



Supplementary_Figure_S2. Summary of piC annotation pipeline. (A) Processing of small RNA library reads to enrich for piRNAs and identification of piRNA cluster-like ‘domains’. **(B)** Manual curation of piC coordinates using IGV browser before remapping to iso-1 coordinates. Strain-specific (piCs coordinates curated for a strain, not that it’s only present in that strain) are created from combined annotations of *proTRAC* and *restrictive* methods.