

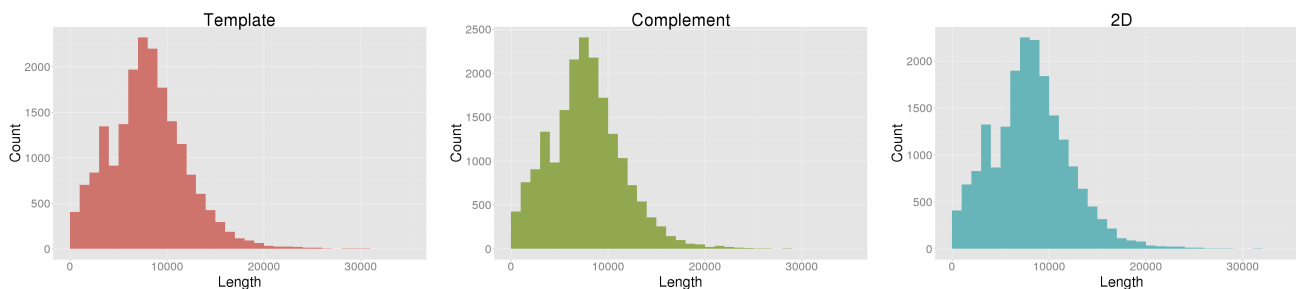
NanoOK report for UCSC_MARC_Phase_Ia_Run_2

Pass and fail counts

Type	Pass	Fail
Template	19169	0
Complement	19169	0
2D	19169	0

Read lengths

Type	NumReads	TotalBases	Mean	Longest	Shortest	N50	N50Count	N90	N90Count
Template	19169	154551900	8062.60	58974	174	9494	6179	5502	14350
Complement	19169	148846277	7764.95	57702	203	9139	6180	5328	14347
2D	19169	156804426	8180.10	59696	194	9626	6182	5611	14344



Template alignments

Number of reads	19169	
Number of reads with alignments	19088	(99.58%)
Number of reads without alignments	81	(0.42%)

ID	Size	Number of Reads	% of Reads	Mean read length	Aligned bases	Mean coverage	Longest Perf Kmer
Control sequence	3560	679	3.54	3139.92	2254575	633.31	67
Escherichia coli	4641652	18409	96.04	8276.55	162488459	35.01	91

Complement alignments

Number of reads	19169	
Number of reads with alignments	19072	(99.49%)
Number of reads without alignments	97	(0.51%)

ID	Size	Number of Reads	% of Reads	Mean read length	Aligned bases	Mean coverage	Longest Perf Kmer
Control sequence	3560	677	3.53	2972.81	2018807	567.08	65
Escherichia coli	4641652	18395	95.96	7977.72	157842948	34.01	70

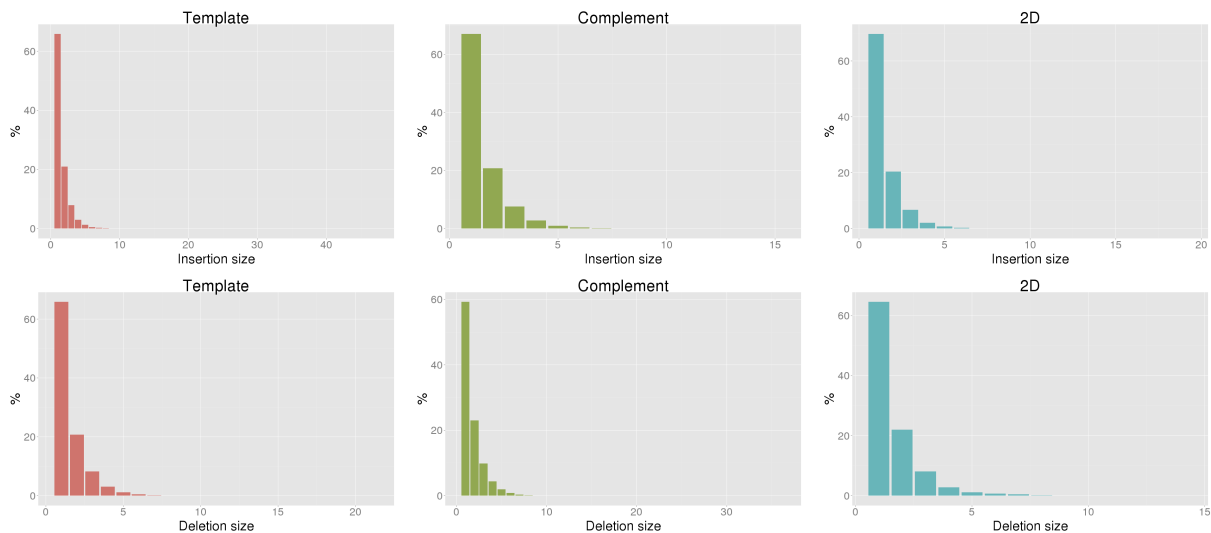
2D alignments

Number of reads	19169	
Number of reads with alignments	19148	(99.89%)
Number of reads without alignments	21	(0.11%)

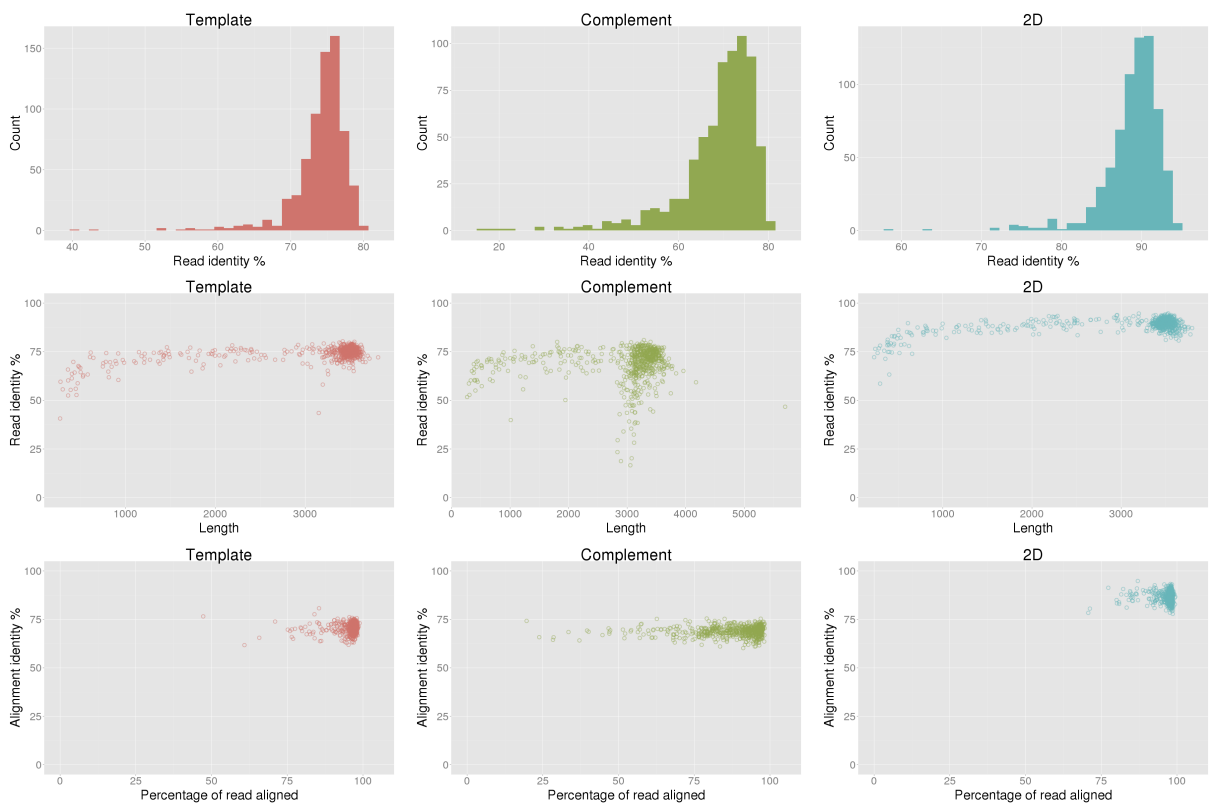
ID	Size	Number of Reads	% of Reads	Mean read length	Aligned bases	Mean coverage	Longest Perf Kmer
Control sequence	3560	693	3.62	3094.63	2215647	622.37	180
Escherichia coli	4641652	18455	96.28	8372.97	159973411	34.46	335

