

Supplemental Table 2: Number of Genes with Annotations for Each Database

<u>Mutant</u>	<u>Tissue</u>	<u>Timepoint</u>	<u>Upload List</u>	<u>GO:BP</u>	<u>Pathways</u>	<u>MPO</u>	<u>Disease</u>
<i>Nadk2</i>	Muscle	Early	557	512 (92%)	273 (49%)	461 (83%)	99 (18%)
<i>Nadk2</i>	Muscle	Late	932	737 (79%)	408 (44%)	604 (65%)	135 (15%)
<i>Nadk2</i>	Brain	Early	5	3 (60%)	2 (40%)	2 (40%)	0 (0%)
<i>Nadk2</i>	Brain	Late	1	0 (0%)	0 (0%)	0 (0%)	0 (0%)
<i>Pla2g6</i>	Muscle	Early	349	325 (93%)	167 (48%)	295 (85%)	63 (18%)
<i>Pla2g6</i>	Muscle	Late	52	49 (94%)	32 (62%)	43 (83%)	12 (23%)
<i>Pla2g6</i>	Brain	Early	14	10 (71%)	7 (50%)	10 (71%)	1 (7%)
<i>Pla2g6</i>	Brain	Late	10	6 (60%)	5 (50%)	5 (50%)	2 (20%)

Supplemental Table 2 – Annotation Statistics for Process and Pathway Enrichment. Differentially expressed genes with FDR < 0.05 and |Log2FC| > 1.5 for each mutant, tissue, and timepoint were uploaded to MouseMine.org, and annotations for each list were retrieved from the Gene Ontology Biological Process (GO:BP), Reactome Pathways (Pathways), Mammalian Phenotype Ontology (MPO), and Disease Ontology (Disease) databases on December 1, 2021. The number of genes with annotations and the percentage of uploaded genes with annotations are reported for each database / tool.