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Data Sheet

Product Name: CancerSeqPlus Paraffin Tissue Curl

Catalog No.: T2235152-SC **Lot No.:** C101119

Species: ■ Human □ Mouse □ Rat □ Monkey (Rh) □ Guinea Pig □ Porcine
□ Bovine □ Hamster □ Dog □ Monkey (Cy) □ Rabbit □ Plant

Tissue Type: □ Normal □ Adult □ Fetal ■ Tumor □ Disease □ Cell line

Tissue Name: Lung

Donor Information:

Male: _____ year(s) old
Female: 51 year(s) old

Pathological Diagnosis: Adenocarcinoma

Tumor Size: 6x3x3 cm

Location: Lung, Right Upper Lobe

Components:
1. 5 curls per package
2. Certificate of Analysis

FOR IN VITRO RESEARCH USE ONLY APPROVED BY: _____

C101119

For CNV mutations, we utilize stringent criteria to confirm copy number variations -- using normal tissues as controls. We may have samples containing additional CNVs not listed here. Please inquire.

tissue type	Lot #	Strong Evidence compared with **GIAB** (NA12878)	Copy Number	STDev of Copy Number	P-value
Lung	C101119	MDM2	3.67	0.73	6.17E-04
		EGFR	8.43	1.18	6.17E-04

symbol	type	chromosome	position	reference	mutation	quality	allele type	Depth	variant frequency	transcript_id	consequence	existing variation
AKT1	snp	chr14	1.05E+08	C	T	237.291	hom	10	1.00	NM_00101	intron_variant	
AKT1	complex	chr14	1.05E+08	TAAAG	GAGATGAG	190.881	hom	10	1.00	NM_00101	intron_variant&feature	
AKT1	mnp	chr14	1.05E+08	CC	GG	200.891	hom	10	1.00	NM_00101	intron_variant	
AKT1	snp	chr14	1.05E+08	G	A	8580.45	het	445	0.70	NM_00101	intron_vari	rs3730344
AKT1	snp	chr14	1.05E+08	T	A	1001.96	hom	41	1.00	NM_00101	intron_vari	rs2494737
AKT1	snp	chr14	1.05E+08	G	A	1426.07	het	114	0.51	NM_00101	intron_vari	rs3563540
ALK	snp	chr2	29445458	G	T	28704	hom	919	1.00	NM_00430	synonymou	rs3795850
APC	snp	chr5	1.12E+08	G	A	9485.35	het	604	0.69	XM_00527	synonymou	rs41115&C
APC	snp	chr5	1.12E+08	G	A	1131.38	het	58	0.74	XM_00527	synonymou	rs42427
APC	snp	chr5	1.12E+08	T	G	1447.63	het	84	0.67	XM_00527	synonymou	rs866006
APC	snp	chr5	1.12E+08	T	A	960.933	het	53	0.74	XM_00527	missense_v	rs459552&
APC	snp	chr5	1.12E+08	G	A	9167.39	het	453	0.75	XM_00527	synonymou	rs465899
ATM	del	chr11	1.08E+08	ATTTTTTTT	ATTTTTTTT	589.289	het	534	0.13	NM_00005	intron_variant&feature	
ATM	snp	chr11	1.08E+08	T	A	440.834	hom	22	1.00	NM_00005	intron_variant	
ATM	snp	chr11	1.08E+08	T	A	557.225	hom	24	1.00	NM_00005	intron_vari	rs642496
ATM	snp	chr11	1.08E+08	C	T	225.925	het	15	0.80	NM_00005	intron_variant	
ATM	snp	chr11	1.08E+08	TTTC	CTTC	9711.89	het	603	0.54	NM_00005	synonymous_variant	
ATM	snp	chr11	1.08E+08	T	C	277.852	hom	11	1.00	NM_00005	intron_vari	rs227075
ATM	snp	chr11	1.08E+08	G	A	266.953	het	20	0.70	NM_00005	intron_variant	
AURKA	snp	chr20	54945783	A	G	549.59	hom	21	1.00	NM_00360	intron_vari	rs1048580

