

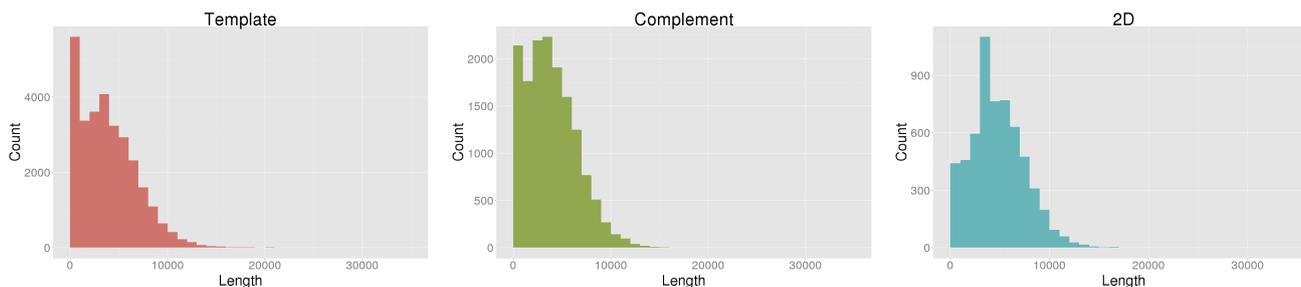
NanoOK report for MARC_1b_042915

Pass and fail counts

Type	Pass	Fail
Template	0	29550
Complement	0	14966
2D	0	5960

Read lengths

Type	NumReads	TotalBases	Mean	Longest	Shortest	N50	N50Count	N90	N90Count
Template	29550	117943730	3991.33	295420	5	5854	7094	2584	18650
Complement	14966	58851294	3932.33	41615	15	5425	3979	2515	10088
2D	5960	28634223	4804.40	76264	138	6109	1765	3140	4332



Template alignments

Number of reads	29550
Number of reads with alignments	13684 (46.31%)
Number of reads without alignments	15866 (53.69%)

ID	Size	Number of Reads	% of Reads	Mean read length	Aligned bases	Mean coverage	Longest Perf Kmer
Control sequence	3560	1133	3.83	2973.57	3212602	902.42	62
Escherichia coli	4641652	12551	42.47	5383.80	61822318	13.32	79

Complement alignments

Number of reads	14966
Number of reads with alignments	7866 (52.56%)
Number of reads without alignments	7100 (47.44%)

ID	Size	Number of Reads	% of Reads	Mean read length	Aligned bases	Mean coverage	Longest Perf Kmer
Control sequence	3560	640	4.28	2751.20	1510945	424.42	46
Escherichia coli	4641652	7226	48.28	4911.21	31607063	6.81	68

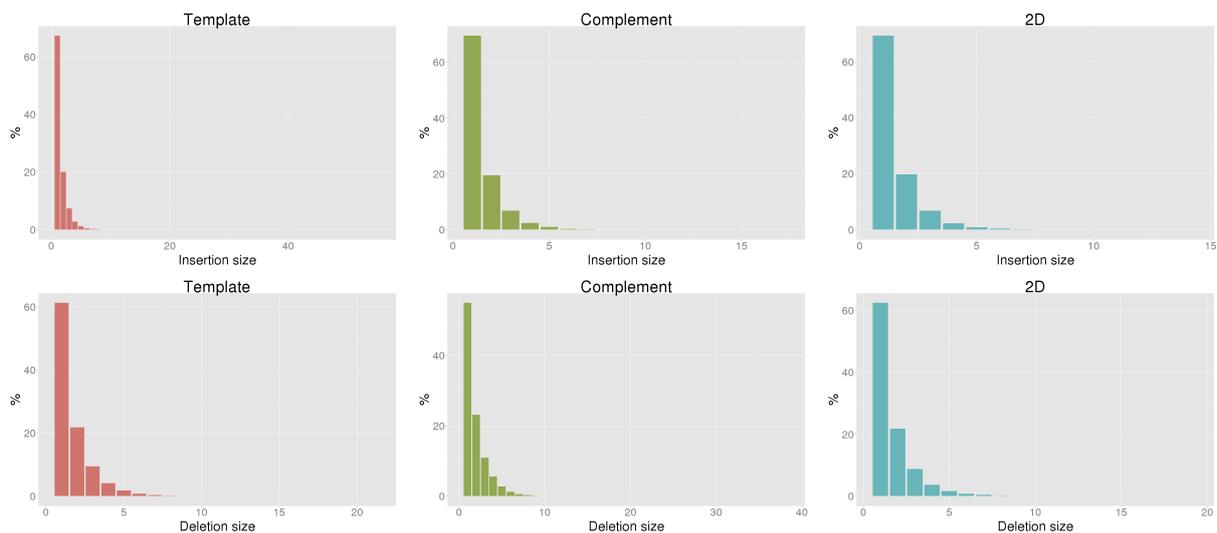
2D alignments

Number of reads	5960
Number of reads with alignments	4938 (82.85%)
Number of reads without alignments	1022 (17.15%)

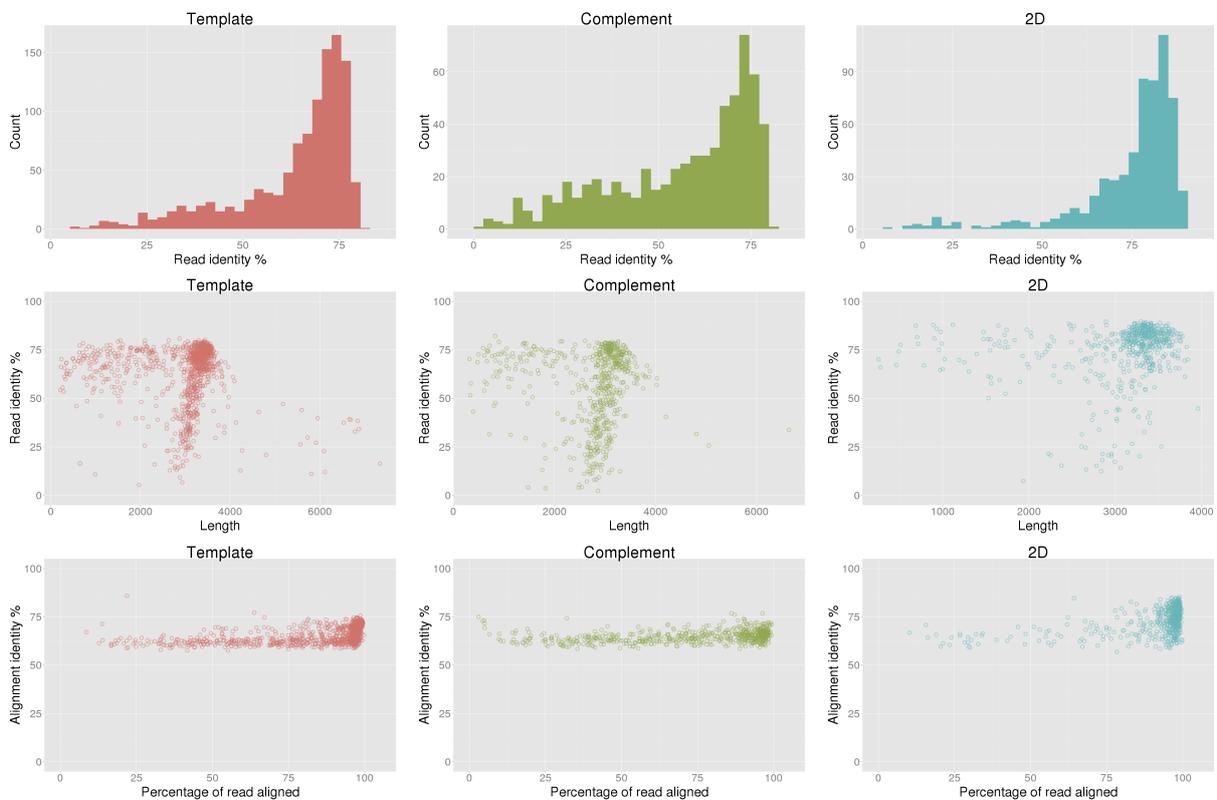
ID	Size	Number of Reads	% of Reads	Mean read length	Aligned bases	Mean coverage	Longest Perf Kmer
Control sequence	3560	610	10.23	3094.86	1916874	538.45	129
Escherichia coli	4641652	4328	72.62	5484.88	24276937	5.23	207

