

**UVB drives different stages of epigenome alterations during progression of skin cancer**

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Table S1 .....	2
Table S2 .....	3
Table S3 .....	6
Table S4 .....	8
Table S5 .....	9
Table S6 .....	15
Figure S1 .....	20
Figure S2.....	21
Figure S3.....	22

**Table S1.** Primers used in qPCR and pyrosequencing

<b>qPCR primers (5' - 3')</b>	
<b>E2f2</b>	
Forward	ACCTGACCGAAGATAATGCC
Reverse	ACTGTCTGCTCCTTGAAGTTG
<b>Il4ra</b>	
Forward	CTGTCTGATTTTGCTGTTGGTG
Reverse	GATGTAGTCAGAGAAGCAGGTG
<b>Mgst2</b>	
Forward	CGCCCGTCACAAGTATTTCTG
Reverse	AAAGTCCAGGTATTCGTTTCAGG
<b>Vegfa</b>	
Forward	GGCAGCTTGAGTTAAACGAAC
Reverse	TGGTGACATGGTTAATCGGTC
<b>Pyrosequencing primers (5' - 3')</b>	
<b>E2f2</b>	
Forward	TTGGATTTGGAGGGTATTGG
Reverse	biotin-TCCTACCTCCTACCACCCACCATAAATA
Sequencing	TGGAGGGTATTGGGA
<b>Il4ra</b>	
Forward	GTGTGTTGGTTTTTTTTGTTGT
Reverse	biotin-ACTTAAAACCAACCCTACTTAACT
Sequencing	TGTTGGTTTTTTTTGTTGTT
<b>Mgst2</b>	
Forward	AGGTTTTTAAGATAGATTTATTAAGATT
Reverse	biotin-CCCCAAAAAACCCTTCTCTATTTAACAAC
Sequencing	ATTTATTAAGATTTGTGTAGTTTAT
<b>Vegfa</b>	
Forward	GGAATTGAAGTTAGGGTGTTAATGG
Reverse	biotin-AAAACAAAATACACCCCTAAATTCT
Sequencing	GGGTGTTAATGGGGG

**Table S2.** Top 56 regulated pathways with  $p < 0.01$  in comparison of UVB (epidermis) vs Control (epidermis)

Ingenuity Canonical Pathways	$-\log(p\text{-value})$	z-score	Molecules
Cyclins and Cell Cycle Regulation	3.0	3.4	CCNH,CDK4,CCNB2,CCND1,CDK1,CCNB1,HDAC5,SKP2,CCNA2,PPP2CB,E2F6,CCNE1,E2F1,FBXL5,GSK3B,E2F2,CDK2,E2F8
Estrogen-mediated S-phase Entry	5.6	2.3	CCNA2,E2F6,CCNE1,E2F1,CDK4,RBL1,CCND1,CDK1,CDK2,E2F2,E2F8,SKP2
Tumoricidal Function of Hepatic Natural Killer Cells	2.1	2.2	M6PR,CASP6,ICAM1,CASP3,CYCS,CASP7,DFFA
Mitotic Roles of Polo-Like Kinase	2.3	2.1	ANAPC2,KIF23,CDC20,PTTG1,PRC1,CDC7,CCNB2,ANAPC10,CDK1,CCNB1,CD25B,PPP2CB,PLK4,CDC26
Actin Nucleation by ARP-WASP Complex	3.5	1.8	ITGB1,RAP2A,PPP1R12C,ARPC1B,GRB2,GNA12,RALB,RAC1,RHOV,RRAS2,RHOQ,PPP1R12A,RHOV,FNBP1,VASP,ARPC4
NRF2-mediated Oxidative Stress Response	4.8	1.6	MAP2K6,RAP2A,PIK3CA,GSTA5,HSPB8,DNAJA4,DNAJC10,DNAJB2,DNAJC15,PIK3R4,DNAJA1,SOD3,CUL3,ABCC1,PMF1/PMF1/BGLAP,GCLM,TXN,GSK3B,NFE2L2,MAP2K1,CBR1,DNAJC9,GRB2,GSTM3,FGFR1,NQO1,RALB,DNAJC1,JUNB,TXNRD1,GSTO1,RRAS2,MGST2,PRKCD,IRS1,PIK3CB,PIK3CD,ENC1,DNAJB5,GSTP1
Ceramide Signaling	4.0	1.5	RAP2A,PIK3CA,S1PR5,BAD,CNKSR1,GRB2,FGFR1,SPHK2,RALB,CERK,PIK3R4,BCL2,S1PR4,S1PR3,PPP2CB,RRAS2,IRS1,SPHK1,PIK3CD,CYCS,PIK3CB,MAP2K1,NSMAF
Cytotoxic T Lymphocyte-mediated Apoptosis of Target Cells	2.5	1.0	CD247,CASP6,CD3G,CASP3,CD3E,CYCS,CASP7,DFFA,BCL2
Role of p14/p19ARF in Tumor Suppression	2.1	1.0	PIK3CA,GRB2,NPM3,IRS1,FGFR1,E2F1,RAC1,PIK3CB,PIK3CD,PIK3R4
Apoptosis Signaling	2.9	0.9	CAPN5,RAP2A,CASP3,BAD,RALB,CDK1,DFFA,BAK1,BCL2,ACIN1,BCL2L1,CASP6,CAPNS1,RRAS2,PLCG2,CAPN2,CAPN9,CYCS,MAP2K1,CASP7
Cell Cycle Regulation by BTG Family Proteins	2.6	0.7	PPP2CB,E2F6,CCNE1,E2F1,CDK4,CCND1,CDK2,E2F2,E2F8,PRMT1
p53 Signaling	4.5	0.7	PIK3CA,SNAI2,JMY,CDK4,HIF1A,PIK3R4,CCND1,BCL2,CCNG1,CASP6,THBS1,PPP1R13B,GSK3B,TOPBP1,GRB2,FGFR1,BIRC5,TP53BP2,BCL2L1,PCNA,IRS1,E2F1,PIK3CD,PIK3CB,PML,CDK2
PTEN Signaling	5.8	0.5	FOXO4,RAP2A,CSNK2A1,PIK3CA,TGFBR1,YWHAH,BAD,CCND1,BCL2,TGFBR2,INPP5B,IGF1R,GSK3B,MAP2K1,ITGB1,CASP3,GRB2,FGFR1,RALB,RAC1,TNFRSF11A,INPP5D,SYNJ2,BCL2L1,MAGI1,GHR,RRAS2,FOXO1,PIK3CD,PIK3CB,INSR
GM-CSF Signaling	2.3	0.5	RAP2A,PIK3CA,GRB2,FGFR1,RALB,JAK2,PIK3R4,CCND1,BCL2L1,CSF2RB,RRAS2,IRS1,PIK3CB,PIK3CD,STAT1,MAP2K1
STAT3 Pathway	4.2	0.4	RAP2A,MAP3K9,IL4R,TGFBR1,FGFR1,RALB,RAC1,IL22RA1,JAK2,TNFRSF11A,MAPK12,BCL2,TGFBR2,VEGFA,CSF2RB,GHR,RRAS2,IGF1R,TGFA,IFNLR1,IL1B,INSR,MAP2K1,SOCS5
Purine Nucleotides Degradation II (Aerobic)	2.8	0.4	GDA,NT5E,XDH,IMPDH1,ADA,NT5C2,ACPP
$\alpha$ -Adrenergic Signaling	2.7	0.3	GNG4,RAP2A,Calm1 (includes others),ADCY3,RALB,GNB5,ADCY6,PHKA2,GNG10,RRAS2,PRKAR2B,PLCG2,PRKCD,ITPR3,PRKAG2,GNG5,MAP2K1,GNG12,PRKAR1A
Regulation of Cellular Mechanics by Calpain Protease	4.5	0.3	CAPN5,ITGB1,RAP2A,GRB2,RALB,CDK4,TLN1,CCND1,CDK1,CCNA2,CCNE1,CAPNS1,RRAS2,TLN2,CAPN2,CAPN9,CDK2,ACTN1
Melanoma Signaling	3.6	0.3	RAP2A,PIK3CA,BAD,GRB2,MITF,FGFR1,RALB,CDK4,PIK3R4,CCND1,RRAS2,IRS1,E2F1,PIK3CB,PIK3CD,MAP2K1
Prolactin Signaling	2.9	0.2	RAP2A,PIK3CA,GRB2,FGFR1,RALB,JAK2,PIK3R4,NR3C1,IRF1,RRAS2,IRS1,PLCG2,PRKCD,NMI,PIK3CD,PIK3CB,STAT1,SOCS5,MAP2K1
Renin-Angiotensin Signaling	3.4	0.2	RAP2A,PIK3CA,JAK2,PIK3R4,SHF,STAT1,MAP2K1,PAK6,GRB2,FGFR1,ADCY3,RALB,RAC1,ADCY6,MAPK12,PRKAR2B,RRAS2,PAK3,IRS1,PLCG2,PRKCD,ITPR3,PRKAG2,PIK3CD,PIK3CB,PRKAR1A
Rac Signaling	4.6	0.2	RAP2A,ABI2,PIK3CA,ARPC1B,PIK3R4,CDK5R1,ARFIP2,MAP2K1,PI4KA,IQGAP3,ITGB1,PAK6,CFL1,GRB2,FGFR1,RALB,RAC1,MCF2L,RRAS2,PAK3,PIP5K1C,IRS1,CD44,PIK3CD,PIK3CB,SH3RF1,PARD3,ARPC4
Glioblastoma Multiforme Signaling	4.6	0.2	RAP2A,PIK3CA,CDK4,PIK3R4,CCND1,E2F6,MTOR,WNT7B,TSC2,RHOV,IGF1R,GSK3B,MAP2K1,E2F8,E2F2,GRB2,FGFR1,RALB,RAC1,RHOV,CCNE1,RHOQ,RRAS2,WNT10A,FOXO1,PRKCD,PLCG2,IRS1,ITPR3,E2F1,FZD6,PIK3CD,PIK3CB,CDK2,FNBP1

