

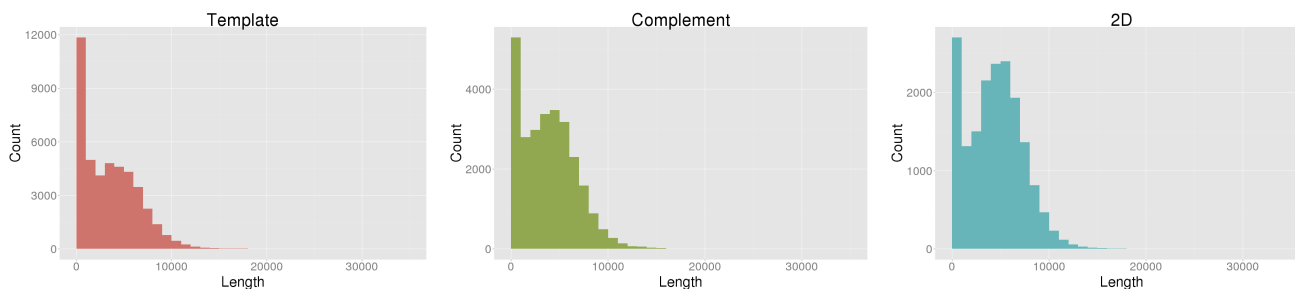
# NanoOK report for JOGrady\_MARC1b\_run1

## Pass and fail counts

Type	Pass	Fail
Template	0	43722
Complement	0	27003
2D	0	17511

## Read lengths

Type	NumReads	TotalBases	Mean	Longest	Shortest	N50	N50Count	N90	N90Count
Template	43722	157618516	3605.02	149041	9	5768	9925	2366	25435
Complement	27003	105678494	3913.58	128049	10	5648	6962	2621	17206
2D	17511	78150592	4462.94	40916	115	6046	4958	3101	11749



## Template alignments

Number of reads	43722
Number of reads with alignments	16003 (36.60%)
Number of reads without alignments	27719 (63.40%)

ID	Size	Number of Reads	% of Reads	Mean read length	Aligned bases	Mean coverage	Longest Perf Kmer
Control sequence	3560	1210	2.77	2880.77	3207424	900.96	50
Escherichia coli	4641652	14793	33.83	5599.23	73155737	15.76	76

## Complement alignments

Number of reads	27003
Number of reads with alignments	11734 (43.45%)
Number of reads without alignments	15269 (56.55%)

ID	Size	Number of Reads	% of Reads	Mean read length	Aligned bases	Mean coverage	Longest Perf Kmer
Control sequence	3560	771	2.86	2807.37	1859901	522.44	46
Escherichia coli	4641652	10963	40.60	5542.89	51528184	11.10	56

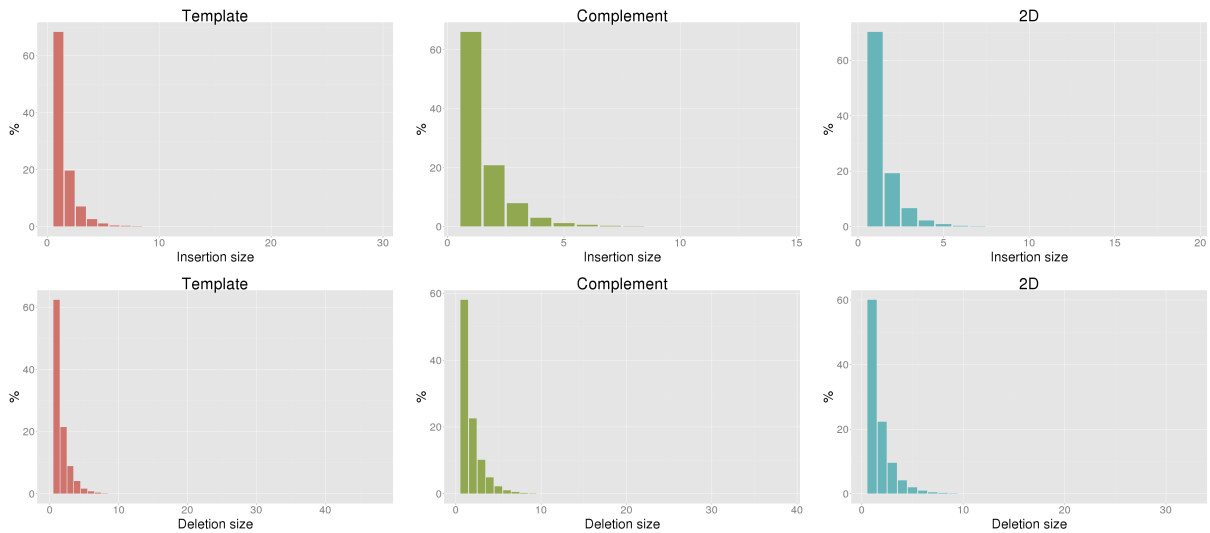
## 2D alignments

Number of reads	17511
Number of reads with alignments	12194 (69.64%)
Number of reads without alignments	5317 (30.36%)

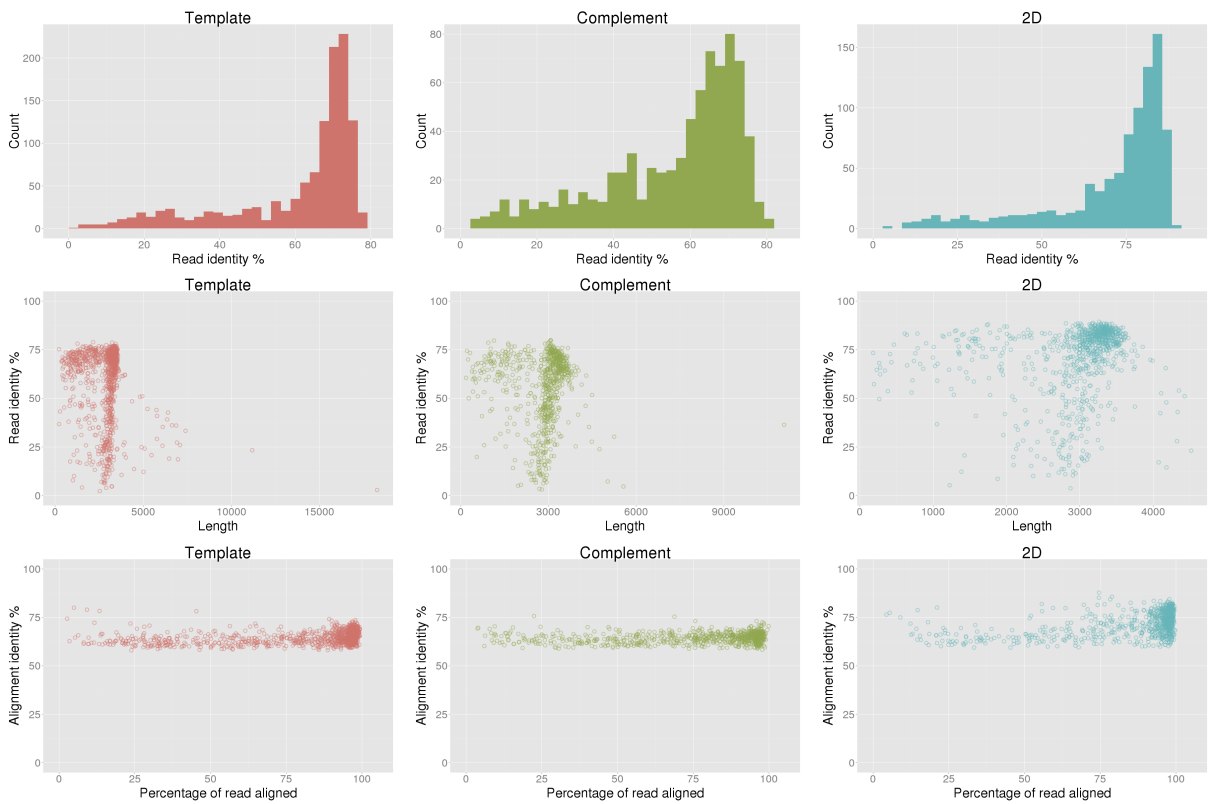
ID	Size	Number of Reads	% of Reads	Mean read length	Aligned bases	Mean coverage	Longest Perf Kmer
Control sequence	3560	904	5.16	2944.02	2604870	731.71	129
Escherichia coli	4641652	11290	64.47	5603.79	61742446	13.30	166

