

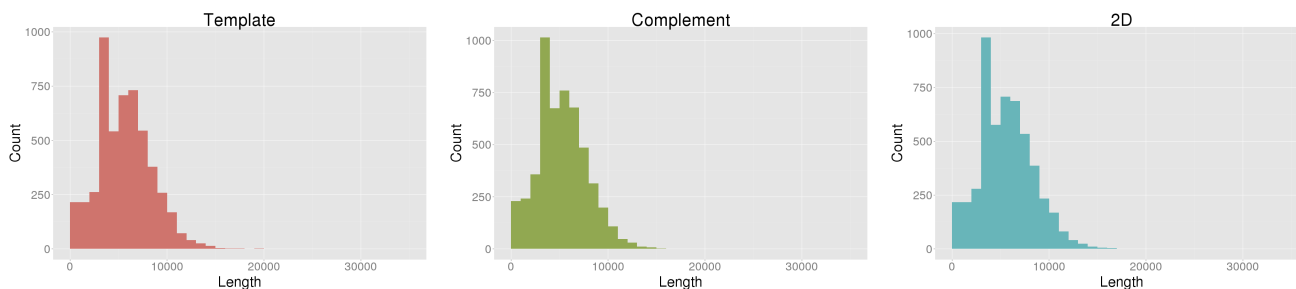
NanoOK report for MARC_1b_042915

Pass and fail counts

Type	Pass	Fail
Template	5165	0
Complement	5165	0
2D	5165	0

Read lengths

Type	NumReads	TotalBases	Mean	Longest	Shortest	N50	N50Count	N90	N90Count
Template	5165	29203780	5654.17	22306	171	6789	1661	3493	3931
Complement	5165	27090557	5245.03	18253	184	6330	1654	3292	3929
2D	5165	28985145	5611.84	20518	177	6766	1655	3505	3933



Template alignments

Number of reads	5165
Number of reads with alignments	5129 (99.30%)
Number of reads without alignments	36 (0.70%)

ID	Size	Number of Reads	% of Reads	Mean read length	Aligned bases	Mean coverage	Longest Perf Kmer
Control sequence	3560	679	13.15	3306.90	2393169	672.24	58
Escherichia coli	4641652	4450	86.16	6053.41	29042742	6.26	77

Complement alignments

Number of reads	5165
Number of reads with alignments	5120 (99.13%)
Number of reads without alignments	45 (0.87%)

ID	Size	Number of Reads	% of Reads	Mean read length	Aligned bases	Mean coverage	Longest Perf Kmer
Control sequence	3560	677	13.11	3089.05	2176953	611.50	54
Escherichia coli	4641652	4443	86.02	5619.19	27144221	5.85	60

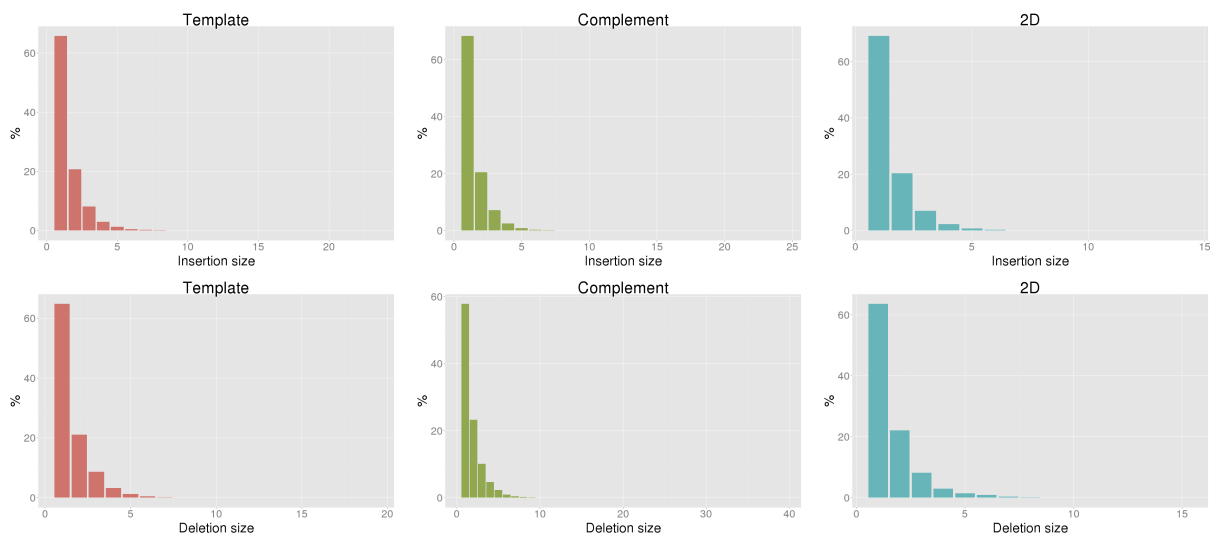
2D alignments

Number of reads	5165
Number of reads with alignments	5163 (99.96%)
Number of reads without alignments	2 (0.04%)

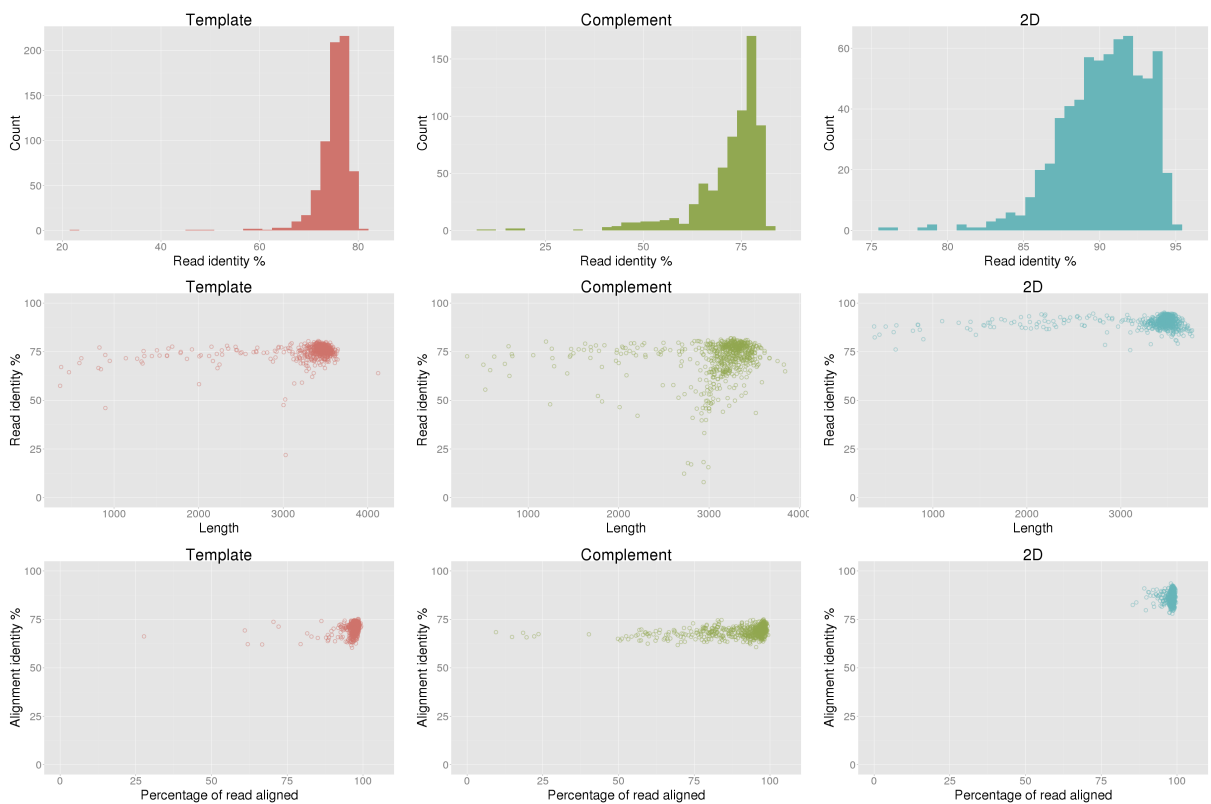
ID	Size	Number of Reads	% of Reads	Mean read length	Aligned bases	Mean coverage	Longest Perf Kmer
Control sequence	3560	680	13.17	3304.77	2338359	656.84	195
Escherichia coli	4641652	4483	86.80	5962.36	27802075	5.99	222

