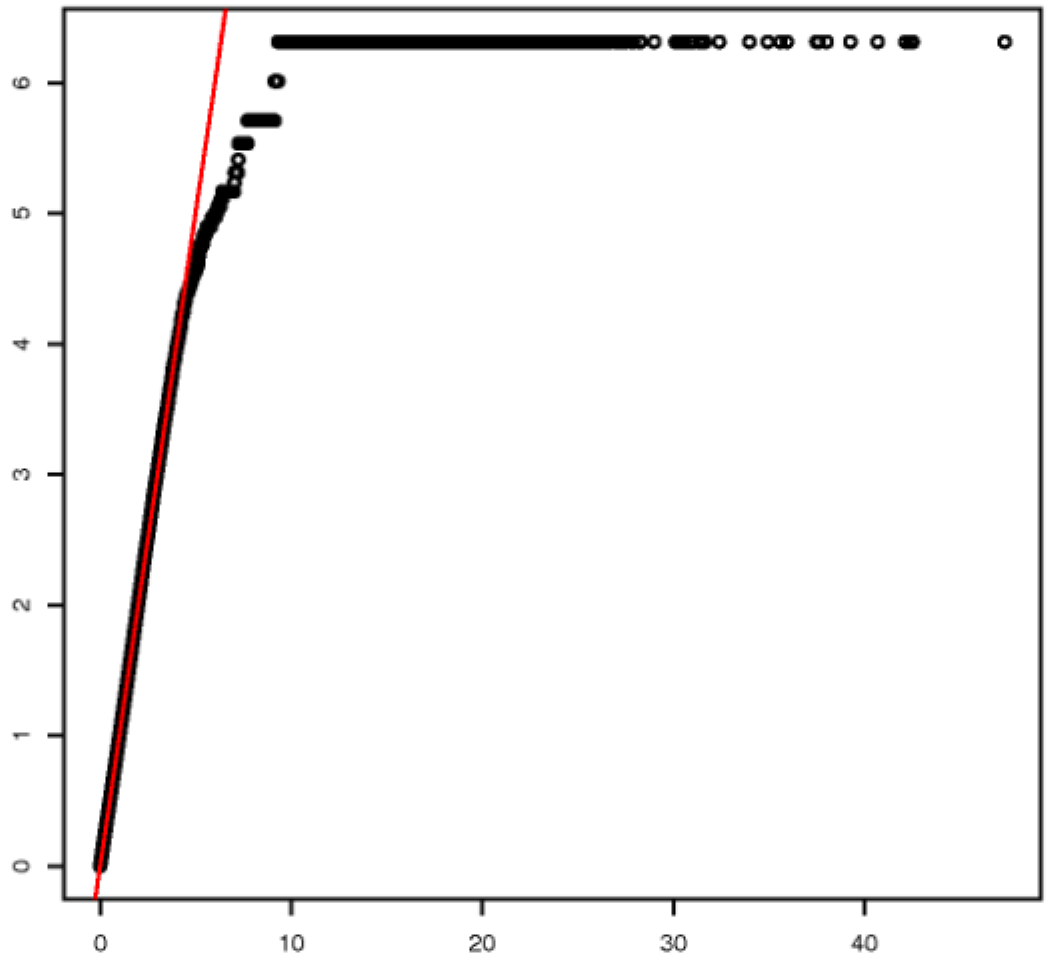


**Figure S1** -log10(GC-corrected P-values) (x-axis) of strain effects vs -log10(permutation based p-values) (y-axis).

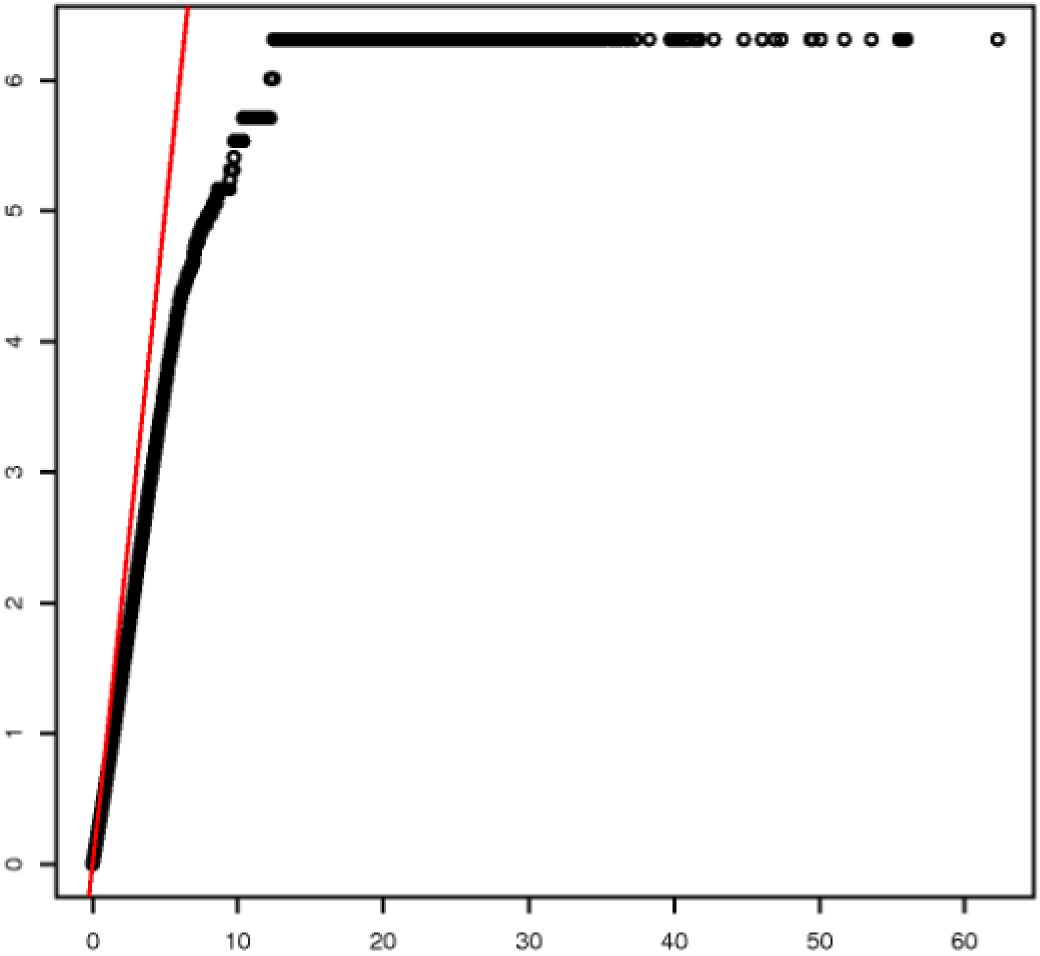


