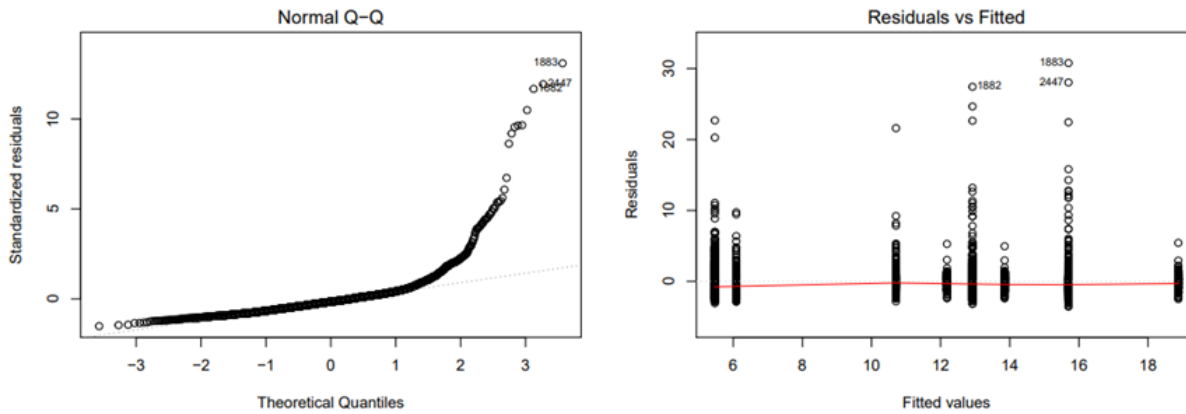
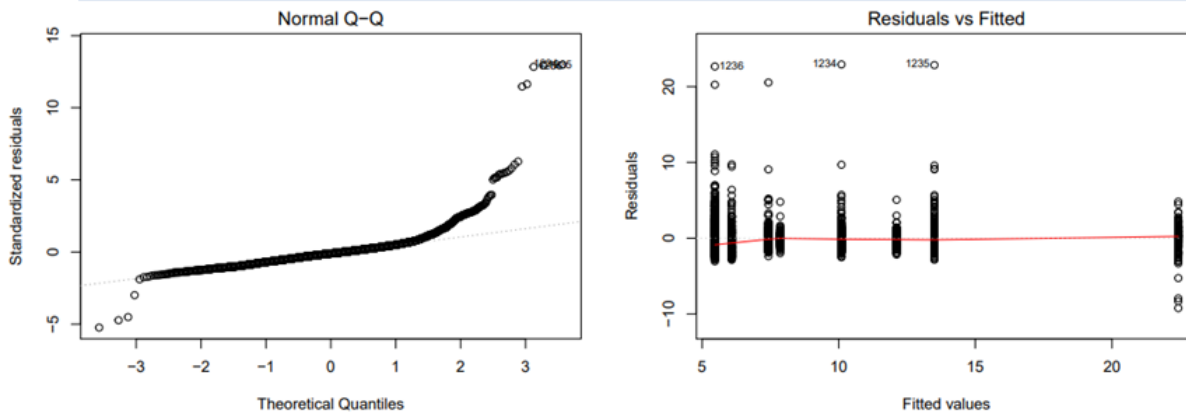


