

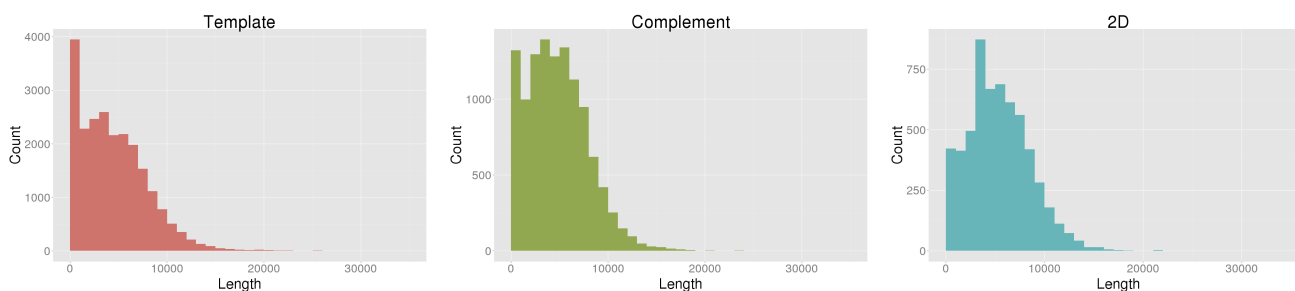
NanoOK report for 20150422_MN02862_FAA40596_BOWDEN05_MdC_MARC_Phase1b.1

Pass and fail counts

Type	Pass	Fail
Template	0	22590
Complement	0	11397
2D	0	5894

Read lengths

Type	NumReads	TotalBases	Mean	Longest	Shortest	N50	N50Count	N90	N90Count
Template	22590	104088643	4607.73	150739	9	6784	5390	2884	14210
Complement	11397	55028540	4828.34	74706	9	6561	3102	3024	7744
2D	5894	31743981	5385.81	21712	149	6994	1723	3321	4225



Template alignments

Number of reads	22590
Number of reads with alignments	8881 (39.31%)
Number of reads without alignments	13709 (60.69%)

ID	Size	Number of Reads	% of Reads	Mean read length	Aligned bases	Mean coverage	Longest Perf Kmer
Control sequence	3560	758	3.36	2879.94	2109246	592.48	48
Escherichia coli	4641652	8123	35.96	6536.10	46609824	10.04	73

Complement alignments

Number of reads	11397
Number of reads with alignments	5734 (50.31%)
Number of reads without alignments	5663 (49.69%)

ID	Size	Number of Reads	% of Reads	Mean read length	Aligned bases	Mean coverage	Longest Perf Kmer
Control sequence	3560	451	3.96	2790.83	1099761	308.92	44
Escherichia coli	4641652	5283	46.35	6091.72	27088048	5.84	52

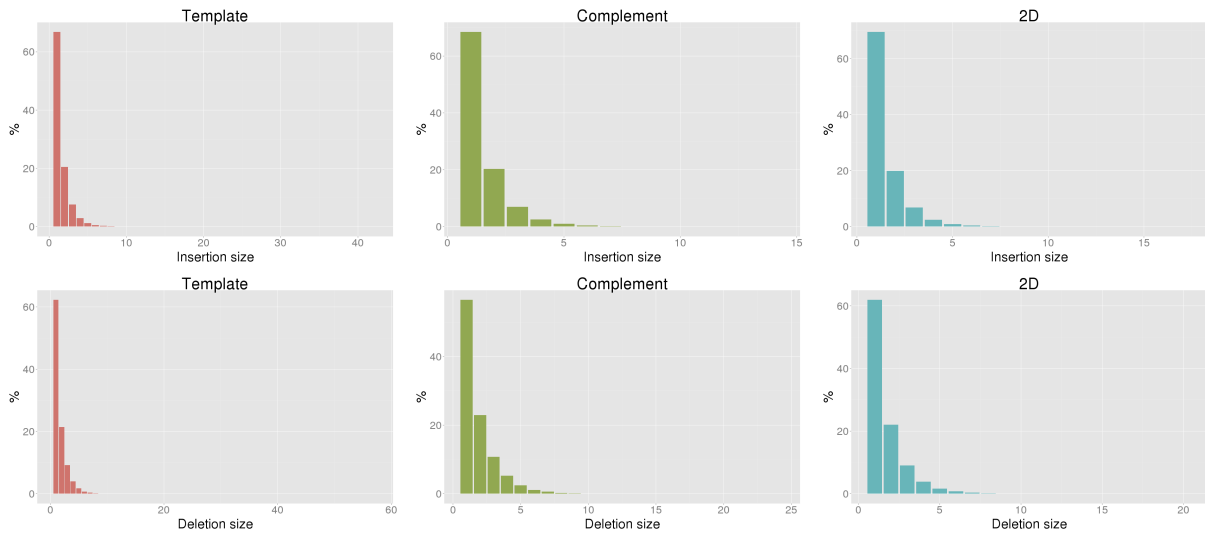
2D alignments

Number of reads	5894
Number of reads with alignments	4929 (83.63%)
Number of reads without alignments	965 (16.37%)

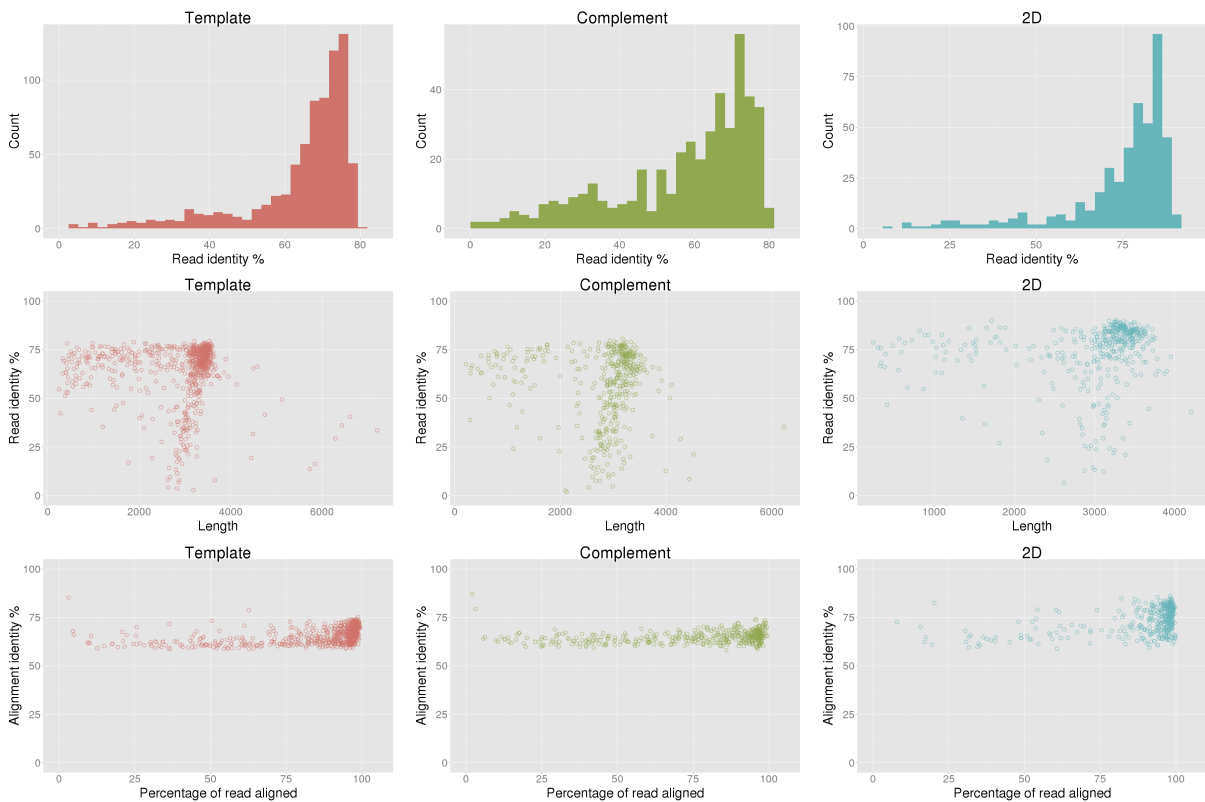
ID	Size	Number of Reads	% of Reads	Mean read length	Aligned bases	Mean coverage	Longest Perf Kmer
Control sequence	3560	458	7.77	2983.22	1369165	384.60	142
Escherichia coli	4641652	4471	75.86	6027.21	27141091	5.85	166

