Supplementary Table S1. Genomic findings by next-generation sequencing

Category	Gene	Nucleotide change	Amino acid change	Variant type	Coverage	VAF (%)	Chromosomal locus	Transcript	Copy No.
Sequence variant	*ATM*	c.8710G>T	p.(E2904*)	Nonsense	1,996	56.66	Chr11:108224531	NM_000051.4	
	NF1	c.702_705delGTACinsATA	p.(Q236Rfs*45)	Frameshift block substitution	153	3.27	Chr17:29508775	NM_01042492.3	
	FGFR4	c.379G>C	p.(D127H)	Missense	1,999	48.47	Chr5:176517769	NM_213647.3	
	MSH6	c.4068_4071dup	p.(K1358Dfs*2)	Frameshift insertion	1,984	50.91	Chr2:48033981	NM_000179.3	
	UGT1A1	c.211G>A	p.(G71R)	Missense	1,999	50.63	Chr2:234669144	NM_000463.3	
	NQO1	c.559C>T	p.(P187S)	Missense	1,999	49.77	Chr16:69745145	NM_000903.3	
	PGD	c.217C>A	p.(L73I)	Missense	1,996	48.85	Chr1:10460582	NM_002631.4	
	KDR	c.3152G>A	p.(R1051Q)	Missense	1,995	51.13	Chr4:55956163	NM_002253.3	
Copy number variant	*CDKN2A*						Chr9:21968178		0.48

VAF, variant allele frequency.