

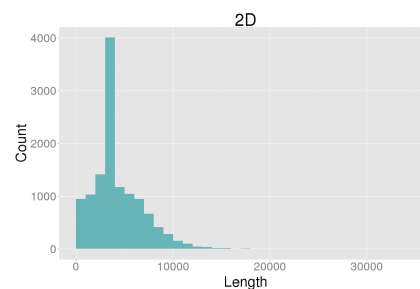
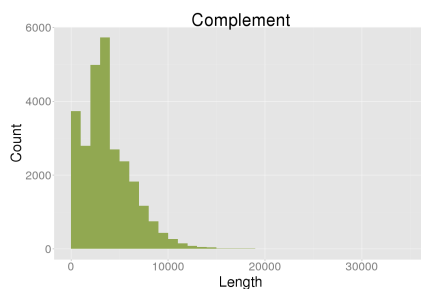
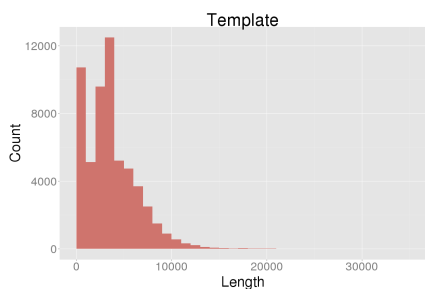
NanoOK report for ZF-screens_MARC_phase_1a_e_coli_run2

Pass and fail counts

Type	Pass	Fail
Template	0	58173
Complement	0	27176
2D	0	12341

Read lengths

Type	NumReads	TotalBases	Mean	Longest	Shortest	N50	N50Count	N90	N90Count
Template	58173	219969974	3781.31	309662	5	5284	13619	2603	37958
Complement	27176	103397631	3804.74	154321	5	5115	6957	2528	18708
2D	12341	52852439	4282.67	92222	95	5295	3445	2946	9078



Template alignments

Number of reads	58173
Number of reads with alignments	26634 (45.78%)
Number of reads without alignments	31539 (54.22%)

ID	Size	Number of Reads	% of Reads	Mean read length	Aligned bases	Mean coverage	Longest Perf Kmer
Control sequence	3560	9461	16.26	2997.22	26659040	7488.49	72
Escherichia coli	4641652	17173	29.52	5728.02	85577098	18.44	94

Complement alignments

Number of reads	27176
Number of reads with alignments	14057 (51.73%)
Number of reads without alignments	13119 (48.27%)

ID	Size	Number of Reads	% of Reads	Mean read length	Aligned bases	Mean coverage	Longest Perf Kmer
Control sequence	3560	4551	16.75	2807.97	10600678	2977.72	52
Escherichia coli	4641652	9506	34.98	5484.15	44369432	9.56	60

