NanoOK report for WTCHG_MARC_Ph1.2

Pass and fail counts

Type	Pass	Fail
Template	17673	0
Complement	17673	0
2D	17673	0

Read lengths

Type	NumReads	TotalBases	Mean	Longest	Shortest	N50	N50Count	N90	N90Count
Template	17673	42530579	2406.53	23038	162	4674	3049	1144	9381
Complement	17673	47729073	2700.68	22446	196	5214	3067	1260	9431
2D	17673	48254325	2730.40	23075	166	5324	3047	1317	9320
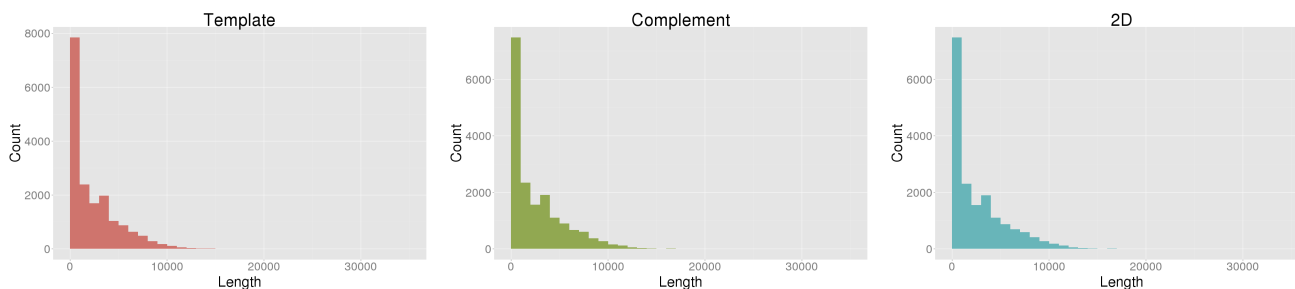
Template alignments

Number of reads	17673	
Number of reads with alignments	12895	(72.96%)
Number of reads without alignments	4778	(27.04%)

ID	Size	Number of Reads	% of Reads	Mean read length	Aligned bases	Mean coverage	Longest Perf Kmer
Control sequence	3560	903	5.11	2902.44	2693644	756.64	52
Escherichia coli	4641652	11992	67.85	3133.53	40448550	8.71	73

Complement alignments

Number of reads	17673	
Number of reads with alignments	14144	(80.03%)
Number of reads without alignments	3529	(19.97%)

ID	Size	Number of Reads	% of Reads	Mean read length	Aligned bases	Mean coverage	Longest Perf Kmer
Control sequence	3560	936	5.30	3273.20	3083307	866.10	56
Escherichia coli	4641652	13208	74.74	3246.95	44450820	9.58	54

2D alignments

Number of reads	17673	
Number of reads with alignments	17642	(99.82%)
Number of reads without alignments	31	(0.18%)

ID	Size	Number of Reads	% of Reads	Mean read length	Aligned bases	Mean coverage	Longest Perf Kmer
Control sequence	3560	951	5.38	3230.37	3155983	886.51	152
Escherichia coli	4641652	16691	94.44	2706.45	46151626	9.94	164

Control sequence error analysis

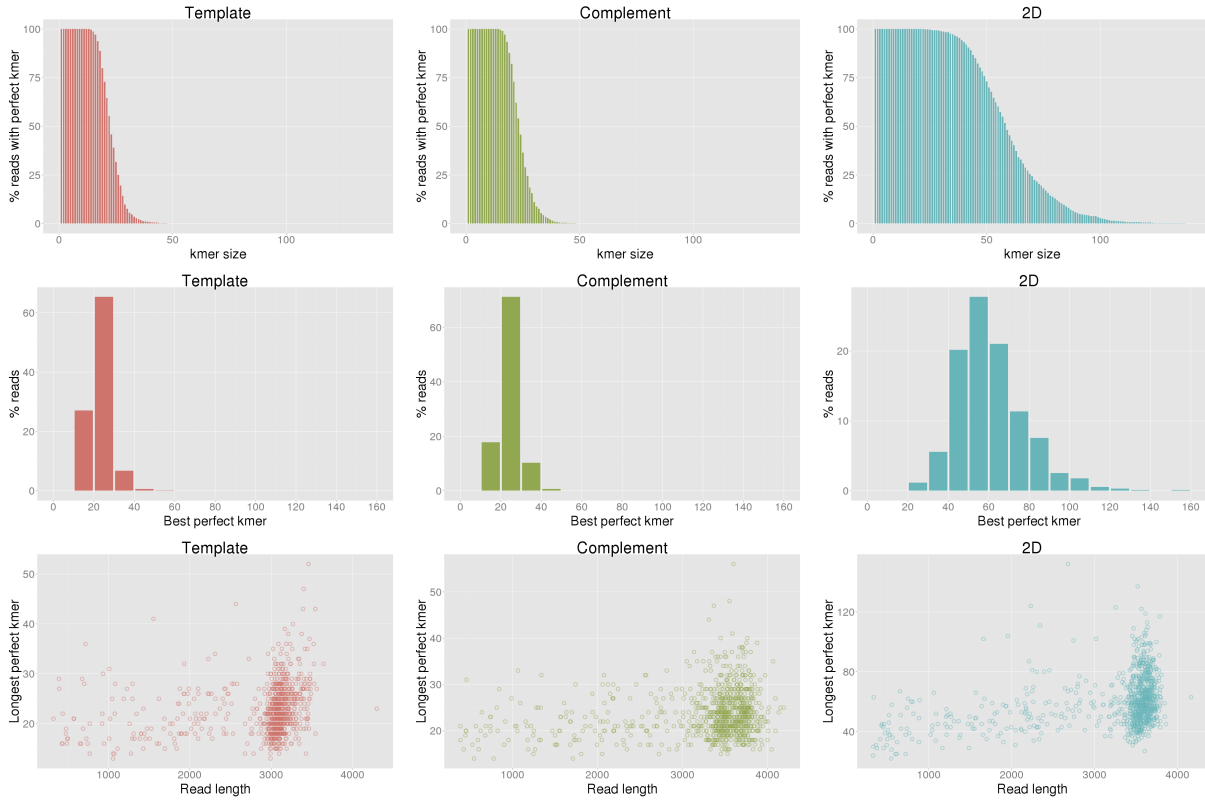|	Template	Complement	2D
Overall base identity (excluding indels)	67.34%	66.63%	83.95%
Aligned base identity (excluding indels)	79.32%	78.96%	91.02%
Identical bases per 100 aligned bases (including indels)	65.53%	66.21%	81.72%
Inserted bases per 100 aligned bases (including indels)	2.31%	7.18%	4.55%
Deleted bases per 100 aligned bases (including indels)	15.08%	8.98%	5.67%
Substitutions per 100 aligned bases (including indels)	17.09%	17.64%	8.06%
Mean insertion size	1.36	1.68	1.54
Mean deletion size	1.68	1.56	1.47
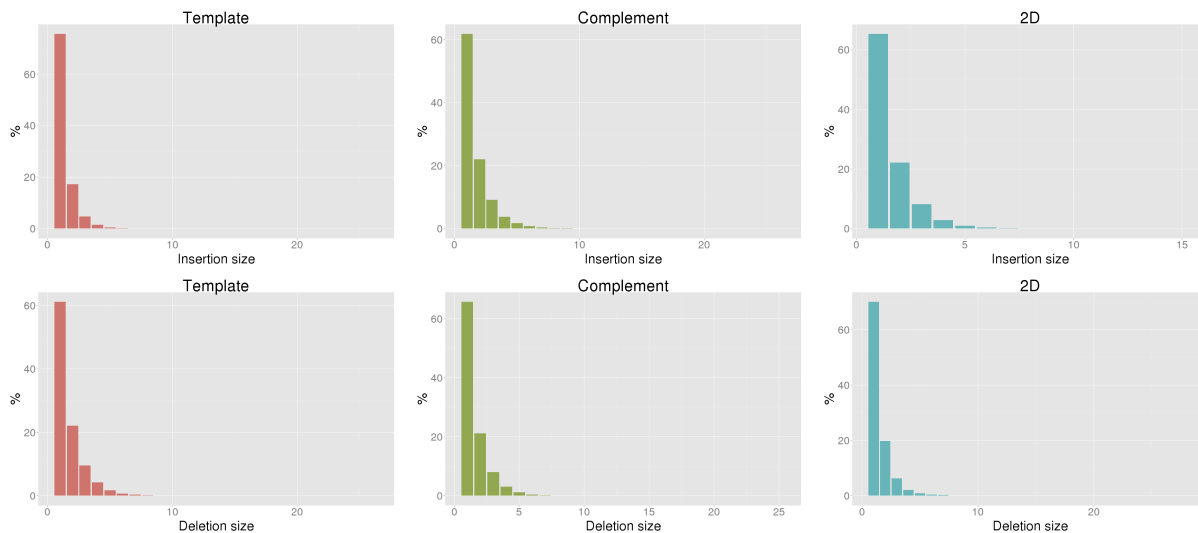
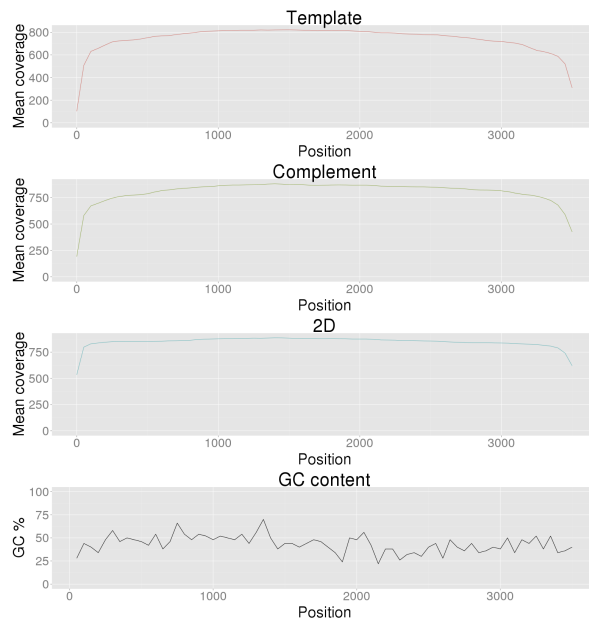# Control sequence read identity

