

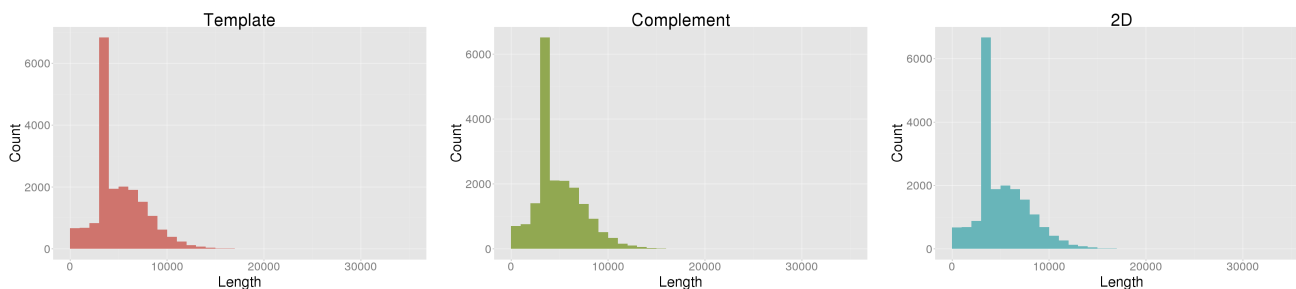
# NanoOK report for ZF-screens\_MARC\_phase\_1a\_e\_coli\_run2

## Pass and fail counts

Type	Pass	Fail
Template	19024	0
Complement	19024	0
2D	19024	0

## Read lengths

Type	NumReads	TotalBases	Mean	Longest	Shortest	N50	N50Count	N90	N90Count
Template	19024	97090096	5103.56	33430	218	6103	5850	3453	14979
Complement	19024	92023023	4837.21	30454	229	5816	5810	3166	14880
2D	19024	98370910	5170.88	34502	204	6211	5821	3473	14940



## Template alignments

Number of reads	19024
Number of reads with alignments	18860 (99.14%)
Number of reads without alignments	164 (0.86%)

ID	Size	Number of Reads	% of Reads	Mean read length	Aligned bases	Mean coverage	Longest Perf Kmer
Control sequence	3560	6273	32.97	3324.70	21944683	6164.24	68
Escherichia coli	4641652	12587	66.16	6043.87	81133277	17.48	89

## Complement alignments

Number of reads	19024
Number of reads with alignments	18838 (99.02%)
Number of reads without alignments	186 (0.98%)

ID	Size	Number of Reads	% of Reads	Mean read length	Aligned bases	Mean coverage	Longest Perf Kmer
Control sequence	3560	6263	32.92	3100.14	19584977	5501.40	61
Escherichia coli	4641652	12575	66.10	5761.27	78257629	16.86	65

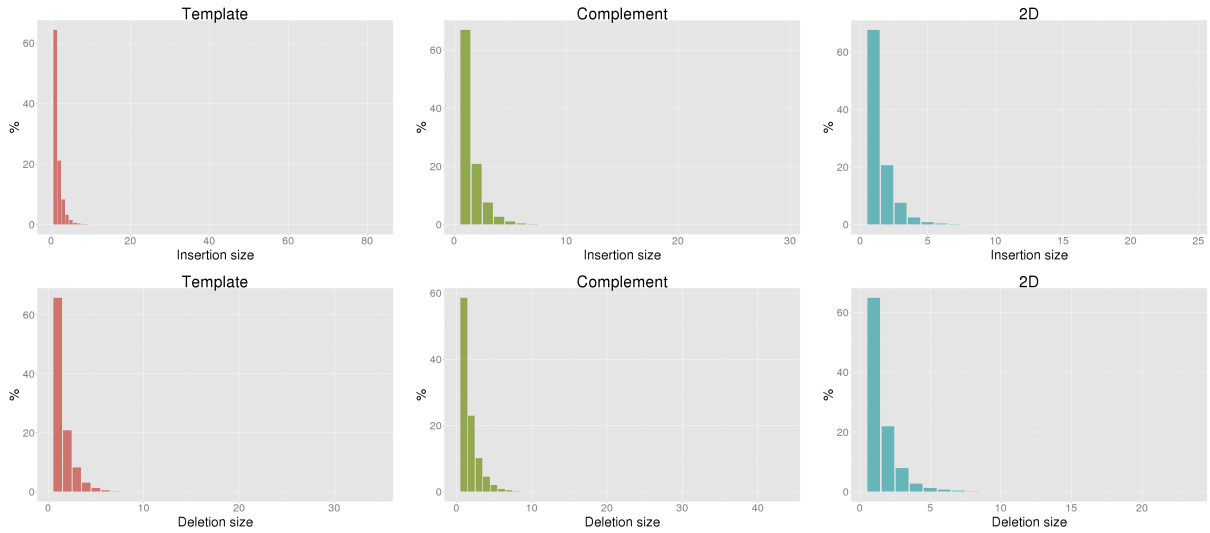
## 2D alignments

Number of reads	19024
Number of reads with alignments	19020 (99.98%)
Number of reads without alignments	4 (0.02%)

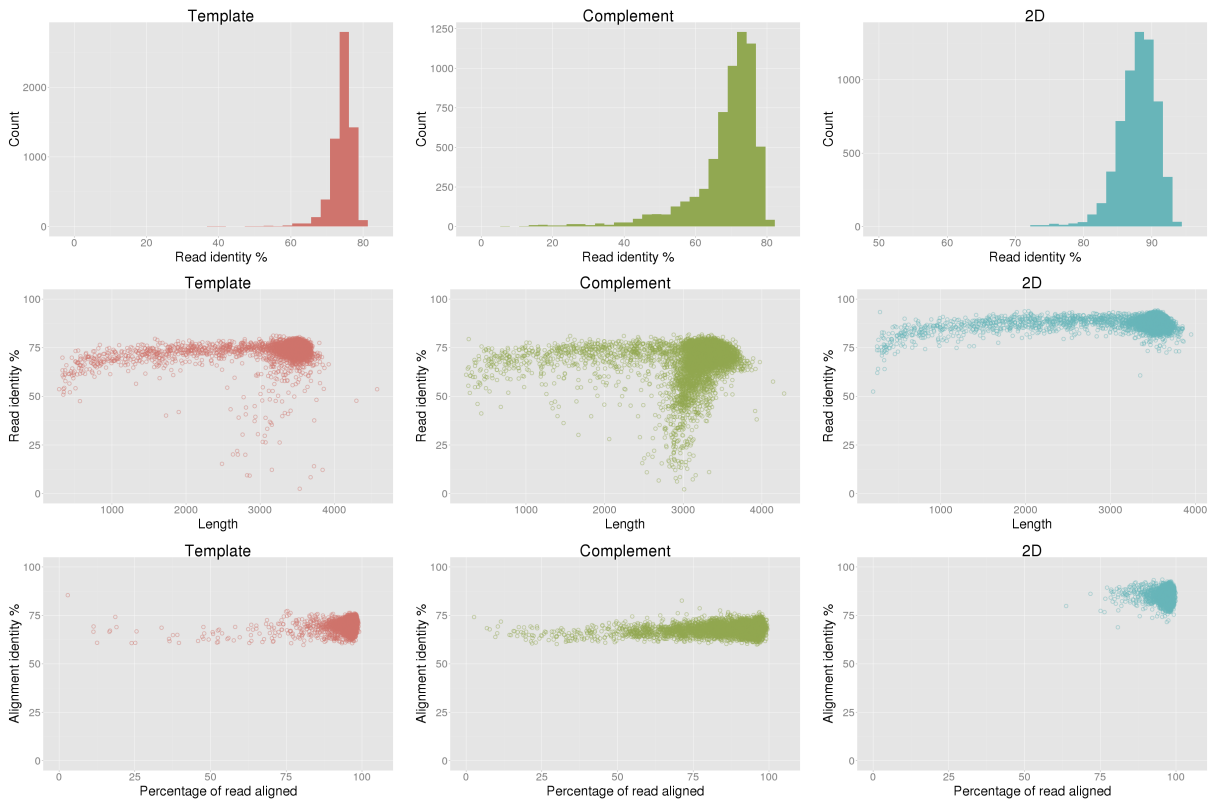
ID	Size	Number of Reads	% of Reads	Mean read length	Aligned bases	Mean coverage	Longest Perf Kmer
Control sequence	3560	6328	33.26	3313.77	21639301	6078.46	203
Escherichia coli	4641652	12692	66.72	6096.40	80242976	17.29	241

