

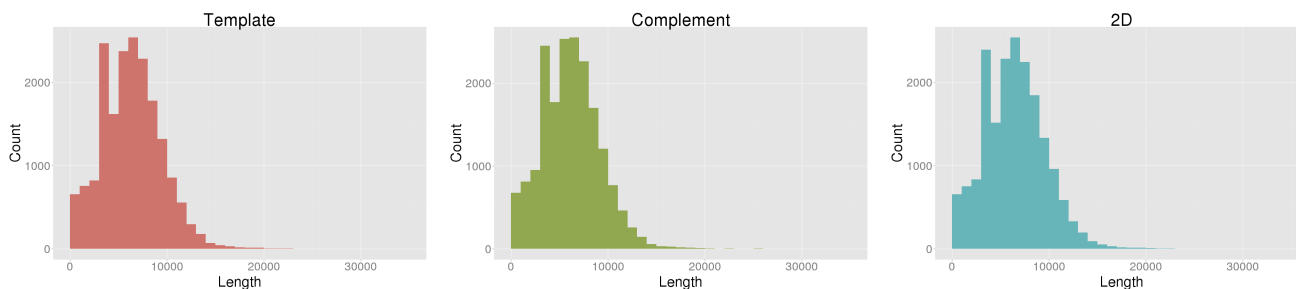
NanoOK report for MA_286_R7.3_MARC_K12_03_27_15

Pass and fail counts

Type	Pass	Fail
Template	18765	0
Complement	18765	0
2D	18765	0

Read lengths

Type	NumReads	TotalBases	Mean	Longest	Shortest	N50	N50Count	N90	N90Count
Template	18765	119627233	6375.02	43561	130	7616	6063	3935	14124
Complement	18765	116000318	6181.74	42351	158	7411	6048	3819	14098
2D	18765	121564632	6478.26	44073	138	7755	6053	4016	14098



Template alignments

Number of reads	18765
Number of reads with alignments	18629 (99.28%)
Number of reads without alignments	136 (0.72%)

ID	Size	Number of Reads	% of Reads	Mean read length	Aligned bases	Mean coverage	Longest Perf Kmer
Control sequence	3560	1777	9.47	3292.50	6173141	1734.03	64
Escherichia coli	4641652	16852	89.81	6744.63	121820827	26.25	78

Complement alignments

Number of reads	18765
Number of reads with alignments	18629 (99.28%)
Number of reads without alignments	136 (0.72%)

ID	Size	Number of Reads	% of Reads	Mean read length	Aligned bases	Mean coverage	Longest Perf Kmer
Control sequence	3560	1772	9.44	3149.84	5631581	1581.90	54
Escherichia coli	4641652	16857	89.83	6544.01	118420676	25.51	91

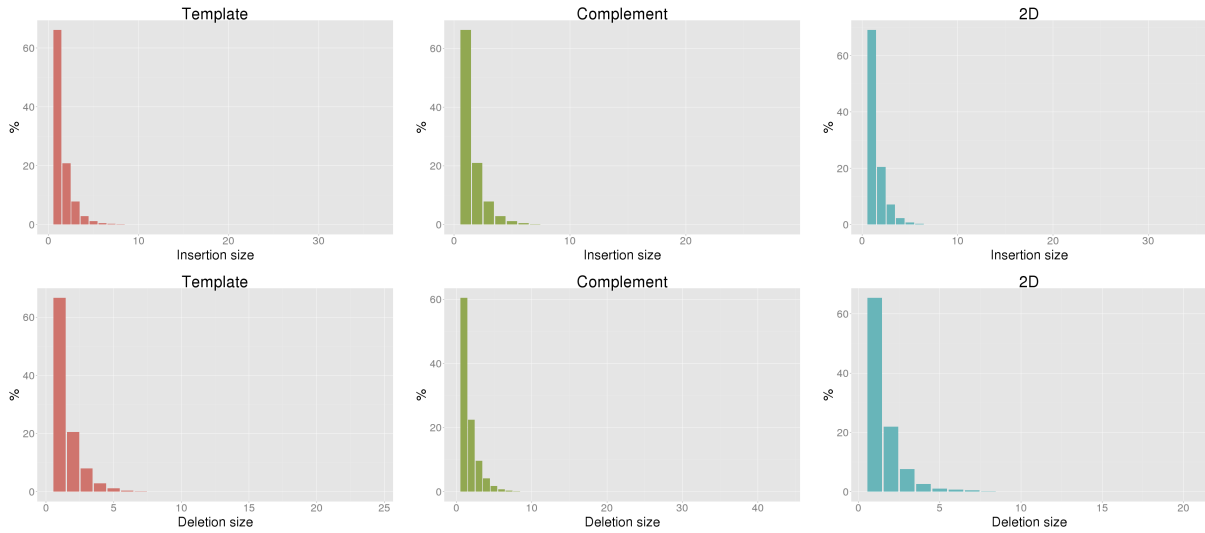
2D alignments

Number of reads	18765
Number of reads with alignments	18760 (99.97%)
Number of reads without alignments	5 (0.03%)

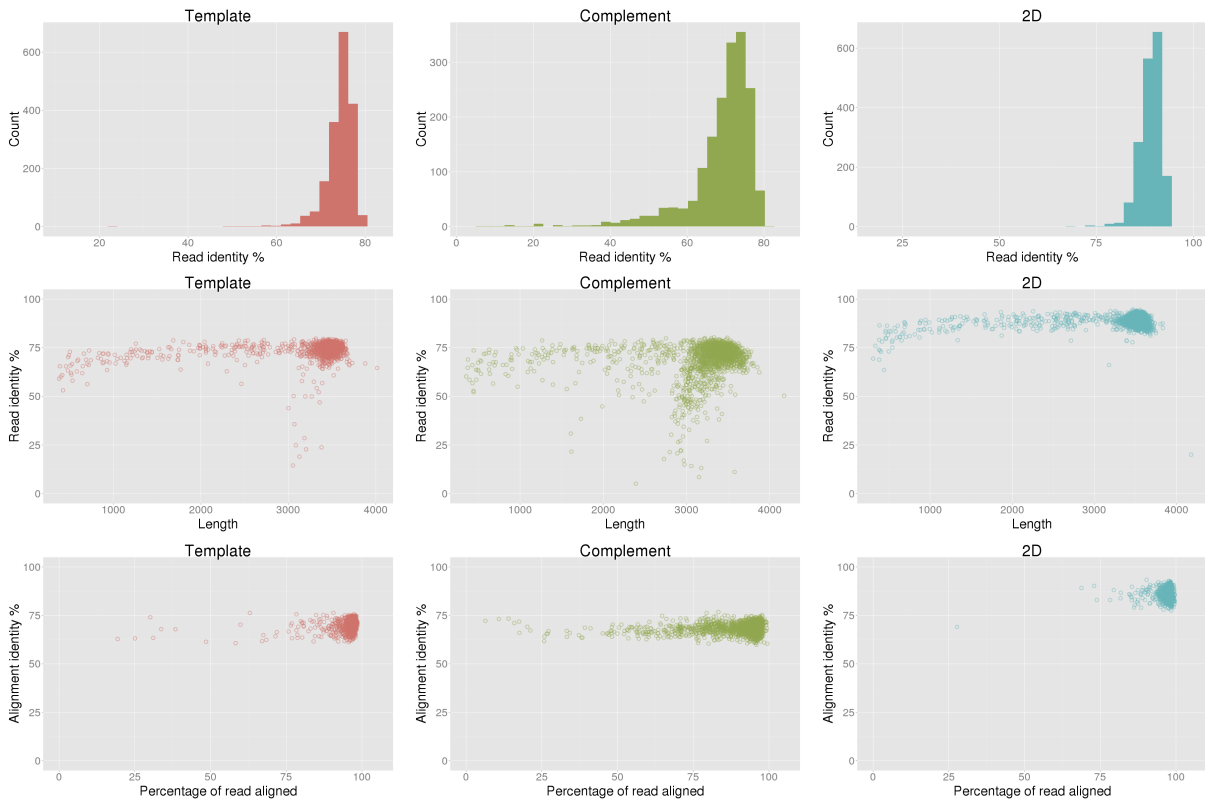
ID	Size	Number of Reads	% of Reads	Mean read length	Aligned bases	Mean coverage	Longest Perf Kmer
Control sequence	3560	1789	9.53	3291.44	6075164	1706.51	212
Escherichia coli	4641652	16971	90.44	6815.07	119826230	25.82	267