2
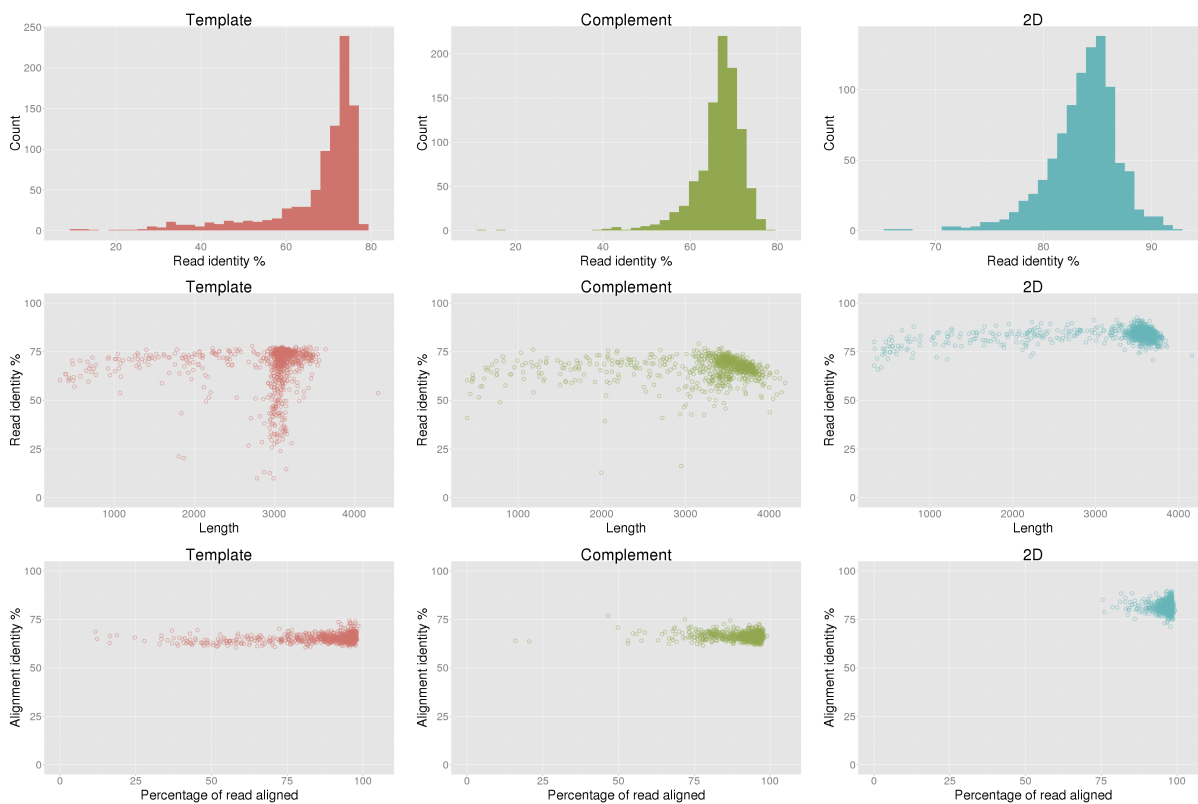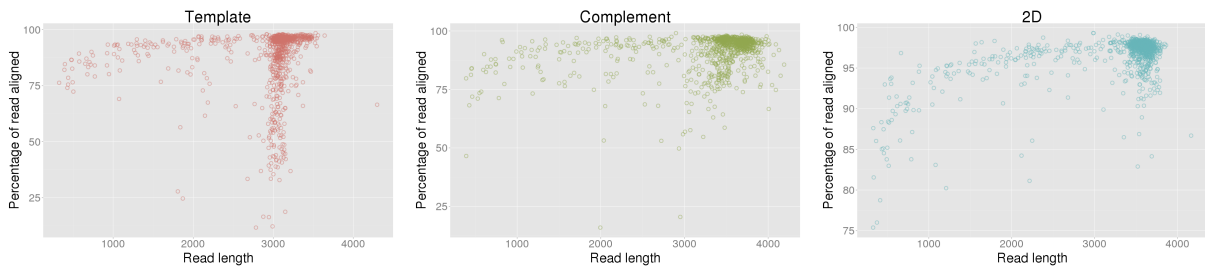
## Control sequence perfect kmers

