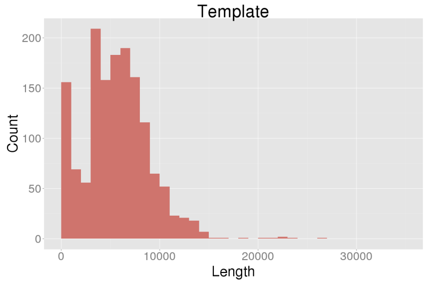
NanoOK report for ZF-screens_MARC_phase_1b_e_coli_run1

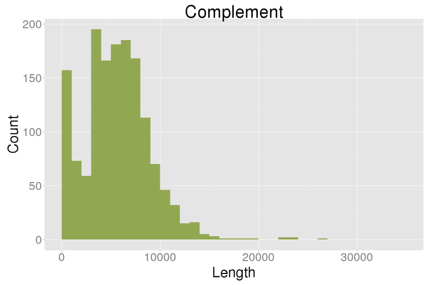
Pass and fail counts

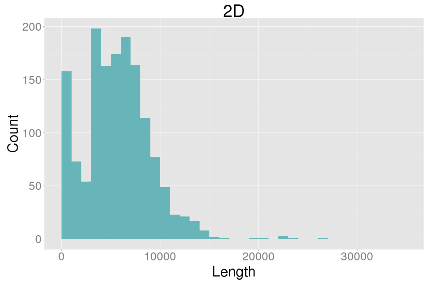
Type	Pass	Fail
Template	1493	0
Complement	1493	0
2D	1493	0

Read lengths

Type	NumReads	TotalBases	Mean	Longest	Shortest	N50	N50Count	N90	N90Count
Template	1493	8396699	5624.04	26382	194	7170	443	3593	1056
Complement	1493	8387902	5618.15	26169	223	7147	445	3668	1056
2D	1493	8445086	5656.45	26653	191	7194	444	3618	1054







Template alignments

Number of reads	1493	
Number of reads with alignments	1439	(96.38%)
Number of reads without alignments	54	(3.62%)

ID	Size	Number of Reads	% of Reads	Mean read length	Aligned bases	Mean coverage	Longest Perf Kmer
Control sequence	3560	133	8.91	3159.63	438993	123.31	44
Escherichia coli	4641652	1306	87.47	6085.56	8596762	1.85	66

Complement alignments

Number of reads	1493	
Number of reads with alignments	1444	(96.72%)
Number of reads without alignments	49	(3.28%)

ID	Size	Number of Reads	% of Reads	Mean read length	Aligned bases	Mean coverage	Longest Perf Kmer
Control sequence	3560	136	9.11	3110.72	442621	124.33	49
Escherichia coli	4641652	1308	87.61	6068.82	8538734	1.84	47

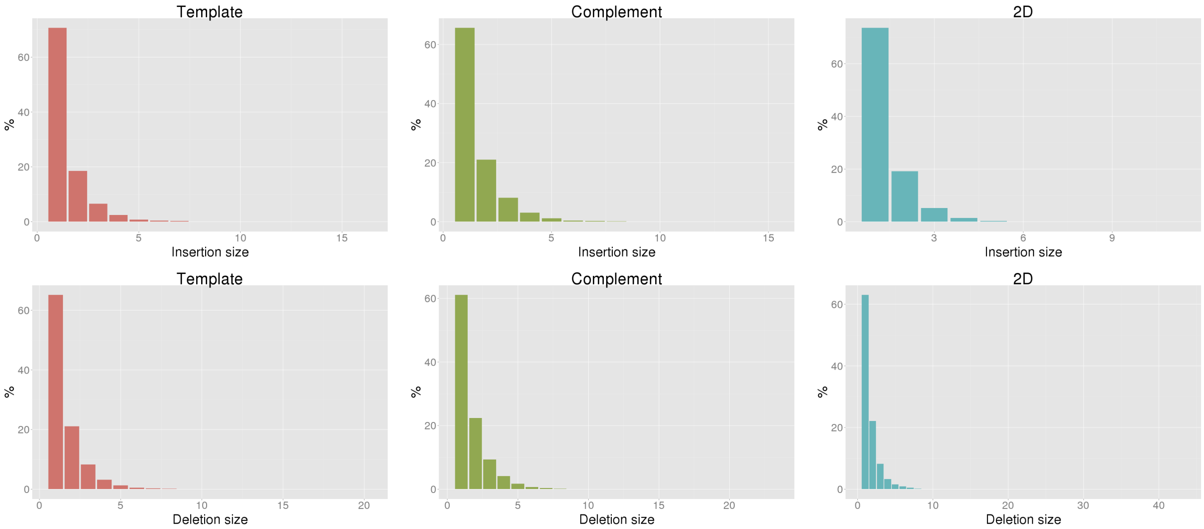
2D alignments

Number of reads	1493	
Number of reads with alignments	1491	(99.87%)
Number of reads without alignments	2	(0.13%)

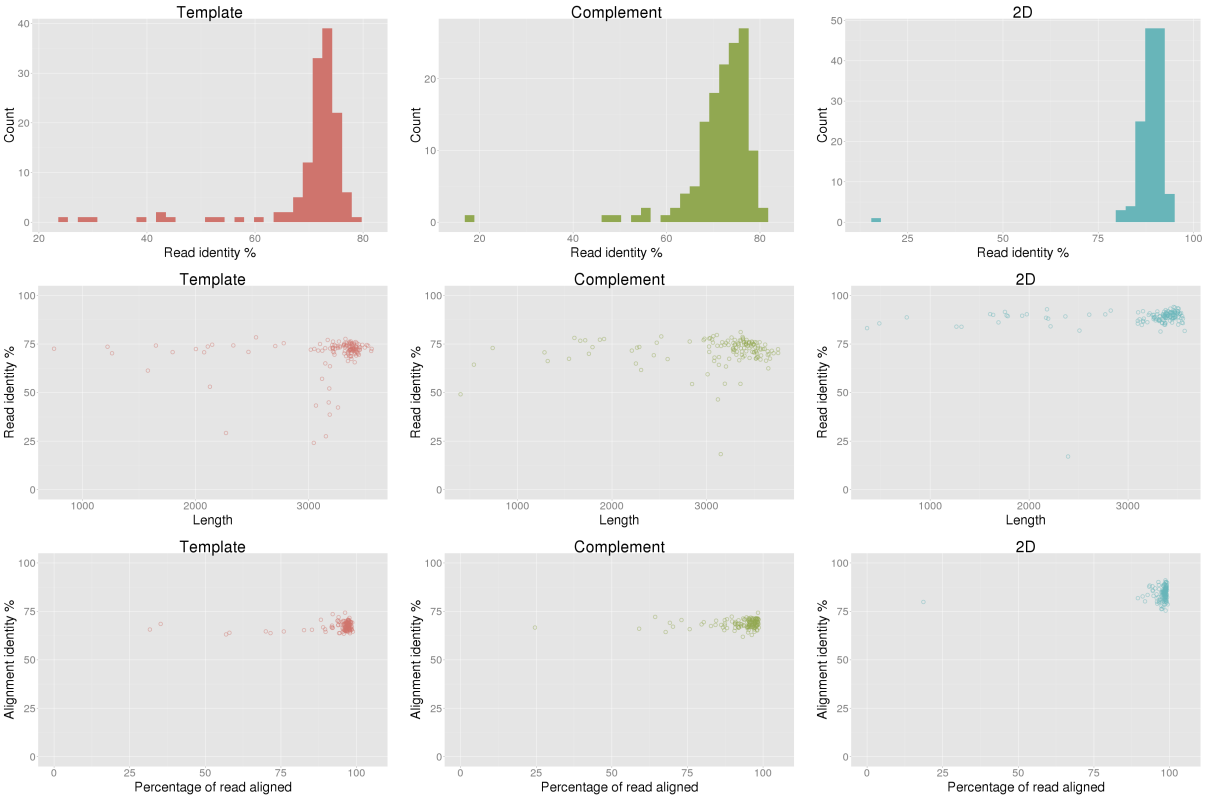
ID	Size	Number of Reads	% of Reads	Mean read length	Aligned bases	Mean coverage	Longest Perf Kmer
Control sequence	3560	136	9.11	3126.21	448263	125.92	132
Escherichia coli	4641652	1355	90.76	5906.66	8493621	1.83	172

