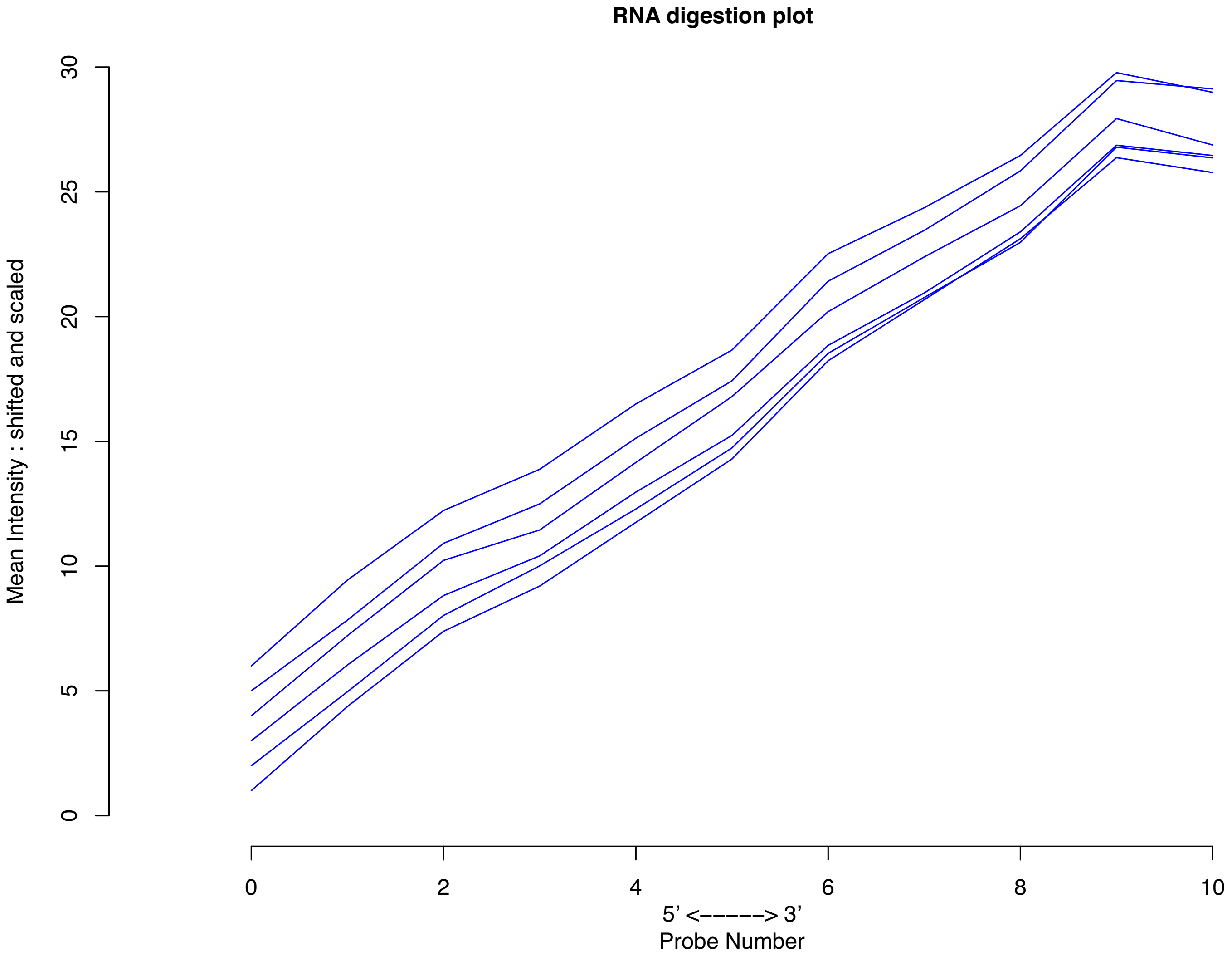
