

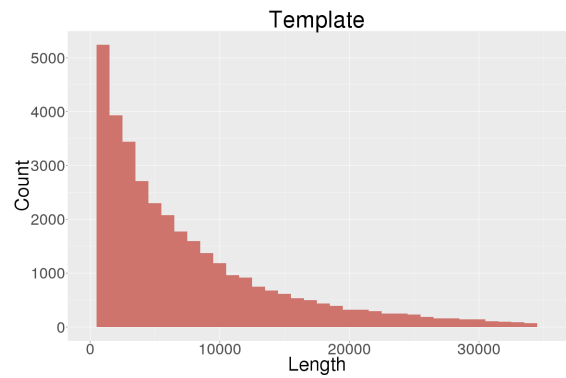
NanoOK report for UBC_MARC_1D_R9_107_Called

Pass and fail counts

Type	Pass	Fail
Template	0	39259

Read lengths

Type	NumReads	TotalBases	Mean	Longest	Shortest	N50	N50Count	N90	N90Count
Template	39259	303312093	7725.93	478773	5	14797	5959	4095	20780



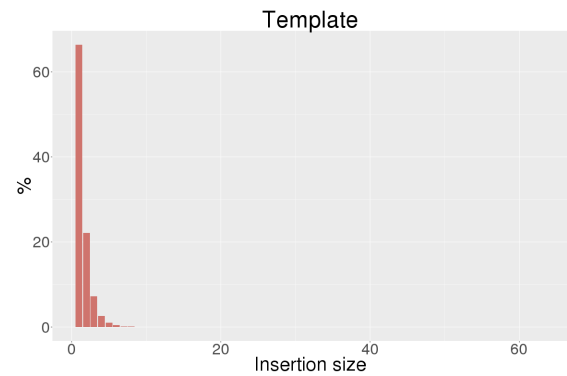
Template alignments

Number of reads	39259
Number of reads with alignments	24578 (62.60%)
Number of reads without alignments	14681 (37.40%)

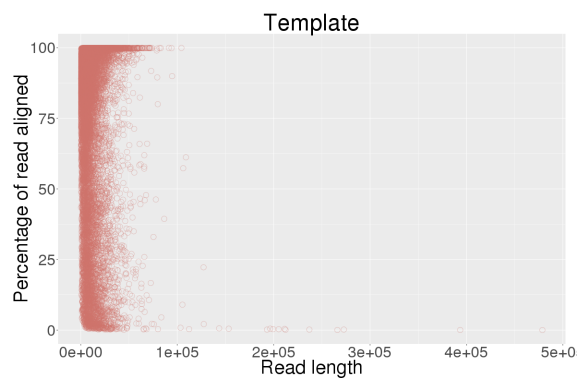
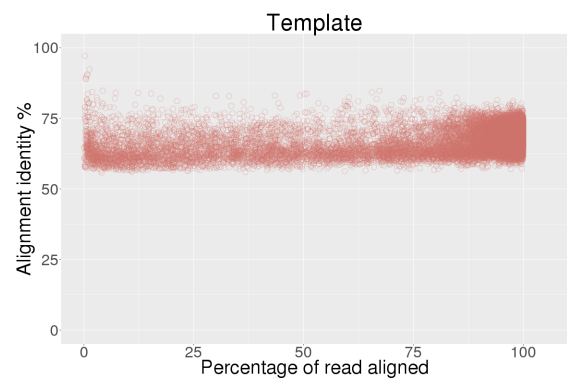
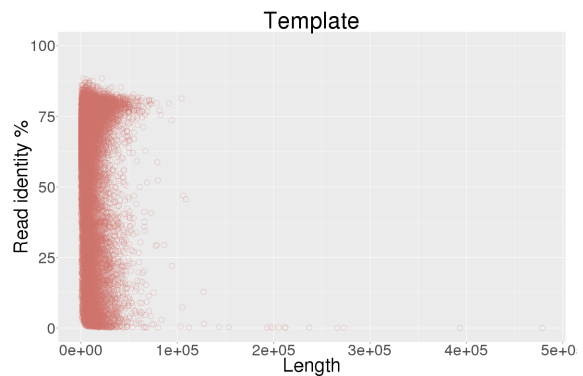
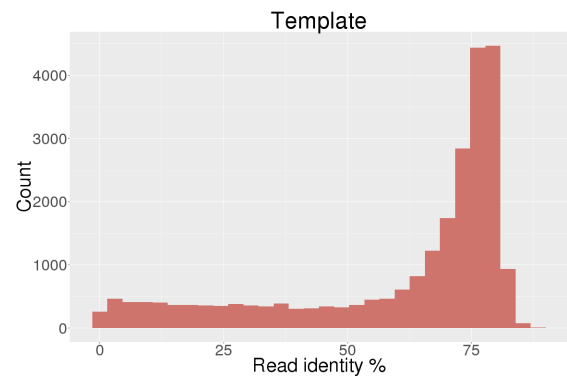
ID	Size	Number of Reads	% of Reads	Mean read length	Aligned bases	Mean coverage	Longest Perf Kmer
Control sequence	3560	0	0.00	0.00	0	0.00	0
Escherichia coli	4641652	24578	62.60	10089.79	202279583	43.58	124