Control sequence coverage

Control sequence 5-mer analysis

Under-represented 5-mers

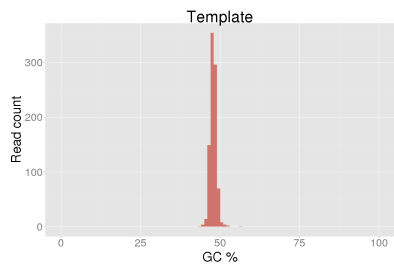| Rank	Template				Complement				2D			
	kmer	Ref %	Read %	Diff %	kmer	Ref %	Read %	Diff %	kmer	Ref %	Read %	Diff %
1	TTTTT	0.759	0.092	-0.666	TTTTT	0.759	0.166	-0.592	TTTTT	0.759	0.078	-0.681
2	AAAAA	0.478	0.066	-0.411	AAAAA	0.478	0.125	-0.353	AAAAA	0.478	0.084	-0.394
3	TGATG	0.393	0.126	-0.268	TGATG	0.393	0.173	-0.221	TGATG	0.393	0.177	-0.217
4	AAAAC	0.337	0.110	-0.227	GATGT	0.309	0.113	-0.196	CTGAT	0.309	0.146	-0.163
5	GATGT	0.309	0.086	-0.223	AAAAC	0.337	0.145	-0.193	GATGT	0.309	0.147	-0.162
6	CTGAT	0.309	0.111	-0.198	GCAAT	0.309	0.121	-0.188	AAAAC	0.337	0.183	-0.154
7	AATAT	0.309	0.117	-0.193	AGTAA	0.253	0.080	-0.173	GCTGA	0.281	0.140	-0.141
8	AGTAA	0.253	0.074	-0.179	TGAAG	0.253	0.087	-0.166	CTTTT	0.253	0.114	-0.139
9	TAAAA	0.225	0.059	-0.165	AACAA	0.281	0.116	-0.165	GCAAT	0.309	0.181	-0.128
10	GCAAT	0.309	0.148	-0.161	TAATA	0.281	0.116	-0.165	TTATC	0.309	0.182	-0.127

Over-represented 5-mers

Rank	Template				Complement				2D			
	kmer	Ref %	Read %	Diff %	kmer	Ref %	Read %	Diff %	kmer	Ref %	Read %	Diff %
1	CTTTG	0.028	0.167	0.139	GAGAG	0.112	0.294	0.182	TCAGC	0.028	0.159	0.131
2	TCTTA	0.000	0.139	0.139	AGAGA	0.140	0.300	0.160	CAGCA	0.056	0.169	0.113
3	TCAGC	0.028	0.154	0.126	ACCCC	0.000	0.160	0.160	ATCAG	0.056	0.167	0.110
4	GTCTT	0.000	0.125	0.125	CCCCA	0.000	0.151	0.151	AACCA	0.028	0.132	0.104
5	AACGT	0.084	0.200	0.115	CGAGA	0.000	0.137	0.137	CATCA	0.112	0.210	0.098
6	GCTCC	0.000	0.114	0.114	ACTCT	0.000	0.136	0.136	CATCT	0.000	0.098	0.098
7	TTCGT	0.084	0.197	0.113	GTATC	0.000	0.135	0.135	ACCAA	0.028	0.124	0.096
8	CATCT	0.000	0.113	0.113	GAGGA	0.000	0.133	0.133	ACATA	0.028	0.115	0.087
9	CAGCA	0.056	0.168	0.112	GTGTG	0.000	0.131	0.131	GACGA	0.000	0.087	0.087
10	GAGGA	0.000	0.111	0.111	CCCGC	0.000	0.125	0.125	CTTTG	0.028	0.114	0.086
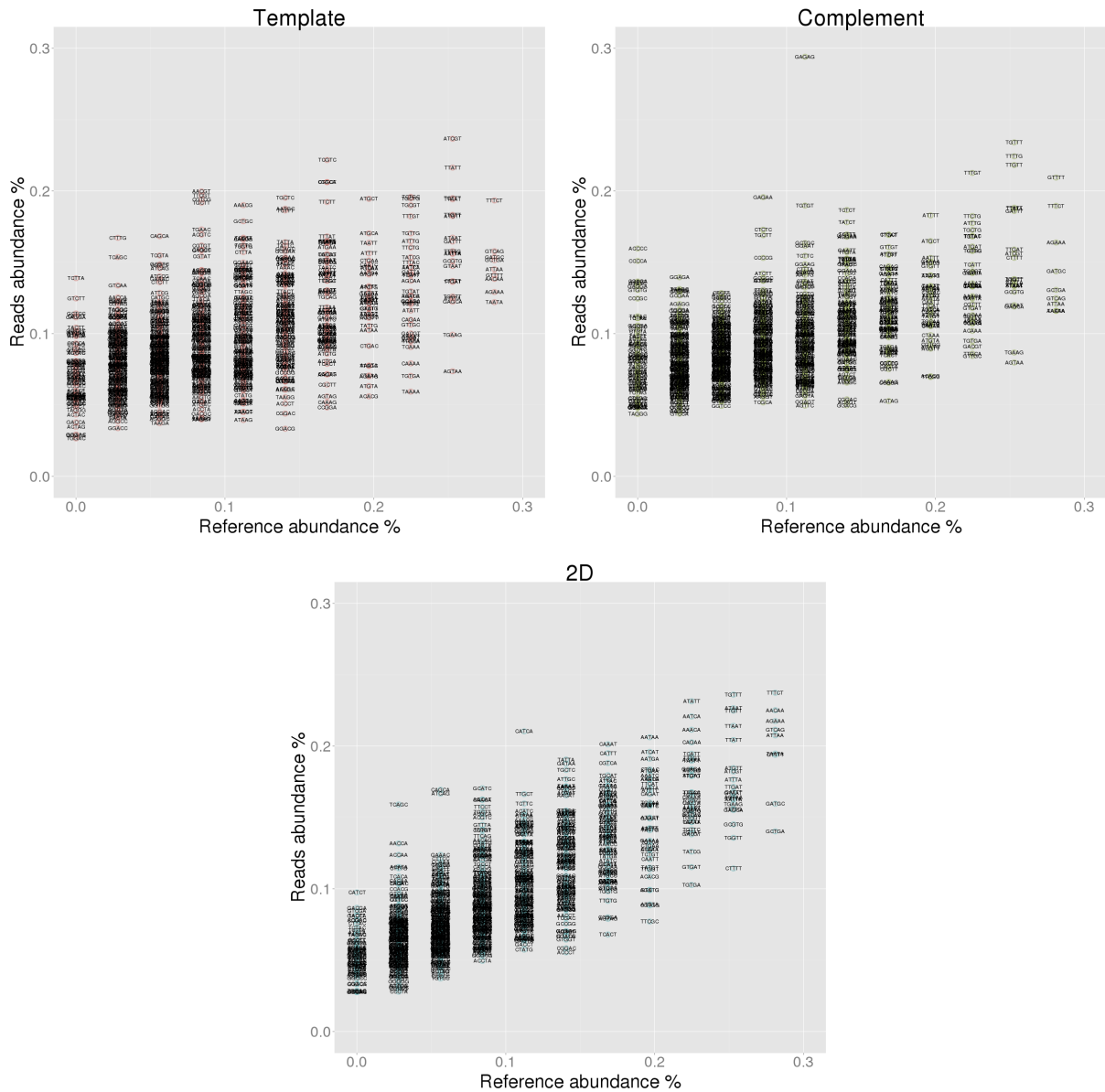
Control sequence GC content
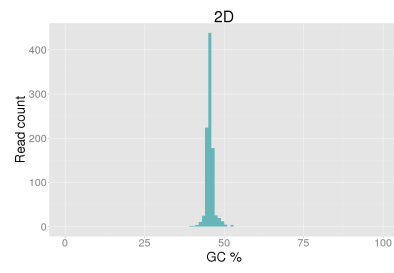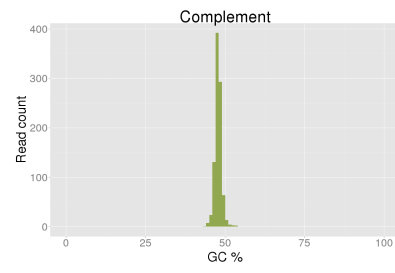
Escherichia coli error analysis

