

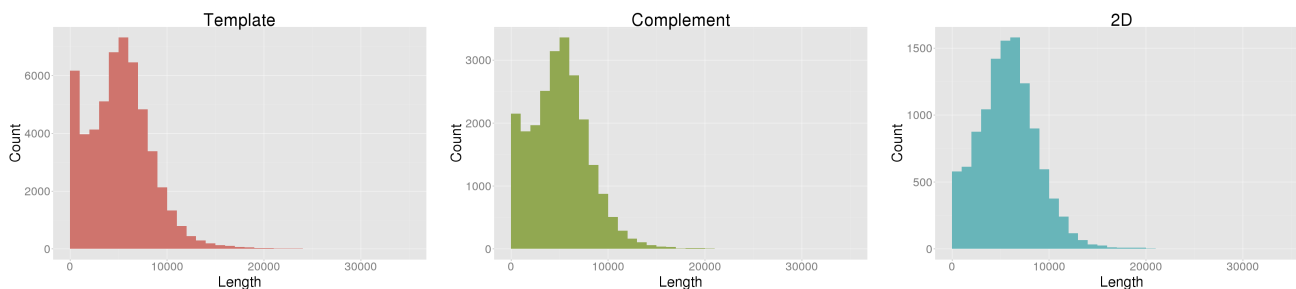
NanoOK report for E.coli_MARC1_run2

Pass and fail counts

Type	Pass	Fail
Template	0	53920
Complement	0	23295
2D	0	11303

Read lengths

Type	NumReads	TotalBases	Mean	Longest	Shortest	N50	N50Count	N90	N90Count
Template	53920	283087734	5250.14	218049	9	6796	15195	3580	36878
Complement	23295	118790374	5099.39	97435	5	6489	6827	3416	16344
2D	11303	65776883	5819.42	49310	135	7053	3563	3887	8329



Template alignments

Number of reads	53920
Number of reads with alignments	25112 (46.57%)
Number of reads without alignments	28808 (53.43%)

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	25112	46.57	6428.63	138170427	29.77	77

Complement alignments

Number of reads	23295
Number of reads with alignments	12901 (55.38%)
Number of reads without alignments	10394 (44.62%)

ID	Size	Number of Reads	% of Reads	Mean read length	Aligned bases	Mean coverage	Longest Perf Kmer
Control sequence	3560	2	0.01	5210.50	2778	0.78	24
Escherichia coli	4641652	12899	55.37	6043.81	64711559	13.94	79

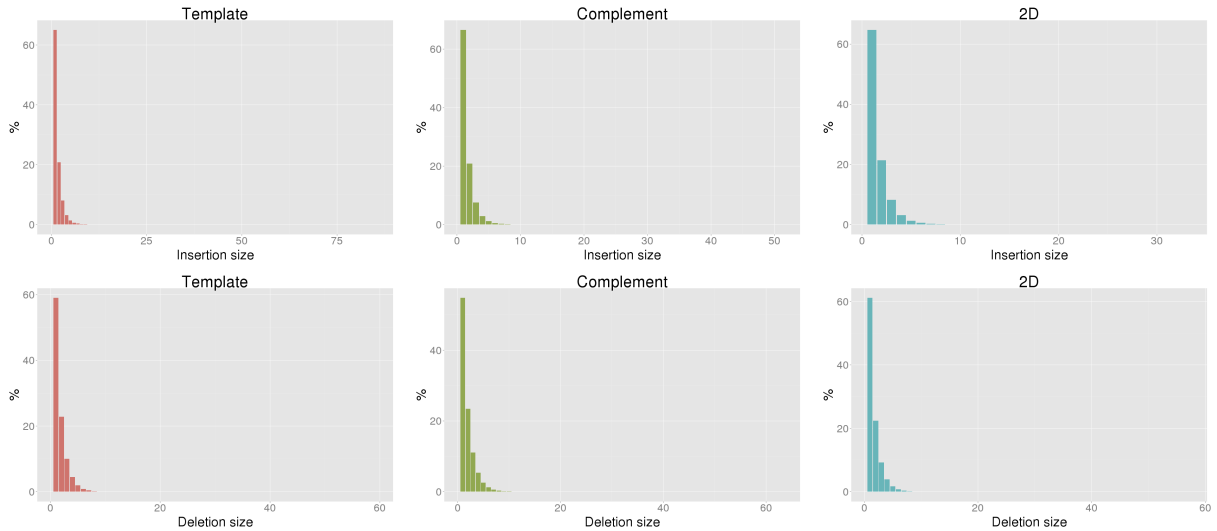
2D alignments

Number of reads	11303
Number of reads with alignments	9369 (82.89%)
Number of reads without alignments	1934 (17.11%)