AURKA	complex	chr20	54963137	GGAAA	AGATTACA	212.018	het	65	0.22	NM_00360	intron_variant&feature	
AURKA	mnp	chr20	54963142	GA	TT	248.562	het	60	0.25	NM_00360	intron_variant	
AURKA	complex	chr20	54963147	CCC	CAATTTA	721.193	het	99	0.35	NM_00360	intron_variant&feature	
AURKA	snp	chr20	54963154	A	T	289.649	het	17	0.88	NM_00360	intron_variant	
AURKA	complex	chr20	54963155	GACC	TATA	166.23	het	12	0.83	NM_00360	intron_variant	
AURKA	complex	chr20	54963163	TCCATG	CACATGGA	198.555	het	20	0.55	NM_00360	intron_variant&feature	
AURKA	snp	chr20	54963170	G	T	450.027	het	20	0.90	NM_00360	intron_variant	
CCND1	del	chr11	69450976	GAAAAAAA	GAAAAAAA	353.33	het	60	0.28	NM_05305	upstream_gene_varian	
CCND1	ins	chr11	69465251	CG	CACTGCGG	153.195	het	105	0.17	NM_05305	intron_variant&feature	
CCNE1	del	chr19	30311542	GTTTTTTTT	GTTTTTTTT	186.917	het	29	0.34	NM_00123	intron_variant&feature	
CDH1	snp	chr16	68771370	CCC	CCT	42616	het	2063	0.68	NM_00436	splice_region_variant&	
CDH1	ins	chr16	68771418	CG	CGCCCCAG	1280.49	het	80	0.63	NM_00436	intron_variant&feature	
CDH1	snp	chr16	68771963	G	A	596.735	hom	26	1.00	NM_00436	intron_variant	
CDH1	snp	chr16	68772208	T	C	232.622	het	13	0.77	NM_00436	synonymous_variant	
CDH1	snp	chr16	68772220	G	A	241.039	het	14	0.71	NM_00436	synonymous_variant	
CDH1	snp	chr16	68844157	T	C	292.215	het	16	0.75	NM_00436	synonymous_variant	
CDH1	del	chr16	68844161	TCAC	TC	295.8	het	16	0.75	NM_00436	frameshift_variant&fea	
CDH1	complex	chr16	68844168	AACCG	TACCGTG	265.587	het	14	0.79	NM_00436	frameshift_variant&fea	
CDH1	complex	chr16	68844177	GAATG	AAATC	247.116	het	13	0.77	NM_00436	missense_variant	
CDH1	complex	chr16	68845494	CCTTT	GCTTA	72.0151	het	151	0.14	NM_00436	intron_variant	
CDH1	complex	chr16	68845502	CCTCAGGG	CAATTCTG	56.6641	het	141	0.14	NM_00436	intron_variant	
CDH1	snp	chr16	68846074	G	C	525.251	het	30	0.67	NM_00436	missense_variant	
CDH1	snp	chr16	68846080	C	G	505.487	het	38	0.50	NM_00436	missense_variant	
CDH1	complex	chr16	68846086	GAGGGG	CAGCAGC	516.6	het	31	0.65	NM_00436	frameshift_variant&fea	
CDK4	snp	chr12	58144665	C	T	2307.62	hom	85	1.00	NM_00007	intron_vari	rs2069502
CDKN2A	snp	chr9	21968199	C	G	110849	hom	3646	1.00	NM_00119	3_prime_U	rs11515&C
CDKN2A	complex	chr9	21968199	CGA	GGG	322.234	hom	14	0.86	NM_00119	3_prime_UTR_variant	
CSF1R	snp	chr5	1.49E+08	C	T	270.849	het	24	0.54	NM_00521	3_prime_UTR_variant	
CSF1R	complex	chr5	1.49E+08	CTCAC	CAGTGAGC	511.619	hom	19	1.00	NM_00521	inframe_insertion	
CSF1R	complex	chr5	1.49E+08	CTGCT	GAGGA	464.591	hom	19	0.95	NM_00521	synonymous_variant	
DDR2	complex	chr1	1.63E+08	CGAAAACT	AGCAAATT	698.382	het	33	0.88	XM_00524	missense_variant	
DDR2	snp	chr1	1.63E+08	T	C	94343.3	hom	3132	1.00	XM_00524	intron_vari	rs1780003
DDR2	snp	chr1	1.63E+08	C	T	16788.3	het	1074	0.53	XM_00524	intron_vari	rs3738807
DDR2	snp	chr1	1.63E+08	G	T	15059.4	hom	491	1.00	XM_00524	intron_vari	rs1355287