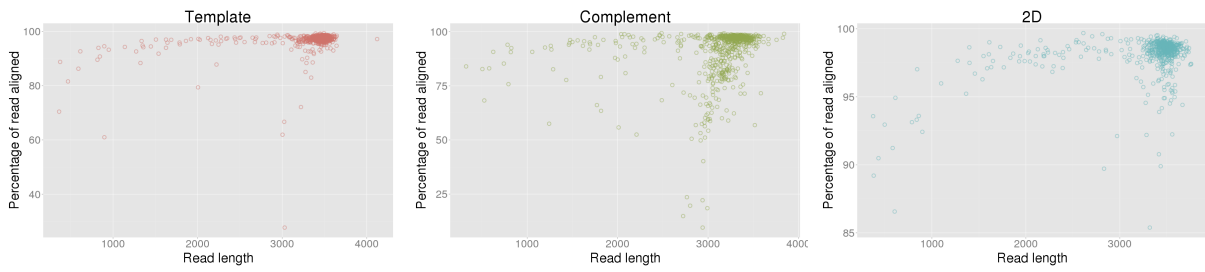
Control sequence error analysis

	Template	Complement	2D
Overall base identity (excluding indels)	75.26%	71.83%	90.31%
Aligned base identity (excluding indels)	82.33%	82.79%	94.76%
Identical bases per 100 aligned bases (including indels)	70.61%	69.00%	86.79%
Inserted bases per 100 aligned bases (including indels)	5.13%	3.82%	2.80%
Deleted bases per 100 aligned bases (including indels)	9.11%	12.83%	5.60%
Substitutions per 100 aligned bases (including indels)	15.15%	14.34%	4.80%
Mean insertion size	1.58	1.50	1.47
Mean deletion size	1.58	1.78	1.62

