

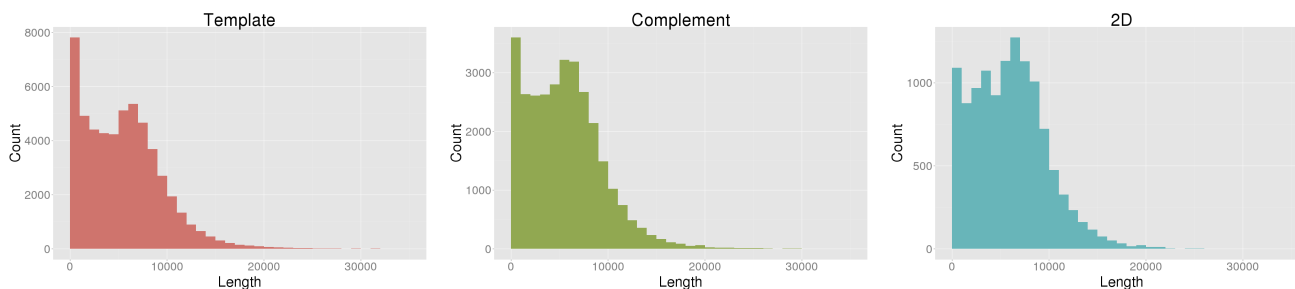
# NanoOK report for UCSC\_MARC\_Phase\_Ib\_Run\_1

## Pass and fail counts

Type	Pass	Fail
Template	0	53826
Complement	0	30515
2D	0	11757

## Read lengths

Type	NumReads	TotalBases	Mean	Longest	Shortest	N50	N50Count	N90	N90Count
Template	53826	300157109	5576.43	383966	5	7887	13494	3529	34200
Complement	30515	171480483	5619.55	300516	10	7649	8002	3567	20132
2D	11757	70434031	5990.82	39770	131	8005	3279	3676	8003



## Template alignments

Number of reads	53826
Number of reads with alignments	28619 (53.17%)
Number of reads without alignments	25207 (46.83%)

ID	Size	Number of Reads	% of Reads	Mean read length	Aligned bases	Mean coverage	Longest Perf Kmer
Control sequence	3560	889	1.65	2801.75	2370402	665.84	59
Escherichia coli	4641652	27730	51.52	7080.97	179805761	38.74	91

## Complement alignments

Number of reads	30515
Number of reads with alignments	17208 (56.39%)
Number of reads without alignments	13307 (43.61%)

ID	Size	Number of Reads	% of Reads	Mean read length	Aligned bases	Mean coverage	Longest Perf Kmer
Control sequence	3560	473	1.55	2652.84	1102342	309.65	45
Escherichia coli	4641652	16735	54.84	6779.40	98926663	21.31	65

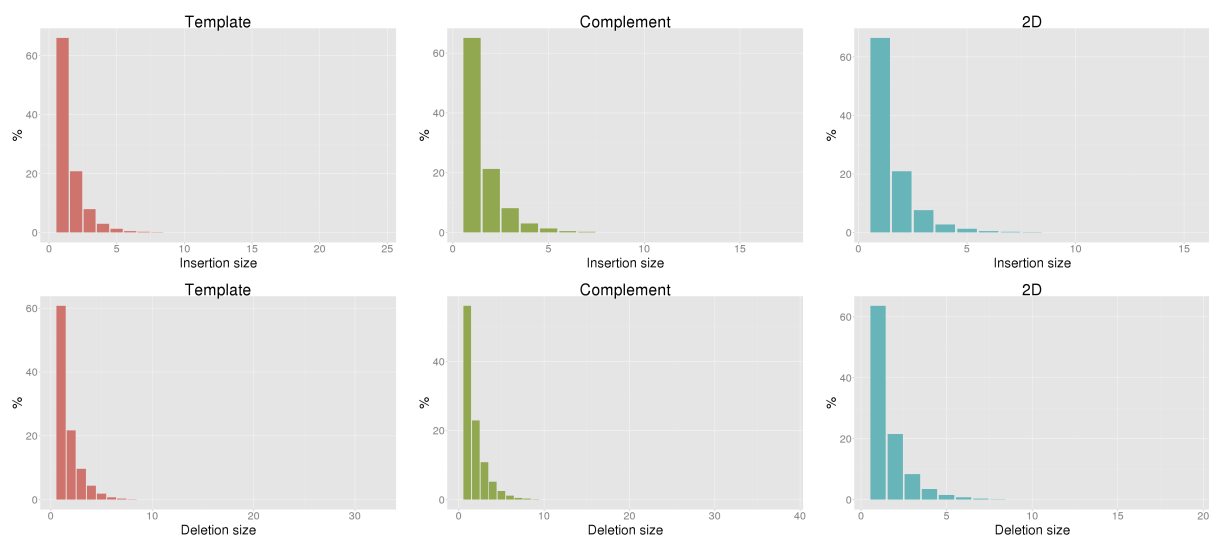
## 2D alignments

Number of reads	11757
Number of reads with alignments	9775 (83.14%)
Number of reads without alignments	1982 (16.86%)

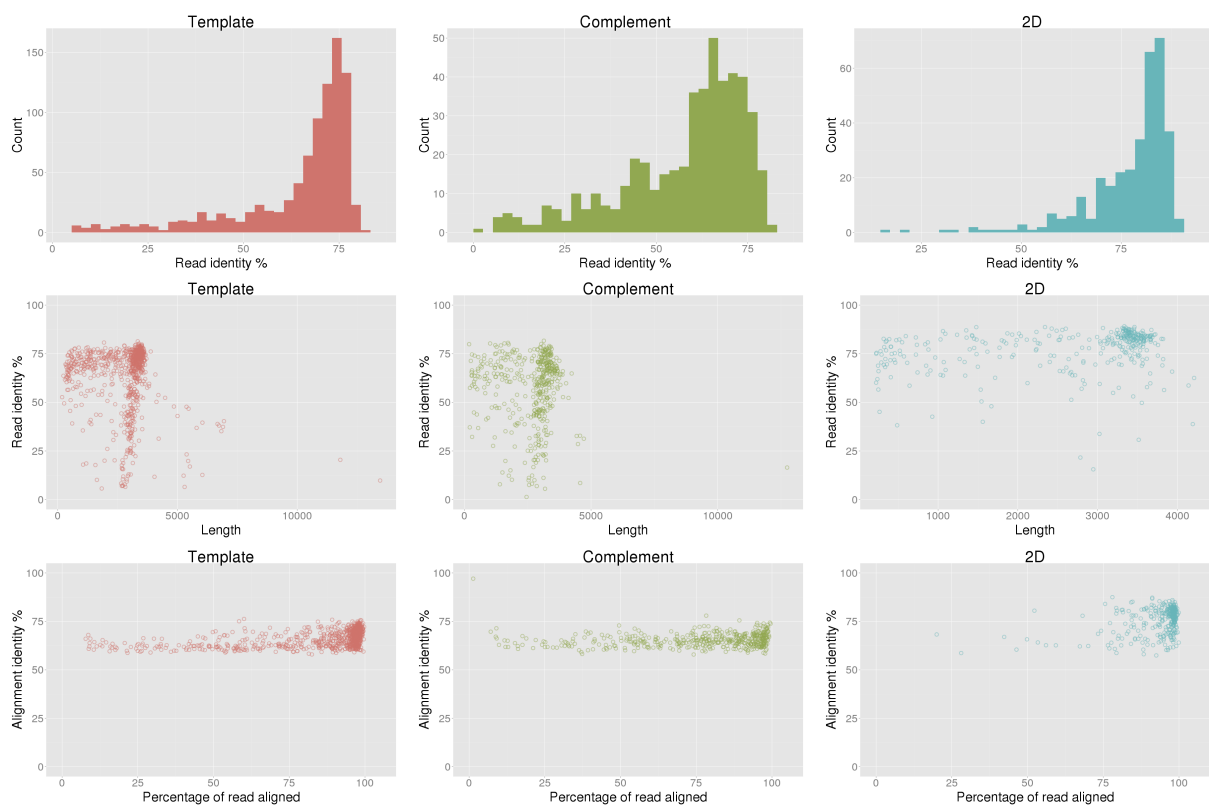
ID	Size	Number of Reads	% of Reads	Mean read length	Aligned bases	Mean coverage	Longest Perf Kmer
Control sequence	3560	347	2.95	2658.17	949637	266.75	141
Escherichia coli	4641652	9428	80.19	6561.60	62837485	13.54	207