## Control sequence error analysis

	Template	Complement	2D
Overall base identity (excluding indels)	74.05%	68.67%	88.01%
Aligned base identity (excluding indels)	82.16%	81.75%	93.62%
Identical bases per 100 aligned bases (including indels)	70.37%	68.08%	85.29%
Inserted bases per 100 aligned bases (including indels)	5.54%	4.37%	3.40%
Deleted bases per 100 aligned bases (including indels)	8.81%	12.35%	5.51%
Substitutions per 100 aligned bases (including indels)	15.28%	15.20%	5.81%
Mean insertion size	1.63	1.54	1.51
Mean deletion size	1.57	1.76	1.59

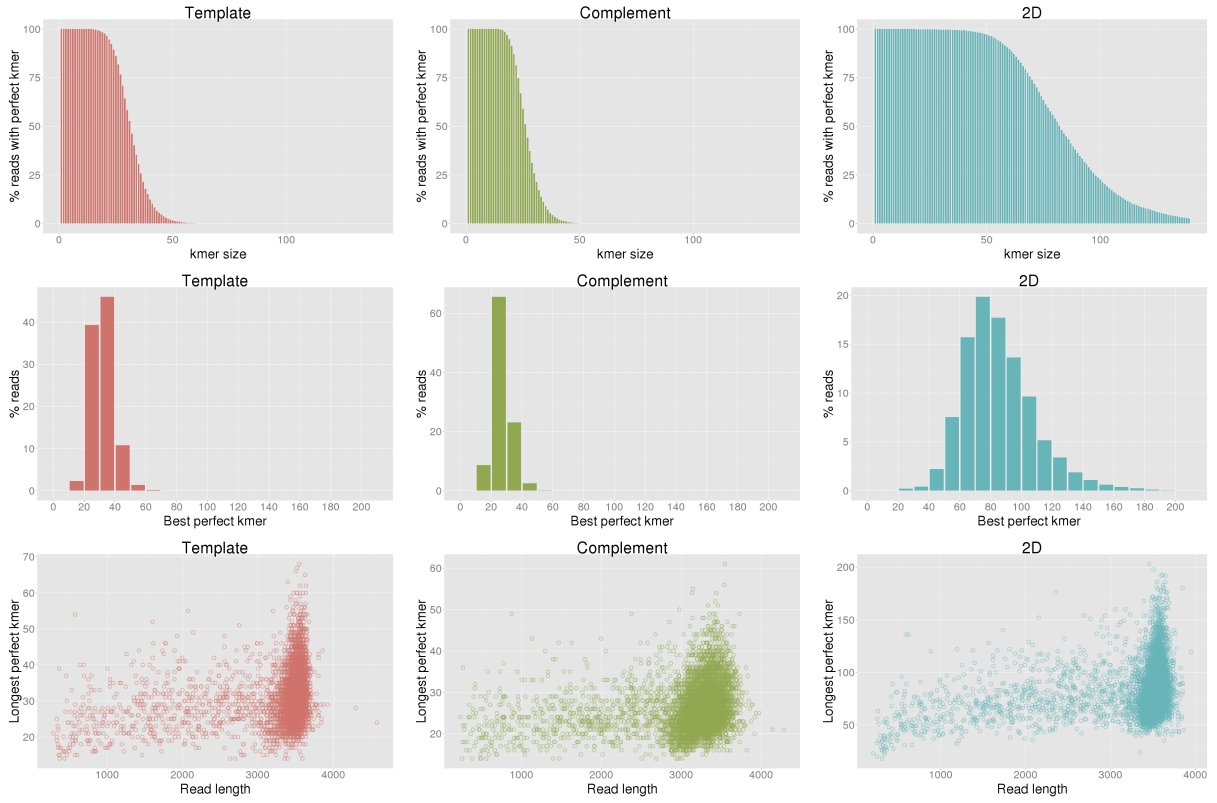


## Control sequence read identity

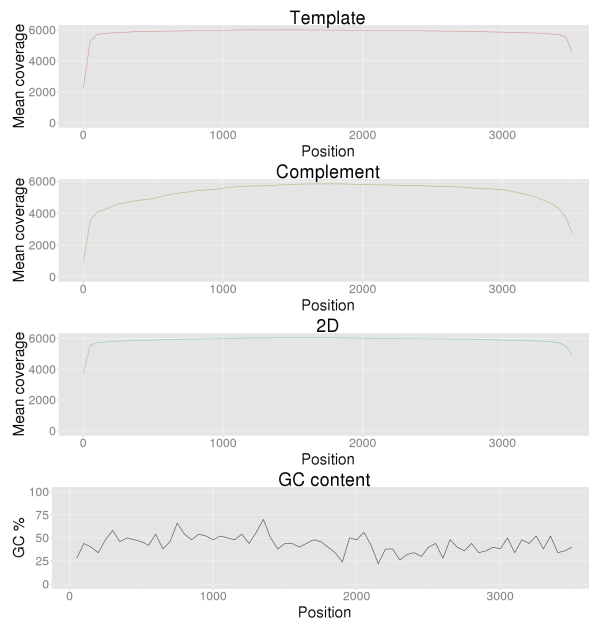




## Control sequence perfect kmers



## Control sequence coverage



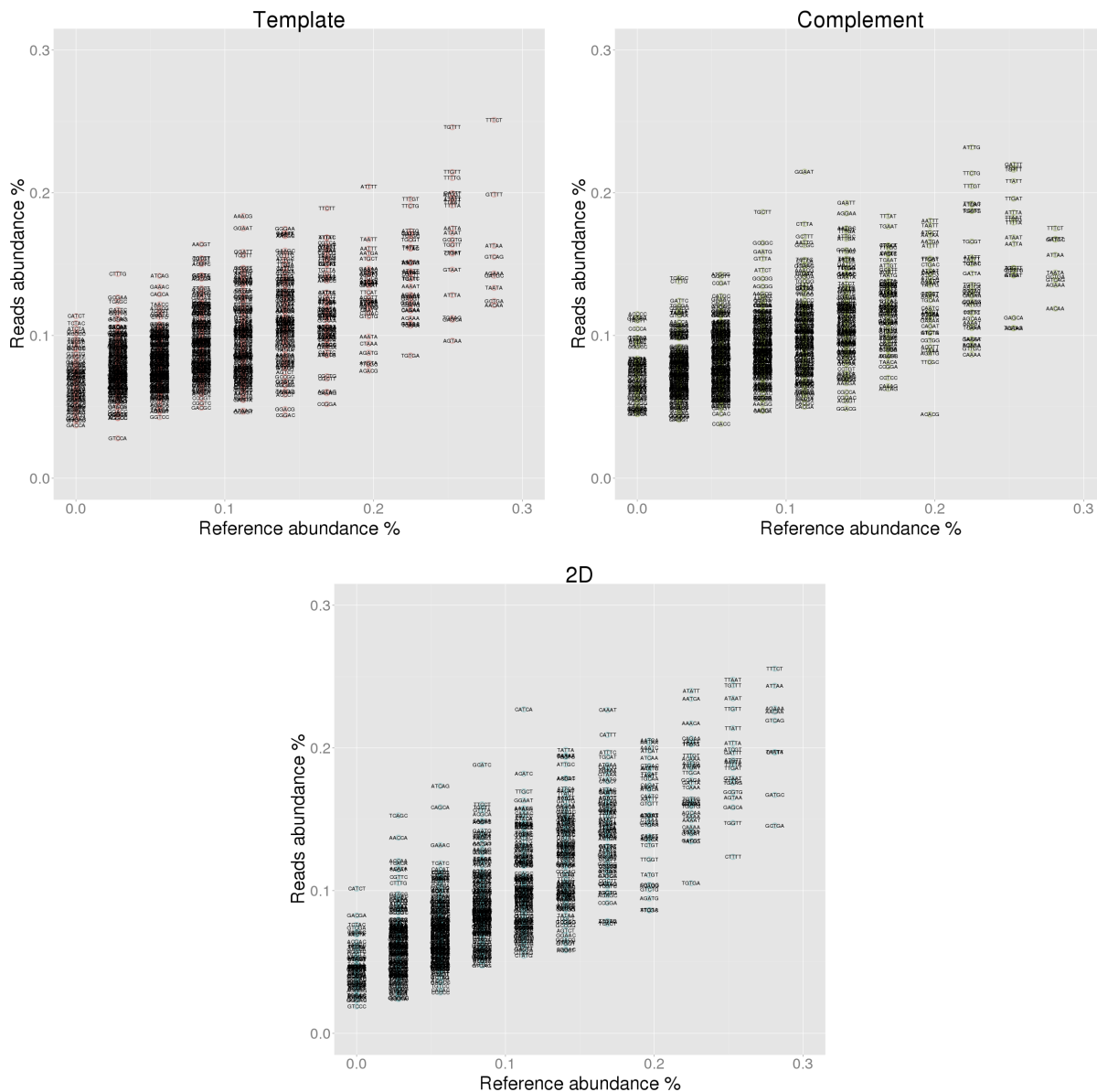
# Control sequence 5-mer analysis

## Under-represented 5-mers

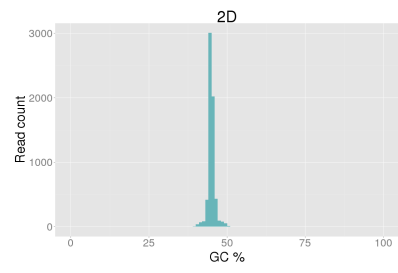
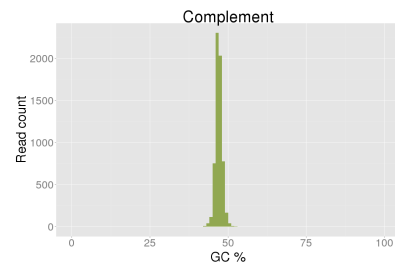
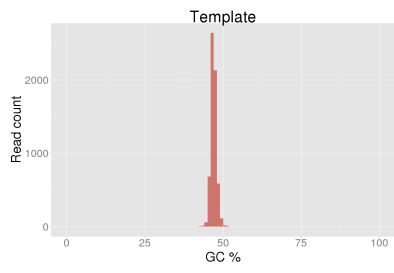
Rank	Template				Complement				2D			
	kmer	Ref %	Read %	Diff %	kmer	Ref %	Read %	Diff %	kmer	Ref %	Read %	Diff %
1	TTTTT	0.759	0.162	-0.597	TTTTT	0.759	0.093	-0.666	TTTTT	0.759	0.062	-0.697
2	AAAAA	0.478	0.119	-0.358	AAAAA	0.478	0.060	-0.418	AAAAA	0.478	0.077	-0.400
3	TGATG	0.393	0.151	-0.243	AAAAC	0.337	0.124	-0.213	TGATG	0.393	0.195	-0.198
4	AAAAC	0.337	0.135	-0.202	GATGT	0.309	0.124	-0.185	CTGAT	0.309	0.155	-0.154