	Template	Complement	2D
Overall base identity (excluding indels)	70.26%	68.93%	83.68%
Aligned base identity (excluding indels)	78.90%	79.36%	91.17%
Identical bases per 100 aligned bases (including indels)	65.27%	66.51%	81.90%
Inserted bases per 100 aligned bases (including indels)	2.71%	6.91%	4.96%
Deleted bases per 100 aligned bases (including indels)	14.56%	9.29%	5.20%
Substitutions per 100 aligned bases (including indels)	17.46%	17.30%	7.94%
Mean insertion size	1.39	1.66	1.57
Mean deletion size	1.68	1.55	1.42
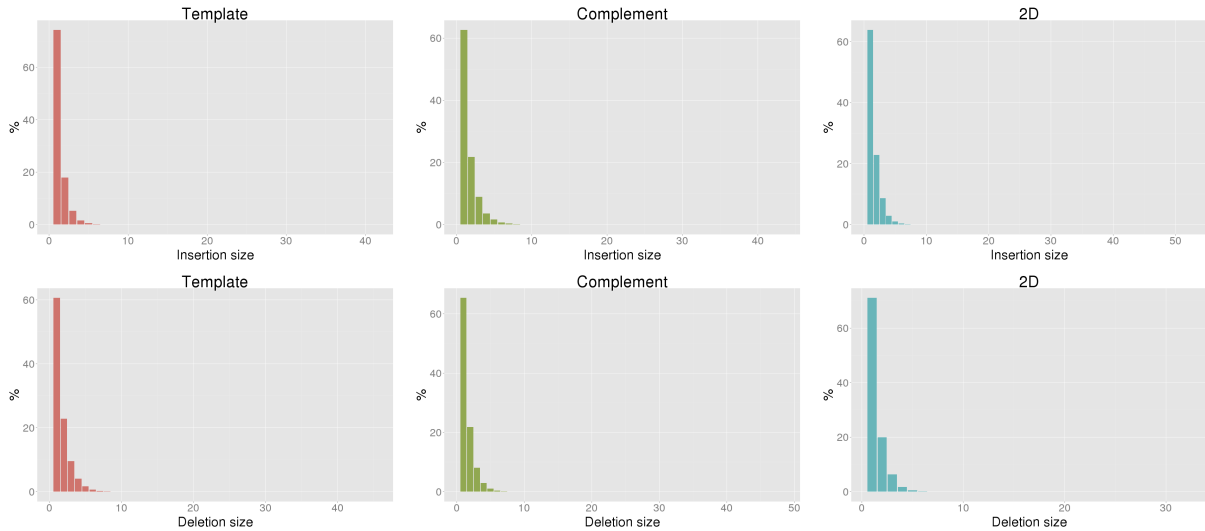
Escherichia coli read identity
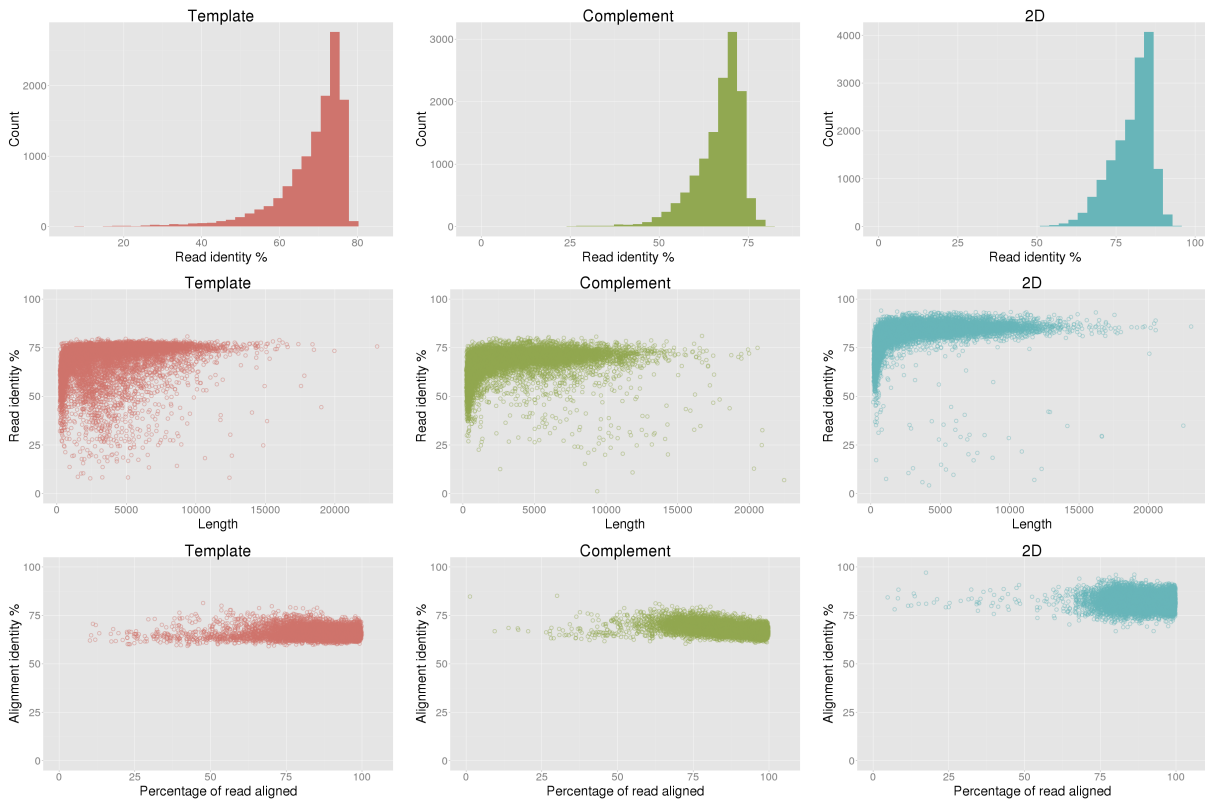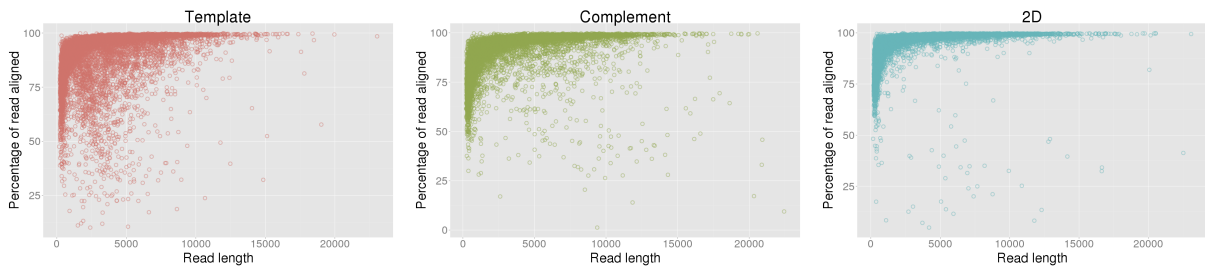
Escherichia coli perfect kmers