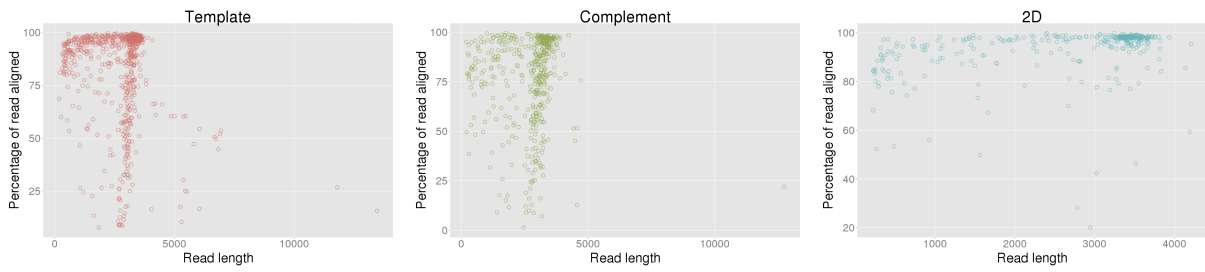
## Control sequence error analysis

	Template	Complement	2D
Overall base identity (excluding indels)	63.45%	57.22%	78.27%
Aligned base identity (excluding indels)	79.76%	79.98%	87.32%
Identical bases per 100 aligned bases (including indels)	66.67%	65.13%	76.03%
Inserted bases per 100 aligned bases (including indels)	4.93%	4.86%	4.91%
Deleted bases per 100 aligned bases (including indels)	11.48%	13.71%	8.03%
Substitutions per 100 aligned bases (including indels)	16.92%	16.30%	11.04%
Mean insertion size	1.58	1.58	1.56
Mean deletion size	1.71	1.85	1.63

