

SUPPLEMENTARY DATA

Table S1

List of top 100 phototherapy affected MVPs (SAM procedure with 5% false discovery rate)

Increased methylation level following phototherapy

probeID	gene	feat.rel	ENHANCER	CONTROL	PRE-UV	MID-UV	POST-UV	Delta-beta (POST-UV vs. PRE-UV)
cg10409253	RNF216	Body_none	NA	0.87	0.20	0.37	0.57	0.37
cg16139316	S100A9	5'UTR_none	NA	0.92	0.34	0.51	0.67	0.34
cg11842073	NA	IGR_none	TRUE	0.79	0.23	0.38	0.57	0.34
cg05435212	NA	IGR_none	TRUE	0.78	0.16	0.30	0.49	0.33
cg20950277	TNIP3	1stExon_none	NA	0.81	0.36	0.50	0.67	0.31
cg03035162	NA	IGR_none	NA	0.88	0.31	0.48	0.62	0.31
cg07964527	PDE8A	Body_none	TRUE	0.83	0.31	0.47	0.61	0.31
cg23598352	C9orf46	5'UTR_shore	NA	0.90	0.30	0.49	0.61	0.30
cg27431500	HN1L	Body_none	NA	0.83	0.31	0.41	0.61	0.30
cg24544808	NA	IGR_none	TRUE	0.74	0.22	0.38	0.52	0.30
cg22946974	SPRR2F	5'UTR_none	NA	0.89	0.42	0.60	0.71	0.29
cg07651316	BTBD12	Body_shelf	NA	0.92	0.44	0.61	0.73	0.29
cg05586676	VNN1	Body_none	TRUE	0.79	0.34	0.46	0.63	0.29
cg05976283	NA	IGR_shelf	NA	0.84	0.31	0.46	0.60	0.29
cg04087571	SIK3	Body_none	TRUE	0.71	0.13	0.25	0.41	0.28
cg27250032	NA	IGR_shelf	NA	0.80	0.25	0.39	0.53	0.28
cg04961225	NA	IGR_none	TRUE	0.90	0.37	0.57	0.65	0.28
cg25367999	NA	IGR_none	TRUE	0.91	0.36	0.50	0.64	0.28
cg19913971	TNIP3	5'UTR_none	NA	0.87	0.41	0.53	0.69	0.28
cg08550523	NA	IGR_none	TRUE	0.83	0.35	0.46	0.62	0.28
cg01655008	C14orf109	Body_shore	NA	0.89	0.38	0.52	0.66	0.27
cg21761639	NA	IGR_none	TRUE	0.61	0.20	0.34	0.47	0.27
cg19846154	NA	IGR_none	TRUE	0.82	0.26	0.40	0.53	0.27
cg21890646	CCDC88C	Body_none	TRUE	0.74	0.21	0.34	0.48	0.27
cg20169988	S100A9	Body_none	NA	0.92	0.44	0.58	0.71	0.27
cg00859858	ZC3H12A	Body_shelf	TRUE	0.76	0.19	0.31	0.46	0.27
cg16125375	PPP2R2B	5'UTR_none	TRUE	0.85	0.35	0.46	0.62	0.27
cg16565031	NA	IGR_none	TRUE	0.63	0.13	0.24	0.39	0.27
cg01973676	CUX1	Body_none	TRUE	0.85	0.25	0.37	0.51	0.26
cg12067024	S100A7A	TSS1500_none	NA	0.65	0.22	0.32	0.49	0.26
cg10649130	NA	IGR_shelf	NA	0.77	0.24	0.36	0.50	0.26
cg04446653	NA	IGR_none	TRUE	0.72	0.23	0.38	0.49	0.26
cg13430755	NA	IGR_none	TRUE	0.80	0.29	0.40	0.55	0.26
cg24870231	NA	IGR_none	TRUE	0.88	0.35	0.44	0.61	0.26
cg24681845	NA	IGR_none	NA	0.62	0.17	0.26	0.43	0.26
cg04076286	NA	IGR_shore	NA	0.74	0.25	0.35	0.51	0.26
cg18477001	NA	IGR_none	TRUE	0.88	0.45	0.60	0.71	0.26
cg22373770	NA	IGR_none	TRUE	0.79	0.24	0.35	0.50	0.26