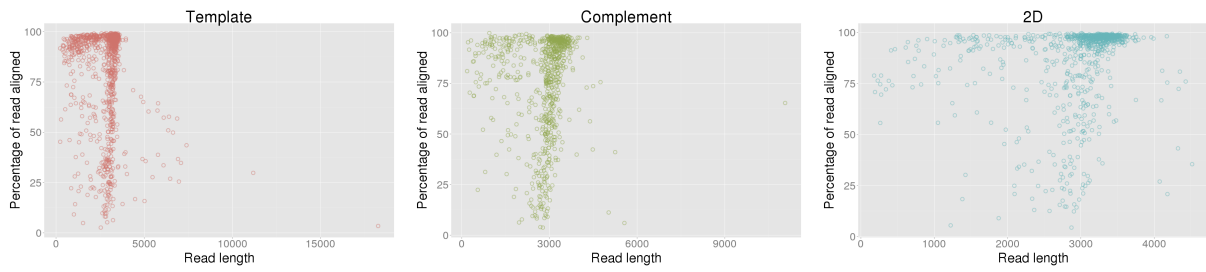
## Control sequence error analysis

	Template	Complement	2D
Overall base identity (excluding indels)	59.71%	55.27%	71.37%
Aligned base identity (excluding indels)	77.84%	78.72%	85.72%
Identical bases per 100 aligned bases (including indels)	64.89%	64.32%	72.92%
Inserted bases per 100 aligned bases (including indels)	4.55%	4.79%	3.53%
Deleted bases per 100 aligned bases (including indels)	12.10%	13.50%	11.41%
Substitutions per 100 aligned bases (including indels)	18.47%	17.39%	12.14%
Mean insertion size	1.53	1.57	1.47
Mean deletion size	1.67	1.80	1.74

