

Refining the Psoriatic Transcriptome: A High-Resolution Bioinformatic Analysis of Four Molecular Hallmarks in GSE13355 Using a Curated Probe-Selection Workflow

Antonio R. Romeu^{1,2}

- ^{1.} University Rovira i Virgili. Tarragona. Spain.
- ^{2.} Corresponding author. Email: antonioramon.romeu@iubilo.urv.cat

SUPPLEMENTARY MATERIAL

Supplementary Table 1S. Curated Pathway Panel Architecture for Canonical TNF- α Signaling.

Gene Symbol	Gene id	Gene Title	System
TNF	7124	tumor necrosis factor	TNF-alpha
TNFRSF1A	7132	TNF receptor superfamily member 1A	TNF-alpha
TNFRSF1B	7133	TNF receptor superfamily member 1B	TNF-alpha
RELA	5970	RELA proto-oncogene. NF-kB subunit	TNF-alpha
NFKB1	4790	nuclear factor kappa B subunit 1	TNF-alpha
IKBKB	3551	inhibitor of nuclear factor kappa B kinase subunit beta	TNF-alpha
CHUK	1147	component of inhibitor of nuclear factor kappa B kinase complex	TNF-alpha
IKBKG	8517	inhibitor of nuclear factor kappa B kinase subunit gamma	TNF-alpha
TRAF2	7186	TNF receptor associated factor 2	TNF-alpha
TRAF1	7185	TNF receptor associated factor 1	TNF-alpha
TRADD	8717	TNFRSF1A associated via death domain	TNF-alpha
FADD	8772	Fas associated via death domain	TNF-alpha
RIPK1	8737	receptor interacting serine/threonine kinase 1	TNF-alpha
CASP8	841	caspase 8	TNF-alpha
MAP3K7	6885	mitogen-activated protein kinase kinase kinase 7	TNF-alpha
TAB1	10454	TGF-beta activated kinase 1 binding protein 1	TNF-alpha
TAB2	23118	TGF-beta activated kinase 1 binding protein 2	TNF-alpha
TNFAIP3	7128	TNF alpha induced protein 3	TNF-alpha

This panel lists the 18 core genomic components curated to map the canonical TNF- α signaling cascade. Gene Symbols and Gene IDs are validated according to the HUGO Gene Nomenclature Committee (HGNC) database.

Supplementary Table 2S. Empirical Bayes Linear Modeling (R-limma) Output for the Canonical TNF- α Architecture in Psoriatic Lesional Skin versus Healthy Controls.