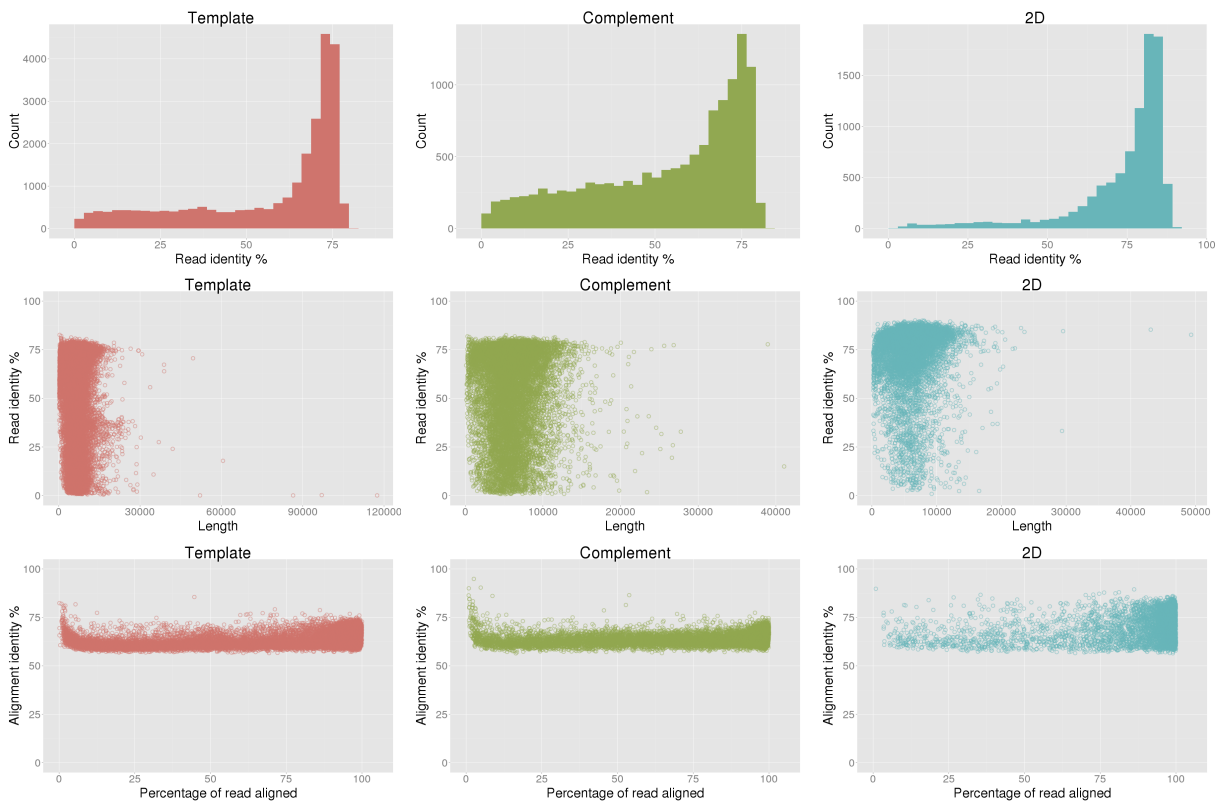
ID	Size	Number of Reads	% of Reads	Mean read length	Aligned bases	Mean coverage	Longest Perf Kmer
Control sequence	3560	0	0.00	0.00	0	0.00	0
Escherichia coli	4641652	9369	82.89	6319.83	59324244	12.78	220

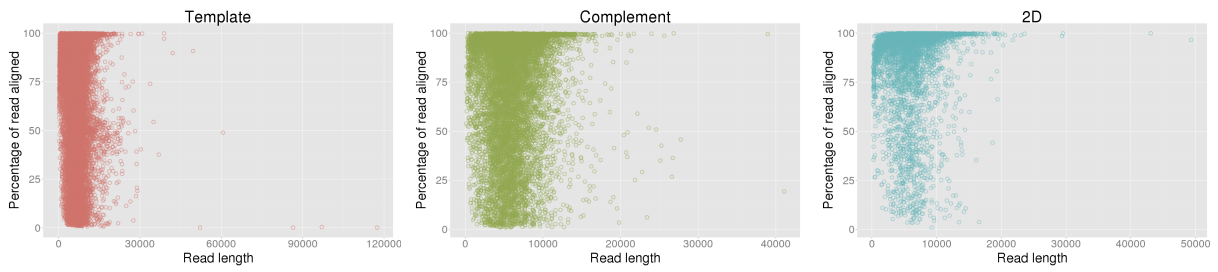
Escherichia coli error analysis

	Template	Complement	2D
Overall base identity (excluding indels)	55.55%	53.25%	73.77%
Aligned base identity (excluding indels)	78.50%	79.45%	85.56%
Identical bases per 100 aligned bases (including indels)	64.91%	64.16%	73.63%
Inserted bases per 100 aligned bases (including indels)	5.33%	4.47%	5.26%
Deleted bases per 100 aligned bases (including indels)	11.98%	14.78%	8.68%
Substitutions per 100 aligned bases (including indels)	17.78%	16.59%	12.43%
Mean insertion size	1.62	1.56	1.60
Mean deletion size	1.74	1.90	1.69