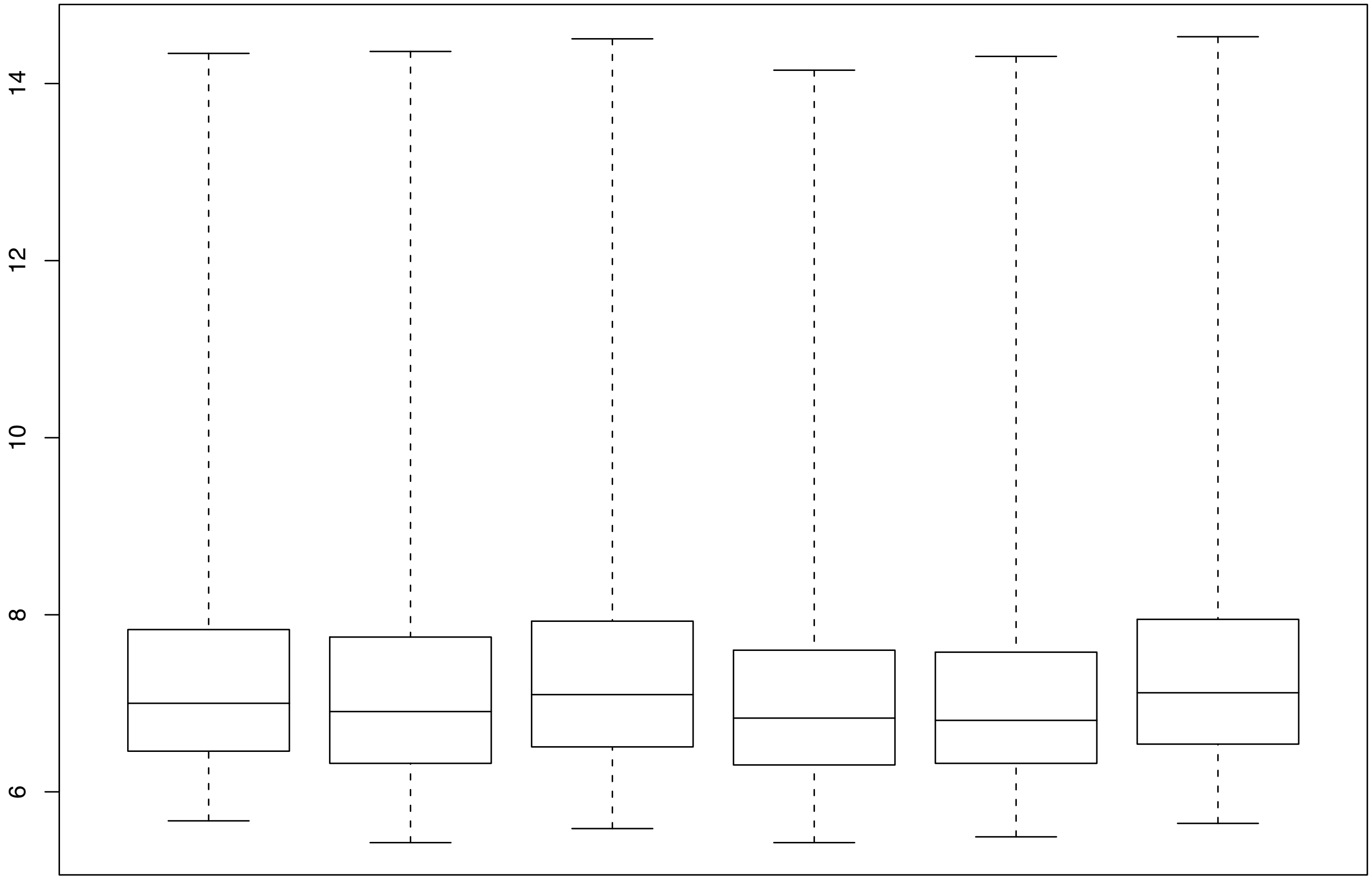
Supplementary Figure 1 (1/4)

