

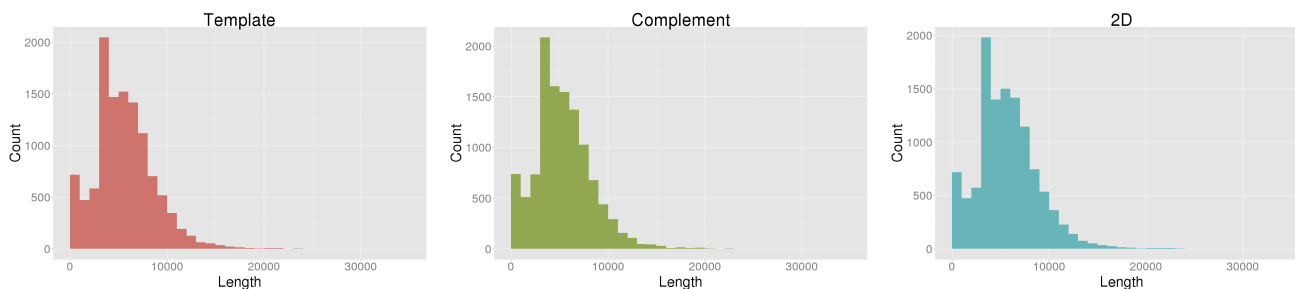
NanoOK report for ZF-screens_MARC_phase_1b_e_coli_run2

Pass and fail counts

Type	Pass	Fail
Template	11484	0
Complement	11484	0
2D	11484	0

Read lengths

Type	NumReads	TotalBases	Mean	Longest	Shortest	N50	N50Count	N90	N90Count
Template	11484	64527325	5618.89	32831	190	6823	3498	3523	8554
Complement	11484	61642109	5367.65	30236	173	6521	3494	3396	8535
2D	11484	65512980	5704.72	32708	175	6934	3492	3543	8534



Template alignments

Number of reads	11484
Number of reads with alignments	11327 (98.63%)
Number of reads without alignments	157 (1.37%)

ID	Size	Number of Reads	% of Reads	Mean read length	Aligned bases	Mean coverage	Longest Perf Kmer
Control sequence	3560	1244	10.83	3208.54	4231282	1188.56	65
Escherichia coli	4641652	10083	87.80	5995.90	65019063	14.01	77

Complement alignments

Number of reads	11484
Number of reads with alignments	11323 (98.60%)
Number of reads without alignments	161 (1.40%)

ID	Size	Number of Reads	% of Reads	Mean read length	Aligned bases	Mean coverage	Longest Perf Kmer
Control sequence	3560	1242	10.82	3030.66	3933162	1104.82	52
Escherichia coli	4641652	10081	87.78	5734.31	62948601	13.56	69

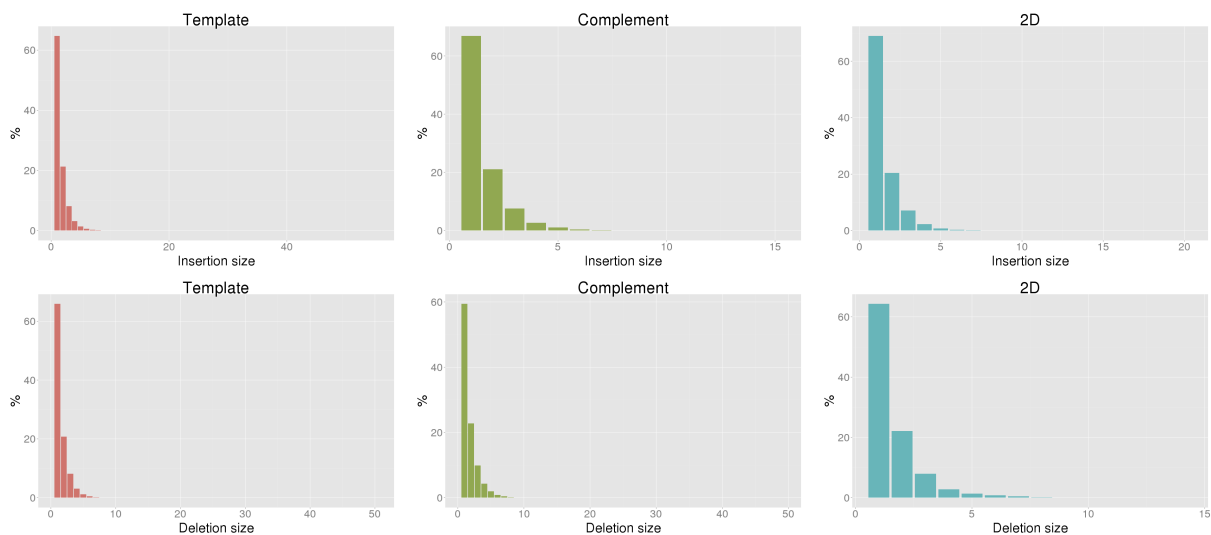
2D alignments

Number of reads	11484
Number of reads with alignments	11479 (99.96%)
Number of reads without alignments	5 (0.04%)

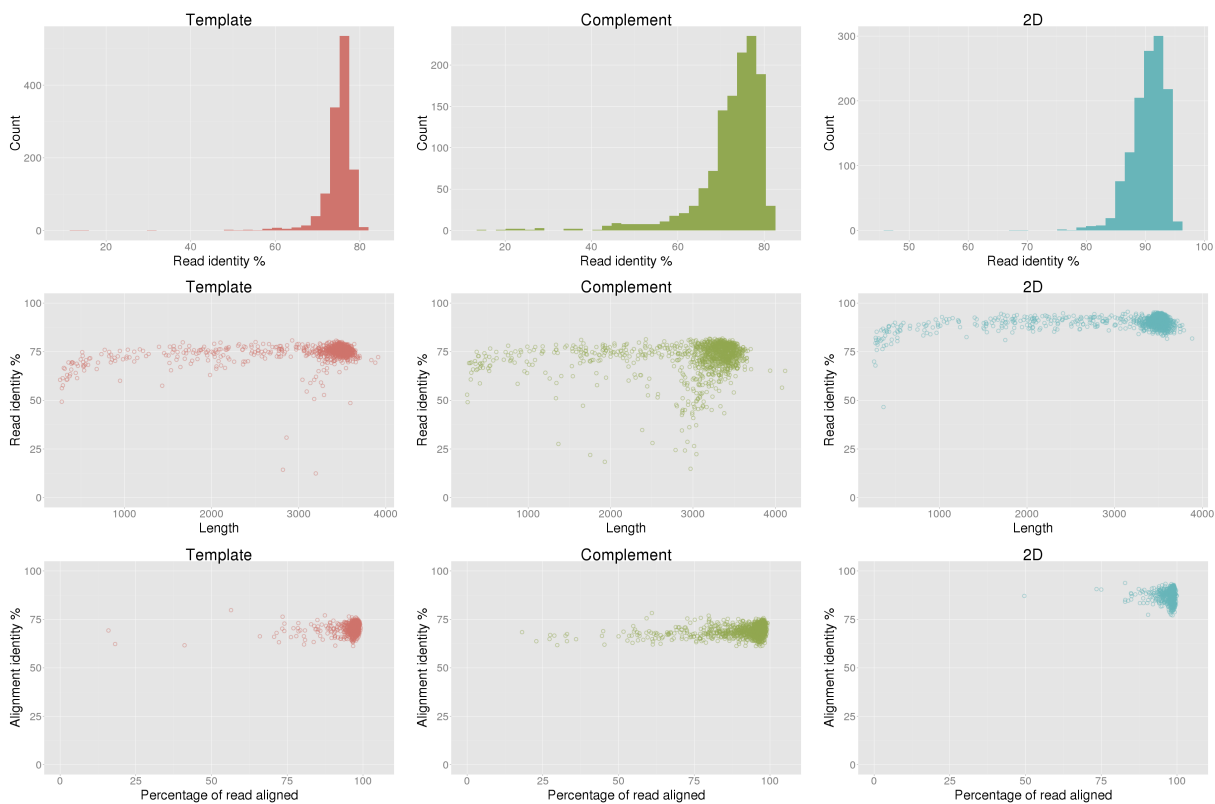
ID	Size	Number of Reads	% of Reads	Mean read length	Aligned bases	Mean coverage	Longest Perf Kmer
Control sequence	3560	1256	10.94	3174.65	4131484	1160.53	210
Escherichia coli	4641652	10223	89.02	6016.10	63693775	13.72	287

