

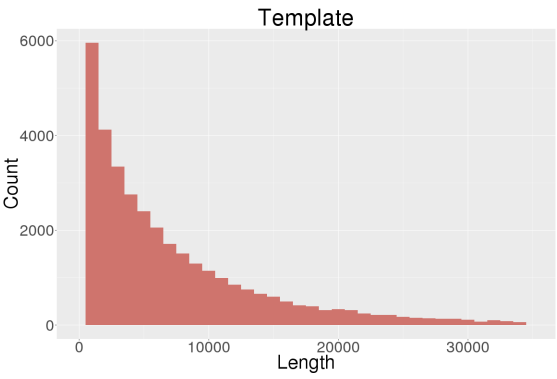
NanoOK report for Nott_R9_run2_1D

Pass and fail counts

Type	Pass	Fail
Template	35306	0

Read lengths

Type	NumReads	TotalBases	Mean	Longest	Shortest	N50	N50Count	N90	N90Count
Template	35306	276269908	7825.01	151217	153	13568	5991	3833	20561



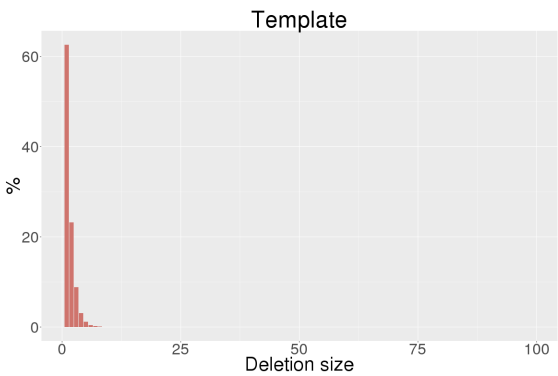
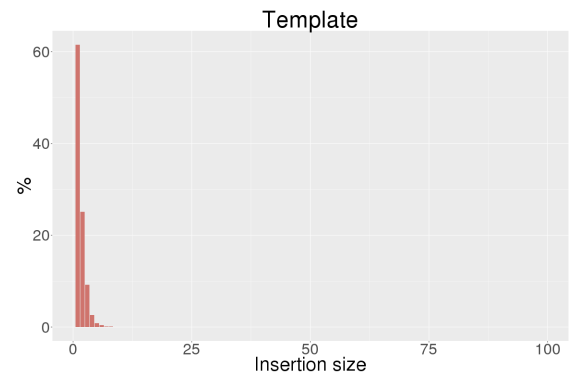
Template alignments

Number of reads	35306
Number of reads with alignments	35253 (99.85%)
Number of reads without alignments	53 (0.15%)

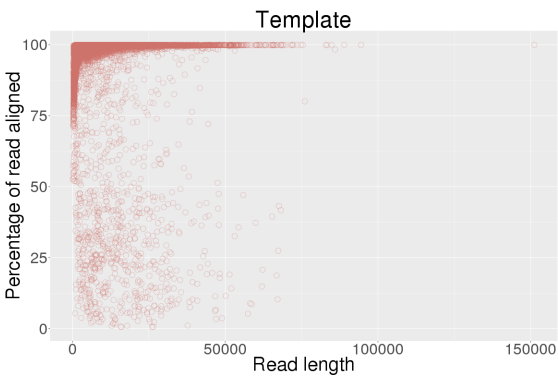
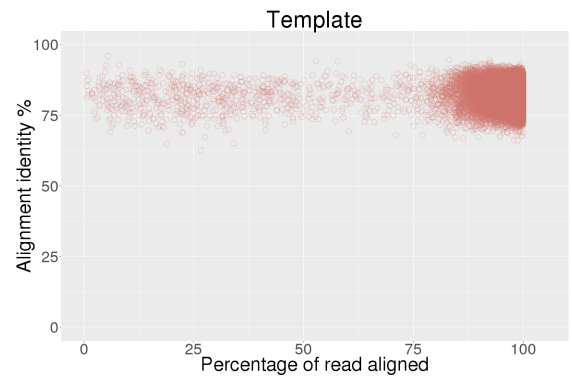
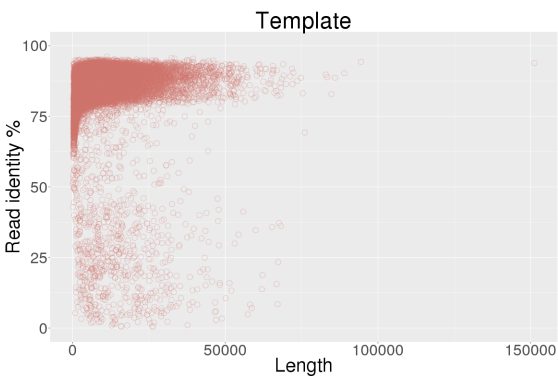
ID	Size	Number of Reads	% of Reads	Mean read length	Aligned bases	Mean coverage	Longest Perf Kmer
Control sequence	3560	0	0.00	0.00	0	0.00	0
Escherichia coli	4641652	35253	99.85	7810.28	282858586	60.94	273

