

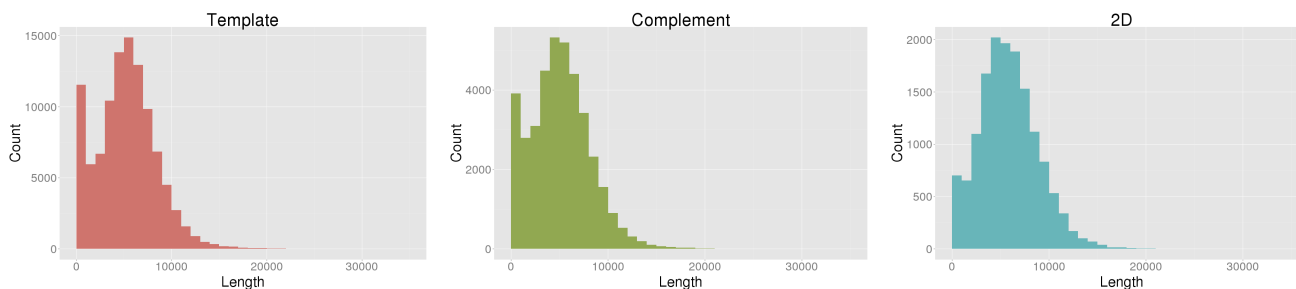
# NanoOK report for E.coli\_MARC1\_run1

## Pass and fail counts

Type	Pass	Fail
Template	0	104397
Complement	0	38840
2D	0	14806

## Read lengths

Type	NumReads	TotalBases	Mean	Longest	Shortest	N50	N50Count	N90	N90Count
Template	104397	557924013	5344.25	278106	5	6801	30481	3763	72702
Complement	38840	199249998	5130.02	55375	5	6589	11245	3459	27135
2D	14806	86850083	5865.87	43570	129	7106	4634	3819	11032



## Template alignments

Number of reads	104397
Number of reads with alignments	46157 (44.21%)
Number of reads without alignments	58240 (55.79%)

ID	Size	Number of Reads	% of Reads	Mean read length	Aligned bases	Mean coverage	Longest Perf Kmer
Control sequence	3560	0	0.00	0.00	0	0.00	0
Escherichia coli	4641652	46157	44.21	6670.13	249952362	53.85	82

## Complement alignments

Number of reads	38840
Number of reads with alignments	19805 (50.99%)
Number of reads without alignments	19035 (49.01%)

ID	Size	Number of Reads	% of Reads	Mean read length	Aligned bases	Mean coverage	Longest Perf Kmer
Control sequence	3560	0	0.00	0.00	0	0.00	0
Escherichia coli	4641652	19805	50.99	6235.84	103310301	22.26	68

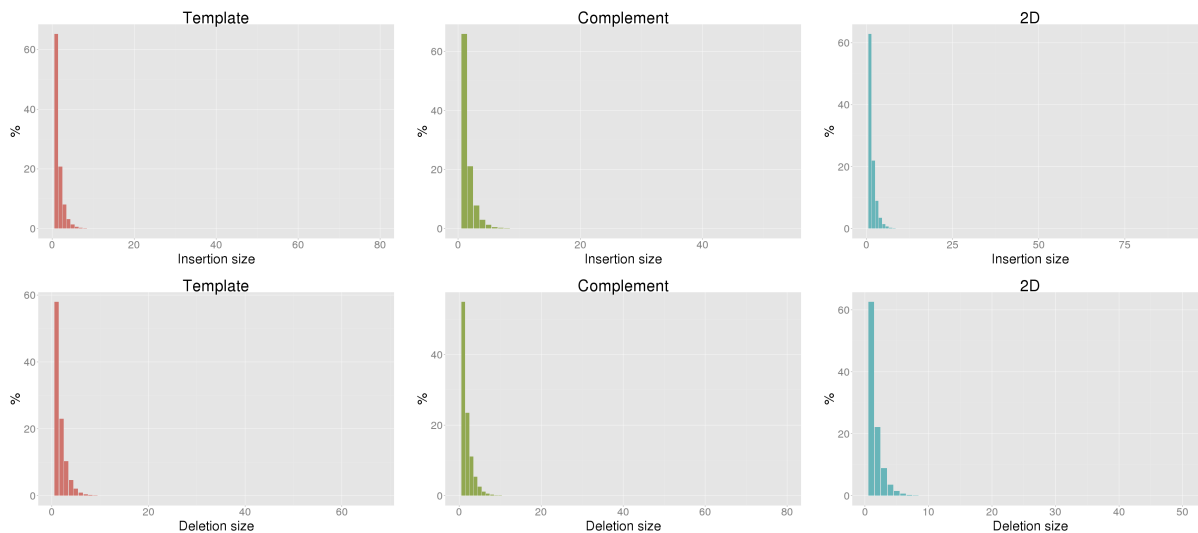
## 2D alignments

Number of reads	14806
Number of reads with alignments	11210 (75.71%)
Number of reads without alignments	3596 (24.29%)

