

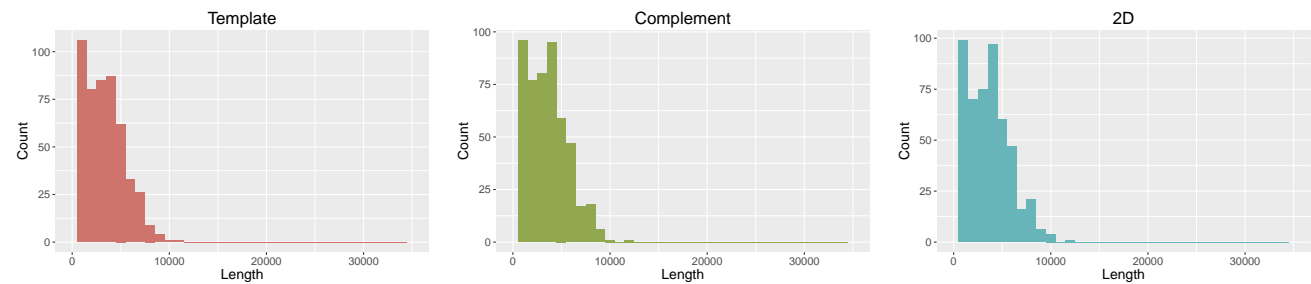
NanoOK report for main

Pass and fail counts

Type	Pass	Fail
Template	500	0
Complement	500	0
2D	500	0

Read lengths

Type	NumReads	TotalBases	Mean	Longest	Shortest	N50	N50Count	N90	N90Count
Template	500	1685124	3370.25	10794	260	4309	144	1969	354
Complement	500	1788780	3577.56	12018	300	4533	146	2014	358
2D	500	1824129	3648.26	12165	297	4672	145	2117	355



Template alignments

Number of reads	500
Number of reads with alignments	471 (94.20%)
Number of reads without alignments	29 (5.80%)

ID	Size	Number of Reads	% of Reads	Mean read length	Aligned bases	Mean coverage	Longest Perf Kmer
DNA CS	3560	17	3.40	3018.24	57853	16.25	47
Escherichia coli	4686137	454	90.80	3492.26	1766480	0.38	59

Complement alignments

Number of reads	500
Number of reads with alignments	479 (95.80%)
Number of reads without alignments	21 (4.20%)

ID	Size	Number of Reads	% of Reads	Mean read length	Aligned bases	Mean coverage	Longest Perf Kmer
DNA CS	3560	17	3.40	3252.59	57967	16.28	47
Escherichia coli	4686137	462	92.40	3660.72	1801633	0.38	47

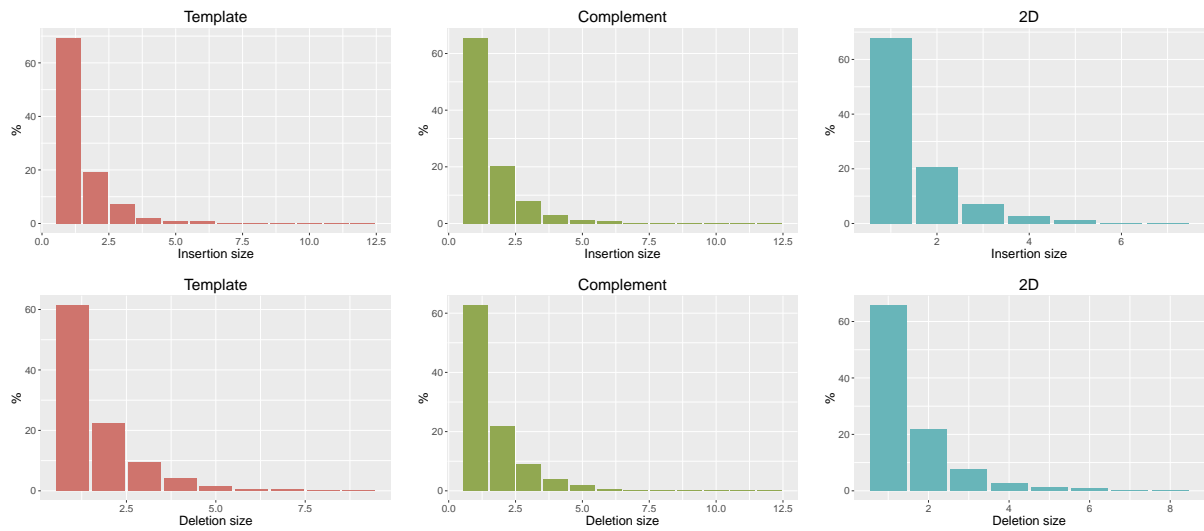
2D alignments

Number of reads	500
Number of reads with alignments	486 (97.20%)
Number of reads without alignments	14 (2.80%)

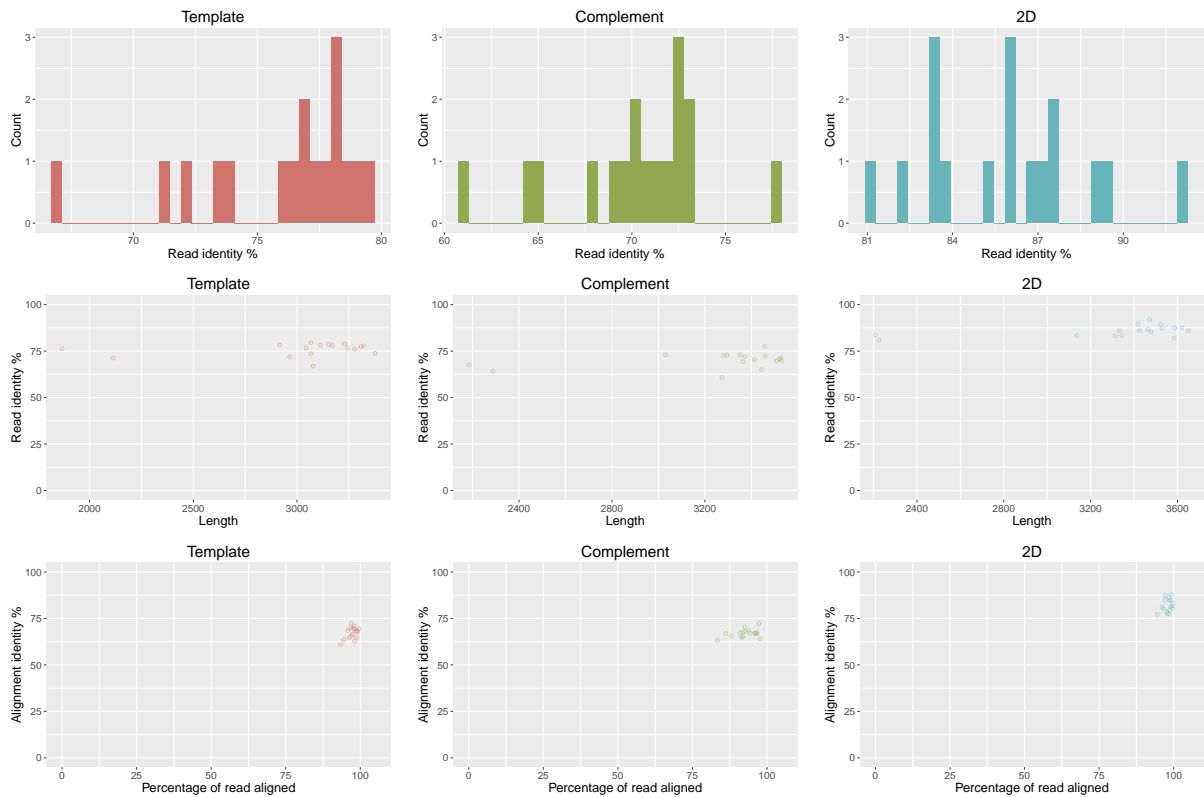
ID	Size	Number of Reads	% of Reads	Mean read length	Aligned bases	Mean coverage	Longest Perf Kmer
DNA CS	3560	17	3.40	3312.65	59003	16.57	87
Escherichia coli	4686137	469	93.80	3692.05	1814283	0.39	182

