

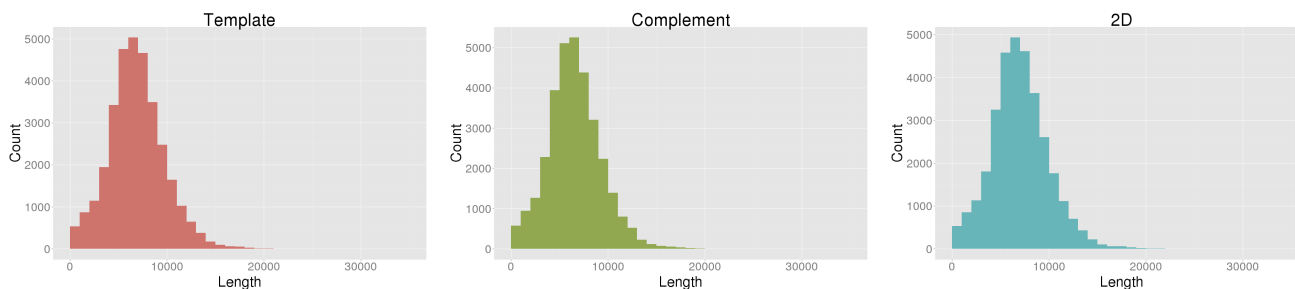
# NanoOK report for E.coli\_MARC1\_run1

## Pass and fail counts

Type	Pass	Fail
Template	32548	0
Complement	32548	0
2D	32548	0

## Read lengths

Type	NumReads	TotalBases	Mean	Longest	Shortest	N50	N50Count	N90	N90Count
Template	32548	224272172	6890.51	57820	205	7744	11264	4753	25558
Complement	32548	214089071	6577.64	56803	193	7412	11245	4534	25533
2D	32548	228371212	7016.44	58704	202	7902	11259	4844	25538



## Template alignments

Number of reads	32548
Number of reads with alignments	32178 (98.86%)
Number of reads without alignments	370 (1.14%)

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	32178	98.86	6929.06	237662440	51.20	88

## Complement alignments

Number of reads	32548
Number of reads with alignments	32127 (98.71%)
Number of reads without alignments	421 (1.29%)

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	32127	98.71	6623.09	228187036	49.16	76

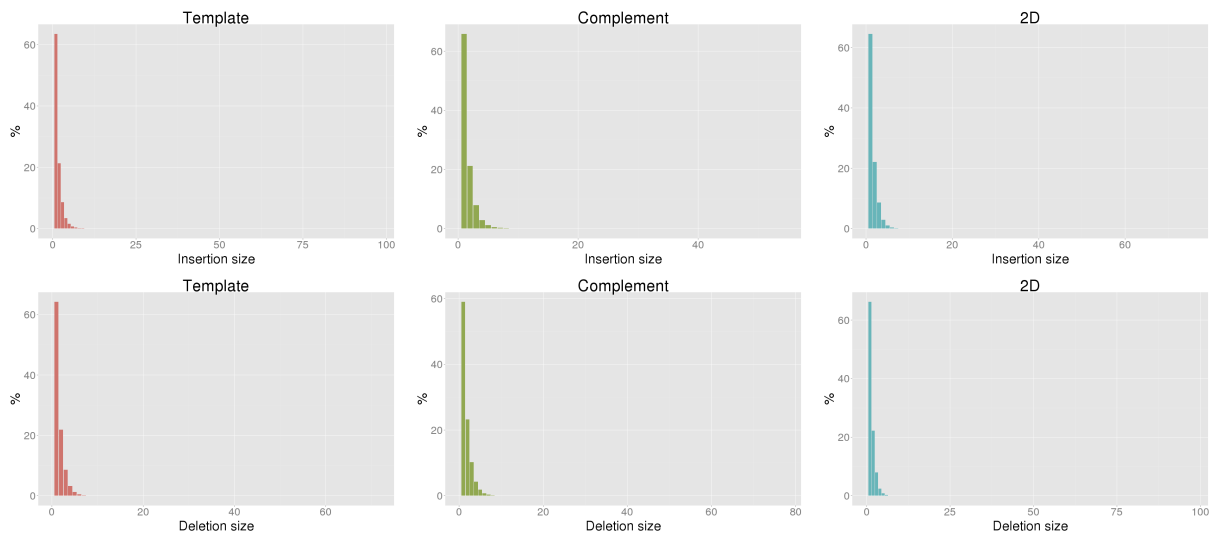
## 2D alignments

Number of reads	32548
Number of reads with alignments	32296 (99.23%)
Number of reads without alignments	252 (0.77%)

