

Table S7. Annotations produced by the HIR V2/GSLA for downregulated genes.

Job Number: GSLA11042831061795

Cutoff used:

Q1: density ≥ 0.01

Q2: $p \leq 0.0005$

Meaning:

Q1: inter-geneset interaction density is greater than expected.

Q2: the observed interaction density can only be observed in the biologically correct interactome topology.

Categories selected: GO biological process

Species: Homo sapiens

Interaction dataset selected: HIR2.0

#Subjob Number: GSLA11042831061795_0

#Description: #top100-down

#Quaried GeneSet: MVB12B, EHD4, APOL3, IRF8, CXCL11, L2HGDH, TLR7, CXCL9, TOMM5, CXCL10, STX17, POMP, CLUAP1, C21orf91, UTP6, TOMM34, SLC31A2, C19orf12, NXF1, WARS, SYCP1, ISCA1, ARHGAP27, PAPD7, TXK, TNFSF10, CYP51A1, SLC38A5, WARS, RNF114, ALPK1, CYP7B1, GAD1, RAB31, HES4, ADAM19, HARS, WDFY2, SP100, CNDP2, C1QB, MASTL, HRASLS2, IGF2R, SLFN12, PELO, IFIT2, SFT2D2, CSTF3, PUS7, HMGCS1, RTP4, PLA1A, SBK1, SRSF4, ISCA1, RGL1, IFIT3, UGGT2, OASL, IFITM2, CD38, LILRA6, IFITM1, BATF2, DOPEY1, CSTF3, TSPAN13, PSMB10, C17orf67, IFIT1, RBMS2, IFI27, SCYL3, CKAP4, CEACAM1, HSH2D, NUP205, ZNF438, MT2A, LYN, CHRN1, ELMO2, ACSL1, STAT1, FAM111A, CCL5, IDO1, RSAD2, FGL2, SP140, EFR3A, CGNL1, N4BP2L2, CLEC2D, KPNA5, RUNX3, TMEM97, QPRT, APOBEC3G

Term type	Term	Description	Term size	P-value	Density	Interaction number	Overlap gene number	Overlap gene(s)	Interactions	Supported term
GO biological process	GO:0043631	RNA polyadenylation	17	3.00E-04	0.0103	17	1	CSTF3	LYN-HGNC:620 STAT1-HGNC:23166 IFIT3-HGNC:23166 SRSF4-HGNC:26184 SRSF4-HGNC:8554 PAPD7-HGNC:25016 PAPD7-HGNC:26184 PAPD7-HGNC:8554 PAPD7-HGNC:25532 PAPD7-HGNC:26776 PAPD7-HGNC:14981 PAPD7-HGNC:14982 PAPD7-HGNC:30401 CSTF3-HGNC:26184 CSTF3-HGNC:8554 CSTF3-HGNC:14981 IFIT1-HGNC:23166	N
GO biological process	GO:0038113	interleukin-9-mediated signaling pathway	9	0	0.0183	16	1	STAT1	LYN-HGNC:11367 LYN-HGNC:11366 LYN-HGNC:11364 LYN-HGNC:6193 LYN-STAT1 STAT1-HGNC:11367 STAT1-HGNC:11366 STAT1-HGNC:11364 STAT1-HGNC:6190 RUNX3-HGNC:6193 IFIT3-STAT1 TXK-HGNC:11367 TXK-HGNC:11366 TXK-STAT1 TXK-HGNC:6190 IFIT1-STAT1	Y
GO biological process	GO:2000563	positive regulation of CD4-positive, alpha-beta T cell proliferation	5	1.00E-04	0.0144	7	0		LYN-HGNC:2665 LYN-HGNC:6570 STAT1-HGNC:11773 CXCL9-HGNC:10645 RUNX3-HGNC:11773 CCL5-HGNC:10645 CXCL10-HGNC:10645	Y
GO biological process	GO:0071677	positive regulation of mononuclear cell migration	19	0	0.0103	19	2	CCL5 CXCL10	LYN-HGNC:6563 LYN-HGNC:1602 LYN-HGNC:1603 LYN-HGNC:25240 LYN-HGNC:3827 STAT1-HGNC:4983 SP100-HGNC:4983 CXCL9-CXCL10 CCL5-HGNC:1603 CCL5-CXCL10 CXCL10-HGNC:9040 CXCL10-HGNC:1602 CXCL10-HGNC:1603 CXCL10-HGNC:4983 CXCL10-HGNC:10609 CXCL10-CCL5 CXCL10-HGNC:8583 CXCL10-HGNC:10672 CXCL11-CXCL10	N
GO biological process	GO:0045236	CXCR chemokine receptor binding	10	0	0.0258	25	3	CXCL9 CXCL11	CXCL9-HGNC:12840 CXCL9-HGNC:6025 CXCL9-HGNC:8861 CXCL9-CXCL10 CXCL9-HGNC:10639 CXCL9-CXCL11 CXCL9-HGNC:10647 WARS-HGNC:12840 CCL5-CXCL10 CCL5-HGNC:10639 CXCL10-HGNC:12840 CXCL10-HGNC:6025 CXCL10-HGNC:8861 CXCL10-CXCL9 CXCL10-HGNC:10639 CXCL10-HGNC:10672 CXCL10-CXCL11 CXCL10-HGNC:10647 CXCL11-HGNC:12840 CXCL11-HGNC:6025 CXCL11-HGNC:8861 CXCL11-CXCL9 CXCL11-CXCL10 CXCL11-HGNC:10639 CXCL11-HGNC:10647	Y

