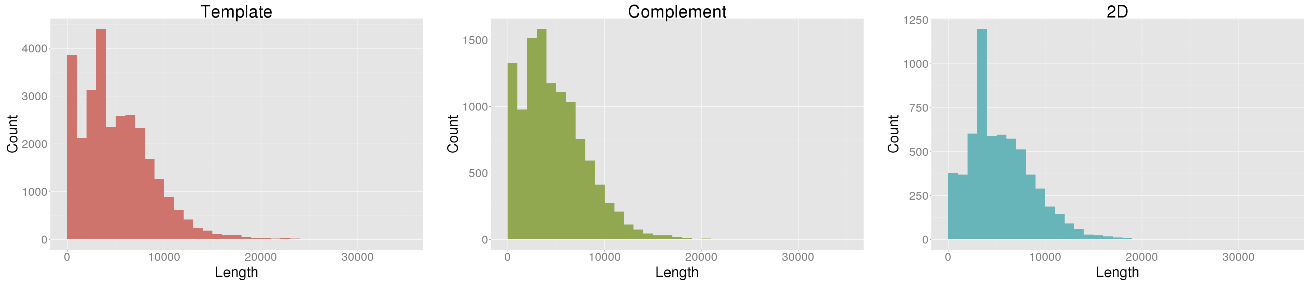
NanoOK report for WTCHG_MARC_Ph1.1

Pass and fail counts

Type	Pass	Fail
Template	0	29318
Complement	0	11331
2D	0	6069

Read lengths

Type	NumReads	TotalBases	Mean	Longest	Shortest	N50	N50Count	N90	N90Count
Template	29318	157955395	5387.66	424544	5	7531	6945	3206	19196
Complement	11331	55665412	4912.67	168511	7	6753	2846	2948	7625
2D	6069	33250166	5478.69	44820	93	7119	1687	3320	4396



Template alignments

Number of reads	29318	
Number of reads with alignments	15019	(51.23%)
Number of reads without alignments	14299	(48.77%)

ID	Size	Number of Reads	% of Reads	Mean read length	Aligned bases	Mean coverage	Longest Perf Kmer
Control sequence	3560	2954	10.08	3048.62	8374533	2352.40	66
Escherichia coli	4641652	12065	41.15	7107.65	72358845	15.59	72

Complement alignments

Number of reads	11331	
Number of reads with alignments	5522	(48.73%)
Number of reads without alignments	5809	(51.27%)

ID	Size	Number of Reads	% of Reads	Mean read length	Aligned bases	Mean coverage	Longest Perf Kmer
Control sequence	3560	1014	8.95	2710.08	2233105	627.28	44
Escherichia coli	4641652	4508	39.78	6425.07	23556520	5.08	70

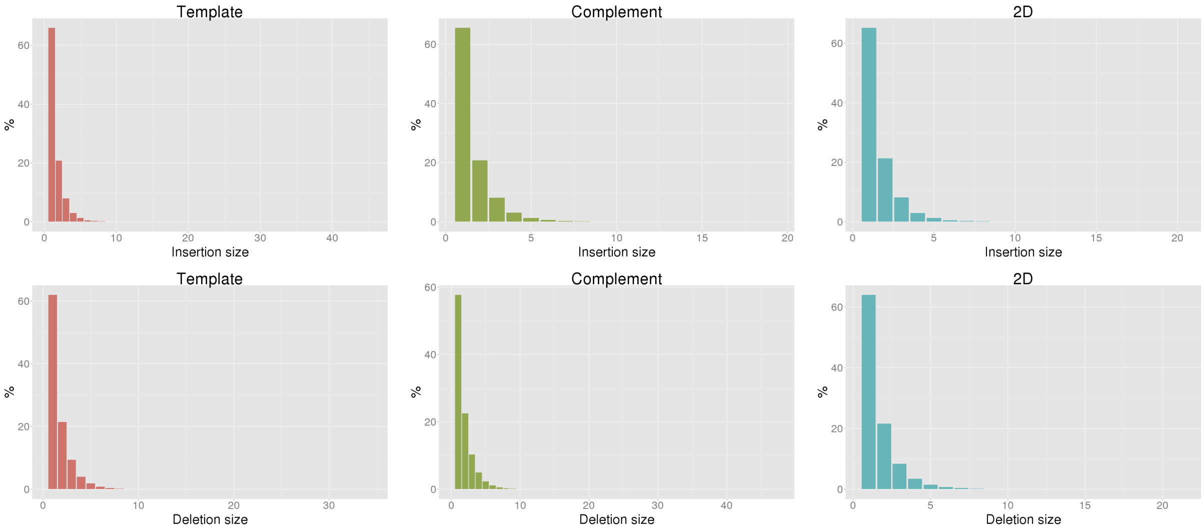
2D alignments

Number of reads	6069	
Number of reads with alignments	4662	(76.82%)
Number of reads without alignments	1407	(23.18%)

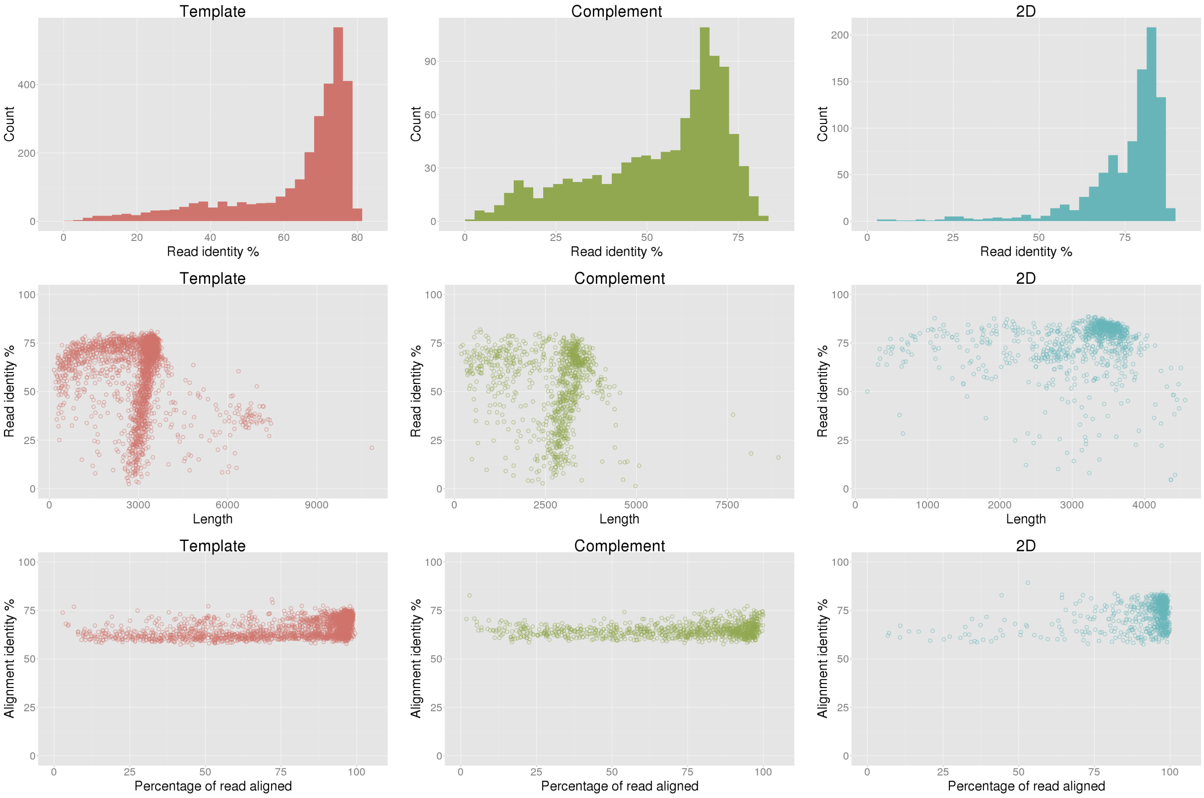
ID	Size	Number of Reads	% of Reads	Mean read length	Aligned bases	Mean coverage	Longest Perf Kmer
Control sequence	3560	942	15.52	3127.56	2961860	831.98	156
Escherichia coli	4641652	3720	61.30	6532.49	23823441	5.13	189