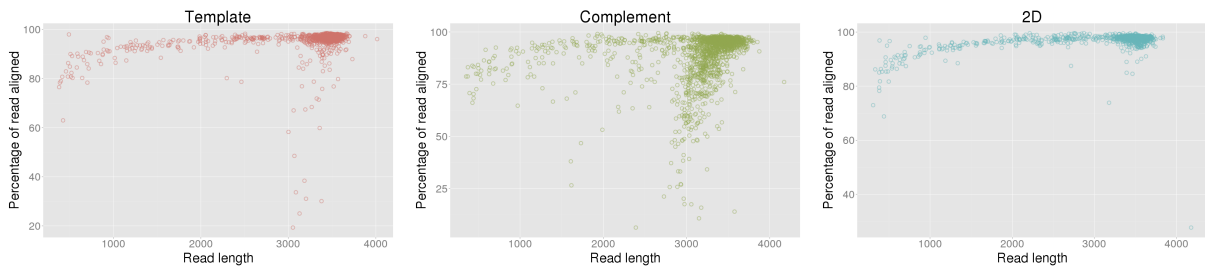
Control sequence error analysis

	Template	Complement	2D
Overall base identity (excluding indels)	74.19%	69.05%	89.00%
Aligned base identity (excluding indels)	81.87%	81.55%	94.23%
Identical bases per 100 aligned bases (including indels)	70.31%	68.43%	86.27%
Inserted bases per 100 aligned bases (including indels)	5.16%	4.76%	2.99%
Deleted bases per 100 aligned bases (including indels)	8.96%	11.32%	5.46%
Substitutions per 100 aligned bases (including indels)	15.57%	15.48%	5.28%
Mean insertion size	1.57	1.55	1.47
Mean deletion size	1.54	1.70	1.57

