

A. Volar epidermis

| Sublist | Category | Term | RT | Genes | Count | % | P-Value | Benjamini |
|--------------------------|---------------|--|----|-------|-------|-----|---------|-----------|
| <input type="checkbox"/> | GOTERM_BP_FAT | cell adhesion | RT | | 9 | 7.3 | 6.9E-2 | 9.1E-1 |
| <input type="checkbox"/> | GOTERM_BP_FAT | biological adhesion | RT | | 9 | 7.3 | 6.9E-2 | 9.0E-1 |
| <input type="checkbox"/> | GOTERM_BP_FAT | ectoderm development | RT | | 7 | 5.6 | 1.5E-3 | 6.2E-1 |
| <input type="checkbox"/> | GOTERM_BP_FAT | cytoskeleton organization | RT | | 7 | 5.6 | 5.4E-2 | 9.2E-1 |
| <input type="checkbox"/> | GOTERM_BP_FAT | steroid metabolic process | RT | | 6 | 4.8 | 8.4E-3 | 7.5E-1 |
| <input type="checkbox"/> | GOTERM_BP_FAT | epithelium development | RT | | 6 | 4.8 | 1.3E-2 | 7.7E-1 |
| <input type="checkbox"/> | GOTERM_BP_FAT | secretion | RT | | 6 | 4.8 | 3.9E-2 | 9.4E-1 |
| <input type="checkbox"/> | GOTERM_BP_FAT | epithelial cell differentiation | RT | | 5 | 4.0 | 1.0E-2 | 7.4E-1 |
| <input type="checkbox"/> | GOTERM_BP_FAT | epidermis development | RT | | 5 | 4.0 | 2.8E-2 | 9.3E-1 |
| <input type="checkbox"/> | GOTERM_BP_FAT | response to hypoxia | RT | | 4 | 3.2 | 5.1E-2 | 9.3E-1 |
| <input type="checkbox"/> | GOTERM_BP_FAT | response to oxygen levels | RT | | 4 | 3.2 | 5.7E-2 | 9.2E-1 |
| <input type="checkbox"/> | GOTERM_BP_FAT | intermediate filament cytoskeleton organization | RT | | 3 | 2.4 | 6.7E-3 | 8.9E-1 |
| <input type="checkbox"/> | GOTERM_BP_FAT | intermediate filament-based process | RT | | 3 | 2.4 | 8.1E-3 | 8.3E-1 |
| <input type="checkbox"/> | GOTERM_BP_FAT | keratinization | RT | | 3 | 2.4 | 2.9E-2 | 9.1E-1 |
| <input type="checkbox"/> | GOTERM_BP_FAT | regulation of proteolysis | RT | | 3 | 2.4 | 4.3E-2 | 9.4E-1 |
| <input type="checkbox"/> | GOTERM_BP_FAT | excretion | RT | | 3 | 2.4 | 5.0E-2 | 9.4E-1 |
| <input type="checkbox"/> | GOTERM_BP_FAT | keratinocyte differentiation | RT | | 3 | 2.4 | 6.3E-2 | 9.2E-1 |
| <input type="checkbox"/> | GOTERM_BP_FAT | regulation of neurotransmitter levels | RT | | 3 | 2.4 | 6.5E-2 | 9.1E-1 |
| <input type="checkbox"/> | GOTERM_BP_FAT | integrin-mediated signaling pathway | RT | | 3 | 2.4 | 7.0E-2 | 9.0E-1 |
| <input type="checkbox"/> | GOTERM_BP_FAT | epidermal cell differentiation | RT | | 3 | 2.4 | 7.4E-2 | 9.0E-1 |
| <input type="checkbox"/> | GOTERM_BP_FAT | steroid biosynthetic process | RT | | 3 | 2.4 | 9.8E-2 | 9.5E-1 |
| <input type="checkbox"/> | GOTERM_BP_FAT | generation of a signal involved in cell-cell signaling | RT | | 3 | 2.4 | 9.8E-2 | 9.5E-1 |
| <input type="checkbox"/> | GOTERM_BP_FAT | wound healing, spreading of epidermal cells | RT | | 2 | 1.6 | 4.9E-2 | 9.5E-1 |
| <input type="checkbox"/> | GOTERM_BP_FAT | intermediate filament organization | RT | | 2 | 1.6 | 6.0E-2 | 9.2E-1 |

