S3 Table. Calculation of tumor mutational burden (TMB)

$$\mathrm{TMB} = \frac{\text{Total eligible variants (N)}}{\text{Total coding region} \geq 50\text{X coverage (N)}}$$

TruSight Oncology 500 and Whole-exome sequencing	
Eligible variants	**Non-eligible variants**
SNVs and indels	
In coding regions	In non-coding regions
In high-confidence regions[a)]	In low-confidence regions
With ≥ 50x coverage	With high COSMIC counts (≥ 50)
With ≥ 5% VAF	Multinucleotide variants
	Filtered germline variants
	Found in germline variant databases[b)]
	Additional variants flagged based on VAF

SNV, single nucleotide variant; indel, insertion and deletion; VAF, variant allele frequency. [a)]High-confidence regions defined as more than 50× coverage, [b)]Germline variant databases include gnomAD, ExAC, and dbSNP.