

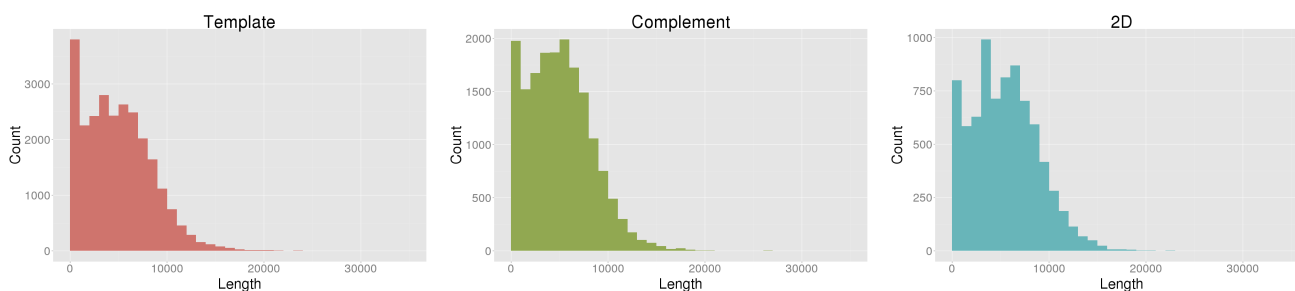
# NanoOK report for WTCHG\_MARC\_Ph1b.2

## Pass and fail counts

Type	Pass	Fail
Template	0	25656
Complement	0	17208
2D	0	7876

## Read lengths

Type	NumReads	TotalBases	Mean	Longest	Shortest	N50	N50Count	N90	N90Count
Template	25656	128517030	5009.24	274311	5	7111	6575	3174	16654
Complement	17208	87574885	5089.20	235142	14	6938	4672	3185	11602
2D	7876	43014234	5461.43	28553	116	7346	2212	3399	5419



## Template alignments

Number of reads	25656
Number of reads with alignments	12937 (50.42%)
Number of reads without alignments	12719 (49.58%)

ID	Size	Number of Reads	% of Reads	Mean read length	Aligned bases	Mean coverage	Longest Perf Kmer
Control sequence	3560	955	3.72	2958.65	2716502	763.06	61
Escherichia coli	4641652	11982	46.70	6591.27	72136239	15.54	71

## Complement alignments

Number of reads	17208
Number of reads with alignments	9790 (56.89%)
Number of reads without alignments	7418 (43.11%)

ID	Size	Number of Reads	% of Reads	Mean read length	Aligned bases	Mean coverage	Longest Perf Kmer
Control sequence	3560	631	3.67	2771.58	1507461	423.44	56
Escherichia coli	4641652	9159	53.23	6271.28	50842285	10.95	63

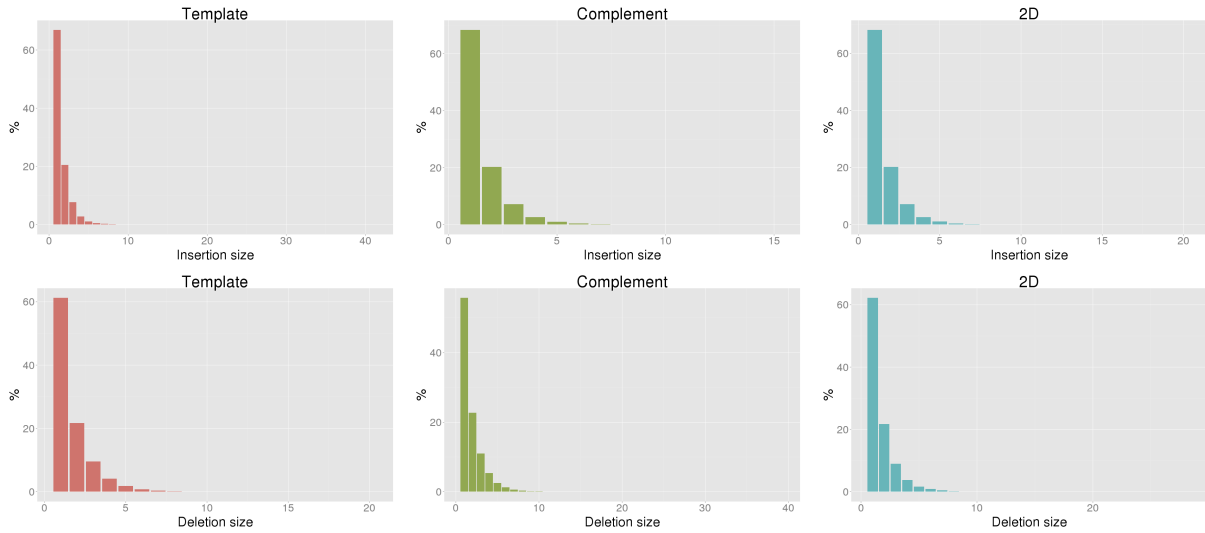
## 2D alignments

Number of reads	7876
Number of reads with alignments	6592 (83.70%)
Number of reads without alignments	1284 (16.30%)

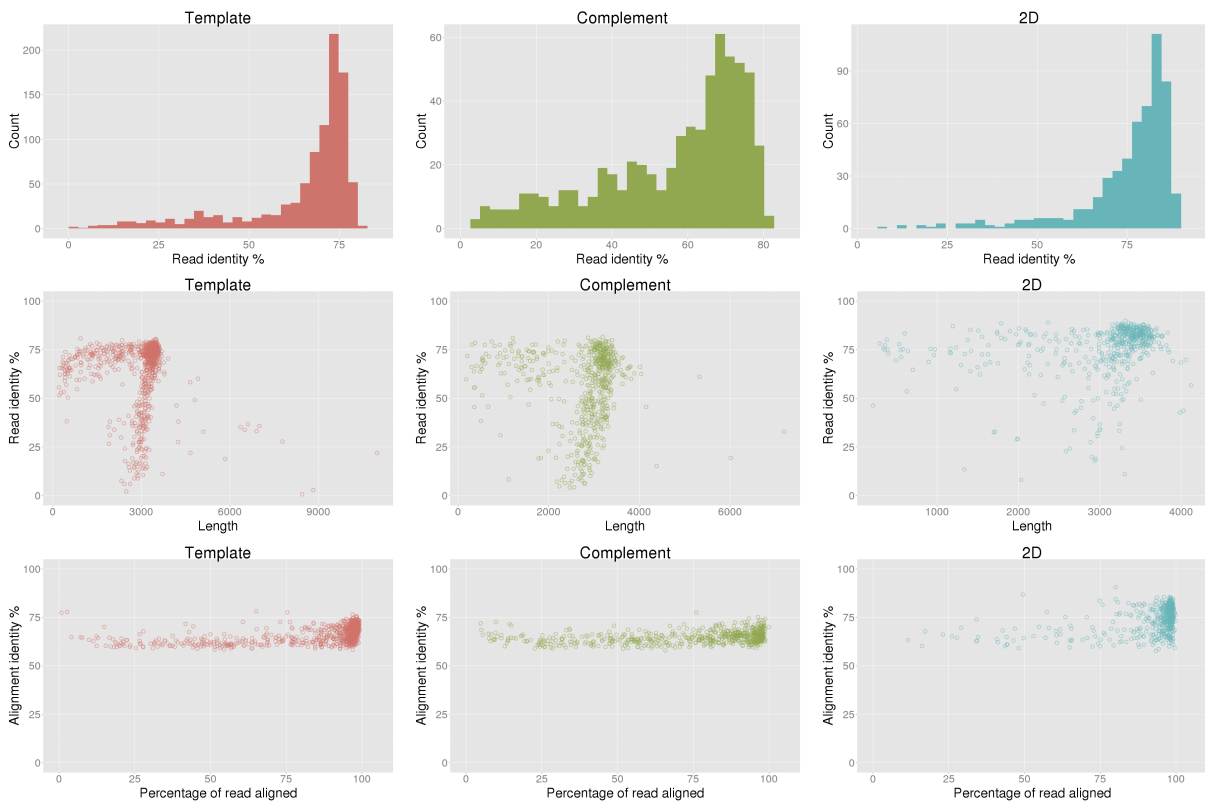
ID	Size	Number of Reads	% of Reads	Mean read length	Aligned bases	Mean coverage	Longest Perf Kmer
Control sequence	3560	547	6.95	3027.41	1682811	472.70	126
Escherichia coli	4641652	6045	76.75	6132.38	37638643	8.11	171

