|  |  |  |  |  |
| --- | --- | --- | --- | --- |
|  |  | **Sensitivity on forward strand** | **Sensitivity on both strands** | **Specificity** |
| **One Stranded Model** | *E.Coli* | 95.7% | 72.4% | 83.5% |
| **One Stranded Model** | *Yeast* | 97.6% | 54.4% | 94.6% |
| **One Stranded Model** | *Arabidopsis* | 55.3% | 36.1% | 94.9% |
| **One Stranded Model** | *Fly* | 21.10% | 12.1% | 93.2% |
| **Two Stranded Model** | *E.Coli* | 95.4% | 95.6% | 79.3% |
| **Two Stranded Model** | *Yeast* | 97.7% | 57.3% | 93.7% |
| **Two Stranded Model** | *Arabidopsis* | 52.2% | 34.7% | 95.4% |
| **Two Stranded Model** | *Fly* | 21.8% | 24.4% | 83.5% |
| **Two Stranded Model with Introns** | *E.Coli\** | 66.4% | 81.1% | 75.1% |
| **Two Stranded Model with Introns** | *Yeast* | 100% | 100% | 0.1% |
| **Two Stranded Model with Introns** | *Arabidopsis* | 12.3% | 11.2% | 96.8% |
| **Two Stranded Model with Introns** | *Fly* | 100.0% | 100.0% | 2.8% |

\* *E.Coli* does not have any introns. With that information, if intron transitions are 0.0 but D-Splice, A-Splice transitions are left intact, this is the result. However, if D-Splice and A-Splice sites do not exist, either, the result would be the same as it was with 2 strands and no introns.