

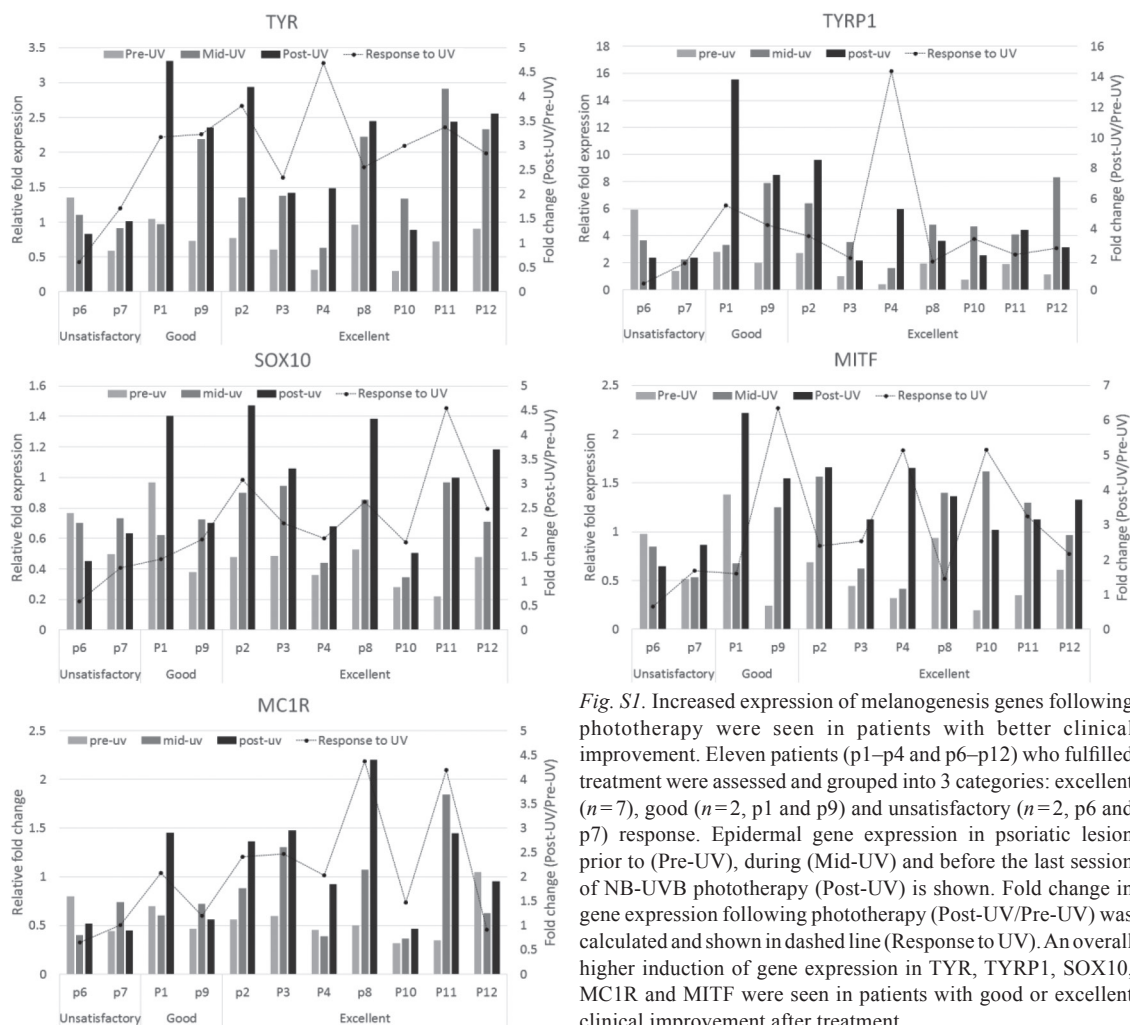


Fig. S1. Increased expression of melanogenesis genes following phototherapy were seen in patients with better clinical improvement. Eleven patients (p1–p4 and p6–p12) who fulfilled treatment were assessed and grouped into 3 categories: excellent ($n=7$), good ($n=2$, p1 and p9) and unsatisfactory ($n=2$, p6 and p7) response. Epidermal gene expression in psoriatic lesion prior to (Pre-UV), during (Mid-UV) and before the last session of NB-UVB phototherapy (Post-UV) is shown. Fold change in gene expression following phototherapy (Post-UV/Pre-UV) was calculated and shown in dashed line (Response to UV). An overall higher induction of gene expression in TYR, TYRP1, SOX10, MC1R and MITF were seen in patients with good or excellent clinical improvement after treatment.

