

## Supplementary Materials for

### **Allele-specific long-distance regulation dictates IL-32 isoform switching and mediates susceptibility to HIV-1**

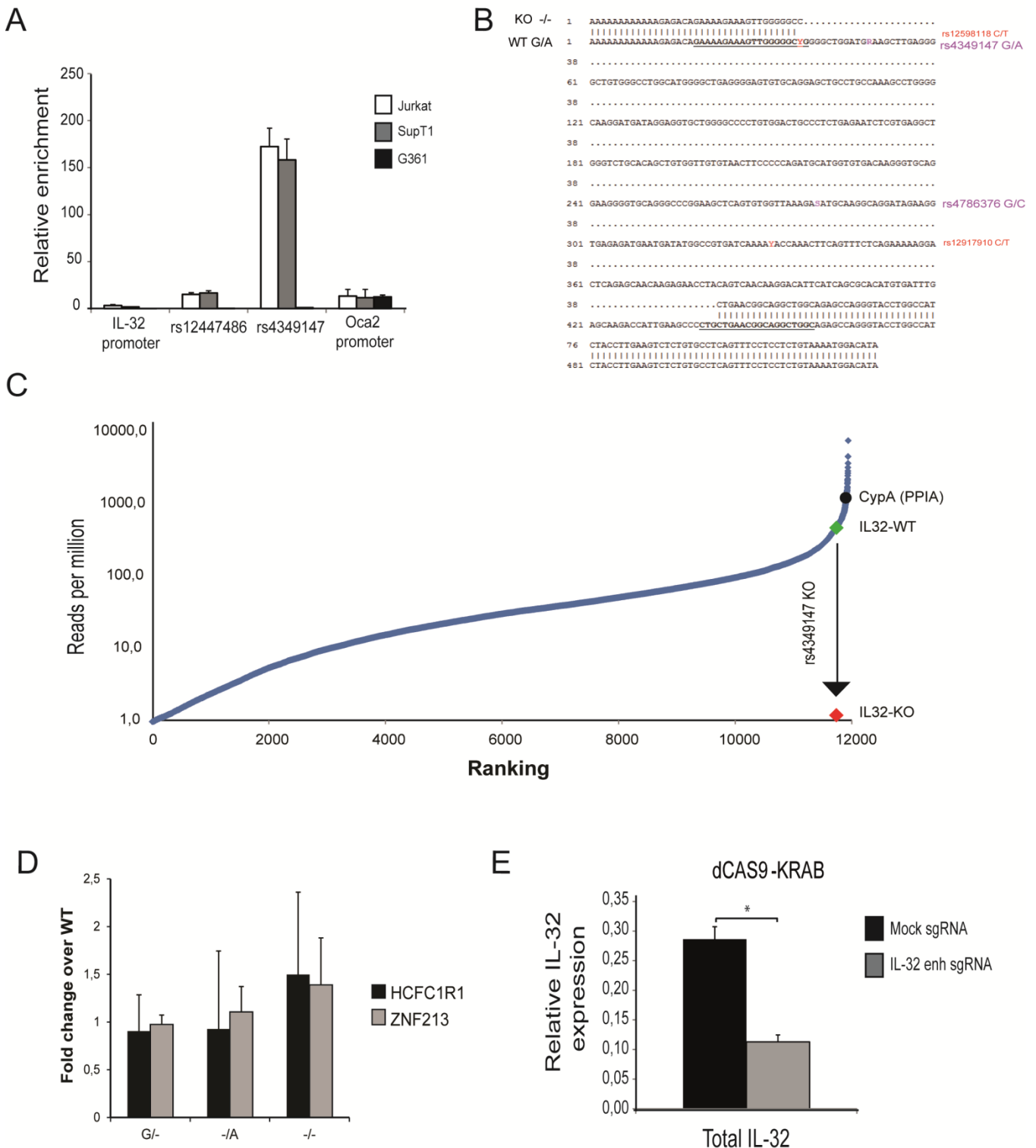
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# Supplementary Figure 1.

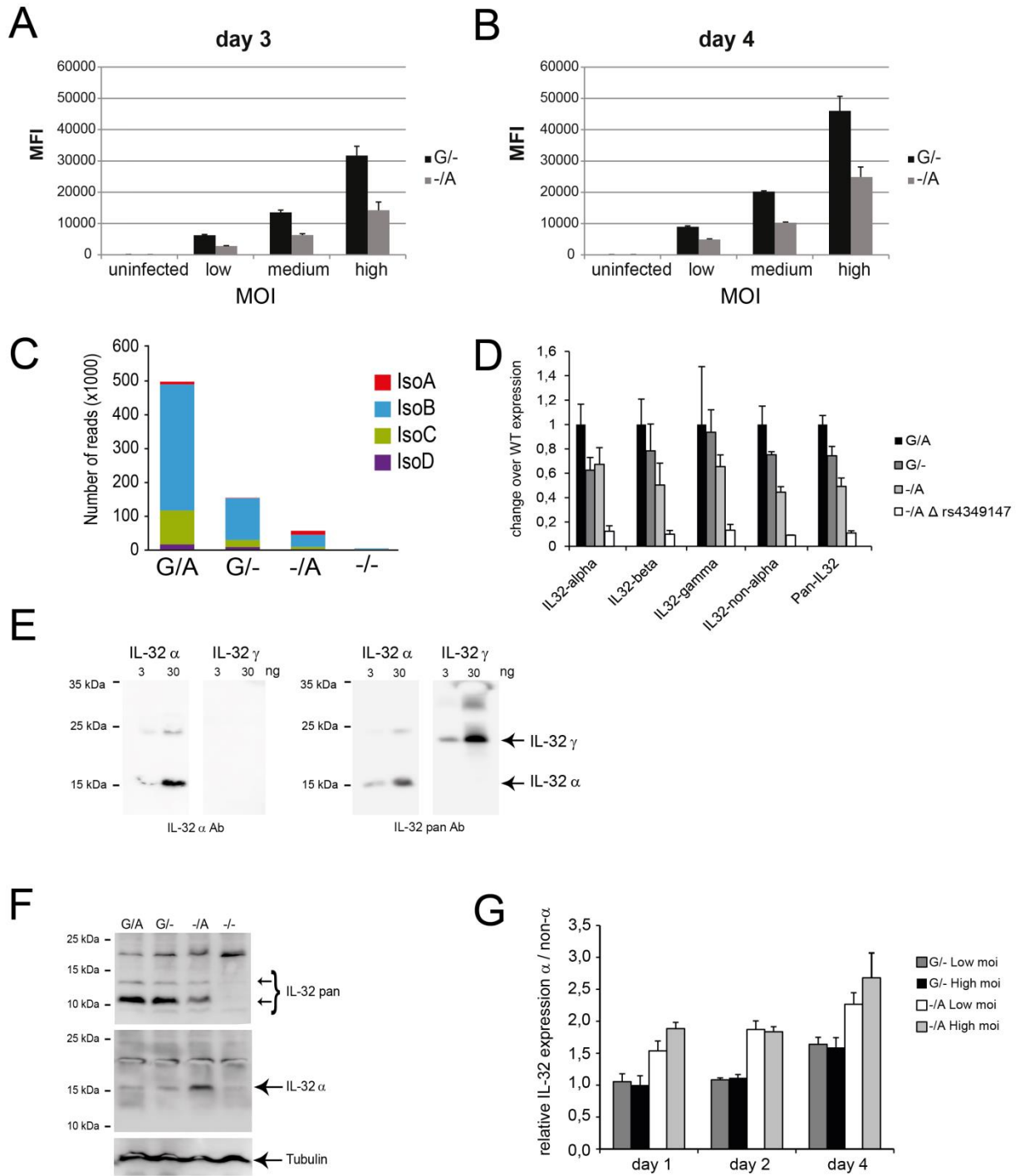


**fig. S1. Characterization of the rs4349147 DHS and the rs4349147 KO clone.** (A) FAIRE analysis of the region surrounding rs4349147 demonstrates significant increase in DNA accessibility indicating this region is depleted of histones and accessible in the T cell derived cell lines Jurkat and SupT1 but not in the melanoma cell line G361. By comparison, control regions rs12447486 and the melanocyte specific Oca2 promoter are less accessible as shown in the FAIRE analysis. (B) Sequencing of PCR

amplicon 1 (see figure 1B) spanning the rs4349147 DHS KO(-/-) line depicts the region deleted using Crispr/CAS9. Top sequence is obtained from the IL-32 rs4349147 DHS KO(-/-) cells; bottom sequence is obtained from the WT(G/A) cells. Sequence of the sgRNA's are indicated by boldface font and underlined. Position of variants is indicated. **(C)** Reads per million of all genes expressed above 1 read per million are ranked in ascending order. In WT(G/A) Jurkat cells IL-32 expression is among the top 5% of highly expressed genes (green diamond) Upon deletion of the rs4349147 regulatory element IL-32 expression drops to the lowest 2% of expressed genes (red diamond). The CypA gene is indicated as reference (black dot). **(D)** Real-time pcr confirmation of invariable expression of surrounding genes. **(E)** Targeting of a dCAS9-KRAB domain fusion to the rs4349147 region in wild type Jurkat cells results in reduced IL-32 expression.