Control sequence error analysis

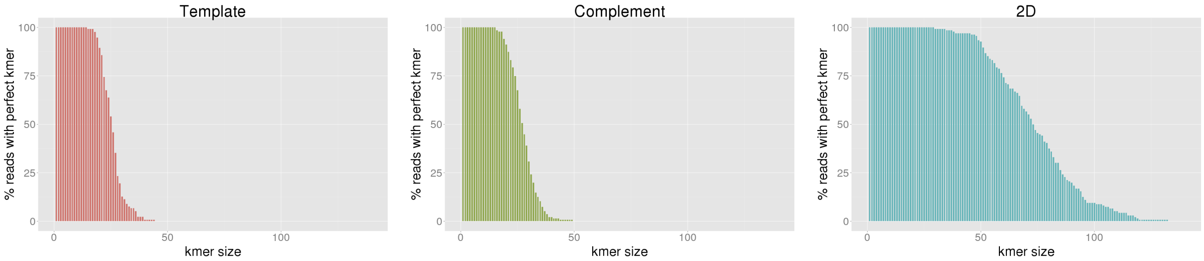
	Template	Complement	2D
Overall base identity (excluding indels)	70.36%	71.73%	88.71%
Aligned base identity (excluding indels)	79.26%	81.60%	93.21%
Identical bases per 100 aligned bases (including indels)	67.35%	68.56%	84.14%
Inserted bases per 100 aligned bases (including indels)	4.23%	5.07%	2.23%
Deleted bases per 100 aligned bases (including indels)	10.79%	10.91%	7.50%
Substitutions per 100 aligned bases (including indels)	17.63%	15.46%	6.12%
Mean insertion size	1.48	1.57	1.37
Mean deletion size	1.58	1.69	1.66

