Supplementary Table S1. Description of whole-exome sequencing data in vulvar squamous cell carcinoma genomes.

Sample ID*	Sequencing reads	Mapped reads	Mapped reads in exon (%)	Coverage (mean)**	Mean Mapping Quality
VSCC2N	130,834,776	129,688,911	99.12%	180.7329	47.69
VSCC2T	121,141,616	119,802,560	98.89%	166.4826	47.67
VSCC1N	108,873,584	101,450,266	93.18%	140.2559	46.35
VSCC1T	102,543,765	91,979,413	89.70%	119.6304	45.78
VSCC9N	93,766,352	80,731,420	86.10%	60.5536	40.09
VSCC9T	107,734,327	90,196,340	83.72%	90.5572	35.48
VSCC10N	127,345,527	114,240,256	89.71%	148.0099	43.24
VSCC10T	96,559,938	85,446,937	88.49%	110.5669	39.3
VSCC11N	128,231,964	111,574,728	87.01%	137.6878	40.73
VSCC11T	132,135,454	120,286,201	91.03%	155.7508	43.61
VSCC3N	117,962,142	97,118,160	82.33%	97.3511	35.3
VSCC3T	127,746,697	113,322,995	88.71%	150.9149	44.38
VSCC12N	109,560,662	97,315,317	88.82%	127.9513	43.53
VSCC12T	110,950,660	102,932,866	92.77%	141.8426	45.37
VSCC4N	128,949,031	116,385,908	90.26%	156.2992	45.86
VSCC4T	111,682,700	103,617,846	92.78%	142.5104	45.19
VSCC13N	104,841,855	95,194,320	90.80%	121.942	45.47
VSCC13T	142,470,621	130,980,313	91.93%	171.4168	45.85
VSCC5N	130,010,952	124,138,090	95.48%	170.2885	46.79
VSCC5T	122,356,923	116,311,880	95.06%	155.882	46.62
VSCC6N	115,809,030	111,841,450	96.57%	152.2072	46.95
VSCC6T	130,244,281	120,012,509	92.14%	157.5839	46.11
VSCC7N	106,964,831	90,652,715	84.75%	108.8077	39
VSCC7T	105,362,712	89,847,664	85.27%	110.4683	39.3923
VSCC8N	106,648,097	86,871,175	81.46%	94.6502	36.846
VSCC8T	115,334,272	101,124,414	87.68%	131.5968	42.6215

VSCC14N	81,411,747	69,071,600	84.84%	88.357	40.058
VSCC14T	97,631,598	88,638,870	90.79%	109.144	40.5631
VSCC15N	74,068,074	71,076,491	95.96%	95.4158	46.7404
VSCC15T	105,699,977	95,696,665	90.54%	112.3625	45.7138

* The vulvar cancer genome and matched normal genome are labeled with the use of characters ‘T’ and ‘N’, respectively.

** The mean coverage was calculated onto the targeted regions (Agilent SureSelect Human All Exome V4).