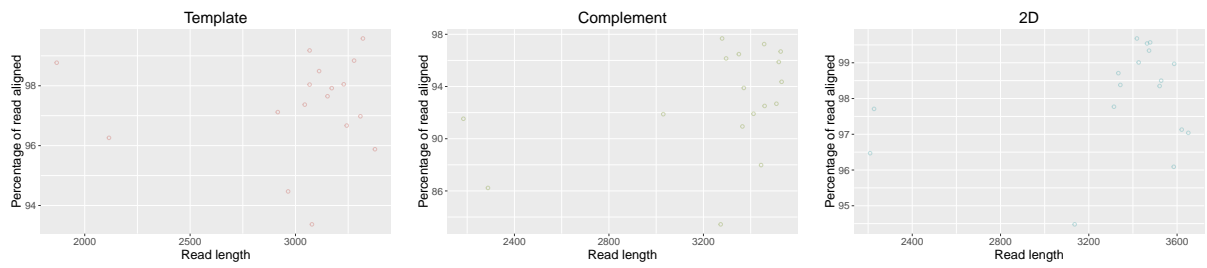
DNA CS error analysis

	Template	Complement	2D
Overall base identity (excluding indels)	76.00%	70.31%	86.06%
Aligned base identity (excluding indels)	80.90%	80.23%	91.54%
Identical bases per 100 aligned bases (including indels)	67.41%	67.07%	82.14%
Inserted bases per 100 aligned bases (including indels)	3.00%	5.09%	3.89%
Deleted bases per 100 aligned bases (including indels)	13.67%	11.31%	6.37%
Substitutions per 100 aligned bases (including indels)	15.92%	16.53%	7.59%
Mean insertion size	1.50	1.61	1.49
Mean deletion size	1.66	1.65	1.55