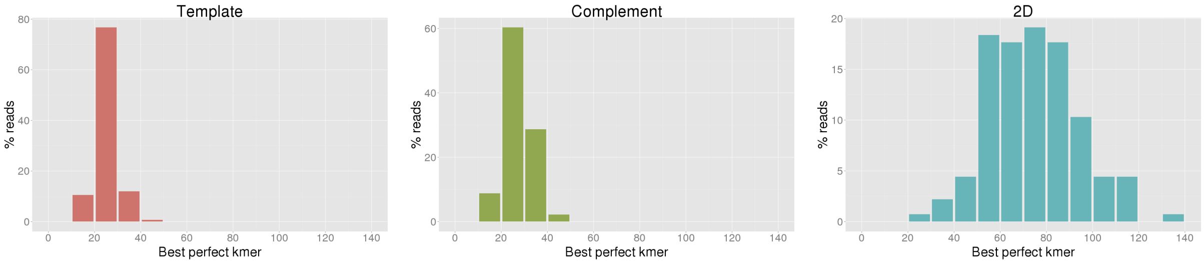


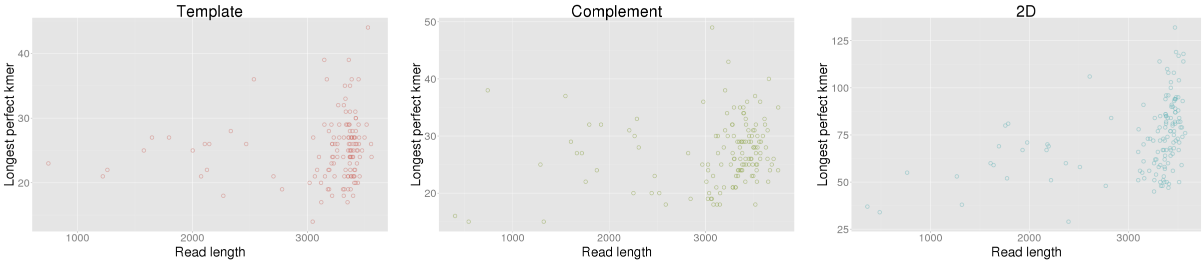
Control sequence read identity



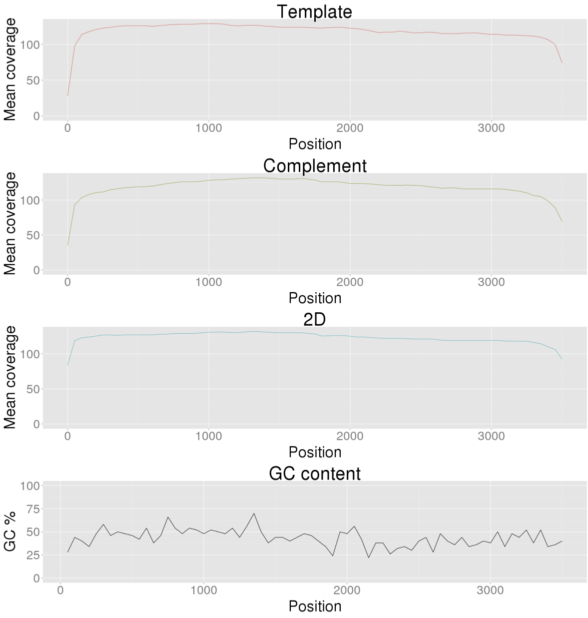
Control sequence perfect kmers







Control sequence coverage



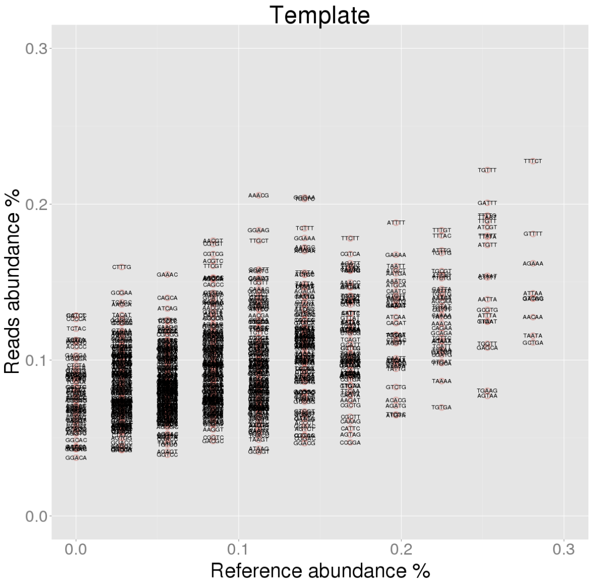
Control sequence 5-mer analysis

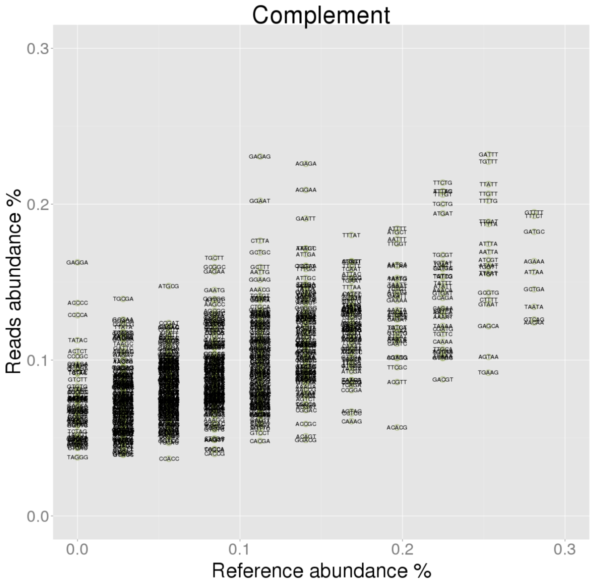
Under-represented 5-mers

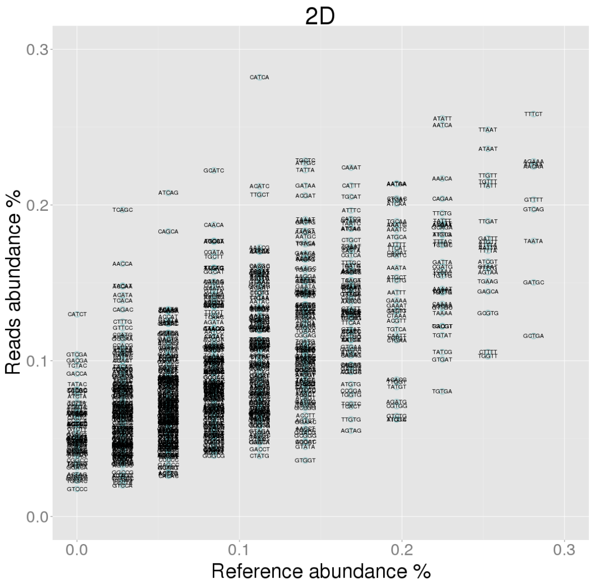
	Template				Complement				2D			
Rank	kmer	Ref %	Read %	Diff %	kmer	Ref %	Read %	Diff %	kmer	Ref %	Read %	Diff %
1	TTTTT	0.759	0.141	-0.618	TTTTT	0.759	0.115	-0.644	TTTTT	0.759	0.058	-0.700
2	AAAAA	0.478	0.117	-0.361	AAAAA	0.478	0.095	-0.383	AAAAA	0.478	0.064	-0.414
3	TGATG	0.393	0.129	-0.264	AAAAC	0.337	0.155	-0.182	TGATG	0.393	0.155	-0.238
4	GATGT	0.309	0.082	-0.228	GATGT	0.309	0.146	-0.163	CTGAT	0.309	0.132	-0.177
5	CTGAT	0.309	0.111	-0.198	TGAAG	0.253	0.092	-0.161	GATGT	0.309	0.133	-0.176
6	AAAAC	0.337	0.144	-0.193	AACAA	0.281	0.124	-0.157	GCTGA	0.281	0.116	-0.165
7	AATAT	0.309	0.117	-0.192	GCAAT	0.309	0.153	-0.156	AAAAC	0.337	0.179	-0.158
8	GCAAT	0.309	0.131	-0.178	GTCAG	0.281	0.126	-0.155	TTATC	0.309	0.152	-0.157
9	AGTAA	0.253	0.077	-0.176	TGATG	0.393	0.241	-0.152	TGGTT	0.253	0.103	-0.150
10	TGAAG	0.253	0.080	-0.173	AGTAA	0.253	0.102	-0.151	CTTTT	0.253	0.106	-0.147

Over-represented 5-mers

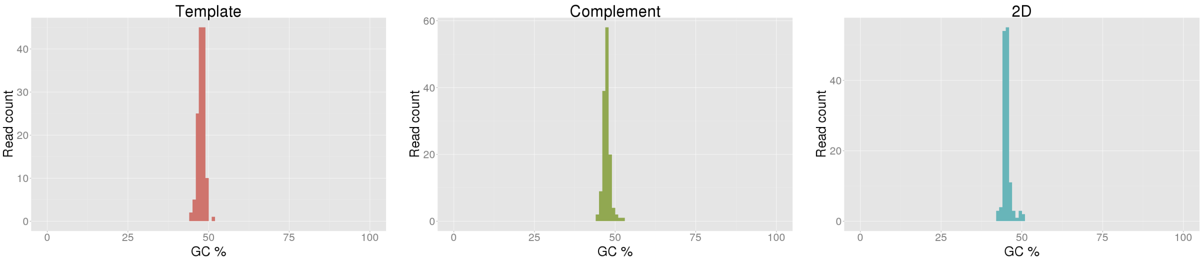
	Template				Complement				2D			
Rank	kmer	Ref %	Read %	Diff %	kmer	Ref %	Read %	Diff %	kmer	Ref %	Read %	Diff %
1	CTTTG	0.028	0.160	0.132	GAGGA	0.000	0.163	0.163	CATCA	0.112	0.282	0.170
2	GCTCC	0.000	0.128	0.128	ACCCC	0.000	0.137	0.137	TCAGC	0.028	0.197	0.169
3	CATCT	0.000	0.128	0.128	CCCCA	0.000	0.129	0.129	ATCAG	0.056	0.208	0.152
4	CCCCA	0.000	0.126	0.126	GAGAG	0.112	0.231	0.118	GCATC	0.084	0.222	0.138
5	TCTAC	0.000	0.120	0.120	TATAC	0.000	0.113	0.113	AACCA	0.028	0.162	0.134
6	GCGAA	0.028	0.143	0.115	TGCGA	0.028	0.139	0.111	CATCT	0.000	0.130	0.130
7	TCTTA	0.000	0.113	0.113	ACTCT	0.000	0.106	0.106	CAGCA	0.056	0.183	0.127
8	ACTCT	0.000	0.112	0.112	CCCGC	0.000	0.102	0.102	TACAT	0.028	0.148	0.120
9	CGAGA	0.000	0.112	0.112	GCGAA	0.028	0.126	0.098	ACCAA	0.028	0.148	0.120
10	CCCGC	0.000	0.111	0.111	CGAGA	0.000	0.098	0.098	ACATA	0.028	0.142	0.114