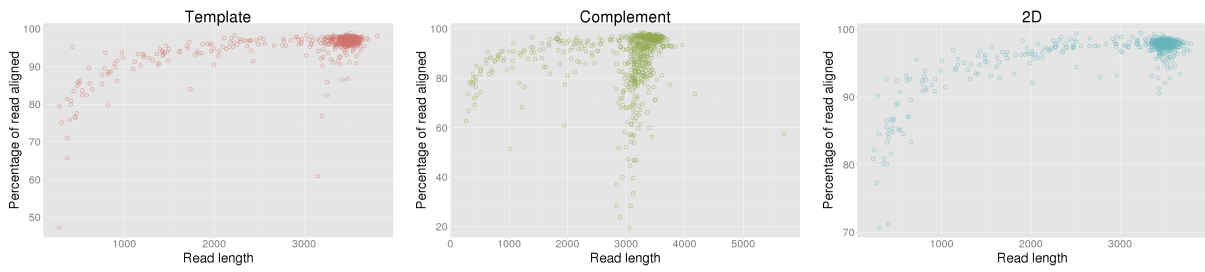
Control sequence error analysis

	Template	Complement	2D
Overall base identity (excluding indels)	74.66%	68.93%	89.43%
Aligned base identity (excluding indels)	82.15%	82.16%	94.49%
Identical bases per 100 aligned bases (including indels)	70.60%	68.72%	86.56%
Inserted bases per 100 aligned bases (including indels)	5.14%	4.35%	2.77%
Deleted bases per 100 aligned bases (including indels)	8.92%	12.01%	5.63%
Substitutions per 100 aligned bases (including indels)	15.34%	14.92%	5.04%
Mean insertion size	1.58	1.53	1.46
Mean deletion size	1.56	1.73	1.59