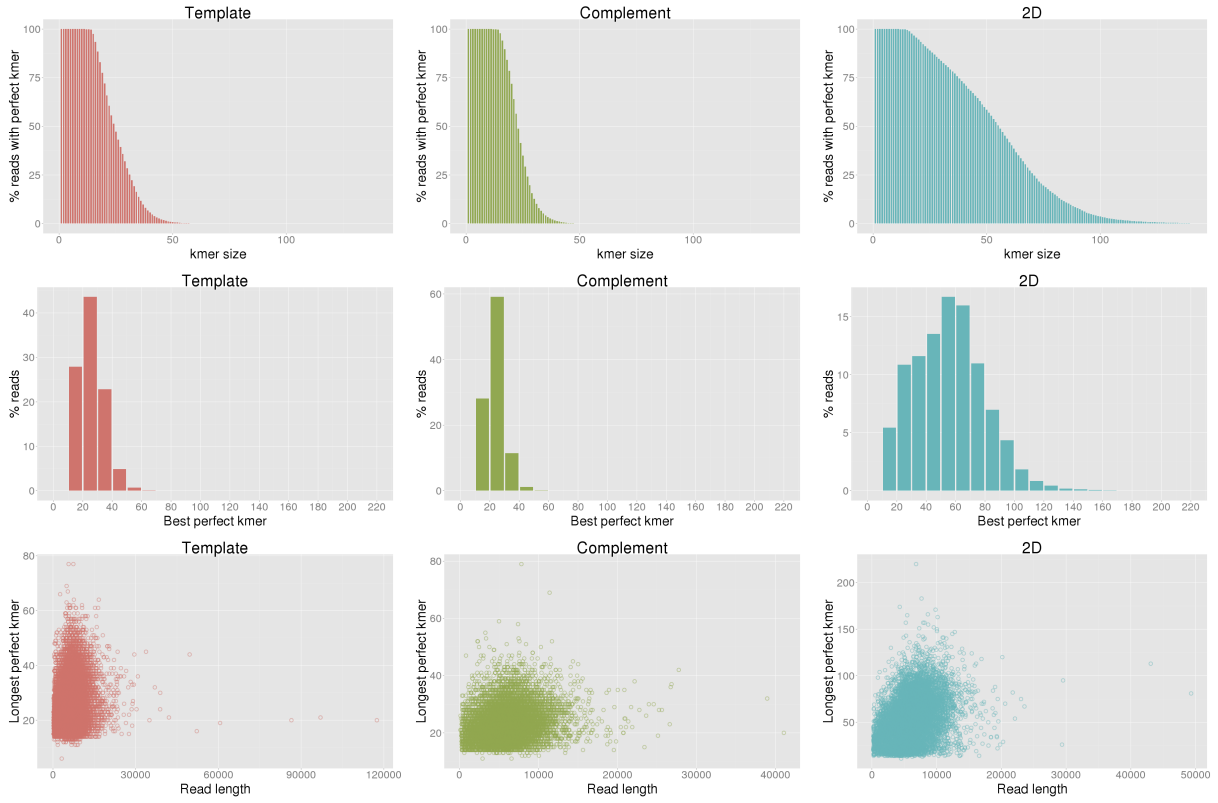


Escherichia coli read identity

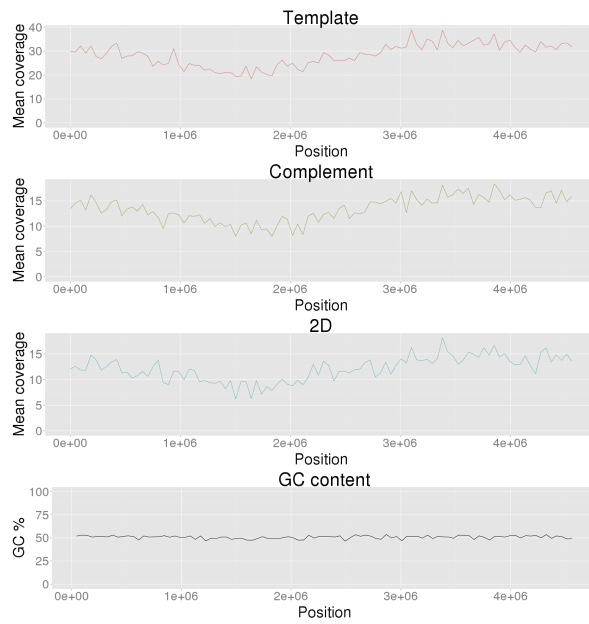




Escherichia coli perfect kmers



Escherichia coli coverage



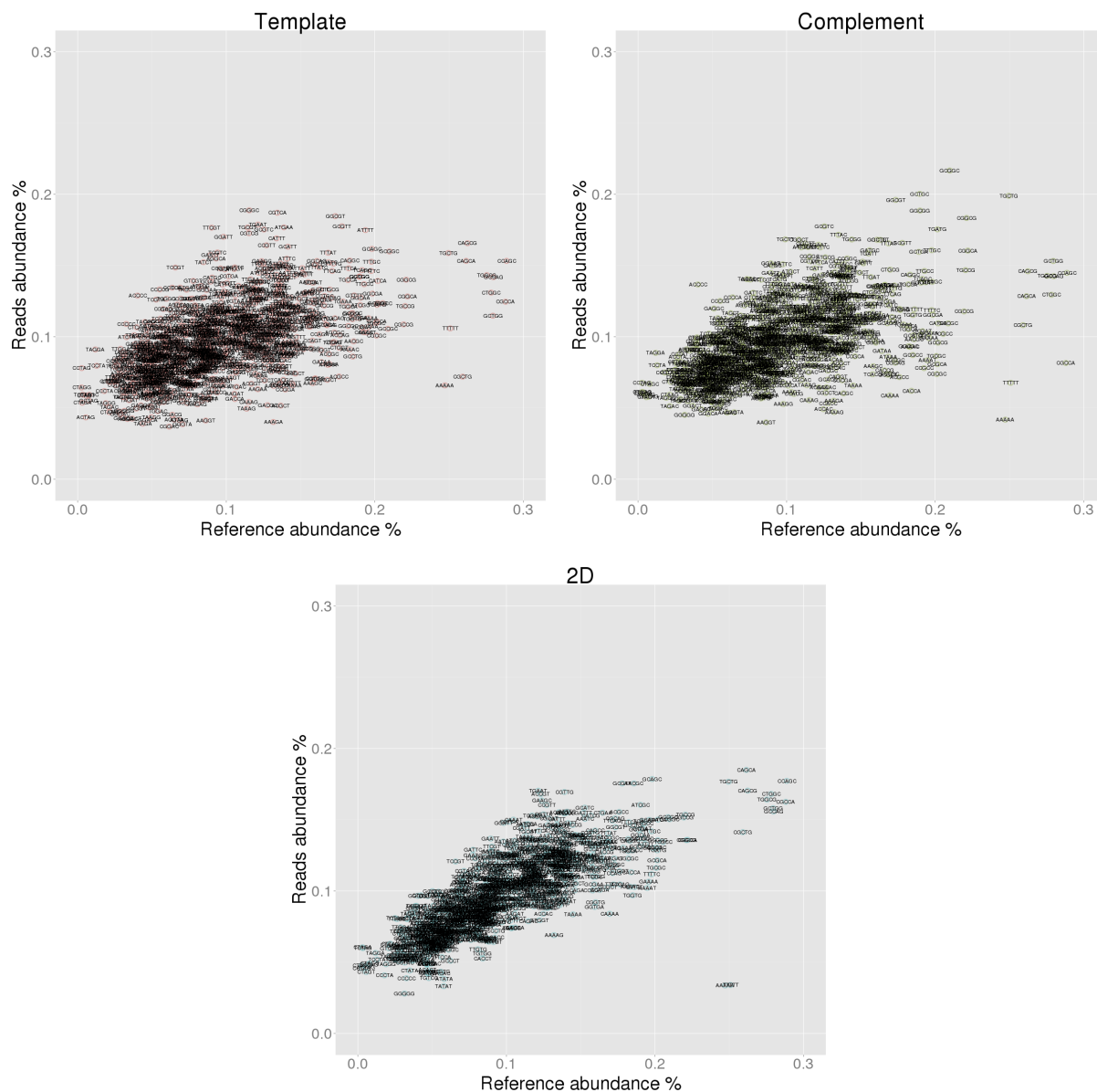
Escherichia coli 5-mer analysis

Under-represented 5-mers

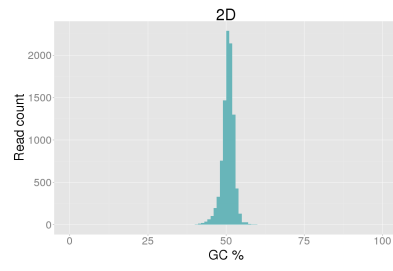
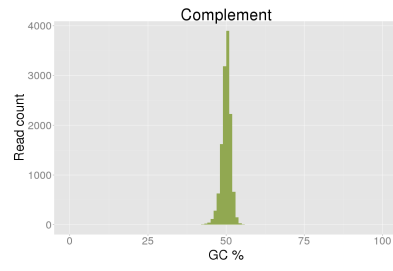
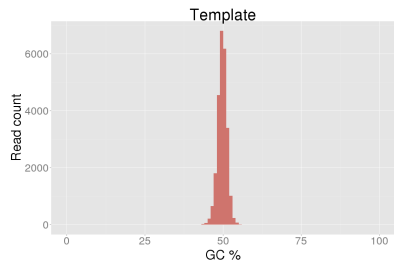
Rank	Template				Complement				2D			
	kmer	Ref %	Read %	Diff %	kmer	Ref %	Read %	Diff %	kmer	Ref %	Read %	Diff %
1	CGCTG	0.259	0.072	-0.187	CGCCA	0.288	0.082	-0.206	TTTTT	0.251	0.034	-0.217
2	AAAAA	0.247	0.066	-0.181	AAAAA	0.247	0.042	-0.205	AAAAA	0.247	0.034	-0.213
3	GCTGG	0.279	0.115	-0.165	TTTTT	0.251	0.068	-0.183	CGCCA	0.288	0.163	-0.125
