Original Article

Characterization of somatic mutations and pathway alterations during hepatocellular carcinoma vascular invasion using next-generation sequencing

Qi Li[1#], Qifan Zhang[2#], Jinzhang Chen[1], Mengya Zang[1], Xiaoyun Hu[1], Rong Li[1], Jinlin Hou[1], Jie Zhou[2]

[1]State Key Laboratory of Organ Failure Research, Guangdong Provincial Key Laboratory of Viral Hepatitis Research, Department of Infectious Diseases, Nanfang Hospital, Southern Medical University, Guangzhou, China; [2]Division of Hepatobiliopancreatic Surgery, Department of General Surgery, Nanfang Hospital, Southern Medical University, Guangzhou, China

Contributions: (I) Conception and design: Q Li, Q Zhang, J Hou, J Zhou; (II) Administrative support: J Hou, J Zhou; (III) Provision of study materials or patients: Q Li, Q Zhang, J Hou, J Zhou; (IV) Collection and assembly of data: Q Li, Q Zhang; (V) Data analysis and interpretation: Q Li, Q Zhang, J Hou, J Zhou; (VI) Manuscript writing: All authors; (VII) Final approval of manuscript: All authors.

[#]These authors contributed equally to this work.

Correspondence to: Jie Zhou. Division of Hepatobiliopancreatic Surgery, Department of General Surgery, Nanfang Hospital, Southern Medical University, Guangzhou 510515, China. Email: jacky@smu.edu.cn; zhoujie_vip01@163.com; Jinlin Hou. State Key Laboratory of Organ Failure Research, Guangdong Provincial Key Laboratory of Viral Hepatitis Research; Department of Infectious Diseases, Nanfang Hospital, Southern Medical University, No. 1838, North Guangzhou Avenue, Guangzhou, Guangdong 510515, China. Email: jlhousmu@163.com.

Background: Vascular invasion is an independent risk factors for recurrence and poor prognosis in patients with hepatocellular carcinoma (HCC). However, the molecular mechanisms of HCC vascular invasion are largely unknown. Deciphering the molecular changes associated with the vascular invasion process will aid in the identification of therapeutic targets and treatment for patients with HCC.

Methods: DNA was extracted from tumor specimens and blood samples collected from 50 patients with HCC. Next-generation sequencing (NGS) was performed to detect HCC gene variants. Bioinformatics methods were used to comprehensively analyze the three sets of sequencing data grouped by vascular invasion, including differences in tumor mutation burden (TMB), mutation characteristics, and alterations in signaling pathways.

Results: Bioinformatics analysis detected a total of 762 single nucleotide variants (SNVs). The TMB was not significantly different between patients with macrovascular invasion, microvascular invasion (MVI), or avascular invasion. Ten genes related to prognosis or recurrence, and one oncogene related to vascular invasion were screened. Compared with the avascular invasion cluster, the variant genes in the macrovascular and MVI clusters were mainly enriched in the thyroid hormone signaling pathway. In addition, macrovascular invasion variant genes were also enriched in the insulin signaling pathway and the Fanconi anemia pathway.

Conclusions: Somatic mutations and pathway changes associated with vascular invasion in HCC were identified. The discovery of the molecular drivers of vascular invasion in HCC provides novel insights that can help guide further patient diagnosis and personalized therapy.

Keywords: Hepatocellular carcinoma (HCC); next-generation sequencing (NGS); vascular invasion; signaling pathway

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Introduction

Hepatocellular carcinoma (HCC) is one of the most common malignant solid tumors worldwide, accounting for more than 90% of primary liver cancers, and is the fourth most common cause of cancer-related deaths (1,2). Due to factors such as hepatitis B virus infection, aflatoxin exposure, alcohol abuse, and environmental pollution, China has become the country with the highest incidence of liver cancer (about 55% of the world's total incidence) and the largest number of deaths (3). Surgical resection and local ablation remain the most commonly used curative treatments for HCC (4,5). However, the tumor recurrence rate is as high as 70% after liver resection and 25% after liver transplantation, and the overall survival (OS) rate remains unsatisfactory, with the 5-year OS rate at 15–20% (6,7).

Vascular invasion is often associated with tumor metastasis, recurrence, and poor prognosis (8). After liver transplantation, patients with microvascular invasion (MVI) experience a more than four-fold increased risk of HCC recurrence (9). Unfortunately, preoperative imaging cannot detect potential microscopic vascular invasion (10). Therefore, identifying the molecular changes associated with vascular invasion to determine the risk of HCC recurrence is a primary task in predicting long-term prognosis. HCC has significant phenotypic and molecular heterogeneity (11). Menyhárt *et al.* found that the *BIRC5*, *CDC20*, and *PLK1* genes could adequately predict the prognosis of Asian patients (12). Vascular invasion is often divided into macrovascular invasion and MVI, however, the molecular changes related to the extent of vascular invasion have been rarely investigated (13). Next-generation sequencing (NGS) technology can realize large-scale parallel sequencing of multiple genes, and fundamentally solve the practical problems of difficult diagnosis caused by heterogeneity of single-gene inheritance, multiple genes, and complex phenotypes.

To identify robust genes related to the prognosis of HCC, 50 patients with HCC were enrolled and screened. Patients were grouped according to the degree of vascular invasion, namely, the no vascular invasion group, the MVI group, and the macrovascular invasion group. Using high-throughput targeted gene sequencing and whole exome sequencing (WES) methods to explore the molecular mechanism changes and pathway changes related to HCC vascular invasion, this information will be useful in guiding auxiliary diagnosis and individualized treatment of Chinese HCC patients. We present the following article in accordance with the REMARK reporting checklist (available at https://jgo.amegroups.com/article/view/10.21037/jgo-22-556/rc).

Methods

Collection of clinical samples

Between 2018 and 2019, a total of 50 HCC patients were enrolled in this study. The median follow-up time was 26.7 months. All tumor samples were estimated for invasive tumor content by two molecular pathologists to ensure that more than 50% of the cells were tumor cells. Avascular invasion was defined as no portal vein, hepatic vein, or inferior vena cava invasion on imaging and no vascular invasion on electron microscopy. MVI refers to the observation of tumor thrombus or cancer cells under the electron microscope without invasion of large blood vessels. Macrovascular invasion refers to the formation of tumor thrombi in the portal vein and its main branches. High-depth targeted gene panel sequencing and WES were performed after passing the nucleic acid quality test. This study was conducted in accordance with the Declaration of Helsinki (as revised in 2013) (14). The protocol was approved by the Ethics Committee of Nanfang Hospital, Southern Medical University (ID of the approval: 2012-092). Written informed consent was obtained from all patients prior to inclusion in the study.

DNA extraction and NGS

DNA was extracted from serial thick sections cut from tumor samples and matched peripheral blood leukocytes as germline DNA control. The invasive tumor content was estimated by pathologists to ensure that more than 50% of cells were tumor cells. DNA was isolated from the formalin-fixed paraffin-embedded (FFPE) tissue blocks and blood samples using the DNeasy Blood and Tissue Kit (69504, QIAGEN, Venlo, Netherlands). Qubit 3.0 (Thermofisher) was used to detect the quality of the DNA. The Generic Library Construction Kit (Cat. No. M0348L, New England Biolabs, USA) and the Hybrid Capture Kit (Cat. No. 1001111E, Naonda (Nanjing) Biotechnology Co., Ltd., Nanjing) were used to capture targeted region sequences from genomic DNA and construct sequencing computer libraries. The captured libraries of targeted gene sequencing and WES were performed as paired end-readings on the

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Table 1 Patient characteristics

Characteristic	No. of cases	Proportion
Total number	n=50	
Age, years (mean)	51.7 [25–80]	
Sex		
Male	46	92%
Female	4	8%
History of hepatitis	42	84%
The history of drinking		
Yes	19	38%
No	31	62%
BCLC staging		
A	19	38%
B	8	16%
C	23	46%
Vascular invasion		
Microvascular	16	32%
Macrovascular	19	38%
Avascular	15	30%
Extrahepatic metastasis		
Yes	6	12%
No	44	88%
Lymphatic metastasis		
Yes	8	16%
No	42	84%
Therapy method		
Excision	31	62%
Medication	19	38%

BCLC, Barcelona Clinic Liver Cancer.

Illumina NoveSeq 6000 sequencing platform.

Variant annotation analysis and visual mapping

Germline variations were identified via SpeedSeq and somatic mutations were identified using Mutect (15). Somatic indels were determined using SomaticIndelDetector (16). The high-quality somatic mutations and indels were selected. The variant data were annotated using ANNOVAR (17) and Oncotator (18), and converted to MAF files using maftools (19). The cancer driver genes were analyzed using Intogen (20), including OncodriveFM and OncodriveCLUST. Based on the fact that tumor development is an evolutionary process, detection of positive selection signals in the pattern of somatic mutation of genes has been used to identify drivers in tumor cohorts.

Statistical analysis

Progress-free survival (PFS) and overall survival (OS) were defined as the time from randomization to disease progression or last follow-up and the time from surgery to death or last follow-up, respectively. All the correlated clinical and biological variables were analyzed using the SPSS Statistics 22.0 package and the ggpubr package (21) in R software (22) by means of Fisher's test or a non-parametric test when necessary. The Kruskal-Wallis test was used to analyze the differences in tumor mutational burden (TMB) between different groups. A P value <0.05 was considered statistically significant.

Results

Patient characteristics

Tumor tissue and corresponding blood samples were collected from 50 HCC patients at the time of diagnosis, including 46 males (92%) and 4 females (8%), with an average age of 51.7 years (range, 25–80 years). Of these, 42 patients had a history of hepatitis and 19 patients had a history of alcohol consumption. According to the Barcelona Clinic Liver Cancer (BCLC) clinical staging system, 19 cases were stage A, 8 cases were stage B, and 23 cases were stage C. There were 35 patients with vascular infiltration, including 16 cases of microvascular infiltration and 19 cases of macrovascular infiltration. The imaging or surgical samples of the other 15 patients showed no vascular infiltration under electron microscopy. In addition, 6 patients presented with extrahepatic metastases and 8 had lymph node metastases. Among the enrolled patients, 31 were treated with radical surgery and the other 19 patients were treated with medical therapy. The detailed clinical characteristics of the patients are shown in *Table 1* and Table S1.

The occurrence of vascular invasion affects the prognosis of hepatocellular patients

According to the degree of vascular invasion of HCC, the

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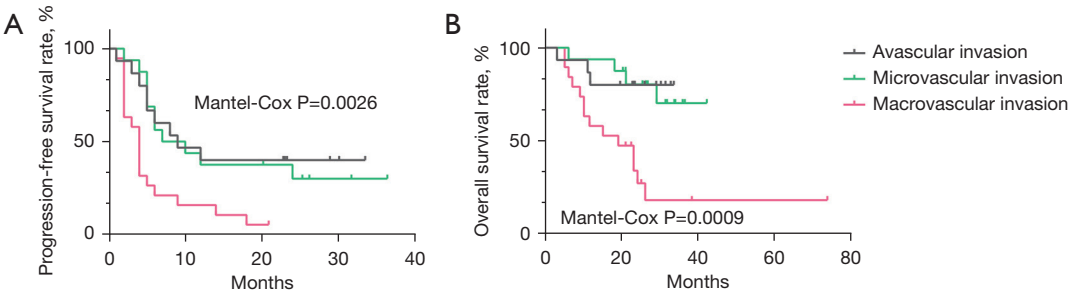

Figure 1 The occurrence of vascular invasion affects the prognosis of patients with hepatocellular carcinoma. (A) PFS in patients with macrovascular invasion, microvascular invasion, and avascular invasion. (B) The OS in patients with macrovascular invasion, the microvascular invasion, and avascular invasion. PFS, progression-free survival; OS, overall survival.

50 patients were divided into the macrovascular invasion group, the MVI group, or the avascular invasion group. Combined with clinical prognostic information, Mantel-Cox tests found that there were significant differences in PFS and OS among the three groups, (P=0.0026 and P=0.0009, respectively) (*Figure 1*). The prognosis of patients with macrovascular invasion was significantly worse than that of patients with MVI and those with no vascular invasion.

Characterization of somatic mutations associated with vascular invasion and tumor mutation burden (TMB)

A total of 50 tumor tissue sections and matched blood DNA samples were collected, of which, 28 underwent whole-exome sequencing and 22 underwent targeted gene sequencing. We successfully analyzed all sections and matched blood second-generation sequencing data using an analysis pipeline of whole exome and targeted sequencing, with an average depth of 203.0X for whole exomes and 572.3X for targeted sequencing samples. A total of 762 somatic mutations were detected by comparing significant changes in non-reference alleles in tumor and control groups (Table S2). Missense mutations were the most common type of mutations, along with frame shift deletion, in frame insertion, frame deletion, and so on. Patient P50 had the most SNVs, followed by patient P23. The top 30 somatic gene mutations are listed according to mutation frequency. The three genes with the highest mutation frequency were *TP53* (28%), *CTNNB1* (14%), and *KMT2B* (10%). Mutations in *CTNNB1*, *CMT2B*, *NF1*, *ZNF595*, and *KMT2D* were found in the avascular invasion group and the MVI group, but not in the macrovascular invasion group. Conversely, mutations in *KIAA2026*, *ALMS1*, *FGFR3*, *LRP1B*, and *PRDM1* were detected in the macrovascular invasion group and the MVI group, but not in the avascular invasion group (*Figure 2A*).

Additionally, the TMB in the whole-exome and target gene sequencing data was calculated using the number of nonsynonymous mutations occurring in somatic cells. Overall, there were large differences in the TMB values across samples within each group. However, there were no significant differences in the TMB among the avascular invasion group, the MVI group, and the macrovascular invasion group (WES data, P=0.67; targeted gene panel, P=0.4; *Figure 2B,2C*).

Candidate biomarkers associated with prognosis in HCC

Combining the recurrence and survival status of patients, 10 genes were found to be significantly associated with OS or PFS (P<0.05). Among these, 5 genes, including *ZNF763*, *FAM71B*, *ZNF616*, *TPR*, and *MYH13*, were significantly associated with both OS and PFS (*Table 2*). As shown in *Figures 3,4* significant genes were selected for survival curve analysis.

Alternations in signaling pathways in vascular invasion

To further characterize the signaling pathway changes in HCC during vascular invasion, vascular invasion patients with SNV binding were divided into three gene clusters by whole exons and targeted sequencing, including an avascular invasion cluster [150], a MVI cluster [190], and a macrovascular invasion cluster [310]. Venn diagrams revealed mutations in *TP53*, *KMT2C*, *AXIN1*, and *ZFHX3* in all three groups. In addition to the crossover gene clusters between groups, there were many genes unique to each cluster, such as 266 mutations specific to the macrovascular

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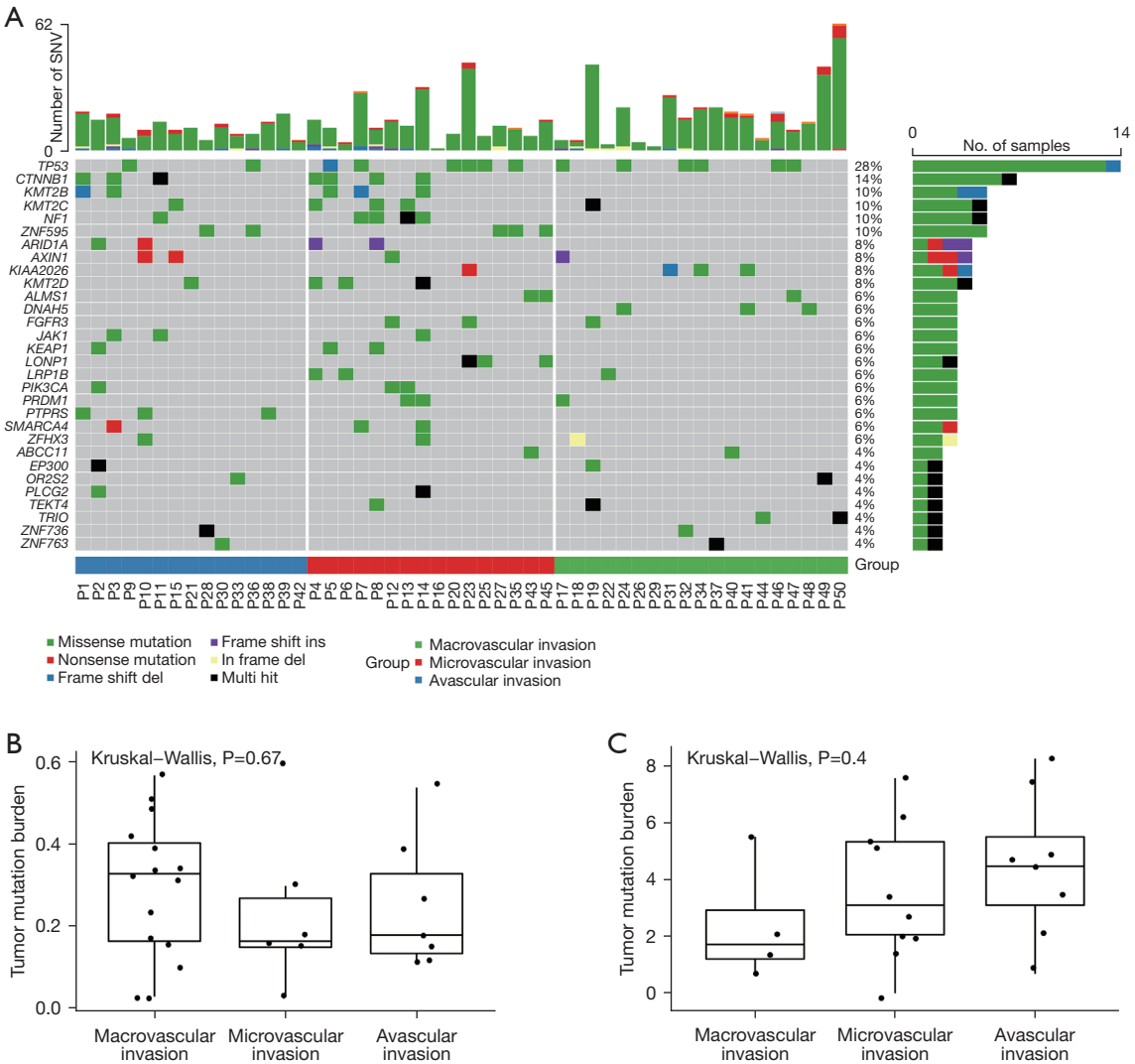

Figure 2 Somatic mutation profiles of hepatocellular carcinoma (HCC) samples and TMB values. (A) The distribution of the top 30 gene mutations in 50 HCC samples. (B) A comparison of the TMB values in the three groups of vascular invasion samples from whole exome sequencing. (C) A comparison of the TMB values among the three groups of vascular invasion in targeted sequencing samples. SNV, single nucleotide variants; HCC, hepatocellular carcinoma; TMB, tumor mutation burden.

invasion group (*Figure 4A*).

The three sets of gene clusters were collectively enriched in epidermal growth factor receptor (EGFR) tyrosine kinase inhibitor resistance, phosphatidylinositol 3-kinase (PI3K)-Akt signaling pathway, and Rap1 signaling pathway. The thyroid hormone signaling pathway was enriched in both the macrovascular invasion and MVI clusters, but not in the avascular invasion clusters. In addition, MVI clusters were independently enriched in the insulin signaling pathway and the Fanconi anemia pathway compared to the MVI cluster and the avascular invasion cluster (*Figure 4B-4D*).

Evaluation of the prognostic value of vascular invasion-related genes

In this study, a total of 35 patients had evidence of vascular invasion, of which, 19 patients presented with macrovascular invasion. Combined with the patient's gene mutation information, a total of 15 genes were found to be associated with vascular invasion. Among these genes, *PTPRS* showed

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Table 2 List of candidate biomarkers that were significantly associated with both OS and PFS

Symbol	Gene name	OS, P (HR)	PFS, P (HR)
ZNF616	Zinc finger protein 616	$5.51E^{-12}$ (101)	$7.21E^{-5}$ (17.5)
MYH13	Myosin heavy chain 13	$7.21E^{-7}$ (20.5)	0.0137 (5.8)
FAM71B	Golgi associated RAB2B interactor family member 3	$5.84E^{-4}$ (9.04)	$7.21E^{-5}$ (17.5)
ZNF763	Zinc finger protein 763	0.00231 (7.3)	$7.21E^{-5}$ (17.5)
TPR	Translocated promoter region, nuclear basket protein	0.0085 (6.03)	0.00898 (6.63)
BLM	BLM RecQ like helicase	0.00246 (7.81)	0.304 (2.01)
UNC13B	Unc-13 homolog B	0.0173 (5.13)	0.424 (1.73)
CPLANE1	Ciliogenesis and planar polarity effector complex subunit 1	0.0179 (5.05)	0.401 (1.89)
EXOC2	Exocyst complex component 2	0.0362 (4.45)	0.0506 (4.62)
PRRC2B	Proline rich coiled-coil 2B	0.05 (4.09)	0.285 (2.32)

PFS, progression-free survival; OS, overall survival.

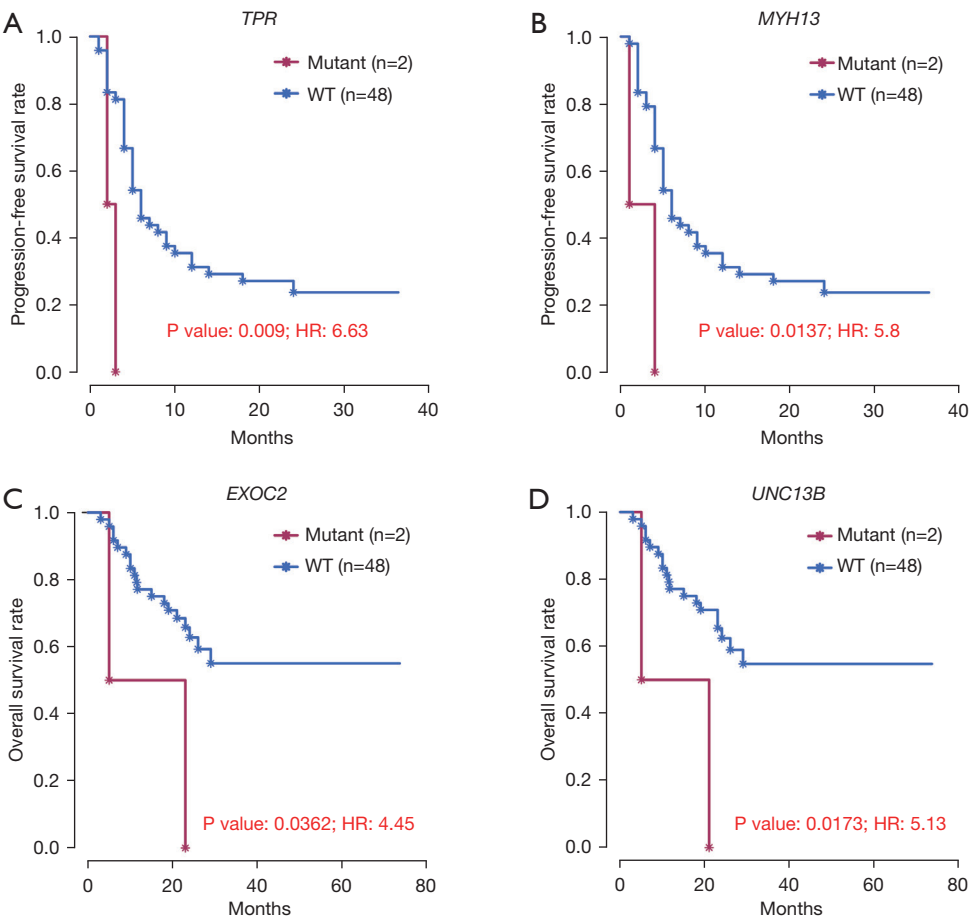

Figure 3 Representative genes associated with PFS and OS. The X-axis represents follow-up time. (A,B) Genes significantly correlated with PFS. (C,D) Genes significantly associated with OS. PFS, progression-free survival; OS, overall survival.

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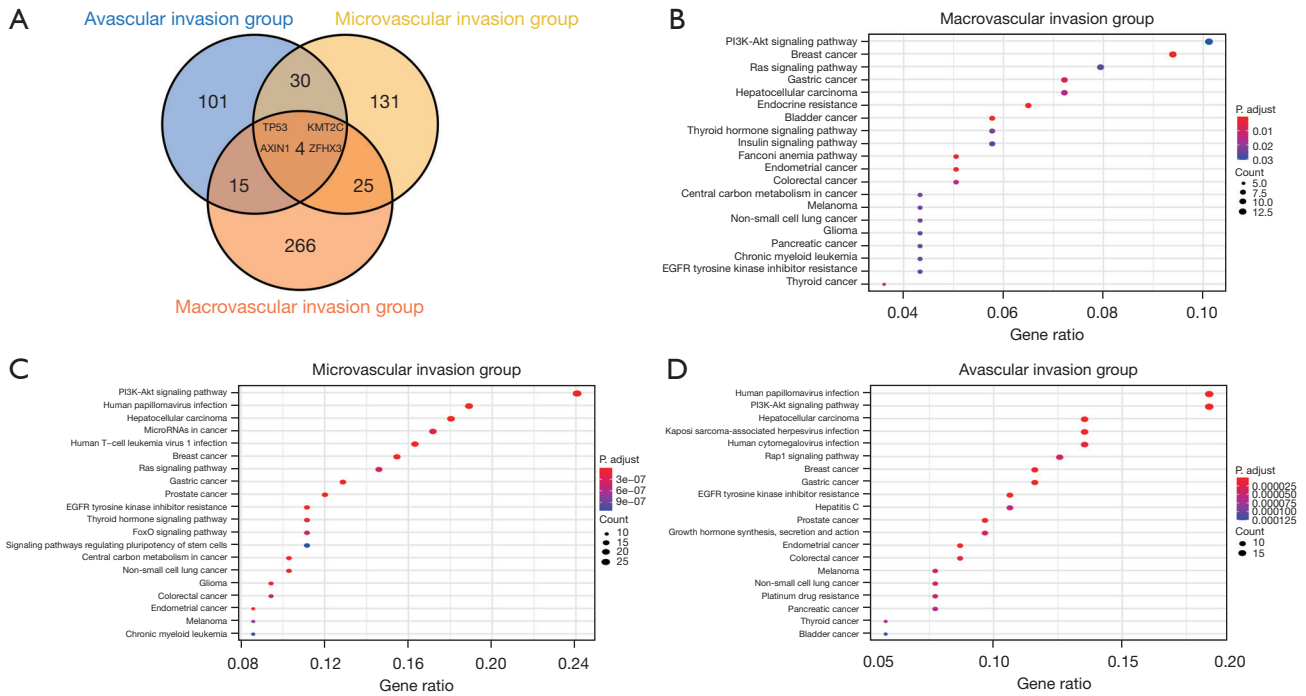

Figure 4 Analysis of the signaling pathways among the macrovascular invasion, microvascular invasion, and avascular invasion clusters. (A) A Venn diagram of the SNVs in clusters of avascular invasion, microvascular invasion, and macrovascular invasion. (B) KEGG signaling pathways enriched by macrovascular invasion cluster variant genes. (C) KEGG signaling pathways enriched by microvascular invasion cluster variant genes. (D) KEGG signaling pathways enriched by avascular invasion cluster variant genes. SNV, single nucleotide variant; KEGG, Kyoto Encyclopedia of Genes and Genomes.

statistical significance (P=0.023; *Table 3*), with no mutation found in the vascular invasion group, but high mutation frequency in the non-vascular invasion group.

Discussion

Vascular invasion in patients with HCC during diagnosis and treatment often predicts poor prognosis or an increased risk of recurrence later in treatment (23). Vascular invasion can be classified as MVI or macrovascular invasion (13). Macrovascular invasion is the result of the evolution of MVI (24). Previous studies have predominantly focused on the impact of the incidence of vascular invasion on tumor recurrence or prognosis (25-27). Guo and Jiang found that overexpression of matrix metalloproteinase 12 (MMP12) is associated with poor prognosis and vascular invasion in HCC, these data suggest that MMP12 may have potential as a therapeutic target and biomarker in HCC (28). However, few studies have examined gene mutations or signaling pathways during vascular invasion. The ability to recognize molecular changes associated with vascular invasion in advance and identify patients at higher risk of recurrence will aid clinical decision-making in the field of HCC treatment.

A total of 50 HCC patients were included in this study, including 19 with macrovascular invasion, 16 with MVI, and 15 with avascular invasion (*Table 1* and Table S1). Similar to a previous study (29), our patients were grouped according to the above vascular invasion status. Analysis of the prognosis and recurrence information of patients revealed significant differences in OS and PFS among the different vascular invasion groups (*Figure 1*). Subsequently, the mutation information of all patients was analyzed through NGS and bioinformatics analysis technology. A total of 762 SNVs were identified (Table S2). Among them, tumor suppressor gene *TP53* and proto-oncogene *CTNNB1* showed the highest mutation frequency (*Figure 2A*). The TMB can indirectly reflect the ability and extent of tumor production of neoantigens, and has been shown to predict the efficacy of immunotherapy for

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Table 3 Hepatocellular carcinoma vascular invasion-related genes

Symbol	Gene name	No. of vascular invasion	No. of avascular invasion	P value
PTPRS	Protein tyrosine phosphatase receptor type S	0	3	0.023214286
TP53	Tumor protein p53	12	2	0.178697863
KIAA2026	KIAA2026	4	0	0.302431611
CTNNB1	Catenin beta 1	4	3	0.414986124
ALMS1	ALMS1 centrosome and basal body associated protein	3	0	0.544642857
DNAH5	Dynein axonemal heavy chain 5	3	0	0.544642857
FGFR3	Fibroblast growth factor receptor 3	3	0	0.544642857
LONP1	Lon peptidase 1, mitochondrial	3	0	0.544642857
LRP1B	LDL receptor related protein 1B	3	0	0.544642857
PRDM1	PR/SET domain 1	3	0	0.544642857
KMT2B	Lysine methyltransferase 2B	3	2	0.629311484
ZNF595	Zinc finger protein 595	3	2	0.629311484
KMT2C	Lysine methyltransferase 2C	4	1	1
KMT2D	Lysine methyltransferase 2D	3	1	1
NF1	Neurofibromin 1	4	1	1

a variety of tumors (30). The TMB values can also reflect the potential of tumor neoantigens in tumors, which are closely related to DNA repair defects (31). Mismatch repair deficient (dMMR) and high microsatellite instability (MSI-H) patients have higher TMB in a variety of tumors (32,33). A study has shown that the TMB obtained from gene panels is overestimated compared to WES data (34), hence, in this study, we calculated the TMB value of the WES and gene panel according to the data source (*Figure 2B,2C*). The macrovascular invasion subgroup analysis of the IMbrave150 study in 2021 showed that atezolizumab combined with bevacizumab was still beneficial in PFS and OS, with a median OS of 24.0 months in the Chinese subgroup (27,35). However, we found no significant difference in the TMB values between the vascular invasion groups, suggesting that the degree of vascular invasion cannot be used as a basis for immunotherapy in HCC, although more data are needed to support this. In addition, with the development of drug therapy, HCC patients who are initially suitable for surgical resection may also benefit from neoadjuvant therapy, and further definitive evidence is required.

