

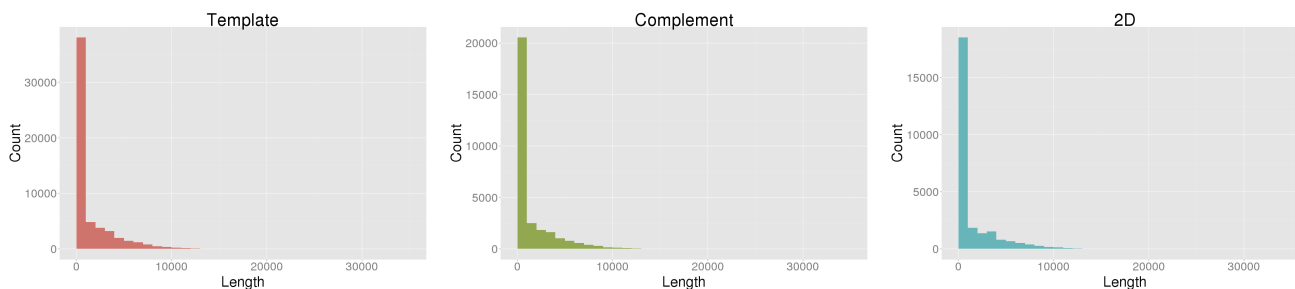
# NanoOK report for WTCHG\_MARC\_Ph1.2

## Pass and fail counts

Type	Pass	Fail
Template	0	56855
Complement	0	30092
2D	0	26351

## Read lengths

Type	NumReads	TotalBases	Mean	Longest	Shortest	N50	N50Count	N90	N90Count
Template	56855	91421954	1607.98	333708	11	4394	6169	477	27478
Complement	30092	46893717	1558.34	245472	6	4190	3371	458	15924
2D	26351	39428613	1496.29	31020	102	4269	2862	420	13862



## Template alignments

Number of reads	56855
Number of reads with alignments	14482 (25.47%)
Number of reads without alignments	42373 (74.53%)

ID	Size	Number of Reads	% of Reads	Mean read length	Aligned bases	Mean coverage	Longest Perf Kmer
Control sequence	3560	1255	2.21	2941.27	3129336	879.03	47
Escherichia coli	4641652	13227	23.26	3368.64	36088673	7.77	55

## Complement alignments

Number of reads	30092
Number of reads with alignments	9021 (29.98%)
Number of reads without alignments	21071 (70.02%)

ID	Size	Number of Reads	% of Reads	Mean read length	Aligned bases	Mean coverage	Longest Perf Kmer
Control sequence	3560	695	2.31	2984.77	1796978	504.77	46
Escherichia coli	4641652	8326	27.67	3016.51	21455749	4.62	52

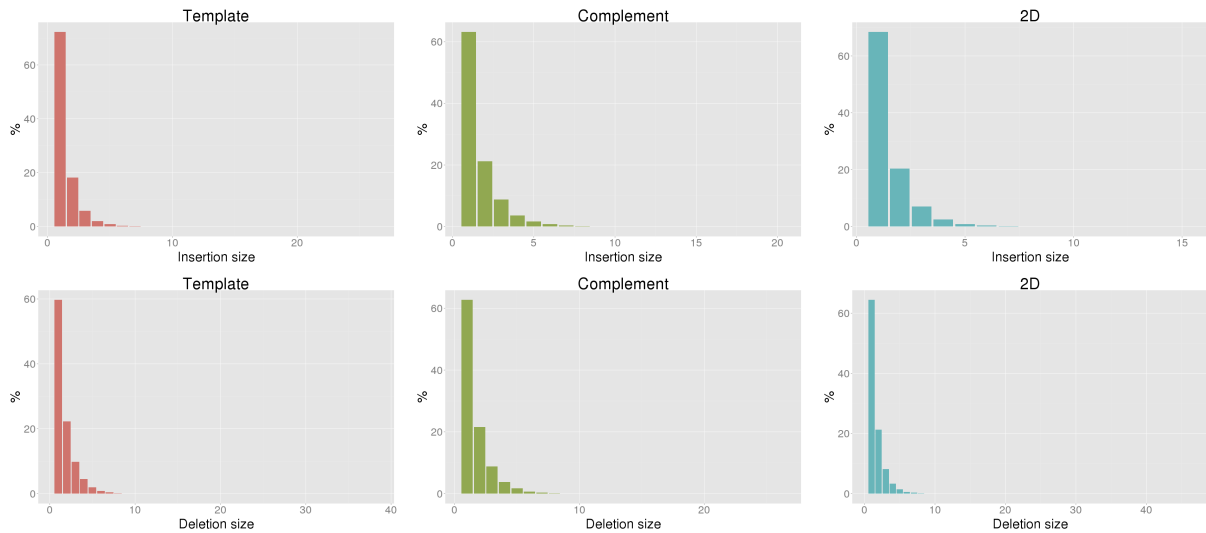
## 2D alignments

Number of reads	26351
Number of reads with alignments	17207 (65.30%)
Number of reads without alignments	9144 (34.70%)

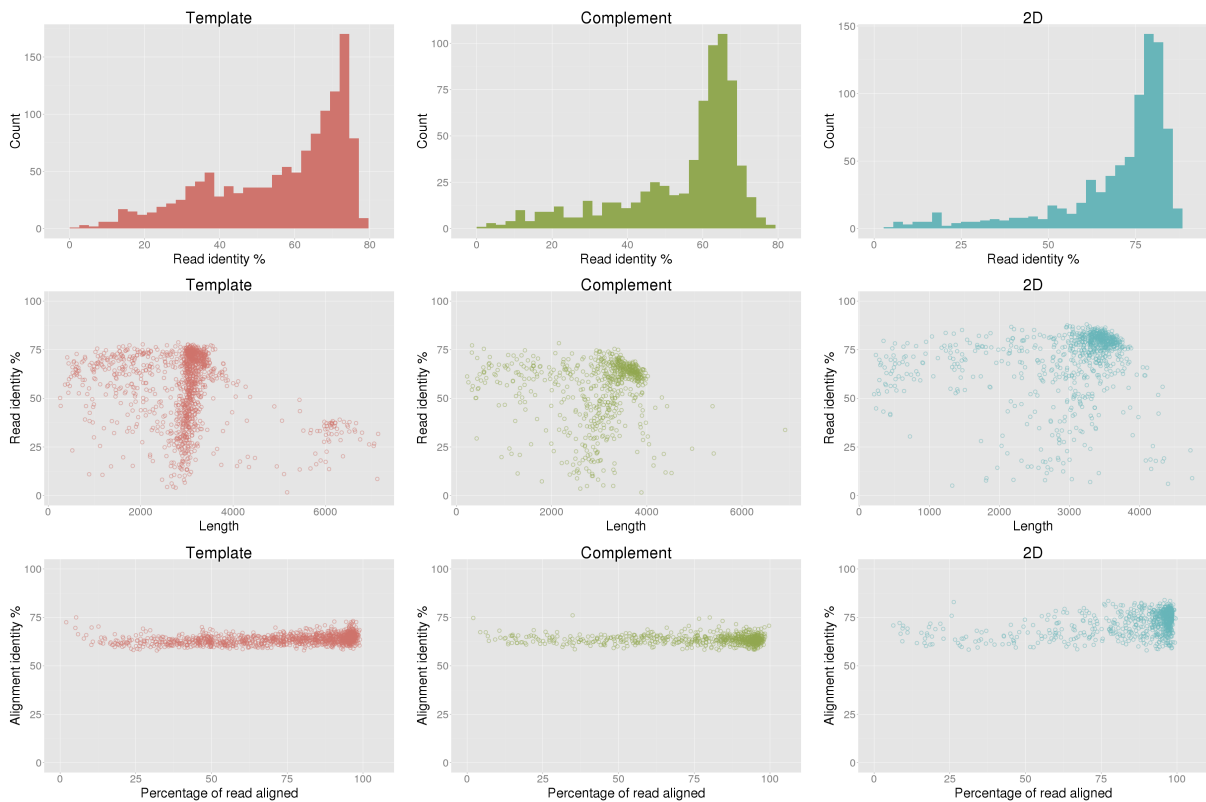
ID	Size	Number of Reads	% of Reads	Mean read length	Aligned bases	Mean coverage	Longest Perf Kmer
Control sequence	3560	832	3.16	2971.72	2377187	667.75	128
Escherichia coli	4641652	16375	62.14	1869.58	28978837	6.24	152

