

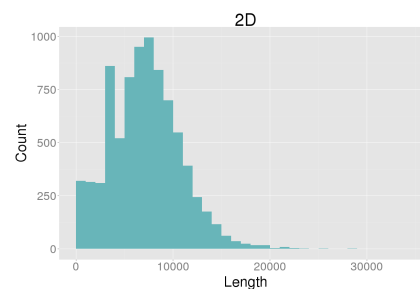
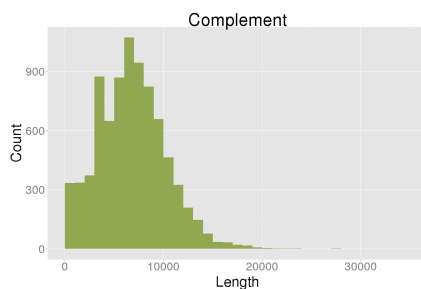
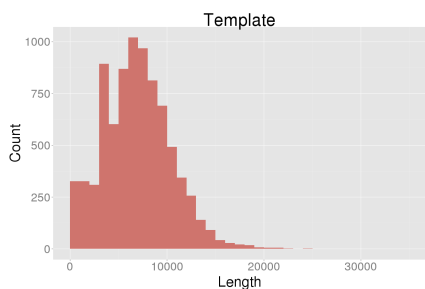
# NanoOK report for MARC\_EColi\_040115

## Pass and fail counts

Type	Pass	Fail
Template	8289	0
Complement	8289	0
2D	8289	0

## Read lengths

Type	NumReads	TotalBases	Mean	Longest	Shortest	N50	N50Count	N90	N90Count
Template	8289	57456459	6931.65	29329	258	8389	2637	4558	6155
Complement	8289	56265872	6788.02	27352	251	8238	2631	4440	6143
2D	8289	59319119	7156.37	29213	249	8685	2636	4694	6146



## Template alignments

Number of reads	8289	
Number of reads with alignments	8218	(99.14%)
Number of reads without alignments	71	(0.86%)

ID	Size	Number of Reads	% of Reads	Mean read length	Aligned bases	Mean coverage	Longest Perf Kmer
Control sequence	3560	682	8.23	3092.08	2234781	627.75	62
Escherichia coli	4641652	7536	90.92	7338.10	59656164	12.85	80

## Complement alignments

Number of reads	8289	
Number of reads with alignments	8204	(98.97%)
Number of reads without alignments	85	(1.03%)

ID	Size	Number of Reads	% of Reads	Mean read length	Aligned bases	Mean coverage	Longest Perf Kmer
Control sequence	3560	679	8.19	2953.75	1991413	559.39	51
Escherichia coli	4641652	7525	90.78	7202.73	58128993	12.52	58

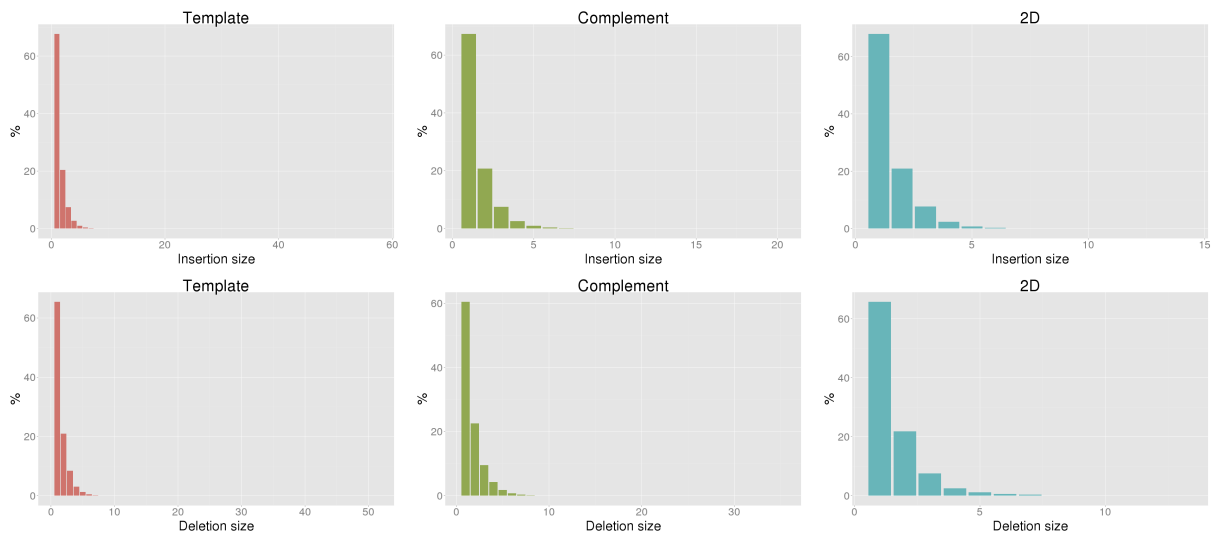
## 2D alignments

Number of reads	8289	
Number of reads with alignments	8289	(100.00%)
Number of reads without alignments	0	(0.00%)

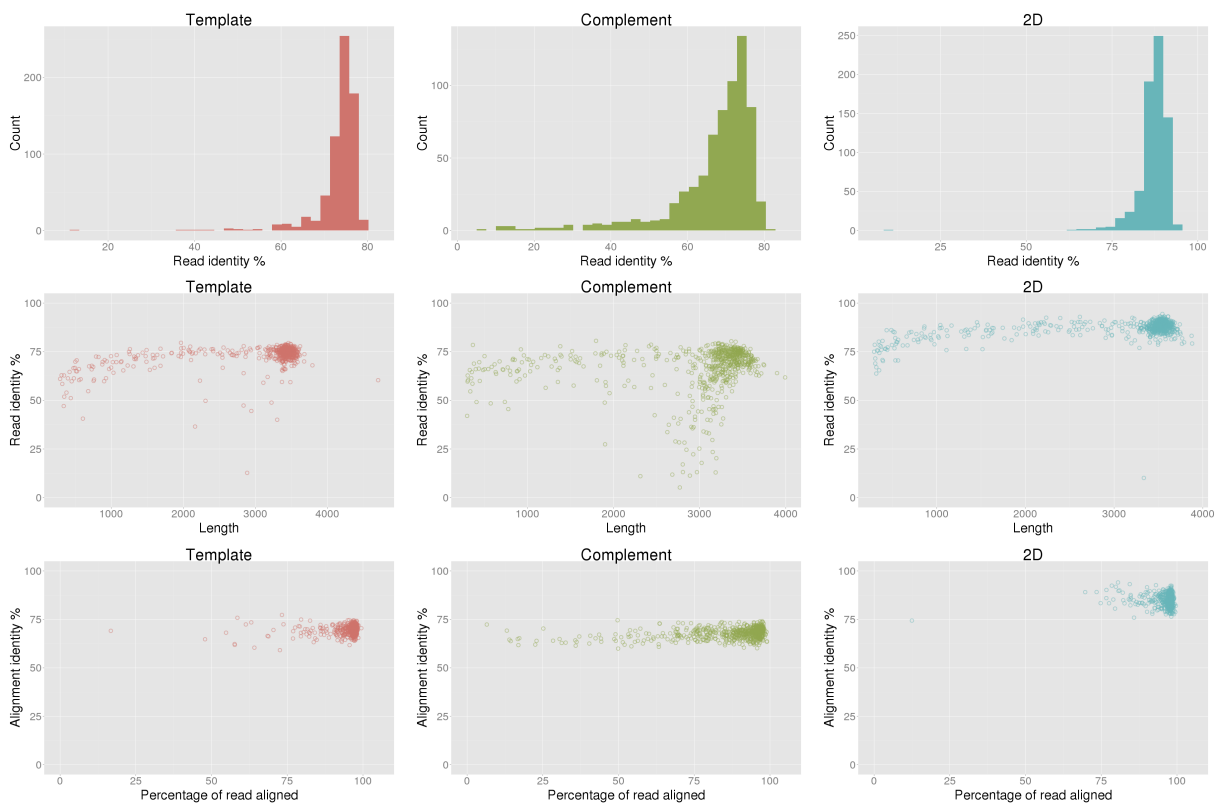
ID	Size	Number of Reads	% of Reads	Mean read length	Aligned bases	Mean coverage	Longest Perf Kmer
Control sequence	3560	699	8.43	3090.59	2224597	624.89	175
Escherichia coli	4641652	7590	91.57	7530.80	59409012	12.80	244

