

## Supplementary Table 2

Sample	Raw GR CHIP-ddPCR data (copies/ $\mu$ l)			Normalisation factors		Normalised <i>Slc3a1</i> site data (copies/ $\mu$ l)	
	Slc3a1 site	Background region	Spike-in	Using background region	Using spike-in	Using background region	Using spike-in
A	36.454	17.783	14.242	0.210	0.516	7.673	18.808
B*	13.864	3.743	7.348	1.000	1.000	13.864	13.864
C	12.437	3.877	7.582	0.965	0.969	12.008	12.054
D	6.155	1.107	2.427	3.380	3.028	20.807	18.637
E	5.624	3.272	2.971	1.144	2.473	6.433	13.909
F	9.593	3.051	2.682	1.227	2.740	11.768	26.282

\*Here, the background and spike-in counts for sample B are nominally chosen as the numerators for calculating other normalisation factors.

Legend: Table showing the raw GR CHIP-ddPCR data (copies/ $\mu$ l) for 6 mouse liver chromatin samples, for a site on chromosome 17 associated with *Slc3a1*, a background (negative) region, and for the spike-in control. Normalisation factors produced from either the background or spike-in values, and the subsequent normalised *Slc3a1* counts are also shown, employing the calculation workflow illustrated in Supplementary Figure 1.