

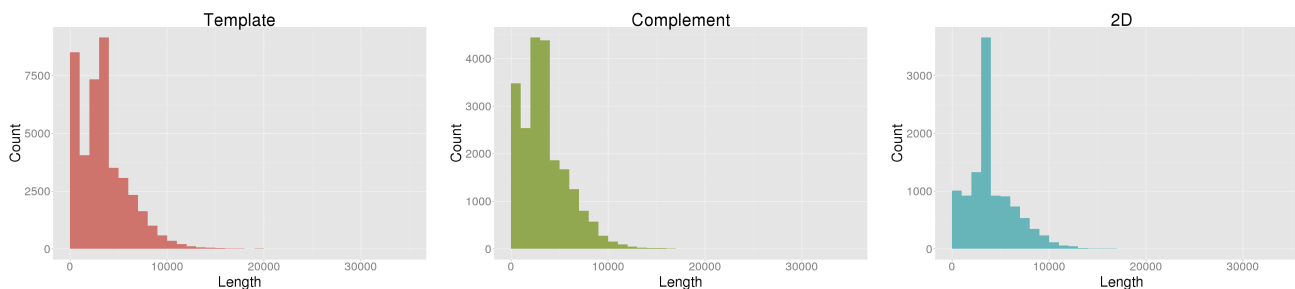
NanoOK report for ZF-screens_MARC_phase_1a_e_coli_run1

Pass and fail counts

Type	Pass	Fail
Template	0	42240
Complement	0	21712
2D	0	10858

Read lengths

Type	NumReads	TotalBases	Mean	Longest	Shortest	N50	N50Count	N90	N90Count
Template	42240	150713664	3568.03	449250	6	4999	9665	2488	27194
Complement	21712	77520815	3570.41	340137	11	4847	5273	2349	14633
2D	10858	44220237	4072.60	30921	122	5033	3004	2859	7912



Template alignments

Number of reads	42240
Number of reads with alignments	19835 (46.96%)
Number of reads without alignments	22405 (53.04%)

ID	Size	Number of Reads	% of Reads	Mean read length	Aligned bases	Mean coverage	Longest Perf Kmer
Control sequence	3560	7718	18.27	2951.98	21411529	6014.47	63
Escherichia coli	4641652	12117	28.69	5499.03	59043707	12.72	66

Complement alignments

Number of reads	21712
Number of reads with alignments	11048 (50.88%)
Number of reads without alignments	10664 (49.12%)

ID	Size	Number of Reads	% of Reads	Mean read length	Aligned bases	Mean coverage	Longest Perf Kmer
Control sequence	3560	4053	18.67	2764.51	9247595	2597.64	52
Escherichia coli	4641652	6995	32.22	5404.19	31670134	6.82	72

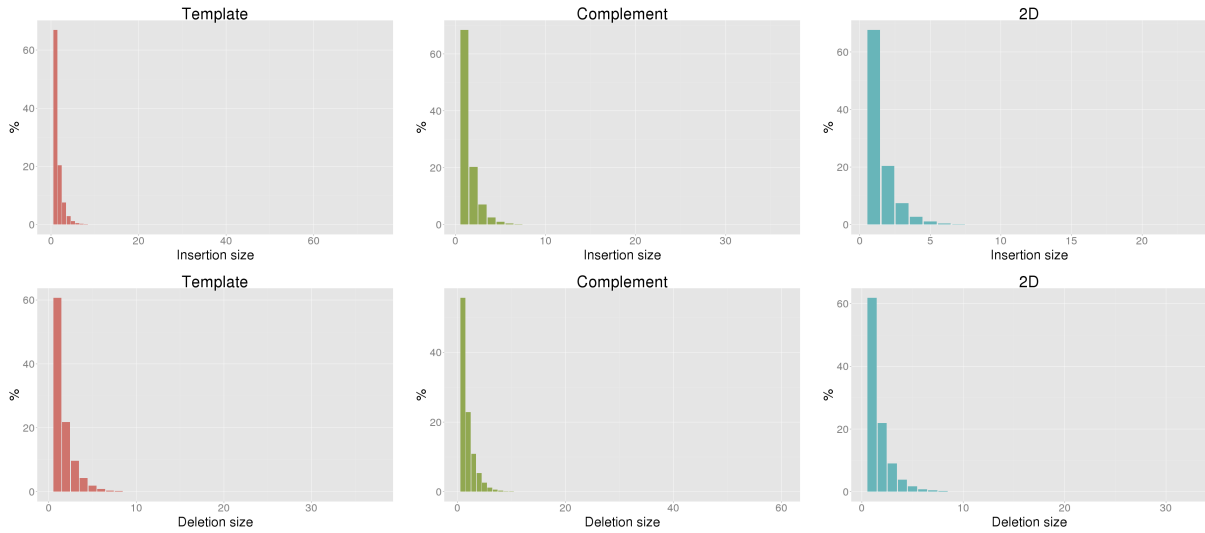
2D alignments

Number of reads	10858
Number of reads with alignments	8823 (81.26%)
Number of reads without alignments	2035 (18.74%)

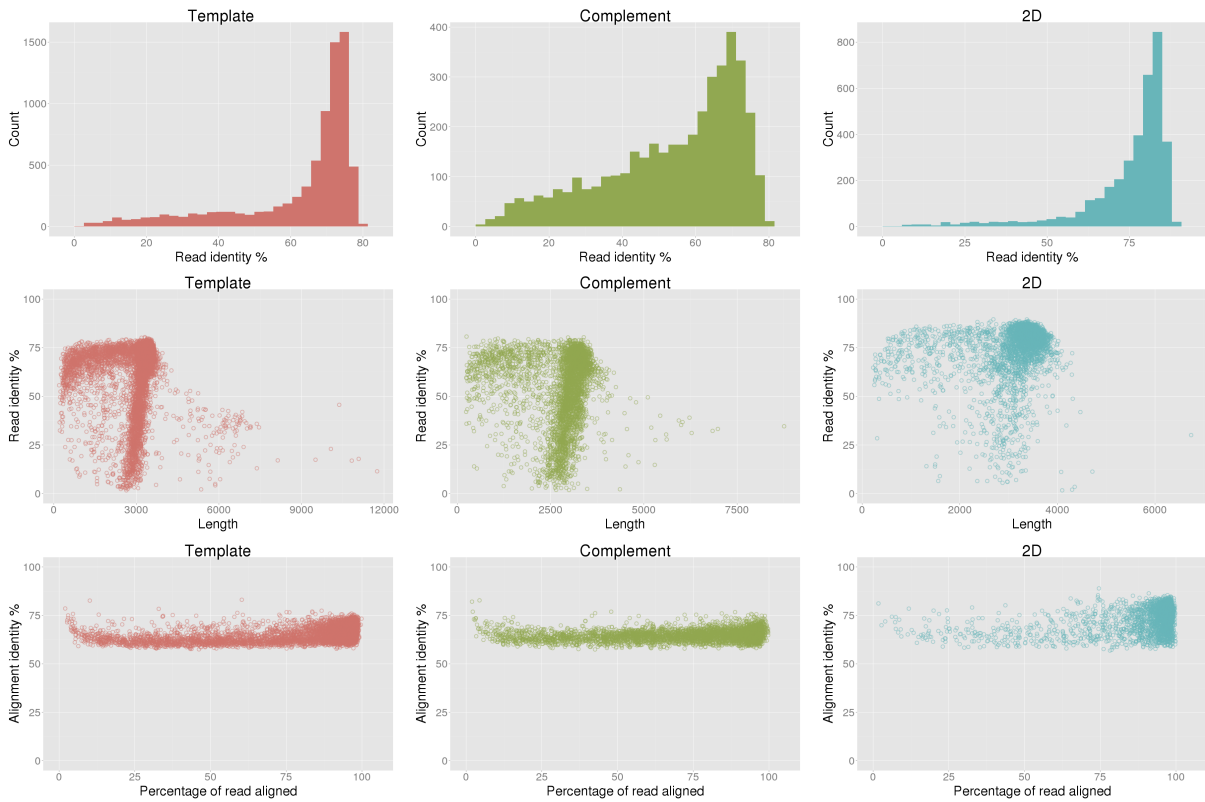
ID	Size	Number of Reads	% of Reads	Mean read length	Aligned bases	Mean coverage	Longest Perf Kmer
Control sequence	3560	3620	33.34	3117.51	11344153	3186.56	167
Escherichia coli	4641652	5203	47.92	5394.57	28221949	6.08	182