<b>Ingenuity Canonical Pathways</b>	<b>-log(p-value)</b>	<b>z-score</b>	<b>Molecules</b>
PDGF Signaling	3.8	0.0	RAP2A,CSNK2A1,PIK3CA,GRB2,FGFR1,SPHK2,RALB,JAK2,PIK3R4,INPP5D,SYNJ2,RRAS2,ABL2,INPP5B,IRS1,PLCG2,SPHK1,PIK3CD,PIK3CB,EIF2AK2,STAT1,MAP2K1
IL-3 Signaling	3.4	0.0	RAP2A,GAB2,PIK3CA,BAD,GRB2,FGFR1,RALB,RAC1,JAK2,PIK3R4,INPP5D,CSF2RB,RRAS2,FOXO1,IRS1,PRKCD,PIK3CB,PIK3CD,STAT1,MAP2K1
Renal Cell Carcinoma Signaling	3.0	0.0	RAP2A,PIK3CA,PAK6,SLC2A1,GRB2,FGFR1,RALB,RAC1,HIF1A,PIK3R4,VEGFA,RRAS2,PAK3,IRS1,TGFA,PIK3CD,PIK3CB,MAP2K1,VHL
CNTF Signaling	2.9	0.0	RAP2A,PIK3CA,GRB2,FGFR1,RALB,JAK2,PIK3R4,LIFR,MTOR,RPS6KA6,RRAS2,IRS1,PIK3CB,PIK3CD,STAT1,MAP2K1
Thrombopoietin Signaling	2.8	0.0	RAP2A,GAB2,PIK3CA,GRB2,FGFR1,RALB,JAK2,PIK3R4,RRAS2,IRS1,PLCG2,PRKCD,PIK3CB,PIK3CD,STAT1,MAP2K1
ErbB2-ErbB3 Signaling	2.6	0.0	RAP2A,PIK3CA,BAD,GRB2,FGFR1,RALB,PIK3R4,CCND1,RRAS2,FOXO1,IRS1,PIK3CB,PIK3CD,ERBB2,GSK3B,MAP2K1
Mitochondrial L-carnitine Shuttle Pathway	2.3	0.0	ACSL3,SLC27A6,CPT2,SLC27A3,CPT1C,ACSL1
Insulin Receptor Signaling	3.9	-0.2	FOXO4,RAP2A,PIK3CA,BAD,JAK2,PIK3R4,EIF4EBP1,MTOR,Ppp1cc,PPP1R12A,PPP1R10,INPP5B,TSC2,GSK3B,MAP2K1,GRB2,FGFR1,RALB,INPP5D,SYNJ2,RRAS2,RHOQ,PRKAR2B,FOXO1,IRS1,PRKAG2,PIK3CD,PIK3CB,INSR,PRKAR1A
CCR3 Signaling in Eosinophils	4.1	-0.2	RAP2A,PIK3CA,MPRIP,Calm1 (includes others),GNB5,PIK3R4,PLA2G4E,PPP1R12A,GNG5,MAP2K1,GNG12,GNG4,PAK6,CFL1,GRB2,FGFR1,RALB,RAC1,PLA2G3,MAPK12,GNG10,RRAS2,PAK3,PLA2G2D,IRS1,PRKCD,ITPR3,PIK3CD,PIK3CB
Ovarian Cancer Signaling	4.1	-0.2	RAP2A,PIK3CA,CDK4,PIK3R4,CCND1,BCL2,RAD51,VEGFA,MTOR,ARRB1,END1,WNT7B,GSK3B,MAP2K1,GRB2,FGFR1,RALB,PTGS1,PRKAR2B,RRAS2,WNT10A,IRS1,E2F1,CD44,PRKAG2,FZD6,BRCA2,PIK3CD,PIK3CB,Tcf7,PRKAR1A
UVA-Induced MAPK Signaling	3.2	-0.3	RAP2A,PARP6,PIK3CA,CASP3,GRB2,PARP10,FGFR1,RALB,PARP8,PARP12,PIK3R4,MAPK12,PARP9,BCL2L1,MTOR,RPS6KA6,RRAS2,PLCG2,IRS1,PIK3CD,CYCS,PIK3CB,STAT1
Endometrial Cancer Signaling	2.4	-0.3	RAP2A,PIK3CA,BAD,GRB2,FGFR1,RALB,PIK3R4,CCND1,RRAS2,IRS1,PIK3CB,PIK3CD,ERBB2,GSK3B,MAP2K1
Guanosine Nucleotides Degradation III	2.4	-0.4	GDA,NT5E,XDH,NT5C2,ACPP
Urate Biosynthesis/Inosine 5'-phosphate Degradation	2.2	-0.4	NT5E,XDH,IMPDH1,NT5C2,ACPP
Non-Small Cell Lung Cancer Signaling	3.8	-0.5	RAP2A,PIK3CA,BAD,GRB2,FGFR1,RALB,CDK4,PIK3R4,CCND1,STK4,RRAS2,IRS1,ITPR3,E2F1,TGFA,PIK3CD,PIK3CB,ERBB2,RASSF5,MAP2K1
Glioma Invasiveness Signaling	2.5	-0.5	RAP2A,PIK3CA,GRB2,FGFR1,HMMR,RALB,PIK3R4,RHOV,RRAS2,RHOQ,IRS1,RHO,CD44,PIK3CB,PIK3CD,FNBP1
Role of BRCA1 in DNA Damage Response	4.5	-0.6	FANCM,RBL2,ARID1A,TOPBP1,RBBP8,ARID2,RBL1,RFC5,SMARCA4,RAD51,E2F6,RFC4,E2F1,RFC2,BRCA2,BLM,STAT1,E2F2,E2F8,PHF10,RFC3
Paxillin Signaling	4.0	-0.7	RAP2A,PIK3CA,ITGA2B,TLN1,ITGB8,PIK3R4,PTPN12,ARFIP2,ACTN1,ITGB1,PARVA,PAK6,GRB2,FGFR1,RALB,RAC1,ITGA6,MAPK12,TLN2,RRAS2,PAK3,IRS1,PIK3CD,PIK3CB,ITGB6,ITGA7
Role of CHK Proteins in Cell Cycle Checkpoint Control	2.4	-0.7	RFC5,CDK1,E2F6,PPP2CB,PCNA,RFC4,E2F1,RFC2,TLK2,CDK2,E2F8,E2F2,RFC3
IL-7 Signaling Pathway	2.8	-0.8	FOXO4,PIK3CA,SLC2A1,BAD,GRB2,FGFR1,PIK3R4,MAPK12,BCL6,CCND1,BAK1,BCL2,FOXO1,IRS1,PIK3CD,PIK3CB,GSK3B,STAT1,CDK2
ErbB Signaling	3.7	-0.9	MAP2K6,RAP2A,PIK3CA,PAK6,BTC,GRB2,FGFR1,RALB,PIK3R4,MAPK12,MTOR,RRAS2,FOXO1,PAK3,PRKCD,PLCG2,IRS1,TGFA,PIK3CD,PIK3CB,ERBB2,GSK3B,MAP2K1
Pyridoxal 5'-phosphate Salvage Pathway	3.3	-1.0	MAP2K6,MAP3K9,DMPK,CDK4,GRK5,CDK1,PNPO,ARAF,PAK3,PRKCD,PRKAA1,EIF2AK2,NEK2,HIPK1,MAP2K1,CDK2
Fatty Acid $\beta$ -oxidation I	2.5	-1.0	ACSL3,ECI2,SLC27A6,SLC27A3,IVD,ACADM,HSD17B4,HADH,ACSL1
Pancreatic Adenocarcinoma Signaling	7.3	-1.2	PIK3CA,TGFBF1,BAD,CDK4,JAK2,PIK3R4,CCND1,BCL2,RAD51,TGFBF2,VEGFA,E2F6,GPLD1,ERBB2,STAT1,MAP2K1,E2F8,E2F2,GRB2,FGFR1,RAC1,MAPK12,RALBP1,BIRC5,BCL2L1,CCNE1,IRS1,E2F1,TGFA,BRCA2,PIK3CD,PIK3CB,CDK2
Small Cell Lung Cancer Signaling	2.8	-1.3	PIK3CA,GRB2,FGFR1,CDK4,PIK3R4,CCND1,BCL2,SKP2,BCL2L1,CCNE1,IRS1,E2F1,CKS1B,CYCS,PIK3CB,PIK3CD,TRAF5,CDK2
Glioma Signaling	4.3	-1.4	RAP2A,RBL2,PIK3CA,Calm1 (includes others),CAMK1D,GRB2,FGFR1,RALB,CDK4,PIK3R4,RBL1,CCND1,IDH1,E2F6,

<b>Ingenuity Canonical Pathways</b>	<b>-log(p-value)</b>	<b>z-score</b>	<b>Molecules</b>
			MTOR,RRAS2,PRKCD,PLCG2,IRS1,E2F1,IGF1R,TGFA,PIK3CB,PIK3CD,MAP2K1,E2F8,E2F2
Amyloid Processing	3.4	-1.4	CAPN5,CSNK2A1,MAPK12,CDK5R1,APP,CAPNS1,PRKAR2B,MAPT,PRKAG2,CAPN2,CAPN9,GSK3B,BACE2,PRKAR1A
Sumoylation Pathway	2.9	-1.5	SUMO3,DNMT3A,RAN,SENP2,MAPK12,RFC5,NR3C1,RHOV,PCNA,RHOQ,RFC4,RCC1,CTBP2,RHO,RFC2,CBX4,PML,FNBP1,ISG20,RFC3
FLT3 Signaling in Hematopoietic Progenitor Cells	2.7	-1.6	RAP2A,GAB2,PIK3CA,BAD,GRB2,FGFR1,RALB,PIK3R4,MAPK12,INPP5D,EIF4EBP1,MTOR,RPS6KA6,RRAS2,IRS1,PIK3CB,PIK3CD,STAT1,MAP2K1
Acute Myeloid Leukemia Signaling	3.6	-1.8	MAP2K6,RAP2A,PIK3CA,BAD,GRB2,FGFR1,RALB,PIK3R4,CCND1,CSF1R,EIF4EBP1,IDH1,CSF2RB,MTOR,RRAS2,ARAF,IRS1,PIK3CD,PIK3CB,PML,Tcf7,MAP2K1
Sphingosine-1-phosphate Signaling	3.6	-1.8	PIK3CA,CASP4,PIK3R4,CASP6,RHO,SPHK1,CASP1,S1PR5,CASP3,GRB2,GN A12,FGFR1,ADCY3,RAC1,ADCY6,S1PR3,S1PR4,RHOV,RHOQ,ACER3,IRS1,PLCG2,PIK3CD,PIK3CB,CASP7,FNBP1
Cell Cycle: G1/S Checkpoint Regulation	3.1	-1.9	RBL2,PAK1IP1,CDK4,RBL1,CCND1,HDAC5,SKP2,E2F6,CCNE1,FOXO1,E2F1,FBXL5,GSK3B,E2F2,CDK2,E2F8
Cell Cycle: G2/M DNA Damage Checkpoint Regulation	2.5	-2.7	CDC25B,YWHAH,PTPMT1,CKS1B,TOP2A,CCNB2,FBXL5,AURKA,CDK1,CCNB1,SKP2,PPM1D

**Table S3.** Top 50 regulated genes with adjusted p-value ( $q$ )  $< 0.01$  in comparison of UVB (tumor) vs Control (whole skin)