Escherichia coli coverage

Escherichia coli 5-mer analysis

Under-represented 5-mers
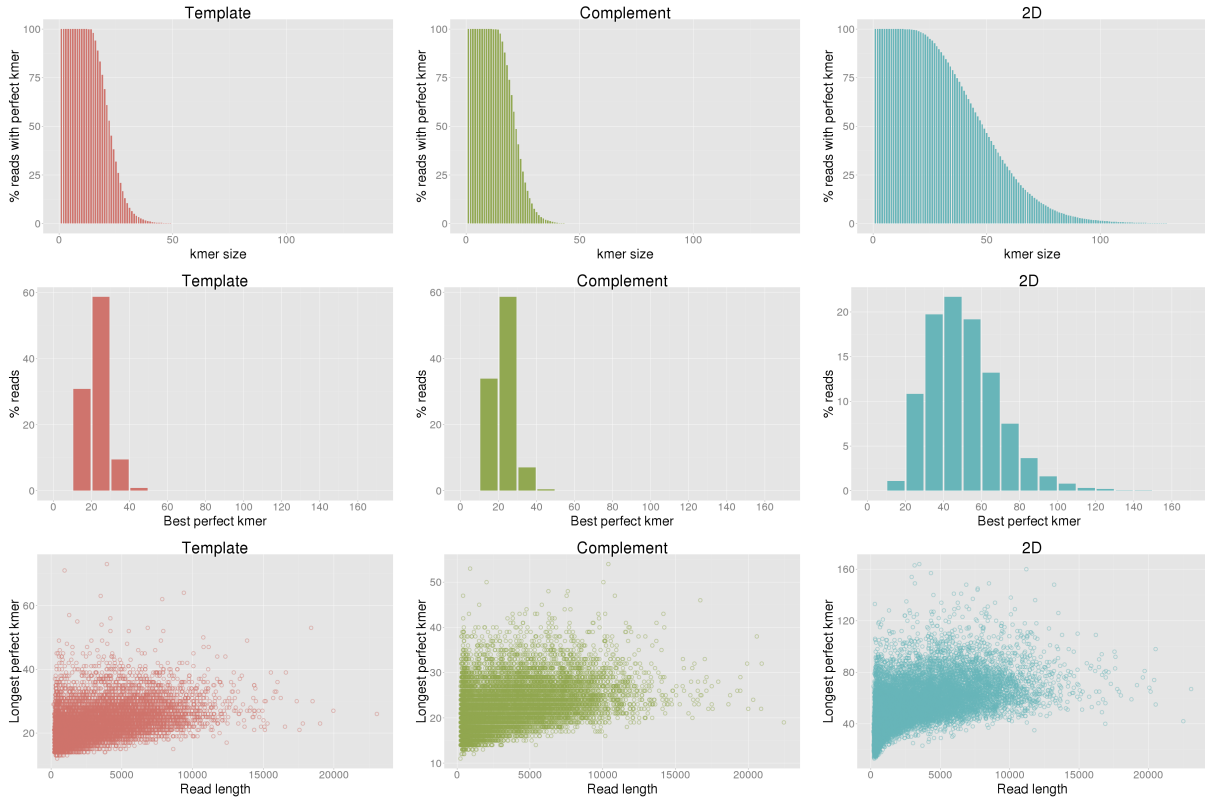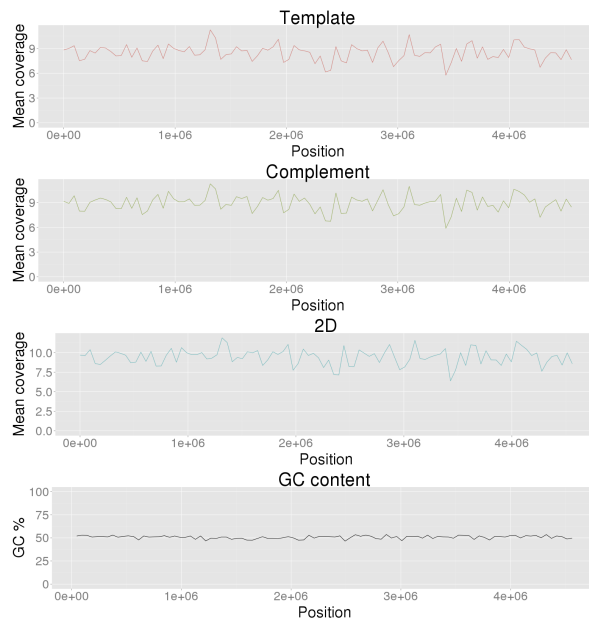
Rank	Template				Complement				2D			
	kmer	Ref %	Read %	Diff %	kmer	Ref %	Read %	Diff %	kmer	Ref %	Read %	Diff %
1	AAAAA	0.247	0.056	-0.191	CGCCA	0.288	0.112	-0.176	TTTTT	0.251	0.053	-0.198
2	TTTTT	0.251	0.070	-0.181	CCAGC	0.289	0.146	-0.142	AAAAA	0.247	0.054	-0.193
3	CGCTG	0.259	0.094	-0.165	CGCTG	0.259	0.121	-0.138	CGCCA	0.288	0.189	-0.099
4	CGCCA	0.288	0.129	-0.159	AAAAA	0.247	0.110	-0.137	TGGCG	0.275	0.181	-0.094
5	GCTGG	0.279	0.133	-0.147	CAGCA	0.261	0.128	-0.134	GCTGG	0.279	0.189	-0.090
6	GCCAG	0.280	0.140	-0.140	CTGGC	0.278	0.146	-0.132	GCCAG	0.280	0.192	-0.088
7	CTGGC	0.278	0.155	-0.124	CACCA	0.184	0.053	-0.131	CCAGC	0.289	0.204	-0.084
8	TGGCG	0.275	0.152	-0.123	GCCAG	0.280	0.153	-0.127	CTGGC	0.278	0.202	-0.076
9	CGCCG	0.219	0.097	-0.122	TTTTT	0.251	0.125	-0.126	AAAAT	0.195	0.124	-0.071
10	ACGCC	0.176	0.063	-0.113	TGGCG	0.275	0.151	-0.125	CGCTG	0.259	0.191	-0.068