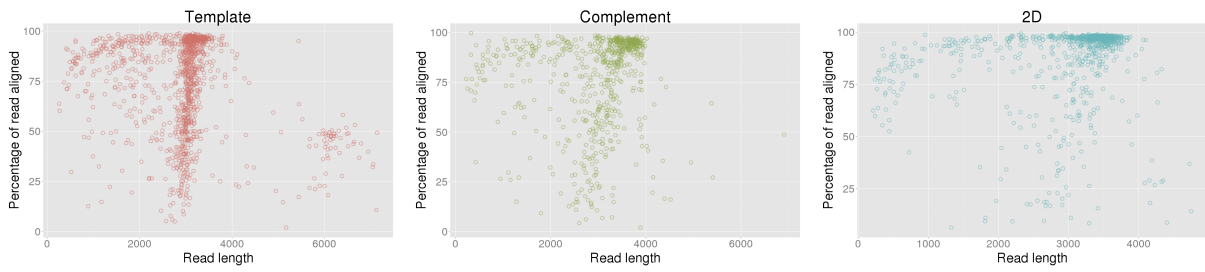
## Control sequence error analysis

	Template	Complement	2D
Overall base identity (excluding indels)	54.23%	54.86%	70.40%
Aligned base identity (excluding indels)	78.11%	76.69%	85.02%
Identical bases per 100 aligned bases (including indels)	63.97%	63.33%	73.23%
Inserted bases per 100 aligned bases (including indels)	3.01%	6.76%	4.55%
Deleted bases per 100 aligned bases (including indels)	15.10%	10.65%	9.32%
Substitutions per 100 aligned bases (including indels)	17.92%	19.25%	12.90%
Mean insertion size	1.45	1.66	1.50
Mean deletion size	1.73	1.66	1.62