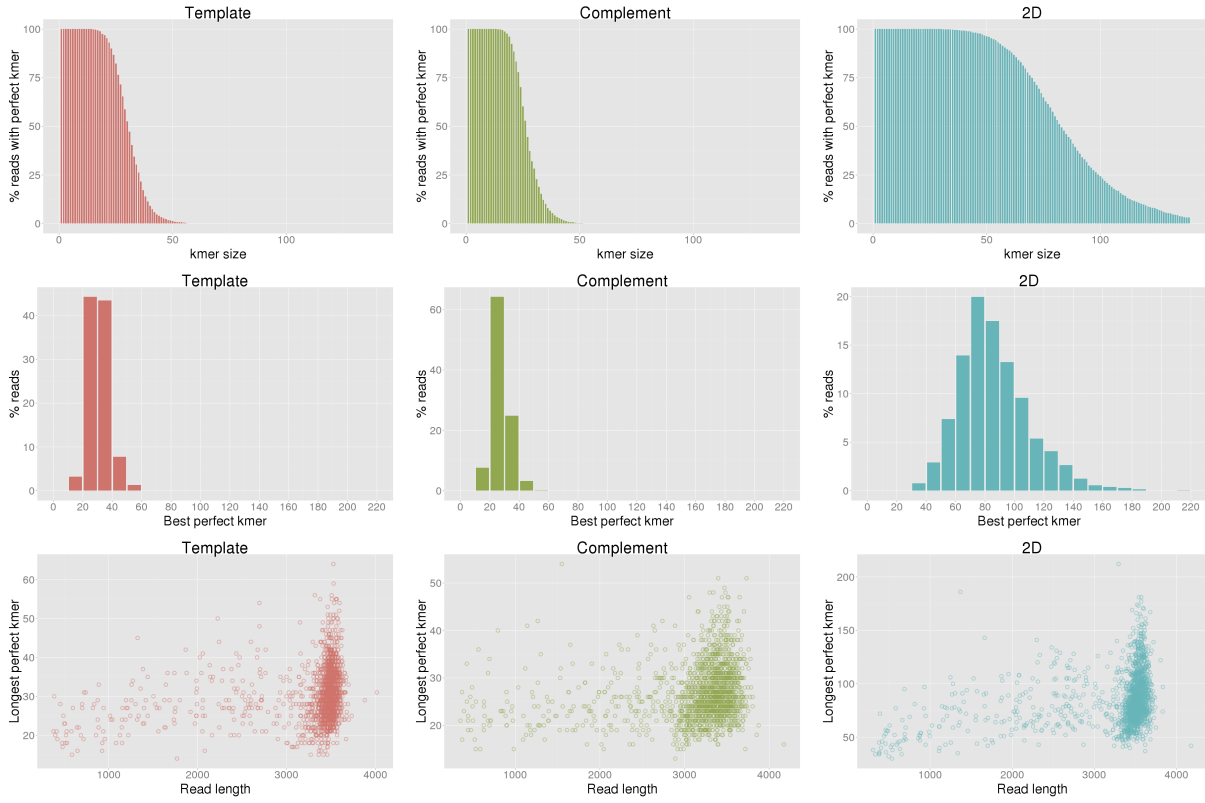


Control sequence read identity

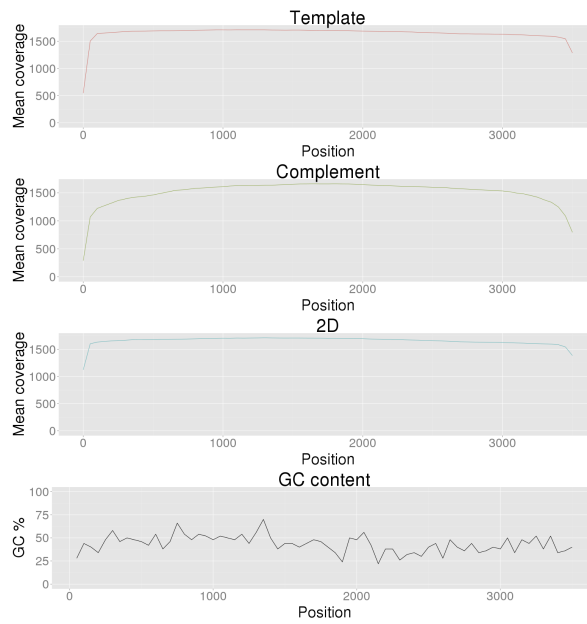




Control sequence perfect kmers



Control sequence coverage



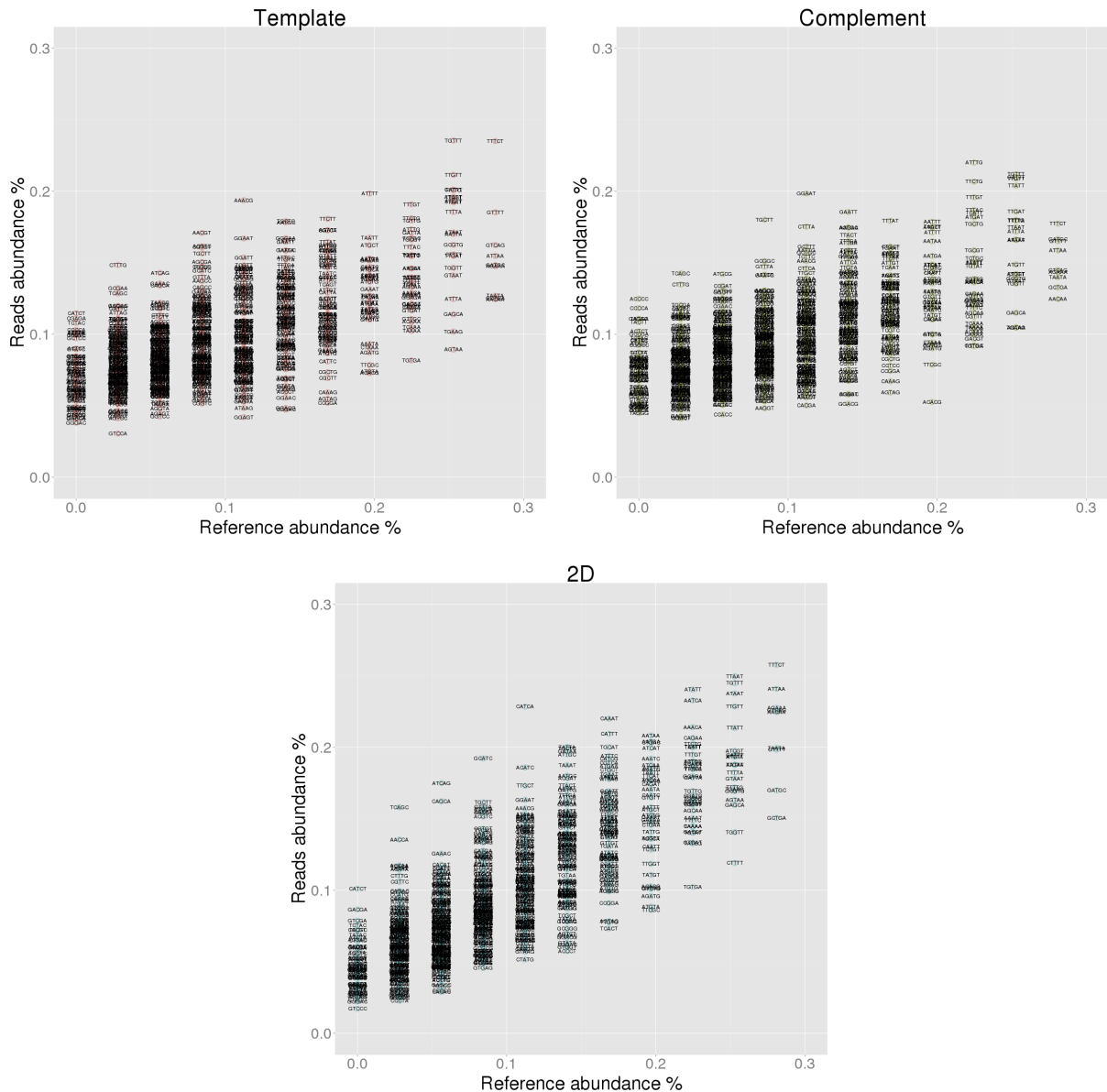
Control sequence 5-mer analysis

Under-represented 5-mers

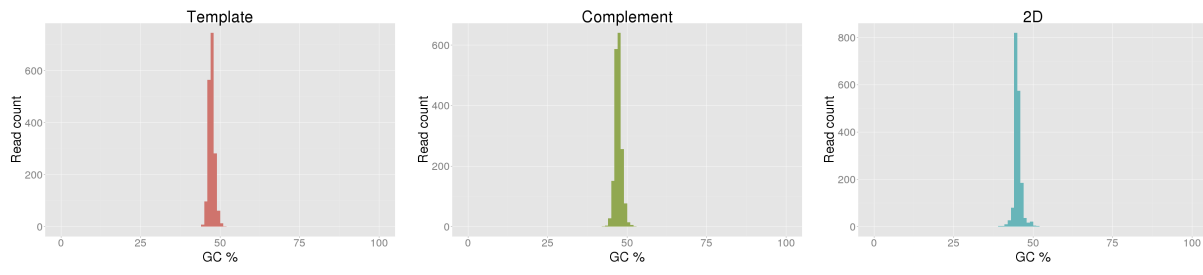
Rank	Template				Complement				2D			
	kmer	Ref %	Read %	Diff %	kmer	Ref %	Read %	Diff %	kmer	Ref %	Read %	Diff %
1	TTTTT	0.759	0.150	-0.609	TTTTT	0.759	0.094	-0.665	TTTTT	0.759	0.056	-0.703
2	AAAAA	0.478	0.121	-0.357	AAAAA	0.478	0.072	-0.406	AAAAA	0.478	0.073	-0.404
3	TGATG	0.393	0.138	-0.256	AAAAC	0.337	0.137	-0.200	TGATG	0.393	0.195	-0.198
4	GATGT	0.309	0.105	-0.204	TGATG	0.393	0.197	-0.197	CTGAT	0.309	0.159	-0.150
5	AAAAC	0.337	0.140	-0.197	GATGT	0.309	0.124	-0.186	GATGT	0.309	0.160	-0.149
6	CTGAT	0.309	0.132	-0.177	GCAAT	0.309	0.143	-0.166	AAAAC	0.337	0.201	-0.136
7	AGTAA	0.253	0.089	-0.164	AACAA	0.281	0.125	-0.156	CTTTT	0.253	0.119	-0.134
8	AATAT	0.309	0.146	-0.163	TTATC	0.309	0.157	-0.153	GCTGA	0.281	0.151	-0.130
9	AACAA	0.281	0.124	-0.156	CTGAT	0.309	0.158	-0.151	TGTGA	0.225	0.102	-0.122
10	GCTGA	0.281	0.126	-0.155	AGTAA	0.253	0.105	-0.148	TTATC	0.309	0.189	-0.120

Over-represented 5-mers

Rank	Template				Complement				2D			
	kmer	Ref %	Read %	Diff %	kmer	Ref %	Read %	Diff %	kmer	Ref %	Read %	Diff %
1	CTTTG	0.028	0.148	0.120	ACCCC	0.000	0.125	0.125	TCAGC	0.028	0.158	0.130
2	CATCT	0.000	0.115	0.115	CCCCA	0.000	0.118	0.118	ATCAG	0.056	0.175	0.119
3	CGAGA	0.000	0.111	0.111	TCAGC	0.028	0.143	0.114	CATCA	0.112	0.229	0.116
4	TCTAC	0.000	0.108	0.108	TATAC	0.000	0.111	0.111	GCATC	0.084	0.192	0.108
5	GCGAA	0.028	0.132	0.104	GAGGA	0.000	0.111	0.111	AACCA	0.028	0.135	0.107
6	CCCCA	0.000	0.103	0.103	TACTT	0.000	0.108	0.108	CAGCA	0.056	0.162	0.106
7	ATCTA	0.000	0.101	0.101	CTTTG	0.028	0.135	0.107	CATCT	0.000	0.101	0.101
8	TCTTA	0.000	0.101	0.101	ACTCT	0.000	0.102	0.102	ACCAA	0.028	0.117	0.089
9	ACCCC	0.000	0.101	0.101	GCCGA	0.000	0.100	0.100	TCACA	0.028	0.117	0.089
10	TCAGC	0.028	0.128	0.100	TCTAC	0.000	0.097	0.097	TACAT	0.028	0.115	0.087