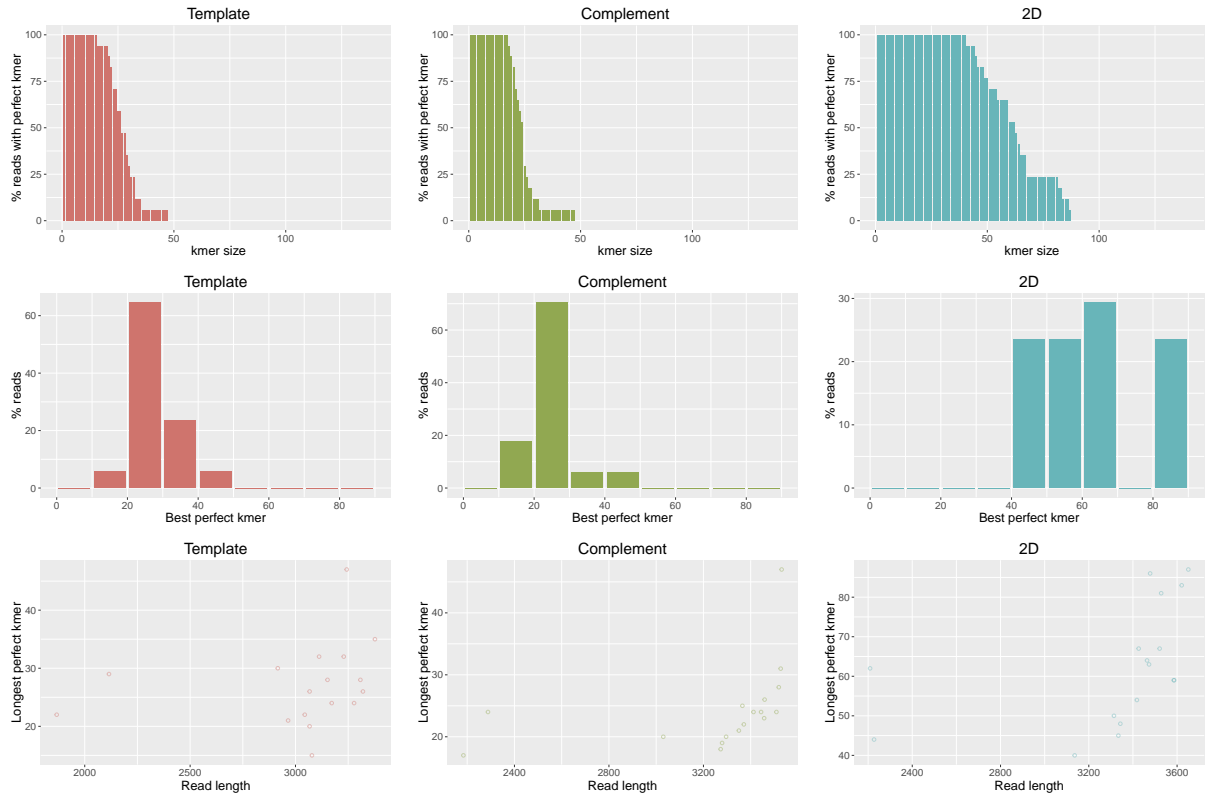


DNA CS read identity

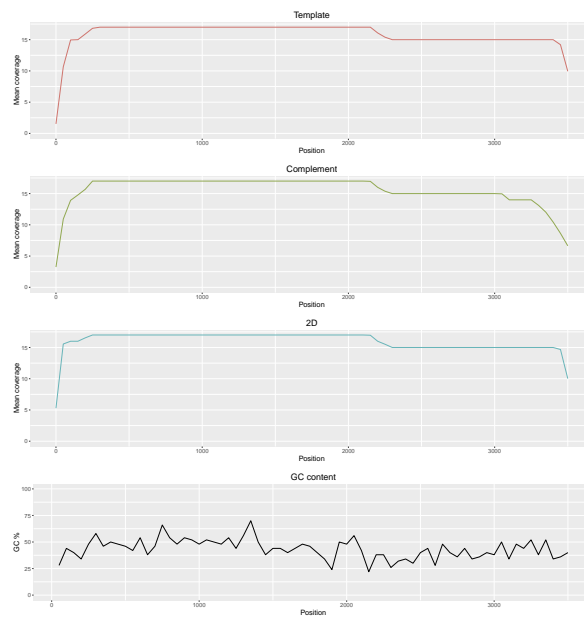




DNA CS perfect kmers



DNA CS coverage



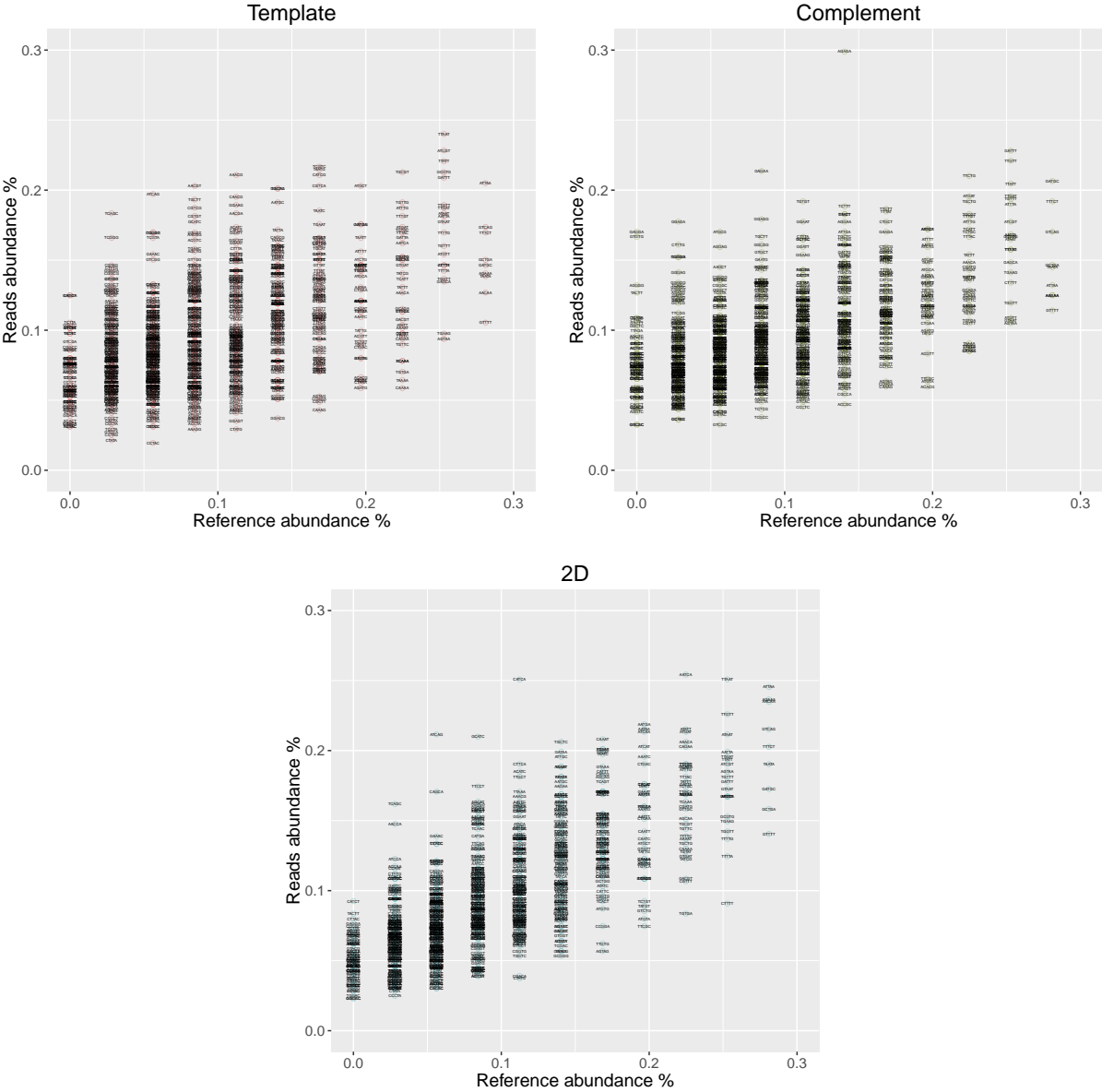
DNA CS 5-mer analysis

Under-represented 5-mers

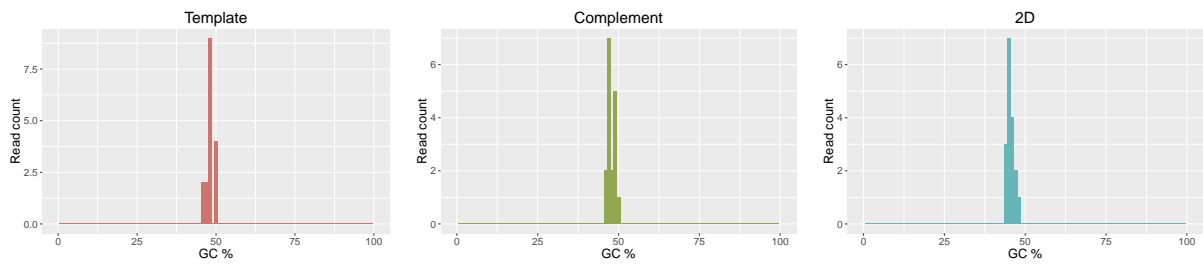
Rank	Template				Complement				2D			
	kmer	Ref %	Read %	Diff %	kmer	Ref %	Read %	Diff %	kmer	Ref %	Read %	Diff %
1	TTTTT	0.759	0.078	-0.681	TTTTT	0.759	0.114	-0.645	TTTTT	0.759	0.039	-0.720
2	AAAAA	0.478	0.057	-0.421	AAAAA	0.478	0.080	-0.398	AAAAA	0.478	0.055	-0.423
3	TGATG	0.393	0.137	-0.257	AAAGG	0.337	0.125	-0.212	TGATG	0.393	0.203	-0.191
4	AAAAC	0.337	0.082	-0.255	GATGT	0.309	0.100	-0.209	CTTTT	0.253	0.091	-0.162
5	GATGT	0.309	0.096	-0.213	TGATG	0.393	0.199	-0.194	GATGT	0.309	0.148	-0.161
6	AATAT	0.309	0.111	-0.198	GTTTT	0.281	0.114	-0.167	AAAAC	0.337	0.180	-0.158
7	CTGAT	0.309	0.123	-0.186	GCAAT	0.309	0.152	-0.157	CTGAT	0.309	0.155	-0.154
8	GTTTT	0.281	0.105	-0.176	AACAA	0.281	0.125	-0.156	GCAAT	0.309	0.158	-0.151
9	CAAAA	0.225	0.059	-0.166	AGAAA	0.281	0.125	-0.156	TTATC	0.309	0.165	-0.144
10	TAAAA	0.225	0.064	-0.160	ATTAA	0.281	0.132	-0.149	TGTGA	0.225	0.084	-0.141

Over-represented 5-mers

Rank	Template				Complement				2D			
	kmer	Ref %	Read %	Diff %	kmer	Ref %	Read %	Diff %	kmer	Ref %	Read %	Diff %
1	TCAGC	0.028	0.184	0.155	GAGAG	0.112	0.306	0.194	ATCAG	0.056	0.212	0.155
2	ATCAG	0.056	0.197	0.141	GAGGA	0.000	0.170	0.170	CATCA	0.112	0.251	0.138
3	TCGGG	0.028	0.166	0.138	GTGTG	0.000	0.167	0.167	TCAGC	0.028	0.162	0.134
4	GAGGA	0.000	0.125	0.125	AGAGA	0.140	0.299	0.158	GCATC	0.084	0.210	0.126
5	CATCT	0.000	0.125	0.125	GGAGA	0.028	0.178	0.149	AACCA	0.028	0.148	0.120
6	AACGT	0.084	0.203	0.119	CTTTG	0.028	0.161	0.133	CAGCA	0.056	0.171	0.115
7	CGTAG	0.028	0.146	0.118	AGGGG	0.000	0.132	0.132	ATCCA	0.028	0.123	0.095
8	CTTTG	0.028	0.144	0.116	GAGAA	0.084	0.214	0.129	CATCT	0.000	0.092	0.092
9	GGGGA	0.028	0.143	0.114	TACTT	0.000	0.127	0.127	TTCCT	0.084	0.174	0.090
10	TCCGT	0.056	0.170	0.114	TCGGG	0.028	0.152	0.124	ACCAA	0.028	0.117	0.089

