

**Supplementary Table 3** BLAST results for HPV genotyping by Sanger sequencing

Sample Info <sup>a</sup>			BLAST statistics <sup>b</sup>													
ID (query)	PAP	AMP	HSP (n)	Lowest E-val	Accession (E-val)	HPV Type <sup>c</sup>	Hit <sup>d</sup>	Total score	Max score	Min E-val	Max bit score	Max id	Max %id	Max pos	Max %pos	
PC_2994	LSIL	E6/E7	16	0	HPV39_A2REF_KC470239	39_A2	Access seq	487	487	0	937.04	531	93.16	531	93.16	
PC (3002	LSIL	E6/E7	3	0	HPV35_A2REF_HQ537727	35_A2	Access seq	540	540	0	1038.94	556	98.06	556	98.06	
PC_3010	LSIL	E6/E7	17	0	HPV39_A2REF_KC470239	39_A2	Access seq	522	522	0	1004.33	553	94.85	553	94.85	
PC_3018	LSIL	E6/E7	1	0	HPV91REF	91	Access seq	521	521	0	1002.41	526	99.43	526	99.43	
PC_3042	LSIL	E6/E7	16	0	HPV39_A2REF_KC470239	39_A2	Access seq	409	409	0	787.07	428	96.83	428	96.83	
PC_3050	LSIL	E6/E7	17	0	HPV39_A2REF_KC470239	39_A2	Access seq	585	585	0	1125.46	585	100	585	100	
PC_3058	LSIL	E6/E7	17	0	HPV39_A2REF_KC470239	39_A2	Access seq	577	577	0	1110.08	578	99.83	578	99.83	
PC_3066	LSIL	E6/E7	17	0	HPV39_A2REF_KC470239	39_A2	Access seq	584	584	0	1123.54	585	99.83	585	99.83	
PC_3074	LSIL	E6/E7	8	0	HPV91REF	91	Access seq	528	528	0	1015.87	533	99.44	533	99.44	
PC_3082	LSIL	L1	231	0	HPV66_B1REF_EF177188	66_B1	Access seq	733	733	0	662.22	370	99.2	370	99.2	
PC_3003	LSIL	E6/E7	9	0	HPV66_B1REF_EF177188	66_B1	Access seq	430	430	0	827.44	470	95.53	470	95.53	
PC_3011	LSIL	E6/E7	11	0	HPV35_A2REF_HQ537727	35_A2	Access seq	531	531	0	1021.63	554	97.71	554	97.71	
PC_3019	LSIL	E6/E7	11	0	HPV16_A1REF_EU_PPH16	16_A1	Access seq	550	550	0	1058.17	560	99.29	560	99.29	
PC_3059	LSIL	E6/E7	17	0	HPV39_A2REF_KC470239	39_A2	Access seq	557	557	0	1071.62	564	99.3	564	99.3	
PC_3067	LSIL	E6/E7	11	0	HPV16_A1REF_EU_PPH16	16_A1	Access seq	514	514	0	988.95	518	99.62	518	99.62	
PC_3075	LSIL	E6/E7	11	0	HPV16_A1REF_EU_PPH16	16_A1	Access seq	385	385	0	740.92	497	90.2	497	90.2	
PC_3083	LSIL	E6/E7	9	0	HPV58_C1REF_HQ537774	58_C1	Access seq	544	544	0	1046.63	553	98.93	553	98.93	
PC_2996	LSIL	E6/E7	1	1.586E-144	HPV62REF	62	Access seq	264	264	1.59E-144	508.28	303	93.52	303	93.52	
