

Figure S1 Density plot of read lengths for all three kits and tissues respectively by site.
Site 2 sequenced to a length of 76 nts, whereas all of Site1 samples were sequenced to <=50 nts.

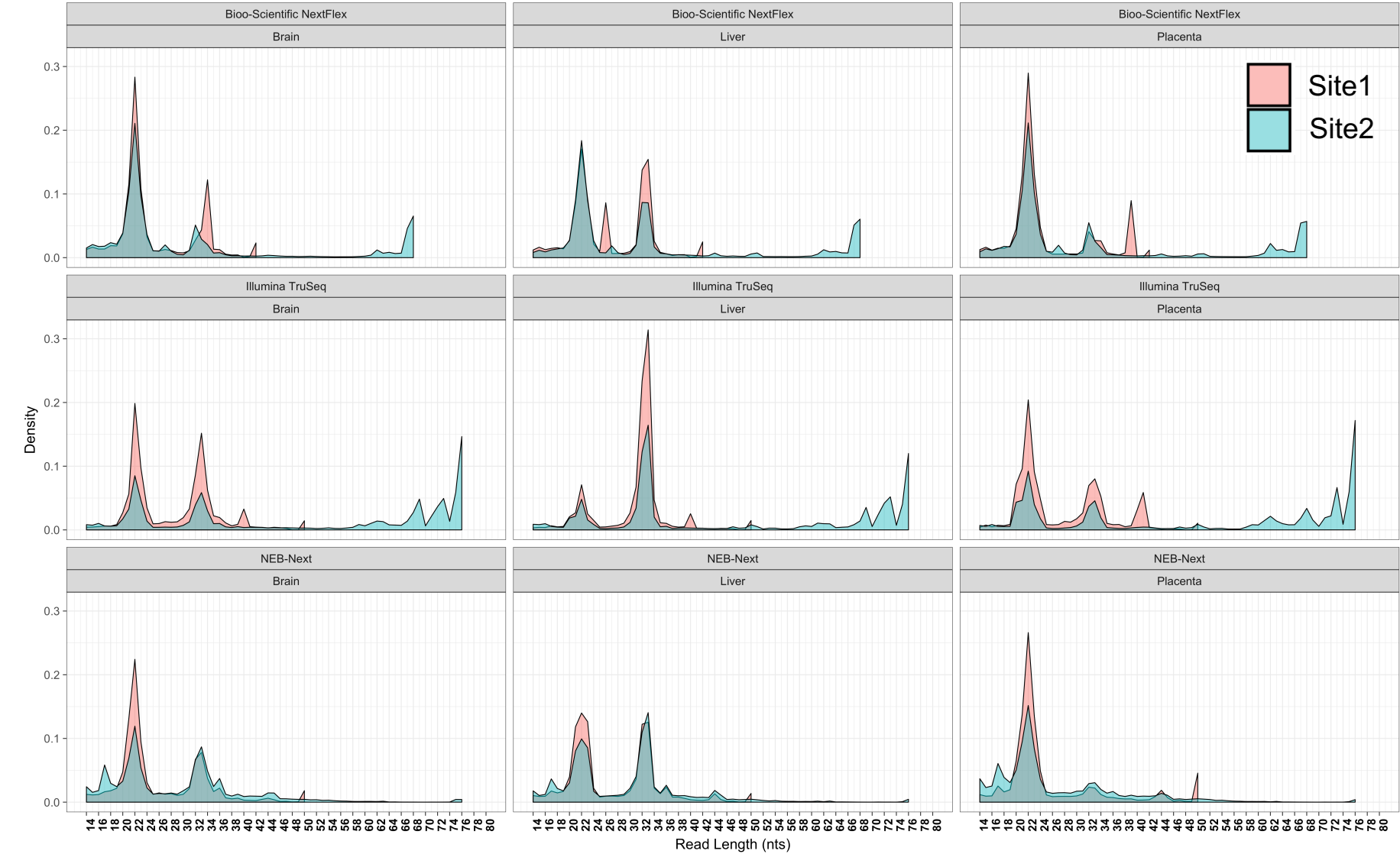


Figure S2 Comparison of percentage of reads assigned to the various RNA biotypes for read length restricted to less than 50 nts versus read length = 76 nts. Site2 sequenced to a length of 76 nts.