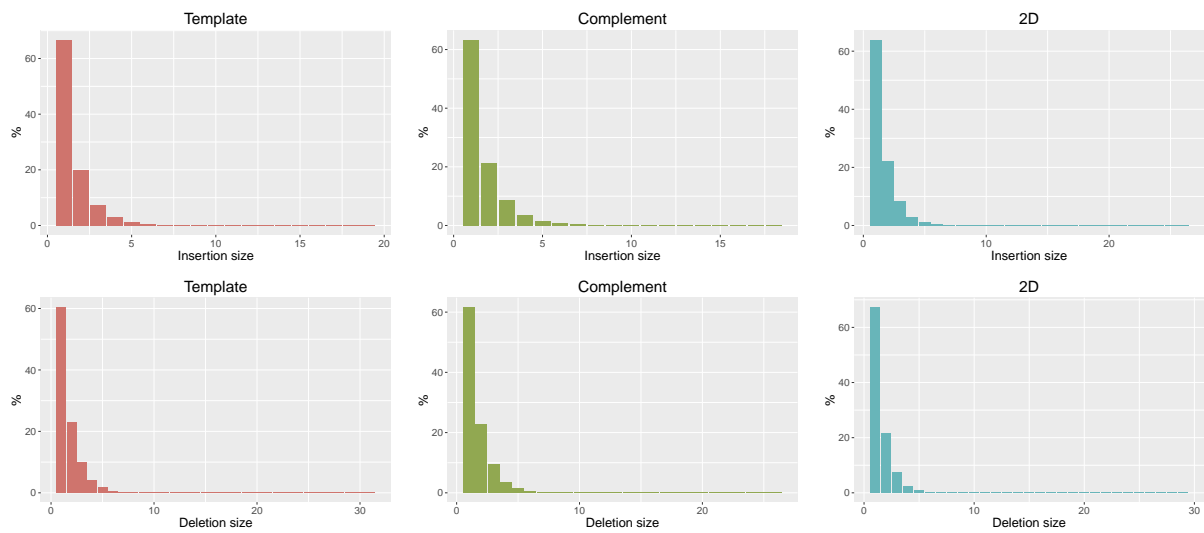


DNA CS GC content

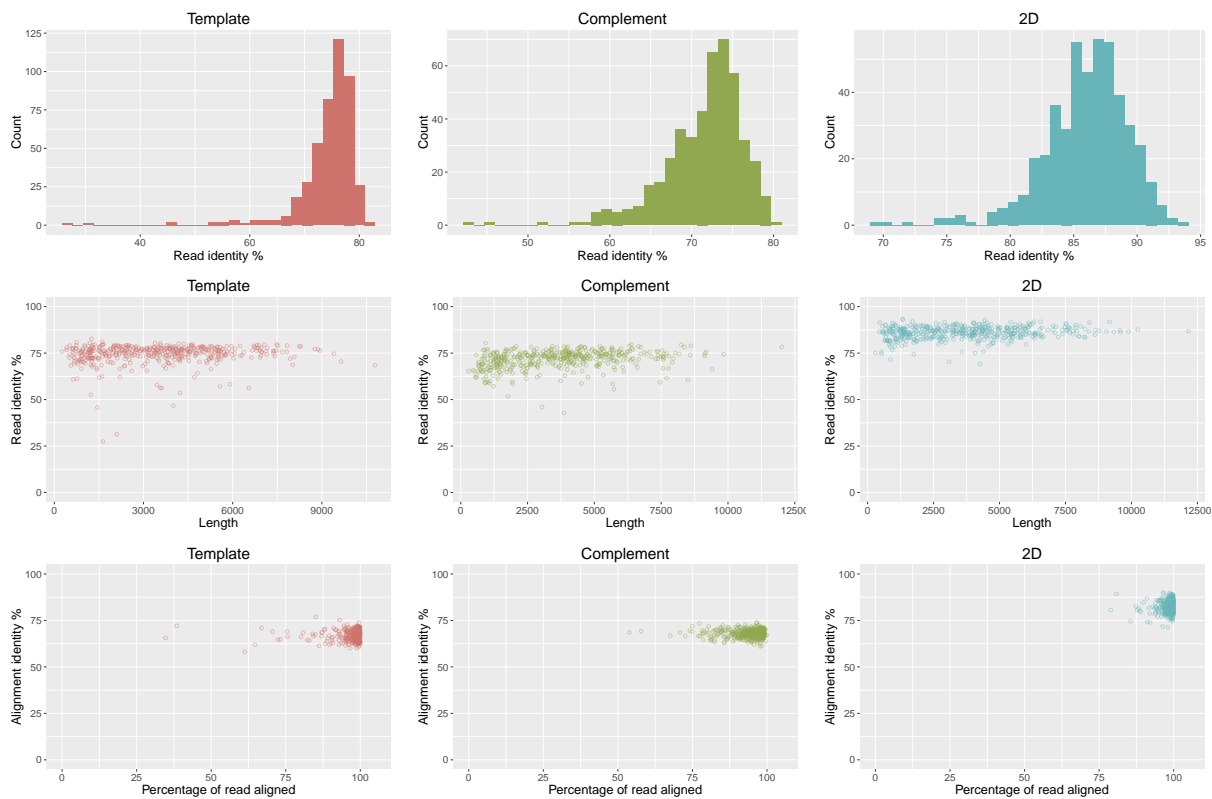


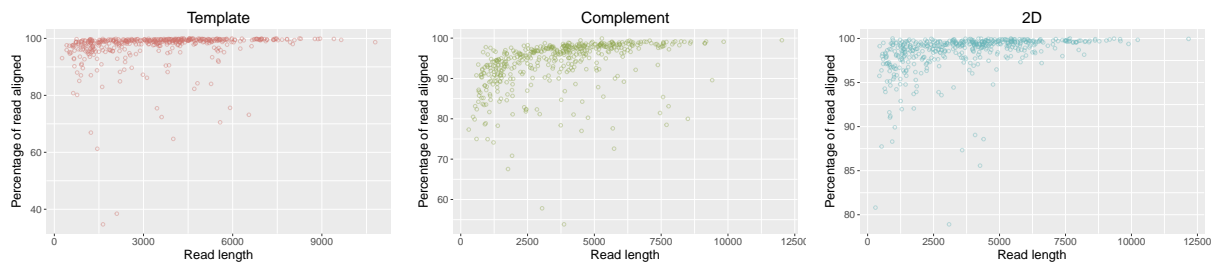
Escherichia coli error analysis

	Template	Complement	2D
Overall base identity (excluding indels)	74.62%	72.29%	86.31%
Aligned base identity (excluding indels)	80.51%	81.26%	91.72%
Identical bases per 100 aligned bases (including indels)	66.97%	67.86%	82.38%
Inserted bases per 100 aligned bases (including indels)	3.89%	5.49%	4.58%
Deleted bases per 100 aligned bases (including indels)	12.92%	10.99%	5.60%
Substitutions per 100 aligned bases (including indels)	16.22%	15.65%	7.44%
Mean insertion size	1.59	1.65	1.60
Mean deletion size	1.68	1.64	1.50

