Case	tissue/plasma	Category	Impacted Gene	Type	Chrom	Pos	Ref Allele	Alt Allele	Allele Frequency	Number of Variant Alleles	Filtered Read Depth (per	Effect	AA
1	tissue-1 Somatic	Category III-Default Categorization	SPEN	SNP	1	16258651	A	G	0.0901	21	233	SYNONYMOUS_CODING(LOW|SILENT|gcA/gcG|A1972|SPEN|mRNA|CODING|NM_015001|NM_015001.ex.11)	A1972
1	tissue-1 Somatic	Category III-Default Categorization	KMT2C	SNP	7	151882657	T	G	0.073	10	137	SYNONYMOUS_CODING(LOW|SILENT|Aga/Cga|R1690|KMT2C|mRNA|CODING|NM_170606|NM_170606.ex.34)	R1690
1	tissue-1 Somatic	Category II-Default Categorization	NOTCH1	SNP	9	139417518	G	A	0.0565	28	496	NON_SYNONYMOUS_CODING(MODERATE|MISSENSE|Cgg/Tgg|R176W|NOTCH1|mRNA|CODING|NM_017617|NM_017617.ex.4),UPSTREAM(MODIFIER||||MIR4673|Non-coding_transcript|NON_CODING|NR_039820|)	R176W
1	Plasma1- 1	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A
1	Plasma1- 2	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A
1	Plasma1-3	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A
2	tissue-2 Somatic	Category II-Default Categorization	PIK3CA	SNP	3	178937755	T	C	0.0254	10	394	NON_SYNONYMOUS_CODING(MODERATE|MISSENSE|Tat/Cat|Y644H|PIK3CA|mRNA|CODING|NM_006218|NM_006218.ex.13)	Y644H
2	tissue-2 Somatic	Category II-Default Categorization	SDHA	SNP	5	251503	A	G	0.0591	11	186	INTRON(MODIFIER||||SDHA|mRNA|CODING|NM_001330758|),NON_SYNONYMOUS_CODING(MODERATE|MISSENSE|Atg/Gtg|M524V|SDHA|mRNA|CODING|NM_001294332|NM_001294332.ex.12),NON_SYNONYMOUS_CODING(MODERATE|MISSENSE|Atg/Gtg|M572V|SDHA|mRNA|CODING|NM_004168|NM_004168.ex.13)	M524V
2	tissue-2 Somatic	Category II-Default Categorization	PCLO	SNP	7	82581494	T	A	0.0444	12	270	NON_SYNONYMOUS_CODING(MODERATE|MISSENSE|gaA/gaT|E2925D|PCLO|mRNA|CODING|NM_014510|NM_014510.ex.5),NON_SYNONYMOUS_CODING(MODERATE|MISSENSE|gaA/gaT|E2925D|PCLO|mRNA|CODING|NM_033026|NM_033026.ex.5)	E2925D
2	tissue-2 Somatic	Category III-Default Categorization	RELN	Deletion	7	103270629	GA	G	0.0813	13	160	INTRON(MODIFIER||||RELN|mRNA|CODING|NM_005045|),INTRON(MODIFIER||||RELN|mRNA|CODING|NM_173054|)	

2	tissue-2 Somatic	Category III-Default Categorization	MGAM	SNP	7	141765547	C	T	0.0943	10	106	INTRON(MODIFIER||||MGAM|mRNA|CODING|NM_004668|)	
2	tissue-2 Somatic	Category III-Default Categorization	MGAM	SNP	7	141767141	G	A	0.104	10	96	INTRON(MODIFIER||||MGAM|mRNA|CODING|NM_004668|)	
2	tissue-2 Somatic	Category II-Default Categorization	KMT2C	SNP	7	151859314	T	C	0.0515	10	194	NON_SYNONYMOUS_CODING(MODERATE|MISSENSE|aAt/aGt|N3783S|KMT2C|mRNA|CODING|NM_170606|NM_170606.ex.43)	N3783S
2	tissue-2 Somatic	Category I-Default Categorization	KMT2C	Deletion	7	151874147	CT	C	0.0512	13	254	FRAME_SHIFT(HIGH||||KMT2C|mRNA|CODING|NM_170606|NM_170606.ex.38)	
2	tissue-2 Somatic	Category II-Default Categorization	KMT2C	SNP	7	151970951	C	T	0.0196	11	561	NON_SYNONYMOUS_CODING(MODERATE|MISSENSE|cGa/cAa|R284Q|KMT2C|mRNA|CODING|NM_170606|NM_170606.ex.7)	R284Q
2	tissue-2 Somatic	Category III-Default Categorization	RAD21	Deletion	8	117868531	TA	T	0.273	18	66	INTRON(MODIFIER||||RAD21|mRNA|CODING|NM_006265|)	
2	tissue-2 Somatic	Category III-Default Categorization	RECQL4	SNP	8	145738768	G	C	0.0591	13	220	DOWNSTREAM(MODIFIER||||MFSD3|Non-coding_transcript|CODING|NM_138431|),DOWNSTREAM(MODIFIER||||MFSD3|Non-coding_transcript|CODING|NR_130120|),INTRON(MODIFIER||||RECQL4|mRNA|CODING|NM_004260|),SPLICE_SITE_ACCEPTOR(HIGH||||RECQL4|mRNA|CODING|NM_004260|),SPLICE_SITE_DONOR(HIGH||||RECQL4|mRNA|CODING|NM_004260|),UPSTREAM(MODIFIER||||LRRC14|mRNA|CODING|NM_001272036|),UPSTREAM(MODIFIER||||LRRC14|mRNA|CODING|NM_014665|)	
2	Plasma2-1	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A
2	Plasma2-2	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A
2	Plasma2-3	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A
3	tissue-3 Somatic	Category III-Default Categorization	STAG1	SNP	3	136141420	A	C	0.671	114	170	SYNONYMOUS_CODING(LOW|SILENT|gtT/gtG|V623|STAG1|mRNA|CODING|NM_005862|NM_005862.ex.19)	V623
3	tissue-3 Somatic	Category III-Default Categorization	ATR	SNP	3	142188404	G	A	0.233	42	180	SYNONYMOUS_CODING(LOW|SILENT|cgC/cgT|R2045|ATR|mRNA|CODING|NM_001354579|NM_001354579.ex.37),SYNONYMOUS_CODING(LOW|SILENT|cgC/cgT|R2109|ATR|mRNA|CODING|NM_001184|NM_001184.ex.38)	R2045

<table>
<tr><td>3</td><td>tissue-3 Somatic</td><td>Category II-Default Categorization</td><td>ETV5</td><td>SNP</td><td>3</td><td>185766490</td><td>C</td><td>T</td><td>0.217</td><td>186</td><td>856</td><td>NON_SYNONYMOUS_CODING(MODERATE|MISSENSE|Gct/Act|A491T|ETV5|mRNA|CODING|NM_004454|NM_004454.ex.13)</td><td>A491T</td></tr>
<tr><td>3</td><td>tissue-3 Somatic</td><td>Category II-Default Categorization</td><td>FAT4</td><td>SNP</td><td>4</td><td>126328257</td><td>C</td><td>T</td><td>0.568</td><td>171</td><td>301</td><td>NON_SYNONYMOUS_CODING(MODERATE|MISSENSE|Ccc/Tcc|P1844S|FAT4|mRNA|CODING|NM_001291285|NM_001291285.ex.3),NON_SYNONYMOUS_CODING(MODERATE|MISSENSE|Ccc/Tcc|P1844S|FAT4|mRNA|CODING|NM_001291303|NM_001291303.ex.3),NON_SYNONYMOUS_CODING(MODERATE|MISSENSE|Ccc/Tcc|P1844S|FAT4|mRNA|CODING|NM_024582|NM_024582.ex.3)</td><td>P1844S</td></tr>
<tr><td>3</td><td>tissue-3 Somatic</td><td>Category III-Default Categorization</td><td>FAT1</td><td>SNP</td><td>4</td><td>187518148</td><td>T</td><td>C</td><td>0.0132</td><td>11</td><td>832</td><td>SYNONYMOUS_CODING(LOW|SILENT|ggA/ggG|G4182|FAT1|mRNA|CODING|NM_005245|NM_005245.ex.25)</td><td>G4182</td></tr>
<tr><td>3</td><td>tissue-3 Somatic</td><td>Category II-Default Categorization</td><td>PCLO</td><td>SNP</td><td>7</td><td>82784336</td><td>C</td><td>G</td><td>0.0108</td><td>17</td><td>1568</td><td>NON_SYNONYMOUS_CODING(MODERATE|MISSENSE|Gct/Cct|A541P|PCLO|mRNA|CODING|NM_014510|NM_014510.ex.2),NON_SYNONYMOUS_CODING(MODERATE|MISSENSE|Gct/Cct|A541P|PCLO|mRNA|CODING|NM_033026|NM_033026.ex.2)</td><td>A541P</td></tr>
<tr><td>3</td><td>tissue-3 Somatic</td><td>Category II-Default Categorization</td><td>PCLO</td><td>SNP</td><td>7</td><td>82784339</td><td>A</td><td>G</td><td>0.00966</td><td>15</td><td>1553</td><td>NON_SYNONYMOUS_CODING(MODERATE|MISSENSE|Tca/Cca|S540P|PCLO|mRNA|CODING|NM_014510|NM_014510.ex.2),NON_SYNONYMOUS_CODING(MODERATE|MISSENSE|Tca/Cca|S540P|PCLO|mRNA|CODING|NM_033026|NM_033026.ex.2)</td><td>S540P</td></tr>
<tr><td>3</td><td>tissue-3 Somatic</td><td>Category III-Default Categorization</td><td>PCLO</td><td>SNP</td><td>7</td><td>82784343</td><td>T</td><td>C</td><td>0.00706</td><td>11</td><td>1557</td><td>SYNONYMOUS_CODING(LOW|SILENT|aaA/aaG|K538|PCLO|mRNA|CODING|NM_014510|NM_014510.ex.2),SYNONYMOUS_CODING(LOW|SILENT|aaA/aaG|K538|PCLO|mRNA|CODING|NM_033026|NM_033026.ex.2)</td><td>K538</td></tr>
<tr><td>3</td><td>tissue-3 Somatic</td><td>Category II-Default Categorization</td><td>PCLO</td><td>SNP</td><td>7</td><td>82784366</td><td>A</td><td>G</td><td>0.0128</td><td>19</td><td>1481</td><td>NON_SYNONYMOUS_CODING(MODERATE|MISSENSE|Tct/Cct|S531P|PCLO|mRNA|CODING|NM_014510|NM_014510.ex.2),NON_SYNONYMOUS_CODING(MODERATE|MISSENSE|Tct/Cct|S531P|PCLO|mRNA|CODING|NM_033026|NM_033026.ex.2)</td><td>S531P</td></tr>
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<tr><td>3</td><td>tissue-3 Somatic</td><td>Category III-Default Categorization</td><td>PCLO</td><td>SNP</td><td>7</td><td>82784373</td><td>T</td><td>C</td><td>0.0114</td><td>16</td><td>1409</td><td>SYNONYMOUS_CODING(LOW|SILENT|aaA/aaG|K528|PCLO|mRNA|CODING|NM_014510|NM_014510.ex.2),SYNONYMOUS_CODING(LOW|SILENT|aaA/aaG|K528|PCLO|mRNA|CODING|NM_033026|NM_033026.ex.2)</td><td>K528</td></tr>
<tr><td>3</td><td>tissue-3 Somatic</td><td>Category II-Default Categorization</td><td>PCLO</td><td>SNP</td><td>7</td><td>82784411</td><td>G</td><td>A</td><td>0.00698</td><td>11</td><td>1577</td><td>NON_SYNONYMOUS_CODING(MODERATE|MISSENSE|Cca/Tca|P516S|PCLO|mRNA|CODING|NM_014510|NM_014510.ex.2),NON_SYNONYMOUS_CODING(MODERATE|MISSENSE|Cca/Tca|P516S|PCLO|mRNA|CODING|NM_033026|NM_033026.ex.2)</td><td>P516S</td></tr>
<tr><td>3</td><td>tissue-3 Somatic</td><td>Category II-Default Categorization</td><td>PCLO</td><td>SNP</td><td>7</td><td>82784498</td><td>C</td><td>T</td><td>0.0108</td><td>15</td><td>1391</td><td>NON_SYNONYMOUS_CODING(MODERATE|MISSENSE|Gca/Aca|A487T|PCLO|mRNA|CODING|NM_014510|NM_014510.ex.2),NON_SYNONYMOUS_CODING(MODERATE|MISSENSE|Gca/Aca|A487T|PCLO|mRNA|CODING|NM_033026|NM_033026.ex.2)</td><td>A487T</td></tr>
<tr><td>3</td><td>tissue-3 Somatic</td><td>Category III-Default Categorization</td><td>RELN</td><td>SNP</td><td>7</td><td>103205778</td><td>C</td><td>T</td><td>0.501</td><td>210</td><td>419</td><td>SYNONYMOUS_CODING(LOW|SILENT|tcG/tcA|S1719|RELN|mRNA|CODING|NM_005045|NM_005045.ex.34),SYNONYMOUS_CODING(LOW|SILENT|tcG/tcA|S1719|RELN|mRNA|CODING|NM_173054|NM_173054.ex.34)</td><td>S1719</td></tr>
<tr><td>3</td><td>tissue-3 Somatic</td><td>Category II-Default Categorization</td><td>KMT2C</td><td>SNP</td><td>7</td><td>151932946</td><td>T</td><td>C</td><td>0.0324</td><td>19</td><td>587</td><td>NON_SYNONYMOUS_CODING(MODERATE|MISSENSE|Agg/Ggg|R909G|KMT2C|mRNA|CODING|NM_170606|NM_170606.ex.16)</td><td>R909G</td></tr>
<tr><td>3</td><td>tissue-3 Somatic</td><td>Category III-Default Categorization</td><td>PC</td><td>SNP</td><td>11</td><td>66618409</td><td>A</td><td>G</td><td>0.00855</td><td>11</td><td>1287</td><td>DOWNSTREAM(MODIFIER||||RCE1|mRNA|CODING|NM_001032279|),DOWNSTREAM(MODIFIER||||RCE1|mRNA|CODING|NM_005133|),INTRON(MODIFIER||||PC|mRNA|CODING|NM_000920|),INTRON(MODIFIER||||PC|mRNA|CODING|NM_001040716|),INTRON(MODIFIER||||PC|mRNA|CODING|NM_022172|)</td><td></td></tr>
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<tr><td>3</td><td>tissue-3 Somatic</td><td>Category III-Default Categorization</td><td>NUMA1</td><td>SNP</td><td>11</td><td>71725030</td><td>C</td><td>T</td><td>0.542</td><td>397</td><td>733</td><td>INTRON(MODIFIER||||NUMA1|mRNA|CODING|NR_104476|),SYNONYMOUS_CODING(LOW|SILENT|gaG/gaA|E1173|NUMA1|mRNA|CODING|NM_001286561|NM_001286561.ex.16),SYNONYMOUS_CODING(LOW|SILENT|gaG/gaA|E1173|NUMA1|mRNA|CODING|NM_006185|NM_006185.ex.15),UPSTREAM(MODIFIER||||LOC100128494|Non-coding_transcript|NON_CODING|NR_104178|)</td><td>E1173</td></tr>
<tr><td>3</td><td>組織3Somatic</td><td>Category II-Default Categorization</td><td>NUMA1</td><td>SNP</td><td>11</td><td>71733433</td><td>C</td><td>T</td><td>0.483</td><td>153</td><td>317</td><td>DOWNSTREAM(MODIFIER||||LOC100128494|Non-coding_transcript|NON_CODING|NR_104178|),NON_SYNONYMOUS_CODING(MODERATE|MISSENSE|atG/atA|M108I|NUMA1|mRNA|CODING|NM_001286561|NM_001286561.ex.8),NON_SYNONYMOUS_CODING(MODERATE|MISSENSE|atG/atA|M108I|NUMA1|mRNA|CODING|NM_006185|NM_006185.ex.7),SYNONYMOUS_STOP(LOW|SILENT|tGa/tAa|*194|NUMA1|mRNA|CODING|NR_104476|NR_104476.ex.7)</td><td>M108I</td></tr>
<tr><td>3</td><td>tissue-3 Somatic</td><td>Category II-Default Categorization</td><td>BIRC3</td><td>SNP</td><td>11</td><td>102196019</td><td>A</td><td>G</td><td>0.56</td><td>195</td><td>348</td><td>NON_SYNONYMOUS_CODING(MODERATE|MISSENSE|aAa/aGa|K260R|BIRC3|mRNA|CODING|NM_001165|NM_001165.ex.2),NON_SYNONYMOUS_CODING(MODERATE|MISSENSE|aAa/aGa|K260R|BIRC3|mRNA|CODING|NM_182962|NM_182962.ex.3)</td><td>K260R</td></tr>
<tr><td>3</td><td>tissue-3 Somatic</td><td>Category III-Default Categorization</td><td>KMT2D</td><td>SNP</td><td>12</td><td>49420740</td><td>C</td><td>T</td><td>0.508</td><td>497</td><td>978</td><td>SYNONYMOUS_CODING(LOW|SILENT|caG/caA|Q5003|KMT2D|mRNA|CODING|NM_003482|NM_003482.ex.48)</td><td>Q5003</td></tr>
<tr><td>3</td><td>tissue-3 Somatic</td><td>Category III-Default Categorization</td><td>KMT2D</td><td>SNP</td><td>12</td><td>49444937</td><td>G</td><td>T</td><td>0.0112</td><td>25</td><td>2226</td><td>SYNONYMOUS_CODING(LOW|SILENT|tcC/tcA|S843|KMT2D|mRNA|CODING|NM_003482|NM_003482.ex.10)</td><td>S843</td></tr>
<tr><td>3</td><td>tissue-3 Somatic</td><td>Category III-Default Categorization</td><td>KMT2D</td><td>SNP</td><td>12</td><td>49444985</td><td>T</td><td>C</td><td>0.00859</td><td>17</td><td>1978</td><td>SYNONYMOUS_CODING(LOW|SILENT|caA/caG|Q827|KMT2D|mRNA|CODING|NM_003482|NM_003482.ex.10)</td><td>Q827</td></tr>
<tr><td>3</td><td>tissue-3 Somatic</td><td>Category III-Default Categorization</td><td>KMT2D</td><td>SNP</td><td>12</td><td>49445372</td><td>T</td><td>C</td><td>0.00698</td><td>17</td><td>2435</td><td>SYNONYMOUS_CODING(LOW|SILENT|acA/acG|T698|KMT2D|mRNA|CODING|NM_003482|NM_003482.ex.10)</td><td>T698</td></tr>
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3	tissue-3 Somatic	Category III-Default Categorization	KMT2D	SNP	12	49445378	G	C	0.00827	22	2661	SYNONYMOUS_CODING(LOW|SILENT|tcC/tcG|S696|KMT2D|mRNA|CODING|NM_003482|NM_003482.ex.10)	S696
3	tissue-3 Somatic	Category III-Default Categorization	KMT2D	SNP	12	49445447	T	A	0.0104	21	2022	SYNONYMOUS_CODING(LOW|SILENT|ccA/ccT|P673|KMT2D|mRNA|CODING|NM_003482|NM_003482.ex.10)	P673
3	tissue-3 Somatic	Category III-Default Categorization	KMT2D	SNP	12	49445546	T	C	0.00732	15	2049	SYNONYMOUS_CODING(LOW|SILENT|gaA/gaG|E640|KMT2D|mRNA|CODING|NM_003482|NM_003482.ex.10)	E640
3	tissue-3 Somatic	Category III-Default Categorization	KMT2D	SNP	12	49445747	A	G	0.00683	12	1758	SYNONYMOUS_CODING(LOW|SILENT|tcT/tcC|S573|KMT2D|mRNA|CODING|NM_003482|NM_003482.ex.10)	S573
3	tissue-3 Somatic	Category II-Default Categorization	KMT2D	SNP	12	49446093	G	A	0.00914	12	1313	NON_SYNONYMOUS_CODING(MODERATE|MISSENSE|aCg/aTg|T458M|KMT2D|mRNA|CODING|NM_003482|NM_003482.ex.10)	T458M
3	tissue-3 Somatic	Category II-Default Categorization	KMT2D	SNP	12	49446102	T	G	0.00905	12	1326	NON_SYNONYMOUS_CODING(MODERATE|MISSENSE|gAa/gCa|E455A|KMT2D|mRNA|CODING|NM_003482|NM_003482.ex.10)	E455A

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<tr><td>3</td><td>tissue-3 Somatic</td><td>Category I-Default Categorization</td><td>TP53</td><td>SNP</td><td>17</td><td>7573982</td><td>C</td><td>A</td><td>0.365</td><td>123</td><td>337</td><td>STOP_GAINED(HIGH|NONSENSE|Gaa/Taa|E190*|TP53|mRNA|CODING|NM_001276697|NM_001276697.ex.6),STOP_GAINED(HIGH|NONSENSE|Gaa/Taa|E217*|TP53|mRNA|CODING|NM_001126115|NM_001126115.ex.6),STOP_GAINED(HIGH|NONSENSE|Gaa/Taa|E310*|TP53|mRNA|CODING|NM_001126118|NM_001126118.ex.9),STOP_GAINED(HIGH|NONSENSE|Gaa/Taa|E310*|TP53|mRNA|CODING|NM_001276760|NM_001276760.ex.10),STOP_GAINED(HIGH|NONSENSE|Gaa/Taa|E310*|TP53|mRNA|CODING|NM_001276761|NM_001276761.ex.10),STOP_GAINED(HIGH|NONSENSE|Gaa/Taa|E349*|TP53|mRNA|CODING|NM_000546|NM_000546.ex.10),STOP_GAINED(HIGH|NONSENSE|Gaa/Taa|E349*|TP53|mRNA|CODING|NM_001126112|NM_001126112.ex.10),UTR_3_PRIME(MODIFIER||||TP53|mRNA|CODING|NM_001126113|NM_001126113.ex.11),UTR_3_PRIME(MODIFIER||||TP53|mRNA|CODING|NM_001126114|NM_001126114.ex.11),UTR_3_PRIME(MODIFIER||||TP53|mRNA|CODING|NM_001126116|NM_001126116.ex.7),UTR_3_PRIME(MODIFIER||||TP53|mRNA|CODING|NM_001126117|NM_001126117.ex.7),UTR_3_PRIME(MODIFIER||||TP53|mRNA|CODING|NM_001276695|NM_001276695.ex.11),UTR_3_PRIME(MODIFIER||||TP53|mRNA|CODING|NM_001276696|NM_001276696.ex.11),UTR_3_PRIME(MODIFIER||||TP53|mRNA|CODING|NM_001276698|NM_001276698.ex.7),UTR_3_PRIME(MODIFIER||||TP53|mRNA|CODING|NM_001276699|NM_001276699.ex.7)</td><td>E190*</td></tr>
<tr><td>3</td><td>Plasma3-1</td><td>Category II-Default Categorization</td><td>PCLO</td><td>SNP</td><td>7</td><td>82784411</td><td>G</td><td>A</td><td>0.0176</td><td>30</td><td>1705</td><td>NON_SYNONYMOUS_CODING(MODERATE|MISSENSE|Cca/Tca|P516S|PCLO|mRNA|CODING|NM_014510|NM_014510.ex.2),NON_SYNONYMOUS_CODING(MODERATE|MISSENSE|Cca/Tca|P516S|PCLO|mRNA|CODING|NM_033026|NM_033026.ex.2)</td><td>P516S</td></tr>
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<tr><td>3</td><td>Plasma3-1</td><td>Category II-Default Categorization</td><td>PCLO</td><td>SNP</td><td>7</td><td>82784498</td><td>C</td><td>T</td><td>0.00941</td><td>21</td><td>2231</td><td>NON_SYNONYMOUS_CODING(MODERATE|MISSENSE|Gca/Aca|A487T|PCLO|mRNA|CODING|NM_014510|NM_014510.ex.2),NON_SYNONYMOUS_CODING(MODERATE|MISSENSE|Gca/Aca|A487T|PCLO|mRNA|CODING|NM_033026|NM_033026.ex.2)</td><td>A487T</td></tr>
<tr><td>3</td><td>Plasma3-2</td><td>Category II-Default Categorization</td><td>PCLO</td><td>SNP</td><td>7</td><td>82784411</td><td>G</td><td>A</td><td>0.0181</td><td>31</td><td>1712</td><td>NON_SYNONYMOUS_CODING(MODERATE|MISSENSE|Cca/Tca|P516S|PCLO|mRNA|CODING|NM_014510|NM_014510.ex.2),NON_SYNONYMOUS_CODING(MODERATE|MISSENSE|Cca/Tca|P516S|PCLO|mRNA|CODING|NM_033026|NM_033026.ex.2)</td><td>P516S</td></tr>
<tr><td>3</td><td>Plasma3-2</td><td>Category II-Default Categorization</td><td>PCLO</td><td>SNP</td><td>7</td><td>82784498</td><td>C</td><td>T</td><td>0.0137</td><td>31</td><td>2259</td><td>NON_SYNONYMOUS_CODING(MODERATE|MISSENSE|Gca/Aca|A487T|PCLO|mRNA|CODING|NM_014510|NM_014510.ex.2),NON_SYNONYMOUS_CODING(MODERATE|MISSENSE|Gca/Aca|A487T|PCLO|mRNA|CODING|NM_033026|NM_033026.ex.2)</td><td>A487T</td></tr>
<tr><td>3</td><td>Plasma3-3</td><td>Category II-Default Categorization</td><td>PCLO</td><td>SNP</td><td>7</td><td>82784336</td><td>C</td><td>G</td><td>0.00839</td><td>16</td><td>1908</td><td>NON_SYNONYMOUS_CODING(MODERATE|MISSENSE|Gct/Cct|A541P|PCLO|mRNA|CODING|NM_014510|NM_014510.ex.2),NON_SYNONYMOUS_CODING(MODERATE|MISSENSE|Gct/Cct|A541P|PCLO|mRNA|CODING|NM_033026|NM_033026.ex.2)</td><td>A541P</td></tr>
<tr><td>3</td><td>Plasma3-3</td><td>Category II-Default Categorization</td><td>PCLO</td><td>SNP</td><td>7</td><td>82784339</td><td>A</td><td>G</td><td>0.0097</td><td>19</td><td>1958</td><td>NON_SYNONYMOUS_CODING(MODERATE|MISSENSE|Tca/Cca|S540P|PCLO|mRNA|CODING|NM_014510|NM_014510.ex.2),NON_SYNONYMOUS_CODING(MODERATE|MISSENSE|Tca/Cca|S540P|PCLO|mRNA|CODING|NM_033026|NM_033026.ex.2)</td><td>S540P</td></tr>
<tr><td>3</td><td>Plasma3-3</td><td>Category II-Default Categorization</td><td>PCLO</td><td>SNP</td><td>7</td><td>82784411</td><td>G</td><td>A</td><td>0.0113</td><td>51</td><td>4509</td><td>NON_SYNONYMOUS_CODING(MODERATE|MISSENSE|Cca/Tca|P516S|PCLO|mRNA|CODING|NM_014510|NM_014510.ex.2),NON_SYNONYMOUS_CODING(MODERATE|MISSENSE|Cca/Tca|P516S|PCLO|mRNA|CODING|NM_033026|NM_033026.ex.2)</td><td>P516S</td></tr>
<tr><td>3</td><td>Plasma3-3</td><td>Category II-Default Categorization</td><td>KMT2C</td><td>SNP</td><td>7</td><td>151932946</td><td>T</td><td>C</td><td>0.00738</td><td>18</td><td>2439</td><td>NON_SYNONYMOUS_CODING(MODERATE|MISSENSE|Agg/Ggg|R909G|KMT2C|mRNA|CODING|NM_170606|NM_170606.ex.16)</td><td>R909G</td></tr>
<tr><td>4</td><td>tissue-4 Somatic</td><td>Category II-Default Categorization</td><td>LRP1B</td><td>SNP</td><td>2</td><td>141143495</td><td>C</td><td>A</td><td>0.211</td><td>47</td><td>223</td><td>NON_SYNONYMOUS_CODING(MODERATE|MISSENSE|Gac/Tac|D3500Y|LRP1B|mRNA|CODING|NM_018557|NM_018557.ex.67)</td><td>D3500Y</td></tr>
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<tr><td>4</td><td>tissue-4 Somatic</td><td>Category III-Default Categorization</td><td>TP63</td><td>Insertion</td><td>3</td><td>189561962</td><td>C</td><td>CT</td><td>0.0588</td><td>13</td><td>221</td><td>INTRON(MODIFIER||||TP63|mRNA|CODING|NM_001114978|),INTRON(MODIFIER||||TP63|mRNA|CODING|NM_001114979|),INTRON(MODIFIER||||TP63|mRNA|CODING|NM_001114980|),INTRON(MODIFIER||||TP63|mRNA|CODING|NM_001114981|),INTRON(MODIFIER||||TP63|mRNA|CODING|NM_001114982|),INTRON(MODIFIER||||TP63|mRNA|CODING|NM_001329144|),INTRON(MODIFIER||||TP63|mRNA|CODING|NM_001329145|),INTRON(MODIFIER||||TP63|mRNA|CODING|NM_001329146|),INTRON(MODIFIER||||TP63|mRNA|CODING|NM_001329148|),INTRON(MODIFIER||||TP63|mRNA|CODING|NM_001329149|),INTRON(MODIFIER||||TP63|mRNA|CODING|NM_001329150|),INTRON(MODIFIER||||TP63|mRNA|CODING|NM_001329964|),INTRON(MODIFIER||||TP63|mRNA|CODING|NM_003722|)</td><td></td></tr>
<tr><td>4</td><td>tissue-4 Somatic</td><td>Category II-Default Categorization</td><td>SDHA</td><td>SNP</td><td>5</td><td>236649</td><td>C</td><td>T</td><td>0.048</td><td>13</td><td>271</td><td>NON_SYNONYMOUS_CODING(MODERATE|MISSENSE|tCg/tTg|S408L|SDHA|mRNA|CODING|NM_001294332|NM_001294332.ex.9),NON_SYNONYMOUS_CODING(MODERATE|MISSENSE|tCg/tTg|S456L|SDHA|mRNA|CODING|NM_001330758|NM_001330758.ex.10),NON_SYNONYMOUS_CODING(MODERATE|MISSENSE|tCg/tTg|S456L|SDHA|mRNA|CODING|NM_004168|NM_004168.ex.10)</td><td>S408L</td></tr>
<tr><td>4</td><td>tissue-4 Somatic</td><td>Category III-Default Categorization</td><td>SDHA</td><td>SNP</td><td>5</td><td>236653</td><td>C</td><td>A</td><td>0.0509</td><td>14</td><td>275</td><td>SYNONYMOUS_CODING(LOW|SILENT|ctC/ctA|L409|SDHA|mRNA|CODING|NM_001294332|NM_001294332.ex.9),SYNONYMOUS_CODING(LOW|SILENT|ctC/ctA|L457|SDHA|mRNA|CODING|NM_001330758|NM_001330758.ex.10),SYNONYMOUS_CODING(LOW|SILENT|ctC/ctA|L457|SDHA|mRNA|CODING|NM_004168|NM_004168.ex.10)</td><td>L409</td></tr>
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<table>
<tr><td>4</td><td>tissue-4 Somatic</td><td>Category II-Default Categorization</td><td>SDHA</td><td>SNP</td><td>5</td><td>236676</td><td>G</td><td>A</td><td>0.0511</td><td>14</td><td>274</td><td>NON_SYNONYMOUS_CODING(MODERATE|MISSENSE|cGg/cAg|R417Q|SDHA|mRNA|CODING|NM_001294332|NM_001294332.ex.9),NON_SYNONYMOUS_CODING(MODERATE|MISSENSE|cGg/cAg|R465Q|SDHA|mRNA|CODING|NM_001330758|NM_001330758.ex.10),NON_SYNONYMOUS_CODING(MODERATE|MISSENSE|cGg/cAg|R465Q|SDHA|mRNA|CODING|NM_004168|NM_004168.ex.10)</td><td>R417Q</td></tr>
<tr><td>4</td><td>tissue-4 Somatic</td><td>Category II-Default Categorization</td><td>SDHA</td><td>SNP</td><td>5</td><td>236678</td><td>G</td><td>A</td><td>0.0519</td><td>14</td><td>270</td><td>NON_SYNONYMOUS_CODING(MODERATE|MISSENSE|Gca/Aca|A418T|SDHA|mRNA|CODING|NM_001294332|NM_001294332.ex.9),NON_SYNONYMOUS_CODING(MODERATE|MISSENSE|Gca/Aca|A466T|SDHA|mRNA|CODING|NM_001330758|NM_001330758.ex.10),NON_SYNONYMOUS_CODING(MODERATE|MISSENSE|Gca/Aca|A466T|SDHA|mRNA|CODING|NM_004168|NM_004168.ex.10)</td><td>A418T</td></tr>
<tr><td>4</td><td>tissue-4 Somatic</td><td>Category III-Default Categorization</td><td>SDHA</td><td>SNP</td><td>5</td><td>236734</td><td>G</td><td>C</td><td>0.0604</td><td>11</td><td>182</td><td>INTRON(MODIFIER||||SDHA|mRNA|CODING|NM_001294332|),INTRON(MODIFIER||||SDHA|mRNA|CODING|NM_001330758|),INTRON(MODIFIER||||SDHA|mRNA|CODING|NM_004168|)</td><td></td></tr>
<tr><td>4</td><td>tissue-4 Somatic</td><td>Category II-Default Categorization</td><td>SDHA</td><td>SNP</td><td>5</td><td>254529</td><td>T</td><td>C</td><td>0.0815</td><td>19</td><td>233</td><td>NON_SYNONYMOUS_CODING(MODERATE|MISSENSE|Tac/Cac|Y525H|SDHA|mRNA|CODING|NM_001330758|NM_001330758.ex.12),NON_SYNONYMOUS_CODING(MODERATE|MISSENSE|Tac/Cac|Y558H|SDHA|mRNA|CODING|NM_001294332|NM_001294332.ex.13),NON_SYNONYMOUS_CODING(MODERATE|MISSENSE|Tac/Cac|Y606H|SDHA|mRNA|CODING|NM_004168|NM_004168.ex.14)</td><td>Y525H</td></tr>
<tr><td>4</td><td>tissue-4 Somatic</td><td>Category II-Default Categorization</td><td>SDHA</td><td>SNP</td><td>5</td><td>254574</td><td>C</td><td>T</td><td>0.0781</td><td>15</td><td>192</td><td>NON_SYNONYMOUS_CODING(MODERATE|MISSENSE|Cac/Tac|H540Y|SDHA|mRNA|CODING|NM_001330758|NM_001330758.ex.12),NON_SYNONYMOUS_CODING(MODERATE|MISSENSE|Cac/Tac|H573Y|SDHA|mRNA|CODING|NM_001294332|NM_001294332.ex.13),NON_SYNONYMOUS_CODING(MODERATE|MISSENSE|Cac/Tac|H621Y|SDHA|mRNA|CODING|NM_004168|NM_004168.ex.14)</td><td>H540Y</td></tr>
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4	tissue-4 Somatic	Category III-Default Categorization	PCLO	SNP	7	82784373	T	C	0.0193	12	623	SYNONYMOUS_CODING(LOW|SILENT|aaA/aaG|K528|PCLO|mRNA|CODING|NM_014510|NM_014510.ex.2),SYNONYMOUS_CODING(LOW|SILENT|aaA/aaG|K528|PCLO|mRNA|CODING|NM_033026|NM_033026.ex.2)	K528
4	tissue-4 Somatic	Category II-Default Categorization	PCLO	SNP	7	82784378	T	C	0.0175	13	743	NON_SYNONYMOUS_CODING(MODERATE|MISSENSE|Aca/Gca|T527A|PCLO|mRNA|CODING|NM_014510|NM_014510.ex.2),NON_SYNONYMOUS_CODING(MODERATE|MISSENSE|Aca/Gca|T527A|PCLO|mRNA|CODING|NM_033026|NM_033026.ex.2)	T527A
4	tissue-4 Somatic	Category II-Default Categorization	PCLO	SNP	7	82784441	A	G	0.0211	12	570	NON_SYNONYMOUS_CODING(MODERATE|MISSENSE|Tca/Cca|S506P|PCLO|mRNA|CODING|NM_014510|NM_014510.ex.2),NON_SYNONYMOUS_CODING(MODERATE|MISSENSE|Tca/Cca|S506P|PCLO|mRNA|CODING|NM_033026|NM_033026.ex.2)	S506P
4	tissue-4 Somatic	Category II-Default Categorization	KMT2C	SNP	7	151932997	C	T	0.0392	10	255	NON_SYNONYMOUS_CODING(MODERATE|MISSENSE|Gga/Aga|G892R|KMT2C|mRNA|CODING|NM_170606|NM_170606.ex.16)	G892R

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<tr><td>4</td><td>tissue-4 Somatic</td><td>Category I-Default Categorization</td><td>FGFR1</td><td>Insertion</td><td>8</td><td>38272121</td><td>T</td><td>TC</td><td>0.0358</td><td>14</td><td>391</td><td>FRAME_SHIFT(HIGH||||FGFR1|mRNA|CODING|NM_001174063|NM_001174063.ex.15),FRAME_SHIFT(HIGH||||FGFR1|mRNA|CODING|NM_001174064|NM_001174064.ex.16),FRAME_SHIFT(HIGH||||FGFR1|mRNA|CODING|NM_001174065|NM_001174065.ex.15),FRAME_SHIFT(HIGH||||FGFR1|mRNA|CODING|NM_001174066|NM_001174066.ex.14),FRAME_SHIFT(HIGH||||FGFR1|mRNA|CODING|NM_001174067|NM_001174067.ex.16),FRAME_SHIFT(HIGH||||FGFR1|mRNA|CODING|NM_001354367|NM_001354367.ex.15),FRAME_SHIFT(HIGH||||FGFR1|mRNA|CODING|NM_001354368|NM_001354368.ex.14),FRAME_SHIFT(HIGH||||FGFR1|mRNA|CODING|NM_001354369|NM_001354369.ex.15),FRAME_SHIFT(HIGH||||FGFR1|mRNA|CODING|NM_001354370|NM_001354370.ex.14),FRAME_SHIFT(HIGH||||FGFR1|mRNA|CODING|NM_015850|NM_015850.ex.15),FRAME_SHIFT(HIGH||||FGFR1|mRNA|CODING|NM_023105|NM_023105.ex.14),FRAME_SHIFT(HIGH||||FGFR1|mRNA|CODING|NM_023106|NM_023106.ex.14),FRAME_SHIFT(HIGH||||FGFR1|mRNA|CODING|NM_023110|NM_023110.ex.15)</td><td></td></tr>
<tr><td>4</td><td>tissue-4 Somatic</td><td>Category III-Default Categorization</td><td>NDRG1</td><td>SNP</td><td>8</td><td>134251253</td><td>T</td><td>G</td><td>0.0192</td><td>13</td><td>676</td><td>SYNONYMOUS_CODING(LOW|SILENT|cgA/cgC|R270|NDRG1|mRNA|CODING|NM_001258433|NM_001258433.ex.15),SYNONYMOUS_CODING(LOW|SILENT|cgA/cgC|R285|NDRG1|mRNA|CODING|NM_001258432|NM_001258432.ex.14),SYNONYMOUS_CODING(LOW|SILENT|cgA/cgC|R351|NDRG1|mRNA|CODING|NM_001135242|NM_001135242.ex.16),SYNONYMOUS_CODING(LOW|SILENT|cgA/cgC|R351|NDRG1|mRNA|CODING|NM_006096|NM_006096.ex.16)</td><td>R270</td></tr>
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4	tissue-4 Somatic	Category III-Default Categorization	RECQL4	SNP	8	145738583	G	T	0.0192	14	730	DOWNSTREAM(MODIFIER||||MFSD3|Non-coding_transcript|CODING|NM_138431|),DOWNSTREAM(MODIFIER||||MFSD3|Non-coding_transcript|CODING|NR_130120|),INTRON(MODIFIER||||RECQL4|mRNA|CODING|NM_004260|),UPSTREAM(MODIFIER||||LRRC14|mRNA|CODING|NM_001272036|),UPSTREAM(MODIFIER||||LRRC14|mRNA|CODING|NM_014665|)	
4	tissue-4 Somatic	Category I-Default Categorization	KMT2D	Insertion	12	49424100	A	ATC	0.219	70	320	FRAME_SHIFT(HIGH||||KMT2D|mRNA|CODING|NM_003482|NM_003482.ex.42)	
4	tissue-4 Somatic	Category III-Default Categorization	KMT2D	SNP	12	49444937	G	T	0.0113	11	977	SYNONYMOUS_CODING(LOW|SILENT|tcC/tcA|S843|KMT2D|mRNA|CODING|NM_003482|NM_003482.ex.10)	S843
4	tissue-4 Somatic	Category II-Default Categorization	KMT2D	SNP	12	49445038	T	G	0.0121	10	829	NON_SYNONYMOUS_CODING(MODERATE|MISSENSE|Act/Cct|T810P|KMT2D|mRNA|CODING|NM_003482|NM_003482.ex.10)	T810P
4	tissue-4 Somatic	Category III-Default Categorization	KMT2D	SNP	12	49445399	G	C	0.0166	18	1086	SYNONYMOUS_CODING(LOW|SILENT|ctC/ctG|L689|KMT2D|mRNA|CODING|NM_003482|NM_003482.ex.10)	L689
4	tissue-4 Somatic	Category III-Default Categorization	KMT2D	SNP	12	49445408	A	T	0.0195	21	1075	SYNONYMOUS_CODING(LOW|SILENT|gcT/gcA|A686|KMT2D|mRNA|CODING|NM_003482|NM_003482.ex.10)	A686
4	tissue-4 Somatic	Category III-Default Categorization	KMT2D	SNP	12	49445420	A	T	0.019	19	998	SYNONYMOUS_CODING(LOW|SILENT|ccT/ccA|P682|KMT2D|mRNA|CODING|NM_003482|NM_003482.ex.10)	P682
4	tissue-4 Somatic	Category III-Default Categorization	KMT2D	SNP	12	49446062	T	G	0.0195	11	565	SYNONYMOUS_CODING(LOW|SILENT|tcA/tcC|S468|KMT2D|mRNA|CODING|NM_003482|NM_003482.ex.10)	S468
4	plasma4-1	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A
4	plasma4-2	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A
4	plasma4-3	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A
5	tissue-5 Somatic	Category I-Default Categorization	SPEN	Deletion	1	16255141	GGA	G	0.0796	37	465	FRAME_SHIFT(HIGH||||SPEN|mRNA|CODING|NM_015001|NM_015001.ex.11)	
5	tissue-5 Somatic	Category III-Default Categorization	LRP1B	SNP	2	141457985	T	A	0.437	240	549	SYNONYMOUS_CODING(LOW|SILENT|ccA/ccT|P2211|LRP1B|mRNA|CODING|NM_018557|NM_018557.ex.41)	P2211

