

Supplemental Figures for: Effect of the environment on horizontal gene transfer between bacteria and archaea by C. A. Fuchsman, R.E. Collins, G. Roca and W.J. Brazelton

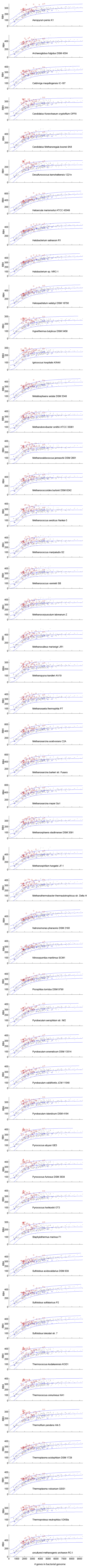


Figure S1. The number of shared genes between archaea and bacteria and bacterial genome size were fitted using non-linear regression (center blue line) and 2 standard deviations from the mean are also shown to visualize the range (upper and lower blue lines). Color scheme of the points reflect growth temperature: thermophiles are red, mesophiles are grey and psychrophiles are blue. The name of the relevant archaea appears on the plot.

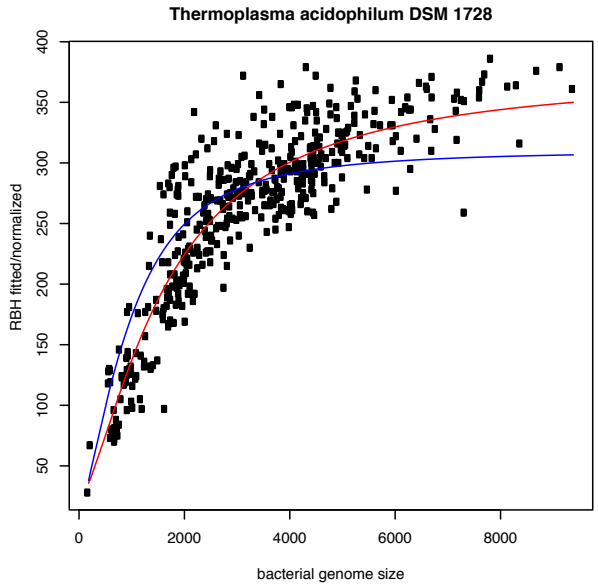
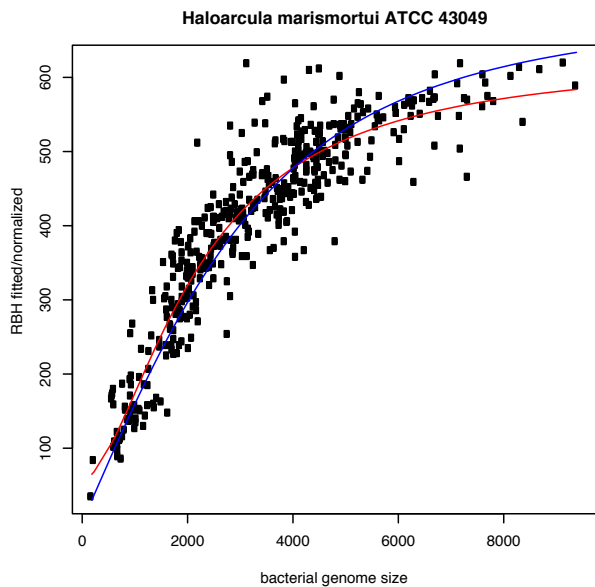
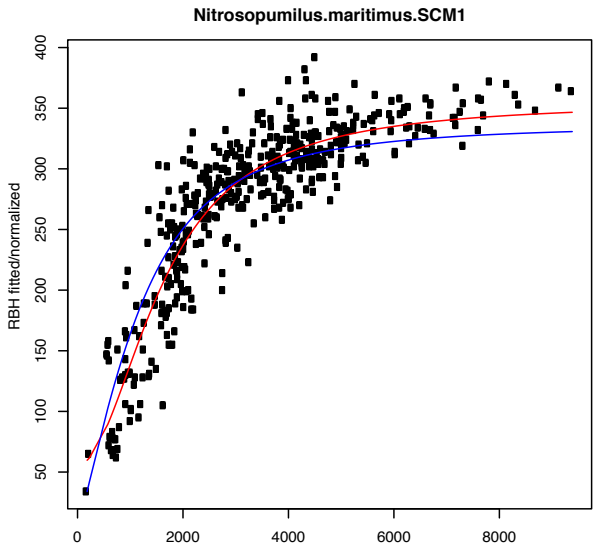
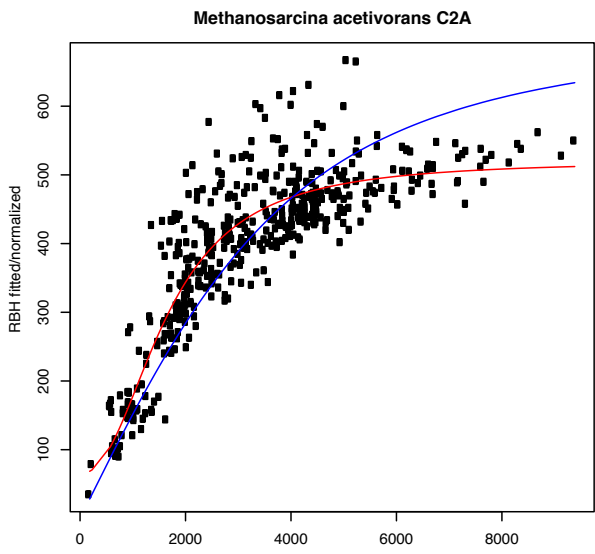
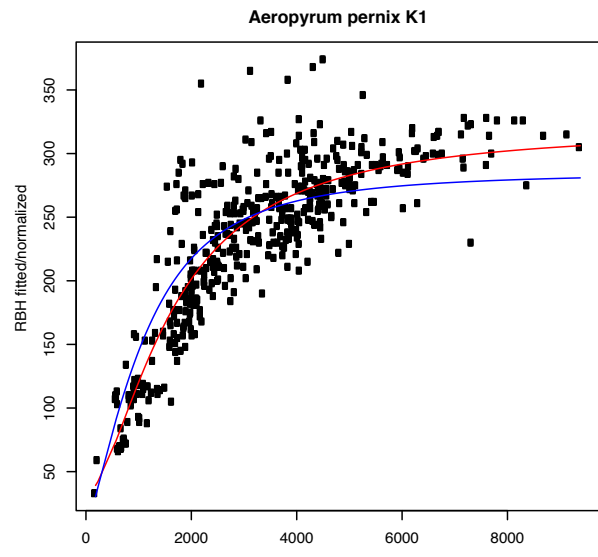
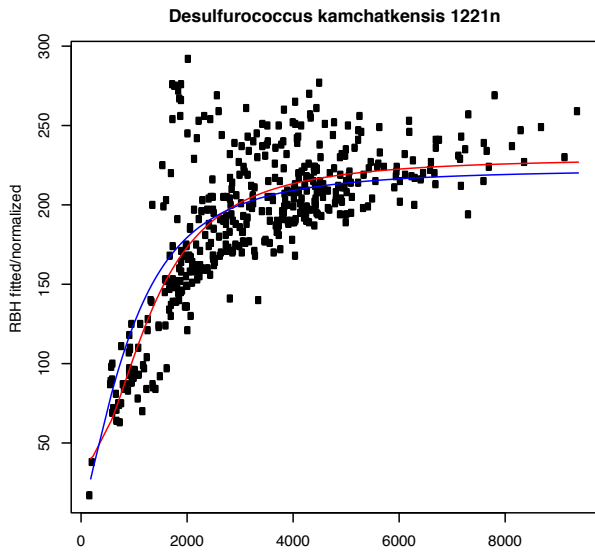
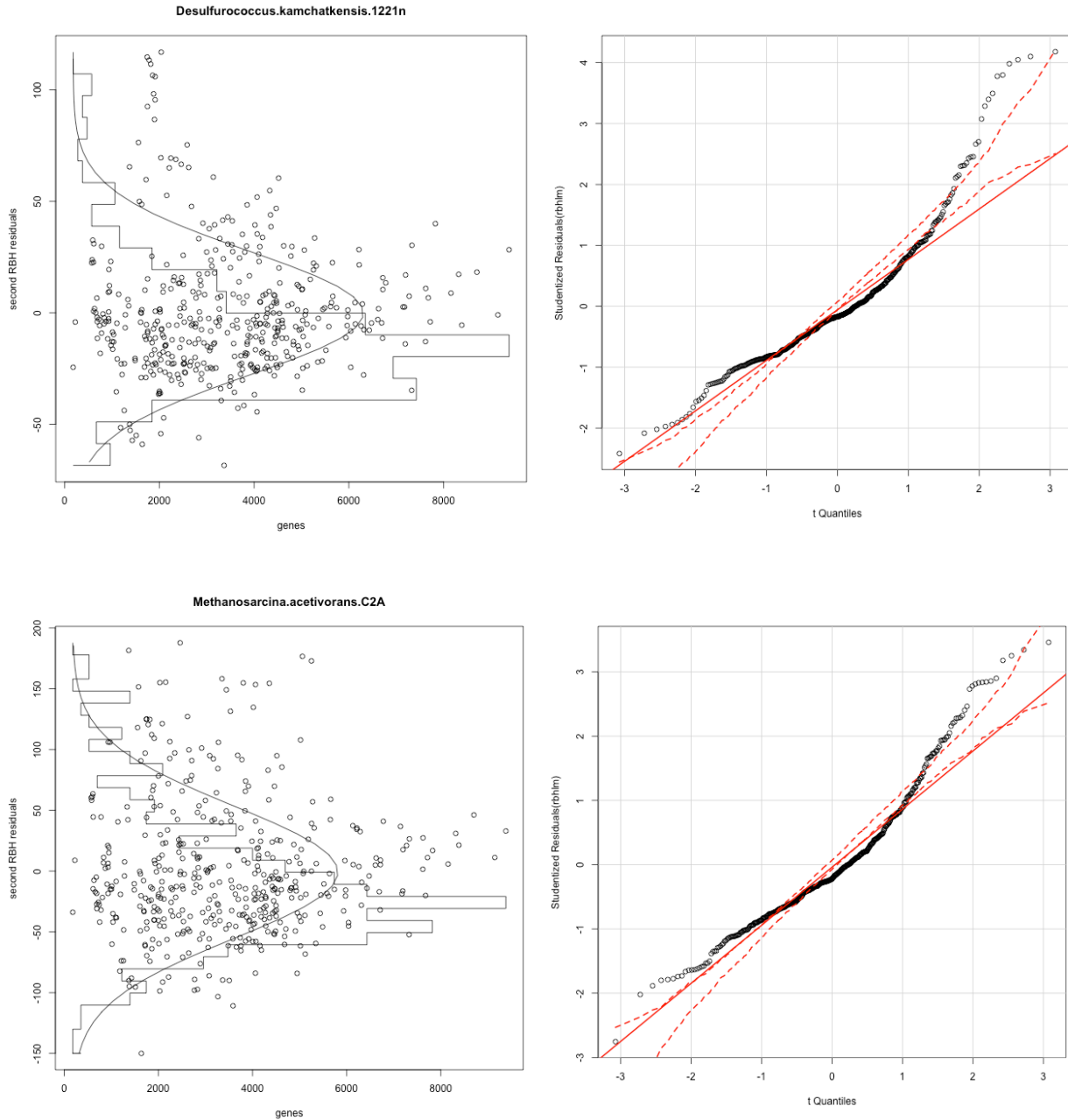