PC_3004	LSIL	E6/E7	17	0	HPV30_A3REF_KF436844	30_A3	Access seq	545	545	0	1048.55	555	98.93	555	98.93	
PC_3020	LSIL	E6/E7	5	2.1342E-176	HPV30_A3REF_KF436844	30_A3	Access seq	319	319	2.13E-176	614.02	439	85.91	439	85.91	
PC_3028	LSIL	E6/E7	18	0	HPV51_B1REF_KF436883	51	Access seq	557	557	0	1071.62	564	99.3	564	99.3	
PC_3036	LSIL	E6/E7	11	0	HPV16_A1REF_EU_PPH16	16_A1	Access seq	549	549	0	1056.24	559	98.59	559	98.59	
PC_3044	LSIL	E6/E7	17	0	HPV39_A2REF_KC470239	39_A2	Access seq	579	579	0	1113.92	586	99.83	586	99.83	
PC_3060	LSIL	E6/E7	17	0	HPV39_A2REF_KC470239	39_A2	Access seq	583	583	0	1121.61	585	99.83	585	99.83	
PC_3076	LSIL	E6/E7	7	2.274E-117	HPV39_A2REF_KC470239	39_A2	Access seq	217	217	2.27E-117	417.91	282	88.12	282	88.12	
PC_3084	LSIL	E6/E7	17	0	HPV39_A2REF_KC470239	39_A2	Access seq	575	575	0	1106.23	585	99.32	585	99.32	
PC_3005	LSIL	L1	267	5.427E-174	HPV53_A1REF_X74482	53_A1	Access seq	671	671	5.43E-174	606.32	340	99.13	340	99.13	
PC_3013	LSIL	E6/E7	17	0	HPV39_A2REF_KC470239	39_A2	Access seq	567	567	0	1090.85	577	98.3	577	98.3	
PC_3029	LSIL	E6/E7	9	0	HPV66_A1REF_HPU31794	66_A1	Access seq	479	479	0	921.65	510	95.68	510	95.68	
PC_3061	LSIL	E6/E7	11	0	HPV16_C1REF_AF2_AF472509	16_C1	Access seq	563	563	0	1083.16	571	98.79	571	98.79	
PC_3069	LSIL	E6/E7	8	0	HPV52_A1REF_X74481	52_A1	Access seq	446	446	0	858.21	486	92.75	486	92.75	
PC_3085	LSIL	E6/E7	4	0	HPV54_A1REF_HPU37488	54_A1	Access seq	525	525	0	1010.1	526	99.81	526	99.81	
PC_2998	LSIL	E6/E7	3	0	HPV35_A2REF_HQ537727	35_A2	Access seq	539	539	0	1037.02	557	98.76	557	98.76	
PC_3006	LSIL	E6/E7	11	0	HPV16_A2REF_EU_AF536179	16_A2	Access seq	538	538	0	1035.09	554	98.23	554	98.23	
PC_3014	LSIL	L1	275	0	HPV53_A1REF_X74482	53_A1	Access seq	740	740	0	668.53	389	97.74	389	97.74	
PC_3030	LSIL	E6/E7	11	0	HPV16_A1REF_EU_PPH16	16_A1	Access seq	561	561	0	1079.32	569	99.3	569	99.3	
PC_3038	LSIL	E6/E7	1	0	HPV91REF	91	Access seq	362	362	0	696.7	414	93.24	414	93.24	
PC_3046	LSIL	E6/E7	2	0	HPV84REF	84	Access seq	398	398	0	765.92	429	95.97	429	95.97	