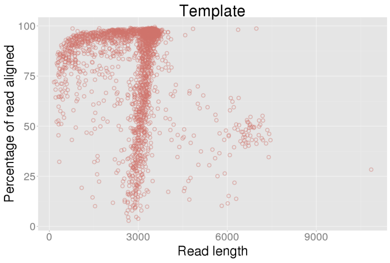
Control sequence error analysis

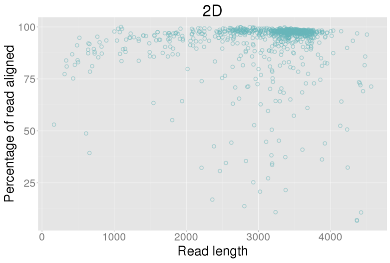
	Template	Complement	2D
Overall base identity (excluding indels)	62.72%	52.38%	75.13%
Aligned base identity (excluding indels)	80.13%	78.75%	86.13%
Identical bases per 100 aligned bases (including indels)	67.44%	64.45%	74.73%
Inserted bases per 100 aligned bases (including indels)	5.07%	5.23%	5.58%
Deleted bases per 100 aligned bases (including indels)	10.76%	12.93%	7.65%
Substitutions per 100 aligned bases (including indels)	16.72%	17.39%	12.04%
Mean insertion size	1.58	1.59	1.58
Mean deletion size	1.68	1.81	1.62



