Profiling Metabolic Genes and Assessing Prognosis – The Dark Horse of *Helicobacter pylori* mediated Gastric Cancer

In conformity with the requirements for the degree of

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IN
BIOMEDICAL ENGINEERING

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Thesis is submitted by

Subhankar Chowdhury

Of

School of Bioscience and Engineering, Jadavpur University

(Registration no: 133734 of 2015-2016, Class Roll No: 001530201003, EXAM Roll No: M4BMD24014)

Under the guidance of

Dr. Piyali Basak
Director
School of Bioscience and Engineering
Jadavpur University,
Kolkata, West Bengal, India

Dr. Oindrilla Mukherjee
Assistant Professor
Department of Biotechnology
National Institute of Technology,
Durgapur, West Bengal, India



August 2024



Certificate of Recommendation:

This is to certify that the thesis entitled "**Profiling of Metabolic Genes and Assessing Genetic Annotations: The Dark Horse of *Helicobater pylori* mediated Gastric Cancer**" is a bona-fide work carried out by **SUBHANKAR CHOWDHURY** (Class roll no: **101530201003,** Examination Roll No. **M4BMD24014,** Registration no: **133734 of 2015-2016**) under our supervision and guidance for the partial fulfilment of the requirements for the award of the degree of Master of Engineering in Biomedical Engineering, attended in the academic session of 2022-2024. Neither the thesis nor any part of the thesis has been formerly submitted for any degree or diploma or any other academic award(s) anywhere.

Piyali Basak.
30th August 2024

Internal Supervisor

Dr. Piyali Basak
Associate Professor
School of Bioscience and Engineering
Jadavpur University,
Kolkata, West Bengal, India

DR. PIYALI BASAK
ASSOCIATE PROFESSOR
SCHOOL OF BIOSCIENCE & ENGG.
JADAVPUR UNIVERSITY
KOLKATA - 700032

Oindrilla Mukherjee, Dr. rer. nat
Assistant Professor
Department of Biotechnology
National Institute of Technology
Durgapur - 713209, West Bengal

External Supervisor

Dr. Oindrilla Mukherjee
Assistant Professor
Department of Biotechnology
National Institute of Technology,
Durgapur, West Bengal, India

Piyali Basak.
30th August 2024

Director,

School of Bioscience and Engineering
Faculty of Interdisciplinary Studies, Law, and Management
Jadavpur University, Kolkata.

Dr. Piyali Basak
Director
School of Bioscience & Engineering
Jadavpur University
Kolkata-700032

30/8/24

Dean,

Faculty of Interdisciplinary Studies, Law, and Management
Jadavpur University, Kolkata.

Dean
Faculty of Interdisciplinary Studies, Law & Management
Jadavpur University, Kolkata-700032

Certificate of Approval*:

The foregoing thesis is hereby approved as a creditable study of an Engineering subject carried out and presented in a manner satisfactory to warrant its acceptance as a prerequisite to the degree for which it has been submitted. It is understood that by this approval the undersigned do not necessarily endorse or approve any statement made opinion expressed or conclusion drawn therein but approve the thesis only for the purpose for which it has been submitted.

Internal Supervisor

Dr. Piyali Basak

Associate Professor
School of Bioscience and Engineering
Jadavpur University,
Kolkata, West Bengal, India

Oindrilla Mukherjee, Dr. rer. nat.
Assistant Professor
Department of Biotechnology
National Institute of Technology
Durgapur - 713209, West Bengal

External Supervisor

Dr. Oindrilla Mukherjee

Assistant Professor
Department of Biotechnology
National Institute of Technology,
Durgapur, West Bengal, India

Signature of Examiner

* Only in case the thesis is approved

Declaration of Originality and Compliance of Academic Ethics

I, SUBHANKAR CHOWDHURY, registered on Jadavpur University (Registration No. 133734 of 2015-2016) do hereby declare that this thesis entitled "Profiling of Metabolic Genes and Assessing Genetic Annotations: The Dark Horse of Gastric Cancer" contains literature survey and original research work done by myself as part of my Masters studies (Master of Engineering in Biomedical Engineering).

All information in this thesis have been obtained and presented in accordance with existing academic rules and ethical conduct. I declare that, as required by these rules and conduct, I have fully cited and referred all materials and results that are not original to this work. I also declare that I have checked this thesis as per the "Policy on Anti Plagiarism, Jadavpur University, 2019", and the level of similarity as checked by Turnitin software is %.

Date: 30/08/2024
Place: Jadavpur, Kolkata.

Name: Subhankar Chowdhury

School of Bioscience and Engineering, Jadavpur University
Registration no: 133734 of 2015-2016,
Class Roll No: 101530201003,
EXAM Roll No: M4BMD24014)

Title of the thesis:
"Profiling Metabolic Genes and Assessing Prognosis – The Dark Horse of *Helicobacter pylori* mediated Gastric Cancer".

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...to the relentless efforts of all the scientists who are fighting against all the tough, deadly and cureless diseases that terrorize mankind...

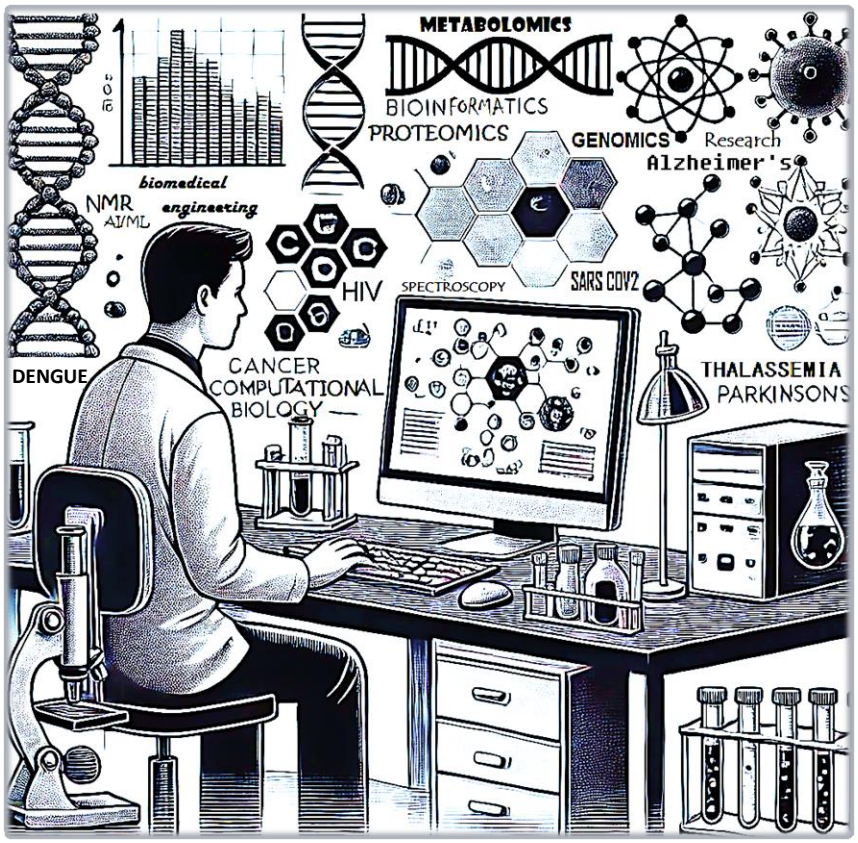


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Abstract:

Gastric cancer is a multifaceted disease with a high mortality rate, making it a significant global health concern. Its pathogenesis is driven by a complex interplay of genetic mutations, metabolic imbalances, and environmental factors. For majority of the cases of gastric cancer worldwide, *Helicobacter pylori* infection remains to be the primary cause. This thesis investigates the roles of metabolic genes and their genetic annotations, aiming to uncover novel insights in the context of *Helicobacter pylori* induced gastric cancer. Through comprehensive profiling and evaluation of metabolic genes in gastric cancer tissues, this study aims to assess genetic annotations to uncover potential biomarkers and therapeutic metabolic targets in gastric cancer. Although metabolic genes are studied in different other types of cancers like cervical cancer, hepatocellular cancer, etc., for finding metabolic therapeutic targets, such research from the perspective of *Helicobacter pylori* induced gastric cancer is attempted for the first time through this thesis. Advanced bioinformatics tools were employed for clinical meta-analysis high-throughput genomic data, leading to the discovery of several previously underexplored yet strong ("dark horse") areas that could play crucial parts in the metabolic reprogramming characteristic of gastric-cancer cells. One of the pivotal findings of this research is the identification of specific metabolic pathways that are significantly altered in gastric cancer. These pathways not only contribute to the aggressive nature of gastric cancer but also present probable targets for developing novel, personalized therapeutic strategies and new technologies. Additionally, this thesis explores the genomic architecture of gastric cancer, shedding light upon the mutations and epigenetic changes that drive the deregulation of these metabolic processes. By integrating genetic annotations with metabolic profiles, the thesis provides a more thorough understanding for the molecular mechanisms underlying gastric cancer. The metabolic gene profiling could revolutionize the current approaches to gastric cancer diagnosis and treatment, this work lays the foundation for the development of targeted therapies that could improve the treatment outcomes and alleviate the burden of this debilitating disease.

CHAPTER: 1

INTRODUCTION

1. Introduction:

Cancer remains a dominant cause of death worldwide, presenting a substantial challenge to improving life expectancy across countries worldwide [204]. As per 2019 evaluations from the World Health Organization (WHO), cancer is 1st or 2nd ranked among the top causes of death before the age of 70, in 112 of 183 countries and ranks 3rd or 4th in 23 more countries (Figure 1) [205]. Globally, the rates of cancer occurrence and mortality are rising swiftly, which can be attributed not only to the aging and expansion of the population, but also shifts in the extent and range of key cancer risk-factors, many of which are linked to socio-economic advancements [206, 207].

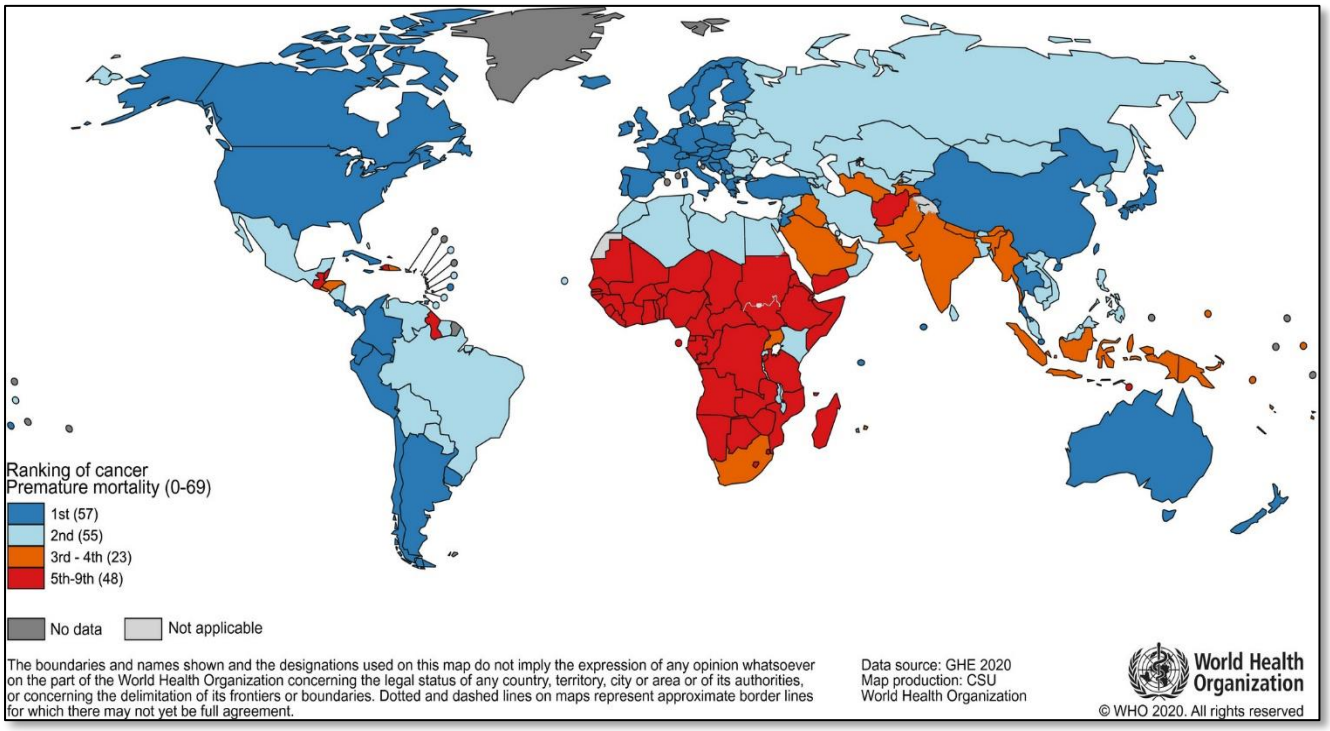


Figure 1: National Ranking for “Cancer as a Cause of Death at Ages <70 Years” I in the year 2019. The number of countries within each ranking category is detailed in the accompanying legend. Source: World Health Organization [208]

Cancer is broadly defined as a category of diseases marked by the unrestrained growth and abnormal division of cells. In addition to that, these diseases can manifest in many forms, with the potential to invade and destroy surrounding tissues, and they can spread to other parts of the body through a process called metastasis. Cancers can progress either rapidly or slowly over time, affecting individuals of any age and originating in nearly any type of cell, tissue, or organ. To date, there are over 200 recognized types of cancer, with new categories continually being identified [1]. The complexity of cancer makes it challenging to fully describe and understand. Consequently, many theories have been proposed to elucidate its origins, and new hypotheses continue to emerge in an effort to uncover the mechanisms behind this "emperor of all maladies" [2]. A number of these theories are closely linked to advances

in medical technology and recent discoveries in the fields of physiology and biology. Hanahan and Weinberg described the hallmarks of cancer to illuminate the mechanisms that drive tumor development, such as the ability to sustain proliferative signaling and evade immune destruction [210]. The intricate nature of cancer, coupled with ongoing technological advancements, continues to test our understanding and treatment approaches, highlighting the critical need for continued research [211].

One of the major and serious malignant tumors of the digestive system has been proven to be the Gastric Cancer (GC). Despite advancements in diagnostic and therapeutic techniques, GC remains a major health concern because of its widespread occurrence, aggressive progression, and the limited likelihood of successful treatment when diagnosed at a symptomatic stage. The rapid evolution of advanced technologies such as computed tomography and gastroscopy has greatly facilitated early detection and treatment, leading to a significant reduction in the progression of GC over the past five decades [10]. Nevertheless, some GC patients still experience atypical patterns of loco-regional and systemic recurrence, and a substantial number of cases progress to advanced and critical stages for various reasons. Consequently, the overall survival (OS) rate of patients with GC remains low at a global level. Indeed, GC ranks as the fifth most prevalent cancer across the globe [3, 47], trailing behind lung, breast, colorectal, and prostate cancers, and it exerts a substantial health burden on a global scale. As per a 2022 report from the World Health Organization (WHO), near about 1.09 million new patients were added to the ever growing list in 2020 (Figure 2), with GC being more prevalent in men than in women (Figure 3) [77].

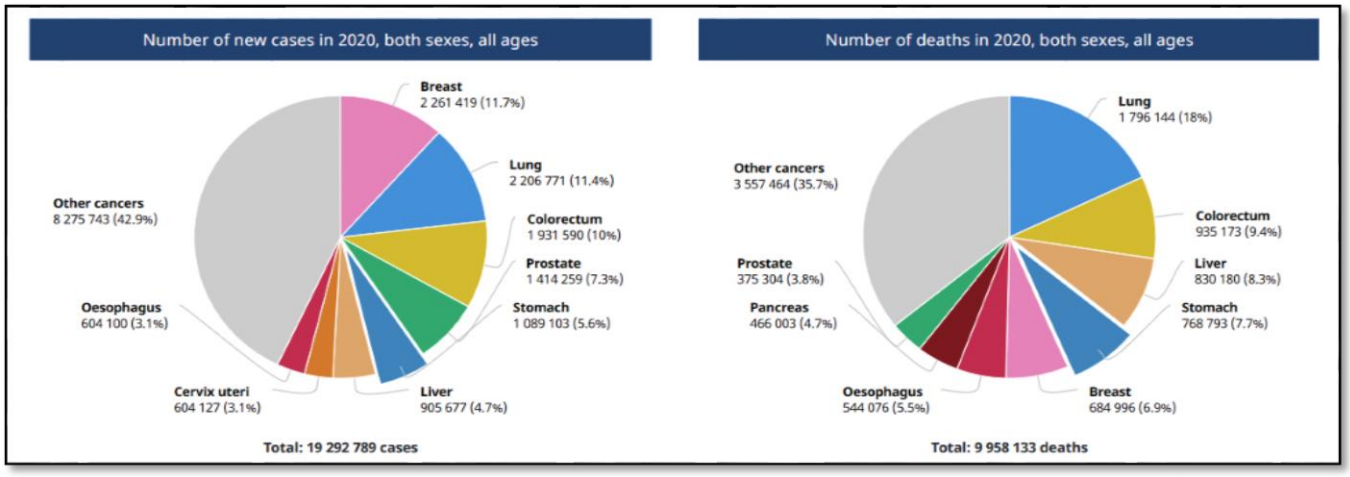
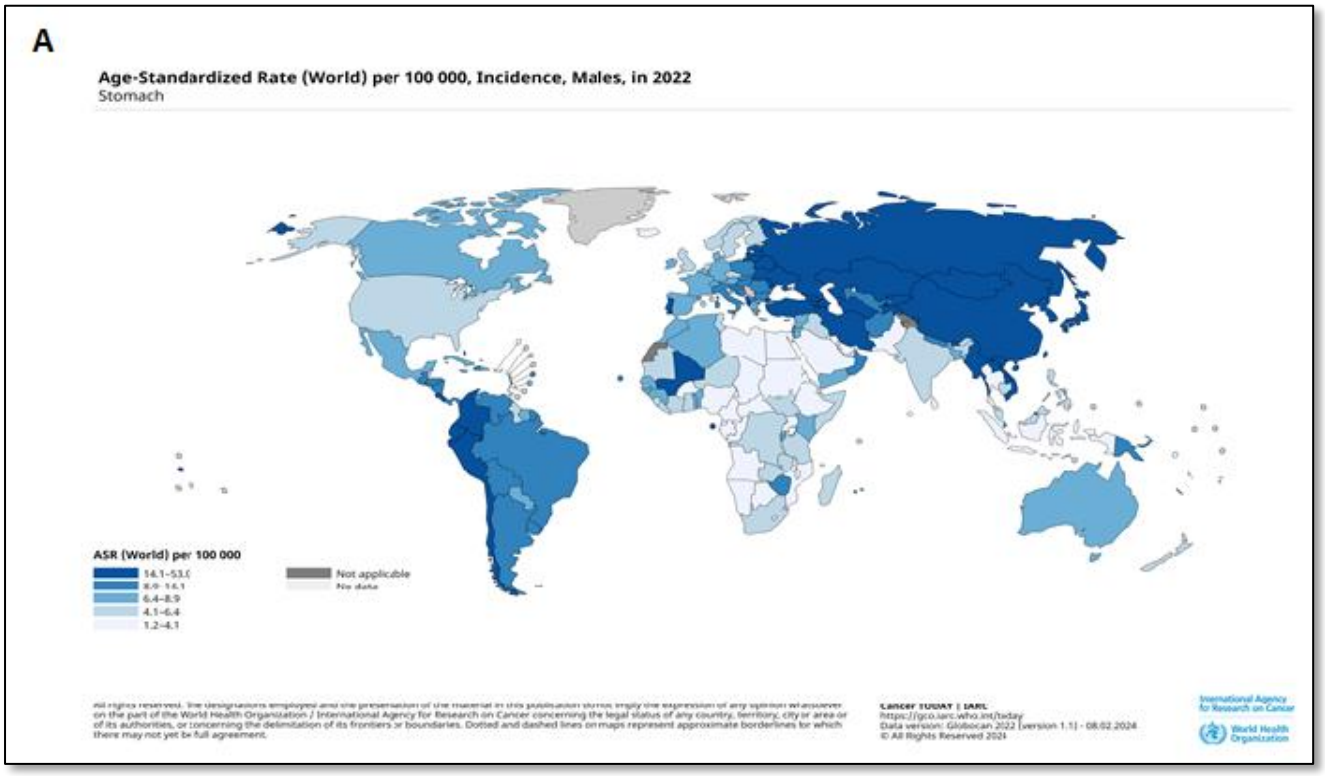


Figure 2: Global status of Gastric/Stomach Cancer (2020) [77]

The incidence rates were about twice as high in males compared to females, with rates, of 15.8 and 7.4 per 100,000 respectively, though these rates vary across different countries [76]. Furthermore, GC is the 2nd highest among the most prevalent causes of cancer related mortality globally [50-53]. Survival rates for GC patients remain precarious. The 5-year relative survival rates vary dramatically depending

on the cancer's stage: 75% for stomach cancer confined to the stomach, 35% for cancer that has spread to nearby lymph nodes or organs, and a dramatically low 7% for metastatic stomach cancer that has reached distant areas of the body [78, 79].



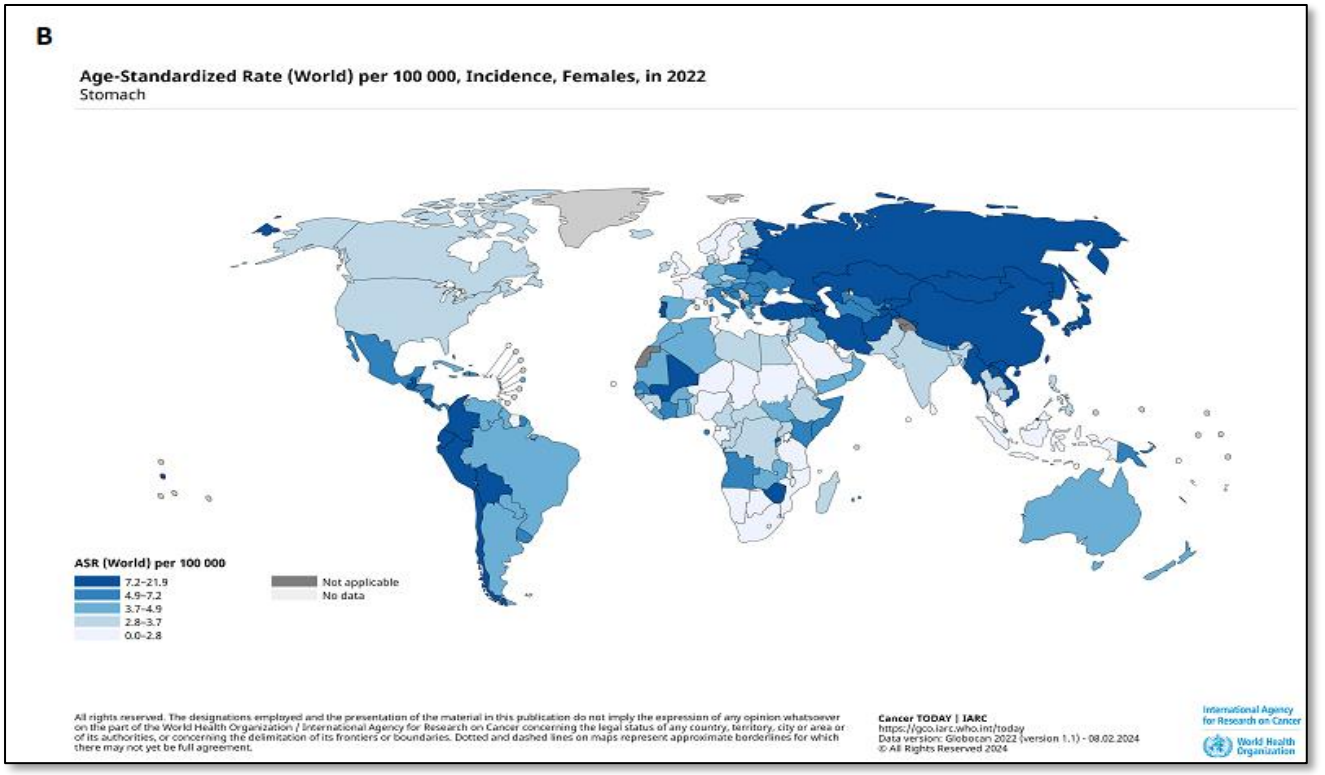


Figure 3: Estimated incidence rates of gastric cancer per 100,000 individuals, differentiated by men (A) and women (B), and adjusted for age using the world population standard for the year 2022. Source: Global Cancer Observatory [212].

Alarmingly, there has been a consistent rise in the incidence of gastric cancer (GC) among younger populations [49]. Research featured by the Harvard Gazette points to a significant increase in early-onset cancers, including GC, starting around 1990. This trend is particularly evident worldwide, especially in more affluent nations, suggesting that lifestyle factors such as diet, alcohol consumption, and obesity play a significant role in this rise [80, 81]. According to Cancer Research UK, cancer incidence rates among individuals aged 25 to 49 increased by 22% between the early 1990s and 2018, a much faster rate than observed in older age groups [81]. While there has been an increase in the occurrence of non-cardia GC among adults under 50 and late-stage GC among Hispanic individuals, the overall rate of GC in the USA has decreased over the last 5 decades. Nevertheless, despite this downward trend in the USA, the global impact of GC is projected to increase by 62% by 2040 [209]. Early detection of stomach cancer significantly enhances the chances of surviving five years post-diagnosis. However, only 29.0% of stomach cancer cases are diagnosed at a localized stage (Figure 4) [79]. Several factors make GC challenging to detect at an early stage, they are as follows: first and foremost important factor is vague or nonspecific symptoms for gastric cancer at the initial stages, signs like indigestion, abdominal discomfort, slight nausea, or a diminished appetite, are often attributed to other common digestive disorders. This misdiagnosis is exacerbated by a general lack of awareness. Moreover, unlike other cancers like cervical cancer, colorectal cancer or breast cancer, there is no widely recommended screening tests for GC in the general population, making early detection even more challenging. Consequently, a significant portion of cases (36%) [79] are already metastatic by the time they are diagnosed.

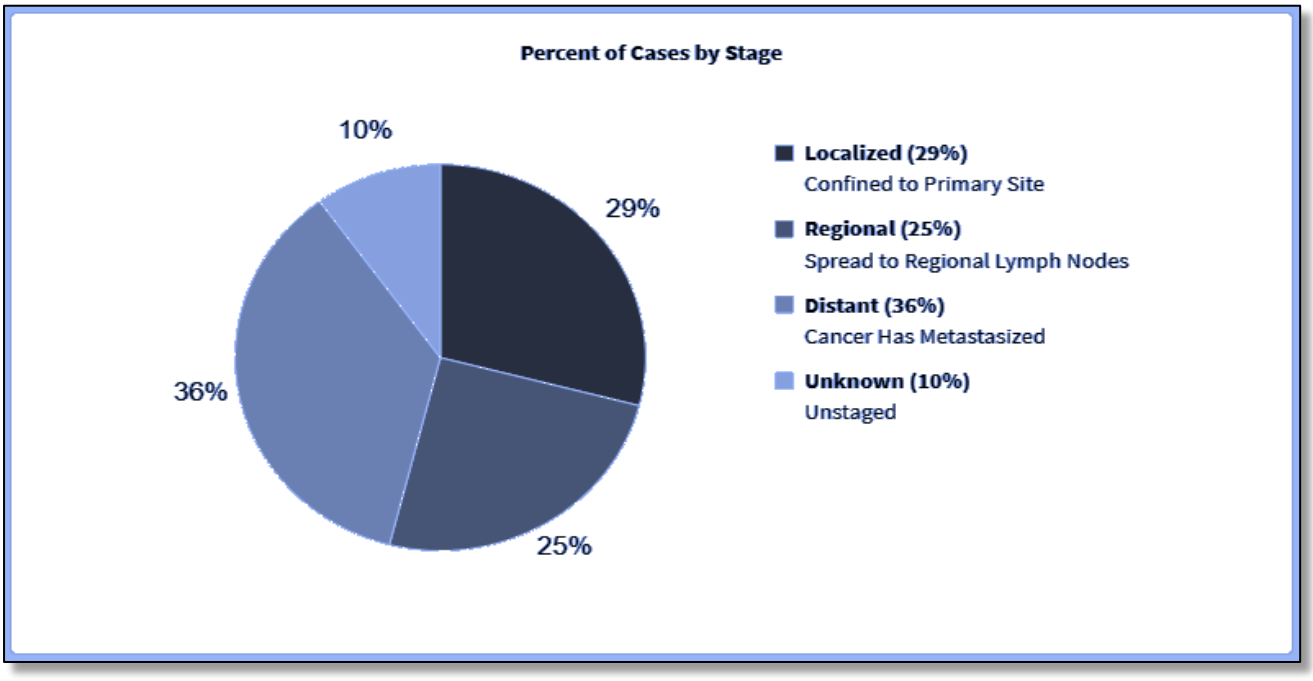


Figure 4: Stage-wise division of Gastric Cancer diagnosis [79]

GC progression also known as gastric carcinogenesis or tumorigenesis is a multifaceted, multistage process influenced by various factors, usually starting with cases of long-term persistent gastritis caused by *Helicobacter pylori (H. pylori)* infection. (Figure 5) [4, 5]. Approximately 70% to 90% of all GCs begin with *H. pylori* infection [17,196] that leads to adenocarcinomas. *H. pylori* (Figure 5A) spiral-shaped, Gram-negative bacteria that infect the gatric lining and is a major contributor to a variety of gastrointestinal disorders, such as gastritis, peptic ulcers, and gastric cancer. It is marked as a Group 1 carcinogen by the International Agency for Research on Cancer (IARC), a part of the WHO [232, 233]. The progression of gastric cancer is often explained using Correa's cascade [6, 7], which describes its gradual progression from a mild form of stomach inflammation (non-active gastritis) to a more severe, ongoing inflammation (chronic active gastritis), precursor lesions of gastric cancer (PLGC: atrophy, intestinal metaplasia, dysplasia), and eventually to stomach adenocarcinoma (STAC), also known as gastric adenocarcinoma (GAC). More than 90% of GC cases are adenocarcinomas [216]. While *H. pylori* infection is commonly an important factor in the development of GC, it remains unclear whether *H. pylori* can directly cause cancer. Earlier research has described gastric cancer as a diverse disease, characterized by genetic and epigenetic changes in key human genes responsible for cell cycle regulation and DNA repair. Environmental influences also play a part in its development and progression [55-58]. Such alterations or mutations are directly linked to the alterations in the cellular metabolic environment, a distinctive feature in several types of cancer. Recent research has uncovered connections between metabolic processes and the onset and advancement of multiple types of cancer, which has led to a growing interest in understanding GC from a metabolic perspective. Recent advances in molecular biology, proteomics, metabolomics and genomics have inaugurated a new era of biomarker discovery for several cancers including GC. Despite the identification of some prognostic biomarkers and their application in clinical treatment [54], there remains an urgent need to discover additional significant genes associated with gastric cancer. This would deepen our understanding of its underlying mechanisms and improve treatment outcomes.

Changes in metabolism contribute to tumorigenesis through several mechanisms, including aerobic glycolysis, diminished oxidative phosphorylation, and heightened production of biosynthetic intermediates [19, 214]. Metabolic genes and related metabolites involved in these processes and pathways show potential as precise biomarkers. In recent years, there have been some studies where gene annotations, correlation analyses, and other such computational tools and methodologies are used to find metabolic genes and metabolites, effectively linking genomics and metabolomics to discover biomarkers and therapeutic targets for various cancers, including hepatocellular, renal, and cervical cancers. However, for *H. pylori* induced gastric cancer we have not found such work yet. This thesis, thus, aims to address this gap by exploring these connections in context of *H. pylori* stimulated gastric

cancer for the first time.

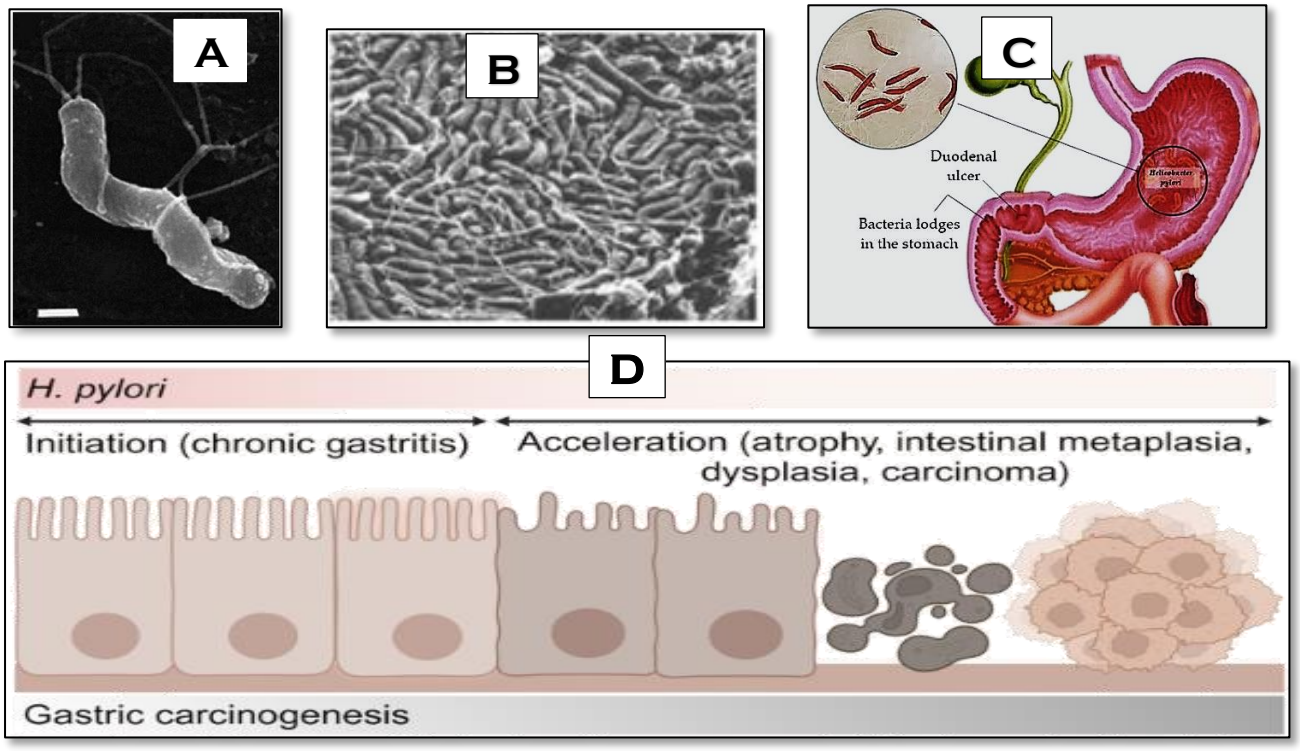


Figure 5: A. Morphology of *Helicobacter pylori* [217, 218], B. *H. pylori* colony (Dennis Kunkel Micro-scopy (http://www.pbrc.hawaii.edu/Vkunkel)) [219], C. *H. pylori* in the stomach [220], D. Gastric carcinogenesis, with *Helicobacter pylori* mainly serving as the trigger for the initiation [215]

CHAPTER: 2

LITERATURE REVIEW

2. Literature review:

Metabolism is a fundamental process in both normal and cancerous cells, with cancer cells relying on metabolic changes to improve their growth and sustain their survival. Metabolites are tiny molecules that act as intermediate or final products of metabolism. Actually, they can be referred to as the down-stream products of the proteome and genome, reflecting how these interact with their surroundings and providing a clear and insightful snapshot of the system's biochemical state [20]. Metabolites include a wide variety of compounds such as sugars, amino acids, nucleotides, and lipids. Metabolic genes are those genes that encode proteins, including enzymes, transporters, and regulators, which are involved in the various metabolic pathways essential for maintaining cellular functions, energy production, and the synthesis and breakdown of metabolites within a cell or organism [221, 222]. Variations in metabolite levels promote carcinogenesis or tumorigenesis in a number of ways, such as, enhanced biosynthetic intermediate synthesis, aerobic glycolysis, and reduced oxidative phosphorylation, [19, 214]. Since the discovery of "oncometabolites" — conventional metabolites that, when abnormally accumulated, gain pro-oncogenic properties and promote tumorigenesis [22], the research of cancer metabolism has progressed well beyond a basic understanding of tumor proliferation and survival.

H. pylori infection is highly prevalent, affecting more than half of the global population [95]. The prevalence of this infection varies by region, being significantly higher in developing countries compared to the developed ones [82]. The infection typically begins in childhood and can persist throughout a person's life if left untreated [83]. *H. pylori* can survive in the general acidic conditions of the stomach, largely because it can produce urease, an enzyme that neutralizes stomach acid [84]. The bacteria can be transmitted through consumption of uncooked or improperly washed or completely unwashed food. The likelihood of developing GC is enhanced by factors such as the consumption of alcoholic beverages and diets high in salty foods. *H. pylori* causes chronic inflammation by damaging the stomach lining, which can lead to ulcers and, over time, significantly heighten the risk of gastric cancer [85]. A large number of people infected with *H. pylori* remain asymptomatic, those who do experience symptoms, may suffer from abdominal pain, bloating, nausea, and loss of appetite [86]. Additional factors contributing to the risk of developing GC include obesity, autoimmune gastritis cigarette smoking, salt-intense diets and processed meats, Epstein–Barr virus infection, and Ménétrier disease [209, 213, 216].

GC has a high mortality rate, especially in cases where the TNM stages— referring to size and extent of the tumor (T), involvement of regional lymph nodes (N), and distant metastasis (M)—are advanced, which usually links to a poor prognosis [9]. The prognosis of GC heavily depends on the tumor stage at the time when it is detected. Diagnosis typically involves procedures such as endoscopy, biopsy,

and pathological examination, with the prognosis closely linked to how advanced the disease is when detected [8]. Unfortunately, gastric cancer in its early stages often presents no symptoms, and for the cases that are diagnosed at leter stages, the 5-year survival rate drops to between 5% and 20% [11, 17].

In the early 1900s, Otto Warburg identified a significant change in the metabolic traits of tumors, observing that oncogenic cells heavily rely on aerobic glycolysis as a means of energy production, the process by which cancer cells, preferentially convert glucose to lactate even in the presence of ample oxygen [64-67]. This groundbreaking discovery, further explored with the rise of what can be called as the “omics era” in biological and biomedical research, has unveiled many new perceptions into cancer cell metabolism. The metabolome, which refers to the complete set of metabolites produced by an organism, plays a critical role in its metabolic processes at specific physiological or developmental stages [12, 13]. Essentially, the metabolome acts as the chemical fingerprint of an organism's metabolism, providing vital information about its physiological state, metabolic pathways, and underlying molecular mechanisms. It encompasses myriad set of molecules, including sugars, lipids, nucleotides, amino acids, hormones, and other organic and inorganic compounds. The field of metabolomics, dedicated to the comprehensive analysis and study of the metabolome, has now become a well-known cornerstone of oncological research [67]. It’s a known that beyond the recognized reliance on glucose metabolism (often referred to as the Warburg effect), relies on various other metabolites, such as glutamine, serine, and fatty acids, for their growth and survival too [68-71]. In addition, the buildup of oncometabolites (e.g., 2-hydroxyglutarate, fumarate etc.), the dysregulation of nutrient transporters (e.g., glucose and monocarboxylate transporters), along with changes in transcriptional modulators, signaling molecules and epigenetic modifications, all play crucial roles in driving altered metabolic processes observed in cancer[65, 72, 73]. A review from the recent times have classified new changes in tumor metabolism into six key hallmarks. These include disrupted glucose and amino acid uptake, increased nitrogen demand, and altered-gene regulation due to the accumulation of specific metabolites such as 2-hydroxyglutarate and acetylcoenzyme A [74]. Various molecular drivers of metabolic dysfunction, including carnitine palmitoyl transferase 1, hexokinases,glucose transporter 1,glutaminase,3-hydroxy-3-methyl-glutaryl-coenzyme A reductase, and isocitrate dehydrogenases, are investigated as potential targets for cancer therapy in both experimental studies and human trials[75, 76]. However, the complete extent and impact of these metabolic changes in cancer cells are not yet fully understood [74, 76], due to the intricate regulation of biochemical pathways and the molecular diversity within and between tumor types. Much of the research has concentrated on the Warburg effect, limiting the exploration of other potentially significant biochemical changes in cancer. Gaining a deeper understanding of the unique metabolic

characteristics of tumors, especially within specific types, will improve tumor categorization and enhance the possibilities for targeting the metabolism in the cancer treatment [74]. Moreover, metabolism plays an important part not only in defining the characteristics of cancer but also in the properties of cancer stem cells, highlighting its significant impact [197].

Cancer metabolism has become a rapidly advancing area of research, resulting in major developments including the creation of positron emission tomography (PET) for tumor imaging [14], the targeting of metabolic enzymes for therapy [15], the discovery and use of oncometabolites [16], and the incorporation of biomarkers of the disease into a personalized treatment strategies[17] These breakthroughs have been instrumental in shaping early detection strategies and treatment approaches for various types of cancer. Our research here aims to help in that pursuit, with a particular focus on GC. Early detection of GC could dramatically improve treatment outcomes, potentially increasing the rate 5-year survival to as much as 90% [17]. This highlights the crucial need for multiomic studies and the development of non-invasive biomarkers to detect early-stage GC, which could lead to better prognostic outcomes. As cancer cells depend on metabolic changes to accelerate their growth and sustain their survival, it is crucial to understand the metabolic gene alterations that repeatedly occur in GC. In this research work we explored and performed a thorough review of a substantial amount of literature to get an extensive list of prognostic biomarkers of GC on one hand, and on the other hand we located a analyzed a large set of genomic data specific to *Helicobacter pylori*-mediated gastric cancer (HpGC) to identify consistently dysregulated metabolic genes with potential clinical relevance. By integrating these data, we explored the relationships between potential oncometabolites and the prognosis of HpGC, aiming to identify potential metabolic targets for therapeutic interventions. While similar studies have been used to identify metabolic targets by analyzing metabolic genes, markers, and pathways in other cancers, such as hepatocellular carcinoma [100, 226, 227], cervical cancer [223, 224, 225] renal cancer [228, 229], but to the best of our knowledge, this approach has not yet been explored for HpGC earlier. This approach poses challenge of managing and analyzing vast amounts of biological data to extract meaningful insights and deduction of conclusions. However this is mollified to a great extent using different computational methods and bioinformatics tools [203] and here in this study we have to used different such resources to achieve our goals.

CHAPTER: 3

AIM & OBJECTIVES

3. Aim and Objectives:

The primary aim of this research is to elucidate consistently dysregulated metabolic genes of potential clinical significance in *H. pylori* mediated gastric cancer (HpGC) and lay the groundwork for the creation of new treatment strategies that could significantly improve patient outcomes. In pursuit of this goal, the thesis seeks to recognise the role of metabolic gene alterations in the development and prognosis of HpGC. This research seeks to uncover metabolic pathways and genetic annotations that contribute to the pathogenesis and prognosis of HpGC, to finally pinpoint specific metabolic genes, pathways and certain metabolites involved in these pathways, which could function as indicators for early detection and as possible targets for therapeutic intervention. With this in mind, the objectives are set as follows:

1. To Identify Differentially Expressed Metabolic Genes (DEMGs) in HpGC:
    - Utilize high-throughput genomic data from publicly available datasets to find metabolic genes, which get differentially expressed in HpGC tissues.
    - Conduct bioinformatics analysis to determine the significance of these gene alterations in the context of HpGC
2. To Analyze Gene Ontology (GO) and Pathway Enrichment:
    - Perform GO and pathway enrichment analysis ascertain the associated biological mechanisms, molecular actions, and cellular elements to the identified elements DEMGs in HpGC.
3. To Explore the Association of the DEMGs with Prognostic Markers:
    - Correlate the expression of identified DEMGs with established prognostic markers of gastric cancer to understand their role in tumor progression and patient outcomes
    - Identify key metabolic pathways that are impacted by these alterations and evaluate their potential as therapeutic targets.
4. To Correlate Metabolic Genes with Prognostic Markers:
    - Investigate the correlation between the identified DEMGs and known prognostic markers of gastric cancer curated from literature, thereby elucidating the potential metabolic pathways involved in tumorigenesis and metastasis.
    - Utilize bioinformatics tools to explore the connection between metabolic gene expression and OS in HpGC patients, aiming to identify potential biomarkers for prognosis.
5. To Identify Potential Oncometabolites and Therapeutic Targets:
    - Analyze the metabolic pathways influenced by the identified DEMGs to determine potential oncometabolites and metabolic targets that could be modulated for therapeutic purposes in HpGC

CHAPTER: 4

METHODOLOGIES

4. Methodologies:

4.1. Dataset Selection and Pre-processing:

To conduct this study, we first searched for microarray data using the keywords "gastric cancer" and "*Homo sapiens*" within the Gene Expression Omnibus (GEO, www.ncbi.nlm.nih.gov/geo/) database, hosted by the National Center for Biotechnology Information (NCBI) (We selected the GSE62254 dataset, which consists of 300 gastric cancer (GC) tissue samples, comprising of 157 non-recurrent and 125 recurrent samples. This dataset was chosen due to its comprehensive coverage and the availability of both recurrent and non-recurrent samples.

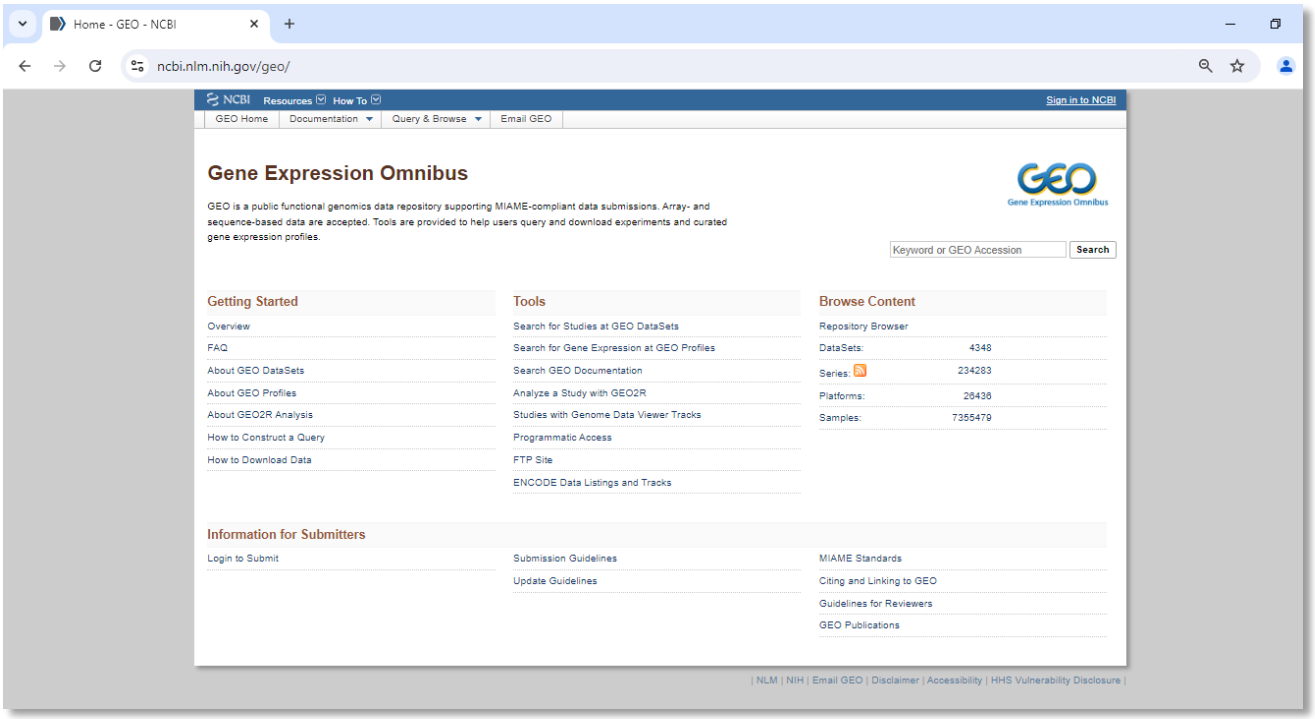


Figure 6: User interface for Gene Expression Omnibus hosted by National Center for Biotechnology Information (https://www.ncbi.nlm.nih.gov/geo/)

4.2. Identification of Differentially Expressed Genes (DEGs):

Using the GEO2R online tool (www.ncbi.nlm.nih.gov/geo/geo2r/), we analyzed the GSE62254 dataset to determine differentially expressed genes (DEGs) in *H. pylori* mediated gastric cancer (HpGC). To find differential expression, GEO2R compares several sample groups within a GEO series. For this study, we included 55 cases of HpGC samples and 72 *H. pylori* negative GC controls from the GSE62254 dataset, which utilizes the GPL570 platform (Affymetrix Human Genome U133 Plus 2.0 Array) [87, 89, 90]. DEGs were identified based on a significance level of $P < 0.05$, with a t-value above 2 (for up-regulated genes) or below -2 (for down-regulated genes), resulting in a list of 1610 genes.

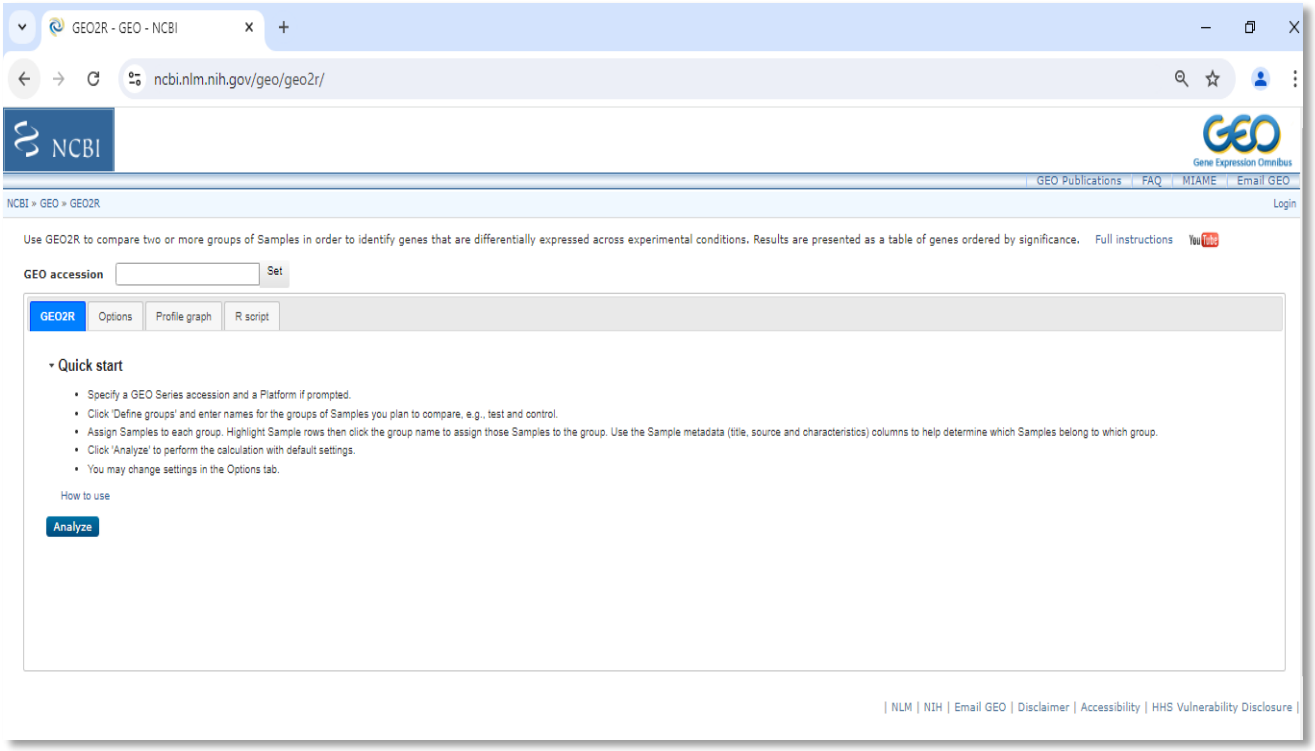


Figure 7: User interface for GEO2R online tool hosted by National Center for Biotechnology Information (http://www.ncbi.nlm.nih.gov/geo/geo2r/)

4.3. Gene Ontology (GO) Analysis:

The next step involved performing Gene Ontology (GO) analysis by using the ShinyGO tool (http://bioinformatics.sdstate.edu/go/), a web-based bioinformatics resource developed by South Dakota State University. ShinyGO facilitates the exploration of GO term enrichment for genomic datasets by comparing the uploaded data against reference gene or protein annotations. Through this comparison, ShinyGO identifies GO terms—such as biological activities, molecular roles, or cellular structures—that are significantly overrepresented (enriched) in the dataset. This is crucial for understanding the biological significance of the data, as it highlights which functions are most relevant or active in the biological context being studied. It offers an interactive visualization of enrichment analysis results, helping researchers identify overrepresented functional categories within their data. We entered the list of 1610 DEGs into ShinyGO, selected "*Homo sapiens*" as the organism, and initiated the pathway enrichment analysis. By exploring the "Pathway Enrichment" section, we identified 131 differentially expressed metabolic genes (DEMGs) related to metabolic pathways. The results were exported for further analysis.

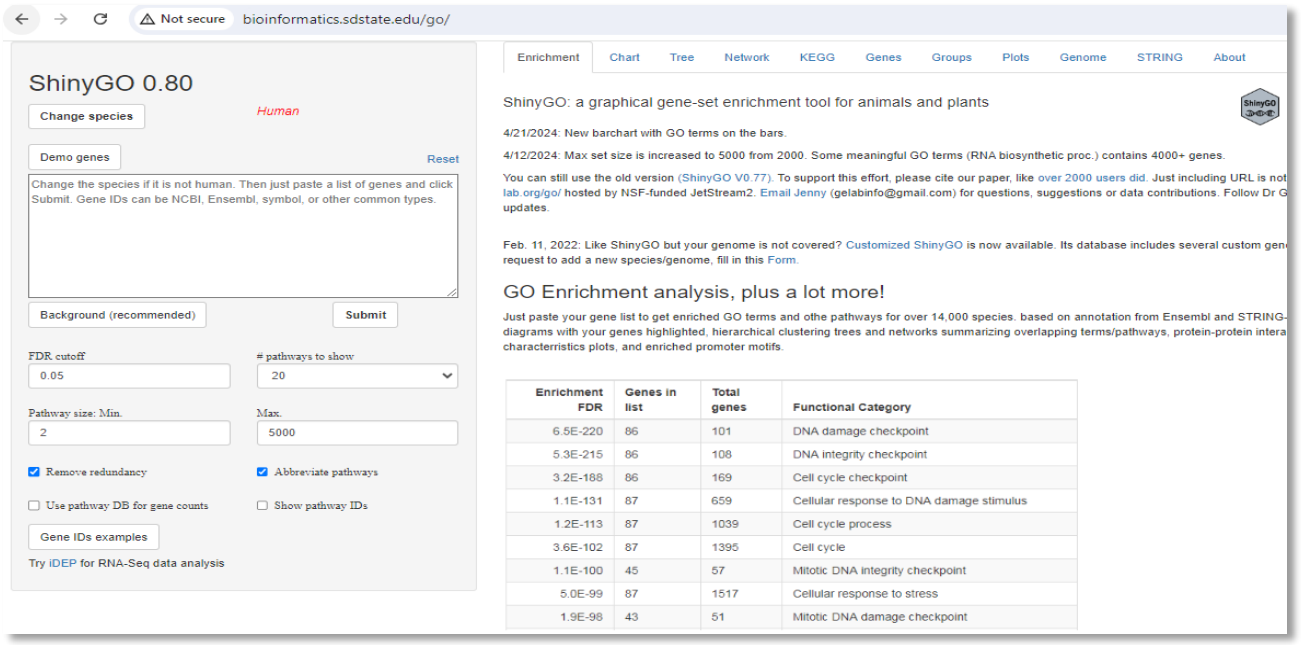


Figure 8: User interface for ShinyGO, online tool for Gene Ontology (http://bioinformatics.sdstate.edu/go/)

4.4. Gene Expression Analysis:

For the analysis the expression levels of the 131 DEMGs based on *H. pylori* infection status, we used the UALCAN portal (https://ualcan.path.uab.edu/analysis.html). UALCAN is a comprehensive, interactive online tool for data analysis on cancer omics, enabling researchers to compare gene expression levels between various tumor groupings based on patient race, tumor grade, pathological cancer stage, and other clinic-pathologic characteristics. In UALCAN, we accessed the TCGA datasets section, provided the list of 131 DEMGs, and selected "Stomach Adenocarcinoma" from the TCGA dataset dropdown. We then examined gene expression based on *H. pylori* infection status.

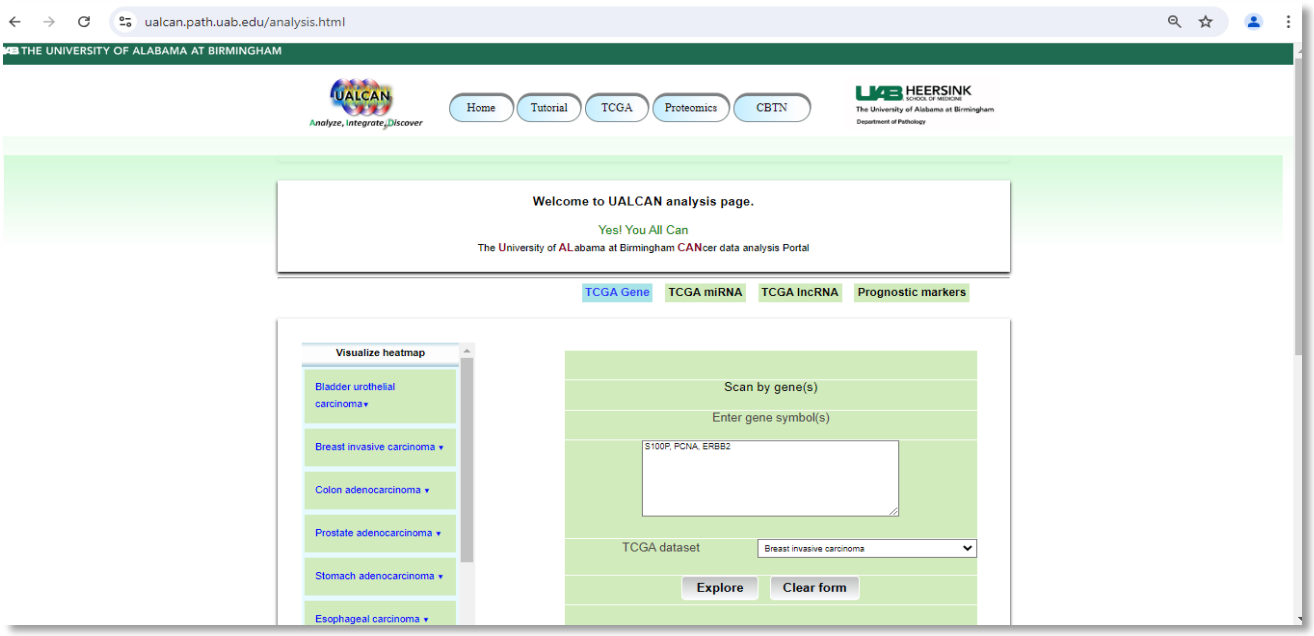


Figure 9: User interface for UALCAN, online tool for analyzing cancer -omics data (https://ualcan.path.uab.edu/analysis.html)

4.5. Prognostic Markers and Gene Expression Profiling:

We manually curated known markers of tumor invasion or metastasis for GC from the literature [59, 60]. From various sources, we identified more than 90 prognostic markers. Gene expression profiling was performed for these markers using the GEPIA2 tool to find Differential Expressed Genes (http://gepia2.cancer-pku.cn/#degenes). GEPIA2 serves as a platform that connects custom user-uploaded data and publicly available cancer genomic data, enabling differential analysis against tumor versus normal data from the TCGA and GTEx projects. We set the analysis parameters as follows: Analysis type: STAD (Stomach adenocarcinoma) vs. Paired Normal sample Analysis, |log2FC| Cutoff = 1, q-value Cutoff = 0.01, Chromosomal Distribution = Both (Over-expressed and Under-expressed), and Differential Methods = LIMMA. Out of the 90 prognostic markers, 22 were found to be differentially expressed. The list of the 22 prognostic markers are mentioned in Table 2.

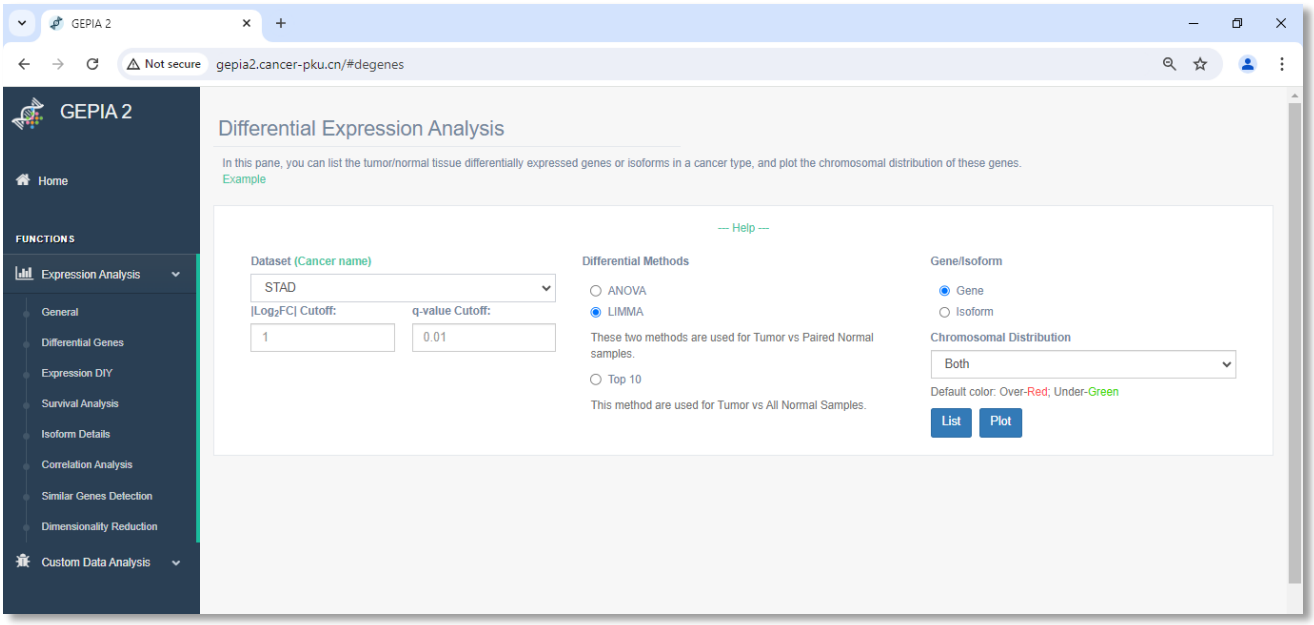


Figure 9: User interface for GEPIA2, differential Expression Analysis (http://gepia2.cancer-pku.cn/#degenes)

4.6. Correlation with Overall Survival:

Next, we tried to access the Kaplan-Meier plotter online database to determine the correlation between the prognostic markers and OS in GC patients. The Kaplan–Meier plot is a standard method used to graphically describe and compare the OS of patient groups. We employed the Gene Expression Profiling Interactive Analysis2 (GEPIA2) web tool (http://gepia2.cancer-pku.cn/#survival)for this purpose, which is also used to check the differential expression of DEMGs between normal tissues and GC cancer tissues. Through this bioinformatics study, we identified several key genes associated with poor prognosis, which could serve as potential therapeutic targets for GC patients.

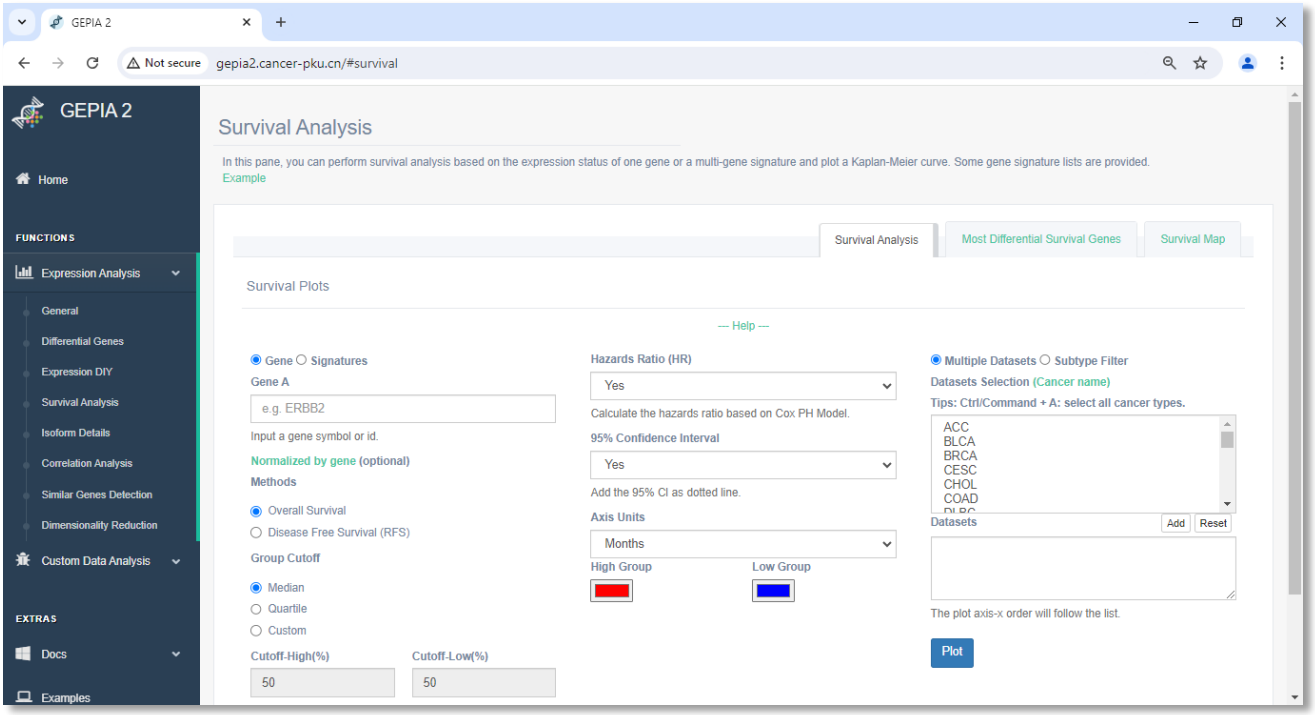


Figure 9: User interface for GEPIA2, Survival Analysis (http://gepia2.cancer-pku.cn/#degenes)

4.7. Correlation Analysis and Pathway Linkage:

We used TCGA's gastric cancer gene expression data as a reference to correlate metabolic genes with the 23 identified prognostic markers. The mRNA expression data were obtained, for each prognostic marker and metabolic genes, through the cBioPortal platform (http://www.cbioportal.org), a widely recognized web resource designed for the exploration of multidimensional cancer genomics data, it allows researchers to easily access, visualize, and analyze large-scale cancer genomics datasets, particularly those related to mRNA expression levels, mutations, copy number variations, and other molecular features across various cancer types. The "co-expression analysis" pane within cBioPortal allows users to calculate correlation coefficients. Using these correlation analyses, we can determine how the expression of a specific metabolic gene or progression marker correlates with the expression of other genes. This can help identify co-regulated genes and suggest functional relationships between the genes that potentially play roles in development or progression of cancer. For instance, if a metabolic gene shows a high positive correlation with a known oncogene, it might suggest that these two genes are co-regulated in a way that promotes tumor growth cBioPortal offers two kinds of correlation coefficients, they are "Pearson's Correlation Coefficient" and "Spearman's Correlation Coefficient". We further scrutinized the progression markers based on a Pearson coefficient, which provides us the linear relationship between two genes, keeping the cutoff as |0.15| and their correlation with at least 10 of the metabolic genes. To establish the linkage between progression markers and prominent metabolic pathways, we conducted KEGG analysis using ShinyGO.

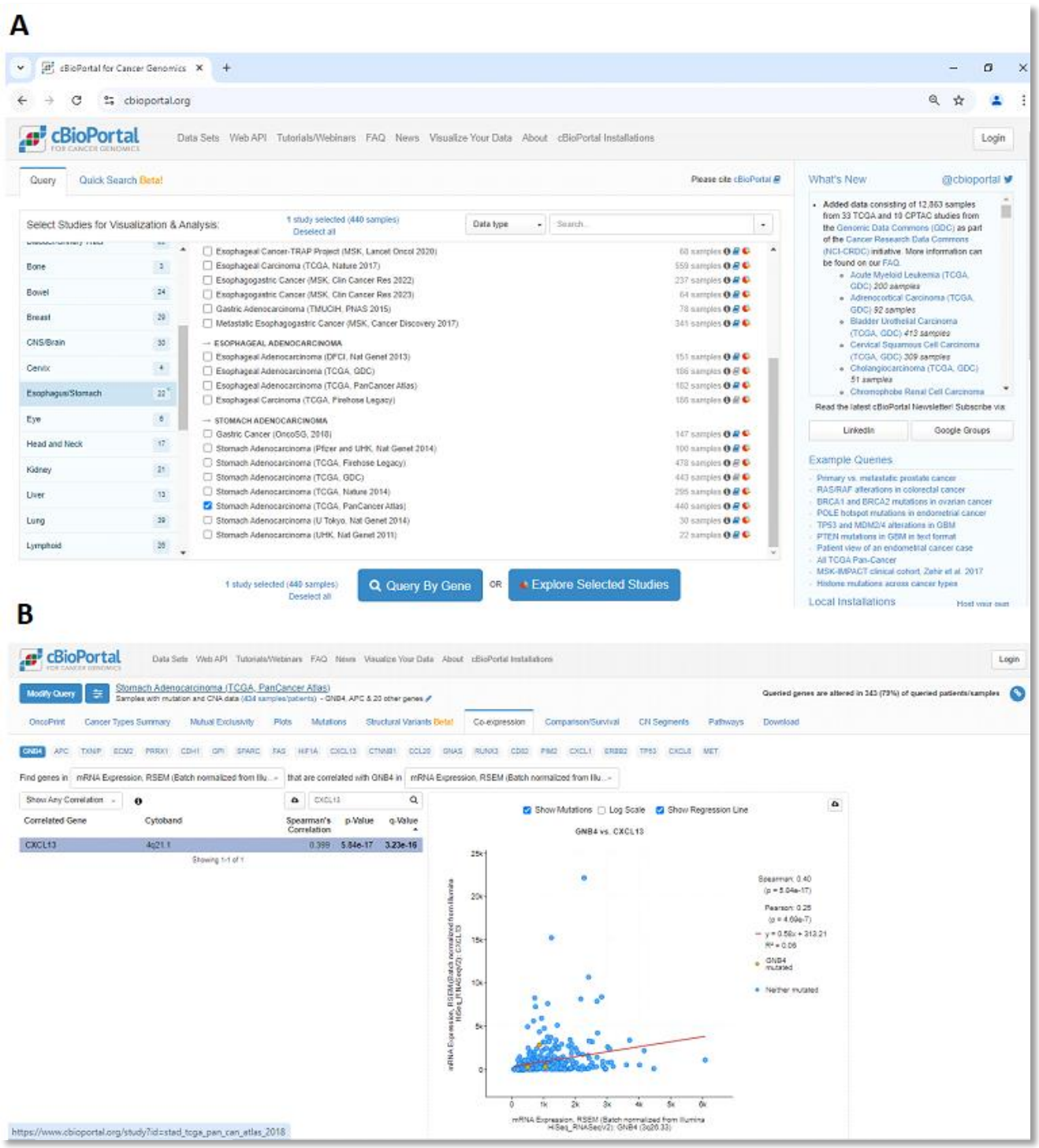


Figure 9: A - User interface for cBioPortal (http://www.cbioportal.org) the online tool that is used for the correlation analysis of genes.
B - User interface for cBioPortal Co-expression analysis pane.

CHAPTER: 5

RESULTS

5. Results:

5.1. Metabolic Genes Altered

To attain a comprehensive understanding of the alterations in metabolic genes within H. pylori-mediated gastric cancer (HpGC), we conducted a comprehensive analysis of the expression patterns for nearly all identified human metabolic genes and transporters, as identified through gene ontology analysis of the GSE62254 dataset. This dataset comprised 1,610 genes, which are detailed in Table 1. Our analysis revealed 131 dysregulated genes within the dataset that impact various metabolic pathways (Table 1). Specifically, the dysregulated metabolic genes in HpGC were associated with essential processes including glycolysis, the pentose phosphate pathway (PPP), the tricarboxylic acid (TCA) cycle also known as Kreb's cycle, glycan metabolism, nucleotide biosynthesis (NB), 'membrane lipid biochemistry', and various transporters as summarized in Table 1 below.

Table 1: Differentially expressed metabolic genes of *H. pylori* mediated Gastric Cancer (as per Gene Ontology Analysis of GSE62254).

#	Gene ID	Gene Name	Significance in Metabolism
1	GPHN	Gephyrin	Involved in clustering and anchoring neurotransmitter receptors to the postsynaptic cytoskeleton. Has an essential role in cellular metabolism and impacts oncological pathways through regulation of cell signaling.
2	CEPT1	Choline/Ethanolamine Phosphotransferase 1	Key enzyme in phospholipid biosynthesis, essential for cell membrane formation. Important for cancer cell proliferation and membrane integrity.
3	ATP5PD	ATP Synthase Peripheral Stalk Subunit Delta	Component of the mitochondrial ATP synthase complex, vital for ATP production. Supports energy metabolism, critical for cancer cell survival.
4	PMVK	Phosphomevalonate Kinase	Participates in the mevalonate pathway, crucial for cholesterol biosynthesis. Implicated in cancer metabolism and cell membrane biosynthesis.
5	ME3	Malic Enzyme 3	Converts malate to pyruvate, providing NADPH for biosynthetic processes. Influences cancer cell growth by regulating metabolic flux.
6	MAN1A2	Mannosidase Alpha Class 1A Member 2	Involved in the processing of N-glycans during glycoprotein maturation. Affects cell-cell interactions and metastasis in cancer.
7	SLC27A5	Solute Carrier Family 27 Member 5	Functions as a fatty acid transporter, playing a role in lipid metabolism. Linked to cancer cell energy supply and growth.
8	TREH	Trehalase	Hydrolyzes trehalose into two glucose molecules, influencing energy metabolism. Important for maintaining cellular energy levels in cancer cells.
9	SDSL	Serine Dehydratase-Like	Involved in the deamination of serine to pyruvate. Affects amino acid metabolism and

			provides intermediates for cancer cell proliferation.
10	ACSM1	Acyl-CoA Synthetase Medium Chain Family Member 1	Activates medium-chain fatty acids by converting them to acyl-CoA that contributes to energy homeostasis and lipid metabolism in cancerous cells.
11	CYP2R1	Cytochrome P450 Family 2 Subfamily R Member 1	A key enzyme in the hydroxylation of vitamin D3, converting it to the active form. Influences cancer prevention and progression through vitamin D metabolism.
12	AFMID	Arylformamidase	Participates in tryptophan metabolism, converting formylkynurenine to kynurenine. Impacts cellular growth and cancer development through metabolic pathways.
13	PIGU	Phosphatidylinositol Glycan Anchor Biosynthesis Class U	Essential for the biosynthesis of glycosylphosphatidylinositol (GPI) anchors. Affects cell surface protein anchoring and communication in cancer cells.
14	COX5B	Cytochrome c Oxidase Subunit 5B	A component of the mitochondrial respiratory chain complex IV. Critical for ATP production and energy metabolism in cancer cells.
15	COX6C	Cytochrome c Oxidase Subunit 6C	Another subunit of complex IV in the mitochondrial respiratory chain. Plays a role in oxidative phosphorylation and energy production in cancer cells.
16	COX7A2	Cytochrome c Oxidase Subunit 7A2	Involved in the formation and operation of cytochrome c oxidase complex IV. Supports mitochondrial energy production essential for cancer cell survival.
17	B3GAT2	Beta-1,3-Glucuronyltransferase 2	Participates in the biosynthesis of glycosaminoglycans (GAGs). Influences cell signaling and extracellular matrix interactions in cancer.
18	COX11	Cytochrome c Oxidase Assembly Protein COX11	Participates in the formation of the cytochrome c oxidase complex. Essential for proper function of mitochondria and energy metabolism.
19	HGSNAT	Heparan-alpha-glucosaminide N-acetyltransferase	Involved in the breakdown of heparan sulfate. Affects cell growth, signaling, and cancer progression through glycan metabolism.
20	NANP	N-Acetylneuraminate Phosphate	Participates in the sialic acid biosynthesis pathway. Impacts cell surface interactions and metastatic potential in cancer.
21	AMDHD1	Amidohydrolase Domain Containing 1	Catalyzes the hydrolysis of N-formyl-L-aspartate. Involved in histidine metabolism, impacting cancer cell growth.
22	UPP2	Uridine Phosphorylase 2	Converts uridine to uracil, participating in pyrimidine metabolism. Crucial for DNA and RNA synthesis in rapidly proliferating cancer cells.
23	VKORC1L1	Vitamin K Epoxide Reductase Complex Subunit 1 Like 1	Also known as aromatase, involved in the biosynthesis of estrogens. Impacts hormone-driven cancers, such as breast cancer.

24	CYP3A5	Cytochrome P450 Family 3 Subfamily A Member 5	Participates in the vitamin K cycle, important for blood coagulation. Involved in cellular growth regulation and cancer progression.
25	CYP19A1	Cytochrome P450 Family 19 Subfamily A Member 1	Metabolizes a variety of xenobiotics and endogenous compounds. Influences cancer drug metabolism and resistance.
26	DHFR2	Dihydrofolate Reductase 2	Essential for folate metabolism and the synthesis of nucleotides. Influences DNA synthesis and repair in cancer cells.
27	ALDOB	Aldolase B	Key enzyme in fructose metabolism, converting fructose-1-phosphate to glyceraldehyde and DHAP. Impacts glycolytic pathways and energy production in cancer cells.
28	PLCH1	Phospholipase C Eta 1	Participates in the hydrolysis of phosphoinositides, generating second messengers. Affects cell signaling and proliferation in cancer.
29	SETD1B	SET Domain Containing 1B	Involved in histone methylation, regulating gene expression. Influences chromatin structure and gene expression for cancer cells.
30	SIRT5	Sirtuin 5	A mitochondrial sirtuin involved in deacetylation and desuccinylation. Plays an important role in cellular metabolism and stress responses in cancer cells.
31	TGDS	TDP-Glucose 4,6-Dehydratase	Participates in the nucleotide-sugar biosynthesis pathway. Affects glycosylation processes in cancer cells.
32	ALOX15	Arachidonate 15-Lipoxygenase	Involved in the metabolism of arachidonic acid to bioactive lipids. Impacts inflammatory responses and cancer progression.
33	GGT7	Gamma-Glutamyltransferase 7	Plays a role in glutathione metabolism, important for cellular redox balance. Influences oxidative stress responses in cancer cells.
34	PDE7B	Phosphodiesterase 7B	Regulates cyclic AMP levels by hydrolyzing cAMP to AMP. Affects cell signaling pathways and cancer cell proliferation.
35	GLS2	Glutaminase 2	Converts glutamine to glutamate, crucial for nitrogen metabolism. Supports energy and biomass production in cancer cells.
36	GLS	Glutaminase	Another enzyme converting glutamine to glutamate, essential for cancer cell growth. Influences cancer's metabolic reprogramming.
37	GLUD1	Glutamate Dehydrogenase 1	Catalyzes the oxidative deamination of glutamate to alpha-ketoglutarate. Involved in energy production and metabolism of amino acids in cancer cells.
38	PGM2L1	Phosphoglucomutase 2 Like 1	Involved in glucose-1-phosphate to glucose-6-phosphate conversion and vice versa. Impacts carbohydrate metabolism and energy pathways in cancer cells.

39	GSS	Glutathione Synthetase	Catalyzes the final step in glutathione biosynthesis. Crucial for maintaining redox balance and detoxification in cancer cells.
40	GSTM5	Glutathione S-Transferase Mu 5	Involved in the conjugation of glutathione to xenobiotics. Affects detoxification processes and cancer cell resistance to therapy.
41	GUCY1A2	Guanylate Cyclase 1 Soluble Subunit Alpha 2	Catalyzes the conversion of GTP to cGMP, a critical second messenger. Participates in signaling pathways and vascular homeostasis in cancer cells.
42	UQCR10	Ubiquinol-Cytochrome c Reductase, Complex III Subunit X	A part in the electron transport chain of the mitochondria. Vital for the synthesis of ATP and oxidative phosphorylation in cancer cells.
43	GUK1	Guanylate Kinase 1	Involved in nucleotide metabolism by converting GMP to GDP. Critical for DNA and RNA synthesis in proliferating cancer cells.
44	ALG5	Asparagine-Linked Glycosylation 5	Participates in the biosynthesis of dolichol-linked oligosaccharides. Essential for protein glycosylation and function in cancer cells.
45	NT5C	5'-Nucleotidase, Cytosolic	Catalyzes the dephosphorylation of nucleotides to nucleosides. Impacts nucleotide metabolism and DNA repair in cancer cells.
46	HMGCR	3-Hydroxy-3-Methylglutaryl-CoA Reductase	Key enzyme in the mevalonate pathway for cholesterol biosynthesis. Influences cell membrane synthesis and proliferation in cancer cells.
47	AOX1	Aldehyde Oxidase 1	Involved in the oxidation of aldehydes and nitrogen-containing compounds. Plays a role in detoxification and metabolic processes in cancer cells.
48	IDI1	Isopentenyl-Diphosphate Delta Isomerase 1	Catalyzes the isomerization of isopentenyl diphosphate to dimethylallyl diphosphate. Important for isoprenoid biosynthesis and cancer cell growth.
49	ITPA	Inosine Triphosphate Pyrophosphatase	Hydrolyzes non-canonical nucleotides to prevent their incorporation into DNA/RNA. Maintains nucleotide pool balance and genomic stability in cancer cells.
50	IVD	Isovaleryl-CoA Dehydrogenase	Participates in leucine catabolism by converting isovaleryl-CoA to 3-methylcrotonyl-CoA. Affects energy production & metabolic pathways in cancer cells.
51	HDDC3	HD Domain Containing 3	Involved in the hydrolysis of nucleotides and nucleic acids. Involved in nucleotide metabolism and cancer cell growth.
52	ACAT2	Acetyl-CoA Acetyltransferase 2	Facilitates the conversion of two acetyl-CoA molecules into acetoacetyl-CoA. Crucial for the energy balance and metabolism of ketone bodies in cancer cells.
53	MGST3	Microsomal Glutathione S-Transferase 3	Catalyzes the conjugation of glutathione to hydrophobic compounds. Influences

			detoxification and hinders cancer cells to accept chemotherapy.
54	KMT2A	Lysine Methyltransferase 2A	Involved in the methylation of histone H3 lysine 4 (H3K4). Controls gene expression and chromatin dynamics in cancer cells.
55	ALG11	Asparagine-Linked Glycosylation 11	Participates in the addition of mannose residues during glycoprotein biosynthesis. Essential for proper protein folding and function in cancer cells.
56	MTHFD2L	Methylenetetrahydrofolate Dehydrogenase 2-Like	Involved in folate metabolism and the synthesis of nucleotides. Crucial for DNA synthesis and repair in rapidly dividing cancer cells.
57	MTAP	Methylthioadenosine Phosphorylase	Catalyzes the conversion of methylthioadenosine to adenine and methylthioribose-1-phosphate. Participates in purine metabolism and cancer cell proliferation.
58	NDUFA4	NADH:Ubiquinone Oxidoreductase Subunit A4	Component in mitochondrial complex I, involved in electron transport and ATP production. Essential for energy metabolism and mitochondrial function in cancer cells.
59	NDUFB1	NADH:Ubiquinone Oxidoreductase Subunit B1	Another subunit of mitochondrial complex I, critical for electron transport chain function. Supports oxidative phosphorylation and energy production in cancer cells.
60	NDUFB2	NADH:Ubiquinone Oxidoreductase Subunit B2	Subunit of complex I, participates in electron transfer and proton gradient formation. Vital for ATP synthesis and cellular energy metabolism in cancer.
61	NDUFV2	NADH:Ubiquinone Oxidoreductase Subunit V2	Involved in the oxidation of NADH in the mitochondrial respiratory chain. Critical for ATP production and energy metabolism in cancer cells.
62	ACO1	Aconitase 1	Enzyme in the TCA cycle, catalyzes the isomerization of citrate to isocitrate. Impacts energy production and redox balance in cancer cells.
63	NT5E	5'-Nucleotidase, Ecto	Hydrolyzes extracellular nucleotides to nucleosides. Affects purine metabolism and cell signaling in the tumor microenvironment.
64	ACOX1	Acyl-CoA Oxidase 1	Initiates the process by which fatty acids are beta-oxidized by peroxisomal beta-oxidation. Affects how fat is metabolized and how energy is produced in cancer cells.
65	NDUFA13	NADH:Ubiquinone Oxidoreductase Subunit A13	Component of mitochondrial complex I, involved in the electron transport chain. Essential for oxidative phosphorylation and energy production in cancer cells.
66	CRYL1	Crystallin Lambda 1	Enzyme has a role in the metabolism of amino acids and sugars. Involved in maintaining metabolic pathways and energy homeostasis in cancer cells.

67	SEPSECS	Sep (O-Phosphoserine) tRNA:Sec (Selenocysteine) tRNA Synthase	Catalyzes the conversion of O-phosphoserine to selenocysteine on its tRNA. Important for selenoprotein synthesis and antioxidant defense in cancer cells.
68	RDH11	Retinol Dehydrogenase 11	Oxidizes retinol to retinal, involved in the visual cycle and retinoid metabolism. Affects cell differentiation and proliferation in cancer.
69	DCXR	Dicarbonyl/L-Xylulose Reductase	Reduces L-xylulose and other sugars, involved in carbohydrate metabolism. Influences energy production and detoxification in cancer cells.
70	ATP5F1E	ATP Synthase F1 Subunit Epsilon	Part of the mitochondrial ATP synthase complex, crucial for ATP production. Supports cellular energy metabolism and survival in cancer cells.
71	PDE3B	Phosphodiesterase 3B	Hydrolyzes cAMP to AMP, regulating cyclic nucleotide levels. Impacts cell signaling pathways and proliferation in cancer cells.
72	PDE4A	Phosphodiesterase 4A	Another enzyme regulating cAMP levels by hydrolyzing it to AMP. Influences cell signaling and growth in cancer.
73	HSD17B7	Hydroxysteroid 17-Beta Dehydrogenase 7	Involved in steroid hormone metabolism, converting estrone to estradiol. Impacts hormone-driven cancers, like prostate and breast cancer.
74	ATP5MC1	ATP Synthase Membrane Subunit C1	Component in the mitochondrial ATP synthase complex, involved in ATP production. Essential for energy metabolism and cellular survival in cancer.
75	PIGT	Phosphatidylinositol Glycan Anchor Biosynthesis Class T	Participates in GPI-anchor biosynthesis, anchoring proteins to cell membranes. Affects cell surface interactions and signaling in cancer.
76	PFKM	Phosphofructokinase, Muscle	A crucial enzyme that changes fructose-6-phosphate into fructose-1,6-bisphosphate during glycolysis. affects the way that cancer cells produce energy and reprogramme their metabolism.
77	ATP6V0C	ATPase H+ Transporting V0 Subunit C	Part of the vacuolar ATPase complex, involved in acidifying intracellular compartments. Impacts cellular pH regulation and survival in cancer cells.
78	PIGF	Phosphatidylinositol Glycan Anchor Biosynthesis Class F	Participates in GPI-anchor biosynthesis, essential for protein anchoring to membranes. Influences cell surface interactions and communication in cancer.
79	PI4KB	Phosphatidylinositol 4-Kinase Beta	Initiates the phosphorylation of phosphatidylinositol to phosphatidylinositol 4-phosphate. Plays an important part in cell signalling and membrane trafficking in cancer cells.
80	PLCB2	Phospholipase C Beta 2	Hydrolyzes phosphatidylinositol 4,5-bisphosphate to produce diacylglycerol and inositol trisphosphate. Involved in intracellular

			signaling and regulation of cell proliferation in cancer.
81	PLCG2	Phospholipase C Gamma 2	Hydrolyzes phosphatidylinositol 4,5-bisphosphate, producing second messengers. Important for cell signaling and immune responses in cancer.
82	PNLIP	Pancreatic Lipase	Hydrolyzes dietary triglycerides into monoglycerides and free fatty acids. Influences lipid metabolism and energy production in cancerous cells.
83	PNMT	Phenylethanolamine N-Methyltransferase	Converts norepinephrine to epinephrine, involved in catecholamine biosynthesis. Affects stress responses and metabolic pathways in cancer.
84	DPM3	Dolichyl-Phosphate Mannosyltransferase Polypeptide 3	Part of the complex that transfers mannose to dolichyl phosphate. Essential for glycoprotein biosynthesis and function in cancer cells.
85	CRLS1	Cardiolipin Synthase 1	Synthesizes cardiolipin, a key phospholipid in mitochondrial membranes. Crucial for mitochondrial function and energy metabolism in cancer cells.
86	PPAT	Phosphoribosyl Pyrophosphate Amidotransferase	Initiates the de novo synthesis of purine nucleotides by catalyzing the initial step. Vital to the synthesis of DNA and RNA in cancer cells that are growing.
87	PNPO	Pyridoxamine 5'-Phosphate Oxidase	Initiates the last step in the biosynthesis of pyridoxal 5'-phosphate (vitamin B6). Important for amino acid metabolism and neurotransmitter synthesis in cancer cells.
88	CHDH	Choline Dehydrogenase	Converts choline to betaine aldehyde in the choline oxidation pathway. Influences cell membrane synthesis and methylation reactions in cancer.
89	ADCY10	Adenylate Cyclase 10	Initiates the conversion of ATP to cAMP, a critical second messenger. Regulates cell signaling and proliferation in cancer cells.
90	PNPLA2	Patatin-Like Phospholipase Domain Containing 2	Hydrolyzes triglycerides into free fatty acids and glycerol. Important for lipid metabolism and energy production in cancer cells.
91	PSPH	Phosphoserine Phosphatase	Initiates the final step in the biosynthesis of serine from 3-phosphoglycerate. Provides essential amino acids for protein synthesis and proliferation in cancer cells.
92	GALNT16	Polypeptide N-Acetylgalactosaminyltransferase 16	Catalyzes the initial step in O-linked glycosylation of proteins. Affects cell surface interactions and signaling in cancer.
93	PYCR1	Pyrroline-5-Carboxylate Reductase 1	Converts pyrroline-5-carboxylate to proline, involved in proline biosynthesis. Influences amino acid metabolism and redox balance in cancer cells.

94	PCYT2	Phosphate Cytidylyltransferase 2, Ethanolamine	Catalyzes the formation of CDP-ethanolamine, a key step in phospholipid biosynthesis. Essential for cell membrane integrity and function in cancer cells.
95	PRUNE1	Prune Exopolyphosphatase 1	Involved in the hydrolysis of polyphosphates to orthophosphate. Affects nucleotide metabolism and cell proliferation in cancer.
96	BCAT1	Branched-Chain Amino Acid Transaminase 1	Catalyzes the reversible transamination of branched-chain amino acids. Provides essential amino acids for protein synthesis and energy production in cancer cells.
97	BCKDHB	Branched Chain Keto Acid Dehydrogenase E1 Subunit Beta	Part of the complex that controls the decarboxylation of branched-chain keto acids. Influences energy production and metabolism in cancerous cells.
98	HPSE2	Heparanase 2	Involved in the degradation of heparan sulfate proteoglycans. Affects cell signaling, growth, and metastasis in cancer.
99	MSMO1	Methylsterol Monooxygenase 1	Controls the demethylation of lanosterol in cholesterol biosynthesis. Influences cell membrane composition and fluidity in cancer cells.
100	PRDM16	PR/SET Domain 16	Engaged in chromatin remodelling to control the gene expressions. Affects cell differentiation and proliferation in cancer.
101	NMNAT1	Nicotinamide Nucleotide Adenylyltransferase 1	Controls the synthesis of NAD from nicotinamide mononucleotide. Essential for cellular metabolism and energy production in cancer cells.
102	NME1-NME2	NME/NM23 Nucleoside Diphosphate Kinase 1 and 2	Controls the conversion of nucleoside diphosphates to triphosphates. Involved in cell signaling and proliferation in cancer.
103	SPR	Sepiapterin Reductase	Catalyzes the reduction of sepiapterin to dihydrobiopterin. Important for the synthesis of tetrahydrobiopterin, a cofactor in neurotransmitter production and cancer cell signaling.
104	UQCRB	Ubiquinol-Cytochrome c Reductase Binding Protein	Component of mitochondrial complex III, involved in electron transport. Essential for oxidative phosphorylation and energy metabolism in cancerous cells.
105	CA3	Carbonic Anhydrase 3	Controls the reversible hydration of carbon dioxide. Helps in pH regulation and cellular metabolism in cancer.
106	DCTPP1	dCTP Pyrophosphatase 1	Hydrolyzes dCTP to dCMP and inorganic pyrophosphate. Maintains nucleotide pool balance and prevents misincorporation into DNA in cancer cells.
107	ALDH5A1	Aldehyde Dehydrogenase 5 Family Member A1	Controls the oxidation of succinic semialdehyde to succinate. Involved in amino acid metabolism and energy production in cancer cells.

108	SRD5A3	Steroid 5 Alpha-Reductase 3	Controls the conversion of testosterone to dihydrotestosterone. Impacts hormone-driven cancers, such as prostate cancer.
109	GALNT12	Polypeptide N-Acetylgalactosaminyltransferase 12	Involved in the beginning steps of O-linked glycosylation. Affects protein function and cell signaling in cancer.
110	AGMAT	Agmatinase	Controls the hydrolysis of agmatine to putrescine. Participates in polyamine metabolism & cell growth in cancer.
111	KMT2D	Lysine Methyltransferase 2D	Involved in the methylation of histone H3 lysine 4 (H3K4). Governs gene expression and chromatin structure in cancer.
112	NPL	N-Acetylneuraminate Lyase	Controls the cleavage of N-acetylneuraminate to pyruvate and N-acetylmannosamine. Influences sialic acid metabolism and cell surface interactions in cancer.
113	CHST9	Carbohydrate Sulfotransferase 9	Controls the transfer of sulfate groups to carbohydrates. Affects glycosaminoglycan biosynthesis and cell signaling in cancer.
114	NUDT12	Nudix Hydrolase 12	Hydrolyzes oxidized nucleotides to prevent their incorporation into DNA/RNA. Maintains nucleotide pool balance and genomic stability in cancer cells.
115	HYAL3	Hyaluronidase 3	Degrades hyaluronan, a major component of the extracellular matrix. Influences cell migration, growth, and metastasis in cancer.
116	SETDB2	SET Domain Bifurcated 2	Involved in histone methylation and gene silencing. Regulates chromatin structure and gene expressions in cancerous cells.
117	ACSS1	Acyl-CoA Synthetase Short-Chain Family Member 1	Activates short-chain fatty acids for metabolism. Participates in metabolism of lipids and energy production in cancer cells.
118	ADO	Adenosine Deaminase, RNA-Specific	Involved in RNA editing, converting adenosine to inosine. Influences gene expression and cellular responses in cancer.
119	KMO	Kynurenine 3-Monooxygenase	Controls the hydroxylation of kynurenine to 3-hydroxykynurenine. Participates in tryptophan metabolism and affects immune response in cancer.
120	PDE5A	Phosphodiesterase 5A	Hydrolyzes cGMP to GMP, regulating cyclic nucleotide levels. Influences cell signaling and growth in cancer cells.
121	SUCLA2	Succinate-CoA Ligase ADP-Forming Beta Subunit	Part of the TCA cycle, converts succinyl-CoA to succinate. Essential for energy production and metabolic balance in cancer cells.
122	SYNJ2	Synaptojanin 2	Involved in phosphoinositide metabolism, regulating membrane dynamics. Affects cell signaling and endocytosis in cancer cells.
123	KYNU	Kynureninase	Controls the hydrolysis of kynurenine to anthranilic acid. Plays a role in tryptophan metabolism and immune modulation in cancer.

124	PAPSS2	3'-Phosphoadenosine 5'-Phosphosulfate Synthase 2	Synthesizes PAPS, a sulfate donor for sulfation reactions. Involved in detoxification and signaling in cancer cells.
125	MTMR6	Myotubularin Related Protein 6	Regulates phosphoinositide metabolism and endosomal trafficking. Influences cell signaling and membrane dynamics in cancer.
126	LARGE1	Like-Glycosyltransferase 1	Participates in the glycosylation of alpha-dystroglycan. Essential for cell adhesion and signaling in cancer.
127	PIGM	Phosphatidylinositol Glycan Anchor Biosynthesis Class M	Involved in the transfer of mannose to GPI anchors. Affects cell surface protein anchoring and communication in cancer.
128	GGPS1	Geranylgeranyl Diphosphate Synthase 1	Controls the synthesis of geranylgeranyl diphosphate. Important for protein prenylation and cell signaling in cancer.
129	PIGL	Phosphatidylinositol Glycan Anchor Biosynthesis Class L	Participates in GPI-anchor biosynthesis, essential for cell surface protein anchoring. Influences cell signaling and communication in cancer.
130	ENTPD2	Ectonucleoside Triphosphate Diphosphohydrolase 2	Hydrolyzes extracellular nucleotides to regulate purinergic signaling. Affects cell communication and immune responses in the tumor microenvironment.
131	ENTPD3	Ectonucleoside Triphosphate Diphosphohydrolase 3	Another enzyme involved in the hydrolysis of extracellular nucleotides. Influences nucleotide metabolism and signalling in cancer cells.

5.2. Curated Prognostic Markers of GC:

In conjunction with the previously mentioned analysis, we conducted an extensive manual literature review to identify numerous genes recognized as significant prognostic biomarkers due to their role in essential cellular functions that propel cancer development Initially, we curated nearly 100 such biomarkers from various literary sources. To determine the most relevant among these, we used the GEPIA2 tool to perform Differential Expression Analysis, which identified several genes as differentially expressed in gastric cancer (GC) and of significant relevance. Guanine Nucleotide Binding Protein Beta 4 (GNB4) is implicated in signal transduction processes mediated by G proteins. Altered expression of GNB4 has been linked to various cancers, including GC, where it may influence tumor progression and patient survival [101, 102]. The tumor suppressing gene Adenomatous Polyposis Coli (APC) is known for controlling cell cycle and adhesion. APC mutations are common in gastrointestinal cancers, including GC, often leading to poor prognosis [103-106]. Thioredoxin Interacting Protein (TXNIP) plays a role in regulating oxidative stress and apoptosis. Downregulation of TXNIP is linked with enhanced tumor growth and worse outcomes in GC [107-110]. Extracellular Matrix Protein 2 (ECM2) is part of the extracellular matrix and affects cell adhesion and migration.

Abnormal expression of ECM2 can contribute to tumor invasiveness and metastasis in GC [111-115]. Paired Related Homeobox 1 (PRRX1) is a transcription factor involved in embryonic maturation and cellular differentiation. Overexpression of PRRX1 has been linked to increased metastasis and poor prognosis in GC [116-120]. E-cadherin (CDH1) encodes E-cadherin, a protein crucial for cell-cell adhesion. Loss of E-cadherin function, often due to CDH1 mutations, is a hallmark of diffuse-type GC, frequently indicating a poor prognosis [121-125, 191]. Glucose-6-Phosphate Isomerase (GPI) participates in glycolysis and gluconeogenesis. Elevated GPI levels are associated with cancer progression and lower survival rates in GC [126-130]. Secreted Protein Acidic and Rich in Cysteine (SPARC) influences cell-matrix interactions and tissue remodeling. High expression of SPARC is associated with heightened tumor aggressiveness and worse prognosis in GC [131-134, 192]. The Fas Cell Surface Death Receptor (FAS) plays a role in apoptotic signaling. Dysregulation of FAS can lead to apoptosis evasion, contributing to tumor survival and poor prognosis in GC [135-138]. Hypoxia-Inducible Factor 1 Alpha (HIF1A) modulates cellular reactions to low oxygen conditions or hypoxia. Overexpression of HIF1A is linked to poor prognosis due to enhanced angiogenesis and tumor progression under hypoxic conditions [139-142]. C-X-C Motif Chemokine Ligand 13 (CXCL13) is involved in attracting B cells to areas of inflammation. While high CXCL13 levels have been associated with better outcomes in some cancers, its role in GC is complex and context-dependent [143-148, 191]. Catenin Beta 1 (CTNNB1) encodes β-catenin, a key player in the Wnt signaling pathway and cell adhesion. Aberrant activation of β-catenin is a marker for poor prognosis due to its role in promoting tumor growth and metastasis [149-153]. C-C Motif Chemokine Ligand 20 (CCL20) plays a part in immune cell trafficking. Elevated CCL20 expression is connected to poor prognosis and tumor progression in GC [154-157]. The GNAS Complex Locus (GNAS) encodes the stimulatory G protein alpha subunit, which participates in signal transduction. Mutations in GNAS are linked to various cancers, including GC, often correlating with aggressive tumor behavior [158-161]. Runt Related Transcription Factor 3 (RUNX3) is a tumor suppressor involved in TGF-β signaling. Loss of RUNX3 function is linked to poor prognosis due to its role in promoting apoptosis and inhibiting proliferation [162-165]. CD82 (KAI1) acts as a metastasis suppressor gene, affecting cell adhesion and migration. Reduced CD82 expression is frequently linked to higher rates of metastasis and worse prognosis in gastric cancer (GC) [166-168].. Pim-2 Proto-Oncogene (PIM2) is a serine/threonine kinase involved in cell survival and proliferation. Overexpression of PIM2 is linked to poor prognosis due to its role in enhancing tumor cell survival [169-171]. C-X-C Motif Chemokine Ligand 1 (CXCL1) is a chemokine involved in neutrophil recruitment and inflammation. Elevated levels of CXCL1 are connected with unfavorable outcomes, largely because of its involvement in enhancing tumor growth and spreading [172-178]. ERBB2 (HER2) is a receptor tyrosine kinase plays crucial part in cell

proliferation and differentiation. Higher expression or amplification of HER2 is linked to poor prognosis but also serves as a target for therapy in GC [179-183, 190]. Tumor Protein p53 (TP53) is a tumor suppressing gene that is involved in a critical role of DNA repair and apoptosis. Mutations in TP53 are common in GC and are often associated with poor prognosis [184-190]. C-X-C Motif Chemokine Ligand 8 (CXCL8), a chemokine that is engaged in neutrophil chemotaxis and activation. Studies show that an elevated serum level of CXCL8 is strongly associated with advanced stages of GC and correlate with poor patient outcomes [230, 231]. Finally, Mesenchymal Epithelial Transition (MET), participates in cellular growth, motility, and differentiation, is frequently overexpressed in GC and serves as a crucial prognostic biomarker. MET overexpression is significantly associated with poor prognosis, including decreased survival rates in GC patients. The detailed information is summarized in Table 2 below for easier comparison with Table 1.

Table 2: Manually curated prognostic markers for Gastric Cancer

#	Marker	Gene Name	Function
1	GNB4	Guanine nucleotide-binding protein subunit beta-4	Involved in signal transduction processes mediated by G proteins.
2	APC	Adenomatous Polyposis Coli	Tumor suppressor gene that controls cell cycle and adhesion.
3	TXNIP	Thioredoxin Interacting Protein	Involved in the regulation of both apoptosis and oxidative stress.
4	ECM2	Extracellular Matrix Protein 2	Component of the extracellular matrix, influences cell adhesion and migration.
5	PRRX1	Paired Related Homeobox 1	Transcription factor involved in embryonic development and cellular differentiation.
6	CDH1	Cadherin 1	Encodes E-cadherin, crucial for cell to cell adhesion.
7	GPI	Glucose-6-Phosphate Isomerase	Plays an essential role in glycolysis and gluconeogenesis.
8	SPARC	Secreted Protein Acidic and Rich in Cysteine	Affects in cell-matrix interactions and tissue remodelling.

9	FAS	Fas Cell Surface Death Receptor	Death receptor involved in apoptotic signalling.
10	HIF1A	Hypoxia Inducible Factor 1 Subunit Alpha	Regulates cellular response to hypoxia.
11	CXCL13	C-X-C Motif Chemokine Ligand 13	Involved in the recruitment of B cells to inflammation sites.
12	CTNNB1	Catenin Beta 1	Encodes β-catenin, involved in the Wnt signalling pathway and cell adhesion.
13	CCL20	C-C Motif Chemokine Ligand 20	Chemokine involved in immune cell trafficking.
14	GNAS	Guanine nucleotide binding protein, alpha stimulating	Encodes the alpha subunit of stimulatory G protein, involved in signal transduction.
15	RUNX3	Runt-Related Transcription Factor 3	Acts as Tumor suppressor and are involved in TGF-β signaling.
16	CD82	Cluster of Differentiation 82	Metastasis suppressor gene involved in cell adhesion and migration.
17	PIM2	Proviral Integrations of Moloney 2	Serine/threonine kinase involved in cell growth and survival.
18	CXCL1	C-X-C Motif Chemokine Ligand 1	Chemokine involved in neutrophil recruitment and inflammation.
19	ERBB2	Erythroblastic oncogene – B Receptor Tyrosine Kinase 2	Involved in cellular differentiation and proliferation.
20	TP53	Tumor Protein p53	Functions as Tumor suppressor gene that affects DNA repair and apoptosis.
21	CXCL8	C-X-C Motif Chemokine Ligand 8	Chemokine involved in neutrophil chemotaxis and activation.
22	MET	Mesenchymal Epithelial Transition	Involved in cellular growth, motility, and differentiation.

5.3. Correlation analysis of Altered Metabolic Genes with Prognostic Markers using cBioPortal:

Investigating the relationship between metabolic targets—specific components or pathways involved in the altered metabolism of cancer cells—and the mediators that drive other critical cancer hallmarks, such as invasion, metastasis, and epithelial-to-mesenchymal transition (EMT), can reveal important underlying connections that might not yet be fully understood. Invasion, metastasis, and EMT are fundamental processes that contribute significantly to the progression of tumors, enabling cancerous cells to propagate from their original location to other body parts. However, while these processes are well-recognized as crucial steps in cancer progression, the way in which changes in cellular metabolism influence or interact with these processes, particularly in the context of *H. pylori* associated gastric cancer (HpGC), remains largely unexplored. Understanding these connections could provide new insights into how metabolic alterations contribute to the aggressive behavior of cancer cells in HpGC, potentially leading to the discovery of novel therapeutic targets. To address this gap, we correlated each of the 131 identified metabolic genes (Table 1) with 22 established prognostic markers (Table 2). In this process we got more than 2800 correlation graph plots each for every unique pair formed of one metabolic gene from Table 1 and one prognostic marker from Table 2. For further analysis we focused on metabolic genes that showed a correlation with the prognostic marker as per the following condition $|\text{Pearson correlation}| > |0.15|$ and p-value < 0.05. This capping in the correlation value helped us to remove the results that had very low or zero correlation and were therefore not considered significant for the correlation analysis and we still had more than 700 correlation graph to continue our analysis. Finally, through our analysis we selected 15 from the 131 metabolic genes (Table 1) which delivered quite crucial results that would be discussed in detail in the next chapter of this thesis. Those 15 metabolic genes are IDI1, ACAT2, AFMID, PDE5A, HMGCR, ITPA, SPR, PDE7B, PPAT, GALNT16, GSS, GSTM5, KMO, PIGF, and PIGU. In this section of the thesis I have showcased, the correlation graph plots for 3 of the top prognostic markers for each of the 15 above mentioned metabolic genes. The remaining of the correlation graph plots, are provided in the "Supplementary Materials" of this thesis.

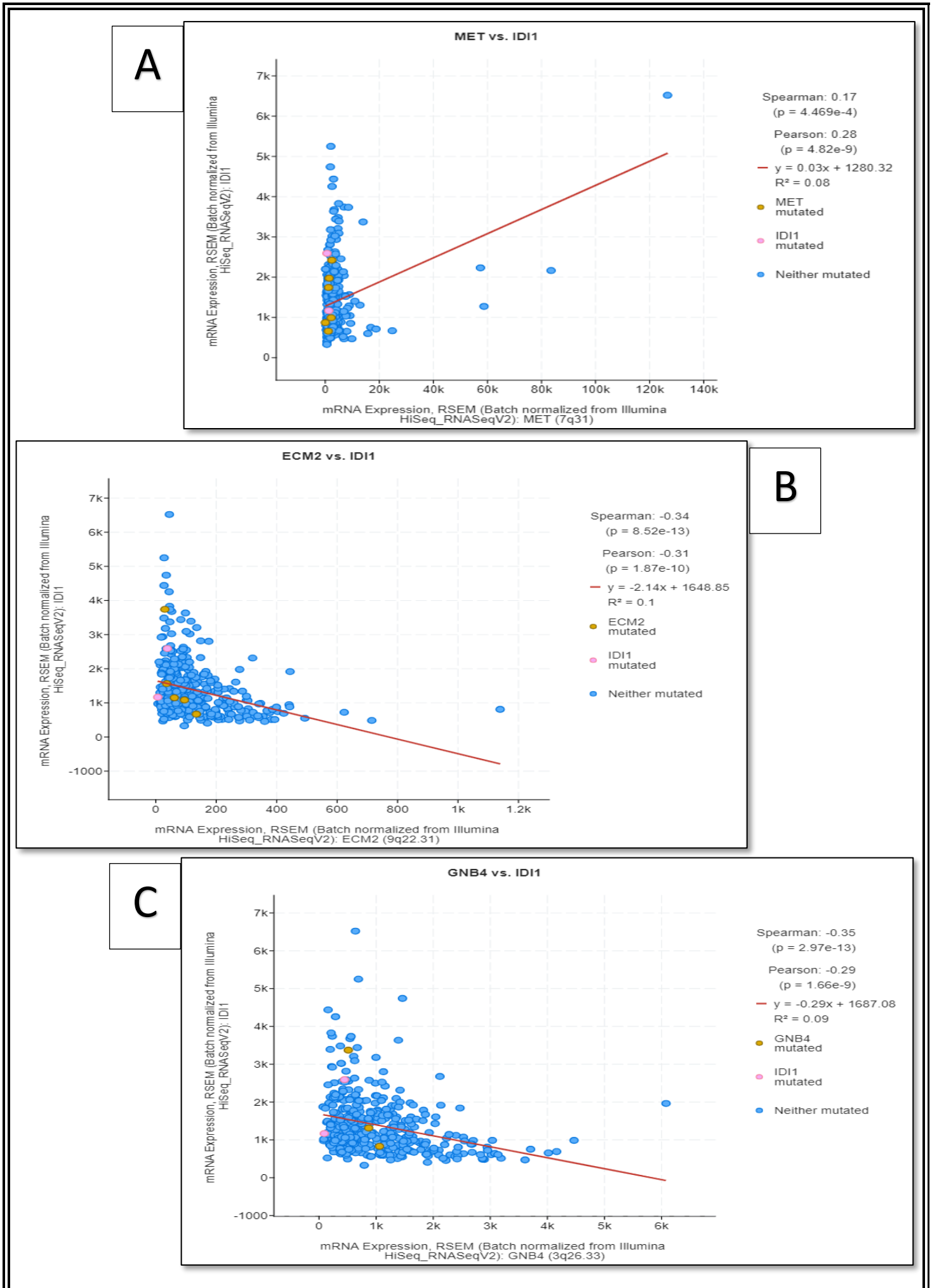
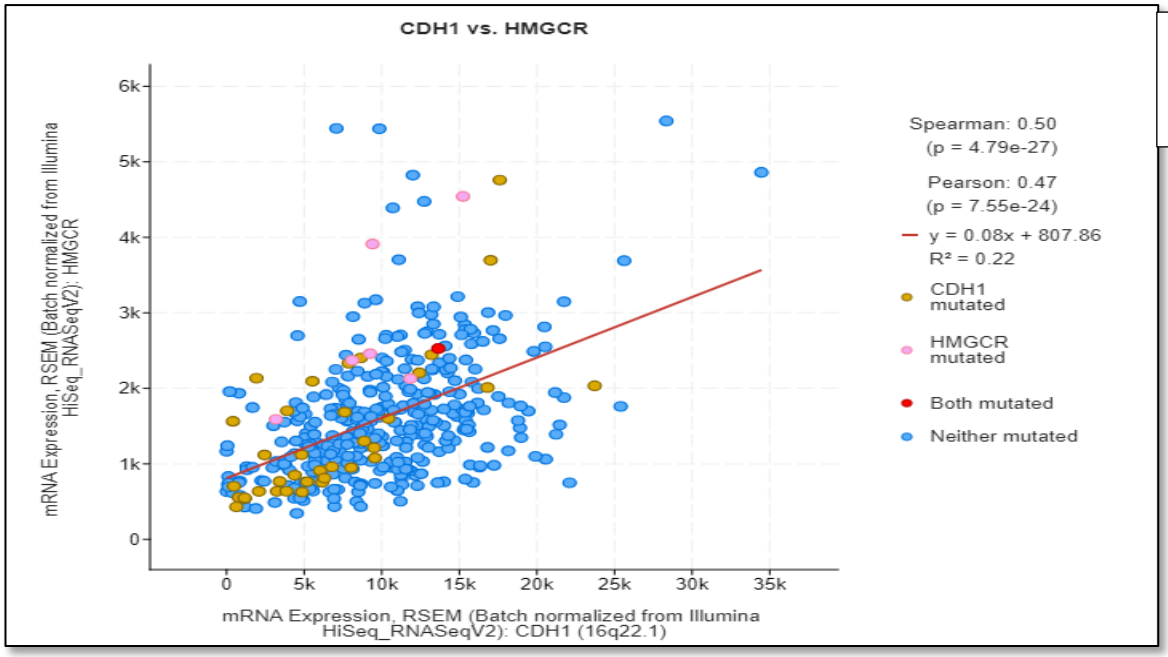
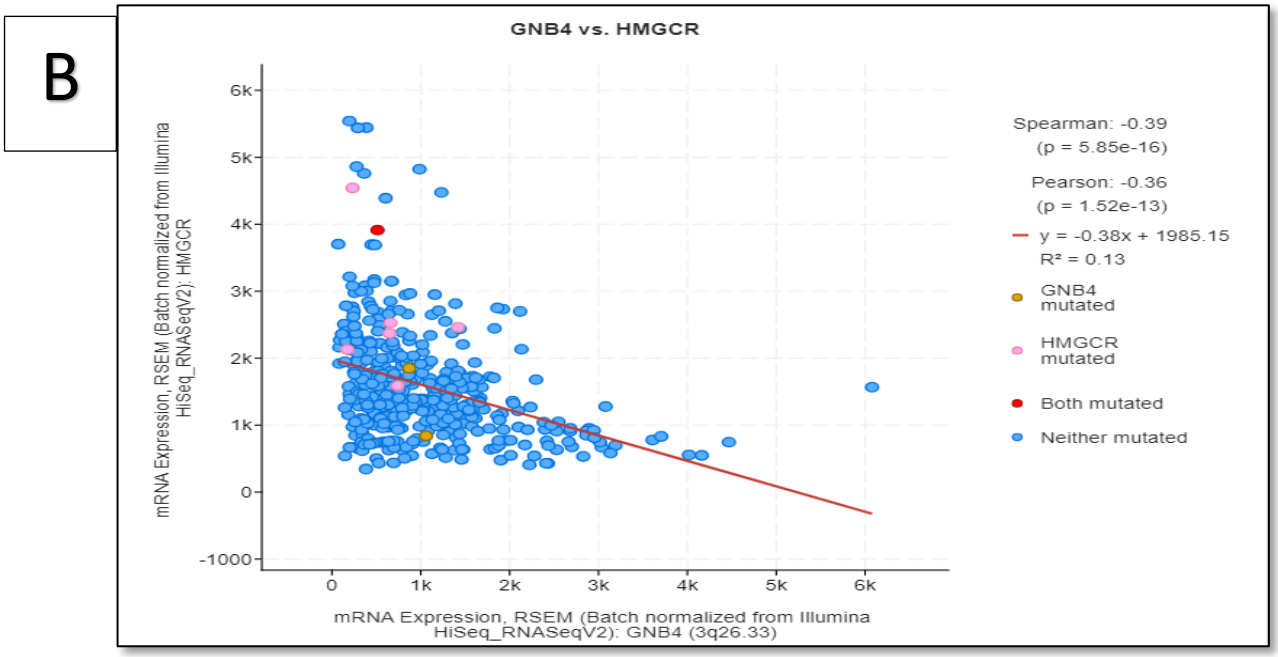


Figure 10: A – Correlation plot between IDI1 and MET, B – Correlation plot between IDI1 and ECM2 & C – Correlation plot between IDI1 and GNB4





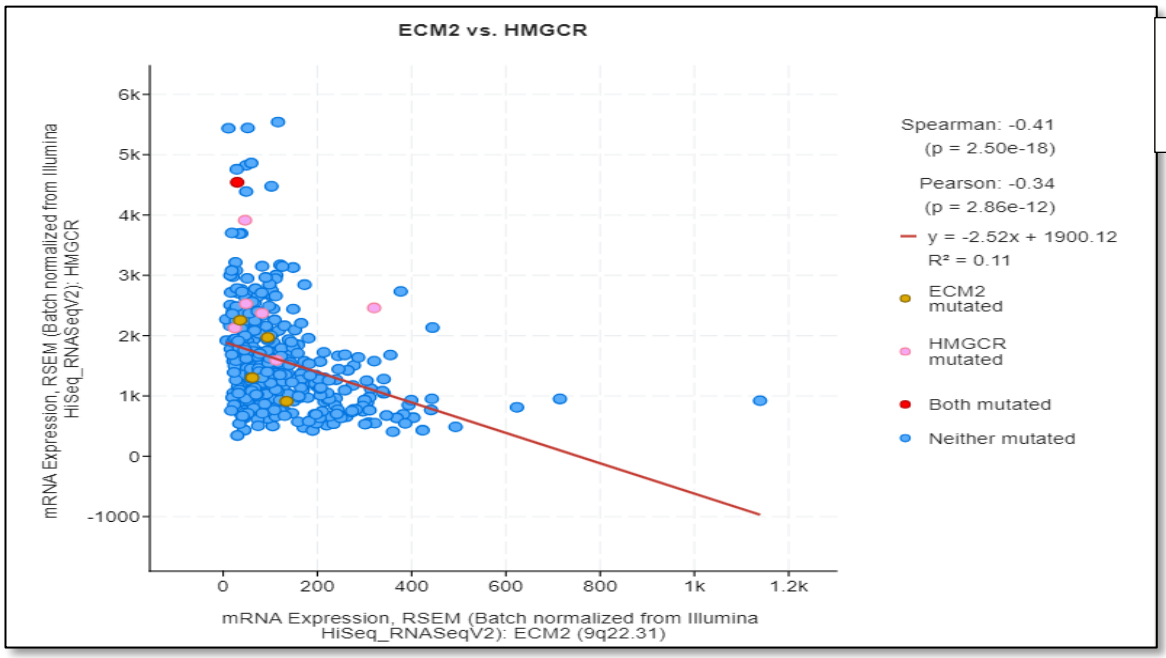
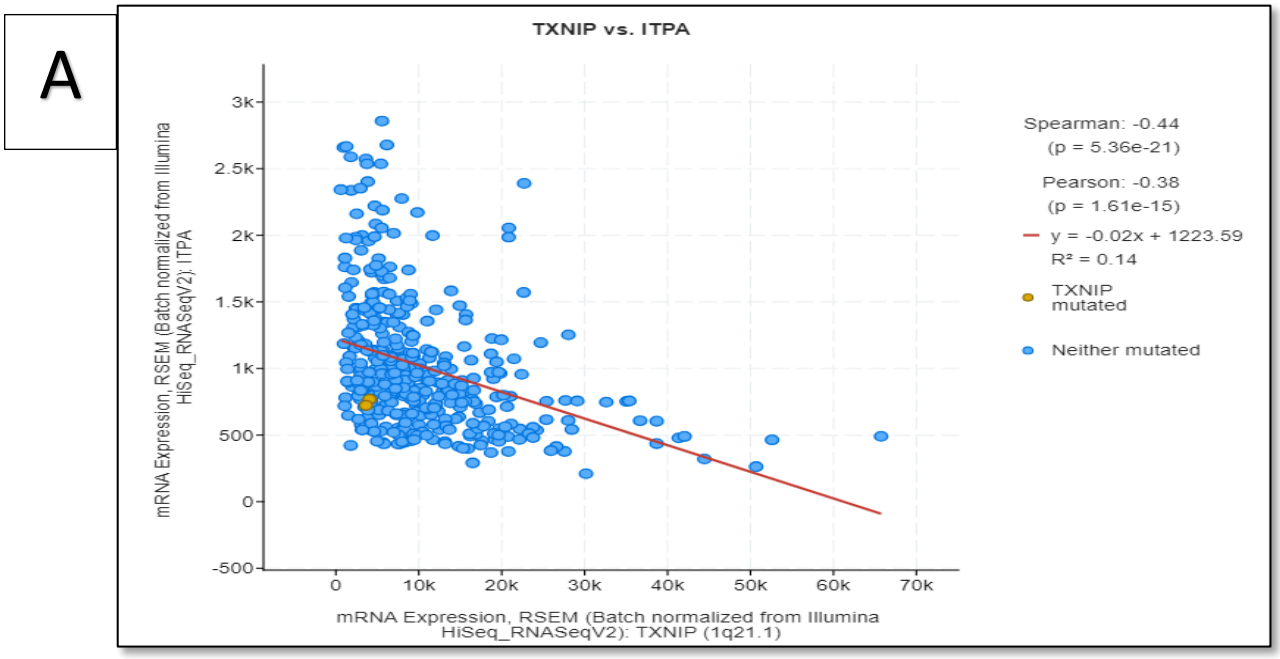
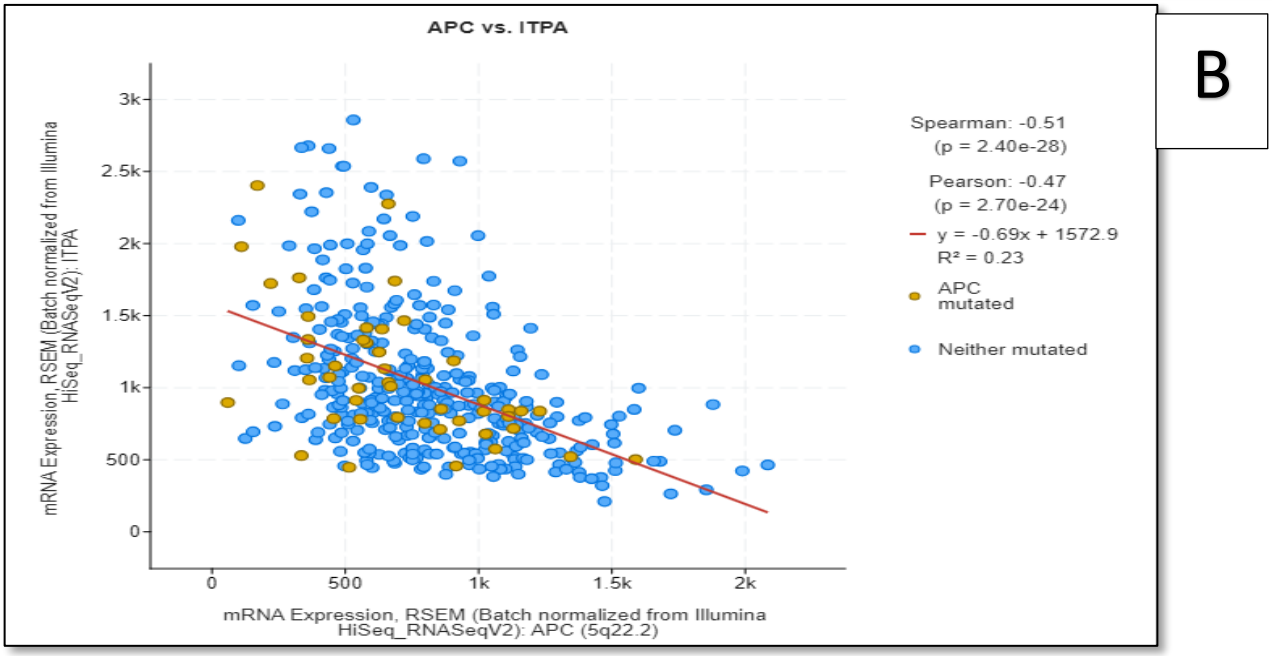


Figure 11: A – Correlation plot between HMGCR and CDH1, B – Correlation plot between HMGCR and GNB4 & C – Correlation plot between HMGCR and ECM2





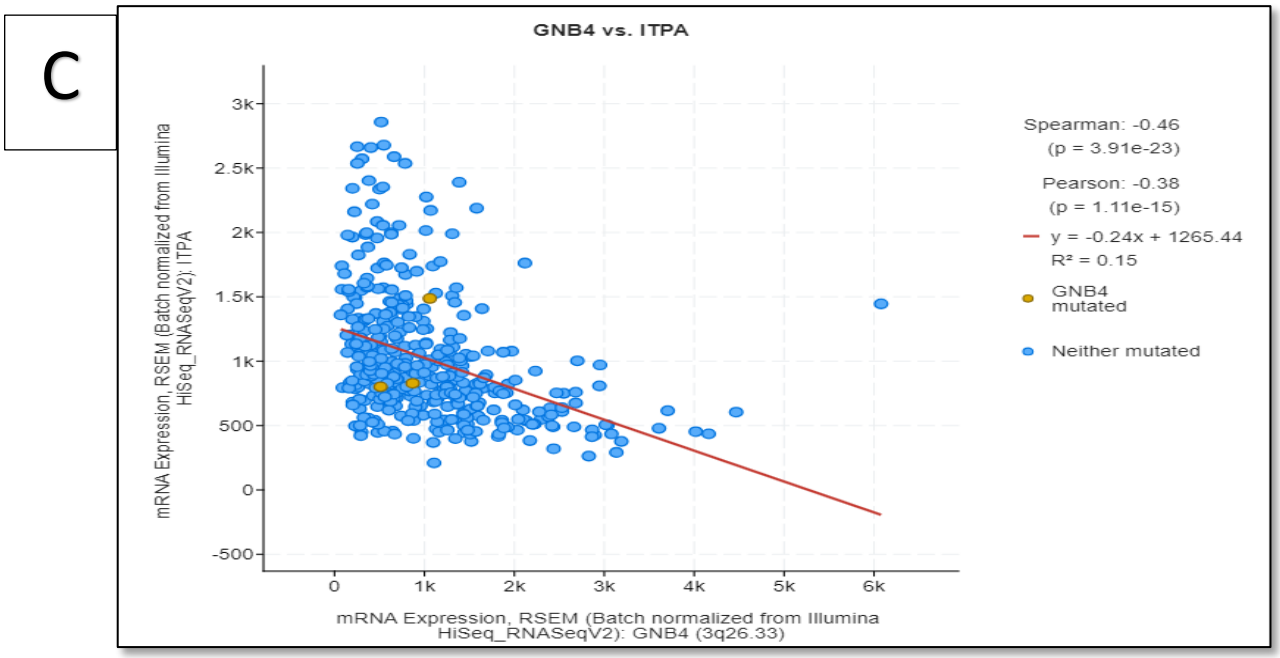
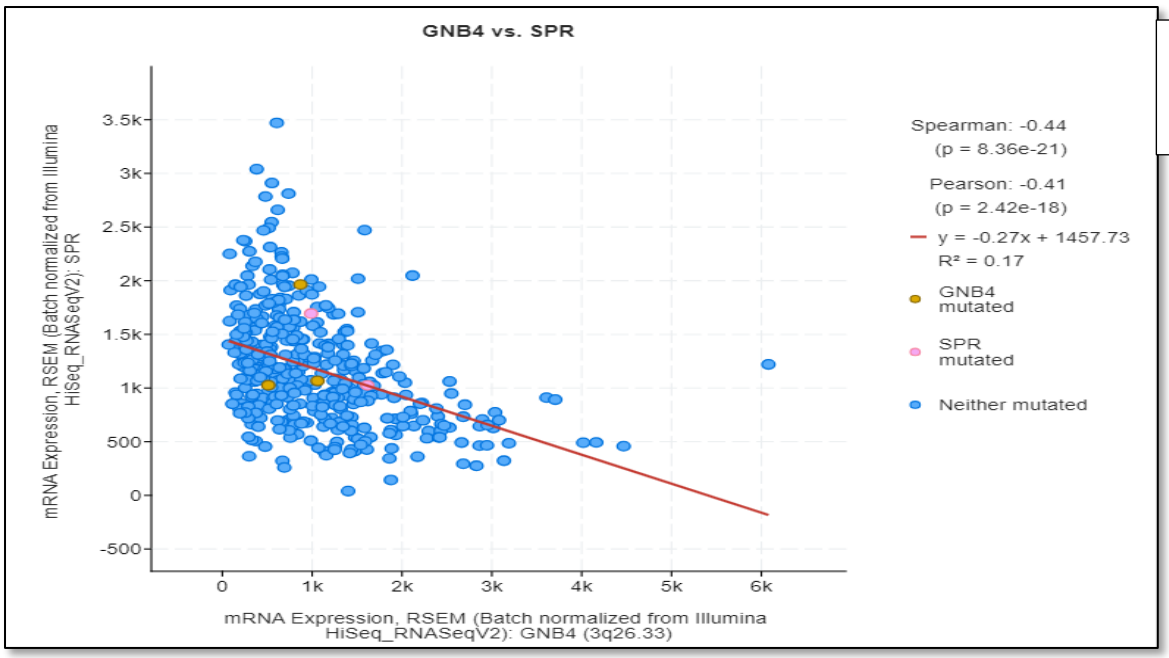
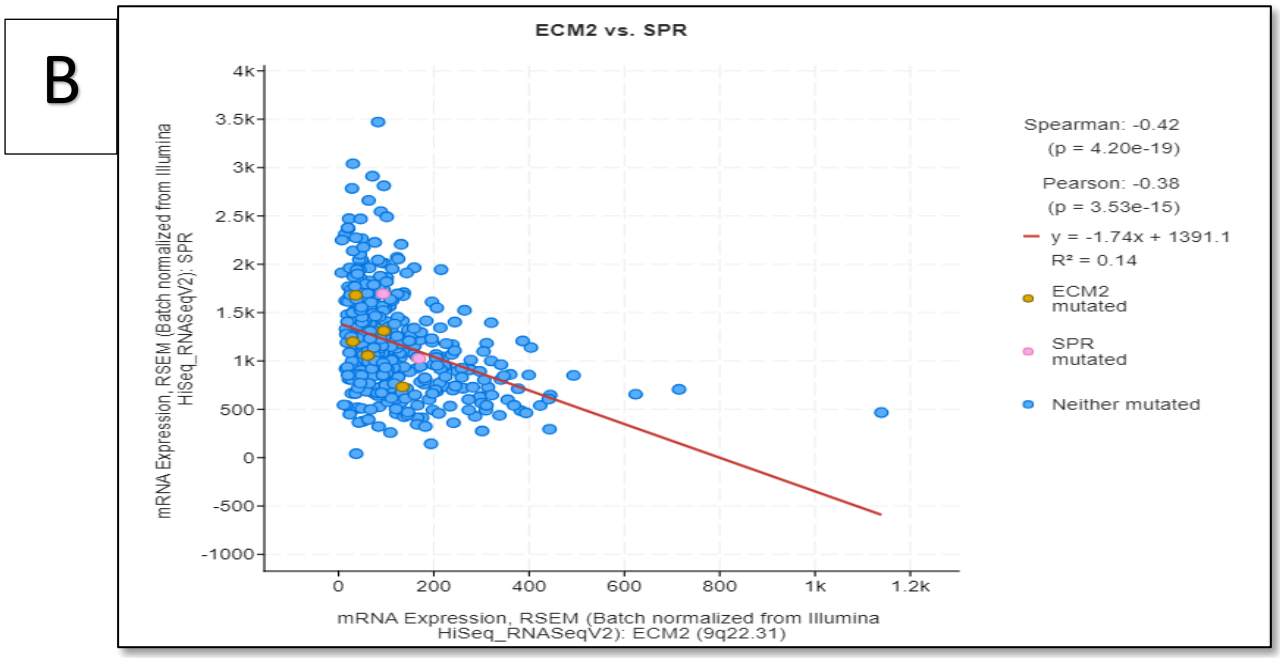


Figure 12: A – Correlation plot between ITPA and CDH1, B – Correlation plot between ITPA and APC & C – Correlation plot between ITPA and GNB4





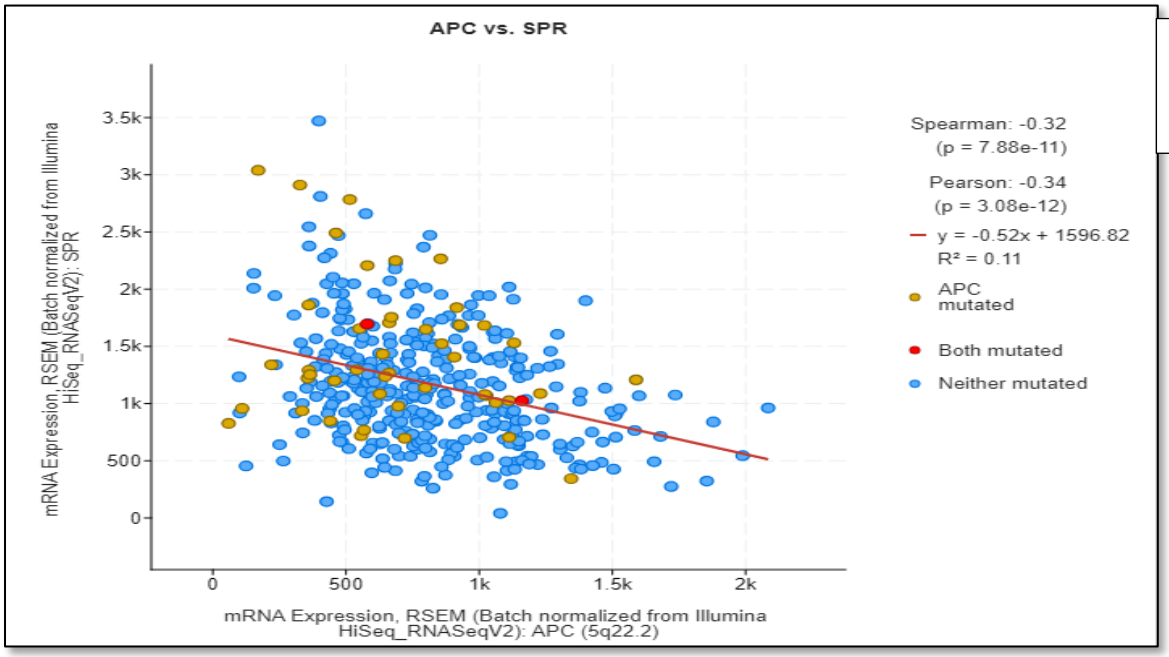


Figure 13: A – Correlation plot between SPR and GNB4, B – Correlation plot between SPR and ECM2 & C – Correlation plot between SPR and APC

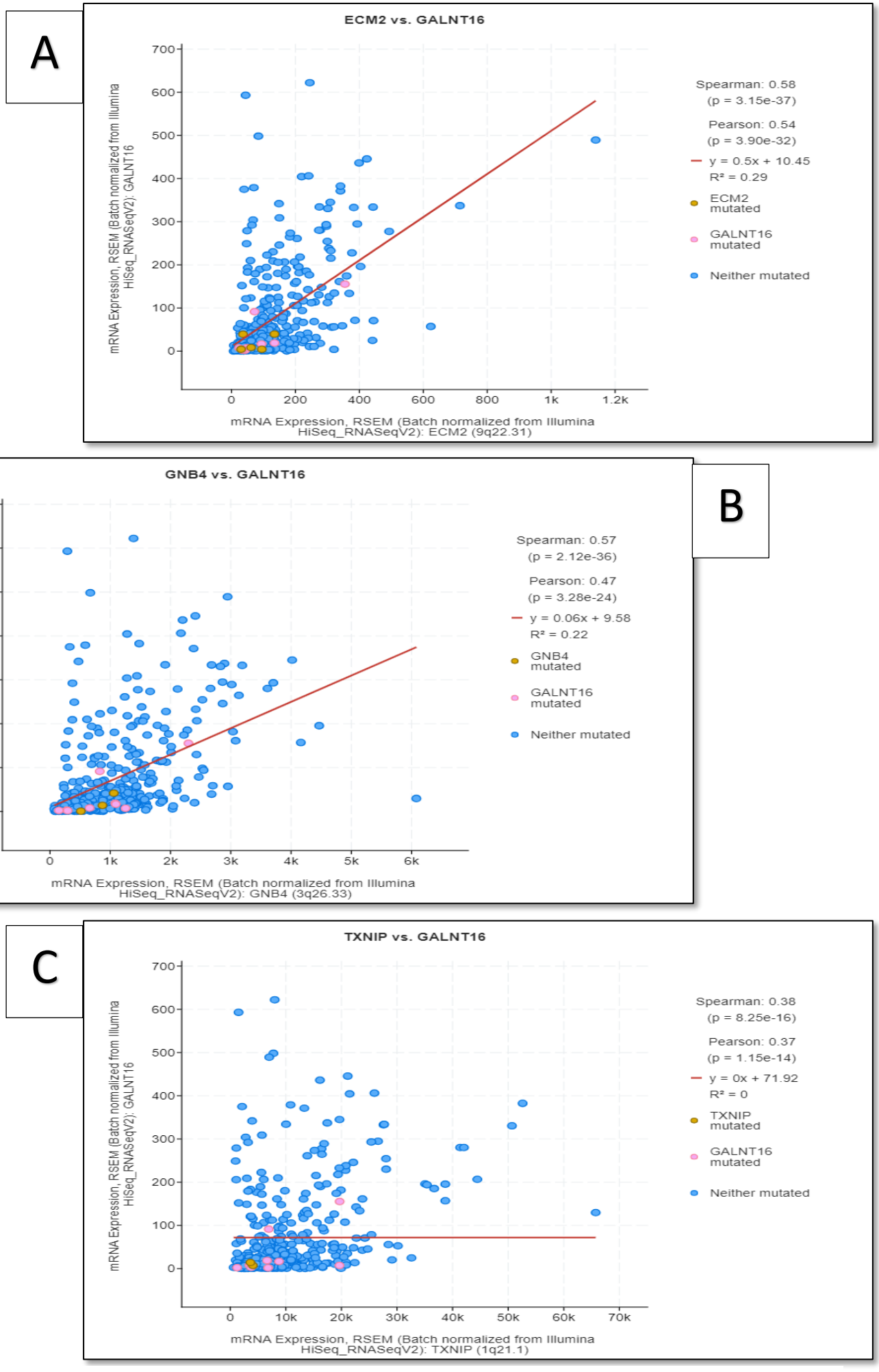
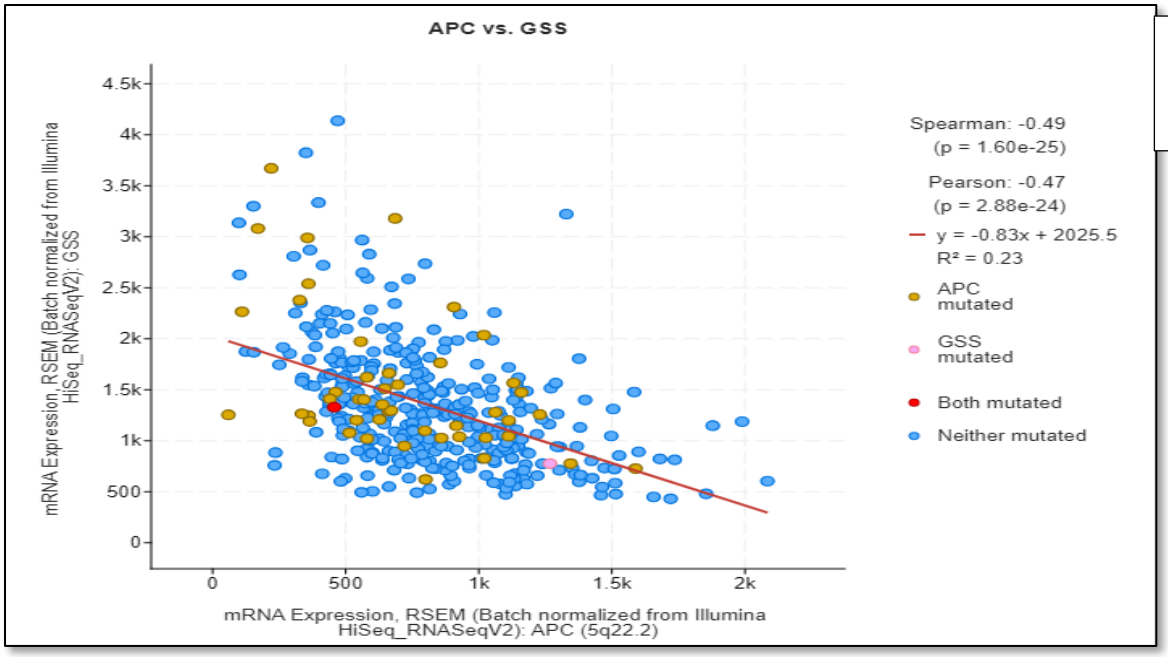
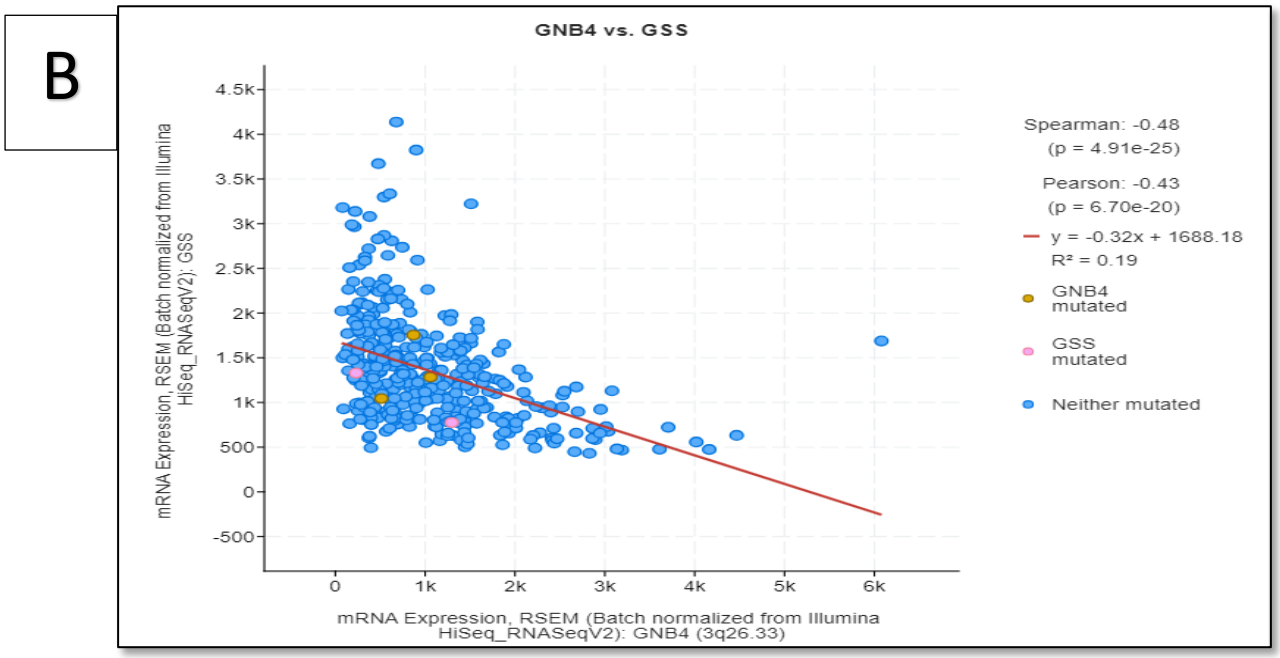


Figure 14: A – Correlation plot between GALMT16 and ECM2, B – Correlation plot between GALMT16 and GNB4 & C – Correlation plot between GALMT16 and TXNIP





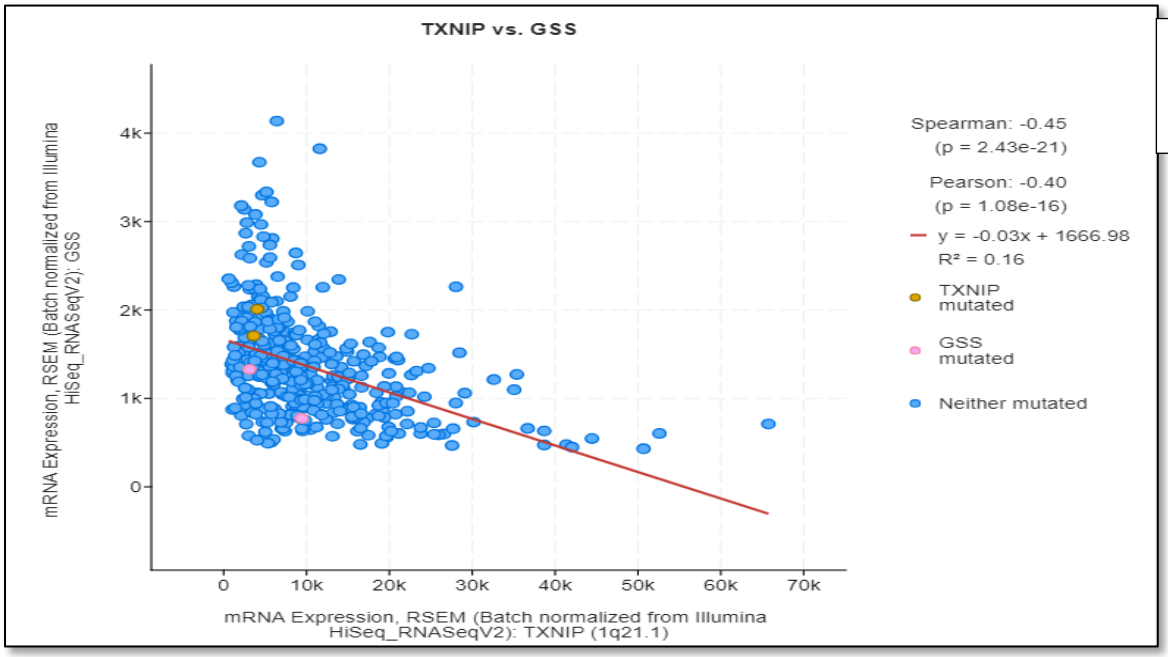


Figure 15: A – Correlation plot between GSS and APC, B – Correlation plot between GSS and GNB4 & C – Correlation plot between GSS and TXNIP

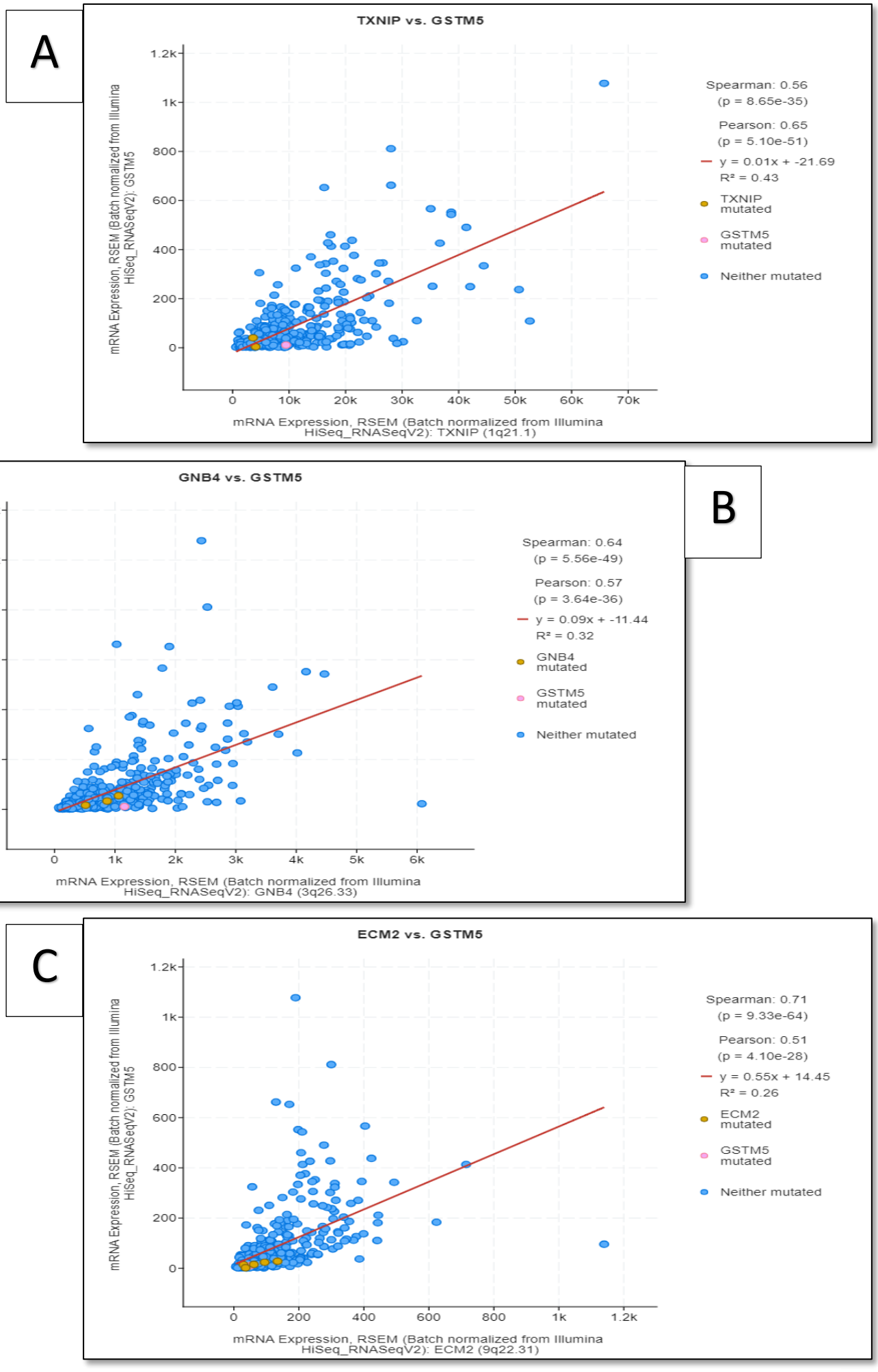
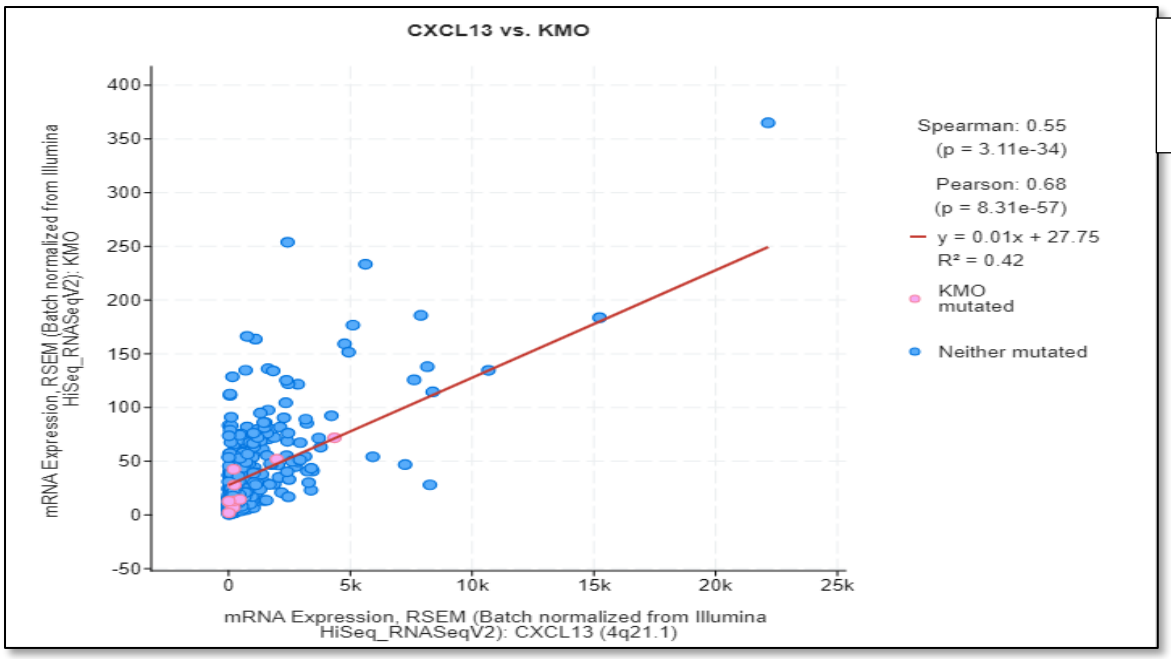
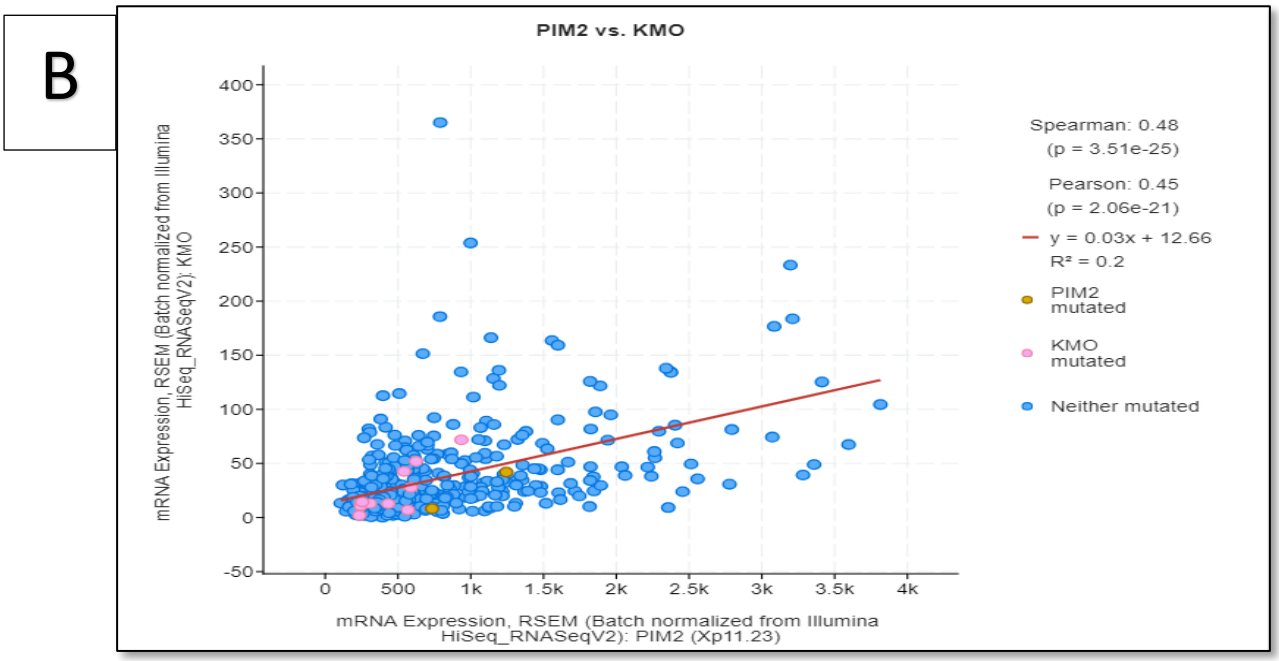


Figure 16: A – Correlation plot between GSTM5 and TXNIP, B – Correlation plot between HMGCR and GNB4 & C – Correlation plot between GSTM5 and ECM2





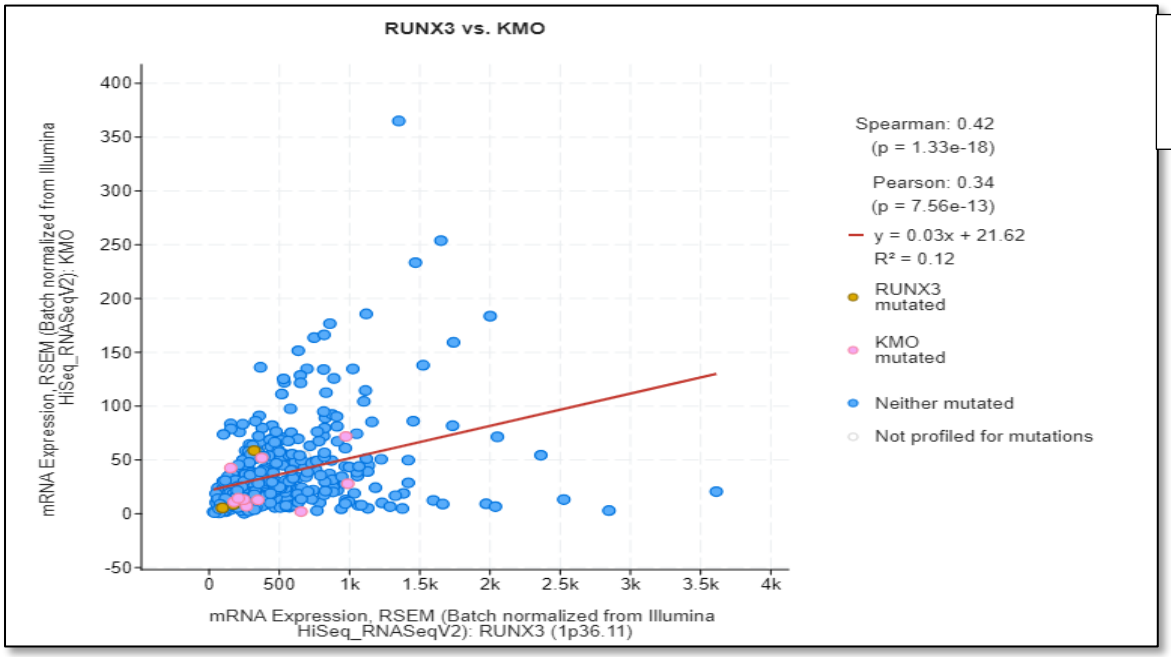


Figure 17: A – Correlation plot between KMO and CXCL13, B – Correlation plot between KMO and PIM2 & C – Correlation plot between KMO and RUNX3

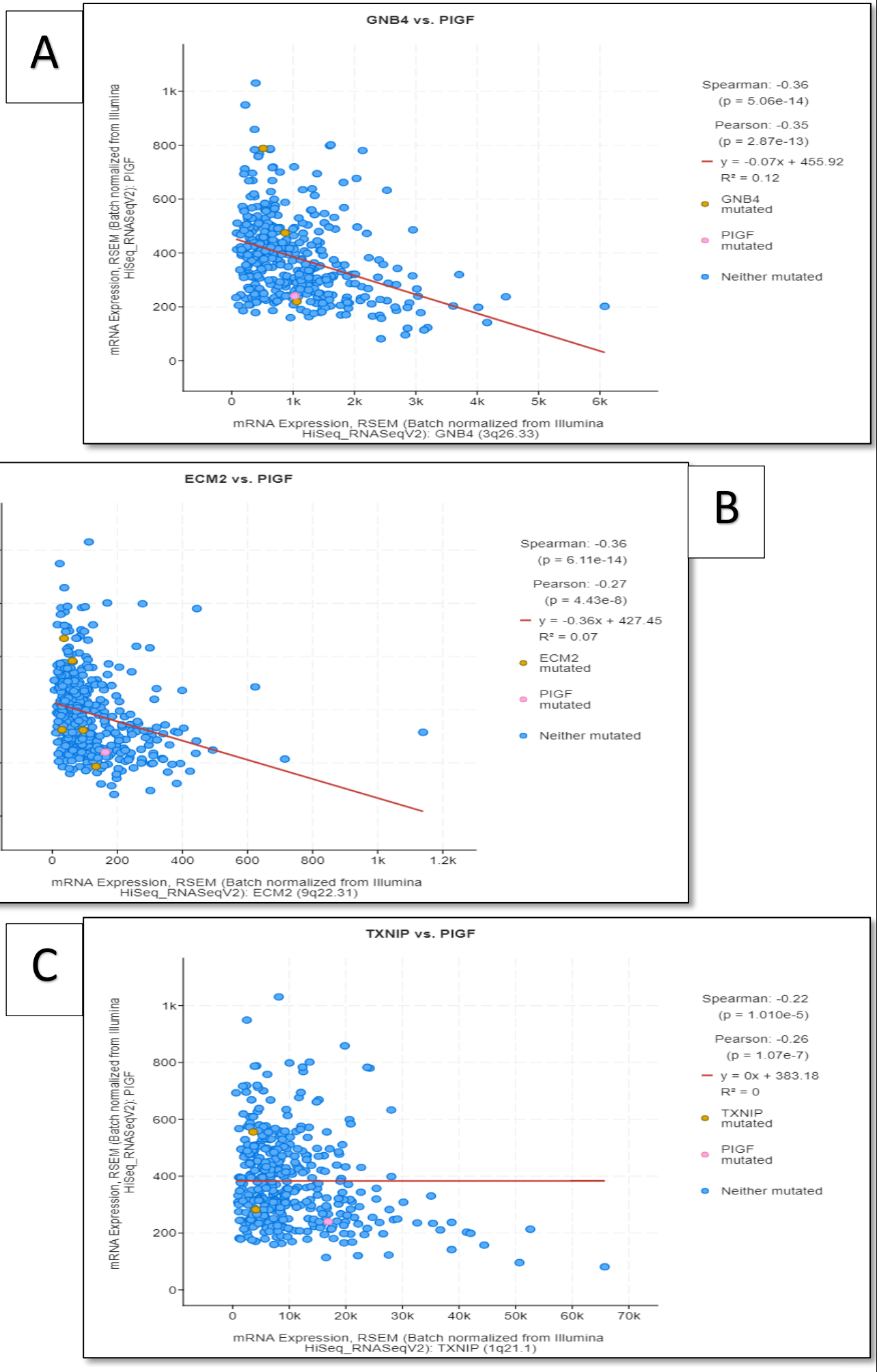
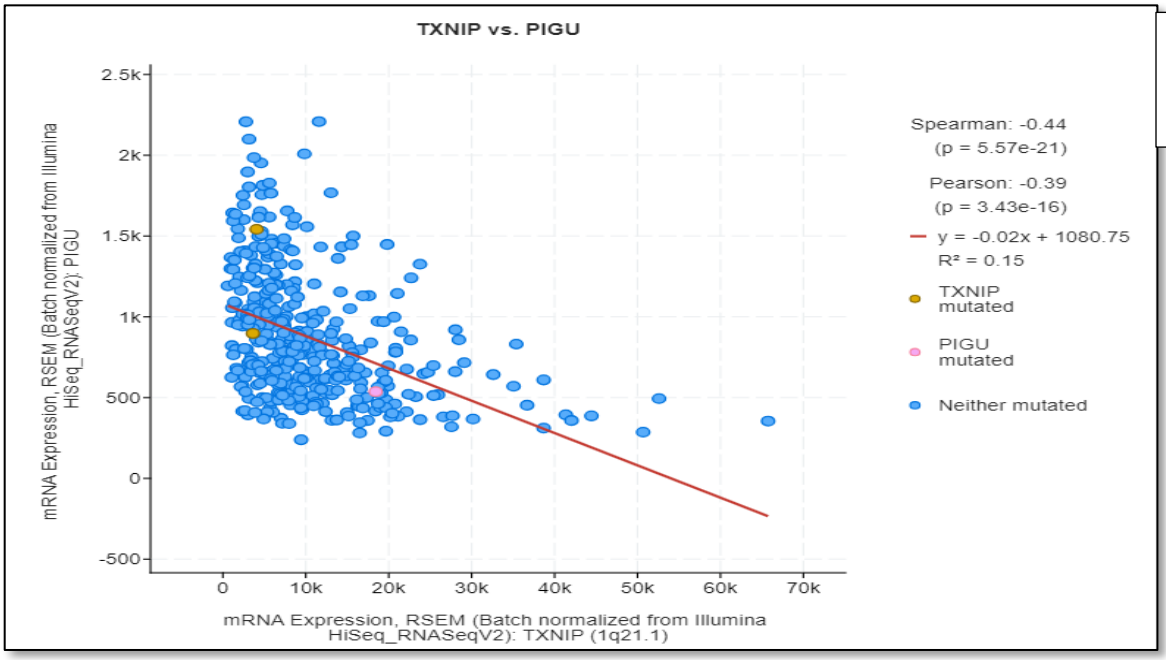
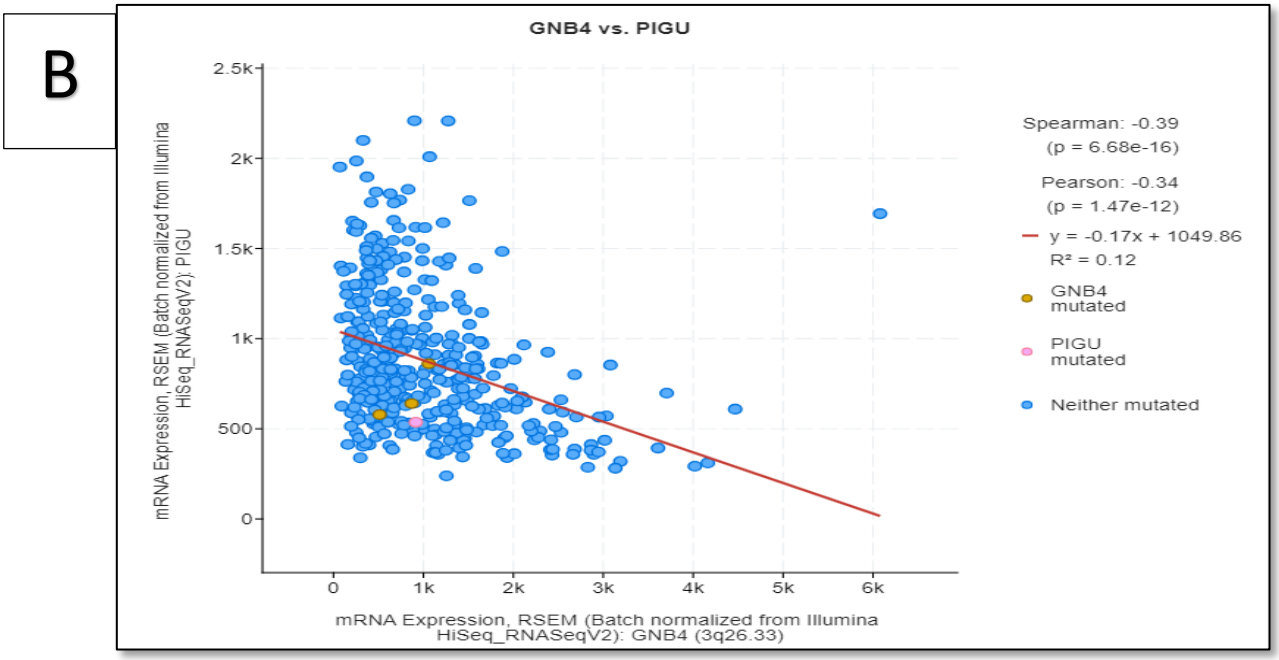