DDR2	snp	chr1	1.63E+08	T	C	4512.1	hom	184	1.00	XM_00524	intron_vari	rs1510315
EGFR	complex	chr7	55211086	ATATG	TTTTCG	202.732	het	35	0.29	NM_00522	frameshift_variant&fea	
EGFR	complex	chr7	55211093	CTACGAAA	GTACATAT	233.5	het	29	0.38	NM_00522	frameshift_variant&fea	
EGFR	snp	chr7	55221447	C	G	837.216	hom	30	1.00	NM_00522	intron_vari	rs12718946
EGFR	snp	chr7	55242112	C	T	869.176	het	72	0.57	NM_00522	intron_variant	
EGFR	complex	chr7	55242537	GGGGTCCA	TGTCCCAA	244.908	het	42	0.26	NM_00522	intron_variant&feature	
EGFR	complex	chr7	55242547	GCTC	CCAG	260.788	het	24	0.46	NM_00522	intron_variant	
EGFR	snp	chr7	55242609	A	G	75061.2	het	3398	0.92	NM_00522	intron_vari	rs2017000
EGFR	snp	chr7	55242782	T	C	1727.98	hom	65	1.00	NM_00522	intron_vari	rs712831
EGFR	snp	chr7	55259515	T	G	411291	het	17143	0.87	NM_00522	missense_v	rs12143456
EGFR	snp	chr7	55259763	A	G	794.332	hom	36	1.00	NM_00522	intron_vari	rs6970262
EGFR	snp	chr7	55259779	G	A	282.123	het	20	0.70	NM_00522	intron_variant	
ERBB3	snp	chr12	56477694	A	T	48216.4	hom	1617	1.00	NM_00198	splice_regi	rs2271194
ERBB3	snp	chr12	56478740	C	T	223.906	het	16	0.63	NM_00198	intron_variant	
ERBB4	del	chr2	2.13E+08	TAAAAAAA	TAAAAAAA	1734.14	het	280	0.26	NM_00523	splice_region_variant&	
ERBB4	snp	chr2	2.13E+08	A	T	13325.7	het	2440	0.22	NM_00523	intron_vari	rs35123918
ERBB4	snp	chr2	2.13E+08	T	C	1301.85	hom	57	0.98	NM_00523	intron_vari	rs839540
ERBB4	snp	chr2	2.13E+08	T	C	4185.86	hom	166	0.98	NM_00523	intron_vari	rs839541
ESR1	snp	chr6	1.52E+08	G	A	32885.1	het	1977	0.53	XM_00526	missense_v	COSM1074
EZH2	snp	chr7	1.49E+08	A	G	6463.86	het	311	0.70	XM_00524	intron_vari	rs2072407
FBXW7	del	chr4	1.53E+08	CTTTTTTTT	CTTTTTTTT	208.703	het	123	0.14	NM_03363	intron_variant&feature	
FBXW7	snp	chr4	1.53E+08	A	G	19520	hom	632	1.00	NM_03363	intron_vari	rs10033601
FBXW7	snp	chr4	1.53E+08	A	G	4513.27	hom	157	1.00	NM_03363	intron_vari	rs2714803
FBXW7	del,del	chr4	1.53E+08	CAAAAAAA	CAAAAAAA	6813.19	het	1009	0.28	NM_03363	splice_region_variant&	
FGFR1	snp	chr8	38272261	A	T	297.21	het	20	0.80	NM_00117	intron_variant	
FGFR1	complex	chr8	38285893	TCTTT	GATGA	308.917	het	25	0.48	NM_00117	missense_variant	
FGFR1	mnp	chr8	38285905	GA	TC	310.999	het	26	0.46	NM_00117	missense_variant	
FGFR2	ins	chr10	1.23E+08	TAT	TAAT	752.574	het	603	0.17	NM_02297	intron_variant&feature	
FGFR3	del	chr4	1806012	TGGGGGG	TGGGGGG	13487.8	het	4528	0.18	NM_00116	intron_variant&feature	
FGFR3	snp	chr4	1807892	ACG	ACA	37341.5	hom	1259	0.99	NM_00116	synonymous_variant	
FGFR3	snp	chr4	1808461	CC	CG	298.242	het	472	0.16	NM_00116	intron_variant	
FGFR3	mnp	chr4	1809145	TG	CA	564.458	hom	24	1.00	NM_00116	3_prime_UTR_variant	
FLT3	del	chr13	28602226	AAGAGAGA	AAGAGAGA	317.928	het	20	0.70	NM_00411	intron_variant&feature	
FLT3	snp	chr13	28609991	T	C	1456.16	hom	58	1.00	NM_00411	intron_vari	rs2491229