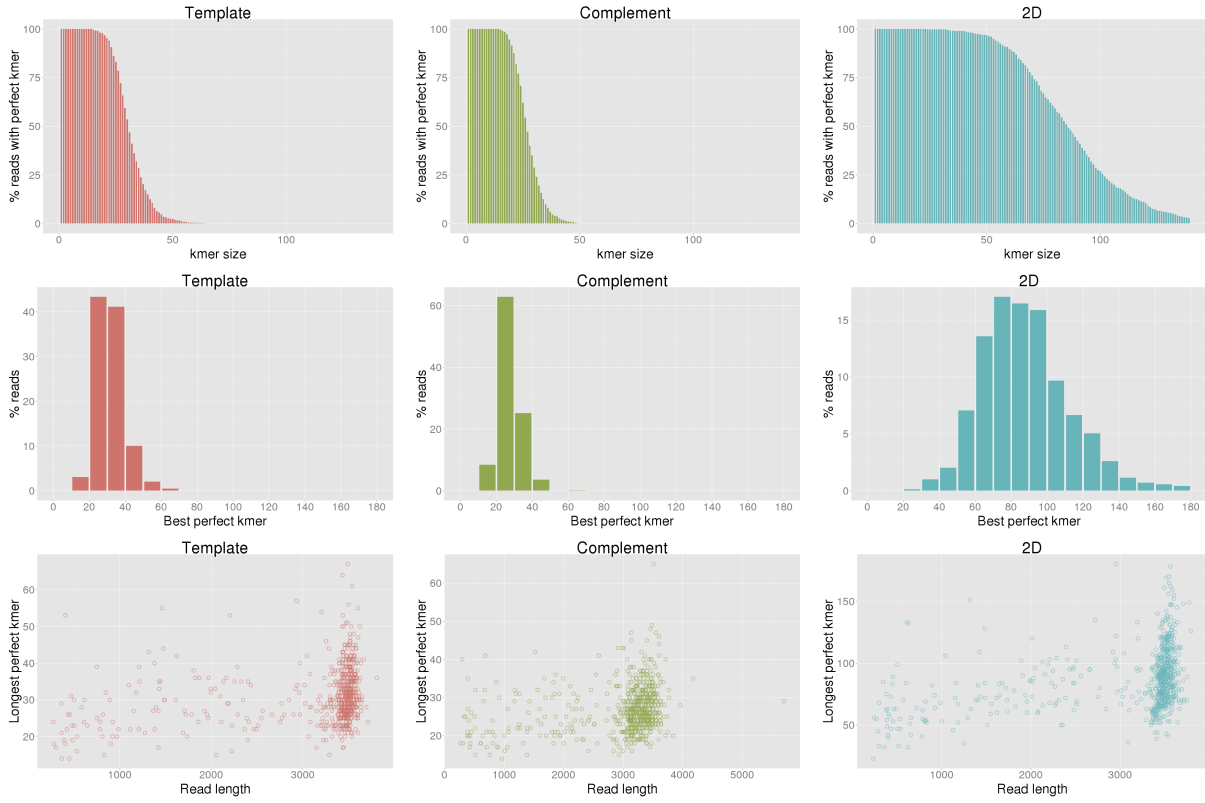


Control sequence read identity

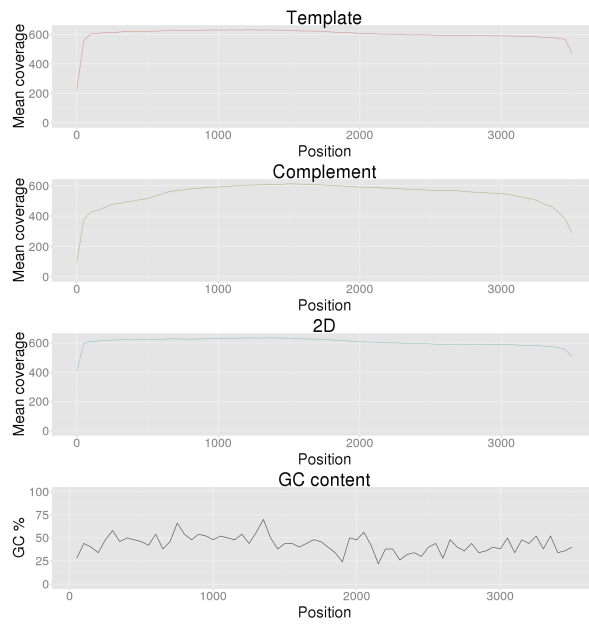




Control sequence perfect kmers



Control sequence coverage



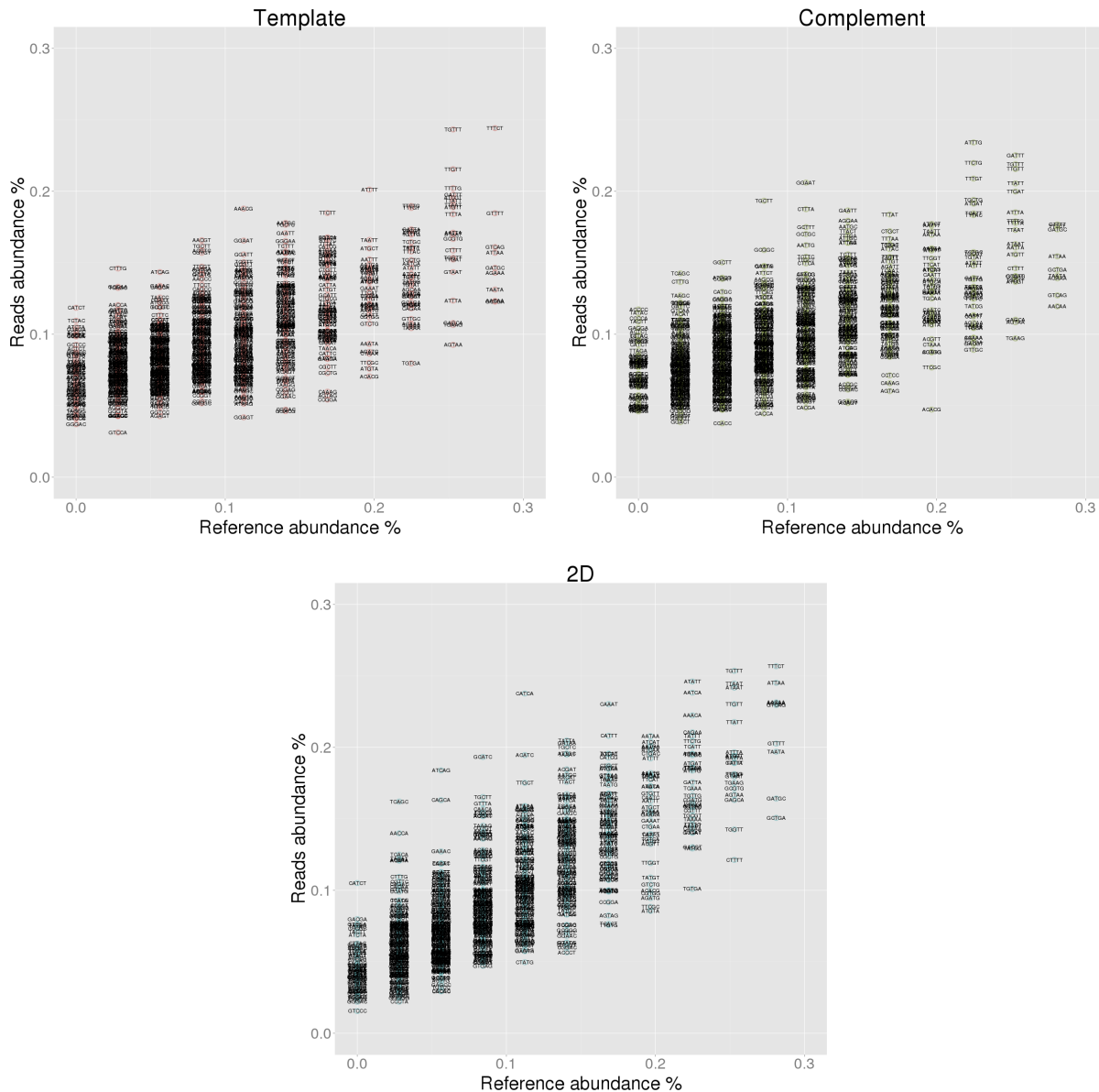
Control sequence 5-mer analysis

Under-represented 5-mers

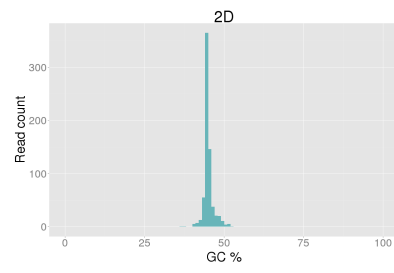
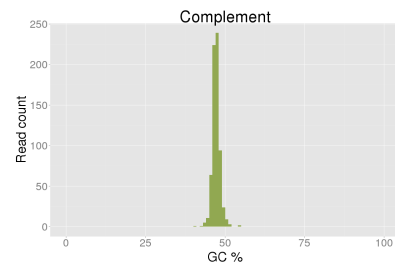
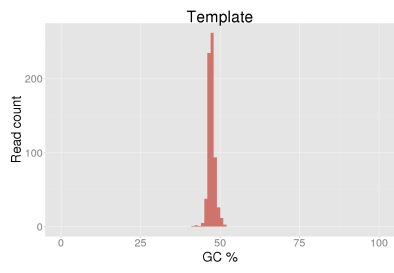
Rank	Template				Complement				2D			
	kmer	Ref %	Read %	Diff %	kmer	Ref %	Read %	Diff %	kmer	Ref %	Read %	Diff %
1	TTTTT	0.759	0.148	-0.611	TTTTT	0.759	0.100	-0.658	TTTTT	0.759	0.059	-0.699
2	AAAAA	0.478	0.122	-0.355	AAAAA	0.478	0.067	-0.411	AAAAA	0.478	0.082	-0.396
3	TGATG	0.393	0.136	-0.257	AAAC	0.337	0.136	-0.201	TGATG	0.393	0.191	-0.203
4	GATGT	0.309	0.105	-0.205	TGATG	0.393	0.217	-0.176	CTGAT	0.309	0.156	-0.153
5	AAAAC	0.337	0.141	-0.196	GATGT	0.309	0.134	-0.175	GATGT	0.309	0.158	-0.151
6	CTGAT	0.309	0.127	-0.182	GCAAT	0.309	0.136	-0.173	CTTTT	0.253	0.121	-0.132
7	AGTAA	0.253	0.093	-0.160	AACAA	0.281	0.119	-0.162	GCTGA	0.281	0.151	-0.130
8	GCTGA	0.281	0.123	-0.158	TTATC	0.309	0.152	-0.157	AAAAC	0.337	0.211	-0.127
9	AACAA	0.281	0.123	-0.158	TGAAG	0.253	0.097	-0.156	TGTGA	0.225	0.101	-0.124
10	GCAAT	0.309	0.152	-0.158	GTCAG	0.281	0.127	-0.154	TTATC	0.309	0.189	-0.120

Over-represented 5-mers

Rank	Template				Complement				2D			
	kmer	Ref %	Read %	Diff %	kmer	Ref %	Read %	Diff %	kmer	Ref %	Read %	Diff %
1	CATCT	0.000	0.118	0.118	ACCCC	0.000	0.117	0.117	TCAGC	0.028	0.162	0.134
2	CTTTG	0.028	0.146	0.118	TATAC	0.000	0.115	0.115	ATCAG	0.056	0.184	0.128
3	TCTAC	0.000	0.110	0.110	TCAGC	0.028	0.143	0.114	CATCA	0.112	0.238	0.125
4	ATCTA	0.000	0.105	0.105	CCCCA	0.000	0.111	0.111	AACCA	0.028	0.140	0.112
5	GCGAA	0.028	0.133	0.105	TGCTT	0.084	0.193	0.109	GCATC	0.084	0.193	0.109
6	TCAGC	0.028	0.132	0.104	TACTT	0.000	0.109	0.109	CAGCA	0.056	0.163	0.107
7	CGAGA	0.000	0.103	0.103	CTTTG	0.028	0.137	0.108	CATCT	0.000	0.105	0.105
8	ACCCC	0.000	0.101	0.101	GAGGA	0.000	0.104	0.104	TCACA	0.028	0.125	0.097
9	TACTT	0.000	0.100	0.100	ACTCT	0.000	0.102	0.102	TACAT	0.028	0.122	0.094
10	TCTTA	0.000	0.099	0.099	TAAGC	0.028	0.127	0.099	ACCAA	0.028	0.121	0.093