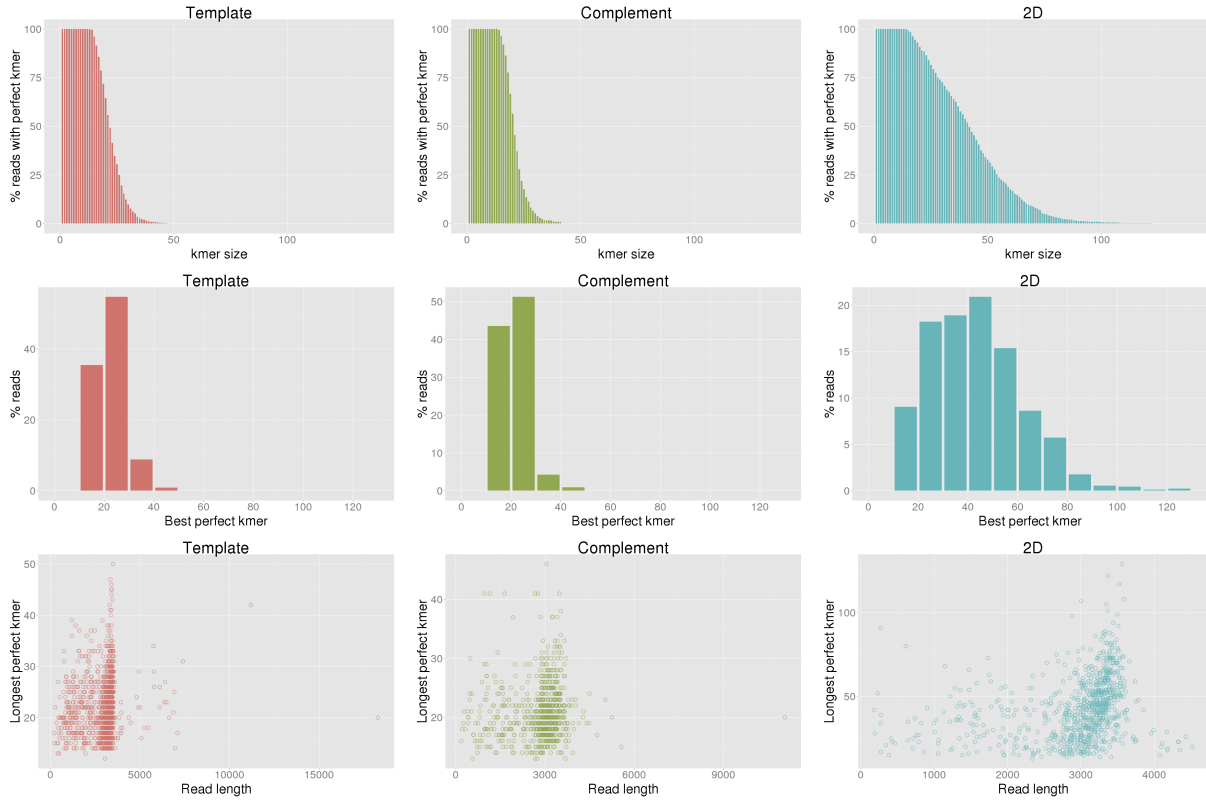


## Control sequence read identity

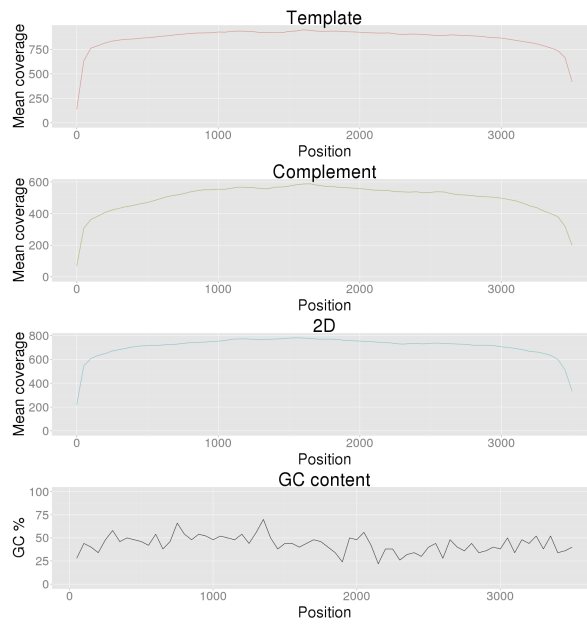




## Control sequence perfect kmers



## Control sequence coverage



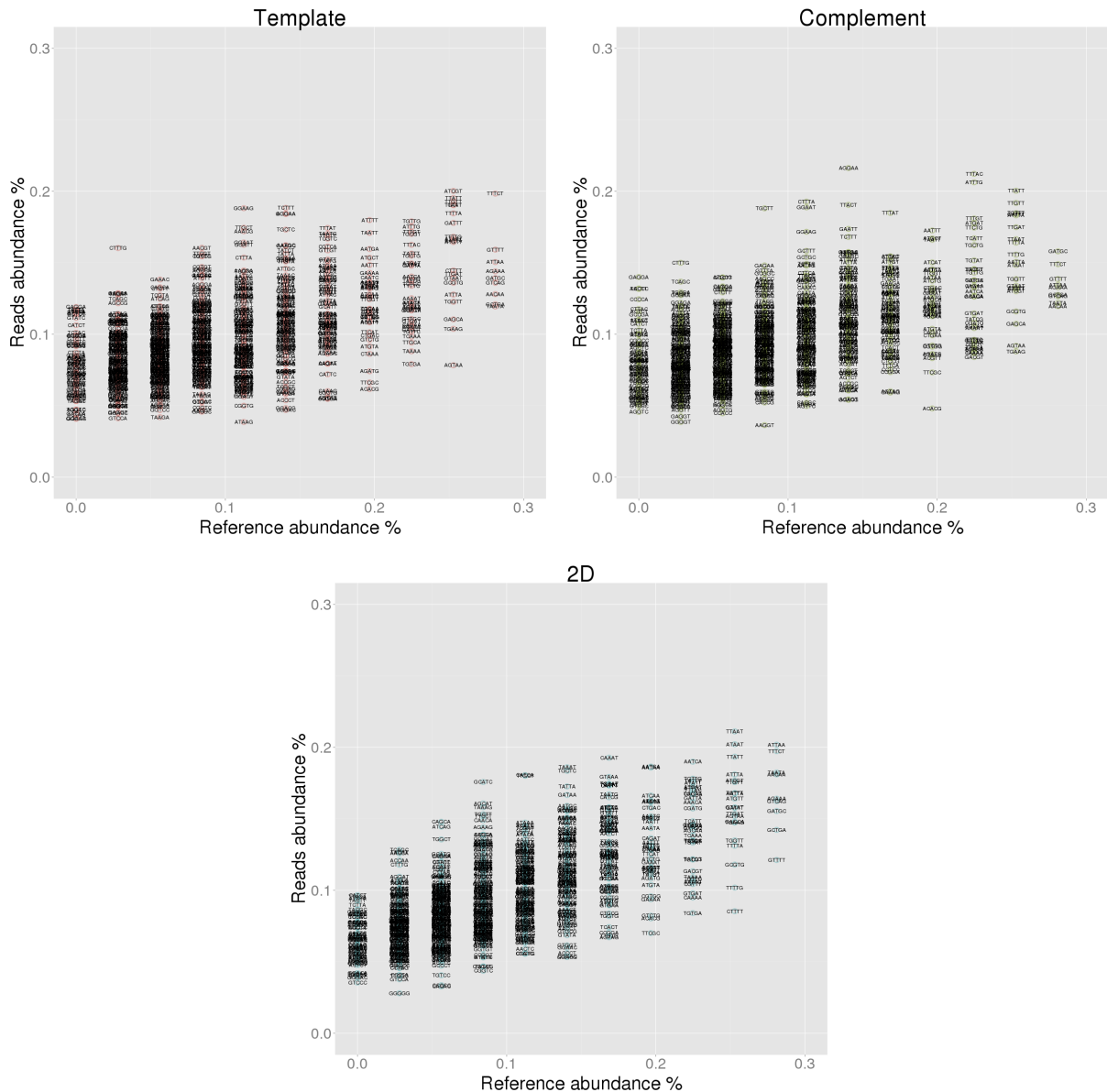
# Control sequence 5-mer analysis

## Under-represented 5-mers

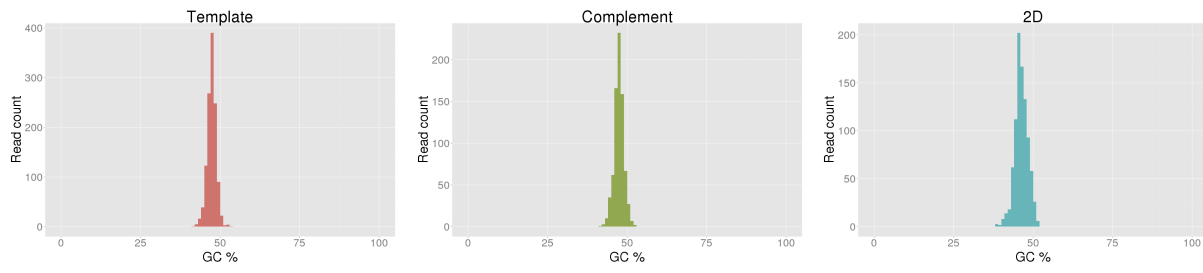
Rank	Template				Complement				2D			
	kmer	Ref %	Read %	Diff %	kmer	Ref %	Read %	Diff %	kmer	Ref %	Read %	Diff %
1	TTTTT	0.759	0.128	-0.631	TTTTT	0.759	0.078	-0.680	TTTTT	0.759	0.035	-0.724
2	AAAAA	0.478	0.098	-0.380	AAAAA	0.478	0.064	-0.414	AAAAA	0.478	0.036	-0.441
3	TGATG	0.393	0.136	-0.257	AAAAC	0.337	0.121	-0.217	TGATG	0.393	0.157	-0.236
4	AAAAC	0.337	0.124	-0.214	TGATG	0.393	0.189	-0.205	AAAAC	0.337	0.123	-0.214
5	GATGT	0.309	0.096	-0.213	GATGT	0.309	0.113	-0.196	GATGT	0.309	0.126	-0.183
6	CTGAT	0.309	0.119	-0.190	GCAAT	0.309	0.127	-0.182	CTGAT	0.309	0.137	-0.172
7	GCAAT	0.309	0.127	-0.182	TGAAG	0.253	0.088	-0.165	CTTTT	0.253	0.085	-0.168
8	AATAT	0.309	0.134	-0.175	AATAT	0.309	0.148	-0.161	GCAAT	0.309	0.148	-0.161
9	AGTAA	0.253	0.078	-0.175	AACAA	0.281	0.120	-0.161	GTTTT	0.281	0.121	-0.160
10	TAATA	0.281	0.119	-0.162	AGTAA	0.253	0.092	-0.161	TTTTG	0.253	0.102	-0.151

## Over-represented 5-mers

Rank	Template				Complement				2D			
	kmer	Ref %	Read %	Diff %	kmer	Ref %	Read %	Diff %	kmer	Ref %	Read %	Diff %
1	CTTTG	0.028	0.160	0.132	GAGGA	0.000	0.140	0.140	TCAGC	0.028	0.128	0.100
2	GAGGA	0.000	0.119	0.119	TACTT	0.000	0.132	0.132	TACAT	0.028	0.127	0.099
3	TACTT	0.000	0.117	0.117	ACCCA	0.000	0.132	0.132	AACCA	0.028	0.126	0.098
4	TCTTA	0.000	0.117	0.117	CCCCA	0.000	0.125	0.125	CATCT	0.000	0.097	0.097
5	CCCCA	0.000	0.116	0.116	CTTTG	0.028	0.150	0.122	TTAGA	0.000	0.096	0.096
6	ATCTA	0.000	0.115	0.115	CTTAC	0.000	0.118	0.118	ATCTA	0.000	0.094	0.094
7	GCTCC	0.000	0.114	0.114	ACTCT	0.000	0.116	0.116	TACTT	0.000	0.093	0.093
8	ACTCT	0.000	0.114	0.114	GCCGA	0.000	0.114	0.114	ACCAA	0.028	0.121	0.093
9	GTATC	0.000	0.112	0.112	ATACT	0.000	0.110	0.110	CAGCA	0.056	0.148	0.092
10	CATCT	0.000	0.106	0.106	TATAC	0.000	0.110	0.110	GCATC	0.084	0.176	0.092