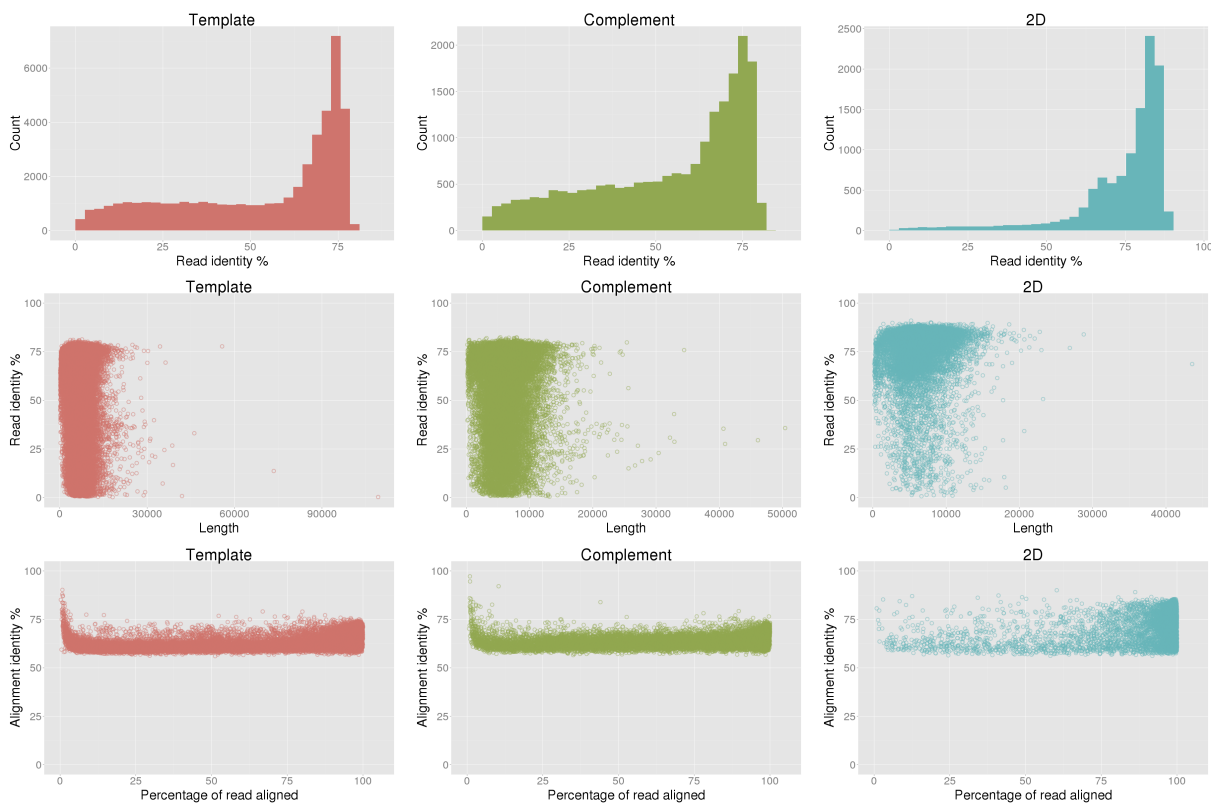
ID	Size	Number of Reads	% of Reads	Mean read length	Aligned bases	Mean coverage	Longest Perf Kmer
Control sequence	3560	0	0.00	0.00	0	0.00	0
Escherichia coli	4641652	11210	75.71	6503.27	73176474	15.77	203

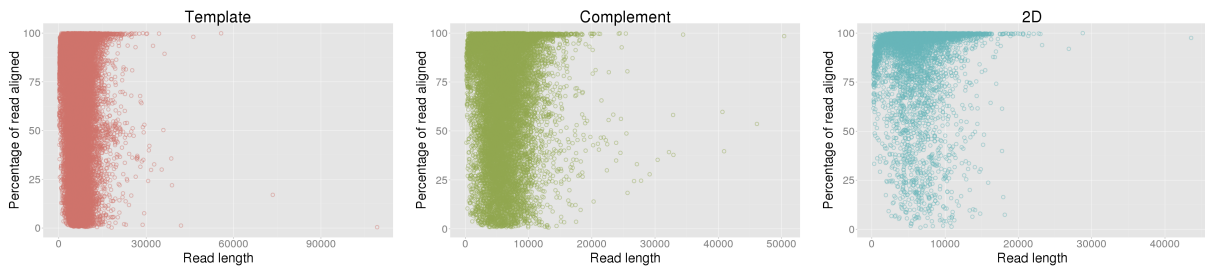
## Escherichia coli error analysis

	Template	Complement	2D
Overall base identity (excluding indels)	52.24%	53.77%	74.38%
Aligned base identity (excluding indels)	78.26%	79.49%	85.83%
Identical bases per 100 aligned bases (including indels)	64.35%	64.27%	74.10%
Inserted bases per 100 aligned bases (including indels)	5.29%	4.76%	5.99%
Deleted bases per 100 aligned bases (including indels)	12.49%	14.38%	7.68%
Substitutions per 100 aligned bases (including indels)	17.87%	16.58%	12.23%
Mean insertion size	1.61	1.57	1.64
Mean deletion size	1.77	1.88	1.64