Probe_ID	Gene	logFC	Fold_Change _Lineal	AveExpr	t	P.Value	adj.P.Val	B
209239_at	NFKB1	0.5161	1.4300	-0.0012	13.1927	2.10E-28	7.15E-27	53.7870
209929_s_at	IKBKKG	0.2820	1.2160	-0.0006	10.8601	1.51E-21	2.57E-20	38.0950
205599_at	TRAF1	0.4417	1.3580	-0.0079	9.9341	6.85E-19	7.77E-18	32.0243
202535_at	FADD	0.3253	1.2530	-0.0052	9.4468	1.61E-17	1.37E-16	28.8935
207643_s_at	TNFRSF1A	0.3236	1.2510	0.0005	9.1321	1.21E-16	8.20E-16	26.9004
207113_s_at	TNF	0.3428	1.2680	-0.0094	9.0240	2.40E-16	1.36E-15	26.2214
205641_s_at	TRADD	0.3246	1.2520	-0.0066	8.2053	3.89E-14	1.89E-13	21.1888
1729_at	TRADD	0.2482	1.1880	-0.0059	8.0027	1.33E-13	5.64E-13	19.9765
203508_at	TNFRSF1B	0.3977	1.3170	-0.0108	7.9399	1.94E-13	6.83E-13	19.6033
206853_s_at	MAP3K7	-0.3708	-1.2930	0.0013	-7.9339	2.01E-13	6.83E-13	19.5677
213373_s_at	CASP8	0.6343	1.5520	-0.0092	7.7989	4.50E-13	1.39E-12	18.7715
207686_s_at	CASP8	0.3711	1.2930	-0.0050	7.6110	1.37E-12	3.88E-12	17.6751
204413_at	TRAF2	0.2572	1.1950	-0.0041	7.1723	1.74E-11	4.55E-11	15.1701
211027_s_at	IKBKB	0.3073	1.2370	0.0029	6.2372	2.98E-09	7.23E-09	10.1238
212184_s_at	TAB2	-0.1777	-1.1310	0.0015	-5.3160	3.05E-07	6.91E-07	5.6123
209666_s_at	CHUK	0.3340	1.2610	-0.0031	5.1645	6.23E-07	1.32E-06	4.9196
36004_at	IKBKKG	0.1273	1.0920	-0.0017	4.0196	8.49E-05	1.70E-04	0.1977
209342_s_at	IKBKB	0.1636	1.1200	-0.0010	3.9775	1.00E-04	1.89E-04	0.0424
235116_at	TRAF1	0.0717	1.0510	-0.0004	3.5002	5.83E-04	1.04E-03	-1.6202
210284_s_at	TAB2	-0.1210	-1.0870	0.0003	-2.9283	3.84E-03	6.53E-03	-3.3646
213443_at	TRADD	0.0843	1.0600	-0.0004	2.6704	8.26E-03	1.34E-02	-4.0589
211537_x_at	MAP3K7	-0.1089	-1.0780	-0.0002	-2.2805	2.37E-02	3.67E-02	-4.9953
209941_at	RIPK1	0.0853	1.0610	0.0022	2.2301	2.70E-02	3.98E-02	-5.1062
235827_at	TAB1	-0.0558	-1.0390	0.0025	-1.8130	7.15E-02	1.01E-01	-5.9330
209341_s_at	IKBKB	-0.0756	-1.0540	0.0021	-1.7572	8.06E-02	1.10E-01	-6.0313
206854_s_at	MAP3K7	-0.0896	-1.0640	-0.0040	-1.6246	1.06E-01	1.39E-01	-6.2527
203901_at	TAB1	-0.0505	-1.0360	0.0024	-1.3783	1.70E-01	2.14E-01	-6.6190
202643_s_at	TNFAIP3	0.0739	1.0530	-0.0075	1.2644	2.08E-01	2.52E-01	-6.7685
226551_at	RIPK1	-0.0101	-1.0070	-0.0008	-0.2911	7.71E-01	9.04E-01	-7.5241
201783_s_at	RELA	-0.0083	-1.0060	0.0030	-0.2257	8.22E-01	9.31E-01	-7.5411
202644_s_at	TNFAIP3	-0.0056	-1.0040	-0.0052	-0.1179	9.06E-01	9.69E-01	-7.5596
209878_s_at	RELA	0.0057	1.0040	0.0075	0.1038	9.17E-01	9.69E-01	-7.5612
211536_x_at	MAP3K7	-0.0034	-1.0020	-0.0031	-0.0749	9.40E-01	9.69E-01	-7.5638
1553306_at	CASP8	0.0009	1.0010	0.0017	0.0367	9.71E-01	9.71E-01	-7.5659

Statistical summaries were generated using the limma package in R based on the NCBI GEO dataset GSE13355 (GPL570 platform). LogFC: log2 fold change; AveExpr: average baseline expression; t: moderated t-statistic; P.Value: raw p-value; adj.P.Val: Benjamini-Hochberg adjusted p-value (FDR); B: log-odds of differential expression (B-statistic). Suffixes _at and _s_at indicate unique and shared probe sets retained via the curation protocol, while cross-hybridizing _x_at probes were systematically excluded.

Supplementary Table 3S. Curated Pathway Panel Components for the Interleukin-6 (IL-6) Transduction Core.

Gene Symbol	Gene id	Gene Title	System
IL6	3569	interleukin 6	IL-6
IL6R	3570	interleukin 6 receptor	IL-6
IL6ST	3572	interleukin 6 cytokine family signal transducer	IL-6
JAK1	3716	Janus kinase 1	IL-6
JAK2	3717	Janus kinase 2	IL-6
STAT3	6774	signal transducer and activator of transcription 3	IL-6
CEBPB	1051	CCAAT enhancer binding protein beta	IL-6
GRB2	2885	growth factor receptor bound protein 2	IL-6
SHC1	6464	SHC adaptor protein 1	IL-6
SOS1	6654	SOS Ras/Rac guanine nucleotide exchange factor 1	IL-6
HRAS	3265	HRas proto-oncogene. GTPase	IL-6
RAF1	5894	Raf-1 proto-oncogene. serine/threonine kinase	IL-6
MAP2K1	5604	mitogen-activated protein kinase kinase 1	IL-6
MAPK3	5595	mitogen-activated protein kinase 3	IL-6
ELK1	2002	ETS transcription factor ELK1	IL-6
FOS	2353	Fos proto-oncogene. AP-1 transcription factor subunit	IL-6
JUN	3725	Jun proto-oncogene. AP-1 transcription factor subunit	IL-6
SOCS3	9006	suppressor of cytokine signaling 3	IL-6

This panel defines the 18 key downstream transducers and adaptors selected to evaluate the core IL-6 framework in human epidermal tissue.

Supplementary Table 4S. Empirical Bayes Linear Modeling (R-limma) Output for the IL-6 Transduction Core in Psoriatic Lesional Skin versus Healthy Controls.

