

Table 4S. Analysis of copper-related gene expression patterns in 5-week-old *Npc1*^{+/+} and *Npc1*^{-/-} mice

Genotype/diet ^a	<i>Ctrl</i>	<i>Atox</i>	<i>Atp7b</i>	<i>Cp</i>	<i>Commd1</i>	<i>Mt1</i>
<i>Npc1</i> ^{+/+} CuA	135.4±6.7 ^b	454.1±35.0	52.6±5.8	873.0±71.3	110.7±5.8	110.0±4.1
<i>Npc1</i> ^{+/+} CuD	153.0±8.2	513.5±23.4	48.2±5.8	770.6±54.7	99.4±6.8	100.0±7.1
<i>Npc1</i> ^{-/-} CuA	150.9±11.8	362.7±32.7	63.5±4.7	1018.2±70.0	105.4±7.3	154.0±11.7
<i>Npc1</i> ^{-/-} CuD	167.3±7.0	411.7±30.0	61.3±3.8	762.6±48.4*	123.1±8.8	66.0±2.1*

^aControl diet (CuA) and copper-deficient diet (CuD).

^bNormalized transcript abundance, expressed as mean ±SEM.

**p* < 0.05 for differences between diets (Mann Whitney-U test), n=5.