Appendix S1

NB-UVB phototherapy

NB-UVB irradiation was administered to the whole body 2–3 times a week using a cabinet (PCL 8000, Puva Combi Light – ARKADE, Heverlee, Belgium) equipped with fluorescent lamps (UVB TL100W/01, Philips, Eindhoven, The Netherlands). Treatment comprising approximately 24 sessions was given during 2–3 months.

Sample processing and microarray hybridisation

Samples were cut into 10 µm thick sections and placed on membrane-covered glass slides (PALM Membrane Slides, PALM Microlaser Technologies, Bernried, Germany). Laser Capture Microdissection (LCM) was then carried out using a PALM® microlaser system (PALM GmbH, Bernried, Germany). Epithelium only was used in further analysis, and RNA extracted using RNAqueous-Micro Kit from Ambion. RNA quality was confirmed by Agilent RNA 6000 Nano kit (Agilent 2100 Bioanalyzer, Agilent Technologies, Santa Clara, CA, USA). RNA with RIN value more than 6 was considered acceptable. Fifty ng of total RNA was used for cRNA production by using the TargetAmp-Nano Labeling Kit for Illumina Expression BeadChip (Epicenter Biotechnologies, Madison, WI, USA). Following the instructions for Illumina Expression BeadChip, a total of 750 ng cRNA was hybridised to Illumina HumanHT-12 v4 Expression BeadChip (Illumina Inc., San Diego, CA, USA). iScan Reader was used to image BeadChips. Images were visualised and intensity data extraction was conducted using GenomeStudio Data Analysis Software. Raw data were deposited in the Gene Expression Omnibus database and are available under the accession number GSE53431.

Microarray data validation

Gene expression data were confirmed by quantitative real-time PCR (qRT-PCR). Two hundred ng of total RNA was used to synthesise cDNA using First-Strand cDNA Synthesis Kit (USB, Cleveland, OH, USA). Real time RT-PCR was performed using an IQ5 multicolor real-time PCR detection system with IQ SYBR Green Supermix (Bio-Rad Laboratories, Hercules, CA, USA). Each sample was measured in duplicate and results normalised in relation to the housekeeping gene *RPL13A*. Primer information is summarised in Table SII¹. Primers for TYR, TYRP1, SOX10, MITF and MC1R were from Real Time Primers (Real Time Primers, LLC, Philadelphia, PA, USA).

In order to study gene expression in non-involved normal skin from psoriasis patients, another set of cDNA samples from heal-

thy controls, non-involved psoriatic skin and lesional psoriatic skin was used, and prepared from whole biopsies as described previously (13). *T*-test was conducted to compare qRT-PCR data and two-tailed *p*-value less than 0.05 was considered statistically significant. For immunohistochemistry, formalin-fixed and paraffin-embedded tissues prepared from the above-mentioned healthy controls, non-involved psoriatic skin and lesional psoriatic skin were used. Immunohistochemical staining was performed using monoclonal antibodies directed against TYR, TYRP1 and MITF (Abcam, Cambridge, UK). Antibodies were used at concentrations 1:50 (TYR), 1:800 (TYRP1) and 1:10 (MITF), respectively. Staining was performed using a Ventana staining machine (Ventana Medical Systems, Tucson, AZ, USA) and reagents according to the supplier's recommendation.

Cell culture and stimuli

Human epidermal keratinocytes adult (HEKa, Life technologies, Carlsbad, USA) were maintained in medium 154 supplemented with human keratinocyte growth supplement (HKGS) (Life technologies) and cultured at 37°C with 5% CO₂. Cells (between passage 3 to 6) were stimulated with Poly(dA:dT)/Lyovect or Poly(I:C) (1 µg/ml, Invivogen, San Diego, CA, USA) in 6-well plates. Experiments were performed in duplicate and repeated in 3 independent experiments. Cells were collected after 24 h and Trizol reagent (Life technologies) was used to isolate RNA. RevertAid H Minus First Strand cDNA Synthesis Kit (Thermo Scientific, Waltham, MA, USA) was used for cDNA synthesis. Real time RT-PCR was performed using an IQ5 multicolor real-time PCR detection system with IQ SYBR Green Supermix (Bio-Rad Laboratories). Primers used are shown in Table SII¹. Statistical analysis for the effect of poly(dA:dT) or poly(I:C) stimulation was assessed by a paired-sample *t*-test, 2-tailed *p*-value < 0.05 was regarded as statistically significant.