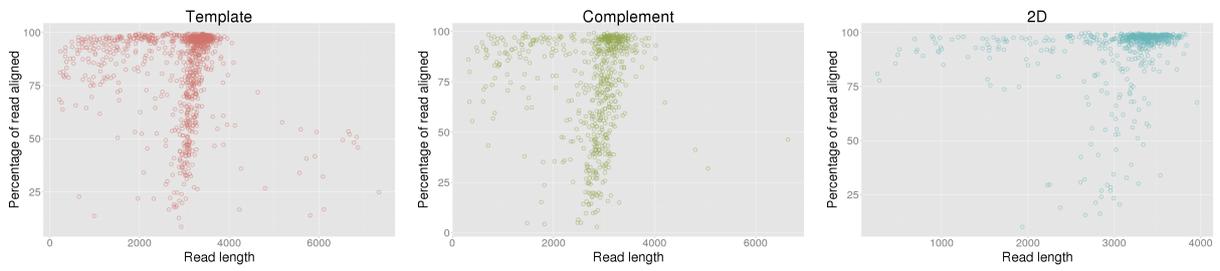
Control sequence error analysis

	Template	Complement	2D
Overall base identity (excluding indels)	62.86%	55.74%	75.17%
Aligned base identity (excluding indels)	78.88%	80.22%	86.00%
Identical bases per 100 aligned bases (including indels)	65.92%	64.96%	74.03%
Inserted bases per 100 aligned bases (including indels)	4.88%	3.73%	4.34%
Deleted bases per 100 aligned bases (including indels)	11.55%	15.29%	9.58%
Substitutions per 100 aligned bases (including indels)	17.65%	16.02%	12.05%
Mean insertion size	1.55	1.48	1.48
Mean deletion size	1.69	1.89	1.66

