

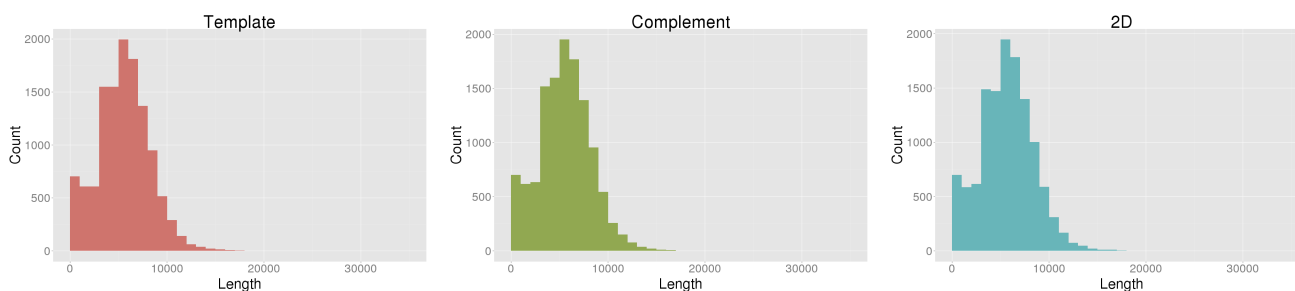
# NanoOK report for JOGrady\_MARC1b\_run1

## Pass and fail counts

Type	Pass	Fail
Template	12258	0
Complement	12258	0
2D	12258	0

## Read lengths

Type	NumReads	TotalBases	Mean	Longest	Shortest	N50	N50Count	N90	N90Count
Template	12258	68123762	5557.49	32654	182	6671	4001	3656	9153
Complement	12258	68119862	5557.18	31734	151	6677	3997	3688	9149
2D	12258	69409047	5662.35	32099	163	6804	3996	3720	9144



## Template alignments

Number of reads	12258
Number of reads with alignments	11682 (95.30%)
Number of reads without alignments	576 (4.70%)

ID	Size	Number of Reads	% of Reads	Mean read length	Aligned bases	Mean coverage	Longest Perf Kmer
Control sequence	3560	839	6.84	3137.38	2796046	785.41	51
Escherichia coli	4641652	10843	88.46	5992.03	70209063	15.13	76

## Complement alignments

Number of reads	12258
Number of reads with alignments	11700 (95.45%)
Number of reads without alignments	558 (4.55%)

ID	Size	Number of Reads	% of Reads	Mean read length	Aligned bases	Mean coverage	Longest Perf Kmer
Control sequence	3560	847	6.91	3090.14	2706387	760.22	51
Escherichia coli	4641652	10853	88.54	5988.96	69762992	15.03	66

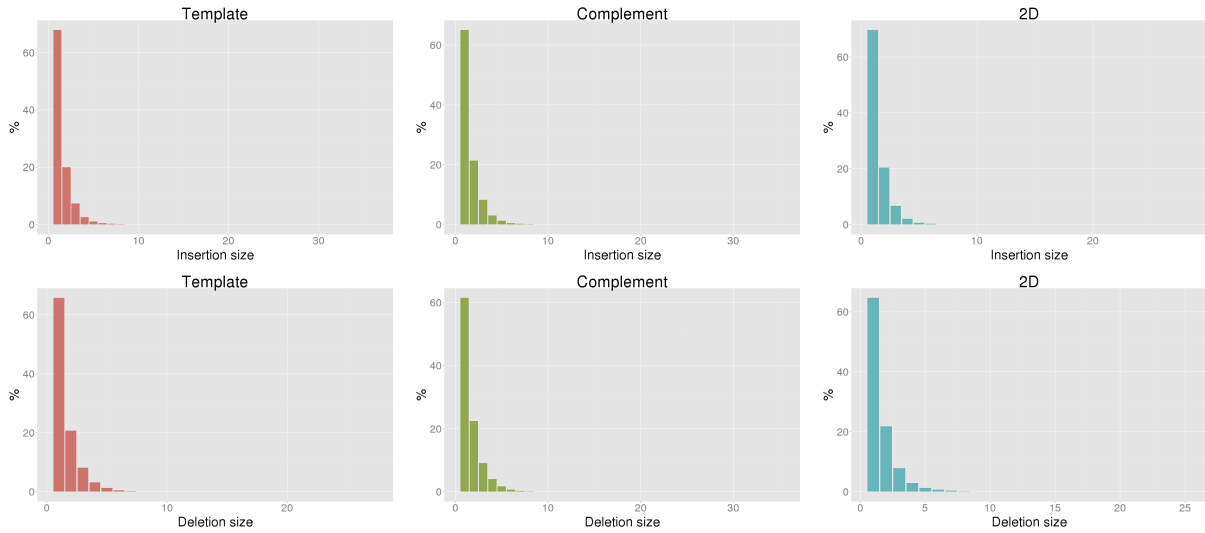
## 2D alignments

Number of reads	12258
Number of reads with alignments	11807 (96.32%)
Number of reads without alignments	451 (3.68%)

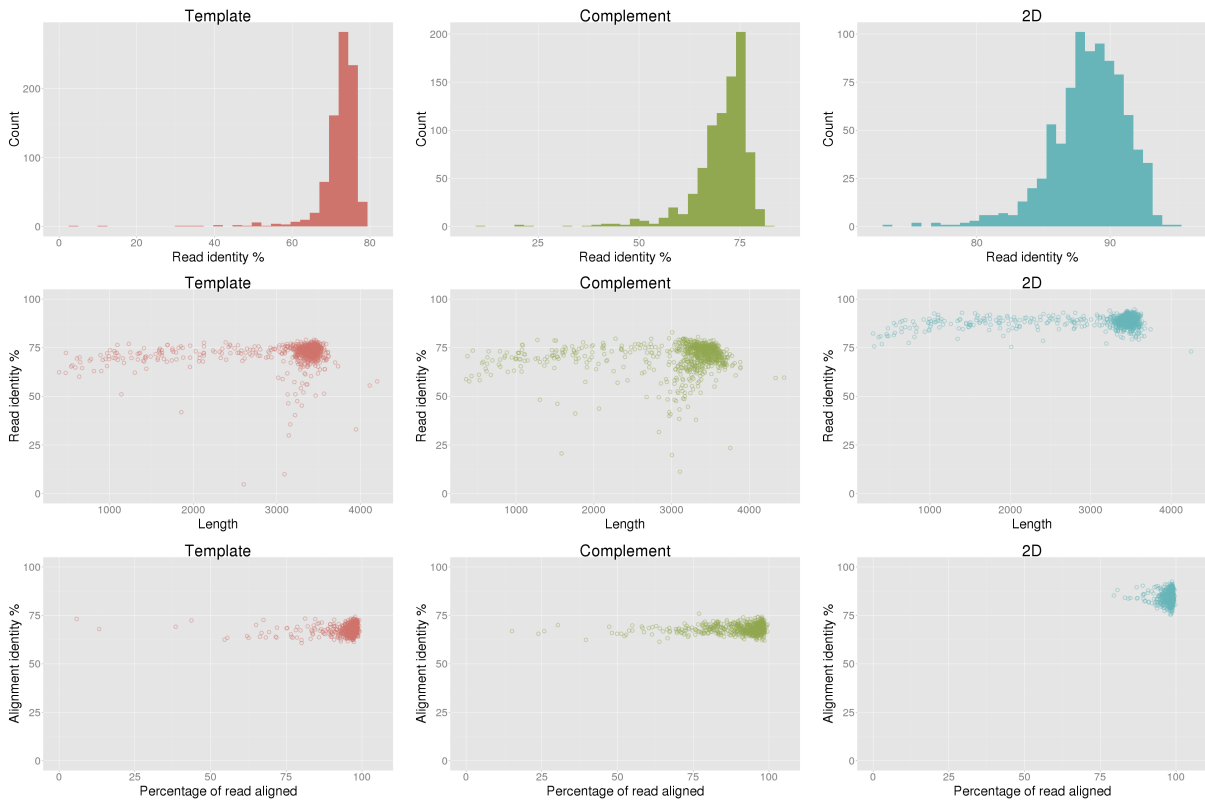
ID	Size	Number of Reads	% of Reads	Mean read length	Aligned bases	Mean coverage	Longest Perf Kmer
Control sequence	3560	854	6.97	3135.98	2804996	787.92	213
Escherichia coli	4641652	10953	89.35	6052.33	69678795	15.01	209