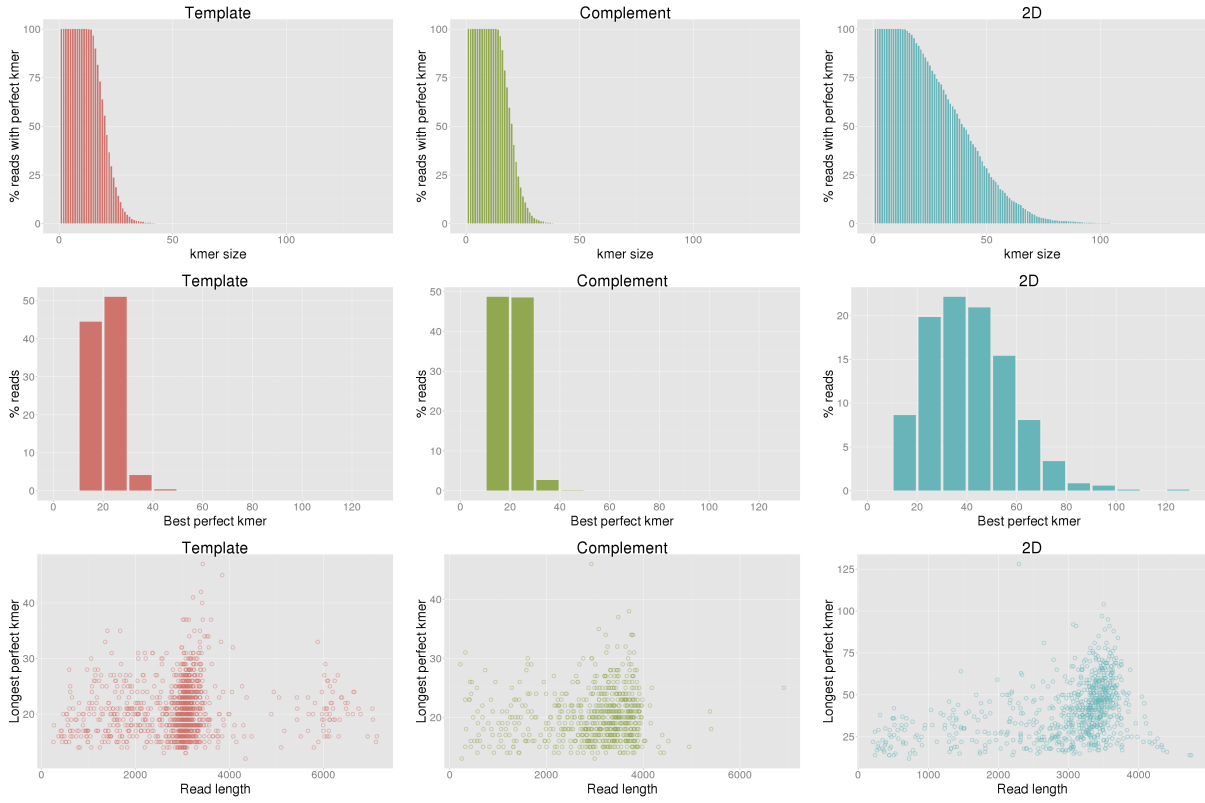


## Control sequence read identity

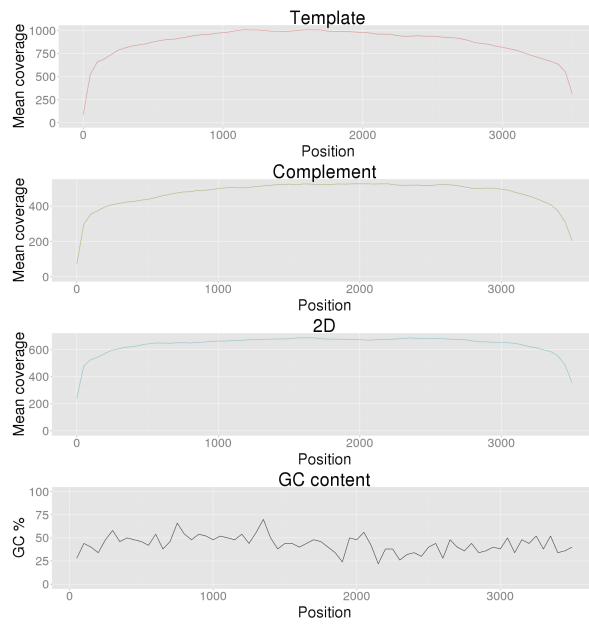




## Control sequence perfect kmers



## Control sequence coverage



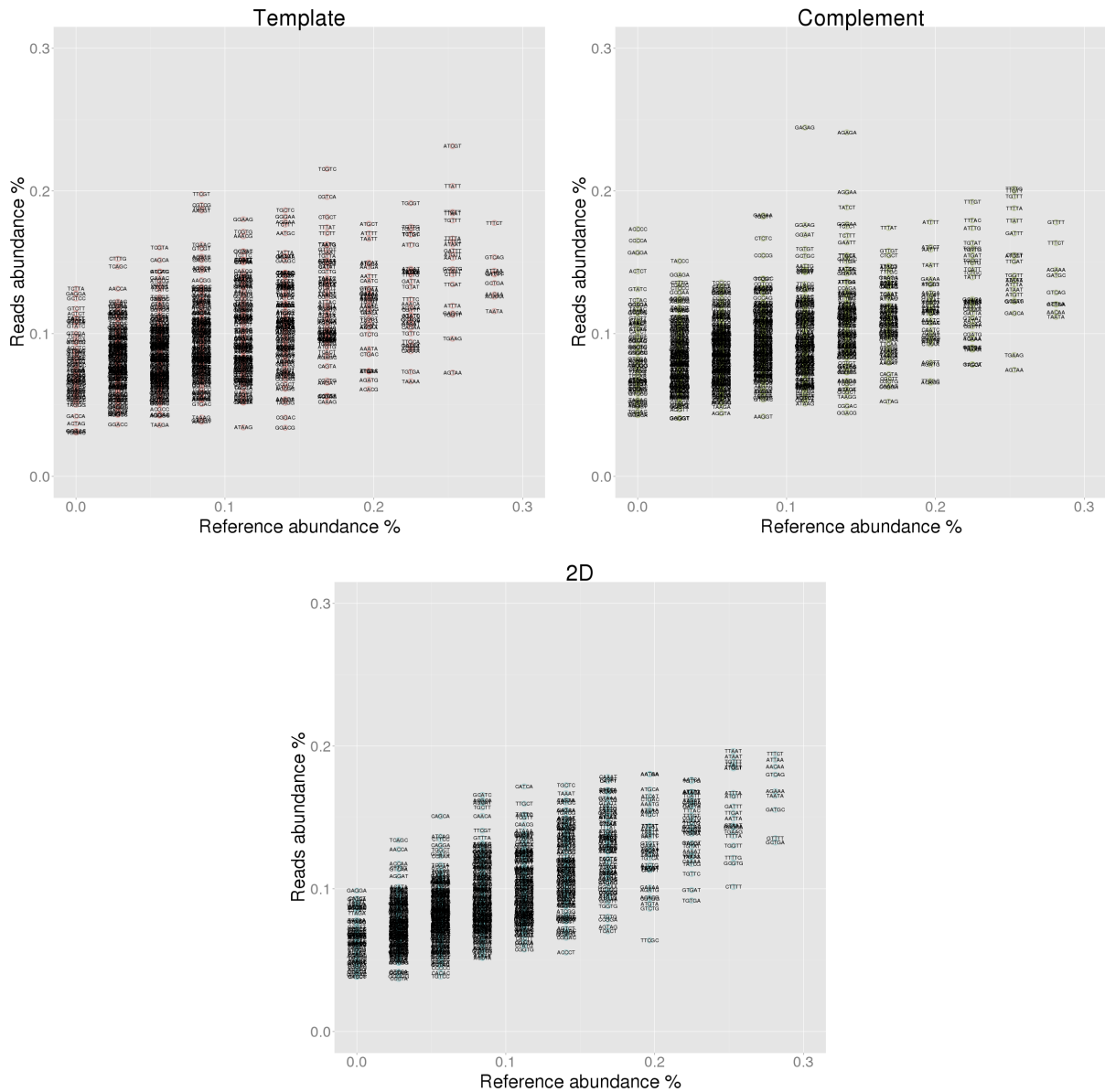
# Control sequence 5-mer analysis

## Under-represented 5-mers

Rank	Template				Complement				2D			
	kmer	Ref %	Read %	Diff %	kmer	Ref %	Read %	Diff %	kmer	Ref %	Read %	Diff %
1	TTTTT	0.759	0.111	-0.648	TTTTT	0.759	0.143	-0.615	TTTTT	0.759	0.053	-0.706
2	AAAAA	0.478	0.074	-0.404	AAAAA	0.478	0.105	-0.373	AAAAA	0.478	0.052	-0.426
3	TGATG	0.393	0.126	-0.268	TGATG	0.393	0.151	-0.243	TGATG	0.393	0.152	-0.242
4	GATGT	0.309	0.079	-0.230	GATGT	0.309	0.089	-0.220	AAAAC	0.337	0.129	-0.208
5	AAAAC	0.337	0.108	-0.229	AAAAC	0.337	0.128	-0.209	GATGT	0.309	0.124	-0.185
6	CTGAT	0.309	0.111	-0.198	GCAAT	0.309	0.113	-0.196	CTGAT	0.309	0.137	-0.173
7	AATAT	0.309	0.119	-0.190	AGTAA	0.253	0.075	-0.178	GCAAT	0.309	0.144	-0.165
8	AGTAA	0.253	0.073	-0.180	TAATA	0.281	0.112	-0.169	CTTTT	0.253	0.101	-0.152
9	GCAAT	0.309	0.129	-0.180	CTGAT	0.309	0.141	-0.168	TTATC	0.309	0.160	-0.149
10	TAATA	0.281	0.116	-0.165	TGAAG	0.253	0.085	-0.168	GCTGA	0.281	0.132	-0.148

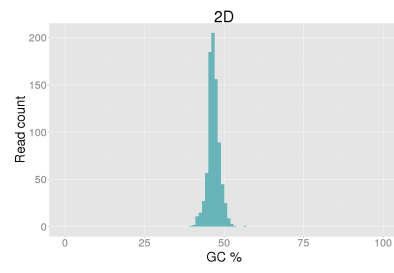
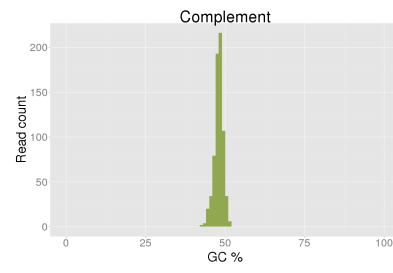
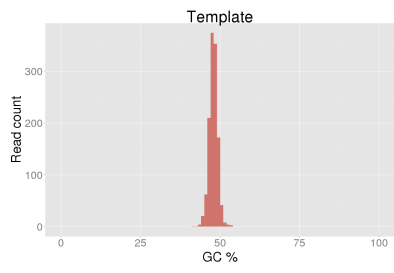
## Over-represented 5-mers

Rank	Template				Complement				2D			
	kmer	Ref %	Read %	Diff %	kmer	Ref %	Read %	Diff %	kmer	Ref %	Read %	Diff %
1	TCTTA	0.000	0.132	0.132	ACCCC	0.000	0.173	0.173	TCAGC	0.028	0.134	0.106
2	GAGGA	0.000	0.128	0.128	CCCCA	0.000	0.165	0.165	AACCA	0.028	0.128	0.100
3	GCTCC	0.000	0.125	0.125	GAGGA	0.000	0.157	0.157	GAGGA	0.000	0.099	0.099
4	CTTTG	0.028	0.153	0.124	ACTCT	0.000	0.144	0.144	CAGCA	0.056	0.151	0.095
5	TCAGC	0.028	0.147	0.119	GAGAG	0.112	0.245	0.132	CATCT	0.000	0.093	0.093
6	GTCTT	0.000	0.118	0.118	GTATC	0.000	0.131	0.131	GTCGA	0.000	0.093	0.093
7	ACTCT	0.000	0.114	0.114	TCTAC	0.000	0.123	0.123	TACTT	0.000	0.091	0.091
8	TTCGT	0.084	0.198	0.114	TACCC	0.028	0.151	0.123	TCTTA	0.000	0.090	0.090
9	TACTT	0.000	0.111	0.111	GCCGA	0.000	0.120	0.120	ACCAA	0.028	0.118	0.090
10	CATCT	0.000	0.111	0.111	CGAGA	0.000	0.120	0.120	GACGA	0.000	0.089	0.089