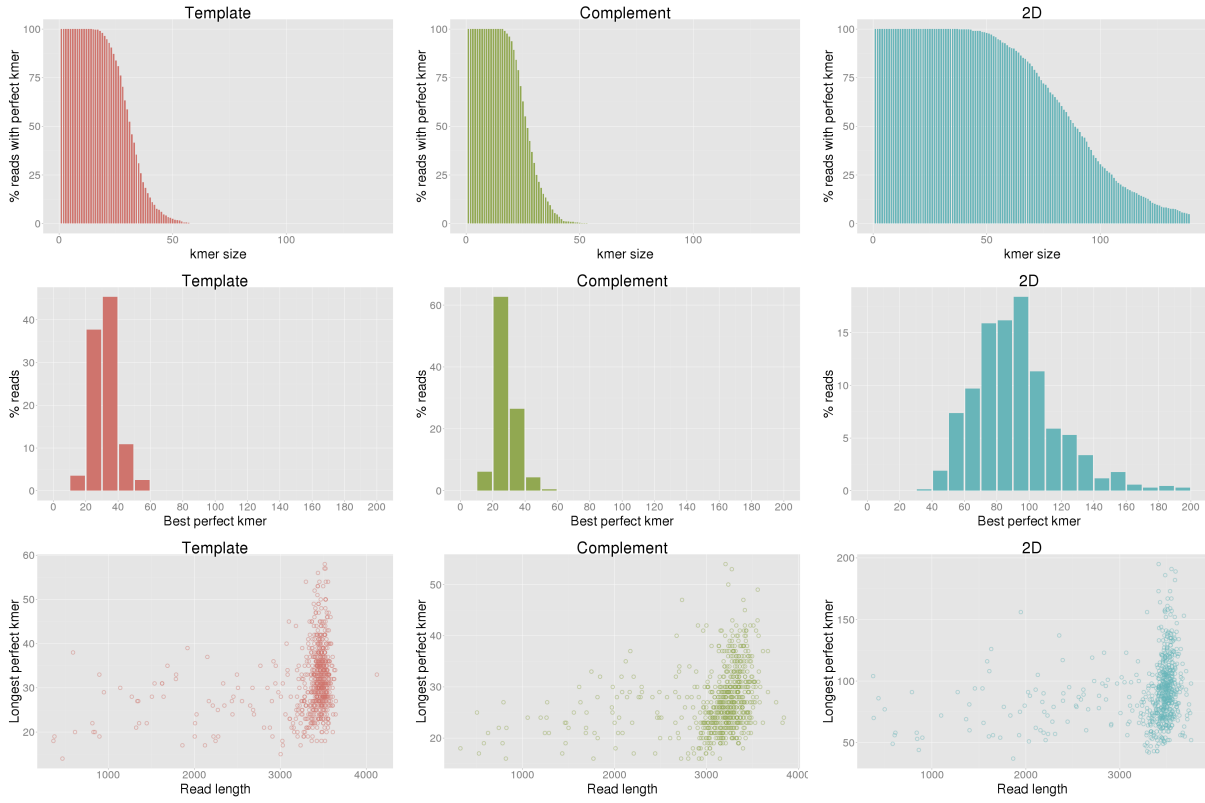


Control sequence read identity

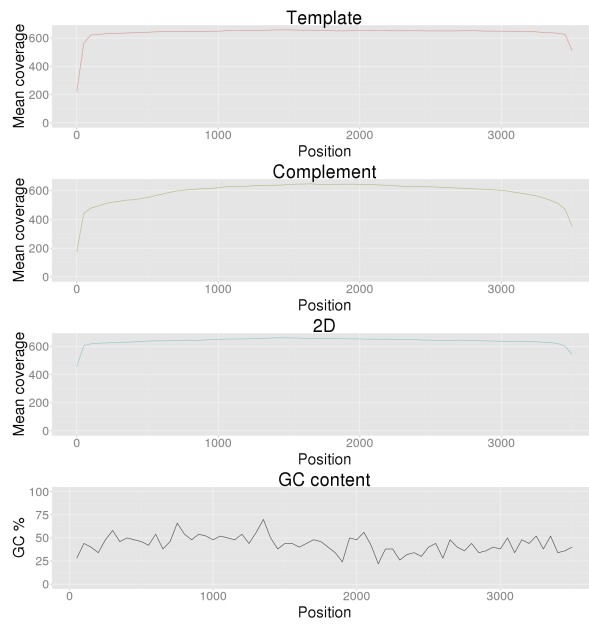




Control sequence perfect kmers



Control sequence coverage



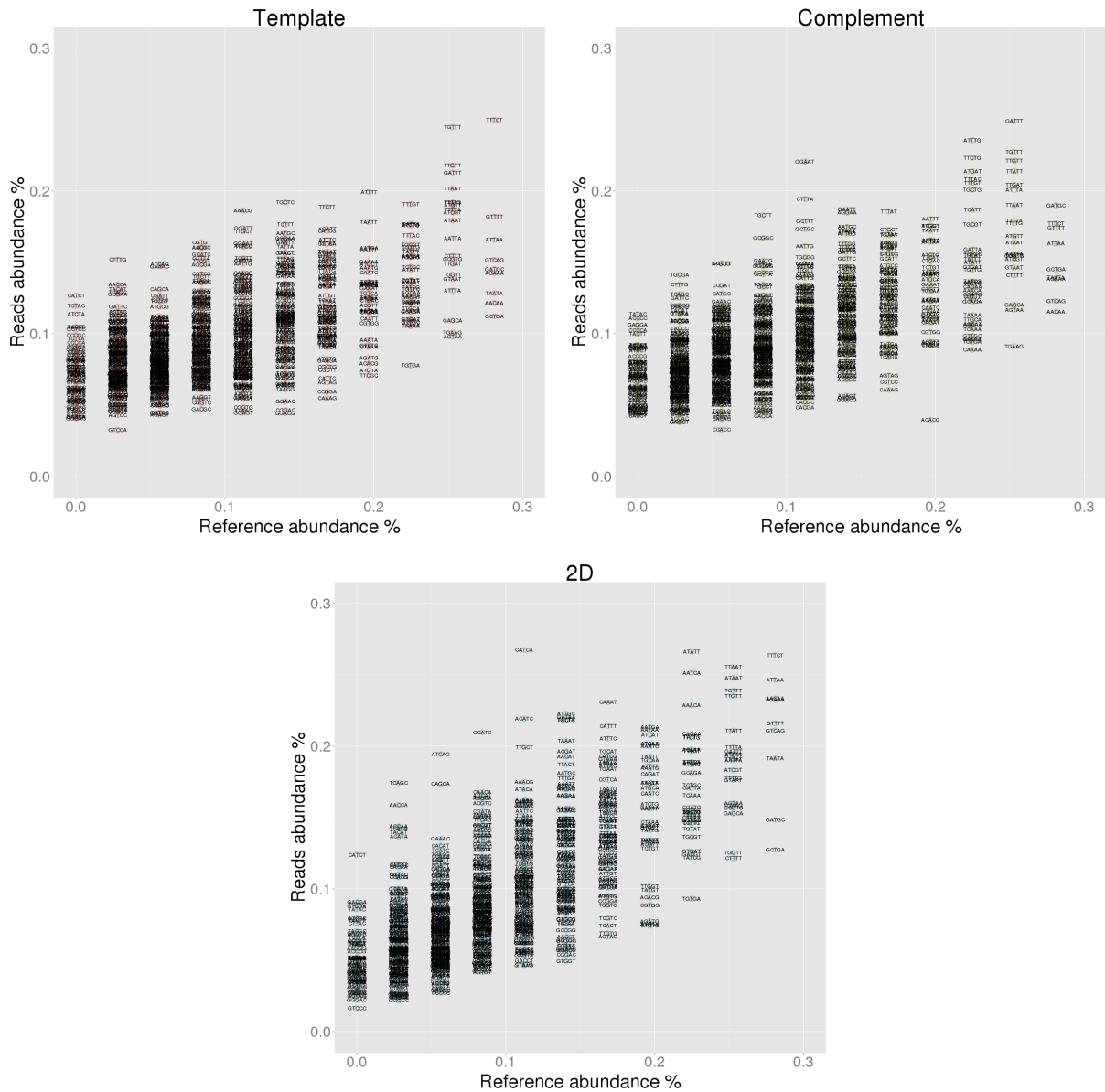
Control sequence 5-mer analysis

Under-represented 5-mers

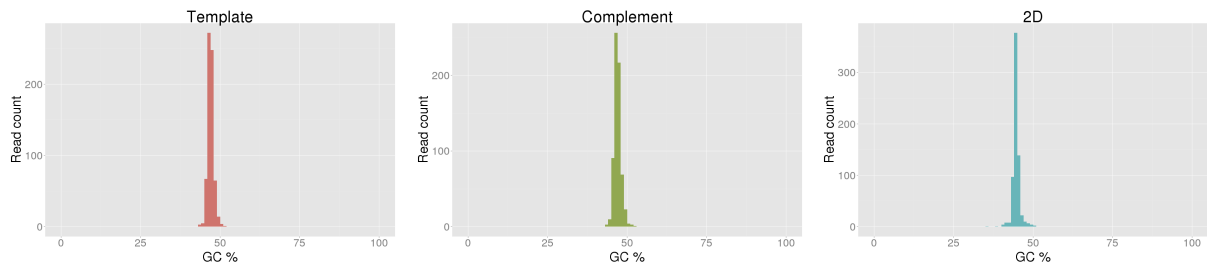
Rank	Template				Complement				2D			
	kmer	Ref %	Read %	Diff %	kmer	Ref %	Read %	Diff %	kmer	Ref %	Read %	Diff %
1	TTTTT	0.759	0.143	-0.616	TTTTT	0.759	0.101	-0.658	TTTTT	0.759	0.066	-0.693
2	AAAAA	0.478	0.118	-0.360	AAAAA	0.478	0.066	-0.412	AAAAA	0.478	0.090	-0.387
3	TGATG	0.393	0.150	-0.243	AAAAC	0.337	0.144	-0.193	TGATG	0.393	0.181	-0.213
4	GATGT	0.309	0.107	-0.202	AACAA	0.281	0.115	-0.166	CTGAT	0.309	0.142	-0.167
5	AAAAC	0.337	0.136	-0.201	GCAAT	0.309	0.145	-0.164	GATGT	0.309	0.150	-0.159
6	CTGAT	0.309	0.119	-0.190	TGAAG	0.253	0.091	-0.162	GCTGA	0.281	0.127	-0.154
7	GCTGA	0.281	0.112	-0.169	GTCAG	0.281	0.123	-0.158	TTATC	0.309	0.175	-0.134
8	GCAAT	0.309	0.142	-0.167	ACACG	0.197	0.040	-0.157	GATGC	0.281	0.148	-0.132
9	AATAT	0.309	0.148	-0.161	GATGT	0.309	0.153	-0.156	TGTGA	0.225	0.093	-0.132
10	AACAA	0.281	0.121	-0.159	TTATC	0.309	0.161	-0.148	CTTTT	0.253	0.121	-0.131

Over-represented 5-mers

Rank	Template				Complement				2D			
	kmer	Ref %	Read %	Diff %	kmer	Ref %	Read %	Diff %	kmer	Ref %	Read %	Diff %
1	CATCT	0.000	0.127	0.127	TATAC	0.000	0.114	0.114	CATCA	0.112	0.267	0.155
2	CTTTG	0.028	0.152	0.124	TGCCA	0.028	0.141	0.113	TCAGC	0.028	0.174	0.146
3	TCTAC	0.000	0.120	0.120	ACCCG	0.000	0.111	0.111	ATCAG	0.056	0.194	0.138
4	ATCTA	0.000	0.114	0.114	GGAAT	0.112	0.221	0.108	AACCA	0.028	0.159	0.131
5	AACCA	0.028	0.134	0.106	CTTTG	0.028	0.134	0.106	GCATC	0.084	0.210	0.125
6	TACTT	0.000	0.105	0.105	GAGGA	0.000	0.106	0.106	CATCT	0.000	0.124	0.124
7	ACCCC	0.000	0.105	0.105	CCCCA	0.000	0.102	0.102	CAGCA	0.056	0.173	0.117
8	TACAT	0.028	0.131	0.103	TACTT	0.000	0.100	0.100	ACCAA	0.028	0.144	0.116
9	GCTCC	0.000	0.103	0.103	TCAGC	0.028	0.128	0.100	TCACA	0.028	0.142	0.114
10	TCAGC	0.028	0.129	0.101	TGCTT	0.084	0.183	0.099	TACAT	0.028	0.140	0.112

