Author Correction: Defining the consequences of genetic variation on a proteome-wide scale

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In this Article, the sample identifiers for two consecutive tandem mass tag (TMT) 10-plexes in the proteomics dataset were inadvertently swapped. We corrected the 18 affected sample identifiers for which we could verify their identity by comparison with the RNA-sequencing data and removed two ambiguous samples. We then re-analysed the corrected dataset and compared the protein quantitative trait loci (pQTL) and mediation results with those originally reported. We verified that every specific pQTL and mediator–target interaction highlighted in the original Article replicated successfully in the new analysis with the corrected proteomics dataset. We identify more significant local and distant pQTLs with the corrected dataset. Nearly 97% of reported local pQTLs replicate after correcting for the sample swaps, and we detect 439 additional significant local pQTLs. Distant pQTLs replicated at a much lower rate, consistent with the replication rate we estimated for distant eQTL (Extended Data Fig. 4) and those reported for other eQTL datasets of similar size[1]. Highly significant distant pQTL replicated at much higher rates, and every distant pQTL individually highlighted in the Article successfully replicated in the corrected dataset. Finally, correcting for the sample swaps resulted in more mediator proteins being identified for more distant pQTL. In summary, the results from our re-analysis of the corrected dataset reinforce the conclusions made in the original Article. We have updated Supplementary Tables 3, 5 and 8 (proteomics dataset, list of pQTLs and mediation results, respectively) of the original Article to reflect these corrections (see Supplementary Information to this Amendment). We regret the oversight and are grateful to B. Zhang and colleagues for bringing it to our attention. The original Article has not been corrected online.

1. Strunz, T. et al. A mega-analysis of expression quantitative trait loci (eQTL) provides insight into the regulatory architecture of gene expression variation in liver. *Sci. Rep.* **8**, 5865 (2018).

Supplementary information is available in the online version of this Amendment.