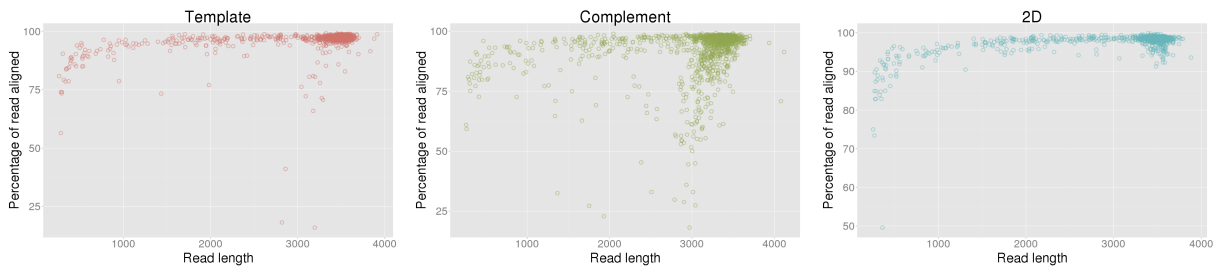
Control sequence error analysis

	Template	Complement	2D
Overall base identity (excluding indels)	75.16%	72.40%	90.67%
Aligned base identity (excluding indels)	82.55%	82.55%	95.11%
Identical bases per 100 aligned bases (including indels)	70.90%	69.28%	87.50%
Inserted bases per 100 aligned bases (including indels)	5.41%	4.42%	2.83%
Deleted bases per 100 aligned bases (including indels)	8.70%	11.65%	5.17%
Substitutions per 100 aligned bases (including indels)	14.99%	14.64%	4.49%
Mean insertion size	1.61	1.53	1.47
Mean deletion size	1.56	1.73	1.60

