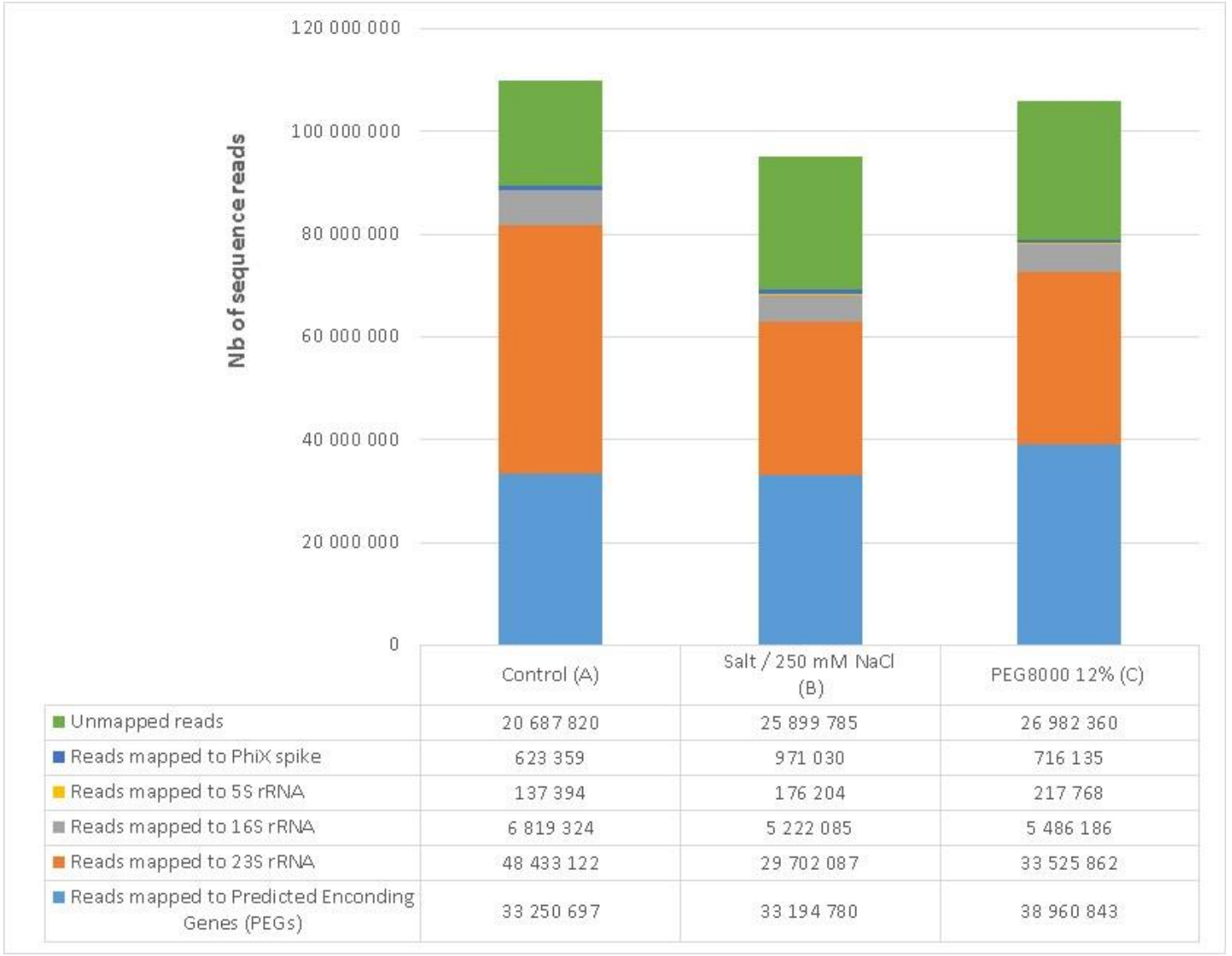

	Control (A)	Salt / 250 mM NaCl (B)	PEG8000 12% (C)
Unmapped reads	20 687 820	25 899 785	26 982 360
Reads mapped to PhiX spike	623 359	971 030	716 135
Reads mapped to 5S rRNA	137 394	176 204	217 768
Reads mapped to 16S rRNA	6 819 324	5 222 085	5 486 186
Reads mapped to 23S rRNA	48 433 122	29 702 087	33 525 862
Reads mapped to Predicted Enconding Genes (PEGs)	33 250 697	33 194 780	38 960 843

Figure S1. Sequencing and Mapping of the 3 RNAseq libraries. Histograms show for the number of sequenced reads obtained by HiSeq for the 3 libraries (indicated at the bottom of each bar. For each bar, the reads that mapped to PEGs, rRNAs, PhiX spike sequence or those were not mapped using 95% sequence identity over 70% of of sequence lengths (other reads) are shown using the color code indicated in the table at the bottom of the histogram together with their respective numbers in the 3 libraries.

