

S4 Table. Gene ontology analysis for identified significant SNPs for the risk of NB using Database for Annotation, Visualization, and Integrated Discovery (DAVID)

GO ID	GO term	p-value	Corrected p-value	Associated gene
GO:0005319	Lipid transporter activity	0.0004	0.01	<i>SETX, TAP2, WRN</i>
GO:0060993	Kidney morphogenesis	0.0006	0.02	<i>EFNA5, PTPRD, SPARCL1</i>
GO:0010743	Regulation of macrophage derived foam cell differentiation	0.0007	0.02	<i>ASPM, LEF1, LRRK2</i>
GO:0010744	Positive regulation of macrophage derived foam cell differentiation	0.0008	0.02	<i>CSF1, HEXB, PDCD6IP, SYNE2</i>
GO:0050909	Sensory perception of taste	0.001	0.03	<i>AGT, PDCD6IP, SETX</i>
GO:0051782	Negative regulation of cell division	0.001	0.03	<i>ALDH1L1, ASPM, GAD2</i>
GO:0090077	Foam cell differentiation	0.002	0.04	<i>AGT, ASPM, NOL6, NRAP, PPARA</i>
GO:0010742	Macrophage derived foam cell differentiation	0.002	0.04	<i>HEXB, LRRK2, TMEM199</i>
GO:0043649	Dicarboxylic acid catabolic process	0.002	0.05	<i>HEXB, LRRK2, TMEM199</i>
GO:0099560	Synaptic membrane adhesion	0.002	0.05	<i>ASPM, PTCH1, WRN</i>
GO:0085029	Extracellular matrix assembly	0.00	0.06	<i>LEF1, PTCH1, TAS2R42, TNFRSF14, TRPM5</i>
GO:0097306	Cellular response to alcohol	0.01	0.11	<i>ANK1, DLG2, PDCD6IP</i>
GO:0055013	Cardiac muscle cell development	0.01	0.11	<i>ANK1, DLG2, PDCD6IP</i>
GO:0008347	Glial cell migration	0.01	0.10	<i>CHST11, HEXB, VCAN</i>
GO:0010611	Regulation of cardiac muscle hypertrophy	0.01	0.10	<i>CHST11, HEXB, VCAN</i>
GO:0014743	Regulation of muscle hypertrophy	0.01	0.11	<i>ANK1, DLG2, PDCD6IP</i>
GO:0030204	Chondroitin sulfate metabolic process	0.01	0.15	<i>AGT, APOB, CSF1</i>
GO:0072078	Nephron tubule morphogenesis	0.01	0.15	<i>AGT, IHH, SMAD3</i>
GO:0072088	Nephron epithelium morphogenesis	0.01	0.15	<i>AGT, PARP1, PPARA, SMAD3</i>
GO:0072028	Nephron morphogenesis	0.01	0.15	<i>AGT, APOB, CSF1, PPARA</i>
GO:0061333	Renal tubule morphogenesis	0.01	0.15	<i>AGT, APOB, CSF1, PPARA</i>
GO:0045332	Phospholipid translocation	0.01	0.14	<i>AGT, LAMA5, PTCH1</i>
GO:0050654	Chondroitin sulfate proteoglycan metabolic process	0.01	0.14	<i>ANO7, ATP10D, ATP8B3</i>
GO:0034204	Lipid translocation	0.01	0.13	<i>ANO7, ATP10D, ATP8B3</i>

GO:0097035	Regulation of membrane lipid distribution	0.02	0.15	<i>AGT, APOB, CSF1, PPARA</i>
GO:0045197	Establishment or maintenance of epithelial cell apical/basal polarity	0.02	0.16	<i>AGT, PARP1, PPARA, SMAD3</i>
GO:0038179	Neurotrophin signaling pathway	0.02	0.14	<i>AGT, FRAS1, LAMA5, LRRK2, PTCH1, WNK4</i>
GO:0051646	Mitochondrion localization	0.02	0.14	<i>AGT, LAMA5, PTCH1, WNK4</i>
GO:0050912	Detection of chemical stimulus involved in sensory perception of taste	0.02	0.14	<i>AGT, LAMA5, PTCH1, WNK4</i>
GO:0061245	Establishment or maintenance of bipolar cell polarity	0.02	0.14	<i>AGT, LAMA5, PTCH1, WNK4</i>
GO:0035088	Establishment or maintenance of apical/basal cell polarity	0.02	0.14	<i>AGT, LAMA5, PTCH1, WNK4</i>
GO:0003678	DNA helicase activity	0.03	0.13	<i>ABCA10, ABCA6, AKR1C4, ANO7, APOB, ATP10D, ATP8B3, SLC27A4</i>
GO:0001658	Branching involved in ureteric bud morphogenesis	0.03	0.11	<i>ANO7, ATP10D, ATP8B3</i>
GO:0080171	Lytic vacuole organization	0.03	0.09	<i>PTCH1, TAS2R42, TNFRSF14</i>
GO:0007040	Lysosome organization	0.03	0.09	<i>CEMIP, HEXB, VCAN</i>
GO:0007405	Neuroblast proliferation	0.03	0.06	<i>EFNA5, MAP4K1, PTCH1, UGGT1, WRN</i>
GO:0006027	Glycosaminoglycan catabolic process	0.03	0.06	<i>BRAT1, LRRK2, SETX</i>

SNP, single nucleotide polymorphism; NB, neuroblastoma.