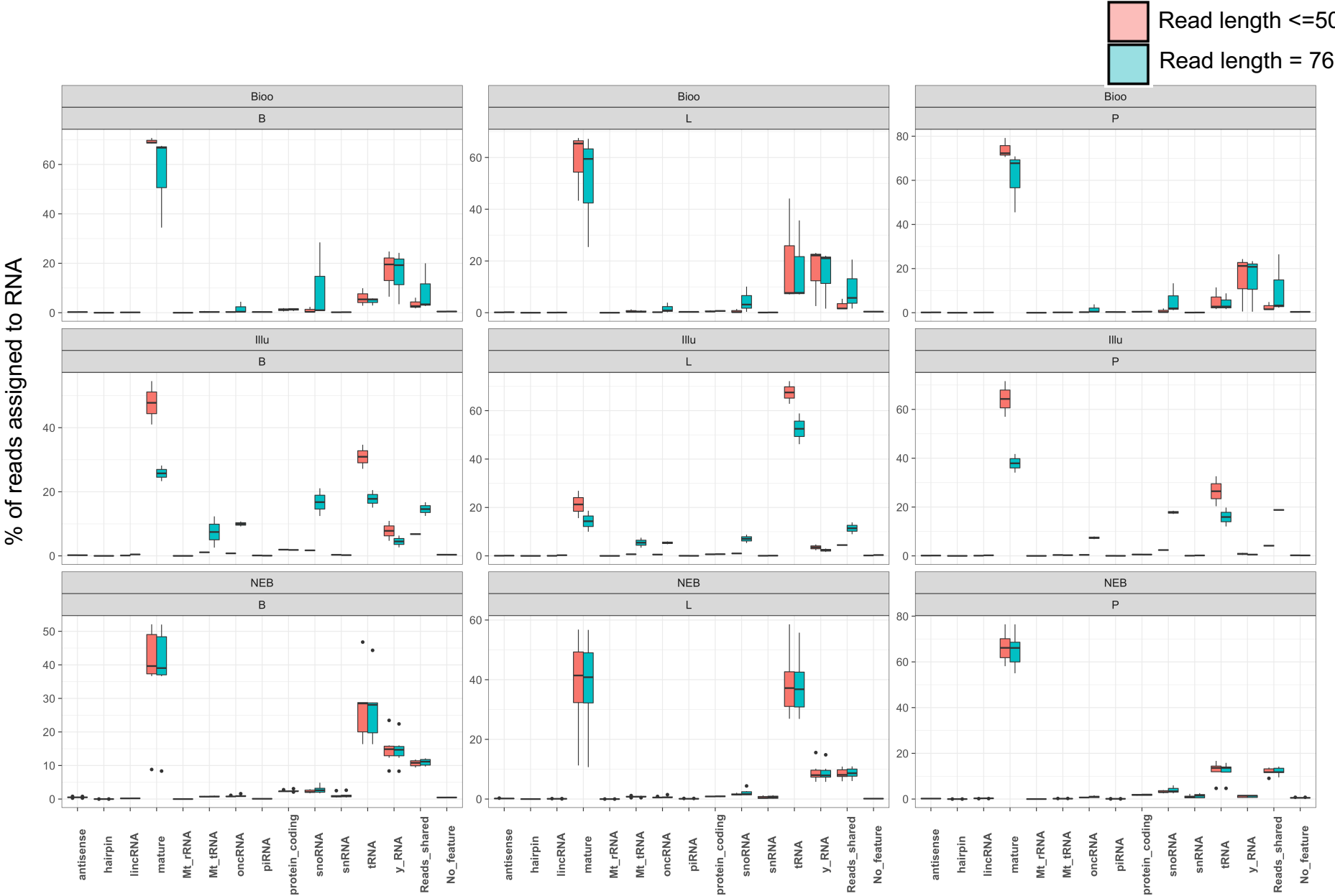


Figure S3. CA plot showing that the BiooScientificNextFlexsamples from Site2 cluster by themselves indicating a batch effect. Also, th

