

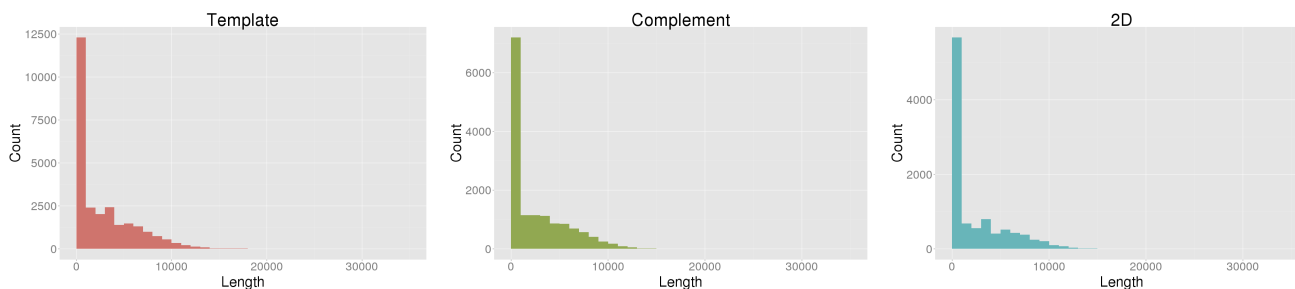
NanoOK report for JOGrady_MARC1b_run2

Pass and fail counts

Type	Pass	Fail
Template	0	26649
Complement	0	14680
2D	0	10162

Read lengths

Type	NumReads	TotalBases	Mean	Longest	Shortest	N50	N50Count	N90	N90Count
Template	26649	77677446	2914.84	201560	8	6313	4192	1846	12225
Complement	14680	39551611	2694.25	68739	21	5995	2347	1661	6623
2D	10162	24734334	2434.00	40646	107	6132	1465	1244	4246



Template alignments

Number of reads	26649
Number of reads with alignments	8102 (30.40%)
Number of reads without alignments	18547 (69.60%)

ID	Size	Number of Reads	% of Reads	Mean read length	Aligned bases	Mean coverage	Longest Perf Kmer
Control sequence	3560	1642	6.16	2910.71	4532627	1273.21	57
Escherichia coli	4641652	6460	24.24	6211.36	37188528	8.01	70

Complement alignments

Number of reads	14680
Number of reads with alignments	4550 (30.99%)
Number of reads without alignments	10130 (69.01%)

ID	Size	Number of Reads	% of Reads	Mean read length	Aligned bases	Mean coverage	Longest Perf Kmer
Control sequence	3560	729	4.97	2656.81	1601979	449.99	43
Escherichia coli	4641652	3821	26.03	5817.08	18527740	3.99	58

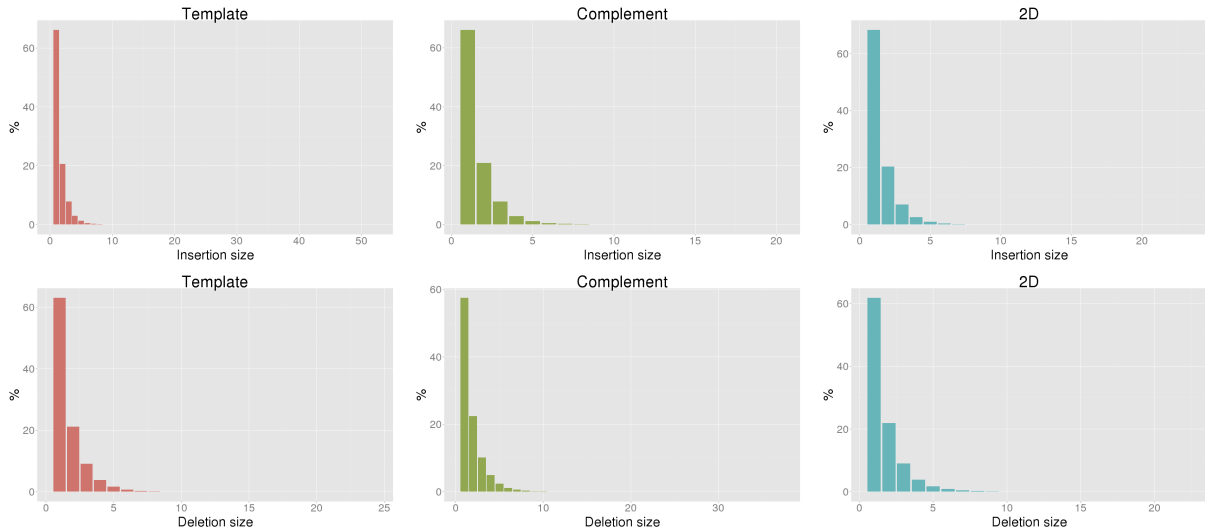
2D alignments

Number of reads	10162
Number of reads with alignments	3850 (37.89%)
Number of reads without alignments	6312 (62.11%)