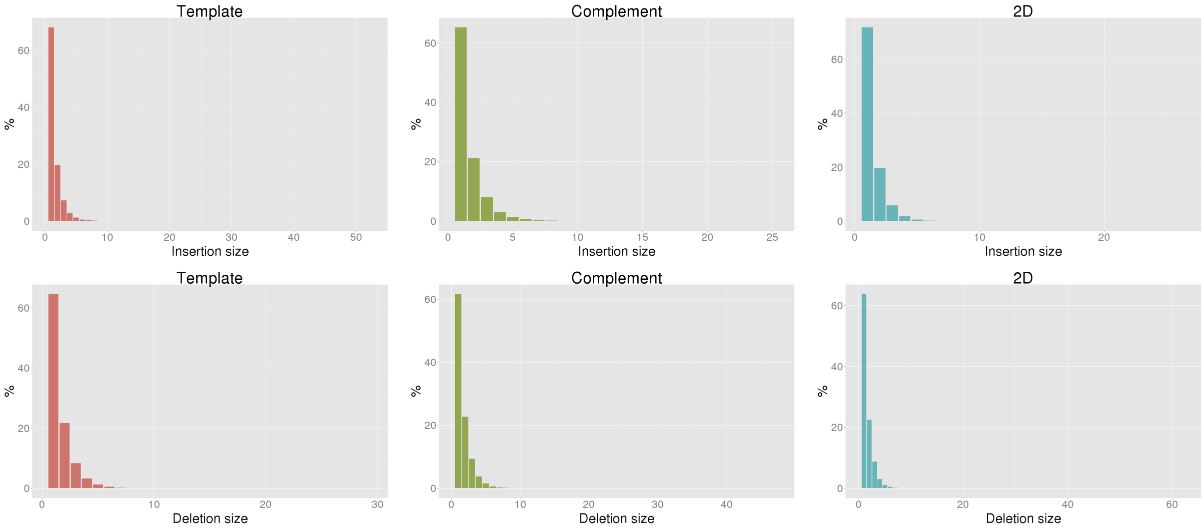


Control sequence GC content

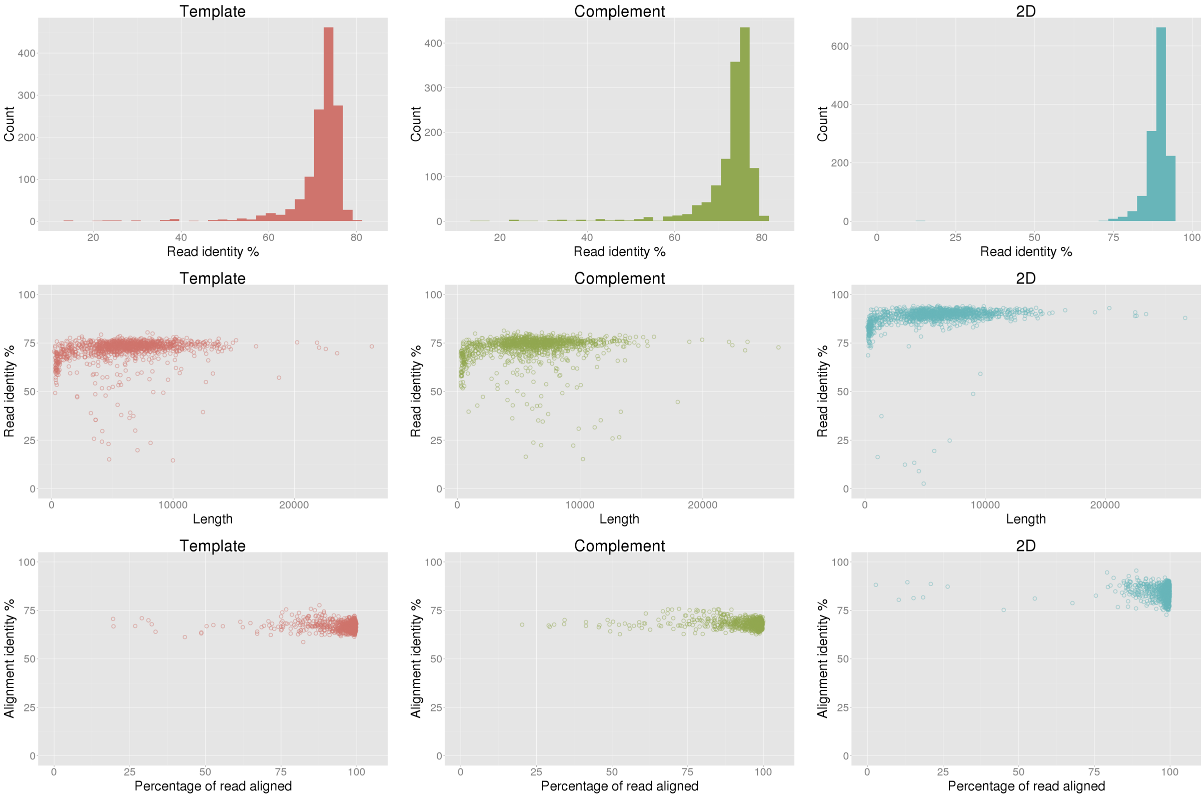


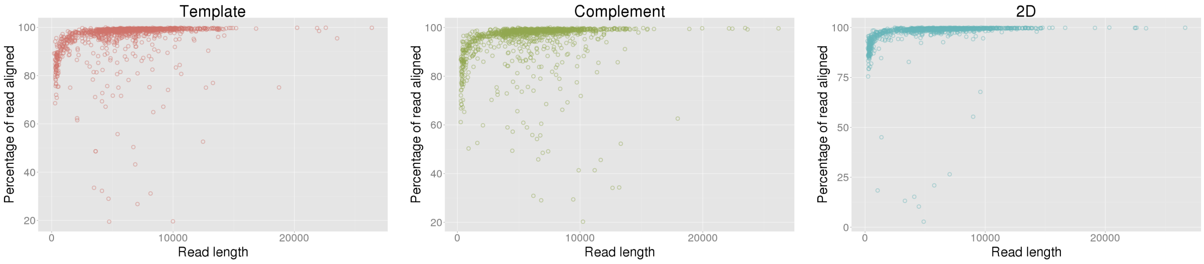
Escherichia coli error analysis

	Template	Complement	2D
Overall base identity (excluding indels)	72.21%	73.09%	89.52%
Aligned base identity (excluding indels)	78.92%	81.09%	93.15%
Identical bases per 100 aligned bases (including indels)	66.76%	67.95%	84.36%
Inserted bases per 100 aligned bases (including indels)	4.93%	5.37%	2.47%
Deleted bases per 100 aligned bases (including indels)	10.47%	10.82%	6.97%
Substitutions per 100 aligned bases (including indels)	17.84%	15.85%	6.20%
Mean insertion size	1.55	1.59	1.41
Mean deletion size	1.59	1.66	1.59