A total of 10 genes were found to be associated with prognostic or recurrence factors for HCC, including *EXOC2*, *PRRC2B*, *PTPRS*, and other genes (*Table 2*). Mutations in *EXOC2* cause defects in human brain development (36). The protein encoded by *EXOC2* is part of the extracellular vesicle complex and is critical for the polarized targeting of extracellular vesicles to specific docking sites on the plasma membrane. This protein has been shown to interact with the Ral subfamily of GTPase to mediate exocytosis by anchoring vesicles to the plasma membrane (37). PRRC2B, which plays an important role in the formation of head and neck tumors, activates RNA binding activity and is involved in cell differentiation (38-40). In addition, the *PTPRS* gene is significantly related to vascular invasion (*Table 3*). The protein encoded by this gene is a member of the protein tyrosine phosphatase (PTP) family, which contains an extracellular domain, a transmembrane segment, and two tandem catalytic domains (41). *PTP* is thought to be a signaling molecule regulating a variety of cellular processes, including cell growth, differentiation, mitotic cycle, and oncogenic transformation (42). Although the above genes have been reported to be involved in tumor formation, transformation, and cancer cell differentiation, whether the mutation of these genes in hepatocytes is the dominant factor affecting hepatocellular carcinogenesis or driving the occurrence of vascular invasion has not been proved.

Mutations or differences in the expression of single or

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multiple genes often lead to perturbation of molecular signals in signaling pathways, including hormones, growth factors, cytokines, neurotransmitters, and other small-molecule compounds. The results of the Kyoto Encyclopedia of Genes and Genomes (KEGG) pathway enrichment analysis showed that when hepatocytes became cancerous, the three signaling pathways including EGFR tyrosine kinase inhibitor resistance, PI3K-Akt signaling pathway, and Rap1 signaling pathway, were significantly altered compared to normal cells (43,44). However, when MVI occurs in HCC, thyroid hormone receives interference from exogenous molecules or dysregulation of the thyroid hormone signaling pathway, which further affects angiogenesis and cancer cell proliferation (45). In the macrovascular invasion group, mutant genes were additionally enriched in the Fanconi anemia pathway and the insulin signaling pathway. Aberrations in the Fanconi anemia pathway are associated with genomic instability and tumorigenesis in a variety of human cancers, especially breast cancer (46). In addition, Fanconi anemia patients are susceptible to human papillomavirus (HPV)-related malignancies, suggesting that loss of Fanconi anemia pathway activity promotes tumorigenesis (47). In physiological functions, insulin mainly regulates the metabolism of glucose and lipids through the insulin signaling cascade (48). However, activation of the insulin receptor (INSR) in cancer cells triggers a signaling cascade of the PI3K-Akt pathway, which promotes cell proliferation and glycolysis, while inhibiting apoptosis (49). This is also one of the reasons for the high incidence of cancer in diabetic patients (50). In addition, due to the limitation of the small sample size, further studies are warranted to further verify the above results.

Conclusions

This investigation demonstrated that patients with macrovascular invasion, MVI, and avascular invasion had significantly different somatic mutations and significant differences in prognosis and risk of recurrence. However, no significant differences in TMB were found between the vascular invasion groups. A total of 10 prognostic-related candidate biomarkers were identified, as well as one oncogene that was significantly associated with vascular invasion. Differences were found in both somatic gene mutations and signaling pathways, indicating that the molecular mechanism of tumor tissue changes at different stages of vascular invasion. Understand the molecular changes associated with the vascular invasion process will aid clinical decision-making in the field of HCC treatment.

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Footnote

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Data Sharing Statement: Available at https://jgo.amegroups.com/article/view/10.21037/jgo-22-556/dss

Conflicts of Interest: All authors have completed the ICMJE uniform disclosure form (available at https://jgo.amegroups.com/article/view/10.21037/jgo-22-556/coif). All authors report that this work has received technical support from Shanghai Tongshu Biotechnology Co., Ltd. The authors have no other conflicts of interest to declare.

Ethical Statement: The authors are accountable for all aspects of the work in ensuring that questions related to the accuracy or integrity of any part of the work are appropriately investigated and resolved. This study was conducted in accordance with the Declaration of Helsinki (as revised in 2013). The protocol was approved by the Ethics Committee of Nanfang Hospital, Southern Medical University (ID of the approval: 2012-092). Written informed consent was obtained from all patients prior to inclusion in the study.

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References

1. Qu J, Luo M, Zhang J, et al. A paradoxical role for sestrin 2 protein in tumor suppression and tumorigenesis. Cancer Cell Int 2021;21:606.
2. Zhou J, Wang W, Li Q. Potential therapeutic targets in the tumor microenvironment of hepatocellular carcinoma: reversing the protumor effect of tumor-associated macrophages. J Exp Clin Cancer Res 2021;40:73.
3. Jin M, Yu Q, Liu Y, et al. Safety and Efficacy of Physical Thermal Ablation Combined Sorafenib for Hepatocellular Carcinoma: A Meta-analysis. J Clin Transl Hepatol 2021;9:149-59.
4. Yang JD, Hainaut P, Gores GJ, et al. A global view of hepatocellular carcinoma: trends, risk, prevention and management. Nat Rev Gastroenterol Hepatol 2019;16:589-604.
5. Hu B, Yang XB, Sang XT. Development and Verification of the Hypoxia-Related and Immune-Associated Prognosis Signature for Hepatocellular Carcinoma. J Hepatocell Carcinoma 2020;7:315-30.
6. He Y, Hu B, Zhu C, et al. A Novel Multimodal Radiomics Model for Predicting Prognosis of Resected Hepatocellular Carcinoma. Front Oncol 2022;12:745258.
7. Cao J, Yang X, Li J, et al. Screening and Identifying Immune-Related Cells and Genes in the Tumor Microenvironment of Bladder Urothelial Carcinoma: Based on TCGA Database and Bioinformatics. Front Oncol 2019;9:1533.
8. Mokdad AA, Singal AG, Marrero JA, et al. Vascular Invasion and Metastasis is Predictive of Outcome in Barcelona Clinic Liver Cancer Stage C Hepatocellular Carcinoma. J Natl Compr Canc Netw 2017;15:197-204.
9. Iwatsuki S, Dvorchik I, Marsh JW, et al. Liver transplantation for hepatocellular carcinoma: a proposal of a prognostic scoring system. J Am Coll Surg 2000;191:389-94.
10. Mínguez B, Hoshida Y, Villanueva A, et al. Gene-expression signature of vascular invasion in hepatocellular carcinoma. J Hepatol 2011;55:1325-31.
11. Wu T, Dong X, Yu D, et al. Natural product pectolinarigenin inhibits proliferation, induces apoptosis, and causes G2/M phase arrest of HCC via PI3K/AKT/mTOR/ERK signaling pathway. Onco Targets Ther 2018;11:8633-42.
12. Menyhárt O, Nagy Á, Győrffy B. Determining consistent prognostic biomarkers of overall survival and vascular invasion in hepatocellular carcinoma. R Soc Open Sci 2018;5:181006.
13. Wang L, Jin YX, Ji YZ, et al. Development and validation of a prediction model for microvascular invasion in hepatocellular carcinoma. World J Gastroenterol 2020;26:1647-59.
14. World Medical Association. World Medical Association Declaration of Helsinki: ethical principles for medical research involving human subjects. JAMA 2013;310:2191-4.
15. Cibulskis K, Lawrence MS, Carter SL, et al. Sensitive detection of somatic point mutations in impure and heterogeneous cancer samples. Nat Biotechnol 2013;31:213-9.
16. DePristo MA, Banks E, Poplin R, et al. A framework for variation discovery and genotyping using next-generation DNA sequencing data. Nat Genet 2011;43:491-8.
17. Wang K, Li M, Hakonarson H. ANNOVAR: functional annotation of genetic variants from high-throughput sequencing data. Nucleic Acids Res 2010;38:e164.
18. Ramos AH, Lichtenstein L, Gupta M, et al. Oncotator: cancer variant annotation tool. Hum Mutat 2015;36:E2423-9.
19. Mayakonda A, Lin DC, Assenov Y, et al. Maftools: efficient and comprehensive analysis of somatic variants in cancer. Genome Res 2018;28:1747-56.
20. Rubio-Perez C, Tamborero D, Schroeder MP, et al. In silico prescription of anticancer drugs to cohorts of 28 tumor types reveals targeting opportunities. Cancer Cell 2015;27:382-96.
21. Kassambara A, Kassambara MA. Package 'ggpubr'. R package version 01 2020;6.
22. Team RC. R: A language and environment for statistical computing. 2013.
23. Zhang X, Jiang D, Yang S, et al. BAP31 Promotes Tumor Cell Proliferation by Stabilizing SERPINE2 in Hepatocellular Carcinoma. Front Cell Dev Biol 2020;8:607906.
24. Yan H, Wang X, Zhou D, et al. Dynamic Nomogram for Predicting Macrovascular Invasion of Patients with Unresectable Hepatocellular Carcinoma after Transarterial Chemoembolization. J Cancer 2022;13:1914-22.
25. Nitta H, Allard MA, Sebagh M, et al. Prognostic Value and Prediction of Extratumoral Microvascular Invasion for Hepatocellular Carcinoma. Ann Surg Oncol 2019;26:2568-76.
26. Lei Z, Li J, Wu D, et al. Nomogram for Preoperative Estimation of Microvascular Invasion Risk in Hepatitis B Virus-Related Hepatocellular Carcinoma Within the Milan Criteria. JAMA Surg 2016;151:356-63.
27. Zhang D, Wei Q, Wu GG, et al. Preoperative Prediction of Microvascular Invasion in Patients With Hepatocellular

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Carcinoma Based on Radiomics Nomogram Using Contrast-Enhanced Ultrasound. Front Oncol 2021;11:709339.
28. Guo ZY, Jiang LP. Matrix metalloproteinase 12 (MMP12) as an adverse prognostic biomarker of vascular invasion in hepatic cell carcinoma. Eur Rev Med Pharmacol Sci 2022;26:2238-49.
29. Amado V, Rodríguez-Perálvarez M, Ferrín G, et al. Selecting patients with hepatocellular carcinoma for liver transplantation: incorporating tumor biology criteria. J Hepatocell Carcinoma 2019;6:1-10.
30. Lobo J, Jerónimo C, Henrique R. Targeting the Immune system and Epigenetic Landscape of Urological Tumors. Int J Mol Sci 2020;21:829.
31. Zhang N, Li P, Wu X, et al. Analysis of Threshold Changes of Tumor Mutation Burden of Gastric Cancer and Its Relationship with Patients' Prognosis. J Oncol 2021;2021:9026610.
32. Shimozaki K, Hayashi H, Tanishima S, et al. Concordance analysis of microsatellite instability status between polymerase chain reaction based testing and next generation sequencing for solid tumors. Sci Rep 2021;11:20003.
33. Li L, Rao X, Wen Z, et al. Implications of driver genes associated with a high tumor mutation burden identified using next-generation sequencing on immunotherapy in hepatocellular carcinoma. Oncol Lett 2020;19:2739-48.
34. Hatakeyama K, Nagashima T, Urakami K, et al. Tumor mutational burden analysis of 2,000 Japanese cancer genomes using whole exome and targeted gene panel sequencing. Biomed Res 2018;39:159-67.
35. Mohr R, Özdirik B, Lambrecht J, et al. From Liver Cirrhosis to Cancer: The Role of Micro-RNAs in Hepatocarcinogenesis. Int J Mol Sci 2021;22:1492.
36. Van Bergen NJ, Ahmed SM, Collins F, et al. Mutations in the exocyst component EXOC2 cause severe defects in human brain development. J Exp Med 2020;217:e20192040.
37. Hazelett CC, Yeaman C. Sec5 and Exo84 mediate distinct aspects of RalA-dependent cell polarization. PLoS One 2012;7:e39602.
38. Xie C, Zhou M, Lin J, et al. EEF1D Promotes Glioma Proliferation, Migration, and Invasion through EMT and PI3K/Akt Pathway. Biomed Res Int 2020;2020:7804706.
39. Manjur ABMK, Lempiäinen JK, Malinen M, et al. BCOR modulates transcriptional activity of a subset of glucocorticoid receptor target genes involved in cell growth and mobility. J Steroid Biochem Mol Biol 2021;210:105873.
40. The International Cancer Congress, Part D: Research and treatment. Proceedings of the 13th International Cancer Congress, September 8-15, 1982, Seattle, Washington. Progress in clinical and biological research 1983:1-521.
41. Huang Y, Zhang Y, Ge L, et al. The Roles of Protein Tyrosine Phosphatases in Hepatocellular Carcinoma. Cancers (Basel) 2018;10:82.
42. Muskiewicz DE, Uhl GR, Hall FS. The Role of Cell Adhesion Molecule Genes Regulating Neuroplasticity in Addiction. Neural Plast 2018;2018:9803764.
43. Chen Z, Chen P, Wu H, et al. Evaluation of Naringenin as a Promising Treatment Option for COPD Based on Literature Review and Network Pharmacology. Biomolecules 2020;10:1644.
44. Zhao CH, Qu L, Zhang H, et al. Identification of breast cancer-related circRNAs by analysis of microarray and RNA-sequencing data: An observational study. Medicine (Baltimore) 2019;98:e18042.
45. Liu YC, Yeh CT, Lin KH. Molecular Functions of Thyroid Hormone Signaling in Regulation of Cancer Progression and Anti-Apoptosis. Int J Mol Sci 2019;20:4986.
46. Fang CB, Wu HT, Zhang ML, et al. Fanconi Anemia Pathway: Mechanisms of Breast Cancer Predisposition Development and Potential Therapeutic Targets. Front Cell Dev Biol 2020;8:160.
47. Spriggs CC, Laimins LA. FANCD2 Binds Human Papillomavirus Genomes and Associates with a Distinct Set of DNA Repair Proteins to Regulate Viral Replication. mBio 2017;8:02340-16.
48. Sommerfeld MR, Müller G, Tschank G, et al. In vitro metabolic and mitogenic signaling of insulin glargine and its metabolites. PLoS One 2010;5:e9540.
49. Wang Y, Wan X, Hao Y, et al. NR6A1 regulates lipid metabolism through mammalian target of rapamycin complex 1 in HepG2 cells. Cell Commun Signal 2019;17:77.
50. Choi Y, Kim TY, Oh DY, et al. The Impact of Diabetes Mellitus and Metformin Treatment on Survival of Patients with Advanced Pancreatic Cancer Undergoing Chemotherapy. Cancer Res Treat 2016;48:171-9.

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Table S1 Patient clinical information

Patient ID	Age	Gender	Clinicopathologic diagnosis	Drinking history	history of hepatitis	Microvascular invasion	Macrovascular invasion	lymphatic metastasis	Extrahepatic metastasis	BCLC staging	CNLC staging	therapy method	Analysis of group
P1_T1	61	M	HCC	Yes	Other	No	No	No	No	B	IIa	excision	Avascular invasion
P2_T1	44	M	HCC	No	HBV	No	No	No	No	A	Ia	excision	Avascular invasion
P3_T1	56	M	HCC	Yes	HBV	No	No	No	No	A	Ib	excision	Avascular invasion
P4_T1	55	M	HCC	Yes	HBV	Yes	No	No	No	A	Ia	excision	Microvascular invasion
P5_T1	74	M	HCC	Yes	HBV	Yes	No	No	No	A	Ia	excision	Microvascular invasion
P6_T1	53	M	HCC	No	HBV	Yes	No	No	No	B	IIb	excision	Microvascular invasion
P7_T1	57	M	HCC	Yes	Other	Yes	No	No	No	A	Ia	excision	Microvascular invasion
P8_T1	61	M	HCC	Yes	Other	Yes	No	No	No	B	IIa	excision	Microvascular invasion
P9_T1	40	M	HCC	Yes	Other	No	No	No	No	A	Ia	excision	Avascular invasion
P10_T1	41	F	HCC	No	HBV	No	No	No	No	A	Ib	excision	Avascular invasion
P11_T1	55	M	HCC	Yes	HBV	No	No	No	No	A	Ia	excision	Avascular invasion
P12_T1	61	M	HCC	Yes	HBV	Yes	No	No	No	A	Ib	excision	Microvascular invasion
P13_T1	54	M	HCC	No	HBV	Yes	No	Yes	No	B	IIa	excision	Microvascular invasion
P14_T1	50	M	HCC	Yes	Other	Yes	No	No	No	C	IIIa	excision	Microvascular invasion
P15_T1	25	M	HCC	No	HBV	No	No	Yes	No	C	IIIa	excision	Avascular invasion
P16_T1	34	M	HCC	Yes	HBV	Yes	No	No	No	A	Ib	excision	Microvascular invasion
P17_T1	40	M	HCC	Yes	HBV	Yes	Yes	Yes	No	C	IIIa	excision	Macrovascular invasion
P18_T1	64	M	HCC	No	Other	Yes	Yes	No	No	C	IIIa	medication	Macrovascular invasion
P19_T1	55	M	HCC	Yes	HBV	Yes	Yes	No	Yes	C	IIIb	medication	Macrovascular invasion
P20_T1	54	M	HCC	No	HBV	Yes	No	No	No	A	Ib	excision	Microvascular invasion
P21_T1	56	F	HCC	No	HBV	No	No	No	No	A	Ib	excision	Avascular invasion
P22_T1	44	M	HCC	No	HBV	Yes	Yes	Yes	No	C	IIIa	medication	Macrovascular invasion
P23_T1	45	M	HCC	No	HBV	Yes	No	Yes	Yes	C	IIIb	medication	Microvascular invasion
P24_T1	71	M	HCC	Yes	Other	Yes	Yes	No	No	C	IIIa	medication	Macrovascular invasion
P25_T1	35	M	HCC	No	HBV	Yes	No	No	Yes	C	IIIb	medication	Microvascular invasion
P26_T1	27	M	HCC	Yes	HBV	Yes	Yes	Yes	No	C	IIIb	medication	Macrovascular invasion
P27_T1	60	M	HCC	Yes	HBV	Yes	No	No	No	A	Ib	excision	Microvascular invasion
P28_T1	40	M	HCC	No	HBV	No	No	No	No	A	Ia	excision	Avascular invasion
P29_T1	46	M	HCC	No	HBV	Yes	Yes	No	No	C	IIIa	medication	Macrovascular invasion
P30_T1	80	M	HCC	No	HBV	No	No	No	No	A	Ib	excision	Avascular invasion
P31_T1	63	M	HCC	No	HBV	Yes	Yes	No	No	C	IIIa	medication	Macrovascular invasion
P32_T1	55	F	HCC	No	HBV	Yes	Yes	No	No	C	IIIa	excision	Macrovascular invasion
P33_T1	64	M	HCC	No	HBV	No	No	No	No	A	Ib	excision	Avascular invasion
P34_T1	60	M	HCC	No	HBV	Yes	Yes	No	No	C	IIIa	medication	Macrovascular invasion
P35_T1	67	M	HCC	No	HBV	Yes	No	No	No	B	IIb	excision	Microvascular invasion
P36_T1	51	M	HCC	No	HBV	No	No	No	No	A	Ib	excision	Avascular invasion
P37_T1	46	M	HCC	No	HBV	Yes	Yes	Yes	Yes	C	IIIb	medication	Macrovascular invasion
P38_T1	41	M	HCC	No	HBV	No	No	No	No	A	Ia	excision	Avascular invasion
P39_T1	50	M	HCC	Yes	HBV	No	No	No	No	B	IIb	medication	Avascular invasion
P40_T1	54	M	HCC	Yes	HBV	Yes	Yes	No	No	C	IIIa	excision	Macrovascular invasion
P41_T1	45	M	HCC	No	HBV	Yes	Yes	No	No	C	IIIa	medication	Macrovascular invasion
P42_T1	46	M	HCC	No	HBV	No	No	No	No	A	Ia	excision	Avascular invasion
P43_T1	71	F	HCC	No	Other	Yes	No	No	Yes	C	IIIb	medication	Microvascular invasion
P44_T1	41	M	HCC	No	HBV	Yes	Yes	No	No	C	IIIa	excision	Macrovascular invasion
P45_T1	35	M	HCC	No	HBV	Yes	No	No	No	B	IIb	excision	Microvascular invasion
P46_T1	63	M	HCC	No	HBV	Yes	Yes	Yes	Yes	C	IIIb	medication	Macrovascular invasion
P47_T1	48	M	HCC	No	HBV	Yes	Yes	No	No	C	IIIa	medication	Macrovascular invasion
P48_T1	47	M	HCC	Yes	HBV	Yes	Yes	No	No	B	IIb	medication	Macrovascular invasion
P49_T1	49	M	HCC	No	HBV	Yes	Yes	No	No	C	IIIa	medication	Macrovascular invasion
P50_T1	52	M	HCC	No	HBV	Yes	Yes	No	No	C	IIIa	medication	Macrovascular invasion

M, male; F, female; HCC, hepatocellular carcinoma; HBV, hepatitis B; BCLC, Barcelona Clinic Liver Cancer; CNLC staging, China liver cancer staging.

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Table S2 Single nucleotide variants detected in all tumor samples.