Figure 18: A – Correlation plot between PIGF and GNB4, B – Correlation plot between PIGF and ECM2 & C – Correlation plot between PIGF and TXNIP





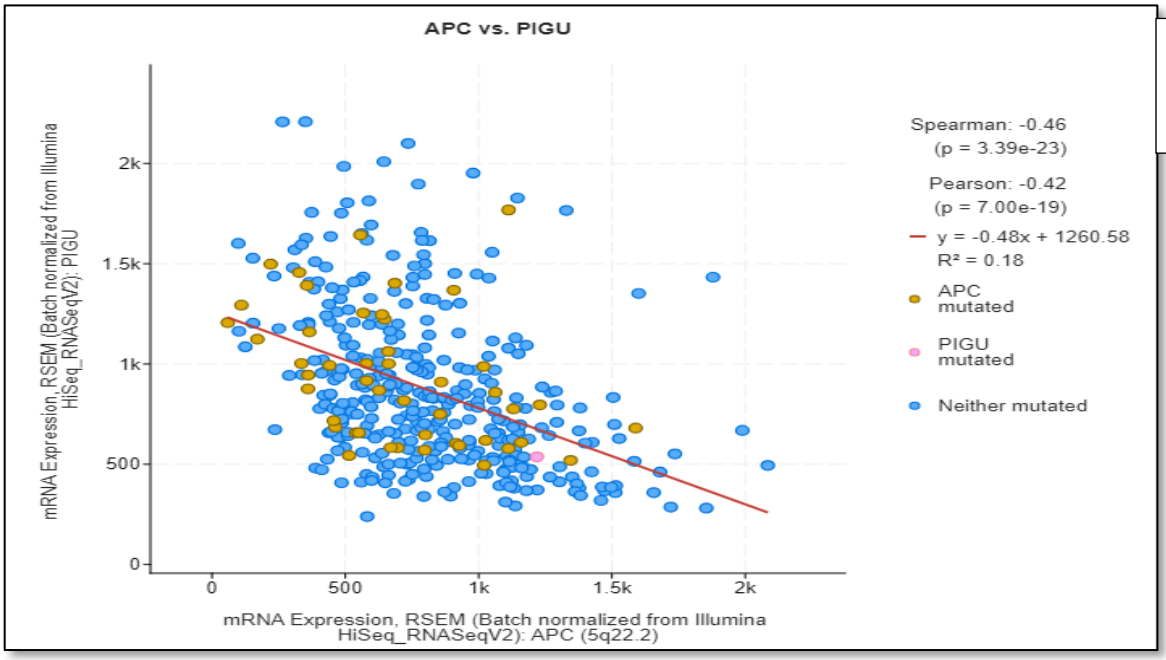


Figure 19: A – Correlation plot between PIGF and TXNIP, B – Correlation plot between PIGF and GNB4 & C – Correlation plot between PIGF and APC

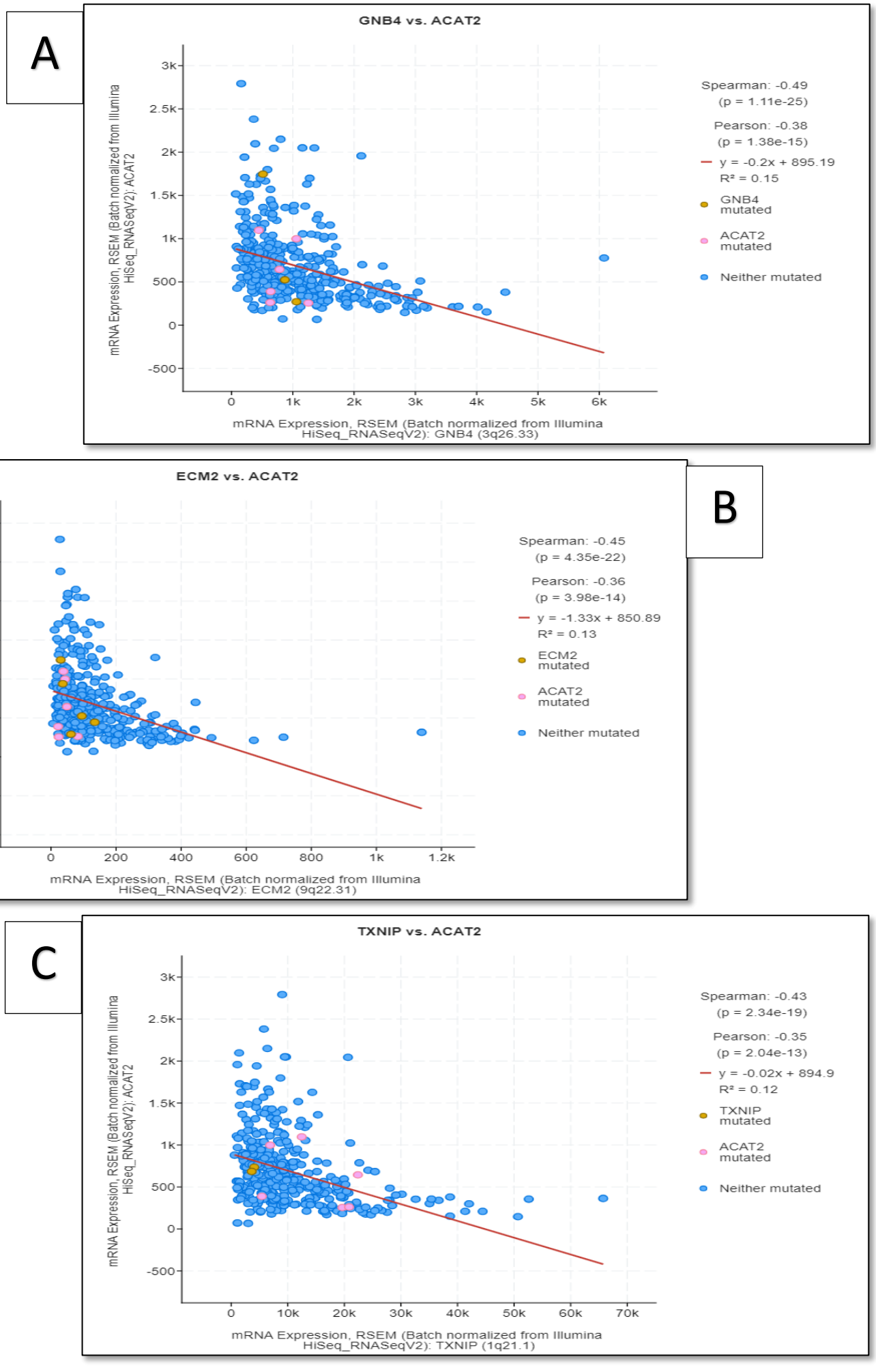
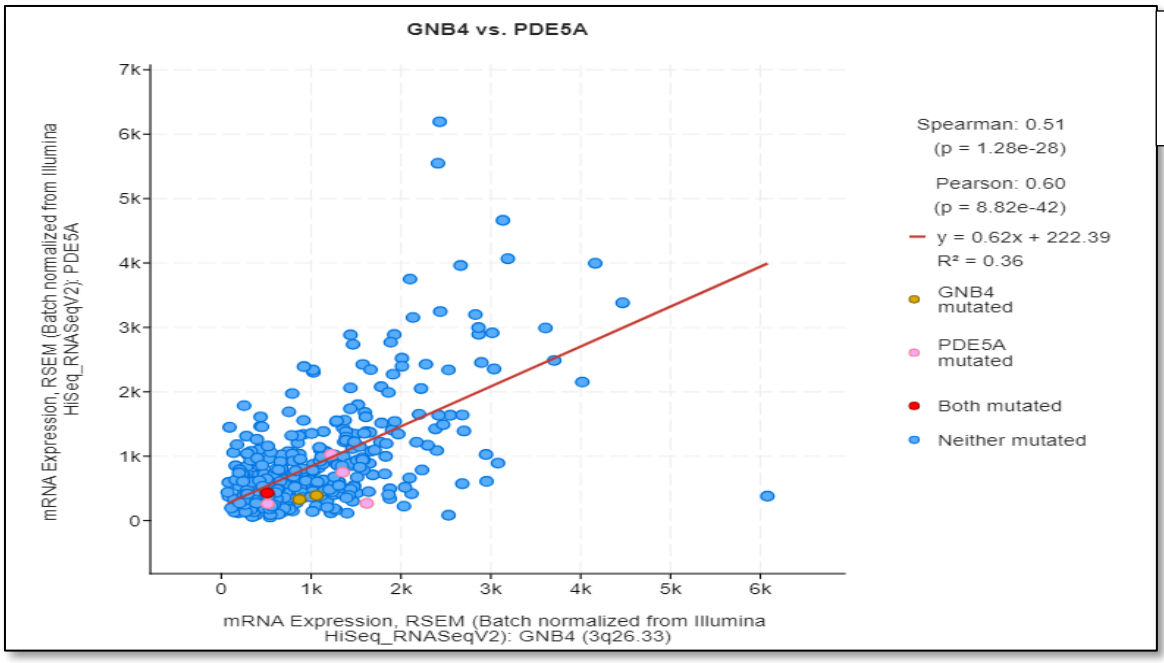
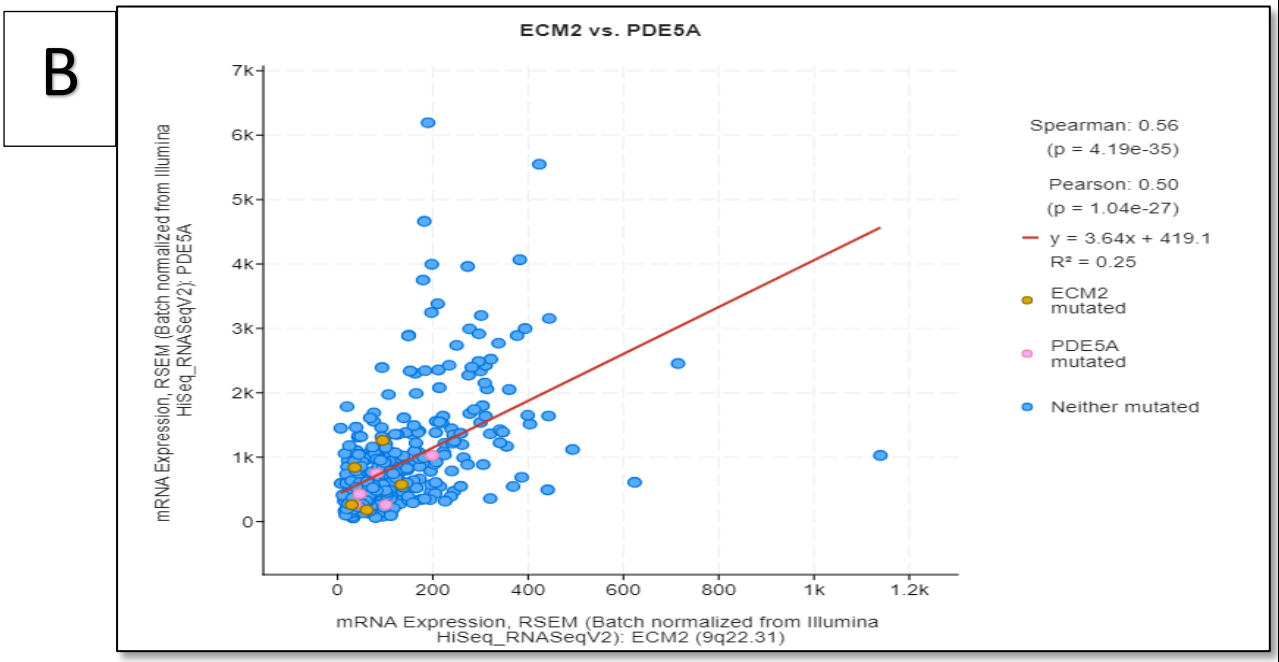


Figure 20: A – Correlation plot between ACAT2 and GNB4, B – Correlation plot between ACAT2 and ECM2 & C – Correlation plot between ACAT2 and TXNIP





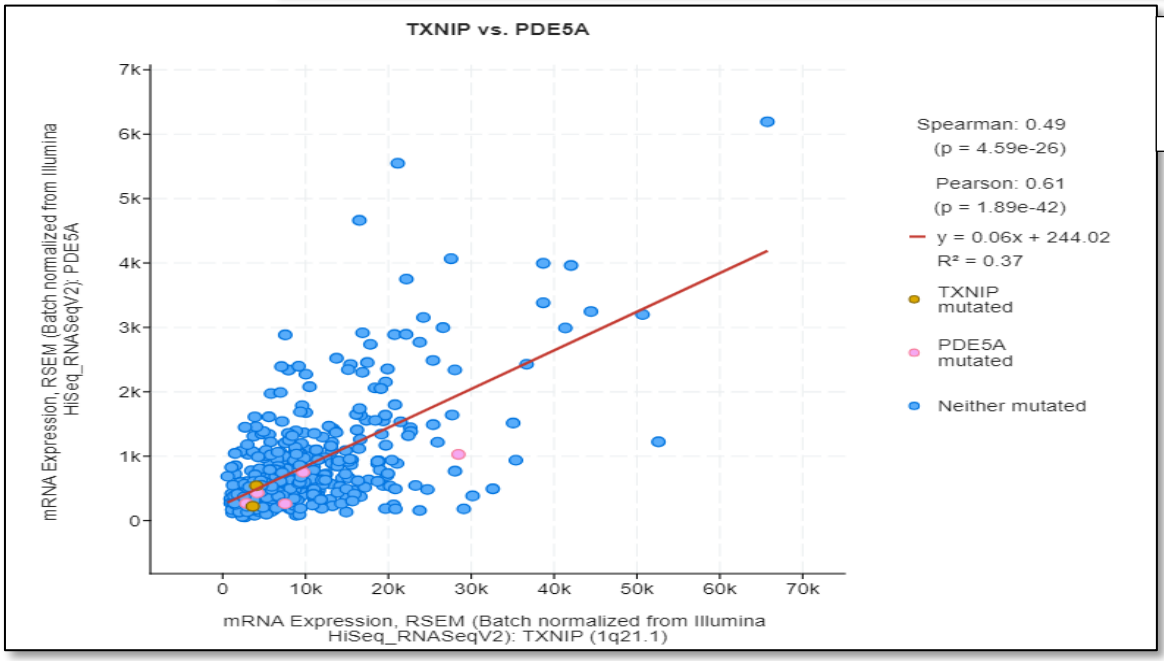
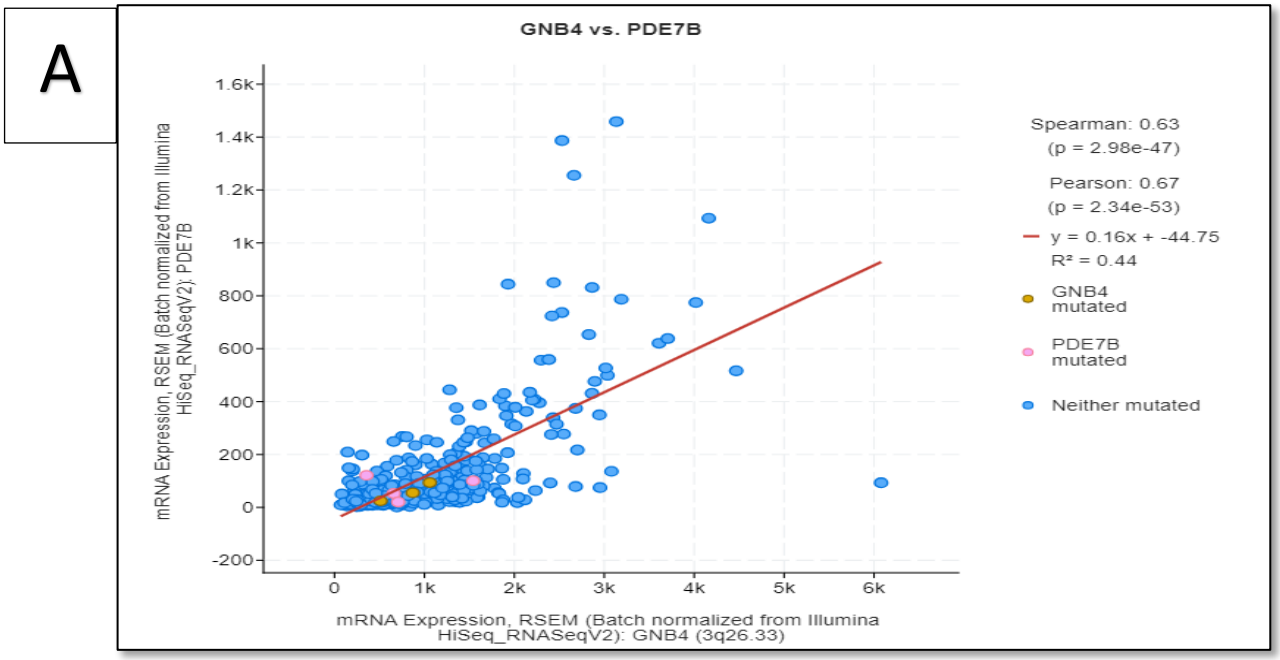
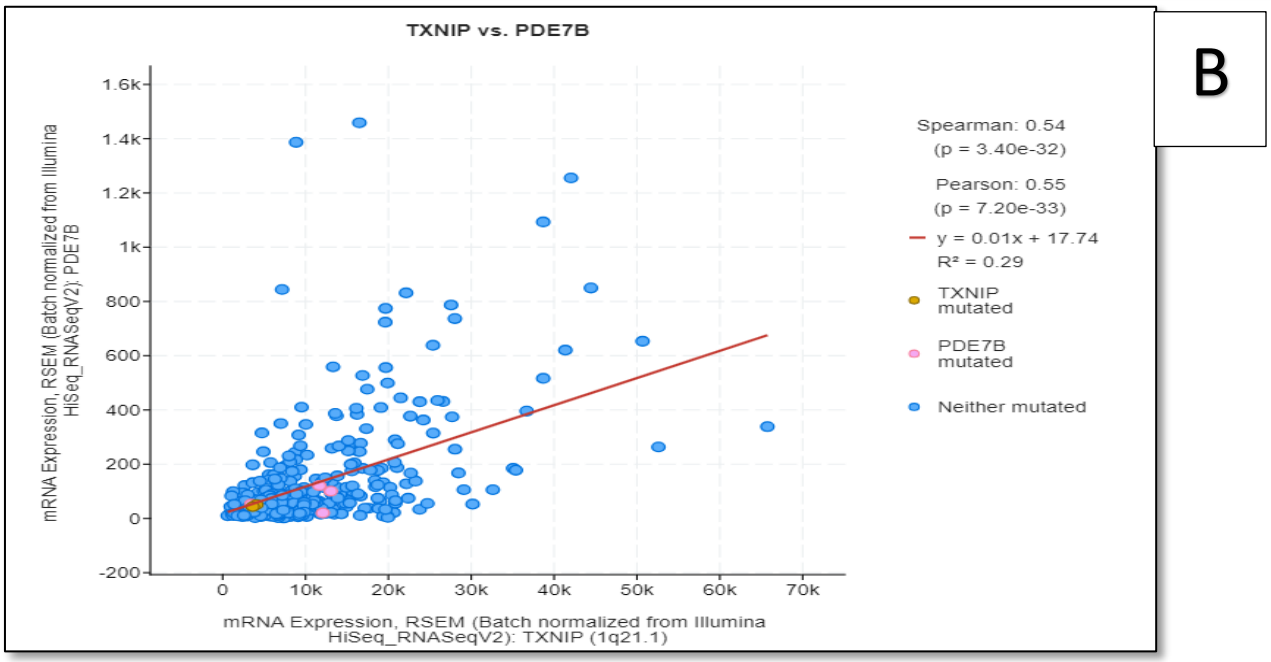


Figure 21: A – Correlation plot between PDE5A and GNB4, B – Correlation plot between PDE5A and ECM2 & C – Correlation plot between PDE5A and TXNIP





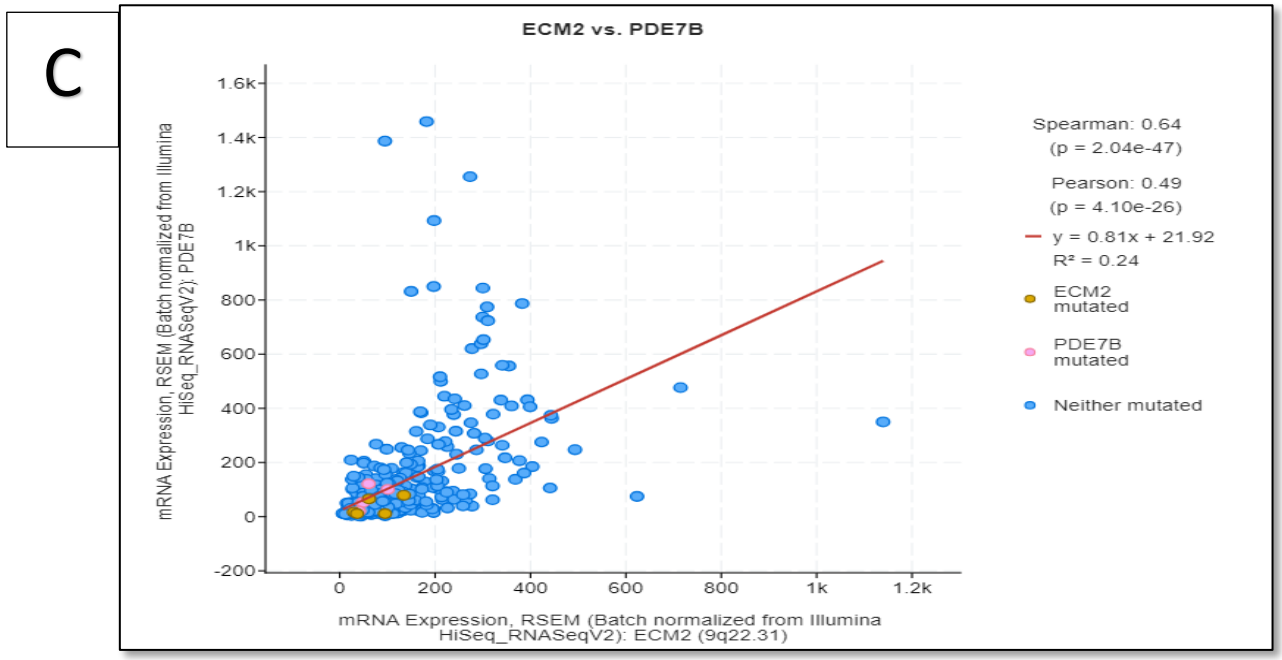
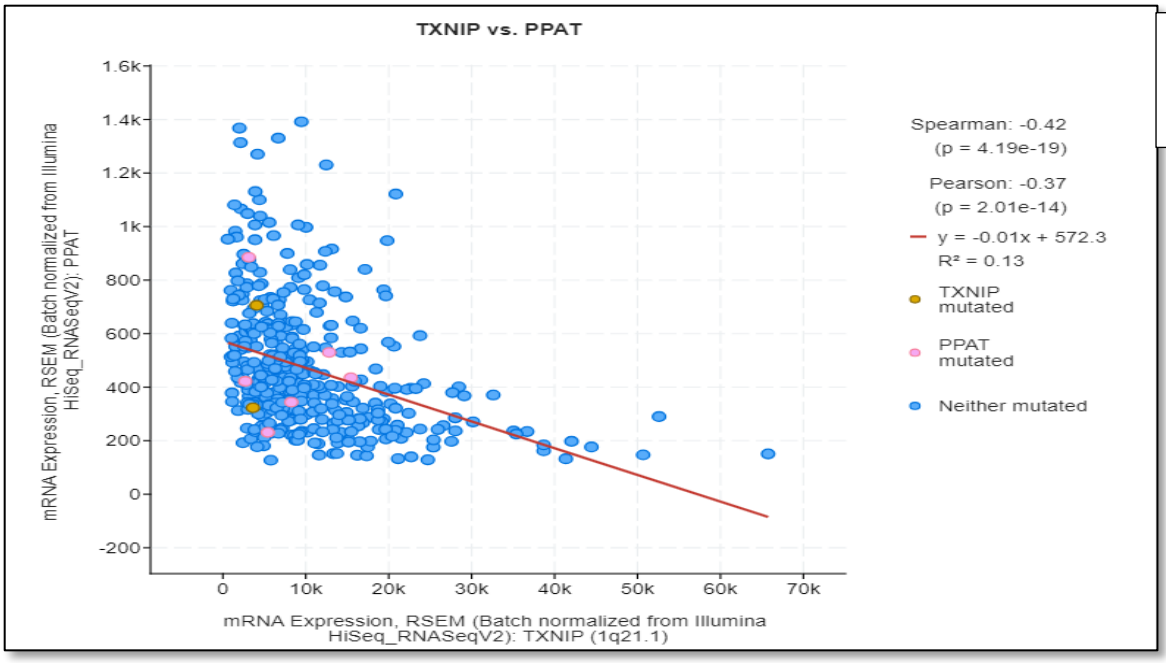
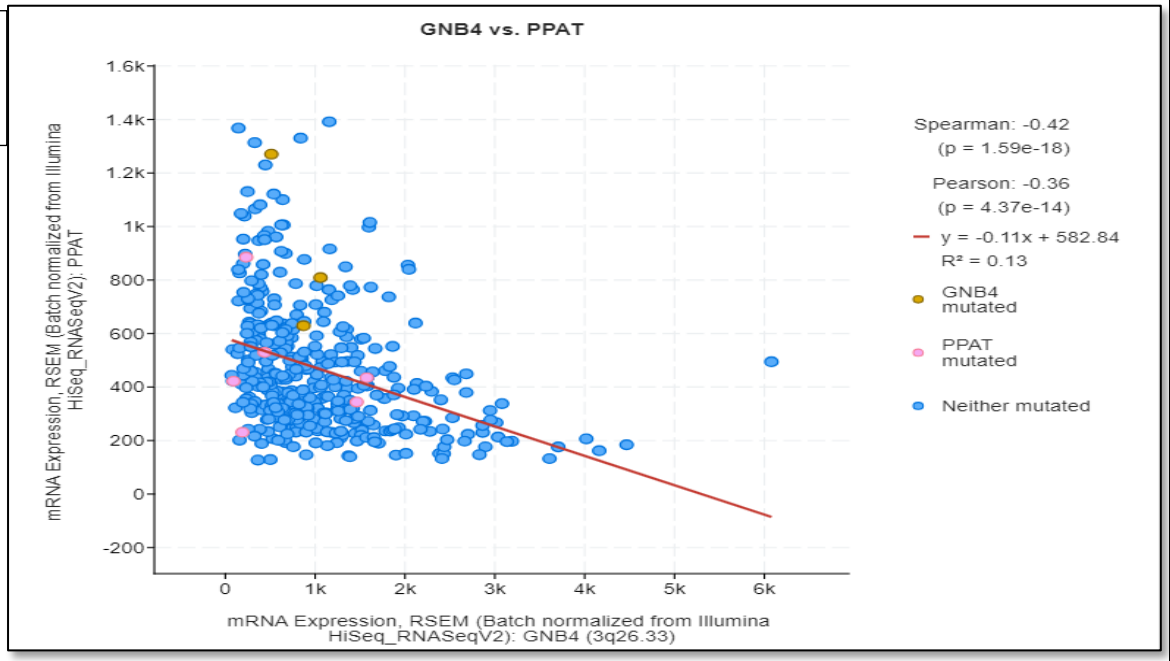


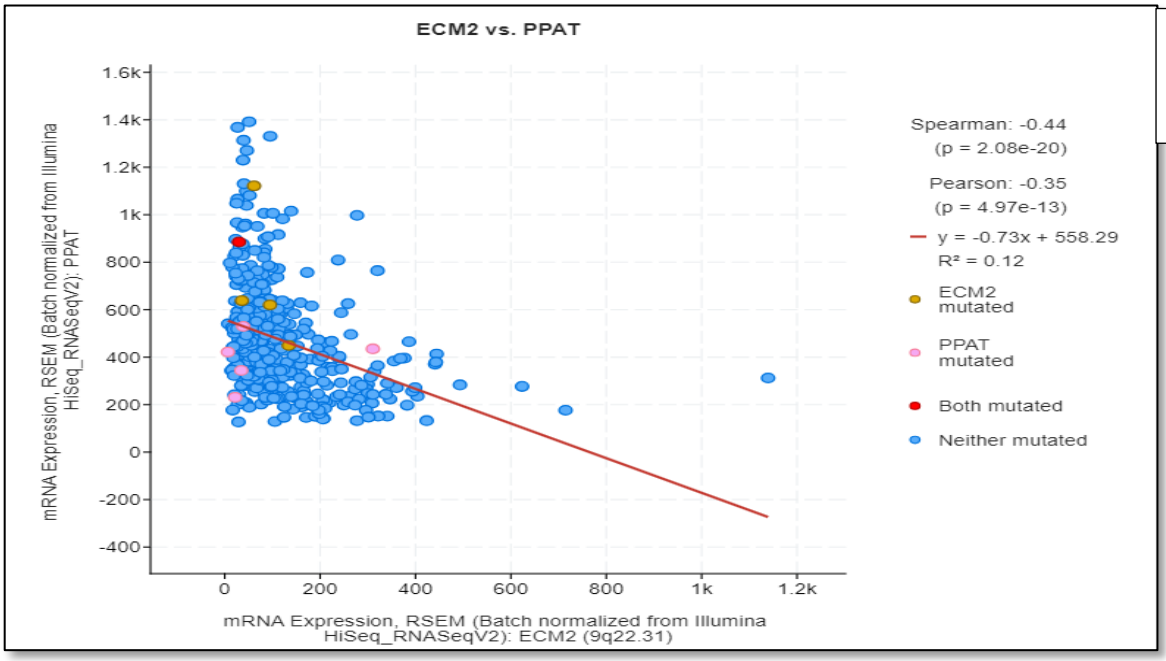
Figure 22: A – Correlation plot between PDE7B and GNB4, B – Correlation plot between PDE7B and ECM2 & C – Correlation plot between PDE7B and TXNIP



A

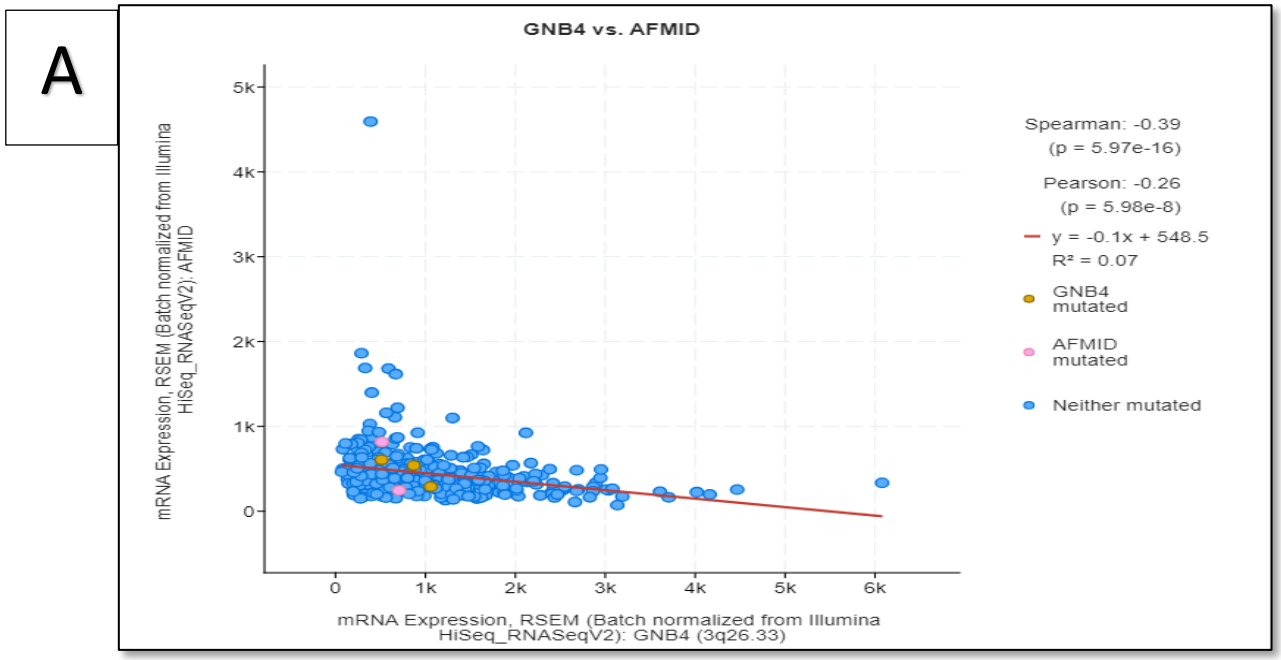


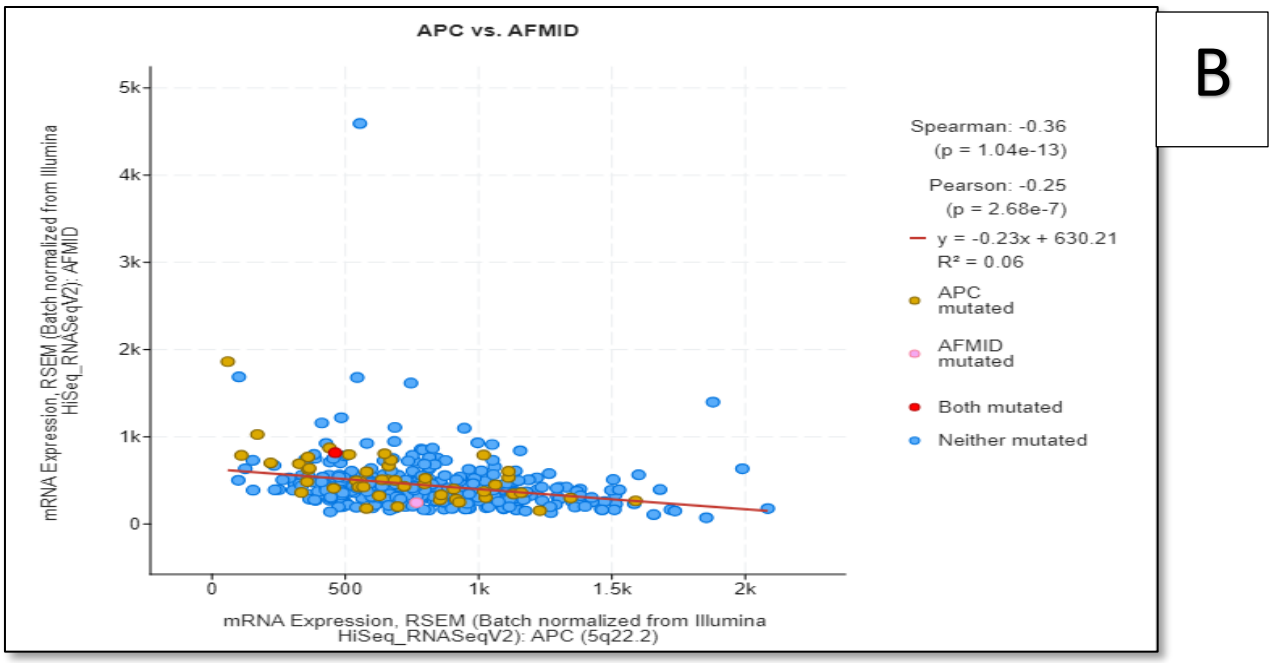
B



C

Figure 23: A – Correlation plot between PPAT and TXNIP, B – Correlation plot between PPAT and GNB4 & C – Correlation plot between PPAT and ECM2





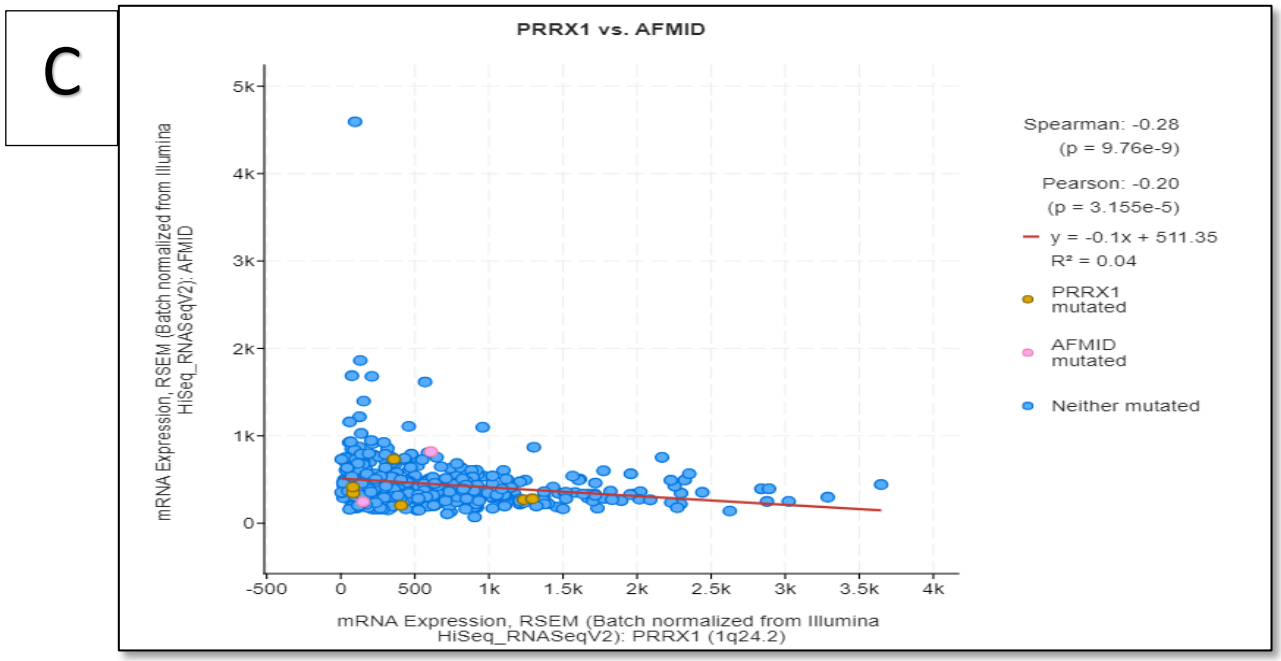


Figure 24: A – Correlation plot between AFMID and GNB4 , B – Correlation plot between AFMID and APC & C – Correlation plot between AFMID and PRRX1

From all the plots we generated, including the ones not demonstrated in this section, we manually created the following table (Table 3) that gives an comprehensive view of the Pearson correlation between each pair of metabolic gene and prognostic marker, which met the condition we had stated above, for the ones we didn't get any value (we didn't get any correlation value for the metabolic gene PNLIP for any of the prognostic markers) or value that was below the cutoff we had set earlier were kept blank.

Table 3: overview of the Pearson correlation between each pair of metabolic gene and prognostic marker

Prognostic markers → / Metabolic genes ↓	GNB4	APC	TXNIP	ECM2	PRRX1	CDH1	GPI	SPARC	FAS	HIF1A	CXCL13	CTNNB1	CCL20	GNAS	RUNX3	CD82	PIM2	CXCL1	ERBB2	TP53	CXCL8	MET
IDI1	-0.29	-0.17	-0.26	-0.31	-0.25	0.24	0.19	-0.19	-0.17		-0.16		0.15		-0.21				0.17			0.28
HMGCR	-0.36	0.19	-0.28	-0.34	-0.24	0.47	0.26	-0.23			-0.22	0.24			-0.23		-0.16		0.17			
ITPA	-0.38	-0.47	-0.38	-0.27	-0.27			-0.17	-0.22	-0.24	-0.16		0.2	0.2			-0.17		0.19			
SPR	-0.41	-0.34	-0.3	-0.38	-0.27	0.22	0.33	-0.16		-16	-0.21	-0.15			-0.15			0.17				
GSS	-0.43	-0.47	-0.4	-0.37	-0.34	0.26	0.2	-0.17	-0.26	-0.18	-0.21								0.2			
GALNT16	0.47	0.23	0.37	0.54	0.32	-0.28	-0.26	0.25			0.15					-0.19		-0.23			-0.16	
GSTM5	0.57	0.21	0.65	0.51	0.39	-0.41	-0.27	0.3			0.28		0.18					-0.16				
KMO	0.28	0.18	0.35	0.24	0.27	-0.17	-0.16		0.22	0.15	0.68				0.34		0.45					
PIGF	-0.35	-0.22	-0.26	-0.27	-0.16	0.18	0.21				-0.18				-0.19		-0.15	0.17			0.16	
PIGU	-0.34	-0.42	-0.39	-0.32	-0.34	0.21		-0.19	-0.24	-23	-0.23		0.2	0.27								
ACAT2	-0.38		-0.35	-0.36	-0.26	0.29	0.26	-0.2	-0.21		-0.2		0.19						0.25			
PDE5A	0.6	0.44	0.61	0.5	0.37	-0.34	-0.26	0.2			0.16		0.2					-0.16				
PDE7B	0.67	0.4	0.55	0.49	0.35	-0.41	-0.29	0.22			0.23		0.2					-0.18				
PPAT	-0.36		-0.37	-0.35	-0.22	0.16	0.33	-0.2			-0.19	0.21				-0.2						0.19
AFMID	-0.26	-0.25	-0.17	-0.18	-0.2	0.15	0.19		-0.15			0.17		0.16								
PLCB2	0.36	0.18	0.36	0.29	0.25	-0.22	-0.15		0.27		0.41				0.39		0.46					
AGMAT	-0.24	-0.18	-0.25	-0.22	-0.25	0.19	0.27	-0.22	-0.2	-0.17									0.16			
COX6C	-0.25	-0.22	-0.24	-0.16					-0.17			-0.16	0.17		-0.18	-0.26	-0.17					
CRLS1	-0.32	-0.26	-0.27		-0.23					-0.24	-0.16		0.32	0.26		-0.17	-0.17					
HSD17B7	-0.37	-0.19	-0.27	-0.32	-0.25	0.27		-0.24	-0.15		-0.16								0.25			
MSMO1	-0.28		-0.24	-0.25	-0.15	0.3			-0.15		-0.19				-0.2		-0.17		0.17			
NANP	-0.26	-0.17	-0.25	-0.21	-0.16				-0.28		-0.21					-0.29	-0.16			-0.17		
PYCR1	-0.39	-0.36	-0.37	-0.31	-0.22	0.18	0.28		-0.2		-0.21	0.16										
ATP5MC1	-0.31	-0.31	-0.29	-0.27	0.22		0.27	-0.18		-0.17			0.19									
ATP5PD	-0.17	-0.3	-0.16	-0.16			0.18					-0.19	0.15	0.16	-0.16							
COX7A2	-0.27	-0.24	-0.25	-0.25	-0.19			-0.16					0.17		-0.21				0.19			
HGSNAT	0.25	0.21	0.28	0.23	0.21	-0.15	-0.21	0.19					-0.22									
KMT2A	0.42	0.47	0.47		0.16	-0.24					0.35				0.16			-0.23			-0.2	
MTHFD2L	-0.22		-0.15	-0.21	-0.19			-0.19					0.18			-0.16	-0.16	0.16				
NT5C	-0.29	-0.45	-0.24	-0.25			0.18			-0.17		-0.16		0.15					0.21			
PCYT2	-0.39	-0.38	-0.28	-0.28	-0.31	0.24	0.21		-0.28					0.17								
RDH11	-0.19	-0.2	-0.25	-0.2		0.16	0.15							0.19	-0.21				0.16			
SLC27A5	-0.19	-0.19	-0.16	-0.17			0.27	-0.15		-24					-0.18	-0.15						
SUCLA2	-0.23		-0.2	-0.19	-0.21	0.2		-0.16	-0.23							-0.22	-0.22					
TGDS	-0.33		-0.26	-0.24	-0.22	0.2		-0.23					0.34			-0.21	-0.17					

UQCR10	-0.25	-0.38	-0.19	-0.23	-0.21		0.21					-0.16	0.16					0.15				
ALG5	-0.29	-0.18	-0.21	-0.21	-0.15	0.19							0.16						0.18			
ATP6V0C	-0.23	-0.38	-0.2	-0.22			0.16					-0.2				0.23		0.18				
CHDH	-0.37		-0.21	-0.27	-0.28	0.29		-0.24	-0.18	-0.18												
COX5B	-0.29	-0.33	-0.2	-0.23	-0.21		0.23					-0.22	0.15									
DCXR	-0.31	-0.4	-0.27	-0.27			0.28		-0.21				0.16	0.17								
GGT7		-0.19			-0.2		-0.2		-0.37	-0.15				0.17				-0.17		-0.19		
GUCY1A2	0.36	0.15		0.36	0.32	-0.15		0.39		0.17											0.16	
HDDC3	-0.26	-0.35	-0.23	-0.23	-0.24		0.15			-0.17				0.15								
PIGT	-0.18	-0.24	-0.16	-0.16		0.18			-0.28		-0.18			0.23								
PNPO	-0.33	-0.21	-0.32	-0.33	-0.22	0.21	0.25	-0.2														
SETDB2		0.2	0.15				-0.2	-0.15			0.2	0.21			0.28			-0.19				
ACSS1	-0.16				-0.24	0.17			-0.3	-0.16			0.15	0.17								
DCTPP1	-0.35	-0.31	-0.28	-0.3	-0.22	0.23	0.46															
PIGM		-0.17			-0.21			-0.17	-0.3	-0.16				0.25				-0.16				
ALG11	-0.2		-0.26	-0.19	-0.18	0.2			-0.25													
NDUFA4	-0.16	-0.31	-0.15							-0.16		-0.21		0.16								
NDUFB2	-0.17	-0.28	-0.16				0.31			-0.18		-0.2										
NDUFV2		-0.18	-0.15									-0.22	0.18		-0.19			0.16				
PLCH1	-0.22			-0.26	-0.28	0.22		-0.29	0.15													
PMVK	-0.15	-0.28							-0.16	-17		-0.19								-0.16		
UQCRB		-0.19										-0.22		0.23	-0.19	-0.24	-0.17					
ACOX1		0.18				0.26		-0.16								0.15				-0.18		
AOX1	0.22		0.21	0.26	0.22			0.21														
CYP19A1	0.15			0.16	0.26			0.21		0.18												
CYP2R1	-0.16			-0.17	-0.2			-0.31					0.24									
ENTPD2	-0.22	0.22		-0.19	-0.17	0.16																
GGPS1		-0.18								-0.22				0.16		-0.19	-0.19					
GPHN	-0.24			-0.21		0.19	0.26							-0.16								
HYAL3	-0.2	-0.24	-0.24	-0.18			0.19															
LARGE1	0.32	0.26	0.29	0.18														-0.17				
MTMR6	0.24	0.4	0.17	0.15	0.18																	
NDUFA13	-0.17	-0.34					0.18			-0.17		-0.21										
NME1-NME2	-0.21	-0.16	-0.26	-0.19			0.19															
PLCG2									0.27		0.17				0.25	0.55	0.24					
PSPH	-0.2	-0.29	-0.25			0.19								0.16								
SETD1B	0.2	0.34	0.3												0.16						-0.17	
SIRT5	-0.18				-0.17			-0.18		-17				0.16								
B3GAT2		0.21						-0.17					-0.21			-0.16						
CA3				0.24						-0.18						-0.15	-0.17					
DHFR2	0.22		0.26	0.21														-0.17				
GLS2	-0.18			-0.17			0.17													0.17		
KMT2D				0.31								0.21			0.22		0.16					
MAN1A2	0.19	0.36	0.19				-0.2															
NDUFB1		-0.23										-0.23	0.18	0.16								
NPL	0.24			0.17					0.17								0.27					
NUDT12		0.33				0.17		0.16							-0.24							
PAPSS2					0.16			0.2		0.24												0.17
PDE4A					0.16	-0.19		0.18							0.15							
PIGL								-0.2	0.15		0.21									0.16		
PRUNE1					-0.17				-0.26			0.15						-0.15				
SEPSECS	-0.16	0.29				0.21		-0.23														

CEPT1									0.26		0.26											
DPM3		-0.32								-0.18		-0.19										
GLS									-0.16				0.27			-0.25						
GUK1		-0.36					0.21					-0.24										
HPSE2	0.24		0.45			-0.19																
KYNU										0.26							0.17	0.21				
ME3			0.15			-0.27										-0.15						
PDE3B						-0.15	-0.15									-0.2						
PFKM	0.22					-0.23										-0.17						
PI4KB			0.16																	-0.15	-0.18	
PNPLA2	-0.17															0.2		0.17				
PRDM16					-0.18				-0.21											-0.15		
VKORC1L1	-0.15										-0.18											0.19
ACSM1					-0.2											0.15						
ALDH5A1					-0.16			-0.17														
ATP5F1E		-0.19												0.73								
BCKDHB		0.19															-0.15					
CHST9					-0.15				-0.15													
CRYL1	-0.19					0.21																
CYP3A5	-0.18					0.32																
IVD								-0.17												0.16		
MGST3	-0.15											-0.19										
NMNAT1								-0.16						-0.16								
NT5E					-0.2																	0.27
PNMT	-0.15																		0.54			
SDSL		-0.27															0.15					
ACO1							0.2															
ADCY10																				-0.17		
ADO												0.15										
AMDHD1															0.21							
BCAT1																					0.31	
GLUD1															-0.15							
MTAP									0.37													
SRD5A3																		0.15				
SYNJ2												0.16										
ALDOB																						
ALOX15																						
COX11																						
GALNT12																						
ENTPD3																						
PGM2L1																						
TREH																						
UPP2																						
PNLIP																						
Total Count	78	67	62	60	57	47	42	41	34	29	27	26	25	23	23	22	21	20	13	10	7	5

5.4. Analysis of the Association of the Altered Metabolic Genes with the Prognostic Markers:

A comprehensive score list based on the Pearson correlation analysis has been compiled (Table 3) and visualized as a heatmap in Figure 27. The heatmap was generated using RStudio (Version: 2023.12.1+402), the code for the same has been added as part of the Supplementary Materials. The prognostic markers that emerged as top performers in this analysis include GNB4, APC, TXNIP, ECM2 and PRRX1 which are involved in critical metabolic pathways such as terpenoid backbone biosynthesis, purine metabolism, cofactors biosynthesis, oxidative phosphorylation, glycosylphosphatidylinositol (GPI) anchor biosynthesis, nucleotide metabolism (Figure 28) etc. On the other way round, the metabolic genes which were top performers in correlation with prognostic markers and effecting crucial metabolic pathways, were IDI1, ACAT2, AFMID, PDE5A, HMGCR, ITPA, SPR, PDE7B, PPAT, GALNT16, GSS, GSTM5, KMO, PIGF, and PIGU. These results indicate that the metabolic processes that are driven by these genes are likely to have a pivotal role in cancer progression. Conversely, genes associated metabolic pathways like, nitrogen metabolism, biosynthesis of unsaturated fatty acids, metabolism of lipoic acid, metabolism of alpha-linolenic acid, biosynthesis of CoA, biosynthesis of N-glycan, arginine metabolism, and biosynthesis of primary bile acid, among others, demonstrated less significant correlations with the prognostic indicators. The correlation patterns are depicted in Figure 27.

Overall, our study highlights that altered expression of metabolic genes are consistently seen in HpGC and are associated with key clinical parameters, and holds significant promise for advancing research in gastric cancer and infection related studies.

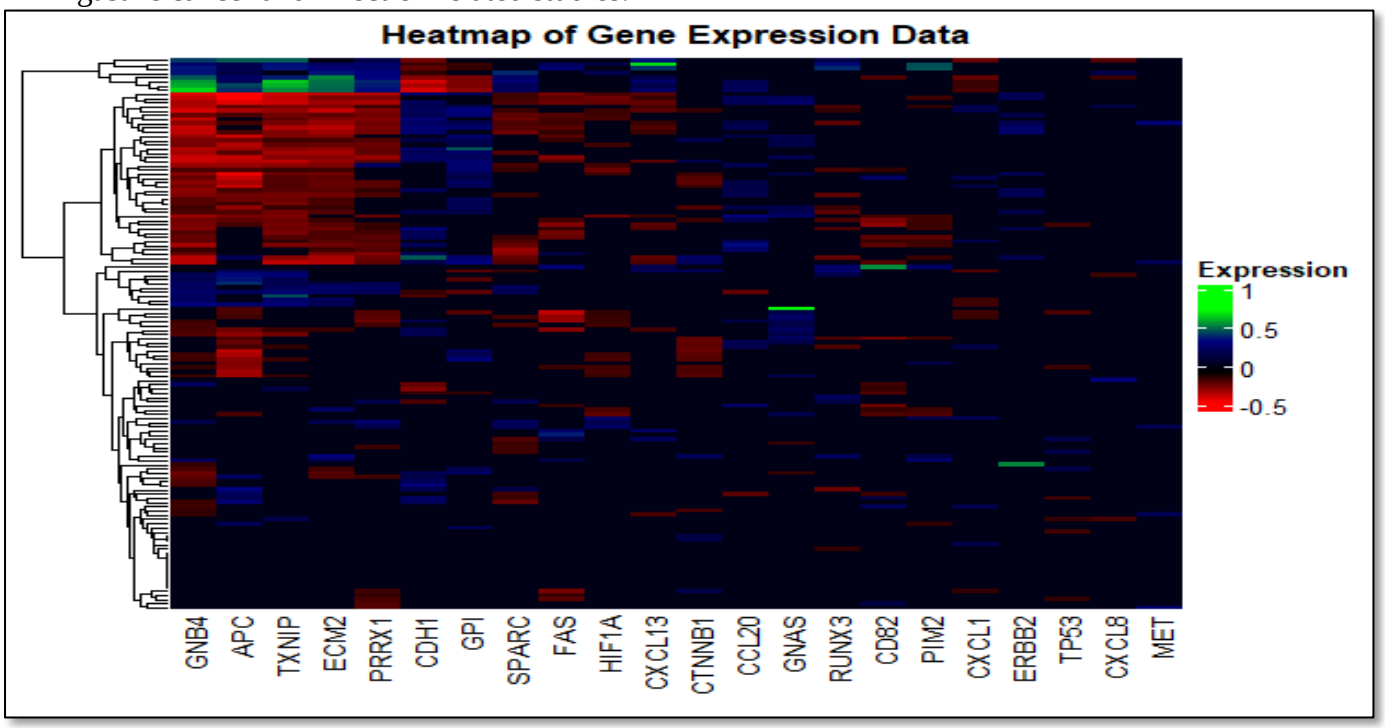
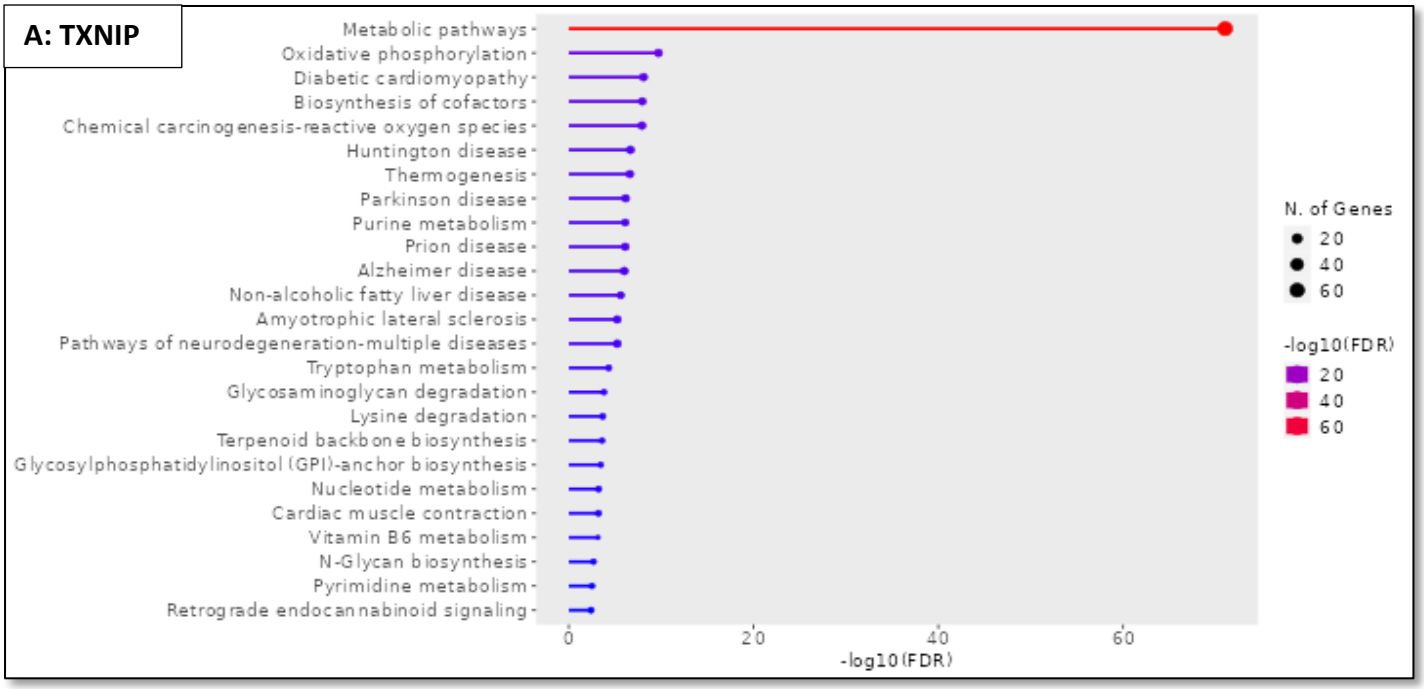
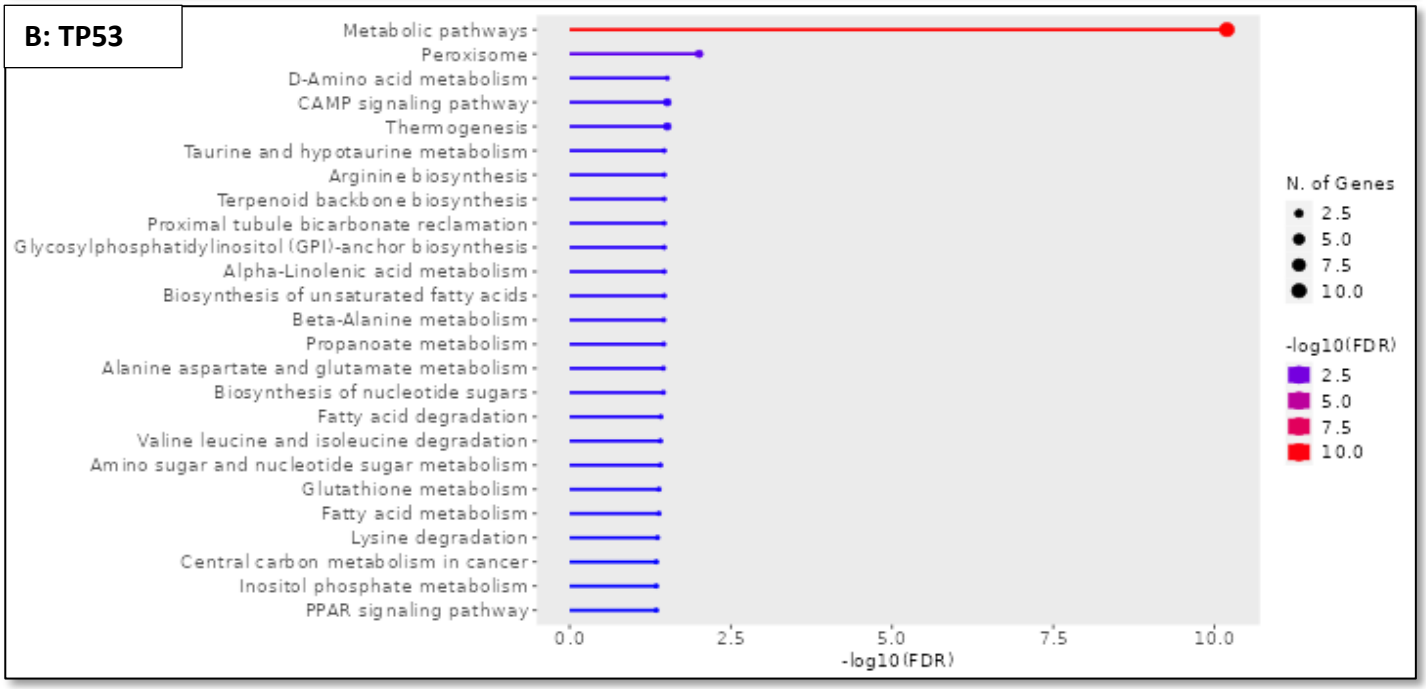


Figure 27: Heatmap of Correlation Analysis of Metabolic Genes and Prognostic Markers, with Pearson's Coefficient >= |0.15|

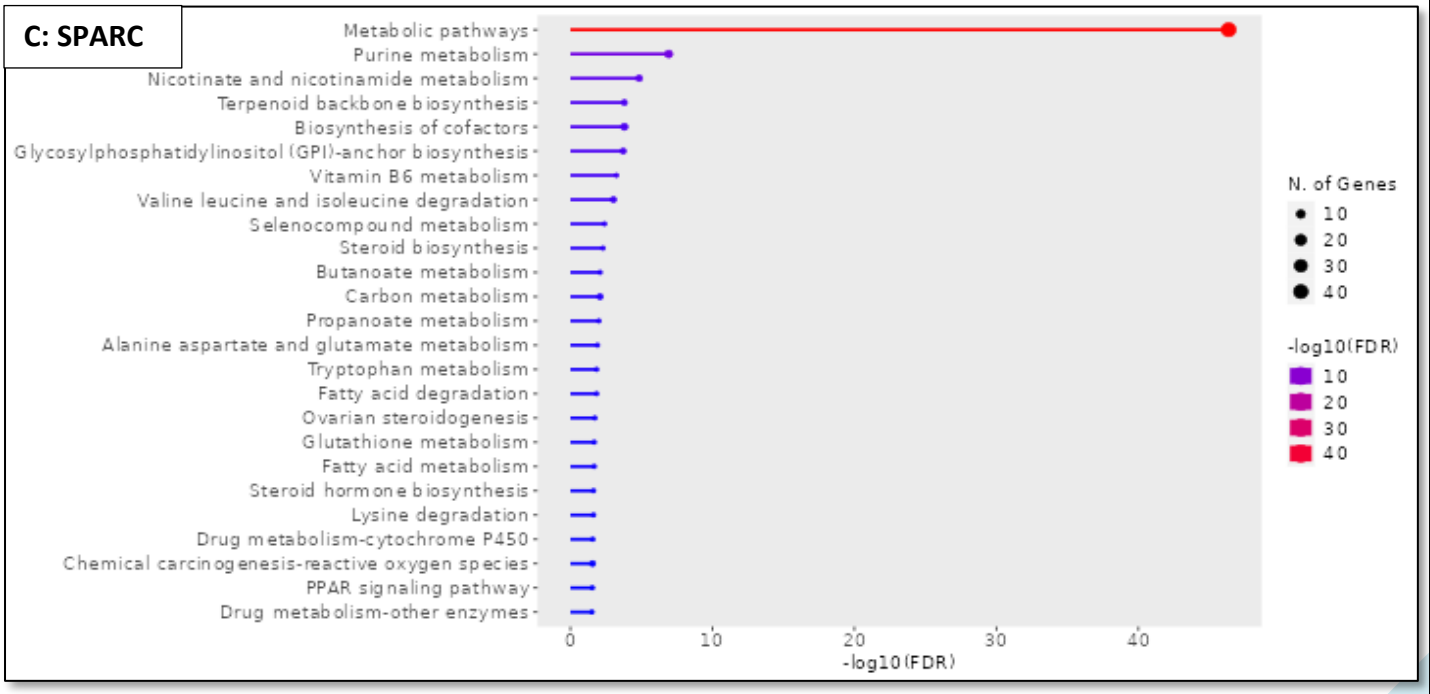
A: TXNIP



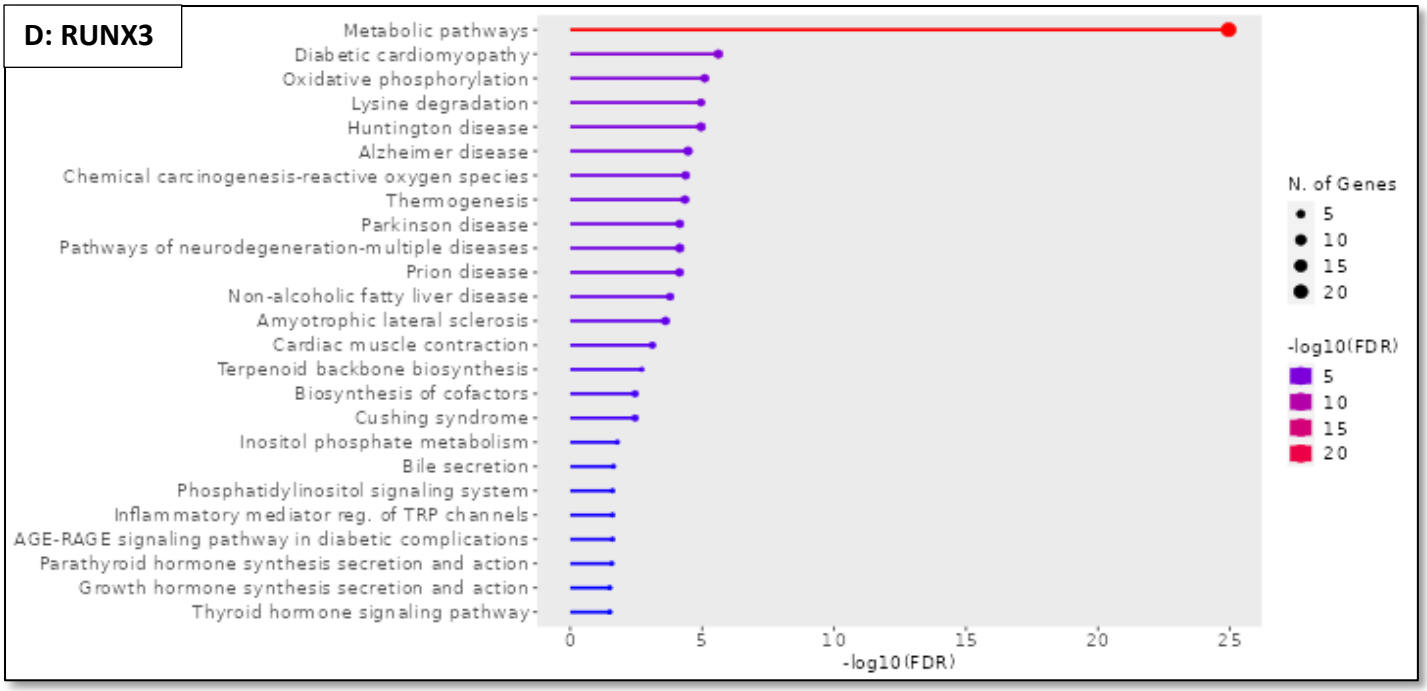
B: TP53



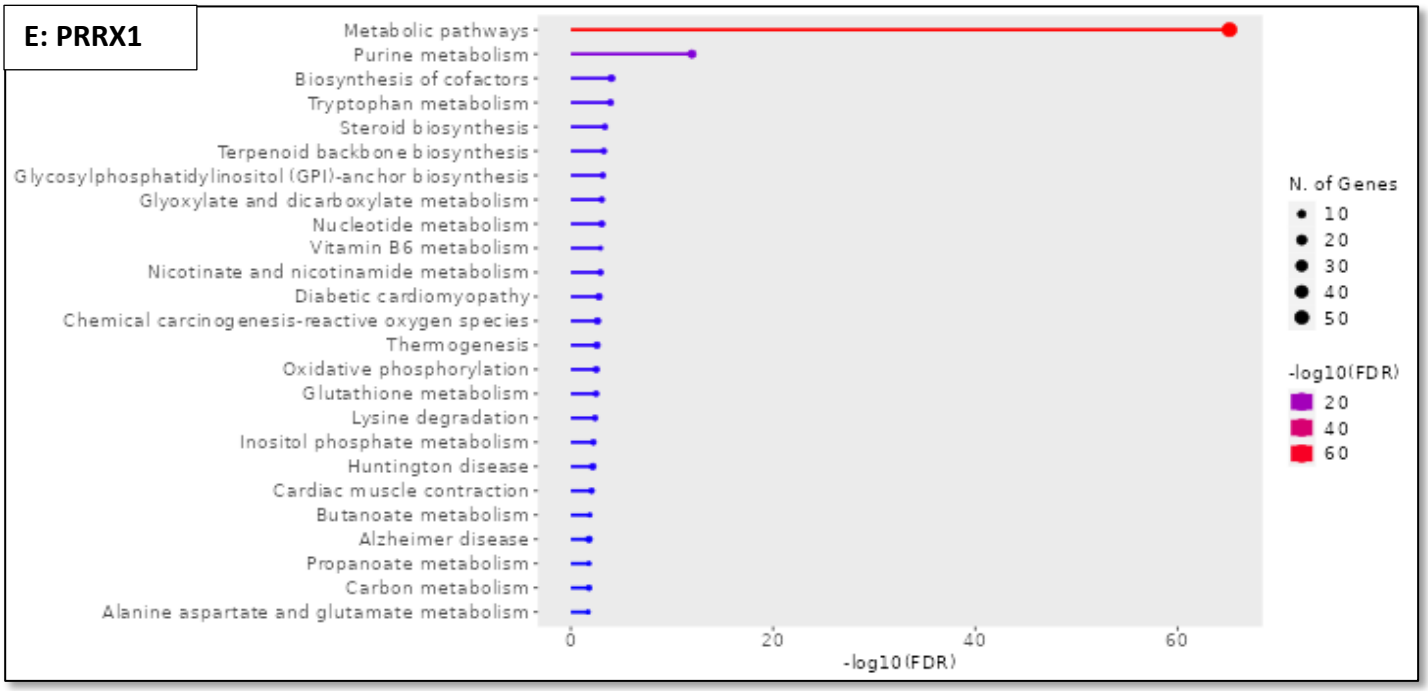
C: SPARC



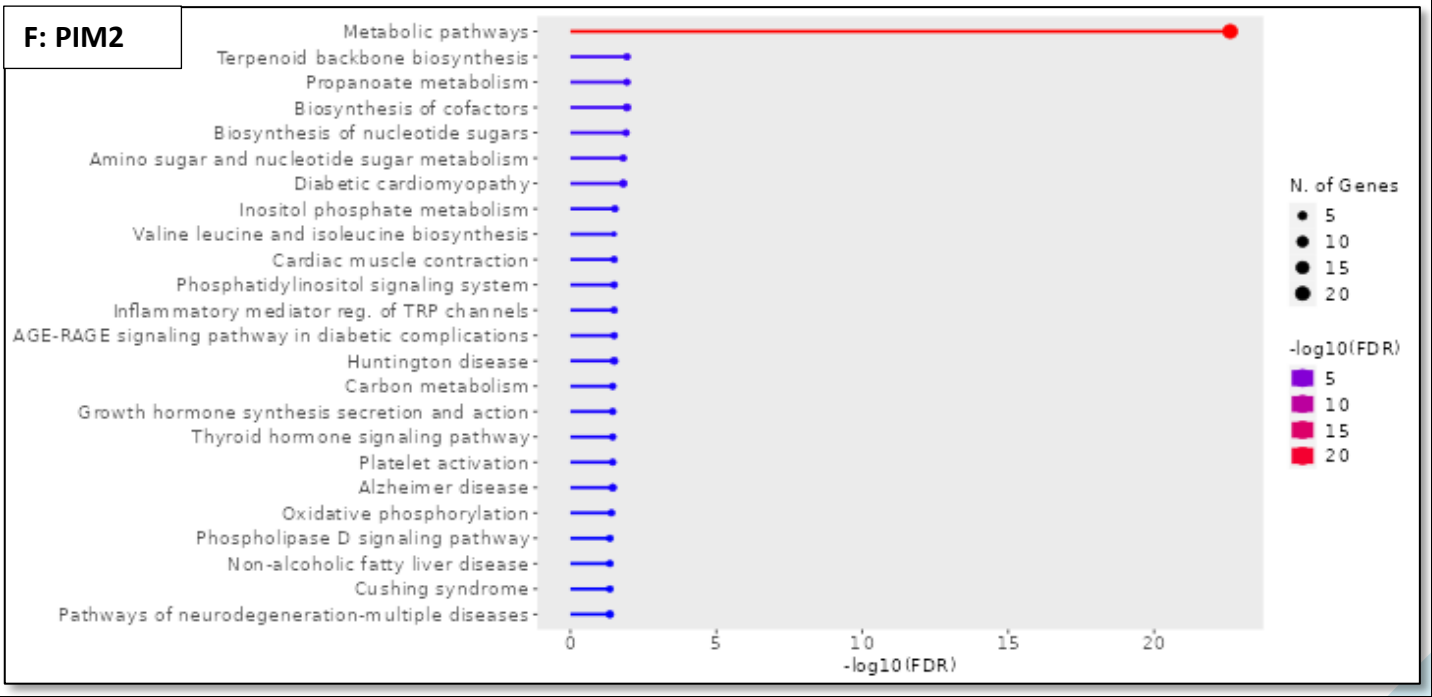
D: RUNX3



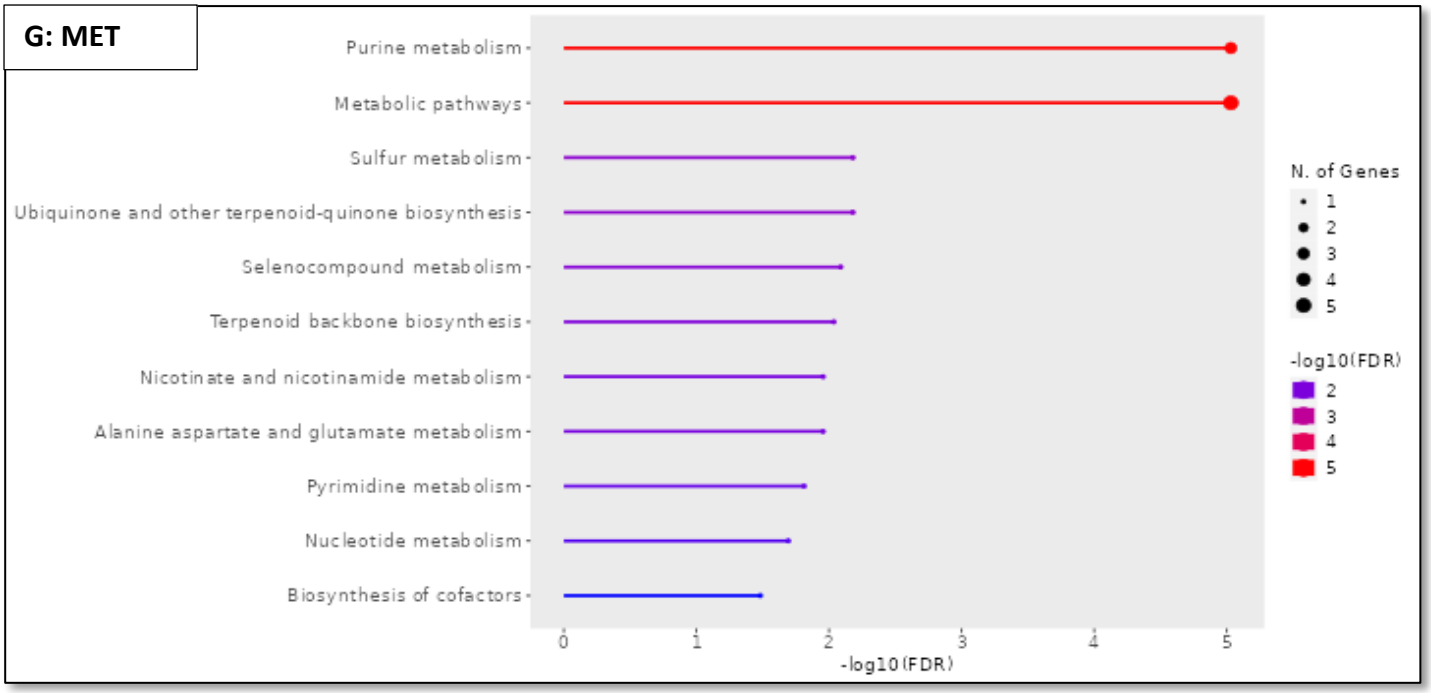
E: PRRX1



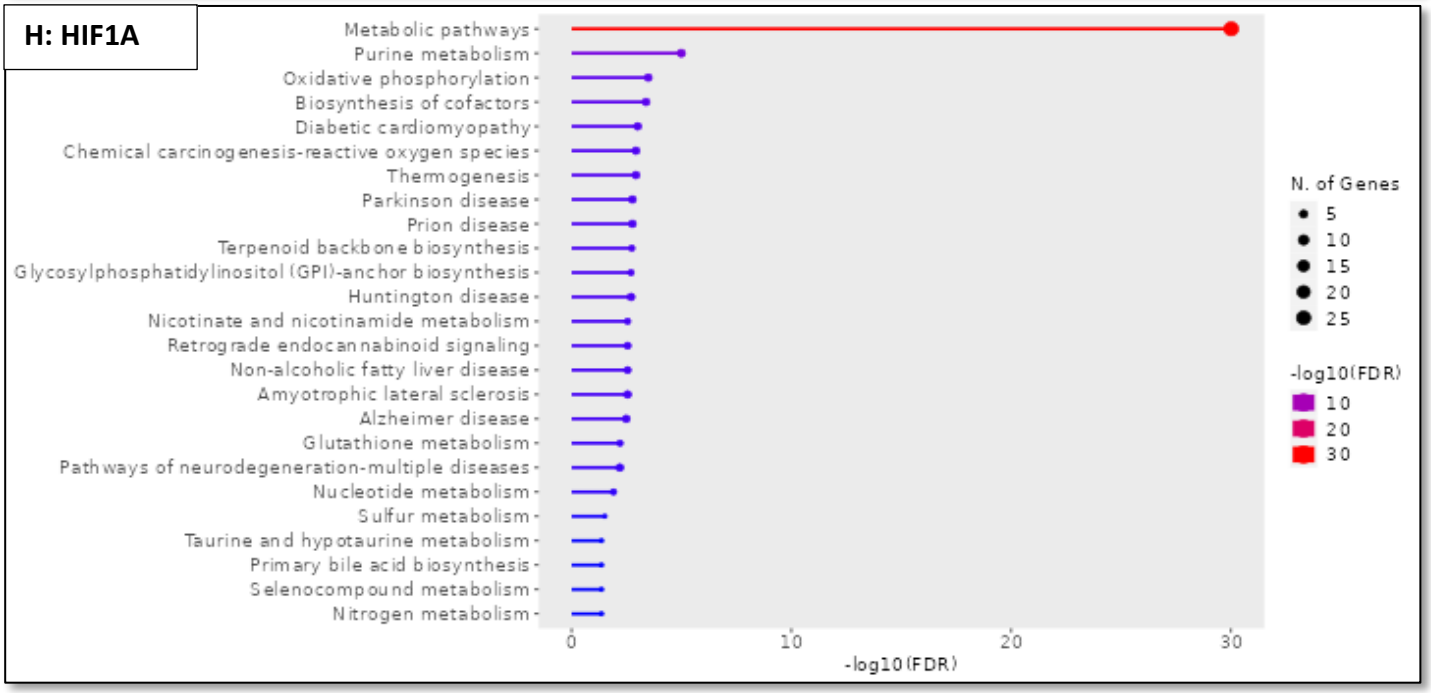
F: PIM2



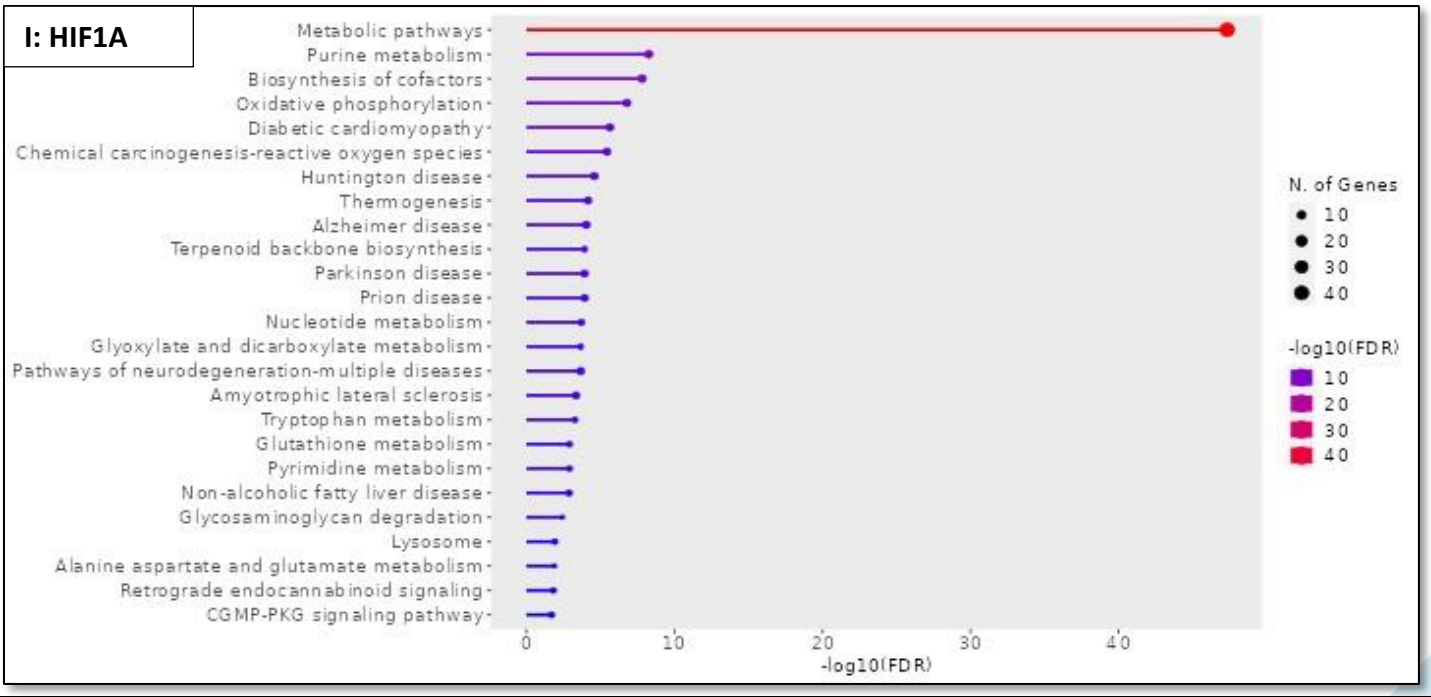
G: MET



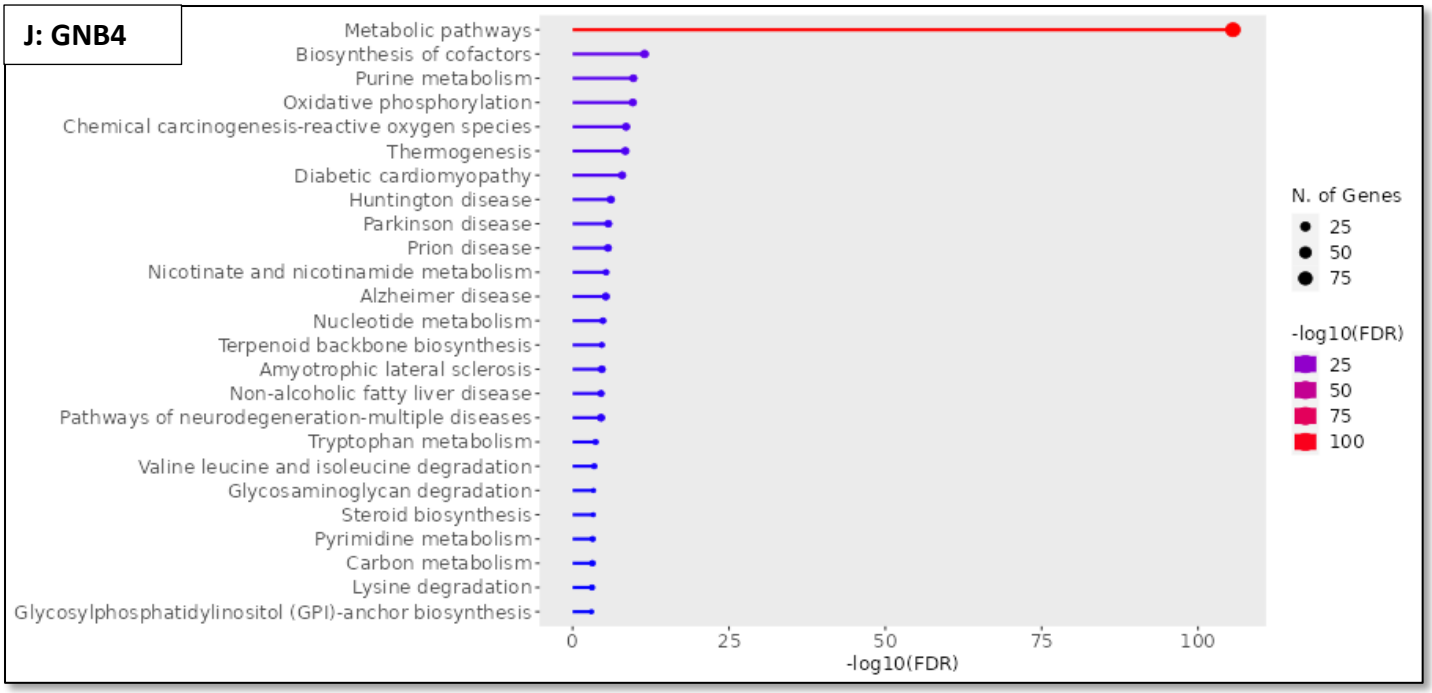
H: HIF1A



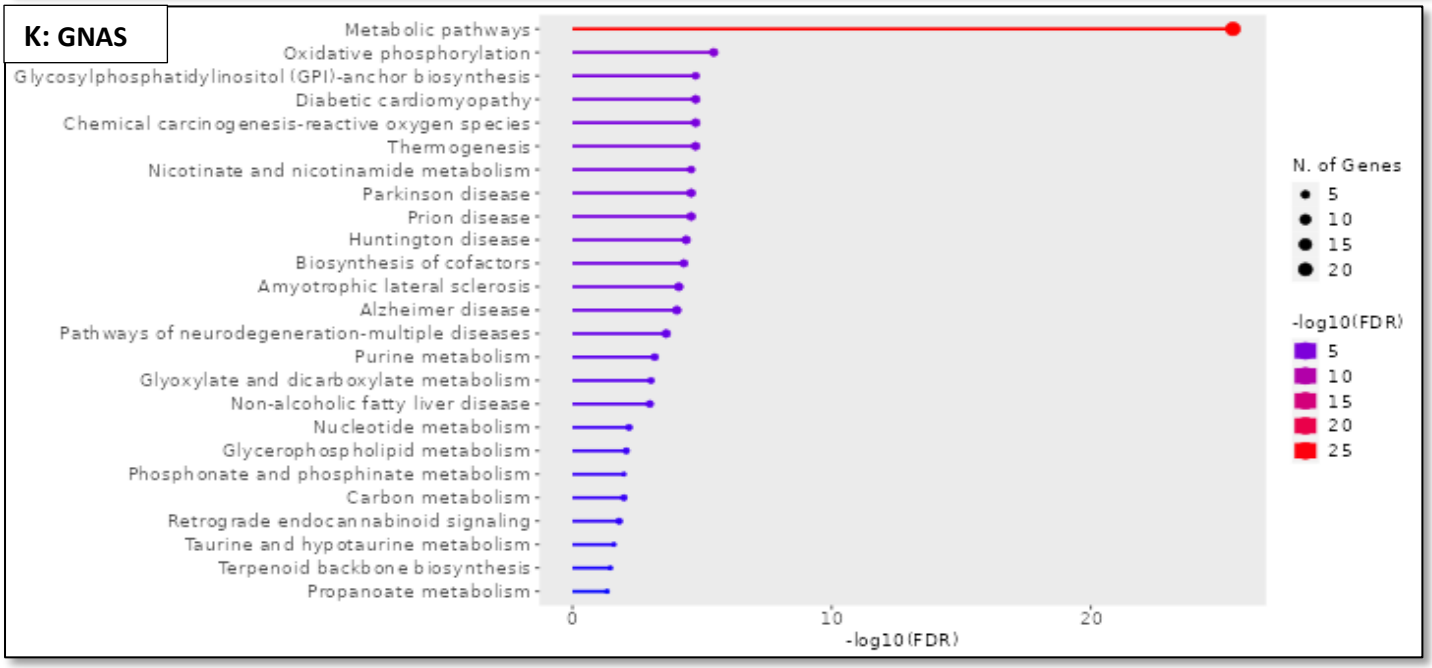
I: HIF1A



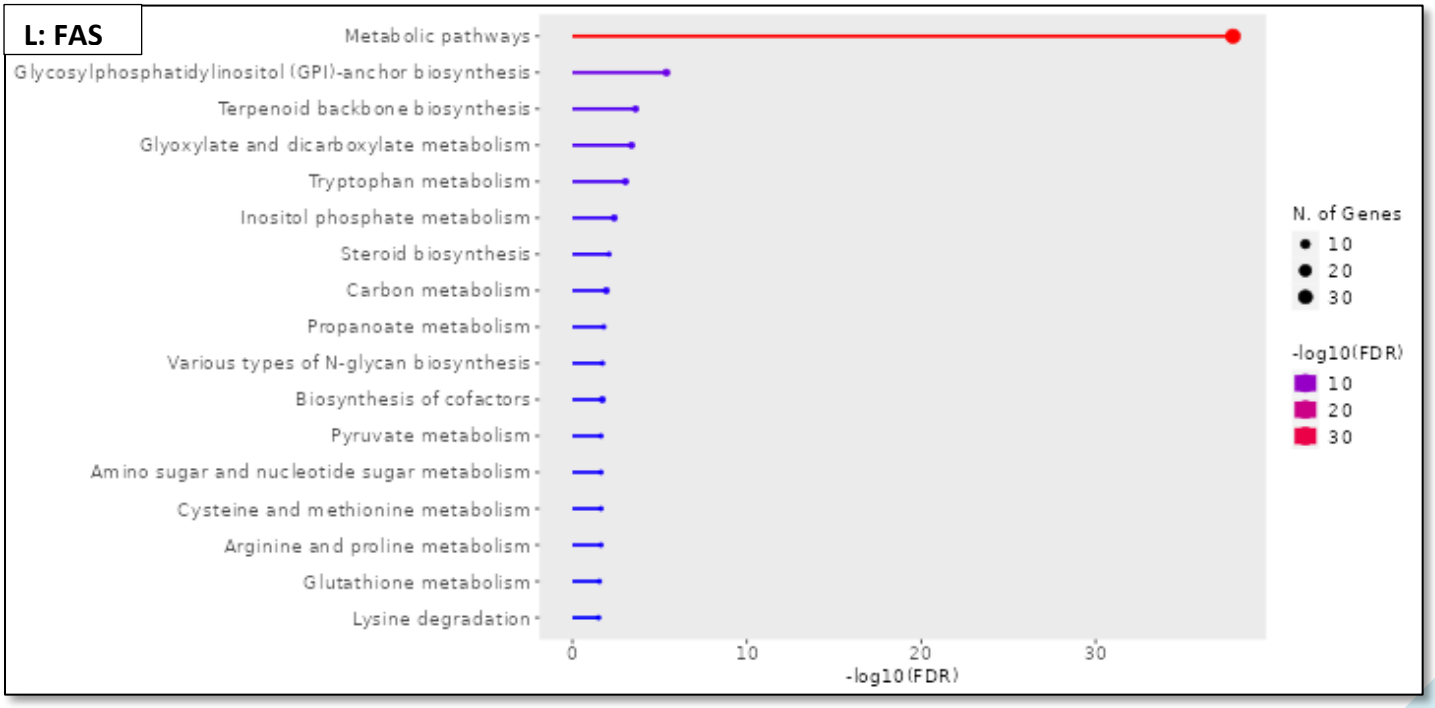
J: GNB4



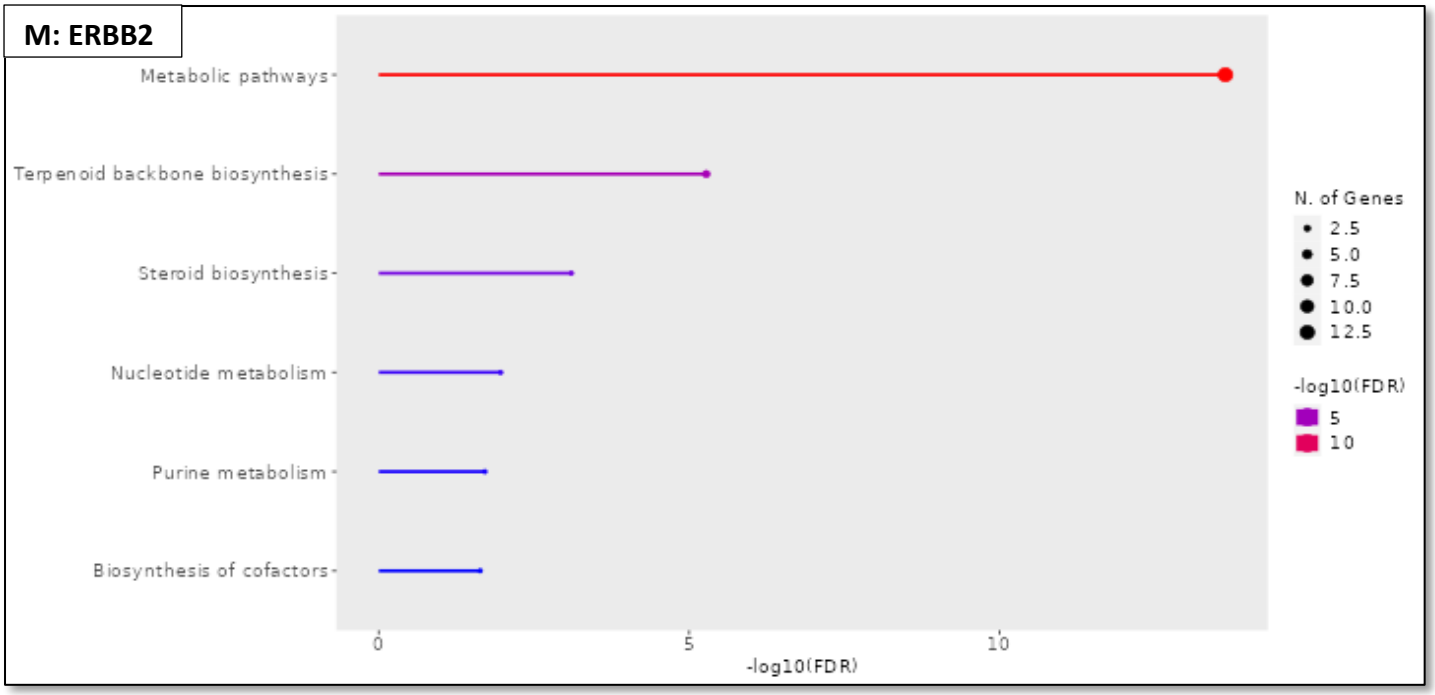
K: GNAS



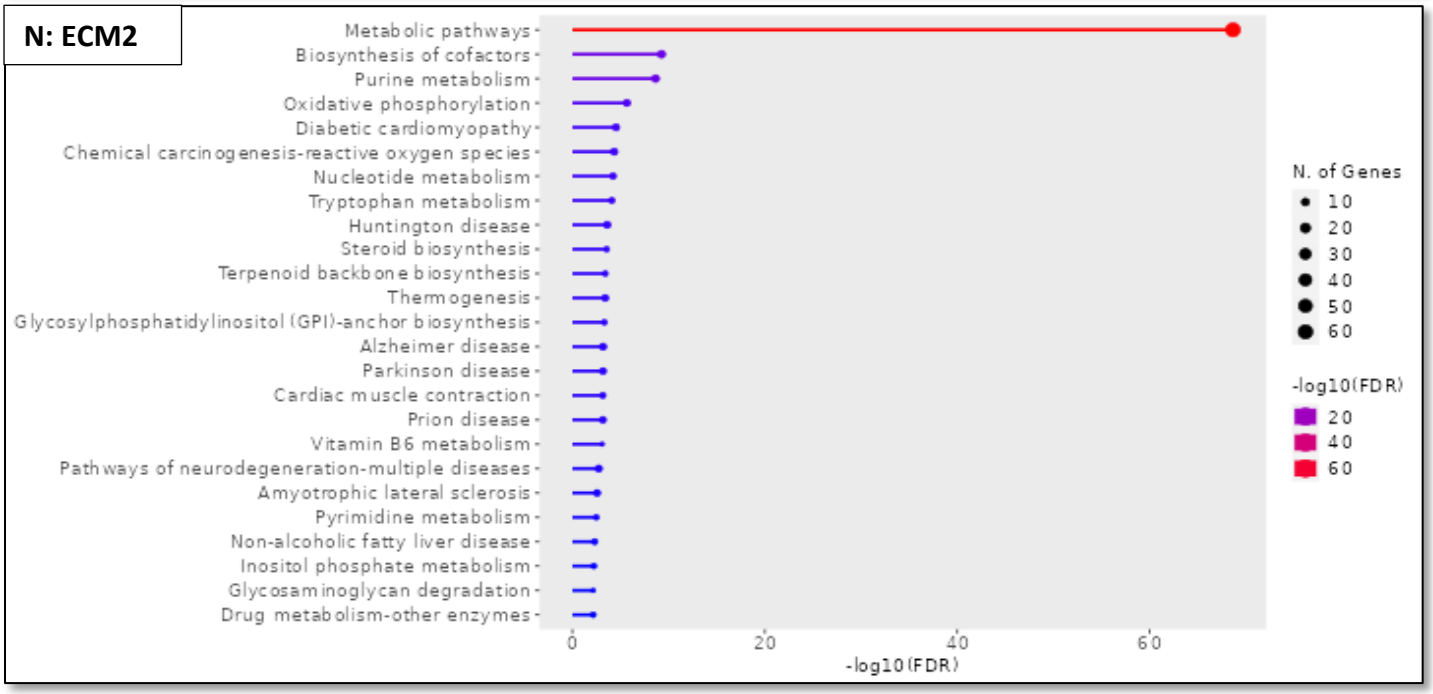
L: FAS



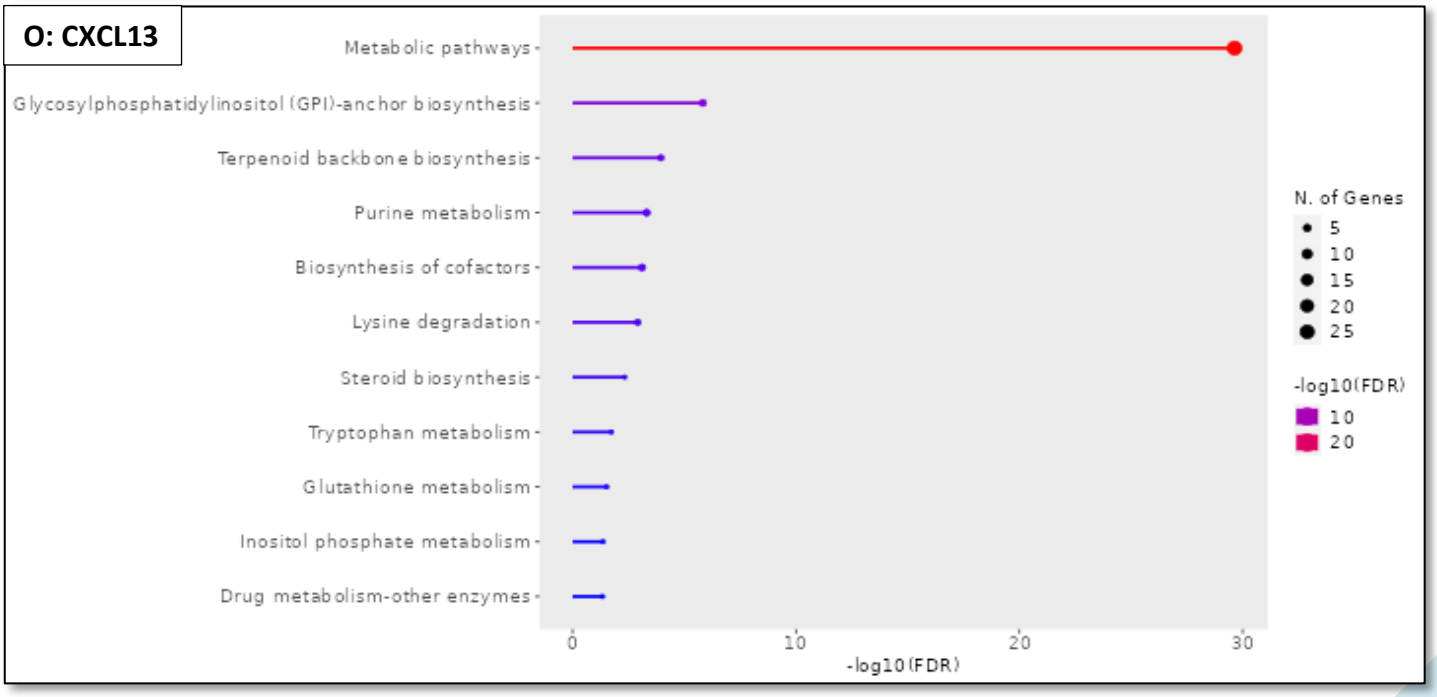
M: ERBB2



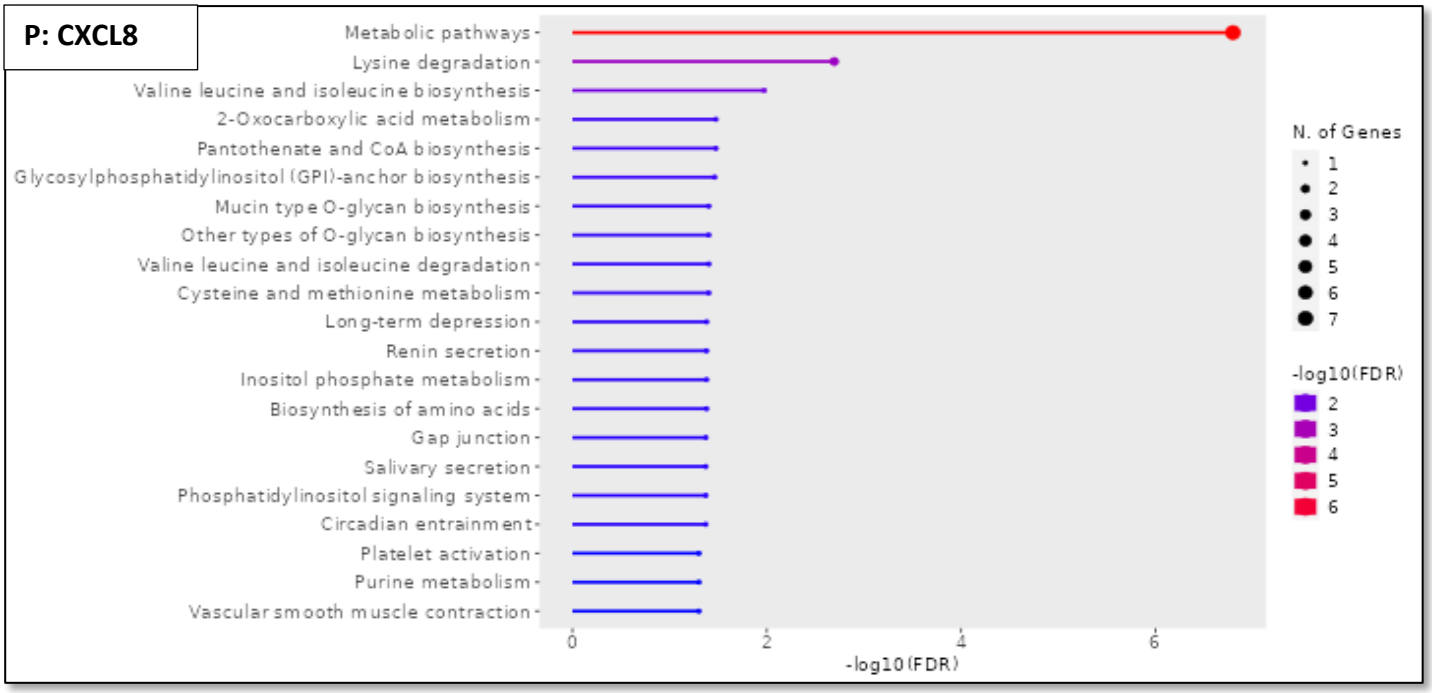
N: ECM2



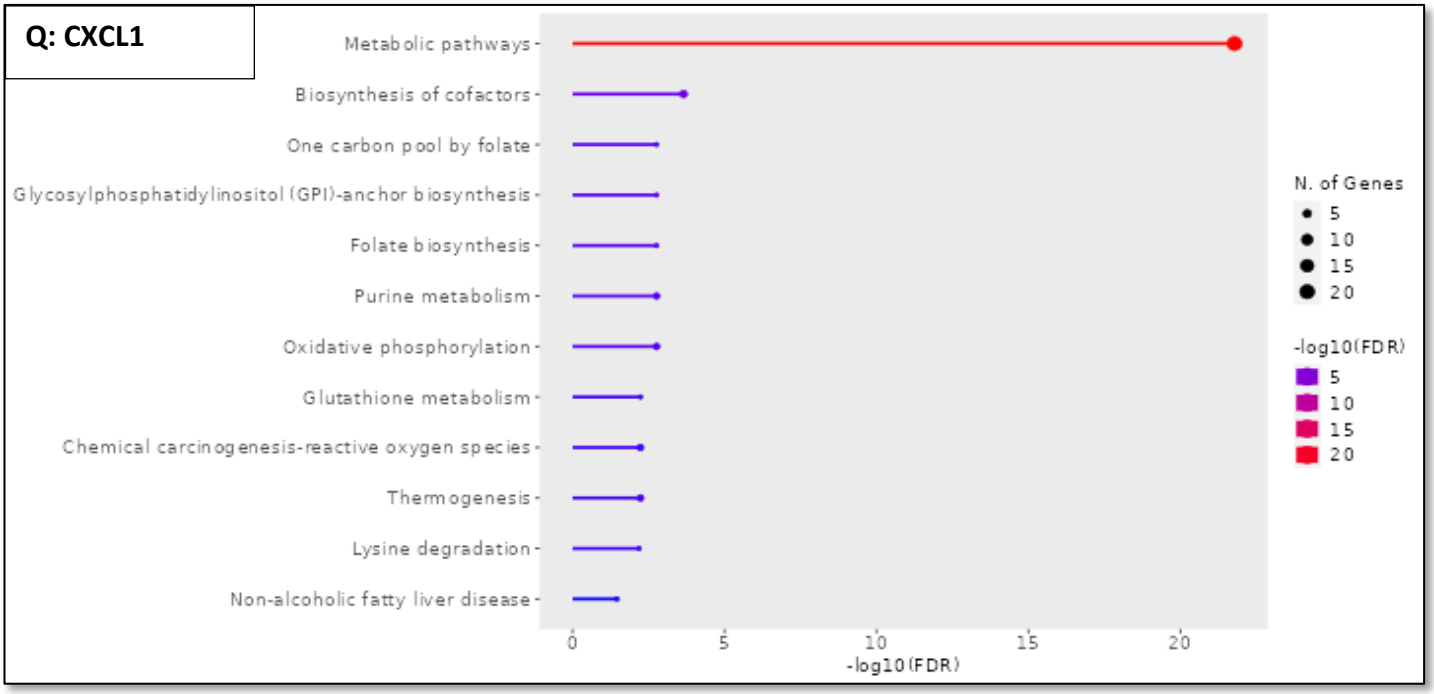
O: CXCL13



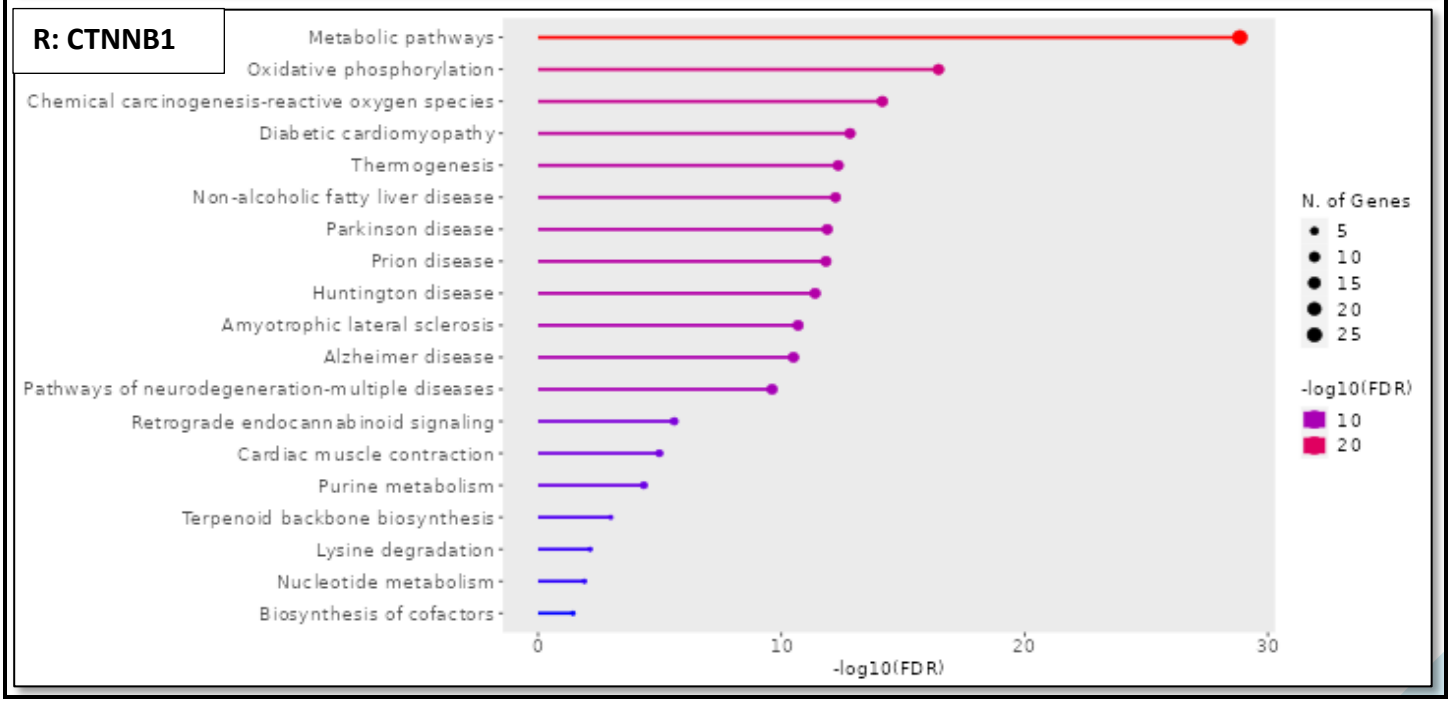
P: CXCL8



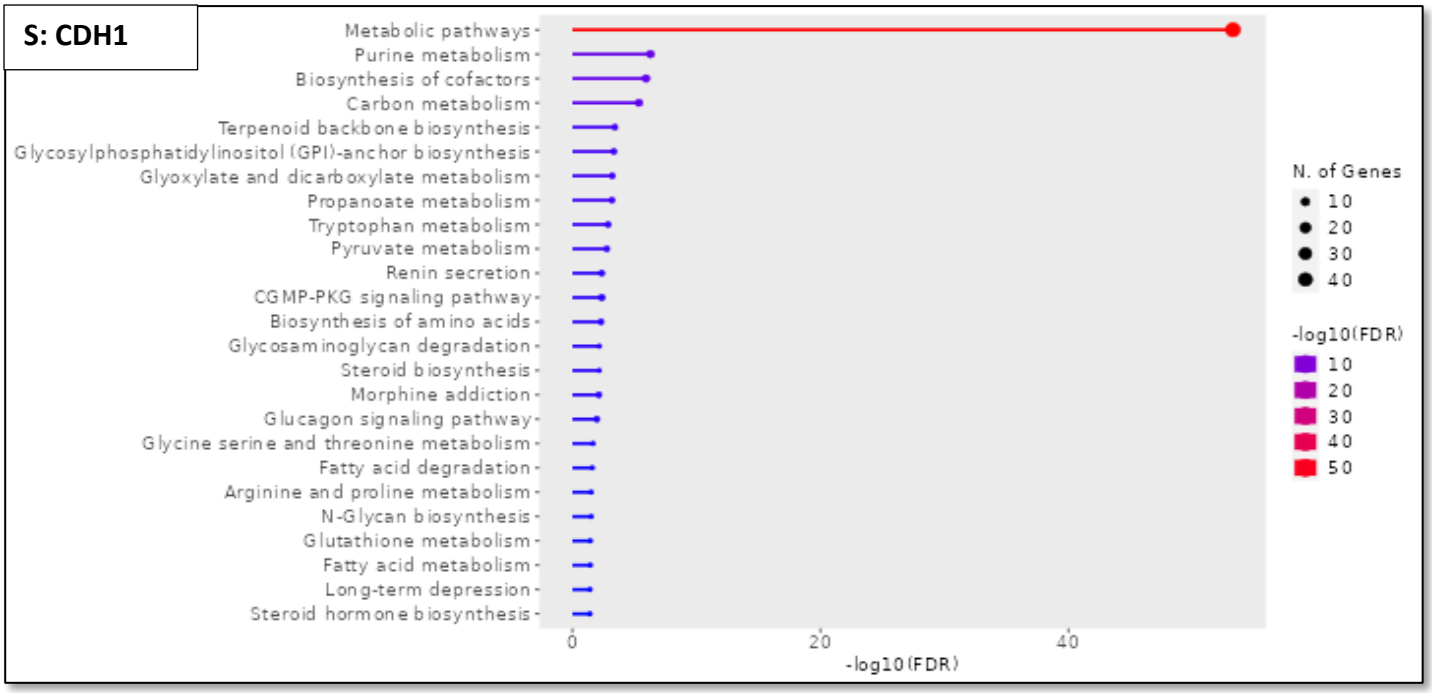
Q: CXCL1



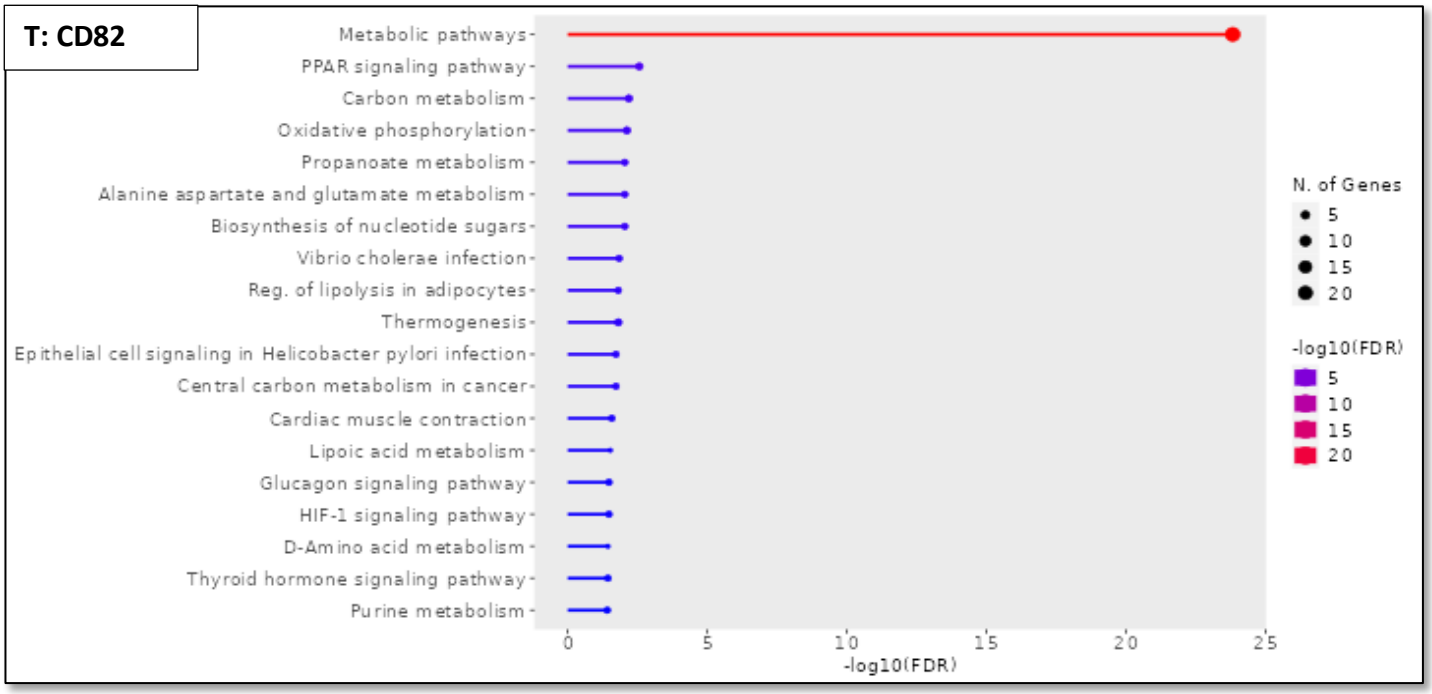
R: CTNNB1



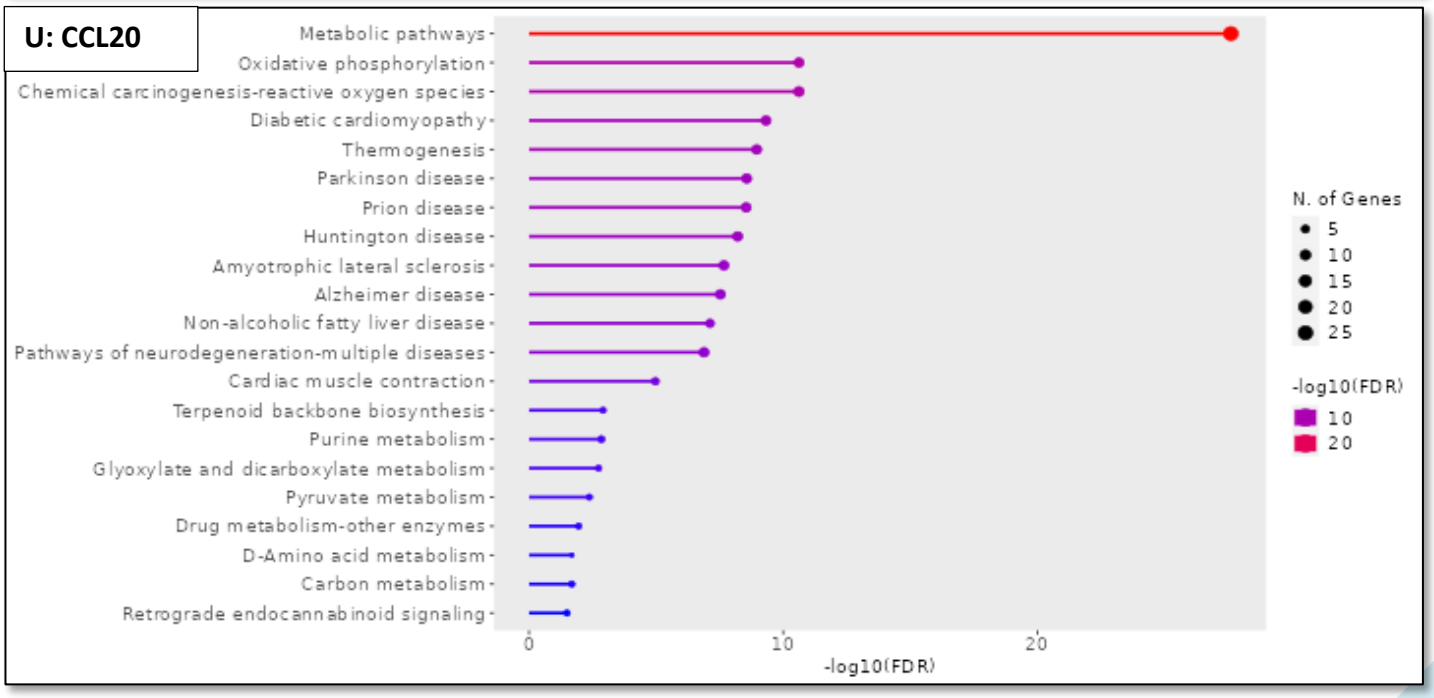
S: CDH1

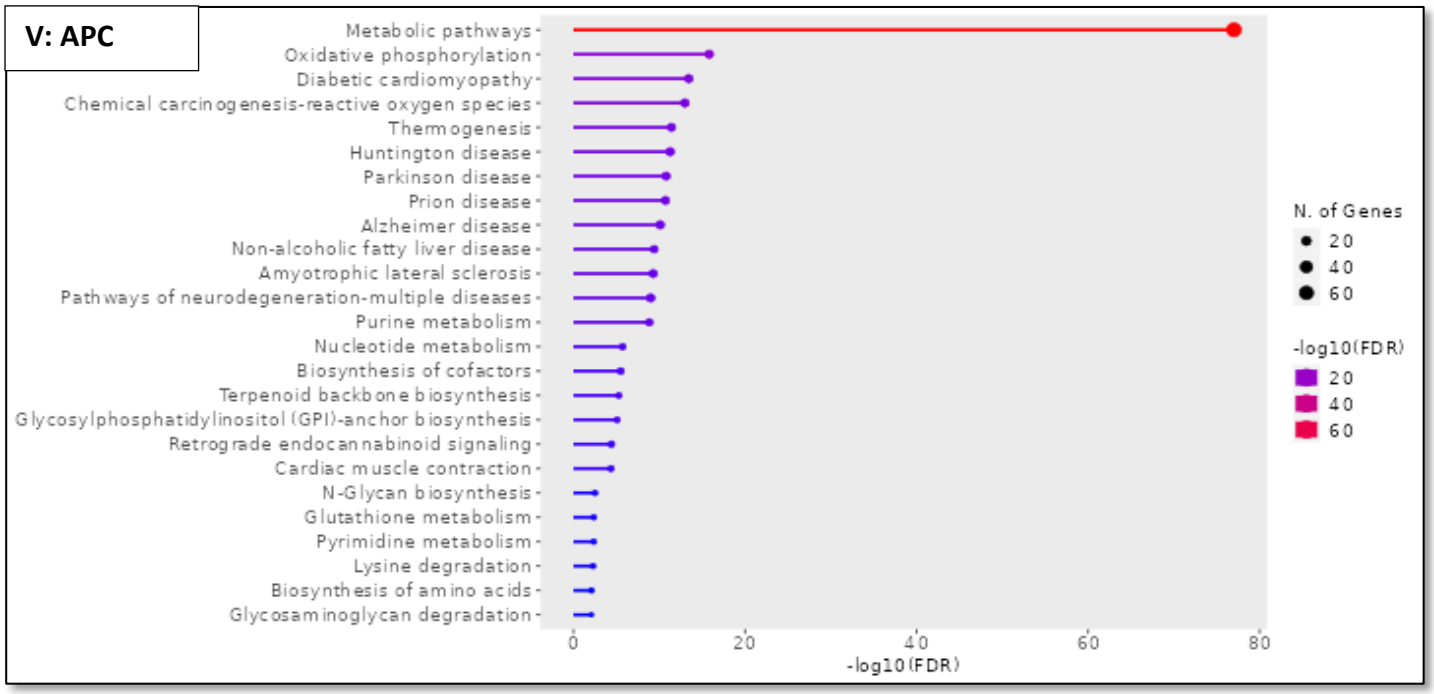


T: CD82



U: CCL20





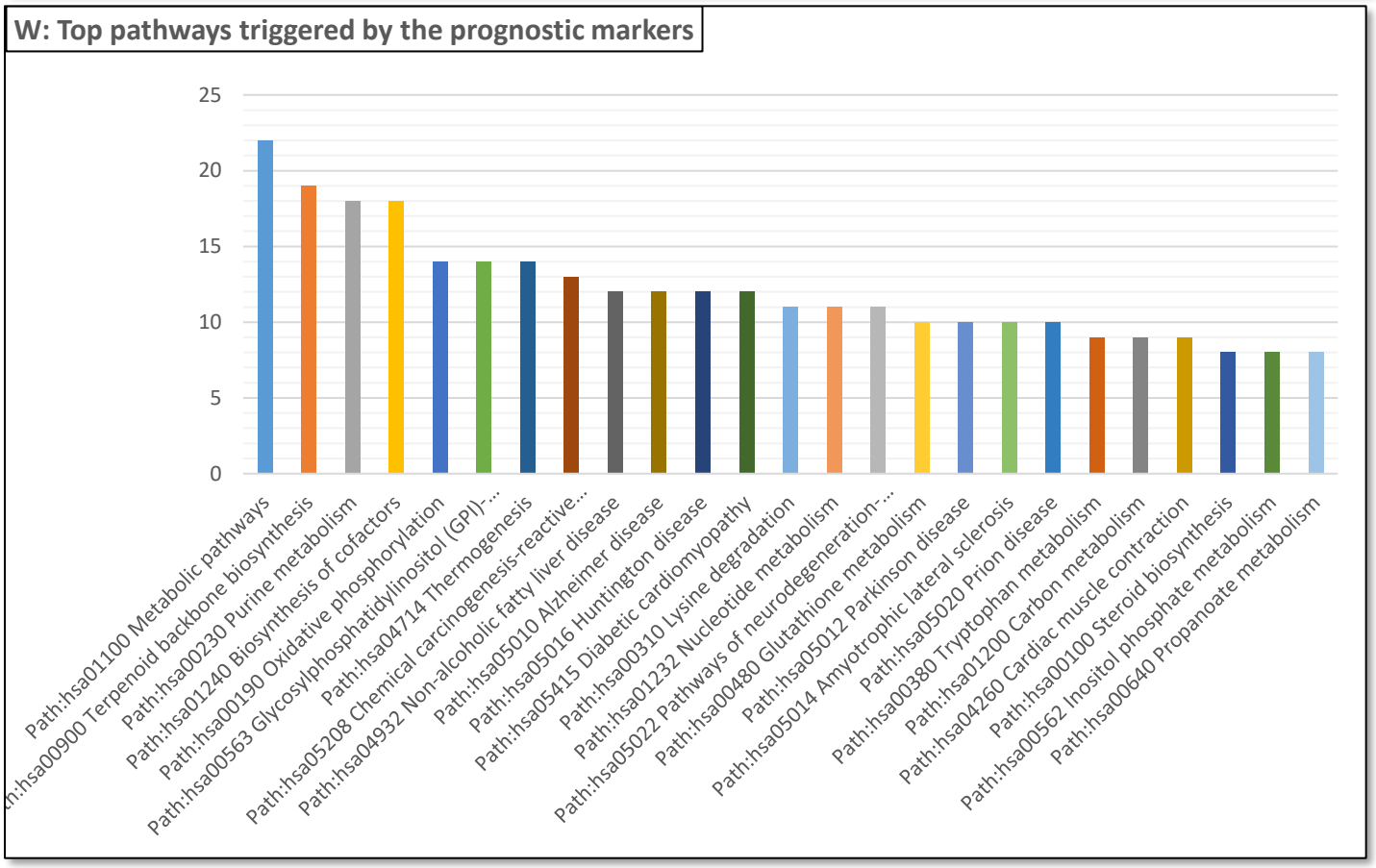


Figure 28: A - V -- Gene Ontology Enrichment pathways charts for the correlated metabolic genes of each Prognostic Markers of HpGC, W- Top Pathways triggered by the Prognostic Markers of HpGC

5.5. Expression Analysis of Metabolic Genes in *H. pylori* induced GC:

UALCAN had been employed for assessing the degree of expression of DEMGs in GC tissue in comparison to normal gastric tissue and, also between *H. pylori* infected cases and non-infected cases, in the TCGA dataset. Understanding these gene expression changes is critical for identifying potential biomarkers for early detection and developing targeted therapies that could inhibit the metabolic adaptations driven by *H. pylori* in gastric cancer. We also observed from the graphs we could generate for the Expression analysis of the metabolic genes in UALCAN is that the expression values (in Transcripts per million) are mostly higher for the genes that are highly correlated to the prognostic markers, and for the ones that are not well correlated the expression values are mostly low. Also in majority of the plots the expression of the metabolic genes showed an increase in median value from normal condition to cancer condition. A few of the plots are being showcased, whereas the other plots that were generated but couldn't be showcased here would be available within the supplementary materials.

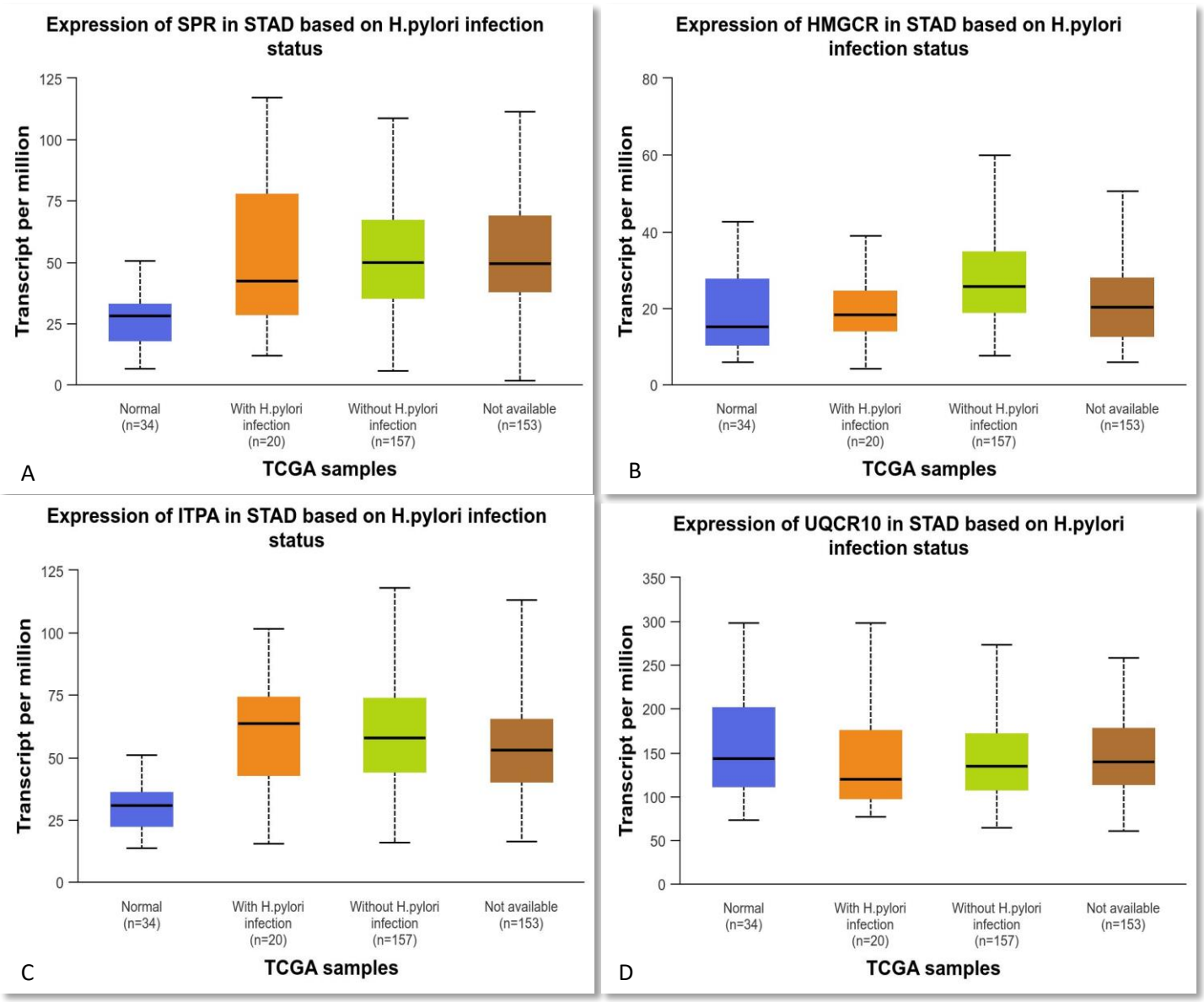


Figure 25: A – Expression analysis of the DEMG SPR, B – Expression analysis of the DEMG HMGCR, C – Expression analysis of the DEMG ITPA & D – Expression analysis of the DEMG UQCR10

5.6. Expression Analysis of Prognostic/Progression markers in HpGC:

The same expression analysis was done for the prognostic markers as well to see how they get expressed in normal different cancer conditions, its was observed among all the prognostic marker for which we could generate the plot, only the one for TXNIP showed that the median value for expression went down in cancer cases than in the normal ones. Again a few of them are showcased here whereas for all the others refer the "Supplementary Materials"

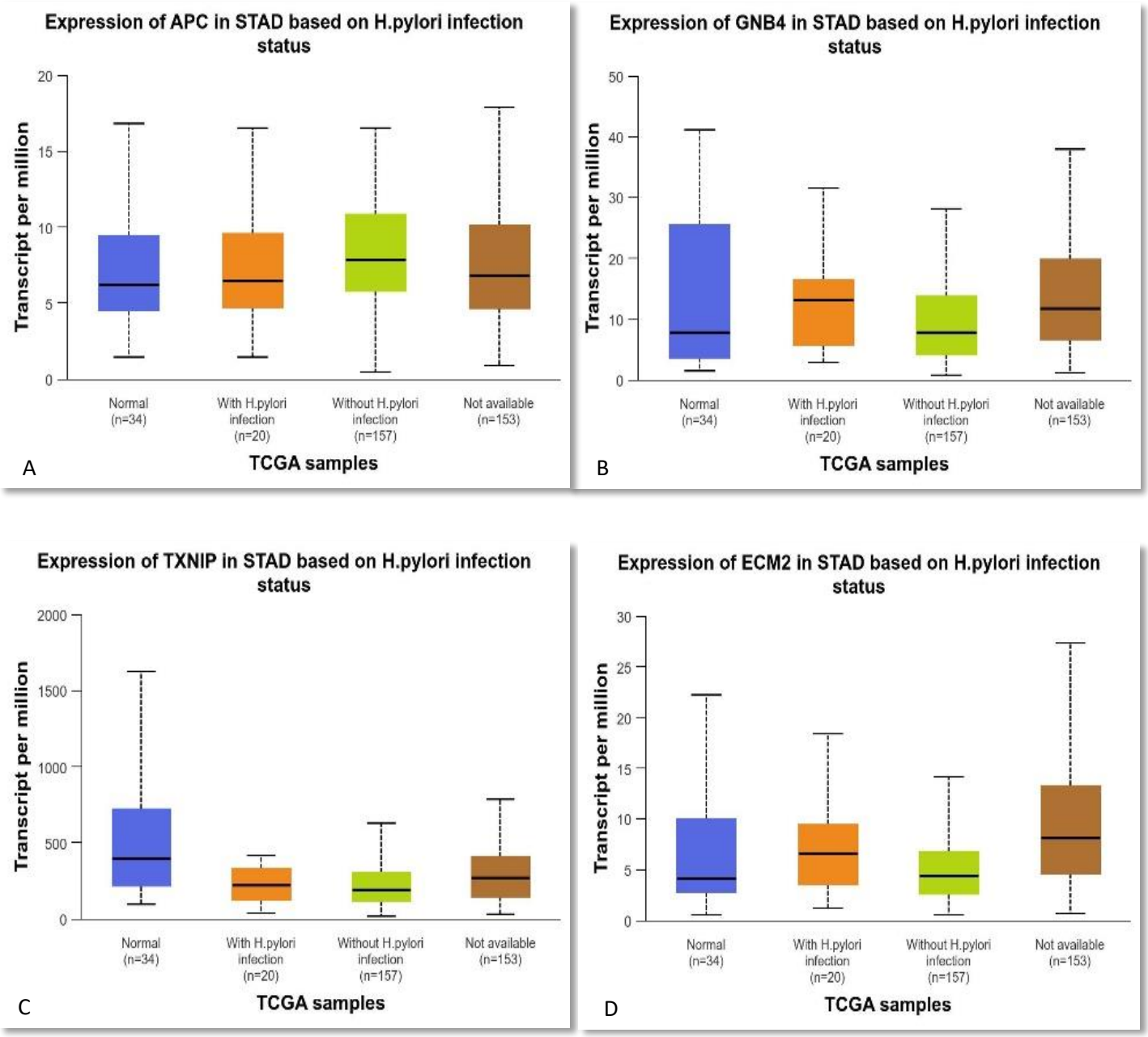


Figure 26: A – Expression analysis of the prognostic marker APC, B – Expression analysis of the DEMG GNB4, C – Expression analysis of the prognostic marker TXNIP & D – Expression analysis of the prognostic marker ECM2

5.7. Cancer Stage response of Metabolic Genes for STAD:

The following plots illustrate the changes in expression levels of aforementioned top metabolic genes across different stages of gastric cancer. This will actually help us understand how the metabolic pathways may get effected in each stage of the cancer. In majority of the metabolic genes we can see, the median gene expression value shoots up from Normal condition to the first stage condition. In very few of them do the expression decreases from the Normal condition to the first stage.

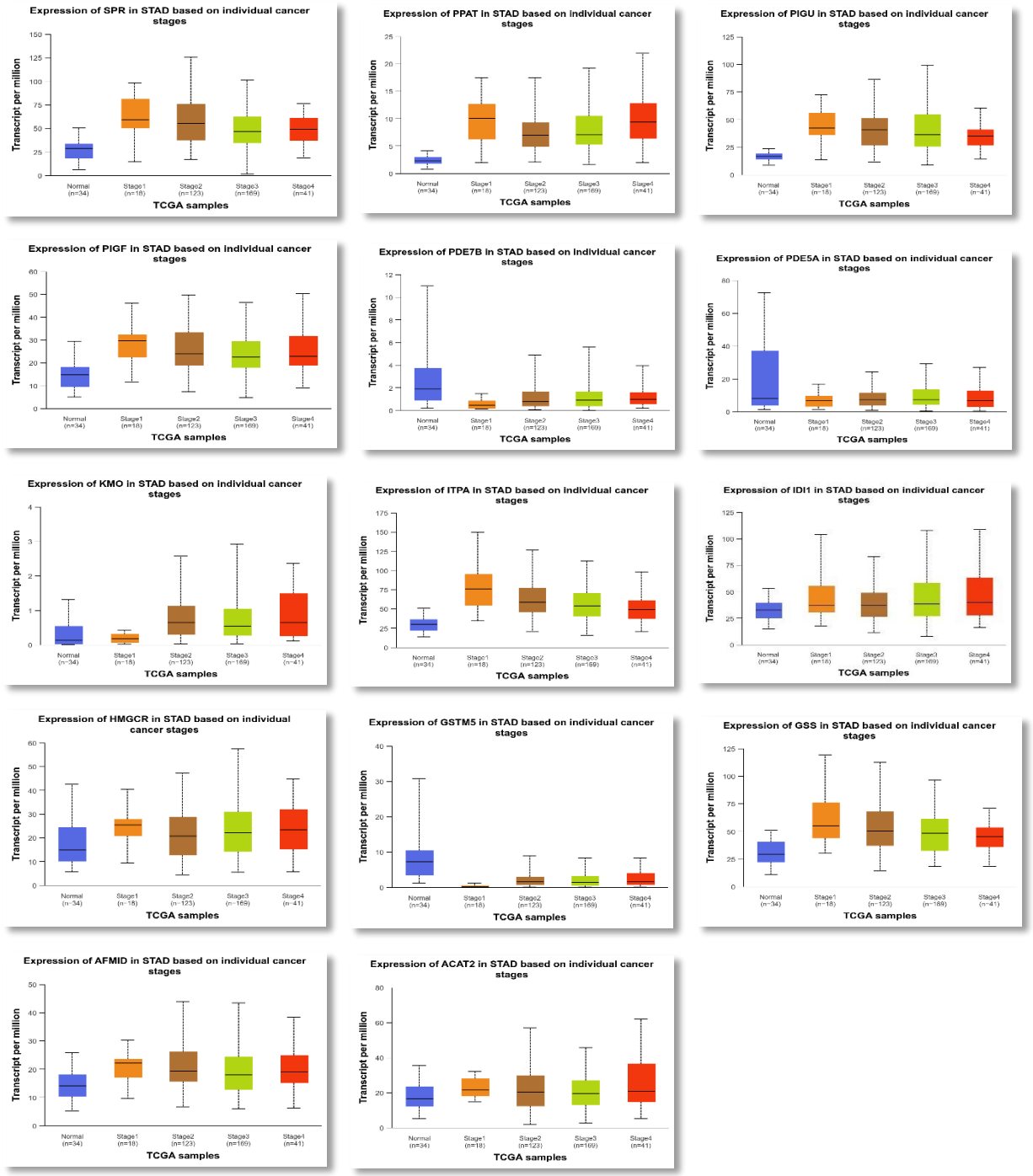
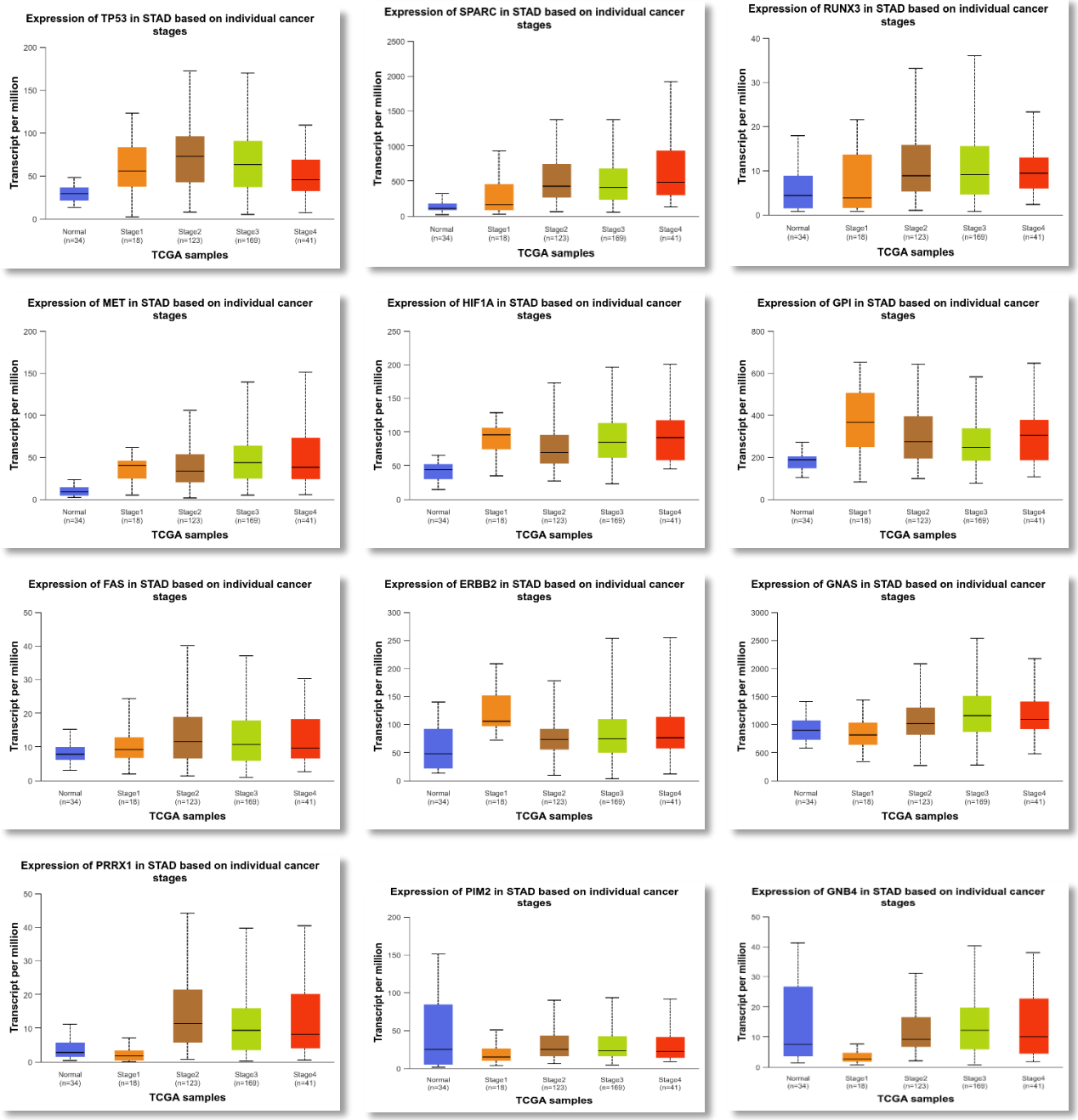


Figure 29: Boxplots shows the change in expression for the metabolic genes with different stages of HpGC

5.8. Cancer Stage response of Prognostic Markers for STAD:

The boxplots provide a visual summary of how prognostic markers'expression levels vary with the progression of gastric cancer. These variations gives us insights into the biological changes occurring at different stages. On analysing the plots we can confirm that these plots actually portrays the fact we have understood earlier, we can see that starting from stage 1 (the 2nd boxplot in every graph), with poor prognosis the expression of the prognostic markers have increased.



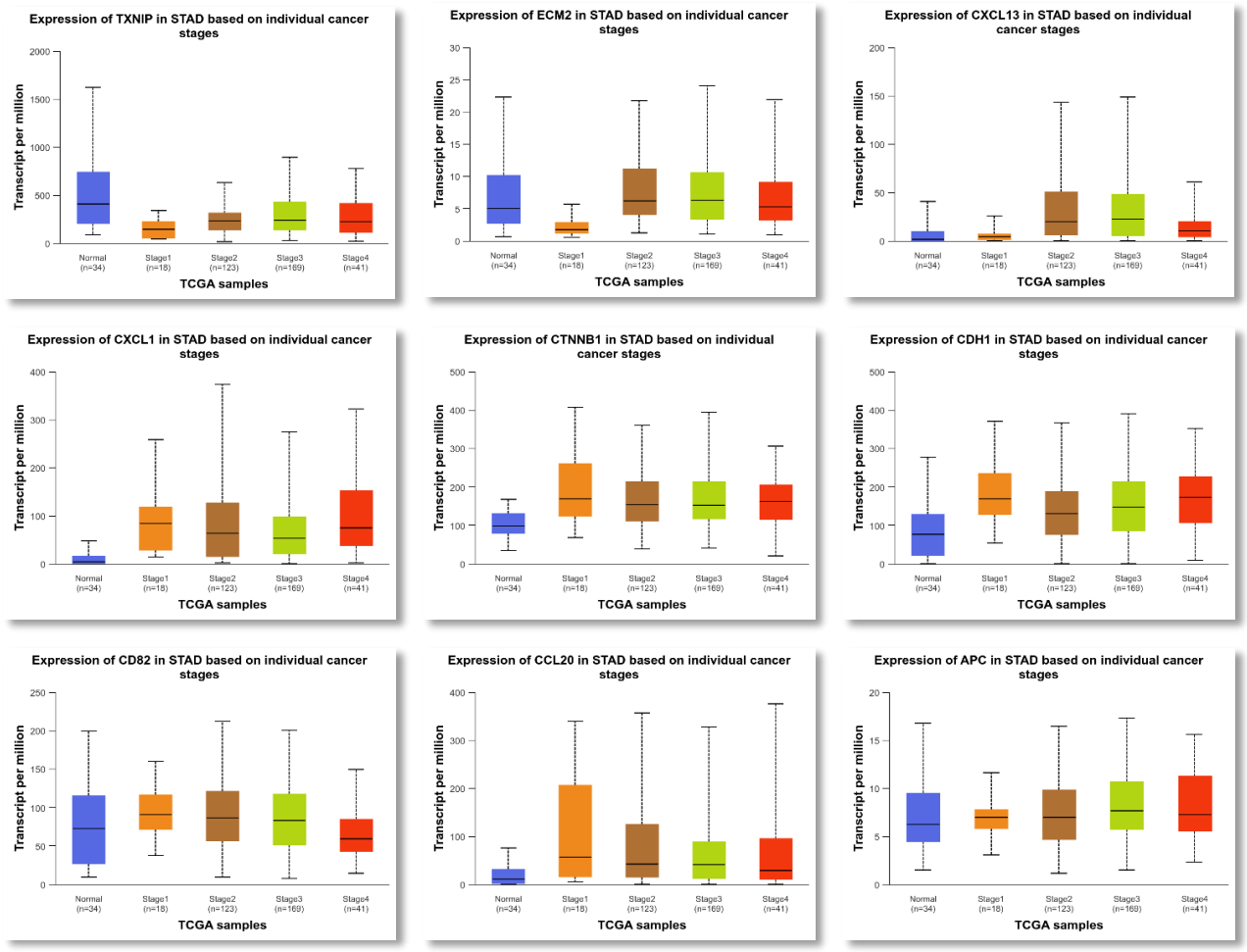


Figure 30: Boxplots shows the change in expression for the prognostic markers with stage different stages of STAD.

5.9. Survival Analysis:

A Kaplan-Meier (KM) plot is a fundamental tool in survival analysis, which is the field of statistics that deals with the time until an event of interest occurs. The KM plot visually represents the probability of surviving past a certain time point based on observed data. The Kaplan-Meier estimator calculates the survival function S(t), which represents the probability of an individual surviving from the beginning of the study to a particular time t. The Kaplan-Meier plot provides several insights like:

1. Survival Probability over Time:
   - The y-axis of the plot shows the survival probability, ranging from 0 to 1 (or 0% to 100%).
   - The x-axis represents time, which can be in days, months, or years, depending on the study.
2. Comparison Between Groups:
   - When comparing survival across different groups (e.g., treatment vs. control), each group has its own KM curve.

- The separation between curves indicates differences in survival rates. For instance, if the treatment group's curve is consistently above the control group's curve, it suggests better survival outcomes for the treatment group.

3. Median Survival Time:
   - The median survival time refers to the point at which half of the participants in the study are projected to have experienced the event of interest. This is identified as the point where the Kaplan-Meier (KM) survival curve intersects with the 50% survival probability line.
   - This value is a critical summary measure of the central tendency of the survival times.

5.9.1. Prognostic Marker Overall Survival Correlation using KM Plot:

Four out of the top performing prognostic markers (GNB4, TXNIP, ECM2 & PRRX1), showed significant HR values in K.M. Plot survival analysis also suggesting that higher expression of these genes are associated with worse survival outcomes in GC patients.

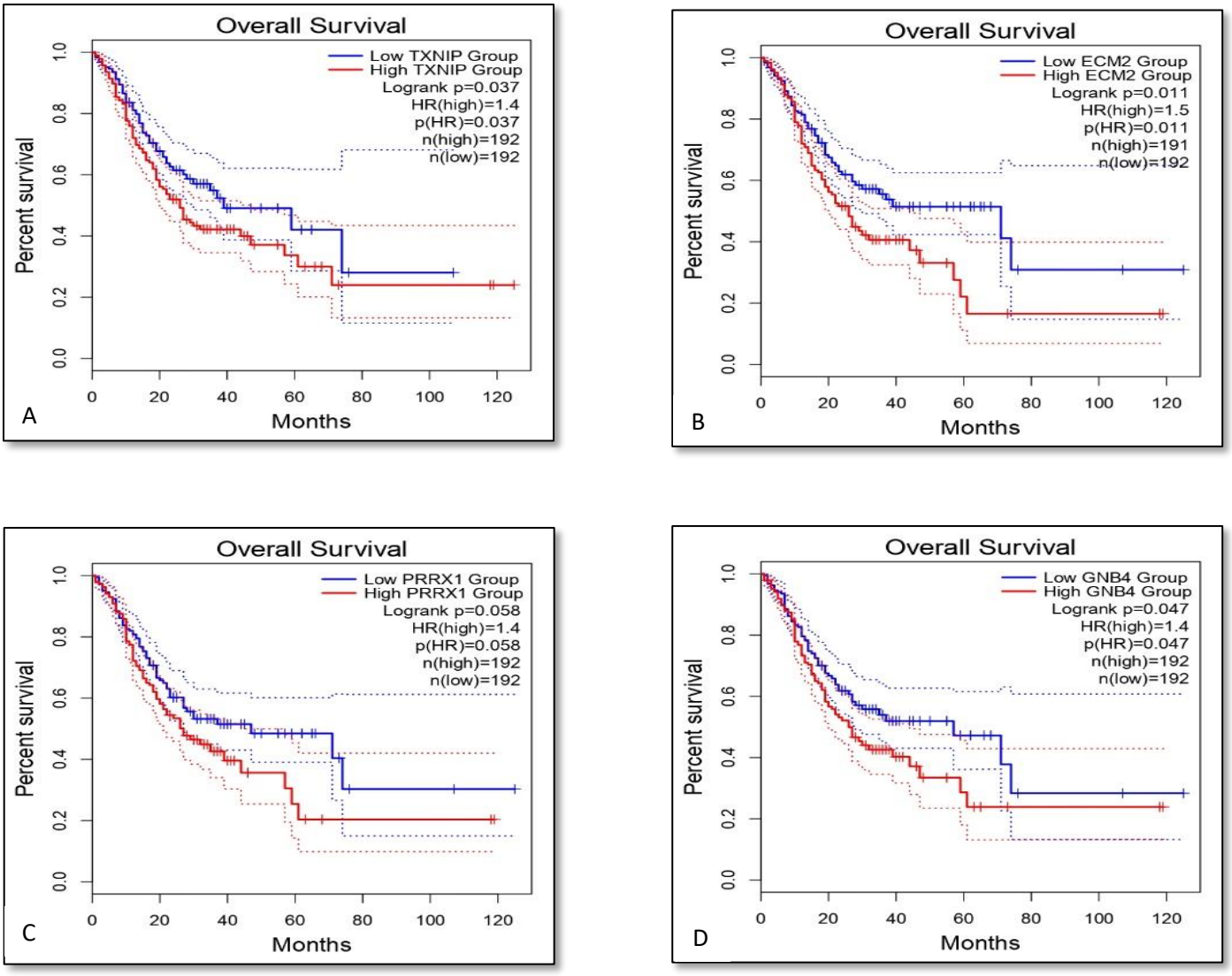


Figure 31: A – KM overall survival plot for TXNIP, B – KM overall survival plot for ECM2, C – KM overall survival plot for PRRX1, & D – KM overall survival plot for GNB4

CHAPTER: 6

DISCUSSION

6. Discussion:

Emerging evidence highlights that *H. pylori* infection significantly affects metabolic alterations within the host [197, 198]. Although the importance of metabolic genes and models based on metabolism in forecasting gastric cancer (GC) survival outcomes has been established [199, 200], the specific metabolic changes associated with HpGC are still largely unexamined. These shifts in metabolic genes enable cancerous cells to reconfigure their metabolic processes to meet the heightened energy needs required for their survival. Therefore, pinpointing metabolic signatures linked to *H. pylori* infection that influence metabolic functions, signalling pathways, and tumor development is essential for gaining deeper insights into HpGC and crafting targeted therapeutic interventions. Tumor cells undergoing rapid proliferation rely on crucial metabolites to support their growth and create an immunosuppressive microenvironment. However, the impact of *H. pylori* infection on immunometabolism remains not fully understood.

GC is a diverse and complex disease, exhibiting a range of clinical behaviours and risk factors. Research involving transcriptomic and genomic analyses has highlighted this diversity, leading to the classification of gastric cancer into distinct molecular subtypes based on specific genetic mutations and expression patterns, which reveal substantial biological variations [201]. To enhance prognostic accuracy, we have developed a metabolic score designed to measure the metabolic characteristics associated with these molecular subtypes. Previous studies have demonstrated that the diffuse histological type and the epithelial-mesenchymal transition (EMT) molecular subtype are closely linked to poorer survival outcomes, while the microsatellite instability (MSI) subtype is associated with more favorable clinical results in gastric cancer [201]

Our study identified 131 potential signature metabolic genes and devised a score to quantify these metabolic patterns. These findings suggest that infection of *H. pylori* that infection might worsen the interaction between the immune environment and metabolic processes. As a result, HpGC patients with lower metabolic scores tend to have poorer prognoses, providing valuable insights into the mechanisms that shape distinct metabolic patterns in HpGC. Recent studies have highlighted that specific metabolic gene transcripts can serve as predictive biomarkers for survival outcomes [202]. In this study 131 consistently dysregulated metabolic genes for HpGC, are exposed. On the other hand, numerous genes have been manually identified from extensive search of literature, as significant prognostic biomarkers because of their participation in essential cellular functions that drive cancer development. Among them, as mentioned earlier the following are found to be differentially expressed in GC and are most relevant: GNB4, APC, TXNIP, ECM2, PRRX1, CDH1, GPI, SPARC, FAS,

HIF1A, CXCL13, CTNNB1, CCL20, GNAS, RUNX3, CD82, PIM2, CXCL1, ERBB2, TP53, CXCL8, and MET. These prognostic biomarkers are related to a number of metabolic pathways that are governed by the metabolic Genes we have discussed earlier. The metabolic pathways where there is significant association of most of the prognostic genes are: Terpenoid biosynthesis pathway (19 of the 22 prognostic genes are associated to this pathway, and the metabolic genes involved in this pathway are PMVK, HMGCR, IDI1, GGPS1, ACAT2), Purine metabolism pathway (18 of the 22 prognostic genes are associated to this pathway, and the metabolic genes involved in this pathway are PDE7B, GUCY1A2, GUK1, NT5C, ITPA, HDDC3, NME1-NME2, PDE5A, ENTPD2, PDE3B, PPAT, PDE4A, PRUNE1, PAPSS2, NT5E), Cofactor biosynthesis pathway (18 of the 22 prognostic genes are associated to this pathway, and the metabolic genes involved in this pathway are AFMID, GSS, RDH11, PNPO, NME1-NME2, SPR, KMO, GPHN, DHFR2, MTHFD2L, KYNU, VKORC1L1, NMNAT1), Oxidative phosphorylation pathway (14 of the 22 prognostic genes are associated to this pathway, and the metabolic genes involved in this pathway are ATP5PD, COX5B, COX6C, COX7A2, UQCR10, NDUFA4, NDUFB1, NDUFB2, NDUFV2, NDUFA13, ATP5F1E, ATP5MC1, ATP6V0C, UQCRB), Glycosyl phosphat idylinositol (GPI)-anchor biosynthesis pathway (14 of the 22 prognostic genes are associated to this pathway, and the metabolic genes involved in this pathway are PIGU, PIGT, PIGF, PIGM, PIGL), Lysine degradation pathway (11 of the 22 prognostic genes are associated to this pathway, and the metabolic genes involved in this pathway are SETD1B, KMT2A, SETDB2, KMT2D, ACAT2, PRDM16), and Nucleotide metabolism (11 of the 22 prognostic genes are associated to this pathway, and the metabolic genes involved in this pathway are GUK1, NT5C, ITPA, NME1-NME2, DCTPP1, ENTPD2, NT5E), among other Metabolic Pathways. Now these metabolic pathways can be controlled by the metabolites that are involved in them, like Glucose, Pyruvate, Aspartate, Glutamate, IMP (Inosine Monophosphate), ADP (Adenosine Diphosphate) AMP (Adenosine monophosphate) If these metabolites can be altered in the body, they would affect the metabolic pathways, and in turn can govern prognosis of Gastric Cancer.

Analysing the above mentioned metabolic pathways we can identify potential Oncometabolites:

1. Terpenoid Backbone Biosynthesis

- Key Metabolites: Geranyl pyrophosphate (GPP), Dimethylallyl pyrophosphate (DMAPP), Farnesyl pyrophosphate (FPP), Isopentenyl pyrophosphate (IPP),
- Oncometabolites: Farnesyl pyrophosphate (FPP) is related to protein farnesylation, which is involved in the post-translational modification of proteins like RAS, a well-known oncogene.

