Supplementary Figure S6:   Quality control of RNA sequencing data from HTG EdgeSeq
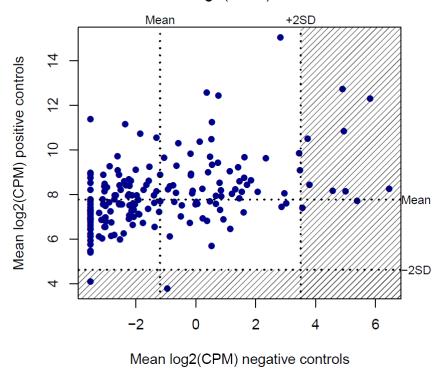
RNA-Seq reads were transformed to counts-per-million and the mean of five negative and four positive internal controls calculated for each sample. A sample was excluded if the mean of its positive controls was below two standard deviations (SDs) of the grand mean across all samples or if the mean of its negative controls were above two SDs from the grand mean (shaded regions in the figure).