NanoOK report for MARC_1b_050814

Pass and fail counts

Type	Pass	Fail
Template	28054	0
Complement	28054	0
2D	28054	0

Read lengths

Type	NumReads	TotalBases	Mean	Longest	Shortest	N50	N50Count	N90	N90Count
Template	28054	193432694	6895.01	45876	187	8498	8638	4851	20202
Complement	28054	204487736	7289.08	48321	211	8995	8644	5140	20215
2D	28054	206510441	7361.18	47741	202	9077	8649	5192	20208
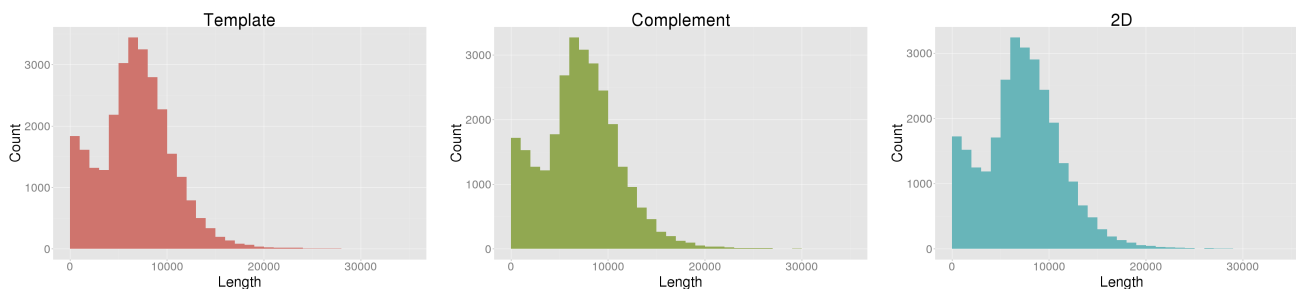
Template alignments

Number of reads	28054	
Number of reads with alignments	27077	(96.52%)
Number of reads without alignments	977	(3.48%)

ID	Size	Number of Reads	% of Reads	Mean read length	Aligned bases	Mean coverage	Longest Perf Kmer
Control sequence	3560	2	0.01	2363.50	5263	1.48	29
Escherichia coli	4641652	27075	96.51	7116.41	211762870	45.62	70

Complement alignments

Number of reads	28054	
Number of reads with alignments	27434	(97.79%)
Number of reads without alignments	620	(2.21%)

ID	Size	Number of Reads	% of Reads	Mean read length	Aligned bases	Mean coverage	Longest Perf Kmer
Control sequence	3560	3	0.01	2840.67	8971	2.52	24
Escherichia coli	4641652	27431	97.78	7439.85	216029166	46.54	64

2D alignments

Number of reads	28054	
Number of reads with alignments	28048	(99.98%)
Number of reads without alignments	6	(0.02%)

ID	Size	Number of Reads	% of Reads	Mean read length	Aligned bases	Mean coverage	Longest Perf Kmer
Control sequence	3560	3	0.01	2768.67	8901	2.50	63
Escherichia coli	4641652	28045	99.97	7361.47	216476115	46.64	281