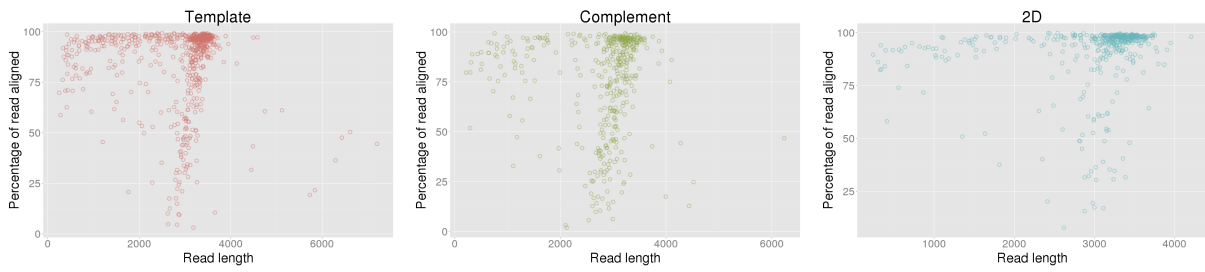
Control sequence error analysis

	Template	Complement	2D
Overall base identity (excluding indels)	63.83%	56.66%	74.92%
Aligned base identity (excluding indels)	78.80%	79.50%	86.71%
Identical bases per 100 aligned bases (including indels)	66.07%	64.85%	74.76%
Inserted bases per 100 aligned bases (including indels)	4.99%	4.09%	3.90%
Deleted bases per 100 aligned bases (including indels)	11.16%	14.34%	9.87%
Substitutions per 100 aligned bases (including indels)	17.78%	16.72%	11.46%
Mean insertion size	1.56	1.50	1.48
Mean deletion size	1.67	1.83	1.67

