

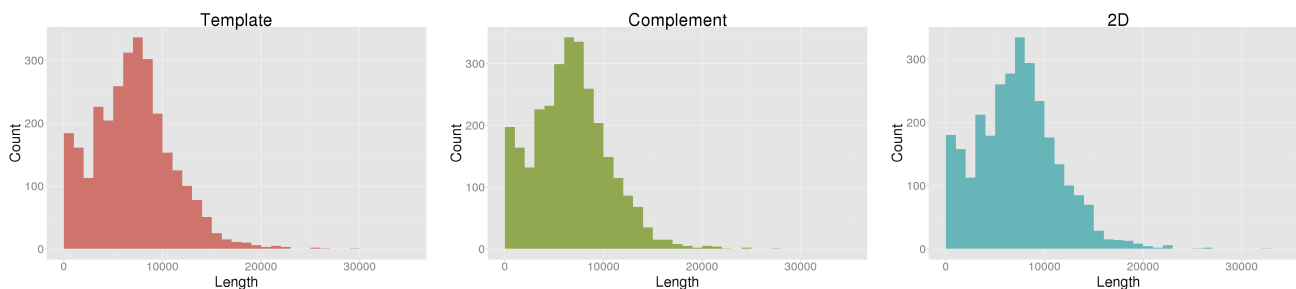
NanoOK report for MARC_ecoli_032615

Pass and fail counts

Type	Pass	Fail
Template	2901	0
Complement	2901	0
2D	2901	0

Read lengths

Type	NumReads	TotalBases	Mean	Longest	Shortest	N50	N50Count	N90	N90Count
Template	2901	20511556	7070.51	29591	246	8762	879	4770	2077
Complement	2901	19458949	6707.67	27901	246	8335	874	4560	2072
2D	2901	21120318	7280.36	32902	266	9056	878	4900	2075



Template alignments

Number of reads	2901	
Number of reads with alignments	2883	(99.38%)
Number of reads without alignments	18	(0.62%)

ID	Size	Number of Reads	% of Reads	Mean read length	Aligned bases	Mean coverage	Longest Perf Kmer
Control sequence	3560	102	3.52	2941.47	315415	88.60	60
Escherichia coli	4641652	2781	95.86	7263.08	21613736	4.66	93

Complement alignments

Number of reads	2901	
Number of reads with alignments	2847	(98.14%)
Number of reads without alignments	54	(1.86%)

ID	Size	Number of Reads	% of Reads	Mean read length	Aligned bases	Mean coverage	Longest Perf Kmer
Control sequence	3560	98	3.38	2757.41	267303	75.09	47
Escherichia coli	4641652	2749	94.76	6965.40	20822231	4.49	77

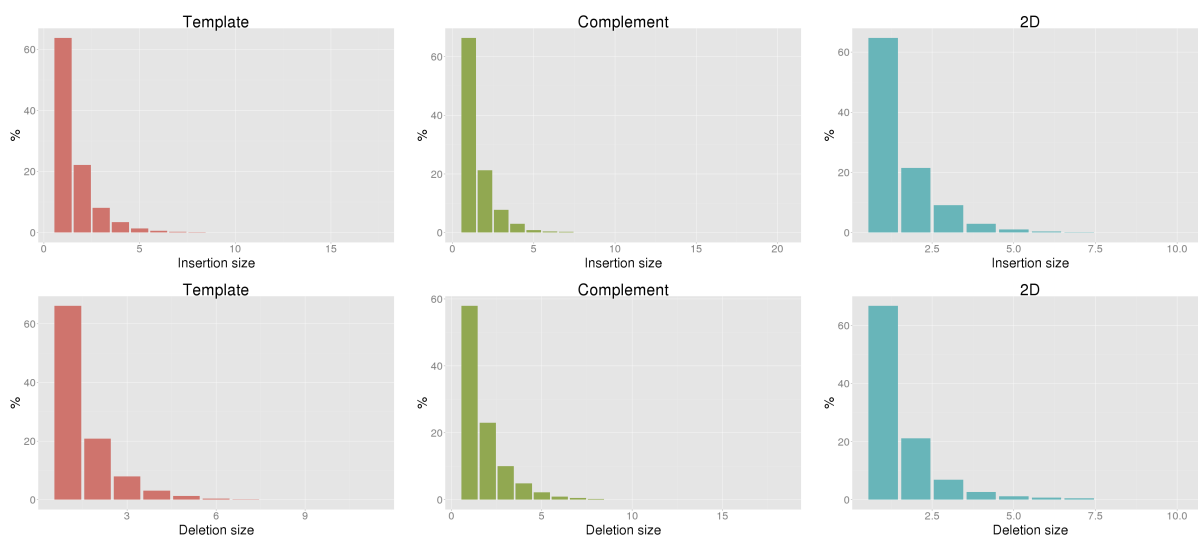
2D alignments

Number of reads	2901	
Number of reads with alignments	2900	(99.97%)
Number of reads without alignments	1	(0.03%)

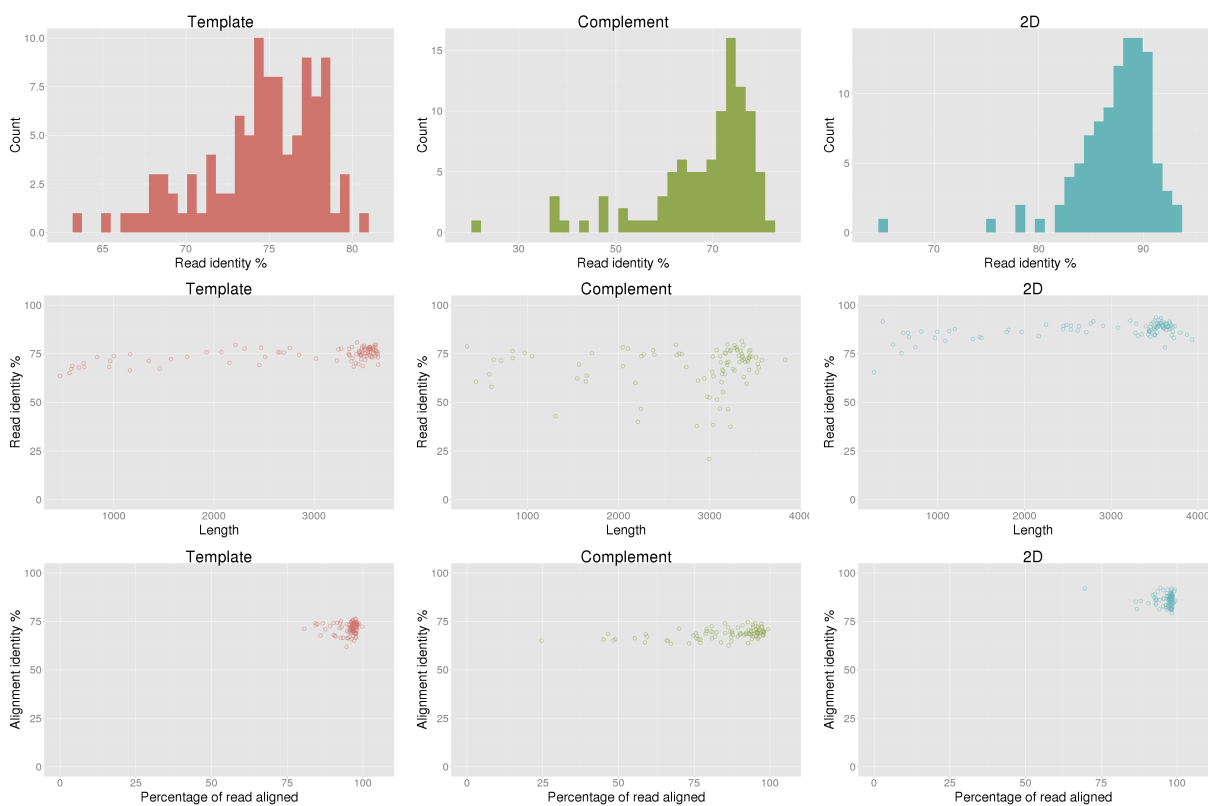
ID	Size	Number of Reads	% of Reads	Mean read length	Aligned bases	Mean coverage	Longest Perf Kmer
Control sequence	3560	103	3.55	2937.47	309284	86.88	170
Escherichia coli	4641652	2797	96.42	7438.07	21387209	4.61	238