Escherichia coli error analysis

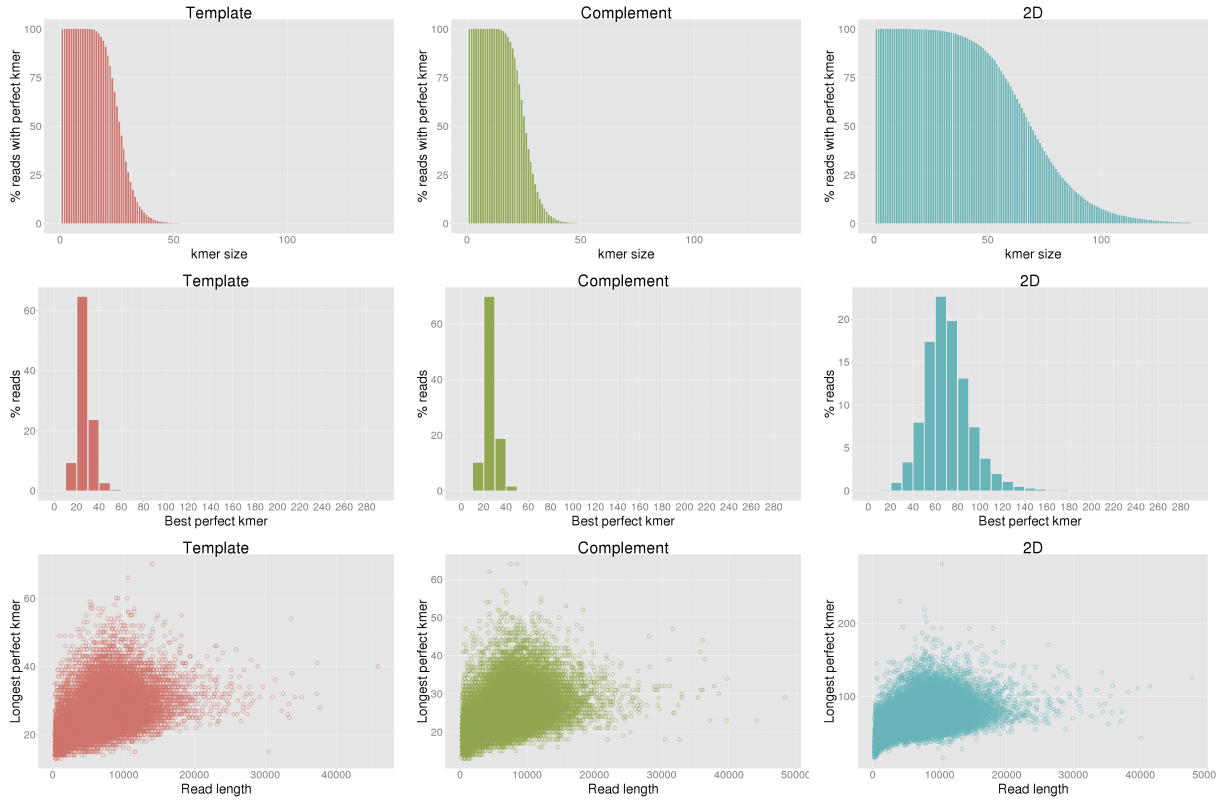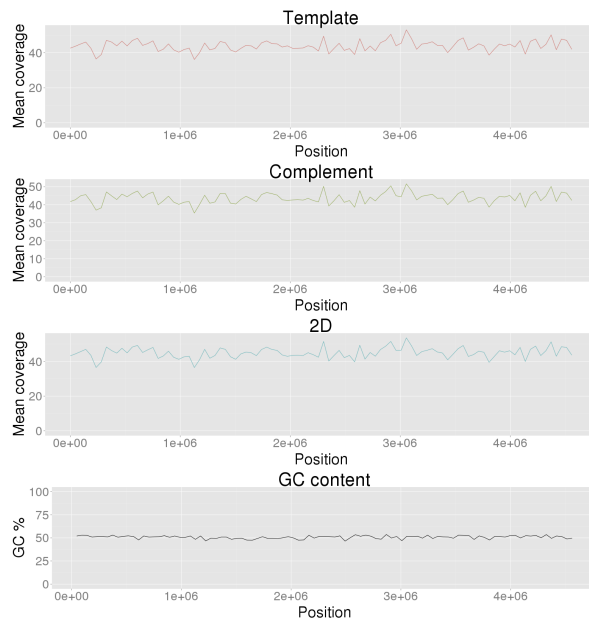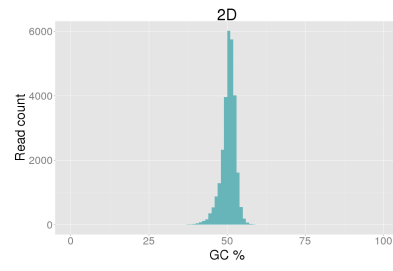|	Template	Complement	2D
Overall base identity (excluding indels)	72.27%	70.71%	87.58%
Aligned base identity (excluding indels)	78.43%	79.84%	92.33%
Identical bases per 100 aligned bases (including indels)	65.76%	66.80%	83.53%
Inserted bases per 100 aligned bases (including indels)	3.81%	6.47%	3.66%