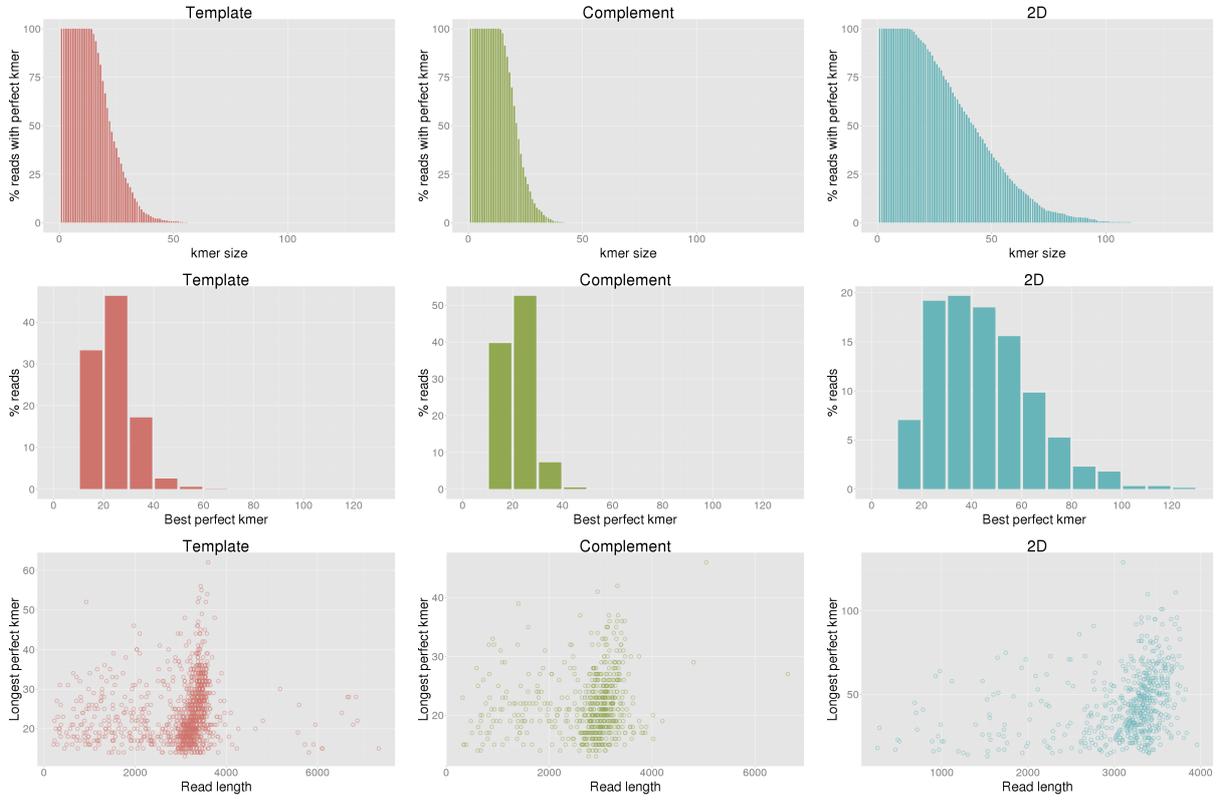


Control sequence read identity

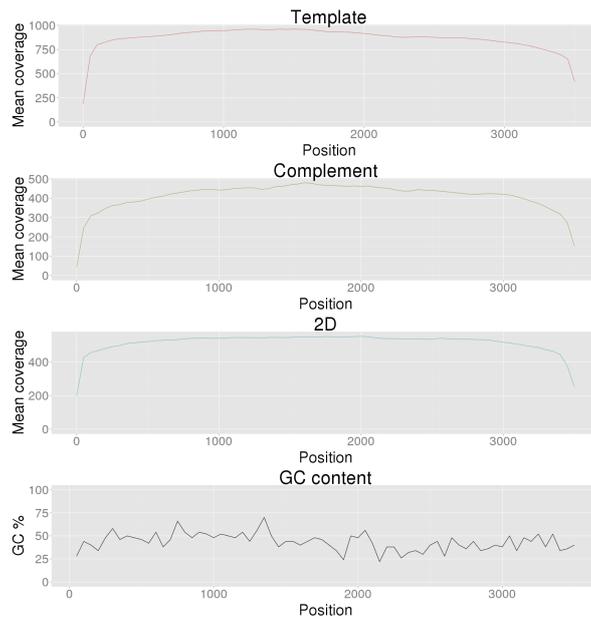




Control sequence perfect kmers



Control sequence coverage



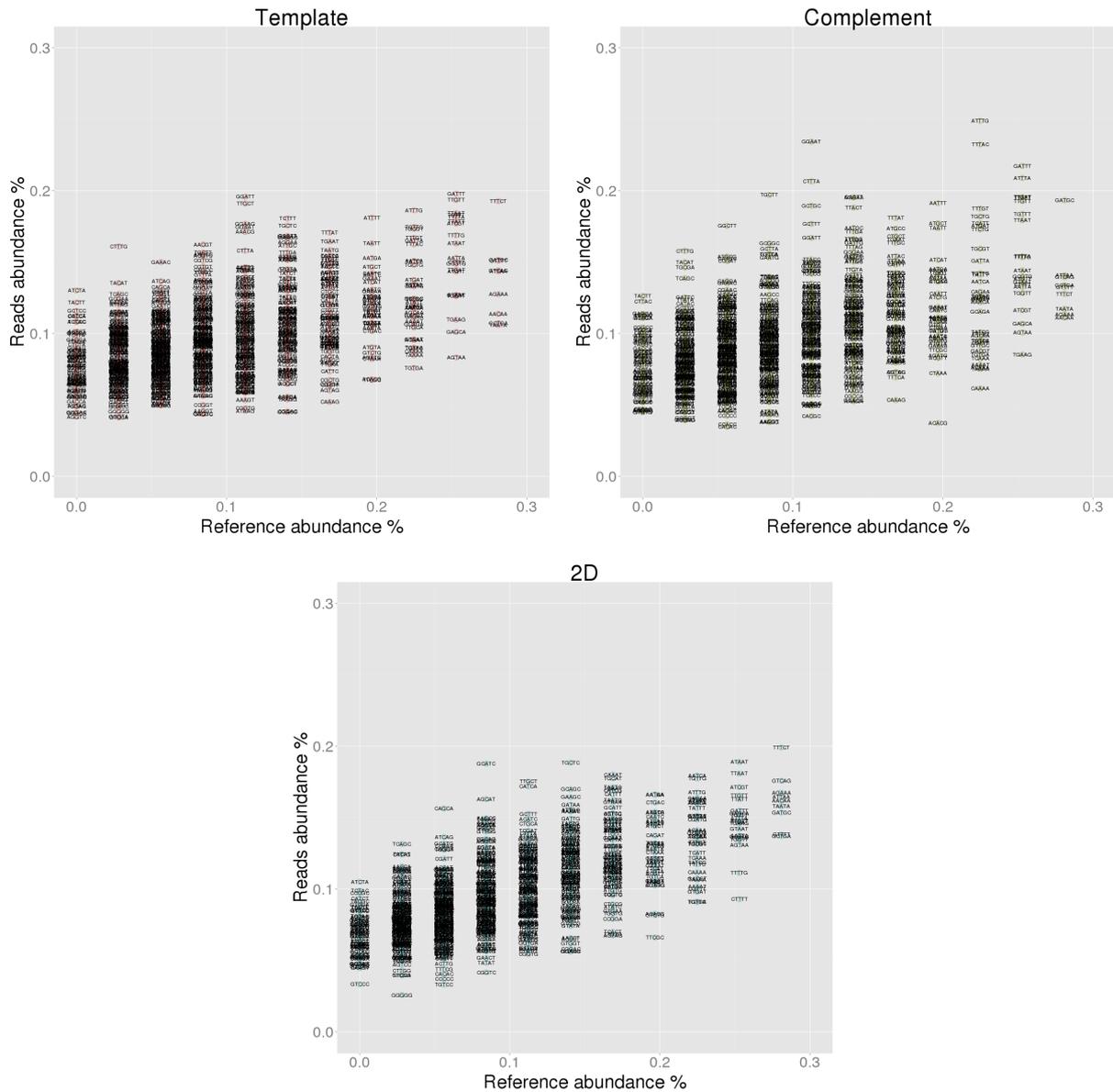
Control sequence 5-mer analysis

Under-represented 5-mers

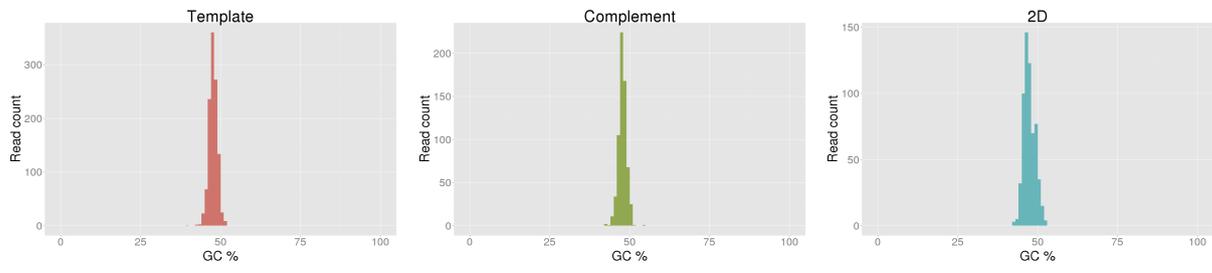
Rank	Template				Complement				2D			
	kmer	Ref %	Read %	Diff %	kmer	Ref %	Read %	Diff %	kmer	Ref %	Read %	Diff %
1	TTTTT	0.759	0.116	-0.643	TTTTT	0.759	0.070	-0.689	TTTTT	0.759	0.040	-0.719
2	AAAAA	0.478	0.081	-0.397	AAAAA	0.478	0.037	-0.440	AAAAA	0.478	0.047	-0.431
3	TGATG	0.393	0.127	-0.266	AAAAC	0.337	0.107	-0.230	TGATG	0.393	0.154	-0.239
4	AAAAC	0.337	0.115	-0.222	GATGT	0.309	0.107	-0.202	AAAAC	0.337	0.137	-0.200
5	GATGT	0.309	0.094	-0.215	TGATG	0.393	0.206	-0.187	GATGT	0.309	0.121	-0.188
6	CTGAT	0.309	0.102	-0.207	GCAAT	0.309	0.126	-0.184	CTGAT	0.309	0.139	-0.171
7	GCAAT	0.309	0.120	-0.189	AATAT	0.309	0.127	-0.182	GCAAT	0.309	0.147	-0.162
8	AATAT	0.309	0.122	-0.187	TTATC	0.309	0.128	-0.181	TTATC	0.309	0.147	-0.162
9	TAATA	0.281	0.106	-0.175	AACAA	0.281	0.111	-0.170	CTTTT	0.253	0.093	-0.160
10	GCTGA	0.281	0.107	-0.174	TGAAG	0.253	0.085	-0.168	TGATT	0.309	0.159	-0.150

Over-represented 5-mers

Rank	Template				Complement				2D			
	kmer	Ref %	Read %	Diff %	kmer	Ref %	Read %	Diff %	kmer	Ref %	Read %	Diff %
1	CTTTG	0.028	0.161	0.133	CTTTG	0.028	0.158	0.130	ATCTA	0.000	0.105	0.105
2	ATCTA	0.000	0.130	0.130	TACTT	0.000	0.126	0.126	GCATC	0.084	0.188	0.104
3	TACTT	0.000	0.122	0.122	CTTAC	0.000	0.123	0.123	TCAGC	0.028	0.132	0.103
4	GCTCC	0.000	0.116	0.116	GGAAT	0.112	0.234	0.122	CAGCA	0.056	0.156	0.100
5	CATCT	0.000	0.112	0.112	TACAT	0.028	0.150	0.122	TCTAC	0.000	0.099	0.099
6	CCCCA	0.000	0.112	0.112	GGCTT	0.056	0.176	0.119	CCCGC	0.000	0.097	0.097
7	ACCCC	0.000	0.108	0.108	TGCGA	0.028	0.146	0.118	TACAT	0.028	0.124	0.096
8	TCTAC	0.000	0.108	0.108	GAGGA	0.000	0.114	0.114	CTTTG	0.028	0.124	0.096
9	TACAT	0.028	0.135	0.107	ACCCC	0.000	0.113	0.113	CATCT	0.000	0.093	0.093
10	ACTCT	0.000	0.101	0.101	TGCTT	0.084	0.197	0.113	TACGC	0.000	0.091	0.091