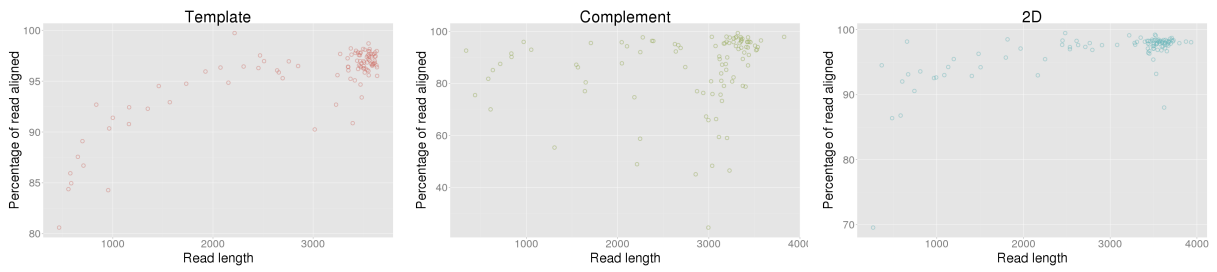
Control sequence error analysis

	Template	Complement	2D
Overall base identity (excluding indels)	75.18%	67.95%	87.99%
Aligned base identity (excluding indels)	83.00%	82.63%	94.32%
Identical bases per 100 aligned bases (including indels)	71.51%	68.70%	86.07%
Inserted bases per 100 aligned bases (including indels)	5.47%	4.13%	4.02%
Deleted bases per 100 aligned bases (including indels)	8.36%	12.73%	4.72%
Substitutions per 100 aligned bases (including indels)	14.65%	14.45%	5.18%
Mean insertion size	1.61	1.54	1.57
Mean deletion size	1.56	1.78	1.55

