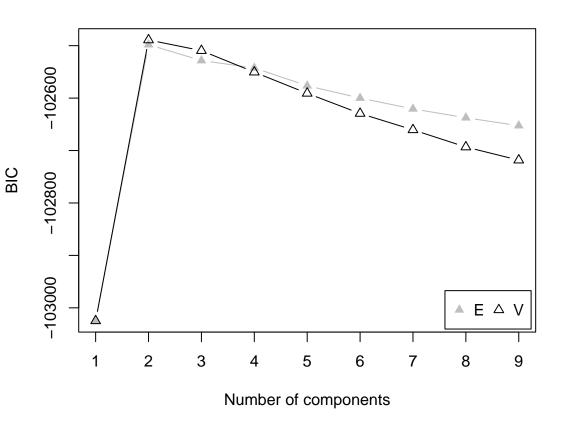
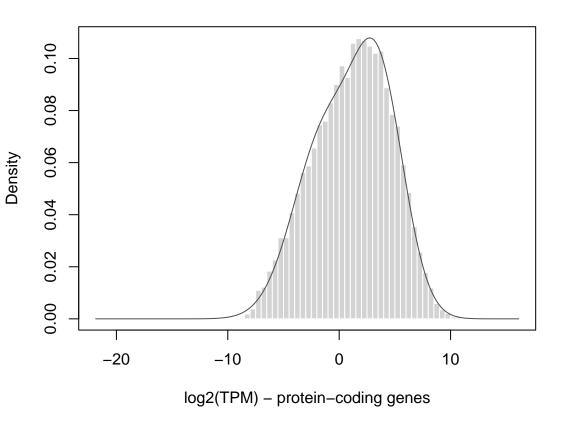
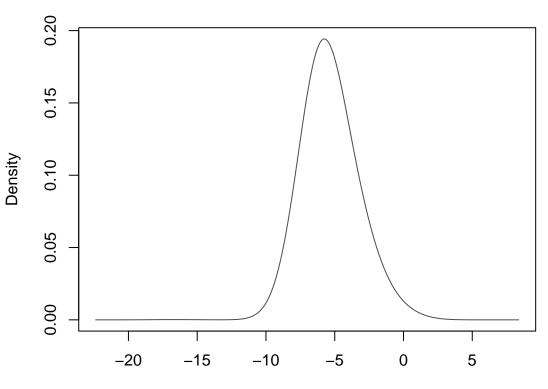


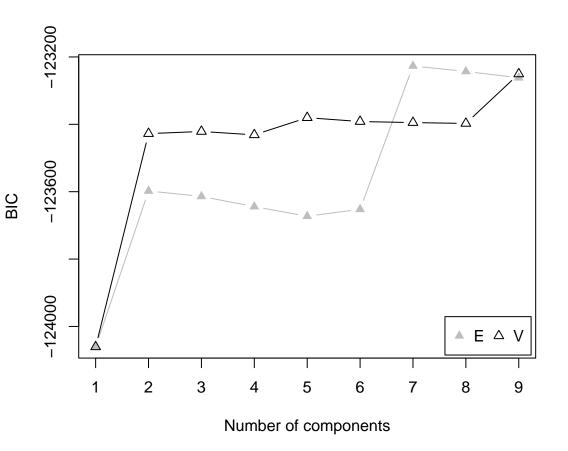
log2(summed\_filtered\$tpm[summed\_filtered\$biotype %in% "protein\_coding"]

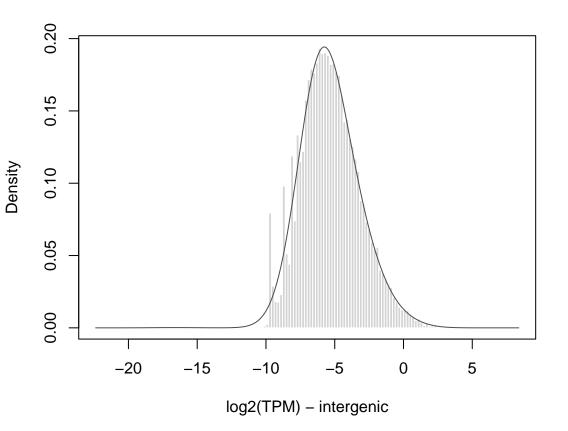






log2(summed\_filtered\$tpm[summed\_filtered\$type == "intergenic"])





## spermatid (1 libraries)

