

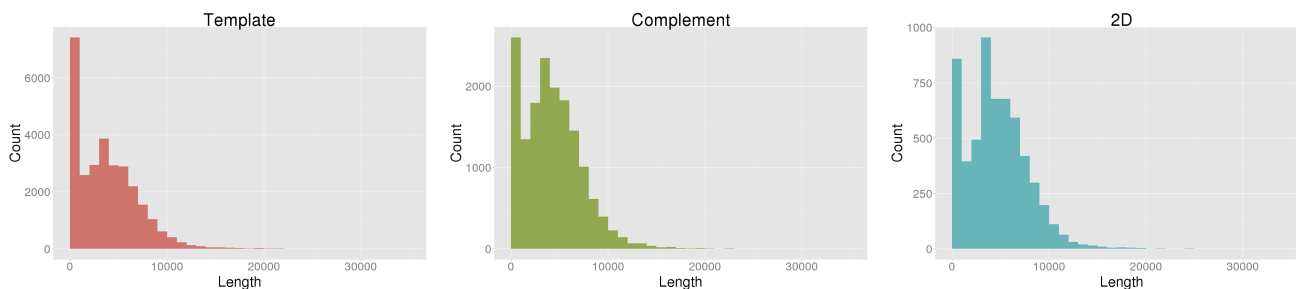
# NanoOK report for ZF-screens\_MARC\_phase\_1b\_e\_coli\_run2

## Pass and fail counts

Type	Pass	Fail
Template	0	29269
Complement	0	16058
2D	0	5856

## Read lengths

Type	NumReads	TotalBases	Mean	Longest	Shortest	N50	N50Count	N90	N90Count
Template	29269	115352699	3941.12	331598	7	6057	6479	2722	17296
Complement	16058	69181648	4308.24	44607	7	5973	4178	2895	10574
2D	5856	27320295	4665.35	43221	134	6297	1587	3218	3948



## Template alignments

Number of reads	29269
Number of reads with alignments	13399 (45.78%)
Number of reads without alignments	15870 (54.22%)

ID	Size	Number of Reads	% of Reads	Mean read length	Aligned bases	Mean coverage	Longest Perf Kmer
Control sequence	3560	1471	5.03	2756.43	3927364	1103.19	57
Escherichia coli	4641652	11928	40.75	5576.79	62115980	13.38	85

## Complement alignments

Number of reads	16058
Number of reads with alignments	8264 (51.46%)
Number of reads without alignments	7794 (48.54%)

ID	Size	Number of Reads	% of Reads	Mean read length	Aligned bases	Mean coverage	Longest Perf Kmer
Control sequence	3560	757	4.71	2660.92	1759929	494.36	41
Escherichia coli	4641652	7507	46.75	5571.93	37594549	8.10	67

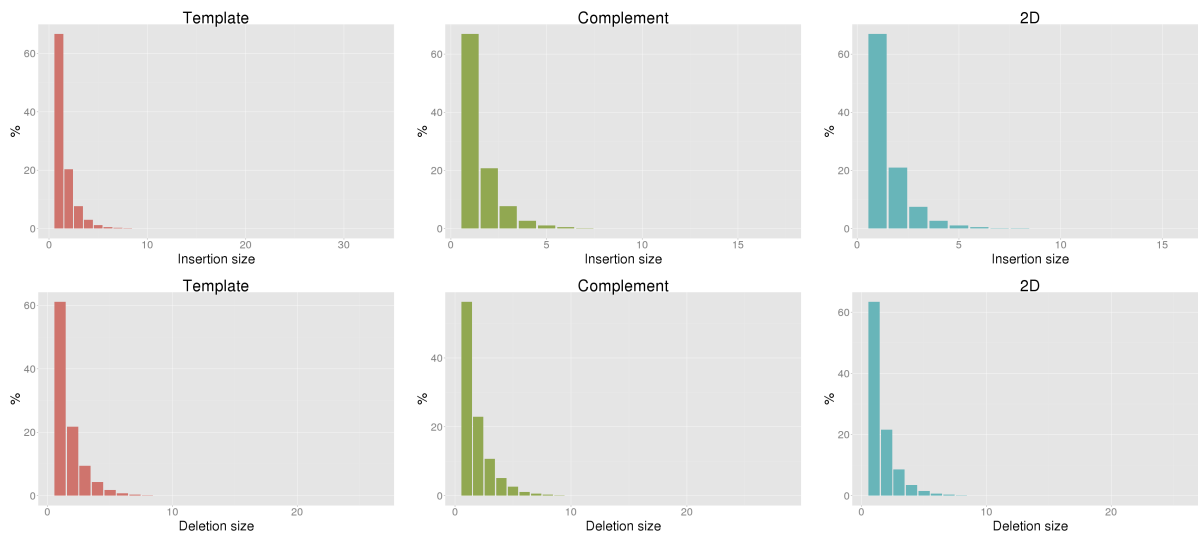
## 2D alignments

Number of reads	5856
Number of reads with alignments	4760 (81.28%)
Number of reads without alignments	1096 (18.72%)

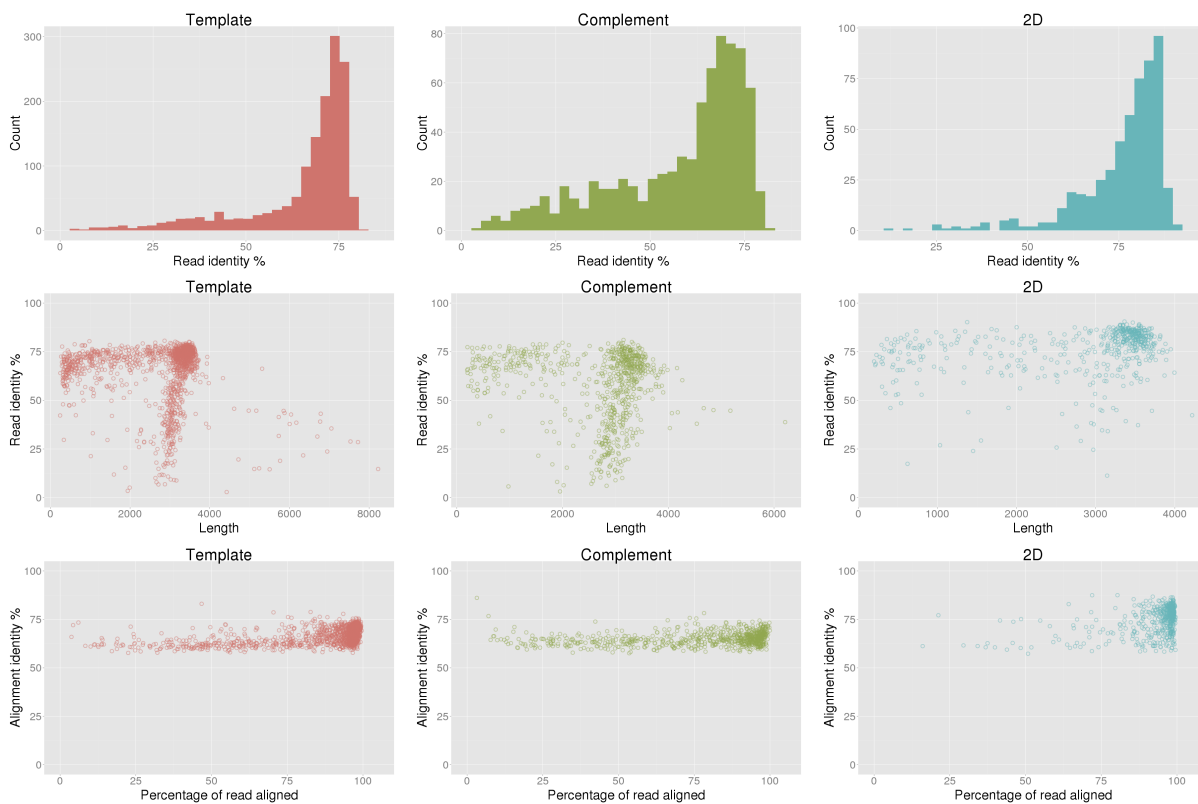
ID	Size	Number of Reads	% of Reads	Mean read length	Aligned bases	Mean coverage	Longest Perf Kmer
Control sequence	3560	538	9.19	2827.80	1555838	437.03	155
Escherichia coli	4641652	4222	72.10	5387.95	23188099	5.00	187