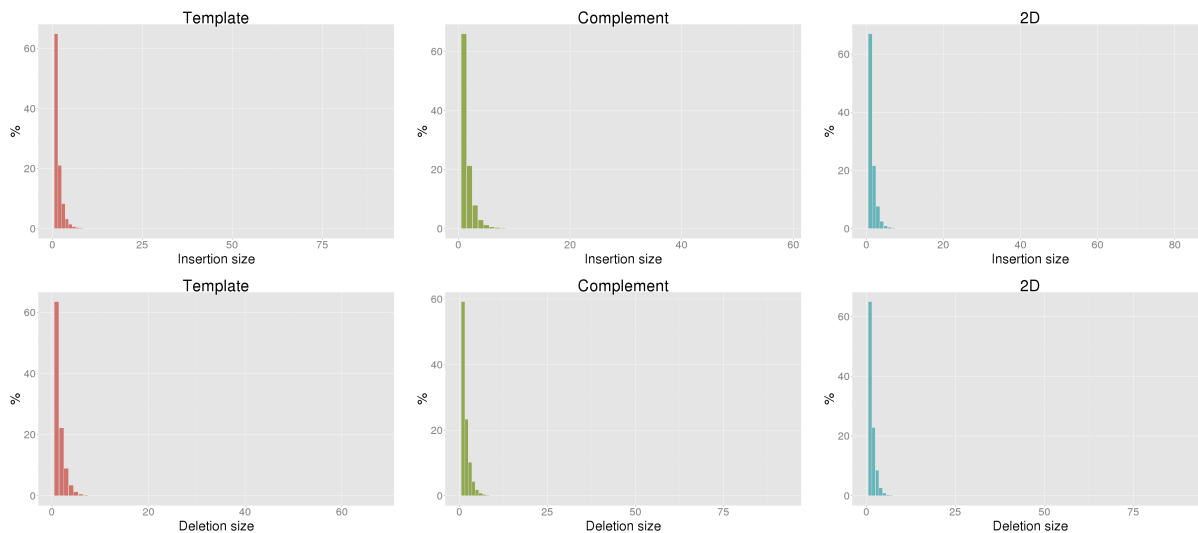


Control sequence GC content

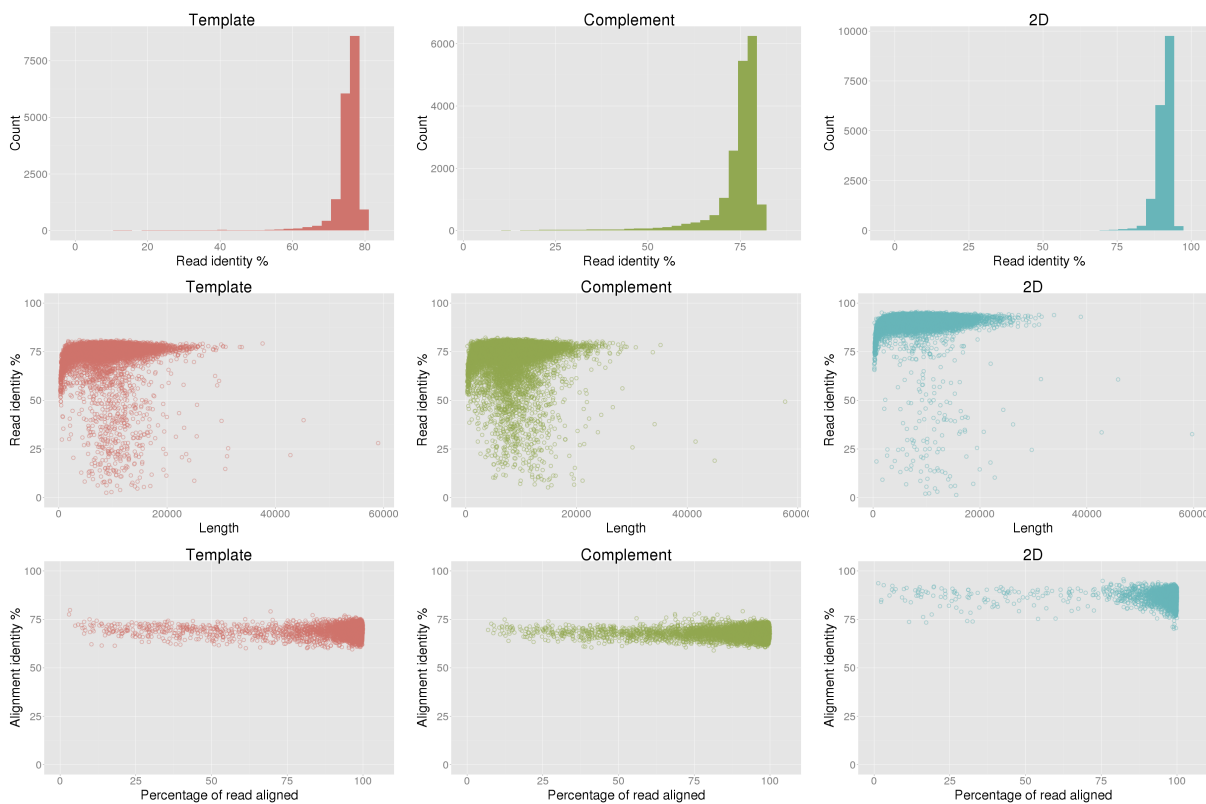


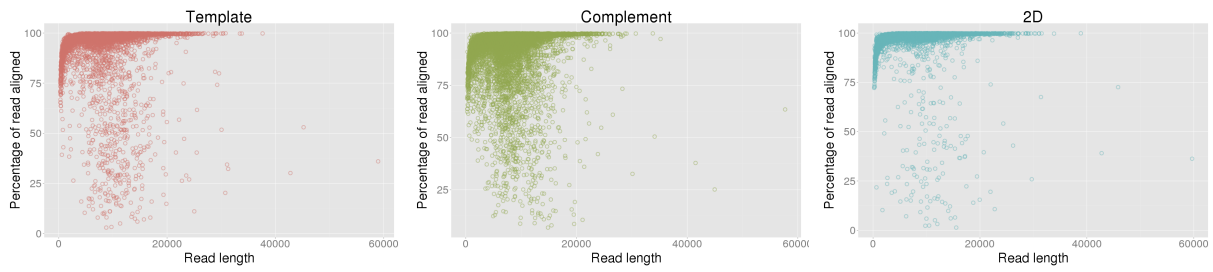
Escherichia coli error analysis

	Template	Complement	2D
Overall base identity (excluding indels)	74.46%	73.85%	90.50%
Aligned base identity (excluding indels)	81.79%	82.14%	94.89%
Identical bases per 100 aligned bases (including indels)	69.82%	68.66%	87.42%
Inserted bases per 100 aligned bases (including indels)	5.38%	4.78%	2.96%
Deleted bases per 100 aligned bases (including indels)	9.26%	11.63%	4.91%
Substitutions per 100 aligned bases (including indels)	15.54%	14.93%	4.71%
Mean insertion size	1.62	1.57	1.52
Mean deletion size	1.60	1.72	1.54