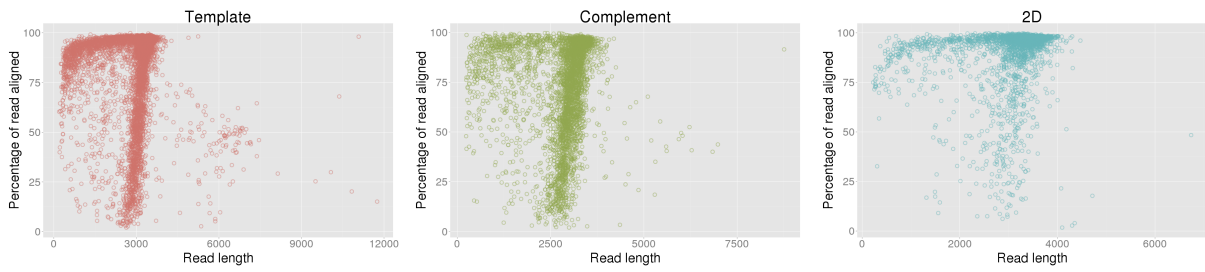
Control sequence error analysis

	Template	Complement	2D
Overall base identity (excluding indels)	62.58%	53.43%	75.16%
Aligned base identity (excluding indels)	79.67%	79.66%	86.51%
Identical bases per 100 aligned bases (including indels)	66.59%	64.74%	74.77%
Inserted bases per 100 aligned bases (including indels)	4.79%	4.03%	4.59%
Deleted bases per 100 aligned bases (including indels)	11.62%	14.70%	8.98%
Substitutions per 100 aligned bases (including indels)	17.00%	16.53%	11.66%
Mean insertion size	1.56	1.50	1.53
Mean deletion size	1.72	1.87	1.69