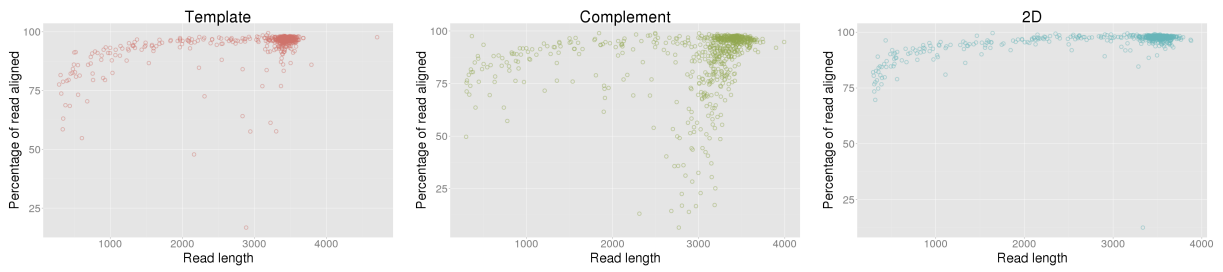
## Control sequence error analysis

	Template	Complement	2D
Overall base identity (excluding indels)	73.91%	67.28%	87.69%
Aligned base identity (excluding indels)	81.35%	80.99%	93.47%
Identical bases per 100 aligned bases (including indels)	69.75%	67.76%	85.16%
Inserted bases per 100 aligned bases (including indels)	4.57%	4.39%	3.25%
Deleted bases per 100 aligned bases (including indels)	9.69%	11.94%	5.63%
Substitutions per 100 aligned bases (including indels)	15.99%	15.90%	5.95%
Mean insertion size	1.52	1.52	1.49
Mean deletion size	1.57	1.70	1.56