Hugo_Symbol	NCBI_Build	Chromosome	Start_Position	End_Position	Strand	Variant_Classification	Reference_Allele	Tumor_Seq_Allele2	dbSNP_RS	Tumor_Sample_Barcode	HGVSc	HGVSp	t_depth	t_ref_count	t_alt_count	n_depth	n_ref_count	n_alt_count	BIOTYPE	CANONICAL	IMPACT	VARIANT_CLASS
RRAGC	GRCh38	chr1	38859556	38859556	+	Nonsense_Mutation	C	A	novel	P1_T1	c.91G>T	p.Glu31Ter	34	30	4	62	62	0	protein_coding	YES	HIGH	SNV
MSH6	GRCh38	chr2	47801150	47801150	+	Missense_Mutation	T	C	novel	P1_T1	c.3167T>C	p.Val1056Ala	177	169	8	70	70	0	protein_coding	YES	MODERATE	SNV
CTNNB1	GRCh38	chr3	41224622	41224622	+	Missense_Mutation	C	T	rs121913403	P1_T1	c.110C>T	p.Ser37Phe	198	192	6	102	102	0	protein_coding	YES	MODERATE	SNV
SETD2	GRCh38	chr3	47123876	47123905	+	In_Frame_Del	TATCTGCTTCTAAAGATTCTGGTACAATTA	-	novel	P1_T1	c.731_760del	p.Ile244_Asp253del	140	124	16	118	118	0	protein_coding	YES	MODERATE	deletion
EPHA3	GRCh38	chr3	89210158	89210158	+	Missense_Mutation	G	A	novel	P1_T1	c.452G>A	p.Ser151Asn	256	213	43	139	139	0	protein_coding	YES	MODERATE	SNV
FGFR4	GRCh38	chr5	1.77E+08	1.77E+08	+	Missense_Mutation	C	T	rs572098218	P1_T1	c.160C>T	p.Arg54Cys	139	134	5	26	26	0	protein_coding	YES	MODERATE	SNV
VEGFA	GRCh38	chr6	43771229	43771229	+	Missense_Mutation	G	A	rs761101895	P1_T1	c.523G>A	p.Gly175Ser	31	26	5	25	25	0	protein_coding	YES	MODERATE	SNV
GRM3	GRCh38	chr7	86838886	86838886	+	Missense_Mutation	A	G	novel	P1_T1	c.1372A>G	p.Thr458Ala	273	264	9	102	102	0	protein_coding	YES	MODERATE	SNV
PPP2R2A	GRCh38	chr8	26361017	26361017	+	Missense_Mutation	C	G	novel	P1_T1	c.533C>G	p.Pro178Arg	263	233	30	75	75	0	protein_coding	YES	MODERATE	SNV
CDH1	GRCh38	chr16	68738376	68738376	+	Missense_Mutation	G	C	novel	P1_T1	c.128G>C	p.Arg43Pro	96	58	38	30	30	0	protein_coding	YES	MODERATE	SNV
CD22	GRCh38	chr19	35337931	35337931	+	Missense_Mutation	G	A	novel	P1_T1	c.895G>A	p.Val299Met	91	87	4	53	53	0	protein_coding	YES	MODERATE	SNV
KMT2B	GRCh38	chr19	35718232	35718253	+	Frame_Shift_Del	GGGCTCCGCCGGGGCCTGCGCC	-	novel	P1_T1	c.216_237del	p.Leu73SerfsTer87	11	8	3	16	16	0	protein_coding	YES	HIGH	deletion
CIC	GRCh38	chr19	42291409	42291409	+	Missense_Mutation	G	A	novel	P1_T1	c.2641G>A	p.Ala881Thr	167	161	6	65	65	0	protein_coding	YES	MODERATE	SNV
ERCC2	GRCh38	chr19	45368955	45368955	+	Missense_Mutation	G	A		P1_T1	c.221C>T	p.Ser74Leu	139	119	20	40	40	0	protein_coding	YES	MODERATE	SNV
ERCC1	GRCh38	chr19	45421188	45421188	+	Missense_Mutation	C	T	novel	P1_T1	c.311G>A	p.Ser104Asn	190	141	49	101	101	0	protein_coding	YES	MODERATE	SNV
NF2	GRCh38	chr22	29678269	29678269	+	Missense_Mutation	T	A	novel	P1_T1	c.1520T>A	p.Phe507Tyr	118	100	18	27	27	0	protein_coding	YES	MODERATE	SNV
NF2	GRCh38	chr22	29678270	29678270	+	Missense_Mutation	C	A	novel	P1_T1	c.1521C>A	p.Phe507Leu	118	100	18	27	27	0	protein_coding	YES	MODERATE	SNV
STAG2	GRCh38	chrX	1.24E+08	1.24E+08	+	Missense_Mutation	G	A	novel	P1_T1	c.1510G>A	p.Glu504Lys	148	144	4	32	32	0	protein_coding	YES	MODERATE	SNV
PTPRS	GRCh38	chr19	5238990	5238990	+	Missense_Mutation	C	T	rs771916005	P1_T1	c.1778G>A	p.Arg593His	68	64	4	43	43	0	protein_coding	YES	MODERATE	SNV
ARID1A	GRCh38	chr1	26732713	26732713	+	Nonsense_Mutation	C	G		P10_T1	c.1841C>G	p.Ser614Ter	274	223	51	51	51	0	protein_coding	YES	HIGH	SNV
NRAS	GRCh38	chr1	1.15E+08	1.15E+08	+	Missense_Mutation	T	C	rs11554290	P10_T1	c.182A>G	p.Gln61Arg	560	436	124	111	111	0	protein_coding	YES	MODERATE	SNV
MGA	GRCh38	chr15	41729294	41729294	+	Nonsense_Mutation	C	A		P10_T1	c.3788C>A	p.Ser1263Ter	574	531	43	122	122	0	protein_coding	YES	HIGH	SNV
MGA	GRCh38	chr15	41729306	41729306	+	Missense_Mutation	A	T	novel	P10_T1	c.3800A>T	p.Gln1267Leu	574	531	43	124	124	0	protein_coding	YES	MODERATE	SNV
AXIN1	GRCh38	chr16	314671	314671	+	Nonsense_Mutation	C	T		P10_T1	c.891G>A	p.Trp297Ter	174	115	59	35	35	0	protein_coding	YES	HIGH	SNV
CDH1	GRCh38	chr16	68819423	68819423	+	Missense_Mutation	A	G	rs1555516592	P10_T1	c.1709A>G	p.Asn570Ser	246	185	61	72	72	0	protein_coding	YES	MODERATE	SNV
ZFHX3	GRCh38	chr16	72950509	72950509	+	Missense_Mutation	G	T		P10_T1	c.3176C>A	p.Thr1059Lys	266	213	53	58	58	0	protein_coding	YES	MODERATE	SNV
PTPRS	GRCh38	chr19	5244314	5244314	+	Missense_Mutation	C	T	novel	P10_T1	c.1157G>A	p.Arg386His	341	232	109	97	97	0	protein_coding	YES	MODERATE	SNV
AXL	GRCh38	chr19	41222011	41222011	+	Missense_Mutation	G	A	novel	P10_T1	c.541G>A	p.Ala181Thr	202	196	6	30	30	0	protein_coding	YES	MODERATE	SNV
AR	GRCh38	chrX	67545197	67545197	+	Missense_Mutation	G	T	rs370971743	P10_T1	c.51G>T	p.Lys17Asn	724	708	16	103	103	0	protein_coding	YES	MODERATE	SNV
JAK1	GRCh38	chr1	64844820	64844820	+	Missense_Mutation	T	A		P11_T1	c.2185A>T	p.Ser729Cys	476	245	231	404	404	0	protein_coding	YES	MODERATE	SNV
TENT5C	GRCh38	chr1	1.18E+08	1.18E+08	+	Missense_Mutation	A	T	novel	P11_T1	c.476A>T	p.Asn159Ile	1206	927	279	738	738	0	protein_coding	YES	MODERATE	SNV
DNMT3A	GRCh38	chr2	25282476	25282476	+	Missense_Mutation	G	A	rs1310158529	P11_T1	c.413C>T	p.Thr138Ile	198	193	5	245	245	0	protein_coding	YES	MODERATE	SNV
XPO1	GRCh38	chr2	61522626	61522626	+	Missense_Mutation	T	C	novel	P11_T1	c.286A>G	p.Arg96Gly	792	671	121	325	325	0	protein_coding	YES	MODERATE	SNV
NFE2L2	GRCh38	chr2	1.77E+08	1.77E+08	+	Missense_Mutation	T	C	novel	P11_T1	c.1751A>G	p.Gln584Arg	2022	1990	32	819	819	0	protein_coding	YES	MODERATE	SNV
CTNNB1	GRCh38	chr3	41224607	41224607	+	Missense_Mutation	A	G	rs121913396	P11_T1	c.95A>G	p.Asp32Gly	1124	1099	25	518	518	0	protein_coding	YES	MODERATE	SNV
CTNNB1	GRCh38	chr3	41224610	41224610	+	Missense_Mutation	C	G	rs121913400	P11_T1	c.98C>G	p.Ser33Cys	1106	930	176	508	508	0	protein_coding	YES	MODERATE	SNV
NSD1	GRCh38	chr5	1.77E+08	1.77E+08	+	Missense_Mutation	G	A	novel	P11_T1	c.3856G>A	p.Glu1286Lys	554	536	18	280	280	0	protein_coding	YES	MODERATE	SNV
TET1	GRCh38	chr10	68646235	68646235	+	Missense_Mutation	A	G	rs756422497	P11_T1	c.3506A>G	p.Gln1169Arg	1266	1046	220	643	643	0	protein_coding	YES	MODERATE	SNV
IRS2	GRCh38	chr13	1.1E+08	1.1E+08	+	Missense_Mutation	C	T	rs1200134173	P11_T1	c.1598G>A	p.Gly533Asp	326	320	6	364	364	0	protein_coding	YES	MODERATE	SNV
NF1	GRCh38	chr17	31169938	31169938	+	Missense_Mutation	A	T		P11_T1	c.527A>T	p.Asp176Val	1126	1096	30	396	396	0	protein_coding	YES	MODERATE	SNV
STAT3	GRCh38	chr17	42338773	42338773	+	Missense_Mutation	C	G	novel	P11_T1	c.508G>C	p.Asp170His	633	334	299	231	231	0	protein_coding	YES	MODERATE	SNV
ZNF217	GRCh38	chr20	53575936	53575936	+	Missense_Mutation	G	C	novel	P11_T1	c.2828C>G	p.Pro943Arg	1201	759	442	832	832	0	protein_coding	YES	MODERATE	SNV
RTEL1	GRCh38	chr20	63689613	63689613	+	Missense_Mutation	G	A	novel	P11_T1	c.1990G>A	p.Asp664Asn	131	126	5	220	220	0	protein_coding	YES	MODERATE	SNV
SPEN	GRCh38	chr1	15919477	15919477	+	Missense_Mutation	A	G	novel	P12_T1	c.1595A>G	p.Tyr532Cys	1000	818	182	138	138	0	protein_coding	YES	MODERATE	SNV
MKNK1	GRCh38	chr1	46558591	46558591	+	Missense_Mutation	G	A	rs373002774	P12_T1	c.1382C>T	p.Pro461Leu	312	308	4	29	29	0	protein_coding	YES	MODERATE	SNV
IRS1	GRCh38	chr2	2.27E+08	2.27E+08	+	Missense_Mutation	A	G	novel	P12_T1	c.845T>C	p.Val282Ala	482	474	8	62	62	0	protein_coding	YES	MODERATE	SNV
PIK3CA	GRCh38	chr3	1.79E+08	1.79E+08	+	Missense_Mutation	A	T	rs121913279	P12_T1	c.3140A>T	p.His1047Leu	589	575	14	122	122	0	protein_coding	YES	MODERATE	SNV
KLHL6	GRCh38	chr3	1.84E+08	1.84E+08	+	Missense_Mutation	A	T	novel	P12_T1	c.437T>A	p.Leu146Gln	736	593	143	80	80	0	protein_coding	YES	MODERATE	SNV
FGFR3	GRCh38	chr4	1804450	1804450	+	Missense_Mutation	G	A	rs761896295	P12_T1	c.1202G>A	p.Arg401His	360	355	5	60	60	0	protein_coding	YES	MODERATE	SNV
KIT	GRCh38	chr4	54725909	54725909	+	Missense_Mutation	C	A	novel	P12_T1	c.1399C>A	p.Pro467Thr	726	500	226	99	99	0	protein_coding	YES	MODERATE	SNV
APC	GRCh38	chr5	1.13E+08	1.13E+08	+	Nonsense_Mutation	G	T		P12_T1	c.2752G>T	p.Glu918Ter	1053	950	103	176	176	0	protein_coding	YES	HIGH	SNV
FLT4	GRCh38	chr5	1.81E+08	1.81E+08	+	Missense_Mutation	C	T	novel	P12_T1	c.3374G>A	p.Cys1125Tyr	229	225	4	33	33	0	protein_coding	YES	MODERATE	SNV
GRM3	GRCh38	chr7	86839787	86839787	+	Missense_Mutation	C	A	rs141671463	P12_T1	c.2273C>A	p.Thr758Lys	1326	665	661	209	209	0	protein_coding	YES	MODERATE	SNV
PTEN	GRCh38	chr10	87933154	87933154	+	Missense_Mutation	G	A	rs121909241	P12_T1	c.395G>A	p.Gly132Asp	788	626	162	192	192	0	protein_coding	YES	MODERATE	SNV
HNF1A	GRCh38	chr12	1.21E+08	1.21E+08	+	Missense_Mutation	G	T		P12_T1	c.1576G>T	p.Asp526Tyr	354	180	174	51	50	1	protein_coding	YES	MODERATE	SNV
LTK	GRCh38	chr15	41507610	41507610	+	Missense_Mutation	C	T	novel	P12_T1	c.1297G>A	p.Ala433Thr	529	521	8	52	52	0	protein_coding	YES	MODERATE	SNV
AXIN1	GRCh38	chr16	297839	297839	+	Missense_Mutation	C	T	novel	P12_T1	c.1667G>A	p.Arg556His	383	377	6	67	67	0	protein_coding	YES	MODERATE	SNV
KDM6A	GRCh38	chrX	45082585	45082586	+	Frame_Shift_Ins	-	A	novel	P12_T1	c.3160dup	p.Arg1054LysfsTer5	399	303	96	90	90	0	protein_coding	YES	HIGH	insertion
PMS1	GRCh38	chr2	1.9E+08	1.9E+08	+	Missense_Mutation	G	A	novel	P13_T1	c.484G>A	p.Ala162Thr	193	189	4	120	120	0	protein_coding	YES	MODERATE	SNV
PIK3CA	GRCh38	chr3	1.79E+08	1.79E+08	+	Missense_Mutation	A	G	novel	P13_T1	c.2210A>G	p.Glu737Gly	196	192	4	123	123	0	protein_coding	YES	MODERATE	SNV
DCUN1D1	GRCh38	chr3	1.83E+08	1.83E+08	+	Missense_Mutation	C	T	novel	P13_T1	c.562G>A	p.Gly188Arg	148	144	4	68	68	0	protein_coding	YES	MODERATE	SNV
PRDM1	GRCh38	chr6	1.06E+08	1.06E+08	+	Missense_Mutation	C	A	rs1250819115	P13_T1	c.1181C>A	p.Pro394His	1044	1030	14	78	78	0	protein_coding	YES	MODERATE	SNV
CFTR	GRCh38	chr7	1.18E+08	1.18E+08	+	Frame_Shift_Del	ATTA	-	rs749854099	P13_T1	c.1333_1336del	p.Asn445SerfsTer3	128	124	4	103	103	0	protein_coding	YES	HIGH	deletion
EZH2	GRCh38	chr7	1.49E+08	1.49E+08	+	Missense_Mutation	G	A	rs771352080	P13_T1	c.52C>T	p.Arg18Cys	119	87	32	101	101	0	protein_coding	YES	MODERATE	SNV
KMT2C	GRCh38	chr7	1.52E+08	1.52E+08	+	Missense_Mutation	C	A	novel	P13_T1	c.4789G>T	p.Ala1597Ser	180	89	91	156	156	0	protein_coding	YES	MODERATE	SNV
PPP2R2A	GRCh38	chr8	26293711	26293711	+	Missense_Mutation	A	G	novel	P13_T1	c.83A>G	p.Lys28Arg	412	407	5	223	223	0	protein_coding	YES	MODERATE	SNV
SOCS1	GRCh38	chr16	11255282	11255282	+	Missense_Mutation	C	T		P13_T1	c.197G>A	p.Arg66His	164	160	4	15	15	0	protein_coding	YES	MODERATE	SNV
NF1	GRCh38	chr17	31200521	31200521	+	Missense_Mutation	G	T		P13_T1	c.988G>T	p.Ala330Ser	186	98	88	79	79	0	protein_coding	YES	MODERATE	SNV
NF1	GRCh38	chr17	31235987	31235987	+	Missense_Mutation	T	G	novel	P13_T1	c.3940T>G	p.Trp1314Gly	407	401	6	146	146	0	protein_coding	YES	MODERATE	SNV
SUZ12	GRCh38	chr17	31975662	31975662	+	Missense_Mutation	G	A	rs748177043	P13_T1	c.772G>A	p.Gly258Arg	292	284	8	160	160	0	protein_coding	YES	MODERATE	SNV
JAK1	GRCh38	chr1	64839716	64839716	+	Missense_Mutation	A	G		P14_T1	c.2729T>C	p.Leu910Pro	469	295	174	41	41	0	protein_coding	YES	MODERATE	SNV
INHA	GRCh38	chr2	2.2E+08	2.2E+08	+	Missense_Mutation	C	T	rs373504529	P14_T1	c.767C>T	p.Pro256Leu	279	275	4	24	24	0	protein_coding	YES	MODERATE	SNV
CTNNB1	GRCh38	chr3	41224633	41224633	+	Missense_Mutation	A	G	rs121913412	P14_T1	c.121A>G	p.Thr41Ala	703	492	211	44	44	0	protein_coding	YES	MODERATE	SNV
PDGFRB	GRCh38	chr5	1.5E+08	1.5E+08	+	Missense_Mutation	G	A	rs1225116257	P14_T1	c.1486C>T	p.Arg496Cys	365	359	6	11	11	0	protein_coding	YES	MODERATE	SNV
PRDM1	GRCh38	chr6	1.06E+08	1.06E+08	+	Missense_Mutation	C	T	rs753673199	P14_T1	c.1553C>T	p.Thr518Met	298	294	4	30	30	0	protein_coding	YES	MODERATE	SNV
RHEB	GRCh38	chr7	1.51E+08	1.51E+08	+	Missense_Mutation	G	A	rs1312383700	P14_T1	c.545C>T	p.Ser182Leu	401	396	5	56	56	0	protein_coding	YES	MODERATE	SNV
RXRA	GRCh38	chr9	1.34E+08	1.34E+08	+	Missense_Mutation	C	T	novel	P14_T1	c.1258C>T	p.Leu420Phe	170	166	4	13	13	0	protein_coding	YES	MODERATE	SNV
RET	GRCh38	chr10	43102437	43102437	+	Missense_Mutation	G	A	rs1311922451	P14_T1	c.433G>A	p.Val145Ile	163	159	4	17	17	0	protein_coding	YES	MODERATE	SNV
FGF3	GRCh38	chr11	69810333	69810333	+	Missense_Mutation	C	T	novel	P14_T1	c.692G>A	p.Gly231Asp	127	123	4	10	10	0	protein_coding	YES	MODERATE	SNV
KMT2D	GRCh38	chr12	49037502	49037502	+	Missense_Mutation	A	G	novel	P14_T1	c.9854T>C	p.Leu3285Pro	135	131	4	13	13	0	protein_coding	YES	MODERATE	SNV
KMT2D	GRCh38	chr12	49048669	49048669	+	Missense_Mutation	A	G	novel	P14_T1	c.4121T>C	p.Val1374Ala	314	310	4	24	24	0	protein_coding	YES	MODERATE	SNV
CREBBP	GRCh38	chr16	3770679	3770679	+	Missense_Mutation	G	A		P14_T1	c.2771C>T	p.Ala924Val	124	120	4	11	11	0	protein_coding	YES	MODERATE	SNV
ZFHX3	GRCh38	chr16	72788023	72788023	+	Missense_Mutation	G	A	novel	P14_T1	c.10253C>T	p.Ser3418Phe	178	174	4	25	25	0	protein_coding	YES	MODERATE	SNV
PLCG2	GRCh38	chr16	81900670	81900670	+	Missense_Mutation	G	A	rs867891510	P14_T1	c.1252G>A	p.Ala418Thr	438	432	6	15	15	0	protein_coding	YES	MODERATE	SNV
PLCG2	GRCh38	chr16	81928606	81928606	+	Missense_Mutation	C	A	novel	P14_T1	c.2563C>A	p.Leu855Ile	300	296	4	30	30	0	protein_coding	YES	MODERATE	SNV
FANCA	GRCh38	chr16	89771797	89771797	+	Missense_Mutation	C	T	novel	P14_T1	c.2032G>A	p.Ala678Thr	211	207	4	27	27	0	protein_coding	YES	MODERATE	SNV
NF1	GRCh38	chr17	31350216	31350216	+	Missense_Mutation	G	A	rs1555536122	P14_T1	c.7355G>A	p.Arg2452His	712	704	8	91	91	0	protein_coding	YES	MODERATE	SNV
MAP3K14	GRCh38	chr17	45265261	45265261	+	Missense_Mutation	C	T	novel	P14_T1	c.2581G>A	p.Val861Met	240	236	4	22	22	0	protein_coding	YES	MODERATE	SNV
MSI2	GRCh38	chr17	57674984	57674984	+	Missense_Mutation	C	T	rs781460110	P14_T1	c.803C>T	p.Ala268Val	196	191	5	29	29	0	protein_coding	YES	MODERATE	SNV
STK11	GRCh38	chr19	1223088	1223088	+	Missense_Mutation	G	A	novel	P14_T1	c.1024G>A	p.Glu342Lys	211	207	4	32	32	0	protein_coding	YES	MODERATE	SNV
DNMT1	GRCh38	chr19	10160393	10160393	+	Missense_Mutation	G	A	novel	P14_T1	c.1034C>T	p.Pro345Leu	237	233	4	77	77	0	protein_coding	YES	MODERATE	SNV
SMARCA4	GRCh38	chr19	10987858	10987858	+	Missense_Mutation	G	A	rs1018881303	P14_T1	c.1052G>A	p.Arg351His	108	105	3	18	18	0	protein_coding	YES	MODERATE	SNV
NOTCH3	GRCh38	chr19	15162553	15162553	+	Missense_Mutation	G	A	novel	P14_T1	c.5825C>T	p.Ala1942Val	72	68	4	31	31	0	protein_coding	YES	MODERATE	SNV
JAK3	GRCh38	chr19	17841689	17841689	+	Missense_Mutation	G	A		P14_T1	c.935C>T	p.Ala312Val	185	181	4	23	23	0	protein_coding	YES	MODERATE	SNV
KMT2B	GRCh38	chr19	35736773	35736773	+	Missense_Mutation	C	T		P14_T1	c.7243C>T	p.Arg2415Cys	315	311	4	19	19	0	protein_coding	YES	MODERATE	SNV
ERF	GRCh38	chr19	42249727	42249727	+	Missense_Mutation	G	T	novel	P14_T1	c.385C>A	p.Pro129Thr	209	205	4	10	10	0	protein_coding	YES	MODERATE	SNV
ASXL1	GRCh38	chr20	32437225	32437225	+	Nonsense_Mutation	C	T	novel	P14_T1	c.4513C>T	p.Gln1505Ter	376	371	5	33	33	0	protein_coding	YES	HIGH	SNV
KDM5C	GRCh38	chrX	53216083	53216083	+	Missense_Mutation	G	A	rs1569278482	P14_T1	c.772C>T	p.Arg258Trp	274	270	4	14	14	0	protein_coding	YES	MODERATE	SNV
AMER1	GRCh38	chrX	64192401	64192401	+	Missense_Mutation	C	T	novel	P14_T1	c.886G>A	p.Gly296Arg	422	414	8	15	15	0	protein_coding	YES	MODERATE	SNV
AR	GRCh38	chrX	67722944	67722944	+	Missense_Mutation	G	A	rs9332971	P14_T1	c.2567G>A	p.Arg856His	399	393	6	29	29	0	protein_coding	YES	MODERATE	SNV
BTK	GRCh38	chrX	1.01E+08	1.01E+08	+	Missense_Mutation	G	A	rs868978699	P14_T1	c.1570C>T	p.Arg524Cys	250	244	6	14	14	0	protein_coding	YES	MODERATE	SNV
MPL	GRCh38	chr1	43340114	43340114	+	Missense_Mutation	C	G	novel	P15_T1	c.841C>G	p.Pro281Ala	556	396	160	37	37	0	protein_coding	YES	MODERATE	SNV
DDR2	GRCh38	chr1	1.63E+08	1.63E+08	+	Nonsense_Mutation	C	T	rs1241709692	P15_T1	c.1021C>T	p.Arg341Ter	2059	1810	249	46	46	0	protein_coding	YES	HIGH	SNV
PPARG	GRCh38	chr3	12416981	12416981	+	Missense_Mutation	G	T	novel	P15_T1	c.1097G>T	p.Gly366Val	724	525	199	39	39	0	protein_coding	YES	MODERATE	SNV
PARP3	GRCh38	chr3	51943359	51943359	+	Missense_Mutation	G	A	rs918761252	P15_T1	c.25G>A	p.Ala9Thr	531	523	8	20	20	0	protein_coding	YES	MODERATE	SNV
PPP4R2	GRCh38	chr3	73065671	73065671	+	Missense_Mutation	A	T		P15_T1	c.1203A>T	p.Glu401Asp	147	143	4	26	26	0	protein_coding	YES	MODERATE	SNV
MSH3	GRCh38	chr5	80672247	80672247	+	Missense_Mutation	G	A		P15_T1	c.796G>A	p.Ala266Thr	130	125	5	23	23	0	protein_coding	YES	MODERATE	SNV
KMT2C	GRCh38	chr7	1.52E+08	1.52E+08	+	Missense_Mutation	T	C	rs4639425	P15_T1	c.2185A>G	p.Asn729Asp	594	581	13	97	97	0	protein_coding	YES	MODERATE	SNV
BIRC3	GRCh38	chr11	1.02E+08	1.02E+08	+	Missense_Mutation	A	G	novel	P15_T1	c.848A>G	p.Tyr283Cys	214	154	60	32	32	0	protein_coding	YES	MODERATE	SNV
BLM	GRCh38	chr15	90749983	90749983	+	Missense_Mutation	G	A	rs200756519	P15_T1	c.715G>A	p.Asp239Asn	405	399	6	65	65	0	protein_coding	YES	MODERATE	SNV
AXIN1	GRCh38	chr16	346590	346590	+	Nonsense_Mutation	G	A		P15_T1	c.436C>T	p.Arg146Ter	801	183	618	60	60	0	protein_coding	YES	HIGH	SNV
ASXL2	GRCh38	chr2	25799447	25799447	+	Missense_Mutation	C	T	NA	P16_T1	c.341G>A	p.Ser114Asn	387	378	9	194	194	0	protein_coding	NA	MODERATE	SNV
NOTCH2	GRCh38	chr1	1.2E+08	1.2E+08	+	Missense_Mutation	C	T	novel	P17_T1	c.356G>A	p.Gly119Asp	338	333	5	474	474	0	protein_coding	YES	MODERATE	SNV
PRDM1	GRCh38	chr6	1.06E+08	1.06E+08	+	Missense_Mutation	C	A	rs767701088	P17_T1	c.365C>A	p.Thr122Asn	580	503	77	508	508	0	protein_coding	YES	MODERATE	SNV
AXIN1	GRCh38	chr16	347011	347012	+	Frame_Shift_Ins	-	TCTTGGAT	novel	P17_T1	c.7_14dup	p.Gln6SerfsTer81	155	89	66	434	434	0	protein_coding	YES	HIGH	insertion
TP53	GRCh38	chr17	7674947	7674947	+	Missense_Mutation	A	G	rs760043106	P17_T1	c.584T>C	p.Ile195Thr	184	126	58	443	443	0	protein_coding	YES	MODERATE	SNV
FANCA	GRCh38	chr16	89805292	89805292	+	Missense_Mutation	C	T		P17_T1	c.697G>A	p.Ala233Thr	159	153	6	217	217	0	protein_coding	YES	MODERATE	SNV
NOTCH2	GRCh38	chr1	1.2E+08	1.2E+08	+	Nonsense_Mutation	C	A	novel	P18_T1	c.5284G>T	p.Glu1762Ter	2414	2288	126	71	71	0	protein_coding	YES	HIGH	SNV
EGFR	GRCh38	chr7	55157710	55157734	+	Frame_Shift_Del	GCCTTTGAGAACCTAGAAATCATAC	-	novel	P18_T1	c.1257_1281del	p.Phe420AlafsTer16	2286	2197	89	62	62	0	protein_coding	YES	HIGH	deletion
MYC	GRCh38	chr8	1.28E+08	1.28E+08	+	Missense_Mutation	G	C	rs61752959	P18_T1	c.144G>C	p.Gln48His	1700	1677	23	64	64	0	protein_coding	YES	MODERATE	SNV
ZFHX3	GRCh38	chr16	72957814	72957816	+	In_Frame_Del	CCA	-	rs768134461	P18_T1	c.2330_2332del	p.Val777del	1416	1370	46	34	34	0	protein_coding	YES	MODERATE	deletion
INSR	GRCh38	chr19	7168084	7168084	+	Missense_Mutation	C	A	novel	P18_T1	c.1494G>T	p.Glu498Asp	1601	1581	20	67	67	0	protein_coding	YES	MODERATE	SNV
BCL10	GRCh38	chr1	85267691	85267691	+	Missense_Mutation	C	T	rs3768235	P19_T1	c.638G>A	p.Gly213Glu	1196	1160	36	93	93	0	protein_coding	YES	MODERATE	SNV
HSD3B1	GRCh38	chr1	1.2E+08	1.2E+08	+	Missense_Mutation	T	C	rs6205	P19_T1	c.856T>C	p.Phe286Leu	1506	1478	28	93	93	0	protein_coding	YES	MODERATE	SNV

Table S2 (*continued*)

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Table S2 (*continued*)

