Cell Reports Methods, Volume *2*

Supplemental information

Enrichment of gut microbiome strains for cultivation-free genome sequencing using droplet microfluidics

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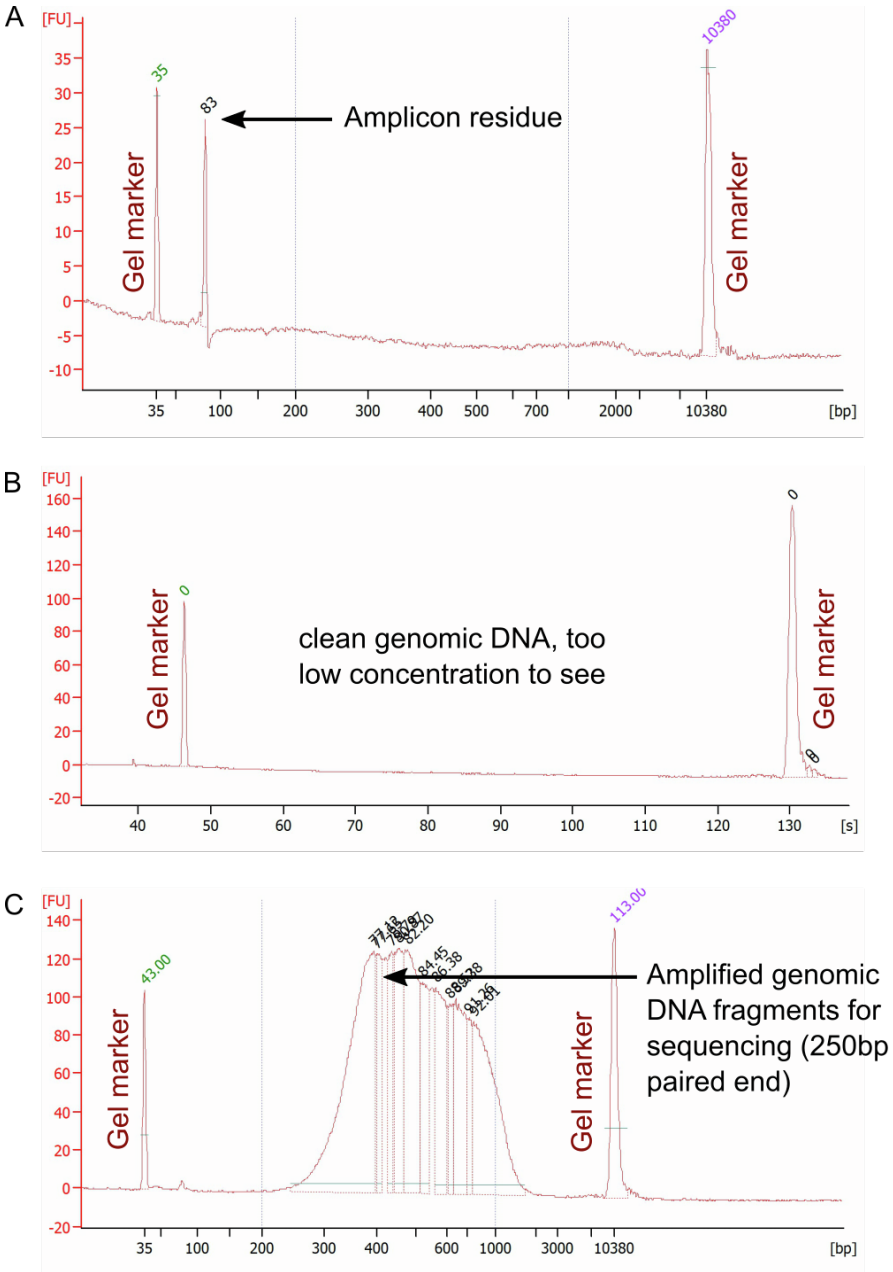
Supplementary Figures



Supplementary Figure 1: **Electropherogram traces recorded with an Agilent Bioanalyzer, related to Figure 1 and STAR Methods section "Amplicon removal and sequencing library preparation".** The x-axis represents the DNA fragment length in base pairs [bp] and the y-axis the amount of DNA detected of such fragments in fluorescence units [FU]. **(A)** DNA from sorted droplets after insufficient Streptavidin beads clean-up; **(B)** Clean genomic DNA that is visibly free of amplicons, but the genome fragment concentration is too low to be detected before amplification; **(C)** Cleaned, amplified (and size selected where needed) genomic sample library, ready for pooling and sequencing. Even without size selection, the genomic DNA recovered from droplets had fragment lengths mostly between 300bp and 3kbp, which indicates fragmentation of the large genome molecules (several Mbp) during thermocycling.