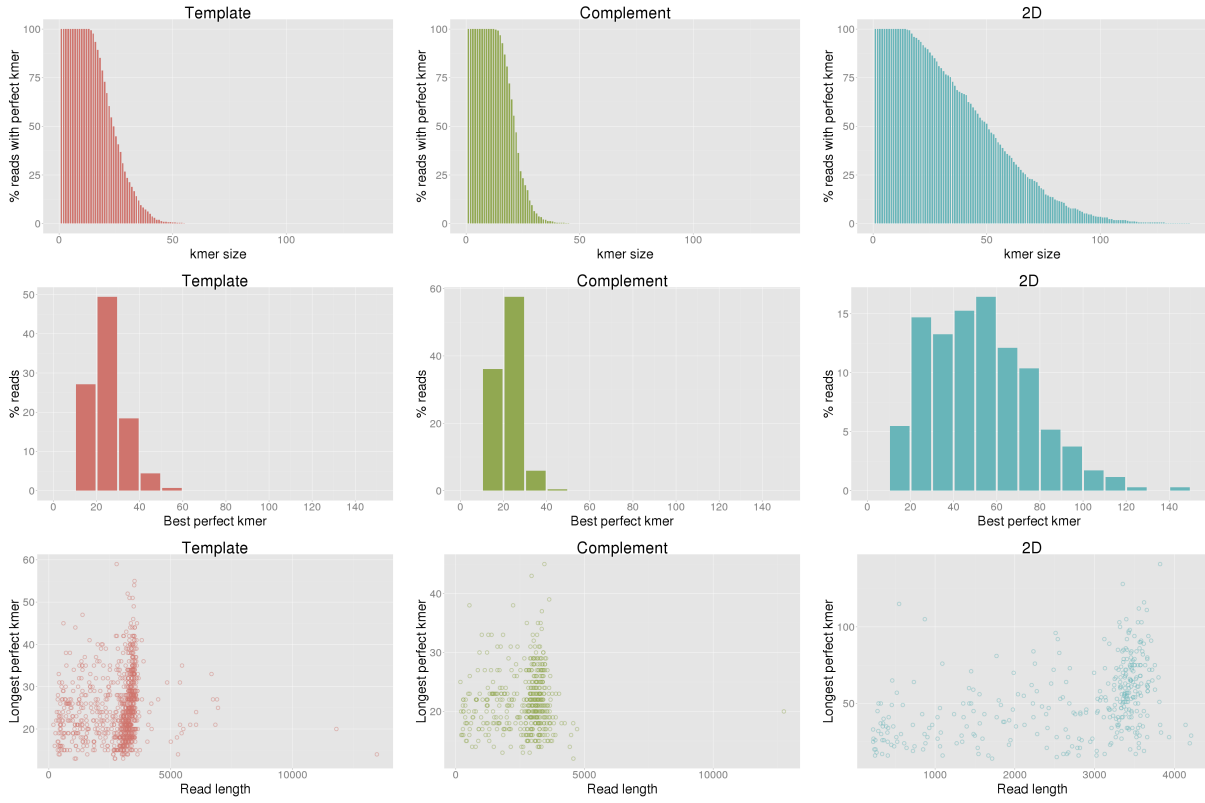


## Control sequence read identity

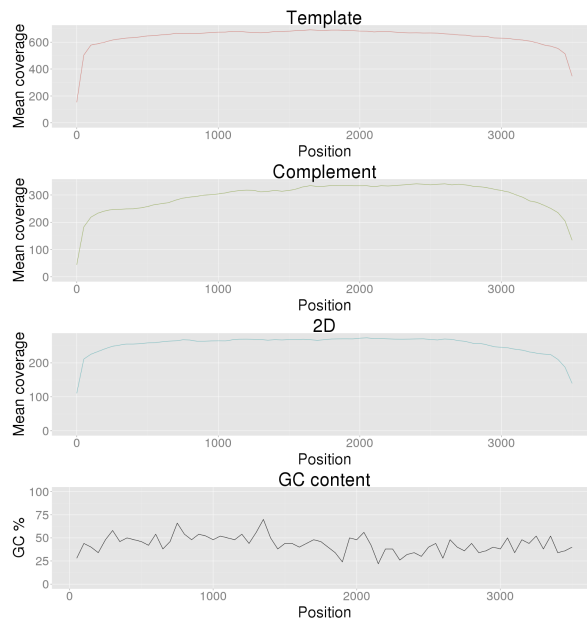




## Control sequence perfect kmers



## Control sequence coverage



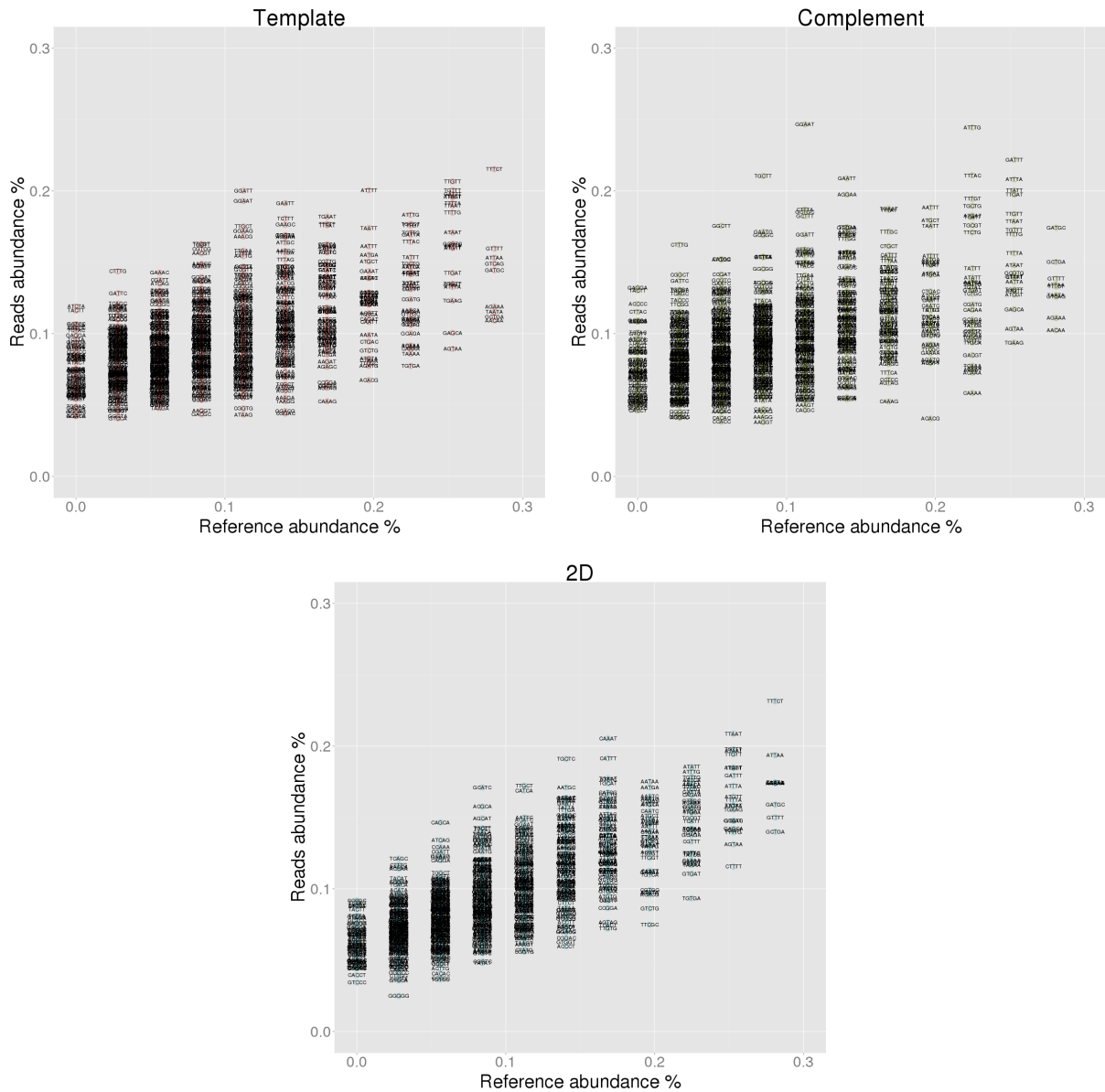
# Control sequence 5-mer analysis

## Under-represented 5-mers

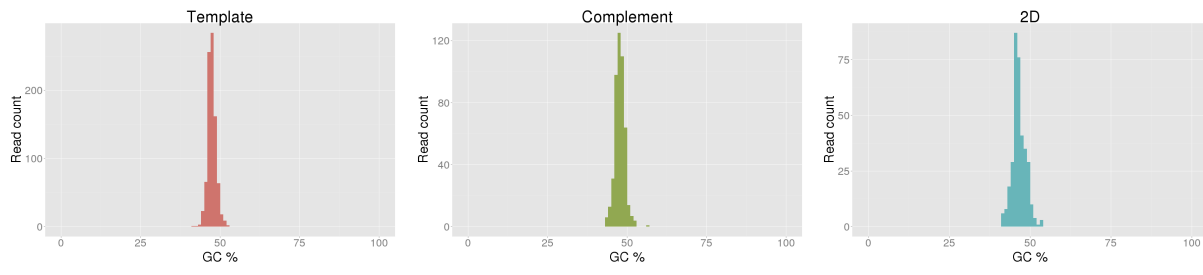
Rank	Template				Complement				2D			
	kmer	Ref %	Read %	Diff %	kmer	Ref %	Read %	Diff %	kmer	Ref %	Read %	Diff %
1	TTTTT	0.759	0.128	-0.631	TTTTT	0.759	0.083	-0.676	TTTTT	0.759	0.050	-0.709
2	AAAAA	0.478	0.083	-0.395	AAAAA	0.478	0.038	-0.439	AAAAA	0.478	0.049	-0.429
3	TGATG	0.393	0.137	-0.256	AAAAC	0.337	0.101	-0.236	TGATG	0.393	0.163	-0.231
4	AAAAC	0.337	0.115	-0.222	GATGT	0.309	0.104	-0.205	AAAAC	0.337	0.146	-0.191
5	GATGT	0.309	0.096	-0.213	TGATG	0.393	0.202	-0.191	GATGT	0.309	0.137	-0.172
6	CTGAT	0.309	0.108	-0.201	GCAAT	0.309	0.123	-0.186	CTGAT	0.309	0.149	-0.160
7	GCAAT	0.309	0.130	-0.180	AACAA	0.281	0.102	-0.179	TTATC	0.309	0.166	-0.143
8	AACAA	0.281	0.109	-0.172	TTATC	0.309	0.133	-0.176	GCTGA	0.281	0.140	-0.141
9	AATAT	0.309	0.138	-0.171	AGAAA	0.281	0.111	-0.170	CTTTT	0.253	0.116	-0.137
10	GCTGA	0.281	0.112	-0.169	CAAAA	0.225	0.059	-0.166	GCAAT	0.309	0.174	-0.136

## Over-represented 5-mers

Rank	Template				Complement				2D			
	kmer	Ref %	Read %	Diff %	kmer	Ref %	Read %	Diff %	kmer	Ref %	Read %	Diff %
1	ATCTA	0.000	0.119	0.119	GGAAT	0.112	0.247	0.134	TCAGC	0.028	0.121	0.093
2	TACTT	0.000	0.116	0.116	CTTTG	0.028	0.162	0.134	CCCGC	0.000	0.092	0.092
3	CTTTG	0.028	0.144	0.116	GAGGA	0.000	0.132	0.132	TCTAC	0.000	0.090	0.090
4	GCTCC	0.000	0.107	0.107	TACTT	0.000	0.130	0.130	CAGCA	0.056	0.147	0.090
5	CCCCA	0.000	0.106	0.106	TGCTT	0.084	0.211	0.126	TACGC	0.000	0.089	0.089
6	CATCT	0.000	0.104	0.104	ACCCC	0.000	0.121	0.121	CTTTG	0.028	0.117	0.088
7	ACCCC	0.000	0.104	0.104	GGCTT	0.056	0.176	0.119	CATCT	0.000	0.088	0.088
8	TCTAC	0.000	0.102	0.102	CTTAC	0.000	0.115	0.115	ATCTA	0.000	0.088	0.088
9	GATTC	0.028	0.128	0.100	CGGCT	0.028	0.141	0.113	AACCA	0.028	0.115	0.087
10	GAGGA	0.000	0.099	0.099	GCCGA	0.000	0.109	0.109	GCATC	0.084	0.171	0.087