Hugo_ Symbol	NCBI_Build	Chromosome	Start_Position	End_Position	Strand	Variant_Classification	Reference_Allele	Tumor_Seq_Allele2	dbSNP_RS	Tumor_Sample_ Barcode	HGVSc	HGVSp	t_depth	t_ref_count	t_alt_count	n_depth	n_ref_count	n_alt_count	BIOTYPE	CANONICAL	IMPACT	VARIANT_ CLASS
H3-3A	GRCh38	chr1	2.26E+08	2.26E+08	+	Missense_Mutation	C	G	rs749423281	P19_T1	c.344C>G	p.Ala115Gly	467	434	33	25	25	0	protein_coding	YES	MODERATE	SNV
PARP1	GRCh38	chr1	2.26E+08	2.26E+08	+	Missense_Mutation	A	G	rs1136410	P19_T1	c.2285T>C	p.Val762Ala	1643	1593	50	62	62	0	protein_coding	YES	MODERATE	SNV
FANCL	GRCh38	chr2	58241253	58241253	+	Missense_Mutation	A	C	novel	P19_T1	c.61T>G	p.Ser21Ala	817	395	422	65	65	0	protein_coding	YES	MODERATE	SNV
TEKT4	GRCh38	chr2	94871827	94871827	+	Missense_Mutation	C	T	rs4854235	P19_T1	c.248C>T	p.Thr83Met	356	346	10	17	17	0	protein_coding	YES	MODERATE	SNV
TEKT4	GRCh38	chr2	94871877	94871877	+	Missense_Mutation	A	G	rs11164112	P19_T1	c.298A>G	p.Ser100Gly	367	350	17	23	23	0	protein_coding	YES	MODERATE	SNV
NFE2L2	GRCh38	chr2	1.77E+08	1.77E+08	+	In_Frame_Del	GTTTCTGACTGGATGTGCTGGGCTGGCT GAATTGGGAGAAATTCACCTGTCTCTTCA TCTAGTTGTAACTGAGCGAAA	-	novel	P19_T1	c.210_287del	p.Phe71_Thr96del	2026	1589	437	285	284	1	protein_coding	YES	MODERATE	deletion
IRS1	GRCh38	chr2	2.27E+08	2.27E+08	+	Missense_Mutation	G	A	rs779584301	P19_T1	c.1360C>T	p.Pro454Ser	1354	1335	19	67	67	0	protein_coding	YES	MODERATE	SNV
VHL	GRCh38	chr3	10146592	10146592	+	Missense_Mutation	T	A		P19_T1	c.419T>A	p.Leu140His	1623	1173	450	85	85	0	protein_coding	YES	MODERATE	SNV
FGFR3	GRCh38	chr4	1801411	1801411	+	Missense_Mutation	C	G	rs577990843	P19_T1	c.490C>G	p.Leu164Val	795	783	12	29	29	0	protein_coding	YES	MODERATE	SNV
FAT1	GRCh38	chr4	1.87E+08	1.87E+08	+	Missense_Mutation	T	C	rs11939575	P19_T1	c.3190A>G	p.Arg1064Gly	1430	1394	36	129	129	0	protein_coding	YES	MODERATE	SNV
FAT1	GRCh38	chr4	1.87E+08	1.87E+08	+	Missense_Mutation	C	G	rs1877731	P19_T1	c.2584G>C	p.Val862Leu	2105	2040	65	217	217	0	protein_coding	YES	MODERATE	SNV
FAT1	GRCh38	chr4	1.87E+08	1.87E+08	+	Missense_Mutation	G	C	rs367863	P19_T1	c.1842C>G	p.Phe614Leu	1330	1293	37	157	157	0	protein_coding	YES	MODERATE	SNV
FAT1	GRCh38	chr4	1.87E+08	1.87E+08	+	Missense_Mutation	C	T	rs3733413	P19_T1	c.1444G>A	p.Val482Ile	2117	2076	41	182	182	0	protein_coding	YES	MODERATE	SNV
FAT1	GRCh38	chr4	1.87E+08	1.87E+08	+	Missense_Mutation	A	C	rs3733414	P19_T1	c.1212T>G	p.Ser404Arg	1568	1522	46	158	158	0	protein_coding	YES	MODERATE	SNV
CCND3	GRCh38	chr6	41941600	41941600	+	Missense_Mutation	G	A	rs1254723551	P19_T1	c.50C>T	p.Pro17Leu	380	283	97	31	31	0	protein_coding	YES	MODERATE	SNV
BRAF	GRCh38	chr7	1.41E+08	1.41E+08	+	Missense_Mutation	T	C	rs121913370	P19_T1	c.1742A>G	p.Asn581Ser	949	721	228	55	55	0	protein_coding	YES	MODERATE	SNV
KMT2C	GRCh38	chr7	1.52E+08	1.52E+08	+	Missense_Mutation	G	A	rs74483926	P19_T1	c.10979C>T	p.Ser3660Leu	2714	2667	47	252	252	0	protein_coding	YES	MODERATE	SNV
KMT2C	GRCh38	chr7	1.52E+08	1.52E+08	+	Missense_Mutation	A	G	rs78004519	P19_T1	c.10639T>C	p.Ser3547Pro	1828	1786	42	178	178	0	protein_coding	YES	MODERATE	SNV
PRDM14	GRCh38	chr8	70068503	70068503	+	Missense_Mutation	T	C	rs3750228	P19_T1	c.730A>G	p.Lys244Glu	854	844	10	56	56	0	protein_coding	YES	MODERATE	SNV
RECQL4	GRCh38	chr8	1.45E+08	1.45E+08	+	Missense_Mutation	T	G	rs535692036	P19_T1	c.1345A>C	p.Thr449Pro	1236	1214	22	53	52	1	protein_coding	YES	MODERATE	SNV
TEK	GRCh38	chr9	27197488	27197488	+	Missense_Mutation	G	T	rs35030851	P19_T1	c.1798G>T	p.Val600Leu	1304	1289	15	137	137	0	protein_coding	YES	MODERATE	SNV
TET1	GRCh38	chr10	68572823	68572823	+	Missense_Mutation	A	G	rs10823229	P19_T1	c.485A>G	p.Asp162Gly	1797	1765	32	156	156	0	protein_coding	YES	MODERATE	SNV
FGFR2	GRCh38	chr10	1.22E+08	1.22E+08	+	Missense_Mutation	T	C		P19_T1	c.130A>G	p.Ile44Val	1625	1135	490	144	144	0	protein_coding	YES	MODERATE	SNV
INPPL1	GRCh38	chr11	72232917	72232917	+	Missense_Mutation	C	A	rs61749195	P19_T1	c.1894C>A	p.Leu632Ile	1090	1072	18	61	61	0	protein_coding	YES	MODERATE	SNV
INPPL1	GRCh38	chr11	72237492	72237492	+	Missense_Mutation	C	G	rs11548491	P19_T1	c.3248C>G	p.Ala1083Gly	1335	1316	19	71	71	0	protein_coding	YES	MODERATE	SNV
FGF23	GRCh38	chr12	4370383	4370383	+	Missense_Mutation	G	A	rs7955866	P19_T1	c.716C>T	p.Thr239Met	2161	2093	68	100	100	0	protein_coding	YES	MODERATE	SNV
PIK3C2G	GRCh38	chr12	18496123	18496123	+	Missense_Mutation	C	T	rs12312266	P19_T1	c.2855C>T	p.Pro952Leu	1177	1158	19	85	85	0	protein_coding	YES	MODERATE	SNV
GLI1	GRCh38	chr12	57472038	57472038	+	Missense_Mutation	G	C	rs2228226	P19_T1	c.3298G>C	p.Glu1100Gln	1419	1398	21	80	80	0	protein_coding	YES	MODERATE	SNV
HNF1A	GRCh38	chr12	1.21E+08	1.21E+08	+	Missense_Mutation	A	C	rs1169288	P19_T1	c.79A>C	p.Ile27Leu	892	875	17	29	28	1	protein_coding	YES	MODERATE	SNV
BRCA2	GRCh38	chr13	32376672	32376672	+	Missense_Mutation	A	G	novel	P19_T1	c.8635A>G	p.Asn2879Asp	561	307	254	42	42	0	protein_coding	YES	MODERATE	SNV
TSHR	GRCh38	chr14	81144239	81144239	+	Missense_Mutation	G	C	rs1991517	P19_T1	c.2181G>C	p.Glu727Asp	1755	1729	26	148	148	0	protein_coding	YES	MODERATE	SNV
BLM	GRCh38	chr15	90751928	90751928	+	Missense_Mutation	C	T	rs751438275	P19_T1	c.941C>T	p.Ser314Phe	817	807	10	88	88	0	protein_coding	YES	MODERATE	SNV
MAPK3	GRCh38	chr16	30118437	30118437	+	Missense_Mutation	C	T	novel	P19_T1	c.455G>A	p.Arg152Gln	1456	1384	72	68	68	0	protein_coding	YES	MODERATE	SNV
ANKRD11	GRCh38	chr16	89279644	89279644	+	Missense_Mutation	C	A	novel	P19_T1	c.6898G>T	p.Ala2300Ser	899	537	362	41	41	0	protein_coding	YES	MODERATE	SNV
AURKB	GRCh38	chr17	8205013	8205013	+	Missense_Mutation	A	G	rs1059476	P19_T1	c.896T>C	p.Met299Thr	1055	1006	49	74	74	0	protein_coding	YES	MODERATE	SNV
SPOP	GRCh38	chr17	49622064	49622064	+	Missense_Mutation	T	C	novel	P19_T1	c.82A>G	p.Lys28Glu	1153	1045	108	54	54	0	protein_coding	YES	MODERATE	SNV
DLL3	GRCh38	chr19	39504071	39504071	+	Missense_Mutation	T	C	rs1110627	P19_T1	c.653T>C	p.Leu218Pro	826	810	16	22	22	0	protein_coding	YES	MODERATE	SNV
AURKA	GRCh38	chr20	56386485	56386485	+	Missense_Mutation	A	T	rs2273535	P19_T1	c.91T>A	p.Phe31Ile	2027	1977	50	96	96	0	protein_coding	YES	MODERATE	SNV
EP300	GRCh38	chr22	41131624	41131624	+	Missense_Mutation	A	G	rs146242251	P19_T1	c.1519A>G	p.Ser507Gly	599	592	7	56	56	0	protein_coding	YES	MODERATE	SNV
KDM6A	GRCh38	chrX	45069832	45069832	+	Missense_Mutation	C	A	rs2230018	P19_T1	c.2177C>A	p.Thr726Lys	512	491	21	57	57	0	protein_coding	YES	MODERATE	SNV
ARID1A	GRCh38	chr1	26774401	26774401	+	Missense_Mutation	C	T	rs758767486	P2_T1	c.4174C>T	p.Pro1392Ser	159	154	5	40	40	0	protein_coding	YES	MODERATE	SNV
MUTYH	GRCh38	chr1	45332179	45332179	+	Missense_Mutation	C	T	rs140156029	P2_T1	c.911G>A	p.Arg304Gln	182	178	4	51	51	0	protein_coding	YES	MODERATE	SNV
PIK3CA	GRCh38	chr3	1.79E+08	1.79E+08	+	Missense_Mutation	G	A		P2_T1	c.1579G>A	p.Asp527Asn	455	424	31	51	51	0	protein_coding	YES	MODERATE	SNV
MAP3K13	GRCh38	chr3	1.85E+08	1.85E+08	+	Missense_Mutation	A	T	novel	P2_T1	c.719A>T	p.Gln240Leu	592	558	34	68	68	0	protein_coding	YES	MODERATE	SNV
TET2	GRCh38	chr4	1.05E+08	1.05E+08	+	Missense_Mutation	A	T		P2_T1	c.5087A>T	p.Tyr1696Phe	811	794	17	100	100	0	protein_coding	YES	MODERATE	SNV
GABRA6	GRCh38	chr5	1.62E+08	1.62E+08	+	Missense_Mutation	C	T	novel	P2_T1	c.395C>T	p.Pro132Leu	528	504	24	78	78	0	protein_coding	YES	MODERATE	SNV
FGF19	GRCh38	chr11	69703344	69703344	+	Missense_Mutation	C	T	rs747918000	P2_T1	c.253G>A	p.Val85Ile	87	83	4	14	14	0	protein_coding	YES	MODERATE	SNV
TYRO3	GRCh38	chr15	41578071	41578071	+	Missense_Mutation	G	A	novel	P2_T1	c.2468G>A	p.Gly823Asp	129	125	4	44	44	0	protein_coding	YES	MODERATE	SNV
PLCG2	GRCh38	chr16	81919504	81919504	+	Missense_Mutation	A	T	rs370718047	P2_T1	c.2075A>T	p.His692Leu	481	462	19	77	77	0	protein_coding	YES	MODERATE	SNV
ALOX12B	GRCh38	chr17	8077024	8077024	+	Missense_Mutation	A	T	novel	P2_T1	c.1241T>A	p.Leu414Gln	174	141	33	55	55	0	protein_coding	YES	MODERATE	SNV
KEAP1	GRCh38	chr19	10491658	10491658	+	Missense_Mutation	C	T	rs1379198956	P2_T1	c.1244G>A	p.Arg415His	205	201	4	81	81	0	protein_coding	YES	MODERATE	SNV
GNAS	GRCh38	chr20	58853458	58853458	+	Missense_Mutation	G	A	novel	P2_T1	c.193G>A	p.Gly65Ser	261	245	16	114	114	0	protein_coding	YES	MODERATE	SNV
RTEL1	GRCh38	chr20	63690199	63690199	+	Missense_Mutation	G	A	novel	P2_T1	c.2254G>A	p.Ala752Thr	122	118	4	45	45	0	protein_coding	YES	MODERATE	SNV
EP300	GRCh38	chr22	41127698	41127698	+	Missense_Mutation	A	T	novel	P2_T1	c.1118A>T	p.Lys373Met	277	221	56	36	36	0	protein_coding	YES	MODERATE	SNV
EP300	GRCh38	chr22	41170414	41170414	+	Missense_Mutation	C	G	novel	P2_T1	c.4295C>G	p.Thr1432Arg	274	227	47	40	40	0	protein_coding	YES	MODERATE	SNV
CSDE1	GRCh38	chr1	1.15E+08	1.15E+08	+	Missense_Mutation	G	T	novel	P20_T1	c.2378C>A	p.Ala793Asp	220	216	4	189	189	0	protein_coding	YES	MODERATE	SNV
NUF2	GRCh38	chr1	1.63E+08	1.63E+08	+	Missense_Mutation	A	T	novel	P20_T1	c.461A>T	p.Gln154Leu	145	108	37	160	160	0	protein_coding	YES	MODERATE	SNV
CDC73	GRCh38	chr1	1.93E+08	1.93E+08	+	Missense_Mutation	C	T	rs754454928	P20_T1	c.1321C>T	p.Arg441Cys	136	127	9	162	161	1	protein_coding	YES	MODERATE	SNV
PIK3C2B	GRCh38	chr1	2.04E+08	2.04E+08	+	Missense_Mutation	T	C	novel	P20_T1	c.2887A>G	p.Lys963Glu	210	206	4	108	108	0	protein_coding	YES	MODERATE	SNV
ZNF703	GRCh38	chr8	37697380	37697380	+	Missense_Mutation	G	T	novel	P20_T1	c.479G>T	p.Gly160Val	922	658	264	116	116	0	protein_coding	YES	MODERATE	SNV
FOXA1	GRCh38	chr14	37591607	37591607	+	Missense_Mutation	G	T		P20_T1	c.1177C>A	p.His393Asn	346	339	7	262	262	0	protein_coding	YES	MODERATE	SNV
IGF1R	GRCh38	chr15	98916831	98916831	+	Missense_Mutation	G	A	rs544049409	P20_T1	c.2156G>A	p.Arg719His	428	422	6	282	282	0	protein_coding	YES	MODERATE	SNV
TP53	GRCh38	chr17	7675071	7675071	+	Missense_Mutation	G	A	rs587782596	P20_T1	c.541C>T	p.Arg181Cys	81	41	40	124	124	0	protein_coding	YES	MODERATE	SNV
PIK3CD	GRCh38	chr1	9724013	9724013	+	Missense_Mutation	C	T	novel	P21_T1	c.2639C>T	p.Ala880Val	195	191	4	42	42	0	protein_coding	YES	MODERATE	SNV
EPHB1	GRCh38	chr3	1.35E+08	1.35E+08	+	Missense_Mutation	C	T	rs756791659	P21_T1	c.196C>T	p.Pro66Ser	683	676	7	135	135	0	protein_coding	YES	MODERATE	SNV
FGF12	GRCh38	chr3	1.92E+08	1.92E+08	+	Missense_Mutation	G	T	novel	P21_T1	c.252C>A	p.Phe84Leu	553	543	10	71	71	0	protein_coding	YES	MODERATE	SNV
KMT2D	GRCh38	chr12	49034814	49034814	+	Missense_Mutation	G	T	novel	P21_T1	c.10353C>A	p.Asn3451Lys	233	228	5	58	58	0	protein_coding	YES	MODERATE	SNV
MSI1	GRCh38	chr12	1.2E+08	1.2E+08	+	Missense_Mutation	G	A	rs778099314	P21_T1	c.833C>T	p.Ala278Val	197	193	4	36	36	0	protein_coding	YES	MODERATE	SNV
RB1	GRCh38	chr13	48459708	48459708	+	Missense_Mutation	C	T	rs137853294	P21_T1	c.1981C>T	p.Arg661Trp	339	331	8	115	115	0	protein_coding	YES	MODERATE	SNV
IRS2	GRCh38	chr13	1.1E+08	1.1E+08	+	Missense_Mutation	C	T	rs779681200	P21_T1	c.1661G>A	p.Arg554His	177	173	4	51	51	0	protein_coding	YES	MODERATE	SNV
TSC2	GRCh38	chr16	2048742	2048742	+	Missense_Mutation	G	A	novel	P21_T1	c.127G>A	p.Glu43Lys	198	137	61	45	45	0	protein_coding	YES	MODERATE	SNV
CTCF	GRCh38	chr16	67621572	67621572	+	Missense_Mutation	A	G	novel	P21_T1	c.1338A>G	p.Ile446Met	292	288	4	94	94	0	protein_coding	YES	MODERATE	SNV
ERBB2	GRCh38	chr17	39707056	39707056	+	Missense_Mutation	G	A	rs144019910	P21_T1	c.140G>A	p.Arg47His	172	168	4	39	39	0	protein_coding	YES	MODERATE	SNV
PPP2R1A	GRCh38	chr19	52211348	52211348	+	Missense_Mutation	C	T	rs755649324	P21_T1	c.359C>T	p.Ser120Leu	275	271	4	50	50	0	protein_coding	YES	MODERATE	SNV
LRP1B	GRCh38	chr2	1.4E+08	1.4E+08	+	Missense_Mutation	A	G	novel	P22_T1	c.13727T>C	p.Leu4576Ser	1251	735	516	492	492	0	protein_coding	YES	MODERATE	SNV
PHOX2B	GRCh38	chr4	41745994	41746011	+	In_Frame_Del	GCCGCCGCCGCTGCCGCG	-	rs771383153	P22_T1	c.741_758del	p.Ala255_Ala260del	118	114	4	42	42	0	protein_coding	YES	MODERATE	deletion
FANCC	GRCh38	chr9	95101832	95101832	+	Missense_Mutation	T	A	novel	P22_T1	c.1552A>T	p.Ile518Leu	177	56	121	185	185	0	protein_coding	YES	MODERATE	SNV
TCEA3	GRCh38	chr1	23397837	23397837	+	Missense_Mutation	G	A	rs370705356	P23_T1	c.562C>T	p.Arg188Trp	295	287	6	97	96	1	protein_coding	YES	MODERATE	SNV
F13B	GRCh38	chr1	1.97E+08	1.97E+08	+	Missense_Mutation	C	T	rs756567129	P23_T1	c.878G>A	p.Arg293His	143	134	6	152	152	0	protein_coding	YES	MODERATE	SNV
USH2A	GRCh38	chr1	2.16E+08	2.16E+08	+	Missense_Mutation	C	T	rs145383772	P23_T1	c.2792G>A	p.Cys931Tyr	206	198	8	177	172	0	protein_coding	YES	MODERATE	SNV
OBSL1	GRCh38	chr2	2.2E+08	2.2E+08	+	Missense_Mutation	G	A		P23_T1	c.3524C>T	p.Ala1175Val	149	142	5	43	42	0	protein_coding	YES	MODERATE	SNV
CSRNP1	GRCh38	chr3	39144199	39144199	+	Missense_Mutation	G	A	rs1411814018	P23_T1	c.718C>T	p.His240Tyr	143	135	6	63	62	0	protein_coding	YES	MODERATE	SNV
CACNA2D2	GRCh38	chr3	50379578	50379578	+	Missense_Mutation	C	T	novel	P23_T1	c.1006G>A	p.Ala336Thr	73	25	48	40	39	0	protein_coding	YES	MODERATE	SNV
NISCH	GRCh38	chr3	52489643	52489643	+	Missense_Mutation	G	A	rs746799481	P23_T1	c.3421G>A	p.Ala1141Thr	111	105	6	35	35	0	protein_coding	YES	MODERATE	SNV
PBRM1	GRCh38	chr3	52563417	52563417	+	Nonsense_Mutation	C	A	novel	P23_T1	c.3952G>T	p.Glu1318Ter	44	8	36	67	67	0	protein_coding	YES	HIGH	SNV
CPA3	GRCh38	chr3	1.49E+08	1.49E+08	+	Missense_Mutation	C	T	rs1479828535	P23_T1	c.616C>T	p.Leu206Phe	92	85	6	80	79	0	protein_coding	YES	MODERATE	SNV
PIGG	GRCh38	chr4	521817	521817	+	Missense_Mutation	C	T	rs755547556	P23_T1	c.1490C>T	p.Ser497Leu	183	173	8	72	72	0	protein_coding	YES	MODERATE	SNV
FGFR3	GRCh38	chr4	1803055	1803055	+	Missense_Mutation	C	T	novel	P23_T1	c.1072C>T	p.Pro358Ser	100	93	6	26	26	0	protein_coding	YES	MODERATE	SNV
FBXL7	GRCh38	chr5	15936626	15936626	+	Missense_Mutation	C	G		P23_T1	c.916C>G	p.Arg306Gly	189	120	67	93	93	0	protein_coding	YES	MODERATE	SNV
ANKHD1-EIF4EBP3	GRCh38	chr5	1.41E+08	1.41E+08	+	Missense_Mutation	C	T	rs1244304804	P23_T1	c.6820C>T	p.Pro2274Ser	243	235	8	216	215	0	protein_coding	YES	MODERATE	SNV
SYNPO	GRCh38	chr5	1.51E+08	1.51E+08	+	Missense_Mutation	G	A	novel	P23_T1	c.2201G>A	p.Arg734Gln	265	255	9	49	47	0	protein_coding	YES	MODERATE	SNV
FOXQ1	GRCh38	chr6	1313066	1313066	+	Missense_Mutation	C	T	rs373880105	P23_T1	c.362C>T	p.Pro121Leu	319	308	10	73	73	0	protein_coding	YES	MODERATE	SNV
STAG3	GRCh38	chr7	1E+08	1E+08	+	Missense_Mutation	G	A	novel	P23_T1	c.2293G>A	p.Ala765Thr	116	82	32	62	62	0	protein_coding	YES	MODERATE	SNV
STAG3	GRCh38	chr7	1E+08	1E+08	+	Missense_Mutation	C	A	novel	P23_T1	c.2294C>A	p.Ala765Asp	116	82	32	62	61	0	protein_coding	YES	MODERATE	SNV
GIMAP1	GRCh38	chr7	1.51E+08	1.51E+08	+	Missense_Mutation	G	A	rs752300708	P23_T1	c.898G>A	p.Val300Ile	184	177	6	69	68	0	protein_coding	YES	MODERATE	SNV
KIAA2026	GRCh38	chr9	5969091	5969091	+	Nonsense_Mutation	C	T	novel	P23_T1	c.1140G>A	p.Trp380Ter	100	94	6	104	104	0	protein_coding	YES	HIGH	SNV
UNC13B	GRCh38	chr9	35390677	35390677	+	Nonsense_Mutation	G	A	novel	P23_T1	c.3024G>A	p.Trp1008Ter	123	116	6	65	65	0	protein_coding	YES	HIGH	SNV
ANO9	GRCh38	chr11	431701	431701	+	Missense_Mutation	C	T	novel	P23_T1	c.532G>A	p.Glu178Lys	117	110	6	30	30	0	protein_coding	YES	MODERATE	SNV
DEAF1	GRCh38	chr11	688364	688364	+	Missense_Mutation	C	T	rs141368610	P23_T1	c.484G>A	p.Gly162Arg	155	147	6	59	59	0	protein_coding	YES	MODERATE	SNV
ABTB2	GRCh38	chr11	34152482	34152482	+	Missense_Mutation	G	A	rs746167793	P23_T1	c.2983C>T	p.Arg995Cys	176	170	6	81	81	0	protein_coding	YES	MODERATE	SNV
AMBRA1	GRCh38	chr11	46397571	46397571	+	Missense_Mutation	G	A	rs1158584653	P23_T1	c.3596C>T	p.Ser1199Phe	205	198	6	85	82	0	protein_coding	YES	MODERATE	SNV
FNBP4	GRCh38	chr11	47753026	47753026	+	Missense_Mutation	G	A	novel	P23_T1	c.527C>T	p.Pro176Leu	101	66	35	57	55	0	protein_coding	YES	MODERATE	SNV
TNKS1BP1	GRCh38	chr11	57313653	57313653	+	Missense_Mutation	G	T	novel	P23_T1	c.1035C>A	p.Asp345Glu	208	146	58	62	62	0	protein_coding	YES	MODERATE	SNV
ADAMTS7	GRCh38	chr15	78765692	78765692	+	Missense_Mutation	G	T	rs768525846	P23_T1	c.4219C>A	p.Pro1407Thr	194	115	78	64	63	0	protein_coding	YES	MODERATE	SNV
WFIKKN1	GRCh38	chr16	631319	631319	+	Missense_Mutation	G	T	novel	P23_T1	c.66G>T	p.Leu22Phe	207	104	101	62	61	0	protein_coding	YES	MODERATE	SNV
SYT17	GRCh38	chr16	19183932	19183932	+	Missense_Mutation	G	A	rs144009523	P23_T1	c.736G>A	p.Gly246Arg	499	485	10	96	93	0	protein_coding	YES	MODERATE	SNV
TP53	GRCh38	chr17	7674216	7674216	+	Missense_Mutation	C	A	rs28934571	P23_T1	c.747G>T	p.Arg249Ser	60	19	41	35	35	0	protein_coding	YES	MODERATE	SNV
FAM174C	GRCh38	chr19	1275763	1275763	+	Missense_Mutation	C	T	novel	P23_T1	c.214C>T	p.Arg72Cys	193	186	6	63	62	0	protein_coding	YES	MODERATE	SNV
EFNA2	GRCh38	chr19	1298560	1298560	+	Missense_Mutation	C	T	novel	P23_T1	c.464C>T	p.Pro155Leu	101	95	6	31	31	0	protein_coding	YES	MODERATE	SNV
NDUFS7	GRCh38	chr19	1390997	1390997	+	Missense_Mutation	G	C	rs766542750	P23_T1	c.355G>C	p.Val119Leu	164	149	13	56	56	0	protein_coding	YES	MODERATE	SNV
THOP1	GRCh38	chr19	2807735	2807735	+	Missense_Mutation	G	A	rs747637020	P23_T1	c.1180G>A	p.Val394Met	114	108	5	46	45	0	protein_coding	YES	MODERATE	SNV
ZNRF4	GRCh38	chr19	5456287	5456287	+	Missense_Mutation	G	A	rs201883665	P23_T1	c.796G>A	p.Val266Ile	142	136	6	55	55	0	protein_coding	YES	MODERATE	SNV
ZNRF4	GRCh38	chr19	5456621	5456621	+	Missense_Mutation	C	T	rs1244900773	P23_T1	c.1130C>T	p.Pro377Leu	102	95	5	39	38	0	protein_coding	YES	MODERATE	SNV
LONP1	GRCh38	chr19	5696142	5696142	+	Missense_Mutation	G	A	rs371606894	P23_T1	c.1925C>T	p.Thr642Met	149	110	38	41	41	0	protein_coding	YES	MODERATE	SNV
LONP1	GRCh38	chr19	5696143	5696143	+	Missense_Mutation	T	G		P23_T1	c.1924A>C	p.Thr642Pro	150	111	38	42	42	0	protein_coding	YES	MODERATE	SNV
LONP1	GRCh38	chr19	5719775	5719775	+	Missense_Mutation	C	G	novel	P23_T1	c.358G>C	p.Val120Leu	177	170	6	67	67	0	protein_coding	YES	MODERATE	SNV
ALKBH7	GRCh38	chr19	6374821	6374821	+	Missense_Mutation	C	T	novel	P23_T1	c.514C>T	p.Arg172Cys	76	70	6	58	57	0	protein_coding	YES	MODERATE	SNV
LSR	GRCh38	chr19	35250587	35250587	+	Missense_Mutation	G	A	rs375353677	P23_T1	c.526G>A	p.Val176Met	248	237	8	53	51	0	protein_coding	YES	MODERATE	SNV
AXL	GRCh38	chr19	41239221	41239221	+	Missense_Mutation	T	C	novel	P23_T1	c.1192T>C	p.Ser398Pro	222	216	5	77	77	0	protein_coding	YES	MODERATE	SNV
FIZ1	GRCh38	chr19	55597762	55597762	+	Missense_Mutation	C	T	rs1260234363	P23_T1	c.104G>A	p.Arg35His	335	325	8	99	95	0	protein_coding	YES	MODERATE	SNV
QSOX1	GRCh38	chr1	1.8E+08	1.8E+08	+	Missense_Mutation	G	A	rs375407780	P24_T1	c.289G>A	p.Ala97Thr	184	152	30	72	70	2	protein_coding	YES	MODERATE	SNV
ARV1	GRCh38	chr1	2.31E+08	2.31E+08	+	Missense_Mutation	A	G	novel	P24_T1	c.163A>G	p.Ile55Val	399	369	30	104	103	0	protein_coding	YES	MODERATE	SNV

Table S2 (*continued*)

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Table S2 (*continued*)

