Supplementary Table S1a

GO Categories of Upregulated Genes in HPV16 Cervix		
GO Term	**Description**	**P-value**
GO:0022402	cell cycle process	1.07E-22
GO:1903047	mitotic cell cycle process	2.44E-22
GO:0051276	chromosome organization	5.57E-18
GO:0006259	DNA metabolic process	8.99E-15
GO:0006281	DNA repair	7.44E-13
GO:0051301	cell division	2.86E-12
GO:0006260	DNA replication	1.22E-11
GO:0007067	mitotic nuclear division	1.31E-11
GO:0006996	organelle organization	6.48E-11
GO:0000280	nuclear division	7.14E-11
GO:0048285	organelle fission	1.61E-10
GO:0044770	cell cycle phase transition	1.86E-10
GO:0006974	cellular response to DNA damage stimulus	3.67E-10
GO:0044772	mitotic cell cycle phase transition	2.23E-09
GO:0007059	chromosome segregation	2.60E-09
GO:0051726	regulation of cell cycle	2.64E-09
GO:0007346	regulation of mitotic cell cycle	3.81E-09
GO:0046483	heterocycle metabolic process	5.34E-09
GO:0033554	cellular response to stress	1.02E-08
GO:0006139	nucleobase-containing compound metabolic process	1.25E-08
GO:0006725	cellular aromatic compound metabolic process	1.47E-08
GO:0007062	sister chromatid cohesion	2.25E-08
GO:0010564	regulation of cell cycle process	4.41E-08
GO:0034641	cellular nitrogen compound metabolic process	6.21E-08
GO:0016043	cellular component organization	8.53E-08
GO:0007017	microtubule-based process	9.46E-08
GO:1901360	organic cyclic compound metabolic process	1.24E-07
GO:0071840	cellular component organization or biogenesis	1.62E-07
GO:0090304	nucleic acid metabolic process	2.15E-07
GO:0044843	cell cycle G1/S phase transition	2.24E-07
GO:0000082	G1/S transition of mitotic cell cycle	2.24E-07
GO:0006807	nitrogen compound metabolic process	2.34E-07
GO:0036297	interstrand cross-link repair	9.58E-07
GO:0045930	negative regulation of mitotic cell cycle	1.03E-06
GO:1901987	regulation of cell cycle phase transition	1.13E-06
GO:1903046	meiotic cell cycle process	1.37E-06
GO:0030261	chromosome condensation	1.44E-06
GO:0098813	nuclear chromosome segregation	1.63E-06
GO:0006312	mitotic recombination	2.55E-06
GO:0045786	negative regulation of cell cycle	2.57E-06
GO:0000722	telomere maintenance via recombination	3.26E-06
GO:0051716	cellular response to stimulus	3.48E-06
GO:1901990	regulation of mitotic cell cycle phase transition	3.57E-06
GO:0006310	DNA recombination	7.55E-06
GO:0006323	DNA packaging	8.43E-06

GO:0000731	DNA synthesis involved in DNA repair	9.75E-06
GO:0006302	double-strand break repair	1.04E-05
GO:0010948	negative regulation of cell cycle process	1.16E-05
GO:0071897	DNA biosynthetic process	1.21E-05
GO:1901991	negative regulation of mitotic cell cycle phase transition	1.31E-05
GO:0042276	error-prone translesion synthesis	1.31E-05
GO:0000726	non-recombinational repair	1.33E-05
GO:0006303	double-strand break repair via nonhomologous end joining	1.33E-05
GO:0007018	microtubule-based movement	1.87E-05
GO:0019985	translesion synthesis	2.34E-05
GO:0051383	kinetochore organization	2.41E-05
GO:0009987	cellular process	2.46E-05
GO:1901988	negative regulation of cell cycle phase transition	2.82E-05
GO:0006270	DNA replication initiation	3.49E-05
GO:0045132	meiotic chromosome segregation	3.66E-05
GO:0007076	mitotic chromosome condensation	3.66E-05
GO:0007088	regulation of mitotic nuclear division	4.28E-05
GO:0006297	nucleotide-excision repair, DNA gap filling	4.41E-05
GO:0007093	mitotic cell cycle checkpoint	4.73E-05
GO:0009157	deoxyribonucleoside monophosphate biosynthetic process	4.92E-05
GO:0022616	DNA strand elongation	5.74E-05
GO:0044260	cellular macromolecule metabolic process	6.03E-05
GO:0071103	DNA conformation change	6.45E-05
GO:0000075	cell cycle checkpoint	6.96E-05
GO:0000723	telomere maintenance	7.24E-05
GO:2000134	negative regulation of G1/S transition of mitotic cell cycle	8.01E-05
GO:0000226	microtubule cytoskeleton organization	9.85E-05
GO:0009177	pyrimidine deoxyribonucleoside monophosphate biosynthetic process	1.02E-04
GO:1902806	regulation of cell cycle G1/S phase transition	1.18E-04
GO:1902807	negative regulation of cell cycle G1/S phase transition	1.19E-04
GO:0051983	regulation of chromosome segregation	1.27E-04
GO:0044237	cellular metabolic process	1.37E-04
GO:0009219	pyrimidine deoxyribonucleotide metabolic process	1.42E-04
GO:0000281	mitotic cytokinesis	1.45E-04
GO:0098840	protein transport along microtubule	1.45E-04
GO:0042073	intraciliary transport	1.45E-04
GO:0009059	macromolecule biosynthetic process	1.76E-04
GO:0009394	2'-deoxyribonucleotide metabolic process	1.78E-04
GO:0006301	postreplication repair	1.81E-04
GO:2000045	regulation of G1/S transition of mitotic cell cycle	1.83E-04
GO:0006271	DNA strand elongation involved in DNA replication	1.88E-04
GO:0051382	kinetochore assembly	2.16E-04
GO:0009162	deoxyribonucleoside monophosphate metabolic process	2.16E-04
GO:0045005	DNA-dependent DNA replication maintenance of fidelity	2.17E-04
GO:0007049	cell cycle	2.38E-04
GO:0045787	positive regulation of cell cycle	2.38E-04
GO:0032200	telomere organization	2.45E-04
GO:0010032	meiotic chromosome condensation	2.50E-04

GO:0007386	compartment pattern specification	2.50E-04
GO:0009176	pyrimidine deoxyribonucleoside monophosphate metabolic process	2.50E-04
GO:0051310	metaphase plate congression	2.52E-04
GO:0044249	cellular biosynthetic process	2.53E-04
GO:0051783	regulation of nuclear division	2.55E-04
GO:0019692	deoxyribose phosphate metabolic process	2.63E-04
GO:0044238	primary metabolic process	2.90E-04
GO:0006298	mismatch repair	3.16E-04
GO:0009262	deoxyribonucleotide metabolic process	3.76E-04
GO:0070925	organelle assembly	3.85E-04
GO:0006220	pyrimidine nucleotide metabolic process	3.87E-04
GO:0061640	cytoskeleton-dependent cytokinesis	4.45E-04
GO:0070986	left/right axis specification	4.47E-04
GO:0000086	G2/M transition of mitotic cell cycle	4.72E-04
GO:1900264	positive regulation of DNA-directed DNA polymerase activity	4.89E-04
GO:1900262	regulation of DNA-directed DNA polymerase activity	4.89E-04
GO:0006545	glycine biosynthetic process	4.89E-04
GO:0045143	homologous chromosome segregation	4.89E-04
GO:1901576	organic substance biosynthetic process	4.92E-04
GO:0044839	cell cycle G2/M phase transition	5.42E-04
GO:0009058	biosynthetic process	6.02E-04
GO:0042769	DNA damage response, detection of DNA damage	6.13E-04
GO:0071704	organic substance metabolic process	6.17E-04
GO:0000070	mitotic sister chromatid segregation	7.41E-04
GO:0000083	regulation of transcription involved in G1/S transition of mitotic cell cycle	7.41E-04
GO:0033047	regulation of mitotic sister chromatid segregation	8.30E-04
GO:0009204	deoxyribonucleoside triphosphate catabolic process	8.37E-04
GO:0009221	pyrimidine deoxyribonucleotide biosynthetic process	8.37E-04
GO:0035735	intraciliary transport involved in cilium assembly	8.37E-04
GO:0006550	isoleucine catabolic process	8.83E-04
GO:0045004	DNA replication proofreading	8.83E-04
GO:0019264	glycine biosynthetic process from serine	8.83E-04
GO:1901874	negative regulation of post-translational protein modification	8.83E-04
GO:1901873	regulation of post-translational protein modification	8.83E-04
GO:0046356	acetyl-CoA catabolic process	8.83E-04
GO:0031102	neuron projection regeneration	8.95E-04
GO:0018130	heterocycle biosynthetic process	9.15E-04
GO:0051052	regulation of DNA metabolic process	9.71E-04
GO Categories of Downregulated Genes in HPV16 Cervix		
GO Term	**Description**	**P-value**
GO:0008544	epidermis development	4.38E-09
GO:0022617	extracellular matrix disassembly	4.44E-07
GO:0033561	regulation of water loss via skin	1.71E-06
GO:0030148	sphingolipid biosynthetic process	2.68E-06
GO:0030216	keratinocyte differentiation	3.99E-06
GO:0009913	epidermal cell differentiation	5.16E-06
GO:0018149	peptide cross-linking	7.85E-06

