

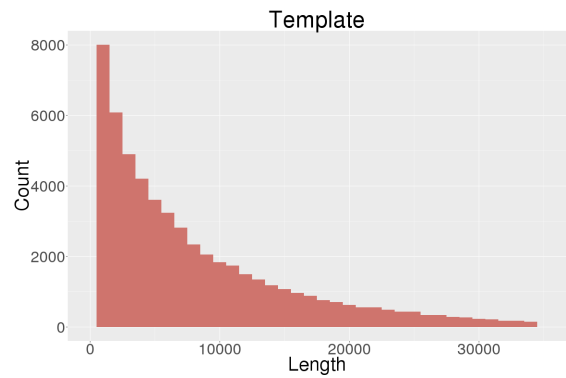
NanoOK report for UBC_MARC_1D_R9_107_Called

Pass and fail counts

Type	Pass	Fail
Template	56904	0

Read lengths

Type	NumReads	TotalBases	Mean	Longest	Shortest	N50	N50Count	N90	N90Count
Template	56904	526340999	9249.63	141200	13	16214	9728	4560	32983



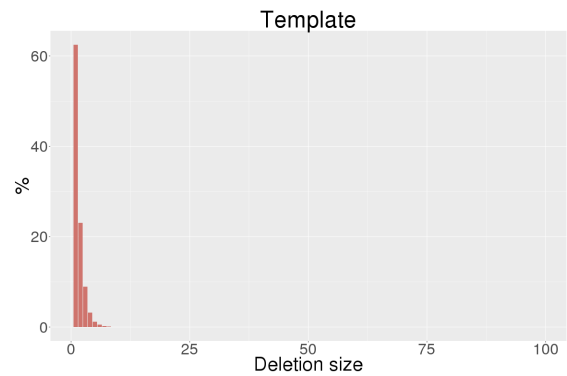
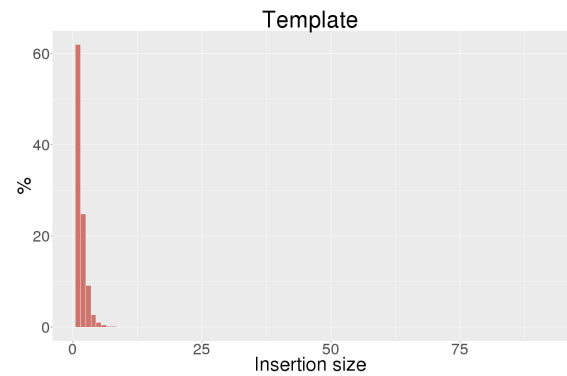
Template alignments

Number of reads	56904
Number of reads with alignments	56830 (99.87%)
Number of reads without alignments	74 (0.13%)