GO biological process	GO:0019773	proteasome core complex, alpha-subunit complex	8	2.00E-04	0.0129	10	0		POMP-HGNC:9531 POMP-HGNC:9532 POMP-HGNC:9536 PSMB10-HGNC:9531 PSMB10-HGNC:9532 PSMB10-HGNC:9533 PSMB10-HGNC:9534 PSMB10-HGNC:9535 PSMB10-HGNC:9536 PSMB10-HGNC:9530	N
GO biological process	GO:2000410	regulation of thymocyte migration	4	2.00E-04	0.0155	6	0		LYN-HGNC:1603 CXCL9-HGNC:10645 CCL5-HGNC:1603 CCL5-HGNC:10645 CXCL10-HGNC:1603 CXCL10-HGNC:10645	N
GO biological process	GO:1901623	regulation of lymphocyte chemotaxis	20	0	0.0119	23	2	CCL5 CXCL10	LYN-HGNC:1603 LYN-HGNC:9612 CXCL9-HGNC:10645 CXCL9-CXCL10 CXCL9-HGNC:10639 TXK-HGNC:9612 CCL5-HGNC:1603 CCL5-HGNC:10630 CCL5-HGNC:10620 CCL5-HGNC:10627 CCL5-HGNC:10645 CCL5-HGNC:10618 CCL5-CXCL10 CCL5-HGNC:10639 CXCL10-HGNC:1603 CXCL10-HGNC:10620 CXCL10-CCL5 CXCL10-HGNC:10645 CXCL10-HGNC:10634 CXCL10-HGNC:10618 CXCL10-HGNC:10639 CXCL11-CXCL10 CXCL11-HGNC:10639	Y
GO biological process	GO:0072307	regulation of metanephric nephron tubule epithelial cell differentiation	4	5.00E-04	0.018	7	1	STAT1	LYN-STAT1 STAT1-HGNC:6596 STAT1-HGNC:8622 STAT1-HGNC:8616 IFIT3-STAT1 TXK-STAT1 IFIT1-STAT1	N
GO biological process	GO:0010820	positive regulation of T cell chemotaxis	12	0	0.0112	13	1	CCL5	LYN-HGNC:1603 CXCL9-HGNC:10645 CXCL9-HGNC:10639 CCL5-HGNC:1603 CCL5-HGNC:10620 CCL5-HGNC:10645 CCL5-HGNC:10639 CXCL10-HGNC:1603 CXCL10-HGNC:10620 CXCL10-HGNC:10645 CXCL10-CCL5 CXCL10-HGNC:10639 CXCL11-HGNC:10639	Y
GO biological process	GO:2000503	positive regulation of natural killer cell chemotaxis	5	0	0.0144	7	1	CCL5	CXCL9-HGNC:10645 CCL5-HGNC:10627 CCL5-HGNC:10630 CCL5-HGNC:10645 CXCL10-HGNC:10645 CXCL10-CCL5 CXCL10-HGNC:10634	Y
GO biological process	GO:0031118	rRNA pseudouridine synthesis	5	2.00E-04	0.0144	7	0		PUS7-HGNC:2890 PUS7-HGNC:25126 PUS7-HGNC:14377 PUS7-HGNC:14378 PUS7-HGNC:14264 PAPD7-HGNC:2890 CSTF3-HGNC:14377	N
GO biological process	GO:0006398	mRNA 3'-end processing by stem-loop binding and cleavage	5	1.00E-04	0.0165	8	0		PAPD7-HGNC:2325 PAPD7-HGNC:2326 PAPD7-HGNC:10904 PAPD7-HGNC:23239 PAPD7-HGNC:30860 NUP205-HGNC:2326 CSTF3-HGNC:2325 CSTF3-HGNC:2326	N
GO biological process	GO:0005839	proteasome core complex	17	0	0.0146	24	1	PSMB10	POMP-HGNC:9531 POMP-HGNC:9544 POMP-HGNC:9532 POMP-HGNC:9542 POMP-HGNC:9536 POMP-HGNC:9537 POMP-HGNC:9546 POMP-HGNC:9541 PSMB10-HGNC:9531 PSMB10-HGNC:9544 PSMB10-HGNC:9532 PSMB10-HGNC:9545 PSMB10-HGNC:9542 PSMB10-HGNC:9533 PSMB10-HGNC:9543 PSMB10-HGNC:9534 PSMB10-HGNC:9535 PSMB10-HGNC:9536 PSMB10-HGNC:9537 PSMB10-HGNC:9546 PSMB10-HGNC:9539 PSMB10-HGNC:9530 PSMB10-HGNC:9541 PSMB10-HGNC:9540	N
GO biological process	GO:0038110	interleukin-2-mediated signaling pathway	11	1.00E-04	0.015	16	0		LYN-HGNC:10840 LYN-HGNC:9612 LYN-HGNC:11367 LYN-HGNC:11366 LYN-HGNC:11491 LYN-HGNC:6193 STAT1-HGNC:11367 STAT1-HGNC:11366 STAT1-HGNC:6190 RUNX3-HGNC:6193 TXK-HGNC:9612 TXK-HGNC:11367 TXK-HGNC:11366 TXK-HGNC:11491 TXK-HGNC:6190 CEACAM1-HGNC:11491	Y