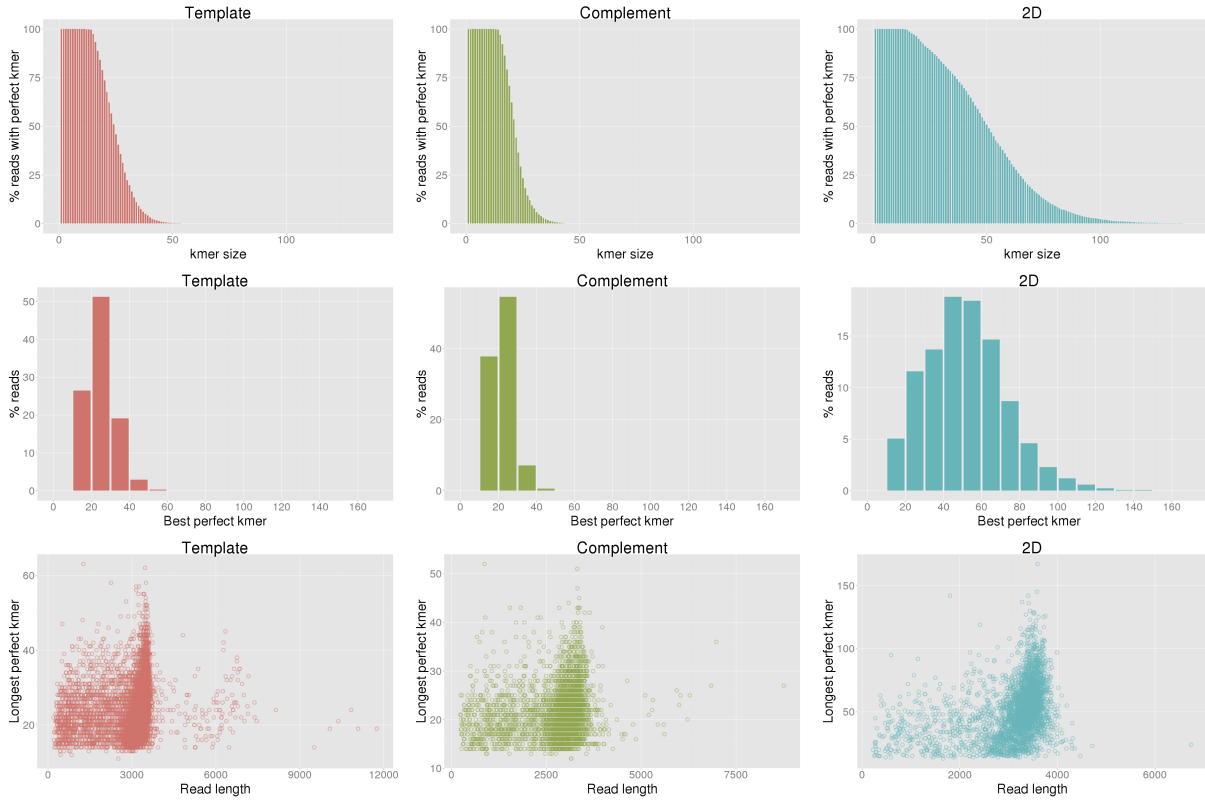


Control sequence read identity

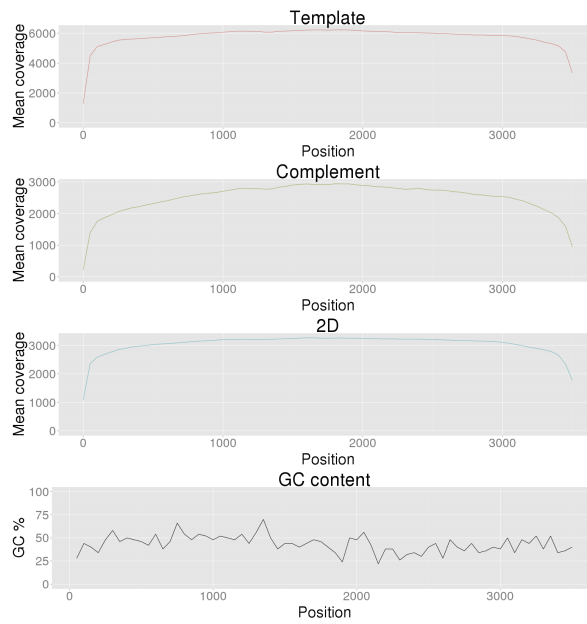




Control sequence perfect kmers



Control sequence coverage



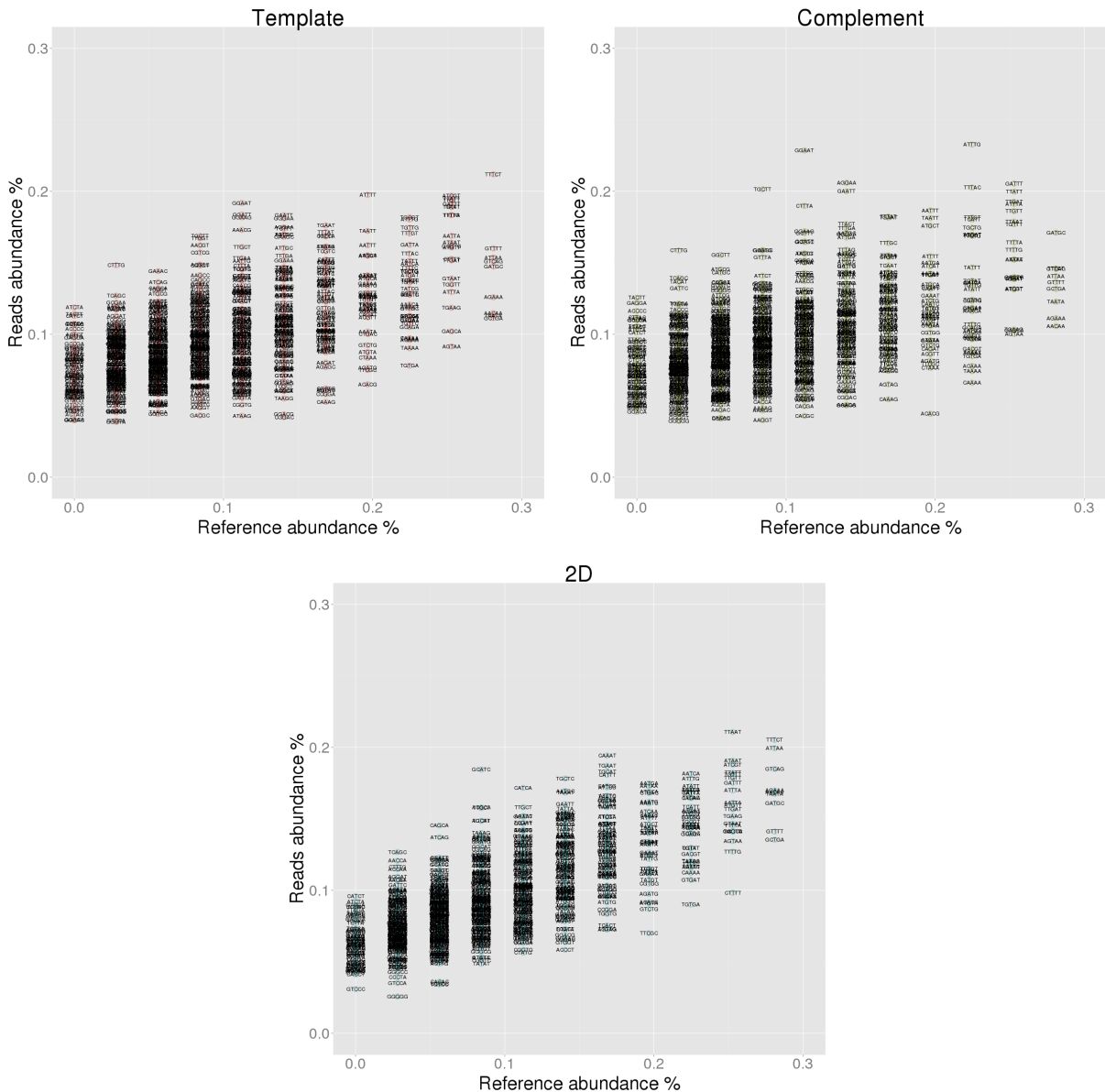
Control sequence 5-mer analysis

Under-represented 5-mers

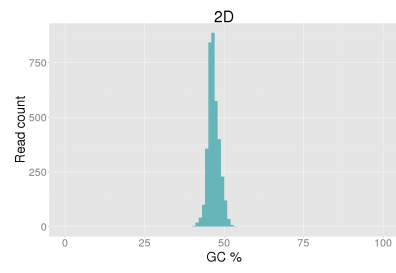
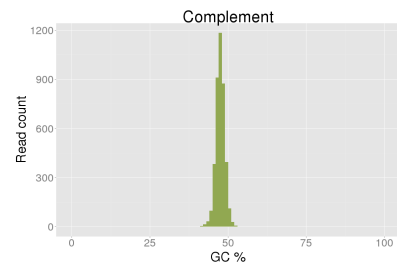
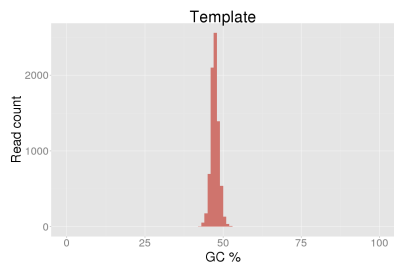
Rank	Template				Complement				2D			
	kmer	Ref %	Read %	Diff %	kmer	Ref %	Read %	Diff %	kmer	Ref %	Read %	Diff %
1	TTTTT	0.759	0.126	-0.633	TTTTT	0.759	0.077	-0.681	TTTTT	0.759	0.045	-0.714
2	AAAAA	0.478	0.091	-0.387	AAAAA	0.478	0.045	-0.433	AAAAA	0.478	0.047	-0.430
3	TGATG	0.393	0.136	-0.257	AAAAC	0.337	0.100	-0.237	TGATG	0.393	0.156	-0.238
4	AAAAC	0.337	0.120	-0.217	TGATG	0.393	0.177	-0.216	AAAAC	0.337	0.143	-0.194
5	GATGT	0.309	0.098	-0.211	GATGT	0.309	0.102	-0.207	GATGT	0.309	0.124	-0.185
6	CTGAT	0.309	0.110	-0.199	GCAAT	0.309	0.126	-0.183	CTGAT	0.309	0.140	-0.169
7	AATAT	0.309	0.134	-0.175	TTATC	0.309	0.133	-0.176	CTTTT	0.253	0.098	-0.155
8	GCAAT	0.309	0.135	-0.174	AACAA	0.281	0.106	-0.175	TTATC	0.309	0.157	-0.152
9	GCTGA	0.281	0.111	-0.170	AATAT	0.309	0.139	-0.170	GCTGA	0.281	0.135	-0.146
10	TAATA	0.281	0.113	-0.168	AGAAA	0.281	0.111	-0.170	GCAAT	0.309	0.164	-0.145

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	CTTTG	0.028	0.159	0.130	GCATC	0.084	0.185	0.100
2	ATCTA	0.000	0.119	0.119	TACTT	0.000	0.126	0.126	TCAGC	0.028	0.127	0.099
3	TACTT	0.000	0.114	0.114	GAGGA	0.000	0.122	0.122	CATCT	0.000	0.096	0.096
4	CACTC	0.000	0.113	0.113	TGCTT	0.084	0.201	0.117	AACCA	0.028	0.121	0.093
5	CCCCA	0.000	0.108	0.108	ACCCC	0.000	0.116	0.116	ATCTA	0.000	0.092	0.092
6	GCTCC	0.000	0.107	0.107	GGAAT	0.112	0.229	0.116	GTCGA	0.000	0.090	0.090
7	TCTAC	0.000	0.107	0.107	CTTAC	0.000	0.112	0.112	CAGCA	0.056	0.145	0.089
8	ACCCC	0.000	0.104	0.104	TCAGC	0.028	0.139	0.111	CCCGC	0.000	0.089	0.089
9	ACTCT	0.000	0.100	0.100	TATAC	0.000	0.111	0.111	TCTAC	0.000	0.088	0.088
10	TCAGC	0.028	0.127	0.099	GCCGA	0.000	0.110	0.110	CTTTG	0.028	0.116	0.088