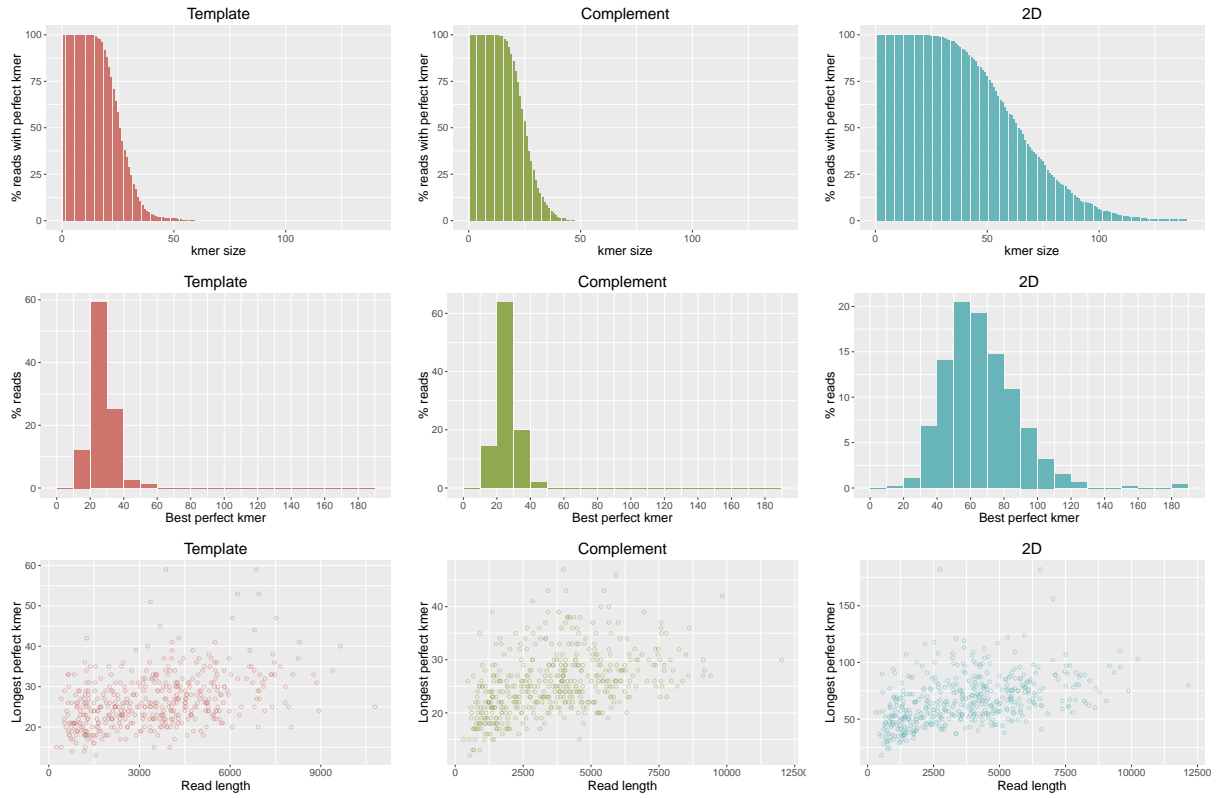


Escherichia coli read identity

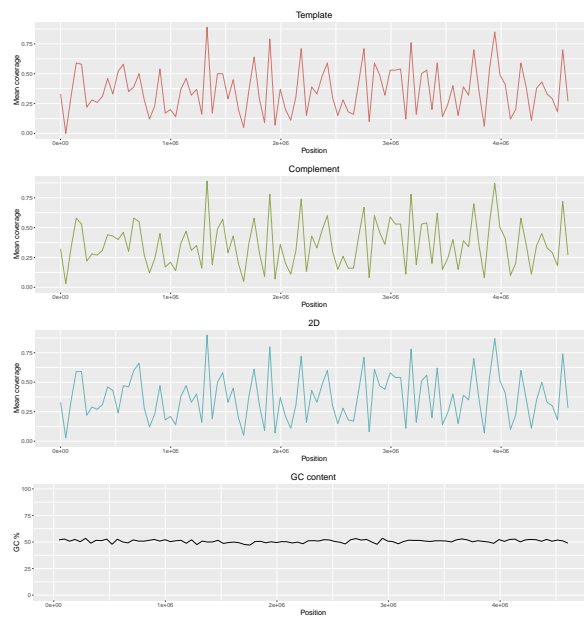




Escherichia coli perfect kmers



Escherichia coli coverage



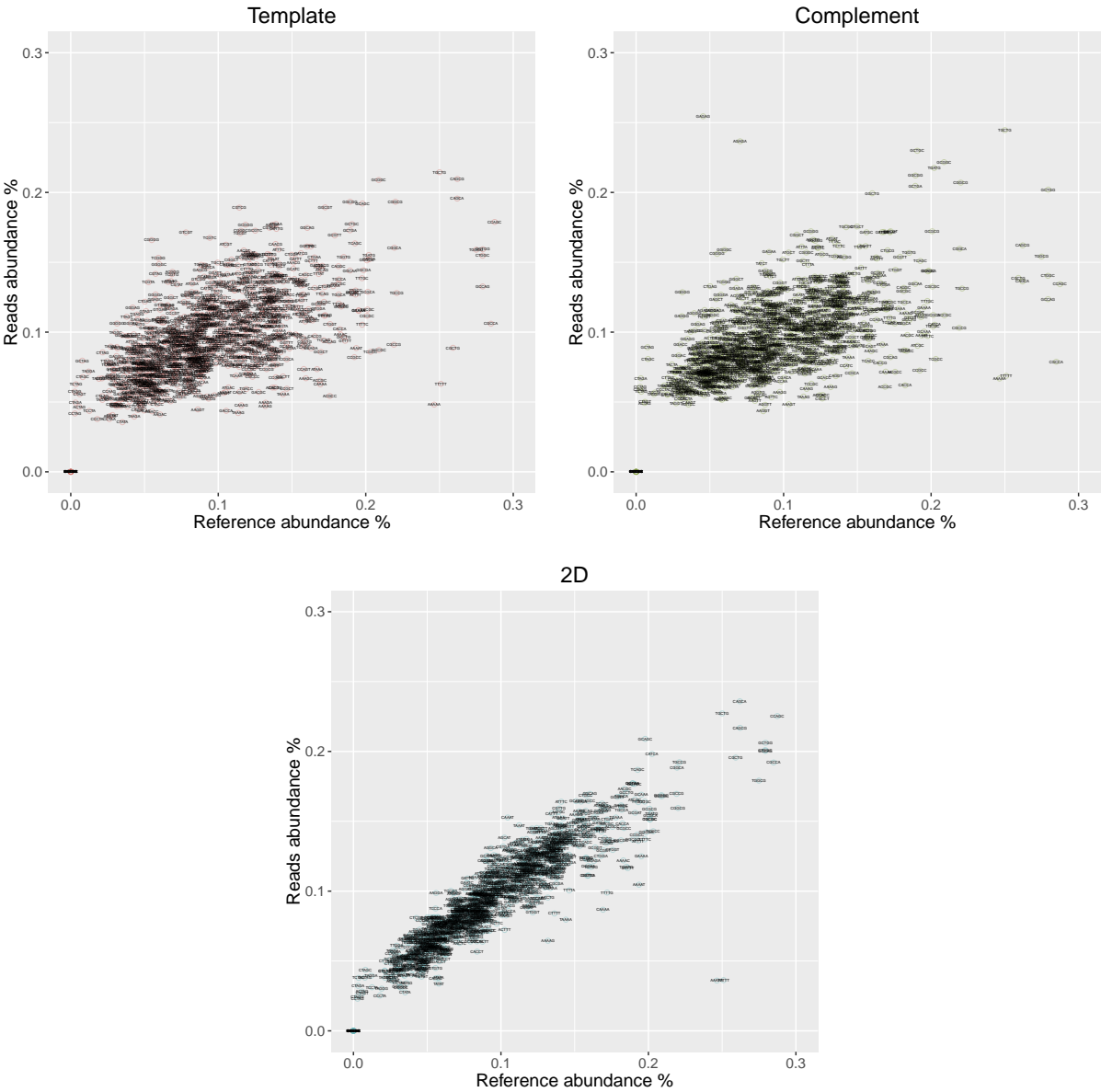
Escherichia coli 5-mer analysis

Under-represented 5-mers

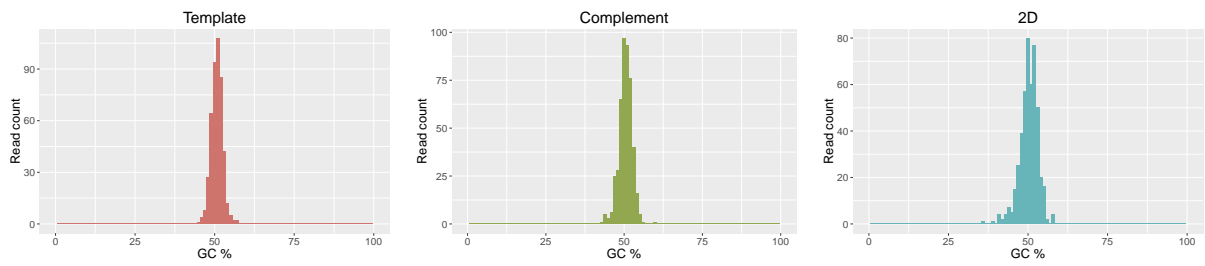
Rank	Template				Complement				2D			
	kmer	Ref %	Read %	Diff %	kmer	Ref %	Read %	Diff %	kmer	Ref %	Read %	Diff %
1	AAAAA	0.246	0.048	-0.198	CGCCA	0.285	0.079	-0.206	TTTTT	0.251	0.036	-0.215
2	TTTTT	0.251	0.063	-0.188	TTTTT	0.251	0.069	-0.182	AAAAA	0.246	0.036	-0.210
3	CGCCA	0.285	0.106	-0.179	AAAAA	0.246	0.067	-0.180	TGGCG	0.275	0.179	-0.096
4	CGCTG	0.259	0.089	-0.170	GCCAG	0.279	0.124	-0.156	CGCCA	0.285	0.192	-0.093
5	GCCAG	0.279	0.133	-0.147	CCAGC	0.287	0.134	-0.153	AAAAT	0.194	0.105	-0.089
6	CGCCG	0.219	0.091	-0.128	CTGGC	0.279	0.140	-0.139	CAAAA	0.169	0.087	-0.082
7	CTGGC	0.279	0.155	-0.124	CAGCA	0.262	0.136	-0.126	GCCAG	0.279	0.200	-0.079
8	GCCGC	0.209	0.087	-0.122	TCGCC	0.203	0.081	-0.122	CTGGC	0.279	0.201	-0.078