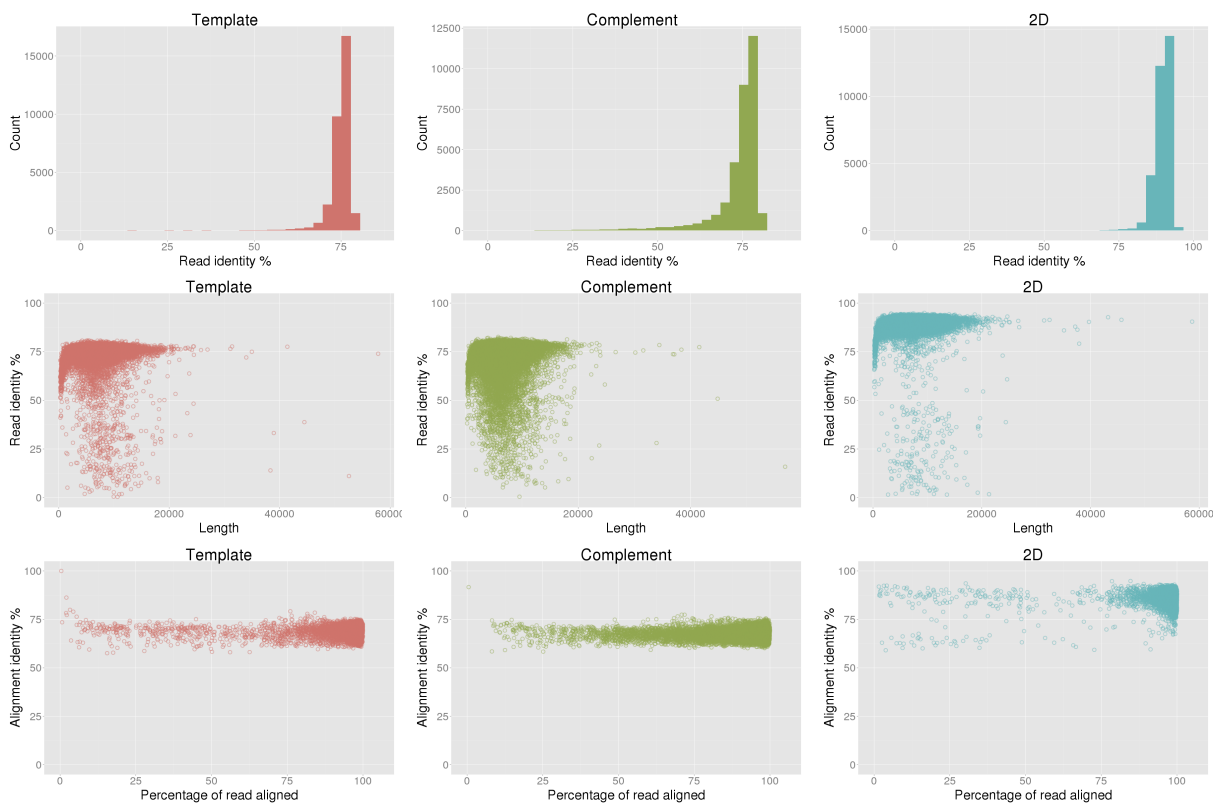
ID	Size	Number of Reads	% of Reads	Mean read length	Aligned bases	Mean coverage	Longest Perf Kmer
Control sequence	3560	0	0.00	0.00	0	0.00	0
Escherichia coli	4641652	32296	99.23	7042.14	234648897	50.55	289

## Escherichia coli error analysis

	Template	Complement	2D
Overall base identity (excluding indels)	74.26%	73.48%	89.28%
Aligned base identity (excluding indels)	81.66%	82.08%	94.36%
Identical bases per 100 aligned bases (including indels)	69.67%	68.52%	86.53%
Inserted bases per 100 aligned bases (including indels)	5.85%	4.79%	3.67%
Deleted bases per 100 aligned bases (including indels)	8.83%	11.73%	4.62%
Substitutions per 100 aligned bases (including indels)	15.65%	14.96%	5.17%
Mean insertion size	1.66	1.57	1.57
Mean deletion size	1.58	1.73	1.51