4	CGCCA	0.288	0.125	-0.163	CGCTG	0.259	0.108	-0.151	GCCAG	0.280	0.156	-0.124
5	CTGGC	0.278	0.131	-0.147	CTGGC	0.278	0.129	-0.149	GCTGG	0.279	0.158	-0.121
6	TTTTT	0.251	0.106	-0.145	CCAGC	0.289	0.145	-0.144	CGCTG	0.259	0.141	-0.118
7	GCCAG	0.280	0.142	-0.138	GCCAG	0.280	0.143	-0.137	CCAGC	0.289	0.177	-0.111
8	CCAGC	0.289	0.153	-0.135	CAGCA	0.261	0.128	-0.133	TGGCG	0.275	0.164	-0.111
9	TGGCG	0.275	0.143	-0.132	TGGCG	0.275	0.143	-0.133	CTGGC	0.278	0.168	-0.110
10	CGCCG	0.219	0.109	-0.111	CGCGC	0.201	0.074	-0.127	AAAAT	0.195	0.102	-0.093

Over-represented 5-mers

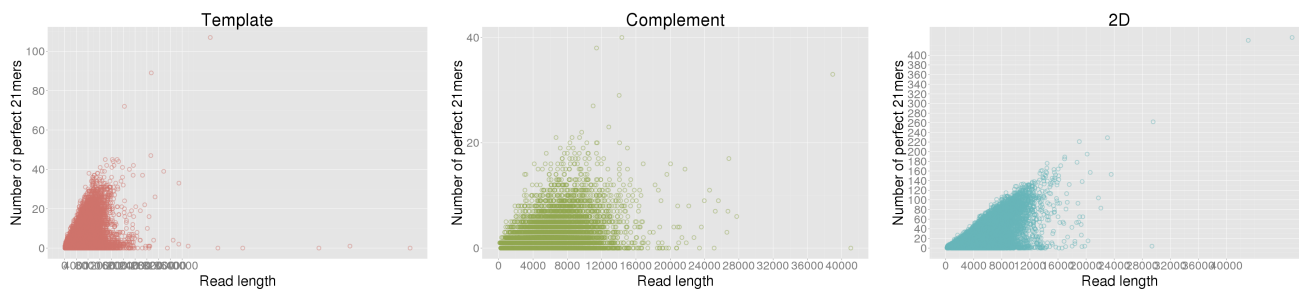
Rank	Template				Complement				2D			
	kmer	Ref %	Read %	Diff %	kmer	Ref %	Read %	Diff %	kmer	Ref %	Read %	Diff %