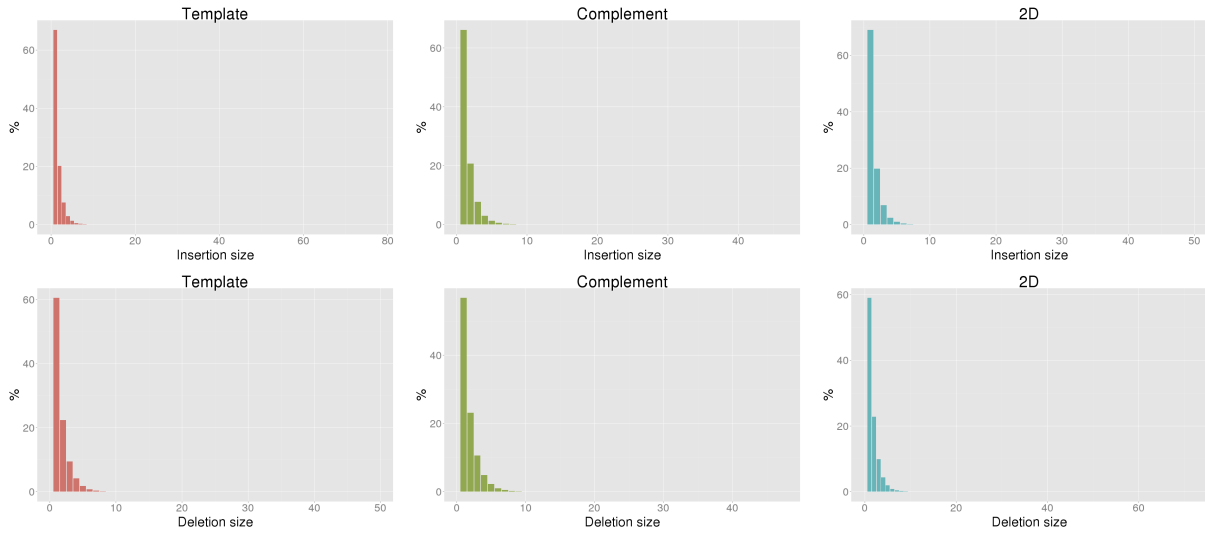


## Control sequence GC content

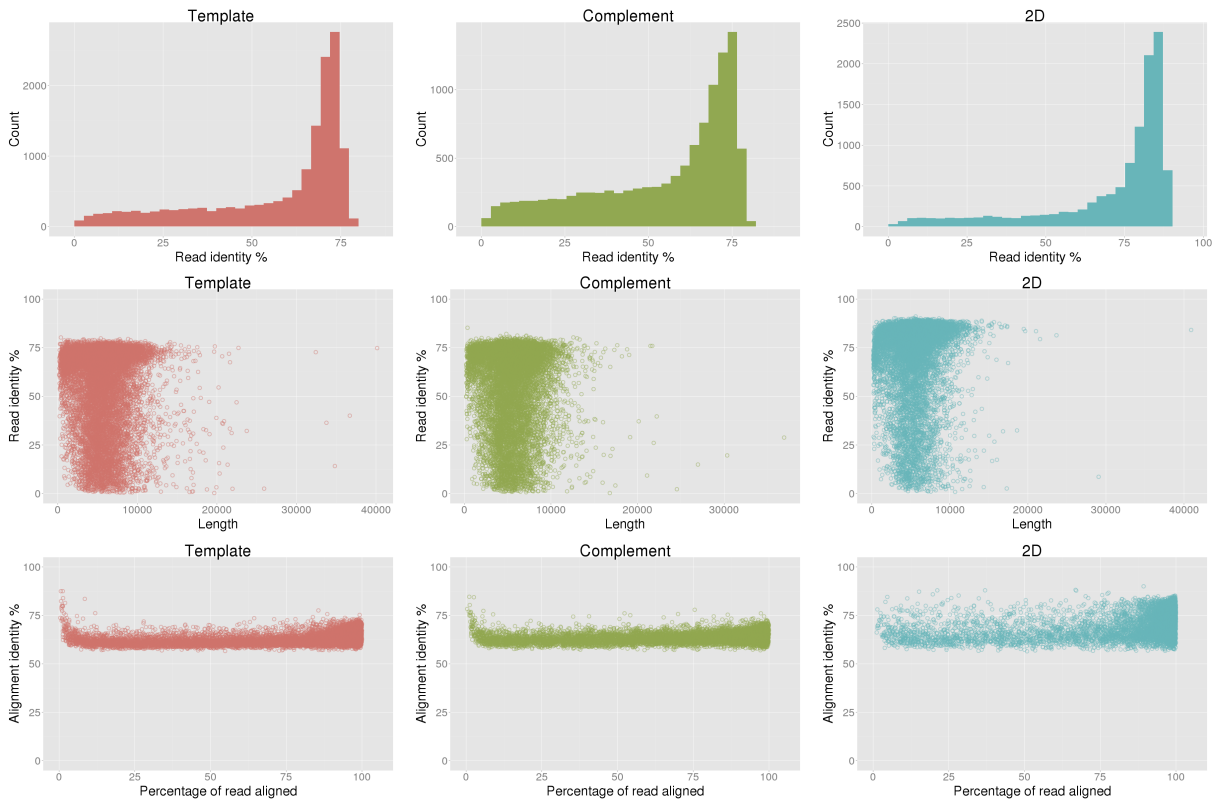


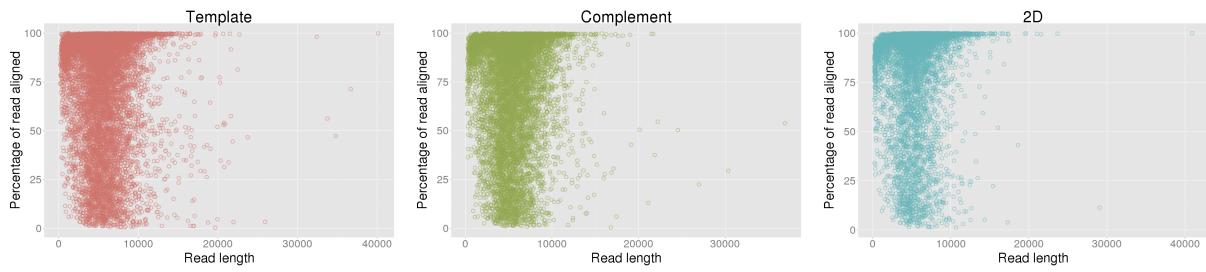
## Escherichia coli error analysis

	Template	Complement	2D
Overall base identity (excluding indels)	56.33%	54.30%	71.43%
Aligned base identity (excluding indels)	77.17%	78.84%	85.92%
Identical bases per 100 aligned bases (including indels)	63.78%	64.04%	73.19%
Inserted bases per 100 aligned bases (including indels)	4.92%	4.78%	3.61%
Deleted bases per 100 aligned bases (including indels)	12.43%	14.00%	11.21%
Substitutions per 100 aligned bases (including indels)	18.87%	17.19%	11.99%
Mean insertion size	1.57	1.58	1.50
Mean deletion size	1.71	1.82	1.76