Over-represented 5-mers

Rank	Template				Complement				2D			
	kmer	Ref %	Read %	Diff %	kmer	Ref %	Read %	Diff %	kmer	Ref %	Read %	Diff %
1	TCGTA	0.053	0.148	0.095	GAGAG	0.046	0.256	0.210	CAAAT	0.105	0.152	0.047
2	TCGTC	0.094	0.182	0.088	AGAGA	0.071	0.253	0.182	GGGGT	0.039	0.085	0.045
3	CGTCT	0.079	0.165	0.086	ACCCC	0.040	0.192	0.152	CTCGT	0.042	0.085	0.043
4	GTCGT	0.078	0.162	0.084	CCCCG	0.055	0.189	0.134	CGGGG	0.054	0.096	0.042
5	CGTAT	0.071	0.147	0.076	CTCTC	0.046	0.167	0.121	CTTGG	0.025	0.064	0.038
6	TTCGT	0.090	0.165	0.075	CCCCA	0.064	0.171	0.107	GCCCC	0.062	0.100	0.038
7	CTCGT	0.042	0.117	0.074	CCCCC	0.033	0.135	0.102	CCCAA	0.047	0.084	0.037
8	CGTAG	0.058	0.131	0.074	TGTGT	0.046	0.136	0.089	TCTAG	0.003	0.040	0.036
9	GTCTT	0.061	0.134	0.073	TCCCC	0.056	0.144	0.088	TTCGT	0.090	0.126	0.036
10	CGTCG	0.115	0.187	0.072	TATCT	0.085	0.170	0.086	TTGGG	0.047	0.082	0.035
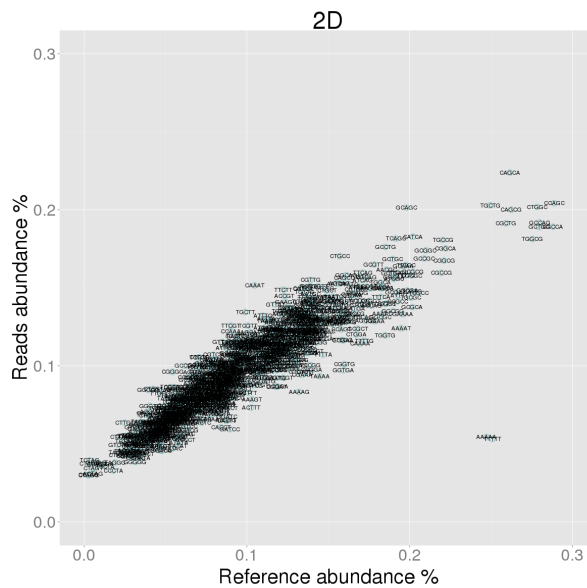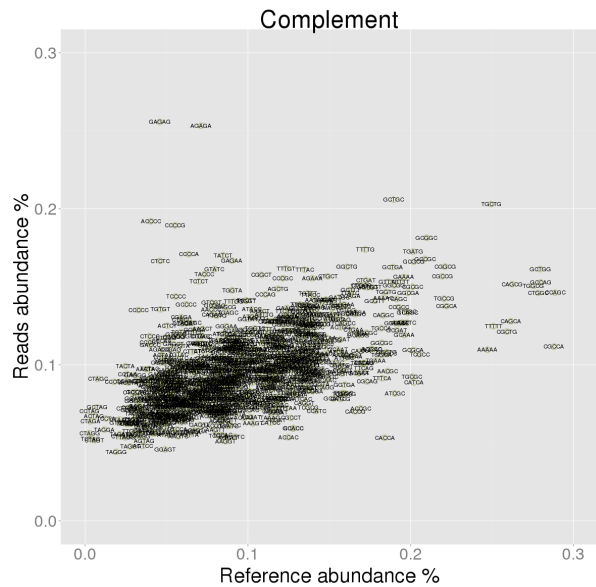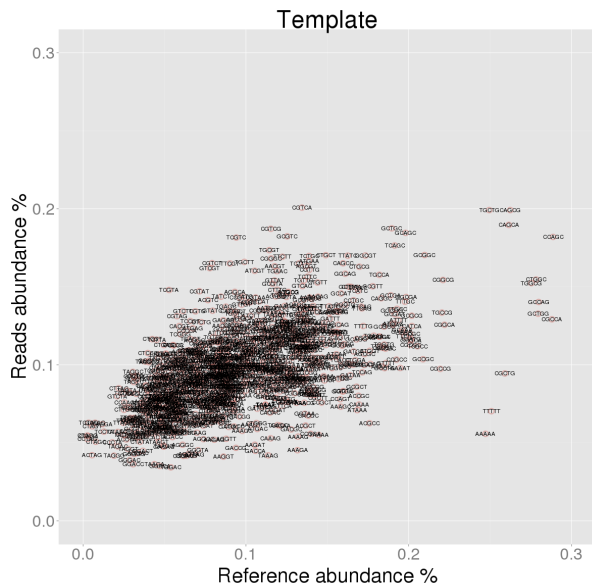
Escherichia coli GC content
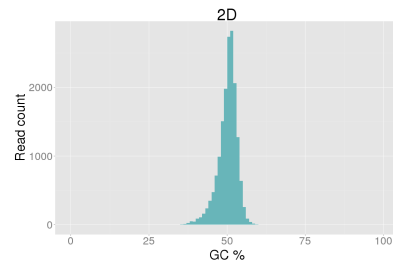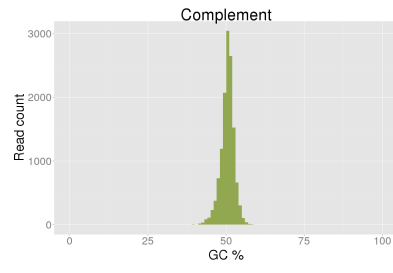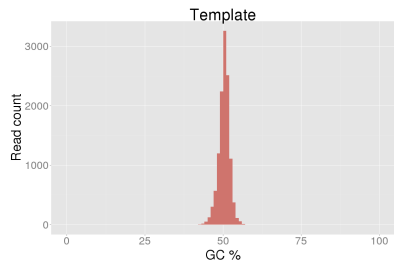
All reference 21mer analysis
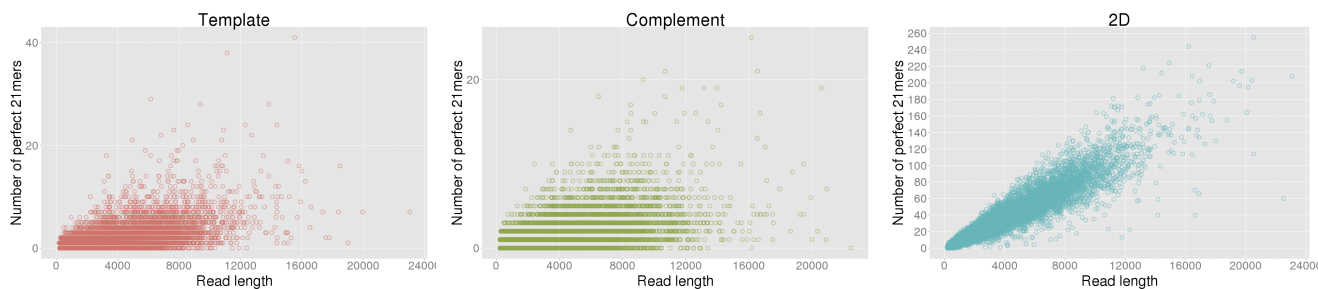
All reference substitutions

		Template substituted %				Complement substituted %				2D substituted %			
		a	c	g	t	a	c	g	t	a	c	g	t
Reference	A	0.00	9.29	9.39	4.45	0.00	9.44	8.72	4.94	0.00	8.78	8.59	3.87
	C	8.29	0.00	9.22	9.68	8.88	0.00	9.00	9.20	8.87	0.00	11.37	8.78
	G	8.98	9.29	0.00	8.08	8.75	9.13	0.00	8.56	8.77	11.53	0.00	8.43
	T	4.99	9.40	8.96	0.00	5.15	8.90	9.34	0.00	3.92	8.53	8.57	0.00