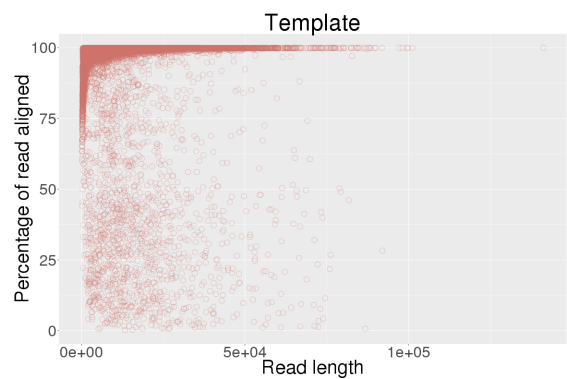
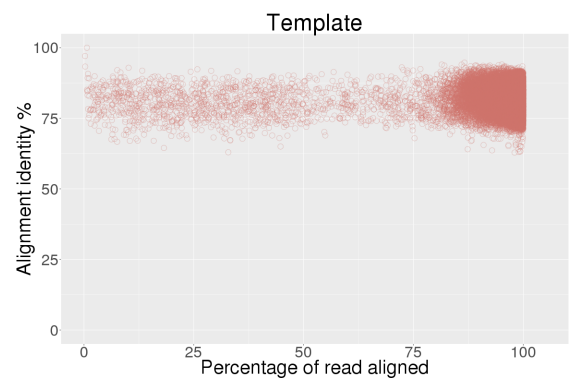
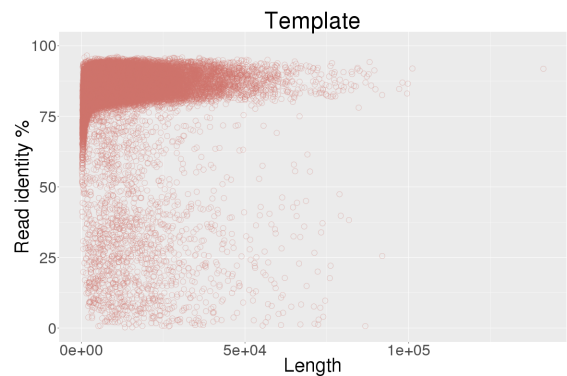
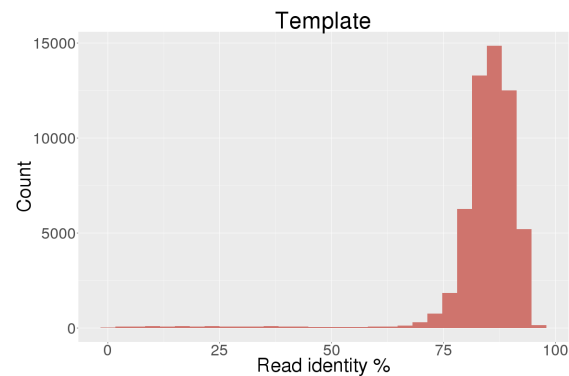
ID	Size	Number of Reads	% of Reads	Mean read length	Aligned bases	Mean coverage	Longest Perf Kmer
Control sequence	3560	0	0.00	0.00	0	0.00	0
Escherichia coli	4641652	56830	99.87	9234.13	539931271	116.32	235

Escherichia coli error analysis

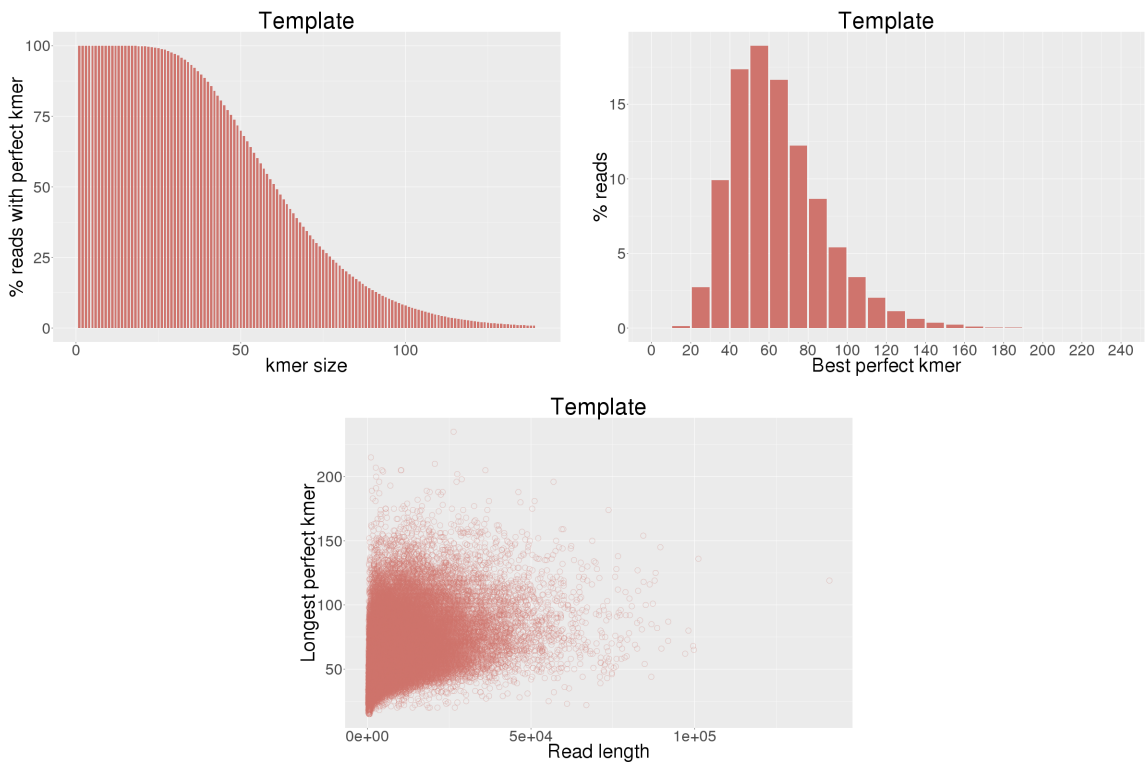
	Template
Overall base identity (excluding indels)	83.81%
Aligned base identity (excluding indels)	90.77%
Identical bases per 100 aligned bases (including indels)	81.46%
Inserted bases per 100 aligned bases (including indels)	3.22%
Deleted bases per 100 aligned bases (including indels)	7.04%
Substitutions per 100 aligned bases (including indels)	8.28%
Mean insertion size	1.59
Mean deletion size	1.63