2. Purine Metabolism

- Key Metabolites: Adenine, Guanine, Hypoxanthine, Xanthine, Inosine, Adenosine, GMP, AMP, Aspartate, Fumarate
- Oncometabolites: Adenosine is involved in signaling pathways that can suppress the immune response against tumors. Fumarate also can accumulate in gastric cancer cells due to mutations in metabolic enzymes. Elevated fumarate levels can contribute to the activation of oncogenic pathways. Thus, elevated levels of purine metabolites are often seen in cancer.

3. Biosynthesis of Cofactors

- Key Metabolites: NAD+, FAD, FADH2, Coenzyme A, Biotin, Tetrahydrofolate, Glucose
- Oncometabolites: NAD+ and FAD are involved in redox reactions and are crucial for maintaining cellular metabolism in cancer cells. The availability of these cofactors is often increased in cancer.

4. Oxidative Phosphorylation

- Key Metabolites: Adenosine triphosphate (ATP), Adenosine diphosphate (ADP), NADH, FADH2, Oxygen, Water, Glucose, Pyruvate, Succinate, Fumarate
- Oncometabolites: Elevated succinate levels have been linked to gastric cancer, where it can act as an oncometabolite by stabilizing hypoxia-inducible factors (HIFs), promoting a hypoxic environment that favors tumor growth. NADH and FADH2 are involved in the electron transport chain, which is often altered in cancer cells to support increased energy demands. ATP itself has role in supporting rapid cell proliferation too. Fumarate produced from succinate in this complex, can also be involved

5. Glycosylphosphatidylinositol (GPI)-Anchor Biosynthesis

- Key Metabolites: Phosphatidylinositol, Dolichol, Ethanolamine, Mannose
- Oncometabolites: No well-known oncometabolites are directly associated with this pathway, though altered GPI-anchor biosynthesis can influence cell signaling and contribute to cancer.

6. Lysine Degradation:

- Key Metabolites: Acetyl-CoA, Crotonyl-CoA, Pipecolate, Saccharopine, Pyruvate, Aspartate, Glutamate, Fumarate
- Oncometabolites: Lysine degradation can produce acetyl-CoA and other intermediates that might feed into the TCA cycle. Acetyl-CoA is a key metabolite that can influence epigenetic modifications such as histone acetylation, which plays a part in cancer advancement. Fumarate particpates in this pathway.

7. Nucleotide Degradation:

- Key Metabolites: Triphosphates, Inosine monophosphate, Carbamoyl phosphate, Glutamate
- Oncometabolites: ATP and other nucleotide triphosphates are critical for DNA replication and repair, which are processes often dysregulated in cancer. Additionally, Deoxyadenosine triphosphate (dATP) and Deoxyguanosine triphosphate (dGTP) are involved in DNA synthesis and are critical for rapidly proliferating cells, including cancer cells.

This study helped us develop and validate a robust metabolic framework specifically for HpGC. Our findings revealed that 15 of 131 metabolic genes are correlated with a high number of the prognostic markers and are involved in crucial metabolic pathways that are closely linked to the cancer, suggesting their potential as targets for personalized treatment strategies in patients with HpGC. Looking ahead, our future research will focus on unraveling the pharmacological mechanisms by which the above mentioned 15 metabolic genes—namely IDI1, ACAT2, AFMID, PDE5A, HMGCR, ITPA, SPR, PDE7B, PPAT, GALNT16, GSS, GSTM5, KMO, PIGF, and PIGU—influence HpGC. We aim to achieve this by modulating their expression to better understand their roles in the disease and to develop more effective therapeutic interventions. Our comprehensive analysis revealed that the metabolic disruptions caused by *H. pylori* infection offer critical insights into the mechanisms of gastric cancer progression. Furthermore, the metabolic genes, along with the associated metabolites and metabolic pathways identified in this research, present a compelling foundation for exploring the metabolic phenotypes of HpGC. These findings hold promise as novel prognostic markers or potential therapeutic targets, opening new avenues for targeted intervention in gastric cancer.

CONCLUSION & FUTURE SCOPES

7. Conclusion

The research presented in this thesis provides a comprehensive analysis of metabolic gene alterations in *Helicobacter pylori*-mediated gastric cancer (HpGC). Through the integration of high-throughput genomic data and advanced bioinformatics tools, this study identifies 131 differentially expressed metabolic genes (DEMGs) that are crucial in understanding the molecular mechanisms underlying HpGC. The findings reveal that these metabolic genes are significantly associated with key pathways such as glycolysis, nucleotide biosynthesis, purine metabolism, and the TCA cycle, all of which play a vital role in cancer cell survival and proliferation.

The correlation analysis between metabolic genes and established prognostic markers underscores the potential of these genes as novel biomarkers for earlier detection and as targets for personalized therapeutic interventions. The study's development of a metabolic score based on the correlation of metabolic genes to prognostic markers and the involvement of those genes in crucial metabolic pathways for gastric cancer as depicted in Table 3, further enhances the classification of HpGC into molecular subtypes, which means classifying cancer in ways other than only the location of occurrence using different molecular characteristics like genomic or metabolomics or biochemical, which is essential for predicting patient outcomes and tailoring precision treatment strategies.

One of the significant contributions of this research is the identification of ten metabolic genes— IDI1, ACAT2, AFMID, PDE5A, HMGCR, ITPA, SPR, PDE7B, PPAT, GALNT16, GSS, GSTM5, KMO, PIGF, and PIGU—as critical drivers of HpGC progression. These genes are strongly correlated with the aggressiveness of gastric cancer, and their dysregulation may provide novel insights into the metabolic reprogramming that characterizes HpGC. Collectively, these genes serve as potential prognostic biomarkers for gastric cancer, highlighting their importance in the molecular pathways that govern cancer development and progression, and underscoring the need for further research to validate their clinical utility.

Overall, this study builds a concrete foundation for understanding the complex metabolic landscape of HpGC, offering valuable insights into the interplay amongst *H. pylori* infection, metabolic alterations, and progression of cancer. Identifying specific metabolic pathways and genes involved in HpGC paves the way for developing targeted therapies and precision medicine strategies, with the goal of enhancing patient outcomes.

8. Future Scopes:

Building on the findings of this research, several future directions can be pursued:

- Pharmacological Targeting of Metabolic Genes: Further research should focus on exploring the pharmacological mechanisms by which the identified metabolic genes (IDI1, ACAT2, AFMID, PDE5A, HMGCR, ITPA, SPR, PDE7B, PPAT, GALNT16, GSS, GSTM5, KMO, PIGF, and PIGU) influence HpGC. This can involve drug screening and validation studies to identify compounds that effectively modulate these genes, providing new avenues for therapeutic intervention.
- Metabolomics and Multi-omics Integration: Integrating metabolomics with other omics data, such as transcriptomics and proteomics, can provide a more holistic understanding of the metabolic reprogramming in HpGC. This approach could aid in uncovering additional metabolic signatures and biomarkers essential for early detection and prognosis.
- Clinical Verification of Biomarkers: The identified metabolic genes and pathways should undergo clinical validation in large patient cohorts to assess their utility as therapeutic targets or prognostic markers. This would involve collaboration with clinical researchers to evaluate the effectiveness of these biomarkers in predicting patient outcomes and guiding treatment decisions
- Development of Diagnostic Tools: Based on the metabolic signatures identified in this study, there is potential to develop minimally-invasive diagnostic tools, such as blood-based, or fecal-based or emetic biomarkers to detect HpGC. Advanced biosensors could be tailored to detect specific metabolic markers associated with HpGC. These biosensors could be integrated into point-of-care devices, enabling rapid and accurate detection of HpGC-related biomarkers. The design of such sensors could leverage advances in microfluidics, nanotechnology, and bioelectronics to achieve high sensitivity and specificity. These tools could significantly improve early detection rates and patient survival.
- Exploration of Immune-Metabolic Interactions: Future research should delve deeper into the interaction between metabolic alterations and the immune microenvironment in HpGC. Understanding how *H. pylori* infection modulates immune-metabolism could uncover new strategies for immunotherapy, potentially enhancing the effectiveness of current treatments.
- Application of Bioinformatics in Personalized Medicine: The bioinformatics approaches used in this study can be further refined and applied to other cancers or diseases where metabolic reprogramming plays a crucial role. This could result in the discovery of new therapeutic targets and the advancement of personalized medicine strategies across different cancer types.

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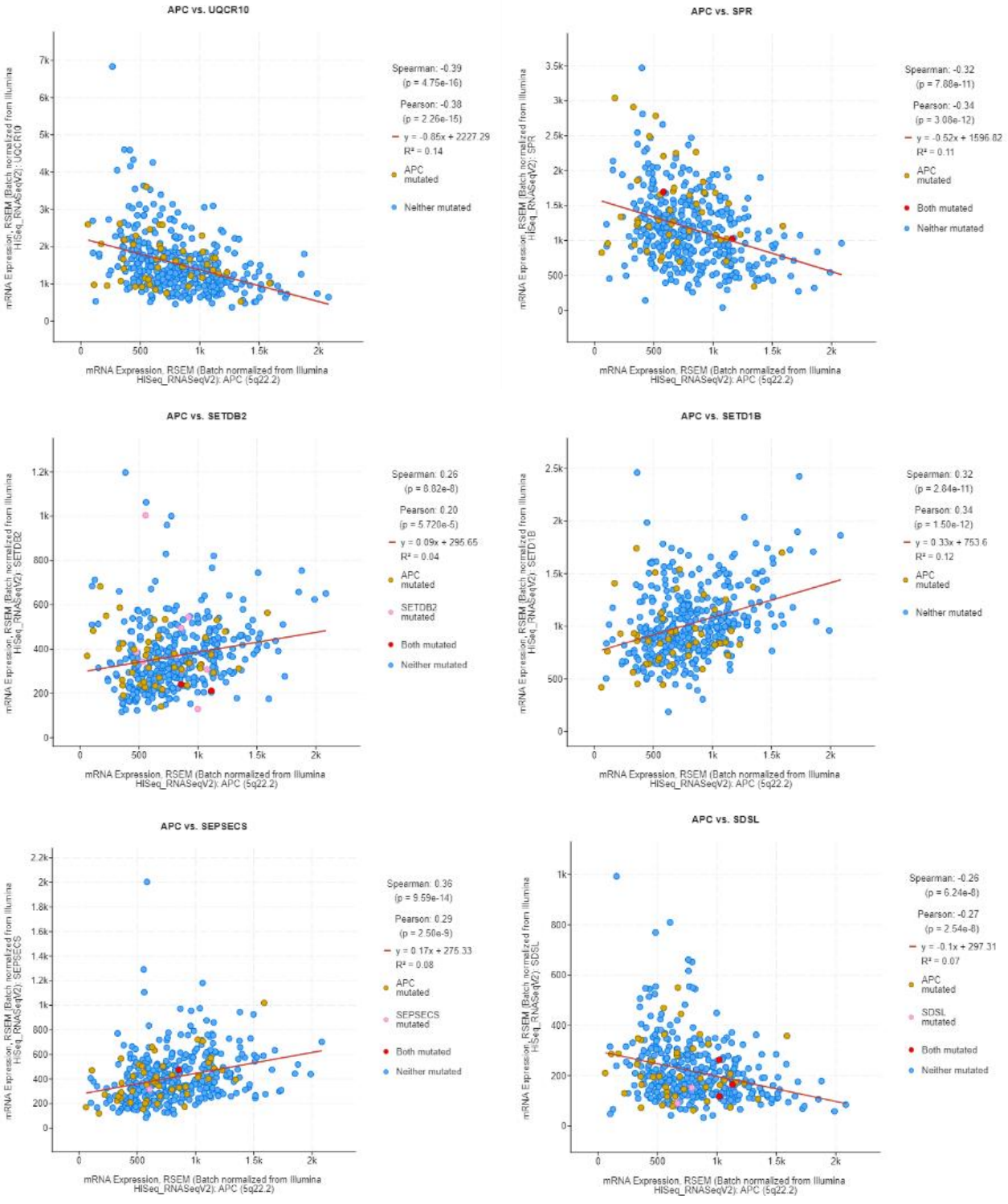
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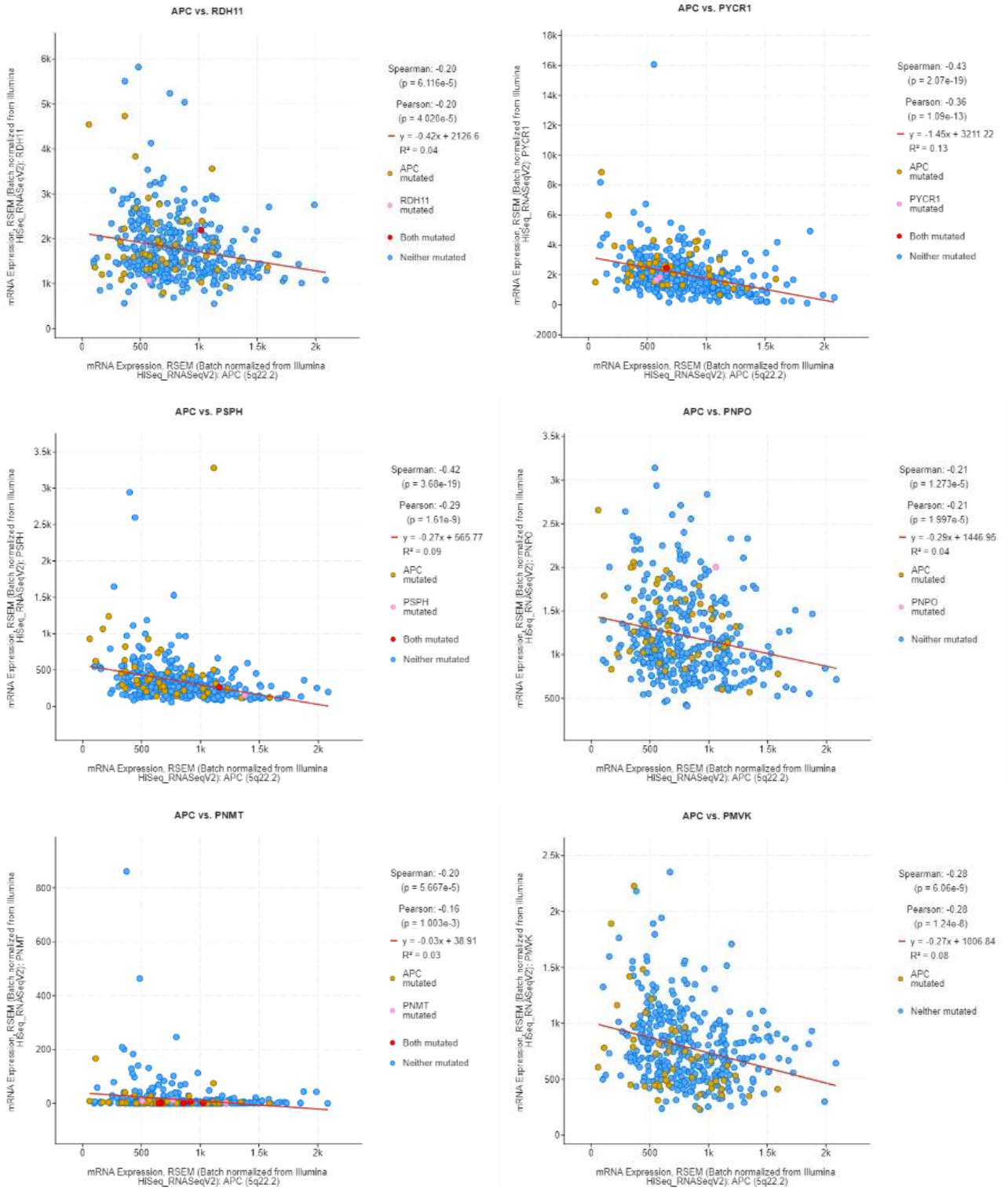
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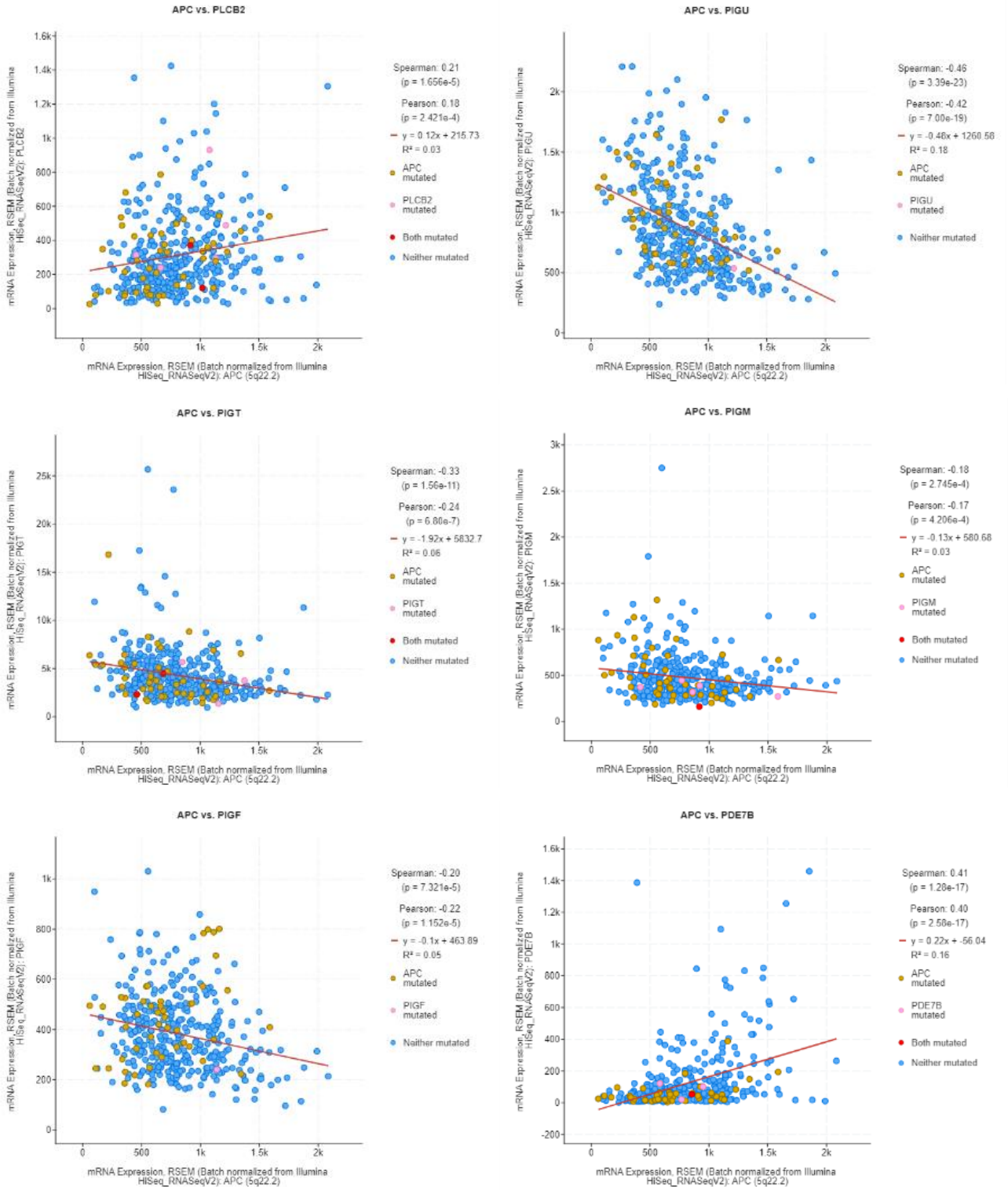
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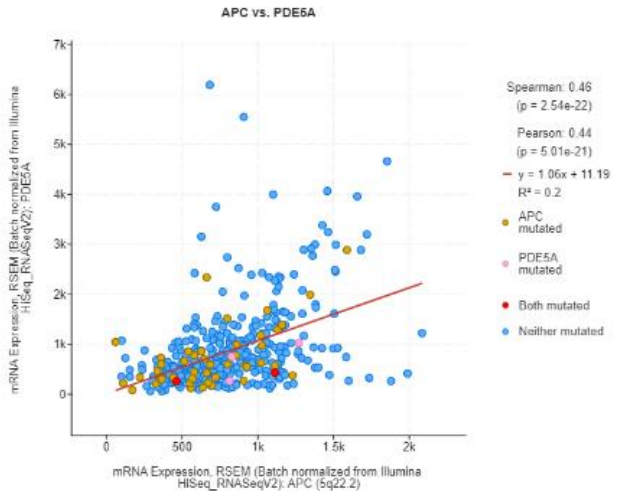
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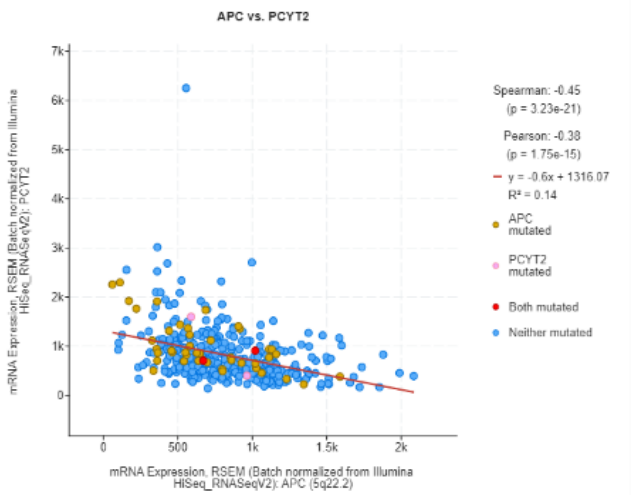
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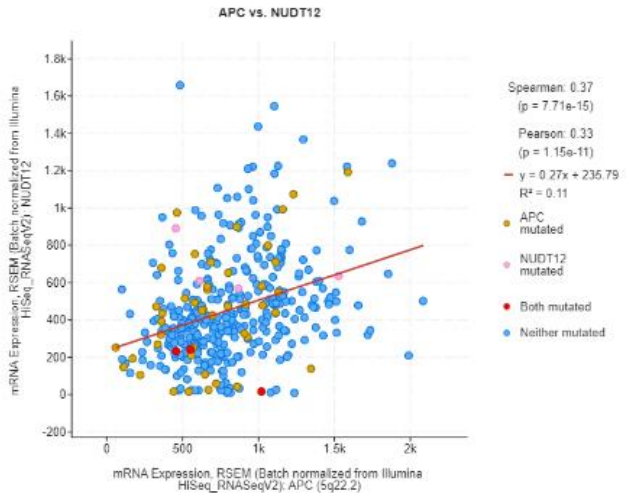


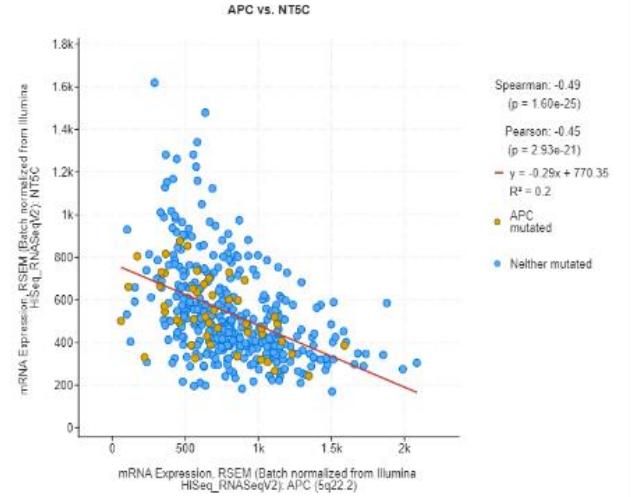

APC vs. RDH11
mRNA Expression, RSEM (Batch normalized from Illumina HiSeq_RNASeqV2): RDH11
mRNA Expression, RSEM (Batch normalized from Illumina HiSeq_RNASeqV2): APC (5q22.2)
Spearman: -0.20
(p = 6.116e-5)
Pearson: -0.20
(p = 4.020e-5)
y = -0.42x + 2126.6
R² = 0.04
APC mutated
RDH11 mutated
Both mutated
Neither mutated
APC vs. PYCR1
mRNA Expression, RSEM (Batch normalized from Illumina HiSeq_RNASeqV2): PYCR1
mRNA Expression, RSEM (Batch normalized from Illumina HiSeq_RNASeqV2): APC (5q22.2)
Spearman: -0.43
(p = 2.07e-19)
Pearson: -0.36
(p = 1.09e-13)
y = -1.45x + 3211.22
R² = 0.13
APC mutated
PYCR1 mutated
Both mutated
Neither mutated
APC vs. PSPH
mRNA Expression, RSEM (Batch normalized from Illumina HiSeq_RNASeqV2): PSPH
mRNA Expression, RSEM (Batch normalized from Illumina HiSeq_RNASeqV2): APC (5q22.2)
Spearman: -0.42
(p = 3.68e-19)
Pearson: -0.29
(p = 1.61e-9)
y = -0.27x + 565.77
R² = 0.09
APC mutated
PSPH mutated
Both mutated
Neither mutated
APC vs. PNPO
mRNA Expression, RSEM (Batch normalized from Illumina HiSeq_RNASeqV2): PNPO
mRNA Expression, RSEM (Batch normalized from Illumina HiSeq_RNASeqV2): APC (5q22.2)
Spearman: -0.21
(p = 1.273e-5)
Pearson: -0.21
(p = 1.997e-5)
y = -0.29x + 1446.95
R² = 0.04
APC mutated
PNPO mutated
Neither mutated
APC vs. PNMT
mRNA Expression, RSEM (Batch normalized from Illumina HiSeq_RNASeqV2): PNMT
mRNA Expression, RSEM (Batch normalized from Illumina HiSeq_RNASeqV2): APC (5q22.2)
Spearman: -0.20
(p = 5.667e-5)
Pearson: -0.16
(p = 1.003e-3)
y = -0.03x + 38.91
R² = 0.03
APC mutated
PNMT mutated
Both mutated
Neither mutated
APC vs. PMVK
mRNA Expression, RSEM (Batch normalized from Illumina HiSeq_RNASeqV2): PMVK
mRNA Expression, RSEM (Batch normalized from Illumina HiSeq_RNASeqV2): APC (5q22.2)
Spearman: -0.28
(p = 6.06e-9)
Pearson: -0.28
(p = 1.24e-8)
y = -0.27x + 1006.84
R² = 0.08
APC mutated
Neither mutated

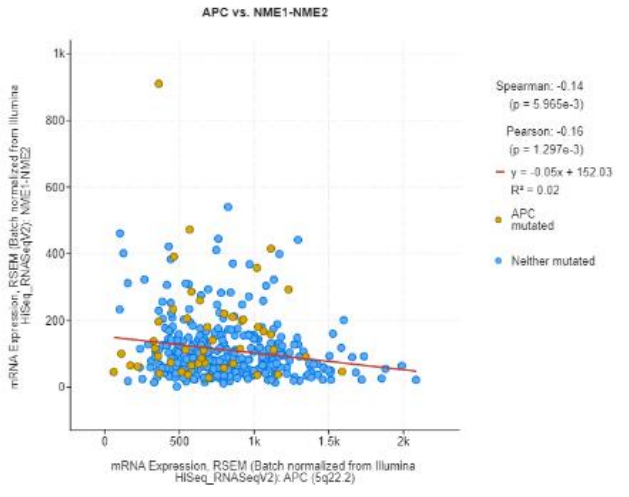

APC vs. PLCB2
mRNA Expression, RSEM (Batch normalized from Illumina HiSeq_RNASeqV2): PLCB2
mRNA Expression, RSEM (Batch normalized from Illumina HiSeq_RNASeqV2): APC (5q22.2)
Spearman: 0.21
(p = 1.656e-5)
Pearson: 0.18
(p = 2.421e-4)
y = 0.12x + 215.73
R² = 0.03
APC mutated
PLCB2 mutated
Both mutated
Neither mutated
APC vs. PIGU
mRNA Expression, RSEM (Batch normalized from Illumina HiSeq_RNASeqV2): PIGU
mRNA Expression, RSEM (Batch normalized from Illumina HiSeq_RNASeqV2): APC (5q22.2)
Spearman: -0.46
(p = 3.39e-23)
Pearson: -0.42
(p = 7.00e-19)
y = -0.46x + 1260.56
R² = 0.18
APC mutated
PIGU mutated
Neither mutated
APC vs. PIGT
mRNA Expression, RSEM (Batch normalized from Illumina HiSeq_RNASeqV2): PIGT
mRNA Expression, RSEM (Batch normalized from Illumina HiSeq_RNASeqV2): APC (5q22.2)
Spearman: -0.33
(p = 1.56e-11)
Pearson: -0.24
(p = 6.86e-7)
y = -1.92x + 5832.7
R² = 0.06
APC mutated
PIGT mutated
Both mutated
Neither mutated
APC vs. PIGM
mRNA Expression, RSEM (Batch normalized from Illumina HiSeq_RNASeqV2): PIGM
mRNA Expression, RSEM (Batch normalized from Illumina HiSeq_RNASeqV2): APC (5q22.2)
Spearman: -0.18
(p = 2.745e-4)
Pearson: -0.17
(p = 4.206e-4)
y = -0.13x + 580.68
R² = 0.03
APC mutated
PIGM mutated
Both mutated
Neither mutated
APC vs. PIGF
mRNA Expression, RSEM (Batch normalized from Illumina HiSeq_RNASeqV2): PIGF
mRNA Expression, RSEM (Batch normalized from Illumina HiSeq_RNASeqV2): APC (5q22.2)
Spearman: -0.20
(p = 7.321e-5)
Pearson: -0.22
(p = 1.152e-5)
y = -0.1x + 463.89
R² = 0.05
APC mutated
PIGF mutated
Neither mutated
APC vs. PDE7B
mRNA Expression, RSEM (Batch normalized from Illumina HiSeq_RNASeqV2): PDE7B
mRNA Expression, RSEM (Batch normalized from Illumina HiSeq_RNASeqV2): APC (5q22.2)
Spearman: 0.41
(p = 1.26e-17)
Pearson: 0.40
(p = 2.56e-17)
y = 0.22x + -56.04
R² = 0.16
APC mutated
PDE7B mutated
Both mutated
Neither mutated

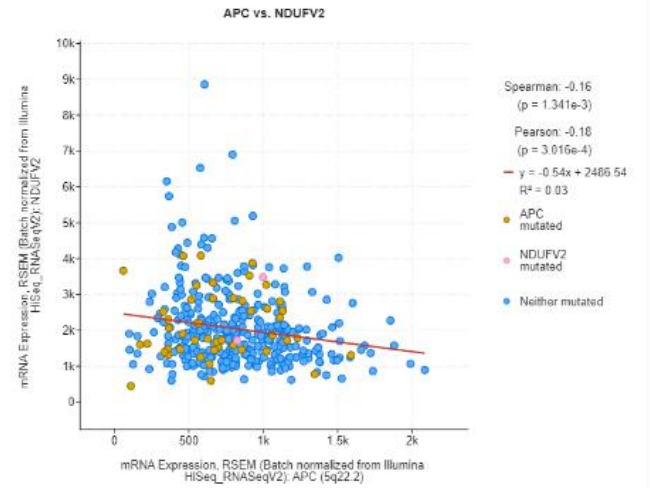

APC vs. PDE5A
mRNA Expression, RSEM (Batch normalized from Illumina HiSeq_RNASeqV2): PDE5A
mRNA Expression, RSEM (Batch normalized from Illumina HiSeq_RNASeqV2): APC (5q22.2)
Spearman: 0.46
(p = 2.54e-22)
Pearson: 0.44
(p = 5.01e-21)
y = 1.06x + 11.19
R² = 0.2
APC mutated
PDE5A mutated
Both mutated
Neither mutated

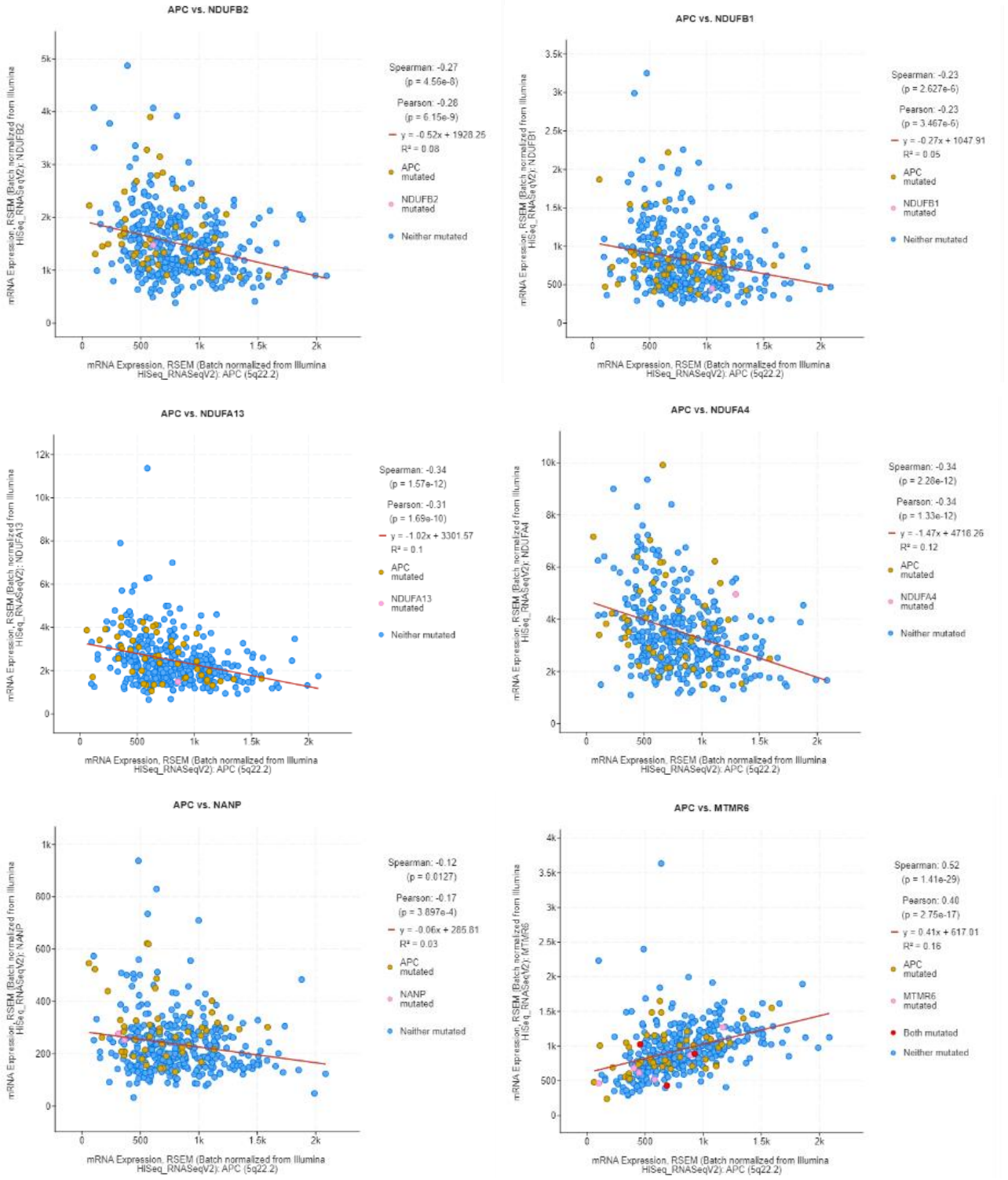

APC vs. PCYT2
mRNA Expression, RSEM (Batch normalized from Illumina HiSeq_RNASeqV2): PCYT2
mRNA Expression, RSEM (Batch normalized from Illumina HiSeq_RNASeqV2): APC (5q22.2)
Spearman: -0.45
(p = 3.23e-21)
Pearson: -0.38
(p = 1.75e-15)
y = -0.6x + 1316.07
R² = 0.14
APC mutated
PCYT2 mutated
Both mutated
Neither mutated

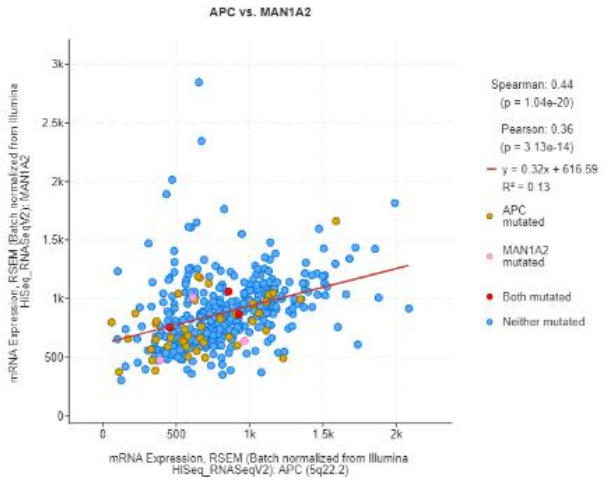

APC vs. NUDT12
mRNA Expression, RSEM (Batch normalized from Illumina HiSeq_RNASeqV2): NUDT12
mRNA Expression, RSEM (Batch normalized from Illumina HiSeq_RNASeqV2): APC (5q22.2)
Spearman: 0.37
(p = 7.71e-15)
Pearson: 0.33
(p = 1.15e-11)
y = 0.27x + 235.79
R² = 0.11
APC mutated
NUDT12 mutated
Both mutated
Neither mutated

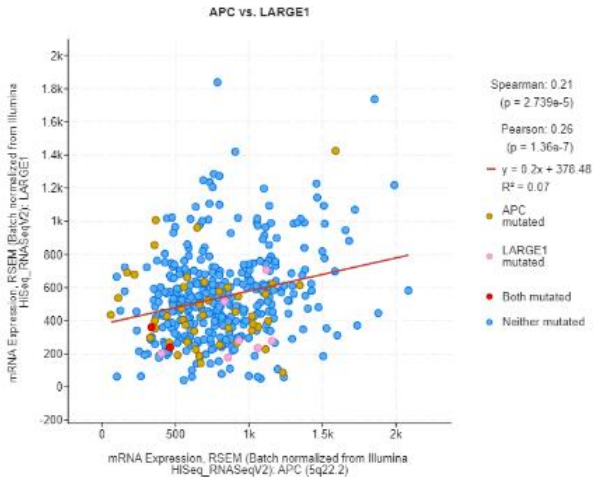

APC vs. NT5C
mRNA Expression, RSEM (Batch normalized from Illumina HiSeq_RNASeqV2): NT5C
mRNA Expression, RSEM (Batch normalized from Illumina HiSeq_RNASeqV2): APC (5q22.2)
Spearman: -0.49
(p = 1.60e-25)
Pearson: -0.45
(p = 2.93e-21)
y = -0.29x + 770.35
R² = 0.2
APC mutated
Neither mutated

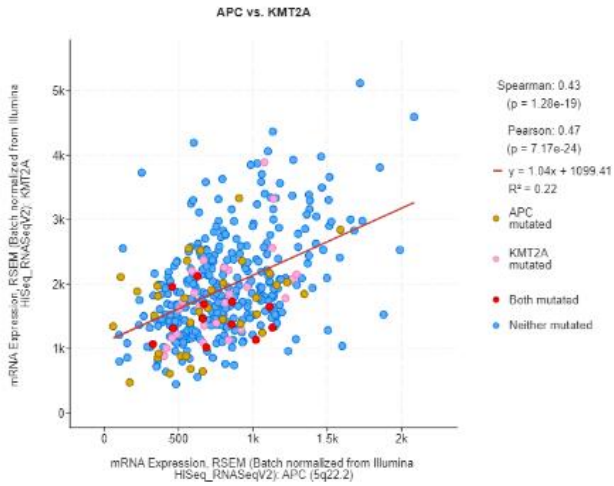

APC vs. NME1-NME2
mRNA Expression, RSEM (Batch normalized from Illumina HiSeq_RNASeqV2): NME1-NME2
mRNA Expression, RSEM (Batch normalized from Illumina HiSeq_RNASeqV2): APC (5q22.2)
Spearman: -0.14
(p = 5.965e-3)
Pearson: -0.16
(p = 1.297e-3)
y = -0.05x + 152.03
R² = 0.02
APC mutated
Neither mutated

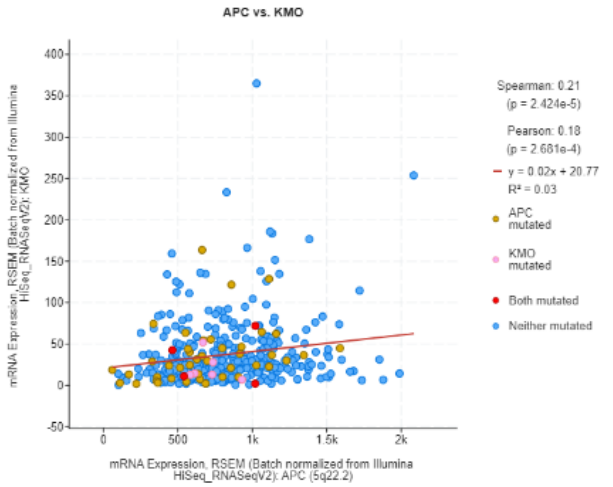

APC vs. NDUFV2
mRNA Expression, RSEM (Batch normalized from Illumina HiSeq_RNASeqV2): NDUFV2
mRNA Expression, RSEM (Batch normalized from Illumina HiSeq_RNASeqV2): APC (5q22.2)
Spearman: -0.16
(p = 1.341e-3)
Pearson: -0.18
(p = 3.016e-4)
y = -0.54x + 2486.54
R² = 0.03
APC mutated
NDUFV2 mutated
Neither mutated

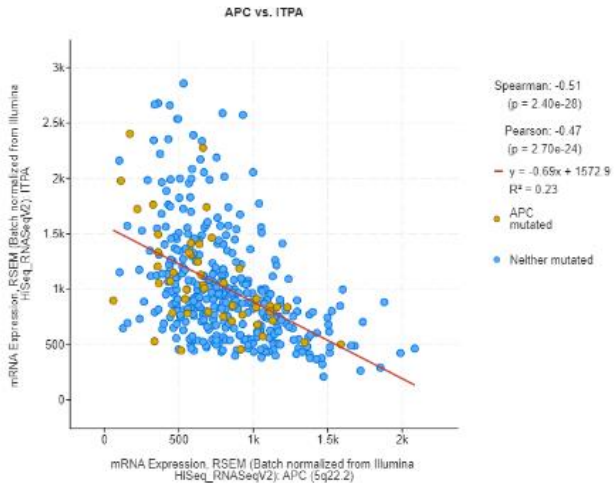

APC vs. NDUFB2
mRNA Expression, RSEM (Batch normalized from Illumina HiSeq_RNASeqV2): NDUFB2
mRNA Expression, RSEM (Batch normalized from Illumina HiSeq_RNASeqV2): APC (5q22.2)
Spearman: -0.27
(p = 4.56e-8)
Pearson: -0.28
(p = 6.15e-9)
y = -0.52x + 1928.25
R² = 0.08
APC mutated
NDUFB2 mutated
Neither mutated
APC vs. NDUFB1
mRNA Expression, RSEM (Batch normalized from Illumina HiSeq_RNASeqV2): NDUFB1
mRNA Expression, RSEM (Batch normalized from Illumina HiSeq_RNASeqV2): APC (5q22.2)
Spearman: -0.23
(p = 2.627e-6)
Pearson: -0.23
(p = 3.467e-6)
y = -0.27x + 1047.91
R² = 0.05
APC mutated
NDUFB1 mutated
Neither mutated
APC vs. NDUFA13
mRNA Expression, RSEM (Batch normalized from Illumina HiSeq_RNASeqV2): NDUFA13
mRNA Expression, RSEM (Batch normalized from Illumina HiSeq_RNASeqV2): APC (5q22.2)
Spearman: -0.34
(p = 1.57e-12)
Pearson: -0.31
(p = 1.69e-10)
y = -1.02x + 3301.57
R² = 0.1
APC mutated
NDUFA13 mutated
Neither mutated
APC vs. NDUFA4
mRNA Expression, RSEM (Batch normalized from Illumina HiSeq_RNASeqV2): NDUFA4
mRNA Expression, RSEM (Batch normalized from Illumina HiSeq_RNASeqV2): APC (5q22.2)
Spearman: -0.34
(p = 2.28e-12)
Pearson: -0.34
(p = 1.33e-12)
y = -1.47x + 4716.26
R² = 0.12
APC mutated
NDUFA4 mutated
Neither mutated
APC vs. NANP
mRNA Expression, RSEM (Batch normalized from Illumina HiSeq_RNASeqV2): NANP
mRNA Expression, RSEM (Batch normalized from Illumina HiSeq_RNASeqV2): APC (5q22.2)
Spearman: -0.12
(p = 0.0127)
Pearson: -0.17
(p = 3.897e-4)
y = -0.06x + 285.81
R² = 0.03
APC mutated
NANP mutated
Neither mutated
APC vs. MTMR6
mRNA Expression, RSEM (Batch normalized from Illumina HiSeq_RNASeqV2): MTMR6
mRNA Expression, RSEM (Batch normalized from Illumina HiSeq_RNASeqV2): APC (5q22.2)
Spearman: 0.52
(p = 1.41e-29)
Pearson: 0.40
(p = 2.75e-17)
y = 0.41x + 617.01
R² = 0.16
APC mutated
MTMR6 mutated
Both mutated
Neither mutated

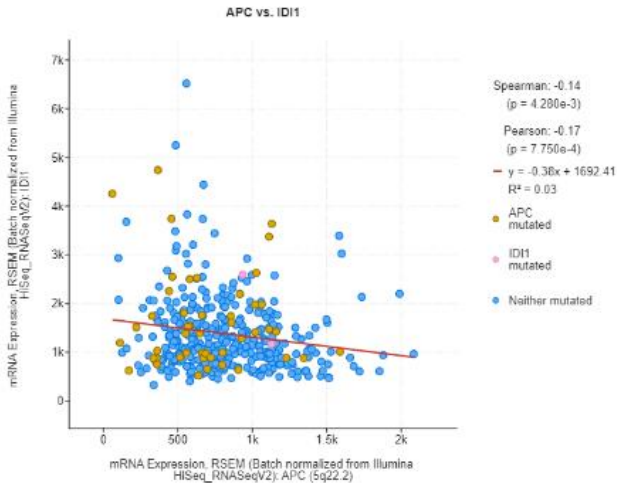

APC vs. MAN1A2
mRNA Expression, RSEM (Batch normalized from Illumina HiSeq_RNASeqV2): MAN1A2
mRNA Expression, RSEM (Batch normalized from Illumina HiSeq_RNASeqV2): APC (5q22.2)
Spearman: 0.44
(p = 1.04e-20)
Pearson: 0.36
(p = 3.13e-14)
y = 0.32x + 616.59
R² = 0.13
APC mutated
MAN1A2 mutated
Both mutated
Neither mutated

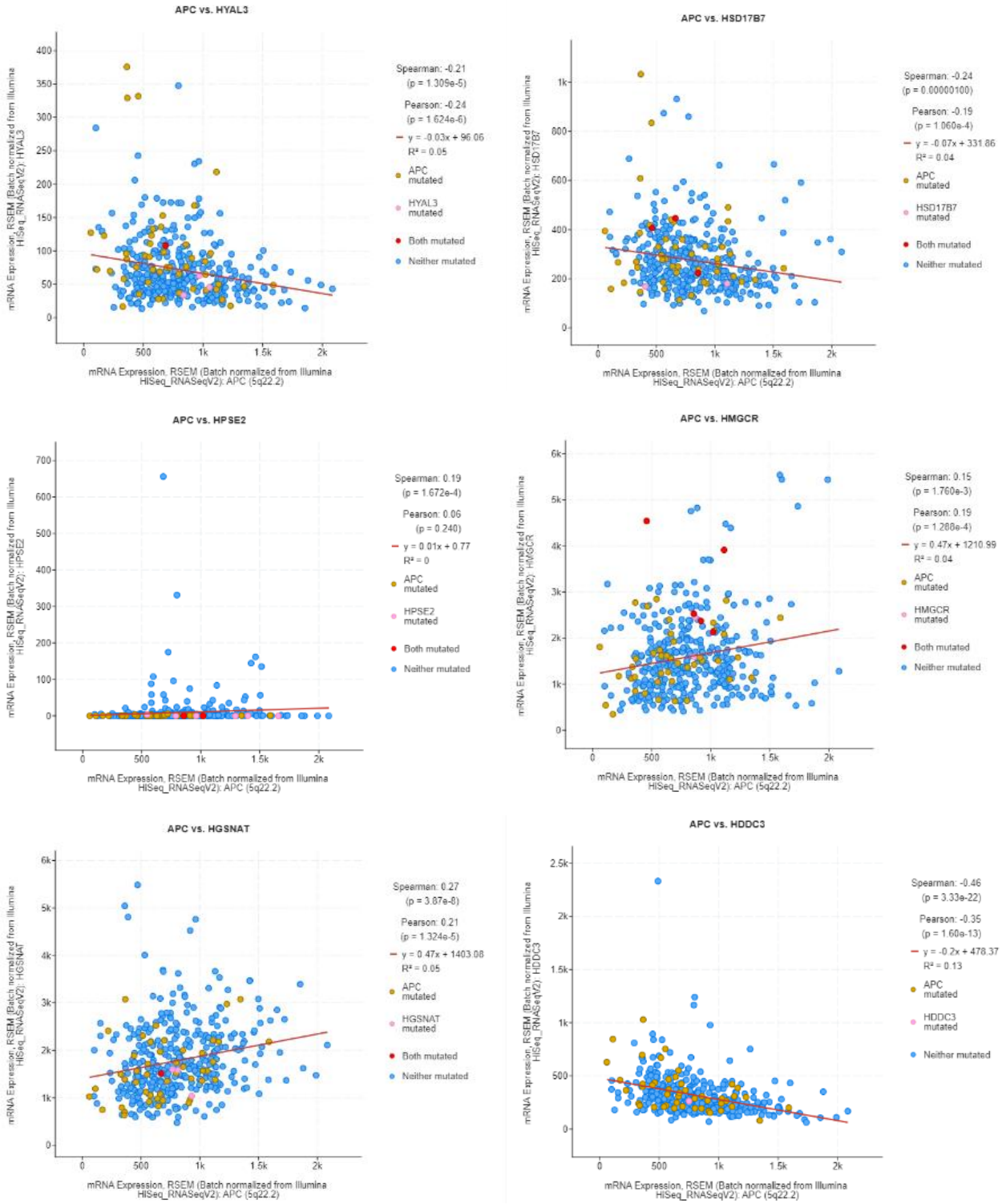

APC vs. LARGE1
mRNA Expression, RSEM (Batch normalized from Illumina HiSeq_RNASeqV2): LARGE1
mRNA Expression, RSEM (Batch normalized from Illumina HiSeq_RNASeqV2): APC (5q22.2)
Spearman: 0.21
(p = 2.739e-5)
Pearson: 0.26
(p = 1.36e-7)
y = 0.2x + 376.48
R² = 0.07
APC mutated
LARGE1 mutated
Both mutated
Neither mutated

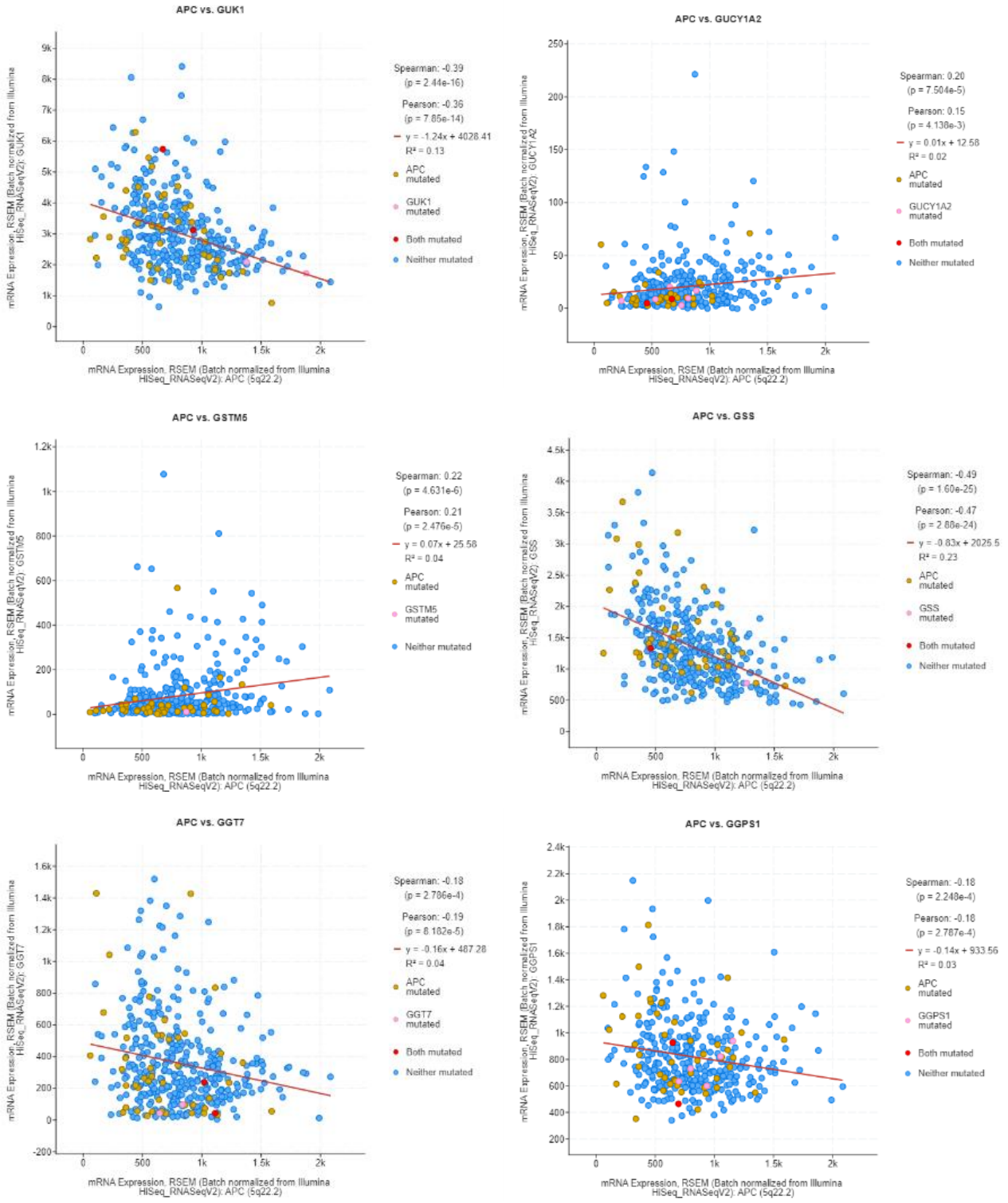

APC vs. KMT2A
mRNA Expression, RSEM (Batch normalized from Illumina HiSeq_RNASeqV2): KMT2A
mRNA Expression, RSEM (Batch normalized from Illumina HiSeq_RNASeqV2): APC (5q22.2)
Spearman: 0.43
(p = 1.28e-19)
Pearson: 0.47
(p = 7.17e-24)
y = 1.04x + 1099.41
R² = 0.22
APC mutated
KMT2A mutated
Both mutated
Neither mutated


APC vs. KMO
mRNA Expression, RSEM (Batch normalized from Illumina HiSeq_RNASeqV2): KMO
mRNA Expression, RSEM (Batch normalized from Illumina HiSeq_RNASeqV2): APC (5q22.2)
Spearman: 0.21
(p = 2.424e-5)
Pearson: 0.18
(p = 2.661e-4)
y = 0.02x + 20.77
R² = 0.03
APC mutated
KMO mutated
Both mutated
Neither mutated

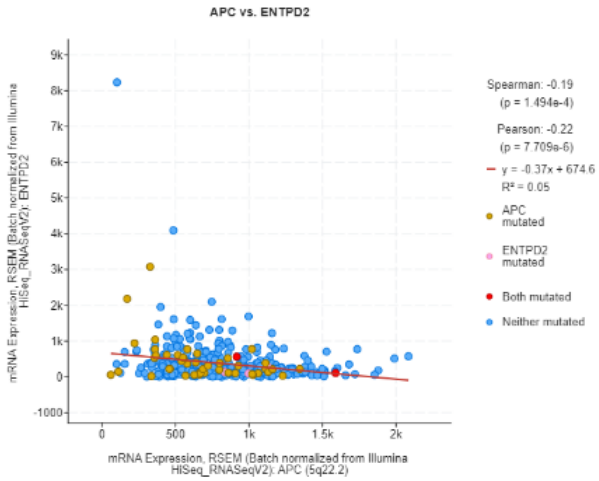

APC vs. ITPA
mRNA Expression, RSEM (Batch normalized from Illumina HiSeq_RNASeqV2): ITPA
mRNA Expression, RSEM (Batch normalized from Illumina HiSeq_RNASeqV2): APC (5q22.2)
Spearman: -0.51
(p = 2.40e-28)
Pearson: -0.47
(p = 2.70e-24)
y = -0.69x + 1572.9
R² = 0.23
APC mutated
Neither mutated

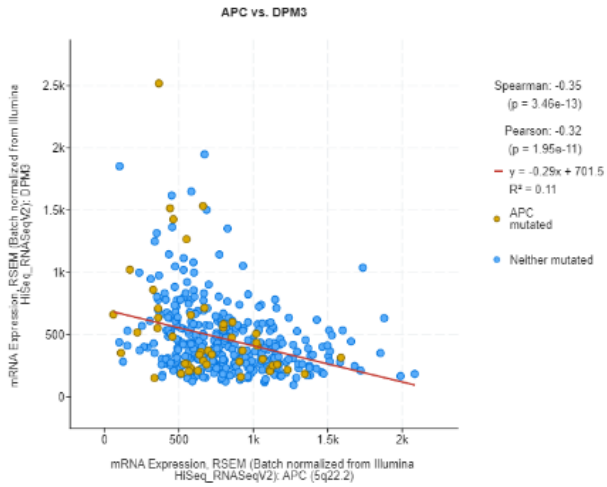

APC vs. IDI1
mRNA Expression, RSEM (Batch normalized from Illumina HiSeq_RNASeqV2): IDI1
mRNA Expression, RSEM (Batch normalized from Illumina HiSeq_RNASeqV2): APC (5q22.2)
Spearman: -0.14
(p = 4.280e-3)
Pearson: -0.17
(p = 7.750e-4)
y = -0.36x + 1692.41
R² = 0.03
APC mutated
IDI1 mutated
Neither mutated

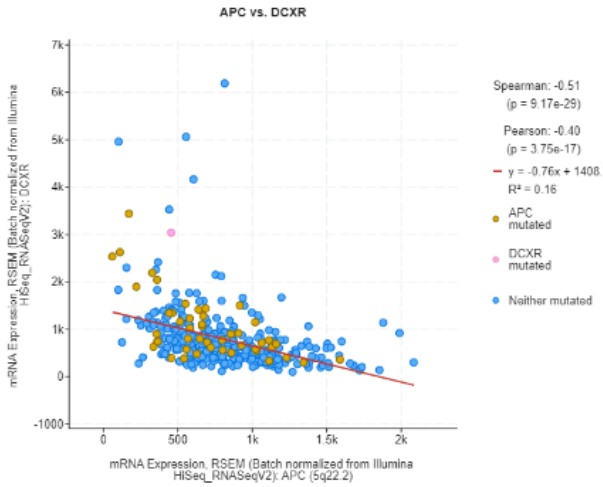

APC vs. HYAL3
mRNA Expression, RSEM (Batch normalized from Illumina HiSeq_RNASeqV2): HYAL3
mRNA Expression, RSEM (Batch normalized from Illumina HiSeq_RNASeqV2): APC (5q22.2)
Spearman: -0.21
(p = 1.309e-5)
Pearson: -0.24
(p = 1.624e-6)
y = -0.03x + 96.06
R² = 0.05
APC mutated
HYAL3 mutated
Both mutated
Neither mutated
APC vs. HSD17B7
mRNA Expression, RSEM (Batch normalized from Illumina HiSeq_RNASeqV2): HSD17B7
mRNA Expression, RSEM (Batch normalized from Illumina HiSeq_RNASeqV2): APC (5q22.2)
Spearman: -0.24
(p = 0.00000100)
Pearson: -0.19
(p = 1.060e-4)
y = -0.07x + 331.86
R² = 0.04
APC mutated
HSD17B7 mutated
Both mutated
Neither mutated
APC vs. HPSE2
mRNA Expression, RSEM (Batch normalized from Illumina HiSeq_RNASeqV2): HPSE2
mRNA Expression, RSEM (Batch normalized from Illumina HiSeq_RNASeqV2): APC (5q22.2)
Spearman: 0.19
(p = 1.672e-4)
Pearson: 0.06
(p = 0.240)
y = 0.01x + 0.77
R² = 0
APC mutated
HPSE2 mutated
Both mutated
Neither mutated
APC vs. HMGCR
mRNA Expression, RSEM (Batch normalized from Illumina HiSeq_RNASeqV2): HMGCR
mRNA Expression, RSEM (Batch normalized from Illumina HiSeq_RNASeqV2): APC (5q22.2)
Spearman: 0.15
(p = 1.760e-3)
Pearson: 0.19
(p = 1.288e-4)
y = 0.47x + 1210.99
R² = 0.04
APC mutated
HMGCR mutated
Both mutated
Neither mutated
APC vs. HGSNAT
mRNA Expression, RSEM (Batch normalized from Illumina HiSeq_RNASeqV2): HGSNAT
mRNA Expression, RSEM (Batch normalized from Illumina HiSeq_RNASeqV2): APC (5q22.2)
Spearman: 0.27
(p = 3.87e-8)
Pearson: 0.21
(p = 1.324e-5)
y = 0.47x + 1403.08
R² = 0.05
APC mutated
HGSNAT mutated
Both mutated
Neither mutated
APC vs. HDDC3
mRNA Expression, RSEM (Batch normalized from Illumina HiSeq_RNASeqV2): HDDC3
mRNA Expression, RSEM (Batch normalized from Illumina HiSeq_RNASeqV2): APC (5q22.2)
Spearman: -0.46
(p = 3.33e-22)
Pearson: -0.35
(p = 1.60e-13)
y = -0.2x + 478.37
R² = 0.13
APC mutated
HDDC3 mutated
Neither mutated

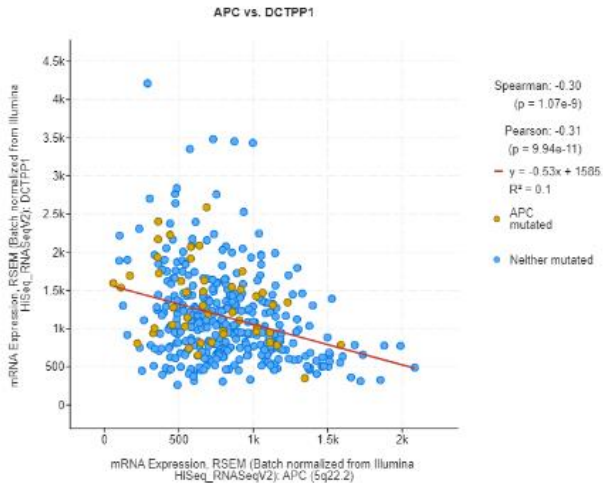

APC vs. GUK1
mRNA Expression, RSEM (Batch normalized from Illumina HiSeq_RNASeqV2): GUK1
mRNA Expression, RSEM (Batch normalized from Illumina HiSeq_RNASeqV2): APC (5q22.2)
Spearman: -0.39
(p = 2.44e-16)
Pearson: -0.36
(p = 7.85e-14)
y = -1.24x + 4028.41
R² = 0.13
APC mutated
GUK1 mutated
Both mutated
Neither mutated
APC vs. GUCY1A2
mRNA Expression, RSEM (Batch normalized from Illumina HiSeq_RNASeqV2): GUCY1A2
mRNA Expression, RSEM (Batch normalized from Illumina HiSeq_RNASeqV2): APC (5q22.2)
Spearman: 0.20
(p = 7.504e-5)
Pearson: 0.15
(p = 4.138e-3)
y = 0.01x + 12.58
R² = 0.02
APC mutated
GUCY1A2 mutated
Both mutated
Neither mutated
APC vs. GSTM5
mRNA Expression, RSEM (Batch normalized from Illumina HiSeq_RNASeqV2): GSTM5
mRNA Expression, RSEM (Batch normalized from Illumina HiSeq_RNASeqV2): APC (5q22.2)
Spearman: 0.22
(p = 4.631e-6)
Pearson: 0.21
(p = 2.476e-5)
y = 0.07x + 25.56
R² = 0.04
APC mutated
GSTM5 mutated
Neither mutated
APC vs. GSS
mRNA Expression, RSEM (Batch normalized from Illumina HiSeq_RNASeqV2): GSS
mRNA Expression, RSEM (Batch normalized from Illumina HiSeq_RNASeqV2): APC (5q22.2)
Spearman: -0.49
(p = 1.60e-25)
Pearson: -0.47
(p = 2.88e-24)
y = -0.83x + 2025.5
R² = 0.23
APC mutated
GSS mutated
Both mutated
Neither mutated
APC vs. GGT7
mRNA Expression, RSEM (Batch normalized from Illumina HiSeq_RNASeqV2): GGT7
mRNA Expression, RSEM (Batch normalized from Illumina HiSeq_RNASeqV2): APC (5q22.2)
Spearman: -0.18
(p = 2.786e-4)
Pearson: -0.19
(p = 8.182e-5)
y = -0.16x + 487.28
R² = 0.04
APC mutated
GGT7 mutated
Both mutated
Neither mutated
APC vs. GGPS1
mRNA Expression, RSEM (Batch normalized from Illumina HiSeq_RNASeqV2): GGPS1
mRNA Expression, RSEM (Batch normalized from Illumina HiSeq_RNASeqV2): APC (5q22.2)
Spearman: -0.18
(p = 2.248e-4)
Pearson: -0.18
(p = 2.787e-4)
y = -0.14x + 933.56
R² = 0.03
APC mutated
GGPS1 mutated
Both mutated
Neither mutated

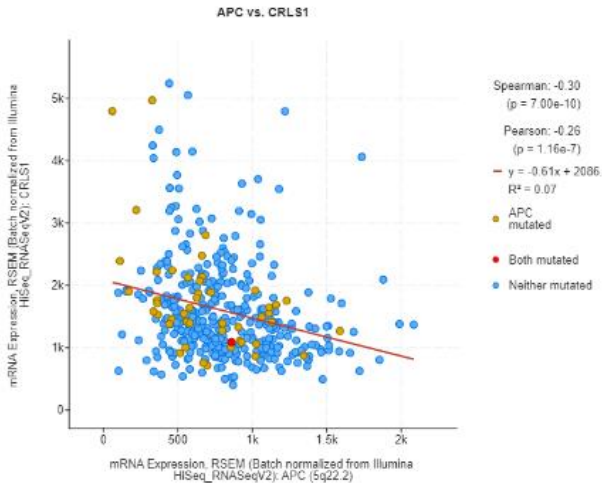

APC vs. GALNT16
mRNA Expression, RSEM (Batch normalized from Illumina HiSeq_RNASeqV2): GALNT16
mRNA Expression, RSEM (Batch normalized from Illumina HiSeq_RNASeqV2): APC (5q22.2)
Spearman: 0.22
(p = 6.293e-6)
Pearson: 0.23
(p = 2.649e-6)
y = 0.07x + 15.43
R² = 0.05
APC mutated
GALNT16 mutated
Both mutated
Neither mutated

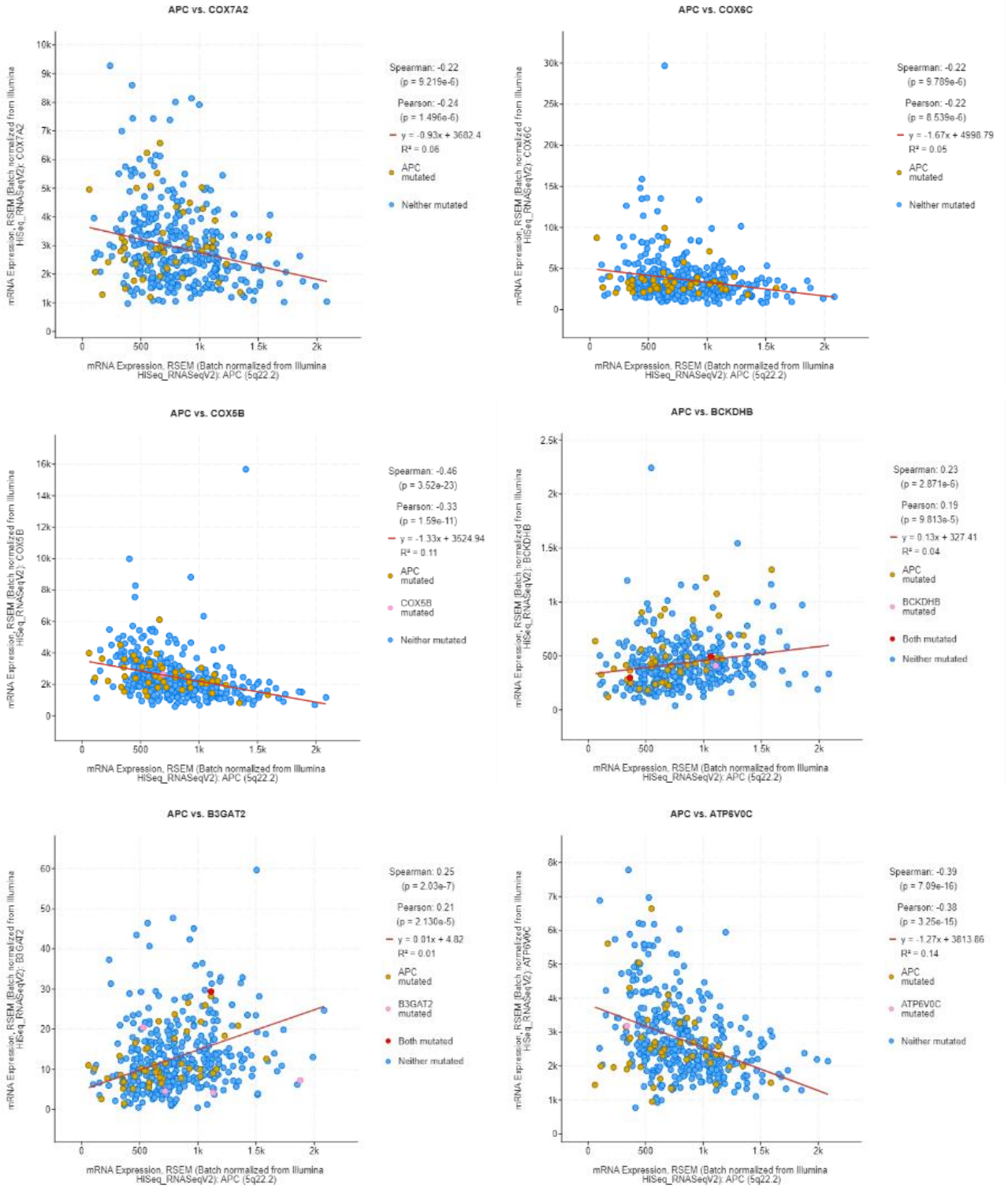

APC vs. ENTPD2
mRNA Expression, RSEM (Batch normalized from Illumina HiSeq_RNASeqV2): ENTPD2
mRNA Expression, RSEM (Batch normalized from Illumina HiSeq_RNASeqV2): APC (5q22.2)
Spearman: -0.19
(p = 1.494e-4)
Pearson: -0.22
(p = 7.709e-6)
y = -0.37x + 674.6
R² = 0.05
APC mutated
ENTPD2 mutated
Both mutated
Neither mutated

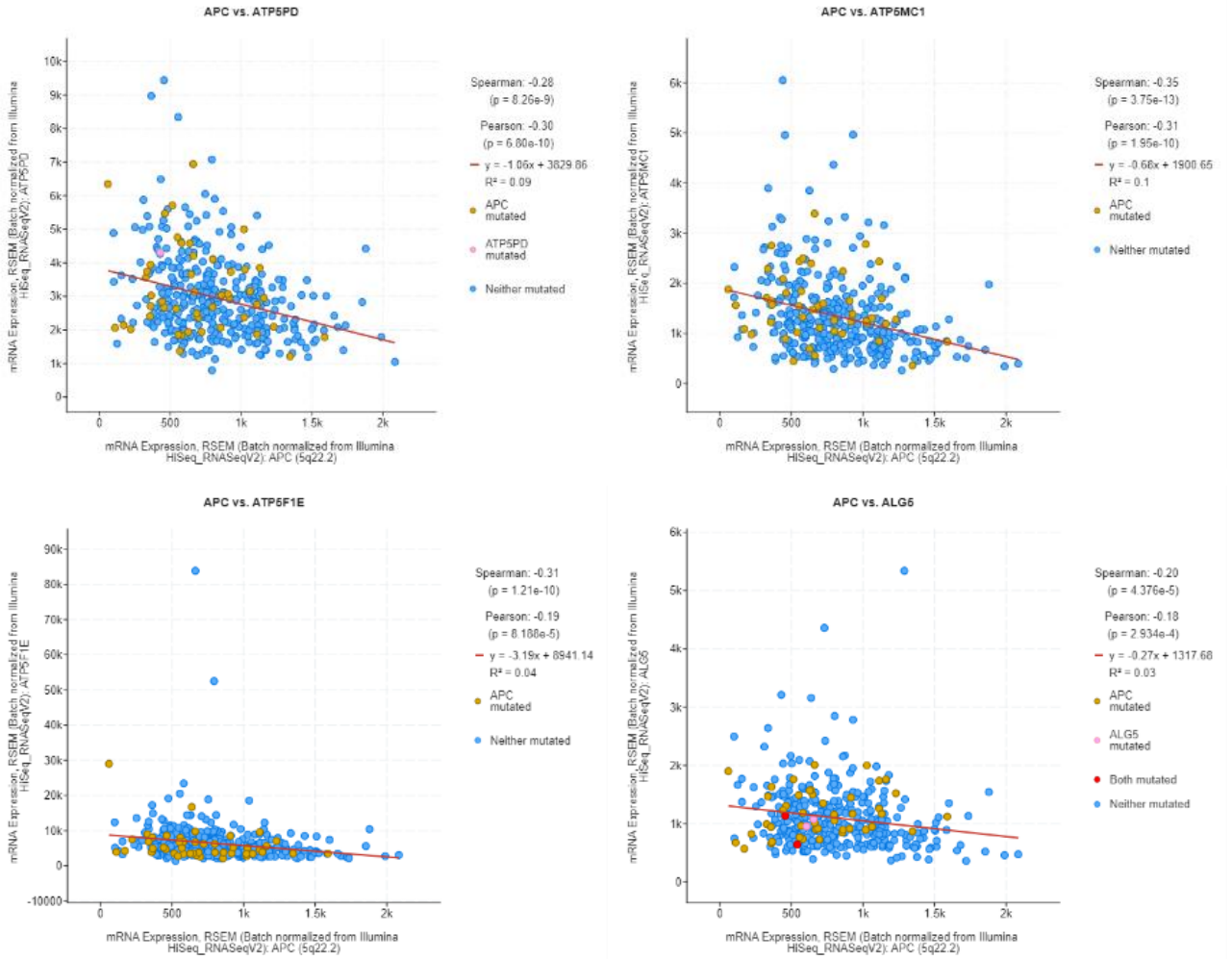

APC vs. DPM3
mRNA Expression, RSEM (Batch normalized from Illumina HiSeq_RNASeqV2): DPM3
mRNA Expression, RSEM (Batch normalized from Illumina HiSeq_RNASeqV2): APC (5q22.2)
Spearman: -0.35
(p = 3.46e-13)
Pearson: -0.32
(p = 1.95e-11)
y = -0.29x + 701.5
R² = 0.11
APC mutated
Neither mutated

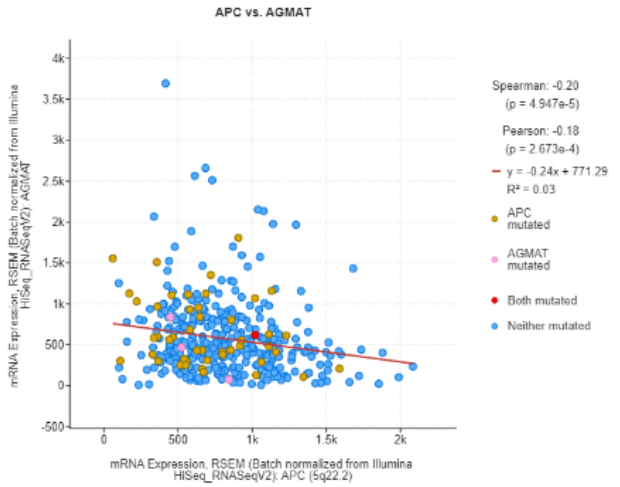

APC vs. DCXR
mRNA Expression, RSEM (Batch normalized from Illumina HiSeq_RNASeqV2): DCXR
mRNA Expression, RSEM (Batch normalized from Illumina HiSeq_RNASeqV2): APC (5q22.2)
Spearman: -0.51
(p = 9.17e-29)
Pearson: -0.40
(p = 3.75e-17)
y = -0.76x + 1408.74
R² = 0.16
APC mutated
DCXR mutated
Neither mutated

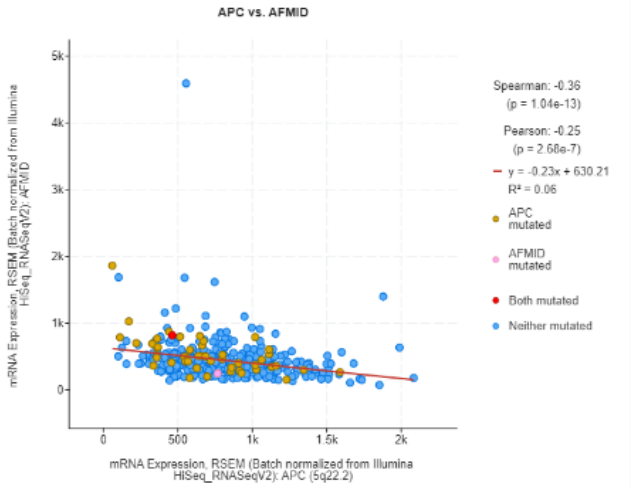

APC vs. DCTPP1
mRNA Expression, RSEM (Batch normalized from Illumina HiSeq_RNASeqV2): DCTPP1
mRNA Expression, RSEM (Batch normalized from Illumina HiSeq_RNASeqV2): APC (5q22.2)
Spearman: -0.30
(p = 1.07e-9)
Pearson: -0.31
(p = 9.94e-11)
y = -0.53x + 1585.85
R² = 0.1
APC mutated
Neither mutated

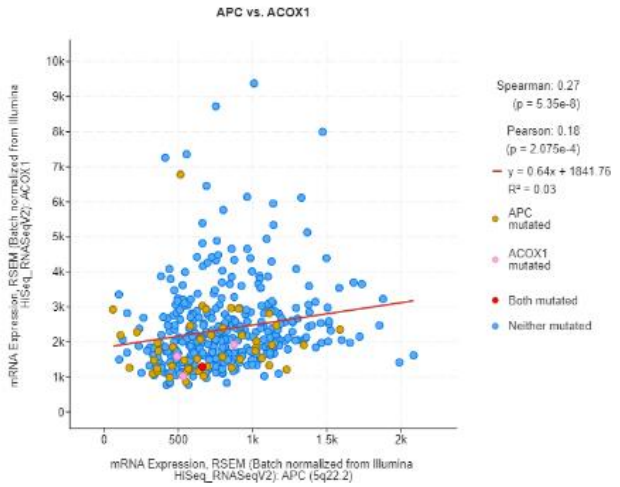

APC vs. CRLS1
mRNA Expression, RSEM (Batch normalized from Illumina HiSeq_RNASeqV2): CRLS1
mRNA Expression, RSEM (Batch normalized from Illumina HiSeq_RNASeqV2): APC (5q22.2)
Spearman: -0.30
(p = 7.00e-10)
Pearson: -0.26
(p = 1.16e-7)
y = -0.61x + 2086.71
R² = 0.07
APC mutated
Both mutated
Neither mutated


APC vs. COX7A2
mRNA Expression, RSEM (Batch normalized from Illumina HiSeq_RNASeqV2): COX7A2
mRNA Expression, RSEM (Batch normalized from Illumina HiSeq_RNASeqV2): APC (5q22.2)
Spearman: -0.22
(p = 9.219e-6)
Pearson: -0.24
(p = 1.496e-6)
y = -0.93x + 3682.4
R² = 0.06
APC mutated
Neither mutated
APC vs. COX6C
mRNA Expression, RSEM (Batch normalized from Illumina HiSeq_RNASeqV2): COX6C
mRNA Expression, RSEM (Batch normalized from Illumina HiSeq_RNASeqV2): APC (5q22.2)
Spearman: -0.22
(p = 9.789e-6)
Pearson: -0.22
(p = 8.539e-6)
y = -1.67x + 4998.79
R² = 0.05
APC mutated
Neither mutated
APC vs. COX5B
mRNA Expression, RSEM (Batch normalized from Illumina HiSeq_RNASeqV2): COX5B
mRNA Expression, RSEM (Batch normalized from Illumina HiSeq_RNASeqV2): APC (5q22.2)
Spearman: -0.46
(p = 3.52e-23)
Pearson: -0.33
(p = 1.59e-11)
y = -1.33x + 3524.94
R² = 0.11
APC mutated
COX5B mutated
Neither mutated
APC vs. BCKDHB
mRNA Expression, RSEM (Batch normalized from Illumina HiSeq_RNASeqV2): BCKDHB
mRNA Expression, RSEM (Batch normalized from Illumina HiSeq_RNASeqV2): APC (5q22.2)
Spearman: 0.23
(p = 2.871e-6)
Pearson: 0.19
(p = 9.813e-5)
y = 0.13x + 327.41
R² = 0.04
APC mutated
BCKDHB mutated
Both mutated
Neither mutated
APC vs. B3GAT2
mRNA Expression, RSEM (Batch normalized from Illumina HiSeq_RNASeqV2): B3GAT2
mRNA Expression, RSEM (Batch normalized from Illumina HiSeq_RNASeqV2): APC (5q22.2)
Spearman: 0.25
(p = 2.03e-7)
Pearson: 0.21
(p = 2.130e-5)
y = 0.01x + 4.82
R² = 0.01
APC mutated
B3GAT2 mutated
Both mutated
Neither mutated
APC vs. ATP6V0C
mRNA Expression, RSEM (Batch normalized from Illumina HiSeq_RNASeqV2): ATP6V0C
mRNA Expression, RSEM (Batch normalized from Illumina HiSeq_RNASeqV2): APC (5q22.2)
Spearman: -0.39
(p = 7.09e-16)
Pearson: -0.38
(p = 3.25e-15)
y = -1.27x + 3813.86
R² = 0.14
APC mutated
ATP6V0C mutated
Neither mutated

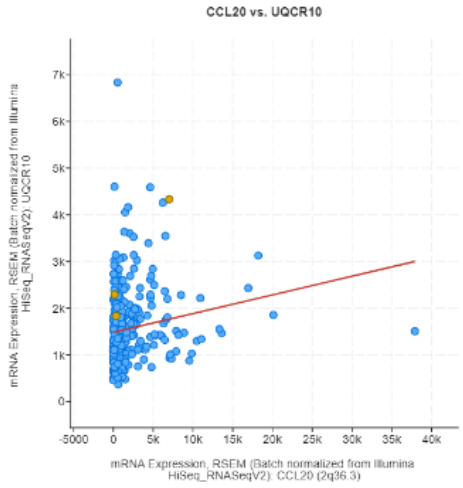

APC vs. ATP5PD
mRNA Expression, RSEM (Batch normalized from Illumina HiSeq_RNASeqV2): ATP5PD
mRNA Expression, RSEM (Batch normalized from Illumina HiSeq_RNASeqV2): APC (5q22.2)
Spearman: -0.28
(p = 8.26e-9)
Pearson: -0.30
(p = 6.60e-10)
y = -1.06x + 3829.86
R² = 0.09
APC mutated
ATP5PD mutated
Neither mutated
APC vs. ATP5MC1
mRNA Expression, RSEM (Batch normalized from Illumina HiSeq_RNASeqV2): ATP5MC1
mRNA Expression, RSEM (Batch normalized from Illumina HiSeq_RNASeqV2): APC (5q22.2)
Spearman: -0.35
(p = 3.75e-13)
Pearson: -0.31
(p = 1.95e-10)
y = -0.68x + 1900.65
R² = 0.1
APC mutated
Neither mutated
APC vs. ATP5F1E
mRNA Expression, RSEM (Batch normalized from Illumina HiSeq_RNASeqV2): ATP5F1E
mRNA Expression, RSEM (Batch normalized from Illumina HiSeq_RNASeqV2): APC (5q22.2)
Spearman: -0.31
(p = 1.21e-10)
Pearson: -0.19
(p = 8.186e-5)
y = -3.19x + 8941.14
R² = 0.04
APC mutated
Neither mutated
APC vs. ALG6
mRNA Expression, RSEM (Batch normalized from Illumina HiSeq_RNASeqV2): ALG6
mRNA Expression, RSEM (Batch normalized from Illumina HiSeq_RNASeqV2): APC (5q22.2)
Spearman: -0.20
(p = 4.376e-5)
Pearson: -0.18
(p = 2.934e-4)
y = -0.27x + 1317.68
R² = 0.03
APC mutated
ALG5 mutated
Both mutated
Neither mutated


APC vs. AGMAT
mRNA Expression, RSEM (Batch normalized from Illumina HiSeq_RNASeqV2): AGMAT
mRNA Expression, RSEM (Batch normalized from Illumina HiSeq_RNASeqV2): APC (5q22.2)
Spearman: -0.20
(p = 4.947e-5)
Pearson: -0.18
(p = 2.673e-4)
y = -0.24x + 771.29
R² = 0.03
APC mutated
AGMAT mutated
Both mutated
Neither mutated

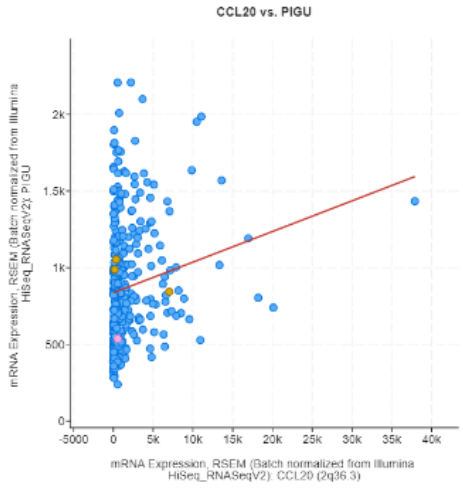

APC vs. AFMID
mRNA Expression, RSEM (Batch normalized from Illumina HiSeq_RNASeqV2): AFMID
mRNA Expression, RSEM (Batch normalized from Illumina HiSeq_RNASeqV2): APC (5q22.2)
Spearman: -0.36
(p = 1.04e-13)
Pearson: -0.25
(p = 2.66e-7)
y = -0.23x + 630.21
R² = 0.06
APC mutated
AFMID mutated
Both mutated
Neither mutated

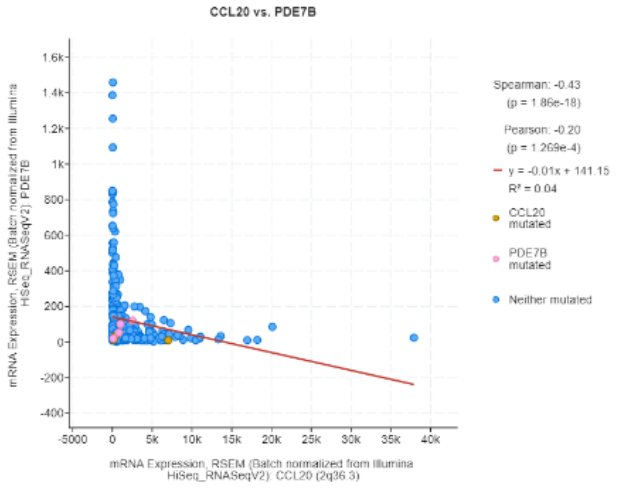

APC vs. ACOX1
mRNA Expression, RSEM (Batch normalized from Illumina HiSeq_RNASeqV2): ACOX1
mRNA Expression, RSEM (Batch normalized from Illumina HiSeq_RNASeqV2): APC (5q22.2)
Spearman: 0.27
(p = 5.35e-8)
Pearson: 0.18
(p = 2.075e-4)
y = 0.64x + 1841.76
R² = 0.03
APC mutated
ACOX1 mutated
Both mutated
Neither mutated

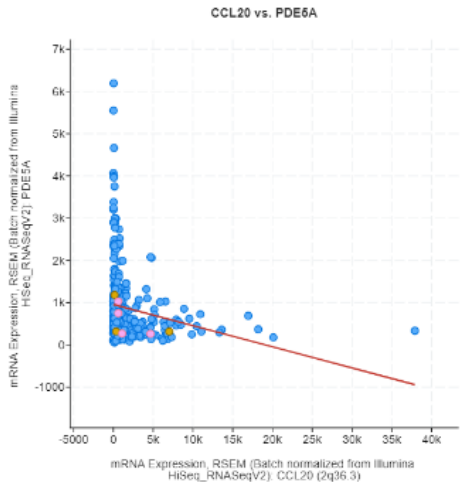
CCL20

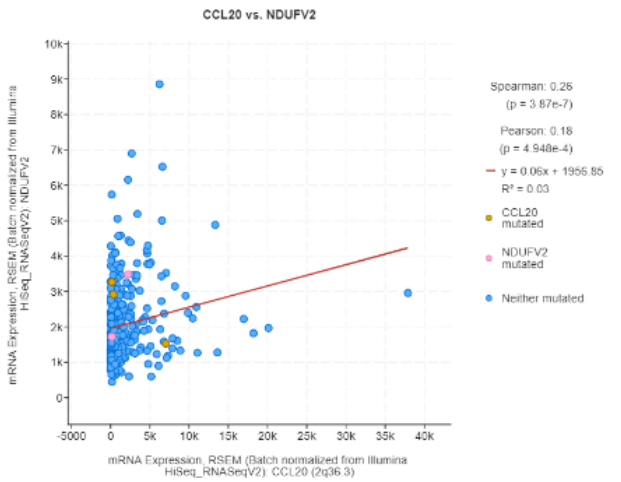

CCL20 vs. UQCR10
mRNA Expression, RSEM (Batch normalized from Illumina HiSeq_RNASeqV2): UQCR10
mRNA Expression, RSEM (Batch normalized from Illumina HiSeq_RNASeqV2): CCL20 (2q36.3)
Spearman: 0.29
(p = 1.53e-8)
Pearson: 0.16
(p = 2.250e-3)
y = 0.04x + 1485.14
R² = 0.02
CCL20 mutated
Neither mutated

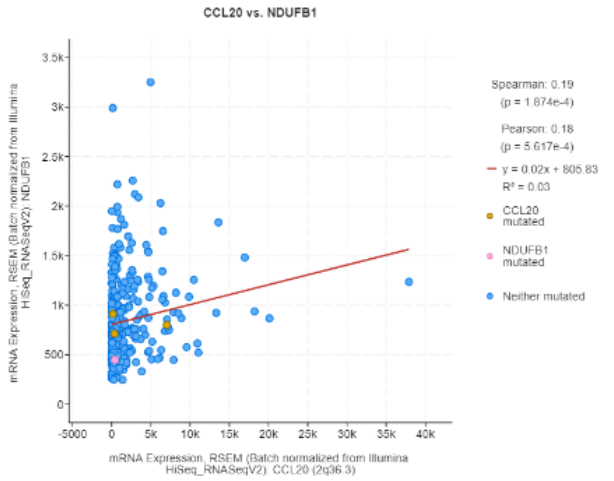

CCL20 vs. TGDS
mRNA Expression, RSEM (Batch normalized from Illumina HiSeq_RNASeqV2): TGDS
mRNA Expression, RSEM (Batch normalized from Illumina HiSeq_RNASeqV2): CCL20 (2q36.3)
Spearman: 0.32
(p = 4.06e-10)
Pearson: 0.34
(p = 1.52e-11)
y = 0.02x + 354.65
R² = 0.11
CCL20 mutated
TGDS mutated
Neither mutated

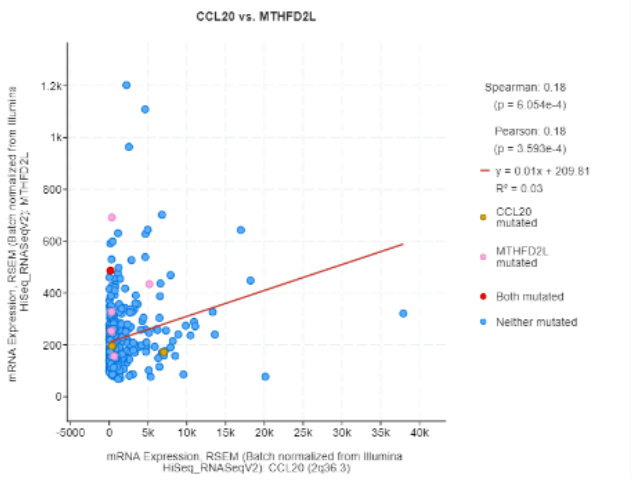

CCL20 vs. PIGU
mRNA Expression, RSEM (Batch normalized from Illumina HiSeq_RNASeqV2): PIGU
mRNA Expression, RSEM (Batch normalized from Illumina HiSeq_RNASeqV2): CCL20 (2q36.3)
Spearman: 0.29
(p = 1.05e-8)
Pearson: 0.20
(p = 1.333e-4)
y = 0.02x + 836.36
R² = 0.04
CCL20 mutated
PIGU mutated
Neither mutated

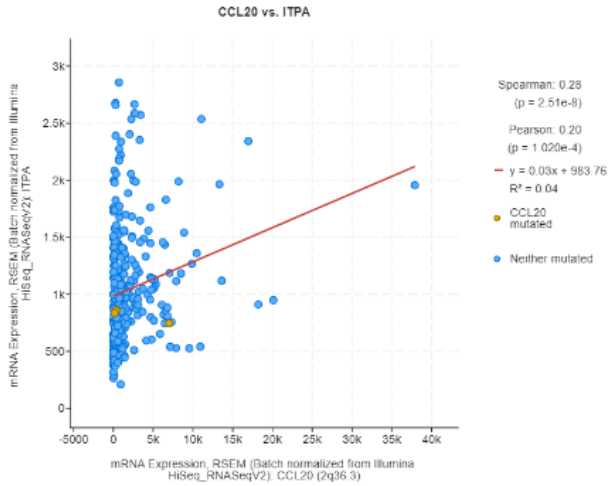

CCL20 vs. PDE7B
mRNA Expression, RSEM (Batch normalized from Illumina HiSeq_RNASeqV2): PDE7B
mRNA Expression, RSEM (Batch normalized from Illumina HiSeq_RNASeqV2): CCL20 (2q36.3)
Spearman: -0.43
(p = 1.86e-18)
Pearson: -0.20
(p = 1.269e-4)
y = -0.01x + 141.15
R² = 0.04
CCL20 mutated
PDE7B mutated
Neither mutated

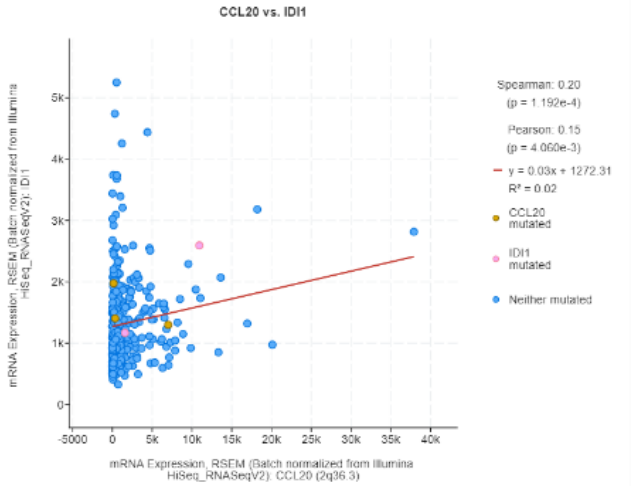

CCL20 vs. PDE5A
mRNA Expression, RSEM (Batch normalized from Illumina HiSeq_RNASeqV2): PDE5A
mRNA Expression, RSEM (Batch normalized from Illumina HiSeq_RNASeqV2): CCL20 (2q36.3)
Spearman: -0.30
(p = 2.83e-9)
Pearson: -0.20
(p = 8.879e-5)
y = -0.05x + 955.53
R² = 0.04
CCL20 mutated
PDE5A mutated
Neither mutated

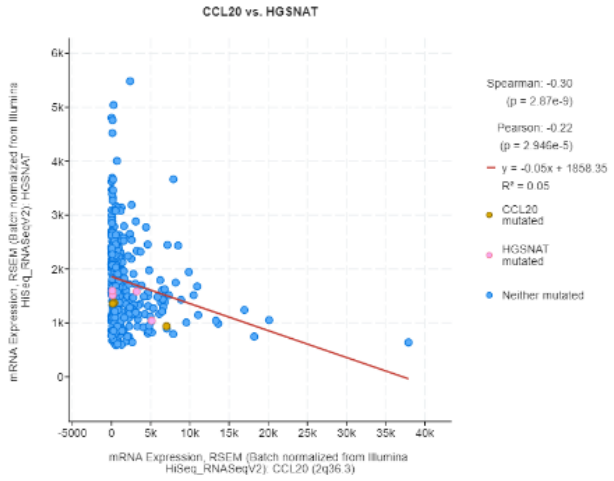

CCL20 vs. NDUFV2
mRNA Expression, RSEM (Batch normalized from Illumina HiSeq_RNASeqV2): NDUFV2
mRNA Expression, RSEM (Batch normalized from Illumina HiSeq_RNASeqV2): CCL20 (2q36.3)
Spearman: 0.26
(p = 3.87e-7)
Pearson: 0.18
(p = 4.948e-4)
y = 0.06x + 1956.85
R² = 0.03
CCL20 mutated
NDUFV2 mutated
Neither mutated

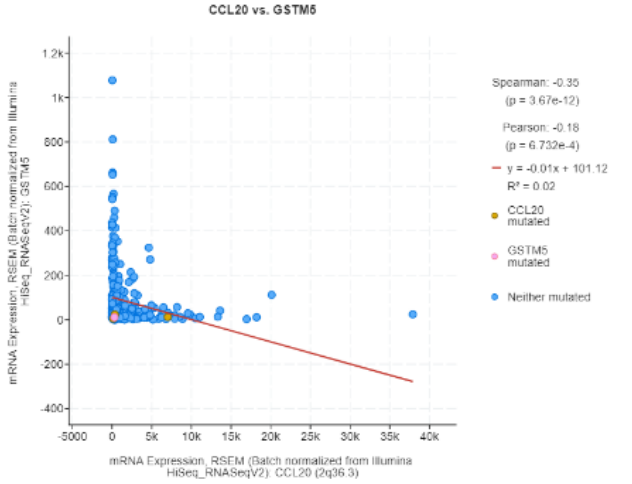

CCL20 vs. NDUFB1
mRNA Expression, RSEM (Batch normalized from Illumina HiSeq_RNASeqV2): NDUFB1
mRNA Expression, RSEM (Batch normalized from Illumina HiSeq_RNASeqV2): CCL20 (2q36.3)
Spearman: 0.19
(p = 1.874e-4)
Pearson: 0.18
(p = 5.617e-4)
y = 0.02x + 805.83
R² = 0.03
CCL20 mutated
NDUFB1 mutated
Neither mutated

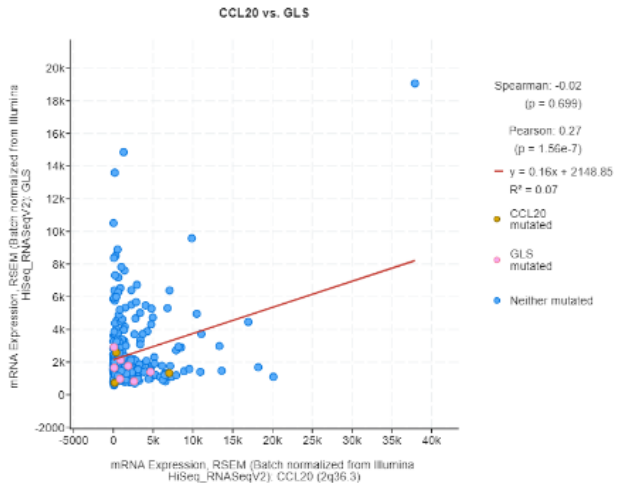

CCL20 vs. MTHFD2L
mRNA Expression, RSEM (Batch normalized from Illumina HiSeq_RNASeqV2): MTHFD2L
mRNA Expression, RSEM (Batch normalized from Illumina HiSeq_RNASeqV2): CCL20 (2q36.3)
Spearman: 0.18
(p = 6.054e-4)
Pearson: 0.18
(p = 3.593e-4)
y = 0.01x + 209.81
R² = 0.03
CCL20 mutated
MTHFD2L mutated
Both mutated
Neither mutated

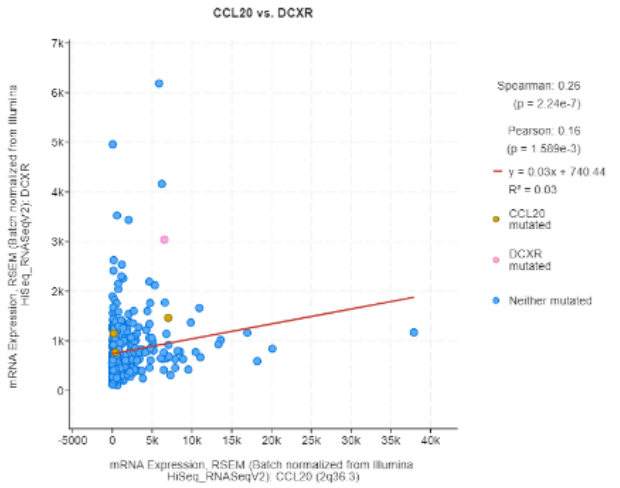

CCL20 vs. ITPA
mRNA Expression, RSEM (Batch normalized from Illumina HiSeq_RNASeqV2): ITPA
mRNA Expression, RSEM (Batch normalized from Illumina HiSeq_RNASeqV2): CCL20 (2q36.3)
Spearman: 0.28
(p = 2.51e-8)
Pearson: 0.20
(p = 1.020e-4)
y = 0.03x + 983.76
R² = 0.04
CCL20 mutated
Neither mutated

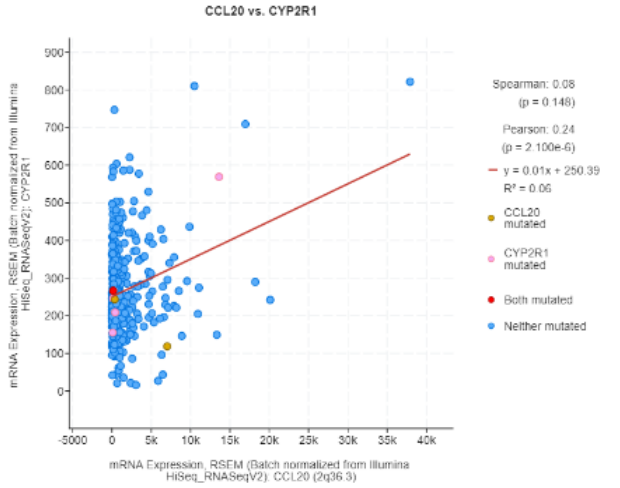

CCL20 vs. IDI1
mRNA Expression, RSEM (Batch normalized from Illumina HiSeq_RNASeqV2): IDI1
mRNA Expression, RSEM (Batch normalized from Illumina HiSeq_RNASeqV2): CCL20 (2q36.3)
Spearman: 0.20
(p = 1.192e-4)
Pearson: 0.15
(p = 4.060e-3)
y = 0.03x + 1272.31
R² = 0.02
CCL20 mutated
IDI1 mutated
Neither mutated

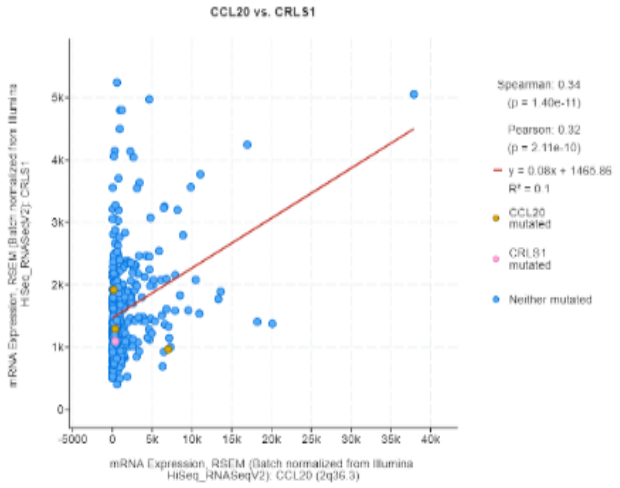

CCL20 vs. HGSNAT
mRNA Expression, RSEM (Batch normalized from Illumina HiSeq_RNASeqV2): HGSNAT
mRNA Expression, RSEM (Batch normalized from Illumina HiSeq_RNASeqV2): CCL20 (2q36.3)
Spearman: -0.30
(p = 2.87e-9)
Pearson: -0.22
(p = 2.946e-5)
y = -0.05x + 1858.35
R² = 0.05
CCL20 mutated
HGSNAT mutated
Neither mutated

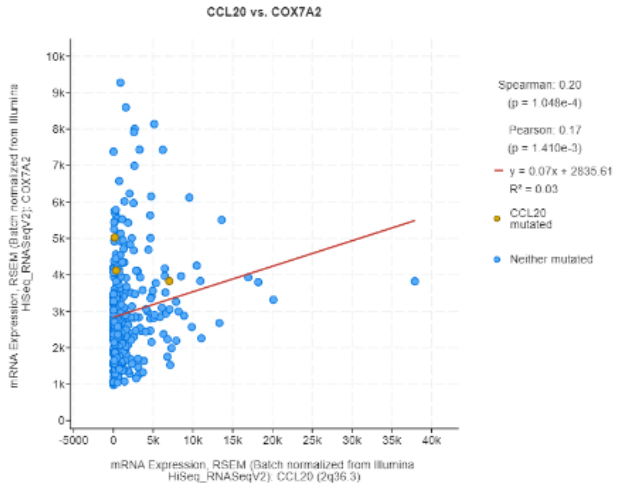

CCL20 vs. GSTM5
mRNA Expression, RSEM (Batch normalized from Illumina HiSeq_RNASeqV2): GSTM5
mRNA Expression, RSEM (Batch normalized from Illumina HiSeq_RNASeqV2): CCL20 (2q36.3)
Spearman: -0.35
(p = 3.67e-12)
Pearson: -0.18
(p = 6.732e-4)
y = -0.01x + 101.12
R² = 0.02
CCL20 mutated
GSTM5 mutated
Neither mutated

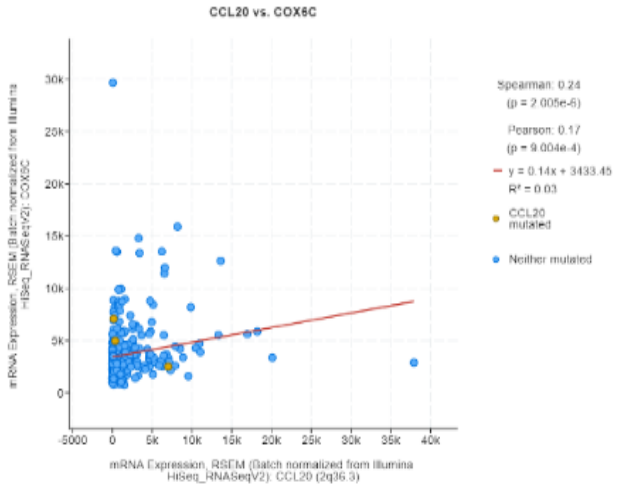

CCL20 vs. GLS
mRNA Expression, RSEM (Batch normalized from Illumina HiSeq_RNASeqV2): GLS
mRNA Expression, RSEM (Batch normalized from Illumina HiSeq_RNASeqV2): CCL20 (2q36.3)
Spearman: -0.02
(p = 0.699)
Pearson: 0.27
(p = 1.56e-7)
y = 0.16x + 2148.85
R² = 0.07
CCL20 mutated
GLS mutated
Neither mutated

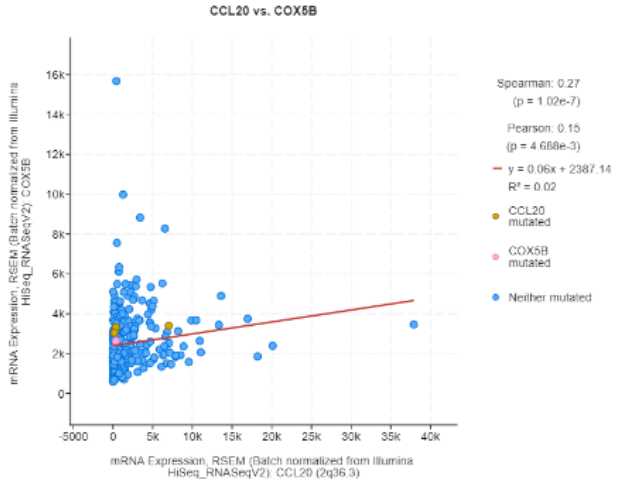

CCL20 vs. DCXR
mRNA Expression, RSEM (Batch normalized from Illumina HiSeq_RNASeqV2): DCXR
mRNA Expression, RSEM (Batch normalized from Illumina HiSeq_RNASeqV2): CCL20 (2q36.3)
Spearman: 0.25
(p = 2.24e-7)
Pearson: 0.16
(p = 1.589e-3)
y = 0.03x + 740.44
R² = 0.03
CCL20 mutated
DCXR mutated
Neither mutated

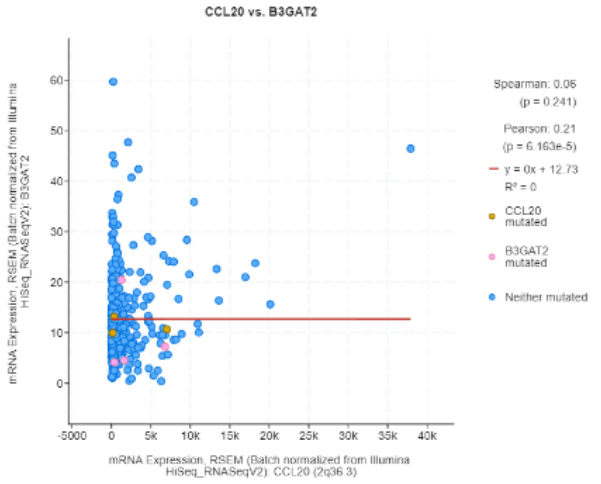

CCL20 vs. CYP2R1
mRNA Expression, RSEM (Batch normalized from Illumina HiSeq_RNASeqV2): CYP2R1
mRNA Expression, RSEM (Batch normalized from Illumina HiSeq_RNASeqV2): CCL20 (2q36.3)
Spearman: 0.08
(p = 0.148)
Pearson: 0.24
(p = 2.100e-6)
y = 0.01x + 250.39
R² = 0.06
CCL20 mutated
CYP2R1 mutated
Both mutated
Neither mutated

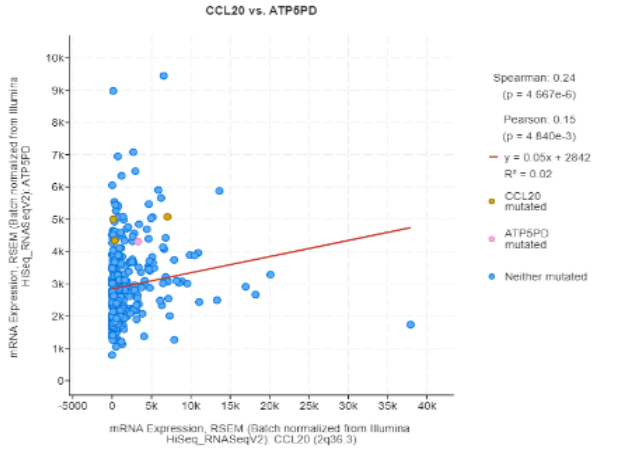

CCL20 vs. CRLS1
mRNA Expression, RSEM (Batch normalized from Illumina HiSeq_RNASeqV2): CRLS1
mRNA Expression, RSEM (Batch normalized from Illumina HiSeq_RNASeqV2): CCL20 (2q36.3)
Spearman: 0.34
(p = 1.40e-11)
Pearson: 0.32
(p = 2.11e-10)
y = 0.08x + 1465.86
R² = 0.1
CCL20 mutated
CRLS1 mutated
Neither mutated

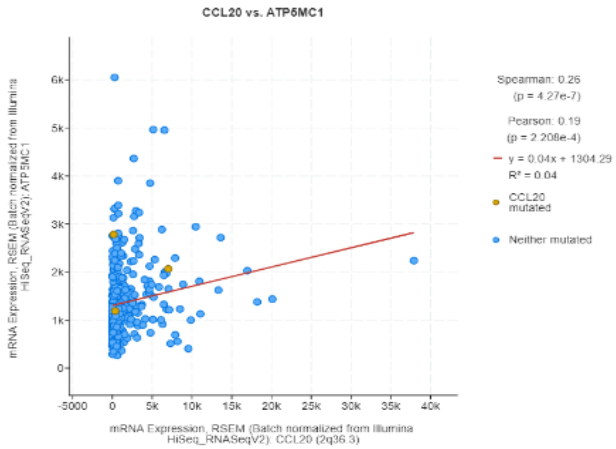

CCL20 vs. COX7A2
mRNA Expression, RSEM (Batch normalized from Illumina HiSeq_RNASeqV2): COX7A2
mRNA Expression, RSEM (Batch normalized from Illumina HiSeq_RNASeqV2): CCL20 (2q36.3)
Spearman: 0.20
(p = 1.048e-4)
Pearson: 0.17
(p = 1.410e-3)
y = 0.07x + 2835.61
R² = 0.03
CCL20 mutated
Neither mutated

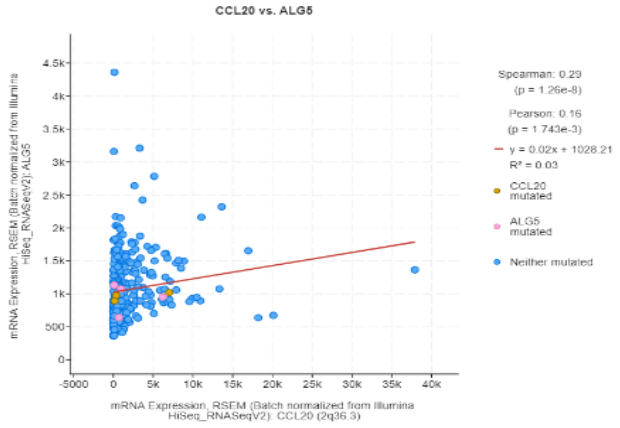

CCL20 vs. COX6C
mRNA Expression, RSEM (Batch normalized from Illumina HiSeq_RNASeqV2): COX6C
mRNA Expression, RSEM (Batch normalized from Illumina HiSeq_RNASeqV2): CCL20 (2q36.3)
Spearman: 0.24
(p = 2.005e-6)
Pearson: 0.17
(p = 9.004e-4)
y = 0.14x + 3433.45
R² = 0.03
CCL20 mutated
Neither mutated

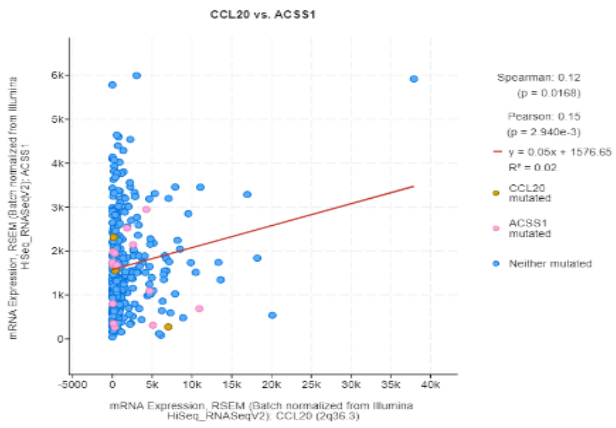

CCL20 vs. COX5B
mRNA Expression, RSEM (Batch normalized from Illumina HiSeq_RNASeqV2): COX5B
mRNA Expression, RSEM (Batch normalized from Illumina HiSeq_RNASeqV2): CCL20 (2q36.3)
Spearman: 0.27
(p = 1.02e-7)
Pearson: 0.15
(p = 4.688e-3)
y = 0.06x + 2387.14
R² = 0.02
CCL20 mutated
COX5B mutated
Neither mutated

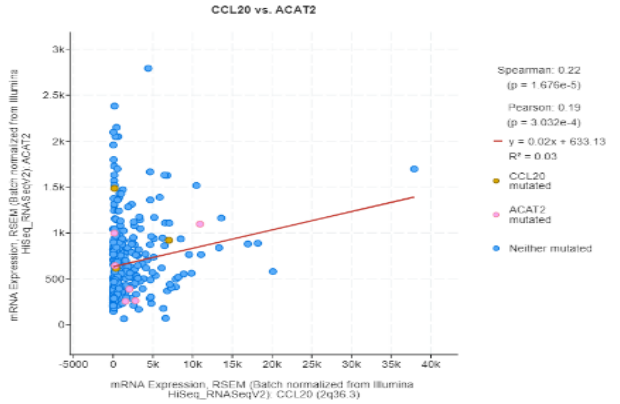

CCL20 vs. B3GAT2
mRNA Expression, RSEM (Batch normalized from Illumina HiSeq_RNASeqV2): B3GAT2
mRNA Expression, RSEM (Batch normalized from Illumina HiSeq_RNASeqV2): CCL20 (2q36.3)
Spearman: 0.05
(p = 0.241)
Pearson: 0.21
(p = 6.163e-5)
y = 0x + 12.73
R² = 0
CCL20 mutated
B3GAT2 mutated
Neither mutated


CCL20 vs. ATP5PD
mRNA Expression, RSEM (Batch normalized from Illumina HiSeq_RNASeqV2): ATP5PD
mRNA Expression, RSEM (Batch normalized from Illumina HiSeq_RNASeqV2): CCL20 (2q36.3)
Spearman: 0.24
(p = 4.667e-6)
Pearson: 0.15
(p = 4.840e-3)
y = 0.05x + 2842
R² = 0.02
CCL20 mutated
ATP5PD mutated
Neither mutated

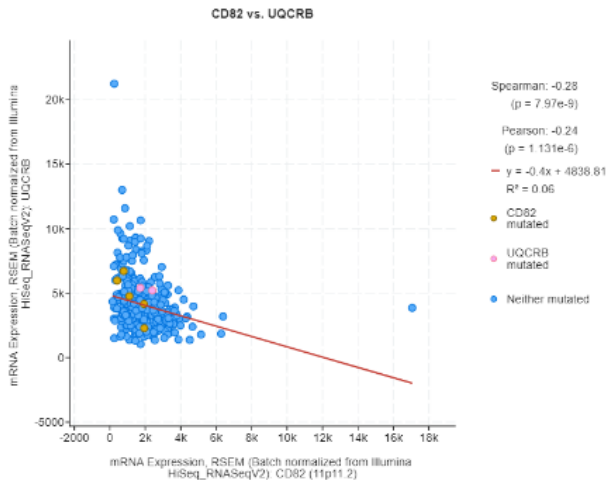

CCL20 vs. ATP6MC1
mRNA Expression, RSEM (Batch normalized from Illumina HiSeq_RNASeqV2): ATP6MC1
mRNA Expression, RSEM (Batch normalized from Illumina HiSeq_RNASeqV2): CCL20 (2q36.3)
Spearman: 0.26
(p = 4.27e-7)
Pearson: 0.19
(p = 2.208e-4)
y = 0.04x + 1304.29
R² = 0.04
CCL20 mutated
Neither mutated


CCL20 vs. ALG5
mRNA Expression, RSEM (Batch normalized from Illumina HiSeq_RNASeqV2): ALG5
mRNA Expression, RSEM (Batch normalized from Illumina HiSeq_RNASeqV2): CCL20 (2q36.3)
Spearman: 0.29
(p = 1.26e-8)
Pearson: 0.16
(p = 1.743e-3)
y = 0.02x + 1028.21
R² = 0.03
CCL20 mutated
ALG5 mutated
Neither mutated

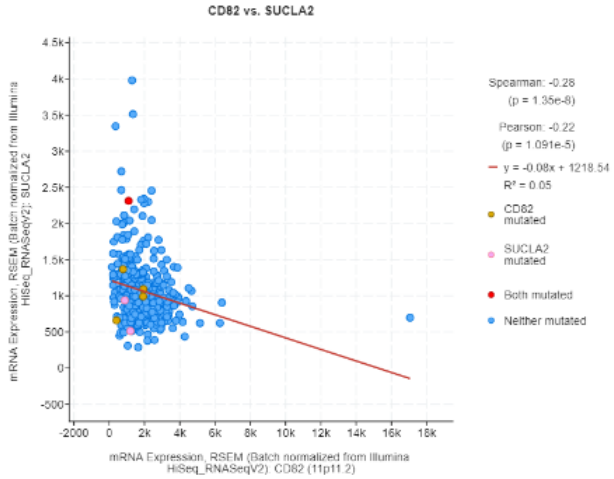

CCL20 vs. ACSS1
mRNA Expression, RSEM (Batch normalized from Illumina HiSeq_RNASeqV2): ACSS1
mRNA Expression, RSEM (Batch normalized from Illumina HiSeq_RNASeqV2): CCL20 (2q36.3)
Spearman: 0.12
(p = 0.0168)
Pearson: 0.15
(p = 2.940e-3)
y = 0.05x + 1576.65
R² = 0.02
CCL20 mutated
ACSS1 mutated
Neither mutated

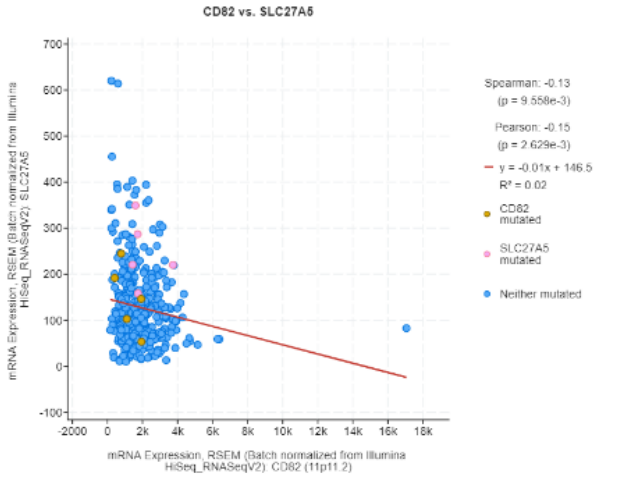

CCL20 vs. ACAT2
mRNA Expression, RSEM (Batch normalized from Illumina HiSeq_RNASeqV2): ACAT2
mRNA Expression, RSEM (Batch normalized from Illumina HiSeq_RNASeqV2): CCL20 (2q36.3)
Spearman: 0.22
(p = 1.676e-5)
Pearson: 0.19
(p = 3.032e-4)
y = 0.02x + 633.13
R² = 0.03
CCL20 mutated
ACAT2 mutated
Neither mutated

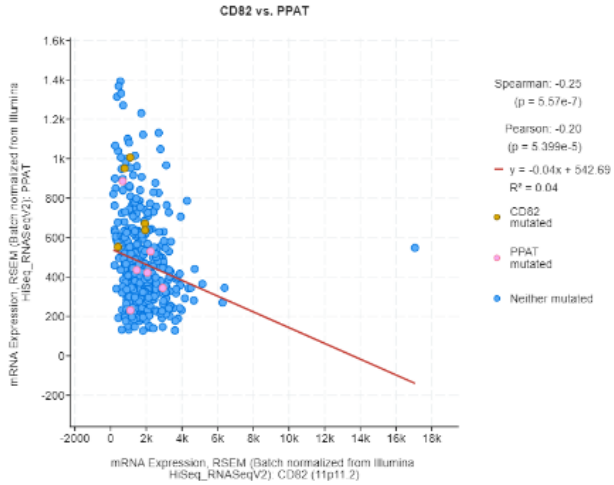
CD82

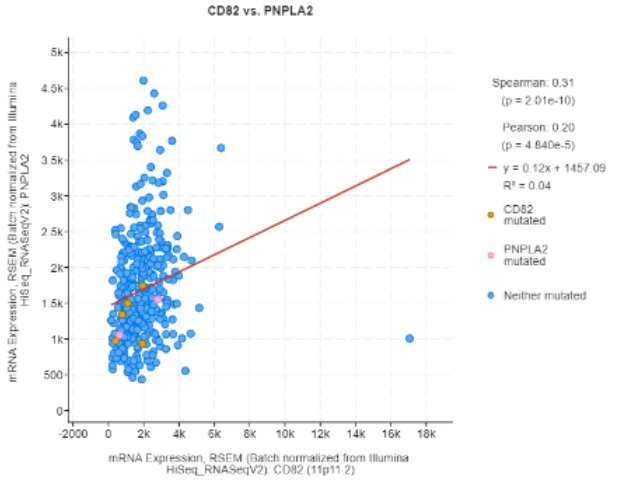

CD82 vs. UQCRB
mRNA Expression, RSEM (Batch normalized from Illumina HiSeq_RNASeqV2): UQCRB
mRNA Expression, RSEM (Batch normalized from Illumina HiSeq_RNASeqV2): CD82 (11p11.2)
Spearman: -0.28
(p = 7.97e-9)
Pearson: -0.24
(p = 1.131e-6)
y = -0.4x + 4838.81
R² = 0.06
CD82 mutated
UQCRB mutated
Neither mutated

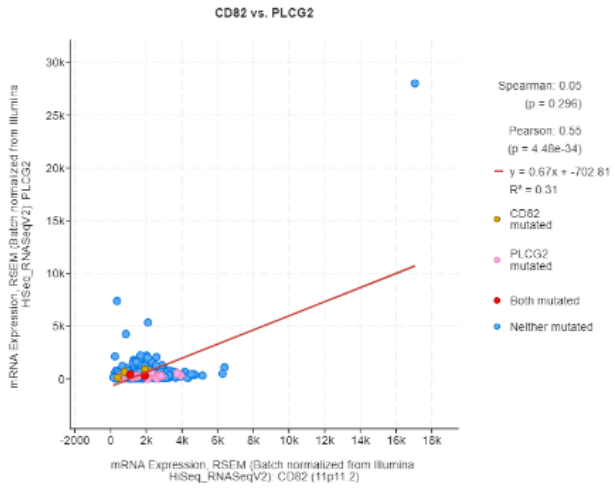

CD82 vs. TGDS
mRNA Expression, RSEM (Batch normalized from Illumina HiSeq_RNASeqV2): TGDS
mRNA Expression, RSEM (Batch normalized from Illumina HiSeq_RNASeqV2): CD82 (11p11.2)
Spearman: -0.23
(p = 2.502e-6)
Pearson: -0.21
(p = 1.983e-5)
y = -0.03x + 452.61
R² = 0.04
CD82 mutated
TGDS mutated
Neither mutated

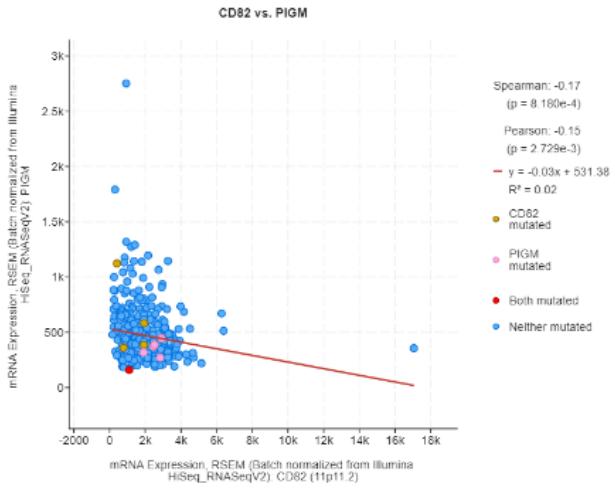

CD82 vs. SUCLA2
mRNA Expression, RSEM (Batch normalized from Illumina HiSeq_RNASeqV2): SUCLA2
mRNA Expression, RSEM (Batch normalized from Illumina HiSeq_RNASeqV2): CD82 (11p11.2)
Spearman: -0.28
(p = 1.35e-8)
Pearson: -0.22
(p = 1.091e-5)
y = -0.08x + 1218.54
R² = 0.05
CD82 mutated
SUCLA2 mutated
Both mutated
Neither mutated

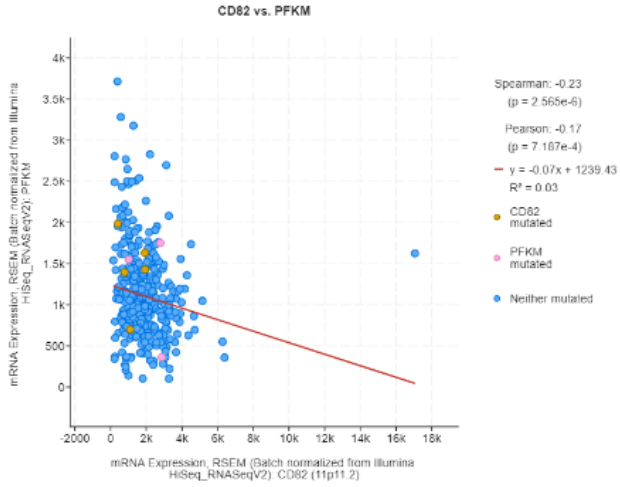

CD82 vs. SLC27A5
mRNA Expression, RSEM (Batch normalized from Illumina HiSeq_RNASeqV2): SLC27A5
mRNA Expression, RSEM (Batch normalized from Illumina HiSeq_RNASeqV2): CD82 (11p11.2)
Spearman: -0.13
(p = 9.558e-3)
Pearson: -0.15
(p = 2.629e-3)
y = -0.01x + 146.5
R² = 0.02
CD82 mutated
SLC27A5 mutated
Neither mutated

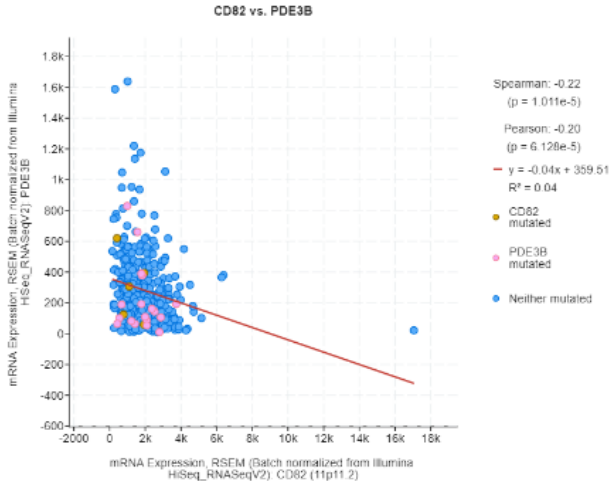

CD82 vs. PPAT
mRNA Expression, RSEM (Batch normalized from Illumina HiSeq_RNASeqV2): PPAT
mRNA Expression, RSEM (Batch normalized from Illumina HiSeq_RNASeqV2): CD82 (11p11.2)
Spearman: -0.25
(p = 5.57e-7)
Pearson: -0.20
(p = 5.399e-5)
y = -0.04x + 542.69
R² = 0.04
CD82 mutated
PPAT mutated
Neither mutated

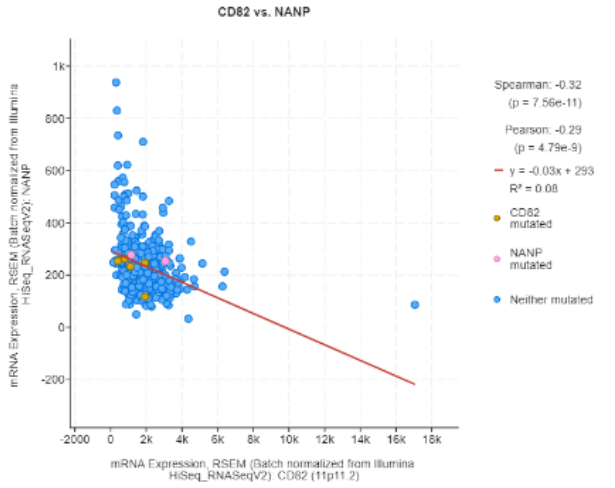

CD82 vs. PNPLA2
mRNA Expression, RSEM (Batch normalized from Illumina HiSeq_RNASeqV2): PNPLA2
mRNA Expression, RSEM (Batch normalized from Illumina HiSeq_RNASeqV2): CD82 (11p11.2)
Spearman: 0.31
(p = 2.01e-10)
Pearson: 0.20
(p = 4.840e-5)
y = 0.12x + 1457.09
R² = 0.04
CD82 mutated
PNPLA2 mutated
Neither mutated

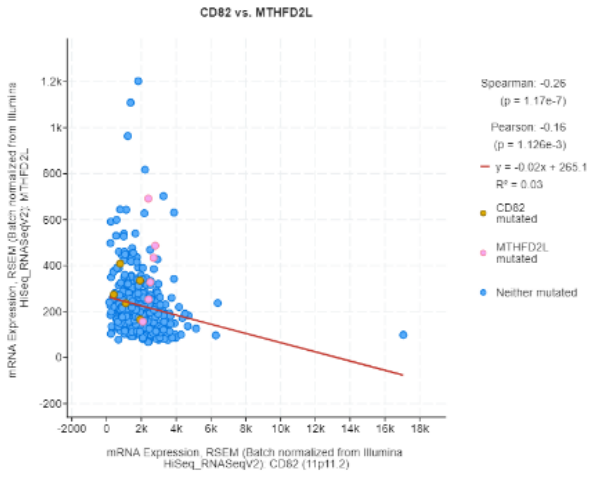

CD82 vs. PLCG2
mRNA Expression, RSEM (Batch normalized from Illumina HiSeq_RNASeqV2): PLCG2
mRNA Expression, RSEM (Batch normalized from Illumina HiSeq_RNASeqV2): CD82 (11p11.2)
Spearman: 0.05
(p = 0.296)
Pearson: 0.55
(p = 4.46e-34)
y = 0.67x + -702.81
R² = 0.31
CD82 mutated
PLCG2 mutated
Both mutated
Neither mutated

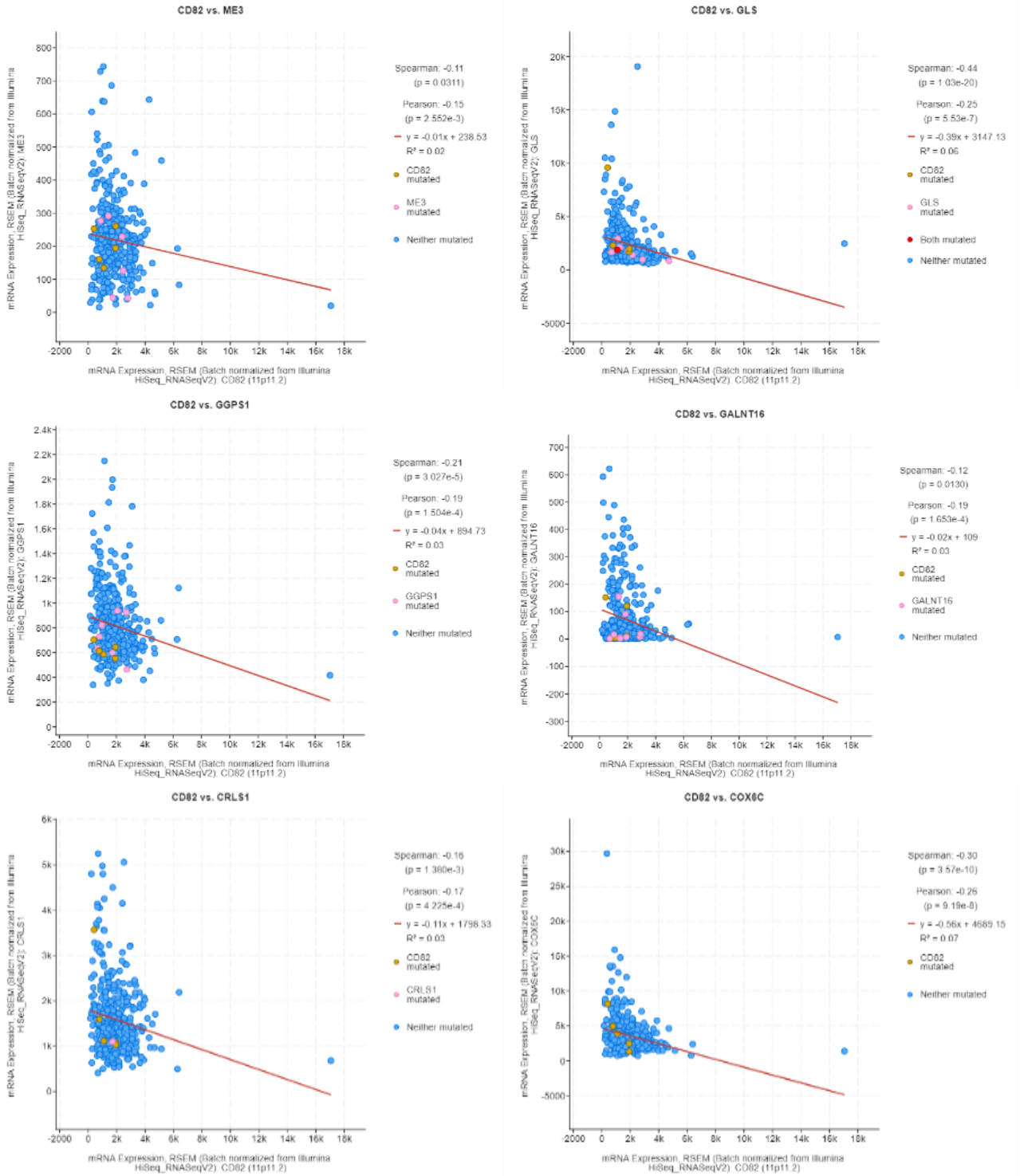

CD82 vs. PIGM
mRNA Expression, RSEM (Batch normalized from Illumina HiSeq_RNASeqV2): PIGM
mRNA Expression, RSEM (Batch normalized from Illumina HiSeq_RNASeqV2): CD82 (11p11.2)
Spearman: -0.17
(p = 8.180e-4)
Pearson: -0.15
(p = 2.729e-3)
y = -0.03x + 531.38
R² = 0.02
CD82 mutated
PIGM mutated
Both mutated
Neither mutated

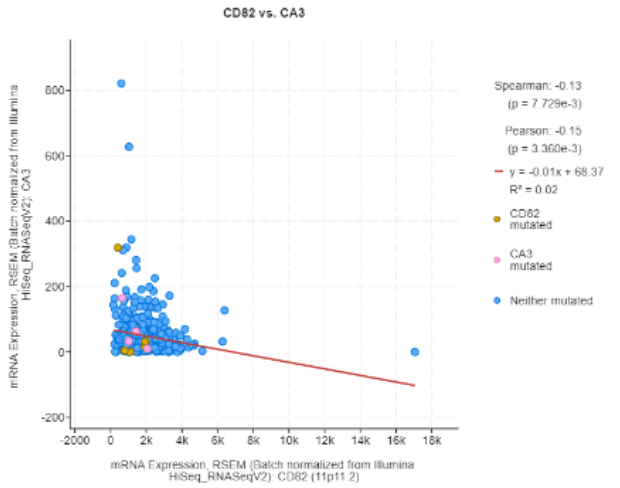

CD82 vs. PFKM
mRNA Expression, RSEM (Batch normalized from Illumina HiSeq_RNASeqV2): PFKM
mRNA Expression, RSEM (Batch normalized from Illumina HiSeq_RNASeqV2): CD82 (11p11.2)
Spearman: -0.23
(p = 2.565e-6)
Pearson: -0.17
(p = 7.167e-4)
y = -0.07x + 1239.43
R² = 0.03
CD82 mutated
PFKM mutated
Neither mutated

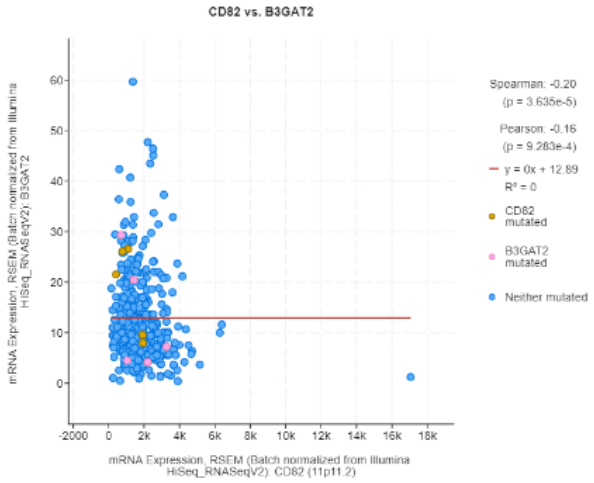

CD82 vs. PDE3B
mRNA Expression, RSEM (Batch normalized from Illumina HiSeq_RNASeqV2): PDE3B
mRNA Expression, RSEM (Batch normalized from Illumina HiSeq_RNASeqV2): CD82 (11p11.2)
Spearman: -0.22
(p = 1.011e-5)
Pearson: -0.20
(p = 6.128e-5)
y = -0.04x + 359.51
R² = 0.04
CD82 mutated
PDE3B mutated
Neither mutated

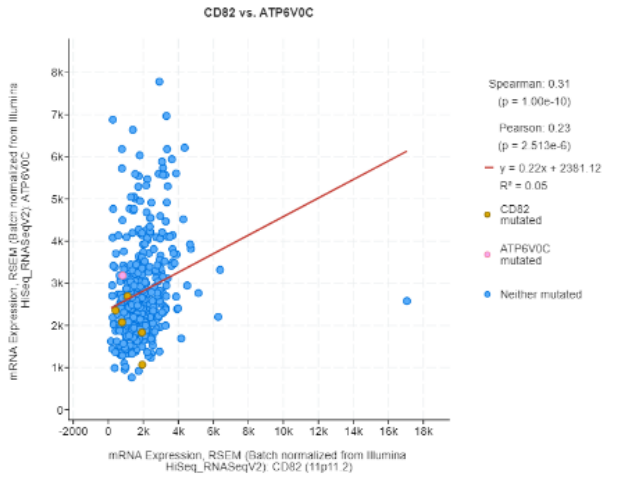

CD82 vs. NANP
mRNA Expression, RSEM (Batch normalized from Illumina HiSeq_RNASeqV2): NANP
mRNA Expression, RSEM (Batch normalized from Illumina HiSeq_RNASeqV2): CD82 (11p11.2)
Spearman: -0.32
(p = 7.56e-11)
Pearson: -0.29
(p = 4.79e-9)
y = -0.03x + 293
R² = 0.08
CD82 mutated
NANP mutated
Neither mutated

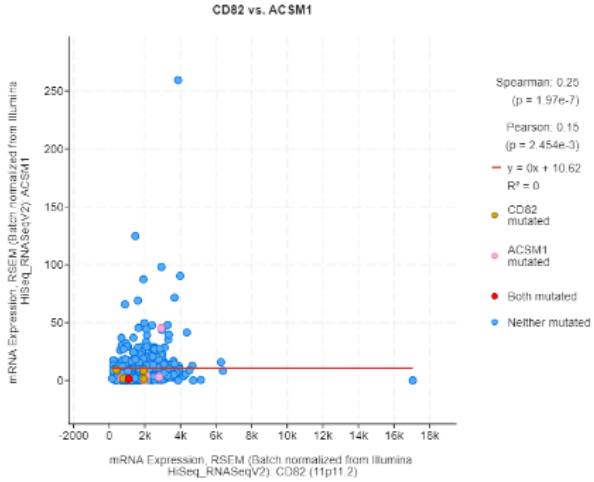

CD82 vs. MTHFD2L
mRNA Expression, RSEM (Batch normalized from Illumina HiSeq_RNASeqV2): MTHFD2L
mRNA Expression, RSEM (Batch normalized from Illumina HiSeq_RNASeqV2): CD82 (11p11.2)
Spearman: -0.26
(p = 1.17e-7)
Pearson: -0.16
(p = 1.126e-3)
y = -0.02x + 265.1
R² = 0.03
CD82 mutated
MTHFD2L mutated
Neither mutated

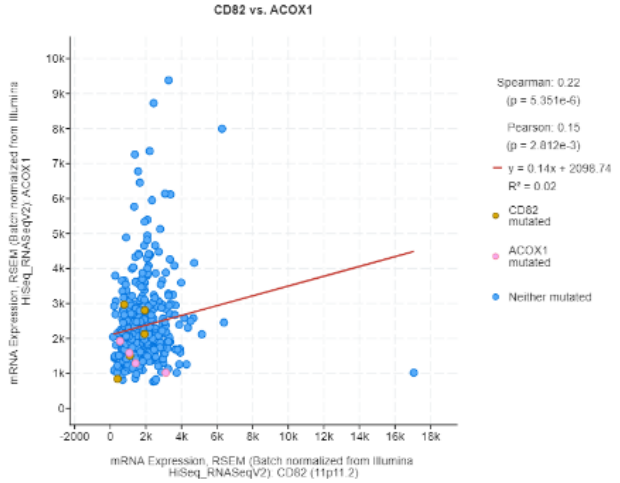

CD82 vs. ME3
mRNA Expression, RSEM (Batch normalized from Illumina HiSeq_RNASeqV2): ME3
mRNA Expression, RSEM (Batch normalized from Illumina HiSeq_RNASeqV2): CD82 (11p11.2)
Spearman: -0.11
(p = 0.0311)
Pearson: -0.15
(p = 2.552e-3)
y = -0.01x + 238.53
R² = 0.02
CD82 mutated
ME3 mutated
Neither mutated
CD82 vs. GLS
mRNA Expression, RSEM (Batch normalized from Illumina HiSeq_RNASeqV2): GLS
mRNA Expression, RSEM (Batch normalized from Illumina HiSeq_RNASeqV2): CD82 (11p11.2)
Spearman: -0.44
(p = 1.03e-20)
Pearson: -0.25
(p = 5.53e-7)
y = -0.39x + 3147.13
R² = 0.06
CD82 mutated
GLS mutated
Both mutated
Neither mutated
CD82 vs. GGPS1
mRNA Expression, RSEM (Batch normalized from Illumina HiSeq_RNASeqV2): GGPS1
mRNA Expression, RSEM (Batch normalized from Illumina HiSeq_RNASeqV2): CD82 (11p11.2)
Spearman: -0.21
(p = 3.027e-5)
Pearson: -0.19
(p = 1.504e-4)
y = -0.04x + 894.73
R² = 0.03
CD82 mutated
GGPS1 mutated
Neither mutated
CD82 vs. GALNT16
mRNA Expression, RSEM (Batch normalized from Illumina HiSeq_RNASeqV2): GALNT16
mRNA Expression, RSEM (Batch normalized from Illumina HiSeq_RNASeqV2): CD82 (11p11.2)
Spearman: -0.12
(p = 0.0130)
Pearson: -0.19
(p = 1.653e-4)
y = -0.02x + 109
R² = 0.03
CD82 mutated
GALNT16 mutated
Neither mutated
CD82 vs. CRLS1
mRNA Expression, RSEM (Batch normalized from Illumina HiSeq_RNASeqV2): CRLS1
mRNA Expression, RSEM (Batch normalized from Illumina HiSeq_RNASeqV2): CD82 (11p11.2)
Spearman: -0.16
(p = 1.380e-3)
Pearson: -0.17
(p = 4.225e-4)
y = -0.11x + 1798.33
R² = 0.03
CD82 mutated
CRLS1 mutated
Neither mutated
CD82 vs. COX6C
mRNA Expression, RSEM (Batch normalized from Illumina HiSeq_RNASeqV2): COX6C
mRNA Expression, RSEM (Batch normalized from Illumina HiSeq_RNASeqV2): CD82 (11p11.2)
Spearman: -0.30
(p = 3.57e-10)
Pearson: -0.26
(p = 9.19e-8)
y = -0.56x + 4689.15
R² = 0.07
CD82 mutated
Neither mutated


CD82 vs. CA3
mRNA Expression, RSEM (Batch normalized from Illumina HiSeq_RNASeqV2): CA3
mRNA Expression, RSEM (Batch normalized from Illumina HiSeq_RNASeqV2): CD82 (11p11.2)
Spearman: -0.13
(p = 7.729e-3)
Pearson: -0.15
(p = 3.360e-3)
y = -0.01x + 68.37
R² = 0.02
CD82 mutated
CA3 mutated
Neither mutated

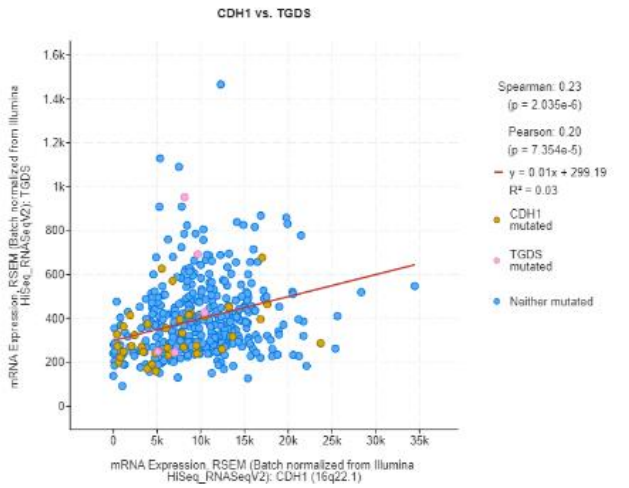

CD82 vs. B3GAT2
mRNA Expression, RSEM (Batch normalized from Illumina HiSeq_RNASeqV2): B3GAT2
mRNA Expression, RSEM (Batch normalized from Illumina HiSeq_RNASeqV2): CD82 (11p11.2)
Spearman: -0.20
(p = 3.635e-5)
Pearson: -0.16
(p = 9.283e-4)
y = 0x + 12.89
R² = 0
CD82 mutated
B3GAT2 mutated
Neither mutated

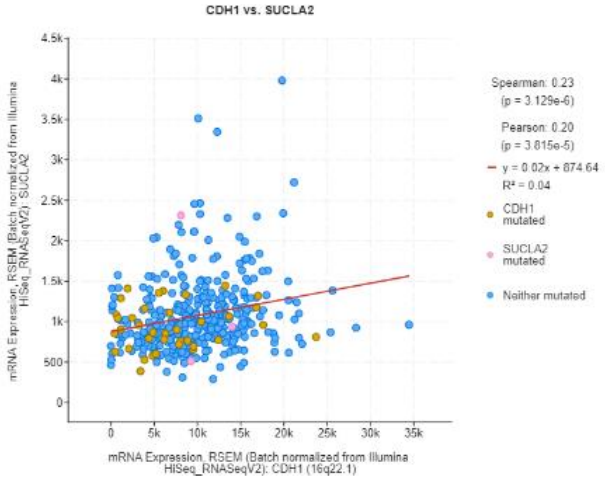

CD82 vs. ATP6V0C
mRNA Expression, RSEM (Batch normalized from Illumina HiSeq_RNASeqV2): ATP6V0C
mRNA Expression, RSEM (Batch normalized from Illumina HiSeq_RNASeqV2): CD82 (11p11.2)
Spearman: 0.31
(p = 1.00e-10)
Pearson: 0.23
(p = 2.513e-6)
y = 0.22x + 2381.12
R² = 0.05
CD82 mutated
ATP6V0C mutated
Neither mutated

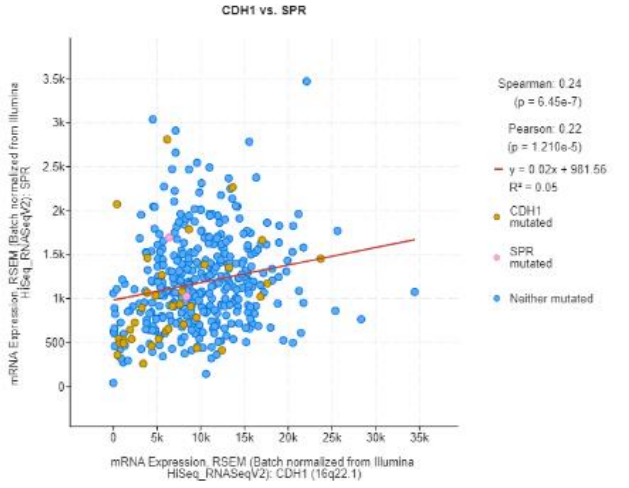

CD82 vs. ACSM1
mRNA Expression, RSEM (Batch normalized from Illumina HiSeq_RNASeqV2): ACSM1
mRNA Expression, RSEM (Batch normalized from Illumina HiSeq_RNASeqV2): CD82 (11p11.2)
Spearman: 0.25
(p = 1.97e-7)
Pearson: 0.15
(p = 2.454e-3)
y = 0x + 10.62
R² = 0
CD82 mutated
ACSM1 mutated
Both mutated
Neither mutated

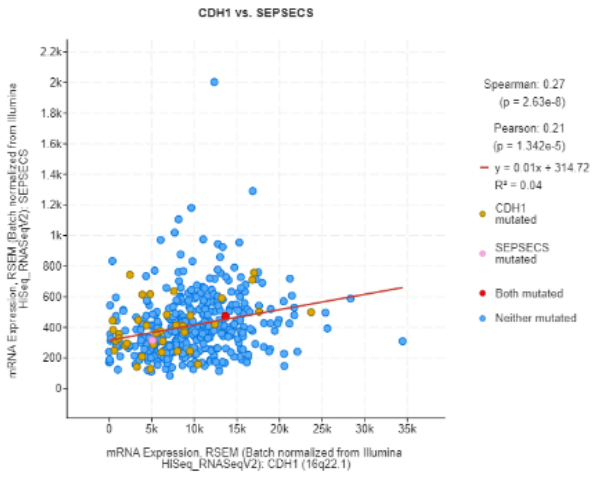

CD82 vs. ACOX1
mRNA Expression, RSEM (Batch normalized from Illumina HiSeq_RNASeqV2): ACOX1
mRNA Expression, RSEM (Batch normalized from Illumina HiSeq_RNASeqV2): CD82 (11p11.2)
Spearman: 0.22
(p = 5.351e-6)
Pearson: 0.15
(p = 2.812e-3)
y = 0.14x + 2098.74
R² = 0.02
CD82 mutated
ACOX1 mutated
Neither mutated

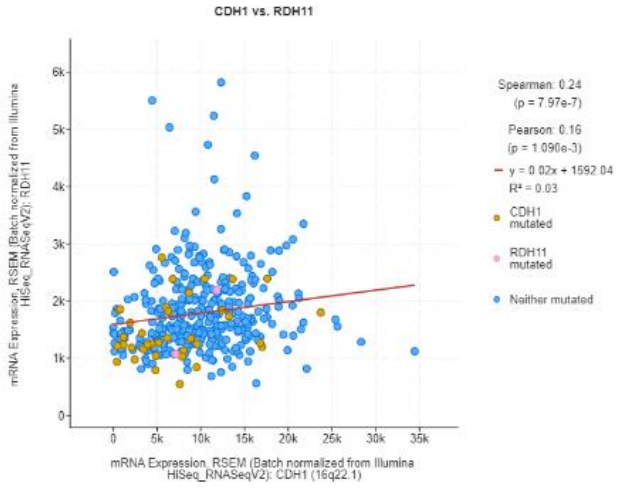
CDH1

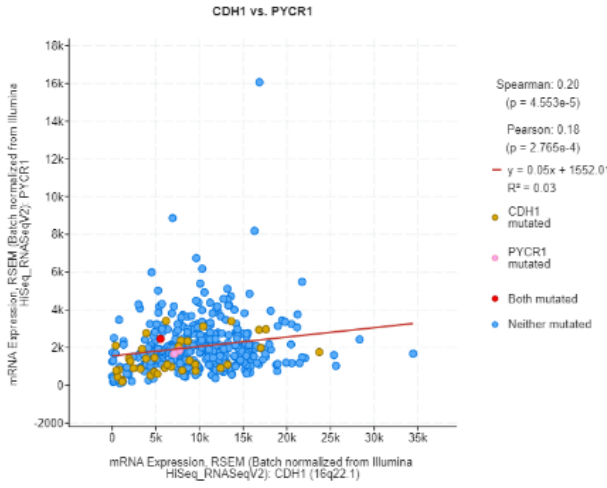

CDH1 vs. TGDS
mRNA Expression, RSEM (Batch normalized from Illumina HiSeq_RNASeqV2): TGDS
mRNA Expression, RSEM (Batch normalized from Illumina HiSeq_RNASeqV2): CDH1 (16q22.1)
Spearman: 0.23
(p = 2.035e-6)
Pearson: 0.20
(p = 7.354e-5)
y = 0.01x + 299.19
R² = 0.03
CDH1 mutated
TGDS mutated
Neither mutated

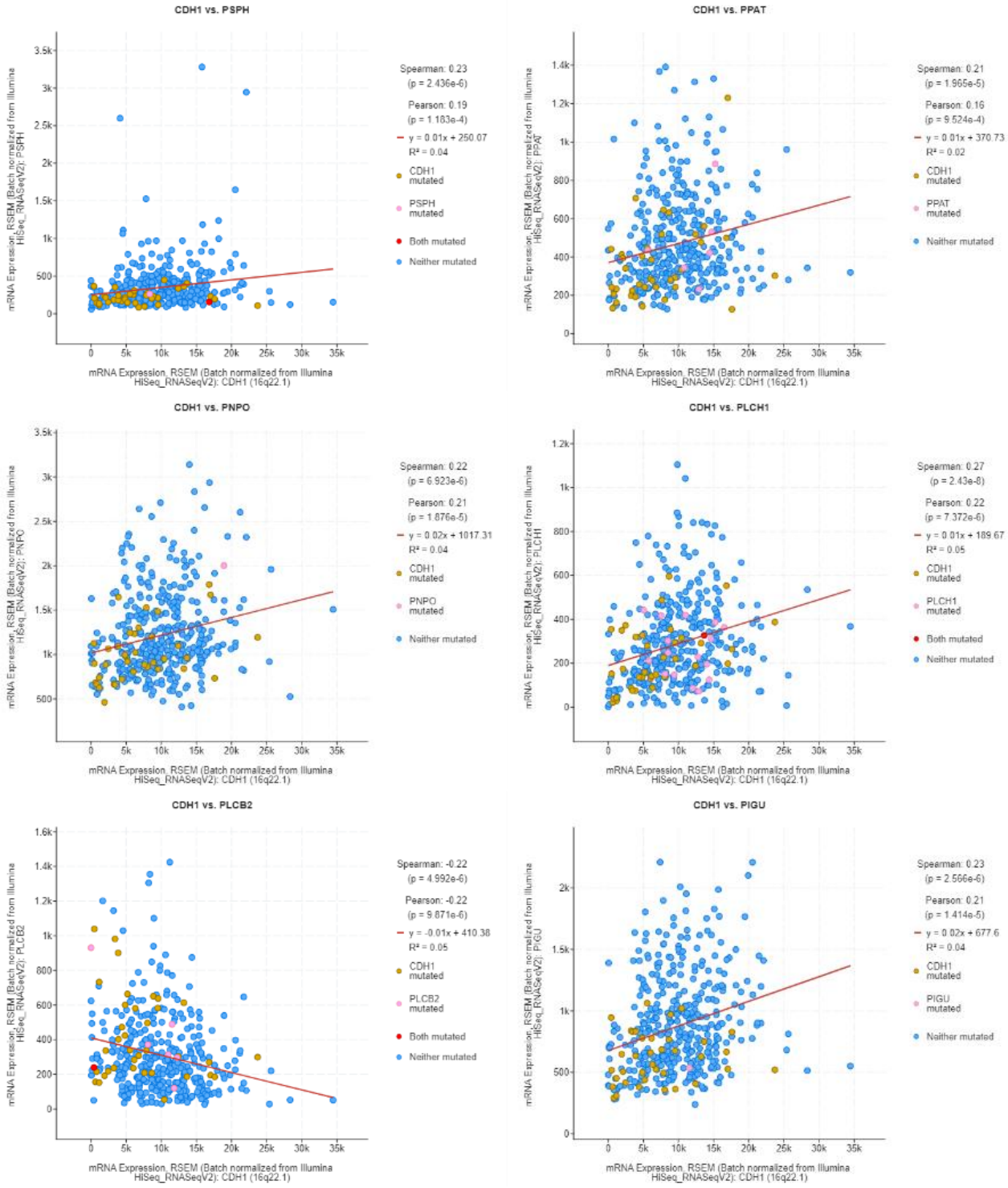

CDH1 vs. SUCLA2
mRNA Expression, RSEM (Batch normalized from Illumina HiSeq_RNASeqV2): SUCLA2
mRNA Expression, RSEM (Batch normalized from Illumina HiSeq_RNASeqV2): CDH1 (16q22.1)
Spearman: 0.23
(p = 3.129e-6)
Pearson: 0.20
(p = 3.815e-5)
y = 0.02x + 874.64
R² = 0.04
CDH1 mutated
SUCLA2 mutated
Neither mutated

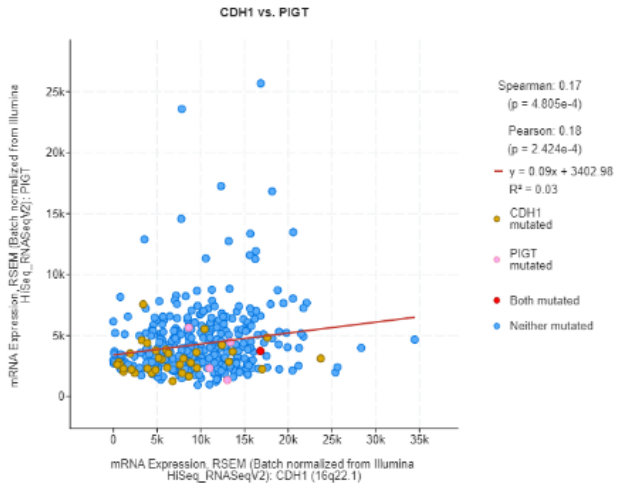

CDH1 vs. SPR
mRNA Expression, RSEM (Batch normalized from Illumina HiSeq_RNASeqV2): SPR
mRNA Expression, RSEM (Batch normalized from Illumina HiSeq_RNASeqV2): CDH1 (16q22.1)
Spearman: 0.24
(p = 6.45e-7)
Pearson: 0.22
(p = 1.210e-5)
y = 0.02x + 981.56
R² = 0.05
CDH1 mutated
SPR mutated
Neither mutated

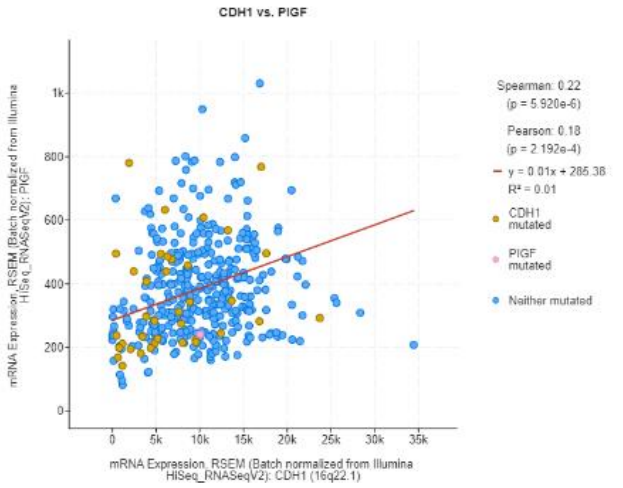

CDH1 vs. SEPSECS
mRNA Expression, RSEM (Batch normalized from Illumina HiSeq_RNASeqV2): SEPSECS
mRNA Expression, RSEM (Batch normalized from Illumina HiSeq_RNASeqV2): CDH1 (16q22.1)
Spearman: 0.27
(p = 2.63e-8)
Pearson: 0.21
(p = 1.342e-5)
y = 0.01x + 314.72
R² = 0.04
CDH1 mutated
SEPSECS mutated
Both mutated
Neither mutated