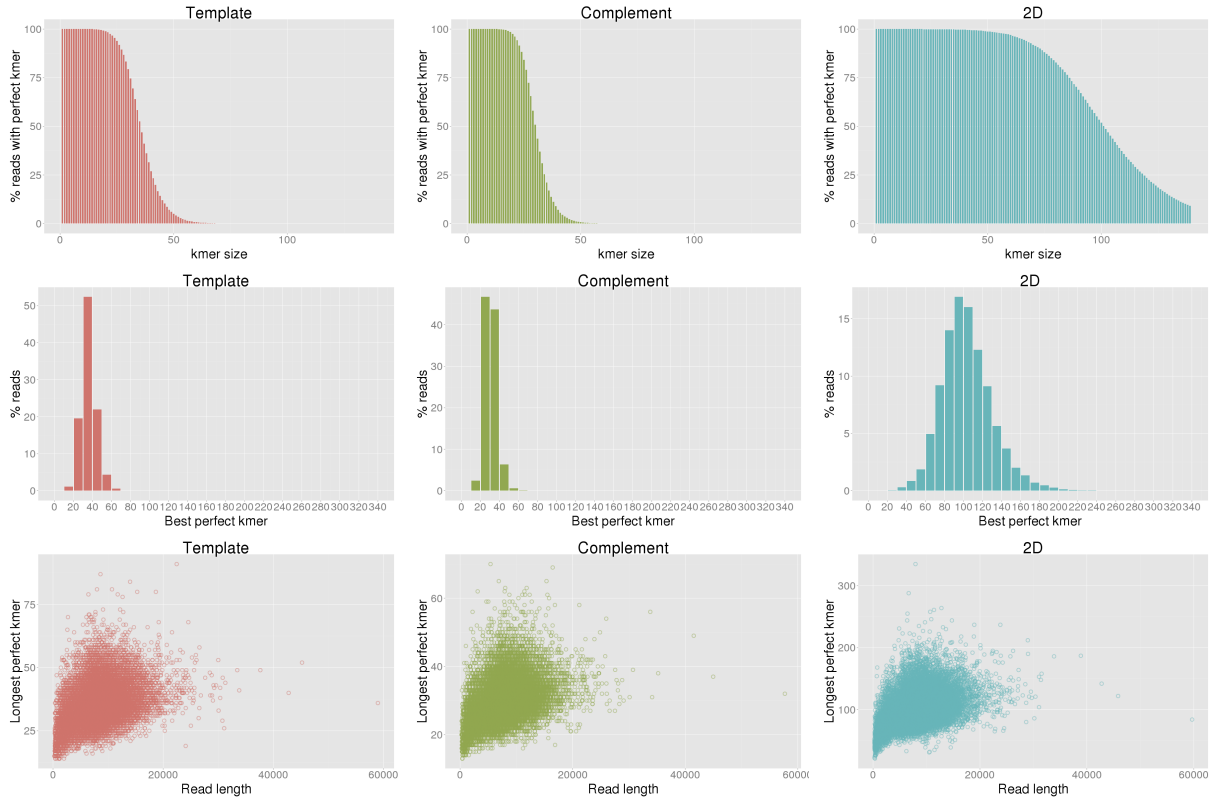


Escherichia coli read identity

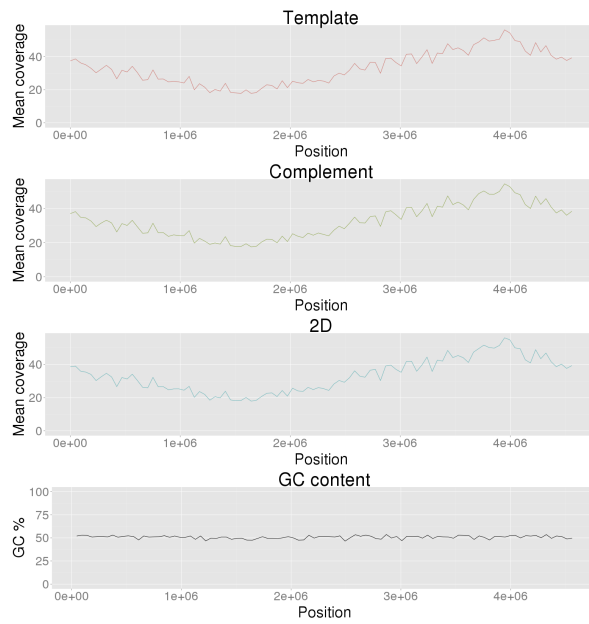




Escherichia coli perfect kmers



Escherichia coli coverage



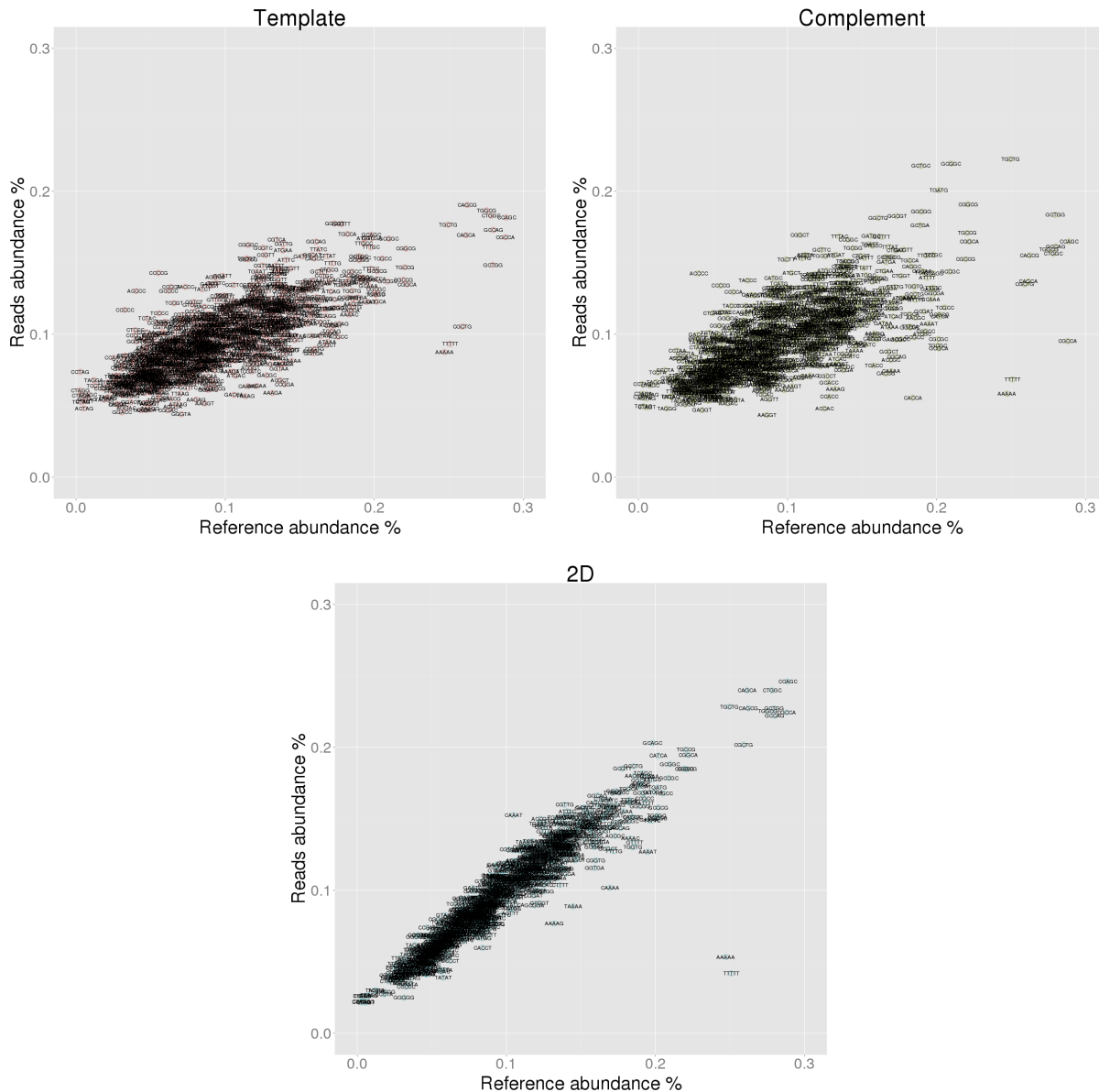
Escherichia coli 5-mer analysis

Under-represented 5-mers

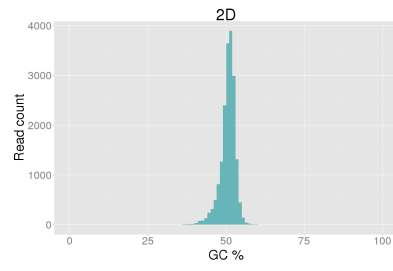
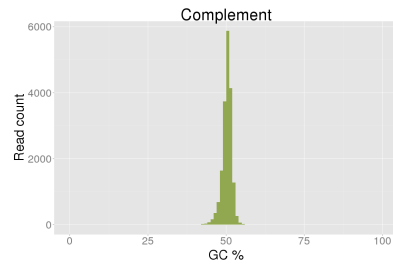
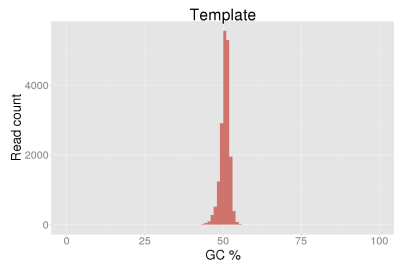
Rank	Template				Complement				2D			
	kmer	Ref %	Read %	Diff %	kmer	Ref %	Read %	Diff %	kmer	Ref %	Read %	Diff %
1	AAAAA	0.247	0.087	-0.160	CGCCA	0.288	0.095	-0.193	TTTTT	0.251	0.042	-0.209
2	TTTTT	0.251	0.093	-0.158	AAAAA	0.247	0.058	-0.189	AAAAA	0.247	0.053	-0.194
3	CGCTG	0.259	0.105	-0.154	TTTTT	0.251	0.068	-0.182	AAAAT	0.195	0.127	-0.068
4	GCTGG	0.279	0.148	-0.131	CACCA	0.184	0.056	-0.128	CAAAA	0.169	0.102	-0.068
5	CGCCA	0.288	0.168	-0.120	CAGCA	0.261	0.137	-0.125	CGCCA	0.288	0.224	-0.064
6	CCAGC	0.289	0.182	-0.107	CGCTG	0.259	0.135	-0.124	GCCAG	0.280	0.222	-0.058
7	GCCAG	0.280	0.173	-0.107	CCAGC	0.289	0.165	-0.124	CGCTG	0.259	0.202	-0.057
8	CTGGC	0.278	0.183	-0.095	CTGGC	0.278	0.156	-0.122	TAAAA	0.145	0.089	-0.056