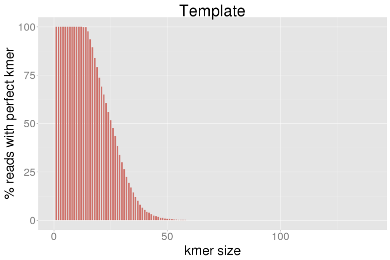
Control sequence read identity

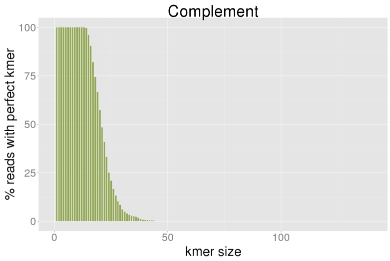


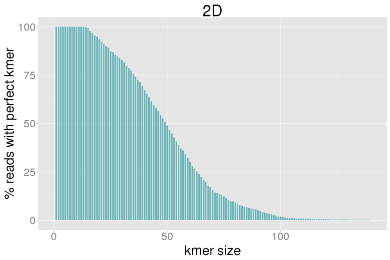


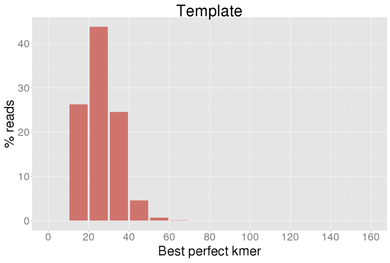


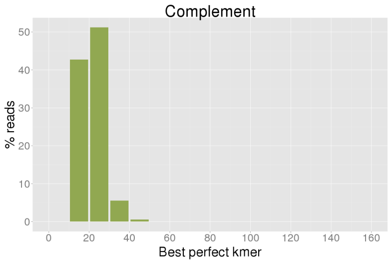
Control sequence perfect kmers

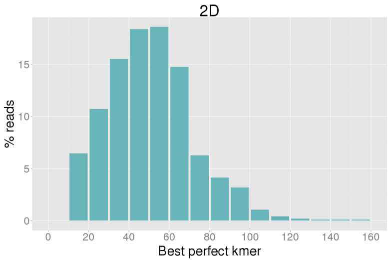


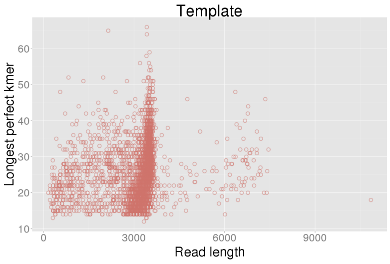


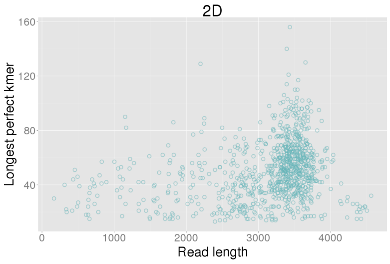




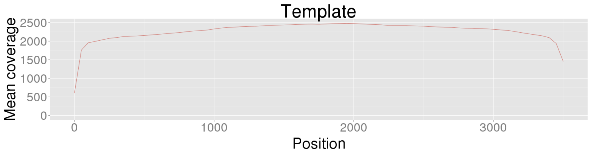


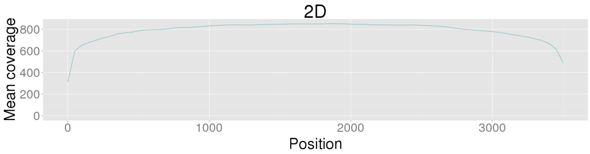


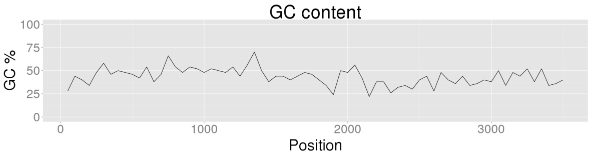




Control sequence coverage







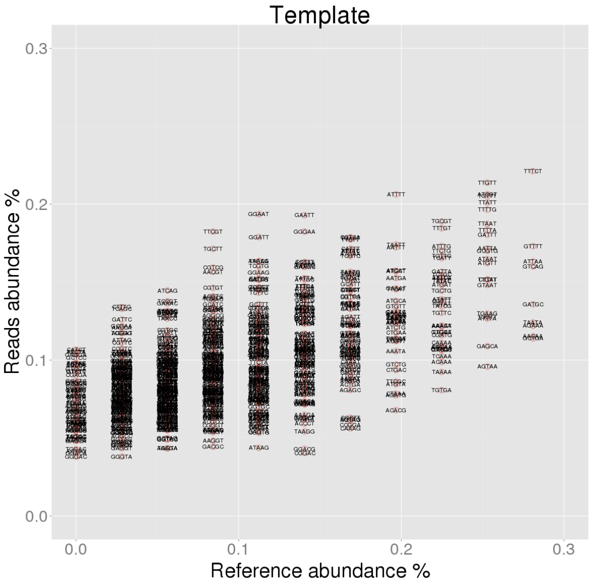
Control sequence 5-mer analysis

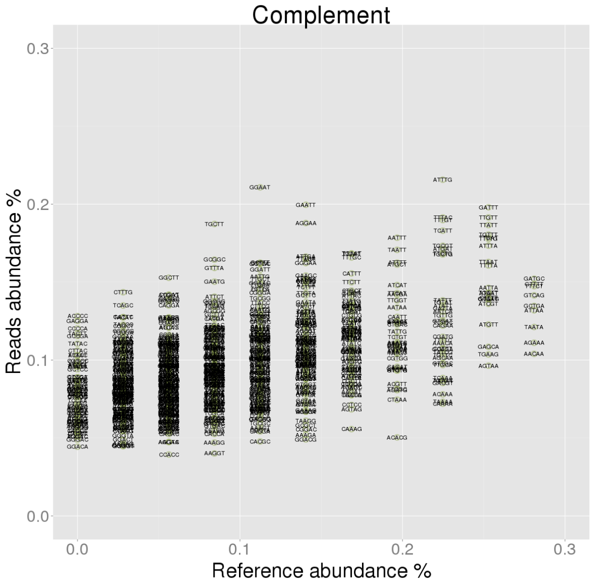
Under-represented 5-mers

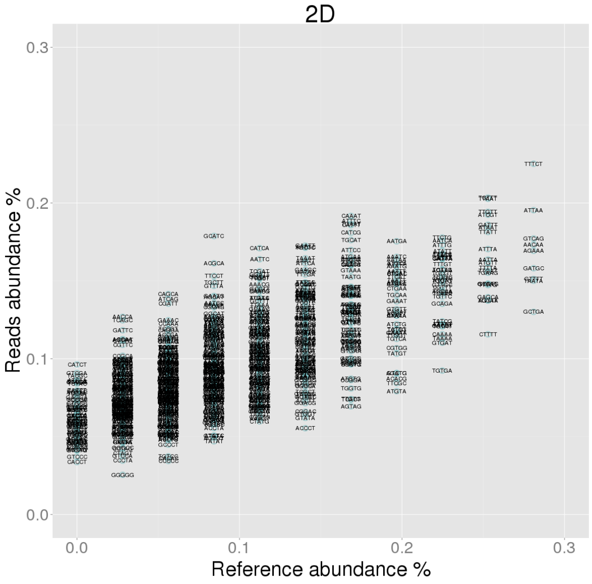
	Template				Complement				2D			
Rank	kmer	Ref %	Read %	Diff %	kmer	Ref %	Read %	Diff %	kmer	Ref %	Read %	Diff %
1	TTTTT	0.759	0.149	-0.610	TTTTT	0.759	0.094	-0.664	TTTTT	0.759	0.050	-0.709
2	AAAAA	0.478	0.103	-0.375	AAAAA	0.478	0.052	-0.426	AAAAA	0.478	0.050	-0.428
3	TGATG	0.393	0.137	-0.256	AAAAC	0.337	0.099	-0.238	TGATG	0.393	0.146	-0.248
4	AAAAC	0.337	0.121	-0.216	TGATG	0.393	0.172	-0.221	AAAAC	0.337	0.142	-0.195
5	GATGT	0.309	0.096	-0.213	GATGT	0.309	0.101	-0.208	GATGT	0.309	0.120	-0.189
6	CTGAT	0.309	0.117	-0.192	GCAAT	0.309	0.119	-0.190	CTGAT	0.309	0.134	-0.175
7	GCAAT	0.309	0.136	-0.173	AACAA	0.281	0.104	-0.177	GCTGA	0.281	0.130	-0.151
8	GCTGA	0.281	0.114	-0.167	TTATC	0.309	0.135	-0.174	TTATC	0.309	0.160	-0.149
9	AACAA	0.281	0.115	-0.166	AGAAA	0.281	0.111	-0.170	AATAT	0.309	0.165	-0.144
10	AATAT	0.309	0.148	-0.161	AATAT	0.309	0.142	-0.167	GCAAT	0.309	0.165	-0.144

Over-represented 5-mers

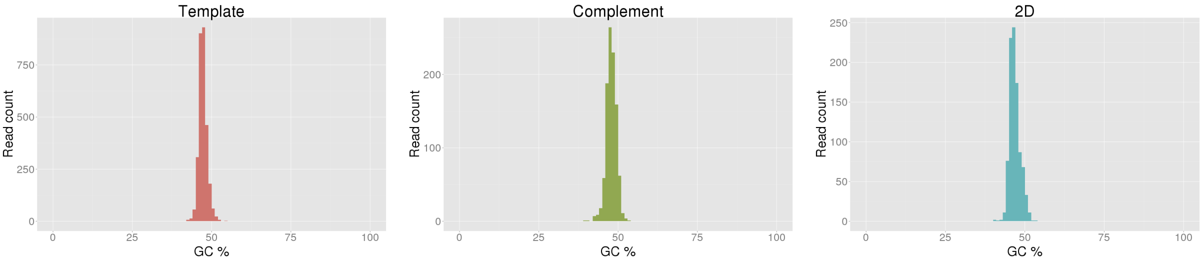
	Template				Complement				2D			
Rank	kmer	Ref %	Read %	Diff %	kmer	Ref %	Read %	Diff %	kmer	Ref %	Read %	Diff %
1	CATCT	0.000	0.107	0.107	ACCCC	0.000	0.128	0.128	AACCA	0.028	0.127	0.099
2	CTTTG	0.028	0.134	0.106	GAGGA	0.000	0.125	0.125	TCAGC	0.028	0.125	0.097
3	ATCTA	0.000	0.105	0.105	CCCCA	0.000	0.120	0.120	CATCT	0.000	0.096	0.096
4	TACTT	0.000	0.105	0.105	TACTT	0.000	0.117	0.117	GCATC	0.084	0.179	0.094
5	TCAGC	0.028	0.133	0.105	GCCGA	0.000	0.115	0.115	GTCGA	0.000	0.091	0.091
6	GAGGA	0.000	0.103	0.103	CTTTG	0.028	0.143	0.115	GATTC	0.028	0.118	0.090
7	GCTCC	0.000	0.101	0.101	TATAC	0.000	0.110	0.110	TACGC	0.000	0.089	0.089
8	TTCGT	0.084	0.182	0.098	TCAGC	0.028	0.135	0.107	ATCTA	0.000	0.086	0.086
9	GATTC	0.028	0.126	0.098	CTTAC	0.000	0.106	0.106	CCCGC	0.000	0.085	0.085
10	TCTAC	0.000	0.098	0.098	TCTAC	0.000	0.103	0.103	TTAGA	0.000	0.085	0.085