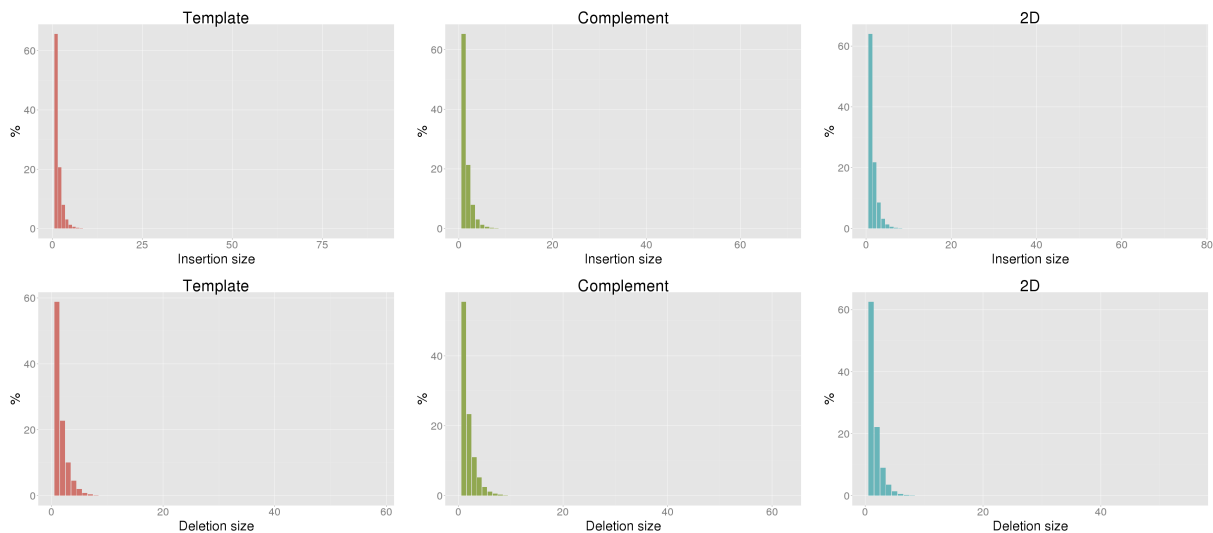


## Control sequence GC content

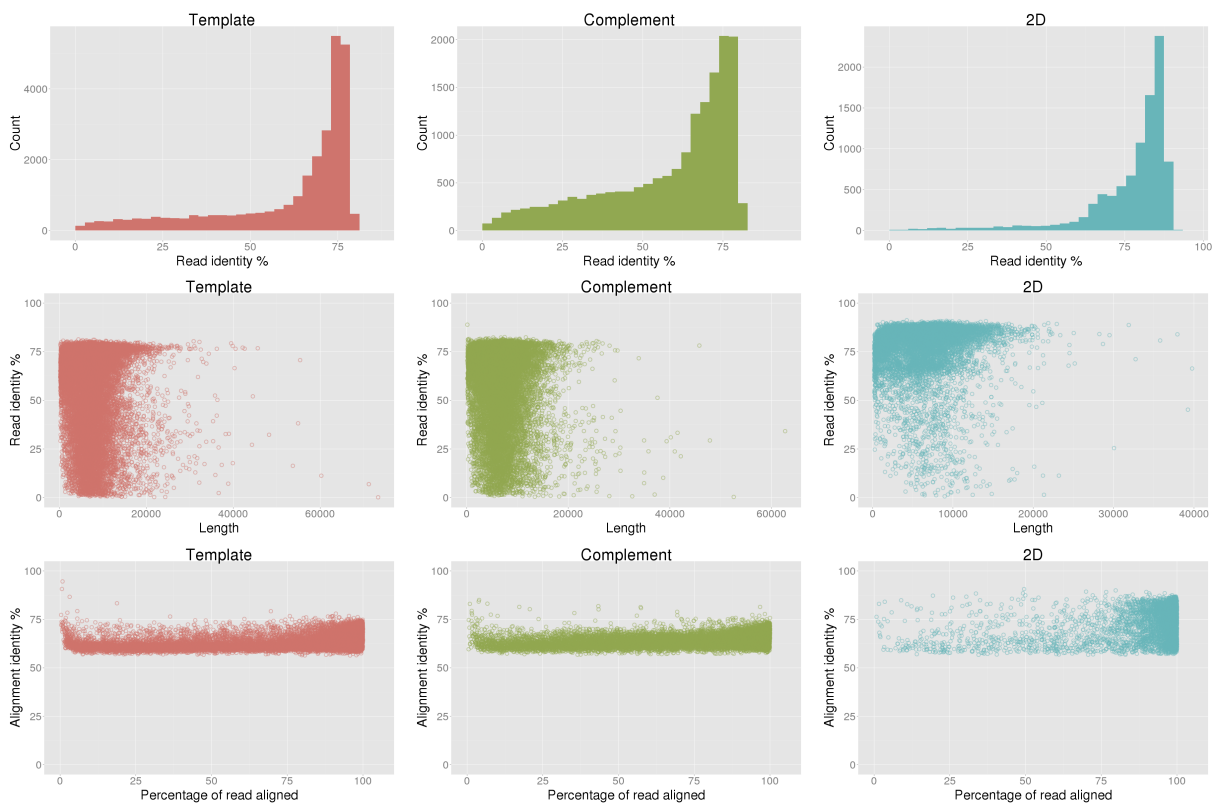


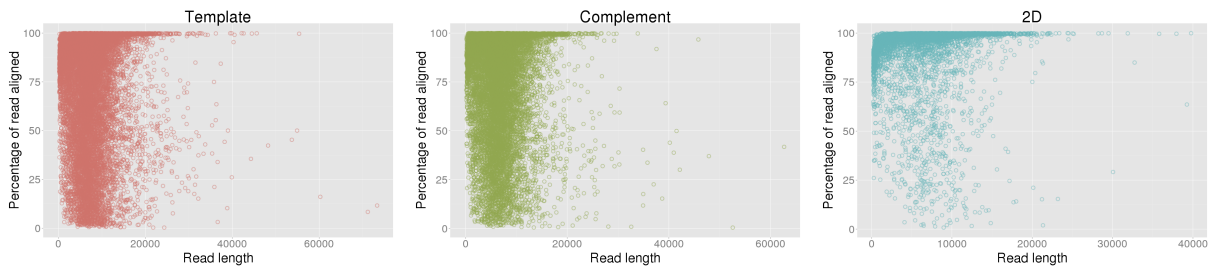
## Escherichia coli error analysis

	Template	Complement	2D
Overall base identity (excluding indels)	59.93%	56.33%	77.06%
Aligned base identity (excluding indels)	79.05%	79.66%	87.14%
Identical bases per 100 aligned bases (including indels)	65.44%	64.60%	75.86%
Inserted bases per 100 aligned bases (including indels)	5.10%	4.93%	5.30%
Deleted bases per 100 aligned bases (including indels)	12.12%	13.97%	7.64%
Substitutions per 100 aligned bases (including indels)	17.34%	16.49%	11.19%
Mean insertion size	1.59	1.59	1.61
Mean deletion size	1.75	1.86	1.64