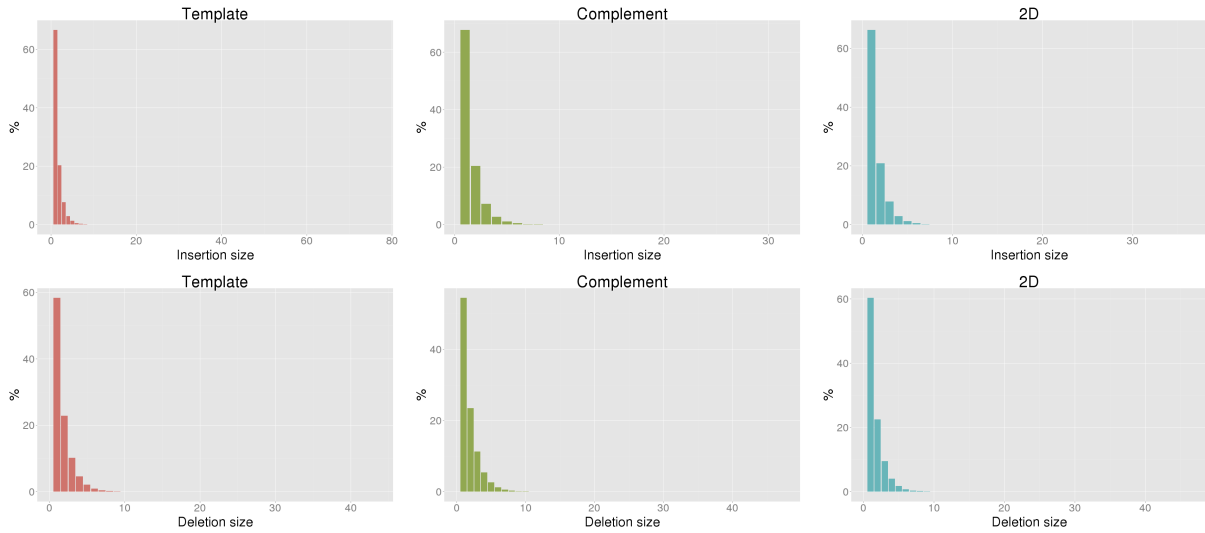


Control sequence GC content

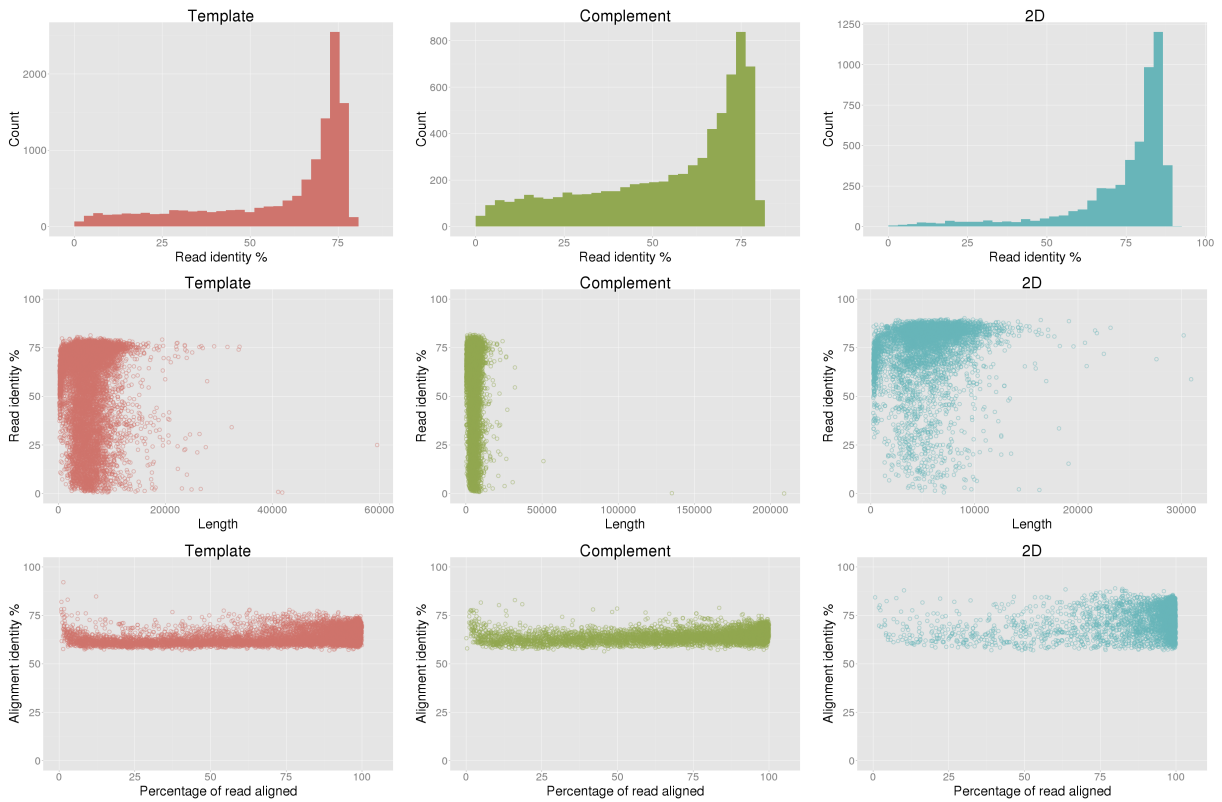


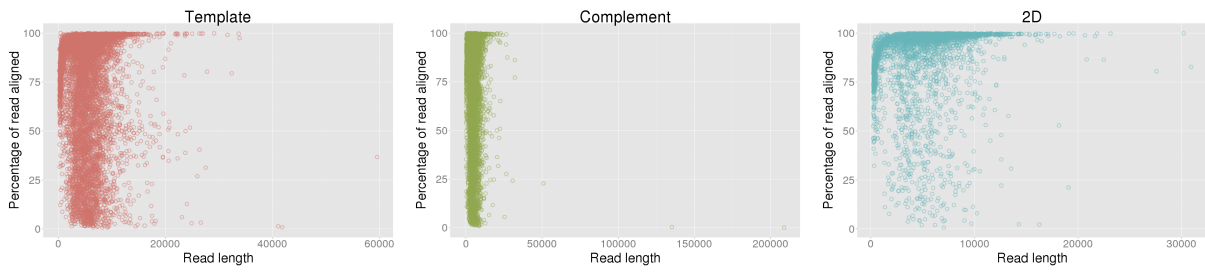
Escherichia coli error analysis

	Template	Complement	2D
Overall base identity (excluding indels)	57.87%	54.03%	75.22%
Aligned base identity (excluding indels)	78.99%	79.84%	86.66%
Identical bases per 100 aligned bases (including indels)	65.31%	64.49%	74.81%
Inserted bases per 100 aligned bases (including indels)	4.78%	4.11%	4.60%
Deleted bases per 100 aligned bases (including indels)	12.54%	15.12%	9.08%
Substitutions per 100 aligned bases (including indels)	17.37%	16.28%	11.51%
Mean insertion size	1.57	1.53	1.56
Mean deletion size	1.76	1.90	1.72