9	CAGCA	0.261	0.169	-0.092	GCCAG	0.280	0.161	-0.118	AAAAG	0.132	0.077	-0.055
10	TGGCG	0.275	0.187	-0.089	TGGCG	0.275	0.160	-0.116	TGGTG	0.185	0.130	-0.055

Over-represented 5-mers

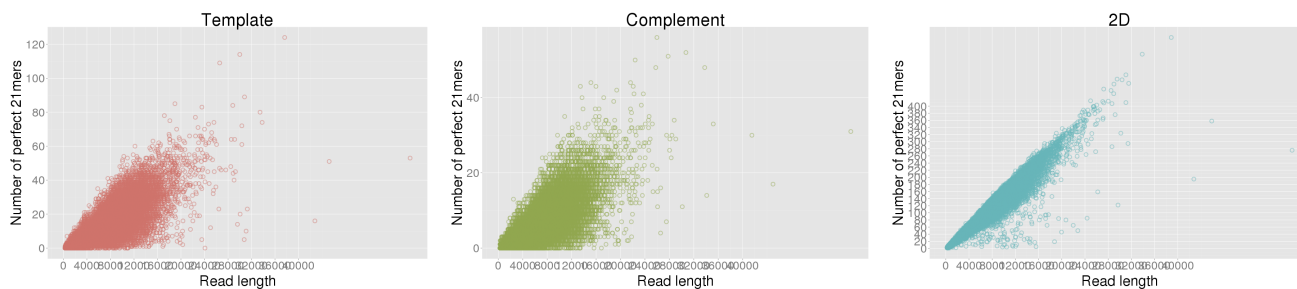
Rank	Template				Complement				2D			
	kmer	Ref %	Read %	Diff %	kmer	Ref %	Read %	Diff %	kmer	Ref %	Read %	Diff %
1	ACCCC	0.040	0.130	0.090	ACCCC	0.040	0.143	0.102	CAAAT	0.105	0.153	0.048
2	CCCCG	0.055	0.143	0.088	CCCCG	0.055	0.134	0.079	GGGTC	0.040	0.069	0.028
3	CCCCC	0.033	0.117	0.084	CCCCA	0.064	0.129	0.066	GGGGT	0.039	0.068	0.028
4	CCTAG	0.003	0.074	0.071	CTGAG	0.050	0.115	0.065	CCCAA	0.047	0.074	0.027
5	CCCCA	0.064	0.133	0.069	TACCC	0.073	0.138	0.064	ACCGT	0.123	0.150	0.027
6	GCCCC	0.062	0.130	0.068	CCTAA	0.026	0.089	0.063	CGTGA	0.102	0.129	0.027
7	TCTAC	0.048	0.111	0.063	CCTAG	0.003	0.065	0.063	CTCGT	0.042	0.068	0.026
8	CTCCC	0.040	0.103	0.063	CGGCT	0.108	0.169	0.061	TGAAT	0.121	0.147	0.025
9	TACCC	0.073	0.133	0.060	TCCTA	0.013	0.073	0.060	CGGGG	0.054	0.080	0.025
10	CCCCT	0.039	0.099	0.060	GACCC	0.040	0.100	0.060	GAATC	0.077	0.102	0.025