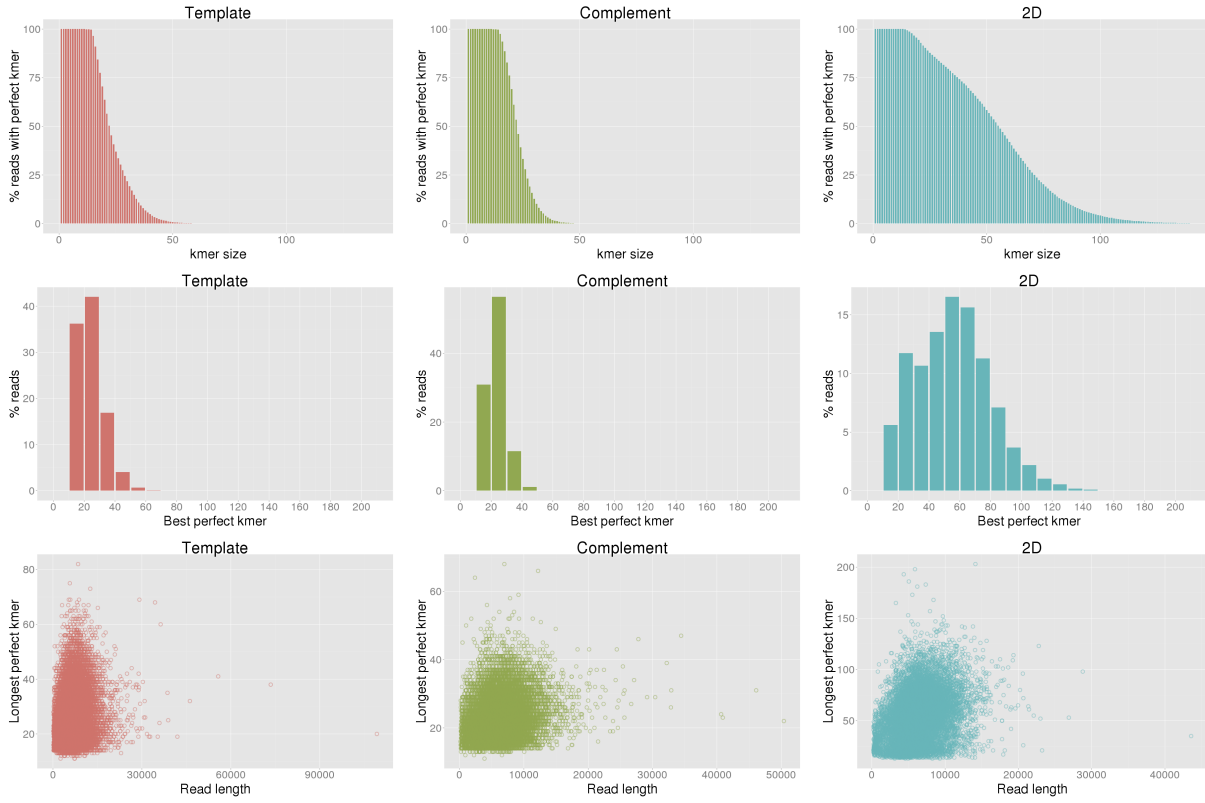


## Escherichia coli read identity

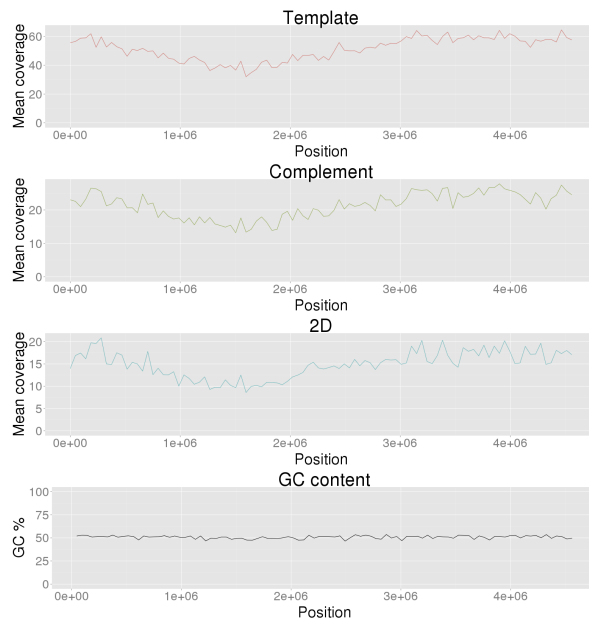




## Escherichia coli perfect kmers



## Escherichia coli coverage



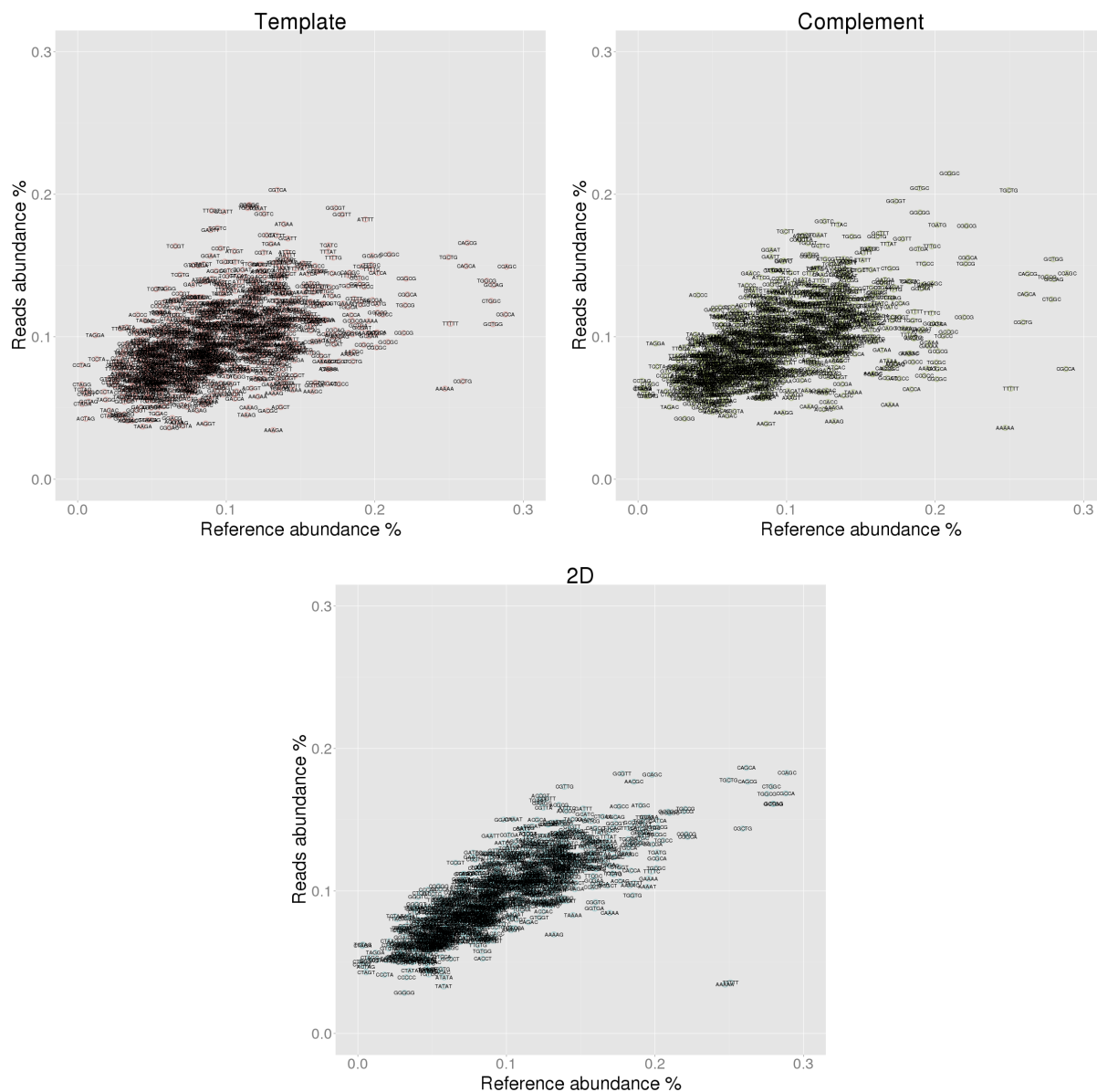
# Escherichia coli 5-mer analysis

## Under-represented 5-mers

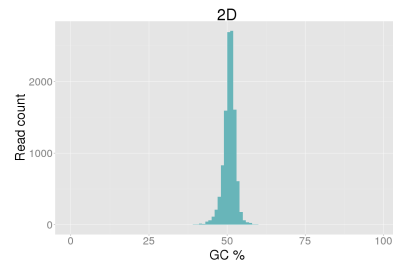
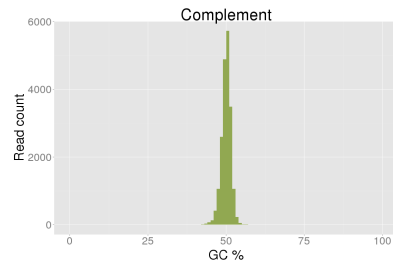
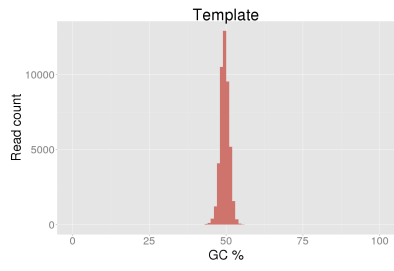
Rank	Template				Complement				2D			
	kmer	Ref %	Read %	Diff %	kmer	Ref %	Read %	Diff %	kmer	Ref %	Read %	Diff %
1	CGCTG	0.259	0.069	-0.190	AAAAA	0.247	0.036	-0.211	TTTTT	0.251	0.036	-0.215
2	AAAAA	0.247	0.064	-0.184	CGCCA	0.288	0.077	-0.211	AAAAA	0.247	0.034	-0.213
3	CGCCA	0.288	0.116	-0.172	TTTTT	0.251	0.064	-0.187	CGCCA	0.288	0.168	-0.120