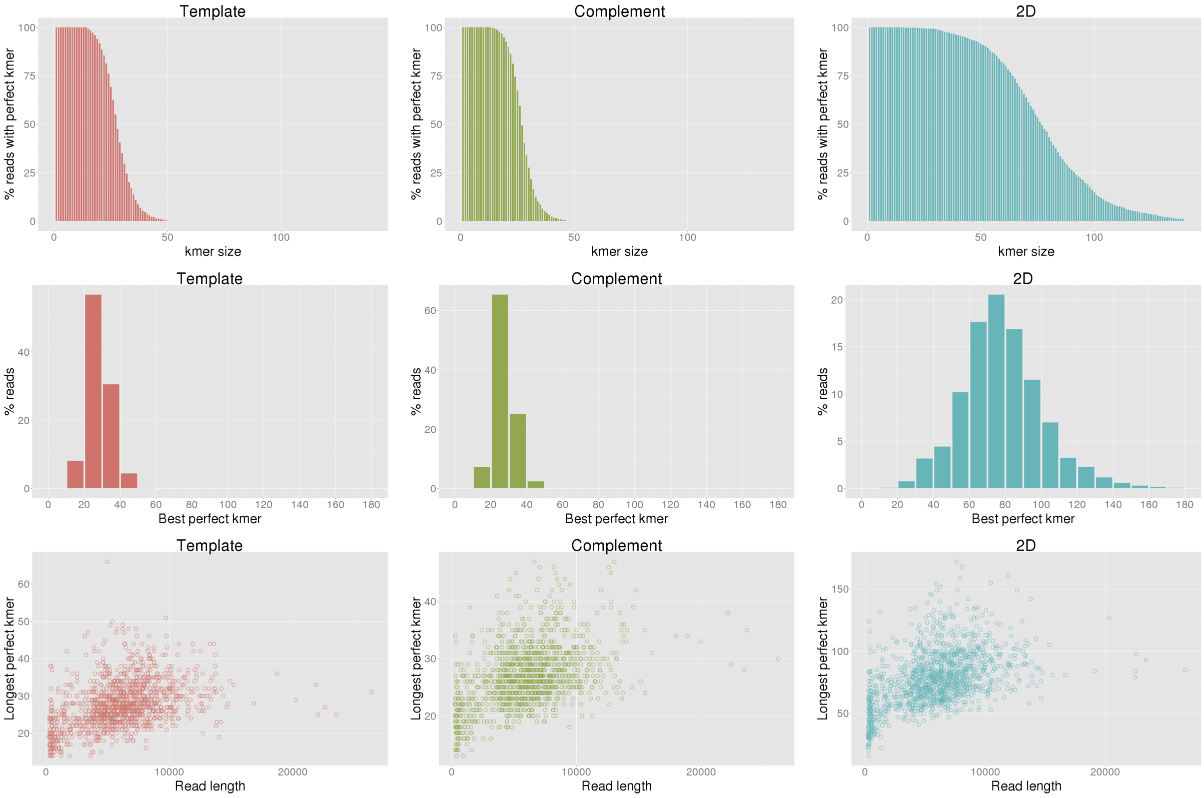


Escherichia coli read identity

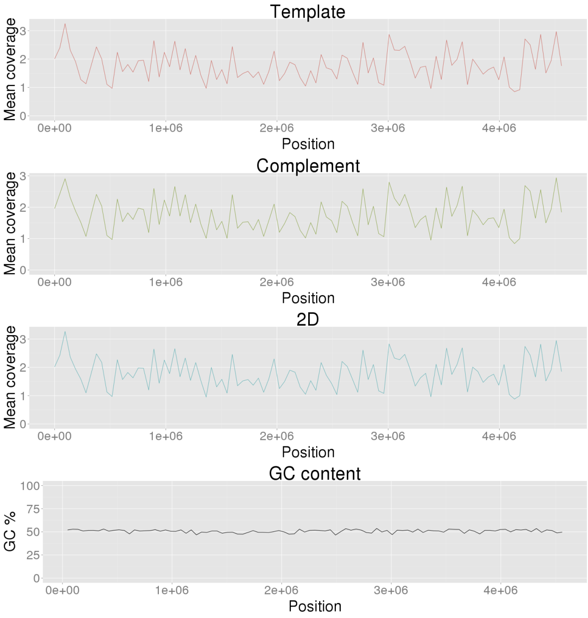




Escherichia coli perfect kmers



Escherichia coli coverage



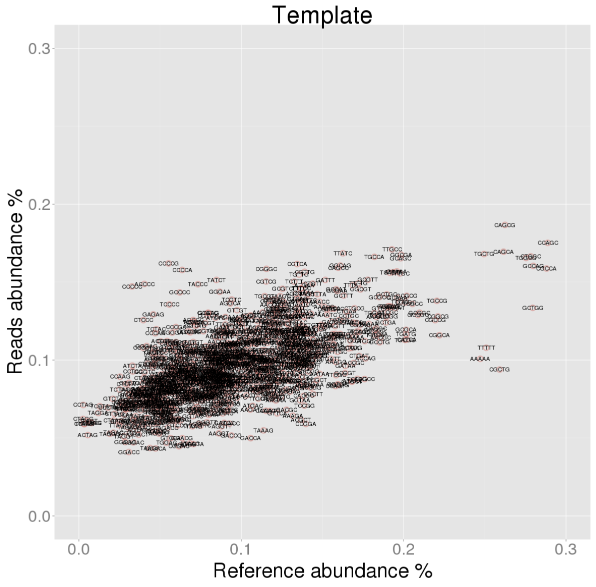
Escherichia coli 5-mer analysis

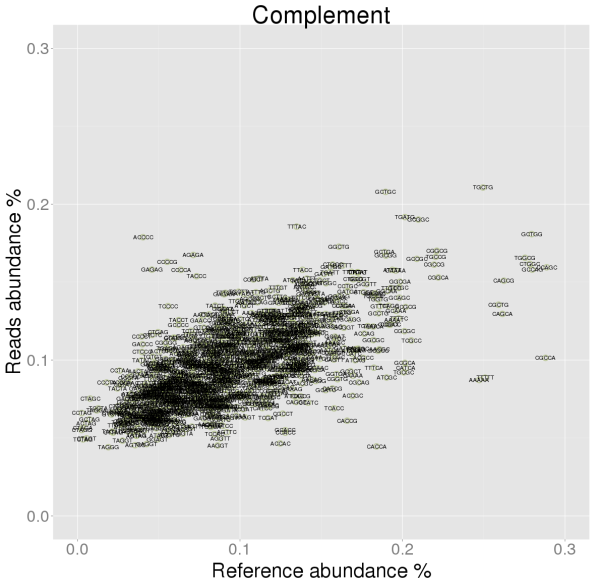
Under-represented 5-mers

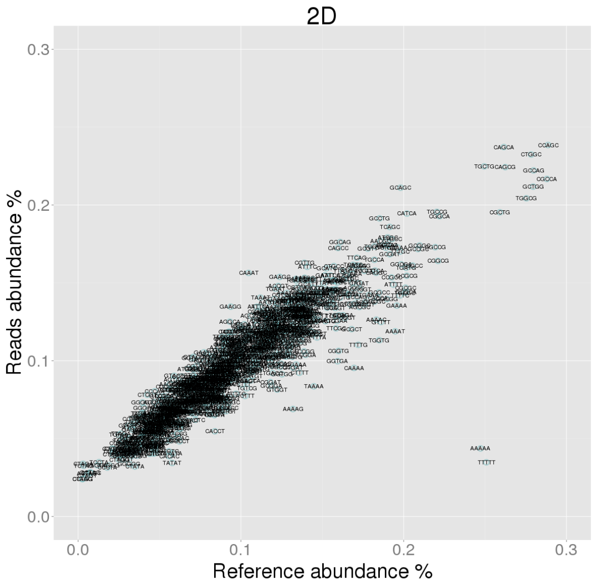
	Template				Complement				2D			
Rank	kmer	Ref %	Read %	Diff %	kmer	Ref %	Read %	Diff %	kmer	Ref %	Read %	Diff %
1	CGCTG	0.259	0.094	-0.165	CGCCA	0.288	0.101	-0.187	TTTTT	0.251	0.035	-0.216
2	AAAAA	0.247	0.101	-0.146	TTTTT	0.251	0.089	-0.162	AAAAA	0.247	0.044	-0.203
3	GCTGG	0.279	0.133	-0.146	AAAAA	0.247	0.087	-0.160	AAAAT	0.195	0.119	-0.076
4	TTTTT	0.251	0.108	-0.143	CACCA	0.184	0.045	-0.139	CAAAA	0.169	0.095	-0.074
5	CGCCA	0.288	0.159	-0.129	CAGCA	0.261	0.130	-0.132	TGGTG	0.185	0.113	-0.072
6	GCCAG	0.280	0.160	-0.119	CCAGC	0.289	0.159	-0.129	CGCCA	0.288	0.217	-0.071
7	CCAGC	0.289	0.175	-0.113	CGCTG	0.259	0.136	-0.124	TGGCG	0.275	0.204	-0.071
8	CTGGC	0.278	0.167	-0.112	GCCAG	0.280	0.158	-0.122	GCTGG	0.279	0.212	-0.068