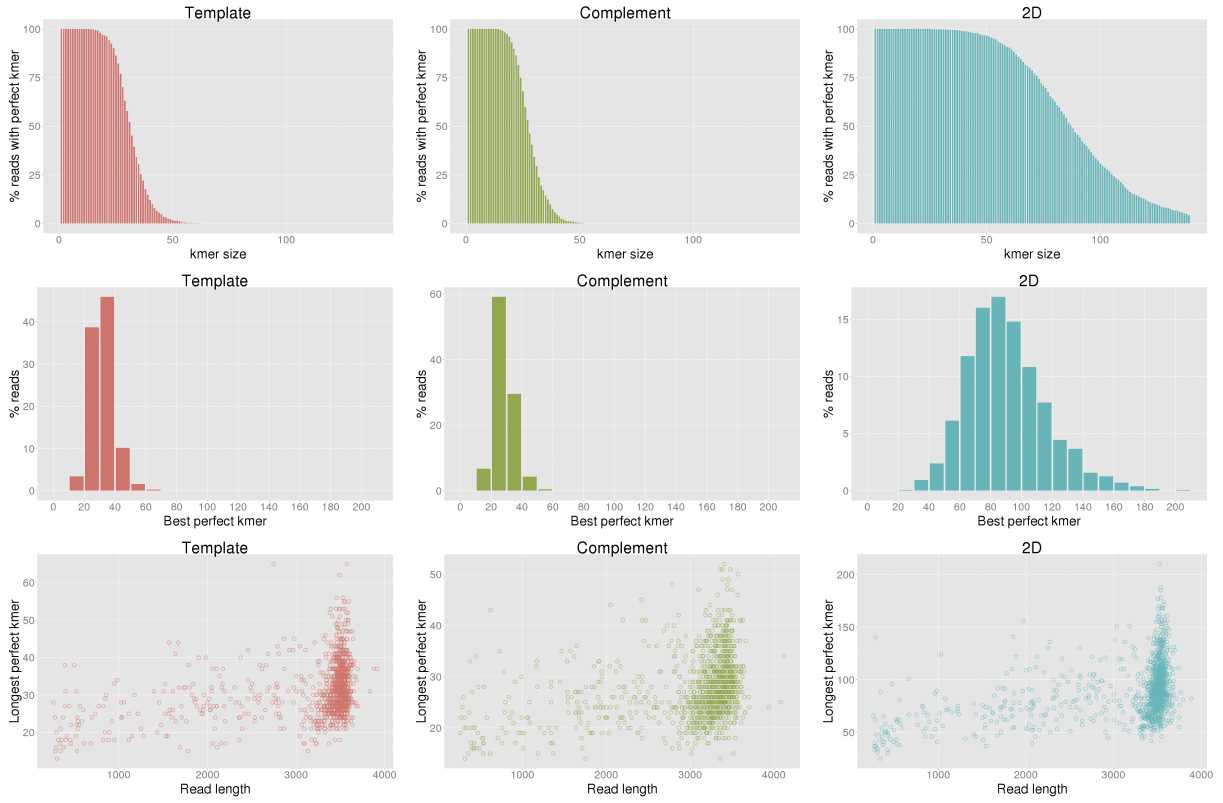


Control sequence read identity

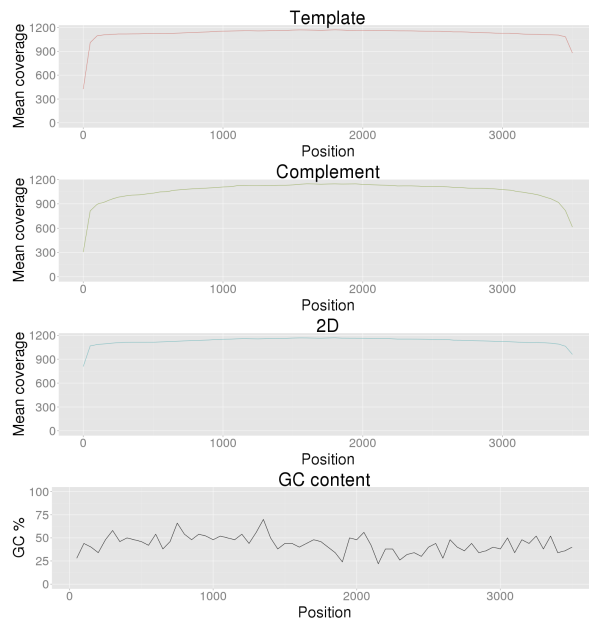




Control sequence perfect kmers



Control sequence coverage



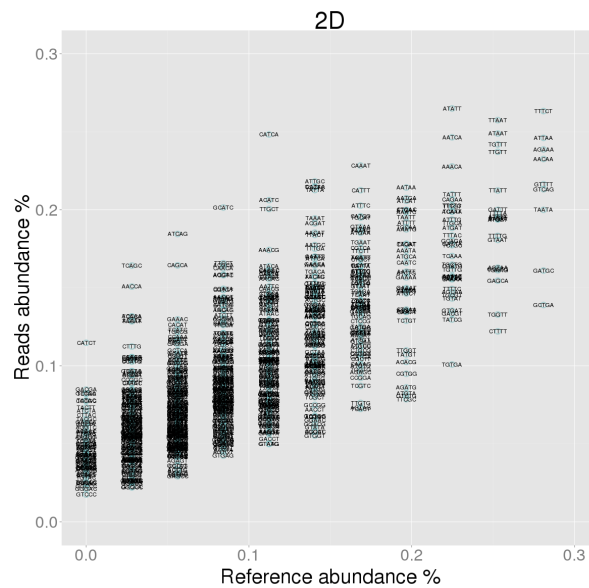
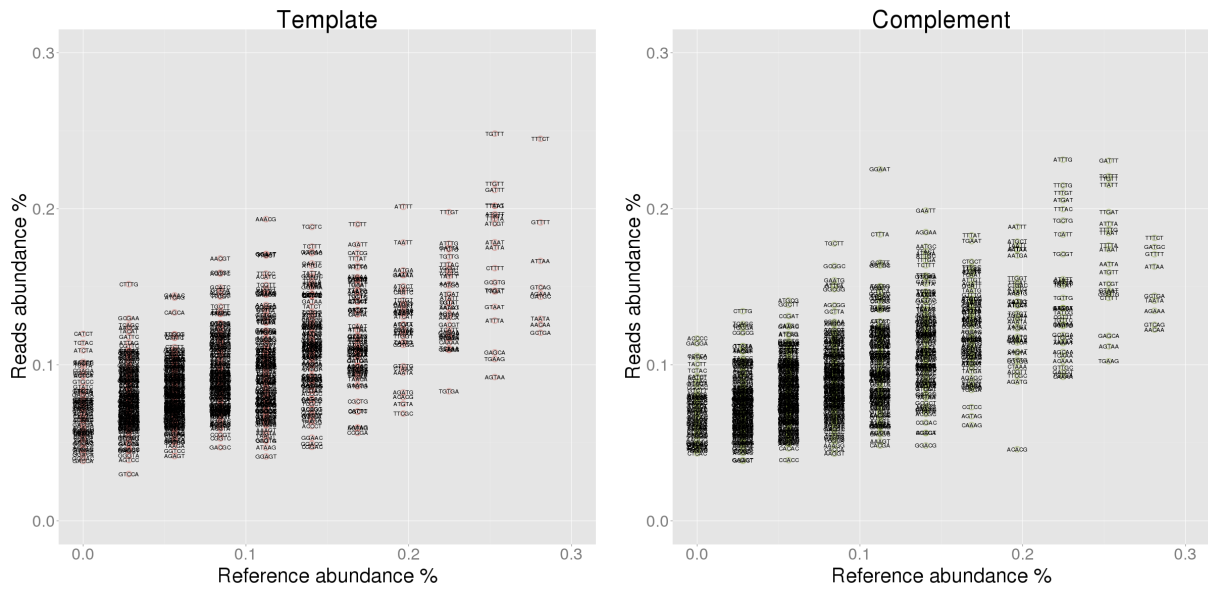
Control sequence 5-mer analysis

Under-represented 5-mers

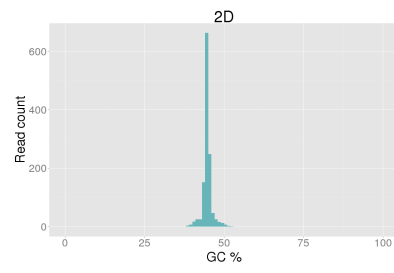
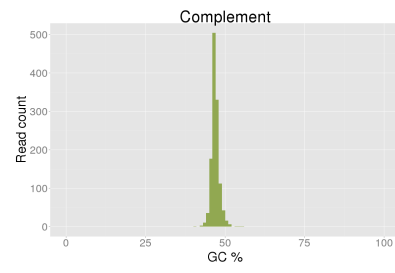
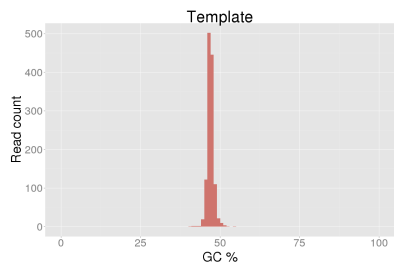
Rank	Template				Complement				2D			
	kmer	Ref %	Read %	Diff %	kmer	Ref %	Read %	Diff %	kmer	Ref %	Read %	Diff %
1	TTTTT	0.759	0.148	-0.611	TTTTT	0.759	0.094	-0.665	TTTTT	0.759	0.067	-0.692
2	AAAAA	0.478	0.122	-0.355	AAAAA	0.478	0.064	-0.413	AAAAA	0.478	0.085	-0.392
3	TGATG	0.393	0.148	-0.246	AAACG	0.337	0.146	-0.191	TGATG	0.393	0.193	-0.201
4	GATGT	0.309	0.108	-0.201	GATGT	0.309	0.138	-0.171	CTGAT	0.309	0.154	-0.155
5	AAAAC	0.337	0.141	-0.196	GCAAT	0.309	0.147	-0.162	GATGT	0.309	0.158	-0.151
6	CTGAT	0.309	0.127	-0.182	TGATG	0.393	0.232	-0.161	GCTGA	0.281	0.139	-0.142
7	AGTAA	0.253	0.092	-0.161	AACAA	0.281	0.123	-0.158	CTTTT	0.253	0.122	-0.131
8	GCTGA	0.281	0.121	-0.160	GTCAG	0.281	0.126	-0.155	TGTGA	0.225	0.101	-0.124
9	AATAT	0.309	0.150	-0.159	ACACG	0.197	0.046	-0.151	TTATC	0.309	0.187	-0.122
10	GCAAT	0.309	0.151	-0.158	TGAAG	0.253	0.102	-0.151	TGGTT	0.253	0.133	-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	0.152	0.124	ACCCC	0.000	0.117	0.117	TCAGC	0.028	0.164	0.136
2	CATCT	0.000	0.120	0.120	GAGGA	0.000	0.114	0.114	CATCA	0.112	0.248	0.136
3	TCTAC	0.000	0.114	0.114	GGAAT	0.112	0.225	0.113	ATCAG	0.056	0.184	0.128
4	ATCTA	0.000	0.109	0.109	CTTTG	0.028	0.134	0.106	AACCA	0.028	0.151	0.123
5	GCTCC	0.000	0.102	0.102	CCCCA	0.000	0.106	0.106	GCATC	0.084	0.201	0.117
6	GCGAA	0.028	0.130	0.102	TATAC	0.000	0.105	0.105	CATCT	0.000	0.115	0.115
7	TACTT	0.000	0.101	0.101	TACTT	0.000	0.101	0.101	CAGCA	0.056	0.164	0.108
8	ACCCC	0.000	0.101	0.101	TCAGC	0.028	0.126	0.098	ACCAA	0.028	0.132	0.104
9	TCTTA	0.000	0.100	0.100	GATTC	0.028	0.125	0.097	TCACA	0.028	0.131	0.103
10	TCAGC	0.028	0.125	0.097	TCTAC	0.000	0.096	0.096	ACATA	0.028	0.129	0.101

