

**Cell Reports, Volume 42**

**Supplemental information**

**Human papillomavirus E5**

**suppresses immunity via inhibition**

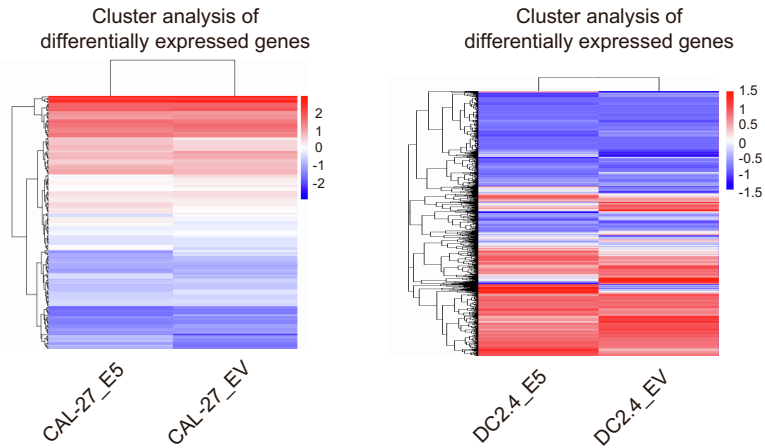
**of the immunoproteasome and STING pathway**

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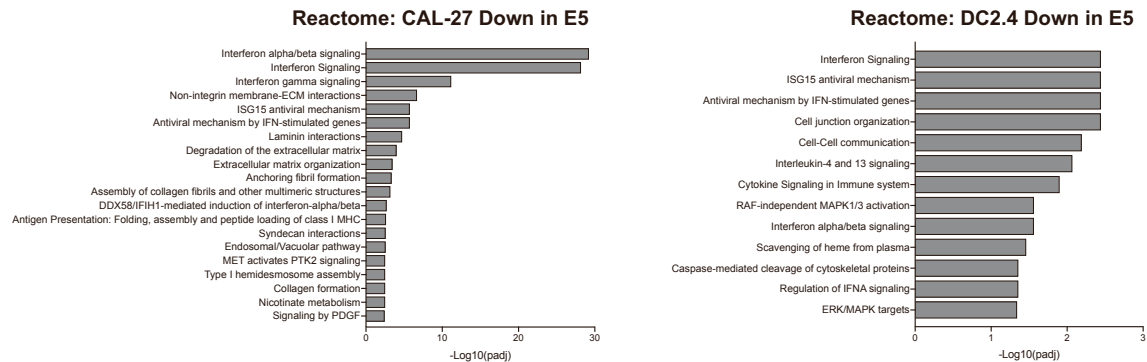
# Supplementary Information

## Supplementary Figure 1

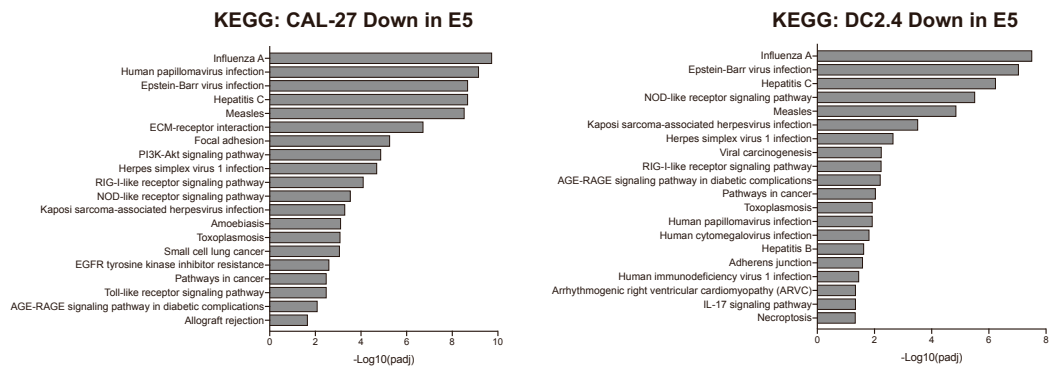
**A**



**B**



**C**



### Supplementary Figure 1: HPV E5 downregulated viral response pathways

**A)** Heatmap of differentially expressed genes. **B)** Reactome analysis of downregulated gene sets. **C)** KEGG analysis of downregulated gene sets.