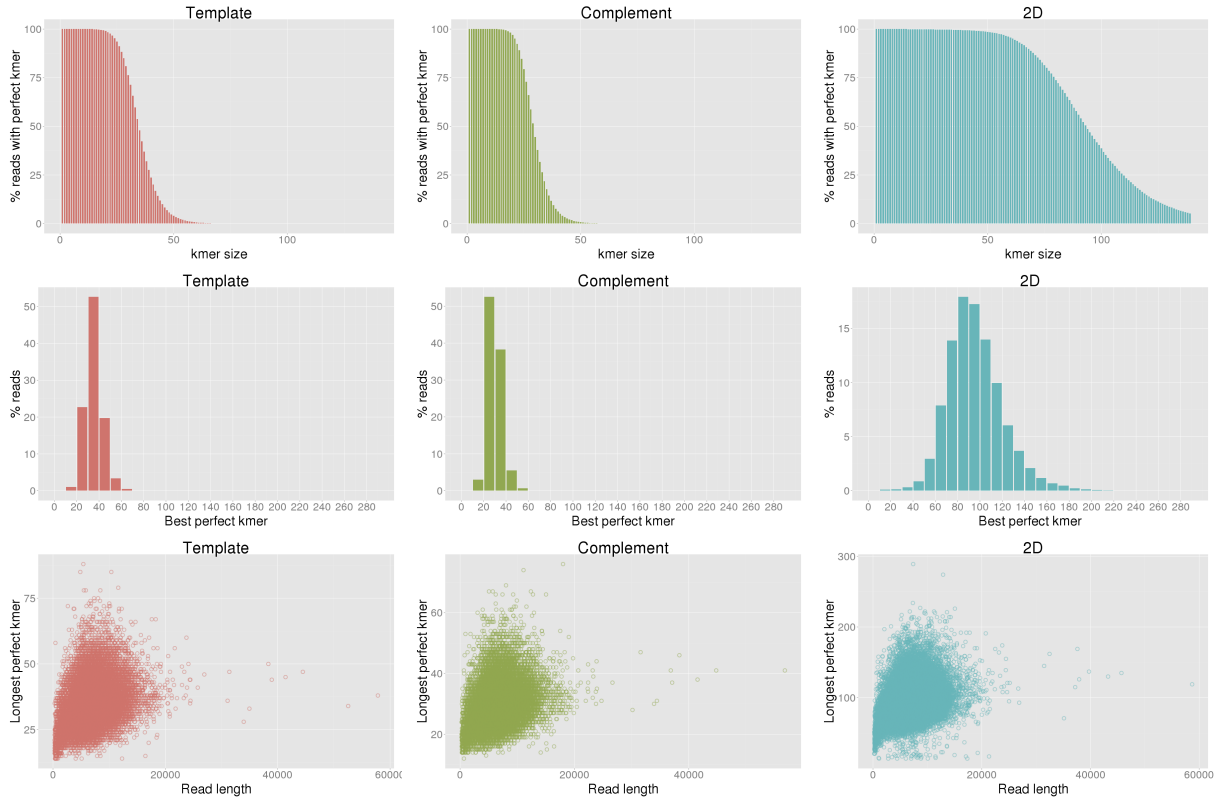


## Escherichia coli read identity

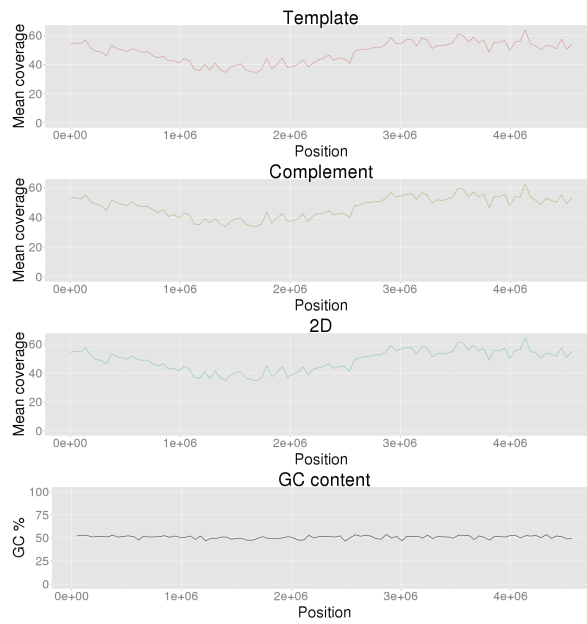




## Escherichia coli perfect kmers



## Escherichia coli coverage



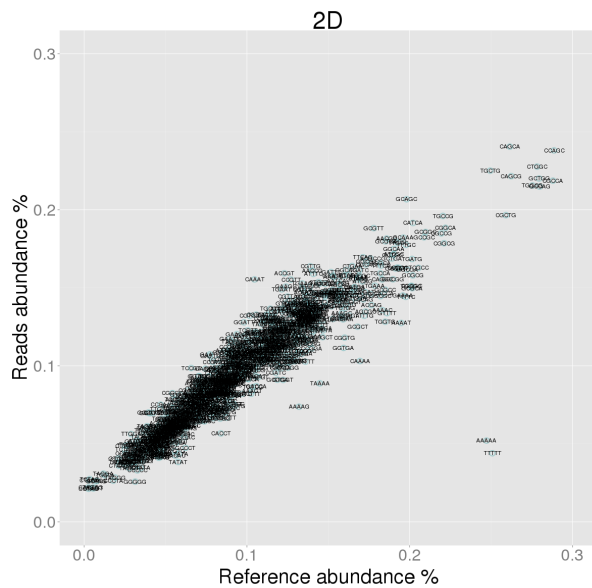
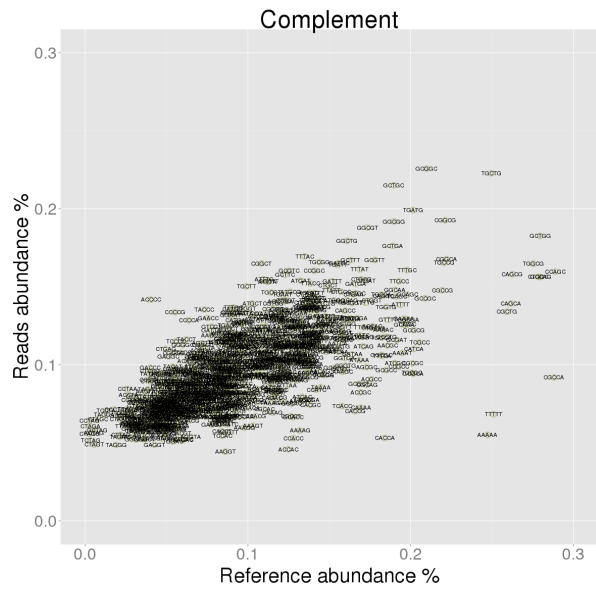
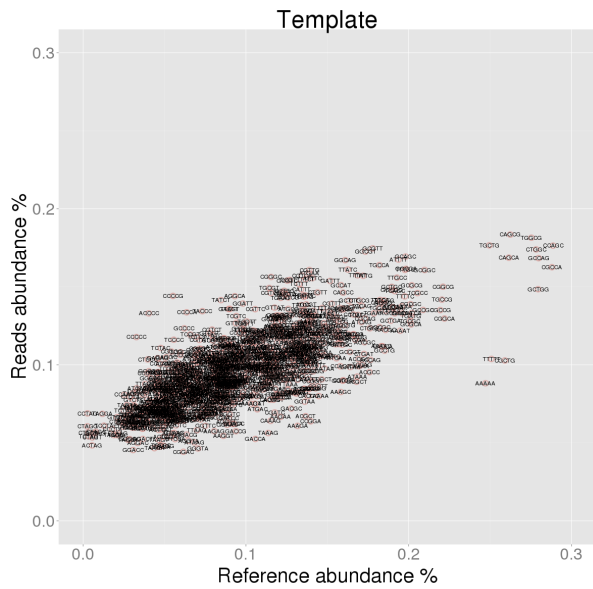
# Escherichia coli 5-mer analysis

## Under-represented 5-mers

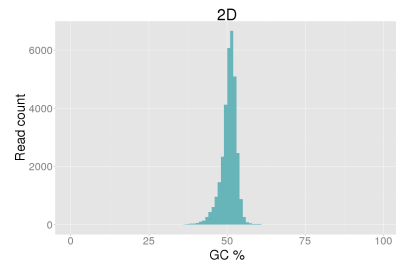
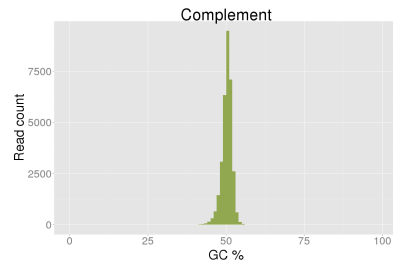
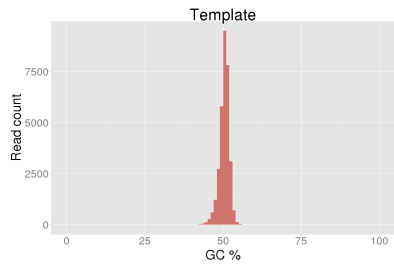
Rank	Template				Complement				2D			
	kmer	Ref %	Read %	Diff %	kmer	Ref %	Read %	Diff %	kmer	Ref %	Read %	Diff %
1	AAAAA	0.247	0.088	-0.159	CGCCA	0.288	0.092	-0.196	TTTTT	0.251	0.044	-0.207