4	GCTGG	0.279	0.109	-0.171	CTGGC	0.278	0.126	-0.152	GCCAG	0.280	0.161	-0.119
5	CTGGC	0.278	0.125	-0.153	CGCTG	0.259	0.110	-0.149	GCTGG	0.279	0.161	-0.118
6	GCCAG	0.280	0.136	-0.143	CCAGC	0.289	0.145	-0.144	CGCTG	0.259	0.144	-0.115
7	TTTTT	0.251	0.109	-0.142	GCCAG	0.280	0.140	-0.139	TGGCG	0.275	0.168	-0.107
8	CCAGC	0.289	0.149	-0.139	TGGCG	0.275	0.142	-0.133	CCAGC	0.289	0.183	-0.106
9	TGGCG	0.275	0.139	-0.136	CAGCA	0.261	0.130	-0.131	CTGGC	0.278	0.173	-0.105
10	CGCCG	0.219	0.103	-0.117	CGCGC	0.201	0.070	-0.131	AAAAT	0.195	0.103	-0.092

## Over-represented 5-mers

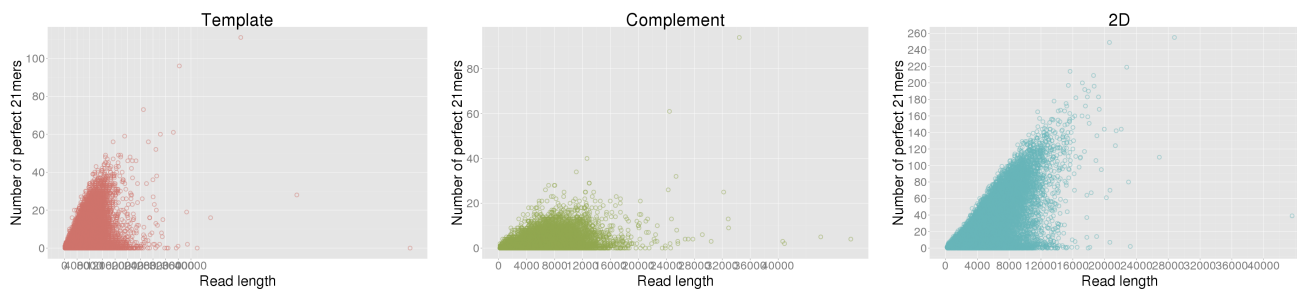
Rank	Template				Complement				2D			
	kmer	Ref %	Read %	Diff %	kmer	Ref %	Read %	Diff %	kmer	Ref %	Read %	Diff %