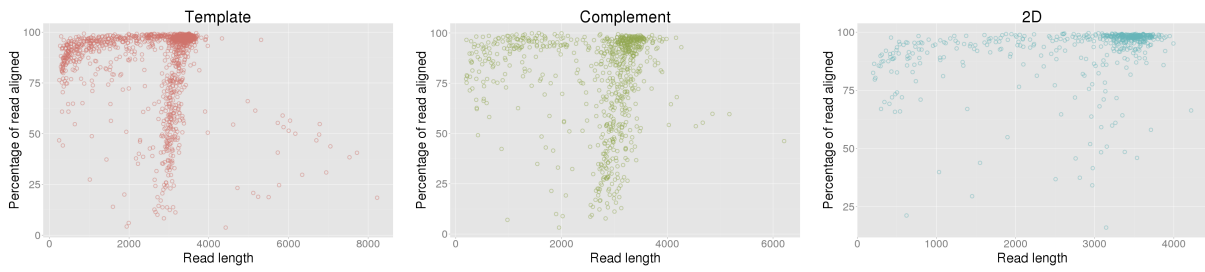
## Control sequence error analysis

	Template	Complement	2D
Overall base identity (excluding indels)	64.90%	56.65%	77.09%
Aligned base identity (excluding indels)	80.00%	79.44%	86.83%
Identical bases per 100 aligned bases (including indels)	67.00%	64.84%	75.38%
Inserted bases per 100 aligned bases (including indels)	4.96%	4.71%	4.94%
Deleted bases per 100 aligned bases (including indels)	11.29%	13.67%	8.26%
Substitutions per 100 aligned bases (including indels)	16.75%	16.78%	11.43%
Mean insertion size	1.57	1.54	1.53
Mean deletion size	1.70	1.84	1.64