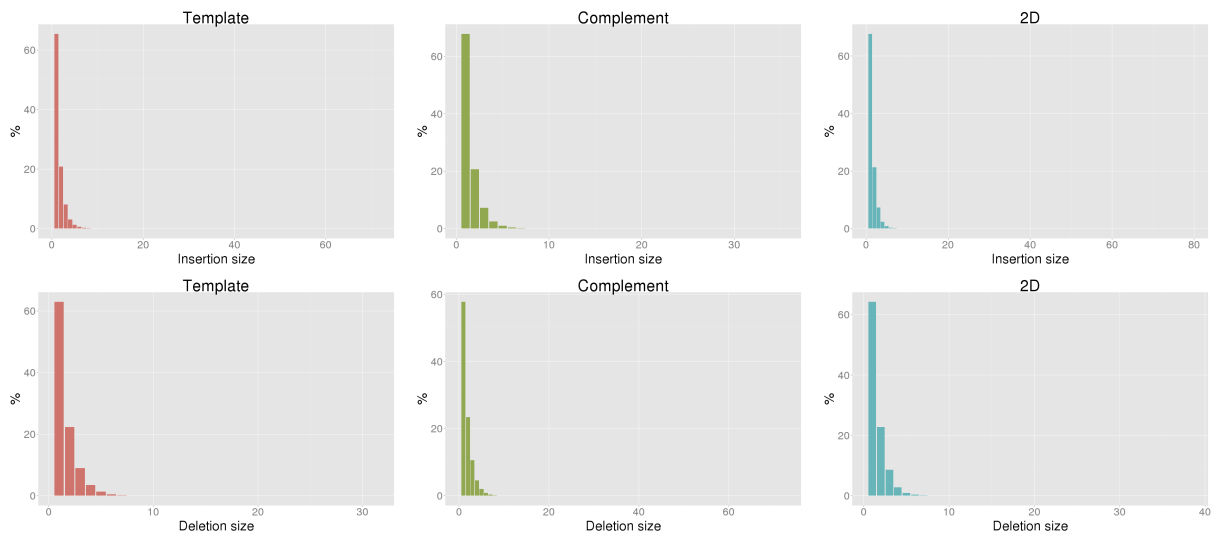


Control sequence GC content

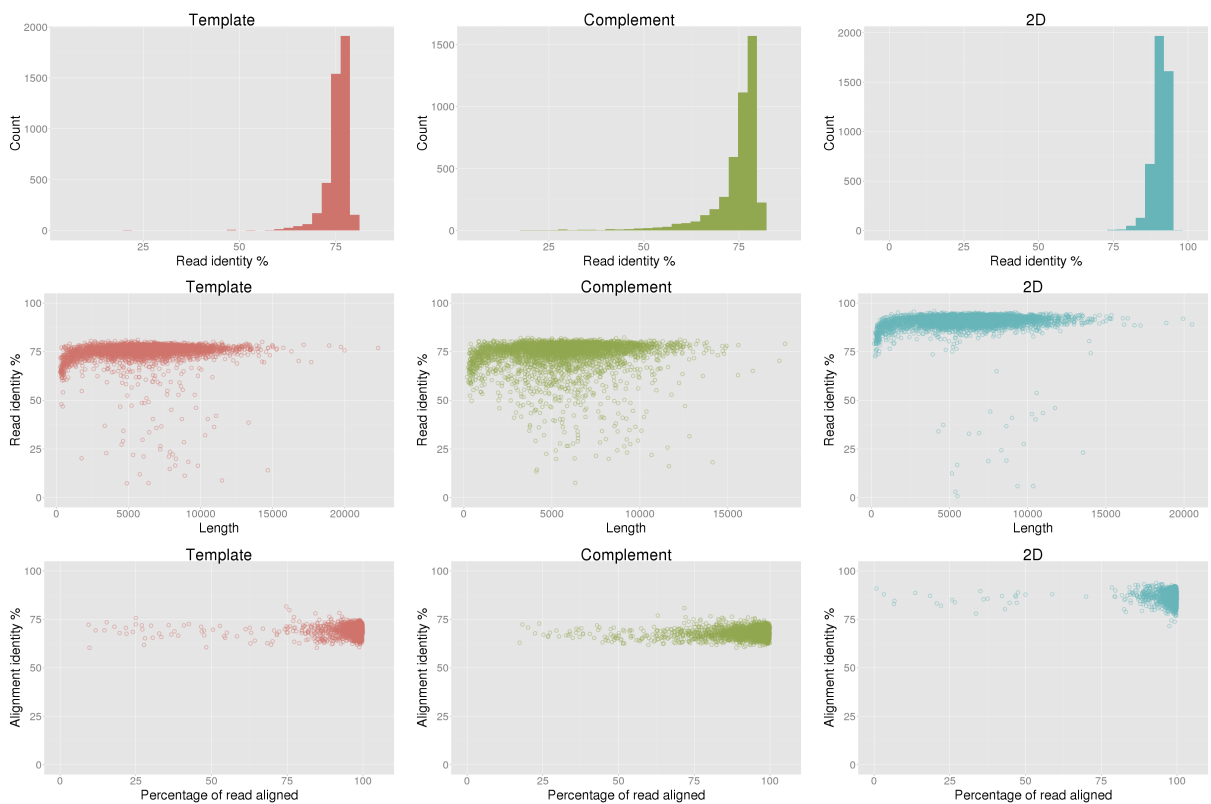


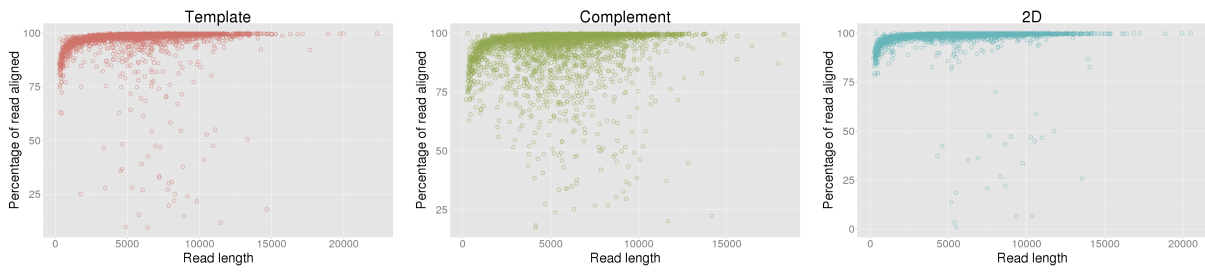
Escherichia coli error analysis

	Template	Complement	2D
Overall base identity (excluding indels)	75.21%	74.28%	90.52%
Aligned base identity (excluding indels)	81.74%	82.18%	94.71%
Identical bases per 100 aligned bases (including indels)	69.76%	68.32%	87.03%
Inserted bases per 100 aligned bases (including indels)	5.29%	4.15%	2.94%
Deleted bases per 100 aligned bases (including indels)	9.36%	12.72%	5.16%
Substitutions per 100 aligned bases (including indels)	15.59%	14.81%	4.87%
Mean insertion size	1.60	1.51	1.50
Mean deletion size	1.61	1.77	1.56

