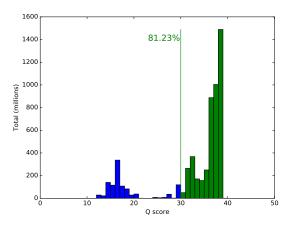
## MiSeq Quality Check

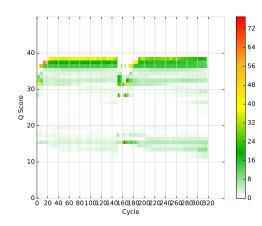
 $160628\_\mathrm{merged}$ 

29/06/2016

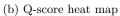
## 1 Quality data

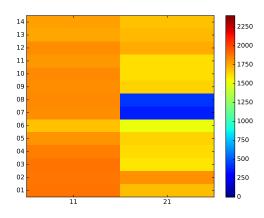
Data	Value	Pass/Fail
Mean Cluster Density (k/mm2)	1650.96	
Clusters passed filter (%)	61.17	
Average $>= Q30$	81.23	
1st full read $>= Q30$	42.56	
2nd full read $\geq$ Q30	37.92	





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





(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	TAAGGCGA	CTCTCTAT	0.0192	
2	CGTACTAG	CTCTCTAT	3.4152	
3	AGGCAGAA	CTCTCTAT	2.6494	5
4	TCCTGAGC	CTCTCTAT	3.4582	
5	GGACTCCT	CTCTCTAT	3.7589	4
6	TAGGCATG	CTCTCTAT	3.7270	
7	CTCTCTAC	CTCTCTAT	3.0917	3
8	CAGAGAGG	CTCTCTAT	2.4057	• • •
9	GCTACGCT	CTCTCTAT	2.9730	sp 2 2
10	CGAGGCTG	CTCTCTAT	3.1706	
11	AAGAGGCA	CTCTCTAT	3.9600	1
12	GTAGAGGA	CTCTCTAT	4.0140	
13	TAAGGCGA	GTAAGGAG	3.5041	
14	CGTACTAG	GTAAGGAG	2.2892	-1
15	AGGCAGAA	GTAAGGAG	2.7785	*0 2 4 6 8 10 12 14 16 18 Sample_ld
16	TCCTGAGC	GTAAGGAG	1.5194	
17	GGACTCCT	GTAAGGAG	2.8356	