



Figure S4. rRNA Sequence Abundance in all samples (LC, LD, P1C, P1D, P2C, P2D, P3C, P3D). Filtered rRNA small subunit sequence reads were clustered and annotated. According to each annotation the reads were summarized in five different groups (Zygnema, Naegleria, other Eukaryota, Bacteria, no BLAST hit) and the read count of each group per sample is displayed in %. Error bars show the standard deviation for each read count. The error bars for P3C and P3D are missing due to missing replicates.