Gene symbol	log <sub>2</sub> FoldChange	Adjusted p-value	Gene description
2300005B03Rik	-1.96	0.00000044	RIKEN cDNA 2300005B03
Aadacl2	1.04	0.00496187	arylacetamide deacetylase like 2
Adh6a	-4.13	0.00649281	alcohol dehydrogenase 6A (class V)
Adrb3	-1.6	0.00037685	adrenergic receptor, beta 3
Arc	2.27	0.00061165	activity regulated cytoskeletal-associated protein
Bace2	0.8	0.00754084	beta-site APP-cleaving enzyme 2
Ccl20	-2.01	0.00552719	chemokine (C-C motif) ligand 20
Cd3g	-2.16	0.00061165	CD3 antigen, gamma polypeptide
Cd7	-2.78	0.00038698	CD7 antigen
Cfap57	-2.38	0.00003786	cilia and flagella associated protein 57
Cldn23	-1.93	0.00020086	claudin 23
Col4a5	-1.56	0.00682342	collagen, type IV, alpha 5
Csrnp1	1.12	0.00087171	cysteine-serine-rich nuclear protein 1
Ctnbp2	-1.81	0.00265291	cortactin binding protein 2
Cyp2b10	0.68	0.00565124	cytochrome P450, family 2, subfamily b, polypeptide 10
Degs2	1.58	0.00682342	delta(4)-desaturase, sphingolipid 2
Dsg1b	1	0.00682342	desmoglein 1 beta
Fam46b	1.19	0.00020073	Family With Sequence Similarity 46 Member B
Galnt6	1.14	0.00106727	polypeptide N-acetylgalactosaminyltransferase 6
Grid2ip	1.86	0.00722759	glutamate receptor, ionotropic, delta 2 (Grid2) interacting protein 1
Hmcn1	-2.41	0.00682342	hemicentin 1
Il4ra	1.2	0.00076271	interleukin 4 receptor, alpha
Junb	1.55	0.00037685	jun B proto-oncogene
Krt77	-3.31	0.00000001	keratin 77
Lgals12	-1.76	0.00000245	lectin, galactose binding, soluble 12
Lypd5	1.37	0.00100465	Ly6/Plaur domain containing 5
Mapk8ip1	-1.39	0.00376888	mitogen-activated protein kinase 8 interacting protein 1
Mpzl3	1.15	0.00682342	myelin protein zero-like 3
Mvk	0.77	0.00625237	mevalonate kinase
Myom3	1.08	0.00376882	myomesin family, member 3
Ocln	-1.43	0.00594436	occludin
Orm1	-1.54	0.00051209	orosomuroid 1
Per3	-1.23	0.0088757	period circadian clock 3
Pkib	-1.02	0.00766542	protein kinase inhibitor beta, cAMP dependent, testis specific
Ptges	0.86	0.00061165	prostaglandin E synthase
Rnf152	1.3	0.00682342	ring finger protein 152
Rnf19b	0.79	0.00682342	ring finger protein 19B
Sbno2	0.96	0.00003896	strawberry notch 2
Scd3	-2.59	0.00061165	stearoyl-coenzyme A desaturase 3
Scnn1g	1.49	0.00582844	sodium channel, nonvoltage-gated 1 gamma
Sema3d	-2.26	0.00001696	sema domain, immunoglobulin domain (Ig), short basic domain, secreted, (semaphorin) 3D

<b>Gene symbol</b>	<b>log<sub>2</sub>FoldChange</b>	<b>Adjusted p-value</b>	<b>Gene description</b>
Skint5	-3.23	0.00000002	selection and upkeep of intraepithelial T cells 5
Skint6	-2.52	0.00000012	selection and upkeep of intraepithelial T cells 6
Skint9	-1.16	0.0007666	selection and upkeep of intraepithelial T cells 9
Slc25a48	1.26	0.00090115	solute carrier family 25, member 48
Slc7a11	1.33	0.00625237	solute carrier family 7 (cationic amino acid transporter, y+ system), member 11
Smox	0.93	0.00934888	spermine oxidase
Sult2b1	0.88	0.00300459	sulfotransferase family, cytosolic, 2B, member 1
Tppp	-1.89	0.00568348	tubulin polymerization promoting protein
Trim25	0.72	0.00683121	tripartite motif-containing 25

**Table S4.** Top 29 regulated pathways with  $p < 0.01$  in comparison of UVB (tumor) vs Control (whole skin)

Ingenuity Canonical Pathways	$-\log(p\text{-value})$	z-score	Molecules
Pancreatic Adenocarcinoma Signaling	5.03	2.1	RELA,PLD3,PIK3R1,HBEGF,STAT3,RALBP1,PLD1,BCL2,TGFBR2,VEGFA,CDKN1A,GPLD1,TGFA,E2F5,STAT1,RALGDS,E2F8,E2F2
LPS/IL-1 Mediated Inhibition of RXR Function	4.11	1.9	PPARA,CYP3A7,TNFRSF1A,MYD88,GSTM3,GSTA5,IL36B,ABCN9,SULT2B1,IL33,GSTZ1,IL36G,SMOX,ALDH1A3,ALDH3A2,CAT,IL1B,SLC27A1,HS3ST1,CYP2B6,SLC27A3,ALDH16A1,ALDH3A1,ALDH6A1
STAT3 Pathway	4.02	1.5	SOCS3,IL4R,IL13RA1,RALB,IL17RC,IL12RB2,IL22RA1,STAT3,IL20RB,BCL2,TGFBR2,VEGFA,GHR,CXCR2,CDKN1A,TGFA,IL1B
Phospholipases	3.97	0.9	PLCD1,PLBD1,PLA2G4E,PLD3,PLA2G2D,ABHD3,PLB1,GPLD1,PNPLA3,PLA2G4F,PLD1
NF- $\kappa$ B Signaling	3.94	2.8	RELA,MAP3K14,TRAF3,BMP4,TNFRSF1A,MYD88,PIK3R1,RALB,IL36B,IL33,TLR2,TGFBR2,IL36G,GHR,UBE2V1,TGFA,IL1B,EIF2AK2,LTBR,TRAF5,IRAK4
Toll-like Receptor Signaling	3.84	3.0	PPARA,TLR2,IL33,MAP3K14,RELA,IL36G,TOLLIP,MYD88,IL1B,EIF2AK2,IRAK4,IL36B
Eicosanoid Signaling	3.66	1.0	PLBD1,PLA2G4E,PTGES,LTB4R,ALOX15B,PLA2G2D,LTB4R2,ABHD3,PLB1,PNPLA3,PLA2G4F
Osteoarthritis Pathway	3.63	1.7	RELA,TCF4,BGLAP,EPAS1,DDIT4,FZD3,PPARD,TNFRSF1A,DLX5,HIF1A,VEGFA,TLR2,TGFBR2,CASP6,ELF3,CXCR2,DDR2,IL1B,SOX9,CASP14,TCF7L2,FZD7
TNFR1 Signaling	3.45	0.3	MAP4K2,MAP3K14,RELA,CASP6,PAK1,PAK6,PAK3,TNFRSF1A,BIRC3
Interferon Signaling	3	1.6	RELA,IRF9,STAT2,IFI35,STAT1,BAK1,BCL2
Noradrenaline and Adrenaline Degradation	2.93	-0.4	ADH7,DHRS9,SMOX,ALDH1A3,Adh6a,ALDH3A2,ALDH3A1
Antioxidant Action of Vitamin C	2.9	-1.2	RELA,PLD3,SLC2A1,ABHD3,PLD1,PLBD1,PLCD1,PLA2G4E,PLA2G2D,PLB1,GPLD1,PNPLA3,PLA2G4F
Phospholipase C Signaling	2.78	1.7	CD247,GNG4,RELA,PLD3,CD3E,RALB,ADCY6,HDAC10,CD3D,PLD1,PLCD1,PLA2G4E,CD3G,RHOV,RHOG,PLA2G2D,HDAC11,GPLD1,GNB2,PLA2G4F,RHOF,RALGDS
Activation of IRF by Cytosolic Pattern Recognition Receptors	2.7	1.7	IFIH1,RELA,IRF7,TRAF3,MAVS,IRF9,STAT2,STAT1,ADAR
IL-8 Signaling	2.63	2.2	GNG4,RELA,ICAM1,PLD3,PIK3R1,RALB,HBEGF,PLD1,BCL2,VEGFA,RHOV,ITGAM,CCND2,RHOG,CXCR2,GPLD1,GNB2,RHOF,IRAK4
Renal Cell Carcinoma Signaling	2.62	0	VEGFA,ETS1,PAK1,PAK6,SLC2A1,PAK3,PIK3R1,RALB,TGFA,EGLN3,HIF1A
Cytotoxic T Lymphocyte-mediated Apoptosis of Target Cells	2.56	-0.8	CD247,CD3G,CASP6,CD3E,CD3D,BCL2
Colorectal Cancer Metastasis Signaling	2.54	1.6	GNG4,RELA,TCF4,FZD3,TNFRSF1A,MMP14,PIK3R1,RALB,ADCY6,STAT3,VEGFA,TLR2,TGFBR2,RHOV,RHOG,GNB2,WNT4,STAT1,RHOF,RALGDS,TCF7L2,FZD7
Retinoate Biosynthesis I	2.42	1.6	SDR9C7,ADH7,DHRS9,ALDH1A3,RDH16,AKR1B10
Ethanol Degradation II	2.42	-0.8	ADH7,DHRS9,ALDH1A3,ALDH3A2,Adh6a,ALDH3A1
Endothelin-1 Signaling	2.39	1.4	PLD3,ABHD3,PIK3R1,RALB,MAPK6,ADCY6,PLD1,PLBD1,PLCD1,CASP6,PLA2G4E,PLA2G2D,EDN1,PLB1,GPLD1,PLA2G4F,PNPLA3,CASP14
Type I Diabetes Mellitus Signaling	2.36	0.6	CD247,SOCS3,CD3G,MAP3K14,RELA,CD3E,MYD88,TNFRSF1A,IL1B,STAT1,CD3D,BCL2
3-phosphoinositide Degradation	2.27	0.8	SOCS3,EPHX2,PPP4R1,STYX,HACD2,PPP4C,PPM1K,DUSP14,ITPK1,DUSP5,PTPRJ,PDXP,PTPN1,SGPP2,MTM1
D-myo-inositol (1,4,5,6)-Tetrakisphosphate Biosynthesis	2.24	1.1	SOCS3,EPHX2,PPP4R1,STYX,HACD2,PPM1K,PPP4C,DUSP14,ITPK1,DUSP5,PTPRJ,PDXP,PTPN1,SGPP2
D-myo-inositol (3,4,5,6)-tetrakisphosphate Biosynthesis	2.24	1.1	SOCS3,EPHX2,PPP4R1,STYX,HACD2,PPM1K,PPP4C,DUSP14,ITPK1,DUSP5,PTPRJ,PDXP,PTPN1,SGPP2
D-myo-inositol-5-phosphate Metabolism	2.17	1.3	SOCS3,EPHX2,PPP4R1,STYX,HACD2,PPP4C,PPM1K,DUSP14,PLCD1,ITPK1,DUSP5,PTPRJ,PDXP,PTPN1,SGPP2
p38 MAPK Signaling	2.15	3.5	TGFBR2,IL33,PLA2G4E,IL36G,PLA2G2D,TNFRSF1A,IL1B,PLA2G4F,RPS6KA4,STAT1,IRAK4,IL36B
Neuroinflammation Signaling Pathway	2.08	1.7	RELA,TRAF3,ICAM1,TNFRSF1A,MYD88,PIK3R1,BIRC6,MAPK6,GABBR1,CSF1R,BCL2,TGFBR2,TLR2,PLA2G4E,IRF7,PLA2G2D,IL34,GLUL,IL1B,PLA2G4F,BACE2,STAT1,BIRC3,IRAK4
Death Receptor Signaling	2.04	1.9	MAP3K14,RELA,CASP6,TNFRSF1A,PARP10,PARP8,PARP12,TNFRSF15,BIRC3,BCL2



**Table S5.** DMRs with inverse DNA methylation change and RNA expression change. Methylation change is expressed as  $R_{UVB} - R_{control}$ , where  $R_{UVB}$  is average methylation ratio in the UVB group and  $R_{control}$  is average methylation ratio in the Control group.