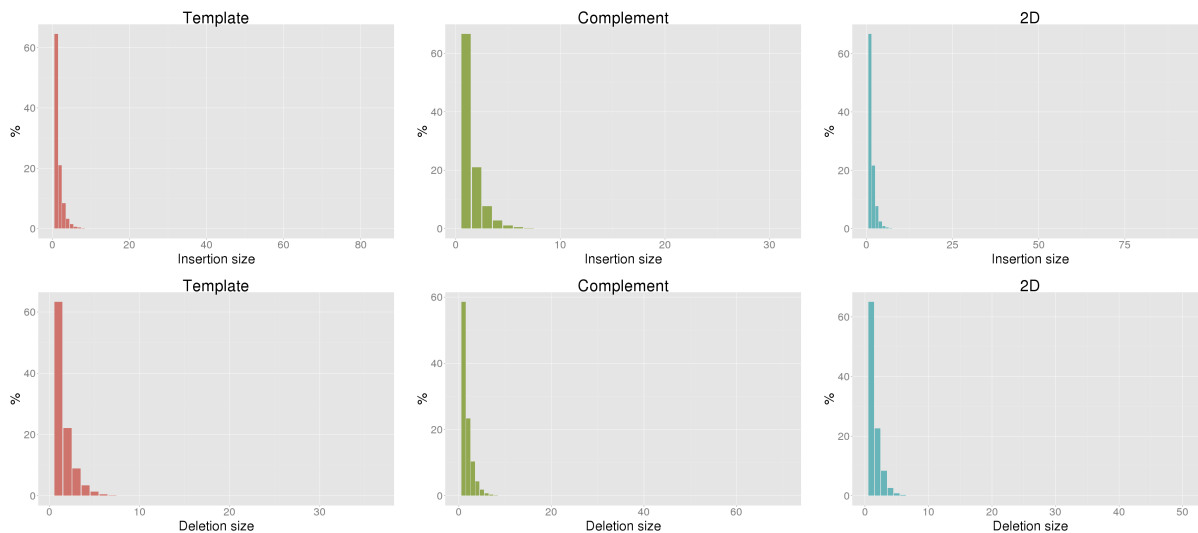


Control sequence GC content

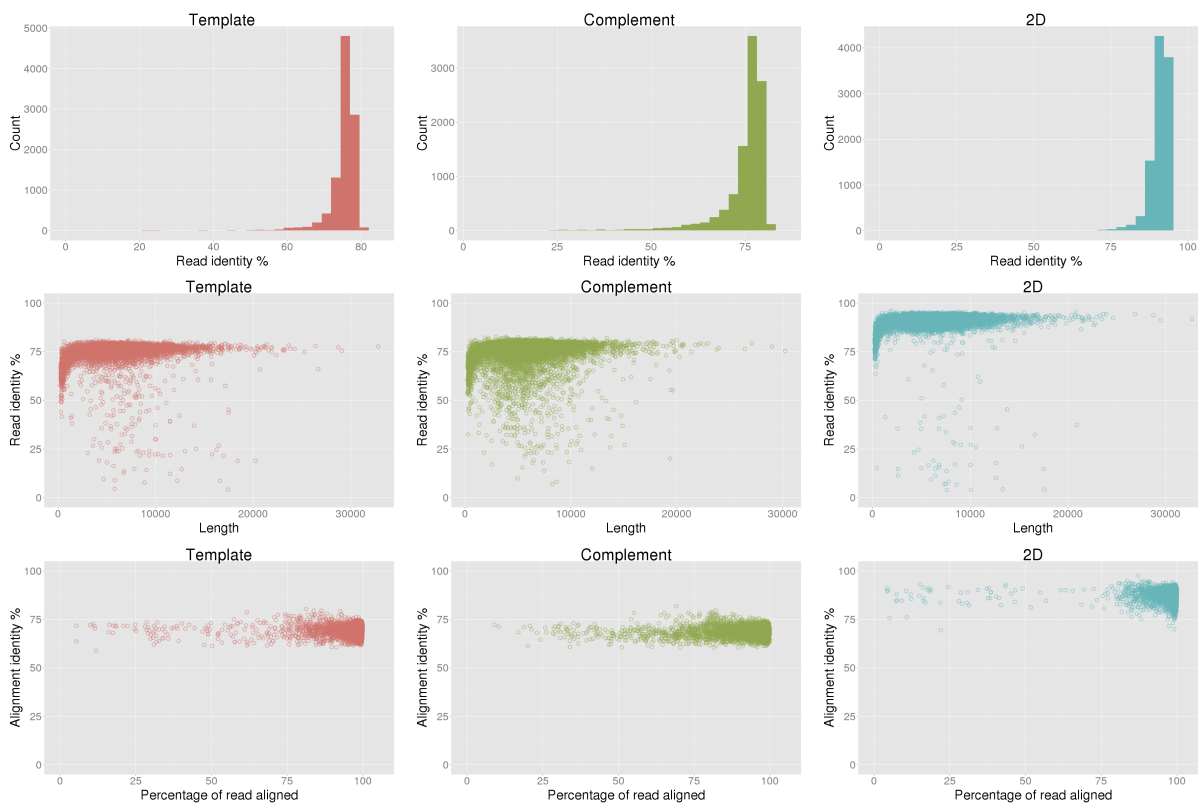


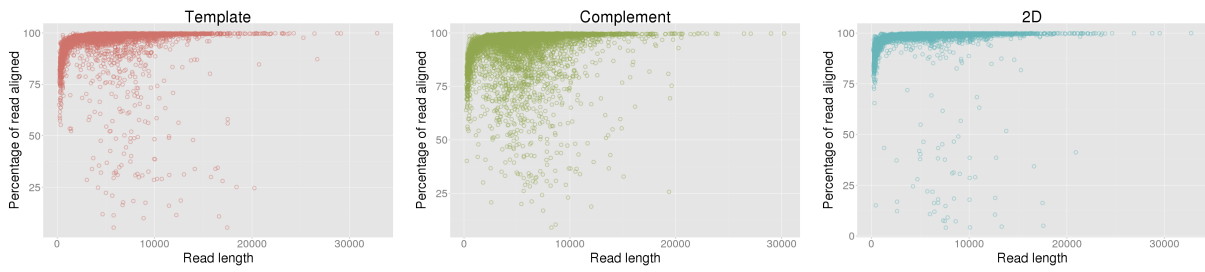
Escherichia coli error analysis

	Template	Complement	2D
Overall base identity (excluding indels)	75.21%	75.10%	90.89%
Aligned base identity (excluding indels)	82.01%	82.56%	95.16%
Identical bases per 100 aligned bases (including indels)	69.94%	68.97%	87.76%
Inserted bases per 100 aligned bases (including indels)	5.52%	4.50%	3.03%
Deleted bases per 100 aligned bases (including indels)	9.20%	11.97%	4.75%
Substitutions per 100 aligned bases (including indels)	15.34%	14.57%	4.46%
Mean insertion size	1.63	1.54	1.52
Mean deletion size	1.61	1.73	1.53

