



Figure 3 - figure supplement 4. (a) Chromosome-wide MNase-Seq coverage along the *T. acidophilum* chromosome (day2, replicate 2), normalized using sonicated DNA to remove replication-associated coverage bias. (b) Multiscale analysis of MNase signal enrichment (see Methods). Significantly enriched or depleted (p -value $< 1.e-15$) segments are colour-coded red and blue, respectively. Scales correspond to increasing window sizes over which enrichment is computed. (c) Enrichment signal of significantly MNase-signal-enriched or -depleted genomic domains at scale 30 as a function GC content. (d) Normalized transcript levels for pooled depleted or enriched domains at scale 30 and (e) corresponding log₂-fold changes in transcript levels.