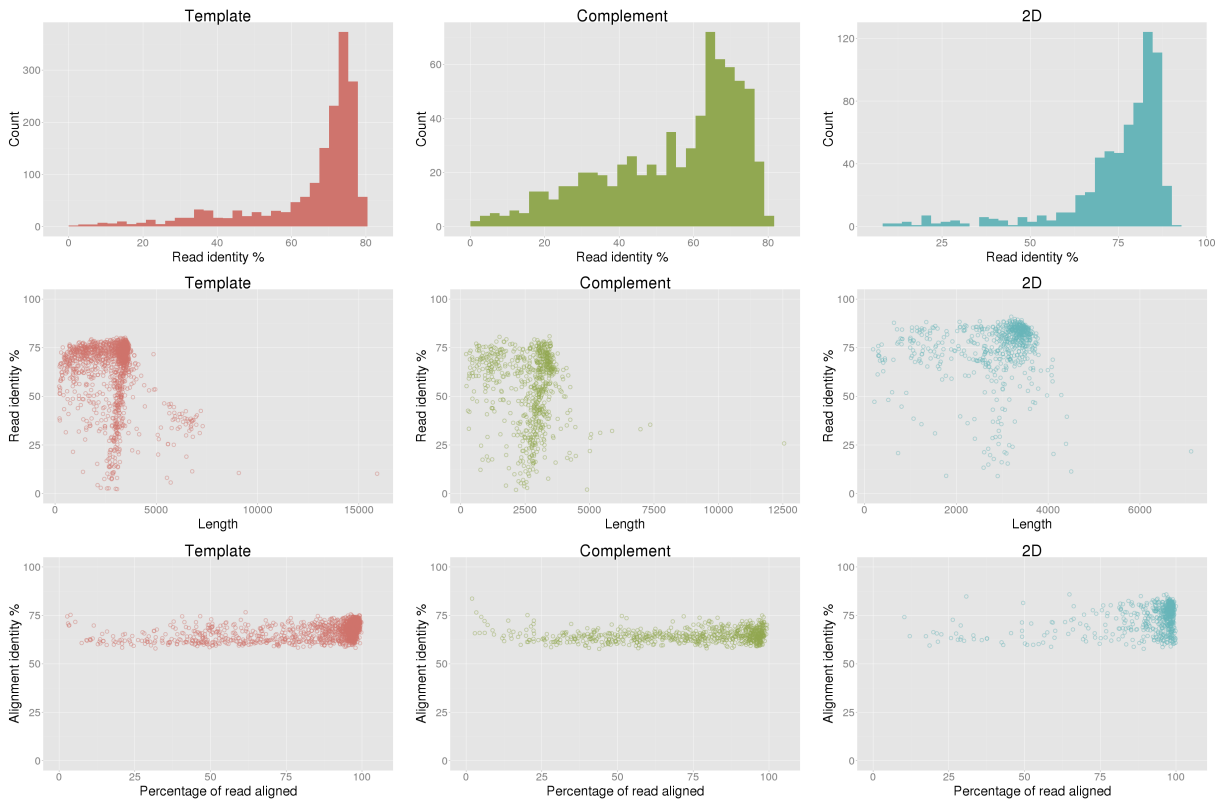
ID	Size	Number of Reads	% of Reads	Mean read length	Aligned bases	Mean coverage	Longest Perf Kmer
Control sequence	3560	667	6.56	2876.34	1936756	544.03	140
Escherichia coli	4641652	3183	31.32	5529.42	17758040	3.83	170

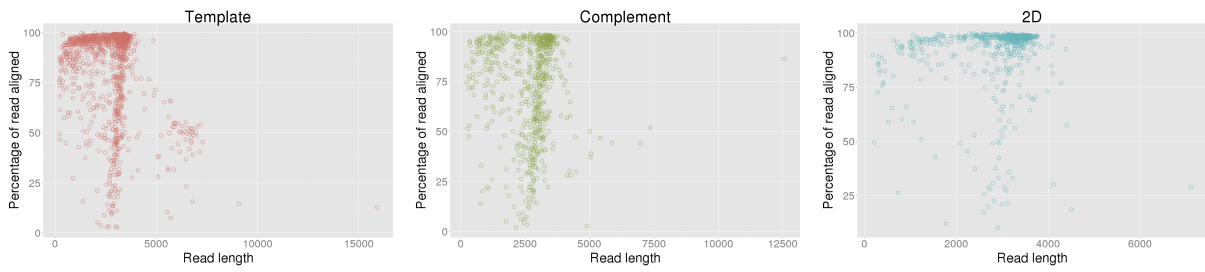
Control sequence error analysis

	Template	Complement	2D
Overall base identity (excluding indels)	64.00%	53.25%	75.14%
Aligned base identity (excluding indels)	79.98%	78.92%	86.17%
Identical bases per 100 aligned bases (including indels)	67.48%	64.38%	74.43%
Inserted bases per 100 aligned bases (including indels)	5.17%	4.92%	4.32%
Deleted bases per 100 aligned bases (including indels)	10.46%	13.51%	9.30%
Substitutions per 100 aligned bases (including indels)	16.89%	17.20%	11.95%
Mean insertion size	1.58	1.57	1.51
Mean deletion size	1.65	1.85	1.69

