

Table 3S. Analysis of iron-related gene expression patterns in 4- and 7-week-old *Npc1*^{+/+} and *Npc1*^{-/-} mice.

Genotype/diet ^a	<i>TfR</i>	<i>FtH</i>	<i>FtL</i>	<i>Dmt1</i>	<i>Fpn</i>	<i>Hepc</i>
<i>Npc1</i> ^{+/+} BM	1127.6±73.5 ^b	3157.2±530.0	3509.4±162.6	31.9±2.7	1317.4±150.5	2434.2±241.6
<i>Npc1</i> ^{-/-} BM	1418.1±67.1*	3094.7±214.5	2584.9±221.9*	36.8±6.4	853.8±60.8*	3229.7±206.9*
<i>Npc1</i> ^{+/+} CuA	1051.4±63.4	3593.9±365.3	2566.1±29.7	30.0±1.3	1250.5±158.7	2388.2±182.1
<i>Npc1</i> ^{-/-} CuA	1841.2±285.0*	3221.9±137.1	2161.6±143.2*	26.5±2.6	800.9±36.9*	1768.2±203.3*

^aBreast milk (BM), control diet (CuA).

^bNormalized transcript abundance, expressed as mean ±SEM.

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