

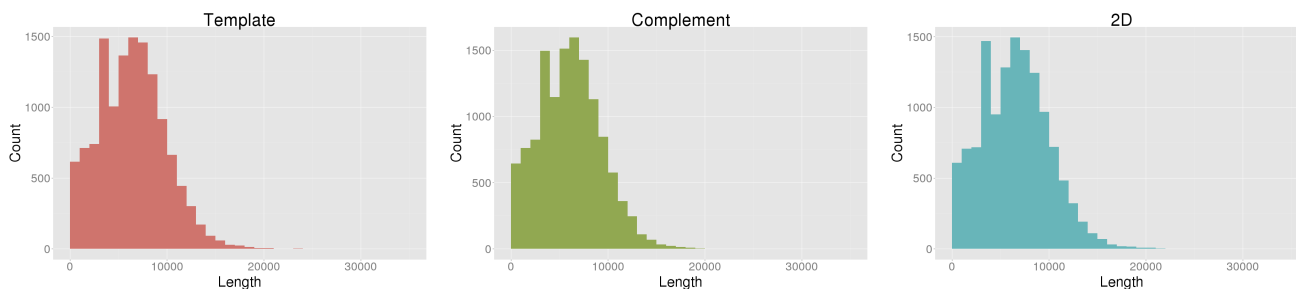
NanoOK report for WTCHG_MARC_Ph1b.2

Pass and fail counts

Type	Pass	Fail
Template	12844	0
Complement	12844	0
2D	12844	0

Read lengths

Type	NumReads	TotalBases	Mean	Longest	Shortest	N50	N50Count	N90	N90Count
Template	12844	82205678	6400.32	29399	169	7996	3976	3922	9356
Complement	12844	78253865	6092.64	27649	213	7621	3972	3751	9347
2D	12844	83844632	6527.92	29713	203	8178	3972	4002	9339



Template alignments

Number of reads	12844	
Number of reads with alignments	12729	(99.10%)
Number of reads without alignments	115	(0.90%)

ID	Size	Number of Reads	% of Reads	Mean read length	Aligned bases	Mean coverage	Longest Perf Kmer
Control sequence	3560	876	6.82	3266.07	3041739	854.42	68
Escherichia coli	4641652	11853	92.28	6686.61	85359508	18.39	99

Complement alignments

Number of reads	12844	
Number of reads with alignments	12725	(99.07%)
Number of reads without alignments	119	(0.93%)

ID	Size	Number of Reads	% of Reads	Mean read length	Aligned bases	Mean coverage	Longest Perf Kmer
Control sequence	3560	881	6.86	3052.29	2829999	794.94	62
Escherichia coli	4641652	11844	92.21	6374.64	82593274	17.79	67

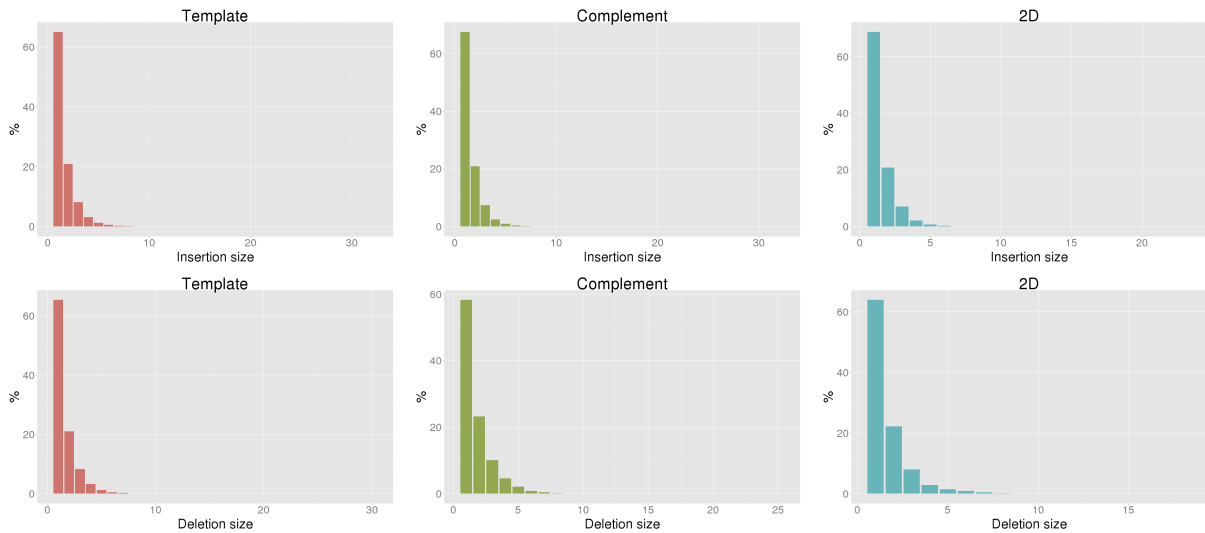
2D alignments

Number of reads	12844	
Number of reads with alignments	12839	(99.96%)
Number of reads without alignments	5	(0.04%)

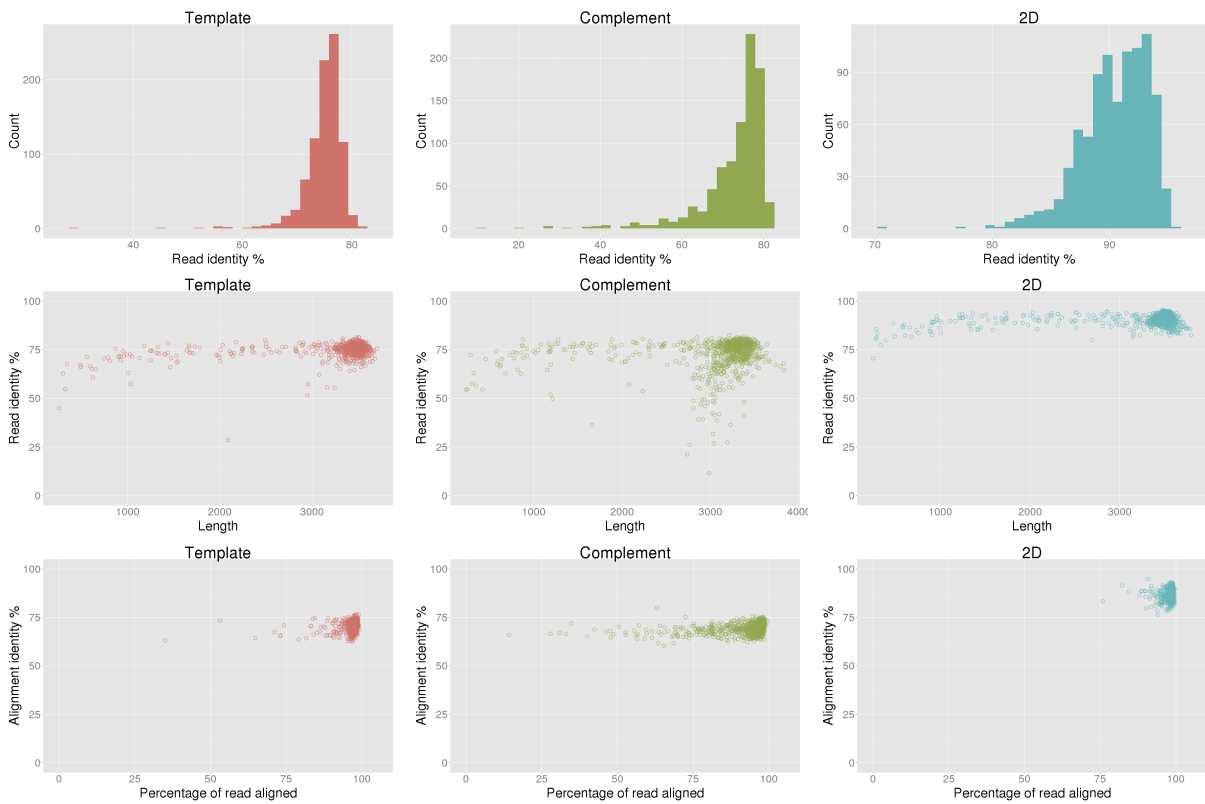
ID	Size	Number of Reads	% of Reads	Mean read length	Aligned bases	Mean coverage	Longest Perf Kmer
Control sequence	3560	887	6.91	3249.52	2990604	840.06	202
Escherichia coli	4641652	11952	93.06	6770.79	84091827	18.12	252