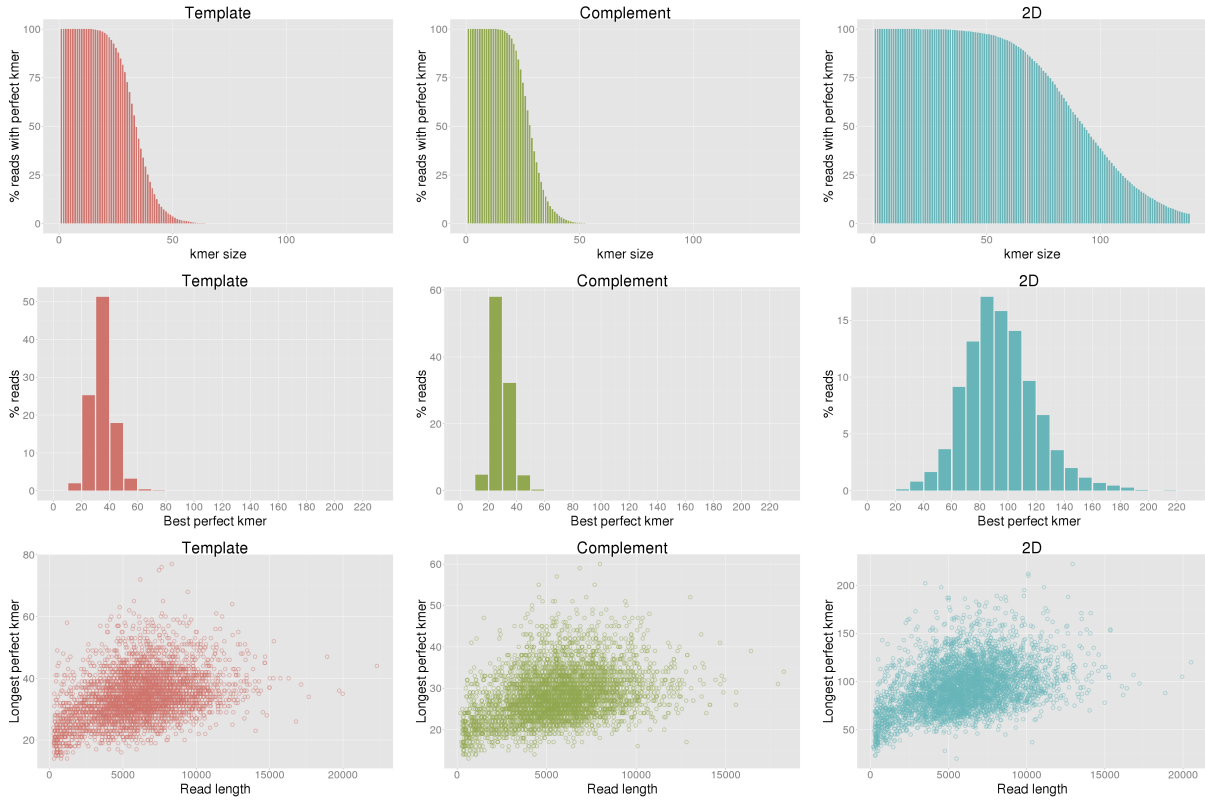


Escherichia coli read identity

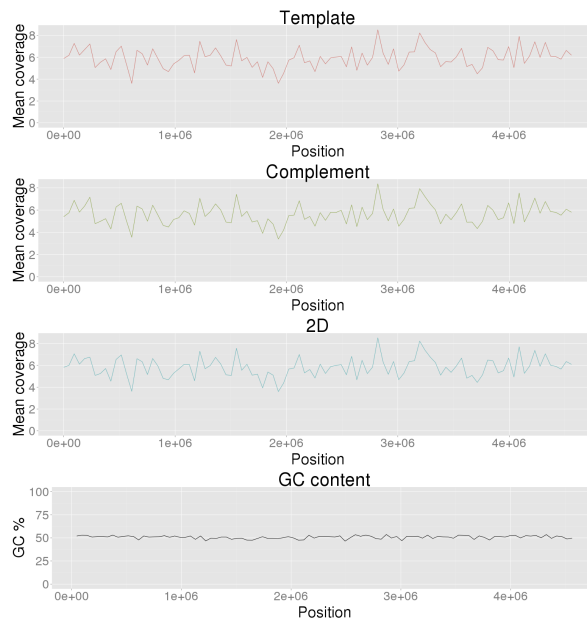




Escherichia coli perfect kmers



Escherichia coli coverage



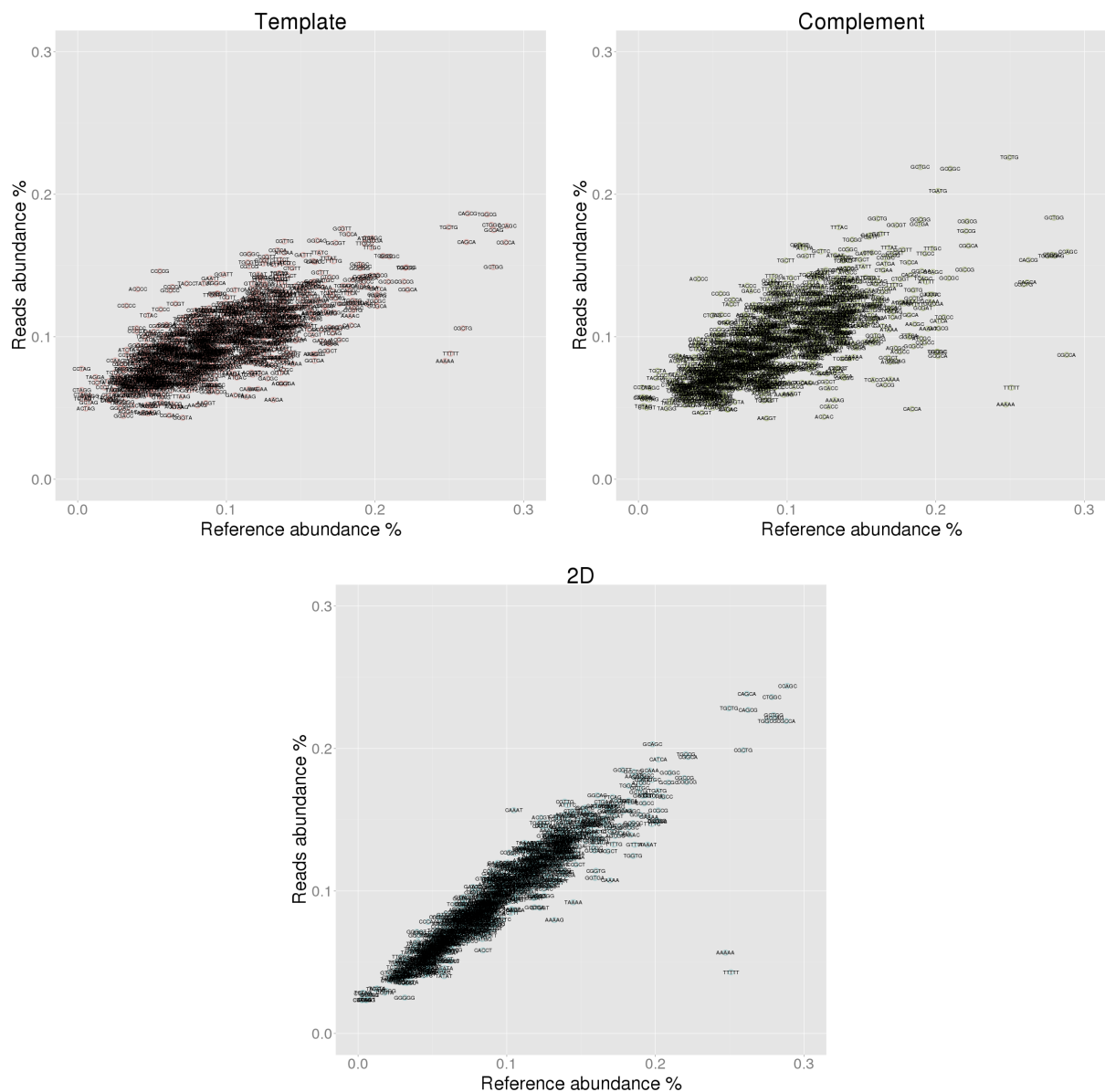
Escherichia coli 5-mer analysis

Under-represented 5-mers

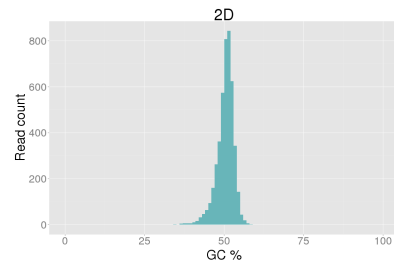
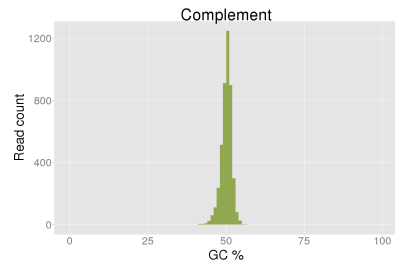
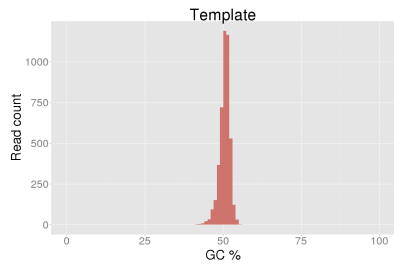
Rank	Template				Complement				2D			
	kmer	Ref %	Read %	Diff %	kmer	Ref %	Read %	Diff %	kmer	Ref %	Read %	Diff %
1	AAAAA	0.247	0.083	-0.164	CGCCA	0.288	0.087	-0.201	TTTTT	0.251	0.043	-0.208
2	TTTTT	0.251	0.088	-0.163	AAAAA	0.247	0.052	-0.195	AAAAA	0.247	0.057	-0.190
3	CGCTG	0.259	0.106	-0.153	TTTTT	0.251	0.064	-0.187	CGCCA	0.288	0.219	-0.069
4	GCTGG	0.279	0.149	-0.131	CACCA	0.184	0.049	-0.135	AAAAT	0.195	0.132	-0.062
5	CGCCA	0.288	0.166	-0.122	CCAGC	0.289	0.160	-0.129	CAAAA	0.169	0.107	-0.062
6	CCAGC	0.289	0.178	-0.111	CAGCA	0.261	0.138	-0.123	TGGTG	0.185	0.125	-0.060
7	GCCAG	0.280	0.175	-0.105	GCCAG	0.280	0.157	-0.123	CGCTG	0.259	0.199	-0.060
8	CTGGC	0.278	0.179	-0.100	CGCTG	0.259	0.137	-0.122	GCCAG	0.280	0.222	-0.058
9	CAGCA	0.261	0.166	-0.095	CTGGC	0.278	0.158	-0.121	GCTGG	0.279	0.223	-0.056
10	TGGCG	0.275	0.186	-0.089	TGGCG	0.275	0.157	-0.119	TGGCG	0.275	0.219	-0.056