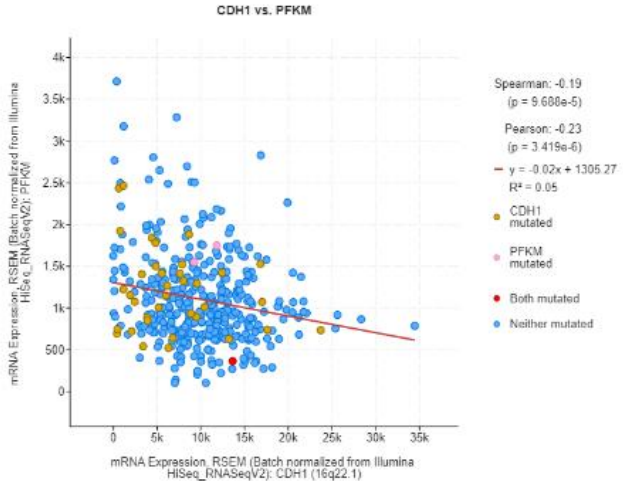

CDH1 vs. RDH11
mRNA Expression, RSEM (Batch normalized from Illumina HiSeq_RNASeqV2): RDH11
mRNA Expression, RSEM (Batch normalized from Illumina HiSeq_RNASeqV2): CDH1 (16q22.1)
Spearman: 0.24
(p = 7.97e-7)
Pearson: 0.16
(p = 1.090e-3)
y = 0.02x + 1592.04
R² = 0.03
CDH1 mutated
RDH11 mutated
Neither mutated

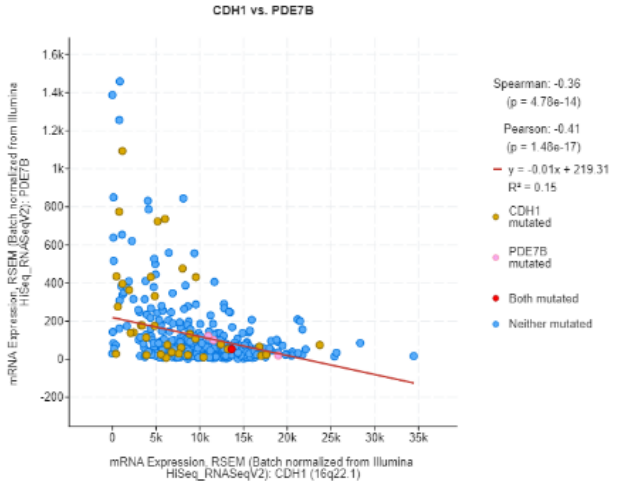

CDH1 vs. PYCR1
mRNA Expression, RSEM (Batch normalized from Illumina HiSeq_RNASeqV2): PYCR1
mRNA Expression, RSEM (Batch normalized from Illumina HiSeq_RNASeqV2): CDH1 (16q22.1)
Spearman: 0.20
(p = 4.553e-5)
Pearson: 0.18
(p = 2.765e-4)
y = 0.05x + 1552.01
R² = 0.03
CDH1 mutated
PYCR1 mutated
Both mutated
Neither mutated

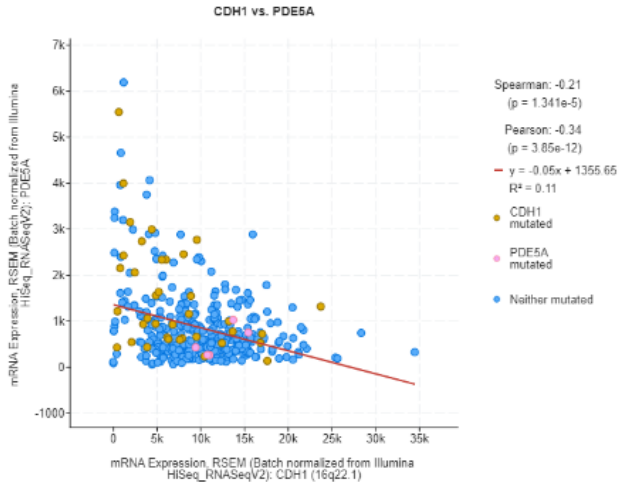

CDH1 vs. PSPH
mRNA Expression, RSEM (Batch normalized from Illumina HiSeq_RNASeqV2): PSPH
mRNA Expression, RSEM (Batch normalized from Illumina HiSeq_RNASeqV2): CDH1 (16q22.1)
Spearman: 0.23
(p = 2.436e-6)
Pearson: 0.19
(p = 1.183e-4)
y = 0.01x + 250.07
R² = 0.04
CDH1 mutated
PSPH mutated
Both mutated
Neither mutated
CDH1 vs. PPAT
mRNA Expression, RSEM (Batch normalized from Illumina HiSeq_RNASeqV2): PPAT
mRNA Expression, RSEM (Batch normalized from Illumina HiSeq_RNASeqV2): CDH1 (16q22.1)
Spearman: 0.21
(p = 1.965e-5)
Pearson: 0.16
(p = 9.524e-4)
y = 0.01x + 370.73
R² = 0.02
CDH1 mutated
PPAT mutated
Neither mutated
CDH1 vs. PNPO
mRNA Expression, RSEM (Batch normalized from Illumina HiSeq_RNASeqV2): PNPO
mRNA Expression, RSEM (Batch normalized from Illumina HiSeq_RNASeqV2): CDH1 (16q22.1)
Spearman: 0.22
(p = 6.923e-6)
Pearson: 0.21
(p = 1.876e-5)
y = 0.02x + 1017.31
R² = 0.04
CDH1 mutated
PNPO mutated
Neither mutated
CDH1 vs. PLCH1
mRNA Expression, RSEM (Batch normalized from Illumina HiSeq_RNASeqV2): PLCH1
mRNA Expression, RSEM (Batch normalized from Illumina HiSeq_RNASeqV2): CDH1 (16q22.1)
Spearman: 0.27
(p = 2.43e-8)
Pearson: 0.22
(p = 7.372e-6)
y = 0.01x + 189.67
R² = 0.05
CDH1 mutated
PLCH1 mutated
Both mutated
Neither mutated
CDH1 vs. PLCB2
mRNA Expression, RSEM (Batch normalized from Illumina HiSeq_RNASeqV2): PLCB2
mRNA Expression, RSEM (Batch normalized from Illumina HiSeq_RNASeqV2): CDH1 (16q22.1)
Spearman: -0.22
(p = 4.992e-6)
Pearson: -0.22
(p = 9.871e-6)
y = -0.01x + 410.38
R² = 0.05
CDH1 mutated
PLCB2 mutated
Both mutated
Neither mutated
CDH1 vs. PIGU
mRNA Expression, RSEM (Batch normalized from Illumina HiSeq_RNASeqV2): PIGU
mRNA Expression, RSEM (Batch normalized from Illumina HiSeq_RNASeqV2): CDH1 (16q22.1)
Spearman: 0.23
(p = 2.566e-6)
Pearson: 0.21
(p = 1.414e-5)
y = 0.02x + 677.6
R² = 0.04
CDH1 mutated
PIGU mutated
Neither mutated

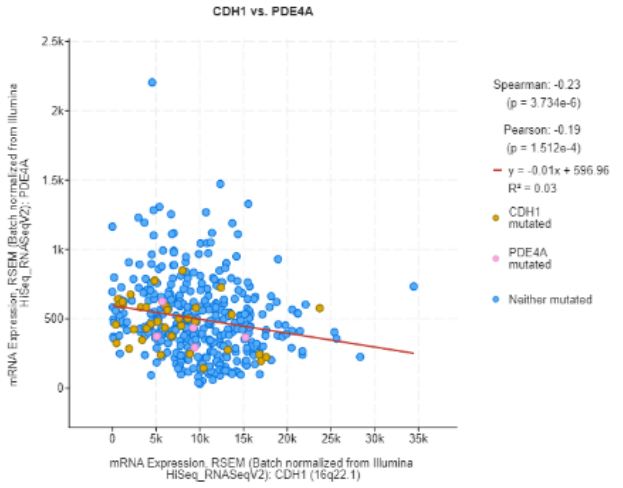

CDH1 vs. PIGT
mRNA Expression, RSEM (Batch normalized from Illumina HiSeq_RNASeqV2): PIGT
mRNA Expression, RSEM (Batch normalized from Illumina HiSeq_RNASeqV2): CDH1 (16q22.1)
Spearman: 0.17
(p = 4.805e-4)
Pearson: 0.18
(p = 2.424e-4)
y = 0.09x + 3402.98
R² = 0.03
CDH1 mutated
PIGT mutated
Both mutated
Neither mutated


CDH1 vs. PIGF
mRNA Expression, RSEM (Batch normalized from Illumina HiSeq_RNASeqV2): PIGF
mRNA Expression, RSEM (Batch normalized from Illumina HiSeq_RNASeqV2): CDH1 (16q22.1)
Spearman: 0.22
(p = 5.920e-6)
Pearson: 0.18
(p = 2.192e-4)
y = 0.01x + 285.38
R² = 0.01
CDH1 mutated
PIGF mutated
Neither mutated

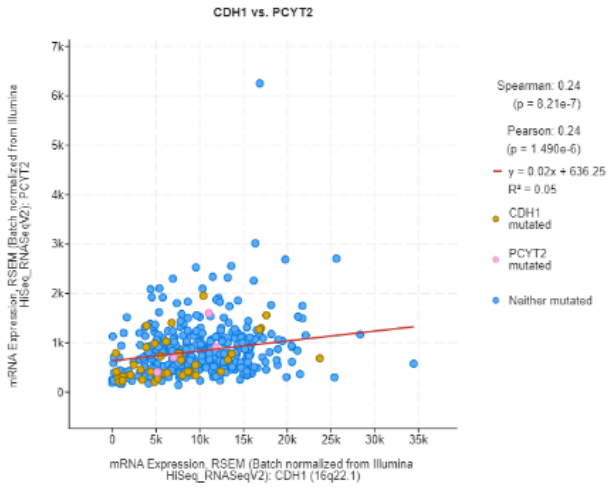

CDH1 vs. PFKM
mRNA Expression, RSEM (Batch normalized from Illumina HiSeq_RNASeqV2): PFKM
mRNA Expression, RSEM (Batch normalized from Illumina HiSeq_RNASeqV2): CDH1 (16q22.1)
Spearman: -0.19
(p = 9.688e-5)
Pearson: -0.23
(p = 3.419e-6)
y = -0.02x + 1305.27
R² = 0.05
CDH1 mutated
PFKM mutated
Both mutated
Neither mutated


CDH1 vs. PDE7B
mRNA Expression, RSEM (Batch normalized from Illumina HiSeq_RNASeqV2): PDE7B
mRNA Expression, RSEM (Batch normalized from Illumina HiSeq_RNASeqV2): CDH1 (16q22.1)
Spearman: -0.36
(p = 4.78e-14)
Pearson: -0.41
(p = 1.48e-17)
y = -0.01x + 219.31
R² = 0.15
CDH1 mutated
PDE7B mutated
Both mutated
Neither mutated

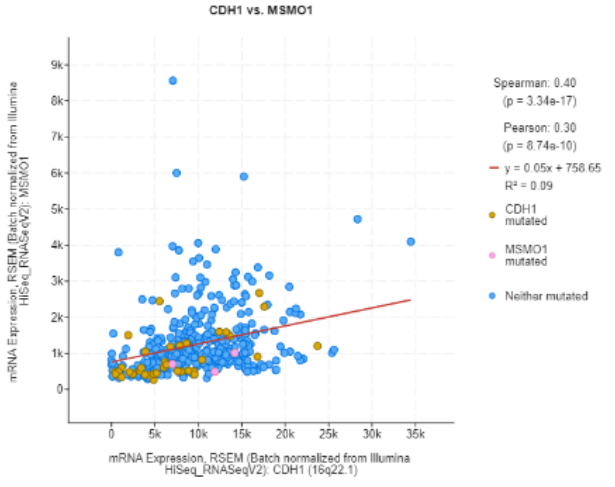

CDH1 vs. PDE5A
mRNA Expression, RSEM (Batch normalized from Illumina HiSeq_RNASeqV2): PDE5A
mRNA Expression, RSEM (Batch normalized from Illumina HiSeq_RNASeqV2): CDH1 (16q22.1)
Spearman: -0.21
(p = 1.341e-5)
Pearson: -0.34
(p = 3.85e-12)
y = -0.05x + 1355.65
R² = 0.11
CDH1 mutated
PDE5A mutated
Neither mutated

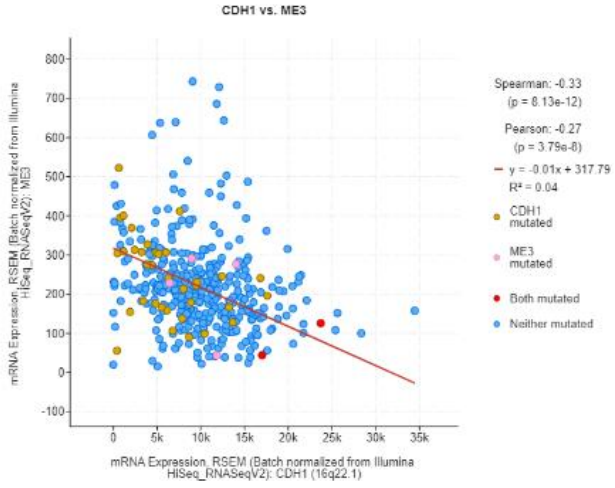

CDH1 vs. PDE4A
mRNA Expression, RSEM (Batch normalized from Illumina HiSeq_RNASeqV2): PDE4A
mRNA Expression, RSEM (Batch normalized from Illumina HiSeq_RNASeqV2): CDH1 (16q22.1)
Spearman: -0.23
(p = 3.734e-6)
Pearson: -0.19
(p = 1.512e-4)
y = -0.01x + 596.96
R² = 0.03
CDH1 mutated
PDE4A mutated
Neither mutated

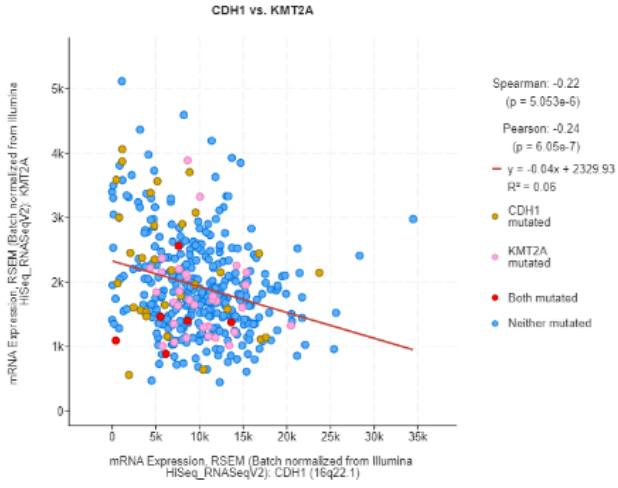

CDH1 vs. PDE3B
mRNA Expression, RSEM (Batch normalized from Illumina HiSeq_RNASeqV2): PDE3B
mRNA Expression, RSEM (Batch normalized from Illumina HiSeq_RNASeqV2): CDH1 (16q22.1)
Spearman: -0.19
(p = 7.715e-5)
Pearson: -0.15
(p = 3.324e-3)
y = -0.01x + 383.17
R² = 0.01
CDH1 mutated
PDE3B mutated
Both mutated
Neither mutated

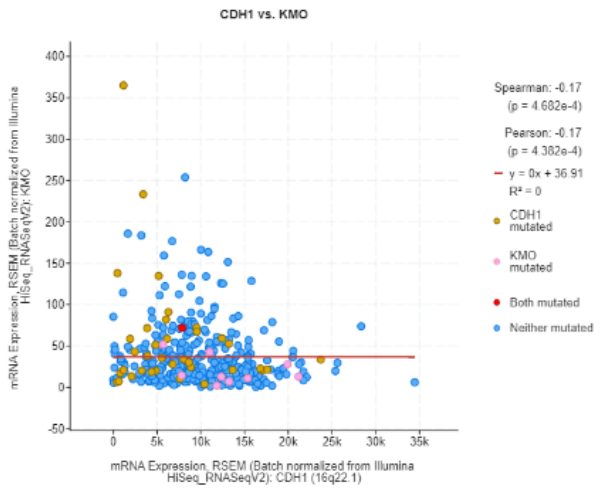

CDH1 vs. PCYT2
mRNA Expression, RSEM (Batch normalized from Illumina HiSeq_RNASeqV2): PCYT2
mRNA Expression, RSEM (Batch normalized from Illumina HiSeq_RNASeqV2): CDH1 (16q22.1)
Spearman: 0.24
(p = 8.21e-7)
Pearson: 0.24
(p = 1.490e-6)
y = 0.02x + 636.25
R² = 0.05
CDH1 mutated
PCYT2 mutated
Neither mutated

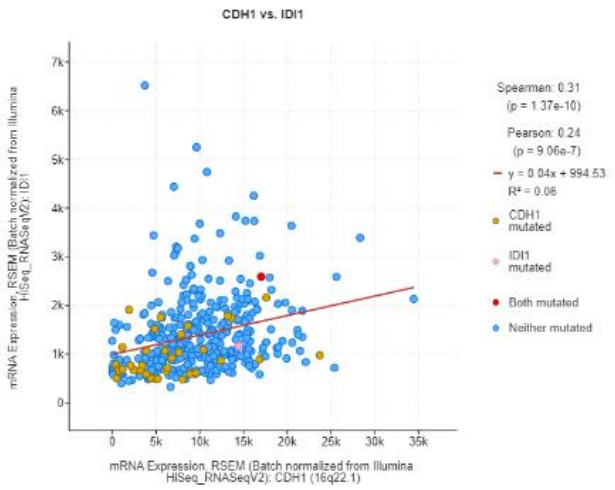

CDH1 vs. NUDT12
mRNA Expression, RSEM (Batch normalized from Illumina HiSeq_RNASeqV2): NUDT12
mRNA Expression, RSEM (Batch normalized from Illumina HiSeq_RNASeqV2): CDH1 (16q22.1)
Spearman: 0.16
(p = 1.415e-3)
Pearson: 0.17
(p = 6.406e-4)
y = 0.01x + 355.69
R² = 0.03
CDH1 mutated
NUDT12 mutated
Neither mutated

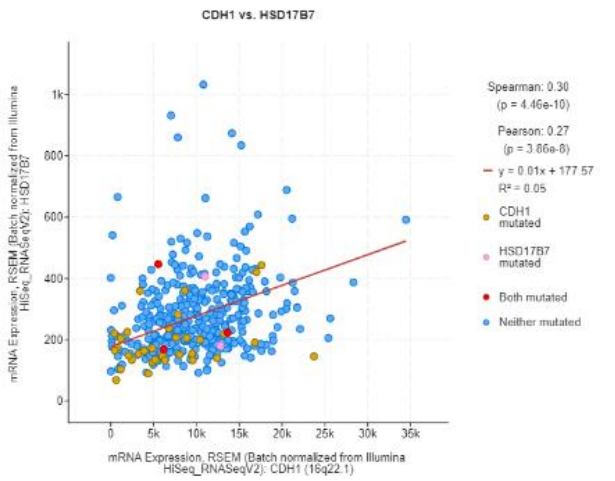

CDH1 vs. MSMO1
mRNA Expression, RSEM (Batch normalized from Illumina HiSeq_RNASeqV2): MSMO1
mRNA Expression, RSEM (Batch normalized from Illumina HiSeq_RNASeqV2): CDH1 (16q22.1)
Spearman: 0.40
(p = 3.34e-17)
Pearson: 0.30
(p = 8.74e-10)
y = 0.05x + 758.65
R² = 0.09
CDH1 mutated
MSMO1 mutated
Neither mutated

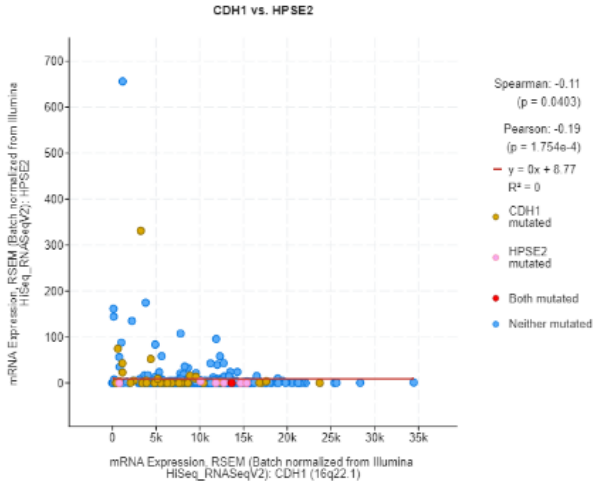

CDH1 vs. ME3
mRNA Expression, RSEM (Batch normalized from Illumina HiSeq_RNASeqV2): ME3
mRNA Expression, RSEM (Batch normalized from Illumina HiSeq_RNASeqV2): CDH1 (16q22.1)
Spearman: -0.33
(p = 8.13e-12)
Pearson: -0.27
(p = 3.79e-8)
y = -0.01x + 317.79
R² = 0.04
CDH1 mutated
ME3 mutated
Both mutated
Neither mutated

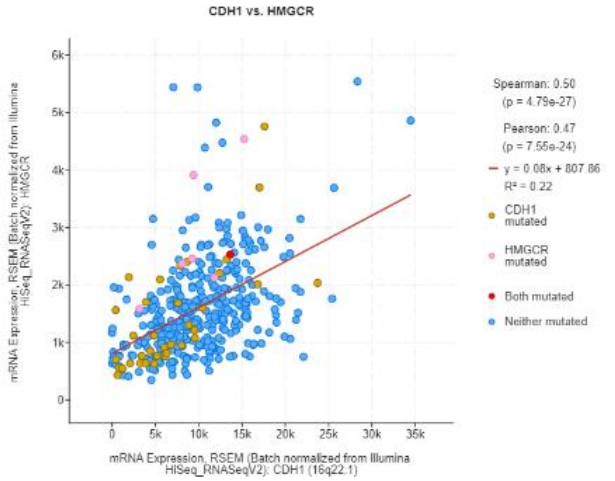

CDH1 vs. KMT2A
mRNA Expression, RSEM (Batch normalized from Illumina HiSeq_RNASeqV2): KMT2A
mRNA Expression, RSEM (Batch normalized from Illumina HiSeq_RNASeqV2): CDH1 (16q22.1)
Spearman: -0.22
(p = 5.053e-6)
Pearson: -0.24
(p = 6.05e-7)
y = -0.04x + 2329.93
R² = 0.06
CDH1 mutated
KMT2A mutated
Both mutated
Neither mutated

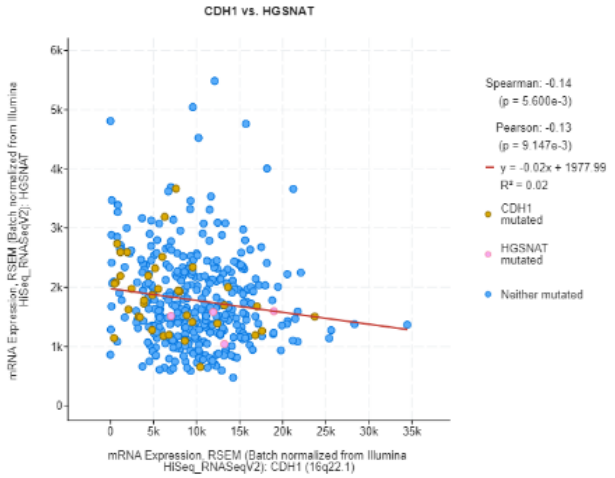

CDH1 vs. KMO
mRNA Expression, RSEM (Batch normalized from Illumina HiSeq_RNASeqV2): KMO
mRNA Expression, RSEM (Batch normalized from Illumina HiSeq_RNASeqV2): CDH1 (16q22.1)
Spearman: -0.17
(p = 4.682e-4)
Pearson: -0.17
(p = 4.382e-4)
y = 0x + 36.91
R² = 0
CDH1 mutated
KMO mutated
Both mutated
Neither mutated

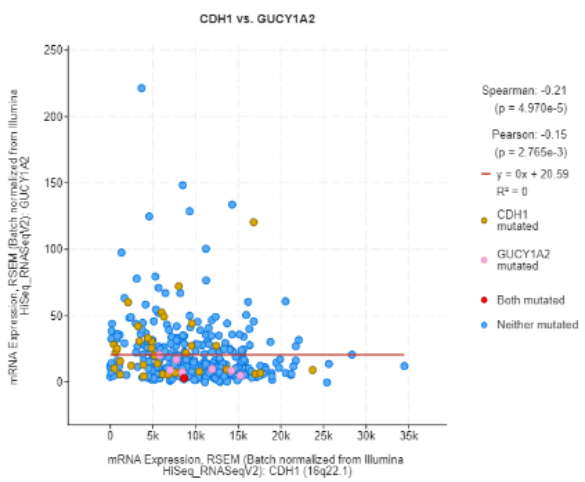

CDH1 vs. IDI1
mRNA Expression, RSEM (Batch normalized from Illumina HiSeq_RNASeqV2): IDI1
mRNA Expression, RSEM (Batch normalized from Illumina HiSeq_RNASeqV2): CDH1 (16q22.1)
Spearman: 0.31
(p = 1.37e-10)
Pearson: 0.24
(p = 9.06e-7)
y = 0.04x + 994.53
R² = 0.06
CDH1 mutated
IDI1 mutated
Both mutated
Neither mutated

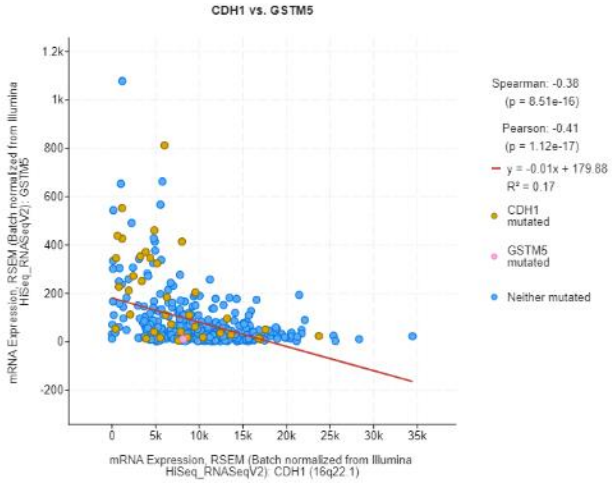

CDH1 vs. HSD17B7
mRNA Expression, RSEM (Batch normalized from Illumina HiSeq_RNASeqV2): HSD17B7
mRNA Expression, RSEM (Batch normalized from Illumina HiSeq_RNASeqV2): CDH1 (16q22.1)
Spearman: 0.30
(p = 4.46e-10)
Pearson: 0.27
(p = 3.66e-8)
y = 0.01x + 177.57
R² = 0.05
CDH1 mutated
HSD17B7 mutated
Both mutated
Neither mutated

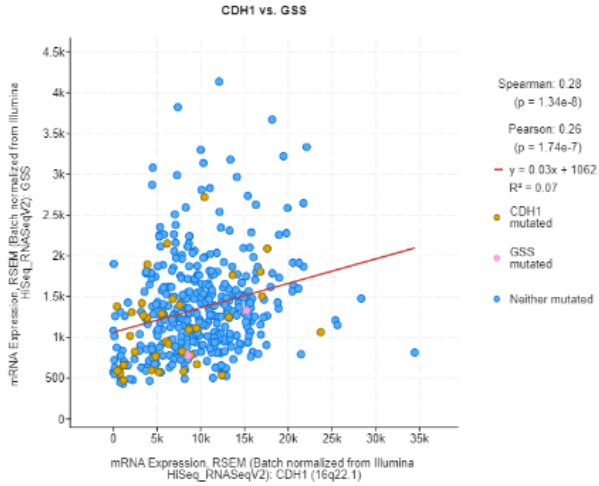

CDH1 vs. HPSE2
mRNA Expression, RSEM (Batch normalized from Illumina HiSeq_RNASeqV2): HPSE2
mRNA Expression, RSEM (Batch normalized from Illumina HiSeq_RNASeqV2): CDH1 (16q22.1)
Spearman: -0.11
(p = 0.0403)
Pearson: -0.19
(p = 1.754e-4)
y = 0x + 8.77
R² = 0
CDH1 mutated
HPSE2 mutated
Both mutated
Neither mutated

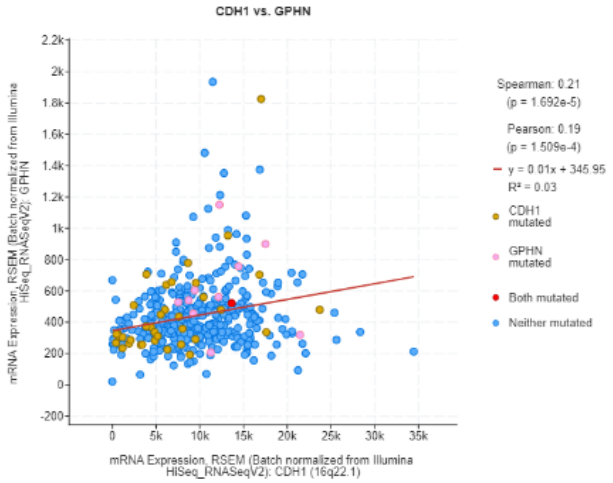

CDH1 vs. HMGCR
mRNA Expression, RSEM (Batch normalized from Illumina HiSeq_RNASeqV2): HMGCR
mRNA Expression, RSEM (Batch normalized from Illumina HiSeq_RNASeqV2): CDH1 (16q22.1)
Spearman: 0.50
(p = 4.79e-27)
Pearson: 0.47
(p = 7.55e-24)
y = 0.08x + 807.86
R² = 0.22
CDH1 mutated
HMGCR mutated
Both mutated
Neither mutated

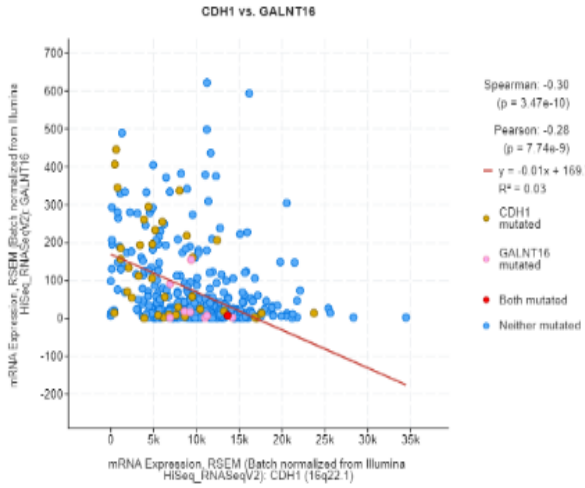

CDH1 vs. HGSNAT
mRNA Expression, RSEM (Batch normalized from Illumina HiSeq_RNASeqV2): HGSNAT
mRNA Expression, RSEM (Batch normalized from Illumina HiSeq_RNASeqV2): CDH1 (16q22.1)
Spearman: -0.14
(p = 5.600e-3)
Pearson: -0.13
(p = 9.147e-3)
y = -0.02x + 1977.99
R² = 0.02
CDH1 mutated
HGSNAT mutated
Neither mutated

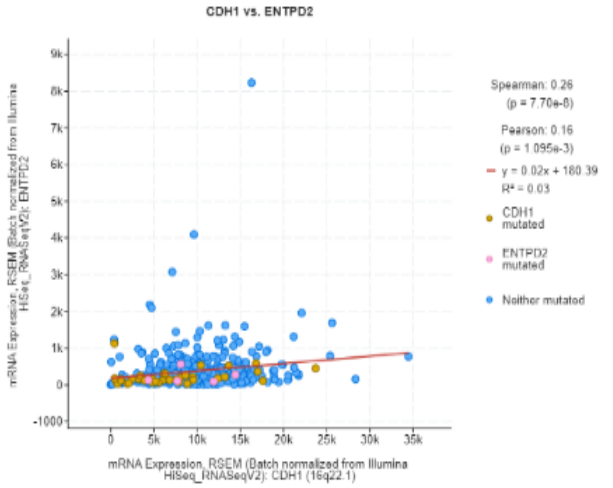

CDH1 vs. GUCY1A2
mRNA Expression, RSEM (Batch normalized from Illumina HiSeq_RNASeqV2): GUCY1A2
mRNA Expression, RSEM (Batch normalized from Illumina HiSeq_RNASeqV2): CDH1 (16q22.1)
Spearman: -0.21
(p = 4.970e-5)
Pearson: -0.15
(p = 2.765e-3)
y = 0x + 20.59
R² = 0
CDH1 mutated
GUCY1A2 mutated
Both mutated
Neither mutated

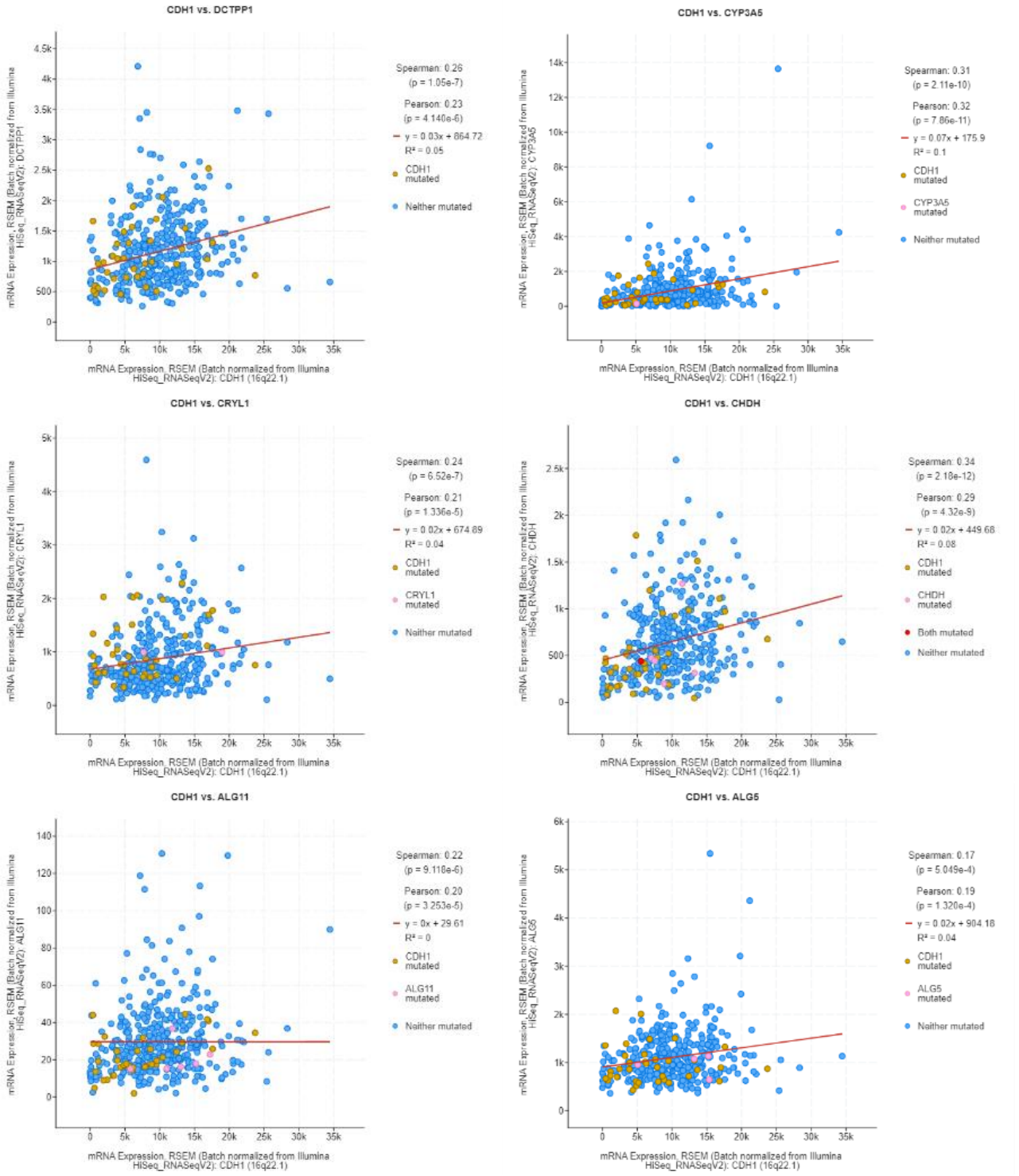

CDH1 vs. GSTM5
mRNA Expression, RSEM (Batch normalized from Illumina HiSeq_RNASeqV2): GSTM5
mRNA Expression, RSEM (Batch normalized from Illumina HiSeq_RNASeqV2): CDH1 (16q22.1)
Spearman: -0.38
(p = 8.51e-16)
Pearson: -0.41
(p = 1.12e-17)
y = -0.01x + 179.88
R² = 0.17
CDH1 mutated
GSTM5 mutated
Neither mutated

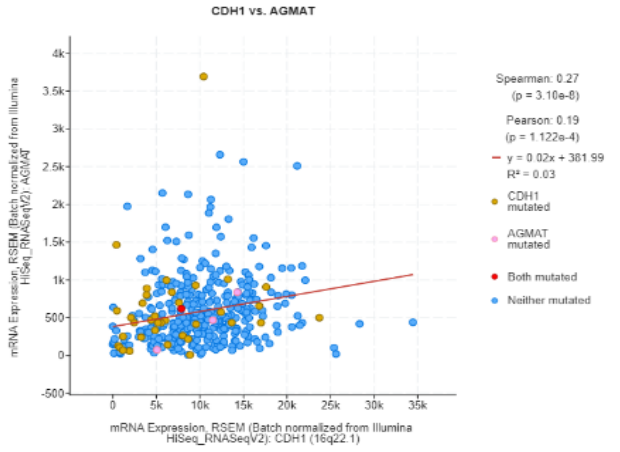

CDH1 vs. GSS
mRNA Expression, RSEM (Batch normalized from Illumina HiSeq_RNASeqV2): GSS
mRNA Expression, RSEM (Batch normalized from Illumina HiSeq_RNASeqV2): CDH1 (16q22.1)
Spearman: 0.28
(p = 1.34e-8)
Pearson: 0.26
(p = 1.74e-7)
y = 0.03x + 1062.26
R² = 0.07
CDH1 mutated
GSS mutated
Neither mutated

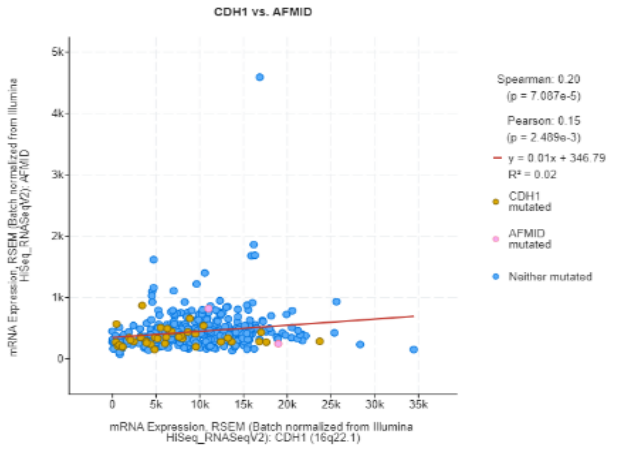

CDH1 vs. GPHN
mRNA Expression, RSEM (Batch normalized from Illumina HiSeq_RNASeqV2): GPHN
mRNA Expression, RSEM (Batch normalized from Illumina HiSeq_RNASeqV2): CDH1 (16q22.1)
Spearman: 0.21
(p = 1.692e-5)
Pearson: 0.19
(p = 1.509e-4)
y = 0.01x + 345.95
R² = 0.03
CDH1 mutated
GPHN mutated
Both mutated
Neither mutated

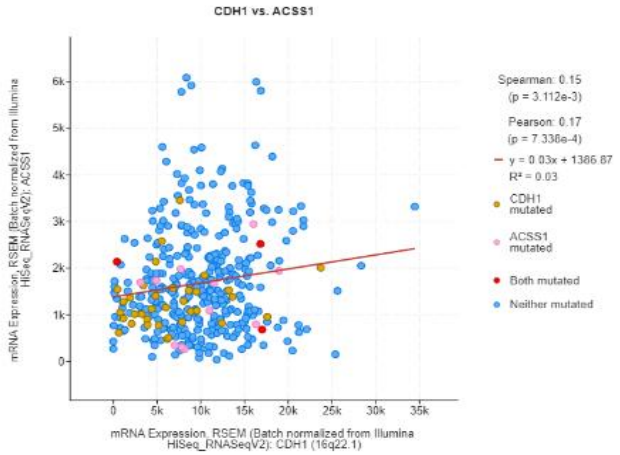

CDH1 vs. GALNT16
mRNA Expression, RSEM (Batch normalized from Illumina HiSeq_RNASeqV2): GALNT16
mRNA Expression, RSEM (Batch normalized from Illumina HiSeq_RNASeqV2): CDH1 (16q22.1)
Spearman: -0.30
(p = 3.47e-10)
Pearson: -0.28
(p = 7.74e-9)
y = -0.01x + 169.73
R² = 0.03
CDH1 mutated
GALNT16 mutated
Both mutated
Neither mutated

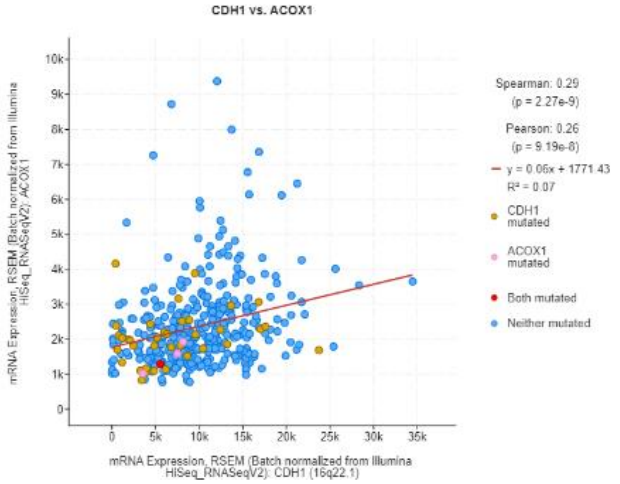

CDH1 vs. ENTPD2
mRNA Expression, RSEM (Batch normalized from Illumina HiSeq_RNASeqV2): ENTPD2
mRNA Expression, RSEM (Batch normalized from Illumina HiSeq_RNASeqV2): CDH1 (16q22.1)
Spearman: 0.26
(p = 7.70e-8)
Pearson: 0.16
(p = 1.095e-3)
y = 0.02x + 180.39
R² = 0.03
CDH1 mutated
ENTPD2 mutated
Neither mutated

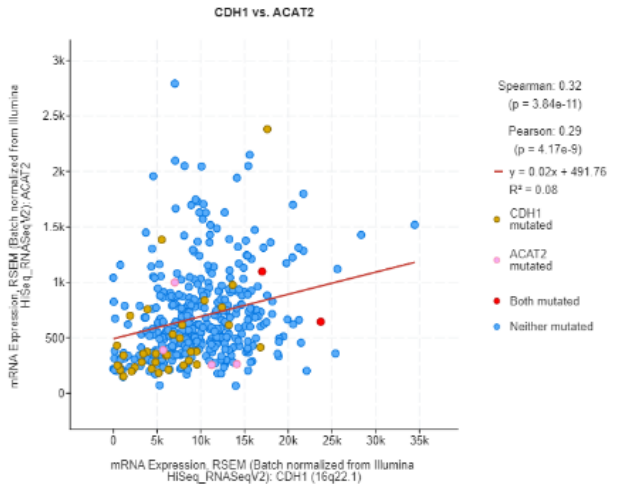

CDH1 vs. DCTPP1
mRNA Expression, RSEM (Batch normalized from Illumina HiSeq_RNASeqV2): DCTPP1
mRNA Expression, RSEM (Batch normalized from Illumina HiSeq_RNASeqV2): CDH1 (16q22.1)
Spearman: 0.26
(p = 1.05e-7)
Pearson: 0.23
(p = 4.140e-6)
y = 0.03x + 864.72
R² = 0.05
CDH1 mutated
Neither mutated
CDH1 vs. CYP3A5
mRNA Expression, RSEM (Batch normalized from Illumina HiSeq_RNASeqV2): CYP3A5
mRNA Expression, RSEM (Batch normalized from Illumina HiSeq_RNASeqV2): CDH1 (16q22.1)
Spearman: 0.31
(p = 2.11e-10)
Pearson: 0.32
(p = 7.86e-11)
y = 0.07x + 175.9
R² = 0.1
CDH1 mutated
CYP3A5 mutated
Neither mutated
CDH1 vs. CRYL1
mRNA Expression, RSEM (Batch normalized from Illumina HiSeq_RNASeqV2): CRYL1
mRNA Expression, RSEM (Batch normalized from Illumina HiSeq_RNASeqV2): CDH1 (16q22.1)
Spearman: 0.24
(p = 6.52e-7)
Pearson: 0.21
(p = 1.336e-5)
y = 0.02x + 674.89
R² = 0.04
CDH1 mutated
CRYL1 mutated
Neither mutated
CDH1 vs. CHDH
mRNA Expression, RSEM (Batch normalized from Illumina HiSeq_RNASeqV2): CHDH
mRNA Expression, RSEM (Batch normalized from Illumina HiSeq_RNASeqV2): CDH1 (16q22.1)
Spearman: 0.34
(p = 2.18e-12)
Pearson: 0.29
(p = 4.32e-9)
y = 0.02x + 449.68
R² = 0.08
CDH1 mutated
CHDH mutated
Both mutated
Neither mutated
CDH1 vs. ALG11
mRNA Expression, RSEM (Batch normalized from Illumina HiSeq_RNASeqV2): ALG11
mRNA Expression, RSEM (Batch normalized from Illumina HiSeq_RNASeqV2): CDH1 (16q22.1)
Spearman: 0.22
(p = 9.118e-6)
Pearson: 0.20
(p = 3.253e-5)
y = 0x + 29.61
R² = 0
CDH1 mutated
ALG11 mutated
Neither mutated
CDH1 vs. ALG5
mRNA Expression, RSEM (Batch normalized from Illumina HiSeq_RNASeqV2): ALG5
mRNA Expression, RSEM (Batch normalized from Illumina HiSeq_RNASeqV2): CDH1 (16q22.1)
Spearman: 0.17
(p = 5.049e-4)
Pearson: 0.19
(p = 1.320e-4)
y = 0.02x + 904.18
R² = 0.04
CDH1 mutated
ALG5 mutated
Neither mutated


CDH1 vs. AGMAT
mRNA Expression, RSEM (Batch normalized from Illumina HiSeq_RNASeqV2): AGMAT
mRNA Expression, RSEM (Batch normalized from Illumina HiSeq_RNASeqV2): CDH1 (16q22.1)
Spearman: 0.27
(p = 3.10e-8)
Pearson: 0.19
(p = 1.122e-4)
y = 0.02x + 381.99
R² = 0.03
CDH1 mutated
AGMAT mutated
Both mutated
Neither mutated

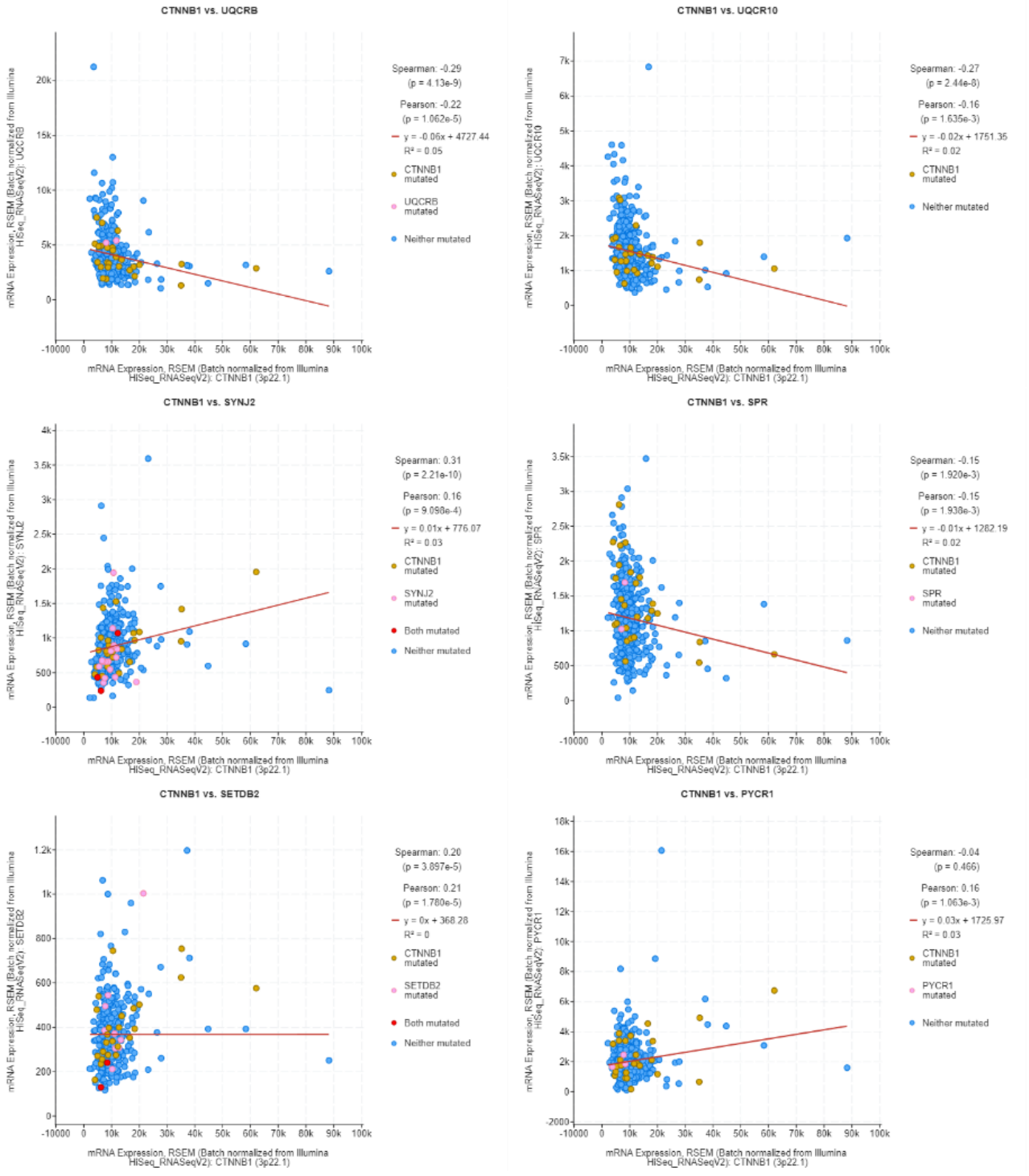

CDH1 vs. AFMID
mRNA Expression, RSEM (Batch normalized from Illumina HiSeq_RNASeqV2): AFMID
mRNA Expression, RSEM (Batch normalized from Illumina HiSeq_RNASeqV2): CDH1 (16q22.1)
Spearman: 0.20
(p = 7.087e-5)
Pearson: 0.15
(p = 2.489e-3)
y = 0.01x + 346.79
R² = 0.02
CDH1 mutated
AFMID mutated
Neither mutated

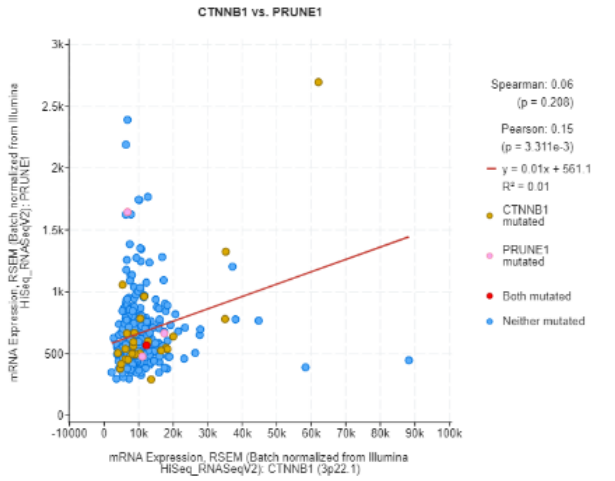

CDH1 vs. ACSS1
mRNA Expression, RSEM (Batch normalized from Illumina HiSeq_RNASeqV2): ACSS1
mRNA Expression, RSEM (Batch normalized from Illumina HiSeq_RNASeqV2): CDH1 (16q22.1)
Spearman: 0.15
(p = 3.112e-3)
Pearson: 0.17
(p = 7.336e-4)
y = 0.03x + 1386.87
R² = 0.03
CDH1 mutated
ACSS1 mutated
Both mutated
Neither mutated

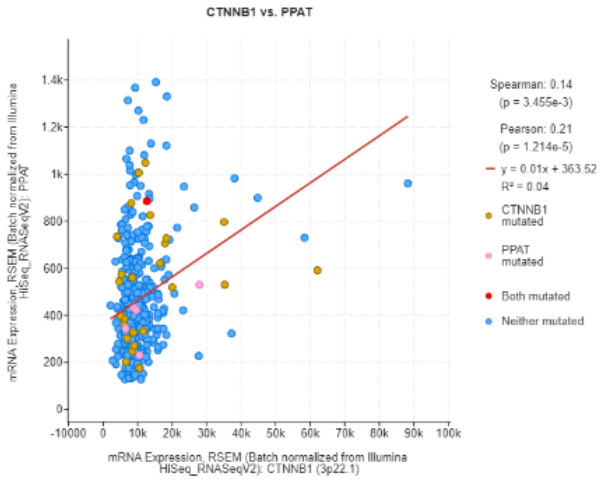

CDH1 vs. ACOX1
mRNA Expression, RSEM (Batch normalized from Illumina HiSeq_RNASeqV2): ACOX1
mRNA Expression, RSEM (Batch normalized from Illumina HiSeq_RNASeqV2): CDH1 (16q22.1)
Spearman: 0.29
(p = 2.27e-9)
Pearson: 0.26
(p = 9.19e-8)
y = 0.06x + 1771.43
R² = 0.07
CDH1 mutated
ACOX1 mutated
Both mutated
Neither mutated

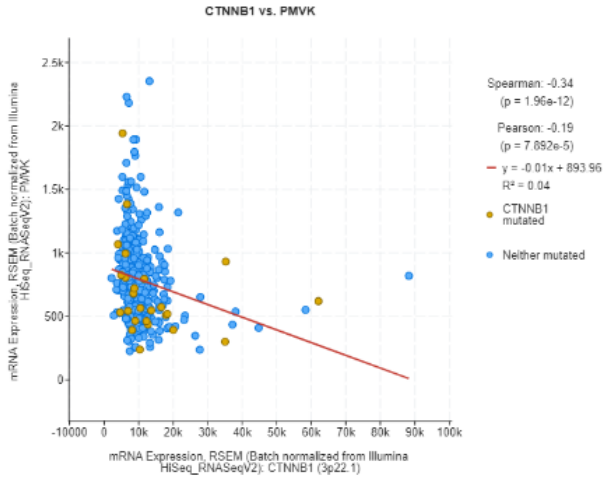

CDH1 vs. ACAT2
mRNA Expression, RSEM (Batch normalized from Illumina HiSeq_RNASeqV2): ACAT2
mRNA Expression, RSEM (Batch normalized from Illumina HiSeq_RNASeqV2): CDH1 (16q22.1)
Spearman: 0.32
(p = 3.84e-11)
Pearson: 0.29
(p = 4.17e-9)
y = 0.02x + 491.76
R² = 0.08
CDH1 mutated
ACAT2 mutated
Both mutated
Neither mutated

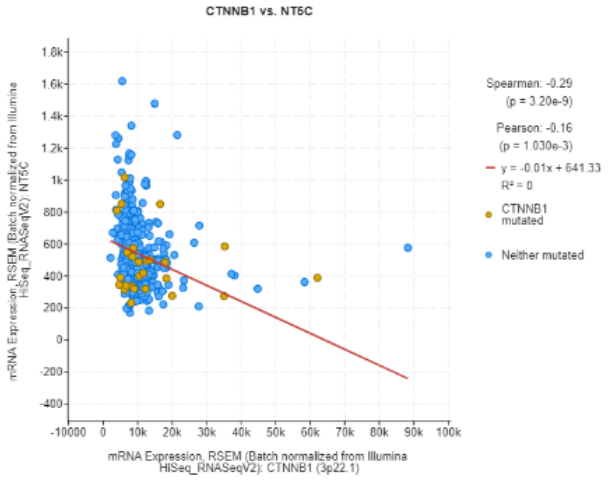
CTNNB1

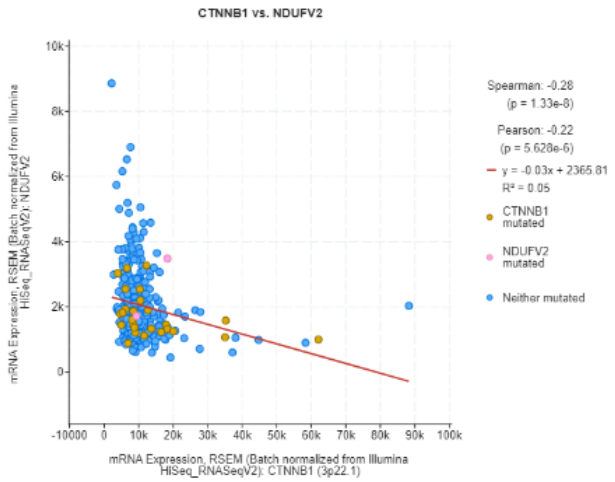

CTNNB1 vs. UQCRB
mRNA Expression, RSEM (Batch normalized from Illumina HiSeq_RNASeqV2): UQCRB
mRNA Expression, RSEM (Batch normalized from Illumina HiSeq_RNASeqV2): CTNNB1 (3p22.1)
Spearman: -0.29
(p = 4.13e-9)
Pearson: -0.22
(p = 1.062e-5)
y = -0.06x + 4727.44
R² = 0.05
CTNNB1 mutated
UQCRB mutated
Neither mutated
CTNNB1 vs. UQCR10
mRNA Expression, RSEM (Batch normalized from Illumina HiSeq_RNASeqV2): UQCR10
mRNA Expression, RSEM (Batch normalized from Illumina HiSeq_RNASeqV2): CTNNB1 (3p22.1)
Spearman: -0.27
(p = 2.44e-8)
Pearson: -0.16
(p = 1.635e-3)
y = -0.02x + 1751.35
R² = 0.02
CTNNB1 mutated
Neither mutated
CTNNB1 vs. SYNJ2
mRNA Expression, RSEM (Batch normalized from Illumina HiSeq_RNASeqV2): SYNJ2
mRNA Expression, RSEM (Batch normalized from Illumina HiSeq_RNASeqV2): CTNNB1 (3p22.1)
Spearman: 0.31
(p = 2.21e-10)
Pearson: 0.16
(p = 9.098e-4)
y = 0.01x + 776.07
R² = 0.03
CTNNB1 mutated
SYNJ2 mutated
Both mutated
Neither mutated
CTNNB1 vs. SPR
mRNA Expression, RSEM (Batch normalized from Illumina HiSeq_RNASeqV2): SPR
mRNA Expression, RSEM (Batch normalized from Illumina HiSeq_RNASeqV2): CTNNB1 (3p22.1)
Spearman: -0.15
(p = 1.920e-3)
Pearson: -0.15
(p = 1.938e-3)
y = -0.01x + 1282.19
R² = 0.02
CTNNB1 mutated
SPR mutated
Neither mutated
CTNNB1 vs. SETDB2
mRNA Expression, RSEM (Batch normalized from Illumina HiSeq_RNASeqV2): SETDB2
mRNA Expression, RSEM (Batch normalized from Illumina HiSeq_RNASeqV2): CTNNB1 (3p22.1)
Spearman: 0.20
(p = 3.897e-5)
Pearson: 0.21
(p = 1.780e-5)
y = 0x + 368.28
R² = 0
CTNNB1 mutated
SETDB2 mutated
Both mutated
Neither mutated
CTNNB1 vs. PYCR1
mRNA Expression, RSEM (Batch normalized from Illumina HiSeq_RNASeqV2): PYCR1
mRNA Expression, RSEM (Batch normalized from Illumina HiSeq_RNASeqV2): CTNNB1 (3p22.1)
Spearman: -0.04
(p = 0.466)
Pearson: 0.16
(p = 1.063e-3)
y = 0.03x + 1725.97
R² = 0.03
CTNNB1 mutated
PYCR1 mutated
Neither mutated

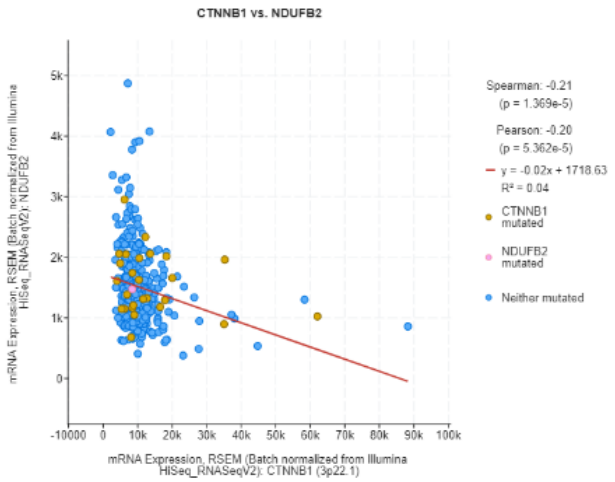

CTNNB1 vs. PRUNE1
Spearman: 0.06
(p = 0.208)
Pearson: 0.15
(p = 3.311e-3)
y = 0.01x + 561.1
R² = 0.01
CTNNB1 mutated
PRUNE1 mutated
Both mutated
Neither mutated
mRNA Expression, RSEM (Batch normalized from Illumina HiSeq_RNASeqV2): PRUNE1
mRNA Expression, RSEM (Batch normalized from Illumina HiSeq_RNASeqV2): CTNNB1 (3p22.1)

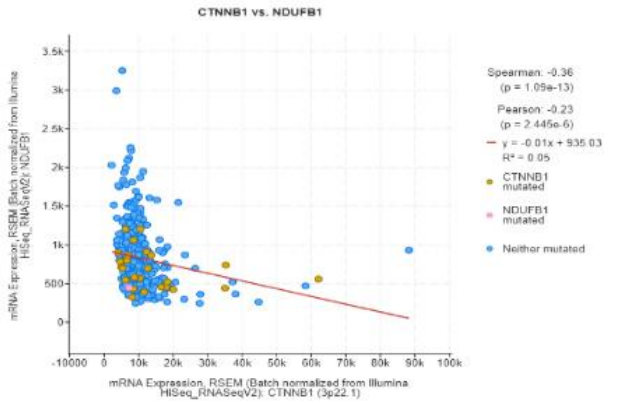

CTNNB1 vs. PPAT
Spearman: 0.14
(p = 3.455e-3)
Pearson: 0.21
(p = 1.214e-5)
y = 0.01x + 363.52
R² = 0.04
CTNNB1 mutated
PPAT mutated
Both mutated
Neither mutated
mRNA Expression, RSEM (Batch normalized from Illumina HiSeq_RNASeqV2): PPAT
mRNA Expression, RSEM (Batch normalized from Illumina HiSeq_RNASeqV2): CTNNB1 (3p22.1)

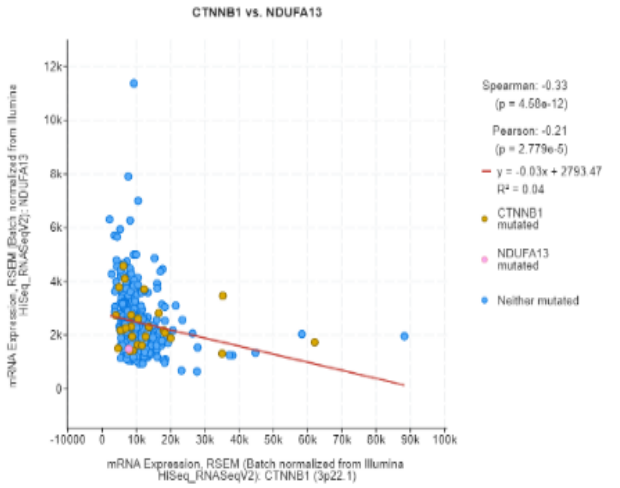

CTNNB1 vs. PMVK
Spearman: -0.34
(p = 1.96e-12)
Pearson: -0.19
(p = 7.892e-5)
y = -0.01x + 893.96
R² = 0.04
CTNNB1 mutated
Neither mutated
mRNA Expression, RSEM (Batch normalized from Illumina HiSeq_RNASeqV2): PMVK
mRNA Expression, RSEM (Batch normalized from Illumina HiSeq_RNASeqV2): CTNNB1 (3p22.1)

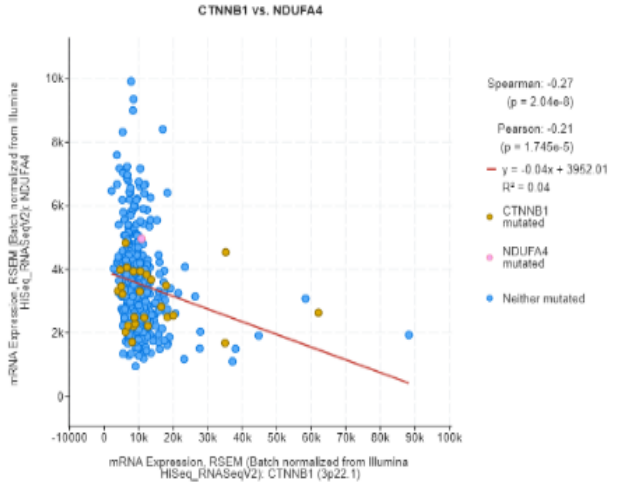

CTNNB1 vs. NT5C
Spearman: -0.29
(p = 3.20e-9)
Pearson: -0.16
(p = 1.030e-3)
y = -0.01x + 641.33
R² = 0
CTNNB1 mutated
Neither mutated
mRNA Expression, RSEM (Batch normalized from Illumina HiSeq_RNASeqV2): NT5C
mRNA Expression, RSEM (Batch normalized from Illumina HiSeq_RNASeqV2): CTNNB1 (3p22.1)

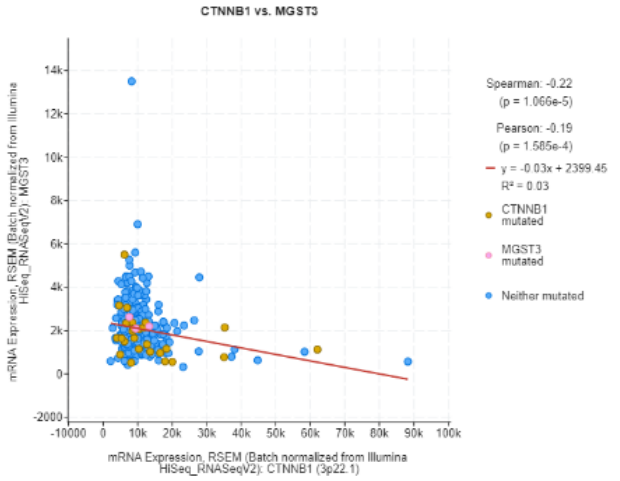

CTNNB1 vs. NDUFV2
Spearman: -0.28
(p = 1.33e-8)
Pearson: -0.22
(p = 5.628e-6)
y = -0.03x + 2365.81
R² = 0.05
CTNNB1 mutated
NDUFV2 mutated
Neither mutated
mRNA Expression, RSEM (Batch normalized from Illumina HiSeq_RNASeqV2): NDUFV2
mRNA Expression, RSEM (Batch normalized from Illumina HiSeq_RNASeqV2): CTNNB1 (3p22.1)

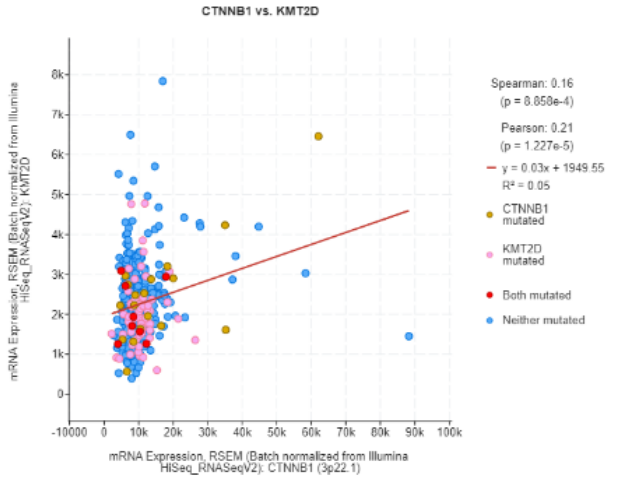

CTNNB1 vs. NDUFB2
Spearman: -0.21
(p = 1.369e-5)
Pearson: -0.20
(p = 5.362e-5)
y = -0.02x + 1718.63
R² = 0.04
CTNNB1 mutated
NDUFB2 mutated
Neither mutated
mRNA Expression, RSEM (Batch normalized from Illumina HiSeq_RNASeqV2): NDUFB2
mRNA Expression, RSEM (Batch normalized from Illumina HiSeq_RNASeqV2): CTNNB1 (3p22.1)

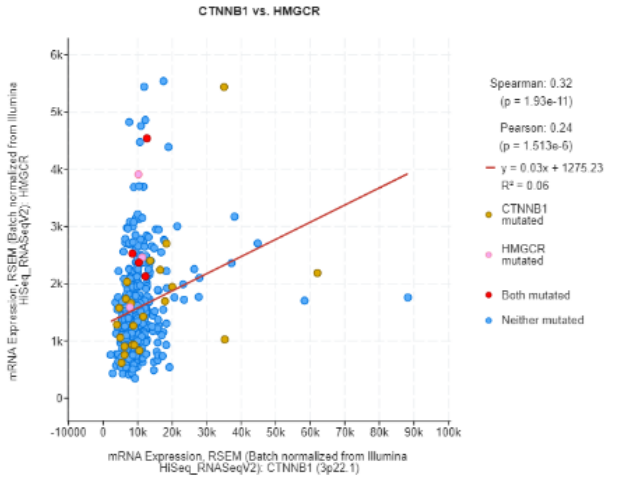

CTNNB1 vs. NDUFB1
Spearman: -0.36
(p = 1.09e-13)
Pearson: -0.23
(p = 2.445e-6)
y = -0.01x + 935.03
R² = 0.05
CTNNB1 mutated
NDUFB1 mutated
Neither mutated
mRNA Expression, RSEM (Batch normalized from Illumina HiSeq_RNASeqV2): NDUFB1
mRNA Expression, RSEM (Batch normalized from Illumina HiSeq_RNASeqV2): CTNNB1 (3p22.1)

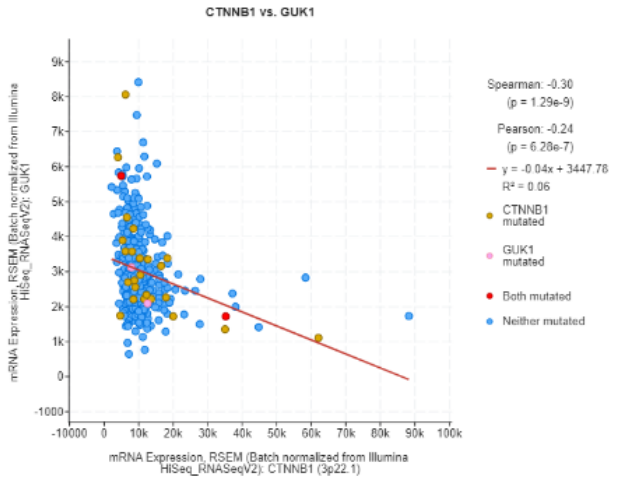

CTNNB1 vs. NDUFA13
Spearman: -0.33
(p = 4.58e-12)
Pearson: -0.21
(p = 2.779e-5)
y = -0.03x + 2793.47
R² = 0.04
CTNNB1 mutated
NDUFA13 mutated
Neither mutated
mRNA Expression, RSEM (Batch normalized from Illumina HiSeq_RNASeqV2): NDUFA13
mRNA Expression, RSEM (Batch normalized from Illumina HiSeq_RNASeqV2): CTNNB1 (3p22.1)

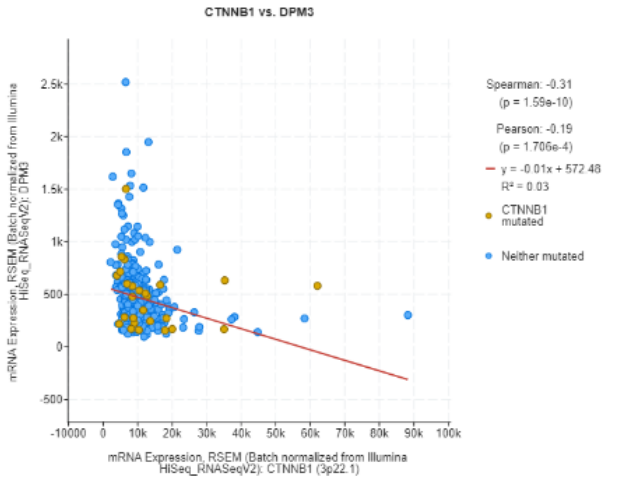

CTNNB1 vs. NDUFA4
Spearman: -0.27
(p = 2.04e-8)
Pearson: -0.21
(p = 1.745e-5)
y = -0.04x + 3952.01
R² = 0.04
CTNNB1 mutated
NDUFA4 mutated
Neither mutated
mRNA Expression, RSEM (Batch normalized from Illumina HiSeq_RNASeqV2): NDUFA4
mRNA Expression, RSEM (Batch normalized from Illumina HiSeq_RNASeqV2): CTNNB1 (3p22.1)

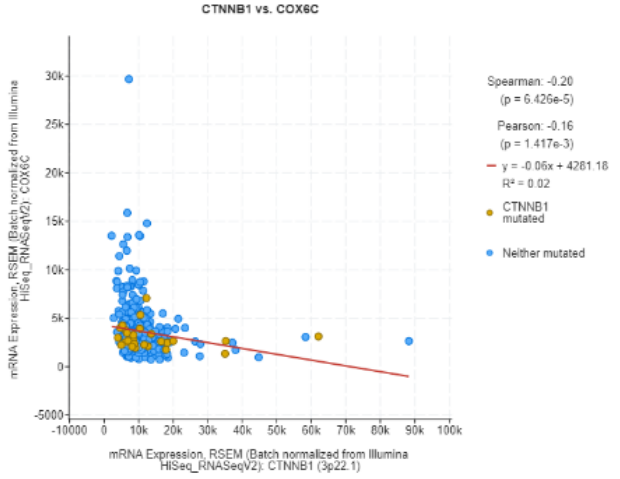

CTNNB1 vs. MGST3
Spearman: -0.22
(p = 1.066e-5)
Pearson: -0.19
(p = 1.585e-4)
y = -0.03x + 2399.45
R² = 0.03
CTNNB1 mutated
MGST3 mutated
Neither mutated
mRNA Expression, RSEM (Batch normalized from Illumina HiSeq_RNASeqV2): MGST3
mRNA Expression, RSEM (Batch normalized from Illumina HiSeq_RNASeqV2): CTNNB1 (3p22.1)

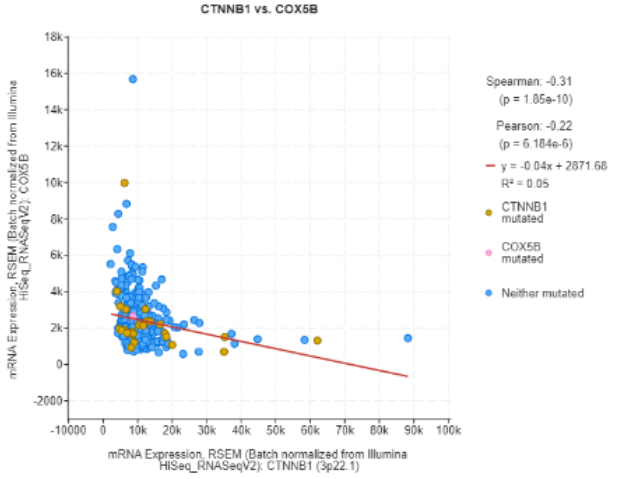

CTNNB1 vs. KMT2D
Spearman: 0.16
(p = 8.658e-4)
Pearson: 0.21
(p = 1.227e-5)
y = 0.03x + 1949.55
R² = 0.05
CTNNB1 mutated
KMT2D mutated
Both mutated
Neither mutated
mRNA Expression, RSEM (Batch normalized from Illumina HiSeq_RNASeqV2): KMT2D
mRNA Expression, RSEM (Batch normalized from Illumina HiSeq_RNASeqV2): CTNNB1 (3p22.1)

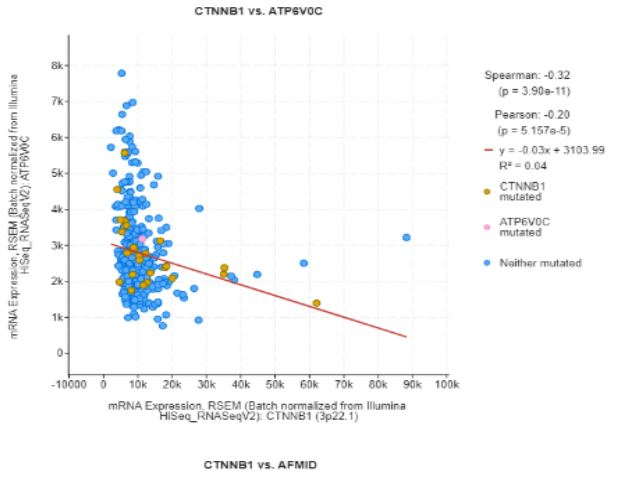

CTNNB1 vs. HMGCR
Spearman: 0.32
(p = 1.93e-11)
Pearson: 0.24
(p = 1.513e-6)
y = 0.03x + 1275.23
R² = 0.06
CTNNB1 mutated
HMGCR mutated
Both mutated
Neither mutated
mRNA Expression, RSEM (Batch normalized from Illumina HiSeq_RNASeqV2): HMGCR
mRNA Expression, RSEM (Batch normalized from Illumina HiSeq_RNASeqV2): CTNNB1 (3p22.1)

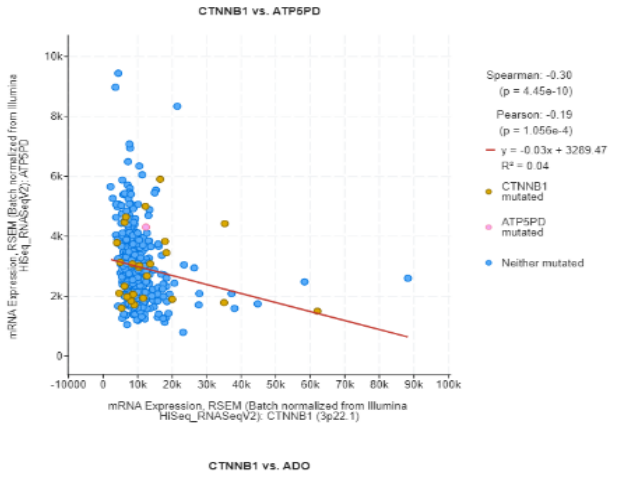

CTNNB1 vs. GUK1
mRNA Expression, RSEM (Batch normalized from Illumina HiSeq_RNASeqV2): GUK1
mRNA Expression, RSEM (Batch normalized from Illumina HiSeq_RNASeqV2): CTNNB1 (3p22.1)
Spearman: -0.30
(p = 1.29e-9)
Pearson: -0.24
(p = 6.28e-7)
y = -0.04x + 3447.78
R² = 0.06
CTNNB1 mutated
GUK1 mutated
Both mutated
Neither mutated

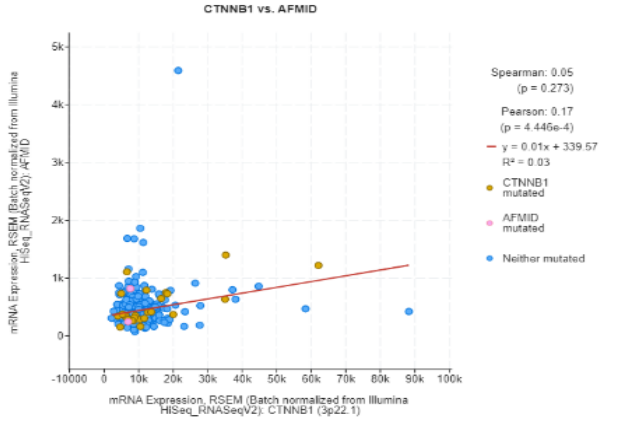

CTNNB1 vs. DPM3
mRNA Expression, RSEM (Batch normalized from Illumina HiSeq_RNASeqV2): DPM3
mRNA Expression, RSEM (Batch normalized from Illumina HiSeq_RNASeqV2): CTNNB1 (3p22.1)
Spearman: -0.31
(p = 1.59e-10)
Pearson: -0.19
(p = 1.706e-4)
y = -0.01x + 572.48
R² = 0.03
CTNNB1 mutated
Neither mutated

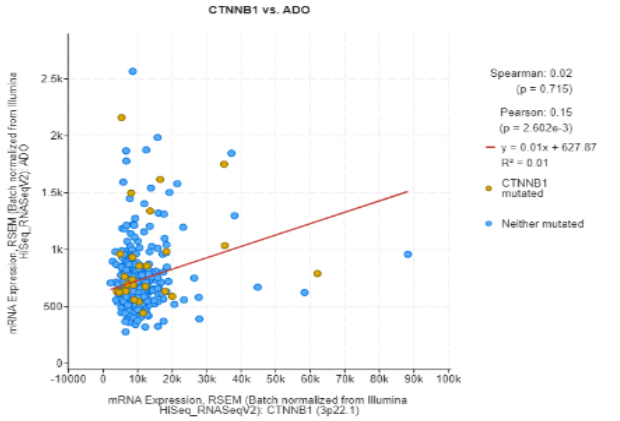

CTNNB1 vs. COX6C
mRNA Expression, RSEM (Batch normalized from Illumina HiSeq_RNASeqV2): COX6C
mRNA Expression, RSEM (Batch normalized from Illumina HiSeq_RNASeqV2): CTNNB1 (3p22.1)
Spearman: -0.20
(p = 6.426e-5)
Pearson: -0.16
(p = 1.417e-3)
y = -0.06x + 4281.18
R² = 0.02
CTNNB1 mutated
Neither mutated


CTNNB1 vs. COX5B
mRNA Expression, RSEM (Batch normalized from Illumina HiSeq_RNASeqV2): COX5B
mRNA Expression, RSEM (Batch normalized from Illumina HiSeq_RNASeqV2): CTNNB1 (3p22.1)
Spearman: -0.31
(p = 1.85e-10)
Pearson: -0.22
(p = 6.184e-6)
y = -0.04x + 2871.68
R² = 0.05
CTNNB1 mutated
COX5B mutated
Neither mutated

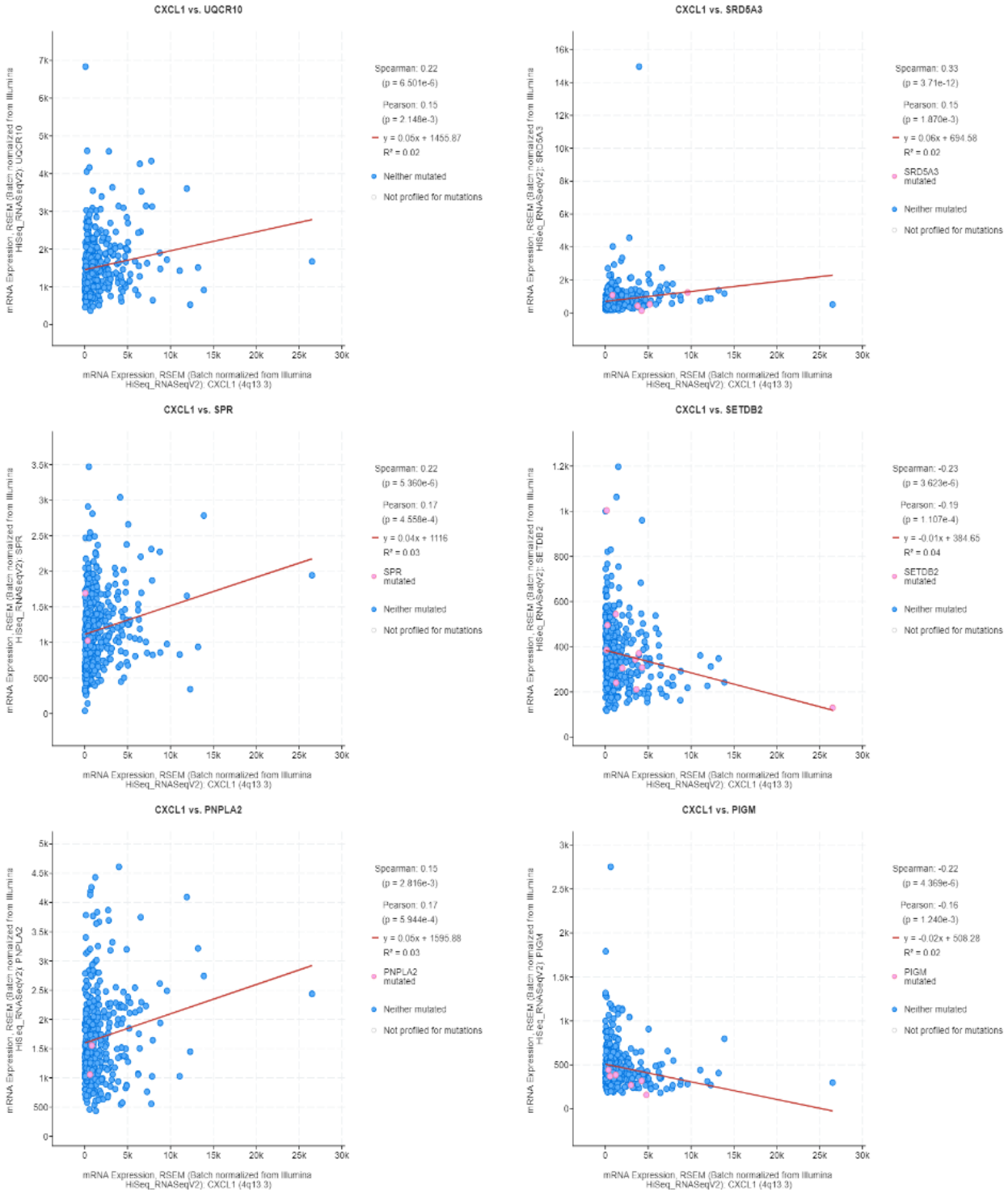

CTNNB1 vs. ATP6V0C
mRNA Expression, RSEM (Batch normalized from Illumina HiSeq_RNASeqV2): ATP6V0C
mRNA Expression, RSEM (Batch normalized from Illumina HiSeq_RNASeqV2): CTNNB1 (3p22.1)
Spearman: -0.32
(p = 3.90e-11)
Pearson: -0.20
(p = 5.157e-5)
y = -0.03x + 3103.99
R² = 0.04
CTNNB1 mutated
ATP6V0C mutated
Neither mutated

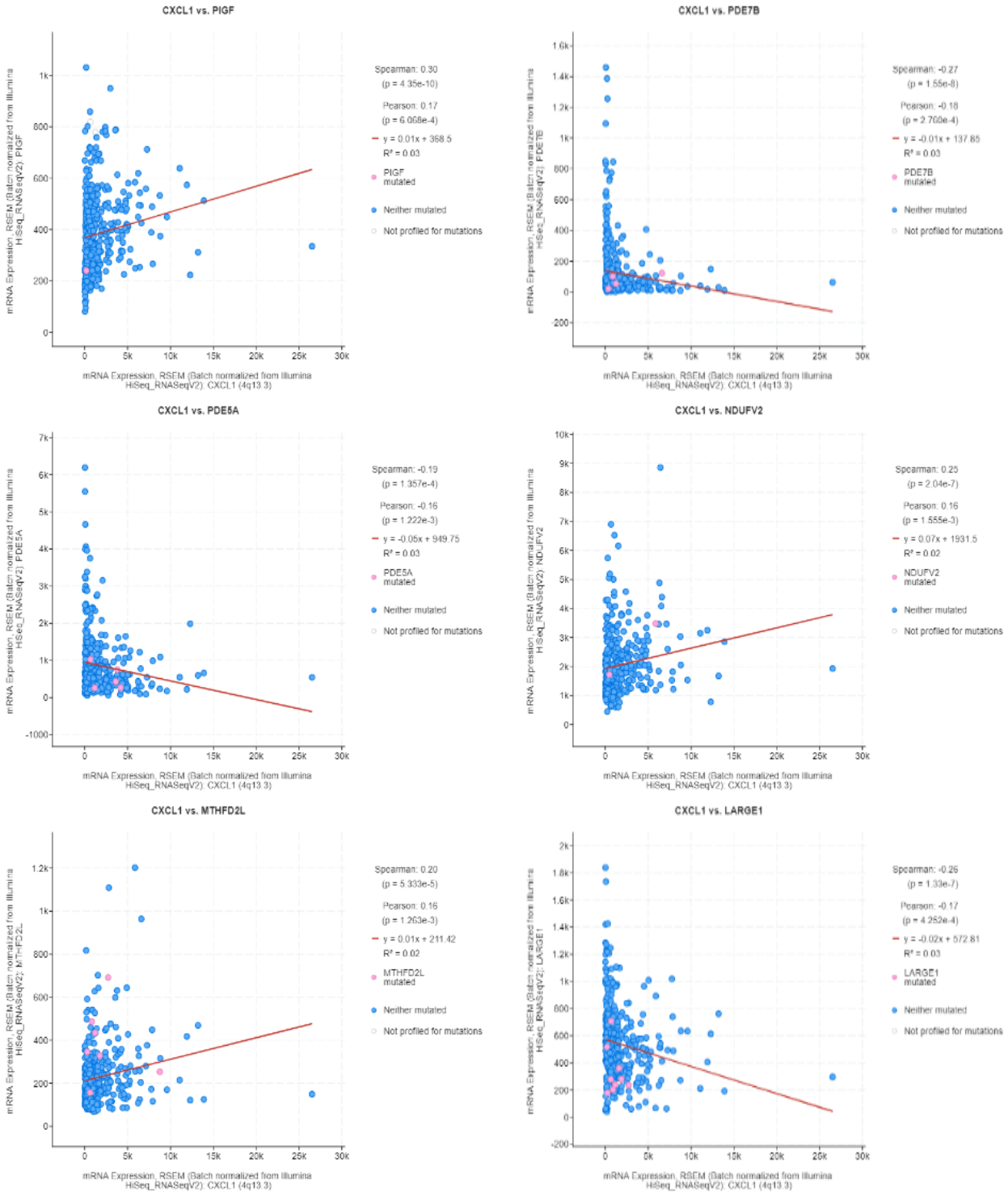

CTNNB1 vs. ATP5PD
mRNA Expression, RSEM (Batch normalized from Illumina HiSeq_RNASeqV2): ATP5PD
mRNA Expression, RSEM (Batch normalized from Illumina HiSeq_RNASeqV2): CTNNB1 (3p22.1)
Spearman: -0.30
(p = 4.45e-10)
Pearson: -0.19
(p = 1.056e-4)
y = -0.03x + 3289.47
R² = 0.04
CTNNB1 mutated
ATP5PD mutated
Neither mutated

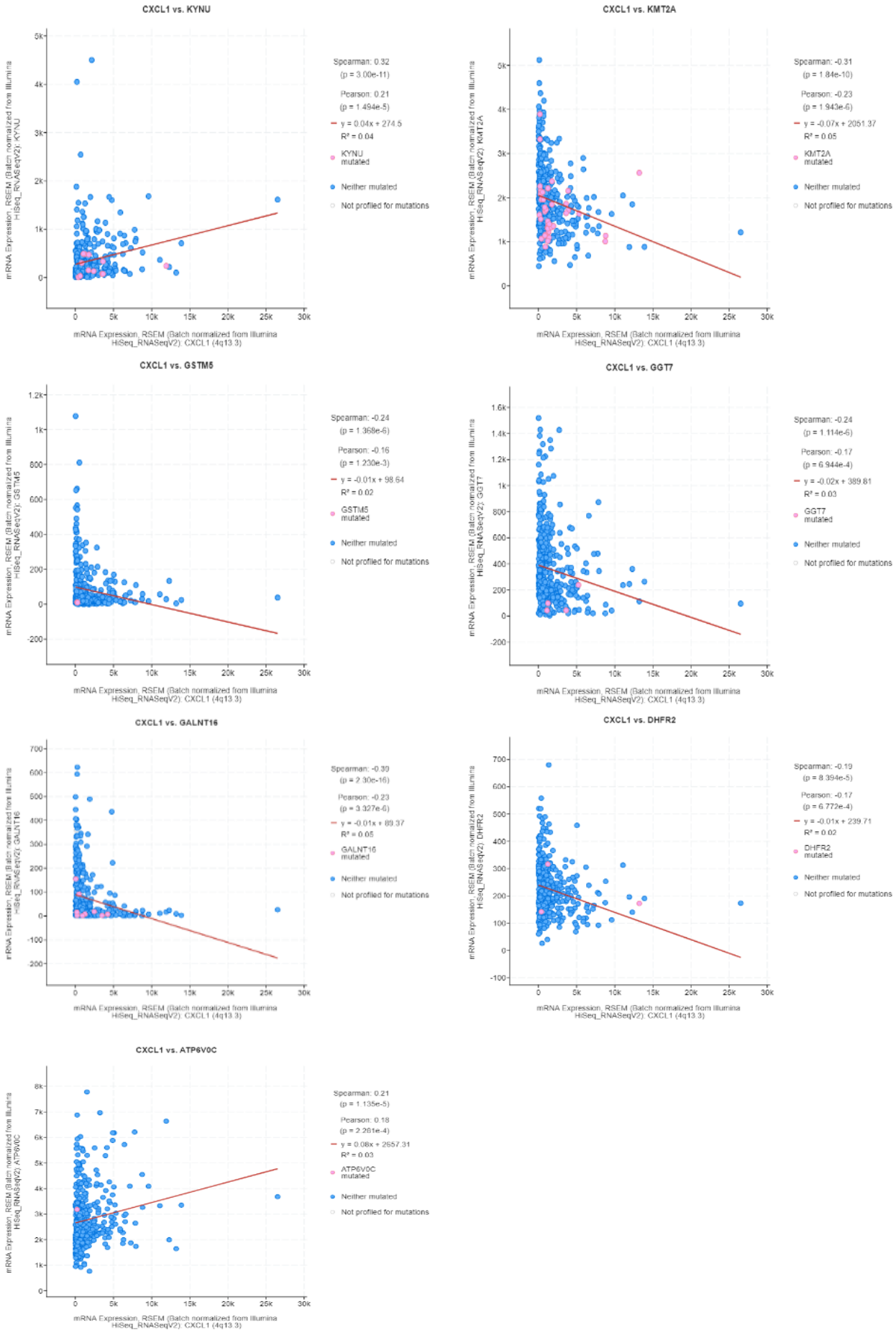

CTNNB1 vs. AFMID
mRNA Expression, RSEM (Batch normalized from Illumina HiSeq_RNASeqV2): AFMID
mRNA Expression, RSEM (Batch normalized from Illumina HiSeq_RNASeqV2): CTNNB1 (3p22.1)
Spearman: 0.05
(p = 0.273)
Pearson: 0.17
(p = 4.446e-4)
y = 0.01x + 339.57
R² = 0.03
CTNNB1 mutated
AFMID mutated
Neither mutated


CTNNB1 vs. ADO
mRNA Expression, RSEM (Batch normalized from Illumina HiSeq_RNASeqV2): ADO
mRNA Expression, RSEM (Batch normalized from Illumina HiSeq_RNASeqV2): CTNNB1 (3p22.1)
Spearman: 0.02
(p = 0.715)
Pearson: 0.15
(p = 2.602e-3)
y = 0.01x + 627.87
R² = 0.01
CTNNB1 mutated
Neither mutated

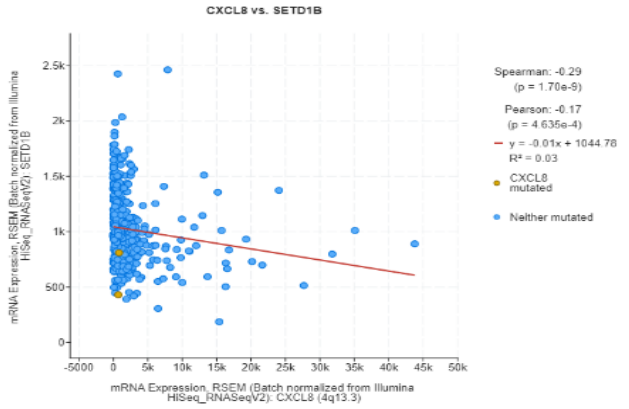
CXCL1

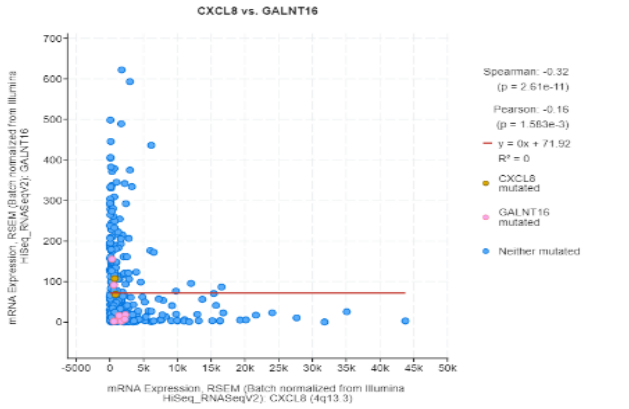

CXCL1 vs. UQCR10
mRNA Expression, RSEM (Batch normalized from Illumina HiSeq_RNASeqV2): UQCR10
mRNA Expression, RSEM (Batch normalized from Illumina HiSeq_RNASeqV2): CXCL1 (4q13.3)
Spearman: 0.22
(p = 6.501e-6)
Pearson: 0.15
(p = 2.148e-3)
y = 0.05x + 1455.87
R² = 0.02
Neither mutated
Not profiled for mutations
CXCL1 vs. SRD5A3
mRNA Expression, RSEM (Batch normalized from Illumina HiSeq_RNASeqV2): SRD5A3
mRNA Expression, RSEM (Batch normalized from Illumina HiSeq_RNASeqV2): CXCL1 (4q13.3)
Spearman: 0.33
(p = 3.71e-12)
Pearson: 0.15
(p = 1.870e-3)
y = 0.06x + 694.58
R² = 0.02
SRD5A3 mutated
Neither mutated
Not profiled for mutations
CXCL1 vs. SPR
mRNA Expression, RSEM (Batch normalized from Illumina HiSeq_RNASeqV2): SPR
mRNA Expression, RSEM (Batch normalized from Illumina HiSeq_RNASeqV2): CXCL1 (4q13.3)
Spearman: 0.22
(p = 5.360e-6)
Pearson: 0.17
(p = 4.558e-4)
y = 0.04x + 1116
R² = 0.03
SPR mutated
Neither mutated
Not profiled for mutations
CXCL1 vs. SETDB2
mRNA Expression, RSEM (Batch normalized from Illumina HiSeq_RNASeqV2): SETDB2
mRNA Expression, RSEM (Batch normalized from Illumina HiSeq_RNASeqV2): CXCL1 (4q13.3)
Spearman: -0.23
(p = 3.623e-6)
Pearson: -0.19
(p = 1.107e-4)
y = -0.01x + 384.65
R² = 0.04
SETDB2 mutated
Neither mutated
Not profiled for mutations
CXCL1 vs. PNPLA2
mRNA Expression, RSEM (Batch normalized from Illumina HiSeq_RNASeqV2): PNPLA2
mRNA Expression, RSEM (Batch normalized from Illumina HiSeq_RNASeqV2): CXCL1 (4q13.3)
Spearman: 0.15
(p = 2.816e-3)
Pearson: 0.17
(p = 5.944e-4)
y = 0.05x + 1595.88
R² = 0.03
PNPLA2 mutated
Neither mutated
Not profiled for mutations
CXCL1 vs. PIGM
mRNA Expression, RSEM (Batch normalized from Illumina HiSeq_RNASeqV2): PIGM
mRNA Expression, RSEM (Batch normalized from Illumina HiSeq_RNASeqV2): CXCL1 (4q13.3)
Spearman: -0.22
(p = 4.369e-6)
Pearson: -0.16
(p = 1.240e-3)
y = -0.02x + 508.28
R² = 0.02
PIGM mutated
Neither mutated
Not profiled for mutations

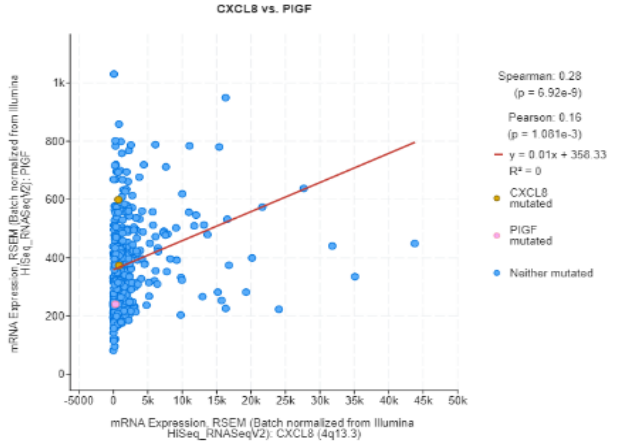

CXCL1 vs. PIGF
mRNA Expression, RSEM (Batch normalized from Illumina HiSeq_RNASeqV2): PIGF
mRNA Expression, RSEM (Batch normalized from Illumina HiSeq_RNASeqV2): CXCL1 (4q13.3)
Spearman: 0.30
(p = 4.35e-10)
Pearson: 0.17
(p = 6.068e-4)
y = 0.01x + 368.5
R² = 0.03
PIGF mutated
Neither mutated
Not profiled for mutations
CXCL1 vs. PDE7B
mRNA Expression, RSEM (Batch normalized from Illumina HiSeq_RNASeqV2): PDE7B
mRNA Expression, RSEM (Batch normalized from Illumina HiSeq_RNASeqV2): CXCL1 (4q13.3)
Spearman: -0.27
(p = 1.55e-8)
Pearson: -0.18
(p = 2.760e-4)
y = -0.01x + 137.85
R² = 0.03
PDE7B mutated
Neither mutated
Not profiled for mutations
CXCL1 vs. PDE5A
mRNA Expression, RSEM (Batch normalized from Illumina HiSeq_RNASeqV2): PDE5A
mRNA Expression, RSEM (Batch normalized from Illumina HiSeq_RNASeqV2): CXCL1 (4q13.3)
Spearman: -0.19
(p = 1.357e-4)
Pearson: -0.16
(p = 1.222e-3)
y = -0.05x + 949.75
R² = 0.03
PDE5A mutated
Neither mutated
Not profiled for mutations
CXCL1 vs. NDUFV2
mRNA Expression, RSEM (Batch normalized from Illumina HiSeq_RNASeqV2): NDUFV2
mRNA Expression, RSEM (Batch normalized from Illumina HiSeq_RNASeqV2): CXCL1 (4q13.3)
Spearman: 0.25
(p = 2.04e-7)
Pearson: 0.16
(p = 1.555e-3)
y = 0.07x + 1931.5
R² = 0.02
NDUFV2 mutated
Neither mutated
Not profiled for mutations
CXCL1 vs. MTHFD2L
mRNA Expression, RSEM (Batch normalized from Illumina HiSeq_RNASeqV2): MTHFD2L
mRNA Expression, RSEM (Batch normalized from Illumina HiSeq_RNASeqV2): CXCL1 (4q13.3)
Spearman: 0.20
(p = 5.333e-5)
Pearson: 0.16
(p = 1.263e-3)
y = 0.01x + 211.42
R² = 0.02
MTHFD2L mutated
Neither mutated
Not profiled for mutations
CXCL1 vs. LARGE1
mRNA Expression, RSEM (Batch normalized from Illumina HiSeq_RNASeqV2): LARGE1
mRNA Expression, RSEM (Batch normalized from Illumina HiSeq_RNASeqV2): CXCL1 (4q13.3)
Spearman: -0.25
(p = 1.33e-7)
Pearson: -0.17
(p = 4.252e-4)
y = -0.02x + 572.81
R² = 0.03
LARGE1 mutated
Neither mutated
Not profiled for mutations

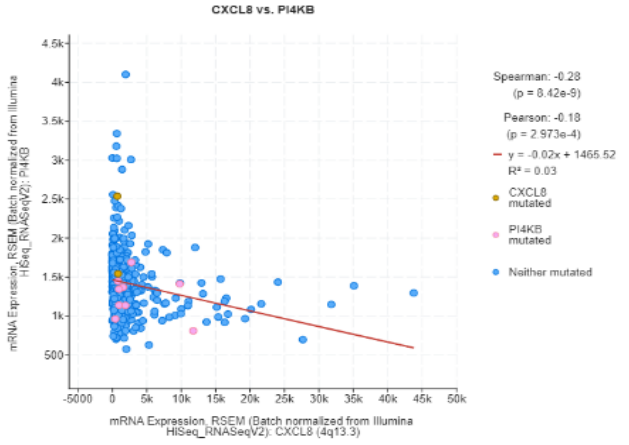

CXCL1 vs. KYNU
mRNA Expression, RSEM (Batch normalized from Illumina HiSeq_RNASeqV2): KYNU
mRNA Expression, RSEM (Batch normalized from Illumina HiSeq_RNASeqV2): CXCL1 (4q13.3)
Spearman: 0.32
(p = 3.00e-11)
Pearson: 0.21
(p = 1.494e-5)
y = 0.04x + 274.5
R² = 0.04
KYNU mutated
Neither mutated
Not profiled for mutations
CXCL1 vs. KMT2A
mRNA Expression, RSEM (Batch normalized from Illumina HiSeq_RNASeqV2): KMT2A
mRNA Expression, RSEM (Batch normalized from Illumina HiSeq_RNASeqV2): CXCL1 (4q13.3)
Spearman: -0.31
(p = 1.84e-10)
Pearson: -0.23
(p = 1.943e-6)
y = -0.07x + 2051.37
R² = 0.05
KMT2A mutated
Neither mutated
Not profiled for mutations
CXCL1 vs. GSTM5
mRNA Expression, RSEM (Batch normalized from Illumina HiSeq_RNASeqV2): GSTM5
mRNA Expression, RSEM (Batch normalized from Illumina HiSeq_RNASeqV2): CXCL1 (4q13.3)
Spearman: -0.24
(p = 1.368e-6)
Pearson: -0.16
(p = 1.230e-3)
y = -0.01x + 98.64
R² = 0.02
GSTM5 mutated
Neither mutated
Not profiled for mutations
CXCL1 vs. GGT7
mRNA Expression, RSEM (Batch normalized from Illumina HiSeq_RNASeqV2): GGT7
mRNA Expression, RSEM (Batch normalized from Illumina HiSeq_RNASeqV2): CXCL1 (4q13.3)
Spearman: -0.24
(p = 1.114e-6)
Pearson: -0.17
(p = 6.944e-4)
y = -0.02x + 389.81
R² = 0.03
GGT7 mutated
Neither mutated
Not profiled for mutations
CXCL1 vs. GALNT16
mRNA Expression, RSEM (Batch normalized from Illumina HiSeq_RNASeqV2): GALNT16
mRNA Expression, RSEM (Batch normalized from Illumina HiSeq_RNASeqV2): CXCL1 (4q13.3)
Spearman: -0.39
(p = 2.30e-16)
Pearson: -0.23
(p = 3.327e-6)
y = -0.01x + 89.37
R² = 0.05
GALNT16 mutated
Neither mutated
Not profiled for mutations
CXCL1 vs. DHFR2
mRNA Expression, RSEM (Batch normalized from Illumina HiSeq_RNASeqV2): DHFR2
mRNA Expression, RSEM (Batch normalized from Illumina HiSeq_RNASeqV2): CXCL1 (4q13.3)
Spearman: -0.19
(p = 8.394e-5)
Pearson: -0.17
(p = 6.772e-4)
y = -0.01x + 239.71
R² = 0.02
DHFR2 mutated
Neither mutated
Not profiled for mutations
CXCL1 vs. ATP6V0C
mRNA Expression, RSEM (Batch normalized from Illumina HiSeq_RNASeqV2): ATP6V0C
mRNA Expression, RSEM (Batch normalized from Illumina HiSeq_RNASeqV2): CXCL1 (4q13.3)
Spearman: 0.21
(p = 1.135e-5)
Pearson: 0.18
(p = 2.261e-4)
y = 0.08x + 2657.31
R² = 0.03
ATP6V0C mutated
Neither mutated
Not profiled for mutations

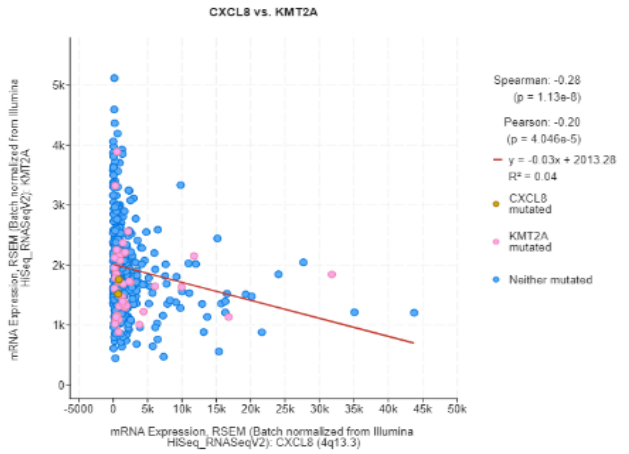
CXCL8

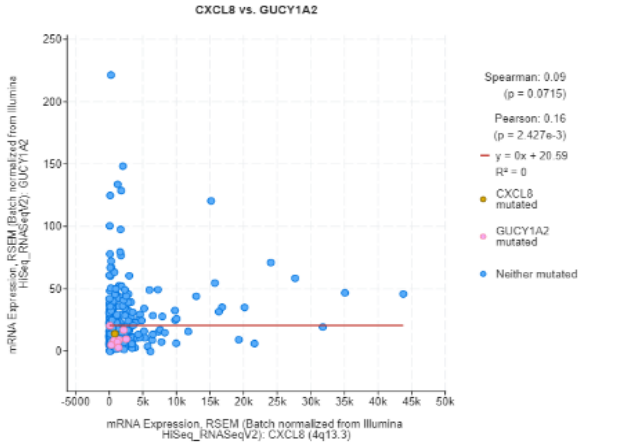

CXCL8 vs. SETD1B
mRNA Expression, RSEM (Batch normalized from Illumina HiSeq_RNASeqV2): SETD1B
mRNA Expression, RSEM (Batch normalized from Illumina HiSeq_RNASeqV2): CXCL8 (4q13.3)
Spearman: -0.29
(p = 1.70e-9)
Pearson: -0.17
(p = 4.635e-4)
y = -0.01x + 1044.76
R² = 0.03
CXCL8 mutated
Neither mutated

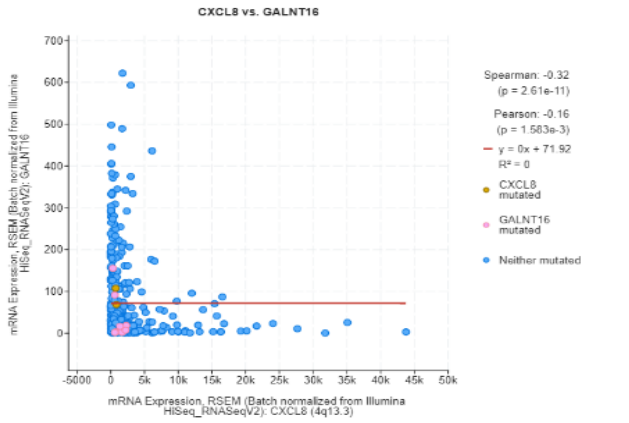

CXCL8 vs. GALNT16
mRNA Expression, RSEM (Batch normalized from Illumina HiSeq_RNASeqV2): GALNT16
mRNA Expression, RSEM (Batch normalized from Illumina HiSeq_RNASeqV2): CXCL8 (4q13.3)
Spearman: -0.32
(p = 2.61e-11)
Pearson: -0.16
(p = 1.583e-3)
y = 0x + 71.92
R² = 0
CXCL8 mutated
GALNT16 mutated
Neither mutated

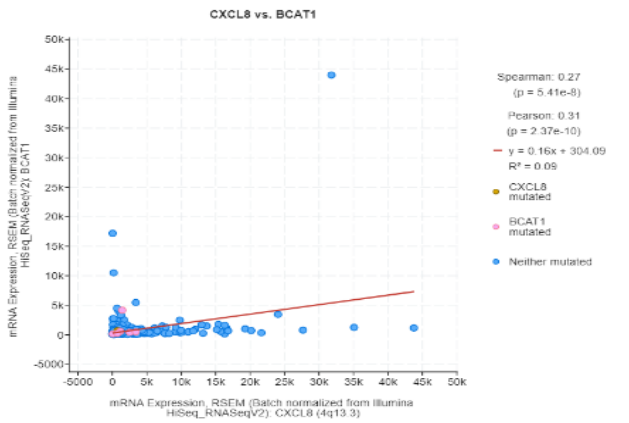

CXCL8 vs. PIGF
mRNA Expression, RSEM (Batch normalized from Illumina HiSeq_RNASeqV2): PIGF
mRNA Expression, RSEM (Batch normalized from Illumina HiSeq_RNASeqV2): CXCL8 (4q13.3)
Spearman: 0.28
(p = 6.92e-9)
Pearson: 0.16
(p = 1.081e-3)
y = 0.01x + 358.33
R² = 0
CXCL8 mutated
PIGF mutated
Neither mutated


CXCL8 vs. PI4KB
mRNA Expression, RSEM (Batch normalized from Illumina HiSeq_RNASeqV2): PI4KB
mRNA Expression, RSEM (Batch normalized from Illumina HiSeq_RNASeqV2): CXCL8 (4q13.3)
Spearman: -0.28
(p = 8.42e-9)
Pearson: -0.18
(p = 2.973e-4)
y = -0.02x + 1465.52
R² = 0.03
CXCL8 mutated
PI4KB mutated
Neither mutated

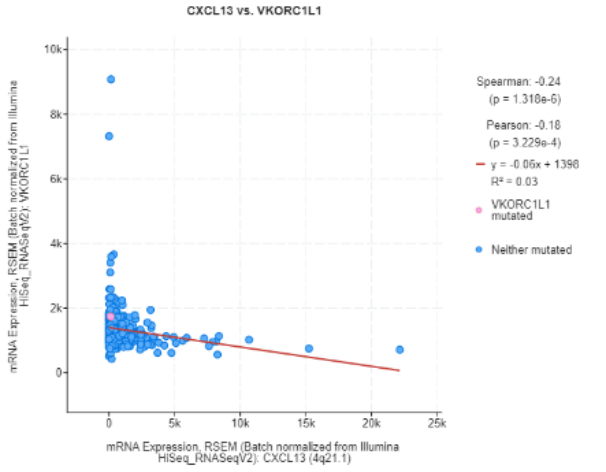

CXCL8 vs. KMT2A
mRNA Expression, RSEM (Batch normalized from Illumina HiSeq_RNASeqV2): KMT2A
mRNA Expression, RSEM (Batch normalized from Illumina HiSeq_RNASeqV2): CXCL8 (4q13.3)
Spearman: -0.28
(p = 1.13e-8)
Pearson: -0.20
(p = 4.046e-5)
y = -0.03x + 2013.28
R² = 0.04
CXCL8 mutated
KMT2A mutated
Neither mutated

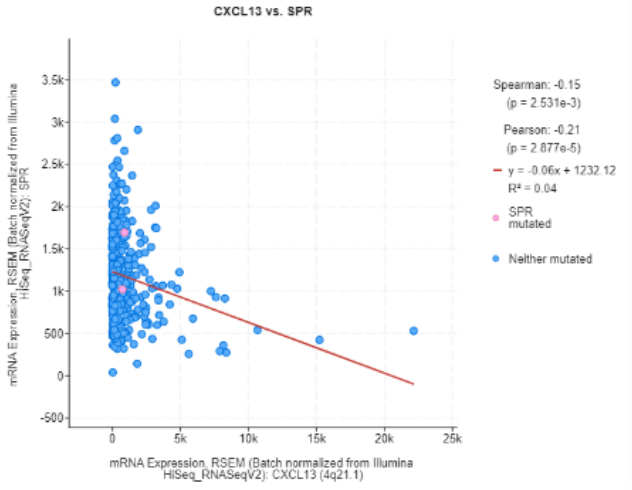

CXCL8 vs. GUCY1A2
mRNA Expression, RSEM (Batch normalized from Illumina HiSeq_RNASeqV2): GUCY1A2
mRNA Expression, RSEM (Batch normalized from Illumina HiSeq_RNASeqV2): CXCL8 (4q13.3)
Spearman: 0.09
(p = 0.0715)
Pearson: 0.16
(p = 2.427e-3)
y = 0x + 20.59
R² = 0
CXCL8 mutated
GUCY1A2 mutated
Neither mutated

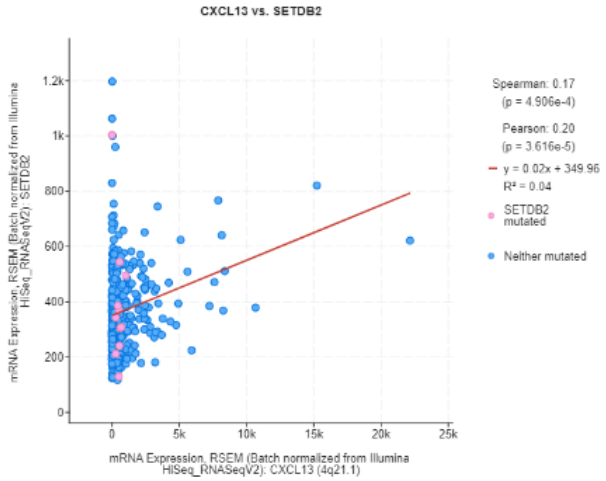

CXCL8 vs. GALNT16
mRNA Expression, RSEM (Batch normalized from Illumina HiSeq_RNASeqV2): GALNT16
mRNA Expression, RSEM (Batch normalized from Illumina HiSeq_RNASeqV2): CXCL8 (4q13.3)
Spearman: -0.32
(p = 2.61e-11)
Pearson: -0.16
(p = 1.583e-3)
y = 0x + 71.92
R² = 0
CXCL8 mutated
GALNT16 mutated
Neither mutated

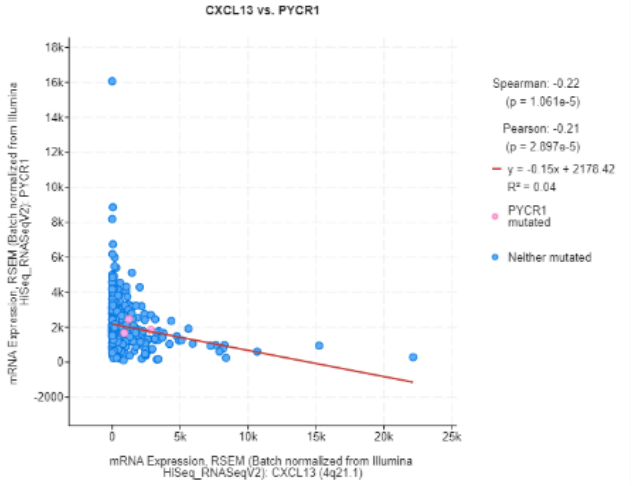

CXCL8 vs. BCAT1
mRNA Expression, RSEM (Batch normalized from Illumina HiSeq_RNASeqV2): BCAT1
mRNA Expression, RSEM (Batch normalized from Illumina HiSeq_RNASeqV2): CXCL8 (4q13.3)
Spearman: 0.27
(p = 5.41e-8)
Pearson: 0.31
(p = 2.37e-10)
y = 0.16x + 304.09
R² = 0.09
CXCL8 mutated
BCAT1 mutated
Neither mutated

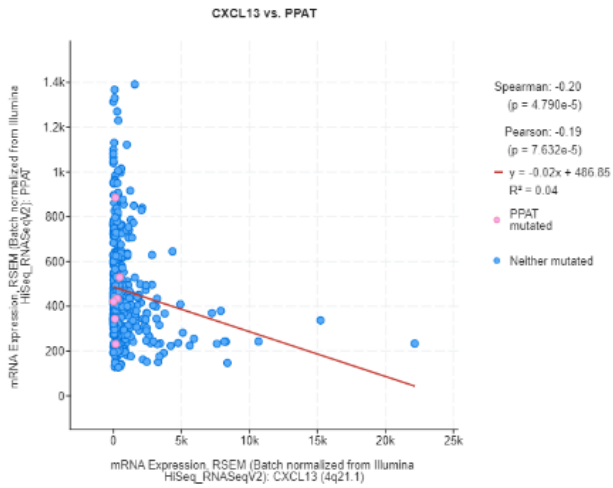
CXCL13

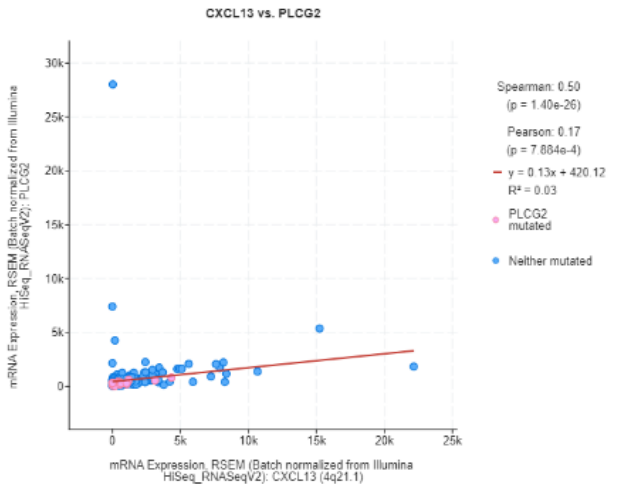

CXCL13 vs. VKORC1L1
Spearman: -0.24
(p = 1.318e-6)
Pearson: -0.18
(p = 3.229e-4)
y = -0.06x + 1396
R² = 0.03
VKORC1L1 mutated
Neither mutated
mRNA Expression, RSEM (Batch normalized from Illumina HiSeq_RNASeqV2): VKORC1L1
mRNA Expression, RSEM (Batch normalized from Illumina HiSeq_RNASeqV2): CXCL13 (4q21.1)

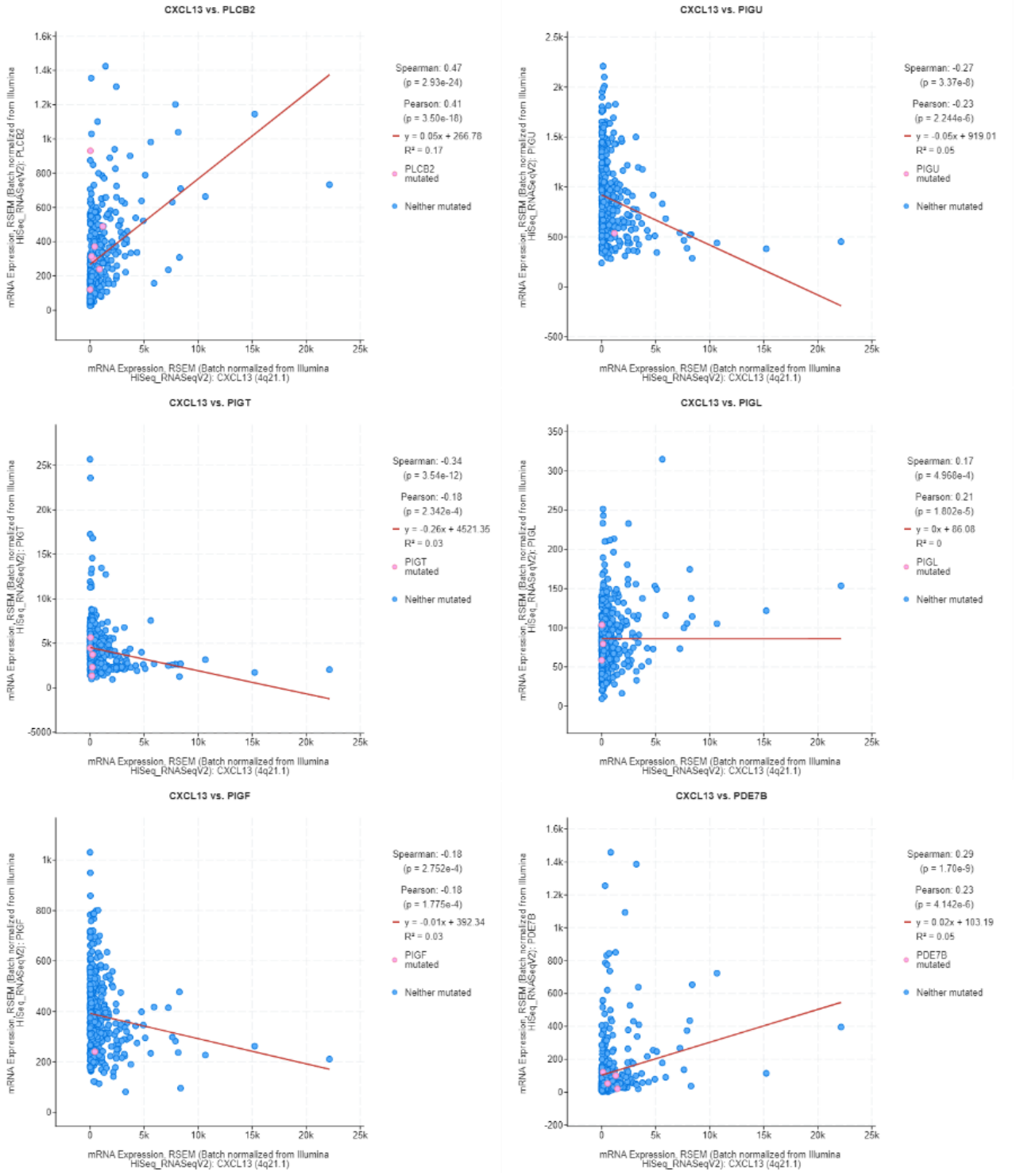

CXCL13 vs. SPR
Spearman: -0.15
(p = 2.531e-3)
Pearson: -0.21
(p = 2.877e-5)
y = -0.06x + 1232.12
R² = 0.04
SPR mutated
Neither mutated
mRNA Expression, RSEM (Batch normalized from Illumina HiSeq_RNASeqV2): SPR
mRNA Expression, RSEM (Batch normalized from Illumina HiSeq_RNASeqV2): CXCL13 (4q21.1)

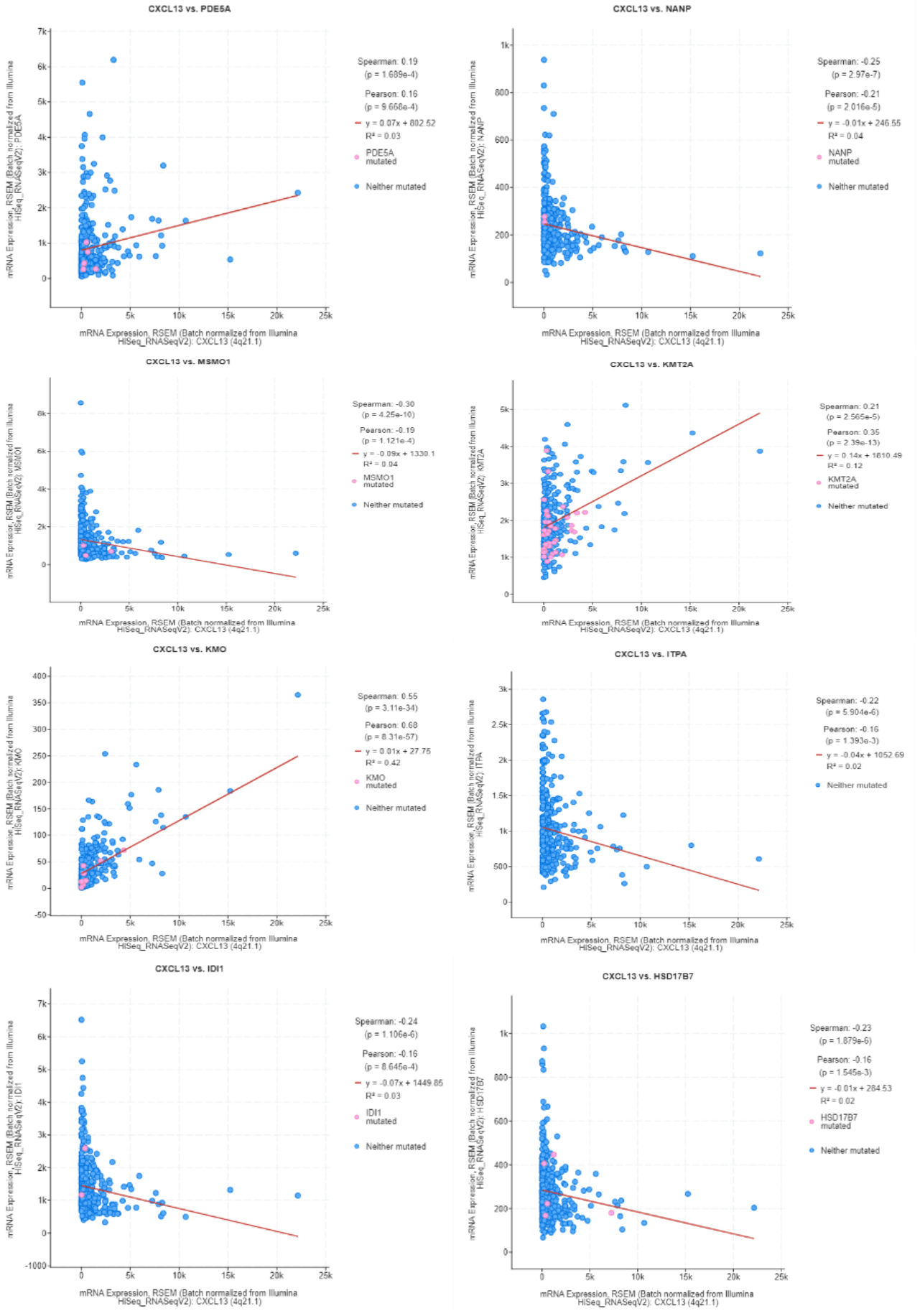

CXCL13 vs. SETDB2
Spearman: 0.17
(p = 4.906e-4)
Pearson: 0.20
(p = 3.616e-5)
y = 0.02x + 349.96
R² = 0.04
SETDB2 mutated
Neither mutated
mRNA Expression, RSEM (Batch normalized from Illumina HiSeq_RNASeqV2): SETDB2
mRNA Expression, RSEM (Batch normalized from Illumina HiSeq_RNASeqV2): CXCL13 (4q21.1)

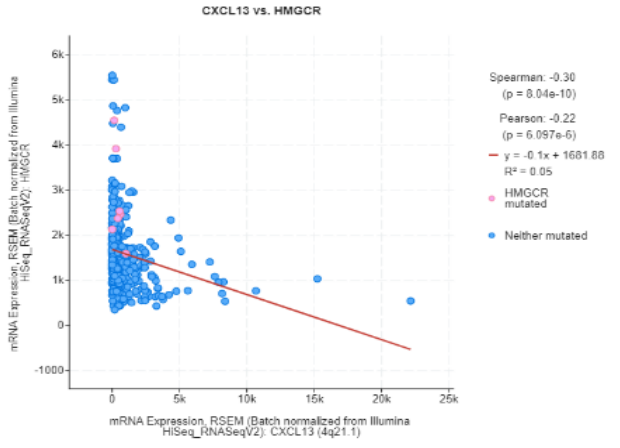

CXCL13 vs. PYCR1
Spearman: -0.22
(p = 1.061e-5)
Pearson: -0.21
(p = 2.897e-5)
y = -0.15x + 2178.42
R² = 0.04
PYCR1 mutated
Neither mutated
mRNA Expression, RSEM (Batch normalized from Illumina HiSeq_RNASeqV2): PYCR1
mRNA Expression, RSEM (Batch normalized from Illumina HiSeq_RNASeqV2): CXCL13 (4q21.1)

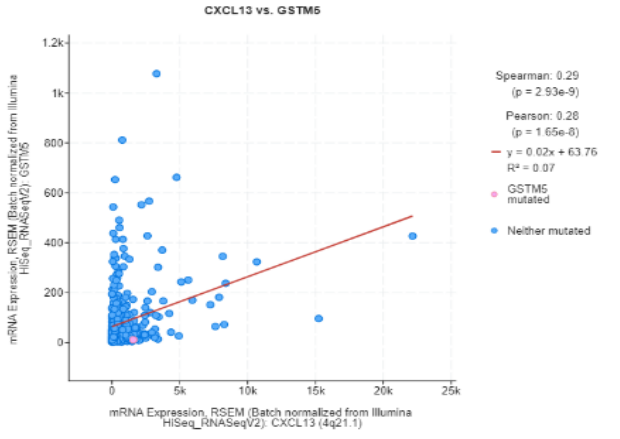

CXCL13 vs. PPAT
Spearman: -0.20
(p = 4.790e-5)
Pearson: -0.19
(p = 7.632e-5)
y = -0.02x + 486.85
R² = 0.04
PPAT mutated
Neither mutated
mRNA Expression, RSEM (Batch normalized from Illumina HiSeq_RNASeqV2): PPAT
mRNA Expression, RSEM (Batch normalized from Illumina HiSeq_RNASeqV2): CXCL13 (4q21.1)

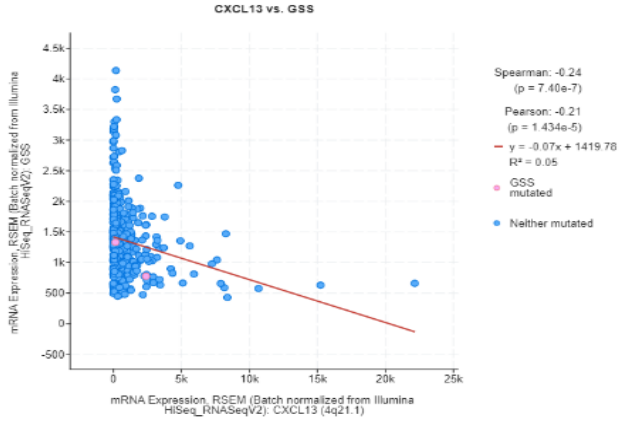

CXCL13 vs. PLCG2
Spearman: 0.50
(p = 1.40e-26)
Pearson: 0.17
(p = 7.884e-4)
y = 0.13x + 420.12
R² = 0.03
PLCG2 mutated
Neither mutated
mRNA Expression, RSEM (Batch normalized from Illumina HiSeq_RNASeqV2): PLCG2
mRNA Expression, RSEM (Batch normalized from Illumina HiSeq_RNASeqV2): CXCL13 (4q21.1)

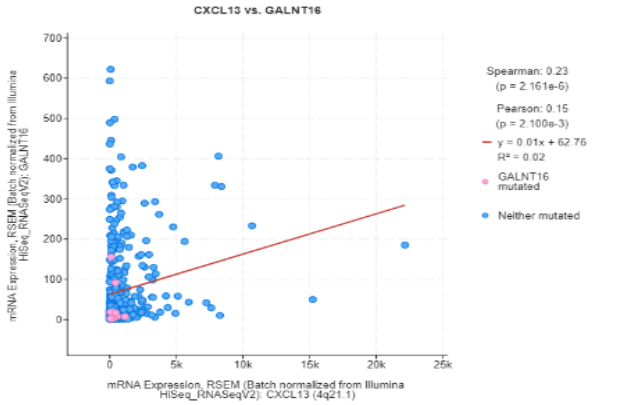

CXCL13 vs. PLCB2
Spearman: 0.47
(p = 2.93e-24)
Pearson: 0.41
(p = 3.50e-18)
y = 0.05x + 266.78
R² = 0.17
PLCB2 mutated
Neither mutated
mRNA Expression, RSEM (Batch normalized from Illumina HiSeq_RNASeqV2): PLCB2
mRNA Expression, RSEM (Batch normalized from Illumina HiSeq_RNASeqV2): CXCL13 (4q21.1)
CXCL13 vs. PIGU
Spearman: -0.27
(p = 3.37e-8)
Pearson: -0.23
(p = 2.244e-6)
y = -0.05x + 919.01
R² = 0.05
PIGU mutated
Neither mutated
mRNA Expression, RSEM (Batch normalized from Illumina HiSeq_RNASeqV2): PIGU
mRNA Expression, RSEM (Batch normalized from Illumina HiSeq_RNASeqV2): CXCL13 (4q21.1)
CXCL13 vs. PIGT
Spearman: -0.34
(p = 3.54e-12)
Pearson: -0.18
(p = 2.342e-4)
y = -0.26x + 4521.35
R² = 0.03
PIGT mutated
Neither mutated
mRNA Expression, RSEM (Batch normalized from Illumina HiSeq_RNASeqV2): PIGT
mRNA Expression, RSEM (Batch normalized from Illumina HiSeq_RNASeqV2): CXCL13 (4q21.1)
CXCL13 vs. PIGL
Spearman: 0.17
(p = 4.968e-4)
Pearson: 0.21
(p = 1.802e-5)
y = 0x + 86.08
R² = 0
PIGL mutated
Neither mutated
mRNA Expression, RSEM (Batch normalized from Illumina HiSeq_RNASeqV2): PIGL
mRNA Expression, RSEM (Batch normalized from Illumina HiSeq_RNASeqV2): CXCL13 (4q21.1)
CXCL13 vs. PIGF
Spearman: -0.18
(p = 2.752e-4)
Pearson: -0.18
(p = 1.775e-4)
y = -0.01x + 392.34
R² = 0.03
PIGF mutated
Neither mutated
mRNA Expression, RSEM (Batch normalized from Illumina HiSeq_RNASeqV2): PIGF
mRNA Expression, RSEM (Batch normalized from Illumina HiSeq_RNASeqV2): CXCL13 (4q21.1)
CXCL13 vs. PDE7B
Spearman: 0.29
(p = 1.70e-9)
Pearson: 0.23
(p = 4.142e-6)
y = 0.02x + 103.19
R² = 0.05
PDE7B mutated
Neither mutated
mRNA Expression, RSEM (Batch normalized from Illumina HiSeq_RNASeqV2): PDE7B
mRNA Expression, RSEM (Batch normalized from Illumina HiSeq_RNASeqV2): CXCL13 (4q21.1)

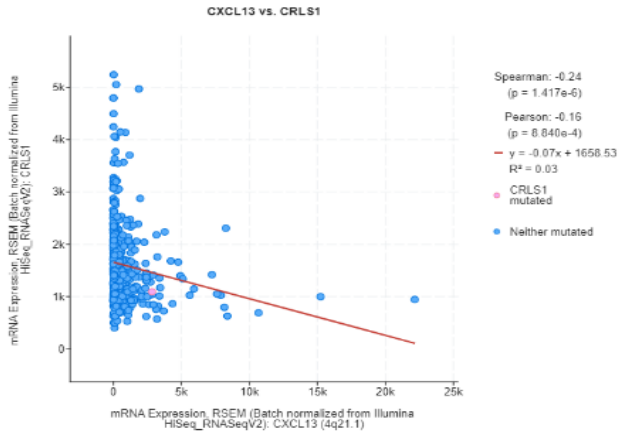

CXCL13 vs. PDE5A
mRNA Expression, RSEM (Batch normalized from Illumina HiSeq_RNASeqV2): PDE5A
mRNA Expression, RSEM (Batch normalized from Illumina HiSeq_RNASeqV2): CXCL13 (4q21.1)
Spearman: 0.19
(p = 1.689e-4)
Pearson: 0.16
(p = 9.668e-4)
y = 0.07x + 802.52
R² = 0.03
PDE5A mutated
Neither mutated
CXCL13 vs. NANP
mRNA Expression, RSEM (Batch normalized from Illumina HiSeq_RNASeqV2): NANP
mRNA Expression, RSEM (Batch normalized from Illumina HiSeq_RNASeqV2): CXCL13 (4q21.1)
Spearman: -0.25
(p = 2.97e-7)
Pearson: -0.21
(p = 2.016e-5)
y = -0.01x + 246.55
R² = 0.04
NANP mutated
Neither mutated
CXCL13 vs. MSMO1
mRNA Expression, RSEM (Batch normalized from Illumina HiSeq_RNASeqV2): MSMO1
mRNA Expression, RSEM (Batch normalized from Illumina HiSeq_RNASeqV2): CXCL13 (4q21.1)
Spearman: -0.30
(p = 4.25e-10)
Pearson: -0.19
(p = 1.121e-4)
y = -0.09x + 1330.1
R² = 0.04
MSMO1 mutated
Neither mutated
CXCL13 vs. KMT2A
mRNA Expression, RSEM (Batch normalized from Illumina HiSeq_RNASeqV2): KMT2A
mRNA Expression, RSEM (Batch normalized from Illumina HiSeq_RNASeqV2): CXCL13 (4q21.1)
Spearman: 0.21
(p = 2.565e-5)
Pearson: 0.35
(p = 2.39e-13)
y = 0.14x + 1610.49
R² = 0.12
KMT2A mutated
Neither mutated
CXCL13 vs. KMO
mRNA Expression, RSEM (Batch normalized from Illumina HiSeq_RNASeqV2): KMO
mRNA Expression, RSEM (Batch normalized from Illumina HiSeq_RNASeqV2): CXCL13 (4q21.1)
Spearman: 0.55
(p = 3.11e-34)
Pearson: 0.68
(p = 8.31e-57)
y = 0.01x + 27.75
R² = 0.42
KMO mutated
Neither mutated
CXCL13 vs. ITPA
mRNA Expression, RSEM (Batch normalized from Illumina HiSeq_RNASeqV2): ITPA
mRNA Expression, RSEM (Batch normalized from Illumina HiSeq_RNASeqV2): CXCL13 (4q21.1)
Spearman: -0.22
(p = 5.904e-6)
Pearson: -0.16
(p = 1.393e-3)
y = -0.04x + 1052.69
R² = 0.02
Neither mutated
CXCL13 vs. IDI1
mRNA Expression, RSEM (Batch normalized from Illumina HiSeq_RNASeqV2): IDI1
mRNA Expression, RSEM (Batch normalized from Illumina HiSeq_RNASeqV2): CXCL13 (4q21.1)
Spearman: -0.24
(p = 1.106e-6)
Pearson: -0.16
(p = 8.645e-4)
y = -0.07x + 1449.85
R² = 0.03
IDI1 mutated
Neither mutated
CXCL13 vs. HSD17B7
mRNA Expression, RSEM (Batch normalized from Illumina HiSeq_RNASeqV2): HSD17B7
mRNA Expression, RSEM (Batch normalized from Illumina HiSeq_RNASeqV2): CXCL13 (4q21.1)
Spearman: -0.23
(p = 1.879e-6)
Pearson: -0.16
(p = 1.545e-3)
y = -0.01x + 284.53
R² = 0.02
HSD17B7 mutated
Neither mutated

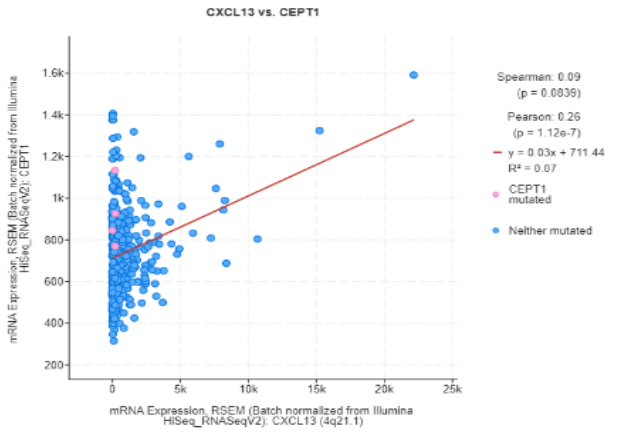

CXCL13 vs. HMGCR
mRNA Expression, RSEM (Batch normalized from Illumina HiSeq_RNASeqV2): HMGCR
mRNA Expression, RSEM (Batch normalized from Illumina HiSeq_RNASeqV2): CXCL13 (4q21.1)
Spearman: -0.30
(p = 8.04e-10)
Pearson: -0.22
(p = 6.097e-6)
y = -0.1x + 1681.88
R² = 0.05
HMGCR mutated
Neither mutated

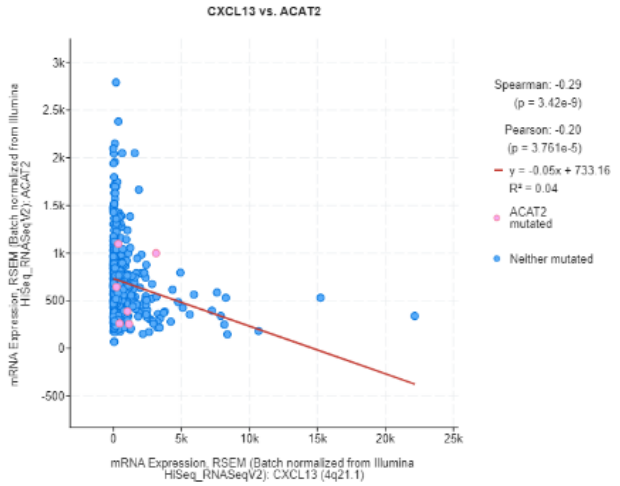

CXCL13 vs. GSTM5
mRNA Expression, RSEM (Batch normalized from Illumina HiSeq_RNASeqV2): GSTM5
mRNA Expression, RSEM (Batch normalized from Illumina HiSeq_RNASeqV2): CXCL13 (4q21.1)
Spearman: 0.29
(p = 2.93e-9)
Pearson: 0.28
(p = 1.65e-8)
y = 0.02x + 63.76
R² = 0.07
GSTM5 mutated
Neither mutated


CXCL13 vs. GSS
mRNA Expression, RSEM (Batch normalized from Illumina HiSeq_RNASeqV2): GSS
mRNA Expression, RSEM (Batch normalized from Illumina HiSeq_RNASeqV2): CXCL13 (4q21.1)
Spearman: -0.24
(p = 7.40e-7)
Pearson: -0.21
(p = 1.434e-5)
y = -0.07x + 1419.78
R² = 0.05
GSS mutated
Neither mutated

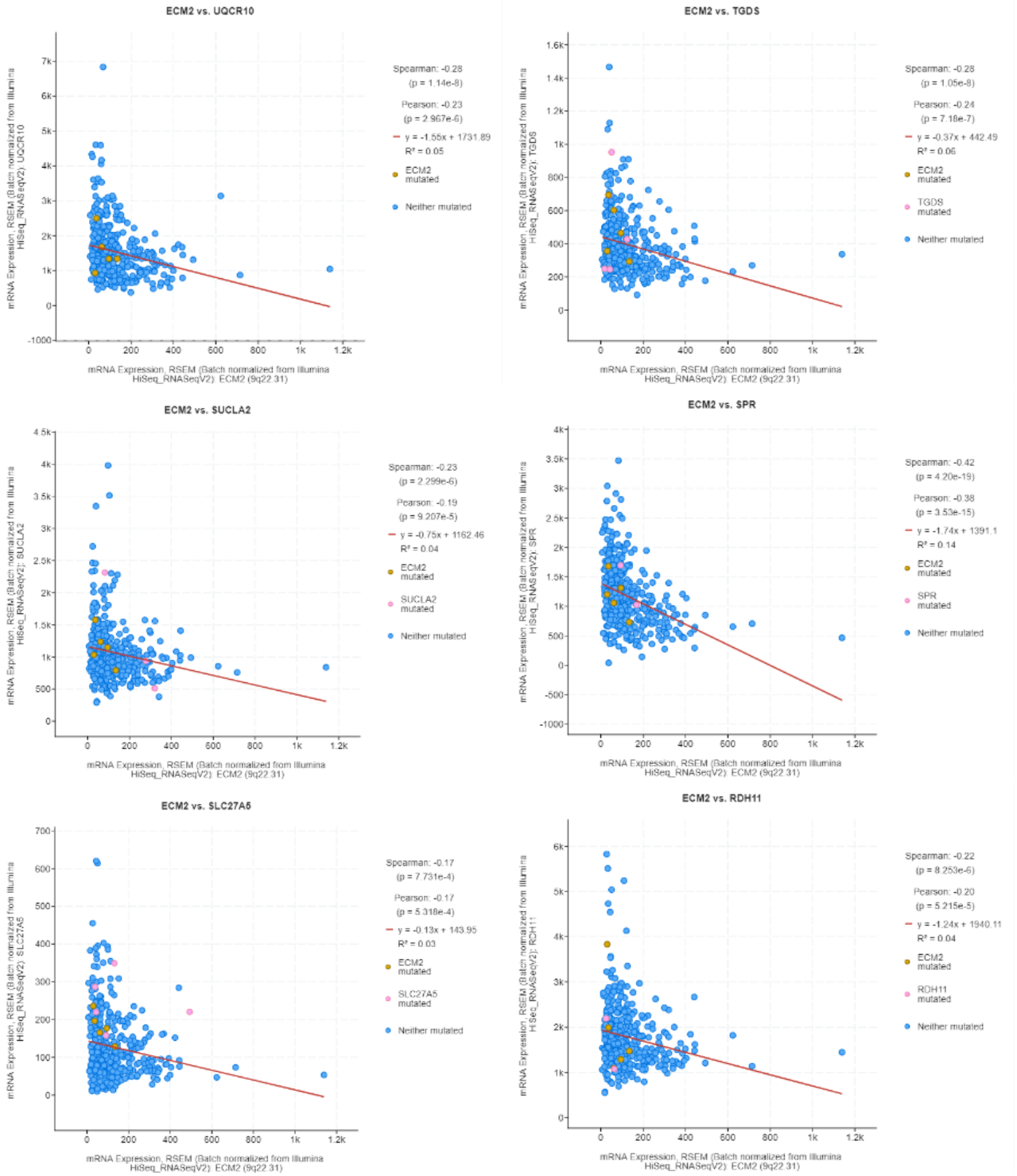

CXCL13 vs. GALNT16
mRNA Expression, RSEM (Batch normalized from Illumina HiSeq_RNASeqV2): GALNT16
mRNA Expression, RSEM (Batch normalized from Illumina HiSeq_RNASeqV2): CXCL13 (4q21.1)
Spearman: 0.23
(p = 2.161e-6)
Pearson: 0.15
(p = 2.100e-3)
y = 0.01x + 62.76
R² = 0.02
GALNT16 mutated
Neither mutated

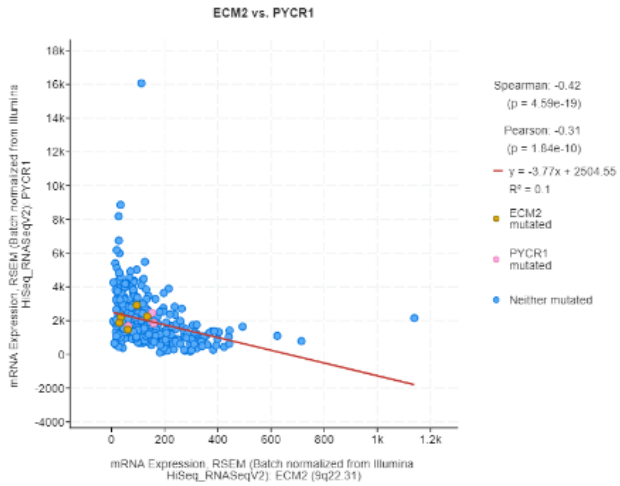

CXCL13 vs. CRLS1
mRNA Expression, RSEM (Batch normalized from Illumina HiSeq_RNASeqV2): CRLS1
mRNA Expression, RSEM (Batch normalized from Illumina HiSeq_RNASeqV2): CXCL13 (4q21.1)
Spearman: -0.24
(p = 1.417e-6)
Pearson: -0.16
(p = 8.840e-4)
y = -0.07x + 1658.53
R² = 0.03
CRLS1 mutated
Neither mutated

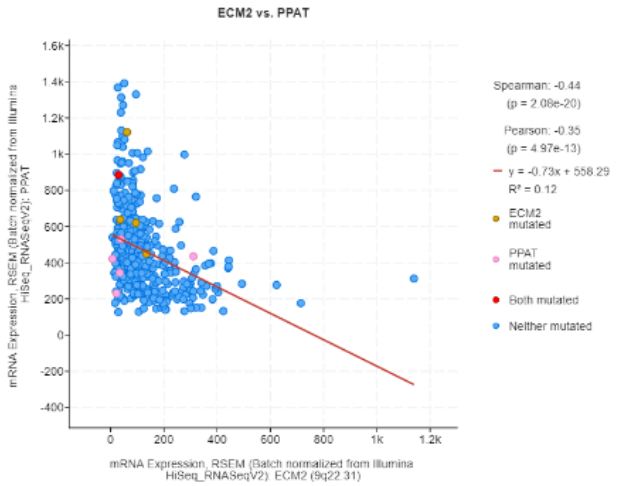

CXCL13 vs. CEPT1
mRNA Expression, RSEM (Batch normalized from Illumina HiSeq_RNASeqV2): CEPT1
mRNA Expression, RSEM (Batch normalized from Illumina HiSeq_RNASeqV2): CXCL13 (4q21.1)
Spearman: 0.09
(p = 0.0839)
Pearson: 0.26
(p = 1.12e-7)
y = 0.03x + 711.44
R² = 0.07
CEPT1 mutated
Neither mutated

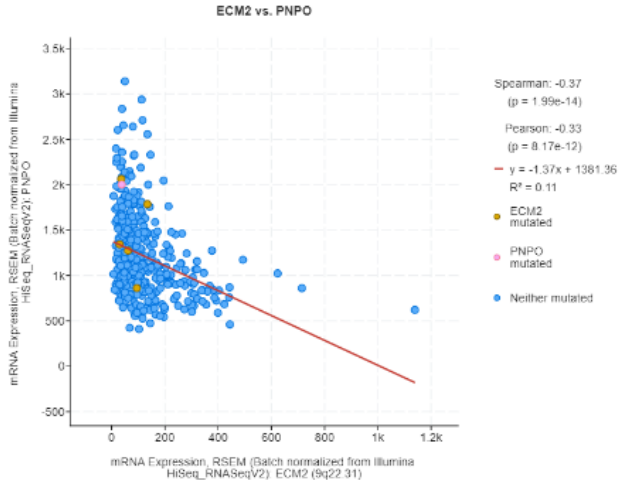

CXCL13 vs. ACAT2
mRNA Expression, RSEM (Batch normalized from Illumina HiSeq_RNASeqV2): ACAT2
mRNA Expression, RSEM (Batch normalized from Illumina HiSeq_RNASeqV2): CXCL13 (4q21.1)
Spearman: -0.29
(p = 3.42e-9)
Pearson: -0.20
(p = 3.761e-5)
y = -0.05x + 733.16
R² = 0.04
ACAT2 mutated
Neither mutated

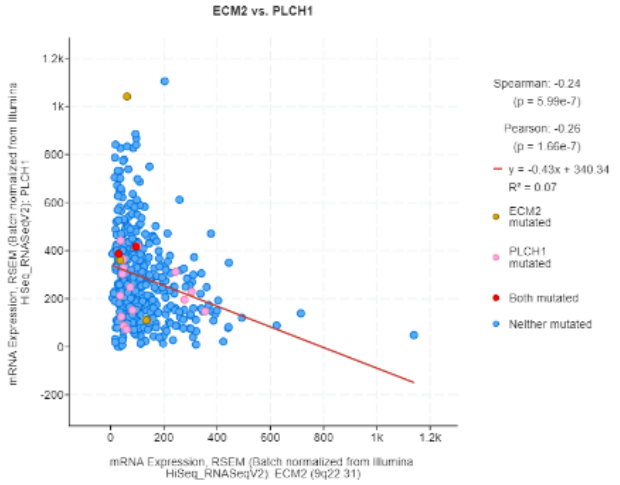
ECM2

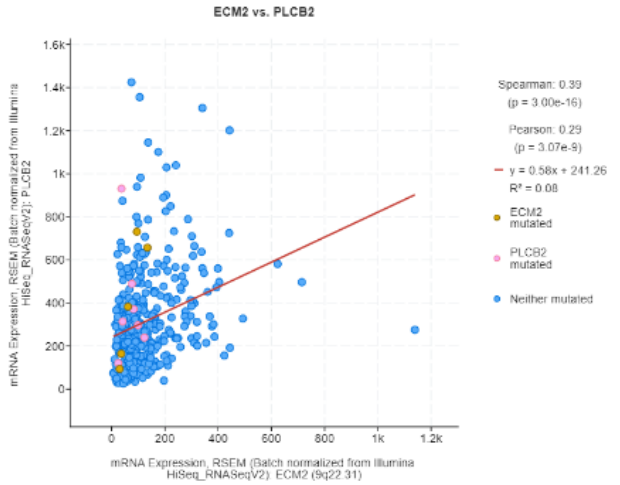

ECM2 vs. UQCR10
mRNA Expression, RSEM (Batch normalized from Illumina HiSeq_RNASeqV2): UQCR10
mRNA Expression, RSEM (Batch normalized from Illumina HiSeq_RNASeqV2): ECM2 (9q22.31)
Spearman: -0.28
(p = 1.14e-8)
Pearson: -0.23
(p = 2.967e-6)
y = -1.55x + 1731.89
R² = 0.05
ECM2 mutated
Neither mutated
ECM2 vs. TGDS
mRNA Expression, RSEM (Batch normalized from Illumina HiSeq_RNASeqV2): TGDS
mRNA Expression, RSEM (Batch normalized from Illumina HiSeq_RNASeqV2): ECM2 (9q22.31)
Spearman: -0.28
(p = 1.05e-8)
Pearson: -0.24
(p = 7.18e-7)
y = -0.37x + 442.49
R² = 0.06
ECM2 mutated
TGDS mutated
Neither mutated
ECM2 vs. SUCLA2
mRNA Expression, RSEM (Batch normalized from Illumina HiSeq_RNASeqV2): SUCLA2
mRNA Expression, RSEM (Batch normalized from Illumina HiSeq_RNASeqV2): ECM2 (9q22.31)
Spearman: -0.23
(p = 2.299e-6)
Pearson: -0.19
(p = 9.207e-5)
y = -0.75x + 1162.46
R² = 0.04
ECM2 mutated
SUCLA2 mutated
Neither mutated
ECM2 vs. SPR
mRNA Expression, RSEM (Batch normalized from Illumina HiSeq_RNASeqV2): SPR
mRNA Expression, RSEM (Batch normalized from Illumina HiSeq_RNASeqV2): ECM2 (9q22.31)
Spearman: -0.42
(p = 4.20e-19)
Pearson: -0.38
(p = 3.53e-15)
y = -1.74x + 1391.1
R² = 0.14
ECM2 mutated
SPR mutated
Neither mutated
ECM2 vs. SLC27A5
mRNA Expression, RSEM (Batch normalized from Illumina HiSeq_RNASeqV2): SLC27A5
mRNA Expression, RSEM (Batch normalized from Illumina HiSeq_RNASeqV2): ECM2 (9q22.31)
Spearman: -0.17
(p = 7.731e-4)
Pearson: -0.17
(p = 5.318e-4)
y = -0.13x + 143.95
R² = 0.03
ECM2 mutated
SLC27A5 mutated
Neither mutated
ECM2 vs. RDH11
mRNA Expression, RSEM (Batch normalized from Illumina HiSeq_RNASeqV2): RDH11
mRNA Expression, RSEM (Batch normalized from Illumina HiSeq_RNASeqV2): ECM2 (9q22.31)
Spearman: -0.22
(p = 8.253e-6)
Pearson: -0.20
(p = 5.215e-5)
y = -1.24x + 1940.11
R² = 0.04
ECM2 mutated
RDH11 mutated
Neither mutated

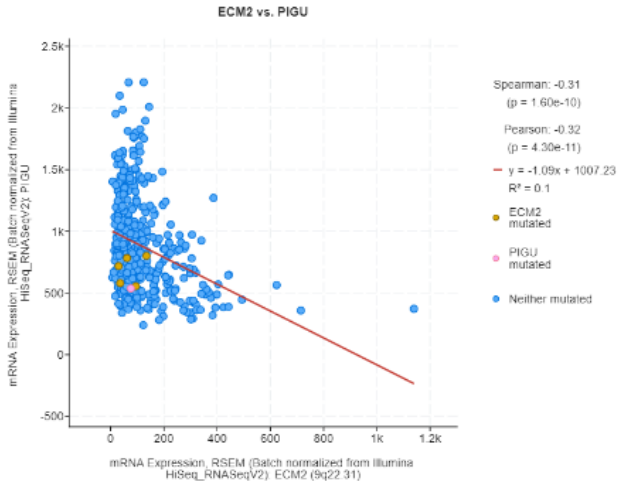

ECM2 vs. PYCR1
mRNA Expression, RSEM (Batch normalized from Illumina HiSeq_RNASeqV2): PYCR1
mRNA Expression, RSEM (Batch normalized from Illumina HiSeq_RNASeqV2): ECM2 (9q22.31)
Spearman: -0.42
(p = 4.59e-19)
Pearson: -0.31
(p = 1.84e-10)
y = -3.77x + 2504.55
R² = 0.1
ECM2 mutated
PYCR1 mutated
Neither mutated

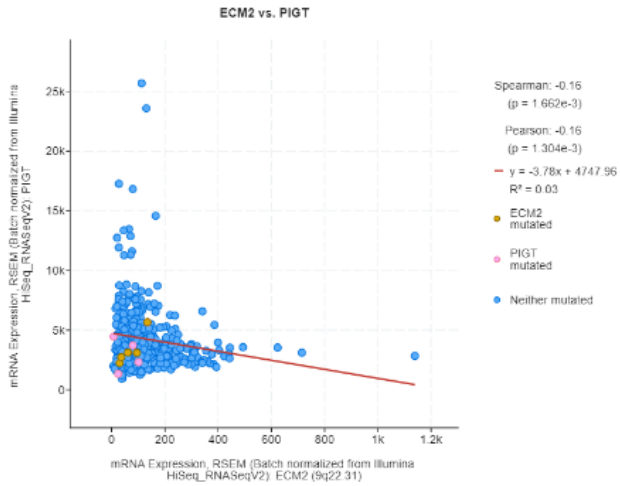

ECM2 vs. PPAT
mRNA Expression, RSEM (Batch normalized from Illumina HiSeq_RNASeqV2): PPAT
mRNA Expression, RSEM (Batch normalized from Illumina HiSeq_RNASeqV2): ECM2 (9q22.31)
Spearman: -0.44
(p = 2.08e-20)
Pearson: -0.35
(p = 4.97e-13)
y = -0.73x + 558.29
R² = 0.12
ECM2 mutated
PPAT mutated
Both mutated
Neither mutated