FLT3	snp	chr13	28609997	T	C	2247.91	hom	91	1.00	NM_00411	intron_vari	rs2491230
FLT3	snp	chr13	28610183	A	G	36049.8	hom	1254	0.99	NM_00411	splice_regi	rs2491231
FOXL2	snp	chr3	1.39E+08	C	G	316.306	hom	17	0.94	NM_02306	missense_v	rs1219083
FOXL2	complex	chr3	1.39E+08	GCCGTC	GTGAACTC	365.724	hom	16	1.00	NM_02306	inframe_insertion	
FOXL2	complex	chr3	1.39E+08	CCGGC	TGGGAG	398.691	hom	18	0.94	NM_02306	frameshift_variant&fea	
FOXL2	complex	chr3	1.39E+08	CAC	CG	948.489	hom	34	1.00	NM_02306	frameshift_variant&fea	
GNA11	snp	chr19	3119184	T	G	640.767	hom	28	1.00	NM_00206	intron_vari	rs308046
GNA11	snp	chr19	3119197	C	T	640.767	hom	28	1.00	NM_00206	splice_regi	rs36969283
GNA11	complex	chr19	3119217	AGAGCAA	GAAGCCT	557.225	hom	24	1.00	NM_00206	missense_variant	
H3F3A	snp	chr1	2.26E+08	C	T	247.789	het	22	0.55	NM_00210	intron_variant	
H3F3A	snp	chr1	2.26E+08	T	A	264.334	het	20	0.90	NM_00210	intron_variant	
HRAS	snp	chr11	534471	G	T	313.396	het	19	0.89	NM_00534	intron_variant	
IDH1	del	chr2	2.09E+08	GAAAAAAA	GAAAAAAA	251.506	het	154	0.15	XM_00524	intron_variant&feature	
IDH1	snp	chr2	2.09E+08	T	G	593.151	het	37	0.62	XM_00524	missense_variant	
IDH1	complex	chr2	2.09E+08	ATTCCCAA	TTTGGGAA	538.606	het	32	0.75	XM_00524	missense_variant	
IDH1	mnp	chr2	2.09E+08	CGT	AAA	352.533	het	31	0.48	XM_00524	missense_variant	
IDH1	del	chr2	2.09E+08	GAAAAAAA	GAAAAAAA	15011	het	2772	0.24	XM_00524	intron_variant&feature	
JAK2	del	chr9	5073681	CTTTTTTTT	CTTTTTTTT	3091.01	het	488	0.25	NM_00497	splice_region_variant&	
KDR	snp	chr4	55955232	T	C	832.321	hom	30	1.00	NM_00225	intron_vari	rs1531289
KDR	snp	chr4	55961159	T	C	24748.4	het	1124	0.76	NM_00225	intron_vari	rs2219471
KDR	snp	chr4	55962310	G	A	356.288	het	34	0.50	NM_00225	intron_variant	
KDR	ins	chr4	55962545	TGG	TGGG	4590.85	het	805	0.27	NM_00225	intron_variant&feature	
KDR	snp	chr4	55972974	T	A	9390.59	het	446	0.75	NM_00225	missense_v	rs18703778
KDR	snp	chr4	55980239	C	T	2921.71	hom	112	1.00	NM_00225	intron_vari	rs7692791
KIT	snp	chr4	55599159	G	A	656.026	hom	33	0.94	XM_00526	intron_vari	rs4864921
KIT	snp	chr4	55599436	T	C	308.56	het	773	0.12	XM_00526	intron_vari	rs1008658
KIT	snp	chr4	55602451	C	T	257.024	hom	11	1.00	XM_00526	intron_vari	rs12649726
MAP2K1	complex	chr15	66727559	TGGTCAT	ATGACCA	318.895	het	15	0.87	NM_00275	missense_variant	
MDM2	snp	chr12	69207162	G	A	746.305	hom	27	1.00	NM_00239	intron_vari	rs1470383
MDM2	snp	chr12	69218455	G	A	271.204	het	25	0.52	NM_00239	intron_variant	
MLH1	complex	chr3	37067091	ATATAT	AGTGGAG	353.272	het	81	0.20	NM_00024	intron_variant&feature	
MLH1	complex	chr3	37067097	ATAT	GGAG	277.692	het	24	0.58	NM_00024	intron_variant	
MPL	mnp	chr1	43814899	GGGT	ACCC	338.613	het	116	0.22	NM_00537	intron_variant	
MYCN	snp	chr2	16080157	C	G	5037.87	hom	166	0.99	NM_00537	upstream_	rs11886063