Over-represented 5-mers

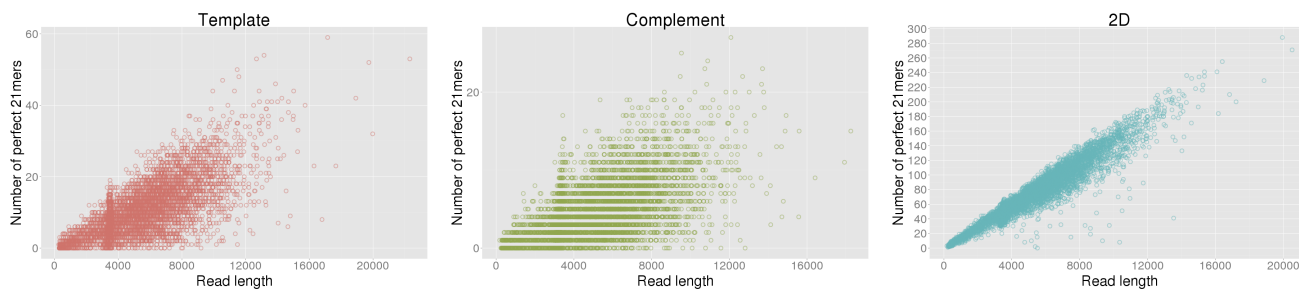
Rank	Template				Complement				2D			
	kmer	Ref %	Read %	Diff %	kmer	Ref %	Read %	Diff %	kmer	Ref %	Read %	Diff %
1	ACCCC	0.040	0.133	0.093	ACCCC	0.040	0.141	0.100	CAAAT	0.105	0.157	0.052
2	CCCCG	0.055	0.146	0.091	CCCCG	0.055	0.130	0.075	GGGGT	0.039	0.071	0.032
3	CCCCC	0.033	0.122	0.089	CTGAG	0.050	0.115	0.065	CCCAA	0.047	0.078	0.031
4	CTTAG	0.003	0.078	0.075	TCCTA	0.013	0.076	0.063	ACCGT	0.123	0.151	0.028
5	CCCCA	0.064	0.135	0.071	TACCC	0.073	0.136	0.063	GGGTC	0.040	0.069	0.028
6	GCCCC	0.062	0.132	0.070	CCCCA	0.064	0.126	0.062	CTCGT	0.042	0.070	0.028
7	TCTAC	0.048	0.115	0.067	CCTAG	0.003	0.064	0.062	CGGGG	0.054	0.082	0.027
8	CTCCC	0.040	0.106	0.066	CCTAA	0.026	0.087	0.061	TGAAT	0.121	0.148	0.026
9	CCCCT	0.039	0.104	0.065	TACCT	0.062	0.123	0.061	TCCCA	0.056	0.082	0.026
10	TACCC	0.073	0.137	0.064	TCCCC	0.056	0.115	0.060	GAAGG	0.094	0.120	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	8.87	9.28	4.70	0.00	9.34	9.01	4.97	0.00	8.43	8.63	3.97
C	8.24	0.00	9.07	9.98	9.22	0.00	8.58	9.49	9.18	0.00	11.00	9.30
G	9.22	9.02	0.00	7.97	8.98	8.78	0.00	8.57	9.09	11.10	0.00	8.46
T	5.00	9.87	8.78	0.00	5.26	8.84	8.96	0.00	4.09	8.58	8.19	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 (3.54%)	AAA (4.16%)	TGC (2.93%)	GCC (3.03%)	AAA (4.01%)	GCA (3.07%)	TGC (2.63%)	AAA (3.84%)
2	AAA (2.85%)	TGC (3.02%)	TTC (3.74%)	GCA (2.74%)	TGC (2.97%)	GCA (3.57%)	TTC (2.78%)	GCC (2.60%)	GCA (3.67%)
3	GCA (2.82%)	GCA (2.81%)	GCA (3.29%)	TTC (2.64%)	AAA (2.78%)	GAA (3.36%)	TCA (2.71%)	TCA (2.49%)	GAA (3.35%)
4	TGC (2.64%)	AAA (2.73%)	GAA (2.96%)	AAA (2.58%)	TTC (2.63%)	TTC (3.21%)	AAA (2.68%)	AAA (2.49%)	TTC (2.98%)
5	ATC (2.56%)	GCC (2.46%)	TTT (2.65%)	CAG (2.46%)	GCA (2.56%)	TTT (2.67%)	ATC (2.41%)	GCA (2.46%)	TTT (2.96%)
6	TCA (2.52%)	GCC (2.38%)	TGC (2.52%)	GGC (2.41%)	GAA (2.41%)	TGC (2.58%)	TGC (2.36%)	TTC (2.45%)	GCC (2.42%)
7	GCC (2.26%)	TCA (2.38%)	AAT (2.38%)	GAA (2.39%)	CAG (2.26%)	TCA (2.43%)	GAA (2.32%)	GCC (2.45%)	AAT (2.28%)
8	TTT (2.23%)	ATC (2.31%)	TCA (2.26%)	TCA (2.35%)	TCA (2.25%)	ATC (2.38%)	GCG (2.17%)	CGC (2.24%)	TCA (2.28%)
9	GAA (2.21%)	AAC (2.22%)	GCC (2.23%)	ATC (2.34%)	GCC (2.23%)	GCC (2.15%)	CGC (2.16%)	ATC (2.22%)	GCG (2.28%)
10	GGC (2.19%)	GCG (2.15%)	CAA (2.19%)	TTT (2.15%)	ATC (2.15%)	GCC (2.07%)	CAG (2.15%)	CAG (2.19%)	GTT (2.28%)
-10	AGT (0.96%)	GTA (0.94%)	GGT (0.92%)	AGT (1.01%)	CTT (0.95%)	CCC (0.94%)	CTT (1.06%)	CCC (1.00%)	CCT (0.90%)
-9	TGT (0.96%)	CCT (0.91%)	GGG (0.91%)	AGA (0.98%)	CGA (0.95%)	CTT (0.89%)	TAC (1.05%)	GTA (0.97%)	ACT (0.89%)
-8	CCC (0.93%)	AGT (0.91%)	AGA (0.83%)	CTC (0.93%)	AGT (0.94%)	AGT (0.87%)	GAG (0.91%)	ACT (0.91%)	TGA (0.84%)
-7	GGA (0.86%)	GAG (0.81%)	AGG (0.82%)	GGA (0.86%)	CCC (0.91%)	AGG (0.84%)	AGG (0.83%)	CGA (0.90%)	GAG (0.73%)
-6	AGA (0.81%)	CTT (0.80%)	AGT (0.78%)	GAG (0.84%)	CTC (0.90%)	CCT (0.78%)	AGA (0.81%)	CCT (0.84%)	CGA (0.71%)