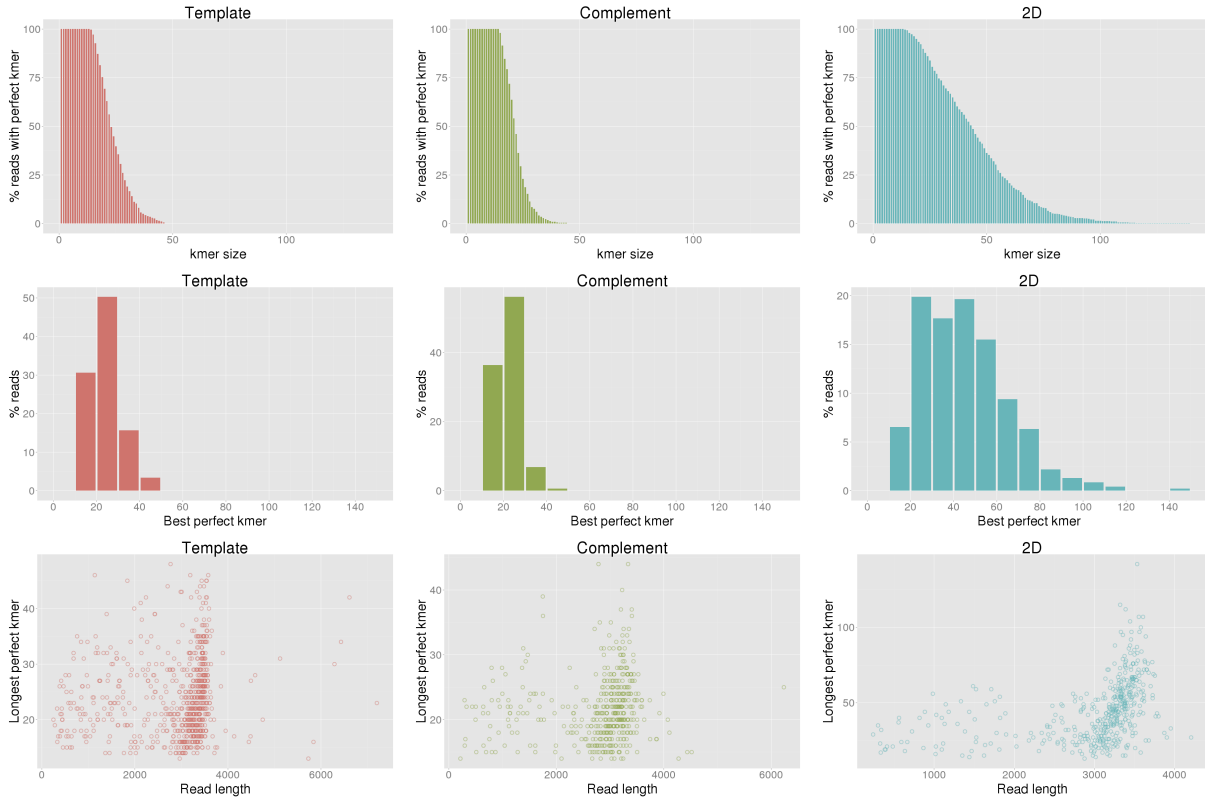


Control sequence read identity

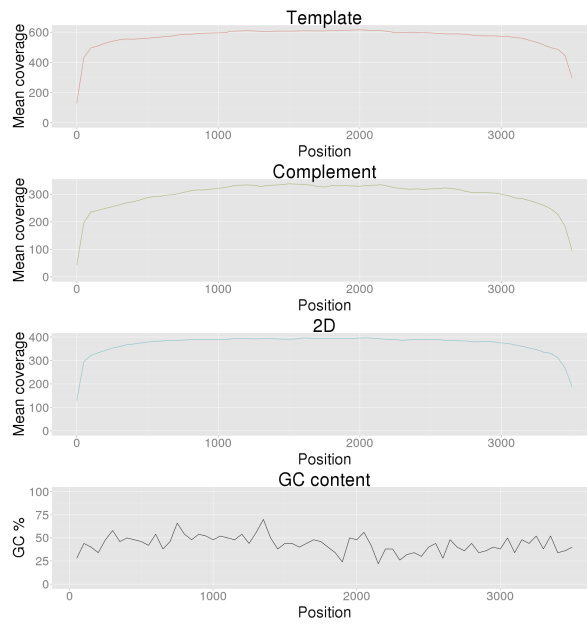




Control sequence perfect kmers



Control sequence coverage



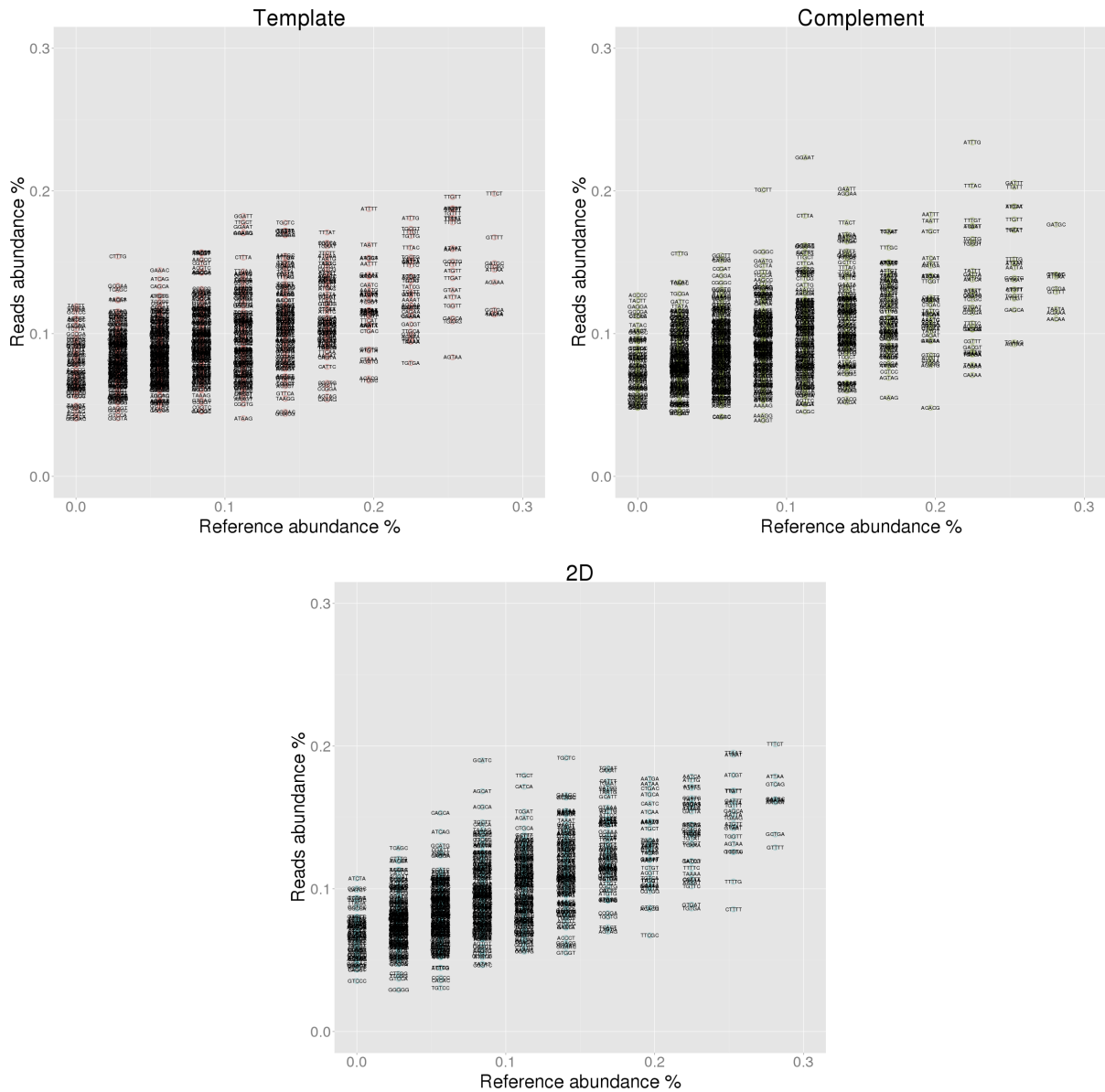
Control sequence 5-mer analysis

Under-represented 5-mers

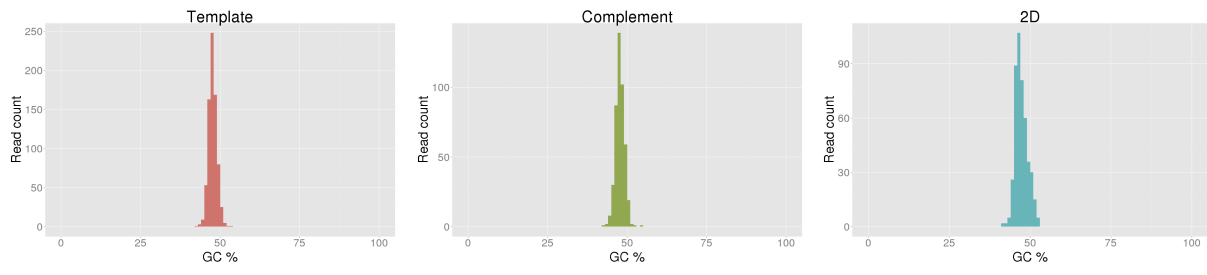
Rank	Template				Complement				2D			
	kmer	Ref %	Read %	Diff %	kmer	Ref %	Read %	Diff %	kmer	Ref %	Read %	Diff %
1	TTTTT	0.759	0.142	-0.617	TTTTT	0.759	0.072	-0.687	TTTTT	0.759	0.040	-0.719
2	AAAAA	0.478	0.107	-0.371	AAAAA	0.478	0.047	-0.431	AAAAA	0.478	0.041	-0.436
3	TGATG	0.393	0.134	-0.260	AAAAC	0.337	0.108	-0.229	TGATG	0.393	0.147	-0.246
4	GATGT	0.309	0.097	-0.212	TGATG	0.393	0.186	-0.207	AAAAC	0.337	0.130	-0.207
5	AAAAC	0.337	0.129	-0.208	GATGT	0.309	0.105	-0.204	GATGT	0.309	0.122	-0.187
6	CTGAT	0.309	0.115	-0.194	GCAAT	0.309	0.124	-0.185	CTGAT	0.309	0.139	-0.170
7	GCAAT	0.309	0.122	-0.187	TTATC	0.309	0.133	-0.176	CTTTT	0.253	0.086	-0.167
8	AATAT	0.309	0.135	-0.174	AATAT	0.309	0.134	-0.175	TTATC	0.309	0.149	-0.160
9	AGTAA	0.253	0.084	-0.169	AACAA	0.281	0.110	-0.171	GCAAT	0.309	0.151	-0.158
10	TAATA	0.281	0.113	-0.168	AGAAA	0.281	0.115	-0.166	GTTTT	0.281	0.129	-0.152

Over-represented 5-mers

Rank	Template				Complement				2D			
	kmer	Ref %	Read %	Diff %	kmer	Ref %	Read %	Diff %	kmer	Ref %	Read %	Diff %
1	CTTTG	0.028	0.154	0.126	CTTTG	0.028	0.156	0.128	ATCTA	0.000	0.107	0.107
2	TACTT	0.000	0.119	0.119	ACCCC	0.000	0.127	0.127	GCATC	0.084	0.190	0.106
3	CCCCA	0.000	0.118	0.118	TACTT	0.000	0.123	0.123	TCAGC	0.028	0.129	0.100
4	ATCTA	0.000	0.117	0.117	GAGGA	0.000	0.119	0.119	CCCGC	0.000	0.100	0.100
5	GCTCC	0.000	0.115	0.115	TGCTT	0.084	0.201	0.116	CATCT	0.000	0.099	0.099
6	ACTCT	0.000	0.111	0.111	GCCGA	0.000	0.115	0.115	CAGCA	0.056	0.153	0.097
7	ACCCC	0.000	0.110	0.110	CTTAC	0.000	0.112	0.112	TCTAC	0.000	0.094	0.094
8	CATCT	0.000	0.110	0.110	CCCCA	0.000	0.112	0.112	GTCGA	0.000	0.093	0.093
9	TCTAC	0.000	0.106	0.106	GGAAT	0.112	0.224	0.111	CTTTG	0.028	0.121	0.093
10	GCGAA	0.028	0.134	0.105	TACAT	0.028	0.136	0.108	TACGC	0.000	0.092	0.092