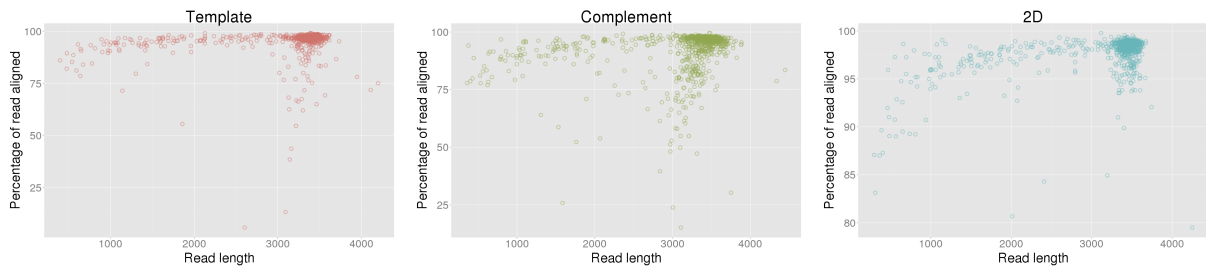
## Control sequence error analysis

	Template	Complement	2D
Overall base identity (excluding indels)	72.17%	70.52%	88.54%
Aligned base identity (excluding indels)	79.91%	81.22%	93.21%
Identical bases per 100 aligned bases (including indels)	67.94%	68.20%	84.53%
Inserted bases per 100 aligned bases (including indels)	4.74%	5.25%	2.86%
Deleted bases per 100 aligned bases (including indels)	10.23%	10.79%	6.45%
Substitutions per 100 aligned bases (including indels)	17.08%	15.77%	6.16%
Mean insertion size	1.54	1.59	1.45
Mean deletion size	1.57	1.67	1.60