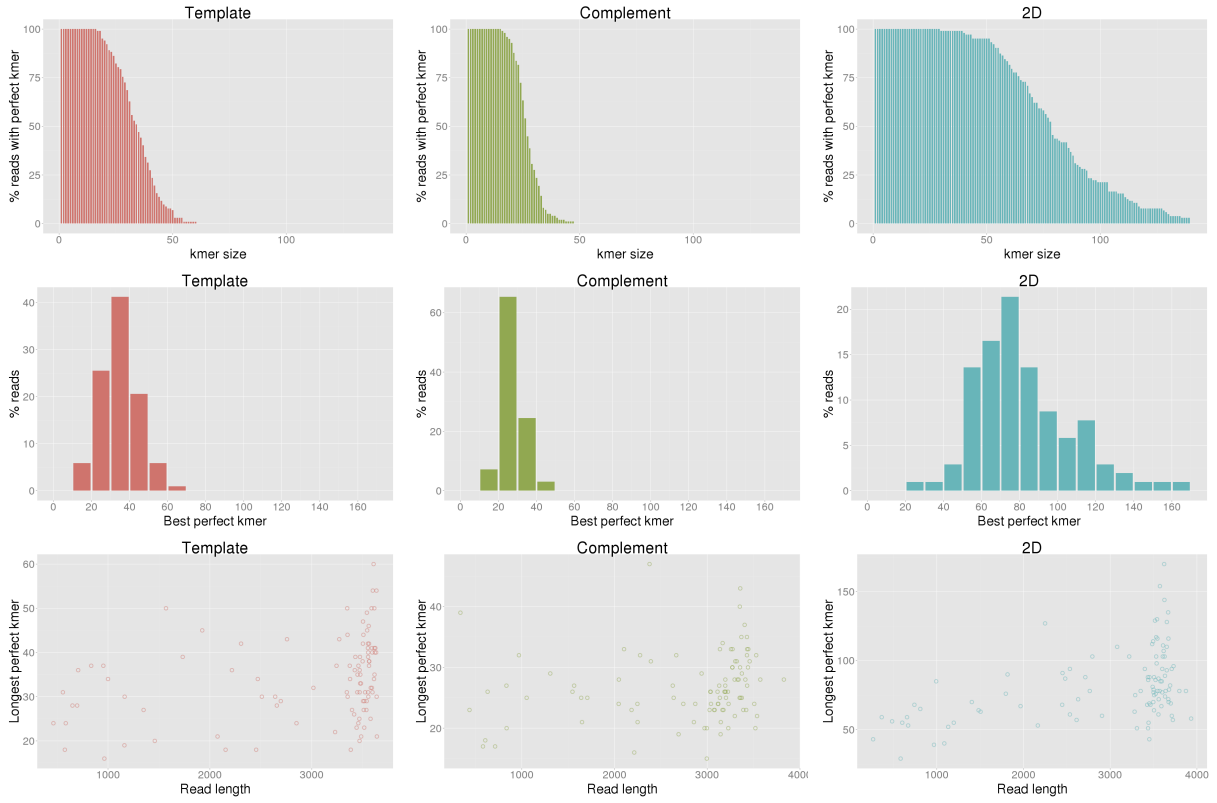


Control sequence read identity

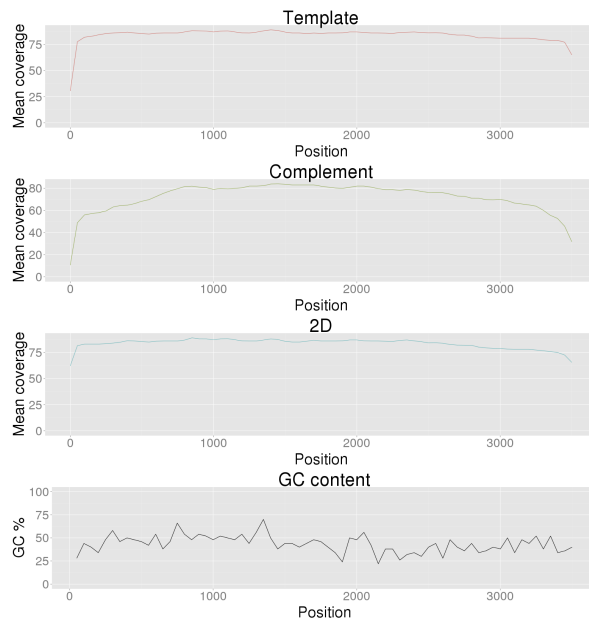




Control sequence perfect kmers



Control sequence coverage



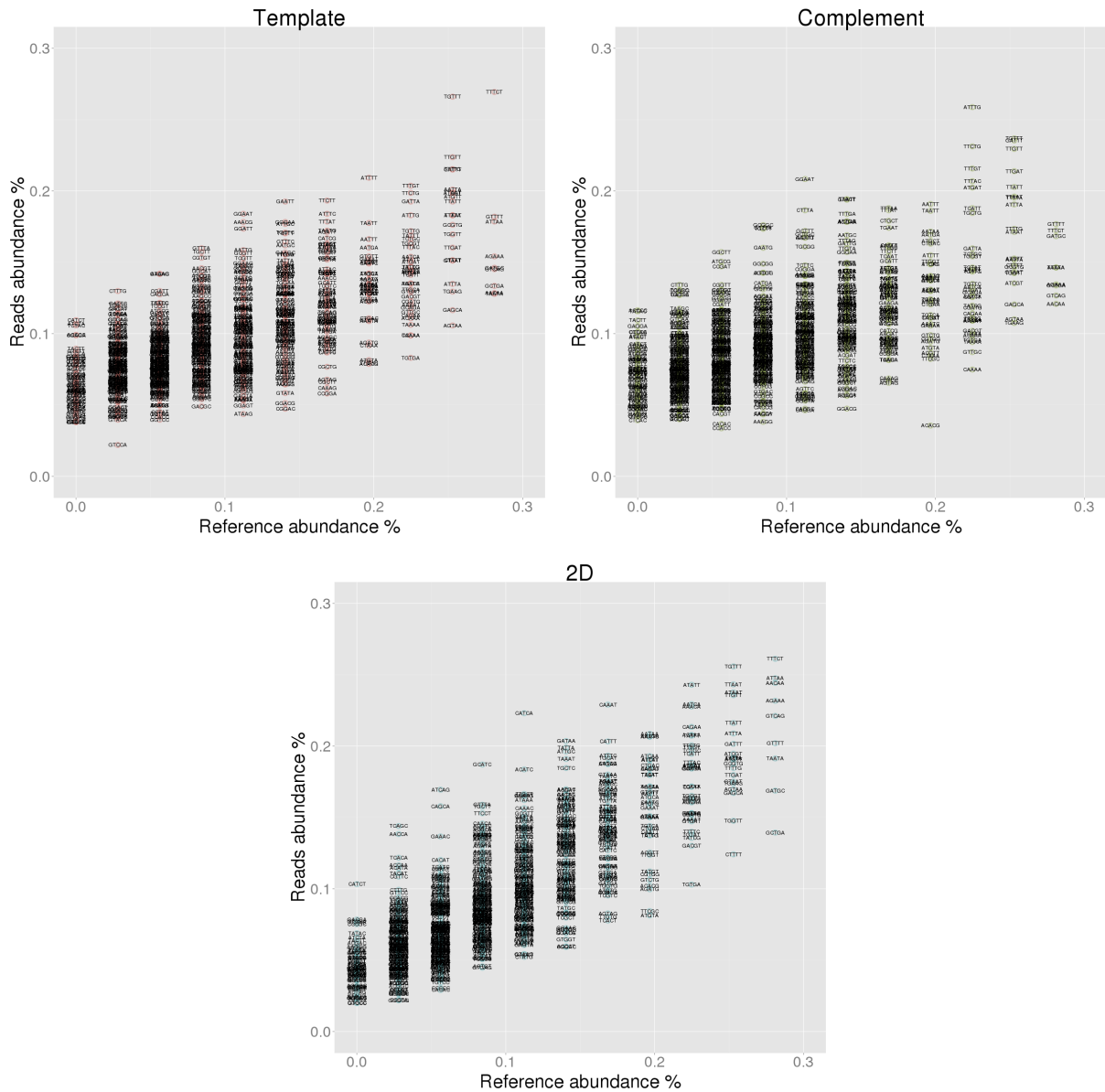
Control sequence 5-mer analysis

Under-represented 5-mers

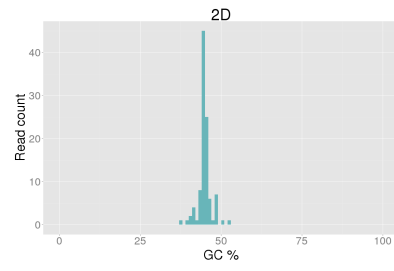
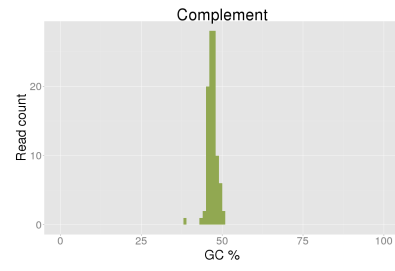
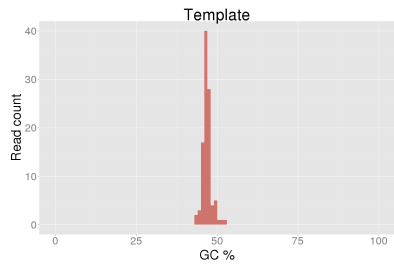
Rank	Template				Complement				2D			
	kmer	Ref %	Read %	Diff %	kmer	Ref %	Read %	Diff %	kmer	Ref %	Read %	Diff %
1	TTTTT	0.759	0.139	-0.619	TTTTT	0.759	0.080	-0.679	TTTTT	0.759	0.068	-0.691
2	AAAAA	0.478	0.106	-0.371	AAAAA	0.478	0.050	-0.428	AAAAA	0.478	0.089	-0.389
3	TGATG	0.393	0.156	-0.238	AAAAC	0.337	0.116	-0.222	TGATG	0.393	0.198	-0.195
4	AAAAC	0.337	0.127	-0.210	GATGT	0.309	0.126	-0.183	GATGT	0.309	0.154	-0.155
5	GATGT	0.309	0.116	-0.193	TGATG	0.393	0.212	-0.181	CTGAT	0.309	0.155	-0.154
6	CTGAT	0.309	0.135	-0.174	GCAAT	0.309	0.136	-0.173	GCTGA	0.281	0.139	-0.142
7	TAATA	0.281	0.128	-0.153	TTATC	0.309	0.148	-0.161	CTTTT	0.253	0.124	-0.129
8	AACAA	0.281	0.129	-0.152	ACACG	0.197	0.036	-0.161	TGTGA	0.225	0.103	-0.122
9	GCAAT	0.309	0.158	-0.151	AACAA	0.281	0.121	-0.160	AAAAC	0.337	0.222	-0.115
10	GCTGA	0.281	0.134	-0.147	GTCAG	0.281	0.127	-0.154	ATGTA	0.197	0.081	-0.115

Over-represented 5-mers

Rank	Template				Complement				2D			
	kmer	Ref %	Read %	Diff %	kmer	Ref %	Read %	Diff %	kmer	Ref %	Read %	Diff %
1	CATCT	0.000	0.110	0.110	ACCCC	0.000	0.116	0.116	TCAGC	0.028	0.144	0.116
2	ATCTA	0.000	0.107	0.107	TATAC	0.000	0.116	0.116	ATCAG	0.056	0.170	0.113
3	TCTAC	0.000	0.106	0.106	TACTT	0.000	0.109	0.109	CATCA	0.112	0.223	0.111
4	CTTTG	0.028	0.130	0.102	CTTTG	0.028	0.134	0.106	AACCA	0.028	0.138	0.110
5	ACCCC	0.000	0.099	0.099	GAGGA	0.000	0.105	0.105	CATCT	0.000	0.103	0.103
6	CGAGA	0.000	0.099	0.099	TCAGC	0.028	0.130	0.102	GCATC	0.084	0.187	0.103
7	GATTC	0.028	0.121	0.093	CGGCG	0.028	0.130	0.102	CAGCA	0.056	0.158	0.102
8	TCAGC	0.028	0.120	0.092	CTTAC	0.000	0.101	0.101	TCACA	0.028	0.122	0.094
9	CGTTC	0.028	0.118	0.090	CCCCA	0.000	0.101	0.101	ACCAA	0.028	0.117	0.088
10	TACTT	0.000	0.089	0.089	GGCTT	0.056	0.157	0.101	ACATA	0.028	0.115	0.086