Deleted bases per 100 aligned bases (including indels)	12.35%	9.86%	5.87%
Substitutions per 100 aligned bases (including indels)	18.09%	16.86%	6.94%
Mean insertion size	1.46	1.63	1.49
Mean deletion size	1.62	1.60	1.47
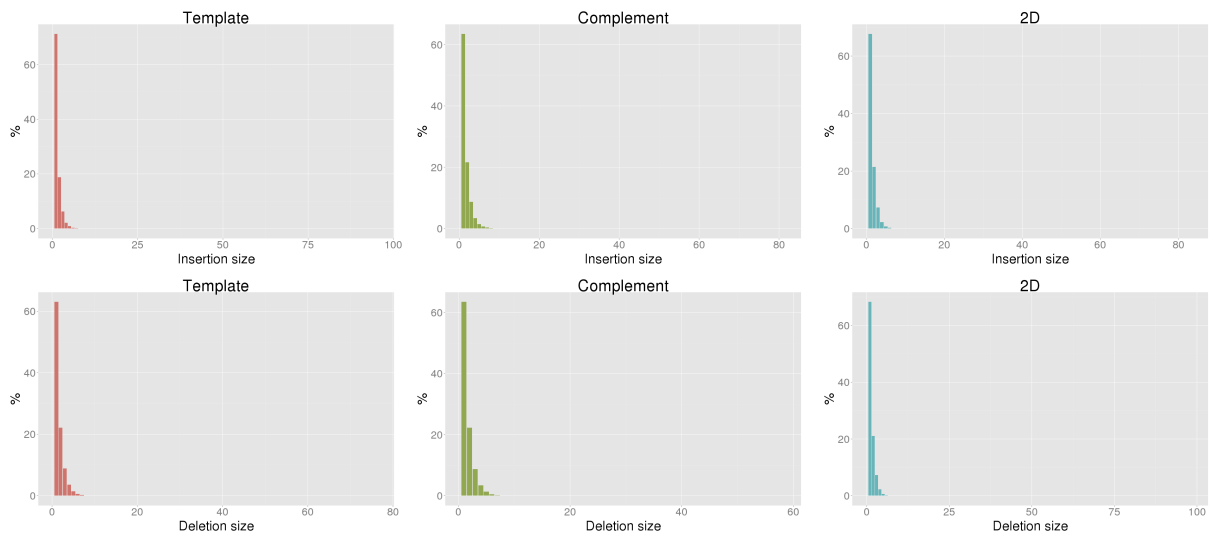
Escherichia coli read identity
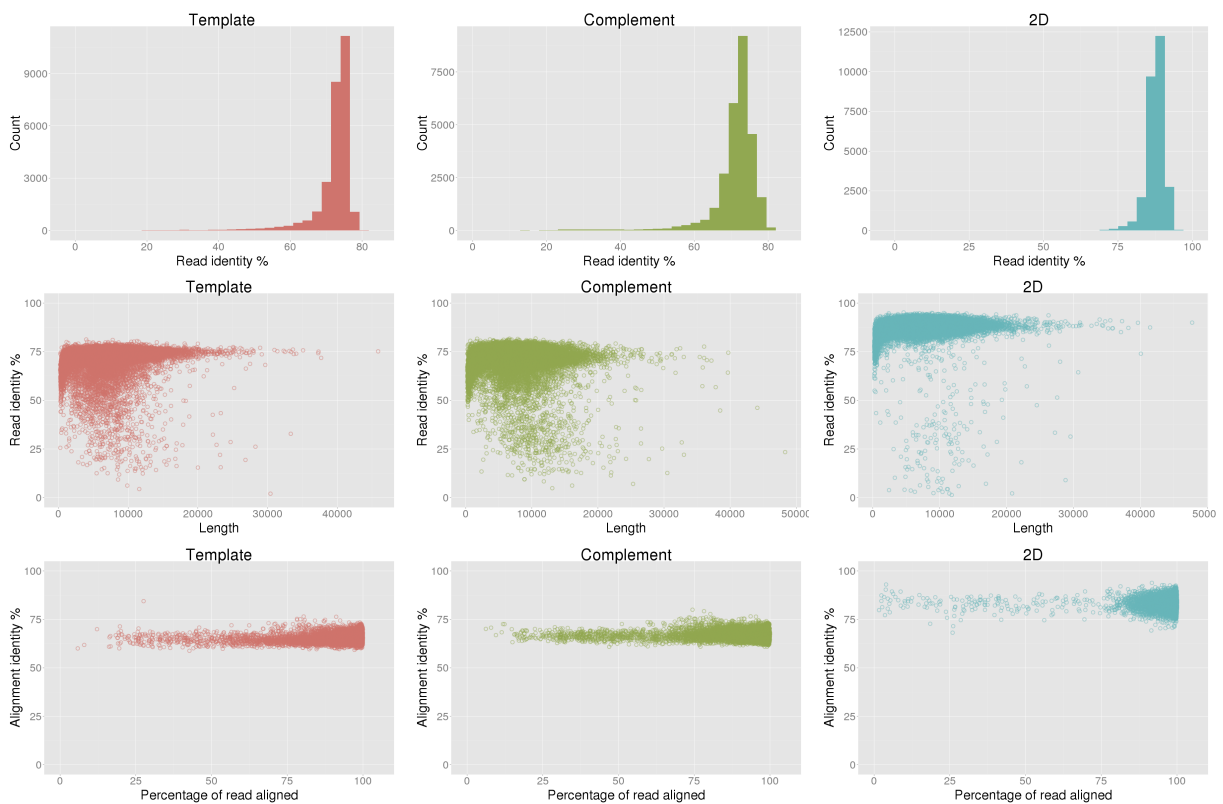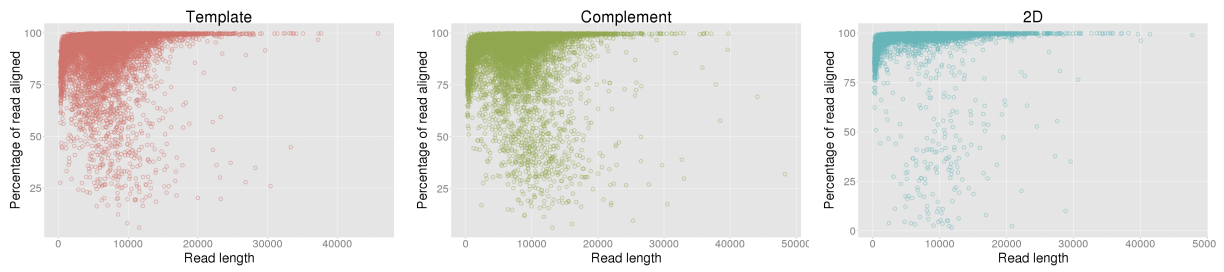
Escherichia coli perfect kmers