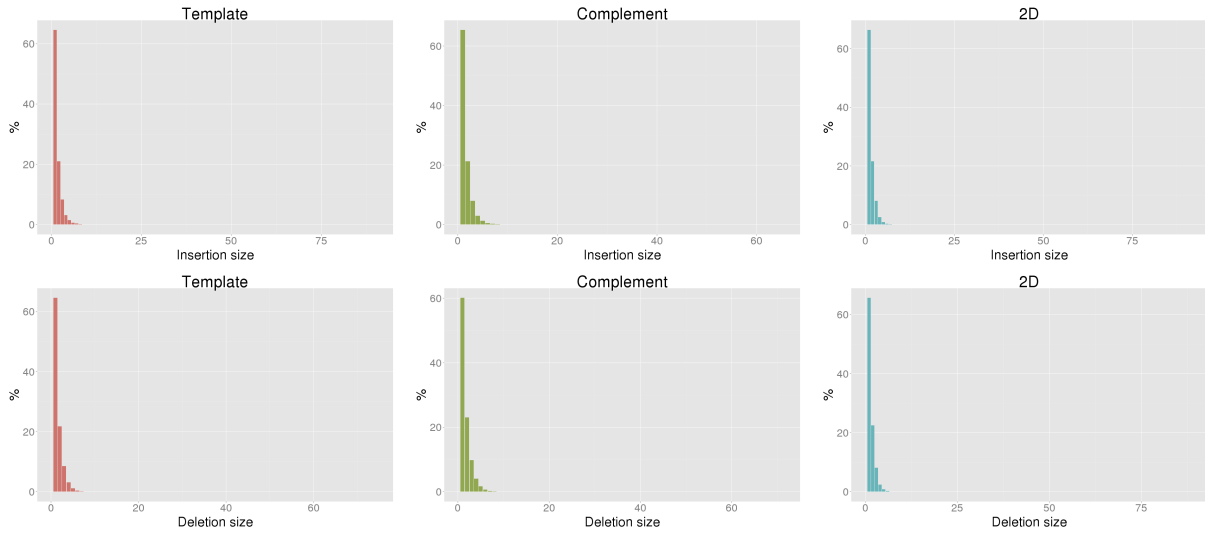


Control sequence GC content

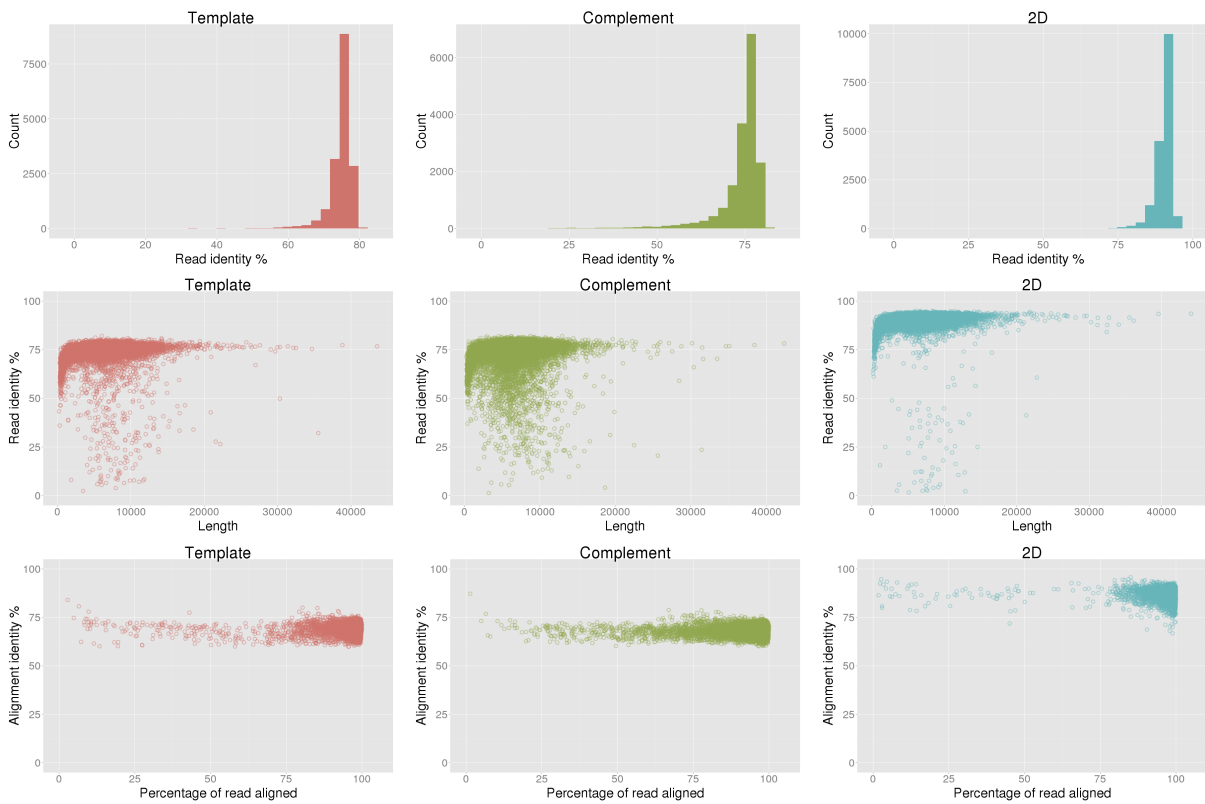


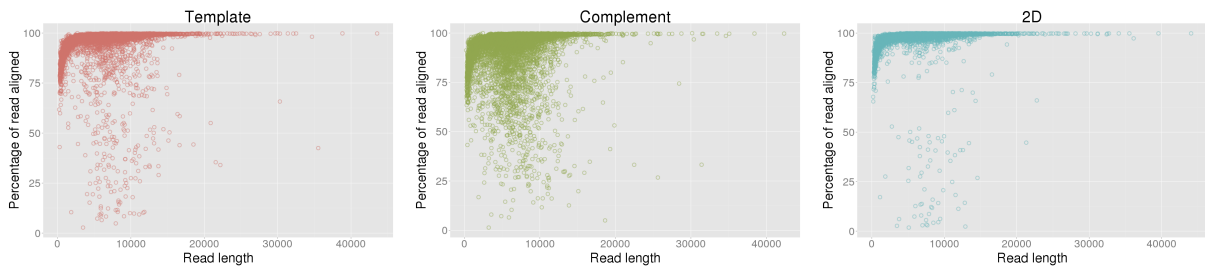
Escherichia coli error analysis

	Template	Complement	2D
Overall base identity (excluding indels)	74.68%	73.86%	90.52%
Aligned base identity (excluding indels)	81.56%	82.11%	94.88%
Identical bases per 100 aligned bases (including indels)	69.67%	68.80%	87.38%
Inserted bases per 100 aligned bases (including indels)	5.55%	5.05%	3.12%
Deleted bases per 100 aligned bases (including indels)	9.03%	11.15%	4.79%
Substitutions per 100 aligned bases (including indels)	15.75%	15.00%	4.72%
Mean insertion size	1.63	1.58	1.52
Mean deletion size	1.57	1.70	1.52