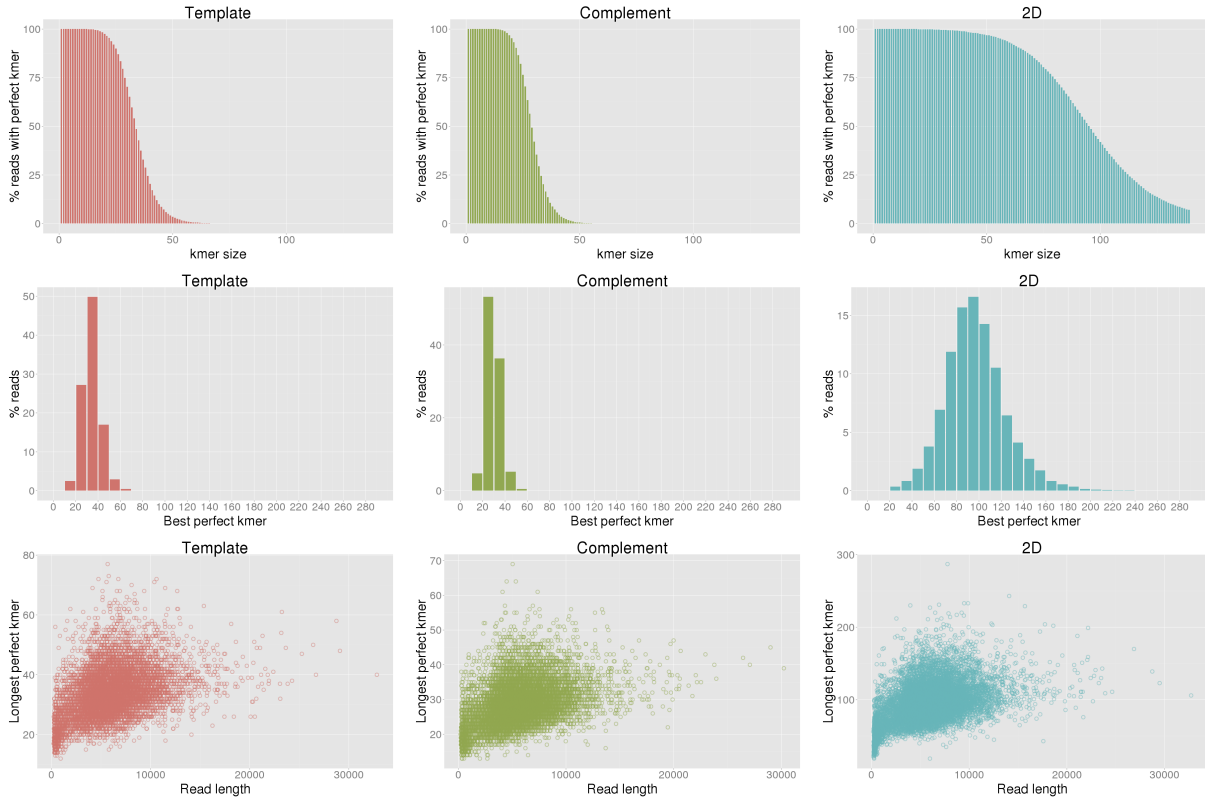


Escherichia coli read identity

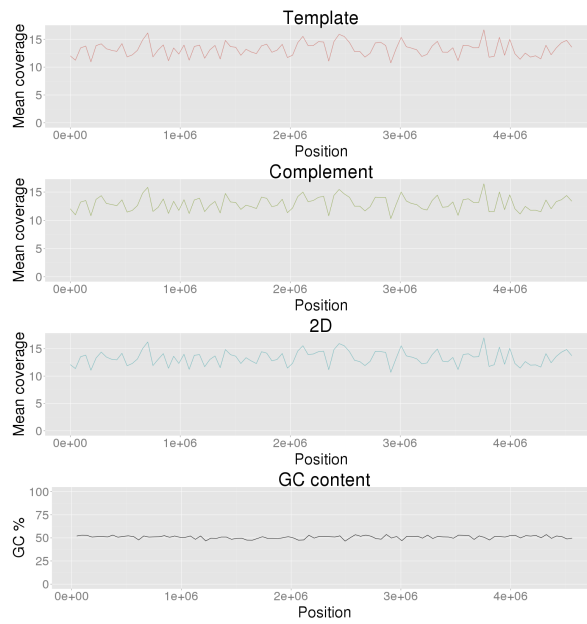




Escherichia coli perfect kmers



Escherichia coli coverage



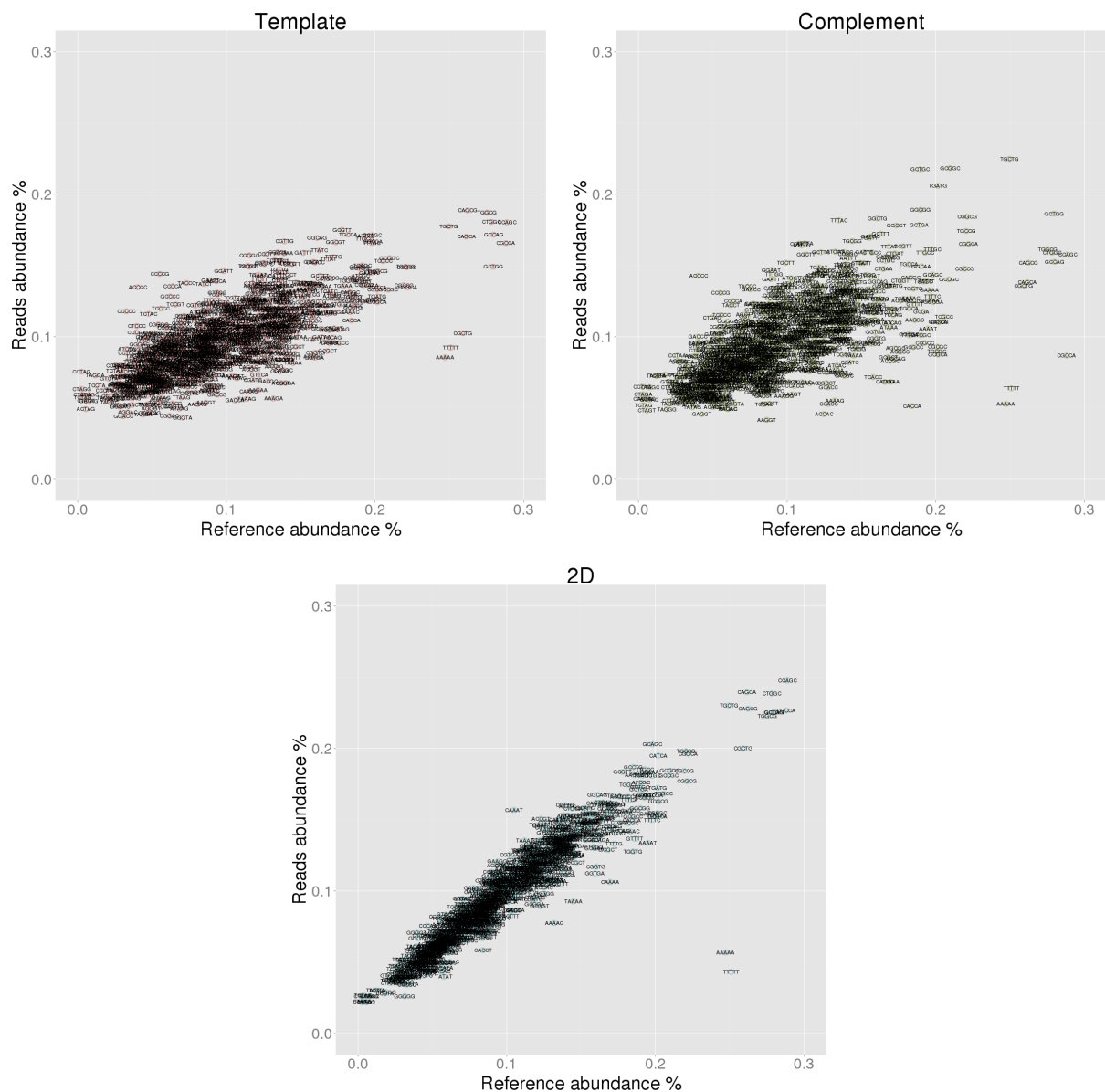
Escherichia coli 5-mer analysis

Under-represented 5-mers

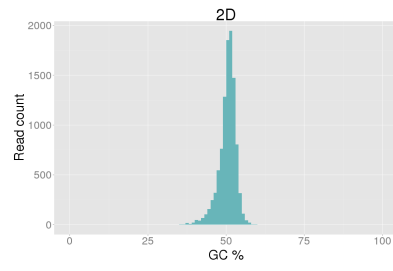
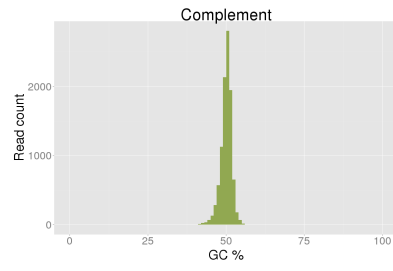
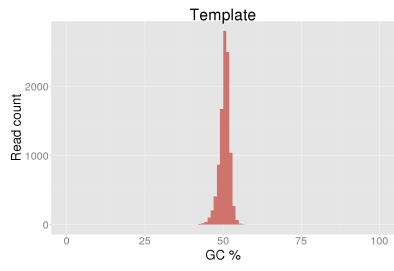
Rank	Template				Complement				2D			
	kmer	Ref %	Read %	Diff %	kmer	Ref %	Read %	Diff %	kmer	Ref %	Read %	Diff %
1	AAAAA	0.247	0.085	-0.162	CGCCA	0.288	0.087	-0.201	TTTTT	0.251	0.043	-0.208
2	TTTTT	0.251	0.092	-0.158	AAAAA	0.247	0.053	-0.194	AAAAA	0.247	0.057	-0.190
3	CGCTG	0.259	0.102	-0.157	TTTTT	0.251	0.064	-0.187	CAAAA	0.169	0.106	-0.063
4	GCTGG	0.279	0.149	-0.130	CACCA	0.184	0.051	-0.133	CGCCA	0.288	0.227	-0.061
5	CGCCA	0.288	0.166	-0.122	CCAGC	0.289	0.158	-0.131	AAAAT	0.195	0.134	-0.061
6	CCAGC	0.289	0.180	-0.108	GCCAG	0.280	0.153	-0.127	CGCTG	0.259	0.200	-0.059
7	GCCAG	0.280	0.172	-0.108	CGCTG	0.259	0.136	-0.123	TGGTG	0.185	0.128	-0.057
8	CTGGC	0.278	0.181	-0.098	CAGCA	0.261	0.138	-0.123	AAAAG	0.132	0.078	-0.054
