

2D Alignment

This report shows the result of aligning 2D reads against the reference genome. Select a row to filter reads with any Exit Status from the rest of the report

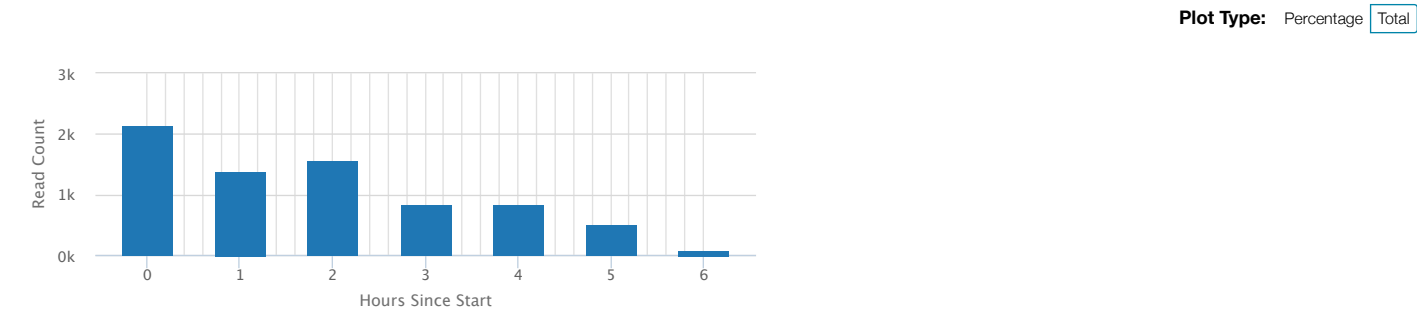
☰ Read Count per Run ID

| Run ID | Read Count | |
|-------------------|------------|------------------|
| NA | 7381 | Showing ✓ |
| Total Read Count: | | 7381 out of 7381 |

☰ Read Count per Exit Status

| Exit Status | Read Count | |
|---------------------|------------|------------------|
| Workflow successful | 7381 | Showing ✓ |
| Total Read Count: | | 7381 out of 7381 |

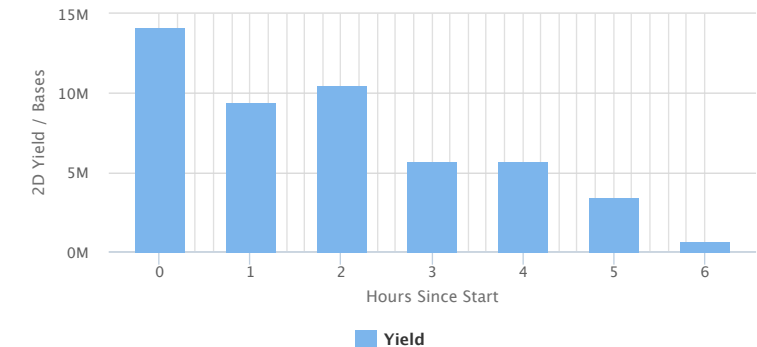
📊 Exit Status vs. Time

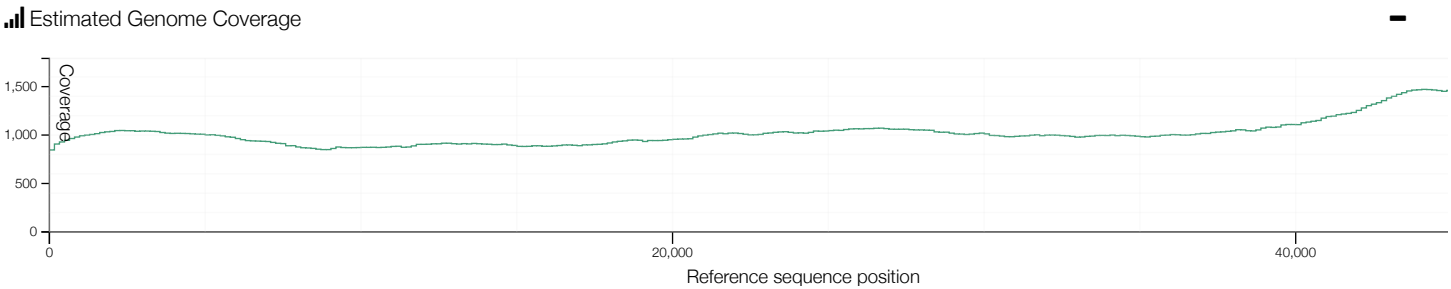


☰ Alignment - Key Figures

| | Unfiltered | Filtered |
|------------------------------|---------------|---------------|
| Alignment Accuracy - Average | 0.87 | 0.87 |
| Alignment Accuracy - Median | 0.88 | 0.88 |
| Alignment Accuracy - Mode | 0.93 | 0.93 |
| Total Aligned 2D Yield | 50.53 M bases | 50.53 M bases |

