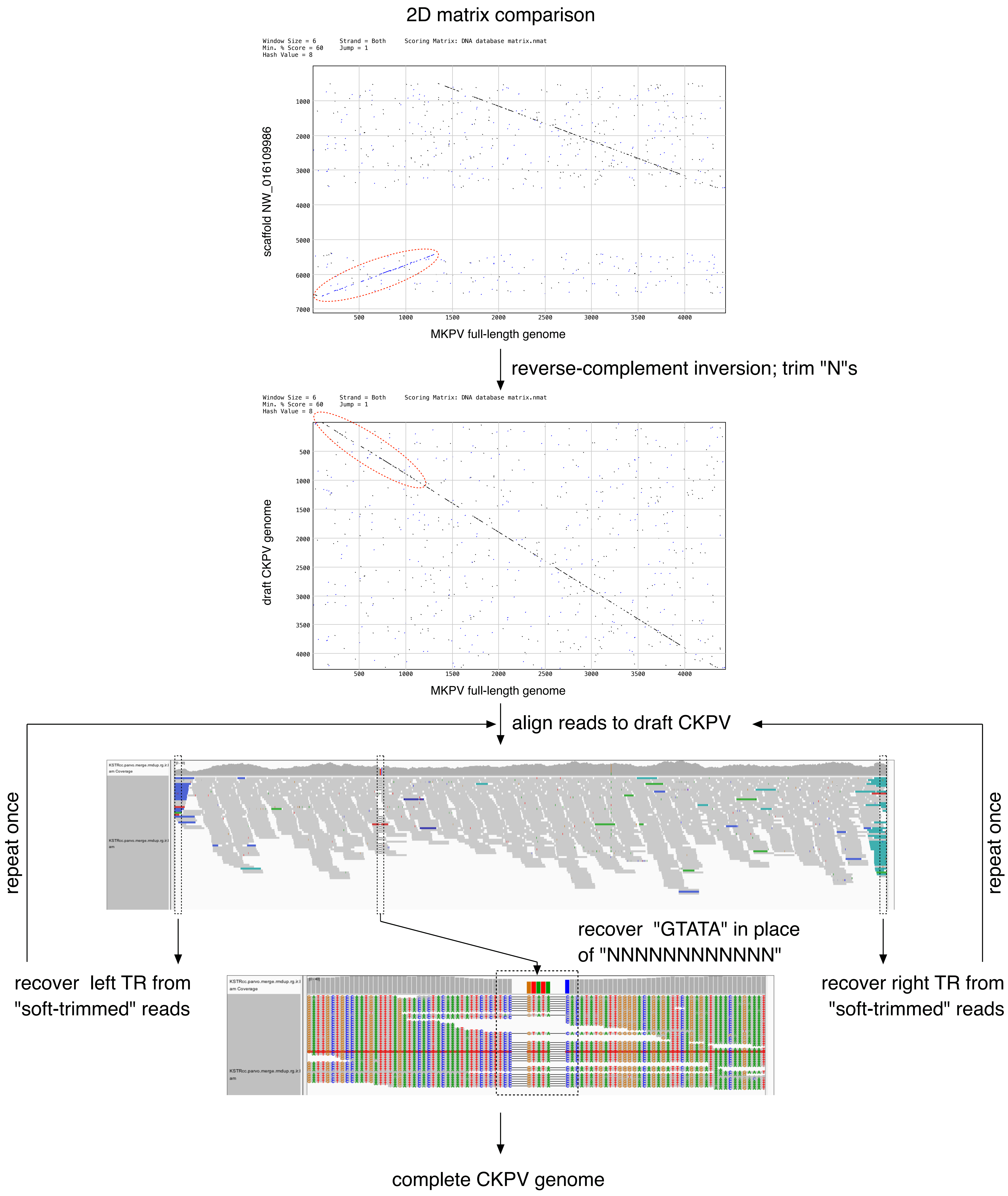
2D matrix comparison
Window Size = 6
Min. % Score = 60
Hash Value = 8
Strand = Both
Jump = 1
Scoring Matrix: DNA database matrix.nmat
scaffold NW_016109986
1000
2000
3000
4000
5000
6000
7000
500
1000
1500
2000
2500
3000
3500
4000
MKPV full-length genome
reverse-complement inversion; trim "N"s
Window Size = 6
Min. % Score = 60
Hash Value = 8
Strand = Both
Jump = 1
Scoring Matrix: DNA database matrix.nmat
draft CKPV genome
500
1000
1500
2000
2500
3000
3500
4000
500
1000
1500
2000
2500
3000
3500
4000
MKPV full-length genome
align reads to draft CKPV
repeat once
repeat once
recover "GTATA" in place of "NNNNNNNNNNNN"
recover left TR from "soft-trimmed" reads
recover right TR from "soft-trimmed" reads
complete CKPV genome