

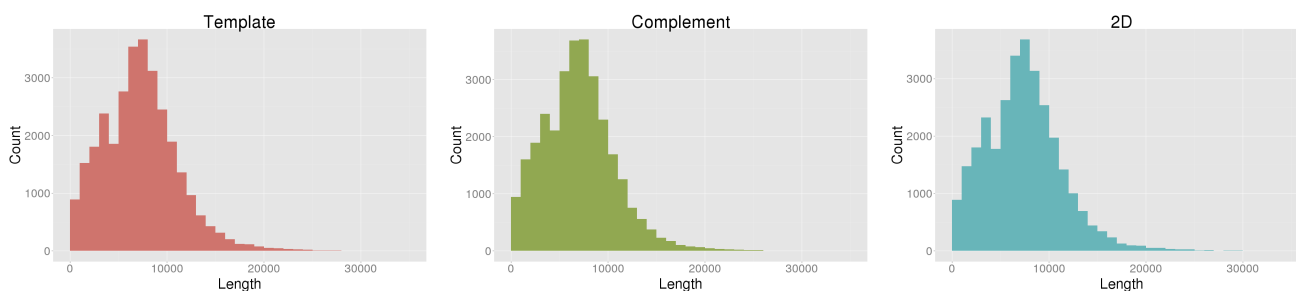
NanoOK report for UCSC_MARC_Phase_Ib_Run_1

Pass and fail counts

Type	Pass	Fail
Template	30364	0
Complement	30364	0
2D	30364	0

Read lengths

Type	NumReads	TotalBases	Mean	Longest	Shortest	N50	N50Count	N90	N90Count
Template	30364	221764757	7303.54	47283	185	8787	9430	4825	22297
Complement	30364	212953040	7013.34	44295	177	8450	9435	4640	22296
2D	30364	225086343	7412.93	45588	183	8931	9443	4905	22290



Template alignments

Number of reads	30364
Number of reads with alignments	30165 (99.34%)
Number of reads without alignments	199 (0.66%)

ID	Size	Number of Reads	% of Reads	Mean read length	Aligned bases	Mean coverage	Longest Perf Kmer
Control sequence	3560	944	3.11	3101.40	3100954	871.05	64
Escherichia coli	4641652	29221	96.24	7483.81	234585188	50.54	89

Complement alignments

Number of reads	30364
Number of reads with alignments	30135 (99.25%)
Number of reads without alignments	229 (0.75%)

ID	Size	Number of Reads	% of Reads	Mean read length	Aligned bases	Mean coverage	Longest Perf Kmer
Control sequence	3560	948	3.12	2916.50	2882270	809.63	62
Escherichia coli	4641652	29187	96.12	7195.33	226596187	48.82	77

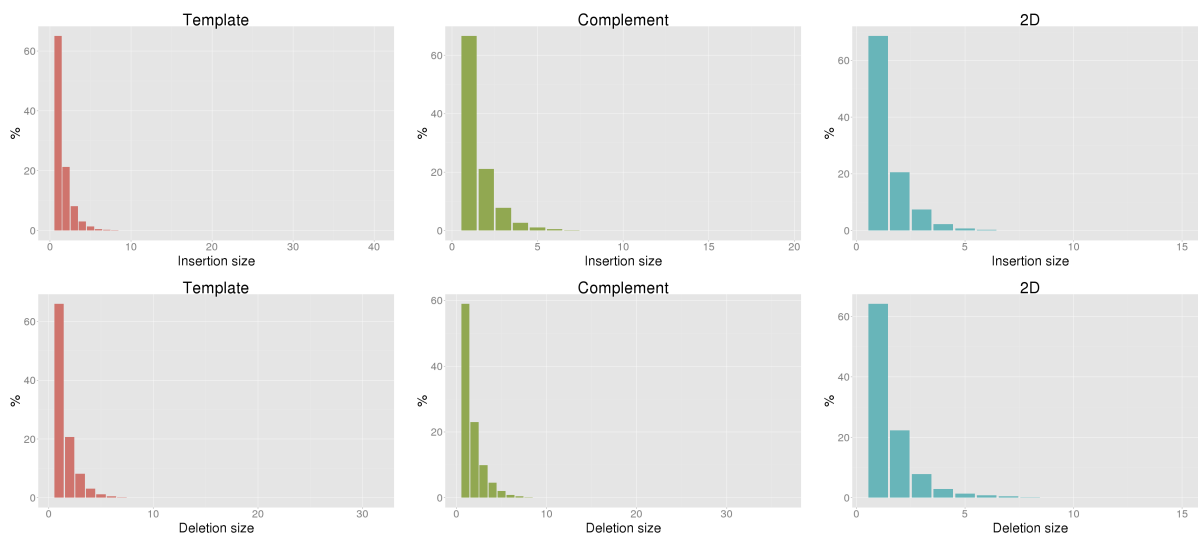
2D alignments

Number of reads	30364
Number of reads with alignments	30301 (99.79%)
Number of reads without alignments	63 (0.21%)

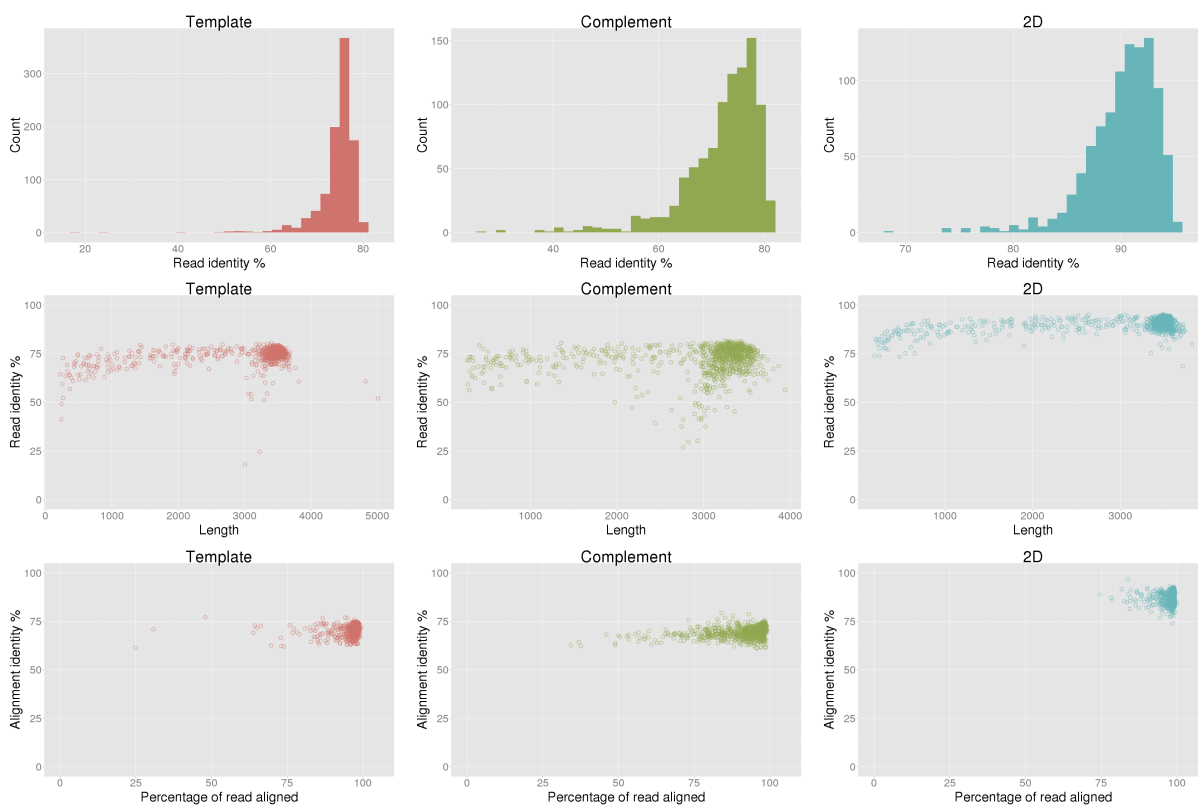
ID	Size	Number of Reads	% of Reads	Mean read length	Aligned bases	Mean coverage	Longest Perf Kmer
Control sequence	3560	961	3.16	3055.96	3046598	855.79	190
Escherichia coli	4641652	29340	96.63	7566.34	230295745	49.62	262