9	ACGCC	0.176	0.054	-0.121	TGGCG	0.275	0.154	-0.121	GCTGG	0.279	0.206	-0.073
10	GCTGG	0.279	0.159	-0.120	CGCTG	0.259	0.139	-0.120	TTTTG	0.172	0.099	-0.073

Over-represented 5-mers

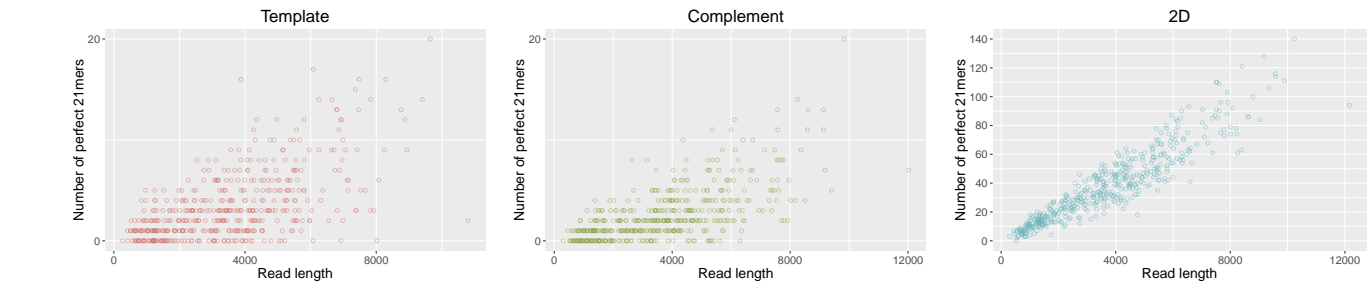
Rank	Template				Complement				2D			
	kmer	Ref %	Read %	Diff %	kmer	Ref %	Read %	Diff %	kmer	Ref %	Read %	Diff %
1	CGGGG	0.055	0.166	0.111	GAGAG	0.045	0.255	0.209	CAAAT	0.105	0.153	0.048
2	TCGGG	0.059	0.153	0.094	AGAGA	0.071	0.237	0.166	AAGGA	0.056	0.099	0.043
3	GTCGT	0.078	0.171	0.093	CGGGG	0.055	0.156	0.101	CTCGT	0.043	0.081	0.038
4	GGGGC	0.060	0.149	0.089	GGGGC	0.060	0.159	0.099	AGGCA	0.093	0.131	0.038
5	CGTAG	0.058	0.142	0.084	GGGGG	0.031	0.129	0.097	AGCAT	0.102	0.138	0.036
6	TCGTA	0.053	0.136	0.083	CTGAG	0.050	0.133	0.083	CTAGC	0.008	0.044	0.036
7	GGGAG	0.042	0.118	0.076	GCTAG	0.008	0.089	0.081	TAAAT	0.112	0.147	0.035
8	CGTCG	0.114	0.189	0.075	GAGGG	0.031	0.111	0.080	GCATG	0.090	0.125	0.035
9	GGGGG	0.031	0.106	0.075	TCGGG	0.059	0.136	0.076	TCTAG	0.004	0.038	0.034
10	ACGGG	0.069	0.143	0.074	AGGGG	0.039	0.114	0.074	TCCGT	0.066	0.100	0.034