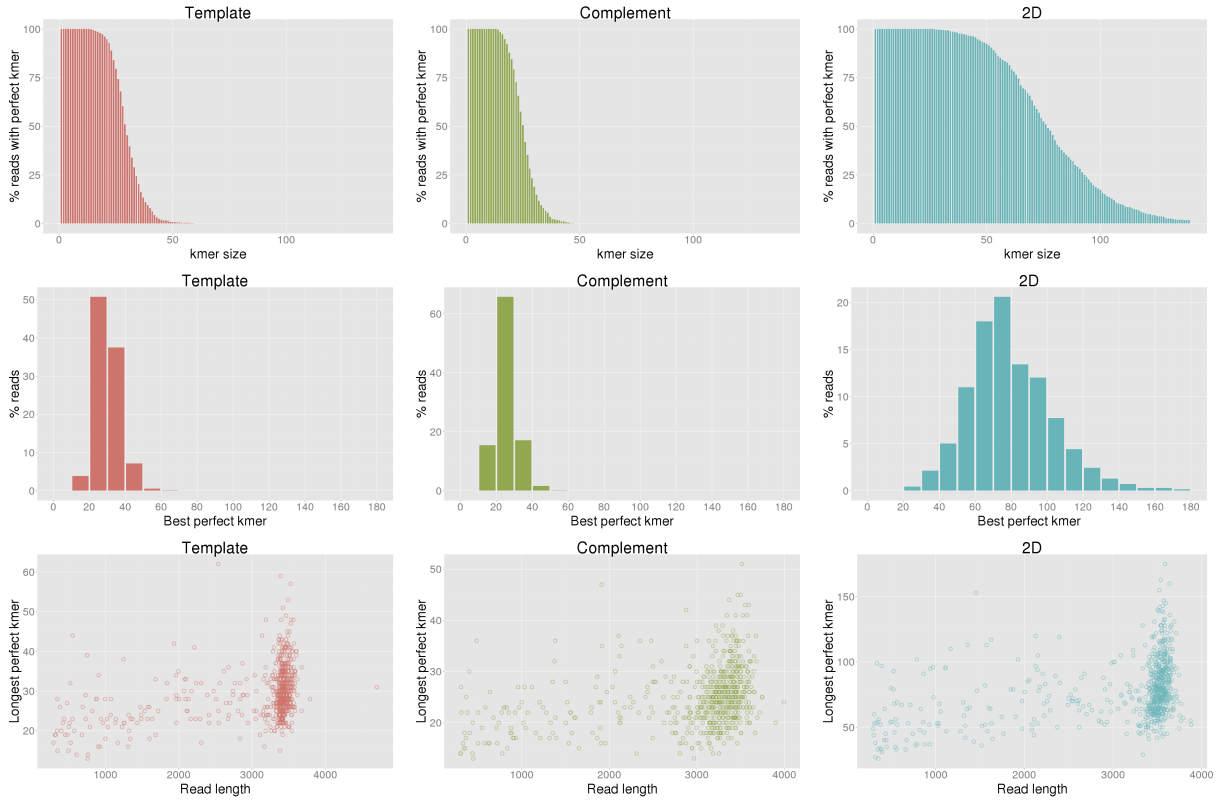


## Control sequence read identity

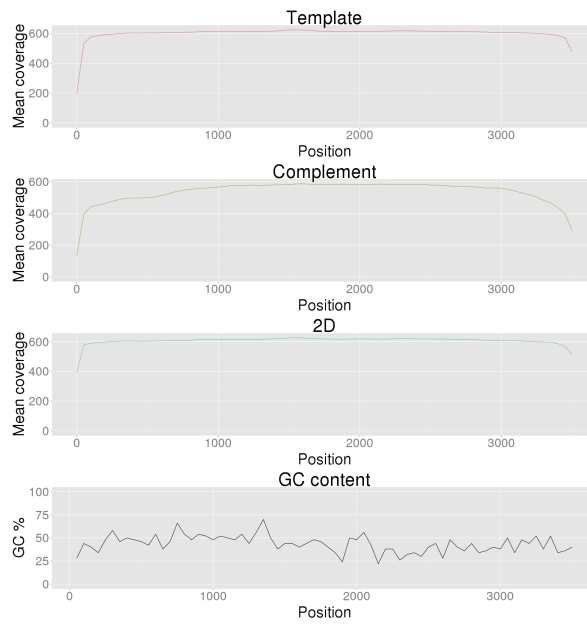




## Control sequence perfect kmers



## Control sequence coverage



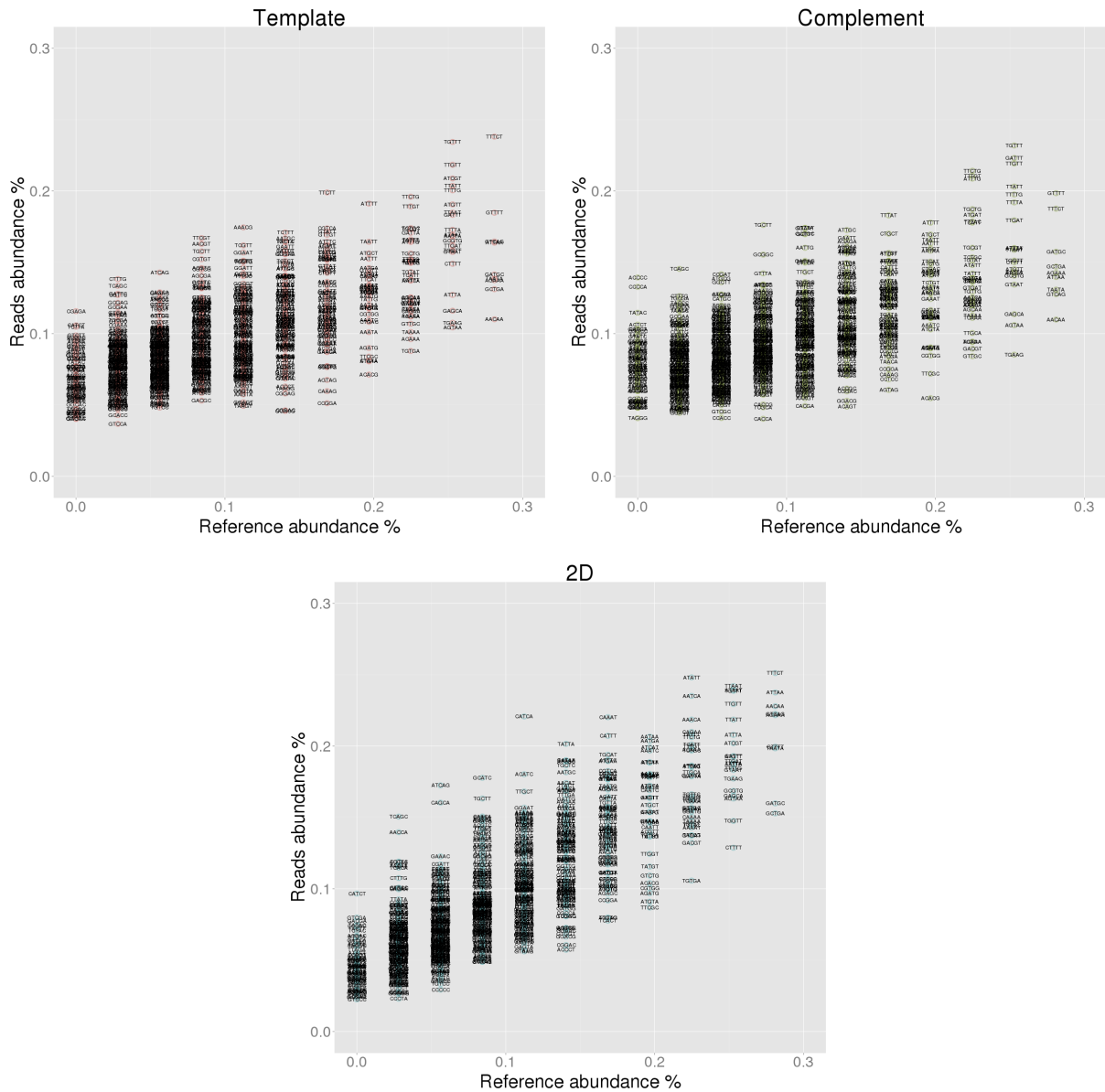
# Control sequence 5-mer analysis

## Under-represented 5-mers

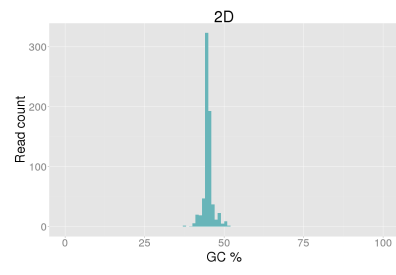
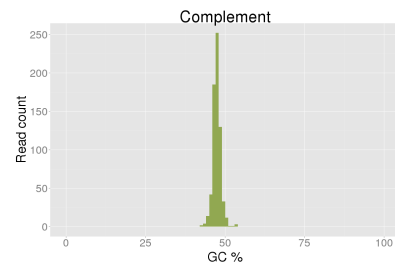
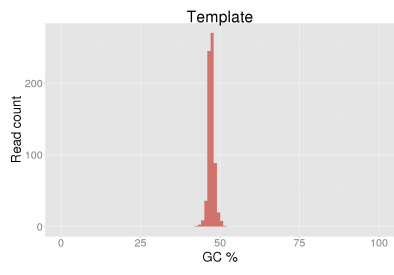
Rank	Template				Complement				2D			
	kmer	Ref %	Read %	Diff %	kmer	Ref %	Read %	Diff %	kmer	Ref %	Read %	Diff %
1	TTTTT	0.759	0.159	-0.600	TTTTT	0.759	0.139	-0.620	TTTTT	0.759	0.077	-0.681
2	AAAAA	0.478	0.118	-0.359	AAAAA	0.478	0.099	-0.379	AAAAA	0.478	0.090	-0.388
3	TGATG	0.393	0.149	-0.245	AAAAC	0.337	0.135	-0.202	TGATG	0.393	0.196	-0.198
4	AAAAC	0.337	0.124	-0.213	TGATG	0.393	0.204	-0.189	GATGT	0.309	0.158	-0.151
5	GATGT	0.309	0.109	-0.201	GATGT	0.309	0.127	-0.182	CTGAT	0.309	0.160	-0.149
6	CTGAT	0.309	0.129	-0.180	GCAAT	0.309	0.129	-0.180	GCTGA	0.281	0.153	-0.128
7	AACAA	0.281	0.110	-0.171	AACAA	0.281	0.110	-0.171	AAAAC	0.337	0.212	-0.125
8	GCAAT	0.309	0.148	-0.161	TGAAG	0.253	0.085	-0.168	CTTTT	0.253	0.129	-0.124
9	GCTGA	0.281	0.131	-0.150	GTCAG	0.281	0.128	-0.153	GATGC	0.281	0.160	-0.121
10	AATAT	0.309	0.160	-0.149	TTATC	0.309	0.157	-0.152	TGTGA	0.225	0.106	-0.119