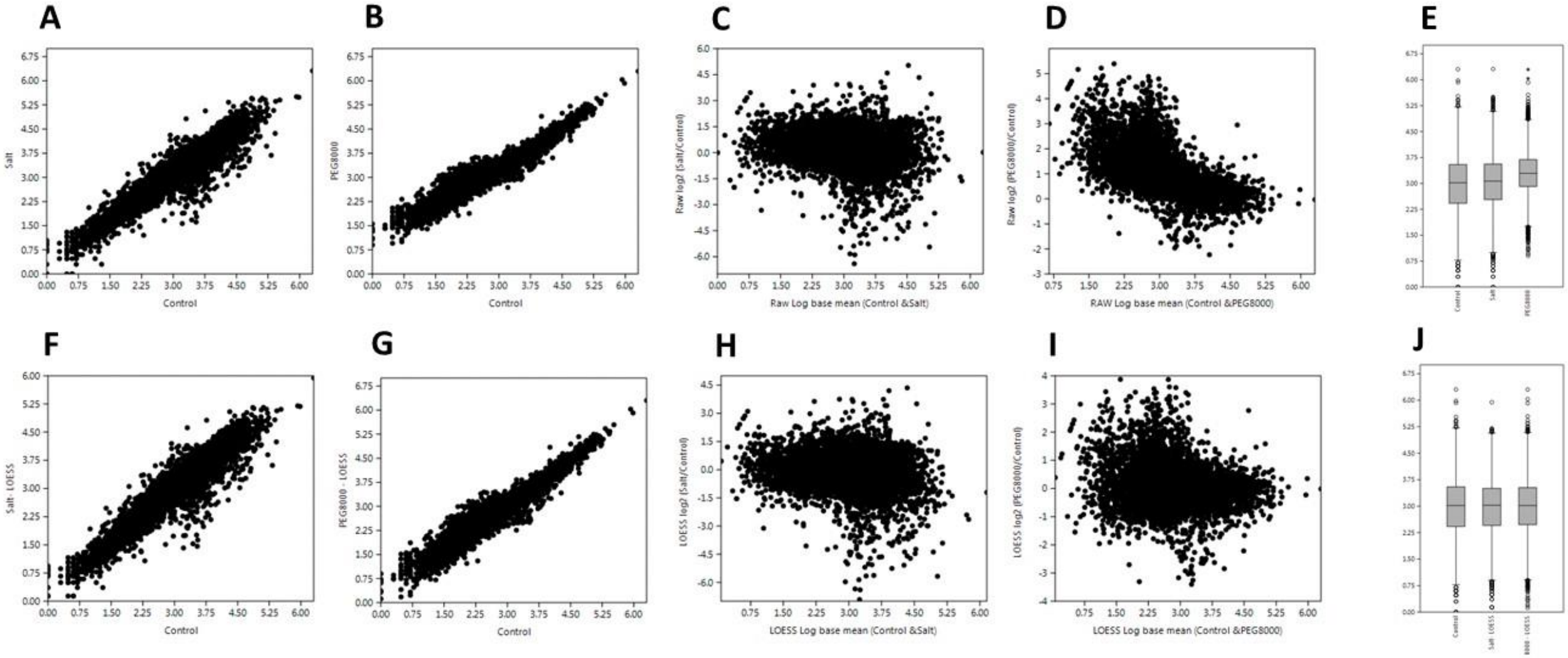

Figure S2. Distributions of RNAseq data. Raw data (A-E) and LOESS normalized data (F-J) are represented using Log scales. Scatter plots show the read counts obtained in control (X axes) and salt stress (A, F) or water stress (B, G) treatments for all predicted PEGs. MA plots for salt stress (C, H) or water stress (D, I) and box plots (E, J) represent the distributions of PEG read counts in each library (Control, salt and PEG8000).