5	tissue-5 Somatic	Category III-Default Categorization	LRP1B	SNP	2	141707868	G	T	0.49	192	392	SYNONYMOUS_CODING(LOW|SILENT|gcC/gcA|A1024|LRP1B|mRNA|CODING|NM_018557|NM_018557.ex.20)	A1024
5	tissue-5 Somatic	Category III-Default Categorization	LRP1B	SNP	2	141709406	T	G	0.49	117	239	INTRON(MODIFIER||||LRP1B|mRNA|CODING|NM_018557|)	
5	tissue-5 Somatic	Category I-Default Categorization	WWTR1	Insertion	3	149238595	C	CTTAA	0.375	117	312	FRAME_SHIFT(HIGH||||WWTR1|mRNA|CODING|NM_001168278|NM_001168278.ex.8),FRAME_SHIFT(HIGH||||WWTR1|mRNA|CODING|NM_001168280|NM_001168280.ex.7),FRAME_SHIFT(HIGH||||WWTR1|mRNA|CODING|NM_001348362|NM_001348362.ex.10),FRAME_SHIFT(HIGH||||WWTR1|mRNA|CODING|NM_015472|NM_015472.ex.7)	
5	tissue-5 Somatic	Category III-Default Categorization	MLF1	SNP	3	158306627	A	G	1	297	297	INTRON(MODIFIER||||MLF1|mRNA|CODING|NM_001130156|),INTRON(MODIFIER||||MLF1|mRNA|CODING|NM_001130157|),INTRON(MODIFIER||||MLF1|mRNA|CODING|NM_001195432|),INTRON(MODIFIER||||MLF1|mRNA|CODING|NM_001195433|),INTRON(MODIFIER||||MLF1|mRNA|CODING|NM_001195434|),INTRON(MODIFIER||||MLF1|mRNA|CODING|NM_022443|)	
5	tissue-5 Somatic	Category III-Default Categorization	MLF1	SNP	3	158320597	T	C	1	285	285	SYNONYMOUS_CODING(LOW|SILENT|agT/agC|S122|MLF1|mRNA|CODING|NM_001195433|NM_001195433.ex.6),SYNONYMOUS_CODING(LOW|SILENT|agT/agC|S165|MLF1|mRNA|CODING|NM_001130156|NM_001130156.ex.6),SYNONYMOUS_CODING(LOW|SILENT|agT/agC|S165|MLF1|mRNA|CODING|NM_001130157|NM_001130157.ex.7),SYNONYMOUS_CODING(LOW|SILENT|agT/agC|S180|MLF1|mRNA|CODING|NM_001195434|NM_001195434.ex.8),SYNONYMOUS_CODING(LOW|SILENT|agT/agC|S190|MLF1|mRNA|CODING|NM_022443|NM_022443.ex.6),SYNONYMOUS_CODING(LOW|SILENT|agT/agC|S221|MLF1|mRNA|CODING|NM_001195432|NM_001195432.ex.8)	S122

<table>
<tr><td>5</td><td>tissue-5 Somatic</td><td>Category II-Default Categorization</td><td>MLF1</td><td>SNP</td><td>3</td><td>158320703</td><td>C</td><td>A</td><td>1</td><td>279</td><td>279</td><td>NON_SYNONYMOUS_CODING(MODERATE|MISSENSE|Cct/Act|P158T|MLF1|mRNA|CODING|NM_001195433|NM_001195433.ex.6),NON_SYNONYMOUS_CODING(MODERATE|MISSENSE|Cct/Act|P201T|MLF1|mRNA|CODING|NM_001130156|NM_001130156.ex.6),NON_SYNONYMOUS_CODING(MODERATE|MISSENSE|Cct/Act|P201T|MLF1|mRNA|CODING|NM_001130157|NM_001130157.ex.7),NON_SYNONYMOUS_CODING(MODERATE|MISSENSE|Cct/Act|P216T|MLF1|mRNA|CODING|NM_001195434|NM_001195434.ex.8),NON_SYNONYMOUS_CODING(MODERATE|MISSENSE|Cct/Act|P226T|MLF1|mRNA|CODING|NM_022443|NM_022443.ex.6),NON_SYNONYMOUS_CODING(MODERATE|MISSENSE|Cct/Act|P257T|MLF1|mRNA|CODING|NM_001195432|NM_001195432.ex.8)</td><td>P158T</td></tr>
<tr><td>5</td><td>tissue-5 Somatic</td><td>Category II-Default Categorization</td><td>MECOM</td><td>SNP</td><td>3</td><td>169098992</td><td>G</td><td>A</td><td>0.482</td><td>264</td><td>548</td><td>INTRON(MODIFIER||||MECOM|mRNA|CODING|NM_001205194|),NON_SYNONYMOUS_CODING(MODERATE|MISSENSE|Ccc/Tcc|P120S|MECOM|mRNA|CODING|NM_004991|NM_004991.ex.2)</td><td>P120S</td></tr>
<tr><td>5</td><td>tissue-5 Somatic</td><td>Category III-Default Categorization</td><td>PIK3CA</td><td>SNP</td><td>3</td><td>178922274</td><td>C</td><td>A</td><td>0.47</td><td>125</td><td>266</td><td>INTRON(MODIFIER||||PIK3CA|mRNA|CODING|NM_006218|)</td><td></td></tr>
<tr><td>5</td><td>tissue-5 Somatic</td><td>Category III-Default Categorization</td><td>PIK3CA</td><td>SNP</td><td>3</td><td>178937877</td><td>A</td><td>G</td><td>0.329</td><td>27</td><td>82</td><td>INTRON(MODIFIER||||PIK3CA|mRNA|CODING|NM_006218|)</td><td></td></tr>
<tr><td>5</td><td>tissue-5 Somatic</td><td>Category III-Default Categorization</td><td>PIK3CA</td><td>SNP</td><td>3</td><td>178938747</td><td>A</td><td>T</td><td>0.567</td><td>51</td><td>90</td><td>INTRON(MODIFIER||||PIK3CA|mRNA|CODING|NM_006218|)</td><td></td></tr>
<tr><td>5</td><td>tissue-5 Somatic</td><td>Category III-Default Categorization</td><td>MAP3K13</td><td>SNP</td><td>3</td><td>185146702</td><td>C</td><td>T</td><td>0.482</td><td>512</td><td>1062</td><td>INTRON(MODIFIER||||MAP3K13|Non-coding_transcript|CODING|NM_001242317|),SYNONYMOUS_CODING(LOW|SILENT|agC/agT|S111|MAP3K13|Non-coding_transcript|CODING|NM_001242314|NM_001242314.ex.3),SYNONYMOUS_CODING(LOW|SILENT|agC/agT|S111|MAP3K13|Non-coding_transcript|CODING|NM_004721|NM_004721.ex.2)</td><td>S111</td></tr>
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5	tissue-5 Somatic	Category III-Default Categorization	LPP	SNP	3	188590446	A	G	0.486	320	658	SYNONYMOUS_CODING(LOW|SILENT|cgA/cgG|R388|LPP|mRNA|CODING|NM_001167672|NM_001167672.ex.9),SYNONYMOUS_CODING(LOW|SILENT|cgA/cgG|R535|LPP|mRNA|CODING|NM_001167671|NM_001167671.ex.10),SYNONYMOUS_CODING(LOW|SILENT|cgA/cgG|R535|LPP|mRNA|CODING|NM_005578|NM_005578.ex.10)	R388

<table>
<tr><td>5</td><td>tissue-5 Somatic</td><td>Category II-Default Categorization</td><td>TP63</td><td>SNP</td><td>3</td><td>189526115</td><td>G</td><td>A</td><td>0.0849</td><td>69</td><td>813</td><td>INTRON(MODIFIER||||TP63|mRNA|CODING|NM_001329146|),INTRON(MODIFIER||||TP63|mRNA|CODING|NM_001329150|),NON_SYNONYMOUS_CODING(MODERATE|MISSENSE|Ggc/Agc|G125S|TP63|mRNA|CODING|NM_001329964|NM_001329964.ex.4),NON_SYNONYMOUS_CODING(MODERATE|MISSENSE|Ggc/Agc|G127S|TP63|mRNA|CODING|NM_001114978|NM_001114978.ex.4),NON_SYNONYMOUS_CODING(MODERATE|MISSENSE|Ggc/Agc|G127S|TP63|mRNA|CODING|NM_001114979|NM_001114979.ex.4),NON_SYNONYMOUS_CODING(MODERATE|MISSENSE|Ggc/Agc|G127S|TP63|mRNA|CODING|NM_001329144|NM_001329144.ex.4),NON_SYNONYMOUS_CODING(MODERATE|MISSENSE|Ggc/Agc|G127S|TP63|mRNA|CODING|NM_001329148|NM_001329148.ex.4),NON_SYNONYMOUS_CODING(MODERATE|MISSENSE|Ggc/Agc|G127S|TP63|mRNA|CODING|NM_003722|NM_003722.ex.4),NON_SYNONYMOUS_CODING(MODERATE|MISSENSE|Ggc/Agc|G33S|TP63|mRNA|CODING|NM_001114980|NM_001114980.ex.2),NON_SYNONYMOUS_CODING(MODERATE|MISSENSE|Ggc/Agc|G33S|TP63|mRNA|CODING|NM_001114981|NM_001114981.ex.2),NON_SYNONYMOUS_CODING(MODERATE|MISSENSE|Ggc/Agc|G33S|TP63|mRNA|CODING|NM_001114982|NM_001114982.ex.2),NON_SYNONYMOUS_CODING(MODERATE|MISSENSE|Ggc/Agc|G33S|TP63|mRNA|CODING|NM_001329145|NM_001329145.ex.2),NON_SYNONYMOUS_CODING(MODERATE|MISSENSE|Ggc/Agc|G33S|TP63|mRNA|CODING|NM_001329149|NM_001329149.ex.2)</td><td>G125S</td></tr>
</table>

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<tr><td>5</td><td>tissue-5 Somatic</td><td>Category II-Default Categorization</td><td>FAT4</td><td>SNP</td><td>4</td><td>126241335</td><td>C</td><td>G</td><td>0.429</td><td>311</td><td>725</td><td>NON_SYNONYMOUS_CODING(MODERATE|MISSENSE|Cag/Gag|Q1257E|FAT4|mRNA|CODING|NM_001291285|NM_001291285.ex.1),NON_SYNONYMOUS_CODING(MODERATE|MISSENSE|Cag/Gag|Q1257E|FAT4|mRNA|CODING|NM_001291303|NM_001291303.ex.1),NON_SYNONYMOUS_CODING(MODERATE|MISSENSE|Cag/Gag|Q1257E|FAT4|mRNA|CODING|NM_024582|NM_024582.ex.1)</td><td>Q1257E</td></tr>
<tr><td>5</td><td>tissue-5 Somatic</td><td>Category III-Default Categorization</td><td>FAT4</td><td>SNP</td><td>4</td><td>126336703</td><td>T</td><td>C</td><td>0.486</td><td>621</td><td>1278</td><td>SYNONYMOUS_CODING(LOW|SILENT|aaT/aaC|N2195|FAT4|mRNA|CODING|NM_001291285|NM_001291285.ex.5),SYNONYMOUS_CODING(LOW|SILENT|aaT/aaC|N2195|FAT4|mRNA|CODING|NM_001291303|NM_001291303.ex.5),SYNONYMOUS_CODING(LOW|SILENT|aaT/aaC|N2195|FAT4|mRNA|CODING|NM_024582|NM_024582.ex.5)</td><td>N2195</td></tr>
<tr><td>5</td><td>tissue-5 Somatic</td><td>Category II-Default Categorization</td><td>FAT4</td><td>SNP</td><td>4</td><td>126372742</td><td>G</td><td>A</td><td>0.463</td><td>416</td><td>898</td><td>NON_SYNONYMOUS_CODING(MODERATE|MISSENSE|gGc/gAc|G3524D|FAT4|mRNA|CODING|NM_024582|NM_024582.ex.9),NON_SYNONYMOUS_CODING(MODERATE|MISSENSE|gGc/gAc|G3526D|FAT4|mRNA|CODING|NM_001291285|NM_001291285.ex.9),NON_SYNONYMOUS_CODING(MODERATE|MISSENSE|gGc/gAc|G3526D|FAT4|mRNA|CODING|NM_001291303|NM_001291303.ex.9)</td><td>G3524D</td></tr>
<tr><td>5</td><td>tissue-5 Somatic</td><td>Category II-Default Categorization</td><td>FBXW7</td><td>SNP</td><td>4</td><td>153249385</td><td>G</td><td>A</td><td>0.0668</td><td>30</td><td>449</td><td>NON_SYNONYMOUS_CODING(MODERATE|MISSENSE|Cgt/Tgt|R347C|FBXW7|mRNA|CODING|NM_001013415|NM_001013415.ex.8),NON_SYNONYMOUS_CODING(MODERATE|MISSENSE|Cgt/Tgt|R385C|FBXW7|mRNA|CODING|NM_018315|NM_018315.ex.8),NON_SYNONYMOUS_CODING(MODERATE|MISSENSE|Cgt/Tgt|R465C|FBXW7|mRNA|CODING|NM_001349798|NM_001349798.ex.11),NON_SYNONYMOUS_CODING(MODERATE|MISSENSE|Cgt/Tgt|R465C|FBXW7|mRNA|CODING|NM_033632|NM_033632.ex.9)</td><td>R347C</td></tr>
<tr><td>5</td><td>tissue-5 Somatic</td><td>Category III-Default Categorization</td><td>FAT1</td><td>SNP</td><td>4</td><td>187516880</td><td>A</td><td>G</td><td>0.436</td><td>184</td><td>422</td><td>SYNONYMOUS_CODING(LOW|SILENT|tcT/tcC|S4367|FAT1|mRNA|CODING|NM_005245|NM_005245.ex.26)</td><td>S4367</td></tr>
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5	tissue-5 Somatic	Category III-Default Categorization	FAT1	SNP	4	187518871	G	A	0.422	121	287	SYNONYMOUS_CODING(LOW|SILENT|gcC/gcT|A4111|FAT1|mRNA|CODING|NM_005245|NM_005245.ex.24)	A4111
5	tissue-5 Somatic	Category II-Default Categorization	FAT1	SNP	4	187525020	A	C	0.456	400	877	NON_SYNONYMOUS_CODING(MODERATE|MISSENSE|Tct/Gct|S3554A|FAT1|mRNA|CODING|NM_005245|NM_005245.ex.19)	S3554A
5	tissue-5 Somatic	Category III-Default Categorization	FAT1	SNP	4	187534363	G	A	0.459	272	593	SYNONYMOUS_CODING(LOW|SILENT|aaC/aaT|N3121|FAT1|mRNA|CODING|NM_005245|NM_005245.ex.13)	N3121
5	tissue-5 Somatic	Category III-Default Categorization	FAT1	SNP	4	187534375	A	G	0.466	280	601	SYNONYMOUS_CODING(LOW|SILENT|gaT/gaC|D3117|FAT1|mRNA|CODING|NM_005245|NM_005245.ex.13)	D3117
5	tissue-5 Somatic	Category III-Default Categorization	FAT1	SNP	4	187538330	G	A	0.509	116	228	SYNONYMOUS_CODING(LOW|SILENT|gcC/gcT|A2968|FAT1|mRNA|CODING|NM_005245|NM_005245.ex.11)	A2968
5	tissue-5 Somatic	Category II-Default Categorization	FAT1	SNP	4	187538942	T	A	0.442	338	765	NON_SYNONYMOUS_CODING(MODERATE|MISSENSE|cAa/cTa|Q2933L|FAT1|mRNA|CODING|NM_005245|NM_005245.ex.10)	Q2933L
5	tissue-5 Somatic	Category III-Default Categorization	FAT1	SNP	4	187629497	G	A	0.462	429	929	SYNONYMOUS_CODING(LOW|SILENT|aaC/aaT|N495|FAT1|mRNA|CODING|NM_005245|NM_005245.ex.2)	N495
5	tissue-5 Somatic	Category II-Default Categorization	FAT1	SNP	4	187629538	C	T	0.459	431	940	NON_SYNONYMOUS_CODING(MODERATE|MISSENSE|Gtc/Atc|V482I|FAT1|mRNA|CODING|NM_005245|NM_005245.ex.2)	V482I
5	tissue-5 Somatic	Category II-Default Categorization	FAT1	SNP	4	187629770	A	C	0.48	412	858	NON_SYNONYMOUS_CODING(MODERATE|MISSENSE|agT/agG|S404R|FAT1|mRNA|CODING|NM_005245|NM_005245.ex.2)	S404R
5	tissue-5 Somatic	Category II-Default Categorization	SDHA	SNP	5	236676	G	A	0.0244	11	451	NON_SYNONYMOUS_CODING(MODERATE|MISSENSE|cGg/cAg|R417Q|SDHA|mRNA|CODING|NM_001294332|NM_001294332.ex.9),NON_SYNONYMOUS_CODING(MODERATE|MISSENSE|cGg/cAg|R465Q|SDHA|mRNA|CODING|NM_001330758|NM_001330758.ex.10),NON_SYNONYMOUS_CODING(MODERATE|MISSENSE|cGg/cAg|R465Q|SDHA|mRNA|CODING|NM_004168|NM_004168.ex.10)	R417Q

5	tissue-5 Somatic	Category II-Default Categorization	SDHA	SNP	5	236678	G	A	0.0264	12	454	NON_SYNONYMOUS_CODING(MODERATE|MISSENSE|Gca/Aca|A418T|SDHA|mRNA|CODING|NM_001294332|NM_001294332.ex.9),NON_SYNONYMOUS_CODING(MODERATE|MISSENSE|Gca/Aca|A466T|SDHA|mRNA|CODING|NM_001330758|NM_001330758.ex.10),NON_SYNONYMOUS_CODING(MODERATE|MISSENSE|Gca/Aca|A466T|SDHA|mRNA|CODING|NM_004168|NM_004168.ex.10)	A418T
5	tissue-5 Somatic	Category II-Default Categorization	SDHA	SNP	5	251503	A	G	0.0262	25	953	INTRON(MODIFIER||||SDHA|mRNA|CODING|NM_001330758|),NON_SYNONYMOUS_CODING(MODERATE|MISSENSE|Atg/Gtg|M524V|SDHA|mRNA|CODING|NM_001294332|NM_001294332.ex.12),NON_SYNONYMOUS_CODING(MODERATE|MISSENSE|Atg/Gtg|M572V|SDHA|mRNA|CODING|NM_004168|NM_004168.ex.13)	M524V
5	tissue-5 Somatic	Category II-Default Categorization	SDHA	SNP	5	254529	T	C	0.0236	11	466	NON_SYNONYMOUS_CODING(MODERATE|MISSENSE|Tac/Cac|Y525H|SDHA|mRNA|CODING|NM_001330758|NM_001330758.ex.12),NON_SYNONYMOUS_CODING(MODERATE|MISSENSE|Tac/Cac|Y558H|SDHA|mRNA|CODING|NM_001294332|NM_001294332.ex.13),NON_SYNONYMOUS_CODING(MODERATE|MISSENSE|Tac/Cac|Y606H|SDHA|mRNA|CODING|NM_004168|NM_004168.ex.14)	Y525H
5	tissue-5 Somatic	Category II-Default Categorization	SDHA	SNP	5	254574	C	T	0.0287	10	349	NON_SYNONYMOUS_CODING(MODERATE|MISSENSE|Cac/Tac|H540Y|SDHA|mRNA|CODING|NM_001330758|NM_001330758.ex.12),NON_SYNONYMOUS_CODING(MODERATE|MISSENSE|Cac/Tac|H573Y|SDHA|mRNA|CODING|NM_001294332|NM_001294332.ex.13),NON_SYNONYMOUS_CODING(MODERATE|MISSENSE|Cac/Tac|H621Y|SDHA|mRNA|CODING|NM_004168|NM_004168.ex.14)	H540Y
5	tissue-5 Somatic	Category I-Default Categorization	SDHA	Deletion	5	256483	CTT	C	0.0635	23	362	FRAME_SHIFT(HIGH||||SDHA|mRNA|CODING|NM_001294332|NM_001294332.ex.14),FRAME_SHIFT(HIGH||||SDHA|mRNA|CODING|NM_001330758|NM_001330758.ex.13),FRAME_SHIFT(HIGH||||SDHA|mRNA|CODING|NM_004168|NM_004168.ex.15)	

<table>
<tr><td>5</td><td>tissue-5 Somatic</td><td>Category III-Default Categorization</td><td>TRIP13</td><td>SNP</td><td>5</td><td>917106</td><td>G</td><td>C</td><td>0.504</td><td>240</td><td>476</td><td>INTRON(MODIFIER||||TRIP13|mRNA|CODING|NM_004237|)</td><td></td></tr>
<tr><td>5</td><td>tissue-5 Somatic</td><td>Category II-Default Categorization</td><td>TERT</td><td>SNP</td><td>5</td><td>1255520</td><td>G</td><td>A</td><td>0.482</td><td>200</td><td>415</td><td>NON_SYNONYMOUS_CODING(MODERATE|MISSENSE|aCg/aTg|T897M|TERT|mRNA|CODING|NR_149163|NR_149163.ex.11),NON_SYNONYMOUS_CODING(MODERATE|MISSENSE|aCg/aTg|T909M|TERT|mRNA|CODING|NR_149162|NR_149162.ex.11),SYNONYMOUS_CODING(LOW|SILENT|caC/caT|H1013|TERT|mRNA|CODING|NM_198253|NM_198253.ex.14),SYNONYMOUS_CODING(LOW|SILENT|caC/caT|H950|TERT|mRNA|CODING|NM_001193376|NM_001193376.ex.13)</td><td>T897M</td></tr>
<tr><td>5</td><td>tissue-5 Somatic</td><td>Category II-Default Categorization</td><td>TERT</td><td>SNP</td><td>5</td><td>1294086</td><td>C</td><td>T</td><td>0.502</td><td>831</td><td>1655</td><td>NON_SYNONYMOUS_CODING(MODERATE|MISSENSE|Ggg/Agg|G325R|TERT|mRNA|CODING|NR_149162|NR_149162.ex.2),NON_SYNONYMOUS_CODING(MODERATE|MISSENSE|Ggg/Agg|G325R|TERT|mRNA|CODING|NR_149163|NR_149163.ex.2),SYNONYMOUS_CODING(LOW|SILENT|gcG/gcA|A305|TERT|mRNA|CODING|NM_001193376|NM_001193376.ex.2),SYNONYMOUS_CODING(LOW|SILENT|gcG/gcA|A305|TERT|mRNA|CODING|NM_198253|NM_198253.ex.2)</td><td>G325R</td></tr>
<tr><td>5</td><td>tissue-5 Somatic</td><td>Category III-Default Categorization</td><td>ROS1</td><td>SNP</td><td>6</td><td>117631414</td><td>G</td><td>A</td><td>0.479</td><td>68</td><td>142</td><td>SYNONYMOUS_CODING(LOW|SILENT|tcC/tcT|S2088|ROS1|mRNA|CODING|NM_002944|NM_002944.ex.40)</td><td>S2088</td></tr>
<tr><td>5</td><td>tissue-5 Somatic</td><td>Category III-Default Categorization</td><td>ROS1</td><td>SNP</td><td>6</td><td>117641016</td><td>G</td><td>A</td><td>0.51</td><td>76</td><td>149</td><td>INTRON(MODIFIER||||ROS1|mRNA|CODING|NM_002944|)</td><td></td></tr>
<tr><td>5</td><td>tissue-5 Somatic</td><td>Category III-Default Categorization</td><td>ROS1</td><td>SNP</td><td>6</td><td>117642418</td><td>A</td><td>C</td><td>0.563</td><td>175</td><td>311</td><td>INTRON(MODIFIER||||ROS1|mRNA|CODING|NM_002944|)</td><td></td></tr>
<tr><td>5</td><td>tissue-5 Somatic</td><td>Category III-Default Categorization</td><td>ROS1</td><td>SNP</td><td>6</td><td>117642457</td><td>G</td><td>A</td><td>0.442</td><td>189</td><td>428</td><td>SYNONYMOUS_CODING(LOW|SILENT|gcC/gcT|A1914|ROS1|mRNA|CODING|NM_002944|NM_002944.ex.35)</td><td>A1914</td></tr>
<tr><td>5</td><td>tissue-5 Somatic</td><td>Category III-Default Categorization</td><td>ROS1</td><td>SNP</td><td>6</td><td>117662682</td><td>A</td><td>G</td><td>0.465</td><td>451</td><td>969</td><td>SYNONYMOUS_CODING(LOW|SILENT|Ttg/Ctg|L1595|ROS1|mRNA|CODING|NM_002944|NM_002944.ex.29)</td><td>L1595</td></tr>
</table>

5	tissue-5 Somatic	Category III-Default Categorization	EGFR	SNP	7	55238087	C	T	0.482	388	805	DOWNSTREAM(MODIFIER||||EGFR|mRNA|CODING|NM_201282|),INTRON(MODIFIER||||EGFR|mRNA|CODING|NM_001346897|),INTRON(MODIFIER||||EGFR|mRNA|CODING|NM_001346898|),INTRON(MODIFIER||||EGFR|mRNA|CODING|NM_001346899|),INTRON(MODIFIER||||EGFR|mRNA|CODING|NM_001346900|),INTRON(MODIFIER||||EGFR|mRNA|CODING|NM_001346941|),INTRON(MODIFIER||||EGFR|mRNA|CODING|NM_005228|),SYNONYMOUS_CODING(LOW|SILENT|caC/caT|H656|EGFR|mRNA|CODING|NM_201284|NM_201284.ex.16)	H656
5	tissue-5 Somatic	Category III-Default Categorization	PCLO	SNP	7	82435033	C	T	0.415	218	525	SYNONYMOUS_CODING(LOW|SILENT|ggG/ggA|G4968|PCLO|mRNA|CODING|NM_033026|NM_033026.ex.21)	G4968
5	tissue-5 Somatic	Category III-Default Categorization	PCLO	SNP	7	82545020	G	A	0.104	115	1107	SYNONYMOUS_CODING(LOW|SILENT|ttC/ttT|F4094|PCLO|mRNA|CODING|NM_014510|NM_014510.ex.7),SYNONYMOUS_CODING(LOW|SILENT|ttC/ttT|F4094|PCLO|mRNA|CODING|NM_033026|NM_033026.ex.7)	F4094
5	tissue-5 Somatic	Category II-Default Categorization	PCLO	SNP	7	82580216	G	A	0.506	307	607	NON_SYNONYMOUS_CODING(MODERATE|MISSENSE|Cgc/Tgc|R3230C|PCLO|mRNA|CODING|NM_014510|NM_014510.ex.6),NON_SYNONYMOUS_CODING(MODERATE|MISSENSE|Cgc/Tgc|R3230C|PCLO|mRNA|CODING|NM_033026|NM_033026.ex.6)	R3230C
5	tissue-5 Somatic	Category II-Default Categorization	PCLO	SNP	7	82764398	C	A	0.477	428	898	NON_SYNONYMOUS_CODING(MODERATE|MISSENSE|cGa/cTa|R823L|PCLO|mRNA|CODING|NM_014510|NM_014510.ex.3),NON_SYNONYMOUS_CODING(MODERATE|MISSENSE|cGa/cTa|R823L|PCLO|mRNA|CODING|NM_033026|NM_033026.ex.3)	R823L
5	tissue-5 Somatic	Category III-Default Categorization	PCLO	SNP	7	82784373	T	C	0.00784	12	1530	SYNONYMOUS_CODING(LOW|SILENT|aaA/aaG|K528|PCLO|mRNA|CODING|NM_014510|NM_014510.ex.2),SYNONYMOUS_CODING(LOW|SILENT|aaA/aaG|K528|PCLO|mRNA|CODING|NM_033026|NM_033026.ex.2)	K528

5	tissue-5 Somatic	Category II-Default Categorization	PCLO	SNP	7	82784489	G	A	0.0135	23	1703	NON_SYNONYMOUS_CODING(MODERATE|MISSENSE|Cca/Tca|P490S|PCLO|mRNA|CODING|NM_014510|NM_014510.ex.2),NON_SYNONYMOUS_CODING(MODERATE|MISSENSE|Cca/Tca|P490S|PCLO|mRNA|CODING|NM_033026|NM_033026.ex.2)	P490S
5	tissue-5 Somatic	Category III-Default Categorization	PCLO	SNP	7	82784493	C	T	0.00929	13	1400	SYNONYMOUS_CODING(LOW|SILENT|aaG/aaA|K488|PCLO|mRNA|CODING|NM_014510|NM_014510.ex.2),SYNONYMOUS_CODING(LOW|SILENT|aaG/aaA|K488|PCLO|mRNA|CODING|NM_033026|NM_033026.ex.2)	K488
5	tissue-5 Somatic	Category II-Default Categorization	PCLO	SNP	7	82785097	T	C	0.484	387	800	NON_SYNONYMOUS_CODING(MODERATE|MISSENSE|gAc/gGc|D287G|PCLO|mRNA|CODING|NM_014510|NM_014510.ex.2),NON_SYNONYMOUS_CODING(MODERATE|MISSENSE|gAc/gGc|D287G|PCLO|mRNA|CODING|NM_033026|NM_033026.ex.2)	D287G
5	tissue-5 Somatic	Category III-Default Categorization	GRM3	SNP	7	86415918	C	T	0.00893	15	1680	SYNONYMOUS_CODING(LOW|SILENT|cgC/cgT|R270|GRM3|mRNA|CODING|NM_000840|NM_000840.ex.3),SYNONYMOUS_CODING(LOW|SILENT|cgC/cgT|R270|GRM3|mRNA|CODING|NM_001363522|NM_001363522.ex.3)	R270
5	tissue-5 Somatic	Category III-Default Categorization	RELN	SNP	7	103124207	T	C	0.488	262	537	INTRON(MODIFIER||||LOC101927870|Non-coding_transcript|NON_CODING|NR_110141|),SYNONYMOUS_CODING(LOW|SILENT|gcA/gcG|A3358|RELN|mRNA|CODING|NM_005045|NM_005045.ex.62),SYNONYMOUS_CODING(LOW|SILENT|gcA/gcG|A3358|RELN|mRNA|CODING|NM_173054|NM_173054.ex.62)	A3358
5	tissue-5 Somatic	Category III-Default Categorization	LOC101927870	SNP	7	103138521	T	G	0.504	208	413	INTRON(MODIFIER||||LOC101927870|Non-coding_transcript|NON_CODING|NR_110141|),INTRON(MODIFIER||||RELN|mRNA|CODING|NM_005045|),INTRON(MODIFIER||||RELN|mRNA|CODING|NM_173054|)	

<table>
<tr><td>5</td><td>tissue-5 Somatic</td><td>Category III-Default Categorization</td><td>RELN</td><td>SNP</td><td>7</td><td>103151436</td><td>T</td><td>C</td><td>0.502</td><td>144</td><td>287</td><td>INTRON(MODIFIER||||LOC101927870|Non-coding_transcript|NON_CODING|NR_110141|),SYNONYMOUS_CODING(LOW|SILENT|ctA/ctG|L2712|RELN|mRNA|CODING|NM_005045|NM_005045.ex.51),SYNONYMOUS_CODING(LOW|SILENT|ctA/ctG|L2712|RELN|mRNA|CODING|NM_173054|NM_173054.ex.51)</td><td>L2712</td></tr>
<tr><td>5</td><td>tissue-5 Somatic</td><td>Category III-Default Categorization</td><td>RELN</td><td>SNP</td><td>7</td><td>103155864</td><td>A</td><td>G</td><td>0.438</td><td>209</td><td>477</td><td>DOWNSTREAM(MODIFIER||||LOC101927870|Non-coding_transcript|NON_CODING|NR_110141|),SYNONYMOUS_CODING(LOW|SILENT|ccT/ccC|P2629|RELN|mRNA|CODING|NM_005045|NM_005045.ex.50),SYNONYMOUS_CODING(LOW|SILENT|ccT/ccC|P2629|RELN|mRNA|CODING|NM_173054|NM_173054.ex.50)</td><td>P2629</td></tr>
<tr><td>5</td><td>tissue-5 Somatic</td><td>Category III-Default Categorization</td><td>RELN</td><td>SNP</td><td>7</td><td>103179595</td><td>A</td><td>G</td><td>0.45</td><td>292</td><td>649</td><td>SYNONYMOUS_CODING(LOW|SILENT|gtT/gtC|V2370|RELN|mRNA|CODING|NM_005045|NM_005045.ex.45),SYNONYMOUS_CODING(LOW|SILENT|gtT/gtC|V2370|RELN|mRNA|CODING|NM_173054|NM_173054.ex.45)</td><td>V2370</td></tr>
<tr><td>5</td><td>tissue-5 Somatic</td><td>Category III-Default Categorization</td><td>MGAM</td><td>SNP</td><td>7</td><td>141732642</td><td>C</td><td>A</td><td>0.529</td><td>156</td><td>295</td><td>SYNONYMOUS_CODING(LOW|SILENT|tcC/tcA|S534|MGAM|mRNA|CODING|NM_004668|NM_004668.ex.14)</td><td>S534</td></tr>
<tr><td>5</td><td>tissue-5 Somatic</td><td>Category III-Default Categorization</td><td>MGAM</td><td>SNP</td><td>7</td><td>141747618</td><td>A</td><td>G</td><td>0.435</td><td>189</td><td>434</td><td>SYNONYMOUS_CODING(LOW|SILENT|ctA/ctG|L844|MGAM|mRNA|CODING|NM_004668|NM_004668.ex.22)</td><td>L844</td></tr>
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<tr><td>5</td><td>tissue-5 Somatic</td><td>Category III-Default Categorization</td><td>MGAM</td><td>SNP</td><td>7</td><td>141755469</td><td>T</td><td>C</td><td>0.0396</td><td>34</td><td>858</td><td>SYNONYMOUS_CODING(LOW|SILENT|taT/taC|Y1142|MGAM|mRNA|CODING|NM_004668|NM_004668.ex.28)</td><td>Y1142</td></tr>
<tr><td>5</td><td>tissue-5 Somatic</td><td>Category III-Default Categorization</td><td>MGAM</td><td>SNP</td><td>7</td><td>141756749</td><td>G</td><td>A</td><td>0.0228</td><td>12</td><td>526</td><td>INTRON(MODIFIER||||MGAM|mRNA|CODING|NM_004668|)</td><td></td></tr>
<tr><td>5</td><td>tissue-5 Somatic</td><td>Category III-Default Categorization</td><td>MGAM</td><td>SNP</td><td>7</td><td>141767153</td><td>C</td><td>T</td><td>0.437</td><td>314</td><td>718</td><td>INTRON(MODIFIER||||MGAM|mRNA|CODING|NM_004668|)</td><td></td></tr>
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5	tissue-5 Somatic	Category III-Default Categorization	MGAM	SNP	7	141767318	G	A	0.44	291	662	INTRON(MODIFIER||||MGAM|mRNA|CODING|NM_004668|)	
5	tissue-5 Somatic	Category III-Default Categorization	MGAM	SNP	7	141776575	T	A	0.448	321	716	INTRON(MODIFIER||||MGAM|mRNA|CODING|NM_004668|)	
5	tissue-5 Somatic	Category III-Default Categorization	MGAM	SNP	7	141778230	A	C	0.505	327	648	INTRON(MODIFIER||||MGAM|mRNA|CODING|NM_004668|)	
5	tissue-5 Somatic	Category III-Default Categorization	MGAM	SNP	7	141778817	G	A	0.481	307	638	INTRON(MODIFIER||||MGAM|mRNA|CODING|NM_004668|)	
5	tissue-5 Somatic	Category III-Default Categorization	MGAM	SNP	7	141780627	G	A	0.446	287	644	INTRON(MODIFIER||||MGAM|mRNA|CODING|NM_004668|)	
5	tissue-5 Somatic	Category III-Default Categorization	MGAM	SNP	7	141781935	G	A	0.524	419	799	INTRON(MODIFIER||||MGAM|mRNA|CODING|NM_004668|)	
5	tissue-5 Somatic	Category III-Default Categorization	MGAM	SNP	7	141781946	C	T	0.531	423	797	INTRON(MODIFIER||||MGAM|mRNA|CODING|NM_004668|)	
5	tissue-5 Somatic	Category III-Default Categorization	MGAM	SNP	7	141782370	G	A	0.465	358	770	INTRON(MODIFIER||||MGAM|mRNA|CODING|NM_004668|)	
5	tissue-5 Somatic	Category III-Default Categorization	MGAM	SNP	7	141783076	G	C	0.117	54	462	INTRON(MODIFIER||||MGAM|mRNA|CODING|NM_004668|)	
5	tissue-5 Somatic	Category III-Default Categorization	MGAM	SNP	7	141783180	A	G	0.489	303	619	INTRON(MODIFIER||||MGAM|mRNA|CODING|NM_004668|)	
5	tissue-5 Somatic	Category III-Default Categorization	MGAM	SNP	7	141783248	T	C	0.481	168	349	INTRON(MODIFIER||||MGAM|mRNA|CODING|NM_004668|)	
5	tissue-5 Somatic	Category III-Default Categorization	MGAM	SNP	7	141784474	G	C	0.486	185	381	INTRON(MODIFIER||||MGAM|mRNA|CODING|NM_004668|)	
5	tissue-5 Somatic	Category III-Default Categorization	MGAM	SNP	7	141786096	T	C	0.473	388	821	INTRON(MODIFIER||||MGAM|mRNA|CODING|NM_004668|)	
5	tissue-5 Somatic	Category III-Default Categorization	MGAM	SNP	7	141796143	C	T	0.0164	11	672	SYNONYMOUS_CODING(LOW|SILENT|gaC/gaT|D1644|MGAM|mRNA|CODING|NM_004668|NM_004668.ex.42)	D1644
5	tissue-5 Somatic	Category II-Default Categorization	KMT2C	SNP	7	151859683	G	A	0.49	456	931	NON_SYNONYMOUS_CODING(MODERATE|MISSENSE|tCg/tTg|S3660L|KMT2C|mRNA|CODING|NM_170606|NM_170606.ex.43)	S3660L
5	tissue-5 Somatic	Category III-Default Categorization	KMT2C	Deletion	7	151919159	GA	G	0.2	15	75	INTRON(MODIFIER||||KMT2C|mRNA|CODING|NM_170606|)	
5	tissue-5 Somatic	Category III-Default Categorization	KMT2C	SNP	7	151919649	T	C	0.055	24	436	INTRON(MODIFIER||||KMT2C|mRNA|CODING|NM_170606|)	

