

Supplementary Table S3. Predicting functional effects of somatic mutations detected in vulvar SCCs.

Gene	Chr:Position*	Allele (Ref/Alt)	Sample	Polyphen-2 score**	Amino acid change	Mutation Allele Frequency
<i>APC</i>	chr5:112179733	G/C	VSCC14	0.998	Lys2814Asn	0.13
<i>APC</i>	chr5:112179816	C/G	VSCC8	1	Ser2842Cys	0.45
<i>APC</i>	chr5:112102982	G/A	VSCC11	0.023	Arg106His	0.06
<i>BCL11B</i>	chr14:99642095	C/A	VSCC4	0.807	Ala289Ser	0.22
<i>BCL11B</i>	chr14:99642095	C/A	VSCC10	0.807	Ala289Ser	0.23
<i>BCORL1</i>	chrX:129162622	G/A	VSCC7	1	Arg1364His	0.06
<i>BRCA2</i>	chr13:32906981	G/C	VSCC12	0.995	Glu456Gln	0.23
<i>BRCA2</i>	chr13:32907084	G/A	VSCC12	0.002	Gly490Glu	0.26
<i>CASC5</i>	chr15:40916432	G/C	VSCC10	0.958	Asp1324His	0.21
<i>CASC5</i>	chr15:40917695	G/C	VSCC10	0.375	Glu1771Gln	0.31
<i>CASP8</i>	chr2:202139642	C/T	VSCC7	0.038	Ser226Leu	0.31
<i>CDK12</i>	chr17:37618494	C/T	VSCC4	0.993	Thr57Ile	0.31
<i>CDK12</i>	chr17:37618494	C/T	VSCC10	0.993	Thr57Ile	0.26
<i>CDKN2A</i>	chr9:21971108	C/A	VSCC14	1	Asp84Tyr	0.07
<i>CDKN2A</i>	chr9:21971186	G/A	VSCC7	0.824	Arg58Tyr	0.3
<i>CHD4</i>	chr12:6709750	C/T	VSCC7	0.987	Arg338His	0.06
<i>CHD4</i>	chr12:6709097	C/T	VSCC9	0.593	Glu442Lys	0.06
<i>COL1A1</i>	chr17:48270014	G/A	VSCC14	0.31	Ser639Phe	0.11
<i>CREBBP</i>	chr16:3777833	C/G	VSCC12	0.99	Gln2405His	0.28
<i>CREBBP</i>	chr16:3823797	C/T	VSCC13	0.192	Met806Ile	0.29
<i>CREBBP</i>	chr16:3781372	C/T	VSCC14	1	Asp1665Asn	0.08
<i>CRTC1</i>	chr19:18864392	G/C	VSCC15	0.946	Lys207Asn	0.25
<i>CRTC1</i>	chr19:18886551	C/T	VSCC9	0.999	Thr509Met	0.2
<i>EGFR</i>	chr7:55233037	C/T	VSCC7	1	Pro596Leu	0.18
<i>ERCC1</i>	chr12:1213924	T/A	VSCC3	0.999	His365Gln	0.34

