PMLB: mutation - Illumina HiSeq 2000, Targeted capture

Molecular Methods Description:

Data output was generated using a gene panel for tumor samples, and matched peripheral blood lymphocytes or normal adjacent, collected from patients as reported by Karamboulas C *et al*. (PMID 30380421).

• Mutations were identified from a custom 112 gene panel was based on the most commonly altered genes from the TCGA cohort of 279 HNSCC samples (Broad Institute). Libraries were designed using Agilent SureSelect XT reagent kits. Paired-end sequencing was performed on the Illumina Hi-Seq 2000.
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Analysis Description:

• Reads were aligned with hg19, and variants were called using Mutect version 1.1.4, indels were called using Strelka version 1.0.14, IndelGenotyper version 36.3336 and Varscan2 version 2.3.6.

Table:

HEADANDNECKGENEPANEL		
EPHB3	EPHB4	EPPK1
ERBB2	ERBB4	FADD
FAM123B	FAT1	FBXW7
FCRL4	FGF3	FGFR1
FGFR3	FLG	MLL2
MLL3	MYC	NAP1L2
NCSTN	NECAB1	NEURL2
NFE2L2	NFIB	NOTCH1
NOTCH2	NOTCH3	NOTCH4
STEAP4	TERT	TGFBR2
TGIF1	TNK2	TP53
TP63	TRAF3	TYMS
YAP1	YEATS4	YES1
ZNF750		