## Over-represented 5-mers

Rank	Template				Complement				2D			
	kmer	Ref %	Read %	Diff %	kmer	Ref %	Read %	Diff %	kmer	Ref %	Read %	Diff %
1	CGAGA	0.000	0.116	0.116	ACCCC	0.000	0.139	0.139	TCAGC	0.028	0.151	0.123
2	CTTTG	0.028	0.138	0.110	CCCCA	0.000	0.133	0.133	ATCAG	0.056	0.172	0.116
3	CATCT	0.000	0.106	0.106	TCAGC	0.028	0.145	0.117	AACCA	0.028	0.140	0.112
4	TCAGC	0.028	0.134	0.106	TATAC	0.000	0.115	0.115	CATCA	0.112	0.221	0.108
5	TCTTA	0.000	0.105	0.105	ACTCT	0.000	0.106	0.106	CAGCA	0.056	0.160	0.104
6	GATTC	0.028	0.128	0.100	GCCGA	0.000	0.103	0.103	CATCT	0.000	0.097	0.097
7	CGTTC	0.028	0.127	0.099	CATCT	0.000	0.103	0.103	GCATC	0.084	0.178	0.093
8	GTCTT	0.000	0.099	0.099	CGGCC	0.000	0.102	0.102	CGTTC	0.028	0.119	0.091
9	CCCGC	0.000	0.097	0.097	TACTT	0.000	0.099	0.099	ACCAA	0.028	0.119	0.091
10	ACCCC	0.000	0.097	0.097	CTTTG	0.028	0.126	0.098	ACATA	0.028	0.116	0.088

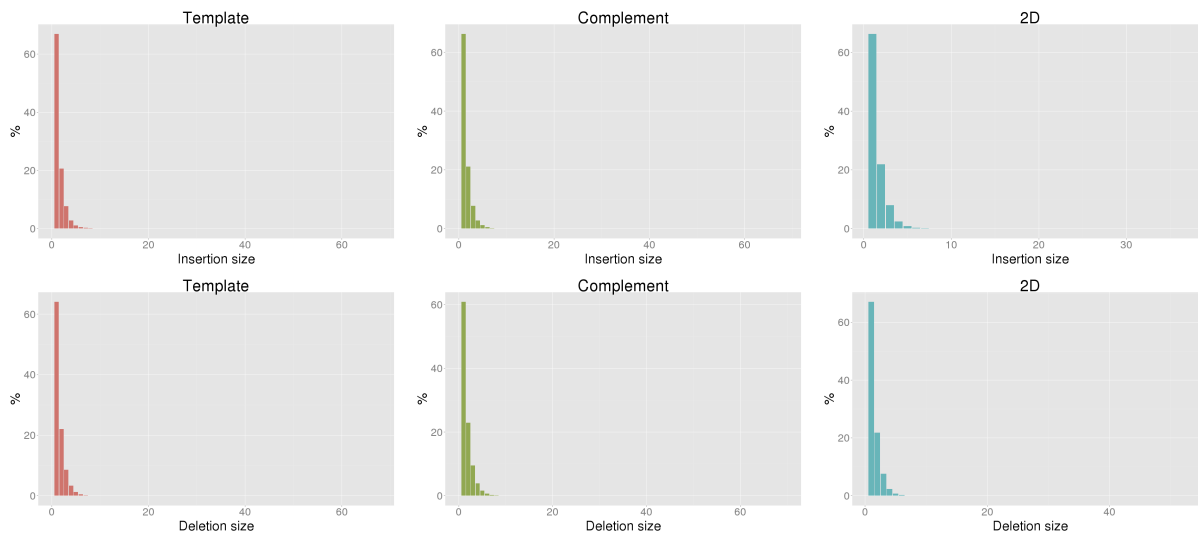


## Control sequence GC content

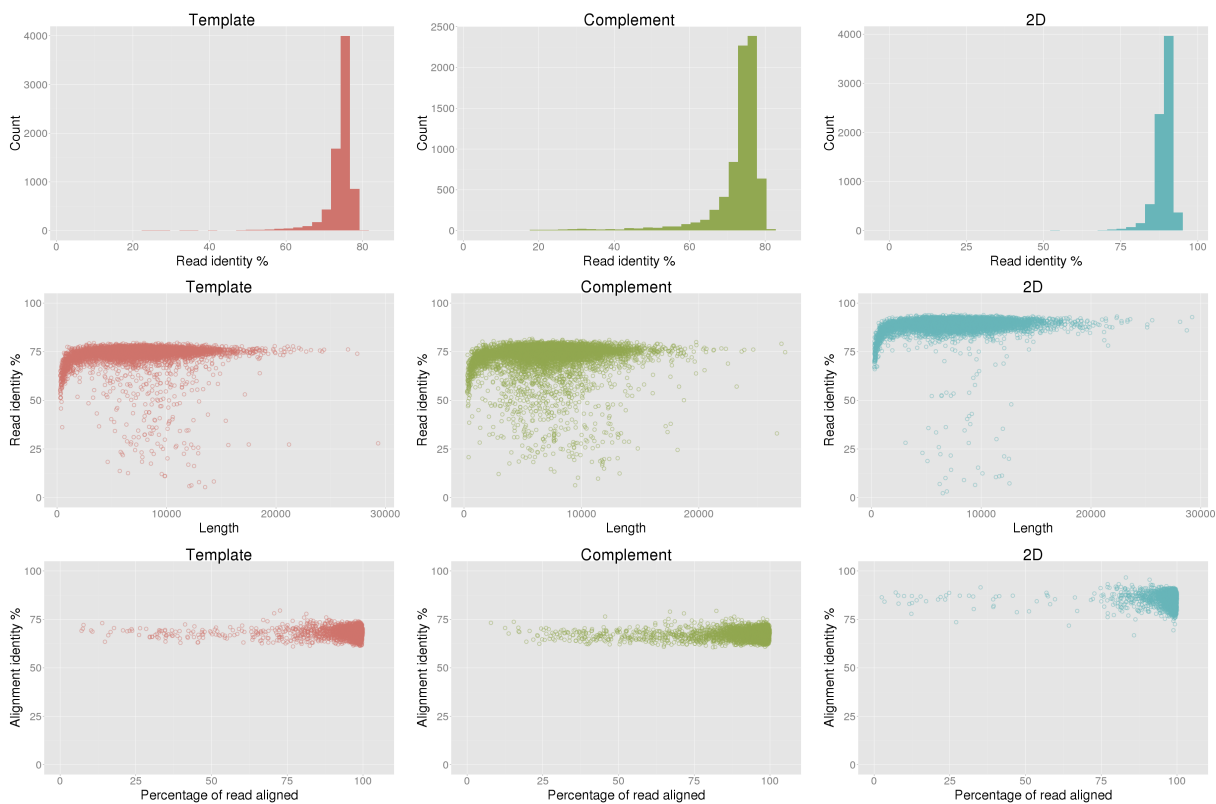


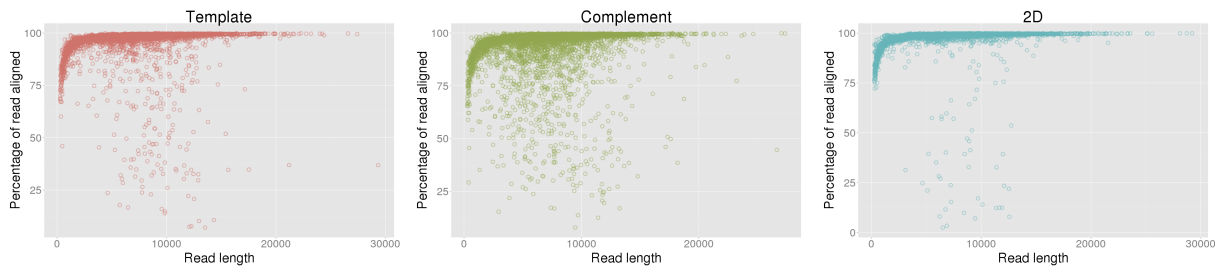
## Escherichia coli error analysis

	Template	Complement	2D
Overall base identity (excluding indels)	73.82%	72.58%	88.88%
Aligned base identity (excluding indels)	80.33%	80.88%	93.54%
Identical bases per 100 aligned bases (including indels)	68.43%	67.67%	85.51%
Inserted bases per 100 aligned bases (including indels)	4.86%	4.87%	3.44%
Deleted bases per 100 aligned bases (including indels)	9.95%	11.46%	5.15%
Substitutions per 100 aligned bases (including indels)	16.76%	16.00%	5.90%
Mean insertion size	1.55	1.55	1.52
Mean deletion size	1.59	1.68	1.50

