fraction of annotated genes that:

|  |  |
| --- | --- |
| perfectly match both ends of one of predicted genes: | 0.37605126151381657 |
| match the start but not the end of a predicted gene: | 0.0 |
| match the end but not the start of a predicted gene: | 0.45694833800560675 |
| do not match either the start or end of a predicted gene: | 0.16700040048057668 |

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