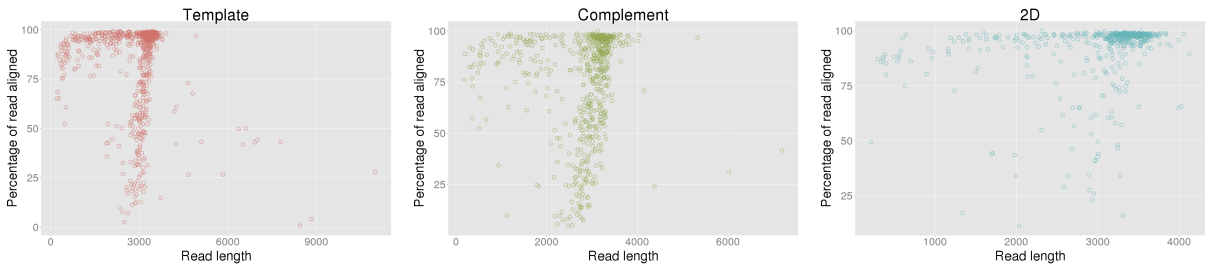
## Control sequence error analysis

	Template	Complement	2D
Overall base identity (excluding indels)	64.24%	55.89%	75.83%
Aligned base identity (excluding indels)	79.75%	79.77%	86.42%
Identical bases per 100 aligned bases (including indels)	66.82%	64.84%	74.62%
Inserted bases per 100 aligned bases (including indels)	4.85%	4.07%	4.49%
Deleted bases per 100 aligned bases (including indels)	11.36%	14.64%	9.16%
Substitutions per 100 aligned bases (including indels)	16.97%	16.45%	11.73%
Mean insertion size	1.56	1.50	1.51
Mean deletion size	1.70	1.87	1.68