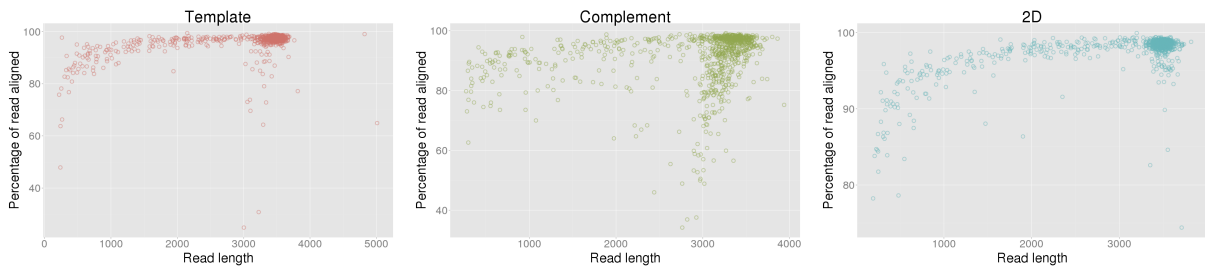
Control sequence error analysis

	Template	Complement	2D
Overall base identity (excluding indels)	74.79%	72.24%	90.50%
Aligned base identity (excluding indels)	82.27%	82.77%	94.97%
Identical bases per 100 aligned bases (including indels)	70.61%	69.30%	87.24%
Inserted bases per 100 aligned bases (including indels)	5.39%	4.29%	2.75%
Deleted bases per 100 aligned bases (including indels)	8.78%	11.99%	5.40%
Substitutions per 100 aligned bases (including indels)	15.22%	14.43%	4.62%
Mean insertion size	1.60	1.54	1.48
Mean deletion size	1.56	1.74	1.60