GO biological process	GO:0010543	regulation of platelet activation	25	0	0.0124	30	2	CEACAM1 LYN	LYN-CEACAM1 LYN-HGNC:9070 LYN-HGNC:429 LYN-HGNC:29605 LYN-HGNC:8803 LYN-HGNC:11719 LYN-HGNC:9393 LYN-HGNC:29602 LYN-HGNC:1709 LYN-HGNC:11491 LYN-HGNC:9414 STAT1-HGNC:9399 STAT1-LYN TLR7-HGNC:11850 MASTL-HGNC:9399 MASTL-HGNC:9393 TXK-LYN TXK-HGNC:11719 TXK-HGNC:11491 CEACAM1-HGNC:3382 CEACAM1-HGNC:9070 CEACAM1-LYN CEACAM1-HGNC:429 CEACAM1-HGNC:9393 CEACAM1-HGNC:29602 CEACAM1-HGNC:1709 CEACAM1-HGNC:11491 CEACAM1-HGNC:8800 CEACAM1-HGNC:9414 IDO1-HGNC:429	N
GO biological process	GO:0004713	protein tyrosine kinase activity	92	0	0.0105	94	2	LYN IGF2R	LYN-HGNC:365 / LYN-HGNC:405 / LYN-HGNC:4840 LYN-HGNC:3655 LYN-HGNC:3697 LYN-HGNC:3223 LYN-HGNC:1079 LYN-HGNC:6906 LYN-HGNC:5465 LYN-HGNC:6524 LYN-HGNC:8804 LYN-HGNC:9611 LYN-HGNC:12841 LYN-HGNC:8803 LYN-HGNC:77 LYN-HGNC:6091 LYN-HGNC:76 LYN-HGNC:9612 LYN-HGNC:9617 LYN-HGNC:3393 LYN-HGNC:3395 LYN-HGNC:6171 LYN-HGNC:11719 LYN-HGNC:2444 LYN-HGNC:10261 LYN-HGNC:3388 LYN-HGNC:11283 LYN-HGNC:3386 LYN-HGNC:3387 LYN-HGNC:1133 LYN-HGNC:3385 LYN-HGNC:2433 LYN-HGNC:19297 LYN-HGNC:3432 LYN-HGNC:12446 LYN-HGNC:3688 LYN-HGNC:6192 LYN-HGNC:6193 LYN-HGNC:1057 LYN-HGNC:12858 LYN-HGNC:6342 LYN-HGNC:6307 LYN-HGNC:3091 LYN-HGNC:11491 LYN-HGNC:3955 STAT1-HGNC:4840 STAT1-HGNC:3655 STAT1-LYN STAT1-HGNC:76 STAT1-HGNC:1133 STAT1-HGNC:3689 STAT1-HGNC:6192 STAT1-HGNC:6190 STAT1-HGNC:3236 SP100-HGNC:961 RUNX3-HGNC:6193 SRSF4-HGNC:3091 MASTL-HGNC:2068 MASTL-HGNC:16870 MASTL-HGNC:3091 TXK-HGNC:3657 TXK-HGNC:4037 TXK-HGNC:3697 TXK-HGNC:1079 TXK-HGNC:6906 TXK-LYN TXK-HGNC:6524 TXK-HGNC:8804 TXK-HGNC:77 TXK-HGNC:76 TXK-HGNC:9612 TXK-HGNC:9617 TXK-HGNC:6171 TXK-HGNC:11719 TXK-HGNC:2444 TXK-HGNC:11283 TXK-HGNC:3765 TXK-HGNC:3386 TXK-HGNC:1133 TXK-HGNC:3385 TXK-HGNC:19297 TXK-HGNC:12446 TXK-HGNC:6192 TXK-HGNC:6190 TXK-HGNC:1057 TXK-HGNC:12858 TXK-LYN-TXK LYN-HGNC:19383 LYN-HGNC:6192 LYN-HGNC:19391 LYN-STAT1 STAT1-HGNC:29933 STAT1-HGNC:9236 STAT1-TXK STAT1-HGNC:19383 STAT1-HGNC:12502 STAT1-HGNC:29232 STAT1-HGNC:6192 STAT1-HGNC:6190 STAT1-HGNC:9650 STAT1-HGNC:5258 STAT1-HGNC:2752 STAT1-HGNC:19391 STAT1-HGNC:24118 MT2A-HGNC:12502 RUNX3-HGNC:19383 RUNX3-HGNC:9650 IFIT3-STAT1 TXK-HGNC:19383 TXK-HGNC:6192 TXK-HGNC:6190 TXK-HGNC:9650 TXK-HGNC:24118 TXK-STAT1 IFIT1-STAT1	N
GO biological process	GO:0060334	regulation of interferon-gamma-mediated signaling pathway	21	0	0.0142	29	2	TXK STAT1	LYN-HGNC:19319 RSAD2-HGNC:6122 STAT1-HGNC:6116 STAT1-HGNC:6122 IFIT3-HGNC:6116 CEACAM1-HGNC:19319 CCL5-HGNC:19319 IFIT1-HGNC:6116	Y
GO biological process	GO:0034124	regulation of MyD88-dependent toll-like receptor signaling pathway	4	0	0.0206	8	0			Y

