

Supplementary table 2: Modulated pathways highlighted by the DAVID functional annotation clustering tool

| <b>Annotation Cluster 1</b> |   | Enrichment Score:<br>3.7008879624375792 |           |  |                 |         |
|-----------------------------|---|---|-----------|--|-----------------|---------|
| Category                    | Term  | Count                                   | PValue    | Genes  | Fold Enrichment | FDR     |
| GOTERM_MF_DIRECT            | <b>GO:0098641~cadherin binding involved in cell-cell adhesion</b> | 9                                       | 1,91E-05  | P57776, P07356, P63101, P52480, Q9Z0P5, P24452, O08992, P06151, P60335 | 7,71            | 0,02467 |
| GOTERM_CC_DIRECT            | <b>GO:0005913~cell-cell adherens junction</b>                     | 9                                       | 2,21E-05  | P57776, P07356, P63101, P52480, Q9Z0P5, P24452, O08992, P06151, P60335 | 7,57            | 0,02725 |
| GOTERM_CC_DIRECT            | <b>GO:0042470~melanosome</b>                                      | 5                                       | 5,44E-04  | P07356, P63101, P24452, O08992, P09103                                 | 13,15           | 0,66861 |
| GOTERM_BP_DIRECT            | <b>GO:0098609~cell-cell adhesion</b>                              | 5                                       | 0,0068431 | P57776, P63101, Q9Z0P5, P24452, P06151                                 | 6,55            | 9,42755 |
| <b>Annotation Cluster 2</b> |   | Enrichment Score:<br>2.961292035066181  |           |  |                 |         |
| Category                    | Term  | Count                                   | PValue    | Genes  | Fold Enrichment | FDR     |
| UP_KEYWORDS                 | <b>Proteasome</b>   | 6                                       | 1,08E-06  | P99026, O35955, O35593, Q9WUP7, Q9R1P4, Q8VDM4                         | 32,40           | 0,00130 |
| GOTERM_CC_DIRECT            | <b>GO:0000502~proteasome complex</b>                              | 6                                       | 4,60E-06  | P99026, O35955, O35593, Q9WUP7, Q9R1P4, Q8VDM4                         | 24,15           | 0,00567 |

|                  |  |    |           |   |       |         |
|------------------|--|----|-----------|---|-------|---------|
| UP_KEYWORDS      | <b>Hydrolase</b>   | 17 | 6,58E-05  | Q9CQ60, P56480, Q8VDK1,<br>P99026, O70370, P97823, P50516,<br>Q9Z1N5, O35955, O35593,<br>Q9D819, Q9WUP7, Q9R1P4,<br>Q8JZV7, Q99KK7, Q9Z0S1, Q9R0P3<br>P99026, O35955, O35593, Q9R1P4,<br>Q8VDM4 | 3,12  | 0,07929 |
| KEGG_PATHWAY     | <b>mmu03050:Proteasome</b>   | 5  | 2,09E-04  | Q9CQ60, P56480, Q8VDK1,<br>P99026, O70370, P97823, P50516,<br>Q9Z1N5, O35955, O35593,<br>Q9D819, Q9WUP7, Q9R1P4,<br>Q8JZV7, Q99KK7, Q9Z0S1, Q9R0P3<br>P99026, O35955, O35593, Q9R1P4,<br>Q8VDM4 | 16,43 | 0,24974 |
| GOTERM_MF_DIRECT | GO:0016787~hydrolase activity  | 17 | 4,22E-04  | Q9CQ60, P56480, Q8VDK1,<br>P99026, O70370, P97823, P50516,<br>Q9Z1N5, O35955, O35593,<br>Q9D819, Q9WUP7, Q9R1P4,<br>Q8JZV7, Q99KK7, Q9Z0S1, Q9R0P3<br>P99026, O35955, O35593, Q9R1P4,<br>Q8VDM4 | 2,65  | 0,54354 |
| GOTERM_MF_DIRECT | GO:0004175~endopeptidase activity  | 5  | 0,0011836 | P99026, O35955, O35593, Q9R1P4,<br>Q8VDM4   | 10,67 | 1,51804 |
| GOTERM_BP_DIRECT | GO:0051603~proteolysis involved in cellular protein catabolic process                                      | 4  | 0,0015182 | P99026, O70370, O35955, Q9R1P4  | 17,38 | 2,16721 |
| UP_KEYWORDS      | Threonine protease   | 3  | 0,0023256 | P99026, O35955, Q9R1P4  | 41,24 | 2,76639 |
| GOTERM_CC_DIRECT | GO:0005839~proteasome core complex   | 3  | 0,0024739 | P99026, O35955, Q9R1P4  | 39,86 | 3,00761 |
| INTERPRO         | IPR001353:Proteasome, subunit alpha/beta   | 3  | 0,0025592 | P99026, O35955, Q9R1P4  | 39,23 | 3,22737 |
| GOTERM_MF_DIRECT | GO:0004298~threonine-type endopeptidase activity   | 3  | 0,0040178 | P99026, O35955, Q9R1P4  | 31,17 | 5,06693 |
| GOTERM_BP_DIRECT | GO:0002479~antigen processing and presentation of exogenous peptide antigen via MHC class I, TAP-dependent | 3  | 0,0063285 | P99026, O35955, Q9R1P4  | 24,77 | 8,74854 |

