

**Figure S1:** Rarefaction curves for bacterial (a-c) and archaeal (d-f) pyrosequencing reads. Data were rarefied for determining the observed species (a & e), Chao1 richness index (b & f), Shannon diversity index (c & g) and Simpson diversity index (d & h).

**Figure S2:** Heatmap showing the relative abundance and distribution of representative 16S rDNA tag sequences classified at the genus level. The setting divergence of  $> 0.5\%$  was used to filter out genera with small differences among the samples. The normalized data were clustered using the complete linkage method and a metric of correlation (uncentered). The color code indicates difference of the relative abundance from mean, ranging from green (-ve, smaller than mean) through black (mean) to red (+ve, larger than mean).

**Figure S3:** RDP classification at the genus level for archaeal amplicons assigned at a 80% confidence level.

**Figure S4:** PCoA plots. a) Weighted-UniFrac based clustering with Jackknife support. b) Unweighted-UniFrac clustering with Jackknife support.

**Figure S5:** PCA plots generated in STAMP (<http://kiwi.cs.dal.ca/Software/STAMP>) based on taxonomy assignment using the default settings on MG-RAST 3.2.5. The best hit classification tabular data at the genus was downloaded and imported into STAMP.

**Figure S6:** Scatter plots showing the correlation between a) ABP-Meta vs ATL-LCL b) DBP-Meta vs DBP-LCL and c) ABP-Meta vs DBP-Meta. The histograms show the number of genera (features).

**Figure S7:** Extended error bars showing the genera that is significantly different in the 2008 vs 2010 samples. Frequencies were tested using the two-sided G-test (w/Yates') and Fisher's while the confidence intervals (CI) were calculated using DP: Asymptotic with continuity corrections. Only genera with p-values above 0.05 are shown. a) p-values not corrected b) Bonferroni-corrected p-values.

**Figure S8:** Singles and Doubles Rarefaction curves for bacterial (A-B) and archaeal (C-D) pyrosequencing reads. Data were rarefied at the smallest size sample. Singles are OTUs that contain a single individual while doubles are OTUs that contain two individuals. Overall, samples from the lower layers of the brine pools contain higher singles and doubles higher diversity and low abundance.