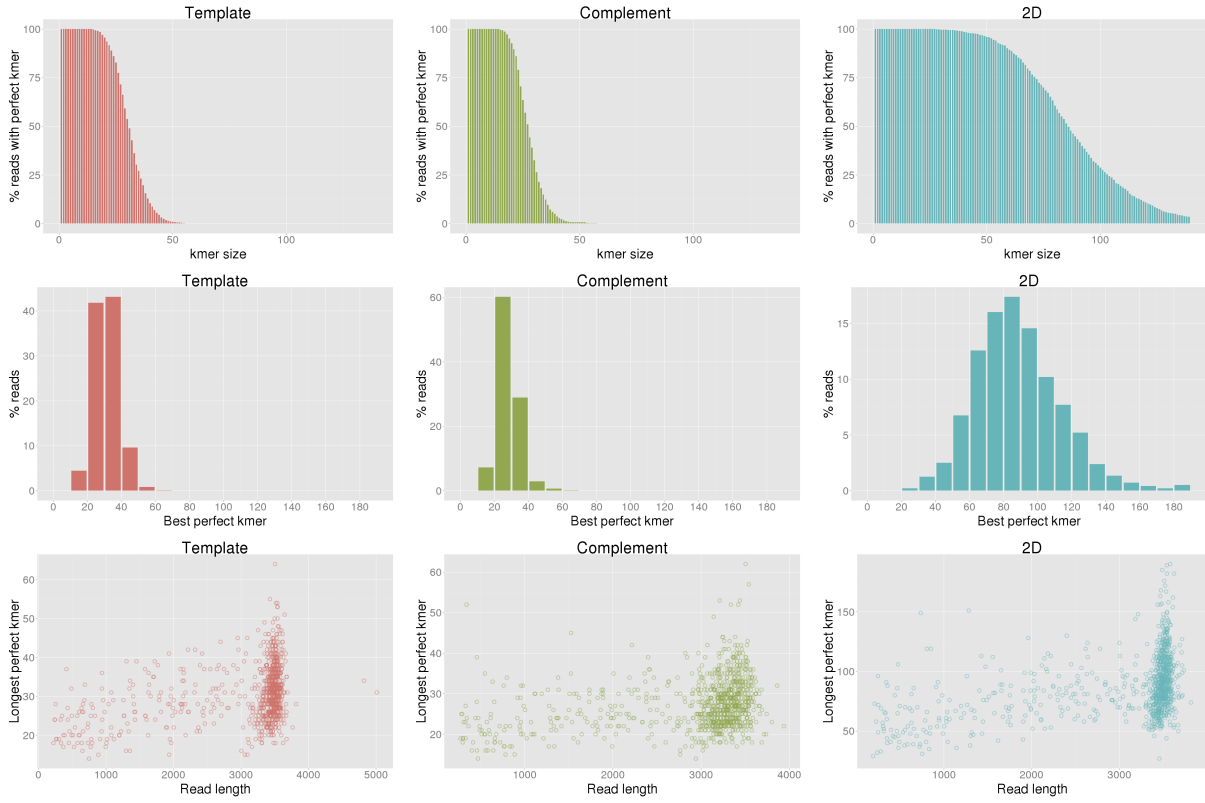


Control sequence read identity

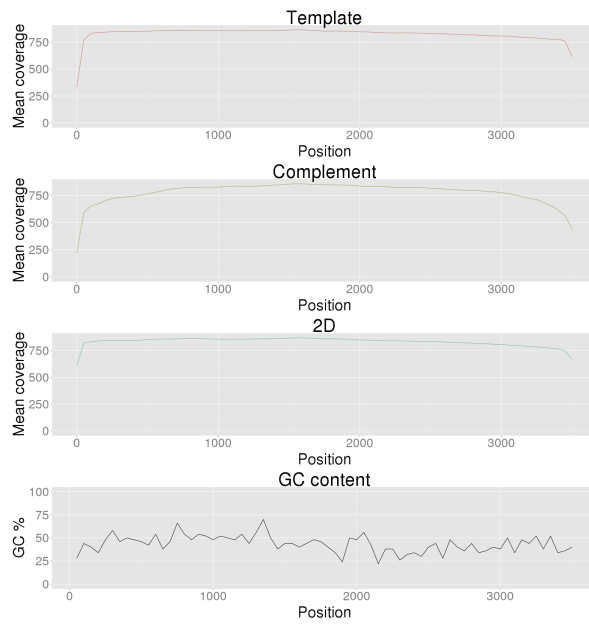




Control sequence perfect kmers



Control sequence coverage



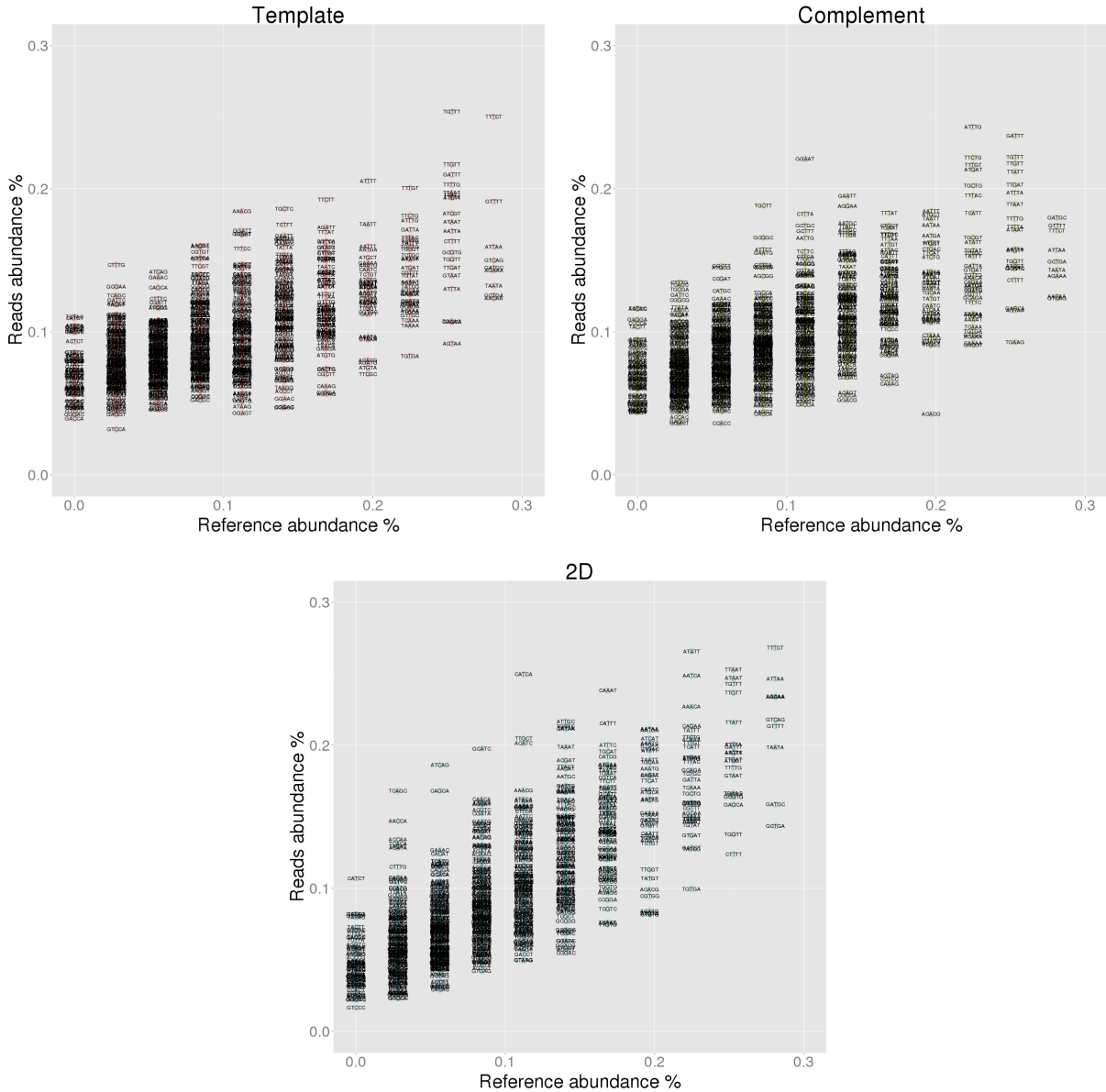
Control sequence 5-mer analysis

Under-represented 5-mers

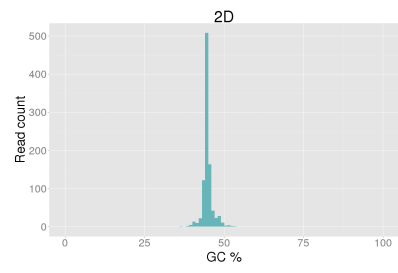
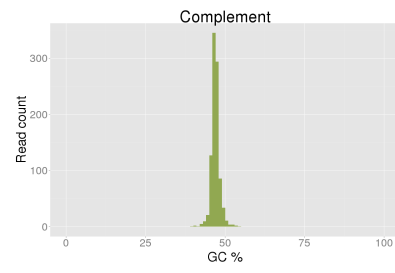
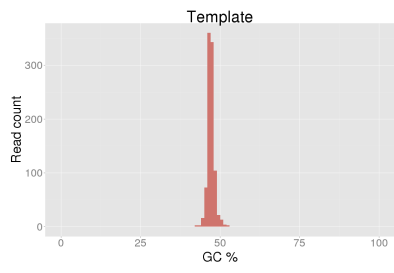
Rank	Template				Complement				2D			
	kmer	Ref %	Read %	Diff %	kmer	Ref %	Read %	Diff %	kmer	Ref %	Read %	Diff %
1	TTTTT	0.759	0.153	-0.605	TTTTT	0.759	0.094	-0.664	TTTTT	0.759	0.065	-0.693
2	AAAAA	0.478	0.119	-0.359	AAAAA	0.478	0.061	-0.416	AAAAA	0.478	0.085	-0.393
3	TGATG	0.393	0.146	-0.247	AAAAC	0.337	0.144	-0.193	TGATG	0.393	0.193	-0.200
4	GATGT	0.309	0.102	-0.207	GCAAT	0.309	0.145	-0.164	CTGAT	0.309	0.153	-0.156
5	AAAAC	0.337	0.134	-0.204	GATGT	0.309	0.146	-0.163	GATGT	0.309	0.155	-0.155
6	CTGAT	0.309	0.129	-0.180	TGAAG	0.253	0.093	-0.160	GCTGA	0.281	0.144	-0.137
7	GCAAT	0.309	0.145	-0.164	GTCAG	0.281	0.123	-0.158	CTTTT	0.253	0.124	-0.129