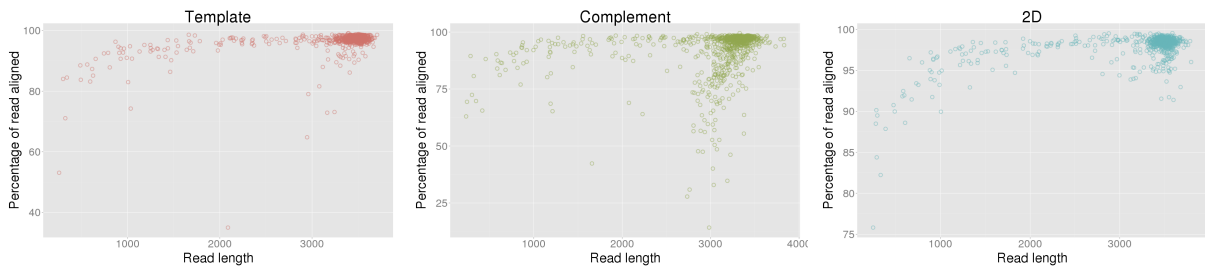
Control sequence error analysis

	Template	Complement	2D
Overall base identity (excluding indels)	75.12%	73.13%	90.59%
Aligned base identity (excluding indels)	82.36%	82.99%	95.03%
Identical bases per 100 aligned bases (including indels)	70.66%	69.48%	87.31%
Inserted bases per 100 aligned bases (including indels)	5.36%	4.04%	2.81%
Deleted bases per 100 aligned bases (including indels)	8.85%	12.23%	5.31%
Substitutions per 100 aligned bases (including indels)	15.14%	14.24%	4.56%
Mean insertion size	1.60	1.51	1.47
Mean deletion size	1.57	1.76	1.61