GO:0048584	positive regulation of response to stimulus	8.29E-06
GO:0030198	extracellular matrix organization	1.00E-05
GO:0043062	extracellular structure organization	1.06E-05
GO:0046467	membrane lipid biosynthetic process	1.13E-05
GO:0061436	establishment of skin barrier	1.35E-05
GO:0043123	positive regulation of I-kappaB kinase/NF-kappaB signaling	1.44E-05
GO:0031424	keratinization	1.44E-05
GO:0043122	regulation of I-kappaB kinase/NF-kappaB signaling	1.62E-05
GO:0046330	positive regulation of JNK cascade	1.89E-05
GO:0090361	regulation of platelet-derived growth factor production	3.20E-05
GO:0000041	transition metal ion transport	3.47E-05
GO:0023056	positive regulation of signaling	3.65E-05
GO:0009967	positive regulation of signal transduction	3.85E-05
GO:0010574	regulation of vascular endothelial growth factor production	4.28E-05
GO:0048583	regulation of response to stimulus	4.43E-05
GO:0010647	positive regulation of cell communication	5.35E-05
GO:0006665	sphingolipid metabolic process	6.02E-05
GO:0090026	positive regulation of monocyte chemotaxis	7.35E-05
GO:0023051	regulation of signaling	8.30E-05
GO:0040017	positive regulation of locomotion	9.74E-05
GO:1902533	positive regulation of intracellular signal transduction	9.81E-05
GO:0010646	regulation of cell communication	9.89E-05
GO:0030335	positive regulation of cell migration	1.07E-04
GO:0032874	positive regulation of stress-activated MAPK cascade	1.11E-04
GO:0046520	sphingoid biosynthetic process	1.12E-04
GO:0001676	long-chain fatty acid metabolic process	1.18E-04
GO:0070304	positive regulation of stress-activated protein kinase signaling cascade	1.20E-04
GO:0080134	regulation of response to stress	1.45E-04
GO:0033559	unsaturated fatty acid metabolic process	1.51E-04
GO:0048871	multicellular organismal homeostasis	1.65E-04
GO:0010575	positive regulation of vascular endothelial growth factor production	1.68E-04
GO:0032101	regulation of response to external stimulus	1.77E-04
GO:0007155	cell adhesion	1.85E-04
GO:2000147	positive regulation of cell motility	1.92E-04
GO:0022610	biological adhesion	2.02E-04
GO:0006643	membrane lipid metabolic process	2.23E-04
GO:0030855	epithelial cell differentiation	2.31E-04
GO:0034330	cell junction organization	2.69E-04
GO:0051272	positive regulation of cellular component movement	2.85E-04
GO:0009966	regulation of signal transduction	3.10E-04
GO:0071677	positive regulation of mononuclear cell migration	3.33E-04
GO:0090025	regulation of monocyte chemotaxis	3.33E-04
GO:0050891	multicellular organismal water homeostasis	3.68E-04
GO:0009888	tissue development	3.94E-04
GO:0008219	cell death	4.52E-04
GO:0001817	regulation of cytokine production	4.76E-04
GO:0016241	regulation of macroautophagy	5.52E-04

GO:0046328	regulation of JNK cascade	5.64E-04
GO:0046519	sphingoid metabolic process	5.75E-04
GO:0032596	protein transport into membrane raft	5.95E-04
GO:0039532	negative regulation of viral-induced cytoplasmic pattern recognition receptor signaling pathway	5.95E-04
GO:0038034	signal transduction in absence of ligand	6.33E-04
GO:0097192	extrinsic apoptotic signaling pathway in absence of ligand	6.33E-04
GO:0045861	negative regulation of proteolysis	6.70E-04
GO:0019369	arachidonic acid metabolic process	7.51E-04
GO:0031347	regulation of defense response	8.02E-04
GO:0040012	regulation of locomotion	8.99E-04
GO:0045087	innate immune response	9.08E-04
GO:0030574	collagen catabolic process	9.17E-04

Supplementary Table S1b

GO Categories of Upregulated Genes in HPV16 Foreskin		
GO Term	**Description**	**P-value**
GO:1903047	mitotic cell cycle process	9.51E-44
GO:0022402	cell cycle process	1.19E-41
GO:0051276	chromosome organization	4.68E-31
GO:0051301	cell division	4.14E-26
GO:0044770	cell cycle phase transition	9.16E-25
GO:0044772	mitotic cell cycle phase transition	2.37E-24
GO:0006259	DNA metabolic process	2.40E-24
GO:0006260	DNA replication	2.94E-23
GO:0044843	cell cycle G1/S phase transition	3.50E-20
GO:0000082	G1/S transition of mitotic cell cycle	3.17E-19
GO:0000280	nuclear division	3.03E-18
GO:0007067	mitotic nuclear division	1.25E-17
GO:0048285	organelle fission	1.55E-17
GO:0051726	regulation of cell cycle	6.75E-17
GO:0006996	organelle organization	1.01E-16
GO:0006270	DNA replication initiation	7.68E-16
GO:0006312	mitotic recombination	6.63E-15
GO:0006281	DNA repair	8.35E-14
GO:0006974	cellular response to DNA damage stimulus	1.08E-13
GO:0007062	sister chromatid cohesion	6.66E-13
GO:0000722	telomere maintenance via recombination	1.38E-12
GO:0010564	regulation of cell cycle process	1.75E-12
GO:1903046	meiotic cell cycle process	5.77E-12
GO:0007059	chromosome segregation	8.08E-12
GO:0006310	DNA recombination	6.76E-11
GO:0016043	cellular component organization	7.98E-11
GO:0051983	regulation of chromosome segregation	9.21E-11
GO:0007017	microtubule-based process	1.33E-10
GO:0007346	regulation of mitotic cell cycle	1.59E-10
GO:0071840	cellular component organization or biogenesis	1.91E-10

