



Figure S4 Expression levels of the 12 most highly expressed GC42 sequences and their (40-nucleotide upstream and 40-nucleotide downstream) flanking sequences. The GC42 sequences are ordered by their average expression levels from panels A-L. The GC42 regions are in red, while the flanking regions in blue. Genome coordinates are based on the *S. cerevisiae* S288c reference mitochondrial genome.