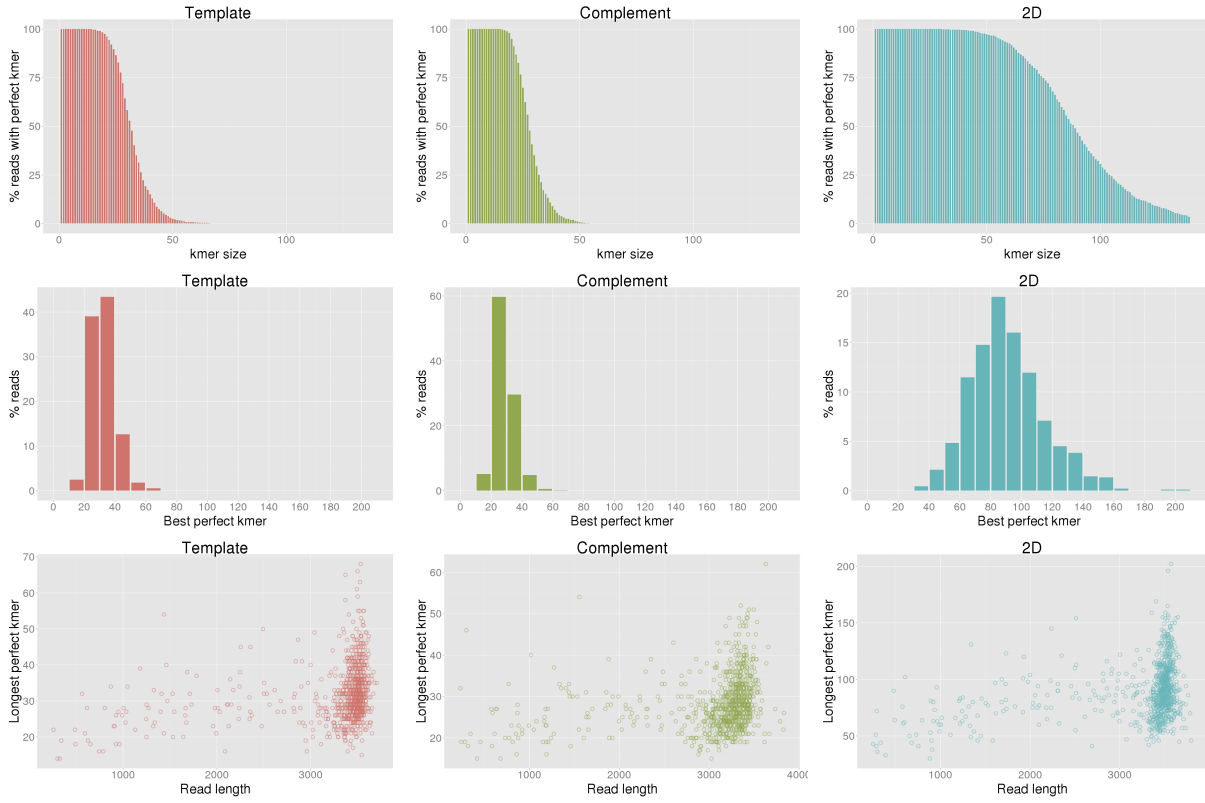


Control sequence read identity

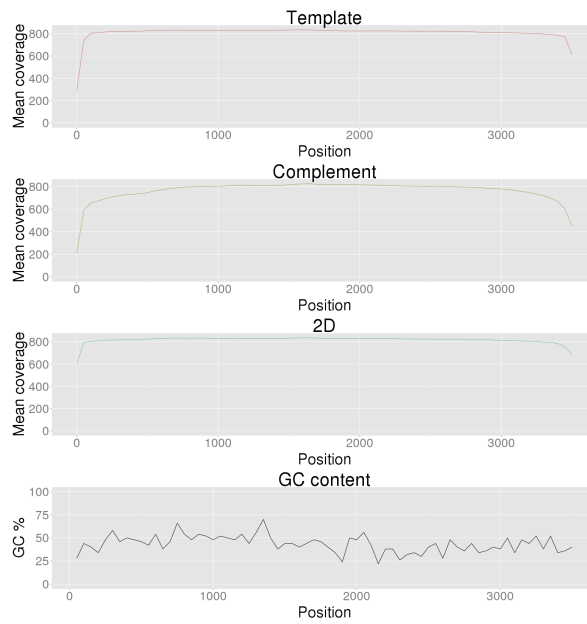




Control sequence perfect kmers



Control sequence coverage



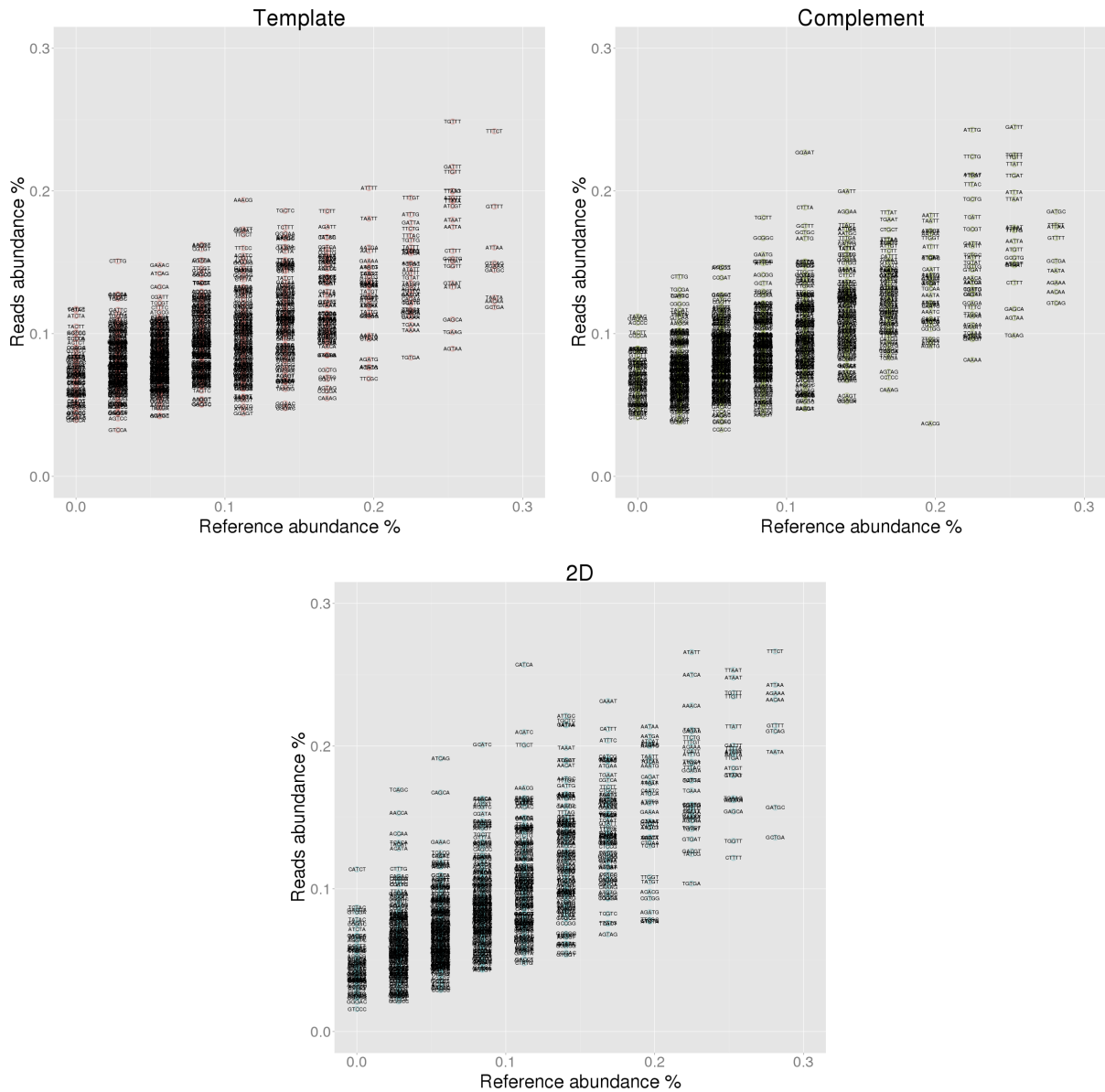
Control sequence 5-mer analysis

Under-represented 5-mers

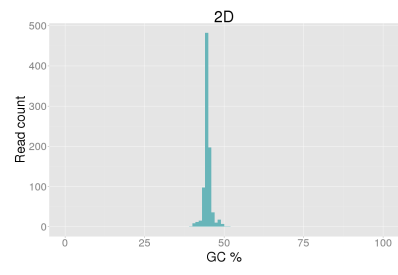
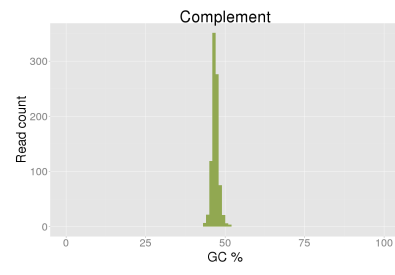
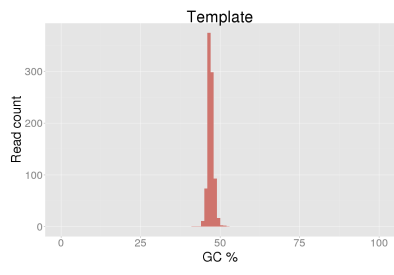
Rank	Template				Complement				2D			
	kmer	Ref %	Read %	Diff %	kmer	Ref %	Read %	Diff %	kmer	Ref %	Read %	Diff %
1	TTTTT	0.759	0.144	-0.614	TTTTT	0.759	0.087	-0.671	TTTTT	0.759	0.065	-0.694
2	AAAAA	0.478	0.114	-0.363	AAAAA	0.478	0.055	-0.423	AAAAA	0.478	0.086	-0.392
3	TGATG	0.393	0.149	-0.244	AAAAC	0.337	0.142	-0.195	TGATG	0.393	0.190	-0.203
4	AAAAC	0.337	0.132	-0.205	GCAAT	0.309	0.146	-0.163	CTGAT	0.309	0.151	-0.158
5	GATGT	0.309	0.112	-0.197	GATGT	0.309	0.147	-0.162	GATGT	0.309	0.155	-0.155
6	CTGAT	0.309	0.121	-0.188	ACACG	0.197	0.037	-0.160	GCTGA	0.281	0.136	-0.145
7	GCAAT	0.309	0.146	-0.164	GTCAG	0.281	0.122	-0.159	CTTTT	0.253	0.122	-0.131
8	AGTAA	0.253	0.090	-0.163	TGAAG	0.253	0.099	-0.154	GATGC	0.281	0.157	-0.124
9	GCTGA	0.281	0.119	-0.162	AACAA	0.281	0.129	-0.152	TTATC	0.309	0.186	-0.123
10	AATAT	0.309	0.149	-0.160	TTATC	0.309	0.161	-0.148	TGTGA	0.225	0.104	-0.121

Over-represented 5-mers

Rank	Template				Complement				2D			
	kmer	Ref %	Read %	Diff %	kmer	Ref %	Read %	Diff %	kmer	Ref %	Read %	Diff %
1	CTTTG	0.028	0.151	0.123	GGAAT	0.112	0.227	0.115	CATCA	0.112	0.257	0.145
2	CATCT	0.000	0.117	0.117	TATAC	0.000	0.112	0.112	TCAGC	0.028	0.169	0.141
3	TCTAC	0.000	0.117	0.117	CTTTG	0.028	0.140	0.112	ATCAG	0.056	0.191	0.135
4	ATCTA	0.000	0.112	0.112	GAGGA	0.000	0.110	0.110	AACCA	0.028	0.153	0.125
5	TACTT	0.000	0.105	0.105	ACCCC	0.000	0.108	0.108	GCATC	0.084	0.201	0.117
6	GCTCC	0.000	0.101	0.101	TGCCA	0.028	0.131	0.103	CATCT	0.000	0.114	0.114
7	ACCCC	0.000	0.100	0.100	TACTT	0.000	0.101	0.101	CAGCA	0.056	0.168	0.111
8	AACCA	0.028	0.128	0.099	TCAGC	0.028	0.127	0.099	ACCAA	0.028	0.139	0.110
9	GCGAA	0.028	0.127	0.099	CCCCA	0.000	0.099	0.099	TCACA	0.028	0.132	0.104
10	TACAT	0.028	0.125	0.097	GATTC	0.028	0.126	0.098	TACAT	0.028	0.131	0.103