GO biological process	GO:0090026	positive regulation of monocyte chemotaxis	17	0	0.0109	18	2	CCL5 CXCL10	LYN-HGNC:1602 LYN-HGNC:1603 LYN-HGNC:25240 LYN-HGNC:3827 STAT1-HGNC:4983 SP100-HGNC:4983 CXCL9-CXCL10 CCL5-HGNC:1603 CCL5-CXCL10 CXCL10-HGNC:9040 CXCL10-HGNC:1602 CXCL10-HGNC:1603 CXCL10-HGNC:4983 CXCL10-HGNC:10609 CXCL10-CCL5 CXCL10-HGNC:8583 CXCL10-HGNC:10672 CXCL11-CXCL10	Y
GO biological process	GO:0016973	poly(A)+ mRNA export from nucleus	7	2.00E-04	0.0103	7	0		POMP-HGNC:24449 SRSF4-HGNC:8565 SRSF4-HGNC:23782 NXF1-HGNC:19073 NXF1-HGNC:23782 NXF1-HGNC:24449 NXF1-HGNC:29093	N
GO biological process	GO:0010793	regulation of mRNA export from nucleus	4	2.00E-04	0.0258	10	0		STAT1-HGNC:18420 SP100-HGNC:18420 SP100-HGNC:11470 SP100-HGNC:12017 SP100-HGNC:25467 NUP205-HGNC:12017 NXF1-HGNC:18420 NXF1-HGNC:11470 NXF1-HGNC:12017 NXF1-HGNC:25467	N
GO biological process	GO:2000564	regulation of CD8-positive, alpha-beta T cell proliferation	6	1.00E-04	0.012	7	0		STAT1-HGNC:6116 CXCL9-HGNC:10645 IFIT3-HGNC:6116 CEACAM1-HGNC:4962 CCL5-HGNC:10645 CXCL10-HGNC:10645 IFIT1-HGNC:6116	Y
GO biological process	GO:0008009	chemokine activity	27	0	0.0115	30	4	CXCL9 CCL5 CXCL10	CXCL9-HGNC:10645 CXCL9-HGNC:10647 CXCL9-HGNC:8861 CXCL9-HGNC:6025 CXCL9-CXCL10 CXCL9-HGNC:10639 CXCL9-CXCL11 CCL5-HGNC:10620 CCL5-HGNC:10627 CCL5-HGNC:10645 CCL5-CXCL10 CCL5-HGNC:10639 CXCL10-HGNC:10620 CXCL10-CXCL9 CXCL10-HGNC:10609 CXCL10-HGNC:10645 CXCL10-HGNC:10647 CXCL10-HGNC:8861 CXCL10-HGNC:6025 CXCL10-CCL5 CXCL10-HGNC:10634 CXCL10-HGNC:10639 CXCL10-CXCL11 CXCL10-HGNC:10672 CXCL11-CXCL9 CXCL11-HGNC:10647 CXCL11-HGNC:8861 CXCL11-HGNC:6025 CXCL11-CXCL10 CXCL11-HGNC:10639	Y
GO biological process	GO:0042494	detection of bacterial lipoprotein	4	0	0.0129	5	0		LYN-HGNC:16711 LYN-HGNC:11847 TLR7-HGNC:16711 TLR7-HGNC:11848 TLR7-HGNC:11847	Y
GO biological process	GO:0004652	polynucleotide adenylyltransferase activity	8	0	0.0103	8	0		SRSF4-HGNC:26184 PAPD7-HGNC:26776 PAPD7-HGNC:26184 PAPD7-HGNC:14981 PAPD7-HGNC:25532 PAPD7-HGNC:14982 CSTF3-HGNC:26184 CSTF3-HGNC:14981	N
GO biological process	GO:0033004	negative regulation of mast cell activation	7	0	0.0103	7	0		LYN-HGNC:3655 LYN-HGNC:3358 LYN-HGNC:19319 LYN-HGNC:6570 STAT1-HGNC:3655 CEACAM1-HGNC:19319 CCL5-HGNC:19319	Y
GO biological process	GO:0034111	negative regulation of homotypic cell-cell adhesion	11	0	0.0103	11	1	CEACAM1	LYN-HGNC:29605 LYN-CEACAM1 LYN-HGNC:1709 LYN-HGNC:9414 LYN-HGNC:429 STAT1-HGNC:9399 MASTL-HGNC:9399 CEACAM1-HGNC:1709 CEACAM1-HGNC:9414 CEACAM1-HGNC:429 IDO1-HGNC:429	N
GO biological process	GO:0031080	nuclear pore outer ring	9	2.00E-04	0.0115	10	0		NUP205-HGNC:21182 NUP205-HGNC:30379 NUP205-HGNC:8734 NUP205-HGNC:8068 NUP205-HGNC:29929 NUP205-HGNC:18017 NUP205-HGNC:29914 NUP205-HGNC:18016 NXF1-HGNC:8068 KPNA5-HGNC:8068	N
GO biological process	GO:0090331	negative regulation of platelet aggregation	9	1.00E-04	0.0126	11	1	CEACAM1	LYN-HGNC:29605 LYN-CEACAM1 LYN-HGNC:1709 LYN-HGNC:9414 LYN-HGNC:429 STAT1-HGNC:9399 MASTL-HGNC:9399 CEACAM1-HGNC:1709 CEACAM1-HGNC:9414 CEACAM1-HGNC:429 IDO1-HGNC:429	N