Probe_ID	Gene	logFC	Fold_Change_ Lineal	AveExpr	t	P.Value	adj.P.Val	B
208992_s_at	STAT3	1,0926	2,1330	-0,0101	17,2303	5,70E-40	2,68E-38	80,1961
214853_s_at	SHC1	0,5640	1,4780	-0,0064	15,0361	1,18E-33	2,77E-32	65,6838
208991_at	STAT3	0,8329	1,7810	-0,0057	14,9496	2,10E-33	3,30E-32	65,1047
212501_at	CEBPB	0,4175	1,3360	-0,0056	14,3693	1,04E-31	1,22E-30	61,2139
225289_at	STAT3	0,6837	1,6060	-0,0091	13,4585	4,84E-29	4,55E-28	55,0864
212983_at	HRAS	0,5884	1,5040	-0,0069	10,9953	7,47E-22	5,85E-21	38,5990
201648_at	JAK1	-0,2891	-1,2220	0,0007	-10,9108	1,31E-21	8,78E-21	38,0414
205207_at	IL6	0,4549	1,3710	-0,0245	10,1166	2,43E-19	1,43E-18	32,8486
201469_s_at	SHC1	0,6788	1,6010	-0,0002	9,9839	5,75E-19	3,00E-18	31,9911
215075_s_at	GRB2	0,5006	1,4150	-0,0166	9,9551	6,93E-19	3,26E-18	31,8054
239695_at	JAK1	-0,3520	-1,2760	0,0005	-8,9848	3,42E-16	1,46E-15	25,6501
212195_at	IL6ST	-0,3193	-1,2480	0,0060	-8,2790	2,70E-14	1,06E-13	21,3243
209189_at	FOS	-1,1199	-2,1730	0,0015	-7,6549	1,13E-12	4,08E-12	17,6343
203617_x_at	ELK1	0,1956	1,1450	-0,0017	6,5170	6,94E-10	2,33E-09	11,3101
1552610_a_at	JAK1	-0,2724	-1,2080	0,0036	-6,3376	1,81E-09	5,68E-09	10,3684
243213_at	STAT3	0,1677	1,1230	-0,0007	6,1245	5,55E-09	1,63E-08	9,2714
1557675_at	RAF1	-0,2451	-1,1850	0,0051	-6,0503	8,15E-09	2,25E-08	8,8956
227426_at	SOS1	-0,2668	-1,2030	-0,0029	-5,4263	1,83E-07	4,79E-07	5,8569
201465_s_at	JUN	-0,3488	-1,2730	0,0031	-4,7485	4,16E-06	1,03E-05	2,8312
204863_s_at	IL6ST	-0,3390	-1,2650	-0,0080	-4,3691	2,10E-05	4,94E-05	1,2748
202670_at	MAP2K1	0,1499	1,1090	-0,0051	4,2409	3,55E-05	7,95E-05	0,7723
201466_s_at	JUN	-0,3320	-1,2590	0,0025	-4,1203	5,76E-05	1,23E-04	0,3110
1552611_a_at	JAK1	-0,1929	-1,1430	-0,0048	-4,0423	7,83E-05	1,60E-04	0,0182
212046_x_at	MAPK3	0,1522	1,1110	0,0018	3,9301	1,21E-04	2,37E-04	-0,3943
201464_x_at	JUN	-0,1991	-1,1480	0,0024	-3,8697	1,52E-04	2,86E-04	-0,6125
1562031_at	JAK2	-0,1573	-1,1150	-0,0012	-3,7773	2,15E-04	3,89E-04	-0,9406
230337_at	SOS1	-0,3507	-1,2750	-0,0029	-3,7066	2,79E-04	4,86E-04	-1,1870
212196_at	IL6ST	-0,1833	-1,1350	0,0052	-3,5845	4,34E-04	7,29E-04	-1,6032
213281_at	JUN	-0,1345	-1,0980	0,0001	-3,5016	5,83E-04	9,45E-04	-1,8788
226333_at	IL6R	0,2050	1,1530	-0,0061	3,3880	8,64E-04	1,35E-03	-2,2475
205945_at	IL6R	0,2530	1,1920	-0,0098	3,2323	1,46E-03	2,21E-03	-2,7352
223049_at	GRB2	0,0800	1,0570	-0,0006	2,8440	4,97E-03	7,30E-03	-3,8619
210850_s_at	ELK1	0,1410	1,1030	-0,0005	2,7755	6,09E-03	8,68E-03	-4,0468
1557354_at	SOS1	-0,0540	-1,0380	0,0008	-2,6816	8,01E-03	1,11E-02	-4,2940
205842_s_at	JAK2	0,1255	1,0910	-0,0080	2,4136	1,68E-02	2,26E-02	-4,9555
212780_at	SOS1	0,1010	1,0730	-0,0015	2,3706	1,88E-02	2,46E-02	-5,0555
210376_x_at	ELK1	0,0794	1,0570	0,0016	1,9826	4,89E-02	6,22E-02	-5,8816
201244_s_at	RAF1	0,0508	1,0360	0,0011	1,9592	5,16E-02	6,39E-02	-5,9268
217489_s_at	IL6R	0,0361	1,0250	-0,0013	1,3680	1,73E-01	2,08E-01	-6,8989
234474_x_at	IL6ST	0,0302	1,0210	-0,0049	1,3397	1,82E-01	2,14E-01	-6,9371
211000_s_at	IL6ST	-0,0977	-1,0700	-0,0119	-1,0565	2,92E-01	3,35E-01	-7,2749
228572_at	GRB2	0,0470	1,0330	0,0016	0,8010	4,24E-01	4,75E-01	-7,5120
234967_at	IL6ST	-0,0160	-1,0110	0,0008	-0,7496	4,54E-01	4,97E-01	-7,5519
205841_at	JAK2	-0,0217	-1,0150	-0,0019	-0,4609	6,45E-01	6,89E-01	-7,7270
212777_at	SOS1	-0,0289	-1,0200	-0,0021	-0,3998	6,90E-01	7,20E-01	-7,7534
204864_s_at	IL6ST	-0,0108	-1,0080	0,0114	-0,1300	8,97E-01	9,16E-01	-7,8251
240613_at	1AK1	-0,0018	-1,0010	0,0029	-0,0644	9,49E-01	9,49E-01	-7,8315

