

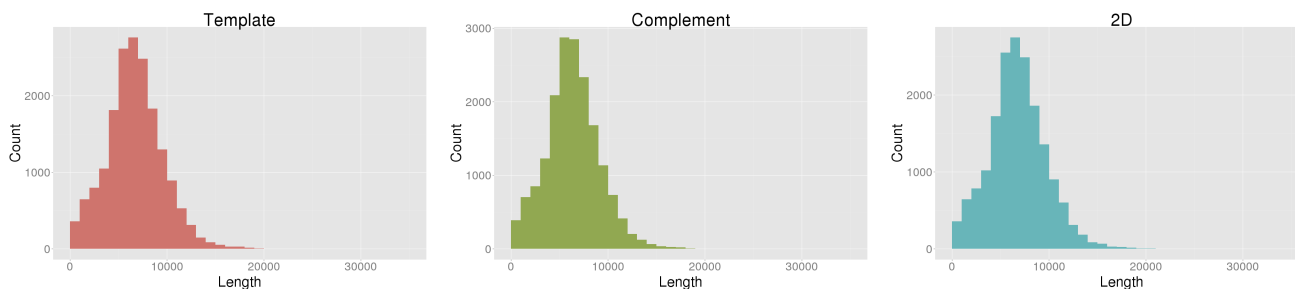
NanoOK report for E.coli_MARC1_run2

Pass and fail counts

Type	Pass	Fail
Template	17805	0
Complement	17805	0
2D	17805	0

Read lengths

Type	NumReads	TotalBases	Mean	Longest	Shortest	N50	N50Count	N90	N90Count
Template	17805	119482001	6710.59	33715	196	7626	6090	4676	13802
Complement	17805	113746865	6388.48	32459	160	7292	6080	4450	13791
2D	17805	120907970	6790.68	34149	147	7740	6087	4729	13792



Template alignments

Number of reads	17805
Number of reads with alignments	17672 (99.25%)
Number of reads without alignments	133 (0.75%)

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	17672	99.25	6747.05	126735516	27.30	82

Complement alignments

Number of reads	17805
Number of reads with alignments	17633 (99.03%)
Number of reads without alignments	172 (0.97%)

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	17633	99.03	6432.70	121525369	26.18	76

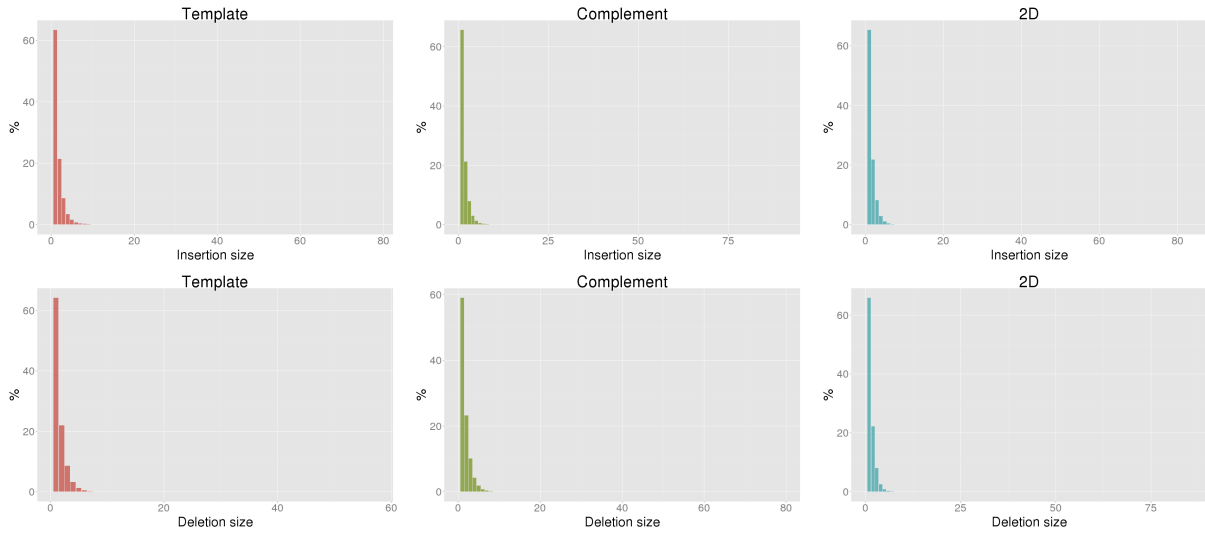
2D alignments

Number of reads	17805
Number of reads with alignments	17733 (99.60%)
Number of reads without alignments	72 (0.40%)