GO biological process	GO:0006999	nuclear pore organization	11	0	0.0141	15	1	NUP205	SP100-HGNC:12017 NUP205-HGNC:30379 NUP205-HGNC:25525 NUP205-HGNC:29577 NUP205-HGNC:14085 NUP205-HGNC:12017 NUP205-HGNC:8068 NUP205-HGNC:29914 NUP205-HGNC:18016 NUP205-HGNC:28958 NUP205-HGNC:8062 NXF1-HGNC:12017 NXF1-HGNC:8068 NXF1-HGNC:28958 KPNA5-HGNC:8068	N
GO biological process	GO:0071221	cellular response to bacterial lipopeptide	6	4.00E-04	0.0103	6	0		LYN-HGNC:16711 LYN-HGNC:17192 LYN-HGNC:11847 TLR7-HGNC:16711 TLR7-HGNC:11848 TLR7-HGNC:11847	Y
GO biological process	GO:0019774	proteasome core complex, beta-subunit complex	11	0	0.0131	14	1	PSMB10	POMP-HGNC:9544 POMP-HGNC:9542 POMP-HGNC:9537 POMP-HGNC:9546 POMP-HGNC:9541 PSMB10-HGNC:9544 PSMB10-HGNC:9545 PSMB10-HGNC:9542 PSMB10-HGNC:9543 PSMB10-HGNC:9537 PSMB10-HGNC:9546 PSMB10-HGNC:9539 PSMB10-HGNC:9541 PSMB10-HGNC:9540	N
GO biological process	GO:0048248	CXCR3 chemokine receptor binding	5	0	0.0289	14	3	CXCL9 CXCL11	CXCL9-HGNC:8861 CXCL9-CXCL10 CXCL9-HGNC:10639 CXCL9-CXCL11 CCL5-CXCL10 CCL5-HGNC:10639 CXCL10-HGNC:8861 CXCL10-CXCL9 CXCL10-HGNC:10639 CXCL10-CXCL11 CXCL11-HGNC:8861 CXCL11-CXCL9 CXCL11-CXCL10 CXCL11-HGNC:10639	Y
GO biological process	GO:2001187	positive regulation of CD8-positive, alpha-beta T cell activation	6	2.00E-04	0.0137	8	1	RUNX3	LYN-HGNC:10471 CXCL9-HGNC:10645 RUNX3-HGNC:1539 RUNX3-HGNC:10471 RUNX3-HGNC:4862 CEACAM1-HGNC:4962 CCL5-HGNC:10645 CXCL10-HGNC:10645	Y
GO biological process	GO:0004715	non-membrane spanning protein tyrosine kinase activity	26	0	0.019	48	1	LYN	LYN-HGNC:11283 LYN-HGNC:3657 LYN-HGNC:3655 LYN-HGNC:3697 LYN-HGNC:1133 LYN-HGNC:1079 LYN-HGNC:9611 LYN-HGNC:12841 LYN-HGNC:77 LYN-HGNC:9612 LYN-HGNC:76 LYN-HGNC:9617 LYN-HGNC:6171 LYN-HGNC:6192 LYN-HGNC:1057 LYN-HGNC:12858 LYN-HGNC:11719 LYN-HGNC:3091 LYN-HGNC:11491 STAT1-HGNC:3655 STAT1-HGNC:1133 STAT1-LYN STAT1-HGNC:76 STAT1-HGNC:6192 STAT1-HGNC:6190 SRSF4-HGNC:3091 MASTL-HGNC:16870 MASTL-HGNC:2068 MASTL-HGNC:3091 TXK-HGNC:11283 TXK-HGNC:3657 TXK-HGNC:3697 TXK-HGNC:1133 TXK-HGNC:1079 TXK-LYN TXK-HGNC:77 TXK-HGNC:9612 TXK-HGNC:76 TXK-HGNC:9617 TXK-HGNC:6171 TXK-HGNC:6192 TXK-HGNC:6190 TXK-HGNC:1057 TXK-HGNC:12858 TXK-HGNC:11719 TXK-HGNC:11491 CEACAM1-LYN CEACAM1-HGNC:11491	N
GO biological process	GO:0035456	response to interferon-beta	19	0	0.0119	22	3	IFITM1 IFITM2	LYN-HGNC:9092 LYN-STAT1 STAT1-HGNC:23166 STAT1-HGNC:6116 STAT1-HGNC:1734 STAT1-HGNC:4914 IFIT3-HGNC:23166 IFIT3-HGNC:6116 IFIT3-HGNC:1734 IFIT3-HGNC:4914 IFIT3-STAT1 IFITM1-IFITM2 IFITM1-HGNC:5414 IFITM2-IFITM1 IFITM2-HGNC:5414 TXK-STAT1 IFIT1-HGNC:23166 IFIT1-HGNC:6116 IFIT1-HGNC:1734 IFIT1-HGNC:4914 IFIT1-HGNC:14348 IFIT1-STAT1	Y
GO biological process	GO:0070757	interleukin-35-mediated signaling pathway	10	3.00E-04	0.0134	13	1	STAT1	LYN-HGNC:11364 LYN-HGNC:6192 LYN-STAT1 STAT1-HGNC:11365 STAT1-HGNC:11364 STAT1-HGNC:6192 STAT1-HGNC:6190 STX17-HGNC:1473 IFIT3-STAT1 TXK-HGNC:6192 TXK-STAT1 TXK-HGNC:6190 IFIT1-STAT1	Y

GO biological process	GO:0032727	positive regulation of interferon-alpha production	17	0	0.0127	21	2	TLR7 STAT1	LYN-STAT1 RSAD2-HGNC:6122 STAT1-HGNC:6118 STAT1-HGNC:18873 STAT1-HGNC:2750 STAT1-HGNC:18420 STAT1-HGNC:6122 STAT1-HGNC:1974 SP100-HGNC:18420 TLR7-HGNC:15633 TLR7-HGNC:15632 TLR7-HGNC:11849 TLR7-HGNC:11850 IFIT3-STAT1 SRSF4-HGNC:2750 TXK-STAT1 NXF1-HGNC:18420 IFIT1-HGNC:19102 IFIT1-HGNC:18873 IFIT1-HGNC:2750 IFIT1-STAT1	Y
GO biological process	GO:0042532	negative regulation of tyrosine phosphorylation of STAT protein	8	0	0.0142	11	0		LYN-HGNC:29605 LYN-HGNC:19383 LYN-HGNC:19391 STAT1-HGNC:9650 STAT1-HGNC:19383 STAT1-HGNC:19391 STAT1-HGNC:29232 RUNX3-HGNC:9650 RUNX3-HGNC:19383 TXK-HGNC:9650 TXK-HGNC:19383	N
GO biological process	GO:0051770	positive regulation of nitric-oxide synthase biosynthetic process	10	1.00E-04	0.0103	10	0		LYN-HGNC:6307 LYN-HGNC:6192 STAT1-HGNC:6192 TLR7-HGNC:15633 TLR7-HGNC:11850 TLR7-HGNC:11848 TXK-HGNC:6192 CEACAM1-HGNC:6307 CCL5-HGNC:10618 CXCL10-HGNC:10618	N
GO biological process	GO:0035458	cellular response to interferon-beta	11	0	0.0159	17	1	STAT1	LYN-STAT1 STAT1-HGNC:23166 STAT1-HGNC:6116 STAT1-HGNC:1734 STAT1-HGNC:4914 IFIT3-HGNC:23166 IFIT3-HGNC:6116 IFIT3-HGNC:1734 IFIT3-HGNC:4914 IFIT3-STAT1 TXK-STAT1 IFIT1-HGNC:23166 IFIT1-HGNC:6116 IFIT1-HGNC:14348 IFIT1-HGNC:1734 IFIT1-HGNC:4914 IFIT1-STAT1	Y
GO biological process	GO:0090330	regulation of platelet aggregation	15	1.00E-04	0.0158	23	2	CEACAM1 LYN	LYN-CEACAM1 LYN-HGNC:429 LYN-HGNC:29605 LYN-HGNC:9393 LYN-HGNC:29602 LYN-HGNC:1709 LYN-HGNC:11491 LYN-HGNC:9414 STAT1-HGNC:9399 STAT1-LYN MASTL-HGNC:9399 MASTL-HGNC:9393 TXK-LYN TXK-HGNC:11491 CEACAM1-HGNC:3382 CEACAM1-LYN CEACAM1-HGNC:429 CEACAM1-HGNC:9393 CEACAM1-HGNC:29602 CEACAM1-HGNC:1709 CEACAM1-HGNC:11491 CEACAM1-HGNC:9414 IDO1-HGNC:429	N
GO biological process	GO:0051292	nuclear pore complex assembly	9	0	0.0149	13	1	NUP205	SP100-HGNC:12017 NUP205-HGNC:25525 NUP205-HGNC:29577 NUP205-HGNC:14085 NUP205-HGNC:12017 NUP205-HGNC:8068 NUP205-HGNC:29914 NUP205-HGNC:28958 NUP205-HGNC:8062 NXF1-HGNC:12017 NXF1-HGNC:8068 NXF1-HGNC:28958 KPNA5-HGNC:8068	N
GO biological process	GO:0033007	negative regulation of mast cell activation involved in immune response	5	0	0.0144	7	0		LYN-HGNC:3655 LYN-HGNC:3358 LYN-HGNC:19319 LYN-HGNC:6570 STAT1-HGNC:3655 CEACAM1-HGNC:19319 CCL5-HGNC:19319	Y
GO biological process	GO:0071044	histone mRNA catabolic process	13	0	0.0127	16	0		SRSF4-HGNC:26184 SRSF4-HGNC:20472 SRSF4-HGNC:11316 PAPD7-HGNC:9962 PAPD7-HGNC:26776 PAPD7-HGNC:18189 PAPD7-HGNC:26184 PAPD7-HGNC:25817 PAPD7-HGNC:20472 PAPD7-HGNC:30654 PAPD7-HGNC:9138 PAPD7-HGNC:11316 PAPD7-HGNC:25532 PAPD7-HGNC:28981 CSTF3-HGNC:26184 PELO-HGNC:9138	N