Escherichia coli coverage

Escherichia coli 5-mer analysis

Under-represented 5-mers

	Template				Complement				2D		
Rank	kmer	Ref %	Read %	Diff %	kmer	Ref %	Read %	Diff %	kmer	Ref %	Read %	Diff %
1	AAAAA	0.247	0.073	-0.174	CGCCA	0.288	0.111	-0.177	TTTTT	0.251	0.051	-0.200
2	CGCTG	0.259	0.099	-0.160	AAAAA	0.247	0.101	-0.146	AAAAA	0.247	0.052	-0.195
3	TTTTT	0.251	0.104	-0.147	CGCTG	0.259	0.126	-0.133	CGCCA	0.288	0.207	-0.081
4	GCTGG	0.279	0.133	-0.147	CACCA	0.184	0.052	-0.132	TGGCG	0.275	0.200	-0.076
5	CGCCA	0.288	0.144	-0.144	CCAGC	0.289	0.158	-0.131	GCTGG	0.279	0.205	-0.074
6	GCCAG	0.280	0.148	-0.132	CAGCA	0.261	0.132	-0.129	GCCAG	0.280	0.208	-0.071
7	CTGGC	0.278	0.163	-0.116	CTGGC	0.278	0.156	-0.123	AAAAT	0.195	0.124	-0.070
8	TGGCG	0.275	0.161	-0.115	TTTTT	0.251	0.129	-0.122	TGGTG	0.185	0.117	-0.068
9	CCAGC	0.289	0.175	-0.113	GCCAG	0.280	0.160	-0.119	CCAGC	0.289	0.224	-0.065
10	CGCCG	0.219	0.116	-0.103	TGGCG	0.275	0.159	-0.116	CAAAA	0.169	0.107	-0.063

Over-represented 5-mers

	Template				Complement				2D		
Rank	kmer	Ref %	Read %	Diff %	kmer	Ref %	Read %	Diff %	kmer	Ref %	Read %	Diff %
1	CCCCG	0.055	0.141	0.086	ACCCC	0.040	0.196	0.155	CAAAT	0.105	0.157	0.053
2	ACCCC	0.040	0.125	0.085	CCCCG	0.055	0.190	0.135	CTCGT	0.042	0.084	0.042
3	CCCCC	0.033	0.113	0.080	GAGAG	0.046	0.165	0.119	GGGGT	0.039	0.080	0.041
4	CTCCC	0.040	0.117	0.078	CCCCA	0.064	0.171	0.108	CCCAA	0.047	0.086	0.039
5	CCCCA	0.064	0.140	0.076	AGAGA	0.071	0.174	0.103	CGGGG	0.054	0.091	0.036
6	TCGTA	0.053	0.127	0.074	TACCC	0.073	0.166	0.093	TCTAG	0.003	0.038	0.034
7	TCCCC	0.056	0.125	0.069	CTCTC	0.046	0.138	0.092	GGTAC	0.070	0.104	0.034
8	TATCT	0.085	0.153	0.068	TCCCC	0.056	0.146	0.090	GCCCC	0.062	0.096	0.034
9	TCTAC	0.048	0.115	0.067	CCCCC	0.033	0.120	0.087	TCGTA	0.053	0.085	0.033
10	CGTAT	0.071	0.139	0.067	CTAGC	0.008	0.086	0.078	CTAGA	0.003	0.036	0.033