2	CGCTG	0.259	0.103	-0.156	AAAAA	0.247	0.055	-0.192	AAAAA	0.247	0.052	-0.195
3	TTTTT	0.251	0.104	-0.147	TTTTT	0.251	0.068	-0.183	CGCCA	0.288	0.219	-0.069
4	GCTGG	0.279	0.148	-0.131	CACCA	0.184	0.053	-0.131	AAAAT	0.195	0.127	-0.067
5	CGCCA	0.288	0.163	-0.125	CCAGC	0.289	0.160	-0.129	CAAAA	0.169	0.103	-0.066
6	CCAGC	0.289	0.176	-0.112	CGCTG	0.259	0.134	-0.125	GCCAG	0.280	0.215	-0.065
7	GCCAG	0.280	0.168	-0.111	GCCAG	0.280	0.156	-0.124	CGCTG	0.259	0.197	-0.062
8	CTGGC	0.278	0.174	-0.104	CAGCA	0.261	0.139	-0.122	TGGCG	0.275	0.216	-0.060
9	TGGCG	0.275	0.182	-0.094	CTGGC	0.278	0.156	-0.122	GCTGG	0.279	0.220	-0.059
10	CAGCA	0.261	0.169	-0.093	TGGCG	0.275	0.165	-0.111	AAAAG	0.132	0.074	-0.058