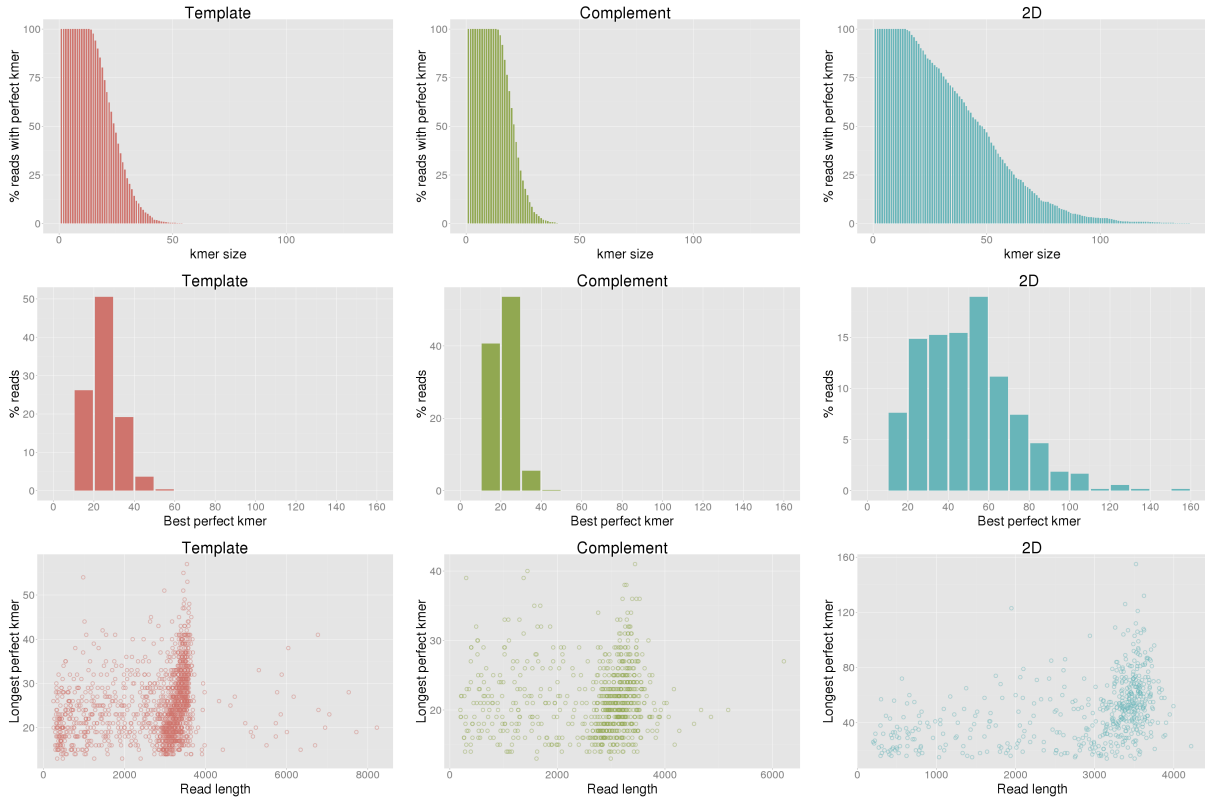


## Control sequence read identity

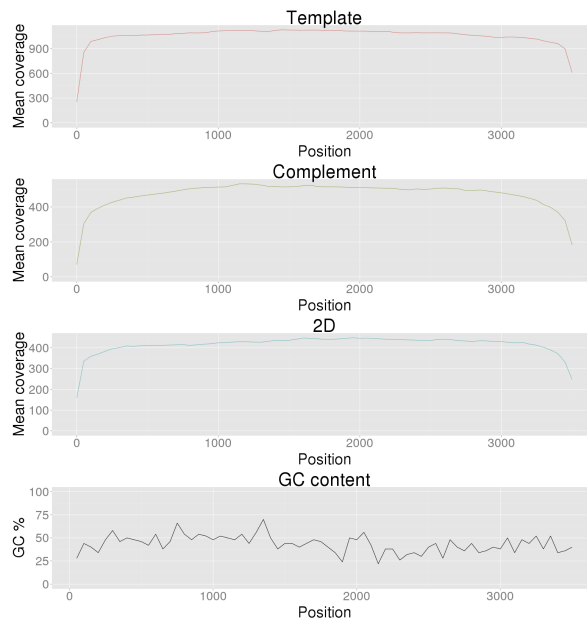




## Control sequence perfect kmers



## Control sequence coverage



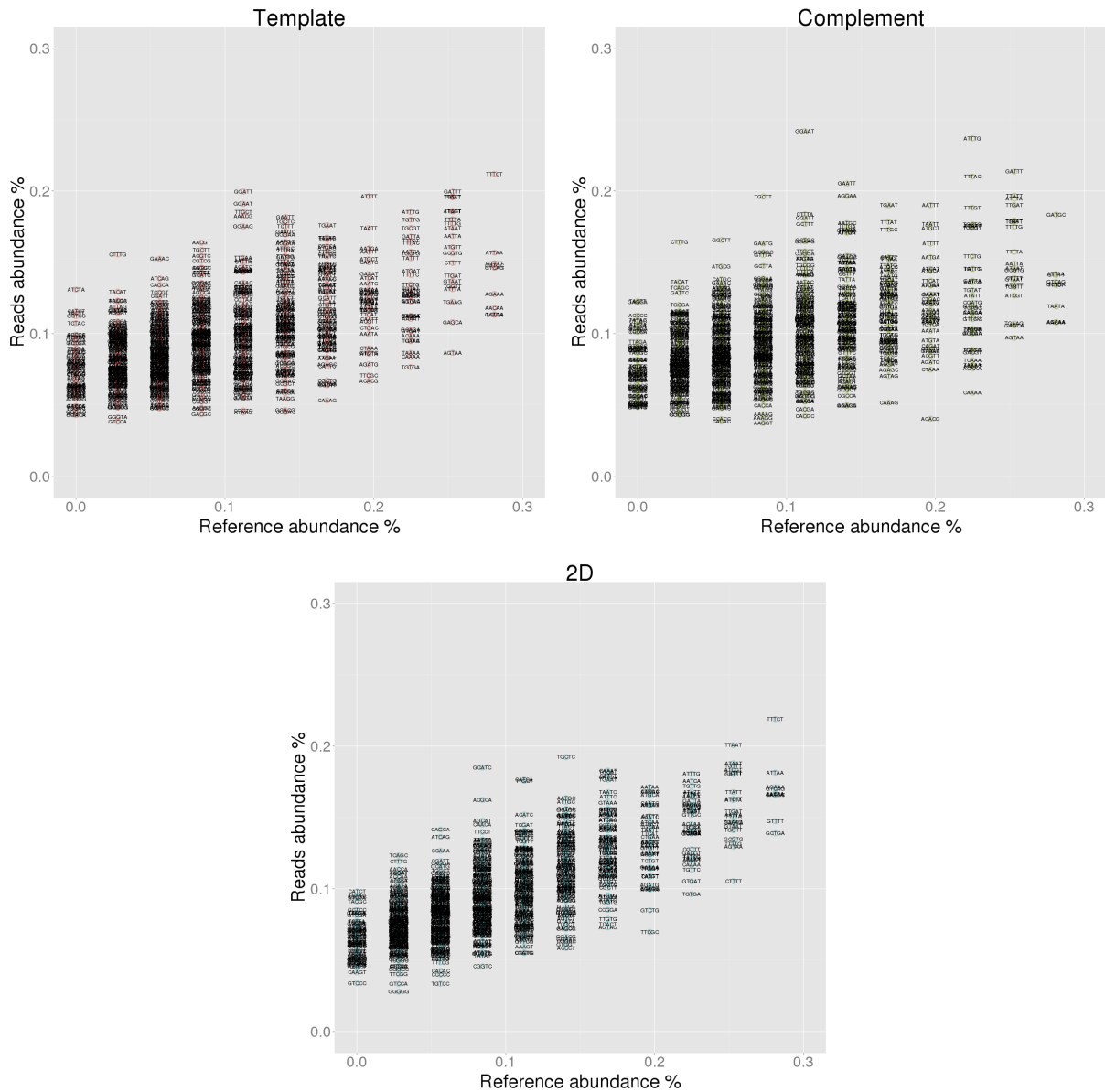
# Control sequence 5-mer analysis

## Under-represented 5-mers

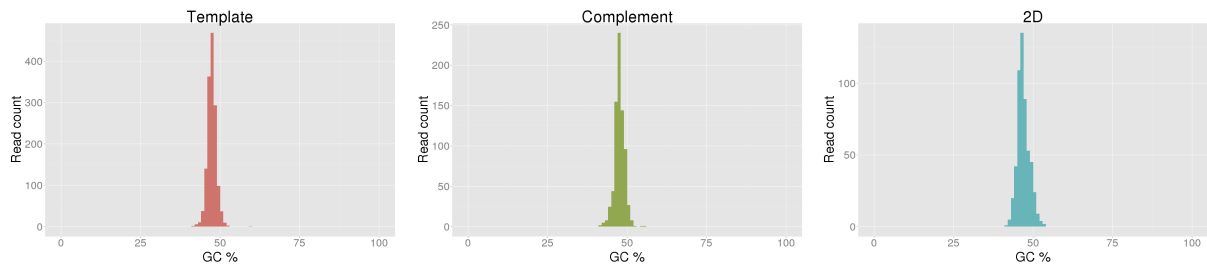
Rank	Template				Complement				2D			
	kmer	Ref %	Read %	Diff %	kmer	Ref %	Read %	Diff %	kmer	Ref %	Read %	Diff %
1	TTTTT	0.759	0.115	-0.644	TTTTT	0.759	0.080	-0.679	TTTTT	0.759	0.047	-0.712
2	AAAAA	0.478	0.079	-0.399	AAAAA	0.478	0.038	-0.440	AAAAA	0.478	0.046	-0.432
3	TGATG	0.393	0.131	-0.262	AAAAC	0.337	0.104	-0.233	TGATG	0.393	0.167	-0.226
4	AAAAC	0.337	0.116	-0.221	GATGT	0.309	0.108	-0.201	AAAAC	0.337	0.148	-0.190
5	GATGT	0.309	0.102	-0.207	TGATG	0.393	0.195	-0.198	GATGT	0.309	0.134	-0.175
6	CTGAT	0.309	0.106	-0.203	TTATC	0.309	0.128	-0.181	CTGAT	0.309	0.151	-0.158
7	AATAT	0.309	0.130	-0.179	GCAAT	0.309	0.132	-0.177	TTATC	0.309	0.159	-0.150
8	GCAAT	0.309	0.139	-0.170	AATAT	0.309	0.135	-0.174	CTTTT	0.253	0.105	-0.147
9	TAATA	0.281	0.113	-0.168	AACAA	0.281	0.108	-0.173	GCAAT	0.309	0.162	-0.147
10	GCTGA	0.281	0.113	-0.167	AGAAA	0.281	0.108	-0.173	GCTGA	0.281	0.139	-0.142

## Over-represented 5-mers

Rank	Template				Complement				2D			
	kmer	Ref %	Read %	Diff %	kmer	Ref %	Read %	Diff %	kmer	Ref %	Read %	Diff %
1	ATCTA	0.000	0.131	0.131	CTTTG	0.028	0.164	0.136	GCATC	0.084	0.185	0.101
2	CTTTG	0.028	0.156	0.127	GGAAT	0.112	0.242	0.129	CATCT	0.000	0.098	0.098
3	CATCT	0.000	0.116	0.116	TACTT	0.000	0.123	0.123	TCAGC	0.028	0.123	0.095
4	TACTT	0.000	0.114	0.114	GAGGA	0.000	0.122	0.122	TCTAC	0.000	0.095	0.095
5	GCTCC	0.000	0.112	0.112	ACCCC	0.000	0.113	0.113	CCCGC	0.000	0.094	0.094
6	TCTAC	0.000	0.107	0.107	TGCTT	0.084	0.196	0.112	ATCTA	0.000	0.094	0.094
7	TACAT	0.028	0.129	0.101	GGCTT	0.056	0.166	0.109	TACGC	0.000	0.091	0.091
8	ACCCC	0.000	0.099	0.099	TATAC	0.000	0.109	0.109	CTTTG	0.028	0.119	0.091
9	CCCCA	0.000	0.099	0.099	CTTAC	0.000	0.109	0.109	AACCA	0.028	0.114	0.085
10	GTGCC	0.000	0.098	0.098	TACAT	0.028	0.136	0.108	CAGCA	0.056	0.142	0.085