5	tissue-5 Somatic	Category III-Default Categorization	KMT2C	SNP	7	151932830	A	T	0.121	46	381	INTRON(MODIFIER||||KMT2C|mRNA|CODING|NM_170606|)	
5	tissue-5 Somatic	Category III-Default Categorization	KMT2C	SNP	7	151932846	T	C	0.11	47	427	INTRON(MODIFIER||||KMT2C|mRNA|CODING|NM_170606|)	
5	tissue-5 Somatic	Category II-Default Categorization	KMT2C	SNP	7	151945225	T	C	0.127	200	1581	NON_SYNONYMOUS_CODING(MODERATE|MISSENSE|gAg/gGg|E765G|KMT2C|mRNA|CODING|NM_170606|NM_170606.ex.14)	E765G
5	tissue-5 Somatic	Category III-Default Categorization	KMT2C	SNP	7	151945313	A	G	0.0458	39	852	SYNONYMOUS_CODING(LOW|SILENT|Ttg/Ctg|L736|KMT2C|mRNA|CODING|NM_170606|NM_170606.ex.14)	L736
5	tissue-5 Somatic	Category I-Default Categorization	KMT2C	SNP	7	151945349	T	A	0.0243	21	863	STOP_GAINED(HIGH|NONSENSE|Aag/Tag|K724*|KMT2C|mRNA|CODING|NM_170606|NM_170606.ex.14)	K724*
5	tissue-5 Somatic	Category II-Default Categorization	KMT2C	SNP	7	151962126	C	T	0.0521	71	1363	NON_SYNONYMOUS_CODING(MODERATE|MISSENSE|tGc/tAc|C394Y|KMT2C|mRNA|CODING|NM_170606|NM_170606.ex.8)	C394Y
5	tissue-5 Somatic	Category I-Default Categorization	KMT2C	SNP	7	151962134	G	T	0.0857	131	1528	STOP_GAINED(HIGH|NONSENSE|tgC/tgA|C391*|KMT2C|mRNA|CODING|NM_170606|NM_170606.ex.8)	C391*
5	tissue-5 Somatic	Category II-Default Categorization	KMT2C	SNP	7	151962168	C	A	0.0902	169	1874	NON_SYNONYMOUS_CODING(MODERATE|MISSENSE|cGt/cTt|R380L|KMT2C|mRNA|CODING|NM_170606|NM_170606.ex.8)	R380L
5	tissue-5 Somatic	Category III-Default Categorization	KMT2C	SNP	7	151962269	C	T	0.0963	125	1298	SYNONYMOUS_CODING(LOW|SILENT|gtG/gtA|V346|KMT2C|mRNA|CODING|NM_170606|NM_170606.ex.8)	V346
5	tissue-5 Somatic	Category II-Default Categorization	KMT2C	SNP	7	151962294	G	A	0.0872	78	895	NON_SYNONYMOUS_CODING(MODERATE|MISSENSE|tCg/tTg|S338L|KMT2C|mRNA|CODING|NM_170606|NM_170606.ex.8)	S338L
5	tissue-5 Somatic	Category I-Default Categorization	KMT2C	SNP	7	151962296	T	C	0.0863	73	846	INTRON(MODIFIER||||KMT2C|mRNA|CODING|NM_170606|),SPLICE_SITE_ACCEPTOR(HIGH||||KMT2C|mRNA|CODING|NM_170606|)	
5	tissue-5 Somatic	Category III-Default Categorization	KMT2C	SNP	7	151970969	A	C	0.0925	91	984	INTRON(MODIFIER||||KMT2C|mRNA|CODING|NM_170606|)	
5	tissue-5 Somatic	Category III-Default Categorization	KMT2C	SNP	7	151970977	C	A	0.122	112	919	INTRON(MODIFIER||||KMT2C|mRNA|CODING|NM_170606|)	

5	tissue-5 Somatic	Category III-Default Categorization	ADGRA2	SNP	8	37698252	G	A	0.442	153	346	DOWNSTREAM(MODIFIER||||BRF2|mRNA|CODING|NM_018310|),INTRON(MODIFIER||||ADGRA2|mRNA|CODING|NM_032777|)	
5	tissue-5 Somatic	Category II-Default Categorization	PRKDC	SNP	8	48809721	C	A	0.118	35	297	NON_SYNONYMOUS_CODING(MODERATE|MISSENSE|Ggc/Tgc|G1200C|PRKDC|mRNA|CODING|NM_001081640|NM_001081640.ex.30),NON_SYNONYMOUS_CODING(MODERATE|MISSENSE|Ggc/Tgc|G1200C|PRKDC|mRNA|CODING|NM_006904|NM_006904.ex.30)	G1200C
5	tissue-5 Somatic	Category III-Default Categorization	RAD21	SNP	8	117869498	C	T	0.431	100	232	INTRON(MODIFIER||||RAD21|mRNA|CODING|NM_006265|)	
5	tissue-5 Somatic	Category III-Default Categorization	NDRG1	SNP	8	134251244	G	C	0.00864	11	1273	SYNONYMOUS_CODING(LOW|SILENT|tcC/tcG|S273|NDRG1|mRNA|CODING|NM_001258433|NM_001258433.ex.15),SYNONYMOUS_CODING(LOW|SILENT|tcC/tcG|S288|NDRG1|mRNA|CODING|NM_001258432|NM_001258432.ex.14),SYNONYMOUS_CODING(LOW|SILENT|tcC/tcG|S354|NDRG1|mRNA|CODING|NM_001135242|NM_001135242.ex.16),SYNONYMOUS_CODING(LOW|SILENT|tcC/tcG|S354|NDRG1|mRNA|CODING|NM_006096|NM_006096.ex.16)	S273
5	tissue-5 Somatic	Category III-Default Categorization	NDRG1	SNP	8	134251274	G	C	0.015	19	1263	SYNONYMOUS_CODING(LOW|SILENT|tcC/tcG|S263|NDRG1|mRNA|CODING|NM_001258433|NM_001258433.ex.15),SYNONYMOUS_CODING(LOW|SILENT|tcC/tcG|S278|NDRG1|mRNA|CODING|NM_001258432|NM_001258432.ex.14),SYNONYMOUS_CODING(LOW|SILENT|tcC/tcG|S344|NDRG1|mRNA|CODING|NM_001135242|NM_001135242.ex.16),SYNONYMOUS_CODING(LOW|SILENT|tcC/tcG|S344|NDRG1|mRNA|CODING|NM_006096|NM_006096.ex.16)	S263
5	tissue-5 Somatic	Category III-Default Categorization	AGO2	SNP	8	141551407	G	A	0.496	271	546	SYNONYMOUS_CODING(LOW|SILENT|cgC/cgT|R630|AGO2|mRNA|CODING|NM_001164623|NM_001164623.ex.15),SYNONYMOUS_CODING(LOW|SILENT|cgC/cgT|R630|AGO2|mRNA|CODING|NM_012154|NM_012154.ex.15)	R630

5	tissue-5 Somatic	Category III-Default Categorization	RECQL4	SNP	8	145737514	G	A	0.453	209	461	DOWNSTREAM(MODIFIER||||GPT|mRNA|CODING|NM_005309|),DOWNSTREAM(MODIFIER||||MFSD3|Non-coding_transcript|CODING|NM_138431|),DOWNSTREAM(MODIFIER||||MFSD3|Non-coding_transcript|CODING|NR_130120|),INTRON(MODIFIER||||RECQL4|mRNA|CODING|NM_004260|)	
5	tissue-5 Somatic	Category II-Default Categorization	RECQL4	SNP	8	145737816	C	T	0.492	569	1156	DOWNSTREAM(MODIFIER||||MFSD3|Non-coding_transcript|CODING|NM_138431|),DOWNSTREAM(MODIFIER||||MFSD3|Non-coding_transcript|CODING|NR_130120|),NON_SYNONYMOUS_CODING(MODERATE|MISSENSE|cGg/cAg|R1005Q|RECQL4|mRNA|CODING|NM_004260|NM_004260.ex.18)	R1005Q
5	tissue-5 Somatic	Category III-Default Categorization	RECQL4	Deletion	8	145738576	CAGTGTGGG	C	0.457	530	1159	DOWNSTREAM(MODIFIER||||MFSD3|Non-coding_transcript|CODING|NM_138431|),DOWNSTREAM(MODIFIER||||MFSD3|Non-coding_transcript|CODING|NR_130120|),INTRON(MODIFIER||||RECQL4|mRNA|CODING|NM_004260|),UPSTREAM(MODIFIER||||LRRC14|mRNA|CODING|NM_001272036|),UPSTREAM(MODIFIER||||LRRC14|mRNA|CODING|NM_014665|)	
5	tissue-5 Somatic	Category III-Default Categorization	RECQL4	SNP	8	145738583	G	T	0.0197	23	1170	DOWNSTREAM(MODIFIER||||MFSD3|Non-coding_transcript|CODING|NM_138431|),DOWNSTREAM(MODIFIER||||MFSD3|Non-coding_transcript|CODING|NR_130120|),INTRON(MODIFIER||||RECQL4|mRNA|CODING|NM_004260|),UPSTREAM(MODIFIER||||LRRC14|mRNA|CODING|NM_001272036|),UPSTREAM(MODIFIER||||LRRC14|mRNA|CODING|NM_014665|)	

<table>
<tr><td>5</td><td>tissue-5 Somatic</td><td>Category III-Default Categorization</td><td>RECQL4</td><td>Deletion</td><td>8</td><td>145738592</td><td>GGT</td><td>G</td><td>0.0303</td><td>26</td><td>858</td><td>DOWNSTREAM(MODIFIER||||MFSD3|Non-coding_transcript|CODING|NM_138431|),DOWNSTREAM(MODIFIER||||MFSD3|Non-coding_transcript|CODING|NR_130120|),INTRON(MODIFIER||||RECQL4|mRNA|CODING|NM_004260|),UPSTREAM(MODIFIER||||LRRC14|mRNA|CODING|NM_001272036|),UPSTREAM(MODIFIER||||LRRC14|mRNA|CODING|NM_014665|)</td><td></td></tr>
<tr><td>5</td><td>tissue-5 Somatic</td><td>Category III-Default Categorization</td><td>RECQL4</td><td>SNP</td><td>8</td><td>145739924</td><td>G</td><td>A</td><td>0.438</td><td>336</td><td>768</td><td>DOWNSTREAM(MODIFIER||||MFSD3|Non-coding_transcript|CODING|NM_138431|),DOWNSTREAM(MODIFIER||||MFSD3|Non-coding_transcript|CODING|NR_130120|),INTRON(MODIFIER||||RECQL4|mRNA|CODING|NM_004260|),UPSTREAM(MODIFIER||||LRRC14|mRNA|CODING|NM_001272036|),UPSTREAM(MODIFIER||||LRRC14|mRNA|CODING|NM_014665|)</td><td></td></tr>
<tr><td>5</td><td>tissue-5 Somatic</td><td>Category II-Default Categorization</td><td>RECQL4</td><td>SNP</td><td>8</td><td>145741702</td><td>C</td><td>G</td><td>0.47</td><td>199</td><td>423</td><td>NON_SYNONYMOUS_CODING(MODERATE|MISSENSE|gaG/gaC|E267D|RECQL4|mRNA|CODING|NM_004260|NM_004260.ex.5),UPSTREAM(MODIFIER||||LRRC14|mRNA|CODING|NM_001272036|),UPSTREAM(MODIFIER||||LRRC14|mRNA|CODING|NM_014665|)</td><td>E267D</td></tr>
<tr><td>5</td><td>tissue-5 Somatic</td><td>Category III-Default Categorization</td><td>RECQL4</td><td>SNP</td><td>8</td><td>145741765</td><td>G</td><td>A</td><td>0.482</td><td>230</td><td>477</td><td>SYNONYMOUS_CODING(LOW|SILENT|agC/agT|S246|RECQL4|mRNA|CODING|NM_004260|NM_004260.ex.5),UPSTREAM(MODIFIER||||LRRC14|mRNA|CODING|NM_001272036|),UPSTREAM(MODIFIER||||LRRC14|mRNA|CODING|NM_014665|)</td><td>S246</td></tr>
<tr><td>5</td><td>tissue-5 Somatic</td><td>Category III-Default Categorization</td><td>RECQL4</td><td>SNP</td><td>8</td><td>145742879</td><td>T</td><td>C</td><td>0.482</td><td>256</td><td>531</td><td>DOWNSTREAM(MODIFIER||||LRRC24|mRNA|CODING|NM_001024678|),SYNONYMOUS_CODING(LOW|SILENT|gaA/gaG|E44|RECQL4|mRNA|CODING|NM_004260|NM_004260.ex.3),UPSTREAM(MODIFIER||||LRRC14|mRNA|CODING|NM_001272036|),UPSTREAM(MODIFIER||||LRRC14|mRNA|CODING|NM_014665|)</td><td>E44</td></tr>
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5	tissue-5 Somatic	Category II-Default Categorization	PTPRD	SNP	9	8485834	G	A	0.46	290	630	INTRON(MODIFIER||||PTPRD|mRNA|CODING|NM_001040712|),INTRON(MODIFIER||||PTPRD|mRNA|CODING|NM_001171025|),INTRON(MODIFIER||||PTPRD|mRNA|CODING|NM_130391|),INTRON(MODIFIER||||PTPRD|mRNA|CODING|NM_130392|),INTRON(MODIFIER||||PTPRD|mRNA|CODING|NM_130393|),NON_SYNONYMOUS_CODING(MODERATE|MISSENSE|Cgt/Tgt|R995C|PTPRD|mRNA|CODING|NM_002839|NM_002839.ex.28)	R995C
5	tissue-5 Somatic	Category III-Default Categorization	PTPRD	SNP	9	8485928	G	A	0.462	439	951	INTRON(MODIFIER||||PTPRD|mRNA|CODING|NM_001040712|),INTRON(MODIFIER||||PTPRD|mRNA|CODING|NM_001171025|),INTRON(MODIFIER||||PTPRD|mRNA|CODING|NM_130391|),INTRON(MODIFIER||||PTPRD|mRNA|CODING|NM_130392|),INTRON(MODIFIER||||PTPRD|mRNA|CODING|NM_130393|),SYNONYMOUS_CODING(LOW|SILENT|atC/atT|I963|PTPRD|mRNA|CODING|NM_002839|NM_002839.ex.28)	I963
5	tissue-5 Somatic	Category III-Default Categorization	PTPRD	SNP	9	8518143	T	C	1	893	893	SYNONYMOUS_CODING(LOW|SILENT|gcA/gcG|A406|PTPRD|mRNA|CODING|NM_001171025|NM_001171025.ex.8),SYNONYMOUS_CODING(LOW|SILENT|gcA/gcG|A410|PTPRD|mRNA|CODING|NM_130393|NM_130393.ex.9),SYNONYMOUS_CODING(LOW|SILENT|gcA/gcG|A413|PTPRD|mRNA|CODING|NM_001040712|NM_001040712.ex.9),SYNONYMOUS_CODING(LOW|SILENT|gcA/gcG|A416|PTPRD|mRNA|CODING|NM_002839|NM_002839.ex.21),SYNONYMOUS_CODING(LOW|SILENT|gcA/gcG|A416|PTPRD|mRNA|CODING|NM_130391|NM_130391.ex.10),SYNONYMOUS_CODING(LOW|SILENT|gcA/gcG|A416|PTPRD|mRNA|CODING|NM_130392|NM_130392.ex.10)	A406
5	tissue-5 Somatic	Category III-Default Categorization	MTAP	SNP	9	21854740	C	T	0.499	331	663	SYNONYMOUS_CODING(LOW|SILENT|cgC/cgT|R187|MTAP|mRNA|CODING|NM_002451|NM_002451.ex.6)	R187

5	tissue-5 Somatic	Category II-Default Categorization	NOTCH1	SNP	9	139401847	C	T	0.453	253	559	NON_SYNONYMOUS_CODING(MODERATE|MISSENSE|Gac/Aac|D1185N|NOTCH1|mRNA|CODING|NM_017617|NM_017617.ex.22)	D1185N
5	tissue-5 Somatic	Category III-Default Categorization	NUMA1	SNP	11	71726212	C	T	0.447	286	640	INTRON(MODIFIER||||NUMA1|mRNA|CODING|NR_104476|),SYNONYMOUS_CODING(LOW|SILENT|caG/caA|Q779|NUMA1|mRNA|CODING|NM_001286561|NM_001286561.ex.16),SYNONYMOUS_CODING(LOW|SILENT|caG/caA|Q779|NUMA1|mRNA|CODING|NM_006185|NM_006185.ex.15),SYNONYMOUS_CODING(LOW|SILENT|gcC/gcT|A292|LOC100128494|Non-coding_transcript|NON_CODING|NR_104178|NR_104178.ex.1)	Q779
5	tissue-5 Somatic	Category II-Default Categorization	INPPL1	SNP	11	71941033	G	C	0.483	431	892	NON_SYNONYMOUS_CODING(MODERATE|MISSENSE|aaG/aaC|K303N|INPPL1|mRNA|CODING|NM_001567|NM_001567.ex.8)	K303N
5	tissue-5 Somatic	Category III-Default Categorization	INPPL1	SNP	11	71941212	A	G	0.467	506	1083	SYNONYMOUS_CODING(LOW|SILENT|tcA/tcG|S329|INPPL1|mRNA|CODING|NM_001567|NM_001567.ex.9)	S329
5	tissue-5 Somatic	Category III-Default Categorization	INPPL1	SNP	11	71941812	C	T	0.487	243	499	INTRON(MODIFIER||||INPPL1|mRNA|CODING|NM_001567|)	
5	tissue-5 Somatic	Category II-Default Categorization	INPPL1	SNP	11	71944152	G	A	0.109	84	769	NON_SYNONYMOUS_CODING(MODERATE|MISSENSE|cGc/cAc|R662H|INPPL1|mRNA|CODING|NM_001567|NM_001567.ex.17)	R662H
5	tissue-5 Somatic	Category III-Default Categorization	INPPL1	SNP	11	71949233	T	C	0.485	302	623	DOWNSTREAM(MODIFIER||||PHOX2A|mRNA|CODING|NM_005169|),INTRON(MODIFIER||||INPPL1|mRNA|CODING|NM_001567|)	
5	tissue-5 Somatic	Category III-Default Categorization	BIRC3	SNP	11	102199609	A	T	0.705	31	44	INTRON(MODIFIER||||BIRC3|mRNA|CODING|NM_001165|),INTRON(MODIFIER||||BIRC3|mRNA|CODING|NM_182962|)	
5	tissue-5 Somatic	Category II-Default Categorization	LRRK2	SNP	12	40757328	G	A	0.443	136	307	NON_SYNONYMOUS_CODING(MODERATE|MISSENSE|Gga/Aga|G2385R|LRRK2|mRNA|CODING|NM_198578|NM_198578.ex.48)	G2385R
5	tissue-5 Somatic	Category III-Default Categorization	KMT2D	SNP	12	49420629	G	A	0.478	552	1156	SYNONYMOUS_CODING(LOW|SILENT|gaC/gaT|D5040|KMT2D|mRNA|CODING|NM_003482|NM_003482.ex.48)	D5040

5	tissue-5 Somatic	Category III-Default Categorization	KMT2D	SNP	12	49424534	G	A	0.416	191	459	SYNONYMOUS_CODING(LOW|SILENT|ccC/ccT|P4563|KMT2D|mRNA|CODING|NM_003482|NM_003482.ex.41)	P4563
5	tissue-5 Somatic	Category III-Default Categorization	KMT2D	SNP	12	49444937	G	T	0.00758	13	1714	SYNONYMOUS_CODING(LOW|SILENT|tcC/tcA|S843|KMT2D|mRNA|CODING|NM_003482|NM_003482.ex.10)	S843
5	tissue-5 Somatic	Category II-Default Categorization	KMT2D	SNP	12	49444945	A	G	0.00741	12	1620	NON_SYNONYMOUS_CODING(MODERATE|MISSENSE|Tgc/Cgc|C841R|KMT2D|mRNA|CODING|NM_003482|NM_003482.ex.10)	C841R
5	tissue-5 Somatic	Category II-Default Categorization	KMT2D	SNP	12	49444957	A	G	0.0166	26	1563	NON_SYNONYMOUS_CODING(MODERATE|MISSENSE|Tct/Cct|S837P|KMT2D|mRNA|CODING|NM_003482|NM_003482.ex.10)	S837P
5	tissue-5 Somatic	Category III-Default Categorization	KMT2D	SNP	12	49444985	T	C	0.00767	12	1565	SYNONYMOUS_CODING(LOW|SILENT|caA/caG|Q827|KMT2D|mRNA|CODING|NM_003482|NM_003482.ex.10)	Q827
5	tissue-5 Somatic	Category III-Default Categorization	KMT2D	SNP	12	49445216	C	T	0.00738	17	2303	SYNONYMOUS_CODING(LOW|SILENT|ccG/ccA|P750|KMT2D|mRNA|CODING|NM_003482|NM_003482.ex.10)	P750
5	tissue-5 Somatic	Category III-Default Categorization	KMT2D	SNP	12	49445399	G	C	0.0206	42	2039	SYNONYMOUS_CODING(LOW|SILENT|ctC/ctG|L689|KMT2D|mRNA|CODING|NM_003482|NM_003482.ex.10)	L689
5	tissue-5 Somatic	Category III-Default Categorization	KMT2D	SNP	12	49445420	A	T	0.0147	28	1903	SYNONYMOUS_CODING(LOW|SILENT|ccT/ccA|P682|KMT2D|mRNA|CODING|NM_003482|NM_003482.ex.10)	P682
5	tissue-5 Somatic	Category III-Default Categorization	KMT2D	SNP	12	49445426	C	A	0.00797	15	1882	SYNONYMOUS_CODING(LOW|SILENT|acG/acT|T680|KMT2D|mRNA|CODING|NM_003482|NM_003482.ex.10)	T680
5	tissue-5 Somatic	Category II-Default Categorization	KMT2D	SNP	12	49445427	G	A	0.0106	20	1893	NON_SYNONYMOUS_CODING(MODERATE|MISSENSE|aCg/aTg|T680M|KMT2D|mRNA|CODING|NM_003482|NM_003482.ex.10)	T680M
5	tissue-5 Somatic	Category II-Default Categorization	KMT2D	SNP	12	49445428	T	G	0.0089	16	1797	NON_SYNONYMOUS_CODING(MODERATE|MISSENSE|Acg/Ccg|T680P|KMT2D|mRNA|CODING|NM_003482|NM_003482.ex.10)	T680P
5	tissue-5 Somatic	Category I-Default Categorization	KMT2D	Deletion	12	49445499	AG	A	0.0123	21	1710	FRAME_SHIFT(HIGH||||KMT2D|mRNA|CODING|NM_003482|NM_003482.ex.10)	

<table>
<tr><td>5</td><td>tissue-5 Somatic</td><td>Category I-Default Categorization</td><td>KMT2D</td><td>Deletion</td><td>12</td><td>49445525</td><td>TG</td><td>T</td><td>0.0112</td><td>19</td><td>1699</td><td>FRAME_SHIFT(HIGH||||KMT2D|mRNA|CODING|NM_003482|NM_003482.ex.10)</td><td></td></tr>
<tr><td>5</td><td>tissue-5 Somatic</td><td>Category III-Default Categorization</td><td>KMT2D</td><td>SNP</td><td>12</td><td>49445564</td><td>A</td><td>G</td><td>0.0075</td><td>12</td><td>1601</td><td>SYNONYMOUS_CODING(LOW|SILENT|ccT/ccC|P634|KMT2D|mRNA|CODING|NM_003482|NM_003482.ex.10)</td><td>P634</td></tr>
<tr><td>5</td><td>tissue-5 Somatic</td><td>Category III-Default Categorization</td><td>KMT2D</td><td>SNP</td><td>12</td><td>49445597</td><td>T</td><td>A</td><td>0.00707</td><td>13</td><td>1838</td><td>SYNONYMOUS_CODING(LOW|SILENT|gcA/gcT|A623|KMT2D|mRNA|CODING|NM_003482|NM_003482.ex.10)</td><td>A623</td></tr>
<tr><td>5</td><td>tissue-5 Somatic</td><td>Category III-Default Categorization</td><td>CREBBP</td><td>SNP</td><td>16</td><td>3778337</td><td>G</td><td>A</td><td>0.534</td><td>473</td><td>885</td><td>SYNONYMOUS_CODING(LOW|SILENT|ccC/ccT|P2199|CREBBP|mRNA|CODING|NM_001079846|NM_001079846.ex.30),SYNONYMOUS_CODING(LOW|SILENT|ccC/ccT|P2237|CREBBP|mRNA|CODING|NM_004380|NM_004380.ex.31)</td><td>P2199</td></tr>
<tr><td>5</td><td>tissue-5 Somatic</td><td>Category III-Default Categorization</td><td>CREBBP</td><td>SNP</td><td>16</td><td>3795292</td><td>G</td><td>T</td><td>0.415</td><td>137</td><td>330</td><td>SYNONYMOUS_CODING(LOW|SILENT|atC/atA|I1262|CREBBP|mRNA|CODING|NM_001079846|NM_001079846.ex.21),SYNONYMOUS_CODING(LOW|SILENT|atC/atA|I1300|CREBBP|mRNA|CODING|NM_004380|NM_004380.ex.22)</td><td>I1262</td></tr>
<tr><td>5</td><td>tissue-5 Somatic</td><td>Category III-Default Categorization</td><td>CREBBP</td><td>SNP</td><td>16</td><td>3795363</td><td>G</td><td>A</td><td>0.404</td><td>138</td><td>342</td><td>INTRON(MODIFIER||||CREBBP|mRNA|CODING|NM_001079846|),INTRON(MODIFIER||||CREBBP|mRNA|CODING|NM_004380|)</td><td></td></tr>
<tr><td>5</td><td>tissue-5 Somatic</td><td>Category III-Default Categorization</td><td>CREBBP</td><td>SNP</td><td>16</td><td>3820667</td><td>C</td><td>T</td><td>0.483</td><td>439</td><td>908</td><td>SYNONYMOUS_CODING(LOW|SILENT|ccG/ccA|P890|CREBBP|mRNA|CODING|NM_001079846|NM_001079846.ex.13),SYNONYMOUS_CODING(LOW|SILENT|ccG/ccA|P928|CREBBP|mRNA|CODING|NM_004380|NM_004380.ex.14)</td><td>P890</td></tr>
<tr><td>5</td><td>tissue-5 Somatic</td><td>Category III-Default Categorization</td><td>CREBBP</td><td>SNP</td><td>16</td><td>3827553</td><td>G</td><td>A</td><td>0.532</td><td>91</td><td>171</td><td>INTRON(MODIFIER||||CREBBP|mRNA|CODING|NM_001079846|),INTRON(MODIFIER||||CREBBP|mRNA|CODING|NM_004380|)</td><td></td></tr>
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5	tissue-5 Somatic	Category II-Default Categorization	TP53	SNP	17	7579472	G	C	0.474	301	635	NON_SYNONYMOUS_CODING(MODERATE|MISSENSE|cCc/cGc|P33R|TP53|mRNA|CODING|NM_001126118|NM_001126118.ex.3),NON_SYNONYMOUS_CODING(MODERATE|MISSENSE|cCc/cGc|P33R|TP53|mRNA|CODING|NM_001276695|NM_001276695.ex.4),NON_SYNONYMOUS_CODING(MODERATE|MISSENSE|cCc/cGc|P33R|TP53|mRNA|CODING|NM_001276696|NM_001276696.ex.4),NON_SYNONYMOUS_CODING(MODERATE|MISSENSE|cCc/cGc|P33R|TP53|mRNA|CODING|NM_001276760|NM_001276760.ex.4),NON_SYNONYMOUS_CODING(MODERATE|MISSENSE|cCc/cGc|P33R|TP53|mRNA|CODING|NM_001276761|NM_001276761.ex.4),NON_SYNONYMOUS_CODING(MODERATE|MISSENSE|cCc/cGc|P72R|TP53|mRNA|CODING|NM_000546|NM_000546.ex.4),NON_SYNONYMOUS_CODING(MODERATE|MISSENSE|cCc/cGc|P72R|TP53|mRNA|CODING|NM_001126112|NM_001126112.ex.4),NON_SYNONYMOUS_CODING(MODERATE|MISSENSE|cCc/cGc|P72R|TP53|mRNA|CODING|NM_001126113|NM_001126113.ex.4),NON_SYNONYMOUS_CODING(MODERATE|MISSENSE|cCc/cGc|P72R|TP53|mRNA|CODING|NM_001126114|NM_001126114.ex.4),UPSTREAM(MODIFIER||||TP53|mRNA|CODING|NM_001126115|),UPSTREAM(MODIFIER||||TP53|mRNA|CODING|NM_001126116|),UPSTREAM(MODIFIER||||TP53|mRNA|CODING|NM_001126117|),UPSTREAM(MODIFIER||||TP53|mRNA|CODING|NM_001276697|),UPSTREAM(MODIFIER||||TP53|mRNA|CODING|NM_001276698|),UPSTREAM(MODIFIER||||TP53|mRNA|CODING|NM_001276699|)	P33R
5	tissue-5 Somatic	Category III-Default Categorization	RNF213	SNP	17	78247230	C	T	0.495	135	273	INTRON(MODIFIER||||RNF213|mRNA|CODING|NM_001256071|),INTRON(MODIFIER||||RNF213|mRNA|CODING|NM_020954|)	

5	tissue-5 Somatic	Category III-Default Categorization	EP300	SNP	22	41523486	C	G	0.0929	38	409	INTRON(MODIFIER||||EP300|mRNA|CODING|NM_001362843|),INTRON(MODIFIER||||EP300|mRNA|CODING|NM_001429|)	
5	tissue-5 Somatic	Category I-Default Categorization	EP300	SNP	22	41523494	C	T	0.0993	44	443	STOP_GAINED(HIGH|NONSENSE|Caa/Taa|Q304*|EP300|mRNA|CODING|NM_001362843|NM_001362843.ex.4), STOP_GAINED(HIGH|NONSENSE|Caa/Taa|Q304*|EP300|mRNA|CODING|NM_001429|NM_001429.ex.4)	Q304*
5	tissue-5 Somatic	Category III-Default Categorization	EP300	SNP	22	41525937	G	A	0.109	43	396	SYNONYMOUS_CODING(LOW|SILENT|aaG/aaA|K404|EP300|mRNA|CODING|NM_001362843|NM_001362843.ex.5),SYNONYMOUS_CODING(LOW|SILENT|aaG/aaA|K404|EP300|mRNA|CODING|NM_001429|NM_001429.ex.5)	K404
5	tissue-5 Somatic	Category III-Default Categorization	EP300	SNP	22	41525976	C	T	0.0971	43	443	SYNONYMOUS_CODING(LOW|SILENT|ctC/ctT|L417|EP300|mRNA|CODING|NM_001362843|NM_001362843.ex.5),SYNONYMOUS_CODING(LOW|SILENT|ctC/ctT|L417|EP300|mRNA|CODING|NM_001429|NM_001429.ex.5)	L417
5	Plasma5-1	Category III-Default Categorization	KMT2D	SNP	12	49444985	T	C	0.0605	13	215	SYNONYMOUS_CODING(LOW|SILENT|caA/caG|Q827|KMT2D|mRNA|CODING|NM_003482|NM_003482.ex.10)	Q827
5	Plasma5-1	Category II-Default Categorization	KMT2D	SNP	12	49445428	T	G	0.0407	10	246	NON_SYNONYMOUS_CODING(MODERATE|MISSENSE|Acg/Ccg|T680P|KMT2D|mRNA|CODING|NM_003482|NM_003482.ex.10)	T680P
5	Plasma5-2	Category II-Default Categorization	KMT2D	SNP	12	49445428	T	G	0.0281	11	391	NON_SYNONYMOUS_CODING(MODERATE|MISSENSE|Acg/Ccg|T680P|KMT2D|mRNA|CODING|NM_003482|NM_003482.ex.10)	T680P
5	Plasma5-3	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A
6	tissue-6 Somatic	Category III-Default Categorization	KMT2D	SNP	12	49444937	G	T	0.0132	10	757	SYNONYMOUS_CODING(LOW|SILENT|tcC/tcA|S843|KMT2D|mRNA|CODING|NM_003482|NM_003482.ex.10)	S843
6	Plasma6-1	Category III-Default Categorization	KMT2D	SNP	12	49444937	G	T	0.0181	20	1105	SYNONYMOUS_CODING(LOW|SILENT|tcC/tcA|S843|KMT2D|mRNA|CODING|NM_003482|NM_003482.ex.10)	S843
6	Plasma6-2	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A
6	Plasma6-3	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A

<table>
<tr><td>7</td><td>tissue-7 somatic</td><td>Category III-Default Categorization</td><td>PCLO</td><td>SNP</td><td>7</td><td>82784373</td><td>T</td><td>C</td><td>0.0131</td><td>10</td><td>763</td><td>SYNONYMOUS_CODING(LOW|SILENT|aaA/aaG|K528|PCLO|mRNA|CODING|NM_014510|NM_014510.ex.2),SYNONYMOUS_CODING(LOW|SILENT|aaA/aaG|K528|PCLO|mRNA|CODING|NM_033026|NM_033026.ex.2)</td><td>K528</td></tr>
<tr><td>7</td><td>tissue-7 somatic</td><td>Category II-Default Categorization</td><td>PCLO</td><td>SNP</td><td>7</td><td>82784378</td><td>T</td><td>C</td><td>0.0161</td><td>14</td><td>868</td><td>NON_SYNONYMOUS_CODING(MODERATE|MISSENSE|Aca/Gca|T527A|PCLO|mRNA|CODING|NM_014510|NM_014510.ex.2),NON_SYNONYMOUS_CODING(MODERATE|MISSENSE|Aca/Gca|T527A|PCLO|mRNA|CODING|NM_033026|NM_033026.ex.2)</td><td>T527A</td></tr>
<tr><td>7</td><td>tissue-7 somatic</td><td>Category III-Default Categorization</td><td>PCLO</td><td>SNP</td><td>7</td><td>82784433</td><td>T</td><td>C</td><td>0.0256</td><td>18</td><td>702</td><td>SYNONYMOUS_CODING(LOW|SILENT|aaA/aaG|K508|PCLO|mRNA|CODING|NM_014510|NM_014510.ex.2),SYNONYMOUS_CODING(LOW|SILENT|aaA/aaG|K508|PCLO|mRNA|CODING|NM_033026|NM_033026.ex.2)</td><td>K508</td></tr>
<tr><td>7</td><td>tissue-7 somatic</td><td>Category II-Default Categorization</td><td>PCLO</td><td>SNP</td><td>7</td><td>82784489</td><td>G</td><td>A</td><td>0.0127</td><td>11</td><td>863</td><td>NON_SYNONYMOUS_CODING(MODERATE|MISSENSE|Cca/Tca|P490S|PCLO|mRNA|CODING|NM_014510|NM_014510.ex.2),NON_SYNONYMOUS_CODING(MODERATE|MISSENSE|Cca/Tca|P490S|PCLO|mRNA|CODING|NM_033026|NM_033026.ex.2)</td><td>P490S</td></tr>
<tr><td>7</td><td>tissue-7 somatic</td><td>Category III-Default Categorization</td><td>NDRG1</td><td>SNP</td><td>8</td><td>134251244</td><td>G</td><td>C</td><td>0.0125</td><td>11</td><td>878</td><td>SYNONYMOUS_CODING(LOW|SILENT|tcC/tcG|S273|NDRG1|mRNA|CODING|NM_001258433|NM_001258433.ex.15),SYNONYMOUS_CODING(LOW|SILENT|tcC/tcG|S288|NDRG1|mRNA|CODING|NM_001258432|NM_001258432.ex.14),SYNONYMOUS_CODING(LOW|SILENT|tcC/tcG|S354|NDRG1|mRNA|CODING|NM_001135242|NM_001135242.ex.16),SYNONYMOUS_CODING(LOW|SILENT|tcC/tcG|S354|NDRG1|mRNA|CODING|NM_006096|NM_006096.ex.16)</td><td>S273</td></tr>
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7	tissue-7 somatic	Category III-Default Categorization	NDRG1	SNP	8	134251274	G	C	0.0202	17	840	SYNONYMOUS_CODING(LOW|SILENT|tcC/tcG|S263|NDRG1|mRNA|CODING|NM_001258433|NM_001258433.ex.15),SYNONYMOUS_CODING(LOW|SILENT|tcC/tcG|S278|NDRG1|mRNA|CODING|NM_001258432|NM_001258432.ex.14),SYNONYMOUS_CODING(LOW|SILENT|tcC/tcG|S344|NDRG1|mRNA|CODING|NM_001135242|NM_001135242.ex.16),SYNONYMOUS_CODING(LOW|SILENT|tcC/tcG|S344|NDRG1|mRNA|CODING|NM_006096|NM_006096.ex.16)	S263
7	tissue-7 somatic	Category III-Default Categorization	KMT2D	SNP	12	49444937	G	T	0.0111	12	1084	SYNONYMOUS_CODING(LOW|SILENT|tcC/tcA|S843|KMT2D|mRNA|CODING|NM_003482|NM_003482.ex.10)	S843
7	tissue-7 somatic	Category II-Default Categorization	KMT2D	SNP	12	49444945	A	G	0.0112	11	979	NON_SYNONYMOUS_CODING(MODERATE|MISSENSE|Tgc/Cgc|C841R|KMT2D|mRNA|CODING|NM_003482|NM_003482.ex.10)	C841R
7	tissue-7 somatic	Category II-Default Categorization	KMT2D	SNP	12	49445202	C	T	0.00893	13	1456	NON_SYNONYMOUS_CODING(MODERATE|MISSENSE|cGg/cAg|R755Q|KMT2D|mRNA|CODING|NM_003482|NM_003482.ex.10)	R755Q
7	tissue-7 somatic	Category III-Default Categorization	KMT2D	SNP	12	49445426	C	A	0.014	15	1069	SYNONYMOUS_CODING(LOW|SILENT|acG/acT|T680|KMT2D|mRNA|CODING|NM_003482|NM_003482.ex.10)	T680
7	tissue-7 somatic	Category II-Default Categorization	KMT2D	SNP	12	49445428	T	G	0.0151	15	993	NON_SYNONYMOUS_CODING(MODERATE|MISSENSE|Acg/Ccg|T680P|KMT2D|mRNA|CODING|NM_003482|NM_003482.ex.10)	T680P
7	tissue-7 somatic	Category III-Default Categorization	KMT2D	SNP	12	49445444	C	T	0.0208	20	960	SYNONYMOUS_CODING(LOW|SILENT|ccG/ccA|P674|KMT2D|mRNA|CODING|NM_003482|NM_003482.ex.10)	P674
7	plasma7-1	Category II-Default Categorization	KMT2D	SNP	12	49445202	C	T	0.0434	22	507	NON_SYNONYMOUS_CODING(MODERATE|MISSENSE|cGg/cAg|R755Q|KMT2D|mRNA|CODING|NM_003482|NM_003482.ex.10)	R755Q
7	plasma7-1	Category II-Default Categorization	KMT2D	SNP	12	49445428	T	G	0.0315	12	381	NON_SYNONYMOUS_CODING(MODERATE|MISSENSE|Acg/Ccg|T680P|KMT2D|mRNA|CODING|NM_003482|NM_003482.ex.10)	T680P
8	tissue-8 somatic	Category I-Default Categorization	SPEN	SNP	1	16254962	C	T	0.0615	24	390	STOP_GAINED(HIGH|NONSENSE|Cag/Tag|Q743*|SPEN|mRNA|CODING|NM_015001|NM_015001.ex.11)	Q743*