DMR	Gene	Location	Feature	DNA Methylation	RNA Expression
				change UVB vs Control	change $\log_2(UVB/Control)$
1	1700017B05Rik	chr9:57268697-57268776	Distal Intergenic	-0.12	1.26
2	1700017B05Rik	chr9:57251575-57251703	Downstream	-0.14	1.26
3	5830416P10Rik	chr19:53461444-53461541	Intron	-0.12	1.08
4	5830416P10Rik	chr19:53482142-53482226	Distal Intergenic	-0.10	1.08
5	5830416P10Rik	chr19:53464577-53464829	Promoter	-0.12	1.08
6	Abca5	chr11:110368147-110368197	Distal Intergenic	0.10	-1.79
7	Actn1	chr12:80213441-80213557	Intron	0.11	-1.22
8	Adamts14	chr10:61242034-61242144	Intron	0.10	-1.15
9	Adamts14	chr10:61248766-61249017	Intron	0.12	-1.15
10	Adap1	chr5:139324548-139324596	Promoter	-0.11	1.04
11	Adap1	chr5:139333563-139334005	Distal Intergenic	-0.11	1.04
12	Adap1	chr5:139315087-139315312	Intron	-0.13	1.04
13	Adap1	chr5:139322634-139322727	Promoter	-0.11	1.04
14	Adcy6	chr15:98602776-98602876	Intron	0.11	-1.64
15	Adcy6	chr15:98602086-98602288	Intron	0.13	-1.64
16	Adcy6	chr15:98602453-98602541	Intron	0.14	-1.64
17	Adh1	chr3:138277418-138277780	Promoter	0.13	-1.83
18	Agfg2	chr5:137673195-137673501	Intron	0.13	-1.47
19	Agps	chr2:75772709-75772960	Distal Intergenic	-0.10	1.14
20	Akr1b8	chr6:34343698-34343748	Distal Intergenic	-0.26	1.68
21	Alox5	chr6:116417447-116417639	Intron	-0.13	1.32
22	Alox5ap	chr5:149274900-149275100	Intron	-0.14	1.24
23	Alox5ap	chr5:149264434-149264508	Promoter	-0.14	1.24
24	Ankrd44	chr1:54888566-54888622	Intron	0.10	-1.76
25	Aqp3	chr4:41073643-41073819	Distal Intergenic	-0.17	1.04
26	Aqp3	chr4:41073441-41073490	Distal Intergenic	-0.21	1.04
27	Arhgap9	chr10:127324191-127324260	Promoter	-0.40	1.12
28	Arl4c	chr1:88698136-88698358	3' UTR	0.20	-1.33
29	Arl4c	chr1:88697731-88697882	Downstream	0.10	-1.33
30	Arntl2	chr6:146776729-146776748	3' UTR	-0.10	1.32
31	Arsa	chr15:89480644-89480688	Intron	0.18	-2.04
32	Arsg	chr11:109553572-109553710	Intron	0.14	-1.21
33	Atic	chr1:71568433-71568563	Intron	-0.12	1.14
34	Atp10b	chr11:42877322-42877420	Distal Intergenic	0.18	-1.03
35	Atp8a1	chr5:67842226-67842291	Intron	0.12	-1.08
36	Auts2	chr5:132501144-132501383	Intron	0.12	-1.06
37	Bmp4	chr14:46397476-46397520	Distal Intergenic	0.13	-1.40
38	Bmp4	chr14:46391579-46391949	Promoter	0.16	-1.40
39	Bmp4	chr14:46418770-46418897	Distal Intergenic	0.12	-1.40
40	Bst1	chr5:43836964-43837007	Intron	0.12	-1.14
41	Camk2n1	chr4:138463107-138463189	Distal Intergenic	0.11	-1.33
42	Capn2	chr1:182465985-182466102	Downstream	-0.12	1.06
43	Car12	chr9:66660030-66660227	Distal Intergenic	-0.17	1.28
44	Casp3	chr8:46640029-46640108	Distal Intergenic	-0.18	1.17
45	Cbx7	chr15:79931675-79931743	Promoter	0.14	-1.43
46	Ccdc88b	chr19:6854160-6854354	Exon	-0.11	1.31
47	Ccdc88b	chr19:6861943-6861974	Distal Intergenic	-0.10	1.31

<b>DMR</b>	<b>Gene</b>	<b>Location</b>	<b>Feature</b>	<b>DNA Methylation change UVB vs Control</b>	<b>RNA Expression change log<sub>2</sub>(UVB/Control)</b>
48	Ccdc88b	chr19:6853901-6854028	Exon	-0.11	1.31
49	Ccng1	chr11:40754087-40754194	Promoter	-0.17	1.35
50	Ccng1	chr11:40871531-40871751	Distal Intergenic	-0.11	1.35
51	Ccng1	chr11:40775411-40775534	Distal Intergenic	-0.10	1.35
52	Cd200	chr16:45426864-45427151	Intron	-0.12	1.79
53	Cdc20	chr4:118445612-118446060	Exon	-0.17	1.60
54	Cdh3	chr8:106507743-106508063	Promoter	-0.20	1.14
55	Cdh3	chr8:106508146-106508403	Promoter	-0.16	1.14
56	Cdk1	chr10:69378523-69378619	Distal Intergenic	-0.19	1.91
57	Cdk1	chr10:69300217-69300282	Distal Intergenic	-0.22	1.91
58	Cdk1	chr10:69299995-69300099	Distal Intergenic	-0.15	1.91
59	Cgn	chr3:94783369-94783471	Intron	0.13	-1.38
60	Chd7	chr4:8799378-8799786	Intron	0.12	-1.08
61	Cks1b	chr3:89416222-89416362	Promoter	-0.20	1.55
62	Clybl	chr14:122202475-122202625	Intron	0.14	-1.06
63	Cotl1	chr8:119844456-119844557	Distal Intergenic	-0.10	1.52
64	Cotl1	chr8:119818010-119818094	Intron	-0.18	1.52
65	Cpne8	chr15:90677962-90677995	Promoter	-0.13	1.59
66	D17H6S56E-5	chr17:34998943-34999270	Promoter	-0.17	1.75
67	D17H6S56E-5	chr17:34998111-34998206	Promoter	-0.11	1.75
68	Dach1	chr14:98181930-98182046	Distal Intergenic	0.15	-1.03
69	Daglb	chr5:143434260-143434286	Distal Intergenic	0.28	-1.99
70	Dapk2	chr9:66214036-66214096	Intron	-0.22	1.74
71	Dapk2	chr9:66183196-66183339	Intron	-0.23	1.74
72	Degs2	chr12:108704127-108704348	Promoter	-0.10	1.39
73	Dio2	chr12:90799069-90799108	Distal Intergenic	-0.16	1.58
74	Dio2	chr12:90365561-90365695	Distal Intergenic	-0.16	1.58
75	Dip2c	chr13:9224480-9224563	Distal Intergenic	0.10	-1.02
76	Dtx3l	chr16:35952012-35952097	Intron	-0.15	1.17
77	Dut	chr2:125263441-125263474	Distal Intergenic	-0.10	1.26
78	E130012A19Rik	chr11:97619854-97620009	Intron	-0.18	1.13
79	E2f1	chr2:154568100-154568334	Promoter	-0.15	1.21
80	Elk3	chr10:93306506-93306700	Intron	-0.24	2.10
81	Elk3	chr10:93273528-93273550	Intron	-0.14	2.10
82	Enah	chr1:182029181-182029580	Distal Intergenic	-0.11	1.11
83	Enah	chr1:182040535-182040634	Distal Intergenic	-0.10	1.11
84	Enah	chr1:182021477-182021534	Promoter	-0.11	1.11
85	Enah	chr1:182064621-182064798	Distal Intergenic	-0.16	1.11
86	Enc1	chr13:97292526-97292731	Distal Intergenic	0.15	-1.51
87	Enc1	chr13:97318006-97318171	Distal Intergenic	0.13	-1.51
88	Fam105a	chr15:27671870-27672064	Intron	-0.12	2.06
89	Fam105a	chr15:27752501-27752579	Intron	-0.11	2.06
90	Fam20c	chr5:138770758-138771051	Intron	-0.24	1.43
91	Fam20c	chr5:138756425-138756804	Promoter	-0.16	1.43
92	Fbln1	chr15:85209524-85209663	Intron	-0.11	1.75
93	Fbln1	chr15:85211656-85211775	Intron	-0.27	1.75
94	Fbln1	chr15:85207425-85207504	Promoter	-0.18	1.75
95	Fchsd2	chr7:101127593-101127748	Intron	0.11	-1.25
96	Fry	chr5:150170844-150170872	Distal Intergenic	0.14	-1.03
97	Fry	chr5:150270058-150270473	Intron	0.14	-1.03
98	Fry	chr5:150233614-150233727	Distal Intergenic	0.16	-1.03

DMR	Gene	Location	Feature	DNA Methylation change UVB vs Control	RNA Expression change $\log_2(\text{UVB}/\text{Control})$
99	Gclm	chr3:122247228-122247651	Promoter	-0.22	1.11
100	Gclm	chr3:122246536-122246657	Promoter	-0.18	1.11
101	Gins1	chr2:150908961-150909081	Promoter	-0.16	1.20
102	Gins1	chr2:150927297-150927555	Intron	-0.17	1.20
103	Gins1	chr2:150955138-150955236	Intron	-0.12	1.20
104	Gnpnat1	chr14:45446984-45447238	Distal Intergenic	-0.11	1.04
105	Gpr146	chr5:139392828-139393155	Promoter	0.19	-2.64
106	Gpr146	chr5:139394619-139394968	3' UTR	0.21	-2.64
107	Grap	chr11:61666292-61666371	Intron	-0.16	1.14
108	Grap	chr11:61637107-61637346	Distal Intergenic	-0.18	1.14
109	Grip1	chr10:119814049-119814086	Intron	-0.16	1.22
110	Grip1	chr10:119456061-119456082	Promoter	-0.26	1.22
111	Gsap	chr5:21255438-21255518	Intron	-0.13	1.04
112	H6pd	chr4:149999379-149999449	Intron	-0.16	2.28
113	H6pd	chr4:149999609-149999860	Intron	-0.10	2.28
114	H6pd	chr4:149999891-150000151	Intron	-0.23	2.28
115	H6pd	chr4:150011683-150011767	Promoter	-0.10	2.28
116	Homer3	chr8:70291827-70291902	Intron	-0.21	1.53
117	Hook3	chr8:26117216-26117385	Promoter	0.12	-1.07
118	Hoxb5	chr11:96301700-96302060	Promoter	0.13	-1.02
119	Hoxb5	chr11:96302102-96302463	Promoter	0.12	-1.02
120	Hoxb5	chr11:96301480-96301566	Promoter	0.15	-1.02
121	Hsf2	chr10:57500015-57500132	Intron	0.11	-1.30
122	Ifitm3	chr7:141007432-141007620	Downstream	-0.12	1.53
123	Igsf3	chr3:101408962-101409433	Intron	-0.11	1.43
124	Impdh1	chr6:29210517-29210667	Promoter	-0.15	1.02
125	Incenp	chr19:9828853-9828907	Distal Intergenic	-0.34	1.08
126	Irf1	chr11:53804025-53804334	Intron	-0.23	1.27
127	Irf1	chr11:53796196-53796234	Intron	-0.12	1.27
128	Irgm2	chr11:58215894-58216068	Promoter	-0.10	1.20
129	Itgax	chr7:128112681-128112774	Exon	-0.15	1.06
130	Itgb6	chr2:60722583-60722788	Promoter	-0.12	1.15
131	Itgb6	chr2:60720276-60720372	Promoter	-0.15	1.15
132	Itgb6	chr2:60720474-60720530	Promoter	-0.11	1.15
133	Itgb6	chr2:60722338-60722469	Promoter	-0.16	1.15
134	Itgb6	chr2:60731343-60731473	Distal Intergenic	-0.11	1.15
135	Itpk1	chr12:102707258-102707383	Promoter	-0.10	2.21
136	Itpk1	chr12:102715580-102715750	Distal Intergenic	-0.15	2.21
137	Itpk1	chr12:102703658-102704076	Promoter	-0.12	2.21
138	Kcnj12	chr11:61027570-61027678	Intron	-0.10	2.11
139	Klhdc7a	chr4:140052667-140052781	Intron	0.11	-1.68
140	Knstrn	chr2:118805287-118805373	Distal Intergenic	-0.10	1.77
141	Krt7	chr15:101421072-101421139	Intron	-0.15	1.88
142	L3hypdh	chr12:72084289-72084684	Promoter	-0.14	1.39
143	L3hypdh	chr12:72082410-72082711	Promoter	-0.16	1.39
144	Lame2	chr1:153101451-153101733	Intron	-0.19	1.03
145	Lame2	chr1:153096178-153096295	Intron	-0.11	1.03
146	Lame2	chr1:153101103-153101403	Intron	-0.14	1.03
147	Large	chr8:73364519-73364649	Distal Intergenic	0.10	-1.18
148	Lgals3bp	chr11:118379374-118379449	Distal Intergenic	-0.15	1.44
149	Lgals9	chr11:78983241-78983393	Promoter	-0.17	1.12