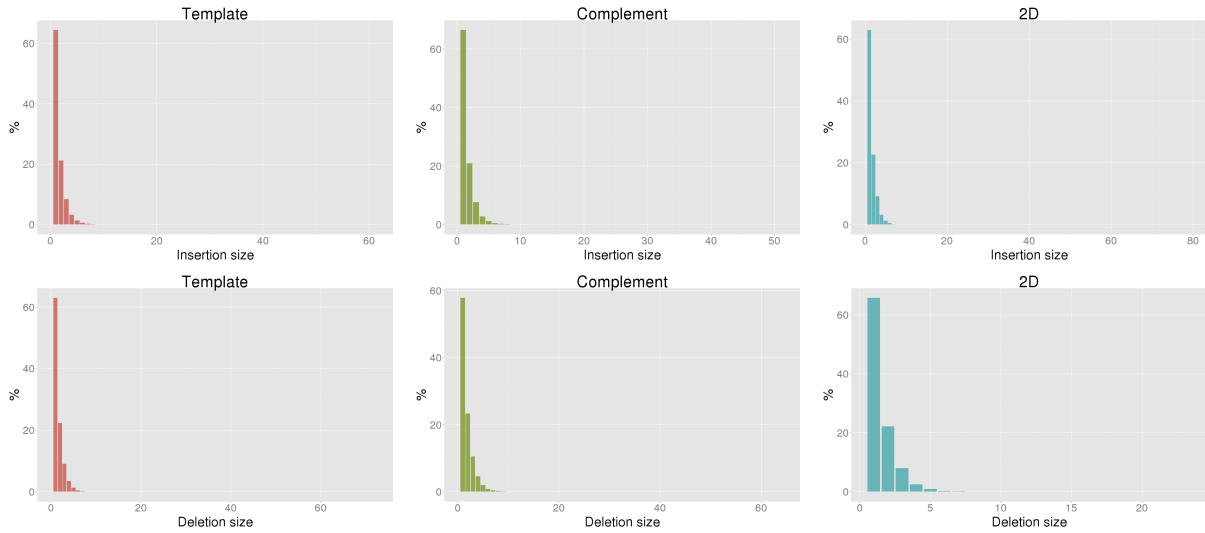


Control sequence GC content

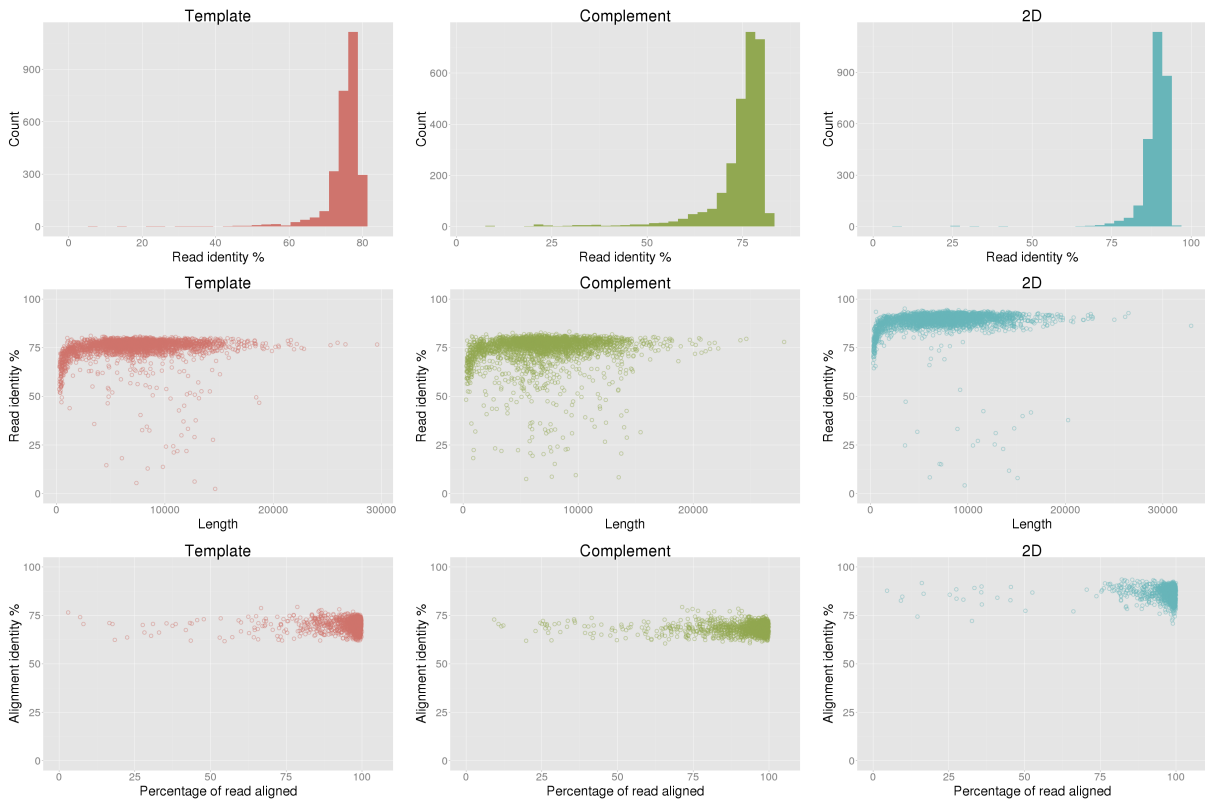


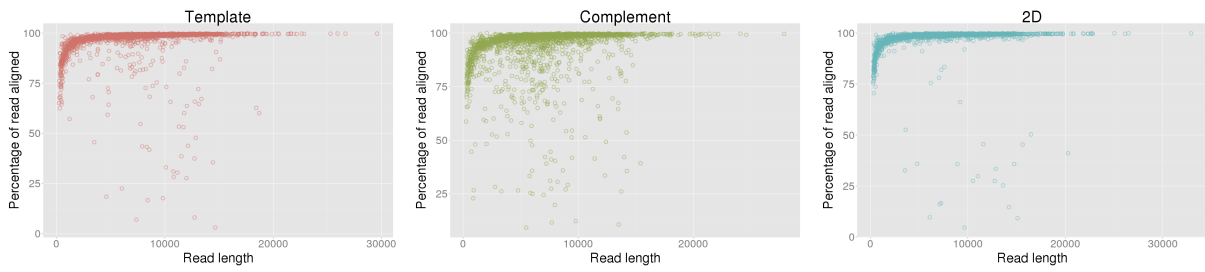
Escherichia coli error analysis

	Template	Complement	2D
Overall base identity (excluding indels)	75.18%	74.49%	89.03%
Aligned base identity (excluding indels)	82.22%	82.41%	94.57%
Identical bases per 100 aligned bases (including indels)	70.26%	68.50%	86.61%
Inserted bases per 100 aligned bases (including indels)	5.48%	4.51%	4.02%
Deleted bases per 100 aligned bases (including indels)	9.07%	12.37%	4.40%
Substitutions per 100 aligned bases (including indels)	15.19%	14.62%	4.97%
Mean insertion size	1.62	1.55	1.61
Mean deletion size	1.61	1.77	1.53