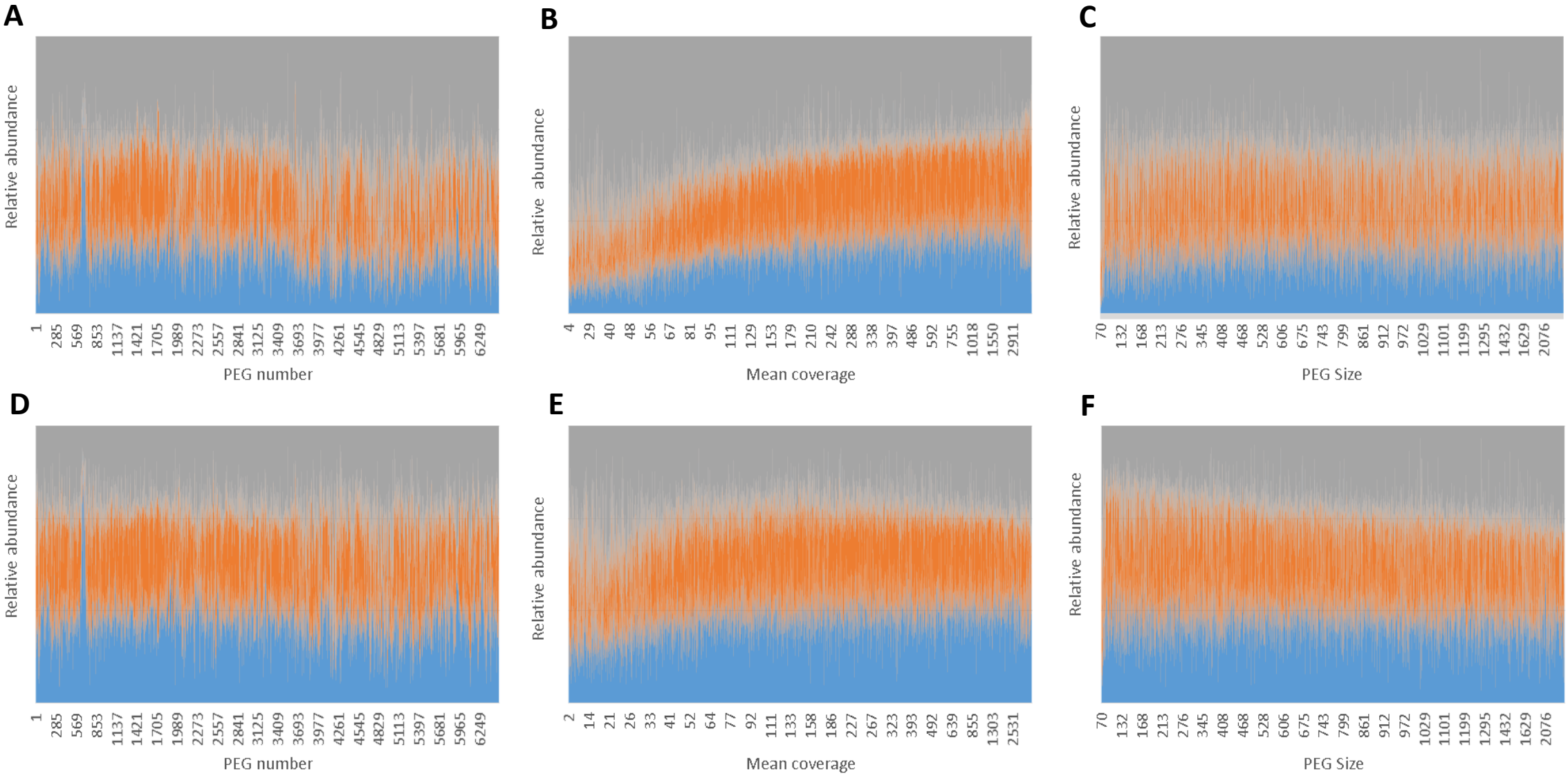

Figure S3. Effect of PEG order, mean coverage or size on the Relative abundance of reads obtained in the 3 libraries Control (Blue), Salt (Orange) PEG8000(Grey). Relative abundances obtained using raw data upon mapping onto PEGs (A-C) and upon LOESS normalization (D-F) are represented using Surface areas 100% piled graphics. Relative abundances obtained upon ordering PEGs according to their predicted position on the genome (A, D) their mean coverage obtained from the three libraires (B, E) or their sizes (C,F) are shown.