1	TTCGT	0.090	0.188	0.098	ACCCC	0.040	0.129	0.089	TCTAG	0.003	0.062	0.059
2	TCCGT	0.066	0.164	0.098	TAGGA	0.012	0.095	0.083	CTAGA	0.003	0.062	0.058
3	GGATT	0.098	0.188	0.090	TGCTT	0.099	0.174	0.075	TCTAA	0.025	0.082	0.057
4	TAGGA	0.012	0.101	0.089	GGAAT	0.089	0.161	0.072	CTCGT	0.042	0.099	0.056
5	GAATT	0.089	0.175	0.086	GAACC	0.075	0.145	0.069	GGGTC	0.040	0.096	0.055
6	TCGTC	0.094	0.176	0.082	GAGGC	0.051	0.119	0.068	TCCGT	0.066	0.120	0.054
7	TCGTA	0.053	0.133	0.081	GAATT	0.089	0.156	0.067	CCCAA	0.047	0.101	0.054
8	CCTAG	0.003	0.080	0.077	CCTAG	0.003	0.069	0.066	TTAGA	0.026	0.080	0.054
9	CGGGC	0.116	0.193	0.077	TCCTA	0.013	0.079	0.066	GGATT	0.098	0.150	0.052
10	TTGGA	0.029	0.106	0.077	CCCCG	0.055	0.121	0.065	TTCTA	0.036	0.088	0.051