Differential expression values were derived from active lesional (PP) skin biopsies compared against healthy reference (NN) templates within the GSE13355 series. Columns display the probe identifier, gene symbol, log2 fold change (logFC), linear fold change, average expression (AveExpr), moderated t-statistic (t), raw p-value, adjusted p-value (adj.P.Val), and B-statistic. Retained _s_at probes capture valid splice variants critical for capturing main STAT3 and SHC1 regulatory signals.

Supplementary Table 5S. Curated Pathway Panel for the S100 Calcium-Binding Protein Family.

Gene Symbol	Gene id	Gene Title	System
S100A1	6271	S100 calcium binding protein A1	Proteínas S100
S100A2	6273	S100 calcium binding protein A2	Proteínas S100
S100A3	6274	S100 calcium binding protein A3	Proteínas S100
S100A4	6275	S100 calcium binding protein A4	Proteínas S100
S100A5	6276	S100 calcium binding protein A5	Proteínas S100
S100A6	6277	S100 calcium binding protein A6	Proteínas S100
S100A7	6278	S100 calcium binding protein A7	Proteínas S100
S100A8	6279	S100 calcium binding protein A8	Proteínas S100
S100A9	6280	S100 calcium binding protein A9	Proteínas S100
S100A10	6281	S100 calcium binding protein A10	Proteínas S100
S100A11	6282	S100 calcium binding protein A11	Proteínas S100
S100A12	6283	S100 calcium binding protein A12	Proteínas S100
S100A13	6284	S100 calcium binding protein A13	Proteínas S100
S100A14	57402	S100 calcium binding protein A14	Proteínas S100
S100A16	142246	S100 calcium binding protein A16	Proteínas S100
S100B	6285	S100 calcium binding protein B	Proteínas S100
S100G	795	S100 calcium binding protein G	Proteínas S100
S100P	6286	S100 calcium binding protein P	Proteínas S100
S100Z	170505	S100 calcium binding protein Z	Proteínas S100

The panel includes 19 functional variables representing the S100 calcium-binding protein family evaluated to map epidermal differentiation defects and alarmin signatures.

Supplementary Table 6S. Empirical Bayes Linear Modeling (R-limma) Output for the S100 Calcium-Binding Family in Psoriatic Lesional Skin versus Healthy Controls.

