# Index of selected raw results

## Quantifying tail length slippage using spike-in standards

- Tail run lengths until the first 1-5 non-A bases in reads mapped to spike-in poly(A) tracts [PDF](PDF)

## Alignment

| Sample | Alignment log | Alignment report |
|---|---|---|
| MUT1A | TXT | PDF |
| MUT1B | TXT | PDF |
| MUT1C | TXT | PDF |
| MUT1D | TXT | PDF |
| MUT2A | TXT | PDF |
| MUT2B | TXT | PDF |
| MUT2C | TXT | PDF |
| MUT2D | TXT | PDF |

## Parsing alignments

| Sample | Parse log | Parse report |
|---|---|---|
| MUT1A | TXT | PDF |
| MUT1B | TXT | PDF |
| MUT1C | TXT | PDF |
| MUT1D | TXT | PDF |
| MUT2A | TXT | PDF |
| MUT2B | TXT | PDF |
| MUT2C | TXT | PDF |
| MUT2D | TXT | PDF |

## Testing differences between wild type and mutant tail runs

| Comparison | Test log | Test report | Results |
|---|---|---|---|
| WT1 vs. MUT1 | TXT | PDF | CSV |
| WT2 vs. MUT2 | TXT | PDF | CSV |

## Tail run distributions from all transcripts with G-tail coverage > 1000

- WT1
- WT2

- [MUT1](#)
- [MUT2](#)

## Cross-study correlation

- [PAL_total vs. WT1](#)
- [PAL_total vs. WT2](#)
- [PAL_total vs. PASTA](#)