Hugo_ Symbol	NCBI_Build	Chromosome	Start_Position	End_Position	Strand	Variant_Classification	Reference_Allele	Tumor_Seq_Allele2	dbSNP_RS	Tumor_Sample_ Barcode	HGVSc	HGVSp	t_depth	t_ref_count	t_alt_count	n_depth	n_ref_count	n_alt_count	BIOTYPE	CANONICAL	IMPACT	VARIANT_ CLASS
DNAH5	GRCh38	chr5	13883053	13883053	+	Missense_Mutation	T	C	rs748538358	P24_T1	c.3025A>G	p.Ile1009Val	404	326	76	163	163	0	protein_coding	YES	MODERATE	SNV
TMEM151B	GRCh38	chr6	44270781	44270783	+	In_Frame_Del	CGG	-	rs1307963698	P24_T1	c.54_56del	p.Gly21del	145	42	8	42	20	0	protein_coding	YES	MODERATE	deletion
ELAVL2	GRCh38	chr9	23762054	23762054	+	Missense_Mutation	T	C	novel	P24_T1	c.268A>G	p.Ser90Gly	277	265	12	152	152	0	protein_coding	YES	MODERATE	SNV
TUSC1	GRCh38	chr9	25677852	25677852	+	Missense_Mutation	A	T	novel	P24_T1	c.470T>A	p.Leu157Gln	248	241	6	93	93	0	protein_coding	YES	MODERATE	SNV
UNC13B	GRCh38	chr9	35390712	35390712	+	Missense_Mutation	A	G	novel	P24_T1	c.3059A>G	p.Glu1020Gly	144	137	5	57	57	0	protein_coding	YES	MODERATE	SNV
VPS13A	GRCh38	chr9	77353484	77353484	+	Missense_Mutation	A	G	rs751982239	P24_T1	c.7495A>G	p.Ile2499Val	221	205	5	99	99	0	protein_coding	YES	MODERATE	SNV
FKBP15	GRCh38	chr9	1.13E+08	1.13E+08	+	Missense_Mutation	G	T	novel	P24_T1	c.2855C>A	p.Pro952Gln	280	274	6	128	127	1	protein_coding	YES	MODERATE	SNV
VPS51	GRCh38	chr11	65108514	65108514	+	Missense_Mutation	A	G	rs1174287312	P24_T1	c.1043A>G	p.Tyr348Cys	323	276	44	100	99	0	protein_coding	YES	MODERATE	SNV
ATP2A2	GRCh38	chr12	1.1E+08	1.1E+08	+	Missense_Mutation	G	A	rs761676527	P24_T1	c.1841G>A	p.Arg614Gln	395	388	6	141	141	0	protein_coding	YES	MODERATE	SNV
ZC3H13	GRCh38	chr13	45969418	45969418	+	Missense_Mutation	C	A	novel	P24_T1	c.3126G>T	p.Leu1042Phe	309	260	49	114	114	0	protein_coding	YES	MODERATE	SNV
METRN	GRCh38	chr16	715660	715660	+	Missense_Mutation	C	A	rs1304352379	P24_T1	c.181C>A	p.Pro61Thr	165	159	6	30	30	0	protein_coding	YES	MODERATE	SNV
TP53	GRCh38	chr17	7674218	7674218	+	Missense_Mutation	T	C	rs587782082	P24_T1	c.745A>G	p.Arg249Gly	114	80	33	51	51	0	protein_coding	YES	MODERATE	SNV
SHC2	GRCh38	chr19	460588	460588	+	Missense_Mutation	G	T	rs1253640609	P24_T1	c.409C>A	p.His137Asn	178	60	117	29	26	3	protein_coding	YES	MODERATE	SNV
HCN2	GRCh38	chr19	615947	615949	+	In_Frame_Del	CCG	-	rs527536363	P24_T1	c.2162_2164del	p.Pro721del	199	53	9	43	18	0	protein_coding	YES	MODERATE	deletion
RANBP3	GRCh38	chr19	5941696	5941696	+	Missense_Mutation	C	G	novel	P24_T1	c.331G>C	p.Glu111Gln	139	131	8	48	48	0	protein_coding	YES	MODERATE	SNV
ZNF225	GRCh38	chr19	44131381	44131381	+	Missense_Mutation	G	C	novel	P24_T1	c.767G>C	p.Gly256Ala	315	263	52	147	147	0	protein_coding	YES	MODERATE	SNV
KLK6	GRCh38	chr19	50963421	50963421	+	Missense_Mutation	A	G	novel	P24_T1	c.326T>C	p.Leu109Pro	196	176	19	101	101	0	protein_coding	YES	MODERATE	SNV
CHGB	GRCh38	chr20	5923424	5923424	+	Missense_Mutation	G	T		P24_T1	c.1280G>T	p.Arg427Leu	265	232	33	81	81	0	protein_coding	YES	MODERATE	SNV
SEC14L2	GRCh38	chr22	30415801	30415801	+	Missense_Mutation	A	G	novel	P24_T1	c.707A>G	p.Gln236Arg	139	108	31	67	67	0	protein_coding	YES	MODERATE	SNV
TERT	GRCh38	chr5	1294866	1294866	+	Missense_Mutation	C	T	novel	P25_T1	c.124G>A	p.Gly42Arg	297	242	55	41	41	0	protein_coding	YES	MODERATE	SNV
CPLANE1	GRCh38	chr5	37224604	37224604	+	Missense_Mutation	A	G	rs886060581	P25_T1	c.2428T>C	p.Cys810Arg	252	208	42	57	57	0	protein_coding	YES	MODERATE	SNV
ZNF853	GRCh38	chr7	6621815	6621815	+	Missense_Mutation	A	T	novel	P25_T1	c.824A>T	p.Gln275Leu	486	316	166	64	64	0	protein_coding	YES	MODERATE	SNV
PIGO	GRCh38	chr9	35094317	35094317	+	Missense_Mutation	A	G	novel	P25_T1	c.554T>C	p.Leu185Pro	340	334	6	26	26	0	protein_coding	YES	MODERATE	SNV
NUP98	GRCh38	chr11	3744548	3744548	+	Missense_Mutation	T	A	novel	P25_T1	c.1369A>T	p.Thr457Ser	298	254	43	41	41	0	protein_coding	YES	MODERATE	SNV
TP53	GRCh38	chr17	7674254	7674254	+	Missense_Mutation	T	C	rs730882004	P25_T1	c.709A>G	p.Met237Val	80	30	50	29	29	0	protein_coding	YES	MODERATE	SNV
LONP1	GRCh38	chr19	5693299	5693299	+	Missense_Mutation	G	A	rs562878082	P25_T1	c.2702C>T	p.Ala901Val	182	133	49	37	37	0	protein_coding	YES	MODERATE	SNV
SLC45A2	GRCh38	chr5	33963895	33963895	+	Missense_Mutation	C	A	novel	P26_T1	c.684G>T	p.Leu228Phe	327	317	10	105	105	0	protein_coding	YES	MODERATE	SNV
MPDZ	GRCh38	chr9	13188812	13188812	+	Missense_Mutation	A	C	novel	P26_T1	c.2336T>G	p.Val779Gly	260	246	12	108	106	0	protein_coding	YES	MODERATE	SNV
PHKG2	GRCh38	chr16	30753263	30753263	+	Missense_Mutation	A	C	novel	P26_T1	c.358A>C	p.Thr120Pro	133	119	12	55	54	1	protein_coding	YES	MODERATE	SNV
ZBTB32	GRCh38	chr19	35716001	35716001	+	Missense_Mutation	C	A		P26_T1	c.1018C>A	p.His340Asn	207	202	5	77	77	0	protein_coding	YES	MODERATE	SNV
ZNF595	GRCh38	chr4	87282	87282	+	Missense_Mutation	C	A		P27_T1	c.1778C>A	p.Thr593Lys	64	59	5	88	88	0	protein_coding	YES	MODERATE	SNV
SRF	GRCh38	chr6	43171747	43171749	+	In_Frame_Del	GGC	-	rs774568148	P27_T1	c.102_104del	p.Gly35del	71	21	7	65	41	0	protein_coding	YES	MODERATE	deletion
ERMP1	GRCh38	chr9	5825128	5825128	+	Missense_Mutation	T	C	rs144810528	P27_T1	c.732A>G	p.Ile244Met	52	9	42	43	43	0	protein_coding	YES	MODERATE	SNV
ODF3	GRCh38	chr11	197363	197363	+	Missense_Mutation	T	A	novel	P27_T1	c.59T>A	p.Met20Lys	29	11	18	25	25	0	protein_coding	YES	MODERATE	SNV
TAT	GRCh38	chr16	71570779	71570779	+	Missense_Mutation	G	T	novel	P27_T1	c.812C>A	p.Pro271His	112	12	99	92	92	0	protein_coding	YES	MODERATE	SNV
CD300LB	GRCh38	chr17	74525762	74525762	+	Missense_Mutation	A	T	novel	P27_T1	c.356T>A	p.Val119Glu	92	87	5	36	36	0	protein_coding	YES	MODERATE	SNV
LAMA1	GRCh38	chr18	7050914	7050914	+	Missense_Mutation	A	T	novel	P27_T1	c.368T>A	p.Ile123Asn	81	51	30	86	86	0	protein_coding	YES	MODERATE	SNV
PPP4R1	GRCh38	chr18	9570603	9570603	+	Missense_Mutation	C	G	novel	P27_T1	c.1127G>C	p.Ser376Thr	131	61	70	90	90	0	protein_coding	YES	MODERATE	SNV
ZNF519	GRCh38	chr18	14104958	14104958	+	Missense_Mutation	G	C	novel	P27_T1	c.1582C>G	p.Arg528Gly	133	127	6	83	82	0	protein_coding	YES	MODERATE	SNV
SHC2	GRCh38	chr19	425168	425168	+	Missense_Mutation	A	T	rs754244054	P27_T1	c.1238T>A	p.Leu413Gln	33	11	22	32	32	0	protein_coding	YES	MODERATE	SNV
ARID3A	GRCh38	chr19	971934	971936	+	In_Frame_Del	GGC	-	rs753131507	P27_T1	c.1666_1668del	p.Gly556del	125	42	6	64	52	0	protein_coding	YES	MODERATE	deletion
CDH4	GRCh38	chr20	61873886	61873886	+	Missense_Mutation	G	T	novel	P27_T1	c.1036G>T	p.Gly346Cys	68	63	5	36	36	0	protein_coding	YES	MODERATE	SNV
ZNF595	GRCh38	chr4	86247	86247	+	Missense_Mutation	A	T		P28_T1	c.743A>T	p.Lys248Ile	431	415	6	91	91	0	protein_coding	YES	MODERATE	SNV
ZNF736	GRCh38	chr7	64348625	64348625	+	Missense_Mutation	C	G		P28_T1	c.762C>G	p.Asp254Glu	119	112	6	49	49	0	protein_coding	YES	MODERATE	SNV
ZNF736	GRCh38	chr7	64348627	64348627	+	Missense_Mutation	G	A		P28_T1	c.764G>A	p.Arg255Lys	115	108	6	49	49	0	protein_coding	YES	MODERATE	SNV
ZBTB5	GRCh38	chr9	37442008	37442008	+	Missense_Mutation	G	A	rs747980674	P28_T1	c.544C>T	p.Arg182Cys	563	415	147	24	24	0	protein_coding	YES	MODERATE	SNV
ABCA7	GRCh38	chr19	1054636	1054636	+	Missense_Mutation	C	A	novel	P28_T1	c.3793C>A	p.His1265Asn	811	446	364	33	33	0	protein_coding	YES	MODERATE	SNV
TPR	GRCh38	chr1	1.86E+08	1.86E+08	+	Missense_Mutation	G	T	novel	P29_T1	c.4445C>A	p.Thr1482Lys	345	337	5	29	29	0	protein_coding	YES	MODERATE	SNV
SPEF2	GRCh38	chr5	35704586	35704586	+	Missense_Mutation	G	T	novel	P29_T1	c.2431G>T	p.Asp811Tyr	192	177	15	21	21	0	protein_coding	YES	MODERATE	SNV
SPEN	GRCh38	chr1	15928906	15928906	+	Missense_Mutation	A	G	novel	P3_T1	c.2666A>G	p.Lys889Arg	470	453	17	154	154	0	protein_coding	YES	MODERATE	SNV
JAK1	GRCh38	chr1	64844820	64844820	+	Missense_Mutation	T	A		P3_T1	c.2185A>T	p.Ser729Cys	922	654	268	136	136	0	protein_coding	YES	MODERATE	SNV
ELF3	GRCh38	chr1	2.02E+08	2.02E+08	+	Missense_Mutation	G	A		P3_T1	c.1093G>A	p.Glu365Lys	1566	1539	27	118	118	0	protein_coding	YES	MODERATE	SNV
REL	GRCh38	chr2	60922488	60922494	+	Frame_Shift_Del	AATGAGC	-	novel	P3_T1	c.1816_1822del	p.Glu606Ter	231	190	41	122	122	0	protein_coding	YES	HIGH	deletion
CTNNB1	GRCh38	chr3	41233420	41233420	+	Missense_Mutation	T	G		P3_T1	c.1161T>G	p.Asn387Lys	329	260	69	153	152	1	protein_coding	YES	MODERATE	SNV
MST1R	GRCh38	chr3	49896889	49896889	+	Missense_Mutation	C	A	novel	P3_T1	c.2185G>T	p.Val729Phe	532	399	133	38	38	0	protein_coding	YES	MODERATE	SNV
PPP4R2	GRCh38	chr3	73065466	73065466	+	Missense_Mutation	T	C	rs1215780330	P3_T1	c.998T>C	p.Leu333Ser	136	131	5	164	164	0	protein_coding	YES	MODERATE	SNV
FBXW7	GRCh38	chr4	1.52E+08	1.52E+08	+	Missense_Mutation	T	C	rs1462861861	P3_T1	c.1625A>G	p.Asn542Ser	56	42	14	180	180	0	protein_coding	YES	MODERATE	SNV
ROS1	GRCh38	chr6	1.17E+08	1.17E+08	+	Missense_Mutation	T	C	novel	P3_T1	c.1282A>G	p.Arg428Gly	305	222	83	115	115	0	protein_coding	YES	MODERATE	SNV
RAD21	GRCh38	chr8	1.17E+08	1.17E+08	+	Missense_Mutation	T	A		P3_T1	c.322A>T	p.Ile108Phe	87	55	32	151	151	0	protein_coding	YES	MODERATE	SNV
PAX5	GRCh38	chr9	36966634	36966634	+	Missense_Mutation	T	A	novel	P3_T1	c.695A>T	p.Gln232Leu	511	360	151	46	46	0	protein_coding	YES	MODERATE	SNV
GNAQ	GRCh38	chr9	77922179	77922179	+	Nonsense_Mutation	G	T	rs200106152	P3_T1	c.303C>A	p.Tyr101Ter	63	55	8	51	51	0	protein_coding	YES	HIGH	SNV
GNAQ	GRCh38	chr9	77922196	77922196	+	Missense_Mutation	T	A	rs753716491	P3_T1	c.286A>T	p.Thr96Ser	73	64	9	58	58	0	protein_coding	YES	MODERATE	SNV
TCF7L2	GRCh38	chr10	1.13E+08	1.13E+08	+	Frame_Shift_Ins	-	C	novel	P3_T1	c.93dup	p.Ser32LeufsTer12	530	358	172	80	80	0	protein_coding	YES	HIGH	insertion
SRSF2	GRCh38	chr17	76736996	76737001	+	In_Frame_Del	GCGGGA	-	novel	P3_T1	c.160_165del	p.Ser54_Arg55del	523	376	147	37	37	0	protein_coding	YES	MODERATE	deletion
SMARCA4	GRCh38	chr19	10994858	10994858	+	Nonsense_Mutation	A	T	novel	P3_T1	c.1450A>T	p.Lys484Ter	697	519	178	67	67	0	protein_coding	YES	HIGH	SNV
KMT2B	GRCh38	chr19	35725332	35725332	+	Missense_Mutation	A	T	novel	P3_T1	c.3641A>T	p.Glu1214Val	889	639	250	47	47	0	protein_coding	YES	MODERATE	SNV
BCORL1	GRCh38	chrX	1.3E+08	1.3E+08	+	Missense_Mutation	A	G	novel	P3_T1	c.2284A>G	p.Thr762Ala	548	527	21	42	42	0	protein_coding	YES	MODERATE	SNV
URB2	GRCh38	chr1	2.3E+08	2.3E+08	+	Missense_Mutation	A	T	novel	P30_T1	c.1022A>T	p.Gln341Leu	324	315	8	47	47	0	protein_coding	YES	MODERATE	SNV
URB2	GRCh38	chr1	2.3E+08	2.3E+08	+	Missense_Mutation	G	T	novel	P30_T1	c.1023G>T	p.Gln341His	326	317	8	47	47	0	protein_coding	YES	MODERATE	SNV
VGLL4	GRCh38	chr3	11643480	11643480	+	Nonsense_Mutation	G	T	novel	P30_T1	c.39C>A	p.Tyr13Ter	238	115	122	33	33	0	protein_coding	YES	HIGH	SNV
QTRT2	GRCh38	chr3	1.14E+08	1.14E+08	+	Missense_Mutation	A	T	novel	P30_T1	c.434A>T	p.Gln145Leu	35	23	12	29	29	0	protein_coding	YES	MODERATE	SNV
PTGER4	GRCh38	chr5	40681187	40681187	+	Missense_Mutation	A	C	novel	P30_T1	c.194A>C	p.Asp65Ala	606	414	191	45	45	0	protein_coding	YES	MODERATE	SNV
CSF1R	GRCh38	chr5	1.5E+08	1.5E+08	+	Nonsense_Mutation	A	T	novel	P30_T1	c.614T>A	p.Leu205Ter	275	196	76	36	36	0	protein_coding	YES	HIGH	SNV
FAM71B	GRCh38	chr5	1.57E+08	1.57E+08	+	Missense_Mutation	C	T	rs764229512	P30_T1	c.1444G>A	p.Glu482Lys	291	279	10	39	39	0	protein_coding	YES	MODERATE	SNV
NPIPB11	GRCh38	chr16	29394063	29394063	+	Missense_Mutation	A	G	novel	P30_T1	c.134T>C	p.Leu45Pro	123	74	42	72	69	0	protein_coding	YES	MODERATE	SNV
NPIPB11	GRCh38	chr16	29394068	29394068	+	Frame_Shift_Del	A	-	novel	P30_T1	c.129del	p.Asn43LysfsTer37	123	61	39	71	68	0	protein_coding	YES	HIGH	deletion
MYH13	GRCh38	chr17	10354763	10354763	+	Missense_Mutation	T	G	novel	P30_T1	c.922A>C	p.Asn308His	29	22	7	27	27	0	protein_coding	YES	MODERATE	SNV
ZNF627	GRCh38	chr19	11617150	11617150	+	Missense_Mutation	G	C	rs765996892	P30_T1	c.647G>C	p.Ser216Thr	87	79	5	35	34	0	protein_coding	YES	MODERATE	SNV
ZNF763	GRCh38	chr19	11978828	11978828	+	Missense_Mutation	C	T	novel	P30_T1	c.913C>T	p.His305Tyr	67	52	12	30	29	0	protein_coding	YES	MODERATE	SNV
ZNF616	GRCh38	chr19	52115592	52115592	+	Missense_Mutation	T	A	rs201736146	P30_T1	c.1572A>T	p.Lys524Asn	242	231	10	78	78	0	protein_coding	YES	MODERATE	SNV
KCNA2	GRCh38	chr1	1.11E+08	1.11E+08	+	Missense_Mutation	T	C	rs768627161	P31_T1	c.1235A>G	p.Asn412Ser	156	88	68	77	77	0	protein_coding	YES	MODERATE	SNV
WDFY1	GRCh38	chr2	2.24E+08	2.24E+08	+	Missense_Mutation	C	A	rs766142606	P31_T1	c.202G>T	p.Ala68Ser	196	175	19	71	71	0	protein_coding	YES	MODERATE	SNV
ICE1	GRCh38	chr5	5464393	5464393	+	Missense_Mutation	G	T	novel	P31_T1	c.5059G>T	p.Asp1687Tyr	320	216	104	149	148	1	protein_coding	YES	MODERATE	SNV
DROSHA	GRCh38	chr5	31515127	31515127	+	Missense_Mutation	T	A	rs1212923687	P31_T1	c.1151A>T	p.Tyr384Phe	424	309	115	122	122	0	protein_coding	YES	MODERATE	SNV
CPLANE1	GRCh38	chr5	37205428	37205428	+	Missense_Mutation	G	T	novel	P31_T1	c.3176C>A	p.Pro1059Gln	245	237	6	79	79	0	protein_coding	YES	MODERATE	SNV
HCN1	GRCh38	chr5	45262132	45262132	+	Missense_Mutation	G	A	rs371602396	P31_T1	c.2462C>T	p.Ala821Val	236	197	39	123	121	1	protein_coding	YES	MODERATE	SNV
HDGFL1	GRCh38	chr6	22569792	22569792	+	Missense_Mutation	C	T		P31_T1	c.217C>T	p.Arg73Cys	201	124	76	104	104	0	protein_coding	YES	MODERATE	SNV
ADGRF2	GRCh38	chr6	47682538	47682538	+	Missense_Mutation	G	A	novel	P31_T1	c.1979G>A	p.Gly660Glu	227	214	13	99	99	0	protein_coding	YES	MODERATE	SNV
KIAA2026	GRCh38	chr9	5922168	5922169	+	Frame_Shift_Del	AT	-	novel	P31_T1	c.3827_3828del	p.Asp1276ValfsTer7	273	121	73	132	114	0	protein_coding	YES	HIGH	deletion
PTPRD	GRCh38	chr9	8518377	8518377	+	Missense_Mutation	G	T	novel	P31_T1	c.1014C>A	p.Ser338Arg	308	301	7	115	115	0	protein_coding	YES	MODERATE	SNV
TYRP1	GRCh38	chr9	12694354	12694354	+	Missense_Mutation	G	T	novel	P31_T1	c.358G>T	p.Ala120Ser	301	185	114	140	140	0	protein_coding	YES	MODERATE	SNV
ADAMTSL1	GRCh38	chr9	18777452	18777452	+	Missense_Mutation	C	A	rs1229156524	P31_T1	c.3223C>A	p.Gln1075Lys	211	205	6	134	134	0	protein_coding	YES	MODERATE	SNV
ADAMTSL1	GRCh38	chr9	18777713	18777713	+	Missense_Mutation	C	A	rs761201169	P31_T1	c.3484C>A	p.Arg1162Ser	275	270	5	145	144	0	protein_coding	YES	MODERATE	SNV
FAM205A	GRCh38	chr9	34725631	34725631	+	Missense_Mutation	A	T	novel	P31_T1	c.1609T>A	p.Trp537Arg	62	43	19	47	47	0	protein_coding	YES	MODERATE	SNV
ALDH1B1	GRCh38	chr9	38396482	38396482	+	Missense_Mutation	C	A	novel	P31_T1	c.734C>A	p.Ala245Glu	154	148	5	112	112	0	protein_coding	YES	MODERATE	SNV
SEC61B	GRCh38	chr9	99227934	99227934	+	Missense_Mutation	G	A	rs759102342	P31_T1	c.137G>A	p.Arg46His	197	191	6	73	73	0	protein_coding	YES	MODERATE	SNV
MFAP1	GRCh38	chr15	43814950	43814950	+	Missense_Mutation	C	T	novel	P31_T1	c.424G>A	p.Asp142Asn	236	170	66	94	94	0	protein_coding	YES	MODERATE	SNV
SLC9A5	GRCh38	chr16	67270819	67270819	+	Missense_Mutation	G	T	rs1449978937	P31_T1	c.2300G>T	p.Gly767Val	116	72	44	82	82	0	protein_coding	YES	MODERATE	SNV
MYH13	GRCh38	chr17	10364435	10364435	+	Missense_Mutation	G	T		P31_T1	c.96C>A	p.Phe32Leu	164	159	5	125	124	0	protein_coding	YES	MODERATE	SNV
APCDD1	GRCh38	chr18	10471976	10471976	+	Missense_Mutation	T	A	novel	P31_T1	c.689T>A	p.Leu230His	158	94	64	107	105	0	protein_coding	YES	MODERATE	SNV
ANKRD30B	GRCh38	chr18	14852323	14852323	+	Missense_Mutation	A	T	novel	P31_T1	c.4022A>T	p.Gln1341Leu	212	149	62	87	85	0	protein_coding	YES	MODERATE	SNV
ATP8B3	GRCh38	chr19	1810658	1810658	+	Nonsense_Mutation	G	A	rs1206695206	P31_T1	c.274C>T	p.Gln92Ter	57	39	18	39	39	0	protein_coding	YES	HIGH	SNV
MUC16	GRCh38	chr19	8974010	8974010	+	Missense_Mutation	A	T	novel	P31_T1	c.7129T>A	p.Ser2377Thr	76	38	38	44	44	0	protein_coding	YES	MODERATE	SNV
CKM	GRCh38	chr19	45317922	45317922	+	Missense_Mutation	A	G	novel	P31_T1	c.251T>C	p.Val84Ala	56	42	13	48	46	0	protein_coding	YES	MODERATE	SNV
KLK4	GRCh38	chr19	50909406	50909406	+	Missense_Mutation	C	A	novel	P31_T1	c.70G>T	p.Val24Phe	96	58	38	69	69	0	protein_coding	YES	MODERATE	SNV
CHKB	GRCh38	chr22	50581537	50581537	+	Missense_Mutation	G	T		P31_T1	c.464C>A	p.Thr155Asn	99	64	35	42	42	0	protein_coding	YES	MODERATE	SNV
RBBP7	GRCh38	chrX	16858701	16858701	+	Missense_Mutation	G	T	novel	P31_T1	c.588C>A	p.Asp196Glu	159	153	6	34	34	0	protein_coding	YES	MODERATE	SNV
VPS13D	GRCh38	chr1	12318228	12318228	+	Missense_Mutation	C	A	novel	P32_T1	c.7305C>A	p.Ser2435Arg	392	385	7	75	75	0	protein_coding	YES	MODERATE	SNV
CYP4B1	GRCh38	chr1	46812604	46812604	+	Missense_Mutation	A	G	novel	P32_T1	c.476A>G	p.Glu159Gly	116	85	31	36	36	0	protein_coding	YES	MODERATE	SNV
PRG4	GRCh38	chr1	1.86E+08	1.86E+08	+	Missense_Mutation	C	A	novel	P32_T1	c.2963C>A	p.Thr988Lys	307	298	7	160	158	0	protein_coding	YES	MODERATE	SNV
KCNT2	GRCh38	chr1	1.96E+08	1.96E+08	+	Missense_Mutation	C	T	rs1261492654	P32_T1	c.1444G>A	p.Gly482Ser	257	251	6	141	141	0	protein_coding	YES	MODERATE	SNV
PLCH1	GRCh38	chr3	1.56E+08	1.56E+08	+	Missense_Mutation	T	A	novel	P32_T1	c.1406A>T	p.Glu469Val	107	92	15	66	64	0	protein_coding	YES	MODERATE	SNV
EPHB3	GRCh38	chr3	1.85E+08	1.85E+08	+	Missense_Mutation	A	G	novel	P32_T1	c.1661A>G	p.Gln554Arg	195	189	6	60	60	0	protein_coding	YES	MODERATE	SNV
PDZD2	GRCh38	chr5	31799505	31799505	+	Missense_Mutation	G	A	novel	P32_T1	c.257G>A	p.Ser86Asn	178	124	52	64	63	0	protein_coding	YES	MODERATE	SNV
ADGRF2	GRCh38	chr6	47681931	47681931	+	Missense_Mutation	A	G	novel	P32_T1	c.1372A>G	p.Ile458Val	212	194	18	92	92	0	protein_coding	YES	MODERATE	SNV
ZNF736	GRCh38	chr7	64348831	64348831	+	Missense_Mutation	A	T	novel	P32_T1	c.968A>T	p.Lys323Met	374	245	125	213	212	0	protein_coding	YES	MODERATE	SNV
TSPAN4	GRCh38	chr11	864443	864445	+	In_Frame_Del	CTG	-	rs753734827	P32_T1	c.274_276del	p.Leu92del	135	65	9	31	22	0	protein_coding	YES	MODERATE	deletion
ANAPC7	GRCh38	chr12	1.1E+08	1.1E+08	+	Nonsense_Mutation	C	A	novel	P32_T1	c.883G>T	p.Glu295Ter	179	135	44	65	65	0	protein_coding	YES	HIGH	SNV
TP53	GRCh38	chr17	7674216	7674216	+	Missense_Mutation	C	A	rs28934571	P32_T1	c.747G>T	p.Arg249Ser	99	53	46	34	34	0	protein_coding	YES	MODERATE	SNV
ANKFN1	GRCh38	chr17	56350773	56350773	+	Missense_Mutation	C	T	rs765737413	P32_T1	c.205C>T	p.Arg69Cys	240	234	5	114	114	0	protein_coding	YES	MODERATE	SNV
LINGO3	GRCh38	chr19	2291325	2291325	+	Missense_Mutation	C	T	novel	P32_T1	c.452G>A	p.Ser151Asn	79	68	11	43	43	0	protein_coding	YES	MODERATE	SNV
ATCAY	GRCh38	chr19	3907817	3907817	+	Missense_Mutation	G	A	rs200021943	P32_T1	c.442G>A	p.Ala148Thr	159	120	39	44	44	0	protein_coding	YES	MODERATE	SNV
CYP4F22	GRCh38	chr19	15540565	15540565	+	Missense_Mutation	A	T	novel	P32_T1	c.787A>T	p.Arg263Trp	404	368	36	80	80	0	protein_coding	YES	MODERATE	SNV
PRDM9	GRCh38	chr5	23522719	23522719	+	Missense_Mutation	C	T	novel	P33_T1	c.716C>T	p.Ala239Val	384	373	7	76	76	0	protein_coding	YES	MODERATE	SNV

Table S2 (*continued*)

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Table S2 (*continued*)