8	AGTAA	0.253	0.092	-0.161	AACAA	0.281	0.125	-0.156	TGTGA	0.225	0.099	-0.125
9	AACAA	0.281	0.123	-0.158	ACACG	0.197	0.042	-0.154	GATGC	0.281	0.159	-0.122
10	AATAT	0.309	0.152	-0.157	TGATG	0.393	0.243	-0.151	TTATC	0.309	0.188	-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	0.147	0.119	TATAC	0.000	0.116	0.116	TCAGC	0.028	0.168	0.140
2	TCTAC	0.000	0.110	0.110	ACCCC	0.000	0.116	0.116	CATCA	0.112	0.250	0.137
3	CATCT	0.000	0.109	0.109	GGAAT	0.112	0.221	0.109	ATCAG	0.056	0.186	0.130
4	ATCTA	0.000	0.104	0.104	GAGGA	0.000	0.108	0.108	AACCA	0.028	0.147	0.119
5	ACCCC	0.000	0.104	0.104	CTTTG	0.028	0.135	0.107	GCATC	0.084	0.198	0.113
6	GCGAA	0.028	0.132	0.103	CCCCA	0.000	0.106	0.106	CAGCA	0.056	0.168	0.112
7	CGAGA	0.000	0.103	0.103	TCAGC	0.028	0.133	0.105	CATCT	0.000	0.107	0.107
8	CCCCA	0.000	0.102	0.102	TGCTT	0.084	0.188	0.104	ACCAA	0.028	0.134	0.106
9	TCTTA	0.000	0.101	0.101	TACTT	0.000	0.103	0.103	TCACA	0.028	0.131	0.103
10	GCTCC	0.000	0.101	0.101	TGCCA	0.028	0.130	0.101	TACAT	0.028	0.129	0.101