**Supplementary Table 1: Top downregulated genes in E5-positive CAL-27**

<b>Gene Name</b>	<b>Fold change</b>	<b>Adjusted P-value</b>	<b>FPKM CAL-27 EV</b>	<b>FPKM CAL-27 E5</b>
OASL	0.20585494	5.28E-116	28.2547705	2.16472548
DDX60	0.27654765	2.07E-88	14.0582601	2.35425262
RSAD2	0.3526967	3.46E-45	7.93781042	0.64969887
IFIT3	0.38804611	9.74E-55	49.6632345	14.7160041
IFIT1	0.40189764	3.23E-38	18.7138658	4.5901364
IFI44	0.42322595	3.44E-44	64.4497237	21.1996557
MX1	0.42398937	1.24E-50	33.2535915	11.5402072
DDX58	0.45426309	8.85E-34	14.4226315	4.96366001
ISG15	0.45697907	9.04E-39	165.093363	61.2381005
IFIT2	0.46245984	1.84E-31	20.8820024	7.26362257
IFI27	0.47067398	1.25E-31	37.0986363	13.5801914
XAF1	0.51819249	2.13E-17	6.3929787	1.74286583
IFI6	0.53665618	3.57E-17	64.3272435	24.6398335
CMPK2	0.53712881	1.24E-15	8.98404844	2.84133502
MX2	0.55431194	5.73E-14	5.74477118	1.84536607
IFI44L	0.55979092	2.89E-15	2.96353893	0.40546305
OAS3	0.5808832	3.99E-30	46.5294403	25.0894155
FGF2	0.58795188	3.84E-11	2.61036847	0.82970054
HELZ2	0.58908185	8.69E-22	18.1552128	9.65857185
OAS2	0.59776901	2.74E-16	19.2031441	10.0204605
SAMHD1	0.59812959	1.37E-14	14.7453687	7.49327483
HERC6	0.60461136	6.25E-10	5.54509733	2.01038865
SAMD9L	0.60815459	3.43E-11	5.76178799	2.75429105
TRIM22	0.60825155	4.96E-10	9.8351385	4.22694954
HERC5	0.61005026	6.44E-11	3.07628624	0.59746944
OAS1	0.62073956	4.70E-09	14.7297645	6.38642767
IL7R	0.64212675	5.28E-14	24.4826588	14.3186334
EPSTI1	0.65724811	7.23E-07	3.27352964	1.21220196
CXCL11	0.66512159	2.09E-06	10.0823504	4.05635429
GBP4	0.6668342	2.73E-06	2.82929781	1.21391394
ZC3HAV1	0.66859293	5.67E-13	20.9096906	12.9883044
PLEKHG4B	0.67100713	1.91E-06	2.90346572	1.5102178
DDX60L	0.6914611	3.37E-05	3.65152642	1.86458059
CCND2	0.69286203	4.12E-05	2.38497946	1.05011191
HLA-B	0.70059374	9.48E-09	137.00686	88.923987
IRF7	0.70527118	0.00013977	7.84847568	3.74171508
STAT2	0.70753332	5.10E-10	44.7714327	29.8922999
CXCL10	0.72080454	0.00023756	8.90919336	3.48256381
DHX58	0.72092446	0.00044284	5.1013706	2.30511518
HLA-DPA1	0.72521466	0.00030729	6.81365709	4.14931752
SAMD9	0.72920684	3.40E-08	22.5532906	15.5921649
FBN2	0.73614405	5.62E-05	6.27815436	4.19834159
LY6E	0.73803442	8.10E-07	164.859424	114.794171
RP11-1E6.1	0.73905826	0.0015712	18.6255058	8.35772182
PARP14	0.74022717	1.14E-07	19.3471161	13.629367
LAPTM5	0.74264261	4.34E-07	60.7685332	42.8497939
ZNF1	0.74478711	4.34E-08	28.342725	20.2228719
AXL	0.74643058	4.53E-07	42.061007	29.8624855
ANKRD10	0.74788067	1.09E-05	42.0754343	29.5137203