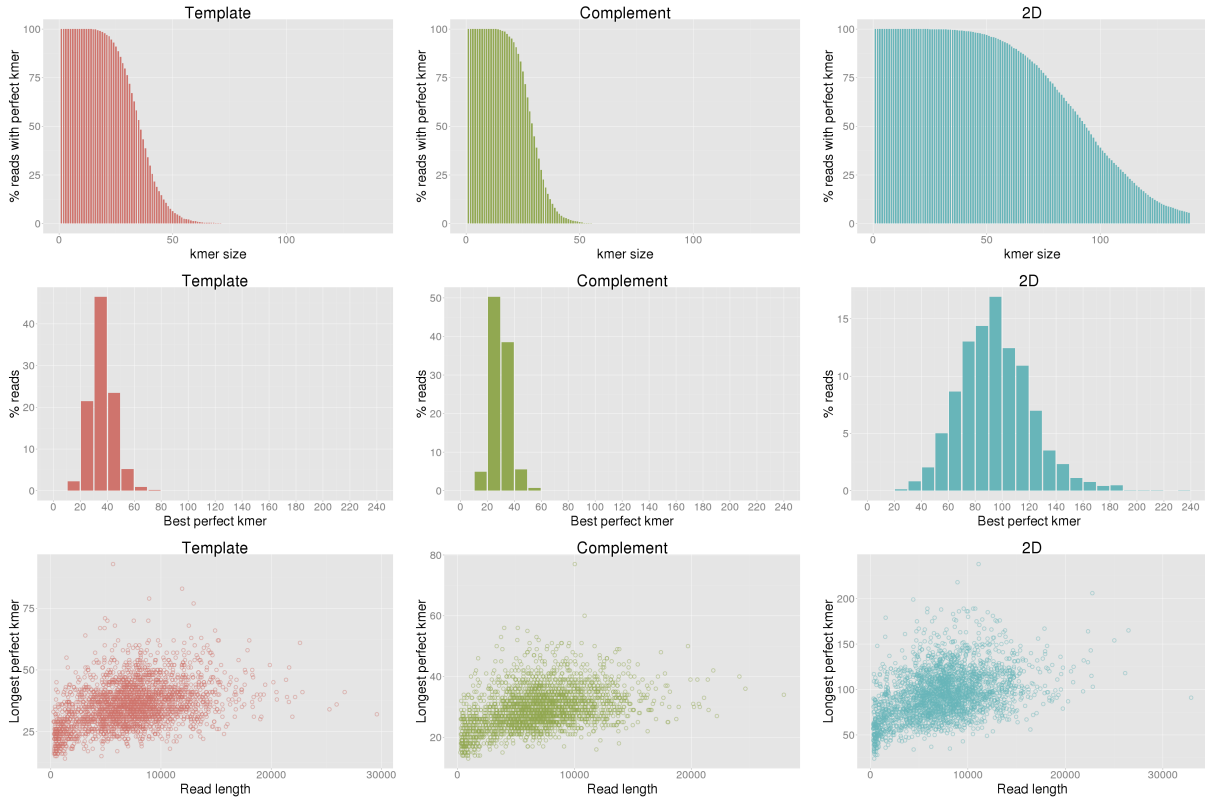


Escherichia coli read identity

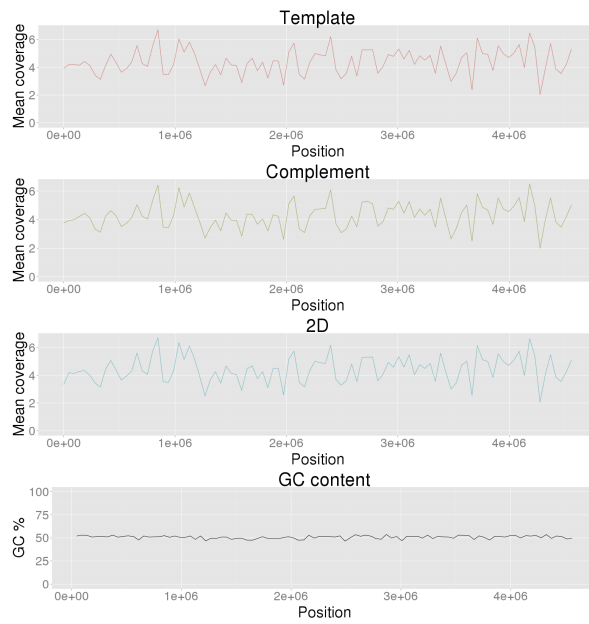




Escherichia coli perfect kmers



Escherichia coli coverage



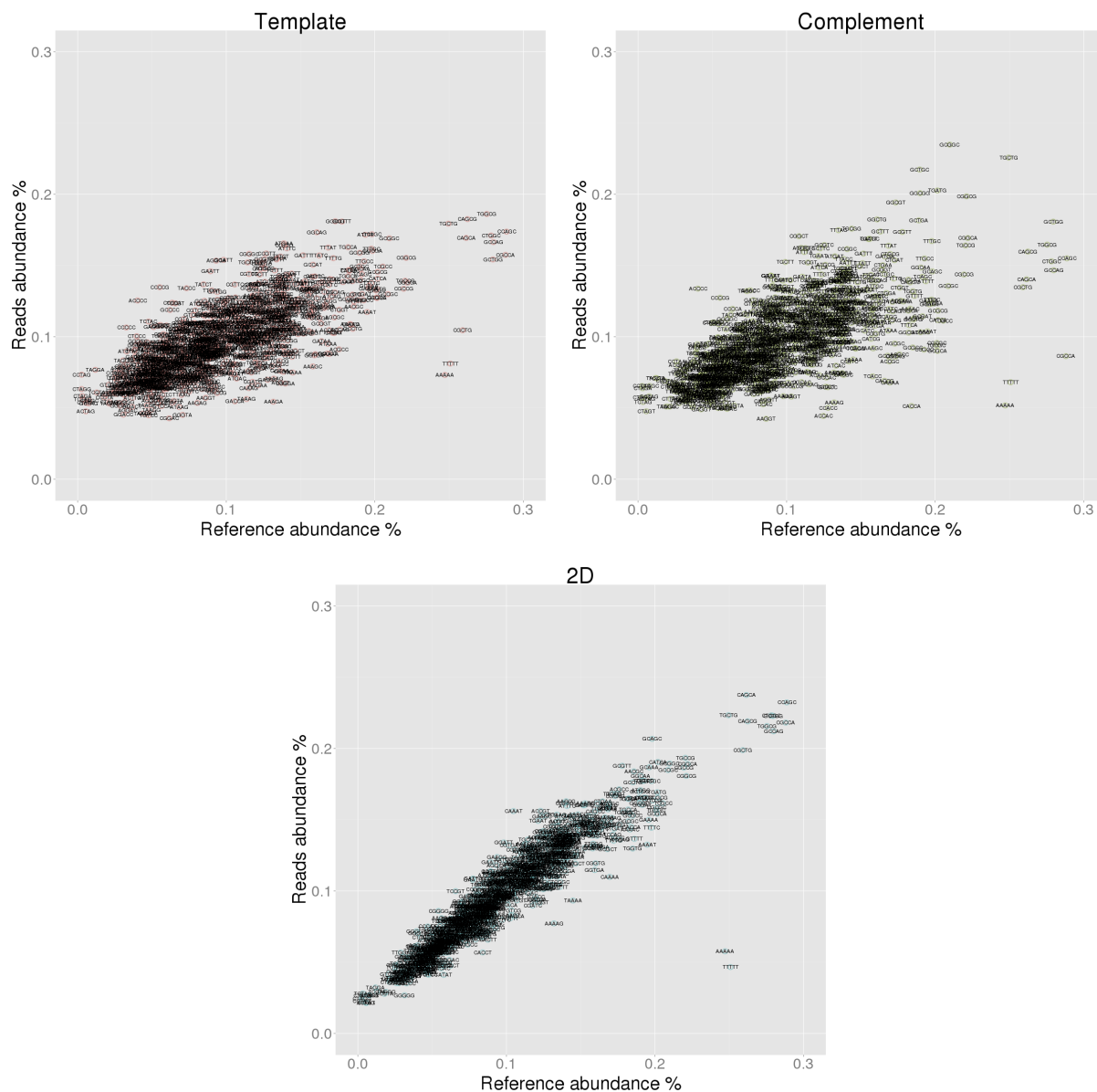
Escherichia coli 5-mer analysis

Under-represented 5-mers

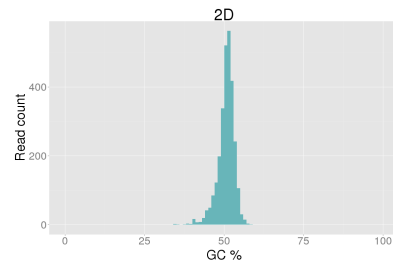
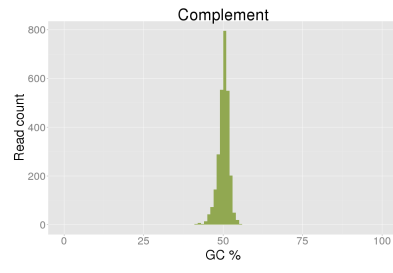
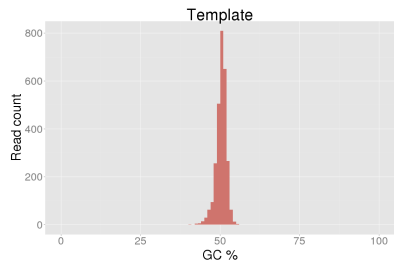
Rank	Template				Complement				2D			
	kmer	Ref %	Read %	Diff %	kmer	Ref %	Read %	Diff %	kmer	Ref %	Read %	Diff %
1	AAAAA	0.247	0.073	-0.174	CGCCA	0.288	0.086	-0.202	TTTTT	0.251	0.047	-0.204
2	TTTTT	0.251	0.081	-0.170	AAAAA	0.247	0.052	-0.195	AAAAA	0.247	0.058	-0.190
3	CGCTG	0.259	0.105	-0.154	TTTTT	0.251	0.068	-0.183	CGCCA	0.288	0.218	-0.070
4	CGCCA	0.288	0.158	-0.130	CCAGC	0.289	0.155	-0.134	GCCAG	0.280	0.212	-0.068
5	GCTGG	0.279	0.154	-0.125	GCCAG	0.280	0.147	-0.133	AAAAT	0.195	0.133	-0.062
6	CCAGC	0.289	0.174	-0.115	CACCA	0.184	0.051	-0.133	CGCTG	0.259	0.199	-0.060
7	GCCAG	0.280	0.166	-0.113	CTGGC	0.278	0.153	-0.125	CAAAA	0.169	0.110	-0.060
8	CTGGC	0.278	0.171	-0.107	CGCTG	0.259	0.135	-0.124	TGGCG	0.275	0.216	-0.060