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	8.60	9.72	5.00	0.00	8.92	9.08	5.18	0.00	8.39	8.45	4.45
	C	8.44	0.00	8.83	9.38	9.42	0.00	8.62	8.86	9.31	0.00	10.04	9.25
	G	9.41	8.91	0.00	8.50	8.86	8.57	0.00	9.31	9.32	9.94	0.00	9.51
	T	4.95	9.78	8.48	0.00	5.28	8.98	8.93	0.00	4.55	8.30	8.52	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 (2.99%)	AAA (3.42%)	AAA (3.60%)	AAA (2.93%)	AAA (3.44%)	AAA (3.75%)	GCA (3.07%)	AAA (5.68%)	AAA (3.90%)
2	GCA (2.59%)	TTC (3.09%)	TTC (3.54%)	GCA (2.77%)	GAA (2.96%)	GCA (3.60%)	AAA (2.80%)	TTT (4.85%)	GCA (3.62%)
3	TCA (2.57%)	TGC (2.94%)	GCA (3.27%)	TGC (2.58%)	TTT (2.74%)	GAA (3.19%)	TTC (2.71%)	GCC (2.76%)	GAA (3.26%)
4	AAA (2.57%)	GCC (2.70%)	GAA (2.82%)	TTT (2.47%)	GCA (2.64%)	TTC (2.85%)	GAA (2.63%)	GAA (2.62%)	TTC (2.80%)
5	ATC (2.51%)	TTT (2.65%)	TCA (2.56%)	GAA (2.40%)	TGC (2.58%)	TTT (2.66%)	TGC (2.55%)	GCA (2.47%)	TCA (2.62%)
6	TGC (2.44%)	GCA (2.59%)	TGC (2.53%)	CAG (2.33%)	TTT (2.39%)	TGC (2.43%)	TCA (2.52%)	GCG (2.38%)	GCC (2.61%)
7	TTT (2.29%)	TCA (2.41%)	ATC (2.30%)	TCA (2.30%)	GGC (2.38%)	TCA (2.39%)	CAG (2.43%)	TGC (2.23%)	TTT (2.54%)
8	GCC (2.23%)	GAA (2.37%)	GCC (2.28%)	GGC (2.17%)	GCC (2.35%)	ATC (2.23%)	ATC (2.34%)	TCA (2.12%)	GCG (2.42%)
9	CAG (2.18%)	GCG (2.17%)	TTT (2.20%)	TTT (2.09%)	CAG (2.27%)	CCA (2.16%)	GCC (2.25%)	TTC (2.10%)	GTT (2.32%)
10	GCG (2.17%)	ACG (2.11%)	ACG (2.19%)	GCC (2.09%)	AGC (2.10%)	GGC (2.16%)	CGC (2.24%)	CAG (2.03%)	TGC (2.24%)
	<div>TTC</div> <div>GCC</div> <div>AAA</div>	<div>TTT</div> <div>GCA</div> <div>AAA</div>	<div>TTT</div> <div>GCA</div> <div>AAA</div>	<div>TTT</div> <div>GCA</div> <div>AAA</div>	<div>TTT</div> <div>GCA</div> <div>AAA</div>	<div>TTT</div> <div>GCA</div> <div>AAA</div>	<div>TTT</div> <div>GCA</div> <div>AAA</div>	<div>TTT</div> <div>GCA</div> <div>AAA</div>	<div>TTT</div> <div>GCA</div> <div>AAA</div>
-10	AGT (0.99%)	GTA (0.95%)	GGG (0.88%)	GAC (1.02%)	AGG (0.98%)	CCC (0.97%)	AGG (0.98%)	CTC (0.93%)	GTA (0.89%)
-9	CCC (0.95%)	GGG (0.95%)	AGG (0.84%)	GTG (1.02%)	GGG (0.98%)	CTT (0.91%)	GGG (0.97%)	GAG (0.93%)	CTT (0.88%)
-8	GGG (0.95%)	ACT (0.94%)	TGT (0.84%)	CTC (0.99%)	AGT (0.95%)	GGG (0.84%)	TAT (0.97%)	AGA (0.83%)	CCT (0.88%)
-7	AGA (0.91%)	CGA (0.91%)	ACT (0.84%)	ACT (0.99%)	GTA (0.89%)	AGG (0.82%)	AGT (0.93%)	GTA (0.82%)	ACT (0.82%)
-6	CTT (0.84%)	AGT (0.80%)	AGT (0.83%)	GGG (0.97%)	CTC (0.86%)	AGT (0.79%)	TGT (0.92%)	CGA (0.80%)	CGA (0.79%)
-5	CTC (0.83%)	GGA (0.76%)	CTT (0.83%)	GGA (0.93%)	CCT (0.85%)	GAG (0.72%)	GAG (0.85%)	CCT (0.69%)	GAG (0.78%)
-4	AGG (0.81%)	GAG (0.72%)	AGA (0.80%)	GAG (0.89%)	GAG (0.81%)	CCT (0.69%)	AGA (0.83%)	ACT (0.66%)	AGA (0.64%)
-3	GAG (0.80%)	AGA (0.71%)	GAG (0.68%)	AGG (0.77%)	ACT (0.77%)	ACT (0.65%)	GGA (0.76%)	GGA (0.58%)	GGA (0.62%)
-2	TAG (0.47%)	TAG (0.52%)	CTA (0.40%)	CTA (0.50%)	CTA (0.53%)	CTA (0.43%)	TAG (0.49%)	CTA (0.57%)	TAG (0.46%)
-1	CTA (0.44%)	CTA (0.42%)	TAG (0.29%)	TAG (0.44%)	TAG (0.42%)	TAG (0.36%)	CTA (0.46%)	TAG (0.55%)	CTA (0.40%)
	<div>TTT</div> <div>GCG</div> <div>AAA</div>	<div>TTT</div> <div>GCG</div> <div>AAA</div>	<div>TTT</div> <div>GCG</div> <div>AAA</div>	<div>TTT</div> <div>GCG</div> <div>AAA</div>	<div>TTT</div> <div>GCG</div> <div>AAA</div>	<div>TTT</div> <div>GCG</div> <div>AAA</div>	<div>TTT</div> <div>GCG</div> <div>AAA</div>	<div>TTT</div> <div>GCG</div> <div>AAA</div>	<div>TTT</div> <div>GCG</div> <div>AAA</div>

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	ATCA (1.10%)	TGCC (1.09%)	GAAA (1.18%)	ATCA (1.02%)	CAGC (1.02%)	AGCA (1.04%)	GGCA (0.97%)	AAAA (1.81%)	AAAA (1.08%)
2	AACG (0.89%)	AAAA (1.02%)	TTTC (1.05%)	CAGC (0.94%)	CAAA (0.97%)	GAAA (1.02%)	GAAA (0.89%)	TTTT (1.72%)	GGCA (1.08%)
3	TGCC (0.89%)	GAAA (1.00%)	AAAA (1.03%)	CTGC (0.86%)	AAAA (0.91%)	CAAA (0.96%)	ATCA (0.89%)	CAAA (1.70%)	GAAA (1.05%)
4	GCTG (0.87%)	TTTC (0.96%)	ATCA (0.92%)	CAAA (0.86%)	TAAA (0.87%)	AAAA (0.95%)	CTGC (0.80%)	TAAA (1.35%)	ATCA (0.98%)
5	CATC (0.83%)	CAAA (0.95%)	CTTC (0.87%)	AGCA (0.85%)	GAAA (0.87%)	CGCA (0.93%)	CCAG (0.80%)	ATTT (1.29%)	TGCC (0.95%)
6	GAAA (0.82%)	TTCA (0.90%)	CGCA (0.86%)	AAAA (0.77%)	TGAA (0.86%)	ATCA (0.91%)	TGCC (0.80%)	CTTT (1.13%)	CAAA (0.93%)
7	TTTC (0.82%)	ATCA (0.89%)	GGCA (0.85%)	GCGC (0.76%)	ATTT (0.84%)	GGCA (0.90%)	CAAA (0.79%)	GAAA (1.09%)	TGAA (0.93%)
8	CGCC (0.82%)	CTGC (0.88%)	GCAA (0.84%)	GCGC (0.76%)	CGCC (0.82%)	CAGC (0.89%)	CGCA (0.75%)	CGCC (0.98%)	CGCC (0.89%)
9	CAAA (0.82%)	TTTT (0.85%)	TGCC (0.84%)	GAAA (0.75%)	TTTT (0.82%)	TGAA (0.87%)	CTGG (0.74%)	GTTT (0.97%)	GGAA (0.89%)
10	GTTC (0.80%)	CAGC (0.85%)	TTCA (0.82%)	ATGC (0.74%)	TGGC (0.80%)	TGCA (0.83%)	AACA (0.74%)	TGCC (0.91%)	AGCA (0.88%)
-10	TAGC (0.10%)	ACTA (0.11%)	TTAG (0.10%)	CGAG (0.13%)	GTGT (0.13%)	CTAA (0.10%)	GGAC (0.12%)	GACT (0.13%)	ACTA (0.10%)
-9	CCCT (0.10%)	CTAT (0.11%)	GGAC (0.09%)	ACTA (0.13%)	CGAG (0.13%)	TAGT (0.10%)	CCCT (0.11%)	TCTA (0.12%)	CTAT (0.10%)
-8	ACTA (0.09%)	CGAG (0.11%)	TCTA (0.09%)	GGAC (0.13%)	TTAG (0.13%)	TAGA (0.10%)	TAGT (0.11%)	ACCT (0.12%)	CTAA (0.10%)
-7	TAGA (0.09%)	TCTA (0.11%)	TAGT (0.08%)	TATA (0.12%)	TCTA (0.12%)	TTAG (0.09%)	TCTA (0.10%)	CACT (0.12%)	ACCT (0.10%)
-6	TCTA (0.07%)	TAGT (0.10%)	ACTA (0.08%)	CTAA (0.12%)	TAGT (0.11%)	TAGG (0.07%)	CTAA (0.09%)	CGGA (0.11%)	TATA (0.08%)
-5	TAGG (0.06%)	CTAA (0.09%)	TATA (0.08%)	CTAT (0.11%)	CCTC (0.10%)	ACTA (0.07%)	TAGG (0.08%)	TAGG (0.09%)	CCCT (0.07%)
-4	CCTA (0.06%)	TAGA (0.08%)	TAGA (0.07%)	GAGG (0.11%)	ACTA (0.09%)	CTAT (0.07%)	TAGA (0.07%)	TAGA (0.08%)	TAGA (0.06%)
-3	TTAG (0.05%)	TAGG (0.06%)	CCTA (0.04%)	CCCT (0.09%)	CCCT (0.09%)	CCCT (0.07%)	CTAT (0.07%)	CCCT (0.08%)	TAGG (0.06%)
-2	TATA (0.04%)	CCTA (0.03%)	TAGG (0.04%)	CCTA (0.06%)	TAGG (0.08%)	CCTA (0.03%)	CCTA (0.04%)	CCTA (0.06%)	CCTA (0.04%)
-1	CTAG (0.02%)	CTAG (0.00%)	CTAG (0.01%)	TAGG (0.04%)	CCTA (0.06%)	CTAG (0.01%)	CTAG (0.03%)	CTAG (0.01%)	CTAG (0.00%)

