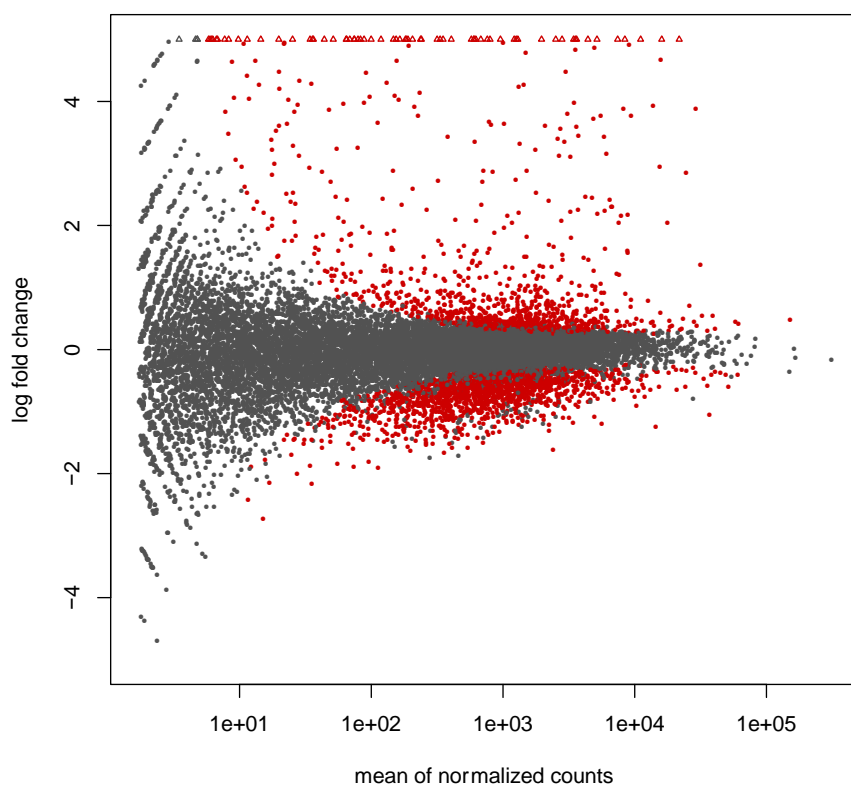


**Supplementary Figure S1.** MA plot providing the two-groups comparison. Each gene is represented as a single dot, where red dots stand for genes with p-adj value<0.01. X axis pictures represent the average expression over all samples, whereas the Y axis shows the  $\log_2$ FC between treatment with siRNA against TG2-lncRNA and siRNA neg (the control).



**Supplementary Figure S2.** Principal Component Analysis (PCA) of normalized read counts obtained from DESeq2 R package output. For each group (“MT” and “WT”), sample to sample distances comprises approximately 84% of variance, providing clustering information based on samples condition.