📊 Aligned 2D Yield vs. Time





Reads per Genome

Read Count ▾

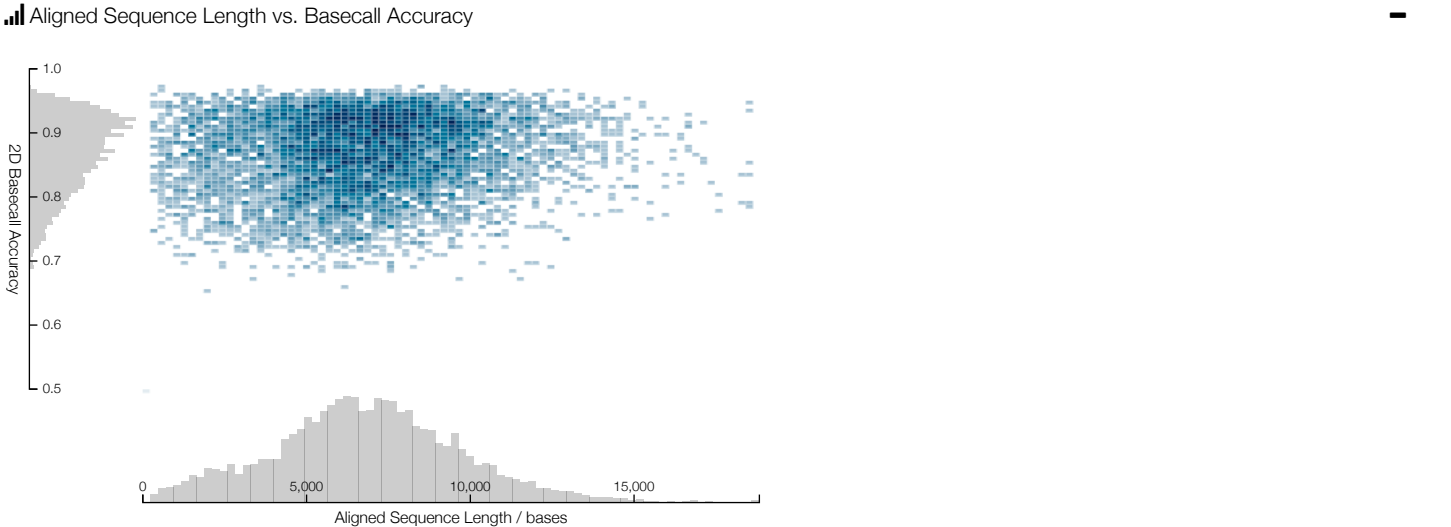
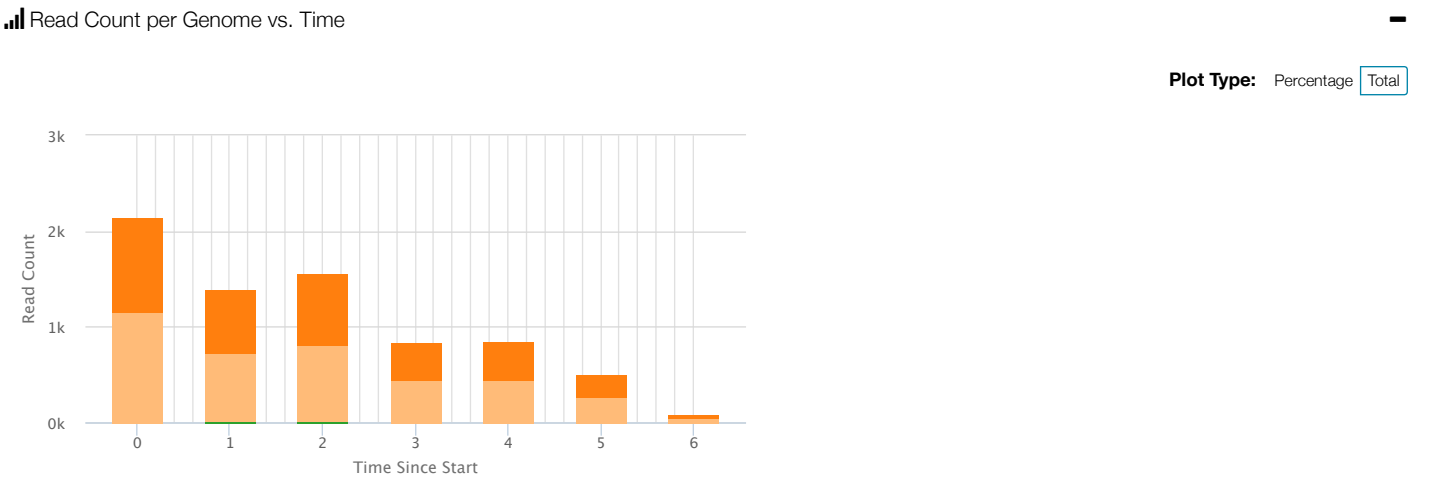
All ☒

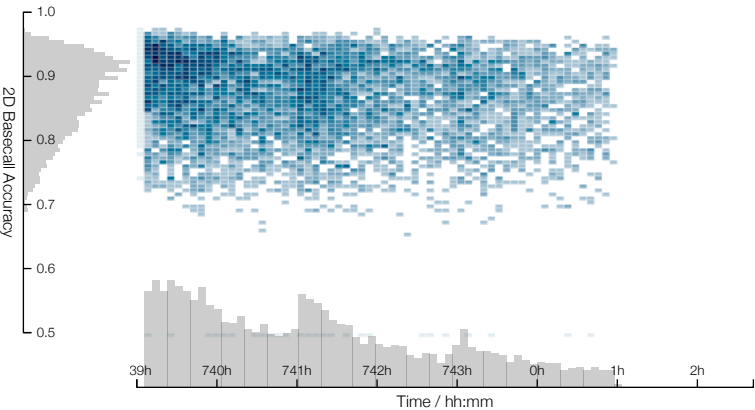
None ☐

| | | |
|----------------------|------|--|
| <div>Lambda_rc</div> | 3867 | <div>Showing <input checked="" type="checkbox"/></div> |
| <div>Lambda</div> | 3477 | <div>Showing <input checked="" type="checkbox"/></div> |
| <div>No Match</div> | 37 | <div>Showing <input checked="" type="checkbox"/></div> |

Total Read Count:

7381 out of 7381





2D Alignment - v1.2.8