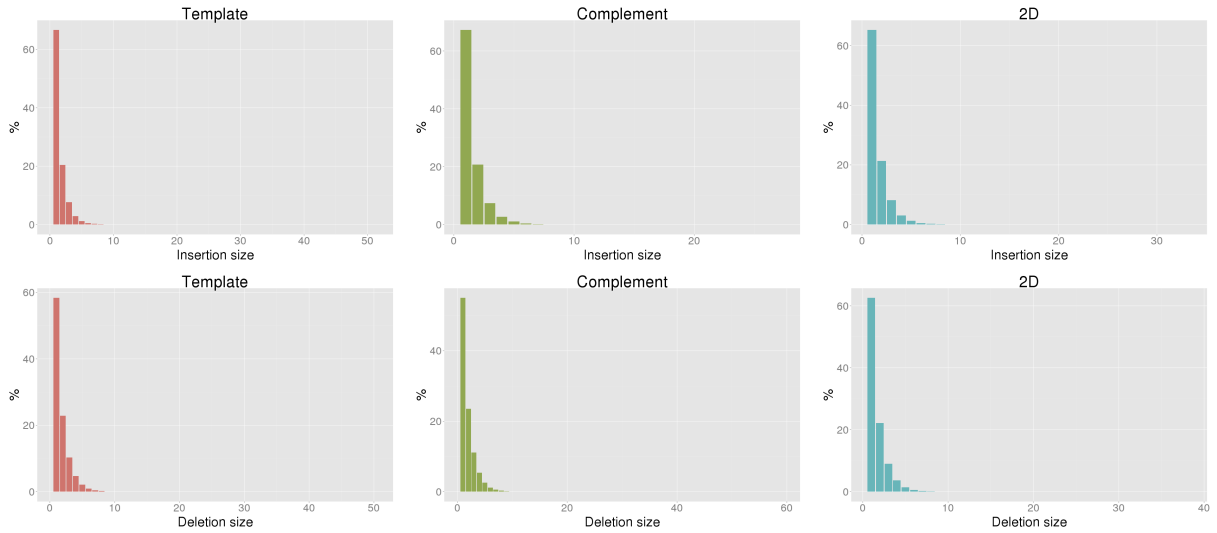


## Control sequence GC content

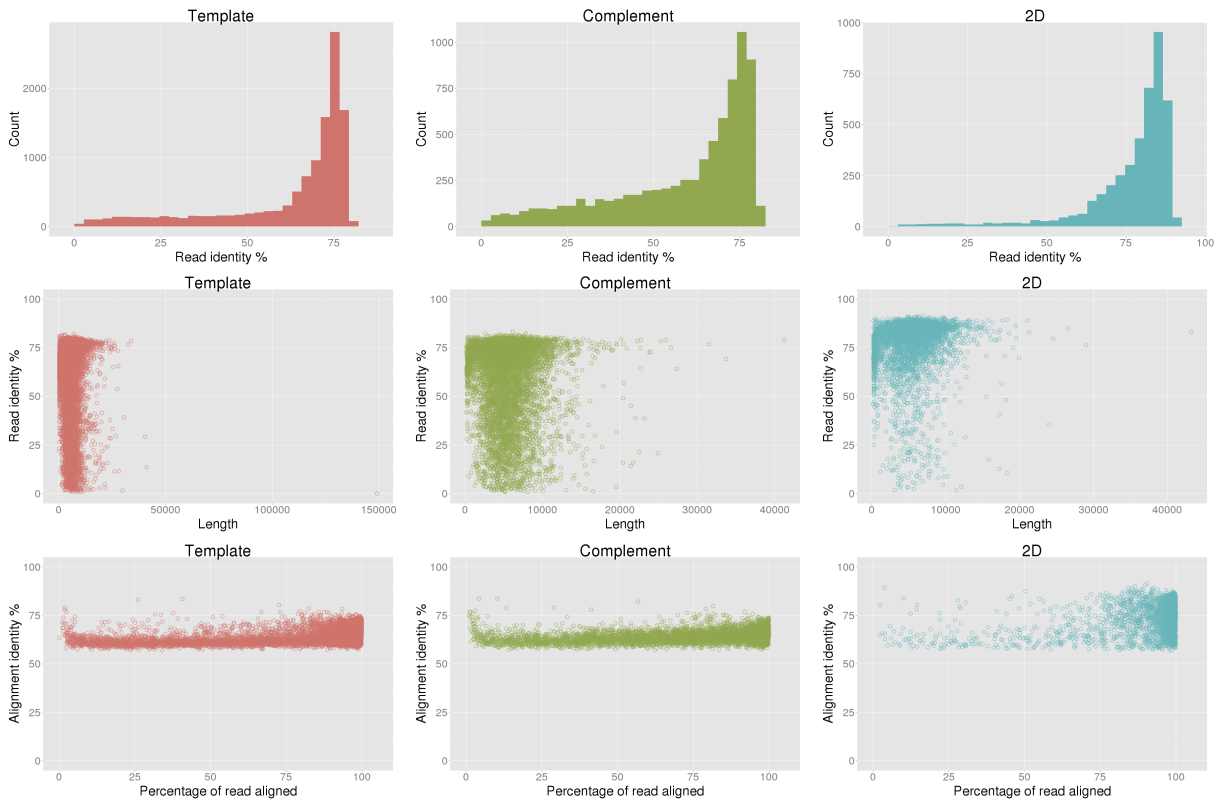


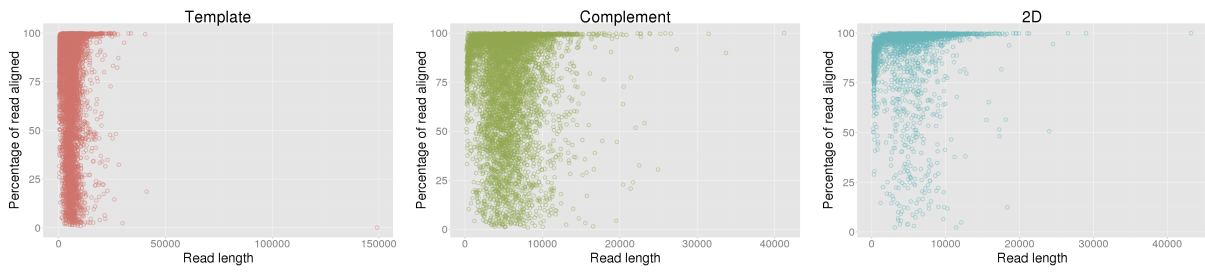
## Escherichia coli error analysis

	Template	Complement	2D
Overall base identity (excluding indels)	61.37%	58.31%	77.49%
Aligned base identity (excluding indels)	79.39%	80.00%	87.32%
Identical bases per 100 aligned bases (including indels)	65.72%	64.88%	76.02%
Inserted bases per 100 aligned bases (including indels)	4.85%	4.46%	5.19%
Deleted bases per 100 aligned bases (including indels)	12.37%	14.44%	7.75%
Substitutions per 100 aligned bases (including indels)	17.06%	16.22%	11.04%
Mean insertion size	1.57	1.53	1.58
Mean deletion size	1.76	1.87	1.64