**Supplementary Table 2: Top upregulated genes in E5-positive CAL-27**

<b>Gene Name</b>	<b>Fold change</b>	<b>Adjusted P-value</b>	<b>FPKM CAL-27_EV</b>	<b>FPKM CAL-27_E5</b>
<b>KRT16</b>	1.62881189	8.68E-22	65.1833556	113.540158
<b>PI3</b>	1.56110762	2.13E-15	211.513756	356.484238
<b>NDRG1</b>	1.5380581	1.07E-10	15.1308274	26.1903942
<b>LUM</b>	1.52260318	8.57E-07	3.08267475	6.85535927
<b>CA12</b>	1.48407088	2.73E-06	2.4746019	4.69918787
<b>SPRR1B</b>	1.46937232	6.29E-07	44.1338198	75.4437704
<b>TNFRSF10D</b>	1.43243532	1.91E-06	9.03672119	14.6092984
<b>TMPRSS11D</b>	1.42016642	0.00011667	4.05690481	7.70654042
<b>KRT17</b>	1.40296595	1.07E-09	271.062116	399.056226
<b>SLPI</b>	1.39983812	6.67E-08	286.91989	427.877323
<b>SPRR1A</b>	1.39911059	0.00028724	21.1559697	38.1828552
<b>GPNMB</b>	1.38536872	0.00036267	6.23736914	10.6161984
<b>DSG3</b>	1.37456011	3.43E-11	34.498636	48.9027974
<b>LTF</b>	1.35281072	3.15E-05	0.35760137	1.91497023
<b>IL1RAP</b>	1.34642139	6.29E-07	29.7671368	41.9652561
<b>ABCA13</b>	1.34146554	0.0002346	2.11981707	3.11482501
<b>AHNAK2</b>	1.33863255	1.43E-06	5.00543432	7.00648461
<b>CLCA2</b>	1.33149776	0.00058978	8.42548094	12.3478012
<b>KRT1</b>	1.32683594	0.0071531	3.61845454	6.61939069
<b>KRT6B</b>	1.32657845	2.16E-05	31.4542266	44.031796
<b>CTSC</b>	1.32497946	1.14E-07	108.070891	147.753696
<b>GJB6</b>	1.31792658	0.0077091	2.70260136	5.40744353
<b>FABP5</b>	1.30589599	0.0018975	54.1001418	77.1381011
<b>LRRC8C</b>	1.30271365	0.0053041	3.64925009	5.29690218