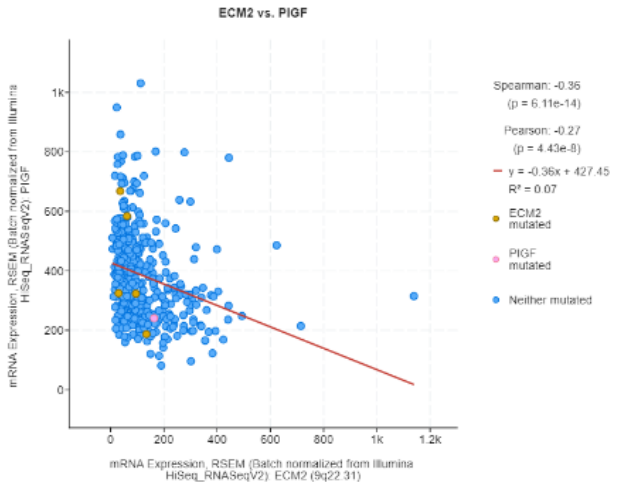

ECM2 vs. PNPO
mRNA Expression, RSEM (Batch normalized from Illumina HiSeq_RNASeqV2): PNPO
mRNA Expression, RSEM (Batch normalized from Illumina HiSeq_RNASeqV2): ECM2 (9q22.31)
Spearman: -0.37
(p = 1.99e-14)
Pearson: -0.33
(p = 8.17e-12)
y = -1.37x + 1381.36
R² = 0.11
ECM2 mutated
PNPO mutated
Neither mutated

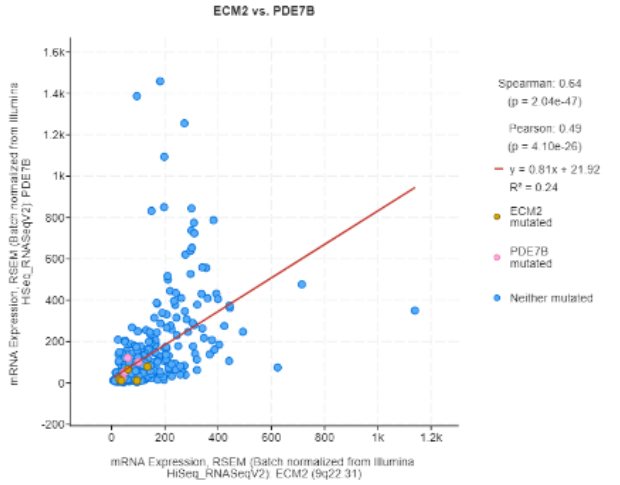

ECM2 vs. PLCH1
mRNA Expression, RSEM (Batch normalized from Illumina HiSeq_RNASeqV2): PLCH1
mRNA Expression, RSEM (Batch normalized from Illumina HiSeq_RNASeqV2): ECM2 (9q22.31)
Spearman: -0.24
(p = 5.99e-7)
Pearson: -0.26
(p = 1.66e-7)
y = -0.43x + 340.34
R² = 0.07
ECM2 mutated
PLCH1 mutated
Both mutated
Neither mutated

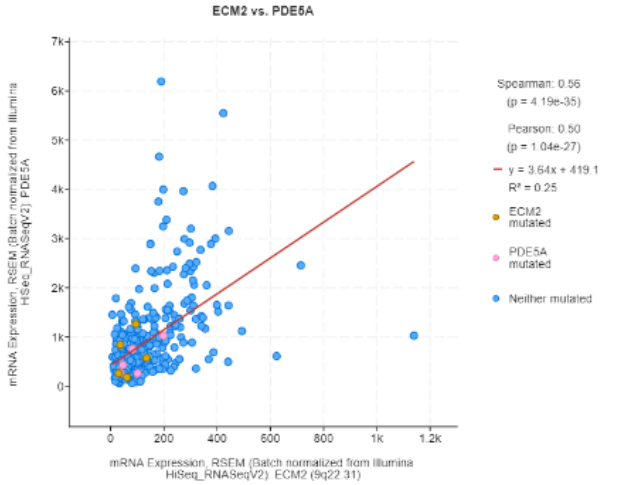

ECM2 vs. PLCB2
mRNA Expression, RSEM (Batch normalized from Illumina HiSeq_RNASeqV2): PLCB2
mRNA Expression, RSEM (Batch normalized from Illumina HiSeq_RNASeqV2): ECM2 (9q22.31)
Spearman: 0.39
(p = 3.00e-16)
Pearson: 0.29
(p = 3.07e-9)
y = 0.58x + 241.26
R² = 0.08
ECM2 mutated
PLCB2 mutated
Neither mutated

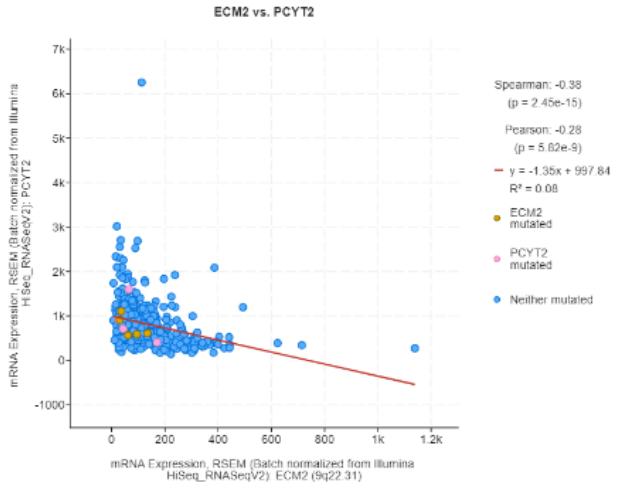

ECM2 vs. PIGU
mRNA Expression, RSEM (Batch normalized from Illumina HiSeq_RNASeqV2): PIGU
mRNA Expression, RSEM (Batch normalized from Illumina HiSeq_RNASeqV2): ECM2 (9q22.31)
Spearman: -0.31
(p = 1.60e-10)
Pearson: -0.32
(p = 4.30e-11)
y = -1.09x + 1007.23
R² = 0.1
ECM2 mutated
PIGU mutated
Neither mutated

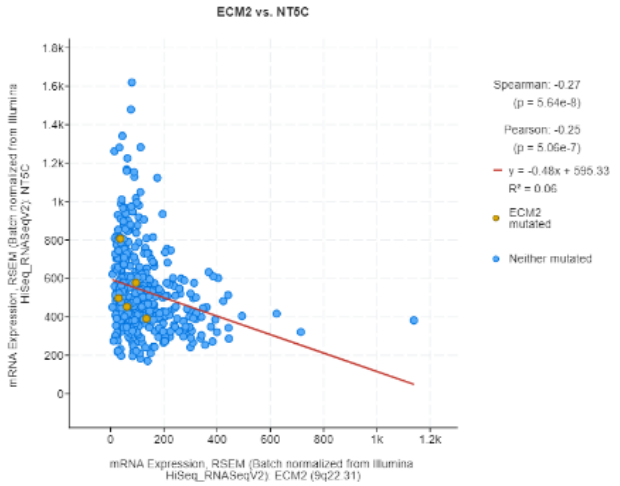

ECM2 vs. PIGT
mRNA Expression, RSEM (Batch normalized from Illumina HiSeq_RNASeqV2): PIGT
mRNA Expression, RSEM (Batch normalized from Illumina HiSeq_RNASeqV2): ECM2 (9q22.31)
Spearman: -0.16
(p = 1.662e-3)
Pearson: -0.16
(p = 1.304e-3)
y = -3.78x + 4747.96
R² = 0.03
ECM2 mutated
PIGT mutated
Neither mutated

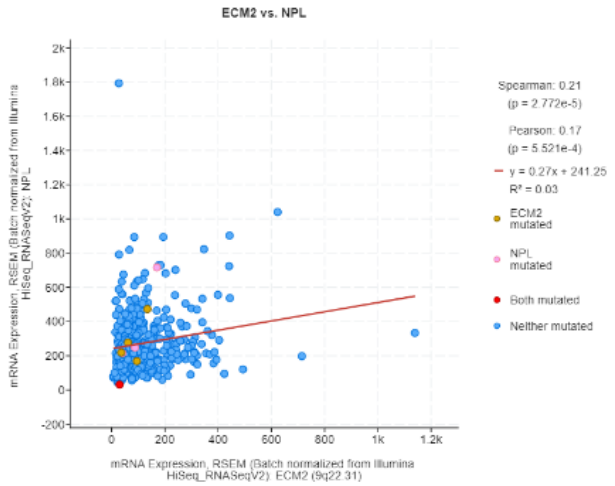

ECM2 vs. PIGF
mRNA Expression, RSEM (Batch normalized from Illumina HiSeq_RNASeqV2): PIGF
mRNA Expression, RSEM (Batch normalized from Illumina HiSeq_RNASeqV2): ECM2 (9q22.31)
Spearman: -0.36
(p = 6.11e-14)
Pearson: -0.27
(p = 4.43e-8)
y = -0.36x + 427.45
R² = 0.07
ECM2 mutated
PIGF mutated
Neither mutated

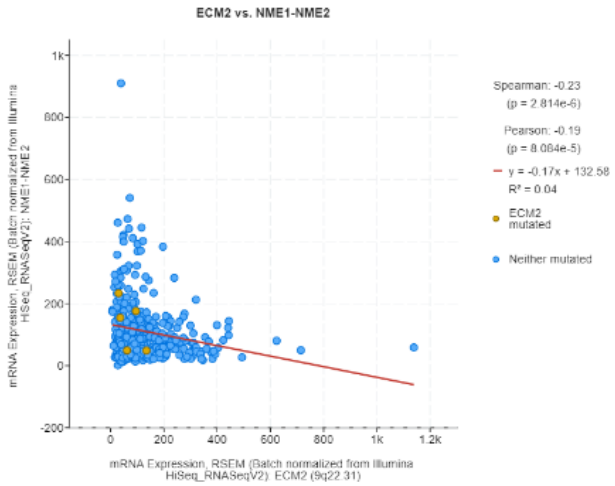

ECM2 vs. PDE7B
mRNA Expression, RSEM (Batch normalized from Illumina HiSeq_RNASeqV2): PDE7B
mRNA Expression, RSEM (Batch normalized from Illumina HiSeq_RNASeqV2): ECM2 (9q22.31)
Spearman: 0.64
(p = 2.04e-47)
Pearson: 0.49
(p = 4.10e-26)
y = 0.81x + 21.92
R² = 0.24
ECM2 mutated
PDE7B mutated
Neither mutated

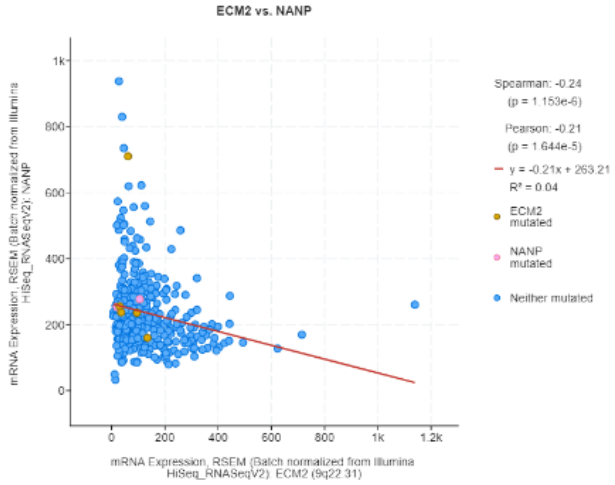

ECM2 vs. PDE5A
mRNA Expression, RSEM (Batch normalized from Illumina HiSeq_RNASeqV2): PDE5A
mRNA Expression, RSEM (Batch normalized from Illumina HiSeq_RNASeqV2): ECM2 (9q22.31)
Spearman: 0.56
(p = 4.19e-35)
Pearson: 0.50
(p = 1.04e-27)
y = 3.64x + 419.1
R² = 0.25
ECM2 mutated
PDE5A mutated
Neither mutated

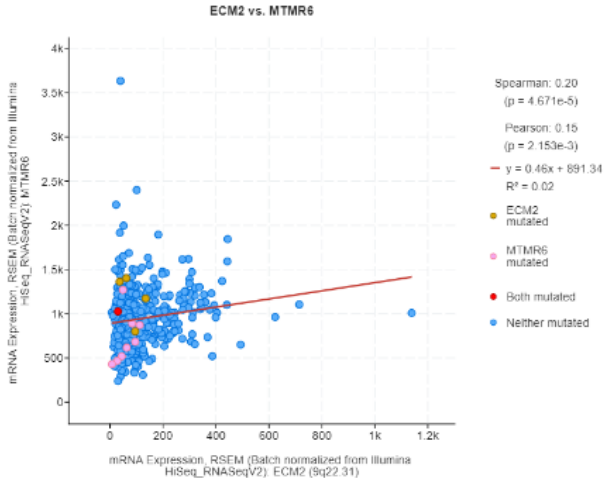

ECM2 vs. PCYT2
mRNA Expression, RSEM (Batch normalized from Illumina HiSeq_RNASeqV2): PCYT2
mRNA Expression, RSEM (Batch normalized from Illumina HiSeq_RNASeqV2): ECM2 (9q22.31)
Spearman: -0.38
(p = 2.45e-15)
Pearson: -0.28
(p = 5.82e-9)
y = -1.35x + 997.84
R² = 0.08
ECM2 mutated
PCYT2 mutated
Neither mutated

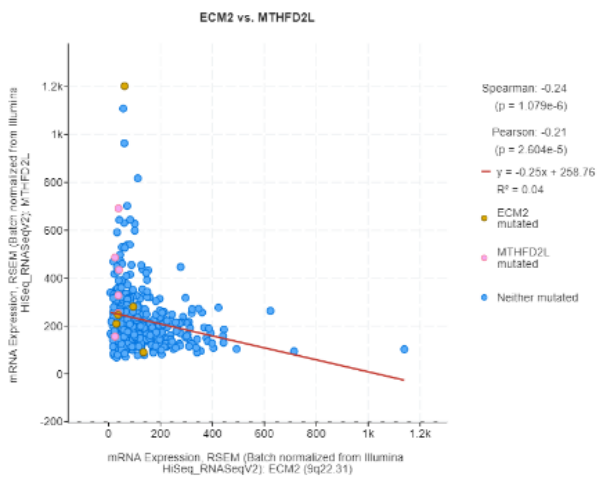

ECM2 vs. NT5C
mRNA Expression, RSEM (Batch normalized from Illumina HiSeq_RNASeqV2): NT5C
mRNA Expression, RSEM (Batch normalized from Illumina HiSeq_RNASeqV2): ECM2 (9q22.31)
Spearman: -0.27
(p = 5.64e-8)
Pearson: -0.25
(p = 5.06e-7)
y = -0.48x + 595.33
R² = 0.06
ECM2 mutated
Neither mutated

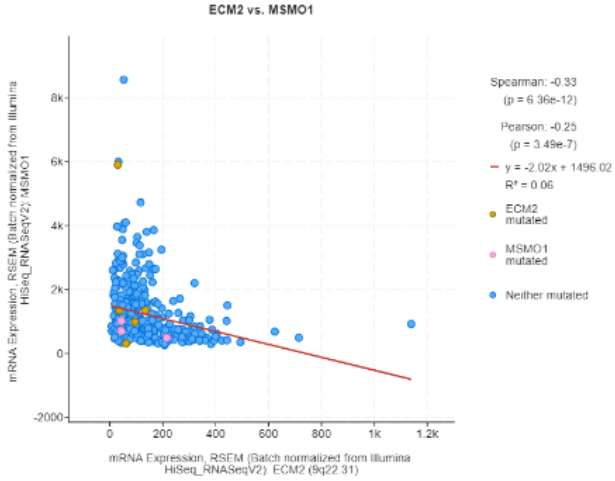

ECM2 vs. NPL
mRNA Expression, RSEM (Batch normalized from Illumina HiSeq_RNASeqV2): NPL
mRNA Expression, RSEM (Batch normalized from Illumina HiSeq_RNASeqV2): ECM2 (9q22.31)
Spearman: 0.21
(p = 2.772e-5)
Pearson: 0.17
(p = 5.521e-4)
y = 0.27x + 241.25
R² = 0.03
ECM2 mutated
NPL mutated
Both mutated
Neither mutated

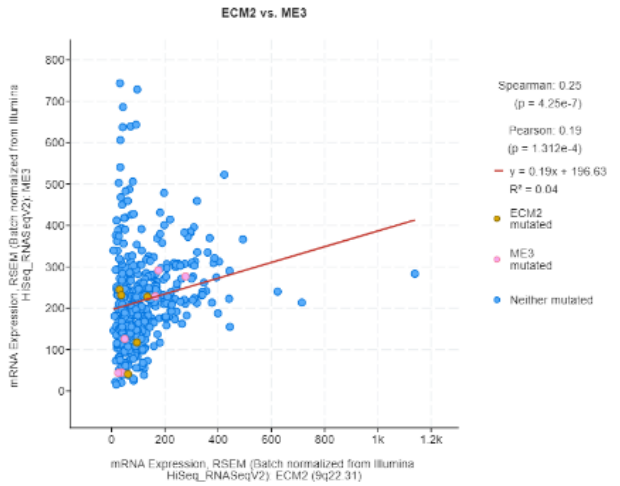

ECM2 vs. NME1-NME2
mRNA Expression, RSEM (Batch normalized from Illumina HiSeq_RNASeqV2): NME1-NME2
mRNA Expression, RSEM (Batch normalized from Illumina HiSeq_RNASeqV2): ECM2 (9q22.31)
Spearman: -0.23
(p = 2.814e-6)
Pearson: -0.19
(p = 8.084e-5)
y = -0.17x + 132.58
R² = 0.04
ECM2 mutated
Neither mutated

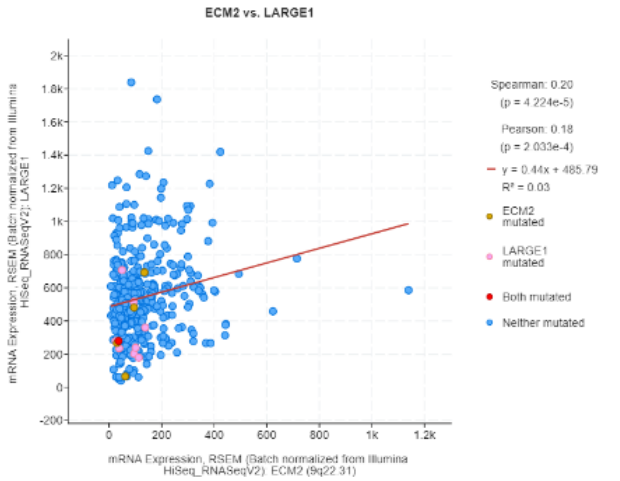

ECM2 vs. NANP
mRNA Expression, RSEM (Batch normalized from Illumina HiSeq_RNASeqV2): NANP
mRNA Expression, RSEM (Batch normalized from Illumina HiSeq_RNASeqV2): ECM2 (9q22.31)
Spearman: -0.24
(p = 1.153e-6)
Pearson: -0.21
(p = 1.644e-5)
y = -0.21x + 263.21
R² = 0.04
ECM2 mutated
NANP mutated
Neither mutated

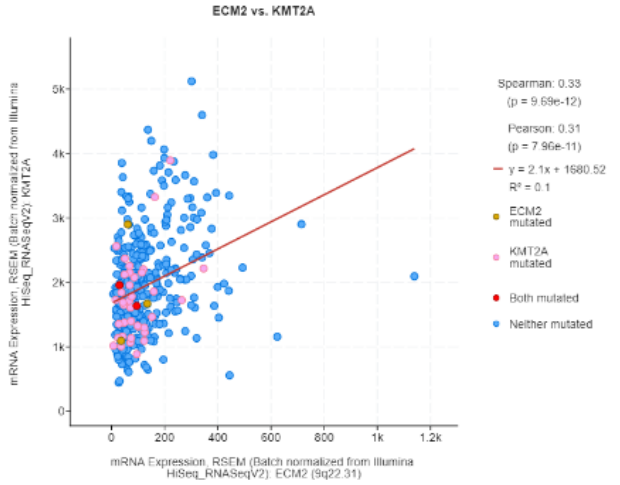

ECM2 vs. MTMR6
mRNA Expression, RSEM (Batch normalized from Illumina HiSeq_RNASeqV2): MTMR6
mRNA Expression, RSEM (Batch normalized from Illumina HiSeq_RNASeqV2): ECM2 (9q22.31)
Spearman: 0.20
(p = 4.671e-5)
Pearson: 0.15
(p = 2.153e-3)
y = 0.46x + 891.34
R² = 0.02
ECM2 mutated
MTMR6 mutated
Both mutated
Neither mutated

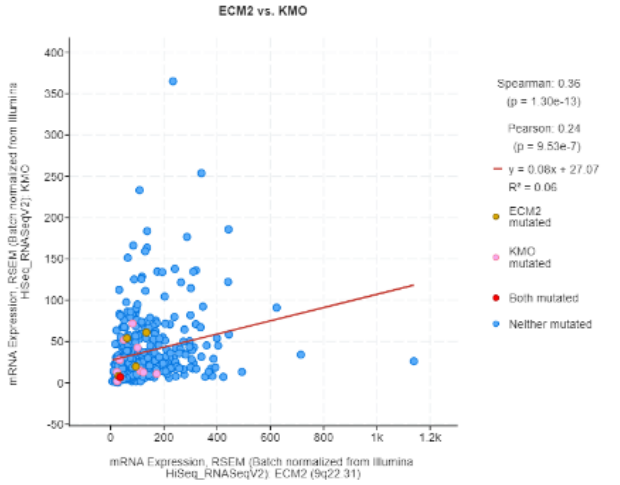

ECM2 vs. MTHFD2L
mRNA Expression, RSEM (Batch normalized from Illumina HiSeq_RNASeqV2): MTHFD2L
mRNA Expression, RSEM (Batch normalized from Illumina HiSeq_RNASeqV2): ECM2 (9q22.31)
Spearman: -0.24
(p = 1.079e-6)
Pearson: -0.21
(p = 2.604e-5)
y = -0.25x + 258.76
R² = 0.04
ECM2 mutated
MTHFD2L mutated
Neither mutated

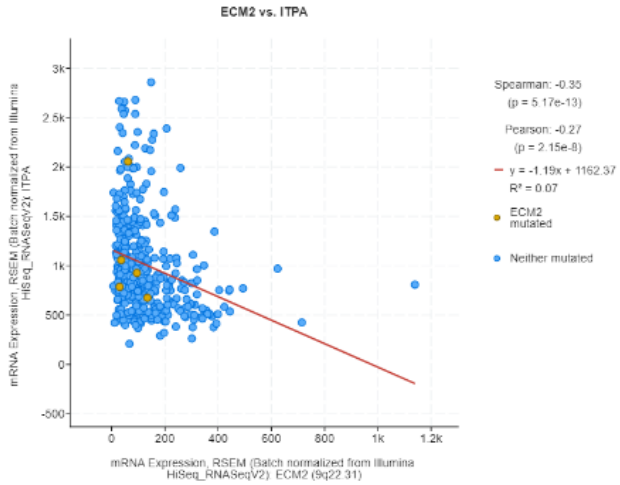

ECM2 vs. MSMO1
mRNA Expression, RSEM (Batch normalized from Illumina HiSeq_RNASeqV2): MSMO1
mRNA Expression, RSEM (Batch normalized from Illumina HiSeq_RNASeqV2): ECM2 (9q22.31)
Spearman: -0.33
(p = 6.36e-12)
Pearson: -0.25
(p = 3.49e-7)
y = -2.02x + 1496.02
R² = 0.06
ECM2 mutated
MSMO1 mutated
Neither mutated

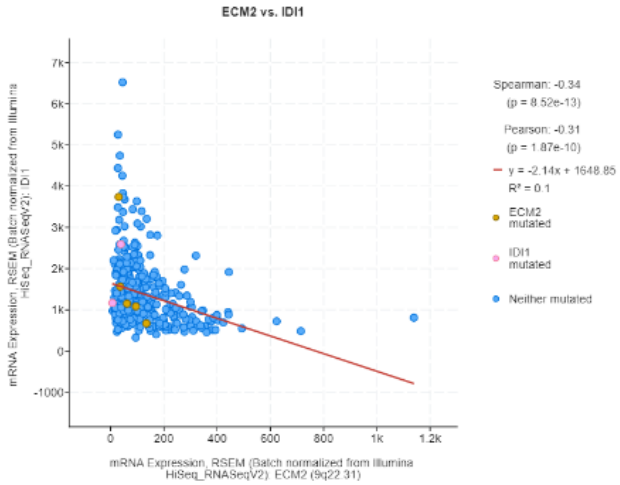

ECM2 vs. ME3
mRNA Expression, RSEM (Batch normalized from Illumina HiSeq_RNASeqV2): ME3
mRNA Expression, RSEM (Batch normalized from Illumina HiSeq_RNASeqV2): ECM2 (9q22.31)
Spearman: 0.25
(p = 4.25e-7)
Pearson: 0.19
(p = 1.312e-4)
y = 0.19x + 196.63
R² = 0.04
ECM2 mutated
ME3 mutated
Neither mutated

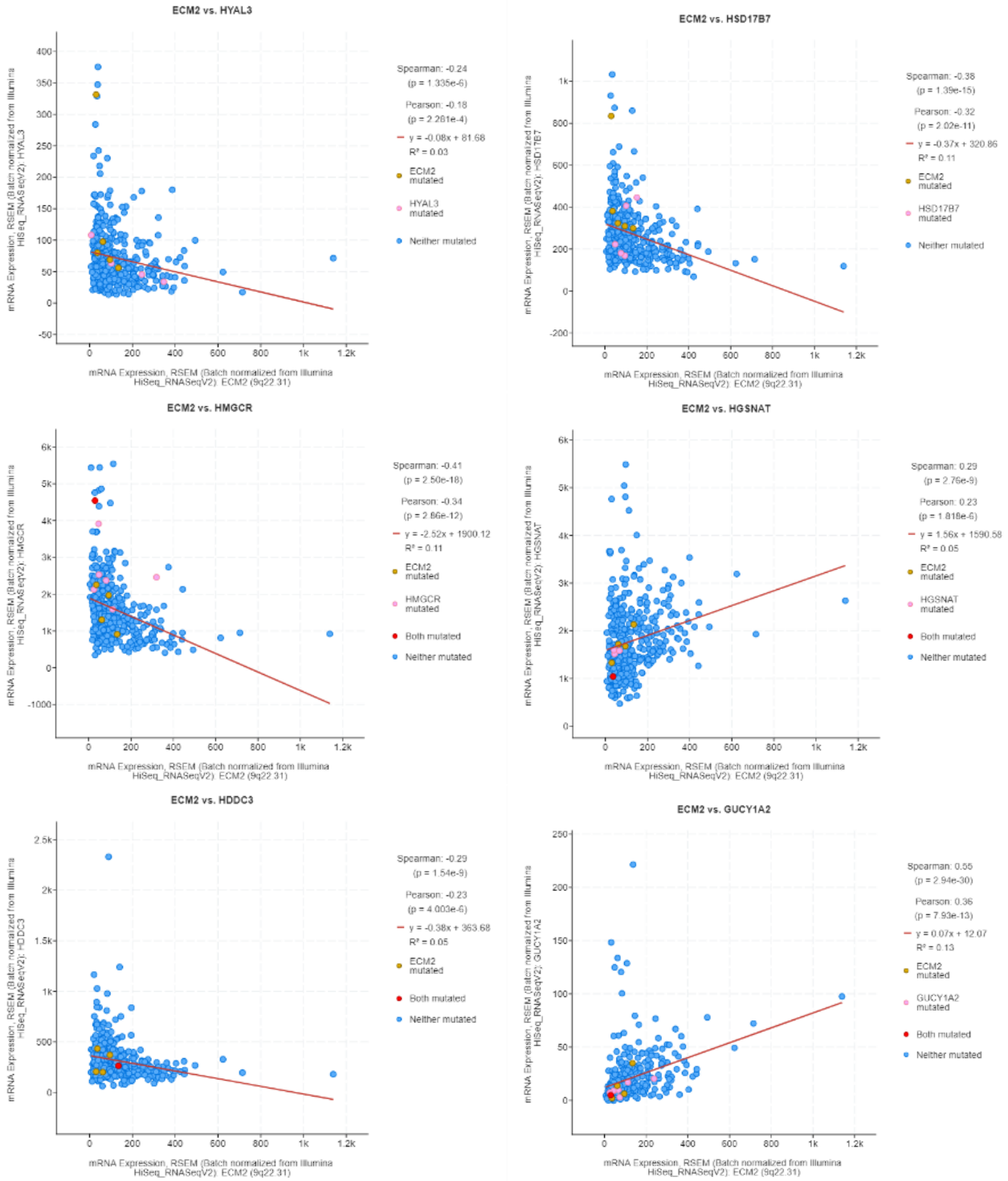

ECM2 vs. LARGE1
mRNA Expression, RSEM (Batch normalized from Illumina HiSeq_RNASeqV2): LARGE1
mRNA Expression, RSEM (Batch normalized from Illumina HiSeq_RNASeqV2): ECM2 (9q22.31)
Spearman: 0.20
(p = 4.224e-5)
Pearson: 0.18
(p = 2.033e-4)
y = 0.44x + 485.79
R² = 0.03
ECM2 mutated
LARGE1 mutated
Both mutated
Neither mutated


ECM2 vs. KMT2A
mRNA Expression, RSEM (Batch normalized from Illumina HiSeq_RNASeqV2): KMT2A
mRNA Expression, RSEM (Batch normalized from Illumina HiSeq_RNASeqV2): ECM2 (9q22.31)
Spearman: 0.33
(p = 9.69e-12)
Pearson: 0.31
(p = 7.96e-11)
y = 2.1x + 1680.52
R² = 0.1
ECM2 mutated
KMT2A mutated
Both mutated
Neither mutated

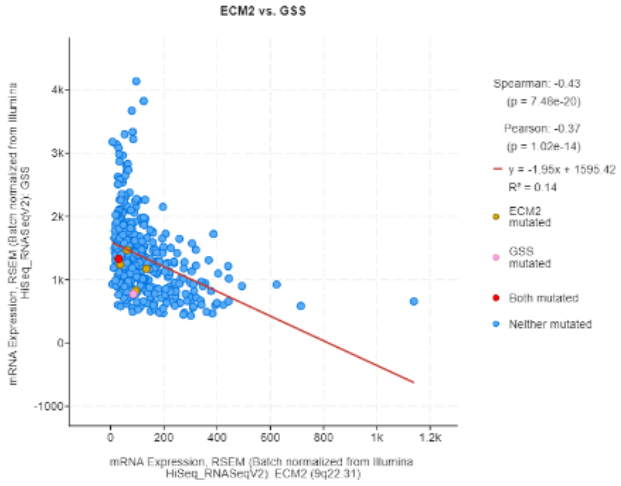

ECM2 vs. KMO
mRNA Expression, RSEM (Batch normalized from Illumina HiSeq_RNASeqV2): KMO
mRNA Expression, RSEM (Batch normalized from Illumina HiSeq_RNASeqV2): ECM2 (9q22.31)
Spearman: 0.36
(p = 1.30e-13)
Pearson: 0.24
(p = 9.53e-7)
y = 0.08x + 27.07
R² = 0.06
ECM2 mutated
KMO mutated
Both mutated
Neither mutated

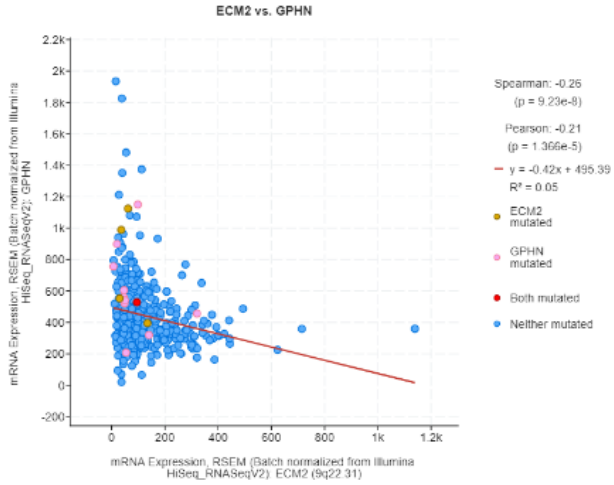

ECM2 vs. ITPA
mRNA Expression, RSEM (Batch normalized from Illumina HiSeq_RNASeqV2): ITPA
mRNA Expression, RSEM (Batch normalized from Illumina HiSeq_RNASeqV2): ECM2 (9q22.31)
Spearman: -0.35
(p = 5.17e-13)
Pearson: -0.27
(p = 2.15e-8)
y = -1.19x + 1162.37
R² = 0.07
ECM2 mutated
Neither mutated

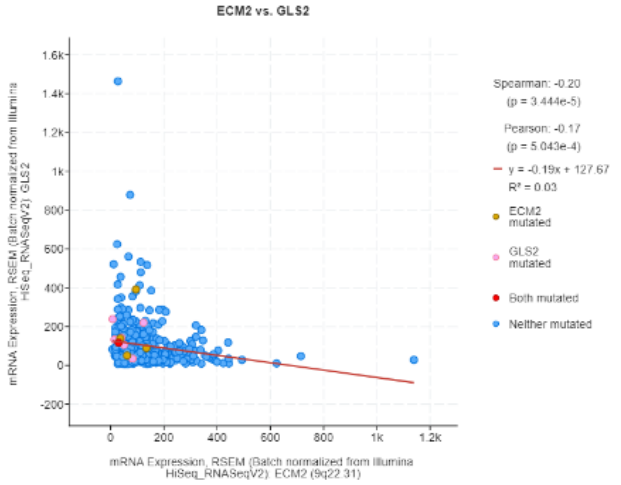

ECM2 vs. IDI1
mRNA Expression, RSEM (Batch normalized from Illumina HiSeq_RNASeqV2): IDI1
mRNA Expression, RSEM (Batch normalized from Illumina HiSeq_RNASeqV2): ECM2 (9q22.31)
Spearman: -0.34
(p = 8.52e-13)
Pearson: -0.31
(p = 1.87e-10)
y = -2.14x + 1648.85
R² = 0.1
ECM2 mutated
IDI1 mutated
Neither mutated

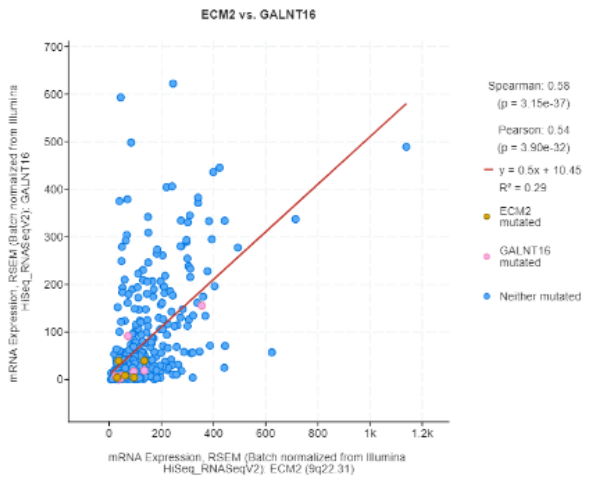

ECM2 vs. HYAL3
mRNA Expression, RSEM (Batch normalized from Illumina HiSeq_RNASeqV2): HYAL3
mRNA Expression, RSEM (Batch normalized from Illumina HiSeq_RNASeqV2): ECM2 (9q22.31)
Spearman: -0.24
(p = 1.335e-6)
Pearson: -0.18
(p = 2.261e-4)
y = -0.08x + 81.68
R² = 0.03
ECM2 mutated
HYAL3 mutated
Neither mutated
ECM2 vs. HSD17B7
mRNA Expression, RSEM (Batch normalized from Illumina HiSeq_RNASeqV2): HSD17B7
mRNA Expression, RSEM (Batch normalized from Illumina HiSeq_RNASeqV2): ECM2 (9q22.31)
Spearman: -0.38
(p = 1.39e-15)
Pearson: -0.32
(p = 2.02e-11)
y = -0.37x + 320.86
R² = 0.11
ECM2 mutated
HSD17B7 mutated
Neither mutated
ECM2 vs. HMGCR
mRNA Expression, RSEM (Batch normalized from Illumina HiSeq_RNASeqV2): HMGCR
mRNA Expression, RSEM (Batch normalized from Illumina HiSeq_RNASeqV2): ECM2 (9q22.31)
Spearman: -0.41
(p = 2.50e-18)
Pearson: -0.34
(p = 2.86e-12)
y = -2.52x + 1900.12
R² = 0.11
ECM2 mutated
HMGCR mutated
Both mutated
Neither mutated
ECM2 vs. HGSNAT
mRNA Expression, RSEM (Batch normalized from Illumina HiSeq_RNASeqV2): HGSNAT
mRNA Expression, RSEM (Batch normalized from Illumina HiSeq_RNASeqV2): ECM2 (9q22.31)
Spearman: 0.29
(p = 2.76e-9)
Pearson: 0.23
(p = 1.818e-6)
y = 1.56x + 1590.58
R² = 0.05
ECM2 mutated
HGSNAT mutated
Both mutated
Neither mutated
ECM2 vs. HDDC3
mRNA Expression, RSEM (Batch normalized from Illumina HiSeq_RNASeqV2): HDDC3
mRNA Expression, RSEM (Batch normalized from Illumina HiSeq_RNASeqV2): ECM2 (9q22.31)
Spearman: -0.29
(p = 1.54e-9)
Pearson: -0.23
(p = 4.003e-6)
y = -0.38x + 363.68
R² = 0.05
ECM2 mutated
Both mutated
Neither mutated
ECM2 vs. GUCY1A2
mRNA Expression, RSEM (Batch normalized from Illumina HiSeq_RNASeqV2): GUCY1A2
mRNA Expression, RSEM (Batch normalized from Illumina HiSeq_RNASeqV2): ECM2 (9q22.31)
Spearman: 0.55
(p = 2.94e-30)
Pearson: 0.36
(p = 7.93e-13)
y = 0.07x + 12.07
R² = 0.13
ECM2 mutated
GUCY1A2 mutated
Both mutated
Neither mutated

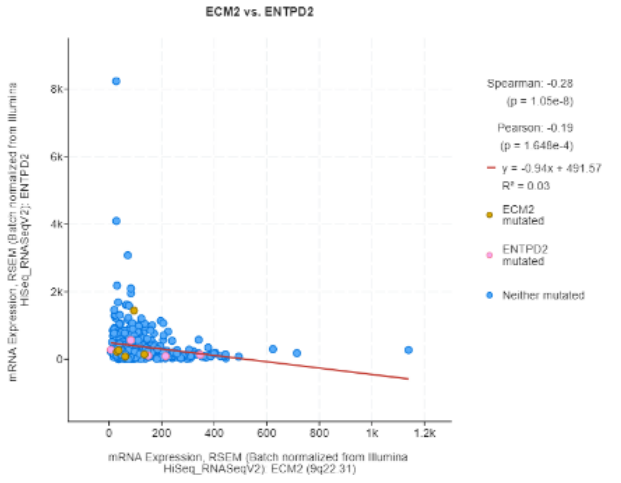

ECM2 vs. GSTM5
mRNA Expression, RSEM (Batch normalized from Illumina HiSeq_RNASeqV2): GSTM5
mRNA Expression, RSEM (Batch normalized from Illumina HiSeq_RNASeqV2): ECM2 (9q22.31)
Spearman: 0.71
(p = 9.33e-64)
Pearson: 0.51
(p = 4.10e-28)
y = 0.55x + 14.45
R² = 0.26
ECM2 mutated
GSTM5 mutated
Neither mutated

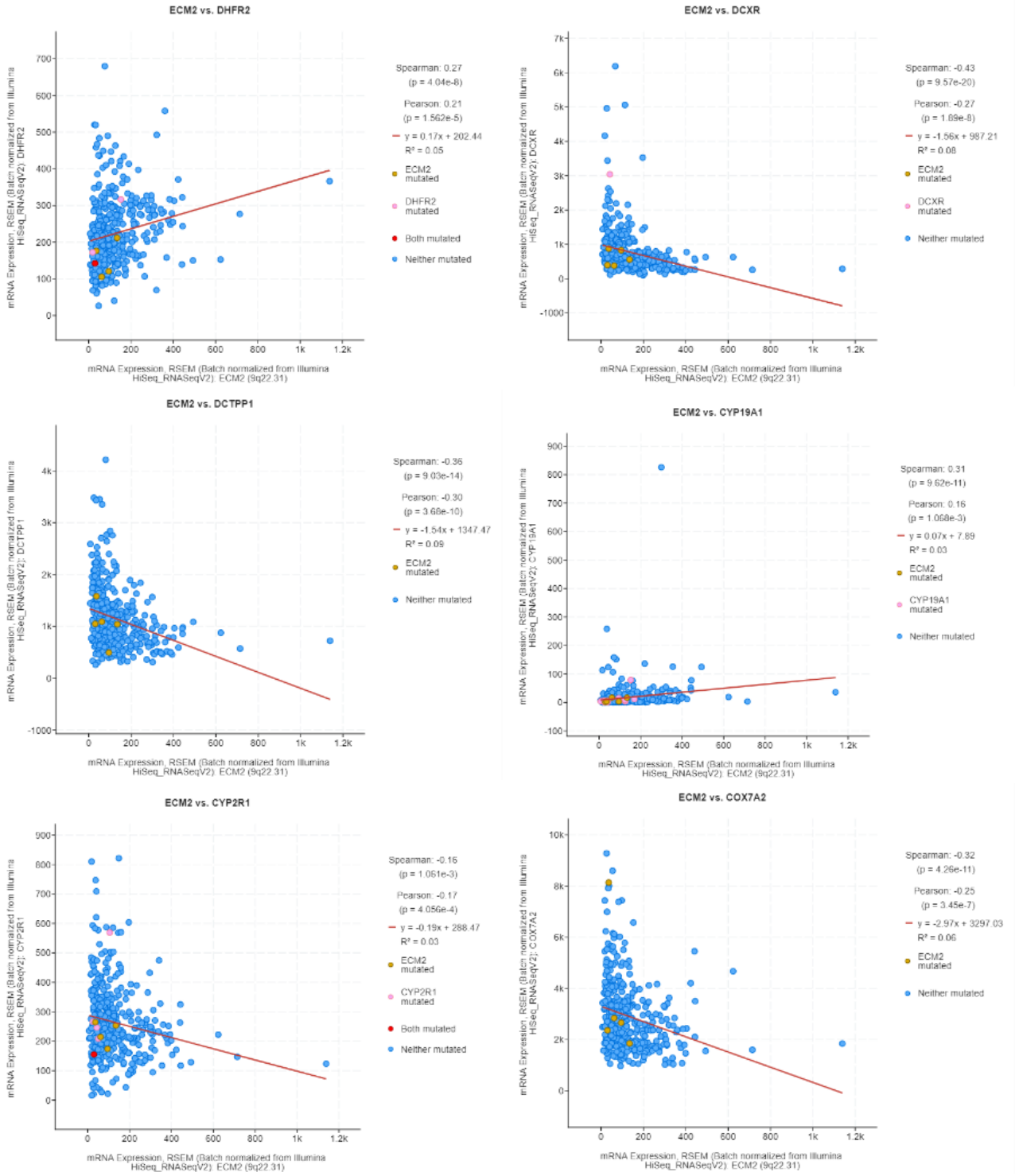

ECM2 vs. GSS
mRNA Expression, RSEM (Batch normalized from Illumina HiSeq_RNASeqV2): GSS
mRNA Expression, RSEM (Batch normalized from Illumina HiSeq_RNASeqV2): ECM2 (9q22.31)
Spearman: -0.43
(p = 7.48e-20)
Pearson: -0.37
(p = 1.02e-14)
y = -1.95x + 1595.42
R² = 0.14
ECM2 mutated
GSS mutated
Both mutated
Neither mutated

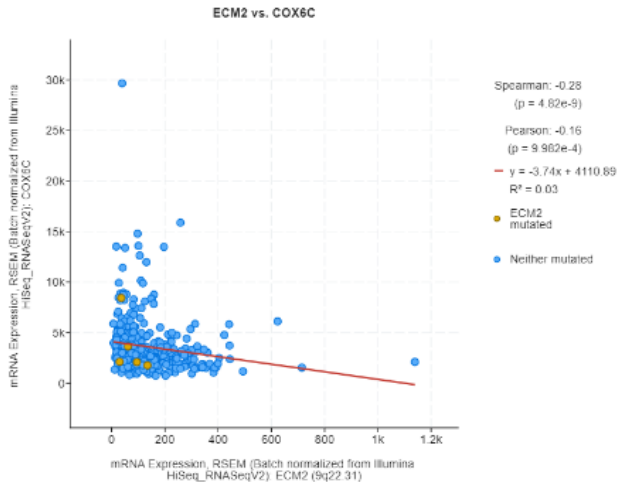

ECM2 vs. GPHN
mRNA Expression, RSEM (Batch normalized from Illumina HiSeq_RNASeqV2): GPHN
mRNA Expression, RSEM (Batch normalized from Illumina HiSeq_RNASeqV2): ECM2 (9q22.31)
Spearman: -0.26
(p = 9.23e-9)
Pearson: -0.21
(p = 1.366e-5)
y = -0.42x + 495.39
R² = 0.05
ECM2 mutated
GPHN mutated
Both mutated
Neither mutated

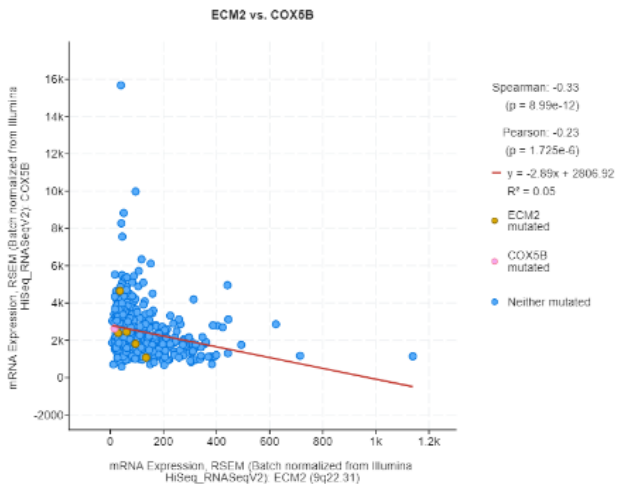

ECM2 vs. GLS2
mRNA Expression, RSEM (Batch normalized from Illumina HiSeq_RNASeqV2): GLS2
mRNA Expression, RSEM (Batch normalized from Illumina HiSeq_RNASeqV2): ECM2 (9q22.31)
Spearman: -0.20
(p = 3.444e-5)
Pearson: -0.17
(p = 5.043e-4)
y = -0.19x + 127.67
R² = 0.03
ECM2 mutated
GLS2 mutated
Both mutated
Neither mutated

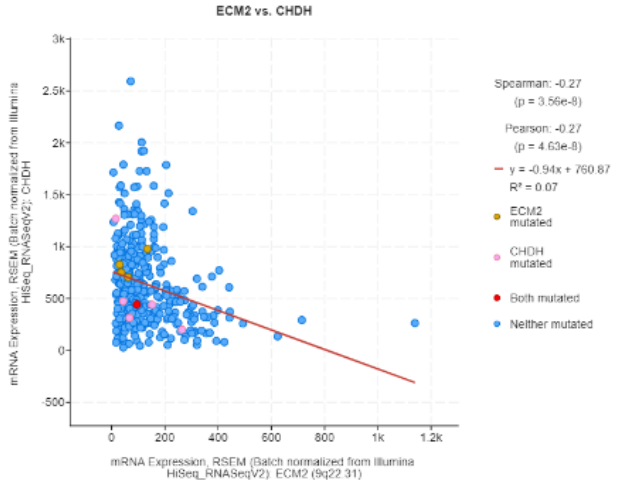

ECM2 vs. GALNT16
mRNA Expression, RSEM (Batch normalized from Illumina HiSeq_RNASeqV2): GALNT16
mRNA Expression, RSEM (Batch normalized from Illumina HiSeq_RNASeqV2): ECM2 (9q22.31)
Spearman: 0.58
(p = 3.15e-37)
Pearson: 0.54
(p = 3.90e-32)
y = 0.5x + 10.45
R² = 0.29
ECM2 mutated
GALNT16 mutated
Neither mutated

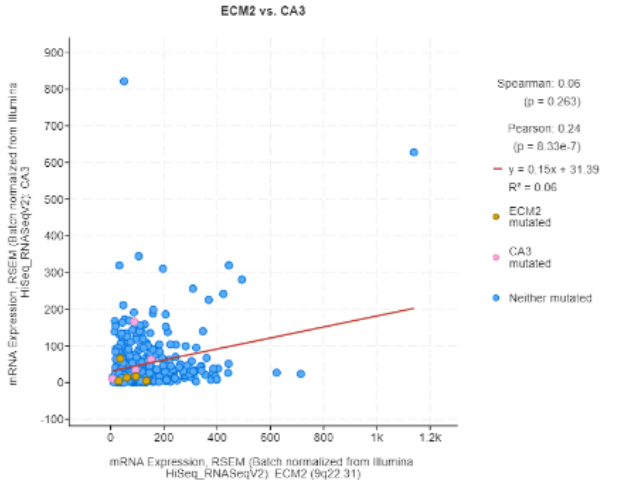

ECM2 vs. ENTPD2
mRNA Expression, RSEM (Batch normalized from Illumina HiSeq_RNASeqV2): ENTPD2
mRNA Expression, RSEM (Batch normalized from Illumina HiSeq_RNASeqV2): ECM2 (9q22.31)
Spearman: -0.28
(p = 1.05e-8)
Pearson: -0.19
(p = 1.648e-4)
y = -0.94x + 491.57
R² = 0.03
ECM2 mutated
ENTPD2 mutated
Neither mutated

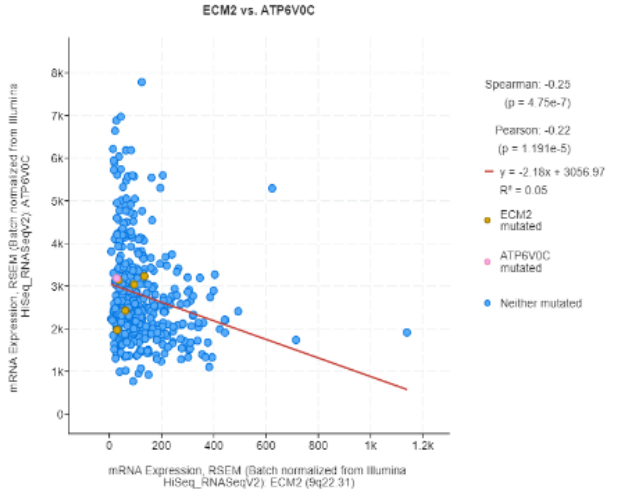

ECM2 vs. DHFR2
mRNA Expression, RSEM (Batch normalized from Illumina HiSeq_RNASeqV2): DHFR2
mRNA Expression, RSEM (Batch normalized from Illumina HiSeq_RNASeqV2): ECM2 (9q22.31)
Spearman: 0.27
(p = 4.04e-8)
Pearson: 0.21
(p = 1.562e-5)
y = 0.17x + 202.44
R² = 0.05
ECM2 mutated
DHFR2 mutated
Both mutated
Neither mutated
ECM2 vs. DCXR
mRNA Expression, RSEM (Batch normalized from Illumina HiSeq_RNASeqV2): DCXR
mRNA Expression, RSEM (Batch normalized from Illumina HiSeq_RNASeqV2): ECM2 (9q22.31)
Spearman: -0.43
(p = 9.57e-20)
Pearson: -0.27
(p = 1.89e-8)
y = -1.56x + 987.21
R² = 0.08
ECM2 mutated
DCXR mutated
Neither mutated
ECM2 vs. DCTPP1
mRNA Expression, RSEM (Batch normalized from Illumina HiSeq_RNASeqV2): DCTPP1
mRNA Expression, RSEM (Batch normalized from Illumina HiSeq_RNASeqV2): ECM2 (9q22.31)
Spearman: -0.36
(p = 9.03e-14)
Pearson: -0.30
(p = 3.68e-10)
y = -1.54x + 1347.47
R² = 0.09
ECM2 mutated
Neither mutated
ECM2 vs. CYP19A1
mRNA Expression, RSEM (Batch normalized from Illumina HiSeq_RNASeqV2): CYP19A1
mRNA Expression, RSEM (Batch normalized from Illumina HiSeq_RNASeqV2): ECM2 (9q22.31)
Spearman: 0.31
(p = 9.62e-11)
Pearson: 0.16
(p = 1.068e-3)
y = 0.07x + 7.89
R² = 0.03
ECM2 mutated
CYP19A1 mutated
Neither mutated
ECM2 vs. CYP2R1
mRNA Expression, RSEM (Batch normalized from Illumina HiSeq_RNASeqV2): CYP2R1
mRNA Expression, RSEM (Batch normalized from Illumina HiSeq_RNASeqV2): ECM2 (9q22.31)
Spearman: -0.16
(p = 1.061e-3)
Pearson: -0.17
(p = 4.056e-4)
y = -0.19x + 288.47
R² = 0.03
ECM2 mutated
CYP2R1 mutated
Both mutated
Neither mutated
ECM2 vs. COX7A2
mRNA Expression, RSEM (Batch normalized from Illumina HiSeq_RNASeqV2): COX7A2
mRNA Expression, RSEM (Batch normalized from Illumina HiSeq_RNASeqV2): ECM2 (9q22.31)
Spearman: -0.32
(p = 4.26e-11)
Pearson: -0.25
(p = 3.45e-7)
y = -2.97x + 3297.03
R² = 0.06
ECM2 mutated
Neither mutated

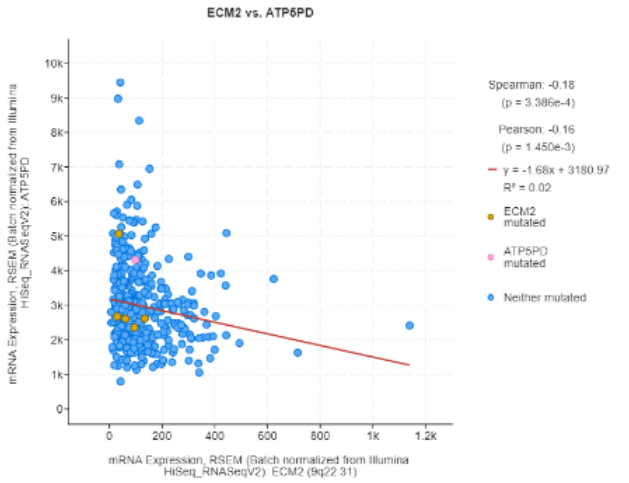

ECM2 vs. COX6C
mRNA Expression, RSEM (Batch normalized from Illumina HiSeq_RNASeqV2): COX6C
mRNA Expression, RSEM (Batch normalized from Illumina HiSeq_RNASeqV2): ECM2 (9q22.31)
Spearman: -0.28
(p = 4.82e-9)
Pearson: -0.16
(p = 9.962e-4)
y = -3.74x + 4110.89
R² = 0.03
ECM2 mutated
Neither mutated

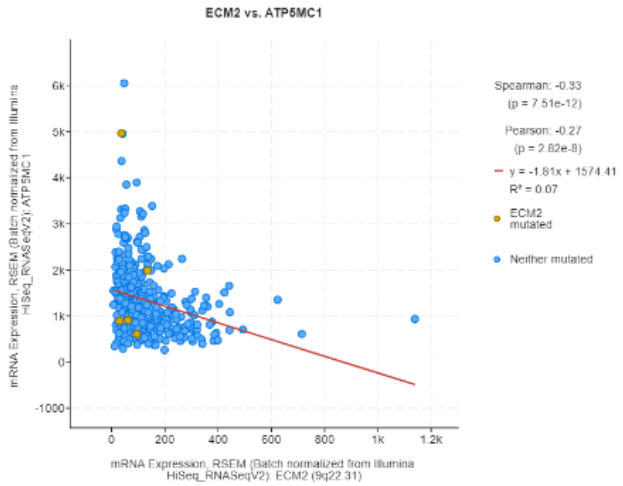

ECM2 vs. COX5B
mRNA Expression, RSEM (Batch normalized from Illumina HiSeq_RNASeqV2): COX5B
mRNA Expression, RSEM (Batch normalized from Illumina HiSeq_RNASeqV2): ECM2 (9q22.31)
Spearman: -0.33
(p = 8.99e-12)
Pearson: -0.23
(p = 1.725e-6)
y = -2.89x + 2806.92
R² = 0.05
ECM2 mutated
COX5B mutated
Neither mutated

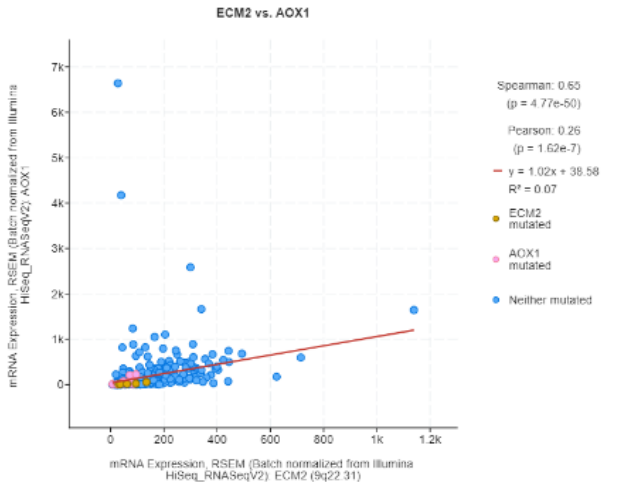

ECM2 vs. CHDH
mRNA Expression, RSEM (Batch normalized from Illumina HiSeq_RNASeqV2): CHDH
mRNA Expression, RSEM (Batch normalized from Illumina HiSeq_RNASeqV2): ECM2 (9q22.31)
Spearman: -0.27
(p = 3.56e-8)
Pearson: -0.27
(p = 4.63e-8)
y = -0.94x + 760.87
R² = 0.07
ECM2 mutated
CHDH mutated
Both mutated
Neither mutated

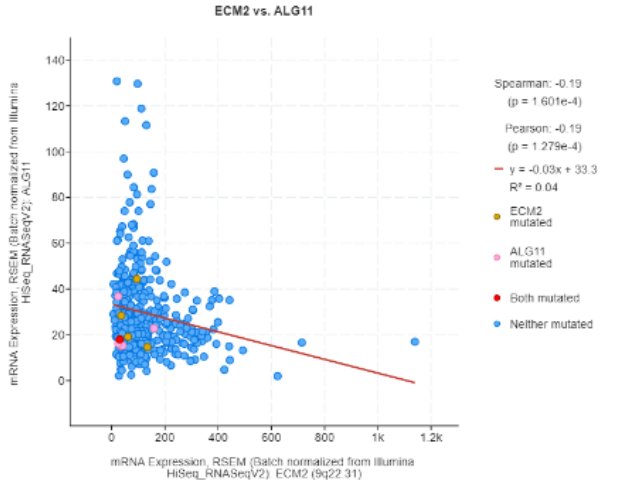

ECM2 vs. CA3
mRNA Expression, RSEM (Batch normalized from Illumina HiSeq_RNASeqV2): CA3
mRNA Expression, RSEM (Batch normalized from Illumina HiSeq_RNASeqV2): ECM2 (9q22.31)
Spearman: 0.06
(p = 0.263)
Pearson: 0.24
(p = 8.33e-7)
y = 0.15x + 31.39
R² = 0.06
ECM2 mutated
CA3 mutated
Neither mutated

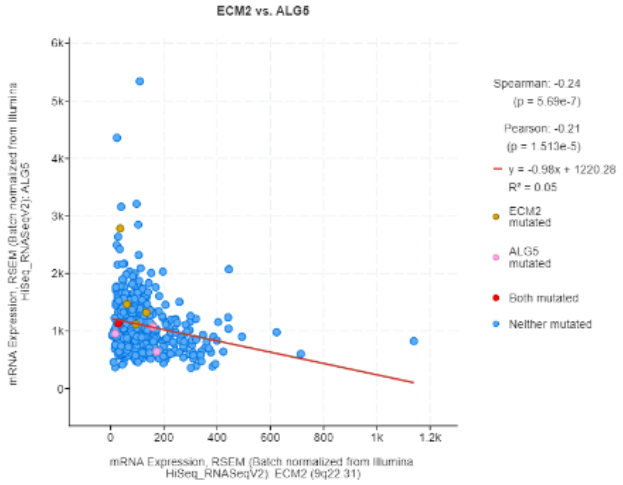

ECM2 vs. ATP6V0C
mRNA Expression, RSEM (Batch normalized from Illumina HiSeq_RNASeqV2): ATP6V0C
mRNA Expression, RSEM (Batch normalized from Illumina HiSeq_RNASeqV2): ECM2 (9q22.31)
Spearman: -0.25
(p = 4.75e-7)
Pearson: -0.22
(p = 1.191e-5)
y = -2.18x + 3056.97
R² = 0.05
ECM2 mutated
ATP6V0C mutated
Neither mutated

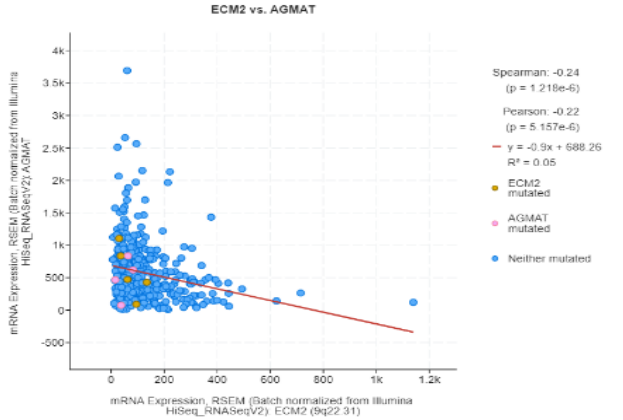

ECM2 vs. ATP5PD
mRNA Expression, RSEM (Batch normalized from Illumina HiSeq_RNASeqV2): ATP5PD
mRNA Expression, RSEM (Batch normalized from Illumina HiSeq_RNASeqV2): ECM2 (9q22.31)
Spearman: -0.18
(p = 3.386e-4)
Pearson: -0.16
(p = 1.450e-3)
y = -1.68x + 3180.97
R² = 0.02
ECM2 mutated
ATP5PD mutated
Neither mutated

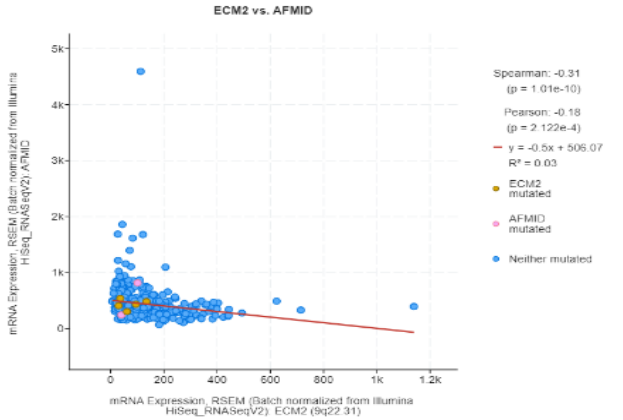

ECM2 vs. ATP5MC1
mRNA Expression, RSEM (Batch normalized from Illumina HiSeq_RNASeqV2): ATP5MC1
mRNA Expression, RSEM (Batch normalized from Illumina HiSeq_RNASeqV2): ECM2 (9q22.31)
Spearman: -0.33
(p = 7.51e-12)
Pearson: -0.27
(p = 2.82e-8)
y = -1.81x + 1574.41
R² = 0.07
ECM2 mutated
Neither mutated

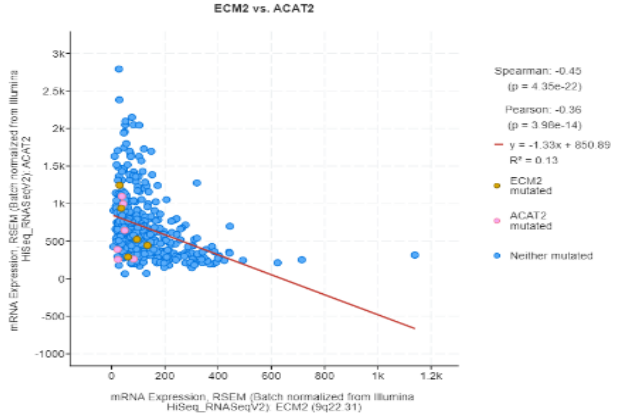

ECM2 vs. AOX1
mRNA Expression, RSEM (Batch normalized from Illumina HiSeq_RNASeqV2): AOX1
mRNA Expression, RSEM (Batch normalized from Illumina HiSeq_RNASeqV2): ECM2 (9q22.31)
Spearman: 0.65
(p = 4.77e-50)
Pearson: 0.26
(p = 1.62e-7)
y = 1.02x + 38.58
R² = 0.07
ECM2 mutated
AOX1 mutated
Neither mutated


ECM2 vs. ALG11
mRNA Expression, RSEM (Batch normalized from Illumina HiSeq_RNASeqV2): ALG11
mRNA Expression, RSEM (Batch normalized from Illumina HiSeq_RNASeqV2): ECM2 (9q22.31)
Spearman: -0.19
(p = 1.601e-4)
Pearson: -0.19
(p = 1.279e-4)
y = -0.03x + 33.3
R² = 0.04
ECM2 mutated
ALG11 mutated
Both mutated
Neither mutated

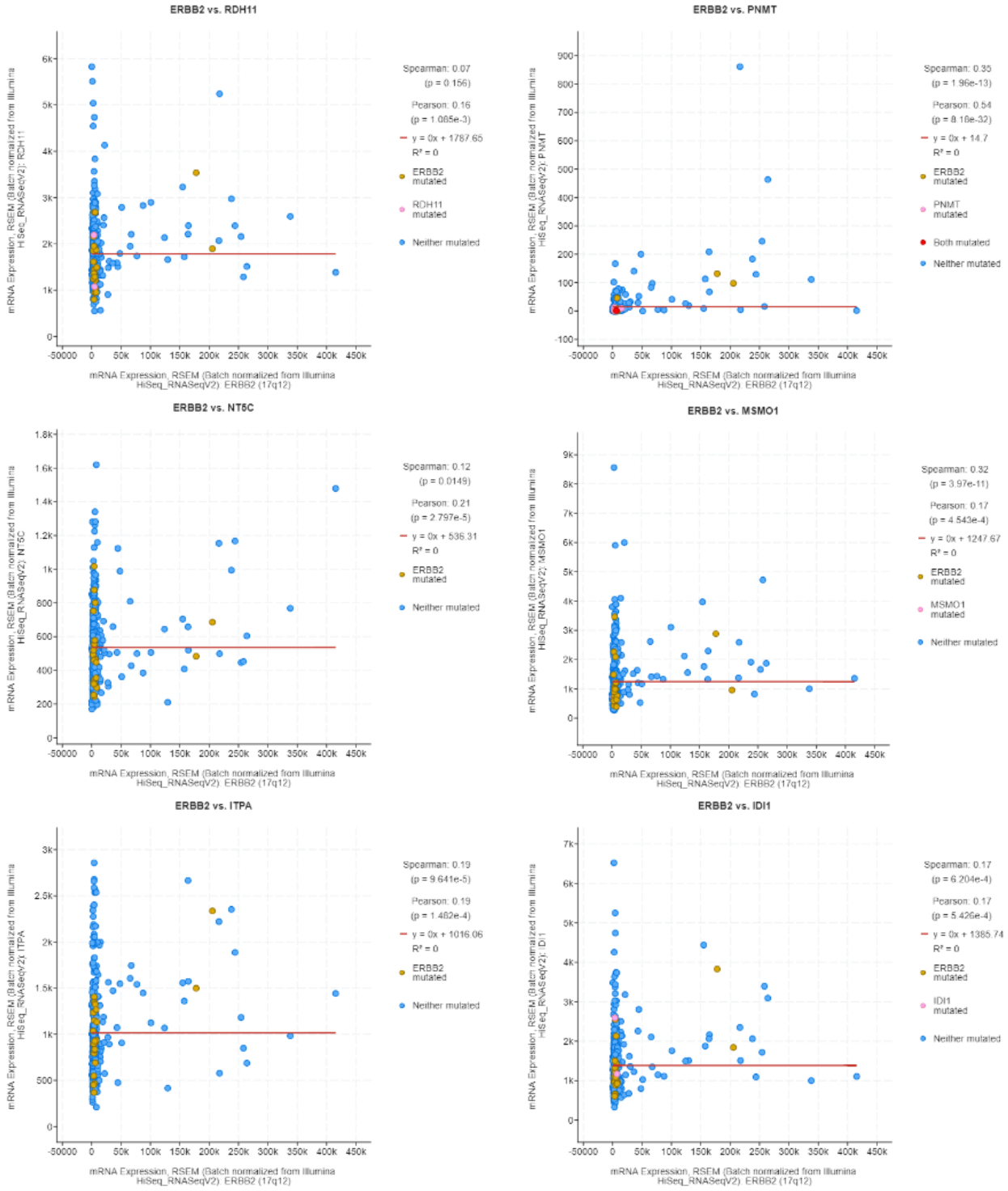

ECM2 vs. ALG5
mRNA Expression, RSEM (Batch normalized from Illumina HiSeq_RNASeqV2): ALG5
mRNA Expression, RSEM (Batch normalized from Illumina HiSeq_RNASeqV2): ECM2 (9q22.31)
Spearman: -0.24
(p = 5.69e-7)
Pearson: -0.21
(p = 1.513e-5)
y = -0.98x + 1220.28
R² = 0.05
ECM2 mutated
ALG5 mutated
Both mutated
Neither mutated

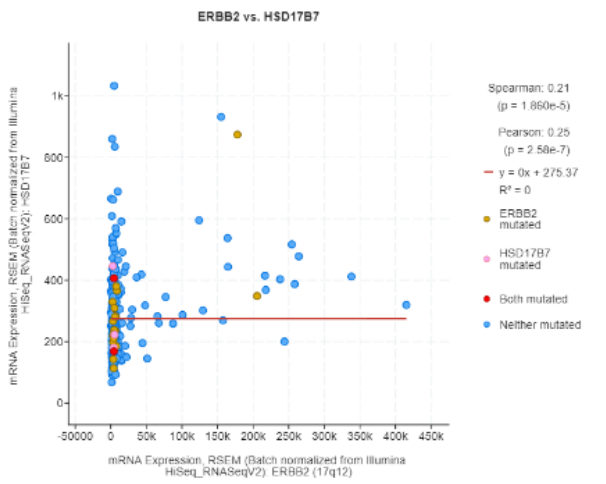

ECM2 vs. AGMAT
mRNA Expression, RSEM (Batch normalized from Illumina HiSeq_RNASeqV2): AGMAT
mRNA Expression, RSEM (Batch normalized from Illumina HiSeq_RNASeqV2): ECM2 (9q22.31)
Spearman: -0.24
(p = 1.218e-6)
Pearson: -0.22
(p = 5.157e-6)
y = -0.9x + 688.26
R² = 0.05
ECM2 mutated
AGMAT mutated
Neither mutated

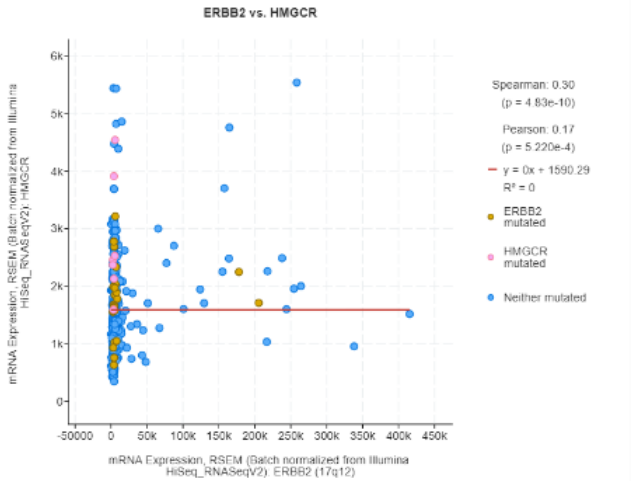

ECM2 vs. AFMID
mRNA Expression, RSEM (Batch normalized from Illumina HiSeq_RNASeqV2): AFMID
mRNA Expression, RSEM (Batch normalized from Illumina HiSeq_RNASeqV2): ECM2 (9q22.31)
Spearman: -0.31
(p = 1.01e-10)
Pearson: -0.18
(p = 2.122e-4)
y = -0.5x + 506.07
R² = 0.03
ECM2 mutated
AFMID mutated
Neither mutated

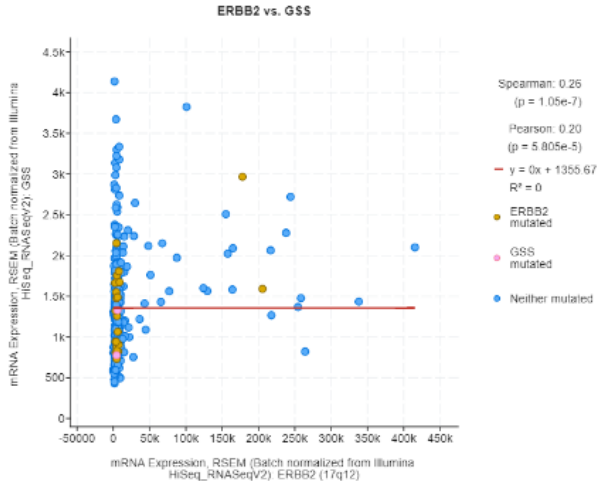

ECM2 vs. ACAT2
mRNA Expression, RSEM (Batch normalized from Illumina HiSeq_RNASeqV2): ACAT2
mRNA Expression, RSEM (Batch normalized from Illumina HiSeq_RNASeqV2): ECM2 (9q22.31)
Spearman: -0.45
(p = 4.35e-22)
Pearson: -0.36
(p = 3.96e-14)
y = -1.33x + 850.89
R² = 0.13
ECM2 mutated
ACAT2 mutated
Neither mutated

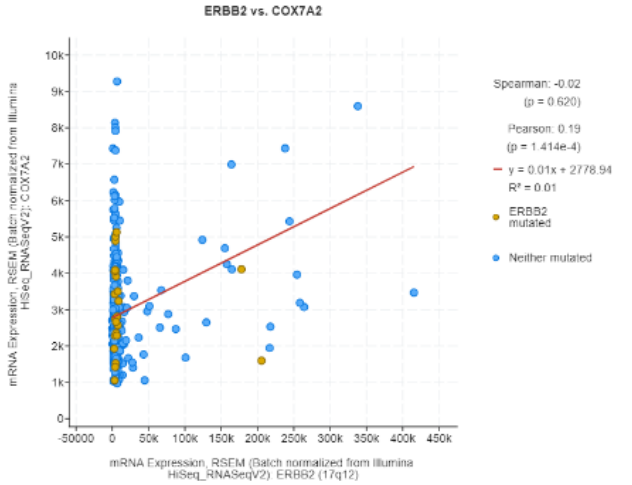
ERBB2

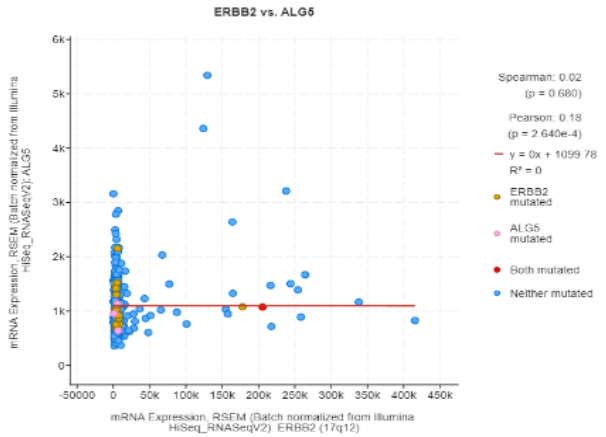

ERBB2 vs. RDH11
mRNA Expression, RSEM (Batch normalized from Illumina HiSeq_RNASeqV2): RDH11
mRNA Expression, RSEM (Batch normalized from Illumina HiSeq_RNASeqV2): ERBB2 (17q12)
Spearman: 0.07
(p = 0.156)
Pearson: 0.16
(p = 1.085e-3)
y = 0x + 1787.65
R² = 0
ERBB2 mutated
RDH11 mutated
Neither mutated
ERBB2 vs. PNMT
mRNA Expression, RSEM (Batch normalized from Illumina HiSeq_RNASeqV2): PNMT
mRNA Expression, RSEM (Batch normalized from Illumina HiSeq_RNASeqV2): ERBB2 (17q12)
Spearman: 0.35
(p = 1.96e-13)
Pearson: 0.54
(p = 8.18e-32)
y = 0x + 14.7
R² = 0
ERBB2 mutated
PNMT mutated
Both mutated
Neither mutated
ERBB2 vs. NT5C
mRNA Expression, RSEM (Batch normalized from Illumina HiSeq_RNASeqV2): NT5C
mRNA Expression, RSEM (Batch normalized from Illumina HiSeq_RNASeqV2): ERBB2 (17q12)
Spearman: 0.12
(p = 0.0149)
Pearson: 0.21
(p = 2.797e-5)
y = 0x + 536.31
R² = 0
ERBB2 mutated
Neither mutated
ERBB2 vs. MSMO1
mRNA Expression, RSEM (Batch normalized from Illumina HiSeq_RNASeqV2): MSMO1
mRNA Expression, RSEM (Batch normalized from Illumina HiSeq_RNASeqV2): ERBB2 (17q12)
Spearman: 0.32
(p = 3.97e-11)
Pearson: 0.17
(p = 4.543e-4)
y = 0x + 1247.67
R² = 0
ERBB2 mutated
MSMO1 mutated
Neither mutated
ERBB2 vs. ITPA
mRNA Expression, RSEM (Batch normalized from Illumina HiSeq_RNASeqV2): ITPA
mRNA Expression, RSEM (Batch normalized from Illumina HiSeq_RNASeqV2): ERBB2 (17q12)
Spearman: 0.19
(p = 9.641e-5)
Pearson: 0.19
(p = 1.482e-4)
y = 0x + 1016.06
R² = 0
ERBB2 mutated
Neither mutated
ERBB2 vs. IDI1
mRNA Expression, RSEM (Batch normalized from Illumina HiSeq_RNASeqV2): IDI1
mRNA Expression, RSEM (Batch normalized from Illumina HiSeq_RNASeqV2): ERBB2 (17q12)
Spearman: 0.17
(p = 6.204e-4)
Pearson: 0.17
(p = 5.426e-4)
y = 0x + 1385.74
R² = 0
ERBB2 mutated
IDI1 mutated
Neither mutated

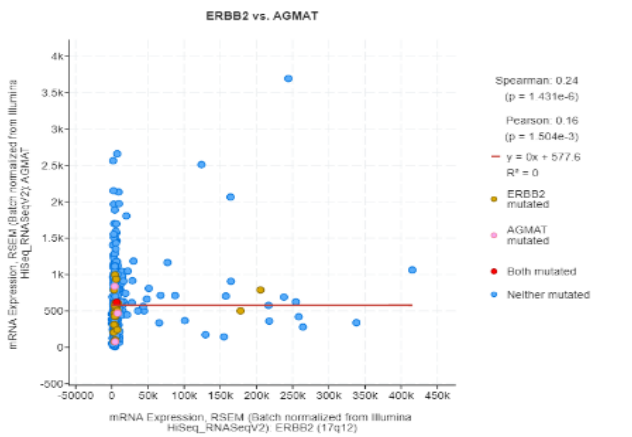

ERBB2 vs. HSD17B7
mRNA Expression, RSEM (Batch normalized from Illumina HiSeq_RNASeqV2): HSD17B7
mRNA Expression, RSEM (Batch normalized from Illumina HiSeq_RNASeqV2): ERBB2 (17q12)
Spearman: 0.21
(p = 1.860e-5)
Pearson: 0.25
(p = 2.58e-7)
y = 0x + 275.37
R² = 0
ERBB2 mutated
HSD17B7 mutated
Both mutated
Neither mutated


ERBB2 vs. HMGCR
mRNA Expression, RSEM (Batch normalized from Illumina HiSeq_RNASeqV2): HMGCR
mRNA Expression, RSEM (Batch normalized from Illumina HiSeq_RNASeqV2): ERBB2 (17q12)
Spearman: 0.30
(p = 4.83e-10)
Pearson: 0.17
(p = 5.220e-4)
y = 0x + 1590.29
R² = 0
ERBB2 mutated
HMGCR mutated
Neither mutated


ERBB2 vs. GSS
mRNA Expression, RSEM (Batch normalized from Illumina HiSeq_RNASeqV2): GSS
mRNA Expression, RSEM (Batch normalized from Illumina HiSeq_RNASeqV2): ERBB2 (17q12)
Spearman: 0.26
(p = 1.05e-7)
Pearson: 0.20
(p = 5.805e-5)
y = 0x + 1355.67
R² = 0
ERBB2 mutated
GSS mutated
Neither mutated

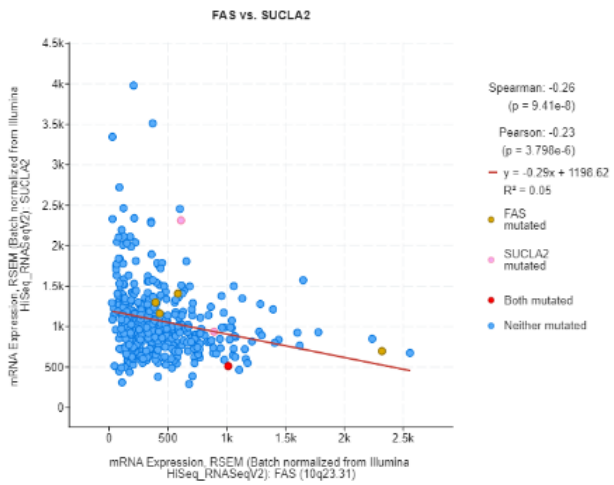

ERBB2 vs. COX7A2
mRNA Expression, RSEM (Batch normalized from Illumina HiSeq_RNASeqV2): COX7A2
mRNA Expression, RSEM (Batch normalized from Illumina HiSeq_RNASeqV2): ERBB2 (17q12)
Spearman: -0.02
(p = 0.620)
Pearson: 0.19
(p = 1.414e-4)
y = 0.01x + 2778.94
R² = 0.01
ERBB2 mutated
Neither mutated

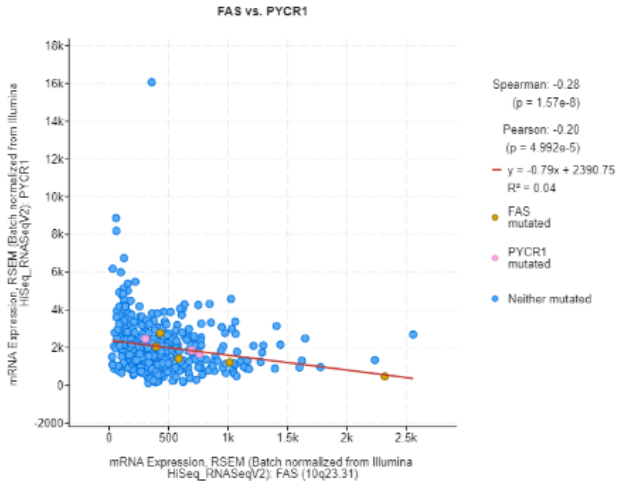

ERBB2 vs. ALG5
mRNA Expression, RSEM (Batch normalized from Illumina HiSeq_RNASeqV2): ALG5
mRNA Expression, RSEM (Batch normalized from Illumina HiSeq_RNASeqV2): ERBB2 (17q12)
Spearman: 0.02
(p = 0.680)
Pearson: 0.18
(p = 2.640e-4)
y = 0x + 1099.78
R² = 0
ERBB2 mutated
ALG5 mutated
Both mutated
Neither mutated

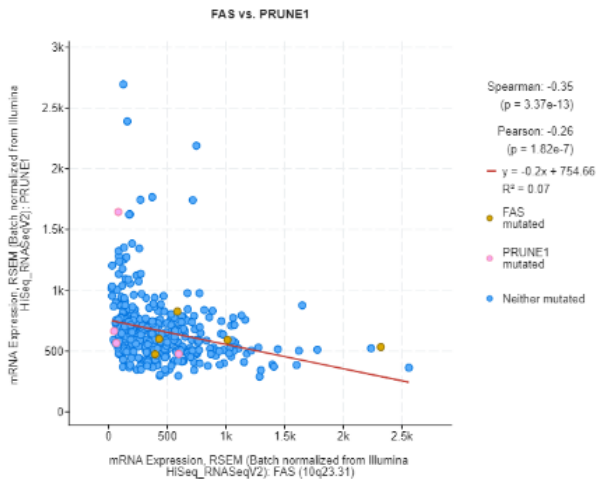

ERBB2 vs. AGMAT
mRNA Expression, RSEM (Batch normalized from Illumina HiSeq_RNASeqV2): AGMAT
mRNA Expression, RSEM (Batch normalized from Illumina HiSeq_RNASeqV2): ERBB2 (17q12)
Spearman: 0.24
(p = 1.431e-6)
Pearson: 0.16
(p = 1.504e-3)
y = 0x + 577.6
R² = 0
ERBB2 mutated
AGMAT mutated
Both mutated
Neither mutated

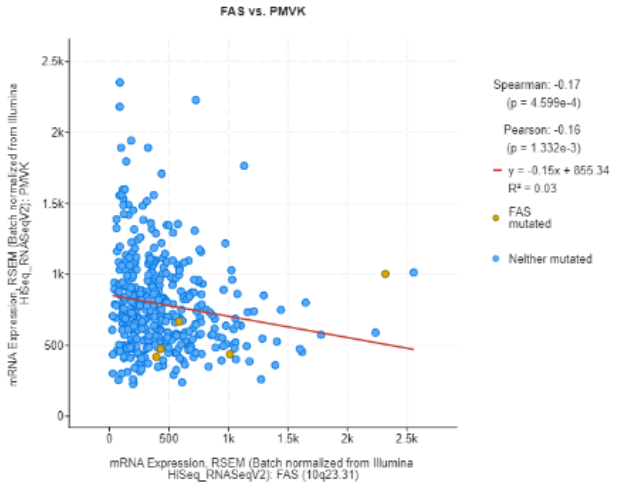

ERBB2 vs. ACAT2
mRNA Expression, RSEM (Batch normalized from Illumina HiSeq_RNASeqV2): ACAT2
mRNA Expression, RSEM (Batch normalized from Illumina HiSeq_RNASeqV2): ERBB2 (17q12)
Spearman: 0.23
(p = 2.174e-6)
Pearson: 0.25
(p = 5.26e-7)
y = 0x + 687.37
R² = 0
ERBB2 mutated
ACAT2 mutated
Neither mutated

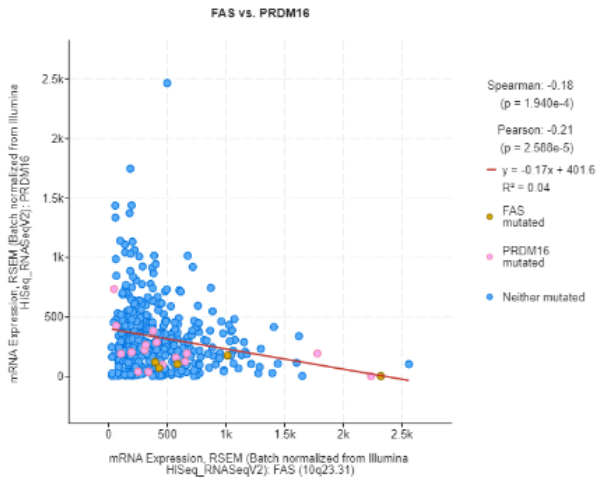
FAS

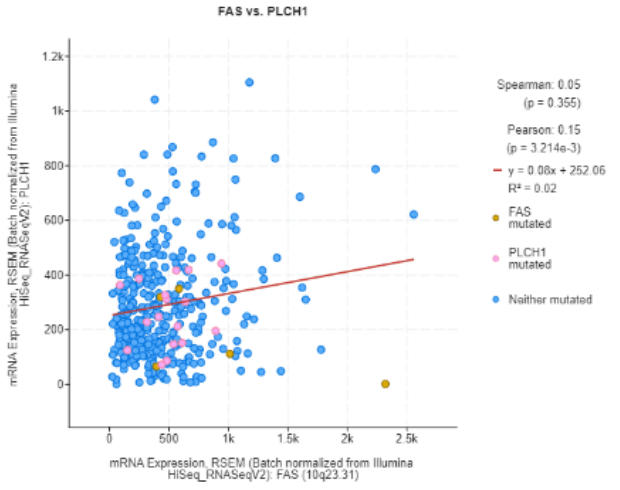

FAS vs. SUCLA2
mRNA Expression, RSEM (Batch normalized from Illumina HiSeq_RNASeqV2): SUCLA2
mRNA Expression, RSEM (Batch normalized from Illumina HiSeq_RNASeqV2): FAS (10q23.31)
Spearman: -0.26
(p = 9.41e-8)
Pearson: -0.23
(p = 3.798e-6)
y = -0.29x + 1198.62
R² = 0.05
FAS mutated
SUCLA2 mutated
Both mutated
Neither mutated

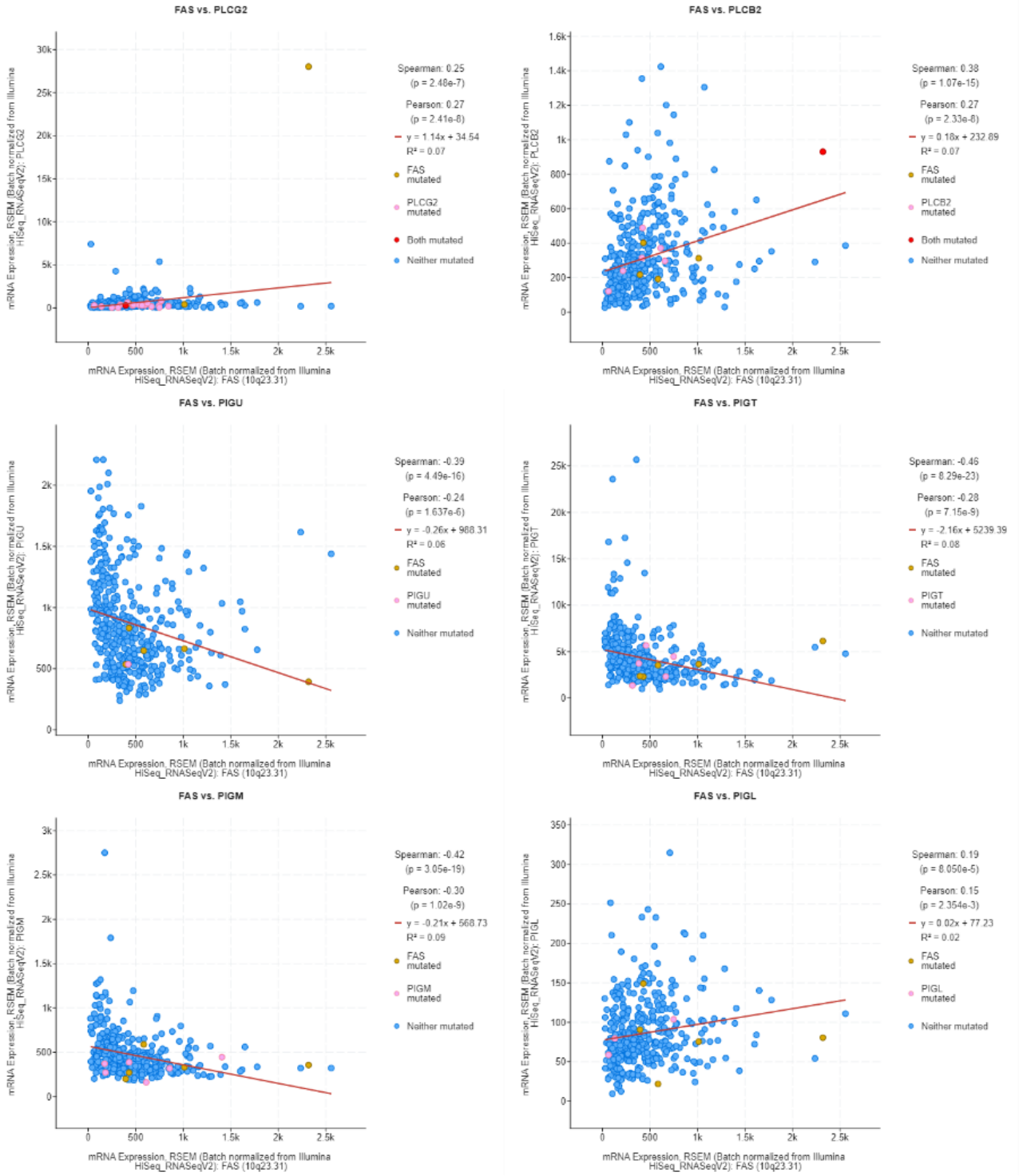

FAS vs. PYCR1
mRNA Expression, RSEM (Batch normalized from Illumina HiSeq_RNASeqV2): PYCR1
mRNA Expression, RSEM (Batch normalized from Illumina HiSeq_RNASeqV2): FAS (10q23.31)
Spearman: -0.28
(p = 1.57e-8)
Pearson: -0.20
(p = 4.992e-5)
y = -0.79x + 2390.75
R² = 0.04
FAS mutated
PYCR1 mutated
Neither mutated

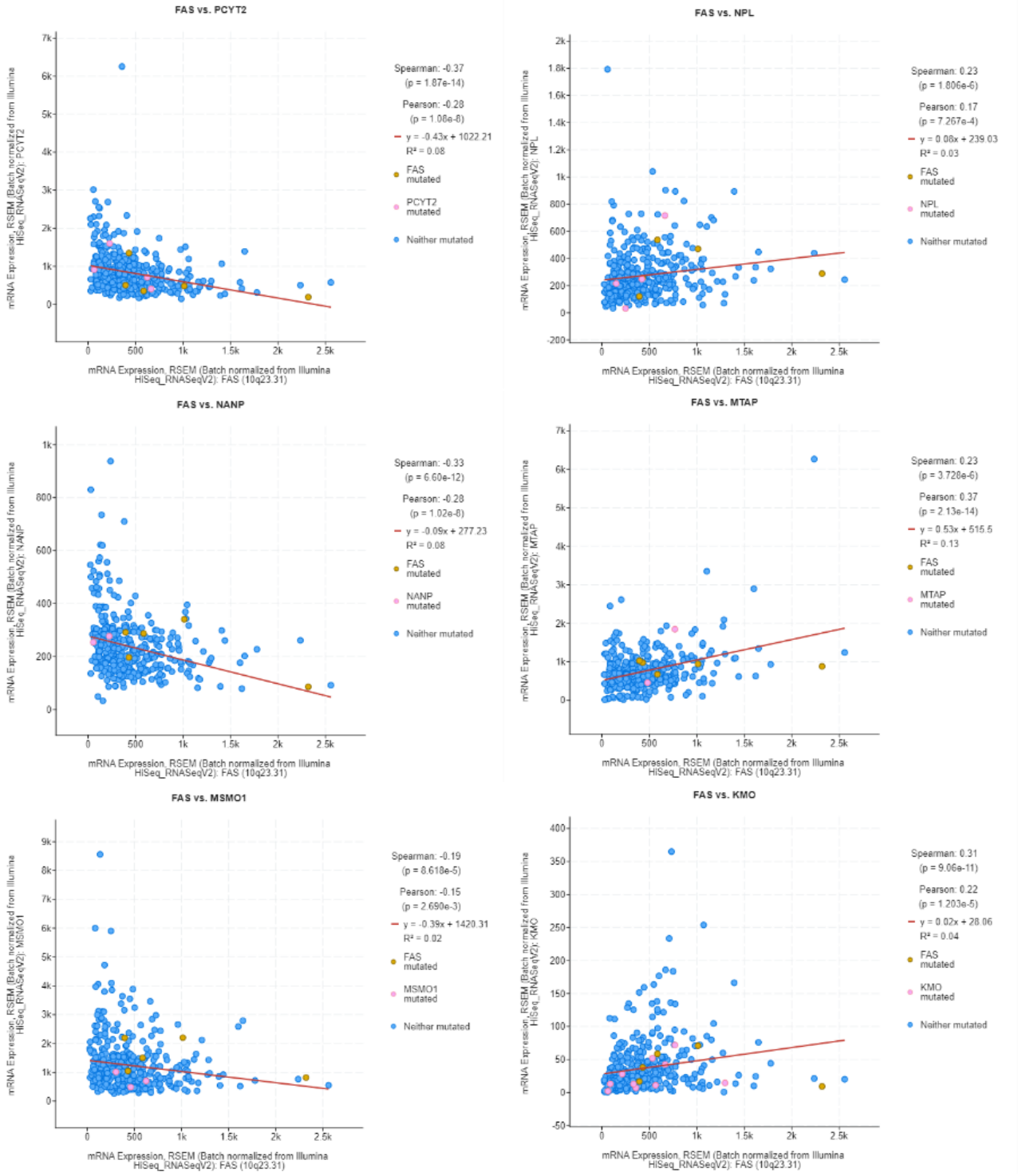

FAS vs. PRUNE1
mRNA Expression, RSEM (Batch normalized from Illumina HiSeq_RNASeqV2): PRUNE1
mRNA Expression, RSEM (Batch normalized from Illumina HiSeq_RNASeqV2): FAS (10q23.31)
Spearman: -0.35
(p = 3.37e-13)
Pearson: -0.26
(p = 1.82e-7)
y = -0.2x + 754.66
R² = 0.07
FAS mutated
PRUNE1 mutated
Neither mutated

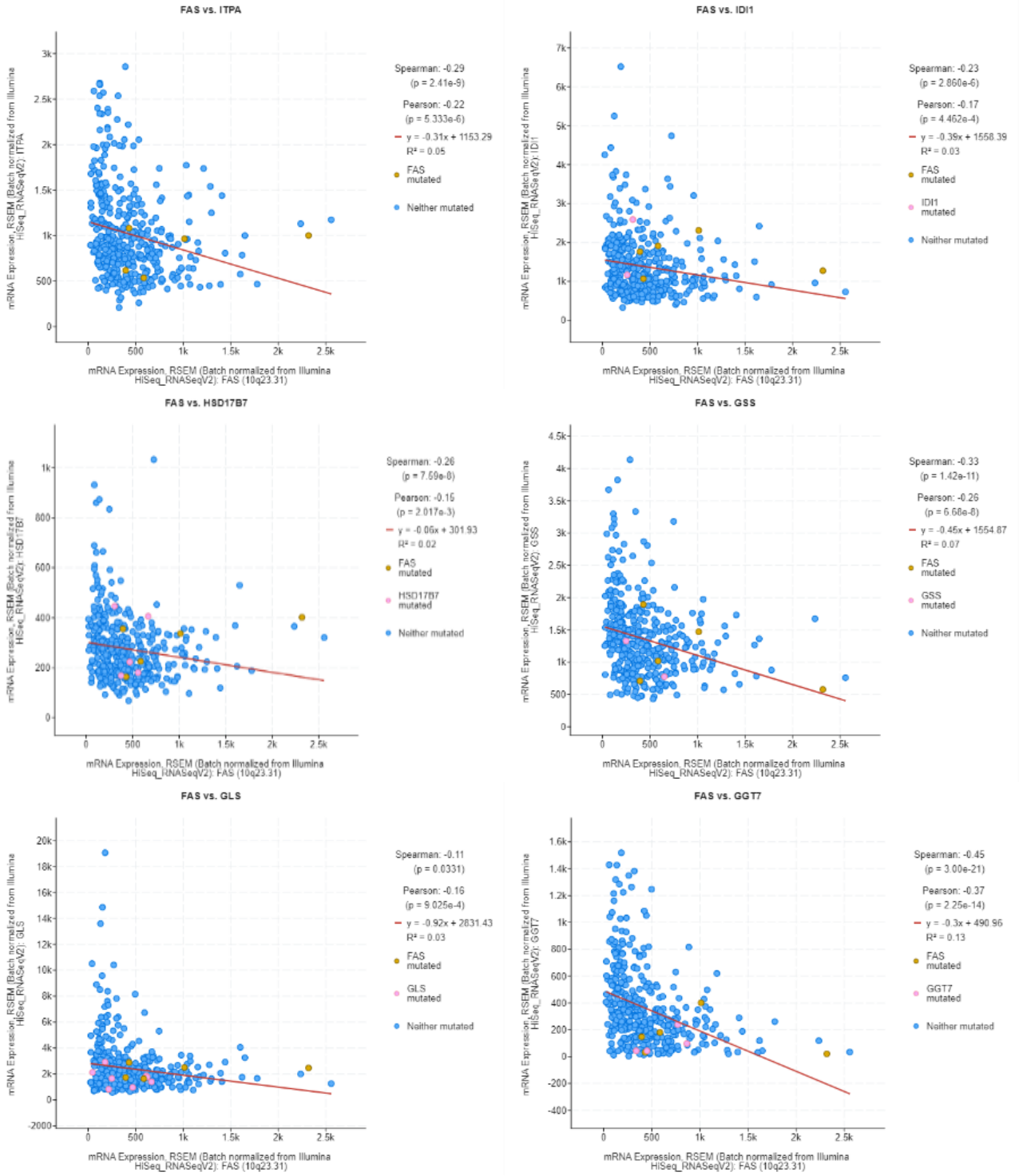

FAS vs. PMVK
mRNA Expression, RSEM (Batch normalized from Illumina HiSeq_RNASeqV2): PMVK
mRNA Expression, RSEM (Batch normalized from Illumina HiSeq_RNASeqV2): FAS (10q23.31)
Spearman: -0.17
(p = 4.599e-4)
Pearson: -0.16
(p = 1.332e-3)
y = -0.15x + 855.34
R² = 0.03
FAS mutated
Neither mutated

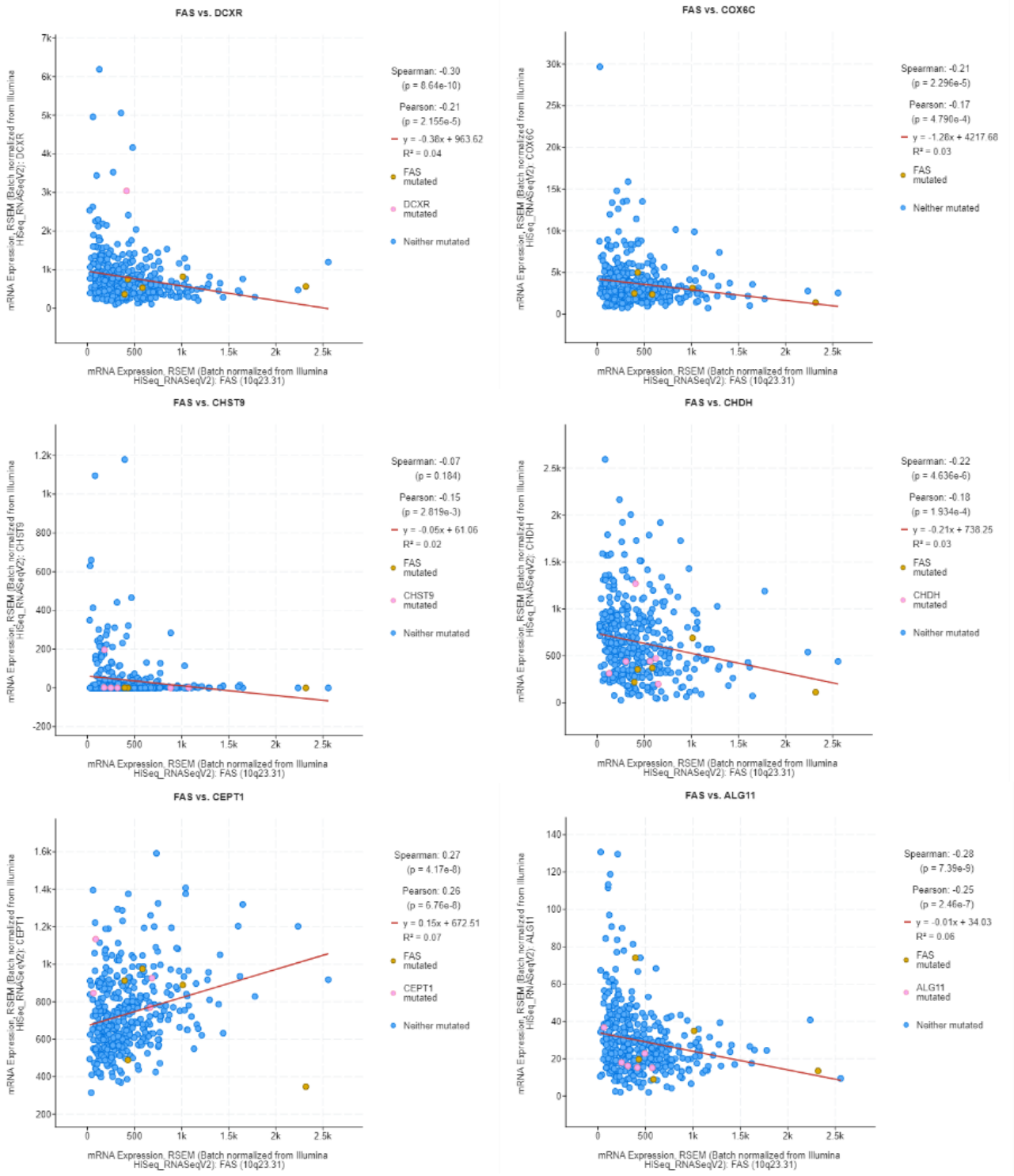

FAS vs. PRDM16
mRNA Expression, RSEM (Batch normalized from Illumina HiSeq_RNASeqV2): PRDM16
mRNA Expression, RSEM (Batch normalized from Illumina HiSeq_RNASeqV2): FAS (10q23.31)
Spearman: -0.18
(p = 1.940e-4)
Pearson: -0.21
(p = 2.568e-5)
y = -0.17x + 401.6
R² = 0.04
FAS mutated
PRDM16 mutated
Neither mutated

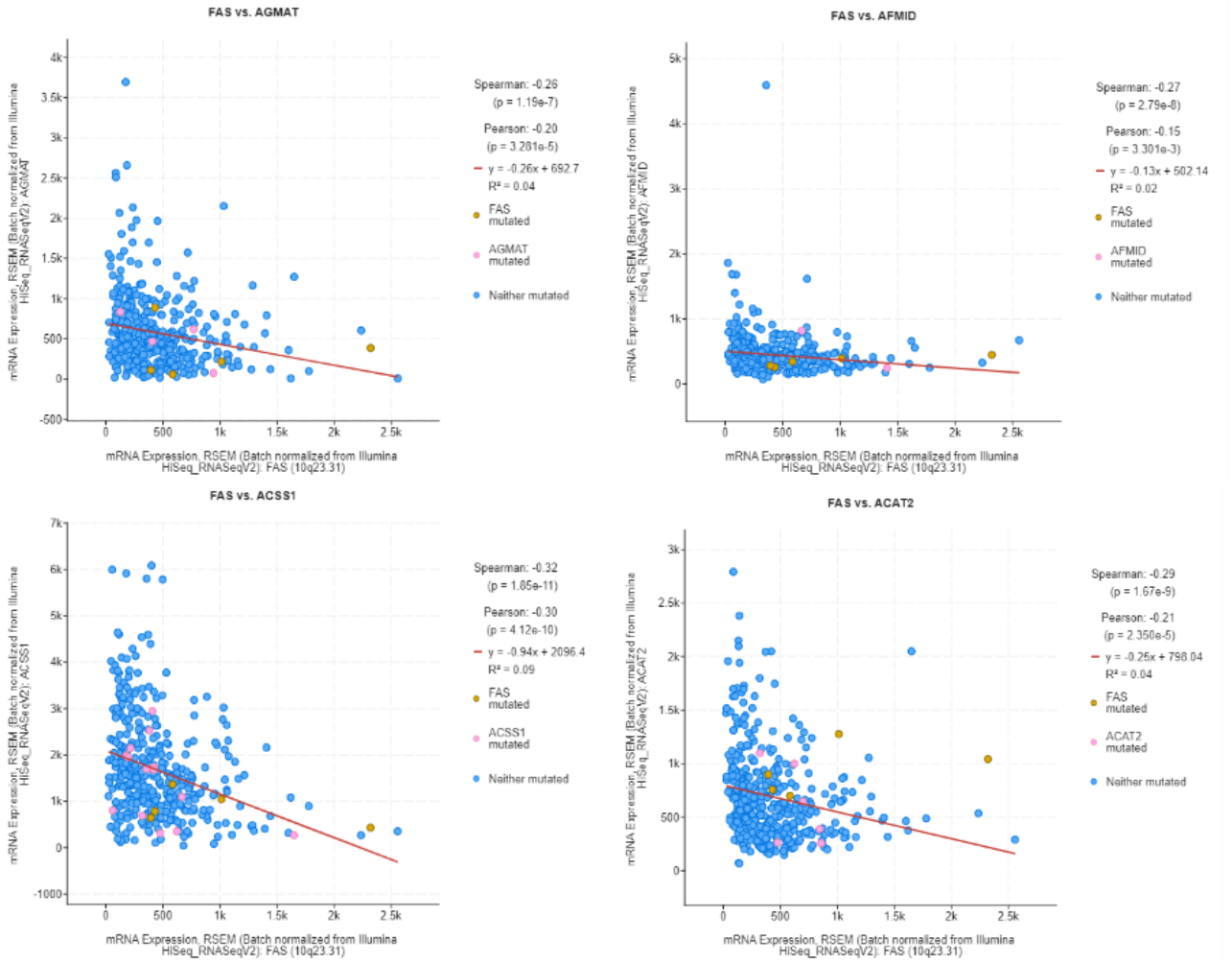

FAS vs. PLCH1
mRNA Expression, RSEM (Batch normalized from Illumina HiSeq_RNASeqV2): PLCH1
mRNA Expression, RSEM (Batch normalized from Illumina HiSeq_RNASeqV2): FAS (10q23.31)
Spearman: 0.05
(p = 0.355)
Pearson: 0.15
(p = 3.214e-3)
y = 0.08x + 252.06
R² = 0.02
FAS mutated
PLCH1 mutated
Neither mutated


FAS vs. PLCG2
mRNA Expression, RSEM (Batch normalized from Illumina HiSeq_RNASeqV2): PLCG2
mRNA Expression, RSEM (Batch normalized from Illumina HiSeq_RNASeqV2): FAS (10q23.31)
Spearman: 0.25
(p = 2.48e-7)
Pearson: 0.27
(p = 2.41e-8)
y = 1.14x + 34.54
R² = 0.07
FAS mutated
PLCG2 mutated
Both mutated
Neither mutated
FAS vs. PLCB2
mRNA Expression, RSEM (Batch normalized from Illumina HiSeq_RNASeqV2): PLCB2
mRNA Expression, RSEM (Batch normalized from Illumina HiSeq_RNASeqV2): FAS (10q23.31)
Spearman: 0.38
(p = 1.07e-15)
Pearson: 0.27
(p = 2.33e-8)
y = 0.18x + 232.89
R² = 0.07
FAS mutated
PLCB2 mutated
Both mutated
Neither mutated
FAS vs. PIGU
mRNA Expression, RSEM (Batch normalized from Illumina HiSeq_RNASeqV2): PIGU
mRNA Expression, RSEM (Batch normalized from Illumina HiSeq_RNASeqV2): FAS (10q23.31)
Spearman: -0.39
(p = 4.49e-16)
Pearson: -0.24
(p = 1.637e-6)
y = -0.26x + 968.31
R² = 0.06
FAS mutated
PIGU mutated
Neither mutated
FAS vs. PIGT
mRNA Expression, RSEM (Batch normalized from Illumina HiSeq_RNASeqV2): PIGT
mRNA Expression, RSEM (Batch normalized from Illumina HiSeq_RNASeqV2): FAS (10q23.31)
Spearman: -0.46
(p = 8.29e-23)
Pearson: -0.28
(p = 7.15e-9)
y = -2.16x + 5239.39
R² = 0.08
FAS mutated
PIGT mutated
Neither mutated
FAS vs. PIGM
mRNA Expression, RSEM (Batch normalized from Illumina HiSeq_RNASeqV2): PIGM
mRNA Expression, RSEM (Batch normalized from Illumina HiSeq_RNASeqV2): FAS (10q23.31)
Spearman: -0.42
(p = 3.05e-19)
Pearson: -0.30
(p = 1.02e-9)
y = -0.21x + 568.73
R² = 0.09
FAS mutated
PIGM mutated
Neither mutated
FAS vs. PIGL
mRNA Expression, RSEM (Batch normalized from Illumina HiSeq_RNASeqV2): PIGL
mRNA Expression, RSEM (Batch normalized from Illumina HiSeq_RNASeqV2): FAS (10q23.31)
Spearman: 0.19
(p = 8.050e-5)
Pearson: 0.15
(p = 2.354e-3)
y = 0.02x + 77.23
R² = 0.02
FAS mutated
PIGL mutated
Neither mutated

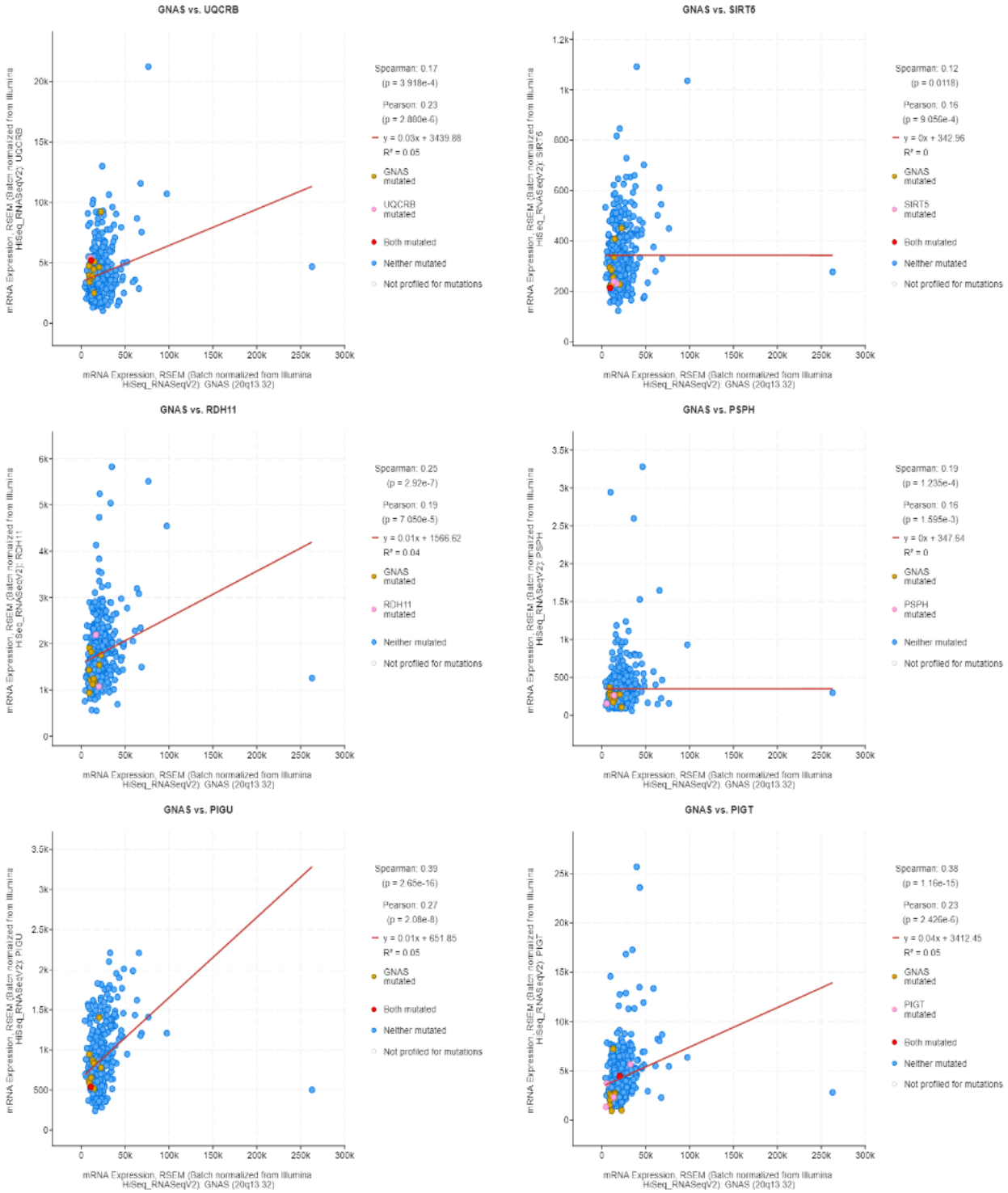

FAS vs. PCYT2
mRNA Expression, RSEM (Batch normalized from Illumina HiSeq_RNASeqV2): PCYT2
mRNA Expression, RSEM (Batch normalized from Illumina HiSeq_RNASeqV2): FAS (10q23.31)
Spearman: -0.37
(p = 1.87e-14)
Pearson: -0.28
(p = 1.08e-8)
y = -0.43x + 1022.21
R² = 0.08
FAS mutated
PCYT2 mutated
Neither mutated
FAS vs. NPL
mRNA Expression, RSEM (Batch normalized from Illumina HiSeq_RNASeqV2): NPL
mRNA Expression, RSEM (Batch normalized from Illumina HiSeq_RNASeqV2): FAS (10q23.31)
Spearman: 0.23
(p = 1.806e-6)
Pearson: 0.17
(p = 7.267e-4)
y = 0.08x + 239.03
R² = 0.03
FAS mutated
NPL mutated
Neither mutated
FAS vs. NANP
mRNA Expression, RSEM (Batch normalized from Illumina HiSeq_RNASeqV2): NANP
mRNA Expression, RSEM (Batch normalized from Illumina HiSeq_RNASeqV2): FAS (10q23.31)
Spearman: -0.33
(p = 6.60e-12)
Pearson: -0.28
(p = 1.02e-8)
y = -0.09x + 277.23
R² = 0.08
FAS mutated
NANP mutated
Neither mutated
FAS vs. MTAP
mRNA Expression, RSEM (Batch normalized from Illumina HiSeq_RNASeqV2): MTAP
mRNA Expression, RSEM (Batch normalized from Illumina HiSeq_RNASeqV2): FAS (10q23.31)
Spearman: 0.23
(p = 3.728e-6)
Pearson: 0.37
(p = 2.13e-14)
y = 0.53x + 515.5
R² = 0.13
FAS mutated
MTAP mutated
Neither mutated
FAS vs. MSMO1
mRNA Expression, RSEM (Batch normalized from Illumina HiSeq_RNASeqV2): MSMO1
mRNA Expression, RSEM (Batch normalized from Illumina HiSeq_RNASeqV2): FAS (10q23.31)
Spearman: -0.19
(p = 8.618e-5)
Pearson: -0.15
(p = 2.690e-3)
y = -0.39x + 1420.31
R² = 0.02
FAS mutated
MSMO1 mutated
Neither mutated
FAS vs. KMO
mRNA Expression, RSEM (Batch normalized from Illumina HiSeq_RNASeqV2): KMO
mRNA Expression, RSEM (Batch normalized from Illumina HiSeq_RNASeqV2): FAS (10q23.31)
Spearman: 0.31
(p = 9.06e-11)
Pearson: 0.22
(p = 1.203e-5)
y = 0.02x + 28.06
R² = 0.04
FAS mutated
KMO mutated
Neither mutated

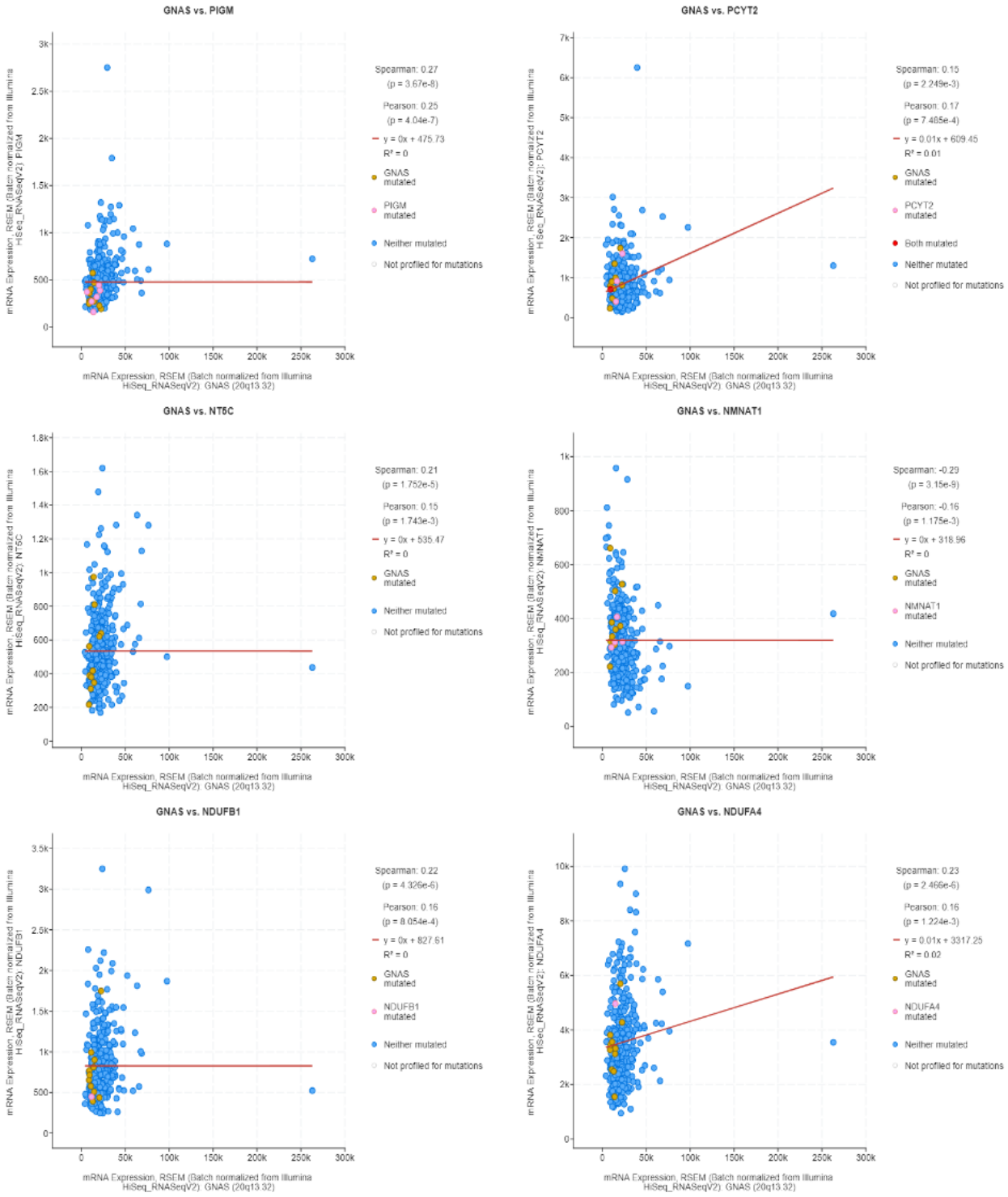

FAS vs. ITPA
Spearman: -0.29
(p = 2.41e-9)
Pearson: -0.22
(p = 5.333e-6)
y = -0.31x + 1153.29
R² = 0.05
FAS mutated
Neither mutated
mRNA Expression, RSEM (Batch normalized from Illumina HiSeq_RNASeqV2): ITPA
mRNA Expression, RSEM (Batch normalized from Illumina HiSeq_RNASeqV2): FAS (10q23.31)
FAS vs. IDI1
Spearman: -0.23
(p = 2.860e-6)
Pearson: -0.17
(p = 4.462e-4)
y = -0.39x + 1558.39
R² = 0.03
FAS mutated
IDI1 mutated
Neither mutated
mRNA Expression, RSEM (Batch normalized from Illumina HiSeq_RNASeqV2): IDI1
mRNA Expression, RSEM (Batch normalized from Illumina HiSeq_RNASeqV2): FAS (10q23.31)
FAS vs. HSD17B7
Spearman: -0.26
(p = 7.59e-8)
Pearson: -0.15
(p = 2.017e-3)
y = -0.06x + 301.93
R² = 0.02
FAS mutated
HSD17B7 mutated
Neither mutated
mRNA Expression, RSEM (Batch normalized from Illumina HiSeq_RNASeqV2): HSD17B7
mRNA Expression, RSEM (Batch normalized from Illumina HiSeq_RNASeqV2): FAS (10q23.31)
FAS vs. GSS
Spearman: -0.33
(p = 1.42e-11)
Pearson: -0.26
(p = 6.66e-8)
y = -0.45x + 1554.87
R² = 0.07
FAS mutated
GSS mutated
Neither mutated
mRNA Expression, RSEM (Batch normalized from Illumina HiSeq_RNASeqV2): GSS
mRNA Expression, RSEM (Batch normalized from Illumina HiSeq_RNASeqV2): FAS (10q23.31)
FAS vs. GLS
Spearman: -0.11
(p = 0.0331)
Pearson: -0.16
(p = 9.025e-4)
y = -0.92x + 2831.43
R² = 0.03
FAS mutated
GLS mutated
Neither mutated
mRNA Expression, RSEM (Batch normalized from Illumina HiSeq_RNASeqV2): GLS
mRNA Expression, RSEM (Batch normalized from Illumina HiSeq_RNASeqV2): FAS (10q23.31)
FAS vs. GGT7
Spearman: -0.45
(p = 3.00e-21)
Pearson: -0.37
(p = 2.25e-14)
y = -0.3x + 490.96
R² = 0.13
FAS mutated
GGT7 mutated
Neither mutated
mRNA Expression, RSEM (Batch normalized from Illumina HiSeq_RNASeqV2): GGT7
mRNA Expression, RSEM (Batch normalized from Illumina HiSeq_RNASeqV2): FAS (10q23.31)


FAS vs. DCXR
mRNA Expression, RSEM (Batch normalized from Illumina HiSeq_RNASeqV2): DCXR
mRNA Expression, RSEM (Batch normalized from Illumina HiSeq_RNASeqV2): FAS (10q23.31)
Spearman: -0.30
(p = 8.64e-10)
Pearson: -0.21
(p = 2.155e-5)
y = -0.36x + 963.62
R² = 0.04
FAS mutated
DCXR mutated
Neither mutated
FAS vs. COX6C
mRNA Expression, RSEM (Batch normalized from Illumina HiSeq_RNASeqV2): COX6C
mRNA Expression, RSEM (Batch normalized from Illumina HiSeq_RNASeqV2): FAS (10q23.31)
Spearman: -0.21
(p = 2.296e-5)
Pearson: -0.17
(p = 4.790e-4)
y = -1.26x + 4217.68
R² = 0.03
FAS mutated
Neither mutated
FAS vs. CHST9
mRNA Expression, RSEM (Batch normalized from Illumina HiSeq_RNASeqV2): CHST9
mRNA Expression, RSEM (Batch normalized from Illumina HiSeq_RNASeqV2): FAS (10q23.31)
Spearman: -0.07
(p = 0.184)
Pearson: -0.15
(p = 2.819e-3)
y = -0.05x + 61.06
R² = 0.02
FAS mutated
CHST9 mutated
Neither mutated
FAS vs. CHDH
mRNA Expression, RSEM (Batch normalized from Illumina HiSeq_RNASeqV2): CHDH
mRNA Expression, RSEM (Batch normalized from Illumina HiSeq_RNASeqV2): FAS (10q23.31)
Spearman: -0.22
(p = 4.636e-6)
Pearson: -0.18
(p = 1.934e-4)
y = -0.21x + 738.25
R² = 0.03
FAS mutated
CHDH mutated
Neither mutated
FAS vs. CEPT1
mRNA Expression, RSEM (Batch normalized from Illumina HiSeq_RNASeqV2): CEPT1
mRNA Expression, RSEM (Batch normalized from Illumina HiSeq_RNASeqV2): FAS (10q23.31)
Spearman: 0.27
(p = 4.17e-8)
Pearson: 0.26
(p = 6.76e-8)
y = 0.15x + 672.51
R² = 0.07
FAS mutated
CEPT1 mutated
Neither mutated
FAS vs. ALG11
mRNA Expression, RSEM (Batch normalized from Illumina HiSeq_RNASeqV2): ALG11
mRNA Expression, RSEM (Batch normalized from Illumina HiSeq_RNASeqV2): FAS (10q23.31)
Spearman: -0.28
(p = 7.39e-9)
Pearson: -0.25
(p = 2.46e-7)
y = -0.01x + 34.03
R² = 0.06
FAS mutated
ALG11 mutated
Neither mutated

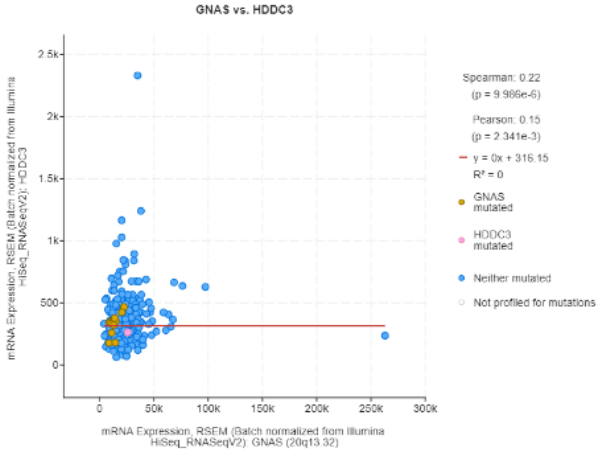

FAS vs. AGMAT
mRNA Expression, RSEM (Batch normalized from Illumina HiSeq_RNASeqV2): AGMAT
mRNA Expression, RSEM (Batch normalized from Illumina HiSeq_RNASeqV2): FAS (10q23.31)
Spearman: -0.26
(p = 1.19e-7)
Pearson: -0.20
(p = 3.281e-5)
y = -0.26x + 692.7
R² = 0.04
FAS mutated
AGMAT mutated
Neither mutated
FAS vs. AFMID
mRNA Expression, RSEM (Batch normalized from Illumina HiSeq_RNASeqV2): AFMID
mRNA Expression, RSEM (Batch normalized from Illumina HiSeq_RNASeqV2): FAS (10q23.31)
Spearman: -0.27
(p = 2.79e-8)
Pearson: -0.15
(p = 3.301e-3)
y = -0.13x + 502.14
R² = 0.02
FAS mutated
AFMID mutated
Neither mutated
FAS vs. ACSS1
mRNA Expression, RSEM (Batch normalized from Illumina HiSeq_RNASeqV2): ACSS1
mRNA Expression, RSEM (Batch normalized from Illumina HiSeq_RNASeqV2): FAS (10q23.31)
Spearman: -0.32
(p = 1.85e-11)
Pearson: -0.30
(p = 4.12e-10)
y = -0.94x + 2096.4
R² = 0.09
FAS mutated
ACSS1 mutated
Neither mutated
FAS vs. ACAT2
mRNA Expression, RSEM (Batch normalized from Illumina HiSeq_RNASeqV2): ACAT2
mRNA Expression, RSEM (Batch normalized from Illumina HiSeq_RNASeqV2): FAS (10q23.31)
Spearman: -0.29
(p = 1.67e-9)
Pearson: -0.21
(p = 2.350e-5)
y = -0.25x + 798.04
R² = 0.04
FAS mutated
ACAT2 mutated
Neither mutated

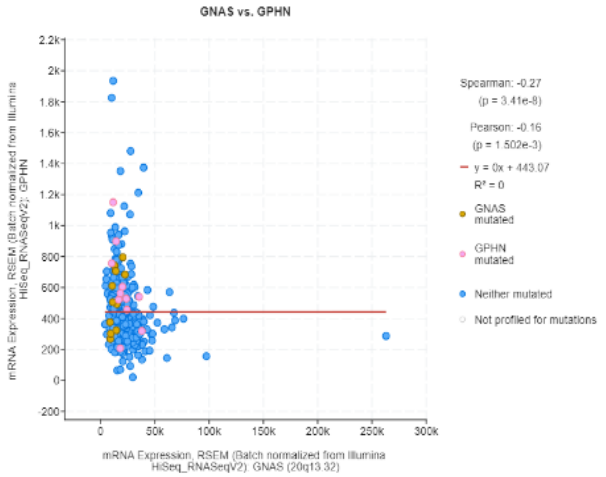
GNAS

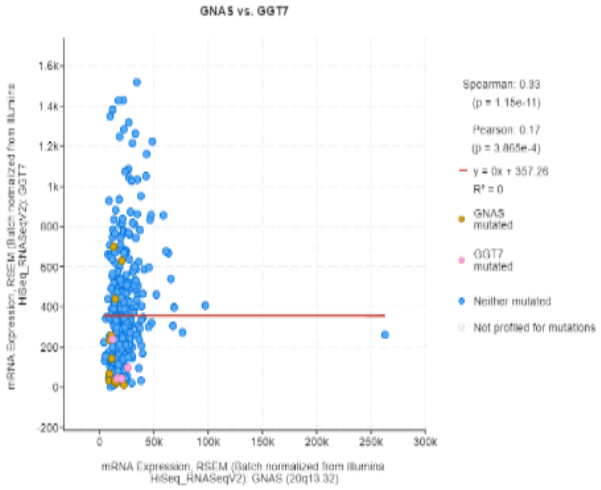

GNAS vs. UQCRB
mRNA Expression, RSEM (Batch normalized from Illumina HiSeq_RNASeqV2); UQCRB
mRNA Expression, RSEM (Batch normalized from Illumina HiSeq_RNASeqV2); GNAS (20q13.32)
Spearman: 0.17
(p = 3.918e-4)
Pearson: 0.23
(p = 2.880e-6)
y = 0.03x + 3439.88
R² = 0.05
GNAS mutated
UQCRB mutated
Both mutated
Neither mutated
Not profiled for mutations
GNAS vs. SIRT5
mRNA Expression, RSEM (Batch normalized from Illumina HiSeq_RNASeqV2); SIRT5
mRNA Expression, RSEM (Batch normalized from Illumina HiSeq_RNASeqV2); GNAS (20q13.32)
Spearman: 0.12
(p = 0.0118)
Pearson: 0.16
(p = 9.056e-4)
y = 0x + 342.96
R² = 0
GNAS mutated
SIRT5 mutated
Both mutated
Neither mutated
Not profiled for mutations
GNAS vs. RDH11
mRNA Expression, RSEM (Batch normalized from Illumina HiSeq_RNASeqV2); RDH11
mRNA Expression, RSEM (Batch normalized from Illumina HiSeq_RNASeqV2); GNAS (20q13.32)
Spearman: 0.25
(p = 2.92e-7)
Pearson: 0.19
(p = 7.050e-5)
y = 0.01x + 1566.62
R² = 0.04
GNAS mutated
RDH11 mutated
Neither mutated
Not profiled for mutations
GNAS vs. PSPH
mRNA Expression, RSEM (Batch normalized from Illumina HiSeq_RNASeqV2); PSPH
mRNA Expression, RSEM (Batch normalized from Illumina HiSeq_RNASeqV2); GNAS (20q13.32)
Spearman: 0.19
(p = 1.235e-4)
Pearson: 0.16
(p = 1.595e-3)
y = 0x + 347.64
R² = 0
GNAS mutated
PSPH mutated
Neither mutated
Not profiled for mutations
GNAS vs. PIGU
mRNA Expression, RSEM (Batch normalized from Illumina HiSeq_RNASeqV2); PIGU
mRNA Expression, RSEM (Batch normalized from Illumina HiSeq_RNASeqV2); GNAS (20q13.32)
Spearman: 0.39
(p = 2.65e-16)
Pearson: 0.27
(p = 2.08e-8)
y = 0.01x + 651.85
R² = 0.05
GNAS mutated
Both mutated
Neither mutated
Not profiled for mutations
GNAS vs. PIGT
mRNA Expression, RSEM (Batch normalized from Illumina HiSeq_RNASeqV2); PIGT
mRNA Expression, RSEM (Batch normalized from Illumina HiSeq_RNASeqV2); GNAS (20q13.32)
Spearman: 0.38
(p = 1.16e-15)
Pearson: 0.23
(p = 2.426e-6)
y = 0.04x + 3412.45
R² = 0.05
GNAS mutated
PIGT mutated
Both mutated
Neither mutated
Not profiled for mutations

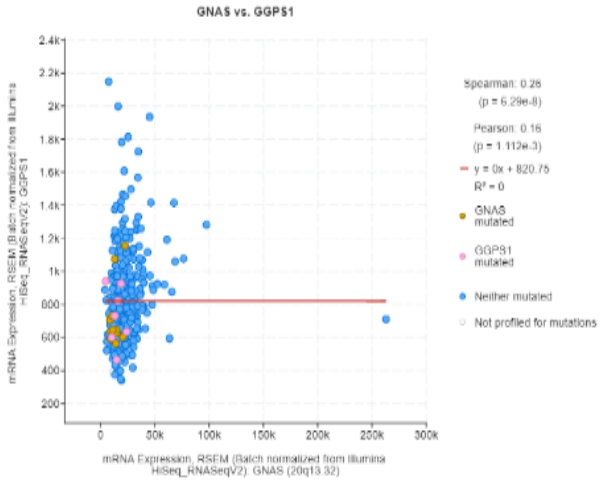

GNAS vs. PIGM
mRNA Expression, RSEM (Batch normalized from Illumina HiSeq_RNASeqV2): PIGM
mRNA Expression, RSEM (Batch normalized from Illumina HiSeq_RNASeqV2): GNAS (20q13.32)
Spearman: 0.27
(p = 3.67e-8)
Pearson: 0.25
(p = 4.04e-7)
y = 0x + 475.73
R² = 0
GNAS mutated
PIGM mutated
Neither mutated
Not profiled for mutations
GNAS vs. PCYT2
mRNA Expression, RSEM (Batch normalized from Illumina HiSeq_RNASeqV2): PCYT2
mRNA Expression, RSEM (Batch normalized from Illumina HiSeq_RNASeqV2): GNAS (20q13.32)
Spearman: 0.15
(p = 2.249e-3)
Pearson: 0.17
(p = 7.465e-4)
y = 0.01x + 609.45
R² = 0.01
GNAS mutated
PCYT2 mutated
Both mutated
Neither mutated
Not profiled for mutations
GNAS vs. NT5C
mRNA Expression, RSEM (Batch normalized from Illumina HiSeq_RNASeqV2): NT5C
mRNA Expression, RSEM (Batch normalized from Illumina HiSeq_RNASeqV2): GNAS (20q13.32)
Spearman: 0.21
(p = 1.752e-5)
Pearson: 0.15
(p = 1.743e-3)
y = 0x + 535.47
R² = 0
GNAS mutated
Neither mutated
Not profiled for mutations
GNAS vs. NMNAT1
mRNA Expression, RSEM (Batch normalized from Illumina HiSeq_RNASeqV2): NMNAT1
mRNA Expression, RSEM (Batch normalized from Illumina HiSeq_RNASeqV2): GNAS (20q13.32)
Spearman: -0.29
(p = 3.15e-9)
Pearson: -0.16
(p = 1.175e-3)
y = 0x + 318.96
R² = 0
GNAS mutated
NMNAT1 mutated
Neither mutated
Not profiled for mutations
GNAS vs. NDUFB1
mRNA Expression, RSEM (Batch normalized from Illumina HiSeq_RNASeqV2): NDUFB1
mRNA Expression, RSEM (Batch normalized from Illumina HiSeq_RNASeqV2): GNAS (20q13.32)
Spearman: 0.22
(p = 4.326e-6)
Pearson: 0.16
(p = 8.054e-4)
y = 0x + 827.61
R² = 0
GNAS mutated
NDUFB1 mutated
Neither mutated
Not profiled for mutations
GNAS vs. NDUFA4
mRNA Expression, RSEM (Batch normalized from Illumina HiSeq_RNASeqV2): NDUFA4
mRNA Expression, RSEM (Batch normalized from Illumina HiSeq_RNASeqV2): GNAS (20q13.32)
Spearman: 0.23
(p = 2.466e-6)
Pearson: 0.16
(p = 1.224e-3)
y = 0.01x + 3317.25
R² = 0.02
GNAS mutated
NDUFA4 mutated
Neither mutated
Not profiled for mutations

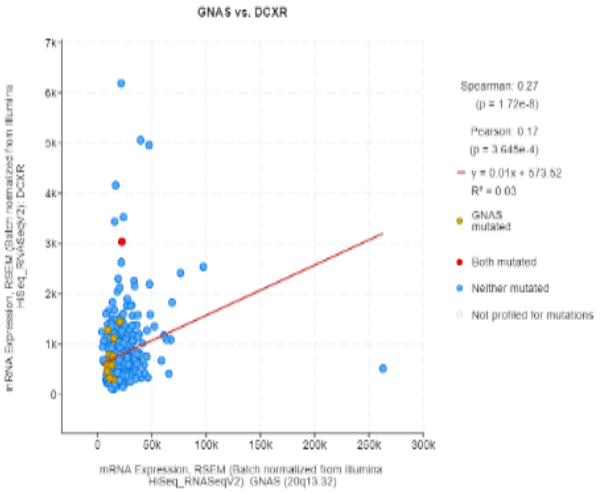

GNAS vs. ITPA
mRNA Expression, RSEM (Batch normalized from Illumina HiSeq_RNASeqV2); ITPA
mRNA Expression, RSEM (Batch normalized from Illumina HiSeq_RNASeqV2); GNAS (20q13.32)
Spearman: 0.28
(p = 9.22e-9)
Pearson: 0.20
(p = 2.904e-5)
y = 0.01x + 793.55
R² = 0.03
GNAS mutated
ITPA mutated
Neither mutated
Not profiled for mutations


GNAS vs. HDDC3
mRNA Expression, RSEM (Batch normalized from Illumina HiSeq_RNASeqV2); HDDC3
mRNA Expression, RSEM (Batch normalized from Illumina HiSeq_RNASeqV2); GNAS (20q13.32)
Spearman: 0.22
(p = 9.986e-6)
Pearson: 0.15
(p = 2.341e-3)
y = 0x + 316.15
R² = 0
GNAS mutated
HDDC3 mutated
Neither mutated
Not profiled for mutations

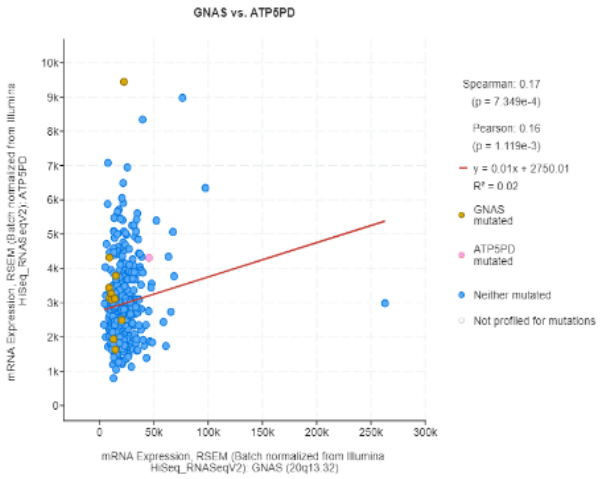

GNAS vs. GPHN
mRNA Expression, RSEM (Batch normalized from Illumina HiSeq_RNASeqV2); GPHN
mRNA Expression, RSEM (Batch normalized from Illumina HiSeq_RNASeqV2); GNAS (20q13.32)
Spearman: -0.27
(p = 3.41e-8)
Pearson: -0.16
(p = 1.502e-3)
y = 0x + 443.07
R² = 0
GNAS mutated
GPHN mutated
Neither mutated
Not profiled for mutations


GNAS vs. GGT7
mRNA Expression, RSEM (Batch normalized from Illumina HiSeq_RNASeqV2); GGT7
mRNA Expression, RSEM (Batch normalized from Illumina HiSeq_RNASeqV2); GNAS (20q13.32)
Spearman: 0.33
(p = 1.15e-11)
Pearson: 0.17
(p = 3.865e-4)
y = 0x + 357.26
R² = 0
GNAS mutated
GGT7 mutated
Neither mutated
Not profiled for mutations

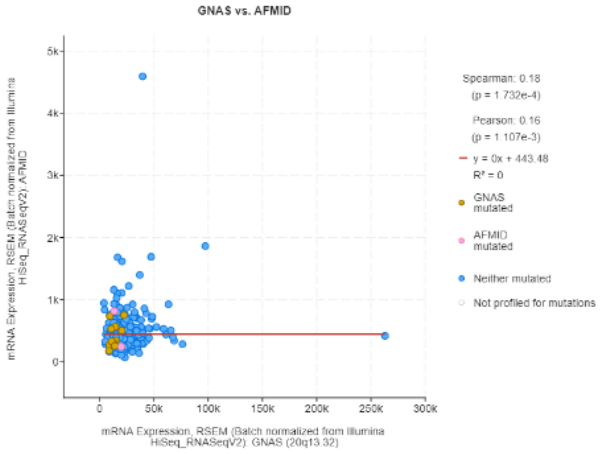

GNAS vs. GGPS1
mRNA Expression, RSEM (Batch normalized from Illumina HiSeq_RNASeqV2); GGPS1
mRNA Expression, RSEM (Batch normalized from Illumina HiSeq_RNASeqV2); GNAS (20q13.32)
Spearman: 0.28
(p = 6.29e-8)
Pearson: 0.16
(p = 1.112e-3)
y = 0x + 820.75
R² = 0
GNAS mutated
GGPS1 mutated
Neither mutated
Not profiled for mutations


GNAS vs. DCXR
mRNA Expression, RSEM (Batch normalized from Illumina HiSeq_RNASeqV2); DCXR
mRNA Expression, RSEM (Batch normalized from Illumina HiSeq_RNASeqV2); GNAS (20q13.32)
Spearman: 0.27
(p = 1.72e-8)
Pearson: 0.17
(p = 3.645e-4)
y = 0.01x + 573.52
R² = 0.03
GNAS mutated
Both mutated
Neither mutated
Not profiled for mutations


GNAS vs. CRLS1
mRNA Expression, RSEM (Batch normalized from Illumina HiSeq_RNASeqV2): CRLS1
mRNA Expression, RSEM (Batch normalized from Illumina HiSeq_RNASeqV2): GNAS (20q13.32)
Spearman: 0.25
(p = 1.61e-7)
Pearson: 0.26
(p = 5.91e-8)
y = 0.01x + 1372.38
R² = 0.07
GNAS mutated
CRLS1 mutated
Neither mutated
Not profiled for mutations

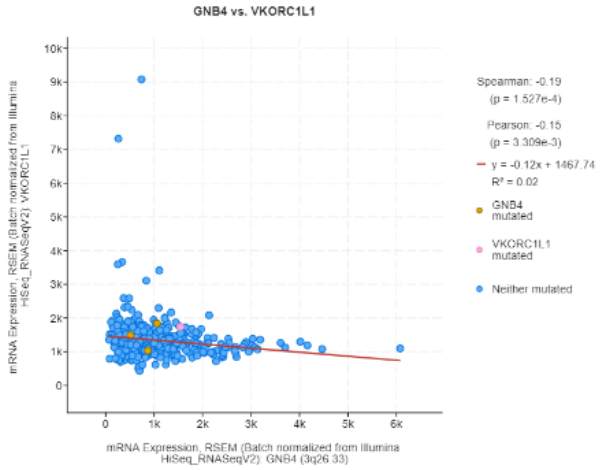

GNAS vs. ATP5PD
mRNA Expression, RSEM (Batch normalized from Illumina HiSeq_RNASeqV2): ATP5PD
mRNA Expression, RSEM (Batch normalized from Illumina HiSeq_RNASeqV2): GNAS (20q13.32)
Spearman: 0.17
(p = 7.349e-4)
Pearson: 0.16
(p = 1.119e-3)
y = 0.01x + 2750.01
R² = 0.02
GNAS mutated
ATP5PD mutated
Neither mutated
Not profiled for mutations

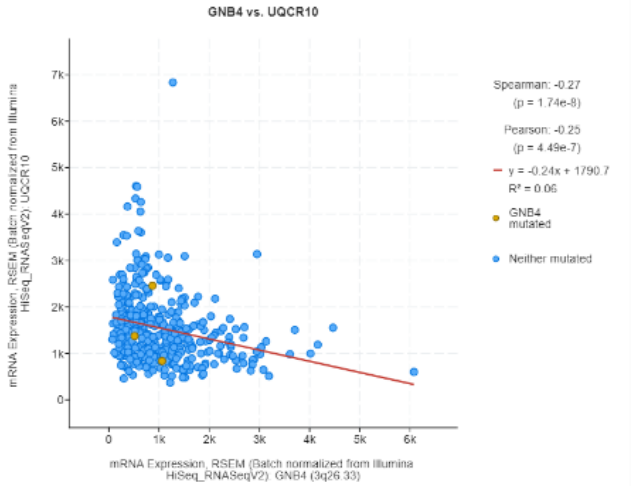

GNAS vs. ATP5F1E
mRNA Expression, RSEM (Batch normalized from Illumina HiSeq_RNASeqV2): ATP5F1E
mRNA Expression, RSEM (Batch normalized from Illumina HiSeq_RNASeqV2): GNAS (20q13.32)
Spearman: 0.53
(p = 4.10e-31)
Pearson: 0.73
(p = 1.46e-69)
y = 0.25x + 848.8
R² = 0.53
GNAS mutated
Neither mutated
Not profiled for mutations

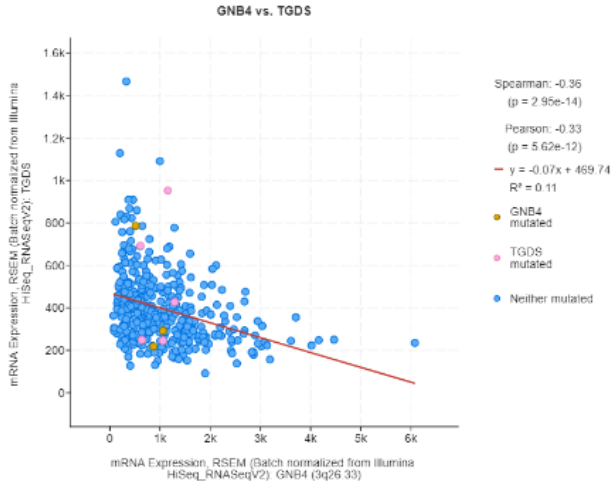

GNAS vs. AFMID
mRNA Expression, RSEM (Batch normalized from Illumina HiSeq_RNASeqV2): AFMID
mRNA Expression, RSEM (Batch normalized from Illumina HiSeq_RNASeqV2): GNAS (20q13.32)
Spearman: 0.18
(p = 1.732e-4)
Pearson: 0.16
(p = 1.107e-3)
y = 0x + 443.48
R² = 0
GNAS mutated
AFMID mutated
Neither mutated
Not profiled for mutations

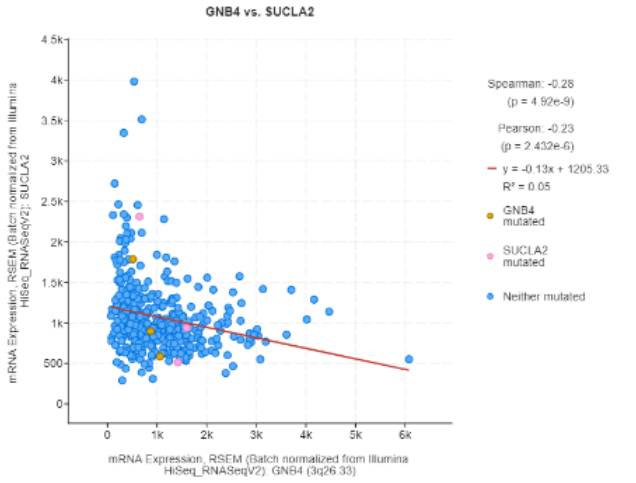

GNAS vs. ACSS1
mRNA Expression, RSEM (Batch normalized from Illumina HiSeq_RNASeqV2): ACSS1
mRNA Expression, RSEM (Batch normalized from Illumina HiSeq_RNASeqV2): GNAS (20q13.32)
Spearman: 0.12
(p = 0.0182)
Pearson: 0.17
(p = 5.533e-4)
y = 0.01x + 1461.82
R² = 0.03
GNAS mutated
ACSS1 mutated
Both mutated
Neither mutated
Not profiled for mutations

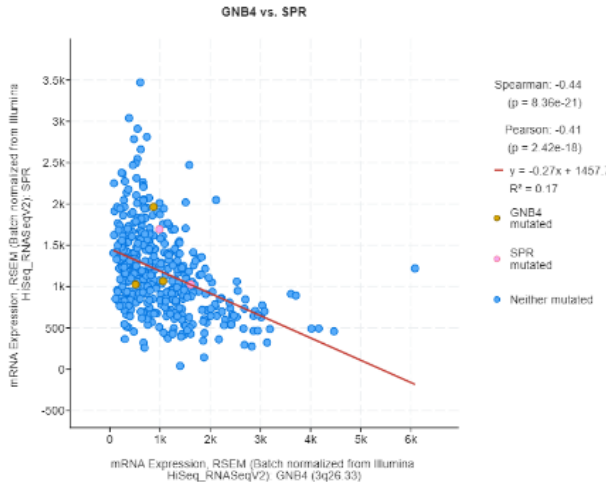
GNB4

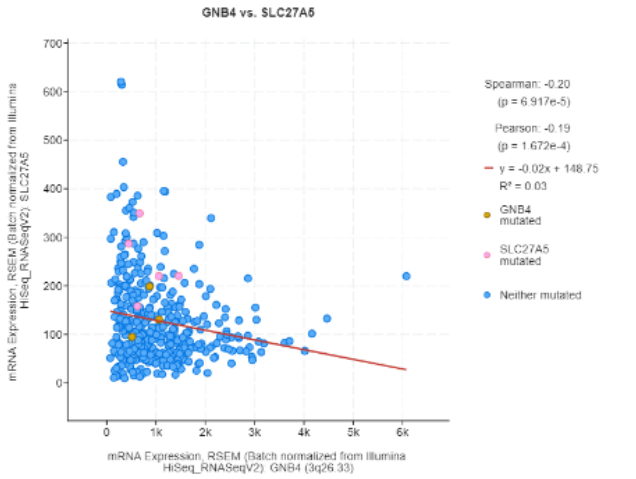

GNB4 vs. VKORC1L1
mRNA Expression, RSEM (Batch normalized from Illumina HiSeq_RNASeqV2): VKORC1L1
mRNA Expression, RSEM (Batch normalized from Illumina HiSeq_RNASeqV2): GNB4 (3q26.33)
Spearman: -0.19
(p = 1.527e-4)
Pearson: -0.15
(p = 3.309e-3)
y = -0.12x + 1467.74
R² = 0.02
GNB4 mutated
VKORC1L1 mutated
Neither mutated

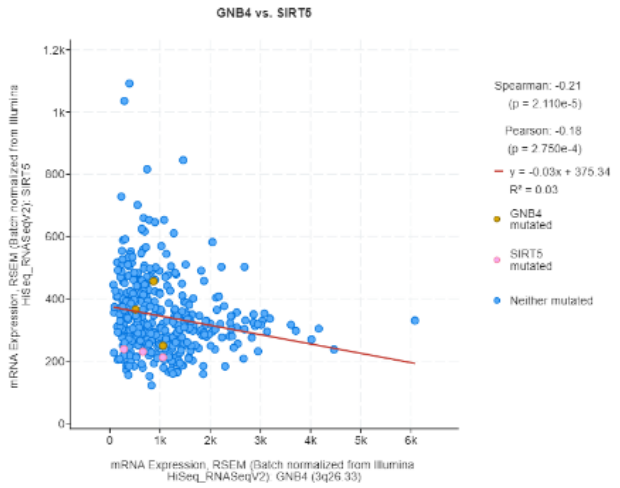

GNB4 vs. UQCR10
mRNA Expression, RSEM (Batch normalized from Illumina HiSeq_RNASeqV2): UQCR10
mRNA Expression, RSEM (Batch normalized from Illumina HiSeq_RNASeqV2): GNB4 (3q26.33)
Spearman: -0.27
(p = 1.74e-8)
Pearson: -0.25
(p = 4.49e-7)
y = -0.24x + 1790.7
R² = 0.06
GNB4 mutated
Neither mutated

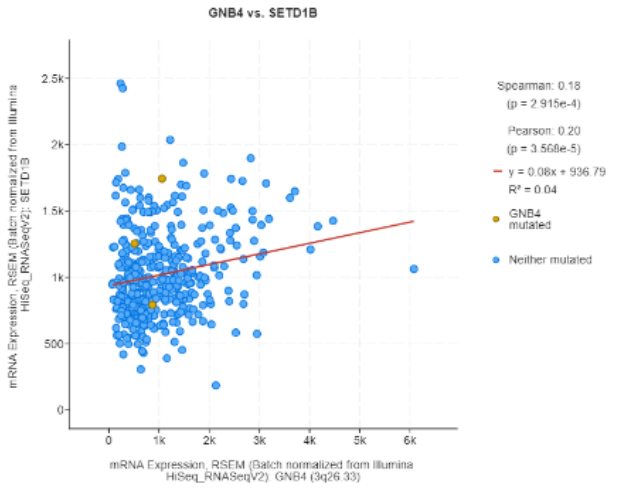

GNB4 vs. TGDS
mRNA Expression, RSEM (Batch normalized from Illumina HiSeq_RNASeqV2): TGDS
mRNA Expression, RSEM (Batch normalized from Illumina HiSeq_RNASeqV2): GNB4 (3q26.33)
Spearman: -0.36
(p = 2.95e-14)
Pearson: -0.33
(p = 5.62e-12)
y = -0.07x + 469.74
R² = 0.11
GNB4 mutated
TGDS mutated
Neither mutated

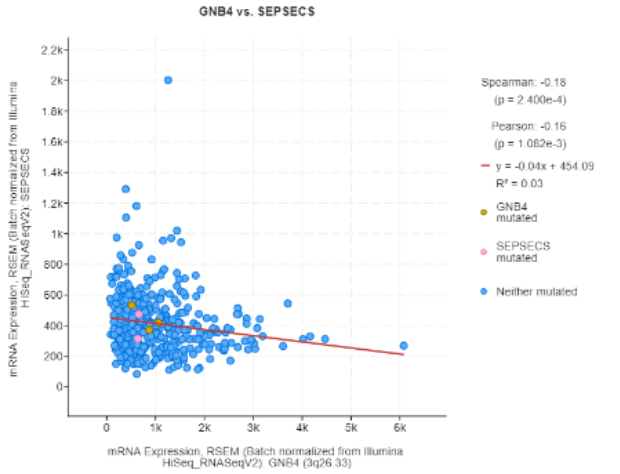

GNB4 vs. SUCLA2
mRNA Expression, RSEM (Batch normalized from Illumina HiSeq_RNASeqV2): SUCLA2
mRNA Expression, RSEM (Batch normalized from Illumina HiSeq_RNASeqV2): GNB4 (3q26.33)
Spearman: -0.28
(p = 4.92e-9)
Pearson: -0.23
(p = 2.432e-6)
y = -0.13x + 1205.33
R² = 0.05
GNB4 mutated
SUCLA2 mutated
Neither mutated

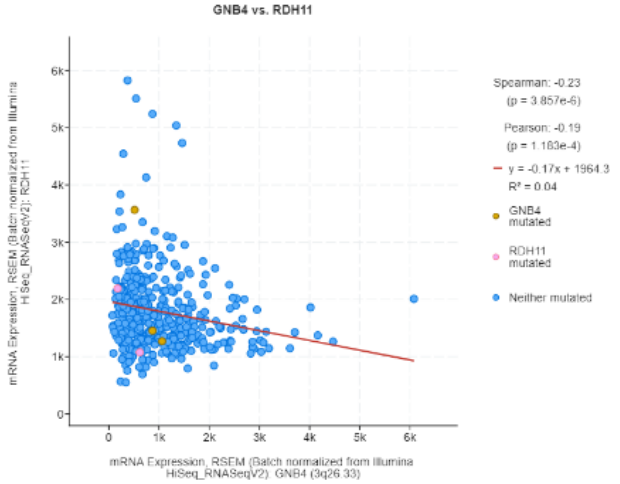

GNB4 vs. SPR
mRNA Expression, RSEM (Batch normalized from Illumina HiSeq_RNASeqV2): SPR
mRNA Expression, RSEM (Batch normalized from Illumina HiSeq_RNASeqV2): GNB4 (3q26.33)
Spearman: -0.44
(p = 8.36e-21)
Pearson: -0.41
(p = 2.42e-18)
y = -0.27x + 1457.73
R² = 0.17
GNB4 mutated
SPR mutated
Neither mutated

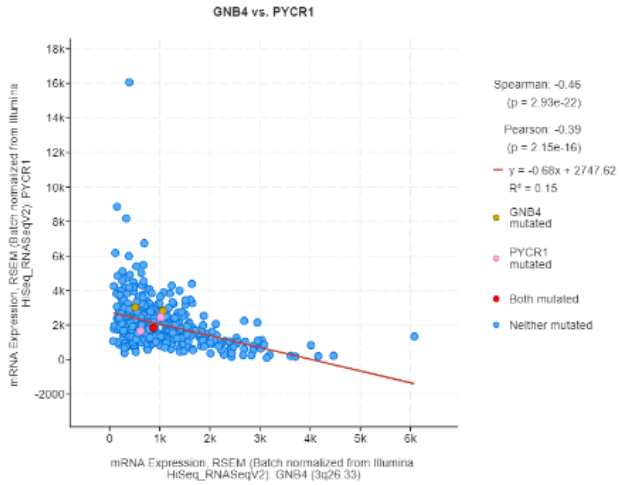

GNB4 vs. SLC27A5
mRNA Expression, RSEM (Batch normalized from Illumina HiSeq_RNASeqV2): SLC27A5
mRNA Expression, RSEM (Batch normalized from Illumina HiSeq_RNASeqV2): GNB4 (3q26.33)
Spearman: -0.20
(p = 6.917e-5)
Pearson: -0.19
(p = 1.672e-4)
y = -0.02x + 148.75
R² = 0.03
GNB4 mutated
SLC27A5 mutated
Neither mutated

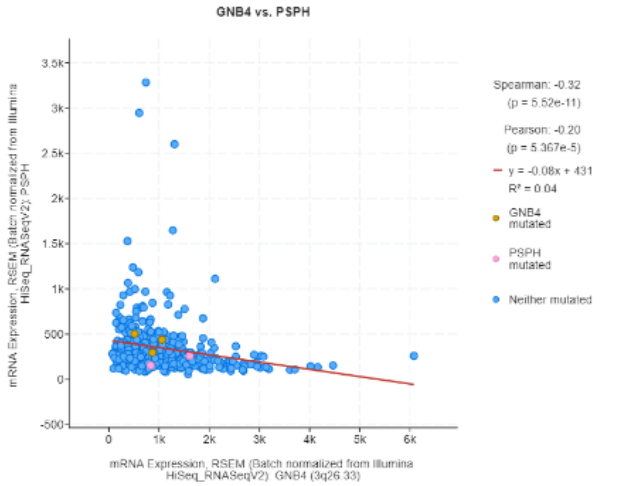

GNB4 vs. SIRT5
mRNA Expression, RSEM (Batch normalized from Illumina HiSeq_RNASeqV2): SIRT5
mRNA Expression, RSEM (Batch normalized from Illumina HiSeq_RNASeqV2): GNB4 (3q26.33)
Spearman: -0.21
(p = 2.110e-5)
Pearson: -0.18
(p = 2.750e-4)
y = -0.03x + 375.34
R² = 0.03
GNB4 mutated
SIRT5 mutated
Neither mutated