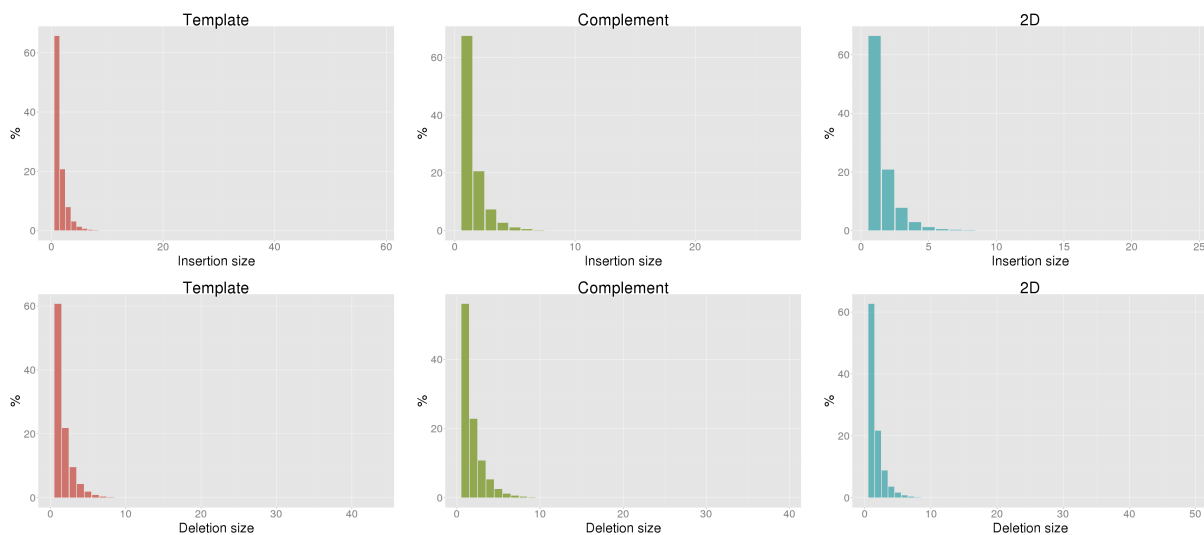
2D alignments

Number of reads	12341
Number of reads with alignments	10024 (81.23%)
Number of reads without alignments	2317 (18.77%)

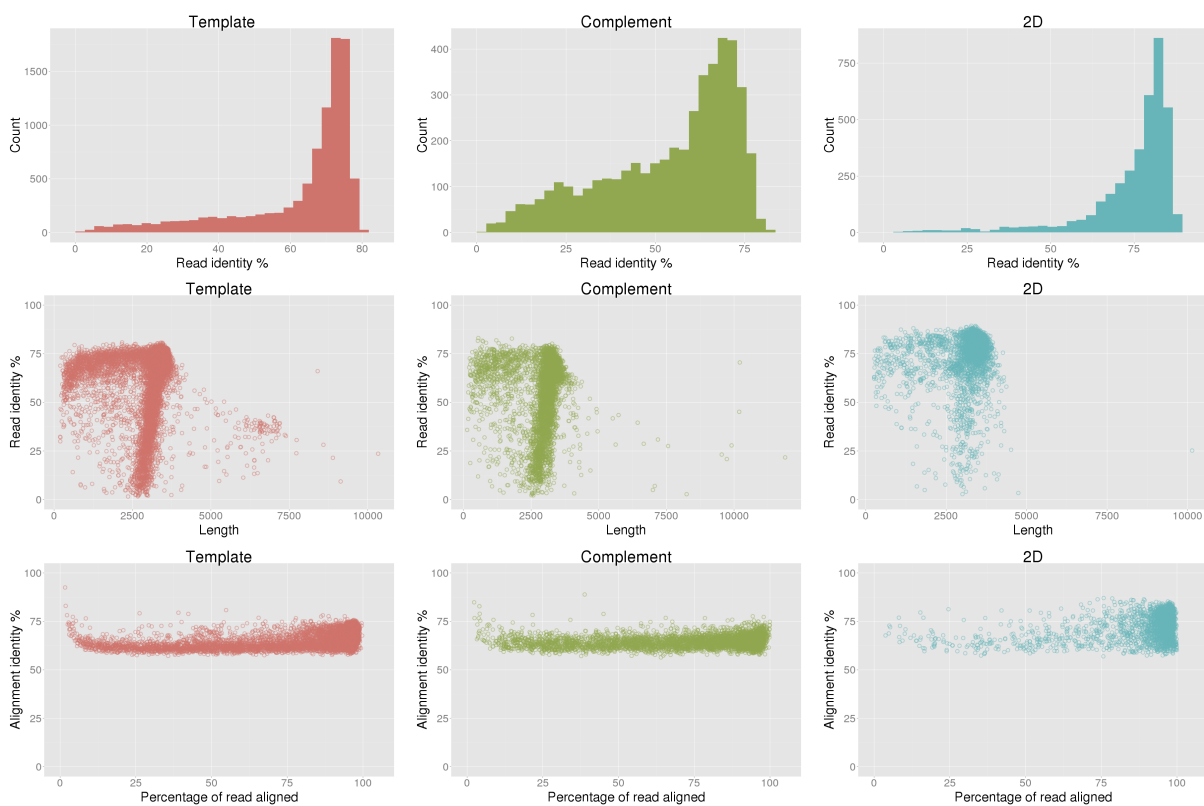
ID	Size	Number of Reads	% of Reads	Mean read length	Aligned bases	Mean coverage	Longest Perf Kmer
Control sequence	3560	3756	30.44	3157.73	11917153	3347.51	175
Escherichia coli	4641652	6268	50.79	5571.96	35160520	7.58	164