9	CAGCA	0.261	0.169	-0.092	CAGCA	0.261	0.140	-0.121	GCTGG	0.279	0.223	-0.057
10	TGGCG	0.275	0.186	-0.089	GCGCA	0.202	0.090	-0.111	CCAGC	0.289	0.232	-0.056

Over-represented 5-mers

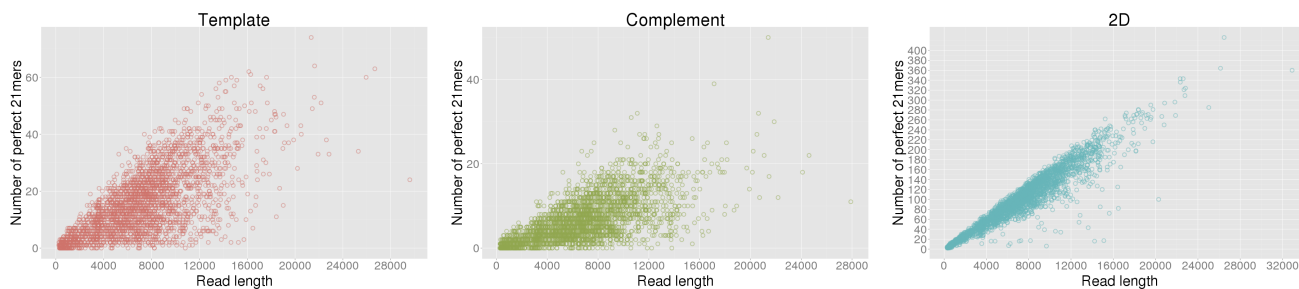
Rank	Template				Complement				2D			
	kmer	Ref %	Read %	Diff %	kmer	Ref %	Read %	Diff %	kmer	Ref %	Read %	Diff %
1	ACCCC	0.040	0.125	0.085	ACCCC	0.040	0.134	0.093	CAAAT	0.105	0.156	0.051
2	CCCCG	0.055	0.135	0.080	CCCCG	0.055	0.127	0.072	GGATT	0.098	0.134	0.036
3	CCCCC	0.033	0.107	0.074	CCTAG	0.003	0.065	0.063	TCCGT	0.066	0.100	0.034
4	CCTAG	0.003	0.073	0.071	CGGCT	0.108	0.171	0.062	ACCGT	0.123	0.156	0.033
5	TAGGA	0.012	0.077	0.065	CTAGA	0.003	0.064	0.061	GGGGT	0.039	0.072	0.032
6	TCTAC	0.048	0.111	0.063	CTGAG	0.050	0.110	0.060	CGGGG	0.054	0.086	0.032
7	TACCC	0.073	0.134	0.061	TAGGA	0.012	0.071	0.059	GATTC	0.078	0.109	0.031
8	CTAGG	0.003	0.063	0.061	GAGGC	0.051	0.110	0.059	GAATT	0.089	0.120	0.031
9	CTCCC	0.040	0.100	0.061	TACCC	0.073	0.132	0.059	GAATC	0.077	0.108	0.031
10	AGGCA	0.093	0.153	0.060	TCCTA	0.013	0.071	0.058	CGTGA	0.102	0.132	0.030