**Supplementary Table 3: Top downregulated genes in E5-positive DC2.4**

Gene Name	Fold change	Adjusted <i>P</i> -value	FPKM DC2.4 EV	FPKM DC2.4 E5
Ly6c2	0.26473117	7.54E-78	37.8857195	8.04235854
Syne2	0.29160755	8.77E-41	1.91561867	0.34139549
Ifit2	0.31514769	1.63E-89	71.8279836	20.36798
Siglec1	0.31707587	9.65E-32	4.62693901	0.78105596
Tinagl1	0.35225693	5.40E-45	41.7094247	12.2062977
Pyhin1	0.3553469	1.41E-24	7.59518274	1.37840744
Ifit3	0.36455288	2.62E-24	16.48767	3.44003573
Erich3	0.37956004	2.32E-22	4.34208926	0
Bcor	0.39291795	2.53E-30	8.71442236	2.75193113
Ifi204	0.39878969	2.33E-27	24.9337321	7.79140053
Ifit1	0.40086823	1.01E-40	50.799994	17.9649303
Apol9b	0.40125743	2.36E-33	56.7842438	19.2443502
Gbp3	0.40460891	2.48E-25	17.3159943	5.39121417
Mpeg1	0.43155011	2.17E-18	7.52927912	2.29161454
Sfn4	0.44590244	1.73E-41	71.6897978	29.6451154
Eya2	0.44794702	7.82E-15	9.4013417	2.58770032
Apol9a	0.44850625	1.83E-26	60.3127618	23.5008423
Ccl2	0.46933827	1.76E-30	217.283927	93.0200214
Ddx60	0.47721126	1.96E-20	11.6463808	4.78296755
Saa3	0.47827093	9.77E-12	35.031086	8.7007943
Gbp7	0.47830408	1.34E-35	34.545993	15.4675027
Lgals9	0.48659723	1.34E-30	92.2877428	41.6883014
Sfn2	0.49076355	1.17E-21	55.8428841	24.3992852
Ephb2	0.49530875	2.99E-11	1.89493123	0.61031994
C3	0.49640859	5.19E-32	40.4331438	18.8604452
Parp14	0.49927272	3.56E-37	37.9631656	18.0431458
Oasl2	0.50325099	4.51E-35	119.93654	57.3541345
Ifi203	0.5056216	1.88E-27	75.8344812	35.7747479
Isg20	0.50563211	1.88E-14	54.0722455	22.6544335
Phf11d	0.50791888	1.05E-27	54.7725304	26.0122539
Ili1b	0.51473436	1.34E-09	8.24508305	1.64070787
Cmpk2	0.5170838	5.66E-20	35.8001685	16.8205316
Gbp2	0.52186914	4.80E-09	5.47303245	1.50450766
Rsad2	0.52362649	2.47E-25	57.4813494	28.2502193
Herc6	0.52449466	3.54E-18	16.265493	7.70851234
Sfn5	0.52705667	7.36E-09	2.79814516	0.63916655
Gimap9	0.53242492	5.21E-09	14.2778844	5.15018576
Cxcl10	0.53397348	1.24E-08	17.3241766	5.82031023
Dhx58	0.53427336	1.20E-18	35.1650595	17.2242221
Irf7	0.53428447	6.53E-39	193.31785	100.129322
Cxcr2	0.53462159	4.85E-09	2.75347903	0.41852435
Ifih1	0.54815659	4.21E-18	20.4669263	10.3956105
Met	0.55145306	6.38E-15	10.6711307	5.33694879
BC007180	0.55150658	1.97E-10	0.97688675	0
Ifitm3	0.55285383	4.77E-19	304.203158	157.187693
Myl1	0.55445797	2.62E-10	5.0722773	0
Igtp	0.55546195	1.20E-10	21.0184571	9.92726236
Map1a	0.55774594	9.50E-09	2.58084022	1.13188839
Isg15	0.55780779	2.45E-24	287.439026	153.227294
Bco2	0.5592247	2.02E-09	15.9099322	7.31125143
Irg1	0.56027227	3.51E-07	4.8189983	1.45549717
Gimap4	0.56090564	7.83E-08	4.26611991	0.70666583
Ly6a	0.56229924	9.48E-08	9.60156683	1.63583036
Trim12c	0.56816426	1.75E-12	18.364503	9.40676187
Ocstamp	0.57405465	7.10E-07	4.80622814	1.91163989
Sp100	0.57554475	2.77E-17	31.7461403	17.2384373
Znfx1	0.57753088	2.08E-29	43.3329523	24.3672103
Stat2	0.57788727	7.18E-17	38.1774272	20.8175429
Tgtp2	0.58163662	2.61E-06	4.98042026	1.7245595
Enpp4	0.58253232	7.92E-13	16.1996997	8.69184534
Sdc3	0.58562945	4.16E-12	14.4249172	7.75142771
Gbp6	0.58673868	2.21E-06	2.25270861	0.55291198
Irgm1	0.58712517	2.94E-21	44.5642732	25.2004588
Samd9l	0.58731647	5.27E-19	33.1728316	18.6533091
Helz2	0.58878793	1.02E-31	55.6672659	32.1154748
Parp9	0.58973552	2.08E-20	50.8941578	28.8836805
Klf2	0.59106553	5.18E-10	28.5261622	15.134781
Phf11b	0.59107373	5.83E-06	9.18529333	2.92554395
Stat1	0.59877255	7.88E-11	13.10114	7.19678653
Xaf1	0.59967802	2.67E-11	27.0890742	15.0021322