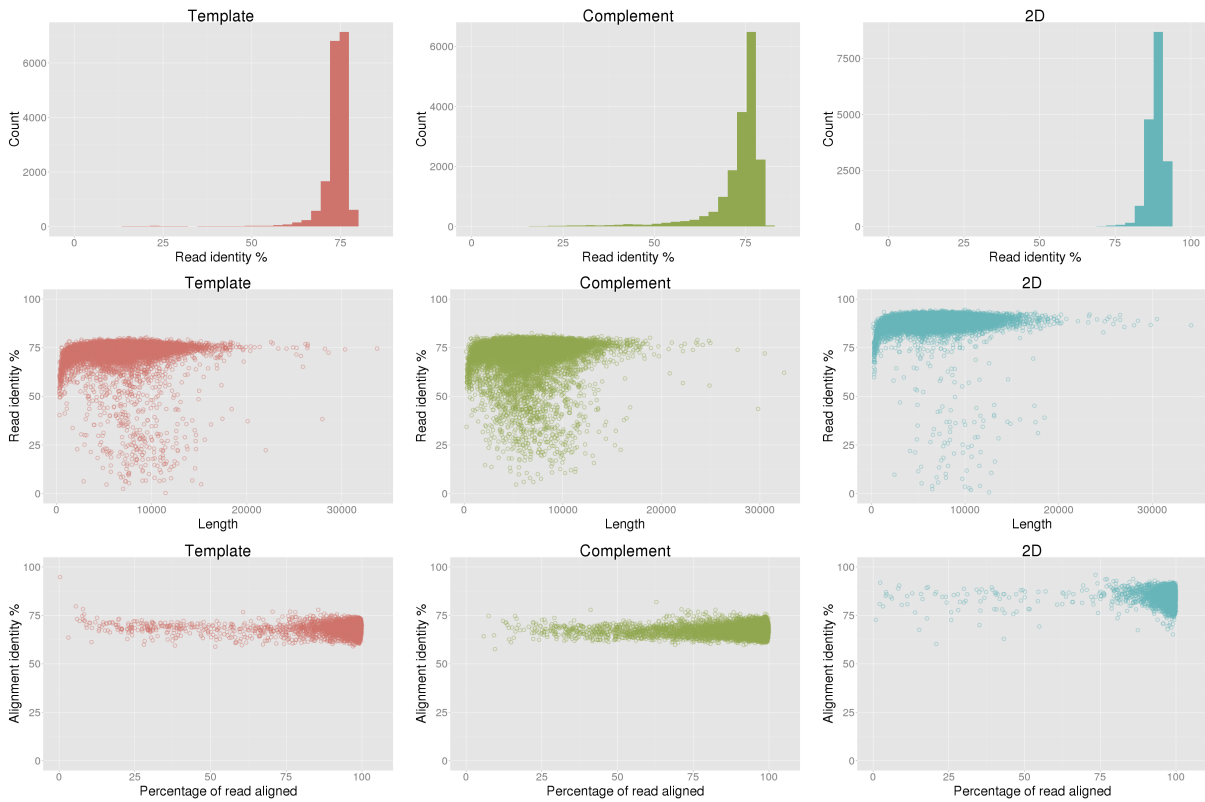
ID	Size	Number of Reads	% of Reads	Mean read length	Aligned bases	Mean coverage	Longest Perf Kmer
Control sequence	3560	0	0.00	0.00	0	0.00	0
Escherichia coli	4641652	17733	99.60	6808.48	125314896	27.00	239

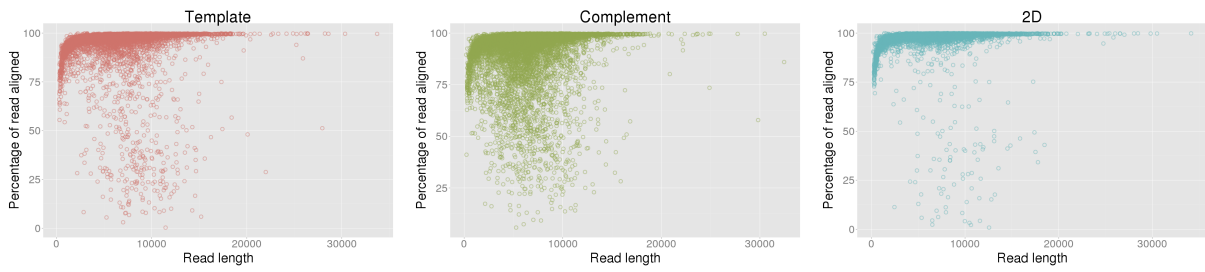
Escherichia coli error analysis

	Template	Complement	2D
Overall base identity (excluding indels)	73.20%	72.72%	88.17%
Aligned base identity (excluding indels)	80.95%	81.54%	93.30%
Identical bases per 100 aligned bases (including indels)	68.86%	67.88%	84.95%
Inserted bases per 100 aligned bases (including indels)	5.98%	4.90%	3.78%
Deleted bases per 100 aligned bases (including indels)	8.95%	11.86%	5.16%
Substitutions per 100 aligned bases (including indels)	16.20%	15.36%	6.10%
Mean insertion size	1.67	1.58	1.56
Mean deletion size	1.59	1.73	1.53