5	GATGT	0.309	0.112	-0.197	TGATG	0.393	0.211	-0.182	GATGT	0.309	0.156	-0.153
6	CTGAT	0.309	0.130	-0.179	GCAAT	0.309	0.142	-0.167	GCTGA	0.281	0.146	-0.135
7	AACAA	0.281	0.121	-0.160	AACAA	0.281	0.119	-0.162	AAAAC	0.337	0.204	-0.133
8	GCTGA	0.281	0.124	-0.157	TTATC	0.309	0.154	-0.155	CTTTT	0.253	0.124	-0.129
9	AGTAA	0.253	0.096	-0.156	ACACG	0.197	0.045	-0.152	TGTGA	0.225	0.105	-0.120
10	GCAAT	0.309	0.154	-0.155	AGTAA	0.253	0.105	-0.148	TTATC	0.309	0.191	-0.118

## Over-represented 5-mers

Rank	Template				Complement				2D			
	kmer	Ref %	Read %	Diff %	kmer	Ref %	Read %	Diff %	kmer	Ref %	Read %	Diff %
1	CTTTG	0.028	0.143	0.115	ACCCC	0.000	0.115	0.115	TCAGC	0.028	0.153	0.125
2	CATCT	0.000	0.114	0.114	TATAC	0.000	0.113	0.113	ATCAG	0.056	0.173	0.117
3	TCTAC	0.000	0.109	0.109	TCAGC	0.028	0.140	0.112	CATCA	0.112	0.227	0.115
4	ATCTA	0.000	0.105	0.105	GAGGA	0.000	0.112	0.112	AACCA	0.028	0.137	0.109
5	CGAGA	0.000	0.102	0.102	TACTT	0.000	0.111	0.111	GCATC	0.084	0.188	0.104
6	ACCCC	0.000	0.101	0.101	CTTTG	0.028	0.138	0.110	CAGCA	0.056	0.159	0.102
7	GCGAA	0.028	0.127	0.099	CCCCA	0.000	0.105	0.105	CATCT	0.000	0.101	0.101
8	TCTTA	0.000	0.097	0.097	GGAAT	0.112	0.215	0.102	ACCAA	0.028	0.121	0.093
9	CCCCA	0.000	0.096	0.096	TGCTT	0.084	0.187	0.102	TCACA	0.028	0.119	0.091
10	TCAGC	0.028	0.124	0.096	TCTAC	0.000	0.098	0.098	ACATA	0.028	0.115	0.087