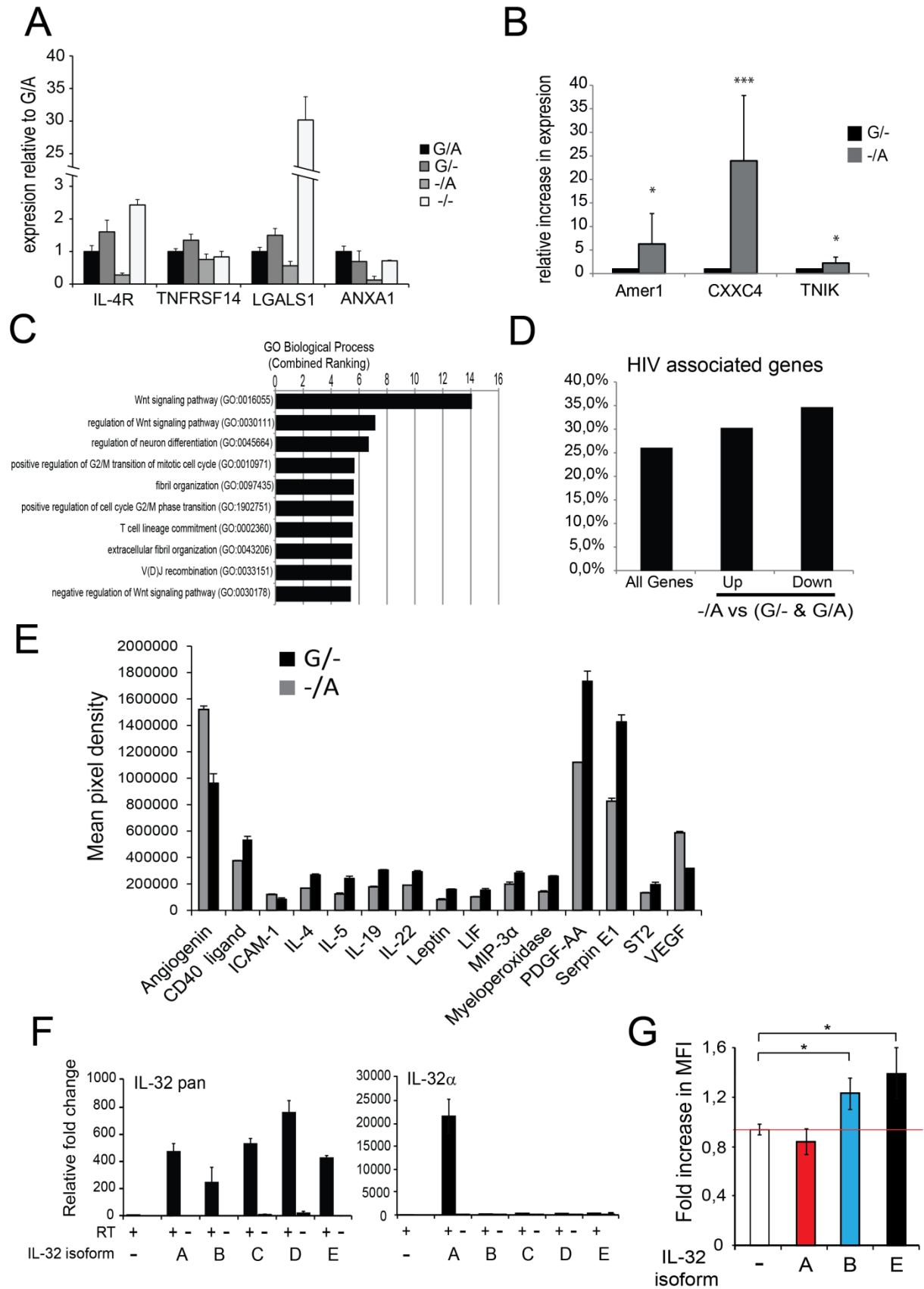
# Supplementary Figure 3.



**fig. S3. HIV infectability and differential expression of IL-32 isoforms between WT, rs4349147 G/-, and rs4349147 -/A clonal Jurkat cell lines. (A, B)** Difference in sensitivity to HIV infection between the rs4349147 -/A and rs4349147 G/- Jurkat cells is independent of MOI and time frame. (A) depicts MFI three days after infection using different MOI and (B) depicts MFI four days after infection using different MOI. Low MOI corresponds to ~20% GFP positive cells, medium MOI to ~50% GFP positive cells and High to ~80% GFP positive cells. (C) IL-32 isoform A expression is relatively elevated in

rs4349147 -/A cells as compared to rs4349147 G/- or WT(G/A) cells. Bar charts show the number of reads for each isoform in the high throughput RNA sequencing analysis **(D)** Relative expression of the IL-32 $\alpha$ , IL-32 $\beta$  and IL-32 $\gamma$  in WT,rs4349147 -/A , rs4349147 G/- and the -/A  $\Delta$ rs4349147 Jurkat cells. The primer pair for IL-32 $\beta$  only recognizes the “short” Var3 isoform originating from the EPD IL32\_1 promoter. **(E)** Determination of specificity of commercial anti-pan IL-32 and anti-IL-32 $\alpha$ -specific antibodies as indicated. Western blot analysis of 3 and 30 ng each of recombinant IL-32 $\alpha$  and IL-32 $\gamma$  protein is shown. **(F)** Western blot analysis using a pan-IL-32 antibody and an antibody specific to IL-32 $\alpha$  in the rs4349147 G/A, G/-, -/A and -/- Jurkat clones. **(G)** The increased ratio of IL-32 $\alpha$  over non- $\alpha$  IL-32 isoforms does not change after infection and is independent of the MOI of infection. Low MOI corresponds to ~20% GFP positive cells and High to ~80% GFP positive cells.

# Supplementary Figure 4.



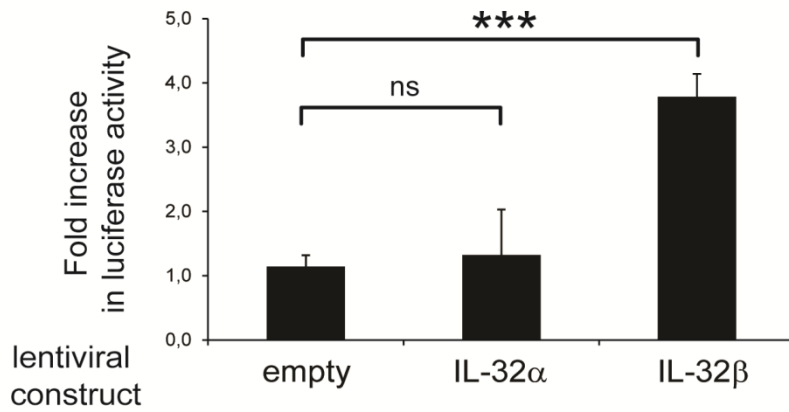
**fig. S4. Analysis of genes that are at least twofold differentially expressed in rs4349147 -/A compared to rs4349147 G/- and WT clonal Jurkat cell lines. (A) Expression of a selection of genes downregulated between rs4349147 -/A and rs4349147 G/- as well as WT(G/A) clonal Jurkat cell lines**

IL-4R, TNFRSF14, LGALS1, and ANXA1 in WT, rs4349147 -/A, rs4349147 G/- and KO Jurkat cells. **(B)** RT-PCR confirmation of a selection of genes upregulated between rs4349147 -/A and rs4349147 G/- as well as WT clonal Jurkat cell lines. **(C)** GO biological process analysis of genes upregulated between rs4349147 -/A and rs4349147 G/- as well as WT clonal Jurkat cell lines. A significant enrichment for factors involved in Wnt signaling and a slight enrichment for factors involved in neuron differentiation is found. **(D)** HIV associated genes, here defined as previously shown to interact with HIV either genetically or via protein-protein interaction (from HIV-1 Human Interaction Database; [www.ncbi.nlm.nih.gov/genome/viruses/retroviruses/hiv-1/interactions/](http://www.ncbi.nlm.nih.gov/genome/viruses/retroviruses/hiv-1/interactions/)) are overrepresented in the downregulated genes when compared to all genes (> 1rpm in Jurkats) and upregulated genes. **(E)** Mean pixel identity as measured by Proteome Profiler Human XL Cytokine Array Kit (R&D systems) in supernatant of rs4349147 -/A Jurkat cells and rs4349147 G/- Jurkat cells. **(F)** RT-PCR confirmation of exogenous expression of distinct IL-32 isoforms in rs4349147 enhancer KO Jurkat cells following nucleofection. Left panel shows IL-32 mRNA expression using PCR primers that detect all isoforms of IL-32. Right panel demonstrates mRNA expression of the IL-32 $\alpha$  isoform using PCR primers that specifically amplify the IL-32 $\alpha$  transcript. **(G)** Levels of infection, measured as fold increase in the MFI, following exogenous expression of IL-32 isoforms A, B, and E in WT Jurkat cells. Color coding is as for Fig. 3h.