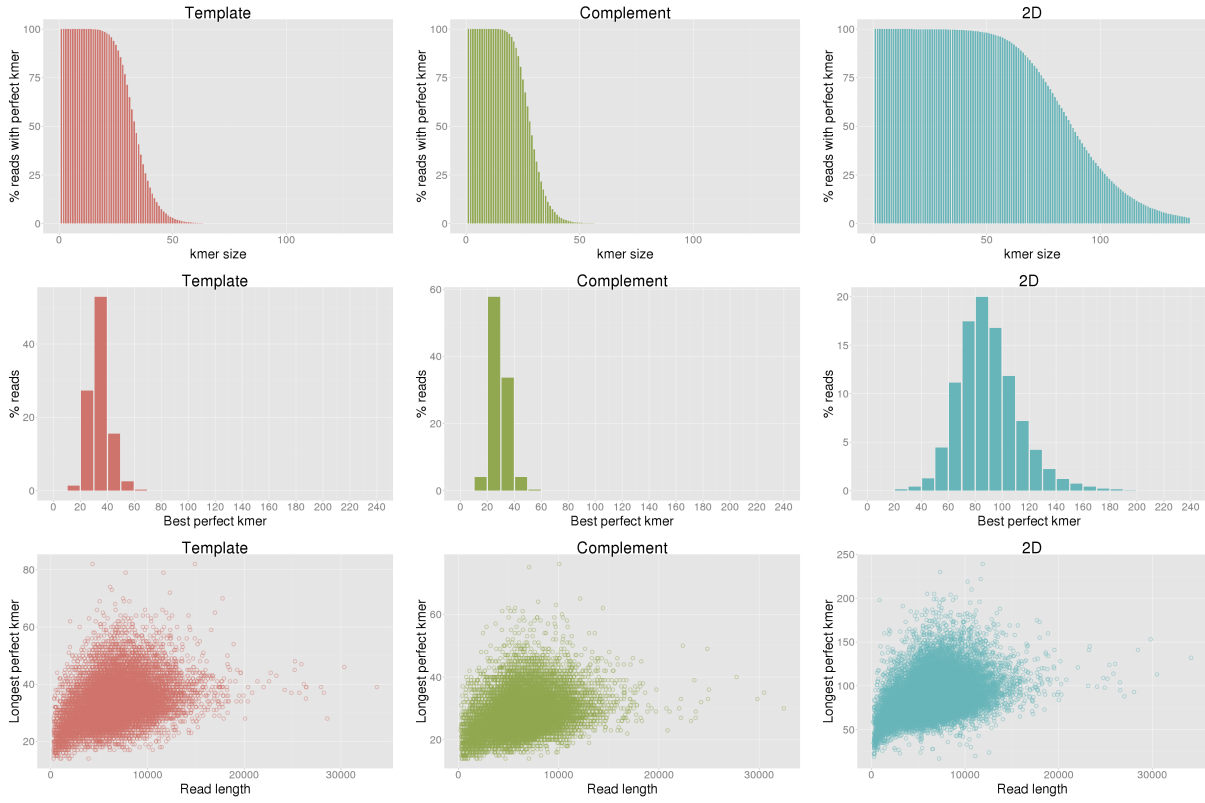


Escherichia coli read identity

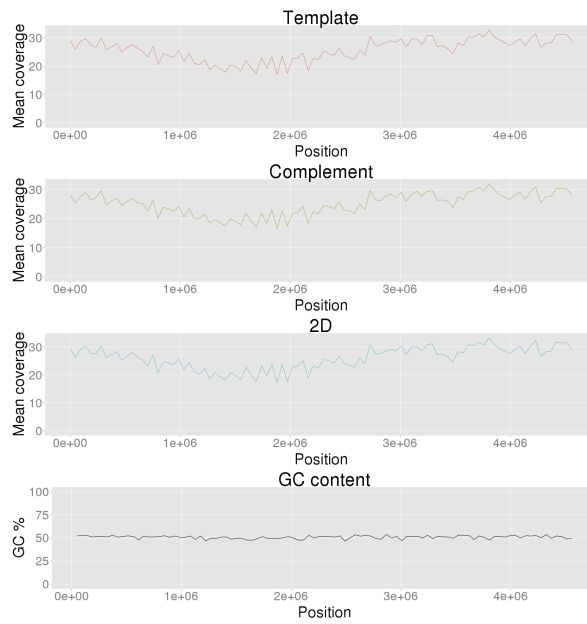




Escherichia coli perfect kmers



Escherichia coli coverage