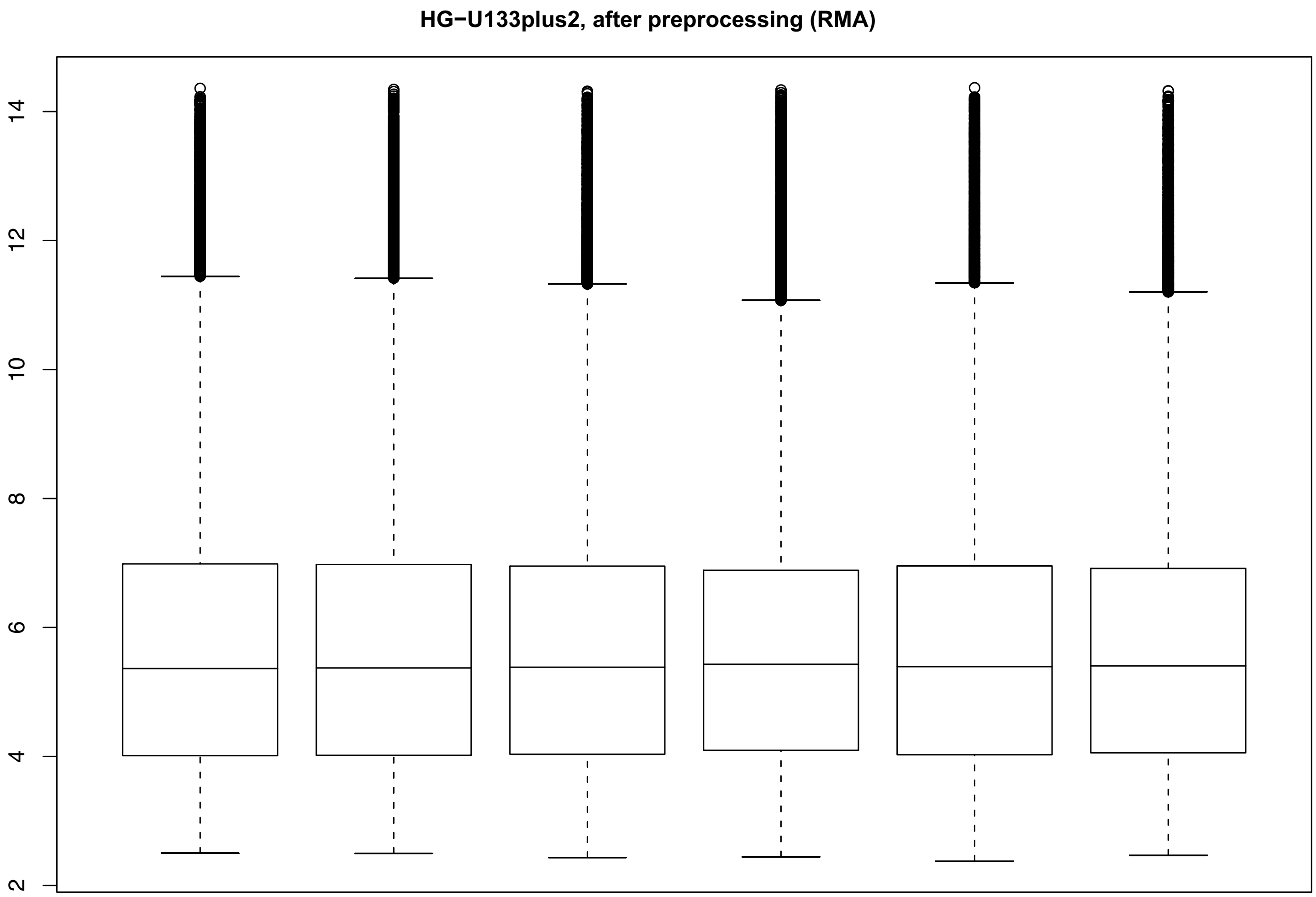


Supplementary Figure 1 (2/4)