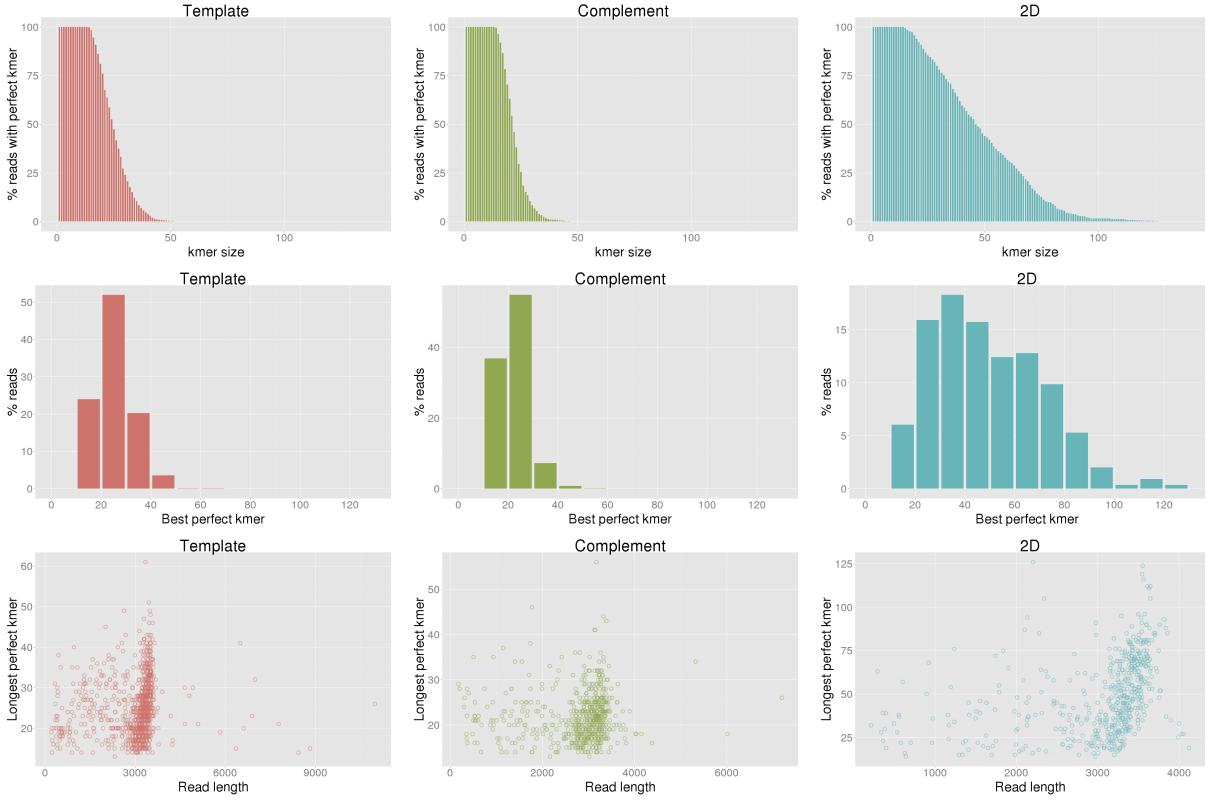


## Control sequence read identity

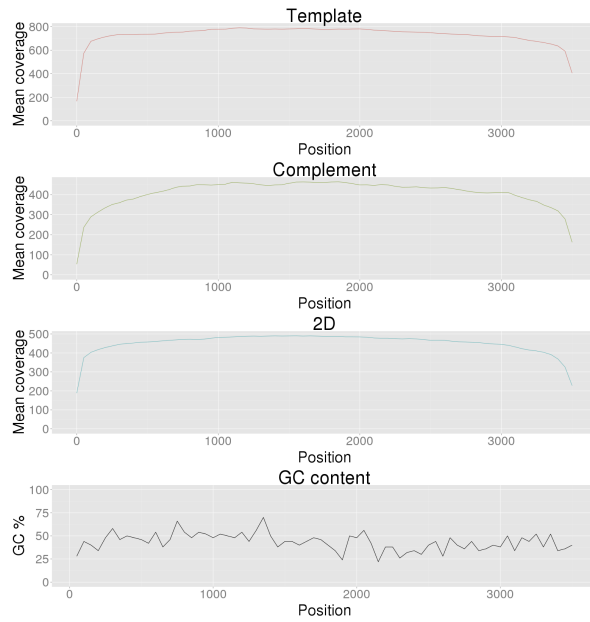




## Control sequence perfect kmers



## Control sequence coverage



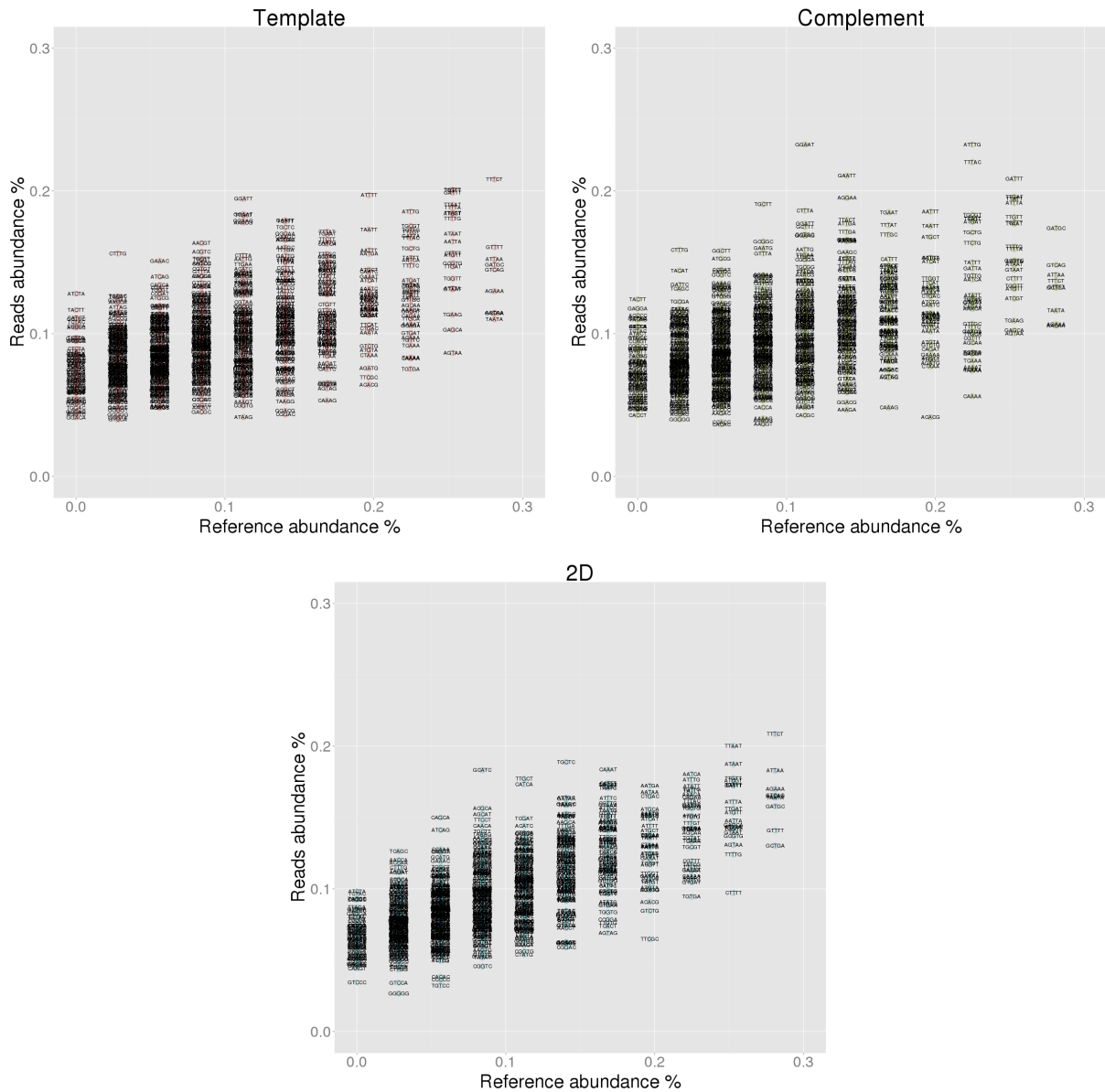
# Control sequence 5-mer analysis

## Under-represented 5-mers

Rank	Template				Complement				2D			
	kmer	Ref %	Read %	Diff %	kmer	Ref %	Read %	Diff %	kmer	Ref %	Read %	Diff %
1	TTTTT	0.759	0.125	-0.634	TTTTT	0.759	0.078	-0.681	TTTTT	0.759	0.045	-0.714
2	AAAAA	0.478	0.079	-0.398	AAAAA	0.478	0.037	-0.440	AAAAA	0.478	0.043	-0.434
3	TGATG	0.393	0.134	-0.260	AA AAC	0.337	0.099	-0.238	TGATG	0.393	0.154	-0.239
4	AAAAC	0.337	0.112	-0.225	TGATG	0.393	0.189	-0.204	AAAAC	0.337	0.136	-0.201
5	GATGT	0.309	0.098	-0.211	GATGT	0.309	0.109	-0.200	GATGT	0.309	0.130	-0.179
6	CTGAT	0.309	0.106	-0.203	GCAAT	0.309	0.126	-0.183	CTGAT	0.309	0.142	-0.167
7	AATAT	0.309	0.128	-0.181	AATAT	0.309	0.131	-0.178	GCAAT	0.309	0.153	-0.156
8	GCAAT	0.309	0.133	-0.176	TTATC	0.309	0.133	-0.176	CTTTT	0.253	0.097	-0.156
9	TAATA	0.281	0.110	-0.171	AACAA	0.281	0.106	-0.175	TTATC	0.309	0.154	-0.155
10	GCTGA	0.281	0.114	-0.167	AGAAA	0.281	0.107	-0.174	GCTGA	0.281	0.130	-0.151

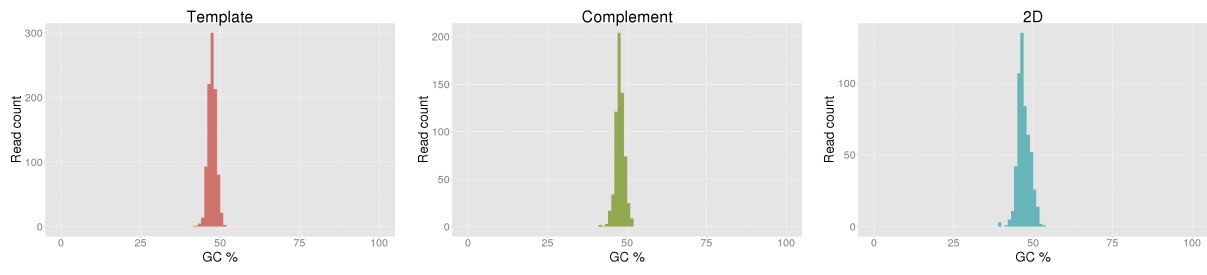
## Over-represented 5-mers

Rank	Template				Complement				2D			
	kmer	Ref %	Read %	Diff %	kmer	Ref %	Read %	Diff %	kmer	Ref %	Read %	Diff %
1	CTTTG	0.028	0.156	0.128	CTTTG	0.028	0.159	0.131	GCATC	0.084	0.183	0.099
2	ATCTA	0.000	0.128	0.128	TACTT	0.000	0.124	0.124	ATCTA	0.000	0.098	0.098
3	TACTT	0.000	0.117	0.117	GGAAT	0.112	0.233	0.120	TCAGC	0.028	0.126	0.098
4	CATCT	0.000	0.111	0.111	GAGGA	0.000	0.118	0.118	TCTAC	0.000	0.097	0.097
5	GCTCC	0.000	0.110	0.110	TACAT	0.028	0.144	0.116	CAGCA	0.056	0.150	0.094
6	TCTAC	0.000	0.108	0.108	ACCCG	0.000	0.113	0.113	TACGC	0.000	0.093	0.093
7	CCCCA	0.000	0.105	0.105	CTTAC	0.000	0.111	0.111	CATCT	0.000	0.093	0.093
8	ACCCC	0.000	0.104	0.104	GCCGA	0.000	0.110	0.110	CCCGC	0.000	0.092	0.092
9	TCAGC	0.028	0.126	0.098	TATAC	0.000	0.110	0.110	AACCA	0.028	0.120	0.092
10	TACAT	0.028	0.126	0.098	TGCTT	0.084	0.191	0.107	ACCAA	0.028	0.118	0.090