1	ACCCC	0.040	0.129	0.089	ACCCC	0.040	0.137	0.096	CTAGA	0.003	0.060	0.057
2	TTCGT	0.090	0.177	0.086	TAGGA	0.012	0.089	0.077	TCTAG	0.003	0.060	0.057
3	TCCGT	0.066	0.149	0.083	CCCCG	0.055	0.125	0.070	GGGTC	0.040	0.097	0.056
4	TAGGA	0.012	0.091	0.079	TGCTT	0.099	0.168	0.069	TCTAA	0.025	0.081	0.056
5	CCCCG	0.055	0.133	0.078	GAGGC	0.051	0.120	0.069	TCCGT	0.066	0.121	0.055
6	CCCCC	0.033	0.109	0.076	TACCC	0.073	0.141	0.067	CTCGT	0.042	0.097	0.054
7	CCTAG	0.003	0.078	0.075	TCCTA	0.013	0.080	0.067	TTAGA	0.026	0.080	0.054
8	TCGTA	0.053	0.126	0.073	CCTAG	0.003	0.068	0.065	GATTC	0.078	0.129	0.051
9	CGGGC	0.116	0.189	0.073	GAACC	0.075	0.140	0.065	TAGAA	0.039	0.089	0.051
10	GGATT	0.098	0.170	0.072	CCCCA	0.064	0.128	0.064	GGGGT	0.039	0.090	0.050