Western blotting

Protein extracted from cultured HEKa cells were separated on 10% ClearPAGE SDS gels (C.B.S. Scientific, San Diego, USA) and transferred to PVDF membranes using the Trans-Blot Turbo Blotting System (Bio-Rad, Hercules, USA). Blots were incubated with 1:400 diluted polyclonal anti-SPATA18 antibody (Atlas antibodies, Stockholm, Sweden). Mouse anti-actin monoclonal antibody from Millipore (Billerica, MA, USA) was used as a loading control at a dilution of 1:20,000. Polyclonal goat anti-rabbit immunoglobulins/HRP or polyclonal rabbit anti-mouse immunoglobulins/HRP (Dako UK Ltd, Cambridgeshire, UK) were used as secondary antibodies at a dilution of 1:50,000 and signals were detected with Amersham ECL select western blotting detection reagent (GE Healthcare, Pittsburgh, PA, USA).

Table SI. Patient clinical data

ID	Sex/Age	Psoriasis since	Biopsy site	Localisation of lesions	Skin type	Given dose	Treatments <i>n</i>	Response
1	M/40	>20 years	Buttock, 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 years	Thighs	Legs, buttocks, left elbow, hands	III	0.3–1.7 J	23	Excellent
4	M/67	<1 years	Buttocks, thigh	Elbows, legs, scalp, buttocks	II–III	0.3–1.5 J	20	Excellent
5	M/26	1 year	Buttocks	Legs, arms, scalp, face, buttocks	I–II	0.1–0.55 J	15 ^a	Unknown
6	M/17	>10 years	Buttocks	Whole body, scalp	IV	0.3–1.7 J ^b	21	Unsatisfactory
7	F/47	>10 years	Buttocks	Whole body	I	0.3–2.2 J	23	Unsatisfactory
8	M/43	>10 years	Buttocks	Lower legs, arms, trunk	III	0.3–2.6 J	25	Excellent
9	F/46	>10 years	Legs	Legs, elbows, hands	III	0.3–2.6 J	30	Good
10	F/74	2 years	Buttocks	Whole body	II	0.3–2.1 J	20	Excellent
11	F/33	>10 years	Buttocks	Whole body	III	0.3–2.0 J	21	Excellent
12	F/28	>10 years	Buttocks	Whole body	I	0.2–1.0 J	19	Excellent

^aStopped treatment half way. ^b0.3–1.7 J, stop 3 weeks, 0.9–1.3 J.

Table SII. Sequences of primers used for qRT-PCR

Gene symbol	Forward primer	Reverse primer
IFI16	AAAGTTCCGAGGTGATGCTG	GAGGGTGCAGGTGAAGTAGC
IFIH1	GTGCATGGAGGAGGAAGTGT	TTCTGAGCAATCAGAGCCTGT
IRF3	GTTCTGTGTGGGGGAGTCAT	GCAGGTAGGCCTTGACTGG
MC1R	GACTTCTCACCAGCAGTCGT	CACCCAGAGACTTCACATCC
MITF	CTGGAACAAGGGAACCATCT	TCACCAAATCTGGAGAGCAG
RPL13A	GTACGCTGTGAAGGCATCAA	GTTGGTGTTTCATCCGCTTG
SOD1	GAAGGTGTGGGGAAGCATTA	CAATAGACACATCGGCCACA
SOD2	CCCTGGAACCTCACATCAAC	GCCGTCAGCTTCTCCTTAAA
SOX10	CCAATTCTGTGCCAATAACC	AGGGGCCATAGAGCCTAGTA
SPATA18	AACTTTACGAACGTTGCAGGA	GGCTGCTGCTGTGAGGAT
TMEM173	AGCCTTGTTCTGCTGAGTG	CAGACCCCGTTTAAACAGCAG
TYR	GTAATGCCTGCTGTGGAGTT	GTTGAATCCCATGAAGTTGC
TYRP1	GGATCCAGAAGCAACTTTGA	GGCGTGTCAAATAAACCAAC