## Over-represented 5-mers

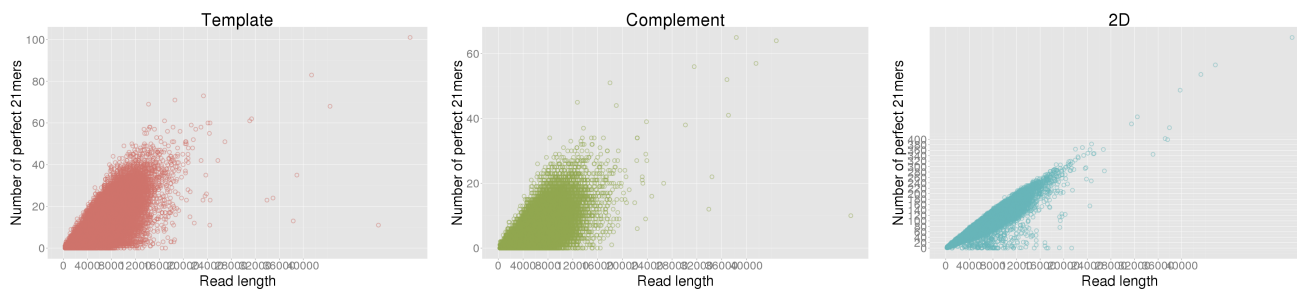
Rank	Template				Complement				2D			
	kmer	Ref %	Read %	Diff %	kmer	Ref %	Read %	Diff %	kmer	Ref %	Read %	Diff %
1	ACCCC	0.040	0.133	0.093	ACCCC	0.040	0.142	0.102	CAAAT	0.105	0.155	0.051
2	CCCCG	0.055	0.144	0.089	CCCCG	0.055	0.134	0.079	ACCGT	0.123	0.159	0.036
3	CCCCC	0.033	0.118	0.085	CCCCA	0.064	0.129	0.065	TCCGT	0.066	0.099	0.033
4	CCCCA	0.064	0.134	0.070	TACCC	0.073	0.136	0.062	GGGGT	0.039	0.070	0.031
5	CCTAG	0.003	0.069	0.066	CCTAG	0.003	0.064	0.062	CGTGA	0.102	0.132	0.030
6	CTCCC	0.040	0.104	0.064	CTGAG	0.050	0.110	0.061	GAATC	0.077	0.107	0.030
7	TCTAC	0.048	0.111	0.063	TCCCC	0.056	0.115	0.059	GGATT	0.098	0.128	0.030
8	GCCCC	0.062	0.123	0.061	CCTAA	0.026	0.085	0.059	GGGTC	0.040	0.070	0.029
9	TACCC	0.073	0.134	0.061	GACCC	0.040	0.098	0.058	GATTC	0.078	0.106	0.029
10	TCCCC	0.056	0.116	0.060	TCCTA	0.013	0.071	0.058	CCGTT	0.127	0.155	0.028