GO biological process	GO:0042379	chemokine receptor binding	42	0	0.0101	41	4	CXCL9 CCL5 C	LYN-HGNC:1603 CXCL9-HGNC:12840 CXCL9-HGNC:10645 CXCL9-HGNC:10647 CXCL9-HGNC:8861 CXCL9-HGNC:6025 CXCL9-CXCL10 CXCL9-HGNC:10639 CXCL9-CXCL11 WARS-HGNC:12840 CCL5-HGNC:10620 CCL5-HGNC:10627 CCL5-HGNC:10645 CCL5-HGNC:10630 CCL5-HGNC:1603 CCL5-CXCL10 CCL5-HGNC:10618 CCL5-HGNC:10639 CXCL10-HGNC:10620 CXCL10-CXCL9 CXCL10-HGNC:12840 CXCL10-HGNC:10609 CXCL10-HGNC:10645 CXCL10-HGNC:10647 CXCL10-HGNC:1603 CXCL10-HGNC:8861 CXCL10-HGNC:6025 CXCL10-CCL5 CXCL10-HGNC:10634 CXCL10-HGNC:10618 CXCL10-HGNC:10619 CXCL10-HGNC:10639 CXCL10-HGNC:10672 CXCL10-CXCL11 CXCL11-CXCL9 CXCL11-HGNC:12840 CXCL11-HGNC:10647 CXCL11-HGNC:8861 CXCL11-HGNC:6025 CXCL11-CXCL10 CXCL11-HGNC:10639	Y
GO biological process	GO:0060330	regulation of response to interferon-gamma	21	0	0.0142	29	2	TXK STAT1	LYN-TXK LYN-HGNC:19383 LYN-HGNC:6192 LYN-HGNC:19391 LYN-STAT1 STAT1-HGNC:29933 STAT1-HGNC:9236 STAT1-TXK STAT1-HGNC:19383 STAT1-HGNC:12502 STAT1-HGNC:29232 STAT1-HGNC:6192 STAT1-HGNC:6190 STAT1-HGNC:9650 STAT1-HGNC:5258 STAT1-HGNC:2752 STAT1-HGNC:19391 STAT1-HGNC:24118 MT2A-HGNC:12502 RUNX3-HGNC:19383 RUNX3-HGNC:9650 IFIT3-STAT1 TXK-HGNC:19383 TXK-HGNC:6192 TXK-HGNC:6190 TXK-HGNC:9650 TXK-HGNC:24118 TXK-STAT1 IFIT1-STAT1	Y
GO biological process	GO:0045309	protein phosphorylated amino acid binding	39	2.00E-04	0.0114	43	0		LYN-HGNC:10840 LYN-HGNC:4840 LYN-HGNC:9066 LYN-HGNC:3697 LYN-HGNC:2362 LYN-HGNC:9658 LYN-HGNC:6524 LYN-HGNC:2363 LYN-HGNC:12841 LYN-HGNC:77 LYN-HGNC:76 LYN-HGNC:12657 LYN-HGNC:12658 LYN-HGNC:9644 LYN-HGNC:12858 LYN-HGNC:10838 LYN-HGNC:4566 LYN-HGNC:11491 LYN-HGNC:9871 STAT1-HGNC:4840 STAT1-HGNC:2363 STAT1-HGNC:76 STAT1-HGNC:12657 STAT1-HGNC:9644 STAT1-HGNC:9871 SP100-HGNC:12851 MASTL-HGNC:12851 TXK-HGNC:9066 TXK-HGNC:3697 TXK-HGNC:2362 TXK-HGNC:9658 TXK-HGNC:6524 TXK-HGNC:2363 TXK-HGNC:77 TXK-HGNC:76 TXK-HGNC:12657 TXK-HGNC:9644 TXK-HGNC:12858 TXK-HGNC:4566 TXK-HGNC:11491 TXK-HGNC:9871 CEACAM1-HGNC:6524 CEACAM1-HGNC:11491	N
GO biological process	GO:0010819	regulation of T cell chemotaxis	13	0	0.0127	16	2	CCL5 CXCL10	LYN-HGNC:1603 CXCL9-HGNC:10645 CXCL9-CXCL10 CXCL9-HGNC:10639 CCL5-HGNC:1603 CCL5-HGNC:10620 CCL5-HGNC:10645 CCL5-CXCL10 CCL5-HGNC:10639 CXCL10-HGNC:1603 CXCL10-HGNC:10620 CXCL10-CCL5 CXCL10-HGNC:10645 CXCL10-HGNC:10639 CXCL11-CXCL10 CXCL11-HGNC:10639	Y