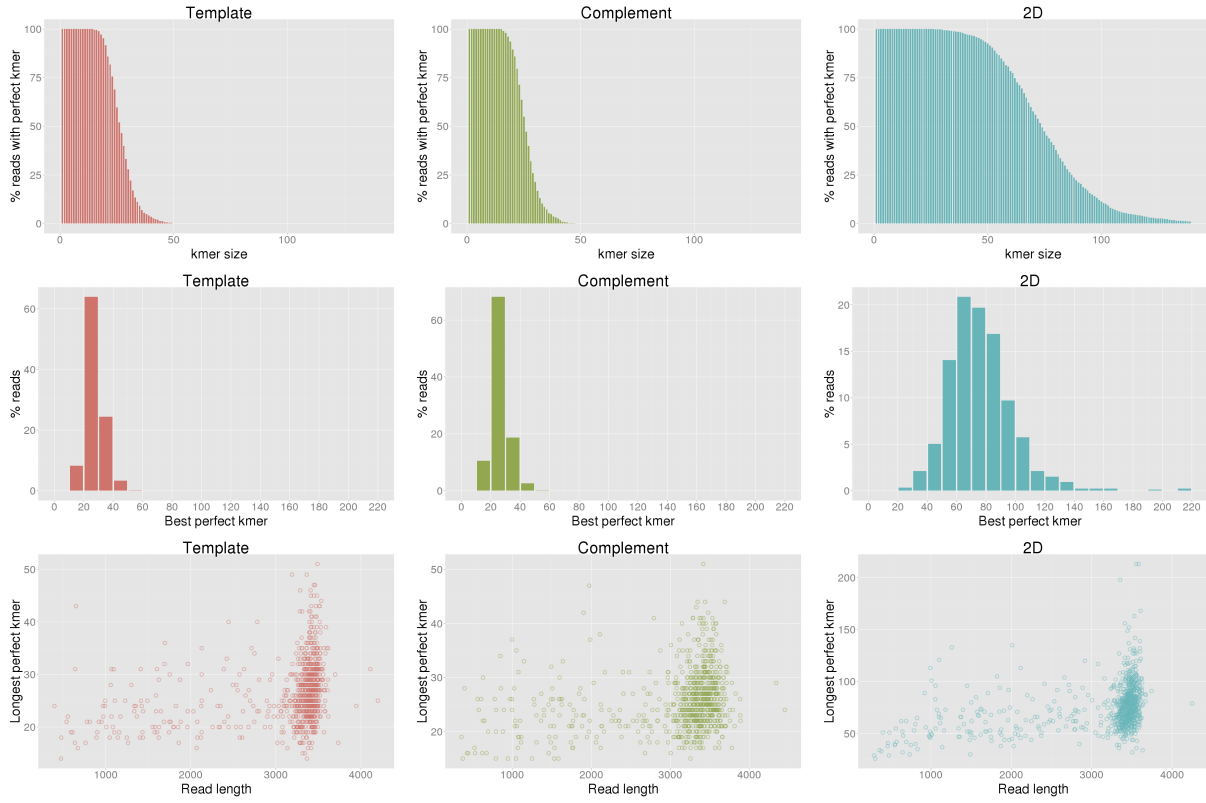


## Control sequence read identity

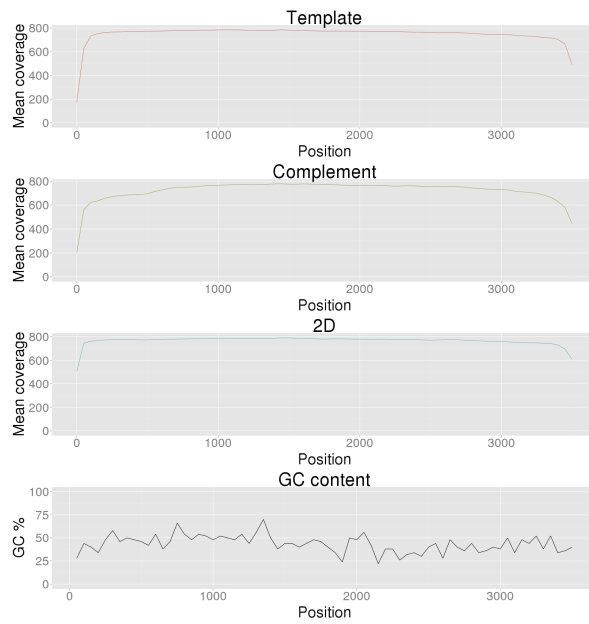




## Control sequence perfect kmers



## Control sequence coverage



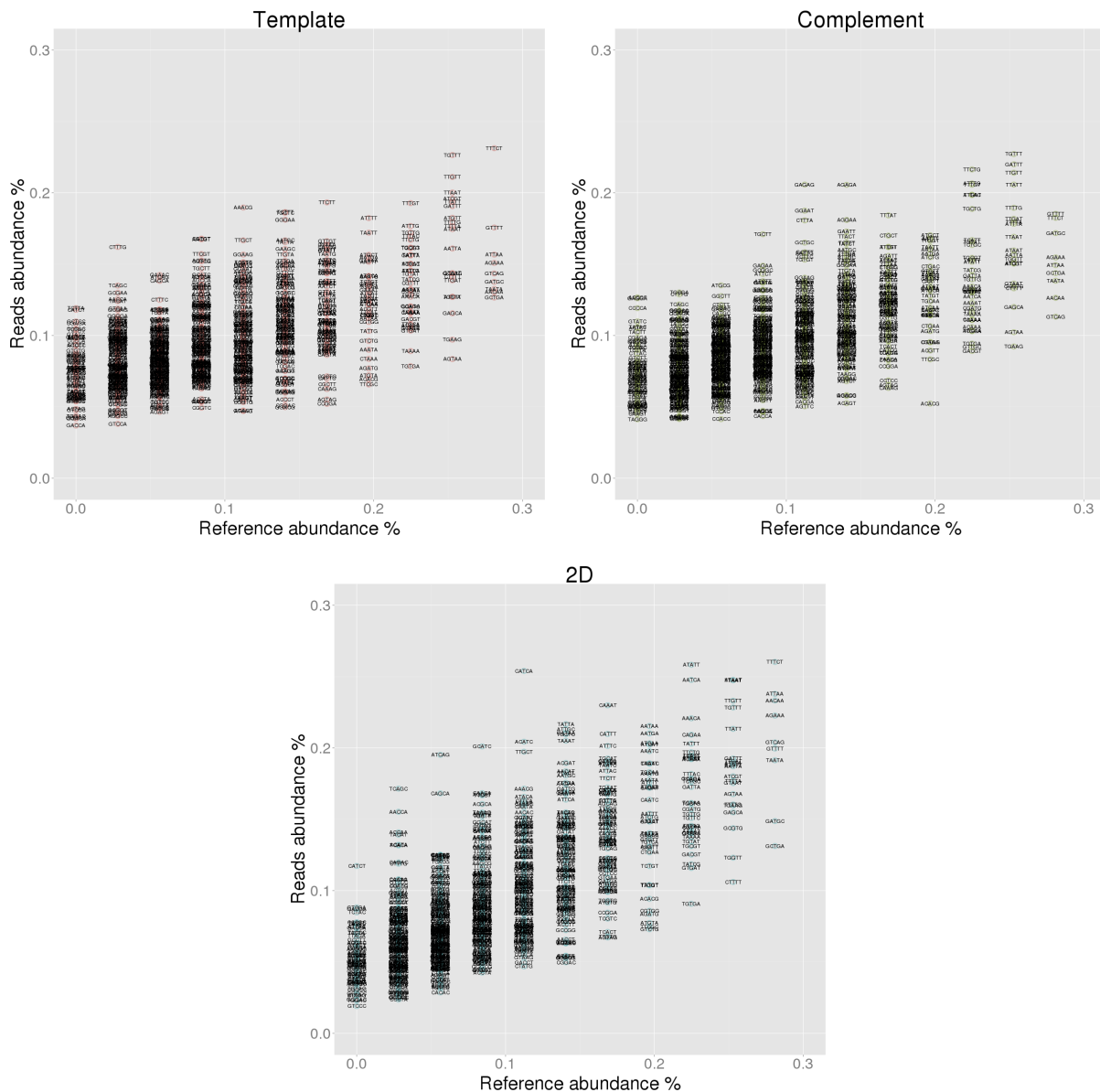
## Control sequence 5-mer analysis

### Under-represented 5-mers

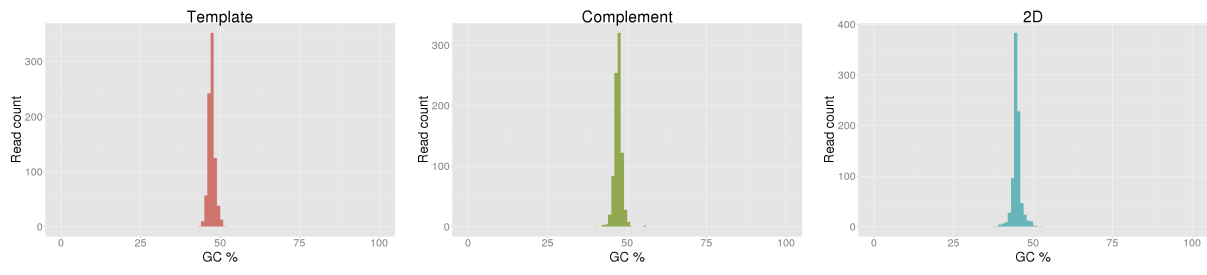
Rank	Template				Complement				2D			
	kmer	Ref %	Read %	Diff %	kmer	Ref %	Read %	Diff %	kmer	Ref %	Read %	Diff %
1	TTTTT	0.759	0.136	-0.623	TTTTT	0.759	0.110	-0.649	TTTTT	0.759	0.056	-0.703
2	AAAAA	0.478	0.109	-0.369	AAAAA	0.478	0.091	-0.387	AAAAA	0.478	0.068	-0.409
3	TGATG	0.393	0.133	-0.260	AAAAC	0.337	0.151	-0.186	TGATG	0.393	0.176	-0.217
4	GATGT	0.309	0.098	-0.211	GCAAT	0.309	0.139	-0.171	GATGT	0.309	0.144	-0.165
5	AAAAC	0.337	0.133	-0.204	GATGT	0.309	0.139	-0.170	CTGAT	0.309	0.144	-0.165
6	CTGAT	0.309	0.122	-0.187	GTCAG	0.281	0.113	-0.168	GCTGA	0.281	0.131	-0.150
7	AATAT	0.309	0.133	-0.176	TGATG	0.393	0.227	-0.167	CTTTT	0.253	0.106	-0.147
8	GCAAT	0.309	0.136	-0.173	TGAAG	0.253	0.092	-0.161	AAAAC	0.337	0.195	-0.142
9	AGTAA	0.253	0.084	-0.169	AACAA	0.281	0.126	-0.155	TGTGA	0.225	0.091	-0.134
10	TGAAG	0.253	0.097	-0.156	AGTAA	0.253	0.102	-0.151	TTATC	0.309	0.175	-0.134

### Over-represented 5-mers

Rank	Template				Complement				2D			
	kmer	Ref %	Read %	Diff %	kmer	Ref %	Read %	Diff %	kmer	Ref %	Read %	Diff %
1	CTTTG	0.028	0.162	0.134	ACCCC	0.000	0.127	0.127	TCAGC	0.028	0.172	0.143
2	TCTTA	0.000	0.119	0.119	GAGGA	0.000	0.126	0.126	CATCA	0.112	0.254	0.142
3	CATCT	0.000	0.118	0.118	CCCCA	0.000	0.119	0.119	ATCAG	0.056	0.195	0.139
4	GCTCC	0.000	0.110	0.110	GTATC	0.000	0.110	0.110	AACCA	0.028	0.155	0.127
5	CGAGA	0.000	0.109	0.109	TATAC	0.000	0.106	0.106	CATCT	0.000	0.117	0.117
6	TCAGC	0.028	0.135	0.107	ACTCT	0.000	0.105	0.105	GCATC	0.084	0.201	0.117
7	CCCGC	0.000	0.105	0.105	TACTT	0.000	0.102	0.102	ACCAA	0.028	0.141	0.113
8	TCTAC	0.000	0.104	0.104	TGCCA	0.028	0.130	0.102	CAGCA	0.056	0.168	0.112
9	GCGAA	0.028	0.130	0.102	CTTTG	0.028	0.129	0.101	TACAT	0.028	0.139	0.111
10	GTATC	0.000	0.101	0.101	CGAGA	0.000	0.098	0.098	ACATA	0.028	0.132	0.104