-5	GAG (0.72%)	CGA (0.76%)	TGT (0.73%)	CCC (0.82%)	GAG (0.87%)	ACT (0.75%)	CCC (0.80%)	CTT (0.83%)	CTT (0.69%)
-4	GGG (0.71%)	AGA (0.68%)	CTT (0.71%)	AGG (0.73%)	CCT (0.85%)	GGG (0.75%)	GGA (0.80%)	AGA (0.77%)	TAG (0.52%)
-3	AGG (0.67%)	GGA (0.67%)	GAG (0.61%)	CTA (0.63%)	GGG (0.76%)	GAG (0.59%)	GGG (0.72%)	GGA (0.75%)	AGA (0.51%)
-2	CTA (0.53%)	TAG (0.55%)	TAG (0.39%)	GGG (0.54%)	TAG (0.54%)	CTA (0.46%)	CTA (0.65%)	CTA (0.71%)	GGA (0.49%)
-1	TAG (0.41%)	CTA (0.52%)	CTA (0.38%)	TAG (0.47%)	CTA (0.54%)	TAG (0.38%)	TAG (0.53%)	TAG (0.65%)	CTA (0.41%)

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 (0.99%)	TTTC (1.13%)	AAAA (1.41%)	CAGC (0.93%)	TGGC (1.11%)	AAAA (1.08%)	ATCA (0.98%)	TGGC (0.95%)	GGCA (1.17%)
2	GAAA (0.92%)	TGCC (0.92%)	TTTT (1.29%)	ATCA (0.93%)	CGGC (1.07%)	CAAA (1.04%)	GGCA (0.82%)	CAGC (0.88%)	AAAA (1.14%)
3	AAAA (0.90%)	TGCC (0.89%)	GAAA (1.13%)	CTGC (0.91%)	CAGC (1.02%)	TGAA (1.00%)	GCCA (0.80%)	TTCA (0.83%)	TGAA (0.99%)
4	ATCA (0.87%)	CTGC (0.89%)	GGCA (0.94%)	TGGC (0.84%)	CTGC (0.94%)	GAAA (0.97%)	AACA (0.79%)	ATCA (0.82%)	TTTT (0.98%)
5	TTCA (0.84%)	CAGC (0.87%)	GTTC (0.93%)	CGGC (0.83%)	TTGC (0.92%)	ATCA (0.96%)	TTCA (0.77%)	CGGC (0.78%)	GAAA (0.96%)
6	TTCT (0.81%)	TTCA (0.87%)	GCAA (0.93%)	TTGC (0.83%)	ATCA (0.82%)	AGCA (0.94%)	TTTC (0.76%)	CTGC (0.76%)	GGAA (0.95%)
7	CAGC (0.79%)	TTGC (0.85%)	TTTT (0.91%)	CCAG (0.79%)	CAAA (0.82%)	GGCA (0.92%)	CAAA (0.76%)	TTGC (0.73%)	TTTC (0.91%)
8	TGCC (0.79%)	AAAA (0.85%)	GGAA (0.85%)	ATGC (0.77%)	TGCC (0.78%)	TTTC (0.91%)	CGCA (0.76%)	TGCC (0.70%)	TGCA (0.90%)
9	GGCA (0.78%)	TTCC (0.85%)	TGCC (0.84%)	CAAA (0.77%)	CTGC (0.75%)	AGAA (0.89%)	CGCC (0.75%)	CAAA (0.70%)	CGCC (0.87%)
10	AACA (0.77%)	GTTC (0.84%)	CAAA (0.83%)	TGAA (0.72%)	TTCC (0.75%)	TAAA (0.87%)	CAGC (0.75%)	GGCC (0.70%)	TGCC (0.84%)
-10	TAGT (0.13%)	GGAC (0.13%)	TTAG (0.11%)	GGGG (0.11%)	CTAT (0.12%)	GGAC (0.11%)	GGGA (0.15%)	CCCC (0.15%)	CCCT (0.11%)
-9	GAGG (0.13%)	CTAT (0.12%)	ACTA (0.10%)	CTAA (0.11%)	CTAA (0.11%)	ACTA (0.11%)	GAGA (0.14%)	CTAT (0.15%)	ACTA (0.11%)
-8	TCTA (0.13%)	TCTA (0.12%)	TAGT (0.10%)	GGAC (0.11%)	ACCT (0.11%)	ACCT (0.11%)	CCCC (0.14%)	GAGA (0.15%)	CGGA (0.11%)
-7	AGGG (0.12%)	CGGA (0.12%)	CGAG (0.09%)	AGGG (0.10%)	CCCC (0.11%)	GTGT (0.10%)	CTAA (0.13%)	ACCT (0.14%)	TCTA (0.10%)
-6	GGAC (0.12%)	TAGT (0.11%)	TAGA (0.09%)	TAGA (0.10%)	TAGA (0.11%)	CGAG (0.09%)	TCTA (0.13%)	CTAA (0.13%)	GGGA (0.09%)
-5	TTAG (0.11%)	CTAA (0.10%)	TCTA (0.09%)	GAGG (0.10%)	GTGT (0.11%)	CTAT (0.08%)	CTAT (0.12%)	TAGG (0.12%)	CTAT (0.09%)
-4	CCTA (0.07%)	TAGG (0.08%)	GGAC (0.08%)	CCCT (0.09%)	TAGG (0.09%)	CCTA (0.07%)	TAGA (0.09%)	CCCT (0.12%)	TAGG (0.08%)
-3	TAGA (0.06%)	TAGA (0.06%)	TAGG (0.07%)	CCTA (0.08%)	CCCT (0.08%)	TAGG (0.07%)	CCTA (0.08%)	CCTA (0.10%)	TAGA (0.06%)
-2	TAGG (0.05%)	CCTA (0.06%)	CCTA (0.05%)	TAGG (0.06%)	CCTA (0.06%)	CCCT (0.05%)	TAGG (0.07%)	TAGA (0.08%)	CCTA (0.04%)
-1	CTAG (0.01%)	CTAG (0.01%)	CTAG (0.01%)	CTAG (0.02%)	CTAG (0.01%)	CTAG (0.01%)	CTAG (0.02%)	CTAG (0.02%)	CTAG (0.02%)