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	8.41	8.85	5.19	0.00	8.61	8.76	5.35	0.00	8.50	8.72	4.90
C	8.99	0.00	9.08	9.86	9.52	0.00	8.65	9.42	9.23	0.00	10.05	8.96
G	9.36	9.10	0.00	8.69	8.84	8.78	0.00	9.15	8.76	10.13	0.00	8.86
T	5.42	8.82	8.23	0.00	5.59	8.75	8.57	0.00	4.93	8.59	8.36	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 (3.44%)	TTC (3.40%)	AAA (4.24%)	TTC (3.01%)	AAA (2.85%)	AAA (4.10%)	TTC (3.07%)	GCA (2.71%)	AAA (3.88%)
2	AAA (2.98%)	AAA (2.91%)	TTC (3.70%)	TGC (2.92%)	GGC (2.82%)	GCA (3.52%)	AAA (3.06%)	AAA (2.70%)	GCA (3.51%)
3	TGC (2.75%)	TGC (2.85%)	GCA (3.33%)	AAA (2.87%)	TGC (2.80%)	GAA (3.37%)	GCA (2.96%)	TTC (2.60%)	GAA (3.21%)
4	GCA (2.68%)	GCA (2.81%)	GAA (3.15%)	GCA (2.74%)	GCA (2.75%)	TTC (3.16%)	TGC (2.65%)	TCA (2.58%)	TTC (3.09%)
5	ATC (2.44%)	TCA (2.52%)	TGC (2.60%)	GAA (2.56%)	TTC (2.66%)	TGC (2.58%)	GAA (2.59%)	GCG (2.56%)	AAT (2.60%)
6	TCA (2.43%)	GCC (2.42%)	AAT (2.52%)	CAG (2.41%)	GAA (2.52%)	TTT (2.48%)	TCA (2.47%)	GGC (2.50%)	TTT (2.48%)
7	GCC (2.42%)	GAA (2.35%)	TTT (2.46%)	TCA (2.34%)	TCA (2.35%)	TCA (2.41%)	CGC (2.43%)	TGC (2.46%)	GCC (2.34%)
8	GAA (2.35%)	AAT (2.35%)	TCA (2.29%)	GGC (2.30%)	GCC (2.34%)	AAT (2.23%)	ATC (2.36%)	GAA (2.40%)	GTT (2.31%)
9	GGC (2.19%)	GGC (2.33%)	GCC (2.25%)	ATC (2.24%)	AAT (2.23%)	ATC (2.22%)	AAT (2.29%)	CGC (2.21%)	TGC (2.28%)
10	CAG (2.12%)	ATC (2.27%)	ATC (2.20%)	GCC (2.24%)	GCG (2.21%)	GCC (2.22%)	GCG (2.28%)	GCC (2.17%)	TCA (2.26%)
-10	TGT (0.98%)	AGT (0.93%)	GGT (0.89%)	AGT (0.96%)	AGT (0.93%)	CTT (0.90%)	CTC (0.98%)	CTC (0.99%)	GGG (0.90%)
-9	CTC (0.94%)	CCT (0.91%)	AGA (0.87%)	AGA (0.94%)	AGG (0.91%)	CTC (0.90%)	TGT (0.96%)	CGA (0.96%)	CGA (0.88%)
-8	CCC (0.89%)	AGG (0.90%)	GGG (0.85%)	CTC (0.89%)	GGA (0.89%)	CCT (0.85%)	AGA (0.82%)	ACT (0.94%)	CCC (0.87%)
-7	AGA (0.82%)	CTT (0.89%)	AGT (0.84%)	CCC (0.84%)	CCC (0.88%)	AGT (0.85%)	CCC (0.81%)	CTT (0.92%)	AGG (0.86%)
-6	GAG (0.76%)	CGA (0.84%)	TGT (0.81%)	GGA (0.83%)	CCT (0.87%)	ACT (0.79%)	GAG (0.78%)	CCC (0.86%)	CTT (0.83%)
-5	GGA (0.75%)	GAG (0.83%)	AGG (0.80%)	GAG (0.75%)	CTC (0.84%)	AGG (0.76%)	GGA (0.78%)	CCT (0.84%)	GAG (0.75%)
-4	AGG (0.71%)	AGA (0.72%)	CTT (0.79%)	AGG (0.69%)	GAG (0.83%)	GGG (0.75%)	AGG (0.74%)	AGA (0.78%)	GGA (0.70%)
-3	GGG (0.66%)	GGA (0.67%)	GAG (0.64%)	GGG (0.58%)	GGG (0.79%)	GAG (0.60%)	GGG (0.64%)	GGA (0.71%)	AGA (0.68%)
-2	CTA (0.50%)	TAG (0.50%)	TAG (0.39%)	CTA (0.54%)	CTA (0.52%)	CTA (0.44%)	CTA (0.54%)	CTA (0.60%)	TAG (0.42%)
-1	TAG (0.44%)	CTA (0.46%)	CTA (0.36%)	TAG (0.45%)	TAG (0.50%)	TAG (0.36%)	TAG (0.46%)	TAG (0.57%)	CTA (0.36%)