8	tissue-8 somatic	Category III-Default Categorization	ETV5	SNP	3	185775177	C	G	0.0333	12	360	INTRON(MODIFIER||||ETV5|mRNA|CODING|NM_004454|)	
8	tissue-8 somatic	Category II-Default Categorization	PCLO	SNP	7	82784366	A	G	0.011	10	909	NON_SYNONYMOUS_CODING(MODERATE|MISSENSE|Tct/Cct|S531P|PCLO|mRNA|CODING|NM_014510|NM_014510.ex.2),NON_SYNONYMOUS_CODING(MODERATE|MISSENSE|Tct/Cct|S531P|PCLO|mRNA|CODING|NM_033026|NM_033026.ex.2)	S531P
8	tissue-8 somatic	Category III-Default Categorization	PCLO	SNP	7	82784373	T	C	0.0118	10	850	SYNONYMOUS_CODING(LOW|SILENT|aaA/aaG|K528|PCLO|mRNA|CODING|NM_014510|NM_014510.ex.2),SYNONYMOUS_CODING(LOW|SILENT|aaA/aaG|K528|PCLO|mRNA|CODING|NM_033026|NM_033026.ex.2)	K528
8	tissue-8 somatic	Category II-Default Categorization	PCLO	SNP	7	82784378	T	C	0.0115	11	953	NON_SYNONYMOUS_CODING(MODERATE|MISSENSE|Aca/Gca|T527A|PCLO|mRNA|CODING|NM_014510|NM_014510.ex.2),NON_SYNONYMOUS_CODING(MODERATE|MISSENSE|Aca/Gca|T527A|PCLO|mRNA|CODING|NM_033026|NM_033026.ex.2)	T527A
8	tissue-8 somatic	Category III-Default Categorization	PCLO	SNP	7	82784433	T	C	0.0183	14	764	SYNONYMOUS_CODING(LOW|SILENT|aaA/aaG|K508|PCLO|mRNA|CODING|NM_014510|NM_014510.ex.2),SYNONYMOUS_CODING(LOW|SILENT|aaA/aaG|K508|PCLO|mRNA|CODING|NM_033026|NM_033026.ex.2)	K508
8	tissue-8 somatic	Category II-Default Categorization	PCLO	SNP	7	82784438	T	C	0.0199	16	804	NON_SYNONYMOUS_CODING(MODERATE|MISSENSE|Aca/Gca|T507A|PCLO|mRNA|CODING|NM_014510|NM_014510.ex.2),NON_SYNONYMOUS_CODING(MODERATE|MISSENSE|Aca/Gca|T507A|PCLO|mRNA|CODING|NM_033026|NM_033026.ex.2)	T507A
8	tissue-8 somatic	Category II-Default Categorization	PCLO	SNP	7	82784441	A	G	0.0239	17	711	NON_SYNONYMOUS_CODING(MODERATE|MISSENSE|Tca/Cca|S506P|PCLO|mRNA|CODING|NM_014510|NM_014510.ex.2),NON_SYNONYMOUS_CODING(MODERATE|MISSENSE|Tca/Cca|S506P|PCLO|mRNA|CODING|NM_033026|NM_033026.ex.2)	S506P

8	tissue-8 somatic	Category III-Default Categorization	PCLO	SNP	7	82784493	C	T	0.0136	10	733	SYNONYMOUS_CODING(LOW|SILENT|aaG/aaA|K488|PCLO|mRNA|CODING|NM_014510|NM_014510.ex.2),SYNONYMOUS_CODING(LOW|SILENT|aaG/aaA|K488|PCLO|mRNA|CODING|NM_033026|NM_033026.ex.2)	K488
8	tissue-8 somatic	Category II-Default Categorization	PCLO	SNP	7	82784501	G	A	0.0157	14	891	NON_SYNONYMOUS_CODING(MODERATE|MISSENSE|Cca/Tca|P486S|PCLO|mRNA|CODING|NM_014510|NM_014510.ex.2),NON_SYNONYMOUS_CODING(MODERATE|MISSENSE|Cca/Tca|P486S|PCLO|mRNA|CODING|NM_033026|NM_033026.ex.2)	P486S
8	tissue-8 somatic	Category III-Default Categorization	NDRG1	SNP	8	134251214	C	G	0.0119	10	839	SYNONYMOUS_CODING(LOW|SILENT|tcG/tcC|S283|NDRG1|mRNA|CODING|NM_001258433|NM_001258433.ex.15),SYNONYMOUS_CODING(LOW|SILENT|tcG/tcC|S298|NDRG1|mRNA|CODING|NM_001258432|NM_001258432.ex.14),SYNONYMOUS_CODING(LOW|SILENT|tcG/tcC|S364|NDRG1|mRNA|CODING|NM_001135242|NM_001135242.ex.16),SYNONYMOUS_CODING(LOW|SILENT|tcG/tcC|S364|NDRG1|mRNA|CODING|NM_006096|NM_006096.ex.16)	S283
8	tissue-8 somatic	Category III-Default Categorization	NDRG1	SNP	8	134251274	G	C	0.0163	14	858	SYNONYMOUS_CODING(LOW|SILENT|tcC/tcG|S263|NDRG1|mRNA|CODING|NM_001258433|NM_001258433.ex.15),SYNONYMOUS_CODING(LOW|SILENT|tcC/tcG|S278|NDRG1|mRNA|CODING|NM_001258432|NM_001258432.ex.14),SYNONYMOUS_CODING(LOW|SILENT|tcC/tcG|S344|NDRG1|mRNA|CODING|NM_001135242|NM_001135242.ex.16),SYNONYMOUS_CODING(LOW|SILENT|tcC/tcG|S344|NDRG1|mRNA|CODING|NM_006096|NM_006096.ex.16)	S263
8	tissue-8 somatic	Category I-Default Categorization	KMT2D	Insertion	12	49420995	A	AG	0.0263	11	418	FRAME_SHIFT(HIGH||||KMT2D|mRNA|CODING|NM_003482|NM_003482.ex.48)	
8	tissue-8 somatic	Category III-Default Categorization	KMT2D	SNP	12	49444937	G	T	0.0108	12	1108	SYNONYMOUS_CODING(LOW|SILENT|tcC/tcA|S843|KMT2D|mRNA|CODING|NM_003482|NM_003482.ex.10)	S843
8	tissue-8 somatic	Category II-Default Categorization	KMT2D	SNP	12	49444944	C	T	0.0102	11	1081	NON_SYNONYMOUS_CODING(MODERATE|MISSENSE|tGc/tAc|C841Y|KMT2D|mRNA|CODING|NM_003482|NM_003482.ex.10)	C841Y

8	tissue-8 somatic	Category II-Default Categorization	KMT2D	SNP	12	49444945	A	G	0.014	15	1068	NON_SYNONYMOUS_CODING(MODERATE|MISSENSE|Tgc/Cgc|C841R|KMT2D|mRNA|CODING|NM_003482|NM_003482.ex.10)	C841R
8	tissue-8 somatic	Category III-Default Categorization	KMT2D	SNP	12	49444946	T	C	0.0112	12	1071	SYNONYMOUS_CODING(LOW|SILENT|ccA/ccG|P840|KMT2D|mRNA|CODING|NM_003482|NM_003482.ex.10)	P840
8	tissue-8 somatic	Category III-Default Categorization	KMT2D	SNP	12	49445216	C	T	0.00858	13	1516	SYNONYMOUS_CODING(LOW|SILENT|ccG/ccA|P750|KMT2D|mRNA|CODING|NM_003482|NM_003482.ex.10)	P750
8	tissue-8 somatic	Category III-Default Categorization	KMT2D	SNP	12	49445420	A	T	0.0183	20	1091	SYNONYMOUS_CODING(LOW|SILENT|ccT/ccA|P682|KMT2D|mRNA|CODING|NM_003482|NM_003482.ex.10)	P682
8	tissue-8 somatic	Category III-Default Categorization	KMT2D	SNP	12	49445426	C	A	0.013	14	1073	SYNONYMOUS_CODING(LOW|SILENT|acG/acT|T680|KMT2D|mRNA|CODING|NM_003482|NM_003482.ex.10)	T680
8	tissue-8 somatic	Category II-Default Categorization	KMT2D	SNP	12	49445428	T	G	0.0145	15	1037	NON_SYNONYMOUS_CODING(MODERATE|MISSENSE|Acg/Ccg|T680P|KMT2D|mRNA|CODING|NM_003482|NM_003482.ex.10)	T680P
8	tissue-8 somatic	Category III-Default Categorization	KMT2D	SNP	12	49445546	T	C	0.0118	11	933	SYNONYMOUS_CODING(LOW|SILENT|gaA/gaG|E640|KMT2D|mRNA|CODING|NM_003482|NM_003482.ex.10)	E640
8	tissue-8 somatic	Category II-Default Categorization	CREBBP	SNP	16	3900518	G	T	0.075	39	520	NON_SYNONYMOUS_CODING(MODERATE|MISSENSE|tCt/tAt|S193Y|CREBBP|mRNA|CODING|NM_001079846|NM_001079846.ex.2),NON_SYNONYMOUS_CODING(MODERATE|MISSENSE|tCt/tAt|S193Y|CREBBP|mRNA|CODING|NM_004380|NM_004380.ex.2)	S193Y

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<tr><td>8</td><td>tissue-8 somatic</td><td>Category II-Default Categorization</td><td>TP53</td><td>SNP</td><td>17</td><td>7577099</td><td>C</td><td>G</td><td>0.0339</td><td>13</td><td>384</td><td>NON_SYNONYMOUS_CODING(MODERATE|MISSENSE|aGa/aCa|R121T|TP53|mRNA|CODING|NM_001276697|NM_001276697.ex.4),NON_SYNONYMOUS_CODING(MODERATE|MISSENSE|aGa/aCa|R121T|TP53|mRNA|CODING|NM_001276698|NM_001276698.ex.4),NON_SYNONYMOUS_CODING(MODERATE|MISSENSE|aGa/aCa|R121T|TP53|mRNA|CODING|NM_001276699|NM_001276699.ex.4),NON_SYNONYMOUS_CODING(MODERATE|MISSENSE|aGa/aCa|R148T|TP53|mRNA|CODING|NM_001126115|NM_001126115.ex.4),NON_SYNONYMOUS_CODING(MODERATE|MISSENSE|aGa/aCa|R148T|TP53|mRNA|CODING|NM_001126116|NM_001126116.ex.4),NON_SYNONYMOUS_CODING(MODERATE|MISSENSE|aGa/aCa|R148T|TP53|mRNA|CODING|NM_001126117|NM_001126117.ex.4),NON_SYNONYMOUS_CODING(MODERATE|MISSENSE|aGa/aCa|R241T|TP53|mRNA|CODING|NM_001126118|NM_001126118.ex.7),NON_SYNONYMOUS_CODING(MODERATE|MISSENSE|aGa/aCa|R241T|TP53|mRNA|CODING|NM_001276695|NM_001276695.ex.8),NON_SYNONYMOUS_CODING(MODERATE|MISSENSE|aGa/aCa|R241T|TP53|mRNA|CODING|NM_001276696|NM_001276696.ex.8),NON_SYNONYMOUS_CODING(MODERATE|MISSENSE|aGa/aCa|R241T|TP53|mRNA|CODING|NM_001276760|NM_001276760.ex.8),NON_SYNONYMOUS_CODING(MODERATE|MISSENSE|aGa/aCa|R241T|TP53|mRNA|CODING|NM_001276761|NM_001276761.ex.8),NON_SYNONYMOUS_CODING(MODERATE|MISSENSE|aGa/aCa|R280T|TP53|mRNA|CODING|NM_000546|NM_000546.ex.8),NON_SYNONYMOUS_CODING(MODERATE|MISSENSE|aGa/aCa|R280T|TP53|mRNA|CODING|NM_001126112|NM_001126112.ex.8),NON_SYNONYMO</td><td>R121T</td></tr>
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<tr><td>8</td><td>Plasma8-1</td><td>Category II-Default Categorization</td><td>PCLO</td><td>SNP</td><td>7</td><td>82784366</td><td>A</td><td>G</td><td>0.0682</td><td>12</td><td>176</td><td>NON_SYNONYMOUS_CODING(MODERATE|MISSENSE|Tct/Cct|S531P|PCLO|mRNA|CODING|NM_014510|NM_014510.ex.2),NON_SYNONYMOUS_CODING(MODERATE|MISSENSE|Tct/Cct|S531P|PCLO|mRNA|CODING|NM_033026|NM_033026.ex.2)</td><td>S531P</td></tr>
<tr><td>8</td><td>Plasma8-2</td><td>Category II-Default Categorization</td><td>PCLO</td><td>SNP</td><td>7</td><td>82784366</td><td>A</td><td>G</td><td>0.0714</td><td>13</td><td>182</td><td>NON_SYNONYMOUS_CODING(MODERATE|MISSENSE|Tct/Cct|S531P|PCLO|mRNA|CODING|NM_014510|NM_014510.ex.2),NON_SYNONYMOUS_CODING(MODERATE|MISSENSE|Tct/Cct|S531P|PCLO|mRNA|CODING|NM_033026|NM_033026.ex.2)</td><td>S531P</td></tr>
<tr><td>8</td><td>Plasma8-3</td><td>N/A</td><td>N/A</td><td>N/A</td><td>N/A</td><td>N/A</td><td>N/A</td><td>N/A</td><td>N/A</td><td>N/A</td><td>N/A</td><td>N/A</td><td>N/A</td></tr>
<tr><td>9</td><td>tissue- 9 somatic</td><td>Category II-Default Categorization</td><td>TIPARP</td><td>SNP</td><td>3</td><td>156395809</td><td>C</td><td>T</td><td>0.0726</td><td>66</td><td>909</td><td>NON_SYNONYMOUS_CODING(MODERATE|MISSENSE|tCt/tTt|S108F|TIPARP|mRNA|CODING|NM_001184717|NM_001184717.ex.2),NON_SYNONYMOUS_CODING(MODERATE|MISSENSE|tCt/tTt|S108F|TIPARP|mRNA|CODING|NM_001184718|NM_001184718.ex.2),NON_SYNONYMOUS_CODING(MODERATE|MISSENSE|tCt/tTt|S108F|TIPARP|mRNA|CODING|NM_015508|NM_015508.ex.2), UPSTREAM(MODIFIER||||TIPARP-AS1|Non-coding_transcript|NON_CODING|NR_027954|)</td><td>S108F</td></tr>
<tr><td>9</td><td>tissue- 9 somatic</td><td>Category II-Default Categorization</td><td>PIK3CA</td><td>SNP</td><td>3</td><td>178916854</td><td>G</td><td>C</td><td>0.0377</td><td>23</td><td>610</td><td>NON_SYNONYMOUS_CODING(MODERATE|MISSENSE|Gaa/Caa|E81Q|PIK3CA|mRNA|CODING|NM_006218|NM_006218.ex.2)</td><td>E81Q</td></tr>
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<tr><td>9</td><td>tissue- 9 somatic</td><td>Category III-Default Categorization</td><td>TP63</td><td>Deletion</td><td>3</td><td>189561962</td><td>CT</td><td>C</td><td>0.134</td><td>11</td><td>82</td><td>INTRON(MODIFIER||||TP63|mRNA|CODING|NM_001114978|),INTRON(MODIFIER||||TP63|mRNA|CODING|NM_001114979|),INTRON(MODIFIER||||TP63|mRNA|CODING|NM_001114980|),INTRON(MODIFIER||||TP63|mRNA|CODING|NM_001114981|),INTRON(MODIFIER||||TP63|mRNA|CODING|NM_001114982|),INTRON(MODIFIER||||TP63|mRNA|CODING|NM_001329144|),INTRON(MODIFIER||||TP63|mRNA|CODING|NM_001329145|),INTRON(MODIFIER||||TP63|mRNA|CODING|NM_001329146|),INTRON(MODIFIER||||TP63|mRNA|CODING|NM_001329148|),INTRON(MODIFIER||||TP63|mRNA|CODING|NM_001329149|),INTRON(MODIFIER||||TP63|mRNA|CODING|NM_001329150|),INTRON(MODIFIER||||TP63|mRNA|CODING|NM_001329964|),INTRON(MODIFIER||||TP63|mRNA|CODING|NM_003722|)</td><td></td></tr>
<tr><td>9</td><td>tissue- 9 somatic</td><td>Category I-Default Categorization</td><td>FBXW7</td><td>SNP</td><td>4</td><td>153259089</td><td>C</td><td>G</td><td>0.041</td><td>10</td><td>244</td><td>INTRON(MODIFIER||||FBXW7|mRNA|CODING|NM_001013415|),INTRON(MODIFIER||||FBXW7|mRNA|CODING|NM_001349798|),INTRON(MODIFIER||||FBXW7|mRNA|CODING|NM_018315|),INTRON(MODIFIER||||FBXW7|mRNA|CODING|NM_033632|),NON_SYNONYMOUS_CODING(MODERATE|MISSENSE|Cta/Gta|L71V|FBXW7-AS1|Non-coding_transcript|NON_CODING|NR_104273|NR_104273.ex.2),SPLICE_SITE_ACCEPTOR(HIGH||||FBXW7|mRNA|CODING|NM_001013415|),SPLICE_SITE_ACCEPTOR(HIGH||||FBXW7|mRNA|CODING|NM_001349798|),SPLICE_SITE_ACCEPTOR(HIGH||||FBXW7|mRNA|CODING|NM_018315|),SPLICE_SITE_ACCEPTOR(HIGH||||FBXW7|mRNA|CODING|NM_033632|)</td><td></td></tr>
<tr><td>9</td><td>tissue- 9 somatic</td><td>Category II-Default Categorization</td><td>PCLO</td><td>SNP</td><td>7</td><td>82585541</td><td>C</td><td>G</td><td>0.0392</td><td>28</td><td>715</td><td>NON_SYNONYMOUS_CODING(MODERATE|MISSENSE|gaG/gaC|E1576D|PCLO|mRNA|CODING|NM_014510|NM_014510.ex.5),NON_SYNONYMOUS_CODING(MODERATE|MISSENSE|gaG/gaC|E1576D|PCLO|mRNA|CODING|NM_033026|NM_033026.ex.5)</td><td>E1576D</td></tr>
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9	tissue- 9 somatic	Category II-Default Categorization	PCLO	SNP	7	82784366	A	G	0.0104	13	1245	NON_SYNONYMOUS_CODING(MODERATE|MISSENSE|Tct/Cct|S531P|PCLO|mRNA|CODING|NM_014510|NM_014510.ex.2),NON_SYNONYMOUS_CODING(MODERATE|MISSENSE|Tct/Cct|S531P|PCLO|mRNA|CODING|NM_033026|NM_033026.ex.2)	S531P
9	tissue- 9 somatic	Category III-Default Categorization	PCLO	SNP	7	82784373	T	C	0.0104	12	1156	SYNONYMOUS_CODING(LOW|SILENT|aaA/aaG|K528|PCLO|mRNA|CODING|NM_014510|NM_014510.ex.2),SYNONYMOUS_CODING(LOW|SILENT|aaA/aaG|K528|PCLO|mRNA|CODING|NM_033026|NM_033026.ex.2)	K528
9	tissue- 9 somatic	Category II-Default Categorization	PCLO	SNP	7	82784378	T	C	0.0106	14	1316	NON_SYNONYMOUS_CODING(MODERATE|MISSENSE|Aca/Gca|T527A|PCLO|mRNA|CODING|NM_014510|NM_014510.ex.2),NON_SYNONYMOUS_CODING(MODERATE|MISSENSE|Aca/Gca|T527A|PCLO|mRNA|CODING|NM_033026|NM_033026.ex.2)	T527A
9	tissue- 9 somatic	Category II-Default Categorization	PCLO	SNP	7	82784489	G	A	0.01	12	1195	NON_SYNONYMOUS_CODING(MODERATE|MISSENSE|Cca/Tca|P490S|PCLO|mRNA|CODING|NM_014510|NM_014510.ex.2),NON_SYNONYMOUS_CODING(MODERATE|MISSENSE|Cca/Tca|P490S|PCLO|mRNA|CODING|NM_033026|NM_033026.ex.2)	P490S
9	tissue- 9 somatic	Category III-Default Categorization	MGAM	SNP	7	141765240	A	G	0.0105	10	956	SYNONYMOUS_CODING(LOW|SILENT|gcA/gcG|A1530|MGAM|mRNA|CODING|NM_004668|NM_004668.ex.38)	A1530
9	tissue- 9 somatic	Category II-Default Categorization	KMT2C	SNP	7	151904410	C	G	0.0794	17	214	NON_SYNONYMOUS_CODING(MODERATE|MISSENSE|aaG/aaC|K1272N|KMT2C|mRNA|CODING|NM_170606|NM_170606.ex.24)	K1272N
9	tissue- 9 somatic	Category II-Default Categorization	KMT2C	SNP	7	151932997	C	T	0.0311	12	386	NON_SYNONYMOUS_CODING(MODERATE|MISSENSE|Gga/Aga|G892R|KMT2C|mRNA|CODING|NM_170606|NM_170606.ex.16)	G892R

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<tr><td>9</td><td>tissue- 9 somatic</td><td>Category II-Default Categorization</td><td>FGFR1</td><td>Deletion</td><td>8</td><td>38272106</td><td>AAATAATGCCTCG</td><td>A</td><td>0.0192</td><td>13</td><td>678</td><td>CODON_CHANGE_PLUS_CODON_DELETION(MODERATE||cccgaggcattattt/cct|PEALF576P|FGFR1|mRNA|CODING|NM_001354368|NM_001354368.ex.14),CODON_CHANGE_PLUS_CODON_DELETION(MODERATE||cccgaggcattattt/cct|PEALF578P|FGFR1|mRNA|CODING|NM_001354370|NM_001354370.ex.14),CODON_CHANGE_PLUS_CODON_DELETION(MODERATE||cccgaggcattattt/cct|PEALF578P|FGFR1|mRNA|CODING|NM_023106|NM_023106.ex.14),CODON_CHANGE_PLUS_CODON_DELETION(MODERATE||cccgaggcattattt/cct|PEALF580P|FGFR1|mRNA|CODING|NM_001174066|NM_001174066.ex.14),CODON_CHANGE_PLUS_CODON_DELETION(MODERATE||cccgaggcattattt/cct|PEALF580P|FGFR1|mRNA|CODING|NM_023105|NM_023105.ex.14),CODON_CHANGE_PLUS_CODON_DELETION(MODERATE||cccgaggcattattt/cct|PEALF659P|FGFR1|mRNA|CODING|NM_001174064|NM_001174064.ex.16),CODON_CHANGE_PLUS_CODON_DELETION(MODERATE||cccgaggcattattt/cct|PEALF665P|FGFR1|mRNA|CODING|NM_001354369|NM_001354369.ex.15),CODON_CHANGE_PLUS_CODON_DELETION(MODERATE||cccgaggcattattt/cct|PEALF667P|FGFR1|mRNA|CODING|NM_001174063|NM_001174063.ex.15),CODON_CHANGE_PLUS_CODON_DELETION(MODERATE||cccgaggcattattt/cct|PEALF667P|FGFR1|mRNA|CODING|NM_001174065|NM_001174065.ex.15),CODON_CHANGE_PLUS_CODON_DELETION(MODERATE||cccgaggcattattt/cct|PEALF667P|FGFR1|mRNA|CODING|NM_001354367|NM_001354367.ex.15),CODON_CHANGE_PLUS_CODON_DELETION(MODERATE||cccgaggcattattt/cct|PEALF667P|FGFR1|mRNA|CODING|NM_015850|NM_015850.ex.15),CODON_CHANGE_PLUS_CODON_DELETION(MODE</td><td>PEALF576P</td></tr>
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9	tissue- 9 somatic	Category III-Default Categorization	NDRG1	SNP	8	134251214	C	G	0.013	18	1389	SYNONYMOUS_CODING(LOW|SILENT|tcG/tcC|S283|NDRG1|mRNA|CODING|NM_001258433|NM_001258433.ex.15),SYNONYMOUS_CODING(LOW|SILENT|tcG/tcC|S298|NDRG1|mRNA|CODING|NM_001258432|NM_001258432.ex.14),SYNONYMOUS_CODING(LOW|SILENT|tcG/tcC|S364|NDRG1|mRNA|CODING|NM_001135242|NM_001135242.ex.16),SYNONYMOUS_CODING(LOW|SILENT|tcG/tcC|S364|NDRG1|mRNA|CODING|NM_006096|NM_006096.ex.16)	S283
9	tissue- 9 somatic	Category III-Default Categorization	NDRG1	SNP	8	134251244	G	C	0.0131	20	1532	SYNONYMOUS_CODING(LOW|SILENT|tcC/tcG|S273|NDRG1|mRNA|CODING|NM_001258433|NM_001258433.ex.15),SYNONYMOUS_CODING(LOW|SILENT|tcC/tcG|S288|NDRG1|mRNA|CODING|NM_001258432|NM_001258432.ex.14),SYNONYMOUS_CODING(LOW|SILENT|tcC/tcG|S354|NDRG1|mRNA|CODING|NM_001135242|NM_001135242.ex.16),SYNONYMOUS_CODING(LOW|SILENT|tcC/tcG|S354|NDRG1|mRNA|CODING|NM_006096|NM_006096.ex.16)	S273

9	tissue- 9 somatic	Category III-Default Categorization	CDKN2A	SNP	9	21994406	C	T	0.0236	11	467	INTRON(MODIFIER||||CDKN2A|mRNA|CODING|NM_001363763|),START_GAINED(LOW||||CDKN2A|mRNA|CODING|NM_058195|NM_058195.ex.1),UPSTREAM(MODIFIER||||CDKN2B-AS1|Non-coding_transcript|NON_CODING|NR_003529|),UPSTREAM(MODIFIER||||CDKN2B-AS1|Non-coding_transcript|NON_CODING|NR_047532|),UPSTREAM(MODIFIER||||CDKN2B-AS1|Non-coding_transcript|NON_CODING|NR_047533|),UPSTREAM(MODIFIER||||CDKN2B-AS1|Non-coding_transcript|NON_CODING|NR_047534|),UPSTREAM(MODIFIER||||CDKN2B-AS1|Non-coding_transcript|NON_CODING|NR_047535|),UPSTREAM(MODIFIER||||CDKN2B-AS1|Non-coding_transcript|NON_CODING|NR_047536|),UPSTREAM(MODIFIER||||CDKN2B-AS1|Non-coding_transcript|NON_CODING|NR_047537|),UPSTREAM(MODIFIER||||CDKN2B-AS1|Non-coding_transcript|NON_CODING|NR_047538|),UPSTREAM(MODIFIER||||CDKN2B-AS1|Non-coding_transcript|NON_CODING|NR_047539|),UPSTREAM(MODIFIER||||CDKN2B-AS1|Non-coding_transcript|NON_CODING|NR_047540|),UPSTREAM(MODIFIER||||CDKN2B-AS1|Non-coding_transcript|NON_CODING|NR_047541|),UPSTREAM(MODIFIER||||CDKN2B-AS1|Non-coding_transcript|NON_CODING|NR_047542|),UPSTREAM(MODIFIER||||CDKN2B-AS1|Non-coding_transcript|NON_CODING|NR_047543|),UPSTREAM(MODIFIER||||CDKN2B-AS1|Non-coding_transcript|NON_CODING|NR_120536|)	
9	tissue- 9 somatic	Category III-Default Categorization	LRRK2	SNP	12	40740742	C	T	0.0938	15	160	INTRON(MODIFIER||||LRRK2|mRNA|CODING|NM_198578|)	
9	tissue- 9 somatic	Category II-Default Categorization	KMT2D	SNP	12	49431941	G	C	0.0479	43	897	NON_SYNONYMOUS_CODING(MODERATE|MISSENSE|ttC/ttG|F3066L|KMT2D|mRNA|CODING|NM_003482|NM_003482.ex.34)	F3066L

9	tissue- 9 somatic	Category III-Default Categorization	KMT2D	SNP	12	49444937	G	T	0.0108	19	1754	SYNONYMOUS_CODING(LOW|SILENT|tcC/tcA|S843|KMT2D|mRNA|CODING|NM_003482|NM_003482.ex.10)	S843
9	tissue- 9 somatic	Category III-Default Categorization	KMT2D	SNP	12	49445216	C	T	0.00893	22	2463	SYNONYMOUS_CODING(LOW|SILENT|ccG/ccA|P750|KMT2D|mRNA|CODING|NM_003482|NM_003482.ex.10)	P750
9	tissue- 9 somatic	Category III-Default Categorization	KMT2D	SNP	12	49445234	T	G	0.00993	23	2317	SYNONYMOUS_CODING(LOW|SILENT|tcA/tcC|S744|KMT2D|mRNA|CODING|NM_003482|NM_003482.ex.10)	S744
9	tissue- 9 somatic	Category III-Default Categorization	KMT2D	SNP	12	49445399	G	C	0.0176	35	1984	SYNONYMOUS_CODING(LOW|SILENT|ctC/ctG|L689|KMT2D|mRNA|CODING|NM_003482|NM_003482.ex.10)	L689
9	tissue- 9 somatic	Category III-Default Categorization	KMT2D	SNP	12	49445408	A	T	0.0155	30	1934	SYNONYMOUS_CODING(LOW|SILENT|gcT/gcA|A686|KMT2D|mRNA|CODING|NM_003482|NM_003482.ex.10)	A686
9	tissue- 9 somatic	Category III-Default Categorization	KMT2D	SNP	12	49445420	A	T	0.0211	39	1847	SYNONYMOUS_CODING(LOW|SILENT|ccT/ccA|P682|KMT2D|mRNA|CODING|NM_003482|NM_003482.ex.10)	P682
9	tissue- 9 somatic	Category II-Default Categorization	KMT2D	SNP	12	49445428	T	G	0.00867	15	1730	NON_SYNONYMOUS_CODING(MODERATE|MISSENSE|Acg/Ccg|T680P|KMT2D|mRNA|CODING|NM_003482|NM_003482.ex.10)	T680P
9	tissue- 9 somatic	Category III-Default Categorization	KMT2D	SNP	12	49445444	C	T	0.0145	25	1727	SYNONYMOUS_CODING(LOW|SILENT|ccG/ccA|P674|KMT2D|mRNA|CODING|NM_003482|NM_003482.ex.10)	P674
9	tissue- 9 somatic	Category III-Default Categorization	KMT2D	SNP	12	49445447	T	A	0.012	20	1669	SYNONYMOUS_CODING(LOW|SILENT|ccA/ccT|P673|KMT2D|mRNA|CODING|NM_003482|NM_003482.ex.10)	P673
9	tissue- 9 somatic	Category II-Default Categorization	KMT2D	SNP	12	49445562	A	G	0.00833	14	1681	NON_SYNONYMOUS_CODING(MODERATE|MISSENSE|aTg/aCg|M635T|KMT2D|mRNA|CODING|NM_003482|NM_003482.ex.10)	M635T
9	tissue- 9 somatic	Category III-Default Categorization	KMT2D	SNP	12	49445564	A	G	0.0166	27	1627	SYNONYMOUS_CODING(LOW|SILENT|ccT/ccC|P634|KMT2D|mRNA|CODING|NM_003482|NM_003482.ex.10)	P634
9	tissue- 9 somatic	Category III-Default Categorization	KMT2D	SNP	12	49445747	A	G	0.00682	10	1467	SYNONYMOUS_CODING(LOW|SILENT|tcT/tcC|S573|KMT2D|mRNA|CODING|NM_003482|NM_003482.ex.10)	S573

9	tissue- 9 somatic	Category III-Default Categorization	KMT2D	SNP	12	49445762	T	C	0.00767	11	1435	SYNONYMOUS_CODING(LOW|SILENT|gaA/gaG|E568|KMT2D|mRNA|CODING|NM_003482|NM_003482.ex.10)	E568
9	tissue- 9 somatic	Category III-Default Categorization	KMT2D	SNP	12	49445771	C	T	0.00726	10	1378	SYNONYMOUS_CODING(LOW|SILENT|ccG/ccA|P565|KMT2D|mRNA|CODING|NM_003482|NM_003482.ex.10)	P565
9	tissue- 9 somatic	Category II-Default Categorization	RNF213	SNP	17	78355519	C	G	0.109	49	451	INTRON(MODIFIER||||LOC100294362|Non-coding_transcript|NON_CODING|NR_029376|),NON_SYNONYMOUS_CODING(MODERATE|MISSENSE|tCt/tGt|S4657C|RNF213|mRNA|CODING|NM_001256071|NM_001256071.ex.57)	S4657C
9	Plasma9-1	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A
9	Plasma9-2	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A
9	Plasma9-3	Category II-Default Categorization	PCLO	SNP	7	82784366	A	G	0.0287	14	488	NON_SYNONYMOUS_CODING(MODERATE|MISSENSE|Tct/Cct|S531P|PCLO|mRNA|CODING|NM_014510|NM_014510.ex.2),NON_SYNONYMOUS_CODING(MODERATE|MISSENSE|Tct/Cct|S531P|PCLO|mRNA|CODING|NM_033026|NM_033026.ex.2)	S531P
10	tissue-10 somatic	Category II-Default Categorization	LRP1B	SNP	2	140995843	G	A	0.509	81	159	NON_SYNONYMOUS_CODING(MODERATE|MISSENSE|Cct/Tct|P4480S|LRP1B|mRNA|CODING|NM_018557|NM_018557.ex.89)	P4480S
10	tissue-10 somatic	Category II-Default Categorization	LRP1B	SNP	2	141113958	C	A	0.373	53	142	NON_SYNONYMOUS_CODING(MODERATE|MISSENSE|cGc/cTc|R3828L|LRP1B|mRNA|CODING|NM_018557|NM_018557.ex.75)	R3828L
10	tissue-10 somatic	Category II-Default Categorization	LRP1B	SNP	2	141128779	C	G	0.42	63	150	NON_SYNONYMOUS_CODING(MODERATE|MISSENSE|gGa/gCa|G3615A|LRP1B|mRNA|CODING|NM_018557|NM_018557.ex.70)	G3615A
10	tissue-10 somatic	Category III-Default Categorization	LRP1B	SNP	2	141130695	C	T	0.414	72	174	SYNONYMOUS_CODING(LOW|SILENT|gaG/gaA|E3550|LRP1B|mRNA|CODING|NM_018557|NM_018557.ex.69)	E3550
10	tissue-10 somatic	Category II-Default Categorization	TERC	SNP	3	169482689	G	C	0.235	89	379	DOWNSTREAM(MODIFIER||||ACTRT3|mRNA|CODING|NM_032487|),NON_SYNONYMOUS_CODING(MODERATE|MISSENSE|Cta/Gta|L54V|TERC|Non-coding_transcript|NON_CODING|NR_001566|NR_001566.ex.1)	L54V