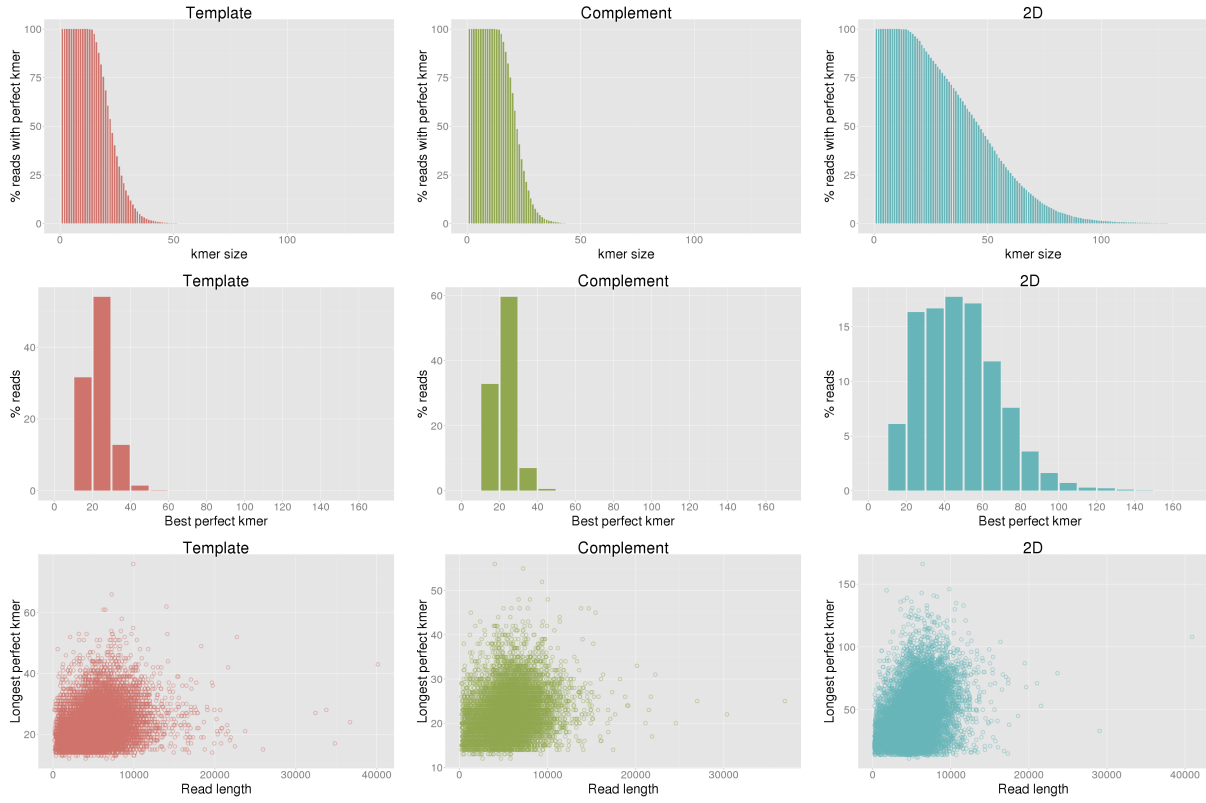


## Escherichia coli read identity

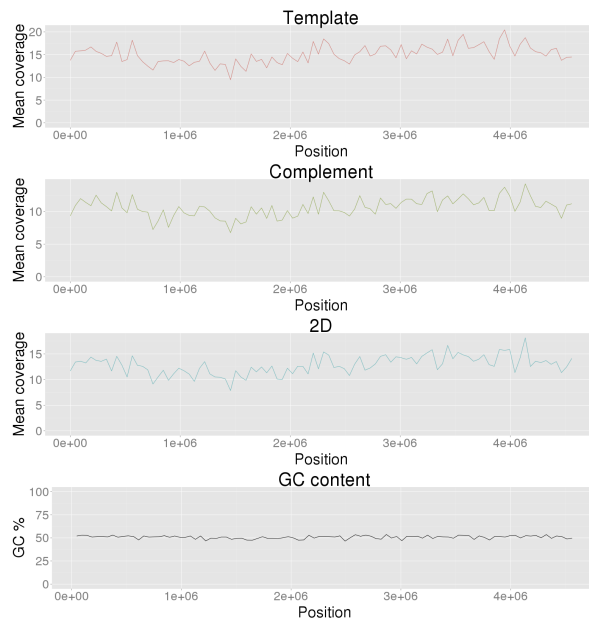




## Escherichia coli perfect kmers



## Escherichia coli coverage



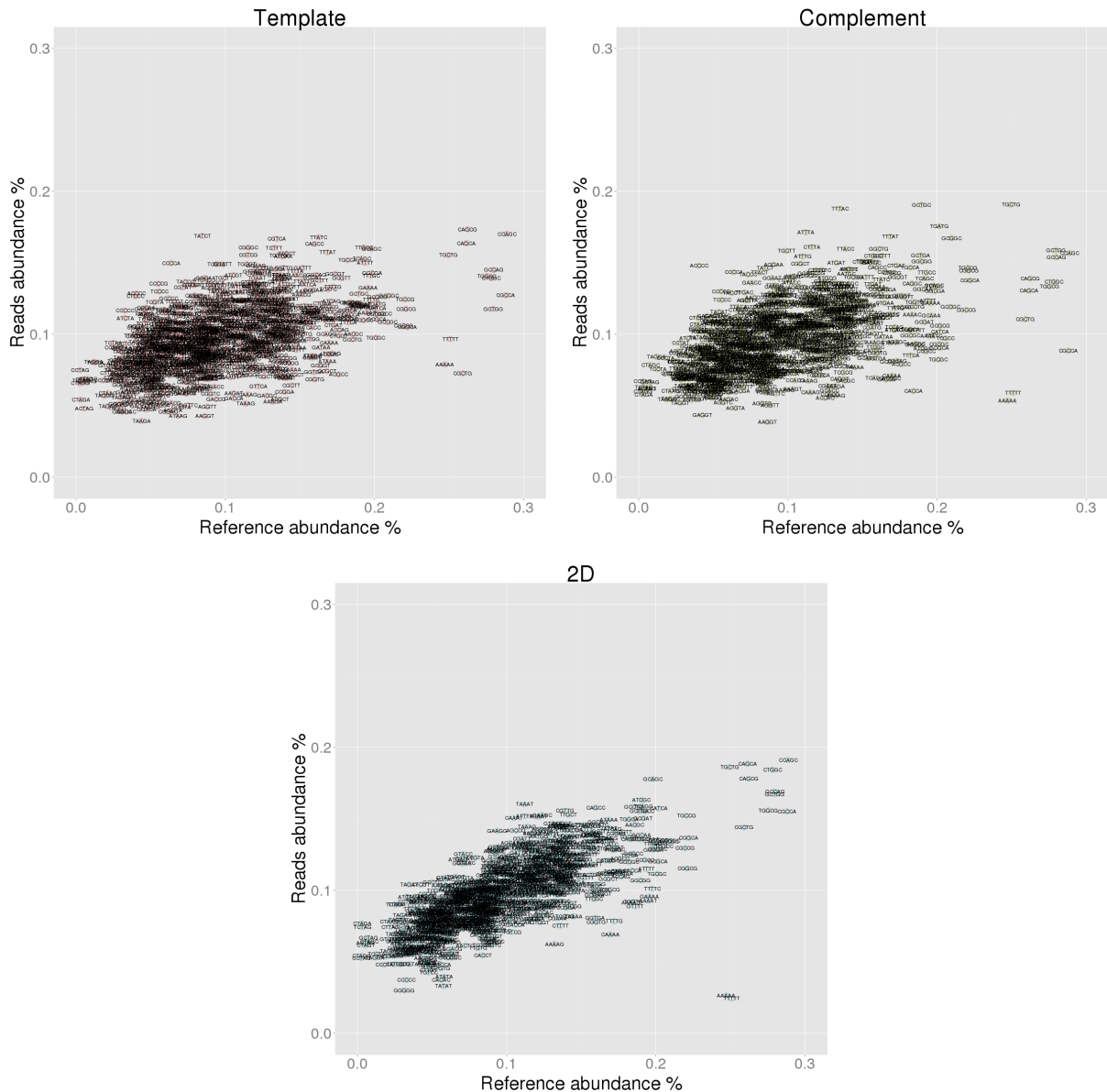
# Escherichia coli 5-mer analysis

## Under-represented 5-mers

Rank	Template				Complement				2D			
	kmer	Ref %	Read %	Diff %	kmer	Ref %	Read %	Diff %	kmer	Ref %	Read %	Diff %
1	CGCTG	0.259	0.073	-0.186	CGCCA	0.288	0.088	-0.200	TTTTT	0.251	0.024	-0.227
2	AAAAA	0.247	0.079	-0.168	AAAAA	0.247	0.054	-0.194	AAAAA	0.247	0.026	-0.221
3	GCTGG	0.279	0.118	-0.162	TTTTT	0.251	0.059	-0.192	CGCCA	0.288	0.155	-0.133
4	CGCCA	0.288	0.127	-0.161	CGCTG	0.259	0.111	-0.149	TGGCG	0.275	0.156	-0.120
5	TTTTT	0.251	0.097	-0.154	TGGCG	0.275	0.133	-0.142	CGCTG	0.259	0.144	-0.115
6	CTGGC	0.278	0.139	-0.139	CTGGC	0.278	0.137	-0.142	GCTGG	0.279	0.167	-0.112
7	GCCAG	0.280	0.145	-0.135	CCAGC	0.289	0.157	-0.132	GCCAG	0.280	0.169	-0.111
8	TGGCG	0.275	0.141	-0.135	CAGCA	0.261	0.131	-0.131	CGGCG	0.221	0.115	-0.106
9	CCAGC	0.289	0.170	-0.118	GCCAG	0.280	0.154	-0.126	AAAAT	0.195	0.093	-0.102