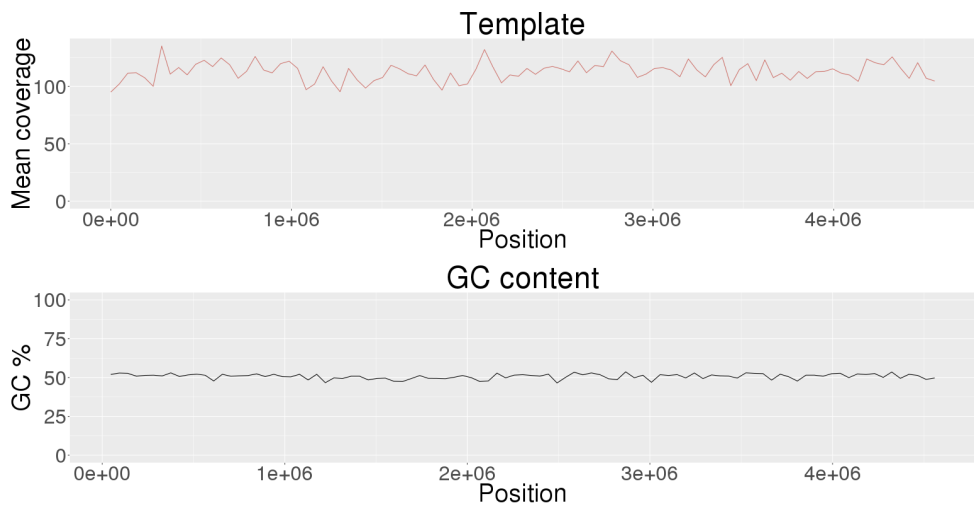
Escherichia coli read identity



Escherichia coli perfect kmers



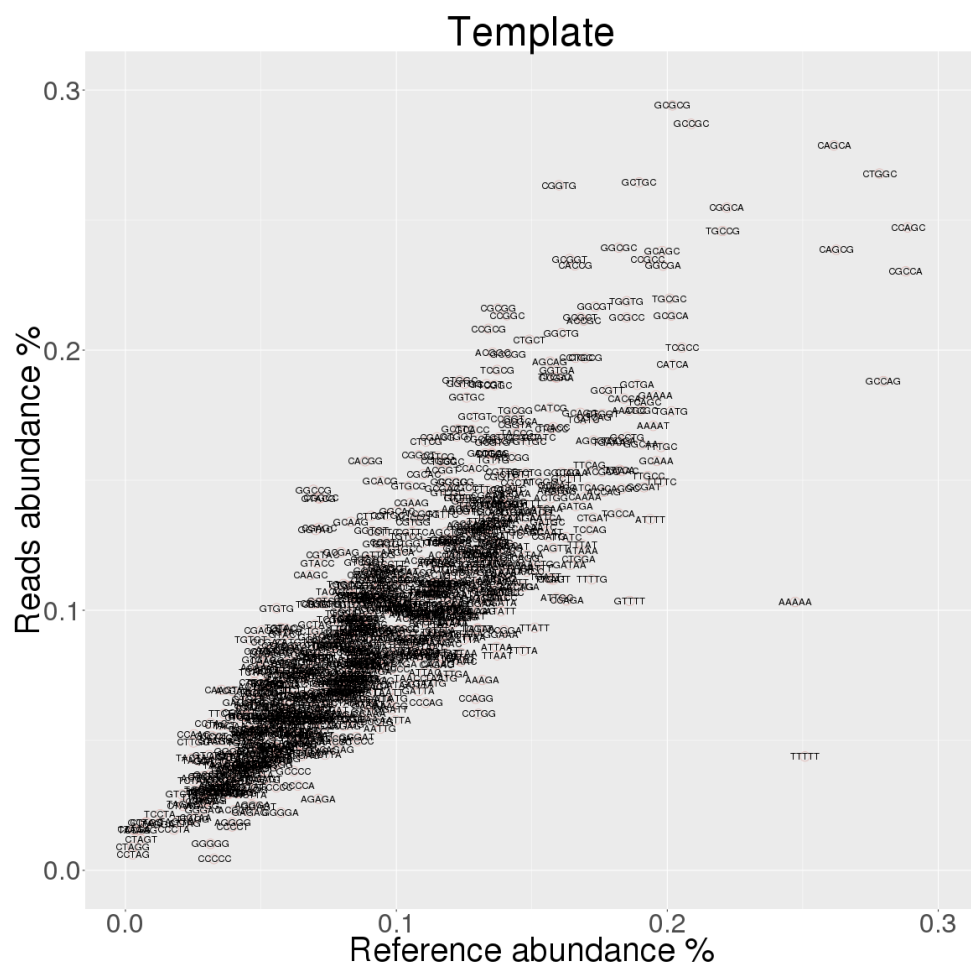
Escherichia coli coverage



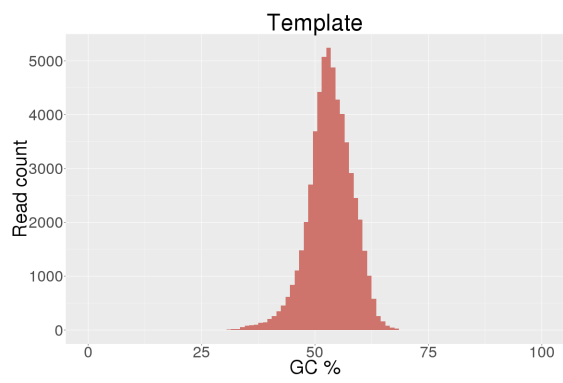
Under-represented 5-mers

Rank	kmer	Template		
		Ref %	Read %	Diff %
1	TTTTT	0.251	0.044	-0.207
2	AAAAA	0.247	0.103	-0.144
3	GCCAG	0.280	0.188	-0.092
4	GTTTT	0.186	0.104	-0.082
5	CCTGG	0.130	0.060	-0.070
6	CCAGG	0.129	0.066	-0.063
7	TTTTA	0.147	0.084	-0.062
8	TTTTG	0.172	0.112	-0.060
9	CCAGA	0.163	0.104	-0.059
10	ATTTT	0.194	0.135	-0.059