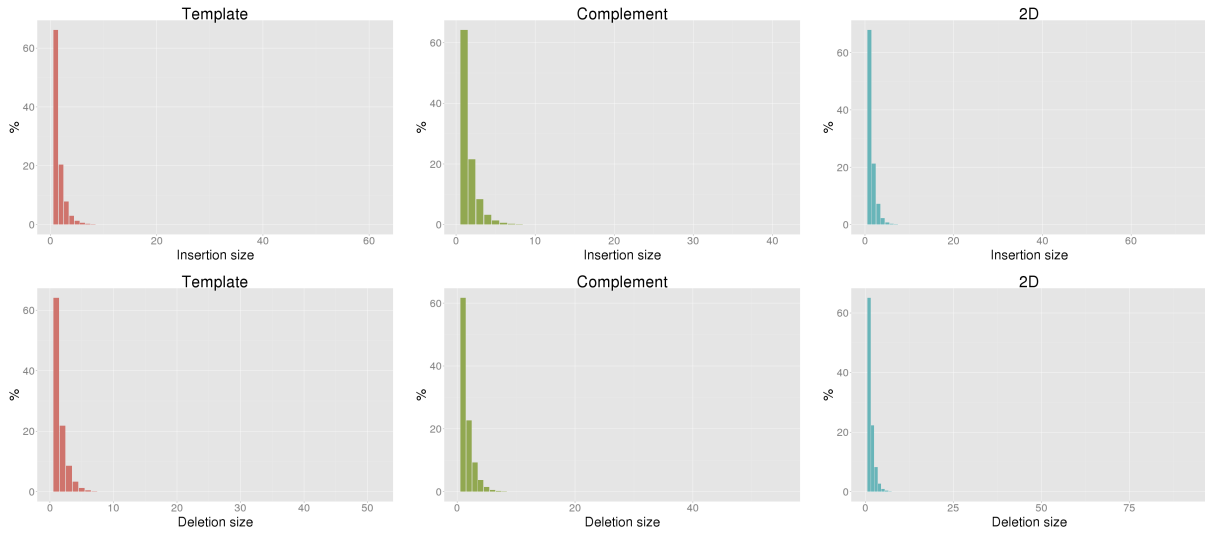


## Control sequence GC content

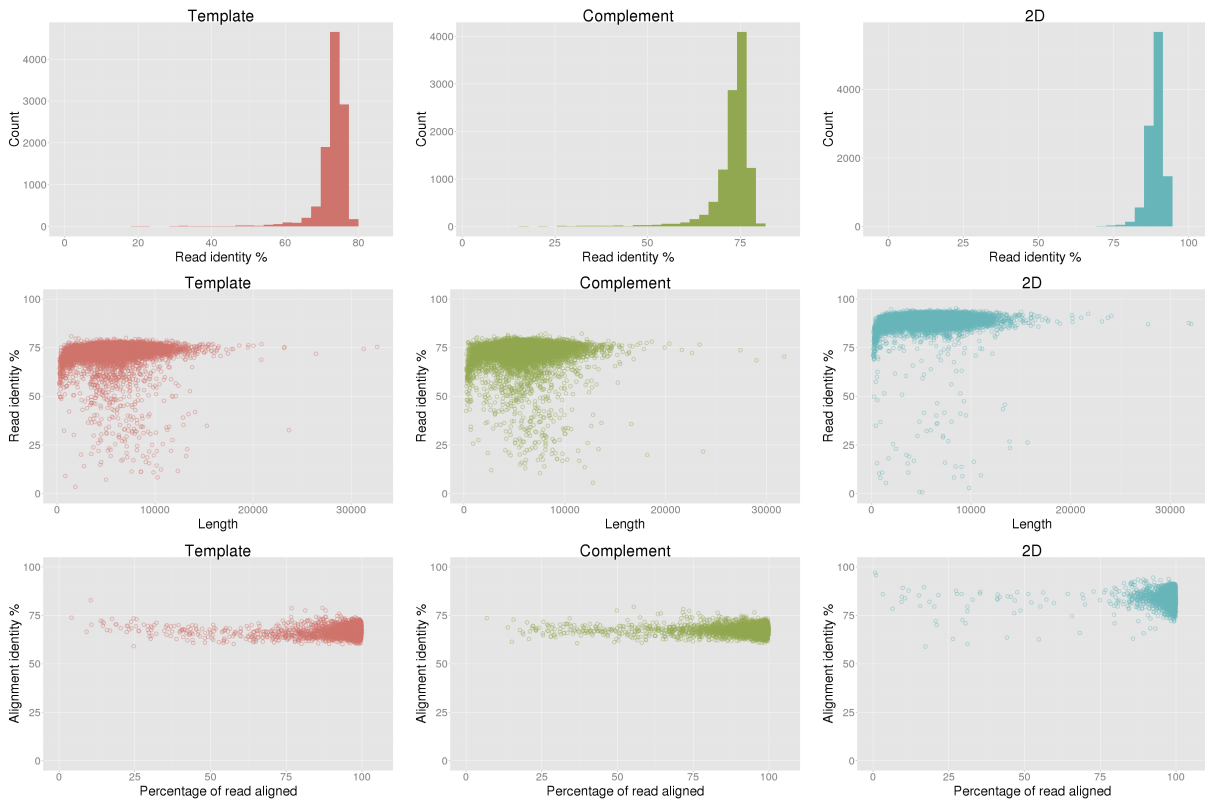


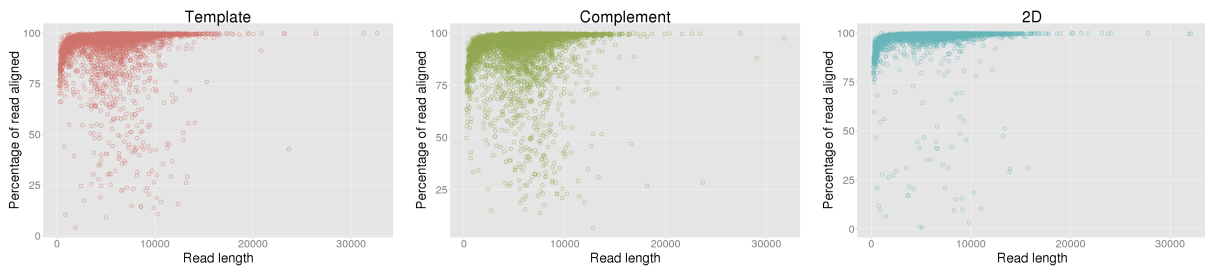
## Escherichia coli error analysis

	Template	Complement	2D
Overall base identity (excluding indels)	72.60%	72.64%	88.77%
Aligned base identity (excluding indels)	79.45%	80.86%	93.02%
Identical bases per 100 aligned bases (including indels)	67.18%	67.68%	84.45%
Inserted bases per 100 aligned bases (including indels)	5.20%	5.70%	3.16%
Deleted bases per 100 aligned bases (including indels)	10.24%	10.60%	6.05%
Substitutions per 100 aligned bases (including indels)	17.37%	16.02%	6.34%
Mean insertion size	1.59	1.62	1.49
Mean deletion size	1.60	1.65	1.55