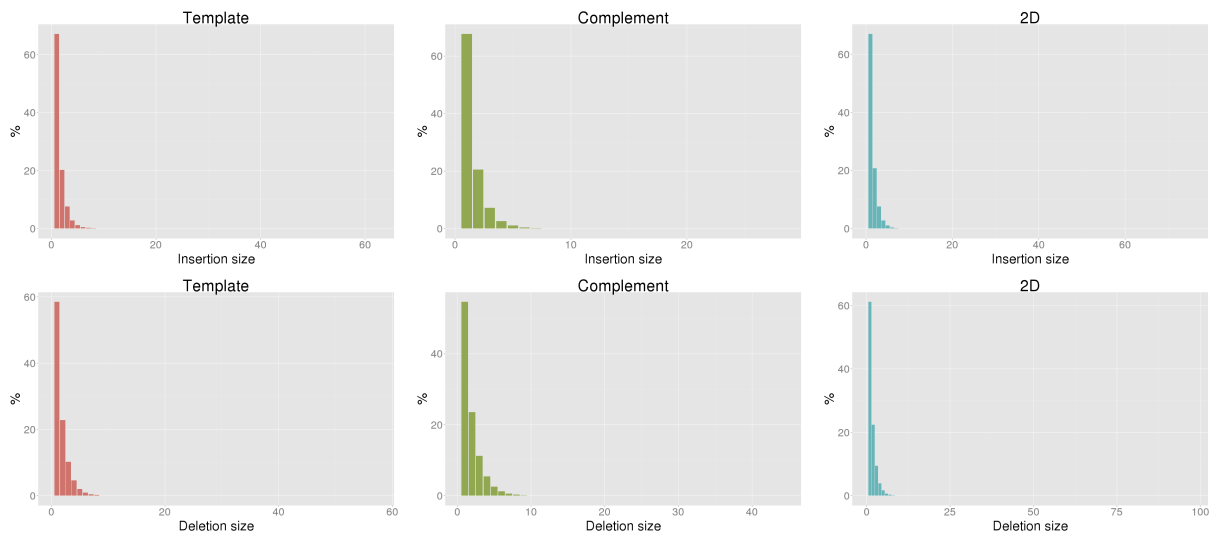


## Control sequence GC content

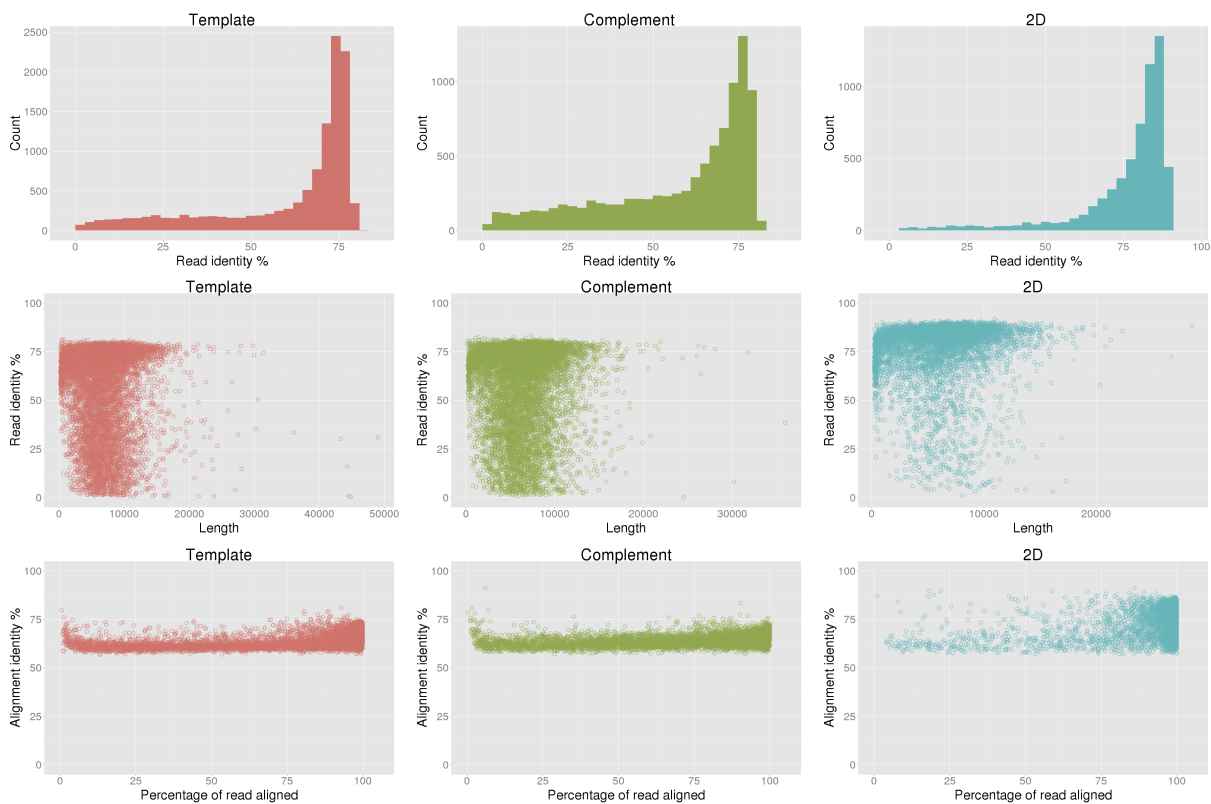


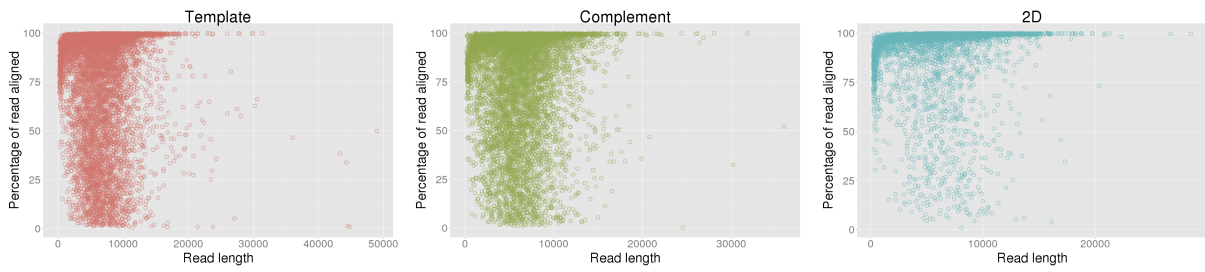
## Escherichia coli error analysis

	Template	Complement	2D
Overall base identity (excluding indels)	59.69%	57.31%	76.46%
Aligned base identity (excluding indels)	78.99%	80.07%	87.02%
Identical bases per 100 aligned bases (including indels)	65.35%	64.75%	75.30%
Inserted bases per 100 aligned bases (including indels)	4.71%	4.19%	4.47%
Deleted bases per 100 aligned bases (including indels)	12.55%	14.96%	9.00%
Substitutions per 100 aligned bases (including indels)	17.38%	16.11%	11.23%
Mean insertion size	1.55	1.52	1.54
Mean deletion size	1.76	1.88	1.69