U133 plus 2, before preprocessing

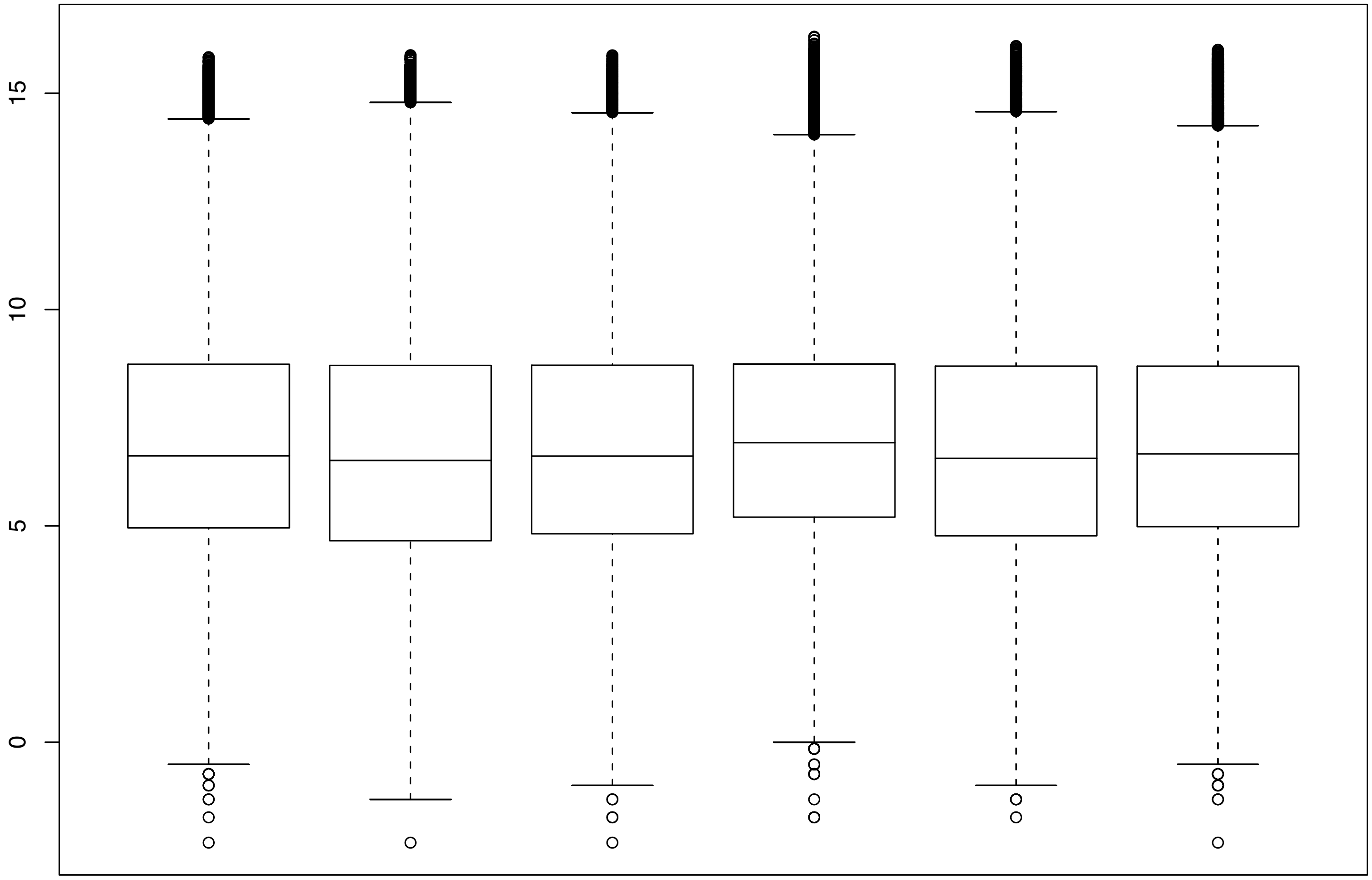


Supplementary Figure 1 (3/4)