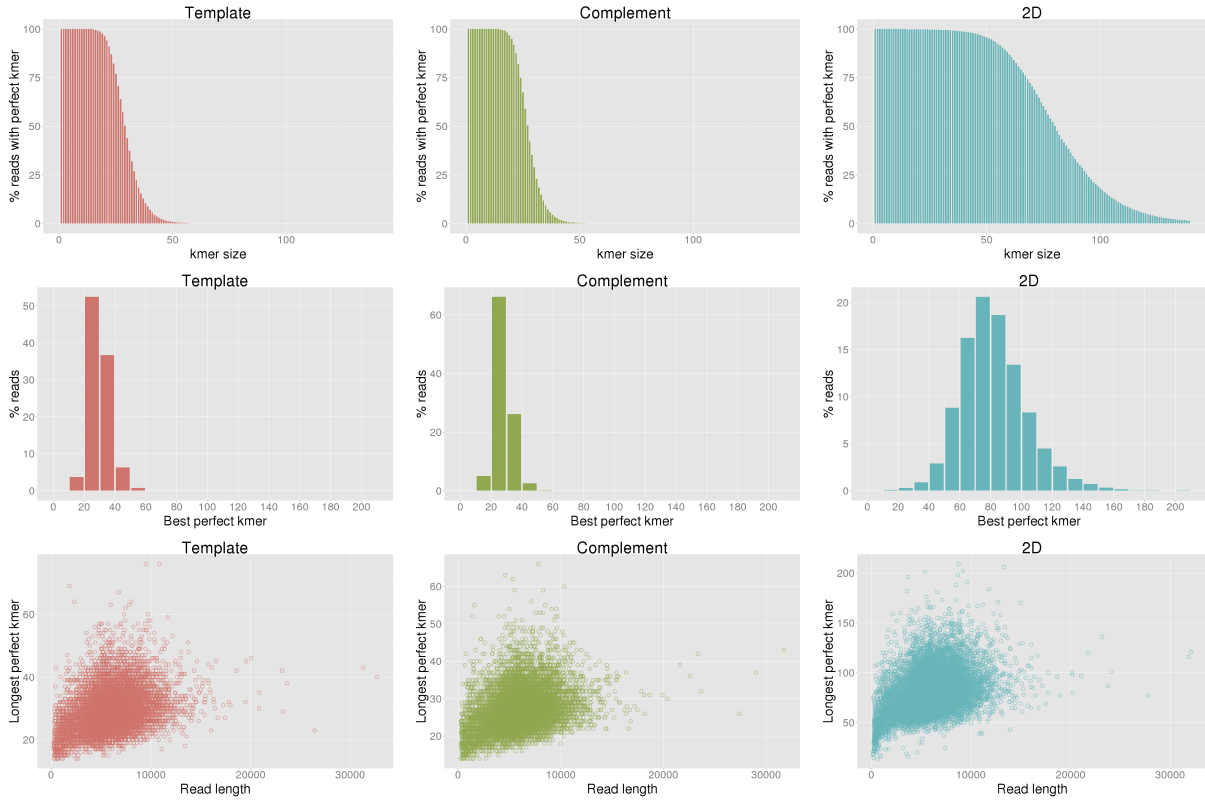


## Escherichia coli read identity

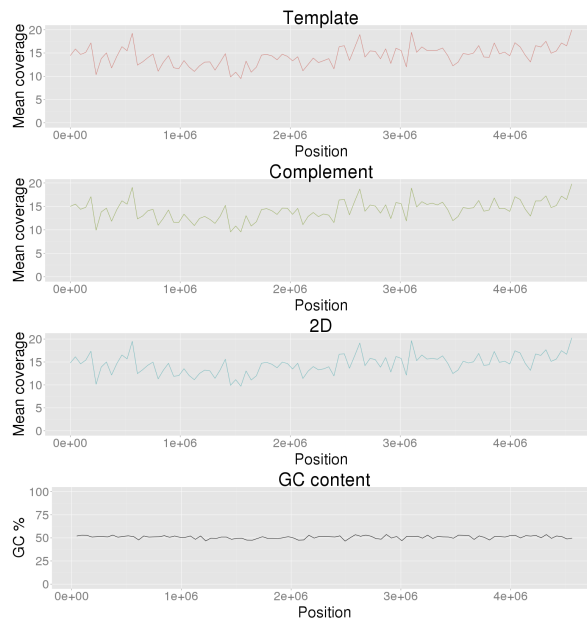




## Escherichia coli perfect kmers



## Escherichia coli coverage



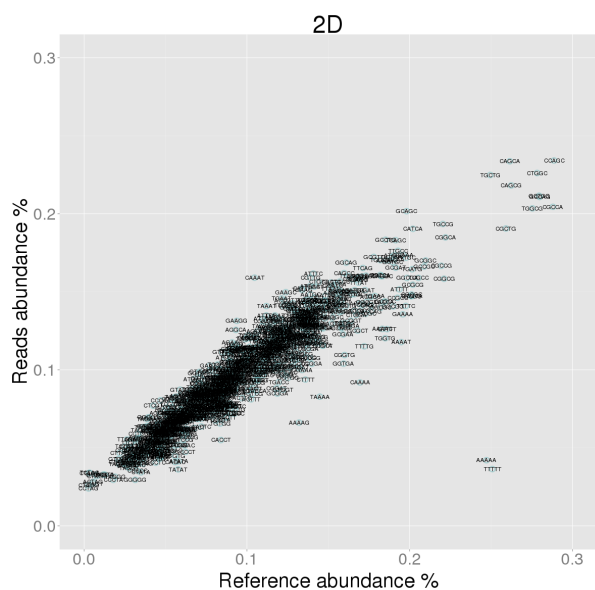
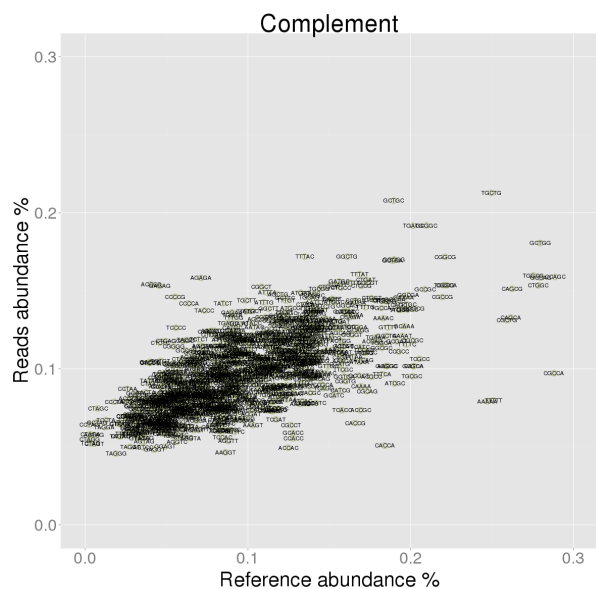
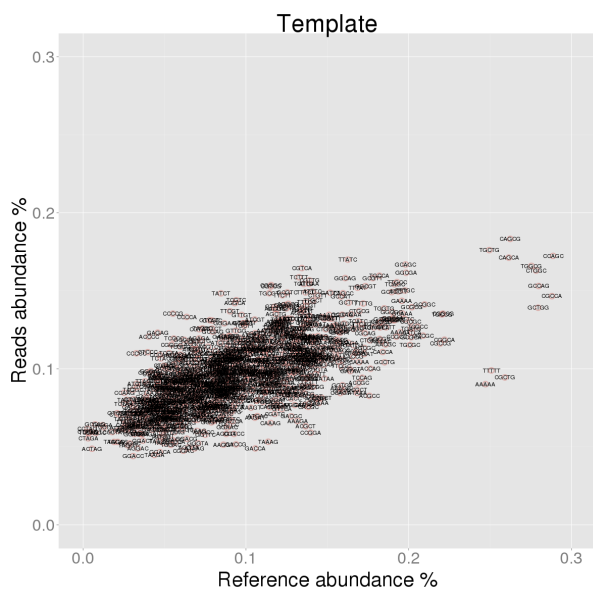
# Escherichia coli 5-mer analysis

