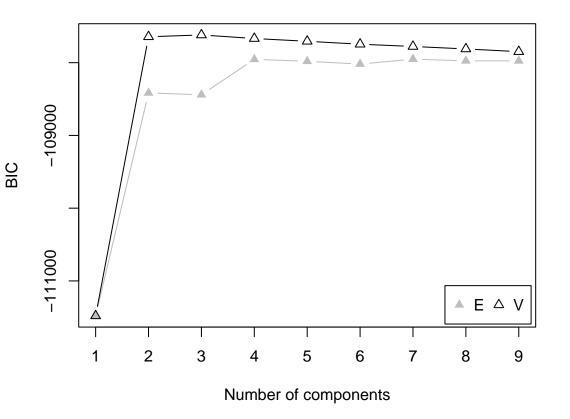
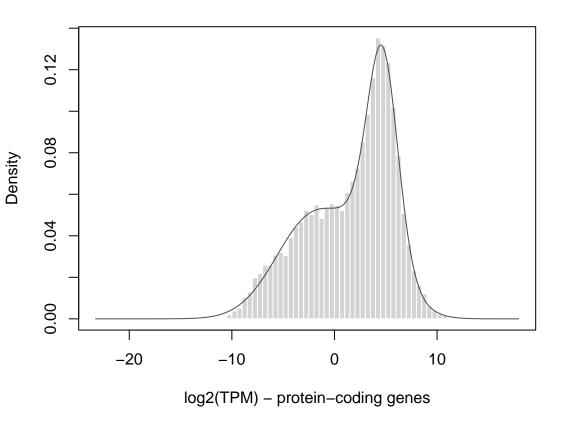
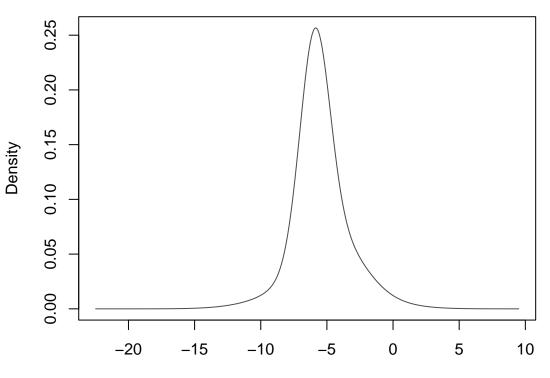


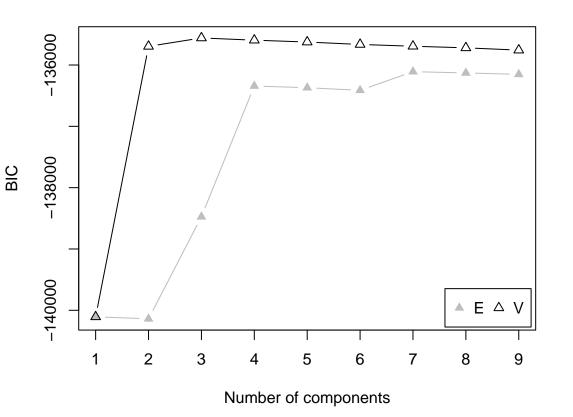
 $log2 (summed_filtered\$tpm[summed_filtered\$biotype~\%in\%~"protein_coding"]$

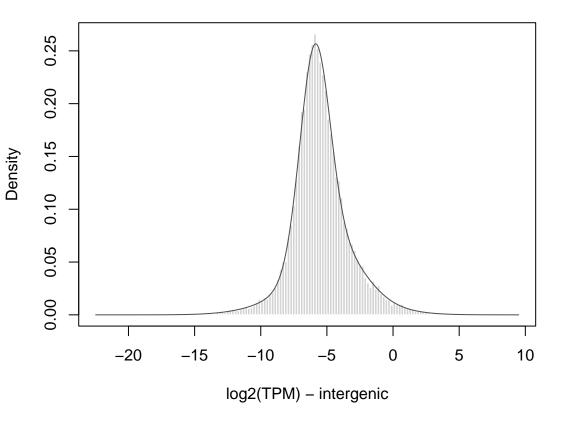




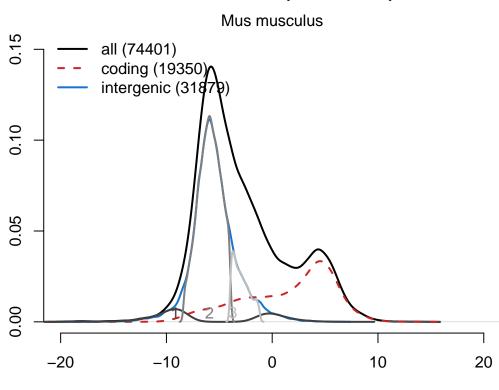


log2(summed_filtered\$tpm[summed_filtered\$type == "intergenic"])





Ammon's horn (25 libraries)



log2(TPM)

Density