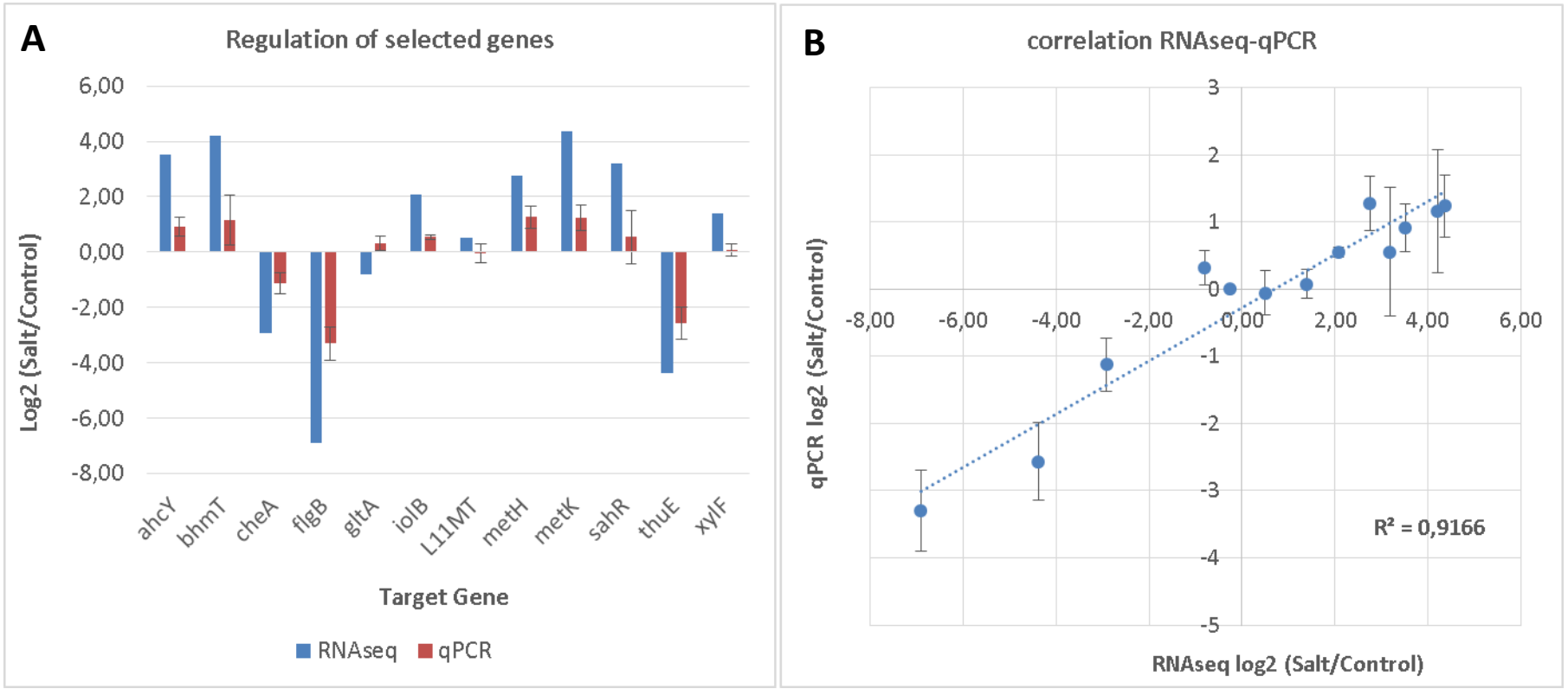

Figure S4: Comparison of the relative expression levels of selected genes by RNAseq and qPCR . The log2 fold changes of expression in salt treated cells as compared to the Control TY cells for the selected genes (Shown bellow bars in histogram) were calculated using the reference genes hrcA. Individual relative expressions for the 12 genes are shown in A; the RNAseq differential expression values are shown as blue bars and red bars bars show the mean relative log2 fold changes (Salt / Control) as analyzed by qPCR using 3 RNA samples, and error bars correspond to standard deviations. The scatter plot (B) shows the average log2 fold changes (Salt / Control) from the RNAseq data (X Axis) against the mean qPCR values from three replicates on RNA samples from 3 biological replicates (Y Axis) which was used to calculate the correlation factors (R2) indicated on the graph.