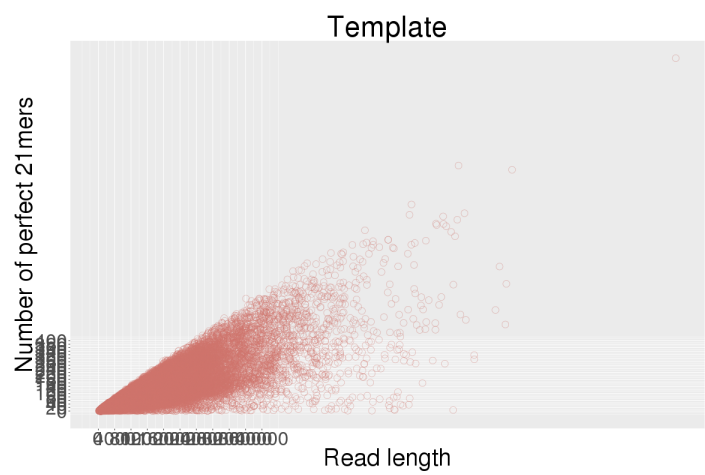
Rank	Template			
	kmer	Ref %	Read %	Diff %
1	CGGCG	0.221	0.381	0.160
2	GCGGC	0.210	0.339	0.130
3	GGCGG	0.190	0.300	0.111
4	CGCGC	0.201	0.308	0.107
5	CGGTG	0.160	0.263	0.103
6	GCGCG	0.202	0.294	0.092
7	CGCCG	0.219	0.305	0.086
8	CGCGG	0.137	0.216	0.079
9	GCCGC	0.209	0.287	0.078
10	GGCCG	0.069	0.146	0.077



Escherichia coli GC content



All reference 21mer analysis



All reference substitutions

Reference		Template substituted %			
		a	c	g	t
Reference	A	0.00	8.14	17.64	4.66
	C	3.48	0.00	3.87	11.82
	G	11.66	4.14	0.00	3.45
	T	4.66	18.24	8.24	0.00







Kmer motifs before errors

3-mer error motif analysis

Rank	Insertion	Deletion	Substitution	Most common
1	TTC (3.27%)	CGC (3.44%)	CGC (4.04%)	
2	CGC (3.02%)	TTC (3.03%)	GCC (3.59%)	
3	ATC (2.84%)	GCC (2.95%)	ATC (3.18%)	
4	TTT (2.67%)	ATC (2.84%)	TGC (3.14%)	
5	GCC (2.64%)	GCG (2.81%)	ACC (3.13%)	
6	TGC (2.37%)	GGC (2.77%)	TTC (3.01%)	
7	GCG (2.33%)	TTT (2.72%)	GGC (2.99%)	
8	ACC (2.32%)	ACC (2.53%)	AAC (2.78%)	
9	GGC (2.19%)	TGC (2.25%)	AGC (2.55%)	
10	CTG (2.07%)	AGC (2.17%)	TTT (2.48%)	
				Least common
-10	TGG (1.07%)	TTA (0.98%)	GTA (0.87%)	
-9	AGT (0.91%)	GTA (0.88%)	ACT (0.84%)	
-8	TAA (0.89%)	GGA (0.86%)	CCT (0.83%)	
-7	GAG (0.87%)	AGT (0.82%)	GAG (0.82%)	
-6	AGA (0.84%)	TAA (0.81%)	AGA (0.66%)	
-5	GGA (0.81%)	AGG (0.77%)	GGG (0.65%)	
-4	AGG (0.74%)	CCT (0.67%)	GGA (0.60%)	
-3	CTA (0.50%)	GGG (0.63%)	AGT (0.59%)	
-2	GGG (0.50%)	TAG (0.39%)	TAG (0.40%)	
-1	TAG (0.43%)	CTA (0.37%)	CTA (0.30%)	