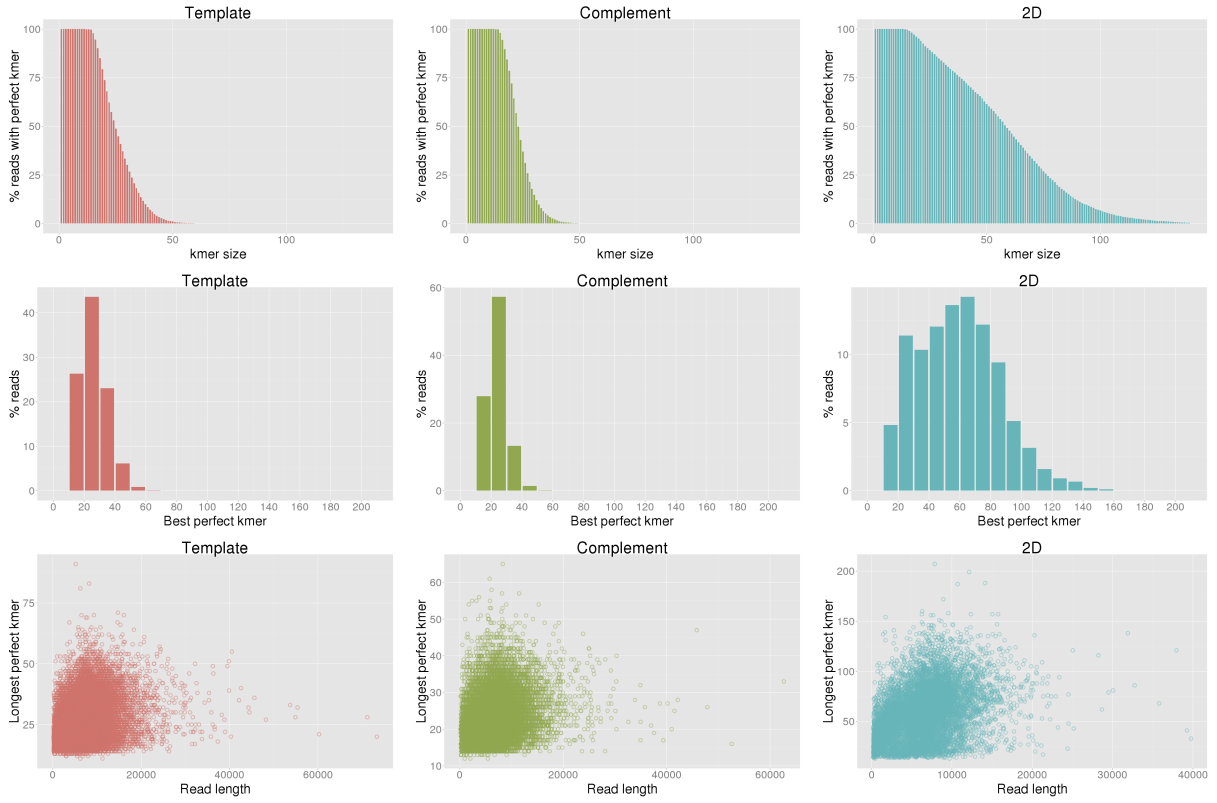


## Escherichia coli read identity

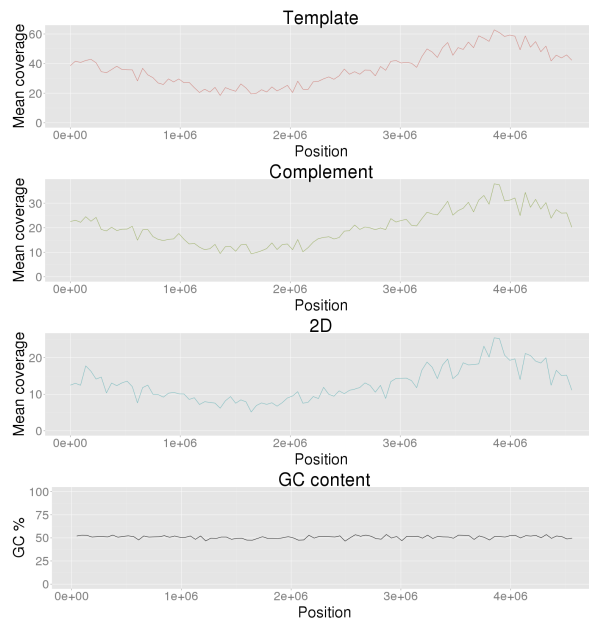




## Escherichia coli perfect kmers



## Escherichia coli coverage



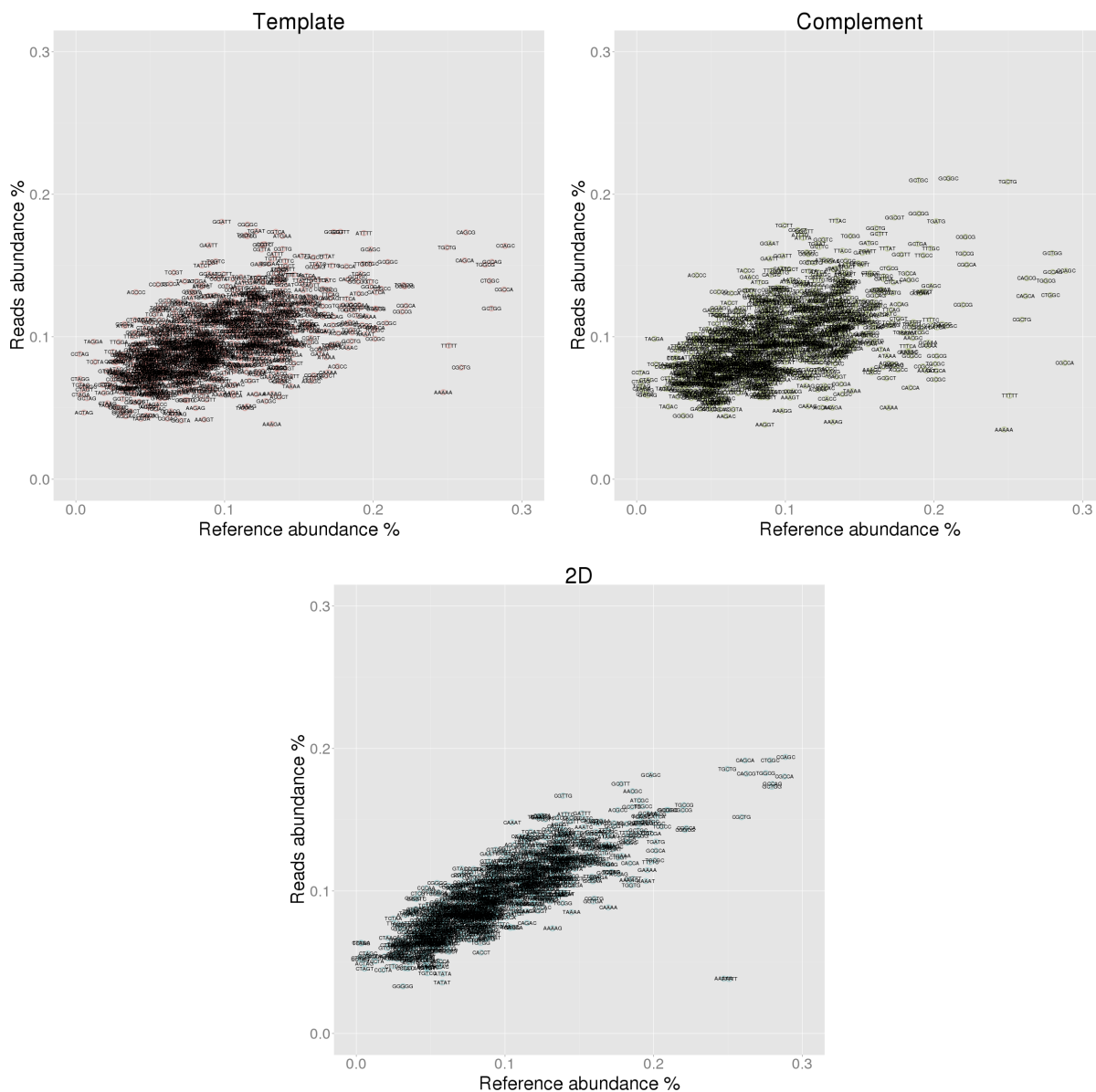
# Escherichia coli 5-mer analysis

## Under-represented 5-mers

Rank	Template				Complement				2D			
	kmer	Ref %	Read %	Diff %	kmer	Ref %	Read %	Diff %	kmer	Ref %	Read %	Diff %
1	AAAAA	0.247	0.061	-0.186	AAAAA	0.247	0.035	-0.212	TTTTT	0.251	0.038	-0.213
2	CGCTG	0.259	0.078	-0.181	CGCCA	0.288	0.082	-0.206	AAAAA	0.247	0.039	-0.209
3	GCTGG	0.279	0.120	-0.160	TTTTT	0.251	0.059	-0.192	CGCCA	0.288	0.180	-0.108
4	TTTTT	0.251	0.094	-0.157	CTGGC	0.278	0.129	-0.149	CGCTG	0.259	0.152	-0.107
5	CGCCA	0.288	0.133	-0.155	CGCTG	0.259	0.112	-0.147	GCTGG	0.279	0.173	-0.106
6	CTGGC	0.278	0.139	-0.139	CCAGC	0.289	0.146	-0.142	GCCAG	0.280	0.175	-0.105
7	GCCAG	0.280	0.153	-0.127	TGGCG	0.275	0.139	-0.136	CCAGC	0.289	0.194	-0.095
8	CCAGC	0.289	0.164	-0.125	GCCAG	0.280	0.145	-0.134	TGGCG	0.275	0.183	-0.093
9	TGGCG	0.275	0.151	-0.125	CAGCA	0.261	0.129	-0.133	AAAAT	0.195	0.107	-0.088
