



**S6 Fig. Replicate-to-replicate MA plot on the 02-A samples for checking the efficiency of the A RPM, B quantile, C DESeq2 and D edgeR normalization methods.** (Sample code: 02h, no rivals, A body part). On the x-axis we represent the average abundance between replicates ( $\log_2$  scale), on the y-axis the FC ( $\log_2$  scale). Although the quantile and the DESeq2 produced very similar distributions of abundances between replicates/samples, the former did not produce a tight MA plot when variability in expression at gene level was assessed. For the comparable results for the subsampling (without replacement) approach, see main Fig 3C.