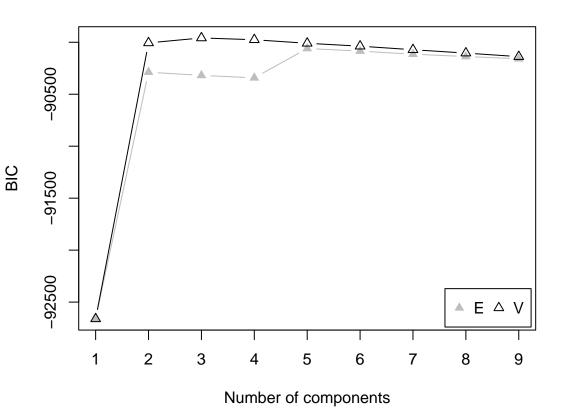
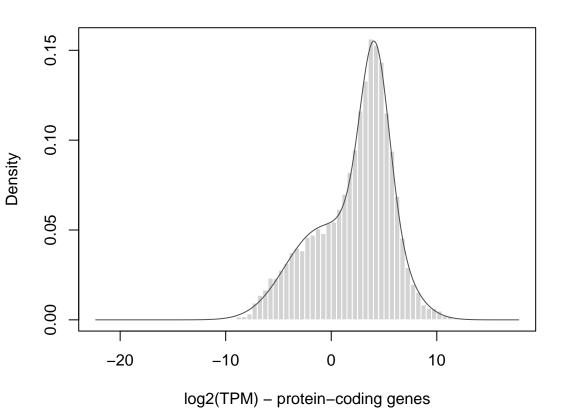
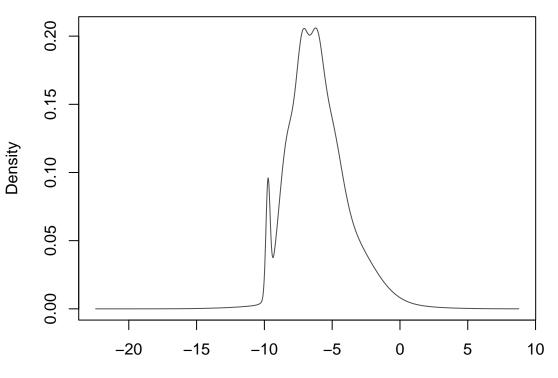


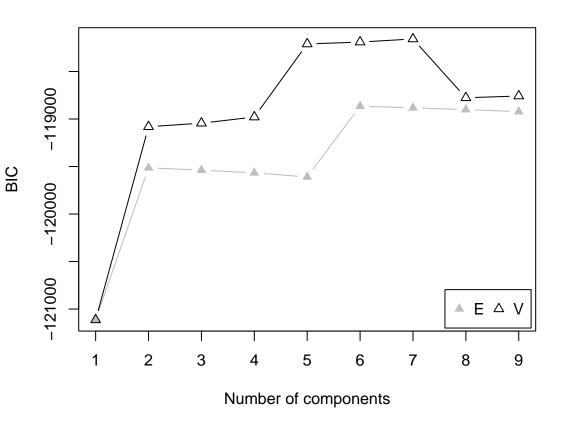
 $log2 (summed\_filtered\$tpm[summed\_filtered\$biotype~\%in\%~"protein\_coding"]$ 

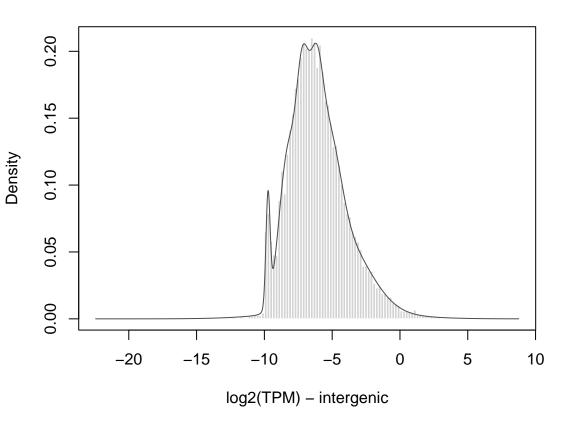






log2(summed\_filtered\$tpm[summed\_filtered\$type == "intergenic"])





## esophagus (3 libraries)