**Annotation Cluster 3** Enrichment Score:  
2.42781337900096

| Category         | Term                                  | Count | PValue    | Genes  | Fold Enrichment | FDR      |
|------------------|---------------------------------------|-------|-----------|--|-----------------|----------|
| KEGG_PATHWAY     | <b>mmu01200:Carbon metabolism</b>     | 7     | 1,07E-04  | Q9CQ60, Q9D2G2, P52480, P28271, Q9R0P3, P09411, P16858 | 8,93            | 0,12794  |
| UP_KEYWORDS      | <b>Glycolysis</b>                     | 3     | 0,0058284 | P52480, P09411, P16858                                 | 25,92           | 6,80087  |
| GOTERM_BP_DIRECT | GO:0006096~glycolytic process         | 3     | 0,0090257 | P52480, P09411, P16858                                 | 20,64           | 12,25596 |
| KEGG_PATHWAY     | mmu00010:Glycolysis / Gluconeogenesis | 4     | 0,0093734 | P52480, P06151, P09411, P16858                         | 8,96            | 10,64844 |
| KEGG_PATHWAY     | mmu01230:Biosynthesis of amino acids  | 4     | 0,0137498 | P52480, P28271, P09411, P16858                         | 7,78            | 15,25506 |

**Annotation Cluster 4** Enrichment Score:  
2.290003037675952

| Category         | Term                               | Count | PValue    | Genes  | Fold Enrichment | FDR      |
|------------------|------------------------------------|-------|-----------|--|-----------------|----------|
| INTERPRO         | IPR016040:NAD(P)-binding domain    | 7     | 8,10E-05  | P50171, Q02053, Q91X52, P06151, Q64105, Q9CY64, P16858                 | 9,66            | 0,10366  |
| UP_KEYWORDS      | NAD                                | 6     | 3,32E-04  | P50171, Q9DCT2, P06151, P24547, Q9CY64, P16858                         | 9,91            | 0,39985  |
| UP_KEYWORDS      | <b>Oxidoreductase</b>              | 9     | 0,0011161 | P20108, P50171, Q91X52, Q9DCT2, P06151, Q64105, P24547, Q9CY64, P16858 | 4,26            | 1,33652  |
| GOTERM_MF_DIRECT | GO:0016491~oxidoreductase activity | 8     | 0,012147  | P20108, P50171, Q91X52, Q9DCT2, P06151, Q64105, P24547, Q9CY64         | 3,17            | 14,60231 |

