



Figure 6 - figure supplement 1. (a) 16% TTS protein gel (Biorad) showing different concentrations of BSA (Biorad) and purified untagged HTa. (b) Bioanalyzer trace of *in vitro* chromatin reconstitution. Two replicates are superimposed. Major peaks are evident at 50bp and ~90bp in both replicates. (c) Distribution of the lengths of fragments from digested *in vitro* reconstitutions mapped to the *T. acidophilum* genome. Note that smaller fragments are much rarer than in (b). We believe this is likely the consequence of preferential amplification of larger fragments during sequencing library preparation. As we sequence to sufficient depth, however, we retain ample read coverage at smaller fragment sizes.