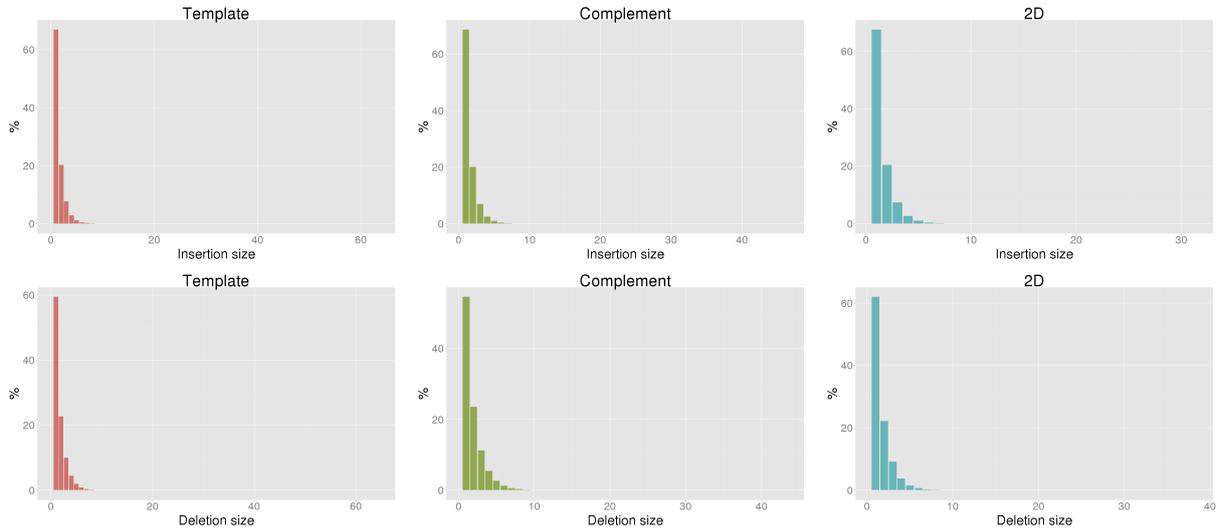


Control sequence GC content

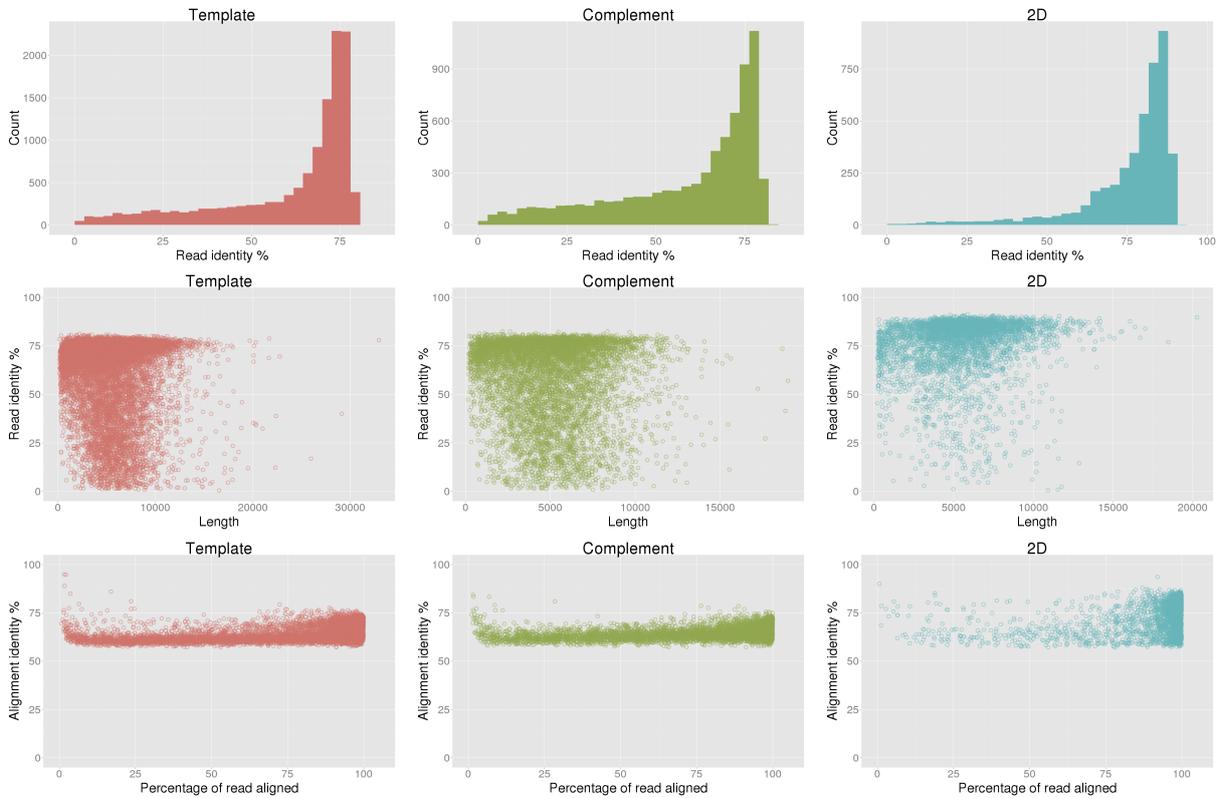


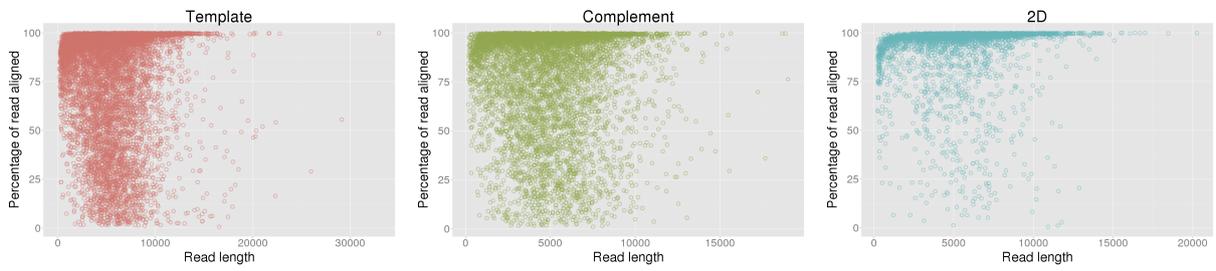
Escherichia coli error analysis

	Template	Complement	2D
Overall base identity (excluding indels)	60.08%	57.69%	76.65%
Aligned base identity (excluding indels)	79.01%	80.11%	86.55%
Identical bases per 100 aligned bases (including indels)	65.66%	64.78%	74.95%
Inserted bases per 100 aligned bases (including indels)	4.90%	3.94%	4.65%
Deleted bases per 100 aligned bases (including indels)	11.99%	15.19%	8.76%
Substitutions per 100 aligned bases (including indels)	17.45%	16.09%	11.65%
Mean insertion size	1.56	1.50	1.53
Mean deletion size	1.73	1.89	1.66