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 (0.36%)	GAAAA (0.48%)	CAGCA (0.38%)	CTGGC (0.42%)	CAGCA (0.52%)	CAGCA (0.37%)	CTGGC (0.39%)	CAGCA (0.41%)
2	TTATC (0.33%)	CAGCA (0.36%)	CAGCA (0.40%)	GCTGC (0.33%)	CAGCA (0.39%)	CGGCA (0.37%)	CGCCA (0.34%)	CATCA (0.30%)	CGGCA (0.41%)
3	CTGGC (0.33%)	TTGCC (0.31%)	CAAAA (0.36%)	CCAGC (0.33%)	GCGGC (0.37%)	GAAAA (0.35%)	CGGCA (0.30%)	CAGCA (0.29%)	TGGCA (0.38%)
4	CGCCA (0.32%)	TTTGC (0.31%)	TGTTT (0.33%)	CATCA (0.31%)	GCTGC (0.33%)	CATCA (0.34%)	CATCA (0.29%)	CGCCA (0.29%)	GAAAA (0.38%)
5	CATCA (0.29%)	ATTTT (0.31%)	AGAAA (0.32%)	CTGGC (0.30%)	CCAGC (0.32%)	ATAAA (0.34%)	CTGGC (0.29%)	CCAGC (0.29%)	CAAAA (0.32%)
6	TTTTT (0.29%)	GCCAG (0.31%)	ATTTT (0.32%)	GATGC (0.30%)	GATGC (0.32%)	AATCA (0.34%)	GCCAG (0.29%)	GCCAG (0.29%)	ATTTT (0.31%)
7	ATTTT (0.29%)	CGCCA (0.31%)	TGGCA (0.32%)	GCGGC (0.30%)	AATCA (0.31%)	CAGAA (0.34%)	GCAAA (0.28%)	GCGGC (0.29%)	TTGCC (0.31%)
8	CCAGC (0.28%)	GCTGC (0.30%)	CGTTT (0.31%)	TTATC (0.29%)	TTTGC (0.31%)	TTATC (0.32%)	TGGCA (0.28%)	TGGCG (0.28%)	CGCCA (0.29%)
9	TGGCA (0.28%)	CATCA (0.30%)	TAAAA (0.31%)	CGGCA (0.29%)	CATCA (0.31%)	AAGAA (0.32%)	GATCA (0.26%)	TTTCA (0.27%)	CTGAA (0.29%)
10	CAAAA (0.28%)	GCAGC (0.30%)	TTTTT (0.31%)	TTTTT (0.28%)	TCAGC (0.29%)	GCAAA (0.31%)	GCGCA (0.26%)	GATGC (0.27%)	GCAAA (0.28%)
-10	GGACC (0.01%)	ACCTA (0.01%)	CTTAG (0.01%)	GGGGG (0.01%)	CCCTA (0.01%)	CCTAT (0.01%)	TAGGA (0.01%)	TCCTA (0.01%)	ACTAG (0.01%)
-9	CCCTA (0.00%)	CCCTA (0.01%)	CCCTA (0.01%)	CTAGC (0.01%)	GCTAG (0.01%)	CCCTA (0.01%)	GCTAG (0.01%)	TAGGA (0.01%)	GCTAG (0.01%)
-8	CTAGT (0.00%)	GCTAG (0.01%)	ACTAG (0.00%)	GCTAG (0.01%)	CTAGC (0.01%)	CTAGC (0.01%)	CCTAG (0.01%)	GCTAG (0.01%)	TCCTA (0.01%)
-7	GCTAG (0.00%)	CTAGC (0.00%)	CTAGC (0.00%)	CCCTA (0.01%)	CCCCC (0.01%)	GCTAG (0.00%)	CCCTA (0.01%)	CTAGC (0.01%)	TAGGA (0.01%)
-6	ACTAG (0.00%)	ACTAG (0.00%)	GCTAG (0.00%)	CTAGT (0.00%)	CTAGT (0.01%)	CTAGA (0.00%)	CTAGC (0.00%)	ACTAG (0.01%)	CTAGT (0.00%)
-5	CTAGA (0.00%)	CTAGT (0.00%)	CTAGT (0.00%)	TCTAG (0.00%)	CTAGA (0.00%)	CTAGT (0.00%)	CTAGT (0.00%)	CTAGT (0.00%)	CTAGC (0.00%)
-4	CTAGC (0.00%)	CTAGG (0.00%)	CCTAG (0.00%)	ACTAG (0.00%)	ACTAG (0.00%)	CTAGG (0.00%)	CTAGA (0.00%)	TCTAG (0.00%)	CCTAG (0.00%)
-3	CCTAG (0.00%)	TCTAG (0.00%)	TCTAG (0.00%)	CTAGA (0.00%)	TCTAG (0.00%)	ACTAG (0.00%)	ACTAG (0.00%)	CTAGA (0.00%)	CTAGG (0.00%)
-2	CTAGG (0.00%)	CCTAG (0.00%)	CTAGG (0.00%)	CCTAG (0.00%)	CCTAG (0.00%)	CCTAG (0.00%)	CTAGG (0.00%)	CTAGG (0.00%)	TCTAG (0.00%)
-1	TCTAG (0.00%)	CTAGA (0.00%)	CTAGA (0.00%)	CTAGG (0.00%)	CTAGG (0.00%)	TCTAG (0.00%)	TCTAG (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%