## Under-represented 5-mers

Rank	Template				Complement				2D			
	kmer	Ref %	Read %	Diff %	kmer	Ref %	Read %	Diff %	kmer	Ref %	Read %	Diff %
1	CGCTG	0.259	0.094	-0.165	CGCCA	0.288	0.097	-0.191	TTTTT	0.251	0.036	-0.214
2	AAAAA	0.247	0.090	-0.157	TTTTT	0.251	0.080	-0.171	AAAAA	0.247	0.042	-0.205
3	TTTTT	0.251	0.099	-0.152	AAAAA	0.247	0.079	-0.168	CGCCA	0.288	0.204	-0.084
4	CGCCA	0.288	0.147	-0.141	CACCA	0.184	0.051	-0.133	CAAAA	0.169	0.092	-0.078
5	GCTGG	0.279	0.139	-0.140	CCAGC	0.289	0.159	-0.130	AAAAT	0.195	0.118	-0.077
6	GCCAG	0.280	0.153	-0.127	CAGCA	0.261	0.133	-0.129	TGGCG	0.275	0.203	-0.072
7	CCAGC	0.289	0.172	-0.116	CGCTG	0.259	0.131	-0.128	GCCAG	0.280	0.211	-0.069
8	CTGGC	0.278	0.163	-0.115	CTGGC	0.278	0.154	-0.125	CGCTG	0.259	0.191	-0.068
9	TGGCG	0.275	0.166	-0.109	GCCAG	0.280	0.159	-0.121	GCTGG	0.279	0.212	-0.068
10	CGGCA	0.222	0.119	-0.103	TGGCG	0.275	0.160	-0.116	AAAAG	0.132	0.066	-0.066

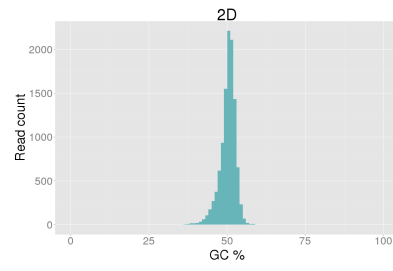
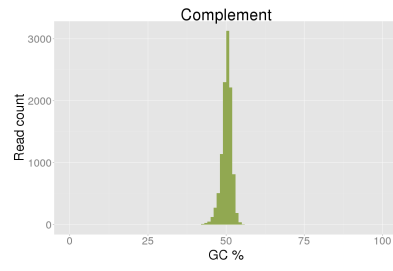
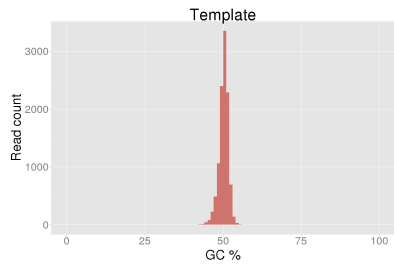
## Over-represented 5-mers

Rank	Template				Complement				2D			
	kmer	Ref %	Read %	Diff %	kmer	Ref %	Read %	Diff %	kmer	Ref %	Read %	Diff %
1	ACCCC	0.040	0.121	0.080	ACCCC	0.040	0.154	0.114	CAAAT	0.105	0.159	0.054
2	CCCCG	0.055	0.135	0.080	GAGAG	0.046	0.153	0.107	GAAGG	0.094	0.131	0.038
3	GAGAG	0.046	0.123	0.077	CCCCG	0.055	0.146	0.091	CTCGT	0.042	0.077	0.035
4	CCCCC	0.033	0.110	0.077	AGAGA	0.071	0.158	0.087	CCCAA	0.047	0.081	0.034
5	CTCCC	0.040	0.111	0.071	CCCCA	0.064	0.142	0.078	AGGCA	0.093	0.126	0.032
6	CCCCA	0.064	0.133	0.070	CTCTC	0.046	0.117	0.071	CTAGA	0.003	0.034	0.031
7	TCCCC	0.056	0.119	0.064	TCCCC	0.056	0.126	0.071	TCTAG	0.003	0.034	0.031
8	TATCT	0.085	0.148	0.064	CTGAG	0.050	0.118	0.068	GGGGT	0.039	0.070	0.030
9	CCCAA	0.047	0.109	0.062	CTAGC	0.008	0.075	0.067	TAGAA	0.039	0.068	0.030
10	CGGGG	0.054	0.116	0.061	CCCCT	0.039	0.104	0.065	TTAGA	0.026	0.055	0.029