B. Non-volar epidermis

| Sublist | Category | Term | RT | Genes | Count | % | P-Value | Benjamini |
|--------------------------|---------------|---|----|-------|-------|------|---------|-----------|
| <input type="checkbox"/> | GOTERM_BP_FAT | cell surface receptor linked signal transduction | RT | | 20 | 14.8 | 4.7E-2 | 7.6E-1 |
| <input type="checkbox"/> | GOTERM_BP_FAT | response to organic substance | RT | | 15 | 11.1 | 3.9E-4 | 2.0E-1 |
| <input type="checkbox"/> | GOTERM_BP_FAT | immune response | RT | | 13 | 9.6 | 2.6E-3 | 4.1E-1 |
| <input type="checkbox"/> | GOTERM_BP_FAT | cell motion | RT | | 11 | 8.1 | 1.5E-3 | 3.7E-1 |
| <input type="checkbox"/> | GOTERM_BP_FAT | regulation of cell proliferation | RT | | 11 | 8.1 | 4.3E-2 | 7.8E-1 |
| <input type="checkbox"/> | GOTERM_BP_FAT | regulation of programmed cell death | RT | | 11 | 8.1 | 5.2E-2 | 7.7E-1 |
| <input type="checkbox"/> | GOTERM_BP_FAT | regulation of cell death | RT | | 11 | 8.1 | 5.3E-2 | 7.6E-1 |
| <input type="checkbox"/> | GOTERM_BP_FAT | positive regulation of macromolecule metabolic process | RT | | 11 | 8.1 | 6.9E-2 | 7.7E-1 |
| <input type="checkbox"/> | GOTERM_BP_FAT | behavior | RT | | 10 | 7.4 | 4.9E-3 | 4.7E-1 |
| <input type="checkbox"/> | GOTERM_BP_FAT | cell death | RT | | 10 | 7.4 | 5.9E-2 | 7.8E-1 |
| <input type="checkbox"/> | GOTERM_BP_FAT | death | RT | | 10 | 7.4 | 6.1E-2 | 7.6E-1 |
| <input type="checkbox"/> | GOTERM_BP_FAT | regulation of transcription from RNA polymerase II promoter | RT | | 10 | 7.4 | 6.2E-2 | 7.6E-1 |
| <input type="checkbox"/> | GOTERM_BP_FAT | lipid biosynthetic process | RT | | 9 | 6.7 | 1.7E-3 | 3.3E-1 |
| <input type="checkbox"/> | GOTERM_BP_FAT | programmed cell death | RT | | 9 | 6.7 | 5.9E-2 | 7.8E-1 |
| <input type="checkbox"/> | GOTERM_BP_FAT | defense response | RT | | 9 | 6.7 | 6.1E-2 | 7.6E-1 |
| <input type="checkbox"/> | GOTERM_BP_FAT | positive regulation of macromolecule biosynthetic process | RT | | 9 | 6.7 | 8.0E-2 | 7.8E-1 |
| <input type="checkbox"/> | GOTERM_BP_FAT | positive regulation of cellular biosynthetic process | RT | | 9 | 6.7 | 9.9E-2 | 7.9E-1 |
| <input type="checkbox"/> | GOTERM_BP_FAT | epidermis development | RT | | 8 | 5.9 | 2.7E-4 | 2.7E-1 |
| <input type="checkbox"/> | GOTERM_BP_FAT | ectoderm development | RT | | 8 | 5.9 | 4.4E-4 | 1.6E-1 |
| <input type="checkbox"/> | GOTERM_BP_FAT | regulation of system process | RT | | 8 | 5.9 | 5.4E-3 | 4.7E-1 |
| <input type="checkbox"/> | GOTERM_BP_FAT | enzyme linked receptor protein signaling pathway | RT | | 8 | 5.9 | 9.2E-3 | 5.7E-1 |
| <input type="checkbox"/> | GOTERM_BP_FAT | positive regulation of cell proliferation | RT | | 8 | 5.9 | 2.4E-2 | 6.8E-1 |
| <input type="checkbox"/> | GOTERM_BP_FAT | reproductive process in a multicellular organism | RT | | 8 | 5.9 | 5.0E-2 | 7.7E-1 |
| <input type="checkbox"/> | GOTERM_BP_FAT | multicellular organism reproduction | RT | | 8 | 5.9 | 5.0E-2 | 7.7E-1 |