Supplementary Table 3 (continued)

ID (query)	PAP	AMP	HSP (n)	Lowest E-val	Accession (E-val)	HPV Type <sup>c</sup>	Hit <sup>d</sup>	Total score	Max score	Min E-val	Max bit score	Max id	Max %id	Max pos	Max %pos
PC_3062	LSIL	E6/E7	18	0	HPV51,_A4REF_KF436875	51,_A4	Access seq	367	367	0	706.31	374	98.68	374	98.68
PC_3086	LSIL	E6/E7	3	0	HPV35,_A2REF_HQ537727	35,_A2	Access seq	481	481	0	925.5	509	95.86	509	95.86
PC_2999	LSIL	E6/E7	7	0	HPV39,_A2REF_KC470239	39,_A2	Access seq	495	495	0	952.42	545	93.8	545	93.8
PC_3007	LSIL	E6/E7	1	0	HPV40REF	40	Access seq	344	344	0	662.09	397	92.76	397	92.76
PC_3023	LSIL	E6/E7	17	0	HPV39,_A2REF_KC470239	39,_A2	Access seq	586	586	0	1127.38	586	100	586	100
PC_3031	LSIL	E6/E7	9	0	HPV58,_A2REF_HQ537752	58,_A2	Access seq	528	528	0	1015.87	539	98.72	539	98.72
PC_3039	LSIL	E6/E7	1	0	HPV81REF	81	Access seq	514	514	0	988.95	536	98.89	536	98.89
PC_3079	LSIL	E6/E7	2	0	HPV43REF	43	Access seq	511	511	0	983.18	529	98.14	529	98.14
PC_3000	LSIL	E6/E7	18	0	HPV51,_A3REF_KF436873	51,_A3	Access seq	348	348	0	669.78	363	98.11	363	98.11
PC_3024	LSIL	E6/E7	17	0	HPV39,_A2REF_KC470239	39,_A2	Access seq	554	554	0	1065.86	568	98.27	568	98.27
PC_3040	LSIL	E6/E7	2	8.2989E-161	HPV74REF	74	Access seq	292	292	8.3E-161	562.11	336	93.59	336	93.59
PC_3048	LSIL	E6/E7	17	0	HPV39,_A2REF_KC470239	39,_A2	Access seq	583	583	0	1121.61	584	99.83	584	99.83
PC_3064	LSIL	E6/E7	9	0	HPV39,_A2REF_KC470239	39,_A2	Access seq	436	436	0	838.98	475	94.43	475	94.43
PC_3072	LSIL	E6/E7	18	0	HPV51,_B2REF_KF436886	51,_B2	Access seq	356	356	0	685.16	383	96.47	383	96.47
PC_3001	LSIL	E6/E7	1	0	HPV40REF	40	Access seq	376	376	0	723.62	471	89.54	471	89.54
PC_3009	LSIL	E6/E7	11	0	HPV16,_C1REF_AF2_AF472509	16,_C1	Access seq	556	556	0	1069.7	559	99.47	559	99.47
PC_3025	LSIL	E6/E7	13	9.9772E-135	HPV67,_A2REF_HQ537780	67,_A2	Access seq	247	247	9.98E-135	475.59	330	87.77	330	87.77
PC_3049	LSIL	E6/E7	18	0	HPV51,A4REF_KF436875	51,_A	Access seq	454	454	0	873.59	502	91.77	502	91.77
PC_3057	LSIL	E6/E7	4	0	HPV54,_A1REF_HPU37488	54,_A1	Access seq	347	347	0	667.86	354	98.33	354	98.33