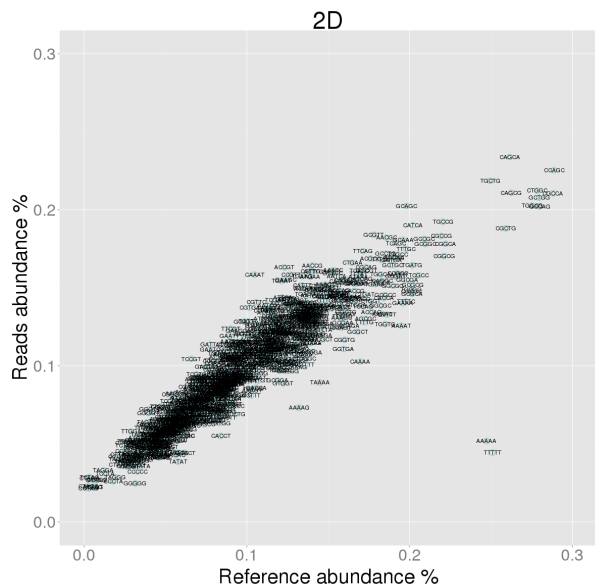
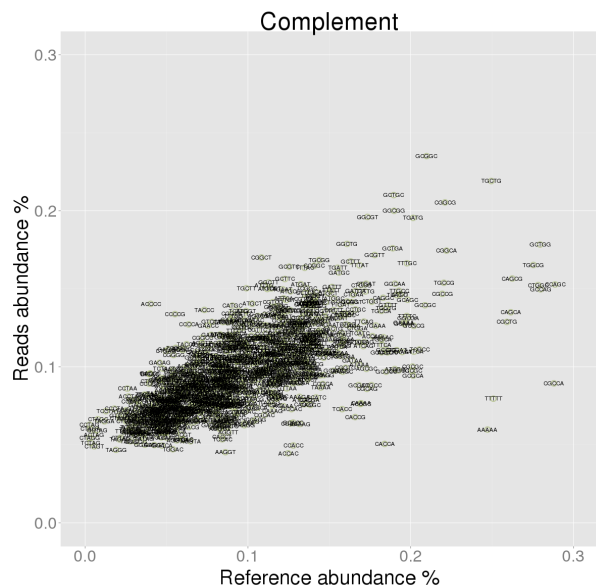
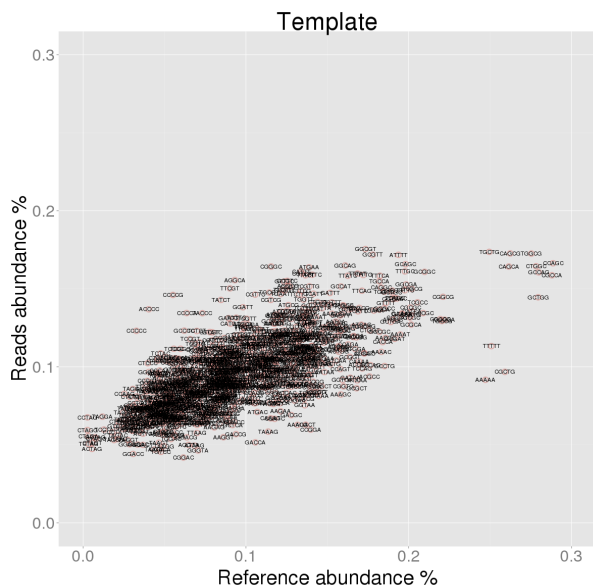
Escherichia coli 5-mer analysis