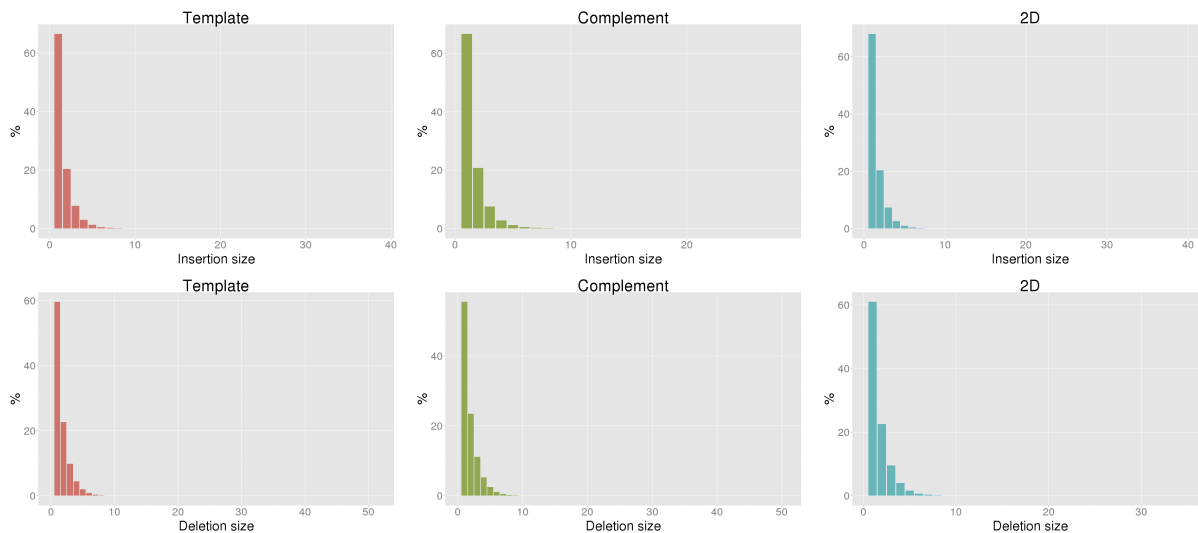


Control sequence GC content

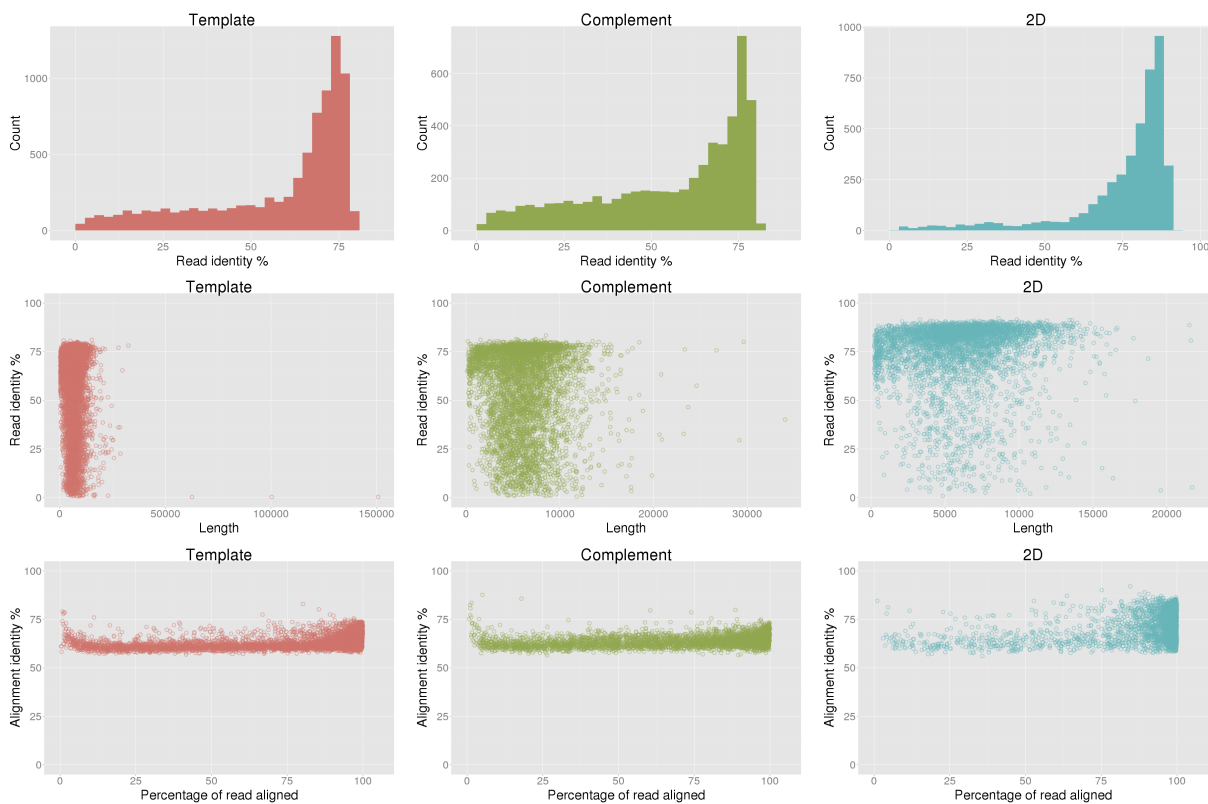


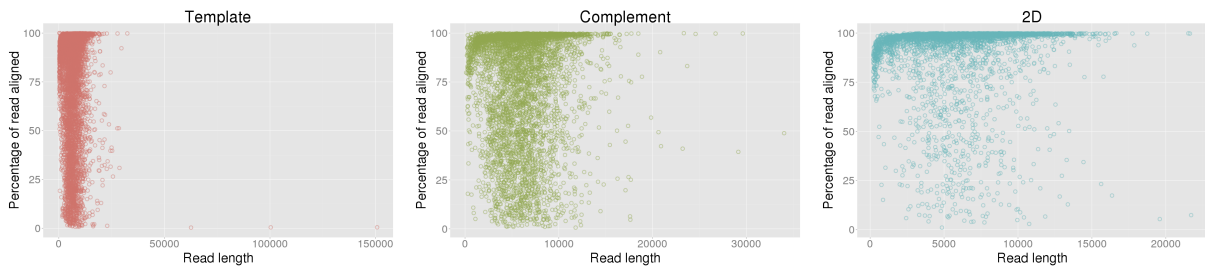
Escherichia coli error analysis

	Template	Complement	2D
Overall base identity (excluding indels)	56.67%	54.28%	75.30%
Aligned base identity (excluding indels)	77.97%	79.62%	86.66%
Identical bases per 100 aligned bases (including indels)	64.55%	64.49%	74.76%
Inserted bases per 100 aligned bases (including indels)	5.09%	4.48%	4.12%
Deleted bases per 100 aligned bases (including indels)	12.12%	14.53%	9.61%
Substitutions per 100 aligned bases (including indels)	18.24%	16.50%	11.50%
Mean insertion size	1.57	1.55	1.51
Mean deletion size	1.73	1.85	1.68