GO:0007051	spindle organization	2.18E-10
GO:0007088	regulation of mitotic nuclear division	3.82E-10
GO:0098813	nuclear chromosome segregation	9.87E-10
GO:0051783	regulation of nuclear division	1.19E-09
GO:0071897	DNA biosynthetic process	1.31E-09
GO:0000226	microtubule cytoskeleton organization	2.03E-09
GO:0071103	DNA conformation change	3.68E-09
GO:0006735	NADH regeneration	3.71E-09
GO:0061718	glucose catabolic process to pyruvate	3.71E-09
GO:0061621	canonical glycolysis	3.71E-09
GO:0061620	glycolytic process through glucose-6-phosphate	5.72E-09
GO:0061615	glycolytic process through fructose-6-phosphate	5.72E-09
GO:0000731	DNA synthesis involved in DNA repair	9.00E-09
GO:0042769	DNA damage response, detection of DNA damage	1.02E-08
GO:0006007	glucose catabolic process	1.28E-08
GO:0006096	glycolytic process	1.41E-08
GO:0006090	pyruvate metabolic process	1.83E-08
GO:0006297	nucleotide-excision repair, DNA gap filling	1.91E-08
GO:0006757	ATP generation from ADP	1.92E-08
GO:0036297	interstrand cross-link repair	2.07E-08
GO:0070192	chromosome organization involved in meiotic cell cycle	2.34E-08
GO:0007052	mitotic spindle organization	2.34E-08
GO:0045786	negative regulation of cell cycle	2.84E-08
GO:1902850	microtubule cytoskeleton organization involved in mitosis	2.93E-08
GO:0033554	cellular response to stress	3.63E-08
GO:0065004	protein-DNA complex assembly	4.58E-08
GO:0051383	kinetochore organization	5.03E-08
GO:0019985	translesion synthesis	6.08E-08
GO:0006734	NADH metabolic process	7.25E-08
GO:0046031	ADP metabolic process	7.93E-08
GO:0044699	single-organism process	7.97E-08
GO:0033045	regulation of sister chromatid segregation	8.38E-08
GO:0006336	DNA replication-independent nucleosome assembly	8.88E-08
GO:0007076	mitotic chromosome condensation	9.77E-08
GO:0042276	error-prone translesion synthesis	9.87E-08
GO:0006094	gluconeogenesis	1.03E-07
GO:0019362	pyridine nucleotide metabolic process	1.04E-07
GO:0046496	nicotinamide nucleotide metabolic process	1.04E-07
GO:0034724	DNA replication-independent nucleosome organization	1.11E-07
GO:0006301	postreplication repair	1.11E-07
GO:0000723	telomere maintenance	1.38E-07
GO:0051052	regulation of DNA metabolic process	1.48E-07
GO:0051716	cellular response to stimulus	1.50E-07
GO:0006266	DNA ligation	1.55E-07
GO:0000086	G2/M transition of mitotic cell cycle	1.70E-07
GO:0030261	chromosome condensation	1.97E-07
GO:0044763	single-organism cellular process	2.11E-07
GO:0019319	hexose biosynthetic process	2.14E-07
GO:0044839	cell cycle G2/M phase transition	2.15E-07

GO:0072524	pyridine-containing compound metabolic process	2.40E-07
GO:0006139	nucleobase-containing compound metabolic process	3.28E-07
GO:0019320	hexose catabolic process	3.37E-07
GO:0034502	protein localization to chromosome	4.20E-07
GO:0071824	protein-DNA complex subunit organization	4.76E-07
GO:0000075	cell cycle checkpoint	5.31E-07
GO:0046034	ATP metabolic process	5.93E-07
GO:0034080	CENP-A containing nucleosome assembly	6.45E-07
GO:0006302	double-strand break repair	6.63E-07
GO:0000819	sister chromatid segregation	7.35E-07
GO:0000083	regulation of transcription involved in G1/S transition of mitotic cell cycle	7.35E-07
GO:0032200	telomere organization	7.57E-07
GO:0034641	cellular nitrogen compound metabolic process	7.70E-07
GO:0043486	histone exchange	7.85E-07
GO:0046364	monosaccharide biosynthetic process	7.85E-07
GO:0019674	NAD metabolic process	7.91E-07
GO:0006733	oxidoreduction coenzyme metabolic process	8.54E-07
GO:0009144	purine nucleoside triphosphate metabolic process	9.00E-07
GO:0006165	nucleoside diphosphate phosphorylation	9.57E-07
GO:0006006	glucose metabolic process	9.62E-07
GO:0060249	anatomical structure homeostasis	1.02E-06
GO:0090068	positive regulation of cell cycle process	1.03E-06
GO:0006333	chromatin assembly or disassembly	1.05E-06
GO:0070987	error-free translesion synthesis	1.25E-06
GO:0006807	nitrogen compound metabolic process	1.27E-06
GO:1901796	regulation of signal transduction by p53 class mediator	1.33E-06
GO:0006323	DNA packaging	1.52E-06
GO:0031055	chromatin remodeling at centromere	1.59E-06
GO:0009141	nucleoside triphosphate metabolic process	1.60E-06
GO:0033044	regulation of chromosome organization	1.82E-06
GO:0051984	positive regulation of chromosome segregation	1.86E-06
GO:0006296	nucleotide-excision repair, DNA incision, 5'-to lesion	1.95E-06
GO:0046605	regulation of centrosome cycle	1.96E-06
GO:0009205	purine ribonucleoside triphosphate metabolic process	2.00E-06
GO:0046483	heterocycle metabolic process	2.22E-06
GO:0046365	monosaccharide catabolic process	2.42E-06
GO:0051225	spindle assembly	2.42E-06
GO:0046939	nucleotide phosphorylation	2.42E-06
GO:0009179	purine ribonucleoside diphosphate metabolic process	2.42E-06
GO:0009135	purine nucleoside diphosphate metabolic process	2.42E-06
GO:0009987	cellular process	2.52E-06
GO:0000281	mitotic cytokinesis	2.60E-06
GO:0033683	nucleotide-excision repair, DNA incision	3.13E-06
GO:0006338	chromatin remodeling	3.19E-06
GO:0009185	ribonucleoside diphosphate metabolic process	3.41E-06
GO:0009199	ribonucleoside triphosphate metabolic process	3.63E-06
GO:0000070	mitotic sister chromatid segregation	3.88E-06
GO:0051297	centrosome organization	3.94E-06

GO:0044238	primary metabolic process	5.26E-06
GO:0006950	response to stress	5.35E-06
GO:0009123	nucleoside monophosphate metabolic process	5.39E-06
GO:0006298	mismatch repair	5.85E-06
GO:0006725	cellular aromatic compound metabolic process	6.19E-06
GO:1901360	organic cyclic compound metabolic process	7.89E-06
GO:0045787	positive regulation of cell cycle	8.56E-06
GO:0006325	chromatin organization	9.57E-06
GO:0001556	oocyte maturation	9.94E-06
GO:0009628	response to abiotic stimulus	1.03E-05
GO:0031023	microtubule organizing center organization	1.04E-05
GO:0009167	purine ribonucleoside monophosphate metabolic process	1.08E-05
GO:0051054	positive regulation of DNA metabolic process	1.10E-05
GO:0045840	positive regulation of mitotic nuclear division	1.10E-05
GO:0009126	purine nucleoside monophosphate metabolic process	1.18E-05
GO:0032787	monocarboxylic acid metabolic process	1.18E-05
GO:0051382	kinetochore assembly	1.34E-05
GO:0008608	attachment of spindle microtubules to kinetochore	1.45E-05
GO:0061640	cytoskeleton-dependent cytokinesis	1.50E-05
GO:0010032	meiotic chromosome condensation	1.52E-05
GO:0044282	small molecule catabolic process	1.58E-05
GO:0044237	cellular metabolic process	2.13E-05
GO:0006271	DNA strand elongation involved in DNA replication	2.23E-05
GO:0043044	ATP-dependent chromatin remodeling	2.33E-05
GO:0009116	nucleoside metabolic process	2.43E-05
GO:0016051	carbohydrate biosynthetic process	2.65E-05
GO:0007063	regulation of sister chromatid cohesion	2.87E-05
GO:0009161	ribonucleoside monophosphate metabolic process	2.88E-05
GO:0033043	regulation of organelle organization	3.03E-05
GO:0033047	regulation of mitotic sister chromatid segregation	3.18E-05
GO:0045930	negative regulation of mitotic cell cycle	3.38E-05
GO:0042278	purine nucleoside metabolic process	3.51E-05
GO:0072698	protein localization to microtubule cytoskeleton	3.70E-05
GO:0006334	nucleosome assembly	3.92E-05
GO:0022414	reproductive process	4.07E-05
GO:0019318	hexose metabolic process	4.14E-05
GO:0090304	nucleic acid metabolic process	4.22E-05
GO:0045931	positive regulation of mitotic cell cycle	4.23E-05
GO:0071704	organic substance metabolic process	4.37E-05
GO:0009058	biosynthetic process	4.58E-05
GO:0009132	nucleoside diphosphate metabolic process	4.92E-05
GO:0071459	protein localization to chromosome, centromeric region	5.35E-05
GO:1901576	organic substance biosynthetic process	5.80E-05
GO:0051310	metaphase plate congression	5.91E-05
GO:0051785	positive regulation of nuclear division	5.93E-05
GO:0000724	double-strand break repair via homologous recombination	6.20E-05
GO:0006268	DNA unwinding involved in DNA replication	6.72E-05
GO:0000725	recombinational repair	6.94E-05
GO:0016052	carbohydrate catabolic process	7.06E-05