PC_3073	LSIL	E6/E7	11	0	HPV16,_A2REF_EU_AF536179	16,_A2	Access seq	560	560	0	1077.39	570	99.13	570	99.13
PC_3081	LSIL	E6/E7	18	0	HPV51,_A3REF_KF436873	51,_A3	Access seq	408	408	0	785.14	444	92.89	444	92.89
PC_2610	LSIL	E6/E7	58	0	HPV39,_A2REF_KC470239	39,_A2	Access seq	1066	1066	0	962.48	562	96.73	562	96.73
PC_2642	LSIL	E6/E7	58	0	HPV39,_A2REF_KC470239	39,_A2	Access seq	1138	1138	0	1027.4	579	98.81	579	98.81
PC_2690	LSIL	E6/E7	58	0	HPV43REF	43	Access seq	974	974	0	879.53	519	97.01	519	97.01
PC_2698	LSIL	E6/E7	58	0	HPV39,_A2REF_KC470239	39,_A2	Access seq	1174	1174	0	1059.86	587	100	587	100
PC_2611	LSIL	E6/E7	47	0	HPV84REF	84	Access seq	894	894	0	807.39	497	95.21	497	95.21
PC_2651	LSIL	E6/E7	60	0	HPV35,_A1REF_X74477	35,_A1	Access seq	1134	1134	0	1023.8	578	98.97	578	98.97
PC_2659	LSIL	E6/E7	57	0	HPV62REF	62	Access seq	964	964	0	870.51	506	97.12	506	97.12
PC_2675	LSIL	E6/E7	59	0	HPV68,_E1REF_KC470277	68,_E1	Access seq	1154	1154	0	1041.83	587	98.82	587	98.82
PC_2683	LSIL	E6/E7	64	0	HPV62REF	62	Access seq	902	902	0	814.61	495	95.01	495	95.01
PC_2612	LSIL	E6/E7	54	0	HPV54,_A1REF_HPU37488	54,_A1	Access seq	1028	1028	0	928.22	531	98.15	531	98.15
PC_2620	LSIL	E6/E7	55	0	HPV16,_A1REF_EU_PPH16	16,_A1	Access seq	1102	1102	0	994.94	570	97.94	570	97.94
PC_2652	LSIL	E6/E7	50	0	HPV18,_A1REF_AY262282	18,_A1	Access seq	1160	1160	0	1047.24	586	99.32	586	99.32
PC_2676	LSIL	E6/E7	15	2.75205E-98	HPV40REF	40	Access seq	392	392	2.75E-98	354.75	393	75.58	393	75.58
PC_2684	LSIL	E6/E7	65	3.8427E-127	HPV58,_A3REF_HQ537758	58,_A3	Access seq	528	498	3.84E-127	450.32	359	82.72	359	82.72
PC_2692	LSIL	E6/E7	61	0	HPV43REF	43	Access seq	1026	1026	0	926.41	529	98.14	529	98.14
PC_2700	LSIL	E6/E7	58	0	HPV39,_A2REF_KC470239	39,_A2	Access seq	1174	1174	0	1059.86	587	100	587	100
PC_2613	LSIL	E6/E7	54	0	HPV54,_A1REF_HPU37488	54,_A1	Access seq	920	920	0	830.84	475	97.74	475	97.74
PC_2621	LSIL	E6/E7	76	1.6181E-113	HPV62REF	62	Access seq	448	448	1.62E-113	405.24	374	79.24	374	79.24
PC_2637	LSIL	E6/E7	51	0	HPV52,_A1REF_X74481	52,_A1	Access seq	1108	1108	0	1000.35	557	99.64	557	99.64