Probe_ID	Gene	logFC	Fold_Change_Lineal	AveExpr	t	P.Value	adj.P.Val	B
205863_at	S100A12	5,8263	56,7400	-0,0644	42,8730	6,44E-96	1,42E-94	208,6490
203535_at	S100A9	5,8228	56,6020	-0,0512	32,8842	1,14E-77	1,26E-76	166,5199
204268_at	S100A2	1,6376	3,1110	-0,0148	22,5283	4,49E-54	3,29E-53	112,0314
200660_at	S100A11	0,6648	1,5850	-0,0063	22,1110	5,27E-53	2,90E-52	109,5626
205916_at	S100A7	4,1945	18,3090	-0,0345	19,6753	1,41E-46	6,22E-46	94,7233
202917_s_at	S100A8	3,5680	11,8600	-0,0323	18,6638	8,15E-44	2,99E-43	88,3533
218677_at	S100A14	0,6363	1,5540	-0,0071	14,8300	6,01E-33	1,89E-32	63,2943
204351_at	S100P	1,2631	2,4000	-0,0137	8,0725	9,83E-14	2,70E-13	19,1780
238909_at	S100A10	-0,5821	-1,4970	0,0064	-6,8501	1,15E-10	2,81E-10	12,1964
203186_s_at	S100A4	-0,3146	-1,2440	-0,0017	-6,7166	2,40E-10	5,28E-10	11,4725
205334_at	S100A1	-0,2814	-1,2150	0,0128	-5,3772	2,35E-07	4,69E-07	4,7257
202598_at	S100A13	-0,2512	-1,1900	0,0058	-5,3259	3,00E-07	5,49E-07	4,4877
217728_at	S100A6	-0,1906	-1,1410	-0,0034	-5,0488	1,09E-06	1,85E-06	3,2319
200872_at	S100A10	-0,1385	-1,1010	0,0005	-4,9233	1,93E-06	3,03E-06	2,6796
213481_at	S100A13	0,1712	1,1260	-0,0002	4,8157	3,12E-06	4,57E-06	2,2150
207763_at	S100A5	0,1290	1,0940	-0,0001	3,5180	5,51E-04	7,58E-04	-2,7300
228923_at	S100A6	-0,0785	-1,0560	0,0006	-2,1883	2,99E-02	3,88E-02	-6,3696
1561521_at	S100B	0,0192	1,0130	-0,0009	1,4444	1,50E-01	1,84E-01	-7,7024
207885_at	S100G	0,0328	1,0230	0,0009	1,3898	1,66E-01	1,93E-01	-7,7794
209686_at	S100B	-0,1106	-1,0800	0,0068	-1,2749	2,04E-01	2,24E-01	-7,9317
214370_at	S100A8	-0,0245	-1,0170	0,0080	-0,2283	8,20E-01	8,59E-01	-8,7189
206027_at	S100A3	-0,0179	-1,0120	-0,0006	-0,1036	9,18E-01	9,18E-01	-8,7397

Data display transcriptomic shifts extracted via R-limma profiling of the GSE13355 dataset. Parameters include Probe ID, Gene Symbol, log2 fold change (logFC), linear fold change, average baseline expression, moderated t-statistic, raw p-value, false discovery rate adjusted p-value (adj.P.Val), and the B-statistic. High absolute magnitudes highlight major alarmin activation profiles.

Supplementary Table 7S. Functional Subgroups and Architecture of the EGFL8 Pathway Grid.

Gene Symbol	Gene id	Gene Title	System
EGFL8	115797	epidermal growth factor like domain multiple 8	General upstream modulator
NOTCH1	4851	notch receptor 1	Notch Signaling
NOTCH2	4853	notch receptor 2	Notch Signaling
HES1	3280	hes family bHLH transcription factor 1	Notch Signaling
HEY1	23462	hes related family bHLH transcription factor with YRPW motif 1	Notch Signaling
MMP2	4313	matrix metalloproteinase 2	Notch Signaling / Invasion
MMP9	4318	matrix metalloproteinase 9	Notch Signaling / Invasion
ZEB1	6935	zinc finger E-box binding homeobox 1	Notch Signaling / EMT
MAPK1	5594	mitogen-activated protein kinase 1 (ERK2)	ERK/MAPK pathway
MAPK3	5595	mitogen-activated protein kinase 3 (ERK1)	ERK/MAPK pathway
RAF1	5894	Raf-1 proto-oncogene. serine/threonine kinase	ERK/MAPK pathway
MAP2K1	5604	mitogen-activated protein kinase kinase 1 (MEK1)	ERK/MAPK pathway
FOS	2353	FOS proto-oncogene. AP-1 transcription factor subunit	ERK/MAPK pathway
JUN	3725	JUN proto-oncogene. AP-1 transcription factor subunit	ERK/MAPK pathway
CDK1	983	cyclin dependent kinase 1	Cell Cycle / Apoptosis
CDK4	1019	cyclin dependent kinase 4	Cell Cycle / Apoptosis
CDK6	1021	cyclin dependent kinase 6	Cell Cycle / Apoptosis
CCND1	595	cyclin D1	Cell Cycle / Apoptosis
BCL2	596	BCL2 apoptosis regulator	Cell Cycle / Apoptosis
BCL2L1	598	BCL2 like 1 (Bcl-xL)	Cell Cycle / Apoptosis
FASLG	356	Fas ligand	Cell Cycle / Apoptosis
VEGFA	7422	vascular endothelial growth factor A	Angiogenesis / Immune Regulation
THBS1	7057	thrombospondin 1	Angiogenesis / Immune Regulation
NRP1	8829	neuropilin 1	Angiogenesis / Immune Regulation
ANGPTL1	9068	angiopoietin like 1	Angiogenesis / Immune Regulation
CXCL5	6374	C-X-C motif chemokine ligand 5	Angiogenesis / Immune Regulation
CXCL10	3627	C-X-C motif chemokine ligand 10	Angiogenesis / Immune Regulation
CXCL16	58191	C-X-C motif chemokine ligand 16	Angiogenesis / Immune Regulation
CCL20	6364	C-C motif chemokine ligand 20	Angiogenesis / Immune Regulation
CD74	972	CD74 molecule	Angiogenesis / Immune Regulation
NFKB2	4791	nuclear factor kappa B subunit 2	Angiogenesis / Immune Regulation
IRF7	3665	interferon regulatory factor 7	Angiogenesis / Immune Regulation