Escherichia coli error analysis

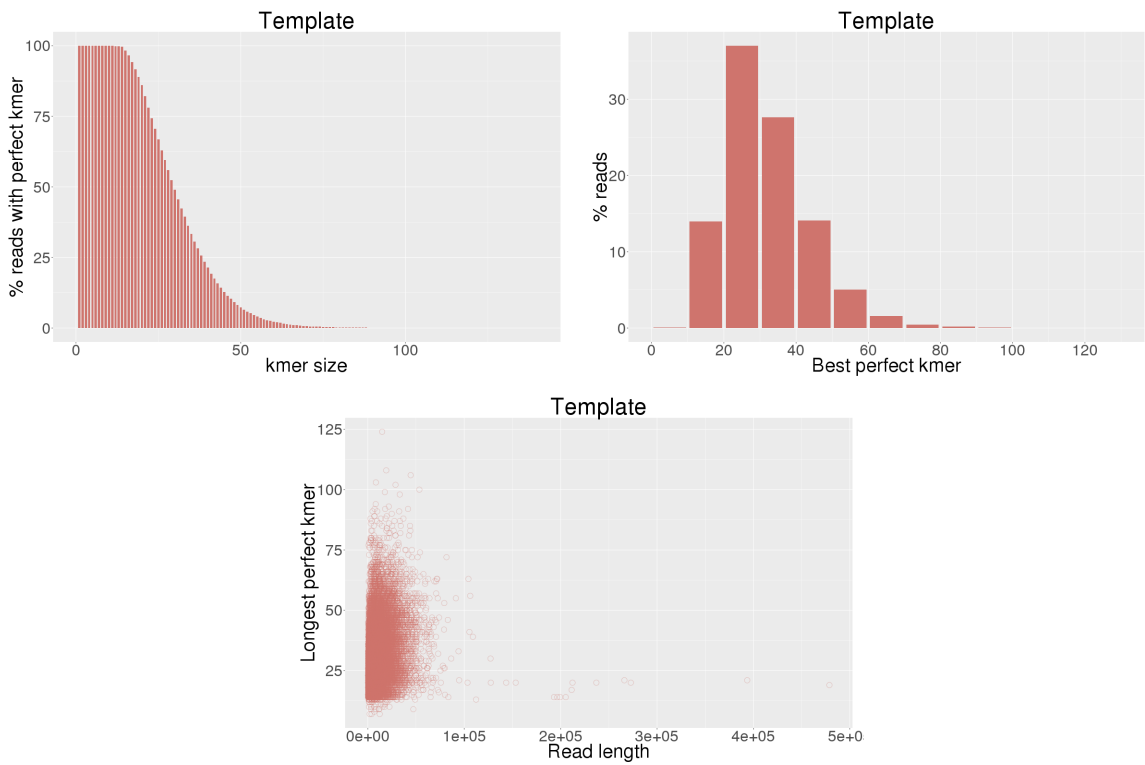
	Template
Overall base identity (excluding indels)	55.79%
Aligned base identity (excluding indels)	80.99%
Identical bases per 100 aligned bases (including indels)	68.40%
Inserted bases per 100 aligned bases (including indels)	4.27%
Deleted bases per 100 aligned bases (including indels)	11.27%
Substitutions per 100 aligned bases (including indels)	16.06%
Mean insertion size	1.53
Mean deletion size	1.79



