

Figure S2

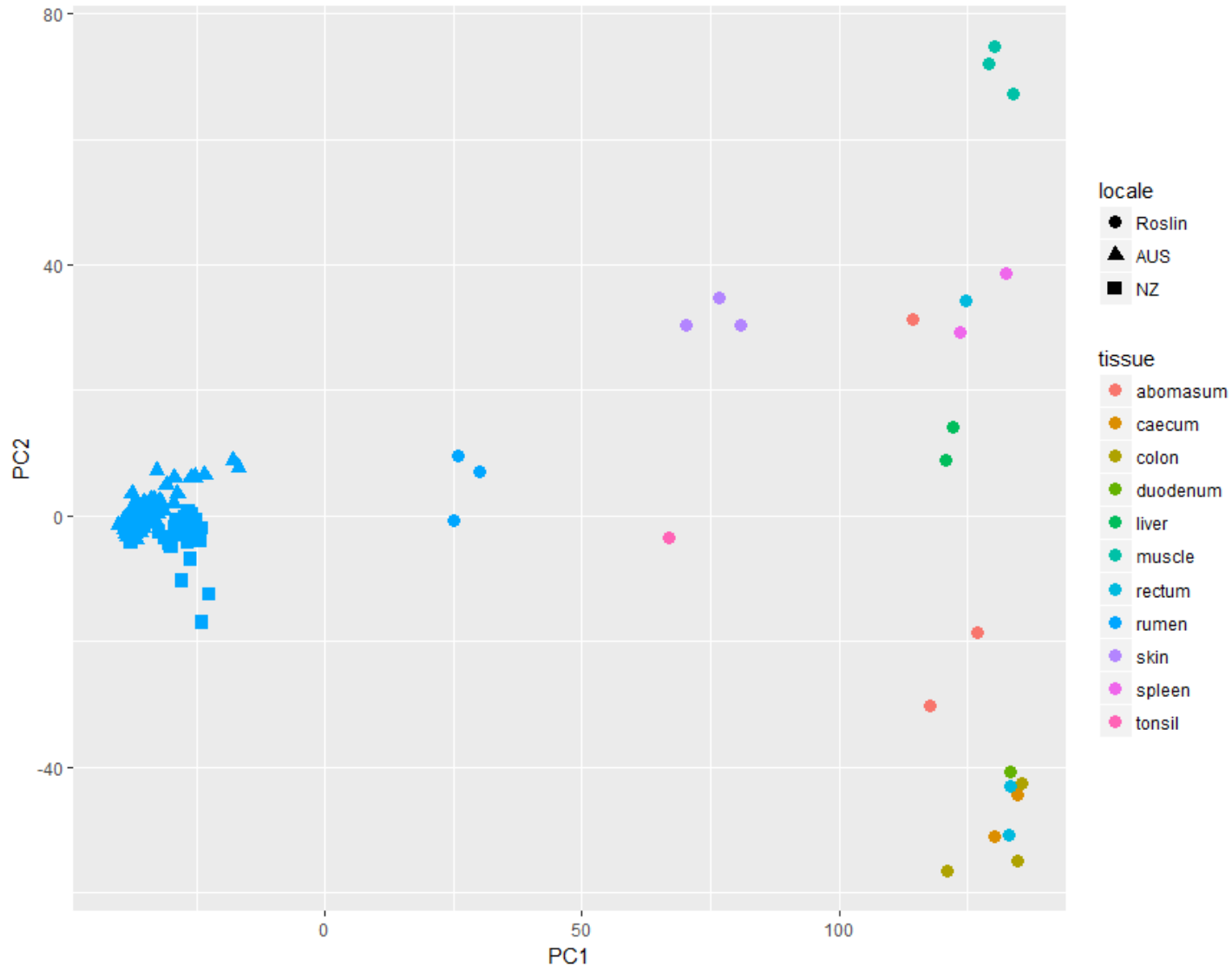


Figure S2: PCA plot of transcriptome data of AUS and NZ with data generated by Roslin institute in studies of [1] and [2]. PCA data were calculated using DESeq2 [3] using default settings.

[1] Jiang, Y., Xie, M., Chen, W., Talbot, R., Maddox, J.F., Faraut, T., et al. (2014). The sheep genome illuminates biology of the rumen and lipid metabolism. *Science* 344(6188), 1168-1173.

[2] Xiang, R., Oddy, V.H., Archibald, A.L., Vercoe, P.E., and Dalrymple, B.P. (2016). Epithelial, metabolic and innate immunity transcriptomic signatures differentiating the rumen from other sheep and mammalian gastrointestinal tract tissues. *PeerJ* 4, e1762.

[3] Love, M.I., Huber, W., and Anders, S. (2014). Moderated estimation of fold change and dispersion for RNA-seq data with DESeq2. *Genome biology* 15(12), 550.