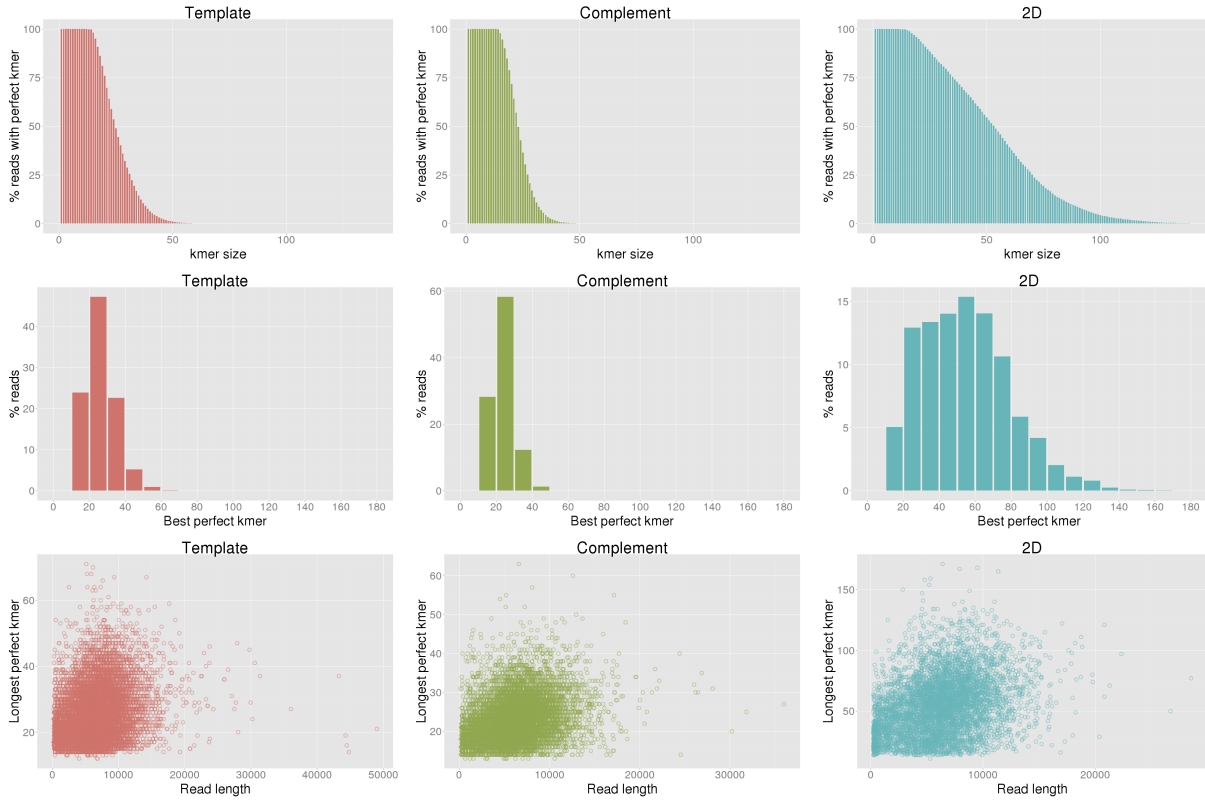


## Escherichia coli read identity

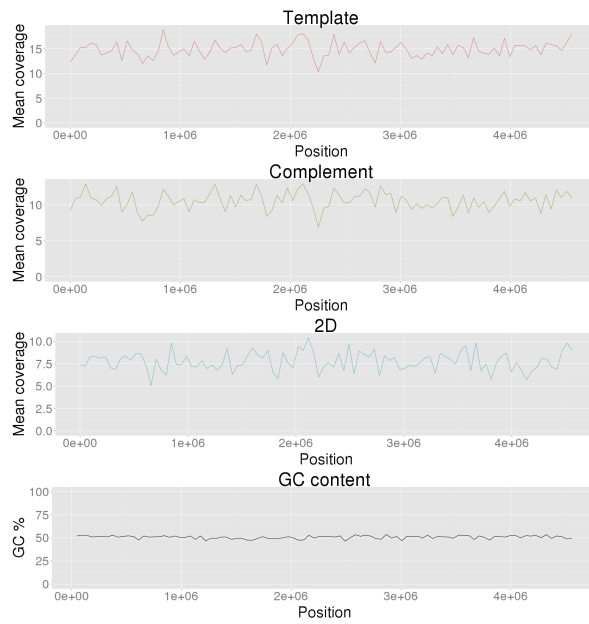




## Escherichia coli perfect kmers



## Escherichia coli coverage



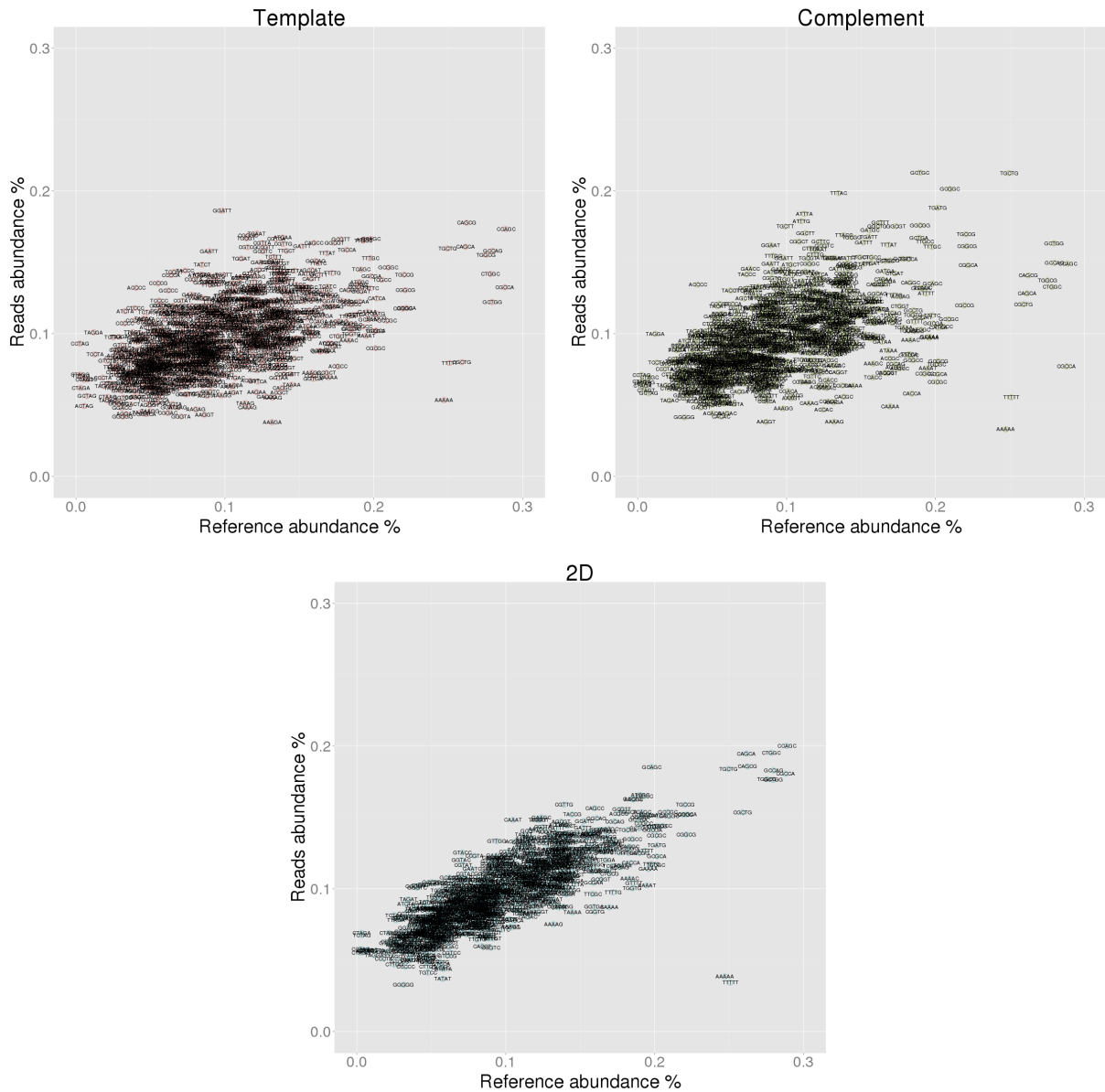
# Escherichia coli 5-mer analysis

## Under-represented 5-mers

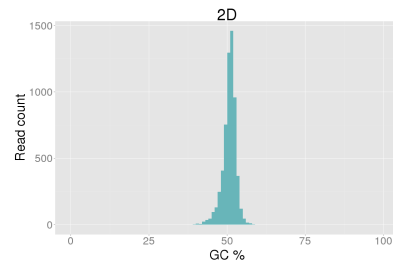
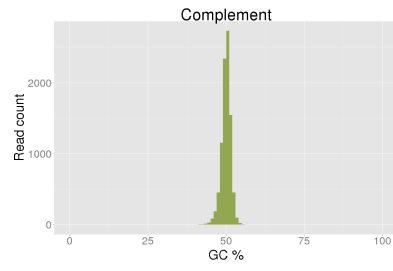
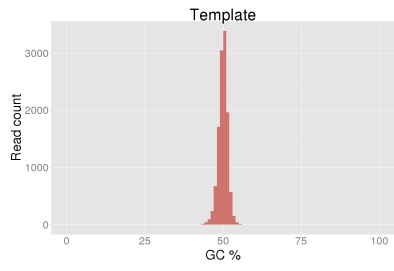
Rank	Template				Complement				2D			
	kmer	Ref %	Read %	Diff %	kmer	Ref %	Read %	Diff %	kmer	Ref %	Read %	Diff %
1	AAAAA	0.247	0.053	-0.194	AAAAA	0.247	0.033	-0.214	TTTTT	0.251	0.034	-0.217
2	CGCTG	0.259	0.080	-0.179	CGCCA	0.288	0.077	-0.211	AAAAA	0.247	0.039	-0.209
3	TTTTT	0.251	0.079	-0.171	TTTTT	0.251	0.055	-0.195	CGCCA	0.288	0.181	-0.107
4	GCTGG	0.279	0.122	-0.157	CTGGC	0.278	0.133	-0.146	CGCTG	0.259	0.154	-0.105
5	CGCCA	0.288	0.133	-0.155	CCAGC	0.289	0.149	-0.140	GCTGG	0.279	0.176	-0.103
6	CTGGC	0.278	0.142	-0.136	CGCTG	0.259	0.121	-0.138	TGGCG	0.275	0.177	-0.098
7	GCCAG	0.280	0.158	-0.122	TGGCG	0.275	0.137	-0.138	GCCAG	0.280	0.183	-0.097
8	TGGCG	0.275	0.155	-0.120	CGCGC	0.201	0.066	-0.135	AAAAT	0.195	0.102	-0.092