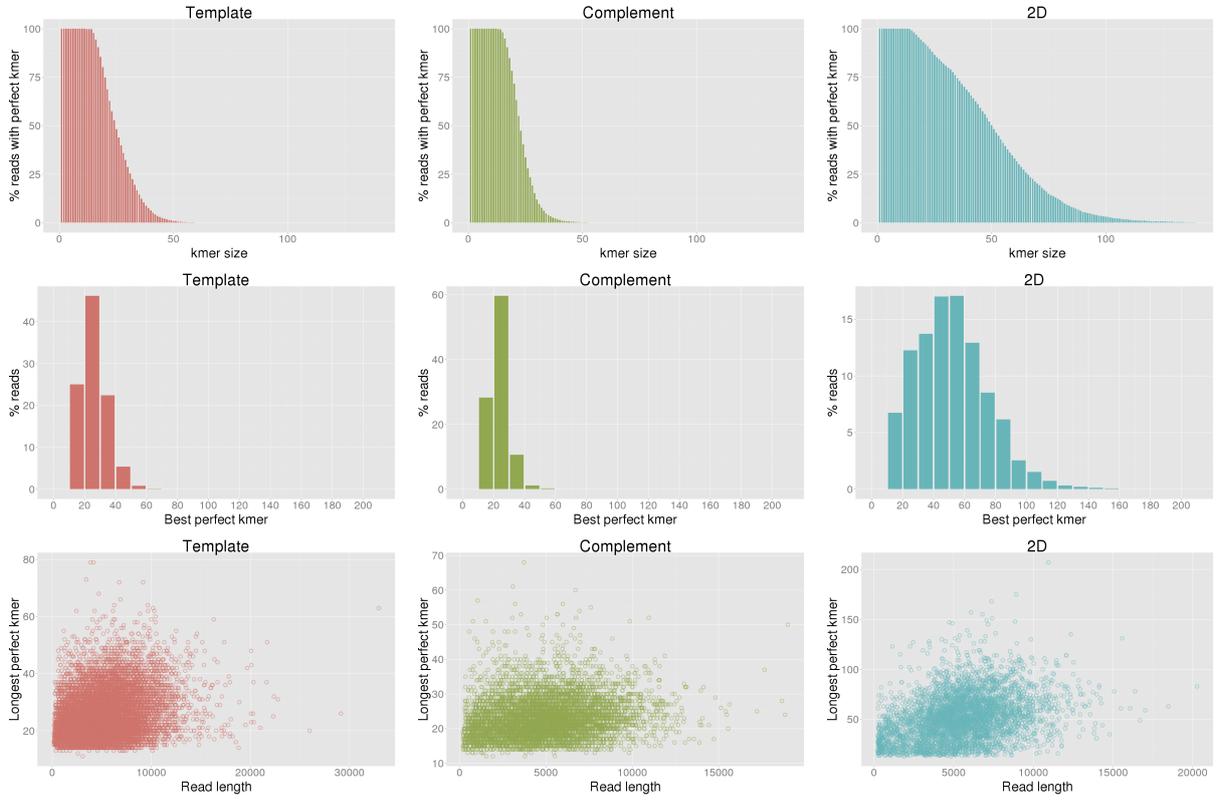


Escherichia coli read identity

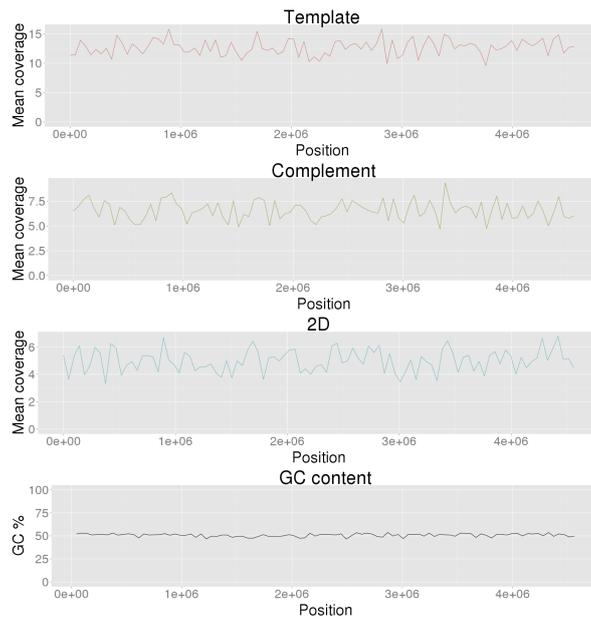




Escherichia coli perfect kmers



Escherichia coli coverage



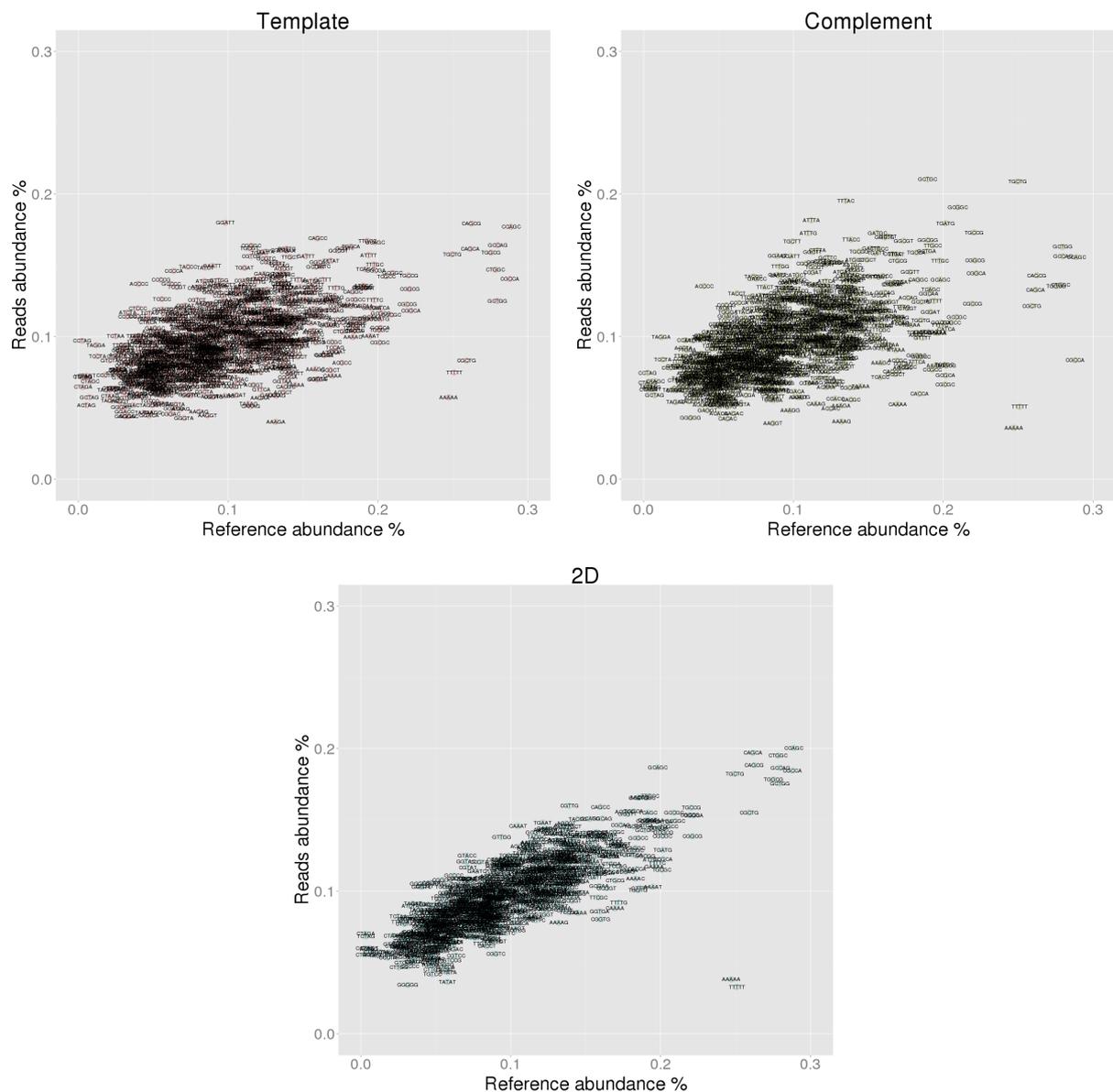
Escherichia coli 5-mer analysis

Under-represented 5-mers

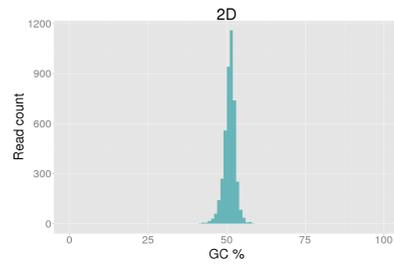
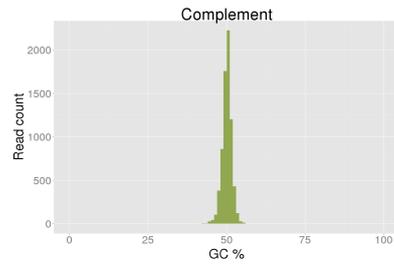
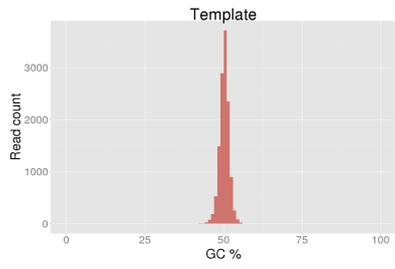
Rank	Template				Complement				2D			
	kmer	Ref %	Read %	Diff %	kmer	Ref %	Read %	Diff %	kmer	Ref %	Read %	Diff %
1	AAAAA	0.247	0.058	-0.190	AAAAA	0.247	0.036	-0.211	TTTTT	0.251	0.033	-0.218
2	TTTTT	0.251	0.075	-0.176	CGCCA	0.288	0.084	-0.204	AAAAA	0.247	0.038	-0.209
3	CGCTG	0.259	0.083	-0.176	TTTTT	0.251	0.051	-0.200	CGCTG	0.259	0.155	-0.104
4	GCTGG	0.279	0.125	-0.155	CTGGC	0.278	0.136	-0.142	GCTGG	0.279	0.176	-0.104
5	CGCCA	0.288	0.140	-0.148	TGGCG	0.275	0.135	-0.140	CGCCA	0.288	0.185	-0.103
6	CTGGC	0.278	0.147	-0.131	CGCTG	0.259	0.122	-0.137	TGGCG	0.275	0.178	-0.097
7	TGGCG	0.275	0.159	-0.116	CGCGC	0.201	0.067	-0.135	GCCAG	0.280	0.187	-0.093
8	GCCAG	0.280	0.164	-0.116	CCAGC	0.289	0.156	-0.133	AAAAT	0.195	0.103	-0.092
