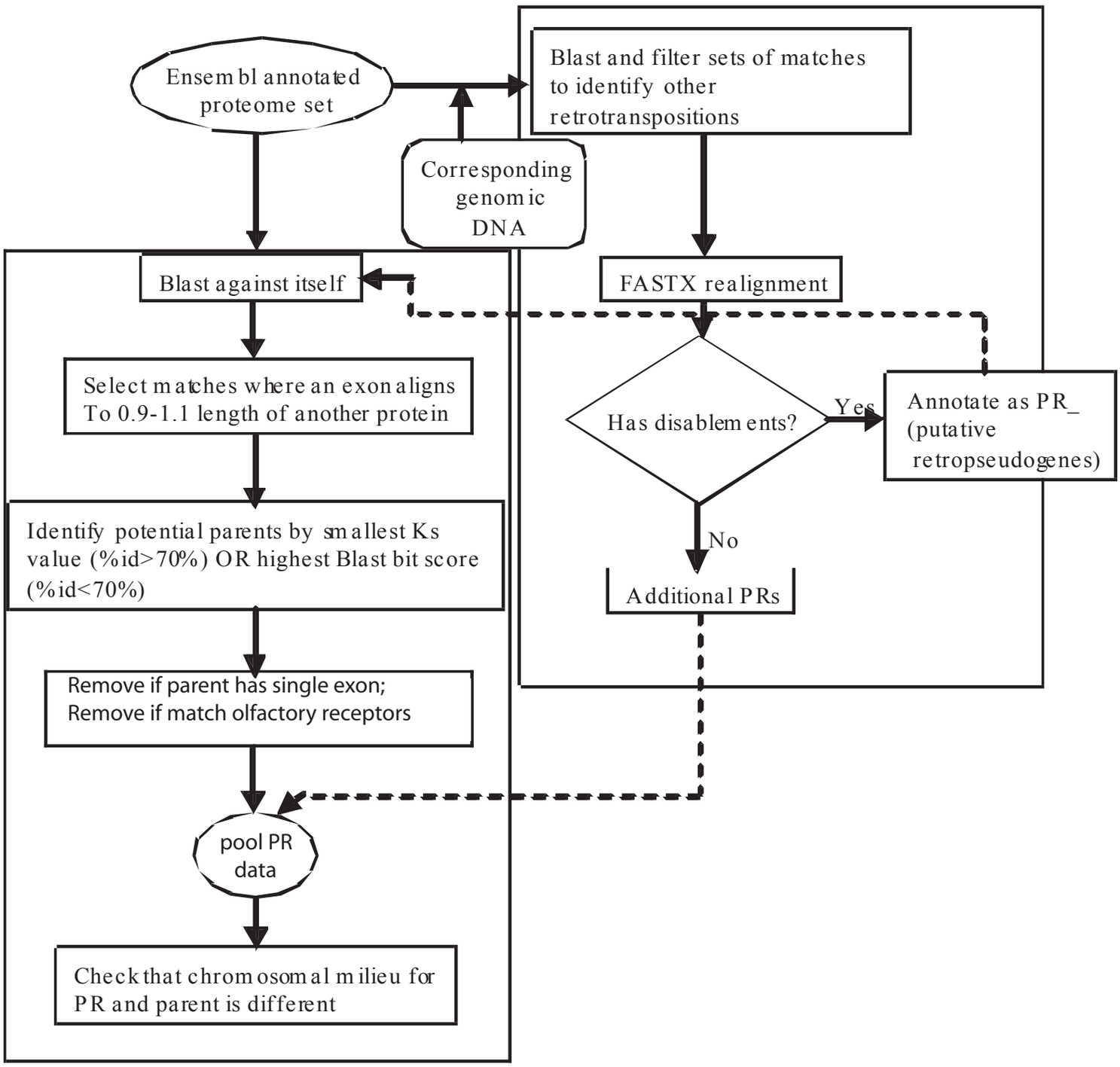
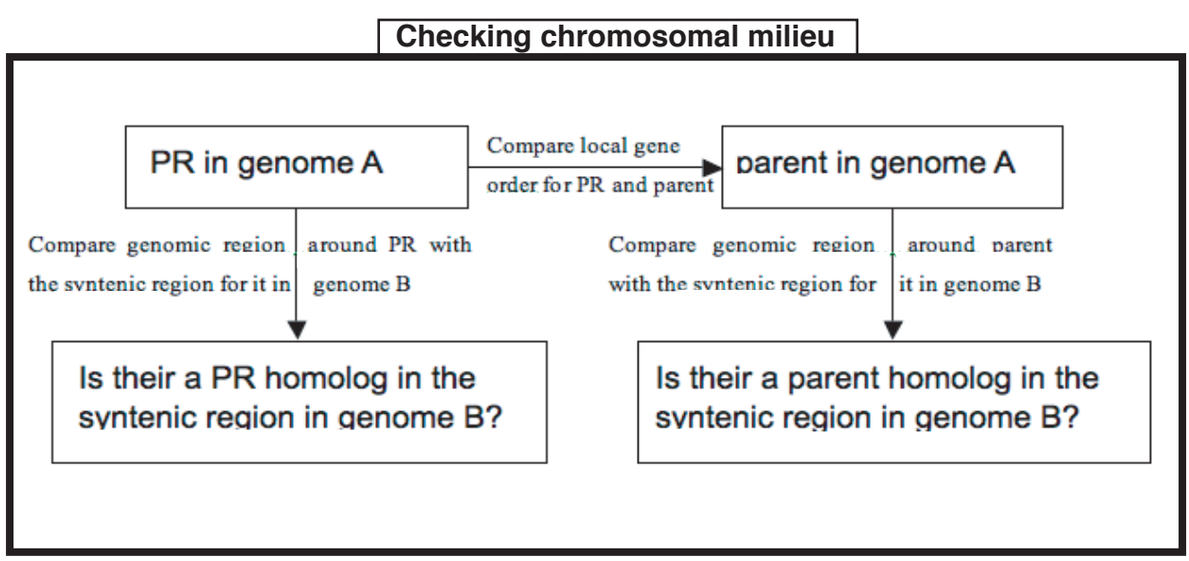

Ensembl annotated proteome set
Blast and filter sets of matches to identify other retrotranspositions
Corresponding genomic DNA
Blast against itself
FASTX realignment
Select matches where an exon aligns To 0.9-1.1 length of another protein
Has disablements?
Yes
Annotate as PR_ (putative retropseudogenes)
No
Additional PRs
Identify potential parents by smallest Ks value (%id>70%) OR highest Blast bit score (%id<70%)
Remove if parent has single exon; Remove if match olfactory receptors
pool PR data
Check that chromosomal milieu for PR and parent is different


Checking chromosomal milieu
PR in genome A
Compare local gene order for PR and parent
parent in genome A
Compare genomic region around PR with the syntenic region for it in genome B
Compare genomic region around parent with the syntenic region for it in genome B
Is their a PR homolog in the syntenic region in genome B?
Is their a parent homolog in the syntenic region in genome B?