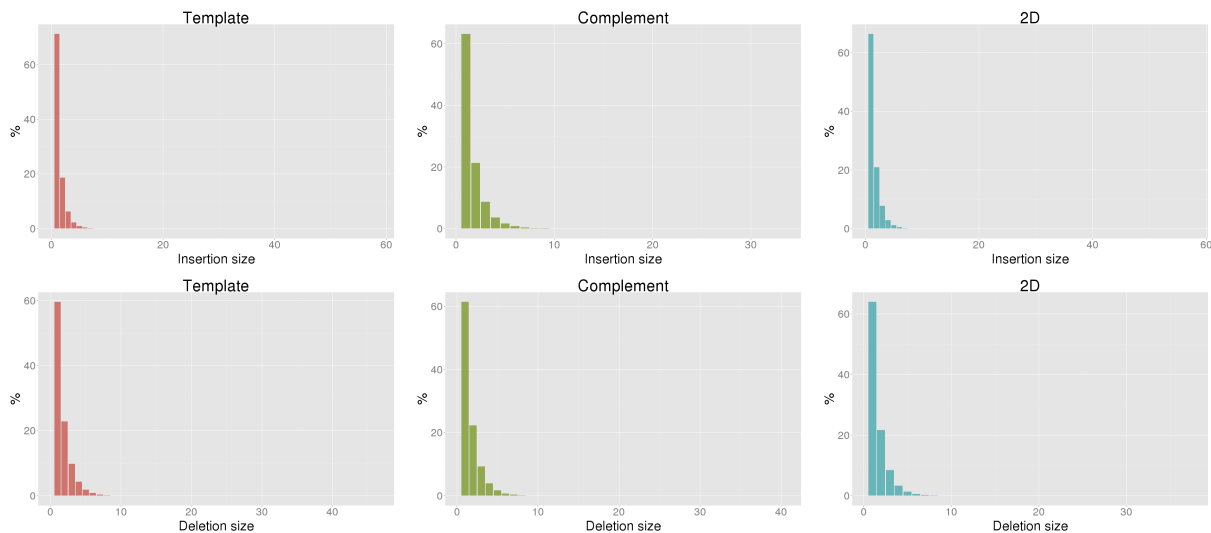


## Control sequence GC content

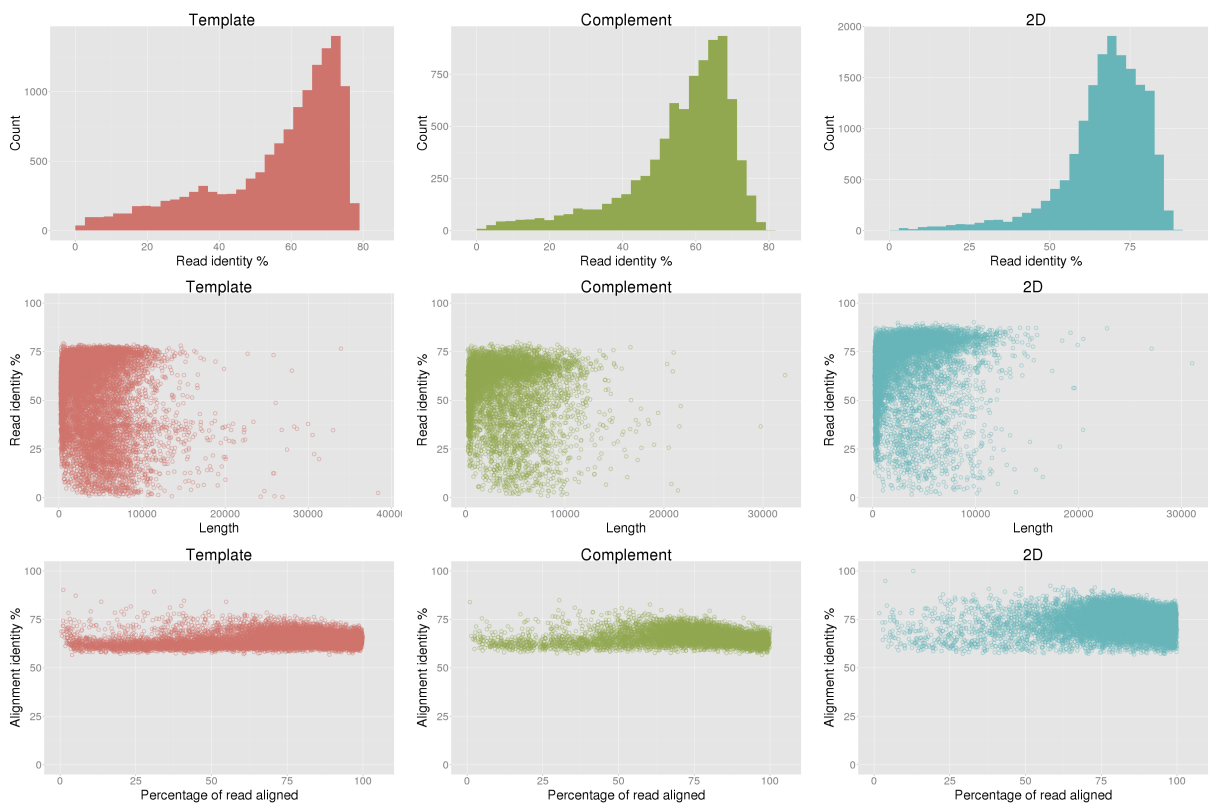


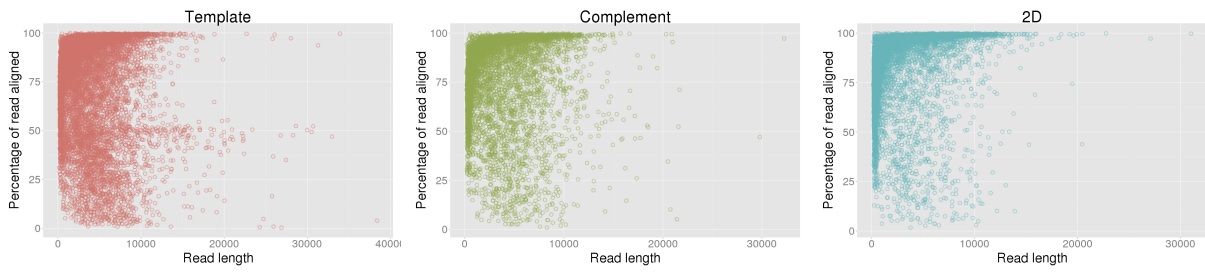
## Escherichia coli error analysis

	Template	Complement	2D
Overall base identity (excluding indels)	51.42%	54.42%	69.21%
Aligned base identity (excluding indels)	77.48%	77.43%	85.03%
Identical bases per 100 aligned bases (including indels)	63.49%	63.70%	73.12%
Inserted bases per 100 aligned bases (including indels)	3.46%	6.51%	4.96%
Deleted bases per 100 aligned bases (including indels)	14.61%	11.21%	9.05%
Substitutions per 100 aligned bases (including indels)	18.45%	18.57%	12.88%
Mean insertion size	1.47	1.66	1.55
Mean deletion size	1.72	1.68	1.61

