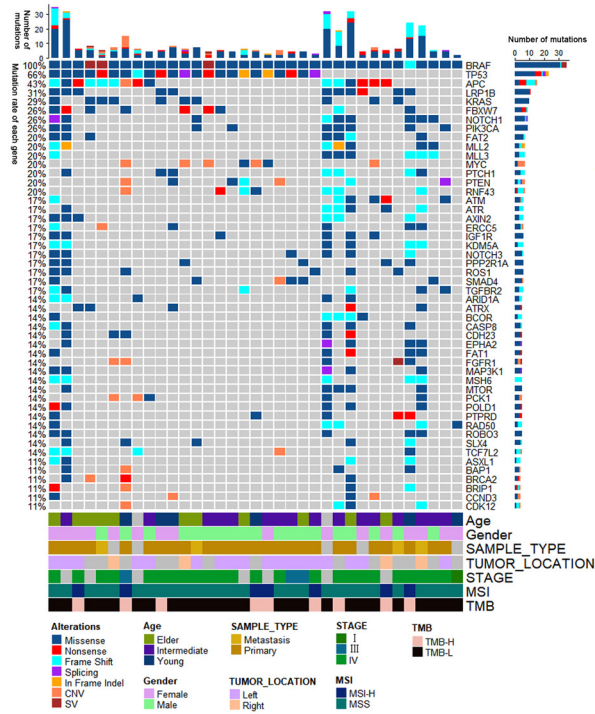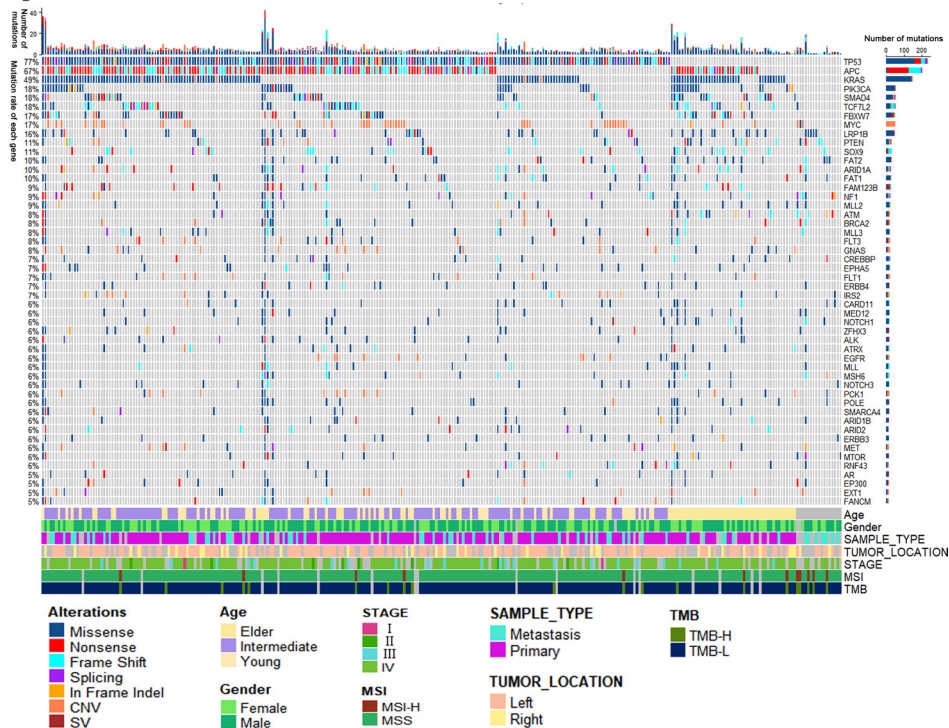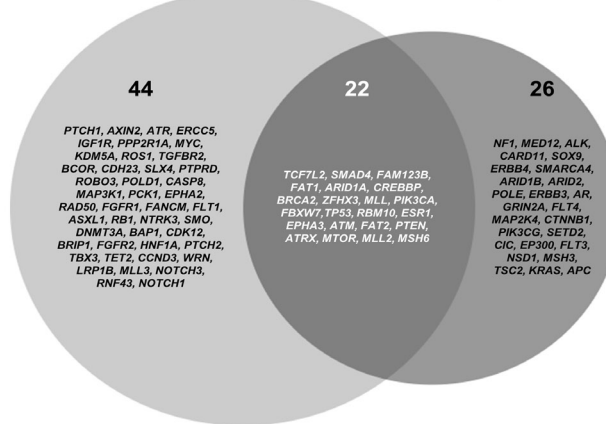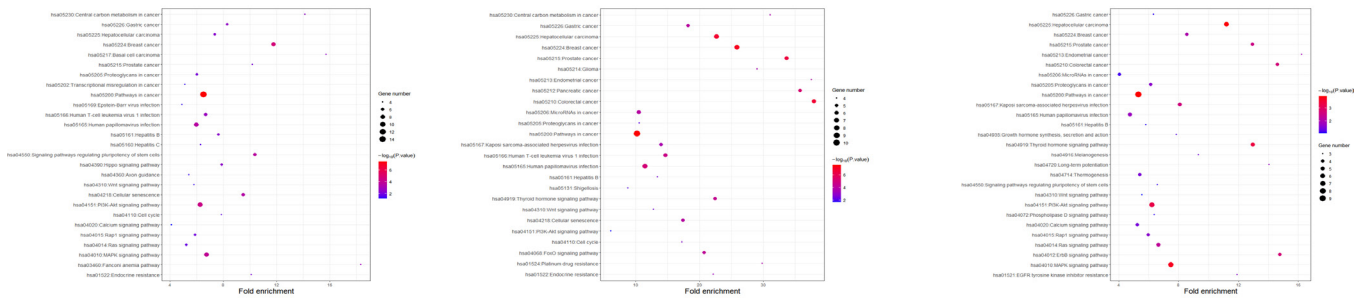Figure S1 Top 50 mutation spectrum of 339 patients in Chinese cohort (A, *BRAF*-mutated; B, *BRAF* wild-type). Each column represents a patient and each row represents a gene. Table on the left represents the mutation rate of each gene. Top plot represents the overall number of mutations a patient carried. Different colors denote different types of mutation. CNV, copy number variation; MSI, microsatellite instability; MSI-H, high MSI; MSS, microsatellite stability; TMB, tumor mutational burden; SV, structural variation.