Table SIII. DAVID functional annotation analysis for dysregulated genes in psoriasis lesional epidermis compared to healthy controls

Category	Term	Count	p-value	Benjamini
Up-regulated genes				
GOTERM_BP_FAT	Generation of precursor metabolites and energy	82	3.00E-21	1.00E-17
GOTERM_BP_FAT	Translation	70	4.60E-13	7.80E-10
GOTERM_BP_FAT	Oxidation reduction	107	2.00E-12	2.20E-09
GOTERM_BP_FAT	Oxidative phosphorylation	32	2.80E-11	2.30E-08
GOTERM_BP_FAT	Mitotic cell cycle	68	6.90E-10	4.60E-07
GOTERM_CC_FAT	Mitochondrion	211	5.40E-34	3.00E-31
GOTERM_CC_FAT	Mitochondrial part	128	2.30E-24	6.40E-22
GOTERM_CC_FAT	Cytosol	198	2.50E-17	4.70E-15
GOTERM_CC_FAT	mitochondrial matrix	59	3.70E-15	5.30E-13
GOTERM_CC_FAT	mitochondrial lumen	59	3.70E-15	5.30E-13
KEGG_PATHWAY	Oxidative phosphorylation	46	5.80E-14	1.00E-11
KEGG_PATHWAY	Alzheimer's disease	48	2.90E-11	2.60E-09
KEGG_PATHWAY	Parkinson's disease	39	1.00E-09	5.90E-08
KEGG_PATHWAY	Proteasome	21	1.20E-08	5.20E-07
KEGG_PATHWAY	Huntington's disease	43	3.10E-07	1.10E-05
Down-regulated genes				
GOTERM_BP_FAT	Regulation of transcription	301	7.40E-14	2.50E-10
GOTERM_BP_FAT	Transcription	251	7.20E-13	1.20E-09
GOTERM_BP_FAT	Regulation of RNA metabolic process	222	2.20E-12	2.40E-09
GOTERM_BP_FAT	Regulation of transcription, DNA-dependent	215	1.50E-11	1.20E-08
GOTERM_BP_FAT	Negative regulation of cellular biosynthetic process	75	6.00E-06	4.00E-03
GOTERM_CC_FAT	Proteinaceous extracellular matrix	54	9.00E-09	4.70E-06
GOTERM_CC_FAT	Extracellular matrix	56	1.90E-08	4.90E-06
GOTERM_CC_FAT	Extracellular matrix part	26	7.10E-07	1.20E-04
GOTERM_CC_FAT	Basement membrane	20	1.90E-06	2.50E-04
GOTERM_CC_FAT	Cell-cell junction	29	2.30E-04	2.40E-02
KEGG_PATHWAY	Pathways in cancer	46	2.10E-05	3.50E-03
KEGG_PATHWAY	Small cell lung cancer	17	3.20E-04	2.60E-02
KEGG_PATHWAY	Endocytosis	28	3.50E-04	1.90E-02
KEGG_PATHWAY	Focal adhesion	28	1.40E-03	5.70E-02
KEGG_PATHWAY	Cytokine-cytokine receptor interaction	32	4.80E-03	1.50E-01

Table SIV. Top 5 biological processes affected by NB-UVB phototherapy in psoriatic epidermis