GO:0044380	protein localization to cytoskeleton	7.14E-05
GO:0008152	metabolic process	7.67E-05
GO:1901990	regulation of mitotic cell cycle phase transition	7.75E-05
GO:0032392	DNA geometric change	7.76E-05
GO:0007093	mitotic cell cycle checkpoint	7.76E-05
GO:0045132	meiotic chromosome segregation	7.82E-05
GO:0051303	establishment of chromosome localization	7.93E-05
GO:1901657	glycosyl compound metabolic process	8.59E-05
GO:0007080	mitotic metaphase plate congression	8.74E-05
GO:0046128	purine ribonucleoside metabolic process	9.09E-05
GO:0055086	nucleobase-containing small molecule metabolic process	9.42E-05
GO:0044260	cellular macromolecule metabolic process	1.10E-04
GO:0009117	nucleotide metabolic process	1.12E-04
GO:0045876	positive regulation of sister chromatid cohesion	1.18E-04
GO:0051315	attachment of mitotic spindle microtubules to kinetochore	1.18E-04
GO:0032508	DNA duplex unwinding	1.25E-04
GO:0019752	carboxylic acid metabolic process	1.30E-04
GO:0044724	single-organism carbohydrate catabolic process	1.42E-04
GO:0006753	nucleoside phosphate metabolic process	1.44E-04
GO:0007131	reciprocal meiotic recombination	1.44E-04
GO:0035825	reciprocal DNA recombination	1.44E-04
GO:0022616	DNA strand elongation	1.53E-04
GO:0007141	male meiosis I	1.53E-04
GO:0050000	chromosome localization	1.55E-04
GO:0006091	generation of precursor metabolites and energy	1.60E-04
GO:0009059	macromolecule biosynthetic process	1.61E-04
GO:0070507	regulation of microtubule cytoskeleton organization	1.83E-04
GO:0009411	response to UV	1.83E-04
GO:0010638	positive regulation of organelle organization	1.95E-04
GO:1901987	regulation of cell cycle phase transition	2.07E-04
GO:0034645	cellular macromolecule biosynthetic process	2.46E-04
GO:0055114	oxidation-reduction process	2.60E-04
GO:0006890	retrograde vesicle-mediated transport, Golgi to ER	2.67E-04
GO:0007049	cell cycle	2.75E-04
GO:0007219	Notch signaling pathway	2.85E-04
GO:0032886	regulation of microtubule-based process	2.89E-04
GO:0044249	cellular biosynthetic process	2.93E-04
GO:0051988	regulation of attachment of spindle microtubules to kinetochore	2.93E-04
GO:0034728	nucleosome organization	2.95E-04
GO:0000727	double-strand break repair via break-induced replication	3.17E-04
GO:0007386	compartment pattern specification	3.17E-04
GO:0043436	oxoacid metabolic process	3.34E-04
GO:0030071	regulation of mitotic metaphase/anaphase transition	3.51E-04
GO:0090329	regulation of DNA-dependent DNA replication	3.51E-04
GO:0044702	single organism reproductive process	3.73E-04
GO:2001252	positive regulation of chromosome organization	3.81E-04
GO:0033365	protein localization to organelle	3.90E-04
GO:0034599	cellular response to oxidative stress	4.07E-04
GO:1902099	regulation of metaphase/anaphase transition of cell cycle	4.08E-04

GO:2000781	positive regulation of double-strand break repair	4.29E-04
GO:0009119	ribonucleoside metabolic process	4.49E-04
GO:2000779	regulation of double-strand break repair	4.71E-04
GO:0010965	regulation of mitotic sister chromatid separation	4.71E-04
GO:0007126	meiotic nuclear division	4.89E-04
GO:0006082	organic acid metabolic process	4.94E-04
GO:0010948	negative regulation of cell cycle process	5.21E-04
GO:0045935	positive regulation of nucleobase-containing compound metabolic process	5.28E-04
GO:0006283	transcription-coupled nucleotide-excision repair	5.42E-04
GO:1905818	regulation of chromosome separation	5.43E-04
GO:0007127	meiosis I	5.69E-04
GO:0005996	monosaccharide metabolic process	5.93E-04
GO:0000910	cytokinesis	6.00E-04
GO:1900264	positive regulation of DNA-directed DNA polymerase activity	6.18E-04
GO:1900262	regulation of DNA-directed DNA polymerase activity	6.18E-04
GO:0051299	centrosome separation	6.18E-04
GO:0007010	cytoskeleton organization	6.41E-04
GO:0043170	macromolecule metabolic process	6.54E-04
GO:0070925	organelle assembly	7.04E-04
GO:0016572	histone phosphorylation	7.08E-04
GO:0006163	purine nucleotide metabolic process	7.48E-04
GO:0044283	small molecule biosynthetic process	7.56E-04
GO:0000278	mitotic cell cycle	7.96E-04
GO:0034622	cellular macromolecular complex assembly	8.12E-04
GO:0010824	regulation of centrosome duplication	9.29E-04
GO:0009150	purine ribonucleotide metabolic process	9.58E-04
GO:0097711	ciliary basal body docking	9.62E-04

GO Categories of Downregulated Genes in HPV16 Foreskin

GO Term	Description	P-value
GO:0060337	type I interferon signaling pathway	1.85E-23
GO:0051707	response to other organism	7.00E-17
GO:0043207	response to external biotic stimulus	7.77E-17
GO:0098542	defense response to other organism	1.73E-16
GO:0002376	immune system process	2.16E-16
GO:0009607	response to biotic stimulus	2.55E-16
GO:0051607	defense response to virus	3.73E-15
GO:0009615	response to virus	6.54E-15
GO:0042221	response to chemical	5.57E-14
GO:0006952	defense response	3.43E-13
GO:0045071	negative regulation of viral genome replication	3.91E-13
GO:0009605	response to external stimulus	3.96E-13
GO:0010033	response to organic substance	3.89E-12
GO:0051704	multi-organism process	5.18E-12
GO:0044710	single-organism metabolic process	5.96E-12
GO:0019221	cytokine-mediated signaling pathway	8.52E-12
GO:0044699	single-organism process	9.20E-12
GO:0002252	immune effector process	1.05E-11
GO:1903901	negative regulation of viral life cycle	2.67E-11