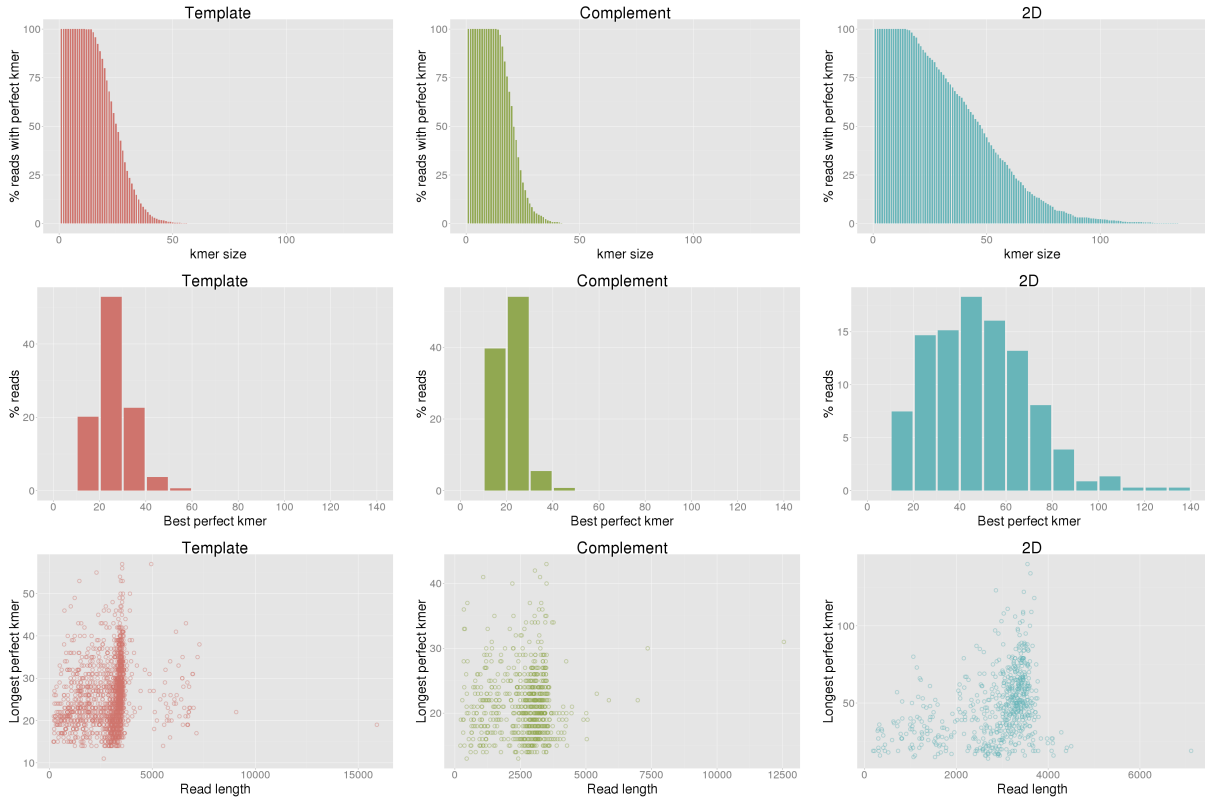


Control sequence read identity

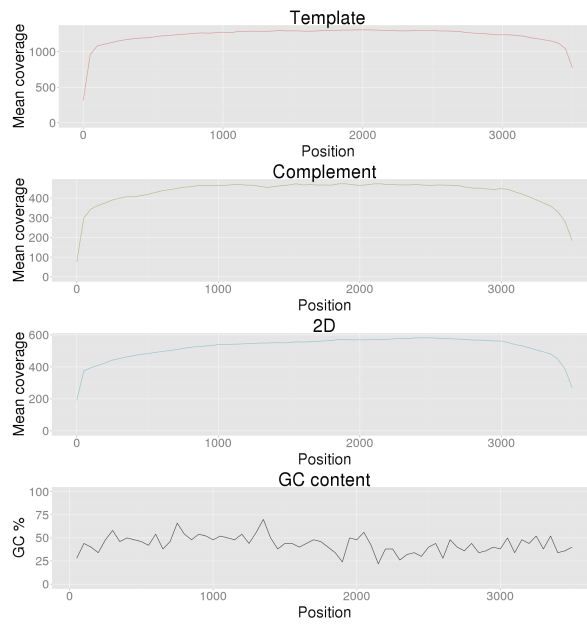




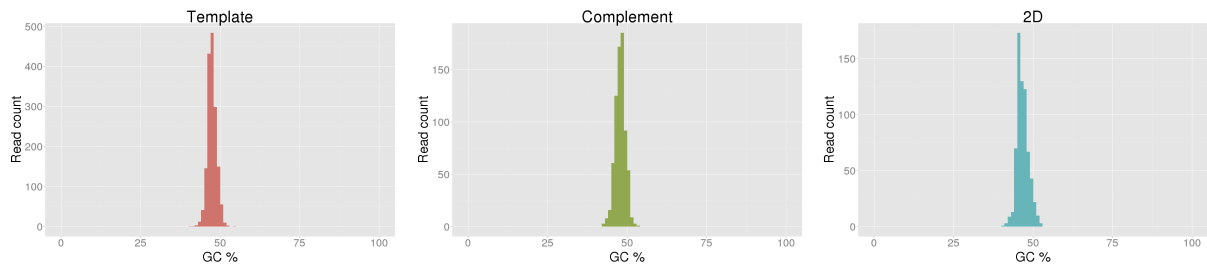
Control sequence perfect kmers



Control sequence coverage

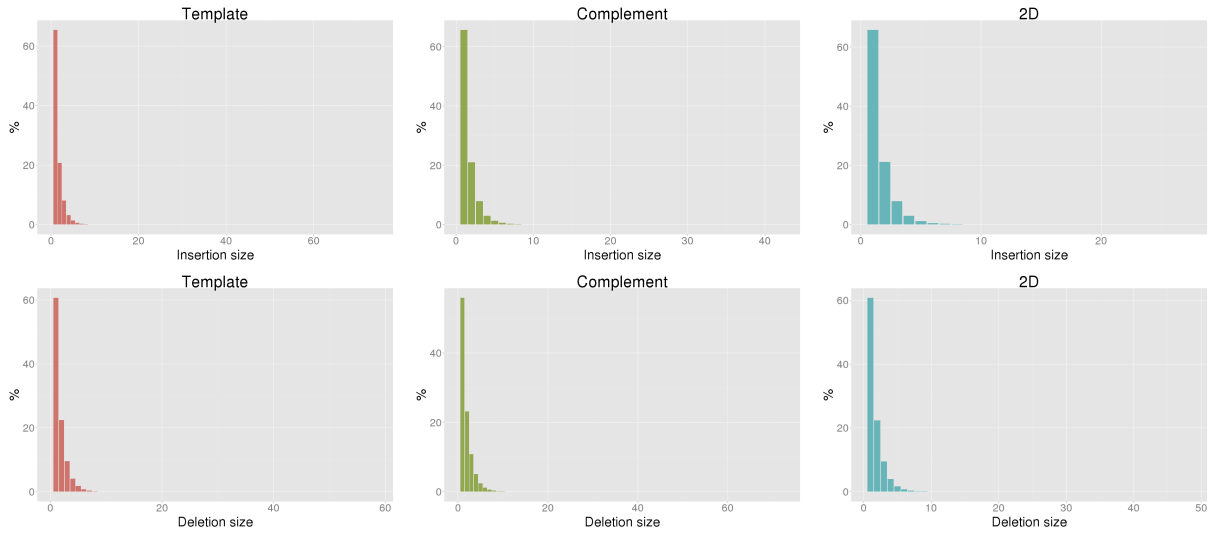


Control sequence GC content

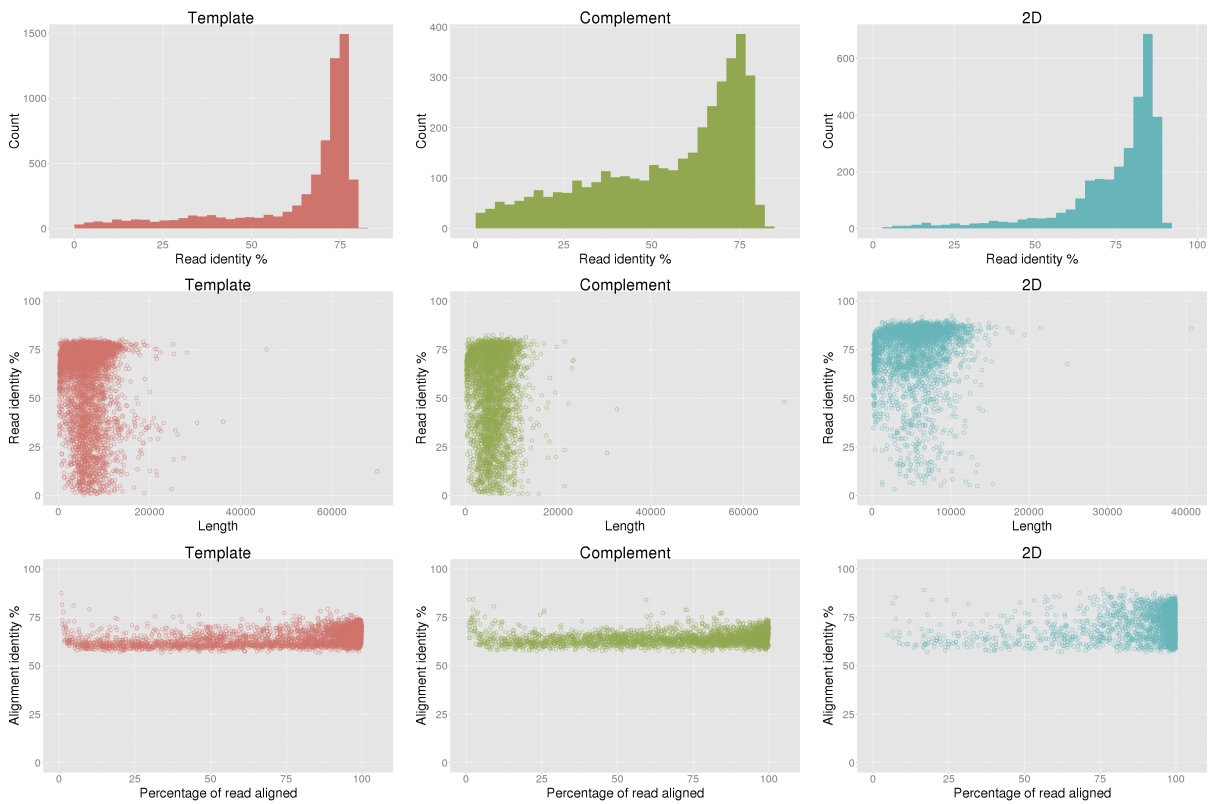


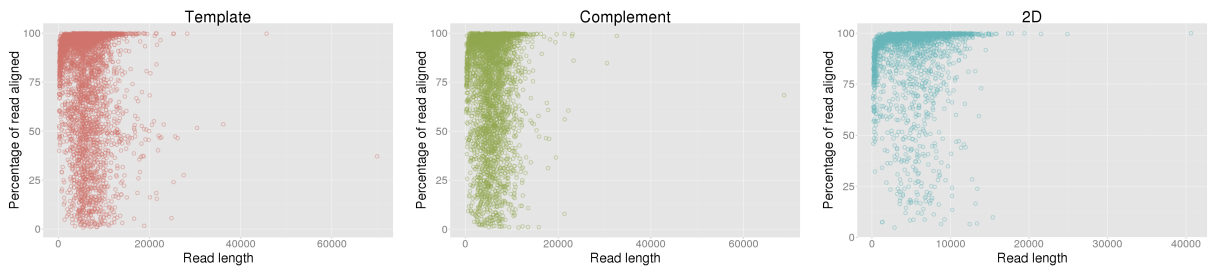
Escherichia coli error analysis

	Template	Complement	2D
Overall base identity (excluding indels)	61.54%	53.69%	74.74%
Aligned base identity (excluding indels)	79.41%	79.41%	86.00%
Identical bases per 100 aligned bases (including indels)	66.40%	64.41%	74.07%
Inserted bases per 100 aligned bases (including indels)	5.31%	4.87%	4.80%
Deleted bases per 100 aligned bases (including indels)	11.07%	14.01%	9.07%
Substitutions per 100 aligned bases (including indels)	17.22%	16.70%	12.06%
Mean insertion size	1.60	1.58	1.57
Mean deletion size	1.69	1.87	1.70