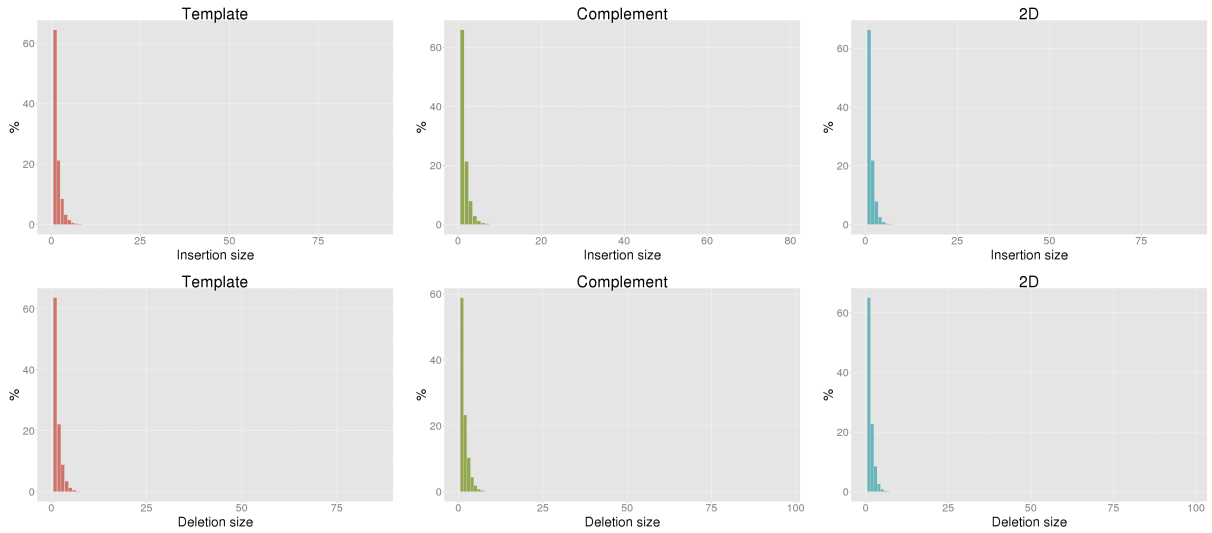


Control sequence GC content

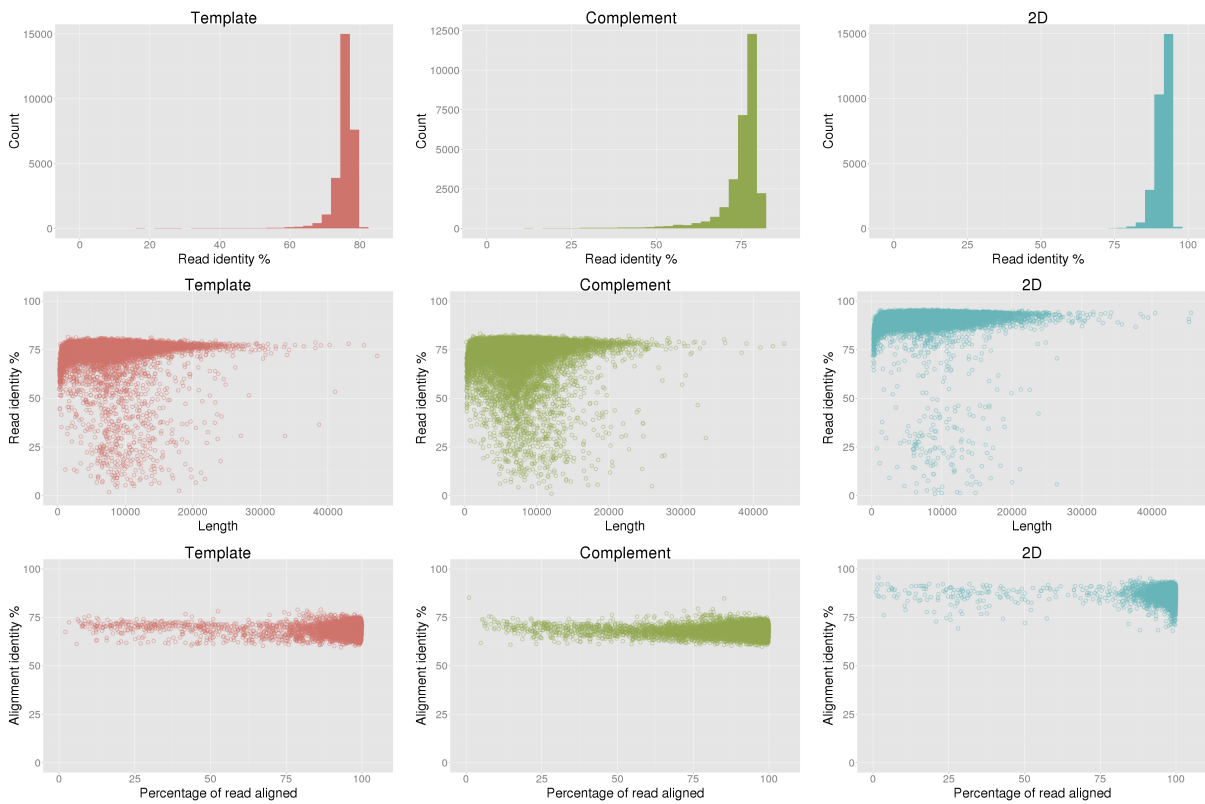


Escherichia coli error analysis

	Template	Complement	2D
Overall base identity (excluding indels)	74.95%	74.38%	91.04%
Aligned base identity (excluding indels)	81.87%	82.46%	95.13%
Identical bases per 100 aligned bases (including indels)	69.87%	68.93%	87.76%
Inserted bases per 100 aligned bases (including indels)	5.48%	4.67%	2.97%
Deleted bases per 100 aligned bases (including indels)	9.18%	11.73%	4.78%
Substitutions per 100 aligned bases (including indels)	15.47%	14.66%	4.49%
Mean insertion size	1.62	1.56	1.52
Mean deletion size	1.60	1.73	1.54