Normality of Tumor Mutational Burden Numbers

Non-somatic mutations filtered using all variants from 1000G and ExAC

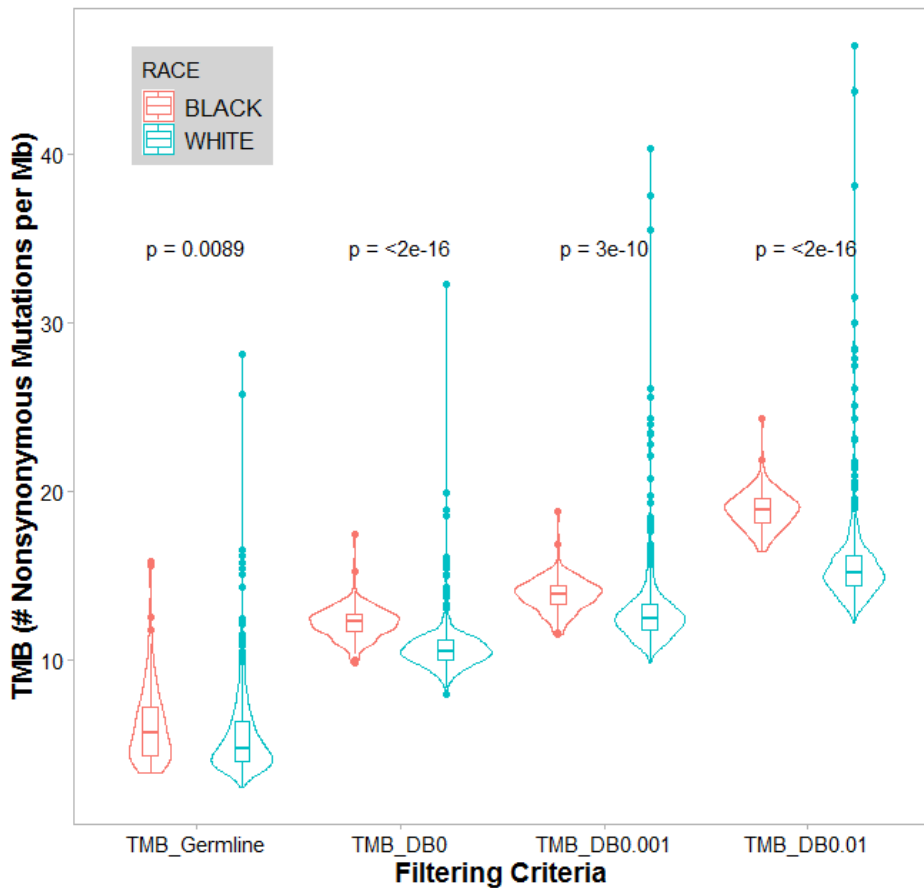


Non-somatic mutations filtered using AFR/EUR variants from 1000G and AFR/NEF variants from ExAC