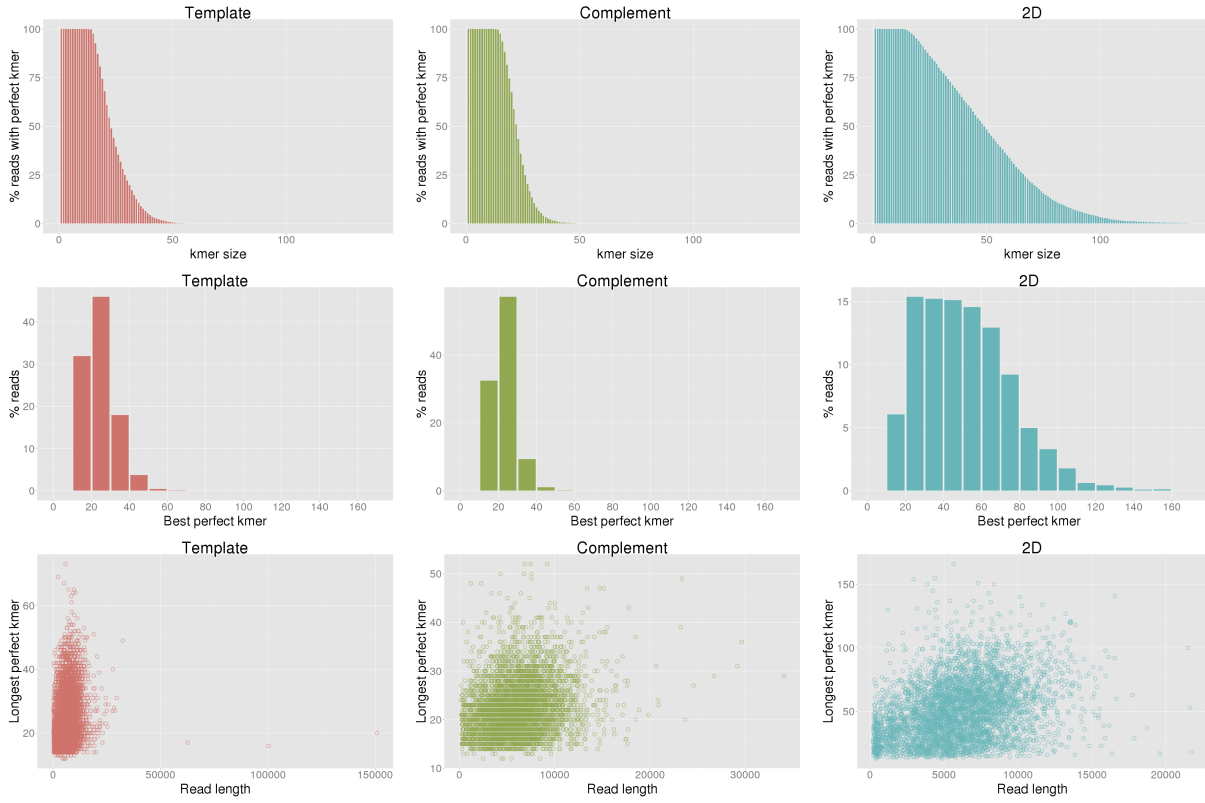


Escherichia coli read identity

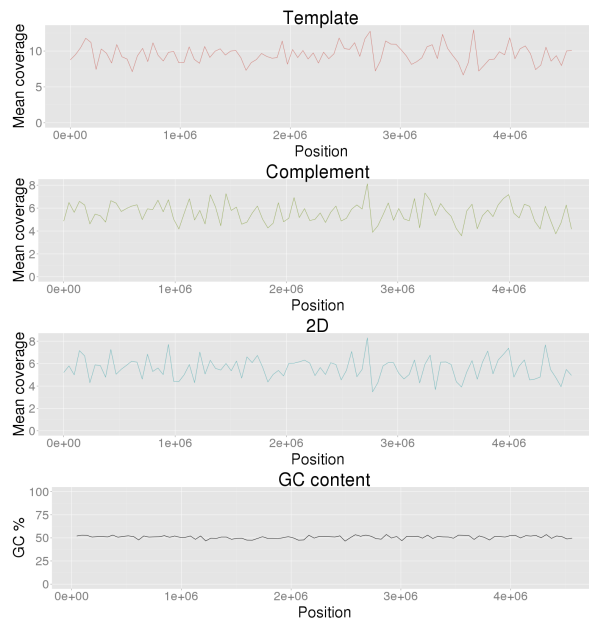




Escherichia coli perfect kmers



Escherichia coli coverage



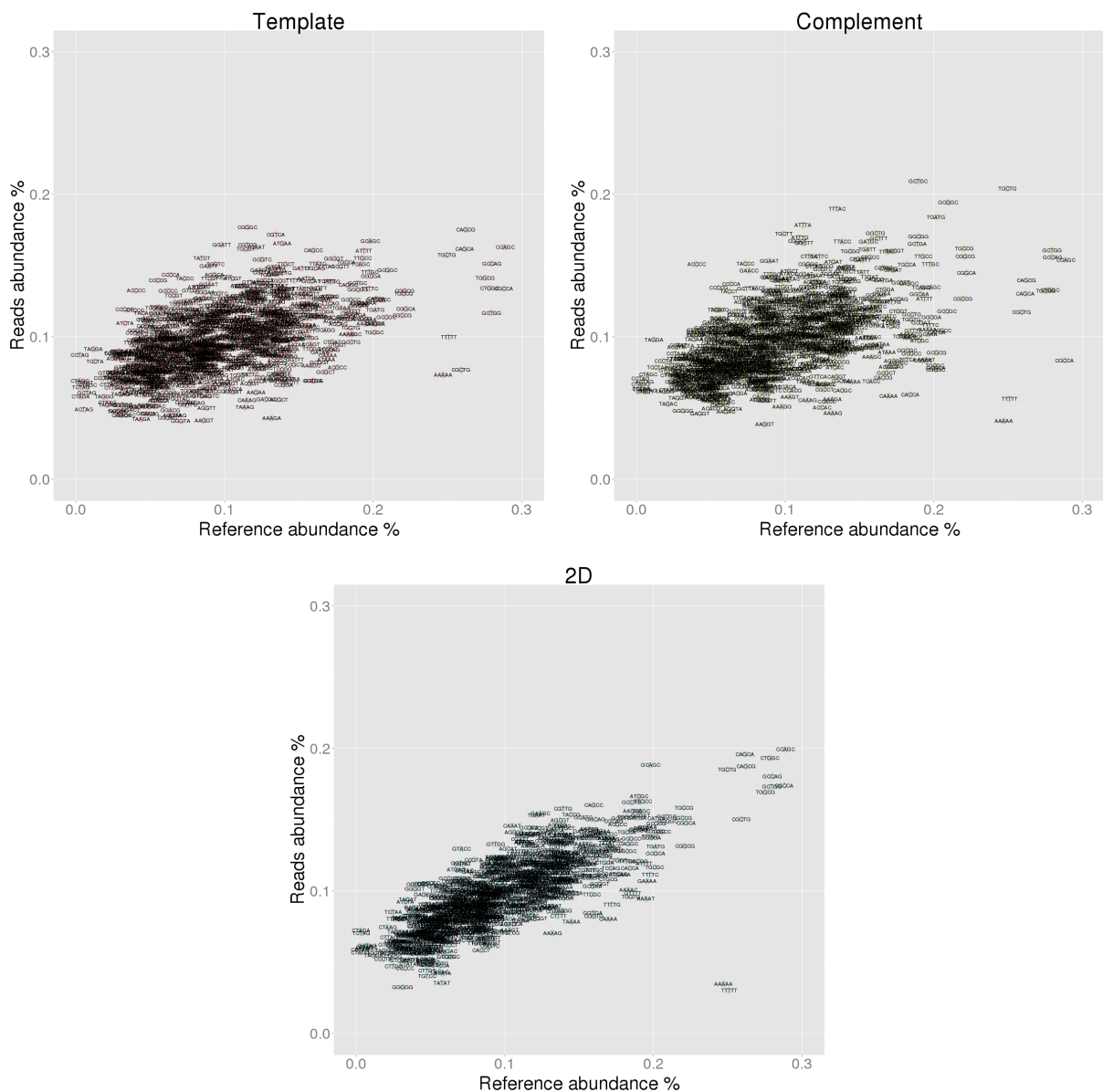
Escherichia coli 5-mer analysis

Under-represented 5-mers

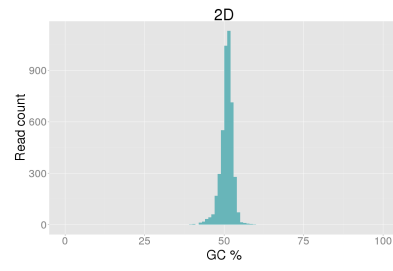
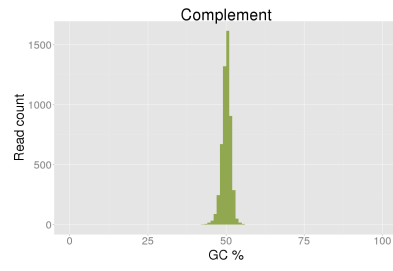
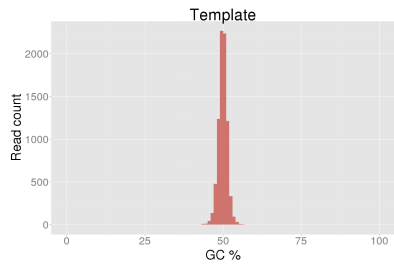
Rank	Template				Complement				2D			
	kmer	Ref %	Read %	Diff %	kmer	Ref %	Read %	Diff %	kmer	Ref %	Read %	Diff %
1	CGCTG	0.259	0.077	-0.182	AAAAA	0.247	0.041	-0.206	TTTTT	0.251	0.030	-0.221
2	AAAAA	0.247	0.073	-0.174	CGCCA	0.288	0.083	-0.205	AAAAA	0.247	0.035	-0.212
3	GCTGG	0.279	0.117	-0.163	TTTTT	0.251	0.056	-0.194	CGCCA	0.288	0.174	-0.114
4	CGCCA	0.288	0.134	-0.154	CTGGC	0.278	0.133	-0.145	CGCTG	0.259	0.150	-0.109
5	TTTTT	0.251	0.100	-0.151	TGGCG	0.275	0.132	-0.143	GCTGG	0.279	0.173	-0.106
6	CTGGC	0.278	0.134	-0.144	CGCTG	0.259	0.117	-0.142	TGGCG	0.275	0.169	-0.106
7	TGGCG	0.275	0.141	-0.134	CCAGC	0.289	0.154	-0.135	AAAAT	0.195	0.094	-0.100
8	GCCAG	0.280	0.151	-0.128	CAGCA	0.261	0.130	-0.131	GCCAG	0.280	0.180	-0.099