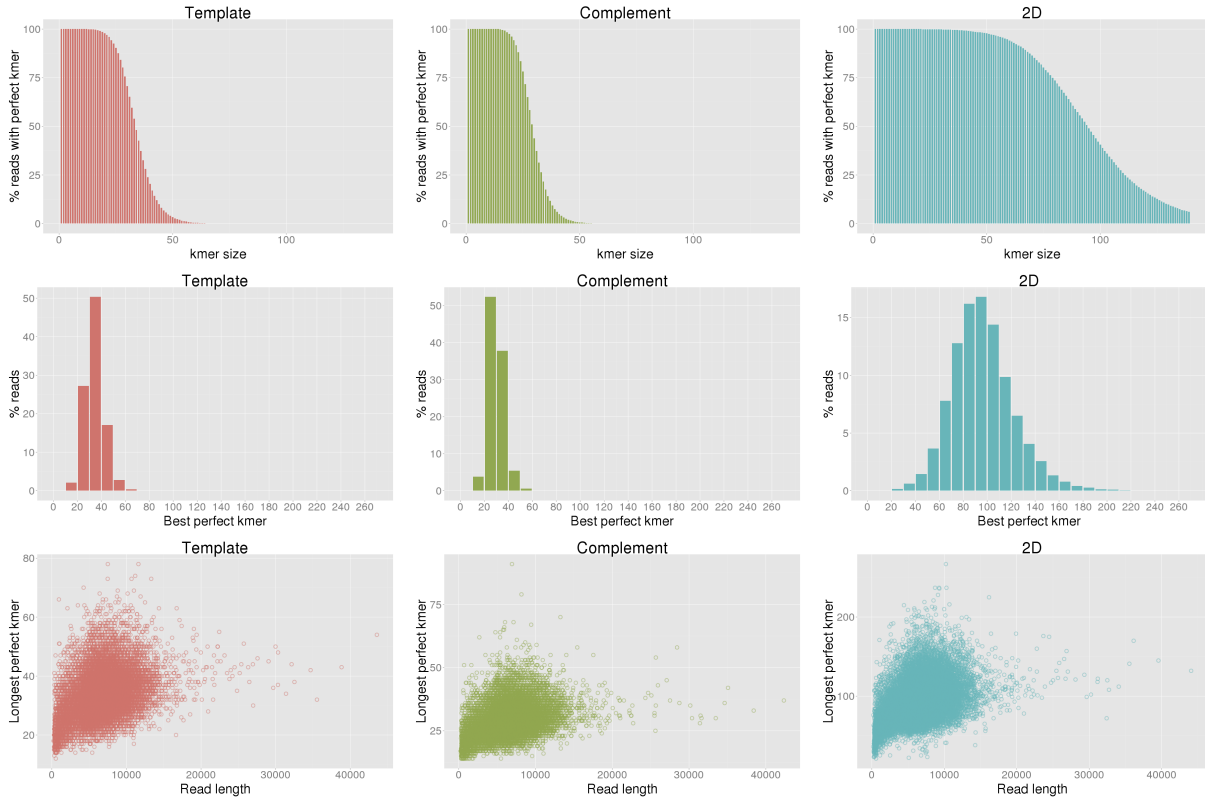


Escherichia coli read identity

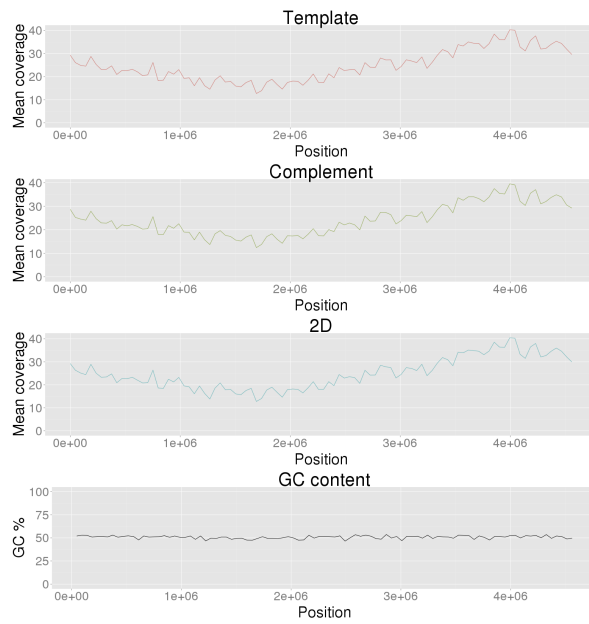




Escherichia coli perfect kmers



Escherichia coli coverage



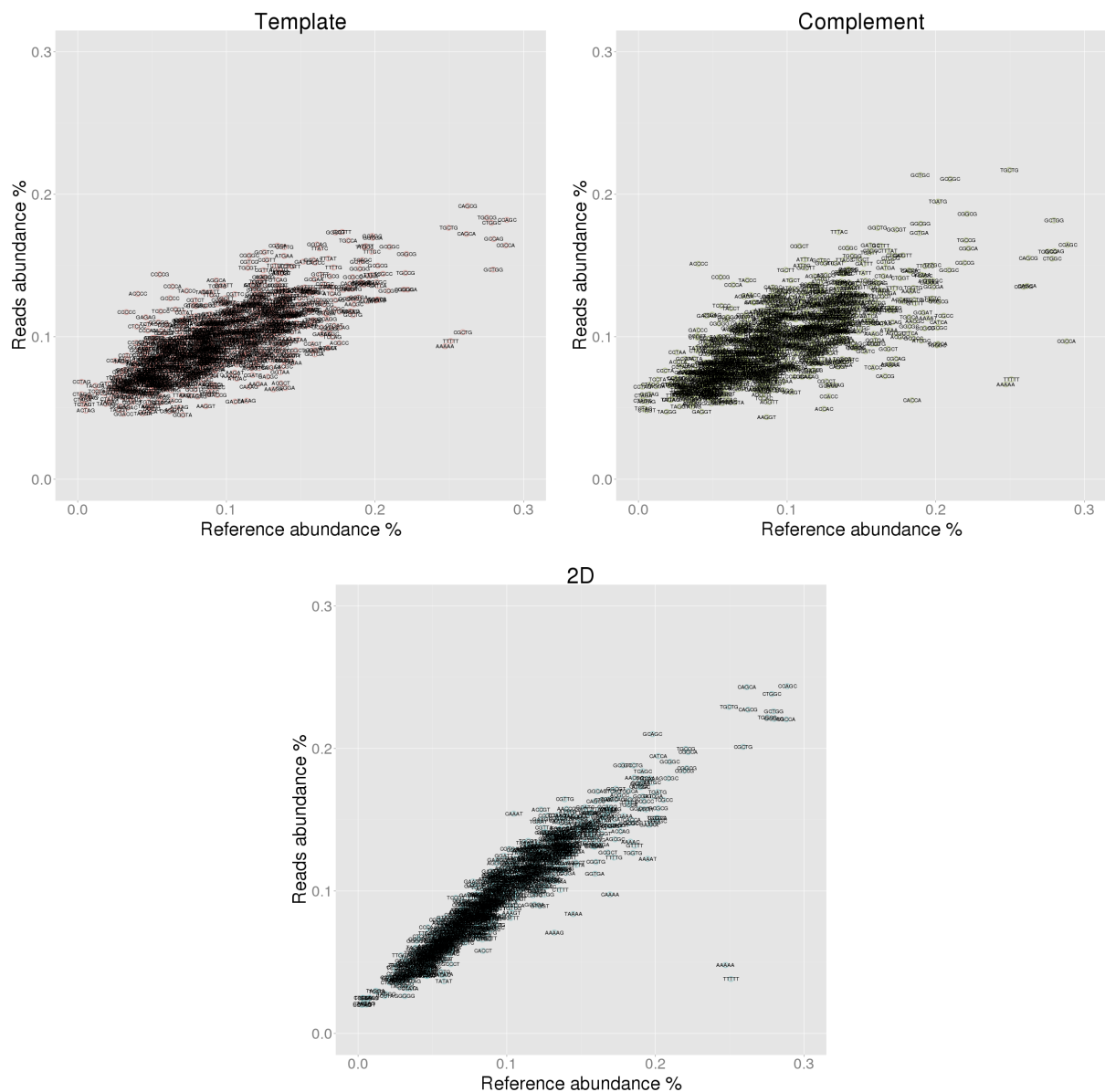
Escherichia coli 5-mer analysis

Under-represented 5-mers

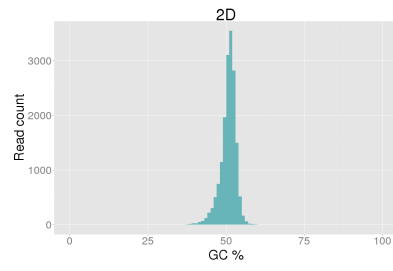
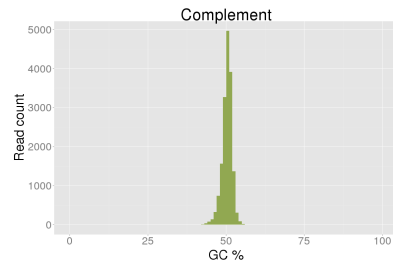
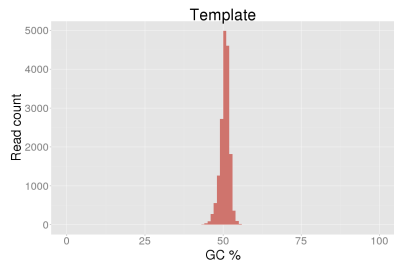
Rank	Template				Complement				2D			
	kmer	Ref %	Read %	Diff %	kmer	Ref %	Read %	Diff %	kmer	Ref %	Read %	Diff %
1	CGCTG	0.259	0.103	-0.156	CGCCA	0.288	0.097	-0.191	TTTTT	0.251	0.038	-0.213
2	TTTTT	0.251	0.097	-0.154	TTTTT	0.251	0.070	-0.181	AAAAA	0.247	0.048	-0.199
3	AAAAA	0.247	0.093	-0.154	AAAAA	0.247	0.067	-0.181	AAAAT	0.195	0.123	-0.072
4	GCTGG	0.279	0.147	-0.132	CACCA	0.184	0.055	-0.129	CAAAA	0.169	0.098	-0.072
5	CGCCA	0.288	0.164	-0.124	CAGCA	0.261	0.136	-0.126	CGCCA	0.288	0.221	-0.067
6	GCCAG	0.280	0.169	-0.111	CCAGC	0.289	0.165	-0.124	AAAAG	0.132	0.071	-0.061
7	CCAGC	0.289	0.182	-0.107	CGCTG	0.259	0.135	-0.124	TAAAA	0.145	0.084	-0.061
8	CTGGC	0.278	0.180	-0.098	CTGGC	0.278	0.155	-0.123	GCCAG	0.280	0.221	-0.059