# 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	8.51	9.32	4.70	0.00	8.76	8.80	4.95	0.00	7.91	8.58	4.10
C	8.65	0.00	9.29	10.04	9.41	0.00	8.74	9.70	9.45	0.00	11.12	9.36
G	9.49	9.23	0.00	8.22	8.93	8.87	0.00	8.95	9.20	11.22	0.00	8.80
T	4.91	9.42	8.22	0.00	5.21	8.96	8.70	0.00	4.10	8.42	7.73	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 (3.24%)	TTC (3.51%)	AAA (4.07%)	TGC (2.84%)	GGC (3.05%)	AAA (3.99%)	GCA (3.09%)	GGC (2.69%)	AAA (3.92%)	Most common
2	AAA (2.82%)	TGC (3.00%)	TTC (3.77%)	GCA (2.73%)	TGC (2.84%)	GCA (3.68%)	TTC (2.75%)	GCG (2.66%)	GCA (3.70%)	
3	GCA (2.74%)	GCA (2.83%)	GCA (3.30%)	TTC (2.71%)	AAA (2.74%)	GAA (3.38%)	AAA (2.75%)	TCA (2.61%)	GAA (3.45%)	
4	TGC (2.70%)	AAA (2.62%)	GAA (3.05%)	AAA (2.64%)	GCA (2.64%)	TTC (3.10%)	TCA (2.56%)	TGC (2.50%)	TTC (2.90%)	
5	ATC (2.56%)	GCC (2.52%)	TGC (2.55%)	CAG (2.54%)	TTC (2.56%)	TGC (2.52%)	TGC (2.54%)	GCA (2.49%)	TTT (2.67%)	
6	TCA (2.48%)	TCA (2.48%)	TTT (2.45%)	GGC (2.45%)	GAA (2.35%)	TTT (2.50%)	GAA (2.47%)	AAA (2.48%)	GCC (2.50%)	
7	GCC (2.39%)	GGC (2.45%)	GCC (2.29%)	GAA (2.41%)	GCC (2.33%)	TCA (2.45%)	ATC (2.43%)	TTC (2.47%)	GCG (2.46%)	
8	GGC (2.34%)	ATC (2.30%)	AAT (2.29%)	TCA (2.35%)	TCA (2.31%)	ATC (2.35%)	CGC (2.40%)	CGC (2.30%)	AAT (2.36%)	
9	GAA (2.27%)	AAC (2.20%)	TCA (2.24%)	ATC (2.31%)	CAG (2.28%)	GCC (2.23%)	CAG (2.26%)	ATC (2.22%)	ATC (2.34%)	
10	CGC (2.22%)	GCG (2.20%)	GCC (2.20%)	GCC (2.21%)	GCG (2.27%)	GCC (2.15%)	GCG (2.25%)	CCA (2.13%)	TCA (2.27%)	
										Least common
-10	AGT (0.97%)	AGG (0.94%)	GGT (0.95%)	GTG (0.99%)	CTT (0.94%)	GTG (0.95%)	TGT (1.02%)	GAG (1.02%)	CCT (0.86%)	
-9	CCC (0.94%)	AGT (0.93%)	GGG (0.93%)	AGT (0.98%)	AGT (0.93%)	CTT (0.88%)	CTC (1.00%)	CGA (0.94%)	ACT (0.86%)	
-8	TGT (0.93%)	CCT (0.88%)	AGA (0.85%)	CTC (0.92%)	GGA (0.91%)	AGT (0.86%)	GAG (0.85%)	ACT (0.90%)	TGA (0.85%)	
-7	AGA (0.83%)	GAG (0.82%)	AGT (0.81%)	GGA (0.87%)	CCC (0.91%)	CCT (0.82%)	CCC (0.83%)	CCC (0.89%)	CGA (0.75%)	
-6	GGA (0.80%)	CTT (0.81%)	AGG (0.79%)	CCC (0.87%)	CTC (0.89%)	AGG (0.81%)	AGA (0.82%)	CTT (0.85%)	CTT (0.73%)	
-5	GAG (0.73%)	CGA (0.78%)	TGT (0.73%)	GAG (0.80%)	CCT (0.86%)	GGG (0.77%)	AGG (0.80%)	AGA (0.78%)	GAG (0.71%)	
-4	AGG (0.69%)	AGA (0.66%)	CTT (0.72%)	AGG (0.72%)	GAG (0.83%)	ACT (0.73%)	GGA (0.80%)	CCT (0.77%)	AGA (0.53%)	
-3	GGG (0.69%)	GGA (0.63%)	GAG (0.60%)	CTA (0.58%)	GGG (0.78%)	GAG (0.59%)	GGG (0.70%)	CTA (0.73%)	GGA (0.50%)	
-2	CTA (0.52%)	CTA (0.52%)	TAG (0.38%)	GGG (0.58%)	CTA (0.55%)	CTA (0.49%)	CTA (0.60%)	GGA (0.71%)	TAG (0.46%)	