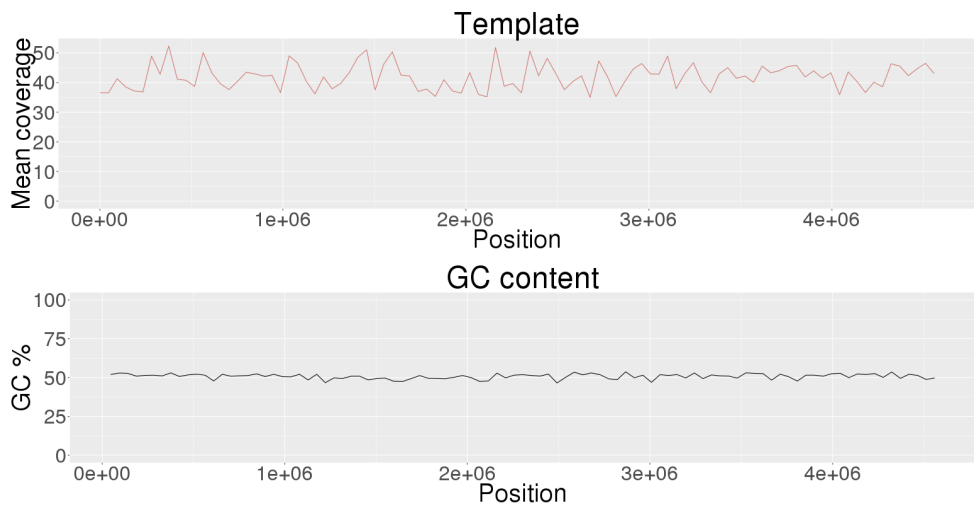
Escherichia coli read identity



Escherichia coli perfect kmers



Escherichia coli coverage



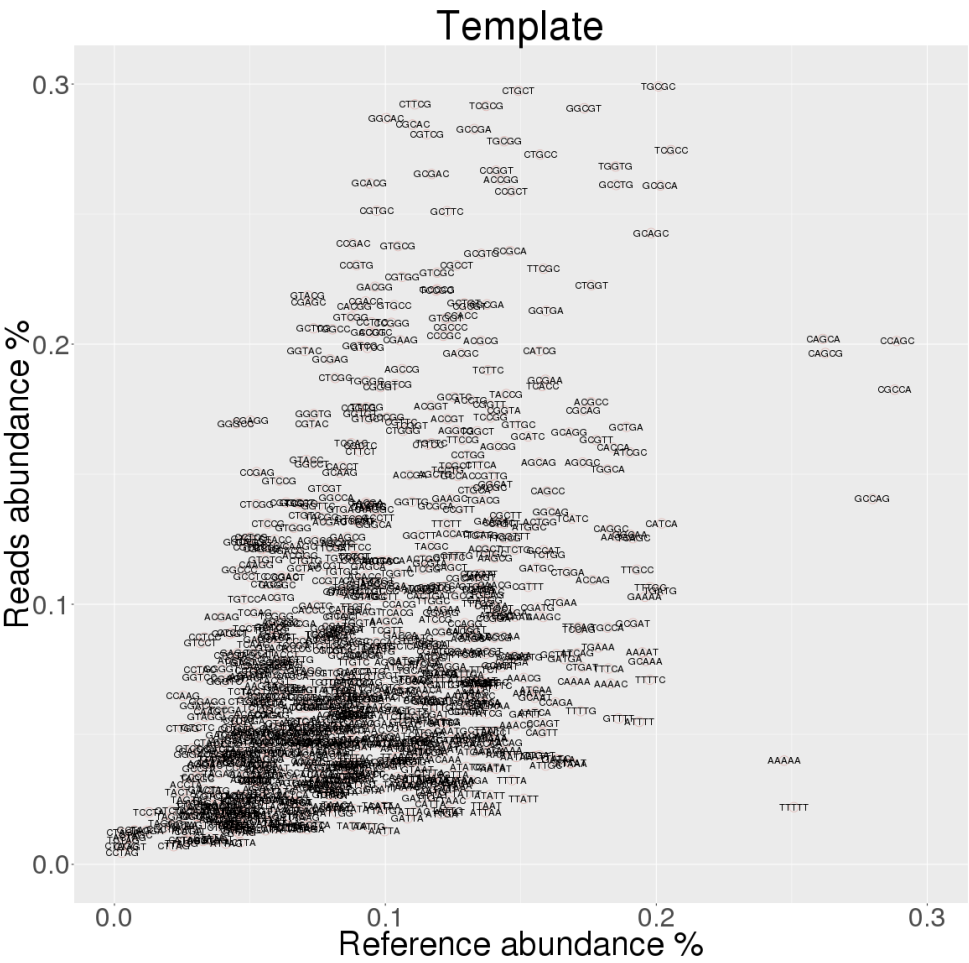
Escherichia coli 5-mer analysis

Under-represented 5-mers

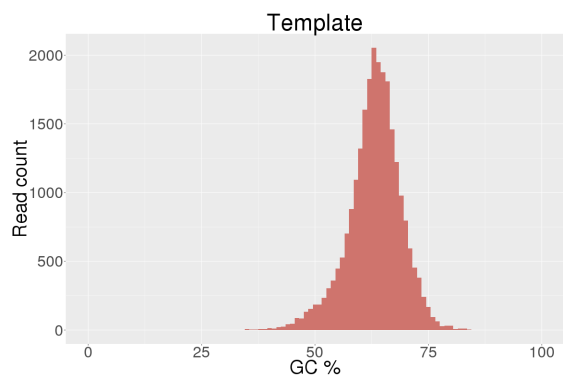
Rank	kmer	Template		
		Ref %	Read %	Diff %
1	TTTTTT	0.251	0.022	-0.229
2	AAAAAA	0.247	0.040	-0.207
3	GCCAG	0.280	0.140	-0.139
4	ATTTT	0.194	0.055	-0.139
5	GTTTT	0.186	0.056	-0.130
6	ATAAA	0.168	0.039	-0.130
7	TTTAT	0.169	0.039	-0.129
8	TTTTC	0.198	0.071	-0.127
9	TTATT	0.151	0.025	-0.126
10	GATAA	0.164	0.040	-0.124

Over-represented 5-mers

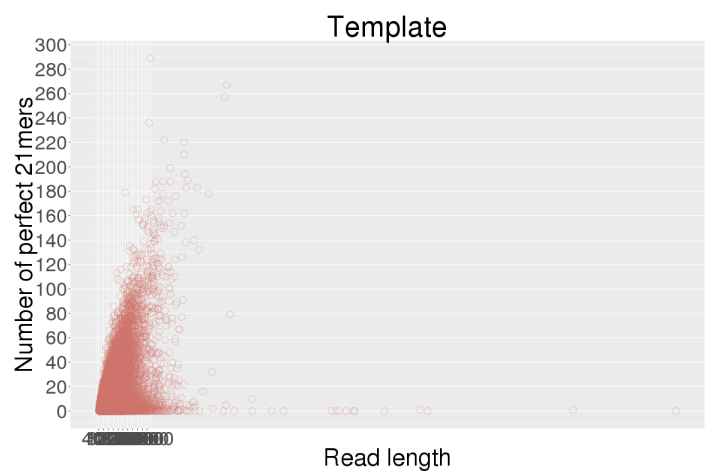
Rank	kmer	Template		
		Ref %	Read %	Diff %
1	CGGCG	0.221	0.884	0.663
2	GCGGC	0.210	0.784	0.574
3	GGCGG	0.190	0.695	0.505
4	CGCCG	0.219	0.679	0.459
5	GCCGC	0.209	0.651	0.442
6	GGCCG	0.069	0.500	0.431
7	CGCGC	0.201	0.603	0.402
8	CCGGC	0.141	0.530	0.389
9	GCGCG	0.202	0.568	0.366
10	GC CGG	0.137	0.504	0.366



Escherichia coli GC content



All reference 21mer analysis