MYCN	snp	chr2	16089359	T	C	307.398	hom	13	1.00	NM_00537	downstrea	rs55912884
MYCN	snp	chr2	16089442	T	A	1220.35	hom	43	1.00	NM_00537	downstrea	rs12619709
MYCN	snp	chr2	16089615	T	C	24524.7	het	1290	0.66	NM_00537	downstrea	rs4669018
NOTCH1	snp	chr9	1.39E+08	C	T	2465.53	hom	103	0.99	NM_01761	3_prime_U	rs3124591
NOTCH1	snp	chr9	1.39E+08	G	A	15158.2	hom	597	1.00	NM_01761	synonymou	rs2229974
NOTCH1	snp	chr9	1.39E+08	G	A	45628.5	hom	1496	1.00	NM_01761	synonymou	rs10521&C
NOTCH1	complex	chr9	1.39E+08	GTC	ATT	224.481	het	19	0.68	NM_01761	missense_variant	
NOTCH1	snp	chr9	1.39E+08	T	A	606.522	het	50	0.60	NM_01761	intron_variant	
NOTCH1	complex	chr9	1.39E+08	CGTCCTCCT	AGTGCCAG	279.38	het	14	0.86	NM_01761	missense_variant	
NPM1	del	chr5	1.71E+08	CTTTTTTTT	CTTTTTTTT	4271.24	het	429	0.39	NM_00252	splice_region_variant&	
NPM1	del	chr5	1.71E+08	CTG	CG	489.416	het	46	0.43	NM_00252	3_prime_UTR_variant&	
NRAS	snp	chr1	1.15E+08	G	A	283.735	hom	10	1.00	NM_00252	intron_vari	rs969273
PDGFRA	complex	chr4	55140854	AGTTCA	CCTTCTCT	309.353	het	46	0.61	NM_00620	intron_variant&feature	
PDGFRA	mnp	chr4	55140864	TTG	CAA	661.897	het	49	0.63	NM_00620	intron_variant	
PDGFRA	snp	chr4	55141055	A	G	134234	hom	4358	1.00	NM_00620	synonymou	rs18737788
PDGFRA	snp	chr4	55144447	T	C	666.849	hom	29	1.00	NM_00620	intron_vari	rs1907820
PDGFRA	snp	chr4	55152040	C	T	23353.3	het	1209	0.66	NM_00620	synonymou	rs22282308