Figure S2. A comparison of fits for select archaeal genomes. The Korbel normalization (blue line) is weighed average $=\sqrt{2} * A * B / (A^2 + B^2)$ where A and B are the genome size of the archaeal and bacterial genomes (Korbel et al 2002). The four-parameter log-logistic function (red line) was used in further analyses.



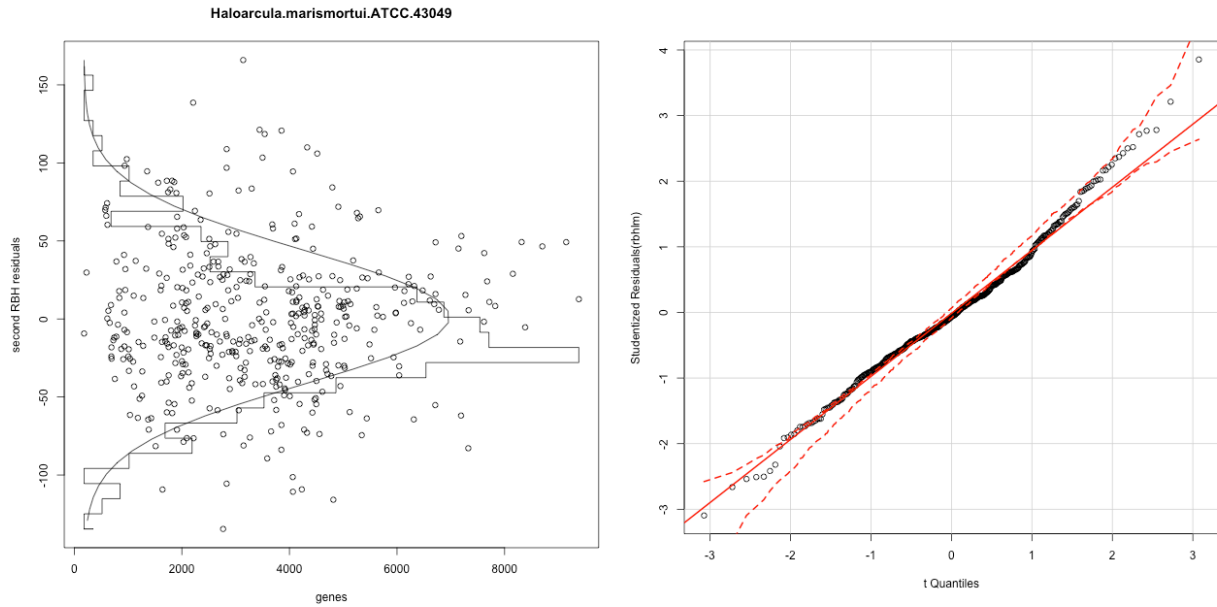
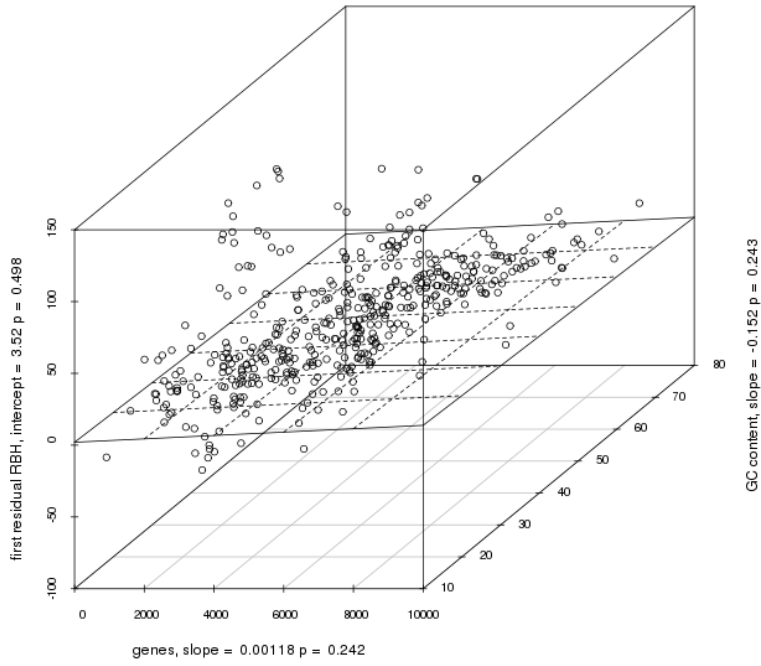


