

Table S14 - IPA canonical pathways unique to EGA3 super-group

Canonical Pathways	p-value <sup>a</sup>	Z-score <sup>b</sup>	Activation State	Total DEGs	Sub-Group
Mitochondrial Dysfunction	4.57E-09			19	EGA3-1
Oxidative Phosphorylation	7.94E-08			14	EGA3-1
LPS/IL-1 Mediated Inhibition of RXR Function	2.95E-03	-1.342		12	EGA3-1
ILK Signaling	9.77E-03	0		10	EGA3-1
Agranulocyte Adhesion and Diapedesis	2.14E-02			9	EGA3-1
Glucocorticoid Receptor Signaling	1.55E-02			6	EGA3-2
Regulation of Actin-based Motility by Rho	4.27E-02	2	Activated	5	EGA3-1
Hypoxia Signaling in the Cardiovascular System	2.19E-02			5	EGA3-1
TCA Cycle II (Eukaryotic)	1.51E-03			4	EGA3-1
Actin Nucleation by ARP-WASP Complex	4.47E-03			3	EGA3-2
Retinoic acid Mediated Apoptosis Signaling	5.89E-03			3	EGA3-2
Glioma Invasiveness Signaling	8.13E-03			3	EGA3-2
Regulation of Actin-based Motility by Rho	1.62E-02			3	EGA3-2
PPAR Signaling	1.86E-02			3	EGA3-2
Mitochondrial L-carnitine Shuttle Pathway	5.25E-03			3	EGA3-1
DNA Double-Strand Break Repair by Homologous Recombination	3.02E-03			2	EGA3-2
Methylglyoxal Degradation III	5.50E-03			2	EGA3-2
Endoplasmic Reticulum Stress Pathway	6.76E-03			2	EGA3-2
Semaphorin Signaling in Neurons	3.89E-02			2	EGA3-2
Cell Cycle Control of Chromosomal Replication	4.37E-02			2	EGA3-2
Glutamate Receptor Signaling	5.13E-04			2	EGA3-4
Interferon Signaling	5.37E-04			2	EGA3-3
Folate Polyglutamylation	4.37E-03			2	EGA3-1
Glycine Cleavage Complex	6.46E-03			2	EGA3-1
Arginine Degradation VI (Arginase 2 Pathway)	6.46E-03			2	EGA3-1
Ceramide Biosynthesis	8.91E-03			2	EGA3-1
Folate Transformations I	1.48E-02			2	EGA3-1

a) The p-value: statistical overlap of differentially expressed gene list and gene set

b) Z-score:  $z > 1.96$  to be significantly activated or increased, and those with  $z < -1.96$  to be significantly inhibited