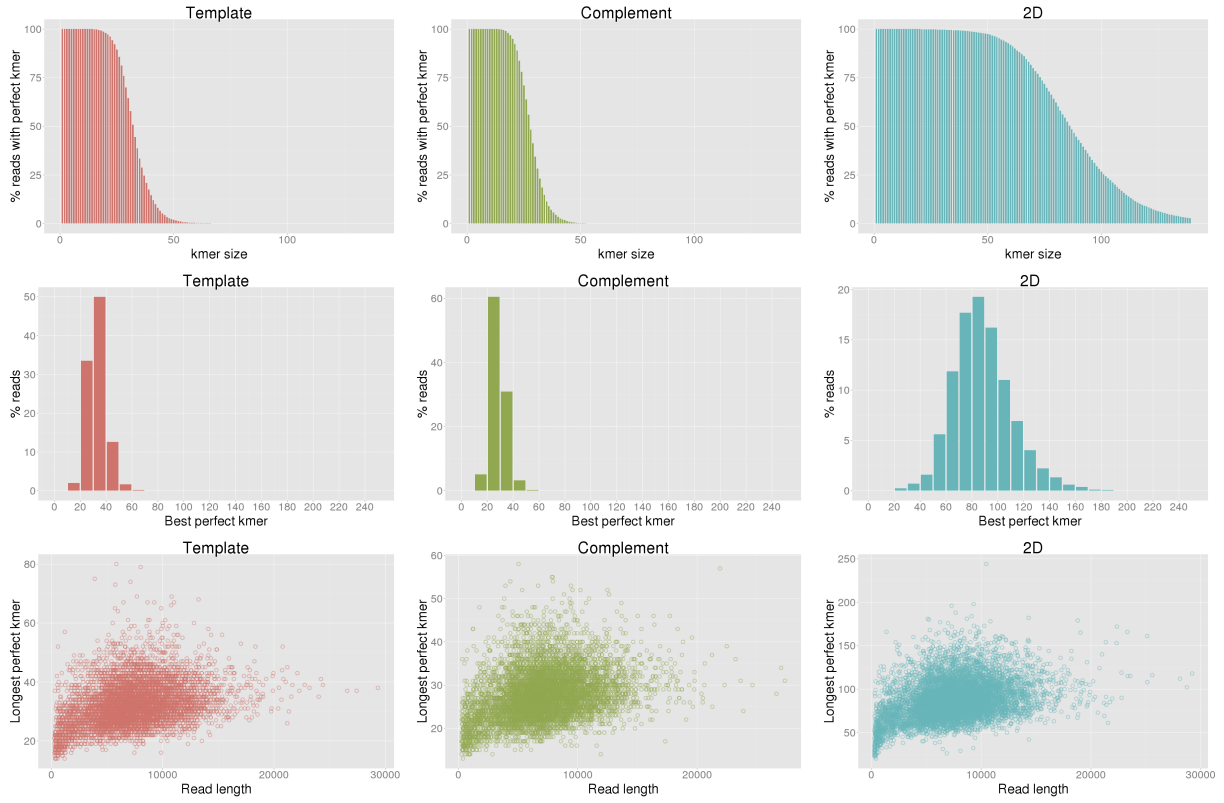


## Escherichia coli read identity

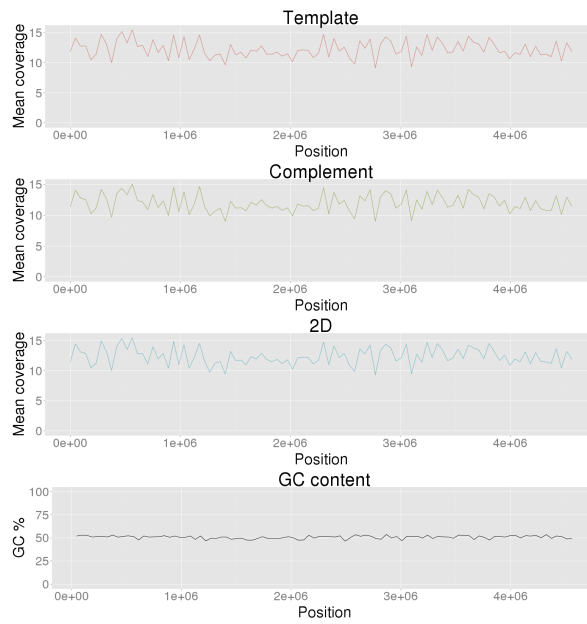




## Escherichia coli perfect kmers



## Escherichia coli coverage



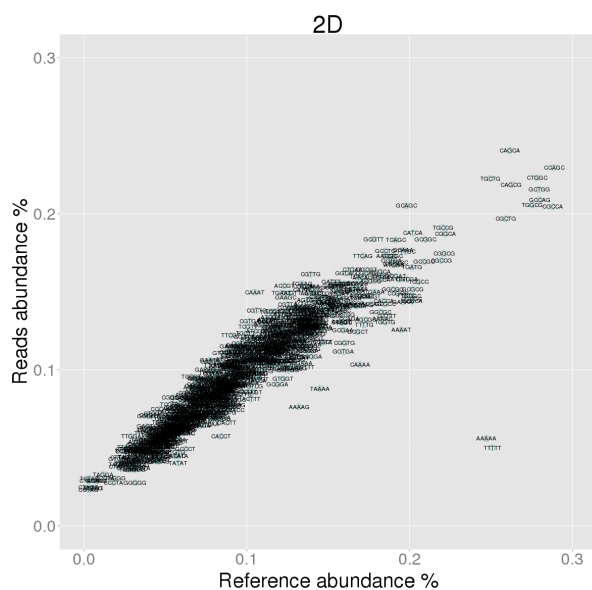
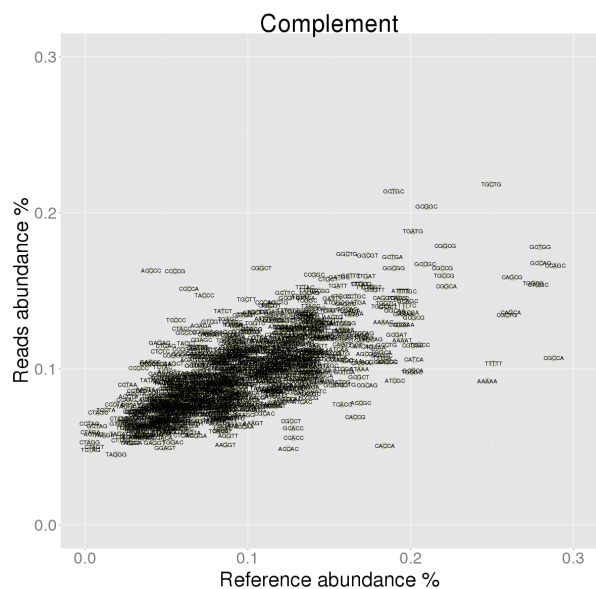
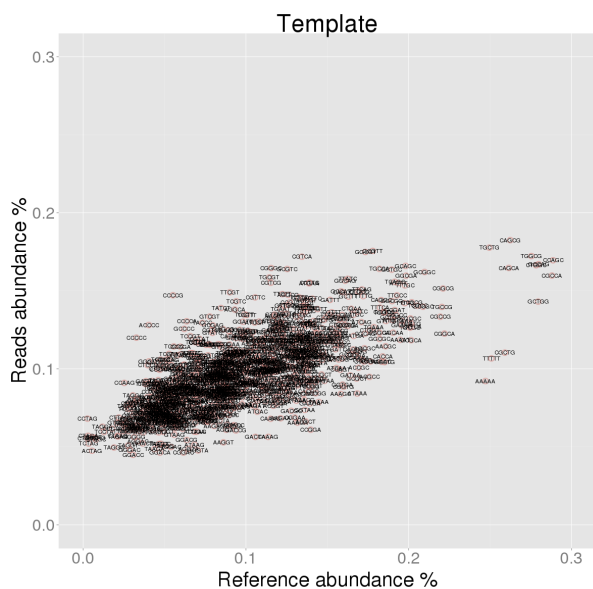
# Escherichia coli 5-mer analysis