Escherichia coli error analysis

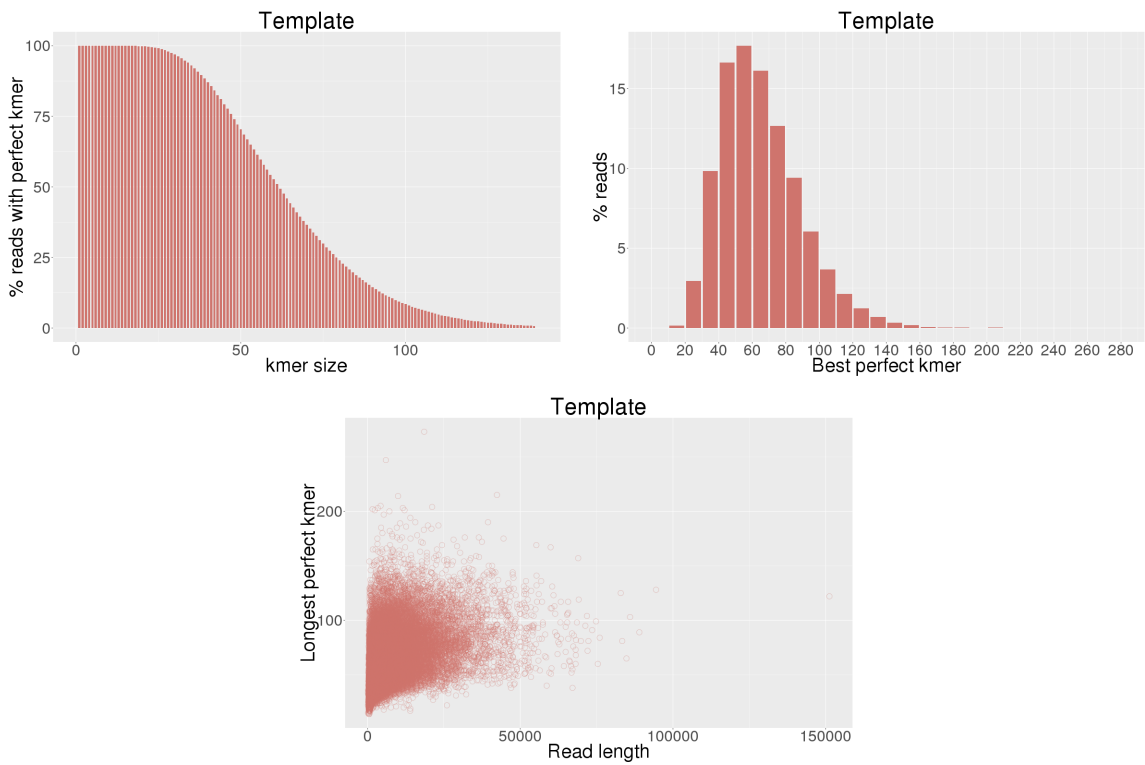
	Template
Overall base identity (excluding indels)	84.58%
Aligned base identity (excluding indels)	91.38%
Identical bases per 100 aligned bases (including indels)	82.33%
Inserted bases per 100 aligned bases (including indels)	3.08%
Deleted bases per 100 aligned bases (including indels)	6.82%
Substitutions per 100 aligned bases (including indels)	7.77%
Mean insertion size	1.59
Mean deletion size	1.62