PDGFRA	snp	chr4	55161391	T	C	8191.75	hom	263	1.00	NM_00620	synonymou	rs7685117
PDGFRA	snp	chr4	55161517	A	G	10147.7	hom	338	1.00	NM_00620	3_prime_U	rs7680422
PIK3CA	del	chr3	1.79E+08	ATTTTTTTT	ATTTTTTTT	4669.79	het	1130	0.19	NM_00621	intron_variant&feature	
PTEN	del	chr10	89720633	CTTTTTTTT	CTTTTTTTT	2491.3	het	886	0.19	NM_00031	splice_acceptor_varian	
PTEN	del	chr10	89725293	CTTTTTTTT	CTTTTTTTT	130.199	het	617	0.11	NM_00031	3_prime_UTR_variant&	
PTEN	snp	chr10	89725379	C	A	274.193	hom	16	1.00	NM_00031	3_prime_UTR_variant	
RB1	snp	chr13	48919358	TTTAC	GTTAC	19881.2	hom	720	0.96	NM_00032	intron_variant	
RB1	complex	chr13	48919358	TTTAC	GTTAT	360.849	het	32	0.50	NM_00032	intron_variant	
RB1	ins	chr13	48953655	CAAAAAAA	CAAAAAAA	1638.19	het	372	0.20	NM_00032	intron_variant&feature	
RB1	snp	chr13	48954021	G	C	648.118	hom	24	1.00	NM_00032	intron_vari	rs2070752
RB1	ins	chr13	48955659	CA	CAAA	1243.22	het	70	0.67	NM_00032	intron_variant&feature	
RB1	snp	chr13	48955676	T	A	2149.14	hom	76	1.00	NM_00032	intron_vari	rs2804086
RB1	snp	chr13	49033747	G	A	641.332	hom	28	0.96	NM_00032	intron_vari	rs198580
RB1	ins	chr13	49034022	ATT	ATTT	4300.5	hom	190	0.93	NM_00032	intron_variant&feature	
RB1	del	chr13	49034085	CTTTTTC	CTTTTC	961.733	hom	48	0.90	NM_00032	intron_variant&feature	
RB1	complex	chr13	49034089	TTCT	CTT	476.355	het	74	0.32	NM_00032	intron_variant&feature	
RB1	ins	chr13	49034095	CTT	CTTT	555.727	het	57	0.47	NM_00032	intron_variant&feature	