Biological process	p-value	Genes						
Up-regulated								
Pigmentation	1.70E-08	<i>BBS2</i>	<i>DCT</i>	<i>EDNRB</i>	<i>KIT</i>	<i>MITF</i>	<i>MLPH</i>	<i>OCA2</i>
		<i>SILV</i>	<i>SLC45A2</i>	<i>SOX10</i>	<i>TYR</i>	<i>TYRP1</i>		
Cell adhesion	5.00E-05	<i>BCAN</i>	<i>CLDN1</i>	<i>CLDN23</i>	<i>CLDN8</i>	<i>COL16A1</i>	<i>COL17A1</i>	<i>COL5A1</i>
		<i>COL7A1</i>	<i>CPXM2</i>	<i>DLC1</i>	<i>DST</i>	<i>ECM2</i>	<i>EPDR1</i>	<i>FBLN7</i>
		<i>FEZ1</i>	<i>GPNMB</i>	<i>HES5</i>	<i>KITLG</i>	<i>LAMA5</i>	<i>LAMB4</i>	<i>LEF1</i>
		<i>PGM5</i>	<i>POSTN</i>	<i>PPFIBP1</i>	<i>PTPRM</i>	<i>RGMB</i>	<i>SORBS1</i>	<i>SRPX</i>
		<i>SSPN</i>	<i>SVEP1</i>	<i>TGFB1</i>				
Regulation of cell motion	1.40E-02	<i>BBS2</i>	<i>DLC1</i>	<i>IGFBP5</i>	<i>KIT</i>	<i>LAMA5</i>	<i>PLD1</i>	<i>PLXNA3</i>
		<i>PTPRM</i>	<i>SERPINE2</i>	<i>TGFBR3</i>				
Cell morphogenesis	2.40E-02	<i>BBS2</i>	<i>DMD</i>	<i>DST</i>	<i>FEZ1</i>	<i>LAMA5</i>	<i>LEF1</i>	<i>LPPR4</i>
		<i>NOTCH1</i>	<i>P2RX7</i>	<i>PLXNA3</i>	<i>PTPRM</i>	<i>SLITRK2</i>	<i>TGFBR3</i>	<i>WNT3A</i>
Oxidation reduction	2.70E-02	<i>ACADL</i>	<i>ADHFE1</i>	<i>CMAH</i>	<i>CYBASC3</i>	<i>CYBRD1</i>	<i>CYP2J2</i>	<i>CYP3A5</i>
		<i>CYP4F12</i>	<i>D2HGDH</i>	<i>GAPDHS</i>	<i>GMPR</i>	<i>GPX8</i>	<i>P4HTM</i>	<i>PHYH</i>
		<i>PLOD3</i>	<i>PPOX</i>	<i>PRODH</i>	<i>RRM2B</i>	<i>SNCA</i>	<i>TYR</i>	<i>TYRP1</i>
Down-regulated								
Ectoderm development	3.80E-08	<i>ALOX12B</i>	<i>ATP2A2</i>	<i>CNFN</i>	<i>CRABP2</i>	<i>FABP5L2</i>	<i>FABP5</i>	<i>IVL</i>
		<i>KRT16</i>	<i>KRT17P3</i>	<i>KRT6A</i>	<i>KRT6B</i>	<i>LCE3A</i>	<i>LCE3D</i>	<i>S100A7</i>
		<i>SPRR1A</i>	<i>SPRR1B</i>	<i>SPRR2A</i>	<i>SPRR2B</i>	<i>SPRR2C</i>	<i>SPRR2D</i>	<i>SPRR2F</i>
		<i>TGM1</i>						
Carbohydrate catabolic process	4.50E-05	<i>ALDOA</i>	<i>CHI3L2</i>	<i>FUT3</i>	<i>G6PD</i>	<i>GPI</i>	<i>HK2</i>	<i>LDHB</i>
		<i>NUDT5</i>	<i>PGAM1</i>	<i>PGAM4</i>	<i>PGD</i>	<i>TP11</i>		
Translation	9.40E-05	<i>EIF2B2</i>	<i>EIF3M</i>	<i>EIF4G2</i>	<i>EIF5</i>	<i>GARS</i>	<i>HNRNP2</i>	<i>MRPL11</i>
		<i>MRPL12</i>	<i>MRPL20</i>	<i>MRPL36</i>	<i>MRPL4</i>	<i>MRPS12</i>	<i>RBM3</i>	<i>RPL10A</i>
		<i>RPL34</i>	<i>RPL36</i>	<i>RPL6</i>	<i>RPLP0</i>	<i>RPS17</i>	<i>RPS21</i>	<i>RPS24</i>
Homeostatic process	3.20E-04	<i>ABCA12</i>	<i>ALDOA</i>	<i>APP</i>	<i>ATP2A2</i>	<i>CACNB4</i>	<i>CCL5</i>	<i>CD24</i>
		<i>CD7</i>	<i>CIDEA</i>	<i>CYB5R4</i>	<i>CYP27B1</i>	<i>EIF2B2</i>	<i>FKBP1A</i>	<i>G6PD</i>
		<i>GLRX3</i>	<i>GNA15</i>	<i>GOT1</i>	<i>HCLS1</i>	<i>HIF1A</i>	<i>KLK6</i>	<i>LOC399804</i>
		<i>LYN</i>	<i>MYC</i>	<i>P2RY2</i>	<i>PDIA6</i>	<i>PRNP</i>	<i>RAC2</i>	<i>RPS17</i>
		<i>RPS24</i>	<i>SCO2</i>	<i>SH3BGR13</i>	<i>SOD2</i>	<i>STAT3</i>	<i>TXNDC5</i>	
Immune response	1.50E-03	<i>AKIRIN2</i>	<i>BCL3</i>	<i>C1QBP</i>	<i>C1R</i>	<i>CCL5</i>	<i>CD14</i>	<i>CD24</i>
		<i>CD7</i>	<i>CD8A</i>	<i>CFB</i>	<i>CNIH</i>	<i>CTSC</i>	<i>CYP27B1</i>	<i>GBP6</i>
		<i>GPI</i>	<i>GZMA</i>	<i>HLA-DRB4</i>	<i>IFITM3</i>	<i>IL1F5</i>	<i>IL1F9</i>	<i>IL4R</i>
		<i>KYNU</i>	<i>LYN</i>	<i>OAS2</i>	<i>OAS3</i>	<i>OASL</i>	<i>PRELID1</i>	<i>LOC728666</i>
		<i>RAET1G</i>	<i>S100A7</i>	<i>XBPI</i>				