Under-represented 5-mers

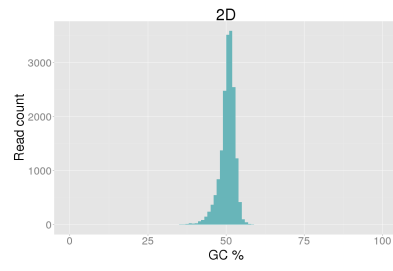
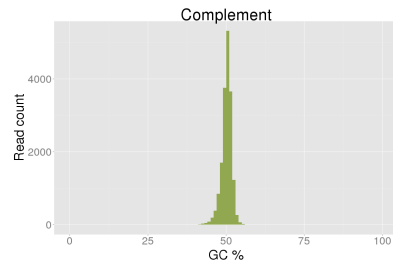
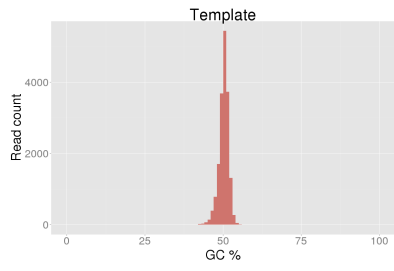
Rank	Template				Complement				2D			
	kmer	Ref %	Read %	Diff %	kmer	Ref %	Read %	Diff %	kmer	Ref %	Read %	Diff %
1	CGCTG	0.259	0.097	-0.162	CGCCA	0.288	0.089	-0.199	TTTTT	0.251	0.044	-0.206
2	AAAAA	0.247	0.092	-0.155	AAAAA	0.247	0.060	-0.187	AAAAA	0.247	0.052	-0.195
3	TTTTT	0.251	0.113	-0.138	TTTTT	0.251	0.080	-0.171	GCCAG	0.280	0.202	-0.078
4	GCTGG	0.279	0.145	-0.135	CCAGC	0.289	0.153	-0.136	CGCCA	0.288	0.211	-0.077
5	CGCCA	0.288	0.159	-0.129	CACCA	0.184	0.051	-0.133	TGGCG	0.275	0.203	-0.073
6	CCAGC	0.289	0.166	-0.122	CGCTG	0.259	0.129	-0.130	GCTGG	0.279	0.208	-0.072
7	GCCAG	0.280	0.161	-0.119	GCCAG	0.280	0.150	-0.130	CGCTG	0.259	0.188	-0.071
8	CTGGC	0.278	0.165	-0.114	CAGCA	0.261	0.135	-0.126	AAAAT	0.195	0.126	-0.069
9	TGGCG	0.275	0.173	-0.103	CTGGC	0.278	0.152	-0.126	CAAAA	0.169	0.103	-0.067
10	CAGCA	0.261	0.164	-0.097	TGGCG	0.275	0.165	-0.110	CTGGC	0.278	0.212	-0.066

Over-represented 5-mers

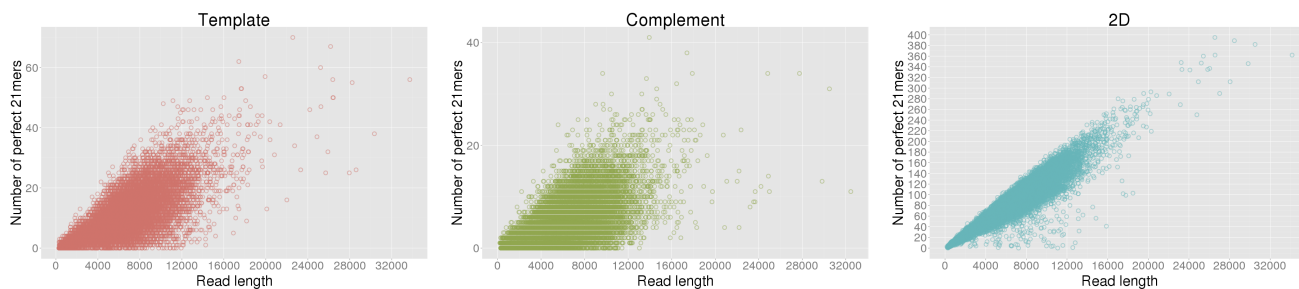
Rank	Template				Complement				2D			
	kmer	Ref %	Read %	Diff %	kmer	Ref %	Read %	Diff %	kmer	Ref %	Read %	Diff %
1	ACCCC	0.040	0.137	0.097	ACCCC	0.040	0.140	0.100	CAAAT	0.105	0.158	0.054
2	CCCCG	0.055	0.146	0.091	CCCCG	0.055	0.134	0.079	ACCGT	0.123	0.163	0.040
3	CCCCC	0.033	0.123	0.090	CCCCC	0.064	0.127	0.064	TCCGT	0.066	0.104	0.039
4	CCCCA	0.064	0.135	0.071	TACCC	0.073	0.136	0.063	GATTC	0.078	0.114	0.036
5	CCTAG	0.003	0.068	0.065	CGGCT	0.108	0.170	0.062	CGTGA	0.102	0.137	0.036
6	CTCCC	0.040	0.102	0.063	CTGAG	0.050	0.110	0.061	CGTTC	0.106	0.141	0.035
7	AGGCA	0.093	0.156	0.062	CCTAA	0.026	0.086	0.060	TTCGT	0.090	0.124	0.034
8	GCCCC	0.062	0.123	0.061	CCTAG	0.003	0.063	0.060	GAATC	0.077	0.110	0.033
9	TACCC	0.073	0.134	0.061	GAGGC	0.051	0.111	0.060	TGAAT	0.121	0.154	0.033
10	TCTAC	0.048	0.109	0.061	TCCTA	0.013	0.072	0.059	GGGTC	0.040	0.072	0.032