Escherichia coli GC content
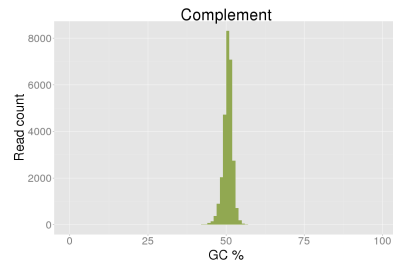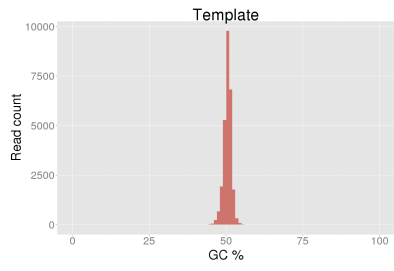
All reference 21mer analysis
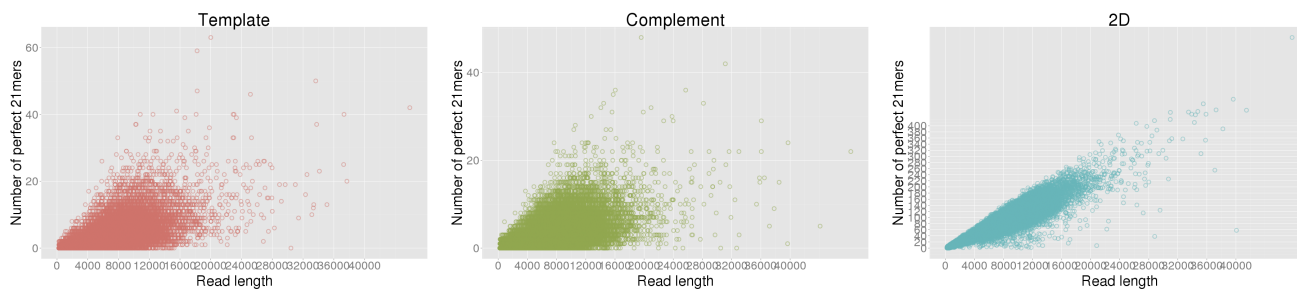
All reference substitutions

		Template substituted %				Complement substituted %				2D substituted %			
		a	c	g	t	a	c	g	t	a	c	g	t
Reference	A	0.00	9.10	9.18	4.54	0.00	9.28	8.53	4.94	0.00	8.60	8.50	3.73
	C	8.47	0.00	9.33	9.83	8.97	0.00	9.08	9.48	9.08	0.00	11.50	9.14
	G	9.30	9.31	0.00	8.19	8.91	9.15	0.00	8.61	9.01	11.69	0.00	8.50
	T	4.93	9.04	8.77	0.00	5.13	8.74	9.18	0.00	3.77	8.17	8.32	0.00