Kmer space for 3-mers: 64 Random chance for any given 3-mer: 1.56%

4-mer error motif analysis







Rank	Insertion	Template Deletion	Substitution
1	CGCC (1.13%)	CGCC (1.28%)	CGCC (1.56%)
2	TTTC (1.12%)	GCGC (1.20%)	GCGC (1.30%)
3	GCGC (1.01%)	GCGC (1.07%)	CAGC (1.20%)
4	CAGC (0.92%)	CAGC (1.06%)	GCGC (1.12%)
5	CATC (0.87%)	TTTC (1.00%)	CATC (1.04%)
6	GCTG (0.85%)	GCGC (0.97%)	CACC (1.02%)
7	CTTC (0.84%)	CATC (0.93%)	ACGC (0.97%)
8	CGGC (0.81%)	CACC (0.87%)	CCGC (0.96%)
9	CACC (0.78%)	CCGC (0.83%)	TGGC (0.94%)
10	GCCA (0.77%)	TGGC (0.83%)	TGCC (0.91%)
			
-10	GGGA (0.11%)	CTTA (0.11%)	GGGG (0.09%)
-9	TCTA (0.11%)	ACTA (0.10%)	CTAA (0.09%)
-8	TTAG (0.10%)	GGGG (0.09%)	TAGT (0.08%)
-7	AGGG (0.09%)	TTAG (0.09%)	ACTA (0.08%)
-6	CTAA (0.08%)	TCTA (0.09%)	GAGT (0.08%)
-5	TAGA (0.08%)	CCCT (0.09%)	TAGG (0.08%)
-4	CCTA (0.07%)	CTAA (0.08%)	TCTA (0.06%)
-3	GGGG (0.07%)	TAGG (0.06%)	TAGA (0.06%)
-2	TAGG (0.06%)	CCTA (0.05%)	CCTA (0.04%)
-1	CTAG (0.01%)	CTAG (0.01%)	CTAG (0.01%)
			

Most common

Least common

Kmer space for 4-mers: 256 Random chance for any given 4-mer: 0.39%

5-mer error motif analysis

Rank	Insertion	Template Deletion	Substitution
1	CGCCA (0.37%)	GCGGC (0.39%)	CCAGC (0.46%)
2	CCAGC (0.35%)	CCAGC (0.38%)	CCGCC (0.43%)
3	ATTTT (0.34%)	GCGGC (0.36%)	TCGCC (0.41%)
4	GCGGC (0.32%)	TCGCC (0.35%)	GCGGC (0.41%)
5	GTTTC (0.31%)	CCGCC (0.34%)	CTGGC (0.40%)
6	CCGCC (0.30%)	TGGCG (0.34%)	GCGCC (0.38%)
7	TCGCC (0.30%)	GCGGC (0.32%)	GCGGC (0.37%)
8	GCGGC (0.29%)	CTGGC (0.32%)	GCGGC (0.37%)
9	CAGCA (0.29%)	GCGGC (0.31%)	ACGCC (0.35%)
10	TGCTG (0.28%)	TGCGC (0.30%)	GCGC (0.35%)
			
-10	CTAGC (0.01%)	CCTGG (0.01%)	CTAGC (0.01%)
-9	CCTGG (0.01%)	CCAGG (0.01%)	GGGGG (0.01%)
-8	ACTAG (0.00%)	CTAGC (0.00%)	TAGGA (0.01%)
-7	GCTAG (0.00%)	CTAGT (0.00%)	ACTAG (0.00%)
-6	GGGGG (0.00%)	ACTAG (0.00%)	CTAGT (0.00%)
-5	CTAGT (0.00%)	GCTAG (0.00%)	GCTAG (0.00%)
-4	TCTAG (0.00%)	TCTAG (0.00%)	TCTAG (0.00%)
-3	CTAGA (0.00%)	CTAGA (0.00%)	CTAGG (0.00%)
-2	CCTAG (0.00%)	CTAGG (0.00%)	CCTAG (0.00%)
-1	CTAGG (0.00%)	CCTAG (0.00%)	CTAGA (0.00%)
			

Most common

Least common

Kmer space for 5-mers: 1024 Random chance for any given 5-mer: 0.10%