

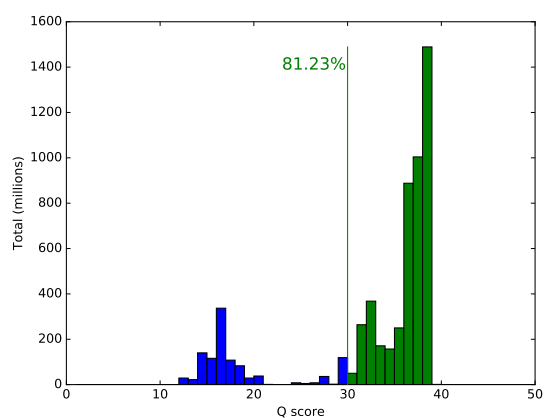
MiSeq Quality Check

<Run_name>

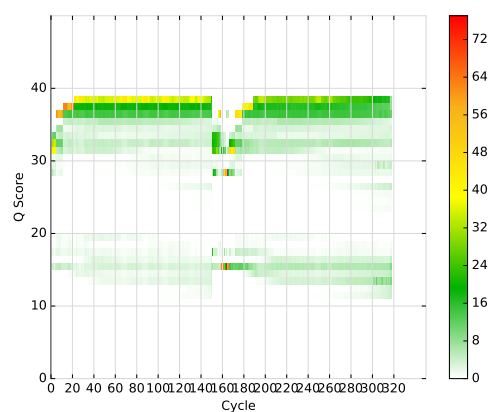
27/05/2016

1 Quality data

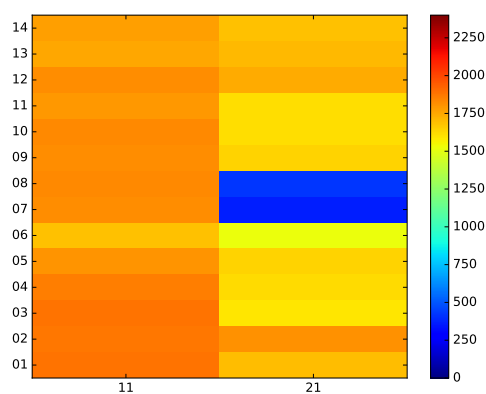
| Data | Value | Pass/Fail |
|------------------------------|---------|-----------|
| Mean Cluster Density (k/mm2) | 1650.96 | |
| Clusters passed filter (%) | 61.17 | |
| Average \geq Q30 | 81.23 | |
| 1st full read \geq Q30 | 42.56 | |
| 2nd full read \geq Q30 | 37.92 | |



(a) Q-score distribution plot (all reads all cycles)



(b) Q-score heat map



(c) Cluster density per tile

2 Phas/Prephas data

| Data | Value | Pass/Fail |
|---------------|---------------|-----------|
| 1st full read | 0.063 / 0.014 | |
| 2nd full read | 0.144 / 0.012 | |

3 Indexing

| Total Reads | PF Reads | % Reads Identified (PF) | Min | Max |
|-------------|----------|-------------------------|--------|--------|
| 6824732 | 3382992 | 49.5696 | 0.0192 | 4.0140 |

| Sample_ID | Index | Index2 | % Reads Identified (PF) |
|-----------|-----------|----------|-------------------------|
| 1 | TAAGGCCGA | CTCTCTAT | 0.0192 |
| 2 | CGTACTAG | CTCTCTAT | 3.4152 |
| 3 | AGGCAGAA | CTCTCTAT | 2.6494 |
| 4 | TCCTGAGC | CTCTCTAT | 3.4582 |
| 5 | GGACTCCT | CTCTCTAT | 3.7589 |
| 6 | TAGGCATG | CTCTCTAT | 3.7270 |
| 7 | CTCTCTAC | CTCTCTAT | 3.0917 |
| 8 | CAGAGAGG | CTCTCTAT | 2.4057 |
| 9 | GCTACGCT | CTCTCTAT | 2.9730 |
| 10 | CGAGGCTG | CTCTCTAT | 3.1706 |
| 11 | AAGAGGCA | CTCTCTAT | 3.9600 |
| 12 | GTAAGGGA | CTCTCTAT | 4.0140 |
| 13 | TAAGGCCGA | GTAAGGAG | 3.5041 |
| 14 | CGTACTAG | GTAAGGAG | 2.2892 |
| 15 | AGGCAGAA | GTAAGGAG | 2.7785 |
| 16 | TCCTGAGC | GTAAGGAG | 1.5194 |
| 17 | GGACTCCT | GTAAGGAG | 2.8356 |