**Supplementary Table 4: Top upregulated genes in E5-positive DC2.4**

Gene Name	Fold change	Adjusted P-value	FPKM DC2.4 EV	FPKM DC2.4 E5
<b>Slc43a3</b>	8.90243502	6.62E-118	0.45956638	20.497042
<b>Chm</b>	6.33392595	5.72E-75	0.00684038	5.83725985
<b>Igf2r</b>	4.62835652	1.45E-112	2.49136084	14.7368281
<b>Hk3</b>	4.12816318	2.05E-58	2.89685488	19.7741695
<b>Inpp4b</b>	3.83174087	3.95E-39	0.1957859	3.90599108
<b>Rgs1</b>	3.78895499	1.14E-44	0.96254556	7.0898984
<b>Itgam</b>	3.7685251	2.76E-71	3.80418986	18.7171052
<b>Chchd10</b>	3.6007564	6.98E-36	0.17291171	16.9110059
<b>Gpmb</b>	3.48824168	8.75E-223	59.2076901	219.178699
<b>Pde3b</b>	3.42190569	7.48E-33	0.08972205	2.57952151
<b>Cd36</b>	3.15054191	1.33E-28	0.47591795	5.33561727
<b>N4bp2</b>	2.93365659	1.25E-25	0.05440088	1.53229408
<b>Lincenc1</b>	2.93284332	2.04E-26	1.54084519	9.60705575
<b>Dock10</b>	2.69260014	5.82E-34	2.65445288	9.16684435
<b>Gpr65</b>	2.68235466	7.64E-24	3.29951312	14.8663267
<b>Ddr2</b>	2.6158866	6.08E-21	0.05574313	1.48401119
<b>Hpgds</b>	2.48457656	5.26E-18	0.43313898	4.00450499
<b>Cst7</b>	2.38700237	2.33E-16	1.99139468	14.6679408
<b>Fam213a</b>	2.17588152	5.27E-13	2.10496534	9.94239511
<b>Rgs2</b>	2.10351193	2.14E-16	5.62612537	15.116801
<b>Atp1a3</b>	2.05523021	1.83E-13	2.79744313	7.84741094
<b>Tle3</b>	1.99563794	2.10E-27	6.57824811	14.3462396
<b>Abcb4</b>	1.96719504	2.56E-10	1.92001438	5.90042111
<b>Arsg</b>	1.96309501	2.62E-15	7.01337978	16.4270845
<b>Lmo2</b>	1.95607271	1.90E-30	55.6084602	116.82351
<b>F5</b>	1.93796162	2.99E-10	0.12774523	1.13828779
<b>Lcp2</b>	1.91276548	4.22E-14	5.94840007	13.5098457
<b>C130026I21Rik</b>	1.90946702	1.83E-09	0.73940969	4.81694464
<b>Bahcc1</b>	1.90228051	2.45E-09	0.15304315	0.96433363
<b>Kcnk13</b>	1.88131314	1.26E-08	1.6054748	5.25074646
<b>Frmd4b</b>	1.85312474	7.92E-10	0.09404738	1.49918252
<b>Fam63a</b>	1.8401457	1.80E-37	42.7628947	82.2399708
<b>Abcd2</b>	1.79244643	7.22E-09	0.09968091	1.32099872
<b>Mcoln2</b>	1.76406045	2.41E-07	3.20327793	8.07017656
<b>Gm15433</b>	1.74023242	1.14E-06	3.52595314	13.2340858
<b>Gpr176</b>	1.72960188	2.39E-07	2.79210121	6.33060458
<b>Selplg</b>	1.71969176	9.85E-07	0.69707114	3.38250772
<b>Btbd3</b>	1.7147283	1.21E-08	0.02022204	1.08431471
<b>Atf3</b>	1.71292264	5.40E-08	9.23745287	19.3484612
<b>Cacna1a</b>	1.70334421	4.14E-06	0.69364653	1.94377867
<b>Rapgef5</b>	1.70237633	1.26E-07	0.12251547	1.46760856
<b>AI504432</b>	1.69101564	1.31E-06	0.23521782	1.32258641
<b>Vwf</b>	1.66199956	1.25E-05	0.3793649	1.25149988
<b>Pou2f2</b>	1.65786898	1.62E-05	0.54999942	1.63248578
<b>Phc1</b>	1.62959109	1.78E-07	0.02338476	1.10937897
<b>Runx3</b>	1.62409948	7.20E-08	7.90820689	14.6084937
<b>Hist1h1c</b>	1.62010801	1.23E-21	97.1804108	163.756222
<b>Tmem176b</b>	1.60993228	5.23E-05	4.63661582	10.8335128