10	CAGCA	0.261	0.154	-0.108	CGCGC	0.201	0.070	-0.131	CTGGC	0.278	0.192	-0.087

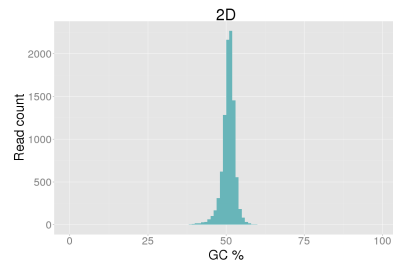
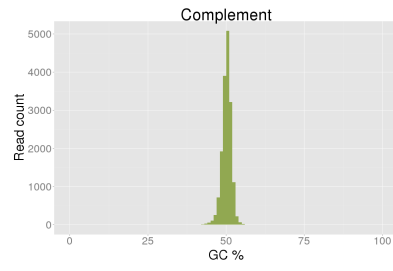
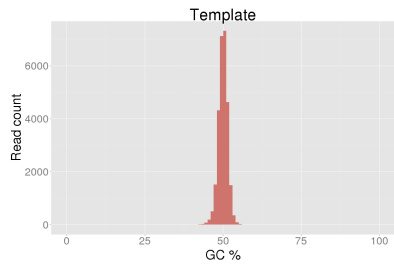
## Over-represented 5-mers

Rank	Template				Complement				2D			
	kmer	Ref %	Read %	Diff %	kmer	Ref %	Read %	Diff %	kmer	Ref %	Read %	Diff %
1	ACCCC	0.040	0.131	0.091	ACCCC	0.040	0.143	0.103	CTAGA	0.003	0.064	0.061
2	CCTAG	0.003	0.088	0.085	TAGGA	0.012	0.099	0.087	TCTAG	0.003	0.063	0.060
3	TAGGA	0.012	0.096	0.085	TGCTT	0.099	0.178	0.079	CTCGT	0.042	0.098	0.056
4	GGATT	0.098	0.181	0.082	GGAAT	0.089	0.166	0.076	TCTAA	0.025	0.081	0.056
5	CCCCG	0.055	0.137	0.082	CCCCG	0.055	0.131	0.076	GGGGT	0.039	0.095	0.055
6	TCCGT	0.066	0.145	0.079	TACCC	0.073	0.146	0.073	CCCAA	0.047	0.102	0.055
7	CCCCC	0.033	0.109	0.076	CCTAG	0.003	0.075	0.072	GGGTC	0.040	0.094	0.054
8	ATCTA	0.033	0.108	0.075	TCCTA	0.013	0.081	0.068	CGGGG	0.054	0.106	0.051
9	GAATT	0.089	0.164	0.075	GAGGC	0.051	0.118	0.067	TTAGA	0.026	0.077	0.051
10	CCCCA	0.064	0.137	0.074	CCCCA	0.064	0.131	0.067	CTAGG	0.003	0.053	0.050