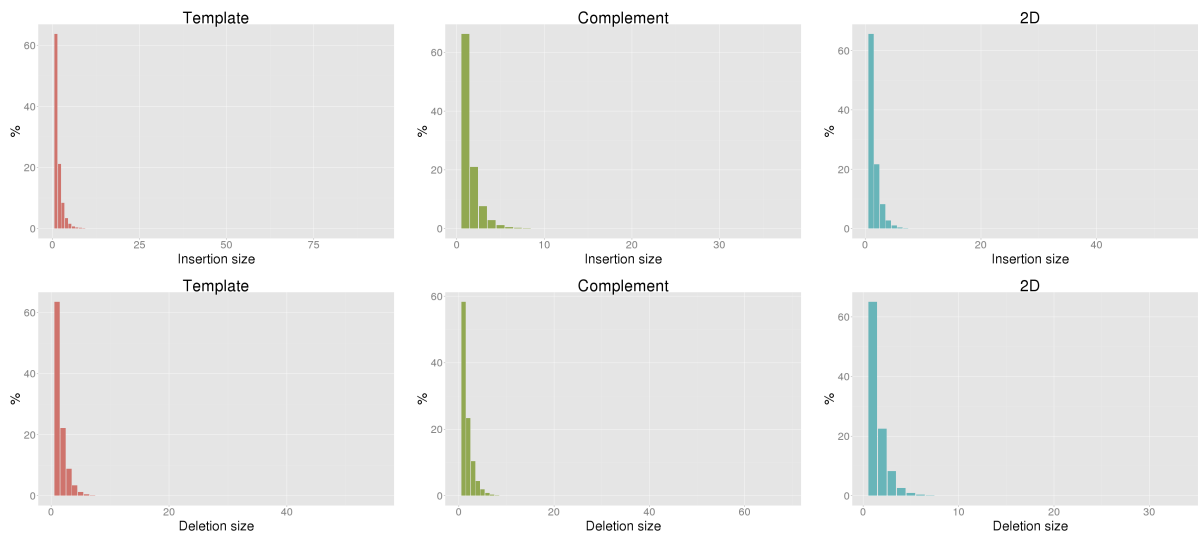


## Control sequence GC content

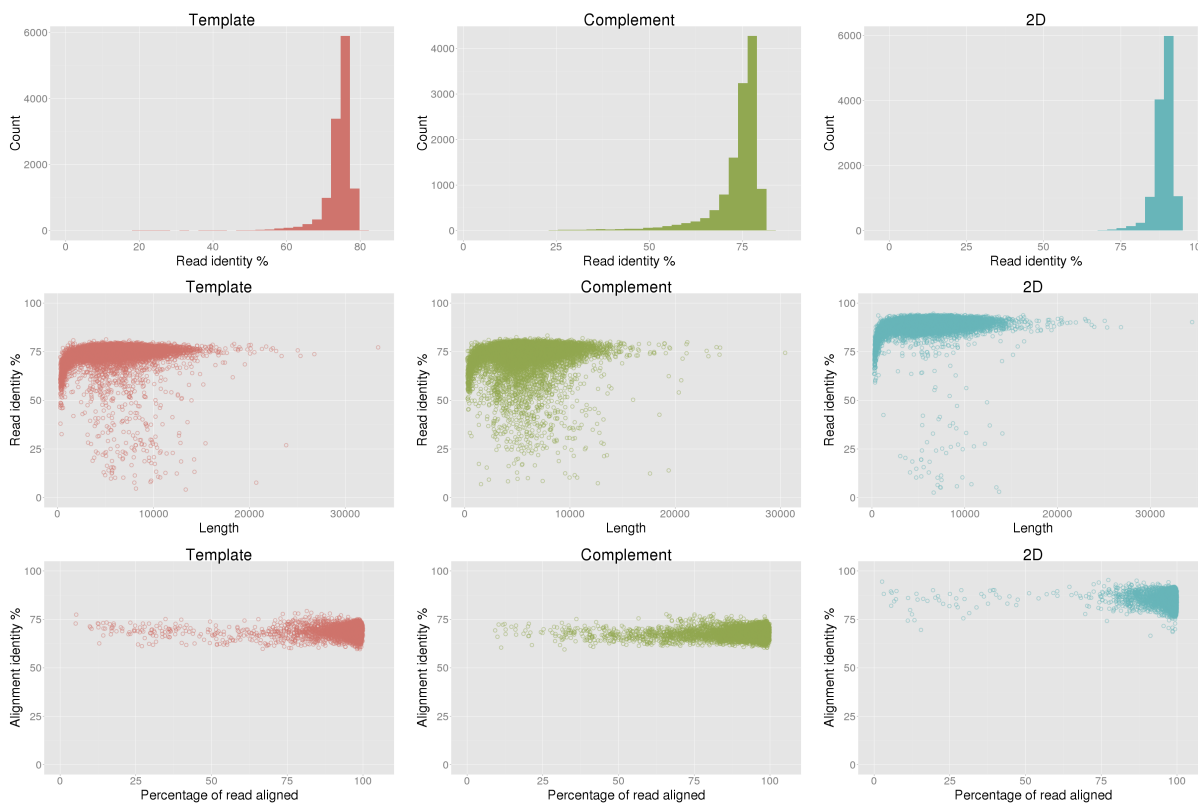


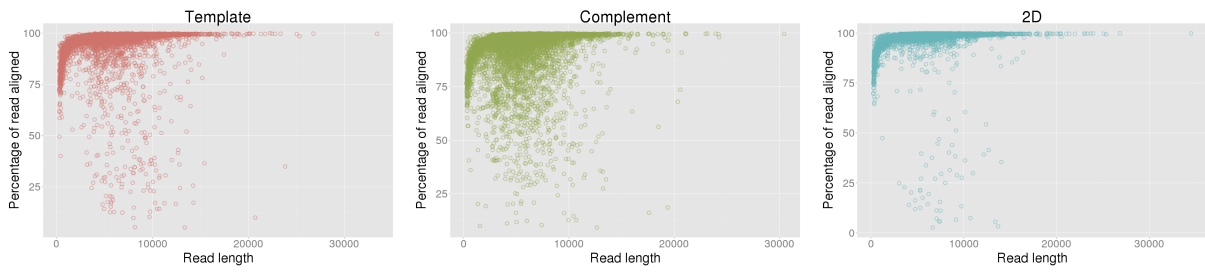
## Escherichia coli error analysis

	Template	Complement	2D
Overall base identity (excluding indels)	73.97%	73.65%	88.93%
Aligned base identity (excluding indels)	81.52%	82.00%	93.87%
Identical bases per 100 aligned bases (including indels)	69.35%	68.18%	85.75%
Inserted bases per 100 aligned bases (including indels)	5.77%	4.60%	3.55%
Deleted bases per 100 aligned bases (including indels)	9.16%	12.25%	5.10%
Substitutions per 100 aligned bases (including indels)	15.72%	14.97%	5.60%
Mean insertion size	1.66	1.56	1.55
Mean deletion size	1.60	1.75	1.54