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	8.35	9.28	4.79	0.00	8.73	8.92	5.04	0.00	7.91	8.59	4.30
C	8.79	0.00	9.25	9.94	9.60	0.00	8.68	9.47	9.64	0.00	10.85	9.16
G	9.24	9.24	0.00	8.44	8.83	8.77	0.00	9.12	8.86	11.01	0.00	9.06
T	5.03	9.50	8.15	0.00	5.26	8.94	8.63	0.00	4.33	8.47	7.81	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 (3.33%)	TTC (3.50%)	AAA (4.25%)	TGC (2.89%)	GCC (3.03%)	AAA (4.11%)	GCA (3.07%)	TCA (2.69%)	AAA (4.05%)
2	AAA (2.98%)	TGC (2.90%)	TTC (3.67%)	TTC (2.74%)	TGC (2.86%)	GCA (3.64%)	AAA (2.90%)	GCC (2.65%)	GCA (3.75%)
3	TGC (2.75%)	GCA (2.86%)	GCA (3.34%)	AAA (2.74%)	AAA (2.75%)	GAA (3.41%)	TTC (2.80%)	GCG (2.64%)	GAA (3.60%)
4	GCA (2.68%)	AAA (2.71%)	GAA (3.18%)	GCA (2.71%)	GCA (2.64%)	TTC (3.10%)	TGC (2.62%)	GCA (2.55%)	TTC (2.89%)
5	ATC (2.51%)	TCA (2.58%)	TGC (2.55%)	CAG (2.51%)	TTC (2.54%)	TGC (2.62%)	TCA (2.58%)	AAA (2.55%)	AAT (2.53%)
6	TCA (2.51%)	GCC (2.48%)	AAT (2.36%)	GCC (2.48%)	GCC (2.35%)	TCA (2.46%)	GAA (2.57%)	TTC (2.51%)	GCC (2.46%)
7	GCC (2.49%)	GGC (2.43%)	GCC (2.35%)	GAA (2.46%)	GAA (2.33%)	TTT (2.44%)	CGC (2.53%)	TGC (2.43%)	GCG (2.44%)
8	GAA (2.33%)	ATC (2.29%)	TTT (2.32%)	TCA (2.34%)	TCA (2.33%)	ATC (2.35%)	ATC (2.43%)	CGC (2.32%)	TTT (2.43%)
9	GGC (2.30%)	AAT (2.24%)	TCA (2.30%)	ATC (2.29%)	GCG (2.33%)	GCC (2.30%)	CAG (2.29%)	ATC (2.26%)	ATC (2.39%)
10	GCG (2.28%)	AAC (2.23%)	CAA (2.16%)	GCC (2.26%)	GCG (2.24%)	GCC (2.22%)	GCG (2.24%)	AAC (2.15%)	TCA (2.37%)
-10	AGT (0.98%)	TGT (0.93%)	GGT (0.93%)	GTG (0.99%)	AGG (0.95%)	GTG (0.93%)	CTC (1.00%)	GAG (0.97%)	CCT (0.88%)
-9	CCC (0.95%)	CCT (0.92%)	GGG (0.91%)	AGT (0.97%)	AGT (0.92%)	CTT (0.90%)	TGT (0.96%)	CGA (0.94%)	ACT (0.87%)
-8	TGT (0.92%)	AGG (0.91%)	AGA (0.87%)	CTC (0.94%)	GGA (0.89%)	AGT (0.85%)	CCC (0.82%)	ACT (0.92%)	TGA (0.86%)
-7	AGA (0.83%)	CTT (0.82%)	AGT (0.84%)	CCC (0.88%)	CTC (0.89%)	CCT (0.82%)	AGA (0.82%)	CTT (0.89%)	CGA (0.76%)
-6	GAG (0.75%)	GAG (0.79%)	AGG (0.78%)	GGA (0.86%)	CCC (0.89%)	AGG (0.78%)	GAG (0.81%)	CCC (0.84%)	CTT (0.76%)
-5	GGA (0.72%)	CGA (0.79%)	TGT (0.72%)	GAG (0.80%)	CCT (0.86%)	GGG (0.76%)	AGG (0.75%)	CCT (0.80%)	GAG (0.68%)
-4	AGG (0.69%)	AGA (0.68%)	CTT (0.72%)	AGG (0.69%)	GAG (0.83%)	ACT (0.73%)	GGA (0.75%)	AGA (0.79%)	AGA (0.55%)
-3	GGG (0.66%)	GGA (0.61%)	GAG (0.59%)	CTA (0.60%)	GGG (0.78%)	GAG (0.59%)	GGG (0.63%)	GGA (0.70%)	GGA (0.50%)
-2	CTA (0.52%)	TAG (0.51%)	CTA (0.39%)	GGG (0.58%)	CTA (0.56%)	CTA (0.49%)	CTA (0.58%)	CTA (0.70%)	TAG (0.43%)
