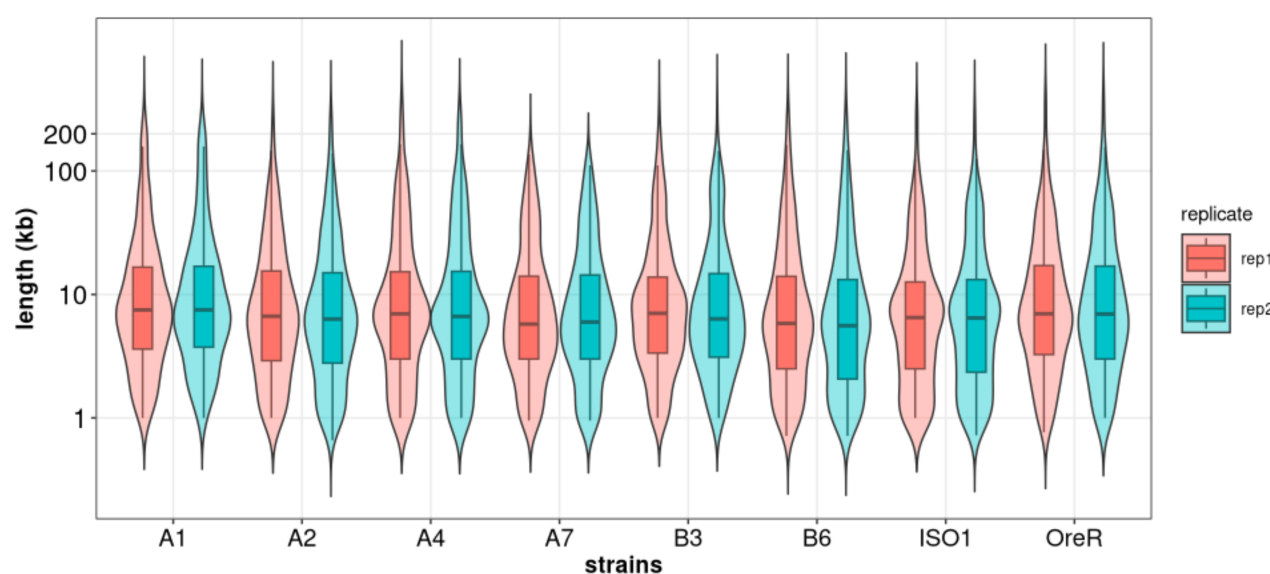
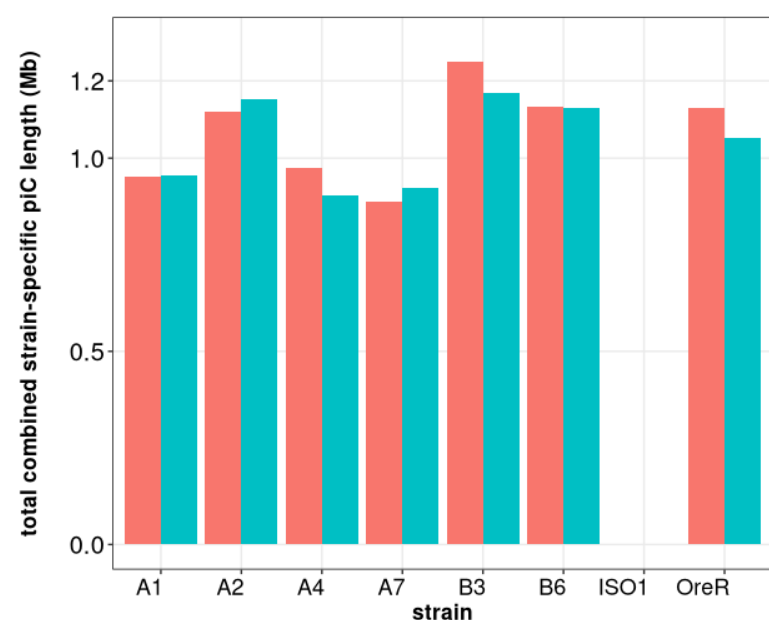
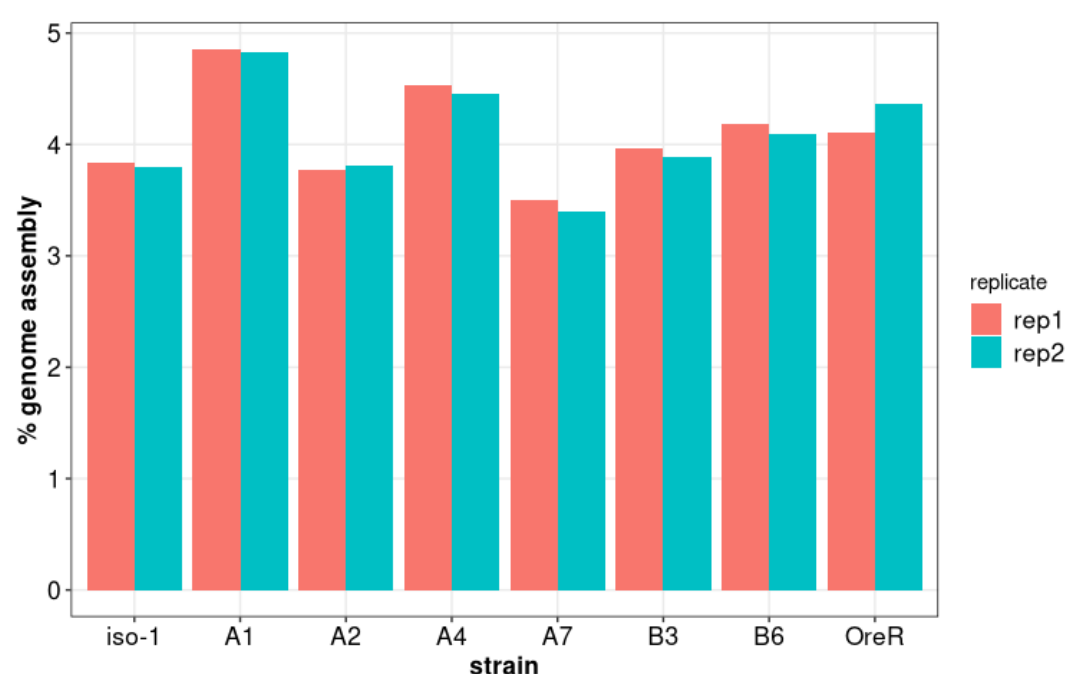
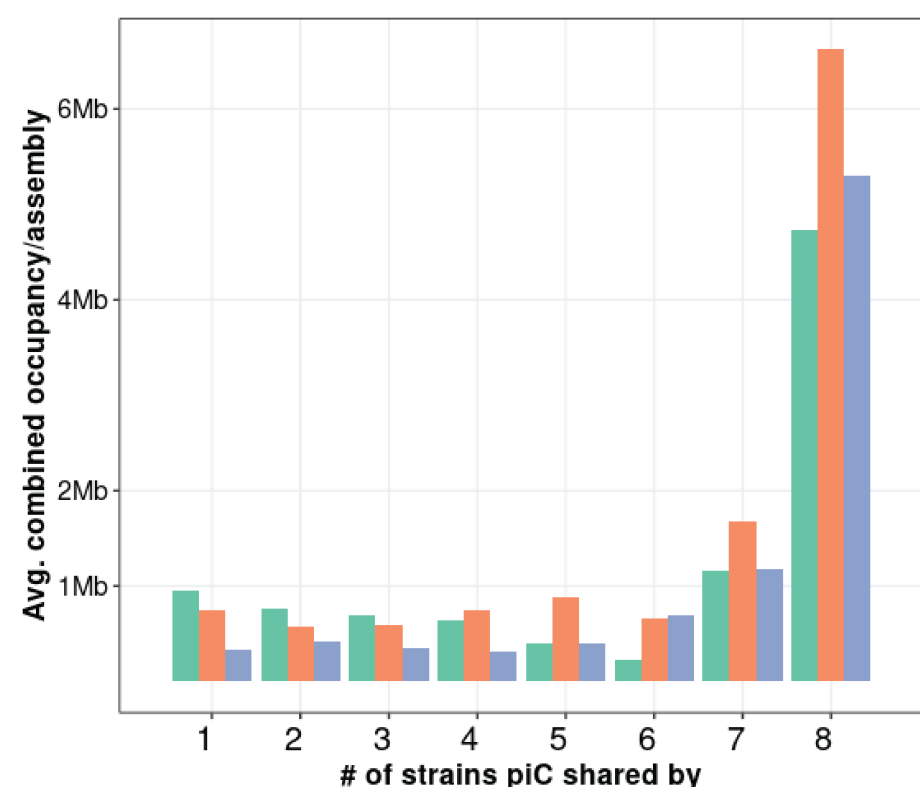


A**B****C****D**

Supplementary_Figure_S4. piC annotation metrics. **(A)** Length distribution of piCs predicted independently from each small RNA library. **(B)** Combined genomic space of strain-specific piCs in the master-list from each strain. **(C)** Combined genomic space of all master-list piCs per replicate per strain in their native genome assemblies. **(D)** Average cumulative piC size from each annotation pipeline and grouped by sharing of piCs among strains post-liftOver (remap).