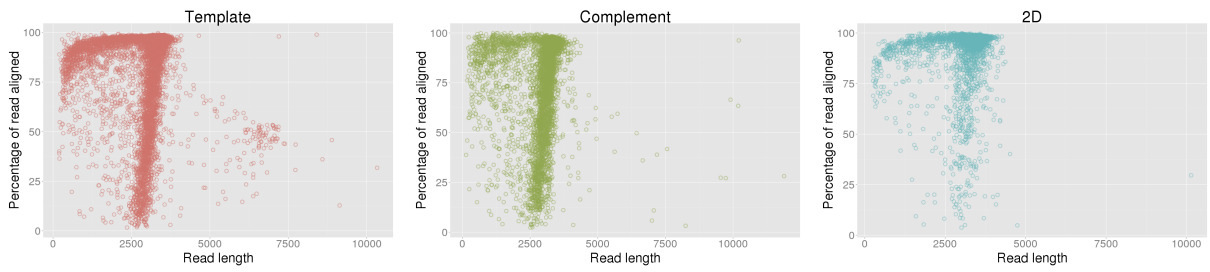
Control sequence error analysis

	Template	Complement	2D
Overall base identity (excluding indels)	62.69%	53.53%	74.91%
Aligned base identity (excluding indels)	79.83%	79.33%	86.23%
Identical bases per 100 aligned bases (including indels)	66.68%	64.53%	74.55%
Inserted bases per 100 aligned bases (including indels)	5.02%	4.37%	5.02%
Deleted bases per 100 aligned bases (including indels)	11.45%	14.29%	8.53%
Substitutions per 100 aligned bases (including indels)	16.84%	16.81%	11.91%
Mean insertion size	1.60	1.53	1.56
Mean deletion size	1.72	1.86	1.66