Hugo_Symbol	NCBI_Build	Chromosome	Start_Position	End_Position	Strand	Variant_Classification	Reference_Allele	Tumor_Seq_Allele2	dbSNP_RS	Tumor_Sample_Barcode	HGVSc	HGVSp	t_depth	t_ref_count	t_alt_count	n_depth	n_ref_count	n_alt_count	BIOTYPE	CANONICAL	IMPACT	VARIANT_CLASS
PIGO	GRCh38	chr9	35091452	35091452	+	Nonsense_Mutation	A	C	novel	P33_T1	c.2435T>G	p.Leu812Ter	141	130	10	66	66	0	protein_coding	YES	HIGH	SNV
OR2S2	GRCh38	chr9	35957559	35957559	+	Missense_Mutation	A	C	novel	P33_T1	c.540T>G	p.Cys180Trp	154	135	17	48	48	0	protein_coding	YES	MODERATE	SNV
KDM5A	GRCh38	chr12	310946	310946	+	Missense_Mutation	G	A	rs761933806	P33_T1	c.3155C>T	p.Ala1052Val	230	224	6	40	40	0	protein_coding	YES	MODERATE	SNV
NOP2	GRCh38	chr12	6560535	6560535	+	Missense_Mutation	T	C	novel	P33_T1	c.1571A>G	p.Gln524Arg	70	52	18	34	33	0	protein_coding	YES	MODERATE	SNV
WDR76	GRCh38	chr15	43857051	43857051	+	Missense_Mutation	A	G	novel	P33_T1	c.1297A>G	p.Arg433Gly	205	196	9	41	41	0	protein_coding	YES	MODERATE	SNV
SLC9A5	GRCh38	chr16	67266114	67266116	+	In_Frame_Del	GAG	-	rs770521682	P33_T1	c.2122_2124del	p.Glu708del	78	36	5	22	20	0	protein_coding	YES	MODERATE	deletion
INTS2	GRCh38	chr17	61869771	61869771	+	Missense_Mutation	G	C	novel	P33_T1	c.3020C>G	p.Ala1007Gly	246	194	51	43	42	0	protein_coding	YES	MODERATE	SNV
FCRL2	GRCh38	chr1	1.58E+08	1.58E+08	+	Missense_Mutation	G	T	novel	P34_T1	c.497C>A	p.Ala166Asp	179	152	27	139	138	1	protein_coding	YES	MODERATE	SNV
RASSF1	GRCh38	chr3	50332057	50332057	+	Missense_Mutation	A	C	novel	P34_T1	c.467T>G	p.Met156Arg	90	78	10	85	85	0	protein_coding	YES	MODERATE	SNV
ARMC8	GRCh38	chr3	1.38E+08	1.38E+08	+	Missense_Mutation	A	T	novel	P34_T1	c.34A>T	p.Ser12Cys	147	123	24	82	82	0	protein_coding	YES	MODERATE	SNV
DGKG	GRCh38	chr3	1.86E+08	1.86E+08	+	Missense_Mutation	C	T	novel	P34_T1	c.520G>A	p.Gly174Arg	254	223	31	127	127	0	protein_coding	YES	MODERATE	SNV
BMP2K	GRCh38	chr4	78870931	78870931	+	Missense_Mutation	G	C	rs1367988852	P34_T1	c.1380G>C	p.Gln460His	421	398	11	286	277	1	protein_coding	YES	MODERATE	SNV
CTNND2	GRCh38	chr5	11098612	11098612	+	Missense_Mutation	G	T	novel	P34_T1	c.2600C>A	p.Ala867Glu	214	179	35	90	90	0	protein_coding	YES	MODERATE	SNV
CDH18	GRCh38	chr5	19838844	19838844	+	Missense_Mutation	T	C	rs765370372	P34_T1	c.143A>G	p.His48Arg	239	201	36	117	117	0	protein_coding	YES	MODERATE	SNV
NADK2	GRCh38	chr5	36197579	36197579	+	Missense_Mutation	T	A	novel	P34_T1	c.1152A>T	p.Arg384Ser	324	295	27	145	143	1	protein_coding	YES	MODERATE	SNV
HIVEP1	GRCh38	chr6	12122002	12122002	+	Missense_Mutation	G	T		P34_T1	c.2207G>T	p.Arg736Leu	222	187	35	159	159	0	protein_coding	YES	MODERATE	SNV
KIAA2026	GRCh38	chr9	5920165	5920165	+	Missense_Mutation	G	T	novel	P34_T1	c.5831C>A	p.Thr1944Lys	232	226	6	164	164	0	protein_coding	YES	MODERATE	SNV
FREM1	GRCh38	chr9	14776161	14776161	+	Missense_Mutation	A	C	novel	P34_T1	c.4485T>G	p.Phe1495Leu	165	157	6	137	136	1	protein_coding	YES	MODERATE	SNV
FRMPD1	GRCh38	chr9	37746375	37746375	+	Missense_Mutation	C	A	novel	P34_T1	c.4343C>A	p.Pro1448Gln	100	80	20	81	80	0	protein_coding	YES	MODERATE	SNV
DCAF10	GRCh38	chr9	37801358	37801358	+	Missense_Mutation	C	A	novel	P34_T1	c.492C>A	p.Ser164Arg	203	197	5	139	138	0	protein_coding	YES	MODERATE	SNV
AHNAK	GRCh38	chr11	62533944	62533944	+	Missense_Mutation	G	A	rs752058736	P34_T1	c.473C>T	p.Thr158Met	131	126	5	60	60	0	protein_coding	YES	MODERATE	SNV
NRXN2	GRCh38	chr11	64713663	64713663	+	Missense_Mutation	G	T	novel	P34_T1	c.37C>A	p.Pro13Thr	52	40	12	25	25	0	protein_coding	YES	MODERATE	SNV
KIF26A	GRCh38	chr14	1.04E+08	1.04E+08	+	Missense_Mutation	G	A		P34_T1	c.1856G>A	p.Gly619Asp	52	45	7	34	34	0	protein_coding	YES	MODERATE	SNV
ARIH1	GRCh38	chr15	72580731	72580731	+	Nonsense_Mutation	C	T	novel	P34_T1	c.1216C>T	p.Arg406Ter	218	212	6	122	121	0	protein_coding	YES	HIGH	SNV
SMG1	GRCh38	chr16	18847864	18847864	+	Missense_Mutation	G	T	novel	P34_T1	c.5793C>A	p.Ser1931Arg	212	207	5	105	105	0	protein_coding	YES	MODERATE	SNV
TP53	GRCh38	chr17	7674216	7674216	+	Missense_Mutation	C	A	rs28934571	P34_T1	c.747G>T	p.Arg249Ser	62	48	14	45	43	2	protein_coding	YES	MODERATE	SNV
ATP8B3	GRCh38	chr19	1806116	1806116	+	Missense_Mutation	C	A	novel	P34_T1	c.731G>T	p.Arg244Leu	56	47	9	45	44	0	protein_coding	YES	MODERATE	SNV
LIPE	GRCh38	chr19	42402036	42402036	+	Missense_Mutation	G	C	novel	P34_T1	c.3007C>G	p.Leu1003Val	97	82	13	58	58	0	protein_coding	YES	MODERATE	SNV
SLC4A7	GRCh38	chr3	27385907	27385907	+	Missense_Mutation	C	G		P35_T1	c.3477G>C	p.Lys1159Asn	222	117	99	101	100	0	protein_coding	YES	MODERATE	SNV
ZNF595	GRCh38	chr4	87359	87359	+	Missense_Mutation	T	C	rs998446351	P35_T1	c.1855T>C	p.Ser619Pro	208	199	9	190	185	0	protein_coding	YES	MODERATE	SNV
SPATS1	GRCh38	chr6	44360444	44360444	+	Splice_Site	A	T	novel	P35_T1	c.288-2A>T		209	119	88	166	166	0	protein_coding	YES	HIGH	SNV
VWDE	GRCh38	chr7	12373194	12373194	+	Missense_Mutation	C	T	rs1354388896	P35_T1	c.1370G>A	p.Arg457His	186	119	67	146	144	0	protein_coding	YES	MODERATE	SNV
CPSF1	GRCh38	chr8	1.44E+08	1.44E+08	+	Missense_Mutation	C	T	novel	P35_T1	c.1064G>A	p.Arg355His	169	161	5	101	98	0	protein_coding	YES	MODERATE	SNV
DOCK8	GRCh38	chr9	340255	340255	+	Missense_Mutation	C	A	novel	P35_T1	c.1613C>A	p.Thr538Lys	289	282	6	161	161	0	protein_coding	YES	MODERATE	SNV
TP53	GRCh38	chr17	7674227	7674227	+	Missense_Mutation	T	C	rs483352695	P35_T1	c.736A>G	p.Met246Val	59	18	40	70	69	0	protein_coding	YES	MODERATE	SNV
HIPK4	GRCh38	chr19	40383997	40383997	+	Missense_Mutation	C	G	novel	P35_T1	c.608G>C	p.Cys203Ser	193	125	67	126	126	0	protein_coding	YES	MODERATE	SNV
TEAD2	GRCh38	chr19	49342583	49342583	+	Missense_Mutation	C	A	novel	P35_T1	c.1097G>T	p.Arg366Leu	255	163	91	156	156	0	protein_coding	YES	MODERATE	SNV
MYBPC2	GRCh38	chr19	50455294	50455294	+	Missense_Mutation	T	A	novel	P35_T1	c.2201T>A	p.Ile734Asn	72	43	29	90	89	0	protein_coding	YES	MODERATE	SNV
TRMT2A	GRCh38	chr22	20114600	20114600	+	Missense_Mutation	G	A	rs764530902	P35_T1	c.1207C>T	p.Arg403Trp	115	72	41	81	78	0	protein_coding	YES	MODERATE	SNV
ZNF595	GRCh38	chr4	87359	87359	+	Missense_Mutation	T	C	rs998446351	P36_T1	c.1855T>C	p.Ser619Pro	485	470	8	111	111	0	protein_coding	YES	MODERATE	SNV
PRLR	GRCh38	chr5	35068236	35068236	+	Missense_Mutation	A	C	novel	P36_T1	c.835T>G	p.Phe279Val	215	202	12	41	41	0	protein_coding	YES	MODERATE	SNV
NUP153	GRCh38	chr6	17629102	17629102	+	Missense_Mutation	G	A	rs1359118646	P36_T1	c.3190C>T	p.Pro1064Ser	190	158	32	44	44	0	protein_coding	YES	MODERATE	SNV
TP53	GRCh38	chr17	7674216	7674216	+	Missense_Mutation	C	A	rs28934571	P36_T1	c.747G>T	p.Arg249Ser	77	55	22	20	20	0	protein_coding	YES	MODERATE	SNV
TLE2	GRCh38	chr19	3009566	3009567	+	Frame_Shift_Ins	-	GAGCT	novel	P36_T1	c.1147_1151dup	p.Val385AlafsTer10	148	49	26	44	29	0	protein_coding	YES	HIGH	insertion
S1PR4	GRCh38	chr19	3179522	3179522	+	Missense_Mutation	C	T	rs768125524	P36_T1	c.730C>T	p.Arg244Cys	107	100	7	57	57	0	protein_coding	YES	MODERATE	SNV
TRIP10	GRCh38	chr19	6743089	6743089	+	Missense_Mutation	A	T	novel	P36_T1	c.320A>T	p.Gln107Leu	215	155	60	45	45	0	protein_coding	YES	MODERATE	SNV
FIZ1	GRCh38	chr19	55592740	55592740	+	Missense_Mutation	C	T	novel	P36_T1	c.1201G>A	p.Gly401Arg	170	157	5	35	33	0	protein_coding	YES	MODERATE	SNV
OR2T8	GRCh38	chr1	2.48E+08	2.48E+08	+	Missense_Mutation	C	T	rs61857491	P37_T1	c.479C>T	p.Ala160Val	27	21	6	21	21	0	protein_coding	YES	MODERATE	SNV
VIT	GRCh38	chr2	36808472	36808472	+	Missense_Mutation	G	A	rs1298488934	P37_T1	c.1390G>A	p.Ala464Thr	158	151	7	73	73	0	protein_coding	YES	MODERATE	SNV
CCDC71	GRCh38	chr3	49163940	49163940	+	Missense_Mutation	G	A	novel	P37_T1	c.269C>T	p.Ala90Val	116	109	5	72	72	0	protein_coding	YES	MODERATE	SNV
AGTR1	GRCh38	chr3	1.49E+08	1.49E+08	+	Missense_Mutation	T	C	novel	P37_T1	c.944T>C	p.Val315Ala	223	216	6	97	97	0	protein_coding	YES	MODERATE	SNV
DNAJB11	GRCh38	chr3	1.87E+08	1.87E+08	+	Missense_Mutation	C	T	novel	P37_T1	c.97C>T	p.Pro33Ser	179	171	8	59	59	0	protein_coding	YES	MODERATE	SNV
SRD5A1	GRCh38	chr5	6633758	6633758	+	Missense_Mutation	T	C	novel	P37_T1	c.182T>C	p.Leu61Pro	153	145	7	90	89	0	protein_coding	YES	MODERATE	SNV
RANBP9	GRCh38	chr6	13711150	13711150	+	Missense_Mutation	G	A	rs773022063	P37_T1	c.356C>T	p.Pro119Leu	151	145	5	53	50	0	protein_coding	YES	MODERATE	SNV
H1-2	GRCh38	chr6	26056058	26056058	+	Missense_Mutation	C	G	rs12111009	P37_T1	c.371G>C	p.Gly124Ala	193	185	7	93	92	0	protein_coding	YES	MODERATE	SNV
H1-3	GRCh38	chr6	26234891	26234891	+	Missense_Mutation	C	G	rs141394027	P37_T1	c.43G>C	p.Ala15Pro	205	196	9	64	64	0	protein_coding	YES	MODERATE	SNV
MLLT3	GRCh38	chr9	20620798	20620798	+	Missense_Mutation	C	T	novel	P37_T1	c.49G>A	p.Ala17Thr	189	182	7	61	61	0	protein_coding	YES	MODERATE	SNV
RUSC2	GRCh38	chr9	35560311	35560311	+	Missense_Mutation	C	T	novel	P37_T1	c.3671C>T	p.Ala1224Val	137	132	5	60	60	0	protein_coding	YES	MODERATE	SNV
ITGA8	GRCh38	chr10	15719714	15719714	+	Missense_Mutation	G	T	novel	P37_T1	c.58C>A	p.Leu20Ile	122	114	5	59	59	0	protein_coding	YES	MODERATE	SNV
KRT1	GRCh38	chr12	52680047	52680047	+	Missense_Mutation	C	A	rs147840212	P37_T1	c.302G>T	p.Gly101Val	507	491	10	218	215	0	protein_coding	YES	MODERATE	SNV
ACAD10	GRCh38	chr12	1.12E+08	1.12E+08	+	Missense_Mutation	G	A	rs148107230	P37_T1	c.2606G>A	p.Cys869Tyr	177	170	6	66	66	0	protein_coding	YES	MODERATE	SNV
FHOD1	GRCh38	chr16	67229967	67229967	+	Missense_Mutation	T	C	rs773670831	P37_T1	c.3238A>G	p.Ile1080Val	138	130	8	76	76	0	protein_coding	YES	MODERATE	SNV
MINK1	GRCh38	chr17	4891601	4891601	+	Missense_Mutation	C	T	rs188278508	P37_T1	c.1886C>T	p.Thr629Met	139	133	6	66	65	0	protein_coding	YES	MODERATE	SNV
DNAH2	GRCh38	chr17	7719798	7719798	+	Missense_Mutation	T	C	novel	P37_T1	c.64T>C	p.Ser22Pro	174	168	5	95	94	0	protein_coding	YES	MODERATE	SNV
MEX3D	GRCh38	chr19	1556899	1556899	+	Missense_Mutation	G	A	novel	P37_T1	c.620C>T	p.Ala207Val	73	66	6	53	52	0	protein_coding	YES	MODERATE	SNV
ZNF763	GRCh38	chr19	11978493	11978493	+	Missense_Mutation	G	A	rs370964246	P37_T1	c.578G>A	p.Arg193His	333	325	7	129	128	0	protein_coding	YES	MODERATE	SNV
ZNF763	GRCh38	chr19	11978723	11978723	+	Missense_Mutation	A	G	rs147184532	P37_T1	c.808A>G	p.Ser270Gly	340	324	14	157	157	0	protein_coding	YES	MODERATE	SNV
SLX4IP	GRCh38	chr20	10623123	10623123	+	Missense_Mutation	T	C	rs754151335	P37_T1	c.971T>C	p.Ile324Thr	332	321	7	105	104	0	protein_coding	YES	MODERATE	SNV
DCST2	GRCh38	chr1	1.55E+08	1.55E+08	+	Missense_Mutation	C	G	novel	P38_T1	c.305G>C	p.Gly102Ala	262	214	48	90	89	0	protein_coding	YES	MODERATE	SNV
PXDN	GRCh38	chr2	1639345	1639345	+	Nonsense_Mutation	C	A	novel	P38_T1	c.4030G>T	p.Glu1344Ter	115	71	44	90	90	0	protein_coding	YES	HIGH	SNV
COL6A6	GRCh38	chr3	1.31E+08	1.31E+08	+	Missense_Mutation	C	A	novel	P38_T1	c.5639C>A	p.Ser1880Tyr	132	107	25	132	132	0	protein_coding	YES	MODERATE	SNV
ZAR1	GRCh38	chr4	48490910	48490910	+	Missense_Mutation	G	A	novel	P38_T1	c.619G>A	p.Gly207Arg	42	19	23	122	122	0	protein_coding	YES	MODERATE	SNV
MRPS30	GRCh38	chr5	44815101	44815101	+	Missense_Mutation	G	T	novel	P38_T1	c.1219G>T	p.Asp407Tyr	81	46	34	98	98	0	protein_coding	YES	MODERATE	SNV
GAL3ST4	GRCh38	chr7	1E+08	1E+08	+	Missense_Mutation	A	C	novel	P38_T1	c.1304T>G	p.Leu435Trp	81	73	7	92	92	0	protein_coding	YES	MODERATE	SNV
SLC26A4	GRCh38	chr7	1.08E+08	1.08E+08	+	Missense_Mutation	A	C	novel	P38_T1	c.2207A>C	p.Gln736Pro	51	43	6	36	34	1	protein_coding	YES	MODERATE	SNV
IFITM3	GRCh38	chr11	320723	320723	+	Missense_Mutation	C	T	rs199582787	P38_T1	c.91G>A	p.Val31Met	137	118	18	89	89	0	protein_coding	YES	MODERATE	SNV
KRT17	GRCh38	chr17	41622377	41622377	+	Missense_Mutation	T	C	novel	P38_T1	c.650A>G	p.Tyr217Cys	38	26	12	64	64	0	protein_coding	YES	MODERATE	SNV
PTPRS	GRCh38	chr19	5225804	5225804	+	Missense_Mutation	G	T		P38_T1	c.2417C>A	p.Ser806Tyr	68	57	11	57	57	0	protein_coding	YES	MODERATE	SNV
FUT5	GRCh38	chr19	5867418	5867418	+	Missense_Mutation	T	C	novel	P38_T1	c.308A>G	p.Asp103Gly	75	58	17	68	67	0	protein_coding	YES	MODERATE	SNV
ACSBG2	GRCh38	chr19	6177240	6177240	+	Missense_Mutation	T	G	rs769535255	P38_T1	c.750T>G	p.Ile250Met	123	116	6	59	59	0	protein_coding	YES	MODERATE	SNV
RNASEH2A	GRCh38	chr19	12807487	12807487	+	Missense_Mutation	A	T	novel	P38_T1	c.392A>T	p.Gln131Leu	76	53	23	41	41	0	protein_coding	YES	MODERATE	SNV
LPAR2	GRCh38	chr19	19626741	19626741	+	Missense_Mutation	C	G		P38_T1	c.544G>C	p.Ala182Pro	70	44	26	75	75	0	protein_coding	YES	MODERATE	SNV
TNFRSF8	GRCh38	chr1	12123750	12123750	+	Missense_Mutation	A	T	novel	P39_T1	c.1076A>T	p.Gln359Leu	119	87	32	30	30	0	protein_coding	YES	MODERATE	SNV
ASPM	GRCh38	chr1	1.97E+08	1.97E+08	+	Missense_Mutation	T	G	novel	P39_T1	c.6512A>C	p.Lys2171Thr	409	227	181	47	47	0	protein_coding	YES	MODERATE	SNV
CACNA2D2	GRCh38	chr3	50379996	50379996	+	Missense_Mutation	G	T	novel	P39_T1	c.865C>A	p.Pro289Thr	47	18	29	25	25	0	protein_coding	YES	MODERATE	SNV
YEATS2	GRCh38	chr3	1.84E+08	1.84E+08	+	Missense_Mutation	A	G	novel	P39_T1	c.1244A>G	p.Gln415Arg	271	139	132	40	40	0	protein_coding	YES	MODERATE	SNV
MUC3A	GRCh38	chr7	1.01E+08	1.01E+08	+	Missense_Mutation	A	G	rs748319946	P39_T1	c.8095A>G	p.Ile2699Val	208	155	53	60	59	0	protein_coding	YES	MODERATE	SNV
JAK2	GRCh38	chr9	5090755	5090755	+	Missense_Mutation	G	A	novel	P39_T1	c.2903G>A	p.Gly968Asp	210	138	72	25	25	0	protein_coding	YES	MODERATE	SNV
IFNA4	GRCh38	chr9	21187225	21187225	+	Missense_Mutation	T	A	novel	P39_T1	c.307A>T	p.Ser103Cys	322	173	148	78	78	0	protein_coding	YES	MODERATE	SNV
MSMP	GRCh38	chr9	35754080	35754080	+	Missense_Mutation	C	A	novel	P39_T1	c.50G>T	p.Gly17Val	99	59	40	40	40	0	protein_coding	YES	MODERATE	SNV
TSPAN4	GRCh38	chr11	865607	865607	+	Missense_Mutation	A	C	novel	P39_T1	c.425A>C	p.Gln142Pro	60	53	6	26	26	0	protein_coding	YES	MODERATE	SNV
SPI1	GRCh38	chr11	47358888	47358888	+	Missense_Mutation	G	A	rs370953870	P39_T1	c.452C>T	p.Ala151Val	82	66	16	38	38	0	protein_coding	YES	MODERATE	SNV
OR9Q2	GRCh38	chr11	58190663	58190663	+	Missense_Mutation	C	T	rs201381322	P39_T1	c.173C>T	p.Pro58Leu	144	99	45	21	21	0	protein_coding	YES	MODERATE	SNV
OR10G3	GRCh38	chr14	21570649	21570649	+	Frame_Shift_Del	A	-	novel	P39_T1	c.96del	p.Leu33Ter	126	62	43	25	17	0	protein_coding	YES	HIGH	deletion
CDK12	GRCh38	chr17	39525933	39525933	+	Missense_Mutation	A	C	novel	P39_T1	c.3377A>C	p.Gln1126Pro	116	109	7	31	31	0	protein_coding	YES	MODERATE	SNV
CDK12	GRCh38	chr17	39525934	39525934	+	Missense_Mutation	A	C		P39_T1	c.3378A>C	p.Gln1126His	115	109	6	31	31	0	protein_coding	YES	MODERATE	SNV
AP3D1	GRCh38	chr19	2121216	2121216	+	Missense_Mutation	C	A	novel	P39_T1	c.1197G>T	p.Lys399Asn	32	8	24	29	29	0	protein_coding	YES	MODERATE	SNV
DOT1L	GRCh38	chr19	2191083	2191083	+	Missense_Mutation	G	T	novel	P39_T1	c.336G>T	p.Gln112His	34	4	30	38	37	0	protein_coding	YES	MODERATE	SNV
PSPN	GRCh38	chr19	6375379	6375379	+	Missense_Mutation	T	G	novel	P39_T1	c.386A>C	p.Tyr129Ser	43	38	5	31	31	0	protein_coding	YES	MODERATE	SNV
TUBB4A	GRCh38	chr19	6495883	6495883	+	Missense_Mutation	C	A	novel	P39_T1	c.616G>T	p.Ala206Ser	97	27	70	71	71	0	protein_coding	YES	MODERATE	SNV
ARID1A	GRCh38	chr1	26762973	26762974	+	Frame_Shift_Ins	-	T	novel	P4_T1	c.2421dup	p.Gly808TrpfsTer9	252	168	84	187	187	0	protein_coding	YES	HIGH	insertion
NTRK1	GRCh38	chr1	1.57E+08	1.57E+08	+	Missense_Mutation	C	T	rs760974854	P4_T1	c.2296C>T	p.Arg766Trp	124	120	4	94	94	0	protein_coding	YES	MODERATE	SNV
LRP1B	GRCh38	chr2	1.4E+08	1.4E+08	+	Missense_Mutation	T	A	novel	P4_T1	c.12658A>T	p.Thr4220Ser	336	331	5	183	183	0	protein_coding	YES	MODERATE	SNV
CUL3	GRCh38	chr2	2.24E+08	2.24E+08	+	Missense_Mutation	A	G	novel	P4_T1	c.2123T>C	p.Val708Ala	610	479	131	491	491	0	protein_coding	YES	MODERATE	SNV
CTNNB1	GRCh38	chr3	41233420	41233420	+	Missense_Mutation	T	G		P4_T1	c.1161T>G	p.Asn387Lys	743	538	205	361	361	0	protein_coding	YES	MODERATE	SNV
SETD2	GRCh38	chr3	47083940	47083953	+	Frame_Shift_Del	CTAGCTTCTATGTT	-	novel	P4_T1	c.5827_5840del	p.Asn1943Ter	665	427	238	757	757	0	protein_coding	YES	HIGH	deletion
BAP1	GRCh38	chr3	52408049	52408049	+	Missense_Mutation	G	A		P4_T1	c.284C>T	p.Ala95Val	334	329	5	145	145	0	protein_coding	YES	MODERATE	SNV
CSF1R	GRCh38	chr5	1.5E+08	1.5E+08	+	Missense_Mutation	T	C	rs757362705	P4_T1	c.1501A>G	p.Ile501Val	172	123	49	149	149	0	protein_coding	YES	MODERATE	SNV
CDKN1A	GRCh38	chr6	36684348	36684355	+	Frame_Shift_Del	CGGCGAGG	-	novel	P4_T1	c.248_255del	p.Arg83ProfsTer3	223	126	97	253	253	0	protein_coding	YES	HIGH	deletion
ARID1B	GRCh38	chr6	1.57E+08	1.57E+08	+	Missense_Mutation	G	A	novel	P4_T1	c.817G>A	p.Ala273Thr	149	144	5	106	106	0	protein_coding	YES	MODERATE	SNV
KMT2C	GRCh38	chr7	1.52E+08	1.52E+08	+	Missense_Mutation	G	A	novel	P4_T1	c.4280C>T	p.Ala1427Val	204	200	4	103	103	0	protein_coding	YES	MODERATE	SNV
KMT2D	GRCh38	chr12	49040266	49040266	+	Missense_Mutation	G	T	novel	P4_T1	c.7504C>A	p.Pro2502Thr	173	103	70	257	257	0	protein_coding	YES	MODERATE	SNV
SH2B3	GRCh38	chr12	1.11E+08	1.11E+08	+	Missense_Mutation	G	A		P4_T1	c.256G>A	p.Gly86Ser	173	169	4	128	128	0	protein_coding	YES	MODERATE	SNV
POLE	GRCh38	chr12	1.33E+08	1.33E+08	+	Missense_Mutation	C	T	rs760942391	P4_T1	c.2173G>A	p.Asp725Asn	261	255	6	225	225	0	protein_coding	YES	MODERATE	SNV
PTPRT	GRCh38	chr20	42110387	42110387	+	Missense_Mutation	C	A		P4_T1	c.3257G>T	p.Arg1086Leu	177	117	60	259	258	1	protein_coding	YES	MODERATE	SNV
NES	GRCh38	chr1	1.57E+08	1.57E+08	+	Missense_Mutation	A	T	novel	P40_T1	c.3802T>A	p.Ser1268Thr	149	122	26	50	50	0	protein_coding	YES	MODERATE	SNV
SLC49A3	GRCh38	chr4	682871	682871	+	Missense_Mutation	T	G	novel	P40_T1	c.1174A>C	p.Ile392Leu	126	114	11	34	34	0	protein_coding	YES	MODERATE	SNV
C6	GRCh38	chr5	41159122	41159122	+	Nonsense_Mutation	G	A	rs191386155	P40_T1	c.1816C>T	p.Arg606Ter	247	238	7	91	91	0	protein_coding	YES	HIGH	SNV
ZAN	GRCh38	chr7	1.01E+08	1.01E+08	+	Missense_Mutation	G	A	rs1223517352	P40_T1	c.5872G>A	p.Val1958Met	214	182	32	80	80	0	protein_coding	YES	MODERATE	SNV
EPPK1	GRCh38	chr8	1.44E+08	1.44E+08	+	Missense_Mutation	T	A	novel	P40_T1	c.5600A>T	p.Gln1867Leu	329	318	8	34	34	0	protein_coding	YES	MODERATE	SNV
RRAGA	GRCh38	chr9	19049891	19049891	+	Nonsense_Mutation	C	T	novel	P40_T1	c.232C>T	p.Arg78Ter	248	242	6	70	70	0	protein_coding	YES	HIGH	SNV
CRTAC1	GRCh38	chr10	97917635	97917635	+	Missense_Mutation	A	T	novel	P40_T1	c.580T>A	p.Tyr194Asn	92	46	46	51	51	0	protein_coding	YES	MODERATE	SNV
EPS8L2	GRCh38	chr11	722771	722771	+	Missense_Mutation	A	G	novel	P40_T1	c.1307A>G	p.Glu436Gly	108	97	10	39	39	0	protein_coding	YES	MODERATE	SNV
SBNO1	GRCh38	chr12	1.23E+08	1.23E+08	+	Missense_Mutation	T	A	novel	P40_T1	c.370A>T	p.Ile124Phe	284	249	35	60	60	0	protein_coding	YES	MODERATE	SNV

Table S2 (*continued*)

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Table S2 (*continued*)