**Supplementary Table 3 (continued)**

ID (query)	PAP	AMP	HSP (n)	Lowest E-val	Accession (E-val)	HPV Type <sup>c</sup>	Hit <sup>d</sup>	Total score	Max score	Min E-val	Max bit score	Max id	Max %id	Max pos	Max %pos
PC_2661	LSIL	E6/E7	54	0	HPV51,_A4REF_KF436875	51,_A4	Access seq	944	944	0	852.48	523	95.26	523	95.26
PC_2669	LSIL	E6/E7	60	0	HPV81REF	81	Access seq	806	806	0	728.04	476	90.49	476	90.49
PC_2677	LSIL	E6/E7	50	0	HPV82,_A2REF_KF436787	82,_A2	Access seq	1070	1070	0	966.09	546	98.56	546	98.56
PC_2685	LSIL	E6/E7	57	0	HPV91REF	91	Access seq	888	888	0	801.98	460	97.46	460	97.46
PC_2693	LSIL	E6/E7	61	0	HPV43REF	43	Access seq	1034	1034	0	933.63	531	98.52	531	98.52
PC_2614	LSIL	E6/E7	58	0	HPV39,_A2REF_KC470239	39,_A2	Access seq	1106	1106	0	998.55	570	97.77	570	97.77
PC_2678	LSIL	E6/E7	51	0	HPV52,_A1REF_X74481	52,_A1	Access seq	1010	1010	0	911.99	525	97.22	525	97.22
PC_2686	LSIL	E6/E7	55	0	HPV16,_A2REF_EU_AF536179	16,_A2	Access seq	1100	1100	0	993.14	569	98.44	569	98.44
PC_2702	LSIL	E6/E7	58	0	HPV39,_A2REF_KC470239	39,_A2	Access seq	1170	1170	0	1056.26	593	99.16	593	99.16
PC_2615	LSIL	E6/E7	50	0	HPV66,_B2REF_EF177187	66,_B2	Access seq	1046	1046	0	944.45	548	97.16	548	97.16
PC_2655	LSIL	E6/E7	65	0	HPV39,_A2REF_KC470239	39,_A2	Access seq	820	820	0	740.67	494	88.69	494	88.69
PC_2663	LSIL	E6/E7	60	0	HPV35,_A2REF_HQ537727	35,_A2	Access seq	1116	1116	0	1007.57	569	98.61	569	98.61
PC_2695	LSIL	E6/E7	58	0	HPV39,_A2REF_KC470239	39,_A2	Access seq	1170	1170	0	1056.26	585	100	585	100
PC_2624	LSIL	E6/E7	58	0	HPV39,_A2REF_KC470239	39,_A2	Access seq	1170	1170	0	1056.26	585	100	585	100
PC_2664	LSIL	E6/E7	52	0	HPV16,_A4REF_ASIA_EA_AF534061	16,_A4	Access seq	728	728	0	657.71	482	85.46	482	85.46
PC_2680	LSIL	E6/E7	51	0	HPV_6,_B1REF_FR751337	6,_B1	Access seq	984	984	0	888.54	510	97.51	510	97.51
PC_2696	LSIL	E6/E7	58	0	HPV39,_A2REF_KC470239	39,_A2	Access seq	1170	1170	0	1056.26	593	99.16	593	99.16
PC_3101	HSIL	E6/E7	11	0	HPV16,_A1REF_EU_PPH16	16,_A1	Access seq	562	562	0	1081.24	574	99.31	574	99.31
PC_3109	HSIL	E6/E7	11	0	HPV16,_A1REF_EU_PPH16	16,_A1	Access seq	537	537	0	1033.17	551	99.1	551	99.1