**Figure S2** -log10(GC-uncorrected P-values) (x-axis) of strain effects vs -log10(permutation based p-values) (y-axis).

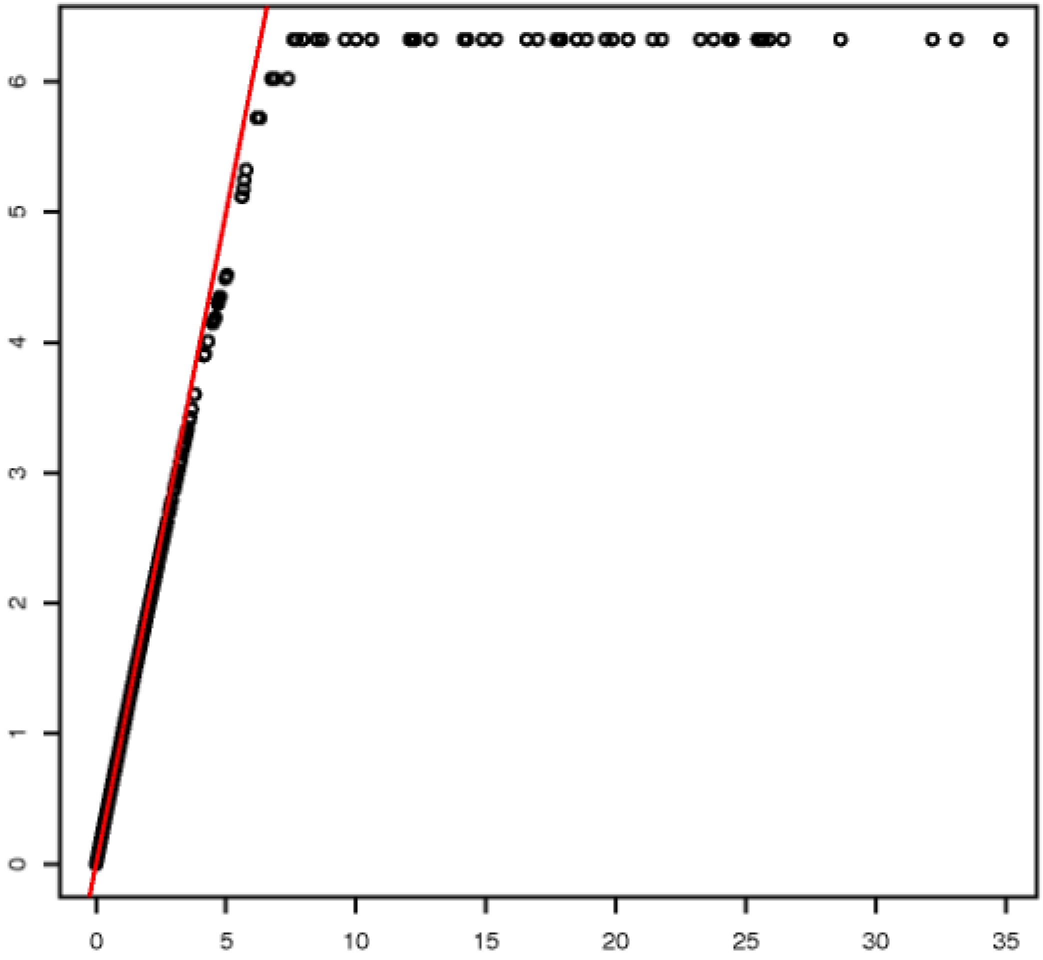


**Figure S3** -log10(GC-corrected