cg20949198	SLC2A12	Body_none	TRUE	0.92	0.49	0.66	0.74	0.26
cg18318006	SORBS1	Body_none	TRUE	0.81	0.38	0.54	0.64	0.26
cg18766755	SPRR2A	5'UTR_none	NA	0.86	0.46	0.63	0.72	0.26
cg25890168	ABHD3	Body_none	TRUE	0.70	0.26	0.40	0.51	0.25
cg03518729	NA	IGR_none	TRUE	0.78	0.37	0.45	0.63	0.25
cg15975676	GPATCH2	Body_none	TRUE	0.91	0.43	0.53	0.69	0.25
cg24004483	NA	IGR_shelf	NA	0.87	0.43	0.58	0.69	0.25
cg20232662	NA	IGR_none	NA	0.81	0.42	0.53	0.67	0.25
cg24687805	RAB27A	Body_none	TRUE	0.54	0.06	0.14	0.31	0.25
cg27092594	NA	IGR_none	NA	0.81	0.30	0.41	0.55	0.25
cg18721397	SUB1	TSS1500_shore	NA	0.84	0.37	0.50	0.62	0.25
cg02284278	NA	IGR_none	TRUE	0.86	0.41	0.52	0.66	0.25

Decreased methylation level following phototherapy

probeID	gene	feat.rel	ENHANCER	CONTROL	PRE-UV	MID-UV	POST-UV	Delta-beta (POST-UV vs. PRE-UV)
cg23999170	TSPAN2	Body_shelf	NA	0.14	0.64	0.53	0.38	-0.26
cg17251713	SERPINB7	5'UTR_none	NA	0.20	0.63	0.43	0.38	-0.25
cg08780218	NA	IGR_shelf	NA	0.12	0.59	0.48	0.34	-0.25
cg24705426	ATG7	Body_none	TRUE	0.35	0.78	0.66	0.56	-0.22
cg00593243	DUSP1	Body_shore	NA	0.12	0.49	0.38	0.26	-0.22
cg09545579	BAHCC1	Body_island	TRUE	0.19	0.60	0.52	0.39	-0.21
cg22801217	TSPO2	TSS200_none	NA	0.34	0.80	0.67	0.58	-0.21
cg00150245	NA	IGR_shelf	NA	0.33	0.78	0.66	0.56	-0.21
cg13001097	UTRN	Body_none	TRUE	0.12	0.54	0.38	0.33	-0.21
cg18421360	GPR98	Body_none	TRUE	0.22	0.80	0.68	0.59	-0.21
cg04071398	IL20RA	Body_shore	NA	0.19	0.63	0.56	0.43	-0.21
cg02711479	STK40	5'UTR_shelf	NA	0.19	0.60	0.51	0.40	-0.20
cg18752854	TNS1	TSS1500_none	NA	0.25	0.60	0.45	0.40	-0.20
cg13983640	TSPO2	TSS1500_none	NA	0.29	0.68	0.58	0.47	-0.20
cg21713780	CHSY1	Body_none	TRUE	0.40	0.73	0.63	0.54	-0.20
cg16312609	NA	IGR_none	TRUE	0.35	0.67	0.58	0.47	-0.20
cg10198568	FRMD4A	Body_none	TRUE	0.24	0.64	0.53	0.45	-0.20
cg02084912	C3orf42	TSS1500_none	NA	0.15	0.58	0.45	0.39	-0.20
cg19370858	NA	IGR_shelf	NA	0.30	0.74	0.61	0.54	-0.20
cg00283857	ZDHHC14	Body_shelf	TRUE	0.39	0.79	0.69	0.60	-0.20
cg17445490	ECE1	Body_none	TRUE	0.24	0.74	0.64	0.55	-0.19
cg02189597	RORA	Body_shelf	NA	0.39	0.68	0.56	0.49	-0.19
cg05484949	NA	IGR_none	NA	0.28	0.64	0.55	0.45	-0.19
cg19221542	NA	IGR_shore	NA	0.24	0.57	0.49	0.38	-0.19
cg04091816	PDK2	Body_shelf	TRUE	0.32	0.69	0.61	0.50	-0.19
cg26777809	LRRC1	Body_none	TRUE	0.24	0.65	0.55	0.46	-0.19
cg06641366	LRRC8C	TSS1500_shore	NA	0.28	0.75	0.66	0.56	-0.19
cg19192626	NA	IGR_none	NA	0.13	0.48	0.38	0.29	-0.19
cg20377447	TSPO2	TSS1500_none	NA	0.29	0.66	0.56	0.47	-0.19
cg05168580	C14orf73	Body_shore	NA	0.28	0.60	0.49	0.41	-0.19
cg05234415	PPP1R14A	Body_shelf	TRUE	0.36	0.70	0.58	0.51	-0.19
cg22821554	CYP3A4	TSS1500_none	NA	0.32	0.71	0.52	0.52	-0.19
cg07803375	HEATR2	Body_shelf	TRUE	0.31	0.67	0.58	0.48	-0.19
cg25533211	TSPO2	TSS1500_none	NA	0.24	0.59	0.51	0.40	-0.19
cg04272613	DAAM1	5'UTR_none	TRUE	0.14	0.49	0.36	0.31	-0.19
cg05021291	NA	IGR_none	TRUE	0.29	0.68	0.56	0.49	-0.19