9	CCAGC	0.289	0.163	-0.126	CACCA	0.184	0.059	-0.125	CGGCG	0.221	0.131	-0.090
10	CGCCG	0.219	0.115	-0.104	CGCGC	0.201	0.077	-0.124	CAAAA	0.169	0.080	-0.089

Over-represented 5-mers

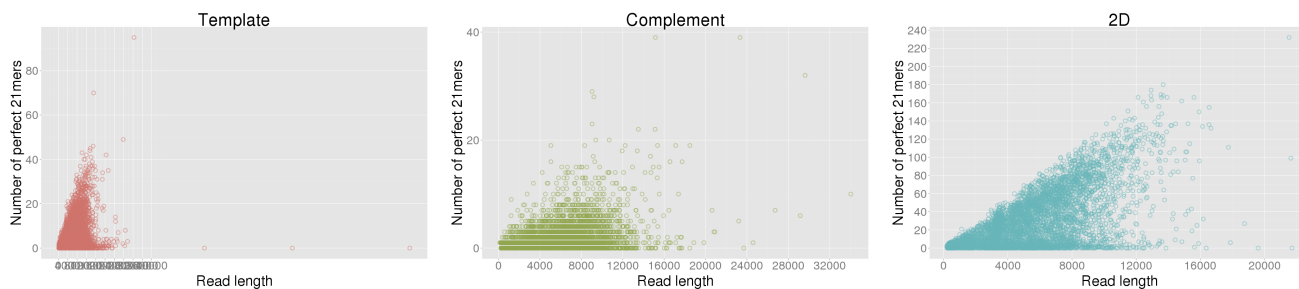
Rank	Template				Complement				2D			
	kmer	Ref %	Read %	Diff %	kmer	Ref %	Read %	Diff %	kmer	Ref %	Read %	Diff %
1	ACCCC	0.040	0.132	0.092	ACCCC	0.040	0.151	0.111	CTAGA	0.003	0.072	0.069
2	CCCCC	0.033	0.119	0.086	TAGGA	0.012	0.098	0.086	TCTAG	0.003	0.070	0.067
3	CCTAG	0.003	0.087	0.085	CCCCG	0.055	0.134	0.079	GGGTC	0.040	0.105	0.064
4	CCCCG	0.055	0.140	0.084	TACCC	0.073	0.151	0.078	CTCGT	0.042	0.105	0.062
5	CCCCA	0.064	0.143	0.080	CCCCA	0.064	0.137	0.074	GGGGT	0.039	0.102	0.062
6	TAGGA	0.012	0.091	0.079	TGCTT	0.099	0.172	0.073	TCTAA	0.025	0.085	0.060
7	CTCCC	0.040	0.119	0.079	GAACC	0.075	0.146	0.071	ATCTA	0.033	0.092	0.059
8	ATCTA	0.033	0.110	0.077	TACCT	0.062	0.132	0.070	TAGAT	0.035	0.094	0.059
9	TACAC	0.045	0.117	0.072	CCTAG	0.003	0.071	0.068	GTACC	0.071	0.130	0.059
10	TATCT	0.085	0.155	0.070	ATTTA	0.112	0.179	0.067	CCCAA	0.047	0.105	0.058