**Supplementary Table 5: Primer sequences (qPCR)**

	Forward	Reverse
<b>hGAPDH</b>	GCAAATTCATGGCACCCTC	TCGCCCCACTTGATTTTGGG
<b>hPSMB8</b>	TTACCTGCTTGGCACCATGT	GCTGCCGACACTGAAATACG
<b>hPSMB9</b>	ACAGCCTTTTGGCATTGGTG	GCAATAGCGTCTGTGGTGAAG
<b>hTAP1</b>	CCAGTGGTCTGTTGACTCCC	AATGTCAGCCCCTGTAGCAC
<b>hTAP2</b>	CCTTGAACAATGTCGGCAGC	AAGTGCAGCACCCCTCCTTAC
<b>hMX1</b>	CAGCCTGCTGACATTGGGTA	CATTACTGGGGACCACCACC
<b>hOAS2</b>	CAGGAACCCGAACAGTTCCC	AGGACAAGGGTACCATCGGA
<b>hSTAT1</b>	CACCTAACGTGCTGTGCGTA	CCACTGAGACATCCTGCCAC
<b>hIFIT1</b>	ATGCGATCTCTGCCTATCGC	CCTGCCTTAGGGGAAGCAA
<b>hDDX58</b>	AGAGCACTTGTGGACGCTTTA	TTGTTTTGCCACGTCCAGTC
<b>hIFIH1</b>	TTGGACTCGGGAATTCGTGG	AACGATGGAGAGGGCAAGTC
<b>hSTING1</b>	CATGGGCTGGCATGGTCATA	CCCCGTAGCAGGTTGTTGTA
<b>hCGAS</b>	CTGGCTTTCAGCAAAAGTTAGG	GATAGCCGCCATGTTTCTTCTTG
<b>hIFNB1</b>	CTTTGCTCTGGCACAACAGG	GTGGAGAAGCACAACAGGAGA
<b>mGapdh</b>	TATGTCGTGGAGTCTACTGG	GAGTTGTCATATTTCTCGTG
<b>mPsmb8</b>	GGAACGCATCTCCGTGTCTG	AGTCCTGGTCCCTTCTTGTC
<b>mPsmb9</b>	CCACACCGGGACAACCATC	GAGGGGAGAGCTTGTCGAAC
<b>mTap1</b>	CTTGATCCGGAAGCCACTCC	GCTGAGCTGCTGGGTGATAA
<b>mTap2</b>	GCAGATTCTGGCTGGAGAGG	ACGTTGCTCAGCATATCCCC
<b>mIfnb1</b>	TGGGAGATGTCCTCAACTGC	CCAGGCGTAGCTGTTGTA