10	CGGCA	0.222	0.105	-0.117	CACCA	0.184	0.060	-0.124	CAAAA	0.169	0.069	-0.100

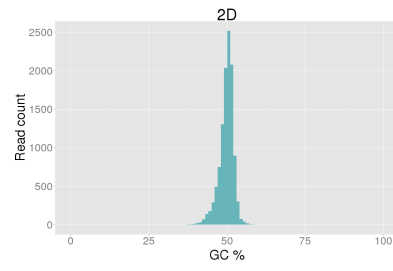
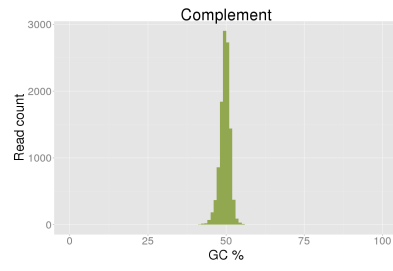
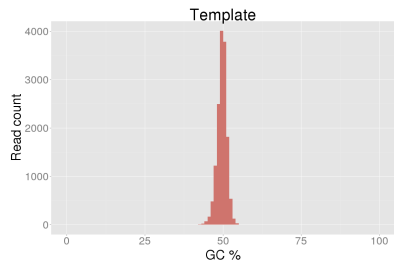
## Over-represented 5-mers

Rank	Template				Complement				2D			
	kmer	Ref %	Read %	Diff %	kmer	Ref %	Read %	Diff %	kmer	Ref %	Read %	Diff %
1	ACCCC	0.040	0.128	0.088	ACCCC	0.040	0.148	0.108	CTAGA	0.003	0.077	0.074
2	CTCCC	0.040	0.127	0.087	CCCCA	0.064	0.143	0.080	TCTAG	0.003	0.074	0.071
3	CCCCA	0.064	0.150	0.086	CCCCG	0.055	0.130	0.075	TAGAT	0.035	0.104	0.070
4	TATCT	0.085	0.169	0.084	TAGGA	0.012	0.084	0.072	TCTAA	0.025	0.090	0.065
5	CCCCC	0.033	0.117	0.084	CTCCC	0.040	0.111	0.072	TTAGA	0.026	0.090	0.064
6	CCCCG	0.055	0.135	0.080	CTAGC	0.008	0.079	0.071	ATCTA	0.033	0.095	0.063
7	ATCTA	0.033	0.111	0.078	TACCC	0.073	0.142	0.069	CTCGT	0.042	0.104	0.062
8	TCCCC	0.056	0.130	0.074	TCCCC	0.056	0.124	0.068	GCTAG	0.007	0.067	0.059
9	CCTAG	0.003	0.075	0.072	CTAAT	0.040	0.107	0.067	CCTCC	0.033	0.092	0.059
10	GAGAG	0.046	0.118	0.072	GAGAG	0.046	0.113	0.067	ACTAG	0.006	0.063	0.058

