

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