9	TGGCG	0.275	0.166	-0.110	CTGGC	0.278	0.162	-0.117	CGCTG	0.259	0.195	-0.064
10	CGGCA	0.222	0.116	-0.106	CAGCG	0.262	0.151	-0.111	AAAAG	0.132	0.069	-0.063

Over-represented 5-mers

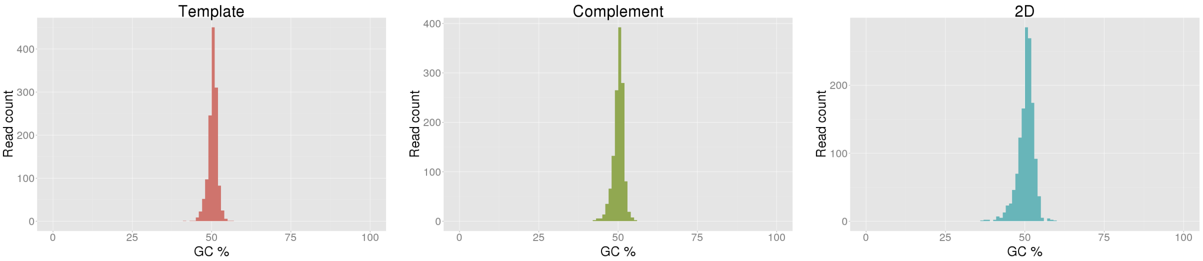
	Template				Complement				2D			
Rank	kmer	Ref %	Read %	Diff %	kmer	Ref %	Read %	Diff %	kmer	Ref %	Read %	Diff %
1	CCCCC	0.033	0.147	0.114	ACCCC	0.040	0.179	0.138	CAAAT	0.105	0.156	0.052
2	ACCCC	0.040	0.149	0.109	GAGAG	0.046	0.158	0.112	GAAGG	0.094	0.135	0.041
3	CCCCG	0.055	0.162	0.107	CCCCG	0.055	0.163	0.108	CTCGT	0.042	0.078	0.036
4	CCCCA	0.064	0.158	0.094	AGAGA	0.071	0.167	0.096	GGGGT	0.039	0.073	0.034
5	CTCCC	0.040	0.126	0.086	CCCCA	0.064	0.158	0.094	CCCAA	0.047	0.080	0.033
6	GAGAG	0.046	0.129	0.083	TACCC	0.073	0.154	0.080	AGGCA	0.093	0.125	0.032
7	GCCCC	0.062	0.143	0.081	TCCCC	0.056	0.135	0.079	GTACC	0.071	0.102	0.032
8	TCCCC	0.056	0.136	0.080	CCCCT	0.039	0.115	0.076	GGTAC	0.070	0.102	0.032
9	TACCC	0.073	0.149	0.075	CTCTC	0.046	0.116	0.070	GTACT	0.059	0.090	0.031
10	TCTAC	0.048	0.120	0.072	GACCC	0.040	0.110	0.070	CTAGA	0.003	0.034	0.031