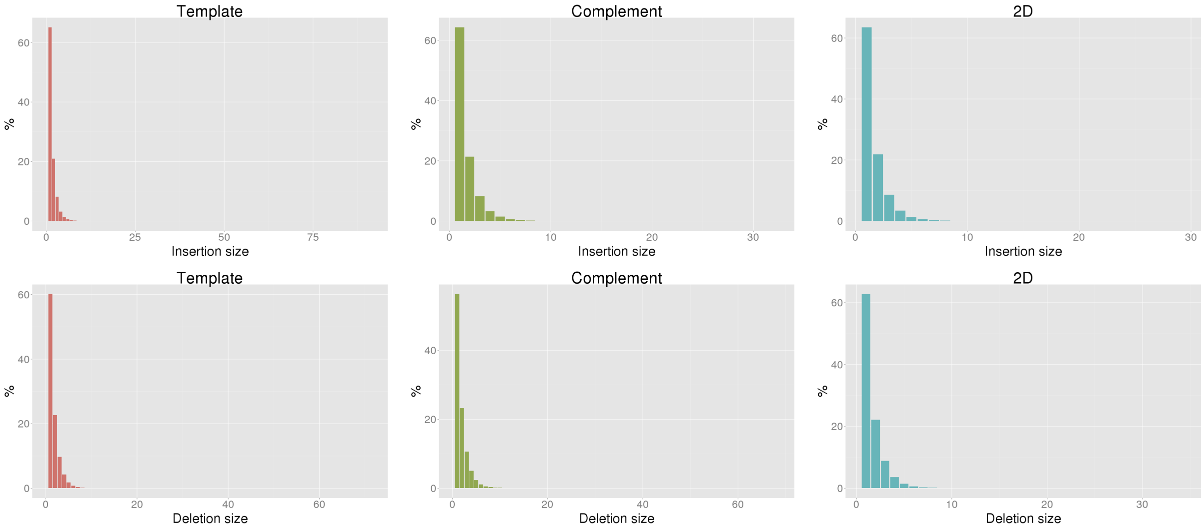


Control sequence GC content

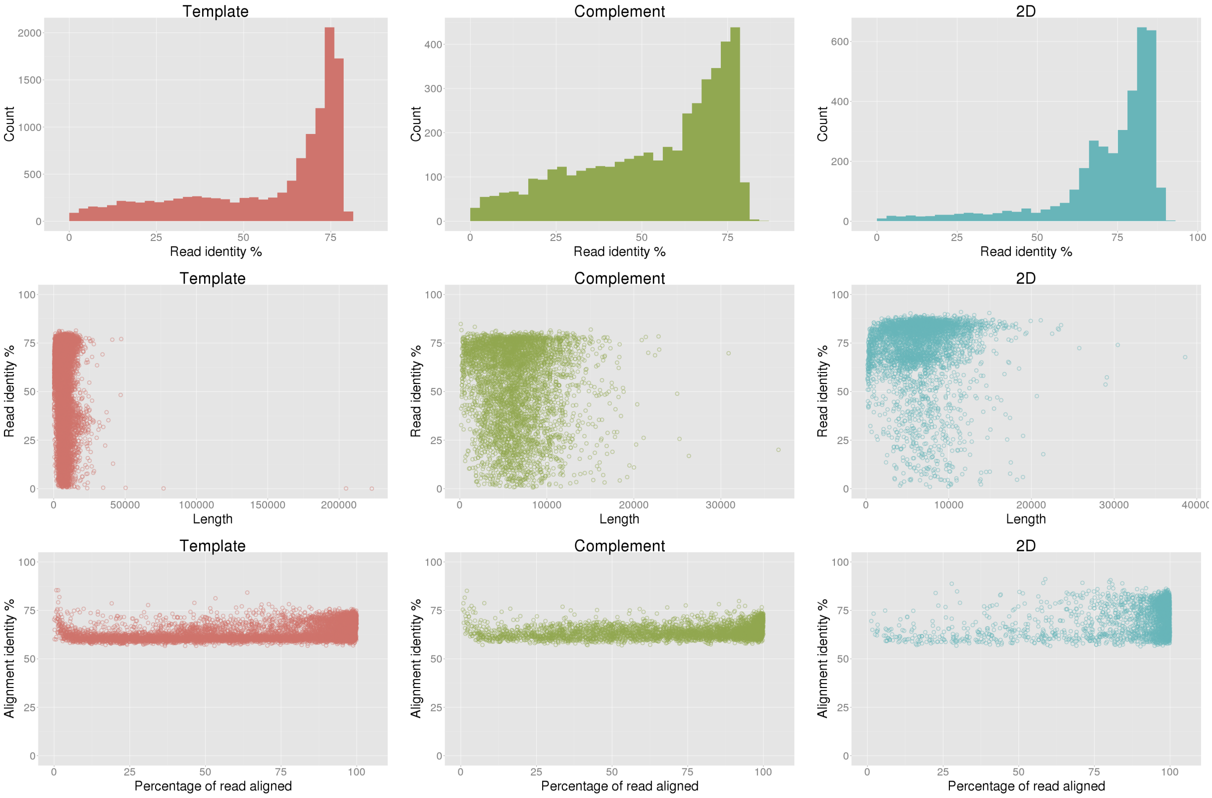


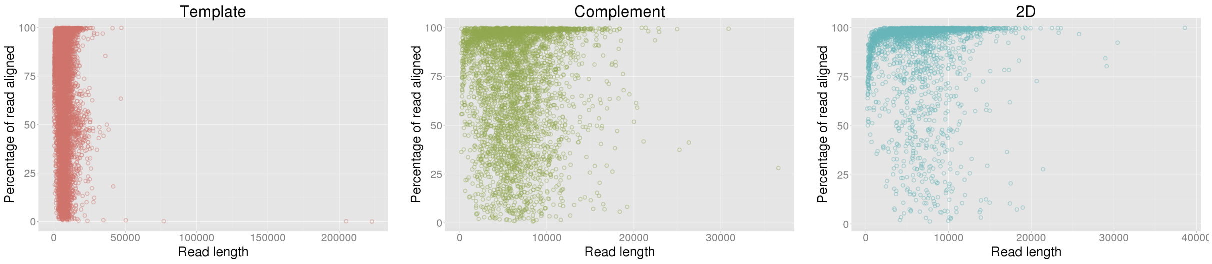
Escherichia coli error analysis

	Template	Complement	2D
Overall base identity (excluding indels)	55.43%	52.30%	71.74%
Aligned base identity (excluding indels)	78.86%	79.14%	84.94%
Identical bases per 100 aligned bases (including indels)	65.69%	64.31%	73.18%
Inserted bases per 100 aligned bases (including indels)	5.44%	5.38%	6.00%
Deleted bases per 100 aligned bases (including indels)	11.25%	13.36%	7.84%
Substitutions per 100 aligned bases (including indels)	17.61%	16.95%	12.98%
Mean insertion size	1.60	1.62	1.62
Mean deletion size	1.71	1.85	1.64