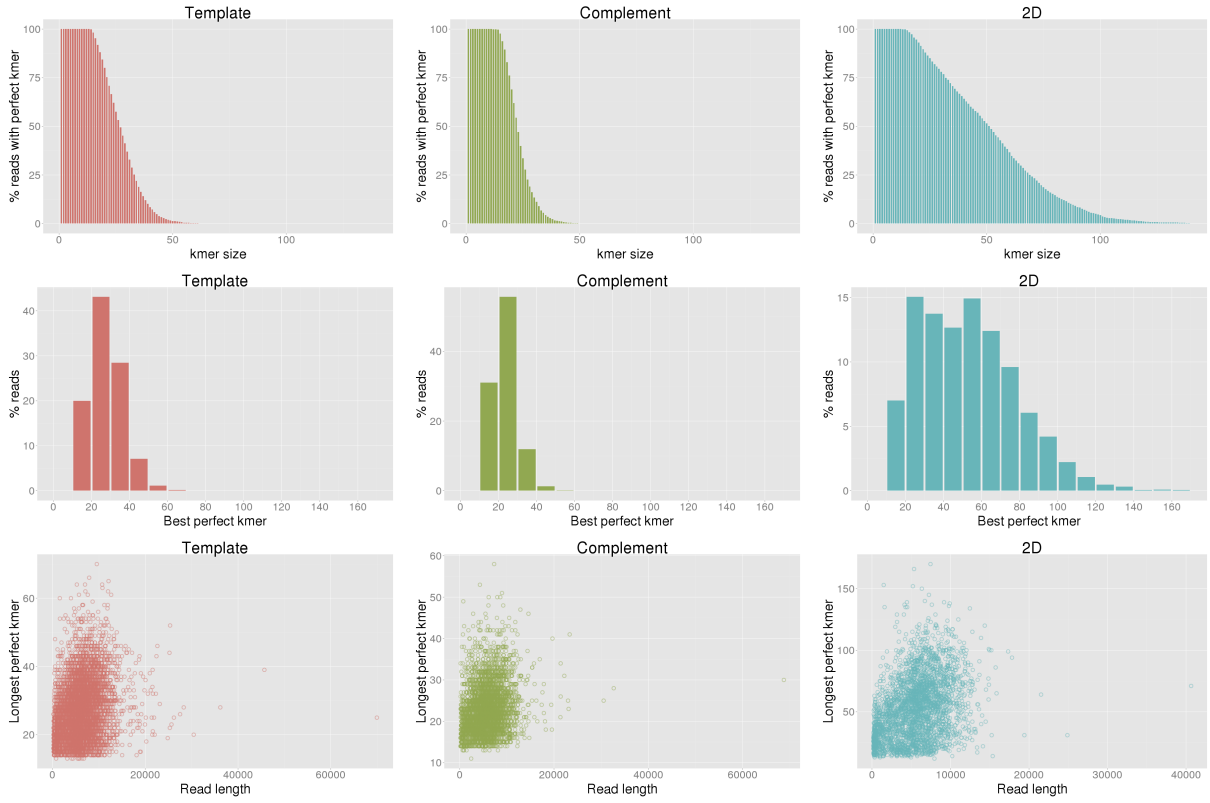


Escherichia coli read identity

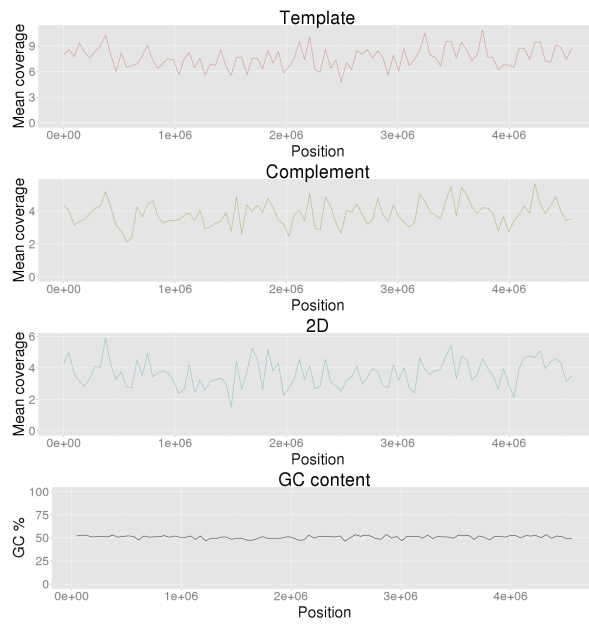




Escherichia coli perfect kmers



Escherichia coli coverage



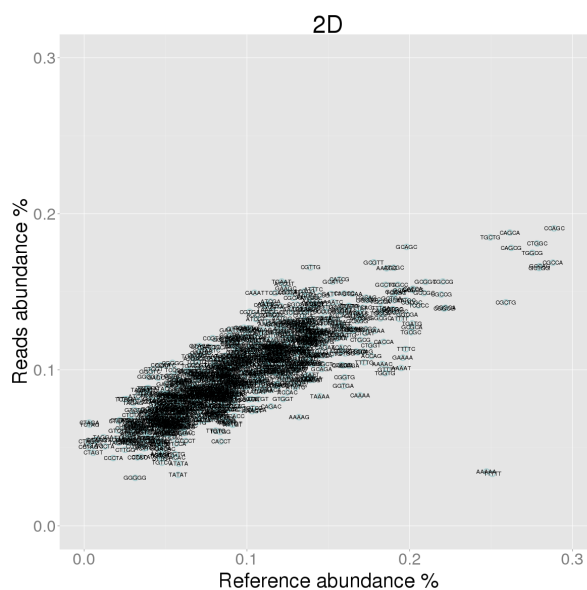
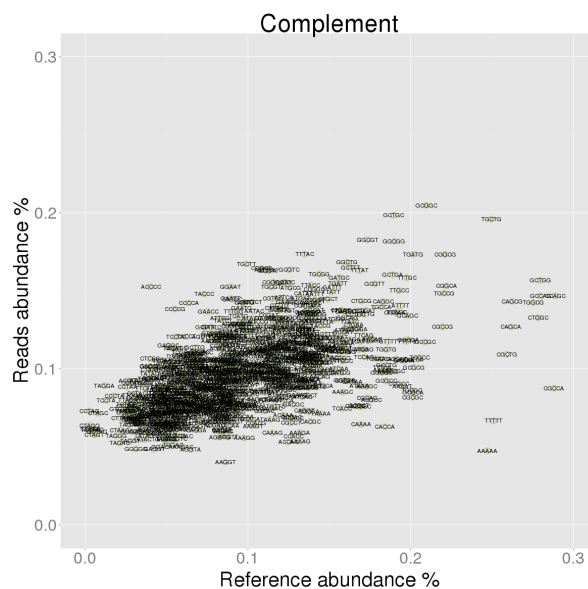
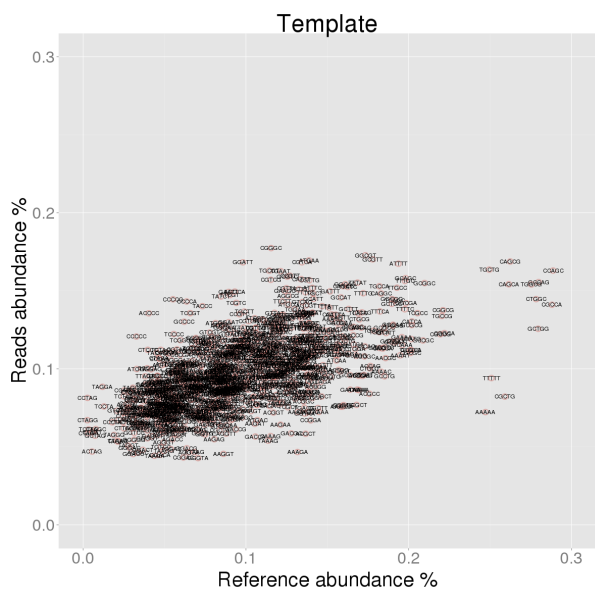
Escherichia coli 5-mer analysis

Under-represented 5-mers

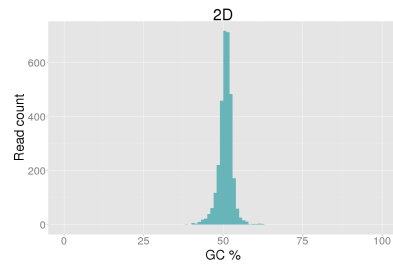
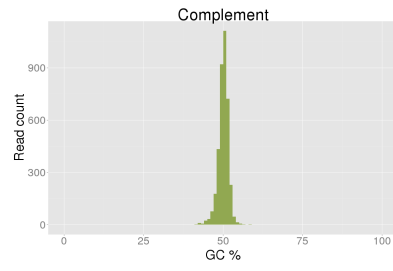
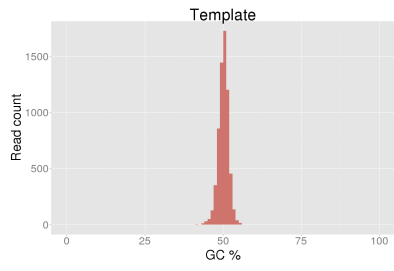
Rank	Template				Complement				2D			
	kmer	Ref %	Read %	Diff %	kmer	Ref %	Read %	Diff %	kmer	Ref %	Read %	Diff %
1	CGCTG	0.259	0.082	-0.177	CGCCA	0.288	0.088	-0.200	TTTTT	0.251	0.033	-0.217
2	AAAAA	0.247	0.072	-0.175	AAAAA	0.247	0.047	-0.200	AAAAA	0.247	0.035	-0.212
3	TTTTT	0.251	0.094	-0.157	TTTTT	0.251	0.067	-0.184	CGCCA	0.288	0.169	-0.119
4	GCTGG	0.279	0.126	-0.154	CGCTG	0.259	0.109	-0.150	CGCTG	0.259	0.143	-0.116
5	CGCCA	0.288	0.141	-0.147	CTGGC	0.278	0.133	-0.146	GCTGG	0.279	0.165	-0.114
6	CTGGC	0.278	0.145	-0.134	CCAGC	0.289	0.147	-0.142	GCCAG	0.280	0.166	-0.113
7	CCAGC	0.289	0.163	-0.126	CAGCA	0.261	0.127	-0.135	TGGCG	0.275	0.175	-0.100
8	GCCAG	0.280	0.156	-0.124	GCCAG	0.280	0.147	-0.133	CCAGC	0.289	0.191	-0.098
9	TGGCG	0.275	0.154	-0.121	TGGCG	0.275	0.143	-0.133	CTGGC	0.278	0.181	-0.097
10	CAGCA	0.261	0.154	-0.107	GCTGG	0.279	0.157	-0.123	AAAAT	0.195	0.101	-0.094