9	TGGCG	0.275	0.184	-0.092	GCCAG	0.280	0.160	-0.120	TGGTG	0.185	0.127	-0.058
10	CAGCA	0.261	0.172	-0.089	TGGCG	0.275	0.160	-0.116	CGCTG	0.259	0.201	-0.058

Over-represented 5-mers

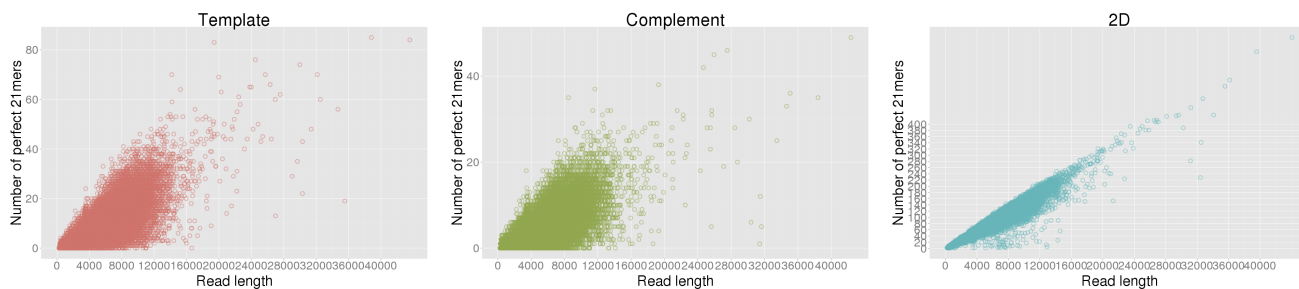
Rank	Template				Complement				2D			
	kmer	Ref %	Read %	Diff %	kmer	Ref %	Read %	Diff %	kmer	Ref %	Read %	Diff %
1	ACCCC	0.040	0.130	0.090	ACCCC	0.040	0.151	0.111	CAAAT	0.105	0.154	0.050
2	CCCCG	0.055	0.144	0.089	CCCCG	0.055	0.142	0.087	ACCGT	0.123	0.157	0.034
3	CCCCC	0.033	0.117	0.085	CCCCC	0.064	0.137	0.073	TCCGT	0.066	0.095	0.030
4	CCCCA	0.064	0.135	0.072	GAGAG	0.046	0.115	0.069	GAATC	0.077	0.107	0.029
5	GAGAG	0.046	0.114	0.068	TACCC	0.073	0.140	0.066	GAAGG	0.094	0.122	0.028
6	CTCCC	0.040	0.107	0.067	TCCCC	0.056	0.122	0.066	CGTGA	0.102	0.130	0.028
7	CCTAG	0.003	0.068	0.066	CTGAG	0.050	0.115	0.066	CCCAA	0.047	0.074	0.028
8	GCCCC	0.062	0.127	0.065	GACCC	0.040	0.105	0.065	TGAAT	0.121	0.149	0.027
9	TCCCC	0.056	0.118	0.062	CCTAA	0.026	0.089	0.063	GGATT	0.098	0.125	0.027
10	TCTAC	0.048	0.109	0.061	CCTAG	0.003	0.065	0.062	GAAGC	0.124	0.150	0.026