All reference substitutions

		Template substituted %			
		a	c	g	t
Reference	A	0.00	11.48	20.60	4.47
	C	2.41	0.00	4.78	6.26
	G	6.34	5.14	0.00	2.36
	T	4.48	20.50	11.19	0.00

Kmer motifs before errors

3-mer error motif analysis

Rank	Insertion	Deletion	Substitution
1	CGC (3.41%)	CGC (4.71%)	CGC (4.60%)
2	GCC (3.11%)	GCG (4.25%)	GCC (3.78%)
3	TTC (2.96%)	GCC (3.76%)	GCG (3.41%)
4	GCG (2.85%)	GGC (3.55%)	GGC (3.40%)
5	ATC (2.60%)	TTC (3.24%)	TTC (2.95%)
6	GGC (2.54%)	ACC (2.86%)	ACC (2.92%)
7	ACC (2.46%)	ATC (2.77%)	ATC (2.86%)
8	GCA (2.35%)	CCG (2.58%)	TGC (2.71%)
9	CCA (2.33%)	CGG (2.44%)	CCG (2.45%)
10	TTT (2.22%)	TGC (2.42%)	CGG (2.44%)
-10	AGA (0.85%)	CAA (0.79%)	CAT (0.77%)
-9	AGG (0.80%)	TGT (0.77%)	AGA (0.74%)
-8	GAG (0.80%)	CCT (0.70%)	ACT (0.67%)
-7	AGT (0.75%)	AGT (0.58%)	ATA (0.59%)
-6	TTA (0.67%)	ATA (0.55%)	TAA (0.53%)
-5	TAT (0.60%)	TTA (0.50%)	AGT (0.52%)
-4	GGG (0.57%)	TAT (0.45%)	TTA (0.50%)
-3	TAA (0.52%)	TAA (0.38%)	TAT (0.44%)
-2	CTA (0.42%)	TAG (0.29%)	TAG (0.30%)
-1	TAG (0.27%)	CTA (0.24%)	CTA (0.22%)