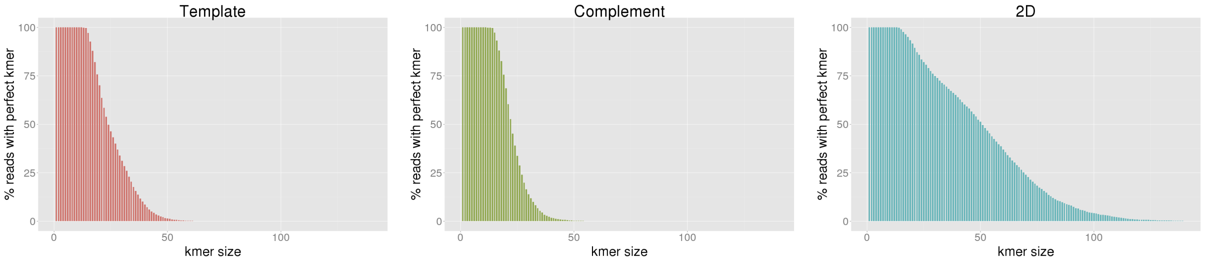


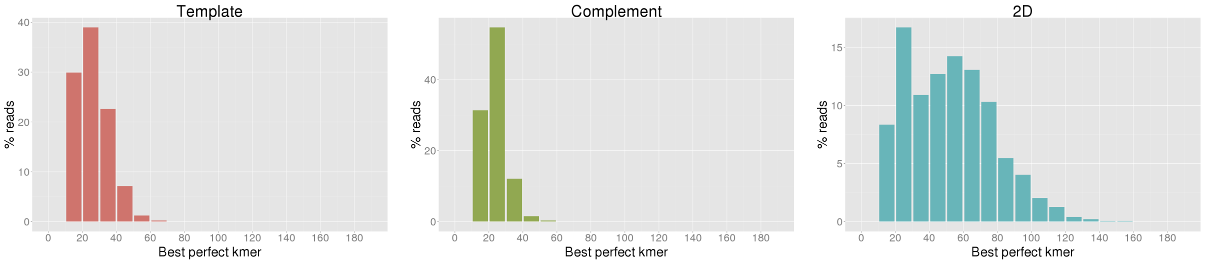
Escherichia coli read identity

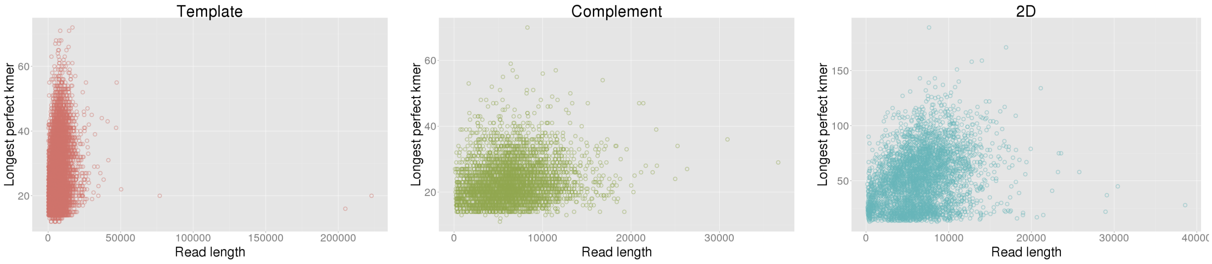




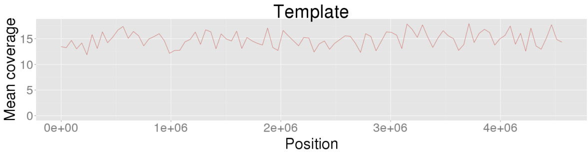
Escherichia coli perfect kmers

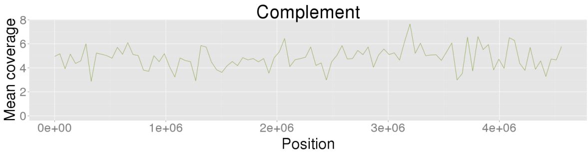


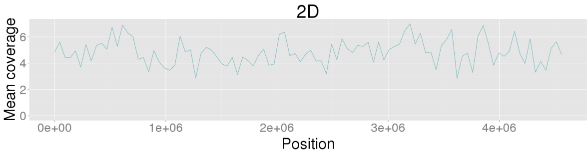


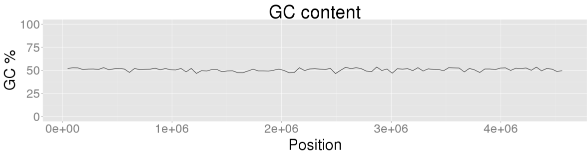


Escherichia coli coverage









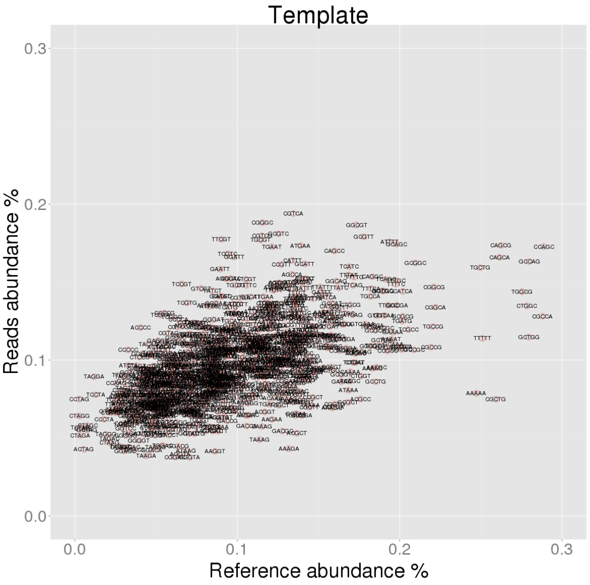
Escherichia coli 5-mer analysis

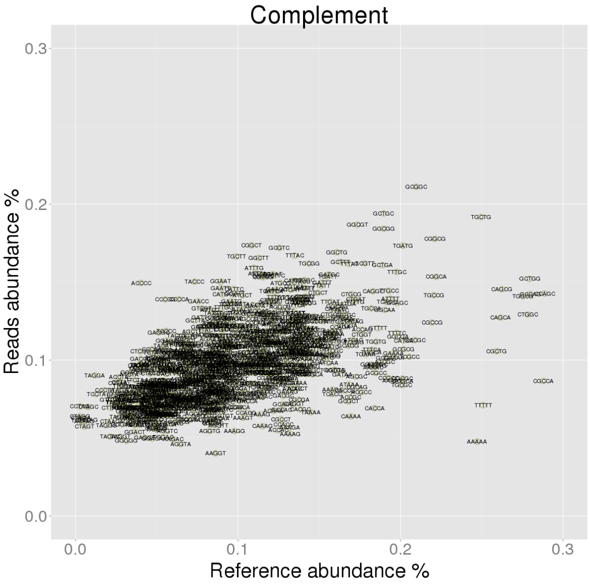
Under-represented 5-mers

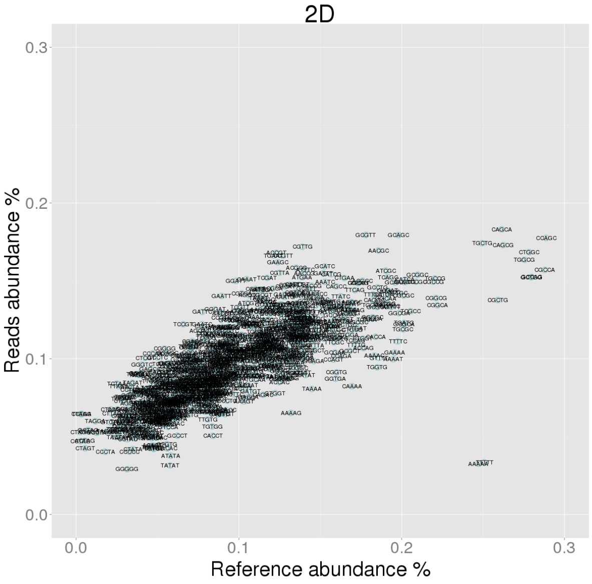
	Template				Complement				2D			
Rank	kmer	Ref %	Read %	Diff %	kmer	Ref %	Read %	Diff %	kmer	Ref %	Read %	Diff %
1	CGCTG	0.259	0.075	-0.184	CGCCA	0.288	0.087	-0.201	TTTTT	0.251	0.034	-0.217
2	AAAAA	0.247	0.079	-0.168	AAAAA	0.247	0.048	-0.199	AAAAA	0.247	0.033	-0.215
3	GCTGG	0.279	0.115	-0.165	TTTTT	0.251	0.071	-0.180	CGCCA	0.288	0.157	-0.131
4	CGCCA	0.288	0.128	-0.160	CGCTG	0.259	0.106	-0.153	GCCAG	0.280	0.152	-0.127
5	CTGGC	0.278	0.135	-0.144	CTGGC	0.278	0.129	-0.149	GCTGG	0.279	0.152	-0.127
6	TTTTT	0.251	0.114	-0.137	CCAGC	0.289	0.143	-0.146	CGCTG	0.259	0.138	-0.121
7	TGGCG	0.275	0.144	-0.131	GCCAG	0.280	0.142	-0.138	TGGCG	0.275	0.164	-0.112
8	GCCAG	0.280	0.163	-0.117	TGGCG	0.275	0.141	-0.134	CCAGC	0.289	0.178	-0.111
9	CCAGC	0.289	0.173	-0.116	CAGCA	0.261	0.127	-0.134	CTGGC	0.278	0.168	-0.110
