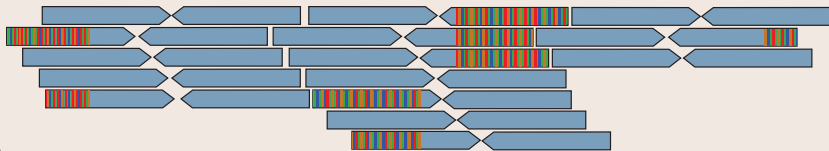


## Complete – Run All Indelible Steps

### Fetch – Identify SRs exome-wide



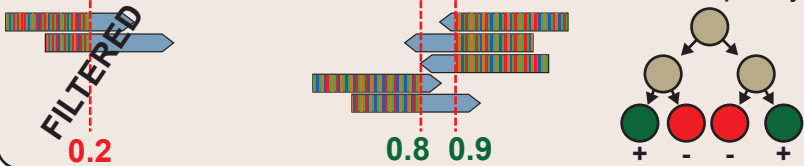
### Aggregate – Merge SRs into clusters



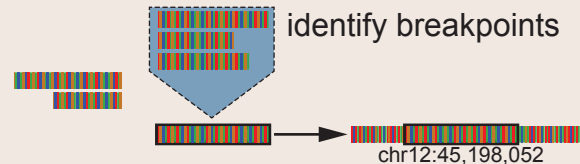
### Train – Retrain RandomForest



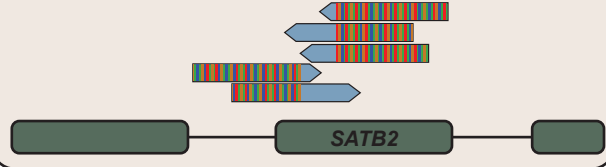
### Score – Use RandomForest to assess cluster quality



### Database – Build MAF database and identify breakpoints



### Annotate – Gene and MAF Annotation



### denovo – Assess parental contribution