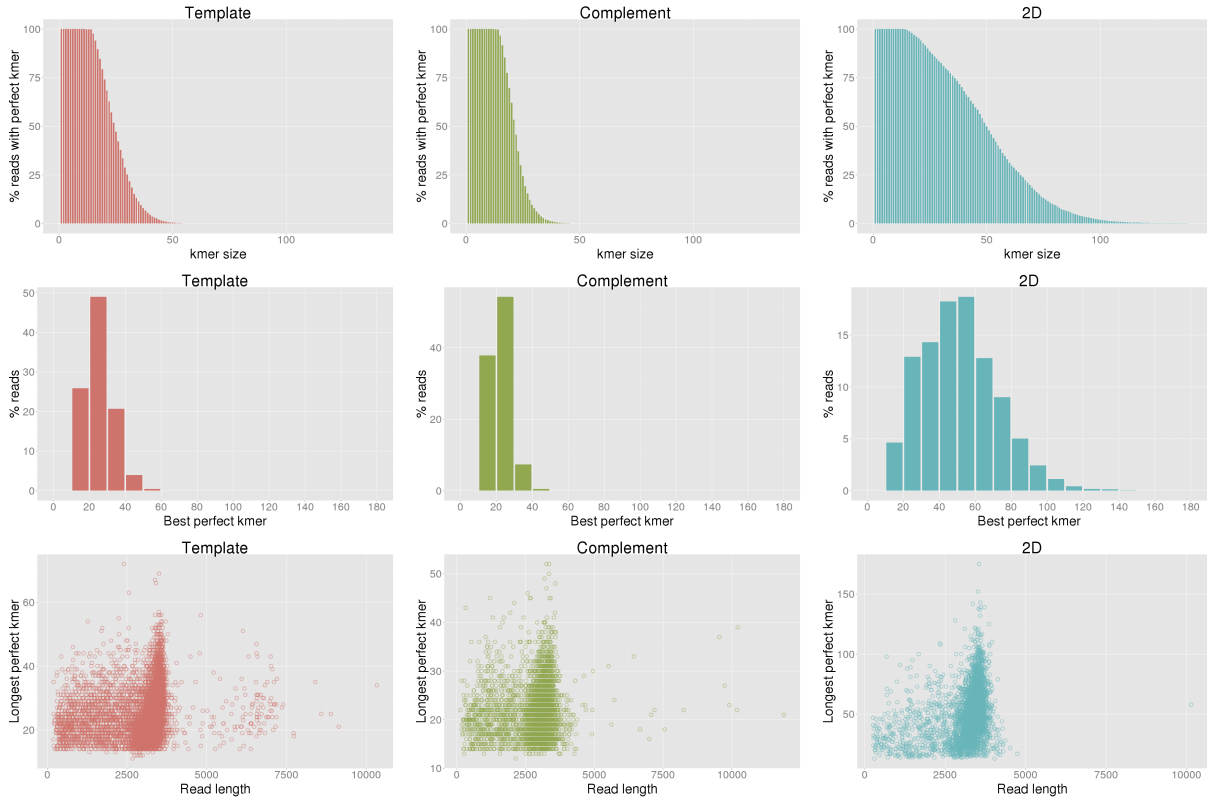


Control sequence read identity

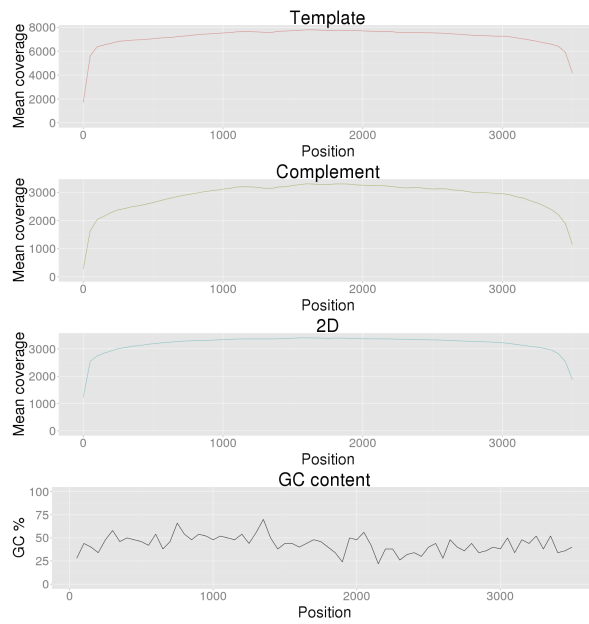




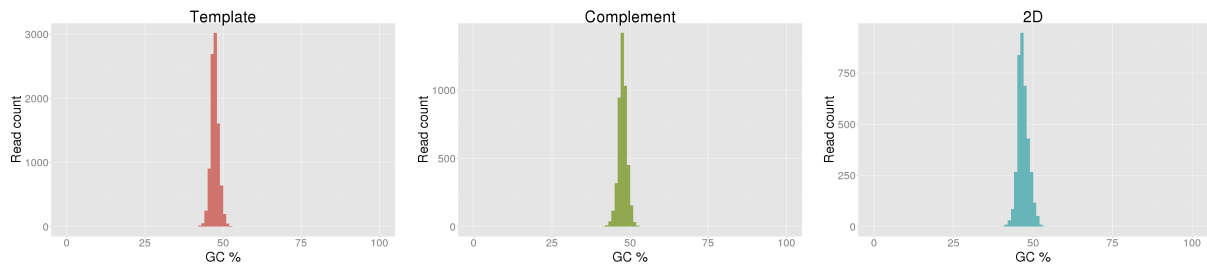
Control sequence perfect kmers



Control sequence coverage

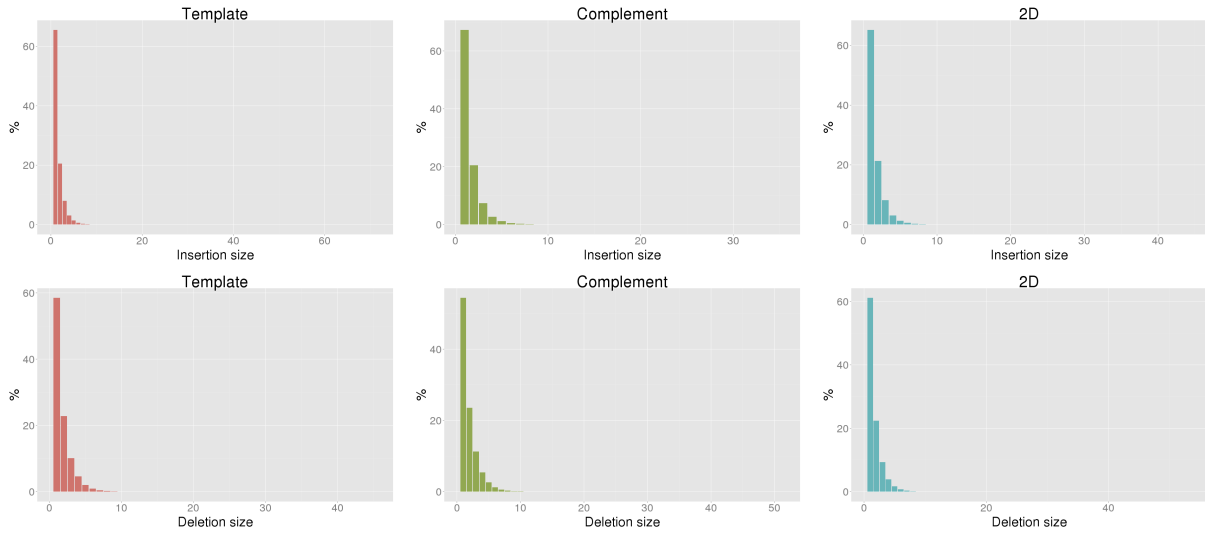


Control sequence GC content