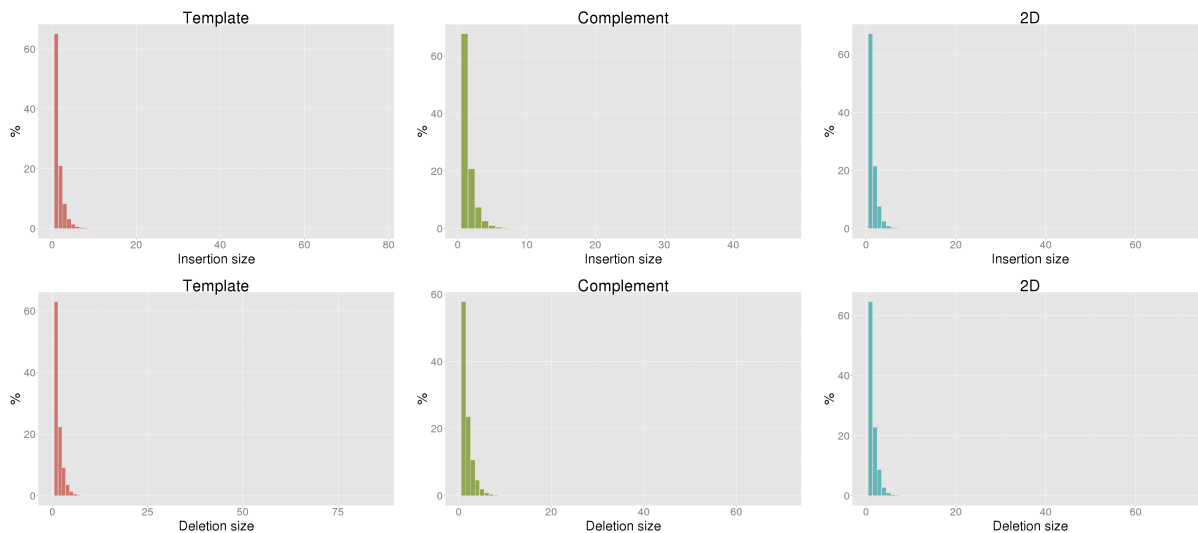


Control sequence GC content

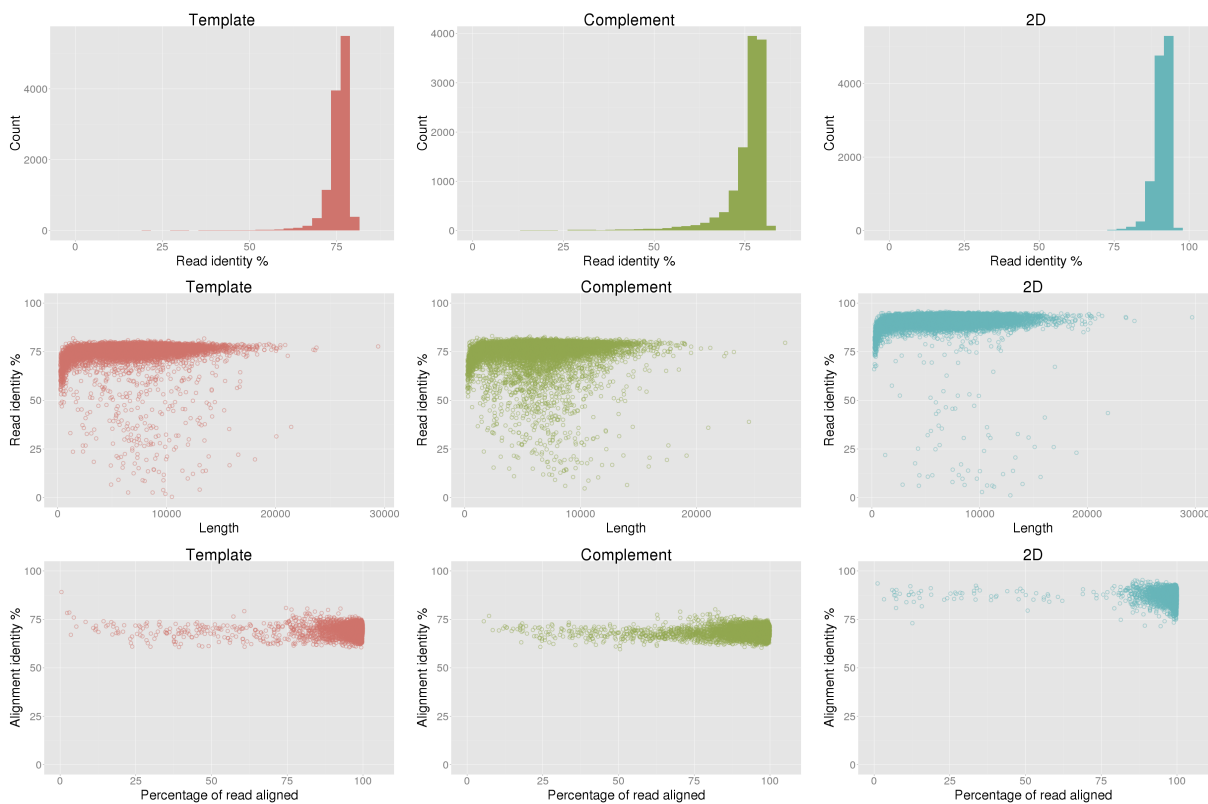


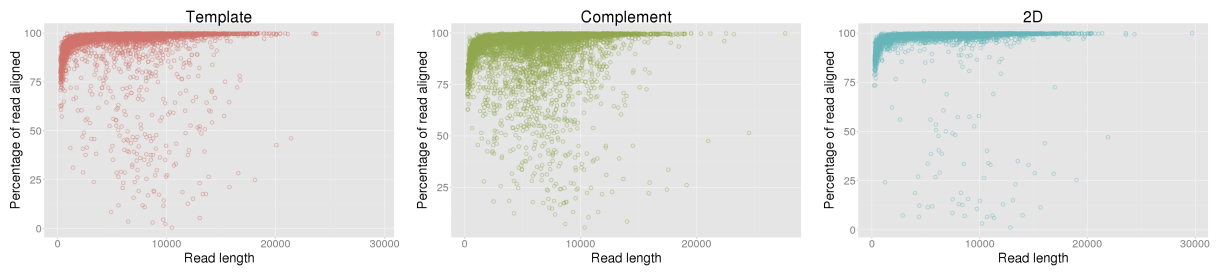
Escherichia coli error analysis

	Template	Complement	2D
Overall base identity (excluding indels)	75.08%	75.26%	90.81%
Aligned base identity (excluding indels)	81.77%	82.58%	94.94%
Identical bases per 100 aligned bases (including indels)	69.71%	68.79%	87.39%
Inserted bases per 100 aligned bases (including indels)	5.36%	4.17%	3.01%
Deleted bases per 100 aligned bases (including indels)	9.39%	12.52%	4.95%
Substitutions per 100 aligned bases (including indels)	15.54%	14.51%	4.65%
Mean insertion size	1.61	1.52	1.51
Mean deletion size	1.62	1.76	1.55