DMR	Gene	Location	Feature	DNA Methylation change UVB vs Control	RNA Expression change log <sub>2</sub> (UVB/Control)
150	Lincppara	chr15:85660742-85661017	Distal Intergenic	0.12	-1.24
151	Lmo1	chr7:109185652-109185861	Distal Intergenic	-0.21	1.21
152	Lmo1	chr7:109144730-109145220	Intron	-0.13	1.21
153	Lnx1	chr5:74618273-74618364	Intron	0.10	-1.74
154	Manba	chr3:135526500-135526642	Intron	-0.48	1.38
155	Marcks	chr10:37223416-37223601	Distal Intergenic	-0.11	1.06
156	Matk	chr10:81252398-81252667	Promoter	0.13	-1.74
157	Mcf2l	chr8:12951235-12951320	Promoter	0.11	-1.01
158	Mcm10	chr2:5011708-5011870	Promoter	-0.11	1.23
159	Mcm5	chr8:75159719-75159804	Distal Intergenic	-0.25	1.61
160	Mcu	chr10:59577713-59577788	Intron	0.12	-1.11
161	Mfge8	chr7:79194601-79195002	Distal Intergenic	-0.11	1.00
162	Mgst2	chr3:51662647-51663039	Promoter	-0.16	1.43
163	Mgst2	chr3:51673443-51673790	Intron	-0.11	1.43
164	Mgst2	chr3:51709631-51709676	Intron	-0.10	1.43
165	Mgst2	chr3:51663161-51663307	Promoter	-0.11	1.43
166	Mis18a	chr16:90673929-90674318	Distal Intergenic	-0.18	1.17
167	Mis18a	chr16:90635591-90635695	Distal Intergenic	-0.13	1.17
168	Mitf	chr6:97888542-97888708	Intron	0.19	-1.43
169	Mllt3	chr4:87668180-87668308	Distal Intergenic	-0.13	1.09
170	Moxd1	chr10:24222840-24222960	Promoter	-0.12	1.16
171	Mylk	chr16:34748457-34748532	Distal Intergenic	0.11	-1.06
172	Myo1d	chr11:80766435-80766518	Intron	0.27	-1.41
173	Myo1d	chr11:80778738-80778869	Promoter	0.10	-1.41
174	Myo1d	chr11:80783618-80783744	Distal Intergenic	0.16	-1.41
175	Myo1d	chr11:80766800-80766876	Intron	0.12	-1.41
176	Myo1d	chr11:80698367-80698555	Intron	0.11	-1.41
177	Ncf2	chr1:152816798-152817258	Exon	-0.12	1.11
178	Nek2	chr1:191815068-191815217	Distal Intergenic	-0.14	1.39
179	Neur11b	chr17:26413292-26413432	Promoter	-0.13	1.02
180	Neur11b	chr17:26416207-26416293	Promoter	-0.19	1.02
181	Nsmce1	chr7:125472677-125472738	Intron	-0.27	1.64
182	Nudt14	chr12:112947197-112947327	Distal Intergenic	-0.13	1.17
183	Nudt7	chr8:114134378-114134640	Promoter	-0.10	1.17
184	Nudt7	chr8:114131588-114131686	Promoter	-0.15	1.17
185	Nudt7	chr8:114093830-114093854	Distal Intergenic	-0.13	1.17
186	Odc1	chr12:17455010-17455209	Distal Intergenic	-0.18	1.21
187	Odc1	chr12:17540059-17540264	Distal Intergenic	-0.15	1.21
188	Odc1	chr12:17481924-17482125	Distal Intergenic	-0.22	1.21
189	Odc1	chr12:17507106-17507203	Distal Intergenic	-0.11	1.21
190	Odc1	chr12:17600778-17600878	Distal Intergenic	-0.14	1.21
191	Odc1	chr12:17507314-17507622	Distal Intergenic	-0.18	1.21
192	Ogfr1l	chr1:23380198-23380588	Promoter	0.15	-1.17
193	Ophn1	chrX:98890004-98890121	Promoter	0.10	-2.09
194	Paqr7	chr4:134494755-134494965	Promoter	0.11	-1.37
195	Parp12	chr6:39116929-39117073	Promoter	-0.14	1.67
196	Parp9	chr16:35920424-35920836	Distal Intergenic	-0.16	1.17
197	Pcdh7	chr5:57855975-57856088	Intron	0.12	-1.24
198	Phgdh	chr3:98348257-98348349	Distal Intergenic	-0.17	1.35
199	Phyhip	chr14:70466273-70466658	Intron	0.15	-1.18
200	Pik3cd	chr4:149691350-149691669	Intron	0.13	-1.06

DMR	Gene	Location	Feature	DNA Methylation change UVB vs Control	RNA Expression change $\log_2(\text{UVB}/\text{Control})$
201	Pik3cd	chr4:149674792-149674841	Promoter	0.11	-1.06
202	Pla2g3	chr11:3489273-3489310	Promoter	0.11	-1.63
203	Plb1	chr5:32313272-32313460	Intron	0.12	-1.85
204	Plb1	chr5:32322521-32322542	Intron	0.16	-1.85
205	Pmaip1	chr18:66429164-66429277	Distal Intergenic	-0.11	1.65
206	Pmaip1	chr18:66467873-66468055	Distal Intergenic	-0.19	1.65
207	Pmaip1	chr18:66468166-66468325	Distal Intergenic	-0.24	1.65
208	Pmaip1	chr18:66459487-66459920	Promoter	-0.13	1.65
209	Ppfia4	chr1:134323025-134323089	Exon	0.12	-2.00
210	Pqlc3	chr12:17000969-17001120	Promoter	-0.16	1.65
211	Prex1	chr2:166712039-166712148	Promoter	-0.12	1.03
212	Prkar2b	chr12:32055112-32055195	Intron	-0.20	1.26
213	Prkar2b	chr12:32050325-32050452	Intron	-0.10	1.26
214	Prkar2b	chr12:32104790-32104882	Distal Intergenic	-0.11	1.26
215	Prkce	chr17:86177659-86177935	Intron	0.13	-1.03
216	Psd3	chr8:68060603-68060734	Distal Intergenic	0.20	-1.63
217	Psd3	chr8:67974409-67974733	Promoter	0.11	-1.63
218	Psd3	chr8:68058684-68058840	Distal Intergenic	0.16	-1.63
219	Psmg4	chr13:34148716-34149013	Distal Intergenic	-0.11	1.32
220	Ptp4a3	chr15:73748834-73749024	Promoter	-0.25	2.07
221	Ptpn21	chr12:98726242-98726434	Intron	0.11	-1.18
222	Pxdc1	chr13:34649946-34650318	Promoter	-0.12	1.08
223	Pxdc1	chr13:34647293-34647726	Intron	-0.13	1.08
224	Rab31	chr17:65771439-65771806	Promoter	-0.22	1.22
225	Rab31	chr17:65771104-65771306	Promoter	-0.15	1.22
226	Rab31	chr17:65727261-65727307	Intron	-0.22	1.22
227	Rab31	chr17:65724196-65724483	Intron	-0.14	1.22
228	Racgap1	chr15:99628210-99628248	Intron	-0.15	1.66
229	Racgap1	chr15:99653511-99653591	Promoter	-0.10	1.66
230	Rbp1	chr9:98418044-98418264	Distal Intergenic	-0.13	1.95
231	Rgs10	chr7:128433713-128433774	Distal Intergenic	0.25	-1.42
232	Rhobtb1	chr10:69269943-69270388	Exon	0.11	-1.93
233	Rilpl1	chr5:124528669-124528773	Promoter	-0.19	1.18
234	Rilpl1	chr5:124530335-124530415	Promoter	-0.23	1.18
235	Rnasel	chr1:153751770-153751984	Promoter	-0.10	2.54
236	Rnf152	chr1:105354982-105355253	Promoter	-0.10	1.28
237	Rnf152	chr1:105357972-105358018	Promoter	-0.46	1.28
238	Rptn	chr3:93378431-93378578	Distal Intergenic	-0.15	1.13
239	Rrm2	chr12:24705658-24705760	Promoter	-0.15	1.39
240	Rtn4r11	chr11:75235334-75235394	Intron	0.36	-1.18
241	Selplg	chr5:113842825-113842911	3' UTR	-0.41	1.31
242	Selplg	chr5:113843037-113843325	3' UTR	-0.27	1.31
243	Selplg	chr5:113843983-113844462	3' UTR	-0.18	1.31
244	Serpinh1	chr7:99329621-99329834	Intron	-0.15	1.09
245	Sfxn5	chr6:85287982-85288069	Intron	0.13	-1.74
246	Shroom3	chr5:92936050-92936265	Intron	0.11	-1.02
247	Siva1	chr12:112648445-112648519	Intron	-0.15	1.68
248	Slc1a1	chr19:28773245-28773324	Distal Intergenic	0.16	-1.40
249	Slc1a5	chr7:16783150-16783292	Promoter	-0.11	1.12
250	Slc1a5	chr7:16780139-16780235	Promoter	-0.11	1.12
251	Slc24a3	chr2:145168809-145168928	Distal Intergenic	0.12	-2.24