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	8.72	9.30	4.66	0.00	8.92	8.75	4.94	0.00	8.02	8.51	4.01
C	8.49	0.00	9.19	10.10	9.38	0.00	8.67	9.80	9.54	0.00	10.94	9.60
G	9.46	9.11	0.00	8.11	9.08	8.80	0.00	8.83	9.28	11.01	0.00	8.83
T	4.92	9.50	8.43	0.00	5.20	8.84	8.78	0.00	4.07	8.36	7.82	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 (3.28%)	TTC (3.48%)	AAA (3.97%)	TGC (2.80%)	GGC (3.06%)	AAA (3.96%)	GCA (3.04%)	GGC (2.71%)	GCA (3.82%)
2	AAA (2.77%)	TGC (3.01%)	TTC (3.73%)	GCA (2.72%)	TGC (2.81%)	GCA (3.64%)	TTC (2.80%)	TCA (2.56%)	AAA (3.76%)
3	GCA (2.75%)	GCA (2.81%)	GCA (3.32%)	TTC (2.72%)	AAA (2.72%)	GAA (3.33%)	TCA (2.64%)	GCG (2.53%)	GAA (3.35%)
4	TGC (2.63%)	AAA (2.65%)	GAA (2.98%)	AAA (2.56%)	GCA (2.62%)	TTC (3.11%)	AAA (2.63%)	TGC (2.52%)	TTC (2.93%)
5	ATC (2.57%)	GCC (2.59%)	TGC (2.54%)	CAG (2.54%)	TTC (2.59%)	TTT (2.55%)	ATC (2.47%)	AAA (2.45%)	TTT (2.74%)
6	TCA (2.50%)	GGC (2.52%)	TTT (2.47%)	GGC (2.45%)	GCC (2.36%)	TGC (2.47%)	TGC (2.38%)	GCA (2.45%)	GCC (2.47%)
7	GCC (2.36%)	TCA (2.44%)	GCC (2.34%)	GAA (2.32%)	GAA (2.36%)	TCA (2.38%)	GAA (2.31%)	TTC (2.44%)	GCG (2.38%)
8	GGC (2.28%)	ATC (2.31%)	AAT (2.30%)	TCA (2.31%)	CAG (2.30%)	ATC (2.36%)	GCG (2.27%)	CGC (2.32%)	ATC (2.32%)
9	GAA (2.21%)	GCG (2.17%)	GGC (2.25%)	ATC (2.31%)	TCA (2.27%)	GCC (2.24%)	CGC (2.27%)	ATC (2.23%)	TCA (2.31%)
10	GCG (2.14%)	AAC (2.16%)	TCA (2.25%)	GCC (2.17%)	CGC (2.19%)	GCC (2.15%)	CAG (2.24%)	CAG (2.22%)	GTT (2.22%)
-10	AGT (0.97%)	GTA (0.96%)	ACT (0.94%)	AGA (1.00%)	CTT (0.95%)	CCC (0.95%)	CTT (1.05%)	GTA (1.02%)	TAT (0.89%)
-9	CCC (0.94%)	AGT (0.93%)	GGG (0.92%)	AGT (0.98%)	AGT (0.93%)	CTT (0.91%)	CTC (1.04%)	CGA (0.94%)	ACT (0.86%)
-8	TGT (0.92%)	CCT (0.91%)	AGA (0.83%)	CTC (0.92%)	GGA (0.92%)	AGT (0.85%)	GAG (0.88%)	ACT (0.92%)	TGA (0.83%)
-7	GGA (0.83%)	CTT (0.81%)	AGT (0.80%)	CCC (0.87%)	CCC (0.92%)	AGG (0.83%)	AGG (0.82%)	CCC (0.89%)	CTT (0.76%)
-6	AGA (0.80%)	CGA (0.80%)	AGG (0.80%)	GGA (0.87%)	CTC (0.89%)	CCT (0.82%)	CCC (0.82%)	CTT (0.88%)	CGA (0.72%)
-5	GAG (0.71%)	GAG (0.80%)	CTT (0.76%)	GAG (0.80%)	CCT (0.89%)	GGG (0.79%)	AGA (0.81%)	CCT (0.81%)	GAG (0.71%)
-4	GGG (0.70%)	AGA (0.66%)	TGT (0.72%)	AGG (0.72%)	GAG (0.83%)	ACT (0.72%)	GGA (0.77%)	AGA (0.80%)	AGA (0.51%)
-3	AGG (0.70%)	GGA (0.65%)	GAG (0.60%)	CTA (0.60%)	GGG (0.77%)	GAG (0.61%)	GGG (0.75%)	GGA (0.73%)	TAG (0.51%)
-2	CTA (0.51%)	TAG (0.52%)	TAG (0.39%)	GGG (0.60%)	CTA (0.55%)	CTA (0.46%)	CTA (0.62%)	CTA (0.73%)	GGA (0.48%)
-1	TAG (0.41%)	CTA (0.52%)	CTA (0.38%)	TAG (0.46%)	TAG (0.54%)	TAG (0.38%)	TAG (0.49%)	TAG (0.66%)	CTA (0.44%)

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 (1.08%)	AAAA (1.31%)	CAGC (0.96%)	CGGC (1.11%)	AAAA (1.07%)	ATCA (0.95%)	TGGC (0.93%)	GGCA (1.21%)
2	GAAA (0.88%)	TGCC (0.98%)	TTTC (1.20%)	ATCA (0.91%)	CAGC (1.07%)	CAAA (1.01%)	GCCA (0.85%)	CAGC (0.92%)	AAAA (1.08%)
3	ATCA (0.88%)	CAGC (0.92%)	GAAA (1.12%)	CGGC (0.90%)	TGGC (1.05%)	GAAA (0.96%)	GGCA (0.84%)	TTCA (0.86%)	TGAA (0.97%)
4	AAAA (0.87%)	TGGC (0.92%)	GGCA (0.98%)	CTGC (0.86%)	CTGC (0.89%)	TGAA (0.96%)	CAGC (0.81%)	CGGC (0.84%)	GAAA (0.95%)
5	TTCA (0.84%)	TTCA (0.89%)	GTTC (0.92%)	CCAG (0.83%)	TTGC (0.85%)	GGCA (0.96%)	CGCA (0.78%)	ATCA (0.84%)	GGAA (0.91%)
6	CAGC (0.84%)	TTGC (0.88%)	GCAA (0.90%)	TGGC (0.80%)	ATCA (0.82%)	ATCA (0.94%)	CGCC (0.77%)	CTGC (0.75%)	CGCA (0.91%)
7	TGCC (0.81%)	CTGC (0.87%)	TGCC (0.89%)	TTGC (0.79%)	CAAA (0.79%)	AGCA (0.93%)	TTCA (0.77%)	GGCC (0.74%)	CGCC (0.90%)
8	CGCC (0.80%)	CGCC (0.84%)	GGAA (0.87%)	CAAA (0.74%)	CGCC (0.76%)	TTTC (0.88%)	AAAC (0.76%)	GGCC (0.74%)	TTTT (0.89%)
9	GGCA (0.80%)	AAAA (0.83%)	TTTT (0.84%)	ATGC (0.72%)	TGCC (0.76%)	AGAA (0.87%)	CCAG (0.75%)	CGCC (0.74%)	TTTC (0.88%)
10	TGCC (0.79%)	TTCC (0.83%)	CTTC (0.82%)	CGCC (0.71%)	TTCC (0.76%)	TAAA (0.87%)	TTTC (0.74%)	GCCA (0.71%)	TGCA (0.87%)
-10	AGGG (0.12%)	TCTA (0.13%)	TTAG (0.12%)	GTGT (0.11%)	CTAT (0.12%)	ACTA (0.11%)	GAGG (0.14%)	ACCT (0.16%)	TGCA (0.11%)
-9	GAGG (0.12%)	CTAT (0.13%)	ACTA (0.11%)	AGGG (0.11%)	CCCC (0.12%)	ACCT (0.11%)	TAGT (0.14%)	CCCC (0.15%)	CTAA (0.10%)
-8	TAGT (0.12%)	CCCT (0.12%)	CGAG (0.10%)	GGAC (0.11%)	ACCT (0.12%)	GTGT (0.10%)	CCCT (0.14%)	GAGA (0.15%)	CCCT (0.10%)
-7	GGAC (0.11%)	TAGT (0.12%)	GGAC (0.09%)	TAGA (0.10%)	GTGT (0.11%)	GGAC (0.10%)	TCTA (0.14%)	CTAT (0.15%)	CGGA (0.10%)
-6	CTAA (0.11%)	CGGA (0.11%)	TAGT (0.09%)	CTAA (0.10%)	CTAA (0.11%)	CTAT (0.10%)	CTAT (0.13%)	CTAA (0.12%)	GGA (0.10%)
-5	TTAG (0.11%)	CTAA (0.10%)	TCTA (0.08%)	GAGG (0.09%)	TAGA (0.11%)	CGAG (0.09%)	CTAA (0.12%)	CCCT (0.10%)	CTAT (0.10%)
-4	TAGA (0.06%)	TAGG (0.07%)	TAGA (0.08%)	CCCT (0.09%)	CCCT (0.08%)	TAGG (0.06%)	TAGA (0.08%)	TAGG (0.10%)	TAGG (0.08%)
-3	CCTA (0.06%)	TAGA (0.06%)	TAGG (0.07%)	CCTA (0.07%)	TAGG (0.08%)	CCCT (0.06%)	CCTA (0.07%)	TAGA (0.10%)	CCTA (0.05%)
-2	TAGG (0.05%)	CCTA (0.06%)	CCTA (0.05%)	TAGG (0.05%)	CCTA (0.06%)	CCTA (0.05%)	TAGG (0.06%)	CCTA (0.08%)	TAGA (0.05%)
-1	CTAG (0.01%)	CTAG (0.01%)	CTAG (0.01%)	CTAG (0.01%)	CTAG (0.01%)	CTAG (0.01%)	CTAG (0.01%)	CTAG (0.02%)	CTAG (0.01%)