Top mutations in BRAFmt

Top mutations in BRAFwt

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PTCH1, AXIN2, ATR, ERCC5, IGF1R, PPP2R1A, MYC, KDM5A, ROS1, TGFBR2, BCOR, CDH23, SLX4, PTPRD, ROBO3, POLD1, CASP8, MAP3K1, PCK1, EPHA2, RAD50, FGFR1, FANCM, FLT1, ASXL1, RB1, NTRK3, SMO, DNMT3A, BAP1, CDK12, BRIP1, FGFR2, HNF1A, PTCH2, TBX3, TET2, CCND3, WRN, LRP1B, MLL3, NOTCH3, RNF43, NOTCH1

22

TCF7L2, SMAD4, FAM123B, FAT1, ARID1A, CREBBP, BRCA2, ZFHX3, MLL, PIK3CA, FBXW7,TP53, RBM10, ESR1, EPHA3, ATM, FAT2, PTEN, ATRX, MTOR, MLL2, MSH6

26

NF1, MED12, ALK, CARD11, SOX9, ERBB4, SMARCA4, ARID1B, ARID2, POLE, ERBB3, AR, GRIN2A, FLT4, MAP2K4, CTNNB1, PIK3CG, SETD2, CIC, EP300, FLT3, NSD1, MSH3, TSC2, KRAS, APC
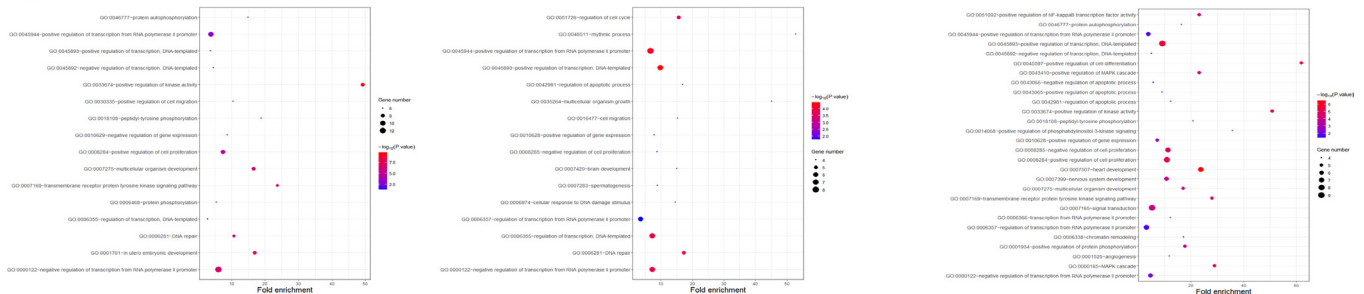
KEGG

GO

Figure S2 Unique and shared mutation analyses between *BRAF* mutations and *BRAF* wild-type to predict carcinogenicity. The Venn diagram shows the unique and shared mutations of *BRAF* mutations and *BRAF* wild-type in the Chinese cohort. GO and KEGG functional enrichment analyses of differentially unique and shared mutations. The left side shows the *BRAF*-mutated unique mutations; the middle shows the shared mutations between *BRAF* mutations and *BRAF* wild-type; the right side shows the *BRAF* wild-type unique mutations. mt, mutation; GO, Gene Ontology; KEGG, Kyoto Encyclopedia of Genes and Genomes.