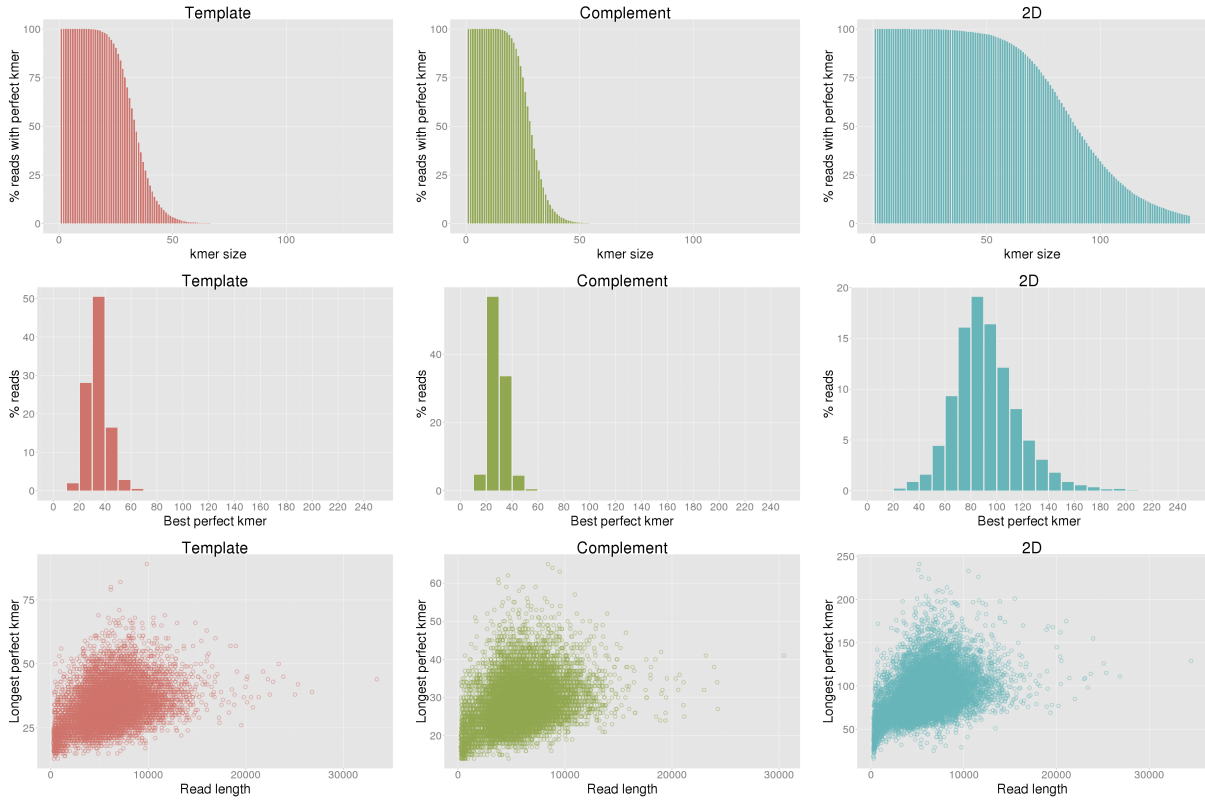


## Escherichia coli read identity

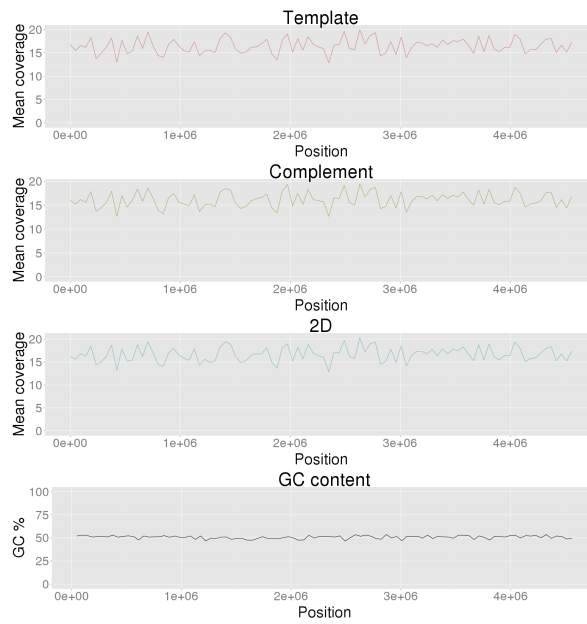




## Escherichia coli perfect kmers



## Escherichia coli coverage



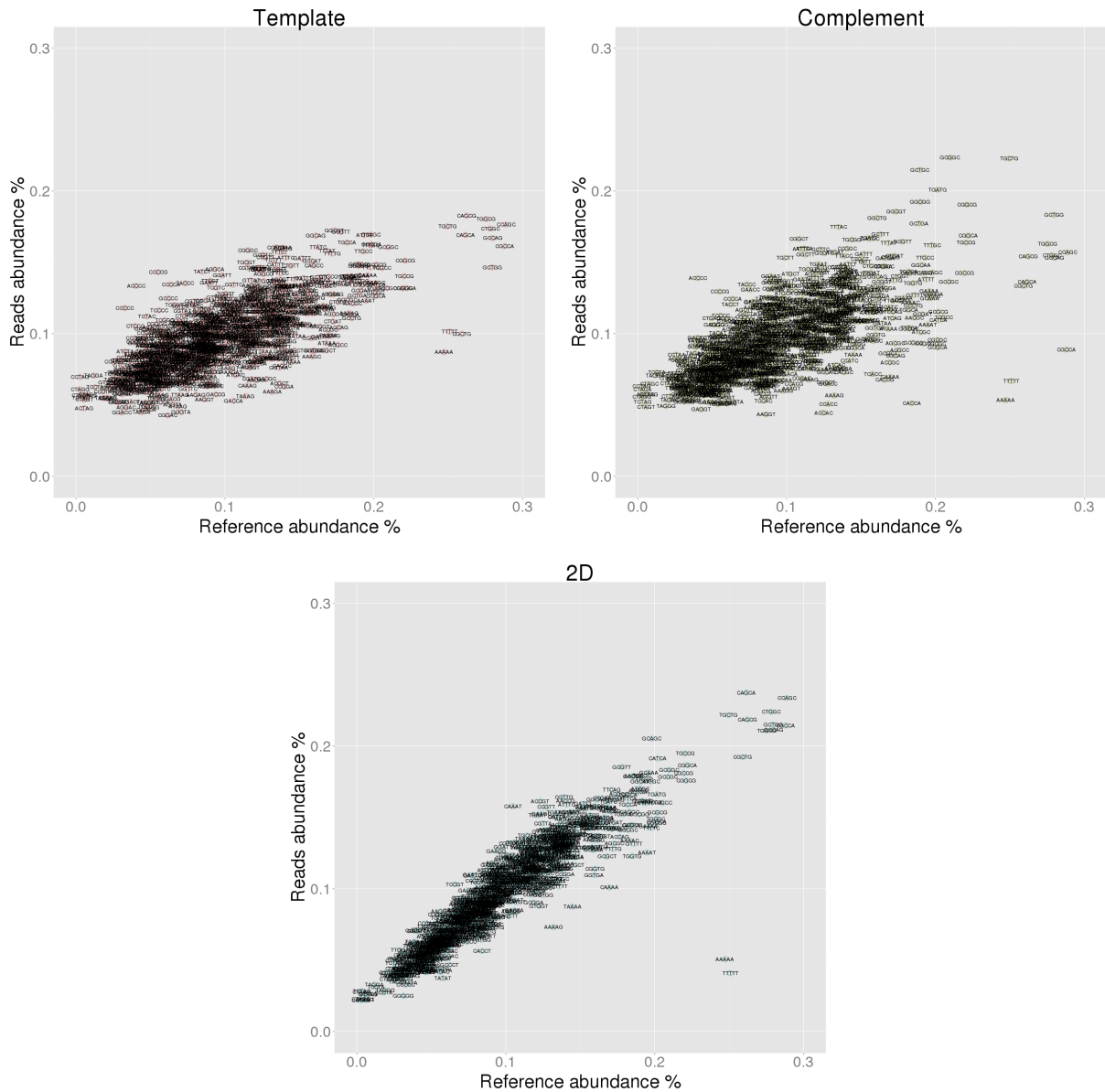
# Escherichia coli 5-mer analysis

## Under-represented 5-mers

Rank	Template				Complement				2D			
	kmer	Ref %	Read %	Diff %	kmer	Ref %	Read %	Diff %	kmer	Ref %	Read %	Diff %
1	AAAAA	0.247	0.087	-0.160	CGCCA	0.288	0.089	-0.199	TTTTT	0.251	0.041	-0.210
2	CGCTG	0.259	0.100	-0.159	AAAAA	0.247	0.054	-0.194	AAAAA	0.247	0.051	-0.196
3	TTTTT	0.251	0.102	-0.149	TTTTT	0.251	0.067	-0.184	CGCCA	0.288	0.214	-0.074
4	GCTGG	0.279	0.147	-0.133	CACCA	0.184	0.051	-0.133	AAAAT	0.195	0.126	-0.069
5	CGCCA	0.288	0.161	-0.127	CCAGC	0.289	0.157	-0.132	CAAAA	0.169	0.101	-0.068
6	GCCAG	0.280	0.167	-0.113	GCCAG	0.280	0.153	-0.127	GCCAG	0.280	0.211	-0.068
7	CCAGC	0.289	0.176	-0.112	CGCTG	0.259	0.134	-0.126	CGCTG	0.259	0.192	-0.067
8	CTGGC	0.278	0.174	-0.105	CAGCA	0.261	0.136	-0.125	GCTGG	0.279	0.215	-0.064
9	TGGCG	0.275	0.180	-0.095	CTGGC	0.278	0.155	-0.123	TGGCG	0.275	0.211	-0.064