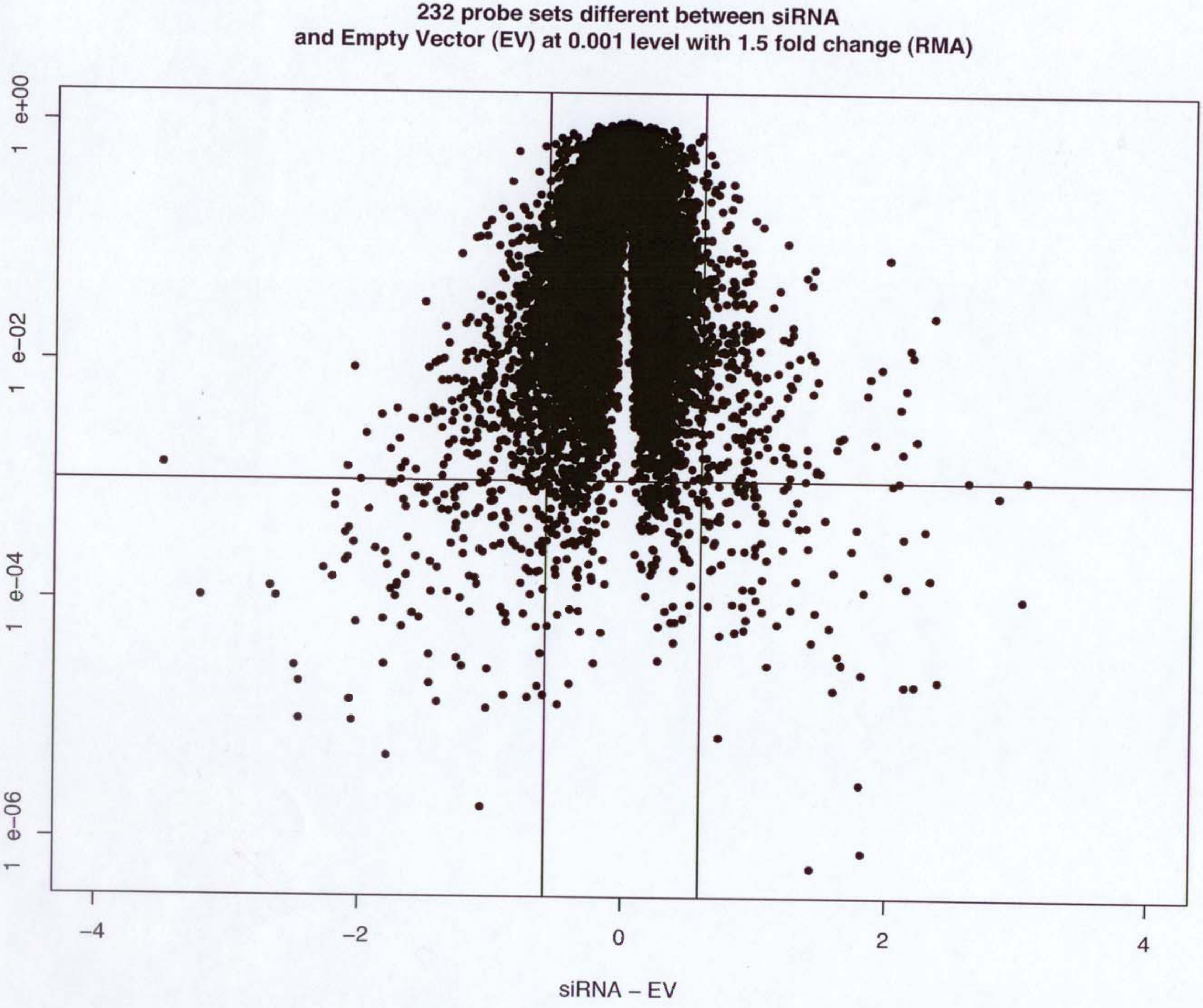


Supplementary Figure 1 (4/4)

HG−U133plus2, after preprocessing (GCOS)