9	CCAGC	0.289	0.173	-0.115	CAGCA	0.261	0.128	-0.133	CCAGC	0.289	0.200	-0.088
10	CGCGC	0.201	0.090	-0.111	GCCAG	0.280	0.150	-0.130	TGGTG	0.185	0.100	-0.085

## Over-represented 5-mers

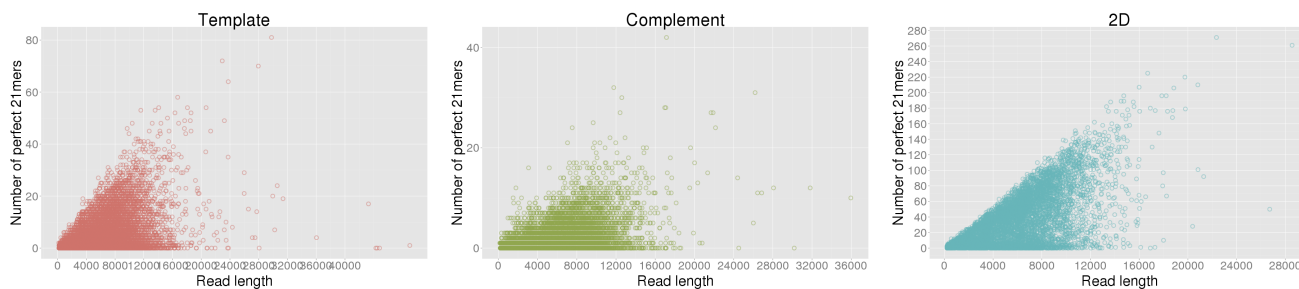
Rank	Template				Complement				2D			
	kmer	Ref %	Read %	Diff %	kmer	Ref %	Read %	Diff %	kmer	Ref %	Read %	Diff %
1	ACCCC	0.040	0.132	0.092	ACCCC	0.040	0.134	0.094	CTAGA	0.003	0.069	0.066
2	CCTAG	0.003	0.093	0.090	TAGGA	0.012	0.100	0.088	TCTAG	0.003	0.068	0.064
3	TAGGA	0.012	0.101	0.089	TGCTT	0.099	0.175	0.076	GGGGT	0.039	0.102	0.062
4	GGATT	0.098	0.186	0.088	GGAAT	0.089	0.162	0.073	GGGTC	0.040	0.101	0.060
5	ATCTA	0.033	0.116	0.083	ATTTA	0.112	0.184	0.072	CTCGT	0.042	0.102	0.060
6	CCCCG	0.055	0.135	0.080	GAACC	0.075	0.145	0.070	TAGAT	0.035	0.093	0.058
7	CTCCC	0.040	0.118	0.078	ATTTG	0.110	0.179	0.069	ATCTA	0.033	0.089	0.057
8	CCCCA	0.064	0.141	0.077	CCTAG	0.003	0.071	0.068	TCTAA	0.025	0.081	0.056
9	TCCGT	0.066	0.143	0.077	TACCC	0.073	0.142	0.068	CCCAA	0.047	0.103	0.056
10	CCCCC	0.033	0.107	0.075	TACCT	0.062	0.130	0.068	CCTAG	0.003	0.058	0.055