PC_3102	HSIL	E6/E7	18	0	HPV51,_A4REF_KF436875	51,_A4	Access seq	352	352	0	677.47	450	87.89	450	87.89
PC_3110	HSIL	E6/E7	17	0	HPV39,_A2REF_KC470239	39,_A2	Access seq	587	587	0	1129.31	587	100	587	100
PC_3142	HSIL	E6/E7	11	0	HPV16,_A1REF_EU_PPH16	16,_A1	Access seq	539	539	0	1037.02	546	99.09	546	99.09
PC_3103	HSIL	E6/E7	11	0	HPV16,_A1REF_EU_PPH16	16,_A1	Access seq	545	545	0	1048.55	557	98.24	557	98.24
PC_3111	HSIL	E6/E7	11	0	HPV16,_A1REF_EU_PPH16	16,_A1	Access seq	561	561	0	1079.32	565	99.65	565	99.65
PC_3119	HSIL	E6/E7	11	0	HPV16,_A1REF_EU_PPH16	16,_A1	Access seq	551	551	0	1060.09	560	98.77	560	98.77
PC_3127	HSIL	E6/E7	6	0	HPV33,_A1REF_PPH33CG	33,_A1	Access seq	504	504	0	969.72	535	96.57	535	96.57
PC_3135	HSIL	E6/E7	11	0	HPV31,_B2REF_HQ537680	31,_B2	Access seq	395	395	0	760.15	460	93.12	460	93.12
PC_3143	HSIL	E6/E7	9	0	HPV58,_A2REF_HQ537752	58,_A2	Access seq	362	362	0	696.7	376	97.66	376	97.66
PC_3104	HSIL	E6/E7	16	0	HPV39,_A2REF_KC470239	39,_A2	Access seq	906	906	0	818.21	488	94.94	488	94.94
PC_3112	HSIL	L1	0		Not Available	NA	Access seq	NA	NA	NA	NA	NA	NA	NA	NA
PC_3120	HSIL	E6/E7	11	0	HPV16,_A1REF_EU_PPH16	16,_A1	Access seq	532	532	0	1023.56	542	98.72	542	98.72
PC_3144	HSIL	E6/E7	16	0	HPV18,_A1REF_AY262282	18,_A1	Access seq	449	449	0	863.97	473	95.36	473	95.36
PC_3121	HSIL	E6/E7	18	0	HPV51,_A2REF_KF436870	51,_A2	Access seq	509	509	0	979.34	514	99.42	514	99.42
PC_3129	HSIL	E6/E7	11	0	HPV16,_A2REF_EU_AF536179	16,_A2	Access seq	563	563	0	1083.16	574	98.8	574	98.8
PC_3137	HSIL	E6/E7	11	0	HPV16,_A1REF_EU_PPH16	16,_A1	Access seq	539	539	0	1037.02	553	97.88	553	97.88
PC_3145	HSIL	E6/E7	9	0	HPV58,_A2REF_HQ537752	58,_A2	Access seq	547	547	0	1052.4	551	99.64	551	99.64
PC_3106	HSIL	E6/E7	9	0	HPV58,_A3REF_HQ537758	58,_A3	Access seq	900	900	0	812.8	502	95.08	502	95.08
PC_3114	HSIL	E6/E7	11	0	HPV16,_A2REF_EU_AF536179	16,_A2	Access seq	1130	1130	0	1020.19	574	98.8	574	98.8
PC_3122	HSIL	E6/E7	8	0	HPV52,_A1REF_X74481	52,_A1	Access seq	502	502	0	965.88	517	98.48	517	98.48
PC_3146	HSIL	E6/E7	11	0	HPV16,_A2REF_EU_AF536179	16,_A2	Access seq	559	559	0	1075.47	569	98.96	569	98.96