This matrix organizes the 32 genes selected to construct the EGFL8 pathway framework, categorized into functional cross-talk groups: General Upstream Modulation, Notch Signaling, Invasion/EMT, ERK/MAPK Pathway, Cell Cycle/Apoptosis, and Angiogenesis/Immune Regulation.

Supplementary Table 8S. Empirical Bayes Linear Modeling (R-limma) Output for the EGFL8 Pathway Grid in Psoriatic Lesional Skin versus Healthy Controls.

Probe_ID	Gene	logFC	Fold_Change_Lineal	AveExpr	t	P.Value	adj.P.Val	B
208436_s_at	CDK1	2,1893	4,5610	-0,0153	27,0887	2,17E-65	1,97E-63	138,4767
205476_at	MAP2K1	2,9684	7,8270	-0,0335	24,3514	7,65E-59	2,84E-57	123,3826
203214_x_at	MAPK1	1,7356	3,3300	-0,0218	24,3160	9,35E-59	2,84E-57	123,1814
203213_at	MAPK1	1,5238	2,8750	-0,0179	22,8465	4,53E-55	1,03E-53	114,6849
210559_s_at	CDK6	1,8785	3,6770	-0,0239	22,8045	5,80E-55	1,06E-53	114,4383
203936_s_at	RAF1	1,5588	2,9460	-0,0279	19,0633	4,81E-45	7,29E-44	91,5736
208712_at	CDK4	-1,0132	-2,0180	0,0139	-18,8037	2,50E-44	3,25E-43	89,9253
223454_at	THBS1	0,7549	1,6870	-0,0071	16,7217	1,76E-38	2,00E-37	76,4485
204533_at	RAF1	2,8182	7,0530	-0,0338	15,8623	5,14E-36	5,20E-35	70,7706
208711_s_at	CDK1	-1,0318	-2,0450	0,0055	-15,7416	1,15E-35	1,04E-34	69,9683
202443_x_at	ZEB1	-0,3367	-1,2630	0,0033	-15,6842	1,68E-35	1,39E-34	69,5867
212377_s_at	VEGFA	-0,3941	-1,3140	0,0051	-15,1903	4,53E-34	3,43E-33	66,2931
203685_at	MAPK3	-1,0401	-2,0560	0,0104	-14,7049	1,17E-32	8,17E-32	63,0436
224621_at	NRP1	-0,2738	-1,2090	0,0025	-11,6342	1,10E-23	7,12E-23	42,4126
212764_at	VEGFA	-0,7406	-1,6710	0,0083	-9,8826	1,14E-18	6,89E-18	30,9078
203395_s_at	MAPK1	-0,4175	-1,3360	0,0043	-9,4727	1,59E-17	9,02E-17	28,2875
202445_s_at	ZEB1	-0,3291	-1,2560	-0,0005	-8,6795	2,34E-15	1,25E-14	23,3278
210865_at	BCL2	0,3862	1,3070	-0,0128	8,5211	6,22E-15	3,14E-14	22,3584
212758_s_at	VEGFA	-0,6431	-1,5620	0,0026	-8,2484	3,29E-14	1,58E-13	20,7066
1552264_a_at	NOTCH1	0,3683	1,2910	-0,0037	7,9924	1,54E-13	7,01E-13	19,1780
209189_at	CDK6	-1,1199	-2,1730	0,0015	-7,6430	1,22E-12	5,30E-12	17,1300