Kmer motifs before errors

3-mer error motif analysis

		Template			Complement			2D			
Rank	Insertion	Deletion	Substitution	Insertion	Deletion	Substitution	Insertion	Deletion	Substitution	
1	TTC (3.09%)	TTC (3.39%)	AAA (3.91%)	AAA (2.77%)	GGC (3.04%)	AAA (4.29%)	GCA (3.19%)	GGC (2.69%)	GCA (3.68%)	Most common
2	GCA (2.96%)	TGC (3.12%)	TTC (3.74%)	GCA (2.70%)	AAA (2.93%)	GCA (3.41%)	TTC (2.76%)	TCA (2.60%)	AAA (3.60%)	
3	AAA (2.66%)	GCA (2.97%)	GCA (3.37%)	TTC (2.58%)	TGC (2.81%)	GAA (3.11%)	TCA (2.63%)	AAA (2.58%)	GAA (3.21%)	
4	TGC (2.55%)	AAA (2.80%)	GAA (2.97%)	TGC (2.55%)	GCA (2.67%)	TTC (3.00%)	AAA (2.52%)	GCA (2.58%)	TTT (2.96%)	
5	ATC (2.49%)	GCC (2.53%)	TTT (2.72%)	CAG (2.48%)	TTC (2.53%)	TTT (2.99%)	ATC (2.43%)	TGC (2.58%)	TTC (2.87%)	
6	TCA (2.32%)	GGC (2.36%)	TGC (2.63%)	GGC (2.41%)	GCC (2.36%)	TGC (2.30%)	TGC (2.34%)	GCG (2.54%)	GTT (2.49%)	
7	GCC (2.27%)	TCA (2.32%)	AAT (2.24%)	TTT (2.30%)	GAA (2.34%)	TCA (2.29%)	GAA (2.31%)	TTC (2.37%)	GCC (2.32%)	
8	GGC (2.26%)	GAA (2.21%)	GCT (2.19%)	GAA (2.26%)	CAG (2.34%)	GCC (2.18%)	CAG (2.22%)	CAG (2.27%)	TCA (2.30%)	
9	GAA (2.18%)	AAC (2.16%)	GCC (2.17%)	GCC (2.21%)	TCA (2.25%)	ATC (2.15%)	GCG (2.19%)	CGC (2.20%)	AAT (2.26%)	
10	GCT (2.13%)	GCG (2.15%)	TCA (2.11%)	ATC (2.20%)	GCG (2.21%)	CAA (2.06%)	CGC (2.09%)	GCC (2.15%)	GCG (2.25%)	
-10	AGT (0.98%)	GGG (0.89%)	GTA (0.93%)	TAC (1.07%)	CGA (0.93%)	CTC (0.97%)	CTT (1.08%)	GTA (0.98%)	GTA (0.91%)	Least common
-9	CTC (0.96%)	CTT (0.88%)	GGT (0.92%)	AGT (0.98%)	CTT (0.93%)	CTT (0.94%)	CTC (1.04%)	ACT (0.93%)	CCT (0.89%)	
-8	AGA (0.93%)	AGT (0.88%)	TGT (0.90%)	CTC (0.96%)	CCC (0.92%)	AGT (0.87%)	GAG (0.90%)	CGA (0.91%)	TGA (0.81%)	
-7	GGA (0.86%)	CCT (0.86%)	CTT (0.86%)	CCC (0.90%)	GGA (0.89%)	GGG (0.86%)	AGA (0.87%)	CTT (0.87%)	CTT (0.80%)	
-6	CCC (0.84%)	GAG (0.84%)	GGG (0.84%)	GGA (0.90%)	CTC (0.88%)	CCT (0.85%)	AGG (0.82%)	CCC (0.87%)	GAG (0.79%)	
-5	GAG (0.74%)	CGA (0.84%)	AGG (0.81%)	GAG (0.86%)	CCT (0.87%)	AGG (0.85%)	GGA (0.79%)	AGA (0.82%)	CGA (0.69%)	
-4	AGG (0.69%)	AGA (0.71%)	AGT (0.79%)	AGG (0.70%)	GAG (0.86%)	ACT (0.77%)	CCC (0.76%)	CCT (0.75%)	AGA (0.57%)	
-3	GGG (0.64%)	GGA (0.62%)	GAG (0.63%)	GGG (0.62%)	GGG (0.81%)	GAG (0.67%)	GGG (0.71%)	CTA (0.72%)	TAG (0.51%)	
-2	CTA (0.49%)	TAG (0.51%)	TAG (0.37%)	CTA (0.58%)	CTA (0.53%)	CTA (0.44%)	CTA (0.61%)	GGA (0.68%)	GGA (0.47%)	