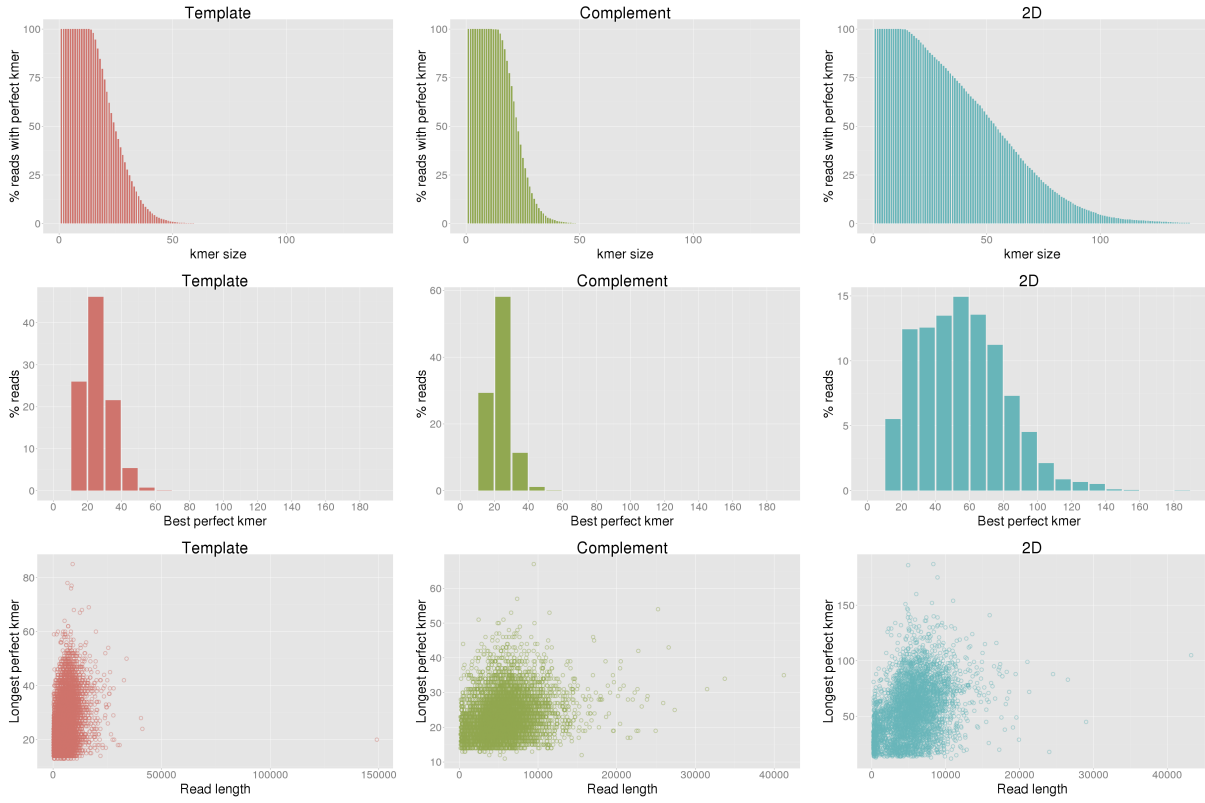


## Escherichia coli read identity

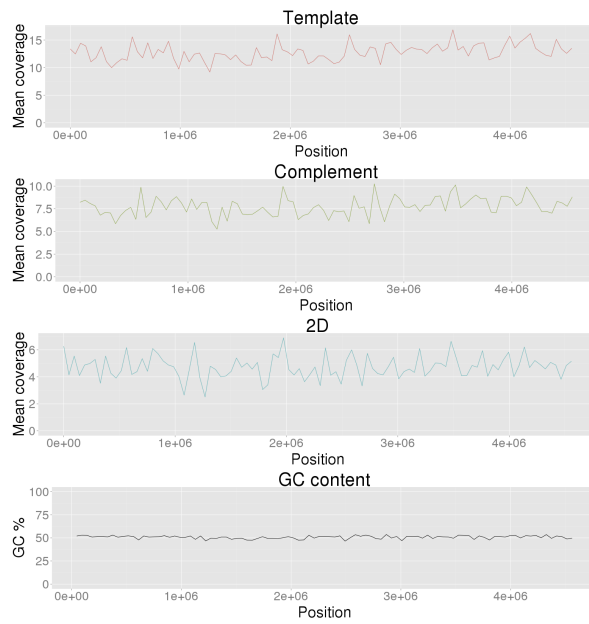




## Escherichia coli perfect kmers



## Escherichia coli coverage



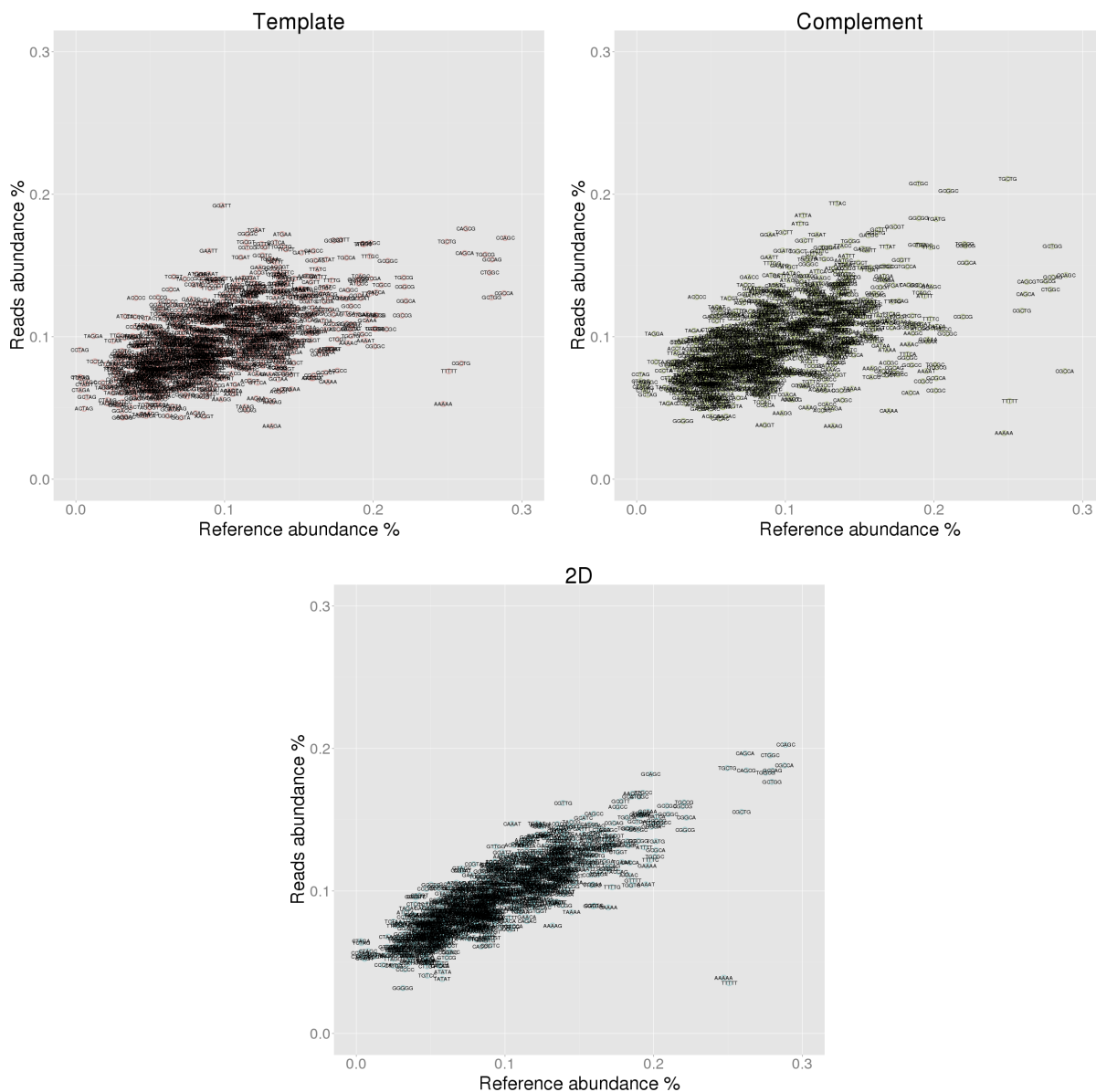
# Escherichia coli 5-mer analysis

## Under-represented 5-mers

Rank	Template				Complement				2D			
	kmer	Ref %	Read %	Diff %	kmer	Ref %	Read %	Diff %	kmer	Ref %	Read %	Diff %
1	AAAAA	0.247	0.053	-0.194	AAAAA	0.247	0.032	-0.215	TTTTT	0.251	0.035	-0.216
2	CGCTG	0.259	0.081	-0.178	CGCCA	0.288	0.076	-0.212	AAAAA	0.247	0.039	-0.208
3	TTTTT	0.251	0.076	-0.175	TTTTT	0.251	0.055	-0.196	CGCTG	0.259	0.155	-0.104
4	CGCCA	0.288	0.130	-0.158	CCAGC	0.289	0.143	-0.145	GCTGG	0.279	0.177	-0.103
5	GCTGG	0.279	0.128	-0.152	CTGGC	0.278	0.133	-0.145	CGCCA	0.288	0.188	-0.100
6	CTGGC	0.278	0.145	-0.133	CGCTG	0.259	0.118	-0.141	GCCAG	0.280	0.184	-0.095
7	GCCAG	0.280	0.154	-0.126	CGCGC	0.201	0.062	-0.139	TGGCG	0.275	0.183	-0.092
8	CCAGC	0.289	0.169	-0.119	GCCAG	0.280	0.142	-0.138	AAAAT	0.195	0.105	-0.090
9	TGGCG	0.275	0.158	-0.118	TGGCG	0.275	0.139	-0.136	CCAGC	0.289	0.203	-0.086
