A

Length distribution of transcripts

B

New transcripts classification

- **c**: Complete match of intron chain
- **i**: Transfrag falling entirely within a reference intron
- **j**: Potentially novel isoform (fragment): at least one splice junction is shared with a reference transcript
- **o**: Generic exonic overlap with a reference transcript
- **u**: Unknown, intergenic transcript
- **x**: Exonic overlap with reference on the opposite strand
- **=**: Complete match of intron chain