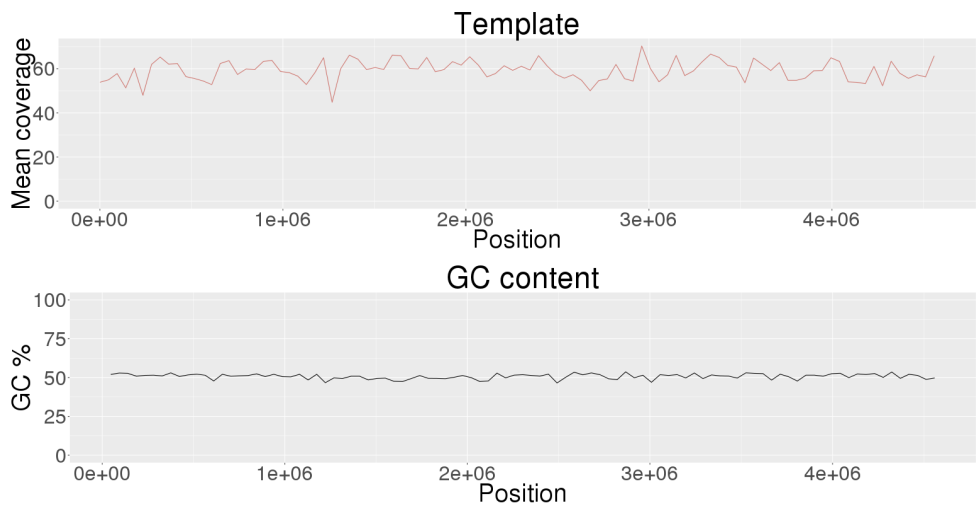
Escherichia coli read identity



Escherichia coli perfect kmers



Escherichia coli coverage



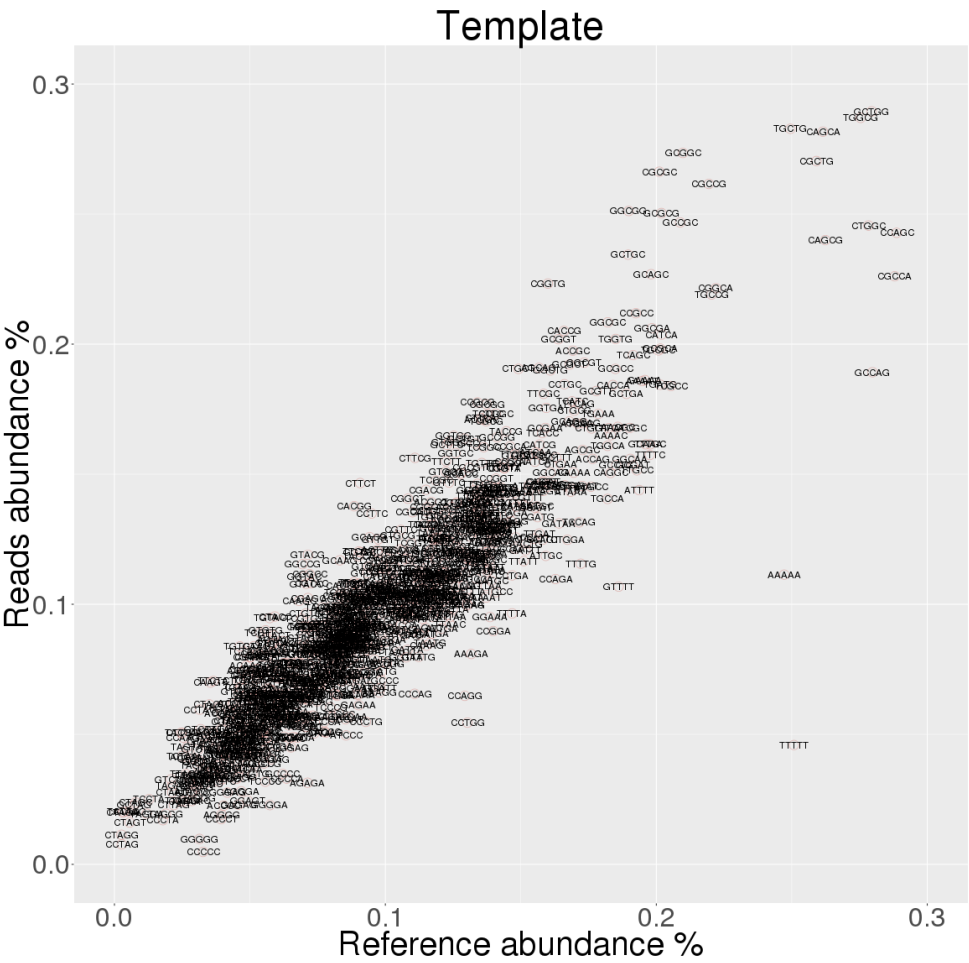
Escherichia coli 5-mer analysis

Under-represented 5-mers

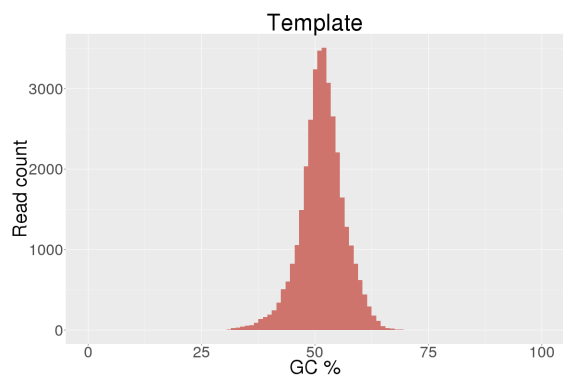
Rank	kmer	Template		
		Ref %	Read %	Diff %
1	TTTTTT	0.251	0.046	-0.205
2	AAAAAA	0.247	0.111	-0.136
3	GCCAG	0.280	0.189	-0.091
4	GTTTT	0.186	0.107	-0.079
5	CCTGG	0.130	0.054	-0.076
6	CCAGG	0.129	0.065	-0.064
7	CGCCA	0.288	0.226	-0.062
8	TTTTTG	0.172	0.116	-0.056
9	CCAGA	0.163	0.110	-0.053
10	AAAGA	0.132	0.081	-0.051