10	CGCCG	0.219	0.108	-0.111	GCTGG	0.279	0.152	-0.127	AAAAT	0.195	0.100	-0.095

Over-represented 5-mers

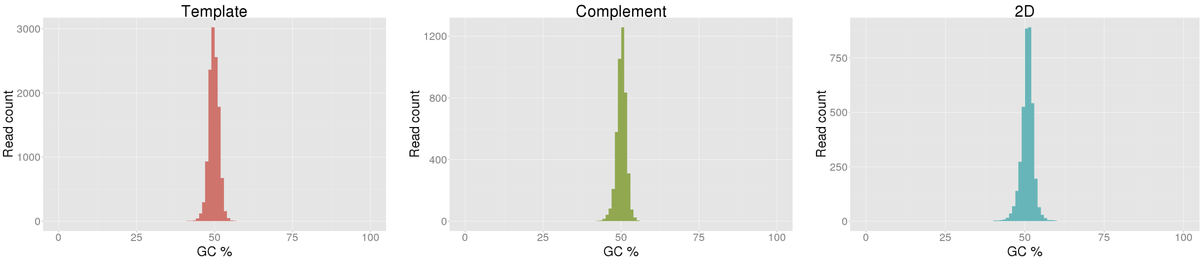
	Template				Complement				2D			
Rank	kmer	Ref %	Read %	Diff %	kmer	Ref %	Read %	Diff %	kmer	Ref %	Read %	Diff %
1	TTCGT	0.090	0.178	0.087	ACCCC	0.040	0.149	0.109	CTAGA	0.003	0.065	0.061
2	TCCGT	0.066	0.149	0.083	CCCCG	0.055	0.139	0.084	TCTAG	0.003	0.065	0.061
3	ACCCC	0.040	0.121	0.080	TAGGA	0.012	0.090	0.078	TCTAA	0.025	0.084	0.059
4	TAGGA	0.012	0.089	0.077	TACCC	0.073	0.150	0.077	CTCGT	0.042	0.101	0.058
5	TCGTA	0.053	0.129	0.076	CCCCA	0.064	0.139	0.075	CCCAA	0.047	0.103	0.056
6	CCCCG	0.055	0.130	0.075	CCTAG	0.003	0.070	0.068	TCCGT	0.066	0.122	0.056
7	TCGTC	0.094	0.168	0.074	TGCTT	0.099	0.166	0.067	TTAGA	0.026	0.082	0.056
8	CCCCC	0.033	0.107	0.074	GAGGC	0.051	0.118	0.067	GGGTC	0.040	0.096	0.056
9	CGGGC	0.116	0.188	0.073	CTCCC	0.040	0.106	0.066	TTCTA	0.036	0.090	0.054
10	CCTAG	0.003	0.075	0.072	TCCTA	0.013	0.078	0.065	GATTC	0.078	0.130	0.053



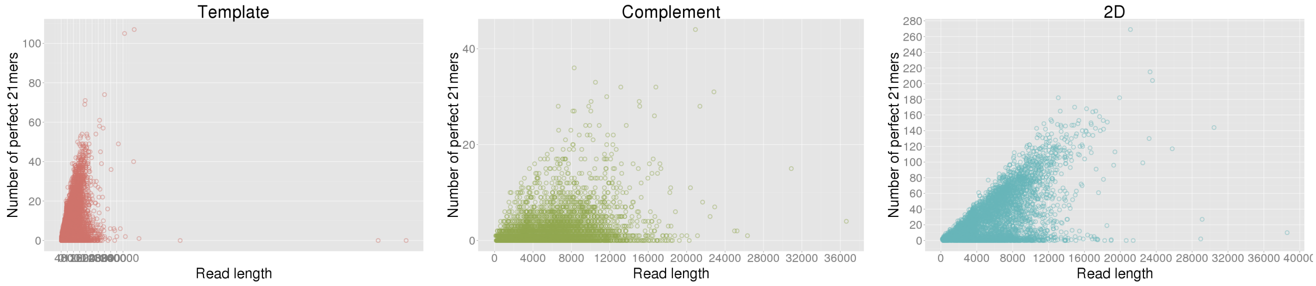




Escherichia coli GC content



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	8.71	9.08	5.15	0.00	8.83	8.90	5.30	0.00	8.70	9.08	4.84
	C	8.75	0.00	8.91	9.66	9.19	0.00	8.65	9.25	8.96	0.00	9.89	8.74
	G	9.28	9.00	0.00	8.45	8.69	8.78	0.00	8.95	8.75	9.95	0.00	8.54
	T	5.39	9.14	8.48	0.00	5.54	9.09	8.83	0.00	4.89	9.09	8.57	0.00

