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| --- | --- | --- | --- | --- | --- | --- |
| **Study** | **Seq. start** | **Plat-form** | **Species** | **% Poly(A) identifying reads** | **Percentage of mapped reads in 3’UTR3** | **Limitations** |
| RNA-Seq | RNA-Seq | HiSeq | *S. cerevisiae* | 0.18% | 19% | Not designed for mapping poly(A) sites |
| Beck *et al.* 2010 | 5’ end | GAII | *H. sapiens* | - | 33-40% | Stringent size selection required, PE reads do not add value |
| Ozsolak *et al.* 2010  (**HELICOS** **DRS**) | 3’ end | Helicos DRS | *S. cerevisiae,*  *H. sapiens* | - | 91% | Short read length, limited availability, lower throughput |
| Yoon & Brem 2010 | 5’ end | GAII | *S. cerevisiae* | - | 35% | Not strand-specific, 50% of reads sequence through a poly(T) stretch resulting in low quality |
| Fox-Walsh *et al.* 2011 | 5’ end | GAII | *H. sapiens* | - | 85% | Stringent size selection required, PE reads do not add value |
| Shepard *et al.* 2011  (**PAS-seq**) | 3’ end | GAII | *H. sapiens* | - | 63% | Decreased quality due to desynchronized sequencing start (polymerase slippage on cluster) |
| Jan *et al.* 2011 | 3’ end | GAII | *C. elegans* | - | - | Protocol includes many RNA manipulation steps, reduced cluster recognition due to remaining A's |
| Pelechano et al. 2012 | 5’ end | HiSeq | *S. cerevisiae* | 47.0% | 89% | Stringent size selection required, PE reads do not add value |
| Derti *et al.* 2012 | 3’ end | GAIIx | *5 mammals* | - | 17-27% | Decreased quality due to desynchronized sequencing start (polymerase slippage on cluster) |
| Wilkening et al. 2012 (**3'FILL**) | 3’ end | HiSeq | *S. cerevisiae* | 74.4% | 92% | Access to cluster station required |
| Hoque et al. 2013 (**3'READS**) | 5’ end | GAIIx | *M. musculus* | 56% | 66.3-91.1% | ? |

**TABLE-1**