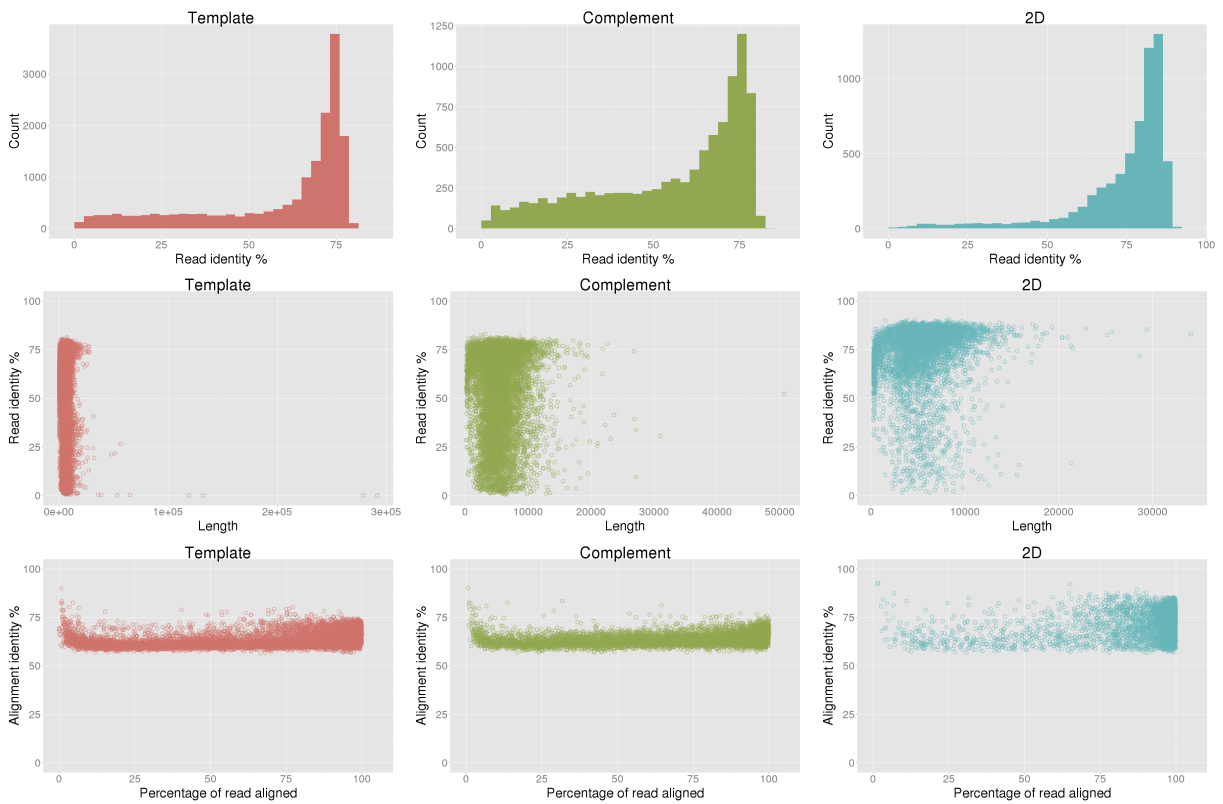


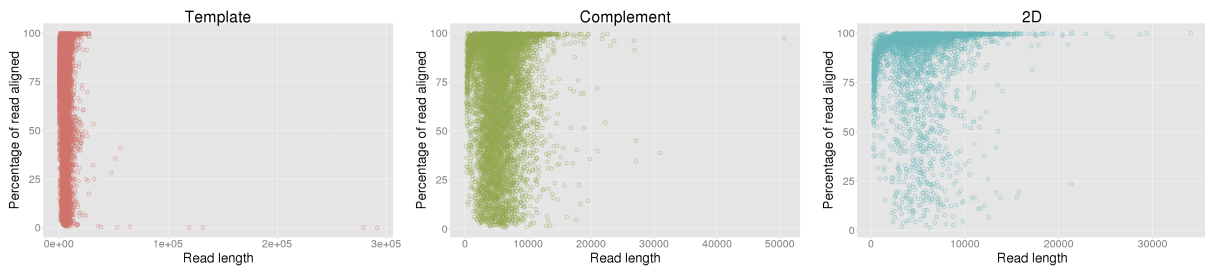
Escherichia coli error analysis

	Template	Complement	2D
Overall base identity (excluding indels)	56.90%	54.85%	74.90%
Aligned base identity (excluding indels)	79.13%	79.87%	86.24%
Identical bases per 100 aligned bases (including indels)	65.40%	64.44%	74.40%
Inserted bases per 100 aligned bases (including indels)	5.06%	4.26%	5.06%
Deleted bases per 100 aligned bases (including indels)	12.28%	15.05%	8.67%
Substitutions per 100 aligned bases (including indels)	17.25%	16.24%	11.87%
Mean insertion size	1.61	1.54	1.59
Mean deletion size	1.76	1.90	1.69