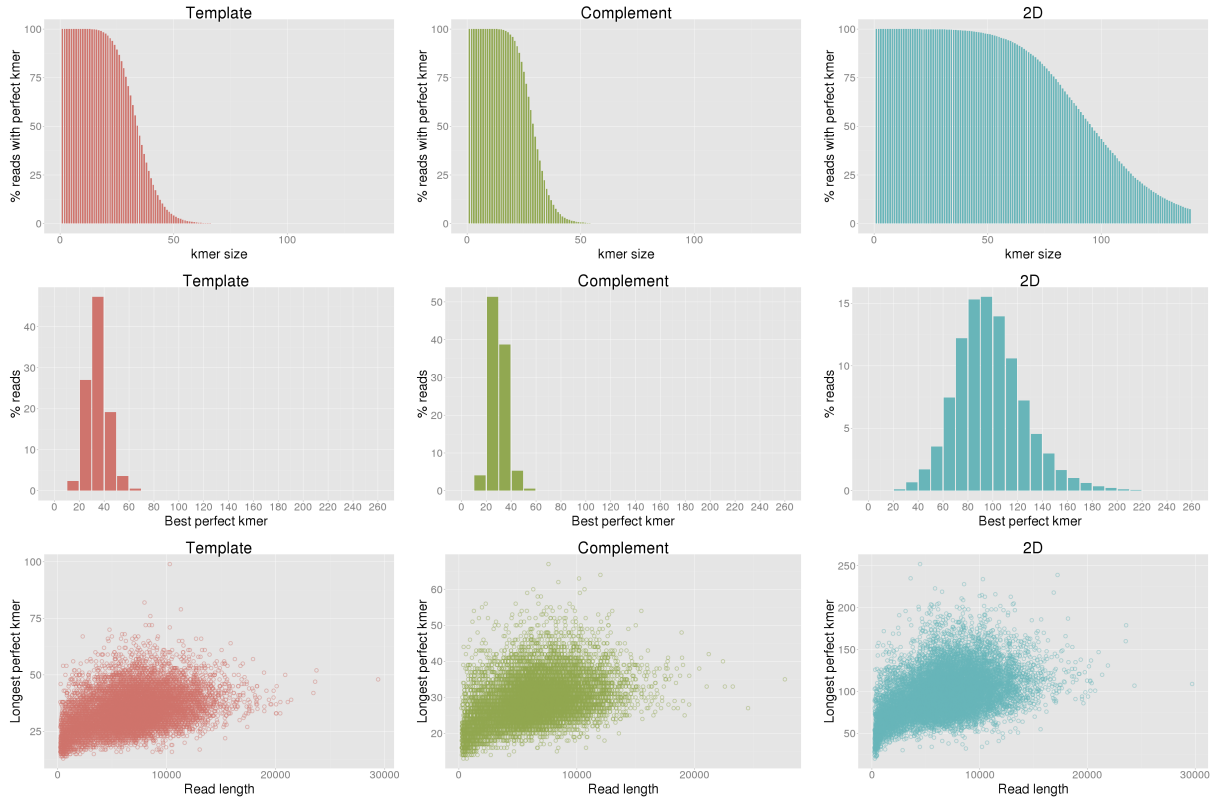


Escherichia coli read identity

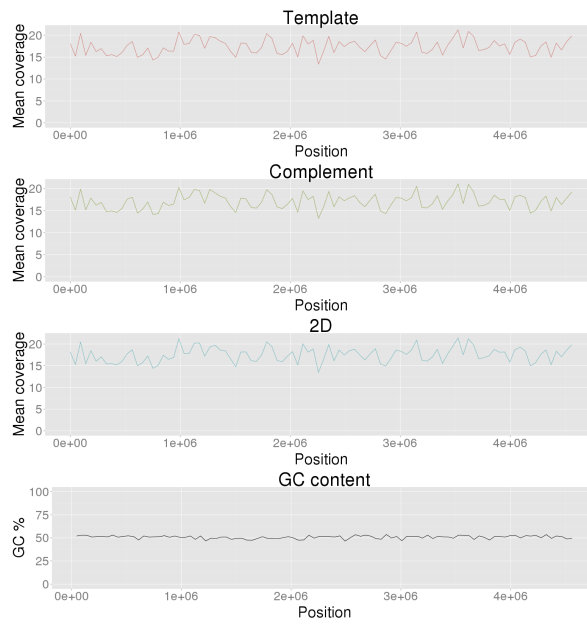




Escherichia coli perfect kmers



Escherichia coli coverage



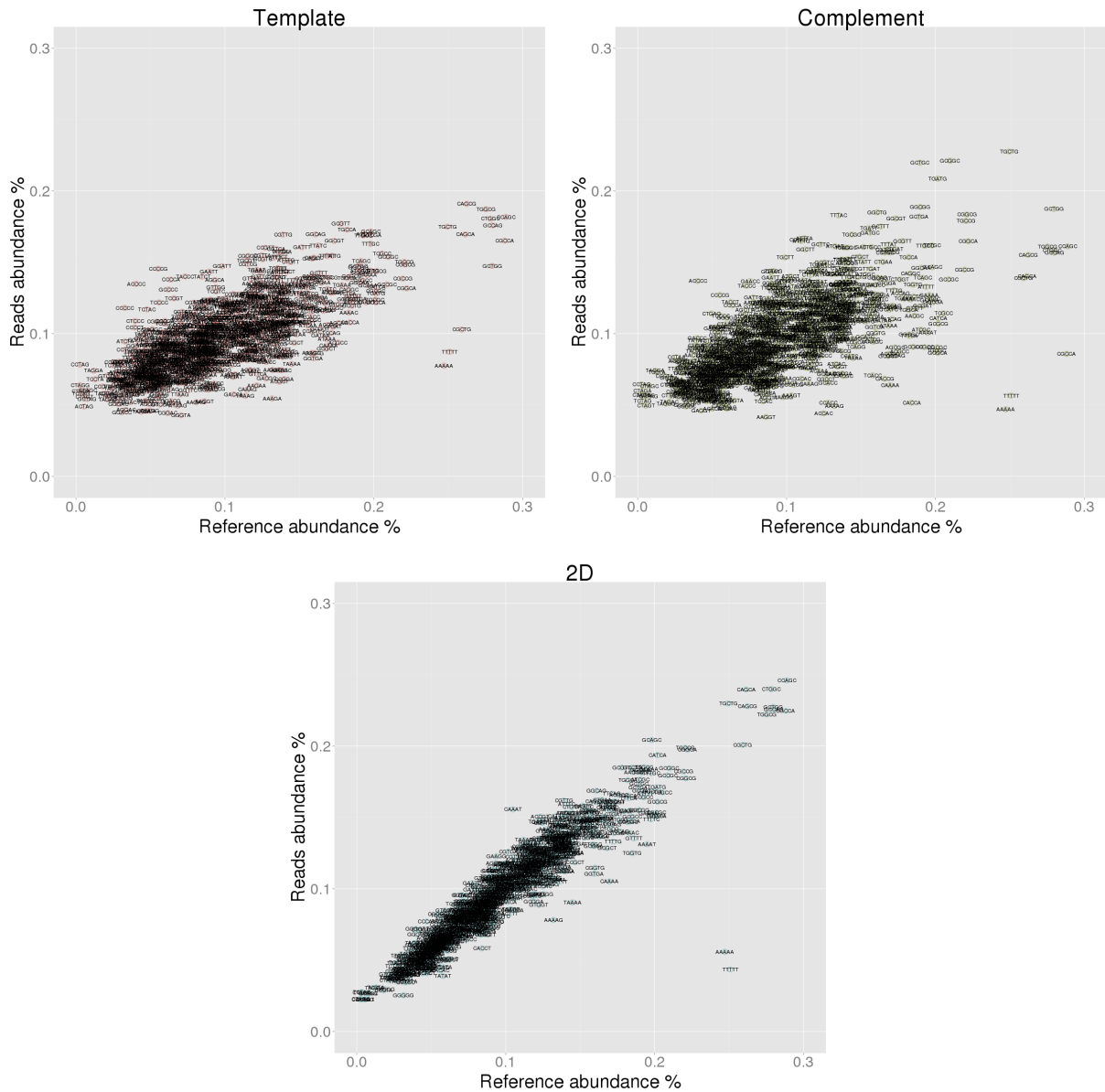
Escherichia coli 5-mer analysis

Under-represented 5-mers

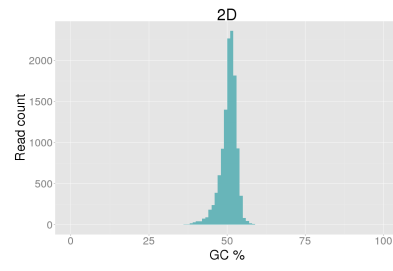
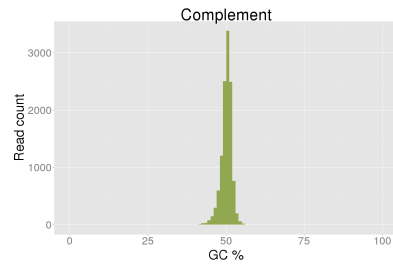
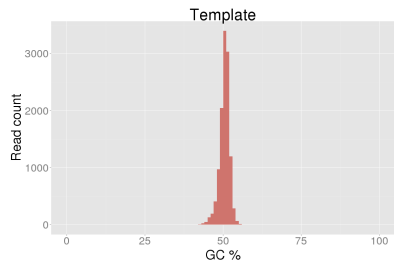
Rank	Template				Complement				2D			
	kmer	Ref %	Read %	Diff %	kmer	Ref %	Read %	Diff %	kmer	Ref %	Read %	Diff %
1	AAAAA	0.247	0.078	-0.170	CGCCA	0.288	0.086	-0.202	TTTTT	0.251	0.043	-0.207
2	TTTTT	0.251	0.087	-0.164	AAAAA	0.247	0.047	-0.200	AAAAA	0.247	0.056	-0.191
3	CGCTG	0.259	0.103	-0.156	TTTTT	0.251	0.057	-0.194	CAAAA	0.169	0.105	-0.064
4	GCTGG	0.279	0.148	-0.132	CACCA	0.184	0.052	-0.132	AAAAT	0.195	0.131	-0.064
5	CGCCA	0.288	0.165	-0.123	CCAGC	0.289	0.161	-0.127	CGCCA	0.288	0.225	-0.063
6	CCAGC	0.289	0.182	-0.107	GCCAG	0.280	0.157	-0.123	TGGTG	0.185	0.125	-0.060
7	GCCAG	0.280	0.176	-0.104	CAGCA	0.261	0.140	-0.121	CGCTG	0.259	0.201	-0.058
8	CTGGC	0.278	0.181	-0.098	CGCTG	0.259	0.139	-0.120	TAAAA	0.145	0.090	-0.054
9	CAGCA	0.261	0.170	-0.092	CTGGC	0.278	0.158	-0.120	GCCAG	0.280	0.226	-0.054
10	CGGCA	0.222	0.132	-0.090	GCGCA	0.202	0.086	-0.115	AAAAG	0.132	0.078	-0.054

Over-represented 5-mers