Over-represented 5-mers

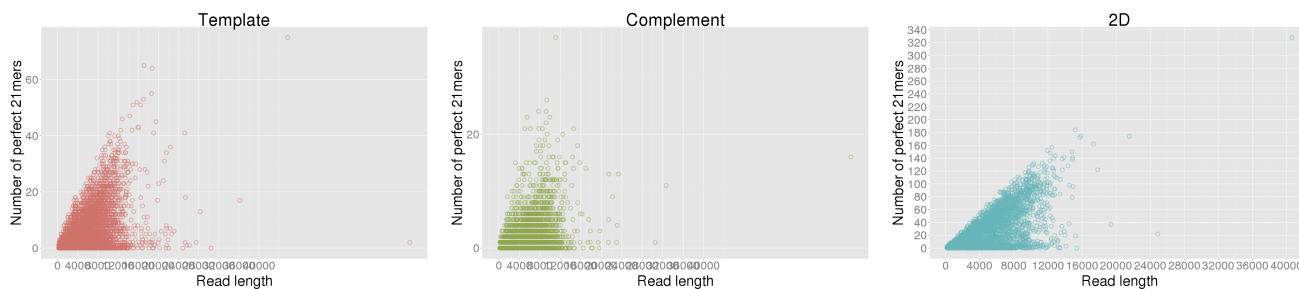
Rank	Template				Complement				2D			
	kmer	Ref %	Read %	Diff %	kmer	Ref %	Read %	Diff %	kmer	Ref %	Read %	Diff %
1	ACCCC	0.040	0.136	0.095	ACCCC	0.040	0.153	0.112	CTAGA	0.003	0.066	0.063
2	CCCCG	0.055	0.145	0.089	CCCCG	0.055	0.138	0.083	TCTAG	0.003	0.065	0.062
3	CCCCC	0.033	0.121	0.088	CCCCC	0.064	0.142	0.079	GGGTC	0.040	0.099	0.058
4	CCCCA	0.064	0.143	0.080	TAGGA	0.012	0.089	0.077	CTCGT	0.042	0.101	0.058
5	CCTAG	0.003	0.081	0.079	TACCC	0.073	0.148	0.075	TCTAA	0.025	0.081	0.056
6	TAGGA	0.012	0.088	0.077	CCTAG	0.003	0.073	0.070	GGGGT	0.039	0.096	0.056
7	CTCCC	0.040	0.112	0.073	TGCTT	0.099	0.167	0.068	CCCAA	0.047	0.103	0.056
8	GGATT	0.098	0.168	0.070	TCCTA	0.013	0.080	0.067	TTAGA	0.026	0.081	0.055
9	TCCGT	0.066	0.136	0.070	CTCCC	0.040	0.106	0.067	GCCTC	0.050	0.103	0.053
10	GCCCC	0.062	0.130	0.068	ACCTA	0.027	0.092	0.066	TAGAT	0.035	0.087	0.053