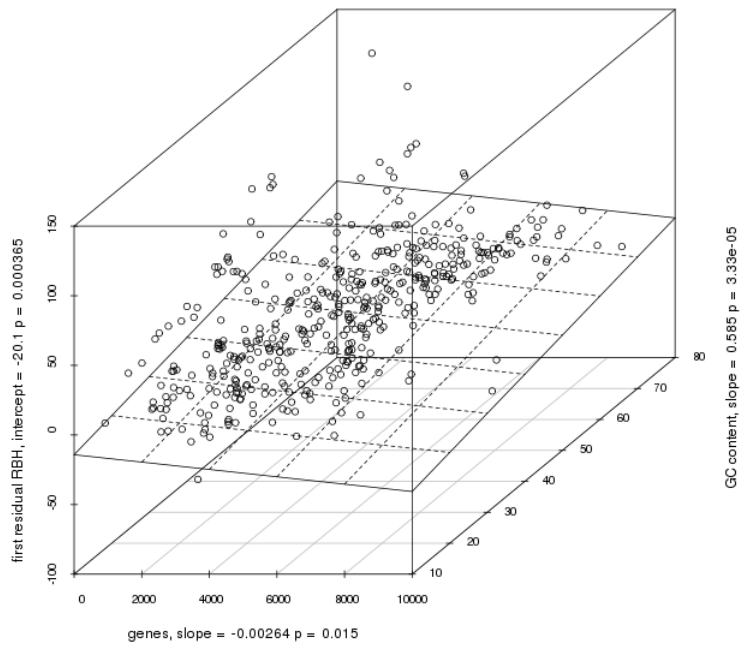
Figure S3. Plots indicating that the distribution of RBH residuals is not normal. The non-normality of the residuals serves as a test of our claim that some bacteria have non-random contributions of archaeal genes from horizontal gene transfer. When more outliers with high RBH are present (as in the case of *Desulfurococcus kamchatkensis*), the distribution of the residuals is skewed, and the QQ plot shows a marked deviation from linearity. In contrast, *Haloarcula marismortui*, which we predict to have had low rates of HGT with bacteria, shows a nearly linear QQ plot and highly normal distribution of RBH with genome size.

Desulfurococcus.kamchatkensis.1221n



Aeropyrum.pernix.K1

B.



C.

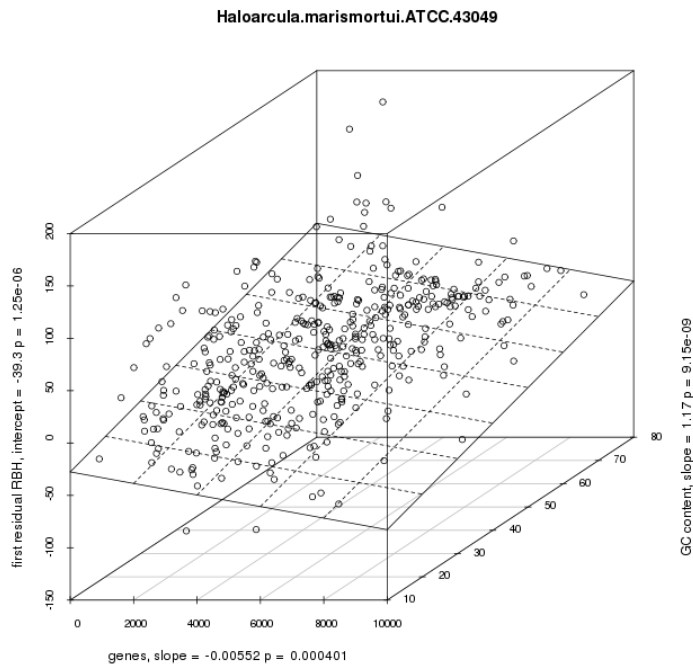


Figure S4. The affect of GC was removed from the residuals for each archaea by fitting a plane to the three axes: number of genes in the bacterial genome, reciprocal BLAST hits, and GC content. Examples include A) anaerobic hyperthermophile *D. kamchatkensis* B) aerobic hyperthermophile *A. pernix* and C) Extremely halophilic aerobic mesophile *H. marismortui*.