Hugo_Symbol	NCBI_Build	Chromosome	Start_Position	End_Position	Strand	Variant_Classification	Reference_Allele	Tumor_Seq_Allele2	dbSNP_RS	Tumor_Sample_Barcode	HGVSc	HGVSp	t_depth	t_ref_count	t_alt_count	n_depth	n_ref_count	n_alt_count	BIOTYPE	CANONICAL	IMPACT	VARIANT_CLASS
ANHX	GRCh38	chr12	1.33E+08	1.33E+08	+	Splice_Site	A	C	novel	P40_T1	c.1053+2T>G		193	184	7	37	37	0	protein_coding	YES	HIGH	SNV
ABCC11	GRCh38	chr16	48210994	48210994	+	Missense_Mutation	T	G	novel	P40_T1	c.1562A>C	p.Asn521Thr	309	297	7	119	119	0	protein_coding	YES	MODERATE	SNV
RNF213	GRCh38	chr17	80273334	80273334	+	Missense_Mutation	T	G	novel	P40_T1	c.191T>G	p.Phe64Cys	306	272	24	69	68	0	protein_coding	YES	MODERATE	SNV
SLC25A23	GRCh38	chr19	6456530	6456530	+	Missense_Mutation	T	A	novel	P40_T1	c.373A>T	p.Met125Leu	88	45	37	38	33	0	protein_coding	YES	MODERATE	SNV
ATP13A1	GRCh38	chr19	19655583	19655583	+	Missense_Mutation	G	T		P40_T1	c.1341C>A	p.Phe447Leu	927	845	80	73	72	0	protein_coding	YES	MODERATE	SNV
ATP13A1	GRCh38	chr19	19656115	19656115	+	Missense_Mutation	G	C	novel	P40_T1	c.1152C>G	p.Ile384Met	953	886	65	66	66	0	protein_coding	YES	MODERATE	SNV
C5AR2	GRCh38	chr19	47341643	47341643	+	Missense_Mutation	G	A	rs200192224	P40_T1	c.844G>A	p.Ala282Thr	256	250	6	46	46	0	protein_coding	YES	MODERATE	SNV
ZNF524	GRCh38	chr19	55602899	55602899	+	Missense_Mutation	C	T	novel	P40_T1	c.787C>T	p.Pro263Ser	289	283	6	82	82	0	protein_coding	YES	MODERATE	SNV
NLRP9	GRCh38	chr19	55711803	55711803	+	Missense_Mutation	A	T	novel	P40_T1	c.2840T>A	p.Leu947Gln	185	121	63	28	28	0	protein_coding	YES	MODERATE	SNV
ZNF543	GRCh38	chr19	57328694	57328694	+	Missense_Mutation	A	T	novel	P40_T1	c.1232A>T	p.Lys411Met	371	262	108	88	86	0	protein_coding	YES	MODERATE	SNV
EIF4G3	GRCh38	chr1	20879466	20879466	+	Missense_Mutation	T	C		P41_T1	c.2419A>G	p.Asn807Asp	354	346	7	61	61	0	protein_coding	YES	MODERATE	SNV
NISCH	GRCh38	chr3	52487998	52487998	+	Missense_Mutation	C	A	novel	P41_T1	c.2506C>A	p.Arg836Ser	172	167	5	48	48	0	protein_coding	YES	MODERATE	SNV
EPHA3	GRCh38	chr3	89449246	89449246	+	Missense_Mutation	T	C	novel	P41_T1	c.2368T>C	p.Trp790Arg	479	460	16	55	55	0	protein_coding	YES	MODERATE	SNV
BMP2K	GRCh38	chr4	78870931	78870931	+	Missense_Mutation	G	C	rs1367988852	P41_T1	c.1380G>C	p.Gln460His	622	602	8	106	105	0	protein_coding	YES	MODERATE	SNV
DNAH5	GRCh38	chr5	13751187	13751187	+	Missense_Mutation	G	A		P41_T1	c.11102C>T	p.Pro3701Leu	400	332	67	36	36	0	protein_coding	YES	MODERATE	SNV
CDH12	GRCh38	chr5	21752076	21752076	+	Missense_Mutation	T	A	novel	P41_T1	c.2046A>T	p.Lys682Asn	437	406	31	48	48	0	protein_coding	YES	MODERATE	SNV
PTGER4	GRCh38	chr5	40681627	40681627	+	Missense_Mutation	C	T	novel	P41_T1	c.634C>T	p.Arg212Cys	402	376	24	68	68	0	protein_coding	YES	MODERATE	SNV
TDP2	GRCh38	chr6	24651015	24651015	+	Missense_Mutation	C	A	novel	P41_T1	c.862G>T	p.Gly288Cys	396	378	7	38	38	0	protein_coding	YES	MODERATE	SNV
HOXA5	GRCh38	chr7	27141888	27141888	+	Missense_Mutation	T	C	novel	P41_T1	c.760A>G	p.Asn254Asp	256	230	26	36	36	0	protein_coding	YES	MODERATE	SNV
DBNL	GRCh38	chr7	44044748	44044748	+	Missense_Mutation	A	G	novel	P41_T1	c.11A>G	p.Asn4Ser	190	158	29	37	37	0	protein_coding	YES	MODERATE	SNV
PLPP6	GRCh38	chr9	4662587	4662587	+	Missense_Mutation	T	C	rs1230036818	P41_T1	c.212T>C	p.Phe71Ser	276	266	5	41	39	0	protein_coding	YES	MODERATE	SNV
KIAA2026	GRCh38	chr9	5968586	5968586	+	Missense_Mutation	G	C	rs1375377845	P41_T1	c.1645C>G	p.Pro549Ala	401	390	10	36	36	0	protein_coding	YES	MODERATE	SNV
TYRP1	GRCh38	chr9	12695648	12695648	+	Missense_Mutation	T	G	novel	P41_T1	c.519T>G	p.Asp173Glu	549	539	10	69	69	0	protein_coding	YES	MODERATE	SNV
FBH1	GRCh38	chr10	5936538	5936538	+	Missense_Mutation	C	T	rs372861811	P41_T1	c.3065C>T	p.Ala1022Val	237	231	5	40	40	0	protein_coding	YES	MODERATE	SNV
HBE1	GRCh38	chr11	5269560	5269560	+	Missense_Mutation	G	T	novel	P41_T1	c.209C>A	p.Thr70Asn	245	220	25	37	37	0	protein_coding	YES	MODERATE	SNV
TRIM44	GRCh38	chr11	35685337	35685337	+	Splice_Site	G	C	novel	P41_T1	c.747+1G>C		279	273	6	23	23	0	protein_coding	YES	HIGH	SNV
TJP3	GRCh38	chr19	3746638	3746638	+	Missense_Mutation	C	T	rs571782628	P41_T1	c.2191C>T	p.Arg731Cys	201	147	54	43	43	0	protein_coding	YES	MODERATE	SNV
ZNF578	GRCh38	chr19	52510655	52510655	+	Nonsense_Mutation	A	T		P41_T1	c.274A>T	p.Arg92Ter	655	576	79	94	94	0	protein_coding	YES	HIGH	SNV
UBR3	GRCh38	chr2	1.7E+08	1.7E+08	+	Missense_Mutation	G	C	novel	P42_T1	c.5596G>C	p.Glu1866Gln	232	138	94	21	21	0	protein_coding	YES	MODERATE	SNV
CRIP3	GRCh38	chr6	43306500	43306500	+	Missense_Mutation	T	C	novel	P42_T1	c.346A>G	p.Thr116Ala	89	81	7	20	20	0	protein_coding	YES	MODERATE	SNV
KANK1	GRCh38	chr9	712006	712006	+	Missense_Mutation	G	A	rs776859009	P42_T1	c.1240G>A	p.Val414Met	206	200	6	52	52	0	protein_coding	YES	MODERATE	SNV
PPP4R1	GRCh38	chr18	9550370	9550371	+	Nonsense_Mutation	TA	-	novel	P42_T1	c.2319_2320del	p.Tyr773Ter	227	67	72	35	20	0	protein_coding	YES	HIGH	deletion
GPX4	GRCh38	chr19	1105695	1105695	+	Missense_Mutation	C	T	rs772822658	P42_T1	c.362C>T	p.Ala121Val	104	86	17	41	39	0	protein_coding	YES	MODERATE	SNV
PLEKHH2	GRCh38	chr2	43712280	43712280	+	Missense_Mutation	A	G	novel	P43_T1	c.2357A>G	p.Glu786Gly	326	319	5	118	118	0	protein_coding	YES	MODERATE	SNV
ALMS1	GRCh38	chr2	73449103	73449103	+	Missense_Mutation	C	A		P43_T1	c.2576C>A	p.Ala859Glu	391	384	6	125	125	0	protein_coding	YES	MODERATE	SNV
DUSP22	GRCh38	chr6	345924	345924	+	Missense_Mutation	C	A	novel	P43_T1	c.259C>A	p.His87Asn	176	170	6	46	46	0	protein_coding	YES	MODERATE	SNV
ZCWPW1	GRCh38	chr7	1E+08	1E+08	+	Missense_Mutation	G	A	novel	P43_T1	c.406C>T	p.Pro136Ser	326	315	6	101	100	0	protein_coding	YES	MODERATE	SNV
PRRC2B	GRCh38	chr9	1.31E+08	1.31E+08	+	Missense_Mutation	C	A	novel	P43_T1	c.3784C>A	p.His1262Asn	169	163	5	61	60	0	protein_coding	YES	MODERATE	SNV
SIRT3	GRCh38	chr11	233128	233128	+	Missense_Mutation	G	T		P43_T1	c.561C>A	p.His187Gln	280	271	6	64	64	0	protein_coding	YES	MODERATE	SNV
ABCC11	GRCh38	chr16	48167523	48167523	+	Missense_Mutation	G	T	novel	P43_T1	c.4029C>A	p.Asp1343Glu	505	478	26	126	126	0	protein_coding	YES	MODERATE	SNV
TRIO	GRCh38	chr5	14497865	14497865	+	Missense_Mutation	A	T	novel	P44_T1	c.8038A>T	p.Ile2680Phe	36	22	14	23	23	0	protein_coding	YES	MODERATE	SNV
FBXL7	GRCh38	chr5	15927947	15927947	+	Missense_Mutation	C	G	novel	P44_T1	c.185C>G	p.Pro62Arg	37	22	13	61	60	0	protein_coding	YES	MODERATE	SNV
RIPK1	GRCh38	chr6	3105907	3105907	+	Missense_Mutation	C	A	rs772895143	P44_T1	c.1432C>A	p.Pro478Thr	25	11	14	54	53	0	protein_coding	YES	MODERATE	SNV
NFX1	GRCh38	chr9	33294796	33294796	+	Missense_Mutation	A	T	novel	P44_T1	c.402A>T	p.Leu134Phe	27	5	22	64	64	0	protein_coding	YES	MODERATE	SNV
TEP1	GRCh38	chr14	20389742	20389742	+	Splice_Site	T	A	novel	P44_T1	c.2335-2A>T		33	23	10	71	71	0	protein_coding	YES	HIGH	SNV
GALK2	GRCh38	chr15	49319737	49319737	+	Missense_Mutation	C	A	novel	P44_T1	c.1101C>A	p.Ser367Arg	32	15	17	70	70	0	protein_coding	YES	MODERATE	SNV
FAM110C	GRCh38	chr2	46181	46181	+	Nonsense_Mutation	T	A	novel	P45_T1	c.205A>T	p.Lys69Ter	42	36	5	72	72	0	protein_coding	YES	HIGH	SNV
ALMS1	GRCh38	chr2	73450719	73450719	+	Missense_Mutation	G	A	rs1445963295	P45_T1	c.4192G>A	p.Gly1398Ser	295	288	7	163	162	0	protein_coding	YES	MODERATE	SNV
ZNF595	GRCh38	chr4	87359	87359	+	Missense_Mutation	T	C	rs998446351	P45_T1	c.1855T>C	p.Ser619Pro	204	196	8	106	106	0	protein_coding	YES	MODERATE	SNV
TMEM129	GRCh38	chr4	1720672	1720672	+	Missense_Mutation	T	G	novel	P45_T1	c.166A>C	p.Thr56Pro	155	147	8	80	80	0	protein_coding	YES	MODERATE	SNV
OXCT1	GRCh38	chr5	41739419	41739419	+	Missense_Mutation	C	T	rs778813276	P45_T1	c.1492G>A	p.Val498Ile	159	154	5	59	59	0	protein_coding	YES	MODERATE	SNV
BAZ1B	GRCh38	chr7	73459553	73459553	+	Missense_Mutation	T	A	novel	P45_T1	c.3415A>T	p.Met1139Leu	219	188	29	75	75	0	protein_coding	YES	MODERATE	SNV
GNB2	GRCh38	chr7	1.01E+08	1.01E+08	+	Missense_Mutation	C	T	rs1193860550	P45_T1	c.746C>T	p.Thr249Met	112	106	6	40	40	0	protein_coding	YES	MODERATE	SNV
TRIM66	GRCh38	chr11	8640870	8640870	+	Missense_Mutation	T	G	novel	P45_T1	c.1505A>C	p.Gln502Pro	163	157	6	129	126	1	protein_coding	YES	MODERATE	SNV
TEP1	GRCh38	chr14	20389638	20389638	+	Missense_Mutation	C	A	novel	P45_T1	c.2437G>T	p.Gly813Cys	131	126	5	111	111	0	protein_coding	YES	MODERATE	SNV
CGNL1	GRCh38	chr15	57545621	57545621	+	Missense_Mutation	G	A	rs1374754601	P45_T1	c.3530G>A	p.Arg1177Gln	142	136	6	57	57	0	protein_coding	YES	MODERATE	SNV
POLRMT	GRCh38	chr19	623575	623575	+	Missense_Mutation	T	A	novel	P45_T1	c.1169A>T	p.His390Leu	125	114	11	79	79	0	protein_coding	YES	MODERATE	SNV
GRIN3B	GRCh38	chr19	1003430	1003430	+	Missense_Mutation	G	T	novel	P45_T1	c.727G>T	p.Ala243Ser	102	97	5	58	58	0	protein_coding	YES	MODERATE	SNV
LONP1	GRCh38	chr19	5719775	5719775	+	Missense_Mutation	C	G	novel	P45_T1	c.358G>C	p.Val120Leu	170	165	5	61	61	0	protein_coding	YES	MODERATE	SNV
ZNF544	GRCh38	chr19	58262337	58262337	+	Missense_Mutation	T	G	rs1430445274	P45_T1	c.1731T>G	p.Asp577Glu	189	184	5	60	60	0	protein_coding	YES	MODERATE	SNV
ZNF544	GRCh38	chr19	58262374	58262374	+	Missense_Mutation	C	G	rs1568503474	P45_T1	c.1768C>G	p.Gln590Glu	195	189	6	76	76	0	protein_coding	YES	MODERATE	SNV
AJAP1	GRCh38	chr1	4772303	4772303	+	Missense_Mutation	G	A	rs267598631	P46_T1	c.941G>A	p.Arg314His	338	330	8	92	92	0	protein_coding	YES	MODERATE	SNV
ASTN1	GRCh38	chr1	1.77E+08	1.77E+08	+	Missense_Mutation	C	T	novel	P46_T1	c.2489G>A	p.Ser830Asn	215	185	29	88	88	0	protein_coding	YES	MODERATE	SNV
IFT172	GRCh38	chr2	27459518	27459518	+	Missense_Mutation	A	G	novel	P46_T1	c.2647T>C	p.Ser883Pro	164	143	21	86	86	0	protein_coding	YES	MODERATE	SNV
ITGA9	GRCh38	chr3	37818987	37818987	+	Nonstop_Mutation	T	A	novel	P46_T1	c.3106T>A	p.Ter1036ArgextTer7	88	78	10	35	34	0	protein_coding	YES	HIGH	SNV
RBM15B	GRCh38	chr3	51393542	51393542	+	Missense_Mutation	G	A	novel	P46_T1	c.2143G>A	p.Ala715Thr	337	327	6	113	113	0	protein_coding	YES	MODERATE	SNV
H2BC6	GRCh38	chr6	26184173	26184173	+	Missense_Mutation	G	C	rs771832548	P46_T1	c.378G>C	p.Lys126Asn	494	484	8	116	115	0	protein_coding	YES	MODERATE	SNV
ABCA13	GRCh38	chr7	48278785	48278785	+	Nonsense_Mutation	A	T	novel	P46_T1	c.7591A>T	p.Lys2531Ter	141	129	11	141	141	0	protein_coding	YES	HIGH	SNV
ANO9	GRCh38	chr11	432043	432043	+	Missense_Mutation	C	T	rs755574497	P46_T1	c.362G>A	p.Arg121Gln	239	207	28	32	32	0	protein_coding	YES	MODERATE	SNV
KDM2A	GRCh38	chr11	67250749	67250749	+	Missense_Mutation	C	T	rs375518283	P46_T1	c.2719C>T	p.Arg907Cys	983	907	36	66	66	0	protein_coding	YES	MODERATE	SNV
TP53	GRCh38	chr17	7674216	7674216	+	Missense_Mutation	C	A	rs28934571	P46_T1	c.747G>T	p.Arg249Ser	180	125	55	27	27	0	protein_coding	YES	MODERATE	SNV
PIEZO2	GRCh38	chr18	10698967	10698967	+	Missense_Mutation	G	A	novel	P46_T1	c.6313C>T	p.Pro2105Ser	359	350	7	102	102	0	protein_coding	YES	MODERATE	SNV
PIEZO2	GRCh38	chr18	10789081	10789081	+	Nonsense_Mutation	G	A	novel	P46_T1	c.2167C>T	p.Gln723Ter	115	98	16	82	82	0	protein_coding	YES	HIGH	SNV
PIEZO2	GRCh38	chr18	10789082	10789082	+	Nonsense_Mutation	G	T	novel	P46_T1	c.2166C>A	p.Tyr722Ter	115	99	15	87	87	0	protein_coding	YES	HIGH	SNV
SPIRE1	GRCh38	chr18	12449649	12449649	+	Missense_Mutation	T	A	novel	P46_T1	c.2260A>T	p.Ser754Cys	240	230	8	48	48	0	protein_coding	YES	MODERATE	SNV
POTEC	GRCh38	chr18	14538151	14538152	+	Frame_Shift_Ins	-	T	rs761185458	P46_T1	c.619dup	p.Arg207LysfsTer14	69	50	11	138	135	1	protein_coding	YES	HIGH	insertion
ANKRD30B	GRCh38	chr18	14848828	14848828	+	Missense_Mutation	T	A	novel	P46_T1	c.2937T>A	p.Asn979Lys	133	112	21	89	88	0	protein_coding	YES	MODERATE	SNV
CBARP	GRCh38	chr19	1235813	1235813	+	Nonsense_Mutation	T	A	novel	P46_T1	c.211A>T	p.Lys71Ter	335	313	21	46	46	0	protein_coding	YES	HIGH	SNV
APC2	GRCh38	chr19	1467007	1467007	+	Missense_Mutation	T	A	novel	P46_T1	c.3706T>A	p.Tyr1236Asn	319	261	58	58	58	0	protein_coding	YES	MODERATE	SNV
SHANK3	GRCh38	chr22	50678879	50678879	+	Missense_Mutation	G	A	rs779287173	P46_T1	c.559G>A	p.Val187Met	346	339	5	77	77	0	protein_coding	YES	MODERATE	SNV
ALMS1	GRCh38	chr2	73450719	73450719	+	Missense_Mutation	G	A	rs1445963295	P47_T1	c.4192G>A	p.Gly1398Ser	97	91	6	52	52	0	protein_coding	YES	MODERATE	SNV
DNAJC21	GRCh38	chr5	34938958	34938958	+	Missense_Mutation	G	A	novel	P47_T1	c.844G>A	p.Gly282Arg	119	112	7	45	45	0	protein_coding	YES	MODERATE	SNV
EXOC2	GRCh38	chr6	629846	629846	+	Missense_Mutation	A	C	novel	P47_T1	c.411T>G	p.Ile137Met	87	79	8	31	31	0	protein_coding	YES	MODERATE	SNV
CNKSR3	GRCh38	chr6	1.54E+08	1.54E+08	+	Missense_Mutation	G	T	novel	P47_T1	c.1057C>A	p.Pro353Thr	60	52	8	39	39	0	protein_coding	YES	MODERATE	SNV
PKD1	GRCh38	chr16	2089957	2089957	+	Nonsense_Mutation	G	A	rs199476095	P47_T1	c.12682C>T	p.Arg4228Ter	227	221	6	25	25	0	protein_coding	YES	HIGH	SNV
SLX4	GRCh38	chr16	3583109	3583109	+	Missense_Mutation	A	C	rs569861974	P47_T1	c.5141T>G	p.Leu1714Trp	109	96	12	25	25	0	protein_coding	YES	MODERATE	SNV
TP53	GRCh38	chr17	7674216	7674216	+	Missense_Mutation	C	A	rs28934571	P47_T1	c.747G>T	p.Arg249Ser	132	118	12	25	25	0	protein_coding	YES	MODERATE	SNV
TMIGD2	GRCh38	chr19	4294792	4294792	+	Missense_Mutation	C	T	rs764768421	P47_T1	c.431G>A	p.Arg144Gln	340	332	7	35	35	0	protein_coding	YES	MODERATE	SNV
PPP1R13L	GRCh38	chr19	45396259	45396259	+	Missense_Mutation	C	T	novel	P47_T1	c.812G>A	p.Arg271His	193	180	12	21	21	0	protein_coding	YES	MODERATE	SNV
ZNF616	GRCh38	chr19	52115449	52115449	+	Missense_Mutation	C	G	rs150574210	P47_T1	c.1715G>C	p.Ser572Thr	113	108	5	64	64	0	protein_coding	YES	MODERATE	SNV
NAXE	GRCh38	chr1	1.57E+08	1.57E+08	+	Missense_Mutation	C	T	novel	P48_T1	c.644C>T	p.Ala215Val	333	324	8	60	59	0	protein_coding	YES	MODERATE	SNV
HMCN1	GRCh38	chr1	1.86E+08	1.86E+08	+	Missense_Mutation	A	T	novel	P48_T1	c.7219A>T	p.Thr2407Ser	289	227	62	48	48	0	protein_coding	YES	MODERATE	SNV
HGFAC	GRCh38	chr4	3447524	3447524	+	Missense_Mutation	G	A	rs894948926	P48_T1	c.1409G>A	p.Gly470Asp	69	45	24	22	22	0	protein_coding	YES	MODERATE	SNV
DNAH5	GRCh38	chr5	13814742	13814742	+	Missense_Mutation	C	T	novel	P48_T1	c.7093G>A	p.Asp2365Asn	287	141	123	44	41	0	protein_coding	YES	MODERATE	SNV
MROH2B	GRCh38	chr5	41049288	41049288	+	Missense_Mutation	G	A	rs750126047	P48_T1	c.1493C>T	p.Thr498Ile	316	287	28	48	48	0	protein_coding	YES	MODERATE	SNV
SPATS1	GRCh38	chr6	44376370	44376370	+	Missense_Mutation	G	T	novel	P48_T1	c.771G>T	p.Trp257Cys	108	102	5	26	26	0	protein_coding	YES	MODERATE	SNV
ZC3HC1	GRCh38	chr7	1.3E+08	1.3E+08	+	Missense_Mutation	T	G	novel	P48_T1	c.938A>C	p.Glu313Ala	193	81	112	69	69	0	protein_coding	YES	MODERATE	SNV
FAM214B	GRCh38	chr9	35106551	35106551	+	Missense_Mutation	A	G		P48_T1	c.1046T>C	p.Leu349Pro	99	74	24	47	47	0	protein_coding	YES	MODERATE	SNV
CCDC62	GRCh38	chr12	1.23E+08	1.23E+08	+	Missense_Mutation	A	T	novel	P48_T1	c.1335A>T	p.Glu445Asp	157	104	51	62	62	0	protein_coding	YES	MODERATE	SNV
RABEP2	GRCh38	chr16	28919881	28919881	+	Missense_Mutation	G	C	novel	P48_T1	c.337C>G	p.Gln113Glu	100	95	5	29	28	0	protein_coding	YES	MODERATE	SNV
MYOM1	GRCh38	chr18	3188951	3188951	+	Missense_Mutation	T	A	rs201810917	P48_T1	c.568A>T	p.Thr190Ser	429	387	11	132	132	0	protein_coding	YES	MODERATE	SNV
PTPRM	GRCh38	chr18	7888361	7888361	+	Missense_Mutation	G	T	novel	P48_T1	c.452G>T	p.Trp151Leu	205	150	53	34	34	0	protein_coding	YES	MODERATE	SNV
C3	GRCh38	chr19	6694622	6694645	+	Splice_Site	GCCACTGGGGTCCCTGCAGCAGGT	-	novel	P48_T1	c.2951-11_2963del		112	33	23	32	21	0	protein_coding	YES	HIGH	deletion
SGK2	GRCh38	chr20	43572075	43572075	+	Missense_Mutation	G	T	novel	P48_T1	c.715G>T	p.Gly239Cys	107	102	5	29	29	0	protein_coding	YES	MODERATE	SNV
ZYG11B	GRCh38	chr1	52821453	52821453	+	Missense_Mutation	A	T	novel	P49_T1	c.2059A>T	p.Ser687Cys	268	122	130	90	87	0	protein_coding	YES	MODERATE	SNV
TPR	GRCh38	chr1	1.86E+08	1.86E+08	+	Missense_Mutation	T	A		P49_T1	c.5651A>T	p.Gln1884Leu	233	89	140	78	78	0	protein_coding	YES	MODERATE	SNV
OBSCN	GRCh38	chr1	2.28E+08	2.28E+08	+	Missense_Mutation	G	T	novel	P49_T1	c.18703G>T	p.Ala6235Ser	87	50	37	69	68	0	protein_coding	YES	MODERATE	SNV
ALPI	GRCh38	chr2	2.32E+08	2.32E+08	+	Missense_Mutation	C	T	novel	P49_T1	c.1175C>T	p.Ser392Phe	124	74	48	104	104	0	protein_coding	YES	MODERATE	SNV
ZNF518B	GRCh38	chr4	10445025	10445025	+	Missense_Mutation	A	G		P49_T1	c.1304T>C	p.Val435Ala	233	226	5	90	89	0	protein_coding	YES	MODERATE	SNV
BOD1L1	GRCh38	chr4	13604976	13604976	+	Missense_Mutation	C	T	rs151278291	P49_T1	c.1924G>A	p.Asp642Asn	321	309	7	132	131	0	protein_coding	YES	MODERATE	SNV
PLEKHG4B	GRCh38	chr5	171408	171408	+	Missense_Mutation	T	A	rs770771633	P49_T1	c.4014T>A	p.Asn1338Lys	171	101	70	80	80	0	protein_coding	YES	MODERATE	SNV
PLEKHG4B	GRCh38	chr5	171409	171409	+	Missense_Mutation	G	C	novel	P49_T1	c.4015G>C	p.Asp1339His	166	97	69	79	79	0	protein_coding	YES	MODERATE	SNV
EXOC3	GRCh38	chr5	453882	453882	+	Missense_Mutation	G	T	novel	P49_T1	c.877G>T	p.Ala293Ser	225	135	88	98	98	0	protein_coding	YES	MODERATE	SNV
SEMA5A	GRCh38	chr5	9190293	9190293	+	Missense_Mutation	A	G	rs368139926	P49_T1	c.1247T>C	p.Leu416Pro	291	280	6	78	78	0	protein_coding	YES	MODERATE	SNV
NNT	GRCh38	chr5	43650500	43650500	+	Missense_Mutation	G	A	rs751998630	P49_T1	c.1630G>A	p.Ala544Thr	285	277	5	78	78	0	protein_coding	YES	MODERATE	SNV
FAM71B	GRCh38	chr5	1.57E+08	1.57E+08	+	Missense_Mutation	A	C	rs781591264	P49_T1	c.1236T>G	p.Asp412Glu	222	214	7	145	144	0	protein_coding	YES	MODERATE	SNV
ZBTB24	GRCh38	chr6	1.09E+08	1.09E+08	+	Missense_Mutation	G	T	rs1245691443	P49_T1	c.31C>A	p.Gln11Lys	197	188	5	69	69	0	protein_coding	YES	MODERATE	SNV
TRRAP	GRCh38	chr7	98983408	98983408	+	Missense_Mutation	G	A	rs1336161275	P49_T1	c.8950G>A	p.Asp2984Asn	207	198	8	96	96	0	protein_coding	YES	MODERATE	SNV
GIGYF1	GRCh38	chr7	1.01E+08	1.01E+08	+	Missense_Mutation	G	A	rs532695822	P49_T1	c.1742C>T	p.Pro581Leu	124	83	21	71	67	0	protein_coding	YES	MODERATE	SNV
DOCK8	GRCh38	chr9	428480	428480	+	Missense_Mutation	G	A	rs775382639	P49_T1	c.4457G>A	p.Arg1486His	176	168	7	100	99	0	protein_coding	YES	MODERATE	SNV
DENND4C	GRCh38	chr9	19346849	19346849	+	Missense_Mutation	G	T	rs560679541	P49_T1	c.4080G>T	p.Lys1360Asn	341	328	10	144	144	0	protein_coding	YES	MODERATE	SNV
CDKN2A	GRCh38	chr9	21971157	21971157	+	Missense_Mutation	C	T		P49_T1	c.202G>A	p.Ala68Thr	205	196	7	129	129	0	protein_coding	YES	MODERATE	SNV
NFX1	GRCh38	chr9	33307295	33307295	+	Missense_Mutation	A	T	novel	P49_T1	c.1372A>T	p.Asn458Tyr	145	45	98	69	69	0	protein_coding	YES	MODERATE	SNV
OR2S2	GRCh38	chr9	35957343	35957343	+	Missense_Mutation	G	C	novel	P49_T1	c.756C>G	p.Phe252Leu	126	120	6	84	84	0	protein_coding	YES	MODERATE	SNV

Table S2 (*continued*)

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Table S2 (*continued*)