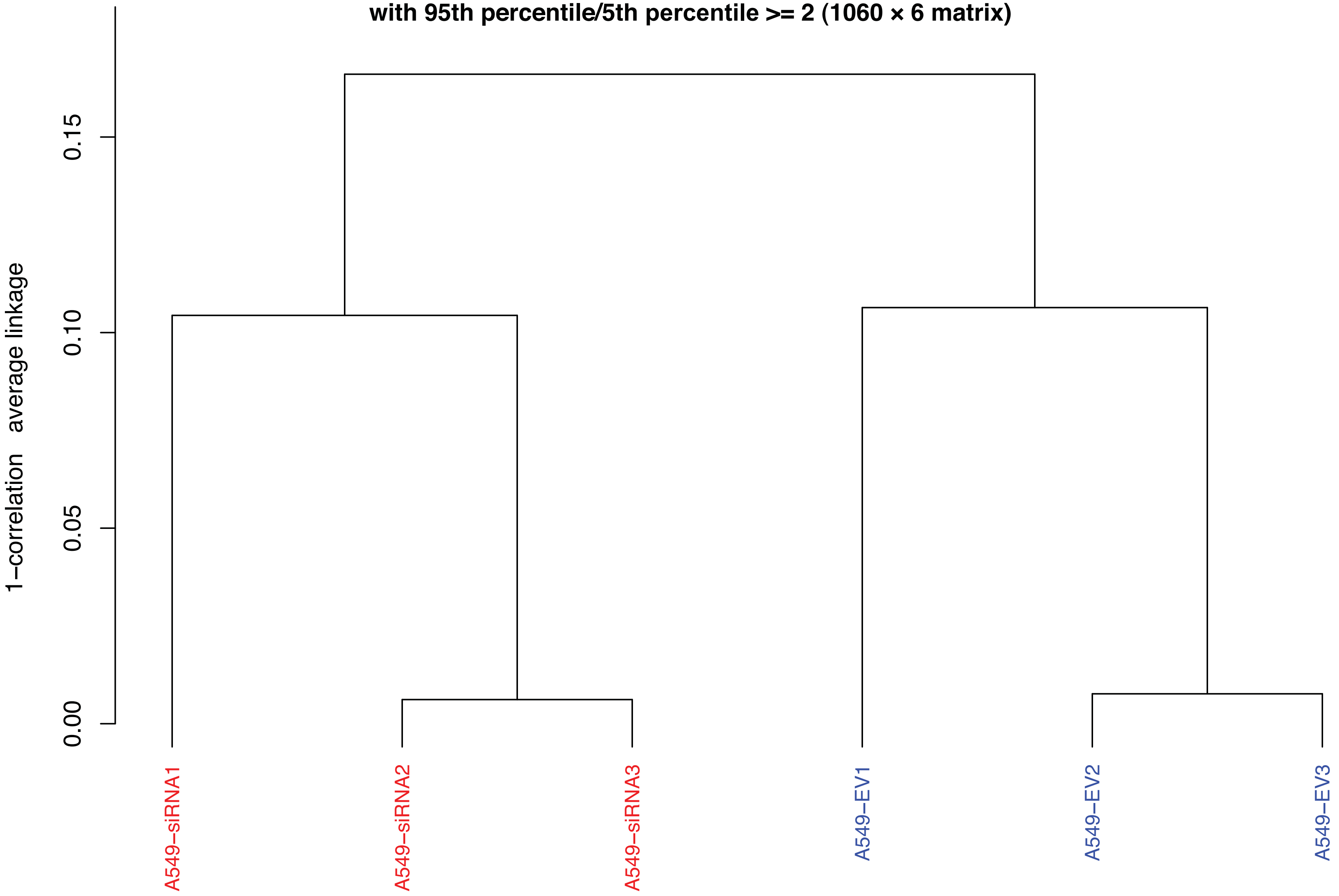
Supplementary Figure 2



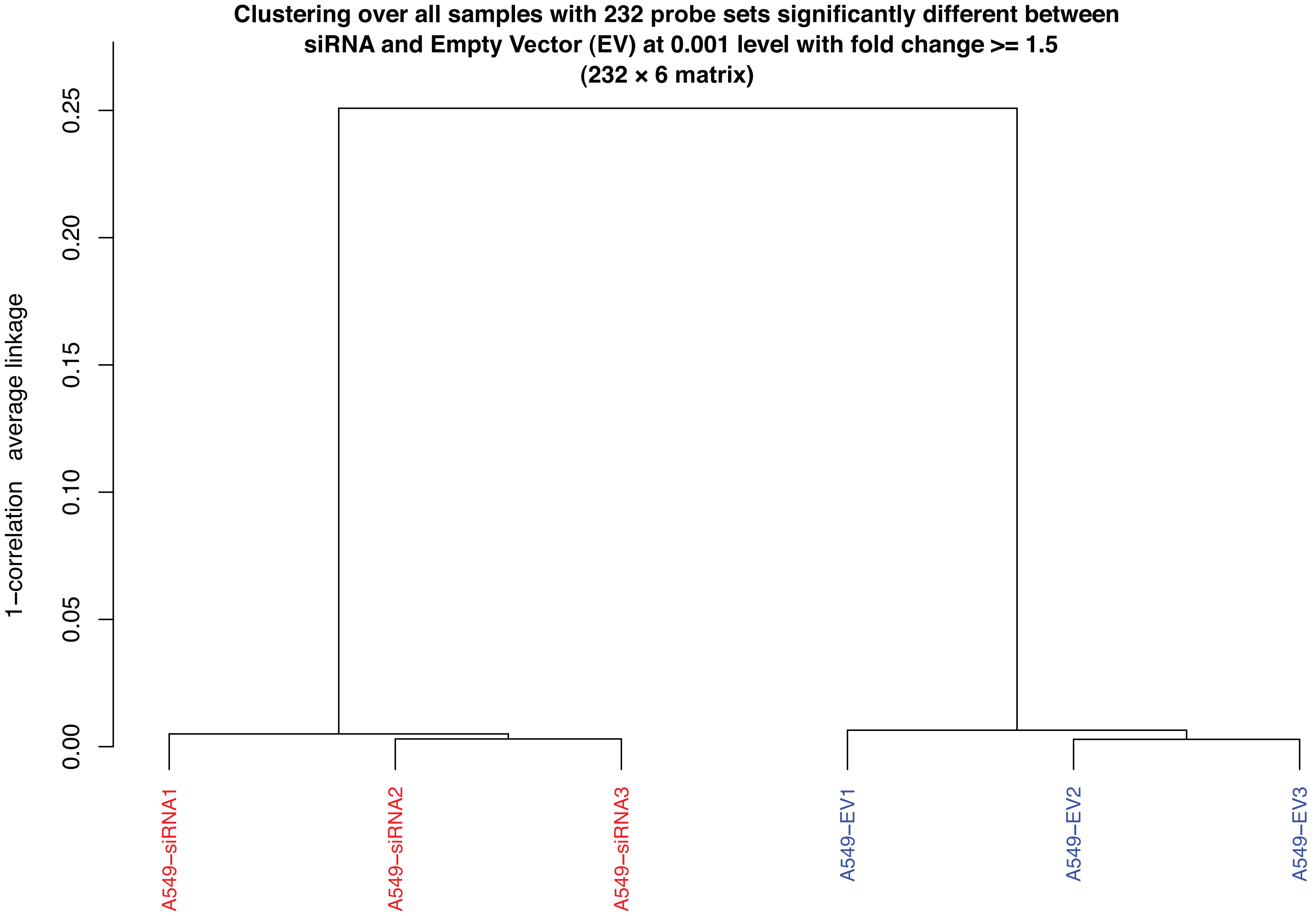
232 probe sets different between siRNA
and Empty Vector (EV) at 0.001 level with 1.5 fold change (RMA)

Supplementary Figure 3 (1/3)

Clustering over all samples of 1060 filtered probe sets
with 95th percentile/5th percentile >= 2 (1060 × 6 matrix)



Supplementary Figure 3 (2/3)



Supplementary Figure 3 (3/3)

Clustering over all samples with 232 probe sets significantly different between siRNA and Empty Vector (EV) at 0.001 level with fold change >= 1.5
Genes are control mean subtracted (232 × 6 matrix)