Supplementary Table 3 (continued)

ID (query)	PAP	AMP	HSP (n)	Lowest E-val	Accession (E-val)	HPV Type <sup>c</sup>	Hit <sup>d</sup>	Total score	Max score	Min E-val	Max bit score	Max id	Max %id	Max pos	Max %pos
PC_3107	HSIL	E6/E7	11	0	HPV16_A2REF_EU_AF536179	16_A2	Access seq	1142	1142	0	1031.01	577	99.14	577	99.14
PC_3123	HSIL	E6/E7	11	0	HPV31_C3REF_HQ537685	31_C3	Access seq	550	550	0	1058.17	559	99.11	559	99.11
PC_3131	HSIL	E6/E7	1	0	HPV62REF	<b>62</b>	Access seq	492	492	0	946.65	515	98.28	515	98.28
PC_3140	HSIL	E6/E7	11	0	HPV16_A1REF_EU_PPH16	16_A1	Access seq	552	552	0	1062.01	563	99.47	563	99.47
PC_3148	HSIL	E6/E7	11	0	HPV16_A2REF_EU_AF536179	16_A2	Access seq	489	489	0	940.88	509	96.77	509	96.77
PC_3125	HSIL	E6/E7	11	0	HPV16_C1REF_AF2_AF472509	16_C1	Access seq	566	566	0	1088.93	569	99.48	569	99.48
PC_1278	HSIL	L1	273	0	HPV16_A4REF_ASIA_EA_AF534061	16_A4	Access seq	814	814	0	735.26	407	100	407	100
PC_3149	HSIL	L1	289	0	HPV58_B2REF_HQ537764	58_B2	Access seq	767	767	0	692.88	394	98.5	394	98.5
PC_3175	HSIL	E6/E7	144	0	HPV16_C1REF_AF2_AF472509	16_C1	Access seq	946	946	0	854.28	497	96.32	497	96.32
PC_3187	HSIL	L1	257	0	HPV16_A4REF_ASIA_EA_AF534061	16_A4	Access seq	786	786	0	710.01	393	100	393	100
PC_3172	HSIL	L1	234	6.74034E-61	HPV16_A4REF_ASIA_EA_AF534061	<b>16_A4</b>	Access seq	255	255	6.74E-61	231.22	236	77.89	236	77.89
PC_3150	HSIL	L1	304	2.7766E-130	HPV61REF	<b>61</b>	Access seq	688	510	2.78E-130	461.14	341	85.89	341	85.89
PC_3163	HSIL	E6/E7	116	0	HPV16_A4REF_ASIA_EA_AF534061	16_A4	Access seq	742	742	0	670.34	427	93.03	427	93.03
PC_3178	HSIL	E6/E7	169	0	HPV16_A1REF_EU_PPH16	16_A1	Access seq	1062	1062	0	958.88	567	96.76	567	96.76
PC_3153	HSIL	E6/E7	129	0	HPV58_A2REF_HQ537752	58_A2	Access seq	794	794	0	717.22	467	91.93	467	91.93
PC_3164	HSIL	E6/E7	178	0	HPV16_C1REF_AF2_AF472509	16_C1	Access seq	1044	1044	0	942.64	560	96.39	560	96.39
PC_3179	HSIL	L1	269	0	HPV73_A1REF_X94165	73_A1	Access seq	728	728	0	657.71	393	95.62	393	95.62
PC_3190	HSIL	E6/E7	157	0	HPV16_A4REF_ASIA_EA_AF534061	16_A4	Access seq	920	920	0	830.84	490	95.52	490	95.52
PC_3154	HSIL	E6/E7	200	0	HPV35_A2REF_HQ537727	35_A2	Access seq	1000	1000	0	902.97	525	97.22	525	97.22
PC_3167	HSIL	E6/E7	198	0	HPV35_A2REF_HQ537727	35_A2	Access seq	1040	1040	0	939.04	538	97.82	538	97.82
PC_3180	HSIL	L1	265	0	HPV16_A4REF_ASIA_EA_AF534061	16_A4	Access seq	785	785	0	709.11	402	98.77	402	98.77
PC_3191	HSIL	L1	280	0	HPV16_A4REF_ASIA_EA_AF534061	16_A4	Access seq	777	777	0	701.89	390	99.74	390	99.74
PC_3155	HSIL	L1	387	4.437E-153	HPV39_A1REF_PPHT39	39_A1	Access seq	1028	594	4.44E-153	536.89	359	90.89	359	90.89
PC_3168	HSIL	E6/E7	159	0	HPV16_A2REF_EU_AF536179	16_A2	Access seq	928	928	0	838.05	525	93.58	525	93.58
PC_3181	HSIL	L1	247	0	HPV16_A4REF_ASIA_EA_AF534061	16_A4	Access seq	783	783	0	707.3	393	99.75	393	99.75
PC_3192	HSIL	E6/E7	177	0	HPV33_A2REF_HQ537698	33_A2	Access seq	1056	1056	0	953.47	545	98.38	545	98.38
PC_3169	HSIL	E6/E7	164	0	HPV16_A1REF_EU_PPH16	16_A1	Access seq	1036	1036	0	935.43	521	99.62	521	99.62
PC_3182	HSIL	E6/E7	207	0	HPV39_A2REF_KC470239	39_A2	Access seq	1016	982	0	886.74	515	96.08	515	96.08
PC_3193	HSIL	E6/E7	150	0	HPV16_A1REF_EU_PPH16	16_A1	Access seq	1064	1064	0	960.68	558	96.37	558	96.37
PC_3157	HSIL	E6/E7	141	0	HPV16_A1REF_EU_PPH16	16_A1	Access seq	1068	1068	0	964.28	549	98.39	549	98.39
PC_3173	HSIL	E6/E7	182	0	HPV35_A2REF_HQ537727	35_A2	Access seq	1100	1100	0	993.14	566	97.92	566	97.92
PC_3184	HSIL	E6/E7	167	0	HPV16_A1REF_EU_PPH16	16_A1	Access seq	1050	1050	0	948.05	545	96.63	545	96.63
PC_3195	HSIL	E6/E7	178	0	HPV18_A2REF_EF202146	18_A2	Access seq	1024	1024	0	924.61	520	99.05	520	99.05
PC_3158	HSIL	E6/E7	145	0	HPV16_A2REF_EU_AF536179	16_A2	Access seq	1000	1000	0	902.97	543	94.11	543	94.11
PC_3174	HSIL	L1	263	0	HPV16_A4REF_ASIA_EA_AF534061	16_A4	Access seq	802	802	0	724.44	401	100	401	100
PC_3186	HSIL	L1	275	0	HPV83REF	<b>83</b>	Access seq	760	760	0	686.57	386	98.97	386	98.97
PC_3171	HSIL	L1	270	0	HPV16_A4REF_ASIA_EA_AF534061	16_A4	Access seq	792	792	0	715.42	400	99.26	400	99.26