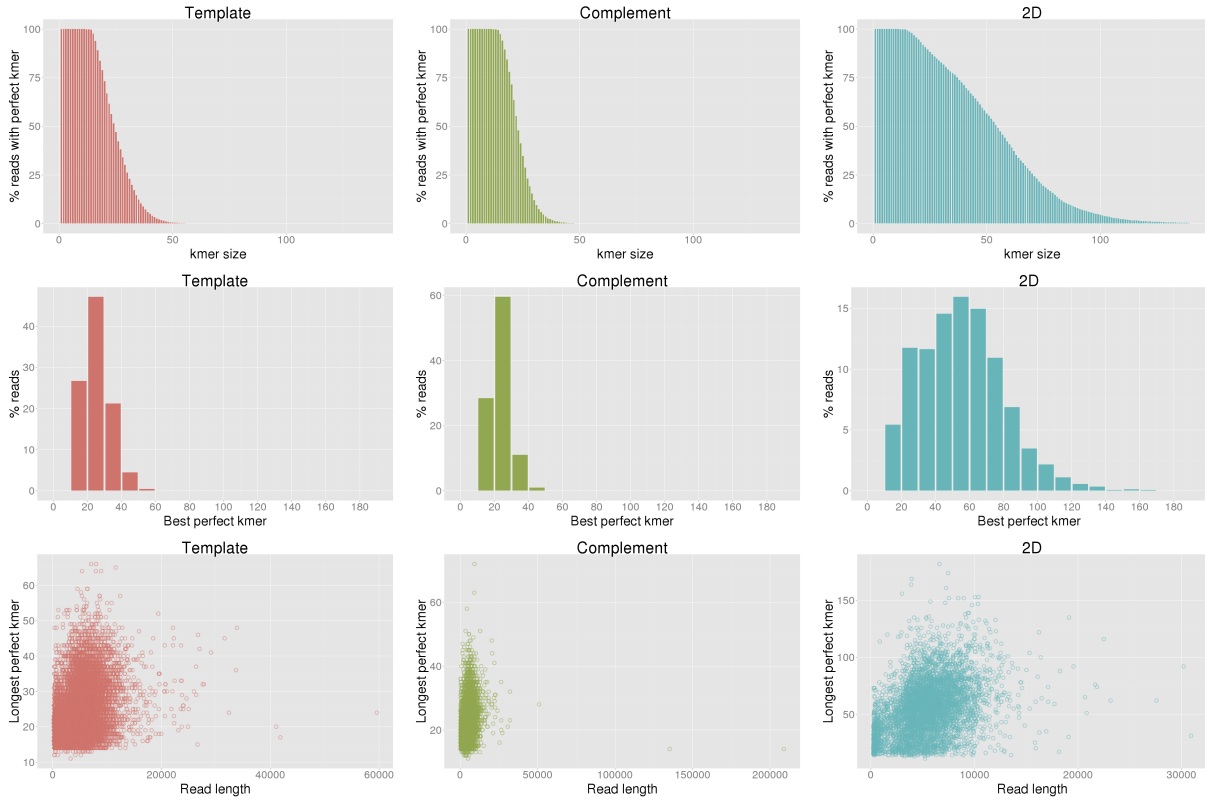


Escherichia coli read identity

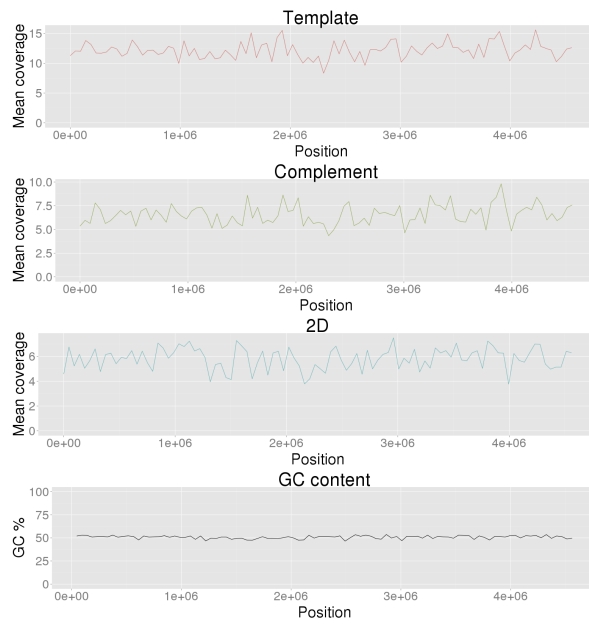




Escherichia coli perfect kmers



Escherichia coli coverage



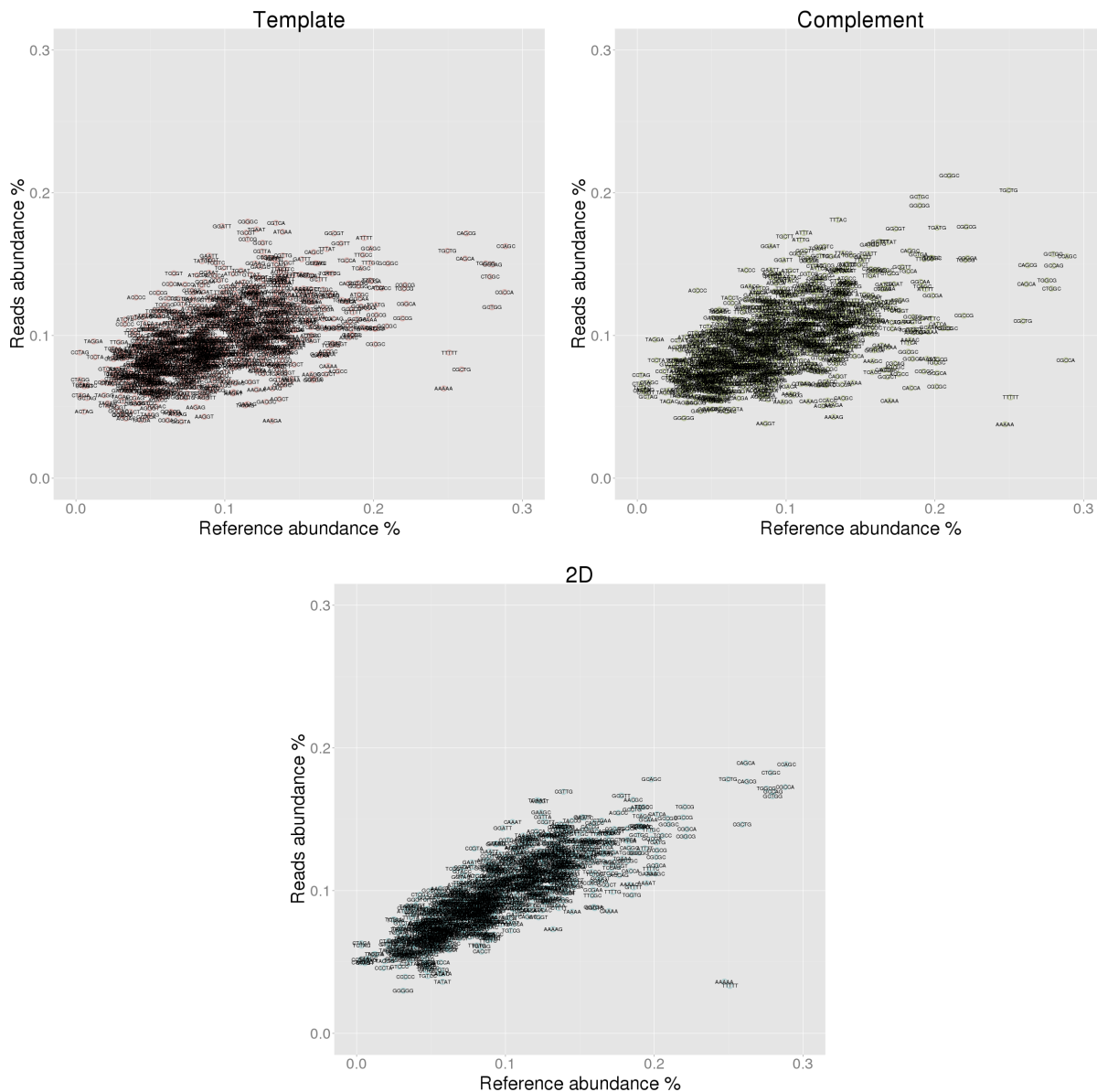
Escherichia coli 5-mer analysis

Under-represented 5-mers

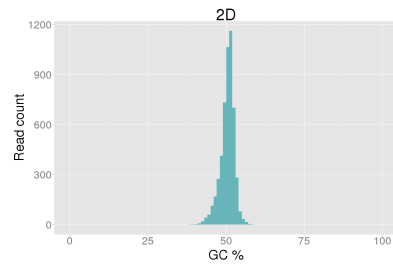
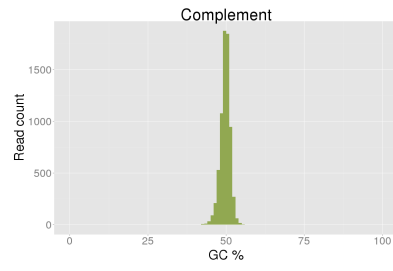
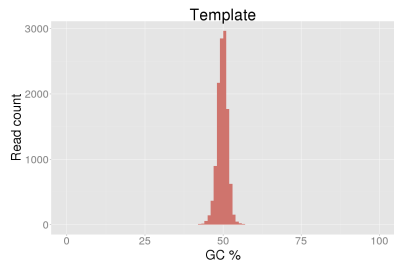
Rank	Template				Complement				2D			
	kmer	Ref %	Read %	Diff %	kmer	Ref %	Read %	Diff %	kmer	Ref %	Read %	Diff %
1	AAAAA	0.247	0.063	-0.184	AAAAA	0.247	0.038	-0.209	TTTTT	0.251	0.033	-0.218
2	CGCTG	0.259	0.076	-0.183	CGCCA	0.288	0.083	-0.205	AAAAA	0.247	0.036	-0.211
3	TTTTT	0.251	0.088	-0.163	TTTTT	0.251	0.057	-0.194	CGCCA	0.288	0.173	-0.115
4	GCTGG	0.279	0.120	-0.160	CGCTG	0.259	0.110	-0.149	GCTGG	0.279	0.166	-0.113
5	CGCCA	0.288	0.130	-0.158	CTGGC	0.278	0.133	-0.145	CGCTG	0.259	0.146	-0.113
6	CTGGC	0.278	0.141	-0.137	CGCGC	0.201	0.064	-0.137	GCCAG	0.280	0.170	-0.110
7	GCCAG	0.280	0.150	-0.130	TGGCG	0.275	0.139	-0.137	TGGCG	0.275	0.172	-0.104
8	CCAGC	0.289	0.163	-0.126	CCAGC	0.289	0.156	-0.133	CCAGC	0.289	0.189	-0.100