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 (1.04%)	AAAA (1.39%)	CAGC (0.90%)	CGGC (1.04%)	AAAA (1.14%)	GAAA (0.94%)	TTCA (0.92%)	GAAA (1.12%)
2	GAAA (0.98%)	TTCA (1.00%)	GAAA (1.25%)	ATCA (0.88%)	CAGC (1.01%)	CAAA (1.13%)	CGCC (0.84%)	TGGC (0.89%)	AAAA (1.09%)
3	AAAA (0.96%)	TGCC (0.93%)	TTTC (1.19%)	TTGC (0.88%)	TGGC (0.97%)	GAAA (1.02%)	TTTC (0.83%)	CAGC (0.89%)	GGCA (1.01%)
4	TTCA (0.88%)	AAAA (0.92%)	GGCA (0.91%)	CTGC (0.86%)	TTGC (0.89%)	TGAA (0.99%)	CAAA (0.82%)	ATCA (0.79%)	TTTC (0.91%)
5	TGCC (0.86%)	TTCC (0.88%)	CAAA (0.91%)	CAAA (0.85%)	CAAA (0.87%)	GGCA (0.90%)	TTCA (0.82%)	CGGC (0.77%)	TGAA (0.91%)
6	CAGC (0.85%)	CAGC (0.86%)	AACG (0.91%)	CGGC (0.82%)	CTGC (0.83%)	TTTC (0.90%)	CAGC (0.82%)	GCCA (0.75%)	CAAA (0.89%)
7	TTGC (0.84%)	GAAA (0.86%)	GCAA (0.90%)	AAAA (0.81%)	ATCA (0.81%)	ATCA (0.89%)	ATCA (0.81%)	CAAA (0.75%)	GGAA (0.89%)
8	AACG (0.82%)	TTGC (0.85%)	TGAA (0.89%)	GAAA (0.79%)	TTCC (0.81%)	AGCA (0.88%)	AACA (0.80%)	CGCC (0.74%)	CGCA (0.87%)
9	GTTC (0.82%)	TGGC (0.82%)	GTTC (0.88%)	TTTC (0.79%)	TTCA (0.80%)	TAAA (0.86%)	TTGC (0.79%)	TGCC (0.73%)	CGCC (0.86%)
10	ATCA (0.81%)	AACG (0.82%)	TTCA (0.88%)	CCAG (0.79%)	TGCC (0.79%)	CGCA (0.84%)	GCCA (0.78%)	CTGC (0.73%)	TGCA (0.84%)
-10	TAGT (0.12%)	TAGT (0.12%)	CCCT (0.11%)	GTGT (0.12%)	GAGG (0.12%)	GTGT (0.10%)	TTAG (0.13%)	GAGA (0.15%)	TATA (0.11%)
-9	AGGG (0.12%)	CTAT (0.12%)	TTAG (0.11%)	CTAA (0.11%)	CCCC (0.12%)	TTAG (0.10%)	GAGG (0.13%)	CGGA (0.15%)	CCCT (0.11%)
-8	CTAA (0.11%)	GGAC (0.12%)	ACTA (0.11%)	AGGG (0.10%)	CTAA (0.11%)	TAGT (0.10%)	CCCT (0.12%)	CCCC (0.14%)	CTAT (0.11%)
-7	TTAG (0.11%)	CGGA (0.11%)	TAGT (0.09%)	CCCT (0.09%)	GTGT (0.11%)	GAGG (0.10%)	AGGG (0.12%)	CTAT (0.14%)	CTAA (0.10%)
-6	GAGG (0.10%)	CCCT (0.10%)	GGAC (0.08%)	GGAC (0.09%)	ACCT (0.11%)	CGAG (0.09%)	CTAT (0.12%)	CTAA (0.12%)	TCTA (0.10%)
-5	GGAC (0.10%)	CTAA (0.10%)	TCTA (0.08%)	GAGG (0.09%)	TAGA (0.10%)	GGAC (0.09%)	CTAA (0.11%)	CCCT (0.10%)	ACTA (0.09%)
-4	TAGA (0.06%)	TAGG (0.07%)	TAGA (0.07%)	TAGA (0.09%)	CCCT (0.07%)	TAGG (0.07%)	TAGA (0.07%)	TAGA (0.09%)	TAGG (0.07%)
-3	CCTA (0.06%)	TAGA (0.06%)	TAGG (0.06%)	CCTA (0.07%)	TAGG (0.06%)	CCCT (0.07%)	CCTA (0.07%)	TAGG (0.08%)	TAGA (0.06%)
-2	TAGG (0.05%)	CCTA (0.05%)	CCTA (0.05%)	TAGG (0.05%)	CCTA (0.06%)	CCTA (0.05%)	TAGG (0.05%)	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 (0.37%)	CAGCA (0.43%)	CAGCA (0.41%)	CAGCA (0.44%)	CAGCA (0.54%)	CAGCA (0.36%)	CAGCA (0.35%)	CAGCA (0.47%)
