

Supplemental Table 5. Molecular pathways and cellular functions associated with significantly altered proteins in *Obscn-ΔIg58/59* atria at 6-months.

<i>Molecular Pathways</i>	
<i>D-myo-GJA (1,4,5,6)-Tetrakisphosphate Biosynthesis (1.64)</i>	
<i>ACP6</i>	Acid phosphatase 6, lysophosphatidic
<i>CAR3</i>	Carbonic anhydrase 3
<i>NUDT4</i>	Nudix (nucleoside diphosphate linked moiety X)-type motif 4
<i>D-myo-inositol (3,4,5,6)-tetrakisphosphate Biosynthesis (1.64)</i>	
<i>ACP6</i>	Acid phosphatase 6, lysophosphatidic
<i>CAR3</i>	Carbonic anhydrase 3
<i>NUDT4</i>	Nudix (nucleoside diphosphate linked moiety X)-type motif 4
<i>3-phosphoinositide Degradation (1.60)</i>	
<i>ACP6</i>	Acid phosphatase 6, lysophosphatidic
<i>CAR3</i>	Carbonic anhydrase 3
<i>NUDT4</i>	Nudix (nucleoside diphosphate linked moiety X)-type motif 4
<i>D-myo-inositol-5-phosphate Metabolism (1.55)</i>	
<i>ACP6</i>	Acid phosphatase 6, lysophosphatidic
<i>CAR3</i>	Carbonic anhydrase 3
<i>NUDT4</i>	Nudix (nucleoside diphosphate linked moiety X)-type motif 4
<i>3-phosphoinositide Biosynthesis (1.51)</i>	
<i>ACP6</i>	Acid phosphatase 6, lysophosphatidic
<i>CAR3</i>	Carbonic anhydrase 3
<i>NUDT4</i>	Nudix (nucleoside diphosphate linked moiety X)-type motif 4
<i>Superpathway of Inositol Phosphate Compounds (1.40)</i>	
<i>ACP6</i>	Acid phosphatase 6, lysophosphatidic
<i>CAR3</i>	Carbonic anhydrase 3
<i>NUDT4</i>	Nudix (nucleoside diphosphate linked moiety X)-type motif 4
<i>Cellular Functions</i>	
<i>Permeabilization of mitochondria (2.73)</i>	
<i>BCL2L13</i>	BCL2-like 13 (apoptosis facilitator)
<i>HK2</i>	Hexokinase 2
<i>PDIA3</i>	Protein disulfide isomerase associated 3
<i>Shape change of fibroblast cell lines (1.69)</i>	
<i>CD151</i>	CD151 antigen
<i>CORO1B</i>	Coronin, actin binding protein 1B
<i>SORBS1</i>	Sorbin and SH3 domain containing 1
<i>Termination of translation of protein (1.64)</i>	
<i>MRPL10</i>	Mitochondrial ribosomal protein L10
<i>MRPS28</i>	Mitochondrial ribosomal protein S28
<i>UPF1</i>	UPF1 regulator of nonsense transcripts homolog (yeast)
<i>Phagocytosis of myeloid cells (1.60)</i>	
<i>GLRX</i>	Glutaredoxin
<i>MFGE8</i>	Milk fat globule EGF and factor V/VIII domain containing (lactadherin)
<i>NHLRC2</i>	NHL repeat containing 2
<i>Transport of monosaccharide (1.51)</i>	

<i>HK2</i>	Hexokinase 2
<i>SORBS1</i>	Sorbin and SH3 domain containing 1
<i>STX16</i>	Syntaxin 16
<i>Phagocytosis of phagocytes (1.51)</i>	
<i>GLRX</i>	Glutaredoxin
<i>MFGE8</i>	Milk fat globule EGF and factor V/VIII domain containing (lactadherin)
<i>NHLRC2</i>	NHL repeat containing 2
<i>Cell viability of neurons (1.40)</i>	
<i>HK2</i>	Hexokinase 2
<i>PDIA3</i>	Protein disulfide isomerase associated 3
<i>UPF1</i>	UPF1 regulator of nonsense transcripts homolog (yeast)
<i>Permeability of vasculature (1.37)</i>	
<i>CAMK2D</i>	Calcium/calmodulin-dependent protein kinase II, delta
<i>CD151</i>	CD151 antigen
<i>MFGE8</i>	Milk fat globule EGF and factor V/VIII domain containing (lactadherin)

Significantly altered proteins and their corresponding gene symbols are listed under the molecular pathway and cellular functions they are associated with. The p-value for each molecular pathway and cellular function is represented as $-\text{Log}_{10}(\text{p-value})$.