<table>
<tr><td>10</td><td>tissue-10 somatic</td><td>Category III-Default Categorization</td><td>TRIP13</td><td>SNP</td><td>5</td><td>912018</td><td>C</td><td>T</td><td>0.582</td><td>152</td><td>261</td><td>DOWNSTREAM(MODIFIER||||TRIP13|mRNA|CODING|NM_001166260|),SYNONYMOUS_CODING(LOW|SILENT|ttC/ttT|F309|TRIP13|mRNA|CODING|NM_004237|NM_004237.ex.10)</td><td>F309</td></tr>
<tr><td>10</td><td>tissue-10 somatic</td><td>Category III-Default Categorization</td><td>ADGRA2</td><td>SNP</td><td>8</td><td>37688433</td><td>C</td><td>T</td><td>0.193</td><td>37</td><td>192</td><td>SYNONYMOUS_CODING(LOW|SILENT|ttC/ttT|F308|ADGRA2|mRNA|CODING|NM_032777|NM_032777.ex.7)</td><td>F308</td></tr>
<tr><td>10</td><td>tissue-10 somatic</td><td>Category III-Default Categorization</td><td>PTPRD</td><td>SNP</td><td>9</td><td>8484103</td><td>C</td><td>G</td><td>0.479</td><td>81</td><td>169</td><td>INTRON(MODIFIER||||PTPRD|mRNA|CODING|NM_001040712|),INTRON(MODIFIER||||PTPRD|mRNA|CODING|NM_001171025|),INTRON(MODIFIER||||PTPRD|mRNA|CODING|NM_002839|),INTRON(MODIFIER||||PTPRD|mRNA|CODING|NM_130391|),INTRON(MODIFIER||||PTPRD|mRNA|CODING|NM_130392|),INTRON(MODIFIER||||PTPRD|mRNA|CODING|NM_130393|)</td><td></td></tr>
<tr><td>10</td><td>tissue-10 somatic</td><td>Category II-Default Categorization</td><td>LRRK2</td><td>SNP</td><td>12</td><td>40757348</td><td>C</td><td>G</td><td>0.47</td><td>77</td><td>164</td><td>NON_SYNONYMOUS_CODING(MODERATE|MISSENSE|caC/caG|H2391Q|LRRK2|mRNA|CODING|NM_198578|NM_198578.ex.48)</td><td>H2391Q</td></tr>
<tr><td>10</td><td>tissue-10 somatic</td><td>Category II-Default Categorization</td><td>KMT2D</td><td>SNP</td><td>12</td><td>49432326</td><td>G</td><td>A</td><td>0.467</td><td>168</td><td>360</td><td>NON_SYNONYMOUS_CODING(MODERATE|MISSENSE|cCg/cTg|P2938L|KMT2D|mRNA|CODING|NM_003482|NM_003482.ex.34)</td><td>P2938L</td></tr>
<tr><td>10</td><td>tissue-10 somatic</td><td>Category II-Default Categorization</td><td>RNF213</td><td>SNP</td><td>17</td><td>78313616</td><td>G</td><td>T</td><td>0.478</td><td>183</td><td>383</td><td>NON_SYNONYMOUS_CODING(MODERATE|MISSENSE|Gtg/Ttg|V1817L|RNF213|mRNA|CODING|NM_001256071|NM_001256071.ex.26)</td><td>V1817L</td></tr>
<tr><td>10</td><td>Plasma10-1</td><td>N/A</td><td>N/A</td><td>N/A</td><td>N/A</td><td>N/A</td><td>N/A</td><td>N/A</td><td>N/A</td><td>N/A</td><td>N/A</td><td>N/A</td><td>N/A</td></tr>
<tr><td>10</td><td>Plasma10-2</td><td>N/A</td><td>N/A</td><td>N/A</td><td>N/A</td><td>N/A</td><td>N/A</td><td>N/A</td><td>N/A</td><td>N/A</td><td>N/A</td><td>N/A</td><td>N/A</td></tr>
<tr><td>10</td><td>Plasma10-3</td><td>N/A</td><td>N/A</td><td>N/A</td><td>N/A</td><td>N/A</td><td>N/A</td><td>N/A</td><td>N/A</td><td>N/A</td><td>N/A</td><td>N/A</td><td>N/A</td></tr>
<tr><td>11</td><td>tissue-11somatic</td><td>Category II-Default Categorization</td><td>PCLO</td><td>SNP</td><td>7</td><td>82784366</td><td>A</td><td>G</td><td>0.00958</td><td>14</td><td>1461</td><td>NON_SYNONYMOUS_CODING(MODERATE|MISSENSE|Tct/Cct|S531P|PCLO|mRNA|CODING|NM_014510|NM_014510.ex.2),NON_SYNONYMOUS_CODING(MODERATE|MISSENSE|Tct/Cct|S531P|PCLO|mRNA|CODING|NM_033026|NM_033026.ex.2)</td><td>S531P</td></tr>
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<table>
<tr><td>11</td><td>tissue-11somatic</td><td>Category III-Default Categorization</td><td>PCLO</td><td>SNP</td><td>7</td><td>82784373</td><td>T</td><td>C</td><td>0.0113</td><td>15</td><td>1324</td><td>SYNONYMOUS_CODING(LOW|SILENT|aaA/aaG|K528|PCLO|mRNA|CODING|NM_014510|NM_014510.ex.2),SYNONYMOUS_CODING(LOW|SILENT|aaA/aaG|K528|PCLO|mRNA|CODING|NM_033026|NM_033026.ex.2)</td><td>K528</td></tr>
<tr><td>11</td><td>tissue-11somatic</td><td>Category II-Default Categorization</td><td>PCLO</td><td>SNP</td><td>7</td><td>82784378</td><td>T</td><td>C</td><td>0.0118</td><td>18</td><td>1531</td><td>NON_SYNONYMOUS_CODING(MODERATE|MISSENSE|Aca/Gca|T527A|PCLO|mRNA|CODING|NM_014510|NM_014510.ex.2),NON_SYNONYMOUS_CODING(MODERATE|MISSENSE|Aca/Gca|T527A|PCLO|mRNA|CODING|NM_033026|NM_033026.ex.2)</td><td>T527A</td></tr>
<tr><td>11</td><td>tissue-11somatic</td><td>Category II-Default Categorization</td><td>PCLO</td><td>SNP</td><td>7</td><td>82784381</td><td>A</td><td>G</td><td>0.00759</td><td>11</td><td>1450</td><td>NON_SYNONYMOUS_CODING(MODERATE|MISSENSE|Tca/Cca|S526P|PCLO|mRNA|CODING|NM_014510|NM_014510.ex.2),NON_SYNONYMOUS_CODING(MODERATE|MISSENSE|Tca/Cca|S526P|PCLO|mRNA|CODING|NM_033026|NM_033026.ex.2)</td><td>S526P</td></tr>
<tr><td>11</td><td>tissue-11somatic</td><td>Category III-Default Categorization</td><td>PCLO</td><td>SNP</td><td>7</td><td>82784433</td><td>T</td><td>C</td><td>0.0163</td><td>19</td><td>1166</td><td>SYNONYMOUS_CODING(LOW|SILENT|aaA/aaG|K508|PCLO|mRNA|CODING|NM_014510|NM_014510.ex.2),SYNONYMOUS_CODING(LOW|SILENT|aaA/aaG|K508|PCLO|mRNA|CODING|NM_033026|NM_033026.ex.2)</td><td>K508</td></tr>
<tr><td>11</td><td>tissue-11somatic</td><td>Category II-Default Categorization</td><td>PCLO</td><td>SNP</td><td>7</td><td>82784438</td><td>T</td><td>C</td><td>0.0172</td><td>22</td><td>1279</td><td>NON_SYNONYMOUS_CODING(MODERATE|MISSENSE|Aca/Gca|T507A|PCLO|mRNA|CODING|NM_014510|NM_014510.ex.2),NON_SYNONYMOUS_CODING(MODERATE|MISSENSE|Aca/Gca|T507A|PCLO|mRNA|CODING|NM_033026|NM_033026.ex.2)</td><td>T507A</td></tr>
<tr><td>11</td><td>tissue-11somatic</td><td>Category II-Default Categorization</td><td>PCLO</td><td>SNP</td><td>7</td><td>82784489</td><td>G</td><td>A</td><td>0.0144</td><td>22</td><td>1529</td><td>NON_SYNONYMOUS_CODING(MODERATE|MISSENSE|Cca/Tca|P490S|PCLO|mRNA|CODING|NM_014510|NM_014510.ex.2),NON_SYNONYMOUS_CODING(MODERATE|MISSENSE|Cca/Tca|P490S|PCLO|mRNA|CODING|NM_033026|NM_033026.ex.2)</td><td>P490S</td></tr>
<tr><td>11</td><td>tissue-11somatic</td><td>Category II-Default Categorization</td><td>KMT2C</td><td>SNP</td><td>7</td><td>151927028</td><td>G</td><td>T</td><td>0.00871</td><td>12</td><td>1377</td><td>NON_SYNONYMOUS_CODING(MODERATE|MISSENSE|Cca/Aca|P986T|KMT2C|mRNA|CODING|NM_170606|NM_170606.ex.18)</td><td>P986T</td></tr>
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<table>
<tr><td>11</td><td>tissue-11somatic</td><td>Category III-Default Categorization</td><td>NDRG1</td><td>SNP</td><td>8</td><td>134251214</td><td>C</td><td>G</td><td>0.00823</td><td>10</td><td>1215</td><td>SYNONYMOUS_CODING(LOW|SILENT|tcG/tcC|S283|NDRG1|mRNA|CODING|NM_001258433|NM_001258433.ex.15),SYNONYMOUS_CODING(LOW|SILENT|tcG/tcC|S298|NDRG1|mRNA|CODING|NM_001258432|NM_001258432.ex.14),SYNONYMOUS_CODING(LOW|SILENT|tcG/tcC|S364|NDRG1|mRNA|CODING|NM_001135242|NM_001135242.ex.16),SYNONYMOUS_CODING(LOW|SILENT|tcG/tcC|S364|NDRG1|mRNA|CODING|NM_006096|NM_006096.ex.16)</td><td>S283</td></tr>
<tr><td>11</td><td>tissue-11somatic</td><td>Category III-Default Categorization</td><td>NDRG1</td><td>SNP</td><td>8</td><td>134251244</td><td>G</td><td>C</td><td>0.0139</td><td>19</td><td>1363</td><td>SYNONYMOUS_CODING(LOW|SILENT|tcC/tcG|S273|NDRG1|mRNA|CODING|NM_001258433|NM_001258433.ex.15),SYNONYMOUS_CODING(LOW|SILENT|tcC/tcG|S288|NDRG1|mRNA|CODING|NM_001258432|NM_001258432.ex.14),SYNONYMOUS_CODING(LOW|SILENT|tcC/tcG|S354|NDRG1|mRNA|CODING|NM_001135242|NM_001135242.ex.16),SYNONYMOUS_CODING(LOW|SILENT|tcC/tcG|S354|NDRG1|mRNA|CODING|NM_006096|NM_006096.ex.16)</td><td>S273</td></tr>
<tr><td>11</td><td>tissue-11somatic</td><td>Category III-Default Categorization</td><td>PC</td><td>SNP</td><td>11</td><td>66618409</td><td>A</td><td>G</td><td>0.0126</td><td>17</td><td>1345</td><td>DOWNSTREAM(MODIFIER||||RCE1|mRNA|CODING|NM_001032279|),DOWNSTREAM(MODIFIER||||RCE1|mRNA|CODING|NM_005133|),INTRON(MODIFIER||||PC|mRNA|CODING|NM_000920|),INTRON(MODIFIER||||PC|mRNA|CODING|NM_001040716|),INTRON(MODIFIER||||PC|mRNA|CODING|NM_022172|)</td><td></td></tr>
<tr><td>11</td><td>tissue-11somatic</td><td>Category III-Default Categorization</td><td>KMT2D</td><td>SNP</td><td>12</td><td>49444937</td><td>G</td><td>T</td><td>0.012</td><td>23</td><td>1912</td><td>SYNONYMOUS_CODING(LOW|SILENT|tcC/tcA|S843|KMT2D|mRNA|CODING|NM_003482|NM_003482.ex.10)</td><td>S843</td></tr>
<tr><td>11</td><td>tissue-11somatic</td><td>Category III-Default Categorization</td><td>KMT2D</td><td>SNP</td><td>12</td><td>49444985</td><td>T</td><td>C</td><td>0.00872</td><td>14</td><td>1605</td><td>SYNONYMOUS_CODING(LOW|SILENT|caA/caG|Q827|KMT2D|mRNA|CODING|NM_003482|NM_003482.ex.10)</td><td>Q827</td></tr>
<tr><td>11</td><td>tissue-11somatic</td><td>Category II-Default Categorization</td><td>KMT2D</td><td>SNP</td><td>12</td><td>49445038</td><td>T</td><td>G</td><td>0.0142</td><td>24</td><td>1685</td><td>NON_SYNONYMOUS_CODING(MODERATE|MISSENSE|Act/Cct|T810P|KMT2D|mRNA|CODING|NM_003482|NM_003482.ex.10)</td><td>T810P</td></tr>
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11	tissue-11somatic	Category II-Default Categorization	KMT2D	SNP	12	49445040	T	C	0.00887	16	1803	NON_SYNONYMOUS_CODING(MODERATE|MISSENSE|cAg/cGg|Q809R|KMT2D|mRNA|CODING|NM_003482|NM_003482.ex.10)	Q809R
11	tissue-11somatic	Category III-Default Categorization	KMT2D	SNP	12	49445420	A	T	0.0133	27	2030	SYNONYMOUS_CODING(LOW|SILENT|ccT/ccA|P682|KMT2D|mRNA|CODING|NM_003482|NM_003482.ex.10)	P682
11	tissue-11somatic	Category II-Default Categorization	KMT2D	SNP	12	49445427	G	A	0.00964	20	2074	NON_SYNONYMOUS_CODING(MODERATE|MISSENSE|aCg/aTg|T680M|KMT2D|mRNA|CODING|NM_003482|NM_003482.ex.10)	T680M
11	tissue-11somatic	Category II-Default Categorization	KMT2D	SNP	12	49445428	T	G	0.0102	20	1953	NON_SYNONYMOUS_CODING(MODERATE|MISSENSE|Acg/Ccg|T680P|KMT2D|mRNA|CODING|NM_003482|NM_003482.ex.10)	T680P
11	tissue-11somatic	Category III-Default Categorization	KMT2D	SNP	12	49445444	C	T	0.0115	22	1906	SYNONYMOUS_CODING(LOW|SILENT|ccG/ccA|P674|KMT2D|mRNA|CODING|NM_003482|NM_003482.ex.10)	P674
11	tissue-11somatic	Category III-Default Categorization	KMT2D	SNP	12	49445447	T	A	0.00821	15	1826	SYNONYMOUS_CODING(LOW|SILENT|ccA/ccT|P673|KMT2D|mRNA|CODING|NM_003482|NM_003482.ex.10)	P673
11	tissue-11somatic	Category III-Default Categorization	KMT2D	SNP	12	49445564	A	G	0.00735	13	1769	SYNONYMOUS_CODING(LOW|SILENT|ccT/ccC|P634|KMT2D|mRNA|CODING|NM_003482|NM_003482.ex.10)	P634
11	tissue-11somatic	Category III-Default Categorization	KMT2D	SNP	12	49445747	A	G	0.00705	11	1561	SYNONYMOUS_CODING(LOW|SILENT|tcT/tcC|S573|KMT2D|mRNA|CODING|NM_003482|NM_003482.ex.10)	S573
11	tissue-11somatic	Category III-Default Categorization	KMT2D	SNP	12	49446062	T	G	0.0242	26	1074	SYNONYMOUS_CODING(LOW|SILENT|tcA/tcC|S468|KMT2D|mRNA|CODING|NM_003482|NM_003482.ex.10)	S468
11	Plasma11-1	Category II-Default Categorization	PCLO	SNP	7	82784366	A	G	0.0159	21	1324	NON_SYNONYMOUS_CODING(MODERATE|MISSENSE|Tct/Cct|S531P|PCLO|mRNA|CODING|NM_014510|NM_014510.ex.2),NON_SYNONYMOUS_CODING(MODERATE|MISSENSE|Tct/Cct|S531P|PCLO|mRNA|CODING|NM_033026|NM_033026.ex.2)	S531P
11	Plasma11-1	Category III-Default Categorization	KMT2D	SNP	12	49444985	T	C	0.00813	14	1722	SYNONYMOUS_CODING(LOW|SILENT|caA/caG|Q827|KMT2D|mRNA|CODING|NM_003482|NM_003482.ex.10)	Q827
11	Plasma11-2	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A

12	tissue-12 Somatic	Category II-Default Categorization	NFE2L2	SNP	2	178096724	C	T	0.0293	25	854	NON_SYNONYMOUS_CODING(MODERATE|MISSENSE|Gaa/Aaa|E103K|NFE2L2|mRNA|CODING|NM_001313904|NM_001313904.ex.5),NON_SYNONYMOUS_CODING(MODERATE|MISSENSE|Gaa/Aaa|E130K|NFE2L2|mRNA|CODING|NM_001313903|NM_001313903.ex.5),NON_SYNONYMOUS_CODING(MODERATE|MISSENSE|Gaa/Aaa|E173K|NFE2L2|mRNA|CODING|NM_001313902|NM_001313902.ex.4),NON_SYNONYMOUS_CODING(MODERATE|MISSENSE|Gaa/Aaa|E180K|NFE2L2|mRNA|CODING|NM_001145413|NM_001145413.ex.5),NON_SYNONYMOUS_CODING(MODERATE|MISSENSE|Gaa/Aaa|E187K|NFE2L2|mRNA|CODING|NM_001145412|NM_001145412.ex.5),NON_SYNONYMOUS_CODING(MODERATE|MISSENSE|Gaa/Aaa|E187K|NFE2L2|mRNA|CODING|NM_001313900|NM_001313900.ex.5),NON_SYNONYMOUS_CODING(MODERATE|MISSENSE|Gaa/Aaa|E187K|NFE2L2|mRNA|CODING|NM_001313901|NM_001313901.ex.5),NON_SYNONYMOUS_CODING(MODERATE|MISSENSE|Gaa/Aaa|E203K|NFE2L2|mRNA|CODING|NM_006164|NM_006164.ex.5)	E103K
12	tissue-12 Somatic	Category II-Default Categorization	PIK3CA	SNP	3	178936091	G	A	0.0235	11	468	NON_SYNONYMOUS_CODING(MODERATE|MISSENSE|Gag/Aag|E545K|PIK3CA|mRNA|CODING|NM_006218|NM_006218.ex.10)	E545K
12	tissue-12 Somatic	Category III-Default Categorization	PIK3CA	SNP	3	178936099	G	A	0.0248	11	443	SYNONYMOUS_CODING(LOW|SILENT|gaG/gaA|E547|PIK3CA|mRNA|CODING|NM_006218|NM_006218.ex.10)	E547
12	tissue-12 Somatic	Category II-Default Categorization	FAT4	SNP	4	126329638	C	G	0.0436	29	665	NON_SYNONYMOUS_CODING(MODERATE|MISSENSE|tCt/tGt|S1870C|FAT4|mRNA|CODING|NM_001291285|NM_001291285.ex.4),NON_SYNONYMOUS_CODING(MODERATE|MISSENSE|tCt/tGt|S1870C|FAT4|mRNA|CODING|NM_001291303|NM_001291303.ex.4),NON_SYNONYMOUS_CODING(MODERATE|MISSENSE|tCt/tGt|S1870C|FAT4|mRNA|CODING|NM_024582|NM_024582.ex.4)	S1870C

12	tissue-12 Somatic	Category II-Default Categorization	SDHA	SNP	5	254529	T	C	0.0365	21	575	NON_SYNONYMOUS_CODING(MODERATE|MISSENSE|Tac/Cac|Y525H|SDHA|mRNA|CODING|NM_001330758|NM_001330758.ex.12),NON_SYNONYMOUS_CODING(MODERATE|MISSENSE|Tac/Cac|Y558H|SDHA|mRNA|CODING|NM_001294332|NM_001294332.ex.13),NON_SYNONYMOUS_CODING(MODERATE|MISSENSE|Tac/Cac|Y606H|SDHA|mRNA|CODING|NM_004168|NM_004168.ex.14)	Y525H
12	tissue-12 Somatic	Category II-Default Categorization	SDHA	SNP	5	254574	C	T	0.0326	14	430	NON_SYNONYMOUS_CODING(MODERATE|MISSENSE|Cac/Tac|H540Y|SDHA|mRNA|CODING|NM_001330758|NM_001330758.ex.12),NON_SYNONYMOUS_CODING(MODERATE|MISSENSE|Cac/Tac|H573Y|SDHA|mRNA|CODING|NM_001294332|NM_001294332.ex.13),NON_SYNONYMOUS_CODING(MODERATE|MISSENSE|Cac/Tac|H621Y|SDHA|mRNA|CODING|NM_004168|NM_004168.ex.14)	H540Y
12	tissue-12 Somatic	Category II-Default Categorization	PCLO	SNP	7	82784366	A	G	0.00789	13	1648	NON_SYNONYMOUS_CODING(MODERATE|MISSENSE|Tct/Cct|S531P|PCLO|mRNA|CODING|NM_014510|NM_014510.ex.2),NON_SYNONYMOUS_CODING(MODERATE|MISSENSE|Tct/Cct|S531P|PCLO|mRNA|CODING|NM_033026|NM_033026.ex.2)	S531P
12	tissue-12 Somatic	Category II-Default Categorization	PCLO	SNP	7	82784486	G	A	0.00882	14	1587	NON_SYNONYMOUS_CODING(MODERATE|MISSENSE|Cct/Tct|P491S|PCLO|mRNA|CODING|NM_014510|NM_014510.ex.2),NON_SYNONYMOUS_CODING(MODERATE|MISSENSE|Cct/Tct|P491S|PCLO|mRNA|CODING|NM_033026|NM_033026.ex.2)	P491S
12	tissue-12 Somatic	Category III-Default Categorization	PCLO	SNP	7	82784493	C	T	0.00781	10	1281	SYNONYMOUS_CODING(LOW|SILENT|aaG/aaA|K488|PCLO|mRNA|CODING|NM_014510|NM_014510.ex.2),SYNONYMOUS_CODING(LOW|SILENT|aaG/aaA|K488|PCLO|mRNA|CODING|NM_033026|NM_033026.ex.2)	K488
12	tissue-12 Somatic	Category II-Default Categorization	PCLO	SNP	7	82784501	G	A	0.0102	17	1670	NON_SYNONYMOUS_CODING(MODERATE|MISSENSE|Cca/Tca|P486S|PCLO|mRNA|CODING|NM_014510|NM_014510.ex.2),NON_SYNONYMOUS_CODING(MODERATE|MISSENSE|Cca/Tca|P486S|PCLO|mRNA|CODING|NM_033026|NM_033026.ex.2)	P486S

<table>
<tr><td>12</td><td>tissue-12 Somatic</td><td>Category III-Default Categorization</td><td>RELN</td><td>Deletion</td><td>7</td><td>103270629</td><td>GA</td><td>G</td><td>0.0307</td><td>14</td><td>456</td><td>INTRON(MODIFIER||||RELN|mRNA|CODING|NM_005045|),INTRON(MODIFIER||||RELN|mRNA|CODING|NM_173054|)</td><td></td></tr>
<tr><td>12</td><td>tissue-12 Somatic</td><td>Category III-Default Categorization</td><td>KMT2C</td><td>Deletion</td><td>7</td><td>151919784</td><td>TG</td><td>T</td><td>0.0292</td><td>16</td><td>548</td><td>INTRON(MODIFIER||||KMT2C|mRNA|CODING|NM_170606|)</td><td></td></tr>
<tr><td>12</td><td>tissue-12 Somatic</td><td>Category I-Default Categorization</td><td>FGFR1</td><td>Insertion</td><td>8</td><td>38272121</td><td>T</td><td>TC</td><td>0.0225</td><td>19</td><td>846</td><td>FRAME_SHIFT(HIGH||||FGFR1|mRNA|CODING|NM_001174063|NM_001174063.ex.15),FRAME_SHIFT(HIGH||||FGFR1|mRNA|CODING|NM_001174064|NM_001174064.ex.16),FRAME_SHIFT(HIGH||||FGFR1|mRNA|CODING|NM_001174065|NM_001174065.ex.15),FRAME_SHIFT(HIGH||||FGFR1|mRNA|CODING|NM_001174066|NM_001174066.ex.14),FRAME_SHIFT(HIGH||||FGFR1|mRNA|CODING|NM_001174067|NM_001174067.ex.16),FRAME_SHIFT(HIGH||||FGFR1|mRNA|CODING|NM_001354367|NM_001354367.ex.15),FRAME_SHIFT(HIGH||||FGFR1|mRNA|CODING|NM_001354368|NM_001354368.ex.14),FRAME_SHIFT(HIGH||||FGFR1|mRNA|CODING|NM_001354369|NM_001354369.ex.15),FRAME_SHIFT(HIGH||||FGFR1|mRNA|CODING|NM_001354370|NM_001354370.ex.14),FRAME_SHIFT(HIGH||||FGFR1|mRNA|CODING|NM_015850|NM_015850.ex.15),FRAME_SHIFT(HIGH||||FGFR1|mRNA|CODING|NM_023105|NM_023105.ex.14),FRAME_SHIFT(HIGH||||FGFR1|mRNA|CODING|NM_023106|NM_023106.ex.14),FRAME_SHIFT(HIGH||||FGFR1|mRNA|CODING|NM_023110|NM_023110.ex.15)</td><td></td></tr>
<tr><td>12</td><td>tissue-12 Somatic</td><td>Category III-Default Categorization</td><td>RAD21</td><td>Deletion</td><td>8</td><td>117868529</td><td>TG</td><td>T</td><td>0.0562</td><td>15</td><td>267</td><td>INTRON(MODIFIER||||RAD21|mRNA|CODING|NM_006265|)</td><td></td></tr>
<tr><td>12</td><td>tissue-12 Somatic</td><td>Category III-Default Categorization</td><td>RAD21</td><td>Insertion</td><td>8</td><td>117868531</td><td>T</td><td>TAA</td><td>0.0758</td><td>15</td><td>198</td><td>INTRON(MODIFIER||||RAD21|mRNA|CODING|NM_006265|)</td><td></td></tr>
<tr><td>12</td><td>tissue-12 Somatic</td><td>Category III-Default Categorization</td><td>RAD21</td><td>Deletion</td><td>8</td><td>117868531</td><td>TA</td><td>T</td><td>0.354</td><td>70</td><td>198</td><td>INTRON(MODIFIER||||RAD21|mRNA|CODING|NM_006265|)</td><td></td></tr>
</table>

<table>
<tr><td>12</td><td>tissue-12 Somatic</td><td>Category III-Default Categorization</td><td>NDRG1</td><td>SNP</td><td>8</td><td>134251244</td><td>G</td><td>C</td><td>0.00717</td><td>13</td><td>1812</td><td>SYNONYMOUS_CODING(LOW|SILENT|tcC/tcG|S273|NDRG1|mRNA|CODING|NM_001258433|NM_001258433.ex.15),SYNONYMOUS_CODING(LOW|SILENT|tcC/tcG|S288|NDRG1|mRNA|CODING|NM_001258432|NM_001258432.ex.14),SYNONYMOUS_CODING(LOW|SILENT|tcC/tcG|S354|NDRG1|mRNA|CODING|NM_001135242|NM_001135242.ex.16),SYNONYMOUS_CODING(LOW|SILENT|tcC/tcG|S354|NDRG1|mRNA|CODING|NM_006096|NM_006096.ex.16)</td><td>S273</td></tr>
<tr><td>12</td><td>tissue-12 Somatic</td><td>Category II-Default Categorization</td><td>CDKN2A</td><td>SNP</td><td>9</td><td>21974759</td><td>C</td><td>A</td><td>0.0495</td><td>44</td><td>889</td><td>INTRON(MODIFIER||||CDKN2A|mRNA|CODING|NM_001363763|),INTRON(MODIFIER||||CDKN2A|mRNA|CODING|NM_058195|),NON_SYNONYMOUS_CODING(MODERATE|MISSENSE|gGt/gTt|G23V|CDKN2A|mRNA|CODING|NM_000077|NM_000077.ex.1),NON_SYNONYMOUS_CODING(MODERATE|MISSENSE|gGt/gTt|G23V|CDKN2A|mRNA|CODING|NM_001195132|NM_001195132.ex.1),NON_SYNONYMOUS_CODING(MODERATE|MISSENSE|gGt/gTt|G23V|CDKN2A|mRNA|CODING|NM_058197|NM_058197.ex.1)</td><td>G23V</td></tr>
<tr><td>12</td><td>tissue-12 Somatic</td><td>Category III-Default Categorization</td><td>KMT2D</td><td>SNP</td><td>12</td><td>49421001</td><td>C</td><td>G</td><td>0.0251</td><td>15</td><td>598</td><td>SYNONYMOUS_CODING(LOW|SILENT|ccG/ccC|P4916|KMT2D|mRNA|CODING|NM_003482|NM_003482.ex.48)</td><td>P4916</td></tr>
<tr><td>12</td><td>tissue-12 Somatic</td><td>Category III-Default Categorization</td><td>KMT2D</td><td>SNP</td><td>12</td><td>49445447</td><td>T</td><td>A</td><td>0.00731</td><td>11</td><td>1504</td><td>SYNONYMOUS_CODING(LOW|SILENT|ccA/ccT|P673|KMT2D|mRNA|CODING|NM_003482|NM_003482.ex.10)</td><td>P673</td></tr>
<tr><td>12</td><td>tissue-12 Somatic</td><td>Category III-Default Categorization</td><td>CREBBP</td><td>SNP</td><td>16</td><td>3779210</td><td>T</td><td>G</td><td>0.023</td><td>10</td><td>435</td><td>SYNONYMOUS_CODING(LOW|SILENT|ccA/ccC|P1908|CREBBP|mRNA|CODING|NM_001079846|NM_001079846.ex.30),SYNONYMOUS_CODING(LOW|SILENT|ccA/ccC|P1946|CREBBP|mRNA|CODING|NM_004380|NM_004380.ex.31)</td><td>P1908</td></tr>
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12	tissue-12 Somatic	Category I-Default Categorization	TP53	Insertion	17	7579392	A	AAGGGACAG	0.0364	33	907	FRAME_SHIFT(HIGH||||TP53|mRNA|CODING|NM_000546|NM_000546.ex.4),FRAME_SHIFT(HIGH||||TP53|mRNA|CODING|NM_001126112|NM_001126112.ex.4),FRAME_SHIFT(HIGH||||TP53|mRNA|CODING|NM_001126113|NM_001126113.ex.4),FRAME_SHIFT(HIGH||||TP53|mRNA|CODING|NM_001126114|NM_001126114.ex.4),FRAME_SHIFT(HIGH||||TP53|mRNA|CODING|NM_001126118|NM_001126118.ex.3),FRAME_SHIFT(HIGH||||TP53|mRNA|CODING|NM_001276695|NM_001276695.ex.4),FRAME_SHIFT(HIGH||||TP53|mRNA|CODING|NM_001276696|NM_001276696.ex.4),FRAME_SHIFT(HIGH||||TP53|mRNA|CODING|NM_001276760|NM_001276760.ex.4),FRAME_SHIFT(HIGH||||TP53|mRNA|CODING|NM_001276761|NM_001276761.ex.4),UPSTREAM(MODIFIER||||TP53|mRNA|CODING|NM_001126115|),UPSTREAM(MODIFIER||||TP53|mRNA|CODING|NM_001126116|),UPSTREAM(MODIFIER||||TP53|mRNA|CODING|NM_001126117|),UPSTREAM(MODIFIER||||TP53|mRNA|CODING|NM_001276697|),UPSTREAM(MODIFIER||||TP53|mRNA|CODING|NM_001276698|),UPSTREAM(MODIFIER||||TP53|mRNA|CODING|NM_001276699|)	
12	Plasma12-1	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A
12	Plasma12-2	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A
12	Plasma12-3	Category II-Default Categorization	PCLO	SNP	7	82784366	A	G	0.0294	11	374	NON_SYNONYMOUS_CODING(MODERATE|MISSENSE|Tct/Cct|S531P|PCLO|mRNA|CODING|NM_014510|NM_014510.ex.2),NON_SYNONYMOUS_CODING(MODERATE|MISSENSE|Tct/Cct|S531P|PCLO|mRNA|CODING|NM_033026|NM_033026.ex.2)	S531P
13	tissue-13 somatic	Category III-Default Categorization	SPEN	SNP	1	16262291	C	T	0.115	222	1938	SYNONYMOUS_CODING(LOW|SILENT|Ctg/Ttg|L3186|SPEN|mRNA|CODING|NM_015001|NM_015001.ex.11)	L3186

13	tissue-13 somatic	Category I-Default Categorization	ATR	Insertion	3	142274739	A	AT	0.018	17	944	FRAME_SHIFT(HIGH||||ATR|mRNA|CODING|NM_001184|NM_001184.ex.10),FRAME_SHIFT(HIGH||||ATR|mRNA|CODING|NM_001354579|NM_001354579.ex.9)	
13	tissue-13 somatic	Category I-Default Categorization	ATR	Deletion	3	142274739	AT	A	0.0117	11	944	FRAME_SHIFT(HIGH||||ATR|mRNA|CODING|NM_001184|NM_001184.ex.10),FRAME_SHIFT(HIGH||||ATR|mRNA|CODING|NM_001354579|NM_001354579.ex.9)	
13	tissue-13 somatic	Category III-Default Categorization	ETV5	SNP	3	185802064	G	A	0.0395	10	253	INTRON(MODIFIER||||ETV5|mRNA|CODING|NM_004454|)	
13	tissue-13 somatic	Category II-Default Categorization	FAT4	SNP	4	126336567	A	C	0.097	254	2619	NON_SYNONYMOUS_CODING(MODERATE|MISSENSE|aAc/aCc|N2150T|FAT4|mRNA|CODING|NM_001291285|NM_001291285.ex.5),NON_SYNONYMOUS_CODING(MODERATE|MISSENSE|aAc/aCc|N2150T|FAT4|mRNA|CODING|NM_001291303|NM_001291303.ex.5),NON_SYNONYMOUS_CODING(MODERATE|MISSENSE|aAc/aCc|N2150T|FAT4|mRNA|CODING|NM_024582|NM_024582.ex.5)	N2150T
13	tissue-13 somatic	Category III-Default Categorization	MGAM	SNP	7	141759688	T	C	0.00794	12	1512	SYNONYMOUS_CODING(LOW|SILENT|ccT/ccC|P1327|MGAM|mRNA|CODING|NM_004668|NM_004668.ex.33)	P1327
13	tissue-13 somatic	Category III-Default Categorization	MGAM	SNP	7	141759733	A	G	0.00761	12	1577	SYNONYMOUS_CODING(LOW|SILENT|aaA/aaG|K1342|MGAM|mRNA|CODING|NM_004668|NM_004668.ex.33)	K1342
13	tissue-13 somatic	Category II-Default Categorization	KMT2C	SNP	7	151919690	C	T	0.0108	10	930	NON_SYNONYMOUS_CODING(MODERATE|MISSENSE|aGc/aAc|S1134N|KMT2C|mRNA|CODING|NM_170606|NM_170606.ex.21)	S1134N
13	tissue-13 somatic	Category III-Default Categorization	KMT2C	SNP	7	151933058	A	C	0.0272	12	441	INTRON(MODIFIER||||KMT2C|mRNA|CODING|NM_170606|)	
13	tissue-13 somatic	Category III-Default Categorization	KMT2C	Deletion	7	152055765	AG	A	0.032	11	344	INTRON(MODIFIER||||KMT2C|mRNA|CODING|NM_170606|)	
13	tissue-13 somatic	Category I-Default Categorization	PRKDC	Insertion	8	48805817	G	GT	0.00923	11	1192	FRAME_SHIFT(HIGH||||PRKDC|mRNA|CODING|NM_001081640|NM_001081640.ex.31),FRAME_SHIFT(HIGH||||PRKDC|mRNA|CODING|NM_006904|NM_006904.ex.31)	

13	tissue-13 somatic	Category III-Default Categorization	RECQL4	SNP	8	145738541	A	G	0.00855	20	2339	DOWNSTREAM(MODIFIER||||MFSD3|Non-coding_transcript|CODING|NM_138431|),DOWNSTREAM(MODIFIER||||MFSD3|Non-coding_transcript|CODING|NR_130120|),INTRON(MODIFIER||||RECQL4|mRNA|CODING|NM_004260|),UPSTREAM(MODIFIER||||LRRC14|mRNA|CODING|NM_001272036|),UPSTREAM(MODIFIER||||LRRC14|mRNA|CODING|NM_014665|)	
13	tissue-13 somatic	Category III-Default Categorization	RECQL4	SNP	8	145738545	T	G	0.00728	16	2197	DOWNSTREAM(MODIFIER||||MFSD3|Non-coding_transcript|CODING|NM_138431|),DOWNSTREAM(MODIFIER||||MFSD3|Non-coding_transcript|CODING|NR_130120|),INTRON(MODIFIER||||RECQL4|mRNA|CODING|NM_004260|),UPSTREAM(MODIFIER||||LRRC14|mRNA|CODING|NM_001272036|),UPSTREAM(MODIFIER||||LRRC14|mRNA|CODING|NM_014665|)	
13	tissue-13 somatic	Category III-Default Categorization	RECQL4	Deletion	8	145738575	GCAGTGTGGG	G	0.649	1668	2572	DOWNSTREAM(MODIFIER||||MFSD3|Non-coding_transcript|CODING|NM_138431|),DOWNSTREAM(MODIFIER||||MFSD3|Non-coding_transcript|CODING|NR_130120|),INTRON(MODIFIER||||RECQL4|mRNA|CODING|NM_004260|),UPSTREAM(MODIFIER||||LRRC14|mRNA|CODING|NM_001272036|),UPSTREAM(MODIFIER||||LRRC14|mRNA|CODING|NM_014665|)	
13	tissue-13 somatic	Category II-Default Categorization	NOTCH1	Deletion	9	139390944	TGTG	T	0.00743	18	2423	CODON_CHANGE_PLUS_CODON_DELETION(MODERATE||ccacag/cag|PQ2415Q|NOTCH1|mRNA|CODING|NM_017617|NM_017617.ex.34)	PQ2415Q
13	tissue-13 somatic	Category I-Default Categorization	KMT2D	SNP	12	49423020	C	T	0.0895	106	1184	INTRON(MODIFIER||||KMT2D|mRNA|CODING|NM_003482|),SPLICE_SITE_ACCEPTOR(HIGH||||KMT2D|mRNA|CODING|NM_003482|)	
13	tissue-13 somatic	Category II-Default Categorization	KMT2D	Deletion	12	49426905	TTGC	T	0.00631	17	2695	CODON_CHANGE_PLUS_CODON_DELETION(MODERATE||cagcaa/caa|QQ3860Q|KMT2D|mRNA|CODING|NM_003482|NM_003482.ex.39)	QQ3860Q
13	tissue-13 somatic	Category III-Default Categorization	KMT2D	SNP	12	49445408	A	T	0.00952	35	3676	SYNONYMOUS_CODING(LOW|SILENT|gcT/gcA|A686|KMT2D|mRNA|CODING|NM_003482|NM_003482.ex.10)	A686

13	tissue-13 somatic	Category III-Default Categorization	KMT2D	SNP	12	49445420	A	T	0.00914	32	3503	SYNONYMOUS_CODING(LOW|SILENT|ccT/ccA|P682|KMT2D|mRNA|CODING|NM_003482|NM_003482.ex.10)	P682
13	tissue-13 somatic	Category II-Default Categorization	KMT2D	SNP	12	49445428	T	G	0.00692	23	3322	NON_SYNONYMOUS_CODING(MODERATE|MISSENSE|Acg/Ccg|T680P|KMT2D|mRNA|CODING|NM_003482|NM_003482.ex.10)	T680P

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<tr><td>13</td><td>Plasma13-1</td><td>Category II-Default Categorization</td><td>KMT2D</td><td>SNP</td><td>12</td><td>49445428</td><td>T</td><td>G</td><td>0.00879</td><td>10</td><td>1138</td><td>NON_SYNONYMOUS_CODING(MODERATE|MISSENSE|Acg/Ccg|T680P|KMT2D|mRNA|CODING|NM_003482|NM_003482.ex.10)</td><td>T680P</td></tr>
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<tr><td>14</td><td>tissue-14 Somatic</td><td>Category II-Default Categorization</td><td>KMT2C</td><td>SNP</td><td>7</td><td>151945060</td><td>G</td><td>A</td><td>0.00867</td><td>10</td><td>1154</td><td>NON_SYNONYMOUS_CODING(MODERATE|MISSENSE|aCt/aTt|T820I|KMT2C|mRNA|CODING|NM_170606|NM_170606.ex.14)</td><td>T820I</td></tr>
<tr><td>14</td><td>tissue-14 Somatic</td><td>Category III-Default Categorization</td><td>RAD21</td><td>Deletion</td><td>8</td><td>117868531</td><td>TA</td><td>T</td><td>0.354</td><td>17</td><td>48</td><td>INTRON(MODIFIER||||RAD21|mRNA|CODING|NM_006265|)</td><td></td></tr>
<tr><td>14</td><td>tissue-14 Somatic</td><td>Category III-Default Categorization</td><td>RECQL4</td><td>Deletion</td><td>8</td><td>145738576</td><td>CAGT</td><td>C</td><td>0.0203</td><td>17</td><td>839</td><td>DOWNSTREAM(MODIFIER||||MFSD3|Non-coding_transcript|CODING|NM_138431|),DOWNSTREAM(MODIFIER||||MFSD3|Non-coding_transcript|CODING|NR_130120|),INTRON(MODIFIER||||RECQL4|mRNA|CODING|NM_004260|),UPSTREAM(MODIFIER||||LRRC14|mRNA|CODING|NM_001272036|),UPSTREAM(MODIFIER||||LRRC14|mRNA|CODING|NM_014665|)</td><td></td></tr>
<tr><td>14</td><td>tissue-14 Somatic</td><td>Category II-Default Categorization</td><td>KMT2D</td><td>SNP</td><td>12</td><td>49445038</td><td>T</td><td>G</td><td>0.01</td><td>11</td><td>1096</td><td>NON_SYNONYMOUS_CODING(MODERATE|MISSENSE|Act/Cct|T810P|KMT2D|mRNA|CODING|NM_003482|NM_003482.ex.10)</td><td>T810P</td></tr>
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<tr><td>15</td><td>tissue-15 somatic</td><td>Category I-Default Categorization</td><td>ATR</td><td>LowAF</td><td>3</td><td>142274739</td><td>AT</td><td>A</td><td>0.0126</td><td>12</td><td>950</td><td>FRAME_SHIFT(HIGH||||ATR|mRNA|CODING|NM_001184|NM_001184.ex.10),FRAME_SHIFT(HIGH||||ATR|mRNA|CODING|NM_001354579|NM_001354579.ex.9)</td><td></td></tr>
<tr><td>15</td><td>tissue-15 somatic</td><td>Category III-Default Categorization</td><td>TP63</td><td>LowAF</td><td>3</td><td>189561962</td><td>C</td><td>CT</td><td>0.0404</td><td>12</td><td>297</td><td>INTRON(MODIFIER||||TP63|mRNA|CODING|NM_001114978|),INTRON(MODIFIER||||TP63|mRNA|CODING|NM_001114979|),INTRON(MODIFIER||||TP63|mRNA|CODING|NM_001114980|),INTRON(MODIFIER||||TP63|mRNA|CODING|NM_001114981|),INTRON(MODIFIER||||TP63|mRNA|CODING|NM_001114982|),INTRON(MODIFIER||||TP63|mRNA|CODING|NM_001329144|),INTRON(MODIFIER||||TP63|mRNA|CODING|NM_001329145|),INTRON(MODIFIER||||TP63|mRNA|CODING|NM_001329146|),INTRON(MODIFIER||||TP63|mRNA|CODING|NM_001329</td><td></td></tr>
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15	tissue-15 somatic	Category III-Default Categorization	TP63	LowAF	3	189561962	CT	C	0.0505	15	297	INTRON(MODIFIER||||TP63|mRNA|CODING|NM_001114978|),INTRON(MODIFIER||||TP63|mRNA|CODING|NM_001114979|),INTRON(MODIFIER||||TP63|mRNA|CODING|NM_001114980|),INTRON(MODIFIER||||TP63|mRNA|CODING|NM_001114981|),INTRON(MODIFIER||||TP63|mRNA|CODING|NM_001114982|),INTRON(MODIFIER||||TP63|mRNA|CODING|NM_001329144|),INTRON(MODIFIER||||TP63|mRNA|CODING|NM_001329145|),INTRON(MODIFIER||||TP63|mRNA|CODING|NM_001329146|),INTRON(MODIFIER||||TP63|mRNA|CODING|NM_001329148|),INTRON(MODIFIER||||TP63|mRNA|CODING|NM_001329149|),INTRON(MODIFIER||||TP63|mRNA|CODING|NM_001329150|),INTRON(MODIFIER||||TP63|mRNA|CODING|NM_001329964|),INTRON(MODIFIER||||TP63|mRNA|CODING|NM_003722|)	
15	tissue-15 somatic	Category I-Default Categorization	FAT1	HET	4	187549899	CTA	C	0.302	115	381	FRAME_SHIFT(HIGH||||FAT1|mRNA|CODING|NM_005245|NM_005245.ex.8)	
15	tissue-15 somatic	Category III-Default Categorization	SDHA	HET	5	225493	G	A	0.165	176	1064	INTRON(MODIFIER||||SDHA|mRNA|CODING|NM_001294332|),INTRON(MODIFIER||||SDHA|mRNA|CODING|NM_001330758|),INTRON(MODIFIER||||SDHA|mRNA|CODING|NM_004168|)	
15	tissue-15 somatic	Category II-Default Categorization	SDHA	LowAF	5	254529	T	C	0.0139	11	793	NON_SYNONYMOUS_CODING(MODERATE|MISSENSE|Tac/Cac|Y525H|SDHA|mRNA|CODING|NM_001330758|NM_001330758.ex.12),NON_SYNONYMOUS_CODING(MODERATE|MISSENSE|Tac/Cac|Y558H|SDHA|mRNA|CODING|NM_001294332|NM_001294332.ex.13),NON_SYNONYMOUS_CODING(MODERATE|MISSENSE|Tac/Cac|Y606H|SDHA|mRNA|CODING|NM_004168|NM_004168.ex.14)	Y525H
15	tissue-15 somatic	Category II-Default Categorization	KMT2C	HET	7	151878079	C	A	0.256	299	1167	NON_SYNONYMOUS_CODING(MODERATE|MISSENSE|cGt/cTt|R2289L|KMT2C|mRNA|CODING|NM_170606|NM_170606.ex.36)	R2289L
15	tissue-15 somatic	Category III-Default Categorization	KMT2C	LowAF	7	151882657	T	G	0.033	10	303	SYNONYMOUS_CODING(LOW|SILENT|Aga/Cga|R1690|KMT2C|mRNA|CODING|NM_170606|NM_170606.ex.34)	R1690