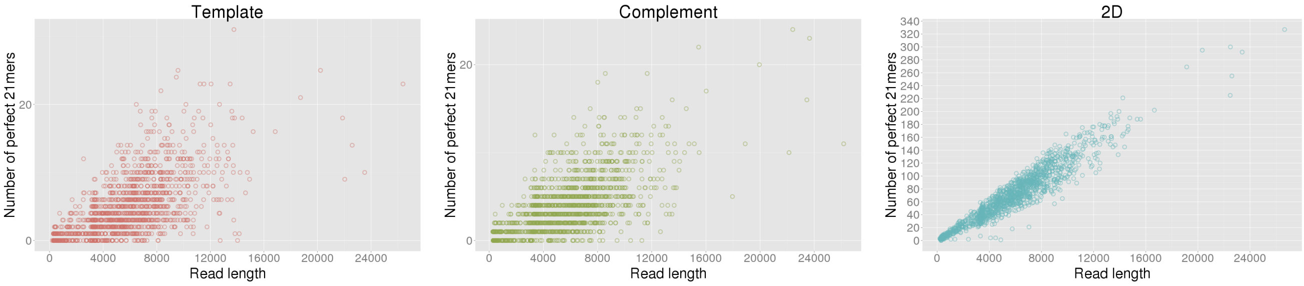




Escherichia coli GC content



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	9.21	8.92	4.77	0.00	9.39	8.55	4.91	0.00	9.27	8.51	3.93
	C	8.32	0.00	9.21	9.85	9.32	0.00	8.73	9.58	9.02	0.00	10.91	8.95
	G	9.25	9.13	0.00	8.14	9.01	8.84	0.00	8.73	8.58	11.30	0.00	8.34
	T	5.09	9.10	9.03	0.00	5.22	8.56	9.18	0.00	4.10	8.19	8.90	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 (3.01%)	TTC (3.31%)	AAA (4.16%)	GCA (2.69%)	GGC (3.04%)	AAA (4.22%)	GCA (3.20%)	TGC (2.64%)	GCA (3.81%)	Most common
2	GCA (2.95%)	TGC (3.05%)	TTC (3.64%)	TGC (2.68%)	AAA (2.88%)	GCA (3.62%)	TTC (2.72%)	AAA (2.63%)	AAA (3.66%)	
3	AAA (2.79%)	GCA (2.90%)	GCA (3.27%)	AAA (2.60%)	TGC (2.84%)	GAA (3.25%)	TCA (2.66%)	GGC (2.63%)	GAA (3.33%)	
4	ATC (2.63%)	AAA (2.84%)	GAA (2.91%)	TTC (2.57%)	GCA (2.65%)	TTC (2.99%)	ATC (2.52%)	TCA (2.60%)	TTC (2.82%)	
5	TGC (2.56%)	GCC (2.52%)	TTT (2.73%)	GGC (2.55%)	TTC (2.49%)	TTT (2.87%)	AAA (2.42%)	GCA (2.56%)	TTT (2.75%)	
6	TCA (2.39%)	TCA (2.33%)	TGC (2.51%)	CAG (2.48%)	GAA (2.45%)	TGC (2.35%)	GAA (2.39%)	GCG (2.44%)	TCA (2.39%)	
7	TTT (2.28%)	GGC (2.26%)	AAT (2.34%)	ATC (2.26%)	GCC (2.27%)	TCA (2.32%)	TGC (2.31%)	TTC (2.28%)	GTT (2.35%)	
8	GCC (2.27%)	GAA (2.16%)	TCA (2.24%)	GAA (2.23%)	CAG (2.27%)	ATC (2.26%)	CAG (2.20%)	CAG (2.27%)	GCC (2.33%)	
9	GGC (2.20%)	AAC (2.13%)	CAA (2.23%)	GCG (2.19%)	TCA (2.27%)	GCC (2.11%)	GCG (2.13%)	CGC (2.22%)	AAT (2.31%)	
10	GAA (2.15%)	GCG (2.08%)	GCC (2.13%)	TCA (2.18%)	AGC (2.15%)	CAA (2.05%)	AAT (2.11%)	GAA (2.14%)	ATC (2.23%)	
										
-10	AGA (0.97%)	GTA (0.93%)	CCT (0.97%)	AGT (0.99%)	AGT (0.96%)	CTC (0.97%)	CTC (1.01%)	GTA (1.00%)	CCT (0.89%)	Least common
-9	CTC (0.96%)	AGT (0.93%)	GTA (0.94%)	CTT (0.96%)	CGA (0.95%)	CCC (0.96%)	TAC (1.01%)	ACT (0.95%)	ACT (0.88%)	
-8	GGA (0.92%)	CCT (0.88%)	GGT (0.92%)	GGA (0.94%)	CTT (0.91%)	AGG (0.86%)	GAG (0.97%)	CGA (0.94%)	GAG (0.84%)	
-7	CCC (0.89%)	GAG (0.85%)	TGT (0.84%)	GAG (0.93%)	CCC (0.90%)	AGT (0.86%)	AGA (0.87%)	CCC (0.92%)	TGA (0.83%)	
-6	AGT (0.89%)	CTT (0.83%)	AGG (0.83%)	CTC (0.90%)	CTC (0.89%)	GGG (0.84%)	AGG (0.83%)	CTT (0.86%)	CTT (0.75%)	
-5	GAG (0.76%)	CGA (0.82%)	CTT (0.80%)	CCC (0.87%)	GAG (0.87%)	CCT (0.79%)	GGA (0.81%)	AGA (0.84%)	CGA (0.71%)	
-4	GGG (0.76%)	AGA (0.72%)	AGT (0.80%)	AGG (0.73%)	CCT (0.86%)	GAG (0.70%)	CCC (0.73%)	CCT (0.79%)	AGA (0.59%)	
-3	AGG (0.69%)	GGA (0.66%)	GAG (0.71%)	GGG (0.62%)	GGG (0.79%)	ACT (0.69%)	GGG (0.72%)	GGA (0.76%)	GGA (0.57%)	
-2	CTA (0.48%)	TAG (0.55%)	TAG (0.40%)	CTA (0.55%)	CTA (0.57%)	CTA (0.42%)	CTA (0.60%)	CTA (0.73%)	TAG (0.54%)	
-1	TAG (0.37%)	CTA (0.52%)	CTA (0.33%)	TAG (0.45%)	TAG (0.51%)	TAG (0.38%)	TAG (0.47%)	TAG (0.66%)	CTA (0.40%)	
										

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 (1.12%)	AAAA (1.40%)	CAGC (1.00%)	TGGC (1.10%)	AAAA (1.21%)	ATCA (0.97%)	TGGC (0.97%)	GGCA (1.19%)	Most common
2	GAAA (0.91%)	TGCC (0.98%)	TTTC (1.32%)	TGGC (0.98%)	CGGC (1.10%)	GAAA (1.03%)	GGCA (0.86%)	CAGC (0.91%)	GAAA (0.97%)	
3	AAAA (0.91%)	TTGC (0.93%)	GAAA (1.15%)	ATCA (0.85%)	CAGC (1.01%)	CAAA (1.01%)	TTCA (0.82%)	TTCA (0.87%)	GGAA (0.96%)	
4	ATCA (0.87%)	CTGC (0.91%)	TTTT (1.00%)	CTGC (0.83%)	CTGC (0.91%)	AGCA (0.98%)	GCCA (0.81%)	ATCA (0.83%)	AAAA (0.95%)	
5	TGCC (0.86%)	AAAA (0.90%)	GGCA (0.98%)	CCAG (0.81%)	TTGC (0.86%)	GGCA (0.96%)	CGCA (0.80%)	CGGC (0.82%)	TGAA (0.94%)	
6	CAGC (0.82%)	CAGC (0.90%)	GCAA (0.96%)	CGGC (0.80%)	CTGG (0.81%)	TTTT (0.94%)	AACA (0.77%)	CTGC (0.77%)	TGCA (0.90%)	
7	TGGC (0.81%)	TGGC (0.88%)	CAAA (0.90%)	TTGC (0.79%)	ATCA (0.80%)	TGAA (0.94%)	CAGC (0.77%)	TTGC (0.76%)	ATCA (0.88%)	
8	TTTT (0.80%)	TTCA (0.85%)	GGAA (0.89%)	CAAA (0.76%)	AAAA (0.79%)	ATCA (0.90%)	TGAA (0.77%)	CAAA (0.75%)	AGCA (0.88%)	
9	GCCA (0.79%)	TTCC (0.82%)	AAAT (0.85%)	AAAA (0.72%)	CAAA (0.79%)	TGCA (0.89%)	TGCA (0.75%)	TGCC (0.74%)	CGCA (0.85%)	
10	CATC (0.78%)	GAAA (0.82%)	CTTC (0.81%)	GGCG (0.72%)	TGCC (0.78%)	AGAA (0.86%)	CGCC (0.75%)	CCAG (0.74%)	TGCC (0.83%)	
										