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	8.39	9.34	4.72	0.00	8.79	8.97	5.06	0.00	7.98	8.70	4.13
C	8.63	0.00	9.13	10.13	9.56	0.00	8.64	9.53	9.27	0.00	11.11	9.22
G	9.34	9.16	0.00	8.25	8.96	8.81	0.00	8.99	9.06	11.20	0.00	8.69
T	4.99	9.70	8.21	0.00	5.25	8.87	8.56	0.00	4.16	8.68	7.79	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 (3.31%)	TTC (3.48%)	AAA (4.18%)	TGC (3.00%)	GCC (3.01%)	AAA (4.01%)	GCA (2.96%)	GGC (2.68%)	AAA (4.00%)
2	AAA (2.85%)	TGC (2.95%)	TTC (3.70%)	TTC (2.74%)	TGC (2.87%)	GCA (3.64%)	AAA (2.80%)	GCG (2.66%)	GCA (3.58%)
3	GCA (2.77%)	GCA (2.76%)	GCA (3.34%)	GCA (2.70%)	AAA (2.68%)	GAA (3.44%)	TTC (2.72%)	TCA (2.54%)	GAA (3.47%)
4	TGC (2.70%)	AAA (2.61%)	GAA (3.11%)	AAA (2.65%)	GCA (2.58%)	TTC (3.12%)	TGC (2.55%)	TGC (2.54%)	TTC (2.90%)
5	ATC (2.60%)	GCC (2.47%)	TGC (2.61%)	CAG (2.48%)	TTC (2.57%)	TGC (2.56%)	CGC (2.50%)	GCA (2.50%)	TTT (2.75%)
6	TCA (2.48%)	TCA (2.46%)	TTT (2.42%)	GAA (2.46%)	GAA (2.37%)	TTT (2.48%)	TCA (2.47%)	TTC (2.48%)	GCG (2.56%)
7	GCC (2.39%)	GGC (2.43%)	AAT (2.37%)	GGC (2.41%)	GCG (2.33%)	TCA (2.41%)	GAA (2.46%)	AAA (2.45%)	GCC (2.54%)
8	GAA (2.33%)	ATC (2.34%)	TCA (2.30%)	ATC (2.36%)	TCA (2.27%)	ATC (2.40%)	ATC (2.41%)	CGC (2.34%)	ATC (2.39%)
9	GGC (2.25%)	AAT (2.24%)	GCC (2.24%)	TCA (2.35%)	GCC (2.27%)	GCC (2.21%)	CAG (2.29%)	ATC (2.27%)	AAT (2.36%)
10	GCG (2.15%)	AAC (2.24%)	ATC (2.20%)	GCC (2.23%)	CAG (2.22%)	GCC (2.18%)	GCG (2.27%)	AAC (2.15%)	TGC (2.23%)
-10	CTC (0.98%)	TGT (0.97%)	GGG (0.94%)	AGA (0.96%)	CTT (0.95%)	CTC (0.96%)	CTC (1.02%)	GAG (1.01%)	CCT (0.88%)
-9	CCC (0.93%)	AGG (0.93%)	CCT (0.93%)	GTG (0.94%)	AGT (0.93%)	CTT (0.87%)	TGT (1.01%)	ACT (0.93%)	TAT (0.85%)
-8	TGT (0.92%)	CCT (0.90%)	AGA (0.85%)	CTC (0.91%)	GGA (0.93%)	AGT (0.87%)	GAG (0.86%)	CGA (0.93%)	ACT (0.83%)
-7	GGA (0.81%)	GAG (0.81%)	AGT (0.81%)	CCC (0.89%)	CCC (0.92%)	CCT (0.82%)	AGA (0.85%)	CCC (0.92%)	CGA (0.73%)
-6	AGA (0.81%)	CTT (0.80%)	AGG (0.78%)	GGA (0.85%)	CTC (0.92%)	AGG (0.80%)	CCC (0.84%)	CTT (0.85%)	CTT (0.71%)
-5	AGG (0.69%)	CGA (0.75%)	CTT (0.70%)	GAG (0.78%)	CCT (0.84%)	GGG (0.75%)	AGG (0.81%)	AGA (0.79%)	GAG (0.69%)
-4	GAG (0.69%)	GGA (0.64%)	TGT (0.70%)	AGG (0.74%)	GAG (0.80%)	ACT (0.70%)	GGA (0.79%)	CCT (0.77%)	AGA (0.52%)
-3	GGG (0.67%)	AGA (0.64%)	GAG (0.59%)	CTA (0.60%)	GGG (0.78%)	GAG (0.60%)	GGG (0.68%)	CTA (0.74%)	GGA (0.50%)
-2	CTA (0.53%)	TAG (0.55%)	TAG (0.39%)	GGG (0.56%)	CTA (0.56%)	CTA (0.48%)	CTA (0.60%)	GGA (0.70%)	TAG (0.43%)
-1	TAG (0.41%)	CTA (0.50%)	CTA (0.39%)	TAG (0.45%)	TAG (0.52%)	TAG (0.37%)	TAG (0.48%)	TAG (0.64%)	CTA (0.43%)