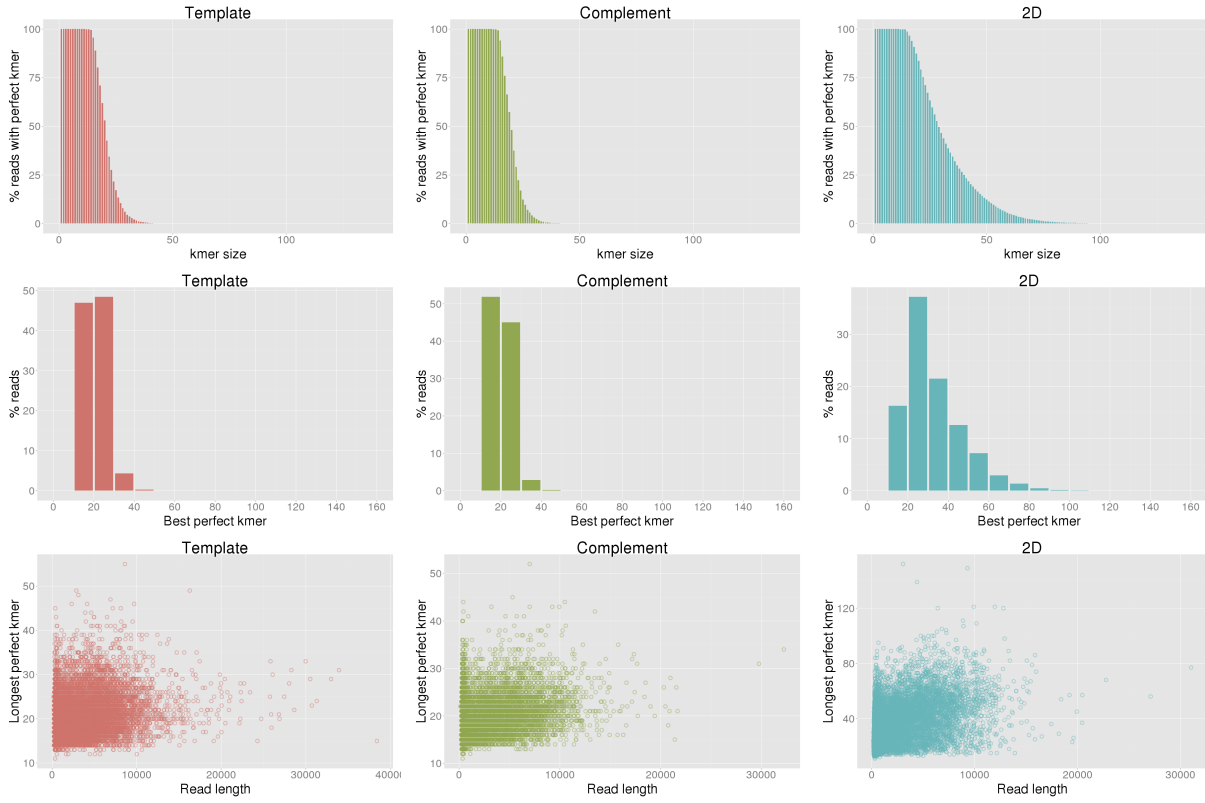


## Escherichia coli read identity

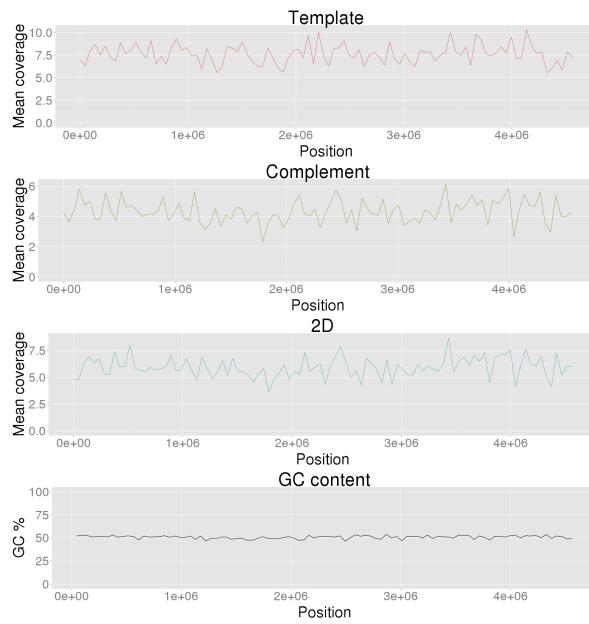




## Escherichia coli perfect kmers



## Escherichia coli coverage



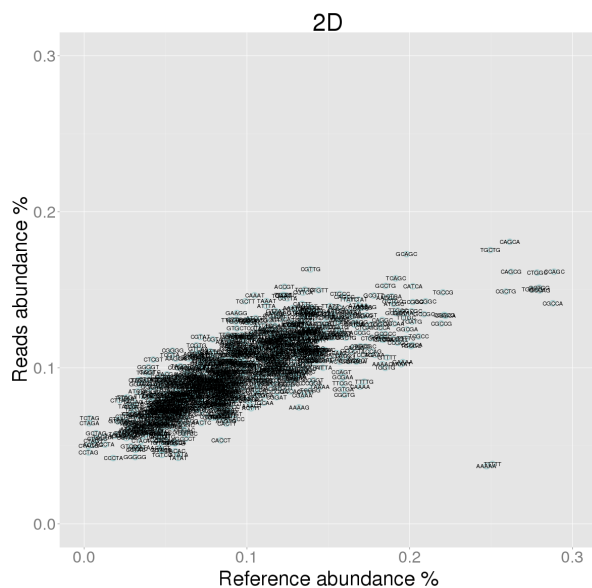
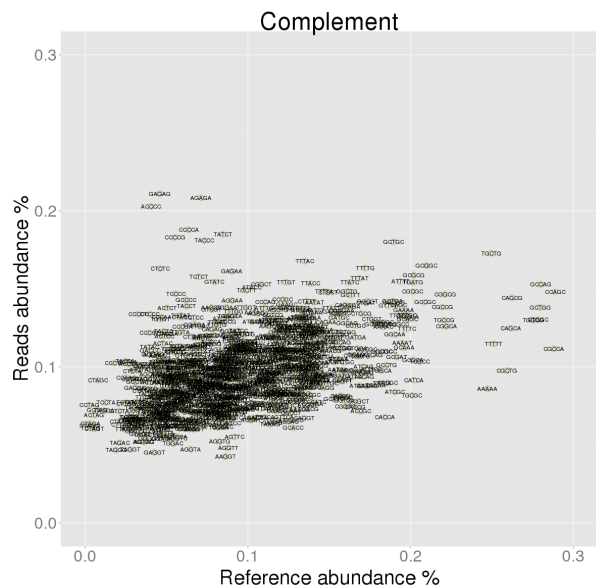
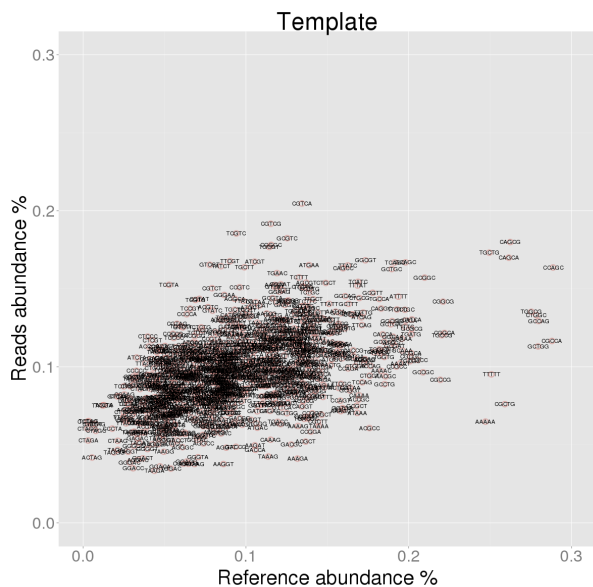
# Escherichia coli 5-mer analysis