cg06935361	BRCA2	Body_none	TRUE	0.34	0.74	0.65	0.55	-0.19
cg10624729	FAM73A	Body_none	TRUE	0.20	0.62	0.49	0.43	-0.18
cg27529668	SLC38A10	Body_none	NA	0.20	0.58	0.51	0.40	-0.18
cg03700171	IREB2	Body_none	TRUE	0.23	0.60	0.54	0.42	-0.18
cg17801930	NA	IGR_none	TRUE	0.42	0.80	0.62	0.62	-0.18
cg26528531	PCDH7	Body_none	TRUE	0.51	0.87	0.72	0.68	-0.18
cg05524458	ANKRD33B	Body_shore	TRUE	0.50	0.87	0.77	0.68	-0.18
cg18634175	ITGB5	Body_none	TRUE	0.31	0.72	0.61	0.54	-0.18
cg22609908	NA	IGR_shelf	NA	0.22	0.55	0.43	0.37	-0.18
cg01821452	NA	IGR_none	TRUE	0.45	0.75	0.65	0.57	-0.18
cg18263455	MIR548H4	Body_none	TRUE	0.23	0.71	0.58	0.53	-0.18
cg04723449	COG7	Body_none	TRUE	0.23	0.67	0.52	0.50	-0.18
cg10221596	ALS2CR12	TSS200_none	NA	0.49	0.72	0.66	0.54	-0.18
cg15881795	NA	IGR_none	TRUE	0.37	0.78	0.66	0.60	-0.18

Table S2

DAVID functional annotation clustering analysis for 2108 phototherapy affected MVPs