## Under-represented 5-mers

Rank	Template				Complement				2D			
	kmer	Ref %	Read %	Diff %	kmer	Ref %	Read %	Diff %	kmer	Ref %	Read %	Diff %
1	AAAAA	0.247	0.092	-0.155	CGCCA	0.288	0.107	-0.181	TTTTT	0.251	0.050	-0.201
2	CGCTG	0.259	0.110	-0.149	AAAAA	0.247	0.092	-0.155	AAAAA	0.247	0.056	-0.191
3	TTTTT	0.251	0.107	-0.144	TTTTT	0.251	0.103	-0.147	CGCCA	0.288	0.205	-0.083
4	GCTGG	0.279	0.143	-0.136	CACCA	0.184	0.051	-0.133	GCCAG	0.280	0.209	-0.071
5	CGCCA	0.288	0.160	-0.128	CAGCA	0.261	0.136	-0.125	TGGCG	0.275	0.206	-0.070
6	CCAGC	0.289	0.170	-0.119	CTGGC	0.278	0.154	-0.124	AAAAT	0.195	0.126	-0.069
7	GCCAG	0.280	0.167	-0.113	CGCTG	0.259	0.135	-0.124	CAAAA	0.169	0.103	-0.066
8	CTGGC	0.278	0.166	-0.112	CCAGC	0.289	0.166	-0.123	GCTGG	0.279	0.216	-0.064
9	TGGCG	0.275	0.172	-0.103	TGGCG	0.275	0.155	-0.121	CGCTG	0.259	0.197	-0.062
10	CGGCA	0.222	0.123	-0.099	GCCAG	0.280	0.168	-0.112	CCAGC	0.289	0.230	-0.059

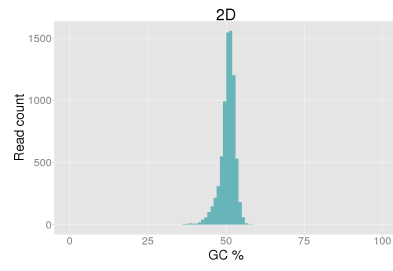
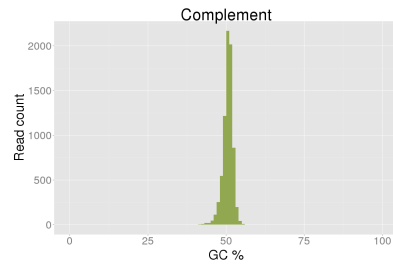
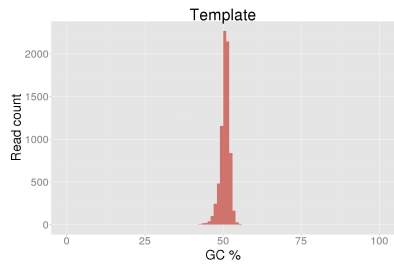
## Over-represented 5-mers

Rank	Template				Complement				2D			
	kmer	Ref %	Read %	Diff %	kmer	Ref %	Read %	Diff %	kmer	Ref %	Read %	Diff %
1	CCCCG	0.055	0.147	0.092	ACCCC	0.040	0.163	0.122	CAAAT	0.105	0.150	0.045
2	ACCCC	0.040	0.128	0.088	CCCCG	0.055	0.163	0.107	CGTTC	0.106	0.138	0.032
3	CCCCC	0.033	0.120	0.087	CCCCA	0.064	0.151	0.088	TTCGT	0.090	0.122	0.032
4	CCCCA	0.064	0.130	0.067	TCCCC	0.056	0.131	0.076	GGGGT	0.039	0.070	0.031
5	CCAAG	0.025	0.091	0.066	TACCC	0.073	0.147	0.074	ACCGT	0.123	0.154	0.031
6	CCTAG	0.003	0.068	0.065	GAGAG	0.046	0.117	0.071	GGGTC	0.040	0.071	0.031
7	GGGTC	0.040	0.105	0.064	CCCCC	0.033	0.101	0.068	CTCGT	0.042	0.072	0.030
8	GCCCC	0.062	0.126	0.064	CTACC	0.059	0.126	0.067	TCCGT	0.066	0.095	0.030
9	CTCCC	0.040	0.102	0.063	CTCTC	0.046	0.111	0.065	CGTGA	0.102	0.131	0.030
10	TTCGT	0.090	0.149	0.059	CTGAG	0.050	0.115	0.065	GAATC	0.077	0.106	0.029

