A

Frequency vs Log$_2$ RPKM of intergenic region

B

Frequency vs Log$_2$ RPKM of exon region

C

RNA sample from S2 cells

Log$_2$ array intensiy vs Log$_2$ expression RPKM

Spearman's rho = 0.8726

Figure S3. RNA-Seq and array expression profiling. We selected an RPKM of 4 as the threshold for expressed versus non-expressed genes based on the distribution of RPKM values in integenic regions (A) relative to transcripts (B). The agreement between expression arrays and RNA-Seq above 4 RPKM was excellent (C).