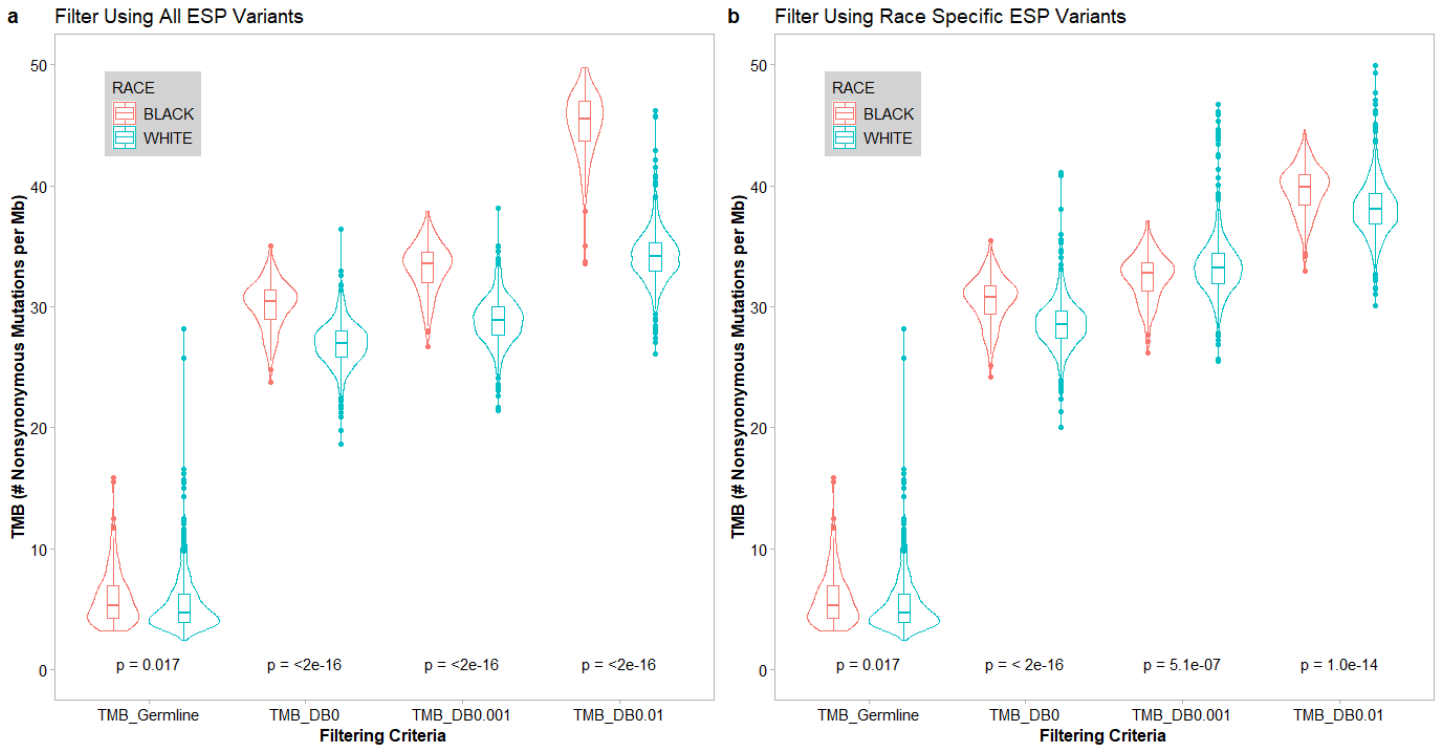


Supplementary Figure 1: Q-Q plot and Residual plot of Tumor Mutational Burden (TMB) values, as calculated as “number of protein-altering somatic mutations per Mb of coding regions”. All TMB values from four different filtering criteria were included: (1) excluding variants in patient-matched germline exome; (2) excluding variants with minor allele frequency (MAF) $\geq 1\%$ in 1000G or ExAC DBs; (3) excluding variants with MAF $\geq 0.1\%$ in 1000G or ExAC; and (4) excluding all variants reported by 1000G or ExAC. The upper panel figures illustrate the TMB normality when non-somatic mutations were filtered using germline or all variants in 1000G/ExAC. The lower panel figures used TMB values when non-somatic mutations were filtered using germline or race-specific variants in 1000G/ExAC

Impact of Variant Filtering Criteria on TMB



Supplementary Figure 2: Violin and Box Plot of Tumor Mutational Burdens (TMB), and Comparisons of TMBs Calculated from All Protein-Coding Genes in Black and White Patients from Four Variant Filtering Criteria. Note that variant MAF of AFR (African) population from 1000G and ExAC were used to filter variants in Black individuals, while MAF of EUR (European) population in 1000G and NFE (Non-Finnish European) in ExAC were used to filter variants in White patients. The TMB values were calculated as number of nonsynonymous mutations per Mb of coding regions. Four criteria were applied to identify patient-specific somatic mutations: (1) TMB_Germline: excluding variants in patient-matched germline exome; (2) TMB_DB0: excluding all variants reported by 1000G or ExAC; (3) TMB_DB0.001: excluding variants with MAF $\geq 0.1\%$ in 1000G or ExAC; and (4) TMB_DB0.01: excluding variants with minor allele frequency (MAF) $\geq 1\%$ in 1000G or ExAC DBs. The violin and box plots in red are TMB values from Black patients, and blue are from White Patients. Note that the 1000 Genome Project uses self-reported race, and ExAC's race definitions are computed from individual genotypes.



Supplementary Figure 3: Violin and Box Plot of Tumor Mutational Burdens (TMB), and Comparisons of TMBs Calculated from All Protein-Coding Genes in Black and White Patients from Four Variant Filtering Criteria Using ESP6500 Database. (a) variant MAF of all ESP6500 variants were used; (b) MAFs of AA (African American, n=2,217) population from ESP6500 were used to filter variants in Black individuals, and MAFs of EA (European American, n=4,298) population in ESP6500 were used to filter variants in White patients. The violin and box plots in red are TMB values from Black patients, and blue are from White Patients.

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ACSL3	2181		
ACSL6	23305		
ACTB	60		
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ACVR1	90	ENST00000263640	NM_001111067.2
ACVR1B	91		
ACVR2A	92		
ADGRA2	25960		
AFDN	4301		
AFF1	4299		
AFF3	3899		
AFF4	27125		
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ALB	213	ENST00000295897	NM_000477.5
ALK	238	ENST00000389048	NM_004304.4
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RXRA	6256	ENST00000481739	NM_002957.4
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SALL4	57167		
SAMHD1	25939	ENST00000262878	NM_015474.3
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MSK-IMPACT	MSK-HEME	FOUNDATION ONE	FOUNDATION ONE HEME	Vogelstein
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