# 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	8.83	8.83	5.10	0.00	8.97	8.69	5.38	0.00	9.31	8.65	4.67
C	8.62	0.00	8.86	10.02	9.24	0.00	8.57	9.49	8.64	0.00	10.15	8.85
G	9.54	8.92	0.00	8.34	9.03	8.73	0.00	8.78	8.79	10.34	0.00	8.25
T	5.36	8.92	8.65	0.00	5.63	8.67	8.81	0.00	4.74	8.52	9.11	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 (3.25%)	TTC (3.33%)	AAA (4.05%)	TGC (2.89%)	GGC (2.84%)	AAA (3.92%)	GCA (3.07%)	AAA (2.68%)	AAA (3.66%)	Most common
2	AAA (2.83%)	TGC (2.94%)	TTC (3.62%)	TTC (2.82%)	AAA (2.83%)	GCA (3.53%)	AAA (2.78%)	GCA (2.65%)	GCA (3.61%)	
3	GCA (2.75%)	AAA (2.88%)	GCA (3.26%)	GCA (2.74%)	TGC (2.80%)	GAA (3.29%)	TTC (2.72%)	GGC (2.65%)	GAA (2.91%)	
4	TGC (2.58%)	GCA (2.73%)	GAA (2.96%)	AAA (2.68%)	GCA (2.72%)	TTC (3.09%)	TCA (2.51%)	TGC (2.58%)	TTT (2.84%)	
5	ATC (2.54%)	GCC (2.46%)	TTT (2.71%)	GAA (2.46%)	TTC (2.60%)	TTT (2.66%)	GAA (2.33%)	GCG (2.41%)	TTC (2.76%)	
6	TCA (2.43%)	GGC (2.32%)	TGC (2.58%)	CAG (2.42%)	GAA (2.54%)	TGC (2.53%)	ATC (2.33%)	TCA (2.34%)	GTT (2.59%)	
7	TTT (2.25%)	TCA (2.32%)	AAT (2.52%)	ATC (2.32%)	CAG (2.28%)	TCA (2.37%)	TGC (2.29%)	CAG (2.30%)	AAT (2.36%)	
8	GAA (2.22%)	AAT (2.23%)	GCC (2.19%)	TCA (2.30%)	GCC (2.26%)	ATC (2.21%)	GCG (2.29%)	TTC (2.30%)	GCC (2.29%)	
9	GCC (2.21%)	ATC (2.23%)	TCA (2.18%)	GGC (2.26%)	TCA (2.25%)	AAT (2.20%)	AAT (2.15%)	GAA (2.27%)	TGC (2.15%)	
10	AAT (2.21%)	GAA (2.20%)	CAA (2.17%)	TTT (2.23%)	AAT (2.21%)	CAA (2.13%)	CAG (2.15%)	CGC (2.20%)	TCA (2.15%)	
										Least common
-10	AGT (0.97%)	AGG (0.97%)	CTC (0.93%)	AGA (0.96%)	AGA (0.95%)	CCC (0.91%)	CTC (1.05%)	CTC (1.01%)	ATG (1.00%)	
-9	CTC (0.91%)	AGT (0.91%)	GGG (0.89%)	GTG (0.95%)	CTT (0.95%)	AGT (0.90%)	CTT (1.05%)	CCC (0.98%)	TGA (0.98%)	
-8	GGA (0.89%)	CCT (0.87%)	AGA (0.86%)	GGA (0.88%)	AGT (0.94%)	CTC (0.87%)	GAG (0.90%)	CGA (0.94%)	ACT (0.94%)	
-7	CCC (0.86%)	GAG (0.86%)	AGG (0.85%)	CTC (0.84%)	CCC (0.91%)	CCT (0.85%)	AGA (0.88%)	CTT (0.89%)	GAG (0.87%)	
-6	AGA (0.81%)	CTT (0.85%)	TGT (0.83%)	CCC (0.79%)	CCT (0.88%)	AGG (0.83%)	GGA (0.87%)	ACT (0.89%)	CTT (0.83%)	
-5	AGG (0.72%)	CGA (0.84%)	AGT (0.79%)	GAG (0.74%)	GAG (0.84%)	ACT (0.77%)	AGG (0.81%)	AGA (0.88%)	CGA (0.81%)	
-4	GGG (0.71%)	AGA (0.73%)	CTT (0.79%)	AGG (0.73%)	CTC (0.81%)	GGG (0.77%)	CCC (0.80%)	CCT (0.82%)	GGA (0.69%)	
-3	GAG (0.70%)	GGA (0.72%)	GAG (0.64%)	GGG (0.57%)	GGG (0.77%)	GAG (0.61%)	GGG (0.75%)	GGA (0.78%)	AGA (0.68%)	
-2	CTA (0.49%)	TAG (0.53%)	TAG (0.39%)	CTA (0.55%)	TAG (0.55%)	CTA (0.43%)	CTA (0.61%)	TAG (0.67%)	TAG (0.52%)	
-1	TAG (0.43%)	CTA (0.48%)	CTA (0.36%)	TAG (0.43%)	CTA (0.52%)	TAG (0.40%)	TAG (0.53%)	CTA (0.66%)	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 (1.07%)	TTTC (1.11%)	AAAA (1.30%)	CAGC (0.91%)	TGGC (1.04%)	CAAA (1.05%)	ATCA (0.87%)	TGGC (1.02%)	GGCA (1.15%)
2	GAAA (0.91%)	TGCC (0.96%)	TTTT (1.30%)	ATCA (0.87%)	CGGC (1.01%)	AAAA (1.05%)	GGCA (0.86%)	CAGC (0.91%)	AAAA (1.04%)
3	AAAA (0.86%)	TTGC (0.90%)	GAAA (1.12%)	CTGC (0.85%)	CAGC (0.99%)	TGAA (0.96%)	GCCA (0.82%)	TTCA (0.82%)	GAAA (0.94%)
4	ATCA (0.84%)	TTCC (0.89%)	GGCA (0.97%)	TTGC (0.85%)	TTGC (0.87%)	GGCA (0.92%)	AACA (0.80%)	CTGC (0.80%)	TTTC (0.91%)
5	TTCA (0.83%)	TGGC (0.89%)	TTTT (0.92%)	CAAA (0.80%)	CTGC (0.86%)	GAAA (0.91%)	TTTT (0.80%)	CGGC (0.77%)	CGTT (0.90%)
6	TGCC (0.79%)	TTCA (0.88%)	AAAT (0.92%)	TGGC (0.79%)	CAAA (0.84%)	ATCA (0.90%)	CAAA (0.77%)	CAAA (0.76%)	GGAA (0.90%)
7	TTGC (0.79%)	CAGC (0.88%)	GCAA (0.90%)	CCAG (0.78%)	ATCA (0.81%)	AGCA (0.90%)	TTCA (0.77%)	GGCA (0.75%)	TGCA (0.88%)
8	GGCA (0.78%)	CTGC (0.85%)	GGAA (0.88%)	ATGC (0.76%)	TGCC (0.81%)	TTTT (0.89%)	GAAA (0.76%)	GCCA (0.75%)	TTTT (0.86%)
9	TGCG (0.77%)	AAAA (0.85%)	CAAA (0.88%)	CGGC (0.76%)	TTCC (0.81%)	TAAA (0.88%)	TGCA (0.76%)	CCAG (0.74%)	CAAA (0.85%)
10	AACG (0.77%)	GAAA (0.83%)	TGCC (0.86%)	ATTC (0.75%)	CCAG (0.77%)	GGAA (0.87%)	TGGC (0.75%)	TGCC (0.74%)	CGCC (0.83%)