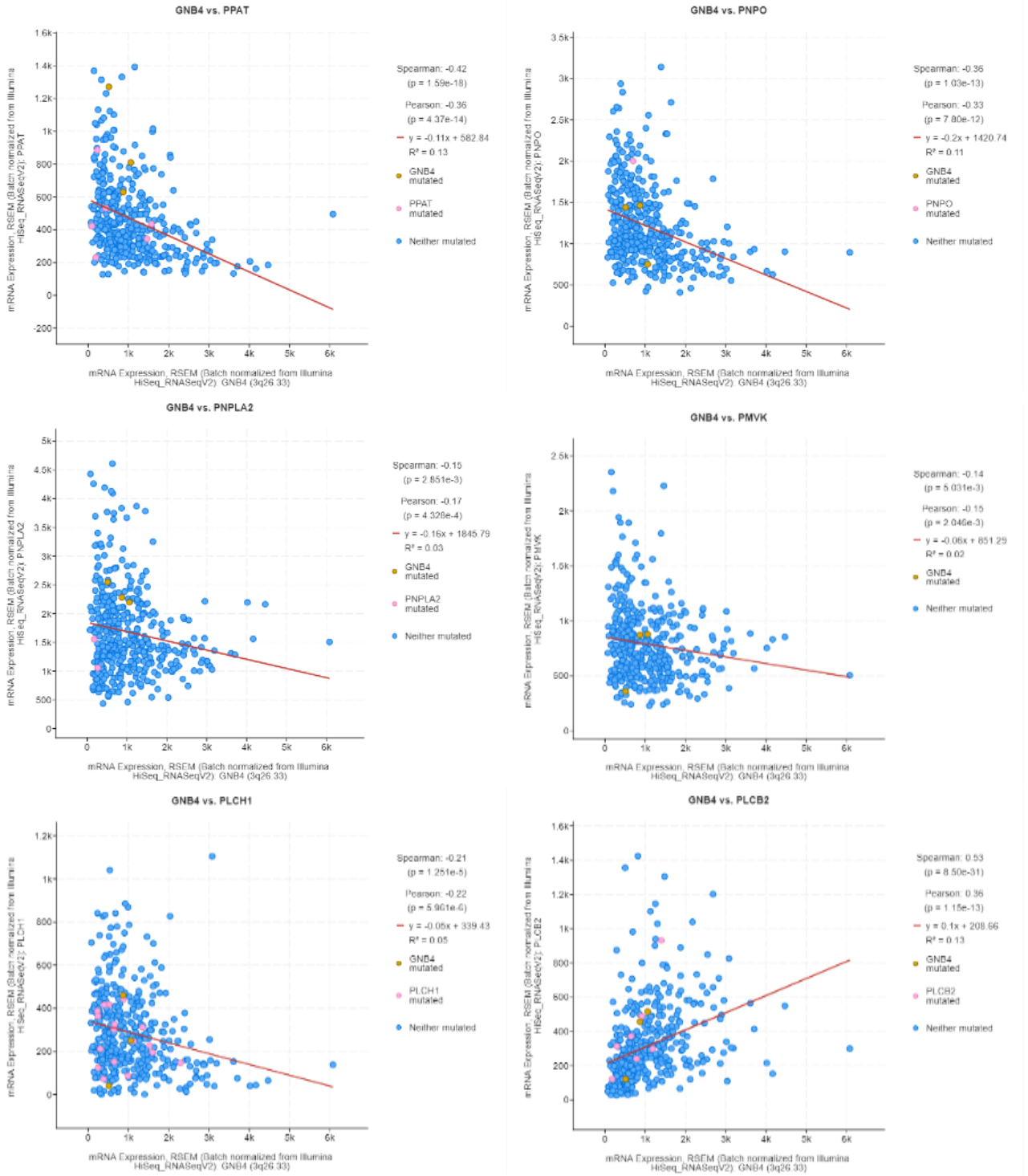

GNB4 vs. SETD1B
mRNA Expression, RSEM (Batch normalized from Illumina HiSeq_RNASeqV2): SETD1B
mRNA Expression, RSEM (Batch normalized from Illumina HiSeq_RNASeqV2): GNB4 (3q26.33)
Spearman: 0.18
(p = 2.915e-4)
Pearson: 0.20
(p = 3.568e-5)
y = 0.08x + 936.79
R² = 0.04
GNB4 mutated
Neither mutated

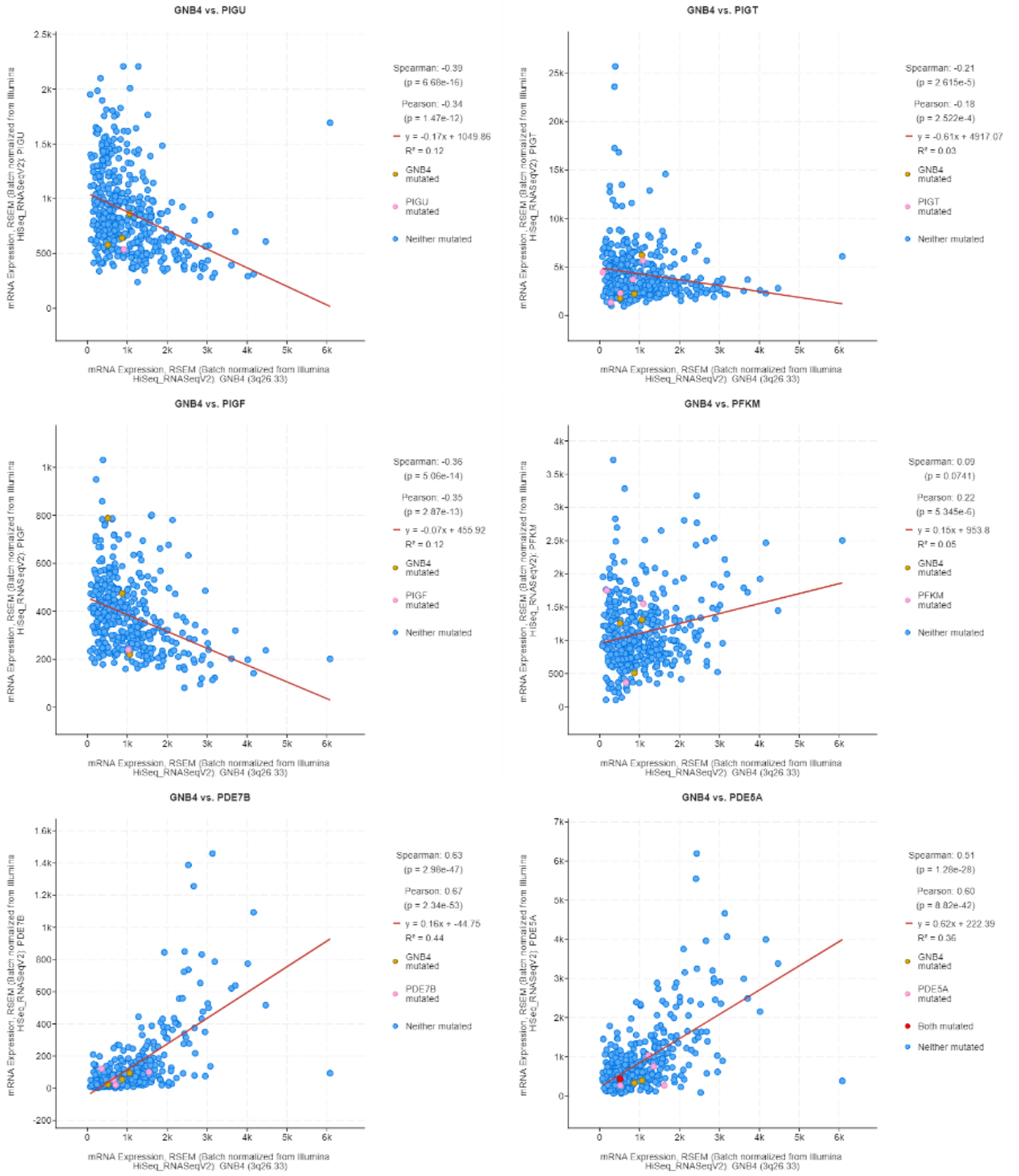

GNB4 vs. SEPSECS
mRNA Expression, RSEM (Batch normalized from Illumina HiSeq_RNASeqV2): SEPSECS
mRNA Expression, RSEM (Batch normalized from Illumina HiSeq_RNASeqV2): GNB4 (3q26.33)
Spearman: -0.18
(p = 2.400e-4)
Pearson: -0.16
(p = 1.082e-3)
y = -0.04x + 454.09
R² = 0.03
GNB4 mutated
SEPSECS mutated
Neither mutated

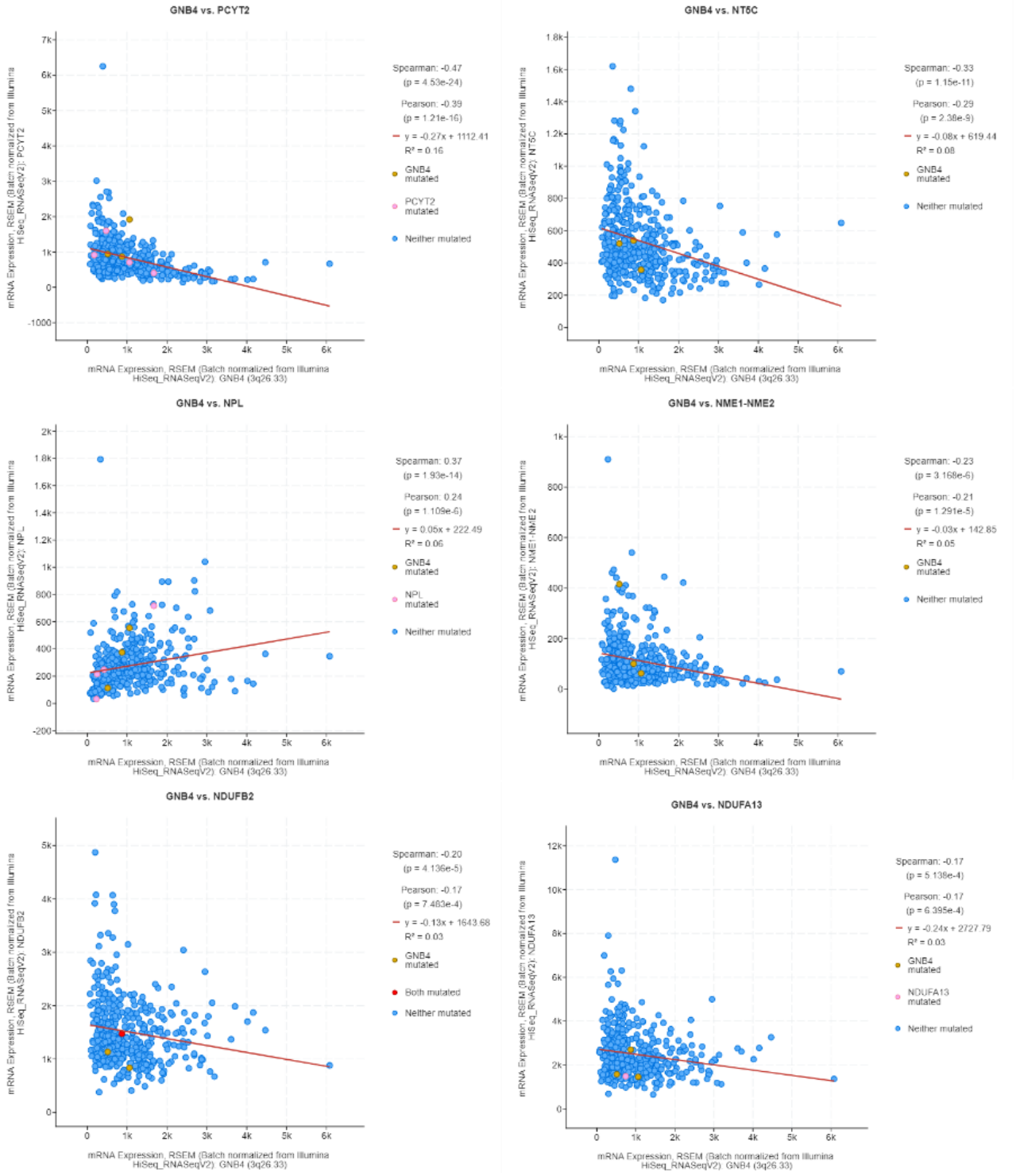

GNB4 vs. RDH11
mRNA Expression, RSEM (Batch normalized from Illumina HiSeq_RNASeqV2): RDH11
mRNA Expression, RSEM (Batch normalized from Illumina HiSeq_RNASeqV2): GNB4 (3q26.33)
Spearman: -0.23
(p = 3.857e-6)
Pearson: -0.19
(p = 1.183e-4)
y = -0.17x + 1964.3
R² = 0.04
GNB4 mutated
RDH11 mutated
Neither mutated

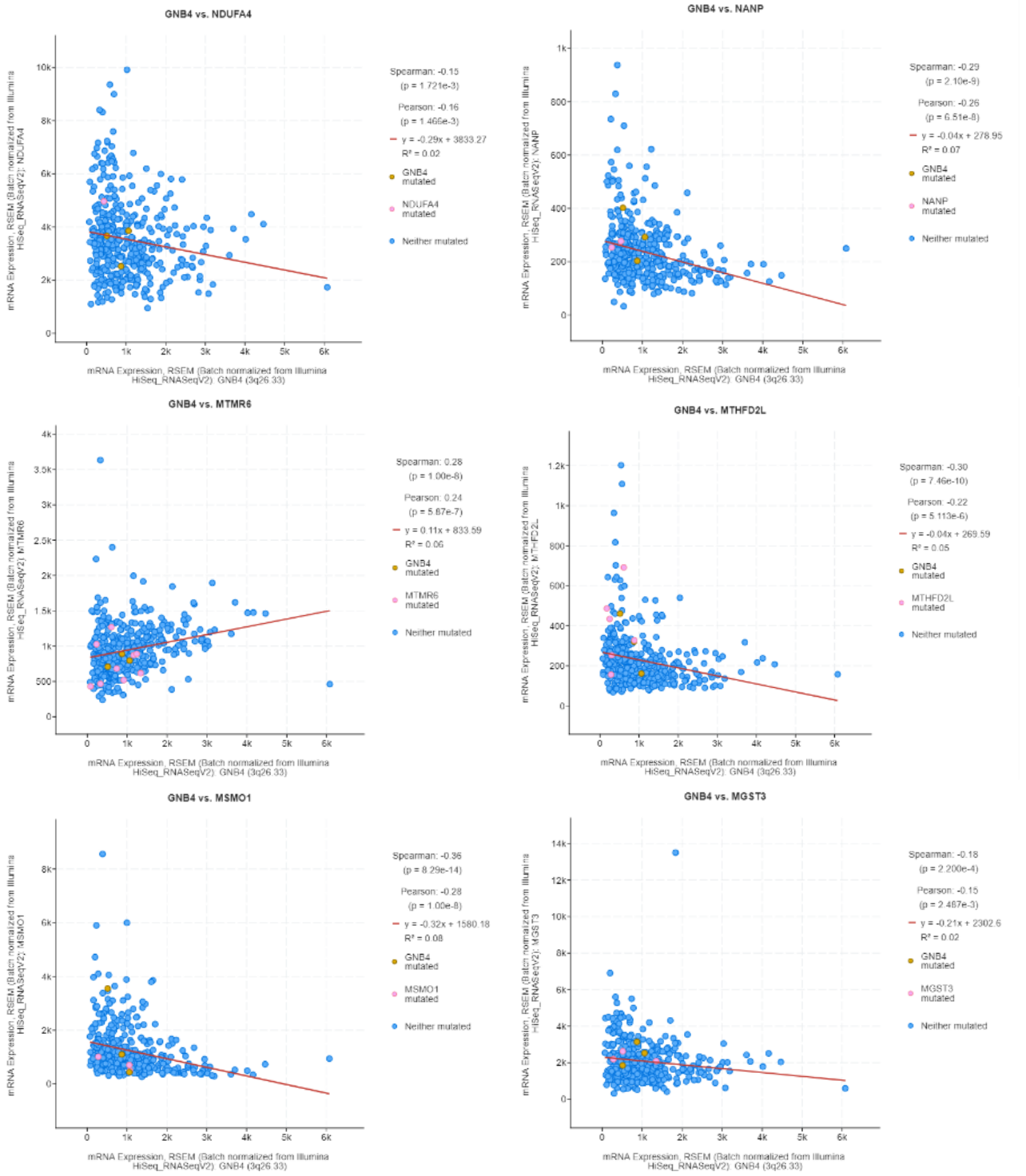

GNB4 vs. PYCR1
mRNA Expression, RSEM (Batch normalized from Illumina HiSeq_RNASeqV2): PYCR1
mRNA Expression, RSEM (Batch normalized from Illumina HiSeq_RNASeqV2): GNB4 (3q26.33)
Spearman: -0.46
(p = 2.93e-22)
Pearson: -0.39
(p = 2.15e-16)
y = -0.68x + 2747.62
R² = 0.15
GNB4 mutated
PYCR1 mutated
Both mutated
Neither mutated

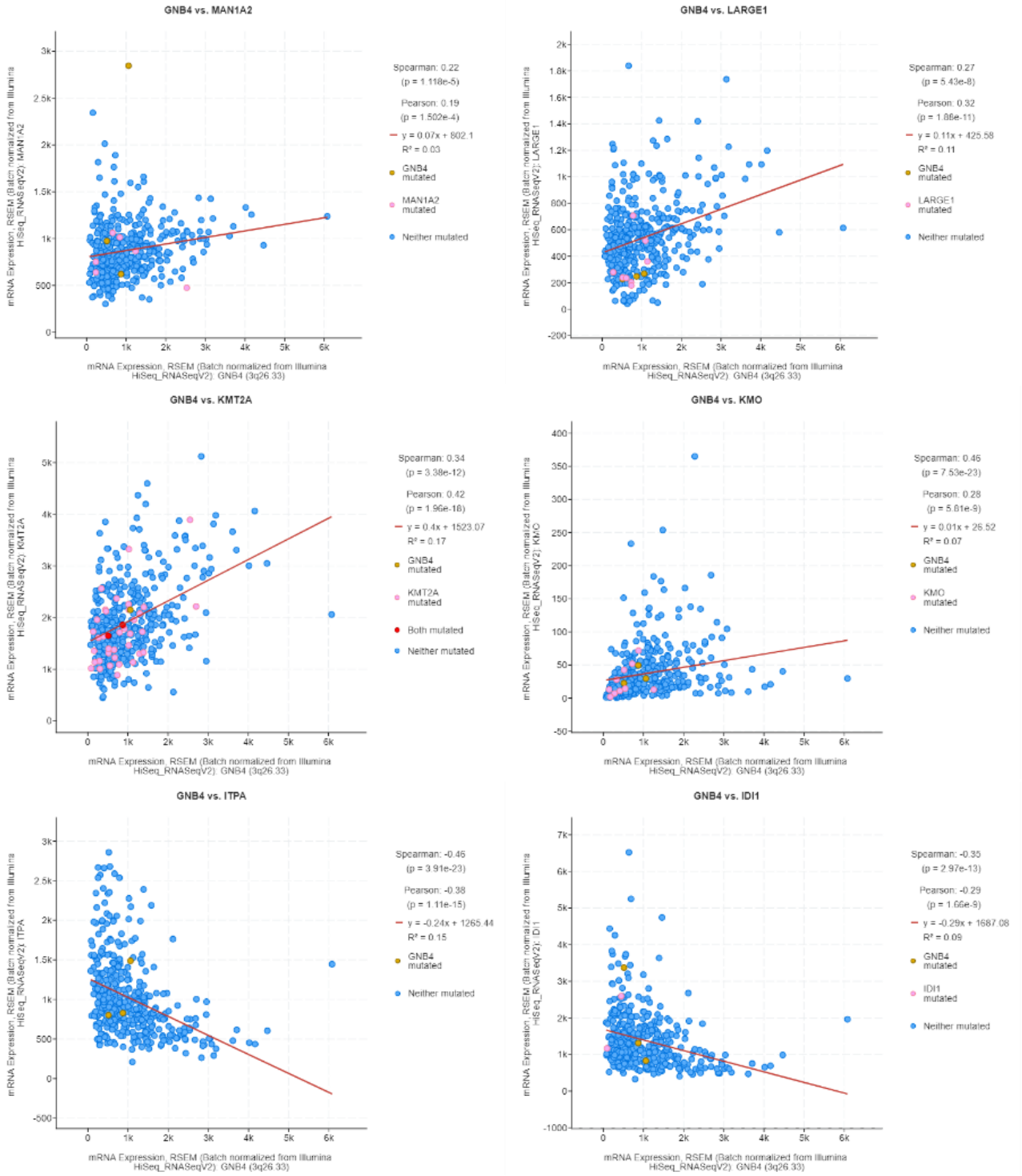

GNB4 vs. PSPH
mRNA Expression, RSEM (Batch normalized from Illumina HiSeq_RNASeqV2): PSPH
mRNA Expression, RSEM (Batch normalized from Illumina HiSeq_RNASeqV2): GNB4 (3q26.33)
Spearman: -0.32
(p = 5.52e-11)
Pearson: -0.20
(p = 5.367e-5)
y = -0.08x + 431
R² = 0.04
GNB4 mutated
PSPH mutated
Neither mutated

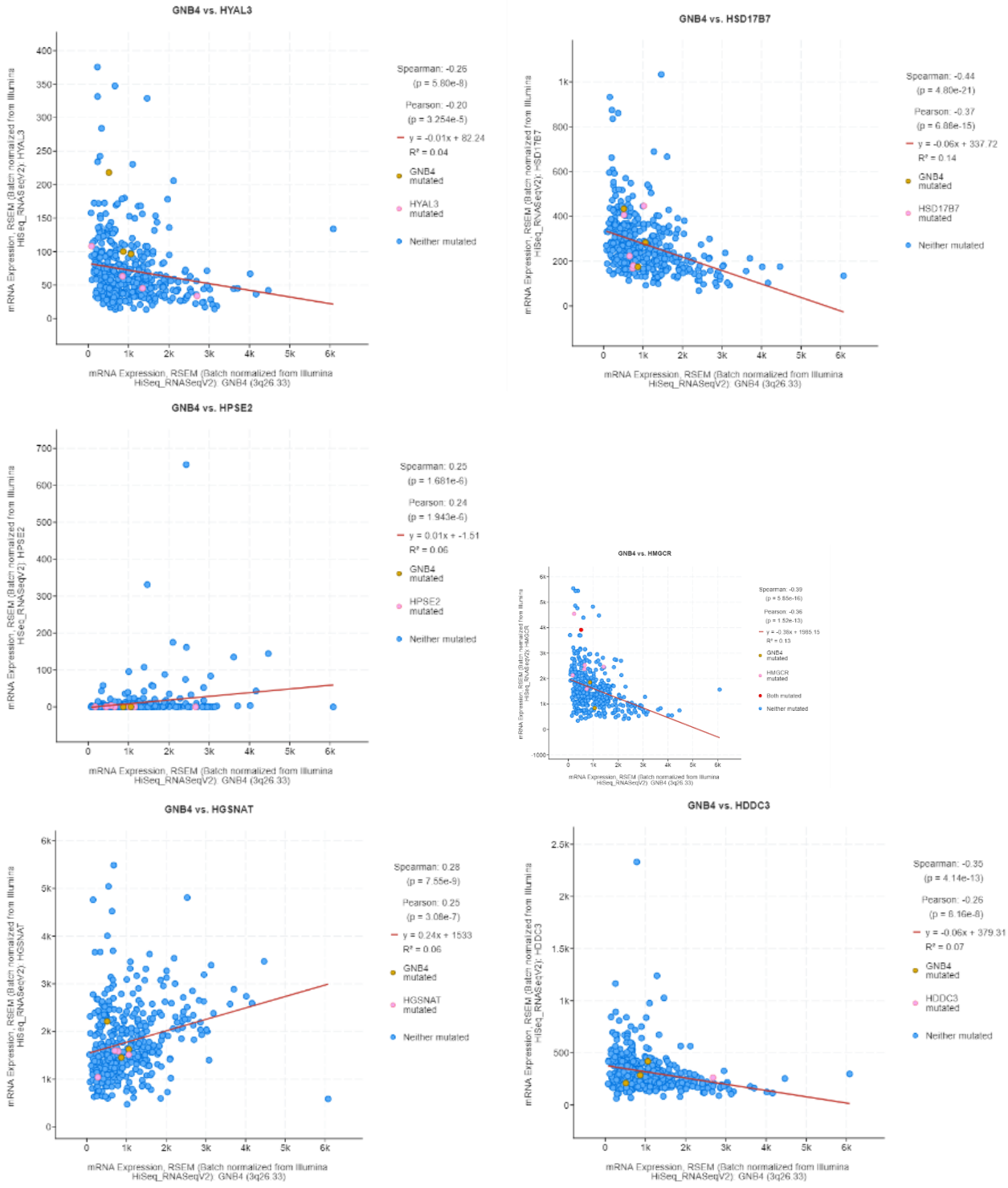

GNB4 vs. PPAT
mRNA Expression, RSEM (Batch normalized from Illumina HiSeq_RNASeqV2): PPAT
mRNA Expression, RSEM (Batch normalized from Illumina HiSeq_RNASeqV2): GNB4 (3q26.33)
Spearman: -0.42
(p = 1.59e-18)
Pearson: -0.36
(p = 4.37e-14)
y = -0.11x + 582.84
R² = 0.13
GNB4 mutated
PPAT mutated
Neither mutated
GNB4 vs. PNPO
mRNA Expression, RSEM (Batch normalized from Illumina HiSeq_RNASeqV2): PNPO
mRNA Expression, RSEM (Batch normalized from Illumina HiSeq_RNASeqV2): GNB4 (3q26.33)
Spearman: -0.36
(p = 1.03e-13)
Pearson: -0.33
(p = 7.80e-12)
y = -0.2x + 1420.74
R² = 0.11
GNB4 mutated
PNPO mutated
Neither mutated
GNB4 vs. PNPLA2
mRNA Expression, RSEM (Batch normalized from Illumina HiSeq_RNASeqV2): PNPLA2
mRNA Expression, RSEM (Batch normalized from Illumina HiSeq_RNASeqV2): GNB4 (3q26.33)
Spearman: -0.15
(p = 2.851e-3)
Pearson: -0.17
(p = 4.328e-4)
y = -0.16x + 1845.79
R² = 0.03
GNB4 mutated
PNPLA2 mutated
Neither mutated
GNB4 vs. PMVK
mRNA Expression, RSEM (Batch normalized from Illumina HiSeq_RNASeqV2): PMVK
mRNA Expression, RSEM (Batch normalized from Illumina HiSeq_RNASeqV2): GNB4 (3q26.33)
Spearman: -0.14
(p = 5.031e-3)
Pearson: -0.15
(p = 2.046e-3)
y = -0.06x + 851.29
R² = 0.02
GNB4 mutated
Neither mutated
GNB4 vs. PLCH1
mRNA Expression, RSEM (Batch normalized from Illumina HiSeq_RNASeqV2): PLCH1
mRNA Expression, RSEM (Batch normalized from Illumina HiSeq_RNASeqV2): GNB4 (3q26.33)
Spearman: -0.21
(p = 1.251e-5)
Pearson: -0.22
(p = 5.961e-6)
y = -0.05x + 339.43
R² = 0.05
GNB4 mutated
PLCH1 mutated
Neither mutated
GNB4 vs. PLCB2
mRNA Expression, RSEM (Batch normalized from Illumina HiSeq_RNASeqV2): PLCB2
mRNA Expression, RSEM (Batch normalized from Illumina HiSeq_RNASeqV2): GNB4 (3q26.33)
Spearman: 0.53
(p = 8.50e-31)
Pearson: 0.36
(p = 1.15e-13)
y = 0.1x + 208.66
R² = 0.13
GNB4 mutated
PLCB2 mutated
Neither mutated

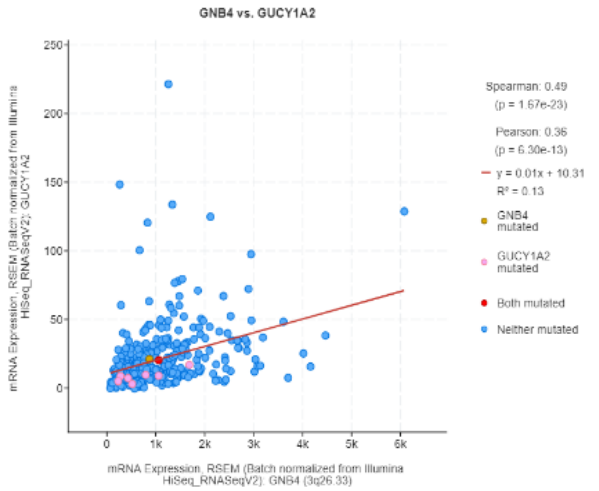

GNB4 vs. PIGU
mRNA Expression, RSEM (Batch normalized from Illumina HiSeq_RNASeqV2): PIGU
mRNA Expression, RSEM (Batch normalized from Illumina HiSeq_RNASeqV2): GNB4 (3q26.33)
Spearman: -0.39
(p = 6.68e-16)
Pearson: -0.34
(p = 1.47e-12)
y = -0.17x + 1049.86
R² = 0.12
GNB4 mutated
PIGU mutated
Neither mutated
GNB4 vs. PIGT
mRNA Expression, RSEM (Batch normalized from Illumina HiSeq_RNASeqV2): PIGT
mRNA Expression, RSEM (Batch normalized from Illumina HiSeq_RNASeqV2): GNB4 (3q26.33)
Spearman: -0.21
(p = 2.615e-5)
Pearson: -0.18
(p = 2.522e-4)
y = -0.61x + 4917.07
R² = 0.03
GNB4 mutated
PIGT mutated
Neither mutated
GNB4 vs. PIGF
mRNA Expression, RSEM (Batch normalized from Illumina HiSeq_RNASeqV2): PIGF
mRNA Expression, RSEM (Batch normalized from Illumina HiSeq_RNASeqV2): GNB4 (3q26.33)
Spearman: -0.36
(p = 5.06e-14)
Pearson: -0.35
(p = 2.87e-13)
y = -0.07x + 455.92
R² = 0.12
GNB4 mutated
PIGF mutated
Neither mutated
GNB4 vs. PFKM
mRNA Expression, RSEM (Batch normalized from Illumina HiSeq_RNASeqV2): PFKM
mRNA Expression, RSEM (Batch normalized from Illumina HiSeq_RNASeqV2): GNB4 (3q26.33)
Spearman: 0.09
(p = 0.0741)
Pearson: 0.22
(p = 5.345e-6)
y = 0.15x + 953.8
R² = 0.05
GNB4 mutated
PFKM mutated
Neither mutated
GNB4 vs. PDE7B
mRNA Expression, RSEM (Batch normalized from Illumina HiSeq_RNASeqV2): PDE7B
mRNA Expression, RSEM (Batch normalized from Illumina HiSeq_RNASeqV2): GNB4 (3q26.33)
Spearman: 0.63
(p = 2.98e-47)
Pearson: 0.67
(p = 2.34e-53)
y = 0.16x + -44.75
R² = 0.44
GNB4 mutated
PDE7B mutated
Neither mutated
GNB4 vs. PDE5A
mRNA Expression, RSEM (Batch normalized from Illumina HiSeq_RNASeqV2): PDE5A
mRNA Expression, RSEM (Batch normalized from Illumina HiSeq_RNASeqV2): GNB4 (3q26.33)
Spearman: 0.51
(p = 1.28e-28)
Pearson: 0.60
(p = 8.82e-42)
y = 0.62x + 222.39
R² = 0.36
GNB4 mutated
PDE5A mutated
Both mutated
Neither mutated


GNB4 vs. PCYT2
mRNA Expression, RSEM (Batch normalized from Illumina HiSeq_RNASeqV2): PCYT2
mRNA Expression, RSEM (Batch normalized from Illumina HiSeq_RNASeqV2): GNB4 (3q26.33)
Spearman: -0.47
(p = 4.53e-24)
Pearson: -0.39
(p = 1.21e-16)
y = -0.27x + 1112.41
R² = 0.16
GNB4 mutated
PCYT2 mutated
Neither mutated
GNB4 vs. NT5C
mRNA Expression, RSEM (Batch normalized from Illumina HiSeq_RNASeqV2): NT5C
mRNA Expression, RSEM (Batch normalized from Illumina HiSeq_RNASeqV2): GNB4 (3q26.33)
Spearman: -0.33
(p = 1.15e-11)
Pearson: -0.29
(p = 2.38e-9)
y = -0.08x + 619.44
R² = 0.08
GNB4 mutated
Neither mutated
GNB4 vs. NPL
mRNA Expression, RSEM (Batch normalized from Illumina HiSeq_RNASeqV2): NPL
mRNA Expression, RSEM (Batch normalized from Illumina HiSeq_RNASeqV2): GNB4 (3q26.33)
Spearman: 0.37
(p = 1.93e-14)
Pearson: 0.24
(p = 1.109e-6)
y = 0.05x + 222.49
R² = 0.06
GNB4 mutated
NPL mutated
Neither mutated
GNB4 vs. NME1-NME2
mRNA Expression, RSEM (Batch normalized from Illumina HiSeq_RNASeqV2): NME1-NME2
mRNA Expression, RSEM (Batch normalized from Illumina HiSeq_RNASeqV2): GNB4 (3q26.33)
Spearman: -0.23
(p = 3.168e-6)
Pearson: -0.21
(p = 1.291e-5)
y = -0.03x + 142.85
R² = 0.05
GNB4 mutated
Neither mutated
GNB4 vs. NDUFB2
mRNA Expression, RSEM (Batch normalized from Illumina HiSeq_RNASeqV2): NDUFB2
mRNA Expression, RSEM (Batch normalized from Illumina HiSeq_RNASeqV2): GNB4 (3q26.33)
Spearman: -0.20
(p = 4.136e-5)
Pearson: -0.17
(p = 7.483e-4)
y = -0.13x + 1643.68
R² = 0.03
GNB4 mutated
Both mutated
Neither mutated
GNB4 vs. NDUFA13
mRNA Expression, RSEM (Batch normalized from Illumina HiSeq_RNASeqV2): NDUFA13
mRNA Expression, RSEM (Batch normalized from Illumina HiSeq_RNASeqV2): GNB4 (3q26.33)
Spearman: -0.17
(p = 5.138e-4)
Pearson: -0.17
(p = 6.395e-4)
y = -0.24x + 2727.79
R² = 0.03
GNB4 mutated
NDUFA13 mutated
Neither mutated

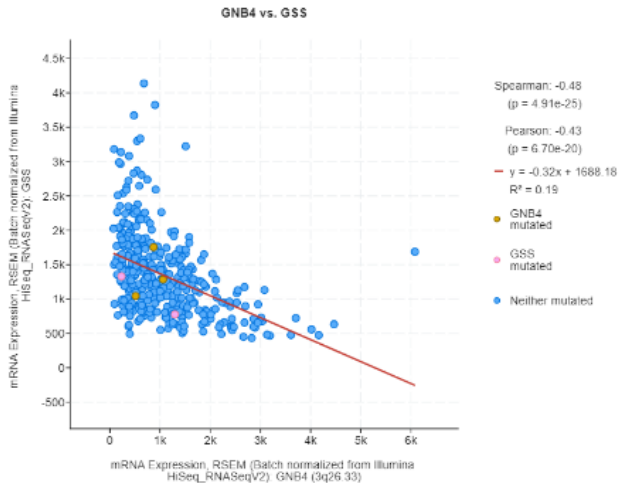

GNB4 vs. NDUFA4
mRNA Expression, RSEM (Batch normalized from Illumina HiSeq_RNASeqV2): NDUFA4
mRNA Expression, RSEM (Batch normalized from Illumina HiSeq_RNASeqV2): GNB4 (3q26.33)
Spearman: -0.15
(p = 1.721e-3)
Pearson: -0.16
(p = 1.466e-3)
y = -0.29x + 3833.27
R² = 0.02
GNB4 mutated
NDUFA4 mutated
Neither mutated
GNB4 vs. NANP
mRNA Expression, RSEM (Batch normalized from Illumina HiSeq_RNASeqV2): NANP
mRNA Expression, RSEM (Batch normalized from Illumina HiSeq_RNASeqV2): GNB4 (3q26.33)
Spearman: -0.29
(p = 2.10e-9)
Pearson: -0.26
(p = 6.51e-8)
y = -0.04x + 278.95
R² = 0.07
GNB4 mutated
NANP mutated
Neither mutated
GNB4 vs. MTMR6
mRNA Expression, RSEM (Batch normalized from Illumina HiSeq_RNASeqV2): MTMR6
mRNA Expression, RSEM (Batch normalized from Illumina HiSeq_RNASeqV2): GNB4 (3q26.33)
Spearman: 0.28
(p = 1.00e-8)
Pearson: 0.24
(p = 5.87e-7)
y = 0.11x + 833.59
R² = 0.06
GNB4 mutated
MTMR6 mutated
Neither mutated
GNB4 vs. MTHFD2L
mRNA Expression, RSEM (Batch normalized from Illumina HiSeq_RNASeqV2): MTHFD2L
mRNA Expression, RSEM (Batch normalized from Illumina HiSeq_RNASeqV2): GNB4 (3q26.33)
Spearman: -0.30
(p = 7.46e-10)
Pearson: -0.22
(p = 5.113e-6)
y = -0.04x + 269.59
R² = 0.05
GNB4 mutated
MTHFD2L mutated
Neither mutated
GNB4 vs. MSMO1
mRNA Expression, RSEM (Batch normalized from Illumina HiSeq_RNASeqV2): MSMO1
mRNA Expression, RSEM (Batch normalized from Illumina HiSeq_RNASeqV2): GNB4 (3q26.33)
Spearman: -0.36
(p = 8.29e-14)
Pearson: -0.28
(p = 1.00e-8)
y = -0.32x + 1580.18
R² = 0.08
GNB4 mutated
MSMO1 mutated
Neither mutated
GNB4 vs. MGST3
mRNA Expression, RSEM (Batch normalized from Illumina HiSeq_RNASeqV2): MGST3
mRNA Expression, RSEM (Batch normalized from Illumina HiSeq_RNASeqV2): GNB4 (3q26.33)
Spearman: -0.18
(p = 2.200e-4)
Pearson: -0.15
(p = 2.467e-3)
y = -0.21x + 2302.6
R² = 0.02
GNB4 mutated
MGST3 mutated
Neither mutated

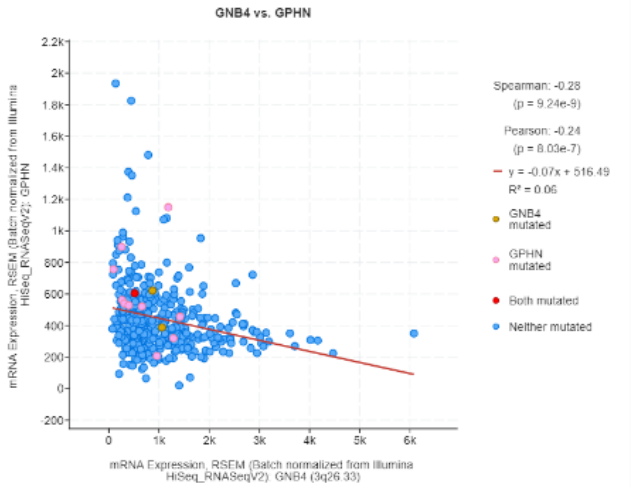

GNB4 vs. MAN1A2
mRNA Expression, RSEM (Batch normalized from Illumina HiSeq_RNASeqV2): MAN1A2
mRNA Expression, RSEM (Batch normalized from Illumina HiSeq_RNASeqV2): GNB4 (3q26.33)
Spearman: 0.22
(p = 1.118e-5)
Pearson: 0.19
(p = 1.502e-4)
y = 0.07x + 802.1
R² = 0.03
GNB4 mutated
MAN1A2 mutated
Neither mutated
GNB4 vs. LARGE1
mRNA Expression, RSEM (Batch normalized from Illumina HiSeq_RNASeqV2): LARGE1
mRNA Expression, RSEM (Batch normalized from Illumina HiSeq_RNASeqV2): GNB4 (3q26.33)
Spearman: 0.27
(p = 5.43e-8)
Pearson: 0.32
(p = 1.86e-11)
y = 0.11x + 425.58
R² = 0.11
GNB4 mutated
LARGE1 mutated
Neither mutated
GNB4 vs. KMT2A
mRNA Expression, RSEM (Batch normalized from Illumina HiSeq_RNASeqV2): KMT2A
mRNA Expression, RSEM (Batch normalized from Illumina HiSeq_RNASeqV2): GNB4 (3q26.33)
Spearman: 0.34
(p = 3.38e-12)
Pearson: 0.42
(p = 1.96e-16)
y = 0.4x + 1523.07
R² = 0.17
GNB4 mutated
KMT2A mutated
Both mutated
Neither mutated
GNB4 vs. KMO
mRNA Expression, RSEM (Batch normalized from Illumina HiSeq_RNASeqV2): KMO
mRNA Expression, RSEM (Batch normalized from Illumina HiSeq_RNASeqV2): GNB4 (3q26.33)
Spearman: 0.46
(p = 7.53e-23)
Pearson: 0.28
(p = 5.81e-9)
y = 0.01x + 26.52
R² = 0.07
GNB4 mutated
KMO mutated
Neither mutated
GNB4 vs. ITPA
mRNA Expression, RSEM (Batch normalized from Illumina HiSeq_RNASeqV2): ITPA
mRNA Expression, RSEM (Batch normalized from Illumina HiSeq_RNASeqV2): GNB4 (3q26.33)
Spearman: -0.46
(p = 3.91e-23)
Pearson: -0.38
(p = 1.11e-15)
y = -0.24x + 1265.44
R² = 0.15
GNB4 mutated
Neither mutated
GNB4 vs. IDI1
mRNA Expression, RSEM (Batch normalized from Illumina HiSeq_RNASeqV2): IDI1
mRNA Expression, RSEM (Batch normalized from Illumina HiSeq_RNASeqV2): GNB4 (3q26.33)
Spearman: -0.35
(p = 2.97e-13)
Pearson: -0.29
(p = 1.66e-9)
y = -0.29x + 1687.08
R² = 0.09
GNB4 mutated
IDI1 mutated
Neither mutated

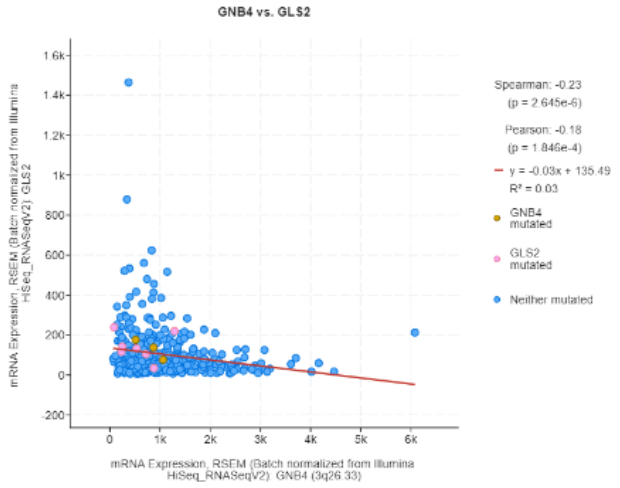

GNB4 vs. HYAL3
mRNA Expression, RSEM (Batch normalized from Illumina HiSeq_RNASeqV2): HYAL3
mRNA Expression, RSEM (Batch normalized from Illumina HiSeq_RNASeqV2): GNB4 (3q26.33)
Spearman: -0.25
(p = 5.80e-8)
Pearson: -0.20
(p = 3.254e-5)
y = -0.01x + 82.24
R² = 0.04
GNB4 mutated
HYAL3 mutated
Neither mutated
GNB4 vs. HSD17B7
mRNA Expression, RSEM (Batch normalized from Illumina HiSeq_RNASeqV2): HSD17B7
mRNA Expression, RSEM (Batch normalized from Illumina HiSeq_RNASeqV2): GNB4 (3q26.33)
Spearman: -0.44
(p = 4.80e-21)
Pearson: -0.37
(p = 6.88e-15)
y = -0.06x + 337.72
R² = 0.14
GNB4 mutated
HSD17B7 mutated
Neither mutated
GNB4 vs. HPSE2
mRNA Expression, RSEM (Batch normalized from Illumina HiSeq_RNASeqV2): HPSE2
mRNA Expression, RSEM (Batch normalized from Illumina HiSeq_RNASeqV2): GNB4 (3q26.33)
Spearman: 0.25
(p = 1.681e-6)
Pearson: 0.24
(p = 1.943e-6)
y = 0.01x + -1.51
R² = 0.06
GNB4 mutated
HPSE2 mutated
Neither mutated
GNB4 vs. HMGCR
GNB4 vs. HGSNAT
mRNA Expression, RSEM (Batch normalized from Illumina HiSeq_RNASeqV2): HGSNAT
mRNA Expression, RSEM (Batch normalized from Illumina HiSeq_RNASeqV2): GNB4 (3q26.33)
Spearman: 0.28
(p = 7.55e-9)
Pearson: 0.25
(p = 3.08e-7)
y = 0.24x + 1533
R² = 0.06
GNB4 mutated
HGSNAT mutated
Neither mutated
GNB4 vs. HDDC3
mRNA Expression, RSEM (Batch normalized from Illumina HiSeq_RNASeqV2): HDDC3
mRNA Expression, RSEM (Batch normalized from Illumina HiSeq_RNASeqV2): GNB4 (3q26.33)
Spearman: -0.35
(p = 4.14e-13)
Pearson: -0.26
(p = 8.16e-8)
y = -0.06x + 379.31
R² = 0.07
GNB4 mutated
HDDC3 mutated
Neither mutated

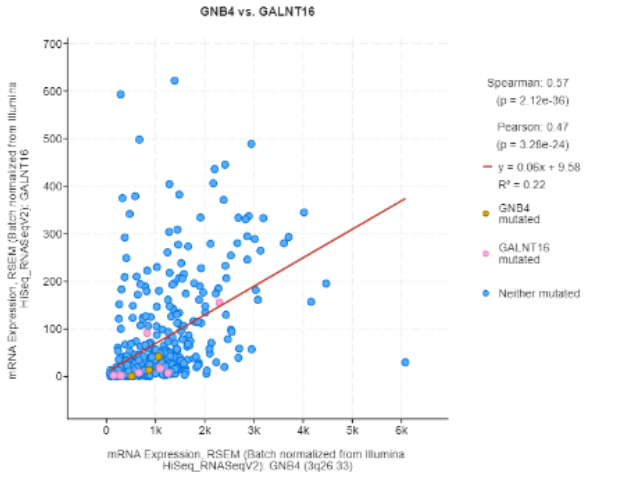

GNB4 vs. GUCY1A2
mRNA Expression, RSEM (Batch normalized from Illumina HiSeq_RNASeqV2): GUCY1A2
mRNA Expression, RSEM (Batch normalized from Illumina HiSeq_RNASeqV2): GNB4 (3q26.33)
Spearman: 0.49
(p = 1.67e-23)
Pearson: 0.36
(p = 6.30e-13)
y = 0.01x + 10.31
R² = 0.13
GNB4 mutated
GUCY1A2 mutated
Both mutated
Neither mutated

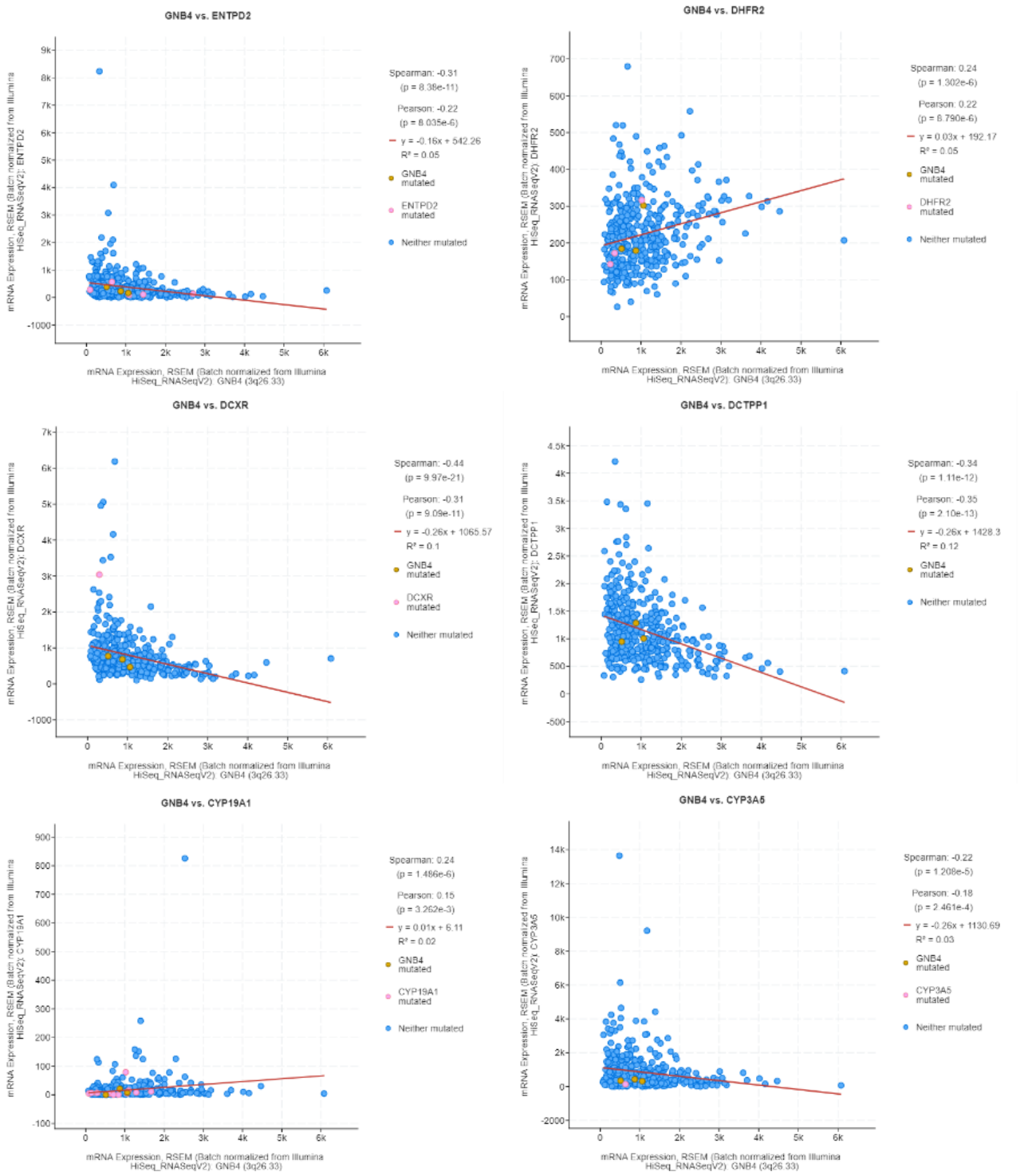

GNB4 vs. GSTM5
mRNA Expression, RSEM (Batch normalized from Illumina HiSeq_RNASeqV2): GSTM5
mRNA Expression, RSEM (Batch normalized from Illumina HiSeq_RNASeqV2): GNB4 (3q26.33)
Spearman: 0.64
(p = 5.56e-49)
Pearson: 0.57
(p = 3.64e-36)
y = 0.09x + -11.44
R² = 0.32
GNB4 mutated
GSTM5 mutated
Neither mutated

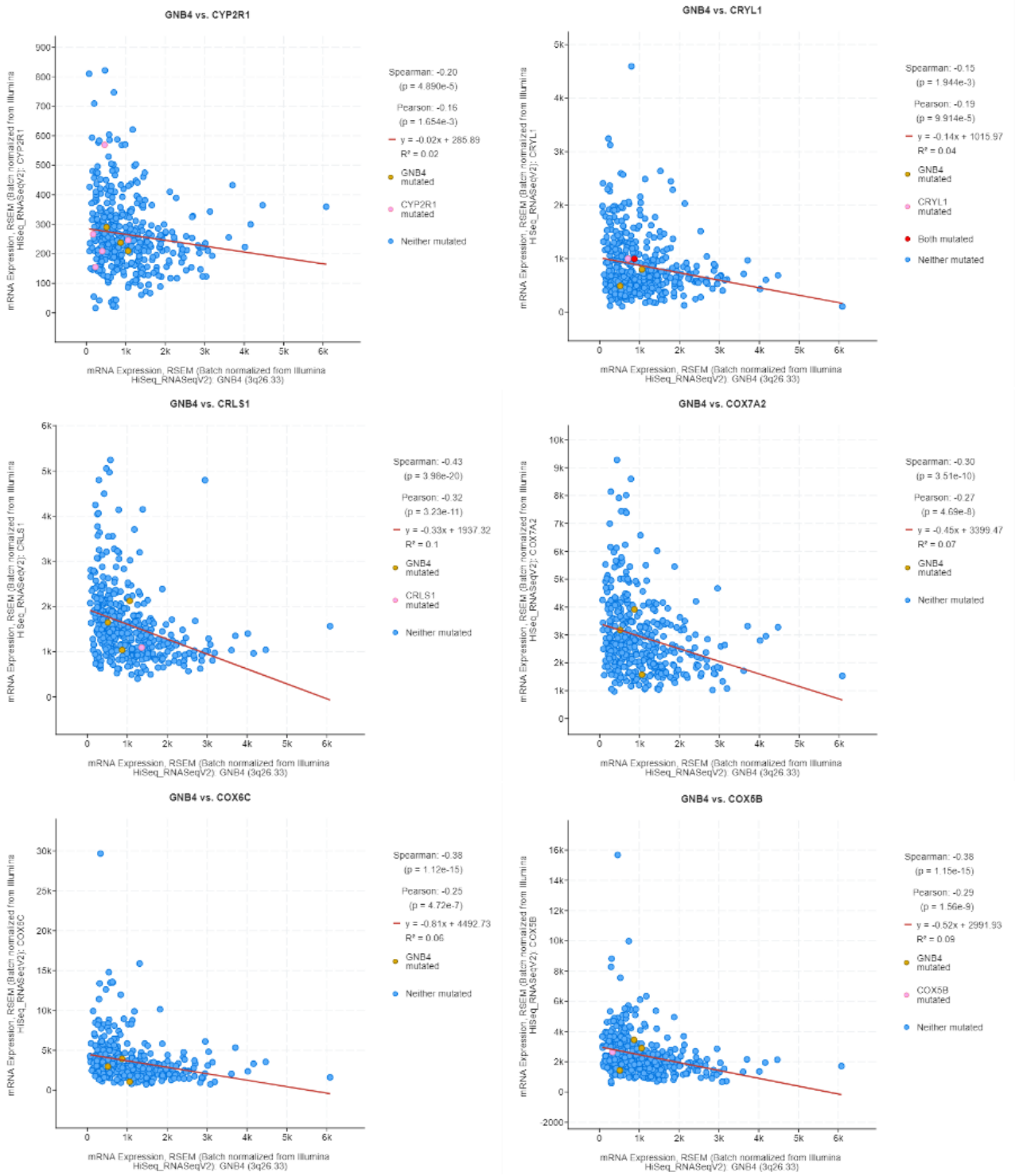

GNB4 vs. GSS
mRNA Expression, RSEM (Batch normalized from Illumina HiSeq_RNASeqV2): GSS
mRNA Expression, RSEM (Batch normalized from Illumina HiSeq_RNASeqV2): GNB4 (3q26.33)
Spearman: -0.48
(p = 4.91e-25)
Pearson: -0.43
(p = 6.70e-20)
y = -0.32x + 1688.18
R² = 0.19
GNB4 mutated
GSS mutated
Neither mutated

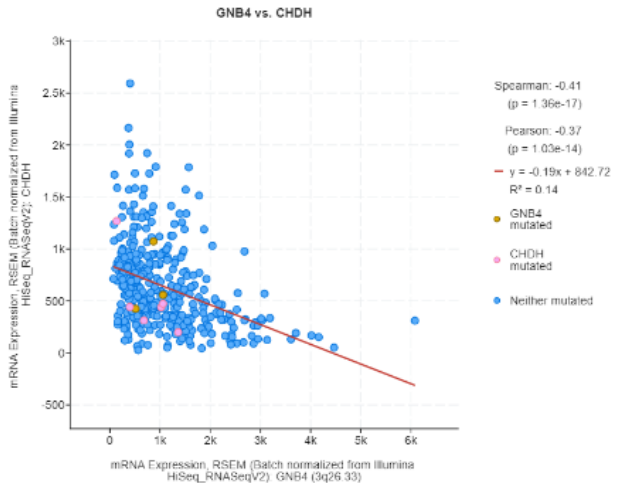

GNB4 vs. GPHN
mRNA Expression, RSEM (Batch normalized from Illumina HiSeq_RNASeqV2): GPHN
mRNA Expression, RSEM (Batch normalized from Illumina HiSeq_RNASeqV2): GNB4 (3q26.33)
Spearman: -0.28
(p = 9.24e-9)
Pearson: -0.24
(p = 8.03e-7)
y = -0.07x + 516.49
R² = 0.06
GNB4 mutated
GPHN mutated
Both mutated
Neither mutated

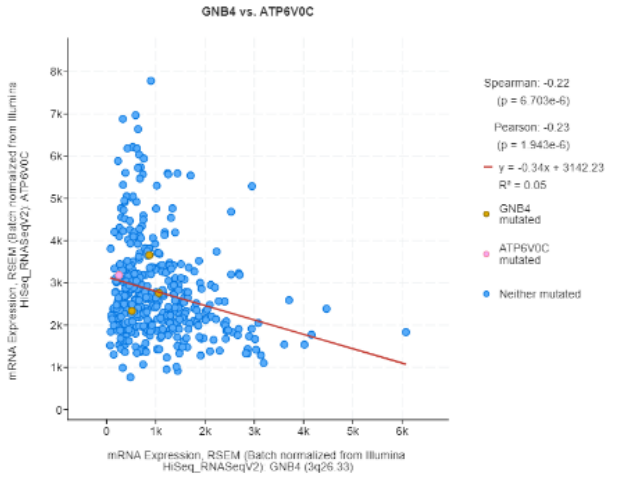

GNB4 vs. GLS2
mRNA Expression, RSEM (Batch normalized from Illumina HiSeq_RNASeqV2): GLS2
mRNA Expression, RSEM (Batch normalized from Illumina HiSeq_RNASeqV2): GNB4 (3q26.33)
Spearman: -0.23
(p = 2.645e-6)
Pearson: -0.18
(p = 1.846e-4)
y = -0.03x + 135.49
R² = 0.03
GNB4 mutated
GLS2 mutated
Neither mutated

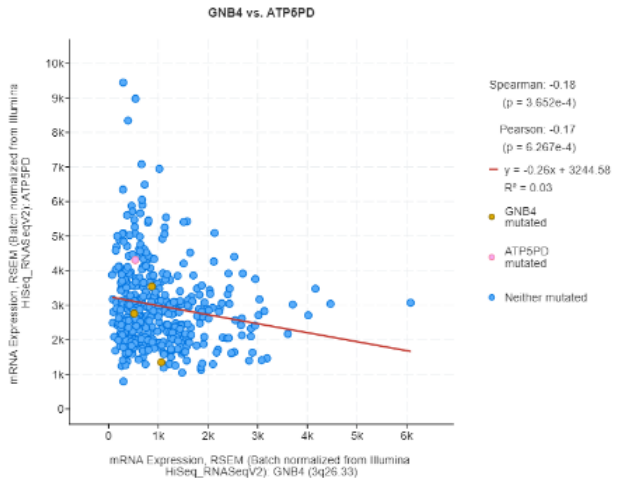

GNB4 vs. GALNT16
mRNA Expression, RSEM (Batch normalized from Illumina HiSeq_RNASeqV2): GALNT16
mRNA Expression, RSEM (Batch normalized from Illumina HiSeq_RNASeqV2): GNB4 (3q26.33)
Spearman: 0.57
(p = 2.12e-36)
Pearson: 0.47
(p = 3.26e-24)
y = 0.06x + 9.58
R² = 0.22
GNB4 mutated
GALNT16 mutated
Neither mutated

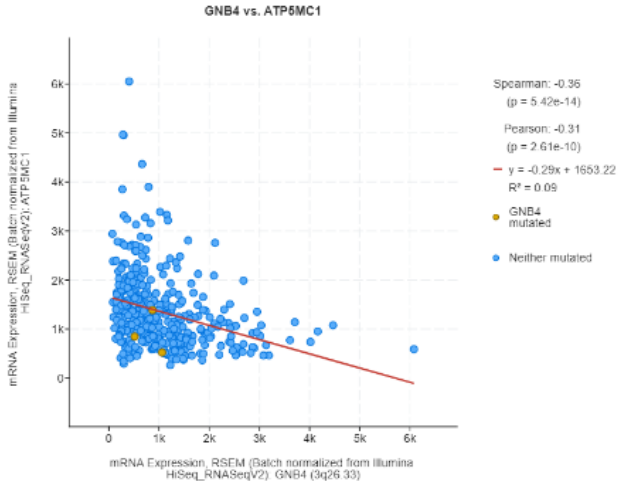

GNB4 vs. ENTPD2
mRNA Expression, RSEM (Batch normalized from Illumina HiSeq_RNASeqV2): ENTPD2
mRNA Expression, RSEM (Batch normalized from Illumina HiSeq_RNASeqV2): GNB4 (3q26.33)
Spearman: -0.31
(p = 8.38e-11)
Pearson: -0.22
(p = 8.035e-6)
y = -0.16x + 542.26
R² = 0.05
GNB4 mutated
ENTPD2 mutated
Neither mutated
GNB4 vs. DHFR2
mRNA Expression, RSEM (Batch normalized from Illumina HiSeq_RNASeqV2): DHFR2
mRNA Expression, RSEM (Batch normalized from Illumina HiSeq_RNASeqV2): GNB4 (3q26.33)
Spearman: 0.24
(p = 1.302e-6)
Pearson: 0.22
(p = 6.790e-6)
y = 0.03x + 192.17
R² = 0.05
GNB4 mutated
DHFR2 mutated
Neither mutated
GNB4 vs. DCXR
mRNA Expression, RSEM (Batch normalized from Illumina HiSeq_RNASeqV2): DCXR
mRNA Expression, RSEM (Batch normalized from Illumina HiSeq_RNASeqV2): GNB4 (3q26.33)
Spearman: -0.44
(p = 9.97e-21)
Pearson: -0.31
(p = 9.09e-11)
y = -0.26x + 1065.57
R² = 0.1
GNB4 mutated
DCXR mutated
Neither mutated
GNB4 vs. DCTPP1
mRNA Expression, RSEM (Batch normalized from Illumina HiSeq_RNASeqV2): DCTPP1
mRNA Expression, RSEM (Batch normalized from Illumina HiSeq_RNASeqV2): GNB4 (3q26.33)
Spearman: -0.34
(p = 1.11e-12)
Pearson: -0.35
(p = 2.10e-13)
y = -0.26x + 1428.3
R² = 0.12
GNB4 mutated
Neither mutated
GNB4 vs. CYP19A1
mRNA Expression, RSEM (Batch normalized from Illumina HiSeq_RNASeqV2): CYP19A1
mRNA Expression, RSEM (Batch normalized from Illumina HiSeq_RNASeqV2): GNB4 (3q26.33)
Spearman: 0.24
(p = 1.486e-6)
Pearson: 0.15
(p = 3.262e-3)
y = 0.01x + 6.11
R² = 0.02
GNB4 mutated
CYP19A1 mutated
Neither mutated
GNB4 vs. CYP3A5
mRNA Expression, RSEM (Batch normalized from Illumina HiSeq_RNASeqV2): CYP3A5
mRNA Expression, RSEM (Batch normalized from Illumina HiSeq_RNASeqV2): GNB4 (3q26.33)
Spearman: -0.22
(p = 1.208e-5)
Pearson: -0.18
(p = 2.461e-4)
y = -0.26x + 1130.69
R² = 0.03
GNB4 mutated
CYP3A5 mutated
Neither mutated

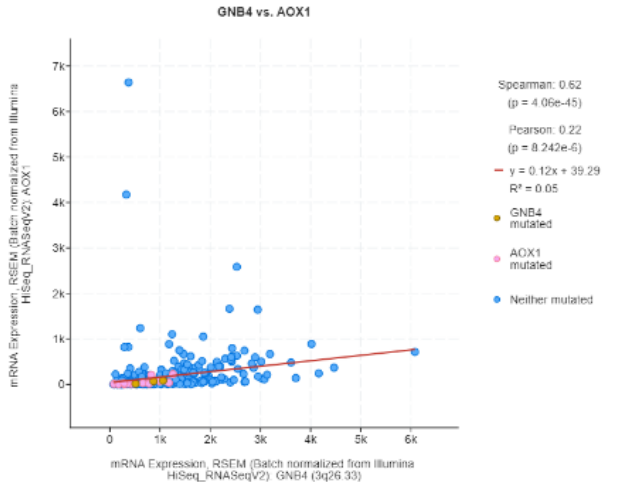

GNB4 vs. CYP2R1
mRNA Expression, RSEM (Batch normalized from Illumina HiSeq_RNASeqV2): CYP2R1
mRNA Expression, RSEM (Batch normalized from Illumina HiSeq_RNASeqV2): GNB4 (3q26.33)
Spearman: -0.20
(p = 4.890e-5)
Pearson: -0.16
(p = 1.654e-3)
y = -0.02x + 285.89
R² = 0.02
GNB4 mutated
CYP2R1 mutated
Neither mutated
GNB4 vs. CRYL1
mRNA Expression, RSEM (Batch normalized from Illumina HiSeq_RNASeqV2): CRYL1
mRNA Expression, RSEM (Batch normalized from Illumina HiSeq_RNASeqV2): GNB4 (3q26.33)
Spearman: -0.15
(p = 1.944e-3)
Pearson: -0.19
(p = 9.914e-5)
y = -0.14x + 1015.97
R² = 0.04
GNB4 mutated
CRYL1 mutated
Both mutated
Neither mutated
GNB4 vs. CRLS1
mRNA Expression, RSEM (Batch normalized from Illumina HiSeq_RNASeqV2): CRLS1
mRNA Expression, RSEM (Batch normalized from Illumina HiSeq_RNASeqV2): GNB4 (3q26.33)
Spearman: -0.43
(p = 3.98e-20)
Pearson: -0.32
(p = 3.23e-11)
y = -0.33x + 1937.32
R² = 0.1
GNB4 mutated
CRLS1 mutated
Neither mutated
GNB4 vs. COX7A2
mRNA Expression, RSEM (Batch normalized from Illumina HiSeq_RNASeqV2): COX7A2
mRNA Expression, RSEM (Batch normalized from Illumina HiSeq_RNASeqV2): GNB4 (3q26.33)
Spearman: -0.30
(p = 3.51e-10)
Pearson: -0.27
(p = 4.69e-8)
y = -0.45x + 3399.47
R² = 0.07
GNB4 mutated
Neither mutated
GNB4 vs. COX6C
mRNA Expression, RSEM (Batch normalized from Illumina HiSeq_RNASeqV2): COX6C
mRNA Expression, RSEM (Batch normalized from Illumina HiSeq_RNASeqV2): GNB4 (3q26.33)
Spearman: -0.38
(p = 1.12e-15)
Pearson: -0.25
(p = 4.72e-7)
y = -0.81x + 4492.73
R² = 0.06
GNB4 mutated
Neither mutated
GNB4 vs. COX5B
mRNA Expression, RSEM (Batch normalized from Illumina HiSeq_RNASeqV2): COX5B
mRNA Expression, RSEM (Batch normalized from Illumina HiSeq_RNASeqV2): GNB4 (3q26.33)
Spearman: -0.38
(p = 1.15e-15)
Pearson: -0.29
(p = 1.56e-9)
y = -0.52x + 2991.93
R² = 0.09
GNB4 mutated
COX5B mutated
Neither mutated

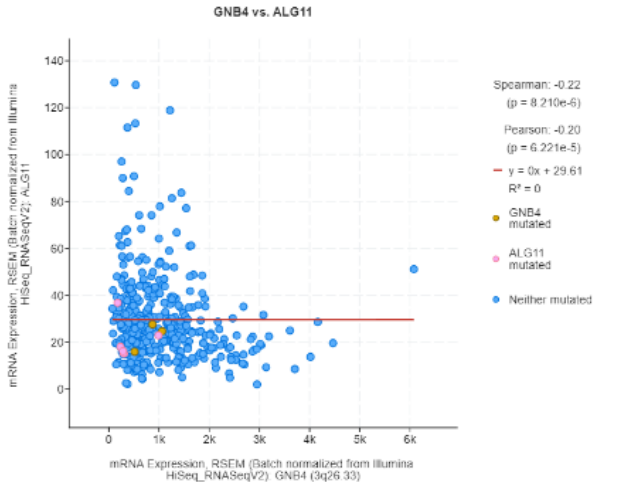

GNB4 vs. CHDH
mRNA Expression, RSEM (Batch normalized from Illumina HiSeq_RNASeqV2): CHDH
mRNA Expression, RSEM (Batch normalized from Illumina HiSeq_RNASeqV2): GNB4 (3q26.33)
Spearman: -0.41
(p = 1.36e-17)
Pearson: -0.37
(p = 1.03e-14)
y = -0.19x + 842.72
R² = 0.14
GNB4 mutated
CHDH mutated
Neither mutated

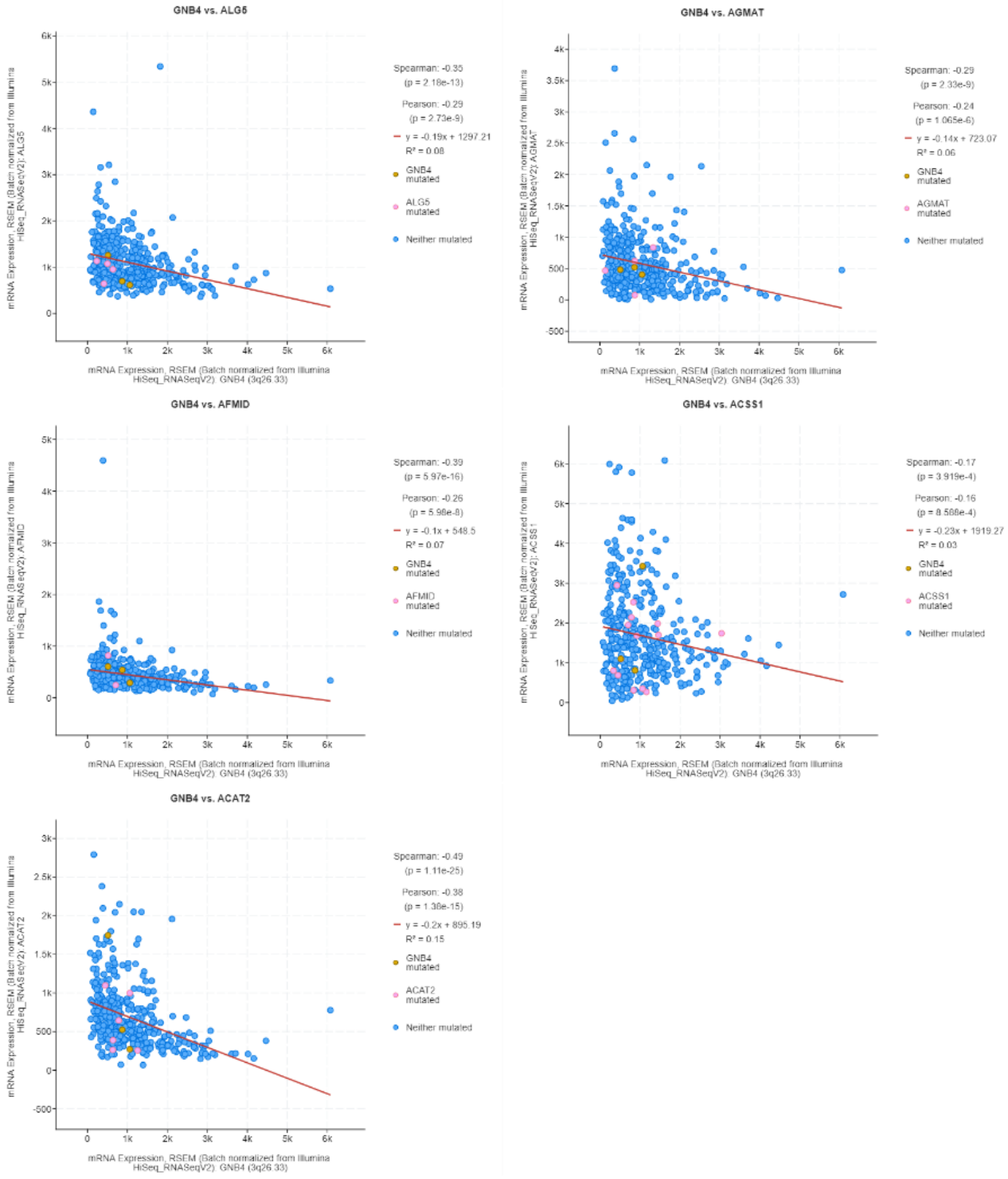

GNB4 vs. ATP6V0C
mRNA Expression, RSEM (Batch normalized from Illumina HiSeq_RNASeqV2): ATP6V0C
mRNA Expression, RSEM (Batch normalized from Illumina HiSeq_RNASeqV2): GNB4 (3q26.33)
Spearman: -0.22
(p = 6.703e-6)
Pearson: -0.23
(p = 1.943e-6)
y = -0.34x + 3142.23
R² = 0.05
GNB4 mutated
ATP6V0C mutated
Neither mutated


GNB4 vs. ATP6PD
mRNA Expression, RSEM (Batch normalized from Illumina HiSeq_RNASeqV2): ATP6PD
mRNA Expression, RSEM (Batch normalized from Illumina HiSeq_RNASeqV2): GNB4 (3q26.33)
Spearman: -0.18
(p = 3.652e-4)
Pearson: -0.17
(p = 6.267e-4)
y = -0.26x + 3244.58
R² = 0.03
GNB4 mutated
ATP6PD mutated
Neither mutated

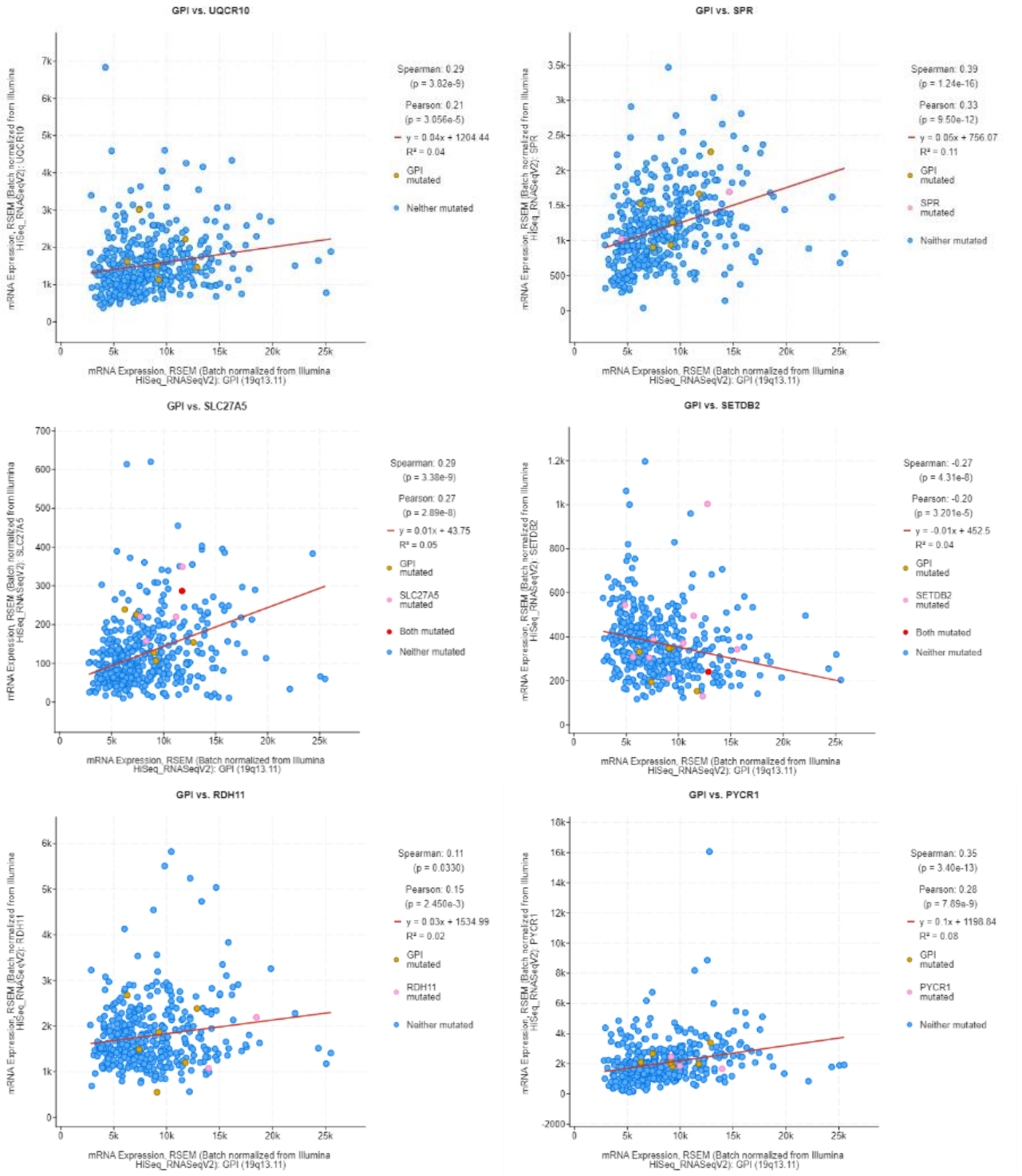

GNB4 vs. ATP5MC1
mRNA Expression, RSEM (Batch normalized from Illumina HiSeq_RNASeqV2): ATP5MC1
mRNA Expression, RSEM (Batch normalized from Illumina HiSeq_RNASeqV2): GNB4 (3q26.33)
Spearman: -0.36
(p = 5.42e-14)
Pearson: -0.31
(p = 2.61e-10)
y = -0.29x + 1653.22
R² = 0.09
GNB4 mutated
Neither mutated

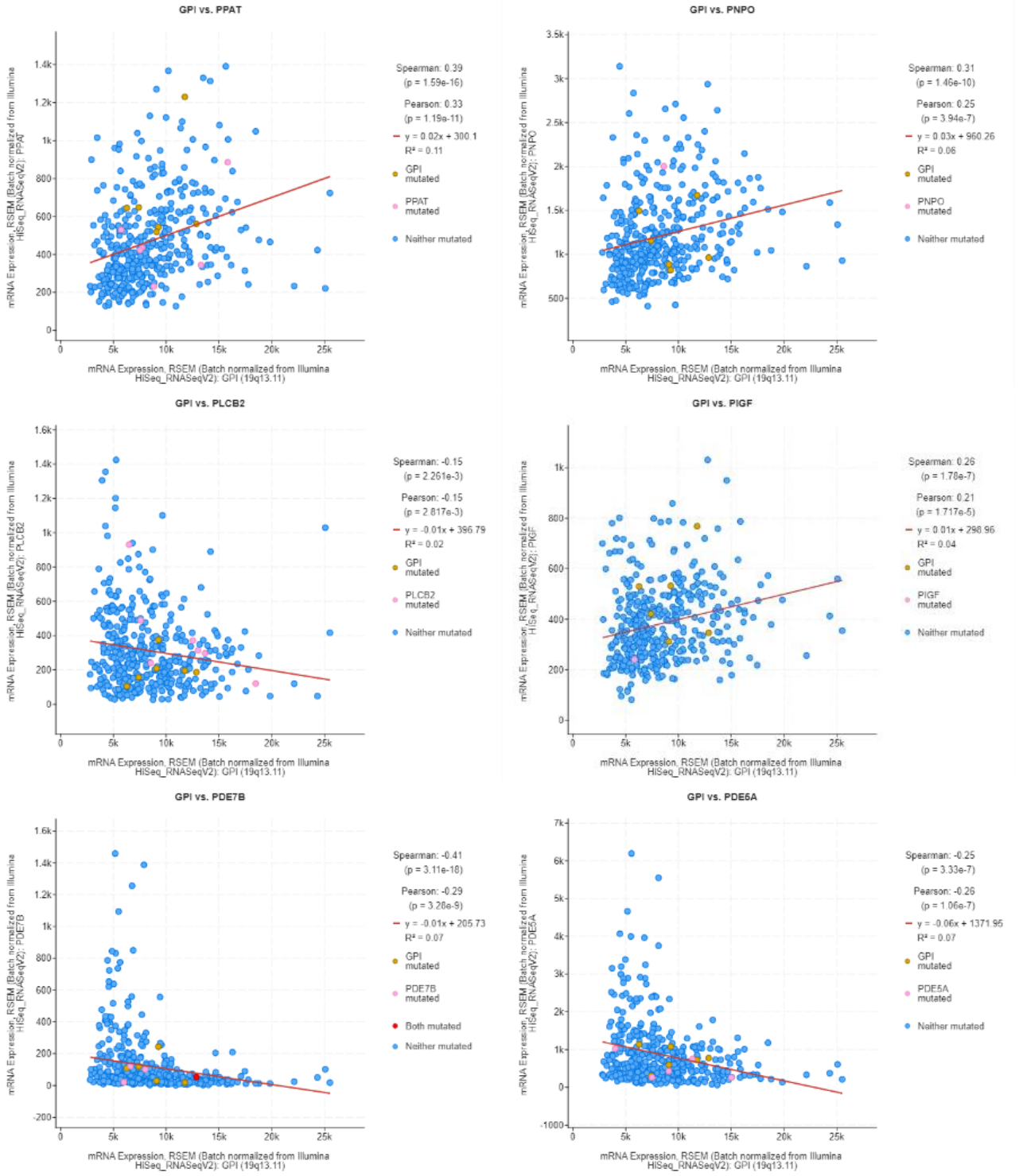

GNB4 vs. AOX1
mRNA Expression, RSEM (Batch normalized from Illumina HiSeq_RNASeqV2): AOX1
mRNA Expression, RSEM (Batch normalized from Illumina HiSeq_RNASeqV2): GNB4 (3q26.33)
Spearman: 0.62
(p = 4.06e-45)
Pearson: 0.22
(p = 8.242e-6)
y = 0.12x + 39.29
R² = 0.05
GNB4 mutated
AOX1 mutated
Neither mutated

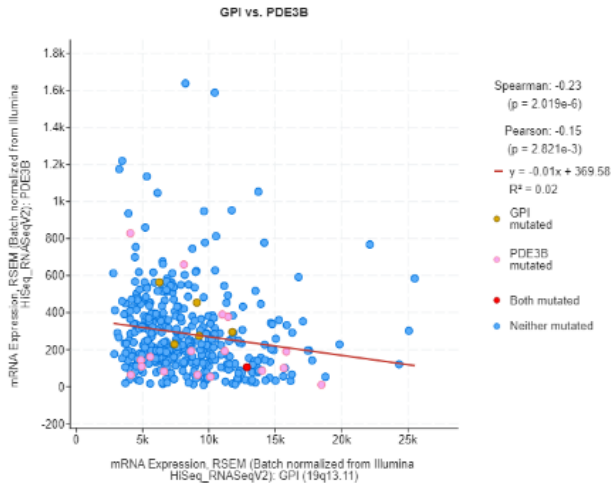

GNB4 vs. ALG11
mRNA Expression, RSEM (Batch normalized from Illumina HiSeq_RNASeqV2): ALG11
mRNA Expression, RSEM (Batch normalized from Illumina HiSeq_RNASeqV2): GNB4 (3q26.33)
Spearman: -0.22
(p = 8.210e-6)
Pearson: -0.20
(p = 6.221e-5)
y = 0x + 29.61
R² = 0
GNB4 mutated
ALG11 mutated
Neither mutated

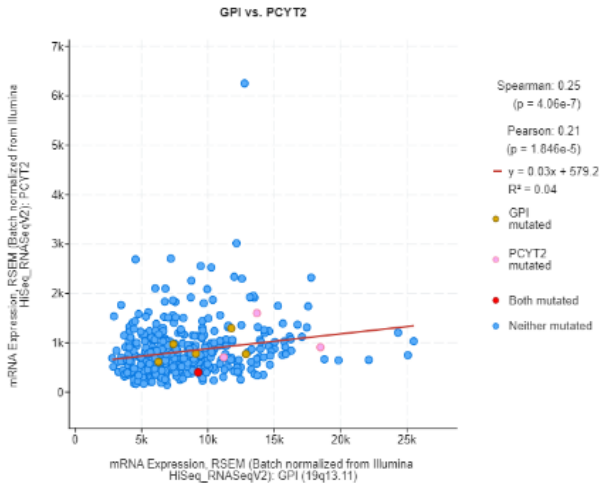

GNB4 vs. ALG5
mRNA Expression, RSEM (Batch normalized from Illumina HiSeq_RNASeqV2): ALG5
mRNA Expression, RSEM (Batch normalized from Illumina HiSeq_RNASeqV2): GNB4 (3q26.33)
Spearman: -0.35
(p = 2.18e-13)
Pearson: -0.29
(p = 2.73e-9)
y = -0.19x + 1297.21
R² = 0.08
GNB4 mutated
ALG5 mutated
Neither mutated
GNB4 vs. AGMAT
mRNA Expression, RSEM (Batch normalized from Illumina HiSeq_RNASeqV2): AGMAT
mRNA Expression, RSEM (Batch normalized from Illumina HiSeq_RNASeqV2): GNB4 (3q26.33)
Spearman: -0.29
(p = 2.33e-9)
Pearson: -0.24
(p = 1.065e-6)
y = -0.14x + 723.07
R² = 0.06
GNB4 mutated
AGMAT mutated
Neither mutated
GNB4 vs. AFMID
mRNA Expression, RSEM (Batch normalized from Illumina HiSeq_RNASeqV2): AFMID
mRNA Expression, RSEM (Batch normalized from Illumina HiSeq_RNASeqV2): GNB4 (3q26.33)
Spearman: -0.39
(p = 5.97e-16)
Pearson: -0.26
(p = 5.98e-8)
y = -0.1x + 548.5
R² = 0.07
GNB4 mutated
AFMID mutated
Neither mutated
GNB4 vs. ACSS1
mRNA Expression, RSEM (Batch normalized from Illumina HiSeq_RNASeqV2): ACSS1
mRNA Expression, RSEM (Batch normalized from Illumina HiSeq_RNASeqV2): GNB4 (3q26.33)
Spearman: -0.17
(p = 3.919e-4)
Pearson: -0.16
(p = 8.568e-4)
y = -0.23x + 1919.27
R² = 0.03
GNB4 mutated
ACSS1 mutated
Neither mutated
GNB4 vs. ACAT2
mRNA Expression, RSEM (Batch normalized from Illumina HiSeq_RNASeqV2): ACAT2
mRNA Expression, RSEM (Batch normalized from Illumina HiSeq_RNASeqV2): GNB4 (3q26.33)
Spearman: -0.49
(p = 1.11e-25)
Pearson: -0.38
(p = 1.38e-15)
y = -0.2x + 895.19
R² = 0.15
GNB4 mutated
ACAT2 mutated
Neither mutated

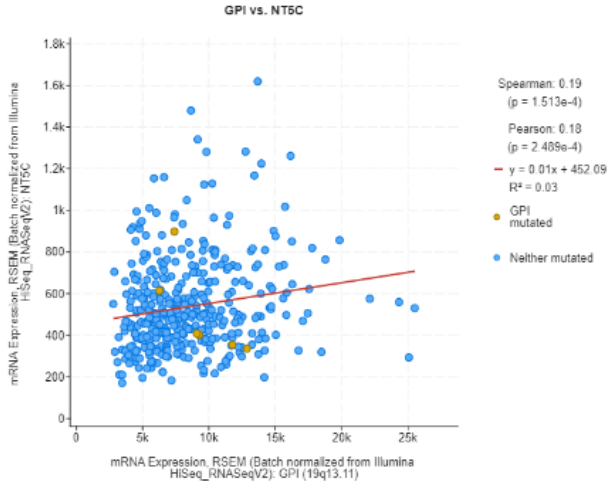
GPI

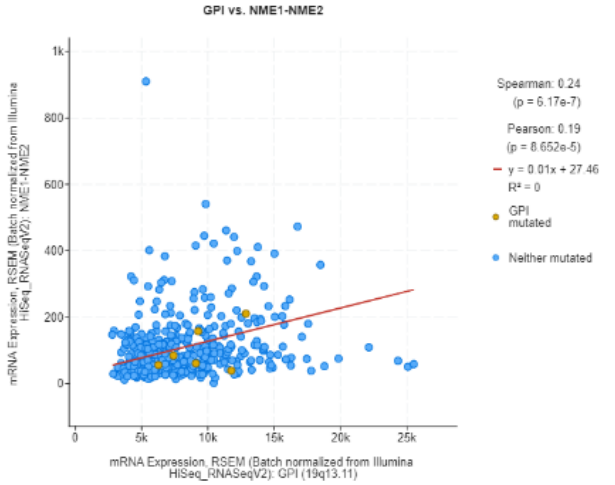

GPI vs. UQCR10
mRNA Expression, RSEM (Batch normalized from Illumina HiSeq_RNASeqV2): UQCR10
mRNA Expression, RSEM (Batch normalized from Illumina HiSeq_RNASeqV2): GPI (19q13.11)
Spearman: 0.29
(p = 3.82e-9)
Pearson: 0.21
(p = 3.056e-5)
y = 0.04x + 1204.44
R² = 0.04
GPI mutated
Neither mutated
GPI vs. SPR
mRNA Expression, RSEM (Batch normalized from Illumina HiSeq_RNASeqV2): SPR
mRNA Expression, RSEM (Batch normalized from Illumina HiSeq_RNASeqV2): GPI (19q13.11)
Spearman: 0.39
(p = 1.24e-16)
Pearson: 0.33
(p = 9.50e-12)
y = 0.05x + 756.07
R² = 0.11
GPI mutated
SPR mutated
Neither mutated
GPI vs. SLC27A5
mRNA Expression, RSEM (Batch normalized from Illumina HiSeq_RNASeqV2): SLC27A5
mRNA Expression, RSEM (Batch normalized from Illumina HiSeq_RNASeqV2): GPI (19q13.11)
Spearman: 0.29
(p = 3.38e-9)
Pearson: 0.27
(p = 2.89e-8)
y = 0.01x + 43.75
R² = 0.05
GPI mutated
SLC27A5 mutated
Both mutated
Neither mutated
GPI vs. SETDB2
mRNA Expression, RSEM (Batch normalized from Illumina HiSeq_RNASeqV2): SETDB2
mRNA Expression, RSEM (Batch normalized from Illumina HiSeq_RNASeqV2): GPI (19q13.11)
Spearman: -0.27
(p = 4.31e-8)
Pearson: -0.20
(p = 3.201e-5)
y = -0.01x + 452.5
R² = 0.04
GPI mutated
SETDB2 mutated
Both mutated
Neither mutated
GPI vs. RDH11
mRNA Expression, RSEM (Batch normalized from Illumina HiSeq_RNASeqV2): RDH11
mRNA Expression, RSEM (Batch normalized from Illumina HiSeq_RNASeqV2): GPI (19q13.11)
Spearman: 0.11
(p = 0.0330)
Pearson: 0.15
(p = 2.450e-3)
y = 0.03x + 1534.99
R² = 0.02
GPI mutated
RDH11 mutated
Neither mutated
GPI vs. PYCR1
mRNA Expression, RSEM (Batch normalized from Illumina HiSeq_RNASeqV2): PYCR1
mRNA Expression, RSEM (Batch normalized from Illumina HiSeq_RNASeqV2): GPI (19q13.11)
Spearman: 0.35
(p = 3.40e-13)
Pearson: 0.28
(p = 7.69e-9)
y = 0.1x + 1198.84
R² = 0.08
GPI mutated
PYCR1 mutated
Neither mutated

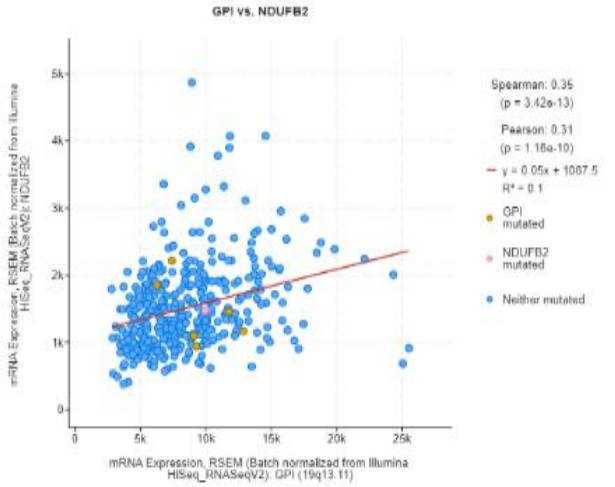

GPI vs. PPAT
mRNA Expression, RSEM (Batch normalized from Illumina HiSeq_RNASeqV2): PPAT
mRNA Expression, RSEM (Batch normalized from Illumina HiSeq_RNASeqV2): GPI (19q13.11)
Spearman: 0.39
(p = 1.59e-16)
Pearson: 0.33
(p = 1.19e-11)
y = 0.02x + 300.1
R² = 0.11
GPI mutated
PPAT mutated
Neither mutated
GPI vs. PNPO
mRNA Expression, RSEM (Batch normalized from Illumina HiSeq_RNASeqV2): PNPO
mRNA Expression, RSEM (Batch normalized from Illumina HiSeq_RNASeqV2): GPI (19q13.11)
Spearman: 0.31
(p = 1.46e-10)
Pearson: 0.25
(p = 3.94e-7)
y = 0.03x + 960.26
R² = 0.06
GPI mutated
PNPO mutated
Neither mutated
GPI vs. PLCB2
mRNA Expression, RSEM (Batch normalized from Illumina HiSeq_RNASeqV2): PLCB2
mRNA Expression, RSEM (Batch normalized from Illumina HiSeq_RNASeqV2): GPI (19q13.11)
Spearman: -0.15
(p = 2.261e-3)
Pearson: -0.15
(p = 2.817e-3)
y = -0.01x + 396.79
R² = 0.02
GPI mutated
PLCB2 mutated
Neither mutated
GPI vs. PIGF
mRNA Expression, RSEM (Batch normalized from Illumina HiSeq_RNASeqV2): PIGF
mRNA Expression, RSEM (Batch normalized from Illumina HiSeq_RNASeqV2): GPI (19q13.11)
Spearman: 0.26
(p = 1.78e-7)
Pearson: 0.21
(p = 1.717e-5)
y = 0.01x + 298.96
R² = 0.04
GPI mutated
PIGF mutated
Neither mutated
GPI vs. PDE7B
mRNA Expression, RSEM (Batch normalized from Illumina HiSeq_RNASeqV2): PDE7B
mRNA Expression, RSEM (Batch normalized from Illumina HiSeq_RNASeqV2): GPI (19q13.11)
Spearman: -0.41
(p = 3.11e-18)
Pearson: -0.29
(p = 3.26e-9)
y = -0.01x + 205.73
R² = 0.07
GPI mutated
PDE7B mutated
Both mutated
Neither mutated
GPI vs. PDE5A
mRNA Expression, RSEM (Batch normalized from Illumina HiSeq_RNASeqV2): PDE5A
mRNA Expression, RSEM (Batch normalized from Illumina HiSeq_RNASeqV2): GPI (19q13.11)
Spearman: -0.25
(p = 3.33e-7)
Pearson: -0.26
(p = 1.06e-7)
y = -0.06x + 1371.95
R² = 0.07
GPI mutated
PDE5A mutated
Neither mutated

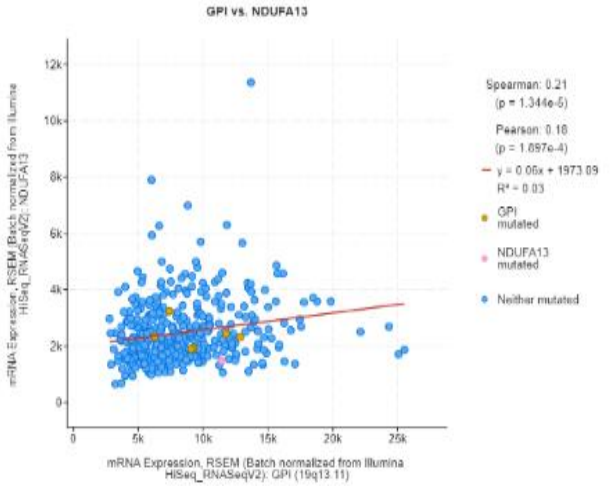

GPI vs. PDE3B
mRNA Expression, RSEM (Batch normalized from Illumina HiSeq_RNASeqV2): PDE3B
mRNA Expression, RSEM (Batch normalized from Illumina HiSeq_RNASeqV2): GPI (19q13.11)
Spearman: -0.23
(p = 2.019e-6)
Pearson: -0.15
(p = 2.821e-3)
y = -0.01x + 369.58
R² = 0.02
GPI mutated
PDE3B mutated
Both mutated
Neither mutated

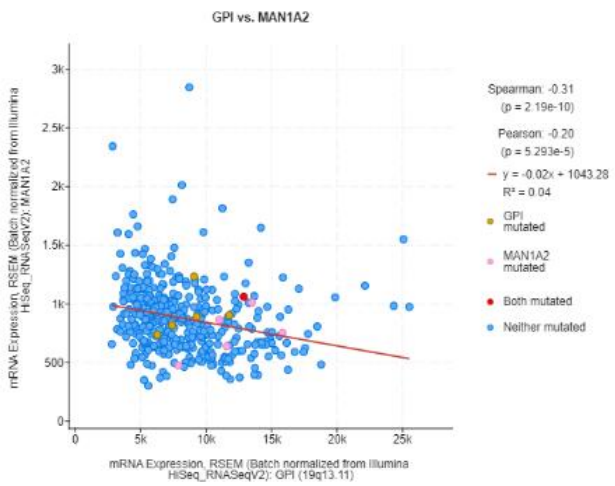

GPI vs. PCYT2
mRNA Expression, RSEM (Batch normalized from Illumina HiSeq_RNASeqV2): PCYT2
mRNA Expression, RSEM (Batch normalized from Illumina HiSeq_RNASeqV2): GPI (19q13.11)
Spearman: 0.25
(p = 4.06e-7)
Pearson: 0.21
(p = 1.846e-5)
y = 0.03x + 579.2
R² = 0.04
GPI mutated
PCYT2 mutated
Both mutated
Neither mutated

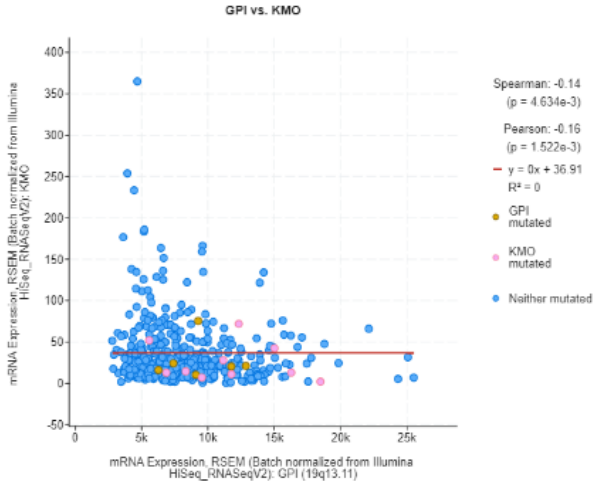

GPI vs. NT5C
mRNA Expression, RSEM (Batch normalized from Illumina HiSeq_RNASeqV2): NT5C
mRNA Expression, RSEM (Batch normalized from Illumina HiSeq_RNASeqV2): GPI (19q13.11)
Spearman: 0.19
(p = 1.513e-4)
Pearson: 0.18
(p = 2.489e-4)
y = 0.01x + 452.09
R² = 0.03
GPI mutated
Neither mutated

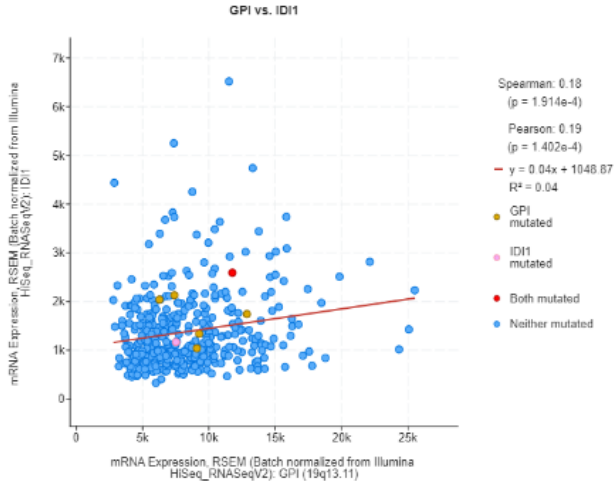

GPI vs. NME1-NME2
mRNA Expression, RSEM (Batch normalized from Illumina HiSeq_RNASeqV2): NME1-NME2
mRNA Expression, RSEM (Batch normalized from Illumina HiSeq_RNASeqV2): GPI (19q13.11)
Spearman: 0.24
(p = 6.17e-7)
Pearson: 0.19
(p = 8.652e-5)
y = 0.01x + 27.46
R² = 0
GPI mutated
Neither mutated


GPI vs. NDUFB2
mRNA Expression, RSEM (Batch normalized from Illumina HiSeq_RNASeqV2): NDUFB2
mRNA Expression, RSEM (Batch normalized from Illumina HiSeq_RNASeqV2): GPI (19q13.11)
Spearman: 0.35
(p = 3.42e-13)
Pearson: 0.31
(p = 1.18e-10)
y = 0.05x + 1067.5
R² = 0.1
GPI mutated
NDUFB2 mutated
Neither mutated

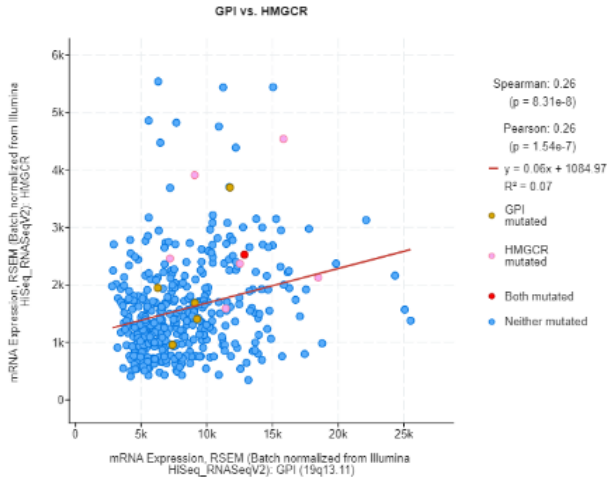

GPI vs. NDUFA13
mRNA Expression, RSEM (Batch normalized from Illumina HiSeq_RNASeqV2): NDUFA13
mRNA Expression, RSEM (Batch normalized from Illumina HiSeq_RNASeqV2): GPI (19q13.11)
Spearman: 0.21
(p = 1.344e-5)
Pearson: 0.16
(p = 1.697e-4)
y = 0.06x + 1973.09
R² = 0.03
GPI mutated
NDUFA13 mutated
Neither mutated

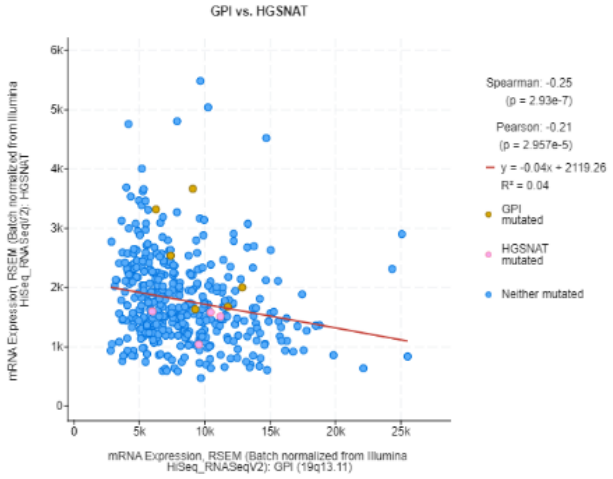

GPI vs. MAN1A2
mRNA Expression, RSEM (Batch normalized from Illumina HiSeq_RNASeqV2): MAN1A2
mRNA Expression, RSEM (Batch normalized from Illumina HiSeq_RNASeqV2): GPI (19q13.11)
Spearman: -0.31
(p = 2.19e-10)
Pearson: -0.20
(p = 5.293e-5)
y = -0.02x + 1043.28
R² = 0.04
GPI mutated
MAN1A2 mutated
Both mutated
Neither mutated

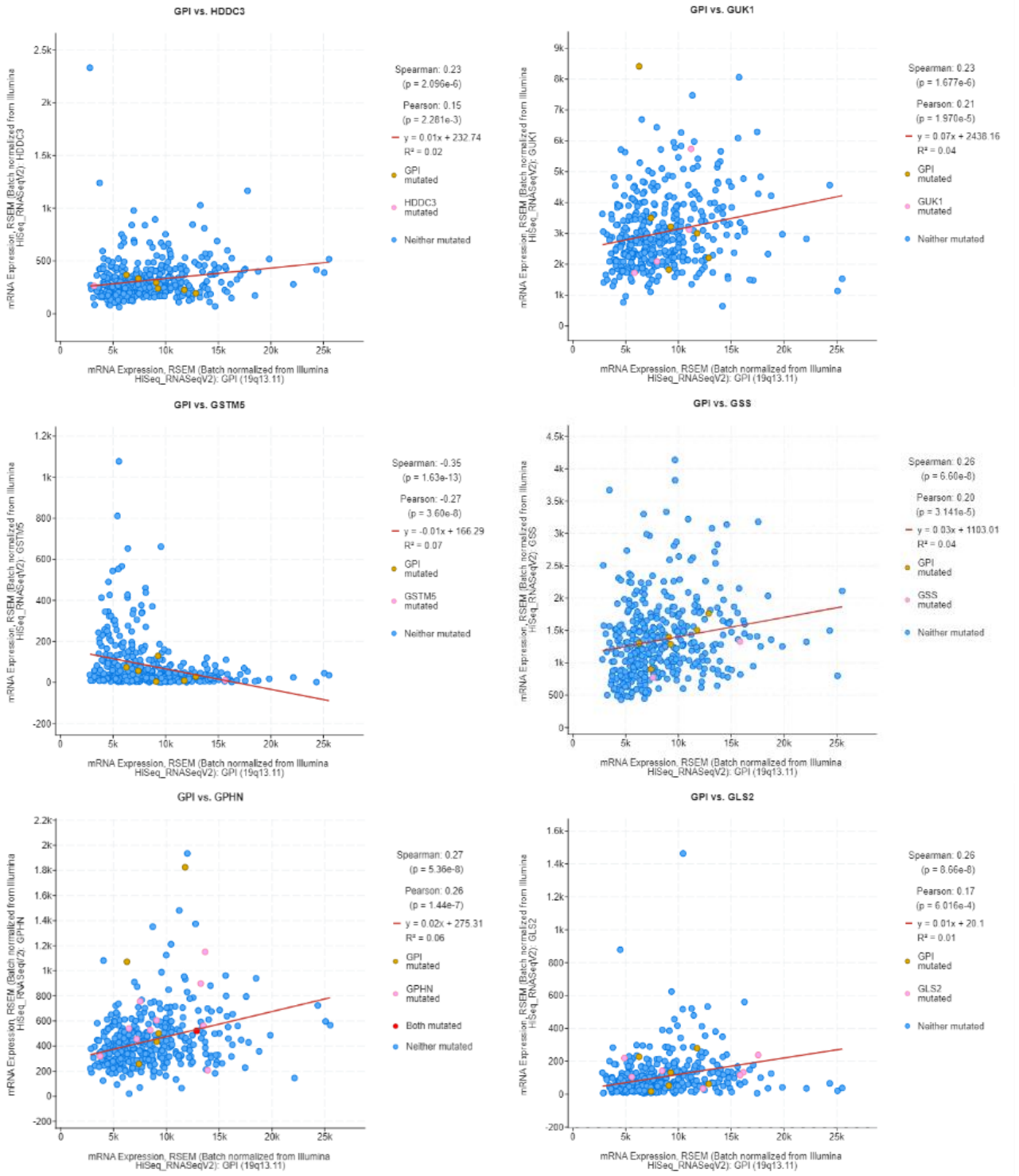

GPI vs. KMO
mRNA Expression, RSEM (Batch normalized from Illumina HiSeq_RNASeqV2): KMO
mRNA Expression, RSEM (Batch normalized from Illumina HiSeq_RNASeqV2): GPI (19q13.11)
Spearman: -0.14
(p = 4.634e-3)
Pearson: -0.16
(p = 1.522e-3)
y = 0x + 36.91
R² = 0
GPI mutated
KMO mutated
Neither mutated

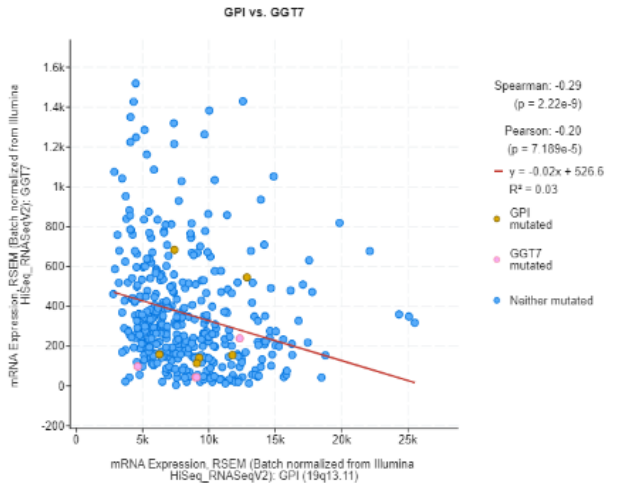

GPI vs. IDI1
mRNA Expression, RSEM (Batch normalized from Illumina HiSeq_RNASeqV2): IDI1
mRNA Expression, RSEM (Batch normalized from Illumina HiSeq_RNASeqV2): GPI (19q13.11)
Spearman: 0.18
(p = 1.914e-4)
Pearson: 0.19
(p = 1.402e-4)
y = 0.04x + 1048.87
R² = 0.04
GPI mutated
IDI1 mutated
Both mutated
Neither mutated

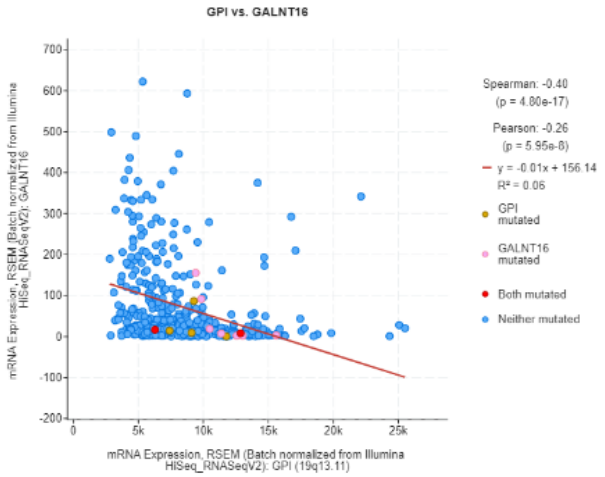

GPI vs. HYAL3
mRNA Expression, RSEM (Batch normalized from Illumina HiSeq_RNASeqV2): HYAL3
mRNA Expression, RSEM (Batch normalized from Illumina HiSeq_RNASeqV2): GPI (19q13.11)
Spearman: 0.21
(p = 1.352e-5)
Pearson: 0.19
(p = 1.703e-4)
y = 0x + 71.85
R² = 0
GPI mutated
HYAL3 mutated
Neither mutated

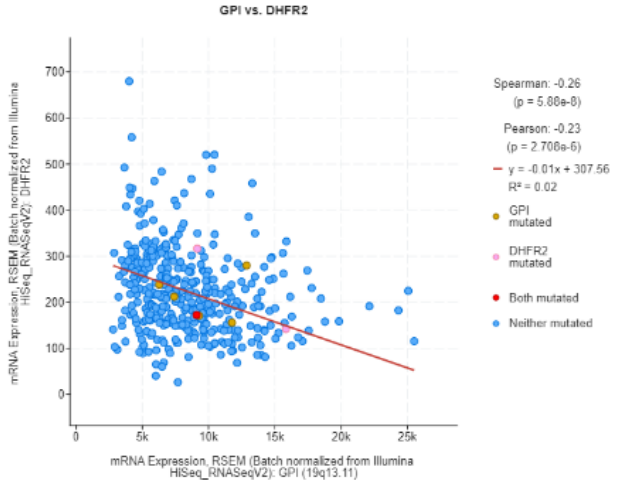

GPI vs. HMGCR
mRNA Expression, RSEM (Batch normalized from Illumina HiSeq_RNASeqV2): HMGCR
mRNA Expression, RSEM (Batch normalized from Illumina HiSeq_RNASeqV2): GPI (19q13.11)
Spearman: 0.26
(p = 8.31e-8)
Pearson: 0.26
(p = 1.54e-7)
y = 0.06x + 1084.97
R² = 0.07
GPI mutated
HMGCR mutated
Both mutated
Neither mutated

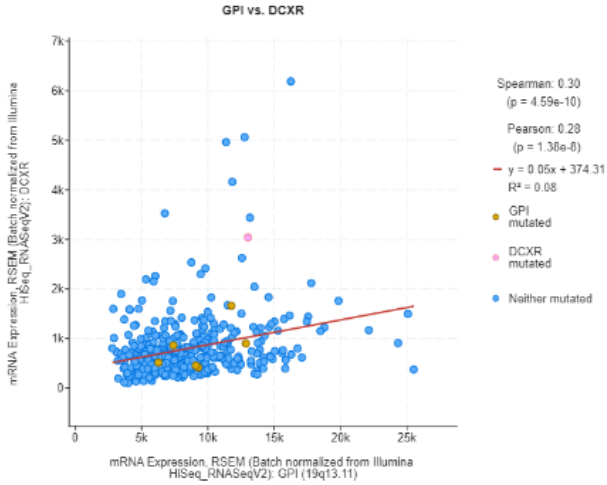

GPI vs. HGSNAT
mRNA Expression, RSEM (Batch normalized from Illumina HiSeq_RNASeqV2): HGSNAT
mRNA Expression, RSEM (Batch normalized from Illumina HiSeq_RNASeqV2): GPI (19q13.11)
Spearman: -0.25
(p = 2.93e-7)
Pearson: -0.21
(p = 2.957e-5)
y = -0.04x + 2119.26
R² = 0.04
GPI mutated
HGSNAT mutated
Neither mutated

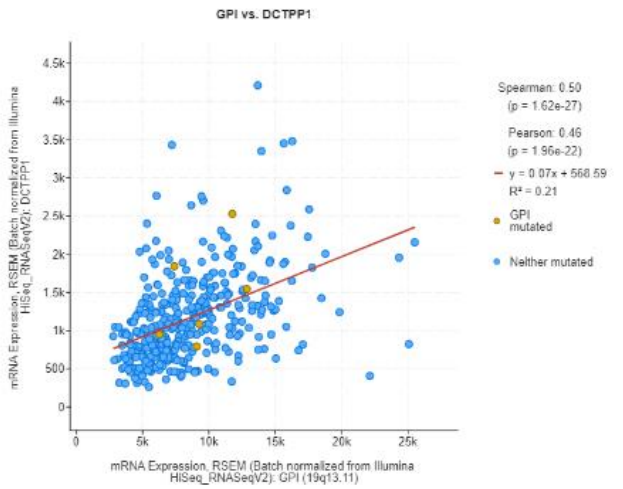

GPI vs. HDDC3
mRNA Expression, RSEM (Batch normalized from Illumina HiSeq_RNASeqV2): HDDC3
mRNA Expression, RSEM (Batch normalized from Illumina HiSeq_RNASeqV2): GPI (19q13.11)
Spearman: 0.23
(p = 2.096e-6)
Pearson: 0.15
(p = 2.281e-3)
y = 0.01x + 232.74
R² = 0.02
GPI mutated
HDDC3 mutated
Neither mutated
GPI vs. GUK1
mRNA Expression, RSEM (Batch normalized from Illumina HiSeq_RNASeqV2): GUK1
mRNA Expression, RSEM (Batch normalized from Illumina HiSeq_RNASeqV2): GPI (19q13.11)
Spearman: 0.23
(p = 1.677e-6)
Pearson: 0.21
(p = 1.970e-5)
y = 0.07x + 2438.16
R² = 0.04
GPI mutated
GUK1 mutated
Neither mutated
GPI vs. GSTM5
mRNA Expression, RSEM (Batch normalized from Illumina HiSeq_RNASeqV2): GSTM5
mRNA Expression, RSEM (Batch normalized from Illumina HiSeq_RNASeqV2): GPI (19q13.11)
Spearman: -0.35
(p = 1.63e-13)
Pearson: -0.27
(p = 3.60e-8)
y = -0.01x + 166.29
R² = 0.07
GPI mutated
GSTM5 mutated
Neither mutated
GPI vs. GSS
mRNA Expression, RSEM (Batch normalized from Illumina HiSeq_RNASeqV2): GSS
mRNA Expression, RSEM (Batch normalized from Illumina HiSeq_RNASeqV2): GPI (19q13.11)
Spearman: 0.26
(p = 6.60e-8)
Pearson: 0.20
(p = 3.141e-5)
y = 0.03x + 1103.01
R² = 0.04
GPI mutated
GSS mutated
Neither mutated
GPI vs. GPHN
mRNA Expression, RSEM (Batch normalized from Illumina HiSeq_RNASeqV2): GPHN
mRNA Expression, RSEM (Batch normalized from Illumina HiSeq_RNASeqV2): GPI (19q13.11)
Spearman: 0.27
(p = 5.36e-8)
Pearson: 0.26
(p = 1.44e-7)
y = 0.02x + 275.31
R² = 0.06
GPI mutated
GPHN mutated
Both mutated
Neither mutated
GPI vs. GLS2
mRNA Expression, RSEM (Batch normalized from Illumina HiSeq_RNASeqV2): GLS2
mRNA Expression, RSEM (Batch normalized from Illumina HiSeq_RNASeqV2): GPI (19q13.11)
Spearman: 0.26
(p = 8.66e-8)
Pearson: 0.17
(p = 6.016e-4)
y = 0.01x + 20.1
R² = 0.01
GPI mutated
GLS2 mutated
Neither mutated

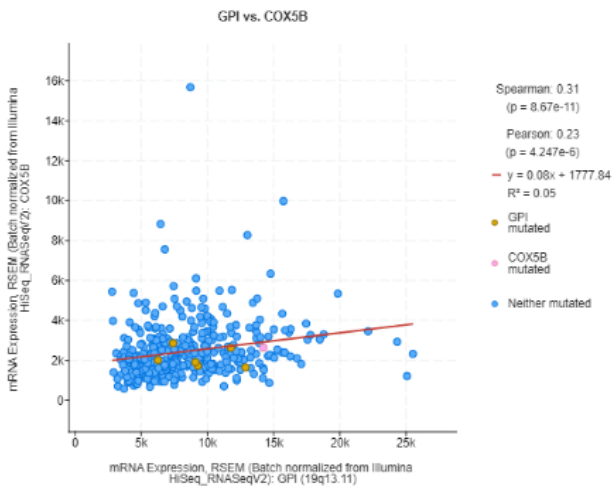

GPI vs. GGT7
mRNA Expression, RSEM (Batch normalized from Illumina HiSeq_RNASeqV2): GGT7
mRNA Expression, RSEM (Batch normalized from Illumina HiSeq_RNASeqV2): GPI (19q13.11)
Spearman: -0.29
(p = 2.22e-9)
Pearson: -0.20
(p = 7.189e-5)
y = -0.02x + 526.6
R² = 0.03
GPI mutated
GGT7 mutated
Neither mutated

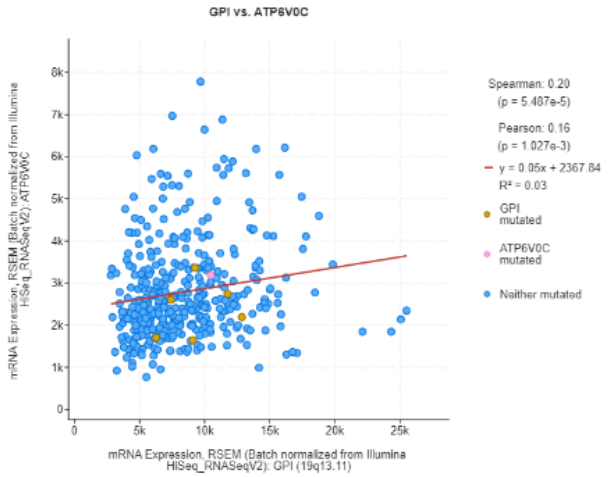

GPI vs. GALNT16
mRNA Expression, RSEM (Batch normalized from Illumina HiSeq_RNASeqV2): GALNT16
mRNA Expression, RSEM (Batch normalized from Illumina HiSeq_RNASeqV2): GPI (19q13.11)
Spearman: -0.40
(p = 4.80e-17)
Pearson: -0.26
(p = 5.95e-8)
y = -0.01x + 156.14
R² = 0.06
GPI mutated
GALNT16 mutated
Both mutated
Neither mutated

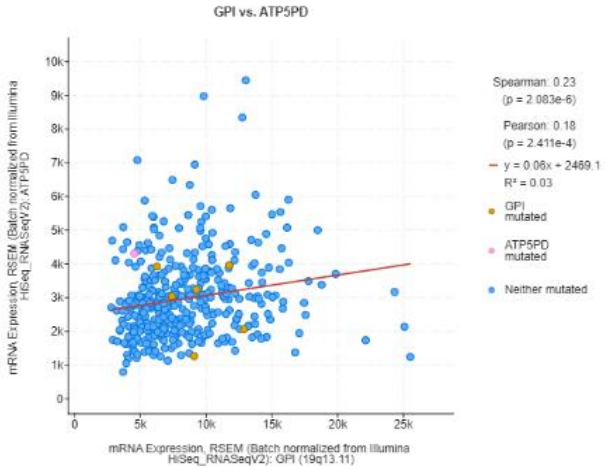

GPI vs. DHFR2
mRNA Expression, RSEM (Batch normalized from Illumina HiSeq_RNASeqV2): DHFR2
mRNA Expression, RSEM (Batch normalized from Illumina HiSeq_RNASeqV2): GPI (19q13.11)
Spearman: -0.26
(p = 5.88e-8)
Pearson: -0.23
(p = 2.706e-6)
y = -0.01x + 307.56
R² = 0.02
GPI mutated
DHFR2 mutated
Both mutated
Neither mutated

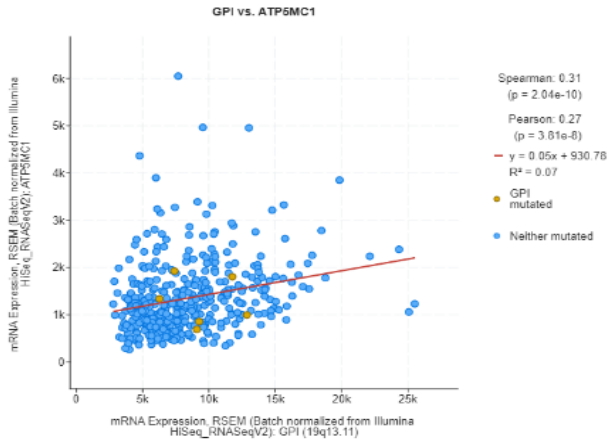

GPI vs. DCXR
mRNA Expression, RSEM (Batch normalized from Illumina HiSeq_RNASeqV2): DCXR
mRNA Expression, RSEM (Batch normalized from Illumina HiSeq_RNASeqV2): GPI (19q13.11)
Spearman: 0.30
(p = 4.59e-10)
Pearson: 0.28
(p = 1.38e-8)
y = 0.05x + 374.31
R² = 0.08
GPI mutated
DCXR mutated
Neither mutated

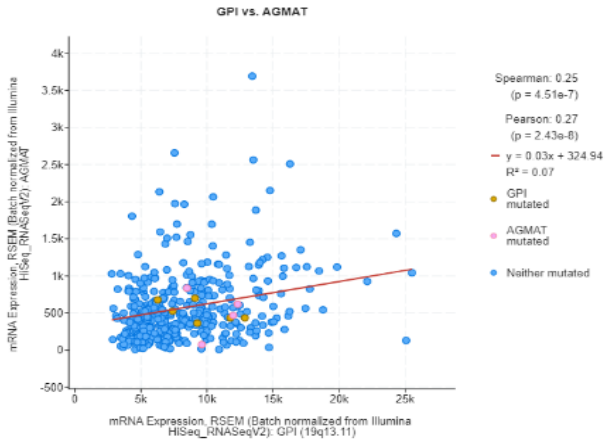

GPI vs. DCTPP1
mRNA Expression, RSEM (Batch normalized from Illumina HiSeq_RNASeqV2): DCTPP1
mRNA Expression, RSEM (Batch normalized from Illumina HiSeq_RNASeqV2): GPI (19q13.11)
Spearman: 0.50
(p = 1.62e-27)
Pearson: 0.46
(p = 1.96e-22)
y = 0.07x + 568.59
R² = 0.21
GPI mutated
Neither mutated

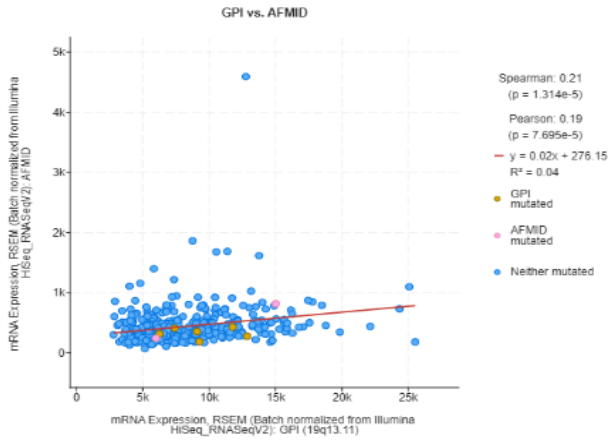

GPI vs. COX5B
mRNA Expression, RSEM (Batch normalized from Illumina HiSeq_RNASeqV2): COX5B
mRNA Expression, RSEM (Batch normalized from Illumina HiSeq_RNASeqV2): GPI (19q13.11)
Spearman: 0.31
(p = 8.67e-11)
Pearson: 0.23
(p = 4.247e-6)
y = 0.08x + 1777.84
R² = 0.05
GPI mutated
COX5B mutated
Neither mutated


GPI vs. ATP6V0C
mRNA Expression, RSEM (Batch normalized from Illumina HiSeq_RNASeqV2): ATP6V0C
mRNA Expression, RSEM (Batch normalized from Illumina HiSeq_RNASeqV2): GPI (19q13.11)
Spearman: 0.20
(p = 5.487e-5)
Pearson: 0.16
(p = 1.027e-3)
y = 0.05x + 2367.84
R² = 0.03
GPI mutated
ATP6V0C mutated
Neither mutated


GPI vs. ATP5PD
mRNA Expression, RSEM (Batch normalized from Illumina HiSeq_RNASeqV2): ATP5PD
mRNA Expression, RSEM (Batch normalized from Illumina HiSeq_RNASeqV2): GPI (19q13.11)
Spearman: 0.23
(p = 2.083e-6)
Pearson: 0.18
(p = 2.411e-4)
y = 0.06x + 2469.1
R² = 0.03
GPI mutated
ATP5PD mutated
Neither mutated


GPI vs. ATP5MC1
mRNA Expression, RSEM (Batch normalized from Illumina HiSeq_RNASeqV2): ATP5MC1
mRNA Expression, RSEM (Batch normalized from Illumina HiSeq_RNASeqV2): GPI (19q13.11)
Spearman: 0.31
(p = 2.04e-10)
Pearson: 0.27
(p = 3.81e-8)
y = 0.05x + 930.78
R² = 0.07
GPI mutated
Neither mutated

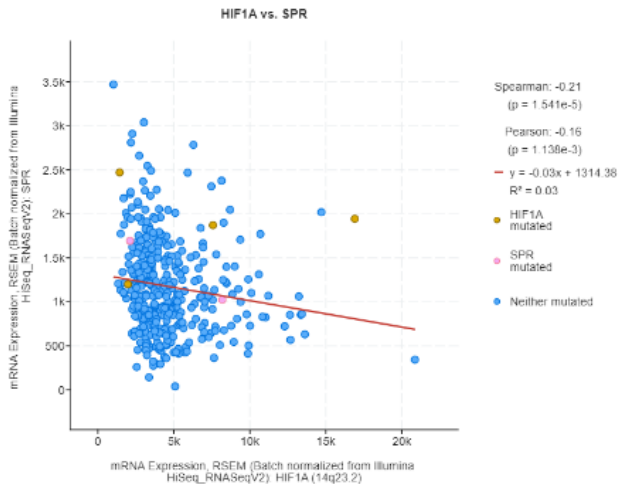

GPI vs. AGMAT
mRNA Expression, RSEM (Batch normalized from Illumina HiSeq_RNASeqV2): AGMAT
mRNA Expression, RSEM (Batch normalized from Illumina HiSeq_RNASeqV2): GPI (19q13.11)
Spearman: 0.25
(p = 4.51e-7)
Pearson: 0.27
(p = 2.43e-8)
y = 0.03x + 324.94
R² = 0.07
GPI mutated
AGMAT mutated
Neither mutated

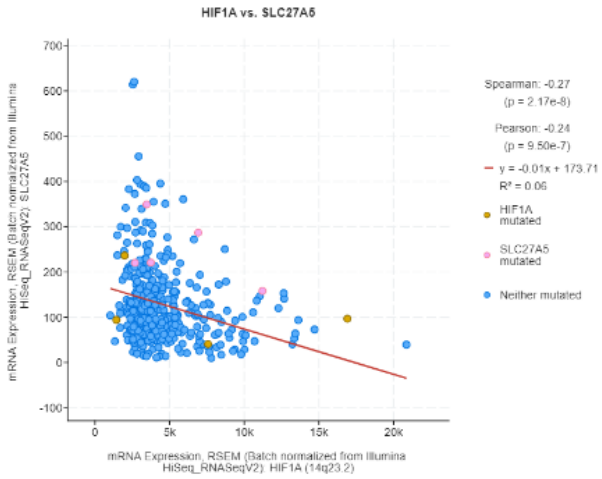

GPI vs. AFMID
mRNA Expression, RSEM (Batch normalized from Illumina HiSeq_RNASeqV2): AFMID
mRNA Expression, RSEM (Batch normalized from Illumina HiSeq_RNASeqV2): GPI (19q13.11)
Spearman: 0.21
(p = 1.314e-5)
Pearson: 0.19
(p = 7.695e-5)
y = 0.02x + 276.15
R² = 0.04
GPI mutated
AFMID mutated
Neither mutated

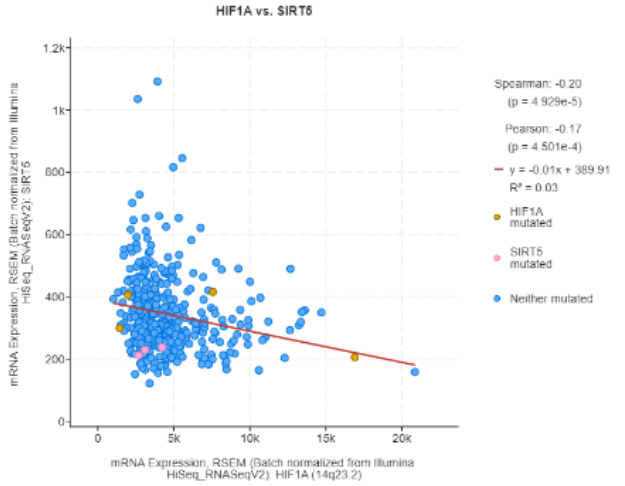

GPI vs. ACO1
mRNA Expression, RSEM (Batch normalized from Illumina HiSeq_RNASeqV2): ACO1
mRNA Expression, RSEM (Batch normalized from Illumina HiSeq_RNASeqV2): GPI (19q13.11)
Spearman: 0.21
(p = 1.556e-5)
Pearson: 0.20
(p = 3.400e-5)
y = 0.04x + 1137.03
R² = 0.04
GPI mutated
ACO1 mutated
Neither mutated

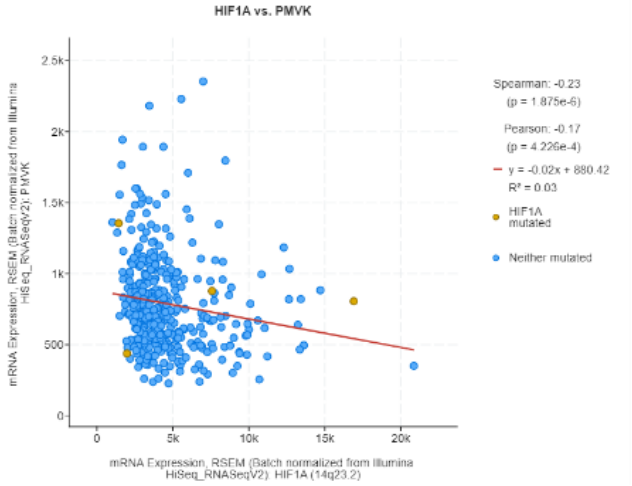

GPI vs. ACAT2
mRNA Expression, RSEM (Batch normalized from Illumina HiSeq_RNASeqV2): ACAT2
mRNA Expression, RSEM (Batch normalized from Illumina HiSeq_RNASeqV2): GPI (19q13.11)
Spearman: 0.33
(p = 5.42e-12)
Pearson: 0.26
(p = 7.37e-8)
y = 0.03x + 434.71
R² = 0.07
GPI mutated
ACAT2 mutated
Both mutated
Neither mutated

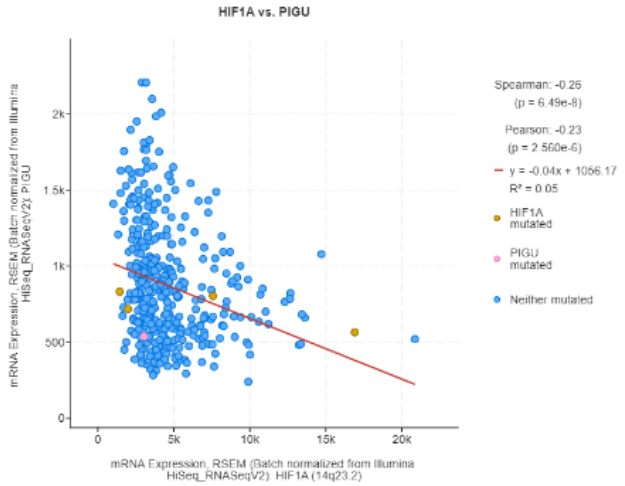
HIF1A

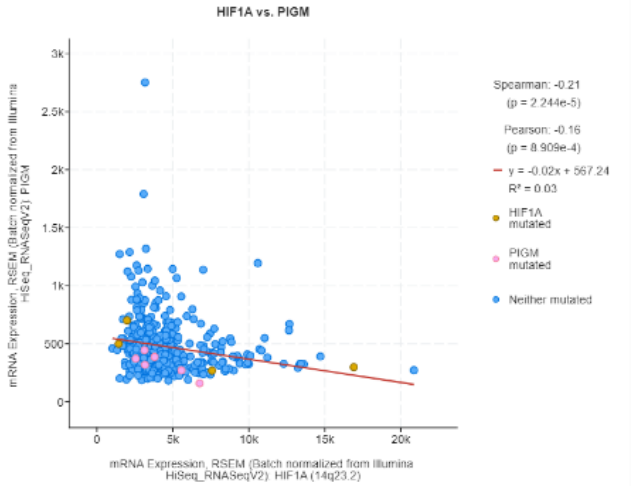

HIF1A vs. SPR
mRNA Expression, RSEM (Batch normalized from Illumina HiSeq_RNASeqV2): SPR
mRNA Expression, RSEM (Batch normalized from Illumina HiSeq_RNASeqV2): HIF1A (14q23.2)
Spearman: -0.21
(p = 1.541e-5)
Pearson: -0.16
(p = 1.138e-3)
y = -0.03x + 1314.38
R² = 0.03
HIF1A mutated
SPR mutated
Neither mutated

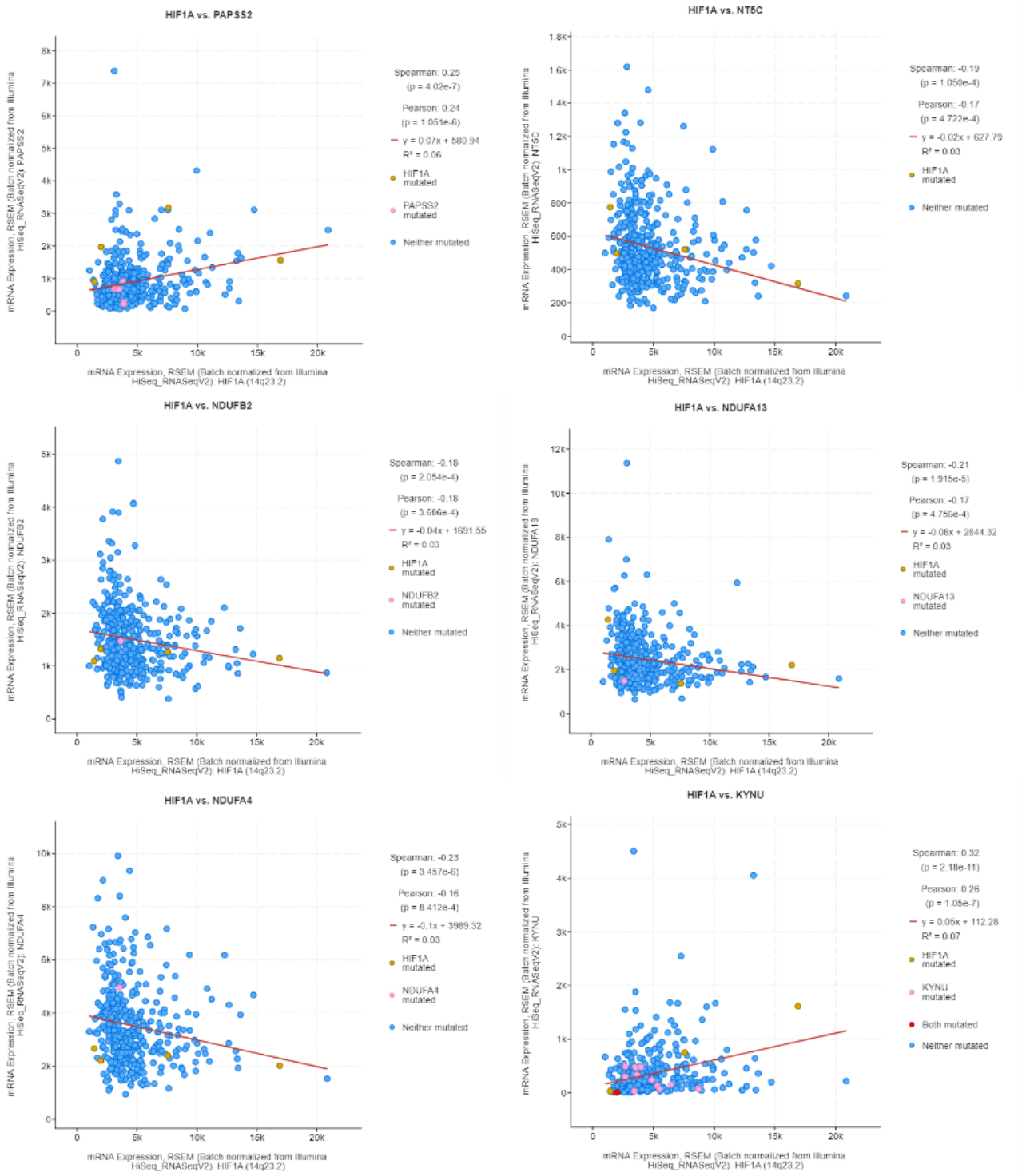

HIF1A vs. SLC27A5
mRNA Expression, RSEM (Batch normalized from Illumina HiSeq_RNASeqV2): SLC27A5
mRNA Expression, RSEM (Batch normalized from Illumina HiSeq_RNASeqV2): HIF1A (14q23.2)
Spearman: -0.27
(p = 2.17e-8)
Pearson: -0.24
(p = 9.50e-7)
y = -0.01x + 173.71
R² = 0.06
HIF1A mutated
SLC27A5 mutated
Neither mutated

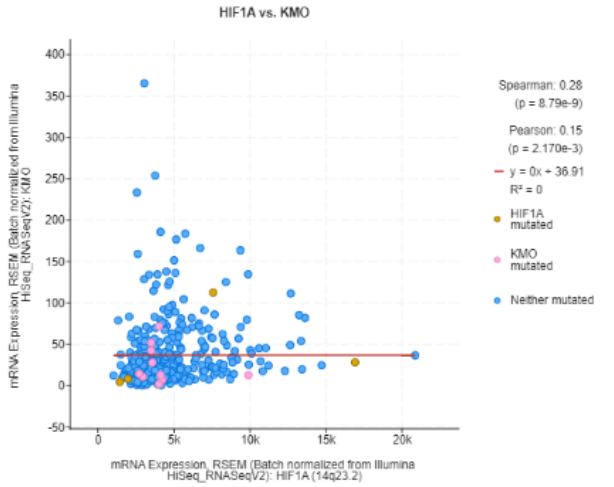

HIF1A vs. SIRT5
mRNA Expression, RSEM (Batch normalized from Illumina HiSeq_RNASeqV2): SIRT5
mRNA Expression, RSEM (Batch normalized from Illumina HiSeq_RNASeqV2): HIF1A (14q23.2)
Spearman: -0.20
(p = 4.929e-5)
Pearson: -0.17
(p = 4.501e-4)
y = -0.01x + 389.91
R² = 0.03
HIF1A mutated
SIRT5 mutated
Neither mutated

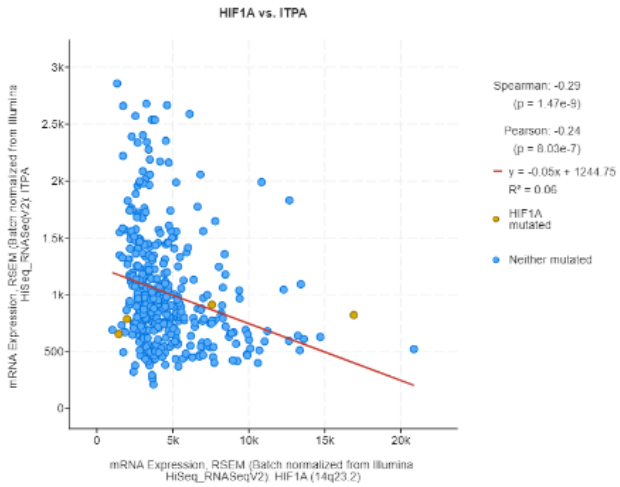

HIF1A vs. PMVK
mRNA Expression, RSEM (Batch normalized from Illumina HiSeq_RNASeqV2): PMVK
mRNA Expression, RSEM (Batch normalized from Illumina HiSeq_RNASeqV2): HIF1A (14q23.2)
Spearman: -0.23
(p = 1.875e-6)
Pearson: -0.17
(p = 4.226e-4)
y = -0.02x + 880.42
R² = 0.03
HIF1A mutated
Neither mutated

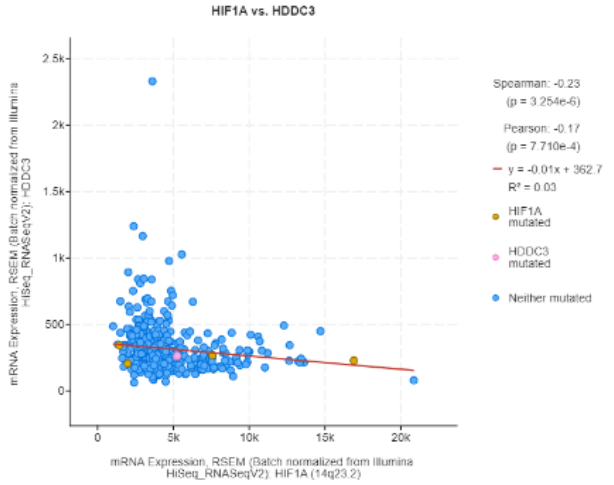

HIF1A vs. PIGU
mRNA Expression, RSEM (Batch normalized from Illumina HiSeq_RNASeqV2): PIGU
mRNA Expression, RSEM (Batch normalized from Illumina HiSeq_RNASeqV2): HIF1A (14q23.2)
Spearman: -0.26
(p = 6.49e-8)
Pearson: -0.23
(p = 2.560e-6)
y = -0.04x + 1056.17
R² = 0.05
HIF1A mutated
PIGU mutated
Neither mutated

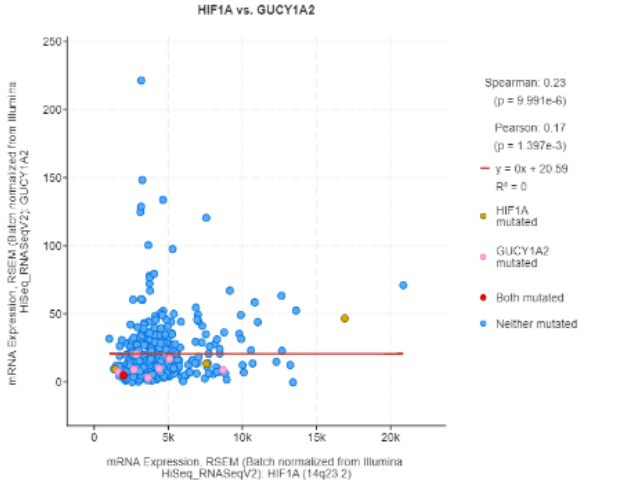

HIF1A vs. PIGM
mRNA Expression, RSEM (Batch normalized from Illumina HiSeq_RNASeqV2): PIGM
mRNA Expression, RSEM (Batch normalized from Illumina HiSeq_RNASeqV2): HIF1A (14q23.2)
Spearman: -0.21
(p = 2.244e-5)
Pearson: -0.16
(p = 8.909e-4)
y = -0.02x + 567.24
R² = 0.03
HIF1A mutated
PIGM mutated
Neither mutated

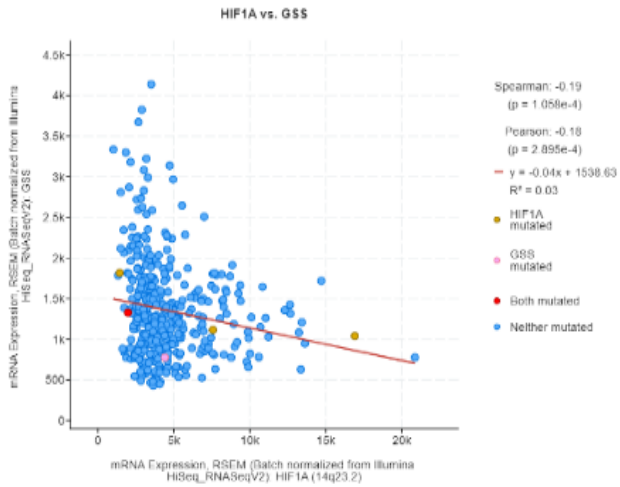

HIF1A vs. PAPSS2
mRNA Expression, RSEM (Batch normalized from Illumina HiSeq_RNASeqV2): PAPSS2
mRNA Expression, RSEM (Batch normalized from Illumina HiSeq_RNASeqV2): HIF1A (14q23.2)
Spearman: 0.25
(p = 4.02e-7)
Pearson: 0.24
(p = 1.051e-6)
y = 0.07x + 580.94
R² = 0.06
HIF1A mutated
PAPSS2 mutated
Neither mutated
HIF1A vs. NT5C
mRNA Expression, RSEM (Batch normalized from Illumina HiSeq_RNASeqV2): NT5C
mRNA Expression, RSEM (Batch normalized from Illumina HiSeq_RNASeqV2): HIF1A (14q23.2)
Spearman: -0.19
(p = 1.050e-4)
Pearson: -0.17
(p = 4.722e-4)
y = -0.02x + 627.79
R² = 0.03
HIF1A mutated
Neither mutated
HIF1A vs. NDUFB2
mRNA Expression, RSEM (Batch normalized from Illumina HiSeq_RNASeqV2): NDUFB2
mRNA Expression, RSEM (Batch normalized from Illumina HiSeq_RNASeqV2): HIF1A (14q23.2)
Spearman: -0.18
(p = 2.054e-4)
Pearson: -0.18
(p = 3.686e-4)
y = -0.04x + 1691.55
R² = 0.03
HIF1A mutated
NDUFB2 mutated
Neither mutated
HIF1A vs. NDUFA13
mRNA Expression, RSEM (Batch normalized from Illumina HiSeq_RNASeqV2): NDUFA13
mRNA Expression, RSEM (Batch normalized from Illumina HiSeq_RNASeqV2): HIF1A (14q23.2)
Spearman: -0.21
(p = 1.915e-5)
Pearson: -0.17
(p = 4.756e-4)
y = -0.08x + 2844.32
R² = 0.03
HIF1A mutated
NDUFA13 mutated
Neither mutated
HIF1A vs. NDUFA4
mRNA Expression, RSEM (Batch normalized from Illumina HiSeq_RNASeqV2): NDUFA4
mRNA Expression, RSEM (Batch normalized from Illumina HiSeq_RNASeqV2): HIF1A (14q23.2)
Spearman: -0.23
(p = 3.457e-6)
Pearson: -0.16
(p = 8.412e-4)
y = -0.1x + 3989.32
R² = 0.03
HIF1A mutated
NDUFA4 mutated
Neither mutated
HIF1A vs. KYNU
mRNA Expression, RSEM (Batch normalized from Illumina HiSeq_RNASeqV2): KYNU
mRNA Expression, RSEM (Batch normalized from Illumina HiSeq_RNASeqV2): HIF1A (14q23.2)
Spearman: 0.32
(p = 2.18e-11)
Pearson: 0.26
(p = 1.05e-7)
y = 0.05x + 112.28
R² = 0.07
HIF1A mutated
KYNU mutated
Both mutated
Neither mutated

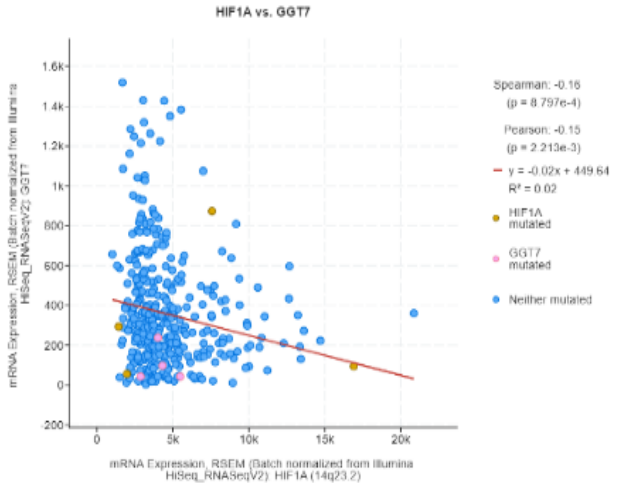

HIF1A vs. KMO
mRNA Expression, RSEM (Batch normalized from Illumina HiSeq_RNASeqV2): KMO
mRNA Expression, RSEM (Batch normalized from Illumina HiSeq_RNASeqV2): HIF1A (14q23.2)
Spearman: 0.28
(p = 8.79e-9)
Pearson: 0.15
(p = 2.170e-3)
y = 0x + 36.91
R² = 0
HIF1A mutated
KMO mutated
Neither mutated

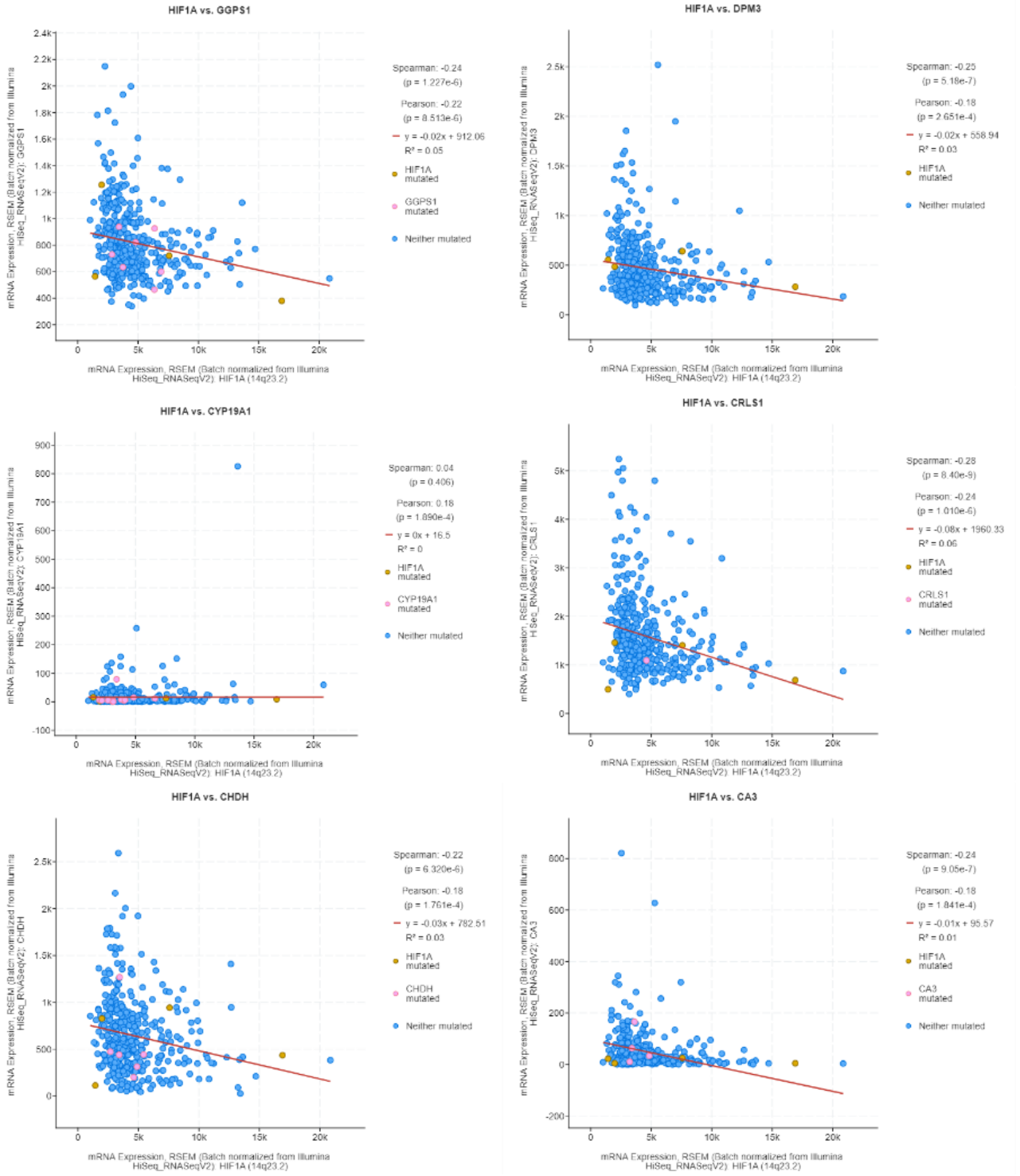

HIF1A vs. ITPA
mRNA Expression, RSEM (Batch normalized from Illumina HiSeq_RNASeqV2): ITPA
mRNA Expression, RSEM (Batch normalized from Illumina HiSeq_RNASeqV2): HIF1A (14q23.2)
Spearman: -0.29
(p = 1.47e-9)
Pearson: -0.24
(p = 8.03e-7)
y = -0.05x + 1244.75
R² = 0.06
HIF1A mutated
Neither mutated

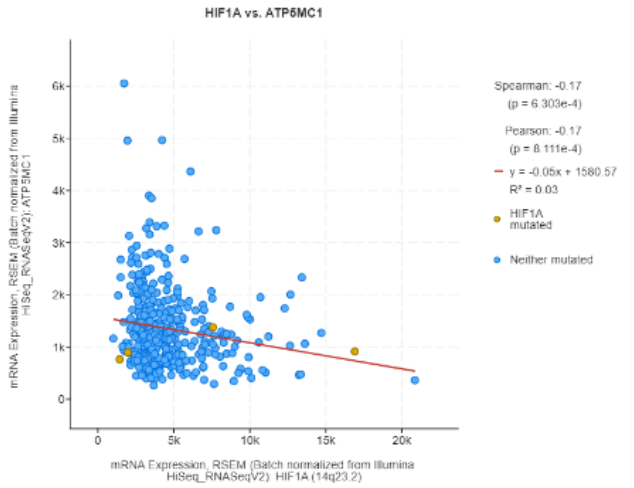

HIF1A vs. HDDC3
mRNA Expression, RSEM (Batch normalized from Illumina HiSeq_RNASeqV2): HDDC3
mRNA Expression, RSEM (Batch normalized from Illumina HiSeq_RNASeqV2): HIF1A (14q23.2)
Spearman: -0.23
(p = 3.254e-6)
Pearson: -0.17
(p = 7.710e-4)
y = -0.01x + 362.7
R² = 0.03
HIF1A mutated
HDDC3 mutated
Neither mutated

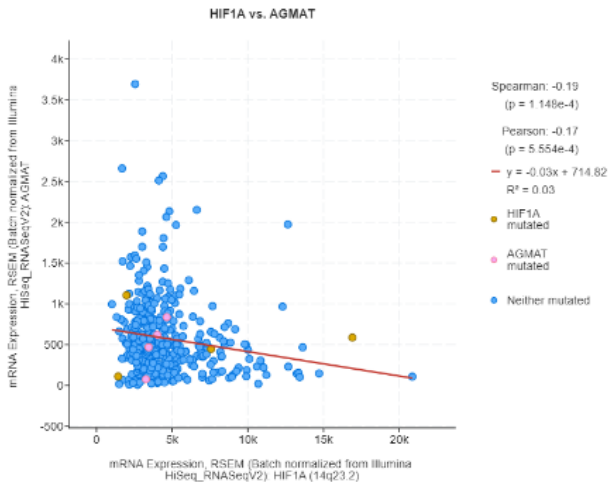

HIF1A vs. GUCY1A2
mRNA Expression, RSEM (Batch normalized from Illumina HiSeq_RNASeqV2): GUCY1A2
mRNA Expression, RSEM (Batch normalized from Illumina HiSeq_RNASeqV2): HIF1A (14q23.2)
Spearman: 0.23
(p = 9.991e-6)
Pearson: 0.17
(p = 1.397e-3)
y = 0x + 20.59
R² = 0
HIF1A mutated
GUCY1A2 mutated
Both mutated
Neither mutated

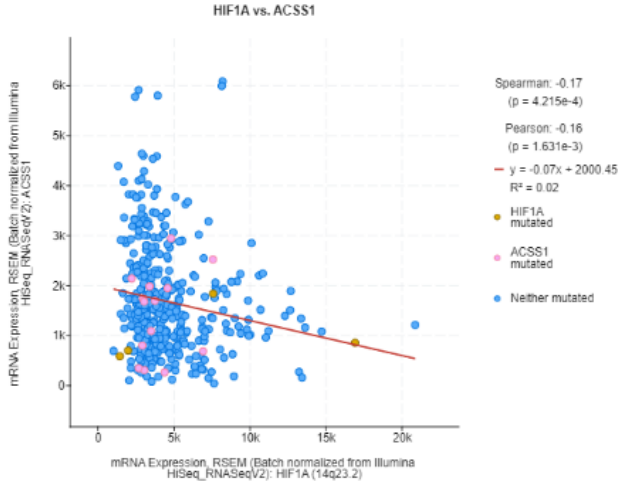

HIF1A vs. GSS
mRNA Expression, RSEM (Batch normalized from Illumina HiSeq_RNASeqV2): GSS
mRNA Expression, RSEM (Batch normalized from Illumina HiSeq_RNASeqV2): HIF1A (14q23.2)
Spearman: -0.19
(p = 1.058e-4)
Pearson: -0.18
(p = 2.895e-4)
y = -0.04x + 1538.63
R² = 0.03
HIF1A mutated
GSS mutated
Both mutated
Neither mutated


HIF1A vs. GGT7
mRNA Expression, RSEM (Batch normalized from Illumina HiSeq_RNASeqV2): GGT7
mRNA Expression, RSEM (Batch normalized from Illumina HiSeq_RNASeqV2): HIF1A (14q23.2)
Spearman: -0.16
(p = 8.797e-4)
Pearson: -0.15
(p = 2.213e-3)
y = -0.02x + 449.64
R² = 0.02
HIF1A mutated
GGT7 mutated
Neither mutated