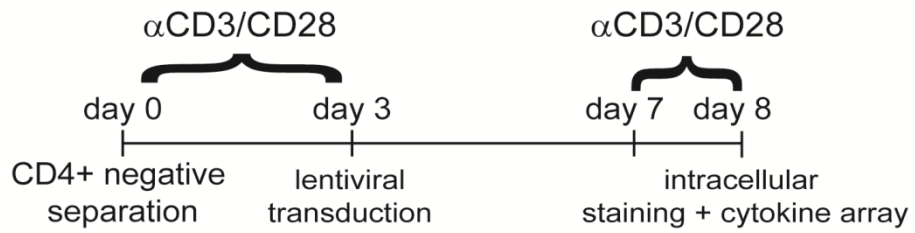


# Supplementary Figure 5.

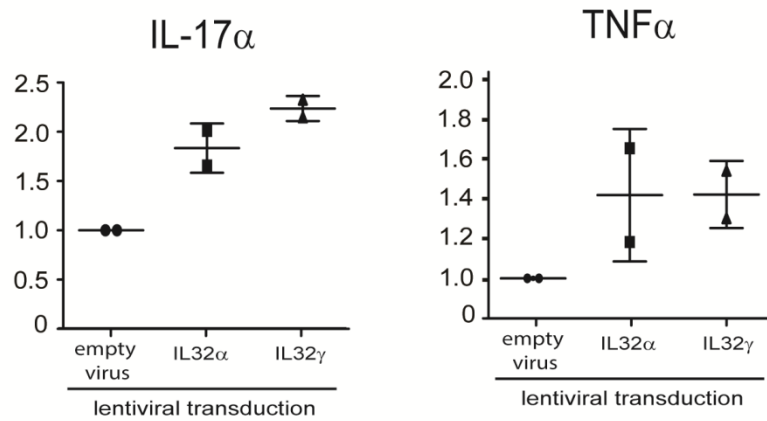
A



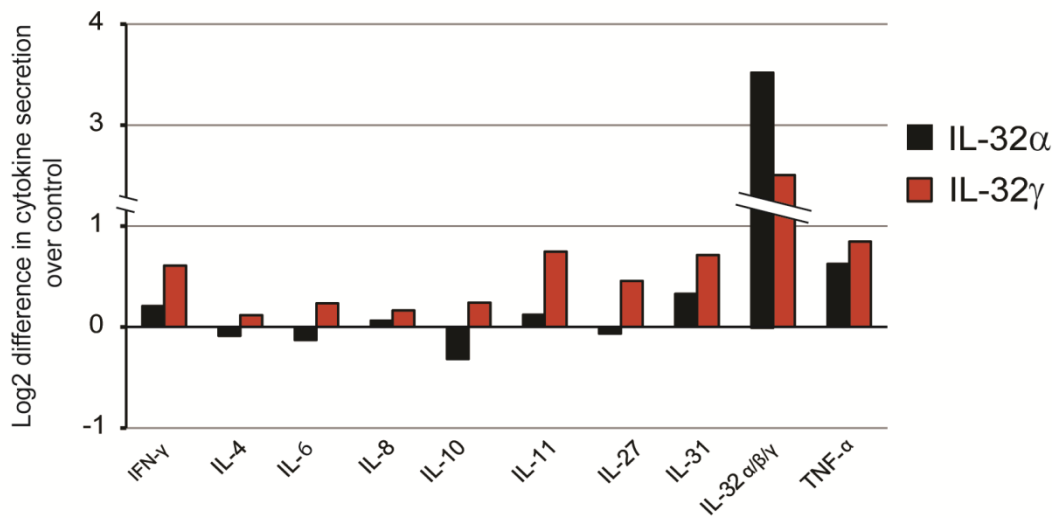
B



C

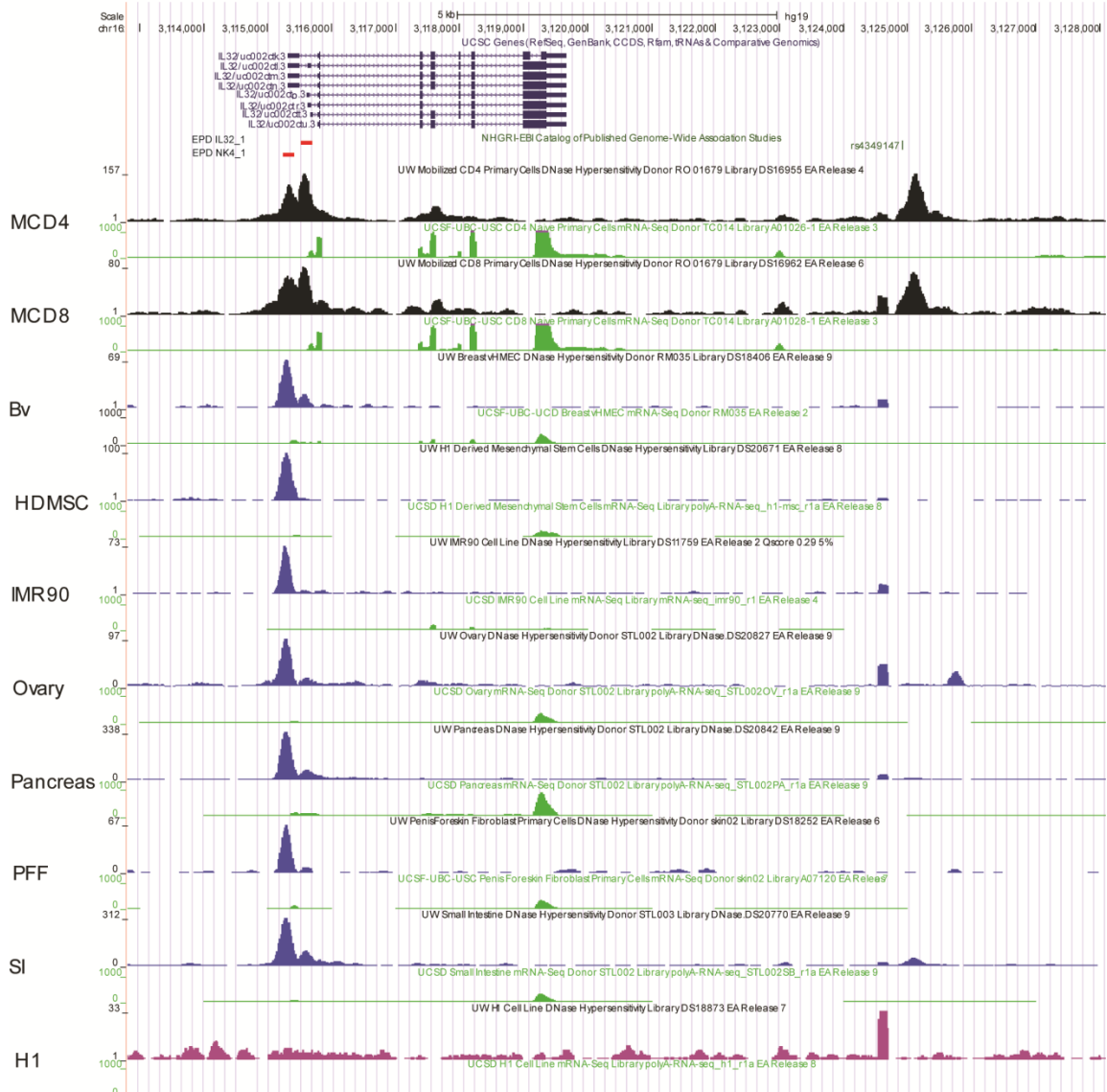


D



**fig. S5. Endogenous lentiviral overexpression of IL-32 isoforms in CD4<sup>+</sup> cells results in altered HIV susceptibility and proinflammatory cytokine expression.** (A) Exogenous lentiviral overexpression of IL-32 $\beta$  results in an increase in HIV infection as compared to CD4<sup>+</sup> T cells overexpressing IL-32 $\alpha$  or control cells infected with an empty lentiviral construct. (B) CD4<sup>+</sup> T cells isolated from two healthy donors were stimulated with CD3-CD28 coated beads and infected with a control lentiviral vector or a lentiviral vector expressing IL-32 $\alpha$  or IL-32 $\gamma$ . After 4 days the cells were re-stimulated for 24h and cytokine levels were determined by intracellular staining or measured using the Proteome Profiler Human XL Cytokine Array Kit (R&D systems) (C) Frequency of IFN $\gamma$  or TNF $\alpha$ -producing live (Annexin V-negative) purified CD4<sup>+</sup> T cells are shown from two different donors. Percentage indicate cytokine positive populations. (D) Cytokine secretion as measured by Proteome Profiler Human XL Cytokine Array Kit (R&D systems) demonstrates increased secretion of pro-inflammatory cytokines in the supernatant of CD4<sup>+</sup>T cells exogenously overexpressing IL-32 $\gamma$  as compared to CD4<sup>+</sup> T cells that overexpress IL-32 $\alpha$ . Values depicted are log<sub>2</sub> fold increase of IL-32 $\alpha$  (black bars) or IL-32 $\gamma$  (red bars) overexpressing cells over control cells. Note that robust overexpression of IL-32 in IL32 $\alpha$  and IL-32 $\gamma$  lentiviral infected CD4<sup>+</sup> cells is evident.