10	CAGCA	0.261	0.169	-0.092	TGGCG	0.275	0.163	-0.112	TGGTG	0.185	0.123	-0.062

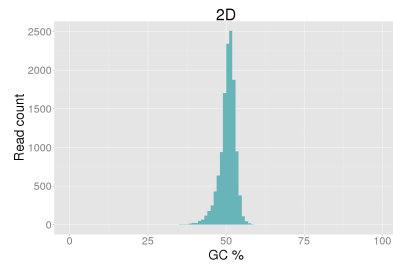
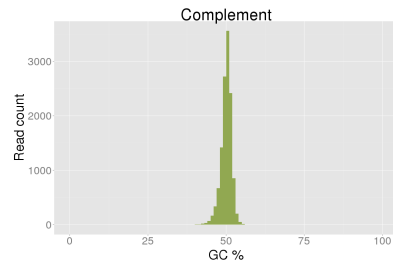
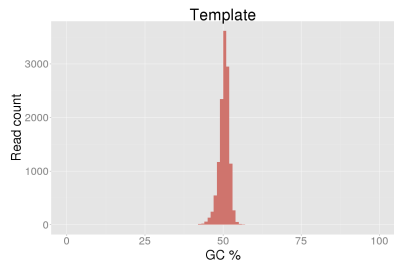
## Over-represented 5-mers

Rank	Template				Complement				2D			
	kmer	Ref %	Read %	Diff %	kmer	Ref %	Read %	Diff %	kmer	Ref %	Read %	Diff %
1	ACCCC	0.040	0.134	0.093	ACCCC	0.040	0.139	0.099	CAAAT	0.105	0.158	0.053
2	CCCCG	0.055	0.143	0.088	CCCCG	0.055	0.129	0.074	ACCGT	0.123	0.161	0.038
3	CCCCC	0.033	0.118	0.085	TACCC	0.073	0.135	0.061	TCCGT	0.066	0.103	0.037
4	CCCCA	0.064	0.135	0.071	CTGAG	0.050	0.111	0.061	GAAGG	0.094	0.126	0.033
5	CCTAG	0.003	0.070	0.067	CCCCA	0.064	0.124	0.061	GAATC	0.077	0.110	0.032
6	CTCCC	0.040	0.105	0.066	CCTAG	0.003	0.063	0.060	GATTC	0.078	0.109	0.032
7	TCTAC	0.048	0.112	0.064	TCCTA	0.013	0.073	0.060	GGGGT	0.039	0.071	0.031
8	GCCCC	0.062	0.125	0.063	CCTAA	0.026	0.085	0.059	GGATT	0.098	0.129	0.031
9	TACCC	0.073	0.135	0.062	TAGGA	0.012	0.071	0.059	CCGTT	0.127	0.157	0.031
10	TCCCC	0.056	0.116	0.061	CGGCT	0.108	0.166	0.058	TGAAT	0.121	0.152	0.030