10	CGCGC	0.201	0.093	-0.108	CAGCA	0.261	0.130	-0.132	CTGGC	0.278	0.195	-0.083

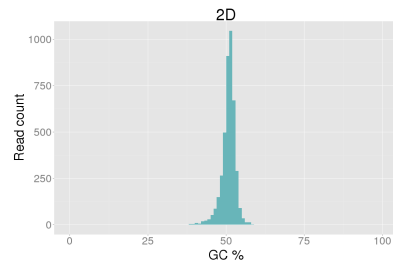
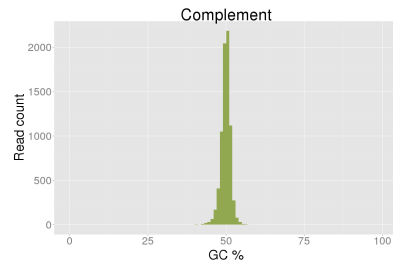
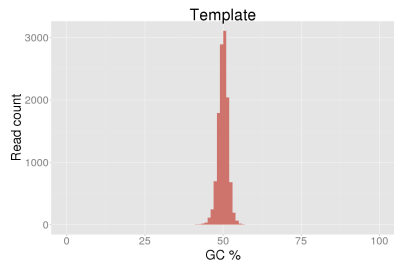
## Over-represented 5-mers

Rank	Template				Complement				2D			
	kmer	Ref %	Read %	Diff %	kmer	Ref %	Read %	Diff %	kmer	Ref %	Read %	Diff %
1	GGATT	0.098	0.192	0.094	TAGGA	0.012	0.102	0.090	CTAGA	0.003	0.065	0.062
2	TAGGA	0.012	0.101	0.089	ACCCC	0.040	0.128	0.088	TCTAG	0.003	0.064	0.060
3	CCTAG	0.003	0.091	0.088	GGAAT	0.089	0.172	0.082	GGGGT	0.039	0.096	0.057
4	ACCCC	0.040	0.127	0.087	TGCTT	0.099	0.173	0.074	GGGTC	0.040	0.096	0.055
5	ATCTA	0.033	0.114	0.081	ATTTA	0.112	0.185	0.073	CTCGT	0.042	0.097	0.055
6	TCCGT	0.066	0.142	0.076	CCTAG	0.003	0.074	0.071	CCCAA	0.047	0.101	0.054
7	CTCCC	0.040	0.114	0.074	ATTTG	0.110	0.180	0.070	GCCTC	0.050	0.105	0.054
8	CCCCG	0.055	0.128	0.073	TCCTA	0.013	0.082	0.070	CCTAG	0.003	0.057	0.054
9	TCTAA	0.025	0.097	0.072	CCTAT	0.028	0.096	0.068	TCTAA	0.025	0.078	0.053
10	TTGGA	0.029	0.101	0.072	TTGGA	0.029	0.096	0.067	TAGAT	0.035	0.088	0.053