15	tissue-15 somatic	Category II-Default Categorization	KMT2C	LowAF	7	151917706	T	C	0.0179	10	560	NON_SYNONYMOUS_CODING(MODERATE|MISSENSE|aAa/aGa|K1205R|KMT2C|mRNA|CODING|NM_170606|NM_170606.ex.23)	K1205R
15	tissue-15 somatic	Category III-Default Categorization	KMT2C	LowAF	7	151917710	A	G	0.0177	10	564	SYNONYMOUS_CODING(LOW|SILENT|Ttg/Ctg|L1204|KMT2C|mRNA|CODING|NM_170606|NM_170606.ex.23)	L1204
15	tissue-15 somatic	Category II-Default Categorization	KMT2C	LowAF	7	151945399	A	G	0.0198	21	1058	NON_SYNONYMOUS_CODING(MODERATE|MISSENSE|aTt/aCt|I707T|KMT2C|mRNA|CODING|NM_170606|NM_170606.ex.14)	I707T
15	tissue-15 somatic	Category III-Default Categorization	KMT2C	LowAF	7	151945401	A	G	0.0171	18	1050	SYNONYMOUS_CODING(LOW|SILENT|agT/agC|S706|KMT2C|mRNA|CODING|NM_170606|NM_170606.ex.14)	S706
15	tissue-15 somatic	Category III-Default Categorization	RAD21	HET	8	117868530	GTA	G	0.293	121	413	INTRON(MODIFIER||||RAD21|mRNA|CODING|NM_006265|)	
15	tissue-15 somatic	Category III-Default Categorization	RECQL4	HET	8	145738575	GCAGTGTGGG	G	0.645	2318	3596	DOWNSTREAM(MODIFIER||||MFSD3|Non-coding_transcript|CODING|NM_138431|),DOWNSTREAM(MODIFIER||||MFSD3|Non-coding_transcript|CODING|NR_130120|),INTRON(MODIFIER||||RECQL4|mRNA|CODING|NM_004260|),UPSTREAM(MODIFIER||||LRRC14|mRNA|CODING|NM_001272036|),UPSTREAM(MODIFIER||||LRRC14|mRNA|CODING|NM_014665|)	
15	tissue-15 somatic	Category III-Default Categorization	KMT2D	LowAF	12	49420995	A	G	0.0302	21	696	SYNONYMOUS_CODING(LOW|SILENT|ccT/ccC|P4918|KMT2D|mRNA|CODING|NM_003482|NM_003482.ex.48)	P4918
15	tissue-15 somatic	Category I-Default Categorization	KMT2D	LowAF	12	49420995	A	AG	0.0158	16	1010	FRAME_SHIFT(HIGH||||KMT2D|mRNA|CODING|NM_003482|NM_003482.ex.48)	
15	tissue-15 somatic	Category II-Default Categorization	KMT2D	LowAF	12	49445428	T	G	0.00693	15	2163	NON_SYNONYMOUS_CODING(MODERATE|MISSENSE|Acg/Ccg|T680P|KMT2D|mRNA|CODING|NM_003482|NM_003482.ex.10)	T680P
15	tissue-15 somatic	Category III-Default Categorization	KMT2D	LowAF	12	49445444	C	T	0.0074	16	2162	SYNONYMOUS_CODING(LOW|SILENT|ccG/ccA|P674|KMT2D|mRNA|CODING|NM_003482|NM_003482.ex.10)	P674

<table>
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<tr><td>15</td><td>tissue-15 somatic</td><td>Category I-Default Categorization</td><td>TP53</td><td>HET</td><td>17</td><td>7576852</td><td>C</td><td>A</td><td>0.705</td><td>486</td><td>689</td><td>INTRON(MODIFIER||||TP53|mRNA|CODING|NM_000546|),INTRON(MODIFIER||||TP53|mRNA|CODING|NM_001126112|),INTRON(MODIFIER||||TP53|mRNA|CODING|NM_001126113|),INTRON(MODIFIER||||TP53|mRNA|CODING|NM_001126114|),INTRON(MODIFIER||||TP53|mRNA|CODING|NM_001126115|),INTRON(MODIFIER||||TP53|mRNA|CODING|NM_001126116|),INTRON(MODIFIER||||TP53|mRNA|CODING|NM_001126117|),INTRON(MODIFIER||||TP53|mRNA|CODING|NM_001126118|),INTRON(MODIFIER||||TP53|mRNA|CODING|NM_001276695|),INTRON(MODIFIER||||TP53|mRNA|CODING|NM_001276696|),INTRON(MODIFIER||||TP53|mRNA|CODING|NM_001276697|),INTRON(MODIFIER||||TP53|mRNA|CODING|NM_001276698|),INTRON(MODIFIER||||TP53|mRNA|CODING|NM_001276699|),INTRON(MODIFIER||||TP53|mRNA|CODING|NM_001276760|),INTRON(MODIFIER||||TP53|mRNA|CODING|NM_001276761|),SPLICE_SITE_DONOR(HIGH||||TP53|mRNA|CODING|NM_000546|),SPLICE_SITE_DONOR(HIGH||||TP53|mRNA|CODING|NM_001126112|),SPLICE_SITE_DONOR(HIGH||||TP53|mRNA|CODING|NM_001126113|),SPLICE_SITE_DONOR(HIGH||||TP53|mRNA|CODING|NM_001126114|),SPLICE_SITE_DONOR(HIGH||||TP53|mRNA|CODING|NM_001126115|),SPLICE_SITE_DONOR(HIGH||||TP53|mRNA|CODING|NM_001126116|),SPLICE_SITE_DONOR(HIGH||||TP53|mRNA|CODING|NM_001126117|),SPLICE_SITE_DONOR(HIGH||||TP53|mRNA|CODING|NM_001126118|),SPLICE_SITE_DONOR(HIGH||||TP53|mRNA|CODING|NM_001276695|),SPLICE_SITE_DONOR(HIGH||||TP53|mRNA|CODING|NM_001276696|),SPLICE_SITE_DONOR(HIGH||||TP53|mRNA|CODING|NM_001276697|),SPLICE_SITE_D</td><td></td></tr>
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<table>
<tr><td>15</td><td>tissue-15 somatic</td><td>Category III-Default Categorization</td><td>TP53</td><td>LowAF</td><td>17</td><td>7579658</td><td>G</td><td>C</td><td>0.0137</td><td>10</td><td>731</td><td>INTRON(MODIFIER||||TP53|mRNA|CODING|NM_000546|),INTRON(MODIFIER||||TP53|mRNA|CODING|NM_001126112|),INTRON(MODIFIER||||TP53|mRNA|CODING|NM_001126113|),INTRON(MODIFIER||||TP53|mRNA|CODING|NM_001126114|),INTRON(MODIFIER||||TP53|mRNA|CODING|NM_001126118|),INTRON(MODIFIER||||TP53|mRNA|CODING|NM_001276695|),INTRON(MODIFIER||||TP53|mRNA|CODING|NM_001276696|),INTRON(MODIFIER||||TP53|mRNA|CODING|NM_001276760|),INTRON(MODIFIER||||TP53|mRNA|CODING|NM_001276761|),UPSTREAM(MODIFIER||||TP53|mRNA|CODING|NM_001126115|),UPSTREAM(MODIFIER||||TP53|mRNA|CODING|NM_001126116|),UPSTREAM(MODIFIER||||TP53|mRNA|CODING|NM_001126117|),UPSTREAM(MODIFIER||||TP53|mRNA|CODING|NM_001276697|),UPSTREAM(MODIFIER||||TP53|mRNA|CODING|NM_001276698|),UPSTREAM(MODIFIER||||TP53|mRNA|CODING|NM_001276699|)</td><td></td></tr>
<tr><td>15</td><td>Plasma15-1</td><td>Category II-Default Categorization</td><td>KMT2D</td><td>SNP</td><td>12</td><td>49445428</td><td>T</td><td>G</td><td>0.0272</td><td>10</td><td>368</td><td>NON_SYNONYMOUS_CODING(MODERATE|MISSENSE|Acg/Ccg|T680P|KMT2D|mRNA|CODING|NM_003482|NM_003482.ex.10)</td><td>T680P</td></tr>
<tr><td>15</td><td>Plasma15-2</td><td>Category III-Default Categorization</td><td>CREBBP</td><td>SNP</td><td>16</td><td>3779204</td><td>C</td><td>G</td><td>0.0118</td><td>12</td><td>1014</td><td>SYNONYMOUS_CODING(LOW|SILENT|ccG/ccC|P1910|CREBBP|mRNA|CODING|NM_001079846|NM_001079846.ex.30),SYNONYMOUS_CODING(LOW|SILENT|ccG/ccC|P1948|CREBBP|mRNA|CODING|NM_004380|NM_004380.ex.31)</td><td>P1910</td></tr>
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<table>
<tr><td>15</td><td>Plasma15-2</td><td>Category I-Default Categorization</td><td>TP53</td><td>SNP</td><td>17</td><td>7576852</td><td>C</td><td>A</td><td>0.126</td><td>11</td><td>87</td><td>INTRON(MODIFIER||||TP53|mRNA|CODING|NM_000546|),INTRON(MODIFIER||||TP53|mRNA|CODING|NM_001126112|),INTRON(MODIFIER||||TP53|mRNA|CODING|NM_001126113|),INTRON(MODIFIER||||TP53|mRNA|CODING|NM_001126114|),INTRON(MODIFIER||||TP53|mRNA|CODING|NM_001126115|),INTRON(MODIFIER||||TP53|mRNA|CODING|NM_001126116|),INTRON(MODIFIER||||TP53|mRNA|CODING|NM_001126117|),INTRON(MODIFIER||||TP53|mRNA|CODING|NM_001126118|),INTRON(MODIFIER||||TP53|mRNA|CODING|NM_001276695|),INTRON(MODIFIER||||TP53|mRNA|CODING|NM_001276696|),INTRON(MODIFIER||||TP53|mRNA|CODING|NM_001276697|),INTRON(MODIFIER||||TP53|mRNA|CODING|NM_001276698|),INTRON(MODIFIER||||TP53|mRNA|CODING|NM_001276699|),INTRON(MODIFIER||||TP53|mRNA|CODING|NM_001276760|),INTRON(MODIFIER||||TP53|mRNA|CODING|NM_001276761|),SPLICE_SITE_DONOR(HIGH||||TP53|mRNA|CODING|NM_000546|),SPLICE_SITE_DONOR(HIGH||||TP53|mRNA|CODING|NM_001126112|),SPLICE_SITE_DONOR(HIGH||||TP53|mRNA|CODING|NM_001126113|),SPLICE_SITE_DONOR(HIGH||||TP53|mRNA|CODING|NM_001126114|),SPLICE_SITE_DONOR(HIGH||||TP53|mRNA|CODING|NM_001126115|),SPLICE_SITE_DONOR(HIGH||||TP53|mRNA|CODING|NM_001126116|),SPLICE_SITE_DONOR(HIGH||||TP53|mRNA|CODING|NM_001126117|),SPLICE_SITE_DONOR(HIGH||||TP53|mRNA|CODING|NM_001126118|),SPLICE_SITE_DONOR(HIGH||||TP53|mRNA|CODING|NM_001276695|),SPLICE_SITE_DONOR(HIGH||||TP53|mRNA|CODING|NM_001276696|),SPLICE_SITE_DONOR(HIGH||||TP53|mRNA|CODING|NM_001276697|),SPLICE_SITE_D</td><td></td></tr>
<tr><td>15</td><td>Plasma15-3</td><td>Category III-Default Categorization</td><td>SDHA</td><td>SNP</td><td>5</td><td>225493</td><td>G</td><td>A</td><td>0.0368</td><td>21</td><td>570</td><td>INTRON(MODIFIER||||SDHA|mRNA|CODING|NM_001294332|),INTRON(MODIFIER||||SDHA|mRNA|CODING|NM_001330758|),INTRON(MODIFIER||||SDHA|mRNA|CODING|NM_004168|)</td><td></td></tr>
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15	Plasma15-3	Category III-Default Categorization	CREBBP	SNP	16	3779204	C	G	0.0144	17	1177	SYNONYMOUS_CODING(LOW|SILENT|ccG/ccC|P1910|CREBBP|mRNA|CODING|NM_001079846|NM_001079846.ex.30),SYNONYMOUS_CODING(LOW|SILENT|ccG/ccC|P1948|CREBBP|mRNA|CODING|NM_004380|NM_004380.ex.31)	P1910

<table>
<tr><td>15</td><td>Plasma15-3</td><td>Category I-Default Categorization</td><td>TP53</td><td>SNP</td><td>17</td><td>7576852</td><td>C</td><td>A</td><td>0.158</td><td>27</td><td>171</td><td>INTRON(MODIFIER||||TP53|mRNA|CODING|NM_000546|),INTRON(MODIFIER||||TP53|mRNA|CODING|NM_001126112|),INTRON(MODIFIER||||TP53|mRNA|CODING|NM_001126113|),INTRON(MODIFIER||||TP53|mRNA|CODING|NM_001126114|),INTRON(MODIFIER||||TP53|mRNA|CODING|NM_001126115|),INTRON(MODIFIER||||TP53|mRNA|CODING|NM_001126116|),INTRON(MODIFIER||||TP53|mRNA|CODING|NM_001126117|),INTRON(MODIFIER||||TP53|mRNA|CODING|NM_001126118|),INTRON(MODIFIER||||TP53|mRNA|CODING|NM_001276695|),INTRON(MODIFIER||||TP53|mRNA|CODING|NM_001276696|),INTRON(MODIFIER||||TP53|mRNA|CODING|NM_001276697|),INTRON(MODIFIER||||TP53|mRNA|CODING|NM_001276698|),INTRON(MODIFIER||||TP53|mRNA|CODING|NM_001276699|),INTRON(MODIFIER||||TP53|mRNA|CODING|NM_001276760|),INTRON(MODIFIER||||TP53|mRNA|CODING|NM_001276761|),SPLICE_SITE_DONOR(HIGH||||TP53|mRNA|CODING|NM_000546|),SPLICE_SITE_DONOR(HIGH||||TP53|mRNA|CODING|NM_001126112|),SPLICE_SITE_DONOR(HIGH||||TP53|mRNA|CODING|NM_001126113|),SPLICE_SITE_DONOR(HIGH||||TP53|mRNA|CODING|NM_001126114|),SPLICE_SITE_DONOR(HIGH||||TP53|mRNA|CODING|NM_001126115|),SPLICE_SITE_DONOR(HIGH||||TP53|mRNA|CODING|NM_001126116|),SPLICE_SITE_DONOR(HIGH||||TP53|mRNA|CODING|NM_001126117|),SPLICE_SITE_DONOR(HIGH||||TP53|mRNA|CODING|NM_001126118|),SPLICE_SITE_DONOR(HIGH||||TP53|mRNA|CODING|NM_001276695|),SPLICE_SITE_DONOR(HIGH||||TP53|mRNA|CODING|NM_001276696|),SPLICE_SITE_DONOR(HIGH||||TP53|mRNA|CODING|NM_001276697|),SPLICE_SITE_D</td><td></td></tr>
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<tbody>
<tr><td>16</td><td>tissue-16 somatic</td><td>Category II-Default Categorization</td><td>NFE2L2</td><td>SNP</td><td>2</td><td>178098960</td><td>C</td><td>G</td><td>0.0198</td><td>19</td><td>962</td><td>NON_SYNONYMOUS_CODING(MODERATE|MISSENSE|Gat/Cat|D13H|NFE2L2|mRNA|CODING|NM_001145412|NM_001145412.ex.2),NON_SYNONYMOUS_CODING(MODERATE|MISSENSE|Gat/Cat|D13H|NFE2L2|mRNA|CODING|NM_001145413|NM_001145413.ex.2),NON_SYNONYMOUS_CODING(MODERATE|MISSENSE|Gat/Cat|D13H|NFE2L2|mRNA|CODING|NM_001313900|NM_001313900.ex.2),NON_SYNONYMOUS_CODING(MODERATE|MISSENSE|Gat/Cat|D13H|NFE2L2|mRNA|CODING|NM_001313901|NM_001313901.ex.2),NON_SYNONYMOUS_CODING(MODERATE|MISSENSE|Gat/Cat|D29H|NFE2L2|mRNA|CODING|NM_001313902|NM_001313902.ex.2),NON_SYNONYMOUS_CODING(MODERATE|MISSENSE|Gat/Cat|D29H|NFE2L2|mRNA|CODING|NM_001313903|NM_001313903.ex.2),NON_SYNONYMOUS_CODING(MODERATE|MISSENSE|Gat/Cat|D29H|NFE2L2|mRNA|CODING|NM_006164|NM_006164.ex.2),START_GAINED(LOW||||NFE2L2|mRNA|CODING|NM_001313904|NM_001313904.ex.2)</td><td>D13H</td></tr>
<tr><td>16</td><td>tissue-16 somatic</td><td>Category I-Default Categorization</td><td>ATR</td><td>Deletion</td><td>3</td><td>142274739</td><td>AT</td><td>A</td><td>0.0143</td><td>15</td><td>1049</td><td>FRAME_SHIFT(HIGH||||ATR|mRNA|CODING|NM_001184|NM_001184.ex.10),FRAME_SHIFT(HIGH||||ATR|mRNA|CODING|NM_001354579|NM_001354579.ex.9)</td><td></td></tr>
<tr><td>16</td><td>tissue-16 somatic</td><td>Category II-Default Categorization</td><td>PIK3CA</td><td>SNP</td><td>3</td><td>178952072</td><td>A</td><td>G</td><td>0.0327</td><td>70</td><td>2139</td><td>NON_SYNONYMOUS_CODING(MODERATE|MISSENSE|Atg/Gtg|M1043V|PIK3CA|mRNA|CODING|NM_006218|NM_006218.ex.21)</td><td>M1043V</td></tr>
<tr><td>16</td><td>tissue-16 somatic</td><td>Category II-Default Categorization</td><td>SDHA</td><td>SNP</td><td>5</td><td>236628</td><td>C</td><td>T</td><td>0.0134</td><td>14</td><td>1042</td><td>NON_SYNONYMOUS_CODING(MODERATE|MISSENSE|gCc/gTc|A401V|SDHA|mRNA|CODING|NM_001294332|NM_001294332.ex.9),NON_SYNONYMOUS_CODING(MODERATE|MISSENSE|gCc/gTc|A449V|SDHA|mRNA|CODING|NM_001330758|NM_001330758.ex.10),NON_SYNONYMOUS_CODING(MODERATE|MISSENSE|gCc/gTc|A449V|SDHA|mRNA|CODING|NM_004168|NM_004168.ex.10)</td><td>A401V</td></tr>
</tbody>
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16	tissue-16 somatic	Category II-Default Categorization	SDHA	SNP	5	236649	C	T	0.0235	25	1064	NON_SYNONYMOUS_CODING(MODERATE|MISSENSE|tCg/tTg|S408L|SDHA|mRNA|CODING|NM_001294332|NM_001294332.ex.9),NON_SYNONYMOUS_CODING(MODERATE|MISSENSE|tCg/tTg|S456L|SDHA|mRNA|CODING|NM_001330758|NM_001330758.ex.10),NON_SYNONYMOUS_CODING(MODERATE|MISSENSE|tCg/tTg|S456L|SDHA|mRNA|CODING|NM_004168|NM_004168.ex.10)	S408L
16	tissue-16 somatic	Category III-Default Categorization	SDHA	SNP	5	236653	C	A	0.0265	28	1055	SYNONYMOUS_CODING(LOW|SILENT|ctC/ctA|L409|SDHA|mRNA|CODING|NM_001294332|NM_001294332.ex.9),SYNONYMOUS_CODING(LOW|SILENT|ctC/ctA|L457|SDHA|mRNA|CODING|NM_001330758|NM_001330758.ex.10),SYNONYMOUS_CODING(LOW|SILENT|ctC/ctA|L457|SDHA|mRNA|CODING|NM_004168|NM_004168.ex.10)	L409
16	tissue-16 somatic	Category II-Default Categorization	SDHA	SNP	5	236676	G	A	0.0289	29	1005	NON_SYNONYMOUS_CODING(MODERATE|MISSENSE|cGg/cAg|R417Q|SDHA|mRNA|CODING|NM_001294332|NM_001294332.ex.9),NON_SYNONYMOUS_CODING(MODERATE|MISSENSE|cGg/cAg|R465Q|SDHA|mRNA|CODING|NM_001330758|NM_001330758.ex.10),NON_SYNONYMOUS_CODING(MODERATE|MISSENSE|cGg/cAg|R465Q|SDHA|mRNA|CODING|NM_004168|NM_004168.ex.10)	R417Q
16	tissue-16 somatic	Category II-Default Categorization	SDHA	SNP	5	236678	G	A	0.0277	28	1010	NON_SYNONYMOUS_CODING(MODERATE|MISSENSE|Gca/Aca|A418T|SDHA|mRNA|CODING|NM_001294332|NM_001294332.ex.9),NON_SYNONYMOUS_CODING(MODERATE|MISSENSE|Gca/Aca|A466T|SDHA|mRNA|CODING|NM_001330758|NM_001330758.ex.10),NON_SYNONYMOUS_CODING(MODERATE|MISSENSE|Gca/Aca|A466T|SDHA|mRNA|CODING|NM_004168|NM_004168.ex.10)	A418T
16	tissue-16 somatic	Category III-Default Categorization	SDHA	SNP	5	236734	G	C	0.0308	19	617	INTRON(MODIFIER||||SDHA|mRNA|CODING|NM_001294332|),INTRON(MODIFIER||||SDHA|mRNA|CODING|NM_001330758|),INTRON(MODIFIER||||SDHA|mRNA|CODING|NM_004168|)	

16	tissue-16 somatic	Category III-Default Categorization	PCLO	SNP	7	82451983	C	T	0.0217	24	1106	SYNONYMOUS_CODING(LOW|SILENT|gaG/gaA|E4873|PCLO|mRNA|CODING|NM_014510|NM_014510.ex.20),SYNONYMOUS_CODING(LOW|SILENT|gaG/gaA|E4873|PCLO|mRNA|CODING|NM_033026|NM_033026.ex.20)	E4873
16	tissue-16 somatic	Category III-Default Categorization	PCLO	SNP	7	82585517	C	T	0.0206	45	2189	SYNONYMOUS_CODING(LOW|SILENT|gaG/gaA|E1584|PCLO|mRNA|CODING|NM_014510|NM_014510.ex.5),SYNONYMOUS_CODING(LOW|SILENT|gaG/gaA|E1584|PCLO|mRNA|CODING|NM_033026|NM_033026.ex.5)	E1584
16	tissue-16 somatic	Category III-Default Categorization	MGAM	SNP	7	141767260	C	T	0.01	13	1300	INTRON(MODIFIER||||MGAM|mRNA|CODING|NM_004668|)	
16	tissue-16 somatic	Category III-Default Categorization	MGAM	SNP	7	141786050	C	T	0.0696	77	1106	INTRON(MODIFIER||||MGAM|mRNA|CODING|NM_004668|)	
16	tissue-16 somatic	Category III-Default Categorization	KMT2C	Deletion	7	151882622	TAG	T	0.0678	27	398	INTRON(MODIFIER||||KMT2C|mRNA|CODING|NM_170606|)	
16	tissue-16 somatic	Category II-Default Categorization	KMT2C	SNP	7	151917706	T	C	0.014	17	1210	NON_SYNONYMOUS_CODING(MODERATE|MISSENSE|aAa/aGa|K1205R|KMT2C|mRNA|CODING|NM_170606|NM_170606.ex.23)	K1205R
16	tissue-16 somatic	Category III-Default Categorization	KMT2C	SNP	7	151917710	A	G	0.014	17	1215	SYNONYMOUS_CODING(LOW|SILENT|Ttg/Ctg|L1204|KMT2C|mRNA|CODING|NM_170606|NM_170606.ex.23)	L1204
16	tissue-16 somatic	Category II-Default Categorization	KMT2C	SNP	7	151917724	C	A	0.0138	16	1161	NON_SYNONYMOUS_CODING(MODERATE|MISSENSE|cGg/cTg|R1199L|KMT2C|mRNA|CODING|NM_170606|NM_170606.ex.23)	R1199L
16	tissue-16 somatic	Category III-Default Categorization	KMT2C	SNP	7	151919649	T	C	0.0333	38	1141	INTRON(MODIFIER||||KMT2C|mRNA|CODING|NM_170606|)	
16	tissue-16 somatic	Category III-Default Categorization	KMT2C	Deletion	7	151919784	TG	T	0.0234	19	811	INTRON(MODIFIER||||KMT2C|mRNA|CODING|NM_170606|)	
16	tissue-16 somatic	Category I-Default Categorization	KMT2C	SNP	7	151921099	C	T	0.0282	22	779	INTRON(MODIFIER||||KMT2C|mRNA|CODING|NM_170606|),SPLICE_SITE_DONOR(HIGH||||KMT2C|mRNA|CODING|NM_170606|)	
16	tissue-16 somatic	Category II-Default Categorization	KMT2C	SNP	7	151921154	C	A	0.0279	33	1183	NON_SYNONYMOUS_CODING(MODERATE|MISSENSE|tGc/tTc|C1090F|KMT2C|mRNA|CODING|NM_170606|NM_170606.ex.20)	C1090F

16	tissue-16 somatic	Category III-Default Categorization	KMT2C	SNP	7	151932822	A	T	0.0309	28	906	INTRON(MODIFIER||||KMT2C|mRNA|CODING|NM_170606|)	
16	tissue-16 somatic	Category II-Default Categorization	KMT2C	SNP	7	151932985	G	A	0.0105	14	1330	NON_SYNONYMOUS_CODING(MODERATE|MISSENSE|Cct/Tct|P896S|KMT2C|mRNA|CODING|NM_170606|NM_170606.ex.16)	P896S
16	tissue-16 somatic	Category II-Default Categorization	KMT2C	SNP	7	151932991	G	A	0.00852	11	1291	NON_SYNONYMOUS_CODING(MODERATE|MISSENSE|Cgg/Tgg|R894W|KMT2C|mRNA|CODING|NM_170606|NM_170606.ex.16)	R894W
16	tissue-16 somatic	Category II-Default Categorization	KMT2C	SNP	7	151933014	C	T	0.0545	55	1010	NON_SYNONYMOUS_CODING(MODERATE|MISSENSE|cGt/cAt|R886H|KMT2C|mRNA|CODING|NM_170606|NM_170606.ex.16)	R886H
16	tissue-16 somatic	Category II-Default Categorization	KMT2C	SNP	7	151945399	A	G	0.0122	27	2210	NON_SYNONYMOUS_CODING(MODERATE|MISSENSE|aTt/aCt|I707T|KMT2C|mRNA|CODING|NM_170606|NM_170606.ex.14)	I707T
16	tissue-16 somatic	Category III-Default Categorization	KMT2C	SNP	7	151945401	A	G	0.0118	26	2209	SYNONYMOUS_CODING(LOW|SILENT|agT/agC|S706|KMT2C|mRNA|CODING|NM_170606|NM_170606.ex.14)	S706
16	tissue-16 somatic	Category III-Default Categorization	ADGRA2	SNP	8	37698379	T	C	0.0116	10	861	DOWNSTREAM(MODIFIER||||BRF2|mRNA|CODING|NM_018310|),INTRON(MODIFIER||||ADGRA2|mRNA|CODING|NM_032777|)	
16	tissue-16 somatic	Category III-Default Categorization	RECQL4	SNP	8	145738583	G	T	0.00776	17	2190	DOWNSTREAM(MODIFIER||||MFSD3|Non-coding_transcript|CODING|NM_138431|),DOWNSTREAM(MODIFIER||||MFSD3|Non-coding_transcript|CODING|NR_130120|),INTRON(MODIFIER||||RECQL4|mRNA|CODING|NM_004260|),UPSTREAM(MODIFIER||||LRRC14|mRNA|CODING|NM_001272036|),UPSTREAM(MODIFIER||||LRRC14|mRNA|CODING|NM_014665|)	
16	tissue-16 somatic	Category II-Default Categorization	NOTCH1	SNP	9	139396851	C	T	0.0181	18	995	NON_SYNONYMOUS_CODING(MODERATE|MISSENSE|Ggg/Agg|G1753R|NOTCH1|mRNA|CODING|NM_017617|NM_017617.ex.28)	G1753R
16	tissue-16 somatic	Category III-Default Categorization	KMT2D	SNP	12	49421001	C	G	0.0241	23	956	SYNONYMOUS_CODING(LOW|SILENT|ccG/ccC|P4916|KMT2D|mRNA|CODING|NM_003482|NM_003482.ex.48)	P4916

16	tissue-16 somatic	Category I-Default Categorization	KMT2D	SNP	12	49424771	G	A	0.0331	35	1057	STOP_GAINED(HIGH|NONSENSE|Cag/Tag|Q4526*|KMT2D|mRNA|CODING|NM_003482|NM_003482.ex.40)	Q4526*
16	tissue-16 somatic	Category I-Default Categorization	KMT2D	SNP	12	49425896	G	A	0.039	88	2259	STOP_GAINED(HIGH|NONSENSE|Cga/Tga|R4198*|KMT2D|mRNA|CODING|NM_003482|NM_003482.ex.39)	R4198*
16	tissue-16 somatic	Category II-Default Categorization	KMT2D	SNP	12	49426759	T	A	0.00712	15	2108	NON_SYNONYMOUS_CODING(MODERATE|MISSENSE|cAg/cTg|Q3910L|KMT2D|mRNA|CODING|NM_003482|NM_003482.ex.39)	Q3910L
16	tissue-16 somatic	Category II-Default Categorization	KMT2D	SNP	12	49434697	C	G	0.0322	39	1212	NON_SYNONYMOUS_CODING(MODERATE|MISSENSE|Gag/Cag|E2286Q|KMT2D|mRNA|CODING|NM_003482|NM_003482.ex.31)	E2286Q
16	Plasma16-1	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A
16	Plasma16-2	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A
17	tissue-17 somatic	Category III-Default Categorization	NFE2L2	SNP	2	178095660	G	C	0.183	117	638	SYNONYMOUS_CODING(LOW|SILENT|ctC/ctG|L457|NFE2L2|mRNA|CODING|NM_001313904|NM_001313904.ex.5),SYNONYMOUS_CODING(LOW|SILENT|ctC/ctG|L484|NFE2L2|mRNA|CODING|NM_001313903|NM_001313903.ex.5),SYNONYMOUS_CODING(LOW|SILENT|ctC/ctG|L527|NFE2L2|mRNA|CODING|NM_001313902|NM_001313902.ex.4),SYNONYMOUS_CODING(LOW|SILENT|ctC/ctG|L534|NFE2L2|mRNA|CODING|NM_001145413|NM_001145413.ex.5),SYNONYMOUS_CODING(LOW|SILENT|ctC/ctG|L541|NFE2L2|mRNA|CODING|NM_001145412|NM_001145412.ex.5),SYNONYMOUS_CODING(LOW|SILENT|ctC/ctG|L541|NFE2L2|mRNA|CODING|NM_001313900|NM_001313900.ex.5),SYNONYMOUS_CODING(LOW|SILENT|ctC/ctG|L541|NFE2L2|mRNA|CODING|NM_001313901|NM_001313901.ex.5),SYNONYMOUS_CODING(LOW|SILENT|ctC/ctG|L557|NFE2L2|mRNA|CODING|NM_006164|NM_006164.ex.5)	L457
17	tissue-17 somatic	Category I-Default Categorization	ATR	Insertion	3	142274739	A	AT	0.0183	14	764	FRAME_SHIFT(HIGH||||ATR|mRNA|CODING|NM_001184|NM_001184.ex.10),FRAME_SHIFT(HIGH||||ATR|mRNA|CODING|NM_001354579|NM_001354579.ex.9)	

17	tissue-17 somatic	Category III-Default Categorization	ETV5	SNP	3	185802016	C	A	0.0274	13	475	INTRON(MODIFIER||||ETV5|mRNA|CODING|NM_004454|)	
17	tissue-17 somatic	Category II-Default Categorization	TERT	SNP	5	1280434	G	C	0.0367	30	817	NON_SYNONYMOUS_CODING(MODERATE|MISSENSE|Cag/Gag|Q597E|TERT|mRNA|CODING|NM_001193376|NM_001193376.ex.4),NON_SYNONYMOUS_CODING(MODERATE|MISSENSE|Cag/Gag|Q597E|TERT|mRNA|CODING|NM_198253|NM_198253.ex.4),NON_SYNONYMOUS_CODING(MODERATE|MISSENSE|gCa/gGa|A616G|TERT|mRNA|CODING|NR_149162|NR_149162.ex.4),NON_SYNONYMOUS_CODING(MODERATE|MISSENSE|gCa/gGa|A616G|TERT|mRNA|CODING|NR_149163|NR_149163.ex.4)	Q597E
17	tissue-17 somatic	Category II-Default Categorization	PCLO	SNP	7	82784339	A	G	0.0091	12	1318	NON_SYNONYMOUS_CODING(MODERATE|MISSENSE|Tca/Cca|S540P|PCLO|mRNA|CODING|NM_014510|NM_014510.ex.2),NON_SYNONYMOUS_CODING(MODERATE|MISSENSE|Tca/Cca|S540P|PCLO|mRNA|CODING|NM_033026|NM_033026.ex.2)	S540P
17	tissue-17 somatic	Category III-Default Categorization	RAD21	Deletion	8	117868529	TG	T	0.0441	12	272	INTRON(MODIFIER||||RAD21|mRNA|CODING|NM_006265|)	
17	tissue-17 somatic	Category III-Default Categorization	RECQL4	Deletion	8	145738592	GGT	G	0.0462	67	1449	DOWNSTREAM(MODIFIER||||MFSD3|Non-coding_transcript|CODING|NM_138431|),DOWNSTREAM(MODIFIER||||MFSD3|Non-coding_transcript|CODING|NR_130120|),INTRON(MODIFIER||||RECQL4|mRNA|CODING|NM_004260|),UPSTREAM(MODIFIER||||LRRC14|mRNA|CODING|NM_001272036|),UPSTREAM(MODIFIER||||LRRC14|mRNA|CODING|NM_014665|)	
17	tissue-17 somatic	Category III-Default Categorization	FGF19	SNP	11	69518386	C	G	0.00679	21	3094	INTRON(MODIFIER||||FGF19|mRNA|CODING|NM_005117|)	
17	tissue-17 somatic	Category III-Default Categorization	FGF19	SNP	11	69518390	C	G	0.00771	25	3241	INTRON(MODIFIER||||FGF19|mRNA|CODING|NM_005117|)	
17	tissue-17 somatic	Category III-Default Categorization	KMT2D	SNP	12	49421001	C	G	0.03	18	600	SYNONYMOUS_CODING(LOW|SILENT|ccG/ccC|P4916|KMT2D|mRNA|CODING|NM_003482|NM_003482.ex.48)	P4916

17	tissue-17 somatic	Category II-Default Categorization	KMT2D	SNP	12	49445517	A	T	0.0082	12	1463	NON_SYNONYMOUS_CODING(MODERATE|MISSENSE|gTa/gAa|V650E|KMT2D|mRNA|CODING|NM_003482|NM_003482.ex.10)	V650E
17	tissue-17 somatic	Category III-Default Categorization	KMT2D	SNP	12	49445564	A	G	0.0105	18	1713	SYNONYMOUS_CODING(LOW|SILENT|ccT/ccC|P634|KMT2D|mRNA|CODING|NM_003482|NM_003482.ex.10)	P634
17	tissue-17 somatic	Category III-Default Categorization	KMT2D	SNP	12	49445771	C	T	0.007	11	1571	SYNONYMOUS_CODING(LOW|SILENT|ccG/ccA|P565|KMT2D|mRNA|CODING|NM_003482|NM_003482.ex.10)	P565
17	tissue-17 somatic	Category III-Default Categorization	CREBBP	SNP	16	3779204	C	G	0.0181	10	553	SYNONYMOUS_CODING(LOW|SILENT|ccG/ccC|P1910|CREBBP|mRNA|CODING|NM_001079846|NM_001079846.ex.30),SYNONYMOUS_CODING(LOW|SILENT|ccG/ccC|P1948|CREBBP|mRNA|CODING|NM_004380|NM_004380.ex.31)	P1910