# 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	8.38	8.74	5.30	0.00	8.62	8.78	5.43	0.00	8.44	8.73	4.84
C	8.95	0.00	8.96	9.96	9.43	0.00	8.66	9.47	9.15	0.00	10.09	9.08
G	9.47	9.00	0.00	8.68	8.93	8.77	0.00	9.06	9.00	10.15	0.00	8.76
T	5.51	8.79	8.28	0.00	5.60	8.76	8.51	0.00	4.83	8.67	8.27	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 (3.40%)	TTC (3.46%)	AAA (4.25%)	TTC (2.92%)	GCC (2.83%)	AAA (4.06%)	AAA (2.99%)	GCA (2.69%)	AAA (3.81%)
2	AAA (2.95%)	AAA (2.97%)	TTC (3.67%)	TGC (2.90%)	TGC (2.81%)	GCA (3.52%)	TTC (2.98%)	AAA (2.68%)	GCA (3.42%)
3	TGC (2.73%)	TGC (2.86%)	GCA (3.26%)	AAA (2.84%)	AAA (2.78%)	GAA (3.31%)	GCA (2.89%)	GCG (2.62%)	GAA (3.14%)
4	GCA (2.73%)	GCA (2.78%)	GAA (3.11%)	GCA (2.71%)	GCA (2.75%)	TTC (3.19%)	TGC (2.62%)	TTC (2.62%)	TTC (3.07%)
5	ATC (2.48%)	TCA (2.47%)	TGC (2.60%)	GAA (2.56%)	TTC (2.69%)	TGC (2.56%)	GAA (2.49%)	TGC (2.52%)	TTT (2.68%)
6	TCA (2.38%)	GAA (2.38%)	AAT (2.60%)	CAG (2.40%)	GAA (2.52%)	TTT (2.53%)	CGC (2.38%)	TCA (2.51%)	AAT (2.50%)
7	GAA (2.36%)	AAT (2.36%)	TTT (2.59%)	TCA (2.31%)	TCA (2.30%)	TCA (2.33%)	TCA (2.37%)	GGC (2.51%)	GCC (2.36%)
8	GCC (2.27%)	GCC (2.33%)	ATC (2.28%)	GGC (2.31%)	GCC (2.28%)	ATC (2.26%)	ATC (2.37%)	GAA (2.31%)	GTT (2.35%)
9	TTT (2.19%)	ATC (2.32%)	TCA (2.25%)	ATC (2.25%)	AAT (2.24%)	AAT (2.24%)	GCG (2.30%)	GCG (2.20%)	GCG (2.31%)
10	AAT (2.16%)	GGC (2.25%)	GCC (2.16%)	GCC (2.17%)	CAG (2.20%)	GCC (2.17%)	AAT (2.24%)	GCC (2.17%)	TGC (2.30%)
-10	TGT (1.00%)	GGG (0.91%)	GGT (0.89%)	GTG (0.96%)	AGA (0.93%)	CCC (0.92%)	CTC (1.01%)	CTC (1.01%)	ACT (0.94%)
-9	CTC (0.92%)	AGG (0.91%)	AGA (0.86%)	AGA (0.94%)	AGG (0.93%)	CTC (0.90%)	TGT (1.00%)	CGA (0.95%)	CCC (0.92%)
-8	CCC (0.85%)	CTT (0.89%)	AGT (0.84%)	GGA (0.89%)	AGT (0.91%)	AGT (0.88%)	AGA (0.83%)	ACT (0.92%)	AGG (0.91%)
-7	AGA (0.83%)	CCT (0.88%)	TGT (0.84%)	CTC (0.86%)	CCC (0.90%)	CCT (0.87%)	CCC (0.83%)	CCC (0.90%)	CGA (0.88%)
-6	GGA (0.80%)	CGA (0.86%)	AGG (0.83%)	CCC (0.82%)	CCT (0.88%)	AGG (0.78%)	GAG (0.82%)	CTT (0.87%)	CTT (0.82%)
-5	GAG (0.74%)	GAG (0.83%)	GGG (0.83%)	GAG (0.73%)	CTC (0.85%)	ACT (0.77%)	GGA (0.81%)	CCT (0.81%)	GAG (0.74%)
-4	AGG (0.73%)	AGA (0.72%)	CTT (0.81%)	AGG (0.70%)	GAG (0.84%)	GGG (0.75%)	AGG (0.78%)	AGA (0.78%)	GGA (0.69%)
-3	GGG (0.66%)	GGA (0.70%)	GAG (0.64%)	GGG (0.57%)	GGG (0.78%)	GAG (0.59%)	GGG (0.69%)	GGA (0.69%)	AGA (0.66%)
-2	CTA (0.49%)	TAG (0.49%)	TAG (0.38%)	CTA (0.51%)	CTA (0.52%)	CTA (0.44%)	CTA (0.54%)	CTA (0.63%)	TAG (0.43%)
-1	TAG (0.42%)	CTA (0.47%)	CTA (0.36%)	TAG (0.43%)	TAG (0.51%)	TAG (0.37%)	TAG (0.46%)	TAG (0.58%)	CTA (0.39%)