-1	TAG (0.38%)	CTA (0.50%)	CTA (0.33%)	TAG (0.43%)	TAG (0.52%)	TAG (0.39%)	TAG (0.46%)	TAG (0.67%)	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 (1.10%)	TTTC (1.30%)	CAGC (0.97%)	TGGC (1.14%)	AAAA (1.38%)	ATCA (0.94%)	TGGC (1.00%)	GGCA (1.18%)	Most common
2	CAGC (0.86%)	TGCC (0.96%)	AAAA (1.29%)	AAAA (0.89%)	CGGC (1.05%)	TTTT (1.08%)	GGCA (0.91%)	CAGC (0.91%)	AAAA (1.04%)	
3	GAAA (0.86%)	CAGC (0.94%)	GAAA (1.13%)	TGGC (0.89%)	CAGC (1.03%)	GAAA (1.04%)	GCCA (0.82%)	TTCA (0.87%)	TTTT (0.95%)	
4	TGGC (0.85%)	CTGC (0.94%)	GGCA (0.96%)	CCAG (0.84%)	AAAA (0.93%)	CAAA (0.98%)	CAGC (0.80%)	CGGC (0.83%)	GAAA (0.94%)	
5	AAAA (0.84%)	TGGC (0.93%)	TTTT (0.93%)	ATCA (0.83%)	CTGC (0.92%)	TTTC (0.96%)	AACA (0.79%)	ATCA (0.83%)	TGAA (0.92%)	
6	ATCA (0.82%)	TTGC (0.93%)	GGAA (0.89%)	CGGC (0.81%)	TTGC (0.84%)	GGCA (0.91%)	TTCA (0.77%)	CTGC (0.81%)	GGAA (0.90%)	
7	GGCA (0.81%)	AAAA (0.90%)	GCAA (0.88%)	CTGC (0.81%)	ATCA (0.80%)	ATCA (0.87%)	CGCA (0.76%)	TGCC (0.73%)	TTTC (0.87%)	
8	TGCC (0.79%)	TTCC (0.85%)	GTTC (0.87%)	TTTT (0.80%)	CCAG (0.79%)	AGCA (0.86%)	CTTC (0.75%)	GGCG (0.73%)	TGCA (0.85%)	
9	TTCT (0.78%)	TTCA (0.85%)	CTTC (0.84%)	CGCC (0.77%)	CTGG (0.78%)	TGAA (0.85%)	TTTC (0.74%)	GCCA (0.73%)	CGCA (0.82%)	
10	TTCA (0.77%)	GAAA (0.83%)	CAAA (0.84%)	TTTC (0.74%)	CGCC (0.78%)	AGAA (0.83%)	TGCA (0.73%)	CCAG (0.72%)	CGTT (0.82%)	
-10	ACTA (0.12%)	TCTA (0.12%)	CGAG (0.10%)	AGGG (0.13%)	ACTA (0.13%)	ACCT (0.11%)	TAGT (0.14%)	CCCC (0.15%)	TCTA (0.10%)	Least common
-9	TAGT (0.12%)	GGAC (0.12%)	TAGT (0.09%)	TTAG (0.11%)	CTAT (0.12%)	TAGA (0.11%)	CCCC (0.14%)	CGGA (0.15%)	CCCT (0.10%)	
-8	TCTA (0.12%)	TAGT (0.12%)	TTAG (0.09%)	CCCT (0.11%)	CCTC (0.12%)	ACTA (0.11%)	CCCT (0.14%)	GGGA (0.14%)	CTAA (0.10%)	
-7	CTAA (0.10%)	CCCT (0.11%)	ACTA (0.09%)	GGAC (0.10%)	ACCT (0.11%)	CGAG (0.10%)	TCTA (0.13%)	ACCT (0.13%)	TCGA (0.10%)	
-6	TTAG (0.09%)	CGGA (0.10%)	GGAC (0.08%)	GAGG (0.09%)	CTAA (0.10%)	CTAT (0.10%)	TTAG (0.13%)	CTAA (0.12%)	GGGA (0.09%)	
-5	GGAC (0.09%)	CTAA (0.10%)	TAGA (0.07%)	CTAA (0.09%)	TAGA (0.10%)	GGAC (0.10%)	CTAA (0.12%)	CCCT (0.10%)	CGGA (0.09%)	
-4	TAGA (0.07%)	TAGG (0.06%)	TCTA (0.07%)	TAGA (0.09%)	CCCT (0.08%)	CCCT (0.08%)	TAGA (0.08%)	TAGG (0.10%)	TAGG (0.08%)	
-3	CCTA (0.05%)	TAGA (0.06%)	TAGG (0.06%)	CCTA (0.06%)	TAGG (0.07%)	TAGG (0.07%)	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 (0.41%)	CAGCA (0.42%)	CAGCA (0.47%)	CAGCA (0.41%)	CTGGC (0.43%)	CAGCA (0.53%)	CAGCA (0.39%)	CTGGC (0.41%)	CAGCA (0.45%)	Most common