DMR	Gene	Location	Feature	DNA Methylation change UVB vs Control	RNA Expression change $\log_2(\text{UVB}/\text{Control})$
252	Slc24a3	chr2:145170090-145170236	Distal Intergenic	0.29	-2.24
253	Slc24a3	chr2:145233006-145233132	Distal Intergenic	0.11	-2.24
254	Slc24a3	chr2:145169073-145169269	Distal Intergenic	0.18	-2.24
255	Slc2a1	chr4:119111465-119111510	Promoter	-0.17	1.08
256	Slc39a14	chr14:70341275-70341597	Intron	-0.10	1.76
257	Slc39a14	chr14:70370733-70370743	Downstream	-0.14	1.76
258	Slc52a3	chr2:152002406-152002471	Promoter	0.15	-1.19
259	Slc9a9	chr9:94691706-94691868	Intron	0.12	-1.86
260	Slfn2	chr11:83066604-83066962	Promoter	-0.12	2.01
261	Slfn2	chr11:83079783-83079891	Distal Intergenic	-0.15	2.01
262	Smim3	chr18:60500264-60500508	Promoter	-0.14	3.01
263	Smim3	chr18:60502924-60503036	Promoter	-0.17	3.01
264	Smyd3	chr1:179198093-179198267	Intron	0.13	-1.30
265	Snn	chr16:11051653-11051744	Distal Intergenic	-0.15	1.36
266	Sorbs1	chr19:40514300-40514417	Promoter	0.27	-1.14
267	Srgn	chr10:62498947-62498997	Intron	-0.28	1.66
268	Srgn	chr10:62505093-62505215	Promoter	-0.10	1.66
269	Srgn	chr10:62517585-62517781	Distal Intergenic	-0.14	1.66
270	Stat1	chr1:52132164-52132297	Intron	-0.11	1.02
271	Stom	chr2:35349083-35349351	Distal Intergenic	-0.11	2.43
272	Stom	chr2:35327466-35327619	Intron	-0.29	2.43
273	Stom	chr2:35339026-35339189	Promoter	-0.16	2.43
274	Stom	chr2:35328072-35328178	Intron	-0.11	2.43
275	Syt8	chr7:142418749-142418905	Distal Intergenic	-0.25	1.09
276	Syt8	chr7:142419052-142419156	Distal Intergenic	-0.20	1.09
277	Tbc1d1	chr5:64236576-64236776	Intron	0.12	-1.23
278	Tk1	chr11:117830243-117830696	Intron	-0.11	1.34
279	Tmem158	chr9:123258764-123259008	Promoter	-0.24	1.21
280	Tmem158	chr9:123259111-123259207	Promoter	-0.18	1.21
281	Tmem229a	chr6:24954595-24954673	Promoter	0.10	-2.14
282	Tmprss11a	chr5:86474051-86474313	Distal Intergenic	-0.21	1.38
283	Tnfrsf11a	chr1:105843217-105843491	Intron	0.11	-1.15
284	Tnxb	chr17:34667889-34667943	Promoter	0.12	-1.20
285	Tspan3	chr9:56264440-56264560	Intron	-0.14	1.87
286	Tubb3	chr8:123413648-123413900	Promoter	-0.12	1.44
287	Upp1	chr11:9120688-9120727	Promoter	0.11	-1.91
288	Vrk1	chr12:105937352-105937733	Distal Intergenic	-0.14	1.01
289	Wwox	chr8:114876284-114876704	Intron	0.11	-1.52
290	Wwox	chr8:114899107-114899524	Intron	0.12	-1.52
291	Xdh	chr17:73893425-73893583	Intron	-0.17	1.11
292	Xdh	chr17:73918894-73918953	Intron	-0.15	1.11
293	Xdh	chr17:73894331-73894436	Intron	-0.18	1.11
294	Xdh	chr17:73894662-73894747	Intron	-0.48	1.11
295	Zfp365	chr10:67786309-67786485	Distal Intergenic	-0.11	1.54
296	Zfp365	chr10:67932461-67932752	Distal Intergenic	-0.12	1.54

**Table S6.** DMRs with non-inverse DNA methylation change and RNA expression change. Methylation change is expressed as  $R_{UVB} - R_{Control}$ , where  $R_{UVB}$  is average methylation ratio in the UVB group and  $R_{Control}$  is average methylation ratio in the Control group.

DMR	Gene	Location	Feature	DNA Methylation	RNA Expression
				change UVB vs Control	change $\log_2(UVB/Control)$
1	1110059E24Rik	chr19:21630639-21630710	Intron	0.12	1.13
2	2700094K13Rik	chr2:84671277-84671379	Promoter	0.10	1.61
3	4930404N11Rik	chr10:81365315-81365451	Promoter	-0.11	-1.02
4	9030617O03Rik	chr12:100835555-100835578	Intron	0.33	1.75
5	A4galt	chr15:83297201-83297389	Downstream	-0.15	-1.18
6	Abi3bp	chr16:56456044-56456112	Distal Intergenic	-0.19	-1.34
7	Ackr3	chr1:90203151-90203164	Promoter	0.21	1.33
8	Ackr3	chr1:90202624-90203050	Promoter	0.12	1.33
9	Actn1	chr12:80223225-80223692	Intron	-0.11	-1.22
10	Actn1	chr12:80224631-80224787	Intron	-0.18	-1.22
11	Actn1	chr12:80257694-80257736	Promoter	-0.14	-1.22
12	Actn1	chr12:80258701-80258888	Promoter	-0.11	-1.22
13	Actn1	chr12:80210019-80210160	Intron	-0.11	-1.22
14	Actn1	chr12:80224903-80224955	Intron	-0.13	-1.22
15	Adam19	chr11:46070375-46070478	Intron	-0.10	-1.52
16	Adam19	chr11:46064845-46065080	5' UTR	-0.19	-1.52
17	Adcy6	chr15:98607865-98607965	Promoter	-0.15	-1.64
18	Adcy6	chr15:98594191-98594686	Exon	-0.14	-1.64
19	Adcy6	chr15:98608467-98608498	Promoter	-0.21	-1.64
20	Adgra2	chr5:50056936-50057076	Promoter	-0.15	-1.47
21	Adgra2	chr5:50057264-50057349	Promoter	-0.12	-1.47
22	Adh1	chr3:138276412-138276431	Promoter	-0.13	-1.83
23	Adh1	chr3:138276547-138276636	Promoter	-0.10	-1.83
24	Akap7	chr10:25295180-25295333	Intron	-0.14	-1.19
25	Aldh1a3	chr7:66498069-66498114	Distal Intergenic	0.19	2.12
26	Alox12	chr11:70273458-70273517	Distal Intergenic	-0.11	-1.21
27	Ankrd23	chr1:36533860-36533913	Promoter	-0.11	-1.78
28	Arhgap44	chr11:65100153-65100423	Intron	-0.10	-1.11
29	Arhgap9	chr10:127323127-127323180	Promoter	0.17	1.12
30	Arl4c	chr1:88705463-88705573	Distal Intergenic	-0.11	-1.33
31	Arsa	chr15:89481039-89481180	Intron	-0.12	-2.04
32	Arsg	chr11:109509183-109509379	Intron	-0.13	-1.21
33	Atp8a1	chr5:67845806-67846293	Promoter	-0.12	-1.08
34	Atp8a1	chr5:67797973-67798070	Intron	-0.21	-1.08
35	Atp8a1	chr5:67845314-67845480	Promoter	-0.12	-1.08
36	Bach2	chr4:32338041-32338144	Distal Intergenic	-0.11	-2.05
37	Bach2	chr4:32245919-32246260	Distal Intergenic	-0.13	-2.05
38	Bach2	chr4:32342286-32342517	Distal Intergenic	-0.10	-2.05
39	Bach2	chr4:32304719-32304791	Distal Intergenic	-0.13	-2.05
40	Bach2	chr4:32249559-32249583	Distal Intergenic	-0.12	-2.05
41	Bmp4	chr14:46389783-46389869	Promoter	-0.15	-1.40
42	Btc	chr5:91404583-91404615	Promoter	-0.13	-1.34
43	C1s1	chr6:124528213-124528384	Downstream	0.17	2.60
44	Camk2n1	chr4:138449132-138449156	Distal Intergenic	-0.15	-1.33
45	Ccdc50	chr16:27423476-27423546	Intron	-0.13	-1.39
46	Ccdc88b	chr19:6857649-6857676	Promoter	0.47	1.31
47	Ccne1	chr7:38074957-38075079	Distal Intergenic	0.33	1.90

DMR	Gene	Location	Feature	DNA Methylation change UVB vs Control	RNA Expression change $\log_2(\text{UVB}/\text{Control})$
48	Chd7	chr4:8745829-8745967	Intron	-0.15	-1.08
49	Chd7	chr4:8692583-8693056	Promoter	-0.11	-1.08
50	Ciita	chr16:10479194-10479229	Promoter	0.10	1.01
51	Cldn23	chr8:35851957-35852077	Distal Intergenic	-0.10	-1.15
52	Cotl1	chr8:119813035-119813053	Intron	0.24	1.52
53	Cryl1	chr14:57332540-57332648	Intron	-0.12	-1.41
54	Cttnbp2	chr6:18435270-18435370	Exon	-0.11	-1.01
55	Cttnbp2	chr6:18434290-18434536	Exon	-0.11	-1.01
56	Cttnbp2	chr6:18436255-18436443	Intron	-0.14	-1.01
57	Cyp39a1	chr17:43685218-43685429	Exon	-0.13	-1.67
58	Dach1	chr14:98166694-98166848	Promoter	-0.14	-1.03
59	Dlgap5	chr14:47406261-47406358	Exon	0.12	1.33
60	Dnaaf3	chr7:4527963-4528065	Exon	0.17	1.21
61	Dnajb5	chr4:42951738-42951848	Promoter	-0.10	-1.09
62	Dnajb5	chr4:42938678-42938744	Exon	-0.25	-1.09
63	Dync2h1	chr9:6801111-6801177	Distal Intergenic	-0.17	-1.30
64	Elk3	chr10:93311708-93311816	Promoter	0.12	2.10
65	Enc1	chr13:97242811-97243012	Promoter	-0.11	-1.51
66	Enc1	chr13:97243900-97244126	Promoter	-0.14	-1.51
67	Enc1	chr13:97299186-97299248	Distal Intergenic	-0.17	-1.51
68	Enc1	chr13:97242379-97242564	Promoter	-0.17	-1.51
69	Enc1	chr13:97244231-97244517	Intron	-0.12	-1.51
70	Enc1	chr13:97249962-97250137	Intron	-0.12	-1.51
71	Fam105a	chr15:27802583-27802770	Intron	0.10	2.06
72	Fam49b	chr15:64118377-64118633	Intron	0.14	1.45
73	Fam49b	chr15:64142554-64142605	Intron	0.21	1.45
74	Fanci	chr7:79424266-79424389	Exon	0.11	1.04
75	Fbln1	chr15:85267106-85267293	Intron	0.13	1.75
76	Fbxo10	chr4:45083159-45083221	Promoter	0.15	1.01
77	Fgd4	chr16:16525392-16525520	Promoter	-0.13	-1.18
78	Gan	chr8:117198525-117198878	Intron	-0.22	-1.31
79	Gjb6	chr14:57131898-57131940	Promoter	0.10	1.31
80	Gnpnat1	chr14:45400134-45400352	Distal Intergenic	0.16	1.04
81	Gnpnat1	chr14:45445039-45445497	Distal Intergenic	0.21	1.04
82	Golga7b	chr19:42257752-42257897	Promoter	-0.19	-2.22
83	Grip1	chr10:119979927-119980347	Intron	0.10	1.22
84	Hddc2	chr10:31209200-31209316	Distal Intergenic	0.22	1.04
85	Helz2	chr2:181244965-181245052	Promoter	0.10	1.04
86	Hsd17b14	chr7:45551806-45551895	Intron	-0.12	-1.48
87	Icosl	chr10:78114727-78114873	Distal Intergenic	0.14	1.99
88	Igsf3	chr3:101464293-101464686	Distal Intergenic	0.11	1.43
89	Il33	chr19:29948048-29948204	Promoter	0.10	2.06
90	Inpp5d	chr1:87673979-87674033	Intron	0.19	1.12
91	Inpp5d	chr1:87620116-87620166	Promoter	0.10	1.12
92	Inpp5d	chr1:87659256-87659487	Intron	0.13	1.12
93	Iqsec2	chrX:152175209-152175327	Intron	-0.11	-1.10
94	Iqsec2	chrX:152147431-152147545	Intron	-0.12	-1.10
95	Irs1	chr1:82287465-82287744	Exon	-0.11	-2.14
96	Isoc2a	chr7:4891220-4891319	Exon	0.10	1.24
97	Isoc2a	chr7:4895339-4895461	3' UTR	0.27	1.24
98	Itga2b	chr11:102487881-102487994	Intron	0.11	2.05

