

The following table represents the data from the bubble chart, where the first column is the Gene Ontology term, the second column is the count from Dataset 1, and the third column is the count from Dataset 2.

| Gene Ontology Term                                | Count 1 | Count 2 |
|---|---------|---------|
| Synaptic signaling (n=46)                         | 8       | 13      |
| Autophagic and endolysosomal pathway (AEL) (n=61) | 13      | 18      |
| Melanosome (n=30)                                 | 7       | 8       |
| Lipid metabolism (n=65)                           | 3       | 10      |
| Nucleotide metabolism (n=38)                      | 2       | 5       |
| Mitochondria organisation (n=46)                  | 3       | 7       |
| Transmembrane transport (n=74)                    | 15      | 12      |
| Peroxisome organisation (n=7)                     |         | 3       |
| Phototransduction (VCPh) (n=32)                   | 3       | 1       |
| Cytoskeleton (n=52)                               | 8       | 3       |
| Cilium (n=83)                                     | 2       | 4       |
| Transcriptional regulation (n=63)                 | 3       | 5       |
| ER / Golgi homeostasis (n=19)                     | 3       | 5       |
| Extracellular matrix (n=29)                       | 4       | 2       |
| Cell adhesion (n=32)                              | 5       | 2       |
| Protein ubiquitination (n=11)                     | 1       | 2       |
| Axonogenesis (n=14)                               | 5       | 3       |
| Protein biosynthesis (n=22)                       |         | 1       |
| RNA splicing (n=19)                               | 1       |         |
| Others (n=35)                                     |         |         |
| Telomere maintenance (n=3)                        |         |         |

