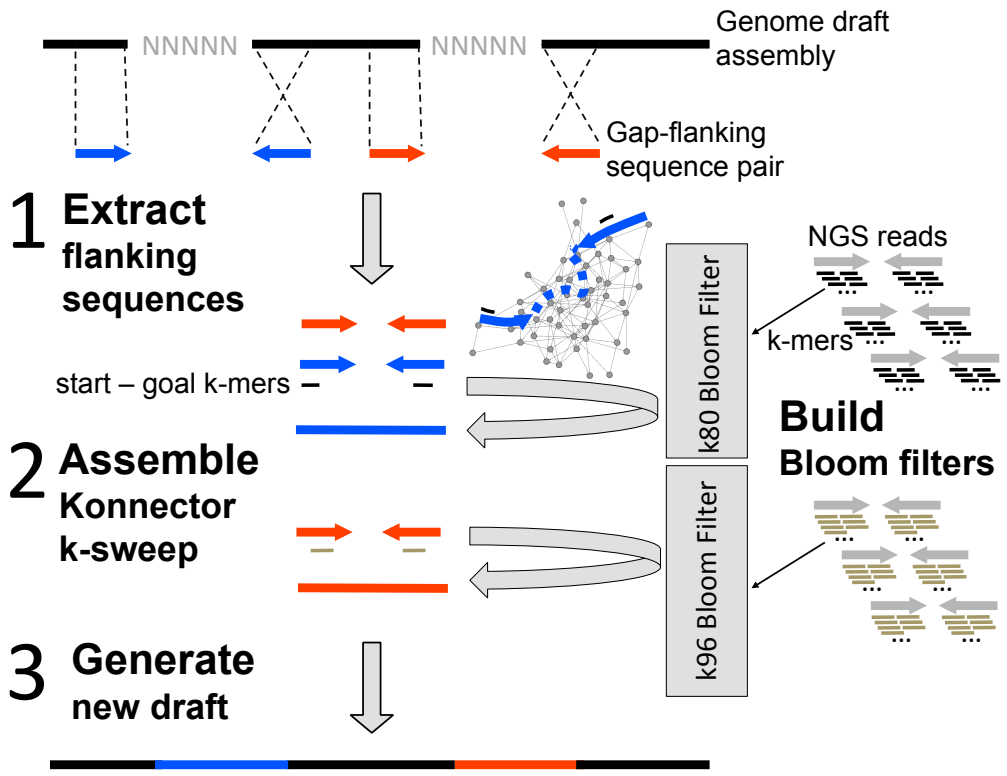

Supplemental figure S1. Steps to gap-filling genome draft assemblies with Sealer. Gaps are first detected from a draft assembly and flanking sequence pairs extracted. Next-generation sequence reads are supplied and *k*-1 overlapping *k-mers* extracted and used to build Bloom filters. Bloom filters are interrogated in turn using start and goal *k-mers* from each flanking pairs and sequences are derived by navigating a de Bruijn graph. Resulting sequences are merged back in the original draft assembly producing a new, gap-filled genome sequence.