Rank	Template				Complement				2D			
	kmer	Ref %	Read %	Diff %	kmer	Ref %	Read %	Diff %	kmer	Ref %	Read %	Diff %
1	ACCCC	0.040	0.135	0.095	ACCCC	0.040	0.137	0.097	CAAAT	0.105	0.156	0.051
2	CCCCG	0.055	0.146	0.090	CCCCG	0.055	0.127	0.072	GGGGT	0.039	0.072	0.032
3	CCCCC	0.033	0.118	0.085	CTGAG	0.050	0.114	0.065	CCCAA	0.047	0.077	0.030
4	CCTAG	0.003	0.078	0.076	TAGGA	0.012	0.074	0.062	GAAGG	0.094	0.123	0.029
5	CCCCA	0.064	0.138	0.074	CCTAG	0.003	0.064	0.062	CTCGT	0.042	0.071	0.029
6	TCTAC	0.048	0.117	0.069	GAACC	0.075	0.137	0.061	CGGGG	0.054	0.082	0.028
7	CTCCC	0.040	0.109	0.069	TCCTA	0.013	0.073	0.060	GGGTC	0.040	0.068	0.028
8	GCCCC	0.062	0.131	0.069	TACCC	0.073	0.134	0.060	ACCGT	0.123	0.151	0.028
9	TACCC	0.073	0.140	0.067	TACCT	0.062	0.122	0.060	GAATC	0.077	0.104	0.027
10	TCCCC	0.056	0.122	0.066	CGGCT	0.108	0.166	0.058	TCCCA	0.056	0.082	0.026



Escherichia coli GC content



All reference 21mer analysis



All reference substitutions

Reference	Template substituted %				Complement substituted %				2D substituted %			
	a	c	g	t	a	c	g	t	a	c	g	t
A	0.00	8.89	9.26	4.73	0.00	8.99	8.79	4.97	0.00	8.40	8.54	4.00
C	8.40	0.00	9.11	10.00	9.32	0.00	8.63	9.74	9.19	0.00	11.08	9.34
G	9.53	9.07	0.00	7.98	8.96	8.77	0.00	8.80	9.16	11.19	0.00	8.48
T	4.97	9.45	8.61	0.00	5.28	8.90	8.86	0.00	4.07	8.40	8.16	0.00