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 (1.05%)	TTTC (1.08%)	AAAA (1.39%)	CAGC (0.90%)	CGGC (1.03%)	AAAA (1.10%)	GAAA (0.90%)	TGGC (0.90%)	AAAA (1.10%)
2	GAAA (0.96%)	TTCA (0.99%)	TTTT (1.23%)	TTGC (0.89%)	TGGC (1.00%)	CAAA (1.10%)	TTTT (0.83%)	TTCA (0.88%)	GAAA (1.07%)
3	AAAA (0.93%)	TTCC (0.95%)	GAAA (1.22%)	CAAA (0.87%)	CAGC (0.98%)	GAAA (0.98%)	CAGC (0.81%)	CAGC (0.85%)	GGCA (1.02%)
4	TTCA (0.87%)	AAAA (0.93%)	AAAT (0.92%)	ATCA (0.86%)	TTGC (0.90%)	TGAA (0.96%)	CAAA (0.80%)	ATCA (0.77%)	TTTC (0.93%)
5	TTGC (0.85%)	TGCC (0.90%)	CAAA (0.92%)	CTGC (0.85%)	CAAA (0.85%)	GGCA (0.90%)	ATCA (0.79%)	CGGC (0.76%)	GGAA (0.90%)
6	ATCA (0.82%)	TTGC (0.89%)	GGCA (0.90%)	CGGC (0.82%)	CTGC (0.84%)	TTTC (0.90%)	AACA (0.79%)	GGCG (0.75%)	TGAA (0.86%)
7	AACG (0.81%)	GAAA (0.88%)	TTTT (0.89%)	CCAG (0.78%)	TTCC (0.82%)	AGCA (0.89%)	CGCC (0.78%)	GCCA (0.75%)	CGCC (0.85%)
8	TTTC (0.81%)	AACG (0.88%)	AACG (0.89%)	TGGC (0.77%)	ATCA (0.80%)	TAAA (0.87%)	GGCA (0.78%)	TTTT (0.75%)	CAAA (0.85%)
9	TGCC (0.81%)	CAGC (0.83%)	GTTC (0.89%)	TTTT (0.77%)	TTCA (0.79%)	ATCA (0.86%)	TTGC (0.77%)	CTGC (0.74%)	CGTT (0.84%)
10	CTTC (0.77%)	GTTC (0.83%)	TTCA (0.88%)	AAAA (0.76%)	TGCC (0.79%)	GGAA (0.85%)	AAAA (0.77%)	CAAA (0.74%)	CGCA (0.83%)
-10	TAGT (0.12%)	CTAT (0.12%)	ACTA (0.10%)	GGGG (0.11%)	TAGT (0.12%)	ACTA (0.11%)	ACTA (0.13%)	ACTT (0.15%)	TATA (0.11%)
-9	AGGG (0.12%)	CGGA (0.12%)	CGAG (0.10%)	GTGT (0.11%)	CCCC (0.12%)	GAGG (0.11%)	TTAG (0.13%)	ACCT (0.14%)	CCCT (0.11%)
-8	TTAG (0.11%)	TAGT (0.12%)	CCCT (0.10%)	CTAA (0.10%)	ACCT (0.11%)	GTGT (0.10%)	CTAT (0.13%)	CGGA (0.14%)	TCTA (0.11%)
-7	CTAA (0.11%)	GGAC (0.11%)	TAGT (0.09%)	GAGG (0.09%)	GTGT (0.11%)	CTAT (0.10%)	CCCT (0.13%)	CTAT (0.14%)	CTAT (0.11%)
-6	GAGG (0.11%)	CTAA (0.10%)	TCTA (0.08%)	GGAC (0.09%)	CTAA (0.11%)	CGAG (0.09%)	TAGT (0.13%)	CTAA (0.11%)	CTAA (0.10%)
-5	GGAC (0.10%)	CCCT (0.10%)	GGAC (0.08%)	CCCT (0.09%)	TAGA (0.10%)	GGAC (0.09%)	CTAA (0.11%)	CCCT (0.10%)	ACTA (0.10%)
-4	TAGA (0.06%)	TAGG (0.07%)	TAGA (0.07%)	TAGA (0.09%)	CCCT (0.08%)	CCCT (0.07%)	TAGA (0.08%)	TAGA (0.09%)	TAGG (0.07%)
-3	CCTA (0.06%)	TAGA (0.06%)	TAGG (0.07%)	CCTA (0.06%)	TAGG (0.07%)	TAGG (0.06%)	CCTA (0.07%)	TAGG (0.08%)	TAGA (0.06%)
-2	TAGG (0.06%)	CCTA (0.05%)	CCTA (0.05%)	TAGG (0.06%)	CCTA (0.06%)	CCTA (0.05%)	TAGG (0.06%)	CCTA (0.07%)	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 (0.34%)	CAGCA (0.36%)	GAAAA (0.41%)	CAGCA (0.39%)	CAGCA (0.44%)	CAGCA (0.54%)	CAGCA (0.36%)	CAGCA (0.36%)	CAGCA (0.44%)