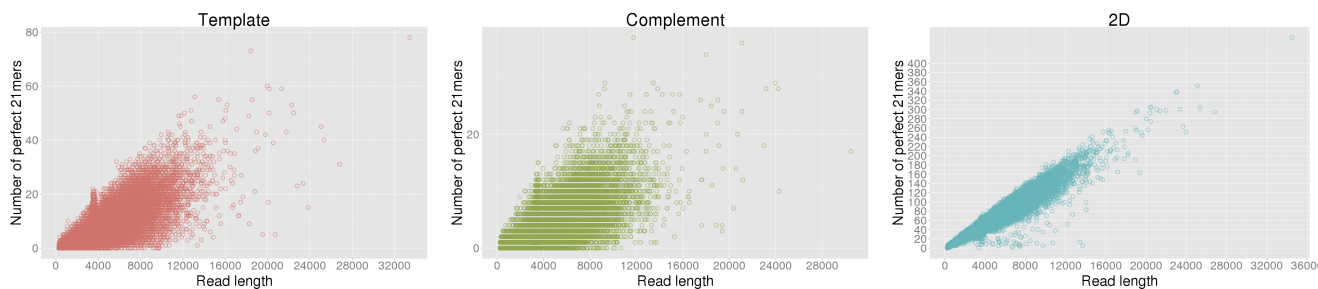




# Escherichia coli GC content



## 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	9.13	9.53	4.80	0.00	9.34	9.13	5.08	0.00	8.72	8.84	4.28
C	8.17	0.00	8.86	9.62	8.98	0.00	8.37	9.19	8.97	0.00	10.55	8.80
G	9.10	8.89	0.00	7.83	8.62	8.63	0.00	8.66	8.72	10.73	0.00	8.44
T	5.20	10.01	8.86	0.00	5.41	9.35	9.24	0.00	4.37	9.03	8.56	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 (3.20%)	TTC (3.66%)	AAA (4.42%)	TGC (2.87%)	TGC (3.01%)	AAA (4.24%)	GCA (3.09%)	TGC (2.75%)	AAA (4.29%)	Most common
2	AAA (2.96%)	TGC (3.11%)	TTC (3.64%)	AAA (2.78%)	AAA (2.92%)	GCA (3.54%)	AAA (3.01%)	AAA (2.65%)	GCA (3.68%)	
3	GCA (2.79%)	GCA (2.84%)	GCA (3.24%)	TTC (2.76%)	GGC (2.75%)	GAA (3.45%)	TTC (2.79%)	TCA (2.62%)	GAA (3.47%)	
4	TGC (2.69%)	AAA (2.80%)	GAA (3.11%)	GCA (2.69%)	TTC (2.67%)	TTC (3.10%)	TCA (2.70%)	TTC (2.45%)	TTT (2.97%)	
5	ATC (2.61%)	TCA (2.44%)	TTT (2.66%)	GAA (2.42%)	GCA (2.50%)	TTT (2.65%)	GAA (2.55%)	GCA (2.44%)	TTC (2.89%)	
6	TCA (2.58%)	ATC (2.28%)	AAT (2.51%)	TCA (2.39%)	GAA (2.42%)	TCA (2.51%)	TGC (2.45%)	GCG (2.36%)	AAT (2.65%)	
7	TTT (2.39%)	GCC (2.28%)	TGC (2.40%)	ATC (2.37%)	TCA (2.32%)	TGC (2.49%)	ATC (2.40%)	GGC (2.33%)	TCA (2.46%)	
8	GAA (2.33%)	GAA (2.26%)	TCA (2.38%)	CAG (2.34%)	AAT (2.29%)	ATC (2.29%)	AAT (2.34%)	ATC (2.27%)	GTT (2.33%)	
9	AAT (2.21%)	GGC (2.23%)	CAA (2.37%)	GGC (2.29%)	CAG (2.21%)	AAT (2.23%)	CGC (2.16%)	GAA (2.27%)	GCC (2.29%)	
10	GCC (2.12%)	AAT (2.20%)	GCC (2.15%)	TTT (2.23%)	ATC (2.15%)	CAA (2.18%)	CAG (2.09%)	CAG (2.18%)	ATC (2.22%)	
										Least common
-10	CGA (0.96%)	AGG (0.96%)	GGT (0.89%)	AGA (1.01%)	CTC (0.94%)	GAC (0.94%)	CTC (1.05%)	GAG (1.05%)	CCT (0.88%)	
-9	AGT (0.95%)	GTA (0.93%)	GGG (0.87%)	AGT (0.98%)	AGG (0.94%)	AGT (0.89%)	CTT (1.00%)	GTA (0.95%)	GTA (0.87%)	
-8	CCC (0.92%)	AGT (0.90%)	AGA (0.86%)	CTC (0.91%)	GGA (0.93%)	CTT (0.87%)	GAG (0.91%)	CCT (0.94%)	ACT (0.85%)	
-7	AGA (0.85%)	GAG (0.83%)	TGT (0.83%)	CCC (0.85%)	CGA (0.92%)	CCT (0.81%)	AGA (0.83%)	ACT (0.88%)	GAG (0.76%)	
-6	GGA (0.84%)	CTT (0.78%)	AGG (0.82%)	GAG (0.84%)	ACT (0.92%)	AGG (0.79%)	CCC (0.82%)	CGA (0.85%)	CTT (0.75%)	
-5	GAG (0.81%)	CGA (0.72%)	AGT (0.81%)	GGA (0.84%)	CCT (0.89%)	GGG (0.74%)	GGA (0.78%)	AGA (0.81%)	CGA (0.66%)	
-4	GGG (0.70%)	AGA (0.68%)	CTT (0.73%)	AGG (0.71%)	GAG (0.87%)	ACT (0.73%)	AGG (0.78%)	CTT (0.81%)	AGA (0.54%)	
-3	AGG (0.68%)	GGA (0.65%)	GAG (0.69%)	CTA (0.64%)	GGG (0.74%)	GAG (0.64%)	GGG (0.70%)	GGA (0.75%)	TAG (0.52%)	
-2	CTA (0.54%)	TAG (0.60%)	TAG (0.42%)	GGG (0.57%)	TAG (0.59%)	CTA (0.48%)	CTA (0.62%)	CTA (0.69%)	GGA (0.52%)	
-1	TAG (0.46%)	CTA (0.54%)	CTA (0.38%)	TAG (0.51%)	CTA (0.52%)	TAG (0.41%)	TAG (0.56%)	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 (0.97%)	TTTC (1.22%)	AAAA (1.60%)	CTGC (0.92%)	TGGC (1.01%)	CAAA (1.18%)	CAAA (0.94%)	ATCA (0.91%)	AAAA (1.29%)
2	GAAA (0.97%)	TTCA (0.90%)	TTTT (1.22%)	ATCA (0.89%)	TTGC (0.96%)	AAAA (1.18%)	ATCA (0.90%)	TTCA (0.84%)	GGCA (1.09%)
3	AAAA (0.93%)	TTGC (0.88%)	GAAA (1.21%)	CAGC (0.87%)	CGGC (0.96%)	TGAA (1.05%)	TGAA (0.81%)	TGGC (0.83%)	GAAA (1.06%)
4	ATCA (0.89%)	TGCC (0.87%)	GCAA (0.98%)	CAAA (0.83%)	CAGC (0.95%)	GAAA (0.99%)	GGCA (0.79%)	ATGC (0.81%)	TGAA (1.02%)
5	TTTT (0.87%)	CTGC (0.86%)	TTTT (0.96%)	TTGC (0.83%)	CTGC (0.93%)	AGCA (0.98%)	TTCA (0.78%)	GGAA (0.81%)	TTTT (0.99%)
6	TTCA (0.86%)	GTTT (0.85%)	TGAA (0.90%)	TGGC (0.82%)	CAAA (0.92%)	AGAA (0.98%)	GAAA (0.77%)	CAAA (0.81%)	GGAA (0.96%)
7	TTGC (0.81%)	TGGC (0.84%)	GTTT (0.88%)	CGGC (0.75%)	ATCA (0.82%)	ATCA (0.94%)	AACA (0.77%)	CAGC (0.78%)	TGCA (0.96%)
8	TGTC (0.78%)	AAAA (0.83%)	GGCA (0.88%)	AAAA (0.75%)	ATGC (0.79%)	TGCA (0.87%)	CGCA (0.77%)	AGCA (0.77%)	CAAA (0.94%)
9	CTGC (0.76%)	GAAA (0.83%)	TGCA (0.85%)	ATGC (0.73%)	TTCA (0.76%)	TAAA (0.87%)	TGCA (0.77%)	TTGC (0.77%)	ATCA (0.88%)
10	TTCT (0.76%)	ATGC (0.82%)	AACG (0.85%)	CCAG (0.73%)	AGCA (0.75%)	TTTT (0.87%)	GCCA (0.73%)	ATCG (0.73%)	TTTT (0.88%)