Over-represented 5-mers

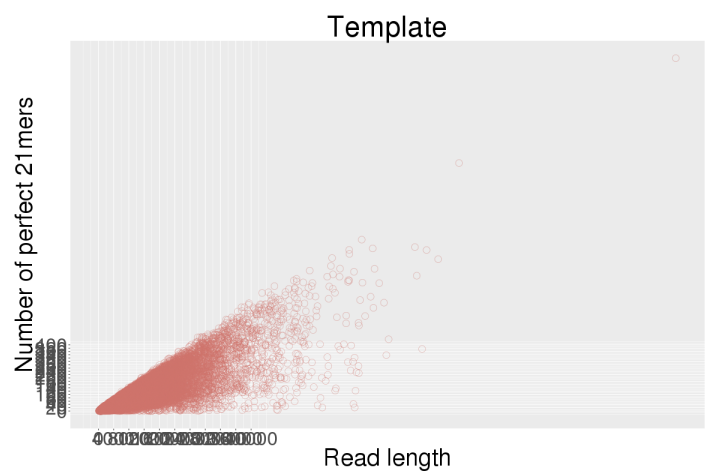
Rank	kmer	Template		
		Ref %	Read %	Diff %
1	CGGCG	0.221	0.304	0.083
2	CGCGC	0.201	0.266	0.065
3	GCGGC	0.210	0.274	0.064
4	CGGTG	0.160	0.223	0.063
5	GGCGG	0.190	0.251	0.061
6	CTTCT	0.091	0.147	0.056
7	CACGG	0.089	0.138	0.049
8	GCGCG	0.202	0.250	0.048
9	GTACG	0.071	0.119	0.048
10	GGCCG	0.069	0.115	0.046



Escherichia coli GC content



All reference 21mer analysis



All reference substitutions

	Reference	Template substituted %			
		a	c	g	t
	A	0.00	7.01	15.29	4.93
	C	4.36	0.00	3.84	14.43
	G	14.24	4.08	0.00	4.25
	T	4.95	15.58	7.04	0.00