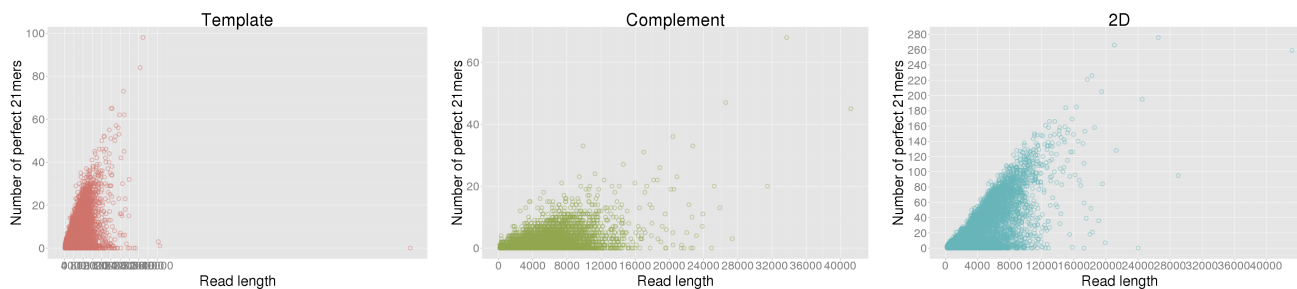




# Escherichia coli GC content



# 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	8.81	8.89	5.13	0.00	8.76	8.54	5.44	0.00	9.20	8.73	4.66
C	8.64	0.00	8.78	10.02	9.34	0.00	8.46	9.68	8.58	0.00	9.99	8.84
G	9.54	8.83	0.00	8.35	9.01	8.59	0.00	8.97	8.80	10.15	0.00	8.31
T	5.40	8.99	8.62	0.00	5.72	8.72	8.77	0.00	4.77	8.85	9.13	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 (3.28%)	TTC (3.31%)	AAA (4.03%)	TGC (2.86%)	TGC (2.80%)	AAA (4.00%)	GCA (3.07%)	AAA (2.72%)	AAA (3.84%)
2	GCA (2.79%)	TGC (2.97%)	TTC (3.56%)	TTC (2.82%)	AAA (2.79%)	GCA (3.53%)	AAA (2.93%)	GCA (2.67%)	GCA (3.65%)
3	AAA (2.79%)	AAA (2.81%)	GCA (3.32%)	GCA (2.77%)	GGC (2.79%)	GAA (3.30%)	TTC (2.71%)	GGC (2.62%)	GAA (3.08%)
4	TGC (2.63%)	GCA (2.77%)	GAA (3.02%)	AAA (2.75%)	GCA (2.71%)	TTC (2.98%)	TCA (2.41%)	TGC (2.56%)	TTT (2.78%)
5	ATC (2.63%)	GCC (2.47%)	TTT (2.67%)	GAA (2.48%)	TTC (2.59%)	TTT (2.65%)	GCG (2.36%)	GCG (2.43%)	TTC (2.74%)
6	TCA (2.46%)	TCA (2.35%)	TGC (2.58%)	CAG (2.38%)	GAA (2.51%)	TGC (2.53%)	GAA (2.34%)	TCA (2.38%)	GTT (2.56%)
7	TTT (2.26%)	GGC (2.32%)	AAT (2.48%)	TCA (2.35%)	CAG (2.28%)	TCA (2.36%)	TGC (2.33%)	GAA (2.33%)	AAT (2.38%)
8	AAT (2.23%)	ATC (2.26%)	TCA (2.22%)	ATC (2.29%)	TCA (2.26%)	AAT (2.25%)	ATC (2.33%)	TTC (2.33%)	GCC (2.34%)
9	GAA (2.22%)	GAA (2.21%)	GCC (2.19%)	AAT (2.24%)	GCC (2.23%)	ATC (2.21%)	AAT (2.19%)	CAG (2.23%)	GCG (2.20%)
10	GCC (2.20%)	AAT (2.20%)	CAA (2.19%)	GGC (2.24%)	AAT (2.21%)	CAA (2.19%)	CAG (2.17%)	GCC (2.20%)	TCA (2.18%)
-10	AGT (0.96%)	AGG (0.98%)	ACT (0.92%)	GTG (0.96%)	AGA (0.96%)	CTT (0.92%)	CTT (1.04%)	CTC (1.04%)	CCT (1.00%)
-9	CTC (0.92%)	AGT (0.93%)	GGG (0.90%)	AGA (0.95%)	CTT (0.94%)	CCC (0.88%)	CTC (1.04%)	CCC (1.00%)	CCC (0.95%)
-8	GGA (0.89%)	GAG (0.88%)	AGA (0.85%)	GGA (0.87%)	ACT (0.93%)	CTC (0.87%)	GAG (0.91%)	CGA (0.92%)	ACT (0.93%)
-7	CCC (0.87%)	CCT (0.87%)	AGG (0.85%)	CTC (0.81%)	CCC (0.92%)	CCT (0.85%)	AGA (0.88%)	ACT (0.91%)	GAG (0.83%)
-6	AGA (0.82%)	CTT (0.84%)	TGT (0.83%)	CCC (0.80%)	CCT (0.89%)	AGG (0.83%)	GGA (0.86%)	CTT (0.86%)	CGA (0.80%)
-5	GAG (0.73%)	CGA (0.84%)	AGT (0.80%)	AGG (0.76%)	GAG (0.88%)	ACT (0.78%)	CCC (0.83%)	AGA (0.85%)	CTT (0.80%)
-4	AGG (0.72%)	AGA (0.72%)	CTT (0.78%)	GAG (0.73%)	CTC (0.85%)	GGG (0.77%)	AGG (0.81%)	CCT (0.84%)	GGA (0.69%)
-3	GGG (0.71%)	GGA (0.71%)	GAG (0.65%)	GGG (0.60%)	GGG (0.78%)	GAG (0.62%)	GGG (0.73%)	GGA (0.74%)	AGA (0.69%)
-2	CTA (0.50%)	TAG (0.55%)	TAG (0.39%)	CTA (0.53%)	TAG (0.55%)	CTA (0.42%)	CTA (0.61%)	CTA (0.69%)	TAG (0.50%)
-1	TAG (0.44%)	CTA (0.50%)	CTA (0.37%)	TAG (0.44%)	CTA (0.51%)	TAG (0.40%)	TAG (0.51%)	TAG (0.64%)	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			Complement			2D		
	Insertion	Deletion	Substitution	Insertion	Deletion	Substitution	Insertion	Deletion	Substitution
1	TTTC (1.04%)	TTTC (1.09%)	AAAA (1.28%)	ATCA (0.88%)	CGGC (1.01%)	CAAA (1.12%)	GGCA (0.86%)	TGGC (0.98%)	GGCA (1.15%)
2	GAAA (0.89%)	TGCC (0.97%)	TTTT (1.26%)	CAGC (0.88%)	TGGC (0.99%)	AAAA (1.07%)	CAAA (0.83%)	CAGC (0.88%)	AAAA (1.10%)
3	TTCA (0.84%)	TTGC (0.91%)	GAAA (1.12%)	CTGC (0.84%)	CAGC (0.98%)	TGAA (0.95%)	GAAA (0.82%)	TTCA (0.80%)	GAAA (1.01%)
4	AAAA (0.84%)	TTCA (0.90%)	GGCA (0.96%)	CAAA (0.84%)	CTGC (0.87%)	GAAA (0.93%)	ATCA (0.82%)	CAAA (0.79%)	GGAA (0.94%)
5	ATCA (0.83%)	TTCC (0.89%)	GCAA (0.92%)	TTGC (0.82%)	TTGC (0.87%)	GGCA (0.91%)	GCCA (0.81%)	CGGC (0.78%)	CAAA (0.90%)
6	TGCC (0.80%)	CAGC (0.88%)	GGAA (0.88%)	TTCA (0.78%)	CAAA (0.86%)	AGCA (0.90%)	AACA (0.80%)	TGCC (0.77%)	TGCA (0.88%)
7	TTGC (0.80%)	TGGC (0.86%)	TGCC (0.88%)	CGGC (0.77%)	TTCC (0.84%)	ATCA (0.89%)	TTTC (0.77%)	CTGC (0.76%)	TTTC (0.87%)
8	AACG (0.78%)	CTGC (0.86%)	TTTT (0.88%)	CCAG (0.77%)	TGCC (0.82%)	GGAA (0.88%)	CGCC (0.76%)	GCCA (0.75%)	CGTT (0.86%)
9	GGCA (0.77%)	GAAA (0.82%)	CAAA (0.87%)	ATGC (0.77%)	ATCA (0.80%)	TAAA (0.87%)	AAAA (0.74%)	ATCA (0.75%)	CGCC (0.84%)
10	CTTC (0.77%)	AAAA (0.79%)	AAAT (0.86%)	TGGC (0.77%)	TTCA (0.77%)	TTTC (0.86%)	TGCA (0.74%)	CGCC (0.74%)	TTTT (0.83%)
-10	AGGG (0.12%)	ACCT (0.13%)	CCCT (0.11%)	CGAG (0.11%)	ACCT (0.11%)	ACCT (0.11%)	CTAT (0.14%)	CTAT (0.16%)	CGGA (0.11%)
-9	ACTA (0.12%)	CGGA (0.12%)	ACTA (0.10%)	AGGG (0.11%)	CTAA (0.11%)	GTGT (0.10%)	ACTA (0.14%)	CGGA (0.15%)	TCTA (0.11%)
-8	CTAA (0.12%)	TAGT (0.12%)	TAGA (0.10%)	GTGT (0.10%)	CTAT (0.11%)	ACTA (0.10%)	TCTA (0.14%)	ACTT (0.14%)	CTTG (0.11%)
-7	TAGT (0.12%)	CCCT (0.11%)	CGAG (0.09%)	TAGA (0.10%)	GTGT (0.11%)	CTAT (0.10%)	TAGT (0.14%)	CTAA (0.14%)	ACTT (0.11%)
-6	GAGG (0.10%)	GGAC (0.11%)	TAGT (0.09%)	GGAC (0.10%)	TAGA (0.11%)	CGAG (0.09%)	GGAC (0.13%)	ACCT (0.13%)	CCCT (0.11%)
-5	GGAC (0.09%)	CTAA (0.10%)	TCTA (0.08%)	GAGG (0.09%)	CCCC (0.11%)	GGAC (0.09%)	CTAA (0.12%)	CCCT (0.11%)	ACTA (0.10%)
-4	TAGA (0.07%)	TAGG (0.08%)	GGAC (0.07%)	CCCT (0.09%)	CCCT (0.08%)	CCCT (0.07%)	TAGA (0.09%)	TAGG (0.10%)	TAGG (0.08%)
-3	CCTA (0.07%)	TAGA (0.06%)	TAGG (0.07%)	CCTA (0.07%)	TAGG (0.08%)	TAGG (0.07%)	CCTA (0.08%)	TAGA (0.10%)	TAGA (0.06%)
-2	TAGG (0.06%)	CCTA (0.06%)	CCTA (0.04%)	TAGG (0.06%)	CCTA (0.06%)	CCTA (0.05%)	TAGG (0.06%)	CCTA (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%)