2	CAAAA (0.31%)	TTGCC (0.33%)	CAGCA (0.41%)	GCTGC (0.33%)	CTGGC (0.37%)	GCAAA (0.38%)	CGCCA (0.32%)	CTGGC (0.35%)	CGGCA (0.38%)
3	ATTTT (0.30%)	TTTTG (0.32%)	CAAAA (0.41%)	CATCA (0.32%)	CGGGC (0.36%)	CGGCA (0.37%)	CTGGC (0.31%)	TGGCG (0.30%)	GAAAA (0.38%)
4	TTATC (0.30%)	CAAAA (0.30%)	GCAAA (0.35%)	GCAAA (0.31%)	CATCA (0.32%)	ATAAA (0.35%)	GCAAA (0.30%)	CGCCA (0.29%)	TGGCA (0.34%)
5	TTTTG (0.30%)	TTTCA (0.30%)	CGTTT (0.35%)	GCGGC (0.30%)	GCTGC (0.32%)	CATCA (0.34%)	CGGCA (0.29%)	CATCA (0.28%)	CAAAA (0.34%)
6	CATCA (0.30%)	CTGGC (0.30%)	TGAAA (0.33%)	CCAGC (0.30%)	CCAGC (0.31%)	AAGAA (0.33%)	GCCAG (0.28%)	GCGGC (0.28%)	GCAAA (0.32%)
7	CGTTT (0.29%)	CGTTT (0.30%)	AGAAA (0.32%)	TTTTG (0.29%)	GCAAA (0.30%)	GAAAA (0.33%)	AACGC (0.28%)	TTTTCA (0.28%)	GCGTT (0.32%)
8	GAAAA (0.29%)	TTTCC (0.30%)	TGTTT (0.31%)	CTGGC (0.29%)	TTTTG (0.30%)	ACGCA (0.32%)	TGGCG (0.28%)	CCAGC (0.27%)	TGAAA (0.30%)
9	CGCCA (0.29%)	TTCCA (0.29%)	TCTTC (0.31%)	TTGCC (0.28%)	ATAAA (0.29%)	CAAAA (0.31%)	CCAGC (0.27%)	GCCAG (0.27%)	TTGCC (0.30%)
10	CTGGC (0.28%)	CATCA (0.29%)	TTGCC (0.31%)	AACGC (0.28%)	TTGCC (0.29%)	TCTTC (0.31%)	CATCA (0.27%)	GCAAA (0.27%)	CGCCA (0.29%)
-10	CCCTA (0.01%)	GGACC (0.01%)	GGACC (0.01%)	ACCTA (0.01%)	ACCTA (0.01%)	ACCTA (0.01%)	CCCTA (0.01%)	CCCTA (0.01%)	TAGGA (0.01%)
-9	GGACC (0.01%)	CCCTA (0.01%)	CCCTA (0.01%)	CCCTA (0.01%)	CCCCC (0.01%)	CCCTA (0.01%)	TAGGA (0.01%)	TAGGA (0.01%)	CCCTA (0.01%)
-8	CTAGC (0.00%)	ACTAG (0.00%)	ACTAG (0.00%)	CTAGC (0.01%)	CTAGC (0.01%)	CTAGC (0.00%)	CTAGC (0.00%)	ACTAG (0.01%)	GCTAG (0.00%)
-7	ACTAG (0.00%)	CTAGC (0.00%)	GCTAG (0.00%)	GCTAG (0.00%)	GCTAG (0.01%)	GCTAG (0.00%)	GCTAG (0.00%)	GCTAG (0.01%)	CTAGC (0.00%)
-6	GCTAG (0.00%)	GCTAG (0.00%)	CTAGC (0.00%)	CTAGT (0.00%)	CTAGT (0.00%)	CTAGT (0.00%)	CTAGT (0.00%)	CTAGC (0.01%)	ACTAG (0.00%)
-5	CTAGT (0.00%)	CTAGT (0.00%)	CTAGG (0.00%)	ACTAG (0.00%)	ACTAG (0.00%)	ACTAG (0.00%)	ACTAG (0.00%)	CTAGT (0.00%)	CTAGT (0.00%)
-4	CCTAG (0.00%)	TCTAG (0.00%)	CTAGT (0.00%)	TCTAG (0.00%)	TCTAG (0.00%)	CTAGA (0.00%)	TCTAG (0.00%)	TCTAG (0.00%)	CTAGG (0.00%)
-3	TCTAG (0.00%)	CTAGG (0.00%)	CCTAG (0.00%)	CTAGG (0.00%)	CTAGG (0.00%)	CCTAG (0.00%)	CCTAG (0.00%)	CTAGG (0.00%)	CCTAG (0.00%)
-2	CTAGG (0.00%)	CCTAG (0.00%)	TCTAG (0.00%)	CCTAG (0.00%)	CCTAG (0.00%)	TCTAG (0.00%)	CTAGG (0.00%)	CCTAG (0.00%)	TCTAG (0.00%)
-1	CTAGA (0.00%)	CTAGA (0.00%)	CTAGA (0.00%)	CTAGA (0.00%)	CTAGA (0.00%)	CTAGG (0.00%)	CTAGA (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%