9	CAGCA	0.261	0.170	-0.091	CTGGC	0.278	0.159	-0.119	GCCAG	0.280	0.226	-0.054
10	TGGCG	0.275	0.187	-0.088	GCGCA	0.202	0.087	-0.114	GCTGG	0.279	0.225	-0.054

Over-represented 5-mers

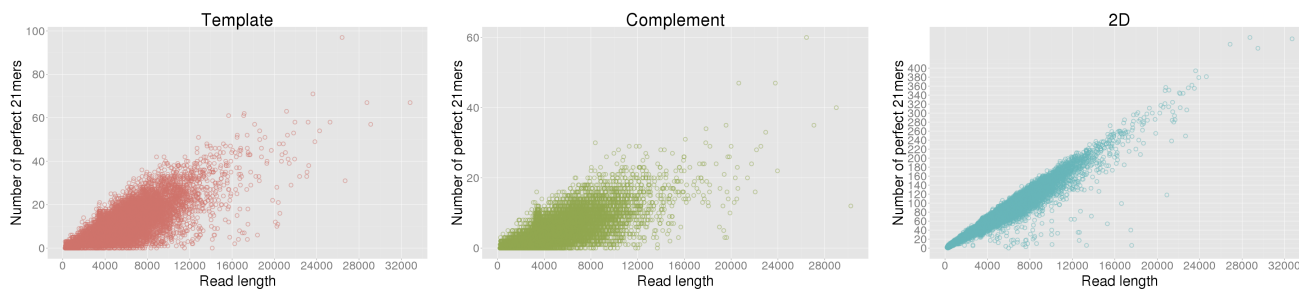
Rank	Template				Complement				2D			
	kmer	Ref %	Read %	Diff %	kmer	Ref %	Read %	Diff %	kmer	Ref %	Read %	Diff %
1	ACCCC	0.040	0.135	0.094	ACCCC	0.040	0.143	0.102	CAAAT	0.105	0.157	0.052
2	CCCCG	0.055	0.144	0.089	CCCCG	0.055	0.131	0.076	GGGGT	0.039	0.071	0.031
3	CCCCC	0.033	0.118	0.085	CTGAG	0.050	0.113	0.064	CCCAA	0.047	0.075	0.029
4	CCTAG	0.003	0.076	0.073	CCTAG	0.003	0.065	0.062	ACCGT	0.123	0.151	0.028
5	CCCCA	0.064	0.136	0.072	TACCC	0.073	0.135	0.062	CGGGG	0.054	0.082	0.028
6	TCTAC	0.048	0.116	0.068	CCCCA	0.064	0.125	0.061	GAAGG	0.094	0.121	0.027
7	CTCCC	0.040	0.108	0.068	CCTAA	0.026	0.087	0.061	GGGTC	0.040	0.067	0.026
8	GCCCC	0.062	0.128	0.066	TAGGA	0.012	0.073	0.061	CTCGT	0.042	0.069	0.026
9	TACCC	0.073	0.138	0.064	GACCC	0.040	0.100	0.060	TCCCA	0.056	0.081	0.025
10	TCCCC	0.056	0.120	0.064	TCCTA	0.013	0.073	0.060	AGGCA	0.093	0.118	0.025