2	CAAAA (0.32%)	TTGCC (0.34%)	CAAAA (0.42%)	GCTGC (0.34%)	GCGGC (0.37%)	GCAAA (0.40%)	CGCCA (0.32%)	CTGGC (0.35%)	CGGCA (0.38%)
3	TTGCC (0.30%)	CTGGC (0.32%)	GAAAA (0.41%)	CATCA (0.34%)	CTGGC (0.35%)	CGGCA (0.38%)	GCAAA (0.31%)	CGCCA (0.30%)	GAAAA (0.36%)
4	TCTTC (0.30%)	TTTGC (0.31%)	GCAAA (0.36%)	GCAAA (0.30%)	CATCA (0.32%)	ATAAA (0.37%)	AACGC (0.30%)	CATCA (0.29%)	TGGCA (0.35%)
5	CGCCA (0.30%)	CGTTC (0.30%)	CGTTC (0.34%)	CCAGC (0.30%)	GCTGC (0.31%)	GAAAA (0.36%)	CGGCA (0.29%)	GCGGC (0.28%)	CAAAA (0.35%)
6	GCAGC (0.30%)	TTTCA (0.30%)	TGAAA (0.34%)	TTTGC (0.30%)	CCAGC (0.31%)	CATCA (0.35%)	CTGGC (0.28%)	TGGCG (0.28%)	GCAAA (0.33%)
7	GAAAA (0.30%)	CAAAA (0.30%)	AGAAA (0.32%)	GCGGC (0.29%)	GCAAA (0.31%)	AAGAA (0.34%)	GCCAG (0.28%)	CCAGC (0.28%)	TGAAA (0.32%)
8	ATTTT (0.30%)	GCAGC (0.29%)	TCTTC (0.32%)	CTGGC (0.28%)	TTTGC (0.30%)	ACGCA (0.33%)	CCAGC (0.28%)	GCAAA (0.28%)	CGCCA (0.31%)
9	CCAGC (0.30%)	GAAAA (0.29%)	TTGCC (0.32%)	TCTTC (0.28%)	ATAAA (0.30%)	CAAAA (0.33%)	CAAAA (0.28%)	TTTCA (0.28%)	AAGAA (0.30%)
10	TTTGC (0.30%)	CATCA (0.29%)	TGTTT (0.31%)	GCCAG (0.28%)	TCAGC (0.30%)	ACAAA (0.31%)	TGAAA (0.27%)	GCAGC (0.27%)	TTGCC (0.30%)
-10	GGACC (0.01%)	TAGGA (0.01%)	CTTAG (0.01%)	ACCTA (0.01%)	CCCTA (0.01%)	CCCTA (0.01%)	CCCTA (0.01%)	CCCTA (0.01%)	ACCTA (0.01%)
-9	TAGGA (0.01%)	CCCTA (0.01%)	CCCTA (0.01%)	TAGGG (0.01%)	CCCCC (0.01%)	ACCTA (0.01%)	CTAGT (0.01%)	TAGGA (0.01%)	CCCTA (0.00%)
-8	CTAGC (0.00%)	ACTAG (0.00%)	ACTAG (0.00%)	CTAGC (0.00%)	CTAGC (0.01%)	CTAGC (0.00%)	TAGGA (0.01%)	GCTAG (0.01%)	GCTAG (0.00%)
-7	ACTAG (0.00%)	GCTAG (0.00%)	GCTAG (0.00%)	ACTAG (0.00%)	CTAGT (0.00%)	GCTAG (0.00%)	CTAGC (0.00%)	CTAGC (0.01%)	CTAGT (0.00%)
-6	GCTAG (0.00%)	CTAGC (0.00%)	CTAGC (0.00%)	GCTAG (0.00%)	GCTAG (0.00%)	CTAGT (0.00%)	GCTAG (0.00%)	ACTAG (0.01%)	CTAGC (0.00%)
-5	CTAGT (0.00%)	CTAGT (0.00%)	CTAGT (0.00%)	CTAGT (0.00%)	ACTAG (0.00%)	ACTAG (0.00%)	ACTAG (0.00%)	CTAGT (0.00%)	CTAGG (0.00%)
-4	CCTAG (0.00%)	CTAGG (0.00%)	CCTAG (0.00%)	TCTAG (0.00%)	CTAGA (0.00%)	CTAGG (0.00%)	CTAGG (0.00%)	TCTAG (0.00%)	ACTAG (0.00%)
-3	TCTAG (0.00%)	TCTAG (0.00%)	CTAGG (0.00%)	CTAGG (0.00%)	CTAGG (0.00%)	CTAGA (0.00%)	CCTAG (0.00%)	CTAGG (0.00%)	CCTAG (0.00%)
-2	CTAGA (0.00%)	CCTAG (0.00%)	TCTAG (0.00%)	CCTAG (0.00%)	CCTAG (0.00%)	TCTAG (0.00%)	TCTAG (0.00%)	CTAGA (0.00%)	TCTAG (0.00%)
-1	CTAGG (0.00%)	CTAGA (0.00%)	CTAGA (0.00%)	CTAGA (0.00%)	TCTAG (0.00%)	CCTAG (0.00%)	CTAGA (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%