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	8.91	9.31	4.62	0.00	9.08	8.72	4.89	0.00	8.41	8.74	3.87
C	8.41	0.00	9.13	10.01	9.22	0.00	8.67	9.73	9.11	0.00	11.02	9.33
G	9.49	9.13	0.00	8.03	9.02	8.85	0.00	8.79	9.14	11.24	0.00	8.43
T	4.91	9.51	8.54	0.00	5.19	8.92	8.92	0.00	3.97	8.60	8.14	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 (3.22%)	TTC (3.52%)	AAA (4.06%)	TGC (2.75%)	GCC (2.97%)	AAA (4.04%)	GCA (3.13%)	GCC (2.67%)	AAA (3.83%)
2	GCA (2.75%)	TGC (3.05%)	TTC (3.71%)	GCA (2.72%)	AAA (2.80%)	GCA (3.56%)	TTC (2.75%)	TCA (2.58%)	GCA (3.78%)
3	AAA (2.72%)	GCA (2.82%)	GCA (3.27%)	TTC (2.66%)	TGC (2.79%)	GAA (3.34%)	AAA (2.61%)	TGC (2.57%)	GAA (3.40%)
4	TGC (2.68%)	AAA (2.68%)	GAA (2.99%)	AAA (2.58%)	GCA (2.62%)	TTC (3.08%)	TCA (2.60%)	AAA (2.55%)	TTC (2.94%)
5	ATC (2.60%)	GCC (2.54%)	TGC (2.55%)	CAG (2.52%)	TTC (2.58%)	TTT (2.60%)	ATC (2.45%)	GCG (2.50%)	TTT (2.80%)
6	TCA (2.49%)	GGC (2.43%)	TTT (2.52%)	GGC (2.43%)	GAA (2.36%)	TGC (2.40%)	TGC (2.42%)	TTC (2.46%)	GCC (2.46%)
7	GCC (2.30%)	TCA (2.43%)	AAT (2.33%)	ATC (2.33%)	GCC (2.32%)	TCA (2.37%)	GAA (2.40%)	GCA (2.44%)	GCG (2.39%)
8	GGC (2.29%)	ATC (2.27%)	GCC (2.29%)	GAA (2.30%)	CAG (2.29%)	ATC (2.33%)	GCG (2.26%)	CGC (2.31%)	AAT (2.38%)
9	GAA (2.18%)	AAC (2.18%)	TCA (2.25%)	TCA (2.29%)	TCA (2.29%)	GCC (2.19%)	CGC (2.21%)	ATC (2.21%)	ATC (2.31%)
10	TTT (2.14%)	GCG (2.13%)	GCC (2.21%)	GCC (2.13%)	AGC (2.15%)	GCC (2.09%)	CAG (2.21%)	CAG (2.21%)	TCA (2.29%)
-10	TGT (0.98%)	AGG (0.96%)	GGT (0.93%)	AGA (1.03%)	ACT (0.95%)	CTC (0.95%)	TAC (1.04%)	GTA (1.01%)	ACT (0.87%)
-9	AGT (0.98%)	AGT (0.92%)	GGG (0.93%)	AGT (0.97%)	AGT (0.94%)	CTT (0.91%)	CTC (1.01%)	CCC (0.93%)	CCT (0.87%)
-8	CCC (0.91%)	CCT (0.92%)	AGA (0.84%)	CTC (0.94%)	CCC (0.93%)	AGT (0.88%)	GAG (0.87%)	CGA (0.91%)	TGA (0.84%)
-7	GGA (0.86%)	CTT (0.82%)	AGG (0.81%)	GGA (0.88%)	CTC (0.91%)	AGG (0.83%)	AGG (0.82%)	ACT (0.90%)	CTT (0.75%)
-6	AGA (0.83%)	GAG (0.81%)	AGT (0.80%)	CCC (0.87%)	GGA (0.91%)	CCT (0.82%)	AGA (0.81%)	CTT (0.85%)	GAG (0.73%)
-5	GAG (0.73%)	CGA (0.78%)	CTT (0.78%)	GAG (0.84%)	CCT (0.89%)	GGG (0.81%)	GGA (0.81%)	CCT (0.82%)	CGA (0.72%)
-4	GGG (0.72%)	AGA (0.68%)	TGT (0.75%)	AGG (0.73%)	GAG (0.82%)	ACT (0.71%)	CCC (0.79%)	AGA (0.81%)	AGA (0.52%)
-3	AGG (0.70%)	GGA (0.64%)	GAG (0.63%)	GGG (0.61%)	GGG (0.77%)	GAG (0.62%)	GGG (0.75%)	CTA (0.74%)	TAG (0.50%)
-2	CTA (0.50%)	TAG (0.53%)	TAG (0.39%)	CTA (0.59%)	CTA (0.55%)	CTA (0.47%)	CTA (0.60%)	GGA (0.73%)	GGA (0.49%)
-1	TAG (0.40%)	CTA (0.53%)	CTA (0.37%)	TAG (0.48%)	TAG (0.55%)	TAG (0.39%)	TAG (0.48%)	TAG (0.67%)	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 (0.99%)	TTTC (1.12%)	AAAA (1.35%)	CAGC (0.97%)	CGGC (1.06%)	AAAA (1.10%)	ATCA (0.94%)	TGGC (0.93%)	GGCA (1.20%)
2	ATCA (0.89%)	TGCC (0.96%)	TTTT (1.22%)	ATCA (0.89%)	TGGC (1.04%)	CAAA (1.03%)	GGCA (0.87%)	CAGC (0.92%)	AAAA (1.09%)
3	GAAA (0.88%)	CAGC (0.90%)	GAAA (1.14%)	CGGC (0.87%)	CAGC (1.03%)	GAAA (0.97%)	GCCA (0.80%)	ATCA (0.85%)	TGAA (1.00%)
4	AAAA (0.85%)	TGGC (0.90%)	GGCA (0.94%)	CTGC (0.86%)	CTGC (0.89%)	TGAA (0.97%)	CGCA (0.79%)	TTCA (0.85%)	GAAA (0.97%)
5	TTCA (0.83%)	TTGC (0.89%)	GTTC (0.92%)	CCAG (0.82%)	TTGC (0.84%)	AGCA (0.94%)	CAGC (0.77%)	CGGC (0.83%)	GGAA (0.94%)
6	CAGC (0.82%)	TTCA (0.89%)	GCAA (0.92%)	TGGC (0.81%)	ATCA (0.83%)	ATCA (0.92%)	CGCC (0.76%)	CTGC (0.75%)	CGCC (0.90%)
7	TTCT (0.80%)	CTGC (0.87%)	TGCC (0.87%)	TTGC (0.76%)	CAAA (0.80%)	GGCA (0.92%)	AACA (0.75%)	CGCC (0.73%)	TTTT (0.89%)
8	TGCC (0.79%)	TTCC (0.83%)	TTTT (0.87%)	CAAA (0.74%)	TTCC (0.76%)	AGAA (0.90%)	CAAA (0.75%)	CAAA (0.73%)	TGCA (0.88%)
9	TGGC (0.79%)	AAAA (0.82%)	GGAA (0.85%)	AGCA (0.71%)	CGCC (0.76%)	TTTC (0.88%)	TTCA (0.74%)	GGCG (0.73%)	TTTC (0.88%)
10	TTGC (0.79%)	CGCC (0.82%)	CAAA (0.81%)	ATGC (0.71%)	CCAG (0.76%)	TAAA (0.86%)	TGAA (0.74%)	GCCG (0.72%)	CGCA (0.87%)