-1	TAG (0.41%)	TAG (0.52%)	CTA (0.37%)	TAG (0.44%)	TAG (0.52%)	TAG (0.37%)	TAG (0.46%)	TAG (0.64%)	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 (1.00%)	TTTC (1.08%)	AAAA (1.34%)	CAGC (0.99%)	CGGC (1.09%)	AAAA (1.07%)	ATCA (0.92%)	TGGC (0.94%)	GGCA (1.15%)
2	GAAA (0.92%)	TGCC (0.97%)	TTTT (1.22%)	ATCA (0.92%)	TGGC (1.08%)	CAAA (1.04%)	CAGC (0.85%)	CAGC (0.92%)	AAAA (1.14%)
3	AAAA (0.90%)	CAGC (0.92%)	GAAA (1.18%)	CGGC (0.89%)	CAGC (1.07%)	TGAA (0.99%)	GCCA (0.84%)	TTCA (0.87%)	GAAA (1.02%)
4	ATCA (0.89%)	TTCA (0.91%)	GGCA (0.97%)	CTGC (0.87%)	CTGC (0.89%)	GAAA (0.97%)	GGCA (0.83%)	CGGC (0.83%)	TGAA (1.00%)
5	CAGC (0.88%)	TGGC (0.90%)	GTTC (0.93%)	CCAG (0.85%)	TTGC (0.87%)	ATCA (0.96%)	CGCC (0.80%)	ATCA (0.83%)	CGAA (0.94%)
6	TGCC (0.83%)	TTGC (0.87%)	GCAA (0.90%)	TGGC (0.82%)	ATCA (0.84%)	AGCA (0.95%)	CGCA (0.80%)	GGCG (0.79%)	CGCC (0.91%)
7	TTCA (0.83%)	CTGC (0.86%)	GGAA (0.89%)	TTGC (0.81%)	CAAA (0.80%)	GGCA (0.94%)	CCAG (0.77%)	CTGC (0.74%)	CGCA (0.90%)
8	TGGC (0.81%)	TTCC (0.83%)	TGCC (0.88%)	CAAA (0.77%)	TTCC (0.76%)	AGAA (0.87%)	GAAA (0.76%)	GCCA (0.74%)	TTTT (0.87%)
9	CGCC (0.80%)	GTTC (0.83%)	TTTT (0.83%)	CGCC (0.74%)	TGCC (0.75%)	CGCA (0.87%)	TGAA (0.76%)	GGCG (0.74%)	TGCC (0.86%)
10	GCCG (0.79%)	ATCA (0.82%)	TGAA (0.83%)	ATGC (0.73%)	TTCA (0.75%)	TTTT (0.87%)	AACA (0.76%)	CGCC (0.72%)	CAAA (0.85%)
-10	TAGT (0.12%)	TCTA (0.13%)	TTAG (0.11%)	AGGG (0.11%)	CCTC (0.12%)	GAGG (0.11%)	TAGT (0.14%)	ACTT (0.16%)	TCTA (0.11%)
-9	AGGG (0.12%)	CTAT (0.13%)	ACTA (0.11%)	GTGT (0.11%)	CCCC (0.12%)	ACCT (0.11%)	CCCT (0.14%)	ACCT (0.15%)	CGGA (0.11%)
-8	GAGG (0.11%)	TAGT (0.13%)	CGAG (0.10%)	GGAC (0.10%)	CTAA (0.11%)	GGAC (0.10%)	GAGG (0.14%)	CTAT (0.15%)	CCCT (0.10%)
-7	GGAC (0.11%)	CCCT (0.12%)	GGAC (0.09%)	CTAA (0.10%)	ACCT (0.11%)	GTGT (0.10%)	TCTA (0.13%)	GAGA (0.15%)	GGGA (0.10%)
-6	TTAG (0.11%)	CGGA (0.11%)	TAGT (0.09%)	TAGA (0.10%)	GTGT (0.11%)	CTAT (0.10%)	CTAT (0.13%)	CTAA (0.12%)	CTAA (0.10%)
-5	CTAA (0.10%)	CTAA (0.10%)	TCTA (0.08%)	GAGG (0.09%)	TAGA (0.10%)	CGAG (0.09%)	CTAA (0.12%)	CCCT (0.10%)	CTAT (0.10%)
-4	TAGA (0.07%)	TAGG (0.07%)	TAGA (0.07%)	CCCT (0.09%)	CCCT (0.07%)	TAGG (0.07%)	TAGA (0.08%)	TAGG (0.10%)	TAGG (0.08%)
-3	CCTA (0.06%)	TAGA (0.06%)	TAGG (0.06%)	CCTA (0.07%)	TAGG (0.07%)	CCCT (0.06%)	CCTA (0.07%)	TAGA (0.09%)	TAGA (0.05%)
-2	TAGG (0.05%)	CCTA (0.05%)	CCTA (0.04%)	TAGG (0.05%)	CCTA (0.06%)	CCTA (0.06%)	TAGG (0.06%)	CCTA (0.08%)	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%)

