

**Supplementary Table 5: Biological function analysis for protein coding genes with positive expressional correlation to lncRNAs of the signature (Only GO biological process terms with Benjamini corrected p value < E-2 are shown).**

Annotation Cluster 1	Enrichment Score:				
Category	Term	Count	PValue	Genes	Benjamini
GOTERM_BP_FAT	GO:0030216~keratinocyte differentiation	22	2.08E-24	LCE3A, LCE3B, LCE3C, LCE3D, ANXA1, SPRR2G, SPRR2F, SPRR2E, SCEL, EVPL, SPRR2C, SPRR2D, SPRR1A, PPL, LCE1C, SPRR1B, SPRR2A, SPRR2B, CNFN, TGM1, LCE3E, CSTA, IVL	2.32E-21
GOTERM_BP_FAT	GO:0031424~keratinization	19	1.24E-23	LCE3A, LCE3B, LCE3C, LCE3D, SPRR2G, SPRR2F, SPRR2E, EVPL, SPRR2C, SPRR2D, SPRR1A, PPL, LCE1C, SPRR1B, SPRR2A, SPRR2B, CNFN, TGM1, LCE3E, IVL	6.92E-21
GOTERM_BP_FAT	GO:0009913~epidermal cell differentiation	22	1.69E-23	LCE3A, LCE3B, LCE3C, LCE3D, ANXA1, SPRR2G, SPRR2F, SPRR2E, SCEL, EVPL, SPRR2C, SPRR2D, SPRR1A, PPL, LCE1C, SPRR1B, SPRR2A, SPRR2B, CNFN, TGM1, LCE3E, CSTA, IVL	6.28E-21
GOTERM_BP_FAT	GO:0007398~ectoderm development	28	1.74E-20	KRT6B, LCE3A, LCE3B, LCE3C, LCE3D, SPRR2G, SPRR2F, SPRR2E, SPRR2C, SPRR2D, PPL, SPRR2A, SPRR2B, TGM1, ALOX12B, TGM5, IVL, ANXA1, GRHL3, SCEL, EVPL, SPRR1A, LCE1C, SPRR1B, CNFN, CSTA, PTCH2, LCE3E, KRT71	4.85E-18
GOTERM_BP_FAT	GO:0008544~epidermis development	27	3.28E-20	LCE3A, LCE3B, LCE3C, LCE3D, SPRR2G, SPRR2F, SPRR2E, SPRR2C, SPRR2D, PPL, SPRR2A, SPRR2B, TGM1, ALOX12B, TGM5, IVL, ANXA1, GRHL3, SCEL, EVPL, SPRR1A, LCE1C, SPRR1B, CNFN, CSTA, PTCH2, LCE3E, KRT71	7.30E-18
GOTERM_BP_FAT	GO:0030855~epithelial cell differentiation	24	1.02E-19	LCE3A, ONECUT1, LCE3B, LCE3C, LCE3D, SPRR2G, SPRR2F, SPRR2E, SPRR2C, SPRR2D, SPRR2A, PPL, TGM1, SPRR2B, IVL, ANXA1, SCEL, EVPL, RHCG, SPRR1A, SPRR1B, LCE1C, CNFN, CSTA, LCE3E	1.90E-17
GOTERM_BP_FAT	GO:0060429~epithelium development	24	1.03E-14	LCE3A, ONECUT1, LCE3B, LCE3C, LCE3D, SPRR2G, SPRR2F, SPRR2E, SPRR2C, SPRR2D, SPRR2A, PPL, TGM1, SPRR2B, IVL, ANXA1, SCEL, EVPL, RHCG, SPRR1A, SPRR1B, LCE1C, CNFN, CSTA, LCE3E	1.64E-12