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	8.86	9.08	4.98	0.00	8.95	8.77	5.27	0.00	8.91	8.88	4.70
C	8.58	0.00	8.95	9.64	9.13	0.00	8.55	9.32	8.74	0.00	9.91	8.76
G	9.16	9.04	0.00	8.36	8.72	8.78	0.00	8.96	8.55	10.08	0.00	8.53
T	5.30	9.38	8.67	0.00	5.59	9.01	8.94	0.00	4.90	9.11	8.92	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 (3.30%)	TTC (3.41%)	AAA (4.31%)	AAA (2.93%)	AAA (2.91%)	AAA (4.24%)	AAA (3.00%)	AAA (2.81%)	AAA (3.98%)
2	AAA (2.91%)	TGC (2.93%)	TTC (3.61%)	TTC (2.86%)	TGC (2.76%)	GCA (3.50%)	GCA (2.96%)	GCA (2.64%)	GCA (3.44%)
3	TGC (2.72%)	AAA (2.87%)	GCA (3.22%)	GCA (2.73%)	GCA (2.72%)	GAA (3.27%)	TTC (2.89%)	TGC (2.59%)	GAA (3.08%)
4	GCA (2.70%)	GCA (2.81%)	GAA (3.02%)	TGC (2.69%)	GGC (2.70%)	TTC (3.08%)	TCA (2.49%)	TTC (2.55%)	TTC (2.90%)
5	ATC (2.51%)	TCA (2.43%)	TTT (2.63%)	GAA (2.43%)	TTC (2.66%)	TTT (2.54%)	GAA (2.48%)	TCA (2.46%)	TTT (2.73%)
6	TCA (2.46%)	GCC (2.37%)	AAT (2.58%)	CAG (2.37%)	GAA (2.52%)	TGC (2.50%)	TGC (2.47%)	GCG (2.46%)	AAT (2.65%)
7	TTT (2.32%)	GAA (2.31%)	TGC (2.52%)	TCA (2.36%)	TCA (2.35%)	TCA (2.37%)	ATC (2.37%)	GGC (2.39%)	GTT (2.43%)
8	GAA (2.28%)	GGC (2.31%)	TCA (2.29%)	ATC (2.28%)	AAT (2.28%)	AAT (2.35%)	AAT (2.33%)	GAA (2.34%)	TGC (2.28%)
9	GCC (2.25%)	AAT (2.30%)	CAA (2.24%)	GGC (2.24%)	GCC (2.28%)	CAA (2.23%)	CGC (2.24%)	CAG (2.19%)	GCC (2.24%)
10	AAT (2.19%)	ATC (2.22%)	GCC (2.22%)	AAT (2.22%)	CAG (2.23%)	GCC (2.17%)	GCG (2.22%)	GCG (2.17%)	TCA (2.23%)
-10	CGA (1.00%)	AGG (0.95%)	GGT (0.90%)	AGA (1.01%)	AGA (0.93%)	CTC (0.91%)	CTT (1.04%)	GTA (1.03%)	GGG (0.96%)
-9	AGT (0.99%)	CCT (0.94%)	GGG (0.88%)	AGT (0.97%)	AGG (0.93%)	CTT (0.91%)	CTC (1.01%)	CCC (0.95%)	AGG (0.93%)
-8	CCC (0.91%)	AGT (0.92%)	AGA (0.87%)	CTC (0.89%)	GGA (0.93%)	AGT (0.90%)	AGA (0.86%)	ACT (0.93%)	CCC (0.91%)
-7	AGA (0.83%)	GAG (0.85%)	TGT (0.86%)	CCC (0.84%)	AGT (0.92%)	CCT (0.86%)	GAG (0.85%)	CGA (0.91%)	CGA (0.82%)
-6	GGA (0.80%)	CTT (0.85%)	AGT (0.82%)	GGA (0.82%)	CCT (0.91%)	AGG (0.79%)	CCC (0.81%)	CCT (0.91%)	CTT (0.80%)
-5	GAG (0.78%)	CGA (0.78%)	AGG (0.82%)	GAG (0.78%)	CTC (0.91%)	ACT (0.78%)	GGA (0.79%)	CTT (0.89%)	GAG (0.80%)
-4	AGG (0.69%)	AGA (0.70%)	CTT (0.78%)	AGG (0.72%)	GAG (0.86%)	GGG (0.78%)	AGG (0.75%)	AGA (0.81%)	GGA (0.71%)
-3	GGG (0.68%)	GGA (0.67%)	GAG (0.67%)	GGG (0.61%)	GGG (0.81%)	GAG (0.64%)	GGG (0.67%)	GGA (0.71%)	AGA (0.65%)
-2	CTA (0.50%)	TAG (0.57%)	TAG (0.41%)	CTA (0.58%)	TAG (0.55%)	CTA (0.43%)	CTA (0.56%)	CTA (0.62%)	TAG (0.45%)
-1	TAG (0.44%)	CTA (0.51%)	CTA (0.36%)	TAG (0.47%)	CTA (0.51%)	TAG (0.40%)	TAG (0.50%)	TAG (0.61%)	CTA (0.43%)