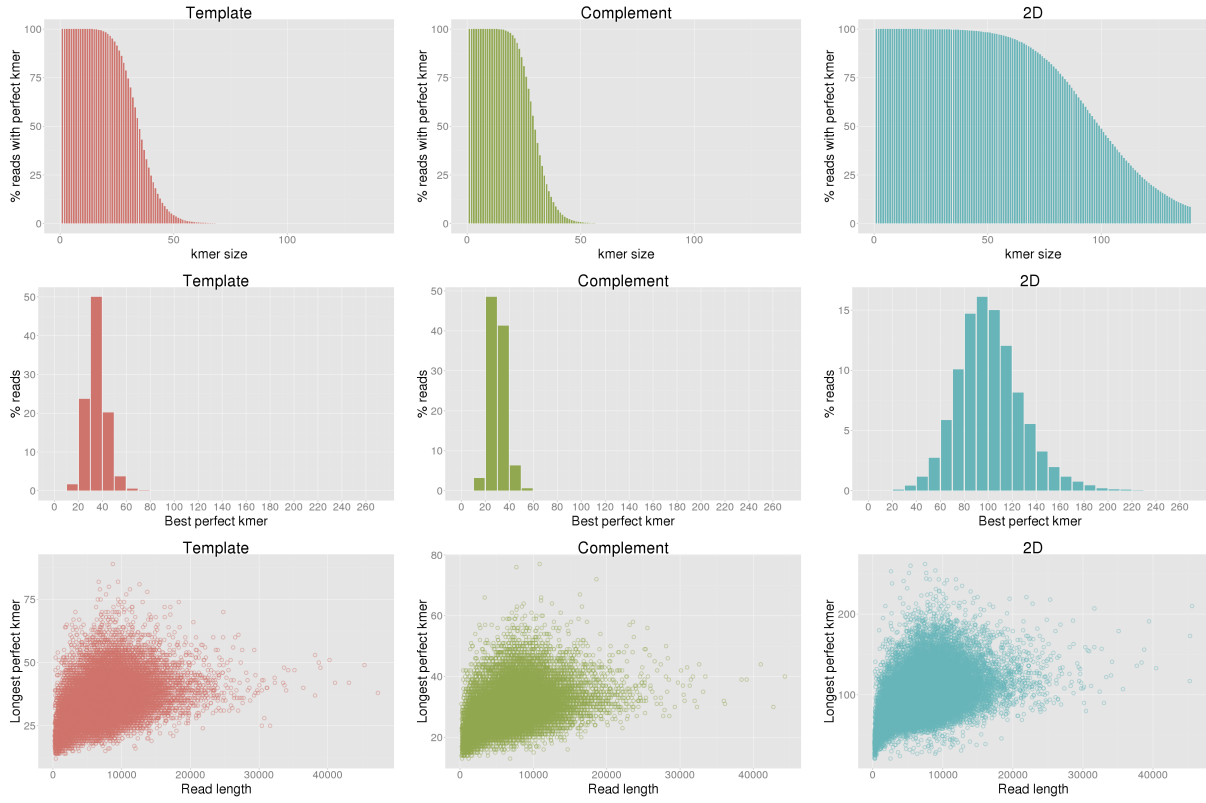


Escherichia coli read identity

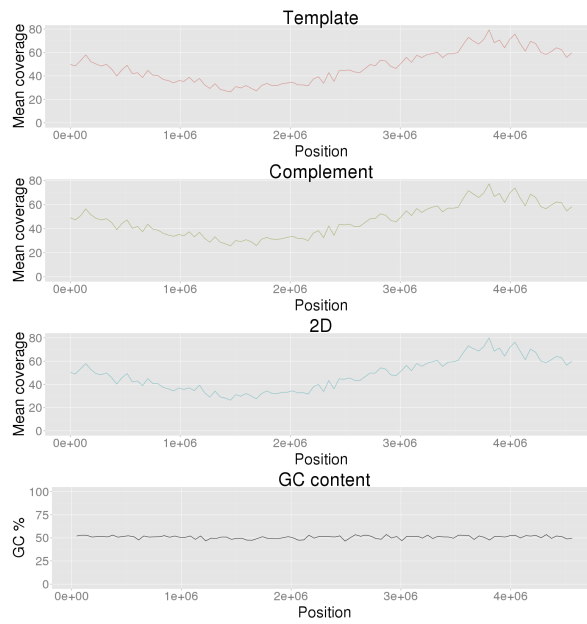




Escherichia coli perfect kmers



Escherichia coli coverage



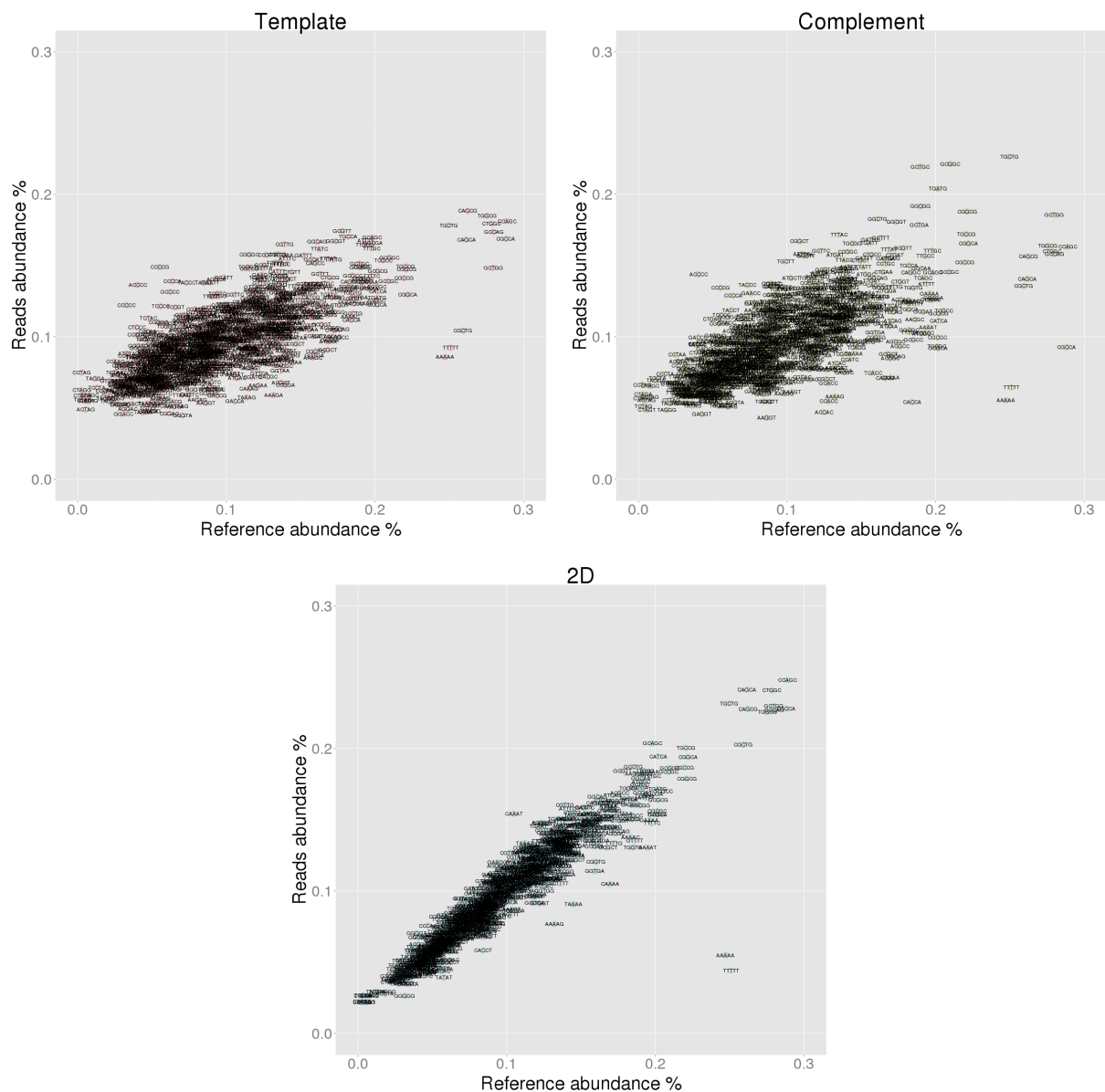
Escherichia coli 5-mer analysis

Under-represented 5-mers

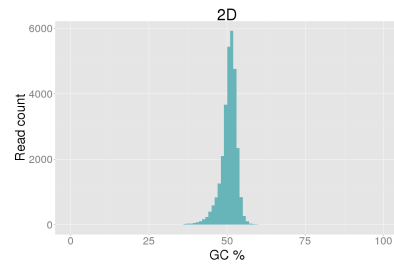
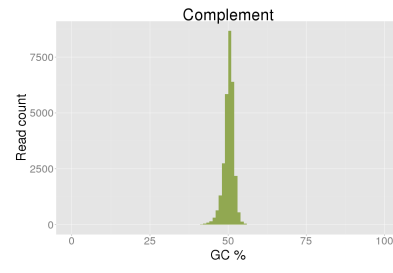
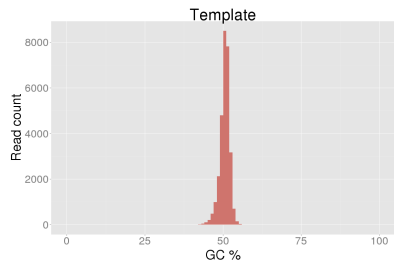
Rank	Template				Complement				2D			
	kmer	Ref %	Read %	Diff %	kmer	Ref %	Read %	Diff %	kmer	Ref %	Read %	Diff %
1	AAAAA	0.247	0.086	-0.161	CGCCA	0.288	0.093	-0.195	TTTTT	0.251	0.044	-0.207
2	TTTTT	0.251	0.092	-0.159	AAAAA	0.247	0.055	-0.192	AAAAA	0.247	0.055	-0.192
3	CGCTG	0.259	0.104	-0.155	TTTTT	0.251	0.064	-0.186	CAAAA	0.169	0.105	-0.065
4	GCTGG	0.279	0.148	-0.131	CACCA	0.184	0.054	-0.130	AAAAT	0.195	0.131	-0.064
5	CGCCA	0.288	0.169	-0.119	CCAGC	0.289	0.163	-0.125	CGCCA	0.288	0.228	-0.060
6	CCAGC	0.289	0.181	-0.107	CGCTG	0.259	0.136	-0.123	CGCTG	0.259	0.203	-0.056
7	GCCAG	0.280	0.174	-0.106	GCCAG	0.280	0.158	-0.122	AAAAG	0.132	0.077	-0.055
8	CTGGC	0.278	0.180	-0.099	CAGCA	0.261	0.141	-0.121	TGGTG	0.185	0.131	-0.054
9	CAGCA	0.261	0.168	-0.093	CTGGC	0.278	0.160	-0.118	TAAAA	0.145	0.091	-0.054
10	CGGCA	0.222	0.130	-0.092	TGGCG	0.275	0.164	-0.112	GCCAG	0.280	0.227	-0.053