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	8.82	8.69	5.11	0.00	9.14	8.67	5.29	0.00	9.40	8.70	4.57
C	8.60	0.00	8.98	9.98	9.17	0.00	8.64	9.49	8.60	0.00	10.22	8.80
G	9.52	9.01	0.00	8.40	9.07	8.81	0.00	8.69	8.68	10.49	0.00	8.24
T	5.36	8.84	8.70	0.00	5.55	8.56	8.92	0.00	4.64	8.54	9.13	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 (3.22%)	TTC (3.30%)	AAA (4.12%)	TGC (2.87%)	AAA (2.86%)	AAA (3.95%)	GCA (3.08%)	AAA (2.71%)	GCA (3.60%)
2	AAA (2.85%)	AAA (2.98%)	TTC (3.54%)	TTC (2.77%)	TGC (2.81%)	GCA (3.44%)	TTC (2.72%)	GCA (2.65%)	AAA (3.54%)
3	GCA (2.74%)	TGC (2.94%)	GCA (3.20%)	AAA (2.67%)	GGC (2.81%)	GAA (3.24%)	AAA (2.71%)	GGC (2.65%)	GAA (2.95%)
4	TGC (2.60%)	GCA (2.73%)	GAA (2.91%)	GCA (2.63%)	GCA (2.69%)	TTC (3.14%)	TCA (2.52%)	TGC (2.59%)	TTC (2.79%)
5	ATC (2.53%)	GCC (2.43%)	TTT (2.74%)	CAG (2.45%)	TTC (2.63%)	TTT (2.70%)	GAA (2.36%)	GCG (2.43%)	TTT (2.73%)
6	TCA (2.36%)	TCA (2.34%)	TGC (2.60%)	GAA (2.40%)	GAA (2.56%)	TGC (2.51%)	TGC (2.33%)	TCA (2.37%)	GTT (2.63%)
7	TTT (2.24%)	GGC (2.27%)	AAT (2.55%)	ATC (2.34%)	CAG (2.30%)	TCA (2.28%)	GCG (2.33%)	GAA (2.37%)	AAT (2.49%)
8	GAA (2.21%)	GAA (2.27%)	TCA (2.19%)	GGC (2.31%)	GCC (2.29%)	AAT (2.23%)	ATC (2.33%)	CAG (2.31%)	GCC (2.27%)
9	AAT (2.20%)	AAT (2.24%)	CAA (2.16%)	TCA (2.24%)	TCA (2.22%)	ATC (2.18%)	AAT (2.20%)	TTC (2.28%)	GCG (2.17%)
10	GCC (2.20%)	ATC (2.23%)	ATC (2.15%)	TTT (2.21%)	AAT (2.19%)	GCC (2.15%)	CAG (2.20%)	GCC (2.20%)	TGC (2.16%)
-10	AGT (1.00%)	GGG (0.93%)	GGT (0.92%)	AGA (0.99%)	CTT (0.95%)	CCC (0.92%)	CTT (1.06%)	CTC (1.00%)	TGA (0.98%)
-9	CTC (0.93%)	AGT (0.92%)	AGA (0.91%)	GTG (0.98%)	ACT (0.95%)	AGT (0.90%)	CTC (1.05%)	CCC (0.98%)	ACT (0.97%)
-8	AGA (0.89%)	CCT (0.89%)	TGT (0.90%)	GGA (0.91%)	AGT (0.94%)	CTC (0.88%)	GAG (0.90%)	CGA (0.94%)	CCC (0.97%)
-7	CCC (0.86%)	CTT (0.88%)	GGG (0.86%)	CTC (0.84%)	CCC (0.94%)	AGG (0.83%)	AGA (0.89%)	CTT (0.92%)	GAG (0.88%)
-6	GGA (0.84%)	GAG (0.87%)	AGG (0.86%)	CCC (0.81%)	CCT (0.89%)	CCT (0.83%)	GGA (0.87%)	ACT (0.91%)	CTT (0.83%)
-5	GAG (0.76%)	CGA (0.85%)	CTT (0.83%)	GAG (0.78%)	GAG (0.86%)	GGG (0.80%)	AGG (0.79%)	AGA (0.87%)	CGA (0.80%)
-4	AGG (0.71%)	AGA (0.74%)	AGT (0.79%)	AGG (0.73%)	CTC (0.84%)	ACT (0.78%)	CCC (0.79%)	CCT (0.82%)	AGA (0.70%)
-3	GGG (0.69%)	GGA (0.70%)	GAG (0.66%)	GGG (0.57%)	GGG (0.79%)	GAG (0.63%)	GGG (0.71%)	GGA (0.75%)	GGA (0.64%)
-2	CTA (0.48%)	TAG (0.55%)	TAG (0.40%)	CTA (0.53%)	TAG (0.54%)	CTA (0.40%)	CTA (0.61%)	TAG (0.68%)	TAG (0.50%)
-1	TAG (0.44%)	CTA (0.49%)	CTA (0.36%)	TAG (0.46%)	CTA (0.51%)	TAG (0.39%)	TAG (0.51%)	CTA (0.68%)	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 (1.06%)	TTTC (1.10%)	AAAA (1.42%)	CAGC (0.89%)	TGGC (1.04%)	AAAA (1.08%)	ATCA (0.87%)	TGGC (0.99%)	GGCA (1.14%)
2	AAAA (0.93%)	AAAA (0.93%)	TTTC (1.28%)	ATCA (0.87%)	CAGC (1.02%)	CAAA (1.05%)	GGCA (0.84%)	CAGC (0.94%)	AAAA (0.96%)
3	GAAA (0.86%)	TGCC (0.93%)	GAAA (1.11%)	CTGC (0.86%)	CGGC (0.99%)	GAAA (0.95%)	CAGC (0.82%)	TTCA (0.82%)	GAAA (0.95%)
4	ATCA (0.84%)	TTTC (0.91%)	TTTT (1.00%)	TGGC (0.83%)	TTGC (0.89%)	TTTC (0.92%)	GCCA (0.79%)	CTGC (0.80%)	GGAA (0.89%)
5	TTGC (0.80%)	TTGC (0.91%)	CAAA (0.91%)	TTGC (0.83%)	CTGC (0.86%)	GGCA (0.92%)	AACA (0.78%)	CGGC (0.78%)	CGTT (0.89%)
6	TTCA (0.80%)	TTCA (0.88%)	AAAT (0.91%)	CCAG (0.81%)	CAAA (0.85%)	TGAA (0.91%)	TTCA (0.77%)	CAAA (0.77%)	TTTC (0.89%)
7	TGCC (0.78%)	TGGC (0.87%)	GGCA (0.89%)	CGGC (0.80%)	TGCC (0.81%)	AGCA (0.88%)	TTTC (0.77%)	CCAG (0.76%)	TGCA (0.88%)
8	TTTT (0.78%)	CAGC (0.86%)	GCAA (0.88%)	CAAA (0.78%)	TTCC (0.81%)	GGAA (0.88%)	CAAA (0.76%)	TGCC (0.75%)	CAAA (0.85%)
9	AACG (0.77%)	GAAA (0.86%)	GGAA (0.84%)	ATGC (0.77%)	ATCA (0.79%)	ATCA (0.85%)	CGCC (0.76%)	ATCA (0.74%)	TGTT (0.83%)
10	CAGC (0.76%)	CTGC (0.85%)	TGCC (0.82%)	TGCC (0.75%)	CTGG (0.77%)	AGAA (0.83%)	TGCA (0.76%)	GGCA (0.73%)	AGCA (0.83%)
-10	ACTA (0.12%)	TCTA (0.12%)	TTAG (0.11%)	GTGT (0.11%)	CCCC (0.12%)	TCTA (0.11%)	ACTA (0.14%)	CTAT (0.15%)	TCGA (0.12%)
-9	CTCG (0.12%)	CCCT (0.12%)	CGAG (0.10%)	GAGG (0.11%)	ACCT (0.12%)	ACCT (0.10%)	CTAT (0.14%)	CCCC (0.15%)	CCCT (0.12%)
-8	GAGG (0.12%)	CGGA (0.12%)	TAGT (0.10%)	AGGG (0.11%)	CCTC (0.12%)	ACTA (0.10%)	TTAG (0.13%)	CGGA (0.14%)	ACTT (0.12%)
-7	TCTA (0.11%)	TAGT (0.11%)	ACTA (0.09%)	GGAC (0.10%)	CTAA (0.12%)	GGAC (0.09%)	CCCT (0.13%)	CTAA (0.14%)	TCTA (0.10%)
-6	TTAG (0.11%)	CTAA (0.11%)	TAGA (0.08%)	CTAA (0.10%)	CTAT (0.11%)	CTAT (0.09%)	GAGG (0.13%)	ACCT (0.13%)	CGGA (0.10%)
-5	GGAC (0.10%)	GGAC (0.10%)	GGAC (0.08%)	TAGA (0.09%)	TAGA (0.10%)	CGAG (0.08%)	CTAA (0.13%)	CCCT (0.11%)	ACTA (0.09%)
-4	TAGA (0.07%)	TAGG (0.07%)	TCTA (0.08%)	CCCT (0.09%)	CCCT (0.08%)	TAGG (0.07%)	TAGA (0.09%)	TAGG (0.09%)	TAGG (0.07%)
-3	CCTA (0.06%)	TAGA (0.06%)	TAGG (0.07%)	CCTA (0.07%)	TAGG (0.08%)	CCCT (0.07%)	CCTA (0.07%)	TAGA (0.09%)	TAGA (0.06%)
-2	TAGG (0.05%)	CCTA (0.06%)	CCTA (0.05%)	TAGG (0.05%)	CCTA (0.06%)	CCTA (0.05%)	TAGG (0.06%)	CCTA (0.09%)	CCTA (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 (0.02%)