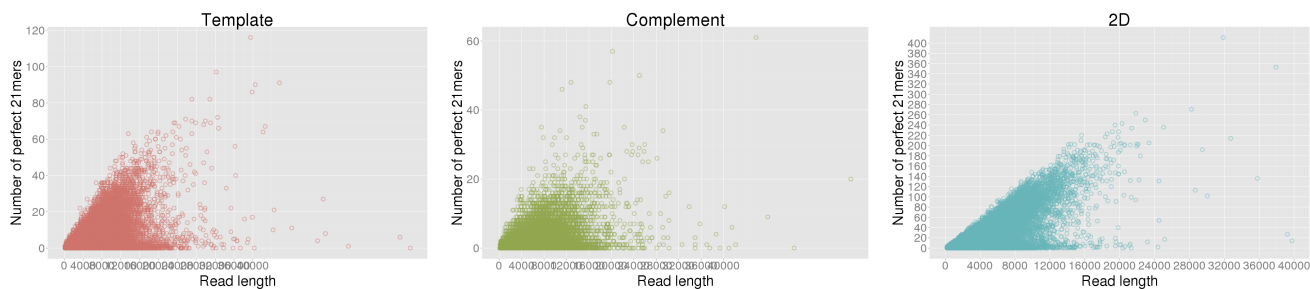




# Escherichia coli GC content



## 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	8.61	8.88	5.13	0.00	8.72	8.72	5.36	0.00	8.64	8.76	4.67
C	8.85	0.00	8.98	9.95	9.37	0.00	8.63	9.48	9.02	0.00	10.18	9.04
G	9.59	9.01	0.00	8.49	8.98	8.78	0.00	9.00	8.96	10.21	0.00	8.61
T	5.35	8.82	8.36	0.00	5.58	8.77	8.59	0.00	4.70	8.71	8.49	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 (3.34%)	TTC (3.38%)	AAA (4.02%)	TGC (2.89%)	GCC (2.82%)	AAA (3.98%)	TTC (2.95%)	AAA (2.63%)	AAA (3.72%)
2	AAA (2.78%)	TGC (2.94%)	TTC (3.74%)	TTC (2.88%)	TGC (2.80%)	GCA (3.47%)	GCA (2.89%)	GCA (2.62%)	GCA (3.44%)
3	TGC (2.70%)	AAA (2.84%)	GCA (3.22%)	AAA (2.73%)	AAA (2.79%)	GAA (3.29%)	AAA (2.82%)	GCC (2.58%)	TTC (3.05%)
4	GCA (2.69%)	GCA (2.75%)	GAA (2.98%)	GCA (2.68%)	GCA (2.73%)	TTC (3.13%)	TGC (2.49%)	GCG (2.57%)	GAA (2.95%)
5	ATC (2.55%)	GCC (2.43%)	TTT (2.67%)	GAA (2.49%)	TTC (2.63%)	TGC (2.56%)	ATC (2.44%)	TGC (2.54%)	TTT (2.77%)
6	TCA (2.37%)	TCA (2.38%)	TGC (2.63%)	CAG (2.40%)	GAA (2.52%)	TTT (2.56%)	TCA (2.40%)	TTC (2.50%)	GTT (2.45%)
7	GCC (2.27%)	GGC (2.34%)	AAT (2.46%)	GGC (2.33%)	GCC (2.34%)	TCA (2.30%)	GCG (2.32%)	TCA (2.42%)	GCC (2.36%)
8	TTT (2.25%)	ATC (2.26%)	ATC (2.19%)	TCA (2.27%)	TCA (2.28%)	AAT (2.23%)	CGC (2.30%)	GAA (2.23%)	AAT (2.35%)
9	GAA (2.24%)	AAT (2.24%)	TCA (2.19%)	ATC (2.25%)	AAT (2.23%)	ATC (2.22%)	GAA (2.28%)	GCC (2.18%)	TGC (2.29%)
10	GGC (2.19%)	GAA (2.23%)	GCC (2.19%)	TTT (2.20%)	CAG (2.22%)	GCC (2.21%)	GCC (2.17%)	CAG (2.17%)	GCG (2.27%)
-10	AGT (0.99%)	AGG (0.97%)	CTC (0.93%)	AGA (0.97%)	AGT (0.94%)	CTT (0.91%)	CTC (1.05%)	CTC (1.04%)	AGG (0.98%)
-9	CTC (0.93%)	AGT (0.92%)	GGG (0.89%)	GTG (0.97%)	GGA (0.93%)	CTC (0.89%)	CTT (1.03%)	CCC (0.94%)	CCC (0.97%)
-8	CCC (0.88%)	CCT (0.88%)	AGA (0.85%)	GGA (0.88%)	AGA (0.93%)	AGT (0.86%)	CCC (0.85%)	CGA (0.92%)	ACT (0.94%)
-7	GGA (0.85%)	CTT (0.87%)	AGG (0.84%)	CTC (0.86%)	CCC (0.93%)	CCT (0.86%)	AGA (0.84%)	ACT (0.92%)	CGA (0.82%)
-6	AGA (0.83%)	GAG (0.85%)	TGT (0.83%)	CCC (0.82%)	CCT (0.89%)	AGG (0.83%)	GAG (0.84%)	CTT (0.87%)	CTT (0.81%)
-5	GAG (0.73%)	CGA (0.84%)	AGT (0.81%)	GAG (0.74%)	CTC (0.85%)	GGG (0.80%)	GGA (0.81%)	CCT (0.85%)	GAG (0.79%)
-4	AGG (0.73%)	AGA (0.71%)	CTT (0.79%)	AGG (0.72%)	GAG (0.85%)	ACT (0.78%)	AGG (0.79%)	AGA (0.77%)	GGA (0.68%)
-3	GGG (0.70%)	GGA (0.71%)	GAG (0.64%)	GGG (0.59%)	GGG (0.81%)	GAG (0.62%)	GGG (0.76%)	GGA (0.70%)	AGA (0.66%)
-2	CTA (0.50%)	TAG (0.52%)	TAG (0.39%)	CTA (0.53%)	TAG (0.53%)	CTA (0.42%)	CTA (0.59%)	CTA (0.66%)	TAG (0.46%)
-1	TAG (0.42%)	CTA (0.48%)	CTA (0.35%)	TAG (0.45%)	CTA (0.53%)	TAG (0.39%)	TAG (0.48%)	TAG (0.62%)	CTA (0.39%)