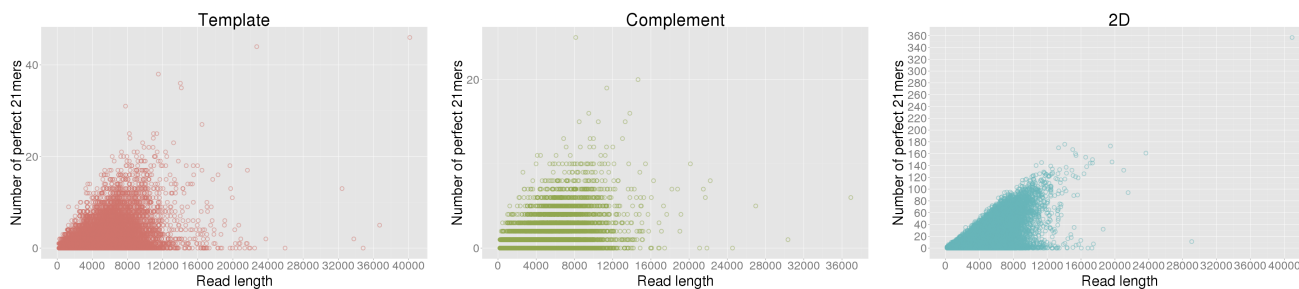




# Escherichia coli GC content



## 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	8.85	8.53	5.09	0.00	9.04	8.34	5.30	0.00	8.93	8.20	4.78
C	8.72	0.00	9.04	9.97	9.27	0.00	8.69	9.65	9.26	0.00	9.90	9.23
G	9.46	9.08	0.00	8.56	9.12	8.89	0.00	8.87	8.98	10.15	0.00	8.90
T	5.41	8.61	8.68	0.00	5.60	8.31	8.92	0.00	4.90	7.99	8.78	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 (3.08%)	TTC (3.23%)	AAA (4.10%)	AAA (2.73%)	AAA (2.97%)	AAA (3.99%)	GCA (3.07%)	AAA (2.72%)	AAA (3.52%)
2	AAA (2.85%)	AAA (2.98%)	TTC (3.52%)	TTC (2.72%)	GCA (2.73%)	GCA (3.38%)	TTC (2.89%)	GCA (2.59%)	GCA (3.49%)
3	GCA (2.74%)	TGC (2.91%)	GCA (3.16%)	TGC (2.72%)	TGC (2.70%)	GAA (3.26%)	AAA (2.76%)	TGC (2.50%)	GAA (2.97%)
4	TGC (2.55%)	GCA (2.75%)	GAA (2.86%)	GCA (2.71%)	GGC (2.70%)	TTC (3.08%)	TCA (2.49%)	TCA (2.48%)	TTC (2.86%)
5	ATC (2.51%)	GCC (2.42%)	TTT (2.78%)	CAG (2.45%)	TTC (2.57%)	TTT (2.75%)	ATC (2.43%)	GCC (2.47%)	TTT (2.72%)
6	TCA (2.35%)	TCA (2.34%)	TGC (2.58%)	GAA (2.40%)	GAA (2.54%)	TGC (2.43%)	TGC (2.41%)	TTC (2.29%)	GTT (2.61%)
7	TTT (2.25%)	GGC (2.23%)	AAT (2.45%)	GGC (2.39%)	TCA (2.32%)	TCA (2.35%)	GAA (2.35%)	CAG (2.27%)	AAT (2.41%)
8	GCC (2.17%)	GAA (2.20%)	TCA (2.18%)	ATC (2.26%)	CAG (2.32%)	CAA (2.16%)	GCG (2.21%)	GAA (2.24%)	TCA (2.23%)
9	GAA (2.17%)	AAT (2.17%)	CAA (2.15%)	TCA (2.19%)	GCC (2.31%)	ATC (2.14%)	CAG (2.20%)	GCG (2.23%)	GCC (2.23%)
10	GGC (2.16%)	ATC (2.13%)	GCC (2.11%)	GCC (2.17%)	AAT (2.20%)	GCC (2.14%)	AAT (2.15%)	GCC (2.17%)	TGC (2.22%)
-10	AGT (0.96%)	CCT (0.92%)	GTA (0.93%)	ACT (1.04%)	ACT (0.94%)	CCC (0.96%)	CTC (1.05%)	CTT (0.99%)	AGG (0.97%)
-9	CTC (0.96%)	AGT (0.92%)	AGA (0.93%)	AGT (0.97%)	CGA (0.94%)	CTC (0.91%)	ACT (1.04%)	ACT (0.98%)	GCG (0.93%)
-8	AGA (0.95%)	GGG (0.91%)	GGT (0.91%)	GGA (0.93%)	AGG (0.94%)	AGT (0.88%)	GAG (0.90%)	GGG (0.97%)	CTT (0.91%)
-7	GGA (0.90%)	CTT (0.90%)	CTT (0.90%)	CTC (0.88%)	CCC (0.93%)	CCT (0.84%)	AGA (0.89%)	CGA (0.90%)	CCC (0.91%)
-6	CCC (0.87%)	GAG (0.84%)	GGG (0.86%)	GAG (0.87%)	CCT (0.91%)	AGG (0.80%)	GGA (0.83%)	CCC (0.88%)	GAG (0.83%)
-5	GAG (0.79%)	CGA (0.83%)	AGG (0.85%)	CCC (0.82%)	GAG (0.85%)	GGG (0.79%)	AGG (0.80%)	AGA (0.88%)	CGA (0.82%)
-4	AGG (0.73%)	AGA (0.76%)	AGT (0.78%)	AGG (0.72%)	CTC (0.84%)	ACT (0.78%)	CCC (0.75%)	CCT (0.86%)	AGA (0.72%)
-3	GGG (0.70%)	GGA (0.67%)	GAG (0.67%)	GGG (0.60%)	GGG (0.77%)	GAG (0.66%)	GGG (0.67%)	GGA (0.72%)	GGA (0.64%)
-2	CTA (0.47%)	TAG (0.54%)	TAG (0.38%)	CTA (0.53%)	CTA (0.52%)	CTA (0.40%)	CTA (0.54%)	CTA (0.66%)	TAG (0.48%)
-1	TAG (0.42%)	CTA (0.48%)	CTA (0.33%)	TAG (0.44%)	TAG (0.52%)	TAG (0.39%)	TAG (0.49%)	TAG (0.65%)	CTA (0.42%)

