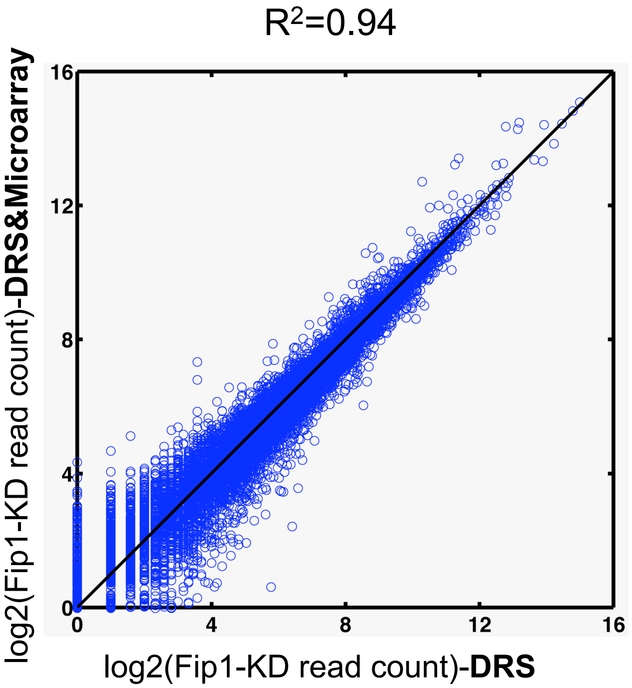

Figure S6. Comparison of gene expression profiling by microarray and by direct RNA sequencing (DRS). X axis: total read count for each gene in Fip1 KD sample based on DRS data; Y axis: total read count for each gene in Fip1 KD based on DRS results of ESC and microarray analyses. The DRS read count for a gene in Fip1 KD sample=(DRS read count for this gene in control ESCs) x (expression fold change for this gene based on microarray analyses: Fip1/ESC). Both X and Y axis are in log scale. r^2=0.94.