Supplementary Figure 1

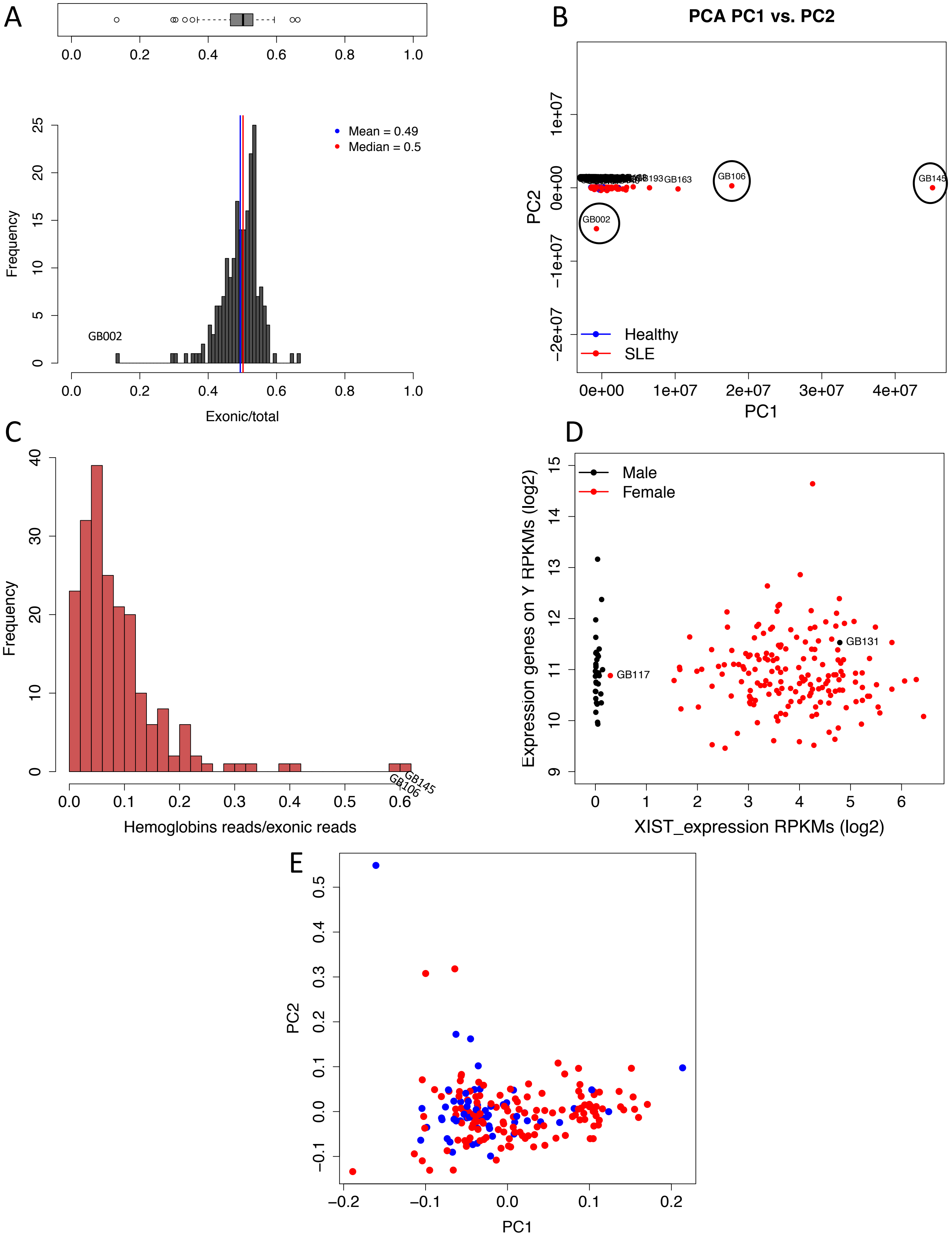

Figure S1. Quality control of RNA-sequencing and genotyping data

(**A**) Fraction of reads mapping to exons per sample. The vertical red line indicates the median and the blue the mean. Samples with less than 0.2 exonic/total reads were considered as technical outliers. (**B**) PCA of gene expression of all the samples. Samples in circles were considered as technical outliers. **(C)** Proportion of reads mapped to haemoglobin genes. Samples above 0.5 were considered as technical outliers (same samples as in B). **(D)** Gender-specific expression: in x-axis RPKMs (log2) of the female specific *XIST* gene versus the sum of RPKMS (log2) of the genes in Y chromosome excluding genes mapped in the pseudo-autosomal region. **(E)** PCA on genotype data to account for genetic ancestry for SLE (red) and healthy (blue) individuals.