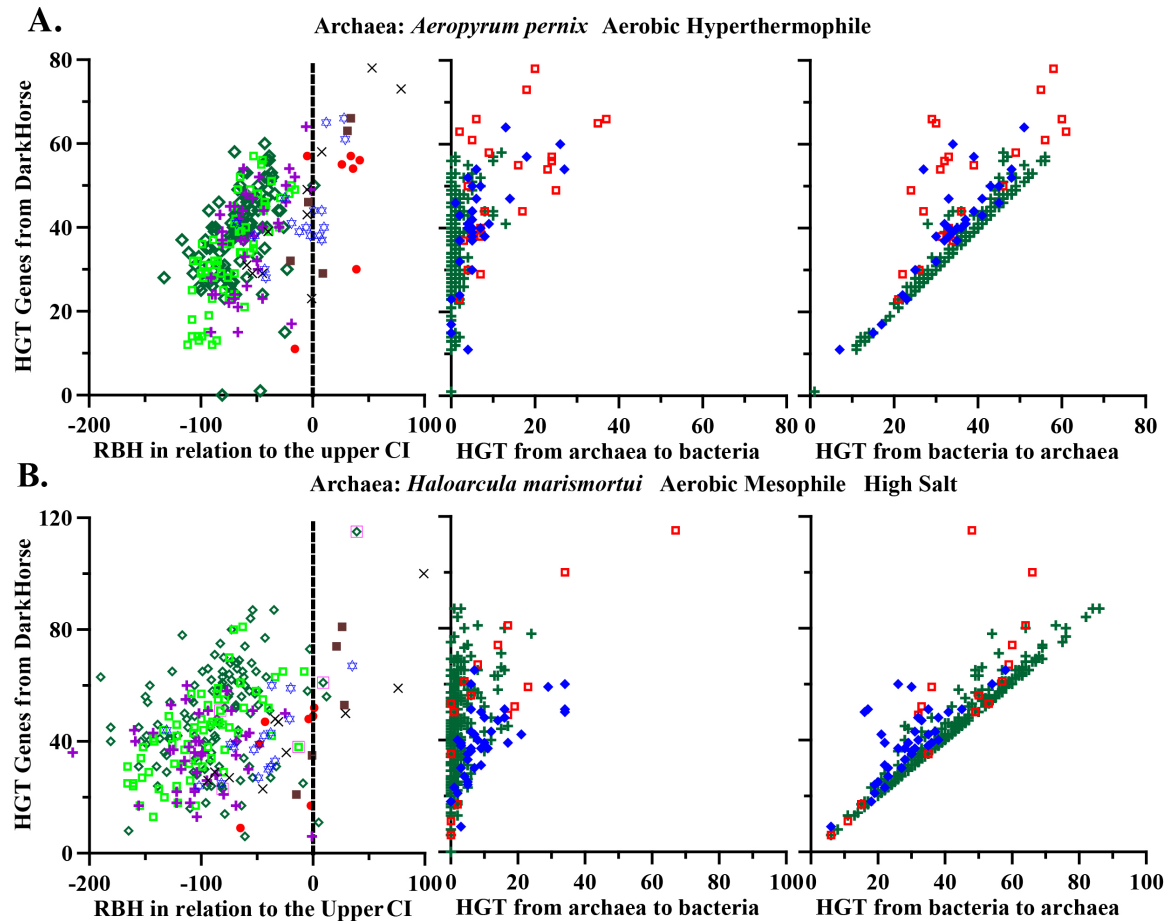


Figure S5. Examples of HGT for aerobic hyperthermophile *Aeropyrum pernix* (A) and the aerobic mesophile but extremely halophilic archaea *Haloarcula marismortui* (B). In the first column the number of potentially horizontally transferred genes as determined from the DarkHorse algorithm is compared to the number of reciprocal best hits between bacteria and each archaeon. A positive value on the x-axis indicates the RBH count was greater than 2 standard deviations from the mean. Color coding describes the lifestyle of the bacteria. A pink box in B indicates extremely halophilic bacteria. In the second column, the number of potentially transferred genes is compared to the number of those genes transferred from archaea to bacteria. In the third column, the number of potentially transferred genes is compared to the number of those genes transferred from bacteria to archaea. Color-coding describes whether the bacterium forms a pair with the archaeon listed (red), with any archaea in this study (blue), or not with any archaea (green).