-10	GTAG (0.12%)	TCTA (0.13%)	CGAG (0.10%)	TTAG (0.12%)	CTAT (0.12%)	CTAT (0.11%)	CTAA (0.13%)	GAGA (0.16%)	CTAT (0.11%)	Least common
-9	ATAG (0.11%)	CCCT (0.13%)	TTAG (0.10%)	CGAG (0.11%)	CGAG (0.12%)	CTAA (0.10%)	TATA (0.13%)	CCCC (0.15%)	GGGA (0.11%)	
-8	CTAA (0.10%)	GGAC (0.12%)	ACTA (0.09%)	GGAC (0.11%)	CTAA (0.12%)	ACCT (0.10%)	GAGG (0.12%)	CTAT (0.14%)	TCGA (0.10%)	
-7	TTAG (0.10%)	TAGT (0.11%)	TAGT (0.09%)	CTAA (0.10%)	CCTC (0.12%)	ACTA (0.10%)	CCCC (0.12%)	CTAA (0.13%)	TCTA (0.09%)	
-6	GGAC (0.10%)	CTAA (0.11%)	GGAC (0.08%)	CCCT (0.10%)	ACCT (0.11%)	GGAC (0.10%)	CCCT (0.12%)	ACCT (0.13%)	CCCT (0.09%)	
-5	TAGT (0.09%)	CGGA (0.10%)	TAGA (0.08%)	TAGA (0.10%)	TAGA (0.11%)	CGAG (0.09%)	CTAT (0.11%)	TAGA (0.10%)	CGGA (0.08%)	
-4	TAGA (0.08%)	TAGG (0.07%)	TCTA (0.07%)	GAGG (0.10%)	TAGG (0.09%)	TAGG (0.07%)	TAGA (0.09%)	TAGG (0.10%)	TAGG (0.07%)	
-3	CCTA (0.06%)	CCTA (0.07%)	TAGG (0.06%)	TAGG (0.07%)	CCCT (0.08%)	CCTA (0.07%)	CCTA (0.07%)	CCCT (0.09%)	CCTA (0.05%)	
-2	TAGG (0.06%)	TAGA (0.05%)	CCTA (0.04%)	CCTA (0.05%)	CCTA (0.07%)	CCCT (0.06%)	TAGG (0.05%)	CCTA (0.08%)	TAGA (0.04%)	
-1	CTAG (0.01%)	CTAG (0.01%)	CTAG (0.01%)	CTAG (0.02%)	CTAG (0.02%)	CTAG (0.01%)	CTAG (0.01%)	CTAG (0.02%)	CTAG (0.01%)	
										

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 (0.37%)	CAGCA (0.38%)	GAAAA (0.43%)	CTGGC (0.40%)	CTGGC (0.43%)	CAGCA (0.56%)	CAGCA (0.40%)	CTGGC (0.40%)	TGGCA (0.45%)	Most common
2	TTATC (0.33%)	CTGGC (0.38%)	CAGCA (0.42%)	CAGCA (0.39%)	CAGCA (0.41%)	GAAAA (0.38%)	CGGCA (0.34%)	CAGCA (0.34%)	CAGCA (0.43%)	
3	CGCCA (0.33%)	TTGCC (0.36%)	GCAAA (0.38%)	CCAGC (0.33%)	GCGGC (0.38%)	CGGCA (0.36%)	CGCCA (0.33%)	GCGGC (0.30%)	CGGCA (0.38%)	
4	GCCAG (0.32%)	GCCAG (0.34%)	TGGCA (0.38%)	CGGCA (0.30%)	CCAGC (0.33%)	TGGCA (0.34%)	CTGGC (0.31%)	TGGCG (0.30%)	GAAAA (0.36%)	
5	TGGCG (0.31%)	CGCCA (0.34%)	CAAAA (0.37%)	CATCA (0.30%)	GCTGC (0.32%)	CATCA (0.34%)	CATCA (0.30%)	GCCAG (0.29%)	GCGTT (0.32%)	
6	TTGCC (0.31%)	GCTGC (0.32%)	TTTTC (0.35%)	GCAGC (0.29%)	CATCA (0.31%)	TTATC (0.33%)	GATCA (0.29%)	CATCA (0.29%)	AGAAA (0.30%)	
7	CAAAA (0.31%)	TTTGC (0.32%)	CGTTT (0.33%)	GCGGC (0.28%)	AATCA (0.30%)	AGAAA (0.31%)	TGGCA (0.28%)	TTTCA (0.28%)	ATTTT (0.29%)	
8	CTGGC (0.30%)	TTTCA (0.32%)	CGCCA (0.32%)	AATCA (0.28%)	TTTGC (0.30%)	ACGCA (0.31%)	GCAAA (0.26%)	CCAGC (0.27%)	CTGCA (0.29%)	
9	GAAAA (0.30%)	GCAGC (0.31%)	AGAAA (0.32%)	CAGGC (0.27%)	TCAGC (0.29%)	AATCA (0.31%)	CAGGC (0.26%)	ATAAA (0.27%)	GCTGG (0.28%)	
10	CCAGC (0.29%)	ATTTC (0.30%)	ATTTC (0.32%)	GCTGC (0.26%)	GCTGG (0.29%)	CAGAA (0.31%)	TTTCA (0.25%)	GCAGC (0.27%)	CAGAA (0.28%)	
										
-10	CCCTA (0.01%)	TAGGA (0.01%)	GGGAC (0.01%)	ACCTA (0.01%)	ACCCT (0.01%)	CCTAT (0.01%)	GGACC (0.01%)	TCCTA (0.01%)	GCTAG (0.01%)	Least common
-9	ACTAG (0.00%)	GGACC (0.01%)	CTTAG (0.01%)	GGACC (0.01%)	TAGGT (0.01%)	ACCCT (0.01%)	TAGGG (0.01%)	TAGGA (0.01%)	TTGGA (0.01%)	
-8	GCTAG (0.00%)	TAGGT (0.01%)	TAGGT (0.01%)	CTAGC (0.01%)	CTAGC (0.01%)	CTAGC (0.01%)	TAGGA (0.01%)	GCTAG (0.01%)	TCCTA (0.00%)	
-7	ACCTA (0.00%)	TTAGA (0.01%)	CCCTA (0.01%)	CTAGA (0.01%)	CCCTA (0.01%)	GCTAG (0.00%)	CCTAT (0.01%)	CTAGC (0.01%)	CTAGT (0.00%)	
-6	GGACC (0.00%)	CCCTA (0.01%)	ACTAG (0.01%)	TCTAG (0.01%)	ACTAG (0.00%)	CTAGA (0.00%)	CCCTA (0.01%)	ACTAG (0.01%)	TTAGA (0.00%)	
-5	CTAGT (0.00%)	GCTAG (0.00%)	TCCTA (0.00%)	CTAGT (0.00%)	CTAGT (0.00%)	TAGGT (0.00%)	CTAGC (0.00%)	CTAGT (0.01%)	ACTAG (0.00%)	
-4	CTAGG (0.00%)	ACTAG (0.00%)	CTAGG (0.00%)	ACTAG (0.00%)	CTAGA (0.00%)	CTAGG (0.00%)	CTAGT (0.00%)	CTAGA (0.00%)	CTAGC (0.00%)	
-3	CTAGC (0.00%)	CCTAG (0.00%)	CTAGA (0.00%)	GCTAG (0.00%)	TCTAG (0.00%)	CTAGT (0.00%)	CTAGA (0.00%)	TCTAG (0.00%)	CTAGG (0.00%)	
-2	CTAGA (0.00%)	CTAGG (0.00%)	GCTAG (0.00%)	CCTAG (0.00%)	CTAGG (0.00%)	CCTAG (0.00%)	ACTAG (0.00%)	CTAGG (0.00%)	TCTAG (0.00%)	
-1	TCTAG (0.00%)	TCTAG (0.00%)	CTAGC (0.00%)	CCCTA (0.00%)	CCTAG (0.00%)	ACTAG (0.00%)	CCTAG (0.00%)	CCTAG (0.00%)	CCTAG (0.00%)	
										

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