DIFF	Hugo_Syn	nł Chromosor	Start_Position E	nd_Position Vari	ant_Cla Varian	t_TyrReferen	ce_ Tumor_	Seq Tumor_San Matched	d_Nt_ref_count	t_alt_count r	n_ref_coun
+	CDCP2	chr1	54605319	54605320 Fran	ne_Shif INS	-	G	s_C_00276(s_C_002	76(87	80	38
+	ALMS1	chr2	73613040	73613041 ln_F	rame_I INS	-	GGA	s_C_00276(s_C_002	76(11	34	9
+	FOXC1	chr6	1612020	1612021 In_F		-	CGG	s_C_00276(s_C_002	76(40	23	17
+	MICA	chr6	31380161	31380162 Fran	me_Shif INS	-	CTGCTG	GCT(s_C_00276(s_C_002	76(0	42	34
+	TBP	chr6	170871055	170871055 Fran	ne_Shif DEL	G	-	s_C_00276(s_C_002	76(21	12	70
+	DLX6	chr7	96635429	96635430 In_F	rame_I INS	-	GCC	s_C_00276(s_C_002	76(12	14	12
+	DCHS1	chr11	6662748	6662749 In_F	rame_I INS	-	CAG	s_C_00276(s_C_002	76(35	36	25
+	DCP1B	chr12	2062324	2062332 In_F	rame_[DEL	TGCTGC	TG(-	s_C_00276(s_C_002	760 14	81	64
+	NOP9	chr14	24769852	24769853 In_F	rame_I INS	-	GAGGA	GG/s_C_00276(s_C_002	76(11	65	47
+	RAI1	chr17	17697102	17697102 Fran	ne_Shif DEL	G	-	s_C_00276(s_C_002	76(97	59	89
+	BPTF	chr17	65955758	65955759 In_F	rame_I INS	-	CCTCCA	.GC(s_C_00276(s_C_002	76(25	16	16
+	CNDP1	chr18	72223594	72223595 In_F	rame_I INS	-	TGC	s_C_00276(s_C_002	76(53	44	27