<table>
<tr><td>17</td><td>tissue-17 somatic</td><td>Category I-Default Categorization</td><td>TP53</td><td>Deletion</td><td>17</td><td>7578284</td><td>CCAGACCTAAGAGCAAT</td><td>C</td><td>0.586</td><td>312</td><td>532</td><td>FRAME_SHIFT(HIGH||||TP53|mRNA|CODING|NM_000546|NM_000546.ex.6),FRAME_SHIFT(HIGH||||TP53|mRNA|CODING|NM_001126112|NM_001126112.ex.6),FRAME_SHIFT(HIGH||||TP53|mRNA|CODING|NM_001126113|NM_001126113.ex.6),FRAME_SHIFT(HIGH||||TP53|mRNA|CODING|NM_001126114|NM_001126114.ex.6),FRAME_SHIFT(HIGH||||TP53|mRNA|CODING|NM_001126115|NM_001126115.ex.2),FRAME_SHIFT(HIGH||||TP53|mRNA|CODING|NM_001126116|NM_001126116.ex.2),FRAME_SHIFT(HIGH||||TP53|mRNA|CODING|NM_001126117|NM_001126117.ex.2),FRAME_SHIFT(HIGH||||TP53|mRNA|CODING|NM_001126118|NM_001126118.ex.5),FRAME_SHIFT(HIGH||||TP53|mRNA|CODING|NM_001276695|NM_001276695.ex.6),FRAME_SHIFT(HIGH||||TP53|mRNA|CODING|NM_001276696|NM_001276696.ex.6),FRAME_SHIFT(HIGH||||TP53|mRNA|CODING|NM_001276697|NM_001276697.ex.2),FRAME_SHIFT(HIGH||||TP53|mRNA|CODING|NM_001276698|NM_001276698.ex.2),FRAME_SHIFT(HIGH||||TP53|mRNA|CODING|NM_001276699|NM_001276699.ex.2),FRAME_SHIFT(HIGH||||TP53|mRNA|CODING|NM_001276760|NM_001276760.ex.6),FRAME_SHIFT(HIGH||||TP53|mRNA|CODING|NM_001276761|NM_001276761.ex.6)</td><td></td></tr>
<tr><td>17</td><td>Plasma17-1</td><td>N/A</td><td>N/A</td><td>N/A</td><td>N/A</td><td>N/A</td><td>N/A</td><td>N/A</td><td>N/A</td><td>N/A</td><td>N/A</td><td>N/A</td><td>N/A</td></tr>
<tr><td>17</td><td>Plasma17-2</td><td>N/A</td><td>N/A</td><td>N/A</td><td>N/A</td><td>N/A</td><td>N/A</td><td>N/A</td><td>N/A</td><td>N/A</td><td>N/A</td><td>N/A</td><td>N/A</td></tr>
<tr><td>17</td><td>Plasma17-3</td><td>Category II-Default Categorization</td><td>PCLO</td><td>SNP</td><td>7</td><td>82784339</td><td>A</td><td>G</td><td>0.0935</td><td>10</td><td>107</td><td>NON_SYNONYMOUS_CODING(MODERATE|MISSENSE|Tca/Cca|S540P|PCLO|mRNA|CODING|NM_014510|NM_014510.ex.2),NON_SYNONYMOUS_CODING(MODERATE|MISSENSE|Tca/Cca|S540P|PCLO|mRNA|CODING|NM_033026|NM_033026.ex.2)</td><td>S540P</td></tr>
<tr><td>18</td><td>tissue-18 somatic</td><td>Category III-Default Categorization</td><td>LRP1B</td><td>SNP</td><td>2</td><td>141459787</td><td>G</td><td>A</td><td>0.369</td><td>139</td><td>377</td><td>SYNONYMOUS_CODING(LOW|SILENT|cgC/cgT|R2075|LRP1B|mRNA|CODING|NM_018557|NM_018557.ex.39)</td><td>R2075</td></tr>
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18	tissue-18 somatic	Category II-Default Categorization	NFE2L2	SNP	2	178098944	C	G	0.367	176	479	INTRON(MODIFIER||||NFE2L2|mRNA|CODING|NM_001313903|),NON_SYNONYMOUS_CODING(MODERATE|MISSENSE|cGa/cCa|R18P|NFE2L2|mRNA|CODING|NM_001145412|NM_001145412.ex.2),NON_SYNONYMOUS_CODING(MODERATE|MISSENSE|cGa/cCa|R18P|NFE2L2|mRNA|CODING|NM_001145413|NM_001145413.ex.2),NON_SYNONYMOUS_CODING(MODERATE|MISSENSE|cGa/cCa|R18P|NFE2L2|mRNA|CODING|NM_001313900|NM_001313900.ex.2),NON_SYNONYMOUS_CODING(MODERATE|MISSENSE|cGa/cCa|R18P|NFE2L2|mRNA|CODING|NM_001313901|NM_001313901.ex.2),NON_SYNONYMOUS_CODING(MODERATE|MISSENSE|cGa/cCa|R34P|NFE2L2|mRNA|CODING|NM_001313902|NM_001313902.ex.2),NON_SYNONYMOUS_CODING(MODERATE|MISSENSE|cGa/cCa|R34P|NFE2L2|mRNA|CODING|NM_006164|NM_006164.ex.2),UTR_5_PRIME(MODIFIER||||NFE2L2|mRNA|CODING|NM_001313904|NM_001313904.ex.2)	R18P
18	tissue-18 somatic	Category I-Default Categorization	ATR	Insertion	3	142274739	A	AT	0.0148	17	1149	FRAME_SHIFT(HIGH||||ATR|mRNA|CODING|NM_001184|NM_001184.ex.10),FRAME_SHIFT(HIGH||||ATR|mRNA|CODING|NM_001354579|NM_001354579.ex.9)	
18	tissue-18 somatic	Category I-Default Categorization	ATR	Deletion	3	142274739	AT	A	0.0122	14	1149	FRAME_SHIFT(HIGH||||ATR|mRNA|CODING|NM_001184|NM_001184.ex.10),FRAME_SHIFT(HIGH||||ATR|mRNA|CODING|NM_001354579|NM_001354579.ex.9)	
18	tissue-18 somatic	Category III-Default Categorization	TIPARP	SNP	3	156413643	C	T	0.0321	10	312	INTRON(MODIFIER||||TIPARP|mRNA|CODING|NM_001184717|),INTRON(MODIFIER||||TIPARP|mRNA|CODING|NM_001184718|),INTRON(MODIFIER||||TIPARP|mRNA|CODING|NM_015508|)	

18	tissue-18 somatic	Category II-Default Categorization	SOX2	SNP	3	181431062	G	A	0.0085	10	1176	INTRON(MODIFIER||||SOX2-OT|Non-coding_transcript|NON_CODING|NR_004053|),INTRON(MODIFIER||||SOX2-OT|Non-coding_transcript|NON_CODING|NR_075089|),INTRON(MODIFIER||||SOX2-OT|Non-coding_transcript|NON_CODING|NR_075090|),INTRON(MODIFIER||||SOX2-OT|Non-coding_transcript|NON_CODING|NR_075091|),INTRON(MODIFIER||||SOX2-OT|Non-coding_transcript|NON_CODING|NR_075092|),INTRON(MODIFIER||||SOX2-OT|Non-coding_transcript|NON_CODING|NR_075093|),NON_SYNONYMOUS_CODING(MODERATE|MISSENSE|gGc/gAc|G305D|SOX2|mRNA|CODING|NM_003106|NM_003106.ex.1)	G305D
18	tissue-18 somatic	Category III-Default Categorization	ETV5	SNP	3	185797800	T	G	0.00703	10	1423	SYNONYMOUS_CODING(LOW|SILENT|ccA/ccC|P152|ETV5|mRNA|CODING|NM_004454|NM_004454.ex.7)	P152
18	tissue-18 somatic	Category III-Default Categorization	ETV5	SNP	3	185802064	G	A	0.0358	15	419	INTRON(MODIFIER||||ETV5|mRNA|CODING|NM_004454|)	
18	tissue-18 somatic	Category III-Default Categorization	LPP	SNP	3	188327536	C	T	0.0215	29	1348	INTRON(MODIFIER||||LPP|mRNA|CODING|NM_001167672|),SYNONYMOUS_CODING(LOW|SILENT|aaC/aaT|N339|LPP|mRNA|CODING|NM_001167671|NM_001167671.ex.6),SYNONYMOUS_CODING(LOW|SILENT|aaC/aaT|N339|LPP|mRNA|CODING|NM_005578|NM_005578.ex.6)	N339

<table>
<tr><td>18</td><td>tissue-18 somatic</td><td>Category II-Default Categorization</td><td>TP63</td><td>SNP</td><td>3</td><td>189507616</td><td>G</td><td>C</td><td>0.172</td><td>121</td><td>702</td><td>INTRON(MODIFIER||||TP63|mRNA|CODING|NM_001114978|),INTRON(MODIFIER||||TP63|mRNA|CODING|NM_001114979|),INTRON(MODIFIER||||TP63|mRNA|CODING|NM_001329144|),INTRON(MODIFIER||||TP63|mRNA|CODING|NM_001329148|),INTRON(MODIFIER||||TP63|mRNA|CODING|NM_001329964|),INTRON(MODIFIER||||TP63|mRNA|CODING|NM_003722|),NON_SYNONYMOUS_CODING(MODERATE|MISSENSE|caG/caC|Q9H|TP63|mRNA|CODING|NM_001114980|NM_001114980.ex.1),NON_SYNONYMOUS_CODING(MODERATE|MISSENSE|caG/caC|Q9H|TP63|mRNA|CODING|NM_001114981|NM_001114981.ex.1),NON_SYNONYMOUS_CODING(MODERATE|MISSENSE|caG/caC|Q9H|TP63|mRNA|CODING|NM_001114982|NM_001114982.ex.1),NON_SYNONYMOUS_CODING(MODERATE|MISSENSE|caG/caC|Q9H|TP63|mRNA|CODING|NM_001329145|NM_001329145.ex.1),NON_SYNONYMOUS_CODING(MODERATE|MISSENSE|caG/caC|Q9H|TP63|mRNA|CODING|NM_001329146|NM_001329146.ex.1),NON_SYNONYMOUS_CODING(MODERATE|MISSENSE|caG/caC|Q9H|TP63|mRNA|CODING|NM_001329149|NM_001329149.ex.1),NON_SYNONYMOUS_CODING(MODERATE|MISSENSE|caG/caC|Q9H|TP63|mRNA|CODING|NM_001329150|NM_001329150.ex.1)</td><td>Q9H</td></tr>
<tr><td>18</td><td>tissue-18 somatic</td><td>Category II-Default Categorization</td><td>FAT1</td><td>SNP</td><td>4</td><td>187518197</td><td>G</td><td>A</td><td>0.415</td><td>364</td><td>877</td><td>NON_SYNONYMOUS_CODING(MODERATE|MISSENSE|gCg/gTg|A4166V|FAT1|mRNA|CODING|NM_005245|NM_005245.ex.25)</td><td>A4166V</td></tr>
<tr><td>18</td><td>tissue-18 somatic</td><td>Category II-Default Categorization</td><td>SDHA</td><td>SNP</td><td>5</td><td>251524</td><td>A</td><td>G</td><td>0.0155</td><td>12</td><td>776</td><td>INTRON(MODIFIER||||SDHA|mRNA|CODING|NM_001330758|),NON_SYNONYMOUS_CODING(MODERATE|MISSENSE|Atc/Gtc|I531V|SDHA|mRNA|CODING|NM_001294332|NM_001294332.ex.12),NON_SYNONYMOUS_CODING(MODERATE|MISSENSE|Atc/Gtc|I579V|SDHA|mRNA|CODING|NM_004168|NM_004168.ex.13)</td><td>I531V</td></tr>
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18	tissue-18 somatic	Category II-Default Categorization	SDHA	SNP	5	251527	T	A	0.0149	12	806	INTRON(MODIFIER||||SDHA|mRNA|CODING|NM_001330758|),NON_SYNONYMOUS_CODING(MODERATE|MISSENSE|Tac/Aac|Y532N|SDHA|mRNA|CODING|NM_001294332|NM_001294332.ex.12),NON_SYNONYMOUS_CODING(MODERATE|MISSENSE|Tac/Aac|Y580N|SDHA|mRNA|CODING|NM_004168|NM_004168.ex.13)	Y532N
18	tissue-18 somatic	Category III-Default Categorization	SDHA	SNP	5	251529	C	T	0.0148	12	810	INTRON(MODIFIER||||SDHA|mRNA|CODING|NM_001330758|),SYNONYMOUS_CODING(LOW|SILENT|taC/taT|Y532|SDHA|mRNA|CODING|NM_001294332|NM_001294332.ex.12),SYNONYMOUS_CODING(LOW|SILENT|taC/taT|Y580|SDHA|mRNA|CODING|NM_004168|NM_004168.ex.13)	Y532
18	tissue-18 somatic	Category II-Default Categorization	ROS1	SNP	6	117710735	C	G	0.0292	23	788	NON_SYNONYMOUS_CODING(MODERATE|MISSENSE|Gat/Cat|D513H|ROS1|mRNA|CODING|NM_002944|NM_002944.ex.12)	D513H
18	tissue-18 somatic	Category II-Default Categorization	PCLO	SNP	7	82784366	A	G	0.00852	10	1174	NON_SYNONYMOUS_CODING(MODERATE|MISSENSE|Tct/Cct|S531P|PCLO|mRNA|CODING|NM_014510|NM_014510.ex.2),NON_SYNONYMOUS_CODING(MODERATE|MISSENSE|Tct/Cct|S531P|PCLO|mRNA|CODING|NM_033026|NM_033026.ex.2)	S531P
18	tissue-18 somatic	Category III-Default Categorization	KMT2C	SNP	7	151927428	G	A	0.0478	12	251	INTRON(MODIFIER||||KMT2C|mRNA|CODING|NM_170606|)	
18	tissue-18 somatic	Category II-Default Categorization	KMT2C	SNP	7	151945400	T	A	0.0106	10	947	NON_SYNONYMOUS_CODING(MODERATE|MISSENSE|Att/Ttt|I707F|KMT2C|mRNA|CODING|NM_170606|NM_170606.ex.14)	I707F
18	tissue-18 somatic	Category III-Default Categorization	KMT2C	SNP	7	151945401	A	G	0.0138	13	940	SYNONYMOUS_CODING(LOW|SILENT|agT/agC|S706|KMT2C|mRNA|CODING|NM_170606|NM_170606.ex.14)	S706
18	tissue-18 somatic	Category II-Default Categorization	KMT2C	SNP	7	151970859	C	A	0.0958	167	1743	NON_SYNONYMOUS_CODING(MODERATE|MISSENSE|Ggc/Tgc|G315C|KMT2C|mRNA|CODING|NM_170606|NM_170606.ex.7)	G315C

<table>
<tr><td>18</td><td>tissue-18 somatic</td><td>Category III-Default Categorization</td><td>NDRG1</td><td>SNP</td><td>8</td><td>134251253</td><td>T</td><td>G</td><td>0.00872</td><td>15</td><td>1720</td><td>SYNONYMOUS_CODING(LOW|SILENT|cgA/cgC|R270|NDRG1|mRNA|CODING|NM_001258433|NM_001258433.ex.15),SYNONYMOUS_CODING(LOW|SILENT|cgA/cgC|R285|NDRG1|mRNA|CODING|NM_001258432|NM_001258432.ex.14),SYNONYMOUS_CODING(LOW|SILENT|cgA/cgC|R351|NDRG1|mRNA|CODING|NM_001135242|NM_001135242.ex.16),SYNONYMOUS_CODING(LOW|SILENT|cgA/cgC|R351|NDRG1|mRNA|CODING|NM_006096|NM_006096.ex.16)</td><td>R270</td></tr>
<tr><td>18</td><td>tissue-18 somatic</td><td>Category III-Default Categorization</td><td>RECQL4</td><td>Deletion</td><td>8</td><td>145738580</td><td>GTGGG</td><td>G</td><td>0.367</td><td>565</td><td>1541</td><td>DOWNSTREAM(MODIFIER||||MFSD3|Non-coding_transcript|CODING|NM_138431|),DOWNSTREAM(MODIFIER||||MFSD3|Non-coding_transcript|CODING|NR_130120|),INTRON(MODIFIER||||RECQL4|mRNA|CODING|NM_004260|),UPSTREAM(MODIFIER||||LRRC14|mRNA|CODING|NM_001272036|),UPSTREAM(MODIFIER||||LRRC14|mRNA|CODING|NM_014665|)</td><td></td></tr>
<tr><td>18</td><td>tissue-18 somatic</td><td>Category III-Default Categorization</td><td>RECQL4</td><td>Deletion</td><td>8</td><td>145738593</td><td>GT</td><td>G</td><td>0.0373</td><td>35</td><td>939</td><td>DOWNSTREAM(MODIFIER||||MFSD3|Non-coding_transcript|CODING|NM_138431|),DOWNSTREAM(MODIFIER||||MFSD3|Non-coding_transcript|CODING|NR_130120|),INTRON(MODIFIER||||RECQL4|mRNA|CODING|NM_004260|),UPSTREAM(MODIFIER||||LRRC14|mRNA|CODING|NM_001272036|),UPSTREAM(MODIFIER||||LRRC14|mRNA|CODING|NM_014665|)</td><td></td></tr>
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18	tissue-18 somatic	Category III-Default Categorization	CDKN2B	SNP	9	22006187	G	A	0.72	409	568	INTRON(MODIFIER||||CDKN2B-AS1|Non-coding_transcript|NON_CODING|NR_003529|),INTRON(MODIFIER||||CDKN2B-AS1|Non-coding_transcript|NON_CODING|NR_047532|),INTRON(MODIFIER||||CDKN2B-AS1|Non-coding_transcript|NON_CODING|NR_047533|),INTRON(MODIFIER||||CDKN2B-AS1|Non-coding_transcript|NON_CODING|NR_047534|),INTRON(MODIFIER||||CDKN2B-AS1|Non-coding_transcript|NON_CODING|NR_047535|),INTRON(MODIFIER||||CDKN2B-AS1|Non-coding_transcript|NON_CODING|NR_047536|),INTRON(MODIFIER||||CDKN2B-AS1|Non-coding_transcript|NON_CODING|NR_047537|),INTRON(MODIFIER||||CDKN2B-AS1|Non-coding_transcript|NON_CODING|NR_047538|),INTRON(MODIFIER||||CDKN2B-AS1|Non-coding_transcript|NON_CODING|NR_047539|),INTRON(MODIFIER||||CDKN2B-AS1|Non-coding_transcript|NON_CODING|NR_047540|),INTRON(MODIFIER||||CDKN2B-AS1|Non-coding_transcript|NON_CODING|NR_047541|),INTRON(MODIFIER||||CDKN2B-AS1|Non-coding_transcript|NON_CODING|NR_047542|),INTRON(MODIFIER||||CDKN2B-AS1|Non-coding_transcript|NON_CODING|NR_047543|),INTRON(MODIFIER||||CDKN2B-AS1|Non-coding_transcript|NON_CODING|NR_120536|),SYNONYMOUS_CODING(LOW|SILENT|ccC/ccT|P72|CDKN2B|mRNA|CODING|NM_004936|NM_004936.ex.2),UTR_3_PRIME(MODIFIER||||CDKN2B|mRNA|CODING|NM_078487|	P72
18	tissue-18 somatic	Category III-Default Categorization	FGF19	SNP	11	69518390	C	G	0.0099	36	3635	INTRON(MODIFIER||||FGF19|mRNA|CODING|NM_005117|)	

18	tissue-18 somatic	Category I-Default Categorization	KMT2D	SNP	12	49437450	G	C	0.427	214	501	STOP_GAINED(HIGH|NONSENSE|tCa/tGa|S1812*|KMT2D|mRNA|CODING|NM_003482|NM_003482.ex.23)	S1812*
18	tissue-18 somatic	Category III-Default Categorization	KMT2D	SNP	12	49445234	T	G	0.00972	14	1441	SYNONYMOUS_CODING(LOW|SILENT|tcA/tcC|S744|KMT2D|mRNA|CODING|NM_003482|NM_003482.ex.10)	S744
18	tissue-18 somatic	Category III-Default Categorization	KMT2D	SNP	12	49445444	C	T	0.0101	10	988	SYNONYMOUS_CODING(LOW|SILENT|ccG/ccA|P674|KMT2D|mRNA|CODING|NM_003482|NM_003482.ex.10)	P674
18	tissue-18 somatic	Category III-Default Categorization	TP53	SNP	17	7579658	G	C	0.0247	10	405	INTRON(MODIFIER||||TP53|mRNA|CODING|NM_000546|),INTRON(MODIFIER||||TP53|mRNA|CODING|NM_001126112|),INTRON(MODIFIER||||TP53|mRNA|CODING|NM_001126113|),INTRON(MODIFIER||||TP53|mRNA|CODING|NM_001126114|),INTRON(MODIFIER||||TP53|mRNA|CODING|NM_001126118|),INTRON(MODIFIER||||TP53|mRNA|CODING|NM_001276695|),INTRON(MODIFIER||||TP53|mRNA|CODING|NM_001276696|),INTRON(MODIFIER||||TP53|mRNA|CODING|NM_001276760|),INTRON(MODIFIER||||TP53|mRNA|CODING|NM_001276761|),UPSTREAM(MODIFIER||||TP53|mRNA|CODING|NM_001126115|),UPSTREAM(MODIFIER||||TP53|mRNA|CODING|NM_001126116|),UPSTREAM(MODIFIER||||TP53|mRNA|CODING|NM_001126117|),UPSTREAM(MODIFIER||||TP53|mRNA|CODING|NM_001276697|),UPSTREAM(MODIFIER||||TP53|mRNA|CODING|NM_001276698|),UPSTREAM(MODIFIER||||TP53|mRNA|CODING|NM_001276699|)	
18	Plasma18-1	Category II-Default Categorization	PCLO	SNP	7	82784366	A	G	0.0702	17	242	NON_SYNONYMOUS_CODING(MODERATE|MISSENSE|Tct/Cct|S531P|PCLO|mRNA|CODING|NM_014510|NM_014510.ex.2),NON_SYNONYMOUS_CODING(MODERATE|MISSENSE|Tct/Cct|S531P|PCLO|mRNA|CODING|NM_033026|NM_033026.ex.2)	S531P

<table>
<tr><td>18</td><td>Plasma18-2</td><td>Category II-Default Categorization</td><td>PCLO</td><td>SNP</td><td>7</td><td>82784366</td><td>A</td><td>G</td><td>0.0331</td><td>12</td><td>363</td><td>NON_SYNONYMOUS_CODING(MODERATE|MISSENSE|Tct/Cct|S531P|PCLO|mRNA|CODING|NM_014510|NM_014510.ex.2),NON_SYNONYMOUS_CODING(MODERATE|MISSENSE|Tct/Cct|S531P|PCLO|mRNA|CODING|NM_033026|NM_033026.ex.2)</td><td>S531P</td></tr>
<tr><td>18</td><td>Plasma18-3</td><td>Category II-Default Categorization</td><td>PCLO</td><td>SNP</td><td>7</td><td>82784366</td><td>A</td><td>G</td><td>0.0385</td><td>12</td><td>312</td><td>NON_SYNONYMOUS_CODING|NM_014510</td><td>S531P</td></tr>
<tr><td>19</td><td>tissue-19 somatic</td><td>Category III-Default Categorization</td><td>SPEN</td><td>Insertion</td><td>1</td><td>16200729</td><td>A</td><td>AT</td><td>0.00756</td><td>13</td><td>1719</td><td>INTRON(MODIFIER||||SPEN|mRNA|CODING|NM_015001|)</td><td></td></tr>
<tr><td>19</td><td>tissue-19 somatic</td><td>Category II-Default Categorization</td><td>LOC100130691</td><td>SNP</td><td>2</td><td>178175729</td><td>A</td><td>G</td><td>0.0139</td><td>12</td><td>866</td><td>DOWNSTREAM(MODIFIER||||MIR6512|Non-coding_transcript|NON_CODING|NR_106767|),NON_SYNONYMOUS_CODING(MODERATE|MISSENSE|aTt/aCt|I281T|LOC100130691|Non-coding_transcript|NON_CODING|NR_026966|NR_026966.ex.8)</td><td>I281T</td></tr>
<tr><td>19</td><td>tissue-19 somatic</td><td>Category II-Default Categorization</td><td>LOC100130691</td><td>SNP</td><td>2</td><td>178175731</td><td>C</td><td>T</td><td>0.0137</td><td>12</td><td>878</td><td>DOWNSTREAM(MODIFIER||||MIR6512|Non-coding_transcript|NON_CODING|NR_106767|),NON_SYNONYMOUS_CODING(MODERATE|MISSENSE|atG/atA|M280I|LOC100130691|Non-coding_transcript|NON_CODING|NR_026966|NR_026966.ex.8)</td><td>M280I</td></tr>
<tr><td>19</td><td>tissue-19 somatic</td><td>Category III-Default Categorization</td><td>LOC100130691</td><td>SNP</td><td>2</td><td>178175734</td><td>G</td><td>T</td><td>0.0124</td><td>12</td><td>968</td><td>DOWNSTREAM(MODIFIER||||MIR6512|Non-coding_transcript|NON_CODING|NR_106767|),SYNONYMOUS_CODING(LOW|SILENT|acC/acA|T279|LOC100130691|Non-coding_transcript|NON_CODING|NR_026966|NR_026966.ex.8)</td><td>T279</td></tr>
<tr><td>19</td><td>tissue-19 somatic</td><td>Category II-Default Categorization</td><td>PRKCI</td><td>SNP</td><td>3</td><td>170002367</td><td>G</td><td>A</td><td>0.174</td><td>256</td><td>1475</td><td>NON_SYNONYMOUS_CODING(MODERATE|MISSENSE|Gac/Aac|D396N|PRKCI|mRNA|CODING|NM_002740|NM_002740.ex.12)</td><td>D396N</td></tr>
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19	tissue-19 somatic	Category II-Default Categorization	SOX2	SNP	3	181431004	C	T	0.168	704	4194	INTRON(MODIFIER||||SOX2-OT|Non-coding_transcript|NON_CODING|NR_004053|),INTRON(MODIFIER||||SOX2-OT|Non-coding_transcript|NON_CODING|NR_075089|),INTRON(MODIFIER||||SOX2-OT|Non-coding_transcript|NON_CODING|NR_075090|),INTRON(MODIFIER||||SOX2-OT|Non-coding_transcript|NON_CODING|NR_075091|),INTRON(MODIFIER||||SOX2-OT|Non-coding_transcript|NON_CODING|NR_075092|),INTRON(MODIFIER||||SOX2-OT|Non-coding_transcript|NON_CODING|NR_075093|),NON_SYNONYMOUS_CODING(MODERATE|MISSENSE|Ccc/Tcc|P286S|SOX2|mRNA|CODING|NM_003106|NM_003106.ex.1)	P286S
19	tissue-19 somatic	Category II-Default Categorization	MAP3K13	SNP	3	185183546	A	G	0.0992	98	988	NON_SYNONYMOUS_CODING(MODERATE|MISSENSE|gAt/gGt|D260G|MAP3K13|Non-coding_transcript|CODING|NM_001242317|NM_001242317.ex.8),NON_SYNONYMOUS_CODING(MODERATE|MISSENSE|gAt/gGt|D467G|MAP3K13|Non-coding_transcript|CODING|NM_001242314|NM_001242314.ex.10),NON_SYNONYMOUS_CODING(MODERATE|MISSENSE|gAt/gGt|D467G|MAP3K13|Non-coding_transcript|CODING|NM_004721|NM_004721.ex.9)	D260G

<table>
<tr><td>19</td><td>tissue-19 somatic</td><td>Category III-Default Categorization</td><td>TP63</td><td>Insertion</td><td>3</td><td>189561962</td><td>C</td><td>CAGTA</td><td>0.0442</td><td>24</td><td>543</td><td>INTRON(MODIFIER||||TP63|mRNA|CODING|NM_001114978|),INTRON(MODIFIER||||TP63|mRNA|CODING|NM_001114979|),INTRON(MODIFIER||||TP63|mRNA|CODING|NM_001114980|),INTRON(MODIFIER||||TP63|mRNA|CODING|NM_001114981|),INTRON(MODIFIER||||TP63|mRNA|CODING|NM_001114982|),INTRON(MODIFIER||||TP63|mRNA|CODING|NM_001329144|),INTRON(MODIFIER||||TP63|mRNA|CODING|NM_001329145|),INTRON(MODIFIER||||TP63|mRNA|CODING|NM_001329146|),INTRON(MODIFIER||||TP63|mRNA|CODING|NM_001329148|),INTRON(MODIFIER||||TP63|mRNA|CODING|NM_001329149|),INTRON(MODIFIER||||TP63|mRNA|CODING|NM_001329150|),INTRON(MODIFIER||||TP63|mRNA|CODING|NM_001329964|),INTRON(MODIFIER||||TP63|mRNA|CODING|NM_003722|)</td><td></td></tr>
<tr><td>19</td><td>tissue-19 somatic</td><td>Category III-Default Categorization</td><td>TP63</td><td>Deletion</td><td>3</td><td>189561962</td><td>CT</td><td>C</td><td>0.0276</td><td>15</td><td>543</td><td>INTRON(MODIFIER||||TP63|mRNA|CODING|NM_001114978|),INTRON(MODIFIER||||TP63|mRNA|CODING|NM_001114979|),INTRON(MODIFIER||||TP63|mRNA|CODING|NM_001114980|),INTRON(MODIFIER||||TP63|mRNA|CODING|NM_001114981|),INTRON(MODIFIER||||TP63|mRNA|CODING|NM_001114982|),INTRON(MODIFIER||||TP63|mRNA|CODING|NM_001329144|),INTRON(MODIFIER||||TP63|mRNA|CODING|NM_001329145|),INTRON(MODIFIER||||TP63|mRNA|CODING|NM_001329146|),INTRON(MODIFIER||||TP63|mRNA|CODING|NM_001329148|),INTRON(MODIFIER||||TP63|mRNA|CODING|NM_001329149|),INTRON(MODIFIER||||TP63|mRNA|CODING|NM_001329150|),INTRON(MODIFIER||||TP63|mRNA|CODING|NM_001329964|),INTRON(MODIFIER||||TP63|mRNA|CODING|NM_003722|)</td><td></td></tr>
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19	tissue-19 somatic	Category II-Default Categorization	SDHA	SNP	5	236628	C	T	0.00905	18	1989	NON_SYNONYMOUS_CODING(MODERATE|MISSENSE|gCc/gTc|A401V|SDHA|mRNA|CODING|NM_001294332|NM_001294332.ex.9),NON_SYNONYMOUS_CODING(MODERATE|MISSENSE|gCc/gTc|A449V|SDHA|mRNA|CODING|NM_001330758|NM_001330758.ex.10),NON_SYNONYMOUS_CODING(MODERATE|MISSENSE|gCc/gTc|A449V|SDHA|mRNA|CODING|NM_004168|NM_004168.ex.10)	A401V
19	tissue-19 somatic	Category II-Default Categorization	SDHA	SNP	5	236649	C	T	0.0141	29	2063	NON_SYNONYMOUS_CODING(MODERATE|MISSENSE|tCg/tTg|S408L|SDHA|mRNA|CODING|NM_001294332|NM_001294332.ex.9),NON_SYNONYMOUS_CODING(MODERATE|MISSENSE|tCg/tTg|S456L|SDHA|mRNA|CODING|NM_001330758|NM_001330758.ex.10),NON_SYNONYMOUS_CODING(MODERATE|MISSENSE|tCg/tTg|S456L|SDHA|mRNA|CODING|NM_004168|NM_004168.ex.10)	S408L
19	tissue-19 somatic	Category III-Default Categorization	SDHA	SNP	5	236653	C	A	0.0183	37	2027	SYNONYMOUS_CODING(LOW|SILENT|ctC/ctA|L409|SDHA|mRNA|CODING|NM_001294332|NM_001294332.ex.9),SYNONYMOUS_CODING(LOW|SILENT|ctC/ctA|L457|SDHA|mRNA|CODING|NM_001330758|NM_001330758.ex.10),SYNONYMOUS_CODING(LOW|SILENT|ctC/ctA|L457|SDHA|mRNA|CODING|NM_004168|NM_004168.ex.10)	L409
19	tissue-19 somatic	Category II-Default Categorization	SDHA	SNP	5	236676	G	A	0.0212	40	1884	NON_SYNONYMOUS_CODING(MODERATE|MISSENSE|cGg/cAg|R417Q|SDHA|mRNA|CODING|NM_001294332|NM_001294332.ex.9),NON_SYNONYMOUS_CODING(MODERATE|MISSENSE|cGg/cAg|R465Q|SDHA|mRNA|CODING|NM_001330758|NM_001330758.ex.10),NON_SYNONYMOUS_CODING(MODERATE|MISSENSE|cGg/cAg|R465Q|SDHA|mRNA|CODING|NM_004168|NM_004168.ex.10)	R417Q

<table>
<tr><td>19</td><td>tissue-19 somatic</td><td>Category II-Default Categorization</td><td>SDHA</td><td>SNP</td><td>5</td><td>236678</td><td>G</td><td>A</td><td>0.0234</td><td>44</td><td>1878</td><td>NON_SYNONYMOUS_CODING(MODERATE|MISSENSE|Gca/Aca|A418T|SDHA|mRNA|CODING|NM_001294332|NM_001294332.ex.9),NON_SYNONYMOUS_CODING(MODERATE|MISSENSE|Gca/Aca|A466T|SDHA|mRNA|CODING|NM_001330758|NM_001330758.ex.10),NON_SYNONYMOUS_CODING(MODERATE|MISSENSE|Gca/Aca|A466T|SDHA|mRNA|CODING|NM_004168|NM_004168.ex.10)</td><td>A418T</td></tr>
<tr><td>19</td><td>tissue-19 somatic</td><td>Category III-Default Categorization</td><td>SDHA</td><td>SNP</td><td>5</td><td>236734</td><td>G</td><td>C</td><td>0.0198</td><td>22</td><td>1111</td><td>INTRON(MODIFIER||||SDHA|mRNA|CODING|NM_001294332|),INTRON(MODIFIER||||SDHA|mRNA|CODING|NM_001330758|),INTRON(MODIFIER||||SDHA|mRNA|CODING|NM_004168|)</td><td></td></tr>
<tr><td>19</td><td>tissue-19 somatic</td><td>Category II-Default Categorization</td><td>SDHA</td><td>SNP</td><td>5</td><td>251524</td><td>A</td><td>G</td><td>0.0101</td><td>35</td><td>3468</td><td>INTRON(MODIFIER||||SDHA|mRNA|CODING|NM_001330758|),NON_SYNONYMOUS_CODING(MODERATE|MISSENSE|Atc/Gtc|I531V|SDHA|mRNA|CODING|NM_001294332|NM_001294332.ex.12),NON_SYNONYMOUS_CODING(MODERATE|MISSENSE|Atc/Gtc|I579V|SDHA|mRNA|CODING|NM_004168|NM_004168.ex.13)</td><td>I531V</td></tr>
<tr><td>19</td><td>tissue-19 somatic</td><td>Category II-Default Categorization</td><td>SDHA</td><td>SNP</td><td>5</td><td>254574</td><td>C</td><td>T</td><td>0.0902</td><td>104</td><td>1153</td><td>NON_SYNONYMOUS_CODING(MODERATE|MISSENSE|Cac/Tac|H540Y|SDHA|mRNA|CODING|NM_001330758|NM_001330758.ex.12),NON_SYNONYMOUS_CODING(MODERATE|MISSENSE|Cac/Tac|H573Y|SDHA|mRNA|CODING|NM_001294332|NM_001294332.ex.13),NON_SYNONYMOUS_CODING(MODERATE|MISSENSE|Cac/Tac|H621Y|SDHA|mRNA|CODING|NM_004168|NM_004168.ex.14)</td><td>H540Y</td></tr>
<tr><td>19</td><td>tissue-19 somatic</td><td>Category III-Default Categorization</td><td>NSD1</td><td>SNP</td><td>5</td><td>176656755</td><td>A</td><td>T</td><td>0.0105</td><td>13</td><td>1237</td><td>INTRON(MODIFIER||||NSD1|mRNA|CODING|NM_022455|),INTRON(MODIFIER||||NSD1|mRNA|CODING|NM_172349|)</td><td></td></tr>
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19	tissue-19 somatic	Category III-Default Categorization	EGFR	SNP	7	55273073	A	T	0.209	953	4565	DOWNSTREAM(MODIFIER||||EGFR|mRNA|CODING|NM_001346897|),DOWNSTREAM(MODIFIER||||EGFR|mRNA|CODING|NM_001346898|),SYNONYMOUS_CODING(LOW|SILENT|gcA/gcT|A1079|EGFR|mRNA|CODING|NM_001346900|NM_001346900.ex.28),SYNONYMOUS_CODING(LOW|SILENT|gcA/gcT|A1087|EGFR|mRNA|CODING|NM_001346899|NM_001346899.ex.27),SYNONYMOUS_CODING(LOW|SILENT|gcA/gcT|A1132|EGFR|mRNA|CODING|NM_005228|NM_005228.ex.28),SYNONYMOUS_CODING(LOW|SILENT|gcA/gcT|A865|EGFR|mRNA|CODING|NM_001346941|NM_001346941.ex.22)	A1079
19	tissue-19 somatic	Category II-Default Categorization	PCLO	SNP	7	82784366	A	G	0.00849	49	5769	NON_SYNONYMOUS_CODING(MODERATE|MISSENSE|Tct/Cct|S531P|PCLO|mRNA|CODING|NM_014510|NM_014510.ex.2),NON_SYNONYMOUS_CODING(MODERATE|MISSENSE|Tct/Cct|S531P|PCLO|mRNA|CODING|NM_033026|NM_033026.ex.2)	S531P
19	tissue-19 somatic	Category III-Default Categorization	PCLO	SNP	7	82784373	T	C	0.00751	43	5727	SYNONYMOUS_CODING(LOW|SILENT|aaA/aaG|K528|PCLO|mRNA|CODING|NM_014510|NM_014510.ex.2),SYNONYMOUS_CODING(LOW|SILENT|aaA/aaG|K528|PCLO|mRNA|CODING|NM_033026|NM_033026.ex.2)	K528
19	tissue-19 somatic	Category II-Default Categorization	PCLO	SNP	7	82784438	T	C	0.0087	51	5865	NON_SYNONYMOUS_CODING(MODERATE|MISSENSE|Aca/Gca|T507A|PCLO|mRNA|CODING|NM_014510|NM_014510.ex.2),NON_SYNONYMOUS_CODING(MODERATE|MISSENSE|Aca/Gca|T507A|PCLO|mRNA|CODING|NM_033026|NM_033026.ex.2)	T507A
19	tissue-19 somatic	Category II-Default Categorization	PCLO	SNP	7	82784489	G	A	0.00787	49	6225	NON_SYNONYMOUS_CODING(MODERATE|MISSENSE|Cca/Tca|P490S|PCLO|mRNA|CODING|NM_014510|NM_014510.ex.2),NON_SYNONYMOUS_CODING(MODERATE|MISSENSE|Cca/Tca|P490S|PCLO|mRNA|CODING|NM_033026|NM_033026.ex.2)	P490S