Kmer motifs before errors

3-mer error motif analysis

	Template			Complement			2D			
Rank	Insertion	Deletion	Substitution	Insertion	Deletion	Substitution	Insertion	Deletion	Substitution	
1	TTC (3.35%)	TTC (3.50%)	AAA (4.30%)	AAA (2.94%)	AAA (2.87%)	AAA (4.24%)	AAA (3.07%)	AAA (2.74%)	AAA (4.02%)	Most common
2	AAA (2.89%)	TGC (2.95%)	TTC (3.69%)	TTC (2.92%)	TGC (2.85%)	GCA (3.39%)	TTC (3.06%)	TTC (2.71%)	GCA (3.39%)	
3	TGC (2.78%)	AAA (2.93%)	GCA (3.20%)	TGC (2.81%)	TTC (2.73%)	GAA (3.26%)	GCA (2.91%)	TGC (2.63%)	TTC (3.15%)	
4	GCA (2.69%)	GCA (2.75%)	GAA (3.07%)	GCA (2.64%)	GCA (2.66%)	TTC (3.17%)	TGC (2.67%)	GCA (2.61%)	GAA (3.12%)	
5	ATC (2.48%)	TCA (2.49%)	TTT (2.67%)	GAA (2.45%)	GGC (2.66%)	TGC (2.54%)	GAA (2.56%)	TCA (2.50%)	TTT (2.75%)	
6	TCA (2.46%)	AAT (2.36%)	AAT (2.63%)	CAG (2.30%)	GAA (2.46%)	TTT (2.48%)	AAT (2.44%)	GCG (2.45%)	AAT (2.75%)	
7	TTT (2.32%)	GAA (2.34%)	TGC (2.59%)	TCA (2.30%)	TCA (2.33%)	AAT (2.41%)	TCA (2.44%)	GAA (2.35%)	TGC (2.34%)	
8	GAA (2.31%)	ATC (2.32%)	TCA (2.31%)	TTT (2.29%)	AAT (2.31%)	TCA (2.34%)	ATC (2.35%)	GGC (2.35%)	GTT (2.33%)	
9	GCC (2.24%)	GCC (2.28%)	ATC (2.25%)	ATC (2.26%)	GCC (2.26%)	ATC (2.22%)	CGC (2.31%)	ATC (2.18%)	GCC (2.26%)	
10	AAT (2.20%)	GGC (2.21%)	CAA (2.19%)	AAT (2.23%)	CAG (2.18%)	CAA (2.18%)	TTT (2.24%)	CAG (2.16%)	TCA (2.24%)	
										
-10	CGA (1.01%)	AGT (0.93%)	GGT (0.89%)	AGA (0.98%)	AGT (0.94%)	CTC (0.91%)	TGT (1.05%)	AGT (0.99%)	GGG (0.90%)	Least common
-9	CTC (0.99%)	AGG (0.91%)	TGT (0.87%)	GTG (0.98%)	CGA (0.94%)	CTT (0.89%)	CTC (1.00%)	CCC (0.97%)	CCC (0.88%)	
-8	CCC (0.87%)	GGG (0.89%)	AGA (0.87%)	CTC (0.90%)	CTC (0.91%)	AGT (0.88%)	CCC (0.83%)	ACT (0.95%)	AGG (0.86%)	
-7	AGA (0.84%)	CTT (0.88%)	AGT (0.86%)	CCC (0.88%)	CCT (0.91%)	CCT (0.87%)	GGA (0.80%)	CGA (0.91%)	CGA (0.85%)	
-6	GGA (0.79%)	GAG (0.83%)	AGG (0.82%)	GGA (0.84%)	GGA (0.90%)	ACT (0.80%)	GAG (0.80%)	CCT (0.91%)	CTT (0.81%)	
-5	GAG (0.78%)	CGA (0.79%)	GGG (0.82%)	GAG (0.76%)	AGG (0.90%)	GGG (0.78%)	AGA (0.80%)	CTT (0.89%)	GAG (0.76%)	
-4	AGG (0.68%)	AGA (0.72%)	CTT (0.81%)	AGG (0.70%)	GAG (0.87%)	AGG (0.76%)	AGG (0.73%)	AGA (0.78%)	GGA (0.75%)	
-3	GGG (0.67%)	GGA (0.68%)	GAG (0.66%)	GGG (0.58%)	GGG (0.80%)	GAG (0.64%)	GGG (0.64%)	GGA (0.70%)	AGA (0.66%)	
-2	CTA (0.51%)	TAG (0.52%)	TAG (0.40%)	CTA (0.55%)	TAG (0.54%)	CTA (0.42%)	CTA (0.56%)	TAG (0.61%)	TAG (0.46%)	
-1	TAG (0.44%)	CTA (0.49%)	CTA (0.36%)	TAG (0.48%)	CTA (0.52%)	TAG (0.37%)	TAG (0.47%)	CTA (0.60%)	CTA (0.38%)	
										

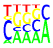
Kmer space for 3-mers: 64 Random chance for any given 3-mer: 1.56%

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 (1.51%)	TTGC (0.89%)	CGGC (0.96%)	AAAA (1.22%)	GAAA (0.94%)	TTCA (0.88%)	AAAA (1.20%)	Most common
2	AAAA (0.94%)	TTCA (0.95%)	TTTC (1.23%)	AAAA (0.86%)	TGGC (0.93%)	CAAA (1.19%)	CAAA (0.87%)	TGGC (0.83%)	GAAA (1.13%)	
3	GAAA (0.93%)	AAAA (0.93%)	GAAA (1.20%)	CAAA (0.85%)	TTGC (0.92%)	GAAA (1.02%)	TTTC (0.83%)	ATCA (0.79%)	GGCA (0.97%)	
4	TTCA (0.87%)	TTGC (0.90%)	TTTT (0.97%)	CAGC (0.85%)	CAGC (0.92%)	TGAA (0.97%)	TTGC (0.81%)	TTTC (0.78%)	TTTC (0.92%)	
5	TTGC (0.84%)	TTCC (0.89%)	CAAA (0.90%)	ATCA (0.85%)	CAAA (0.87%)	TTTC (0.91%)	TTCA (0.81%)	CAGC (0.77%)	CAAA (0.88%)	
6	ATCA (0.83%)	TGCC (0.88%)	TGAA (0.90%)	CTGC (0.80%)	CTGC (0.84%)	AGCA (0.86%)	AACA (0.81%)	CAAA (0.77%)	GGAA (0.87%)	
7	TTTT (0.82%)	GAAA (0.86%)	GTTC (0.90%)	GAAA (0.80%)	TTCC (0.83%)	ATCA (0.85%)	AAAA (0.80%)	TTGC (0.76%)	TGCA (0.86%)	
8	TGCC (0.82%)	GTTC (0.84%)	GCAA (0.89%)	TGGC (0.78%)	TTCA (0.80%)	GGCA (0.84%)	GTTC (0.77%)	GAAA (0.75%)	AAAT (0.85%)	
9	GTTC (0.82%)	AACG (0.83%)	AAAT (0.87%)	TTTC (0.76%)	ATCA (0.79%)	TAAA (0.83%)	TGAA (0.77%)	CTGC (0.72%)	TGAA (0.85%)	
10	AACG (0.81%)	ATCA (0.81%)	AACG (0.87%)	CGGC (0.76%)	TTTC (0.77%)	AGAA (0.83%)	ATCA (0.76%)	TGCC (0.71%)	CGCC (0.84%)	
										