GO:0050896	response to stimulus	3.60E-11
GO:0060333	interferon-gamma-mediated signaling pathway	5.22E-11
GO:0045069	regulation of viral genome replication	6.29E-11
GO:0019752	carboxylic acid metabolic process	3.06E-10
GO:0048525	negative regulation of viral process	4.21E-10
GO:0006955	immune response	5.59E-10
GO:0043901	negative regulation of multi-organism process	9.00E-10
GO:0016032	viral process	1.79E-09
GO:0044403	symbiosis, encompassing mutualism through parasitism	1.79E-09
GO:0006082	organic acid metabolic process	2.41E-09
GO:0044764	multi-organism cellular process	2.70E-09
GO:0006950	response to stress	2.83E-09
GO:0044419	interspecies interaction between organisms	3.50E-09
GO:0070268	cornification	3.65E-09
GO:0043436	oxoacid metabolic process	5.74E-09
GO:0044763	single-organism cellular process	8.67E-09
GO:0044281	small molecule metabolic process	9.69E-09
GO:0034097	response to cytokine	1.00E-08
GO:0035455	response to interferon-alpha	1.23E-08
GO:0001817	regulation of cytokine production	1.24E-08
GO:0043903	regulation of symbiosis, encompassing mutualism through parasitism	1.27E-08
GO:0050792	regulation of viral process	1.95E-08
GO:0016053	organic acid biosynthetic process	2.14E-08
GO:0046394	carboxylic acid biosynthetic process	2.14E-08
GO:0008544	epidermis development	2.43E-08
GO:0043900	regulation of multi-organism process	8.13E-08
GO:0034340	response to type I interferon	1.32E-07
GO:0008285	negative regulation of cell proliferation	1.47E-07
GO:0044283	small molecule biosynthetic process	1.65E-07
GO:0035456	response to interferon-beta	1.72E-07
GO:0044711	single-organism biosynthetic process	1.75E-07
GO:1903900	regulation of viral life cycle	1.99E-07
GO:0006629	lipid metabolic process	2.10E-07
GO:0002480	antigen processing and presentation of exogenous peptide antigen via MHC class I, TAP-independent	3.83E-07
GO:0001819	positive regulation of cytokine production	6.06E-07
GO:0016042	lipid catabolic process	7.37E-07
GO:0032675	regulation of interleukin-6 production	8.44E-07
GO:0042127	regulation of cell proliferation	1.01E-06
GO:0002474	antigen processing and presentation of peptide antigen via MHC class I	1.31E-06
GO:1901564	organonitrogen compound metabolic process	1.49E-06
GO:0002682	regulation of immune system process	1.56E-06
GO:0032787	monocarboxylic acid metabolic process	1.77E-06
GO:0012501	programmed cell death	1.88E-06
GO:0072330	monocarboxylic acid biosynthetic process	1.90E-06
GO:0008219	cell death	1.95E-06
GO:0031581	hemidesmosome assembly	1.96E-06

GO:0002479	antigen processing and presentation of exogenous peptide antigen via MHC class I, TAP-dependent	2.58E-06
GO:0019730	antimicrobial humoral response	2.58E-06
GO:0009913	epidermal cell differentiation	2.71E-06
GO:0043651	linoleic acid metabolic process	2.83E-06
GO:0006631	fatty acid metabolic process	3.59E-06
GO:0042590	antigen processing and presentation of exogenous peptide antigen via MHC class I	4.16E-06
GO:0048523	negative regulation of cellular process	4.58E-06
GO:0044712	single-organism catabolic process	4.69E-06
GO:0009056	catabolic process	5.32E-06
GO:0014070	response to organic cyclic compound	6.21E-06
GO:0048584	positive regulation of response to stimulus	6.66E-06
GO:0030216	keratinocyte differentiation	7.37E-06
GO:0050776	regulation of immune response	1.07E-05
GO:0032755	positive regulation of interleukin-6 production	1.10E-05
GO:0044255	cellular lipid metabolic process	1.11E-05
GO:0007166	cell surface receptor signaling pathway	1.15E-05
GO:0048583	regulation of response to stimulus	1.23E-05
GO:0009395	phospholipid catabolic process	1.28E-05
GO:0051239	regulation of multicellular organismal process	1.31E-05
GO:0002702	positive regulation of production of molecular mediator of immune response	1.80E-05
GO:0031349	positive regulation of defense response	1.83E-05
GO:0009968	negative regulation of signal transduction	1.83E-05
GO:0006959	humoral immune response	1.98E-05
GO:0032479	regulation of type I interferon production	2.19E-05
GO:0045087	innate immune response	2.20E-05
GO:0023057	negative regulation of signaling	2.31E-05
GO:0042178	xenobiotic catabolic process	2.60E-05
GO:0050778	positive regulation of immune response	2.89E-05
GO:0001676	long-chain fatty acid metabolic process	2.89E-05
GO:0002684	positive regulation of immune system process	2.94E-05
GO:0008150	biological_process	3.01E-05
GO:0002366	leukocyte activation involved in immune response	3.08E-05
GO:0002263	cell activation involved in immune response	3.35E-05
GO:0010648	negative regulation of cell communication	3.61E-05
GO:0006633	fatty acid biosynthetic process	4.02E-05
GO:0048585	negative regulation of response to stimulus	4.07E-05
GO:0019885	antigen processing and presentation of endogenous peptide antigen via MHC class I	4.17E-05
GO:0008610	lipid biosynthetic process	4.78E-05
GO:0006693	prostaglandin metabolic process	5.22E-05
GO:0006692	prostanoid metabolic process	5.22E-05
GO:0048519	negative regulation of biological process	5.29E-05
GO:0030855	epithelial cell differentiation	5.59E-05
GO:0018149	peptide cross-linking	5.62E-05
GO:0018916	nitrobenzene metabolic process	7.17E-05
GO:0070458	cellular detoxification of nitrogen compound	7.17E-05

GO:0046942	carboxylic acid transport	7.49E-05
GO:0050707	regulation of cytokine secretion	7.93E-05
GO:0032649	regulation of interferon-gamma production	8.59E-05
GO:1901615	organic hydroxy compound metabolic process	8.63E-05
GO:0045089	positive regulation of innate immune response	8.71E-05
GO:0048518	positive regulation of biological process	8.77E-05
GO:0002483	antigen processing and presentation of endogenous peptide antigen	9.40E-05
GO:0043122	regulation of I-kappaB kinase/NF-kappaB signaling	9.46E-05
GO:0006869	lipid transport	1.05E-04
GO:0044242	cellular lipid catabolic process	1.13E-04
GO:0055114	oxidation-reduction process	1.14E-04
GO:0050715	positive regulation of cytokine secretion	1.21E-04
GO:0015849	organic acid transport	1.22E-04
GO:0043123	positive regulation of I-kappaB kinase/NF-kappaB signaling	1.29E-04
GO:1901566	organonitrogen compound biosynthetic process	1.35E-04
GO:0032481	positive regulation of type I interferon production	1.38E-04
GO:0042742	defense response to bacterium	1.43E-04
GO:1905039	carboxylic acid transmembrane transport	1.68E-04
GO:0031347	regulation of defense response	1.79E-04
GO:0030638	polyketide metabolic process	1.82E-04
GO:0044598	doxorubicin metabolic process	1.82E-04
GO:0044597	daunorubicin metabolic process	1.82E-04
GO:0045088	regulation of innate immune response	1.82E-04
GO:0097164	ammonium ion metabolic process	1.87E-04
GO:0051241	negative regulation of multicellular organismal process	1.88E-04
GO:0050830	defense response to Gram-positive bacterium	1.92E-04
GO:0033559	unsaturated fatty acid metabolic process	2.26E-04
GO:0048660	regulation of smooth muscle cell proliferation	2.26E-04
GO:0070887	cellular response to chemical stimulus	2.41E-04
GO:0040012	regulation of locomotion	2.50E-04
GO:0022617	extracellular matrix disassembly	2.59E-04
GO:0034375	high-density lipoprotein particle remodeling	2.60E-04
GO:0042119	neutrophil activation	2.63E-04
GO:0097113	AMPA glutamate receptor clustering	2.78E-04
GO:0002741	positive regulation of cytokine secretion involved in immune response	2.78E-04
GO:0097688	glutamate receptor clustering	2.78E-04
GO:0043588	skin development	2.84E-04
GO:0010574	regulation of vascular endothelial growth factor production	2.84E-04
GO:0002720	positive regulation of cytokine production involved in immune response	2.84E-04
GO:0036230	granulocyte activation	2.85E-04
GO:0051716	cellular response to stimulus	2.87E-04
GO:0009888	tissue development	2.91E-04
GO:0048522	positive regulation of cellular process	2.91E-04
GO:0033993	response to lipid	3.02E-04
GO:0071223	cellular response to lipoteichoic acid	3.16E-04
GO:0030647	aminoglycoside antibiotic metabolic process	3.16E-04