Kmer motifs before errors

3-mer error motif analysis

Rank	Template			Complement			2D		
	Insertion	Deletion	Substitution	Insertion	Deletion	Substitution	Insertion	Deletion	Substitution
1	TTC (3.23%)	TTC (3.53%)	AAA (4.06%)	TGC (2.88%)	GCC (3.03%)	AAA (3.97%)	GCA (3.06%)	GCC (2.70%)	AAA (3.75%)
2	GCA (2.79%)	TGC (3.05%)	TTC (3.82%)	GCA (2.75%)	TGC (2.85%)	GCA (3.68%)	TTC (2.74%)	TGC (2.59%)	GCA (3.72%)
3	AAA (2.78%)	GCA (2.75%)	GCA (3.26%)	TTC (2.65%)	AAA (2.76%)	GAA (3.41%)	TCA (2.63%)	TCA (2.53%)	GAA (3.28%)
4	ATC (2.60%)	AAA (2.68%)	GAA (2.98%)	AAA (2.57%)	TTC (2.60%)	TTC (3.11%)	AAA (2.63%)	GCG (2.52%)	TTT (2.95%)
5	TGC (2.59%)	GCC (2.55%)	TTT (2.64%)	CAG (2.52%)	GCA (2.60%)	TTT (2.59%)	ATC (2.48%)	GCA (2.46%)	TTC (2.94%)
6	TCA (2.49%)	GGC (2.44%)	TGC (2.53%)	GCC (2.41%)	GAA (2.38%)	TGC (2.47%)	TGC (2.33%)	AAA (2.46%)	GCC (2.46%)
7	GCC (2.29%)	TCA (2.40%)	AAT (2.34%)	GAA (2.39%)	CAG (2.29%)	TCA (2.46%)	GCG (2.27%)	TTT (2.41%)	GCG (2.37%)
8	GGC (2.29%)	ATC (2.28%)	GCC (2.26%)	TCA (2.37%)	TCA (2.26%)	ATC (2.36%)	GAA (2.25%)	CGC (2.27%)	ATC (2.29%)
9	TTT (2.23%)	AAC (2.19%)	GCC (2.24%)	ATC (2.32%)	GCC (2.22%)	GCC (2.16%)	CAG (2.24%)	CAG (2.21%)	GTT (2.28%)
10	GAA (2.18%)	GCG (2.18%)	TCA (2.24%)	GCC (2.13%)	AAT (2.17%)	GCC (2.07%)	GCG (2.24%)	ATC (2.17%)	TCA (2.24%)
-10	AGT (0.95%)	GTA (0.94%)	GGT (0.93%)	AGT (0.97%)	GGA (0.95%)	CCC (0.92%)	TAC (1.07%)	GTA (1.00%)	TAT (0.89%)
-9	TGT (0.95%)	AGT (0.92%)	GGG (0.93%)	GTG (0.96%)	AGT (0.94%)	CTT (0.89%)	CTT (1.05%)	CCC (0.94%)	ACT (0.87%)
-8	CCC (0.92%)	CCT (0.87%)	AGA (0.85%)	CTC (0.91%)	CTT (0.94%)	AGT (0.86%)	GAG (0.92%)	CGA (0.92%)	TGA (0.84%)
-7	GGA (0.89%)	GAG (0.82%)	AGG (0.81%)	GGA (0.89%)	CCC (0.91%)	AGG (0.83%)	CCC (0.82%)	ACT (0.89%)	GAG (0.76%)
-6	AGA (0.81%)	CGA (0.79%)	AGT (0.77%)	CCC (0.84%)	CTC (0.87%)	CCT (0.83%)	AGA (0.82%)	CTT (0.84%)	CTT (0.72%)
-5	GAG (0.71%)	CTT (0.79%)	TGT (0.74%)	GAG (0.81%)	CCT (0.86%)	GGG (0.77%)	AGG (0.82%)	AGA (0.79%)	CGA (0.71%)
-4	GGG (0.71%)	GGA (0.68%)	CTT (0.73%)	AGG (0.73%)	GAG (0.84%)	ACT (0.72%)	GGA (0.80%)	CCT (0.78%)	TAG (0.51%)
-3	AGG (0.68%)	AGA (0.67%)	GAG (0.61%)	CTA (0.60%)	GGG (0.77%)	GAG (0.60%)	GGG (0.76%)	GGA (0.74%)	AGA (0.51%)
-2	CTA (0.52%)	TAG (0.53%)	TAG (0.39%)	GGG (0.56%)	TAG (0.56%)	CTA (0.47%)	CTA (0.62%)	CTA (0.72%)	GGA (0.49%)
-1	TAG (0.41%)	CTA (0.53%)	CTA (0.37%)	TAG (0.45%)	CTA (0.54%)	TAG (0.38%)	TAG (0.51%)	TAG (0.67%)	CTA (0.43%)

