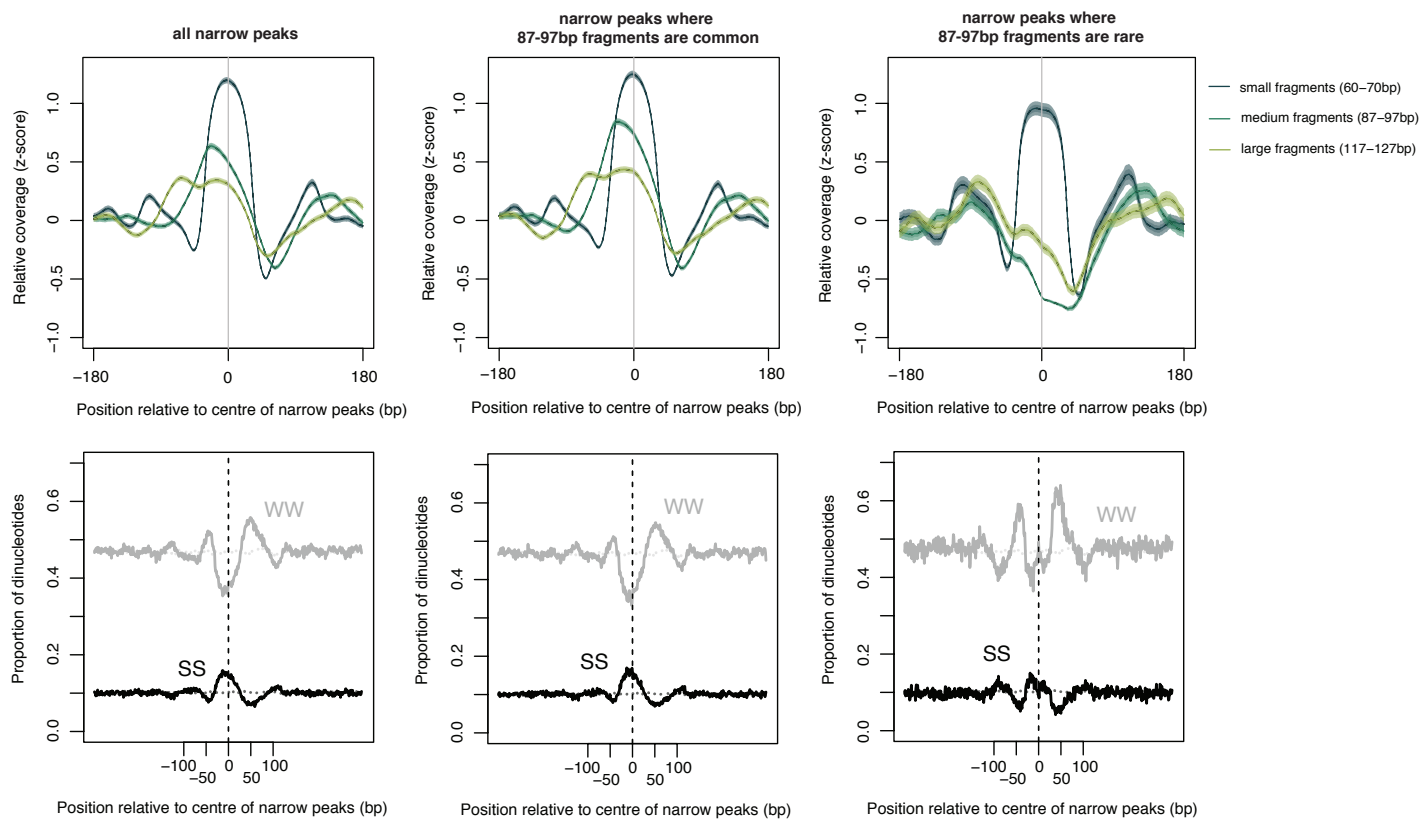


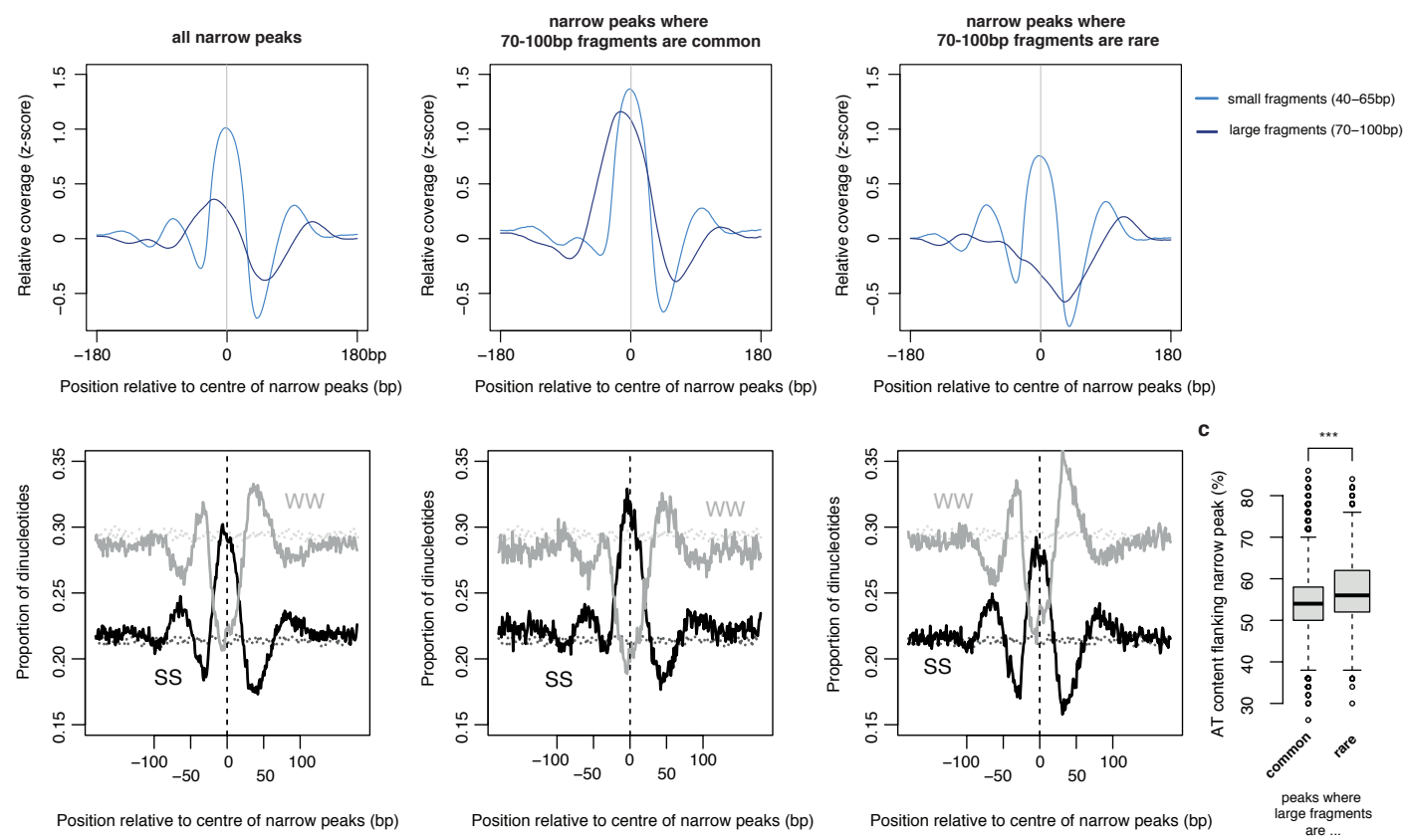
a

M. fervidus



b

T. acidophilum



c

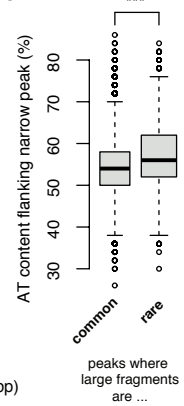


Figure 4 - figure supplement 2. Normalized MNase-Seq coverage relative to the centre of narrow peaks oriented according to the abundance of (a) 87-97bp fragments in *M. fervidus* and (b) 70-100bp fragments in *T. acidophilum*. Middle and right panels are focused on peaks where 87-97bp (70-100bp) fragments are common or rare, respectively. Lower panels display the proportion of SS (=CCICGICIGG) and WW (=AAIATTAITTT) dinucleotides at locations matching the upper panels. Dotted lines indicate the proportion of SS or WW dinucleotides expected by chance, estimated by randomly sampling 25000 regions per genome. (c) AT content in the flanks of narrow peaks (defined across the two windows 25-50bp either side of the centre of the peak) is higher at peaks where large fragments are rare (t-test, *** $P < 2.2 \times 10^{-16}$).