P-values) (x-axis) of PoO vs -log10(permutation based p-values) (y-axis).

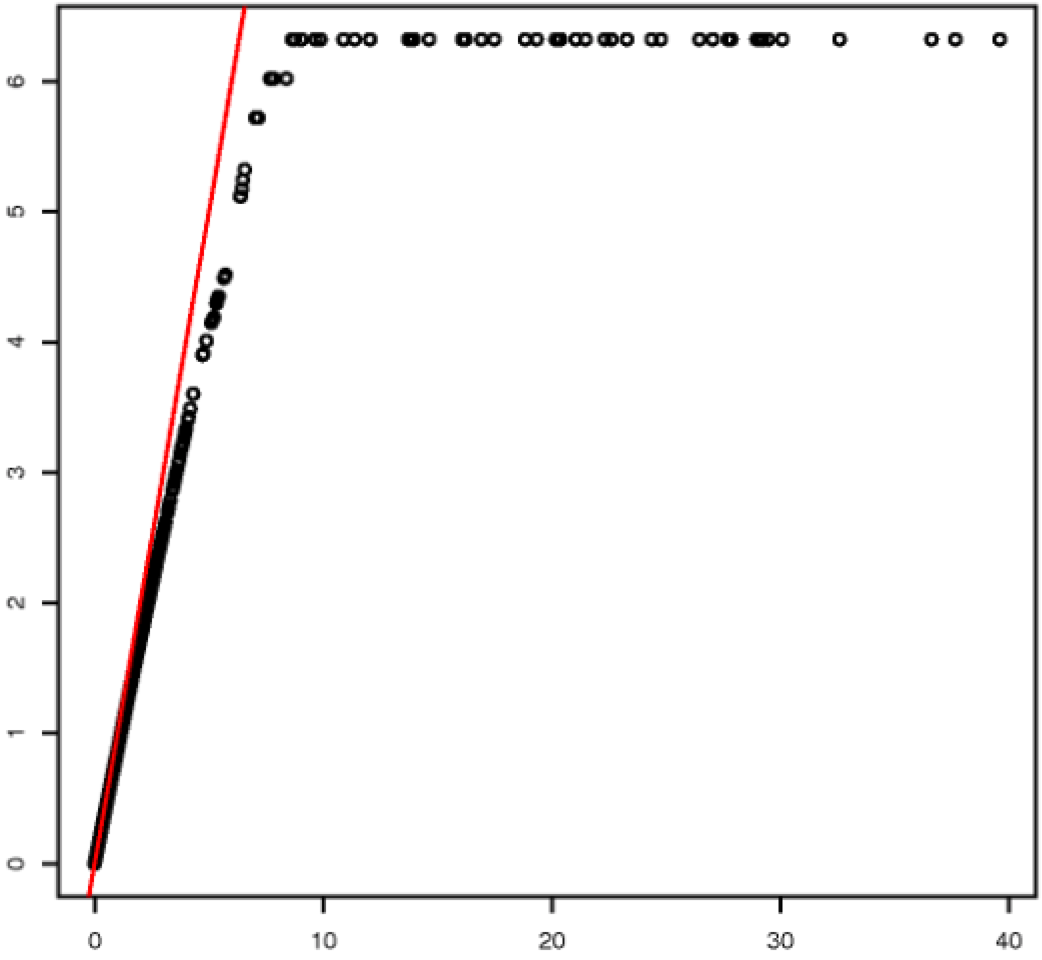


**Figure S4** -log10(GC-uncorrected P-values) (x-axis) of PoO vs -log10(permutation based p-values) (y-axis).