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 (1.08%)	TTTC (1.10%)	TTTC (1.31%)	CAGC (0.90%)	CGGC (1.02%)	CAAA (1.10%)	TTTC (0.85%)	TGGC (0.96%)	AAAA (1.08%)
2	GAAA (0.89%)	TGCC (0.94%)	AAAA (1.30%)	ATCA (0.88%)	TGGC (1.00%)	AAAA (1.06%)	ATCA (0.82%)	CAGC (0.86%)	GGCA (1.07%)
3	AAAA (0.86%)	TTCA (0.93%)	GAAA (1.12%)	TTGC (0.87%)	CAGC (0.99%)	TGAA (0.95%)	GAAA (0.81%)	TTCA (0.84%)	GAAA (1.02%)
4	TTCA (0.84%)	TTCC (0.90%)	GGCA (0.93%)	CAAA (0.85%)	TTGC (0.88%)	GAAA (0.95%)	GGCA (0.80%)	ATCA (0.76%)	TTTC (0.98%)
5	ATCA (0.82%)	TTGC (0.89%)	TTTT (0.92%)	CGGC (0.84%)	CAAA (0.86%)	TTTC (0.91%)	CAGC (0.79%)	CGGC (0.76%)	GGAA (0.87%)
6	TTGC (0.82%)	TGGC (0.86%)	GTTC (0.89%)	CTGC (0.84%)	CTGC (0.85%)	GGCA (0.91%)	AACA (0.78%)	GGCG (0.75%)	CGTT (0.86%)
7	TGCG (0.81%)	AAAA (0.86%)	AAAT (0.89%)	TGGC (0.80%)	TGCC (0.83%)	AGCA (0.88%)	CGCC (0.78%)	GCCA (0.75%)	CGCC (0.85%)
8	CAGC (0.79%)	CAGC (0.85%)	GGAA (0.87%)	CCAG (0.78%)	TTCC (0.82%)	ATCA (0.87%)	GCCA (0.78%)	CTGC (0.75%)	TTTT (0.84%)
9	CTTC (0.78%)	CTGC (0.84%)	GCAA (0.86%)	TGCC (0.76%)	ATCA (0.80%)	GGAA (0.85%)	TTCA (0.76%)	TGCC (0.75%)	CAAA (0.84%)
10	AACG (0.76%)	GAAA (0.83%)	CAAA (0.85%)	ATGC (0.75%)	TTCA (0.77%)	TAAA (0.85%)	TGGC (0.75%)	TTTT (0.74%)	TGCC (0.82%)
-10	AGGG (0.12%)	CTAT (0.13%)	CCCT (0.11%)	CGAG (0.11%)	CCTC (0.12%)	TTAG (0.11%)	ACTA (0.14%)	ACTT (0.15%)	TATA (0.12%)
-9	TAGT (0.12%)	TAGT (0.12%)	CGAG (0.10%)	AGGG (0.11%)	ACCT (0.12%)	GTGT (0.11%)	CTAT (0.14%)	CTAT (0.14%)	CCCT (0.11%)
-8	TTAG (0.11%)	CGGA (0.12%)	ACTA (0.10%)	GTGT (0.11%)	CCCC (0.12%)	ACTA (0.10%)	GGAC (0.14%)	CCCC (0.14%)	CTAA (0.11%)
-7	CTAA (0.11%)	GGAC (0.11%)	TAGT (0.09%)	TAGA (0.10%)	GTGT (0.11%)	CTAT (0.10%)	CCCT (0.14%)	CGGA (0.14%)	CTAT (0.11%)
-6	GAGG (0.11%)	CCCT (0.11%)	TCTA (0.08%)	GAGG (0.09%)	CTAA (0.11%)	GGAC (0.09%)	GAGG (0.13%)	CTAA (0.12%)	ACTA (0.10%)
-5	GGAC (0.10%)	CTAA (0.10%)	TAGA (0.08%)	GGAC (0.09%)	TAGA (0.10%)	CGAG (0.09%)	CTAA (0.11%)	CCCT (0.11%)	TCTA (0.10%)
-4	TAGA (0.07%)	TAGG (0.08%)	GGAC (0.08%)	CCCT (0.09%)	CCCT (0.08%)	TAGG (0.07%)	TAGA (0.08%)	TAGG (0.09%)	TAGG (0.08%)
-3	CCTA (0.07%)	TAGA (0.07%)	TAGG (0.07%)	CCTA (0.06%)	TAGG (0.07%)	CCCT (0.07%)	CCTA (0.07%)	TAGA (0.08%)	TAGA (0.05%)
-2	TAGG (0.06%)	CCTA (0.05%)	CCTA (0.05%)	TAGG (0.06%)	CCTA (0.06%)	CCTA (0.05%)	TAGG (0.05%)	CCTA (0.08%)	CCTA (0.05%)
-1	CTAG (0.01%)	CTAG (0.01%)	CTAG (0.01%)	CTAG (0.01%)	CTAG (0.01%)	CTAG (0.01%)	CTAG (0.01%)	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	CAGCA (0.33%)	CAGCA (0.35%)	GAAAA (0.40%)	CAGCA (0.40%)	CAGCA (0.43%)	CAGCA (0.53%)	CAGCA (0.35%)	CTGGC (0.39%)	CAGCA (0.42%)
2	ATTTT (0.31%)	CTGGC (0.34%)	CAGCA (0.40%)	CATCA (0.34%)	CTGGC (0.38%)	CGGCA (0.37%)	CGCCA (0.32%)	CAGCA (0.33%)	TGGCA (0.38%)
3	CTGGC (0.31%)	TTGCC (0.33%)	CAAAA (0.37%)	GCTGC (0.33%)	CGGGC (0.35%)	GCAAA (0.36%)	CTGGC (0.32%)	TGGCG (0.31%)	CGGCA (0.37%)
4	TTATC (0.30%)	TTTGC (0.32%)	CGTTC (0.34%)	CCAGC (0.31%)	CCAGC (0.32%)	CATCA (0.35%)	TGGCG (0.29%)	CGCCA (0.30%)	GAAAA (0.36%)
5	CATCA (0.29%)	TTTCA (0.30%)	ATTTT (0.32%)	CTGGC (0.31%)	CATCA (0.32%)	ATAAA (0.35%)	CGGCA (0.29%)	CCAGC (0.29%)	GCGTT (0.33%)
6	CGCCA (0.29%)	GCTGC (0.30%)	TGGCA (0.32%)	GCGGC (0.31%)	GCTGC (0.31%)	AAGAA (0.33%)	GCAAA (0.28%)	GCGGC (0.28%)	CAAAA (0.32%)
7	CAAAA (0.28%)	TTTCC (0.30%)	GCAAA (0.32%)	GCAAA (0.29%)	TTGCC (0.31%)	GAAAA (0.33%)	GCCAG (0.28%)	GCCAG (0.28%)	GCAAA (0.30%)
8	TTTGC (0.28%)	CGCCA (0.29%)	TGTTT (0.32%)	TTTGC (0.28%)	AATCA (0.30%)	ACGCA (0.32%)	CATCA (0.27%)	CATCA (0.27%)	CGCCA (0.30%)
9	TGGCG (0.28%)	GCAGC (0.29%)	TTGCC (0.31%)	AATCA (0.28%)	TTTGC (0.30%)	ACAAA (0.31%)	TGGCA (0.27%)	TTTCA (0.27%)	ATTTT (0.30%)
10	TTGCC (0.27%)	CGTTC (0.28%)	TTTGC (0.31%)	CGGCA (0.27%)	ATAAA (0.29%)	ATGAA (0.31%)	CCAGC (0.26%)	ATAAA (0.26%)	TTGCC (0.30%)
-10	TAGGA (0.01%)	GGACC (0.01%)	CTTAG (0.01%)	GGGGG (0.01%)	CCCTA (0.01%)	CCCTA (0.01%)	CCCTA (0.01%)	TCCTA (0.01%)	CCCTA (0.01%)
-9	GGACC (0.01%)	CCCTA (0.01%)	CCCTA (0.01%)	CCCTA (0.01%)	CCCCC (0.01%)	ACCTA (0.01%)	TAGGA (0.01%)	TAGGA (0.01%)	TAGGA (0.01%)
-8	CTAGC (0.00%)	ACTAG (0.00%)	ACTAG (0.00%)	CTAGC (0.01%)	CTAGC (0.01%)	GCTAG (0.00%)	CTAGT (0.00%)	GCTAG (0.01%)	GCTAG (0.00%)
-7	CTAGT (0.00%)	GCTAG (0.00%)	GCTAG (0.00%)	GCTAG (0.00%)	GCTAG (0.01%)	CTAGT (0.00%)	GCTAG (0.00%)	ACTAG (0.01%)	ACTAG (0.00%)
-6	GCTAG (0.00%)	CTAGT (0.00%)	CTAGC (0.00%)	ACTAG (0.00%)	CTAGT (0.00%)	CTAGC (0.00%)	ACTAG (0.00%)	CTAGC (0.00%)	CTAGC (0.00%)
-5	ACTAG (0.00%)	CTAGC (0.00%)	CTAGG (0.00%)	CTAGT (0.00%)	ACTAG (0.00%)	CTAGA (0.00%)	CTAGC (0.00%)	CTAGT (0.00%)	CTAGT (0.00%)
-4	CTAGA (0.00%)	TCTAG (0.00%)	CTAGT (0.00%)	TCTAG (0.00%)	CTAGG (0.00%)	ACTAG (0.00%)	TCTAG (0.00%)	CTAGG (0.00%)	TCTAG (0.00%)
-3	TCTAG (0.00%)	CTAGG (0.00%)	CCTAG (0.00%)	CTAGA (0.00%)	TCTAG (0.00%)	CTAGG (0.00%)	CCTAG (0.00%)	CCTAG (0.00%)	CCTAG (0.00%)
-2	CCTAG (0.00%)	CCTAG (0.00%)	TCTAG (0.00%)	CCTAG (0.00%)	CTAGA (0.00%)	CCTAG (0.00%)	CTAGA (0.00%)	TCTAG (0.00%)	CTAGG (0.00%)
-1	CTAGG (0.00%)	CTAGA (0.00%)	CTAGA (0.00%)	CTAGG (0.00%)	CCTAG (0.00%)	TCTAG (0.00%)	CTAGG (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%