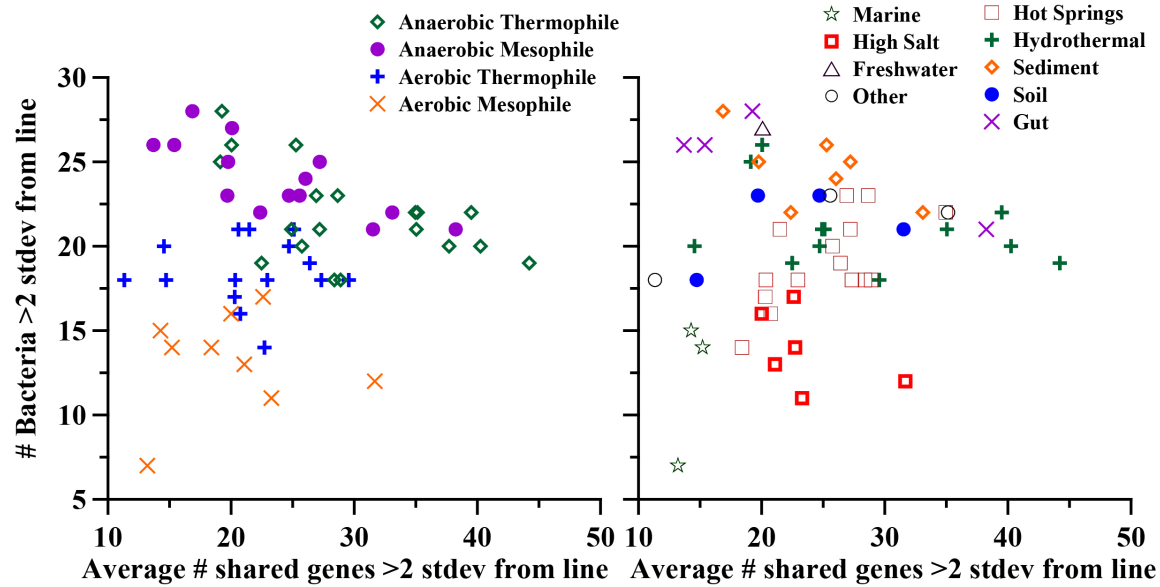


Figure S6. The number of archaea-bacteria pairs enriched in shared genes (RBHs) and the average number of reciprocal best hits in each pair, plotted by archaeon. In A) color coding describes the phenotypes of the archaea. In B) color coding describes the environments the archaea were isolated from.

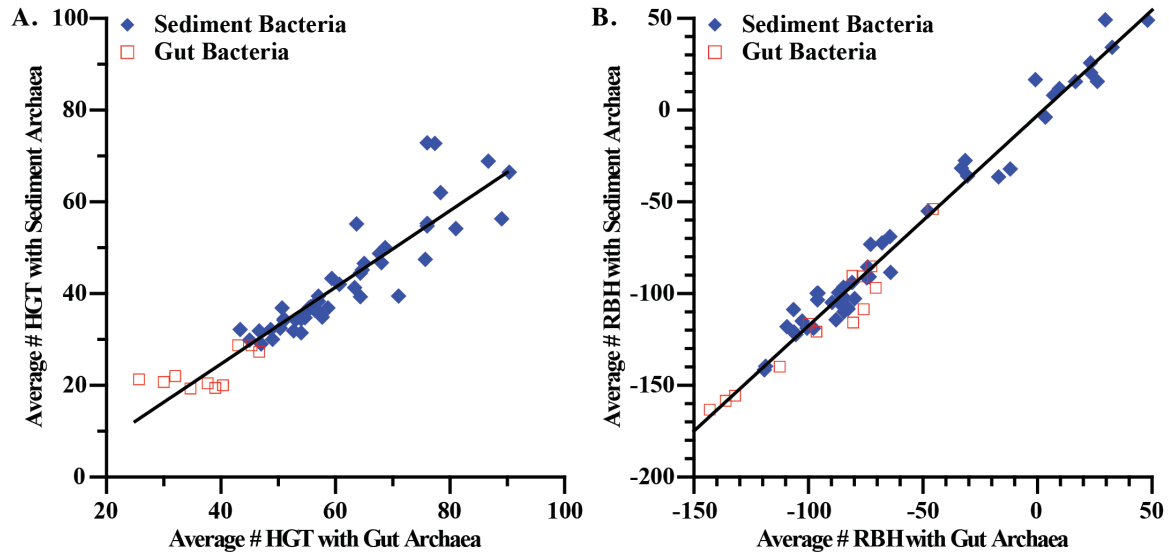


Figure S7. Comparison of transferred (A.) and shared (B.) genes with habitat. Particularly, we compare genes in sediment and gut bacteria and sediment and gut archaea. HGT stands for horizontally transferred genes, and RBH stands for reciprocal best hits or shared genes.