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 (0.46%)	TTGCC (0.42%)	CAGCA (0.42%)	CAGCA (0.57%)	CAGCA (0.42%)	CAGCA (0.57%)	CAGCA (0.41%)	ATTTT (0.71%)	CAGCA (0.45%)
2	CATCA (0.40%)	CAGCA (0.37%)	GAAAA (0.39%)	CCAGC (0.40%)	TCAGC (0.38%)	ATAAA (0.43%)	CGGCA (0.37%)	GAAAA (0.61%)	CGGCA (0.40%)
3	ATTTT (0.34%)	ATTTT (0.34%)	GCGCA (0.36%)	CATCA (0.33%)	ATAAA (0.35%)	CAGAA (0.38%)	GCTGG (0.34%)	GCAAA (0.59%)	TTGCC (0.37%)
4	CTGGC (0.34%)	CAAAA (0.34%)	CAAAA (0.36%)	GCTGC (0.31%)	CTGGC (0.33%)	CGGCA (0.35%)	GCAAA (0.32%)	ATAAA (0.58%)	GAAAA (0.36%)
5	TTATC (0.33%)	GCAAA (0.33%)	CATCA (0.36%)	ATAAA (0.31%)	GCTGC (0.31%)	CATCA (0.34%)	CATCA (0.29%)	TAAAA (0.56%)	CGCCA (0.36%)
6	GCAAA (0.31%)	GCTGC (0.33%)	AGAAA (0.33%)	GCGGC (0.31%)	GCAAA (0.31%)	CTGCA (0.34%)	ATTTT (0.29%)	CAAAA (0.51%)	CAAAA (0.34%)
7	GCATC (0.31%)	GAAAA (0.33%)	GGAAA (0.32%)	CGGCA (0.31%)	ACGCC (0.31%)	ACGCA (0.32%)	GCGCA (0.28%)	CTTTT (0.49%)	TGGCA (0.32%)
8	ATTTT (0.31%)	CATCA (0.32%)	GCAAA (0.31%)	ATTTT (0.31%)	ATTTT (0.31%)	CGCCA (0.32%)	TGGCA (0.28%)	ACAAA (0.43%)	GCAAA (0.31%)
9	TTGCC (0.31%)	CGCCA (0.32%)	CGGCA (0.31%)	ACAAA (0.30%)	CGGCA (0.31%)	GCTGC (0.32%)	TCTTC (0.28%)	TCTTT (0.42%)	TGAAA (0.31%)
10	CGCTG (0.30%)	TGCTG (0.30%)	TGCTG (0.31%)	CTGGC (0.29%)	GAAAA (0.31%)	TTATC (0.32%)	TGTTT (0.27%)	GATTT (0.39%)	CATCA (0.30%)
-10	ATAGG (0.01%)	TCTAT (0.01%)	TAGGT (0.01%)	ATATA (0.01%)	CCCTT (0.01%)	CTAGT (0.01%)	ACTAG (0.01%)	GTCCT (0.01%)	ATAGG (0.01%)
-9	CGAGT (0.01%)	CGAGT (0.01%)	TAGGG (0.01%)	ACTTG (0.01%)	GGACT (0.01%)	CTAGC (0.01%)	ACCTA (0.00%)	TAGGA (0.01%)	CCCTG (0.01%)
-8	CCGAG (0.01%)	GGACC (0.01%)	GGGAC (0.01%)	CTACT (0.01%)	CTACT (0.01%)	TAGAT (0.01%)	CCCCC (0.00%)	GCCCT (0.01%)	CCCTA (0.01%)
-7	TTTAG (0.01%)	TAGT (0.01%)	CTTGG (0.01%)	TAGGG (0.01%)	TAGGG (0.01%)	CCCTC (0.01%)	CTAGT (0.00%)	TCCTA (0.01%)	GCTAG (0.00%)
-6	TACTA (0.01%)	CTTAG (0.01%)	CTAAC (0.01%)	TAGGA (0.01%)	CTAAG (0.01%)	GGTCC (0.00%)	CTAGA (0.00%)	CTAGT (0.01%)	ACCTA (0.00%)
-5	CTGAG (0.01%)	TTGGA (0.01%)	GTCCA (0.01%)	GGGAC (0.01%)	CACTC (0.01%)	CTAGG (0.00%)	CTTGT (0.00%)	CTAGC (0.01%)	CTAGC (0.00%)
-4	ACTCG (0.01%)	GCTAG (0.00%)	TACTA (0.01%)	CTAAG (0.01%)	CTAGT (0.00%)	CTAGA (0.00%)	CCTAT (0.00%)	TCGGA (0.01%)	CTAGA (0.00%)
-3	GAGGG (0.01%)	CTAGC (0.00%)	TAAGA (0.00%)	CGAGG (0.01%)	CTAGC (0.00%)	TATAG (0.00%)	CCTAG (0.00%)	ACTAG (0.01%)	TAGGG (0.00%)
-2	GTAGC (0.01%)	TAGAT (0.00%)	CTAGC (0.00%)	TTTAG (0.01%)	CTAGA (0.00%)	TAGGT (0.00%)	TCGGA (0.00%)	CTAGA (0.00%)	TAGGA (0.00%)
-1	ACTAC (0.01%)	CCCTA (0.00%)	CCTAT (0.00%)	GAGGT (0.01%)	ACCCT (0.00%)	CCCTA (0.00%)	ACTAT (0.00%)	TCTAG (0.00%)	CTTAG (0.00%)

Most common

Least common

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