-10	TCTA (0.12%)	CTAT (0.12%)	CCCT (0.11%)	GTGT (0.10%)	CTAA (0.11%)	GAGG (0.11%)	CCCC (0.15%)	CCCC (0.15%)	TGCA (0.13%)
-9	CTAA (0.12%)	CGGA (0.12%)	CGAG (0.10%)	TAGA (0.10%)	CCTC (0.11%)	GTGT (0.10%)	TCTA (0.15%)	ACTT (0.15%)	ACTT (0.12%)
-8	TTAG (0.11%)	CCCT (0.11%)	ACTA (0.09%)	CTAA (0.10%)	GTGT (0.11%)	ACTA (0.10%)	GAGG (0.14%)	CTAT (0.15%)	CTAA (0.12%)
-7	TAGT (0.11%)	TAGT (0.11%)	TAGT (0.09%)	CGAG (0.10%)	CCCC (0.11%)	GGAC (0.09%)	CCCT (0.14%)	ACCT (0.13%)	CGGA (0.11%)
-6	GAGC (0.11%)	GGAC (0.11%)	TAGA (0.09%)	GAGG (0.10%)	ACCT (0.10%)	CTAT (0.09%)	GGAC (0.13%)	CTAA (0.12%)	TCTA (0.11%)
-5	GGAC (0.09%)	CTAA (0.10%)	TCTA (0.08%)	GGAC (0.10%)	TAGA (0.10%)	CGAG (0.08%)	CTAA (0.13%)	CCCT (0.11%)	ACTA (0.10%)
-4	TAGA (0.08%)	TAGG (0.08%)	GGAC (0.07%)	CCCT (0.08%)	CCCT (0.08%)	TAGG (0.07%)	TAGA (0.09%)	TAGG (0.10%)	TAGG (0.08%)
-3	CCTA (0.06%)	TAGA (0.06%)	TAGG (0.07%)	CCTA (0.07%)	TAGG (0.07%)	CCCT (0.07%)	CCTA (0.07%)	TAGA (0.09%)	TAGA (0.06%)
-2	TAGG (0.05%)	CCTA (0.05%)	CCTA (0.04%)	TAGG (0.05%)	CCTA (0.06%)	CCTA (0.05%)	TAGG (0.06%)	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 (0.33%)	CTGGC (0.37%)	GAAAA (0.42%)	CAGCA (0.43%)	CAGCA (0.43%)	CAGCA (0.54%)	CAGCA (0.36%)	CTGGC (0.43%)	CAGCA (0.44%)
2	CTGGC (0.32%)	CAGCA (0.36%)	CAGCA (0.41%)	CATCA (0.33%)	CTGGC (0.40%)	CGGCA (0.37%)	CGCCA (0.34%)	CAGCA (0.34%)	TGGCA (0.43%)
3	ATTTT (0.31%)	TTGCC (0.34%)	CAAAA (0.37%)	CCAGC (0.31%)	GCGGC (0.35%)	CATCA (0.36%)	CTGGC (0.33%)	GCCAG (0.31%)	CGGCA (0.40%)
4	TTATC (0.31%)	TTTGC (0.32%)	TGGCA (0.34%)	GCTGC (0.31%)	CCAGC (0.33%)	GAAAA (0.34%)	CGGCA (0.31%)	CGCCA (0.30%)	GAAAA (0.36%)
5	CATCA (0.30%)	GCTGC (0.31%)	GCAAA (0.32%)	CGGCA (0.30%)	CATCA (0.32%)	ATAAA (0.34%)	TGGCA (0.30%)	CCAGC (0.30%)	GCGTT (0.35%)
6	CAAAA (0.28%)	CCAGC (0.30%)	CGTTT (0.32%)	CTGGC (0.29%)	GCTGC (0.32%)	AATCA (0.33%)	CATCA (0.29%)	TGGCG (0.29%)	GCAAA (0.30%)
7	TGGCG (0.28%)	GCAGC (0.30%)	ATTTT (0.31%)	GCGGC (0.29%)	AATCA (0.32%)	CAGAA (0.32%)	TGGCG (0.29%)	GCGGC (0.28%)	TGGCG (0.29%)
8	CGCCA (0.28%)	TTTCA (0.30%)	GCCAG (0.31%)	AATCA (0.29%)	TTTGC (0.29%)	GCAAA (0.32%)	GCAAA (0.28%)	GCAGC (0.28%)	CTGCA (0.29%)
9	GAAAA (0.28%)	CGCCA (0.29%)	TTGCC (0.31%)	TTTTG (0.28%)	CGGCA (0.29%)	AAGAA (0.32%)	GCCAG (0.26%)	TTTTCA (0.27%)	CAAAA (0.29%)
10	TGGCA (0.28%)	GCCAG (0.29%)	CGTTC (0.31%)	TTGCC (0.27%)	TTGCC (0.28%)	TTACC (0.31%)	CTGCA (0.26%)	GCTGC (0.27%)	ATTTT (0.29%)
-10	CCCTA (0.01%)	CCCTA (0.01%)	CCCTA (0.01%)	GGGGG (0.01%)	CCCTA (0.01%)	ACCTA (0.01%)	GGACC (0.01%)	TCCTA (0.01%)	TAGGA (0.01%)
-9	GGACC (0.01%)	GGACC (0.01%)	CTTAG (0.01%)	CTAGC (0.01%)	CCCCC (0.01%)	CTAGC (0.00%)	CCCTA (0.01%)	TAGGA (0.01%)	CCCTA (0.01%)
-8	CTAGC (0.00%)	GCTAG (0.00%)	GCTAG (0.00%)	CCCTA (0.01%)	GCTAG (0.01%)	CCCTA (0.00%)	CTAGC (0.00%)	GCTAG (0.01%)	GCTAG (0.01%)
-7	ACTAG (0.00%)	ACTAG (0.00%)	CTAGG (0.00%)	GCTAG (0.00%)	CTAGC (0.01%)	GCTAG (0.00%)	CCTAG (0.00%)	CTAGC (0.01%)	CTAGT (0.00%)
-6	GCTAG (0.00%)	CTAGC (0.00%)	CTAGC (0.00%)	CTAGT (0.00%)	CTAGT (0.00%)	CTAGT (0.00%)	GCTAG (0.00%)	ACTAG (0.00%)	CTAGC (0.00%)
-5	CTAGT (0.00%)	CTAGG (0.00%)	ACTAG (0.00%)	CTAGA (0.00%)	ACTAG (0.00%)	CTAGA (0.00%)	ACTAG (0.00%)	CTAGT (0.00%)	ACTAG (0.00%)
-4	CTAGA (0.00%)	TCTAG (0.00%)	CCTAG (0.00%)	ACTAG (0.00%)	TCTAG (0.00%)	CTAGG (0.00%)	CTAGT (0.00%)	TCTAG (0.00%)	CCTAG (0.00%)
-3	CCTAG (0.00%)	CTAGT (0.00%)	TCTAG (0.00%)	TCTAG (0.00%)	CTAGA (0.00%)	TCTAG (0.00%)	CTAGA (0.00%)	CTAGG (0.00%)	CTAGG (0.00%)
-2	TCTAG (0.00%)	CCTAG (0.00%)	CTAGT (0.00%)	CTAGG (0.00%)	CCTAG (0.00%)	CCTAG (0.00%)	TCTAG (0.00%)	CCTAG (0.00%)	TCTAG (0.00%)
-1	CTAGG (0.00%)	CTAGA (0.00%)	CTAGA (0.00%)	CCTAG (0.00%)	CTAGG (0.00%)	ACTAG (0.00%)	CTAGG (0.00%)	CTAGA (0.00%)	CTAGA (0.00%)

Most common

Least common

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