## Under-represented 5-mers

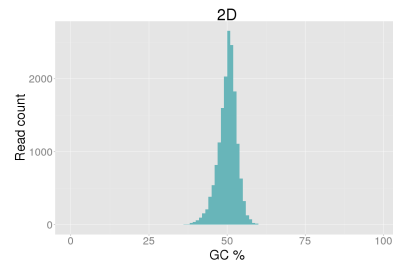
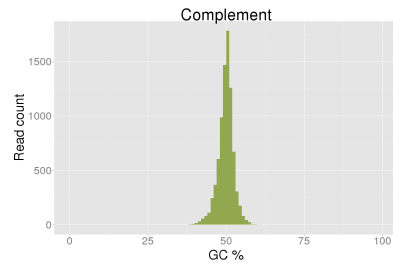
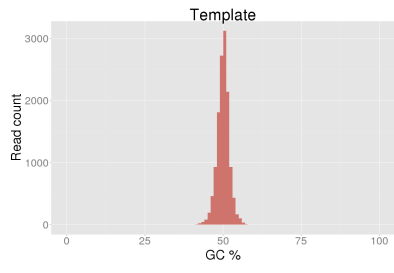
Rank	Template				Complement				2D			
	kmer	Ref %	Read %	Diff %	kmer	Ref %	Read %	Diff %	kmer	Ref %	Read %	Diff %
1	CGCTG	0.259	0.076	-0.183	CGCCA	0.288	0.112	-0.176	TTTTT	0.251	0.038	-0.212
2	AAAAA	0.247	0.065	-0.182	CGCTG	0.259	0.098	-0.161	AAAAA	0.247	0.037	-0.210
3	CGCCA	0.288	0.117	-0.171	AAAAA	0.247	0.086	-0.161	CGCCA	0.288	0.141	-0.147
4	GCTGG	0.279	0.113	-0.166	CTGGC	0.278	0.130	-0.148	GCCAG	0.280	0.150	-0.130
5	TTTTT	0.251	0.095	-0.156	TGGCG	0.275	0.130	-0.145	GCTGG	0.279	0.151	-0.128
6	GCCAG	0.280	0.129	-0.150	GCTGG	0.279	0.138	-0.141	CCAGC	0.289	0.162	-0.127
7	CTGGC	0.278	0.133	-0.145	CCAGC	0.289	0.148	-0.141	TGGCG	0.275	0.150	-0.125
8	TGGCG	0.275	0.135	-0.140	CAGCA	0.261	0.125	-0.137	CTGGC	0.278	0.161	-0.117
9	CGCCG	0.219	0.092	-0.128	TTTTT	0.251	0.115	-0.136	CGCTG	0.259	0.149	-0.110
10	CCAGC	0.289	0.164	-0.125	GCCAG	0.280	0.153	-0.127	CAGCG	0.262	0.161	-0.101

## Over-represented 5-mers

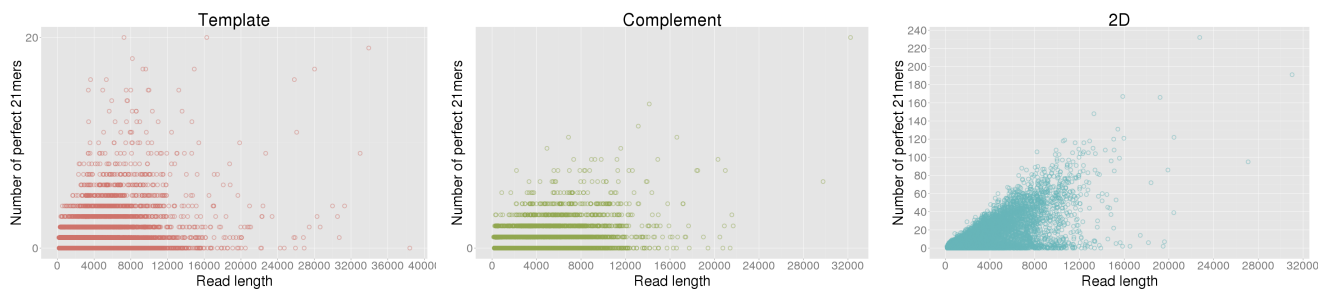
Rank	Template				Complement				2D			
	kmer	Ref %	Read %	Diff %	kmer	Ref %	Read %	Diff %	kmer	Ref %	Read %	Diff %
1	TCGTA	0.053	0.153	0.100	GAGAG	0.046	0.211	0.165	TCTAG	0.003	0.068	0.064
2	TCGTC	0.094	0.185	0.091	ACCCC	0.040	0.203	0.162	CTCGT	0.042	0.105	0.063
3	GTCGT	0.078	0.165	0.088	AGAGA	0.071	0.208	0.137	CTAGA	0.003	0.065	0.061
4	TATCT	0.085	0.165	0.080	CCCCG	0.055	0.183	0.128	GGGGT	0.039	0.100	0.061
5	CTCCC	0.040	0.119	0.080	CCCCA	0.064	0.188	0.124	CCTCC	0.033	0.092	0.059
6	TTCGT	0.090	0.168	0.078	CTCTC	0.046	0.163	0.117	TTAGT	0.038	0.097	0.059
7	CGTCG	0.115	0.192	0.076	TACCC	0.073	0.181	0.108	TAGAT	0.035	0.092	0.058
8	CTCGT	0.042	0.117	0.075	CCCCC	0.033	0.134	0.101	CTTAG	0.022	0.079	0.057
9	TCGTG	0.069	0.143	0.074	TATCT	0.085	0.185	0.100	CGGGG	0.054	0.111	0.057
10	ATCTA	0.033	0.106	0.073	CTCCC	0.040	0.134	0.094	GGGTC	0.040	0.097	0.057