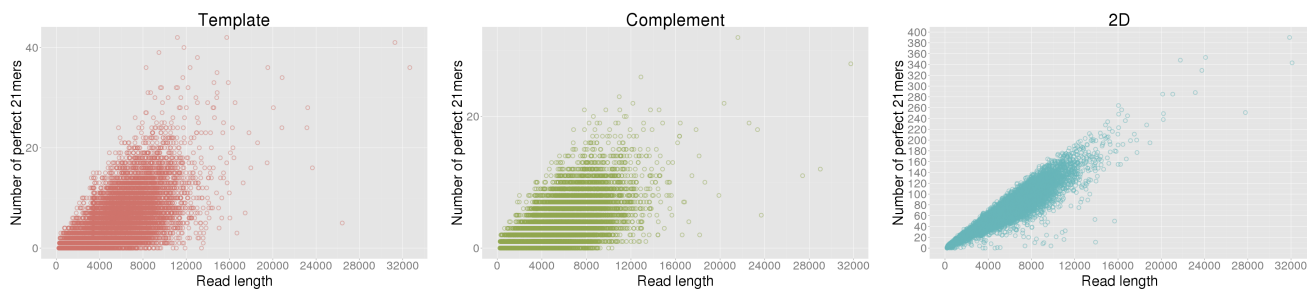




# Escherichia coli GC content



## 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	8.92	9.14	4.76	0.00	9.15	8.60	4.98	0.00	8.63	8.37	4.11
C	8.58	0.00	9.23	9.79	9.22	0.00	8.76	9.62	9.38	0.00	10.91	9.17
G	9.33	9.19	0.00	8.23	8.88	8.89	0.00	8.84	8.91	11.03	0.00	8.79
T	5.07	9.16	8.59	0.00	5.24	8.77	9.04	0.00	4.19	8.12	8.39	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 (3.21%)	TTC (3.46%)	AAA (4.00%)	TGC (2.71%)	GGC (2.85%)	AAA (4.04%)	GCA (3.13%)	TCA (2.63%)	GCA (3.74%)
2	GCA (2.81%)	TGC (3.05%)	TTC (3.72%)	GCA (2.71%)	AAA (2.84%)	GCA (3.52%)	TTC (2.83%)	GGC (2.56%)	AAA (3.70%)
3	AAA (2.74%)	GCA (2.85%)	GCA (3.27%)	AAA (2.63%)	TGC (2.75%)	GAA (3.30%)	TCA (2.67%)	AAA (2.54%)	GAA (3.29%)
4	TGC (2.67%)	AAA (2.72%)	GAA (2.96%)	TTC (2.61%)	GCA (2.67%)	TTC (3.01%)	ATC (2.55%)	TGC (2.54%)	TTC (2.91%)
5	ATC (2.58%)	GCC (2.46%)	TTT (2.67%)	CAG (2.53%)	TTC (2.54%)	TTT (2.70%)	AAA (2.54%)	GCA (2.51%)	TTT (2.78%)
6	TCA (2.43%)	TCA (2.45%)	TGC (2.58%)	GGC (2.49%)	GAA (2.40%)	TCA (2.41%)	TGC (2.44%)	TTC (2.41%)	GCC (2.41%)
7	GGC (2.27%)	GGC (2.28%)	AAT (2.31%)	GAA (2.31%)	TCA (2.35%)	TGC (2.38%)	GAA (2.35%)	GCG (2.37%)	TCA (2.39%)
8	GCC (2.27%)	ATC (2.24%)	TCA (2.26%)	ATC (2.29%)	CAG (2.34%)	ATC (2.29%)	CAG (2.24%)	CAG (2.25%)	ATC (2.30%)
9	GAA (2.20%)	AAC (2.19%)	GCC (2.21%)	TCA (2.26%)	GCC (2.32%)	GCC (2.13%)	GCG (2.23%)	CGC (2.18%)	GTT (2.29%)
10	TTT (2.18%)	GAA (2.12%)	ATC (2.14%)	GCC (2.14%)	AGC (2.14%)	GCC (2.07%)	CGC (2.20%)	ATC (2.15%)	AAT (2.25%)
-10	CTC (0.98%)	GGG (0.93%)	GGT (0.95%)	ACT (1.05%)	ACT (0.95%)	CTC (0.96%)	CTC (1.04%)	GTA (1.02%)	ACT (0.92%)
-9	AGT (0.98%)	CCT (0.91%)	AGA (0.89%)	AGT (0.98%)	CCC (0.94%)	CTT (0.94%)	CTT (1.04%)	ACT (0.95%)	CCT (0.92%)
-8	CCC (0.92%)	AGT (0.91%)	GGG (0.88%)	CTC (0.95%)	CGA (0.93%)	AGT (0.87%)	GAG (0.92%)	CGA (0.90%)	TGA (0.82%)
-7	AGA (0.89%)	CTT (0.86%)	TGT (0.85%)	GAG (0.89%)	GGA (0.92%)	AGG (0.84%)	AGA (0.84%)	CTT (0.90%)	CTT (0.81%)
-6	GGA (0.86%)	GAG (0.82%)	CTT (0.82%)	GGA (0.89%)	CTC (0.91%)	GGG (0.82%)	AGG (0.82%)	CCC (0.89%)	GAG (0.78%)
-5	GAG (0.74%)	CGA (0.78%)	AGG (0.80%)	CCC (0.87%)	CCT (0.88%)	CCT (0.82%)	GGA (0.79%)	AGA (0.83%)	CGA (0.72%)
-4	GGG (0.68%)	AGA (0.69%)	AGT (0.80%)	AGG (0.71%)	GAG (0.84%)	ACT (0.72%)	CCC (0.79%)	CCT (0.81%)	AGA (0.57%)
-3	AGG (0.68%)	GGA (0.62%)	GAG (0.63%)	GGG (0.61%)	GGG (0.80%)	GAG (0.66%)	GGG (0.73%)	GGA (0.73%)	GGA (0.52%)
-2	CTA (0.47%)	TAG (0.54%)	TAG (0.39%)	CTA (0.56%)	CTA (0.55%)	CTA (0.46%)	CTA (0.59%)	CTA (0.71%)	TAG (0.49%)
-1	TAG (0.40%)	CTA (0.52%)	CTA (0.34%)	TAG (0.47%)	TAG (0.53%)	TAG (0.38%)	TAG (0.49%)	TAG (0.66%)	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 (1.03%)	TTTC (1.11%)	AAAA (1.26%)	CAGC (1.00%)	CAGC (1.05%)	AAAA (1.10%)	ATCA (0.94%)	TGGC (0.92%)	GGCA (1.13%)
2	GAAA (0.89%)	TGCC (0.97%)	TTTT (1.26%)	ATCA (0.88%)	TGGC (1.03%)	CAAA (1.02%)	GGCA (0.87%)	CAGC (0.91%)	GAAA (0.98%)
3	ATCA (0.87%)	CAGC (0.92%)	GAAA (1.17%)	TGGC (0.88%)	CGGC (0.99%)	GAAA (1.01%)	CAGC (0.86%)	TTCA (0.90%)	TGAA (0.96%)
4	CAGC (0.87%)	TTCA (0.91%)	GGCA (0.91%)	CTGC (0.86%)	CTGC (0.89%)	TGAA (0.94%)	GCCA (0.81%)	ATCA (0.85%)	AAAA (0.96%)
5	AAAA (0.84%)	TTGC (0.90%)	GTTC (0.91%)	CGGC (0.84%)	ATCA (0.85%)	ATCA (0.94%)	TTCA (0.79%)	CGGC (0.79%)	TGCA (0.91%)
6	TTCA (0.82%)	TGGC (0.88%)	GCAA (0.89%)	CCAG (0.82%)	TTGC (0.82%)	AGAA (0.92%)	AACA (0.77%)	CTGC (0.76%)	GGAA (0.91%)
7	TGCC (0.81%)	CTGC (0.88%)	TTTT (0.88%)	CAAA (0.75%)	CAAA (0.80%)	AGCA (0.91%)	CGCA (0.77%)	CAAA (0.73%)	AGCA (0.86%)
8	TGGC (0.81%)	TTCC (0.84%)	GGAA (0.87%)	TTGC (0.75%)	CTGG (0.77%)	GGCA (0.91%)	TTTT (0.74%)	TGCC (0.73%)	CAAA (0.85%)
9	CTTC (0.78%)	GAAA (0.83%)	CAAA (0.85%)	AGCA (0.71%)	TTCA (0.77%)	TAAA (0.86%)	TGAA (0.73%)	CGCC (0.72%)	CGCC (0.85%)
10	GGCA (0.77%)	AAAA (0.81%)	TGCC (0.84%)	AAAA (0.71%)	CCAG (0.77%)	TGCA (0.83%)	CTTC (0.73%)	GCCA (0.72%)	TGCC (0.84%)