## Supplementary Figure 6.



**fig. S6. UCSC genome browser graphic of DNase I hypersensitivity (upper track, black, blue, purple) and mRNA sequencing (lower track, green) data obtained from the Human Epigenome Atlas.** In T-cells, which express high levels of IL-32 (green tracks), a DNaseI HS peak (black tracks) is present at the location of rs4349147 and a double DNaseI HS peak is present at the IL-32 promoter region indicating the presence of two separate promoters for IL-32. In cell types that lack a DNaseI HS peak at the location of rs4349147 (blue tracks) but still express low levels of IL-32 (corresponding green tracks) a single DNaseI HS peak is present at the IL-32 promoter for the long IL-32 transcripts. In H1 human ES cells no DNaseI HS peaks are detected in the IL-32 locus and the IL-32 gene is not expressed. mRNA-seq tracks are delimited to 1000 to emphasize differences in expression levels, while DNaseI HS tracks are not delimited to emphasize IL-32 promoter region peaks. <http://www.genboree.org/epigenomeatlas/index.rhtml>. Promoters as defined by the Eukaryotic Promoter Database (EPD; <http://epd.vital-it.ch>) are indicated as red bars.

table S1. Overview of SNPs.

SNP	Celltype	Chromosome	start	end
rs2796163	Th0;Th1	chr1	234978473	234979377
rs2802978	Th1	chr1	234978473	234979377
rs62000984	Th0;Th1	chr6	26017665	26018290
rs41266783	Th0;Th1	chr6	26031942	26032652
rs2230654	Th0;Th1	chr6	26033518	26034104
rs11751732	Th0;Th1	chr6	26043567	26044256
rs9468842	Th0;Th1	chr6	30851403	30854679
rs6901464	Th0;Th1	chr6	30851403	30854679
rs1049622	Th1	chr6	30858647	30859161
rs1049628	Th1	chr6	30866998	30867470
rs2074510	Th0;Th1	chr6	30875522	30876336
rs1052693	Th0;Th1	chr6	30875522	30876336
rs3828917	Th0;Th1	chr6	31465194	31466193
rs3093661	Th1	chr6	31542110	31543783
rs9368699	Th0;Th1	chr6	31802108	31803075
rs8192583	Th0;Th1	chr6	32162969	32164095
rs6990319	Th0;Th1	chr8	66862573	66863027
rs11998618	Th0	chr8	66858410	66858738
rs12447486	Th0;Th1	chr16	3121836	3123558
rs4349147	Th0;Th1	chr16	3124834	3125437
rs2015620	Th0	chr16	3123504	3123607
GRCh37/hg19	assembly			

table S2. List of differentially regulated genes.

GENE	WT (RPM)	G/- (RPM)	-/A (RPM)	-/- (RPM)
OR3A2	1,9237	1,4648	0,0000	0,2341
RTP4	0,8630	1,2101	0,0000	0,8993
CARNS1	0,9448	0,5732	0,0000	0,9532
TNS3	0,8009	0,3821	0,0000	0,3086
NIPSNAP3B	0,6478	0,3821	0,0000	0,7406
LGR6	0,5721	0,3821	0,0000	0,2341
GCSAML	0,7887	0,2548	0,0000	0,6926
LRRTM2	0,6880	0,1911	0,0000	0,3938
ZP1	0,8630	0,1274	0,0000	0,2929
CRISPLD1	0,7266	0,0637	0,0000	0,0000
ZCCHC16	0,7206	0,0637	0,0000	0,2929
DPP6	0,6819	0,0637	0,0000	1,2676
ANO9	3,5611	4,0761	0,0622	4,0703
LARGE	3,6491	2,9297	0,0622	3,0995
FAAH2	1,3979	2,6112	0,0622	3,8195
ZNF697	2,5314	3,4392	0,1244	1,9113
C10orf107	6,5094	8,0885	0,3111	14,7982
GPR158	12,6412	7,7064	0,3111	0,3517
TMEM151B	2,0996	2,8023	0,1244	8,8842
ANGPTL6	1,2169	2,0380	0,1244	2,2473
GBGT1	2,2579	1,7833	0,1244	2,5137
TUBA4A	16,4543	31,9081	2,2399	19,5230
TMOD1	1,8556	1,5922	0,1244	1,9808
F2RL2	5,2113	6,7510	0,5600	2,6107
PIANP	4,3288	4,1398	0,3733	3,9537
FXVD2	4,7035	0,6369	0,0622	4,3849
GCA	3,5505	0,6369	0,0622	2,1630
<b>ANXA1</b>	<b>232,6092</b>	<b>158,1394</b>	<b>15,8040</b>	<b>113,4199</b>
PYGL	8,5059	3,6940	0,3733	11,2002
ATP2B2	3,3594	0,5732	0,0622	7,5129
ITGA6	8,0081	26,3035	2,8621	12,5178
GZMA	37,1217	19,3614	2,1155	37,1296
UBXN10	5,5305	8,8528	0,9955	12,4539
LSP1	2,9489	3,1844	0,3733	1,8485
PTCRA	1,6450	1,0190	0,1244	0,8092
<b>TNFRSF14</b>	<b>9,9424</b>	<b>12,4193</b>	<b>1,6177</b>	<b>11,6105</b>
SLC25A21	1,5866	1,4012	0,1867	1,8270
SIGLEC6	5,6690	2,2928	0,3111	1,3156
ITGB2-AS1	5,5804	10,8908	1,4933	5,7023
PCBP3	3,9832	3,6303	0,4978	18,6150
BCAM	1,3267	1,3375	0,1867	1,6673
GPR68	2,7633	2,9934	0,4355	4,4210
GSTM3	37,5542	22,9917	3,3599	18,8696
BST2	44,9524	104,5134	15,3685	66,2490

IER3	8,4907	7,7700	1,1822	5,5692
TRPM2	5,8159	6,4326	0,9955	10,6309
<b>STAT5A</b>	13,3907	17,6418	2,8621	6,8289
LOC90246	1,7427	1,1464	0,1867	0,5114
SMAP1	31,5560	21,7179	3,7955	27,1142
PI16	29,3594	49,1678	8,6487	11,7409
GFRA3	2,1927	2,1017	0,3733	1,3205
CRIM1	1,5820	0,7006	0,1244	1,0972
CD69	12,0947	12,2283	2,2399	12,0202
CTSW	36,0529	52,0338	9,5820	101,1831
EFNB3	3,6847	2,2928	0,4355	2,0768
PLCH1	21,9898	19,9346	3,9821	19,4173
CST7	26,6965	26,3035	5,3510	117,9958
PLEK	54,0085	14,5211	2,9866	106,6130
GNLY	4,6648	0,8916	0,1867	18,0264
PRKCH	198,9677	305,3880	64,2116	196,0620
ADCYAP1	20,7476	20,2531	4,2932	4,2035
CD300A	2,4352	0,5732	0,1244	0,4369
PDE9A	6,0229	8,4069	1,8666	4,0478
IFI35	12,2411	13,6931	3,0488	16,1884
USP40	17,5236	25,5392	5,7243	19,9463
GAS7	94,4084	139,4786	32,3547	101,6567
HECW1	7,2178	2,6749	0,6222	1,8535
LPCAT2	10,7652	10,8908	2,6133	17,6029
<b>LGALS1</b>	63,0176	4,9040	1,1822	107,6043
AKAP7	4,4551	2,8023	0,6844	4,2487
DENND2D	3,8718	3,5666	0,8711	3,7715
SMPD3	3,1254	1,7196	0,4355	0,5701
C16orf74	2,3966	2,4202	0,6222	8,1015
PCCA	11,8957	13,7568	3,5466	14,7032
TNFSF10	14,1815	15,0306	3,9199	21,9496
TDRD9	35,7427	21,4631	5,6621	28,5570
EGR1	10,0812	8,0248	2,1777	11,5017
C19orf59	1,9435	0,8916	0,2489	1,3156
LAIR1	109,1083	81,8402	23,3327	75,0209
LST1	6,2562	5,1588	1,4933	4,6297
SLC2A3	15,1188	13,6294	3,9821	9,4554
KLHL29	20,2388	24,3928	7,1554	40,9360
<b>IL4R</b>	8,4943	11,6551	3,4221	25,3313
BMP10	6,0146	4,0124	1,1822	6,8975
IFI30	22,0016	29,1695	8,8353	29,6365
CHRNA3	24,9003	35,7931	11,0753	52,4075
DPEP2	2,2761	1,4012	0,4355	1,0972
FAM101B	35,2872	54,8361	17,0484	39,8864
NRBP2	9,7002	5,5409	1,7422	11,6457
GPA33	12,0305	14,1389	4,4799	13,1544
SIRPB1	8,5868	5,4136	1,7422	15,4232
MSH5-SAPCD1	5,0689	4,5219	1,4933	5,7269
H6PD	52,2552	60,9502	20,3461	39,6230
HLF	6,9214	2,4202	0,8089	2,6685