Table SV. Top 100 best discriminators

Var ID (Primary)	Symbol	0.998512 *M2.pq[1]	0.728203 *M2.poso[1]	Var ID (Primary)	Symbol	0.998512 *M2.pq[1]	0.728203 *M2.poso[1]
ILMN_1662839	PLEKHA1	-0.0324	0.0080	ILMN_1787265	ZNF503	0.0351	-0.0001
ILMN_1735798	OSBPL3	-0.0315	0.0044	ILMN_2149494	NPL	0.0327	-0.0049
ILMN_1809208	KIAA1543	-0.0314	0.0108	ILMN_1866954	NA	0.0324	-0.0084
ILMN_1667948	SPATA18	-0.0312	0.0088	ILMN_3239060	KRBA1	0.0319	-0.0027
ILMN_1791067	TESK1	-0.0308	0.0072	ILMN_1778755	TRIL	0.0309	-0.0071
ILMN_1815086	NINJ1	-0.0305	0.0069	ILMN_1781360	MPHOSPH6	0.0305	-0.0086
ILMN_1747020	SGK3	-0.0304	0.0116	ILMN_2120222	SERPINB3	0.0302	-0.0108
ILMN_2086612	CMAH	-0.0302	0.0118	ILMN_2103107	ADAMDEC1	0.0301	-0.0090
ILMN_2170595	RRM2B	-0.0301	-0.0013	ILMN_1664001	ARSF	0.0300	-0.0109
ILMN_3242709	LOC100130422	-0.0301	0.0085	ILMN_1794046	MTX2	0.0298	-0.0094
ILMN_3273996	LOC100129148	-0.0301	0.0059	ILMN_1814465	UBE2G1	0.0294	-0.0114
ILMN_1722294	CPNE8	-0.0298	0.0038	ILMN_1741264	MRPS33	0.0293	-0.0116
ILMN_1882590	NA	-0.0296	-0.0019	ILMN_1746517	KYNU	0.0292	-0.0122
ILMN_1804461	MYH14	-0.0295	0.0074	ILMN_1672295	ZC3H12A	0.0290	-0.0121
ILMN_1653836	C11orf41	-0.0293	0.0113	ILMN_1782070	NPL	0.0289	-0.0109
ILMN_1754507	IRF4	-0.0291	-0.0011	ILMN_1775111	SND1	0.0287	-0.0073
ILMN_1730639	SLC22A15	-0.0290	0.0054	ILMN_1676014	LOC728635	0.0286	-0.0064
ILMN_1714567	AHNAK	-0.0290	0.0130	ILMN_1727098	PPP1R16B	0.0285	-0.0014
ILMN_2057573	FAM62B	-0.0290	0.0134	ILMN_2136495	A2ML1	0.0285	-0.0119
ILMN_1760855	OCRL	-0.0289	0.0138	ILMN_1661695	IRAK3	0.0284	-0.0103
ILMN_1692824	ASPA	-0.0289	0.0048	ILMN_1689831	FLJ11235	0.0284	-0.0055
ILMN_2113606	CCL27	-0.0288	0.0099	ILMN_2157219	AASS	0.0280	-0.0031
ILMN_1666894	CSPG4	-0.0285	0.0045	ILMN_2370091	NGFRAP1	0.0279	-0.0078
ILMN_2093500	ZBED5	-0.0285	0.0107	ILMN_1795507	ABCA6	0.0278	-0.0025
