

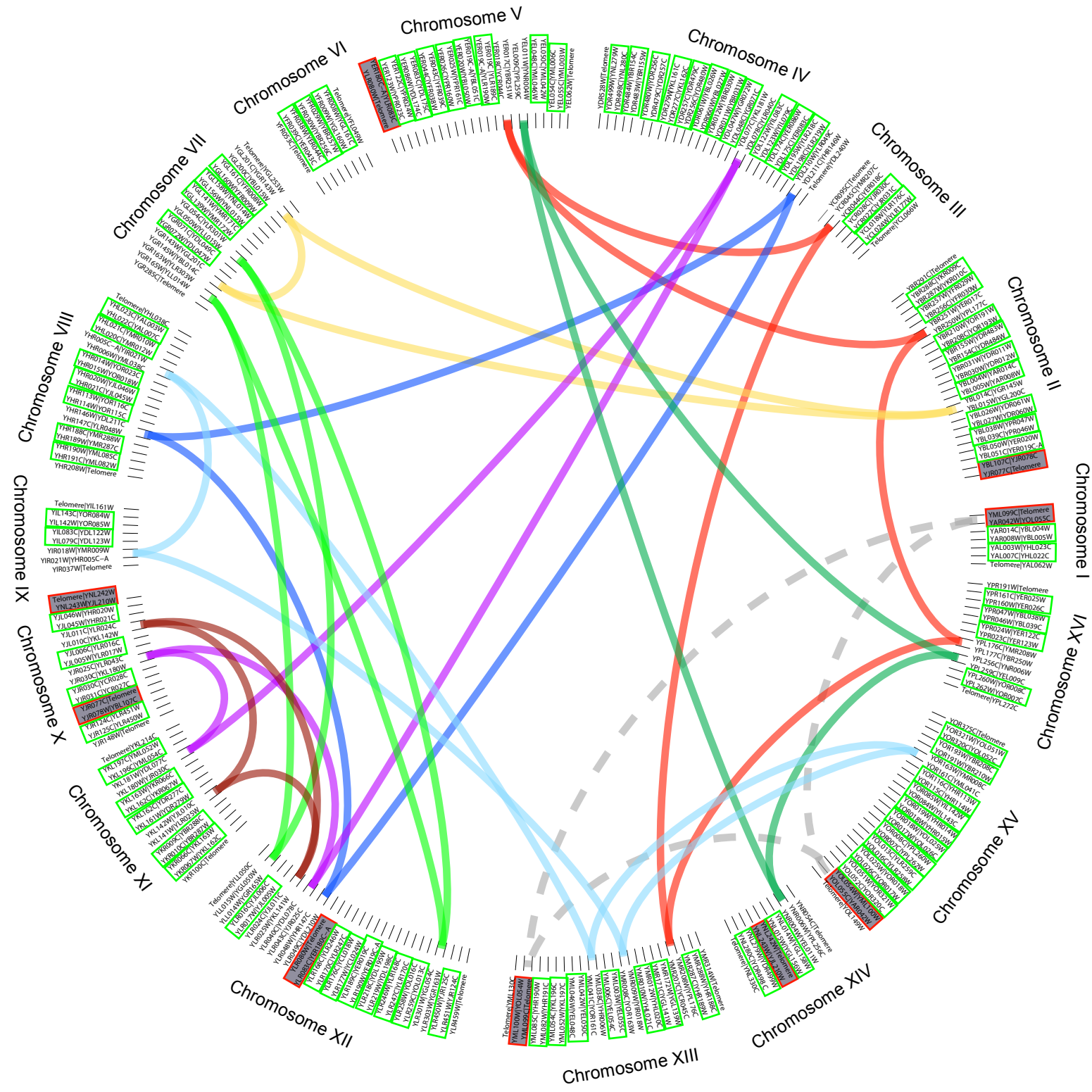


Figure S2.1 Breakpoints between *S. cerevisiae* synteny blocks relative to the ancestral genome and arranged by their order along each extant *S. cerevisiae* chromosome. Each pair of genes separated with a “|” represent adjacent genes in the ancestral genome that were separated by a reciprocal translocation in the *S. cerevisiae* lineage. Each breakpoint is drawn twice because each rearrangement created breakpoints at two different genomic locations in *S. cerevisiae*. A green box has been drawn around each pair of breakpoints that were formed by one reciprocal translocation event with no breakpoint reuse. In these cases, the genes bordering the same side of each breakpoint (as ordered) are adjacent in the current *S. cerevisiae* genome (e.g. YPR161C|YER025W (from ANC7B) and YPR160W|YER026C (from ANC3B)). In cases of breakpoint reuse, the genes on one side of the pair of breakpoints are adjacent in *S. cerevisiae*, while the genes on the other side are not. By iteratively linking each of the non-matching genes to the gene that is adjacent to them in the *S. cerevisiae* genome, we can describe reciprocal translocation cycles (coloured lines) that link breakpoints which have been used more than once. For a cycle with n lines there are n breakpoints locations and $n-1$ reciprocal translocation events. The breakpoint reuse for each cycle is $n/(n-1)$. We observed 1 event where a Robertsonian translocation breakpoint was reused (dashed grey line). Telomeric Robertsonian translocation events are depicted as grey shaded red boxes. Figure generated in part by Gavin Conant.