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Supplementary Table S5. Transcription factors with overrepresented binding site motifs among genes differentially expressed in psoriatic keratinocytes (PP vs. H) genes differentially expressed in psoriatic keratinocytes (PP vs. H).

Transcription Factor	TF gene name	N. of target genes	p-value	z-score
E2F4	E2F transcription factor 4	121	2.14E-59	22.72
FOXM1	Forkhead box M1	62	9.53E-37	18.52
HIF1A	Hypoxia inducible factor 1 alpha subunit	151	2.51E-40	16.50
c-Jun	Jun proto-oncogene, AP-1 transcription factor subunit	160	1.97E-38	15.83
IRF4	Interferon regulatory factor 4	100	1.86E-31	14.87
STAT3	Signal transducer and activator of transcription 3	133	2.66E-30	13.86
b-Myb	MYB proto-oncogene like 2	38	2.86E-20	13.06
STAT1	Signal transducer and activator of transcription 1	82	9.35E-25	12.98
NF-kB1 (p50)	Nuclear factor kappa B subunit 1	91	5.06E-23	12.14
KLF4	Kruppel like factor 4	69	5.04E-19	11.07
E2F8	E2F transcription factor 8	16	3.34E-12	10.71
EGR1	Early growth response 1	82	2.42E-18	10.53
FKHR	Forkhead box O1	62	4.85E-17	10.40
E2F7	E2F transcription factor 7	19	2.79E-11	9.54
STAT2	Signal transducer and activator of transcription 2	24	5.35E-12	9.50
MITF	Melanogenesis associated transcription factor	35	6.17E-13	9.33
GATA-3	GATA binding protein 3	94	4.63E-15	9.06
C/EBP zeta	DNA damage inducible transcript 3	25	4.61E-10	8.15
BMAL1	Aryl hydrocarbon receptor nuclear translocator like	28	3.28E-10	8.07
NF-kB p50/p50	Nuclear receptor subfamily 1 group D member 1	20	2.93E-09	7.97
XBP1	X-box binding protein 1	32	1.54E-09	7.48
JunD	JunD proto-oncogene, AP-1 transcription factor subunit	36	5.31E-09	7.03
ATF-3	Activating transcription factor 3	32	8.53E-09	7.02
c-Fos	Fos proto-oncogene, AP-1 transcription factor subunit	53	2.68E-09	6.88
CLOCK	Clock circadian regulator	20	2.39E-07	6.56
REV-ERBa1alpha	Nuclear receptor subfamily 1 group D member 1	14	2.47E-06	6.18
GLI-2	GLI family zinc finger 2	14	4.94E-06	5.91
ZNF652	Zinc finger protein 652	5	1.50E-04	5.86
ZNF145	Zinc finger and BTB domain containing 16	12	1.92E-05	5.55
NF-kB1 (p105)	Nuclear receptor subfamily 1 group D member 1	16	9.16E-06	5.54
TRPS1	Transcriptional repressor GATA binding 1	7	1.07E-04	5.47
ROR-alpha	RAR related orphan receptor A	19	7.92E-06	5.44
EGR2 (Krox20)	Early growth response 2	21	7.70E-06	5.37
ESE3	ETS homologous factor	8	9.68E-05	5.33
SOX4	SRY-box 4	19	4.12E-05	4.85
LHX2	LIM homeobox 2	45	1.46E-05	4.75
SMARCA3	Helicase like transcription factor	3	3.75E-03	4.54
TR-alpha	Thyroid hormone receptor, alpha	19	1.49E-04	4.39
HEY2	Hes related family bHLH transcription factor with YRPW motif 2	7	1.65E-03	4.00
SIP1 (ZFX1B)	Zinc finger E-box binding homeobox 2	7	1.65E-03	4.00
DACH1	Dachshund family transcription factor 1	4	4.31E-03	3.99
ELF1	Elongation Factor Like GTPase 1 (EFL1)	14	6.44E-04	3.97
ROR-gamma	RAR related orphan receptor C	8	1.59E-03	3.91
GATA-6	GATA binding protein 6	17	6.12E-04	3.90
SOHLH1	Spermatogenesis and oogenesis specific basic helix-loop-helix 1	2	1.99E-02	3.71
PAX3	Paired box 3	8	2.65E-03	3.65
CTIP2	Atlastin GTPase 1	7	4.94E-03	3.40
SOX5	SRY-box 5	6	7.87E-03	3.23
TIEG1	Kruppel like factor 10	6	9.27E-03	3.14
EGR3	Early growth response 3	6	1.09E-02	3.04
HES1	Hes family bHLH transcription factor 1	11	7.33E-03	2.97
FosB	FosB proto-oncogene, AP-1 transcription factor subunit	9	1.24E-02	2.78
NF-AT1(NFATC2)	Nuclear factor of activated T cells 2	14	1.11E-02	2.69
SMAD1	SMAD family member 1	15	1.65E-02	2.48

54 transcription factors whose binding site motifs showed the highest enrichment are shown (TF = transcription factor; N. of target genes = number of target genes in PP vs H comparison; p-value = for the given predicted N. of target genes; z-score = Actual N. of target genes – Expected N. of target genes / sqrt(variance)).