19	tissue-19 somatic	Category II-Default Categorization	PCLO	SNP	7	82784501	G	A	0.01	60	5978	NON_SYNONYMOUS_CODING(MODERATE|MISSENSE|Cca/Tca|P486S|PCLO|mRNA|CODING|NM_014510|NM_014510.ex.2),NON_SYNONYMOUS_CODING(MODERATE|MISSENSE|Cca/Tca|P486S|PCLO|mRNA|CODING|NM_033026|NM_033026.ex.2)	P486S
19	tissue-19 somatic	Category II-Default Categorization	MGAM	SNP	7	141758010	G	C	0.0118	15	1272	NON_SYNONYMOUS_CODING(MODERATE|MISSENSE|gGc/gCc|G1234A|MGAM|mRNA|CODING|NM_004668|NM_004668.ex.31)	G1234A
19	tissue-19 somatic	Category III-Default Categorization	MGAM	SNP	7	141767260	C	T	0.02	67	3351	INTRON(MODIFIER||||MGAM|mRNA|CODING|NM_004668|)	
19	tissue-19 somatic	Category II-Default Categorization	KMT2C	SNP	7	151917706	T	C	0.0162	27	1663	NON_SYNONYMOUS_CODING(MODERATE|MISSENSE|aAa/aGa|K1205R|KMT2C|mRNA|CODING|NM_170606|NM_170606.ex.23)	K1205R
19	tissue-19 somatic	Category III-Default Categorization	KMT2C	SNP	7	151917710	A	G	0.0157	26	1656	SYNONYMOUS_CODING(LOW|SILENT|Ttg/Ctg|L1204|KMT2C|mRNA|CODING|NM_170606|NM_170606.ex.23)	L1204
19	tissue-19 somatic	Category II-Default Categorization	KMT2C	SNP	7	151917724	C	A	0.0163	26	1591	NON_SYNONYMOUS_CODING(MODERATE|MISSENSE|cGg/cTg|R1199L|KMT2C|mRNA|CODING|NM_170606|NM_170606.ex.23)	R1199L
19	tissue-19 somatic	Category II-Default Categorization	KMT2C	SNP	7	151919670	G	A	0.0284	37	1303	NON_SYNONYMOUS_CODING(MODERATE|MISSENSE|Cct/Tct|P1141S|KMT2C|mRNA|CODING|NM_170606|NM_170606.ex.21)	P1141S
19	tissue-19 somatic	Category II-Default Categorization	KMT2C	SNP	7	151927028	G	T	0.0106	52	4903	NON_SYNONYMOUS_CODING(MODERATE|MISSENSE|Cca/Aca|P986T|KMT2C|mRNA|CODING|NM_170606|NM_170606.ex.18)	P986T
19	tissue-19 somatic	Category III-Default Categorization	KMT2C	SNP	7	151932822	A	T	0.0458	41	896	INTRON(MODIFIER||||KMT2C|mRNA|CODING|NM_170606|)	
19	tissue-19 somatic	Category II-Default Categorization	KMT2C	SNP	7	151932997	C	T	0.0265	57	2153	NON_SYNONYMOUS_CODING(MODERATE|MISSENSE|Gga/Aga|G892R|KMT2C|mRNA|CODING|NM_170606|NM_170606.ex.16)	G892R
19	tissue-19 somatic	Category III-Default Categorization	KMT2C	SNP	7	151945602	G	A	0.0271	38	1403	SYNONYMOUS_CODING(LOW|SILENT|ggC/ggT|G639|KMT2C|mRNA|CODING|NM_170606|NM_170606.ex.14)	G639
19	tissue-19 somatic	Category III-Default Categorization	RAD21	Deletion	8	117868529	TG	T	0.0208	15	721	INTRON(MODIFIER||||RAD21|mRNA|CODING|NM_006265|)	

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<tbody>
<tr><td>19</td><td>tissue-19 somatic</td><td>Category III-Default Categorization</td><td>NDRG1</td><td>SNP</td><td>8</td><td>134251274</td><td>G</td><td>C</td><td>0.008</td><td>42</td><td>5253</td><td>SYNONYMOUS_CODING(LOW|SILENT|tcC/tcG|S263|NDRG1|mRNA|CODING|NM_001258433|NM_001258433.ex.15),SYNONYMOUS_CODING(LOW|SILENT|tcC/tcG|S278|NDRG1|mRNA|CODING|NM_001258432|NM_001258432.ex.14),SYNONYMOUS_CODING(LOW|SILENT|tcC/tcG|S344|NDRG1|mRNA|CODING|NM_001135242|NM_001135242.ex.16),SYNONYMOUS_CODING(LOW|SILENT|tcC/tcG|S344|NDRG1|mRNA|CODING|NM_006096|NM_006096.ex.16)</td><td>S263</td></tr>
<tr><td>19</td><td>tissue-19 somatic</td><td>Category III-Default Categorization</td><td>RECQL4</td><td>Deletion</td><td>8</td><td>145738580</td><td>GTGGG</td><td>G</td><td>0.34</td><td>1429</td><td>4209</td><td>DOWNSTREAM(MODIFIER||||MFSD3|Non-coding_transcript|CODING|NM_138431|),DOWNSTREAM(MODIFIER||||MFSD3|Non-coding_transcript|CODING|NR_130120|),INTRON(MODIFIER||||RECQL4|mRNA|CODING|NM_004260|),UPSTREAM(MODIFIER||||LRRC14|mRNA|CODING|NM_001272036|),UPSTREAM(MODIFIER||||LRRC14|mRNA|CODING|NM_014665|)</td><td></td></tr>
<tr><td>19</td><td>tissue-19 somatic</td><td>Category I-Default Categorization</td><td>CDKN2A</td><td>SNP</td><td>9</td><td>21971028</td><td>C</td><td>T</td><td>0.144</td><td>554</td><td>3854</td><td>DOWNSTREAM(MODIFIER||||CDKN2A-DT|Non-coding_transcript|NON_CODING|NR_024274|),NON_SYNONYMOUS_CODING(MODERATE|MISSENSE|Ggg/Agg|G125R|CDKN2A|mRNA|CODING|NM_058195|NM_058195.ex.2),STOP_GAINED(HIGH|NONSENSE|tgG/tgA|W110*|CDKN2A|mRNA|CODING|NM_000077|NM_000077.ex.2),STOP_GAINED(HIGH|NONSENSE|tgG/tgA|W110*|CDKN2A|mRNA|CODING|NM_001195132|NM_001195132.ex.2),STOP_GAINED(HIGH|NONSENSE|tgG/tgA|W59*|CDKN2A|mRNA|CODING|NM_001363763|NM_001363763.ex.2),UTR_3_PRIME(MODIFIER||||CDKN2A|mRNA|CODING|NM_058197|NM_058197.ex.2)</td><td>W110*</td></tr>
<tr><td>19</td><td>tissue-19 somatic</td><td>Category II-Default Categorization</td><td>NOTCH1</td><td>Deletion</td><td>9</td><td>139390944</td><td>TGTG</td><td>T</td><td>0.00508</td><td>19</td><td>3739</td><td>CODON_CHANGE_PLUS_CODON_DELETION(MODERATE||ccacag/cag|PQ2415Q|NOTCH1|mRNA|CODING|NM_017617|NM_017617.ex.34)</td><td>PQ2415Q</td></tr>
<tr><td>19</td><td>tissue-19 somatic</td><td>Category III-Default Categorization</td><td>FGF4</td><td>SNP</td><td>11</td><td>69589502</td><td>G</td><td>T</td><td>0.0228</td><td>100</td><td>4386</td><td>INTRON(MODIFIER||||FGF4|mRNA|CODING|NM_002007|)</td><td></td></tr>
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19	tissue-19 somatic	Category III-Default Categorization	INPPL1	SNP	11	71945558	A	C	0.0157	17	1085	DOWNSTREAM(MODIFIER||||PHOX2A|mRNA|CODING|NM_005169|),INTRON(MODIFIER||||INPPL1|mRNA|CODING|NM_001567|)	
19	tissue-19 somatic	Category III-Default Categorization	INPPL1	SNP	11	71945564	A	C	0.0236	29	1228	DOWNSTREAM(MODIFIER||||PHOX2A|mRNA|CODING|NM_005169|),INTRON(MODIFIER||||INPPL1|mRNA|CODING|NM_001567|)	
19	tissue-19 somatic	Category I-Default Categorization	INPPL1	SNP	11	71945569	A	C	0.0106	14	1319	DOWNSTREAM(MODIFIER||||PHOX2A|mRNA|CODING|NM_005169|),INTRON(MODIFIER||||INPPL1|mRNA|CODING|NM_001567|),SPLICE_SITE_ACCEPTOR(HIGH||||INPPL1|mRNA|CODING|NM_001567|)	
19	tissue-19 somatic	Category I-Default Categorization	KMT2D	Insertion	12	49420993	G	GA	0.00528	11	2085	FRAME_SHIFT(HIGH||||KMT2D|mRNA|CODING|NM_003482|NM_003482.ex.48)	
19	tissue-19 somatic	Category III-Default Categorization	KMT2D	SNP	12	49445069	A	G	0.00802	31	3865	SYNONYMOUS_CODING(LOW|SILENT|ccT/ccC|P799|KMT2D|mRNA|CODING|NM_003482|NM_003482.ex.10)	P799
19	tissue-19 somatic	Category III-Default Categorization	CREBBP	SNP	16	3779192	A	G	0.00776	12	1547	SYNONYMOUS_CODING(LOW|SILENT|ccT/ccC|P1914|CREBBP|mRNA|CODING|NM_001079846|NM_001079846.ex.30),SYNONYMOUS_CODING(LOW|SILENT|ccT/ccC|P1952|CREBBP|mRNA|CODING|NM_004380|NM_004380.ex.31)	P1914
19	tissue-19 somatic	Category III-Default Categorization	CREBBP	SNP	16	3779204	C	G	0.0118	15	1267	SYNONYMOUS_CODING(LOW|SILENT|ccG/ccC|P1910|CREBBP|mRNA|CODING|NM_001079846|NM_001079846.ex.30),SYNONYMOUS_CODING(LOW|SILENT|ccG/ccC|P1948|CREBBP|mRNA|CODING|NM_004380|NM_004380.ex.31)	P1910

19	tissue-19 somatic	Category II-Default Categorization	TP53	SNP	17	7577141	C	T	0.132	190	1441	NON_SYNONYMOUS_CODING(MODERATE|MISSENSE|gGa/gAa|G107E|TP53|mRNA|CODING|NM_001276697|NM_001276697.ex.4),NON_SYNONYMOUS_CODING(MODERATE|MISSENSE|gGa/gAa|G107E|TP53|mRNA|CODING|NM_001276698|NM_001276698.ex.4),NON_SYNONYMOUS_CODING(MODERATE|MISSENSE|gGa/gAa|G107E|TP53|mRNA|CODING|NM_001276699|NM_001276699.ex.4),NON_SYNONYMOUS_CODING(MODERATE|MISSENSE|gGa/gAa|G134E|TP53|mRNA|CODING|NM_001126115|NM_001126115.ex.4),NON_SYNONYMOUS_CODING(MODERATE|MISSENSE|gGa/gAa|G134E|TP53|mRNA|CODING|NM_001126116|NM_001126116.ex.4),NON_SYNONYMOUS_CODING(MODERATE|MISSENSE|gGa/gAa|G134E|TP53|mRNA|CODING|NM_001126117|NM_001126117.ex.4),NON_SYNONYMOUS_CODING(MODERATE|MISSENSE|gGa/gAa|G227E|TP53|mRNA|CODING|NM_001126118|NM_001126118.ex.7),NON_SYNONYMOUS_CODING(MODERATE|MISSENSE|gGa/gAa|G227E|TP53|mRNA|CODING|NM_001276695|NM_001276695.ex.8),NON_SYNONYMOUS_CODING(MODERATE|MISSENSE|gGa/gAa|G227E|TP53|mRNA|CODING|NM_001276696|NM_001276696.ex.8),NON_SYNONYMOUS_CODING(MODERATE|MISSENSE|gGa/gAa|G227E|TP53|mRNA|CODING|NM_001276760|NM_001276760.ex.8),NON_SYNONYMOUS_CODING(MODERATE|MISSENSE|gGa/gAa|G227E|TP53|mRNA|CODING|NM_001276761|NM_001276761.ex.8),NON_SYNONYMOUS_CODING(MODERATE|MISSENSE|gGa/gAa|G266E|TP53|mRNA|CODING|NM_000546|NM_000546.ex.8),NON_SYNONYMOUS_CODING(MODERATE|MISSENSE|gGa/gAa|G266E|TP53|mRNA|CODING|NM_001126112|NM_001126112.ex.8),NON_SYNONYMO	G107E

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<tr><td>19</td><td>tissue-19 somatic</td><td>Category III-Default Categorization</td><td>TP53</td><td>SNP</td><td>17</td><td>7579659</td><td>T</td><td>C</td><td>0.0138</td><td>20</td><td>1445</td><td>INTRON(MODIFIER||||TP53|mRNA|CODING|NM_000546|),INTRON(MODIFIER||||TP53|mRNA|CODING|NM_001126112|),INTRON(MODIFIER||||TP53|mRNA|CODING|NM_001126113|),INTRON(MODIFIER||||TP53|mRNA|CODING|NM_001126114|),INTRON(MODIFIER||||TP53|mRNA|CODING|NM_001126118|),INTRON(MODIFIER||||TP53|mRNA|CODING|NM_001276695|),INTRON(MODIFIER||||TP53|mRNA|CODING|NM_001276696|),INTRON(MODIFIER||||TP53|mRNA|CODING|NM_001276760|),INTRON(MODIFIER||||TP53|mRNA|CODING|NM_001276761|),UPSTREAM(MODIFIER||||TP53|mRNA|CODING|NM_001126115|),UPSTREAM(MODIFIER||||TP53|mRNA|CODING|NM_001126116|),UPSTREAM(MODIFIER||||TP53|mRNA|CODING|NM_001126117|),UPSTREAM(MODIFIER||||TP53|mRNA|CODING|NM_001276697|),UPSTREAM(MODIFIER||||TP53|mRNA|CODING|NM_001276698|),UPSTREAM(MODIFIER||||TP53|mRNA|CODING|NM_001276699|)</td><td></td></tr>
<tr><td>19</td><td>tissue-19 somatic</td><td>Category III-Default Categorization</td><td>EP300</td><td>Insertion</td><td>22</td><td>41550984</td><td>C</td><td>CTT</td><td>0.0181</td><td>11</td><td>607</td><td>INTRON(MODIFIER||||EP300|mRNA|CODING|NM_001362843|),INTRON(MODIFIER||||EP300|mRNA|CODING|NM_001429|)</td><td></td></tr>
<tr><td>19</td><td>Plasma19-1</td><td>Category III-Default Categorization</td><td>PCLO</td><td>SNP</td><td>7</td><td>82784373</td><td>T</td><td>C</td><td>0.0474</td><td>12</td><td>253</td><td>SYNONYMOUS_CODING(LOW|SILENT|aaA/aaG|K528|PCLO|mRNA|CODING|NM_014510|NM_014510.ex.2),SYNONYMOUS_CODING(LOW|SILENT|aaA/aaG|K528|PCLO|mRNA|CODING|NM_033026|NM_033026.ex.2)</td><td>K528</td></tr>
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<tr><td>19</td><td>Plasma19-2</td><td>Category III-Default Categorization</td><td>EGFR</td><td>SNP</td><td>7</td><td>55273073</td><td>A</td><td>T</td><td>0.188</td><td>26</td><td>138</td><td>DOWNSTREAM(MODIFIER||||EGFR|mRNA|CODING|NM_001346897|),DOWNSTREAM(MODIFIER||||EGFR|mRNA|CODING|NM_001346898|),SYNONYMOUS_CODING(LOW|SILENT|gcA/gcT|A1079|EGFR|mRNA|CODING|NM_001346900|NM_001346900.ex.28),SYNONYMOUS_CODING(LOW|SILENT|gcA/gcT|A1087|EGFR|mRNA|CODING|NM_001346899|NM_001346899.ex.27),SYNONYMOUS_CODING(LOW|SILENT|gcA/gcT|A1132|EGFR|mRNA|CODING|NM_005228|NM_005228.ex.28),SYNONYMOUS_CODING(LOW|SILENT|gcA/gcT|A865|EGFR|mRNA|CODING|NM_001346941|NM_001346941.ex.22)</td><td>A1079</td></tr>
<tr><td>19</td><td>Plasma19-3</td><td>N/A</td><td>N/A</td><td>N/A</td><td>N/A</td><td>N/A</td><td>N/A</td><td>N/A</td><td>N/A</td><td>N/A</td><td>N/A</td><td>N/A</td><td>N/A</td></tr>
<tr><td>20</td><td>tissue-20 somatic</td><td>Category II-Default Categorization</td><td>LRP1B</td><td>SNP</td><td>2</td><td>141232735</td><td>G</td><td>T</td><td>0.177</td><td>80</td><td>451</td><td>NON_SYNONYMOUS_CODING(MODERATE|MISSENSE|agC/agA|S3199R|LRP1B|mRNA|CODING|NM_018557|NM_018557.ex.60)</td><td>S3199R</td></tr>
<tr><td>20</td><td>tissue-20 somatic</td><td>Category II-Default Categorization</td><td>NFE2L2</td><td>SNP</td><td>2</td><td>178098810</td><td>C</td><td>T</td><td>0.0661</td><td>36</td><td>545</td><td>INTRON(MODIFIER||||NFE2L2|mRNA|CODING|NM_001313903|),NON_SYNONYMOUS_CODING(MODERATE|MISSENSE|Gag/Aag|E63K|NFE2L2|mRNA|CODING|NM_001145412|NM_001145412.ex.2),NON_SYNONYMOUS_CODING(MODERATE|MISSENSE|Gag/Aag|E63K|NFE2L2|mRNA|CODING|NM_001145413|NM_001145413.ex.2),NON_SYNONYMOUS_CODING(MODERATE|MISSENSE|Gag/Aag|E63K|NFE2L2|mRNA|CODING|NM_001313900|NM_001313900.ex.2),NON_SYNONYMOUS_CODING(MODERATE|MISSENSE|Gag/Aag|E63K|NFE2L2|mRNA|CODING|NM_001313901|NM_001313901.ex.2),NON_SYNONYMOUS_CODING(MODERATE|MISSENSE|Gag/Aag|E79K|NFE2L2|mRNA|CODING|NM_001313902|NM_001313902.ex.2),NON_SYNONYMOUS_CODING(MODERATE|MISSENSE|Gag/Aag|E79K|NFE2L2|mRNA|CODING|NM_006164|NM_006164.ex.2),SYNONYMOUS_CODING(LOW|SILENT|aaG/aaA|K2|NFE2L2|mRNA|CODING|NM_001313904|NM_001313904.ex.2)</td><td>E63K</td></tr>
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<tr><td>20</td><td>tissue-20 somatic</td><td>Category III-Default Categorization</td><td>LPP</td><td>SNP</td><td>3</td><td>188327230</td><td>C</td><td>T</td><td>0.101</td><td>181</td><td>1792</td><td>INTRON(MODIFIER||||LPP|mRNA|CODING|NM_001167672|),SYNONYMOUS_CODING(LOW|SILENT|gcC/gcT|A237|LPP|mRNA|CODING|NM_001167671|NM_001167671.ex.6),SYNONYMOUS_CODING(LOW|SILENT|gcC/gcT|A237|LPP|mRNA|CODING|NM_005578|NM_005578.ex.6)</td><td>A237</td></tr>
<tr><td>20</td><td>tissue-20 somatic</td><td>Category III-Default Categorization</td><td>TP63</td><td>SNP</td><td>3</td><td>189349287</td><td>C</td><td>T</td><td>0.0512</td><td>33</td><td>645</td><td>INTRON(MODIFIER||||TP63|mRNA|CODING|NM_001329964|),UTR_5_PRIME(MODIFIER||||TP63|mRNA|CODING|NM_001114978|NM_001114978.ex.1),UTR_5_PRIME(MODIFIER||||TP63|mRNA|CODING|NM_001114979|NM_001114979.ex.1),UTR_5_PRIME(MODIFIER||||TP63|mRNA|CODING|NM_001329144|NM_001329144.ex.1),UTR_5_PRIME(MODIFIER||||TP63|mRNA|CODING|NM_001329148|NM_001329148.ex.1),UTR_5_PRIME(MODIFIER||||TP63|mRNA|CODING|NM_003722|NM_003722.ex.1)</td><td></td></tr>
<tr><td>20</td><td>tissue-20 somatic</td><td>Category II-Default Categorization</td><td>SDHA</td><td>SNP</td><td>5</td><td>251524</td><td>A</td><td>G</td><td>0.00729</td><td>10</td><td>1371</td><td>INTRON(MODIFIER||||SDHA|mRNA|CODING|NM_001330758|),NON_SYNONYMOUS_CODING(MODERATE|MISSENSE|Atc/Gtc|I531V|SDHA|mRNA|CODING|NM_001294332|NM_001294332.ex.12),NON_SYNONYMOUS_CODING(MODERATE|MISSENSE|Atc/Gtc|I579V|SDHA|mRNA|CODING|NM_004168|NM_004168.ex.13)</td><td>I531V</td></tr>
<tr><td>20</td><td>tissue-20 somatic</td><td>Category II-Default Categorization</td><td>SDHA</td><td>SNP</td><td>5</td><td>254529</td><td>T</td><td>C</td><td>0.0551</td><td>37</td><td>672</td><td>NON_SYNONYMOUS_CODING(MODERATE|MISSENSE|Tac/Cac|Y525H|SDHA|mRNA|CODING|NM_001330758|NM_001330758.ex.12),NON_SYNONYMOUS_CODING(MODERATE|MISSENSE|Tac/Cac|Y558H|SDHA|mRNA|CODING|NM_001294332|NM_001294332.ex.13),NON_SYNONYMOUS_CODING(MODERATE|MISSENSE|Tac/Cac|Y606H|SDHA|mRNA|CODING|NM_004168|NM_004168.ex.14)</td><td>Y525H</td></tr>
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20	tissue-20 somatic	Category II-Default Categorization	SDHA	SNP	5	254574	C	T	0.07	38	543	NON_SYNONYMOUS_CODING(MODERATE|MISSENSE|Cac/Tac|H540Y|SDHA|mRNA|CODING|NM_001330758|NM_001330758.ex.12),NON_SYNONYMOUS_CODING(MODERATE|MISSENSE|Cac/Tac|H573Y|SDHA|mRNA|CODING|NM_001294332|NM_001294332.ex.13),NON_SYNONYMOUS_CODING(MODERATE|MISSENSE|Cac/Tac|H621Y|SDHA|mRNA|CODING|NM_004168|NM_004168.ex.14)	H540Y
20	tissue-20 somatic	Category II-Default Categorization	ROS1	SNP	6	117710848	T	A	0.161	157	978	NON_SYNONYMOUS_CODING(MODERATE|MISSENSE|cAa/cTa|Q475L|ROS1|mRNA|CODING|NM_002944|NM_002944.ex.12)	Q475L
20	tissue-20 somatic	Category II-Default Categorization	PCLO	SNP	7	82784441	A	G	0.0162	24	1479	NON_SYNONYMOUS_CODING(MODERATE|MISSENSE|Tca/Cca|S506P|PCLO|mRNA|CODING|NM_014510|NM_014510.ex.2),NON_SYNONYMOUS_CODING(MODERATE|MISSENSE|Tca/Cca|S506P|PCLO|mRNA|CODING|NM_033026|NM_033026.ex.2)	S506P
20	tissue-20 somatic	Category III-Default Categorization	PCLO	SNP	7	82784493	C	T	0.00939	14	1491	SYNONYMOUS_CODING(LOW|SILENT|aaG/aaA|K488|PCLO|mRNA|CODING|NM_014510|NM_014510.ex.2),SYNONYMOUS_CODING(LOW|SILENT|aaG/aaA|K488|PCLO|mRNA|CODING|NM_033026|NM_033026.ex.2)	K488
20	tissue-20 somatic	Category III-Default Categorization	GRM3	SNP	7	86415945	C	T	0.0231	58	2507	SYNONYMOUS_CODING(LOW|SILENT|gaC/gaT|D279|GRM3|mRNA|CODING|NM_000840|NM_000840.ex.3),SYNONYMOUS_CODING(LOW|SILENT|gaC/gaT|D279|GRM3|mRNA|CODING|NM_001363522|NM_001363522.ex.3)	D279

<table>
<tr><td>20</td><td>tissue-20 somatic</td><td>Category I-Default Categorization</td><td>FGFR1</td><td>Insertion</td><td>8</td><td>38272121</td><td>T</td><td>TC</td><td>0.0108</td><td>11</td><td>1017</td><td>FRAME_SHIFT(HIGH||||FGFR1|mRNA|CODING|NM_001174063|NM_001174063.ex.15),FRAME_SHIFT(HIGH||||FGFR1|mRNA|CODING|NM_001174064|NM_001174064.ex.16),FRAME_SHIFT(HIGH||||FGFR1|mRNA|CODING|NM_001174065|NM_001174065.ex.15),FRAME_SHIFT(HIGH||||FGFR1|mRNA|CODING|NM_001174066|NM_001174066.ex.14),FRAME_SHIFT(HIGH||||FGFR1|mRNA|CODING|NM_001174067|NM_001174067.ex.16),FRAME_SHIFT(HIGH||||FGFR1|mRNA|CODING|NM_001354367|NM_001354367.ex.15),FRAME_SHIFT(HIGH||||FGFR1|mRNA|CODING|NM_001354368|NM_001354368.ex.14),FRAME_SHIFT(HIGH||||FGFR1|mRNA|CODING|NM_001354369|NM_001354369.ex.15),FRAME_SHIFT(HIGH||||FGFR1|mRNA|CODING|NM_001354370|NM_001354370.ex.14),FRAME_SHIFT(HIGH||||FGFR1|mRNA|CODING|NM_015850|NM_015850.ex.15),FRAME_SHIFT(HIGH||||FGFR1|mRNA|CODING|NM_023105|NM_023105.ex.14),FRAME_SHIFT(HIGH||||FGFR1|mRNA|CODING|NM_023106|NM_023106.ex.14),FRAME_SHIFT(HIGH||||FGFR1|mRNA|CODING|NM_023110|NM_023110.ex.15)</td><td></td></tr>
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<tr><td>20</td><td>tissue-20 somatic</td><td>Category II-Default Categorization</td><td>FGFR1</td><td>Insertion</td><td>8</td><td>38272124</td><td>C</td><td>CGTATCATTAAAA</td><td>0.0132</td><td>14</td><td>1061</td><td>CODON_CHANGE_PLUS_CODON_INSERTION(MODERATE||atg/aTTTTAATGATACtg|M574ILMIL|FGFR1|mRNA|CODING|NM_001354368|NM_001354368.ex.14),CODON_CHANGE_PLUS_CODON_INSERTION(MODERATE||atg/aTTTTAATGATACtg|M576ILMIL|FGFR1|mRNA|CODING|NM_001354370|NM_001354370.ex.14),CODON_CHANGE_PLUS_CODON_INSERTION(MODERATE||atg/aTTTTAATGATACtg|M576ILMIL|FGFR1|mRNA|CODING|NM_023106|NM_023106.ex.14),CODON_CHANGE_PLUS_CODON_INSERTION(MODERATE||atg/aTTTTAATGATACtg|M578ILMIL|FGFR1|mRNA|CODING|NM_001174066|NM_001174066.ex.14),CODON_CHANGE_PLUS_CODON_INSERTION(MODERATE||atg/aTTTTAATGATACtg|M578ILMIL|FGFR1|mRNA|CODING|NM_023105|NM_023105.ex.14),CODON_CHANGE_PLUS_CODON_INSERTION(MODERATE||atg/aTTTTAATGATACtg|M657ILMIL|FGFR1|mRNA|CODING|NM_001174064|NM_001174064.ex.16),CODON_CHANGE_PLUS_CODON_INSERTION(MODERATE||atg/aTTTTAATGATACtg|M663ILMIL|FGFR1|mRNA|CODING|NM_001354369|NM_001354369.ex.15),CODON_CHANGE_PLUS_CODON_INSERTION(MODERATE||atg/aTTTTAATGATACtg|M665ILMIL|FGFR1|mRNA|CODING|NM_001174063|NM_001174063.ex.15),CODON_CHANGE_PLUS_CODON_INSERTION(MODERATE||atg/aTTTTAATGATACtg|M665ILMIL|FGFR1|mRNA|CODING|NM_001174065|NM_001174065.ex.15),CODON_CHANGE_PLUS_CODON_INSERTION(MODERATE||atg/aTTTTAATGATACtg|M665ILMIL|FGFR1|mRNA|CODING|NM_001354367|NM_001354367.ex.15),CODON_CHANGE_PLUS_CODON_INSERTION(MODERATE||atg/aTTTTAATGATACtg|M665ILMIL|FGFR1|mRNA|CODING|NM_015850|NM_015850.ex.</td><td>M574ILMIL</td></tr>
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<tr><td>20</td><td>tissue-20 somatic</td><td>Category III-Default Categorization</td><td>PTPRD</td><td>Deletion</td><td>9</td><td>8341685</td><td>AC</td><td>A</td><td>0.27</td><td>93</td><td>345</td><td>INTRON(MODIFIER||||PTPRD|mRNA|CODING|NM_001040712|),INTRON(MODIFIER||||PTPRD|mRNA|CODING|NM_001171025|),INTRON(MODIFIER||||PTPRD|mRNA|CODING|NM_002839|),INTRON(MODIFIER||||PTPRD|mRNA|CODING|NM_130391|),INTRON(MODIFIER||||PTPRD|mRNA|CODING|NM_130392|),INTRON(MODIFIER||||PTPRD|mRNA|CODING|NM_130393|)</td><td></td></tr>
<tr><td>20</td><td>tissue-20 somatic</td><td>Category II-Default Categorization</td><td>CDKN2A</td><td>SNP</td><td>9</td><td>21971160</td><td>G</td><td>A</td><td>0.0114</td><td>10</td><td>881</td><td>DOWNSTREAM(MODIFIER||||CDKN2A-DT|Non-coding_transcript|NON_CODING|NR_024274|),NON_SYNONYMOUS_CODING(MODERATE|MISSENSE|Cgg/Tgg|R81W|CDKN2A|mRNA|CODING|NM_058195|NM_058195.ex.2),SYNONYMOUS_CODING(LOW|SILENT|caC/caT|H15|CDKN2A|mRNA|CODING|NM_001363763|NM_001363763.ex.2),SYNONYMOUS_CODING(LOW|SILENT|caC/caT|H66|CDKN2A|mRNA|CODING|NM_000077|NM_000077.ex.2),SYNONYMOUS_CODING(LOW|SILENT|caC/caT|H66|CDKN2A|mRNA|CODING|NM_001195132|NM_001195132.ex.2),UTR_3_PRIME(MODIFIER||||CDKN2A|mRNA|CODING|NM_058197|NM_058197.ex.2)</td><td>R81W</td></tr>
<tr><td>20</td><td>tissue-20 somatic</td><td>Category II-Default Categorization</td><td>NOTCH1</td><td>SNP</td><td>9</td><td>139399790</td><td>C</td><td>A</td><td>0.00715</td><td>11</td><td>1539</td><td>NON_SYNONYMOUS_CODING(MODERATE|MISSENSE|Gac/Tac|D1520Y|NOTCH1|mRNA|CODING|NM_017617|NM_017617.ex.25)</td><td>D1520Y</td></tr>
<tr><td>20</td><td>tissue-20 somatic</td><td>Category III-Default Categorization</td><td>FGF19</td><td>SNP</td><td>11</td><td>69518386</td><td>C</td><td>G</td><td>0.00715</td><td>10</td><td>1399</td><td>INTRON(MODIFIER||||FGF19|mRNA|CODING|NM_005117|)</td><td></td></tr>
<tr><td>20</td><td>tissue-20 somatic</td><td>Category I-Default Categorization</td><td>INPPL1</td><td>Deletion</td><td>11</td><td>71939786</td><td>AGCCCCCGCTGCCCCCGCGCTCTGGCTCCACCAGCATTTCT</td><td>A</td><td>0.0264</td><td>35</td><td>1325</td><td>FRAME_SHIFT(HIGH||||INPPL1|mRNA|CODING|NM_001567|NM_001567.ex.4)</td><td></td></tr>
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20	tissue-20 somatic	Category III-Default Categorization	INPPL1	SNP	11	71945564	A	C	0.0164	10	610	DOWNSTREAM(MODIFIER||||PHOX2A|mRNA|CODING|NM_005169|),INTRON(MODIFIER||||INPPL1|mRNA|CODING|NM_001567|)	
20	tissue-20 somatic	Category II-Default Categorization	YAP1	SNP	11	102100541	G	A	0.0145	10	691	NON_SYNONYMOUS_CODING(MODERATE|MISSENSE|gGa/gAa|G284E|YAP1|mRNA|CODING|NM_001195045|NM_001195045.ex.9),NON_SYNONYMOUS_CODING(MODERATE|MISSENSE|gGa/gAa|G408E|YAP1|mRNA|CODING|NM_006106|NM_006106.ex.7),NON_SYNONYMOUS_CODING(MODERATE|MISSENSE|gGa/gAa|G412E|YAP1|mRNA|CODING|NM_001282098|NM_001282098.ex.7),NON_SYNONYMOUS_CODING(MODERATE|MISSENSE|gGa/gAa|G424E|YAP1|mRNA|CODING|NM_001282097|NM_001282097.ex.8),NON_SYNONYMOUS_CODING(MODERATE|MISSENSE|gGa/gAa|G428E|YAP1|mRNA|CODING|NM_001282099|NM_001282099.ex.8),NON_SYNONYMOUS_CODING(MODERATE|MISSENSE|gGa/gAa|G446E|YAP1|mRNA|CODING|NM_001195044|NM_001195044.ex.8),NON_SYNONYMOUS_CODING(MODERATE|MISSENSE|gGa/gAa|G450E|YAP1|mRNA|CODING|NM_001282100|NM_001282100.ex.8),NON_SYNONYMOUS_CODING(MODERATE|MISSENSE|gGa/gAa|G462E|YAP1|mRNA|CODING|NM_001130145|NM_001130145.ex.9),NON_SYNONYMOUS_CODING(MODERATE|MISSENSE|gGa/gAa|G466E|YAP1|mRNA|CODING|NM_001282101|NM_001282101.ex.9)	G284E
20	tissue-20 somatic	Category III-Default Categorization	KMT2D	SNP	12	49421001	C	G	0.0253	16	632	SYNONYMOUS_CODING(LOW|SILENT|ccG/ccC|P4916|KMT2D|mRNA|CODING|NM_003482|NM_003482.ex.48)	P4916
20	tissue-20 somatic	Category III-Default Categorization	KMT2D	SNP	12	49445420	A	T	0.00952	20	2100	SYNONYMOUS_CODING(LOW|SILENT|ccT/ccA|P682|KMT2D|mRNA|CODING|NM_003482|NM_003482.ex.10)	P682
20	tissue-20 somatic	Category II-Default Categorization	KMT2D	SNP	12	49445427	G	A	0.00703	15	2135	NON_SYNONYMOUS_CODING(MODERATE|MISSENSE|aCg/aTg|T680M|KMT2D|mRNA|CODING|NM_003482|NM_003482.ex.10)	T680M

20	tissue-20 somatic	Category II-Default Categorization	KMT2D	SNP	12	49445428	T	G	0.00797	16	2008	NON_SYNONYMOUS_CODING(MODERATE|MISSENSE|Acg/Ccg|T680P|KMT2D|mRNA|CODING|NM_003482|NM_003482.ex.10)	T680P
20	tissue-20 somatic	Category III-Default Categorization	CREBBP	SNP	16	3779210	T	G	0.0247	12	486	SYNONYMOUS_CODING(LOW|SILENT|ccA/ccC|P1908|CREBBP|mRNA|CODING|NM_001079846|NM_001079846.ex.30),SYNONYMOUS_CODING(LOW|SILENT|ccA/ccC|P1946|CREBBP|mRNA|CODING|NM_004380|NM_004380.ex.31)	P1908
20	tissue-20 somatic	Category I-Default Categorization	TP53	Deletion	17	7577070	GGA	G	0.294	224	761	FRAME_SHIFT(HIGH||||TP53|mRNA|CODING|NM_000546|NM_000546.ex.8),FRAME_SHIFT(HIGH||||TP53|mRNA|CODING|NM_001126112|NM_001126112.ex.8),FRAME_SHIFT(HIGH||||TP53|mRNA|CODING|NM_001126113|NM_001126113.ex.8),FRAME_SHIFT(HIGH||||TP53|mRNA|CODING|NM_001126114|NM_001126114.ex.8),FRAME_SHIFT(HIGH||||TP53|mRNA|CODING|NM_001126115|NM_001126115.ex.4),FRAME_SHIFT(HIGH||||TP53|mRNA|CODING|NM_001126116|NM_001126116.ex.4),FRAME_SHIFT(HIGH||||TP53|mRNA|CODING|NM_001126117|NM_001126117.ex.4),FRAME_SHIFT(HIGH||||TP53|mRNA|CODING|NM_001126118|NM_001126118.ex.7),FRAME_SHIFT(HIGH||||TP53|mRNA|CODING|NM_001276695|NM_001276695.ex.8),FRAME_SHIFT(HIGH||||TP53|mRNA|CODING|NM_001276696|NM_001276696.ex.8),FRAME_SHIFT(HIGH||||TP53|mRNA|CODING|NM_001276697|NM_001276697.ex.4),FRAME_SHIFT(HIGH||||TP53|mRNA|CODING|NM_001276698|NM_001276698.ex.4),FRAME_SHIFT(HIGH||||TP53|mRNA|CODING|NM_001276699|NM_001276699.ex.4),FRAME_SHIFT(HIGH||||TP53|mRNA|CODING|NM_001276760|NM_001276760.ex.8),FRAME_SHIFT(HIGH||||TP53|mRNA|CODING|NM_001276761|NM_001276761.ex.8)	

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<tr><td>20</td><td>tissue-20 somatic</td><td>Category II-Default Categorization</td><td>TP53</td><td>SNP</td><td>17</td><td>7578449</td><td>C</td><td>T</td><td>0.0239</td><td>28</td><td>1173</td><td>NON_SYNONYMOUS_CODING(MODERATE|MISSENSE|Gcc/Acc|A122T|TP53|mRNA|CODING|NM_001126118|NM_001126118.ex.4),NON_SYNONYMOUS_CODING(MODERATE|MISSENSE|Gcc/Acc|A122T|TP53|mRNA|CODING|NM_001276695|NM_001276695.ex.5),NON_SYNONYMOUS_CODING(MODERATE|MISSENSE|Gcc/Acc|A122T|TP53|mRNA|CODING|NM_001276696|NM_001276696.ex.5),NON_SYNONYMOUS_CODING(MODERATE|MISSENSE|Gcc/Acc|A122T|TP53|mRNA|CODING|NM_001276760|NM_001276760.ex.5),NON_SYNONYMOUS_CODING(MODERATE|MISSENSE|Gcc/Acc|A122T|TP53|mRNA|CODING|NM_001276761|NM_001276761.ex.5),NON_SYNONYMOUS_CODING(MODERATE|MISSENSE|Gcc/Acc|A161T|TP53|mRNA|CODING|NM_000546|NM_000546.ex.5),NON_SYNONYMOUS_CODING(MODERATE|MISSENSE|Gcc/Acc|A161T|TP53|mRNA|CODING|NM_001126112|NM_001126112.ex.5),NON_SYNONYMOUS_CODING(MODERATE|MISSENSE|Gcc/Acc|A161T|TP53|mRNA|CODING|NM_001126113|NM_001126113.ex.5),NON_SYNONYMOUS_CODING(MODERATE|MISSENSE|Gcc/Acc|A161T|TP53|mRNA|CODING|NM_001126114|NM_001126114.ex.5),NON_SYNONYMOUS_CODING(MODERATE|MISSENSE|Gcc/Acc|A29T|TP53|mRNA|CODING|NM_001126115|NM_001126115.ex.1),NON_SYNONYMOUS_CODING(MODERATE|MISSENSE|Gcc/Acc|A29T|TP53|mRNA|CODING|NM_001126116|NM_001126116.ex.1),NON_SYNONYMOUS_CODING(MODERATE|MISSENSE|Gcc/Acc|A29T|TP53|mRNA|CODING|NM_001126117|NM_001126117.ex.1),NON_SYNONYMOUS_CODING(MODERATE|MISSENSE|Gcc/Acc|A2T|TP53|mRNA|CODING|NM_001276697|NM_001276697.ex.1),NON_SYNONYMOUS_CODING</td><td>A122T</td></tr>
<tr><td>20</td><td>Plasma20-1</td><td>Category II-Default Categorization</td><td>SDHA</td><td>SNP</td><td>5</td><td>251524</td><td>A</td><td>G</td><td>0.0322</td><td>11</td><td>342</td><td>NON_SYNONYMOUS_CODING|NM_001294332</td><td>I531V</td></tr>
<tr><td>20</td><td>Plasma20-2</td><td>N/A</td><td>N/A</td><td>N/A</td><td>N/A</td><td>N/A</td><td>N/A</td><td>N/A</td><td>N/A</td><td>N/A</td><td>N/A</td><td>N/A</td><td>N/A</td></tr>
<tr><td>20</td><td>Plasma20-3</td><td>N/A</td><td>N/A</td><td>N/A</td><td>N/A</td><td>N/A</td><td>N/A</td><td>N/A</td><td>N/A</td><td>N/A</td><td>N/A</td><td>N/A</td><td>N/A</td></tr>
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