GO:0070391	response to lipoteichoic acid	3.16E-04
GO:0044707	single-multicellular organism process	3.41E-04
GO:0022408	negative regulation of cell-cell adhesion	3.62E-04
GO:0019372	lipoxygenase pathway	3.66E-04
GO:1901700	response to oxygen-containing compound	3.72E-04
GO:0048002	antigen processing and presentation of peptide antigen	3.75E-04
GO:0002700	regulation of production of molecular mediator of immune response	3.75E-04
GO:0030334	regulation of cell migration	4.03E-04
GO:0043330	response to exogenous dsRNA	4.05E-04
GO:0034341	response to interferon-gamma	4.10E-04
GO:0071827	plasma lipoprotein particle organization	4.22E-04
GO:0071310	cellular response to organic substance	4.46E-04
GO:1903825	organic acid transmembrane transport	4.52E-04
GO:0034367	macromolecular complex remodeling	4.56E-04
GO:0034368	protein-lipid complex remodeling	4.56E-04
GO:0034369	plasma lipoprotein particle remodeling	4.56E-04
GO:0036152	phosphatidylethanolamine acyl-chain remodeling	4.56E-04
GO:0042886	amide transport	4.65E-04
GO:0009966	regulation of signal transduction	4.84E-04
GO:1901617	organic hydroxy compound biosynthetic process	4.84E-04
GO:0043691	reverse cholesterol transport	5.01E-04
GO:0009070	serine family amino acid biosynthetic process	5.01E-04
GO:0006066	alcohol metabolic process	5.06E-04
GO:0006563	L-serine metabolic process	5.10E-04
GO:0019883	antigen processing and presentation of endogenous antigen	5.10E-04
GO:0002275	myeloid cell activation involved in immune response	5.50E-04
GO:1901575	organic substance catabolic process	5.67E-04
GO:0008202	steroid metabolic process	5.70E-04
GO:0009617	response to bacterium	5.71E-04
GO:1902533	positive regulation of intracellular signal transduction	5.79E-04
GO:0009967	positive regulation of signal transduction	6.08E-04
GO:0015711	organic anion transport	6.09E-04
GO:0015804	neutral amino acid transport	6.09E-04
GO:0019731	antibacterial humoral response	6.09E-04
GO:2000145	regulation of cell motility	6.20E-04
GO:0044272	sulfur compound biosynthetic process	6.24E-04
GO:0001818	negative regulation of cytokine production	6.36E-04
GO:0035584	calcium-mediated signaling using intracellular calcium source	6.70E-04
GO:0030581	symbiont intracellular protein transport in host	6.73E-04
GO:0019060	intracellular transport of viral protein in host cell	6.73E-04
GO:0051410	detoxification of nitrogen compound	6.73E-04
GO:0051708	intracellular protein transport in other organism involved in symbiotic interaction	6.73E-04
GO:0019882	antigen processing and presentation	6.75E-04
GO:0048661	positive regulation of smooth muscle cell proliferation	6.78E-04
GO:0010035	response to inorganic substance	7.09E-04
GO:0010575	positive regulation of vascular endothelial growth factor production	7.10E-04
GO:0002218	activation of innate immune response	7.16E-04

GO:0071825	protein-lipid complex subunit organization	7.24E-04
GO:0090196	regulation of chemokine secretion	7.75E-04
GO:0010646	regulation of cell communication	7.84E-04
GO:0009108	coenzyme biosynthetic process	7.92E-04
GO:0023051	regulation of signaling	7.99E-04
GO:0002699	positive regulation of immune effector process	8.02E-04
GO:0043299	leukocyte degranulation	8.27E-04
GO:0043312	neutrophil degranulation	8.30E-04
GO:0043331	response to dsRNA	8.58E-04
GO:0032722	positive regulation of chemokine production	8.58E-04
GO:0002283	neutrophil activation involved in immune response	8.61E-04
GO:0046596	regulation of viral entry into host cell	8.72E-04
GO:0006520	cellular amino acid metabolic process	8.77E-04
GO:0032373	positive regulation of sterol transport	8.78E-04
GO:0032376	positive regulation of cholesterol transport	8.78E-04
GO:0055094	response to lipoprotein particle	8.78E-04
GO:0046597	negative regulation of viral entry into host cell	8.78E-04
GO:0006954	inflammatory response	8.89E-04
GO:0002274	myeloid leukocyte activation	8.89E-04
GO:0006690	icosanoid metabolic process	9.01E-04
GO:1901568	fatty acid derivative metabolic process	9.01E-04
GO:1904951	positive regulation of establishment of protein localization	9.21E-04
GO:0040013	negative regulation of locomotion	9.24E-04
GO:0051222	positive regulation of protein transport	9.29E-04

Supplementary Table S1c

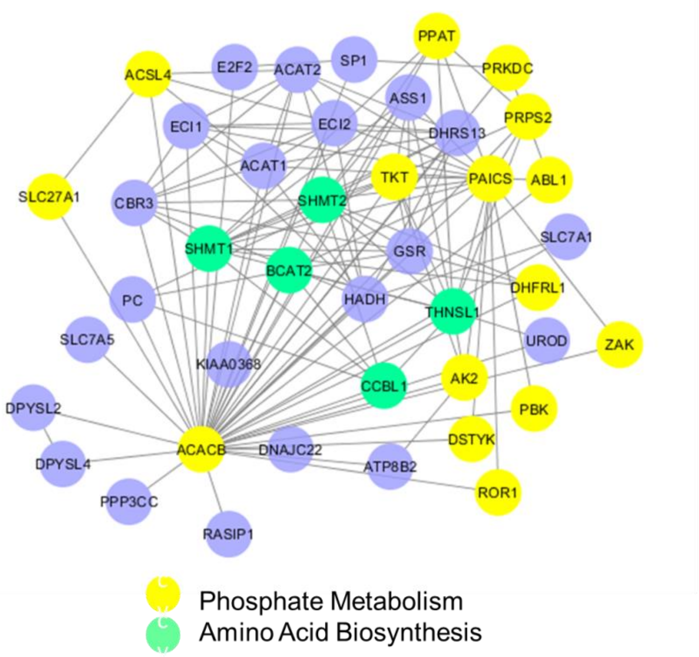
GO Categories of Upregulated Genes in HPV16 Tonsil		
GO Term	**Description**	**P-value**
GO:0022402	cell cycle process	1.25E-12
GO:1903047	mitotic cell cycle process	1.99E-09
GO:0051726	regulation of cell cycle	8.36E-08
GO:0006259	DNA metabolic process	1.61E-07
GO:0051301	cell division	3.21E-07
GO:0000280	nuclear division	6.09E-07
GO:0007067	mitotic nuclear division	9.92E-07
GO:0048285	organelle fission	1.23E-06
GO:0065004	protein-DNA complex assembly	5.43E-06
GO:0051276	chromosome organization	8.96E-06
GO:0071824	protein-DNA complex subunit organization	1.22E-05
GO:0010564	regulation of cell cycle process	1.57E-05
GO:0006260	DNA replication	1.79E-05
GO:1903046	meiotic cell cycle process	2.20E-05
GO:0006281	DNA repair	2.47E-05
GO:0006336	DNA replication-independent nucleosome assembly	3.02E-05