GO biological process	GO:0046831	regulation of RNA export from nucleus	10	5.00E-04	0.0206	20	0		STAT1-HGNC:2750 STAT1-HGNC:18420 SP100-HGNC:18420 SP100-HGNC:11470 SP100-HGNC:12017 SP100-HGNC:25467 SRSF4-HGNC:7659 SRSF4-HGNC:13871 SRSF4-HGNC:18116 SRSF4-HGNC:2750 NUP205-HGNC:13871 NUP205-HGNC:12017 NUP205-HGNC:8062 CSTF3-HGNC:7659 CSTF3-HGNC:13871 NXF1-HGNC:18420 NXF1-HGNC:11470 NXF1-HGNC:12017 NXF1-HGNC:25467 IFIT1-HGNC:2750	N
GO biological process	GO:0001784	phosphotyrosine residue binding	32	5.00E-04	0.0132	41	0		LYN-HGNC:10840 LYN-HGNC:9066 LYN-HGNC:4840 LYN-HGNC:3697 LYN-HGNC:2362 LYN-HGNC:9658 LYN-HGNC:6524 LYN-HGNC:2363 LYN-HGNC:12841 LYN-HGNC:77 LYN-HGNC:76 LYN-HGNC:12657 LYN-HGNC:12658 LYN-HGNC:9644 LYN-HGNC:10838 LYN-HGNC:12858 LYN-HGNC:4566 LYN-HGNC:11491 LYN-HGNC:9871 STAT1-HGNC:4840 STAT1-HGNC:2363 STAT1-HGNC:76 STAT1-HGNC:12657 STAT1-HGNC:9644 STAT1-HGNC:9871 TXK-HGNC:9066 TXK-HGNC:3697 TXK-HGNC:2362 TXK-HGNC:9658 TXK-HGNC:6524 TXK-HGNC:2363 TXK-HGNC:77 TXK-HGNC:76 TXK-HGNC:12657 TXK-HGNC:9644 TXK-HGNC:12858 TXK-HGNC:4566 TXK-HGNC:11491 TXK-HGNC:9871 CEACAM1-HGNC:6524 CEACAM1-HGNC:11491	N
GO biological process	GO:0008334	histone mRNA metabolic process	26	0	0.0123	31	0		SRSF4-HGNC:11161 SRSF4-HGNC:11160 SRSF4-HGNC:11316 SRSF4-HGNC:20472 SRSF4-HGNC:26184 SRSF4-HGNC:11153 SRSF4-HGNC:7659 SRSF4-HGNC:7658 PAPD7-HGNC:2325 PAPD7-HGNC:2326 PAPD7-HGNC:30654 PAPD7-HGNC:11316 PAPD7-HGNC:25532 PAPD7-HGNC:30860 PAPD7-HGNC:9962 PAPD7-HGNC:25817 PAPD7-HGNC:20472 PAPD7-HGNC:9138 PAPD7-HGNC:23239 PAPD7-HGNC:26184 PAPD7-HGNC:28981 PAPD7-HGNC:26776 PAPD7-HGNC:18189 PAPD7-HGNC:10904 NUP205-HGNC:2326 CSTF3-HGNC:2325 CSTF3-HGNC:2326 CSTF3-HGNC:26184 CSTF3-HGNC:7659 CSTF3-HGNC:7658 PELO-HGNC:9138	N
GO biological process	GO:0010818	T cell chemotaxis	11	0	0.0103	11	2	CXCL10 CXCL	LYN-HGNC:1603 LYN-HGNC:8978 LYN-HGNC:8977 CXCL9-CXCL10 CXCL9-CXCL11 CCL5-HGNC:10627 CCL5-HGNC:1603 CCL5-CXCL10 CXCL10-HGNC:1603 CXCL10-CXCL11 CXCL11-CXCL10	Y