Most common

Least common

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 (1.11%)	AAAA (1.48%)	CAAA (0.91%)	CGGC (0.98%)	AAAA (1.21%)	CAAA (0.85%)	TGGC (0.87%)	GAAA (1.13%)
2	AAAA (0.95%)	TTCA (0.94%)	TTTT (1.24%)	ATCA (0.86%)	TGGC (0.95%)	CAAA (1.18%)	GAAA (0.84%)	TTCA (0.87%)	AAAA (1.11%)
3	GAAA (0.92%)	TGCC (0.90%)	GAAA (1.23%)	AAAA (0.84%)	CAGC (0.94%)	GAAA (1.01%)	ATCA (0.83%)	CAGC (0.84%)	GGCA (0.99%)
4	TTCA (0.86%)	AAAA (0.89%)	GCAA (0.93%)	CAGC (0.81%)	CAAA (0.90%)	TGAA (0.97%)	TTTC (0.82%)	CAAA (0.80%)	CAAA (0.92%)
5	TTGC (0.83%)	TTGC (0.89%)	TTTT (0.91%)	TTGC (0.81%)	TTGC (0.88%)	AGCA (0.91%)	TTCA (0.81%)	ATCA (0.78%)	TTTT (0.90%)
6	TGCC (0.82%)	GAAA (0.85%)	CAAA (0.90%)	CTGC (0.81%)	CTGC (0.83%)	ATCA (0.90%)	AACA (0.80%)	GAAA (0.76%)	TGCA (0.88%)
7	ATCA (0.80%)	TGGC (0.85%)	GGCA (0.90%)	TGGC (0.80%)	ATCA (0.83%)	GGCA (0.89%)	TGAA (0.79%)	TTTC (0.74%)	TGAA (0.86%)
8	TTTT (0.79%)	TTCC (0.84%)	TGCC (0.87%)	TTTT (0.75%)	TTCC (0.82%)	TTTC (0.89%)	GGCA (0.78%)	TTGC (0.73%)	GGAA (0.86%)
9	CAGC (0.79%)	CAGC (0.80%)	GTTC (0.86%)	CGGC (0.74%)	TTCA (0.80%)	AGAA (0.87%)	AAAA (0.78%)	CGCC (0.72%)	CGTT (0.84%)
10	AACG (0.77%)	GTTC (0.80%)	AAAT (0.85%)	TTCA (0.73%)	TGCC (0.80%)	TAAA (0.86%)	CGCC (0.77%)	GCCA (0.72%)	CGCC (0.83%)
-10	TAGT (0.13%)	TAGT (0.12%)	CTAT (0.11%)	CTAA (0.12%)	ACTA (0.12%)	TCTA (0.11%)	CTTG (0.14%)	CGGA (0.15%)	TATA (0.12%)
-9	TTAG (0.12%)	TCTA (0.12%)	TAGT (0.11%)	CGAG (0.12%)	TAGT (0.12%)	GTGT (0.11%)	CCCT (0.14%)	CCCC (0.14%)	TTAG (0.12%)
-8	TCTA (0.12%)	CTAT (0.12%)	ACTA (0.10%)	AGGG (0.12%)	ACCT (0.12%)	ACTA (0.10%)	GGAC (0.14%)	TAGT (0.14%)	CTTG (0.12%)
-7	AGGG (0.12%)	CGGA (0.12%)	CGAG (0.10%)	GAGG (0.11%)	GGAC (0.12%)	CGAG (0.10%)	CTAT (0.13%)	CTAT (0.13%)	ACTA (0.11%)
-6	GAGG (0.11%)	GGAC (0.12%)	TAGA (0.09%)	CCCT (0.10%)	CTAA (0.11%)	CTAT (0.10%)	CTAA (0.13%)	CTAA (0.12%)	TCTA (0.10%)
-5	GGAC (0.10%)	CTAA (0.10%)	GGAC (0.08%)	TAGA (0.10%)	CCCT (0.11%)	GGAC (0.09%)	AGGG (0.12%)	CCCT (0.12%)	CTAT (0.10%)
-4	TAGA (0.07%)	TAGG (0.09%)	TCTA (0.08%)	GGAC (0.10%)	TAGA (0.10%)	CCCT (0.07%)	TAGA (0.09%)	TAGG (0.09%)	TAGG (0.07%)
-3	CCTA (0.07%)	TAGA (0.06%)	TAGG (0.07%)	CCTA (0.08%)	TAGG (0.08%)	TAGG (0.06%)	CCTA (0.06%)	CCTA (0.08%)	TAGA (0.05%)
-2	TAGG (0.06%)	CCTA (0.06%)	CCTA (0.04%)	TAGG (0.06%)	CCTA (0.06%)	CCTA (0.05%)	TAGG (0.06%)	TAGA (0.08%)	CCTA (0.05%)
-1	CTAG (0.01%)	CTAG (0.01%)	CTAG (0.01%)	CTAG (0.01%)	CTAG (0.01%)	CTAG (0.01%)	CTAG (0.02%)	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	TTATC (0.33%)	CAGCA (0.35%)	GAAAA (0.45%)	CAGCA (0.41%)	CAGCA (0.40%)	CAGCA (0.51%)	CAGCA (0.34%)	CTGGC (0.37%)	CAGCA (0.39%)
2	CAGCA (0.32%)	CTGGC (0.34%)	CAAAA (0.40%)	GCAAA (0.31%)	CTGGC (0.36%)	GCAAA (0.39%)	CGCCA (0.31%)	CAGCA (0.33%)	GAAAA (0.38%)
3	CAAAA (0.32%)	TTTGC (0.32%)	CAGCA (0.39%)	CATCA (0.31%)	GCGGC (0.34%)	GAAAA (0.38%)	CTGGC (0.30%)	TGGCG (0.29%)	TGGCA (0.37%)
4	CGTTT (0.31%)	TTGCC (0.31%)	AGAAA (0.35%)	TTATC (0.30%)	CATCA (0.33%)	AAGAA (0.36%)	CGGCA (0.29%)	CATCA (0.29%)	CGGCA (0.33%)
5	CTGGC (0.30%)	TTTCA (0.31%)	GCAAA (0.34%)	GCGGC (0.29%)	TTTGC (0.31%)	ATAAA (0.35%)	CATCA (0.28%)	GATGC (0.29%)	CAAAA (0.33%)
6	ATTTT (0.30%)	ATTTT (0.30%)	TAAAA (0.33%)	CGGCA (0.29%)	AATCA (0.30%)	CAAAA (0.35%)	GCAAA (0.28%)	TTTCA (0.28%)	GCAAA (0.32%)
7	CGCCA (0.29%)	GCCAG (0.29%)	ATTTT (0.33%)	GCTGC (0.29%)	TTGCC (0.30%)	CGGCA (0.35%)	CAAAA (0.28%)	GCCAG (0.28%)	AGAAA (0.31%)
8	GAAAA (0.29%)	CATCA (0.28%)	TTGCC (0.33%)	CTGGC (0.28%)	GCTGC (0.30%)	ACAAA (0.35%)	TGGCA (0.27%)	CGCCA (0.28%)	AAGAA (0.31%)
9	CATCA (0.27%)	GAAAA (0.28%)	TGTTT (0.32%)	AATCA (0.28%)	GCAAA (0.29%)	AATCA (0.32%)	AACGC (0.26%)	GCGGC (0.27%)	TGAAA (0.31%)
10	CCAGC (0.27%)	TGTTT (0.28%)	TGGCA (0.32%)	GAAAA (0.28%)	CCAGC (0.29%)	CAGAA (0.32%)	GCCAG (0.26%)	CCAGC (0.27%)	GCGTT (0.30%)
-10	GGACC (0.01%)	GGACC (0.01%)	CCCTA (0.01%)	GGACC (0.01%)	CCCCC (0.01%)	CCCTT (0.01%)	CCTAG (0.01%)	TAGGA (0.01%)	CCCTA (0.01%)
-9	CTAGT (0.01%)	CCCTA (0.01%)	ACCTA (0.00%)	CTAGT (0.01%)	CCCTA (0.01%)	TAGGG (0.01%)	TAGGA (0.01%)	TCCTA (0.01%)	CTAGT (0.01%)
-8	CCCTA (0.00%)	GCTAG (0.00%)	GCTAG (0.00%)	GCTAG (0.01%)	CTAGC (0.01%)	CCCTA (0.00%)	CCCTA (0.01%)	GCTAG (0.01%)	GCTAG (0.00%)
-7	ACTAG (0.00%)	ACTAG (0.00%)	ACTAG (0.00%)	CCCTA (0.00%)	GCTAG (0.01%)	CTAGT (0.00%)	GCTAG (0.00%)	ACTAG (0.01%)	TTAGA (0.00%)
-6	GCTAG (0.00%)	CTAGT (0.00%)	CTAGC (0.00%)	CTAGA (0.00%)	CTAGT (0.00%)	ACTAG (0.00%)	CTAGA (0.00%)	CTAGC (0.00%)	CTAGG (0.00%)
-5	CTAGC (0.00%)	CTAGC (0.00%)	CTAGA (0.00%)	TCTAG (0.00%)	CTAGA (0.00%)	CTAGC (0.00%)	CTAGT (0.00%)	CTAGT (0.00%)	CTAGA (0.00%)
-4	CTAGA (0.00%)	CTAGG (0.00%)	CTAGT (0.00%)	CTAGC (0.00%)	ACTAG (0.00%)	CCTAG (0.00%)	ACTAG (0.00%)	CTAGA (0.00%)	ACTAG (0.00%)
-3	CCTAG (0.00%)	CCTAG (0.00%)	TCTAG (0.00%)	CCTAG (0.00%)	TCTAG (0.00%)	CTAG (0.00%)	CTAGC (0.00%)	CTAGG (0.00%)	CTAGC (0.00%)
-2	CTAGG (0.00%)	TCTAG (0.00%)	CTAGG (0.00%)	CTAGG (0.00%)	CTAGG (0.00%)	TCTAG (0.00%)	CTAGG (0.00%)	TCTAG (0.00%)	TCTAG (0.00%)
-1	TCTAG (0.00%)	CTAGA (0.00%)	CCTAG (0.00%)	ACTAG (0.00%)	CCTAG (0.00%)	CTAGG (0.00%)	TCTAG (0.00%)	CCTAG (0.00%)	CCTAG (0.00%)

Most common

Least common

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