Annotation Cluster 1	Enrichment Score: 4.96	Count	P_Value	Benjamini
GOTERM_BP_FAT	inflammatory response	42	5.50E-07	1.70E-03
GOTERM_BP_FAT	defense response	59	3.80E-05	2.30E-02
GOTERM_BP_FAT	response to wounding	52	6.60E-05	2.80E-02
Annotation Cluster 2	Enrichment Score: 4.05	Count	P_Value	Benjamini
GOTERM_BP_FAT	cytoskeleton organization	47	1.60E-05	1.60E-02
GOTERM_BP_FAT	actin filament-based process	29	1.50E-04	4.40E-02
GOTERM_BP_FAT	actin cytoskeleton organization	27	2.90E-04	4.40E-02
Annotation Cluster 3	Enrichment Score: 2.92	Count	P_Value	Benjamini
GOTERM_BP_FAT	response to hormone stimulus	40	6.00E-05	3.00E-02
GOTERM_BP_FAT	cellular response to hormone stimulus	20	1.20E-04	4.40E-02
GOTERM_BP_FAT	response to endogenous stimulus	41	2.40E-04	4.40E-02
GOTERM_BP_FAT	response to organic substance	63	2.90E-04	4.60E-02
GOTERM_BP_FAT	insulin receptor signaling pathway	8	3.60E-03	2.00E-01
GOTERM_BP_FAT	response to peptide hormone stimulus	17	1.10E-02	3.60E-01
GOTERM_BP_FAT	cellular response to insulin stimulus	10	1.20E-02	3.70E-01
GOTERM_BP_FAT	response to insulin stimulus	12	2.10E-02	4.70E-01
Annotation Cluster 4	Enrichment Score: 2.91	Count	P_Value	Benjamini
GOTERM_BP_FAT	regulation of cell motion	25	1.50E-04	4.10E-02
GOTERM_BP_FAT	regulation of locomotion	23	8.80E-04	8.80E-02
GOTERM_BP_FAT	regulation of cell migration	21	9.90E-04	9.30E-02
GOTERM_BP_FAT	positive regulation of locomotion	14	2.70E-03	1.80E-01
GOTERM_BP_FAT	positive regulation of cell motion	14	2.70E-03	1.80E-01
GOTERM_BP_FAT	positive regulation of cell migration	13	3.40E-03	1.90E-01
Annotation Cluster 5	Enrichment Score: 2.79	Count	P_Value	Benjamini
GOTERM_BP_FAT	regulation of programmed cell death	70	1.80E-04	4.20E-02
GOTERM_BP_FAT	regulation of cell death	70	2.10E-04	4.40E-02
GOTERM_BP_FAT	regulation of apoptosis	69	2.30E-04	4.60E-02
GOTERM_BP_FAT	apoptosis	55	2.50E-04	4.40E-02
GOTERM_BP_FAT	cell death	63	2.60E-04	4.30E-02
GOTERM_BP_FAT	death	63	3.20E-04	4.50E-02
GOTERM_BP_FAT	programmed cell death	55	3.60E-04	4.70E-02
GOTERM_BP_FAT	positive regulation of programmed cell death	42	4.70E-04	5.70E-02
GOTERM_BP_FAT	positive regulation of cell death	42	5.20E-04	6.10E-02
GOTERM_BP_FAT	positive regulation of apoptosis	41	7.90E-04	8.20E-02
GOTERM_BP_FAT	induction of programmed cell death	31	3.20E-03	1.90E-01
GOTERM_BP_FAT	induction of apoptosis by extracellular signals	15	3.30E-03	1.90E-01
GOTERM_BP_FAT	induction of apoptosis	30	5.70E-03	2.60E-01
GOTERM_BP_FAT	negative regulation of programmed cell death	30	2.40E-02	5.00E-01
GOTERM_BP_FAT	negative regulation of cell death	30	2.50E-02	5.00E-01
GOTERM_BP_FAT	negative regulation of apoptosis	29	3.40E-02	5.50E-01
GOTERM_BP_FAT	anti-apoptosis	15	2.40E-01	9.10E-01

Table S3**Overall methylation improvement at the end of phototherapy based on 2108 MVPs**

Clinical improvement	Excellent							Good		Unsatisfactory	
	P2	P3	P4	P8	P10	P11	P12	P1	P9	P6	P7
% methylation improvement (POST-UV vs. PRE-UV, increased)	109.39	136.00	11.36	38.62	93.25	30.54	71.13	62.00	14.66	11.52	9.40
% methylation improvement (POST-UV vs. PRE-UV, decreased)	40.15	27.94	10.01	10.70	48.27	42.49	15.92	38.56	5.92	4.88	5.71
Absolute methylation difference (POST-UV vs. Control)	0.15	0.11	0.16	0.12	0.07	0.07	0.16	0.09	0.37	0.30	0.33

Table S4

List of MVPs that responded to phototherapy and strongly correlated with gene expression