GO biological process	GO:0018108	peptidyl-tyrosine phosphorylation	58	0	0.0121	68	1	LYN	LYN-HGNC:3657 LYN-HGNC:4840 LYN-HGNC:4037 LYN-HGNC:3655 LYN-HGNC:3697 LYN-HGNC:5465 LYN-HGNC:6524 LYN-HGNC:9658 LYN-HGNC:9611 LYN-HGNC:8804 LYN-HGNC:8803 LYN-HGNC:77 LYN-HGNC:6091 LYN-HGNC:76 LYN-HGNC:9612 LYN-HGNC:9617 LYN-HGNC:3393 LYN-HGNC:11719 LYN-HGNC:3388 LYN-HGNC:11283 LYN-HGNC:3387 LYN-HGNC:1133 LYN-HGNC:3385 LYN-HGNC:2433 LYN-HGNC:3432 LYN-HGNC:3688 LYN-HGNC:6192 LYN-HGNC:6193 LYN-HGNC:1057 LYN-HGNC:6342 LYN-HGNC:12858 LYN-HGNC:6307 LYN-HGNC:3091 STAT1-HGNC:4840 STAT1-HGNC:3655 STAT1-LYN STAT1-HGNC:76 STAT1-HGNC:1133 STAT1-HGNC:3689 STAT1-HGNC:6192 STAT1-HGNC:3236 RUNX3-HGNC:6193 SRSF4-HGNC:3091 MASTL-HGNC:3091 TXK-HGNC:3657 TXK-HGNC:4037 TXK-HGNC:3697 TXK-LYN TXK-HGNC:6524 TXK-HGNC:9658 TXK-HGNC:8804 TXK-HGNC:77 TXK-HGNC:76 TXK-HGNC:9612 TXK-HGNC:9617 TXK-HGNC:11719 TXK-HGNC:3765 TXK-HGNC:11283 TXK-HGNC:1133 TXK-HGNC:3385 TXK-HGNC:6192 TXK-HGNC:1057 TXK-HGNC:12858 CEACAM1-LYN CEACAM1-HGNC:6524 CEACAM1-HGNC:8800 CEACAM1-HGNC:3767 CEACAM1-HGNC:6307	N
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GO biological process	GO:0039528	cytoplasmic pattern recognition receptor signaling pathway in response 4 to virus	4	0	0.0155	6	0		RSAD2-HGNC:6122 STAT1-HGNC:18873 STAT1-HGNC:6122 STAT1-HGNC:6118 IFIT1-HGNC:18873 IFIT1-HGNC:19102	Y
GO biological process	GO:0035754	B cell chemotaxis	5	1.00E-04	0.0103	5	1	CYP7B1	LYN-HGNC:8977 CXCL9-HGNC:10639 CCL5-HGNC:10639 CXCL10-HGNC:10639 CXCL11-HGNC:10639	Y
GO biological process	GO:0035723	interleukin-15-mediated signaling pathway	13	2.00E-04	0.0127	16	0		LYN-HGNC:10840 LYN-HGNC:6193 LYN-HGNC:4566 LYN-HGNC:11367 LYN-HGNC:11366 LYN-HGNC:11364 STAT1-HGNC:6190 STAT1-HGNC:11367 STAT1-HGNC:11366 STAT1-HGNC:11364 RUNX3-HGNC:6193 IFITM1-HGNC:1678 TXK-HGNC:6190 TXK-HGNC:4566 TXK-HGNC:11367 TXK-HGNC:11366	Y
GO biological process	GO:0070102	interleukin-6-mediated signaling pathway	16	0	0.0148	23	1	STAT1	LYN-HGNC:3655 LYN-HGNC:6192 LYN-HGNC:9644 LYN-HGNC:1541 LYN-HGNC:19391 LYN-HGNC:11364 LYN-STAT1 RSAD2-HGNC:6018 STAT1-HGNC:3655 STAT1-HGNC:16850 STAT1-HGNC:6192 STAT1-HGNC:9644 STAT1-HGNC:6190 STAT1-HGNC:19391 STAT1-HGNC:6770 STAT1-HGNC:11364 IFIT3-STAT1 TXK-HGNC:6192 TXK-HGNC:9644 TXK-HGNC:6190 TXK-STAT1 NXF1-HGNC:1833 IFIT1-STAT1	Y
GO biological process	GO:0031727	CCR2 chemokine receptor binding	4	2.00E-04	0.0129	5	0		LYN-HGNC:1603 CCL5-HGNC:1603 CCL5-HGNC:10618 CXCL10-HGNC:1603 CXCL10-HGNC:10618	Y
GO biological process	GO:0031957	very long-chain fatty acid-CoA ligase activity	5	1.00E-04	0.0103	5	0		ACSL1-HGNC:10999 ACSL1-HGNC:3571 ACSL1-HGNC:29567 ACSL1-HGNC:10996 STX17-HGNC:3571	N
GO biological process	GO:0038114	interleukin-21-mediated signaling pathway	7	5.00E-04	0.0162	11	1	STAT1	LYN-HGNC:11364 LYN-HGNC:6193 LYN-STAT1 STAT1-HGNC:11365 STAT1-HGNC:11364 STAT1-HGNC:6190 RUNX3-HGNC:6193 IFIT3-STAT1 TXK-STAT1 TXK-HGNC:6190 IFIT1-STAT1	Y

GO biological process	GO:0033634	positive regulation of cell-cell adhesion mediated by integrin	6	0	0.0155	9	1	CCL5	LYN-HGNC:15605 CXCL9-HGNC:10639 TXK-HGNC:15605 CCL5-HGNC:9171 CCL5-HGNC:15605 CCL5-HGNC:10639 CXCL10-HGNC:10639 CXCL10-HGNC:10639 CXCL11-HGNC:10639	N
GO biological process	GO:0017056	structural constituent of nuclear pore	10	0	0.0155	15	1	NUP205	SP100-HGNC:12017 NUP205-HGNC:13722 NUP205-HGNC:25525 NUP205-HGNC:12017 NUP205-HGNC:8068 NUP205-HGNC:18017 NUP205-HGNC:29914 NUP205-HGNC:18016 NUP205-HGNC:28958 NUP205-HGNC:8062 NXF1-HGNC:13722 NXF1-HGNC:12017 NXF1-HGNC:8068 NXF1-HGNC:28958 KPNA5-HGNC:8068	N
GO biological process	GO:0090661	box H/ACA telomerase RNP complex	4	4.00E-04	0.0155	6	0		PUS7-HGNC:2890 PUS7-HGNC:14377 PUS7-HGNC:14378 PUS7-HGNC:14264 PAPD7-HGNC:2890 CSTF3-HGNC:14377	N
GO biological process	GO:0034513	box H/ACA snoRNA binding	4	4.00E-04	0.0155	6	0		PUS7-HGNC:2890 PUS7-HGNC:14377 PUS7-HGNC:14378 PUS7-HGNC:14264 PAPD7-HGNC:2890 CSTF3-HGNC:14377	N
GO biological process	GO:0044615	nuclear pore nuclear basket	11	3.00E-04	0.0112	12	0		POMP-HGNC:24449 SP100-HGNC:12017 NUP205-HGNC:12017 NUP205-HGNC:8068 NUP205-HGNC:9848 NUP205-HGNC:6763 NUP205-HGNC:8062 NXF1-HGNC:25653 NXF1-HGNC:12017 NXF1-HGNC:8068 NXF1-HGNC:24449 KPNA5-HGNC:8068	N