SLC16A3	9,5840	9,3623	3,1732	9,0361
AIG1	64,4390	91,5846	31,1103	62,6788
GLDC	34,5223	31,8444	10,8886	23,0093
GALNT6	15,5484	18,6608	6,4709	14,8100
DHX32	22,6168	21,2084	7,4042	26,5959
PTPN3	52,0431	49,8684	17,4840	38,9746
<b>ITGAL</b>	26,2732	30,9528	10,8886	27,9478
KLHL35	5,5144	2,1017	0,7466	1,2725
IL32	621,6479	144,5737	53,5719	1,5067
CD244	7,0395	5,5409	2,0533	11,2276
SQRDL	35,7659	36,5574	13,5641	44,7357
RGS2	3,3898	1,3375	0,4978	1,3950
LIMD2	58,5659	42,7989	16,3640	51,4402
RAET1E	11,4925	9,1712	3,5466	17,3982
EMID1	12,1328	12,1646	4,7288	12,6283
SLA	478,0886	376,9743	146,5916	462,1445
TTC16	27,7892	29,0421	11,3241	15,9542
LACTB2	11,5229	7,0058	2,7377	8,2769
SPINK2	2,4459	0,3184	0,1244	0,4849
SKAP1	18,3071	19,4888	7,6531	20,7486
GVINP1	47,6777	45,6649	18,1062	50,8067
DNTT	37,2784	9,8718	3,9199	66,5260
FLOT1	89,8745	90,6929	36,5235	70,0579
KIAA0125	17,8081	12,9288	5,2265	17,1609
PTPN6	210,8397	164,6357	66,5760	185,7251
<b>HES1</b>	19,0670	16,4317	6,7820	4,6797
TSHZ3	18,5028	20,7626	8,6487	23,3220
CPA4	12,1662	3,5666	1,4933	34,1661
RMRP	19,3306	3,1208	1,3066	1,0600
ZAP70	451,6591	396,3994	166,0044	585,9785
MAL	42,5390	25,5392	10,7642	20,1643
TEX19	26,7968	8,4069	3,5466	9,1418
FAIM3	15,6537	7,6427	3,2355	10,2714
ADC	6,7821	5,8594	2,4888	6,7760
SPSB1	12,3570	10,6360	4,5421	7,0886
CCDC102B	11,6085	5,6683	2,4266	10,3204
RHBDL3	5,6440	3,5666	1,5555	6,2941
ZNF616	12,6664	11,5277	5,0399	12,0964
ABI3	8,4846	7,5153	3,3599	7,8194
<b>JAK3</b>	25,9808	23,6923	10,7642	21,2217
APOBEC3B	26,9777	25,2845	11,5108	25,3480
TSPAN9	9,7492	8,2796	3,7955	10,9797
ERP27	5,5296	3,3755	1,5555	3,8509
LAT	68,6253	69,2935	32,1058	70,2288
LOC100130476	6,2766	4,2035	1,9911	7,7332
CECR1	44,9476	43,6269	20,8439	62,8255
IL16	28,6884	16,8139	8,0887	27,0064
RCBTB2	25,6701	14,3937	6,9687	15,2813
NDFIP2	36,9922	14,6484	7,0931	41,5746
CD82	295,4044	198,7729	96,2552	206,1652

BIN2	78,8526	59,2943	28,8081	89,3595
LPAR5	17,7956	12,4193	6,0354	27,9518
LOC440354	3,2565	1,4012	0,6844	2,6195
MAGEB18	3,5566	0,7643	0,3733	2,2904
C1orf186	3,4482	1,5285	0,7466	3,0368
UGT3A2	5,9909	0,3821	0,1867	5,0902
GYPC	189,0652	170,5587	83,6244	244,8064
HPGD	15,1422	4,7767	2,3644	5,3419
LIMS2	4,3642	9,9355	20,0972	3,9724
ATP2B3	0,0000	2,6749	5,5998	0,1225
DNAJC12	0,0773	0,8916	1,8666	0,0960
SLC9A7	8,6081	12,9288	27,6881	13,0369
TMEM100	0,0000	0,3184	0,6844	0,5055
ZNF211	15,7289	17,2597	37,7057	10,5536
TNIK	28,6610	46,8113	102,6017	26,1868
RAG2	13,0955	17,3234	38,7012	13,9145
TGFB3	3,4467	5,2862	11,8219	4,9706
FAM84B	9,5688	11,4640	25,8837	9,0263
IKZF3	3,7142	5,2225	11,8219	28,8514
MFAP4	0,1129	5,4136	12,3197	2,9055
FKBP9L	0,0000	0,1911	0,4355	0,3194
EPHB6	44,3400	40,1877	92,5842	34,7260
HYDIN	2,5792	3,6303	8,5864	1,9485
PPP2R2B	0,4948	0,9553	2,3022	0,5858
SRGAP1	1,7366	2,8660	6,9065	5,8083
SLC12A6	19,7711	17,8329	43,1811	49,0547
MAT1A	3,5082	5,3499	13,3774	1,0717
TLE1	25,9050	25,4755	64,2738	30,8435
MIR181B1	0,0000	0,1911	0,4978	0,0852
TMEM178B	0,7175	2,1654	5,6621	1,1236
CKM	0,0000	0,4458	1,1822	0,1489
OR2C1	0,0000	0,2548	0,6844	0,0960
IFI44L	0,0386	0,3821	1,0577	0,0372
RGS4	0,0000	0,2548	0,7466	0,1225
ACTC1	0,0000	0,2548	0,7466	0,0000
AP1B1	26,9615	38,0222	113,0547	32,0132
PLEKHG1	0,9835	1,8470	5,8487	0,9640
NYNRIN	0,1531	0,9553	3,0488	0,4154
ADAMTS3	0,1546	0,3821	1,2444	1,8436
SPTLC3	1,8261	2,0380	6,8443	5,4957
ZNF83	15,6750	11,8461	40,0700	0,1969
ZBBX	0,0000	0,1274	0,4355	0,0000
LGALS3BP	0,6509	5,9868	22,7727	3,0995
PSD3	0,3819	0,6369	2,4266	0,6446
CD79A	6,0222	4,4582	17,2351	13,5326
PBX1	0,0758	0,4458	1,7422	0,5006
PRKAA2	0,0742	0,2548	1,0577	0,0000
PHLDB2	7,0419	9,5533	41,8122	19,3164
EOMES	1,3888	2,2291	10,2042	38,4467
GALC	2,0305	1,7833	8,2753	0,3674