2	CTGGC (0.36%)	CTGGC (0.39%)	GAAAA (0.40%)	CTGGC (0.36%)	CAGCA (0.43%)	GAAAA (0.38%)	CGGCA (0.34%)	CAGCA (0.34%)	CGGCA (0.42%)	
3	TTATC (0.33%)	GCTGC (0.36%)	CAAAA (0.36%)	CCAGC (0.33%)	GCGGC (0.37%)	CGGCA (0.37%)	CGCCA (0.33%)	GCGGC (0.31%)	TGGCA (0.41%)	
4	CGCCA (0.31%)	TTTGC (0.34%)	TCTTC (0.35%)	CATCA (0.32%)	CCAGC (0.34%)	AGAAA (0.33%)	CTGGC (0.31%)	TGGCG (0.30%)	GAAAA (0.35%)	
5	GCCAG (0.29%)	TTGCC (0.33%)	CTGGC (0.34%)	GCTGC (0.31%)	GCTGC (0.33%)	CATCA (0.33%)	TGGCA (0.31%)	CGCCA (0.29%)	GCGTT (0.29%)	
6	GAAAA (0.29%)	CGCCA (0.32%)	TGGCA (0.34%)	GCGGC (0.30%)	CATCA (0.32%)	CAAAA (0.33%)	CATCA (0.31%)	CATCA (0.29%)	ATTTT (0.29%)	
7	TGGCG (0.29%)	GCAGC (0.31%)	GCAAA (0.33%)	CGGCA (0.30%)	TTTGC (0.31%)	AAAAA (0.32%)	GCCAG (0.28%)	CCAGC (0.29%)	TTGCC (0.28%)	
8	GCAGC (0.29%)	GCCAG (0.30%)	TGTTC (0.32%)	GCAGC (0.28%)	AATCA (0.30%)	CAGAA (0.32%)	TGGCG (0.26%)	GCCAG (0.28%)	TGGCG (0.28%)	
9	TGGCA (0.28%)	TTTCC (0.30%)	CGTTC (0.32%)	GCCAG (0.28%)	TCAGC (0.30%)	ATAAA (0.32%)	TCTTC (0.26%)	GCTGC (0.27%)	CGCCA (0.27%)	
10	CATCA (0.28%)	GAAAA (0.29%)	GCCAG (0.32%)	CGCCA (0.27%)	TTGGC (0.29%)	TGGCA (0.32%)	CCAGC (0.26%)	ATAAA (0.27%)	CATCA (0.27%)	
-10	CCCTA (0.01%)	CCCTA (0.01%)	CCCTA (0.01%)	CCCTA (0.01%)	ACCTA (0.01%)	ACCTA (0.01%)	CCCTA (0.01%)	TCCTA (0.01%)	CCCTA (0.01%)	Least common
-9	GGACC (0.00%)	TAGGA (0.01%)	ACCTA (0.01%)	TAGGG (0.01%)	CCCTA (0.01%)	CCCTA (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 (0.01%)	GCTAG (0.01%)	CTAGC (0.00%)	
-7	CTAGT (0.00%)	CTGAC (0.00%)	CTGAC (0.00%)	CTAGT (0.00%)	GCTAG (0.00%)	GCTAG (0.00%)	GCTAG (0.00%)	CTAGC (0.01%)	GCTAG (0.00%)	
-6	ACTAG (0.00%)	ACTAG (0.00%)	GCTAG (0.00%)	GCTAG (0.00%)	CTAGT (0.00%)	CTAGT (0.00%)	CTAGT (0.00%)	ACTAG (0.01%)	CTAGT (0.00%)	
-5	GCTAG (0.00%)	CTAGT (0.00%)	CTAGT (0.00%)	ACTAG (0.00%)	ACTAG (0.00%)	ACTAG (0.00%)	ACTAG (0.00%)	CTAGT (0.00%)	ACTAG (0.00%)	
-4	CTAGG (0.00%)	CTAGG (0.00%)	CTAGG (0.00%)	TCTAG (0.00%)	TCTAG (0.00%)	CTAGG (0.00%)	TCTAG (0.00%)	TCTAG (0.00%)	CTAGG (0.00%)	
-3	TCTAG (0.00%)	TCTAG (0.00%)	CTAGA (0.00%)	CCTAG (0.00%)	CTAGG (0.00%)	CTAGA (0.00%)	CTAGG (0.00%)	CTAGG (0.00%)	TCTAG (0.00%)	
-2	CTAGA (0.00%)	CCTAG (0.00%)	TCTAG (0.00%)	CTAGA (0.00%)	CTAGA (0.00%)	CCTAG (0.00%)	CCTAG (0.00%)	CCTAG (0.00%)	CTAGA (0.00%)	
-1	CCTAG (0.00%)	CTAGA (0.00%)	CCTAG (0.00%)	CTAGG (0.00%)	CCTAG (0.00%)	TCTAG (0.00%)	CTAGA (0.00%)	CTAGA (0.00%)	CTAGA (0.00%)	

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