-1	TAG (0.43%)	CTA (0.49%)	TAG (0.38%)	TAG (0.44%)	TAG (0.51%)	TAG (0.35%)	TAG (0.46%)	TAG (0.60%)	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	GAAG (0.99%)	TTTC (1.04%)	AAAA (1.42%)	CAGC (0.99%)	CGGC (1.12%)	AAAA (1.14%)	ATCA (0.89%)	TGGC (0.91%)	AAAA (1.18%)
2	TTTC (0.98%)	TTCA (0.98%)	GAAA (1.28%)	CGGC (0.92%)	CAGC (1.05%)	CAAA (1.07%)	CAGC (0.88%)	CAGC (0.91%)	GGCA (1.11%)
3	AAAA (0.97%)	TGCC (0.96%)	TTTC (1.14%)	ATCA (0.90%)	TGGC (1.05%)	TGAA (1.03%)	CGCC (0.85%)	TTCA (0.89%)	GAAA (1.07%)
4	CAGC (0.90%)	CAGC (0.91%)	GGCA (0.93%)	CTGC (0.86%)	TTGC (0.89%)	GAAA (1.00%)	GCCA (0.84%)	ATCA (0.85%)	TGAA (1.07%)
5	TGCC (0.88%)	AAAA (0.86%)	GCAA (0.92%)	TTGC (0.85%)	CTGC (0.86%)	AGCA (0.96%)	GAAA (0.83%)	CGGC (0.84%)	CGCA (0.95%)
6	ATCA (0.88%)	TGCC (0.86%)	TGCC (0.91%)	CCAG (0.83%)	ATCA (0.84%)	ATCA (0.95%)	CGCA (0.81%)	GGCG (0.75%)	GGAA (0.93%)
7	TTCA (0.86%)	GTTC (0.83%)	TGAA (0.90%)	TGGC (0.81%)	CAA (0.81%)	GGCA (0.91%)	GGCA (0.79%)	GCCA (0.75%)	CGCC (0.93%)
8	CGCC (0.85%)	CTGC (0.83%)	GTTC (0.86%)	CAAA (0.79%)	CGCC (0.77%)	TAAA (0.88%)	TGAA (0.79%)	GCGC (0.74%)	CAAA (0.90%)
9	TTGC (0.80%)	ATCA (0.83%)	AACG (0.85%)	AAAA (0.78%)	AAAA (0.77%)	AGAA (0.88%)	CAAA (0.79%)	CGCC (0.73%)	CGAA (0.84%)
10	GCCG (0.80%)	TTGC (0.83%)	GGAA (0.85%)	CGCC (0.75%)	TTCC (0.75%)	CGCA (0.87%)	AACA (0.77%)	CTGC (0.72%)	AGCA (0.84%)
-10	TAGT (0.12%)	CTAT (0.13%)	ACTA (0.11%)	GTGT (0.12%)	CCTC (0.13%)	GAGG (0.10%)	CTTG (0.13%)	GGGA (0.15%)	CTTG (0.11%)
-9	AGGG (0.12%)	TAGT (0.13%)	TTAG (0.11%)	AGGG (0.11%)	CCCC (0.13%)	GGAC (0.10%)	TCTA (0.13%)	CTAT (0.15%)	CGGA (0.11%)
-8	GGAC (0.11%)	TCTA (0.12%)	CGAG (0.11%)	GGAC (0.11%)	CTAA (0.12%)	CTAT (0.10%)	GAGG (0.13%)	CCCC (0.15%)	GGGA (0.10%)
-7	GAGG (0.11%)	CCCT (0.12%)	GGAG (0.10%)	CTAA (0.10%)	ACCT (0.11%)	ACCT (0.10%)	CCCT (0.13%)	GAGA (0.15%)	CCCT (0.10%)
-6	TTAG (0.11%)	CGGA (0.11%)	TAGT (0.10%)	GAGG (0.10%)	GTGT (0.11%)	GTGT (0.10%)	CTAT (0.12%)	CTAA (0.12%)	CTAT (0.10%)
-5	CTAA (0.10%)	CTAA (0.10%)	TCTA (0.09%)	TAGA (0.09%)	TAGA (0.10%)	CGAG (0.09%)	CTAA (0.11%)	CCCT (0.10%)	CTAA (0.10%)
-4	TAGA (0.06%)	TAGG (0.07%)	TAGA (0.07%)	CCCT (0.08%)	CCCT (0.07%)	CCCT (0.06%)	TAGA (0.08%)	TAGA (0.09%)	TAGG (0.07%)
-3	CCTA (0.06%)	TAGA (0.06%)	TAGG (0.06%)	CCTA (0.07%)	TAGG (0.07%)	TAGG (0.06%)	CCTA (0.08%)	TAGG (0.09%)	TAGA (0.04%)
-2	TAGG (0.05%)	CCTA (0.06%)	CCTA (0.05%)	TAGG (0.05%)	CCTA (0.06%)	CCTA (0.06%)	TAGG (0.05%)	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%)