ILMN_1776998	DNAJA4	-0.0283	0.0098	ILMN_1674038	CTSD	0.0277	-0.0061
ILMN_1653750	SOX10	-0.0283	0.0085	ILMN_1740170	CHCHD10	0.0277	-0.0118
ILMN_1701424	LAMC2	-0.0283	0.0121	ILMN_1714384	PCCA	0.0276	-0.0001
ILMN_1756784	FREQ	-0.0283	0.0054	ILMN_1779470	ABCG4	0.0276	-0.0110
ILMN_1702105	EF3	-0.0283	0.0086	ILMN_1779324	GZMA	0.0276	-0.0100
ILMN_1752117	TMEM55A	-0.0282	0.0115	ILMN_1797822	SEL1L3	0.0275	-0.0103
ILMN_1723536	USP33	-0.0282	0.0009	ILMN_1801377	SLC29A4	0.0275	-0.0074
ILMN_2208777	NHLH2	-0.0282	0.0053	ILMN_2133205	GPX2	0.0275	-0.0106
ILMN_2091310	TMEM16A	-0.0282	0.0049	ILMN_1804415	SMAGP	0.0273	-0.0140
ILMN_3243156	AHNAK2	-0.0281	0.0130	ILMN_1719661	SEPX1	0.0273	-0.0124
ILMN_1712705	RAB40C	-0.0281	0.0128	ILMN_1742813	TMEM167A	0.0271	-0.0137
ILMN_2183692	PHYHD1	-0.0281	0.0125	ILMN_1874613	NA	0.0270	-0.0125
ILMN_2219512	NPHP4	-0.0281	0.0072	ILMN_3305849	LOC728431	0.0270	-0.0134
ILMN_1759326	P2RX7	-0.0280	0.0105	ILMN_1769388	GJB2	0.0270	-0.0147
ILMN_1722718	BMP2	-0.0278	0.0132	ILMN_1779852	LOC387934	0.0269	-0.0143
ILMN_1854384	NA	-0.0278	0.0064	ILMN_1698804	ATP10B	0.0268	-0.0059
ILMN_3234775	SLAIN2	-0.0278	0.0051	ILMN_1782015	FCRLB	0.0268	-0.0125
ILMN_2399174	TRAK1	-0.0278	0.0044	ILMN_1702197	C9orf140	0.0268	-0.0091
ILMN_1702384	ZNF706	-0.0278	0.0083	ILMN_1678454	CASP4	0.0268	-0.0146
ILMN_1723021	ICMT	-0.0278	-0.0105	ILMN_2091347	IDH1	0.0268	-0.0097
ILMN_1712914	SEMA6B	-0.0277	0.0086	ILMN_3266606	FABP5L2	0.0268	-0.0145
ILMN_1664466	KLHL9	-0.0277	-0.0050	ILMN_1696302	FABP5	0.0267	-0.0139
ILMN_3181411	ATL1	-0.0276	0.0135	ILMN_1652721	LOC648758	0.0267	-0.0135
ILMN_1701933	SNCA	-0.0276	0.0080	ILMN_1805228	LRG1	0.0267	-0.0132
ILMN_1763638	BCAR3	-0.0276	0.0052	ILMN_1788607	RPL23A	0.0266	-0.0115
ILMN_1789384	QSOX2	-0.0276	0.0045	ILMN_2219002	KRT6A	0.0266	-0.0132