PCED1B-AS1	0,1515	0,5732	2,7377	0,7563
CYTH4	0,1485	0,5732	2,7377	2,6549
GPC5	0,3448	0,9553	4,9154	0,0000
TLL1	2,6519	2,2291	11,5108	3,3601
ZNF385B	2,0117	1,1464	5,9732	3,4983
ZNF772	0,6478	3,2481	16,9862	1,6820
RGPD3	2,4769	2,1017	11,1997	0,3409
PRUNE2	1,0236	1,1464	6,5332	0,1440
BEST1	0,0371	0,3821	2,3022	0,6867
SMARCA1	2,1322	6,6873	41,1900	22,0886
EVPLL	0,0742	0,1911	1,1822	0,0480
<b>AMER1</b>	<b>23,2847</b>	<b>10,6360</b>	<b>66,2649</b>	<b>29,5464</b>
CLEC11A	1,7192	4,5219	28,2481	1,3587
SDC2	0,6448	0,3821	2,4266	8,3542
HHEX	0,0773	0,2548	1,6177	0,0000
STX1B	0,1887	0,1911	1,3066	0,3037
LIN28B	0,3864	0,5095	3,5466	0,3252
DBH	0,0000	0,0637	0,4978	0,0000
TC2N	0,1902	0,3821	3,0488	0,0000
PTPRG	0,3046	1,2101	9,8931	1,3685
C11orf74	0,0386	0,5095	4,2310	0,5065
AKR1C6P	5,4213	1,7833	15,3063	1,4538
C2orf16	0,0000	0,0637	0,5600	0,0372
ADAMTS18	2,6595	0,8280	7,2798	15,1500
RAG1	13,1222	10,9545	105,0905	9,2377
PPAP2B	0,0758	0,1911	1,8666	0,0852
RNF43	0,5319	0,3821	3,7332	0,8680
COBL	0,1129	0,3821	3,8577	0,0480
AKR1C3	0,0371	0,1274	1,3066	0,0480
TRPS1	0,0386	0,2548	2,8621	0,4526
<b>CXXC4</b>	<b>0,3804</b>	<b>0,1911</b>	<b>2,3022</b>	<b>0,0745</b>
PTPRD	0,0758	1,9107	23,9549	0,3781
IRF4	0,0386	0,0637	0,8089	0,0852
SORBS2	0,0000	0,5732	7,2798	0,0480
GABRB2	7,0139	3,0571	48,4076	12,4824
HLA-DOA	1,3994	0,5732	9,0842	3,3983
TRIM29	0,0000	0,0637	1,2444	0,2341
STARD13	0,0773	0,0637	1,7422	1,1501
SOX5	0,1485	0,6369	18,1684	0,0745
APP	0,1856	0,1274	3,9821	0,6495
CACNB2	0,0000	0,0637	2,0533	0,2929
TSPEAR	0,3016	0,0637	2,2399	0,0480
RASEF	0,0371	0,3184	14,1241	0,9855
GABRA3	0,0773	0,0637	3,8577	1,8270
INPP4B	0,0000	0,0000	0,4355	0,0000
FLRT3	0,0000	0,0000	0,4355	0,0000
VN1R1	0,0000	0,0000	0,4978	0,0000
PLD1	0,0000	0,0000	0,4978	0,0000
ROR2	0,0000	0,0000	0,5600	0,1225
SCEL	0,0000	0,0000	0,5600	0,0000

HCG23	0,0000	0,0000	0,6222	0,0000
LIX1	0,0758	0,0000	0,8711	0,0000
CAPN6	0,0000	0,0000	0,9333	0,0000
SDSL	0,2258	0,0000	1,5555	1,3156
CREB5	0,1144	0,0000	3,3599	0,0480

table S3. GO term analysis of -/A versus WT and G/- down-regulated genes.

Go-term analysis ( <a href="http://amp.pharm.mssm.edu/Enrichr/">http://amp.pharm.mssm.edu/Enrichr/</a> )												
-/A vs WT & G/- down regulated genes												
Term	Overlap	P-value	Adjusted P-value	Old P-value	Old Adjusted P-value	Z-score	Combined Score	Genes				
negative regulation of alpha-beta T cell activation (GO:0046636)	4/19	1.14E-05	0.007110384	2.306E-05	0.008985301	-2.81977	13.94712595	IL4R	CD300A	TNFRSF14	JAK3	
regulation of cell activation (GO:0050865)	13/420	2.01E-05	0.007420925	1.946E-05	0.008985301	-2.52287	12.37074968	STAT5A	IL4R	CD300A	LST1	PLEK ITGAL ZAP70 LGALS1 TNFRSF14 PTPN6 HES1 JAK3 LAT
regulation of lymphocyte activation (GO:0051249)	12/344	1.31E-05	0.007110384	1.329E-05	0.008985301	-2.50051	12.36803498	STAT5A	ZAP70	LGALS1	IL4R	CD300A LST1 HES1 TNFRSF14 PTPN6 ITGAL JAK3 LAT
regulation of leukocyte activation (GO:0002694)	12/390	4.47E-05	0.007420925	4.394E-05	0.011542311	-2.513	12.32234948	STAT5A	ZAP70	LGALS1	IL4R	CD300A LST1 TNFRSF14 PTPN6 HES1 ITGAL JAK3 LAT
regulation of T cell activation (GO:0050863)	11/259	4.81E-06	0.007110384	5.283E-06	0.008626579	-2.461	12.17259303	STAT5A	ZAP70	LGALS1	IL4R	CD300A TNFRSF14 PTPN6 HES1 ITGAL JAK3 LAT
negative regulation of immune system process (GO:0002683)	11/211	2.67E-05	0.007420925	2.751E-05	0.008985301	-2.45097	12.01821632	BST2	STAT5A	ADCYAP1	IL4R	GPR68 CD300A LST1 TNFRSF14 PTPN6 HES1 JAK3
negative regulation of muscle hypertrophy (GO:0014741)	3/10	4.97E-05	0.007420925	0.0001087	0.01389582	-2.40784	11.8067472	BMP10	RG52	PI16		
regulation of lymphocyte proliferation (GO:0050670)	8/170	4.8E-05	0.007420925	5.435E-05	0.011542311	-2.39045	11.72147707	STAT5A	ZAP70	CD300A	LST1	TNFRSF14 PTPN6 HES1 ITGAL
regulation of mononuclear cell proliferation (GO:0032944)	8/171	5E-05	0.007420925	5.655E-05	0.011542311	-2.38645	11.7018626	STAT5A	ZAP70	CD300A	LST1	TNFRSF14 PTPN6 HES1 ITGAL
negative regulation of cardiac muscle hypertrophy (GO:0010614)	3/9	3.5E-05	0.007420925	8.408E-05	0.01248172	-2.35276	11.53665581	BMP10	RG52	PI16		
regulation of leukocyte proliferation (GO:0070653)	8/176	6.13E-05	0.00833752	6.866E-05	0.012458499	-2.38568	11.4200588	STAT5A	ZAP70	CD300A	LST1	TNFRSF14 PTPN6 HES1 ITGAL
thrombin receptor signaling pathway (GO:0070493)	3/9	3.5E-05	0.007420925	8.408E-05	0.01248172	-2.31554	11.35414795	HPGD	PLEK	F2RL2		
negative regulation of leukocyte mediated immunity (GO:0002704)	4/34	0.000125	0.01234564	0.0001764	0.016949509	-2.50356	11.00176688	BST2	CD300A	PTPN6	JAK3	
regulation of B cell receptor signaling pathway (GO:0050855)	3/13	0.000116	0.01234564	0.0002094	0.018991166	-2.48029	10.89953766	PRKCH	CD300A	PTPN6	HES1	
regulation of glial cell proliferation (GO:0060251)	3/15	0.000183	0.015739091	0.0003019	0.020539492	-2.48753	10.32725119	ADCYAP1	PRKCH	HES1		
positive regulation of T cell activation (GO:0050870)	8/189	0.000101	0.01234564	0.0001106	0.01389582	-2.31267	10.16290134	STAT5A	ZAP70	LGALS1	IL4R	TNFRSF14 PTPN6 HES1 ITGAL
negative regulation of lymphocyte activation (GO:0051250)	6/102	0.000129	0.01234564	0.0001531	0.016435011	-2.25827	9.923840189	IL4R	CD300A	LST1	TNFRSF14 PTPN6 JAK3	
negative regulation of immune response (GO:0050777)	6/103	0.000136	0.01234564	0.0001611	0.016435011	-2.20943	9.682862807	BST2	ADCYAP1	IL4R	CD300A	PTPN6 JAK3
positive regulation of cell activation (GO:0050867)	9/272	0.000241	0.01871675	0.0002474	0.019649793	-2.39548	9.530006345	STAT5A	ZAP70	LGALS1	IL4R	PLEK TNFRSF14 PTPN6 HES1 ITGAL
regulation of alpha-beta T cell activation (GO:0046634)	5/63	0.000117	0.01234564	0.0001496	0.016435011	-2.1497	9.446745115	ZAP70	IL4R	CD300A	TNFRSF14 JAK3	
-/A vs WT & G/- up regulated genes												
Term	Overlap	P-value	Adjusted P-value	Old P-value	Old Adjusted P-value	Z-score	Combined Score	Genes				
Wnt signaling pathway (GO:0016055)	9/234	2.06E-06	0.002406062	5.877E-06	0.006864484	-2.33521	14.08078829	AMER1	RNF43	HHEX	TLE1	PRKAA2 PPAP2B ROR2 TNIK CXCC4
regulation of Wnt signaling pathway (GO:0030111)	7/214	8.28E-05	0.048337881	0.0001808	0.105590527	-2.36183	7.155267604	AMER1	RNF43	HHEX	TLE1	PPAP2B ROR2 CXCC4
regulation of neuron differentiation (GO:0045664)	9/405	0.000156	0.060574599	0.0003627	0.141229462	-2.38555	6.888663217	EOMES	PTPRD	APP	SDC2	COBL TNIK PBX1 SOX5 PTPRG
positive regulation of G2/M transition of mitotic cell cycle (GO:0010971)	2/14	0.00204	0.113441367	0.0032522	0.180882111	-2.60583	5.671502706	APP	PBX1			
fibril organization (GO:0097435)	2/14	0.00204	0.113441367	0.0032522	0.180882111	-2.58071	5.616844562	MFAP4	ADAMT3S			
positive regulation of cell cycle G2/M phase transition (GO:1902751)	2/14	0.00204	0.113441367	0.0032522	0.180882111	-2.56874	5.590794407	APP	PBX1			
T cell lineage commitment (GO:0002360)	2/12	0.001489	0.110363586	0.0024834	0.180882111	-2.5128	5.53850311	IRF4	RAG2			
extracellular fibril organization (GO:0043206)	2/12	0.001489	0.110363586	0.0024834	0.180882111	-2.49737	5.504152017	MFAP4	ADAMT3S			
VDJ recombination (GO:0033151)	2/16	0.002673	0.130069855	0.0041178	0.206030672	-2.68048	5.467338683	RAG2	RAG1			
negative regulation of Wnt signaling pathway (GO:0030178)	5/126	0.000372	0.093354279	0.0006877	0.172060453	-2.27836	5.402793201	AMER1	RNF43	TLE1	ROR2	CXCC4
response to light stimulus (GO:0009416)	7/322	0.000979	0.110363586	0.0019082	0.180882111	-2.38069	5.246975331	MFAP4	APP	SDC2	AKR1C3	GPC5 DBH BEST1
B cell activation (GO:0042113)	5/128	0.0004	0.093354279	0.0007366	0.172060453	-2.16852	5.142322765	CD79A	HHEX	RAG2	IKZF3	RAG1
lymphocyte activation (GO:0046649)	7/304	0.000699	0.108841518	0.0013843	0.180882111	-2.31394	5.131909594	EOMES	CD79A	HHEX	IRF4	RAG2 IKZF3 RAG1
leukocyte differentiation (GO:0002521)	6/251	0.001404	0.110363586	0.0025603	0.180882111	-2.32475	5.123683466	EOMES	CD79A	HHEX	IRF4	RAG2 RAG1
leukocyte activation (GO:0045321)	7/373	0.002265	0.12026623	0.0024489	0.206030672	-2.32584	4.927011656	EOMES	CD79A	HHEX	IRF4	RAG2 IKZF3 RAG1
lymphocyte differentiation (GO:0030098)	5/172	0.001512	0.110363586	0.0026111	0.180882111	-2.22511	4.90408891	EOMES	CD79A	HHEX	RAG2	RAG1
regulation of dendrite development (GO:0050773)	4/89	0.000926	0.110363586	0.0015626	0.180882111	-2.20161	4.852287074	PTPRD	SDC2	COBL	TNIK	
B cell differentiation (GO:0030183)	4/80	0.00062	0.108841518	0.0010709	0.180882111	-2.18121	4.83763109	CD79A	HHEX	RAG2	RAG1	
detection of visible light (GO:0009584)	4/104	0.00165	0.113382092	0.0026998	0.180882111	-2.18116	4.74837213	SDC2	AKR1C3	GPC5	BEST1	
anion transmembrane transport (GO:0098656)	5/172	0.001512	0.110363586	0.0026111	0.180882111	-2.14829	4.734778726	GABRR2	PRKAA2	GABRA3	SLC12A6	BEST1