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 (1.44%)	CGCC (1.79%)	CGCC (1.79%)
2	GCGC (1.12%)	GCGC (1.68%)	GCGC (1.52%)
3	GCTG (1.04%)	GCGC (1.59%)	CGGC (1.41%)
4	CGGC (1.01%)	CGGC (1.53%)	CCGC (1.26%)
5	GGCG (0.95%)	CCGC (1.30%)	GGCG (1.20%)
6	CAGC (0.95%)	CAGC (1.22%)	CAGC (1.14%)
7	GCCA (0.94%)	CACC (1.12%)	CACC (1.12%)
8	CTTC (0.93%)	GCGC (1.11%)	GCTG (1.11%)
9	CACC (0.92%)	GCCG (1.06%)	CATC (1.06%)
10	CCGC (0.91%)	CTTC (1.05%)	GCCG (0.96%)
-10	TAAG (0.08%)	ACTA (0.06%)	TATA (0.06%)
-9	CTTA (0.08%)	TCTA (0.06%)	TAAG (0.06%)
-8	CCTA (0.07%)	CTAT (0.06%)	CTAT (0.05%)
-7	CTAT (0.07%)	TATA (0.05%)	TAGA (0.05%)
-6	TAGA (0.07%)	TTAG (0.05%)	CTTA (0.05%)
-5	ATAG (0.06%)	TAGG (0.05%)	TAGT (0.05%)
-4	TTAG (0.06%)	CTTA (0.05%)	TCTA (0.05%)
-3	CTAA (0.05%)	CCTA (0.04%)	CTAA (0.05%)
-2	TAGG (0.05%)	CTAA (0.04%)	CCTA (0.04%)
-1	CTAG (0.01%)	CTAG (0.00%)	CTAG (0.00%)

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 (0.50%)	CGGCG (0.59%)	CGGCC (0.54%)
2	CCGCC (0.42%)	GCGGC (0.58%)	GCGGC (0.53%)
3	CCAGC (0.40%)	CCGCC (0.53%)	GCCGC (0.49%)
4	GCGGC (0.39%)	GCGGC (0.53%)	GCGGC (0.47%)
5	CGGCG (0.37%)	CCAGC (0.50%)	CGGCG (0.47%)
6	GCGGC (0.36%)	GCGGC (0.48%)	CCAGC (0.47%)
7	CAGCA (0.36%)	TGGCG (0.47%)	CGCGC (0.46%)
8	CGCTG (0.35%)	GCGGC (0.47%)	TCGCC (0.44%)
9	TCGCC (0.34%)	CGCCG (0.46%)	CGCCG (0.42%)
10	GCCGC (0.34%)	TCGCC (0.43%)	GCGCC (0.42%)
-10	TAGGA (0.01%)	TCCTA (0.01%)	TCCTA (0.00%)
-9	GGGGG (0.01%)	CCTAA (0.01%)	TAGGA (0.00%)
-8	CTAGC (0.00%)	CTAGC (0.00%)	CTAGC (0.00%)
-7	GCTAG (0.00%)	ACTAG (0.00%)	TCTAG (0.00%)
-6	CTAGT (0.00%)	CTAGT (0.00%)	ACTAG (0.00%)
-5	TCTAG (0.00%)	GCTAG (0.00%)	CTAGT (0.00%)
-4	ACTAG (0.00%)	TCTAG (0.00%)	GCTAG (0.00%)
-3	CTAGA (0.00%)	CTAGA (0.00%)	CCTAG (0.00%)
-2	CCTAG (0.00%)	CTAGG (0.00%)	CTAGA (0.00%)
-1	CTAGG (0.00%)	CCTAG (0.00%)	CTAGG (0.00%)

Most common

Least common

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