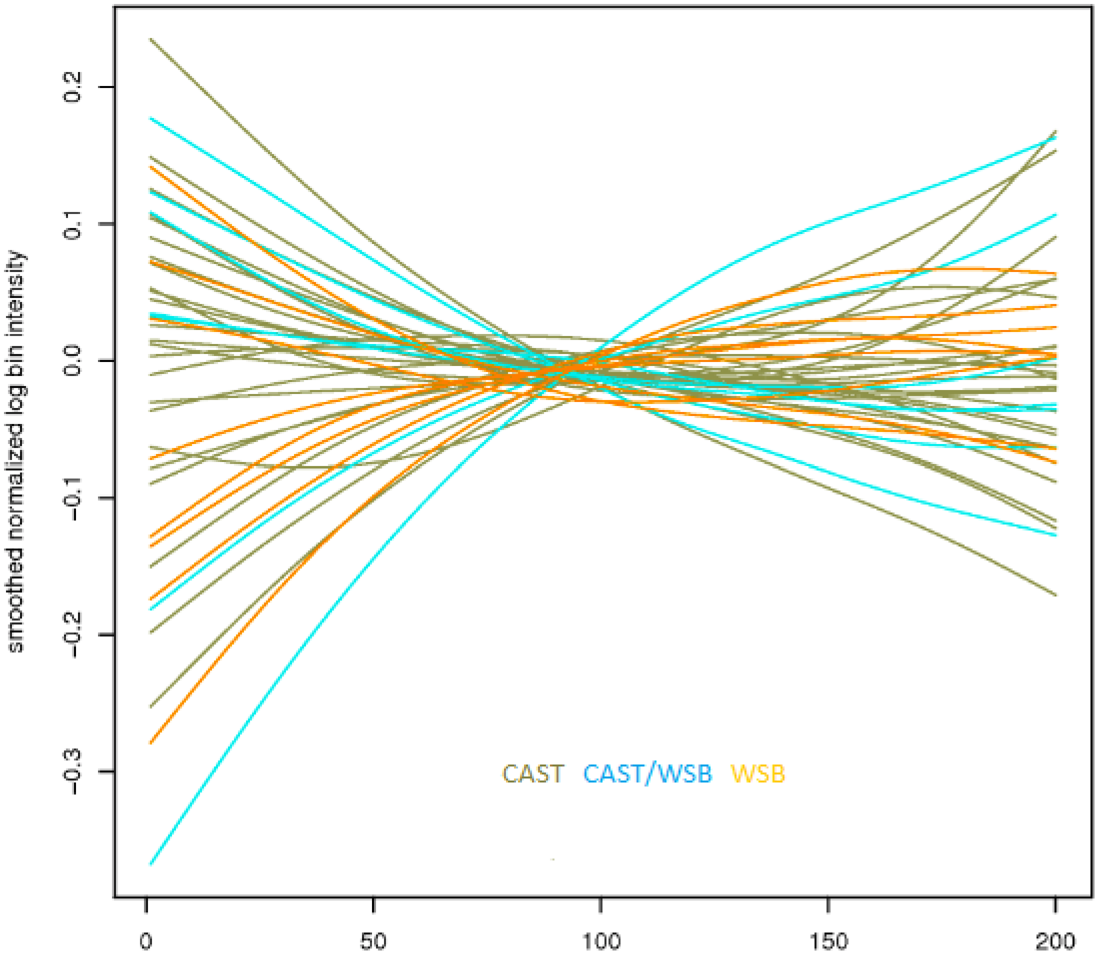
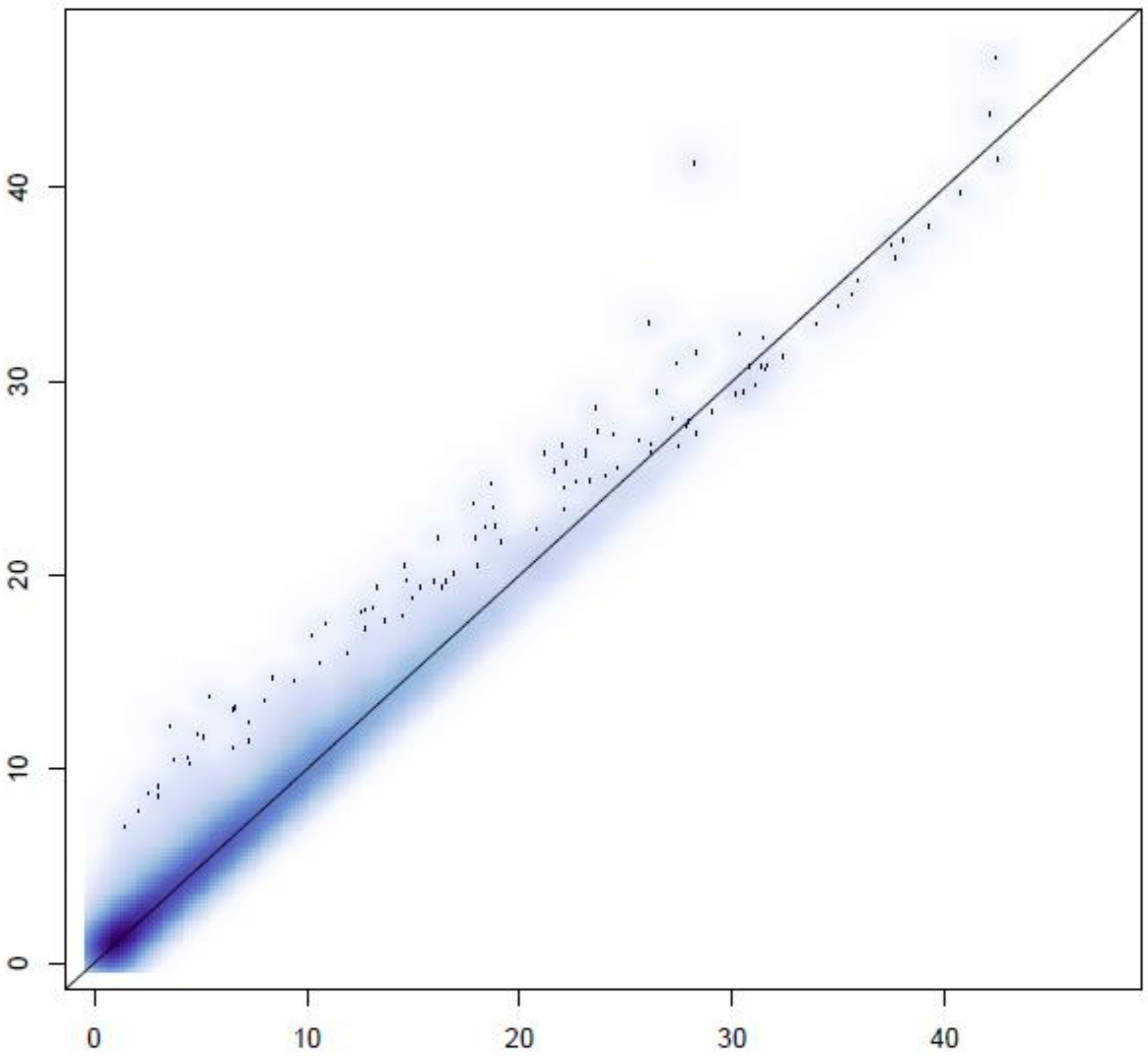
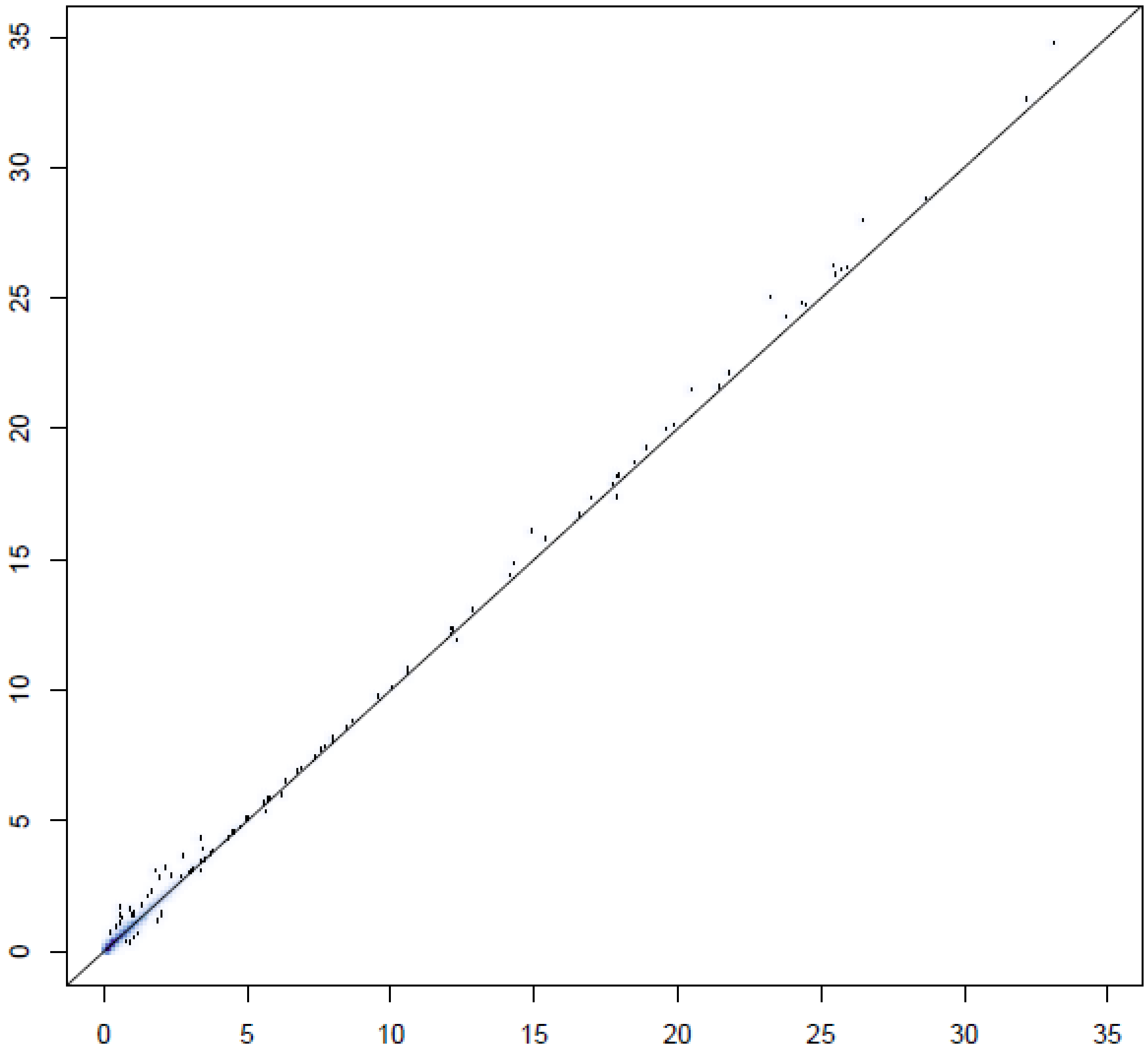


**Figure S5** The %GC-content vs the smoothed normalized log intensity. The X-axis refers the bin number where total of 200 bins are used to divide genes. The lower the bin #, the lower the %GC content.



**CƛƎǳǊŜ {c** Scatter plot of -log10(P-values) of strain effects with (y-axis) and without (x-axis) correction of %GC-content.



**CΆ∃dzǊŜ {τ** Scatter plot of -log10(P-values) of PoO with (y-axis) and without (x-axis) correction of %GC-content.