**table S5. Cytokine secretion in CD4+ T cells after stimulation and infection with HIV as measured by Proteome Profiler Human XL Cytokine Array kit.**

Label	Control	CD4-alpha	CD4-gamma	control		CD4-alpha		CD4-gamma	
				Average	Stdev	Average	Stdev	Average	Stdev
A1 Reference	777490	640384	439183	779017	27237	629767	42295	629767	42295
A2 Reference	777492	640386	439185	779019	27239	629769	42297	629769	42297
A3 Reference	777494	640388	439187	779021	27241	629771	42299	629771	42299
A4 Reference	777496	640390	439189	779023	27243	629773	42301	629773	42301
A5 Reference	777498	640392	439191	779025	27245	629775	42303	629775	42303
A6 Reference	777500	640394	439193	779027	27247	629777	42305	629777	42305
A7 Reference	777502	640396	439195	779029	27249	629779	42307	629779	42307
A8 Reference	777504	640398	439197	779031	27251	629781	42309	629781	42309
A9 Reference	777506	640400	439199	779033	27253	629783	42311	629783	42311
A10 Reference	777508	640402	439201	779035	27255	629785	42313	629785	42313
A11 Reference	777510	640404	439203	779037	27257	629787	42315	629787	42315
A12 Reference	777512	640406	439205	779039	27259	629789	42317	629789	42317
A13 Reference	777514	640408	439207	779041	27261	629791	42319	629791	42319
A14 Reference	777516	640410	439209	779043	27263	629793	42321	629793	42321
A15 Reference	777518	640412	439211	779045	27265	629795	42323	629795	42323
A16 Reference	777520	640414	439213	779047	27267	629797	42325	629797	42325
A17 Reference	777522	640416	439215	779049	27269	629799	42327	629799	42327
A18 Reference	777524	640418	439217	779051	27271	629801	42329	629801	42329
A19 Reference	777526	640420	439219	779053	27273	629803	42331	629803	42331
A20 Reference	777528	640422	439221	779055	27275	629805	42333	629805	42333
A21 Reference	777530	640424	439223	779057	27277	629807	42335	629807	42335
A22 Reference	777532	640426	439225	779059	27279	629809	42337	629809	42337
A23 Reference	777534	640428	439227	779061	27281	629811	42339	629811	42339
A24 Reference	777536	640430	439229	779063	27283	629813	42341	629813	42341
A25 Reference	777538	640432	439231	779065	27285	629815	42343	629815	42343
A26 Reference	777540	640434	439233	779067	27287	629817	42345	629817	42345
A27 Reference	777542	640436	439235	779069	27289	629819	42347	629819	42347
A28 Reference	777544	640438	439237	779071	27291	629821	42349	629821	42349
A29 Reference	777546	640440	439239	779073	27293	629823	42351	629823	42351
A30 Reference	777548	640442	439241	779075	27295	629825	42353	629825	42353
A31 Reference	777550	640444	439243	779077	27297	629827	42355	629827	42355
A32 Reference	777552	640446	439245	779079	27299	629829	42357	629829	42357
A33 Reference	777554	640448	439247	779081	27301	629831	42359	629831	42359
A34 Reference	777556	640450	439249	779083	27303	629833	42361	629833	42361
A35 Reference	777558	640452	439251	779085	27305	629835	42363	629835	42363
A36 Reference	777560	640454	439253	779087	27307	629837	42365	629837	42365
A37 Reference	777562	640456	439255	779089	27309	629839	42367	629839	42367
A38 Reference	777564	640458	439257	779091	27311	629841	42369	629841	42369
A39 Reference	777566	640460	439259	779093	27313	629843	42371	629843	42371
A40 Reference	777568	640462	439261	779095	27315	629845	42373	629845	42373
A41 Reference	777570	640464	439263	779097	27317	629847	42375	629847	42375
A42 Reference	777572	640466	439265	779099	27319	629849	42377	629849	42377
A43 Reference	777574	640468	439267	779101	27321	629851	42379	629851	42379
A44 Reference	777576	640470	439269	779103	27323	629853	42381	629853	42381
A45 Reference	777578	640472	439271	779105	27325	629855	42383	629855	42383
A46 Reference	777580	640474	439273	779107	27327	629857	42385	629857	42385
A47 Reference	777582	640476	439275	779109	27329	629859	42387	629859	42387
A48 Reference	777584	640478	439277	779111	27331	629861	42389	629861	42389
A49 Reference	777586	640480	439279	779113	27333	629863	42391	629863	42391
A50 Reference	777588	640482	439281	779115	27335	629865	42393	629865	42393
A51 Reference	777590	640484	439283	779117	27337	629867	42395	629867	42395
A52 Reference	777592	640486	439285	779119	27339	629869	42397	629869	42397
A53 Reference	777594	640488	439287	779121	27341	629871	42399	629871	42399
A54 Reference	777596	640490	439289	779123	27343	629873	42401	629873	42401
A55 Reference	777598	640492	439291	779125	27345	629875	42403	629875	42403
A56 Reference	777600	640494	439293	779127	27347	629877	42405	629877	42405
A57 Reference	777602	640496	439295	779129	27349	629879	42407	629879	42407
A58 Reference	777604	640498	439297	779131	27351	629881	42409	629881	42409
A59 Reference	777606	640500	439299	779133	27353	629883	42411	629883	42411
A60 Reference	777608	640502	439301	779135	27355	629885	42413	629885	42413
A61 Reference	777610	640504	439303	779137	27357	629887	42415	629887	42415
A62 Reference	777612	640506	439305	779139	27359	629889	42417	629889	42417
A63 Reference	777614	640508	439307	779141	27361	629891	42419	629891	42419
A64 Reference	777616	640510	439309	779143	27363	629893	42421	629893	42421
A65 Reference	777618	640512	439311	779145	27365	629895	42423	629895	42423
A66 Reference	777620	640514	439313	779147	27367	629897	42425	629897	42425
A67 Reference	777622	640516	439315	779149	27369	629899	42427	629899	42427
A68 Reference	777624	640518	439317	779151	27371	629901	42429	629901	42429
A69 Reference	777626	640520	439319	779153	27373	629903	42431	629903	42431
A70 Reference	777628	640522	439321	779155	27375	629905	42433	629905	42433
A71 Reference	777630	640524	439323	779157	27377	629907	42435	629907	42435
A72 Reference	777632	640526	439325	779159	27379	629909	42437	629909	42437
A73 Reference	777634	640528	439327	779161	27381	629911	42439	629911	42439
A74 Reference	777636	640530	439329	779163	27383	629913	42441	629913	42441
A75 Reference	777638	640532	439331	779165	27385	629915	42443	629915	42443
A76 Reference	777640	640534	439333	779167	27387	629917	42445	629917	42445
A77 Reference	777642	640536	439335	779169	27389	629919	42447	629919	42447
A78 Reference	777644	640538	439337	779171	27391	629921	42449	629921	42449
A79 Reference	777646	640540	439339	779173	27393	629923	42451	629923	42451
A80 Reference	777648	640542	439341	779175	27395	629925	42453	629925	42453
A81 Reference	777650	640544	439343	779177	27397	629927	42455	629927	42455
A82 Reference	777652	640546	439345	779179	27399	629929	42457	629929	42457
A83 Reference	777654	640548	439347	779181	27401	629931	42459	629931	42459
A84 Reference	777656	640550	439349	779183	27403	629933	42461	629933	42461
A85 Reference	777658	640552	439351	779185	27405	629935	42463	629935	42463
A86 Reference	777660	640554	439353	779187	27407	629937	42465	629937	42465
A87 Reference	777662	640556	439355	779189	27409	629939	42467	629939	42467
A88 Reference	777664	640558	439357	779191	27411	629941	42469	629941	42469
A89 Reference	777666	640560	439359	779193	27413	629943	42471	629943	42471
A90 Reference	777668	640562	439361	779195	27415	629945	42473	629945	42473
A91 Reference	777670	640564	439363	779197	27417	629947	42475	629947	42475
A92 Reference	777672	640566	439365	779199	27419	629949	42477	629949	42477
A93 Reference	777674	640568	439367	779201	27421	629951	42479	629951	42479
A94 Reference	777676	640570	439369	779203	27423	629953	42481	629953	42481
A95 Reference	777678	640572	439371	779205	27425	629955	42483	629955	42483
A96 Reference	777680	640574	439373	779207	27427	629957	42485	629957	42485
A97 Reference	777682	640576	439375	779209	27429	629959	42487	629959	42487
A98 Reference	777684	640578	439377	779211	27431	629961	42489	629961	42489
A99 Reference	777686	640580	439379	779213	27433	629963	42491	629963	42491
A100 Reference	777688	640582	439381	779215	27435	629965	42493	629965	42493
A101 Reference	777690	640584	439383	779217	27437	629967	42495	629967	42495
A102 Reference	777692	640586	439385	779219	27439	629969	42497	629969	42497
A103 Reference	777694	640588	439387	779221	27441	629971	42499	629971	42499
A104 Reference	777696	640590	439389	779223	27443	629973	42501	629973	42501
A105 Reference	777698	640592	439391	779225	27445	629975	42503	629975	42503
A106 Reference	777700	640594	439393	779227	27447	629977	42505	629977	42505
A107 Reference	777702	640596	439395	779229	27449	629979	42507	629979	42507
A108 Reference	777704	640598	439397	779231	27451	629981	42509	629981	42509
A109 Reference	777706	640600	439399	779233	27453	629983	42511	629983	42511
A110 Reference	777708	640602	439401	779235	27455	629985	42513	629985	42513
A111 Reference	777710	640604	439403	779237	27457	629987	42515	629987	42515
A112 Reference	777712								