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 (1.05%)	TTTC (1.10%)	AAAA (1.32%)	CAGC (0.97%)	TGGC (1.02%)	AAAA (1.08%)	GGCA (0.87%)	TGGC (0.95%)	GGCA (1.08%)
2	GAAA (0.92%)	TGCC (0.94%)	TTTT (1.30%)	TGGC (0.88%)	CAGC (1.01%)	CAAA (1.02%)	ATCA (0.85%)	CAGC (0.90%)	GAAA (0.97%)
3	AAAA (0.88%)	TTGC (0.92%)	GAAA (1.17%)	ATCA (0.83%)	CGGC (0.92%)	GAAA (1.01%)	TTTC (0.82%)	TTCA (0.86%)	TTTC (0.89%)
4	ATCA (0.84%)	GAAA (0.90%)	TTTT (0.94%)	CTGC (0.83%)	CTGC (0.87%)	TTTC (0.92%)	CAGC (0.81%)	ATCA (0.80%)	CAAA (0.88%)
5	CAGC (0.81%)	CAGC (0.89%)	CAAA (0.92%)	CGGC (0.80%)	CAAA (0.86%)	GGCA (0.90%)	CAAA (0.80%)	CAAA (0.78%)	CGTT (0.87%)
6	TGGC (0.80%)	AAAA (0.88%)	GGCA (0.90%)	CAAA (0.78%)	ATCA (0.84%)	TGAA (0.89%)	TTCA (0.80%)	CTGC (0.78%)	GGAA (0.86%)
7	TTCA (0.79%)	TGGC (0.87%)	GCAA (0.89%)	TTGC (0.78%)	TGCC (0.84%)	ATCA (0.88%)	GAAA (0.79%)	TGCC (0.76%)	TGCA (0.85%)
8	AACG (0.79%)	TTCC (0.87%)	AAAT (0.83%)	CCAG (0.76%)	TTGC (0.81%)	AGAA (0.88%)	CTTC (0.78%)	TAAA (0.74%)	TGTT (0.85%)
9	TTGC (0.77%)	TTCA (0.87%)	GGAA (0.83%)	AAAA (0.75%)	TTCC (0.80%)	AGCA (0.86%)	GCCA (0.77%)	GCCA (0.74%)	AAAA (0.84%)
10	TGCC (0.77%)	CTGC (0.82%)	TTCC (0.82%)	TGCC (0.75%)	TTCA (0.77%)	GGAA (0.86%)	AACA (0.76%)	CGGC (0.73%)	AGCA (0.82%)
-10	TAGT (0.12%)	CCCT (0.12%)	TTAG (0.11%)	TTAG (0.12%)	CCTC (0.12%)	TCTA (0.10%)	TCTA (0.13%)	CTAT (0.15%)	TCGA (0.12%)
-9	GAGG (0.12%)	TAGT (0.12%)	CGAG (0.10%)	AGGG (0.11%)	GGAC (0.12%)	CTAT (0.10%)	GTAG (0.13%)	CCCC (0.14%)	CCCT (0.11%)
-8	TTAG (0.11%)	TCTA (0.12%)	TAGT (0.09%)	GAGG (0.11%)	CTAT (0.12%)	ACCT (0.10%)	CCCC (0.13%)	ACCT (0.14%)	CGGA (0.11%)
-7	CTAA (0.11%)	GGAC (0.11%)	ACTA (0.08%)	CTAA (0.10%)	ACCT (0.11%)	CGAG (0.09%)	ACTA (0.13%)	CGGA (0.13%)	TATA (0.11%)
-6	TCTA (0.10%)	CGGA (0.11%)	TAGA (0.08%)	GGAC (0.09%)	CTAA (0.11%)	GGAC (0.09%)	CTAA (0.12%)	CTAA (0.13%)	TCTA (0.10%)
-5	GGAC (0.09%)	CTAA (0.10%)	GGAC (0.07%)	CCCT (0.09%)	TAGA (0.10%)	ACTA (0.09%)	CCCT (0.12%)	CCCT (0.10%)	ACTA (0.10%)
-4	TAGA (0.07%)	TAGG (0.07%)	TCTA (0.07%)	TAGA (0.09%)	CCCT (0.08%)	CCCT (0.07%)	TAGA (0.09%)	TAGA (0.09%)	TAGG (0.06%)
-3	CCTA (0.06%)	TAGA (0.06%)	TAGG (0.06%)	CCTA (0.07%)	TAGG (0.07%)	TAGG (0.06%)	CCTA (0.06%)	TAGG (0.08%)	TAGA (0.06%)
-2	TAGG (0.05%)	CCTA (0.05%)	CCTA (0.04%)	TAGG (0.05%)	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 (0.02%)	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 (0.37%)	CAGCA (0.38%)	CAGCA (0.42%)	CAGCA (0.42%)	CAGCA (0.43%)	CAGCA (0.51%)	CAGCA (0.39%)	CTGGC (0.39%)	CAGCA (0.46%)
2	TTATC (0.33%)	CTGGC (0.35%)	GAAAA (0.41%)	CTGGC (0.34%)	CTGGC (0.39%)	GAAAA (0.35%)	TGGCA (0.32%)	CAGCA (0.35%)	TGGCA (0.42%)
3	CTGGC (0.33%)	TTGGC (0.35%)	CAAAA (0.37%)	CCAGC (0.33%)	CCAGC (0.33%)	CGGCA (0.35%)	CGGCA (0.31%)	CCAGC (0.29%)	CGGCA (0.37%)
4	ATTTTC (0.29%)	TTTTGC (0.33%)	AGAAA (0.33%)	GCGGC (0.31%)	AATCA (0.33%)	ATAAA (0.34%)	CGCCA (0.31%)	GCCAG (0.29%)	GCGTT (0.31%)
5	TTTTCT (0.29%)	TTTTCC (0.32%)	GCAAA (0.33%)	GCTGC (0.30%)	CATCA (0.32%)	CATCA (0.33%)	CTGGC (0.31%)	ATAAA (0.28%)	GAAAA (0.31%)
6	CAAAA (0.29%)	GCTGC (0.31%)	TGGCA (0.33%)	CATCA (0.30%)	GCGGC (0.31%)	CAGAA (0.33%)	TCTTC (0.29%)	CGCCA (0.28%)	GCAAA (0.30%)
7	CATCA (0.28%)	GCCAG (0.29%)	TCTTC (0.32%)	GCAGC (0.29%)	GCTGC (0.31%)	AAGAA (0.33%)	CATCA (0.28%)	TTTTCA (0.28%)	TTGCC (0.29%)
8	GAAAA (0.28%)	CGCCA (0.29%)	CGTTT (0.31%)	TCTTC (0.28%)	ATAAA (0.30%)	TCTTC (0.32%)	GCAAA (0.27%)	CATCA (0.28%)	AAGAA (0.29%)
9	TGGCG (0.28%)	GCAGC (0.29%)	TTTTCC (0.31%)	TTATC (0.28%)	GCAGC (0.29%)	AGAAA (0.32%)	CCAGC (0.27%)	GCAGC (0.27%)	TCTTC (0.29%)
10	TTGCC (0.27%)	ATTTTC (0.29%)	TTATC (0.31%)	CGGCA (0.27%)	TCAGC (0.29%)	AATCA (0.32%)	TGGCG (0.26%)	TGGCG (0.26%)	CTGCA (0.28%)
-10	ACCTA (0.01%)	CCCTA (0.01%)	CCCTA (0.01%)	CTAGC (0.01%)	CCCTA (0.01%)	CCCTA (0.01%)	GGACC (0.01%)	CCCTA (0.01%)	ACCTA (0.01%)
-9	GGACC (0.00%)	GGACC (0.01%)	ACCTA (0.00%)	TAGGG (0.01%)	ACCTA (0.01%)	ACCTA (0.01%)	CCCTA (0.01%)	TAGGA (0.01%)	TAGGA (0.01%)
-8	CTAGC (0.00%)	GCTAG (0.00%)	GCTAG (0.00%)	CTAGT (0.01%)	CTAGC (0.01%)	GCTAG (0.01%)	GCTAG (0.01%)	GCTAG (0.01%)	ACTAG (0.00%)
-7	ACTAG (0.00%)	ACTAG (0.00%)	CTAGC (0.00%)	GCTAG (0.01%)	GCTAG (0.00%)	CTAGC (0.00%)	CCTAG (0.01%)	ACTAG (0.01%)	GCTAG (0.00%)
-6	CCTAG (0.00%)	CTAGC (0.00%)	ACTAG (0.00%)	CCCTA (0.00%)	CTAGT (0.00%)	ACTAG (0.00%)	CTAGC (0.00%)	CTAGC (0.01%)	CTAGC (0.00%)
-5	CTAGT (0.00%)	CTAGT (0.00%)	CTAGT (0.00%)	ACTAG (0.00%)	ACTAG (0.00%)	CTAGT (0.00%)	CTAGT (0.00%)	CTAGT (0.00%)	CTAGT (0.00%)
-4	GCTAG (0.00%)	TCTAG (0.00%)	CCTAG (0.00%)	CTAGA (0.00%)	CTAGG (0.00%)	CTAGA (0.00%)	ACTAG (0.00%)	TCTAG (0.00%)	CTAGG (0.00%)
-3	TCTAG (0.00%)	CCTAG (0.00%)	CTAGG (0.00%)	CTAGG (0.00%)	CCTAG (0.00%)	TCTAG (0.00%)	TCTAG (0.00%)	CTAGA (0.00%)	CTAGA (0.00%)
-2	CTAGG (0.00%)	CTAGG (0.00%)	CTAGA (0.00%)	CCTAG (0.00%)	CTAGA (0.00%)	CTAGG (0.00%)	CTAGA (0.00%)	CTAGG (0.00%)	TCTAG (0.00%)
-1	CTAG (0.00%)	CTAG (0.00%)	TCTAG (0.00%)	TCTAG (0.00%)	TCTAG (0.00%)	CCTAG (0.00%)	CTAGG (0.00%)	CCTAG (0.00%)	CCTAG (0.00%)

Most common

Least common

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