-10	GAGG (0.12%)	GGAC (0.13%)	TTAG (0.11%)	CTAT (0.13%)	CGAG (0.13%)	GTAG (0.11%)	TATA (0.14%)	CCCC (0.15%)	TCGA (0.11%)
-9	AGGG (0.12%)	CTAT (0.13%)	ACTA (0.10%)	AGGG (0.12%)	CCTC (0.12%)	GGAC (0.10%)	GTGT (0.14%)	CTAT (0.15%)	GGGA (0.11%)
-8	CTAA (0.11%)	TCTA (0.12%)	CGAG (0.10%)	GAGG (0.11%)	GTGT (0.12%)	ACCT (0.10%)	CCCT (0.13%)	GAGA (0.15%)	ACTA (0.11%)
-7	GGAC (0.11%)	TAGT (0.12%)	TAGT (0.09%)	GGAC (0.10%)	CTAA (0.12%)	ACTA (0.10%)	CTAT (0.13%)	ACCT (0.14%)	TCTA (0.11%)
-6	TCTA (0.11%)	CGGA (0.10%)	GGAC (0.09%)	TAGA (0.10%)	ACCT (0.11%)	CTAT (0.10%)	TCTA (0.13%)	CTAA (0.13%)	CTAT (0.10%)
-5	TTAG (0.10%)	CTAA (0.10%)	TAGA (0.07%)	CTAA (0.10%)	TAGA (0.10%)	CGAG (0.09%)	CTAA (0.12%)	CCCT (0.10%)	CGGA (0.09%)
-4	TAGA (0.07%)	TAGG (0.07%)	TCTA (0.07%)	CCCT (0.10%)	CCCT (0.08%)	CCCT (0.06%)	TAGA (0.08%)	TAGG (0.09%)	TAGG (0.07%)
-3	CCTA (0.06%)	CCTA (0.06%)	TAGG (0.06%)	CCTA (0.07%)	TAGG (0.07%)	CCTA (0.06%)	CCTA (0.07%)	TAGA (0.09%)	CCTA (0.05%)
-2	TAGG (0.04%)	TAGA (0.05%)	CCTA (0.04%)	TAGG (0.05%)	CCTA (0.06%)	TAGG (0.06%)	TAGG (0.05%)	CCTA (0.09%)	TAGA (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 (0.39%)	CAGCA (0.43%)	CAGCA (0.41%)	CAGCA (0.43%)	CAGCA (0.53%)	CAGCA (0.39%)	CTGGC (0.37%)	CAGCA (0.47%)
2	TTATC (0.34%)	CTGGC (0.36%)	GAAAA (0.39%)	CCAGC (0.35%)	CTGGC (0.39%)	CGGCA (0.35%)	CGCCA (0.33%)	CAGCA (0.33%)	CGGCA (0.41%)
3	CTGGC (0.33%)	TTGGC (0.34%)	CAAAA (0.35%)	CTGGC (0.33%)	CTAGC (0.33%)	ATAAA (0.35%)	CGGCA (0.33%)	CATCA (0.31%)	TGGCA (0.38%)
4	CGCCA (0.30%)	GCTGC (0.32%)	TGTTT (0.33%)	CATCA (0.32%)	GCGGC (0.33%)	CAGAA (0.35%)	CTGGC (0.30%)	GCGGC (0.29%)	GAAAA (0.34%)
5	GCAGC (0.29%)	TTTGC (0.31%)	CGTTT (0.32%)	GCTGC (0.31%)	CATCA (0.33%)	CATCA (0.34%)	CCAGC (0.29%)	CCAGC (0.29%)	GCAAA (0.30%)
6	ATTTT (0.29%)	CGCCA (0.31%)	TGGCA (0.32%)	GCGGC (0.30%)	TCAGC (0.31%)	AAGAA (0.34%)	TGGCA (0.29%)	CGCCA (0.29%)	CGCCA (0.29%)
7	CATCA (0.28%)	GCAGC (0.31%)	GCAAA (0.32%)	TTATC (0.28%)	AATCA (0.31%)	GAAAA (0.33%)	CATCA (0.29%)	TTTTT (0.28%)	ATTTT (0.28%)
8	TCTTC (0.28%)	TTTCA (0.30%)	TCTTC (0.32%)	CGGCA (0.28%)	GCTGC (0.30%)	AATCA (0.33%)	GCCAG (0.27%)	GCCAG (0.28%)	TGAAA (0.28%)
9	CCAGC (0.28%)	CATCA (0.30%)	AGAAA (0.31%)	AATCA (0.28%)	ATAAA (0.30%)	TTATC (0.32%)	GCAAA (0.26%)	ATAAA (0.26%)	TTGCC (0.28%)
10	TGGCG (0.28%)	ATTTT (0.29%)	CTGGC (0.31%)	GCAGC (0.27%)	TTTTT (0.28%)	AGAAA (0.32%)	GCGCA (0.25%)	TGGCG (0.26%)	AAGAA (0.28%)
-10	GGACC (0.01%)	GGACC (0.01%)	CCCTA (0.01%)	CTAGC (0.01%)	CCCTT (0.01%)	CCCTA (0.01%)	TAGGA (0.01%)	TCCTA (0.01%)	TCCTA (0.01%)
-9	CCCTA (0.01%)	TAGGA (0.01%)	ACCTA (0.01%)	ACCTA (0.01%)	CCCTA (0.01%)	CTAGC (0.01%)	CCCTA (0.01%)	GCTAG (0.01%)	CCCTA (0.01%)
-8	CTAGC (0.00%)	GCTAG (0.00%)	ACTAG (0.00%)	CCCTA (0.01%)	CTAGC (0.01%)	ACCTA (0.01%)	GCTAG (0.01%)	TAGGA (0.01%)	GCTAG (0.01%)
-7	CTAGT (0.00%)	CTAGC (0.00%)	GCTAG (0.00%)	GCTAG (0.01%)	GCTAG (0.01%)	GCTAG (0.00%)	CTAGC (0.00%)	ACTAG (0.01%)	CTAGC (0.01%)
-6	CCTAG (0.00%)	ACTAG (0.00%)	CTAGC (0.00%)	CTAGT (0.00%)	CTAGT (0.00%)	CTAGA (0.00%)	ACTAG (0.00%)	CTAGC (0.01%)	CTAGT (0.00%)
-5	GCTAG (0.00%)	CTAGT (0.00%)	CTAGT (0.00%)	ACTAG (0.00%)	CTAGA (0.00%)	CTAGT (0.00%)	CTAGT (0.00%)	CTAGT (0.00%)	ACTAG (0.00%)
-4	ACTAG (0.00%)	TCTAG (0.00%)	CTAGA (0.00%)	TCTAG (0.00%)	ACTAG (0.00%)	CTAGG (0.00%)	CCTAG (0.00%)	TCTAG (0.00%)	CTAGG (0.00%)
-3	TCTAG (0.00%)	CTAGG (0.00%)	CTAGG (0.00%)	CTAGA (0.00%)	CTAGG (0.00%)	TCTAG (0.00%)	TCTAG (0.00%)	CTAGA (0.00%)	TCTAG (0.00%)
-2	CTAGG (0.00%)	CTAG (0.00%)	CCTAG (0.00%)	CCTAG (0.00%)	CCTAG (0.00%)	ACTAG (0.00%)	CTAG (0.00%)	CTAGG (0.00%)	CCTAG (0.00%)
-1	CTAGA (0.00%)	CCTAG (0.00%)	TCTAG (0.00%)	CTAGG (0.00%)	TCTAG (0.00%)	CCTAG (0.00%)	CTAGG (0.00%)	CCTAG (0.00%)	CTAGA (0.00%)

Most common

Least common

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