**table S6. Primer sequences used.**

Primer Name	Sequence
IL-32 enhancer amplicon 1 forward	ACATGGTGAAATCCCGTCCC
IL-32 enhancer amplicon 1 reverse	CCCTAAAACCACTAGCTGAGCA
IL-32 enhancer amplicon 2 forward	TGAGAATCTCGTGAGGCTGG
IL-32 enhancer amplicon 2 reverse	ACTTCTACCAAACCTGTCC
Total IL-32 forward	AGGACGTGGACAGGTGATGTC
Total IL-32 reverse	GTCTCCAGGTAGCCCTCTTTGA
Cyclophilin A (CypA/PPIA) forward	TCATCTGCACTGCCAAGACTG
Cyclophilin A (CypA/PPIA) reverse	CATGCCTTCTTTCACITTTGCC
β2-microglobulin (B2M)-fw	ATGAGTATGCCTGCCGTGTG
β2-microglobulin (B2M)-rev	CCAAATGCGGCATCTTCAAAC
3C primer A	CCTCTATGTGTTCTCTGGGTCG
3C primer rs4349147	GCAGGATAGAAGGTGAGAGATGAAT
3C primer B	GGGAACCTGACCTCAGACAG
3C primer C	GCACCCCTGTTGTTTCTCA
3C primer IL32 promoter	GAGGGAAAGTCCAGACTCGG
3C primer D	TCAGCCAAGCTCAGACAGC
3C primer E	GTGGCTTCCTTCTGTCTCCC
IL4R forward	CGTGGTCAGTGGGATAACTA
IL4R reverse	TGGTGTGAACTGTACAGTTTC
TNFRSF14 forward	GTGCAGTCCAGGTTATCGTGT
TNFRSF14 reverse	CACTTGCTTAGGCCATTGAGG
STAT5A forward	CGACGGGACCTTCTTGTG
STAT5A reverse	GTTCCGGGGAGTCAAACCTCC
LGALS1 forward	TCGCCAGCAACCTGAATCTC
LGALS1 reverse	GCACGAAGCTCTTAGCGTCA
ANXA1 forward	GCAGGCCTGGTTTATTGAAA
ANXA1 reverse	GCTGTGCATTGTTTCGCTTA
IL-32 enhancer gRNA 1 forward	ACCGGAAAAGAAAGTTGGGGCCG
IL-32 enhancer gRNA 1 reverse	ACCGCCAGCCTGCCGTTACGAG
IL-32 enhancer gRNA 2 forward	AAACCGGCCCCCACTTTCTTTTC
IL-32 enhancer gRNA 2 reverse	AAACCTGCTGAACGGCAGGCTGGC
IL-32 promoter forward	GTGGAGCTGGGTCACTCAG
IL-32 promoter reverse	CATGGCGGCCAAAAGTTCAA
rs12447486 forward	AGATCTGGCTGGATCCTGGT
rs12447486 reverse	TACTCATGCCTGCCTTCTGC
rs4349147 forward	CCTGGGGCAAGGATGATAGG
rs4349147 reverse	AGACCCAGCCTCACGAGATT
Oca2 promoter forward	TAAACCTCCCTGCCTGTT
Oca2 promoter reverse	CCCTCTGAGTTCTTACTTCG
Mock sgRNA 1 forward	ACCGGTCAAGGTGCACTCAATCGC
Mock sgRNA 1 reverse	AAACGCGATTGAGTGACCTTGAC
Mock sgRNA 2 forward	ACCGCTATCATCATCAGGGGCCG
Mock sgRNA 2 reverse	AAACCGGCCCTGATGATGATAGC
Amer1 forward	AGTACCCGTGAACAAACAGCA
Amer1 reverse	AGGCAGAGTACAGATACCCCTTC
CXXC4 forward	ATGCACCACCGAAACGACTC
CXXC4 reverse	GCAGTGTTCAGGGGATAAGGT
TNIK forward	TAAGGGTCGTCATGTCAAACG
TNIK reverse	CCATGCCTGGTGGGTTCTTT
IL-32 non-alpha forward	TCTTCA TGCCCTCTTTCCAGTCCTA
IL-32 non-alpha reverse	AAGGTGGTGTGAGTATCTTCATTTG
IL-32 alpha forward	CTTTTGGCCGCCATGTG
IL-32 alpha reverse	GTGCATTCGGGCCTTCAG
IL-32 beta forward	GAAGACTGCGTGCAGAAGGT
IL-32 beta reverse	CTTTCTATGGCCTGGTGCAT
IL-32 gamma forward	AGGCCGAATGGTAAATGCT
IL-32 gamma reverse	CTGTCTCAGGTAGCCCTCT