GO:0034724	DNA replication-independent nucleosome organization	3.25E-05
GO:0006996	organelle organization	7.05E-05
GO:0006334	nucleosome assembly	1.01E-04
GO:0006270	DNA replication initiation	1.85E-04
GO:0034728	nucleosome organization	2.33E-04
GO:0006333	chromatin assembly or disassembly	2.40E-04
GO:0007059	chromosome segregation	2.50E-04
GO:0034080	CENP-A containing nucleosome assembly	3.81E-04
GO:0000082	G1/S transition of mitotic cell cycle	4.65E-04
GO:0044843	cell cycle G1/S phase transition	4.81E-04
GO:0031055	chromatin remodeling at centromere	4.98E-04
GO:0006974	cellular response to DNA damage stimulus	5.05E-04
GO:0046605	regulation of centrosome cycle	5.31E-04
GO:0034622	cellular macromolecular complex assembly	7.25E-04
GO:0043486	histone exchange	7.56E-04
GO:0051383	kinetochore organization	8.51E-04
GO:0071103	DNA conformation change	8.59E-04
GO:0072091	regulation of stem cell proliferation	9.84E-04
GO:0046599	regulation of centriole replication	9.90E-04
GO Categories of Downregulated Genes in HPV16 Tonsil		
GO Term	**Description**	**P-value**
GO:0030198	extracellular matrix organization	9.64E-07
GO:0043062	extracellular structure organization	9.92E-07
GO:0031581	hemidesmosome assembly	7.48E-06
GO:0008544	epidermis development	1.07E-05
GO:0007155	cell adhesion	4.44E-05
GO:0022610	biological adhesion	4.70E-05
GO:0042127	regulation of cell proliferation	6.60E-05
GO:0030335	positive regulation of cell migration	6.82E-05
GO:0050921	positive regulation of chemotaxis	7.62E-05
GO:0032967	positive regulation of collagen biosynthetic process	7.78E-05
GO:0010714	positive regulation of collagen metabolic process	8.87E-05
GO:0044253	positive regulation of multicellular organismal metabolic process	8.87E-05
GO:2000147	positive regulation of cell motility	8.94E-05
GO:0051272	positive regulation of cellular component movement	1.06E-04
GO:0030334	regulation of cell migration	1.25E-04
GO:0090023	positive regulation of neutrophil chemotaxis	1.27E-04
GO:0001887	selenium compound metabolic process	1.30E-04
GO:0040017	positive regulation of locomotion	1.41E-04
GO:0006954	inflammatory response	1.48E-04
GO:0022617	extracellular matrix disassembly	1.61E-04

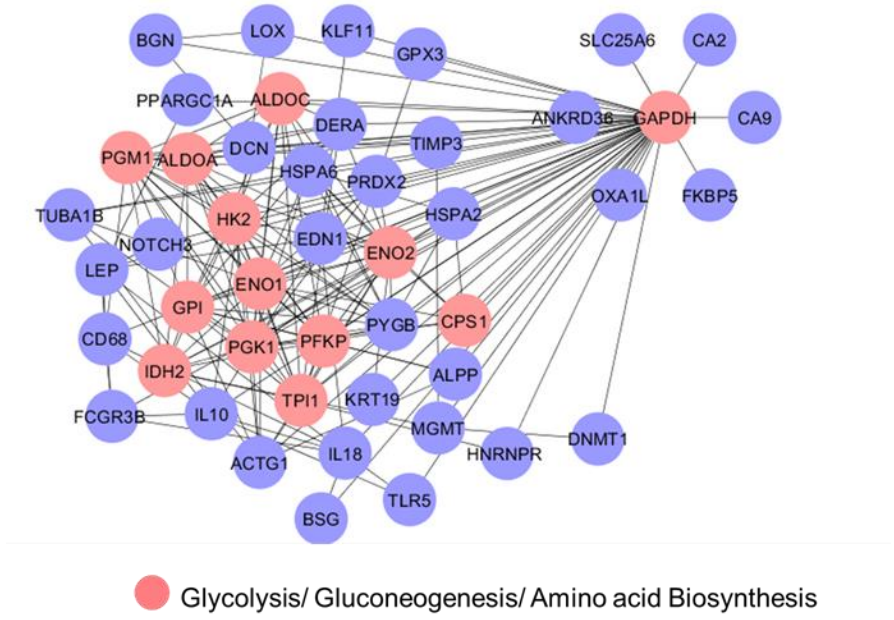
GO:0048870	cell motility	1.74E-04
GO:0071624	positive regulation of granulocyte chemotaxis	1.75E-04
GO:1902624	positive regulation of neutrophil migration	1.75E-04
GO:0032965	regulation of collagen biosynthetic process	1.75E-04
GO:0090022	regulation of neutrophil chemotaxis	2.13E-04
GO:1901342	regulation of vasculature development	2.18E-04
GO:0002690	positive regulation of leukocyte chemotaxis	2.28E-04
GO:2000145	regulation of cell motility	2.29E-04
GO:0010712	regulation of collagen metabolic process	2.79E-04
GO:1902622	regulation of neutrophil migration	2.79E-04
GO:0044246	regulation of multicellular organismal metabolic process	3.03E-04
GO:0050920	regulation of chemotaxis	3.28E-04
GO:0016477	cell migration	3.47E-04
GO:0044763	single-organism cellular process	3.81E-04
GO:0060326	cell chemotaxis	3.98E-04
GO:0007044	cell-substrate junction assembly	4.15E-04
GO:0032940	secretion by cell	4.33E-04
GO:0051270	regulation of cellular component movement	4.41E-04
GO:0032496	response to lipopolysaccharide	4.47E-04
GO:0002688	regulation of leukocyte chemotaxis	4.50E-04
GO:0040011	locomotion	4.58E-04
GO:0040012	regulation of locomotion	4.59E-04
GO:0006935	chemotaxis	5.42E-04
GO:0042330	taxis	5.52E-04
GO:0071622	regulation of granulocyte chemotaxis	5.89E-04
GO:0002237	response to molecule of bacterial origin	5.95E-04
GO:0090303	positive regulation of wound healing	6.28E-04
GO:0002687	positive regulation of leukocyte migration	6.96E-04
GO:1903036	positive regulation of response to wounding	9.52E-04
GO:0033993	response to lipid	9.84E-04

Supplementary Figure S1: Protein interaction networks depict metabolism related pathways enriched in the HPV16 cervical (a) and foreskin (b) tissue, among the upregulated genes. (a) Highlighted in yellow and green are proteins involved in phosphate metabolism and amino acid biosynthesis, respectively. (b) Highlighted in peach are proteins with overlapping functions in glycolysis, gluconeogenesis and amino acid biosynthesis.

a. Upregulated Genes HPV16 cervical tissue



b. Upregulated Genes in HPV16 foreskin tissue



Supplementary Figure S2: Protein interaction network depicts Fanconi Anemia pathway and DNA repair proteins to be upregulated in the HPV16 foreskin tissue.