9	CCAGC	0.289	0.177	-0.112	GCGCA	0.202	0.073	-0.129	CCAGC	0.289	0.200	-0.088
10	CGCGC	0.201	0.096	-0.105	CAGCA	0.261	0.133	-0.129	TGCGC	0.201	0.115	-0.086

Over-represented 5-mers

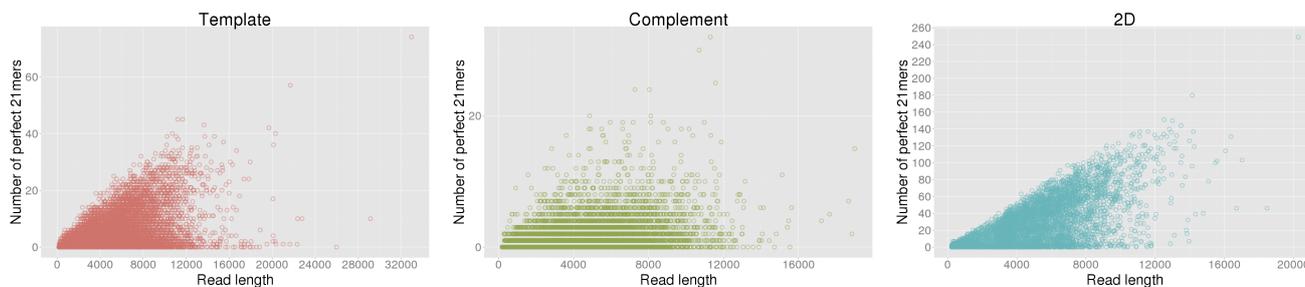
Rank	Template				Complement				2D			
	kmer	Ref %	Read %	Diff %	kmer	Ref %	Read %	Diff %	kmer	Ref %	Read %	Diff %
1	ACCCC	0.040	0.137	0.097	ACCCC	0.040	0.136	0.095	CTAGA	0.003	0.070	0.067
2	CCTAG	0.003	0.097	0.094	TAGGA	0.012	0.100	0.088	GGGTT	0.039	0.105	0.066
3	CCCCG	0.055	0.140	0.085	CCTAG	0.003	0.075	0.072	TCTAG	0.003	0.068	0.065
4	ATCTA	0.033	0.117	0.084	TCCTA	0.013	0.084	0.071	GGGTC	0.040	0.103	0.063
5	CCCCA	0.064	0.146	0.083	ATTTA	0.112	0.182	0.070	CTCGT	0.042	0.104	0.061
6	TAGGA	0.012	0.094	0.082	CCTAT	0.028	0.098	0.070	CCCAA	0.047	0.106	0.059
7	GGATT	0.098	0.180	0.082	TACCC	0.073	0.142	0.069	TCTAA	0.025	0.082	0.057
8	CCCCC	0.033	0.114	0.081	TACCT	0.062	0.130	0.068	CCTAG	0.003	0.060	0.057
9	CTCCC	0.040	0.120	0.080	TGCTT	0.099	0.167	0.068	ATCTA	0.033	0.090	0.057
10	TACCC	0.073	0.149	0.076	GGAAT	0.089	0.157	0.067	TAGAT	0.035	0.091	0.057