Kmer motifs before errors

3-mer error motif analysis

Rank	Insertion	Deletion	Substitution	Most common
1	TTC (3.43%)	CGC (3.02%)	CGC (3.79%)	
2	CGC (3.04%)	TTT (3.02%)	GCC (3.46%)	
3	ATC (2.89%)	TTT (2.97%)	ACC (3.25%)	
4	TTT (2.77%)	ATC (2.94%)	ATC (3.20%)	
5	GCC (2.62%)	GCC (2.74%)	TGC (3.11%)	
6	TGC (2.43%)	GCG (2.51%)	TTC (2.98%)	
7	ACC (2.37%)	GGC (2.50%)	AAC (2.97%)	
8	GCG (2.21%)	ACC (2.49%)	GGC (2.79%)	
9	GGC (2.19%)	ATT (2.16%)	TTT (2.66%)	
10	AAC (2.17%)	TGC (2.13%)	AGC (2.63%)	
				Least common
-10	TGG (1.10%)	AGA (0.96%)	CGA (0.88%)	
-9	TAA (0.95%)	TAA (0.93%)	TGA (0.86%)	
-8	AGT (0.94%)	GTA (0.86%)	GTA (0.84%)	
-7	AGA (0.83%)	AGT (0.84%)	GAG (0.81%)	
-6	GAG (0.81%)	GGA (0.81%)	AGA (0.62%)	
-5	GGA (0.75%)	AGG (0.77%)	GGG (0.61%)	
-4	AGG (0.74%)	CCT (0.72%)	AGT (0.59%)	
-3	CTA (0.49%)	GGG (0.59%)	GGA (0.51%)	
-2	GGG (0.48%)	TAG (0.43%)	TAG (0.44%)	
-1	TAG (0.45%)	CTA (0.40%)	CTA (0.32%)	







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	TTTC (1.22%)	CGCC (1.15%)	CGCC (1.45%)
2	CGCC (1.10%)	GCGC (1.04%)	CAGC (1.22%)
3	GCGC (1.01%)	TTTC (1.01%)	GCGC (1.21%)
4	CAGC (0.95%)	CAGC (0.99%)	CACC (1.01%)
5	CTTC (0.88%)	CATC (0.92%)	CATC (0.99%)
6	CATC (0.84%)	CGGC (0.91%)	CGGC (0.97%)
7	GCTG (0.83%)	GGCG (0.84%)	ACGC (0.93%)
8	TTTT (0.78%)	GTTT (0.83%)	ATCC (0.93%)
9	CGGC (0.78%)	ATTT (0.83%)	AACC (0.92%)
10	CACC (0.77%)	CACC (0.83%)	TTTC (0.91%)
			
-10	TTAG (0.12%)	TAGA (0.11%)	TAGT (0.09%)
-9	TCTA (0.11%)	TTAG (0.11%)	ACTA (0.09%)
-8	AGGG (0.10%)	ACTA (0.10%)	GGGG (0.08%)
-7	GGGA (0.10%)	TCTA (0.10%)	TAGG (0.08%)
-6	CTAA (0.09%)	CTAA (0.09%)	GAGT (0.08%)
-5	TAGA (0.09%)	CCCT (0.09%)	GGGA (0.08%)
-4	CCTA (0.07%)	GGGG (0.09%)	TCTA (0.07%)
-3	GGGG (0.07%)	TAGG (0.06%)	TAGA (0.06%)
-2	TAGG (0.06%)	CCTA (0.06%)	CCTA (0.04%)
-1	CTAG (0.01%)	CTAG (0.01%)	CTAG (0.01%)
			

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	ATTTTC (0.36%)	CCAGC (0.35%)	CCAGC (0.47%)
2	CCAGC (0.36%)	GCGGC (0.33%)	TCGCC (0.40%)
3	GTTTTC (0.34%)	TCGCC (0.32%)	CCGCC (0.39%)
4	CGCCA (0.34%)	GGCGC (0.31%)	CTGGC (0.38%)
5	CGCGC (0.31%)	CCGCC (0.30%)	GCGGC (0.36%)
6	TTTTTC (0.30%)	TGGCG (0.30%)	GCGCC (0.35%)
7	TCGCC (0.29%)	CTGGC (0.30%)	ACGCC (0.34%)
8	TCTTC (0.29%)	CGCCA (0.29%)	CGCGC (0.34%)
9	CCGCC (0.29%)	TTTTTC (0.29%)	CAGCC (0.34%)
10	GCGGC (0.28%)	TCATC (0.28%)	TCACC (0.34%)
			
-10	TAGGA (0.01%)	CCAGG (0.01%)	TCCTA (0.01%)
-9	CTAGC (0.01%)	GGGGG (0.01%)	GGGGG (0.01%)
-8	GGGGG (0.00%)	CTAGC (0.00%)	TAGGA (0.00%)
-7	ACTAG (0.00%)	CTAGT (0.00%)	ACTAG (0.00%)
-6	GCTAG (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	CTAGG (0.00%)	CTAGG (0.00%)	CCTAG (0.00%)
-1	CCTAG (0.00%)	CCTAG (0.00%)	CTAGA (0.00%)
			

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