Access seq, Accession sequence name; E6/E7, HPV E6/E7 gene amplified by PCR; HSIL, high-grade squamous intraepithelial lesion; HPV, human papillomavirus; Info, information; ID, sample identification; L1, HPV L1 gene amplified by PCR; LSIL, low-grade squamous intraepithelial lesion; NA, not available/sequenceable; PAP, Pap smear; PCR, polymerase chain reaction; Query, sequence used for BLAST search; Seq, Sanger (dideoxy) sequencing

<sup>a</sup> Sample ID of LSIL ( $n = 95$ ) and HSIL ( $n = 60$ ) cervical cytology samples subjected to HPV E6/E7 or L1 gene amplification by PCR. The amplified nucleotide sequences i.e., query sequences were BLAST-aligned for HPV genotyping.

<sup>b</sup> BLAST statistics nomenclature and definitions from left to right of table columns [33].

HSP (n), Number of high scoring pairs from the source database.

Lowest E-val, Lowest Expect value.

Accession (E-val), Accession name of the matched database sequence with the lowest E-value.

HPV Type, HPV genotype (numeral), variant and sub-lineage (alphanumeric) of the Accession sequence.

Hit, Name of the sequence found in the BLAST search with the max score.

Total score, Total alignment score for all HSPs.

Max score, Maximum (best) score or highest alignment score of all HSPs.

Min E-value, Minimum (best) e-value of all HSPs.

Max bit score, Maximum (best) bit score of all HSPs.

Max id, Maximum number of identical residues in the query and Hit sequence.

Max %id, Percentage of maximum identical residues in the query and Hit sequence.

Max pos, Maximum number of similar but not necessarily identical residues in the query and Hit sequence.

Max %pos, Percentage of maximum similar but not necessarily identical residues in the query and Hit sequence.

<sup>c</sup> HPV genotype as determined by BLAST alignment of E6/E7 amplicon/Sanger-based sequences and assigned according to the best Hit result. HPV genotypes are in numerals; variant lineage and sublineage are in alphanumeric values, respectively. For non-sequenceable or interpretable E6/E7 results, HPV L1 sequencing results ( $n = 16$ ) were used alternatively for genotype determination. Samples (9/155 samples, 5.81%) with discordant HPV typing results by Sanger sequencing/BLAST and deep sequencing/taxonomic profiling are in bold.

<sup>d</sup> Hit result with the max bit score were identical to the Accession sequence.