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 (0.34%)	CTGGC (0.38%)	CAGCA (0.42%)	CAGCA (0.41%)	CAGCA (0.41%)	CAGCA (0.54%)	CAGCA (0.38%)	CTGGC (0.37%)	CAGCA (0.46%)
2	CTGGC (0.33%)	CAGCA (0.37%)	GAAAA (0.40%)	CATCA (0.33%)	CTGGC (0.38%)	CGGCA (0.39%)	CGCCA (0.36%)	CAGCA (0.31%)	CGGCA (0.43%)
3	CGCCA (0.32%)	TTGCC (0.34%)	CAAAA (0.36%)	CCAGC (0.32%)	GCGGC (0.36%)	ATAAA (0.35%)	CGGCA (0.33%)	GCGGC (0.30%)	TGGCA (0.38%)
4	CATCA (0.31%)	CGCCA (0.33%)	CGTTC (0.34%)	GCGGC (0.32%)	CCAGC (0.34%)	CATCA (0.35%)	CTGGC (0.30%)	CCAGC (0.30%)	GAAAA (0.36%)
5	TTATC (0.30%)	CATCA (0.32%)	TGTTT (0.33%)	GCTGC (0.32%)	TCAGC (0.32%)	GAAAA (0.33%)	CATCA (0.29%)	CATCA (0.29%)	ATTTT (0.31%)
6	ATTTT (0.29%)	TTTGC (0.31%)	TGGCA (0.33%)	CTGGC (0.30%)	CATCA (0.32%)	AAGAA (0.32%)	GCCAG (0.28%)	CGCCA (0.29%)	GCGCA (0.30%)
7	GCCAG (0.28%)	CCAGC (0.31%)	GCCAG (0.32%)	CGGCA (0.29%)	GCTGC (0.31%)	GCAAA (0.31%)	CCAGC (0.27%)	TGGCG (0.29%)	TTGCC (0.30%)
8	CCAGC (0.28%)	GCTGC (0.30%)	TTGCC (0.32%)	AATCA (0.28%)	AATCA (0.30%)	CAGAA (0.31%)	TGGCA (0.27%)	TTTTT (0.28%)	CGCCA (0.30%)
9	CAAAA (0.28%)	GCAGC (0.30%)	GCAAA (0.31%)	GCAGC (0.27%)	CAGGC (0.29%)	ACGCA (0.31%)	GCAAA (0.27%)	GCCAG (0.27%)	GCAAA (0.29%)
10	TGGCG (0.28%)	GCCAG (0.30%)	CGCCA (0.31%)	TTATC (0.27%)	ATAAA (0.29%)	AATCA (0.31%)	GCGCA (0.27%)	CAGCG (0.26%)	CAAAA (0.29%)
-10	GGACC (0.01%)	CCCTA (0.01%)	CTTAG (0.01%)	ACCTA (0.01%)	CCCTA (0.01%)	CCCTA (0.01%)	CCCTA (0.01%)	TCCTA (0.01%)	TTAGA (0.01%)
-9	CCCTA (0.01%)	TAGGA (0.01%)	CCCTA (0.01%)	CCCTA (0.01%)	CTAGC (0.01%)	ACCTA (0.01%)	TAGGA (0.01%)	TAGGA (0.01%)	TAGGA (0.01%)
-8	GCTAG (0.00%)	GCTAG (0.00%)	ACTAG (0.00%)	CTAGC (0.01%)	CCCC (0.01%)	CTAGC (0.01%)	CTAGC (0.00%)	GCTAG (0.01%)	GCTAG (0.00%)
-7	CTAGC (0.00%)	CTAGC (0.00%)	GCTAG (0.00%)	GCTAG (0.01%)	GCTAG (0.01%)	GCTAG (0.00%)	GCTAG (0.00%)	CTAGC (0.01%)	ACTAG (0.00%)
-6	ACTAG (0.00%)	CTAGT (0.00%)	CTAGC (0.00%)	CTAGT (0.00%)	CTAGT (0.00%)	CTAGT (0.00%)	ACTAG (0.00%)	ACTAG (0.01%)	CTAGC (0.00%)
-5	CTAGT (0.00%)	ACTAG (0.00%)	CTAGG (0.00%)	ACTAG (0.00%)	ACTAG (0.00%)	ACTAG (0.00%)	CTAGT (0.00%)	CTAGT (0.00%)	CTAGT (0.00%)
-4	CTAGG (0.00%)	TAGG (0.00%)	CTAGT (0.00%)	CTAGG (0.00%)	CTAGG (0.00%)	CTAGA (0.00%)	CCTAG (0.00%)	TCTAG (0.00%)	CTAGG (0.00%)
-3	CTAGA (0.00%)	TCTAG (0.00%)	CCTAG (0.00%)	CCTAG (0.00%)	CTAGA (0.00%)	CTAGG (0.00%)	TCTAG (0.00%)	CTAGG (0.00%)	CCTAG (0.00%)
-2	TCTAG (0.00%)	CCTAG (0.00%)	TCTAG (0.00%)	CTAGA (0.00%)	TCTAG (0.00%)	TCTAG (0.00%)	CTAGG (0.00%)	CCTAG (0.00%)	TCTAG (0.00%)
-1	CCTAG (0.00%)	CTAGA (0.00%)	CTAGA (0.00%)	TCTAG (0.00%)	CCTAG (0.00%)	CCTAG (0.00%)	CTAGA (0.00%)	CTAGA (0.00%)	CTAGA (0.00%)

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