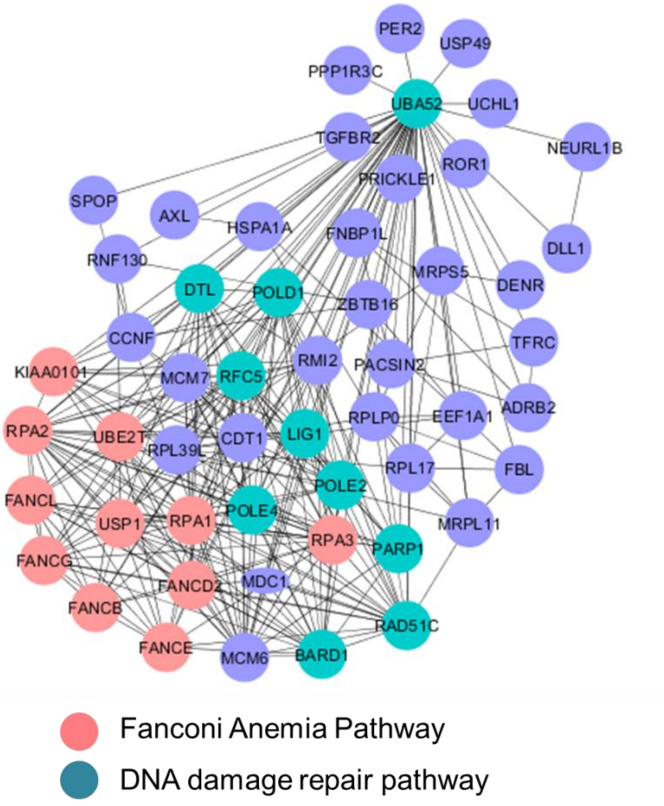


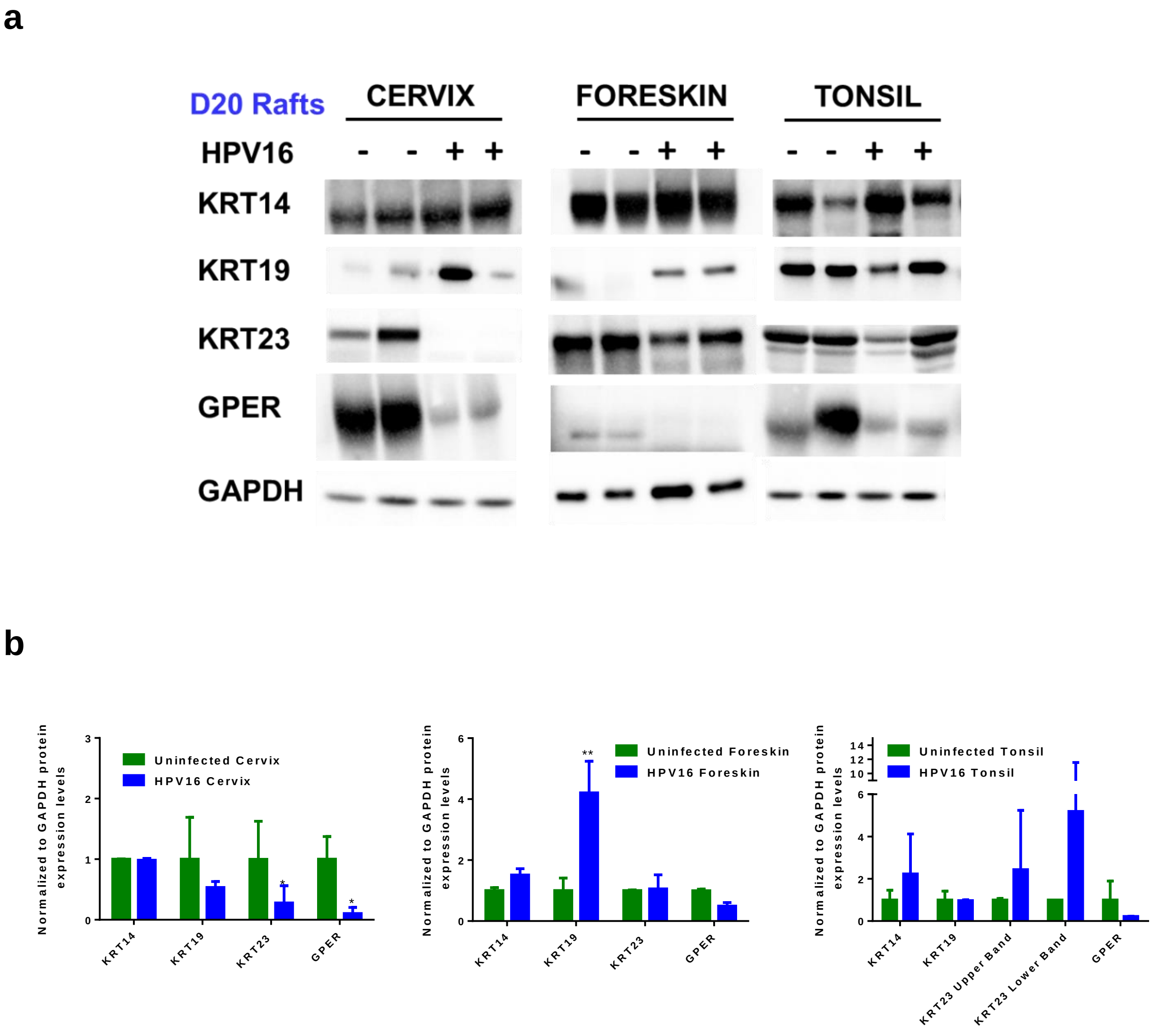
Table S2: Fanconi Anemia Complementation Group (FANC) genes upregulated in the HPV16 cervical, foreskin and tonsil tissue. The fold changes are included within brackets.

HPV16 Cervix	HPV16 Foreskin	HPV16 Tonsil
FANCC (1.68)	FANCB (2.16)	FANCE (1.74)
FANCD2 (2.06)	FANCD2 (1.63)	
FANCE (4.18)	FANCE (1.55)	
	FANCG (1.99)	
	FANCL (1.65)	

Supplementary Table S3: Table shows the progeny virus titers obtained from the rafts used for RT-PCR and western blot validation experiments. Virus titers were determined using established protocols in the laboratory, from rafts harvested at D20.

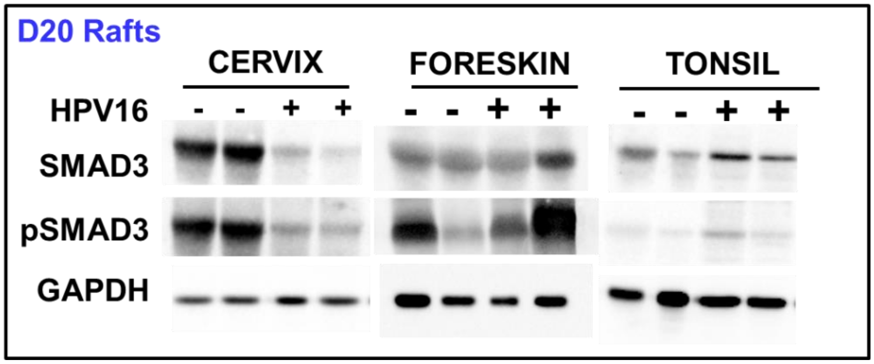
Raft Identification	No. of virus particles per raft
HPV16 Cervical raft #1	9.38×10^7
HPV16 Cervical raft #2	5.25×10^8
HPV16 Foreskin raft #1	7.7×10^6
HPV16 Foreskin raft #2	3.15×10^7
HPV16 Tonsil raft #1	3.6×10^7
HPV16 Tonsil raft #2	4.28×10^7

Supplementary Figure S3: Western blot analysis for KRT14, KRT19, KRT23 and GPER from D20 rafts of uninfected and infected cervix, foreskin and tonsil. Cell lysates from two uninfected and HPV16 infected rafts were used for western blot analysis. (a) Representative western blots indicating the protein levels of KRT14, KRT19, KRT23 and GPER. GAPDH is used as a loading control. (b) The histograms represent average expression levels of the proteins normalized to GAPDH levels (Mean + SEM), for each of the tissue types, obtained from at least three independent experiments. * indicates p value<0.05.



Supplementary Figure S4: Western Blot showing SMAD3/pSMAD3 expression levels in rafts harvested at D20 from uninfected and HPV16 infected cervical, foreskin and tonsil tissue. Cell lysates from two uninfected and HPV16 infected rafts for each tissue types, were used for western blot analysis. (a) Representative blot images showing protein expression levels of SMAD3, pSMAD3 in the uninfected and HPV16 positive cervix, tonsil and foreskin rafts. GAPDH is used as a loading control. (b) Histograms represent average ratios of SMAD3 and pSMAD3 levels normalized to GAPDH (Mean + SEM), obtained from at least three independent experiments. * indicates p value<0.05.

a



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