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%)	CAGCA (0.37%)	GAAAA (0.44%)	CAGCA (0.40%)	CAGCA (0.41%)	CAGCA (0.52%)	CAGCA (0.40%)	CTGGC (0.41%)	CAGCA (0.45%)
2	TTATC (0.32%)	CTGGC (0.34%)	CAGCA (0.40%)	CATCA (0.33%)	CTGGC (0.39%)	GAAAA (0.37%)	TGGCA (0.33%)	CAGCA (0.34%)	TGGCA (0.43%)
3	CTGGC (0.31%)	TTGGC (0.33%)	CAAAA (0.39%)	GCTGC (0.33%)	CCAGC (0.35%)	CGGCA (0.37%)	CGCCA (0.32%)	GCCAG (0.31%)	CGGCA (0.41%)
4	GAAAA (0.30%)	TTTGC (0.33%)	GCAAA (0.34%)	CTGGC (0.32%)	GCGGC (0.33%)	ATAAA (0.34%)	CTGGC (0.31%)	CCAGC (0.31%)	GAAAA (0.35%)
5	CAAAA (0.29%)	TTTCC (0.32%)	TGCCA (0.31%)	CCAGC (0.32%)	GCTGC (0.31%)	CATCA (0.33%)	TGGCG (0.30%)	TGGCG (0.30%)	GCGTT (0.34%)
6	ATTTT (0.29%)	GCTGC (0.30%)	AGAAA (0.31%)	TTATC (0.29%)	AATCA (0.31%)	CAGAA (0.33%)	CGGCA (0.29%)	GCAGC (0.30%)	GCAAA (0.30%)
7	TTTTT (0.28%)	GAAAA (0.30%)	TCTTC (0.31%)	TTTTT (0.28%)	CATCA (0.31%)	TTACC (0.32%)	CCAGC (0.28%)	CGCCA (0.28%)	TGGCG (0.30%)
8	GCAAA (0.28%)	GCAGC (0.30%)	TTTTT (0.31%)	GCCAG (0.28%)	GCAGC (0.31%)	AAGAA (0.32%)	CATCA (0.27%)	GCGGC (0.28%)	TGCA (0.29%)
9	TGGCG (0.28%)	CGCCA (0.29%)	CGTTT (0.30%)	TTGCC (0.28%)	TTTTG (0.30%)	GCAAA (0.32%)	GCCAG (0.27%)	GCTGC (0.27%)	AGGAA (0.29%)
10	CGCCA (0.28%)	TTTCA (0.29%)	TTTGC (0.30%)	GATGC (0.28%)	ATAAA (0.29%)	ACAAA (0.31%)	CTGCA (0.27%)	CAGGC (0.27%)	AAGAA (0.28%)
-10	GGACC (0.01%)	GGACC (0.01%)	TACTA (0.01%)	CTTAG (0.01%)	CCCTT (0.01%)	CCCTA (0.01%)	CCCTA (0.01%)	TCCTA (0.01%)	TTAGA (0.01%)
-9	CTTAG (0.01%)	CCCTA (0.01%)	CCCTA (0.01%)	CCCTA (0.01%)	CTAGC (0.01%)	ACCTA (0.01%)	GGACC (0.01%)	TAGGA (0.01%)	CTAGT (0.01%)
-8	CTAGC (0.01%)	GCTAG (0.00%)	GCTAG (0.00%)	CTAGC (0.01%)	CCCCC (0.01%)	GCTAG (0.00%)	GCTAG (0.01%)	GCTAG (0.01%)	TCCTA (0.01%)
-7	CTAGT (0.00%)	ACTAG (0.00%)	ACTAG (0.00%)	GCTAG (0.01%)	GCTAG (0.00%)	CTAGC (0.00%)	CCTAG (0.01%)	CTAGC (0.01%)	GCTAG (0.01%)
-6	GCTAG (0.00%)	CCTAG (0.00%)	CTAGC (0.00%)	CTAGT (0.01%)	ACTAG (0.00%)	CTAGT (0.00%)	CTAGC (0.00%)	ACTAG (0.01%)	ACTAG (0.00%)
-5	ACTAG (0.00%)	CTAGG (0.00%)	CTAGG (0.00%)	CTAGA (0.00%)	CTAGT (0.00%)	CTAGA (0.00%)	TAGA (0.00%)	CTAGT (0.00%)	TCTAG (0.00%)
-4	CTAGG (0.00%)	CTAGT (0.00%)	CTAGT (0.00%)	ACTAG (0.00%)	TCTAG (0.00%)	CTAGG (0.00%)	TCTAG (0.00%)	TCTAG (0.00%)	CCTAG (0.00%)
-3	CTAGA (0.00%)	CTAGC (0.00%)	CTAGA (0.00%)	CTAGG (0.00%)	CTAGG (0.00%)	TCTAG (0.00%)	ACTAG (0.00%)	CCTAG (0.00%)	CTAGC (0.00%)
-2	TCTAG (0.00%)	TCTAG (0.00%)	CCTAG (0.00%)	CCTAG (0.00%)	CTAGA (0.00%)	ACTAG (0.00%)	CTAGT (0.00%)	CTAGA (0.00%)	CTAGC (0.00%)
-1	CCTAG (0.00%)	CTAGA (0.00%)	TCTAG (0.00%)	TCTAG (0.00%)	CCTAG (0.00%)	CCTAG (0.00%)	CTAGG (0.00%)	CTAGG (0.00%)	CTAGA (0.00%)

Most common

Least common

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