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	9.28	4.70	0.00	9.07	8.85	4.98	0.00	8.34	8.59	3.95
C	8.32	0.00	9.03	10.01	9.34	0.00	8.55	9.68	9.18	0.00	11.02	9.41
G	9.42	9.03	0.00	7.95	8.99	8.73	0.00	8.81	9.21	11.12	0.00	8.47
T	4.99	9.66	8.68	0.00	5.26	8.88	8.86	0.00	4.03	8.56	8.13	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 (3.20%)	TTC (3.50%)	AAA (4.10%)	TGC (2.90%)	GGC (2.99%)	AAA (4.05%)	GCA (3.07%)	GGC (2.63%)	AAA (3.80%)
2	GCA (2.83%)	TGC (3.08%)	TTC (3.76%)	GCA (2.72%)	TGC (2.88%)	GCA (3.60%)	TTC (2.70%)	TGC (2.58%)	GCA (3.78%)
3	AAA (2.81%)	GCA (2.79%)	GCA (3.28%)	TTC (2.68%)	AAA (2.76%)	GAA (3.37%)	TCA (2.66%)	TCA (2.52%)	GAA (3.34%)
4	TGC (2.63%)	AAA (2.68%)	GAA (2.99%)	AAA (2.57%)	TTC (2.60%)	TTC (3.09%)	AAA (2.65%)	GCG (2.49%)	TTT (2.95%)
5	ATC (2.59%)	GCC (2.53%)	TTT (2.64%)	CAG (2.51%)	GCA (2.58%)	TTT (2.60%)	ATC (2.46%)	GCA (2.48%)	TTC (2.89%)
6	TCA (2.53%)	TCA (2.42%)	TGC (2.50%)	GGC (2.42%)	GAA (2.39%)	TGC (2.47%)	TGC (2.33%)	AAA (2.48%)	GCC (2.45%)
7	GCC (2.28%)	GGC (2.41%)	AAT (2.34%)	TCA (2.37%)	TCA (2.28%)	TCA (2.43%)	GAA (2.28%)	TTC (2.38%)	GCG (2.35%)
8	TTT (2.24%)	ATC (2.29%)	TCA (2.28%)	GAA (2.32%)	CAG (2.26%)	ATC (2.35%)	CAG (2.25%)	CGC (2.27%)	GTT (2.30%)
9	GGC (2.21%)	AAC (2.19%)	GCC (2.22%)	ATC (2.31%)	GCC (2.23%)	GGC (2.12%)	CGC (2.21%)	ATC (2.19%)	TCA (2.28%)
10	GAA (2.20%)	GCG (2.12%)	CAA (2.21%)	TTT (2.11%)	AAT (2.17%)	GCC (2.11%)	GCG (2.21%)	CAG (2.19%)	AAT (2.27%)
-10	AGT (0.97%)	GTA (0.96%)	GGG (0.93%)	AGA (0.99%)	CTT (0.96%)	CCC (0.93%)	CTC (1.06%)	GTA (1.00%)	CCT (0.87%)
-9	TGT (0.96%)	AGT (0.92%)	GGT (0.92%)	AGT (0.97%)	ACT (0.95%)	CTT (0.88%)	TAC (1.02%)	CCC (0.97%)	ACT (0.86%)
-8	CCC (0.93%)	CCT (0.89%)	AGA (0.84%)	CTC (0.90%)	AGT (0.94%)	AGT (0.88%)	GAG (0.94%)	CGA (0.91%)	TGA (0.84%)
-7	GGA (0.87%)	GAG (0.83%)	AGG (0.83%)	GGA (0.87%)	CCC (0.93%)	AGG (0.86%)	AGG (0.83%)	ACT (0.90%)	GAG (0.76%)
-6	AGA (0.83%)	CTT (0.79%)	AGT (0.77%)	CCC (0.85%)	CTC (0.88%)	CCT (0.80%)	CCC (0.82%)	CTT (0.84%)	CTT (0.71%)
-5	GAG (0.73%)	CGA (0.77%)	TGT (0.74%)	GAG (0.82%)	CCT (0.84%)	GGG (0.78%)	AGA (0.82%)	CCT (0.80%)	CGA (0.71%)
-4	GGG (0.73%)	GGA (0.67%)	CTT (0.73%)	AGG (0.75%)	GAG (0.84%)	ACT (0.70%)	GGA (0.79%)	AGA (0.79%)	TAG (0.52%)
-3	AGG (0.68%)	AGA (0.67%)	GAG (0.62%)	CTA (0.61%)	GGG (0.77%)	GAG (0.62%)	GGG (0.78%)	GGA (0.76%)	AGA (0.52%)
-2	CTA (0.52%)	TAG (0.54%)	TAG (0.39%)	GGG (0.60%)	TAG (0.57%)	CTA (0.47%)	CTA (0.61%)	CTA (0.74%)	GGA (0.47%)
-1	TAG (0.42%)	CTA (0.54%)	CTA (0.38%)	TAG (0.46%)	CTA (0.55%)	TAG (0.38%)	TAG (0.53%)	TAG (0.68%)	CTA (0.45%)

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 (1.01%)	TTTC (1.13%)	AAAA (1.39%)	CAGC (0.96%)	TGGC (1.06%)	AAAA (1.08%)	ATCA (0.97%)	TGGC (0.93%)	GGCA (1.21%)
2	AAAA (0.90%)	TGCC (0.95%)	TTTT (1.30%)	ATCA (0.93%)	CGGC (1.06%)	CAAA (1.05%)	GGCA (0.83%)	CAGC (0.85%)	AAAA (1.12%)
3	ATCA (0.88%)	TGCC (0.91%)	GAAA (1.14%)	CTGC (0.90%)	CAGC (1.03%)	TGAA (1.00%)	GCCA (0.83%)	TTCA (0.84%)	TTTT (1.00%)
4	GAAA (0.88%)	TTGC (0.90%)	GGCA (0.96%)	CGGC (0.86%)	TTGC (0.90%)	ATCA (0.96%)	CGCA (0.79%)	ATCA (0.83%)	TGAA (0.99%)
5	TTCA (0.83%)	TTCA (0.88%)	TTTT (0.92%)	TGGC (0.84%)	CTGC (0.89%)	GAAA (0.94%)	CAGC (0.77%)	CGGC (0.80%)	GGAA (0.95%)
6	TGCC (0.81%)	CTGC (0.88%)	GCAA (0.91%)	CCAG (0.82%)	ATCA (0.82%)	AGCA (0.94%)	CGCC (0.77%)	CTGC (0.74%)	GAAA (0.94%)
7	GGCA (0.81%)	CAGC (0.86%)	GTTT (0.90%)	TTGC (0.82%)	CAAA (0.82%)	GGCA (0.93%)	CCAG (0.77%)	TTGC (0.73%)	TTTT (0.90%)
8	TTTT (0.79%)	TTCC (0.84%)	GGAA (0.88%)	ATGC (0.76%)	TTCC (0.77%)	AGAA (0.90%)	AACA (0.77%)	GGCG (0.72%)	TGCA (0.89%)
9	CAGC (0.79%)	AAAA (0.82%)	TGCC (0.84%)	CAAA (0.76%)	TGCC (0.76%)	TAAA (0.88%)	CAAA (0.74%)	TGCC (0.72%)	CGCC (0.88%)
10	TTGC (0.77%)	CGCC (0.82%)	AAAT (0.83%)	TGAA (0.70%)	TTCA (0.75%)	TTTT (0.88%)	TTCA (0.74%)	CAAA (0.71%)	CGCA (0.86%)
-10	TCTA (0.12%)	GGAC (0.13%)	TTAG (0.11%)	CGAG (0.12%)	CCTC (0.12%)	GGAC (0.11%)	GAGG (0.15%)	CCCC (0.15%)	TGGA (0.11%)
-9	CTAA (0.12%)	TCTA (0.13%)	ACTA (0.10%)	GTGT (0.11%)	CTAA (0.11%)	ACTA (0.11%)	GAGA (0.15%)	CTAT (0.14%)	TCTA (0.10%)
-8	TAGT (0.12%)	CTAT (0.13%)	CGAG (0.09%)	CTAA (0.11%)	TAGA (0.11%)	GTGT (0.10%)	GGGA (0.15%)	GAGA (0.14%)	ACTT (0.10%)
-7	GAGG (0.12%)	TAGT (0.11%)	TAGT (0.09%)	GAGG (0.11%)	CCCC (0.11%)	ACCT (0.10%)	CTAT (0.13%)	ACCT (0.14%)	CGGA (0.10%)
-6	TTAG (0.11%)	CGGA (0.11%)	GGAC (0.09%)	TAGA (0.11%)	ACCT (0.11%)	CGAG (0.09%)	TCTA (0.13%)	CTAA (0.13%)	GGGA (0.09%)
-5	GGAC (0.10%)	CTAA (0.10%)	TAGA (0.08%)	GGAC (0.10%)	GTGT (0.11%)	CTAT (0.09%)	CTAA (0.13%)	TAGG (0.11%)	CTAT (0.09%)
-4	TAGA (0.07%)	TAGG (0.08%)	TCTA (0.08%)	CCCT (0.09%)	CCCT (0.08%)	TAGG (0.07%)	TAGA (0.08%)	CCCT (0.11%)	TAGG (0.08%)
-3	CCTA (0.07%)	CCTA (0.06%)	TAGG (0.06%)	CCTA (0.08%)	TAGG (0.08%)	CCTA (0.06%)	CCTA (0.08%)	CCTA (0.10%)	TAGA (0.05%)
-2	TAGG (0.05%)	TAGA (0.06%)	CCTA (0.04%)	TAGG (0.06%)	CCTA (0.07%)	CCCT (0.06%)	TAGG (0.06%)	TAGA (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%)