-10	GAGG (0.13%)	TAGT (0.12%)	TAGT (0.11%)	TAGA (0.12%)	CTAT (0.12%)	GGGT (0.11%)	CGAG (0.14%)	TAGG (0.14%)	ACTA (0.11%)
-9	TAGT (0.13%)	GGAC (0.12%)	CTAT (0.11%)	GGAC (0.11%)	TAGA (0.12%)	ACCT (0.11%)	CTTG (0.14%)	ACCT (0.14%)	GAGA (0.10%)
-8	TCTA (0.12%)	CTAT (0.11%)	TAGA (0.11%)	GGGG (0.11%)	CCCT (0.12%)	ACTA (0.10%)	GAGG (0.14%)	CTAT (0.13%)	TCTA (0.10%)
-7	AGGG (0.12%)	CTAA (0.11%)	ACTA (0.10%)	AGGG (0.11%)	ACTA (0.12%)	GGAC (0.10%)	GGGA (0.14%)	CTAA (0.13%)	CGGA (0.10%)
-6	TTAG (0.12%)	TCTA (0.11%)	CGAG (0.10%)	CGAG (0.11%)	CCCC (0.11%)	CGAG (0.09%)	CTAT (0.13%)	CCCC (0.13%)	GGGA (0.10%)
-5	GGAC (0.11%)	CGGA (0.11%)	GGAC (0.09%)	GAGG (0.11%)	CGAG (0.11%)	CTAT (0.08%)	TCTA (0.12%)	GAGA (0.13%)	CTAT (0.08%)
-4	TAGA (0.08%)	TAGG (0.11%)	TCTA (0.09%)	CCCT (0.11%)	ACCT (0.10%)	CCCT (0.07%)	TAGA (0.09%)	CCCT (0.12%)	TAGG (0.07%)
-3	CCTA (0.07%)	CCTA (0.08%)	TAGG (0.06%)	CCTA (0.10%)	TAGG (0.10%)	CCTA (0.06%)	CCTA (0.09%)	CCTA (0.12%)	TAGA (0.05%)
-2	TAGG (0.05%)	TAGA (0.05%)	CCTA (0.04%)	TAGG (0.06%)	CCTA (0.07%)	TAGG (0.06%)	TAGG (0.06%)	TAGA (0.09%)	CCTA (0.05%)
-1	CTAG (0.01%)	CTAG (0.01%)	CTAG (0.01%)	CTAG (0.02%)	CTAG (0.02%)	CTAG (0.01%)	CTAG (0.03%)	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	TTATC (0.35%)	GATGC (0.37%)	GAAAA (0.50%)	CAGCA (0.36%)	CTGGC (0.40%)	CAGCA (0.48%)	CAGCA (0.32%)	TATCG (0.44%)	GAAAA (0.40%)
2	CGTTT (0.32%)	CAGCA (0.37%)	CAAAA (0.40%)	GCTGC (0.32%)	GATGC (0.37%)	ACAAA (0.39%)	TCAAA (0.32%)	GATGC (0.41%)	CAGCA (0.39%)
3	CTGGC (0.31%)	CTGGC (0.37%)	AGAAA (0.39%)	TTATC (0.30%)	CAGCA (0.36%)	AAGAA (0.39%)	CGCCA (0.31%)	CTGGC (0.35%)	CGGCA (0.38%)
4	CAAAA (0.30%)	ATTTC (0.36%)	TAAAA (0.37%)	GATGC (0.29%)	ACAAA (0.36%)	CAGAA (0.38%)	GCAAA (0.31%)	CATCA (0.35%)	CAAAA (0.37%)
5	AGAAA (0.30%)	GTTC (0.34%)	CAGCA (0.36%)	CTGGC (0.29%)	GCGGC (0.33%)	GAAAA (0.37%)	TGTTC (0.29%)	ACAAA (0.35%)	TGGCA (0.37%)
6	CAGCA (0.30%)	TGTTT (0.34%)	TGTTT (0.32%)	CCAGC (0.29%)	TGATG (0.33%)	AATCA (0.35%)	CGGCA (0.29%)	TGGAA (0.33%)	CTGAA (0.33%)
7	TTTCT (0.29%)	TATCG (0.33%)	CGTTT (0.32%)	AATCA (0.29%)	ATTGC (0.31%)	AGAAA (0.33%)	GCAAT (0.28%)	GCGAC (0.31%)	AATGG (0.32%)
8	GTTGC (0.29%)	GCCAG (0.32%)	TTTTT (0.32%)	GCGGC (0.28%)	TTTGC (0.30%)	ATGAA (0.33%)	CTGGC (0.27%)	GCCAG (0.30%)	GCAAT (0.32%)
9	GAAAA (0.29%)	GCAGC (0.32%)	CTGAA (0.31%)	CATCA (0.27%)	GCAGC (0.30%)	CGGCA (0.32%)	CAGGC (0.27%)	TTTTCA (0.29%)	AGAAA (0.31%)
10	CGCCA (0.28%)	TTTCA (0.32%)	ATTTC (0.31%)	ATATC (0.27%)	AATCA (0.30%)	GCAAA (0.32%)	CGTCA (0.27%)	TTATT (0.29%)	TAAAA (0.31%)
-10	CCCTA (0.01%)	TCCTA (0.01%)	TAGGT (0.01%)	GGGAC (0.01%)	CCCTT (0.01%)	CTAGA (0.01%)	CTTGG (0.01%)	TCCTA (0.01%)	TCCTA (0.01%)
-9	GGACC (0.01%)	CCCTA (0.01%)	CCCTA (0.01%)	CCCTA (0.01%)	CCCTA (0.01%)	GCTAG (0.01%)	TAGGA (0.01%)	GCTAG (0.01%)	GCTAG (0.01%)
-8	GCTAG (0.00%)	GCTAG (0.00%)	GCTAG (0.00%)	TAGGG (0.01%)	CCCC (0.01%)	CCCTT (0.01%)	GCTAG (0.01%)	TAGGA (0.01%)	TTAGA (0.01%)
-7	CTAGT (0.00%)	CTAGT (0.00%)	ACTAG (0.00%)	CTAGA (0.01%)	CTAGA (0.01%)	CCCTA (0.01%)	CCCTA (0.01%)	CTAGA (0.00%)	CTAGC (0.00%)
-6	CTAGC (0.00%)	CTAGC (0.00%)	CTAGC (0.00%)	CTAGC (0.01%)	CTAGC (0.01%)	CTAGC (0.00%)	CTAGA (0.01%)	CTAGC (0.00%)	CCTAG (0.00%)
-5	CCTAG (0.00%)	ACTAG (0.00%)	CTAGT (0.00%)	CTAGT (0.00%)	CTAGT (0.00%)	CTAGT (0.00%)	CTAGT (0.00%)	ACTAG (0.00%)	CTAGT (0.00%)
-4	CTAGA (0.00%)	CCTAG (0.00%)	CCTAG (0.00%)	CCTAG (0.00%)	ACTAG (0.00%)	ACTAG (0.00%)	CTAGC (0.00%)	CTAGT (0.00%)	ACTAG (0.00%)
-3	ACTAG (0.00%)	CTAGA (0.00%)	CTAGG (0.00%)	ACTAG (0.00%)	TCTAG (0.00%)	TCTAG (0.00%)	ACTAG (0.00%)	TCTAG (0.00%)	CTAGG (0.00%)
-2	CTAGG (0.00%)	CTAGG (0.00%)	TCTAG (0.00%)	TCTAG (0.00%)	CCTAG (0.00%)	CCTAG (0.00%)	TCTAG (0.00%)	CTAGG (0.00%)	CTAGG (0.00%)
-1	TCTAG (0.00%)	TCTAG (0.00%)	CTAGA (0.00%)	CTAGG (0.00%)	CTAGG (0.00%)	CTAGG (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%