

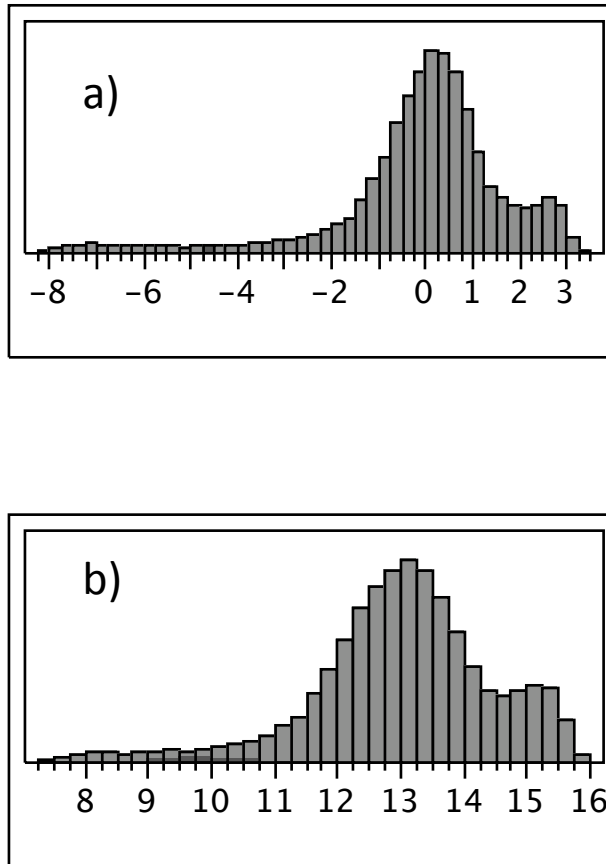


Fig. S1. Comparizon of ANOVA and RMA normalization methods for *Littorina* aCGH.

Overall signal distributions in one sample after normalization by a) ANOVA and b) RMA methods. X axis represents log2-transformed signals with subtracted average (a) or log2-transformed signals after RMA normalization (b). Note very similar shapes of the two distributions. Correlation between signal levels per gene model, produced by the two normalization methods, is $R^2=0.967$, $p<0.00001$.