# 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	9.12	8.85	4.82	0.00	9.29	8.50	5.17	0.00	9.13	8.63	4.48
C	8.50	0.00	9.06	9.78	8.79	0.00	8.96	9.24	8.84	0.00	10.32	8.69
G	9.18	9.17	0.00	8.41	8.83	9.07	0.00	8.63	8.60	10.65	0.00	8.55
T	5.29	8.93	8.89	0.00	5.44	8.73	9.35	0.00	4.60	8.52	8.99	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 (3.04%)	TTC (3.30%)	AAA (3.97%)	AAA (3.00%)	AAA (3.08%)	AAA (4.45%)	GCA (3.08%)	AAA (2.74%)	AAA (3.78%)
2	GCA (2.97%)	TGC (3.05%)	TTC (3.47%)	TTC (2.67%)	TGC (2.77%)	GCA (3.16%)	AAA (2.88%)	GCA (2.60%)	GCA (3.41%)
3	AAA (2.72%)	GCA (2.94%)	GCA (3.34%)	GCA (2.64%)	GCA (2.72%)	TTT (3.09%)	TTC (2.78%)	TGC (2.57%)	GAA (3.07%)
4	TGC (2.55%)	AAA (2.93%)	GAA (2.98%)	TGC (2.51%)	TTC (2.65%)	TTC (3.05%)	GAA (2.56%)	TCA (2.54%)	TTT (2.90%)
5	ATC (2.49%)	TCA (2.37%)	TTT (2.75%)	TTT (2.44%)	GGC (2.60%)	GAA (3.04%)	TCA (2.49%)	TTC (2.41%)	TTC (2.88%)
6	TCA (2.35%)	GCC (2.35%)	TGC (2.65%)	CAG (2.34%)	GAA (2.45%)	TGC (2.35%)	TGC (2.42%)	GAA (2.31%)	GTT (2.63%)
7	TTT (2.29%)	GAA (2.33%)	AAT (2.47%)	GAA (2.30%)	CAG (2.27%)	TCA (2.26%)	ATC (2.32%)	GGC (2.28%)	AAT (2.54%)
8	GAA (2.26%)	AAC (2.20%)	TCA (2.24%)	ATC (2.18%)	GCC (2.27%)	AAT (2.15%)	AAT (2.23%)	GCG (2.27%)	TCA (2.28%)
9	GCC (2.13%)	ATC (2.14%)	CAA (2.16%)	GGC (2.15%)	TCA (2.24%)	CAA (2.15%)	TTT (2.22%)	CAG (2.23%)	TGC (2.24%)
10	AAT (2.13%)	GGC (2.13%)	ATC (2.10%)	TCA (2.14%)	AAT (2.22%)	GCC (2.11%)	CAG (2.14%)	GCC (2.13%)	GCC (2.20%)
-10	AGA (0.99%)	GTA (0.92%)	CCT (0.93%)	ACT (1.08%)	ACT (0.95%)	CTC (0.99%)	ACT (1.03%)	GGG (1.00%)	GGG (0.93%)
-9	AGT (0.97%)	CCT (0.91%)	CTT (0.91%)	AGT (0.98%)	AGG (0.95%)	CTT (0.96%)	CTC (1.01%)	ACT (0.98%)	CCC (0.92%)
-8	CTC (0.95%)	AGT (0.89%)	GTA (0.90%)	CTC (0.97%)	CTC (0.91%)	AGT (0.89%)	AGA (0.94%)	CTT (0.97%)	GTA (0.92%)
-7	GGA (0.83%)	GAG (0.86%)	GGT (0.86%)	GAG (0.91%)	CCT (0.90%)	GGG (0.88%)	GAG (0.87%)	CCC (0.88%)	CTT (0.91%)
-6	CCC (0.82%)	CGA (0.84%)	AGG (0.85%)	GGA (0.86%)	GAG (0.89%)	CCT (0.88%)	GGA (0.81%)	CGA (0.87%)	GAG (0.84%)
-5	GAG (0.79%)	GGG (0.82%)	AGT (0.81%)	CCC (0.85%)	CGA (0.88%)	ACT (0.83%)	AGG (0.79%)	AGA (0.87%)	CGA (0.77%)
-4	AGG (0.74%)	AGA (0.76%)	GGG (0.78%)	AGG (0.73%)	GGA (0.85%)	AGG (0.81%)	CCC (0.73%)	CCT (0.86%)	AGA (0.72%)
-3	GGG (0.62%)	GGA (0.65%)	GAG (0.67%)	GGG (0.64%)	GGG (0.82%)	GAG (0.71%)	GGG (0.67%)	GGA (0.67%)	GGA (0.63%)
-2	CTA (0.50%)	TAG (0.53%)	TAG (0.39%)	CTA (0.58%)	TAG (0.54%)	TAG (0.41%)	CTA (0.56%)	CTA (0.64%)	TAG (0.46%)
-1	TAG (0.43%)	CTA (0.47%)	CTA (0.33%)	TAG (0.49%)	CTA (0.50%)	CTA (0.41%)	TAG (0.47%)	TAG (0.64%)	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 (0.99%)	TTTC (1.10%)	AAAA (1.28%)	AAAA (1.04%)	TGGC (1.03%)	AAAA (1.53%)	GGCA (0.82%)	TGGC (0.89%)	AAAA (1.06%)
2	AAAA (0.88%)	AAAA (0.93%)	TTTC (1.25%)	CAGC (0.90%)	AAAA (0.96%)	TTTT (1.12%)	ATCA (0.82%)	TTCA (0.86%)	GAAA (1.01%)
3	GAAA (0.87%)	CTGC (0.92%)	GAAA (1.15%)	TTTT (0.88%)	CAGC (0.94%)	CAAA (1.06%)	GAAA (0.81%)	CAGC (0.85%)	GGCA (0.99%)
4	CAGC (0.81%)	TGCG (0.91%)	TTTT (0.98%)	TGGC (0.81%)	CTGC (0.89%)	GAAA (1.06%)	CAAA (0.80%)	ATCA (0.80%)	TTTC (0.91%)
5	ATCA (0.80%)	TTCA (0.89%)	CAAA (0.91%)	CAAA (0.81%)	CGGC (0.85%)	TTTT (1.01%)	AACA (0.80%)	CTGC (0.79%)	TGTT (0.90%)
6	TTTT (0.80%)	TTCC (0.89%)	GGCA (0.89%)	TTTC (0.81%)	TTCC (0.84%)	GGAA (0.83%)	TTCA (0.80%)	CAAA (0.77%)	TTTT (0.87%)
7	TTCA (0.80%)	TTGC (0.89%)	GCAA (0.88%)	GAAA (0.78%)	CAAA (0.84%)	ATCA (0.82%)	TTTC (0.79%)	TGCC (0.74%)	TGAA (0.87%)
8	AACG (0.80%)	CAGC (0.88%)	TGCA (0.87%)	CTGC (0.77%)	TTGC (0.83%)	GGCA (0.81%)	TGAA (0.78%)	TTGC (0.72%)	CAAA (0.87%)
9	TTGC (0.79%)	GAAA (0.88%)	AAAT (0.87%)	CCAG (0.77%)	TTTT (0.82%)	AGAA (0.81%)	CAGC (0.76%)	TAAA (0.71%)	TGCA (0.86%)
10	TGCC (0.77%)	TGGC (0.83%)	AACG (0.82%)	ATCA (0.77%)	GAAA (0.78%)	TGAA (0.80%)	TGCA (0.76%)	TGAA (0.70%)	GGAA (0.86%)
-10	ACTA (0.12%)	CTAT (0.12%)	GGGT (0.10%)	TTAG (0.13%)	ACTA (0.12%)	CTAT (0.11%)	ACTA (0.14%)	CTAT (0.14%)	CCCT (0.12%)
-9	TAGT (0.12%)	CCCT (0.12%)	TAGT (0.10%)	AGGG (0.12%)	CTAT (0.12%)	TCTA (0.10%)	GTCC (0.14%)	ACCT (0.14%)	CTAT (0.12%)
-8	AGGG (0.12%)	TCTA (0.11%)	CGAG (0.09%)	CCCT (0.12%)	GGAC (0.11%)	TAGA (0.10%)	GGAC (0.13%)	CCCC (0.13%)	TCGA (0.11%)
-7	TCTA (0.11%)	CGGA (0.10%)	TAGA (0.09%)	GAGG (0.12%)	CTAA (0.11%)	CCCT (0.10%)	TTAG (0.13%)	CTAA (0.13%)	CGGA (0.11%)
-6	TTAG (0.10%)	GGAC (0.10%)	ACTA (0.09%)	CTAA (0.11%)	ACCT (0.10%)	ACTA (0.09%)	CTAA (0.13%)	CGGA (0.13%)	ACTA (0.10%)
-5	TAGA (0.08%)	CTAA (0.10%)	GGAC (0.08%)	TAGA (0.09%)	CCCT (0.10%)	CGAG (0.09%)	TCTA (0.12%)	CCCT (0.10%)	TCTA (0.09%)
-4	GGAC (0.08%)	TAGG (0.07%)	TCTA (0.06%)	GGAC (0.08%)	TAGA (0.09%)	GGAC (0.08%)	TAGA (0.09%)	TAGA (0.08%)	TAGG (0.06%)
-3	CCTA (0.06%)	TAGA (0.06%)	TAGG (0.06%)	CCTA (0.08%)	TAGG (0.07%)	TAGG (0.07%)	CCTA (0.07%)	CCTA (0.08%)	TAGA (0.06%)
-2	TAGG (0.06%)	CCTA (0.06%)	CCTA (0.04%)	TAGG (0.06%)	CCTA (0.06%)	CCTA (0.05%)	TAGG (0.05%)	TAGG (0.08%)	CCTA (0.04%)
-1	CTAG (0.00%)	CTAG (0.01%)	CTAG (0.01%)	CTAG (0.02%)	CTAG (0.01%)	CTAG (0.01%)	CTAG (0.02%)	CTAG (0.02%)	CTAG (0.01%)