Over-represented 5-mers

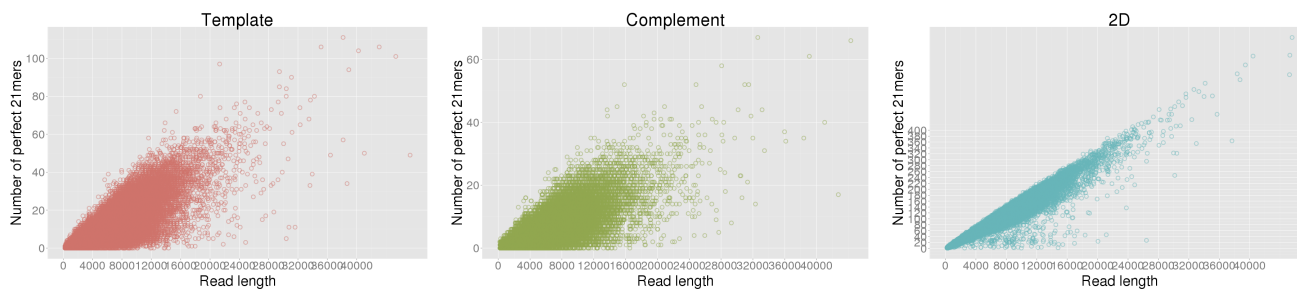
Rank	Template				Complement				2D			
	kmer	Ref %	Read %	Diff %	kmer	Ref %	Read %	Diff %	kmer	Ref %	Read %	Diff %
1	ACCCC	0.040	0.137	0.096	ACCCC	0.040	0.144	0.104	CAAAT	0.105	0.154	0.049
2	CCCCG	0.055	0.149	0.094	CCCCG	0.055	0.135	0.079	GGGGT	0.039	0.070	0.031
3	CCCCC	0.033	0.122	0.089	CCCCA	0.064	0.129	0.065	CCCAA	0.047	0.076	0.029
4	CCCCA	0.064	0.139	0.075	CCTAG	0.003	0.066	0.064	CGGGG	0.054	0.082	0.028
5	CCTAG	0.003	0.075	0.072	CTGAG	0.050	0.113	0.063	GGGTC	0.040	0.067	0.027
6	GCCCC	0.062	0.131	0.069	TACCC	0.073	0.136	0.063	GAAGG	0.094	0.120	0.026
7	CTCCC	0.040	0.107	0.067	CCTAA	0.026	0.087	0.062	CTCGT	0.042	0.068	0.025
8	TCCCC	0.056	0.121	0.066	GACCC	0.040	0.100	0.060	CGTGA	0.102	0.127	0.025
9	TCTAC	0.048	0.113	0.065	TCCCC	0.056	0.115	0.059	ACCGT	0.123	0.148	0.025
10	TACCC	0.073	0.138	0.065	CGGCT	0.108	0.167	0.059	TCCCA	0.056	0.080	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	8.70	9.31	4.66	0.00	8.84	8.77	4.92	0.00	8.07	8.55	3.94
C	8.56	0.00	9.22	10.01	9.40	0.00	8.69	9.82	9.42	0.00	11.17	9.46
G	9.49	9.19	0.00	8.12	9.03	8.83	0.00	8.90	9.24	11.28	0.00	8.66
T	4.90	9.45	8.40	0.00	5.19	8.90	8.73	0.00	3.99	8.39	7.84	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 (3.26%)	TTC (3.48%)	AAA (4.00%)	TGC (2.85%)	GGC (3.05%)	AAA (3.96%)	GCA (3.02%)	GGC (2.70%)	GCA (3.73%)
2	AAA (2.75%)	TGC (3.02%)	TTC (3.80%)	GCA (2.72%)	TGC (2.82%)	GCA (3.67%)	TTC (2.76%)	GCG (2.60%)	AAA (3.68%)
3	GCA (2.72%)	GCA (2.79%)	GCA (3.28%)	TTC (2.67%)	AAA (2.70%)	GAA (3.38%)	TCA (2.60%)	TCA (2.53%)	GAA (3.32%)
4	TGC (2.67%)	AAA (2.62%)	GAA (2.96%)	AAA (2.58%)	GCA (2.63%)	TTC (3.07%)	AAA (2.58%)	TGC (2.52%)	TTC (2.90%)
5	ATC (2.59%)	GCC (2.54%)	TGC (2.57%)	CAG (2.55%)	TTC (2.57%)	TTT (2.52%)	ATC (2.48%)	GCA (2.46%)	TTT (2.81%)
6	TCA (2.46%)	GGC (2.47%)	TTT (2.56%)	GGC (2.49%)	GAA (2.37%)	TGC (2.50%)	TGC (2.40%)	AAA (2.42%)	GCC (2.49%)
7	GCC (2.37%)	TCA (2.43%)	AAT (2.29%)	GAA (2.34%)	GCC (2.32%)	TCA (2.41%)	CGC (2.32%)	TTC (2.41%)	GCG (2.48%)
8	GGC (2.33%)	ATC (2.29%)	GCC (2.29%)	ATC (2.33%)	CAG (2.28%)	ATC (2.35%)	GCG (2.30%)	CGC (2.29%)	ATC (2.30%)
9	GAA (2.18%)	GCG (2.19%)	GGC (2.25%)	TCA (2.33%)	TCA (2.28%)	GCC (2.22%)	CAG (2.26%)	ATC (2.19%)	TCA (2.23%)
10	GCG (2.15%)	AAC (2.15%)	TCA (2.20%)	GCC (2.17%)	GCG (2.21%)	GCC (2.14%)	GGC (2.25%)	CAG (2.17%)	GTT (2.22%)
-10	AGT (0.98%)	GTA (0.96%)	CCT (0.96%)	AGT (0.99%)	ACT (0.94%)	CCC (0.95%)	CTT (1.06%)	GTA (1.03%)	ACT (0.86%)
-9	CCC (0.94%)	AGT (0.92%)	GGG (0.95%)	AGA (0.99%)	AGT (0.94%)	CTT (0.89%)	TAC (1.06%)	CGA (0.93%)	TAT (0.86%)
-8	TGT (0.93%)	CCT (0.89%)	AGA (0.85%)	CTC (0.92%)	GGA (0.93%)	AGG (0.85%)	GAG (0.89%)	CCC (0.91%)	TGA (0.83%)
-7	GGA (0.84%)	GAG (0.82%)	AGG (0.81%)	GGA (0.88%)	CCC (0.92%)	AGT (0.85%)	AGG (0.84%)	ACT (0.89%)	GAG (0.74%)
-6	AGA (0.81%)	CTT (0.81%)	AGT (0.79%)	CCC (0.86%)	CTC (0.89%)	CCT (0.80%)	CCC (0.84%)	CTT (0.86%)	CTT (0.74%)
-5	GAG (0.72%)	CGA (0.78%)	CTT (0.73%)	GAG (0.80%)	CCT (0.87%)	GGG (0.80%)	AGA (0.82%)	AGA (0.79%)	CGA (0.73%)
-4	GGG (0.72%)	AGA (0.66%)	TGT (0.73%)	AGG (0.73%)	GAG (0.84%)	ACT (0.71%)	GGA (0.78%)	CCT (0.78%)	AGA (0.51%)
-3	AGG (0.70%)	GGA (0.65%)	GAG (0.60%)	GGG (0.59%)	GGG (0.79%)	GAG (0.61%)	GGG (0.76%)	CTA (0.73%)	TAG (0.49%)
-2	CTA (0.51%)	CTA (0.53%)	TAG (0.39%)	CTA (0.59%)	CTA (0.56%)	CTA (0.48%)	CTA (0.62%)	GGA (0.72%)	GGA (0.49%)
-1	TAG (0.41%)	TAG (0.52%)	CTA (0.38%)	TAG (0.45%)	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 (1.10%)	AAAA (1.32%)	CAGC (0.99%)	CGGC (1.09%)	AAAA (1.04%)	ATCA (0.95%)	TGGC (0.94%)	GGCA (1.19%)
2	GAAA (0.89%)	TGCC (0.97%)	TTTT (1.27%)	ATCA (0.92%)	TGGC (1.08%)	CAAA (1.04%)	GCCA (0.86%)	CAGC (0.91%)	AAAA (1.07%)
3	ATCA (0.88%)	TGGC (0.92%)	GAAA (1.13%)	CGGC (0.89%)	CAGC (1.05%)	TGAA (0.99%)	CAGC (0.85%)	TTCA (0.85%)	TGAA (0.96%)
4	CAGC (0.86%)	CAGC (0.90%)	GGCA (0.99%)	CTGC (0.87%)	CTGC (0.88%)	GGCA (0.96%)	GGCA (0.83%)	CGGC (0.83%)	TTTT (0.94%)
5	AAAA (0.84%)	TTCA (0.89%)	GTTC (0.95%)	CCAG (0.84%)	TTGC (0.87%)	ATCA (0.95%)	CGCC (0.78%)	ATCA (0.82%)	GGAA (0.93%)
6	TGCC (0.82%)	TTGC (0.88%)	GCAA (0.89%)	TGGC (0.84%)	ATCA (0.83%)	AGCA (0.95%)	CGCA (0.78%)	GGCG (0.77%)	GAAA (0.93%)