-10	TAGT (0.12%)	CCCT (0.14%)	TTAG (0.11%)	CGAG (0.12%)	CCTC (0.13%)	GTGT (0.11%)	GAGG (0.14%)	ACCT (0.15%)	GAGA (0.11%)
-9	GAGG (0.12%)	TCTA (0.13%)	ACTA (0.10%)	AGGG (0.12%)	ACCT (0.12%)	ACTA (0.11%)	CCCC (0.14%)	CCCC (0.15%)	CTAA (0.11%)
-8	TCTA (0.12%)	CTAT (0.12%)	CGAG (0.10%)	GGAC (0.11%)	CGAG (0.12%)	ACCT (0.10%)	GTGT (0.14%)	CTAT (0.15%)	CGGA (0.10%)
-7	GGAC (0.12%)	TAGT (0.12%)	TAGT (0.09%)	CTAA (0.10%)	GTGT (0.12%)	GGAC (0.10%)	CTAT (0.13%)	GAGA (0.14%)	CCCT (0.10%)
-6	CTAA (0.12%)	CGGA (0.11%)	GGAC (0.09%)	GAGG (0.10%)	CTAA (0.11%)	CTAT (0.09%)	TCTA (0.13%)	CTAA (0.13%)	CTAT (0.10%)
-5	TTAG (0.10%)	CTAA (0.10%)	TAGA (0.08%)	TAGA (0.10%)	TAGA (0.10%)	CGAG (0.09%)	CTAA (0.12%)	CCCT (0.11%)	GGGA (0.09%)
-4	TAGA (0.06%)	TAGG (0.08%)	TCTA (0.08%)	CCCT (0.10%)	CCCT (0.09%)	TAGG (0.07%)	TAGA (0.08%)	TAGG (0.11%)	TAGG (0.08%)
-3	CCTA (0.06%)	CCTA (0.06%)	TAGG (0.06%)	CCTA (0.07%)	TAGG (0.08%)	CCCT (0.06%)	CCTA (0.07%)	TAGA (0.10%)	TAGA (0.05%)
-2	TAGG (0.05%)	TAGA (0.06%)	CCTA (0.05%)	TAGG (0.06%)	CCTA (0.07%)	CCTA (0.06%)	TAGG (0.06%)	CCTA (0.09%)	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	CAGCA (0.34%)	CAGCA (0.38%)	GAAAA (0.42%)	CAGCA (0.40%)	CAGCA (0.41%)	CAGCA (0.51%)	CAGCA (0.37%)	CTGGC (0.38%)	CAGCA (0.45%)
2	CTGGC (0.33%)	CTGGC (0.37%)	CAGCA (0.41%)	CCAGC (0.33%)	CTGGC (0.38%)	CGGCA (0.37%)	CGCCA (0.34%)	CAGCA (0.31%)	CGGCA (0.42%)
3	TTATC (0.31%)	TTGCC (0.34%)	CAAAA (0.37%)	CATCA (0.31%)	GCGGC (0.35%)	GAAAA (0.35%)	CGGCA (0.34%)	CATCA (0.30%)	TGGCA (0.39%)
4	CGCCA (0.31%)	TTTGC (0.31%)	TGTTT (0.34%)	GCTGC (0.31%)	CCAGC (0.33%)	ATAAA (0.35%)	CATCA (0.29%)	GCGGC (0.30%)	GAAAA (0.37%)
5	CATCA (0.30%)	CGCCA (0.31%)	CGTTT (0.33%)	GCGGC (0.30%)	CATCA (0.32%)	CAGAA (0.33%)	CTGGC (0.29%)	CCAGC (0.30%)	GCAAA (0.30%)
6	TGGCG (0.28%)	CATCA (0.31%)	TGGCA (0.32%)	CGGCA (0.29%)	TCAGC (0.30%)	AAGAA (0.33%)	TGGCA (0.28%)	CGCCA (0.29%)	TTGCC (0.29%)
7	ATTTT (0.28%)	GCTGC (0.31%)	GCCAG (0.32%)	CTGGC (0.29%)	GCTGC (0.30%)	CATCA (0.33%)	GCGCA (0.27%)	TGGCG (0.29%)	GCGCA (0.29%)
8	CCAGC (0.27%)	TTTCA (0.31%)	CTGGC (0.31%)	TTATC (0.28%)	AATCA (0.30%)	AATCA (0.31%)	GCAAA (0.27%)	TTTTT (0.28%)	CGCCA (0.29%)
9	CAAAA (0.27%)	CCAGC (0.30%)	GCAAA (0.31%)	GCAGC (0.27%)	TTTTT (0.28%)	TTATC (0.31%)	GCCAG (0.27%)	GCCAG (0.28%)	ATTTT (0.29%)
10	TTTTT (0.27%)	ATTTT (0.30%)	TTGCC (0.31%)	AATCA (0.26%)	ATAAA (0.28%)	GCAAA (0.30%)	GATCA (0.26%)	GCAGC (0.26%)	CAAAA (0.29%)
-10	GGACC (0.01%)	TAGGA (0.01%)	CTTAG (0.01%)	ACCTA (0.01%)	CCCTA (0.01%)	CCCTA (0.01%)	CCCTA (0.01%)	TCCTA (0.01%)	TAGGA (0.01%)
-9	CCCTA (0.01%)	CCCTA (0.01%)	CCCTA (0.01%)	CCCTA (0.01%)	CCCCC (0.01%)	ACCTA (0.01%)	TAGGA (0.01%)	TAGGA (0.01%)	CCCTA (0.01%)
-8	CTAGC (0.00%)	GCTAG (0.00%)	GCTAG (0.00%)	CTAGC (0.01%)	CTAGC (0.01%)	CTAGC (0.01%)	GCTAG (0.01%)	GCTAG (0.01%)	GCTAG (0.01%)
-7	GCTAG (0.00%)	CTAGC (0.00%)	ACTAG (0.00%)	GCTAG (0.01%)	GCTAG (0.01%)	GCTAG (0.01%)	CTAGT (0.00%)	CTAGC (0.01%)	CTAGC (0.00%)
-6	ACTAG (0.00%)	ACTAG (0.00%)	CTAGC (0.00%)	CTAGT (0.01%)	CTAGT (0.00%)	CTAGT (0.00%)	CTAGC (0.00%)	ACTAG (0.01%)	CTAGT (0.00%)
-5	CTAGT (0.00%)	CTAGT (0.00%)	CTAGT (0.00%)	CTAGA (0.00%)	ACTAG (0.00%)	CTAGA (0.00%)	CCTAG (0.00%)	CTAGT (0.00%)	ACTAG (0.00%)
-4	CCTAG (0.00%)	CCTAG (0.00%)	CTAGG (0.00%)	ACTAG (0.00%)	CTAGA (0.00%)	ACTAG (0.00%)	ACTAG (0.00%)	CTAGA (0.00%)	CTAGG (0.00%)
-3	CTAGG (0.00%)	TCTAG (0.00%)	TCTAG (0.00%)	CCTAG (0.00%)	CTAGG (0.00%)	CTAGG (0.00%)	CTAGA (0.00%)	TCTAG (0.00%)	CCTAG (0.00%)
-2	CTAGA (0.00%)	CTAGG (0.00%)	CTAGA (0.00%)	TCTAG (0.00%)	CCTAG (0.00%)	TCTAG (0.00%)	TCTAG (0.00%)	CTAGG (0.00%)	TCTAG (0.00%)
-1	TCTAG (0.00%)	CTAGA (0.00%)	CCTAG (0.00%)	CTAGG (0.00%)	TCTAG (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%