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 (0.38%)	CAGCA (0.41%)	CAGCA (0.45%)	CAGCA (0.40%)	CTGGC (0.41%)	CAGCA (0.47%)	CAGCA (0.38%)	CTGGC (0.35%)	CAGCA (0.42%)
2	TTATC (0.34%)	GCTGC (0.34%)	GAAAA (0.42%)	CTGGC (0.33%)	CAGCA (0.40%)	GAAAA (0.42%)	CGGCA (0.30%)	CAGCA (0.34%)	TGGCA (0.38%)
3	CTGGC (0.31%)	CTGGC (0.34%)	CAAAA (0.36%)	GAAAA (0.32%)	TTTGC (0.32%)	AGAAA (0.37%)	TGGCA (0.29%)	GCAGC (0.28%)	GAAAA (0.38%)
4	CAAAA (0.30%)	GCAGC (0.33%)	TCTTC (0.35%)	CAAAA (0.31%)	CATCA (0.31%)	CAAAA (0.36%)	GCAAA (0.29%)	CATCA (0.28%)	CGGCA (0.34%)
5	CGTTT (0.29%)	TTGCC (0.32%)	AGAAA (0.35%)	TTATC (0.31%)	GCTGC (0.31%)	AAAAA (0.35%)	TCTTC (0.29%)	CGCCA (0.27%)	AGAAA (0.31%)
6	GCAGC (0.29%)	GAAAA (0.32%)	GCAAA (0.34%)	CCAGC (0.31%)	GCGGC (0.30%)	GCAAA (0.33%)	CGCCA (0.28%)	TTTCA (0.27%)	AAGAA (0.30%)
7	CGCCA (0.29%)	TTTCC (0.32%)	TTTTTC (0.32%)	TTTCT (0.29%)	CCAGC (0.29%)	ACAAA (0.33%)	TTATC (0.28%)	GCAGC (0.27%)	GCAAA (0.30%)
8	GAAAA (0.28%)	TTTGC (0.31%)	TGGCA (0.32%)	GCAAA (0.29%)	GCAGC (0.29%)	TCTTC (0.32%)	CATCA (0.27%)	CCAGC (0.26%)	GCGTT (0.30%)
9	GCAAA (0.28%)	TTTCA (0.31%)	TTATC (0.32%)	GTTTT (0.28%)	ATAAA (0.29%)	ATAAA (0.32%)	CTGGC (0.27%)	ATAAA (0.26%)	TTGTT (0.29%)
10	ATTTT (0.28%)	TTATC (0.30%)	CGTTT (0.31%)	ATTTT (0.27%)	AATCA (0.28%)	CAGAA (0.31%)	GAAAA (0.27%)	GCTGC (0.26%)	TTGCC (0.28%)
-10	TAGGG (0.01%)	CCCTA (0.01%)	TAGGT (0.01%)	GGACC (0.01%)	TAGGG (0.01%)	TAGGG (0.01%)	GGACC (0.01%)	TCCTA (0.01%)	TTAGA (0.01%)
-9	CTTAG (0.01%)	TAGGG (0.01%)	CCCTA (0.01%)	ACCTA (0.01%)	CCCTA (0.01%)	GCTAG (0.01%)	CCCTA (0.01%)	GCTAG (0.01%)	TAGGA (0.01%)
-8	GGACC (0.00%)	GCTAG (0.00%)	GCTAG (0.00%)	CCCTA (0.01%)	CTAGC (0.01%)	CCCTA (0.00%)	CTAGA (0.01%)	TAGGA (0.01%)	ACCTA (0.01%)
-7	GCTAG (0.00%)	ACTAG (0.00%)	CTAGC (0.00%)	GCTAG (0.01%)	GCTAG (0.01%)	CTAGT (0.00%)	GCTAG (0.00%)	ACTAG (0.01%)	CCCTA (0.01%)
-6	CTAGT (0.00%)	CTAGT (0.00%)	ACTAG (0.00%)	CTAGT (0.01%)	CTAGT (0.00%)	ACTAG (0.00%)	CTAGC (0.00%)	CTAGC (0.00%)	CTAGC (0.00%)
-5	CTAGC (0.00%)	CTAGC (0.00%)	CCTAG (0.00%)	CTAGA (0.00%)	ACTAG (0.00%)	CTAGC (0.00%)	CCTAG (0.00%)	CTAGT (0.00%)	CTAGT (0.00%)
-4	ACTAG (0.00%)	CCTAG (0.00%)	CTAGT (0.00%)	ACTAG (0.00%)	CTAGA (0.00%)	CTAGC (0.00%)	ACTAG (0.00%)	CTAGA (0.00%)	ACTAG (0.00%)
-3	CTAGG (0.00%)	CTAGA (0.00%)	CTAGA (0.00%)	CTAGG (0.00%)	TCTAG (0.00%)	CTAGA (0.00%)	CTAGT (0.00%)	CCTAG (0.00%)	CTAGG (0.00%)
-2	CTAGA (0.00%)	TCTAG (0.00%)	TCTAG (0.00%)	CTAGG (0.00%)	CTAGG (0.00%)	CCTAG (0.00%)	CTAGG (0.00%)	TCTAG (0.00%)	CTAGG (0.00%)
-1	CCTAG (0.00%)	CTAGG (0.00%)	CTAGG (0.00%)	CCTAG (0.00%)	CCTAG (0.00%)	TCTAG (0.00%)	TCTAG (0.00%)	CTAGG (0.00%)	TCTAG (0.00%)

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