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 (0.35%)	CAGCA (0.38%)	CAGCA (0.45%)	CAGCA (0.42%)	CAGCA (0.42%)	CAGCA (0.57%)	CAGCA (0.39%)	CTGGC (0.36%)	CAGCA (0.47%)
2	CGCCA (0.32%)	CTGGC (0.34%)	CAAAA (0.41%)	GCGGC (0.34%)	GCGGC (0.38%)	ATAAA (0.38%)	CGCCA (0.35%)	CAGCA (0.34%)	CGGCA (0.42%)
3	CAAAA (0.32%)	TTGCC (0.33%)	GAAAA (0.40%)	GCTGC (0.34%)	TTGGC (0.38%)	CGGCA (0.37%)	CGGCA (0.31%)	GCGGC (0.31%)	GAAAA (0.39%)
4	CCAGC (0.32%)	CGCCA (0.32%)	TGAAA (0.35%)	CATCA (0.33%)	TCAGC (0.34%)	GCAAA (0.35%)	GCAAA (0.31%)	CGCCA (0.30%)	TGGCA (0.34%)
5	CTGGC (0.31%)	CATCA (0.32%)	GCAAA (0.35%)	CCAGC (0.32%)	CCAGC (0.33%)	CATCA (0.34%)	CCAGC (0.30%)	CATCA (0.30%)	GCAAA (0.34%)
6	CATCA (0.31%)	TTTCA (0.31%)	AGAAA (0.33%)	CTGGC (0.30%)	CATCA (0.32%)	AAGAA (0.34%)	CATCA (0.29%)	TGGCG (0.29%)	CAAAA (0.33%)
7	GCAGC (0.30%)	CCAGC (0.30%)	CGCCA (0.33%)	GCAAA (0.28%)	GCTGC (0.32%)	GAAAA (0.33%)	CTGGC (0.29%)	CCAGC (0.28%)	TGAAA (0.32%)
8	TTGCC (0.30%)	GCAGC (0.29%)	TTGCC (0.32%)	TCAGC (0.28%)	TTTGC (0.30%)	CAGAA (0.33%)	GCCAG (0.28%)	TTTCA (0.28%)	GCGCA (0.32%)
9	TTTTGC (0.29%)	GCTGC (0.29%)	CGTTC (0.32%)	GCAGC (0.27%)	AATCA (0.29%)	ACGCA (0.31%)	GCGCA (0.27%)	ATAAA (0.27%)	GCGAA (0.31%)
10	GAAAA (0.28%)	CGTTC (0.29%)	GCCAG (0.31%)	AACGC (0.27%)	ATAAA (0.29%)	TTATC (0.31%)	GCGGC (0.27%)	CAGCG (0.26%)	CGCCA (0.31%)
-10	TAGGA (0.01%)	TAGGA (0.01%)	ACCTA (0.01%)	ACCTA (0.01%)	CCCC (0.01%)	ACCTA (0.01%)	CCCTA (0.01%)	TCCTA (0.01%)	CCCTA (0.01%)
-9	CCCTA (0.01%)	CCCTA (0.01%)	CCCTA (0.01%)	CCCTA (0.01%)	ACCTA (0.01%)	CCCT (0.01%)	TAGGA (0.01%)	CTAGC (0.01%)	TAGGA (0.00%)
-8	ACTAG (0.00%)	ACTAG (0.00%)	ACTAG (0.00%)	CTAGC (0.01%)	CTAGC (0.01%)	CCCTA (0.01%)	CTAGC (0.01%)	TAGGA (0.01%)	CTAGT (0.00%)
-7	CTAGC (0.00%)	GCTAG (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%)	CTAGC (0.00%)	CTAGC (0.00%)	CTAGT (0.00%)	CTAGT (0.00%)	CTAGT (0.00%)	CTAGT (0.00%)	ACTAG (0.01%)	GCTAG (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 (0.01%)	ACTAG (0.00%)
-4	CCTAG (0.00%)	CTAGG (0.00%)	TCTAG (0.00%)	TCTAG (0.00%)	TCTAG (0.00%)	CTAGA (0.00%)	TCTAG (0.00%)	TCTAG (0.00%)	CTAGG (0.00%)
-3	CTAGG (0.00%)	CCTAG (0.00%)	CTAGG (0.00%)	CTAGA (0.00%)	CTAGA (0.00%)	CTAGG (0.00%)	CCTAG (0.00%)	CTAGG (0.00%)	TCTAG (0.00%)
-2	TCTAG (0.00%)	TCTAG (0.00%)	CCTAG (0.00%)	CCTAG (0.00%)	CCTAG (0.00%)	TCTAG (0.00%)	CTAGA (0.00%)	CTAGA (0.00%)	CCTAG (0.00%)
-1	CTAGA (0.00%)	CTAGA (0.00%)	CTAGA (0.00%)	CTAGG (0.00%)	CTAGG (0.00%)	CCTAG (0.00%)	CTAGG (0.00%)	CCTAG (0.00%)	CTAGA (0.00%)

Most common

Least common

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