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 (1.03%)	AAAA (1.34%)	CAGC (0.99%)	CGGC (1.08%)	CAAA (1.07%)	ATCA (0.88%)	TGGC (0.93%)	AAAA (1.24%)
2	GAAA (0.95%)	TGCC (0.98%)	GAAA (1.23%)	ATCA (0.91%)	CAGC (1.06%)	TGAA (1.05%)	CAGC (0.84%)	CAGC (0.90%)	GGCA (1.12%)
3	TGCC (0.87%)	CAGC (0.92%)	TTTC (1.17%)	CTGC (0.90%)	TGGC (1.05%)	AAAA (1.04%)	CGCC (0.83%)	TTCA (0.84%)	TGAA (1.02%)
4	ATCA (0.87%)	TTCA (0.89%)	GGCA (0.94%)	CGGC (0.87%)	TTGC (0.90%)	GAAA (0.96%)	GCCA (0.82%)	ATCA (0.83%)	GAAA (1.01%)
5	AAAA (0.87%)	TTGC (0.86%)	GCAA (0.92%)	TTGT (0.87%)	CTGC (0.88%)	AGCA (0.94%)	CCAG (0.81%)	CGGC (0.82%)	CGCC (0.96%)
6	CAGC (0.85%)	TGGC (0.85%)	GTTC (0.90%)	CCAG (0.82%)	ATCA (0.81%)	ATCA (0.93%)	CAAA (0.80%)	GCGC (0.76%)	GGAA (0.94%)
7	TTCA (0.84%)	CTGC (0.84%)	TGCC (0.86%)	TGGC (0.80%)	CAAA (0.81%)	GGCA (0.92%)	GGCA (0.79%)	GCGC (0.75%)	TTTT (0.91%)
8	CATC (0.82%)	GTTC (0.82%)	TGAA (0.85%)	CAAA (0.80%)	TTCC (0.78%)	TAAA (0.90%)	CGCA (0.78%)	TTGC (0.74%)	CGCA (0.88%)
9	TTGC (0.79%)	TTCC (0.82%)	GGAA (0.84%)	ATGC (0.76%)	TGCC (0.75%)	AGAA (0.89%)	TGAA (0.77%)	GCCA (0.74%)	TGCC (0.86%)
10	GGCA (0.79%)	GCCA (0.81%)	CAAA (0.84%)	AGCA (0.73%)	TTCA (0.74%)	CGCA (0.85%)	GAAA (0.77%)	CTGC (0.71%)	CAAA (0.86%)
-10	AGGG (0.12%)	TCTA (0.13%)	TTAG (0.11%)	GGGG (0.12%)	CTAT (0.12%)	TTAG (0.11%)	CTTG (0.15%)	CTAT (0.15%)	CGGA (0.11%)
-9	TAGT (0.12%)	CTAT (0.13%)	ACTA (0.11%)	GTGT (0.11%)	CGAG (0.12%)	ACCT (0.11%)	TTAG (0.14%)	ACTT (0.15%)	TCGA (0.10%)
-8	GGAC (0.11%)	TAGT (0.12%)	TCTA (0.09%)	GGAC (0.10%)	CTAA (0.11%)	GGAC (0.10%)	GTGT (0.14%)	GAGA (0.15%)	CCCT (0.10%)
-7	GAGG (0.10%)	CGGA (0.12%)	CGAG (0.09%)	GAGG (0.10%)	TAGA (0.11%)	CGAG (0.09%)	TCTA (0.13%)	ACCT (0.15%)	GGGA (0.10%)
-6	CTAA (0.10%)	CCCT (0.12%)	GGAC (0.09%)	CTAA (0.10%)	ACCT (0.11%)	CTAT (0.09%)	CTAT (0.13%)	CTAA (0.12%)	CTAA (0.09%)
-5	TTAG (0.10%)	CTAA (0.10%)	TAGT (0.09%)	TAGA (0.09%)	GTGT (0.09%)	GTGT (0.09%)	CTAA (0.13%)	TAGG (0.10%)	CTAT (0.09%)
-4	CCTA (0.08%)	TAGG (0.08%)	TAGA (0.08%)	CCCT (0.08%)	CCCT (0.08%)	CCCT (0.07%)	TAGA (0.08%)	TAGA (0.09%)	TAGG (0.08%)
-3	TAGA (0.07%)	TAGA (0.06%)	TAGG (0.06%)	CCTA (0.07%)	TAGG (0.07%)	TAGG (0.06%)	CCTA (0.07%)	CCCT (0.09%)	CCTA (0.05%)
-2	TAGG (0.05%)	CCTA (0.06%)	CCTA (0.05%)	TAGG (0.05%)	CCTA (0.06%)	CCTA (0.06%)	TAGG (0.06%)	CCTA (0.09%)	TAGA (0.04%)
-1	CTAG (0.01%)	CTAG (0.01%)	CTAG (0.01%)	CTAG (0.02%)	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 (0.37%)	CAGCA (0.43%)	CAGCA (0.43%)	CAGCA (0.41%)	CAGCA (0.58%)	CAGCA (0.37%)	CTGGC (0.38%)	CAGCA (0.43%)
2	CATCA (0.33%)	CGCCA (0.34%)	GAAAA (0.42%)	GCTGC (0.36%)	CTGGC (0.39%)	ATAAA (0.37%)	CGCCA (0.35%)	CAGCA (0.31%)	GAAAA (0.41%)
3	TTGCC (0.30%)	CTGGC (0.34%)	CAAAA (0.37%)	CATCA (0.35%)	GCGGC (0.37%)	CGGCA (0.37%)	GCCAG (0.31%)	CGCCA (0.31%)	CGGCA (0.40%)
4	ATTTT (0.30%)	TTGCC (0.34%)	GCAAA (0.34%)	CCAGC (0.32%)	GCTGC (0.32%)	CATCA (0.36%)	GCAAA (0.31%)	CATCA (0.30%)	CAAAA (0.37%)
5	TTATC (0.30%)	CCAGC (0.31%)	TGAAA (0.32%)	GCGGC (0.31%)	CCAGC (0.32%)	GCAAA (0.34%)	CGGCA (0.30%)	CCAGC (0.30%)	TGGCA (0.36%)
6	CTGGC (0.30%)	CATCA (0.31%)	CGTTT (0.32%)	CTGGC (0.31%)	CATCA (0.32%)	CAGAA (0.34%)	CTGGC (0.29%)	GCGGC (0.30%)	TTGCC (0.32%)
7	GCCAG (0.30%)	TTTCA (0.30%)	CGGCA (0.32%)	GCAAA (0.29%)	TCAGC (0.32%)	GAAAA (0.33%)	CAGGC (0.29%)	TGGCG (0.28%)	GCAAA (0.32%)
8	CCAGC (0.30%)	GCAGC (0.30%)	TGTTT (0.31%)	CGGCA (0.28%)	TTTGC (0.29%)	AAGAA (0.33%)	CATCA (0.28%)	AATCA (0.27%)	CGCCA (0.31%)
9	CGCCA (0.29%)	GCTGC (0.30%)	TGGCA (0.31%)	GCAGC (0.27%)	AATCA (0.29%)	ATGAA (0.32%)	CCAGC (0.28%)	TTTCA (0.26%)	ATTTT (0.31%)
10	GCAGC (0.29%)	ATTTT (0.30%)	ATTTT (0.31%)	AATGC (0.27%)	GCAAA (0.28%)	ACAAA (0.31%)	GCGCA (0.27%)	GCCAG (0.26%)	GCGAA (0.30%)
-10	TAGGG (0.01%)	ACCTA (0.01%)	TAGGA (0.01%)	CTAGC (0.01%)	CCCCC (0.01%)	CCCCT (0.01%)	CCCTA (0.01%)	TCCGA (0.02%)	CCCTA (0.01%)
-9	TAGGA (0.01%)	TAGGA (0.01%)	CCCTA (0.01%)	ACCTA (0.01%)	CCCTA (0.01%)	GCTAG (0.01%)	TAGGA (0.01%)	GCTAG (0.01%)	ACTAG (0.01%)
-8	CTAGT (0.00%)	GCTAG (0.00%)	ACTAG (0.01%)	GGGGG (0.01%)	GCTAG (0.01%)	CTAGC (0.01%)	CTAGC (0.01%)	TAGGA (0.01%)	GCTAG (0.00%)
-7	CTAGC (0.00%)	ACTAG (0.00%)	GCTAG (0.00%)	CCCCT (0.01%)	CTAGC (0.01%)	ACCTA (0.00%)	GCTAG (0.01%)	ACTAG (0.01%)	TAGGA (0.00%)
-6	GCTAG (0.00%)	CTAGC (0.00%)	CTAGC (0.00%)	GCTAG (0.01%)	CTAGT (0.00%)	CTAGA (0.00%)	CTAGT (0.00%)	CTAGC (0.01%)	CTAGC (0.00%)
-5	ACTAG (0.00%)	CTAGT (0.00%)	CTAGA (0.00%)	CTAGT (0.01%)	ACTAG (0.00%)	CTAGT (0.00%)	ACTAG (0.00%)	CTAGT (0.01%)	CTAGT (0.00%)
-4	CTAGA (0.00%)	CCTAG (0.00%)	TCTAG (0.00%)	CTAGA (0.00%)	TCTAG (0.00%)	CTAGG (0.00%)	CTAGA (0.00%)	TCTAG (0.00%)	CTAGG (0.00%)
-3	CCTAG (0.00%)	CTAGA (0.00%)	CTAGT (0.00%)	CCTAG (0.00%)	CTAGA (0.00%)	CCTAG (0.00%)	CTAGG (0.00%)	CTAGA (0.00%)	TCTAG (0.00%)
-2	TCTAG (0.00%)	TCTAG (0.00%)	CTAGG (0.00%)	ACTAG (0.00%)	CTAGG (0.00%)	ACTAG (0.00%)	TCTAG (0.00%)	CCTAG (0.00%)	CCTAG (0.00%)
-1	CTAGG (0.00%)	CTAGG (0.00%)	CCTAG (0.00%)	TCTAG (0.00%)	CCTAG (0.00%)	TCTAG (0.00%)	CCTAG (0.00%)	CTAGG (0.00%)	CTAGA (0.00%)

Most common

Least common

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