210756_s_at	CCND1	-0,3150	-1,2440	0,0049	-7,3876	5,40E-12	2,23E-11	15,6623
224851_at	ANGPTL1	-0,3553	-1,2790	0,0078	-7,2571	1,14E-11	4,52E-11	14,9223
211333_s_at	BCL2	0,1747	1,1290	-0,0022	7,1656	1,92E-11	7,30E-11	14,4081
210875_s_at	BCL2	-0,6571	-1,5770	0,0156	-7,1290	2,37E-11	8,62E-11	14,2038
201069_at	HES1	-0,4931	-1,4080	0,0060	-6,9170	7,79E-11	2,73E-10	13,0295
239183_at	CD74	-0,8154	-1,7600	0,0108	-6,8364	1,22E-10	4,11E-10	12,5882
208351_s_at	CDK1	0,3486	1,2730	-0,0012	6,7717	1,74E-10	5,66E-10	12,2365
214974_x_at	THBS1	0,2507	1,1900	-0,0169	6,6794	2,89E-10	9,08E-10	11,7381
229847_at	CXCL5	0,2297	1,1730	-0,0023	6,6042	4,36E-10	1,32E-09	11,3352
212298_at	FASLG	-0,4127	-1,3310	0,0003	-6,5005	7,63E-10	2,24E-09	10,7838
202246_s_at	ZEB1	0,1727	1,1270	-0,0026	6,4807	8,49E-10	2,41E-09	10,6792
203394_s_at	MAPK1	-0,4479	-1,3640	0,0068	-6,4726	8,86E-10	2,44E-09	10,6369
207535_s_at	JUN	0,2047	1,1520	0,0018	6,1256	5,54E-09	1,48E-08	8,8376
1557675_at	NOTCH2	-0,2451	-1,1850	0,0051	-6,0442	8,45E-09	2,20E-08	8,4249
231534_at	CXCL16	0,1219	1,0880	-0,0029	5,9289	1,53E-08	3,86E-08	7,8463
231773_at	CCL20	-0,6294	-1,5470	0,0112	-5,8369	2,43E-08	5,98E-08	7,3905
224339_s_at	NRP1	-0,6637	-1,5840	0,0138	-5,8004	2,92E-08	7,00E-08	7,2106
209636_at	CDK6	0,2639	1,2010	-0,0016	5,6135	7,40E-08	1,73E-07	6,3030
243000_at	NFKB2	-0,3631	-1,2860	-0,0022	-5,4483	1,65E-07	3,76E-07	5,5188
1552263_at	NOTCH1	0,2954	1,2270	-0,0078	4,9847	1,45E-06	3,15E-06	3,4083
215101_s_at	THBS1	0,1472	1,1070	-0,0074	4,9843	1,45E-06	3,15E-06	3,4064
210513_s_at	CDK6	0,2361	1,1780	-0,0031	4,8131	3,14E-06	6,64E-06	2,6629
201465_s_at	MMP9	-0,3488	-1,2730	0,0031	-4,7417	4,30E-06	8,89E-06	2,3589
44783_s_at	IRF7	-0,3196	-1,2480	0,0079	-4,7222	4,68E-06	9,47E-06	2,2761
212271_at	BCL2L1	0,1895	1,1400	-0,0025	4,6394	6,71E-06	1,33E-05	1,9290
207004_at	JUN	0,2082	1,1550	0,0006	4,6171	7,38E-06	1,43E-05	1,8365
218839_at	THBS1	-0,2818	-1,2160	0,0068	-4,5992	7,97E-06	1,51E-05	1,7624
211527_x_at	BCL2L1	0,2131	1,1590	-0,0030	4,5823	8,57E-06	1,59E-05	1,6927
224847_at	ANGPTL1	-0,1665	-1,1220	-0,0005	-4,3843	1,98E-05	3,60E-05	0,8902