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	8.96	8.87	5.06	0.00	9.04	8.56	5.28	0.00	9.54	8.71	4.66
C	8.59	0.00	8.88	9.91	9.03	0.00	8.57	9.77	8.42	0.00	10.09	8.72
G	9.61	8.94	0.00	8.29	9.07	8.72	0.00	8.71	8.75	10.31	0.00	8.08
T	5.31	8.87	8.72	0.00	5.57	8.64	9.03	0.00	4.75	8.64	9.33	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 (3.24%)	TTC (3.24%)	AAA (4.01%)	TGC (2.83%)	AAA (2.89%)	AAA (3.98%)	GCA (3.17%)	AAA (2.74%)	GCA (3.69%)
2	AAA (2.80%)	TGC (3.00%)	TTC (3.59%)	GCA (2.81%)	GGC (2.80%)	GCA (3.55%)	AAA (2.82%)	GGC (2.68%)	AAA (3.67%)
3	GCA (2.78%)	AAA (2.84%)	GCA (3.26%)	TTC (2.78%)	TGC (2.80%)	GAA (3.26%)	TTC (2.64%)	GCA (2.63%)	GAA (3.00%)
4	TGC (2.59%)	GCA (2.73%)	GAA (2.90%)	AAA (2.65%)	GCA (2.72%)	TTC (3.07%)	TCA (2.52%)	TGC (2.61%)	TTT (2.87%)
5	ATC (2.56%)	GCC (2.54%)	TTT (2.71%)	CAG (2.49%)	TTC (2.58%)	TTT (2.69%)	GAA (2.39%)	GAA (2.35%)	GTT (2.68%)
6	TCA (2.38%)	GGC (2.40%)	TGC (2.60%)	GAA (2.40%)	GAA (2.57%)	TGC (2.47%)	GCG (2.28%)	GCG (2.35%)	TTC (2.64%)
7	GAA (2.26%)	TCA (2.28%)	AAT (2.43%)	TCA (2.32%)	CAG (2.36%)	TCA (2.29%)	TGC (2.26%)	TCA (2.30%)	AAT (2.46%)
8	TTT (2.24%)	ATC (2.18%)	GCC (2.24%)	GGC (2.30%)	GCC (2.24%)	AAT (2.23%)	ATC (2.24%)	CAG (2.30%)	GCC (2.23%)
9	GCC (2.23%)	GAA (2.18%)	CAA (2.15%)	ATC (2.24%)	TCA (2.21%)	CAA (2.16%)	AAT (2.19%)	TTC (2.23%)	TCA (2.14%)
10	GGC (2.17%)	AAT (2.15%)	ATC (2.15%)	AAT (2.18%)	AAT (2.18%)	ATC (2.15%)	CAG (2.17%)	GCC (2.22%)	TGC (2.10%)
-10	AGT (0.96%)	AGG (0.99%)	GGT (0.93%)	AGT (0.98%)	AGT (0.96%)	CCC (0.89%)	TAC (1.03%)	GTA (1.04%)	TGA (1.01%)
-9	CTC (0.93%)	AGT (0.90%)	GGG (0.89%)	AGA (0.97%)	ACT (0.95%)	AGT (0.89%)	CTT (1.00%)	CCC (1.03%)	CCT (0.99%)
-8	GGA (0.92%)	CCT (0.89%)	AGA (0.87%)	GGA (0.93%)	CTT (0.95%)	CCT (0.86%)	GGA (0.92%)	CGA (0.93%)	ACT (0.95%)
-7	CCC (0.90%)	GAG (0.88%)	AGG (0.86%)	CTC (0.83%)	CCC (0.94%)	AGG (0.85%)	GAG (0.92%)	AGA (0.90%)	GAG (0.90%)
-6	AGA (0.84%)	CTT (0.86%)	TGT (0.84%)	CCC (0.81%)	CCT (0.88%)	CTC (0.84%)	AGA (0.88%)	ACT (0.88%)	CGA (0.82%)
-5	GAG (0.73%)	CGA (0.84%)	CTT (0.79%)	AGG (0.75%)	GAG (0.86%)	ACT (0.79%)	AGG (0.83%)	CTT (0.86%)	CTT (0.80%)
-4	GGG (0.71%)	AGA (0.73%)	AGT (0.77%)	GAG (0.74%)	CTC (0.83%)	GGG (0.76%)	CCC (0.78%)	CCT (0.82%)	AGA (0.72%)
-3	AGG (0.70%)	GGA (0.72%)	GAG (0.63%)	GGG (0.59%)	GGG (0.78%)	GAG (0.61%)	GGG (0.73%)	GGA (0.79%)	GGA (0.68%)
-2	CTA (0.51%)	TAG (0.54%)	TAG (0.40%)	CTA (0.52%)	TAG (0.54%)	TAG (0.40%)	CTA (0.63%)	TAG (0.69%)	TAG (0.52%)
-1	TAG (0.43%)	CTA (0.49%)	CTA (0.36%)	TAG (0.43%)	CTA (0.50%)	CTA (0.39%)	TAG (0.53%)	CTA (0.66%)	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 (1.06%)	TTTC (1.10%)	TTTC (1.31%)	CAGC (0.89%)	TGGC (1.03%)	AAAA (1.03%)	GGCA (0.87%)	TGGC (1.04%)	GGCA (1.23%)
2	GAAA (0.89%)	TGCC (0.97%)	AAAA (1.29%)	ATCA (0.86%)	CAGC (1.00%)	CAAA (1.03%)	ATCA (0.87%)	CAGC (0.92%)	AAAA (1.02%)
3	AAAA (0.86%)	TGCC (0.93%)	GAAA (1.10%)	CTGC (0.86%)	CGGC (0.99%)	GAAA (0.96%)	GCCA (0.83%)	CTGC (0.81%)	GGAA (0.97%)
4	TTCA (0.82%)	TTGC (0.92%)	GGCA (0.97%)	TGGC (0.85%)	CTGC (0.89%)	GGCA (0.94%)	AACA (0.82%)	TTCA (0.80%)	GAAA (0.97%)
5	ATCA (0.81%)	CAGC (0.90%)	TTTT (0.91%)	CCAG (0.81%)	CAAA (0.87%)	AGCA (0.94%)	TTTT (0.79%)	CAAA (0.80%)	CGTT (0.90%)
6	TGCC (0.81%)	CTGC (0.87%)	GCAA (0.91%)	TTGC (0.80%)	TTGC (0.86%)	TGAA (0.93%)	CAAA (0.79%)	CGGC (0.79%)	TGCA (0.90%)
7	TGCG (0.80%)	TTCC (0.87%)	GGAA (0.88%)	CAAA (0.78%)	TTCC (0.82%)	TTTT (0.93%)	GAAA (0.79%)	TGCC (0.77%)	CAAA (0.88%)
8	GGCA (0.78%)	TTCA (0.86%)	CAAA (0.88%)	CGGC (0.74%)	TGCC (0.80%)	GGAA (0.87%)	TGGC (0.76%)	GGAA (0.75%)	TTTT (0.88%)
9	TTGC (0.78%)	AAAA (0.83%)	AAAT (0.87%)	TTCA (0.74%)	CCAG (0.78%)	ATCA (0.86%)	TTCA (0.76%)	CCAG (0.74%)	TGTT (0.87%)
10	CAGC (0.77%)	GAAA (0.81%)	TGCC (0.86%)	GGCA (0.74%)	ATCA (0.77%)	TAAA (0.85%)	TGCA (0.76%)	GGCA (0.73%)	TTTT (0.82%)
-10	TCTA (0.12%)	CCCT (0.12%)	CTAT (0.11%)	GGGG (0.12%)	ACCT (0.11%)	TAGA (0.11%)	TCTA (0.15%)	ACTA (0.15%)	TATA (0.13%)
-9	CTAA (0.12%)	CTAT (0.12%)	CGAG (0.10%)	GTGT (0.11%)	ACTA (0.11%)	TCTA (0.10%)	CCCC (0.14%)	CGGA (0.15%)	CCCT (0.11%)
-8	TTAG (0.11%)	CGGA (0.12%)	TAGT (0.09%)	CGAG (0.11%)	TAGA (0.11%)	ACTA (0.10%)	CTAA (0.14%)	CTAA (0.14%)	CGGA (0.11%)
-7	TAGT (0.11%)	GGAC (0.11%)	TAGA (0.09%)	GGAC (0.10%)	CTAT (0.11%)	CTAT (0.10%)	GGAC (0.14%)	ACCT (0.14%)	ACCT (0.11%)
-6	GAGC (0.10%)	TAGT (0.11%)	ACTA (0.09%)	TAGA (0.10%)	CTAA (0.11%)	GGAC (0.09%)	ACTA (0.14%)	ACCT (0.13%)	TCTA (0.11%)
-5	GGAC (0.09%)	CTAA (0.10%)	TCTA (0.08%)	GAGG (0.10%)	CCCC (0.10%)	CGAG (0.09%)	CCCT (0.13%)	CCCT (0.11%)	ACTA (0.10%)
-4	TAGA (0.07%)	TAGG (0.08%)	GGAC (0.08%)	CCCT (0.10%)	CCCT (0.09%)	CCCT (0.07%)	TAGA (0.10%)	TAGG (0.10%)	TAGG (0.08%)
-3	CCTA (0.07%)	TAGA (0.06%)	TAGG (0.07%)	CCTA (0.06%)	TAGG (0.07%)	TAGG (0.06%)	CCTA (0.09%)	TAGA (0.10%)	TAGA (0.07%)
-2	TAGG (0.05%)	CCTA (0.05%)	CCTA (0.05%)	TAGG (0.06%)	CCTA (0.06%)	CCTA (0.05%)	TAGG (0.06%)	CCTA (0.08%)	CCTA (0.06%)
-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%)