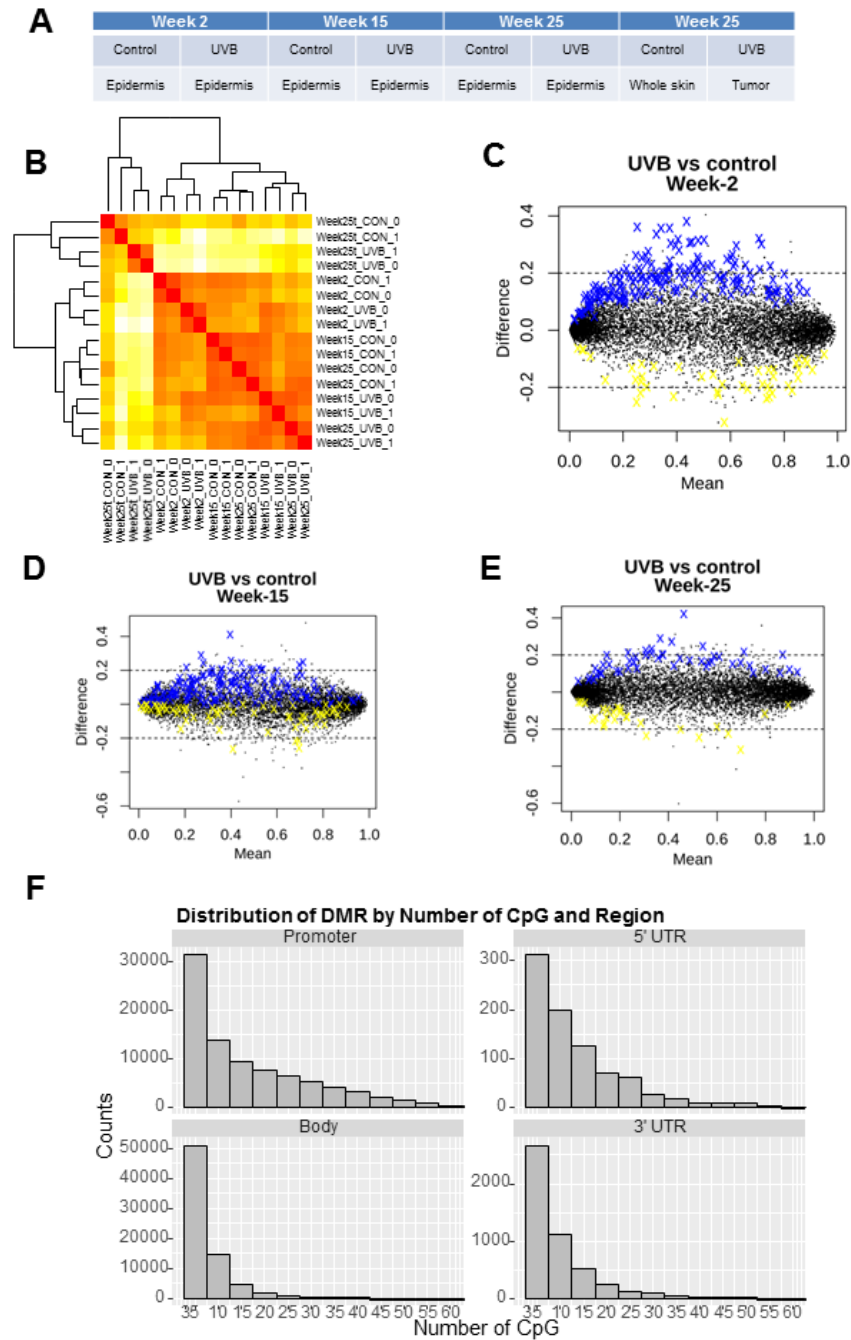


DMR	Gene	Location	Feature	DNA Methylation	RNA Expression
				change UVB vs Control	change log <sub>2</sub> (UVB/Control)
99	Kazald1	chr19:45078046-45078428	Promoter	-0.12	-1.72
100	Kazald1	chr19:45067475-45067794	Distal Intergenic	-0.12	-1.72
101	Kcnab3	chr11:69327749-69327824	Promoter	-0.13	-1.20
102	Kcnj15	chr16:95341494-95341506	Distal Intergenic	0.12	1.14
103	Lamc2	chr1:153073284-153073372	Intron	0.13	1.03
104	Large	chr8:73750700-73750898	Distal Intergenic	-0.12	-1.18
105	Ldlrad3	chr2:102126620-102126716	Intron	-0.11	-1.46
106	Lincppara	chr15:85654071-85654262	Distal Intergenic	-0.15	-1.24
107	Lmo1	chr7:109168720-109168916	Promoter	0.12	1.21
108	Lnx1	chr5:74796561-74796651	Distal Intergenic	-0.10	-1.74
109	Lnx1	chr5:74703553-74703661	Promoter	-0.15	-1.74
110	Magi1	chr6:93445575-93445732	Distal Intergenic	-0.10	-1.79
111	Magi1	chr6:93924567-93924601	Intron	-0.18	-1.79
112	Magi1	chr6:93445163-93445197	Distal Intergenic	-0.11	-1.79
113	Mapt	chr11:104305929-104306016	Intron	-0.13	-1.51
114	Mapt	chr11:104310749-104310881	Intron	-0.11	-1.51
115	Mareks	chr10:37232065-37232191	Distal Intergenic	0.12	1.06
116	Matk	chr10:81258230-81258384	Promoter	-0.11	-1.74
117	Mcf2l	chr8:12891253-12891569	Distal Intergenic	-0.13	-1.01
118	Mcm2	chr6:88893915-88894109	Intron	0.10	1.34
119	Mdfi	chr17:47815256-47815412	3' UTR	0.13	1.03
120	Mdfi	chr17:47821591-47821682	Intron	0.17	1.03
121	Mdfi	chr17:47811409-47811630	Distal Intergenic	0.12	1.03
122	Mgst2	chr3:51668716-51668875	Intron	0.11	1.43
123	Mitf	chr6:97855635-97855780	Intron	-0.19	-1.43
124	Mllt3	chr4:87930772-87930931	Intron	0.10	1.09
125	Mtmr12	chr15:12194302-12194388	Distal Intergenic	-0.12	-1.01
126	Myo5a	chr9:75085667-75085751	Intron	-0.11	-1.15
127	Nceh1	chr3:27237695-27237890	Intron	0.14	1.37
128	Ncf2	chr1:152816584-152816660	Intron	0.13	1.11
129	Ncf2	chr1:152815265-152815368	Intron	0.11	1.11
130	Pde1b	chr15:103518974-103519011	Intron	-0.14	-1.01
131	Pde1b	chr15:103504235-103504257	Promoter	-0.13	-1.01
132	Pdzn3	chr6:101293433-101293490	Intron	-0.14	-1.16
133	Pdzn3	chr6:101289866-101289960	Intron	-0.16	-1.16
134	Pik3cd	chr4:149702620-149703047	Promoter	-0.15	-1.06
135	Plet1	chr9:50443710-50444001	Distal Intergenic	-0.10	-1.11
136	Pmaip1	chr18:66427199-66427337	Distal Intergenic	0.12	1.65
137	Pnkd	chr1:74331588-74331810	Promoter	-0.11	-1.19
138	Pnkd	chr1:74335237-74335306	Promoter	-0.12	-1.19
139	Ppfia4	chr1:134328334-134328417	Exon	-0.12	-2.00
140	Prkar2b	chr12:32111822-32112005	Distal Intergenic	0.14	1.26
141	Prkar2b	chr12:32113157-32113364	Distal Intergenic	0.18	1.26
142	Ptp4a3	chr15:73717486-73717526	Distal Intergenic	0.16	2.07
143	Pvrl3	chr16:46592795-46592971	Distal Intergenic	-0.11	-1.37
144	Pxdc1	chr13:34635983-34636067	Intron	0.14	1.08
145	Rab44	chr17:29169101-29169162	Intron	-0.22	-1.61
146	Rapgef2	chr3:79066505-79066869	Exon	-0.11	-1.30
147	Rapgef2	chr3:78933105-78933237	Distal Intergenic	-0.11	-1.30
148	Rapgef2	chr3:79086277-79086445	Intron	-0.16	-1.30
149	Rapgef4	chr2:72137248-72137297	Exon	-0.13	-1.03

DMR	Gene	Location	Feature	DNA Methylation	RNA Expression
				change UVB vs Control	change log <sub>2</sub> (UVB/Control)
150	Rgs10	chr7:128399063-128399169	Intron	-0.23	-1.42
151	Rhobtb1	chr10:69218958-69219273	Intron	-0.10	-1.93
152	Rnf152	chr1:105095406-105095612	Distal Intergenic	0.11	1.28
153	Rtn4r11	chr11:75215291-75215353	Intron	-0.14	-1.18
154	Sema6a	chr18:47330180-47330227	Intron	-0.12	-1.61
155	Sh3tc2	chr18:61955953-61956043	Promoter	-0.17	-1.92
156	Sigirr	chr7:141096881-141096966	Intron	-0.17	-1.22
157	Siva1	chr12:112634472-112634631	Exon	0.10	1.68
158	Slc1a1	chr19:28862439-28862574	Intron	-0.19	-1.40
159	Slc1a5	chr7:16760471-16760668	Distal Intergenic	0.19	1.12
160	Slc46a1	chr11:78454697-78454967	Distal Intergenic	-0.11	-1.04
161	Slc46a1	chr11:78454355-78454646	Distal Intergenic	-0.13	-1.04
162	Slc52a3	chr2:152020753-152020937	Distal Intergenic	-0.19	-1.19
163	Slc9a9	chr9:94681213-94681297	Intron	-0.21	-1.86
164	Slfn8	chr11:83019924-83019950	Promoter	0.16	1.13
165	Smyd3	chr1:179108432-179108532	Intron	-0.13	-1.30
166	Sntb1	chr15:55758521-55758659	Intron	-0.13	-1.51
167	Sntb1	chr15:55877289-55877408	Intron	-0.10	-1.51
168	Snx10	chr6:51586532-51586635	Intron	0.10	1.51
169	Sorbs1	chr19:40464776-40464971	Intron	-0.13	-1.14
170	Sorbs1	chr19:40477185-40477335	Intron	-0.18	-1.14
171	Srgap1	chr10:121902628-121902858	Intron	-0.13	-1.10
172	St3gal2	chr8:110946947-110947002	Intron	0.14	1.03
173	St3gal2	chr8:110949588-110949756	Intron	0.26	1.03
174	St6galnac2	chr11:116695641-116696027	Promoter	-0.11	-1.14
175	St6galnac2	chr11:116697752-116697916	Distal Intergenic	-0.12	-1.14
176	St6galnac2	chr11:116696229-116696521	Promoter	-0.19	-1.14
177	Stat1	chr1:52146669-52146811	Intron	0.15	1.02
178	Stat1	chr1:52149935-52150413	Intron	0.11	1.02
179	Syne1	chr10:4996424-4996482	Intron	-0.13	-2.31
180	Tbc1d24	chr17:24199377-24199484	Promoter	-0.23	-1.87
181	Tbc1d24	chr17:24207100-24207257	Promoter	-0.14	-1.87
182	Tesc	chr5:118063416-118063477	Downstream	-0.15	-1.70
183	Tmem177	chr1:119894947-119895026	Distal Intergenic	-0.11	-1.59
184	Tmem229a	chr6:24913589-24913696	Distal Intergenic	-0.14	-2.14
185	Tnxb	chr17:34671449-34671914	Promoter	-0.14	-1.20
186	Tnxb	chr17:34670964-34671437	Promoter	-0.11	-1.20
187	Tnxb	chr17:34671928-34672387	Promoter	-0.12	-1.20
188	Trappc9	chr15:73003893-73003991	Intron	-0.10	-1.19
189	Trim2	chr3:84294301-84294329	Intron	-0.17	-1.65
190	Trim2	chr3:84271821-84272109	Promoter	-0.15	-1.65
191	Ttll7	chr3:147335188-147335364	Distal Intergenic	0.16	1.69
192	Ttll7	chr3:147098353-147098567	Distal Intergenic	0.13	1.69
193	Tubb6	chr18:67396783-67396949	Intron	0.12	1.81
194	Vrk1	chr12:106034558-106034619	Intron	0.12	1.01
195	Vrk1	chr12:106199489-106199568	Distal Intergenic	0.11	1.01
196	Wnt10a	chr1:74793878-74794026	Promoter	0.11	1.02
197	Wwox	chr8:114440604-114440769	Promoter	-0.10	-1.52
198	Wwox	chr8:114452425-114452516	Intron	-0.27	-1.52
199	Wwox	chr8:114883032-114883182	Intron	-0.11	-1.52
200	Wwox	chr8:114837977-114838106	Intron	-0.16	-1.52

