**S1 Table: Summary of association results for liver Slc22a1 mRNA expression with relevant traits among inbred strains of mice.**

|  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- |
| **Mouse Sex** | **Tissue** | **Gene** | **Trait** | **bicor** | **p value** |
| Male | Liver | Slc22a1 | Liver Wt | 0.28710 | 0.00001 |
| Male | Liver | Slc22a1 | Liver/NMR\_Mass\_8wks | 0.22799 | 0.00055 |
| Male | Liver | Slc22a1 | Triglycerides (liver) | 0.28966 | 0.00195 |
| Male | Liver | Slc22a1 | Fat Mass\_Percent Growth\_2 to 4 wks | -0.20046 | 0.00361 |
| Male | Liver | Slc22a1 | Fat Mass\_Percent Growth\_2 to 8 wks | -0.24932 | 0.00022 |
| Male | Liver | Slc22a1 | Fat Mass\_Percent Growth\_2 to 6 wks | -0.21814 | 0.00163 |
| Male | Liver | Slc22a1 | Fat Mass\_Percent Growth\_4 to 8 wks | -0.20299 | 0.00243 |
| Male | Liver | Slc22a1 | Fat Mass\_Percent Growth\_6 to 8 wks | -0.26390 | 0.00008 |
| Male | Liver | Slc22a1 | BF\_Percent Growth\_0 to 4 wks | -0.20476 | 0.00249 |
| Male | Liver | Slc22a1 | BF\_Percent Growth\_0 to 6 wks | -0.21771 | 0.00128 |
| Male | Liver | Slc22a1 | BF\_Percent Growth\_0 to 8 wks | -0.23787 | 0.00033 |
| Male | Liver | Slc22a1 | BF\_Percent Growth\_2 to 4wks | -0.26685 | 0.00011 |
| Male | Liver | Slc22a1 | BF\_Percent Growth\_2 to 6wks | -0.27034 | 0.00008 |
| Male | Liver | Slc22a1 | BF\_Percent Growth\_2 to 8wks | -0.29944 | 0.00001 |
| Male | Liver | Slc22a1 | BF\_Percent Growth\_6 to 8 wks | -0.25616 | 0.00014 |
| Female | Liver | Slc22a1 | Gonadal Fat Wt | -0.21670 | 0.00176 |
| Female | Liver | Slc22a1 | Visceral Fat | -0.19663 | 0.00472 |
| Female | Liver | Slc22a1 | Visceral Fat/NMR\_Mass\_8wks | -0.19662 | 0.00472 |
| Female | Liver | Slc22a1 | Gonadal\_Fat/NMR\_Mass\_8wks | -0.21762 | 0.00168 |

\* The data were obtained from previous studies conducted by Aldon J. Lusis laboratory[1-3]. Correlations were calculated with the biweight midcorrelation (bicor), which is robust to outliers and was used in the studies performed by Aldons J. Lusis laboratory[1]. A positive bicor means that the higher expression level of Slc22a1 mRNA is associated with higher levels of the measured trait. A negative bicor means that the higher expression level of Slc22a1 mRNA is associated with lower levels of the measured trait.

**Supplemental references**

1. Hui, S.T., et al., *The genetic architecture of NAFLD among inbred strains of mice.* Elife, 2015. **4**: p. e05607.

2. Parks, B.W., et al., *Genetic control of obesity and gut microbiota composition in response to high-fat, high-sucrose diet in mice.* Cell Metab, 2013. **17**(1): p. 141-52.

3. Parks, B.W., et al., *Genetic architecture of insulin resistance in the mouse.* Cell Metab, 2015. **21**(2): p. 334-46.