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 (0.35%)	CAGCA (0.38%)	CAGCA (0.43%)	CAGCA (0.42%)	CAGCA (0.42%)	CAGCA (0.57%)	CAGCA (0.39%)	CTGGC (0.38%)	CAGCA (0.46%)
2	CTGGC (0.33%)	CTGGC (0.36%)	GAAAA (0.40%)	CATCA (0.34%)	CTGGC (0.40%)	CGGCA (0.38%)	CGCCA (0.35%)	CAGCA (0.32%)	CGGCA (0.41%)
3	CGCCA (0.32%)	TTGCC (0.33%)	CAAAA (0.38%)	GCTGC (0.34%)	GCGGC (0.36%)	CATCA (0.36%)	GCGCA (0.32%)	TGGCG (0.30%)	GAAAA (0.37%)
4	CATCA (0.32%)	CGCCA (0.32%)	CGTTC (0.34%)	CCAGC (0.33%)	CCAGC (0.34%)	ATAAA (0.35%)	CTGGC (0.30%)	GCGGC (0.30%)	TGGCA (0.37%)
5	CCAGC (0.30%)	CATCA (0.31%)	GCAAA (0.33%)	GCGGC (0.31%)	CATCA (0.33%)	GCAAA (0.34%)	CATCA (0.29%)	CCAGC (0.30%)	CAAAA (0.32%)
6	TTATC (0.29%)	TTTTGC (0.31%)	TGTTT (0.33%)	CTGGC (0.31%)	TCAGC (0.32%)	CAGAA (0.33%)	CCAGC (0.29%)	CGCCA (0.30%)	GCAAA (0.31%)
7	CAAAA (0.29%)	GCTGC (0.31%)	GCCAG (0.33%)	GCAGC (0.29%)	GCTGC (0.32%)	GAAAA (0.32%)	GCCAG (0.29%)	CATCA (0.29%)	TTGCC (0.31%)
8	GCAGC (0.29%)	CCAGC (0.30%)	TGGCA (0.32%)	CGGCA (0.28%)	AATCA (0.30%)	AAGAA (0.32%)	GCAAA (0.29%)	TTTTT (0.27%)	GCGAA (0.30%)
9	ATTTT (0.28%)	TTTTCA (0.30%)	CGCCA (0.31%)	GCCAG (0.28%)	TTTTGC (0.29%)	ACGCA (0.32%)	GCGCA (0.27%)	CAGCG (0.27%)	CGCCA (0.30%)
10	GCCAG (0.28%)	CGTTC (0.29%)	TGAAA (0.31%)	TTATC (0.27%)	ATAAA (0.29%)	TGGCA (0.31%)	TGGCA (0.27%)	ATAAA (0.27%)	GCGCA (0.29%)
-10	TAGGA (0.01%)	CCCTA (0.01%)	ACCTA (0.01%)	ACCTA (0.01%)	CCCTA (0.01%)	ACCTA (0.01%)	CCCTA (0.01%)	TCCTA (0.01%)	CCCTA (0.01%)
-9	GGACC (0.01%)	TAGGA (0.01%)	CCCTA (0.01%)	CCCTA (0.01%)	CCCCC (0.01%)	CCCTT (0.01%)	TAGGA (0.01%)	TAGGA (0.01%)	TAGGA (0.01%)
-8	CTAGC (0.00%)	GCTAG (0.00%)	ACTAG (0.00%)	CTAGC (0.01%)	CTAGC (0.01%)	CTAGC (0.01%)	CTAGC (0.00%)	GCTAG (0.01%)	CTAGC (0.01%)
-7	ACTAG (0.00%)	ACTAG (0.00%)	GCTAG (0.00%)	CTAGT (0.00%)	GCTAG (0.01%)	GCTAG (0.00%)	CTAGT (0.00%)	CTAGC (0.01%)	GCTAG (0.00%)
-6	GCTAG (0.00%)	CTAGC (0.00%)	CTAGC (0.00%)	GCTAG (0.00%)	CTAGT (0.00%)	CTAGT (0.00%)	GCTAG (0.00%)	ACTAG (0.01%)	ACTAG (0.00%)
-5	CTAGT (0.00%)	CTAGT (0.00%)	CTAGT (0.00%)	ACTAG (0.00%)	ACTAG (0.00%)	ACTAG (0.00%)	ACTAG (0.00%)	CTAGT (0.00%)	CTAGT (0.00%)
-4	CTAGG (0.00%)	TCTAG (0.00%)	CTAGG (0.00%)	TCTAG (0.00%)	TCTAG (0.00%)	CTAGG (0.00%)	CCTAG (0.00%)	CTAGG (0.00%)	CTAGG (0.00%)
-3	CTAGA (0.00%)	CTAGG (0.00%)	TCTAG (0.00%)	CTAGG (0.00%)	CTAGA (0.00%)	CTAGA (0.00%)	TCTAG (0.00%)	TCTAG (0.00%)	TCTAG (0.00%)
-2	TCTAG (0.00%)	CCTAG (0.00%)	CCTAG (0.00%)	CCTAG (0.00%)	CCTAG (0.00%)	TCTAG (0.00%)	CTAGA (0.00%)	CTAGA (0.00%)	CCTAG (0.00%)
-1	CCTAG (0.00%)	CTAGA (0.00%)	CTAGA (0.00%)	CTAGA (0.00%)	CTAGG (0.00%)	CCTAG (0.00%)	CTAGG (0.00%)	CCTAG (0.00%)	CTAGA (0.00%)

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