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%)	CTGGC (0.37%)	GAAAA (0.44%)	CAGCA (0.39%)	CAGCA (0.39%)	CAGCA (0.53%)	CAGCA (0.37%)	CTGGC (0.38%)	CAGCA (0.43%)
2	CTGGC (0.32%)	CAGCA (0.36%)	CAGCA (0.39%)	CATCA (0.33%)	CTGGC (0.39%)	CGGCA (0.36%)	CGCCA (0.35%)	CAGCA (0.31%)	CGGCA (0.42%)
3	TTATC (0.32%)	CGCCA (0.33%)	CAAAA (0.38%)	GCTGC (0.32%)	GCGGC (0.36%)	GAAAA (0.34%)	CGGCA (0.31%)	CATCA (0.30%)	TGGCA (0.41%)
4	CGCCA (0.31%)	TTGCC (0.33%)	TGGCA (0.32%)	CCAGC (0.31%)	CCAGC (0.32%)	CAGAA (0.34%)	CTGGC (0.29%)	GCGGC (0.30%)	GAAAA (0.37%)
5	CATCA (0.31%)	TTTGC (0.32%)	TGTTT (0.32%)	CTGGC (0.31%)	CATCA (0.32%)	AATCA (0.34%)	GCCAG (0.29%)	CGCCA (0.29%)	ATTTT (0.32%)
6	CAAAA (0.29%)	GCCAG (0.31%)	CGTTT (0.31%)	GCGGC (0.30%)	TCAGC (0.30%)	ATAAA (0.34%)	CATCA (0.28%)	TTTTA (0.28%)	CAAAA (0.30%)
7	TTTTT (0.29%)	ATTTT (0.30%)	GCCAG (0.31%)	AATCA (0.29%)	TTTTT (0.30%)	CATCA (0.34%)	TGGCA (0.27%)	TGGCG (0.28%)	TTGCC (0.30%)
8	CGTTT (0.29%)	GCTGC (0.30%)	AGAAA (0.31%)	CGGCA (0.28%)	GCTGC (0.30%)	AAGAA (0.33%)	GCAAA (0.27%)	GCCAG (0.28%)	GCGCA (0.29%)
9	GAAAA (0.28%)	TTTTA (0.30%)	GCAAA (0.31%)	GATGC (0.28%)	AATCA (0.30%)	GCAAA (0.32%)	GATCA (0.27%)	CCAGC (0.27%)	TGGCG (0.28%)
10	TGGCA (0.28%)	CATCA (0.30%)	ATTTT (0.30%)	GCCGC (0.28%)	GATGC (0.29%)	TTATC (0.31%)	GCGCA (0.27%)	GATGC (0.25%)	CGCCA (0.28%)
-10	GGACC (0.01%)	TAGGG (0.01%)	CTTAG (0.01%)	GGGGG (0.01%)	CCCTA (0.01%)	ACCTA (0.01%)	CCCTA (0.01%)	TCCTA (0.02%)	TAGGA (0.01%)
-9	CCCTA (0.01%)	ACCTA (0.01%)	CCCTA (0.01%)	CCCTA (0.01%)	CTAGC (0.01%)	CCCTT (0.01%)	TAGGA (0.01%)	TAGGA (0.01%)	GCTAG (0.01%)
-8	CTAGT (0.00%)	GCTAG (0.01%)	GCTAG (0.00%)	GCTAG (0.01%)	GCTAG (0.01%)	CTAGC (0.01%)	GCTAG (0.01%)	GCTAG (0.01%)	TTAGA (0.01%)
-7	GCTAG (0.00%)	CTAGC (0.00%)	CTAGC (0.00%)	CTAGT (0.01%)	CCCCC (0.01%)	GCTAG (0.00%)	CCTAG (0.00%)	ACTAG (0.01%)	CTAGC (0.00%)
-6	CTAGC (0.00%)	ACTAG (0.00%)	ACTAG (0.00%)	CTAGC (0.01%)	CTAGT (0.00%)	CTAGA (0.00%)	CTAGC (0.00%)	CTAGC (0.01%)	CTAGG (0.00%)
-5	CCTAG (0.00%)	CTAGT (0.00%)	CTAGT (0.00%)	CTAGA (0.00%)	CTAGA (0.00%)	ACTAG (0.00%)	ACTAG (0.00%)	CTAGT (0.00%)	CTAGT (0.00%)
-4	ACTAG (0.00%)	CTAGG (0.00%)	CTAGG (0.00%)	ACTAG (0.00%)	ACTAG (0.00%)	CTAGT (0.00%)	CTAGT (0.00%)	TCTAG (0.00%)	ACTAG (0.00%)
-3	CTAGG (0.00%)	TCTAG (0.00%)	CCTAG (0.00%)	CTAGG (0.00%)	CCTAG (0.00%)	CTAGG (0.00%)	CTAGG (0.00%)	CTAGA (0.00%)	CCTAG (0.00%)
-2	CTAGA (0.00%)	CTAGA (0.00%)	CTAGA (0.00%)	CCTAG (0.00%)	CTAGC (0.00%)	TCTAG (0.00%)	TCTAG (0.00%)	CTAGC (0.00%)	TCTAG (0.00%)
-1	TCTAG (0.00%)	CCTAG (0.00%)	TCTAG (0.00%)	TCTAG (0.00%)	TCTAG (0.00%)	CCTAG (0.00%)	CTAGA (0.00%)	CCTAG (0.00%)	CTAGA (0.00%)

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