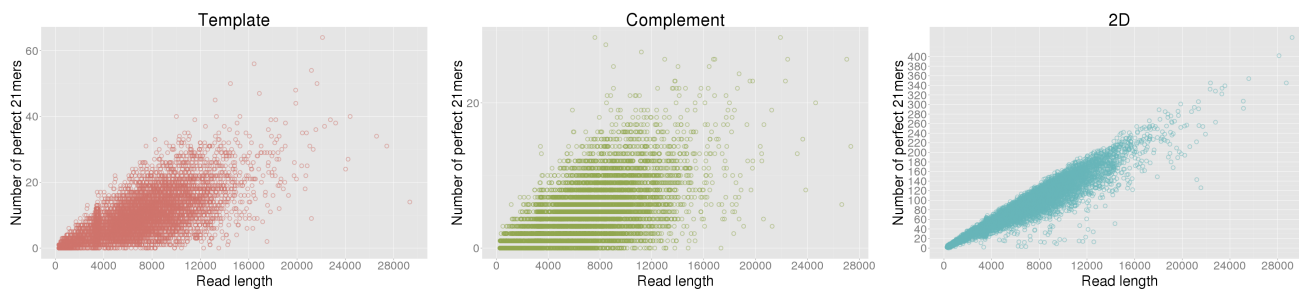




# Escherichia coli GC content



## 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	8.69	9.51	4.58	0.00	9.20	8.90	4.79	0.00	8.12	8.69	3.94
C	8.39	0.00	9.45	9.70	8.93	0.00	9.01	9.44	9.24	0.00	11.46	9.00
G	9.12	9.40	0.00	8.11	8.87	9.14	0.00	8.50	8.88	11.53	0.00	8.65
T	4.88	9.72	8.46	0.00	5.07	9.02	9.12	0.00	3.97	8.54	7.98	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 (3.33%)	TTC (3.49%)	AAA (3.93%)	TGC (2.76%)	GGC (3.05%)	AAA (4.02%)	GCA (3.03%)	GGC (2.64%)	AAA (3.70%)
2	GCA (2.76%)	TGC (3.04%)	TTC (3.76%)	TTC (2.65%)	TGC (2.87%)	GCA (3.45%)	TTC (2.80%)	GCG (2.57%)	GCA (3.53%)
3	AAA (2.76%)	GCA (2.87%)	GCA (3.30%)	GCA (2.63%)	AAA (2.75%)	GAA (3.19%)	TCA (2.71%)	TCA (2.57%)	GAA (3.27%)
4	TGC (2.73%)	AAA (2.66%)	GAA (2.94%)	AAA (2.62%)	GCA (2.61%)	TTC (3.17%)	AAA (2.62%)	TGC (2.54%)	TTC (3.00%)
5	TCA (2.58%)	TCA (2.46%)	TGC (2.57%)	CAG (2.55%)	TTC (2.54%)	TTT (2.72%)	TGC (2.58%)	TTC (2.52%)	TTT (2.78%)
6	ATC (2.42%)	GCC (2.41%)	TTT (2.46%)	GGC (2.45%)	GCC (2.34%)	TGC (2.49%)	GAA (2.49%)	GCA (2.44%)	AAT (2.40%)
7	GCC (2.35%)	GGC (2.38%)	AAT (2.35%)	GAA (2.28%)	CAG (2.31%)	ATC (2.38%)	ATC (2.38%)	AAA (2.42%)	ATC (2.35%)
8	GAA (2.25%)	ATC (2.32%)	TCA (2.28%)	ATC (2.27%)	GCG (2.26%)	TCA (2.34%)	CAG (2.25%)	ATC (2.27%)	GCC (2.32%)
9	GGC (2.24%)	AAC (2.22%)	GCC (2.24%)	TCA (2.24%)	TCA (2.25%)	GCC (2.20%)	CGC (2.21%)	CAG (2.24%)	GCG (2.27%)
10	GCG (2.22%)	GCG (2.21%)	ATC (2.20%)	GCC (2.17%)	GAA (2.23%)	GCC (2.13%)	GCG (2.20%)	GCG (2.23%)	TCA (2.27%)
-10	CTT (1.00%)	CCT (0.93%)	GGA (0.92%)	GTG (1.07%)	AGT (0.94%)	GTG (0.98%)	CTC (1.03%)	ACT (0.98%)	CCT (0.90%)
-9	TGT (0.99%)	GTA (0.93%)	AGA (0.85%)	AGT (1.02%)	CGA (0.93%)	CTT (0.93%)	CTT (1.02%)	GAG (0.97%)	GTA (0.90%)
-8	CCC (0.95%)	AGT (0.88%)	GGG (0.84%)	CTC (0.98%)	CCC (0.93%)	AGT (0.88%)	GAG (0.84%)	CCC (0.91%)	TGA (0.82%)
-7	AGA (0.83%)	CTT (0.83%)	AGT (0.84%)	CCC (0.90%)	CTC (0.90%)	CCT (0.84%)	AGA (0.83%)	CGA (0.89%)	CTT (0.77%)
-6	GGA (0.75%)	CGA (0.79%)	AGG (0.80%)	GGA (0.87%)	GGA (0.88%)	AGG (0.80%)	CCC (0.82%)	CTT (0.86%)	CGA (0.72%)
-5	GAG (0.72%)	GAG (0.78%)	TGT (0.80%)	GAG (0.83%)	CCT (0.87%)	ACT (0.80%)	AGG (0.78%)	CCT (0.82%)	GAG (0.66%)
-4	AGG (0.68%)	AGA (0.65%)	CTT (0.77%)	AGG (0.69%)	GAG (0.82%)	GGG (0.74%)	GGA (0.75%)	AGA (0.77%)	AGA (0.51%)
-3	GGG (0.63%)	GGA (0.63%)	GAG (0.59%)	CTA (0.67%)	GGG (0.77%)	GAG (0.61%)	GGG (0.69%)	GGA (0.69%)	GGA (0.50%)
-2	CTA (0.56%)	TAG (0.53%)	TAG (0.39%)	GGG (0.56%)	TAG (0.54%)	CTA (0.47%)	CTA (0.62%)	CTA (0.65%)	TAG (0.45%)
-1	TAG (0.43%)	CTA (0.49%)	CTA (0.37%)	TAG (0.47%)	CTA (0.51%)	TAG (0.39%)	TAG (0.49%)	TAG (0.63%)	CTA (0.41%)