Kmer space for 3-mers: 64

Random chance for any given 3-mer: 1.56%

4-mer error motif analysis

Rank	Template			Complement			2D		
	Insertion	Deletion	Substitution	Insertion	Deletion	Substitution	Insertion	Deletion	Substitution
1	TTTC (1.02%)	TTTC (1.15%)	AAAA (1.34%)	CAGC (0.99%)	TGGC (1.08%)	CAAA (1.05%)	ATCA (0.95%)	TGGC (0.96%)	GGCA (1.18%)
2	ATCA (0.89%)	TGCC (0.98%)	TTTC (1.30%)	ATCA (0.92%)	CGGC (1.08%)	AAAA (1.02%)	GGCA (0.85%)	CAGC (0.88%)	AAAA (1.11%)
3	GAAA (0.88%)	TGGC (0.92%)	GAAA (1.13%)	CTGC (0.91%)	CAGC (1.05%)	TGAA (1.00%)	GCCA (0.85%)	TTCA (0.84%)	TTTT (0.98%)
4	AAAA (0.87%)	CAGC (0.90%)	GGCA (0.98%)	CGGC (0.84%)	CTGC (0.90%)	ATCA (0.98%)	CAGC (0.80%)	ATCA (0.83%)	TGAA (0.96%)
5	TTCA (0.83%)	TTGC (0.89%)	GTTC (0.96%)	CCAG (0.83%)	TTGC (0.89%)	AGCA (0.96%)	CGCA (0.78%)	CGGC (0.81%)	GAAA (0.93%)
6	TGGC (0.81%)	CTGC (0.88%)	GGAA (0.90%)	TGGC (0.83%)	ATCA (0.82%)	GGCA (0.96%)	CCAG (0.78%)	CTGC (0.76%)	GGAA (0.93%)
7	GGCA (0.80%)	TTCA (0.88%)	TTTT (0.90%)	TTGC (0.81%)	CAAA (0.81%)	GAAA (0.95%)	AACA (0.77%)	TTGC (0.74%)	TTTT (0.92%)
8	CAGC (0.80%)	TTCC (0.86%)	GCAA (0.90%)	ATGC (0.76%)	TTCC (0.78%)	AGAA (0.89%)	CGCC (0.77%)	GGCG (0.73%)	CGCC (0.88%)
9	TGCC (0.80%)	AAAA (0.83%)	TGCC (0.86%)	CAAA (0.75%)	CCAG (0.77%)	TAAA (0.87%)	TTTC (0.75%)	GCCA (0.72%)	CGCA (0.86%)
10	CATC (0.79%)	GTTC (0.82%)	AAAT (0.84%)	AGCA (0.73%)	TGCC (0.76%)	TTTC (0.87%)	TTCA (0.74%)	TGCC (0.71%)	TGCC (0.85%)
-10	AGGG (0.13%)	ACCT (0.13%)	TTAG (0.11%)	GGAC (0.11%)	CTAT (0.12%)	ACCT (0.11%)	TAGT (0.15%)	ACTT (0.15%)	CTAA (0.11%)
-9	CTAA (0.12%)	CCCT (0.13%)	ACTA (0.10%)	AGGG (0.11%)	CTAA (0.11%)	GGAC (0.11%)	CCCC (0.14%)	CTAT (0.15%)	CCCT (0.11%)
-8	GAGG (0.11%)	CTAT (0.12%)	CGAG (0.09%)	CTAA (0.10%)	ACCT (0.11%)	GAGG (0.10%)	GAGG (0.14%)	GAGA (0.15%)	ACTT (0.11%)
-7	TAGT (0.11%)	TAGT (0.12%)	TAGT (0.09%)	GTGT (0.10%)	CCCC (0.11%)	GTGT (0.09%)	TCTA (0.13%)	ACCT (0.14%)	GGGA (0.10%)
-6	TTAG (0.11%)	CGGA (0.11%)	TAGA (0.08%)	TAGA (0.10%)	TAGA (0.11%)	CTAT (0.09%)	CTAT (0.13%)	CTAA (0.12%)	CGGA (0.10%)
-5	GGAC (0.10%)	CTAA (0.10%)	TCTA (0.08%)	GAGG (0.09%)	GTGT (0.10%)	CGAG (0.09%)	CTAA (0.12%)	TAGG (0.11%)	CTAT (0.09%)
-4	TAGA (0.07%)	TAGG (0.08%)	GGAC (0.08%)	CCCT (0.09%)	TAGG (0.08%)	TAGG (0.07%)	TAGA (0.08%)	CCCT (0.10%)	TAGG (0.08%)
-3	CCTA (0.06%)	TAGA (0.06%)	TAGG (0.07%)	CCTA (0.08%)	CCCT (0.08%)	CCCT (0.06%)	CCTA (0.08%)	CCTA (0.09%)	TAGA (0.05%)
-2	TAGG (0.05%)	CCTA (0.06%)	CCTA (0.05%)	TAGG (0.06%)	CCTA (0.06%)	CCTA (0.06%)	TAGG (0.06%)	TAGA (0.09%)	CCTA (0.04%)
-1	CTAG (0.01%)	CTAG (0.01%)	CTAG (0.01%)	CTAG (0.01%)	CTAG (0.01%)	CTAG (0.01%)	CTAG (0.02%)	CTAG (0.02%)	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	Template			Complement			2D		
	Insertion	Deletion	Substitution	Insertion	Deletion	Substitution	Insertion	Deletion	Substitution
1	CAGCA (0.35%)	CTGGC (0.37%)	GAAAA (0.42%)	CAGCA (0.41%)	CAGCA (0.40%)	CAGCA (0.55%)	CAGCA (0.36%)	CTGGC (0.38%)	CAGCA (0.44%)
2	CTGGC (0.34%)	CAGCA (0.36%)	CAGCA (0.40%)	GCTGC (0.34%)	CTGGC (0.39%)	CGGCA (0.38%)	CGCCA (0.36%)	CAGCA (0.31%)	CGGCA (0.41%)
3	CATCA (0.32%)	TTGCC (0.33%)	CAAAA (0.38%)	CATCA (0.33%)	GCGGC (0.37%)	CATCA (0.37%)	CGGCA (0.32%)	CGCCA (0.30%)	TGGCA (0.40%)
4	CGCCA (0.32%)	GCTGC (0.32%)	TGTTT (0.35%)	CCAGC (0.33%)	CCAGC (0.33%)	CAGAA (0.34%)	CTGGC (0.30%)	CATCA (0.30%)	GAAAA (0.36%)
5	TTATC (0.29%)	TTTGC (0.32%)	CGTTT (0.34%)	CTGGC (0.31%)	CATCA (0.32%)	ATAAA (0.34%)	TGGCA (0.29%)	GCGGC (0.29%)	ATTTT (0.33%)
6	CAAAA (0.28%)	CGCCA (0.31%)	TGGCA (0.34%)	CGGCA (0.30%)	GCTGC (0.32%)	GAAAA (0.33%)	GCCAG (0.29%)	TGGCG (0.29%)	TTGCC (0.30%)
7	ATTTT (0.28%)	CATCA (0.30%)	GCCAG (0.33%)	GCGGC (0.28%)	TCAGC (0.31%)	AATCA (0.33%)	CATCA (0.29%)	GCCAG (0.28%)	CAAAA (0.30%)
8	GAAAA (0.28%)	TTTTC (0.30%)	CTGGC (0.33%)	GCAGC (0.28%)	AATCA (0.30%)	AAGAA (0.32%)	CCAGC (0.27%)	CCAGC (0.28%)	CGCCA (0.29%)
9	TTTTT (0.28%)	GCCAG (0.30%)	CGGCA (0.31%)	GATGC (0.28%)	TTTTG (0.29%)	GCAAA (0.32%)	GCAAA (0.27%)	TTTTT (0.28%)	CGGCA (0.29%)
10	CGTTT (0.28%)	CCAGC (0.30%)	TTGCC (0.30%)	AATCA (0.28%)	GCAGC (0.29%)	TGGCA (0.32%)	GCGCA (0.26%)	ATAAA (0.25%)	GCAAA (0.28%)
-10	GGACC (0.01%)	CCCTA (0.01%)	CTTAG (0.01%)	CCCTA (0.01%)	ACCTA (0.01%)	CCCTT (0.01%)	CCCTA (0.01%)	TCCTA (0.02%)	TCCTA (0.01%)
-9	CCCTA (0.01%)	TAGGA (0.01%)	CCCTA (0.01%)	GGGGG (0.01%)	CCCTA (0.01%)	CCCTA (0.01%)	TAGGA (0.01%)	TAGGA (0.01%)	CCCTA (0.01%)
-8	CTAGC (0.00%)	GCTAG (0.00%)	ACTAG (0.00%)	CTAGC (0.01%)	GCTAG (0.01%)	CTAGC (0.00%)	GCTAG (0.01%)	GCTAG (0.01%)	GCTAG (0.00%)
-7	GCTAG (0.00%)	ACTAG (0.00%)	GCTAG (0.00%)	GCTAG (0.00%)	CCCCC (0.01%)	CTAGT (0.00%)	CTAGT (0.00%)	CTAGC (0.01%)	CTAGC (0.00%)
-6	CTAGT (0.00%)	CTAGC (0.00%)	CTAGC (0.00%)	CTAGT (0.00%)	ACTAG (0.00%)	GCTAG (0.00%)	CCTAG (0.00%)	ACTAG (0.01%)	ACTAG (0.00%)
-5	ACTAG (0.00%)	CTAGT (0.00%)	CTAGG (0.00%)	ACTAG (0.00%)	CTAGT (0.00%)	CTAGA (0.00%)	CTAGC (0.00%)	CTAGT (0.00%)	CTAGG (0.00%)
-4	CTAGA (0.00%)	TCTAG (0.00%)	TCTAG (0.00%)	CTAGA (0.00%)	CTAGA (0.00%)	ACTAG (0.00%)	ACTAG (0.00%)	CTAGG (0.00%)	CTAGT (0.00%)
-3	CCTAG (0.00%)	CCTAG (0.00%)	CTAGT (0.00%)	TCTAG (0.00%)	CCTAG (0.00%)	CTAGG (0.00%)	TCTAG (0.00%)	TCTAG (0.00%)	TCTAG (0.00%)
-2	TCTAG (0.00%)	CTAGG (0.00%)	CCTAG (0.00%)	CTAGG (0.00%)	CTAGG (0.00%)	TCTAG (0.00%)	CTAGG (0.00%)	CTAGA (0.00%)	CCTAG (0.00%)
-1	CTAGG (0.00%)	CTAGA (0.00%)	CTAGA (0.00%)	CCTAG (0.00%)	TCTAG (0.00%)	CCTAG (0.00%)	CTAGA (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%