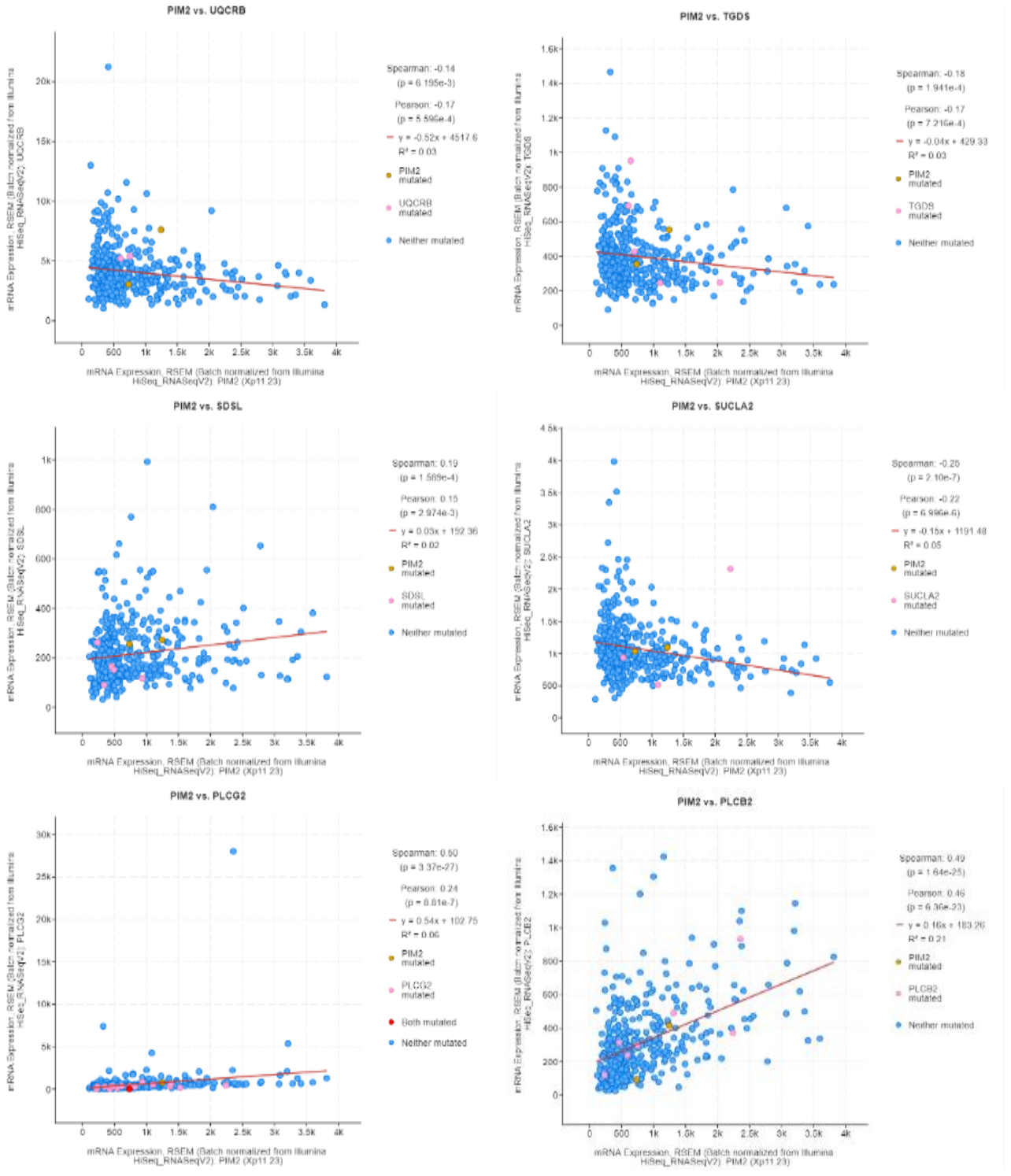

HIF1A vs. GGPS1
mRNA Expression, RSEM (Batch normalized from Illumina HiSeq_RNASeqV2): GGPS1
mRNA Expression, RSEM (Batch normalized from Illumina HiSeq_RNASeqV2): HIF1A (14q23.2)
Spearman: -0.24
(p = 1.227e-6)
Pearson: -0.22
(p = 8.513e-6)
y = -0.02x + 912.06
R² = 0.05
HIF1A mutated
GGPS1 mutated
Neither mutated
HIF1A vs. DPM3
mRNA Expression, RSEM (Batch normalized from Illumina HiSeq_RNASeqV2): DPM3
mRNA Expression, RSEM (Batch normalized from Illumina HiSeq_RNASeqV2): HIF1A (14q23.2)
Spearman: -0.25
(p = 5.18e-7)
Pearson: -0.18
(p = 2.651e-4)
y = -0.02x + 558.94
R² = 0.03
HIF1A mutated
Neither mutated
HIF1A vs. CYP19A1
mRNA Expression, RSEM (Batch normalized from Illumina HiSeq_RNASeqV2): CYP19A1
mRNA Expression, RSEM (Batch normalized from Illumina HiSeq_RNASeqV2): HIF1A (14q23.2)
Spearman: 0.04
(p = 0.406)
Pearson: 0.18
(p = 1.899e-4)
y = 0x + 16.5
R² = 0
HIF1A mutated
CYP19A1 mutated
Neither mutated
HIF1A vs. CRLS1
mRNA Expression, RSEM (Batch normalized from Illumina HiSeq_RNASeqV2): CRLS1
mRNA Expression, RSEM (Batch normalized from Illumina HiSeq_RNASeqV2): HIF1A (14q23.2)
Spearman: -0.28
(p = 8.40e-9)
Pearson: -0.24
(p = 1.010e-6)
y = -0.08x + 1960.33
R² = 0.06
HIF1A mutated
CRLS1 mutated
Neither mutated
HIF1A vs. CHDH
mRNA Expression, RSEM (Batch normalized from Illumina HiSeq_RNASeqV2): CHDH
mRNA Expression, RSEM (Batch normalized from Illumina HiSeq_RNASeqV2): HIF1A (14q23.2)
Spearman: -0.22
(p = 6.320e-6)
Pearson: -0.18
(p = 1.761e-4)
y = -0.03x + 782.51
R² = 0.03
HIF1A mutated
CHDH mutated
Neither mutated
HIF1A vs. CA3
mRNA Expression, RSEM (Batch normalized from Illumina HiSeq_RNASeqV2): CA3
mRNA Expression, RSEM (Batch normalized from Illumina HiSeq_RNASeqV2): HIF1A (14q23.2)
Spearman: -0.24
(p = 9.05e-7)
Pearson: -0.18
(p = 1.841e-4)
y = -0.01x + 95.57
R² = 0.01
HIF1A mutated
CA3 mutated
Neither mutated

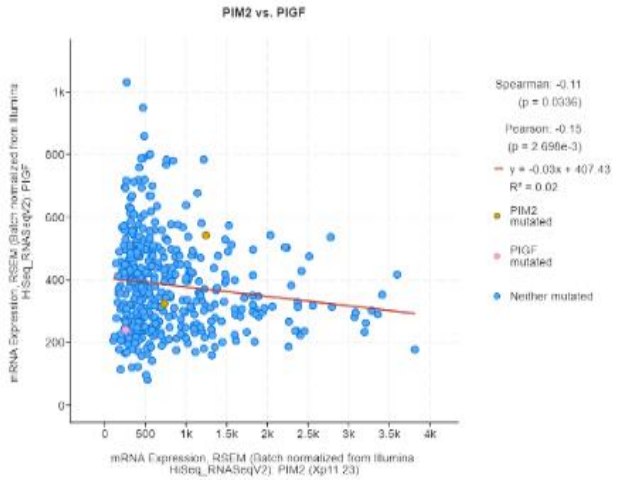

HIF1A vs. ATP5MC1
mRNA Expression, RSEM (Batch normalized from Illumina HiSeq_RNASeqV2): ATP5MC1
mRNA Expression, RSEM (Batch normalized from Illumina HiSeq_RNASeqV2): HIF1A (14q23.2)
Spearman: -0.17
(p = 6.303e-4)
Pearson: -0.17
(p = 8.111e-4)
y = -0.05x + 1580.57
R² = 0.03
HIF1A mutated
Neither mutated

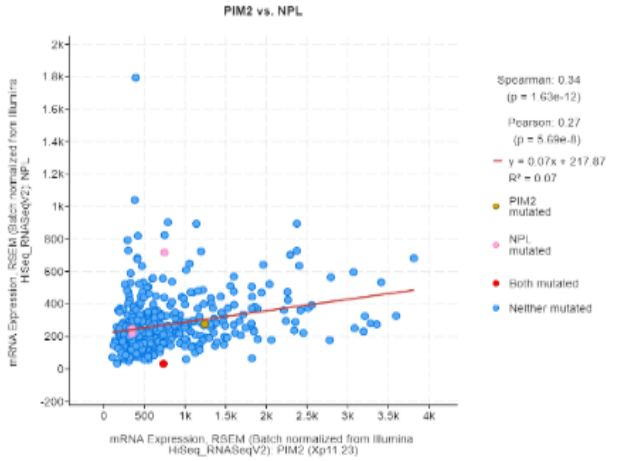

HIF1A vs. AGMAT
mRNA Expression, RSEM (Batch normalized from Illumina HiSeq_RNASeqV2): AGMAT
mRNA Expression, RSEM (Batch normalized from Illumina HiSeq_RNASeqV2): HIF1A (14q23.2)
Spearman: -0.19
(p = 1.148e-4)
Pearson: -0.17
(p = 5.554e-4)
y = -0.03x + 714.82
R² = 0.03
HIF1A mutated
AGMAT mutated
Neither mutated

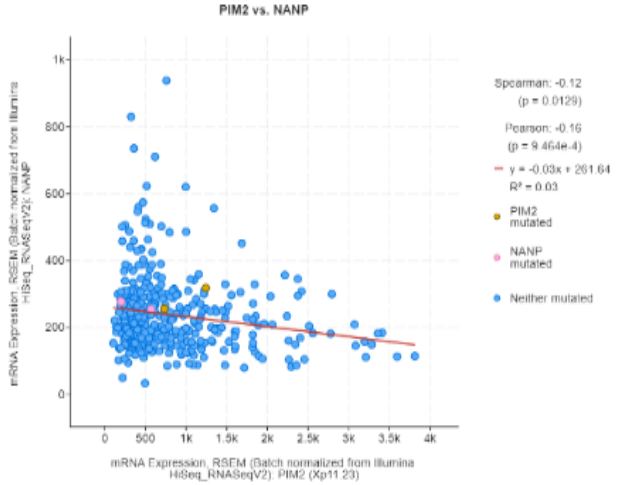

HIF1A vs. ACSS1
mRNA Expression, RSEM (Batch normalized from Illumina HiSeq_RNASeqV2): ACSS1
mRNA Expression, RSEM (Batch normalized from Illumina HiSeq_RNASeqV2): HIF1A (14q23.2)
Spearman: -0.17
(p = 4.215e-4)
Pearson: -0.16
(p = 1.631e-3)
y = -0.07x + 2000.45
R² = 0.02
HIF1A mutated
ACSS1 mutated
Neither mutated

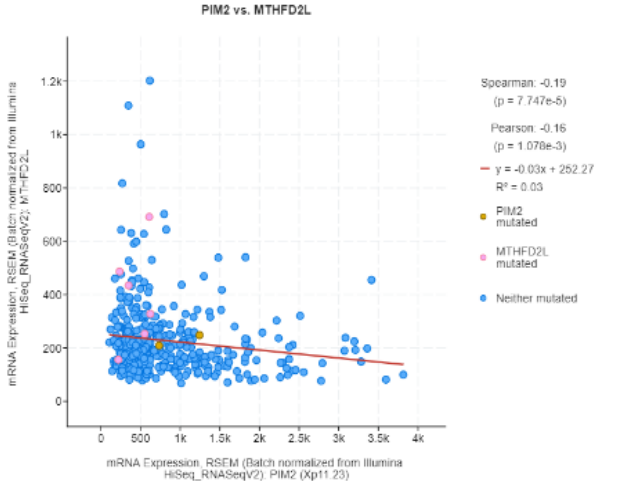
PIM2

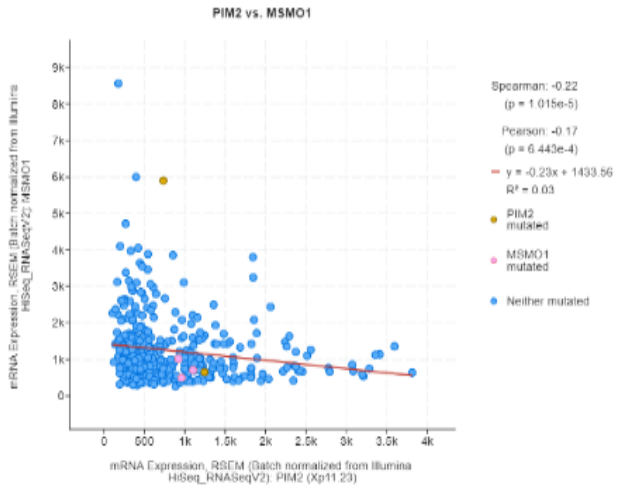

PIM2 vs. UQCRB
Spearman: -0.14
(p = 6.195e-3)
Pearson: -0.17
(p = 5.596e-4)
y = -0.52x + 4517.6
R² = 0.03
PIM2 mutated
UQCRB mutated
Neither mutated
PIM2 vs. TGDS
Spearman: -0.18
(p = 1.941e-4)
Pearson: -0.17
(p = 7.216e-4)
y = -0.04x + 429.33
R² = 0.03
PIM2 mutated
TGDS mutated
Neither mutated
PIM2 vs. SDSL
Spearman: 0.19
(p = 1.569e-4)
Pearson: 0.15
(p = 2.974e-3)
y = 0.03x + 192.36
R² = 0.02
PIM2 mutated
SDSL mutated
Neither mutated
PIM2 vs. SUCLA2
Spearman: -0.25
(p = 2.10e-7)
Pearson: -0.22
(p = 6.986e-6)
y = -0.15x + 1191.48
R² = 0.05
PIM2 mutated
SUCLA2 mutated
Neither mutated
PIM2 vs. PLCG2
Spearman: 0.60
(p = 3.37e-27)
Pearson: 0.24
(p = 8.81e-7)
y = 0.54x + 102.75
R² = 0.06
PIM2 mutated
PLCG2 mutated
Both mutated
Neither mutated
PIM2 vs. PLCB2
Spearman: 0.49
(p = 1.64e-25)
Pearson: 0.46
(p = 6.36e-23)
y = 0.16x + 183.26
R² = 0.21
PIM2 mutated
PLCB2 mutated
Neither mutated
mRNA Expression, RSEM (Batch normalized from Illumina HiSeq_RNASeqV2): PIM2 (Xp11.23)

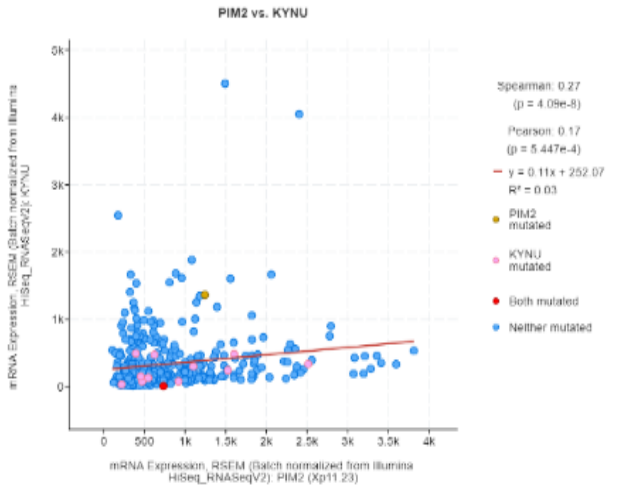

PIM2 vs. PIGF
Spearman: -0.11
(p = 0.0336)
Pearson: -0.15
(p = 2.696e-3)
y = -0.03x + 407.43
R² = 0.02
PIM2 mutated
PIGF mutated
Neither mutated
mRNA Expression, RSEM (Batch normalized from Illumina HiSeq_RNASeqV2): PIM2 (Xp11.23)

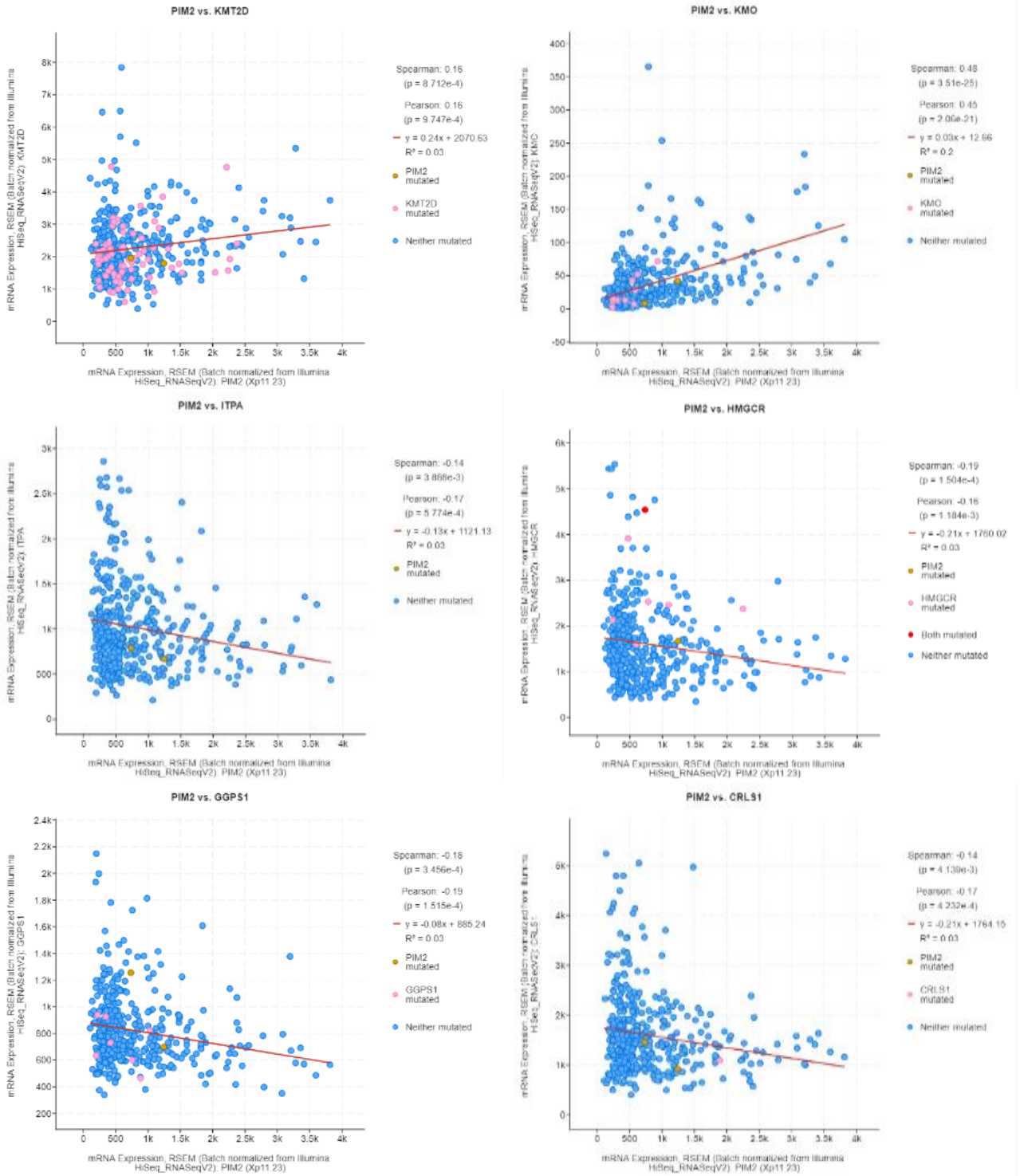

PIM2 vs. NPL
Spearman: 0.34
(p = 1.63e-12)
Pearson: 0.27
(p = 5.69e-8)
y = 0.07x + 217.87
R² = 0.07
PIM2 mutated
NPL mutated
Both mutated
Neither mutated
mRNA Expression, RSEM (Batch normalized from Illumina HiSeq_RNASeqV2): PIM2 (Xp11.23)

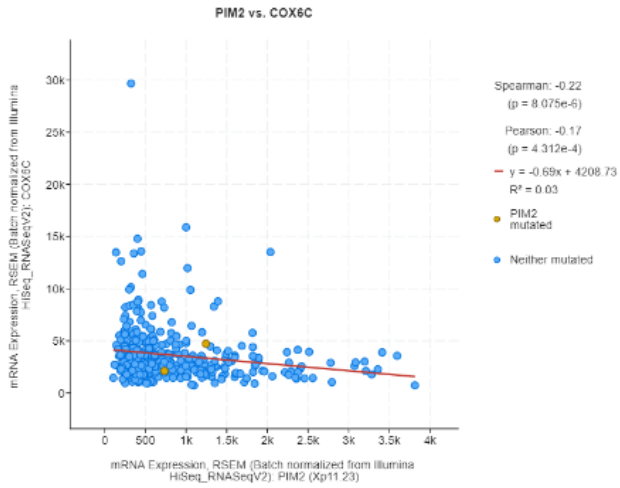

PIM2 vs. NANP
Spearman: -0.12
(p = 0.0129)
Pearson: -0.16
(p = 9.464e-4)
y = -0.03x + 261.64
R² = 0.03
PIM2 mutated
NANP mutated
Neither mutated
mRNA Expression, RSEM (Batch normalized from Illumina HiSeq_RNASeqV2): PIM2 (Xp11.23)

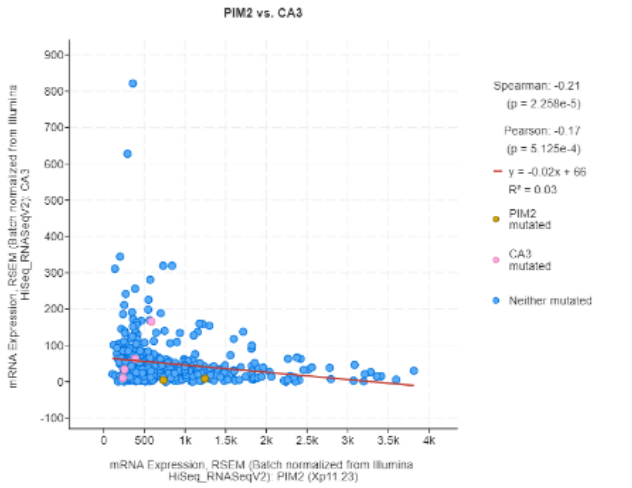

PIM2 vs. MTHFD2L
Spearman: -0.19
(p = 7.747e-5)
Pearson: -0.16
(p = 1.078e-3)
y = -0.03x + 252.27
R² = 0.03
PIM2 mutated
MTHFD2L mutated
Neither mutated
mRNA Expression, RSEM (Batch normalized from Illumina HiSeq_RNASeqV2): PIM2 (Xp11.23)

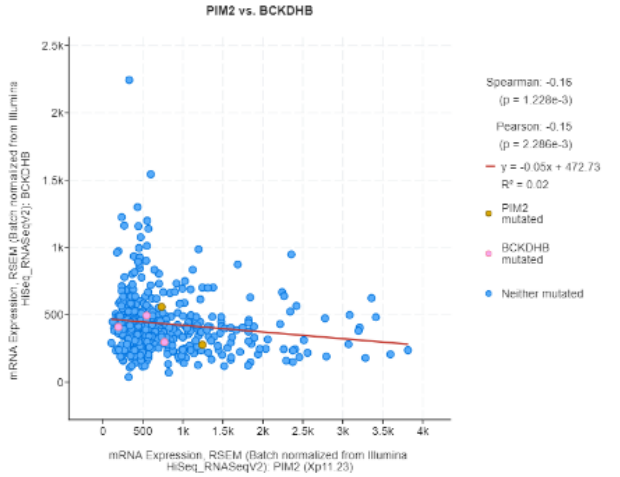

PIM2 vs. MSMO1
Spearman: -0.22
(p = 1.015e-5)
Pearson: -0.17
(p = 6.443e-4)
y = -0.23x + 1433.56
R² = 0.03
PIM2 mutated
MSMO1 mutated
Neither mutated
mRNA Expression, RSEM (Batch normalized from Illumina HiSeq_RNASeqV2): PIM2 (Xp11.23)


PIM2 vs. KYNU
Spearman: 0.27
(p = 4.09e-8)
Pearson: 0.17
(p = 5.447e-4)
y = 0.11x + 252.07
R² = 0.03
PIM2 mutated
KYNU mutated
Both mutated
Neither mutated
mRNA Expression, RSEM (Batch normalized from Illumina HiSeq_RNASeqV2): PIM2 (Xp11.23)

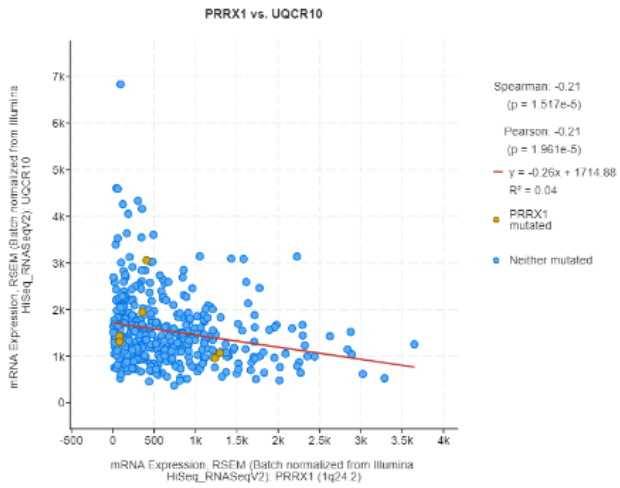

PIM2 vs. KMT2D
mRNA Expression, RSEM (Batch normalized from Illumina HiSeq_RNASeqV2): KMT2D
mRNA Expression, RSEM (Batch normalized from Illumina HiSeq_RNASeqV2): PIM2 (Xp11.23)
Spearman: 0.16
(p = 8.712e-4)
Pearson: 0.16
(p = 9.747e-4)
y = 0.24x + 2070.63
R² = 0.03
PIM2 mutated
KMT2D mutated
Neither mutated
PIM2 vs. KMO
mRNA Expression, RSEM (Batch normalized from Illumina HiSeq_RNASeqV2): KMO
mRNA Expression, RSEM (Batch normalized from Illumina HiSeq_RNASeqV2): PIM2 (Xp11.23)
Spearman: 0.48
(p = 3.51e-25)
Pearson: 0.45
(p = 2.06e-21)
y = 0.03x + 12.66
R² = 0.2
PIM2 mutated
KMO mutated
Neither mutated
PIM2 vs. ITPA
mRNA Expression, RSEM (Batch normalized from Illumina HiSeq_RNASeqV2): ITPA
mRNA Expression, RSEM (Batch normalized from Illumina HiSeq_RNASeqV2): PIM2 (Xp11.23)
Spearman: -0.14
(p = 3.868e-3)
Pearson: -0.17
(p = 5.774e-4)
y = -0.13x + 1121.13
R² = 0.03
PIM2 mutated
Neither mutated
PIM2 vs. HMGCR
mRNA Expression, RSEM (Batch normalized from Illumina HiSeq_RNASeqV2): HMGCR
mRNA Expression, RSEM (Batch normalized from Illumina HiSeq_RNASeqV2): PIM2 (Xp11.23)
Spearman: -0.19
(p = 1.504e-4)
Pearson: -0.16
(p = 1.184e-3)
y = -0.21x + 1760.02
R² = 0.03
PIM2 mutated
HMGCR mutated
Both mutated
Neither mutated
PIM2 vs. GGPS1
mRNA Expression, RSEM (Batch normalized from Illumina HiSeq_RNASeqV2): GGPS1
mRNA Expression, RSEM (Batch normalized from Illumina HiSeq_RNASeqV2): PIM2 (Xp11.23)
Spearman: -0.18
(p = 3.456e-4)
Pearson: -0.19
(p = 1.515e-4)
y = -0.08x + 885.24
R² = 0.03
PIM2 mutated
GGPS1 mutated
Neither mutated
PIM2 vs. CRLS1
mRNA Expression, RSEM (Batch normalized from Illumina HiSeq_RNASeqV2): CRLS1
mRNA Expression, RSEM (Batch normalized from Illumina HiSeq_RNASeqV2): PIM2 (Xp11.23)
Spearman: -0.14
(p = 4.139e-3)
Pearson: -0.17
(p = 4.232e-4)
y = -0.21x + 1764.15
R² = 0.03
PIM2 mutated
CRLS1 mutated
Neither mutated

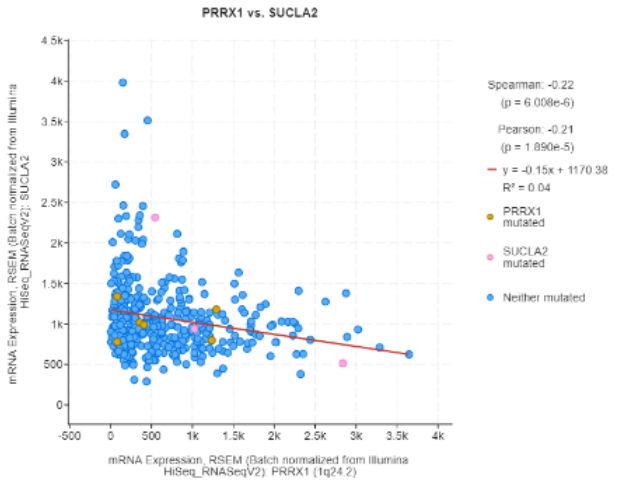

PIM2 vs. COX6C
mRNA Expression, RSEM (Batch normalized from Illumina HiSeq_RNASeqV2): COX6C
mRNA Expression, RSEM (Batch normalized from Illumina HiSeq_RNASeqV2): PIM2 (Xp11.23)
Spearman: -0.22
(p = 8.075e-6)
Pearson: -0.17
(p = 4.312e-4)
y = -0.69x + 4208.73
R² = 0.03
PIM2 mutated
Neither mutated

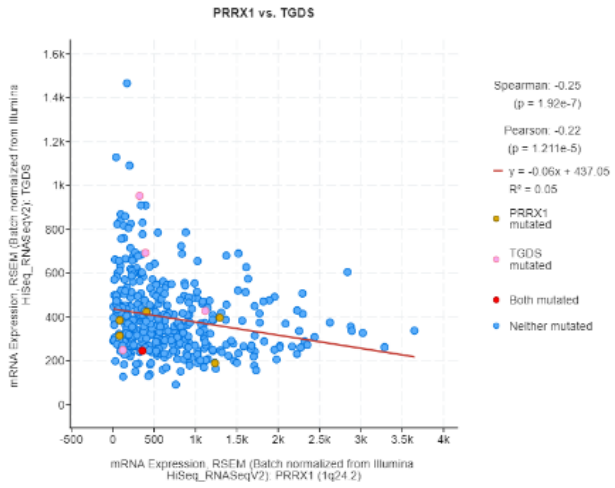

PIM2 vs. CA3
mRNA Expression, RSEM (Batch normalized from Illumina HiSeq_RNASeqV2): CA3
mRNA Expression, RSEM (Batch normalized from Illumina HiSeq_RNASeqV2): PIM2 (Xp11.23)
Spearman: -0.21
(p = 2.258e-5)
Pearson: -0.17
(p = 5.125e-4)
y = -0.02x + 66
R² = 0.03
PIM2 mutated
CA3 mutated
Neither mutated

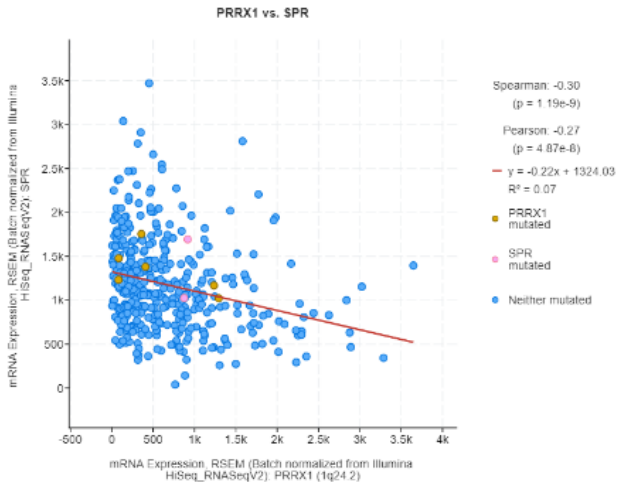

PIM2 vs. BCKDHB
mRNA Expression, RSEM (Batch normalized from Illumina HiSeq_RNASeqV2): BCKDHB
mRNA Expression, RSEM (Batch normalized from Illumina HiSeq_RNASeqV2): PIM2 (Xp11.23)
Spearman: -0.16
(p = 1.228e-3)
Pearson: -0.15
(p = 2.286e-3)
y = -0.05x + 472.73
R² = 0.02
PIM2 mutated
BCKDHB mutated
Neither mutated

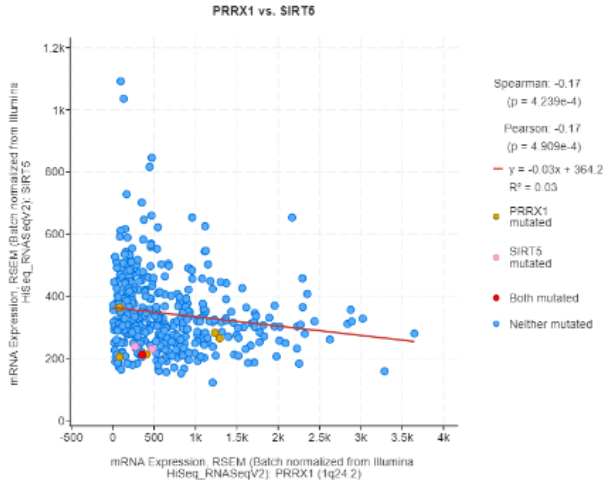
PRRX1

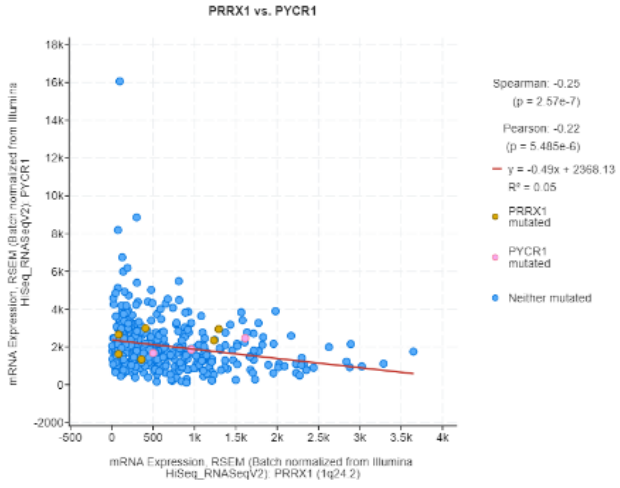

PRRX1 vs. UQCR10
mRNA Expression, RSEM (Batch normalized from Illumina HiSeq_RNASeqV2): UQCR10
mRNA Expression, RSEM (Batch normalized from Illumina HiSeq_RNASeqV2): PRRX1 (1q24.2)
Spearman: -0.21
(p = 1.517e-5)
Pearson: -0.21
(p = 1.961e-5)
y = -0.26x + 1714.88
R² = 0.04
PRRX1 mutated
Neither mutated

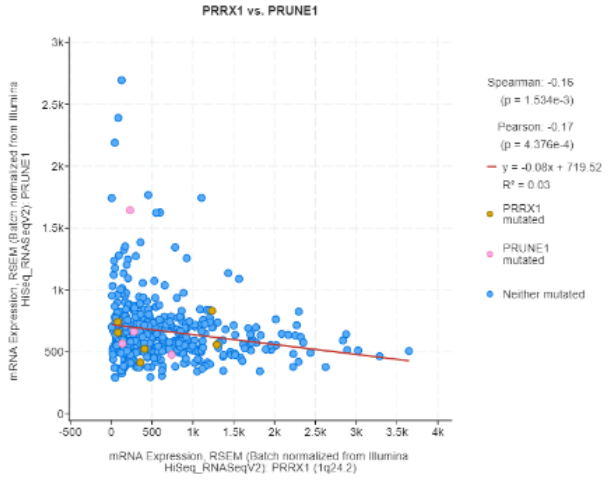

PRRX1 vs. SUCLA2
mRNA Expression, RSEM (Batch normalized from Illumina HiSeq_RNASeqV2): SUCLA2
mRNA Expression, RSEM (Batch normalized from Illumina HiSeq_RNASeqV2): PRRX1 (1q24.2)
Spearman: -0.22
(p = 6.008e-6)
Pearson: -0.21
(p = 1.890e-5)
y = -0.15x + 1170.38
R² = 0.04
PRRX1 mutated
SUCLA2 mutated
Neither mutated

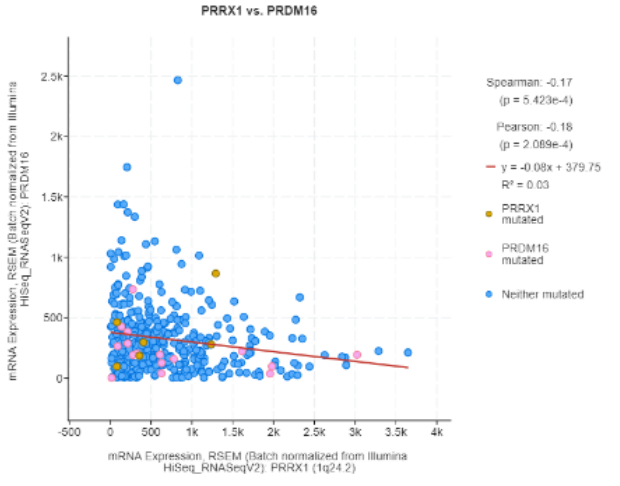

PRRX1 vs. TGDS
mRNA Expression, RSEM (Batch normalized from Illumina HiSeq_RNASeqV2): TGDS
mRNA Expression, RSEM (Batch normalized from Illumina HiSeq_RNASeqV2): PRRX1 (1q24.2)
Spearman: -0.25
(p = 1.92e-7)
Pearson: -0.22
(p = 1.211e-5)
y = -0.06x + 437.05
R² = 0.05
PRRX1 mutated
TGDS mutated
Both mutated
Neither mutated

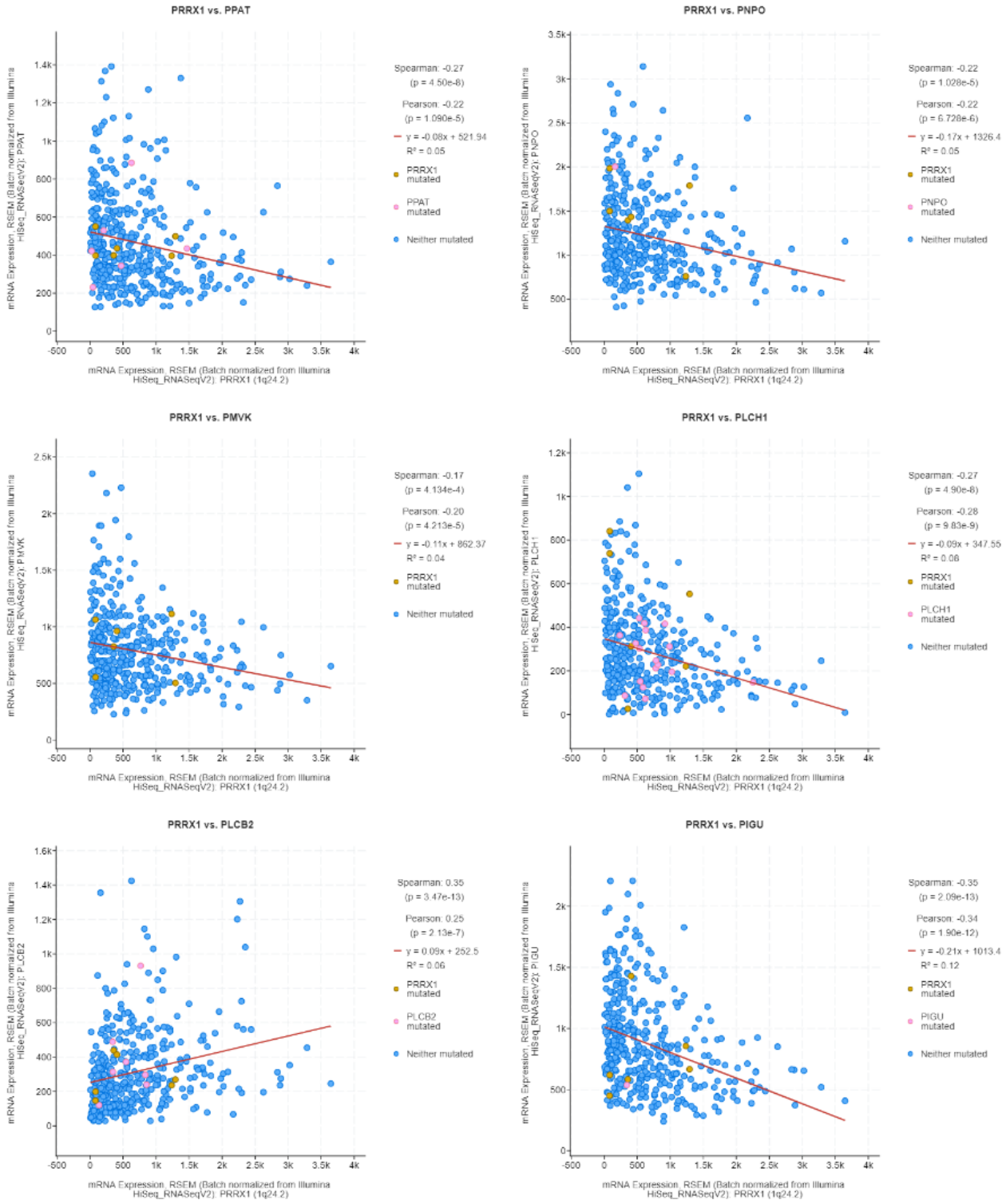

PRRX1 vs. SPR
mRNA Expression, RSEM (Batch normalized from Illumina HiSeq_RNASeqV2): SPR
mRNA Expression, RSEM (Batch normalized from Illumina HiSeq_RNASeqV2): PRRX1 (1q24.2)
Spearman: -0.30
(p = 1.19e-9)
Pearson: -0.27
(p = 4.87e-8)
y = -0.22x + 1324.03
R² = 0.07
PRRX1 mutated
SPR mutated
Neither mutated

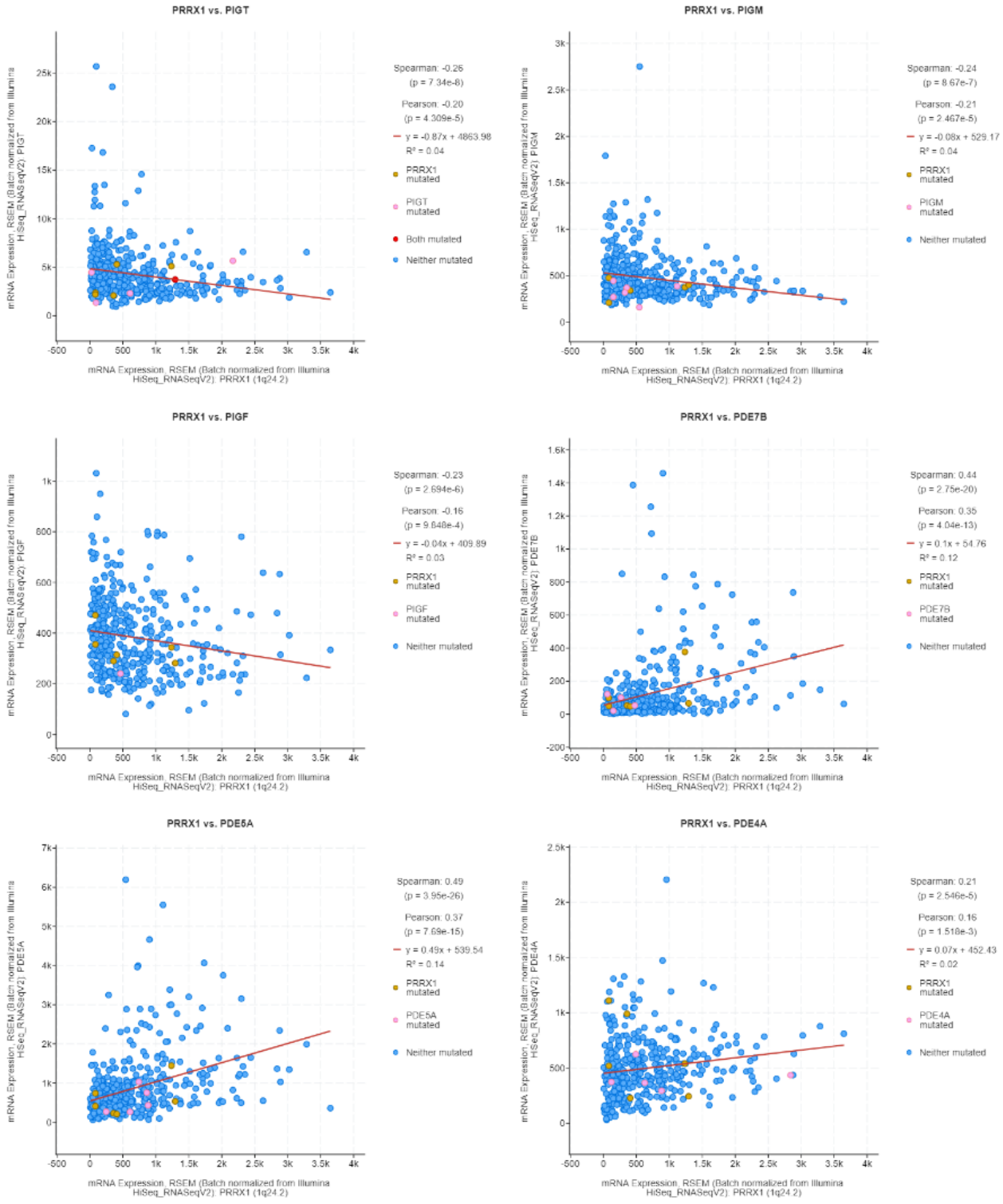

PRRX1 vs. SIRT5
mRNA Expression, RSEM (Batch normalized from Illumina HiSeq_RNASeqV2): SIRT5
mRNA Expression, RSEM (Batch normalized from Illumina HiSeq_RNASeqV2): PRRX1 (1q24.2)
Spearman: -0.17
(p = 4.239e-4)
Pearson: -0.17
(p = 4.909e-4)
y = -0.03x + 364.2
R² = 0.03
PRRX1 mutated
SIRT5 mutated
Both mutated
Neither mutated

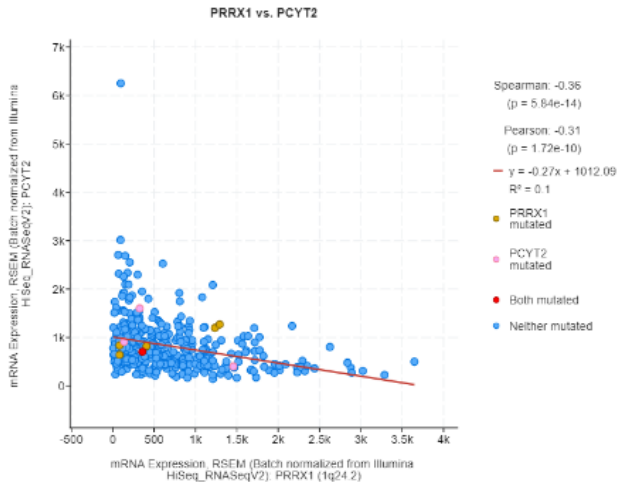

PRRX1 vs. PYCR1
mRNA Expression, RSEM (Batch normalized from Illumina HiSeq_RNASeqV2): PYCR1
mRNA Expression, RSEM (Batch normalized from Illumina HiSeq_RNASeqV2): PRRX1 (1q24.2)
Spearman: -0.25
(p = 2.57e-7)
Pearson: -0.22
(p = 5.485e-6)
y = -0.49x + 2368.13
R² = 0.05
PRRX1 mutated
PYCR1 mutated
Neither mutated

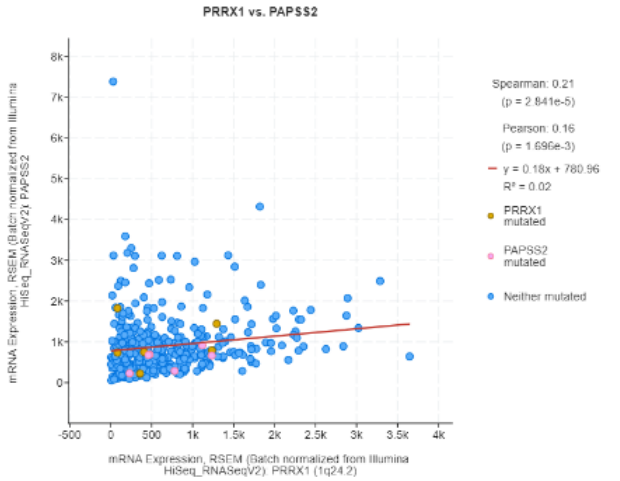

PRRX1 vs. PRUNE1
mRNA Expression, RSEM (Batch normalized from Illumina HiSeq_RNASeqV2): PRUNE1
mRNA Expression, RSEM (Batch normalized from Illumina HiSeq_RNASeqV2): PRRX1 (1q24.2)
Spearman: -0.16
(p = 1.534e-3)
Pearson: -0.17
(p = 4.376e-4)
y = -0.08x + 719.52
R² = 0.03
PRRX1 mutated
PRUNE1 mutated
Neither mutated

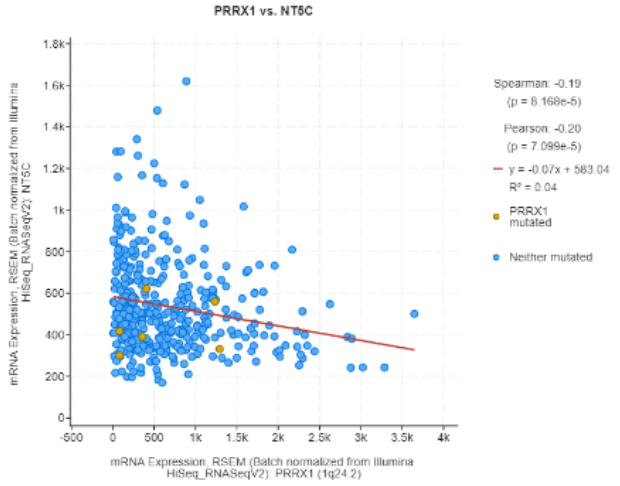

PRRX1 vs. PRDM16
mRNA Expression, RSEM (Batch normalized from Illumina HiSeq_RNASeqV2): PRDM16
mRNA Expression, RSEM (Batch normalized from Illumina HiSeq_RNASeqV2): PRRX1 (1q24.2)
Spearman: -0.17
(p = 5.423e-4)
Pearson: -0.18
(p = 2.089e-4)
y = -0.08x + 379.75
R² = 0.03
PRRX1 mutated
PRDM16 mutated
Neither mutated

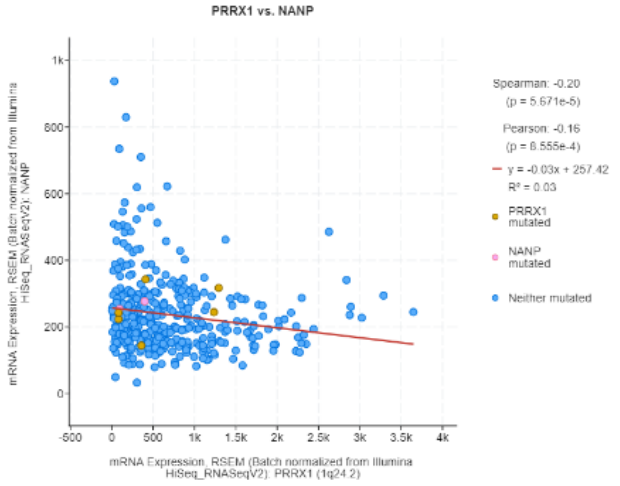

PRRX1 vs. PPAT
mRNA Expression, RSEM (Batch normalized from Illumina HiSeq_RNASeqV2): PPAT
mRNA Expression, RSEM (Batch normalized from Illumina HiSeq_RNASeqV2): PRRX1 (1q24.2)
Spearman: -0.27
(p = 4.50e-8)
Pearson: -0.22
(p = 1.090e-5)
y = -0.08x + 521.94
R² = 0.05
PRRX1 mutated
PPAT mutated
Neither mutated
PRRX1 vs. PNPO
mRNA Expression, RSEM (Batch normalized from Illumina HiSeq_RNASeqV2): PNPO
mRNA Expression, RSEM (Batch normalized from Illumina HiSeq_RNASeqV2): PRRX1 (1q24.2)
Spearman: -0.22
(p = 1.028e-5)
Pearson: -0.22
(p = 6.728e-6)
y = -0.17x + 1326.4
R² = 0.05
PRRX1 mutated
PNPO mutated
Neither mutated
PRRX1 vs. PMVK
mRNA Expression, RSEM (Batch normalized from Illumina HiSeq_RNASeqV2): PMVK
mRNA Expression, RSEM (Batch normalized from Illumina HiSeq_RNASeqV2): PRRX1 (1q24.2)
Spearman: -0.17
(p = 4.134e-4)
Pearson: -0.20
(p = 4.213e-5)
y = -0.11x + 862.37
R² = 0.04
PRRX1 mutated
Neither mutated
PRRX1 vs. PLCH1
mRNA Expression, RSEM (Batch normalized from Illumina HiSeq_RNASeqV2): PLCH1
mRNA Expression, RSEM (Batch normalized from Illumina HiSeq_RNASeqV2): PRRX1 (1q24.2)
Spearman: -0.27
(p = 4.90e-8)
Pearson: -0.28
(p = 9.83e-9)
y = -0.09x + 347.55
R² = 0.08
PRRX1 mutated
PLCH1 mutated
Neither mutated
PRRX1 vs. PLCB2
mRNA Expression, RSEM (Batch normalized from Illumina HiSeq_RNASeqV2): PLCB2
mRNA Expression, RSEM (Batch normalized from Illumina HiSeq_RNASeqV2): PRRX1 (1q24.2)
Spearman: 0.35
(p = 3.47e-13)
Pearson: 0.25
(p = 2.13e-7)
y = 0.09x + 252.5
R² = 0.06
PRRX1 mutated
PLCB2 mutated
Neither mutated
PRRX1 vs. PIGU
mRNA Expression, RSEM (Batch normalized from Illumina HiSeq_RNASeqV2): PIGU
mRNA Expression, RSEM (Batch normalized from Illumina HiSeq_RNASeqV2): PRRX1 (1q24.2)
Spearman: -0.35
(p = 2.09e-13)
Pearson: -0.34
(p = 1.90e-12)
y = -0.21x + 1013.4
R² = 0.12
PRRX1 mutated
PIGU mutated
Neither mutated

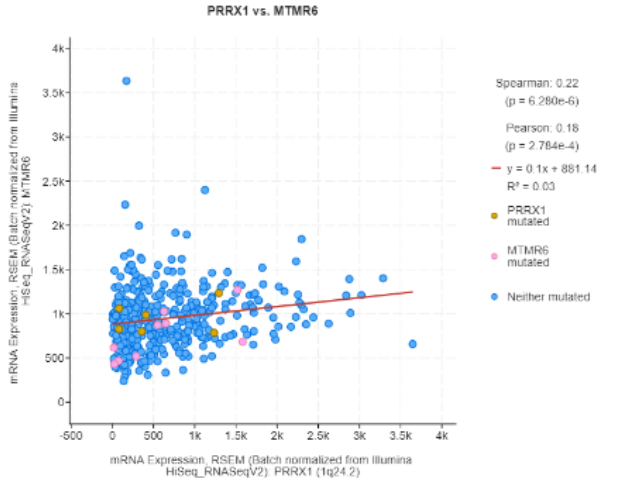

PRRX1 vs. PIGT
mRNA Expression, RSEM (Batch normalized from Illumina HiSeq_RNASeqV2): PIGT
mRNA Expression, RSEM (Batch normalized from Illumina HiSeq_RNASeqV2): PRRX1 (1q24.2)
Spearman: -0.26
(p = 7.34e-8)
Pearson: -0.20
(p = 4.309e-5)
y = -0.87x + 4863.98
R² = 0.04
PRRX1 mutated
PIGT mutated
Both mutated
Neither mutated
PRRX1 vs. PIGM
mRNA Expression, RSEM (Batch normalized from Illumina HiSeq_RNASeqV2): PIGM
mRNA Expression, RSEM (Batch normalized from Illumina HiSeq_RNASeqV2): PRRX1 (1q24.2)
Spearman: -0.24
(p = 8.67e-7)
Pearson: -0.21
(p = 2.467e-5)
y = -0.08x + 529.17
R² = 0.04
PRRX1 mutated
PIGM mutated
Neither mutated
PRRX1 vs. PIGF
mRNA Expression, RSEM (Batch normalized from Illumina HiSeq_RNASeqV2): PIGF
mRNA Expression, RSEM (Batch normalized from Illumina HiSeq_RNASeqV2): PRRX1 (1q24.2)
Spearman: -0.23
(p = 2.684e-6)
Pearson: -0.16
(p = 9.648e-4)
y = -0.04x + 409.89
R² = 0.03
PRRX1 mutated
PIGF mutated
Neither mutated
PRRX1 vs. PDE7B
mRNA Expression, RSEM (Batch normalized from Illumina HiSeq_RNASeqV2): PDE7B
mRNA Expression, RSEM (Batch normalized from Illumina HiSeq_RNASeqV2): PRRX1 (1q24.2)
Spearman: 0.44
(p = 2.75e-20)
Pearson: 0.35
(p = 4.04e-13)
y = 0.1x + 54.76
R² = 0.12
PRRX1 mutated
PDE7B mutated
Neither mutated
PRRX1 vs. PDE5A
mRNA Expression, RSEM (Batch normalized from Illumina HiSeq_RNASeqV2): PDE5A
mRNA Expression, RSEM (Batch normalized from Illumina HiSeq_RNASeqV2): PRRX1 (1q24.2)
Spearman: 0.49
(p = 3.95e-26)
Pearson: 0.37
(p = 7.69e-15)
y = 0.49x + 539.54
R² = 0.14
PRRX1 mutated
PDE5A mutated
Neither mutated
PRRX1 vs. PDE4A
mRNA Expression, RSEM (Batch normalized from Illumina HiSeq_RNASeqV2): PDE4A
mRNA Expression, RSEM (Batch normalized from Illumina HiSeq_RNASeqV2): PRRX1 (1q24.2)
Spearman: 0.21
(p = 2.546e-5)
Pearson: 0.16
(p = 1.518e-3)
y = 0.07x + 452.43
R² = 0.02
PRRX1 mutated
PDE4A mutated
Neither mutated

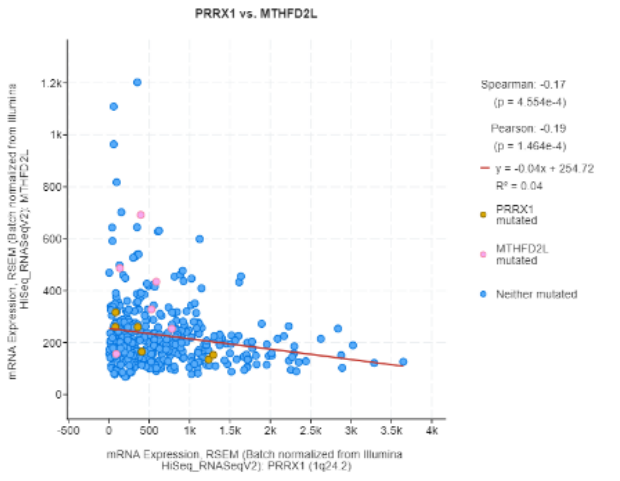

PRRX1 vs. PCYT2
mRNA Expression, RSEM (Batch normalized from Illumina HiSeq_RNASeqV2): PCYT2
mRNA Expression, RSEM (Batch normalized from Illumina HiSeq_RNASeqV2): PRRX1 (1q24.2)
Spearman: -0.36
(p = 5.84e-14)
Pearson: -0.31
(p = 1.72e-10)
y = -0.27x + 1012.09
R² = 0.1
PRRX1 mutated
PCYT2 mutated
Both mutated
Neither mutated

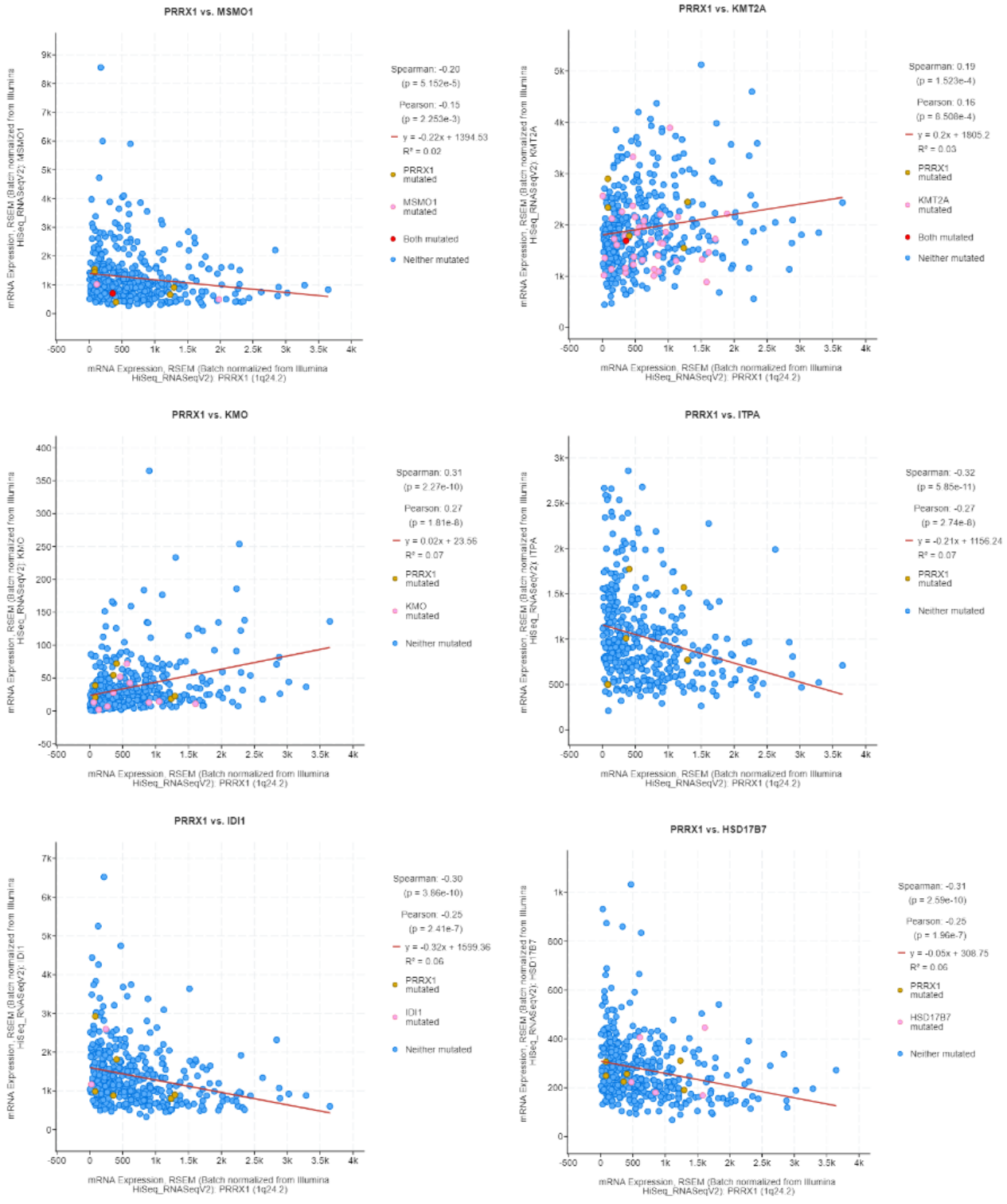

PRRX1 vs. PAPSS2
mRNA Expression, RSEM (Batch normalized from Illumina HiSeq_RNASeqV2): PAPSS2
mRNA Expression, RSEM (Batch normalized from Illumina HiSeq_RNASeqV2): PRRX1 (1q24.2)
Spearman: 0.21
(p = 2.841e-5)
Pearson: 0.16
(p = 1.696e-3)
y = 0.18x + 780.96
R² = 0.02
PRRX1 mutated
PAPSS2 mutated
Neither mutated

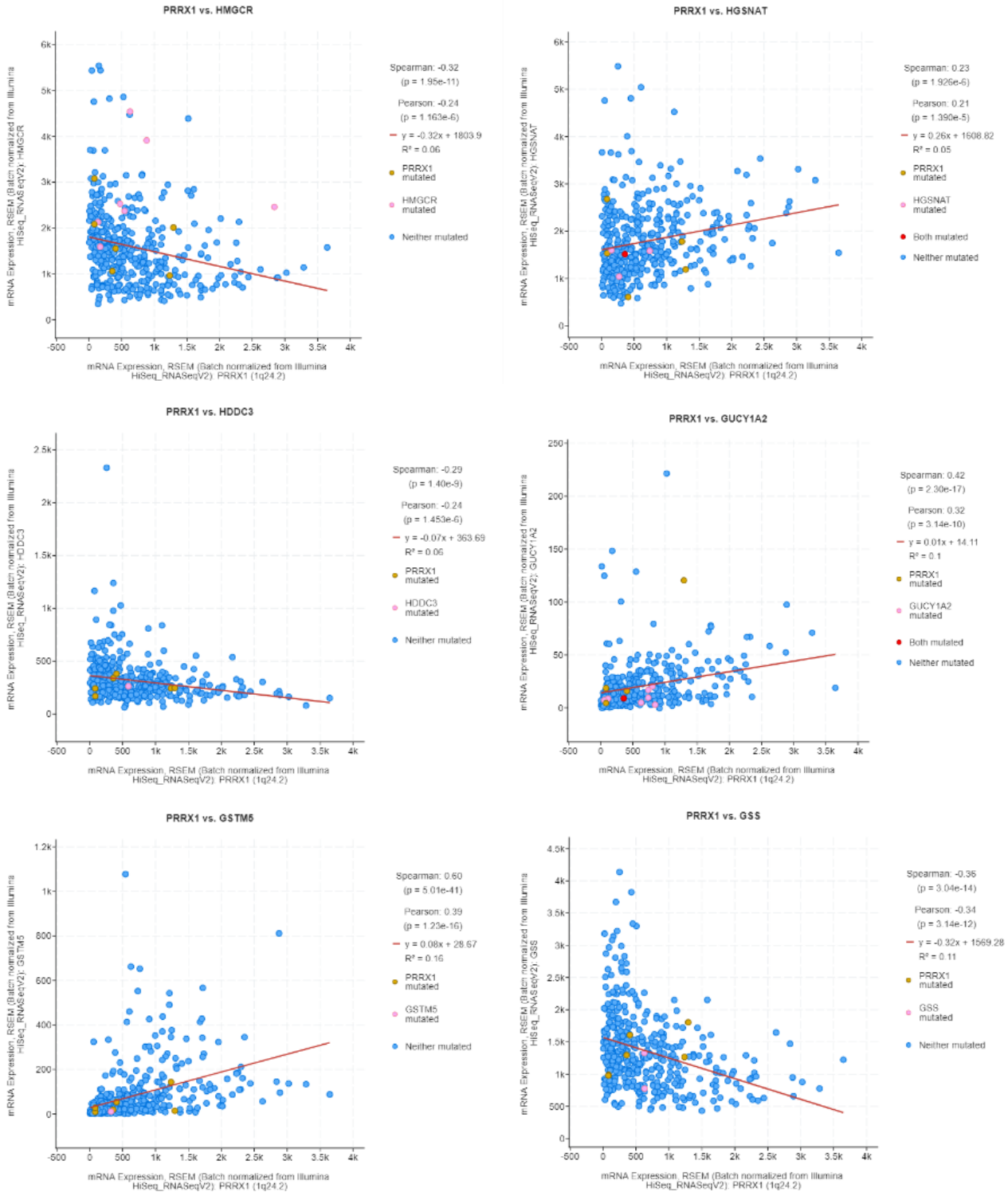

PRRX1 vs. NT5C
mRNA Expression, RSEM (Batch normalized from Illumina HiSeq_RNASeqV2): NT5C
mRNA Expression, RSEM (Batch normalized from Illumina HiSeq_RNASeqV2): PRRX1 (1q24.2)
Spearman: -0.19
(p = 8.168e-5)
Pearson: -0.20
(p = 7.099e-5)
y = -0.07x + 583.04
R² = 0.04
PRRX1 mutated
Neither mutated

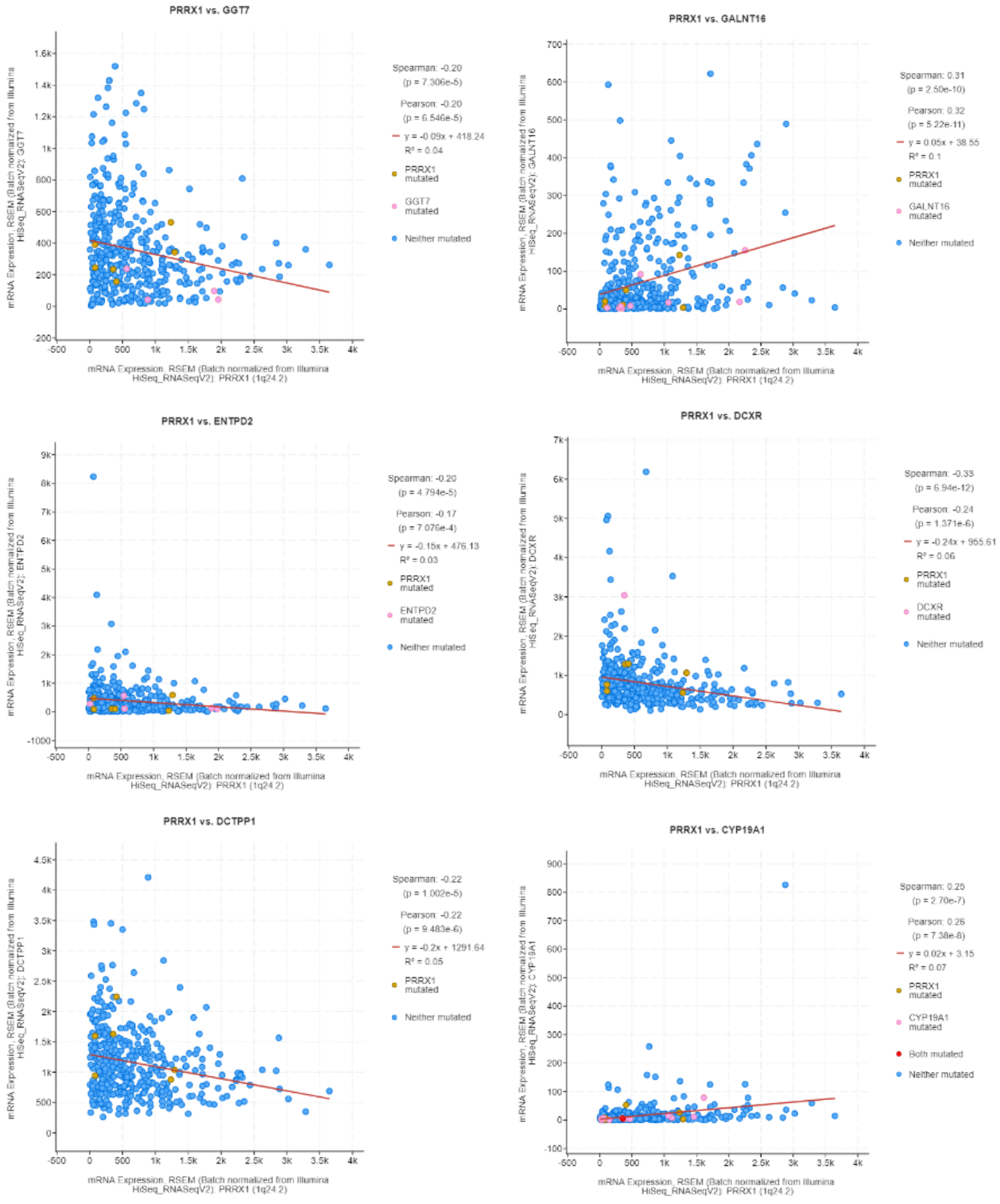

PRRX1 vs. NANP
mRNA Expression, RSEM (Batch normalized from Illumina HiSeq_RNASeqV2): NANP
mRNA Expression, RSEM (Batch normalized from Illumina HiSeq_RNASeqV2): PRRX1 (1q24.2)
Spearman: -0.20
(p = 5.671e-5)
Pearson: -0.16
(p = 8.555e-4)
y = -0.03x + 257.42
R² = 0.03
PRRX1 mutated
NANP mutated
Neither mutated

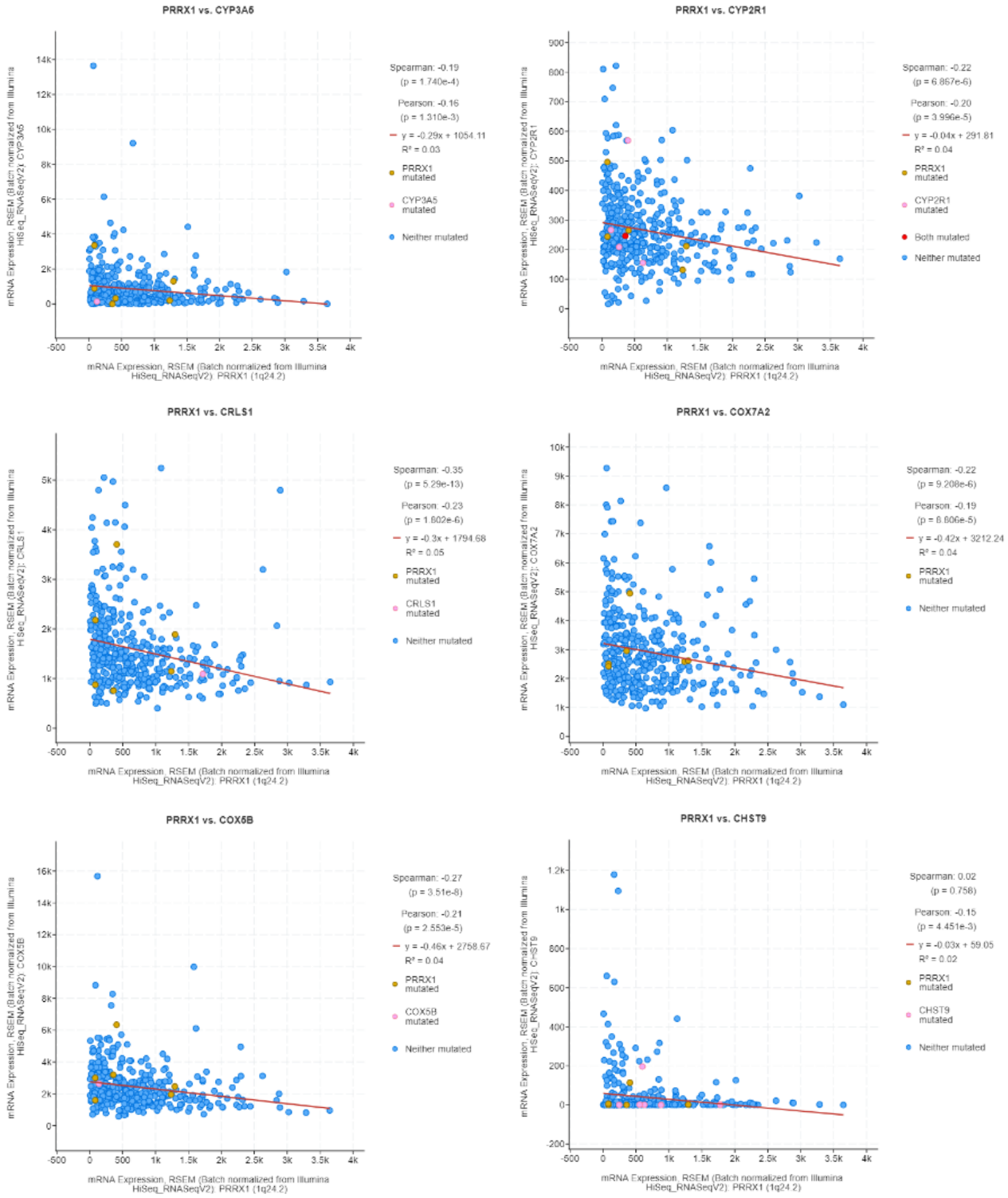

PRRX1 vs. MTMR6
mRNA Expression, RSEM (Batch normalized from Illumina HiSeq_RNASeqV2): MTMR6
mRNA Expression, RSEM (Batch normalized from Illumina HiSeq_RNASeqV2): PRRX1 (1q24.2)
Spearman: 0.22
(p = 6.280e-6)
Pearson: 0.18
(p = 2.784e-4)
y = 0.1x + 881.14
R² = 0.03
PRRX1 mutated
MTMR6 mutated
Neither mutated

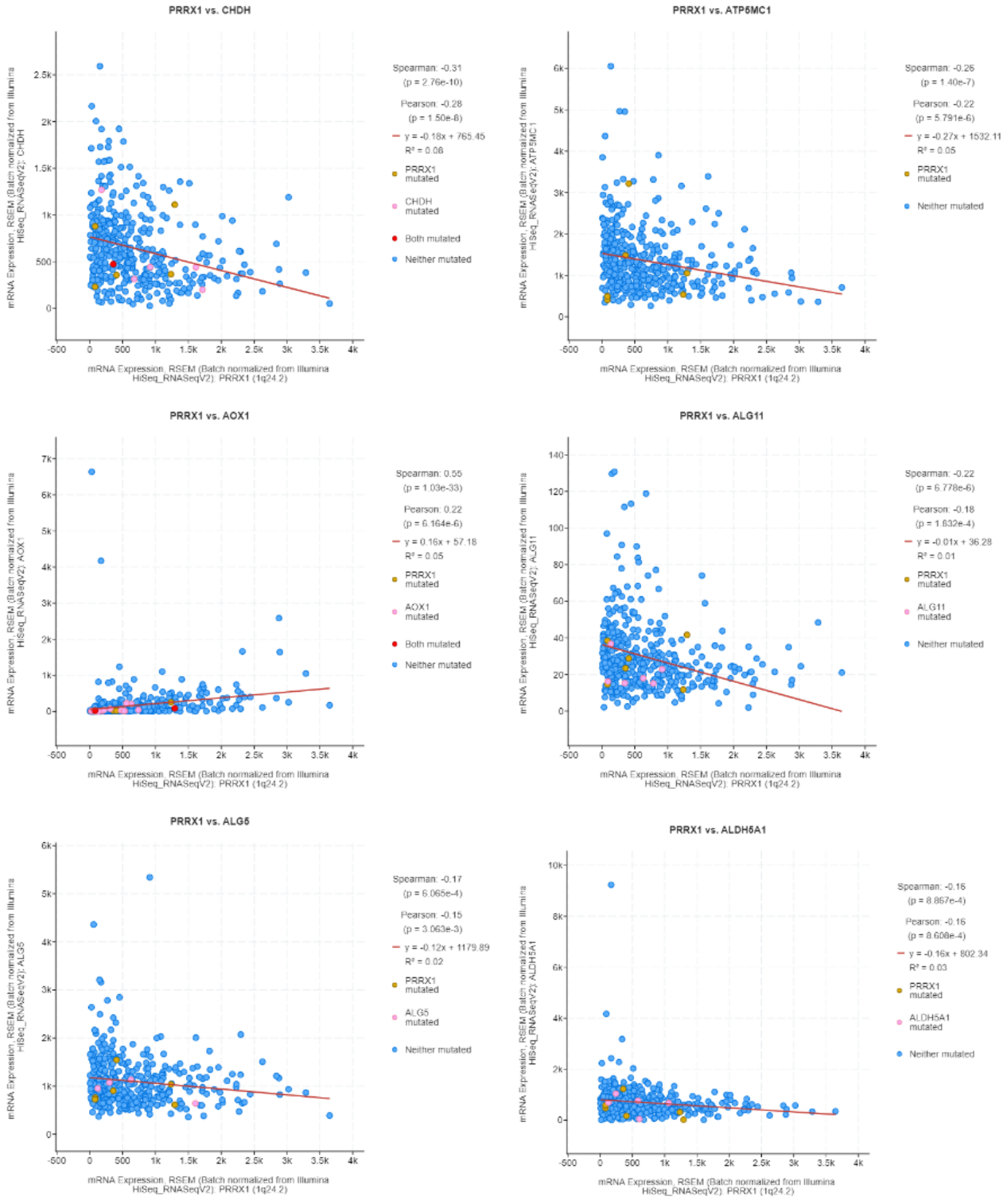

PRRX1 vs. MTHFD2L
mRNA Expression, RSEM (Batch normalized from Illumina HiSeq_RNASeqV2): MTHFD2L
mRNA Expression, RSEM (Batch normalized from Illumina HiSeq_RNASeqV2): PRRX1 (1q24.2)
Spearman: -0.17
(p = 4.554e-4)
Pearson: -0.19
(p = 1.464e-4)
y = -0.04x + 254.72
R² = 0.04
PRRX1 mutated
MTHFD2L mutated
Neither mutated

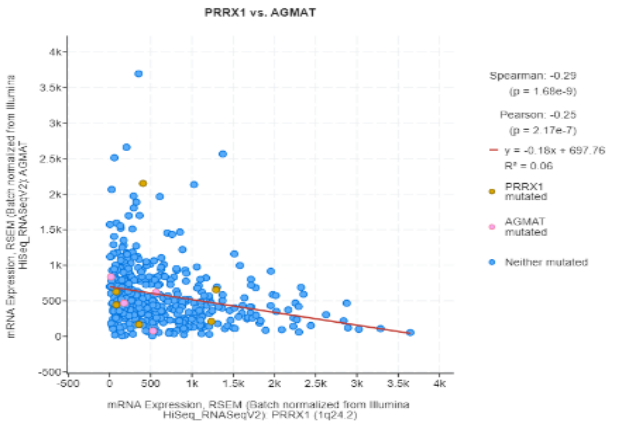

PRRX1 vs. MSMO1
mRNA Expression, RSEM (Batch normalized from Illumina HiSeq_RNASeqV2): MSMO1
mRNA Expression, RSEM (Batch normalized from Illumina HiSeq_RNASeqV2): PRRX1 (1q24.2)
Spearman: -0.20
(p = 5.152e-5)
Pearson: -0.15
(p = 2.253e-3)
y = -0.22x + 1394.53
R² = 0.02
PRRX1 mutated
MSMO1 mutated
Both mutated
Neither mutated
PRRX1 vs. KMT2A
mRNA Expression, RSEM (Batch normalized from Illumina HiSeq_RNASeqV2): KMT2A
mRNA Expression, RSEM (Batch normalized from Illumina HiSeq_RNASeqV2): PRRX1 (1q24.2)
Spearman: 0.19
(p = 1.523e-4)
Pearson: 0.16
(p = 6.508e-4)
y = 0.2x + 1805.2
R² = 0.03
PRRX1 mutated
KMT2A mutated
Both mutated
Neither mutated
PRRX1 vs. KMO
mRNA Expression, RSEM (Batch normalized from Illumina HiSeq_RNASeqV2): KMO
mRNA Expression, RSEM (Batch normalized from Illumina HiSeq_RNASeqV2): PRRX1 (1q24.2)
Spearman: 0.31
(p = 2.27e-10)
Pearson: 0.27
(p = 1.81e-8)
y = 0.02x + 23.56
R² = 0.07
PRRX1 mutated
KMO mutated
Neither mutated
PRRX1 vs. ITPA
mRNA Expression, RSEM (Batch normalized from Illumina HiSeq_RNASeqV2): ITPA
mRNA Expression, RSEM (Batch normalized from Illumina HiSeq_RNASeqV2): PRRX1 (1q24.2)
Spearman: -0.32
(p = 5.85e-11)
Pearson: -0.27
(p = 2.74e-8)
y = -0.21x + 1156.24
R² = 0.07
PRRX1 mutated
Neither mutated
PRRX1 vs. IDI1
mRNA Expression, RSEM (Batch normalized from Illumina HiSeq_RNASeqV2): IDI1
mRNA Expression, RSEM (Batch normalized from Illumina HiSeq_RNASeqV2): PRRX1 (1q24.2)
Spearman: -0.30
(p = 3.86e-10)
Pearson: -0.25
(p = 2.41e-7)
y = -0.32x + 1599.36
R² = 0.06
PRRX1 mutated
IDI1 mutated
Neither mutated
PRRX1 vs. HSD17B7
mRNA Expression, RSEM (Batch normalized from Illumina HiSeq_RNASeqV2): HSD17B7
mRNA Expression, RSEM (Batch normalized from Illumina HiSeq_RNASeqV2): PRRX1 (1q24.2)
Spearman: -0.31
(p = 2.59e-10)
Pearson: -0.26
(p = 1.96e-7)
y = -0.05x + 308.75
R² = 0.06
PRRX1 mutated
HSD17B7 mutated
Neither mutated

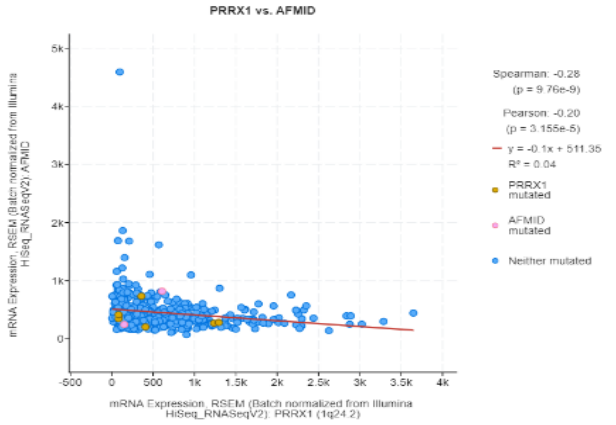

PRRX1 vs. HMGCR
mRNA Expression, RSEM (Batch normalized from Illumina HiSeq_RNASeqV2): HMGCR
mRNA Expression, RSEM (Batch normalized from Illumina HiSeq_RNASeqV2): PRRX1 (1q24.2)
Spearman: -0.32
(p = 1.95e-11)
Pearson: -0.24
(p = 1.163e-6)
y = -0.32x + 1803.9
R² = 0.06
PRRX1 mutated
HMGCR mutated
Neither mutated
PRRX1 vs. HGSNAT
mRNA Expression, RSEM (Batch normalized from Illumina HiSeq_RNASeqV2): HGSNAT
mRNA Expression, RSEM (Batch normalized from Illumina HiSeq_RNASeqV2): PRRX1 (1q24.2)
Spearman: 0.23
(p = 1.926e-6)
Pearson: 0.21
(p = 1.390e-5)
y = 0.26x + 1608.82
R² = 0.05
PRRX1 mutated
HGSNAT mutated
Both mutated
Neither mutated
PRRX1 vs. HDDC3
mRNA Expression, RSEM (Batch normalized from Illumina HiSeq_RNASeqV2): HDDC3
mRNA Expression, RSEM (Batch normalized from Illumina HiSeq_RNASeqV2): PRRX1 (1q24.2)
Spearman: -0.29
(p = 1.40e-9)
Pearson: -0.24
(p = 1.453e-6)
y = -0.07x + 363.69
R² = 0.06
PRRX1 mutated
HDDC3 mutated
Neither mutated
PRRX1 vs. GUCY1A2
mRNA Expression, RSEM (Batch normalized from Illumina HiSeq_RNASeqV2): GUCY1A2
mRNA Expression, RSEM (Batch normalized from Illumina HiSeq_RNASeqV2): PRRX1 (1q24.2)
Spearman: 0.42
(p = 2.30e-17)
Pearson: 0.32
(p = 3.14e-10)
y = 0.01x + 14.11
R² = 0.1
PRRX1 mutated
GUCY1A2 mutated
Both mutated
Neither mutated
PRRX1 vs. GSTM5
mRNA Expression, RSEM (Batch normalized from Illumina HiSeq_RNASeqV2): GSTM5
mRNA Expression, RSEM (Batch normalized from Illumina HiSeq_RNASeqV2): PRRX1 (1q24.2)
Spearman: 0.60
(p = 5.01e-41)
Pearson: 0.39
(p = 1.23e-16)
y = 0.08x + 28.67
R² = 0.16
PRRX1 mutated
GSTM5 mutated
Neither mutated
PRRX1 vs. GSS
mRNA Expression, RSEM (Batch normalized from Illumina HiSeq_RNASeqV2): GSS
mRNA Expression, RSEM (Batch normalized from Illumina HiSeq_RNASeqV2): PRRX1 (1q24.2)
Spearman: -0.36
(p = 3.04e-14)
Pearson: -0.34
(p = 3.14e-12)
y = -0.32x + 1569.28
R² = 0.11
PRRX1 mutated
GSS mutated
Neither mutated

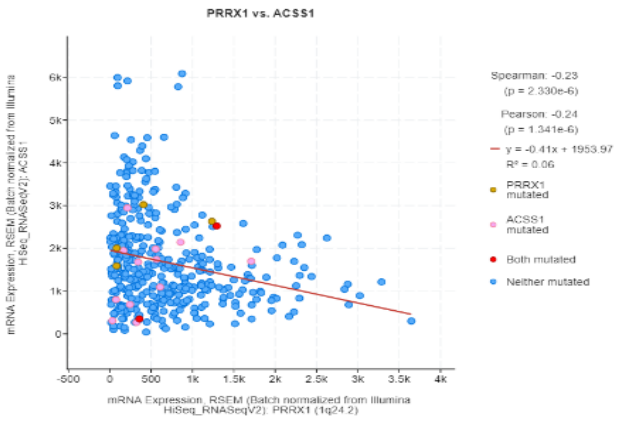

PRRX1 vs. GGT7
mRNA Expression, RSEM (Batch normalized from Illumina HiSeq_RNASeqV2): GGT7
mRNA Expression, RSEM (Batch normalized from Illumina HiSeq_RNASeqV2): PRRX1 (1q24.2)
Spearman: -0.20
(p = 7.306e-5)
Pearson: -0.20
(p = 6.546e-5)
y = -0.09x + 418.24
R² = 0.04
PRRX1 mutated
GGT7 mutated
Neither mutated
PRRX1 vs. GALNT16
mRNA Expression, RSEM (Batch normalized from Illumina HiSeq_RNASeqV2): GALNT16
mRNA Expression, RSEM (Batch normalized from Illumina HiSeq_RNASeqV2): PRRX1 (1q24.2)
Spearman: 0.31
(p = 2.50e-10)
Pearson: 0.32
(p = 5.22e-11)
y = 0.05x + 38.55
R² = 0.1
PRRX1 mutated
GALNT16 mutated
Neither mutated
PRRX1 vs. ENTPD2
mRNA Expression, RSEM (Batch normalized from Illumina HiSeq_RNASeqV2): ENTPD2
mRNA Expression, RSEM (Batch normalized from Illumina HiSeq_RNASeqV2): PRRX1 (1q24.2)
Spearman: -0.20
(p = 4.794e-5)
Pearson: -0.17
(p = 7.076e-4)
y = -0.15x + 476.13
R² = 0.03
PRRX1 mutated
ENTPD2 mutated
Neither mutated
PRRX1 vs. DCXR
mRNA Expression, RSEM (Batch normalized from Illumina HiSeq_RNASeqV2): DCXR
mRNA Expression, RSEM (Batch normalized from Illumina HiSeq_RNASeqV2): PRRX1 (1q24.2)
Spearman: -0.33
(p = 6.94e-12)
Pearson: -0.24
(p = 1.371e-6)
y = -0.24x + 955.61
R² = 0.06
PRRX1 mutated
DCXR mutated
Neither mutated
PRRX1 vs. DCTPP1
mRNA Expression, RSEM (Batch normalized from Illumina HiSeq_RNASeqV2): DCTPP1
mRNA Expression, RSEM (Batch normalized from Illumina HiSeq_RNASeqV2): PRRX1 (1q24.2)
Spearman: -0.22
(p = 1.002e-5)
Pearson: -0.22
(p = 9.483e-6)
y = -0.2x + 1291.64
R² = 0.05
PRRX1 mutated
Neither mutated
PRRX1 vs. CYP19A1
mRNA Expression, RSEM (Batch normalized from Illumina HiSeq_RNASeqV2): CYP19A1
mRNA Expression, RSEM (Batch normalized from Illumina HiSeq_RNASeqV2): PRRX1 (1q24.2)
Spearman: 0.25
(p = 2.70e-7)
Pearson: 0.26
(p = 7.38e-8)
y = 0.02x + 3.15
R² = 0.07
PRRX1 mutated
CYP19A1 mutated
Both mutated
Neither mutated

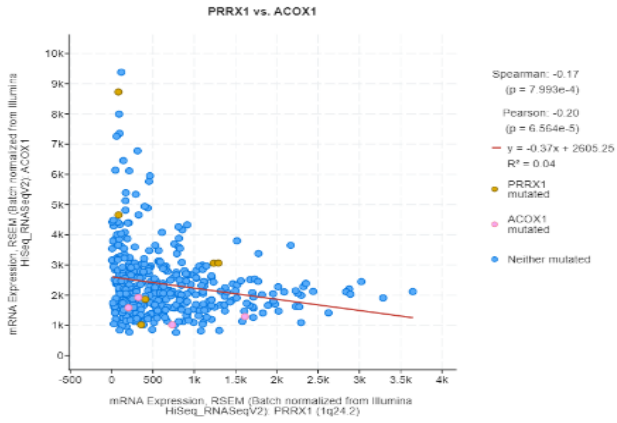

PRRX1 vs. CYP3A5
mRNA Expression, RSEM (Batch normalized from Illumina HiSeq_RNASeqV2): CYP3A5
mRNA Expression, RSEM (Batch normalized from Illumina HiSeq_RNASeqV2): PRRX1 (1q24.2)
Spearman: -0.19
(p = 1.740e-4)
Pearson: -0.16
(p = 1.310e-3)
y = -0.29x + 1054.11
R² = 0.03
PRRX1 mutated
CYP3A5 mutated
Neither mutated
PRRX1 vs. CYP2R1
mRNA Expression, RSEM (Batch normalized from Illumina HiSeq_RNASeqV2): CYP2R1
mRNA Expression, RSEM (Batch normalized from Illumina HiSeq_RNASeqV2): PRRX1 (1q24.2)
Spearman: -0.22
(p = 6.867e-6)
Pearson: -0.20
(p = 3.996e-5)
y = -0.04x + 291.81
R² = 0.04
PRRX1 mutated
CYP2R1 mutated
Both mutated
Neither mutated
PRRX1 vs. CRLS1
mRNA Expression, RSEM (Batch normalized from Illumina HiSeq_RNASeqV2): CRLS1
mRNA Expression, RSEM (Batch normalized from Illumina HiSeq_RNASeqV2): PRRX1 (1q24.2)
Spearman: -0.35
(p = 5.29e-13)
Pearson: -0.23
(p = 1.802e-6)
y = -0.3x + 1794.68
R² = 0.05
PRRX1 mutated
CRLS1 mutated
Neither mutated
PRRX1 vs. COX7A2
mRNA Expression, RSEM (Batch normalized from Illumina HiSeq_RNASeqV2): COX7A2
mRNA Expression, RSEM (Batch normalized from Illumina HiSeq_RNASeqV2): PRRX1 (1q24.2)
Spearman: -0.22
(p = 9.208e-6)
Pearson: -0.19
(p = 8.806e-5)
y = -0.42x + 3212.24
R² = 0.04
PRRX1 mutated
Neither mutated
PRRX1 vs. COX5B
mRNA Expression, RSEM (Batch normalized from Illumina HiSeq_RNASeqV2): COX5B
mRNA Expression, RSEM (Batch normalized from Illumina HiSeq_RNASeqV2): PRRX1 (1q24.2)
Spearman: -0.27
(p = 3.51e-8)
Pearson: -0.21
(p = 2.553e-5)
y = -0.46x + 2758.67
R² = 0.04
PRRX1 mutated
COX5B mutated
Neither mutated
PRRX1 vs. CHST9
mRNA Expression, RSEM (Batch normalized from Illumina HiSeq_RNASeqV2): CHST9
mRNA Expression, RSEM (Batch normalized from Illumina HiSeq_RNASeqV2): PRRX1 (1q24.2)
Spearman: 0.02
(p = 0.758)
Pearson: -0.15
(p = 4.451e-3)
y = -0.03x + 59.05
R² = 0.02
PRRX1 mutated
CHST9 mutated
Neither mutated

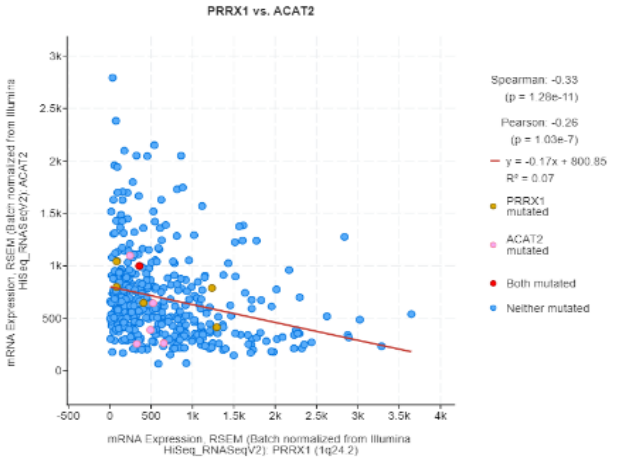

PRRX1 vs. CHDH
mRNA Expression, RSEM (Batch normalized from Illumina HiSeq_RNASeqV2): CHDH
mRNA Expression, RSEM (Batch normalized from Illumina HiSeq_RNASeqV2): PRRX1 (1q24.2)
Spearman: -0.31
(p = 2.76e-10)
Pearson: -0.28
(p = 1.50e-8)
y = -0.18x + 765.45
R² = 0.08
PRRX1 mutated
CHDH mutated
Both mutated
Neither mutated
PRRX1 vs. ATP5MC1
mRNA Expression, RSEM (Batch normalized from Illumina HiSeq_RNASeqV2): ATP5MC1
mRNA Expression, RSEM (Batch normalized from Illumina HiSeq_RNASeqV2): PRRX1 (1q24.2)
Spearman: -0.26
(p = 1.40e-7)
Pearson: -0.22
(p = 5.791e-6)
y = -0.27x + 1532.11
R² = 0.05
PRRX1 mutated
Neither mutated
PRRX1 vs. AOX1
mRNA Expression, RSEM (Batch normalized from Illumina HiSeq_RNASeqV2): AOX1
mRNA Expression, RSEM (Batch normalized from Illumina HiSeq_RNASeqV2): PRRX1 (1q24.2)
Spearman: 0.55
(p = 1.03e-33)
Pearson: 0.22
(p = 6.164e-6)
y = 0.16x + 57.18
R² = 0.05
PRRX1 mutated
AOX1 mutated
Both mutated
Neither mutated
PRRX1 vs. ALG11
mRNA Expression, RSEM (Batch normalized from Illumina HiSeq_RNASeqV2): ALG11
mRNA Expression, RSEM (Batch normalized from Illumina HiSeq_RNASeqV2): PRRX1 (1q24.2)
Spearman: -0.22
(p = 6.778e-6)
Pearson: -0.18
(p = 1.632e-4)
y = -0.01x + 36.28
R² = 0.01
PRRX1 mutated
ALG11 mutated
Neither mutated
PRRX1 vs. ALG5
mRNA Expression, RSEM (Batch normalized from Illumina HiSeq_RNASeqV2): ALG5
mRNA Expression, RSEM (Batch normalized from Illumina HiSeq_RNASeqV2): PRRX1 (1q24.2)
Spearman: -0.17
(p = 6.065e-4)
Pearson: -0.15
(p = 3.063e-3)
y = -0.12x + 1179.89
R² = 0.02
PRRX1 mutated
ALG5 mutated
Neither mutated
PRRX1 vs. ALDH5A1
mRNA Expression, RSEM (Batch normalized from Illumina HiSeq_RNASeqV2): ALDH5A1
mRNA Expression, RSEM (Batch normalized from Illumina HiSeq_RNASeqV2): PRRX1 (1q24.2)
Spearman: -0.16
(p = 8.867e-4)
Pearson: -0.16
(p = 8.608e-4)
y = -0.16x + 802.34
R² = 0.03
PRRX1 mutated
ALDH5A1 mutated
Neither mutated


PRRX1 vs. AGMAT
mRNA Expression, RSEM (Batch normalized from Illumina HiSeq_RNASeqV2): AGMAT
mRNA Expression, RSEM (Batch normalized from Illumina HiSeq_RNASeqV2): PRRX1 (1q24.2)
Spearman: -0.29
(p = 1.68e-9)
Pearson: -0.25
(p = 2.17e-7)
y = -0.18x + 697.76
R² = 0.06
PRRX1 mutated
AGMAT mutated
Neither mutated

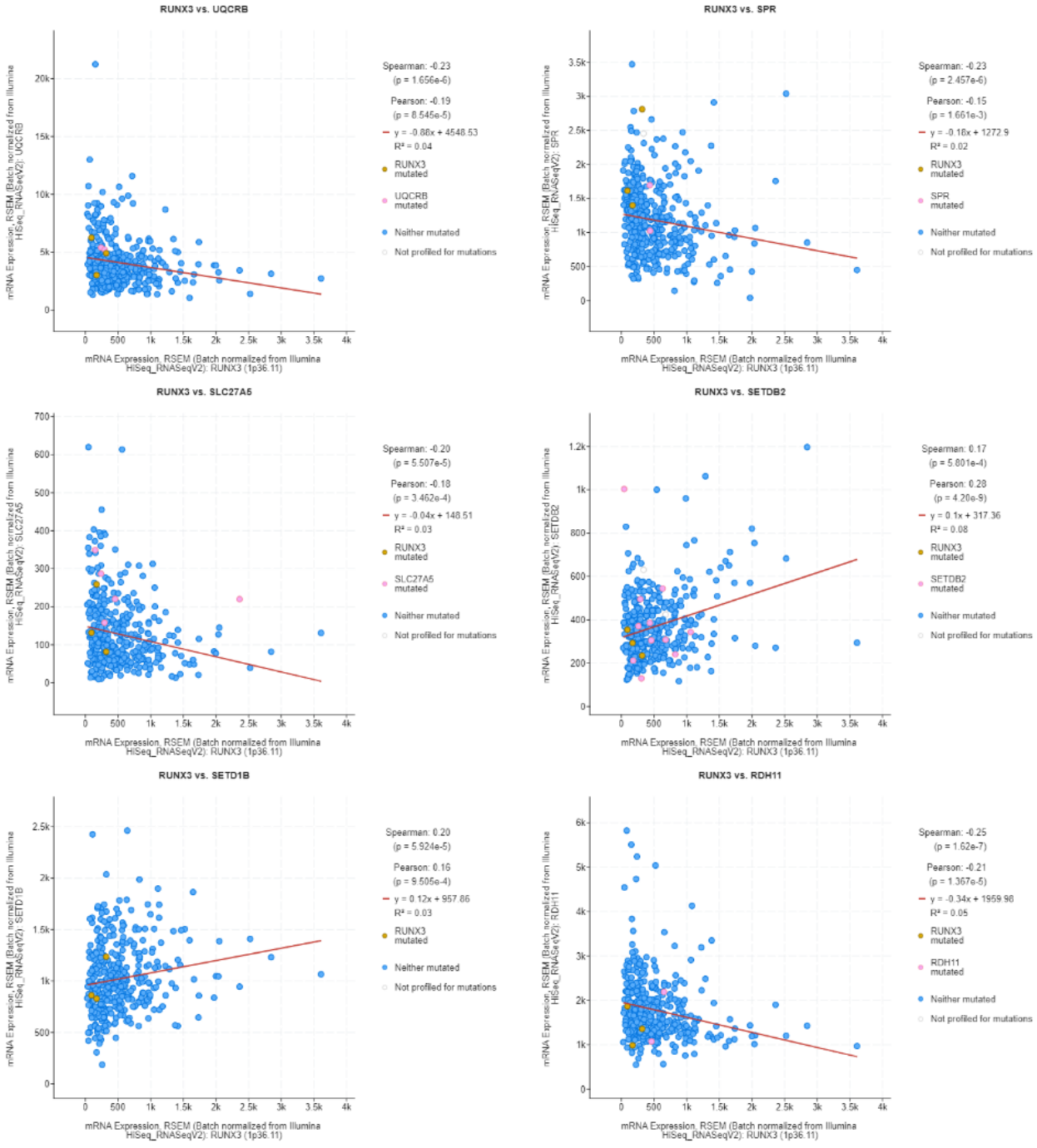

PRRX1 vs. AFMID
mRNA Expression, RSEM (Batch normalized from Illumina HiSeq_RNASeqV2): AFMID
mRNA Expression, RSEM (Batch normalized from Illumina HiSeq_RNASeqV2): PRRX1 (1q24.2)
Spearman: -0.28
(p = 9.76e-9)
Pearson: -0.20
(p = 3.155e-5)
y = -0.1x + 511.35
R² = 0.04
PRRX1 mutated
AFMID mutated
Neither mutated

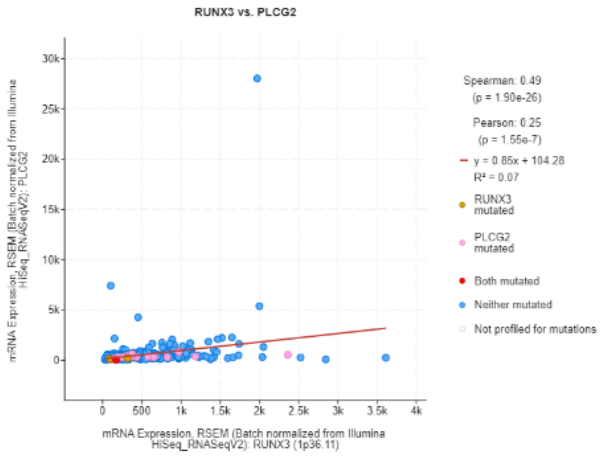

PRRX1 vs. ACSS1
mRNA Expression, RSEM (Batch normalized from Illumina HiSeq_RNASeqV2): ACSS1
mRNA Expression, RSEM (Batch normalized from Illumina HiSeq_RNASeqV2): PRRX1 (1q24.2)
Spearman: -0.23
(p = 2.330e-6)
Pearson: -0.24
(p = 1.341e-6)
y = -0.41x + 1953.97
R² = 0.06
PRRX1 mutated
ACSS1 mutated
Both mutated
Neither mutated

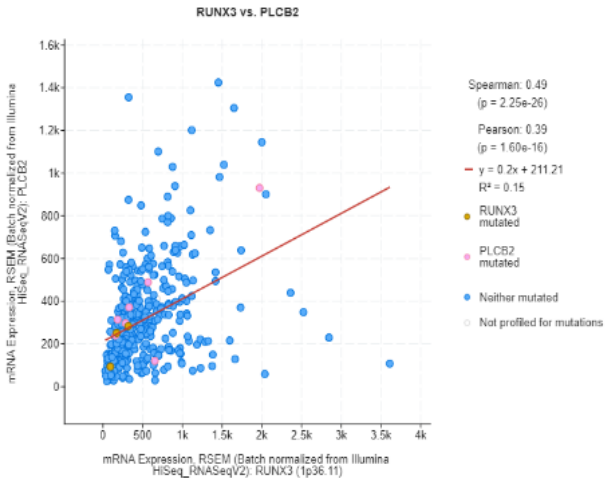

PRRX1 vs. ACOX1
mRNA Expression, RSEM (Batch normalized from Illumina HiSeq_RNASeqV2): ACOX1
mRNA Expression, RSEM (Batch normalized from Illumina HiSeq_RNASeqV2): PRRX1 (1q24.2)
Spearman: -0.17
(p = 7.993e-4)
Pearson: -0.20
(p = 6.564e-5)
y = -0.37x + 2605.25
R² = 0.04
PRRX1 mutated
ACOX1 mutated
Neither mutated

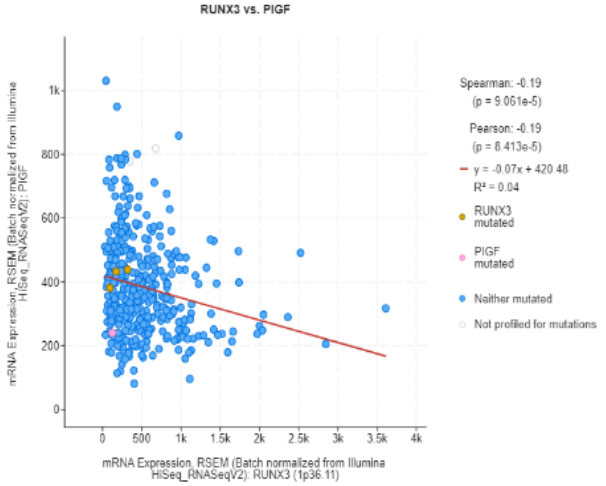

PRRX1 vs. ACAT2
mRNA Expression, RSEM (Batch normalized from Illumina HiSeq_RNASeqV2): ACAT2
mRNA Expression, RSEM (Batch normalized from Illumina HiSeq_RNASeqV2): PRRX1 (1q24.2)
Spearman: -0.33
(p = 1.28e-11)
Pearson: -0.26
(p = 1.03e-7)
y = -0.17x + 800.85
R² = 0.07
PRRX1 mutated
ACAT2 mutated
Both mutated
Neither mutated

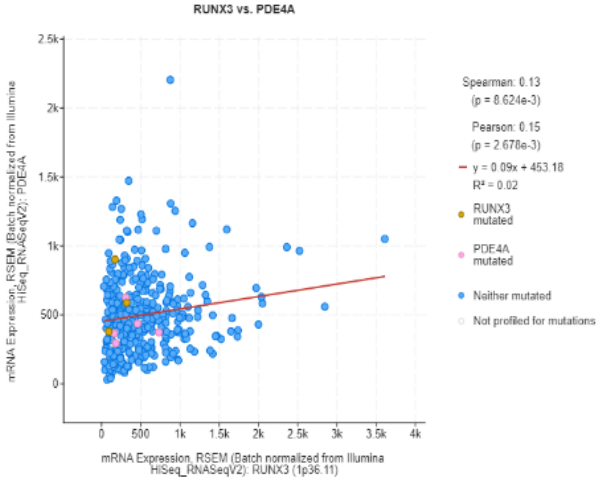
RUNX3

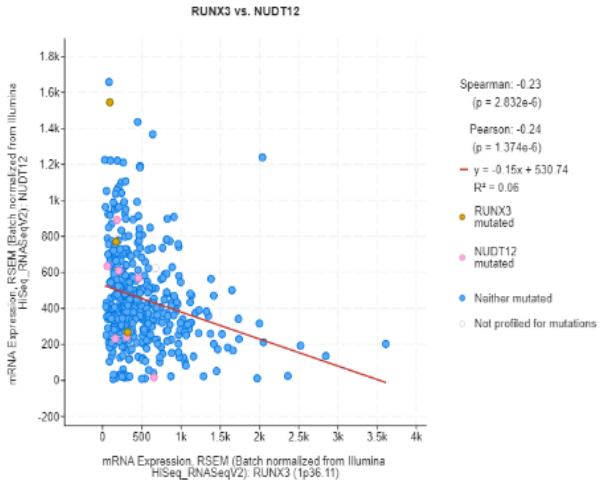

RUNX3 vs. UQCRB
mRNA Expression, RSEM (Batch normalized from Illumina HiSeq_RNASeqV2): UQCRB
mRNA Expression, RSEM (Batch normalized from Illumina HiSeq_RNASeqV2): RUNX3 (1p36.11)
Spearman: -0.23
(p = 1.656e-6)
Pearson: -0.19
(p = 8.545e-5)
y = -0.86x + 4548.53
R² = 0.04
RUNX3 mutated
UQCRB mutated
Neither mutated
Not profiled for mutations
RUNX3 vs. SPR
mRNA Expression, RSEM (Batch normalized from Illumina HiSeq_RNASeqV2): SPR
mRNA Expression, RSEM (Batch normalized from Illumina HiSeq_RNASeqV2): RUNX3 (1p36.11)
Spearman: -0.23
(p = 2.457e-6)
Pearson: -0.15
(p = 1.661e-3)
y = -0.16x + 1272.9
R² = 0.02
RUNX3 mutated
SPR mutated
Neither mutated
Not profiled for mutations
RUNX3 vs. SLC27A5
mRNA Expression, RSEM (Batch normalized from Illumina HiSeq_RNASeqV2): SLC27A5
mRNA Expression, RSEM (Batch normalized from Illumina HiSeq_RNASeqV2): RUNX3 (1p36.11)
Spearman: -0.20
(p = 5.507e-5)
Pearson: -0.18
(p = 3.462e-4)
y = -0.04x + 148.51
R² = 0.03
RUNX3 mutated
SLC27A5 mutated
Neither mutated
Not profiled for mutations
RUNX3 vs. SETDB2
mRNA Expression, RSEM (Batch normalized from Illumina HiSeq_RNASeqV2): SETDB2
mRNA Expression, RSEM (Batch normalized from Illumina HiSeq_RNASeqV2): RUNX3 (1p36.11)
Spearman: 0.17
(p = 5.801e-4)
Pearson: 0.28
(p = 4.20e-9)
y = 0.1x + 317.36
R² = 0.08
RUNX3 mutated
SETDB2 mutated
Neither mutated
Not profiled for mutations
RUNX3 vs. SETD1B
mRNA Expression, RSEM (Batch normalized from Illumina HiSeq_RNASeqV2): SETD1B
mRNA Expression, RSEM (Batch normalized from Illumina HiSeq_RNASeqV2): RUNX3 (1p36.11)
Spearman: 0.20
(p = 5.924e-5)
Pearson: 0.16
(p = 9.505e-4)
y = 0.12x + 957.86
R² = 0.03
RUNX3 mutated
Neither mutated
Not profiled for mutations
RUNX3 vs. RDH11
mRNA Expression, RSEM (Batch normalized from Illumina HiSeq_RNASeqV2): RDH11
mRNA Expression, RSEM (Batch normalized from Illumina HiSeq_RNASeqV2): RUNX3 (1p36.11)
Spearman: -0.25
(p = 1.62e-7)
Pearson: -0.21
(p = 1.367e-5)
y = -0.34x + 1959.98
R² = 0.05
RUNX3 mutated
RDH11 mutated
Neither mutated
Not profiled for mutations

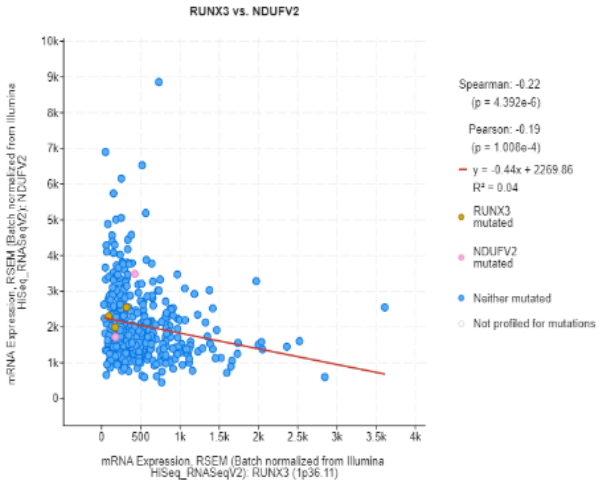

RUNX3 vs. PLCG2
mRNA Expression, RSEM (Batch normalized from Illumina HiSeq_RNASeqV2): PLCG2
mRNA Expression, RSEM (Batch normalized from Illumina HiSeq_RNASeqV2): RUNX3 (1p36.11)
Spearman: 0.49
(p = 1.90e-26)
Pearson: 0.25
(p = 1.55e-7)
y = 0.85x + 104.28
R² = 0.07
RUNX3 mutated
PLCG2 mutated
Both mutated
Neither mutated
Not profiled for mutations

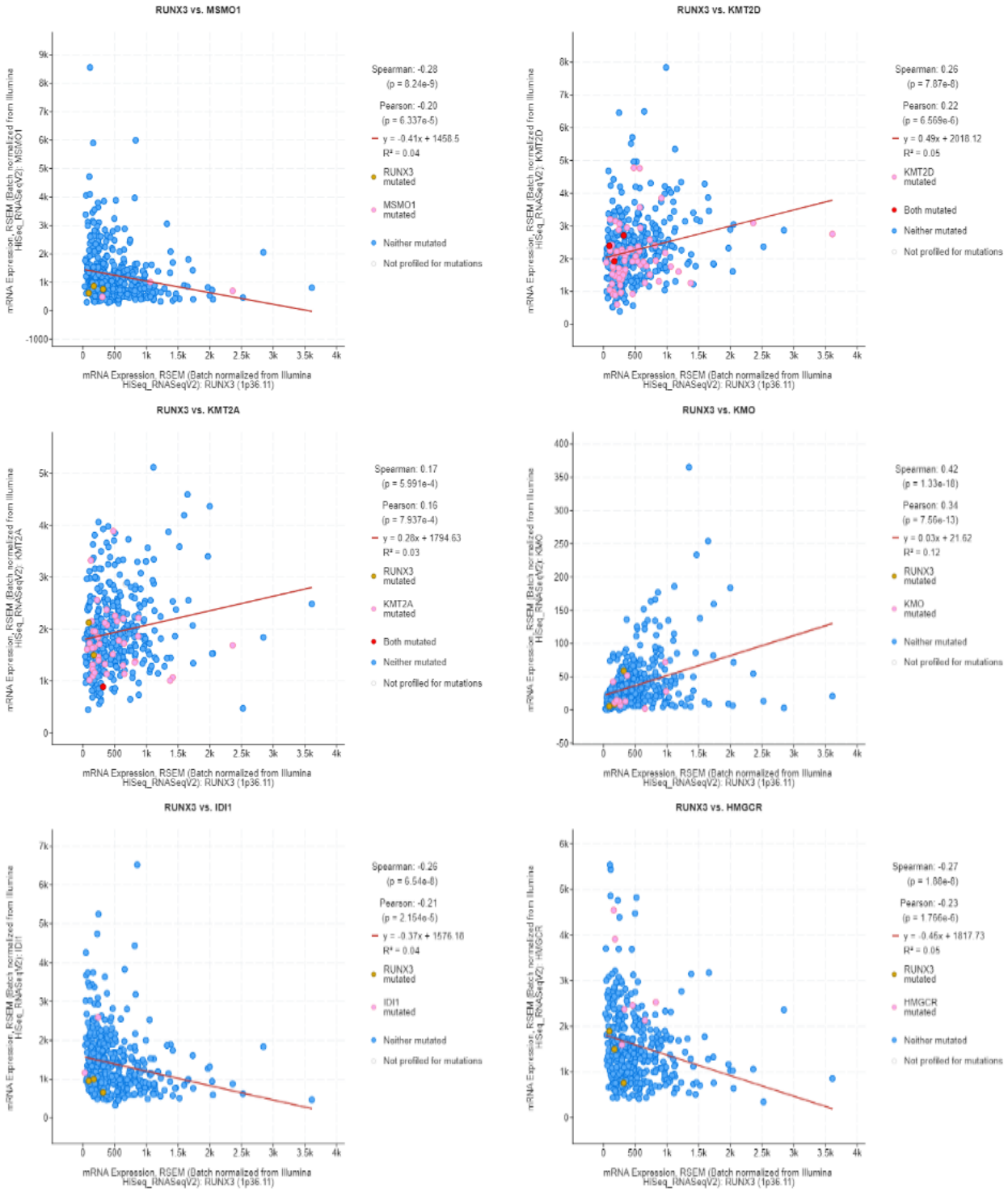

RUNX3 vs. PLCB2
mRNA Expression, RSEM (Batch normalized from Illumina HiSeq_RNASeqV2): PLCB2
mRNA Expression, RSEM (Batch normalized from Illumina HiSeq_RNASeqV2): RUNX3 (1p36.11)
Spearman: 0.49
(p = 2.25e-26)
Pearson: 0.39
(p = 1.60e-16)
y = 0.2x + 211.21
R² = 0.15
RUNX3 mutated
PLCB2 mutated
Neither mutated
Not profiled for mutations

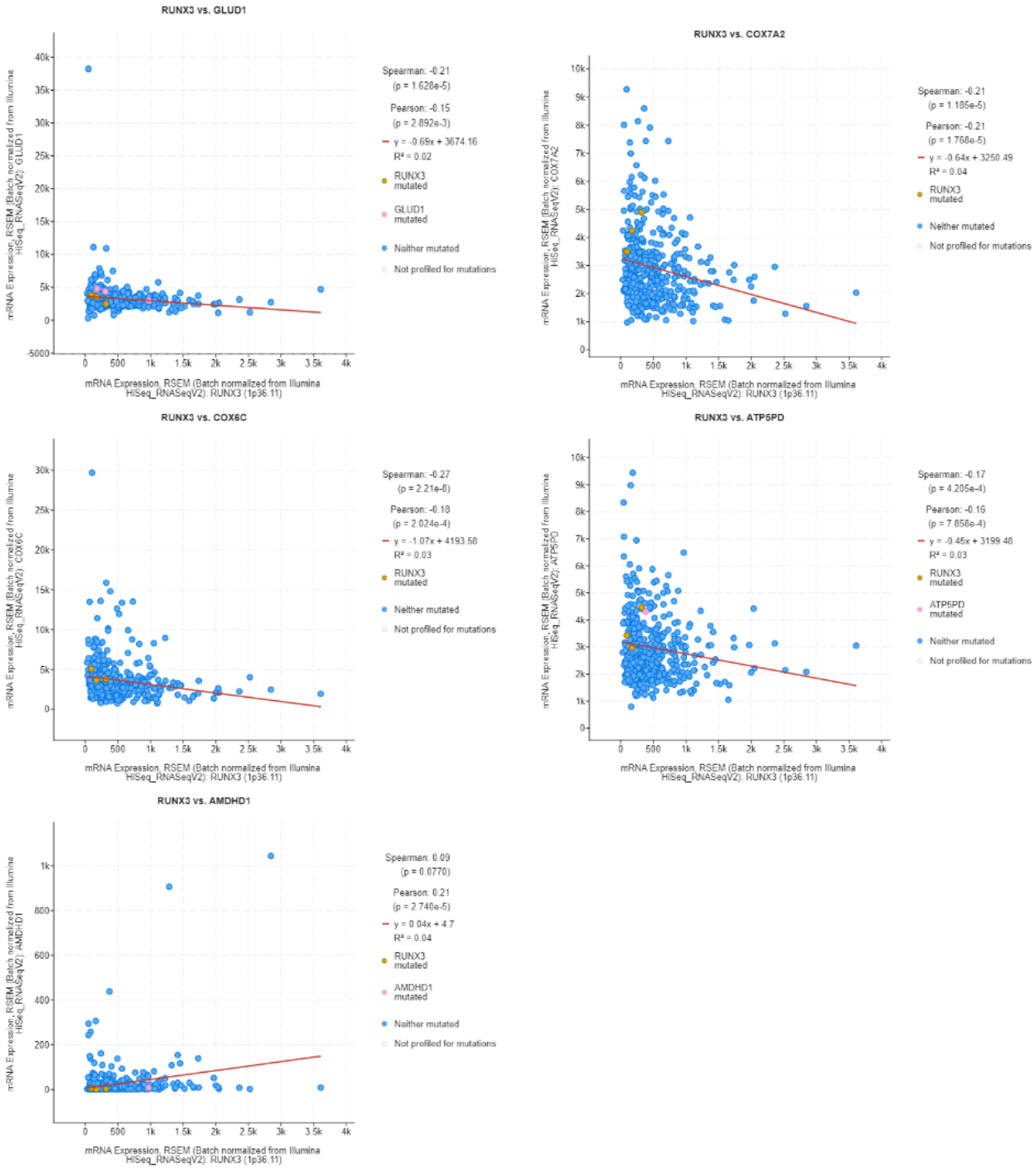

RUNX3 vs. PIGF
mRNA Expression, RSEM (Batch normalized from Illumina HiSeq_RNASeqV2): PIGF
mRNA Expression, RSEM (Batch normalized from Illumina HiSeq_RNASeqV2): RUNX3 (1p36.11)
Spearman: -0.19
(p = 9.061e-5)
Pearson: -0.19
(p = 8.413e-5)
y = -0.07x + 420.48
R² = 0.04
RUNX3 mutated
PIGF mutated
Neither mutated
Not profiled for mutations


RUNX3 vs. PDE4A
mRNA Expression, RSEM (Batch normalized from Illumina HiSeq_RNASeqV2): PDE4A
mRNA Expression, RSEM (Batch normalized from Illumina HiSeq_RNASeqV2): RUNX3 (1p36.11)
Spearman: 0.13
(p = 8.624e-3)
Pearson: 0.15
(p = 2.678e-3)
y = 0.09x + 453.18
R² = 0.02
RUNX3 mutated
PDE4A mutated
Neither mutated
Not profiled for mutations

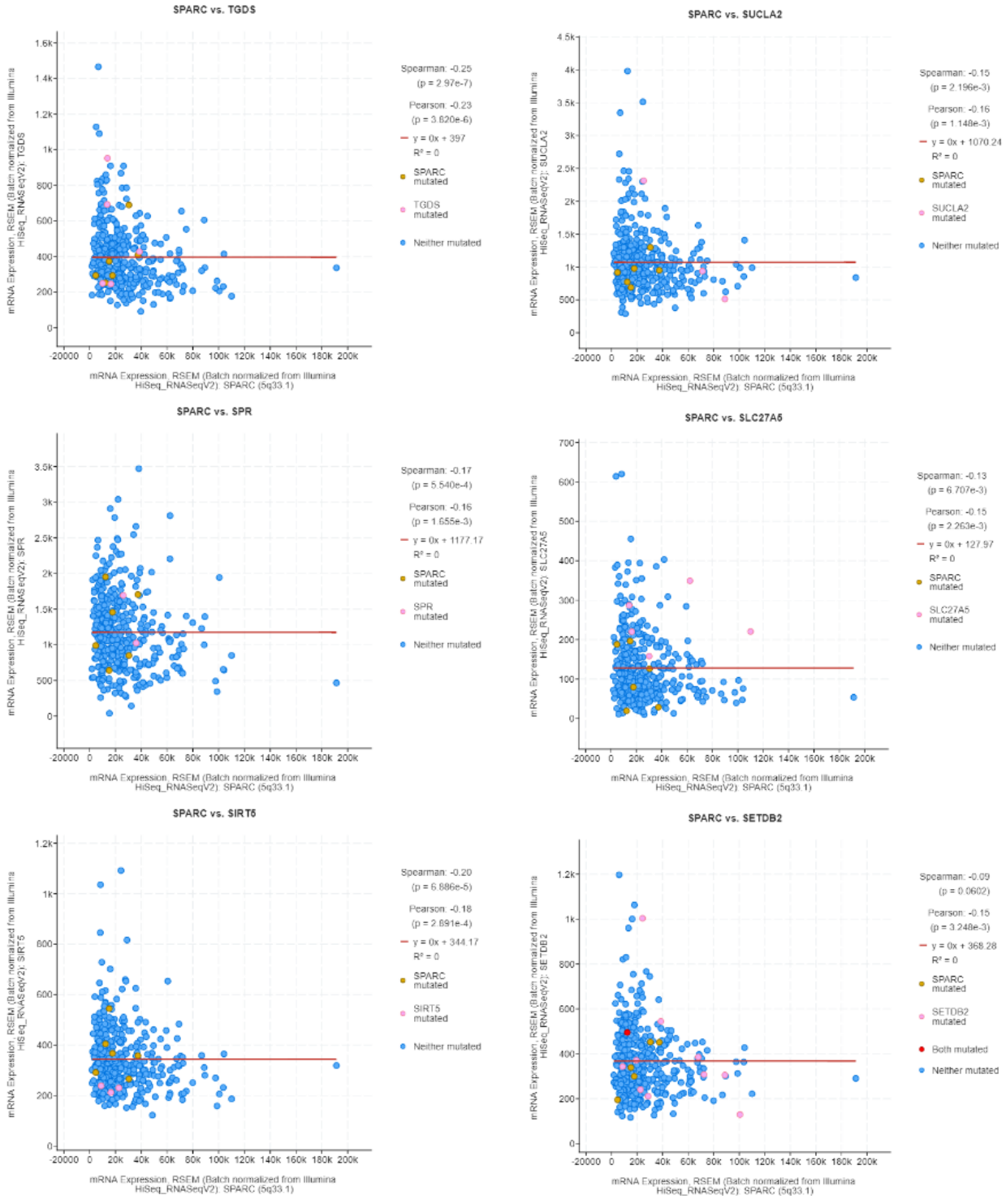

RUNX3 vs. NUDT12
mRNA Expression, RSEM (Batch normalized from Illumina HiSeq_RNASeqV2): NUDT12
mRNA Expression, RSEM (Batch normalized from Illumina HiSeq_RNASeqV2): RUNX3 (1p36.11)
Spearman: -0.23
(p = 2.832e-6)
Pearson: -0.24
(p = 1.374e-6)
y = -0.15x + 530.74
R² = 0.06
RUNX3 mutated
NUDT12 mutated
Neither mutated
Not profiled for mutations

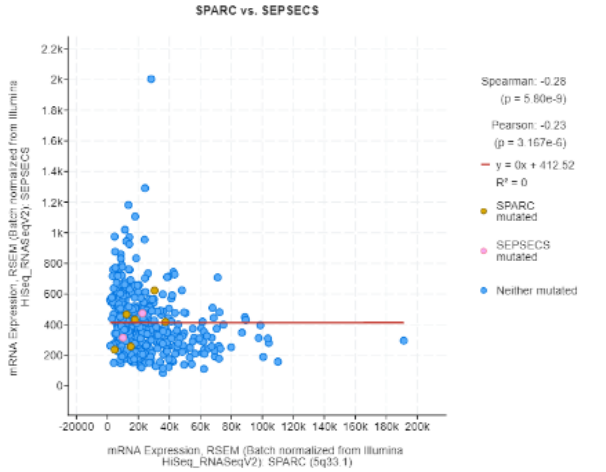

RUNX3 vs. NDUFV2
mRNA Expression, RSEM (Batch normalized from Illumina HiSeq_RNASeqV2): NDUFV2
mRNA Expression, RSEM (Batch normalized from Illumina HiSeq_RNASeqV2): RUNX3 (1p36.11)
Spearman: -0.22
(p = 4.392e-6)
Pearson: -0.19
(p = 1.008e-4)
y = -0.44x + 2269.86
R² = 0.04
RUNX3 mutated
NDUFV2 mutated
Neither mutated
Not profiled for mutations

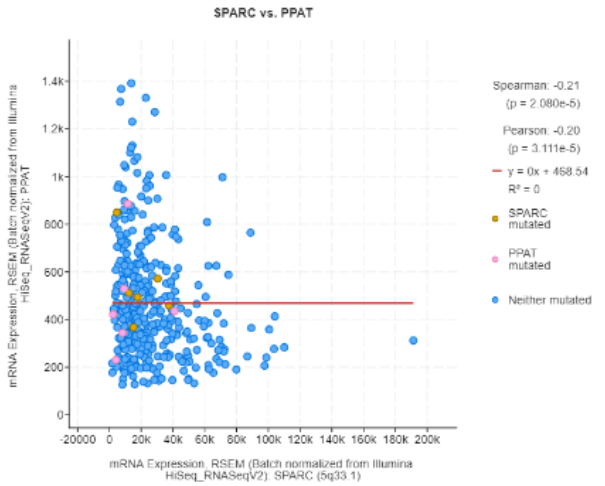

RUNX3 vs. MSMO1
mRNA Expression, RSEM (Batch normalized from Illumina HiSeq_RNASeqV2): MSMO1
mRNA Expression, RSEM (Batch normalized from Illumina HiSeq_RNASeqV2): RUNX3 (1p36.11)
Spearman: -0.28
(p = 8.24e-9)
Pearson: -0.20
(p = 6.337e-5)
y = -0.41x + 1458.5
R² = 0.04
RUNX3 mutated
MSMO1 mutated
Neither mutated
Not profiled for mutations
RUNX3 vs. KMT2D
mRNA Expression, RSEM (Batch normalized from Illumina HiSeq_RNASeqV2): KMT2D
mRNA Expression, RSEM (Batch normalized from Illumina HiSeq_RNASeqV2): RUNX3 (1p36.11)
Spearman: 0.26
(p = 7.87e-8)
Pearson: 0.22
(p = 6.569e-6)
y = 0.49x + 2018.12
R² = 0.05
KMT2D mutated
Both mutated
Neither mutated
Not profiled for mutations
RUNX3 vs. KMT2A
mRNA Expression, RSEM (Batch normalized from Illumina HiSeq_RNASeqV2): KMT2A
mRNA Expression, RSEM (Batch normalized from Illumina HiSeq_RNASeqV2): RUNX3 (1p36.11)
Spearman: 0.17
(p = 5.991e-4)
Pearson: 0.16
(p = 7.937e-4)
y = 0.28x + 1794.63
R² = 0.03
RUNX3 mutated
KMT2A mutated
Both mutated
Neither mutated
Not profiled for mutations
RUNX3 vs. KMO
mRNA Expression, RSEM (Batch normalized from Illumina HiSeq_RNASeqV2): KMO
mRNA Expression, RSEM (Batch normalized from Illumina HiSeq_RNASeqV2): RUNX3 (1p36.11)
Spearman: 0.42
(p = 1.33e-18)
Pearson: 0.34
(p = 7.56e-13)
y = 0.03x + 21.62
R² = 0.12
RUNX3 mutated
KMO mutated
Neither mutated
Not profiled for mutations
RUNX3 vs. IDI1
mRNA Expression, RSEM (Batch normalized from Illumina HiSeq_RNASeqV2): IDI1
mRNA Expression, RSEM (Batch normalized from Illumina HiSeq_RNASeqV2): RUNX3 (1p36.11)
Spearman: -0.26
(p = 6.54e-8)
Pearson: -0.21
(p = 2.154e-5)
y = -0.37x + 1576.18
R² = 0.04
RUNX3 mutated
IDI1 mutated
Neither mutated
Not profiled for mutations
RUNX3 vs. HMGCR
mRNA Expression, RSEM (Batch normalized from Illumina HiSeq_RNASeqV2): HMGCR
mRNA Expression, RSEM (Batch normalized from Illumina HiSeq_RNASeqV2): RUNX3 (1p36.11)
Spearman: -0.27
(p = 1.06e-8)
Pearson: -0.23
(p = 1.766e-6)
y = -0.46x + 1817.73
R² = 0.05
RUNX3 mutated
HMGCR mutated
Neither mutated
Not profiled for mutations

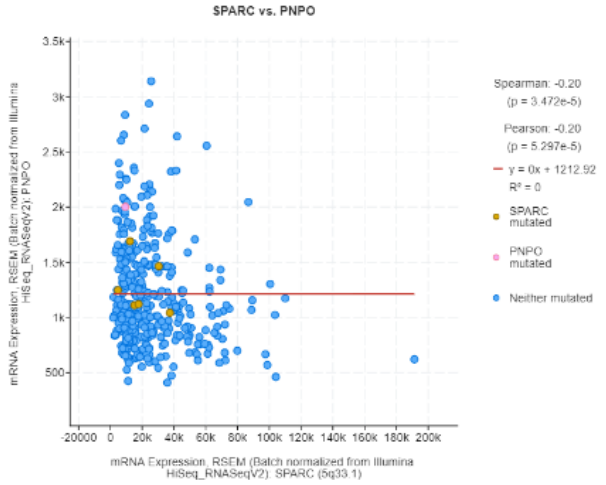

RUNX3 vs. GLUD1
mRNA Expression, RSEM (Batch normalized from Illumina HiSeq_RNASeqV2): GLUD1
mRNA Expression, RSEM (Batch normalized from Illumina HiSeq_RNASeqV2): RUNX3 (1p36.11)
Spearman: -0.21
(p = 1.628e-5)
Pearson: -0.15
(p = 2.892e-3)
y = -0.69x + 3674.16
R² = 0.02
RUNX3 mutated
GLUD1 mutated
Neither mutated
Not profiled for mutations
RUNX3 vs. COX7A2
mRNA Expression, RSEM (Batch normalized from Illumina HiSeq_RNASeqV2): COX7A2
mRNA Expression, RSEM (Batch normalized from Illumina HiSeq_RNASeqV2): RUNX3 (1p36.11)
Spearman: -0.21
(p = 1.185e-5)
Pearson: -0.21
(p = 1.768e-5)
y = -0.64x + 3250.49
R² = 0.04
RUNX3 mutated
Neither mutated
Not profiled for mutations
RUNX3 vs. COX6C
mRNA Expression, RSEM (Batch normalized from Illumina HiSeq_RNASeqV2): COX6C
mRNA Expression, RSEM (Batch normalized from Illumina HiSeq_RNASeqV2): RUNX3 (1p36.11)
Spearman: -0.27
(p = 2.21e-8)
Pearson: -0.18
(p = 2.024e-4)
y = -1.07x + 4193.58
R² = 0.03
RUNX3 mutated
Neither mutated
Not profiled for mutations
RUNX3 vs. ATP5PD
mRNA Expression, RSEM (Batch normalized from Illumina HiSeq_RNASeqV2): ATP5PD
mRNA Expression, RSEM (Batch normalized from Illumina HiSeq_RNASeqV2): RUNX3 (1p36.11)
Spearman: -0.17
(p = 4.205e-4)
Pearson: -0.16
(p = 7.858e-4)
y = -0.45x + 3199.48
R² = 0.03
RUNX3 mutated
ATP5PD mutated
Neither mutated
Not profiled for mutations
RUNX3 vs. AMDHD1
mRNA Expression, RSEM (Batch normalized from Illumina HiSeq_RNASeqV2): AMDHD1
mRNA Expression, RSEM (Batch normalized from Illumina HiSeq_RNASeqV2): RUNX3 (1p36.11)
Spearman: 0.09
(p = 0.0770)
Pearson: 0.21
(p = 2.740e-5)
y = 0.04x + 4.7
R² = 0.04
RUNX3 mutated
AMDHD1 mutated
Neither mutated
Not profiled for mutations

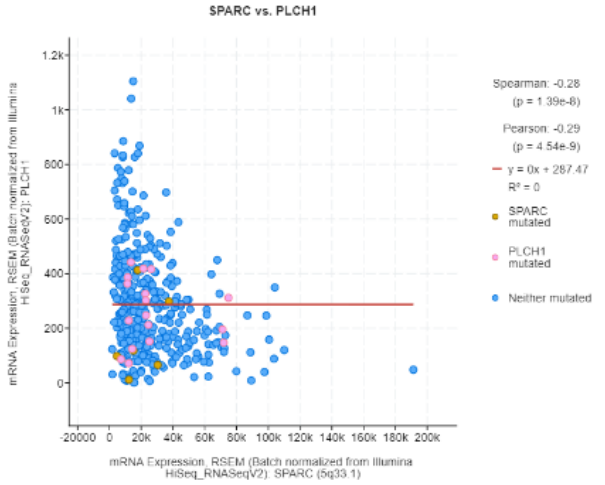
SPARC

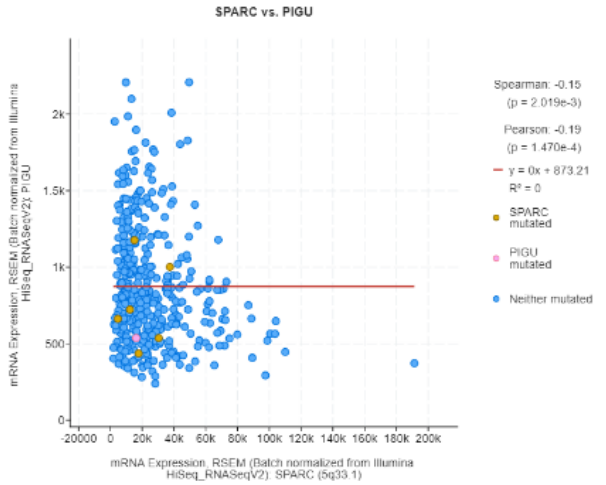

SPARC vs. TGDS
mRNA Expression, RSEM (Batch normalized from Illumina HiSeq_RNASeqV2): TGDS
mRNA Expression, RSEM (Batch normalized from Illumina HiSeq_RNASeqV2): SPARC (5q33.1)
Spearman: -0.25
(p = 2.97e-7)
Pearson: -0.23
(p = 3.820e-6)
y = 0x + 397
R² = 0
SPARC mutated
TGDS mutated
Neither mutated
SPARC vs. SUCLA2
mRNA Expression, RSEM (Batch normalized from Illumina HiSeq_RNASeqV2): SUCLA2
mRNA Expression, RSEM (Batch normalized from Illumina HiSeq_RNASeqV2): SPARC (5q33.1)
Spearman: -0.15
(p = 2.196e-3)
Pearson: -0.16
(p = 1.148e-3)
y = 0x + 1070.24
R² = 0
SPARC mutated
SUCLA2 mutated
Neither mutated
SPARC vs. SPR
mRNA Expression, RSEM (Batch normalized from Illumina HiSeq_RNASeqV2): SPR
mRNA Expression, RSEM (Batch normalized from Illumina HiSeq_RNASeqV2): SPARC (5q33.1)
Spearman: -0.17
(p = 5.540e-4)
Pearson: -0.16
(p = 1.655e-3)
y = 0x + 1177.17
R² = 0
SPARC mutated
SPR mutated
Neither mutated
SPARC vs. SLC27A5
mRNA Expression, RSEM (Batch normalized from Illumina HiSeq_RNASeqV2): SLC27A5
mRNA Expression, RSEM (Batch normalized from Illumina HiSeq_RNASeqV2): SPARC (5q33.1)
Spearman: -0.13
(p = 6.707e-3)
Pearson: -0.15
(p = 2.263e-3)
y = 0x + 127.97
R² = 0
SPARC mutated
SLC27A5 mutated
Neither mutated
SPARC vs. SIRT5
mRNA Expression, RSEM (Batch normalized from Illumina HiSeq_RNASeqV2): SIRT5
mRNA Expression, RSEM (Batch normalized from Illumina HiSeq_RNASeqV2): SPARC (5q33.1)
Spearman: -0.20
(p = 6.886e-5)
Pearson: -0.18
(p = 2.691e-4)
y = 0x + 344.17
R² = 0
SPARC mutated
SIRT5 mutated
Neither mutated
SPARC vs. SETDB2
mRNA Expression, RSEM (Batch normalized from Illumina HiSeq_RNASeqV2): SETDB2
mRNA Expression, RSEM (Batch normalized from Illumina HiSeq_RNASeqV2): SPARC (5q33.1)
Spearman: -0.09
(p = 0.0602)
Pearson: -0.15
(p = 3.248e-3)
y = 0x + 368.28
R² = 0
SPARC mutated
SETDB2 mutated
Both mutated
Neither mutated

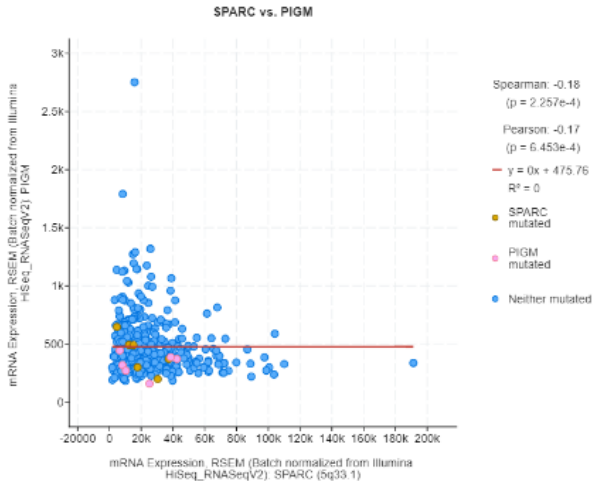

SPARC vs. SEPSECS
mRNA Expression, RSEM (Batch normalized from Illumina HiSeq_RNASeqV2): SEPSECS
mRNA Expression, RSEM (Batch normalized from Illumina HiSeq_RNASeqV2): SPARC (5q33.1)
Spearman: -0.28
(p = 5.80e-9)
Pearson: -0.23
(p = 3.167e-6)
y = 0x + 412.52
R² = 0
SPARC mutated
SEPSECS mutated
Neither mutated

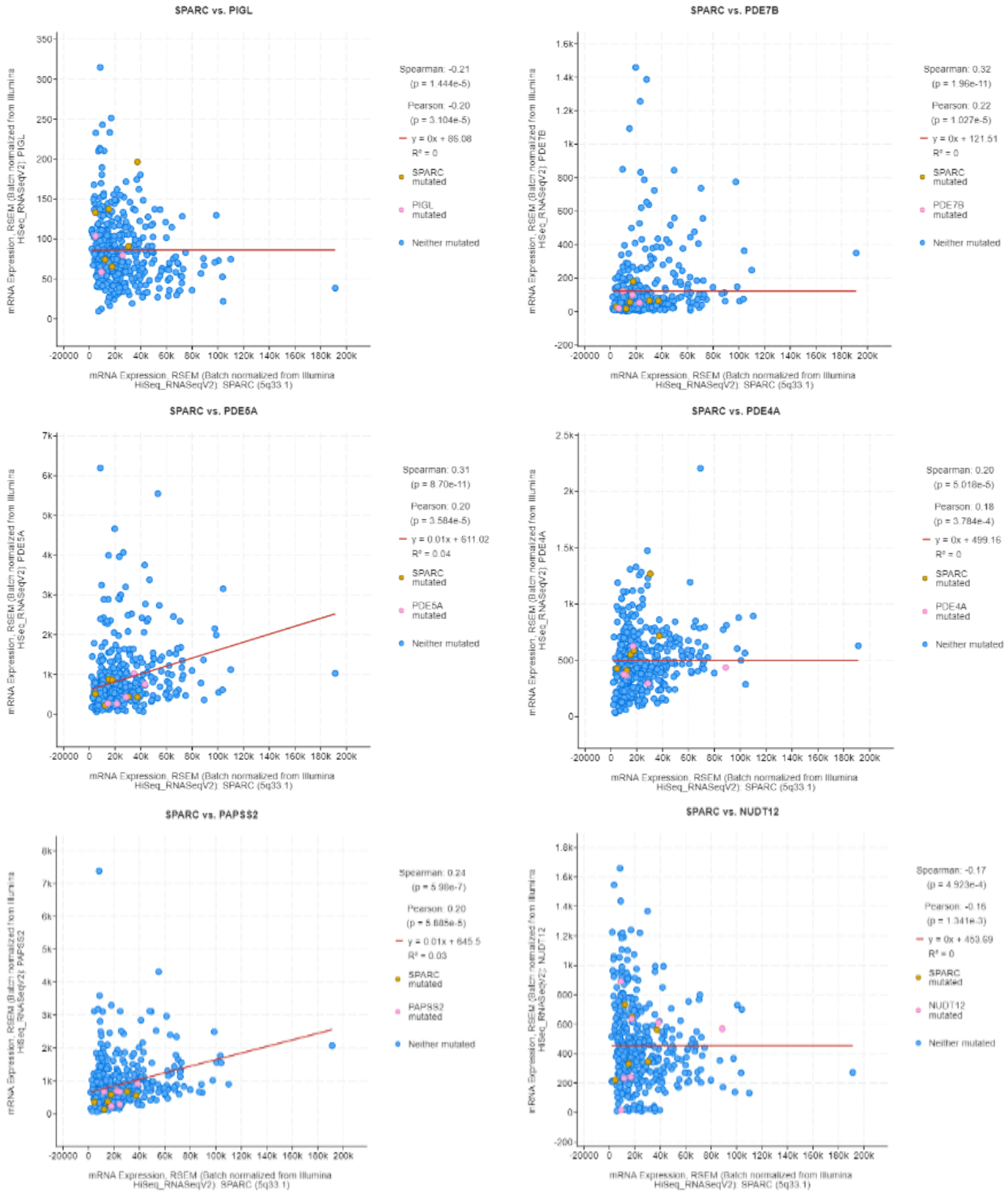

SPARC vs. PPAT
mRNA Expression, RSEM (Batch normalized from Illumina HiSeq_RNASeqV2): PPAT
mRNA Expression, RSEM (Batch normalized from Illumina HiSeq_RNASeqV2): SPARC (5q33.1)
Spearman: -0.21
(p = 2.080e-5)
Pearson: -0.20
(p = 3.111e-5)
y = 0x + 468.54
R² = 0
SPARC mutated
PPAT mutated
Neither mutated

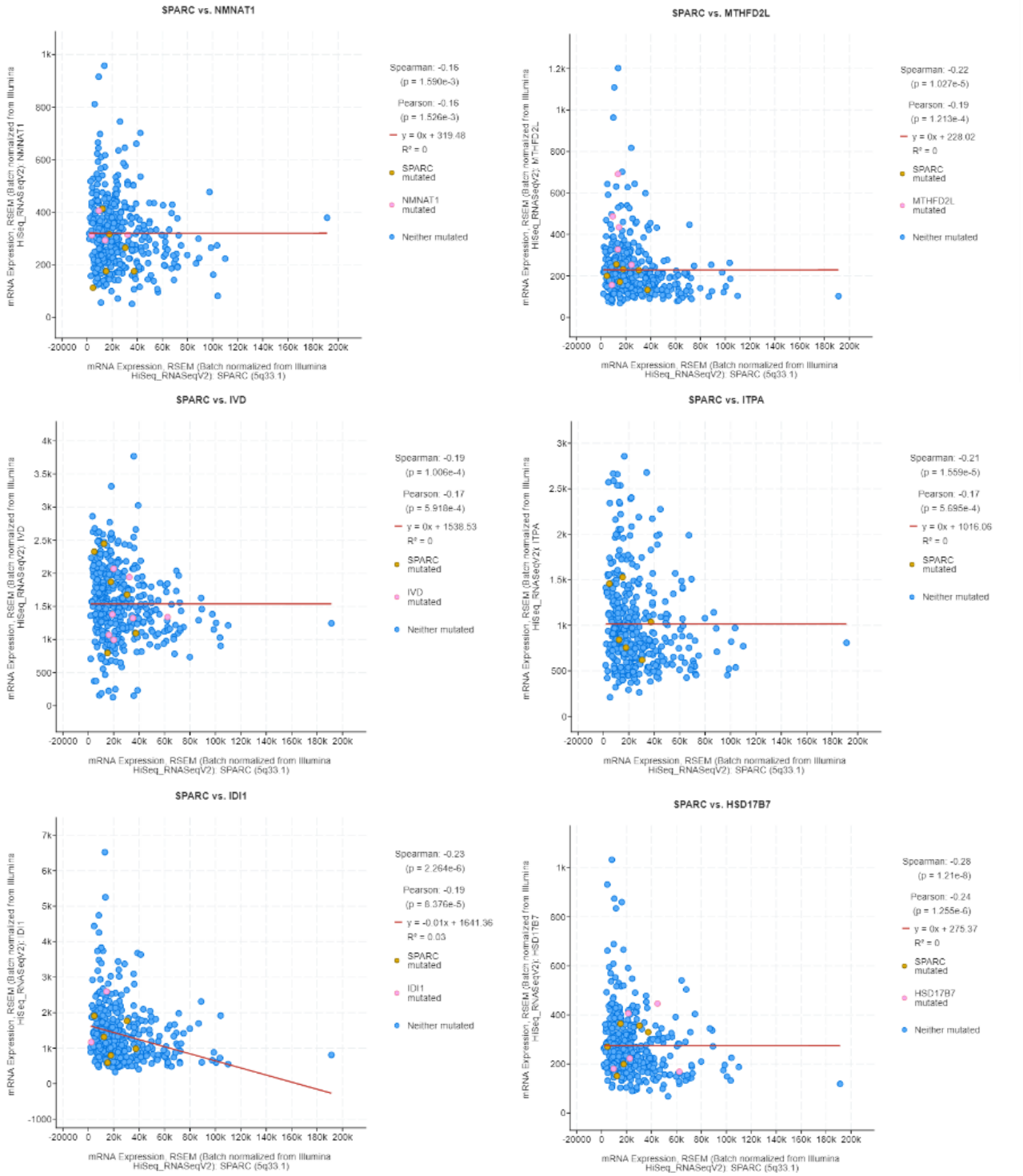

SPARC vs. PNPO
mRNA Expression, RSEM (Batch normalized from Illumina HiSeq_RNASeqV2): PNPO
mRNA Expression, RSEM (Batch normalized from Illumina HiSeq_RNASeqV2): SPARC (5q33.1)
Spearman: -0.20
(p = 3.472e-5)
Pearson: -0.20
(p = 5.297e-5)
y = 0x + 1212.92
R² = 0
SPARC mutated
PNPO mutated
Neither mutated

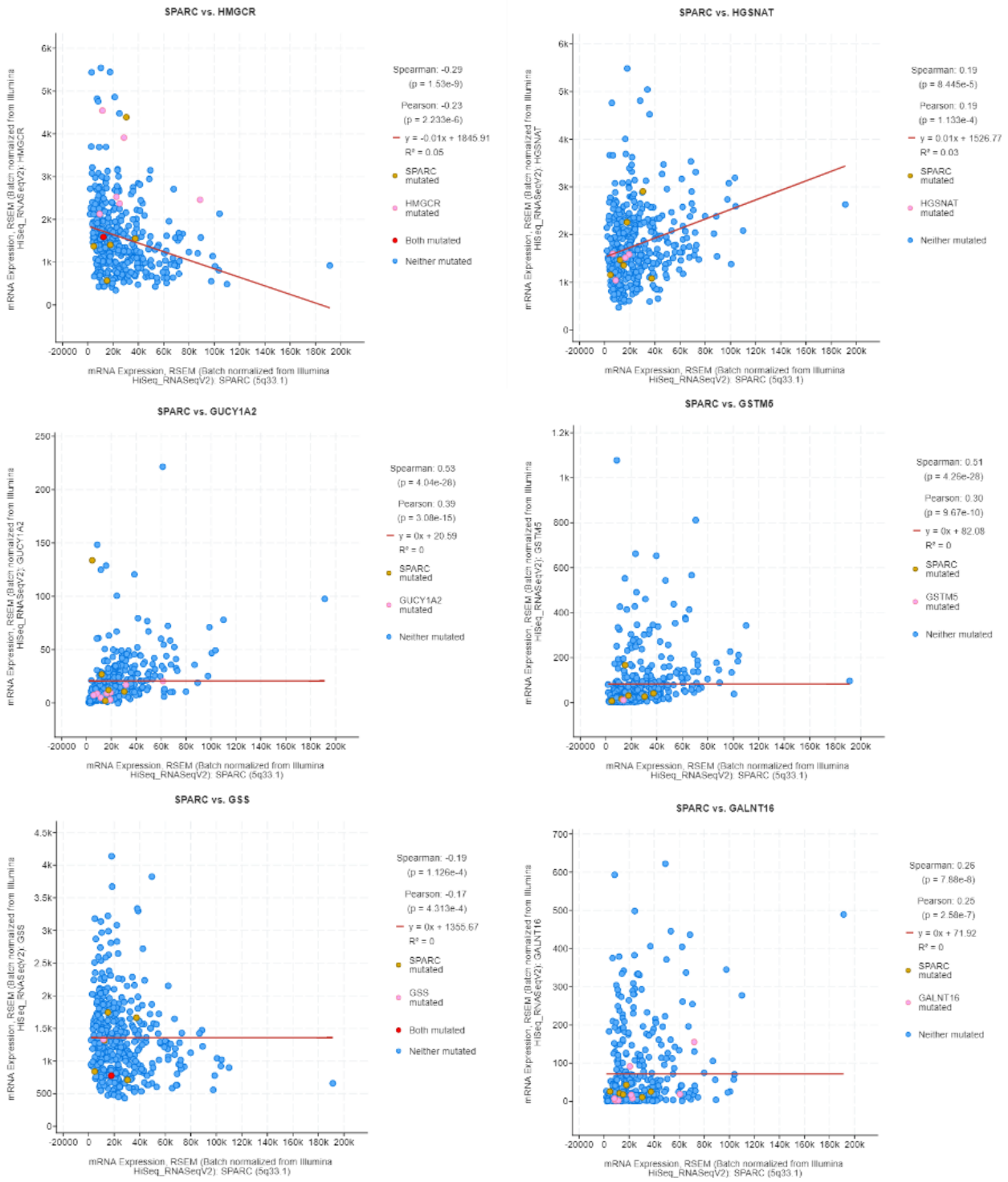

SPARC vs. PLCH1
mRNA Expression, RSEM (Batch normalized from Illumina HiSeq_RNASeqV2): PLCH1
mRNA Expression, RSEM (Batch normalized from Illumina HiSeq_RNASeqV2): SPARC (5q33.1)
Spearman: -0.28
(p = 1.39e-8)
Pearson: -0.29
(p = 4.54e-9)
y = 0x + 287.47
R² = 0
SPARC mutated
PLCH1 mutated
Neither mutated

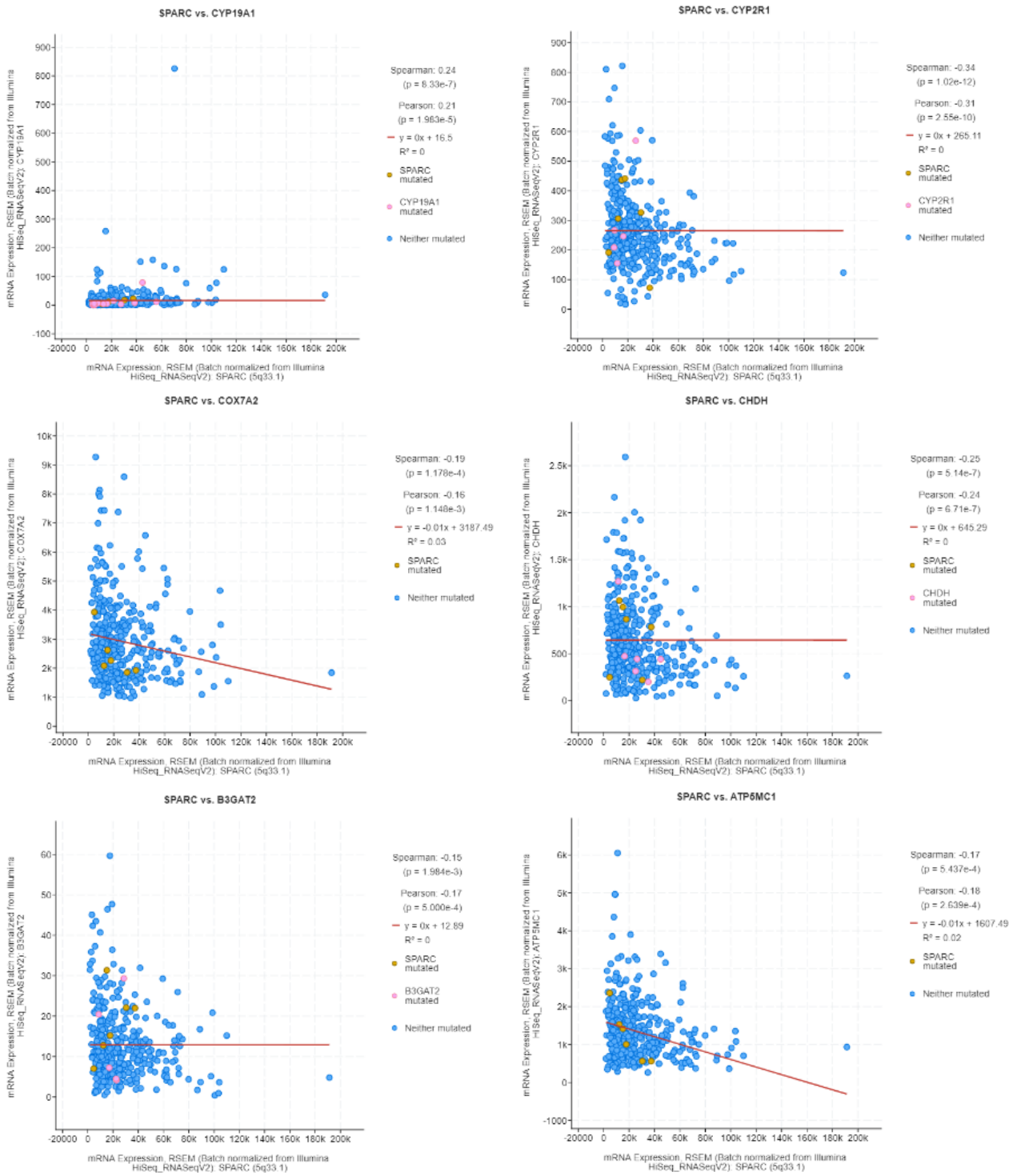

SPARC vs. PIGU
mRNA Expression, RSEM (Batch normalized from Illumina HiSeq_RNASeqV2): PIGU
mRNA Expression, RSEM (Batch normalized from Illumina HiSeq_RNASeqV2): SPARC (5q33.1)
Spearman: -0.15
(p = 2.019e-3)
Pearson: -0.19
(p = 1.470e-4)
y = 0x + 873.21
R² = 0
SPARC mutated
PIGU mutated
Neither mutated

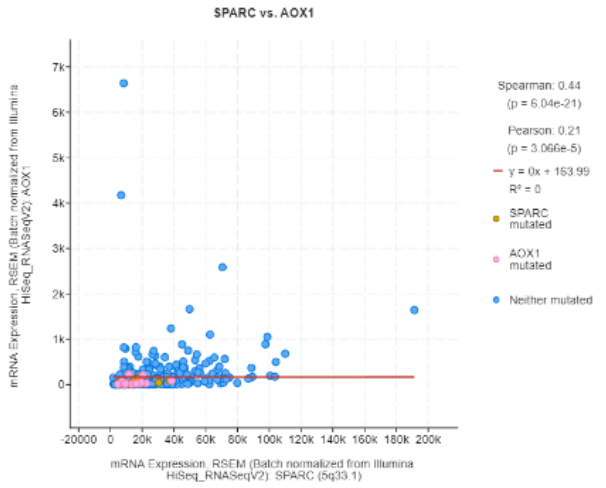

SPARC vs. PIGM
mRNA Expression, RSEM (Batch normalized from Illumina HiSeq_RNASeqV2): PIGM
mRNA Expression, RSEM (Batch normalized from Illumina HiSeq_RNASeqV2): SPARC (5q33.1)
Spearman: -0.18
(p = 2.257e-4)
Pearson: -0.17
(p = 6.453e-4)
y = 0x + 475.76
R² = 0
SPARC mutated
PIGM mutated
Neither mutated

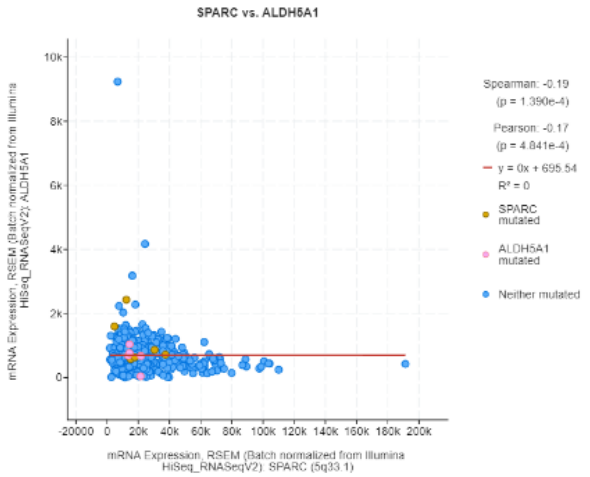

SPARC vs. PIGL
mRNA Expression, RSEM (Batch normalized from Illumina HiSeq_RNASeqV2): PIGL
mRNA Expression, RSEM (Batch normalized from Illumina HiSeq_RNASeqV2): SPARC (5q33.1)
Spearman: -0.21
(p = 1.444e-5)
Pearson: -0.20
(p = 3.104e-5)
y = 0x + 86.08
R² = 0
SPARC mutated
PIGL mutated
Neither mutated
SPARC vs. PDE7B
mRNA Expression, RSEM (Batch normalized from Illumina HiSeq_RNASeqV2): PDE7B
mRNA Expression, RSEM (Batch normalized from Illumina HiSeq_RNASeqV2): SPARC (5q33.1)
Spearman: 0.32
(p = 1.96e-11)
Pearson: 0.22
(p = 1.027e-5)
y = 0x + 121.51
R² = 0
SPARC mutated
PDE7B mutated
Neither mutated
SPARC vs. PDE5A
mRNA Expression, RSEM (Batch normalized from Illumina HiSeq_RNASeqV2): PDE5A
mRNA Expression, RSEM (Batch normalized from Illumina HiSeq_RNASeqV2): SPARC (5q33.1)
Spearman: 0.31
(p = 8.70e-11)
Pearson: 0.20
(p = 3.584e-5)
y = 0.01x + 611.02
R² = 0.04
SPARC mutated
PDE5A mutated
Neither mutated
SPARC vs. PDE4A
mRNA Expression, RSEM (Batch normalized from Illumina HiSeq_RNASeqV2): PDE4A
mRNA Expression, RSEM (Batch normalized from Illumina HiSeq_RNASeqV2): SPARC (5q33.1)
Spearman: 0.20
(p = 5.018e-5)
Pearson: 0.18
(p = 3.784e-4)
y = 0x + 499.16
R² = 0
SPARC mutated
PDE4A mutated
Neither mutated
SPARC vs. PAPSS2
mRNA Expression, RSEM (Batch normalized from Illumina HiSeq_RNASeqV2): PAPSS2
mRNA Expression, RSEM (Batch normalized from Illumina HiSeq_RNASeqV2): SPARC (5q33.1)
Spearman: 0.24
(p = 5.98e-7)
Pearson: 0.20
(p = 5.885e-5)
y = 0.01x + 645.5
R² = 0.03
SPARC mutated
PAPSS2 mutated
Neither mutated
SPARC vs. NUDT12
mRNA Expression, RSEM (Batch normalized from Illumina HiSeq_RNASeqV2): NUDT12
mRNA Expression, RSEM (Batch normalized from Illumina HiSeq_RNASeqV2): SPARC (5q33.1)
Spearman: -0.17
(p = 4.923e-4)
Pearson: -0.16
(p = 1.341e-3)
y = 0x + 453.69
R² = 0
SPARC mutated
NUDT12 mutated
Neither mutated