9	TGGCG	0.275	0.151	-0.125	GCCAG	0.280	0.149	-0.131	CTGGC	0.278	0.183	-0.096
10	CAGCA	0.261	0.154	-0.108	GCGCA	0.202	0.074	-0.128	AAAAT	0.195	0.105	-0.090

Over-represented 5-mers

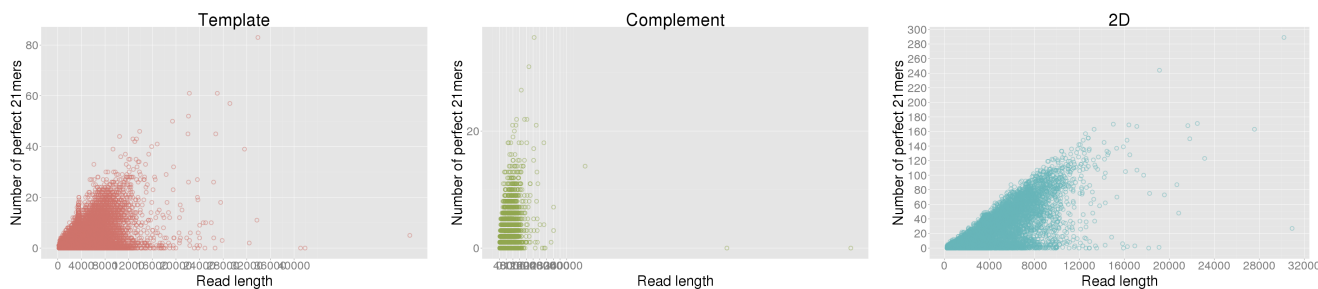
Rank	Template				Complement				2D			
	kmer	Ref %	Read %	Diff %	kmer	Ref %	Read %	Diff %	kmer	Ref %	Read %	Diff %
1	ACCCC	0.040	0.127	0.086	ACCCC	0.040	0.132	0.091	CTAGA	0.003	0.063	0.060
2	CCTAG	0.003	0.088	0.085	TAGGA	0.012	0.097	0.085	TCTAG	0.003	0.061	0.058
3	TAGGA	0.012	0.096	0.084	GGAAT	0.089	0.163	0.073	TCTAA	0.025	0.080	0.055
4	GGATT	0.098	0.177	0.078	TACCC	0.073	0.146	0.072	CTCGT	0.042	0.097	0.055
5	ATCTA	0.033	0.111	0.078	TGCTT	0.099	0.169	0.070	CCTCC	0.033	0.088	0.055
6	TCCGT	0.066	0.144	0.078	TCCTA	0.013	0.083	0.070	TAGAT	0.035	0.089	0.054
7	CCCCC	0.033	0.108	0.075	CCTAG	0.003	0.072	0.070	GGGTC	0.040	0.094	0.053
8	CCCCG	0.055	0.130	0.075	CCTAT	0.028	0.097	0.069	ATCTA	0.033	0.085	0.053
9	CTCCC	0.040	0.113	0.073	ATCTA	0.033	0.099	0.066	TTAGA	0.026	0.079	0.053
10	CCCCA	0.064	0.136	0.072	ACCTA	0.027	0.092	0.065	CCGTA	0.079	0.130	0.051