Kmer motifs before errors

3-mer error motif analysis

Rank	Template Insertion	Template Deletion	Template Substitution	Complement Insertion	Complement Deletion	Complement Substitution	2D Insertion	2D Deletion	2D Substitution	
1	GCA (3.15%)	TTC (3.37%)	AAA (3.75%)	AAA (2.79%)	AAA (2.92%)	AAA (4.29%)	GCA (3.12%)	TCA (2.63%)	AAA (3.78%)	Most common
2	TTC (3.03%)	TGC (3.17%)	TTC (3.65%)	GCA (2.61%)	GGC (2.86%)	GCA (3.27%)	TTC (2.78%)	AAA (2.60%)	GCA (3.55%)	
3	TGC (2.63%)	GCA (3.06%)	GCA (3.53%)	TTC (2.60%)	TGC (2.83%)	TTT (3.08%)	AAA (2.62%)	TGC (2.60%)	GAA (3.24%)	
4	AAA (2.55%)	AAA (2.75%)	GAA (3.05%)	TGC (2.57%)	GCA (2.64%)	GAA (3.07%)	TCA (2.55%)	GGC (2.57%)	TTT (3.09%)	
5	ATC (2.49%)	GCC (2.43%)	TGC (2.73%)	CAG (2.44%)	TTC (2.51%)	TTC (2.99%)	TGC (2.50%)	GCA (2.52%)	TTC (2.83%)	
6	TCA (2.32%)	TCA (2.38%)	TTT (2.58%)	TTT (2.37%)	CAG (2.30%)	TGC (2.35%)	GAA (2.42%)	GCG (2.48%)	GTT (2.48%)	
7	GAA (2.31%)	GAA (2.27%)	AAT (2.36%)	GAA (2.30%)	GCC (2.29%)	TCA (2.29%)	ATC (2.35%)	TTC (2.38%)	AAT (2.36%)	
8	GGC (2.20%)	GGC (2.22%)	TCA (2.24%)	GGC (2.28%)	GAA (2.29%)	ATC (2.23%)	CAG (2.24%)	CAG (2.26%)	TCA (2.32%)	
9	GCC (2.18%)	AAC (2.18%)	GCT (2.16%)	ATC (2.19%)	TCA (2.27%)	GCC (2.08%)	GCG (2.18%)	GAA (2.16%)	GCC (2.28%)	
10	TTT (2.17%)	GCG (2.12%)	GCC (2.11%)	TCA (2.12%)	GCG (2.16%)	CAA (2.03%)	TTT (2.17%)	GCC (2.15%)	TGC (2.23%)	
-10	AGT (0.96%)	CTT (0.89%)	AGA (0.94%)	TAC (1.06%)	CTC (0.94%)	GTG (1.01%)	TAC (1.06%)	ACT (0.96%)	GTA (0.90%)	Least common
-9	AGA (0.93%)	CCT (0.89%)	GTA (0.90%)	CTC (1.00%)	CCC (0.93%)	CTT (0.97%)	CTC (1.03%)	GTA (0.96%)	CCT (0.87%)	
-8	CTC (0.93%)	AGT (0.87%)	GGT (0.87%)	AGT (1.00%)	AGG (0.93%)	AGT (0.90%)	AGA (0.91%)	CCC (0.90%)	TGA (0.85%)	
-7	GGA (0.90%)	GAG (0.84%)	CTT (0.86%)	GAG (0.92%)	CGA (0.89%)	GGG (0.86%)	GAG (0.91%)	CTT (0.86%)	CTT (0.80%)	
-6	CCC (0.75%)	GGG (0.83%)	AGT (0.82%)	CCC (0.90%)	GAG (0.88%)	AGG (0.84%)	GGA (0.81%)	CGA (0.85%)	GAG (0.79%)	
-5	GAG (0.72%)	CGA (0.82%)	AGG (0.79%)	GGA (0.88%)	GGA (0.87%)	CCT (0.83%)	AGG (0.81%)	AGA (0.83%)	CGA (0.70%)	
-4	AGG (0.69%)	AGA (0.73%)	GGG (0.74%)	AGG (0.70%)	CCT (0.86%)	ACT (0.78%)	CCC (0.74%)	CCT (0.79%)	AGA (0.62%)	
-3	GGG (0.62%)	GGA (0.61%)	GAG (0.64%)	CTA (0.62%)	GGG (0.81%)	GAG (0.72%)	GGG (0.69%)	CTA (0.72%)	GGA (0.51%)	
-2	CTA (0.47%)	TAG (0.53%)	TAG (0.36%)	GGG (0.61%)	TAG (0.54%)	CTA (0.44%)	CTA (0.59%)	GGA (0.66%)	TAG (0.48%)	
-1	TAG (0.38%)	CTA (0.47%)	CTA (0.33%)	TAG (0.45%)	CTA (0.53%)	TAG (0.39%)	TAG (0.47%)	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 Insertion	Template Deletion	Template Substitution	Complement Insertion	Complement Deletion	Complement Substitution	2D Insertion	2D Deletion	2D Substitution	
1	TTTC (0.94%)	TTTC (1.06%)	TTTC (1.20%)	CAGC (0.95%)	TGGC (1.10%)	AAAA (1.39%)	ATCA (0.89%)	TGGC (0.95%)	AAAA (1.12%)	Most common
2	GAAA (0.87%)	CTGC (0.98%)	AAAA (1.17%)	AAAA (0.89%)	CAGC (0.99%)	TTTT (1.12%)	GGCA (0.86%)	CAGC (0.87%)	GGCA (1.06%)	
3	CAGC (0.84%)	CAGC (0.94%)	GAAA (1.12%)	TGGC (0.86%)	CGGC (0.96%)	GAAA (1.03%)	CAGC (0.78%)	ATCA (0.87%)	TTTT (1.02%)	
4	GGCA (0.83%)	TGCC (0.94%)	GGCA (0.94%)	CTGC (0.84%)	AAAA (0.91%)	CAAA (1.02%)	AACA (0.77%)	TTCA (0.87%)	GAAA (0.96%)	
5	ATCA (0.81%)	TTCA (0.88%)	TGCA (0.90%)	TTTT (0.84%)	CTGC (0.90%)	TTTC (0.92%)	CTTC (0.76%)	CGGC (0.79%)	TGAA (0.94%)	
6	TGGC (0.80%)	TTGC (0.87%)	GGAA (0.89%)	CCAG (0.80%)	TTGC (0.83%)	ATCA (0.87%)	CTGC (0.76%)	CTGC (0.79%)	GGAA (0.91%)	
7	TGCA (0.79%)	TGGC (0.87%)	GCAA (0.87%)	ATCA (0.77%)	ATCA (0.81%)	AGCA (0.86%)	GCCA (0.75%)	CAAA (0.76%)	TGCA (0.88%)	
8	TGCC (0.79%)	GAAA (0.86%)	GTTC (0.87%)	CGGC (0.75%)	TTCC (0.79%)	TGAA (0.85%)	TTCA (0.75%)	CGCC (0.74%)	TTTC (0.84%)	
9	AACG (0.79%)	TTCC (0.85%)	CAAA (0.86%)	CAAA (0.75%)	CAAA (0.79%)	AGAA (0.84%)	CGCA (0.74%)	TGCC (0.73%)	CAAA (0.83%)	
10	AACA (0.79%)	AAAA (0.82%)	CTGC (0.85%)	TTTC (0.75%)	CTGG (0.79%)	GGCA (0.84%)	TGCA (0.74%)	CCAG (0.71%)	ATCA (0.82%)	
-10	AGGG (0.12%)	TCTA (0.12%)	TAGT (0.10%)	CGAG (0.13%)	CCTC (0.13%)	ACCT (0.11%)	CTAT (0.14%)	CCCC (0.14%)	CCGA (0.11%)	Least common
-9	ATAG (0.12%)	GGAC (0.12%)	CGAG (0.10%)	TTAG (0.12%)	CTAT (0.13%)	ACTA (0.11%)	CCCC (0.14%)	GGGA (0.14%)	GGGA (0.11%)	
-8	CTAA (0.11%)	CCCT (0.11%)	GGAC (0.09%)	CCCT (0.12%)	ACTA (0.12%)	TCTA (0.11%)	TTAG (0.14%)	CTAT (0.14%)	CTAT (0.10%)	
-7	TCTA (0.11%)	TAGT (0.11%)	TTAG (0.09%)	CTAA (0.11%)	ACCT (0.11%)	CTAT (0.10%)	CCCT (0.13%)	ACCT (0.13%)	TCGA (0.10%)	
-6	GGAC (0.09%)	CTAA (0.10%)	ACTA (0.09%)	GAGG (0.10%)	CTAA (0.11%)	CGAG (0.10%)	TCTA (0.12%)	CTAA (0.12%)	CCCT (0.10%)	
-5	TTAG (0.09%)	CGGA (0.10%)	TAGA (0.08%)	TAGA (0.10%)	TAGA (0.09%)	GGAC (0.09%)	CTAA (0.12%)	CCCT (0.10%)	CGGA (0.09%)	
-4	TAGA (0.07%)	TAGG (0.07%)	TCTA (0.07%)	GGAC (0.10%)	CCCT (0.09%)	CCCT (0.07%)	TAGA (0.09%)	TAGG (0.10%)	TAGG (0.08%)	
-3	CCTA (0.05%)	TAGA (0.06%)	TAGG (0.05%)	CCTA (0.08%)	TAGG (0.07%)	TAGG (0.06%)	CCTA (0.06%)	CCTA (0.09%)	TAGA (0.05%)	
-2	TAGG (0.04%)	CCTA (0.06%)	CCTA (0.04%)	TAGG (0.05%)	CCTA (0.06%)	CCTA (0.06%)	TAGG (0.06%)	TAGA (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 (0.01%)	