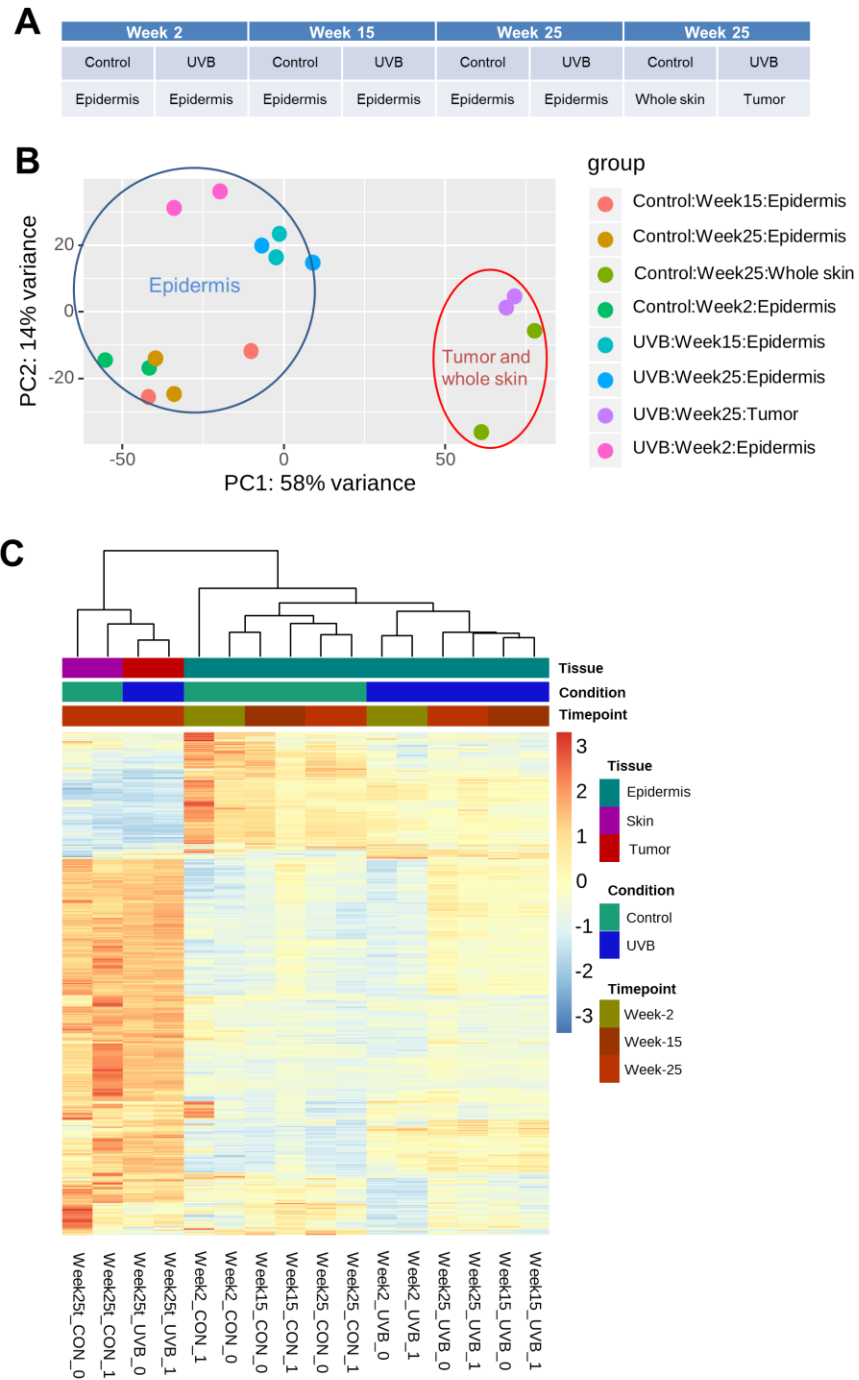
<b>DMR</b>	<b>Gene</b>	<b>Location</b>	<b>Feature</b>	<b>DNA Methylation change UVB vs Control</b>	<b>RNA Expression change log<sub>2</sub>(UVB/Control)</b>
201	Wwox	chr8:114629899-114630153	Intron	-0.12	-1.52
202	Wwox	chr8:114716494-114716803	Intron	-0.13	-1.52
203	Wwox	chr8:114591920-114592220	Intron	-0.15	-1.52
204	Wwox	chr8:114591725-114591791	Intron	-0.17	-1.52
205	Ypel2	chr11:86906564-86906648	Intron	-0.17	-1.30
206	Ypel2	chr11:86937873-86938071	3' UTR	-0.16	-1.30

**Figure S1**



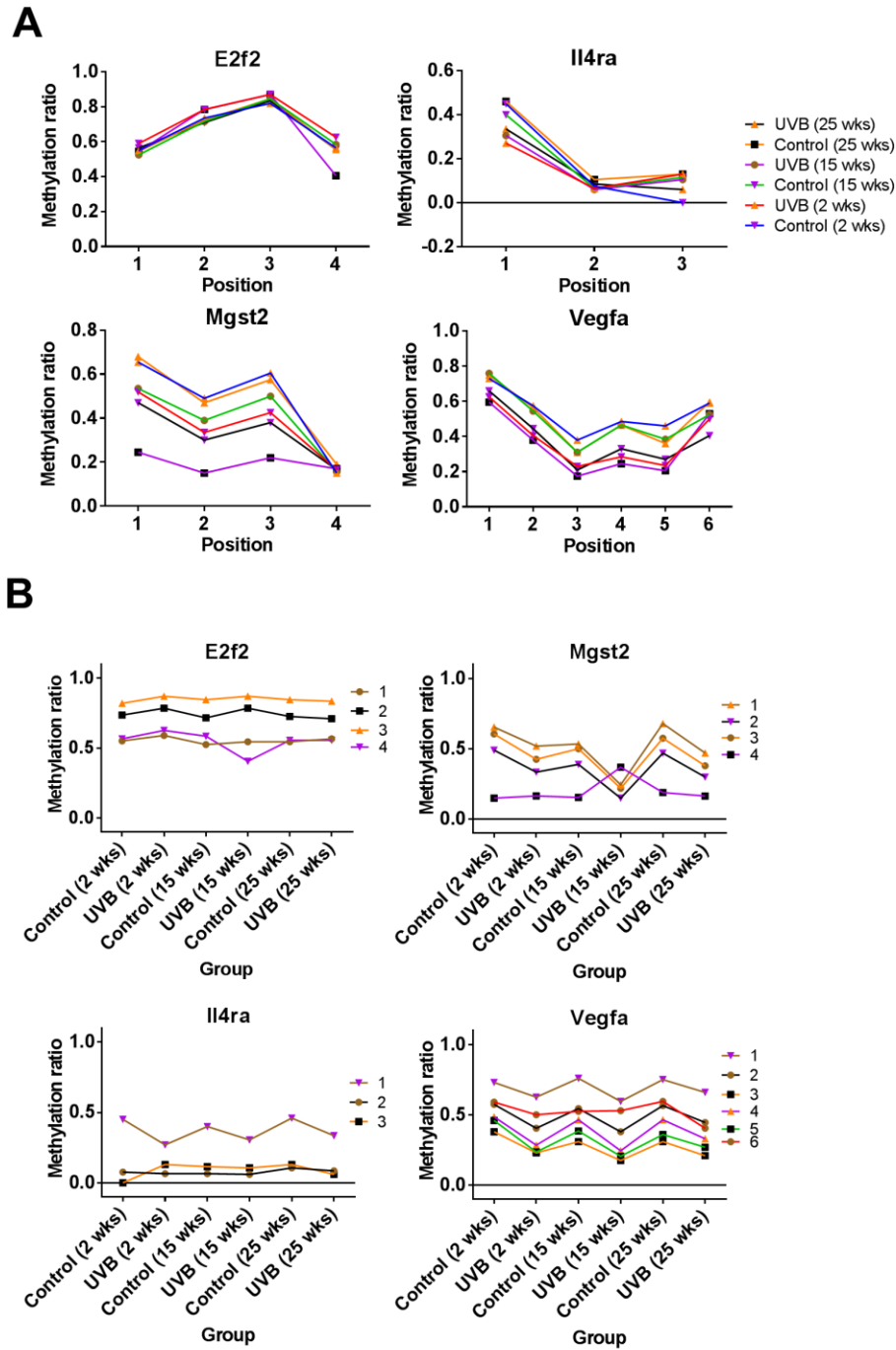
**Figure S1:** Methylation analysis on Methyl-seq data. (A) Sample collection scheme for the animal study. (B) Dendrogram clustering by Euclidean distance of 16 samples including epidermis, whole skin, and tumors. (C-E) MA plots showing methylation changes between UVB and Control conditions at different time points. (F) (E) Distribution of DMRs by CpG numbers and locations.

**Figure S2**



**Figure S2:** Gene expression analysis on RNA-seq data. (A) Sample collection scheme for the animal study (same as Figure S1A). (B) Principal component analysis (PCA) on RNA expression of the 16 samples. (C) Heatmap showing top 1000 regulated genes across all samples.

Figure S3



**Figure S3.** Single CpG methylation profiles of the 4 genes that were validated by pyrosequencing. (A) Data with CpG sites shown on x-axis. (B) Same data with groups shown on x-axis.