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 (0.34%)	CAGCA (0.36%)	GAAAA (0.43%)	CAGCA (0.39%)	CAGCA (0.41%)	CAGCA (0.51%)	CAGCA (0.35%)	CTGGC (0.40%)	TGGCA (0.43%)
2	TTATC (0.32%)	CTGGC (0.35%)	CAGCA (0.43%)	CATCA (0.34%)	CTGGC (0.38%)	CGGCA (0.38%)	CGCCA (0.34%)	CAGCA (0.32%)	CGGCA (0.42%)
3	ATTTT (0.32%)	TTGCC (0.35%)	CAAAA (0.34%)	GCTGC (0.31%)	GCGGC (0.37%)	GCAAA (0.35%)	CTGGC (0.32%)	GCGGC (0.30%)	CAGCA (0.41%)
4	CTGGC (0.31%)	TTTGC (0.32%)	TGGCA (0.33%)	CCAGC (0.31%)	GCTGC (0.32%)	CATCA (0.35%)	CGGCA (0.32%)	CGCCA (0.30%)	GAAAA (0.40%)
5	CATCA (0.30%)	GCAGC (0.31%)	TTGCC (0.32%)	CGGCA (0.30%)	CATCA (0.32%)	GAAAA (0.35%)	TGGCA (0.30%)	GCCAG (0.29%)	GCAAA (0.34%)
6	TTGCC (0.29%)	GCTGC (0.31%)	AGAAA (0.32%)	GCGGC (0.30%)	CCAGC (0.31%)	CAGAA (0.34%)	GCAAA (0.29%)	TGGCG (0.29%)	GCGTT (0.33%)
7	GAAAA (0.29%)	GCCAG (0.30%)	CGTTT (0.31%)	CTGGC (0.28%)	AATCA (0.31%)	ATAAA (0.34%)	GCCAG (0.28%)	CATCA (0.29%)	CGCCA (0.30%)
8	CGCCA (0.29%)	TTTCA (0.30%)	CGGCA (0.31%)	AATCA (0.27%)	TTGCC (0.30%)	AATCA (0.33%)	TGGCG (0.28%)	CCAGC (0.28%)	CAAAA (0.30%)
9	CGTTT (0.28%)	TTTTCC (0.30%)	ATTTT (0.31%)	AACGC (0.27%)	TTTTGC (0.29%)	ACAAA (0.32%)	CAACA (0.26%)	GCAGC (0.27%)	AGAAA (0.30%)
10	CAAAA (0.27%)	CCAGC (0.29%)	CGTTC (0.30%)	ATAAA (0.27%)	GCAGC (0.29%)	ACGCA (0.32%)	CCAGC (0.26%)	GCAAA (0.26%)	ATTTT (0.29%)
-10	CCCTA (0.01%)	CCCTA (0.01%)	CTTAG (0.01%)	GGACC (0.01%)	CCCCC (0.01%)	CCCTA (0.01%)	TAGGA (0.01%)	TCCTA (0.01%)	TTAGA (0.01%)
-9	GGACC (0.01%)	GGACC (0.01%)	ACCTA (0.01%)	CCCTA (0.00%)	GCTAG (0.01%)	CCCCT (0.01%)	GGACC (0.01%)	TAGGA (0.01%)	CCCTA (0.01%)
-8	CTAGT (0.00%)	GCTAG (0.00%)	GCTAG (0.00%)	CTAGT (0.00%)	CCCTA (0.01%)	CTAGC (0.01%)	CCTAG (0.01%)	GCTAG (0.01%)	CTAGC (0.00%)
-7	GCTAG (0.00%)	ACTAG (0.00%)	ACTAG (0.00%)	CTAGC (0.00%)	CTAGC (0.01%)	GCTAG (0.00%)	CTAGA (0.01%)	CTAGC (0.01%)	ACTAG (0.00%)
-6	ACTAG (0.00%)	CTAGC (0.00%)	CTAGT (0.00%)	CTAGA (0.00%)	ACTAG (0.00%)	CTAGA (0.00%)	GCTAG (0.00%)	ACTAG (0.00%)	GCTAG (0.00%)
-5	CTAGC (0.00%)	CTAGT (0.00%)	CTAGG (0.00%)	ACTAG (0.00%)	CTAGT (0.00%)	CCTAG (0.00%)	ACTAG (0.00%)	CTAGT (0.00%)	CCTAG (0.00%)
-4	CTAGG (0.00%)	CCTAG (0.00%)	CTAGC (0.00%)	GCTAG (0.00%)	CTAGA (0.00%)	CTAGT (0.00%)	CTAGT (0.00%)	CTAGG (0.00%)	CTAGT (0.00%)
-3	CCTAG (0.00%)	CTAGG (0.00%)	CTAGA (0.00%)	CTAGG (0.00%)	CTAGG (0.00%)	CTAGG (0.00%)	TCTAG (0.00%)	CTAGA (0.00%)	CTAGG (0.00%)
-2	TCTAG (0.00%)	CTAGA (0.00%)	CCTAG (0.00%)	CCTAG (0.00%)	CCTAG (0.00%)	ACTAG (0.00%)	CTAGC (0.00%)	TCTAG (0.00%)	CTAGA (0.00%)
-1	CTAGA (0.00%)	TCTAG (0.00%)	TCTAG (0.00%)	TCTAG (0.00%)	TCTAG (0.00%)	TCTAG (0.00%)	CTAGG (0.00%)	CCTAG (0.00%)	TCTAG (0.00%)

Most common

Least common

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