Kmer space for 4-mers: 256   Random chance for any given 4-mer: 0.39%

5-mer error motif analysis

Rank	Template Insertion	Template Deletion	Template Substitution	Complement Insertion	Complement Deletion	Complement Substitution	2D Insertion	2D Deletion	2D Substitution	
1	CAGCA (0.44%)	CAGCA (0.43%)	CAGCA (0.50%)	CAGCA (0.40%)	CTGGC (0.42%)	CAGCA (0.49%)	CAGCA (0.37%)	CTGGC (0.38%)	CAGCA (0.41%)	Most common
2	CTGGC (0.36%)	CTGGC (0.38%)	GAAAA (0.40%)	CTGGC (0.33%)	CAGCA (0.41%)	GAAAA (0.39%)	CGGCA (0.31%)	CAGCA (0.33%)	GAAAA (0.39%)	
3	TTATC (0.32%)	GCTGC (0.37%)	TCTTC (0.37%)	CCAGC (0.32%)	GCGGC (0.32%)	TTATC (0.34%)	TGGCA (0.30%)	CATCA (0.31%)	TGGCA (0.38%)	
4	TGGCA (0.31%)	GCAGC (0.35%)	CAAAA (0.34%)	GCTGC (0.31%)	CATCA (0.32%)	AGAAA (0.34%)	CGCCA (0.29%)	GCGGC (0.29%)	CGGCA (0.37%)	
5	CGCCA (0.30%)	TTGCC (0.31%)	TGTTC (0.33%)	GCGGC (0.29%)	GCTGC (0.31%)	CGGCA (0.32%)	CATCA (0.28%)	TGGCG (0.28%)	ATTTT (0.31%)	
6	CGTTT (0.30%)	TTTGC (0.30%)	TGGCA (0.32%)	CATCA (0.29%)	CCAGC (0.31%)	CAAAA (0.32%)	CTGGC (0.28%)	CGCCA (0.28%)	GCGTT (0.30%)	
7	TCTTC (0.30%)	TTTTC (0.30%)	GCAAA (0.32%)	TTATC (0.28%)	AATCA (0.30%)	ACAAA (0.32%)	TCTTC (0.27%)	CCAGC (0.27%)	AAGAA (0.29%)	
8	GCAGC (0.29%)	CGCCA (0.29%)	GCTGC (0.32%)	GCAGC (0.27%)	TCAGC (0.29%)	ATAAA (0.32%)	GCCAG (0.26%)	GCCAG (0.27%)	CAAAA (0.29%)	
9	ATTTC (0.28%)	CCAGC (0.29%)	CTGGC (0.31%)	TCTTC (0.27%)	TTTGC (0.29%)	ATTTT (0.32%)	GCAAA (0.25%)	TTTCA (0.27%)	GCAAA (0.28%)	
10	CGTTG (0.28%)	GAAAA (0.29%)	CGGCA (0.30%)	CAAAA (0.26%)	GCAGC (0.28%)	AAGAA (0.32%)	GCGCA (0.25%)	ATAAA (0.26%)	TTGCC (0.27%)	
-10	CCCTA (0.00%)	CCCTA (0.01%)	ACCTA (0.01%)	TAGGG (0.01%)	CCCTA (0.01%)	CTTAG (0.01%)	TCCTA (0.01%)	TCCTA (0.01%)	CCCTA (0.01%)	Least common
-9	GCTAG (0.00%)	ACCTA (0.01%)	TAGGT (0.01%)	CCCTA (0.01%)	ACCTA (0.01%)	ACCTA (0.01%)	CCCTA (0.01%)	GCTAG (0.01%)	TAGGA (0.01%)	
-8	ACCTA (0.00%)	GCTAG (0.00%)	GCTAG (0.00%)	CTAGT (0.01%)	CTAGC (0.01%)	CTAGA (0.01%)	GCTAG (0.01%)	TAGGA (0.01%)	ACTAG (0.01%)	
-7	GGACC (0.00%)	CTGAG (0.00%)	ACTAG (0.00%)	CTAGC (0.01%)	GCTAG (0.01%)	GCTAG (0.01%)	CTAGC (0.01%)	CTAGC (0.01%)	GCTAG (0.01%)	
-6	ACTAG (0.00%)	ACTAG (0.00%)	CTAGT (0.00%)	GCTAG (0.00%)	CTAGT (0.00%)	CTAGC (0.00%)	CTAGT (0.01%)	CTAGT (0.00%)	CTAGC (0.00%)	
-5	CTAGC (0.00%)	CTAGT (0.00%)	CTAGC (0.00%)	CTAGA (0.00%)	CTAGA (0.00%)	CTAGT (0.00%)	CCTAG (0.00%)	CTAGA (0.00%)	CTAGT (0.00%)	
-4	CCTAG (0.00%)	CTAGG (0.00%)	CTAGG (0.00%)	CCTAG (0.00%)	ACTAG (0.00%)	ACTAG (0.00%)	ACTAG (0.00%)	CCTAG (0.00%)	CTAGG (0.00%)	
-3	CTAGG (0.00%)	CTAGA (0.00%)	CTAGA (0.00%)	CTAGG (0.00%)	CTAGG (0.00%)	CTAGG (0.00%)	CTAGA (0.00%)	ACTAG (0.00%)	CTAGA (0.00%)	
-2	CTAGA (0.00%)	CCTAG (0.00%)	CCTAG (0.00%)	ACTAG (0.00%)	CCTAG (0.00%)	CCTAG (0.00%)	TCTAG (0.00%)	CCTAG (0.00%)	CTAGG (0.00%)	
-1	TCTAG (0.00%)	TCTAG (0.00%)	TCTAG (0.00%)	TCTAG (0.00%)	TCTAG (0.00%)	TCTAG (0.00%)	CTAGG (0.00%)	CTAGG (0.00%)	CCTAG (0.00%)	

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