RB1	ins	chr13	49034099	CTT	CTTT	474.446	het	52	0.42	NM_00032	intron_variant&feature	
RB1	snp	chr13	49037976	G	A	271.204	het	26	0.50	NM_00032	splice_regi	CS910460&
RET	snp	chr10	43610281	G	A	425.683	het	28	0.89	NM_02097	intron_variant	
RET	complex	chr10	43615494	CATGGC	GAGGGT	678.138	het	52	0.52	NM_02097	intron_variant	
RHOA	snp	chr3	49406080	T	C	1321.21	hom	57	1.00	NM_00166	intron_vari	rs2878298
SMAD4	complex	chr18	48581249	CCACCAAG	GCACGATT	302.468	hom	12	1.00	NM_00535	missense_variant	
SMAD4	del	chr18	48584855	ATTTTTTTT	ATTTTTTTT	166.658	het	60	0.18	NM_00535	intron_variant&feature	
SMAD4	snp	chr18	48593175	C	T	1238.55	hom	53	1.00	NM_00535	intron_variant	
SMAD4	complex	chr18	48603044	CAGCAGGC	TAGCCGCC	301.292	het	20	0.60	NM_00535	stop_gained	
SMO	snp	chr7	1.29E+08	CGG	CCG	32790.1	het	2021	0.54	NM_00563	intron_variant	
SMO	snp	chr7	1.29E+08	T	C	470.982	hom	20	1.00	NM_00563	intron_vari	rs2075779
SMO	snp	chr7	1.29E+08	GTGGG	GTGGC	18670.4	het	1228	0.49	NM_00563	synonymous_variant	
SMO	snp	chr7	1.29E+08	A	G	1576.46	het	82	0.89	NM_00563	intron_vari	rs2735842
SRC	snp	chr20	36031559	TCG	TCC	25368.4	het	1916	0.44	NM_00541	intron_variant	
STK11	del	chr19	1206796	CTTTTTTTT	CTTTTTTTT	211.817	het	47	0.23	XM_00525	5_prime_UTR_variant&	
STK11	snp	chr19	1219553	G	T	550.896	hom	24	1.00	XM_00525	intron_vari	rs1108488
STK11	snp	chr19	1220321	T	C	21748.2	het	1371	0.50	XM_00525	intron_vari	rs2075606
STK11	snp	chr19	1221161	C	T	1374.76	het	85	0.65	XM_00525	intron_vari	rs9282860
STK11	snp	chr19	1221484	C	T	1821.82	hom	79	1.00	XM_00525	intron_vari	rs741764
STK11	snp	chr19	1222268	A	G	1454.07	hom	65	1.00	XM_00525	intron_vari	rs60977562
TERT	mnp	chr5	1295349	AA	GG	186.064	het	15	0.67	NM_19825	upstream_gene_variar	
TERT	snp	chr5	1295349	A	G	141468	hom	4440	1.00	NM_19825	upstream_	rs2853669
TP53	del	chr17	7576853	CTGAAGGG	CT	33691.8	het	4148	0.32	NM_00054	frameshift_variant&sp	
TP53	snp	chr17	7577407	A	C	11001.7	het	819	0.50	NM_00054	intron_vari	rs1295105
TP53	snp	chr17	7578115	T	C	401.657	hom	16	1.00	NM_00054	intron_vari	rs1625895
TP53	snp	chr17	7579619	GGAC	TGAC	27402.4	het	1979	0.52	NM_00054	intron_variant	
TP53	snp	chr17	7579619	G	T	6088.57	het	320	0.64	NM_00054	intron_vari	rs1788332
TP53	del	chr17	7579643	CCCCCAGC	CC	1990.59	het	966	0.19	NM_00054	intron_variant&feature	
TP53	complex	chr17	7579668	CTCCAG	CAACCCTT	5925.5	het	1050	0.29	NM_00054	intron_variant&feature	
TP53	complex	chr17	7579678	CCAG	TTAC	5339.22	het	1101	0.29	NM_00054	intron_variant	
TP53	snp	chr17	7580052	C	T	18088.6	het	942	0.70	NM_00054	intron_vari	rs8079544
TP53	complex	chr17	7590817	AACTTTTA	GACTG	311.917	het	15	0.87	NM_00054	5_prime_UTR_variant&	
TP53	complex	chr17	7590828	CCAGTC	CTAAAAGT	302.241	het	18	0.72	NM_00054	5_prime_UTR_variant&	
VHL	snp	chr3	10188428	T	G	1629.28	hom	61	1.00	NM_00055	intron_vari	rs1678607