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	9.36	9.21	5.16	0.00	9.22	8.82	5.36	0.00	9.47	8.92	4.84
C	8.23	0.00	8.56	9.35	8.68	0.00	8.28	9.21	8.34	0.00	9.56	8.37
G	9.14	8.72	0.00	7.98	8.58	8.60	0.00	8.67	8.45	9.90	0.00	8.18
T	5.62	9.55	9.14	0.00	5.78	9.41	9.39	0.00	5.11	9.29	9.56	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 (3.46%)	AAA (4.44%)	AAA (2.92%)	AAA (3.06%)	AAA (4.42%)	AAA (3.17%)	AAA (2.88%)	AAA (4.19%)	Most common
2	AAA (2.94%)	TGC (3.06%)	TTC (3.56%)	TTC (2.88%)	TGC (2.88%)	GCA (3.42%)	GCA (3.06%)	TGC (2.71%)	GCA (3.47%)	
3	GCA (2.76%)	AAA (2.97%)	GCA (3.22%)	TGC (2.81%)	TTC (2.75%)	GAA (3.38%)	TTC (2.79%)	GCA (2.55%)	GAA (3.15%)	
4	TGC (2.64%)	GCA (2.78%)	GAA (3.09%)	GCA (2.74%)	GCA (2.66%)	TTC (3.11%)	TCA (2.60%)	GAA (2.47%)	TTT (3.00%)	
5	ATC (2.58%)	TCA (2.37%)	TTT (2.84%)	GAA (2.52%)	GAA (2.61%)	TTT (2.67%)	GAA (2.57%)	TTC (2.43%)	TTC (2.86%)	
6	TCA (2.56%)	GAA (2.36%)	AAT (2.76%)	TCA (2.40%)	GGC (2.48%)	AAT (2.53%)	AAT (2.49%)	TCA (2.43%)	AAT (2.84%)	
7	TTT (2.55%)	AAT (2.31%)	TGC (2.46%)	AAT (2.39%)	AAT (2.40%)	TCA (2.43%)	TGC (2.35%)	CAG (2.21%)	GTT (2.65%)	
8	AAT (2.41%)	ATC (2.22%)	TCA (2.40%)	ATC (2.34%)	TCA (2.32%)	TGC (2.41%)	TTT (2.32%)	GCG (2.17%)	TCA (2.33%)	
9	GAA (2.33%)	GCC (2.22%)	CAA (2.37%)	TTT (2.33%)	CAG (2.20%)	CAA (2.30%)	ATC (2.30%)	GCC (2.14%)	GCC (2.12%)	
10	GCC (2.02%)	AAC (2.14%)	ATC (2.12%)	CAG (2.23%)	ATC (2.13%)	ATC (2.13%)	GCG (2.05%)	ATC (2.09%)	TGC (2.10%)	
										Least common
-10	CTC (0.96%)	ACT (0.95%)	CGA (0.89%)	AGA (0.98%)	GGA (0.95%)	AGT (0.90%)	CTT (0.98%)	GTA (1.02%)	GTA (0.97%)	
-9	CGA (0.93%)	GGG (0.94%)	AGA (0.88%)	CGA (0.97%)	AGG (0.93%)	CTT (0.90%)	CGA (0.96%)	GGG (1.00%)	CCC (0.97%)	
-8	GGA (0.89%)	AGT (0.89%)	GGT (0.86%)	GGA (0.86%)	CCT (0.92%)	CCT (0.86%)	GAG (0.90%)	CCT (0.96%)	ACT (0.90%)	
-7	AGA (0.85%)	GAG (0.88%)	AGG (0.85%)	CTC (0.82%)	CGA (0.91%)	CTC (0.86%)	AGA (0.86%)	AGA (0.92%)	GAG (0.86%)	
-6	CCC (0.85%)	CTT (0.85%)	GGG (0.83%)	CCC (0.78%)	CTC (0.89%)	ACT (0.80%)	GGA (0.85%)	ACT (0.88%)	CTT (0.82%)	
-5	GAG (0.82%)	AGA (0.76%)	AGT (0.79%)	AGG (0.75%)	ACT (0.89%)	AGG (0.79%)	AGG (0.78%)	CTT (0.87%)	CGA (0.73%)	
-4	AGG (0.70%)	CGA (0.76%)	CTT (0.78%)	GAG (0.75%)	GAG (0.89%)	GGG (0.75%)	CCC (0.78%)	CGA (0.83%)	GGA (0.71%)	
-3	GGG (0.69%)	GGA (0.73%)	GAG (0.72%)	GGG (0.60%)	GGG (0.75%)	GAG (0.65%)	GGG (0.69%)	GGA (0.79%)	AGA (0.68%)	
-2	CTA (0.55%)	TAG (0.61%)	TAG (0.44%)	CTA (0.58%)	TAG (0.61%)	TAG (0.42%)	TAG (0.62%)	TAG (0.71%)	TAG (0.55%)	
-1	TAG (0.50%)	CTA (0.52%)	CTA (0.37%)	TAG (0.49%)	CTA (0.47%)	CTA (0.42%)	CTA (0.62%)	CTA (0.64%)	CTA (0.44%)	

