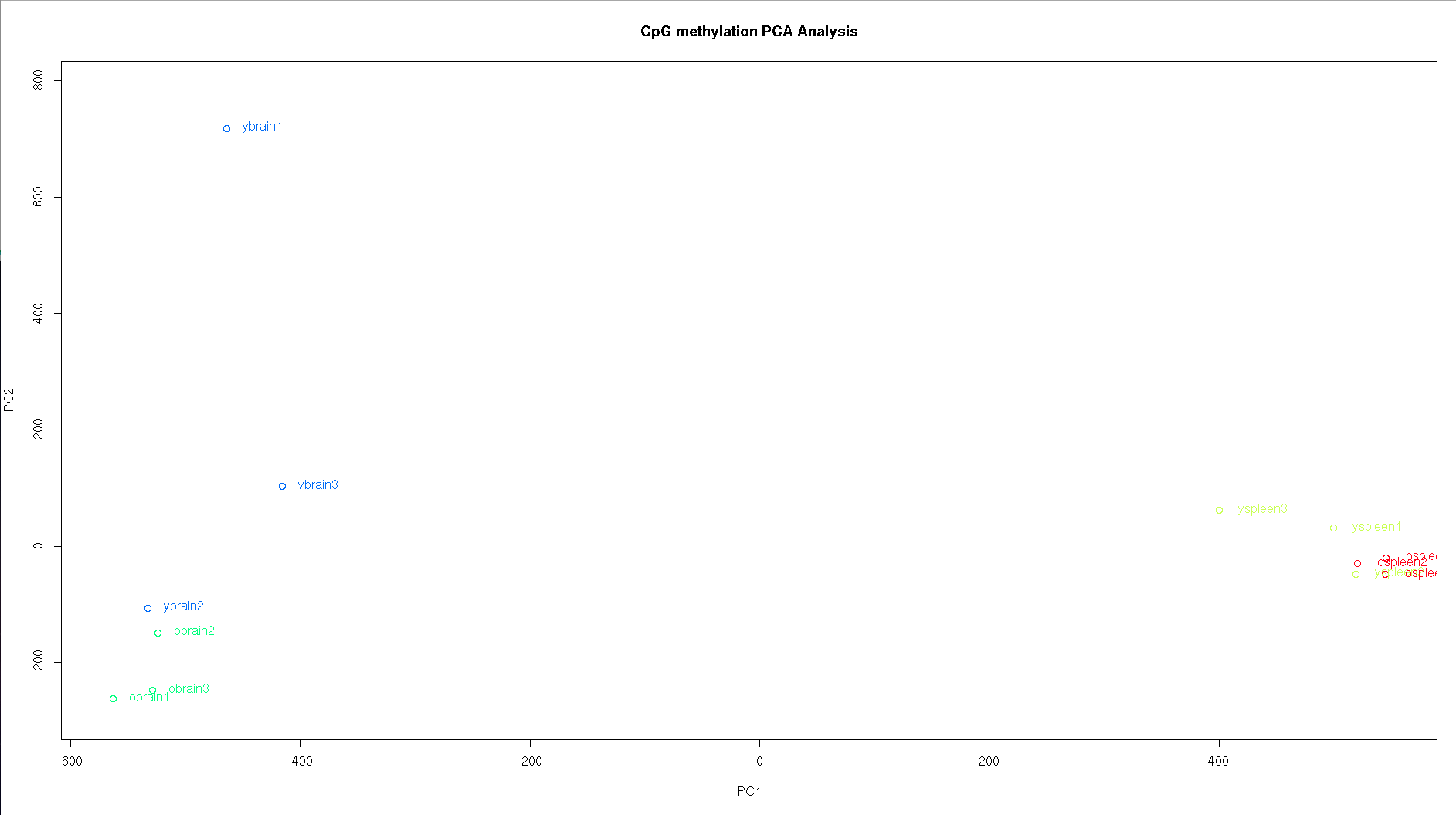
**Supplementary Figure 1 (S1 Fig). Principal component analysis.** Sequencing results generating sample-specific methylation profiles were clustered by principal component analysis according to differentially methylated cytosines (DMCs). As expected, given the large number of tissue-specific DMCs, the tissue types clustered quite distinctly with less resolution due to age. ****