**Annotation Cluster 5** Enrichment Score:  
2.221007657916773

| Category         | Term  | Count | PValue    | Genes  | Fold Enrichment | FDR      |
|------------------|---|-------|-----------|--|-----------------|----------|
| GOTERM_BP_DIRECT | <b>GO:0051016~barbed-end actin filament capping</b> | 3     | 0,0018097 | P47754, Q9Z0P5, P24452                         | 46,44           | 2,57830  |
| UP_KEYWORDS      | <b>Actin-binding</b>                                | 5     | 0,0093274 | Q6IRU2, P40124, P47754, Q9Z0P5, P24452         | 6,00            | 10,67718 |
| GOTERM_MF_DIRECT | GO:0003779~actin binding                            | 6     | 0,0128705 | Q9CQI3, Q6IRU2, P40124, P47754, Q9Z0P5, P24452 | 4,24            | 15,40666 |

**Annotation Cluster 6** Enrichment Score:  
1.7532557305124994

| Category       | Term                               | Count | PValue    | Genes                  | Fold Enrichment | FDR      |
|----------------|------------------------------------|-------|-----------|------------------------|-----------------|----------|
| UP_SEQ_FEATURE | metal ion-binding site:Magnesium 2 | 3     | 0,0140917 | Q9D819, Q920E5, Q9Z0S1 | 16,37           | 16,94066 |
| UP_SEQ_FEATURE | metal ion-binding site:Magnesium 1 | 3     | 0,0140917 | Q9D819, Q920E5, Q9Z0S1 | 16,37           | 16,94066 |

**Annotation Cluster 7** Enrichment Score:  
1.554843385372

| Category         | Term                              | Count | PValue    | Genes                  | Fold Enrichment | FDR      |
|------------------|-----------------------------------|-------|-----------|------------------------|-----------------|----------|
| INTERPRO         | IPR013766:Thioredoxin domain      | 3     | 0,0090962 | P20108, Q9CQM9, P09103 | 20,59           | 11,04033 |
| GOTERM_BP_DIRECT | GO:0045454~cell redox homeostasis | 3     | 0,0276759 | P20108, Q9CQM9, P09103 | 11,43           | 33,28426 |
| INTERPRO         | IPR012336:Thioredoxin-like fold   | 3     | 0,086002  | P20108, Q9CQM9, P09103 | 6,06            | 68,37724 |

**Annotation Cluster 8** Enrichment Score:  
1.3970844114629328

| Category         | Term                                    | Count | PValue    | Genes  | Fold Enrichment | FDR      |
|------------------|---|-------|-----------|--|-----------------|----------|
| UP_KEYWORDS      | <b>Mitochondrion</b>                    | 10    | 0,007354  | P56480, Q9D2G2, P20108, P67778, P50171, Q8VVK1, Q02053, Q9DCT2, P53395, Q8BK08 | 2,86            | 8,50955  |
| UP_KEYWORDS      | Mitochondrion inner membrane            | 4     | 0,050366  | P56480, P67778, Q9DCT2, Q8BK08   | 4,76            | 46,34913 |
| GOTERM_CC_DIRECT | GO:0005743~mitochondrial inner membrane | 4     | 0,1738136 | P56480, P67778, Q9DCT2, Q8BK08   | 2,75            | 90,50128 |

**Annotation Cluster 9** Enrichment Score:  
1.345122814366088

| Category       | Term                          | Count | PValue    | Genes  | Fold Enrichment | FDR      |
|----------------|-------------------------------|-------|-----------|--|-----------------|----------|
| UP_KEYWORDS    | <b>Mitochondrion</b>          | 10    | 0,007354  | P56480, Q9D2G2, P20108, P67778, P50171, Q8VVK1, Q02053, Q9DCT2, P53395, Q8BK08 | 2,86            | 8,50955  |
| UP_KEYWORDS    | Transit peptide               | 5     | 0,0853392 | P56480, Q9D2G2, P20108, Q9DCT2, P53395   | 2,96            | 65,86303 |
| UP_SEQ_FEATURE | transit peptide:Mitochondrion | 5     | 0,1468782 | P56480, Q9D2G2, P20108, Q9DCT2, P53395   | 2,42            | 87,47729 |