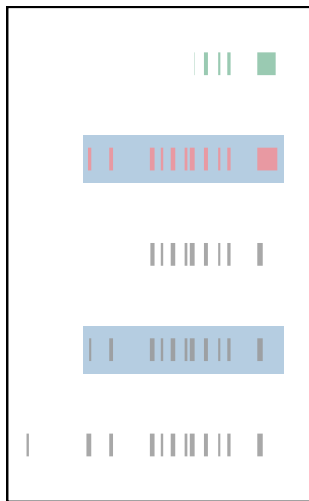


Bma-gar-3



Structural Category

- Full-Splice Match
- Incomplete-Splice Match
- Reference Transcripts

0.1875

0.1872

0.1869

0.1866

Chr X Position (Mb)