7	TTCA (0.81%)	CTGC (0.86%)	GGAA (0.89%)	TTGC (0.80%)	CAAA (0.80%)	GAAA (0.94%)	CCAG (0.77%)	CTGC (0.74%)	CGCC (0.90%)
8	TGGC (0.81%)	TTCC (0.84%)	TGCC (0.86%)	CAAA (0.77%)	TTCC (0.76%)	AGAA (0.89%)	AACA (0.75%)	GCGC (0.73%)	TTTC (0.89%)
9	CGCC (0.79%)	GTTC (0.82%)	TTTT (0.86%)	ATGC (0.74%)	TGCC (0.76%)	TAAA (0.87%)	TTTC (0.74%)	GCCA (0.72%)	CGCA (0.88%)
10	GGCA (0.79%)	GCCA (0.81%)	AAAT (0.83%)	CGCC (0.71%)	CCAG (0.76%)	CGCA (0.87%)	TGGC (0.74%)	CGCC (0.72%)	TGCC (0.84%)
-10	TCTA (0.12%)	TCTA (0.13%)	TTAG (0.11%)	AGGG (0.12%)	CCTC (0.12%)	TTAG (0.11%)	CCCT (0.15%)	CCCC (0.15%)	TGCA (0.11%)
-9	TAGT (0.12%)	CTAT (0.13%)	ACTA (0.11%)	GTGT (0.11%)	CCCC (0.12%)	ACCT (0.10%)	TAGT (0.14%)	CTAT (0.15%)	CTAA (0.10%)
-8	GAGG (0.11%)	TAGT (0.12%)	CGAG (0.10%)	GGAC (0.11%)	ACCT (0.12%)	GGAC (0.10%)	GAGG (0.14%)	ACCT (0.15%)	CCCT (0.10%)
-7	CTAA (0.11%)	CCCT (0.12%)	GGAC (0.09%)	CTAA (0.10%)	CTAA (0.11%)	GTGT (0.10%)	CTAT (0.14%)	GAGA (0.15%)	GGGA (0.10%)
-6	GGAC (0.11%)	CGGA (0.11%)	TAGT (0.09%)	GAGG (0.10%)	TAGA (0.11%)	CTAT (0.09%)	TCTA (0.13%)	CTAA (0.13%)	CGGA (0.10%)
-5	TTAG (0.11%)	CTAA (0.10%)	TCTA (0.08%)	TAGA (0.10%)	GTGT (0.11%)	CGAG (0.09%)	CTAA (0.12%)	TAGG (0.11%)	CTAT (0.09%)
-4	TAGA (0.07%)	TAGG (0.08%)	TAGA (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 (0.06%)	CCTA (0.07%)	CCCT (0.08%)	CCCT (0.06%)	CCTA (0.07%)	TAGA (0.09%)	CCTA (0.05%)
-2	TAGG (0.05%)	CCTA (0.06%)	CCTA (0.05%)	TAGG (0.06%)	CCTA (0.06%)	CCTA (0.06%)	TAGG (0.06%)	CCTA (0.09%)	TAGA (0.05%)
-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	CTGGC (0.34%)	CTGGC (0.38%)	CAGCA (0.41%)	CAGCA (0.42%)	CAGCA (0.42%)	CAGCA (0.55%)	CAGCA (0.37%)	CTGGC (0.38%)	CAGCA (0.46%)
2	CAGCA (0.34%)	CAGCA (0.37%)	GAAAA (0.40%)	CATCA (0.34%)	CTGGC (0.39%)	CGGCA (0.39%)	CGCCA (0.36%)	CAGCA (0.31%)	CGGCA (0.42%)
3	CATCA (0.31%)	TTGCC (0.33%)	CAAAA (0.37%)	GCTGC (0.33%)	GCGGC (0.37%)	ATAAA (0.36%)	CGGCA (0.32%)	TGGCG (0.31%)	TGGCA (0.38%)
4	CGCCA (0.31%)	TTTGC (0.32%)	TGTTT (0.35%)	CCAGC (0.33%)	CCAGC (0.33%)	CATCA (0.36%)	CTGGC (0.31%)	CCAGC (0.30%)	GAAAA (0.35%)
5	CCAGC (0.30%)	CGCCA (0.32%)	CGTTT (0.34%)	GCGGC (0.32%)	CATCA (0.33%)	AAGAA (0.33%)	CATCA (0.29%)	GCGGC (0.30%)	ATTTT (0.32%)
6	TTATC (0.29%)	CCAGC (0.31%)	TGGCA (0.33%)	CTGGC (0.32%)	TCAGC (0.31%)	CAGAA (0.33%)	CCAGC (0.29%)	CGCCA (0.30%)	CGCCA (0.30%)
7	ATTTT (0.29%)	CATCA (0.30%)	GCCAG (0.32%)	CGGCA (0.29%)	GCTGC (0.31%)	GCAAA (0.32%)	GCCAG (0.29%)	CATCA (0.29%)	GCGCA (0.30%)
8	GCCAG (0.28%)	GCTGC (0.30%)	CTGGC (0.32%)	GCAGC (0.28%)	AATCA (0.30%)	GAAAA (0.32%)	GCAAA (0.27%)	TTTTT (0.27%)	TTGCC (0.30%)
9	TGGCG (0.28%)	TTTTT (0.29%)	CGGCA (0.31%)	AATCA (0.27%)	TTTTT (0.29%)	AATCA (0.32%)	GCGCA (0.27%)	GCCAG (0.27%)	TGGCG (0.29%)
10	GCAGC (0.28%)	GCCAG (0.29%)	GCAAA (0.31%)	TCAGC (0.27%)	CAGGC (0.28%)	TGGCA (0.31%)	TGGCA (0.27%)	CAGCG (0.26%)	GCAAA (0.29%)
-10	CCCTA (0.01%)	GGACC (0.01%)	TAGGT (0.01%)	ACCTA (0.01%)	ACCTA (0.01%)	ACCTA (0.01%)	CCCTA (0.01%)	TCCTA (0.01%)	TCCTA (0.01%)
-9	GGACC (0.01%)	TAGGA (0.01%)	CCCTA (0.01%)	CCCTA (0.01%)	CCCCC (0.01%)	CCCTA (0.01%)	TAGGA (0.01%)	TAGGA (0.01%)	GCTAG (0.01%)
-8	CTAGC (0.00%)	GCTAG (0.00%)	ACTAG (0.00%)	CTAGC (0.01%)	CTAGC (0.01%)	CTAGC (0.01%)	CTAGC (0.01%)	GCTAG (0.01%)	TAGGA (0.01%)
-7	ACTAG (0.00%)	CTAGC (0.00%)	GCTAG (0.00%)	GCTAG (0.00%)	GCTAG (0.01%)	GCTAG (0.00%)	GCTAG (0.01%)	ACTAG (0.01%)	ACTAG (0.01%)
-6	CTAGT (0.00%)	ACTAG (0.00%)	CTAGC (0.00%)	CTAGT (0.00%)	CTAGT (0.00%)	CTAGT (0.00%)	ACTAG (0.00%)	CTAGC (0.01%)	CTAGC (0.00%)
-5	GCTAG (0.00%)	CTAGT (0.00%)	CTAGG (0.00%)	ACTAG (0.00%)	ACTAG (0.00%)	ACTAG (0.00%)	CTAGT (0.00%)	CTAGT (0.00%)	CTAGG (0.00%)
-4	CTAGG (0.00%)	TCTAG (0.00%)	CTAGT (0.00%)	TCTAG (0.00%)	CTAGA (0.00%)	CTAGA (0.00%)	CCTAG (0.00%)	CTAGG (0.00%)	CTAGT (0.00%)
-3	CTAGA (0.00%)	CTAGG (0.00%)	TCTAG (0.00%)	CTAGA (0.00%)	TCTAG (0.00%)	CTAGG (0.00%)	TCTAG (0.00%)	TCTAG (0.00%)	TCTAG (0.00%)
-2	TCTAG (0.00%)	CCTAG (0.00%)	CCTAG (0.00%)	CTAGG (0.00%)	CTAGG (0.00%)	CCTAG (0.00%)	CTAGG (0.00%)	CCTAG (0.00%)	CCTAG (0.00%)
-1	CCTAG (0.00%)	CTAGA (0.00%)	CTAGA (0.00%)	CCTAG (0.00%)	CCTAG (0.00%)	TCTAG (0.00%)	CTAGA (0.00%)	CTAGA (0.00%)	CTAGA (0.00%)

Most common

Least common

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