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 (1.09%)	AAAA (1.34%)	CAGC (0.98%)	TGGC (1.12%)	AAAA (1.24%)	ATCA (0.95%)	TGGC (0.95%)	AAAA (1.11%)
2	GAAA (0.91%)	TGCC (0.92%)	TTTT (1.19%)	ATCA (0.86%)	CAGC (1.08%)	CAAA (0.99%)	GGCA (0.84%)	CAGC (0.92%)	GGCA (1.10%)
3	ATCA (0.90%)	CAGC (0.91%)	GAAA (1.13%)	CCAG (0.85%)	CGGC (1.06%)	GAAA (0.96%)	CAGC (0.83%)	ATCA (0.85%)	TGAA (0.97%)
4	AAAA (0.90%)	TTCA (0.91%)	GTTC (0.96%)	CTGC (0.85%)	CTGC (0.92%)	TTTT (0.95%)	TTCA (0.79%)	TTCA (0.85%)	TTTT (0.93%)
5	CAGC (0.89%)	TGGC (0.90%)	GGCA (0.93%)	TGGC (0.85%)	TTGC (0.87%)	TGAA (0.93%)	TGAA (0.79%)	CGGC (0.81%)	GAAA (0.91%)
6	TTCA (0.86%)	CTGC (0.88%)	TTTT (0.87%)	CGGC (0.83%)	AAAA (0.83%)	TTTC (0.93%)	AACA (0.78%)	CTGC (0.76%)	GGAA (0.89%)
7	TGCC (0.81%)	AAAA (0.86%)	TGCC (0.85%)	AAAA (0.81%)	ATCA (0.80%)	AGCA (0.91%)	GCCA (0.78%)	GGCG (0.74%)	TTTC (0.86%)
8	TGGC (0.80%)	GTTC (0.86%)	GCAA (0.85%)	TGTC (0.80%)	CTGG (0.77%)	GGCA (0.90%)	TTTT (0.76%)	TGCC (0.72%)	TGCA (0.83%)
9	CTTC (0.79%)	TTGC (0.85%)	TGCA (0.83%)	CGCC (0.73%)	CAAA (0.77%)	ATCA (0.89%)	CTGC (0.74%)	CGCC (0.71%)	CGCC (0.83%)
10	TTCT (0.79%)	TTCC (0.82%)	TGAA (0.82%)	TTTT (0.73%)	CCAG (0.77%)	AGAA (0.83%)	CGCA (0.74%)	TTGC (0.70%)	CAAA (0.81%)
-10	GGGG (0.12%)	GAGA (0.13%)	GGAC (0.11%)	CGAG (0.13%)	CGAG (0.13%)	GTAG (0.11%)	TTAG (0.15%)	ACCT (0.15%)	CGGA (0.11%)
-9	AGGG (0.12%)	TAGT (0.12%)	ACTA (0.11%)	AGGG (0.12%)	CTAT (0.12%)	ACCT (0.11%)	GGGA (0.14%)	CCCC (0.15%)	CCCT (0.11%)
-8	GGAC (0.12%)	CTAT (0.12%)	TAGT (0.11%)	CTAA (0.11%)	GTGT (0.12%)	GAGG (0.11%)	GAGG (0.13%)	GAGA (0.14%)	GGGA (0.10%)
-7	CTAA (0.12%)	TCTA (0.12%)	TTAG (0.11%)	GGAC (0.10%)	CTAA (0.12%)	GGAC (0.10%)	CTAT (0.13%)	CTAT (0.13%)	CTAA (0.10%)
-6	GAGG (0.11%)	CGGA (0.11%)	CGAG (0.10%)	TAGA (0.10%)	ACCT (0.11%)	CTAT (0.09%)	TCTA (0.13%)	CTAA (0.12%)	TCTA (0.09%)
-5	TTAG (0.11%)	CTAA (0.10%)	TCTA (0.08%)	CCCT (0.10%)	TAGA (0.09%)	CGAG (0.09%)	CTAA (0.12%)	CCCT (0.11%)	CTAT (0.09%)
-4	TAGA (0.07%)	TAGG (0.07%)	TAGA (0.07%)	GAGG (0.09%)	CCCT (0.08%)	CCCT (0.07%)	TAGA (0.08%)	TAGG (0.10%)	TAGG (0.07%)
-3	CCTA (0.06%)	TAGA (0.06%)	TAGG (0.06%)	CCTA (0.08%)	TAGG (0.08%)	CCTA (0.06%)	CCTA (0.08%)	TAGA (0.08%)	TAGA (0.05%)
-2	TAGG (0.06%)	CCTA (0.06%)	CCTA (0.04%)	TAGG (0.05%)	CCTA (0.06%)	TAGG (0.06%)	TAGG (0.06%)	CCTA (0.08%)	CCTA (0.04%)
-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 (0.36%)	CAGCA (0.38%)	CAGCA (0.42%)	CAGCA (0.41%)	CAGCA (0.42%)	CAGCA (0.52%)	CAGCA (0.37%)	CTGGC (0.38%)	CAGCA (0.44%)
2	CATCA (0.32%)	CTGGC (0.36%)	GAAAA (0.40%)	CTGGC (0.34%)	CTGGC (0.41%)	CGGCA (0.35%)	CGCCA (0.32%)	CAGCA (0.31%)	CGGCA (0.39%)
3	CGCCA (0.32%)	GCTGC (0.32%)	CAAAA (0.38%)	CCAGC (0.32%)	GCGGC (0.34%)	GAAAA (0.35%)	CTGGC (0.31%)	CATCA (0.30%)	GAAAA (0.35%)
4	CTGGC (0.32%)	TTTGC (0.31%)	TGTTT (0.35%)	GCTGC (0.31%)	CCAGC (0.34%)	ATAAA (0.34%)	CGGCA (0.31%)	CCAGC (0.29%)	TGGCA (0.35%)
5	GCAGC (0.30%)	CATCA (0.30%)	CGTTC (0.34%)	CATCA (0.30%)	TCAGC (0.32%)	TTATC (0.33%)	TGGCA (0.28%)	TGGCG (0.29%)	CAAAA (0.30%)
6	TTATC (0.30%)	TTGCC (0.30%)	TGGCA (0.33%)	GCGGC (0.29%)	CATCA (0.31%)	CATCA (0.31%)	CATCA (0.28%)	GCGGC (0.29%)	GCAAAA (0.30%)
7	CAAAA (0.29%)	TTTCA (0.30%)	GCAAA (0.32%)	TTATC (0.29%)	GCTGC (0.31%)	AAGAA (0.31%)	GCAAA (0.28%)	CGCCA (0.28%)	ATTTT (0.29%)
8	CCAGC (0.29%)	GCAGC (0.30%)	GCCAG (0.31%)	GCCAG (0.27%)	TTTGC (0.30%)	TGTTT (0.31%)	CCAGC (0.27%)	TTTCA (0.27%)	TAAAA (0.27%)
9	ATTTT (0.28%)	CCAGC (0.30%)	TGAAA (0.31%)	TCAGC (0.27%)	GCAGC (0.29%)	TGGCA (0.31%)	GCCAG (0.26%)	GCCAG (0.27%)	TTGCC (0.27%)
10	GCCAG (0.28%)	CGTTC (0.29%)	CTGGC (0.31%)	TCTTC (0.27%)	AATCA (0.29%)	CAAAA (0.31%)	AATCA (0.25%)	CAGCG (0.26%)	ATGAA (0.27%)
-10	TAGGA (0.01%)	ACCTA (0.01%)	ACCTA (0.01%)	CCCTA (0.01%)	CCCCT (0.01%)	ACCTA (0.01%)	TAGGA (0.01%)	TCCTA (0.01%)	TAGGA (0.01%)
-9	CCCTA (0.01%)	TAGGA (0.01%)	CCCTA (0.01%)	TAGGG (0.01%)	CTAGC (0.01%)	CCCTA (0.01%)	CCCTA (0.01%)	TAGGA (0.01%)	CTAGC (0.01%)
-8	CTAGC (0.00%)	GCTAG (0.00%)	GCTAG (0.00%)	CTAGC (0.01%)	ACCTA (0.01%)	CTAGC (0.01%)	CTAGC (0.01%)	GCTAG (0.01%)	TTAGA (0.01%)
-7	GCTAG (0.00%)	CTAGC (0.00%)	ACTAG (0.00%)	CTAGT (0.01%)	GCTAG (0.01%)	GCTAG (0.01%)	GCTAG (0.00%)	CTAGC (0.01%)	GCTAG (0.01%)
-6	ACTAG (0.00%)	CTAGT (0.00%)	CTAGC (0.00%)	GCTAG (0.00%)	CTAGT (0.00%)	CTAGT (0.00%)	CCTAG (0.00%)	ACTAG (0.01%)	CTAGT (0.00%)
-5	CTAGT (0.00%)	ACTAG (0.00%)	CTAGG (0.00%)	CTAGA (0.00%)	ACTAG (0.00%)	CTAGA (0.00%)	CTAGT (0.00%)	CTAGT (0.01%)	ACTAG (0.00%)
-4	CCTAG (0.00%)	CTAGG (0.00%)	CTAGT (0.00%)	CCTAG (0.00%)	TAGA (0.00%)	CTAGG (0.00%)	ACTAG (0.00%)	CTAGG (0.00%)	CTAGG (0.00%)
-3	CTAGG (0.00%)	CCTAG (0.00%)	CCTAG (0.00%)	TCTAG (0.00%)	CTAGG (0.00%)	ACTAG (0.00%)	CTAGA (0.00%)	TCTAG (0.00%)	CCTAG (0.00%)
-2	TCTAG (0.00%)	TCTAG (0.00%)	TCTAG (0.00%)	ACTAG (0.00%)	CCTAG (0.00%)	TCTAG (0.00%)	CTAGG (0.00%)	CTAGA (0.00%)	TCTAG (0.00%)
-1	CTAGA (0.00%)	CTAGA (0.00%)	CTAGA (0.00%)	CTAGG (0.00%)	TCTAG (0.00%)	CCTAG (0.00%)	TCTAG (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%