ProbeID	Gene symbol	Correlation r *	Enhancer	Feat.rel	CONTROL	PRE-UV	MID-UV	POST-UV
cg06355720	S100A9	-0.8898	NA	3'UTR_none	0.93	0.52	0.67	0.76
cg20169988	S100A9	-0.8717	NA	Body_none	0.92	0.44	0.58	0.71
cg16139316	S100A9	-0.8701	NA	5'UTR_none	0.92	0.34	0.51	0.67
cg22952459	C10orf99	-0.8683	NA	TSS1500_none	0.82	0.48	0.57	0.66
cg23092820	S100A9	-0.8679	NA	TSS1500_none	0.86	0.61	0.69	0.73
cg20161089	IFI27	-0.8627	NA	5'UTR_none	0.91	0.44	0.53	0.68
cg15467116	S100A9	-0.8545	NA	Body_none	0.95	0.73	0.82	0.85
cg03165378	S100A9	-0.8517	NA	TSS1500_none	0.86	0.48	0.59	0.67
cg03514239	S100A9	-0.8409	NA	TSS1500_none	0.49	0.17	0.23	0.30
cg01431057	S100A8	-0.8344	NA	Body_none	0.64	0.20	0.29	0.43
cg22946974	SPRR2F	-0.8334	NA	5'UTR_none	0.89	0.42	0.60	0.71
cg18766755	SPRR2A	-0.8177	NA	5'UTR_none	0.86	0.46	0.63	0.72
cg04112417	VSNL1	-0.8108	TRUE	Body_none	0.74	0.41	0.47	0.57
cg03404572	SERPINB3	-0.8015	NA	TSS200_none	0.68	0.22	0.28	0.38
cg22204954	SPRR2F	-0.7929	NA	TSS200_none	0.56	0.16	0.27	0.36
cg02892624	S100A7	-0.7875	NA	5'UTR_none	0.89	0.60	0.71	0.76
cg09174555	S100A8	-0.7870	NA	TSS1500_none	0.43	0.16	0.22	0.31
cg07290257	LASS6	-0.7830	TRUE	Body_none	0.40	0.76	0.61	0.59
cg08036899	IFI27	-0.7792	NA	5'UTR_none	0.93	0.68	0.74	0.82
cg20335425	S100A8	-0.7732	NA	5'UTR_none	0.49	0.19	0.24	0.35
cg22933439	S100A7A	-0.7683	NA	TSS1500_none	0.79	0.53	0.64	0.71
cg00859858	ZC3H12A	-0.7662	TRUE	Body_shelf	0.76	0.19	0.31	0.46
cg04452195	GJB2	-0.7659	NA	3'UTR_shelf	0.83	0.43	0.52	0.66
cg18443806	IFI27	-0.7612	NA	TSS1500_none	0.87	0.62	0.69	0.77
cg18145090	GJB6	-0.7445	NA	5'UTR_shore	0.84	0.56	0.61	0.69
cg26127113	CGNL1	-0.7427	TRUE	Body_none	0.30	0.75	0.59	0.57
cg04880990	KRT6A	-0.7377	NA	TSS1500_none	0.71	0.33	0.41	0.51
cg22377389	GJB6	-0.7371	TRUE	5'UTR_shore	0.49	0.21	0.28	0.36
cg17304678	RGMB	-0.7360	TRUE	Body_none	0.18	0.54	0.43	0.40
cg24036517	SOX7	-0.7335	NA	Body_shore	0.71	0.34	0.43	0.50
cg24790676	KLK10	-0.7324	NA	TSS1500_shore	0.75	0.53	0.60	0.63
cg07798731	C10orf99	-0.7322	NA	TSS1500_none	0.46	0.23	0.29	0.36
cg01440333	CHI3L2	-0.7282	NA	TSS200_none	0.46	0.25	0.31	0.39
cg20393620	SGK1	-0.7272	TRUE	Body_none	0.82	0.41	0.53	0.64
cg07813495	ZC3H12A	-0.7256	NA	Body_none	0.54	0.27	0.35	0.41
cg20256009	S100A8	-0.7210	NA	5'UTR_none	0.36	0.11	0.12	0.22
cg06051311	TRIM15	-0.7166	TRUE	5'UTR_none	0.83	0.52	0.62	0.67
cg03473518	GJB6	-0.7161	TRUE	5'UTR_shore	0.50	0.22	0.28	0.37
cg15662902	TNNI2	-0.7160	NA	TSS1500_none	0.40	0.65	0.58	0.50
cg12869351	GJB2	-0.7137	NA	5'UTR_shelf	0.95	0.63	0.70	0.83
cg12067024	S100A7A	-0.7135	NA	TSS1500_none	0.65	0.22	0.32	0.49
cg01011918	SPRR2D	-0.7131	NA	1stExon_none	0.81	0.40	0.47	0.56
cg26808583	S100A12	-0.7118	NA	Body_none	0.89	0.67	0.74	0.78
cg27229484	ZC3H12A	-0.7106	NA	Body_none	0.61	0.23	0.33	0.42