-10	TAGT (0.13%)	TAGT (0.12%)	CTAT (0.11%)	CTCG (0.13%)	CTAT (0.13%)	TTAG (0.11%)	CTAT (0.13%)	ACTT (0.15%)	CTAA (0.12%)	Least common
-9	AGGG (0.12%)	TCTA (0.12%)	TAGT (0.10%)	GAGG (0.11%)	CCCC (0.13%)	ACTA (0.11%)	GGGG (0.13%)	ACCT (0.14%)	CTTG (0.11%)	
-8	GAGG (0.12%)	GGAC (0.12%)	CGAG (0.10%)	AGGG (0.11%)	GGAC (0.12%)	CTAT (0.11%)	GAGG (0.13%)	TAGT (0.14%)	TATA (0.11%)	
-7	TCTA (0.12%)	CGGA (0.12%)	ACTA (0.10%)	CGAG (0.11%)	ACCT (0.11%)	TCTA (0.10%)	CTAA (0.13%)	CCCT (0.13%)	CTAT (0.11%)	
-6	TTAG (0.11%)	CTAT (0.11%)	TCTA (0.08%)	CCCT (0.10%)	CTAA (0.11%)	CGAG (0.10%)	AGGG (0.12%)	CTAT (0.13%)	ACTA (0.09%)	
-5	GGAC (0.10%)	CTAA (0.10%)	TAGA (0.08%)	GGAC (0.10%)	CCCT (0.10%)	GGAC (0.09%)	TCTA (0.12%)	CTAA (0.12%)	TCTA (0.09%)	
-4	CCTA (0.06%)	TAGG (0.08%)	GGAC (0.08%)	TAGA (0.09%)	TAGA (0.10%)	CCCT (0.08%)	CCTA (0.07%)	TAGG (0.09%)	TAGG (0.06%)	
-3	TAGA (0.06%)	CCTA (0.06%)	TAGG (0.06%)	CCTA (0.09%)	TAGG (0.07%)	TAGG (0.06%)	TAGA (0.07%)	CCTA (0.08%)	TAGA (0.05%)	
-2	TAGG (0.05%)	TAGA (0.06%)	CCTA (0.05%)	TAGG (0.06%)	CCTA (0.06%)	CCTA (0.05%)	TAGG (0.05%)	TAGA (0.07%)	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 (0.02%)	
										

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 (0.32%)	CAGCA (0.35%)	GAAAA (0.44%)	CAGCA (0.38%)	CAGCA (0.39%)	CAGCA (0.49%)	CAGCA (0.34%)	CTGGC (0.33%)	CAGCA (0.41%)	Most common
2	CAAAA (0.31%)	CTGGC (0.33%)	CAAAA (0.43%)	CATCA (0.32%)	CTGGC (0.36%)	ACAAA (0.38%)	GCAAA (0.31%)	CAGCA (0.31%)	GAAAA (0.40%)	
3	TTATC (0.31%)	TTTGC (0.31%)	CAGCA (0.39%)	GCGGC (0.30%)	GCGGC (0.35%)	GCAAA (0.37%)	CAAAA (0.30%)	CATCA (0.30%)	CAAAA (0.39%)	
4	CTGGC (0.30%)	TGTTC (0.31%)	AGAAA (0.36%)	TTATC (0.29%)	CATCA (0.32%)	CAAAA (0.36%)	CGCCA (0.29%)	GATGC (0.30%)	TGGCA (0.35%)	
5	TGTTC (0.29%)	TTTCA (0.31%)	GCAAA (0.33%)	TTTGC (0.29%)	TTTGC (0.31%)	GAAAA (0.36%)	TTTGC (0.29%)	CGCCA (0.29%)	AGAAA (0.34%)	
6	TTTGC (0.29%)	ATTTC (0.31%)	TGTTC (0.33%)	GCAAA (0.29%)	GCTGC (0.30%)	ATAAA (0.35%)	TGTTC (0.28%)	GCCAG (0.28%)	CGGCA (0.33%)	
7	TTGCC (0.28%)	TTGCC (0.31%)	TAAAA (0.33%)	CTGGC (0.28%)	ACAAA (0.29%)	AAGAA (0.34%)	AACGC (0.28%)	TTTCA (0.28%)	TGAAA (0.31%)	
8	GAAAA (0.28%)	TTATC (0.30%)	TGAAA (0.32%)	GCTGC (0.28%)	CCAGC (0.28%)	CGGCA (0.33%)	CGGCA (0.27%)	GCGGC (0.28%)	GCAAA (0.31%)	
9	CGTTT (0.28%)	CATCA (0.29%)	TTTTC (0.31%)	TTGCC (0.27%)	GCAAA (0.28%)	TCTTC (0.32%)	CTGGC (0.27%)	ACAAA (0.27%)	TAAAA (0.30%)	
10	ATTTC (0.27%)	GAAAA (0.29%)	ATTTC (0.31%)	TCTTC (0.27%)	AATCA (0.28%)	CAGAA (0.31%)	TGAAA (0.26%)	TGGCG (0.27%)	TTGCC (0.29%)	
										
-10	CCCTA (0.01%)	ACCTA (0.01%)	CTTAG (0.01%)	GGACC (0.01%)	CCCCT (0.01%)	CTTAG (0.01%)	GGACC (0.01%)	TAGGG (0.01%)	TTAGA (0.01%)	Least common
-9	GGACC (0.01%)	CCCTA (0.01%)	CCCTA (0.01%)	ACCTA (0.01%)	CCCTA (0.01%)	CCCTA (0.01%)	CCCTA (0.01%)	GCTAG (0.01%)	TCCTA (0.01%)	
-8	GCTAG (0.00%)	GCTAG (0.00%)	GCTAG (0.00%)	GCTAG (0.01%)	GCTAG (0.01%)	CTAGT (0.00%)	TAGGA (0.01%)	ACTAG (0.01%)	ACTAG (0.01%)	
-7	CTAGT (0.00%)	CTAGT (0.00%)	ACTAG (0.00%)	CTAGA (0.00%)	CTAGA (0.00%)	GCTAG (0.00%)	GCTAG (0.01%)	TAGGA (0.01%)	CCCTA (0.00%)	
-6	CTAGC (0.00%)	ACTAG (0.00%)	CTAGC (0.00%)	CTAGT (0.00%)	CTAGT (0.00%)	CTAGC (0.00%)	CTAGC (0.00%)	CTAGC (0.00%)	CTAGC (0.00%)	
-5	ACTAG (0.00%)	CTAGC (0.00%)	CTAGG (0.00%)	ACTAG (0.00%)	CTAGC (0.00%)	CTAGA (0.00%)	CTAGA (0.00%)	TCTAG (0.00%)	CTAGG (0.00%)	
-4	CTAGA (0.00%)	CTAGA (0.00%)	CTAGA (0.00%)	CTAGC (0.00%)	ACTAG (0.00%)	TCTAG (0.00%)	CTAGT (0.00%)	CTAGA (0.00%)	CTAGT (0.00%)	
-3	CCTAG (0.00%)	CCTAG (0.00%)	TCTAG (0.00%)	TCTAG (0.00%)	TCTAG (0.00%)	ACTAG (0.00%)	ACTAG (0.00%)	CTAGT (0.00%)	CCTAG (0.00%)	
-2	CTAGG (0.00%)	CTAGG (0.00%)	CTAGT (0.00%)	CCTAG (0.00%)	CTAGG (0.00%)	CTAGG (0.00%)	CTAGG (0.00%)	CTAGG (0.00%)	CTAGA (0.00%)	
-1	TCTAG (0.00%)	TCTAG (0.00%)	CCTAG (0.00%)	CTAGG (0.00%)	CCTAG (0.00%)	CCTAG (0.00%)	TCTAG (0.00%)	CCTAG (0.00%)	TCTAG (0.00%)	
										

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