Hugo_Symbol	NCBI_Build	Chromosome	Start_Position	End_Position	Strand	Variant_Classification	Reference_Allele	Tumor_Seq_Allele2	dbSNP_RS	Tumor_Sample_Barcode	HGVSc	HGVSp	t_depth	t_ref_count	t_alt_count	n_depth	n_ref_count	n_alt_count	BIOTYPE	CANONICAL	IMPACT	VARIANT_CLASS
OR2S2	GRCh38	chr9	35957457	35957457	+	Missense_Mutation	G	C	novel	P49_T1	c.642C>G	p.Phe214Leu	117	110	5	77	77	0	protein_coding	YES	MODERATE	SNV
OR2S2	GRCh38	chr9	35957877	35957877	+	Missense_Mutation	G	C	novel	P49_T1	c.222C>G	p.Phe74Leu	147	140	5	87	86	0	protein_coding	YES	MODERATE	SNV
OR2S2	GRCh38	chr9	35957930	35957930	+	Missense_Mutation	G	A	rs1194862600	P49_T1	c.169C>T	p.His57Tyr	132	124	8	85	85	0	protein_coding	YES	MODERATE	SNV
OR2S2	GRCh38	chr9	35957991	35957991	+	Nonsense_Mutation	G	C	rs144882847	P49_T1	c.108C>G	p.Tyr36Ter	168	162	6	95	94	1	protein_coding	YES	HIGH	SNV
DIP2C	GRCh38	chr10	327110	327110	+	Missense_Mutation	C	T	rs780701624	P49_T1	c.3820G>A	p.Ala1274Thr	324	315	5	115	112	0	protein_coding	YES	MODERATE	SNV
CRACR2B	GRCh38	chr11	830110	830110	+	Missense_Mutation	G	T	rs557608054	P49_T1	c.583G>T	p.Gly195Cys	123	117	6	78	78	0	protein_coding	YES	MODERATE	SNV
PDHX	GRCh38	chr11	34916702	34916702	+	Missense_Mutation	A	C	rs118136428	P49_T1	c.47A>C	p.Tyr16Ser	141	133	6	89	88	0	protein_coding	YES	MODERATE	SNV
PAFAH1B2	GRCh38	chr11	1.17E+08	1.17E+08	+	Missense_Mutation	C	T	rs757287568	P49_T1	c.554C>T	p.Ala185Val	174	167	7	77	76	0	protein_coding	YES	MODERATE	SNV
KCNJ1	GRCh38	chr11	1.29E+08	1.29E+08	+	Missense_Mutation	A	T	novel	P49_T1	c.692T>A	p.Leu231Gln	178	141	34	84	84	0	protein_coding	YES	MODERATE	SNV
MYO1A	GRCh38	chr12	57038921	57038921	+	Missense_Mutation	T	A		P49_T1	c.1421A>T	p.Gln474Leu	221	101	118	74	73	0	protein_coding	YES	MODERATE	SNV
NDN	GRCh38	chr15	23687132	23687132	+	Nonsense_Mutation	G	T		P49_T1	c.86C>A	p.Ser29Ter	240	231	7	143	141	0	protein_coding	YES	HIGH	SNV
UBE2O	GRCh38	chr17	76399587	76399587	+	Missense_Mutation	G	T		P49_T1	c.1490C>A	p.Ser497Tyr	146	140	6	93	93	0	protein_coding	YES	MODERATE	SNV
L3MBTL4	GRCh38	chr18	6243399	6243399	+	Missense_Mutation	C	T	rs202225584	P49_T1	c.355G>A	p.Asp119Asn	250	242	7	88	86	0	protein_coding	YES	MODERATE	SNV
CEP76	GRCh38	chr18	12699071	12699071	+	Missense_Mutation	C	T	rs202117013	P49_T1	c.428G>A	p.Arg143Gln	320	312	7	77	77	0	protein_coding	YES	MODERATE	SNV
ARID3A	GRCh38	chr19	964859	964859	+	Missense_Mutation	A	T	novel	P49_T1	c.977A>T	p.Glu326Val	89	35	53	57	57	0	protein_coding	YES	MODERATE	SNV
ATP5F1D	GRCh38	chr19	1244417	1244417	+	Missense_Mutation	C	A	rs865966395	P49_T1	c.487C>A	p.Leu163Met	116	109	6	95	95	0	protein_coding	YES	MODERATE	SNV
DUS3L	GRCh38	chr19	5790316	5790316	+	Nonsense_Mutation	G	A	novel	P49_T1	c.118C>T	p.Gln40Ter	121	115	6	50	49	0	protein_coding	YES	HIGH	SNV
TMEM205	GRCh38	chr19	11342865	11342865	+	Missense_Mutation	T	C	novel	P49_T1	c.520A>G	p.Ser174Gly	112	105	6	78	78	0	protein_coding	YES	MODERATE	SNV
PSMC4	GRCh38	chr19	39972540	39972540	+	Missense_Mutation	G	A	novel	P49_T1	c.307G>A	p.Val103Met	140	132	6	67	67	0	protein_coding	YES	MODERATE	SNV
SNX21	GRCh38	chr20	45841242	45841242	+	Nonsense_Mutation	C	T	novel	P49_T1	c.1051C>T	p.Gln351Ter	226	201	7	118	109	0	protein_coding	YES	HIGH	SNV
TAF1	GRCh38	chrX	71401711	71401711	+	Missense_Mutation	A	T	novel	P49_T1	c.4030A>T	p.Ile1344Phe	175	40	134	50	50	0	protein_coding	YES	MODERATE	SNV
CTNNB1	GRCh38	chr3	41224612	41224612	+	Missense_Mutation	G	A	rs121913399	P5_T1	c.100G>A	p.Gly34Arg	323	236	87	195	195	0	protein_coding	YES	MODERATE	SNV
TIPARP	GRCh38	chr3	1.57E+08	1.57E+08	+	Missense_Mutation	C	T	novel	P5_T1	c.380C>T	p.Ser127Phe	407	282	125	225	225	0	protein_coding	YES	MODERATE	SNV
PHOX2B	GRCh38	chr4	41745994	41746011	+	In_Frame_Del	GCCGCCGCCGCTGCCGCG	-	rs771383153	P5_T1	c.741_758del	p.Ala255_Ala260del	41	38	3	31	31	0	protein_coding	YES	MODERATE	deletion
ROS1	GRCh38	chr6	1.17E+08	1.17E+08	+	Missense_Mutation	C	G	novel	P5_T1	c.5854G>C	p.Gly1952Arg	301	116	185	264	264	0	protein_coding	YES	MODERATE	SNV
QKI	GRCh38	chr6	1.64E+08	1.64E+08	+	Missense_Mutation	G	T	novel	P5_T1	c.964G>T	p.Asp322Tyr	329	129	200	181	180	1	protein_coding	YES	MODERATE	SNV
EPHB4	GRCh38	chr7	1.01E+08	1.01E+08	+	Missense_Mutation	C	A	rs759227832	P5_T1	c.950G>T	p.Gly317Val	287	155	132	71	71	0	protein_coding	YES	MODERATE	SNV
BIVM-ERCC5	GRCh38	chr13	1.03E+08	1.03E+08	+	Missense_Mutation	T	G	novel	P5_T1	c.3835T>G	p.Phe1279Val	452	330	122	108	108	0	protein_coding	YES	MODERATE	SNV
TRAF7	GRCh38	chr16	2172259	2172259	+	Missense_Mutation	G	C	novel	P5_T1	c.544G>C	p.Gly182Arg	331	300	31	53	53	0	protein_coding	YES	MODERATE	SNV
TP53	GRCh38	chr17	7675206	7675206	+	Frame_Shift_Del	G	-		P5_T1	c.406del	p.Gln136AsnfsTer34	247	60	187	89	89	0	protein_coding	YES	HIGH	deletion
KEAP1	GRCh38	chr19	10499694	10499694	+	Missense_Mutation	C	T		P5_T1	c.340G>A	p.Gly114Arg	314	72	242	93	93	0	protein_coding	YES	MODERATE	SNV
KMT2B	GRCh38	chr19	35727506	35727506	+	Missense_Mutation	G	A	novel	P5_T1	c.4186G>A	p.Ala1396Thr	262	54	208	19	19	0	protein_coding	YES	MODERATE	SNV
SRRM1	GRCh38	chr1	24645985	24645985	+	Missense_Mutation	G	A		P50_T1	c.23G>A	p.Gly8Glu	270	254	15	80	79	0	protein_coding	YES	MODERATE	SNV
PRRC2C	GRCh38	chr1	1.72E+08	1.72E+08	+	Missense_Mutation	A	T	novel	P50_T1	c.2930A>T	p.Glu977Val	213	205	7	129	128	0	protein_coding	YES	MODERATE	SNV
LGR6	GRCh38	chr1	2.02E+08	2.02E+08	+	Missense_Mutation	A	G	rs376357186	P50_T1	c.515A>G	p.Asn172Ser	126	120	5	67	67	0	protein_coding	YES	MODERATE	SNV
CNTN2	GRCh38	chr1	2.05E+08	2.05E+08	+	Nonsense_Mutation	C	T	novel	P50_T1	c.124C>T	p.Gln42Ter	175	169	6	73	72	0	protein_coding	YES	HIGH	SNV
TAF5L	GRCh38	chr1	2.3E+08	2.3E+08	+	Missense_Mutation	C	T	rs55655740	P50_T1	c.721G>A	p.Val241Ile	287	275	9	158	156	1	protein_coding	YES	MODERATE	SNV
XPC	GRCh38	chr3	14158112	14158112	+	Missense_Mutation	T	A	rs751819500	P50_T1	c.1771A>T	p.Thr591Ser	329	321	8	149	148	0	protein_coding	YES	MODERATE	SNV
TTC21A	GRCh38	chr3	39133205	39133205	+	Missense_Mutation	A	G	rs199602060	P50_T1	c.2737A>G	p.Lys913Glu	170	165	5	70	70	0	protein_coding	YES	MODERATE	SNV
USP4	GRCh38	chr3	49335472	49335472	+	Missense_Mutation	A	G	novel	P50_T1	c.226T>C	p.Ser76Pro	294	274	16	82	81	0	protein_coding	YES	MODERATE	SNV
YEATS2	GRCh38	chr3	1.84E+08	1.84E+08	+	Missense_Mutation	T	C	rs759145989	P50_T1	c.2165T>C	p.Val722Ala	237	229	5	120	117	0	protein_coding	YES	MODERATE	SNV
SLAIN2	GRCh38	chr4	48422058	48422058	+	Nonsense_Mutation	G	A		P50_T1	c.1727G>A	p.Trp576Ter	179	173	6	84	83	0	protein_coding	YES	HIGH	SNV
SDHA	GRCh38	chr5	226048	226048	+	Splice_Site	G	A	novel	P50_T1	c.621+1G>A		154	148	5	86	85	0	protein_coding	YES	HIGH	SNV
ICE1	GRCh38	chr5	5462500	5462500	+	Missense_Mutation	C	T	rs751117948	P50_T1	c.3166C>T	p.Pro1056Ser	152	141	10	111	110	0	protein_coding	YES	MODERATE	SNV
TRIO	GRCh38	chr5	14389321	14389321	+	Missense_Mutation	A	T	novel	P50_T1	c.3981A>T	p.Glu1327Asp	217	208	6	80	80	0	protein_coding	YES	MODERATE	SNV
TRIO	GRCh38	chr5	14507220	14507220	+	Missense_Mutation	G	A	rs182365882	P50_T1	c.8711G>A	p.Arg2904Gln	183	169	13	102	99	0	protein_coding	YES	MODERATE	SNV
PDZD2	GRCh38	chr5	32087307	32087307	+	Missense_Mutation	G	A	rs755562193	P50_T1	c.3859G>A	p.Glu1287Lys	145	122	7	84	80	0	protein_coding	YES	MODERATE	SNV
SPEF2	GRCh38	chr5	35806787	35806787	+	Missense_Mutation	A	T	novel	P50_T1	c.5091A>T	p.Lys1697Asn	340	322	16	127	125	0	protein_coding	YES	MODERATE	SNV
HMGCS1	GRCh38	chr5	43291166	43291166	+	Missense_Mutation	G	T	rs754716585	P50_T1	c.1528C>A	p.Pro510Thr	175	165	6	23	23	0	protein_coding	YES	MODERATE	SNV
EXOC2	GRCh38	chr6	576850	576850	+	Missense_Mutation	G	A	novel	P50_T1	c.1225C>T	p.Leu409Phe	212	205	6	102	102	0	protein_coding	YES	MODERATE	SNV
SLC17A1	GRCh38	chr6	25811758	25811758	+	Missense_Mutation	A	G	novel	P50_T1	c.910T>C	p.Ser304Pro	293	286	6	115	113	0	protein_coding	YES	MODERATE	SNV
PPP1R17	GRCh38	chr7	31695547	31695547	+	Missense_Mutation	T	A	novel	P50_T1	c.161T>A	p.Leu54Gln	167	160	6	102	99	0	protein_coding	YES	MODERATE	SNV
ZAN	GRCh38	chr7	1.01E+08	1.01E+08	+	Missense_Mutation	A	G	rs78193191	P50_T1	c.5765A>G	p.His1922Arg	228	189	13	70	65	0	protein_coding	YES	MODERATE	SNV
ADCK5	GRCh38	chr8	1.44E+08	1.44E+08	+	In_Frame_Ins	-	GGGGGTGCAAGGTGA	rs148509143	P50_T1	c.1260_1267+7dup		164	74	12	80	59	0	protein_coding	YES	MODERATE	insertion
DMRT1	GRCh38	chr9	841965	841965	+	Missense_Mutation	A	T	novel	P50_T1	c.127A>T	p.Ser43Cys	94	89	5	69	67	0	protein_coding	YES	MODERATE	SNV
TPD52L3	GRCh38	chr9	6328768	6328768	+	Missense_Mutation	G	C	novel	P50_T1	c.173G>C	p.Gly58Ala	246	233	10	140	137	0	protein_coding	YES	MODERATE	SNV
FREM1	GRCh38	chr9	14792751	14792751	+	Nonsense_Mutation	G	A	novel	P50_T1	c.3973C>T	p.Gln1325Ter	98	92	6	58	57	0	protein_coding	YES	HIGH	SNV
PSIP1	GRCh38	chr9	15474124	15474124	+	Missense_Mutation	G	A	rs188943134	P50_T1	c.743C>T	p.Pro248Leu	334	324	8	163	156	0	protein_coding	YES	MODERATE	SNV
KLHL9	GRCh38	chr9	21333466	21333466	+	Missense_Mutation	C	T	rs191333137	P50_T1	c.1394G>A	p.Cys465Tyr	248	241	6	155	153	0	protein_coding	YES	MODERATE	SNV
DMRTA1	GRCh38	chr9	22451796	22451796	+	Missense_Mutation	G	A	rs148090498	P50_T1	c.1400G>A	p.Arg467Gln	402	388	12	162	162	0	protein_coding	YES	MODERATE	SNV
TMEM215	GRCh38	chr9	32784718	32784718	+	Missense_Mutation	G	A	rs1204273965	P50_T1	c.535G>A	p.Val179Ile	115	106	7	112	110	0	protein_coding	YES	MODERATE	SNV
UBAP1	GRCh38	chr9	34179202	34179202	+	Missense_Mutation	C	T	rs1196295221	P50_T1	c.188C>T	p.Thr63Ile	220	210	6	77	77	0	protein_coding	YES	MODERATE	SNV
MYORG	GRCh38	chr9	34372875	34372875	+	Nonsense_Mutation	G	C	rs4879782	P50_T1	c.69C>G	p.Tyr23Ter	221	208	8	71	71	0	protein_coding	YES	HIGH	SNV
MELK	GRCh38	chr9	36599466	36599466	+	Nonsense_Mutation	A	T	novel	P50_T1	c.547A>T	p.Lys183Ter	145	137	8	63	61	0	protein_coding	YES	HIGH	SNV
SPATA31A1	GRCh38	chr9	39359837	39359837	+	Missense_Mutation	G	A	rs1289947663	P50_T1	c.2072G>A	p.Arg691Gln	127	107	19	262	258	0	protein_coding	YES	MODERATE	SNV
PRRC2B	GRCh38	chr9	1.31E+08	1.31E+08	+	Missense_Mutation	G	A	rs183123525	P50_T1	c.4333G>A	p.Val1445Ile	136	129	6	47	47	0	protein_coding	YES	MODERATE	SNV
INPP5E	GRCh38	chr9	1.36E+08	1.36E+08	+	Missense_Mutation	G	C	rs745450500	P50_T1	c.386C>G	p.Ser129Cys	166	159	6	59	59	0	protein_coding	YES	MODERATE	SNV
AGPAT2	GRCh38	chr9	1.37E+08	1.37E+08	+	Missense_Mutation	C	A	rs746809573	P50_T1	c.315G>T	p.Met105Ile	233	211	19	55	54	0	protein_coding	YES	MODERATE	SNV
DMBT1	GRCh38	chr10	1.23E+08	1.23E+08	+	Missense_Mutation	G	A	rs193149514	P50_T1	c.7118G>A	p.Arg2373His	182	174	6	96	94	0	protein_coding	YES	MODERATE	SNV
TMEM80	GRCh38	chr11	695803	695803	+	Missense_Mutation	C	G	rs1045405533	P50_T1	c.195C>G	p.Asp65Glu	249	231	17	58	58	0	protein_coding	YES	MODERATE	SNV
CRACR2B	GRCh38	chr11	831572	831572	+	Missense_Mutation	T	A	rs530911961	P50_T1	c.1063T>A	p.Cys355Ser	300	286	13	57	57	0	protein_coding	YES	MODERATE	SNV
DNHD1	GRCh38	chr11	6498396	6498396	+	Missense_Mutation	C	A	novel	P50_T1	c.181C>A	p.Leu61Met	239	232	6	112	111	0	protein_coding	YES	MODERATE	SNV
DCHS1	GRCh38	chr11	6640157	6640157	+	Missense_Mutation	G	A	rs147698268	P50_T1	c.1457C>T	p.Ala486Val	276	267	6	91	90	0	protein_coding	YES	MODERATE	SNV
DDB1	GRCh38	chr11	61313524	61313524	+	Missense_Mutation	G	A	novel	P50_T1	c.2044C>T	p.Leu682Phe	171	164	6	101	100	1	protein_coding	YES	MODERATE	SNV
AHNAK	GRCh38	chr11	62529201	62529201	+	Missense_Mutation	G	A	rs774112416	P50_T1	c.5216C>T	p.Ala1739Val	258	245	10	153	150	0	protein_coding	YES	MODERATE	SNV
RIN1	GRCh38	chr11	66332407	66332407	+	Missense_Mutation	C	T	novel	P50_T1	c.2221G>A	p.Val741Ile	162	154	5	70	68	0	protein_coding	YES	MODERATE	SNV
MYH7	GRCh38	chr14	23417183	23417183	+	Missense_Mutation	T	C	novel	P50_T1	c.4489A>G	p.Thr1497Ala	124	118	5	96	96	0	protein_coding	YES	MODERATE	SNV
SYNDIG1L	GRCh38	chr14	74407606	74407606	+	Missense_Mutation	C	A	rs541607278	P50_T1	c.646G>T	p.Val216Leu	188	175	12	89	89	0	protein_coding	YES	MODERATE	SNV
SPTBN5	GRCh38	chr15	41863931	41863931	+	Missense_Mutation	G	A	rs186967701	P50_T1	c.7012C>T	p.Arg2338Trp	116	110	6	45	45	0	protein_coding	YES	MODERATE	SNV
TELO2	GRCh38	chr16	1497103	1497103	+	Missense_Mutation	G	C	rs139365746	P50_T1	c.681G>C	p.Gln227His	128	120	7	35	35	0	protein_coding	YES	MODERATE	SNV
MEFV	GRCh38	chr16	3254652	3254652	+	Missense_Mutation	G	T	rs575678784	P50_T1	c.416C>A	p.Ala139Asp	108	102	5	77	76	0	protein_coding	YES	MODERATE	SNV
SETD1A	GRCh38	chr16	30964788	30964788	+	Missense_Mutation	C	T	rs746239302	P50_T1	c.1046C>T	p.Ser349Leu	142	133	7	65	65	0	protein_coding	YES	MODERATE	SNV
ENOSF1	GRCh38	chr18	677370	677370	+	Missense_Mutation	A	C		P50_T1	c.1123T>G	p.Ser375Ala	130	125	5	64	63	1	protein_coding	YES	MODERATE	SNV
TXNDC2	GRCh38	chr18	9887859	9887859	+	Missense_Mutation	G	C	rs750926186	P50_T1	c.1380G>C	p.Glu460Asp	229	216	11	159	157	0	protein_coding	YES	MODERATE	SNV
CBARP	GRCh38	chr19	1230955	1230955	+	Missense_Mutation	C	T	rs778716668	P50_T1	c.1300G>A	p.Gly434Arg	183	159	14	40	37	0	protein_coding	YES	MODERATE	SNV
PWWP3A	GRCh38	chr19	1360907	1360907	+	Missense_Mutation	C	T	rs1451800136	P50_T1	c.989C>T	p.Pro330Leu	290	281	8	80	78	0	protein_coding	YES	MODERATE	SNV
LMNB2	GRCh38	chr19	2434880	2434880	+	Missense_Mutation	C	T	rs776112679	P50_T1	c.889G>A	p.Asp297Asn	144	135	8	50	49	0	protein_coding	YES	MODERATE	SNV
ANKRD24	GRCh38	chr19	4219684	4219684	+	Missense_Mutation	G	A	rs546339422	P50_T1	c.3097G>A	p.Glu1033Lys	213	201	10	84	83	0	protein_coding	YES	MODERATE	SNV
C3	GRCh38	chr19	6694601	6694601	+	Missense_Mutation	A	C	novel	P50_T1	c.2984T>G	p.Val995Gly	390	366	18	46	46	0	protein_coding	YES	MODERATE	SNV
CC2D1A	GRCh38	chr19	13919860	13919860	+	Missense_Mutation	A	T	novel	P50_T1	c.1265A>T	p.Gln422Leu	200	189	9	47	47	0	protein_coding	YES	MODERATE	SNV
DHX34	GRCh38	chr19	47353506	47353506	+	Missense_Mutation	G	A	rs116000939	P50_T1	c.476G>A	p.Arg159Gln	264	251	11	99	98	0	protein_coding	YES	MODERATE	SNV
SIGLEC6	GRCh38	chr19	51530858	51530858	+	Missense_Mutation	G	A	rs200369206	P50_T1	c.529C>T	p.Pro177Ser	121	113	7	98	94	0	protein_coding	YES	MODERATE	SNV
ZNF211	GRCh38	chr19	57642071	57642071	+	Nonsense_Mutation	A	T	novel	P50_T1	c.1780A>T	p.Arg594Ter	236	222	13	182	180	0	protein_coding	YES	HIGH	SNV
NCOA3	GRCh38	chr20	47639723	47639723	+	Missense_Mutation	C	G	novel	P50_T1	c.2854C>G	p.Pro952Ala	220	212	7	125	125	0	protein_coding	YES	MODERATE	SNV
LRP1B	GRCh38	chr2	1.41E+08	1.41E+08	+	Missense_Mutation	T	C	novel	P6_T1	c.7868A>G	p.Lys2623Arg	461	455	6	130	130	0	protein_coding	YES	MODERATE	SNV
IL7R	GRCh38	chr5	35873498	35873498	+	Missense_Mutation	A	G	novel	P6_T1	c.556A>G	p.Thr186Ala	227	173	54	60	60	0	protein_coding	YES	MODERATE	SNV
RICTOR	GRCh38	chr5	38953068	38953068	+	Nonsense_Mutation	C	T	novel	P6_T1	c.2814G>A	p.Trp938Ter	631	483	148	154	154	0	protein_coding	YES	HIGH	SNV
KMT2D	GRCh38	chr12	49049869	49049869	+	Missense_Mutation	A	C	novel	P6_T1	c.3719T>G	p.Met1240Arg	147	144	3	53	53	0	protein_coding	YES	MODERATE	SNV
PIK3CD	GRCh38	chr1	9721979	9721979	+	Missense_Mutation	A	G		P7_T1	c.2060A>G	p.Glu687Gly	516	510	6	21	21	0	protein_coding	YES	MODERATE	SNV
CDC73	GRCh38	chr1	1.93E+08	1.93E+08	+	Missense_Mutation	G	T	novel	P7_T1	c.1355G>T	p.Trp452Leu	347	255	92	30	30	0	protein_coding	YES	MODERATE	SNV
MSH2	GRCh38	chr2	47403349	47403349	+	Missense_Mutation	C	T	rs1456393710	P7_T1	c.158C>T	p.Ala53Val	279	275	4	22	22	0	protein_coding	YES	MODERATE	SNV
ATR	GRCh38	chr3	1.43E+08	1.43E+08	+	Missense_Mutation	A	T	novel	P7_T1	c.4410T>A	p.Asp1470Glu	267	263	4	60	60	0	protein_coding	YES	MODERATE	SNV
RICTOR	GRCh38	chr5	39002634	39002634	+	Missense_Mutation	T	C	novel	P7_T1	c.293A>G	p.Glu98Gly	227	223	4	43	43	0	protein_coding	YES	MODERATE	SNV
INHBA	GRCh38	chr7	41689954	41689954	+	Frame_Shift_Del	A	-	novel	P7_T1	c.977del	p.Phe326SerfsTer33	351	302	49	36	36	0	protein_coding	YES	HIGH	deletion
SMO	GRCh38	chr7	1.29E+08	1.29E+08	+	Missense_Mutation	G	T	novel	P7_T1	c.454G>T	p.Gly152Cys	187	183	4	18	18	0	protein_coding	YES	MODERATE	SNV
RAD21	GRCh38	chr8	1.17E+08	1.17E+08	+	Missense_Mutation	C	T	rs780692465	P7_T1	c.1757G>A	p.Arg586Gln	727	695	32	89	89	0	protein_coding	YES	MODERATE	SNV
NOTCH1	GRCh38	chr9	1.36E+08	1.36E+08	+	Missense_Mutation	C	T	rs375073677	P7_T1	c.6457G>A	p.Val2153Met	290	286	4	19	19	0	protein_coding	YES	MODERATE	SNV
RET	GRCh38	chr10	43126724	43126724	+	Splice_Site	T	C	novel	P7_T1	c.3187+2T>C		529	477	52	45	45	0	protein_coding	YES	HIGH	SNV
ETV6	GRCh38	chr12	11869700	11869700	+	Missense_Mutation	C	T	rs144782370	P7_T1	c.740C>T	p.Ala247Val	290	285	5	22	22	0	protein_coding	YES	MODERATE	SNV
ARID2	GRCh38	chr12	45860807	45860807	+	Missense_Mutation	C	T	rs146219095	P7_T1	c.4780C>T	p.Pro1594Ser	349	345	4	60	60	0	protein_coding	YES	MODERATE	SNV
GLI1	GRCh38	chr12	57465131	57465131	+	Missense_Mutation	C	T	rs145283539	P7_T1	c.410C>T	p.Ala137Val	274	269	5	38	38	0	protein_coding	YES	MODERATE	SNV
BRCA2	GRCh38	chr13	32362644	32362644	+	Missense_Mutation	G	A	rs1566244896	P7_T1	c.7927G>A	p.Ala2643Thr	297	293	4	65	65	0	protein_coding	YES	MODERATE	SNV
NFKBIA	GRCh38	chr14	35404631	35404631	+	Missense_Mutation	G	A	novel	P7_T1	c.14C>T	p.Ala5Val	205	201	4	14	14	0	protein_coding	YES	MODERATE	SNV
MAP2K1	GRCh38	chr15	66485009	66485009	+	Missense_Mutation	C	T	novel	P7_T1	c.713C>T	p.Thr238Ile	368	363	5	27	27	0	protein_coding	YES	MODERATE	SNV
TSC2	GRCh38	chr16	2062994	2062994	+	Missense_Mutation	C	T	rs397515261	P7_T1	c.1384C>T	p.Arg462Cys	268	264	4	14	14	0	protein_coding	YES	MODERATE	SNV
TP53	GRCh38	chr17	7674216	7674216	+	Missense_Mutation	C	A	rs28934571	P7_T1	c.747G>T	p.Arg249Ser	187	161	26	30	30	0	protein_coding	YES	MODERATE	SNV
NF1	GRCh38	chr17	31349236	31349236	+	Missense_Mutation	G	T		P7_T1	c.7306G>T	p.Val2436Leu	440	414	26	57	57	0	protein_coding	YES	MODERATE	SNV
SMARCA4	GRCh38	chr19	11030750	11030750	+	Missense_Mutation	C	T		P7_T1	c.3403C>T	p.Arg1135Trp	323	308	15	41	41	0	protein_coding	YES	MODERATE	SNV
CALR	GRCh38	chr19	12940279	12940279	+	Missense_Mutation	C	T	rs1451773406	P7_T1	c.529C>T	p.Arg177Trp	521	516	5	66	66	0	protein_coding	YES	MODERATE	SNV
CALR	GRCh38	chr19	12943621	12943621	+	Missense_Mutation	G	A	rs144233437	P7_T1	c.1045G>A	p.Val349Ile	306	302	4	52	52	0	protein_coding	YES	MODERATE	SNV
PIK3R2	GRCh38	chr19	18169106	18169106	+	Missense_Mutation	C	T	rs1480103403	P7_T1	c.1999C>T	p.His667Tyr	313	309	4	16	16	0	protein_coding	YES	MODERATE	SNV
UPF1	GRCh38	chr19	18850208	18850208	+	Missense_Mutation	G	A		P7_T1	c.595G>A	p.Ala199Thr	378	373	5	27	27	0	protein_coding	YES	MODERATE	SNV
UPF1	GRCh38	chr19	18853257	18853257	+	Missense_Mutation	C	T	novel	P7_T1	c.1096C>T	p.Arg366Trp	419	413	6	31	31	0	protein_coding	YES	MODERATE	SNV
KMT2B	GRCh38	chr19	35723995	35723999	+	Frame_Shift_Del	CCCCG	-	novel	P7_T1	c.3322_3326del	p.Pro1108ArgfsTer3	298	279	19	12	12	0	protein_coding	YES	HIGH	deletion

Table S2 (*continued*)

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Table S2 (*continued*)

Hugo_ Symbol	NCBI_Build	Chromosome	Start_Position	End_Position	Strand	Variant_Classification	Reference_Allele	Tumor_Seq_Allele2	dbSNP_RS	Tumor_Sample_ Barcode	HGVSc	HGVSp	t_depth	t_ref_count	t_alt_count	n_depth	n_ref_count	n_alt_count	BIOTYPE	CANONICAL	IMPACT	VARIANT_ CLASS
CD79A	GRCh38	chr19	41880940	41880940	+	Missense_Mutation	G	A	novel	P7_T1	c.641G>A	p.Gly214Asp	209	205	4	18	17	1	protein_coding	YES	MODERATE	SNV
STAG2	GRCh38	chrX	1.24E+08	1.24E+08	+	Missense_Mutation	C	T	rs1375196362	P7_T1	c.899C>T	p.Ala300Val	171	167	4	27	26	1	protein_coding	YES	MODERATE	SNV
BCORL1	GRCh38	chrX	1.3E+08	1.3E+08	+	Missense_Mutation	G	A	novel	P7_T1	c.3233G>A	p.Gly1078Asp	276	271	5	17	17	0	protein_coding	YES	MODERATE	SNV
ARID1A	GRCh38	chr1	26780655	26780656	+	Frame_Shift_Ins	-	TG	novel	P8_T1	c.6759_6760dup	p.Tyr2254CysfsTer14	951	382	569	19	19	0	protein_coding	YES	HIGH	insertion
ALK	GRCh38	chr2	29239753	29239753	+	Missense_Mutation	C	T	novel	P8_T1	c.2282G>A	p.Gly761Asp	1454	915	539	53	53	0	protein_coding	YES	MODERATE	SNV
TEKT4	GRCh38	chr2	94871614	94871614	+	Missense_Mutation	G	A	novel	P8_T1	c.35G>A	p.Cys12Tyr	382	376	6	16	16	0	protein_coding	YES	MODERATE	SNV
CTNNB1	GRCh38	chr3	41224609	41224609	+	Missense_Mutation	T	C	rs1057519886	P8_T1	c.97T>C	p.Ser33Pro	1499	874	625	44	44	0	protein_coding	YES	MODERATE	SNV
PLK2	GRCh38	chr5	58459774	58459782	+	In_Frame_Del	ATGGTGGTG	-	rs1561217633	P8_T1	c.178_186del	p.His60_His62del	782	520	262	10	10	0	protein_coding	YES	MODERATE	deletion
KMT2C	GRCh38	chr7	1.52E+08	1.52E+08	+	Missense_Mutation	A	G	rs761007667	P8_T1	c.2882T>C	p.Val961Ala	834	751	83	30	30	0	protein_coding	YES	MODERATE	SNV
TGFBR1	GRCh38	chr9	99137956	99137956	+	Nonsense_Mutation	G	A	rs201021249	P8_T1	c.684G>A	p.Trp228Ter	1853	1211	642	73	73	0	protein_coding	YES	HIGH	SNV
NF1	GRCh38	chr17	31343055	31343055	+	Missense_Mutation	A	T	novel	P8_T1	c.7109A>T	p.His2370Leu	1824	1128	696	62	62	0	protein_coding	YES	MODERATE	SNV
STAT5A	GRCh38	chr17	42301381	42301381	+	Frame_Shift_Del	C	-	rs759027671	P8_T1	c.1102del	p.Gln368ArgfsTer2	1573	1552	21	34	34	0	protein_coding	YES	HIGH	deletion
KEAP1	GRCh38	chr19	10489753	10489753	+	Missense_Mutation	C	A	novel	P8_T1	c.1426G>T	p.Gly476Trp	890	377	513	86	86	0	protein_coding	YES	MODERATE	SNV
CCNE1	GRCh38	chr19	29817491	29817491	+	Missense_Mutation	C	A	novel	P8_T1	c.412C>A	p.Pro138Thr	1934	1233	701	117	117	0	protein_coding	YES	MODERATE	SNV
MST1R	GRCh38	chr3	49902534	49902534	+	Missense_Mutation	C	T	novel	P9_T1	c.1076G>A	p.Gly359Asp	1191	938	253	90	90	0	protein_coding	YES	MODERATE	SNV
FOXL2	GRCh38	chr3	1.39E+08	1.39E+08	+	Frame_Shift_Del	GGGCTCGGCGGCGGCCCTTCTGGCTCC TTGACTGTGCGACCGGTCTCTGGGGCCA GCAGGGCCCCCGCCGCGTCCTC	-	novel	P9_T1	c.25_101del	p.Glu9ArgfsTer61	698	691	7	62	62	0	protein_coding	YES	HIGH	deletion
ARID1B	GRCh38	chr6	1.57E+08	1.57E+08	+	Missense_Mutation	C	G	rs797045270	P9_T1	c.1379C>G	p.Ala460Gly	372	363	9	17	17	0	protein_coding	YES	MODERATE	SNV
FGF4	GRCh38	chr11	69774909	69774909	+	Missense_Mutation	G	A	novel	P9_T1	c.176C>T	p.Pro59Leu	959	913	46	39	39	0	protein_coding	YES	MODERATE	SNV
TP53	GRCh38	chr17	7674216	7674216	+	Missense_Mutation	C	A	rs28934571	P9_T1	c.747G>T	p.Arg249Ser	580	427	153	84	84	0	protein_coding	YES	MODERATE	SNV
NOTCH3	GRCh38	chr19	15186963	15186963	+	Missense_Mutation	G	C		P9_T1	c.1866C>G	p.Asp622Glu	671	530	141	80	80	0	protein_coding	YES	MODERATE	SNV

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