

Supplemental Table S2: Top 10 significantly enriched GO biological processes (gene set overlaps investigated in GSEA and Molecular Signature Database, FDRq-value <0.05). Genes from selected subclusters from the spaghetti plot showing a pattern of significantly **increased** or **decreased** genes for Rods, Cones, and RGCs were used as input data.

(A) Rod Photoreceptor: One subcluster with 37 genes showing significant late **increase** (day 5)

Pathways / Gene Set Name	# Genes in Overlap	p-value	FDRq-value
Homeostatic Process	12	7.75 e ⁻⁹	4.08 e ⁻⁵
Nervous system process	11	3.51 e ⁻⁸	1.23 e ⁻⁴
Establishment of protein localization	11	8.81 e ⁻⁸	1.55 e ⁻⁴
Tissue homeostasis	6	8.84 e ⁻⁸	1.55 e ⁻⁴
Cellular Homeostasis	8	2.65 e ⁻⁷	3.11 e ⁻⁴
Regulation of cardiac muscle contraction by regulation of the release of sequestered calcium ion	3	8.5 e ⁻⁷	8.01 e ⁻⁴
Microtubule based process	8	1.01 e ⁻⁶	8.19 e ⁻⁴
Sensory perception of light stimulus	5	1.28 e ⁻⁶	9.24 e ⁻⁴
Regulation of cardiac muscle contraction by calcium ion signaling	3	1.43 e ⁻⁶	9.43 e ⁻⁴
Regulation of transport	10	1.75 e ⁻⁶	1.03 e ⁻³

(B) Rod Photoreceptor: Two subcluster with 170 genes showing significant late **decrease** (day 5)

Pathways / Gene Set Name	# of Genes in Overlap	p-value	FDRq-value
Cytoplasmic translation	65	3.95 e ⁻¹¹⁷	3.06 e ⁻¹¹³
Peptide biosynthetic process	70	5.03 e ⁻⁷⁵	1.95 e ⁻⁷¹
Amide biosynthetic process	71	6.69 e ⁻⁷²	1.73 e ⁻⁶⁸
Peptide metabolic process	71	9.36 e ⁻⁷¹	1.82 e ⁻⁶⁷
Organonitrogen biosynthetic process	83	3.92 e ⁻⁶⁷	6.08 e ⁻⁶⁴
Cellular amide metabolic process	72	2.13 e ⁻⁶⁴	2.75 e ⁻⁶¹
Cellular macromolecule biosynthetic process	70	7.7 e ⁻⁶²	8.54 e ⁻⁵⁹
Ribosome biogenesis	25	2.95 e ⁻²⁵	2.86 e ⁻²²
Ribonucleoprotein complex biogenesis	28	3.77 e ⁻²⁴	3.25 e ⁻²¹
rRNA metabolic process	21	4.33 e ⁻²¹	3.36 e ⁻¹⁸

(C) Cone Photoreceptor: One subcluster with 22 genes showing significant late **decrease** (day 5)

Pathways / Gene Set Name	# of Genes in Overlap	p-value	FDRq-value
Organonitrogen compound biosynthetic process	13	8.54 e ⁻¹³	6.63 e ⁻⁹
ATP biosynthetic process	6	8.54 e ⁻¹³	6.63 e ⁻⁹
Purine containing compound biosynthetic process	7	4.66 e ⁻¹¹	1.21 e ⁻⁷
Nucleoside triphosphate biosynthetic process	6	7.76 e ⁻¹¹	1.51 e ⁻⁷

Oxidative phosphorylation	6	1.36 e ⁻¹⁰	2.11 e ⁻⁷
Nucleoside phosphate biosynthetic process	7	1.86 e ⁻¹⁰	2.41 e ⁻⁷
Cytoplasmic translation	6	2.36 e ⁻¹⁰	2.62 e ⁻⁷
Proton motive force driven ATP synthesis	5	4.91 e ⁻¹⁰	4.76 e ⁻⁷
Ribosomal small subunit biogenesis	5	5.61 e ⁻¹⁰	4.84 e ⁻⁷
Aerobic respiration	6	7.26 e ⁻¹⁰	5.64 e ⁻⁷

Note: There was **no** subcluster pattern with significantly **increased** genes in cones.

(D) Retinal Ganglion Cells (RGCs): Three subclusters with 189 genes showing significant late **decrease** (day 5)

Pathways / Gene Set Name	# of Genes in Overlap	p-value	FDRq-value
Cytoplasmic translation	57	3.5 e ⁻⁹⁴	2.72 e ⁻⁹⁰
Organonitrogen compound biosynthetic process	91	1.62 e ⁻⁷¹	6.27 e ⁻⁶⁸
Peptide metabolic process	71	8.42 e ⁻⁶⁶	2.18 e ⁻⁶²
Peptide biosynthetic process	67	1.28 e ⁻⁶⁵	2.48 e ⁻⁶²
Amide biosynthetic process	67	3.34 e ⁻⁶¹	5.19 e ⁻⁵⁸
Cellular amide metabolic process	72	2.04 e ⁻⁵⁹	2.64 e ⁻⁵⁶
Cellular macromolecule biosynthetic process	69	9.66 e ⁻⁵⁶	1.07 e ⁻⁵²
Oxidative phosphorylation	34	1.82 e ⁻⁴⁸	1.77 e ⁻⁴⁵
Aerobic respiration	34	5.59 e ⁻⁴⁴	4.82 e ⁻⁴¹
Cellular respiration	35	2.7 e ⁻⁴²	2.09 e ⁻³⁹

Note: One subcluster pattern in RGCs with 20 genes showing significant late **increase** resulted in **no** GO-biological process overlaps.