203684_s_at	MAPK1	-0,1492	-1,1090	-0,0028	-4,2708	3,15E-05	5,62E-05	0,4432
202670_at	MAPK1	0,1499	1,1090	-0,0051	4,2374	3,61E-05	6,31E-05	0,3135
207005_s_at	JUN	0,2331	1,1750	-0,0002	4,1223	5,72E-05	9,82E-05	-0,1273
201466_s_at	ZEB1	-0,3320	-1,2590	0,0025	-4,1144	5,90E-05	9,95E-05	-0,1571
215037_s_at	THBS1	0,2575	1,1950	0,0065	4,0513	7,57E-05	1,25E-04	-0,3941
212046_x_at	BCL2L1	0,1522	1,1110	0,0018	3,9264	1,23E-04	1,99E-04	-0,8541
201464_x_at	MMP2	-0,1991	-1,1480	0,0024	-3,8649	1,55E-04	2,47E-04	-1,0759
213281_at	VEGFA	-0,1345	-1,0980	0,0001	-3,4983	5,90E-04	9,26E-04	-2,3370
223508_at	NRP1	0,1595	1,1170	0,0015	3,4298	7,49E-04	1,16E-03	-2,5605
231228_at	CXCL10	0,1188	1,0860	-0,0011	3,1474	1,93E-03	2,92E-03	-3,4407
210510_s_at	CDK6	-0,1566	-1,1150	-0,0032	-3,0036	3,05E-03	4,55E-03	-3,8631
235287_at	CD74	-0,2902	-1,2230	-0,0037	-2,8991	4,21E-03	6,18E-03	-4,1588
207143_at	JUN	-0,1294	-1,0940	-0,0020	-2,8354	5,10E-03	7,37E-03	-4,3341
239952_at	NFKB2	-0,0879	-1,0630	0,0021	-2,8062	5,56E-03	7,88E-03	-4,4133
207852_at	CDK1	0,0415	1,0290	-0,0012	2,8025	5,63E-03	7,88E-03	-4,4234
215775_at	THBS1	0,0814	1,0580	-0,0011	2,7454	6,66E-03	9,18E-03	-4,5761
224620_at	NRP1	0,1156	1,0830	0,0008	2,5870	1,05E-02	1,42E-02	-4,9844
1561365_at	NOTCH2	-0,0633	-1,0450	0,0015	-2,4296	1,61E-02	2,15E-02	-5,3676
201107_s_at	HES1	0,1112	1,0800	-0,0012	2,3035	2,24E-02	2,95E-02	-5,6585
206665_s_at	FOS	0,1242	1,0900	0,0063	2,2486	2,58E-02	3,35E-02	-5,7806
201109_s_at	HEY1	-0,2590	-1,1970	-0,0036	-2,2409	2,63E-02	3,37E-02	-5,7975
212171_x_at	BCL2L1	0,0945	1,0680	-0,0015	2,2035	2,88E-02	3,64E-02	-5,8787
201110_s_at	MMP2	-0,2379	-1,1790	-0,0027	-2,0550	4,13E-02	5,15E-02	-6,1886
201244_s_at	MMP2	0,0508	1,0360	0,0011	1,9589	5,17E-02	6,35E-02	-6,3782
227067_x_at	CXCL5	0,1424	1,1040	0,0028	1,9260	5,57E-02	6,76E-02	-6,4412
235086_at	CD74	0,0877	1,0630	-0,0092	1,7295	8,54E-02	1,02E-01	-6,7954
224848_at	ANGPTL1	-0,0750	-1,0530	-0,0004	-1,7107	8,89E-02	1,05E-01	-6,8274
231198_at	CXCL5	0,0812	1,0580	0,0020	1,6803	9,46E-02	1,10E-01	-6,8784
1567627_at	NOTCH2 /// NOTCH2NL	0,0939	1,0670	-0,0010	1,6075	1,10E-01	1,26E-01	-6,9969
201108_s_at	HEY1	-0,1155	-1,0830	-0,0054	-1,3922	1,66E-01	1,88E-01	-7,3174
1566678_at	NOTCH2	0,0542	1,0380	0,0005	1,2231	2,23E-01	2,50E-01	-7,5375
210615_at	CCND1	-0,0269	-1,0190	-0,0013	-1,0833	2,80E-01	3,11E-01	-7,6983
212312_at	FASLG	0,0322	1,0230	0,0010	0,8669	3,87E-01	4,24E-01	-7,9092
218902_at	THBS1	-0,0403	-1,0280	0,0039	-0,7712	4,42E-01	4,78E-01	-7,9876
210512_s_at	CDK6	-0,0335	-1,0230	-0,0019	-0,5542	5,80E-01	6,21E-01	-8,1318
1567628_at	HES1	0,0511	1,0360	0,0132	0,5190	6,04E-01	6,40E-01	-8,1508
209619_at	CDK6	0,0270	1,0190	0,0058	0,4267	6,70E-01	6,98E-01	-8,1946
203393_at	MAPK1	0,0136	1,0090	-0,0024	0,4204	6,75E-01	6,98E-01	-8,1973
1566677_at	NOTCH2	-0,0049	-1,0030	-0,0007	-0,2104	8,34E-01	8,52E-01	-8,2638
239336_at	NFKB2	-0,0016	-1,0010	-0,0017	-0,0485	9,61E-01	9,72E-01	-8,2848
211524_at	BCL2	-0,0006	-1,0000	-0,0006	-0,0294	9,77E-01	9,77E-01	-8,2856

Table values track full differential expression indices across the multi-functional EGFL8 pathway network using the limma linear modeling framework on the GSE13355 series. Statistical annotations list specific probe designations, target gene labels, log2 fold changes, linear ratios, base expression means, moderated t-statistics, adjusted significance metrics (adj.P.Val), and the corresponding log-odds (B). Redundant multiple probes are retained and presented for alternative transcript tracking.