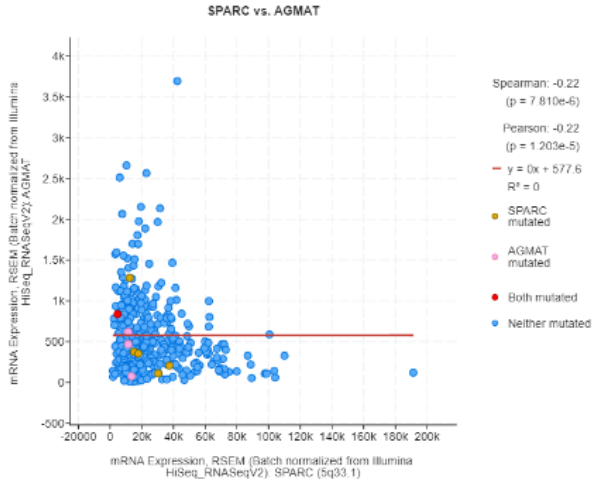

SPARC vs. NMNAT1
mRNA Expression, RSEM (Batch normalized from Illumina HiSeq_RNASeqV2): NMNAT1
mRNA Expression, RSEM (Batch normalized from Illumina HiSeq_RNASeqV2): SPARC (5q33.1)
Spearman: -0.15
(p = 1.590e-3)
Pearson: -0.16
(p = 1.526e-3)
y = 0x + 319.48
R² = 0
SPARC mutated
NMNAT1 mutated
Neither mutated
SPARC vs. MTHFD2L
mRNA Expression, RSEM (Batch normalized from Illumina HiSeq_RNASeqV2): MTHFD2L
mRNA Expression, RSEM (Batch normalized from Illumina HiSeq_RNASeqV2): SPARC (5q33.1)
Spearman: -0.22
(p = 1.027e-5)
Pearson: -0.19
(p = 1.213e-4)
y = 0x + 228.02
R² = 0
SPARC mutated
MTHFD2L mutated
Neither mutated
SPARC vs. IVD
mRNA Expression, RSEM (Batch normalized from Illumina HiSeq_RNASeqV2): IVD
mRNA Expression, RSEM (Batch normalized from Illumina HiSeq_RNASeqV2): SPARC (5q33.1)
Spearman: -0.19
(p = 1.006e-4)
Pearson: -0.17
(p = 5.918e-4)
y = 0x + 1538.53
R² = 0
SPARC mutated
IVD mutated
Neither mutated
SPARC vs. ITPA
mRNA Expression, RSEM (Batch normalized from Illumina HiSeq_RNASeqV2): ITPA
mRNA Expression, RSEM (Batch normalized from Illumina HiSeq_RNASeqV2): SPARC (5q33.1)
Spearman: -0.21
(p = 1.559e-5)
Pearson: -0.17
(p = 5.695e-4)
y = 0x + 1016.06
R² = 0
SPARC mutated
Neither mutated
SPARC vs. IDI1
mRNA Expression, RSEM (Batch normalized from Illumina HiSeq_RNASeqV2): IDI1
mRNA Expression, RSEM (Batch normalized from Illumina HiSeq_RNASeqV2): SPARC (5q33.1)
Spearman: -0.23
(p = 2.264e-6)
Pearson: -0.19
(p = 8.376e-5)
y = -0.01x + 1641.36
R² = 0.03
SPARC mutated
IDI1 mutated
Neither mutated
SPARC vs. HSD17B7
mRNA Expression, RSEM (Batch normalized from Illumina HiSeq_RNASeqV2): HSD17B7
mRNA Expression, RSEM (Batch normalized from Illumina HiSeq_RNASeqV2): SPARC (5q33.1)
Spearman: -0.28
(p = 1.21e-8)
Pearson: -0.24
(p = 1.255e-6)
y = 0x + 275.37
R² = 0
SPARC mutated
HSD17B7 mutated
Neither mutated

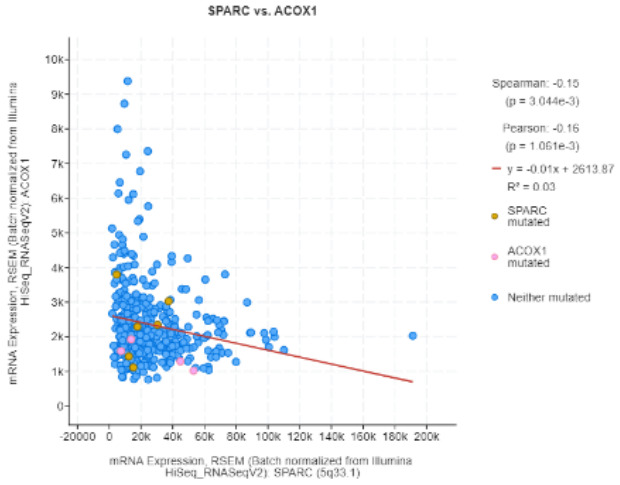

SPARC vs. HMGCR
mRNA Expression, RSEM (Batch normalized from Illumina HiSeq_RNASeqV2): HMGCR
mRNA Expression, RSEM (Batch normalized from Illumina HiSeq_RNASeqV2): SPARC (5q33.1)
Spearman: -0.29
(p = 1.53e-9)
Pearson: -0.23
(p = 2.233e-6)
y = -0.01x + 1845.91
R² = 0.05
SPARC mutated
HMGCR mutated
Both mutated
Neither mutated
SPARC vs. HGSNAT
mRNA Expression, RSEM (Batch normalized from Illumina HiSeq_RNASeqV2): HGSNAT
mRNA Expression, RSEM (Batch normalized from Illumina HiSeq_RNASeqV2): SPARC (5q33.1)
Spearman: 0.19
(p = 8.445e-5)
Pearson: 0.19
(p = 1.133e-4)
y = 0.01x + 1526.77
R² = 0.03
SPARC mutated
HGSNAT mutated
Neither mutated
SPARC vs. GUCY1A2
mRNA Expression, RSEM (Batch normalized from Illumina HiSeq_RNASeqV2): GUCY1A2
mRNA Expression, RSEM (Batch normalized from Illumina HiSeq_RNASeqV2): SPARC (5q33.1)
Spearman: 0.53
(p = 4.04e-28)
Pearson: 0.39
(p = 3.08e-15)
y = 0x + 20.59
R² = 0
SPARC mutated
GUCY1A2 mutated
Neither mutated
SPARC vs. GSTM5
mRNA Expression, RSEM (Batch normalized from Illumina HiSeq_RNASeqV2): GSTM5
mRNA Expression, RSEM (Batch normalized from Illumina HiSeq_RNASeqV2): SPARC (5q33.1)
Spearman: 0.51
(p = 4.26e-28)
Pearson: 0.30
(p = 9.67e-10)
y = 0x + 82.08
R² = 0
SPARC mutated
GSTM5 mutated
Neither mutated
SPARC vs. GSS
mRNA Expression, RSEM (Batch normalized from Illumina HiSeq_RNASeqV2): GSS
mRNA Expression, RSEM (Batch normalized from Illumina HiSeq_RNASeqV2): SPARC (5q33.1)
Spearman: -0.19
(p = 1.126e-4)
Pearson: -0.17
(p = 4.313e-4)
y = 0x + 1355.67
R² = 0
SPARC mutated
GSS mutated
Both mutated
Neither mutated
SPARC vs. GALNT16
mRNA Expression, RSEM (Batch normalized from Illumina HiSeq_RNASeqV2): GALNT16
mRNA Expression, RSEM (Batch normalized from Illumina HiSeq_RNASeqV2): SPARC (5q33.1)
Spearman: 0.26
(p = 7.88e-8)
Pearson: 0.25
(p = 2.58e-7)
y = 0x + 71.92
R² = 0
SPARC mutated
GALNT16 mutated
Neither mutated

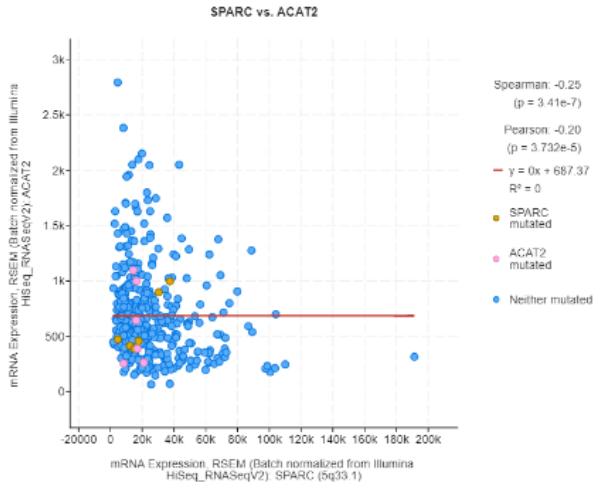

SPARC vs. CYP19A1
mRNA Expression, RSEM (Batch normalized from Illumina HiSeq_RNASeqV2): CYP19A1
mRNA Expression, RSEM (Batch normalized from Illumina HiSeq_RNASeqV2): SPARC (5q33.1)
Spearman: 0.24
(p = 8.33e-7)
Pearson: 0.21
(p = 1.983e-5)
y = 0x + 16.5
R² = 0
SPARC mutated
CYP19A1 mutated
Neither mutated
SPARC vs. CYP2R1
mRNA Expression, RSEM (Batch normalized from Illumina HiSeq_RNASeqV2): CYP2R1
mRNA Expression, RSEM (Batch normalized from Illumina HiSeq_RNASeqV2): SPARC (5q33.1)
Spearman: -0.34
(p = 1.02e-12)
Pearson: -0.31
(p = 2.55e-10)
y = 0x + 265.11
R² = 0
SPARC mutated
CYP2R1 mutated
Neither mutated
SPARC vs. COX7A2
mRNA Expression, RSEM (Batch normalized from Illumina HiSeq_RNASeqV2): COX7A2
mRNA Expression, RSEM (Batch normalized from Illumina HiSeq_RNASeqV2): SPARC (5q33.1)
Spearman: -0.19
(p = 1.178e-4)
Pearson: -0.16
(p = 1.148e-3)
y = -0.01x + 3187.49
R² = 0.03
SPARC mutated
Neither mutated
SPARC vs. CHDH
mRNA Expression, RSEM (Batch normalized from Illumina HiSeq_RNASeqV2): CHDH
mRNA Expression, RSEM (Batch normalized from Illumina HiSeq_RNASeqV2): SPARC (5q33.1)
Spearman: -0.25
(p = 5.14e-7)
Pearson: -0.24
(p = 6.71e-7)
y = 0x + 645.29
R² = 0
SPARC mutated
CHDH mutated
Neither mutated
SPARC vs. B3GAT2
mRNA Expression, RSEM (Batch normalized from Illumina HiSeq_RNASeqV2): B3GAT2
mRNA Expression, RSEM (Batch normalized from Illumina HiSeq_RNASeqV2): SPARC (5q33.1)
Spearman: -0.15
(p = 1.984e-3)
Pearson: -0.17
(p = 5.000e-4)
y = 0x + 12.89
R² = 0
SPARC mutated
B3GAT2 mutated
Neither mutated
SPARC vs. ATP5MC1
mRNA Expression, RSEM (Batch normalized from Illumina HiSeq_RNASeqV2): ATP5MC1
mRNA Expression, RSEM (Batch normalized from Illumina HiSeq_RNASeqV2): SPARC (5q33.1)
Spearman: -0.17
(p = 5.437e-4)
Pearson: -0.18
(p = 2.639e-4)
y = -0.01x + 1607.49
R² = 0.02
SPARC mutated
Neither mutated


SPARC vs. AOX1
mRNA Expression, RSEM (Batch normalized from Illumina HiSeq_RNASeqV2): AOX1
mRNA Expression, RSEM (Batch normalized from Illumina HiSeq_RNASeqV2): SPARC (5q33.1)
Spearman: 0.44
(p = 6.04e-21)
Pearson: 0.21
(p = 3.066e-5)
y = 0x + 163.99
R² = 0
SPARC mutated
AOX1 mutated
Neither mutated

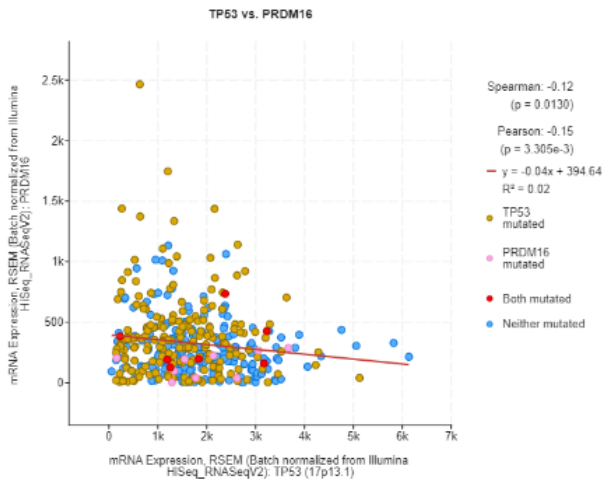

SPARC vs. ALDH5A1
mRNA Expression, RSEM (Batch normalized from Illumina HiSeq_RNASeqV2): ALDH5A1
mRNA Expression, RSEM (Batch normalized from Illumina HiSeq_RNASeqV2): SPARC (5q33.1)
Spearman: -0.19
(p = 1.390e-4)
Pearson: -0.17
(p = 4.841e-4)
y = 0x + 695.54
R² = 0
SPARC mutated
ALDH5A1 mutated
Neither mutated

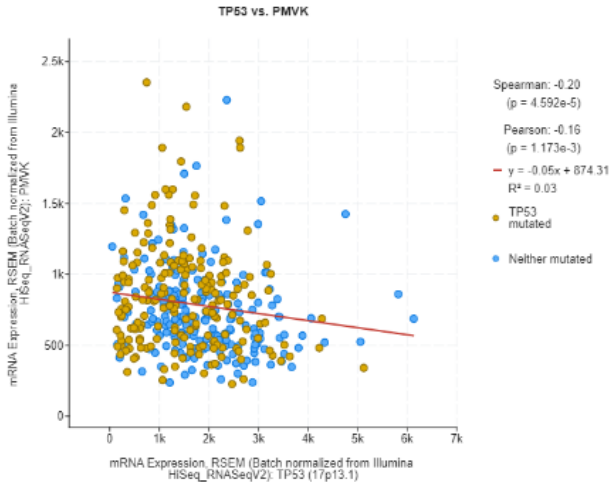

SPARC vs. AGMAT
mRNA Expression, RSEM (Batch normalized from Illumina HiSeq_RNASeqV2): AGMAT
mRNA Expression, RSEM (Batch normalized from Illumina HiSeq_RNASeqV2): SPARC (5q33.1)
Spearman: -0.22
(p = 7.810e-6)
Pearson: -0.22
(p = 1.203e-5)
y = 0x + 577.6
R² = 0
SPARC mutated
AGMAT mutated
Both mutated
Neither mutated

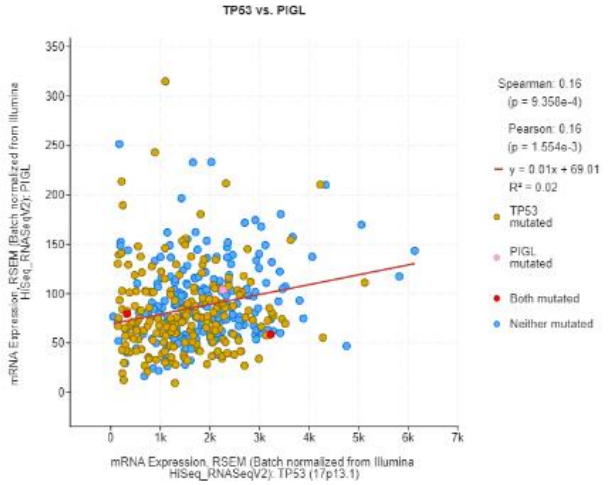

SPARC vs. ACOX1
mRNA Expression, RSEM (Batch normalized from Illumina HiSeq_RNASeqV2): ACOX1
mRNA Expression, RSEM (Batch normalized from Illumina HiSeq_RNASeqV2): SPARC (5q33.1)
Spearman: -0.15
(p = 3.044e-3)
Pearson: -0.16
(p = 1.061e-3)
y = -0.01x + 2613.87
R² = 0.03
SPARC mutated
ACOX1 mutated
Neither mutated

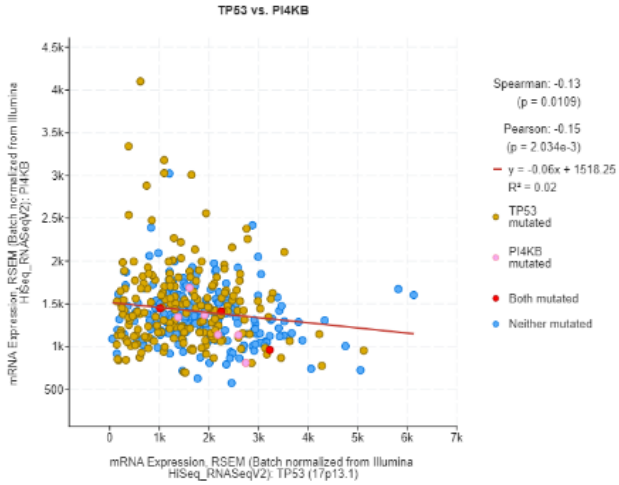

SPARC vs. ACAT2
mRNA Expression, RSEM (Batch normalized from Illumina HiSeq_RNASeqV2): ACAT2
mRNA Expression, RSEM (Batch normalized from Illumina HiSeq_RNASeqV2): SPARC (5q33.1)
Spearman: -0.25
(p = 3.41e-7)
Pearson: -0.20
(p = 3.732e-5)
y = 0x + 687.37
R² = 0
SPARC mutated
ACAT2 mutated
Neither mutated

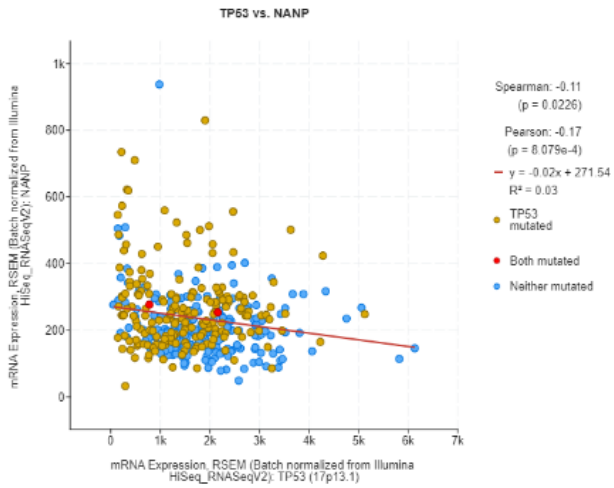
TP53

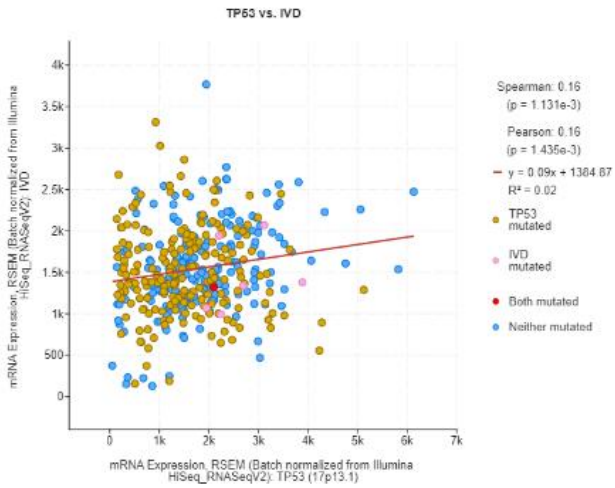

TP53 vs. PRDM16
mRNA Expression, RSEM (Batch normalized from Illumina HiSeq_RNASeqV2): PRDM16
mRNA Expression, RSEM (Batch normalized from Illumina HiSeq_RNASeqV2): TP53 (17p13.1)
Spearman: -0.12
(p = 0.0130)
Pearson: -0.15
(p = 3.305e-3)
y = -0.04x + 394.64
R² = 0.02
TP53 mutated
PRDM16 mutated
Both mutated
Neither mutated

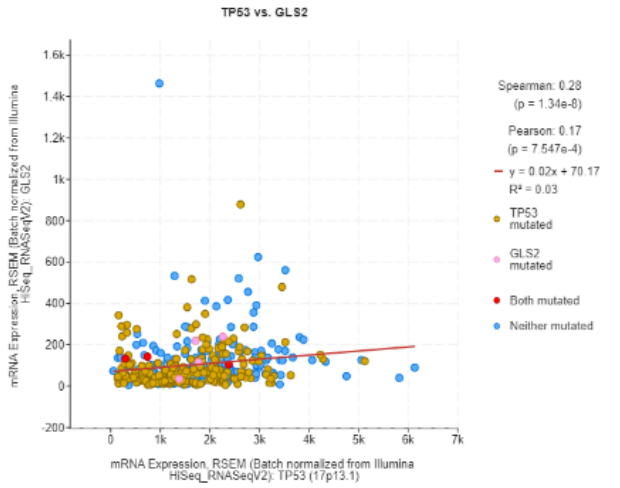

TP53 vs. PMVK
mRNA Expression, RSEM (Batch normalized from Illumina HiSeq_RNASeqV2): PMVK
mRNA Expression, RSEM (Batch normalized from Illumina HiSeq_RNASeqV2): TP53 (17p13.1)
Spearman: -0.20
(p = 4.592e-5)
Pearson: -0.16
(p = 1.173e-3)
y = -0.05x + 874.31
R² = 0.03
TP53 mutated
Neither mutated

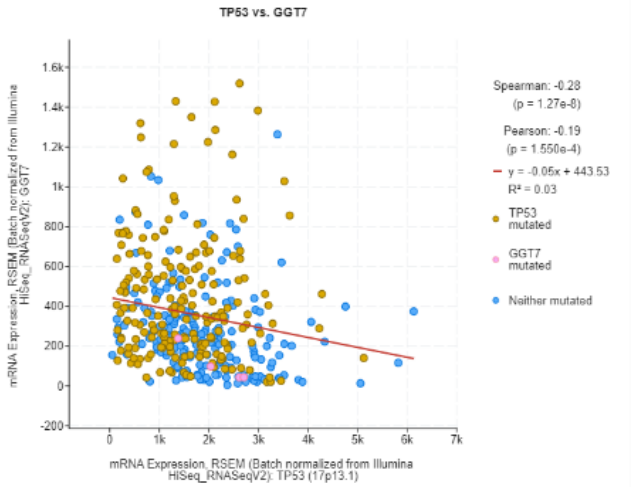

TP53 vs. PIGL
mRNA Expression, RSEM (Batch normalized from Illumina HiSeq_RNASeqV2): PIGL
mRNA Expression, RSEM (Batch normalized from Illumina HiSeq_RNASeqV2): TP53 (17p13.1)
Spearman: 0.16
(p = 9.358e-4)
Pearson: 0.16
(p = 1.554e-3)
y = 0.01x + 69.01
R² = 0.02
TP53 mutated
PIGL mutated
Both mutated
Neither mutated

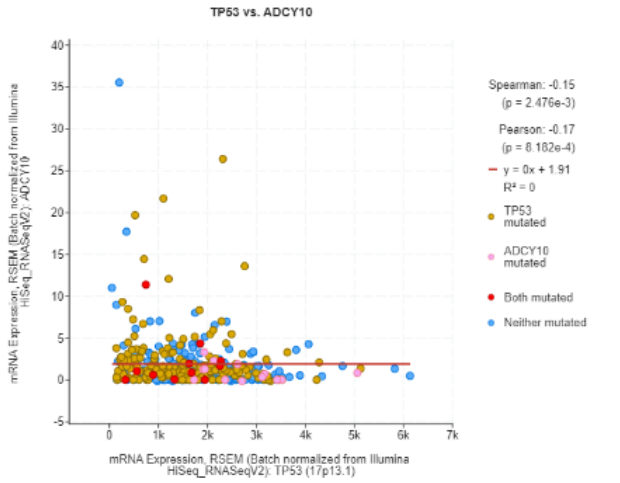

TP53 vs. PI4KB
mRNA Expression, RSEM (Batch normalized from Illumina HiSeq_RNASeqV2): PI4KB
mRNA Expression, RSEM (Batch normalized from Illumina HiSeq_RNASeqV2): TP53 (17p13.1)
Spearman: -0.13
(p = 0.0109)
Pearson: -0.15
(p = 2.034e-3)
y = -0.06x + 1518.25
R² = 0.02
TP53 mutated
PI4KB mutated
Both mutated
Neither mutated

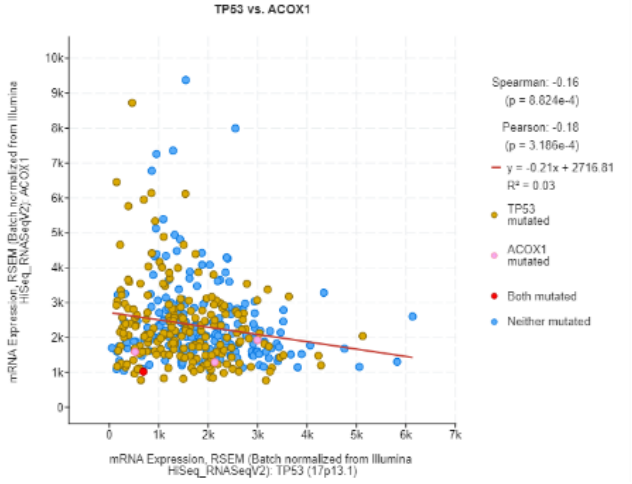

TP53 vs. NANP
mRNA Expression, RSEM (Batch normalized from Illumina HiSeq_RNASeqV2): NANP
mRNA Expression, RSEM (Batch normalized from Illumina HiSeq_RNASeqV2): TP53 (17p13.1)
Spearman: -0.11
(p = 0.0226)
Pearson: -0.17
(p = 8.079e-4)
y = -0.02x + 271.54
R² = 0.03
TP53 mutated
Both mutated
Neither mutated


TP53 vs. IVD
mRNA Expression, RSEM (Batch normalized from Illumina HiSeq_RNASeqV2): IVD
mRNA Expression, RSEM (Batch normalized from Illumina HiSeq_RNASeqV2): TP53 (17p13.1)
Spearman: 0.16
(p = 1.131e-3)
Pearson: 0.16
(p = 1.435e-3)
y = 0.09x + 1384.87
R² = 0.02
TP53 mutated
IVD mutated
Both mutated
Neither mutated

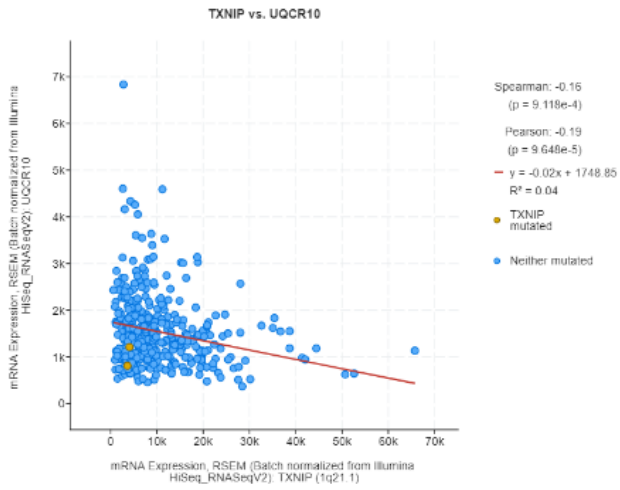

TP53 vs. GLS2
mRNA Expression, RSEM (Batch normalized from Illumina HiSeq_RNASeqV2): GLS2
mRNA Expression, RSEM (Batch normalized from Illumina HiSeq_RNASeqV2): TP53 (17p13.1)
Spearman: 0.28
(p = 1.34e-8)
Pearson: 0.17
(p = 7.547e-4)
y = 0.02x + 70.17
R² = 0.03
TP53 mutated
GLS2 mutated
Both mutated
Neither mutated

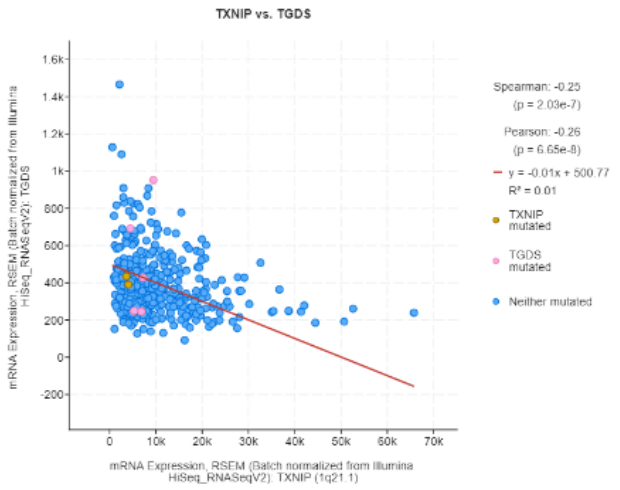

TP53 vs. GGT7
mRNA Expression, RSEM (Batch normalized from Illumina HiSeq_RNASeqV2): GGT7
mRNA Expression, RSEM (Batch normalized from Illumina HiSeq_RNASeqV2): TP53 (17p13.1)
Spearman: -0.28
(p = 1.27e-8)
Pearson: -0.19
(p = 1.550e-4)
y = -0.05x + 443.53
R² = 0.03
TP53 mutated
GGT7 mutated
Neither mutated

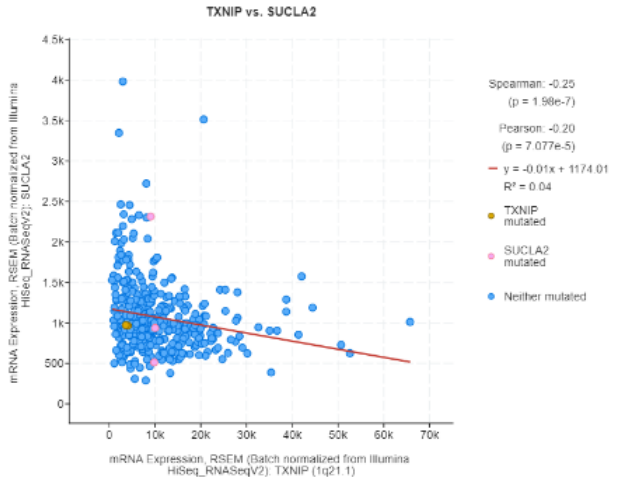

TP53 vs. ADCY10
mRNA Expression, RSEM (Batch normalized from Illumina HiSeq_RNASeqV2): ADCY10
mRNA Expression, RSEM (Batch normalized from Illumina HiSeq_RNASeqV2): TP53 (17p13.1)
Spearman: -0.15
(p = 2.476e-3)
Pearson: -0.17
(p = 8.182e-4)
y = 0x + 1.91
R² = 0
TP53 mutated
ADCY10 mutated
Both mutated
Neither mutated

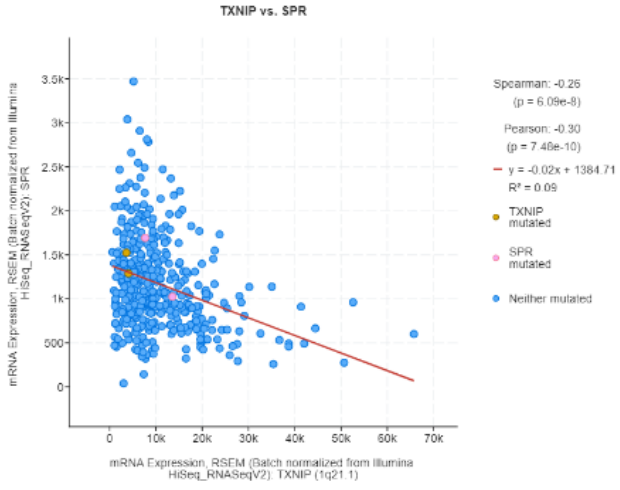

TP53 vs. ACOX1
mRNA Expression, RSEM (Batch normalized from Illumina HiSeq_RNASeqV2): ACOX1
mRNA Expression, RSEM (Batch normalized from Illumina HiSeq_RNASeqV2): TP53 (17p13.1)
Spearman: -0.16
(p = 8.824e-4)
Pearson: -0.18
(p = 3.186e-4)
y = -0.21x + 2716.81
R² = 0.03
TP53 mutated
ACOX1 mutated
Both mutated
Neither mutated

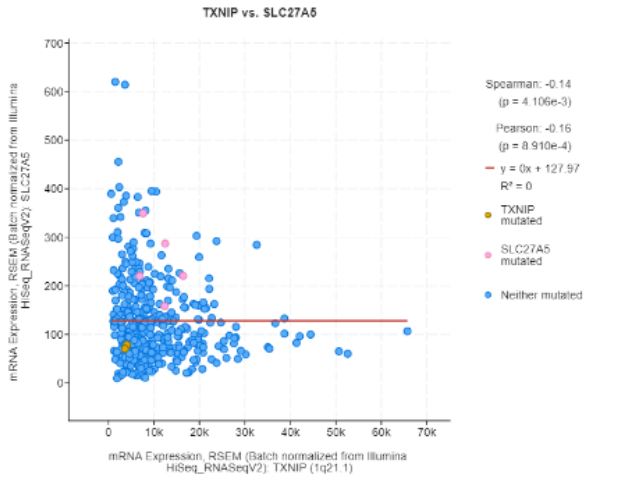
TXNIP

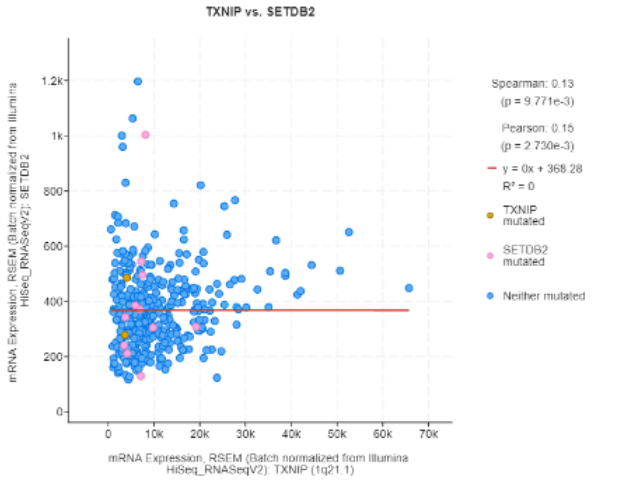

TXNIP vs. UQCR10
mRNA Expression, RSEM (Batch normalized from Illumina HiSeq_RNASeqV2): UQCR10
mRNA Expression, RSEM (Batch normalized from Illumina HiSeq_RNASeqV2): TXNIP (1q21.1)
Spearman: -0.16
(p = 9.118e-4)
Pearson: -0.19
(p = 9.648e-5)
y = -0.02x + 1748.85
R² = 0.04
TXNIP mutated
Neither mutated

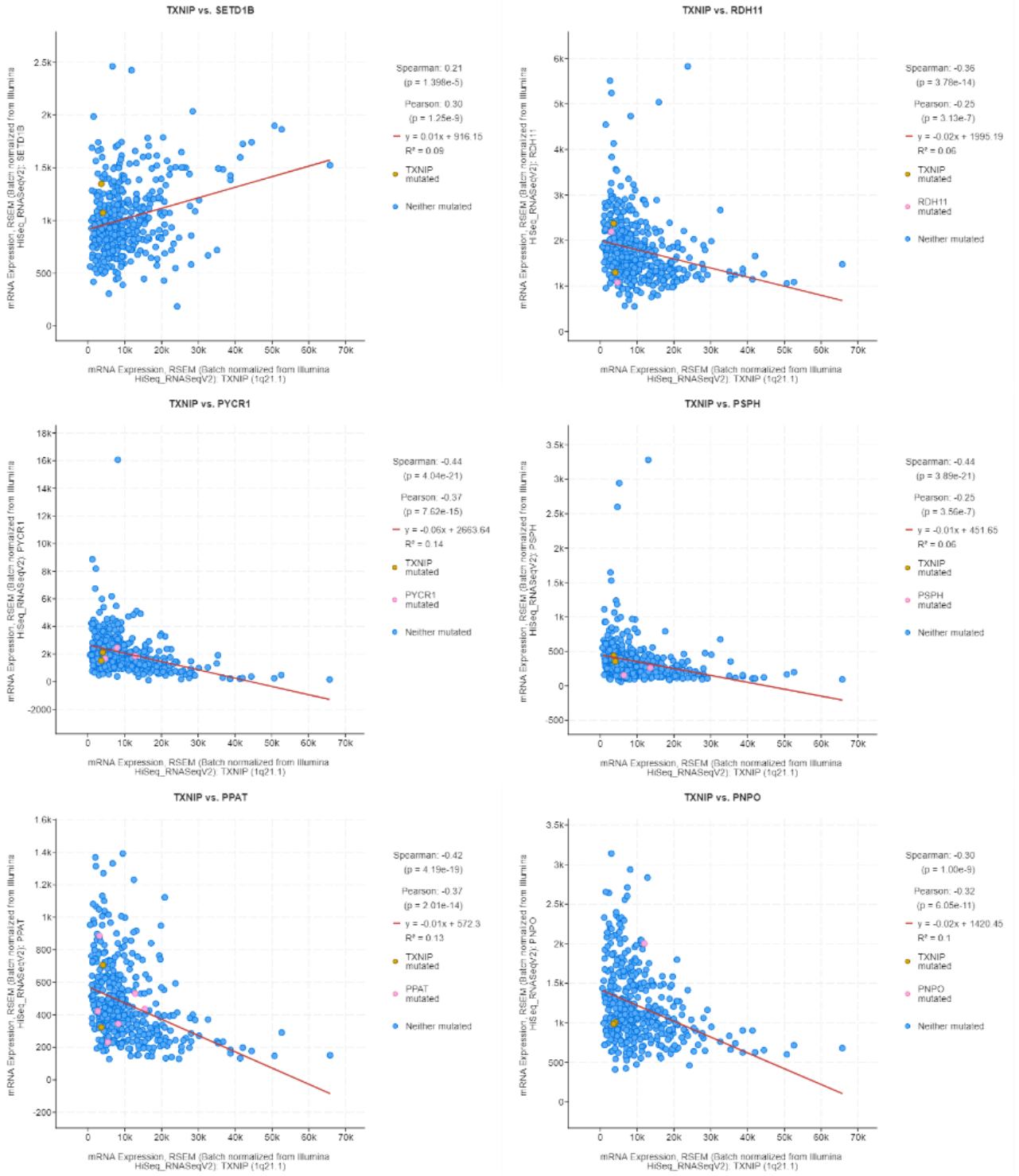

TXNIP vs. TGDS
mRNA Expression, RSEM (Batch normalized from Illumina HiSeq_RNASeqV2): TGDS
mRNA Expression, RSEM (Batch normalized from Illumina HiSeq_RNASeqV2): TXNIP (1q21.1)
Spearman: -0.25
(p = 2.03e-7)
Pearson: -0.26
(p = 6.65e-8)
y = -0.01x + 500.77
R² = 0.01
TXNIP mutated
TGDS mutated
Neither mutated

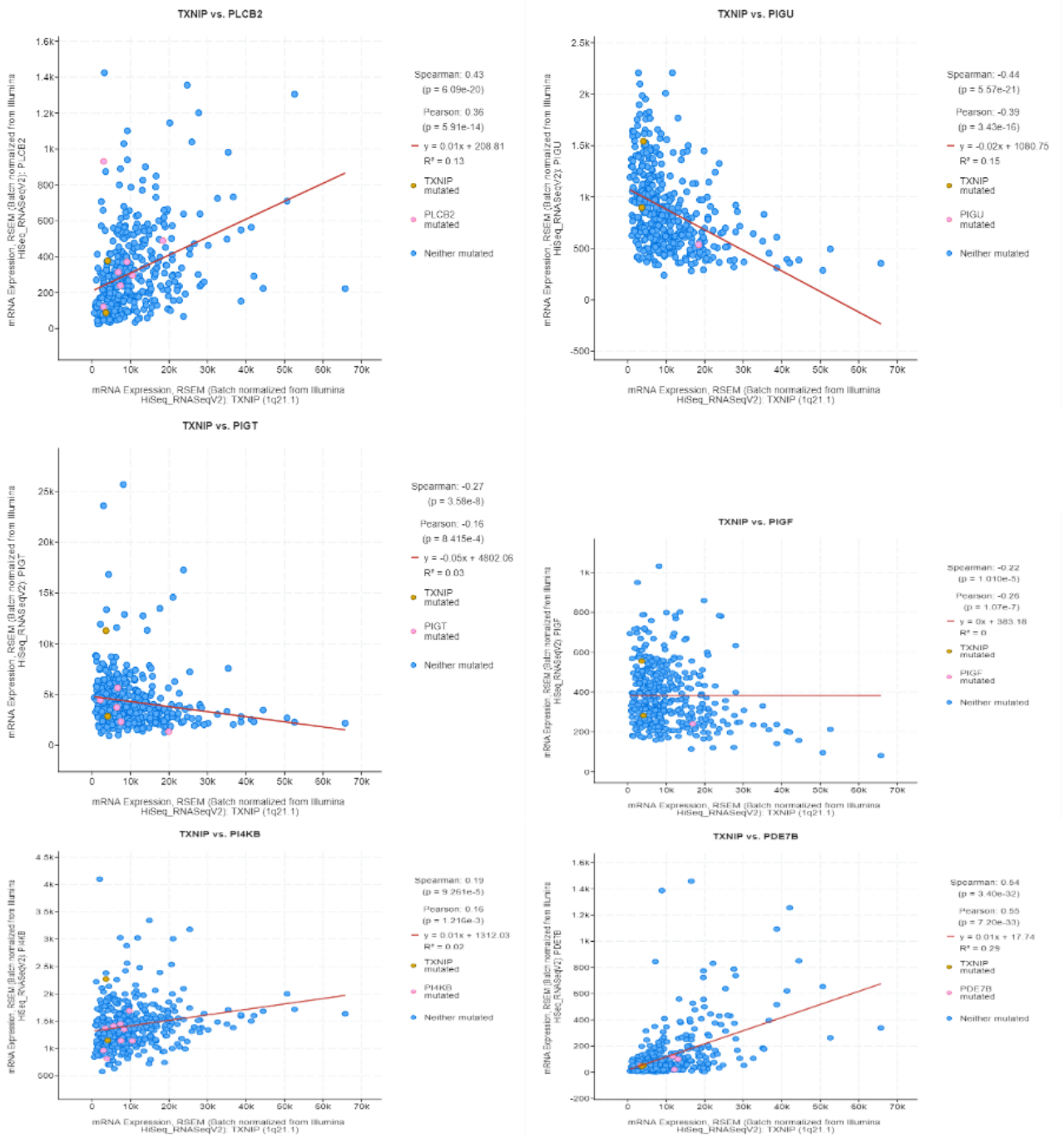

TXNIP vs. SUCLA2
mRNA Expression, RSEM (Batch normalized from Illumina HiSeq_RNASeqV2): SUCLA2
mRNA Expression, RSEM (Batch normalized from Illumina HiSeq_RNASeqV2): TXNIP (1q21.1)
Spearman: -0.25
(p = 1.98e-7)
Pearson: -0.20
(p = 7.077e-5)
y = -0.01x + 1174.01
R² = 0.04
TXNIP mutated
SUCLA2 mutated
Neither mutated

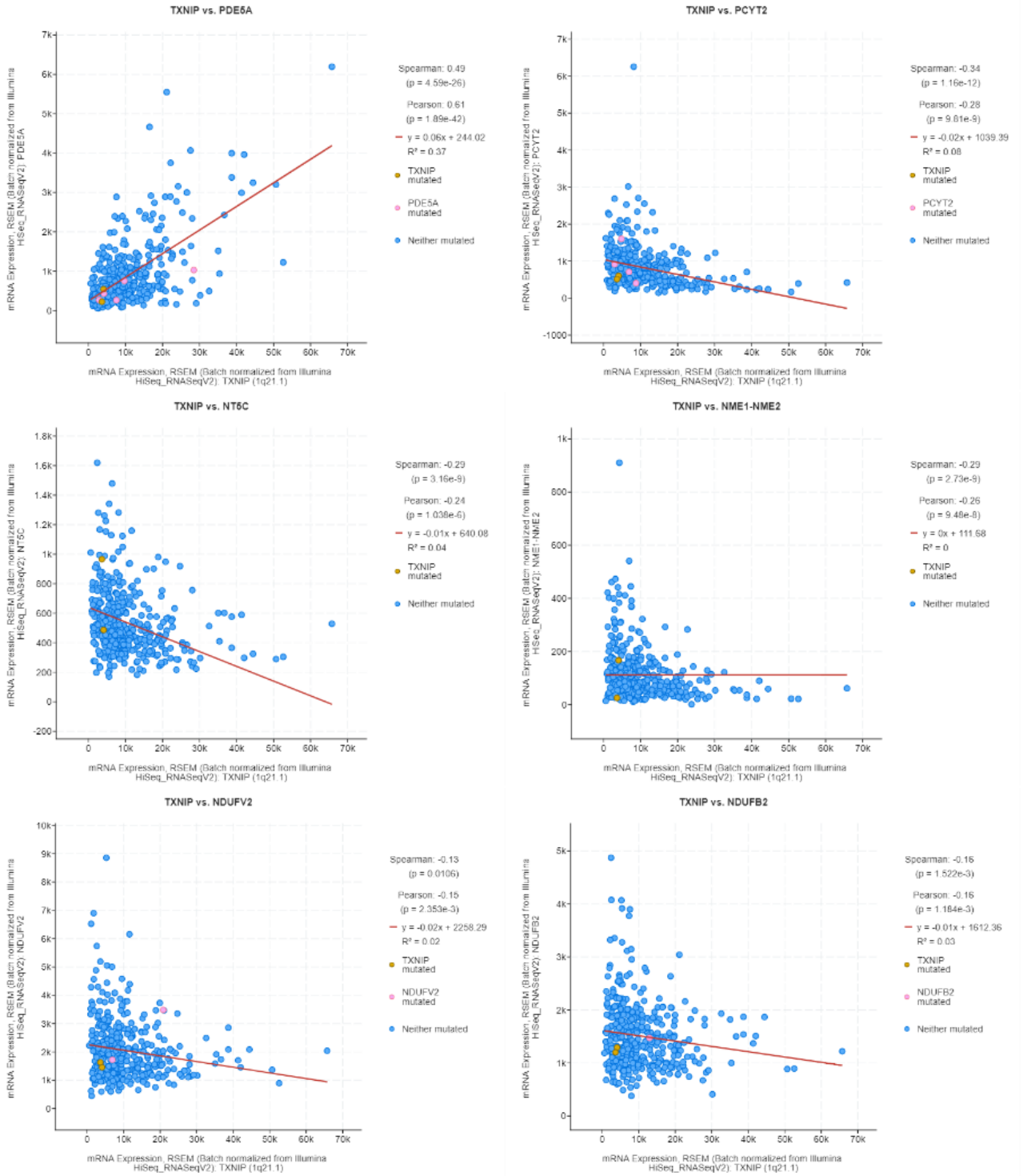

TXNIP vs. SPR
mRNA Expression, RSEM (Batch normalized from Illumina HiSeq_RNASeqV2): SPR
mRNA Expression, RSEM (Batch normalized from Illumina HiSeq_RNASeqV2): TXNIP (1q21.1)
Spearman: -0.26
(p = 6.09e-8)
Pearson: -0.30
(p = 7.48e-10)
y = -0.02x + 1384.71
R² = 0.09
TXNIP mutated
SPR mutated
Neither mutated

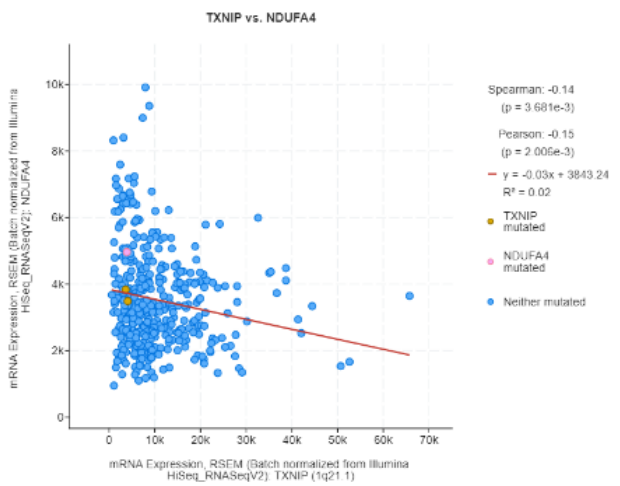

TXNIP vs. SLC27A5
mRNA Expression, RSEM (Batch normalized from Illumina HiSeq_RNASeqV2): SLC27A5
mRNA Expression, RSEM (Batch normalized from Illumina HiSeq_RNASeqV2): TXNIP (1q21.1)
Spearman: -0.14
(p = 4.106e-3)
Pearson: -0.16
(p = 8.910e-4)
y = 0x + 127.97
R² = 0
TXNIP mutated
SLC27A5 mutated
Neither mutated

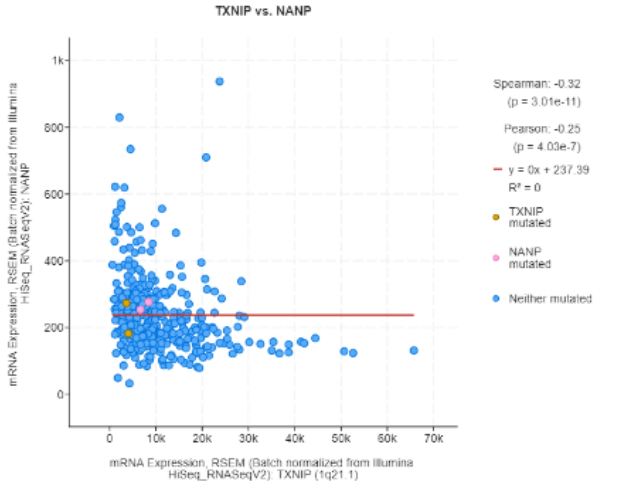

TXNIP vs. SETDB2
mRNA Expression, RSEM (Batch normalized from Illumina HiSeq_RNASeqV2): SETDB2
mRNA Expression, RSEM (Batch normalized from Illumina HiSeq_RNASeqV2): TXNIP (1q21.1)
Spearman: 0.13
(p = 9.771e-3)
Pearson: 0.15
(p = 2.730e-3)
y = 0x + 368.28
R² = 0
TXNIP mutated
SETDB2 mutated
Neither mutated

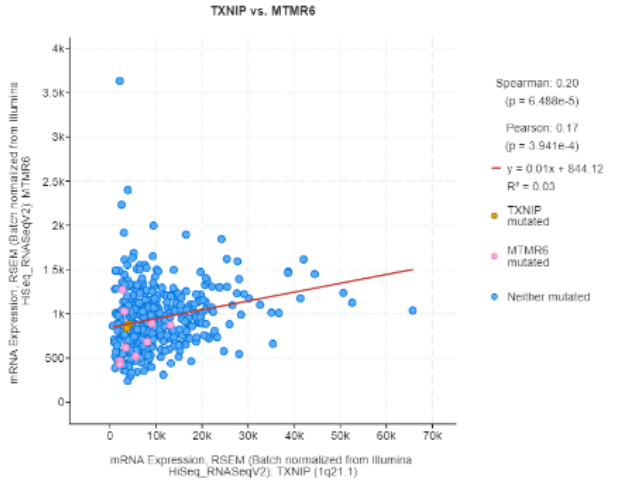

TXNIP vs. SETD1B
mRNA Expression, RSEM (Batch normalized from Illumina HiSeq_RNASeqV2): SETD1B
mRNA Expression, RSEM (Batch normalized from Illumina HiSeq_RNASeqV2): TXNIP (1q21.1)
Spearman: 0.21
(p = 1.398e-5)
Pearson: 0.30
(p = 1.25e-9)
y = 0.01x + 916.15
R² = 0.09
TXNIP mutated
Neither mutated
TXNIP vs. RDH11
mRNA Expression, RSEM (Batch normalized from Illumina HiSeq_RNASeqV2): RDH11
mRNA Expression, RSEM (Batch normalized from Illumina HiSeq_RNASeqV2): TXNIP (1q21.1)
Spearman: -0.36
(p = 3.78e-14)
Pearson: -0.25
(p = 3.13e-7)
y = -0.02x + 1995.19
R² = 0.06
TXNIP mutated
RDH11 mutated
Neither mutated
TXNIP vs. PYCR1
mRNA Expression, RSEM (Batch normalized from Illumina HiSeq_RNASeqV2): PYCR1
mRNA Expression, RSEM (Batch normalized from Illumina HiSeq_RNASeqV2): TXNIP (1q21.1)
Spearman: -0.44
(p = 4.04e-21)
Pearson: -0.37
(p = 7.62e-15)
y = -0.06x + 2663.64
R² = 0.14
TXNIP mutated
PYCR1 mutated
Neither mutated
TXNIP vs. PSPH
mRNA Expression, RSEM (Batch normalized from Illumina HiSeq_RNASeqV2): PSPH
mRNA Expression, RSEM (Batch normalized from Illumina HiSeq_RNASeqV2): TXNIP (1q21.1)
Spearman: -0.44
(p = 3.89e-21)
Pearson: -0.25
(p = 3.56e-7)
y = -0.01x + 451.65
R² = 0.06
TXNIP mutated
PSPH mutated
Neither mutated
TXNIP vs. PPAT
mRNA Expression, RSEM (Batch normalized from Illumina HiSeq_RNASeqV2): PPAT
mRNA Expression, RSEM (Batch normalized from Illumina HiSeq_RNASeqV2): TXNIP (1q21.1)
Spearman: -0.42
(p = 4.19e-19)
Pearson: -0.37
(p = 2.01e-14)
y = -0.01x + 572.3
R² = 0.13
TXNIP mutated
PPAT mutated
Neither mutated
TXNIP vs. PNPO
mRNA Expression, RSEM (Batch normalized from Illumina HiSeq_RNASeqV2): PNPO
mRNA Expression, RSEM (Batch normalized from Illumina HiSeq_RNASeqV2): TXNIP (1q21.1)
Spearman: -0.30
(p = 1.00e-9)
Pearson: -0.32
(p = 6.05e-11)
y = -0.02x + 1420.45
R² = 0.1
TXNIP mutated
PNPO mutated
Neither mutated

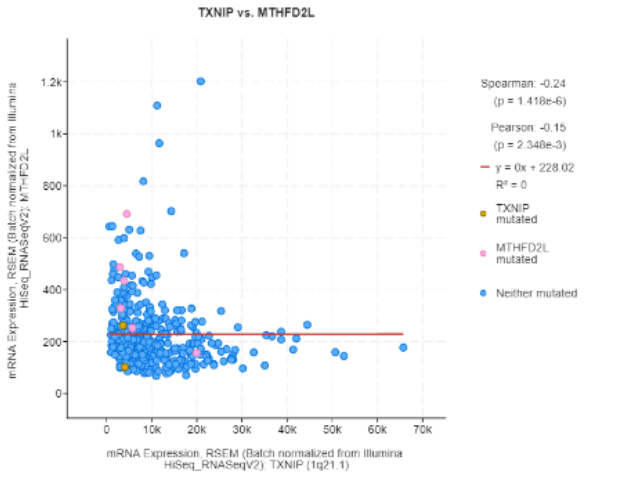

TXNIP vs. PLCB2
mRNA Expression, RSEM (Batch normalized from Illumina HiSeq_RNASeqV2): PLCB2
mRNA Expression, RSEM (Batch normalized from Illumina HiSeq_RNASeqV2): TXNIP (1q21.1)
Spearman: 0.43
(p = 6.09e-20)
Pearson: 0.36
(p = 5.91e-14)
y = 0.01x + 208.81
R² = 0.13
TXNIP mutated
PLCB2 mutated
Neither mutated
TXNIP vs. PIGU
mRNA Expression, RSEM (Batch normalized from Illumina HiSeq_RNASeqV2): PIGU
mRNA Expression, RSEM (Batch normalized from Illumina HiSeq_RNASeqV2): TXNIP (1q21.1)
Spearman: -0.44
(p = 5.57e-21)
Pearson: -0.39
(p = 3.43e-16)
y = -0.02x + 1080.75
R² = 0.15
TXNIP mutated
PIGU mutated
Neither mutated
TXNIP vs. PIGT
mRNA Expression, RSEM (Batch normalized from Illumina HiSeq_RNASeqV2): PIGT
mRNA Expression, RSEM (Batch normalized from Illumina HiSeq_RNASeqV2): TXNIP (1q21.1)
Spearman: -0.27
(p = 3.58e-8)
Pearson: -0.16
(p = 8.415e-4)
y = -0.05x + 4802.06
R² = 0.03
TXNIP mutated
PIGT mutated
Neither mutated
TXNIP vs. PIGF
mRNA Expression, RSEM (Batch normalized from Illumina HiSeq_RNASeqV2): PIGF
mRNA Expression, RSEM (Batch normalized from Illumina HiSeq_RNASeqV2): TXNIP (1q21.1)
Spearman: -0.22
(p = 1.010e-5)
Pearson: -0.26
(p = 1.07e-7)
y = 0x + 383.18
R² = 0
TXNIP mutated
PIGF mutated
Neither mutated
TXNIP vs. PI4KB
mRNA Expression, RSEM (Batch normalized from Illumina HiSeq_RNASeqV2): PI4KB
mRNA Expression, RSEM (Batch normalized from Illumina HiSeq_RNASeqV2): TXNIP (1q21.1)
Spearman: 0.19
(p = 9.261e-5)
Pearson: 0.16
(p = 1.216e-3)
y = 0.01x + 1312.03
R² = 0.02
TXNIP mutated
PI4KB mutated
Neither mutated
TXNIP vs. PDE7B
mRNA Expression, RSEM (Batch normalized from Illumina HiSeq_RNASeqV2): PDE7B
mRNA Expression, RSEM (Batch normalized from Illumina HiSeq_RNASeqV2): TXNIP (1q21.1)
Spearman: 0.64
(p = 3.40e-32)
Pearson: 0.55
(p = 7.20e-33)
y = 0.01x + 17.74
R² = 0.29
TXNIP mutated
PDE7B mutated
Neither mutated

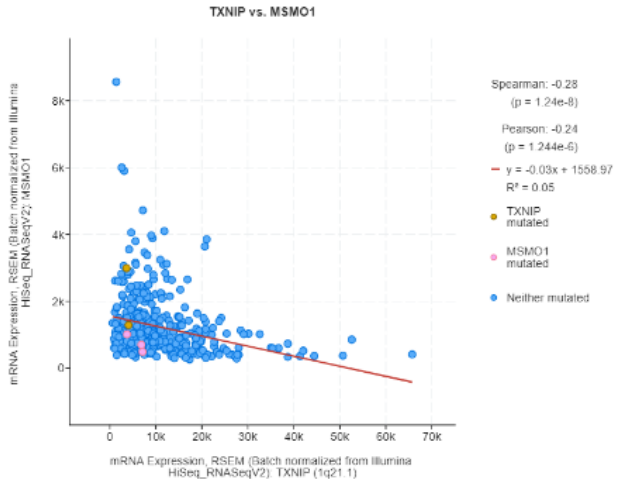

TXNIP vs. PDE5A
mRNA Expression, RSEM (Batch normalized from Illumina HiSeq_RNASeqV2): PDE5A
mRNA Expression, RSEM (Batch normalized from Illumina HiSeq_RNASeqV2): TXNIP (1q21.1)
Spearman: 0.49
(p = 4.59e-26)
Pearson: 0.61
(p = 1.89e-42)
y = 0.06x + 244.02
R² = 0.37
TXNIP mutated
PDE5A mutated
Neither mutated
TXNIP vs. PCYT2
mRNA Expression, RSEM (Batch normalized from Illumina HiSeq_RNASeqV2): PCYT2
mRNA Expression, RSEM (Batch normalized from Illumina HiSeq_RNASeqV2): TXNIP (1q21.1)
Spearman: -0.34
(p = 1.16e-12)
Pearson: -0.28
(p = 9.81e-9)
y = -0.02x + 1039.39
R² = 0.08
TXNIP mutated
PCYT2 mutated
Neither mutated
TXNIP vs. NT5C
mRNA Expression, RSEM (Batch normalized from Illumina HiSeq_RNASeqV2): NT5C
mRNA Expression, RSEM (Batch normalized from Illumina HiSeq_RNASeqV2): TXNIP (1q21.1)
Spearman: -0.29
(p = 3.16e-9)
Pearson: -0.24
(p = 1.038e-6)
y = -0.01x + 640.08
R² = 0.04
TXNIP mutated
Neither mutated
TXNIP vs. NME1-NME2
mRNA Expression, RSEM (Batch normalized from Illumina HiSeq_RNASeqV2): NME1-NME2
mRNA Expression, RSEM (Batch normalized from Illumina HiSeq_RNASeqV2): TXNIP (1q21.1)
Spearman: -0.29
(p = 2.73e-9)
Pearson: -0.26
(p = 9.48e-8)
y = 0x + 111.68
R² = 0
TXNIP mutated
Neither mutated
TXNIP vs. NDUFV2
mRNA Expression, RSEM (Batch normalized from Illumina HiSeq_RNASeqV2): NDUFV2
mRNA Expression, RSEM (Batch normalized from Illumina HiSeq_RNASeqV2): TXNIP (1q21.1)
Spearman: -0.13
(p = 0.0106)
Pearson: -0.15
(p = 2.353e-3)
y = -0.02x + 2258.29
R² = 0.02
TXNIP mutated
NDUFV2 mutated
Neither mutated
TXNIP vs. NDUFB2
mRNA Expression, RSEM (Batch normalized from Illumina HiSeq_RNASeqV2): NDUFB2
mRNA Expression, RSEM (Batch normalized from Illumina HiSeq_RNASeqV2): TXNIP (1q21.1)
Spearman: -0.16
(p = 1.522e-3)
Pearson: -0.16
(p = 1.184e-3)
y = -0.01x + 1612.36
R² = 0.03
TXNIP mutated
NDUFB2 mutated
Neither mutated

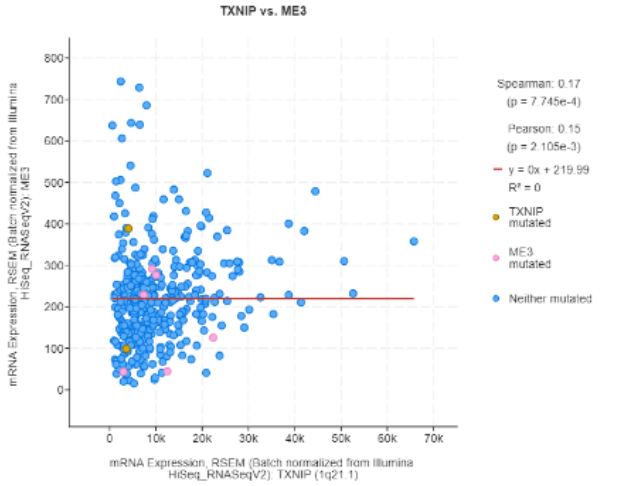

TXNIP vs. NDUFA4
mRNA Expression, RSEM (Batch normalized from Illumina HiSeq_RNASeqV2): NDUFA4
mRNA Expression, RSEM (Batch normalized from Illumina HiSeq_RNASeqV2): TXNIP (1q21.1)
Spearman: -0.14
(p = 3.681e-3)
Pearson: -0.15
(p = 2.006e-3)
y = -0.03x + 3843.24
R² = 0.02
TXNIP mutated
NDUFA4 mutated
Neither mutated

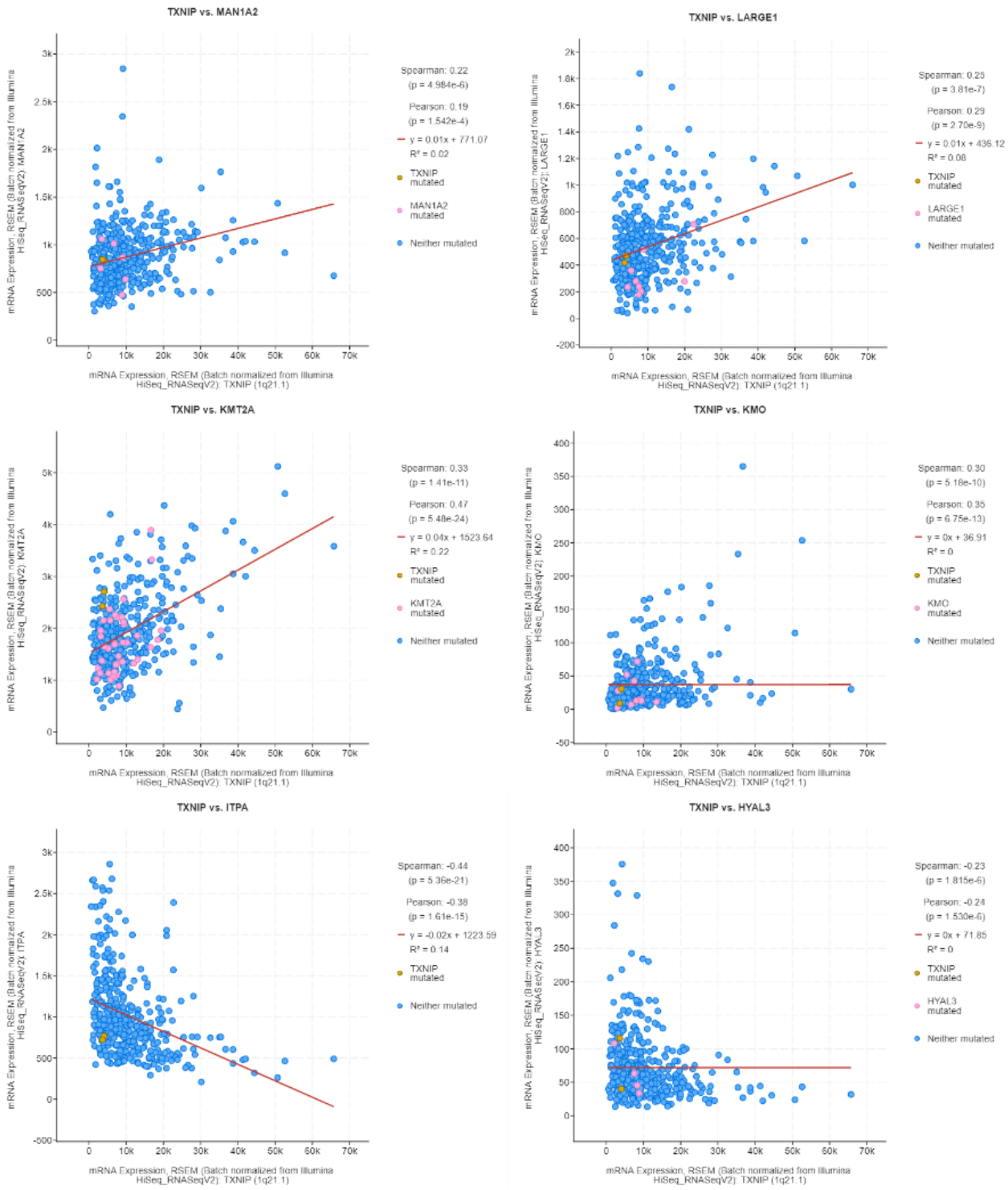

TXNIP vs. NANP
mRNA Expression, RSEM (Batch normalized from Illumina HiSeq_RNASeqV2): NANP
mRNA Expression, RSEM (Batch normalized from Illumina HiSeq_RNASeqV2): TXNIP (1q21.1)
Spearman: -0.32
(p = 3.01e-11)
Pearson: -0.25
(p = 4.03e-7)
y = 0x + 237.39
R² = 0
TXNIP mutated
NANP mutated
Neither mutated

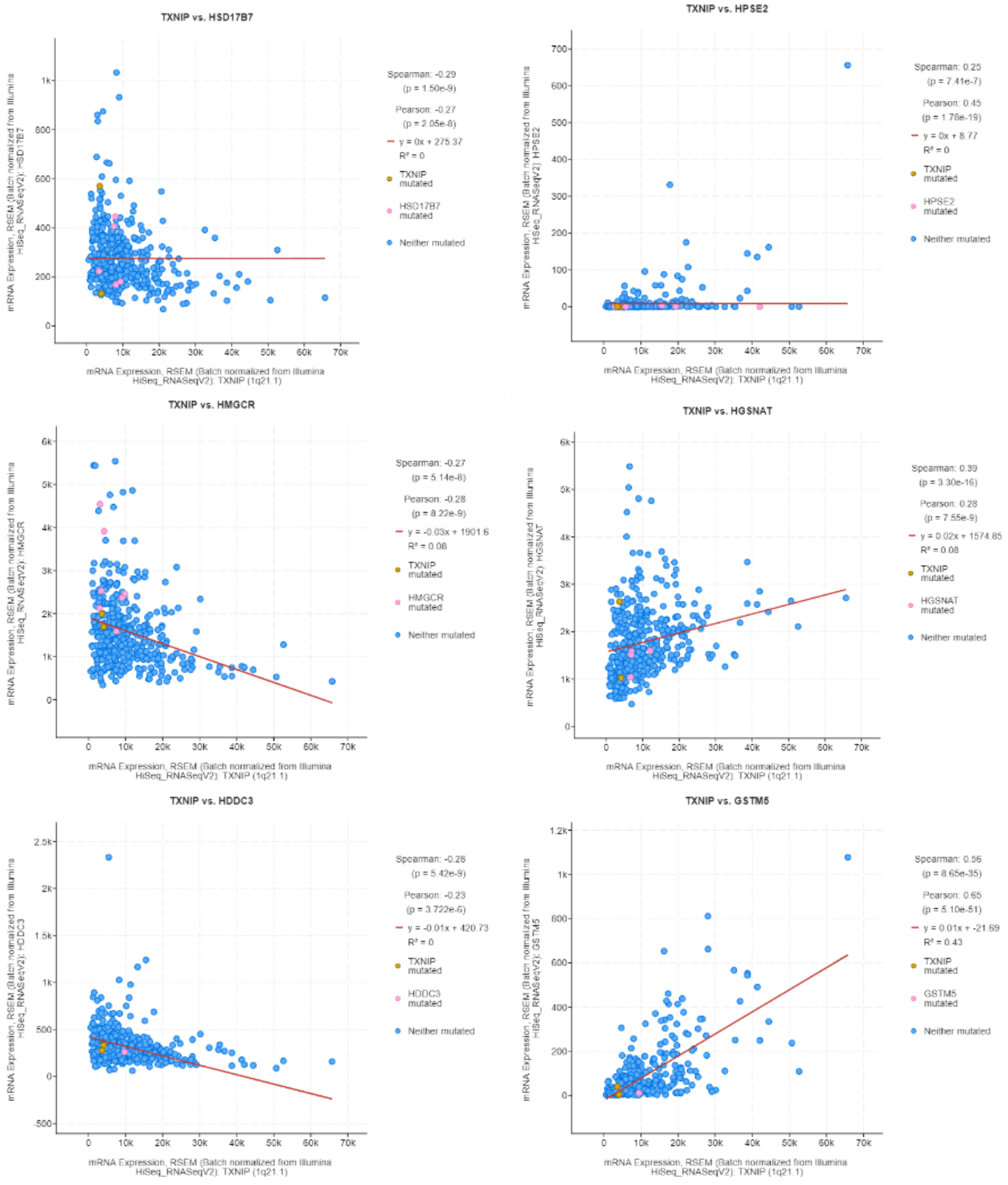

TXNIP vs. MTMR6
mRNA Expression, RSEM (Batch normalized from Illumina HiSeq_RNASeqV2): MTMR6
mRNA Expression, RSEM (Batch normalized from Illumina HiSeq_RNASeqV2): TXNIP (1q21.1)
Spearman: 0.20
(p = 6.488e-5)
Pearson: 0.17
(p = 3.941e-4)
y = 0.01x + 844.12
R² = 0.03
TXNIP mutated
MTMR6 mutated
Neither mutated

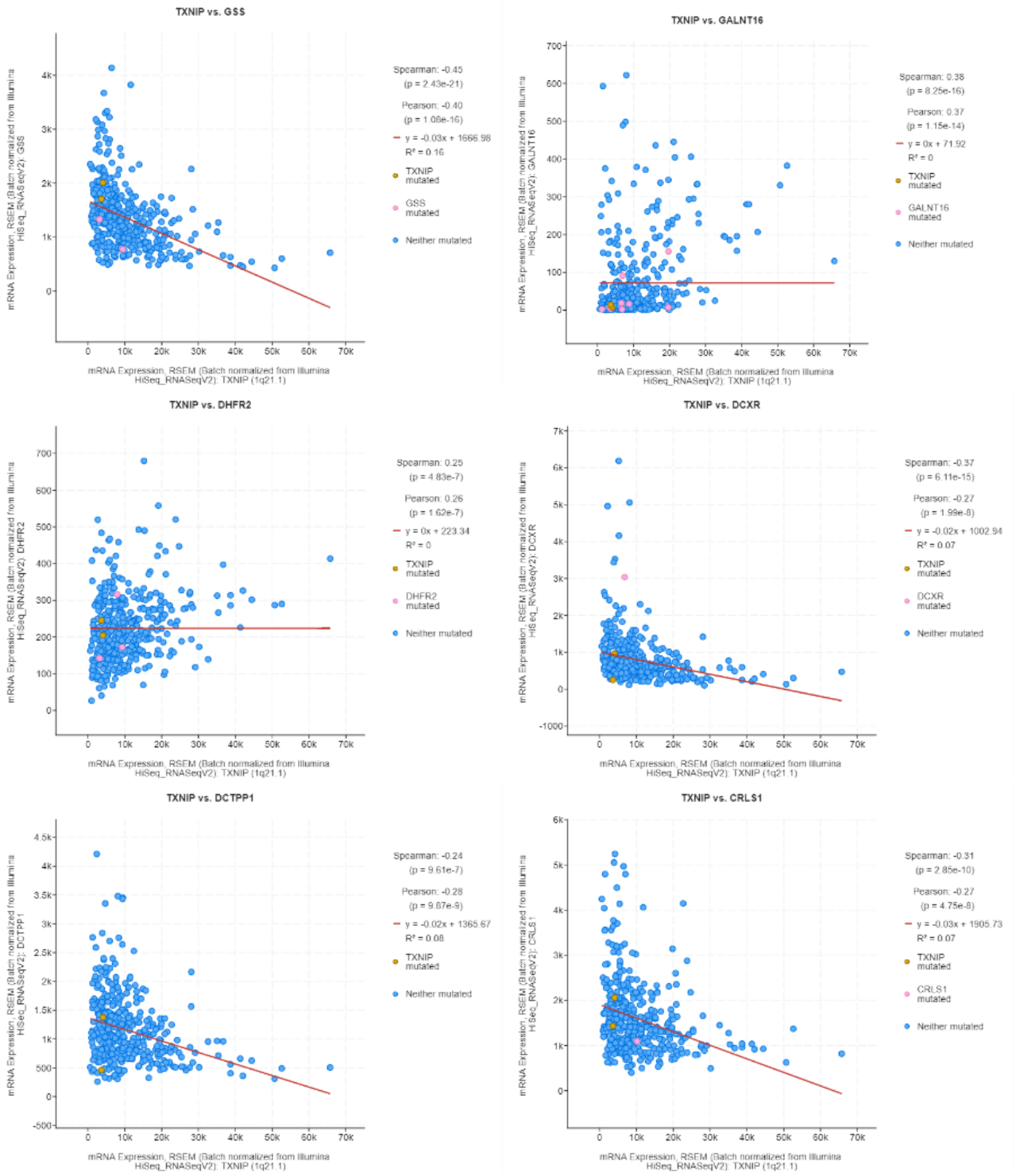

TXNIP vs. MTHFD2L
mRNA Expression, RSEM (Batch normalized from Illumina HiSeq_RNASeqV2): MTHFD2L
mRNA Expression, RSEM (Batch normalized from Illumina HiSeq_RNASeqV2): TXNIP (1q21.1)
Spearman: -0.24
(p = 1.418e-6)
Pearson: -0.15
(p = 2.348e-3)
y = 0x + 228.02
R² = 0
TXNIP mutated
MTHFD2L mutated
Neither mutated

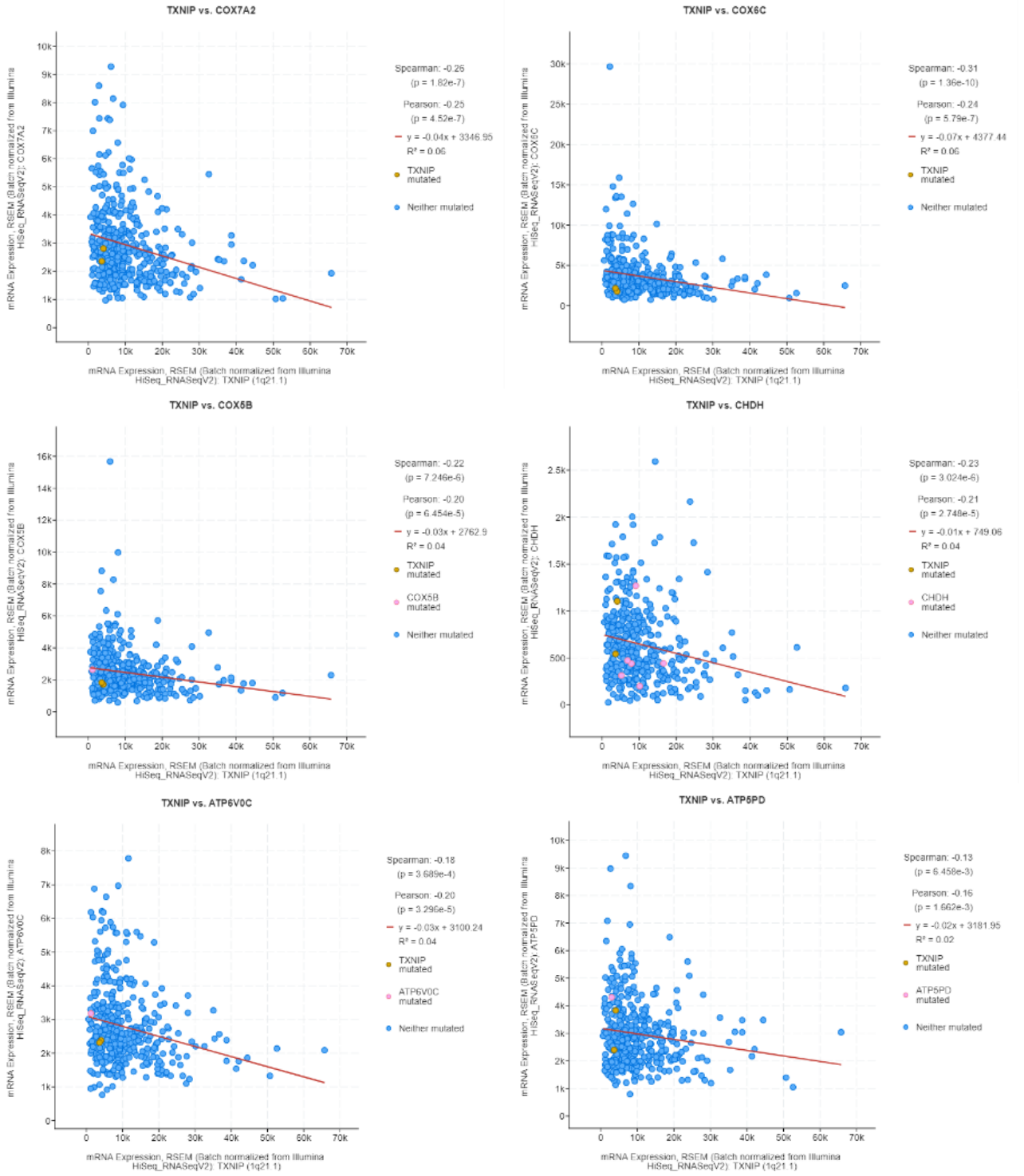

TXNIP vs. MSMO1
mRNA Expression, RSEM (Batch normalized from Illumina HiSeq_RNASeqV2): MSMO1
mRNA Expression, RSEM (Batch normalized from Illumina HiSeq_RNASeqV2): TXNIP (1q21.1)
Spearman: -0.28
(p = 1.24e-8)
Pearson: -0.24
(p = 1.244e-6)
y = -0.03x + 1558.97
R² = 0.05
TXNIP mutated
MSMO1 mutated
Neither mutated

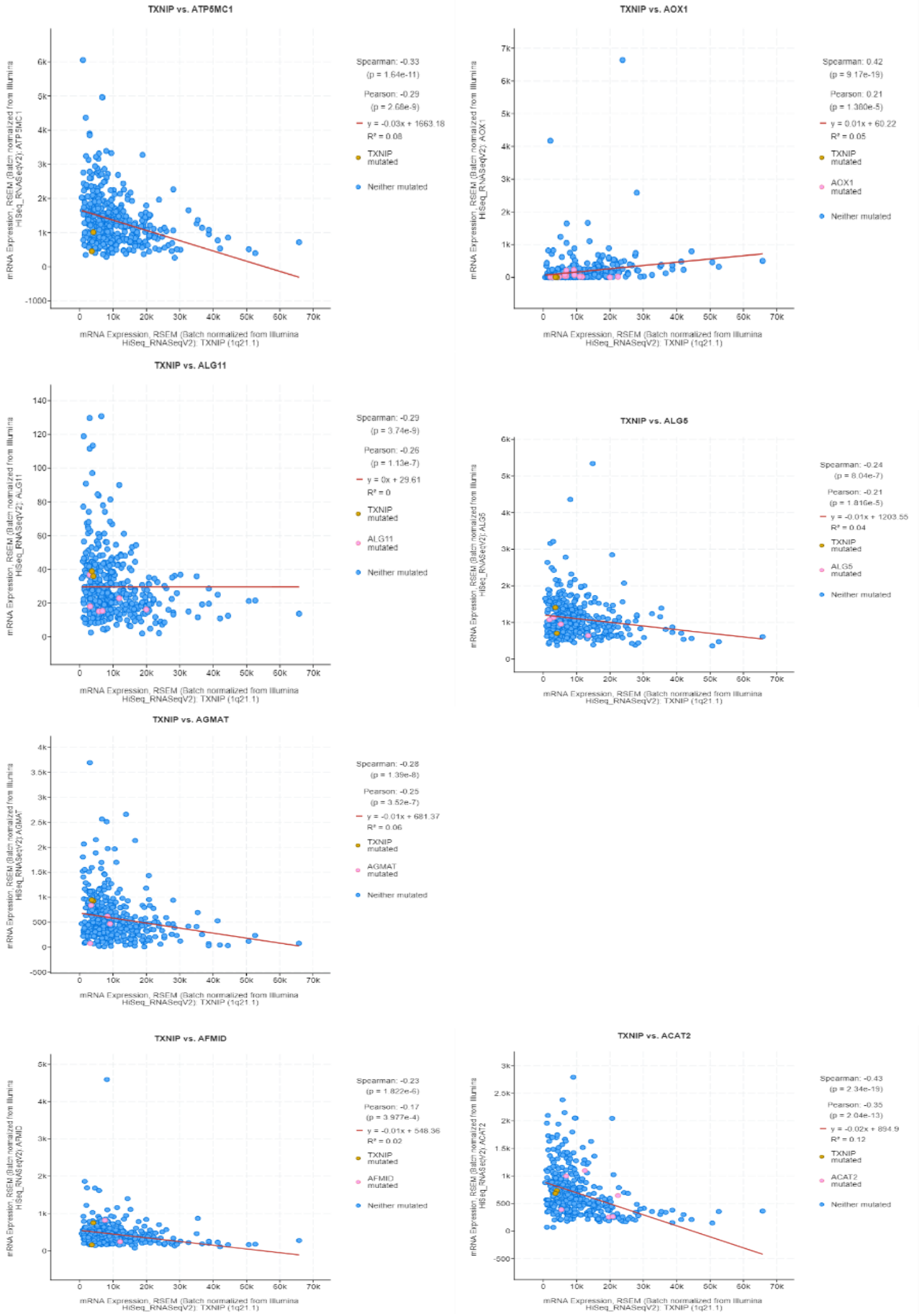

TXNIP vs. ME3
mRNA Expression, RSEM (Batch normalized from Illumina HiSeq_RNASeqV2): ME3
mRNA Expression, RSEM (Batch normalized from Illumina HiSeq_RNASeqV2): TXNIP (1q21.1)
Spearman: 0.17
(p = 7.745e-4)
Pearson: 0.15
(p = 2.105e-3)
y = 0x + 219.99
R² = 0
TXNIP mutated
ME3 mutated
Neither mutated


TXNIP vs. MAN1A2
mRNA Expression, RSEM (Batch normalized from Illumina HiSeq_RNASeqV2): MAN1A2
mRNA Expression, RSEM (Batch normalized from Illumina HiSeq_RNASeqV2): TXNIP (1q21.1)
Spearman: 0.22
(p = 4.984e-6)
Pearson: 0.19
(p = 1.542e-4)
y = 0.01x + 771.07
R² = 0.02
TXNIP mutated
MAN1A2 mutated
Neither mutated
TXNIP vs. LARGE1
mRNA Expression, RSEM (Batch normalized from Illumina HiSeq_RNASeqV2): LARGE1
mRNA Expression, RSEM (Batch normalized from Illumina HiSeq_RNASeqV2): TXNIP (1q21.1)
Spearman: 0.25
(p = 3.81e-7)
Pearson: 0.29
(p = 2.70e-9)
y = 0.01x + 436.12
R² = 0.08
TXNIP mutated
LARGE1 mutated
Neither mutated
TXNIP vs. KMT2A
mRNA Expression, RSEM (Batch normalized from Illumina HiSeq_RNASeqV2): KMT2A
mRNA Expression, RSEM (Batch normalized from Illumina HiSeq_RNASeqV2): TXNIP (1q21.1)
Spearman: 0.33
(p = 1.41e-11)
Pearson: 0.47
(p = 5.48e-24)
y = 0.04x + 1523.64
R² = 0.22
TXNIP mutated
KMT2A mutated
Neither mutated
TXNIP vs. KMO
mRNA Expression, RSEM (Batch normalized from Illumina HiSeq_RNASeqV2): KMO
mRNA Expression, RSEM (Batch normalized from Illumina HiSeq_RNASeqV2): TXNIP (1q21.1)
Spearman: 0.30
(p = 5.18e-10)
Pearson: 0.35
(p = 6.75e-13)
y = 0x + 36.91
R² = 0
TXNIP mutated
KMO mutated
Neither mutated
TXNIP vs. ITPA
mRNA Expression, RSEM (Batch normalized from Illumina HiSeq_RNASeqV2): ITPA
mRNA Expression, RSEM (Batch normalized from Illumina HiSeq_RNASeqV2): TXNIP (1q21.1)
Spearman: -0.44
(p = 5.36e-21)
Pearson: -0.38
(p = 1.61e-15)
y = -0.02x + 1223.59
R² = 0.14
TXNIP mutated
Neither mutated
TXNIP vs. HYAL3
mRNA Expression, RSEM (Batch normalized from Illumina HiSeq_RNASeqV2): HYAL3
mRNA Expression, RSEM (Batch normalized from Illumina HiSeq_RNASeqV2): TXNIP (1q21.1)
Spearman: -0.23
(p = 1.815e-6)
Pearson: -0.24
(p = 1.530e-6)
y = 0x + 71.85
R² = 0
TXNIP mutated
HYAL3 mutated
Neither mutated

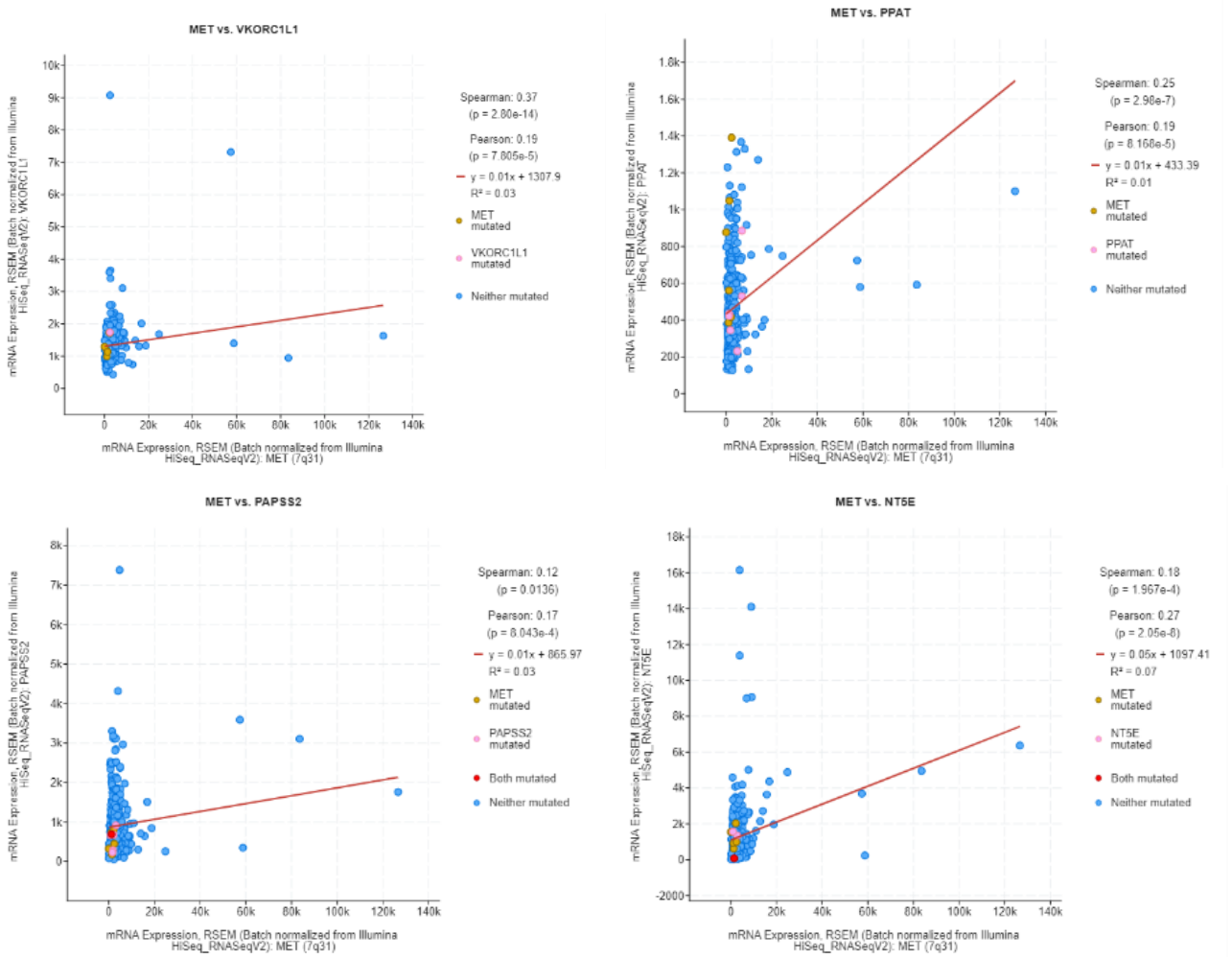

TXNIP vs. HSD17B7
mRNA Expression, RSEM (Batch normalized from Illumina HiSeq_RNASeqV2): HSD17B7
mRNA Expression, RSEM (Batch normalized from Illumina HiSeq_RNASeqV2): TXNIP (1q21.1)
Spearman: -0.29
(p = 1.50e-9)
Pearson: -0.27
(p = 2.05e-8)
y = 0x + 275.37
R² = 0
TXNIP mutated
HSD17B7 mutated
Neither mutated
TXNIP vs. HPSE2
mRNA Expression, RSEM (Batch normalized from Illumina HiSeq_RNASeqV2): HPSE2
mRNA Expression, RSEM (Batch normalized from Illumina HiSeq_RNASeqV2): TXNIP (1q21.1)
Spearman: 0.25
(p = 7.41e-7)
Pearson: 0.45
(p = 1.78e-19)
y = 0x + 8.77
R² = 0
TXNIP mutated
HPSE2 mutated
Neither mutated
TXNIP vs. HMGCR
mRNA Expression, RSEM (Batch normalized from Illumina HiSeq_RNASeqV2): HMGCR
mRNA Expression, RSEM (Batch normalized from Illumina HiSeq_RNASeqV2): TXNIP (1q21.1)
Spearman: -0.27
(p = 5.14e-8)
Pearson: -0.28
(p = 8.22e-9)
y = -0.03x + 1901.6
R² = 0.08
TXNIP mutated
HMGCR mutated
Neither mutated
TXNIP vs. HGSNAT
mRNA Expression, RSEM (Batch normalized from Illumina HiSeq_RNASeqV2): HGSNAT
mRNA Expression, RSEM (Batch normalized from Illumina HiSeq_RNASeqV2): TXNIP (1q21.1)
Spearman: 0.39
(p = 3.30e-16)
Pearson: 0.28
(p = 7.55e-9)
y = 0.02x + 1574.85
R² = 0.08
TXNIP mutated
HGSNAT mutated
Neither mutated
TXNIP vs. HDDC3
mRNA Expression, RSEM (Batch normalized from Illumina HiSeq_RNASeqV2): HDDC3
mRNA Expression, RSEM (Batch normalized from Illumina HiSeq_RNASeqV2): TXNIP (1q21.1)
Spearman: -0.28
(p = 5.42e-9)
Pearson: -0.23
(p = 3.722e-6)
y = -0.01x + 420.73
R² = 0
TXNIP mutated
HDDC3 mutated
Neither mutated
TXNIP vs. GSTM5
mRNA Expression, RSEM (Batch normalized from Illumina HiSeq_RNASeqV2): GSTM5
mRNA Expression, RSEM (Batch normalized from Illumina HiSeq_RNASeqV2): TXNIP (1q21.1)
Spearman: 0.56
(p = 8.65e-35)
Pearson: 0.65
(p = 5.10e-51)
y = 0.01x + -21.69
R² = 0.43
TXNIP mutated
GSTM5 mutated
Neither mutated


TXNIP vs. GSS
mRNA Expression, RSEM (Batch normalized from Illumina HiSeq_RNASeqV2): GSS
mRNA Expression, RSEM (Batch normalized from Illumina HiSeq_RNASeqV2): TXNIP (1q21.1)
Spearman: -0.45
(p = 2.43e-21)
Pearson: -0.40
(p = 1.08e-16)
y = -0.03x + 1666.98
R² = 0.16
TXNIP mutated
GSS mutated
Neither mutated
TXNIP vs. GALNT16
mRNA Expression, RSEM (Batch normalized from Illumina HiSeq_RNASeqV2): GALNT16
mRNA Expression, RSEM (Batch normalized from Illumina HiSeq_RNASeqV2): TXNIP (1q21.1)
Spearman: 0.38
(p = 8.25e-16)
Pearson: 0.37
(p = 1.15e-14)
y = 0x + 71.92
R² = 0
TXNIP mutated
GALNT16 mutated
Neither mutated
TXNIP vs. DHFR2
mRNA Expression, RSEM (Batch normalized from Illumina HiSeq_RNASeqV2): DHFR2
mRNA Expression, RSEM (Batch normalized from Illumina HiSeq_RNASeqV2): TXNIP (1q21.1)
Spearman: 0.25
(p = 4.83e-7)
Pearson: 0.26
(p = 1.62e-7)
y = 0x + 223.34
R² = 0
TXNIP mutated
DHFR2 mutated
Neither mutated
TXNIP vs. DCXR
mRNA Expression, RSEM (Batch normalized from Illumina HiSeq_RNASeqV2): DCXR
mRNA Expression, RSEM (Batch normalized from Illumina HiSeq_RNASeqV2): TXNIP (1q21.1)
Spearman: -0.37
(p = 6.11e-15)
Pearson: -0.27
(p = 1.99e-8)
y = -0.02x + 1002.94
R² = 0.07
TXNIP mutated
DCXR mutated
Neither mutated
TXNIP vs. DCTPP1
mRNA Expression, RSEM (Batch normalized from Illumina HiSeq_RNASeqV2): DCTPP1
mRNA Expression, RSEM (Batch normalized from Illumina HiSeq_RNASeqV2): TXNIP (1q21.1)
Spearman: -0.24
(p = 9.61e-7)
Pearson: -0.28
(p = 9.87e-9)
y = -0.02x + 1365.67
R² = 0.08
TXNIP mutated
Neither mutated
TXNIP vs. CRLS1
mRNA Expression, RSEM (Batch normalized from Illumina HiSeq_RNASeqV2): CRLS1
mRNA Expression, RSEM (Batch normalized from Illumina HiSeq_RNASeqV2): TXNIP (1q21.1)
Spearman: -0.31
(p = 2.85e-10)
Pearson: -0.27
(p = 4.75e-8)
y = -0.03x + 1905.73
R² = 0.07
TXNIP mutated
CRLS1 mutated
Neither mutated


TXNIP vs. COX7A2
mRNA Expression, RSEM (Batch normalized from Illumina HiSeq_RNASeqV2): COX7A2
mRNA Expression, RSEM (Batch normalized from Illumina HiSeq_RNASeqV2): TXNIP (1q21.1)
Spearman: -0.25
(p = 1.82e-7)
Pearson: -0.25
(p = 4.52e-7)
y = -0.04x + 3346.95
R² = 0.06
TXNIP mutated
Neither mutated
TXNIP vs. COX6C
mRNA Expression, RSEM (Batch normalized from Illumina HiSeq_RNASeqV2): COX6C
mRNA Expression, RSEM (Batch normalized from Illumina HiSeq_RNASeqV2): TXNIP (1q21.1)
Spearman: -0.31
(p = 1.36e-10)
Pearson: -0.24
(p = 5.79e-7)
y = -0.07x + 4377.44
R² = 0.06
TXNIP mutated
Neither mutated
TXNIP vs. COX5B
mRNA Expression, RSEM (Batch normalized from Illumina HiSeq_RNASeqV2): COX5B
mRNA Expression, RSEM (Batch normalized from Illumina HiSeq_RNASeqV2): TXNIP (1q21.1)
Spearman: -0.22
(p = 7.246e-6)
Pearson: -0.20
(p = 6.454e-5)
y = -0.03x + 2762.9
R² = 0.04
TXNIP mutated
COX5B mutated
Neither mutated
TXNIP vs. CHDH
mRNA Expression, RSEM (Batch normalized from Illumina HiSeq_RNASeqV2): CHDH
mRNA Expression, RSEM (Batch normalized from Illumina HiSeq_RNASeqV2): TXNIP (1q21.1)
Spearman: -0.23
(p = 3.024e-6)
Pearson: -0.21
(p = 2.748e-5)
y = -0.01x + 749.06
R² = 0.04
TXNIP mutated
CHDH mutated
Neither mutated
TXNIP vs. ATP6V0C
mRNA Expression, RSEM (Batch normalized from Illumina HiSeq_RNASeqV2): ATP6V0C
mRNA Expression, RSEM (Batch normalized from Illumina HiSeq_RNASeqV2): TXNIP (1q21.1)
Spearman: -0.18
(p = 3.689e-4)
Pearson: -0.20
(p = 3.296e-5)
y = -0.03x + 3100.24
R² = 0.04
TXNIP mutated
ATP6V0C mutated
Neither mutated
TXNIP vs. ATP5PD
mRNA Expression, RSEM (Batch normalized from Illumina HiSeq_RNASeqV2): ATP5PD
mRNA Expression, RSEM (Batch normalized from Illumina HiSeq_RNASeqV2): TXNIP (1q21.1)
Spearman: -0.13
(p = 6.458e-3)
Pearson: -0.16
(p = 1.662e-3)
y = -0.02x + 3181.95
R² = 0.02
TXNIP mutated
ATP5PD mutated
Neither mutated


TXNIP vs. ATP5MC1
Spearman: -0.33
(p = 1.64e-11)
Pearson: -0.29
(p = 2.68e-9)
y = -0.03x + 1663.18
R² = 0.08
TXNIP mutated
Neither mutated
TXNIP vs. AOX1
Spearman: 0.42
(p = 9.17e-19)
Pearson: 0.21
(p = 1.380e-5)
y = 0.01x + 60.22
R² = 0.05
TXNIP mutated
AOX1 mutated
Neither mutated
TXNIP vs. ALG11
Spearman: -0.29
(p = 3.74e-9)
Pearson: -0.26
(p = 1.13e-7)
y = 0x + 29.61
R² = 0
TXNIP mutated
ALG11 mutated
Neither mutated
TXNIP vs. ALG5
Spearman: -0.24
(p = 8.04e-7)
Pearson: -0.21
(p = 1.816e-5)
y = -0.01x + 1203.55
R² = 0.04
TXNIP mutated
ALG5 mutated
Neither mutated
TXNIP vs. AGMAT
Spearman: -0.28
(p = 1.39e-8)
Pearson: -0.25
(p = 3.52e-7)
y = -0.01x + 681.37
R² = 0.06
TXNIP mutated
AGMAT mutated
Neither mutated
TXNIP vs. AFMID
Spearman: -0.23
(p = 1.822e-6)
Pearson: -0.17
(p = 3.977e-4)
y = -0.01x + 548.36
R² = 0.02
TXNIP mutated
AFMID mutated
Neither mutated
TXNIP vs. ACAT2
Spearman: -0.43
(p = 2.34e-19)
Pearson: -0.35
(p = 2.04e-13)
y = -0.02x + 894.9
R² = 0.12
TXNIP mutated
ACAT2 mutated
Neither mutated
mRNA Expression, RSEM (Batch normalized from Illumina HiSeq_RNASeqV2): TXNIP (1q21.1)

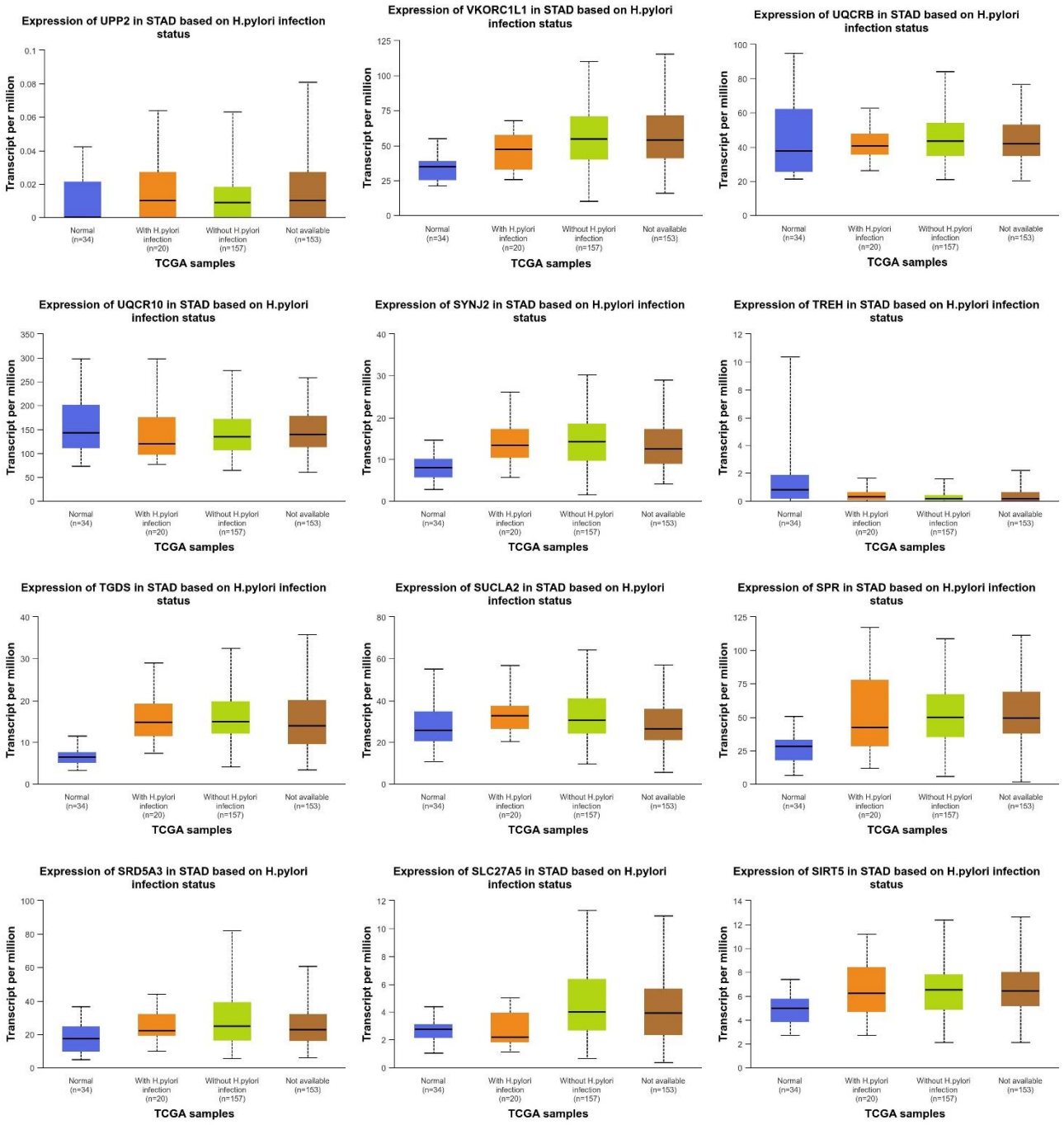
MET

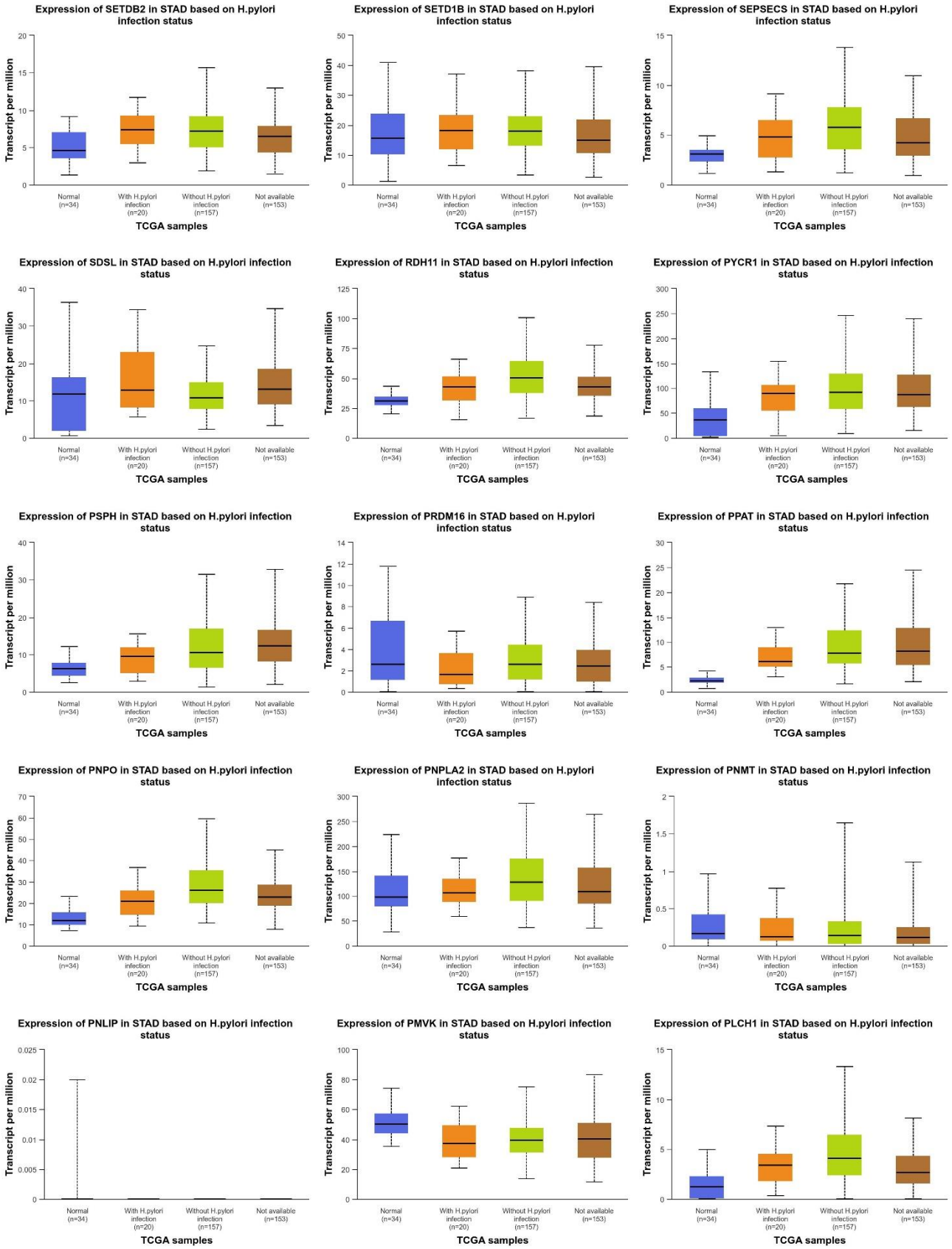


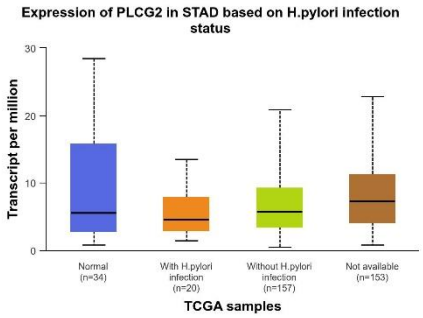
11.2. Code for Heatmap generation using R:

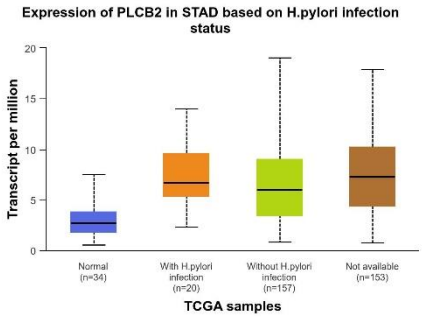
Heatmap.R

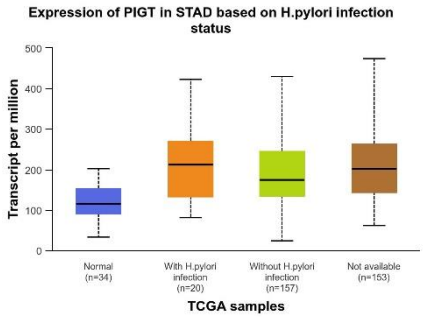
11.3. Expression analysis for Metabolic genes using UALCAN:

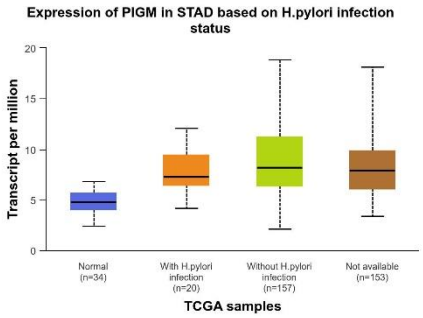


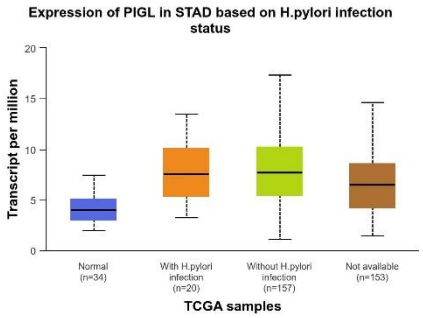

Expression of SETDB2 in STAD based on H.pylori infection status
Expression of SETD1B in STAD based on H.pylori infection status
Expression of SEPSECS in STAD based on H.pylori infection status
Expression of SDSL in STAD based on H.pylori infection status
Expression of RDH11 in STAD based on H.pylori infection status
Expression of PYCR1 in STAD based on H.pylori infection status
Expression of PSPH in STAD based on H.pylori infection status
Expression of PRDM16 in STAD based on H.pylori infection status
Expression of PPAT in STAD based on H.pylori infection status
Expression of PNPO in STAD based on H.pylori infection status
Expression of PNPLA2 in STAD based on H.pylori infection status
Expression of PNMT in STAD based on H.pylori infection status
Expression of PNLIP in STAD based on H.pylori infection status
Expression of PMVK in STAD based on H.pylori infection status
Expression of PLCH1 in STAD based on H.pylori infection status
Transcript per million
Normal (n=34)
With H.pylori infection (n=20)
Without H.pylori infection (n=157)
Not available (n=153)
TCGA samples

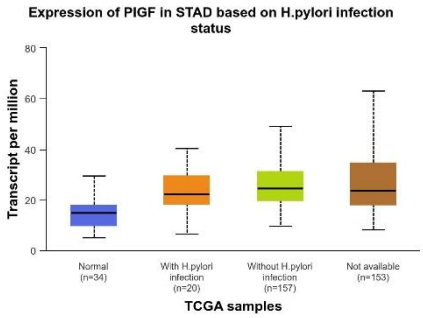

Expression of PLCG2 in STAD based on H.pylori infection status
Transcript per million
Normal (n=34)
With H.pylori infection (n=20)
Without H.pylori infection (n=157)
Not available (n=153)
TCGA samples

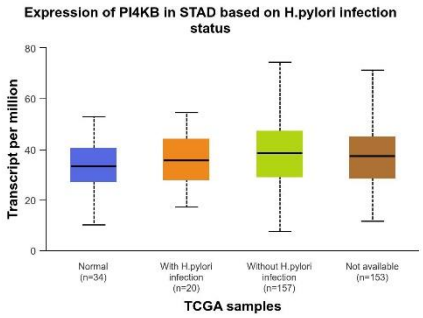

Expression of PLCB2 in STAD based on H.pylori infection status
Transcript per million
Normal (n=34)
With H.pylori infection (n=20)
Without H.pylori infection (n=157)
Not available (n=153)
TCGA samples

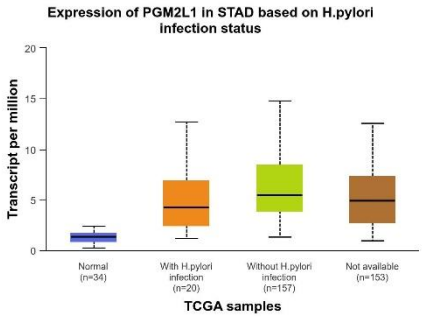

Expression of PIGT in STAD based on H.pylori infection status
Transcript per million
Normal (n=34)
With H.pylori infection (n=20)
Without H.pylori infection (n=157)
Not available (n=153)
TCGA samples

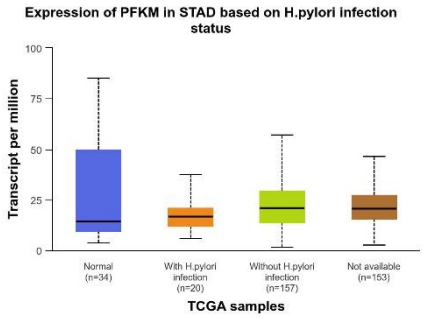

Expression of PIGM in STAD based on H.pylori infection status
Transcript per million
Normal (n=34)
With H.pylori infection (n=20)
Without H.pylori infection (n=157)
Not available (n=153)
TCGA samples

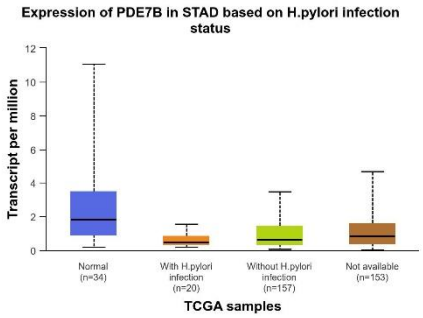

Expression of PIGL in STAD based on H.pylori infection status
Transcript per million
Normal (n=34)
With H.pylori infection (n=20)
Without H.pylori infection (n=157)
Not available (n=153)
TCGA samples

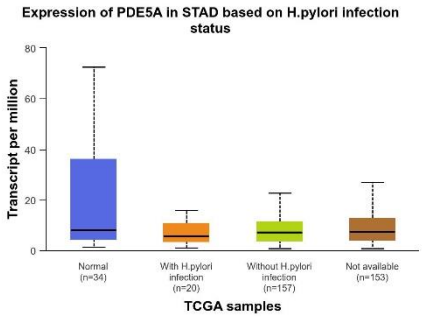

Expression of PIGF in STAD based on H.pylori infection status
Transcript per million
Normal (n=34)
With H.pylori infection (n=20)
Without H.pylori infection (n=157)
Not available (n=153)
TCGA samples

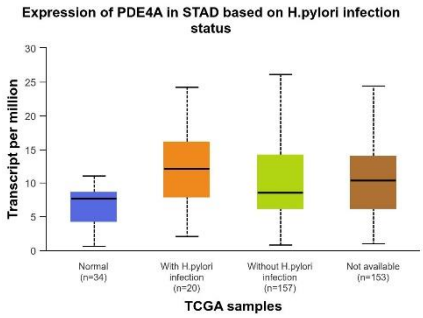

Expression of PI4KB in STAD based on H.pylori infection status
Transcript per million
Normal (n=34)
With H.pylori infection (n=20)
Without H.pylori infection (n=157)
Not available (n=153)
TCGA samples

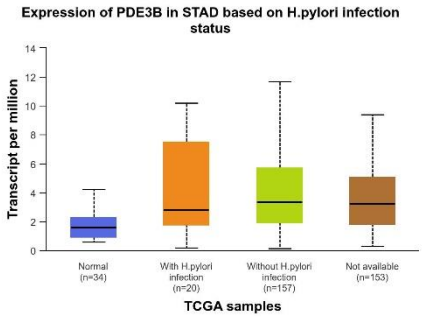

Expression of PGM2L1 in STAD based on H.pylori infection status
Transcript per million
Normal (n=34)
With H.pylori infection (n=20)
Without H.pylori infection (n=157)
Not available (n=153)
TCGA samples

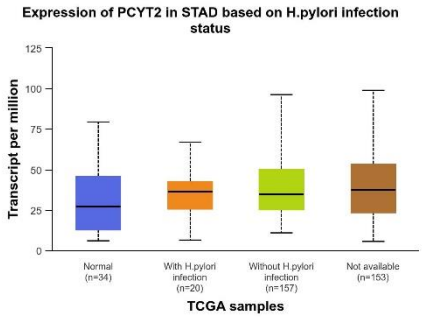

Expression of PFKM in STAD based on H.pylori infection status
Transcript per million
Normal (n=34)
With H.pylori infection (n=20)
Without H.pylori infection (n=157)
Not available (n=153)
TCGA samples

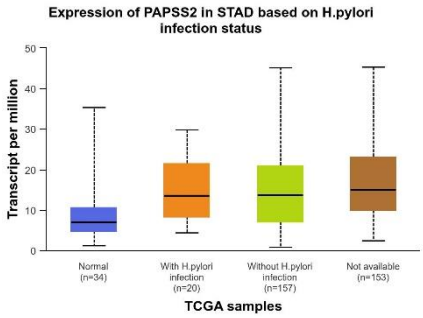

Expression of PDE7B in STAD based on H.pylori infection status
Transcript per million
Normal (n=34)
With H.pylori infection (n=20)
Without H.pylori infection (n=157)
Not available (n=153)
TCGA samples

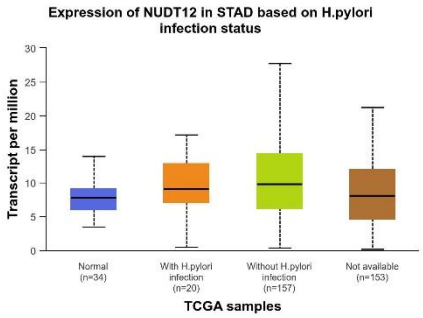

Expression of PDE5A in STAD based on H.pylori infection status
Transcript per million
Normal (n=34)
With H.pylori infection (n=20)
Without H.pylori infection (n=157)
Not available (n=153)
TCGA samples

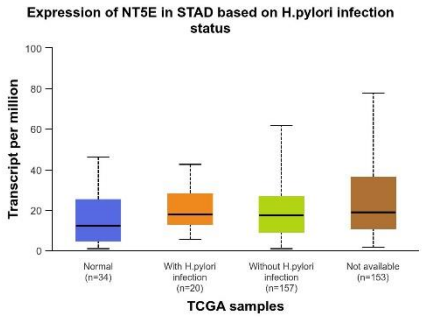

Expression of PDE4A in STAD based on H.pylori infection status
Transcript per million
Normal (n=34)
With H.pylori infection (n=20)
Without H.pylori infection (n=157)
Not available (n=153)
TCGA samples

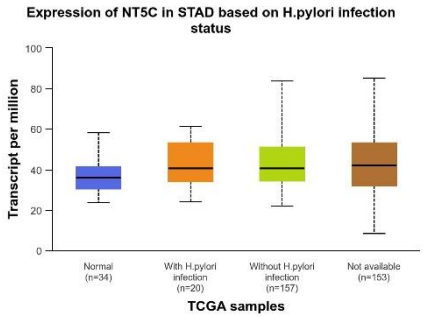

Expression of PDE3B in STAD based on H.pylori infection status
Transcript per million
Normal (n=34)
With H.pylori infection (n=20)
Without H.pylori infection (n=157)
Not available (n=153)
TCGA samples

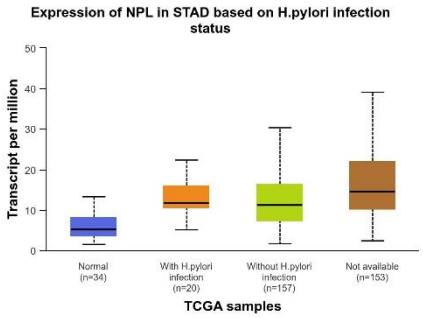

Expression of PCYT2 in STAD based on H.pylori infection status
Transcript per million
Normal (n=34)
With H.pylori infection (n=20)
Without H.pylori infection (n=157)
Not available (n=153)
TCGA samples

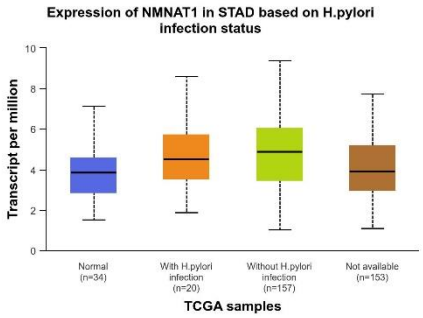

Expression of PAPSS2 in STAD based on H.pylori infection status
Transcript per million
Normal (n=34)
With H.pylori infection (n=20)
Without H.pylori infection (n=157)
Not available (n=153)
TCGA samples

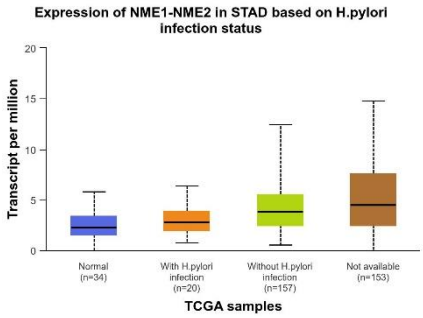

Expression of NUDT12 in STAD based on H.pylori infection status
Transcript per million
Normal (n=34)
With H.pylori infection (n=20)
Without H.pylori infection (n=157)
Not available (n=153)
TCGA samples

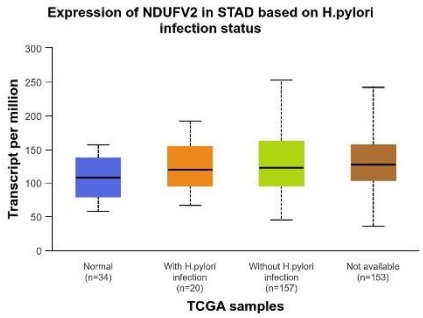

Expression of NT5E in STAD based on H.pylori infection status
Transcript per million
Normal (n=34)
With H.pylori infection (n=20)
Without H.pylori infection (n=157)
Not available (n=153)
TCGA samples

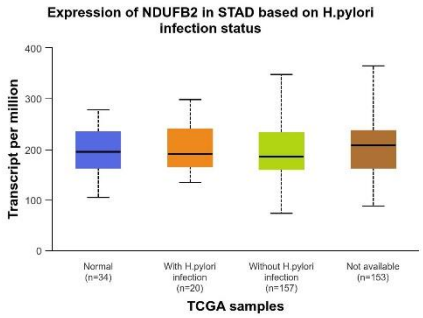

Expression of NT5C in STAD based on H.pylori infection status
Transcript per million
Normal (n=34)
With H.pylori infection (n=20)
Without H.pylori infection (n=157)
Not available (n=153)
TCGA samples

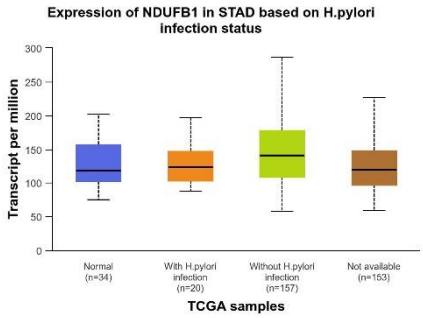

Expression of NPL in STAD based on H.pylori infection status
Transcript per million
Normal (n=34)
With H.pylori infection (n=20)
Without H.pylori infection (n=157)
Not available (n=153)
TCGA samples

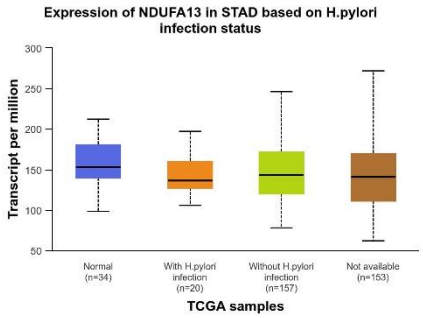

Expression of NMNAT1 in STAD based on H.pylori infection status
Transcript per million
Normal (n=34)
With H.pylori infection (n=20)
Without H.pylori infection (n=157)
Not available (n=153)
TCGA samples

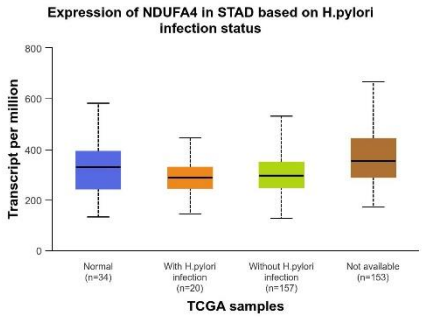

Expression of NME1-NME2 in STAD based on H.pylori infection status
Transcript per million
Normal (n=34)
With H.pylori infection (n=20)
Without H.pylori infection (n=157)
Not available (n=153)
TCGA samples

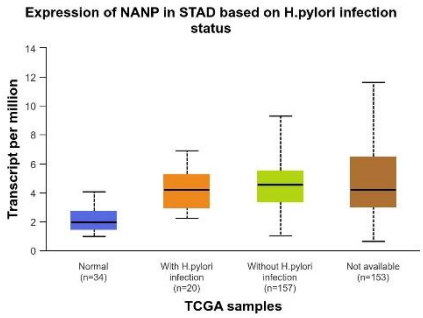

Expression of NDUFV2 in STAD based on H.pylori infection status
Transcript per million
Normal (n=34)
With H.pylori infection (n=20)
Without H.pylori infection (n=157)
Not available (n=153)
TCGA samples

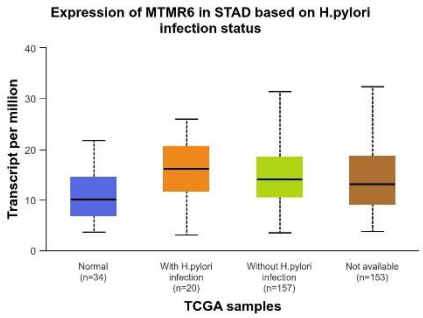

Expression of NDUFB2 in STAD based on H.pylori infection status
Transcript per million
Normal (n=34)
With H.pylori infection (n=20)
Without H.pylori infection (n=157)
Not available (n=153)
TCGA samples

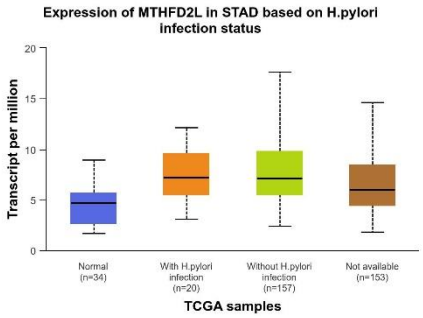

Expression of NDUFB1 in STAD based on H.pylori infection status
Transcript per million
Normal (n=34)
With H.pylori infection (n=20)
Without H.pylori infection (n=157)
Not available (n=153)
TCGA samples

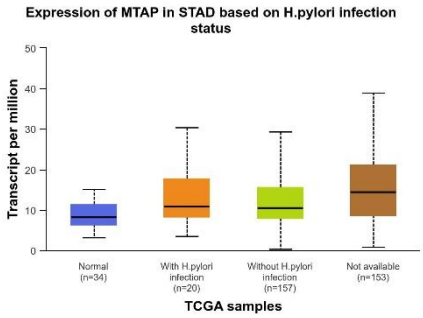

Expression of NDUFA13 in STAD based on H.pylori infection status
Transcript per million
Normal (n=34)
With H.pylori infection (n=20)
Without H.pylori infection (n=157)
Not available (n=153)
TCGA samples

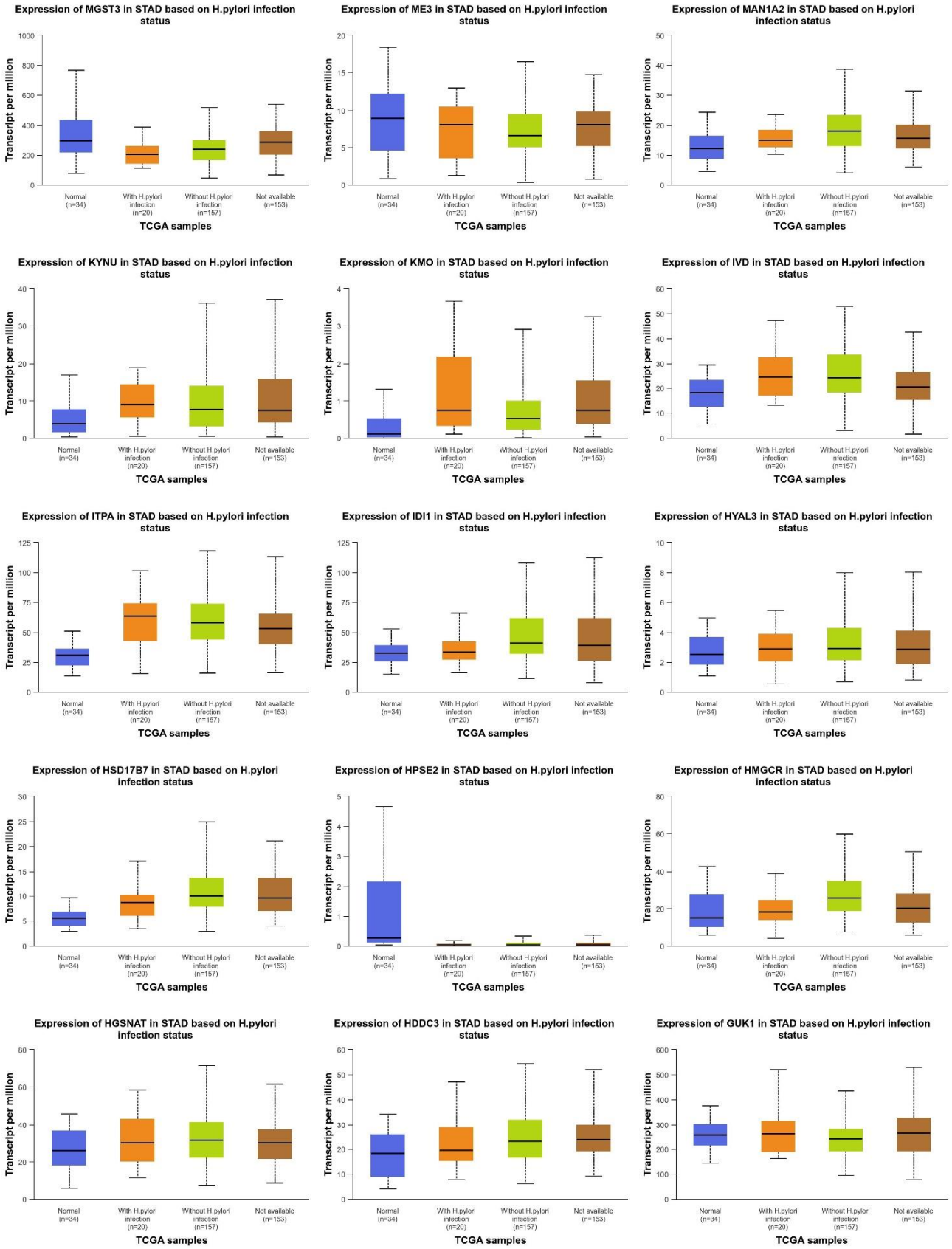

Expression of NDUFA4 in STAD based on H.pylori infection status
Transcript per million
Normal (n=34)
With H.pylori infection (n=20)
Without H.pylori infection (n=157)
Not available (n=153)
TCGA samples

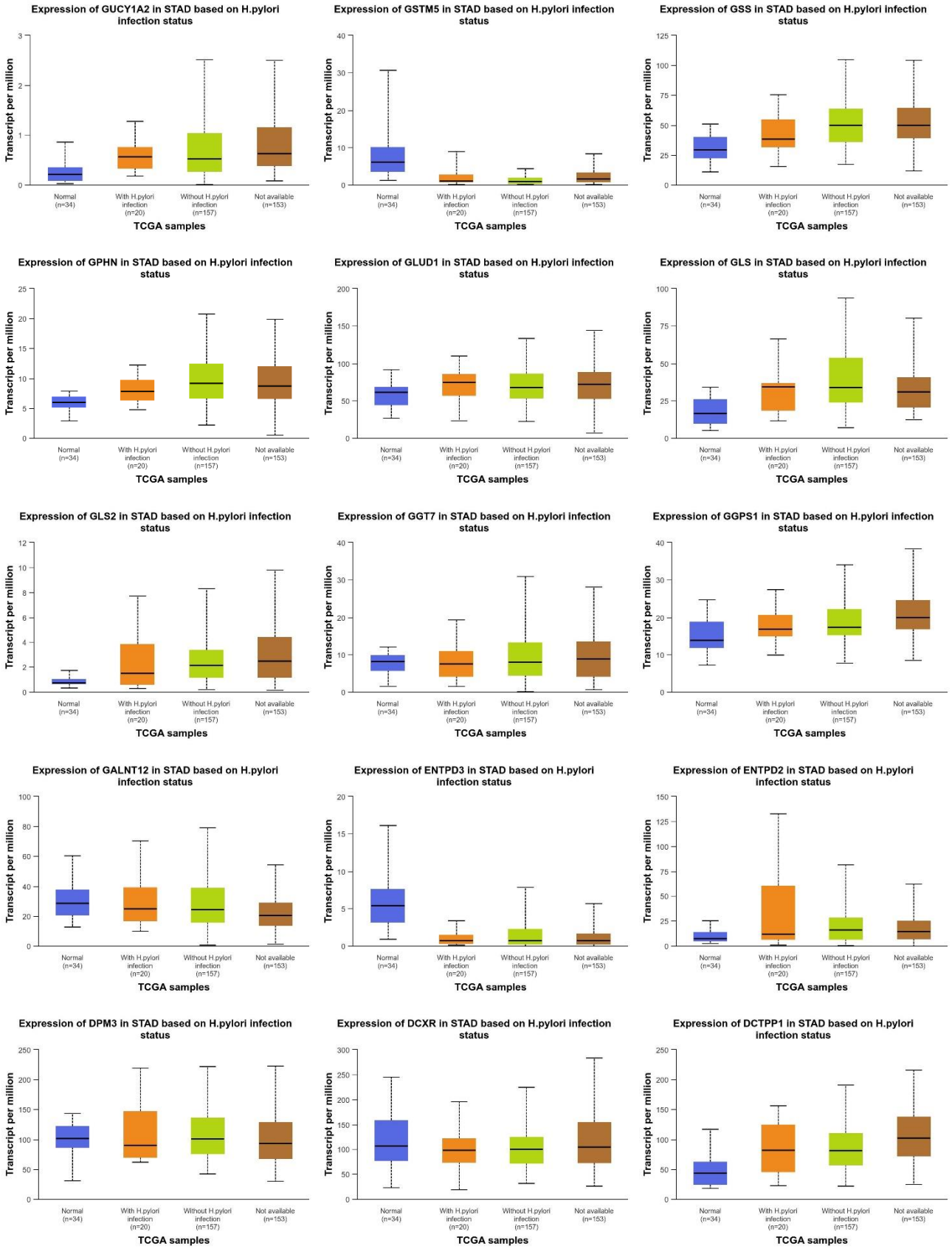

Expression of NANP in STAD based on H.pylori infection status
Transcript per million
Normal (n=34)
With H.pylori infection (n=20)
Without H.pylori infection (n=157)
Not available (n=153)
TCGA samples

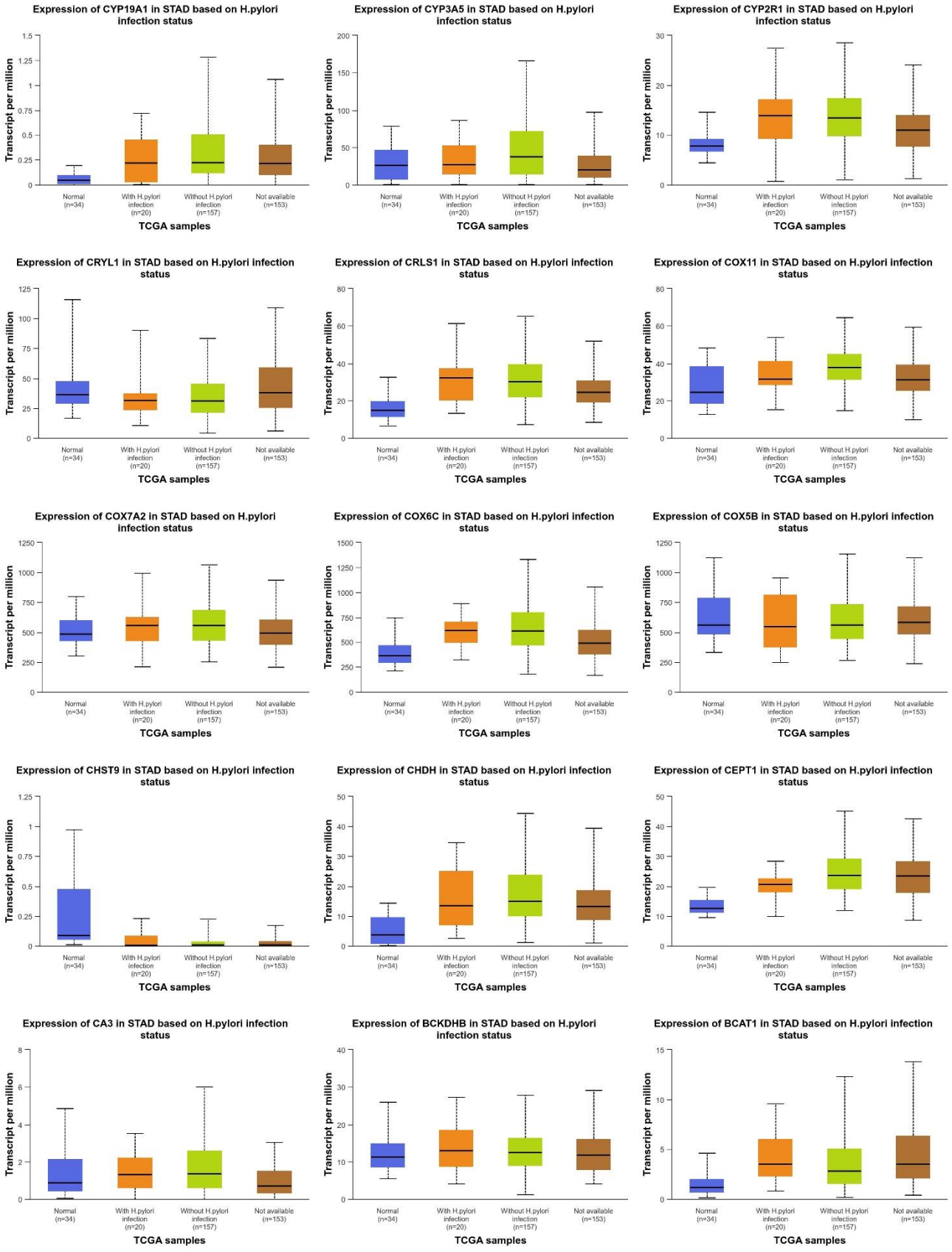

Expression of MTMR6 in STAD based on H.pylori infection status
Transcript per million
Normal (n=34)
With H.pylori infection (n=20)
Without H.pylori infection (n=157)
Not available (n=153)
TCGA samples

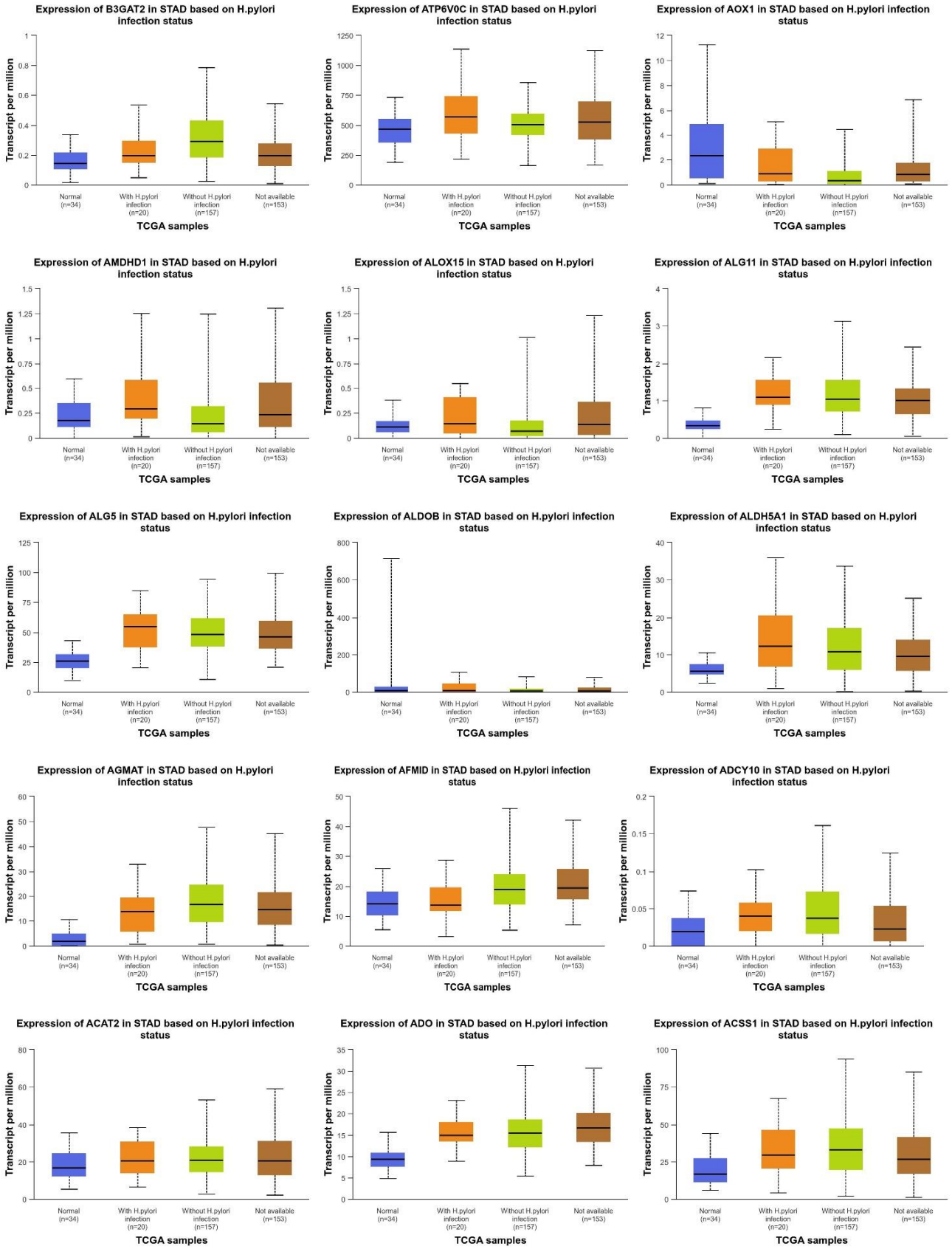

Expression of MTHFD2L in STAD based on H.pylori infection status
Transcript per million
Normal (n=34)
With H.pylori infection (n=20)
Without H.pylori infection (n=157)
Not available (n=153)
TCGA samples

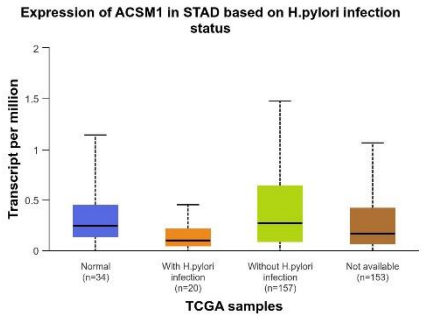

Expression of MTAP in STAD based on H.pylori infection status
Transcript per million
Normal (n=34)
With H.pylori infection (n=20)
Without H.pylori infection (n=157)
Not available (n=153)
TCGA samples

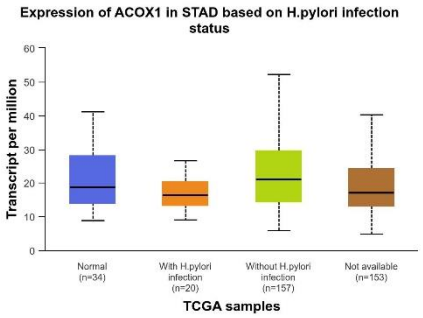

Expression of MGST3 in STAD based on H.pylori infection status
Expression of ME3 in STAD based on H.pylori infection status
Expression of MAN1A2 in STAD based on H.pylori infection status
Expression of KYNU in STAD based on H.pylori infection status
Expression of KMO in STAD based on H.pylori infection status
Expression of IVD in STAD based on H.pylori infection status
Expression of ITPA in STAD based on H.pylori infection status
Expression of IDI1 in STAD based on H.pylori infection status
Expression of HYAL3 in STAD based on H.pylori infection status
Expression of HSD17B7 in STAD based on H.pylori infection status
Expression of HPSE2 in STAD based on H.pylori infection status
Expression of HMGCR in STAD based on H.pylori infection status
Expression of HGSNAT in STAD based on H.pylori infection status
Expression of HDDC3 in STAD based on H.pylori infection status
Expression of GUK1 in STAD based on H.pylori infection status
Transcript per million
Normal (n=34)
With H.pylori infection (n=20)
Without H.pylori infection (n=157)
Not available (n=153)
TCGA samples

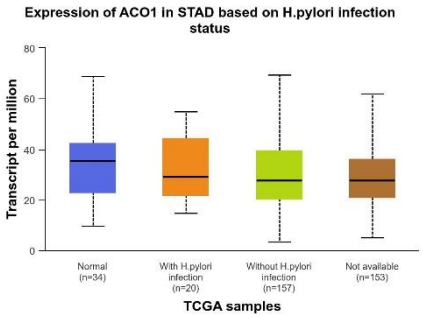

Expression of GUCY1A2 in STAD based on H.pylori infection status
Expression of GSTM5 in STAD based on H.pylori infection status
Expression of GSS in STAD based on H.pylori infection status
Expression of GPHN in STAD based on H.pylori infection status
Expression of GLUD1 in STAD based on H.pylori infection status
Expression of GLS in STAD based on H.pylori infection status
Expression of GLS2 in STAD based on H.pylori infection status
Expression of GGT7 in STAD based on H.pylori infection status
Expression of GGPS1 in STAD based on H.pylori infection status
Expression of GALNT12 in STAD based on H.pylori infection status
Expression of ENTPD3 in STAD based on H.pylori infection status
Expression of ENTPD2 in STAD based on H.pylori infection status
Expression of DPM3 in STAD based on H.pylori infection status
Expression of DCXR in STAD based on H.pylori infection status
Expression of DCTPP1 in STAD based on H.pylori infection status
Transcript per million
Normal (n=34)
With H.pylori infection (n=20)
Without H.pylori infection (n=157)
Not available (n=153)
TCGA samples


Expression of CYP19A1 in STAD based on H.pylori infection status
Expression of CYP3A5 in STAD based on H.pylori infection status
Expression of CYP2R1 in STAD based on H.pylori infection status
Expression of CRYL1 in STAD based on H.pylori infection status
Expression of CRLS1 in STAD based on H.pylori infection status
Expression of COX11 in STAD based on H.pylori infection status
Expression of COX7A2 in STAD based on H.pylori infection status
Expression of COX6C in STAD based on H.pylori infection status
Expression of COX5B in STAD based on H.pylori infection status
Expression of CHST9 in STAD based on H.pylori infection status
Expression of CHDH in STAD based on H.pylori infection status
Expression of CEPT1 in STAD based on H.pylori infection status
Expression of CA3 in STAD based on H.pylori infection status
Expression of BCKDHB in STAD based on H.pylori infection status
Expression of BCAT1 in STAD based on H.pylori infection status
Transcript per million
Normal (n=34)
With H.pylori infection (n=20)
Without H.pylori infection (n=157)
Not available (n=153)
TCGA samples

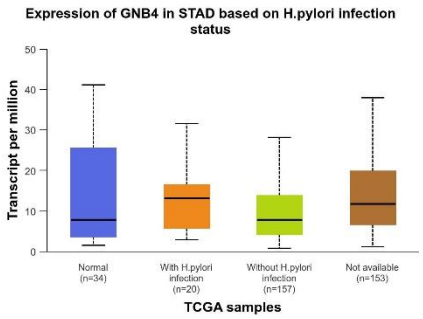

Expression of B3GAT2 in STAD based on H.pylori infection status
Expression of ATP6V0C in STAD based on H.pylori infection status
Expression of AOX1 in STAD based on H.pylori infection status
Expression of AMDHD1 in STAD based on H.pylori infection status
Expression of ALOX15 in STAD based on H.pylori infection status
Expression of ALG11 in STAD based on H.pylori infection status
Expression of ALG5 in STAD based on H.pylori infection status
Expression of ALDOB in STAD based on H.pylori infection status
Expression of ALDH5A1 in STAD based on H.pylori infection status
Expression of AGMAT in STAD based on H.pylori infection status
Expression of AFMID in STAD based on H.pylori infection status
Expression of ADCY10 in STAD based on H.pylori infection status
Expression of ACAT2 in STAD based on H.pylori infection status
Expression of ADO in STAD based on H.pylori infection status
Expression of ACSS1 in STAD based on H.pylori infection status
Transcript per million
Normal (n=34)
With H.pylori infection (n=20)
Without H.pylori infection (n=157)
Not available (n=153)
TCGA samples

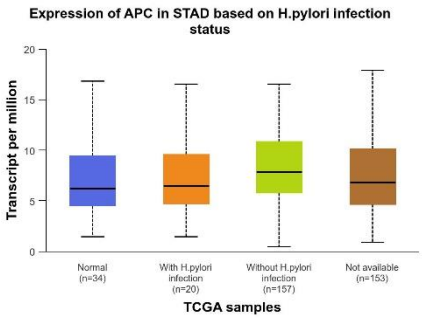


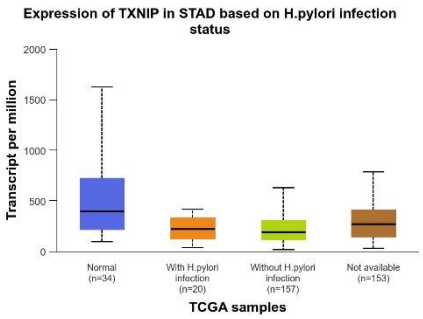


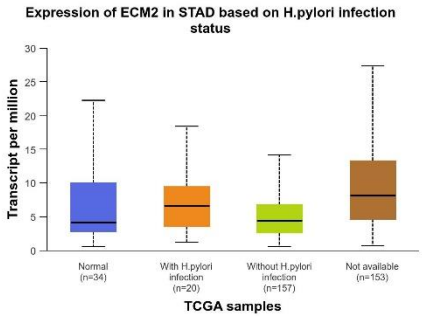


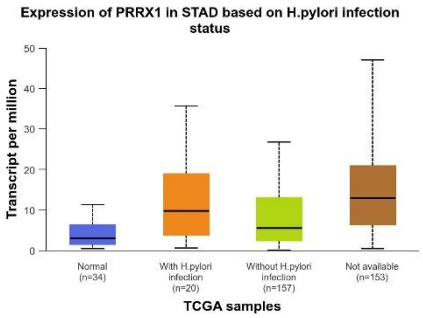
11.4. Expression analysis for Prognostic marker using UALCAN:

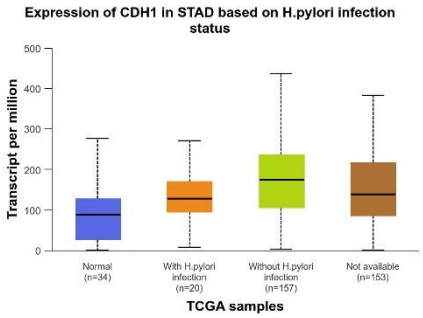


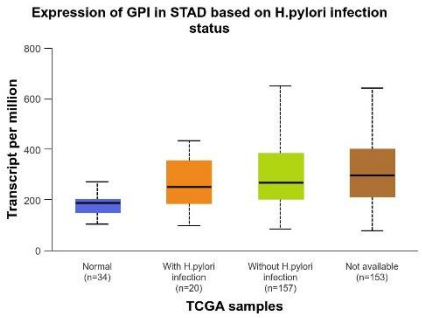


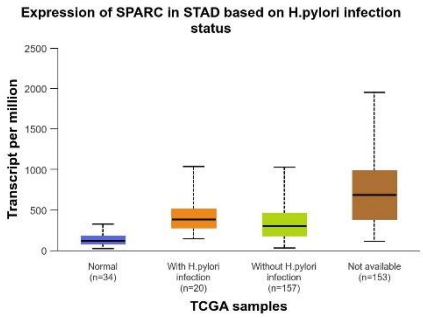


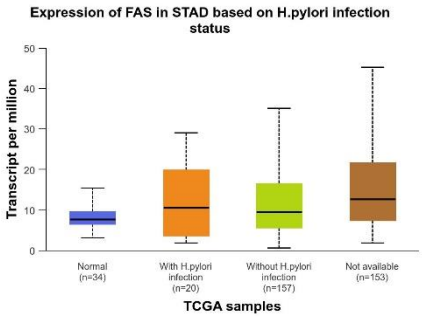


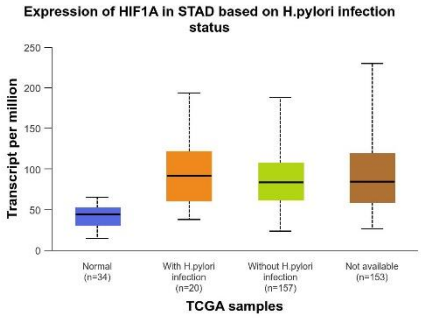


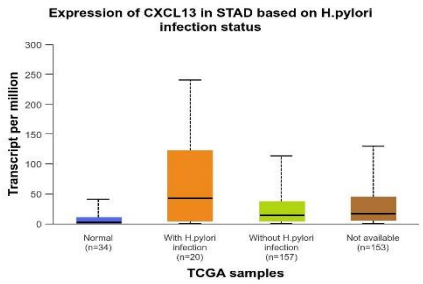


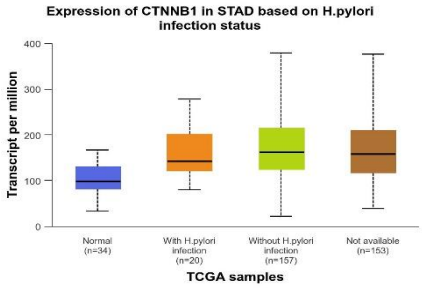

Expression of GPI in STAD based on H.pylori infection status
Transcript per million
800
600
400
200
0
Normal (n=34)
With H.pylori infection (n=20)
Without H.pylori infection (n=157)
Not available (n=153)
TCGA samples

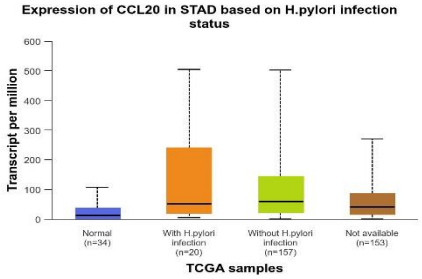

Expression of SPARC in STAD based on H.pylori infection status
Transcript per million
2500
2000
1500
1000
500
0
Normal (n=34)
With H.pylori infection (n=20)
Without H.pylori infection (n=157)
Not available (n=153)
TCGA samples

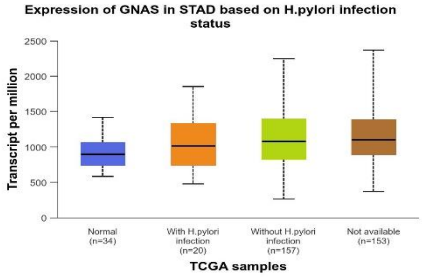

Expression of FAS in STAD based on H.pylori infection status
Transcript per million
50
40
30
20
10
0
Normal (n=34)
With H.pylori infection (n=20)
Without H.pylori infection (n=157)
Not available (n=153)
TCGA samples

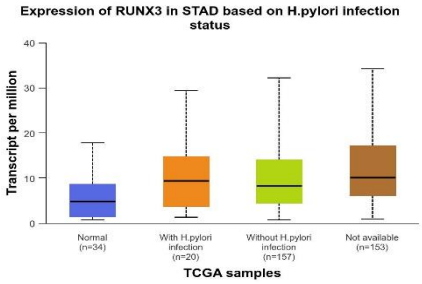

Expression of HIF1A in STAD based on H.pylori infection status
Transcript per million
250
200
150
100
50
0
Normal (n=34)
With H.pylori infection (n=20)
Without H.pylori infection (n=157)
Not available (n=153)
TCGA samples

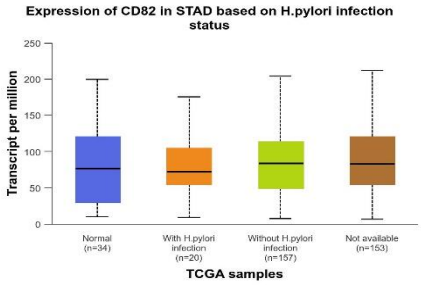

Expression of CXCL13 in STAD based on H.pylori infection status
Transcript per million
300
250
200
150
100
50
0
Normal (n=34)
With H.pylori infection (n=20)
Without H.pylori infection (n=157)
Not available (n=153)
TCGA samples

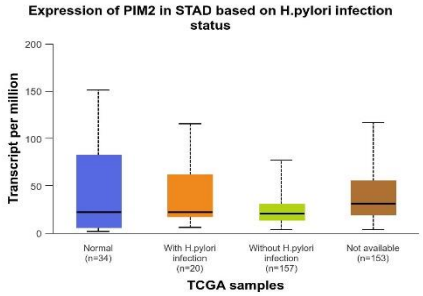

Expression of CTNNB1 in STAD based on H.pylori infection status
Transcript per million
400
300
200
100
0
Normal (n=34)
With H.pylori infection (n=20)
Without H.pylori infection (n=157)
Not available (n=153)
TCGA samples

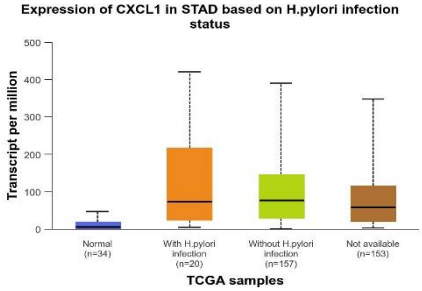

Expression of CCL20 in STAD based on H.pylori infection status
Transcript per million
600
500
400
300
200
100
0
Normal (n=34)
With H.pylori infection (n=20)
Without H.pylori infection (n=157)
Not available (n=153)
TCGA samples

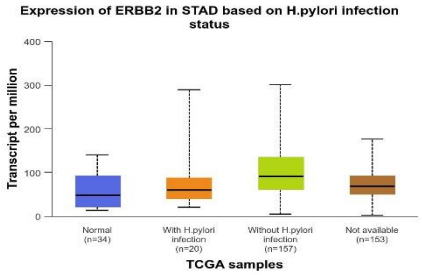

Expression of GNAS in STAD based on H.pylori infection status
Transcript per million
2500
2000
1500
1000
500
0
Normal (n=34)
With H.pylori infection (n=20)
Without H.pylori infection (n=157)
Not available (n=153)
TCGA samples

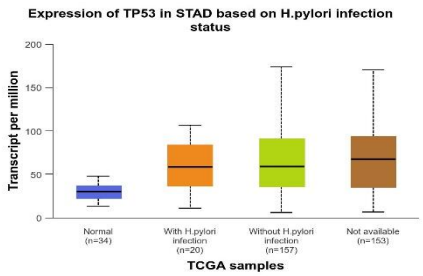

Expression of RUNX3 in STAD based on H.pylori infection status
Transcript per million
40
30
20
10
0
Normal (n=34)
With H.pylori infection (n=20)
Without H.pylori infection (n=157)
Not available (n=153)
TCGA samples

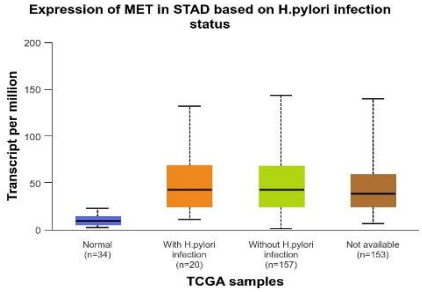

Expression of CD82 in STAD based on H.pylori infection status
Transcript per million
250
200
150
100
50
0
Normal (n=34)
With H.pylori infection (n=20)
Without H.pylori infection (n=157)
Not available (n=153)
TCGA samples


Expression of PIM2 in STAD based on H.pylori infection status
Transcript per million
200
150
100
50
0
Normal (n=34)
With H.pylori infection (n=20)
Without H.pylori infection (n=157)
Not available (n=153)
TCGA samples


Expression of CXCL1 in STAD based on H.pylori infection status
Transcript per million
500
400
300
200
100
0
Normal (n=34)
With H.pylori infection (n=20)
Without H.pylori infection (n=157)
Not available (n=153)
TCGA samples


Expression of ERBB2 in STAD based on H.pylori infection status
Transcript per million
400
300
200
100
0
Normal (n=34)
With H.pylori infection (n=20)
Without H.pylori infection (n=157)
Not available (n=153)
TCGA samples


Expression of TP53 in STAD based on H.pylori infection status
Transcript per million
200
150
100
50
0
Normal (n=34)
With H.pylori infection (n=20)
Without H.pylori infection (n=157)
Not available (n=153)
TCGA samples


Expression of MET in STAD based on H.pylori infection status
Transcript per million
200
150
100
50
0
Normal (n=34)
With H.pylori infection (n=20)
Without H.pylori infection (n=157)
Not available (n=153)
TCGA samples