cg17496887	S100A7A	-0.7081	NA	TSS1500_none	0.61	0.17	0.22	0.33
cg11668844	MCF2L	-0.7068	TRUE	Body_shore	0.14	0.56	0.47	0.42
cg18116418	LCE3D	-0.7054	NA	TSS1500_none	0.58	0.33	0.40	0.45
cg17967059	GJB2	-0.7039	NA	Body_shelf	0.71	0.33	0.41	0.53
cg00863378	BBS2	-0.7032	NA	Body_shelf	0.15	0.35	0.25	0.24
cg00012692	GJB6	-0.7031	TRUE	5'UTR_shore	0.47	0.26	0.30	0.38
cg25212571	SPRR2C	-0.7004	NA	TSS200_none	0.88	0.51	0.62	0.69
cg11692307	PLCH2	0.7381	NA	Body_none	0.75	0.39	0.45	0.55
cg18318006	SORBS1	0.7647	TRUE	Body_none	0.81	0.38	0.54	0.64
cg23553762	GALNTL1	0.8721	TRUE	Body_none	0.64	0.28	0.35	0.43

*Correlation between levels of gene expression and DNA methylation (n=47)

Table S5**Summary of feature and correlation with gene expression for 2108 MVPs**

	Total MVPs (2108)			Enhancer-located MVPs (1098)		
	Count	Count (strong/moderate correlation)	%	Count	Count (strong/moderate correlation)	%
Promoter	510	72	14.12%	151	17	11.26%
Gene body	832	73	8.77%	460	26	5.65%
3'UTR	78	5	6.41%	14	0	0
IGR	688	0	0	473	0	0
Total	2108	150	7.12%	1098	43	3.92%

Table S6**Clinical data of twelve patients with psoriasis**

ID	Sex	Age	Psoriasis since	Biopsy site	Localisation of lesions	Skin type	Given dose	No of treatments	Response	others
1	M	40	> 20 y	Buttocks, lower back	Whole body	I - II	0.3 – 1.4 J	34	Good	
2	F	73	unknown	Arms	Arms, back, soles, scalp	III	0.3 – 2.0 J	20	Excellent	
3	M	59	> 20 y	Thighs	Legs, buttocks, left elbow, hands	III	0.3 – 1.7 J	23	Excellent	Hypertonia
4	M	67	< 1 y	Buttocks, thigh	Elbows, legs, scalp, buttocks	II - III	0.3 – 1.5 J	20	Excellent	
5	M	26	~1 y	Buttocks	Legs, arms, scalp, face, buttocks	I – II	0.1 – 0.55 J	15 Stopped	unknown (light sensitive)	
6	M	17	> 10 y	Buttocks	Whole body, scalp	IV	0.3 – 1.7 J Stopped 3 weeks 0.9 – 1.3 J	21	Unsatisfactory	
7	F	47	> 10 y	buttocks	Whole body	I	0.3 – 2.2 J	23	Unsatisfactory	Psoriatic arthritis
8	M	43	> 10 y	buttocks	Lower legs, arms, trunk	III	0.3 – 2.6 J	25	Excellent	
9	F	46	> 10 y	legs	Legs, elbows, hands	III	0.3 – 2.6 J	30	Good	Psoriatic arthritis
10	F	74	2 y	buttocks	Whole body	II	0.3 – 2.1 J	20	Excellent	Hypertonia
11	F	33	> 10 y	Buttocks	Whole body	III	0.3 – 2.0 J	21	Excellent	
12	F	28	> 10y	Buttocks	Whole body	I	0.2 – 1.0 J	19	Excellent	

Table S7**Primers for OneStep qMethyl DNA methylation analysis**

ProbeID	Gene	Forward	Reverse	product size
cg20161089	IFI27	AAAGCTTCTGACCTGGAGCA	GGCTGCTTTCTTTCTCCTGA	263 bp
cg27431500	HN1L	AAACAGTCCAGCCTTGTGCT	TGCAAGGTGAAACAGGAAGA	193 bp
cg11802666	IRF2	ATGGAGGCTGAGAAGTCAA	AGGGGTAGGATTGTGGCTTT	175 bp
cg04091816	PDK2	CTCATCCTCTCCCCTCCATT	GGCTGCTCAACAACCCTAGA	178 bp

Figure S1

Validation of 450K BeadChip data by OneStep qMethyl analysis. Four CpG sites were selected for data validation. Results from two methods were consistent based on Pearson's correlation coefficient (r).