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 (0.38%)	GAAAA (0.43%)	CAGCA (0.43%)	CAGCA (0.42%)	CAGCA (0.54%)	CAGCA (0.39%)	CTGGC (0.44%)	TGGCA (0.47%)
2	TTATC (0.33%)	CAGCA (0.34%)	CAGCA (0.40%)	CATCA (0.32%)	CTGGC (0.41%)	CGGCA (0.37%)	CGCCA (0.36%)	CAGCA (0.32%)	CAGCA (0.43%)
3	CTGGC (0.32%)	TTGCC (0.34%)	CAAAA (0.35%)	CCAGC (0.31%)	CCAGC (0.33%)	GAAAA (0.35%)	CTGGC (0.34%)	GCGGC (0.31%)	CGGCA (0.41%)
4	ATTTT (0.31%)	TTTGC (0.33%)	TGGCA (0.34%)	GCTGC (0.31%)	GCGGC (0.33%)	CATCA (0.33%)	TGGCA (0.32%)	GCCAG (0.30%)	GAAAA (0.38%)
5	TGGCG (0.30%)	GCTGC (0.32%)	CGTTT (0.32%)	CTGGC (0.31%)	GCTGC (0.32%)	TGGCA (0.32%)	CGGCA (0.31%)	TGGCG (0.30%)	GCGTT (0.36%)
6	CATCA (0.29%)	GCAGC (0.31%)	CTGGC (0.32%)	GCGGC (0.29%)	CATCA (0.31%)	CAGAA (0.32%)	TGGCG (0.30%)	GCAGC (0.30%)	TGGCG (0.32%)
7	CGCCA (0.29%)	CGCCA (0.31%)	CGTTC (0.32%)	CGGCA (0.29%)	TTTGC (0.30%)	ATAAA (0.32%)	GCAAA (0.29%)	CCAGC (0.29%)	GCAAA (0.30%)
8	CGTTT (0.28%)	GCCAG (0.31%)	TGTTT (0.31%)	AATCA (0.28%)	GCTGG (0.30%)	AAGAA (0.32%)	CATCA (0.28%)	CGCCA (0.28%)	TGCA (0.30%)
9	TTTCT (0.28%)	TTTCA (0.29%)	TTGCC (0.31%)	TTTTG (0.28%)	AATCA (0.30%)	AATCA (0.32%)	CTGCA (0.26%)	TGGCA (0.27%)	AGGAA (0.30%)
10	GAAAA (0.28%)	TTTCC (0.29%)	GCAAA (0.30%)	GCCAG (0.27%)	GCAGC (0.30%)	ACGCA (0.31%)	GAAAA (0.26%)	GCTGC (0.27%)	TGGAA (0.29%)
-10	CTTAG (0.01%)	GGACC (0.01%)	CCCTA (0.01%)	GGGGG (0.01%)	TAGGG (0.01%)	TAGGG (0.01%)	CCCTA (0.01%)	TAGGA (0.01%)	CCCTA (0.01%)
-9	GGACC (0.01%)	CCCTA (0.01%)	TAGGT (0.01%)	CTAGT (0.01%)	CCCCC (0.01%)	CCCCC (0.01%)	GGACC (0.01%)	TCCTA (0.01%)	TTAGA (0.01%)
-8	GCTAG (0.00%)	GCTAG (0.00%)	ACTAG (0.00%)	CCCTA (0.01%)	CTAGC (0.01%)	CCCTA (0.01%)	GCTAG (0.01%)	GCTAG (0.01%)	ACTAG (0.01%)
-7	ACTAG (0.00%)	CTAGC (0.00%)	GCTAG (0.00%)	CTAGC (0.00%)	ACTAG (0.00%)	GCTAG (0.00%)	CTAGC (0.00%)	CTAGC (0.01%)	GCTAG (0.00%)
-6	CTAGT (0.00%)	ACTAG (0.00%)	CTAGC (0.00%)	GCTAG (0.00%)	GCTAG (0.00%)	CTAGC (0.00%)	CCTAG (0.00%)	ACTAG (0.01%)	CTAGC (0.00%)
-5	CTAGG (0.00%)	CTAGT (0.00%)	CTAGG (0.00%)	CTAGA (0.00%)	CTAGG (0.00%)	CTAGT (0.00%)	ACTAG (0.00%)	CTAGT (0.00%)	CTAGA (0.00%)
-4	CCTAG (0.00%)	CCTAG (0.00%)	CTAGT (0.00%)	TCTAG (0.00%)	CTAGT (0.00%)	CTAGG (0.00%)	CTAGA (0.00%)	CTAGA (0.00%)	CTAGT (0.00%)
-3	CTAGC (0.00%)	TCTAG (0.00%)	CTAGA (0.00%)	ACTAG (0.00%)	CTAGA (0.00%)	ACTAG (0.00%)	CTAGT (0.00%)	CTAGG (0.00%)	CTAGG (0.00%)
-2	CTAGA (0.00%)	CTAGA (0.00%)	CCTAG (0.00%)	CTAGG (0.00%)	CCTAG (0.00%)	TCTAG (0.00%)	TCTAG (0.00%)	TCTAG (0.00%)	TCTAG (0.00%)
-1	TCTAG (0.00%)	CTAGG (0.00%)	TCTAG (0.00%)	CCTAG (0.00%)	TCTAG (0.00%)	CTAGA (0.00%)	CTAGG (0.00%)	CCTAG (0.00%)	CCTAG (0.00%)

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