<i>EXT2</i>	chr11:44146343	C/T	VSCC11	1	Arg250Trp	0.1
<i>FAT1</i>	chr4:187524435	C/T	VSCC9	0.661	Asp3751Asn	0.07
<i>FBXW7</i>	chr4:153247175	T/C	VSCC12	1	Arg463Gly	0.32
<i>FBXW7</i>	chr4:153247366	C/T	VSCC5	1	Arg399Gln	0.65
<i>HOOK3</i>	chr8:42865534	G/C	VSCC14	1	Glu609Gln	0.07
<i>HOOK3</i>	chr8:42865517	G/A	VSCC8	1	Arg603Gln	0.06
<i>HRAS</i>	chr11:534289	C/T	VSCC13	0.831	Gly12Ser	0.5
<i>KAT6B</i>	chr10:76789215	G/A	VSCC7	0.999	Val1545Ile	0.04
<i>KMT2C</i>	chr7:151970951	C/T	VSCC13	0.984	Arg284Gln	0.09
<i>KMT2C</i>	chr7:151860394	C/G	VSCC8	1	Arg3423Thr	0.32
<i>KMT2C</i>	chr7:151877851	G/A	VSCC8	0.985	Thr2365Ile	0.55
<i>KMT2C</i>	chr7:151860342	C/G	VSCC10	0.979	Glu3440Asp	0.16
<i>LRP1B</i>	chr2:141473652	A/T	VSCC13	1	Asp1971Glu	0.22
<i>LRP1B</i>	chr2:141665596	C/G	VSCC7	1	Asp1124His	0.09
<i>MLLT6</i>	chr17:36865522	G/A	VSCC7	1	Val151Ile	0.09
<i>NCOA1</i>	chr2:24914466	C/T	VSCC4	1	Arg217Cys	0.3
<i>NCOA1</i>	chr2:24914466	C/T	VSCC10	1	Arg217Cys	0.1
<i>NCOR2</i>	chr12:124835222	G/A	VSCC10	1	Pro1259Leu	0.06
<i>NOTCH1</i>	chr9:139413049	G/A	VSCC12	1	Arg365Cys	0.51
<i>NOTCH1</i>	chr9:139414012	T/G	VSCC13	0.861	Thr250Pro	0.07
<i>NOTCH1</i>	chr9:139414013	G/T	VSCC13	0.999	Phe249Leu	0.07
<i>NOTCH1</i>	chr9:139414014	A/C	VSCC13	1	Phe249Cys	0.06
<i>NRG1</i>	chr8:32621592	A/G	VSCC4	1	Glu532Gly	0.27
<i>NRG1</i>	chr8:32621592	A/G	VSCC10	1	Glu532Gly	0.12
<i>PIK3CA</i>	chr3:178936091	G/A	VSCC4	0.991	Glu545Lys	0.21
<i>PIK3CA</i>	chr3:178936091	G/A	VSCC1	0.991	Glu545Lys	0.49
<i>PMS2</i>	chr7:6026988	G/A	VSCC9	0.018	Pro470Ser	0.13
<i>POLE</i>	chr12:133236034	C/T	VSCC9	0.998	Arg1041Gln	0.05
<i>PTPRB</i>	chr12:70949923	C/T	VSCC11	0.995	Asp1356Asn	0.34

<i>PTPRK</i>	chr6:128410991	C/T	VSCC9	0.046	Glu437Lys	0.07
<i>RNF213</i>	chr17:78319136	G/A	VSCC9	0	Ser407Asn	0.09
<i>SMARCA4</i>	chr19:11144179	G/A	VSCC7	0.998	Glu1254Lys	0.09
<i>SPEN</i>	chr1:16258542	G/A	VSCC9	0.063	Arg1936Gln	0.06
<i>TLX1</i>	chr10:102891414	G/A	VSCC13	0.999	Arg39His	0.08
<i>TP53</i>	chr17:7577511	A/C	VSCC12	1	Leu257Arg	0.64
<i>TP53</i>	chr17:7577539	G/A	VSCC15	1	Arg248Trp	0.13
<i>TP53</i>	chr17:7577559	G/T	VSCC7	1	Ser241Tyr	0.32
<i>TP53</i>	chr17:7577538	C/G	VSCC11	1	Arg248Pro	0.35
<i>TP53</i>	chr17:7577539	G/A	VSCC11	1	Arg248Trp	0.36
<i>TRRAP</i>	chr7:98548550	G/A	VSCC15	0.968	Glu1771Lys	0.18
<i>TRRAP</i>	chr7:98552761	G/A	VSCC10	1	Arg1899Gln	0.06
<i>UBR5</i>	chr8:103424438	G/A	VSCC15	0.659	His9Tyr	0.08
<i>ZFHX3</i>	chr16:72993621	A/T	VSCC4	1	Tyr142Asn	0.17
<i>ZFHX3</i>	chr16:72830616	C/T	VSCC7	1	Gly1989Ser	0.05
<i>ZFHX3</i>	chr16:72993621	A/T	VSCC10	1	Tyr142Asn	0.22

* UCSC GRCh37/hg19

** Probably damaging (≥ 0.957), possibly damaging ($0.453 \leq \text{score} \leq 0.956$), or benign (≤ 0.452)