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 (1.22%)	AAAA (1.58%)	CAAA (0.89%)	CAAA (0.96%)	CAAA (1.25%)	CAAA (0.96%)	CAAA (0.86%)	AAAA (1.26%)
2	TTTT (0.97%)	TTGC (0.91%)	TTTT (1.28%)	CTGC (0.85%)	TGGC (0.93%)	AAAA (1.24%)	GAAA (0.87%)	GGAA (0.86%)	GAAA (1.07%)
3	GAAA (0.93%)	TTCA (0.89%)	GAAA (1.20%)	ATCA (0.85%)	TTGC (0.92%)	GAAA (1.02%)	AACA (0.83%)	TTCA (0.83%)	TGCA (1.03%)
4	AAAA (0.92%)	GAAA (0.88%)	TTTT (1.03%)	TTGC (0.82%)	CTGC (0.88%)	TGAA (1.00%)	TGCA (0.82%)	TGGC (0.80%)	GGCA (1.00%)
5	TTCA (0.87%)	AAAA (0.87%)	GCAA (0.97%)	AAAA (0.78%)	CAGC (0.88%)	AGAA (0.95%)	ATCA (0.80%)	ATGC (0.80%)	CAAA (0.97%)
6	TTGC (0.84%)	TGCC (0.86%)	CAAA (0.94%)	GAAA (0.77%)	CGGC (0.86%)	AGCA (0.93%)	AAAA (0.79%)	ATCA (0.77%)	GGAA (0.96%)
7	ATCA (0.83%)	CTGC (0.86%)	TGAA (0.90%)	CAGC (0.76%)	TTCC (0.82%)	TTTC (0.91%)	TTCA (0.79%)	CAGC (0.77%)	TGTT (0.92%)
8	GTTT (0.80%)	TTCC (0.86%)	GTTT (0.89%)	TTTC (0.76%)	TTCA (0.80%)	TAAA (0.91%)	TGAA (0.79%)	GAAA (0.76%)	TTTC (0.91%)
9	AACG (0.79%)	TGGC (0.81%)	TGCA (0.88%)	ATTC (0.76%)	AGCA (0.79%)	ATCA (0.88%)	GGCA (0.77%)	AGCA (0.76%)	TTTT (0.91%)
10	TGCA (0.79%)	ATGC (0.79%)	AAAT (0.87%)	TGGC (0.75%)	TTTC (0.79%)	TGCA (0.86%)	TTTC (0.76%)	CTGC (0.76%)	CGTT (0.87%)
-10	TAGT (0.13%)	CGAG (0.12%)	GGGT (0.11%)	TAGT (0.13%)	GGGG (0.12%)	TCTA (0.11%)	CTTG (0.15%)	ACTA (0.14%)	CGGA (0.12%)
-9	GAGG (0.13%)	CTAA (0.12%)	CTAT (0.11%)	TAGA (0.13%)	CGAG (0.12%)	GTGT (0.11%)	CGAG (0.15%)	CCCT (0.14%)	ACTA (0.12%)
-8	TCTA (0.13%)	TCTA (0.11%)	TAGT (0.11%)	CCCT (0.12%)	CTAT (0.11%)	CTAT (0.09%)	GGAC (0.14%)	ACCT (0.14%)	CCCT (0.11%)
-7	CGAG (0.12%)	CTAT (0.11%)	ACTA (0.10%)	GAGG (0.11%)	ACCT (0.11%)	GGAC (0.09%)	CCCC (0.14%)	CCGA (0.14%)	CTTG (0.11%)
-6	AGGG (0.12%)	TAGT (0.11%)	CGAG (0.09%)	AGGG (0.11%)	ACTA (0.11%)	ACTA (0.09%)	TCTA (0.13%)	CCCC (0.13%)	CTAT (0.11%)
-5	CCTA (0.09%)	TAGG (0.10%)	TCTA (0.08%)	CCTA (0.11%)	TAGA (0.11%)	CCCT (0.08%)	CTAT (0.13%)	CCTA (0.12%)	TCTA (0.10%)
-4	GGAC (0.08%)	GGAC (0.09%)	GGAC (0.07%)	GGAC (0.10%)	CCCC (0.10%)	CGAG (0.08%)	TAGA (0.09%)	CTAT (0.12%)	TAGA (0.08%)
-3	TAGA (0.08%)	CCTA (0.08%)	TAGG (0.06%)	CGAG (0.10%)	TAGG (0.10%)	TAGG (0.06%)	CCTA (0.09%)	TAGG (0.12%)	TAGG (0.07%)
-2	TAGG (0.06%)	TAGA (0.06%)	CCTA (0.05%)	TAGG (0.08%)	CCTA (0.06%)	CCTA (0.05%)	TAGG (0.06%)	TAGA (0.09%)	CCTA (0.06%)
-1	CTAG (0.01%)	CTAG (0.01%)	CTAG (0.01%)	CTAG (0.01%)	CTAG (0.02%)	CTAG (0.01%)	CTAG (0.04%)	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	TTATC (0.38%)	GATGC (0.38%)	GAAA (0.54%)	CAGCA (0.35%)	CAGCA (0.38%)	CAGCA (0.45%)	TCAA (0.33%)	GATGC (0.42%)	GAAA (0.42%)
2	CGTTT (0.36%)	ATTTT (0.35%)	AGAAA (0.43%)	CATCA (0.30%)	CTGGC (0.36%)	GAAA (0.43%)	CGTCA (0.31%)	TATCG (0.37%)	TGGCA (0.41%)
3	GTTGC (0.32%)	CTGGC (0.35%)	CAAAA (0.39%)	CGTTT (0.29%)	ACAAA (0.36%)	ACAAA (0.42%)	GCAAT (0.31%)	ACAAA (0.37%)	CAAAA (0.39%)
4	ATTTT (0.32%)	CAGCA (0.33%)	CGTTT (0.35%)	ACAAA (0.29%)	GATGC (0.35%)	AAGAA (0.38%)	GCAAA (0.30%)	CTGGC (0.35%)	AGAAA (0.38%)
5	AGAAA (0.32%)	GTTTC (0.33%)	TAAAA (0.35%)	TTATC (0.29%)	TGATG (0.31%)	CAGAA (0.36%)	CAGCA (0.30%)	TTATT (0.32%)	GCAAT (0.35%)
6	CAAAA (0.31%)	TTTCA (0.32%)	ATTTT (0.34%)	GCTGC (0.28%)	AATCA (0.31%)	AATCA (0.35%)	TTGCA (0.30%)	GCCAG (0.30%)	CAGCA (0.34%)
7	TTTTT (0.31%)	TGTTT (0.32%)	GCAAT (0.34%)	AATCA (0.28%)	ATTTT (0.30%)	AGAAA (0.35%)	TGGCA (0.29%)	TGGAA (0.29%)	CGGCA (0.33%)
8	CTGGC (0.30%)	GCCAG (0.32%)	CAGCA (0.34%)	GATGC (0.28%)	GCGGC (0.30%)	ATGAA (0.34%)	CGCCA (0.28%)	CATCA (0.29%)	AGGAA (0.33%)
9	GAAA (0.30%)	TTTTG (0.32%)	TTTTT (0.33%)	CTGGC (0.28%)	GCGC (0.30%)	CAAAA (0.33%)	AGAAA (0.28%)	TTTTA (0.29%)	CTGCA (0.32%)
10	GTTTT (0.29%)	TATCG (0.31%)	CTGAA (0.33%)	GCAAA (0.27%)	ATTGC (0.29%)	GCAAA (0.33%)	TGTTT (0.28%)	TCTTT (0.28%)	ACAAA (0.31%)
-10	TAGGG (0.01%)	TAGGG (0.01%)	CTTAG (0.01%)	GGACC (0.01%)	CCCTT (0.01%)	TAGGT (0.01%)	CTTGG (0.01%)	TCCTA (0.01%)	CCCTA (0.01%)
-9	CTAGT (0.01%)	CCCTA (0.01%)	TAGGG (0.01%)	TAGGG (0.01%)	ACCTA (0.01%)	CCCTA (0.01%)	TAGGG (0.01%)	CCCTA (0.01%)	GCTAG (0.01%)
-8	GCTAG (0.00%)	GCTAG (0.00%)	GCTAG (0.00%)	CTAGA (0.01%)	CCCTA (0.01%)	GCTAG (0.00%)	CCCTA (0.01%)	GCTAG (0.01%)	TTAGA (0.01%)
-7	GGACC (0.00%)	CTAGA (0.00%)	ACTAG (0.00%)	GCTAG (0.01%)	CTAGA (0.00%)	CTAGT (0.00%)	GGACC (0.01%)	CTAGA (0.01%)	CTAGA (0.00%)
-6	CCTAG (0.00%)	ACTAG (0.00%)	CTAGC (0.00%)	CTAGT (0.01%)	CTAGT (0.00%)	CTAGA (0.00%)	CTAGA (0.01%)	ACTAG (0.00%)	CCTAG (0.00%)
-5	CTAGA (0.00%)	CCTAG (0.00%)	CCTAG (0.00%)	CTAGC (0.00%)	CTAGC (0.00%)	ACTAG (0.00%)	CTAGT (0.00%)	CTAGC (0.00%)	CTAGC (0.00%)
-4	CTAGC (0.00%)	CTAGC (0.00%)	CTAGT (0.00%)	CCTAG (0.00%)	ACTAG (0.00%)	CTAGC (0.00%)	CTAGC (0.00%)	CTAGT (0.00%)	TCTAG (0.00%)
-3	ACTAG (0.00%)	CTAGT (0.00%)	CTAGA (0.00%)	CTAGG (0.00%)	CCTAG (0.00%)	CTAGG (0.00%)	ACTAG (0.00%)	TCTAG (0.00%)	CTAGT (0.00%)
-2	CTAGG (0.00%)	TCTAG (0.00%)	CTAGG (0.00%)	ACTAG (0.00%)	TCTAG (0.00%)	CCTAG (0.00%)	CTAGG (0.00%)	CCTAG (0.00%)	CTAGG (0.00%)
-1	TCTAG (0.00%)	CTAGG (0.00%)	TCTAG (0.00%)	TCTAG (0.00%)	CTAGG (0.00%)	TCTAG (0.00%)	TCTAG (0.00%)	CTAGG (0.00%)	ACTAG (0.00%)

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