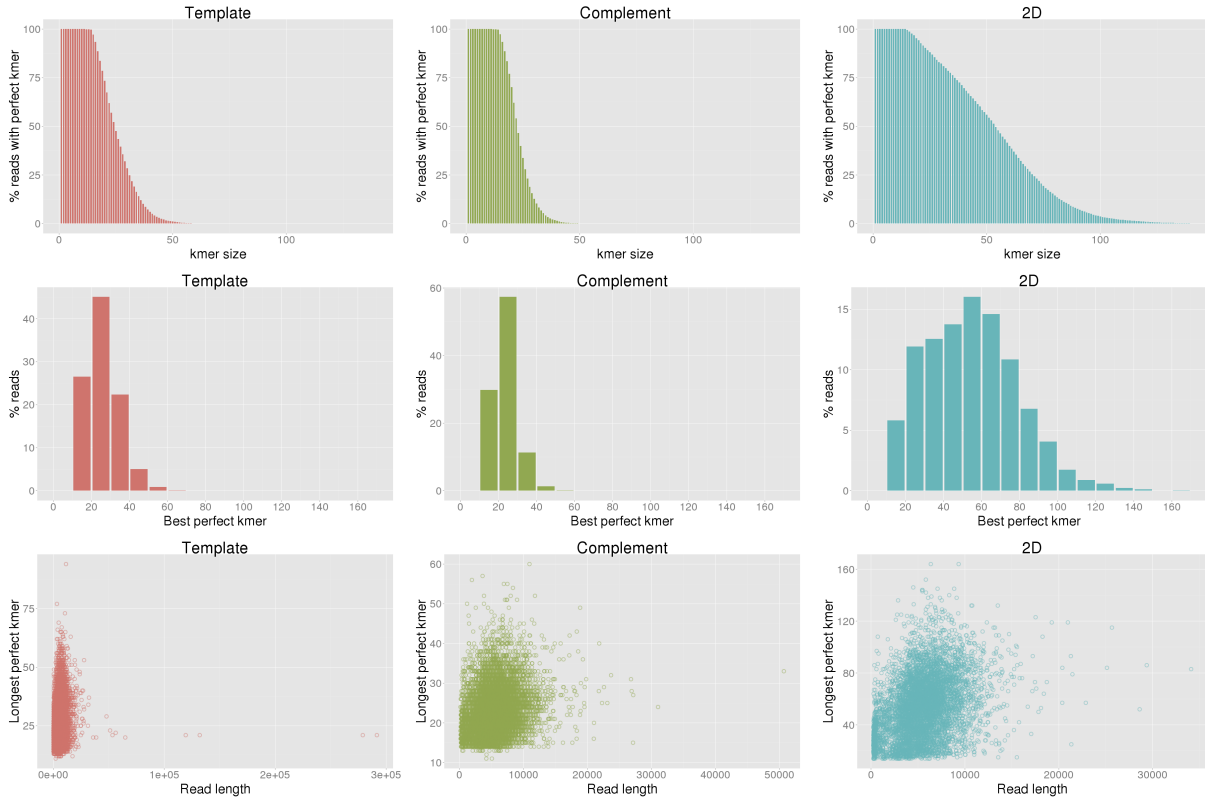


Escherichia coli read identity

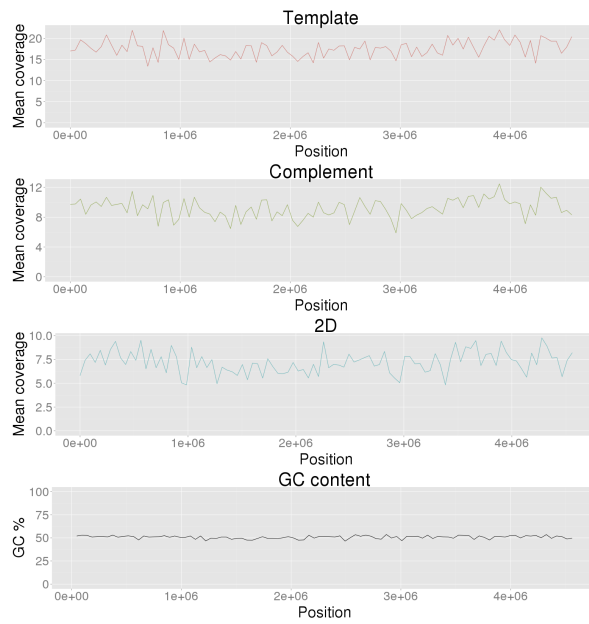




Escherichia coli perfect kmers



Escherichia coli coverage



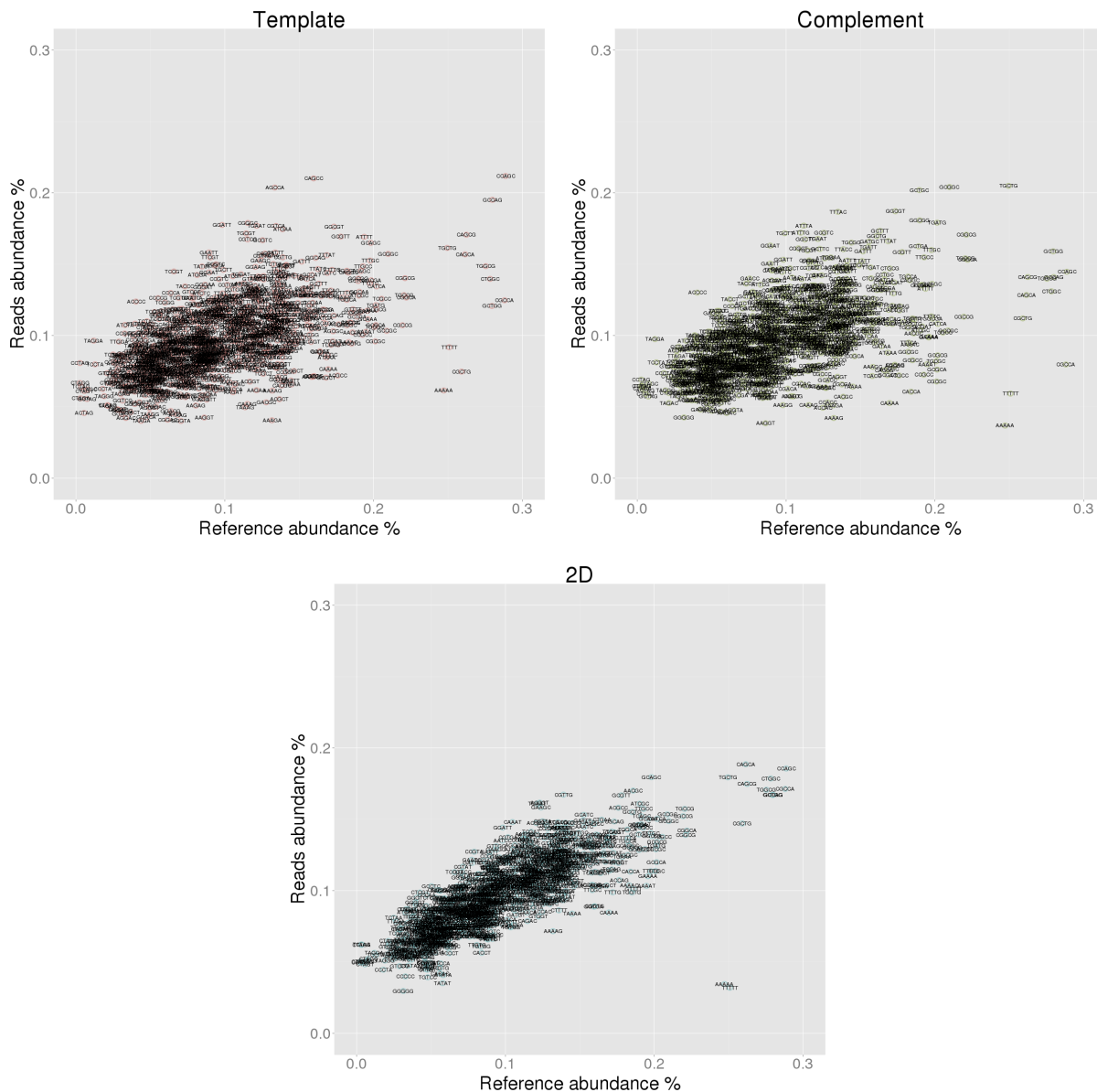
Escherichia coli 5-mer analysis

Under-represented 5-mers

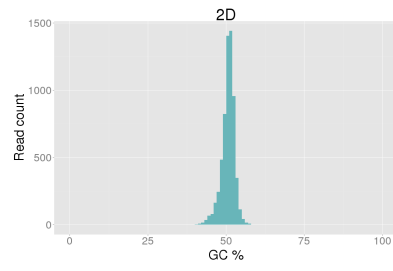
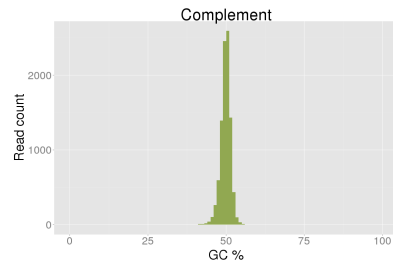
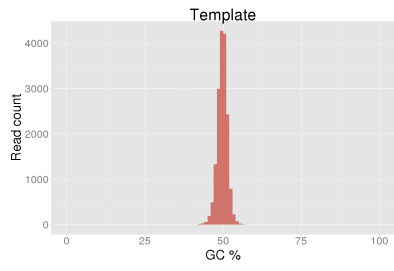
Rank	Template				Complement				2D			
	kmer	Ref %	Read %	Diff %	kmer	Ref %	Read %	Diff %	kmer	Ref %	Read %	Diff %
1	AAAAA	0.247	0.062	-0.186	AAAAA	0.247	0.037	-0.210	TTTTT	0.251	0.032	-0.219
2	CGCTG	0.259	0.075	-0.184	CGCCA	0.288	0.080	-0.208	AAAAA	0.247	0.035	-0.213
3	CGCCA	0.288	0.125	-0.163	TTTTT	0.251	0.059	-0.192	CGCCA	0.288	0.171	-0.117
4	TTTTT	0.251	0.092	-0.159	CTGGC	0.278	0.131	-0.147	GCCAG	0.280	0.167	-0.113
5	GCTGG	0.279	0.121	-0.159	CGCTG	0.259	0.112	-0.147	GCTGG	0.279	0.167	-0.112
6	CTGGC	0.278	0.140	-0.139	CCAGC	0.289	0.145	-0.144	CGCTG	0.259	0.147	-0.112
7	TGGCG	0.275	0.149	-0.127	GCCAG	0.280	0.141	-0.139	TGGCG	0.275	0.171	-0.105
8	CGCCG	0.219	0.107	-0.112	TGGCG	0.275	0.140	-0.136	CCAGC	0.289	0.186	-0.103
9	GCCGC	0.209	0.103	-0.105	CGCGC	0.201	0.068	-0.133	CTGGC	0.278	0.179	-0.100
10	CGCGC	0.201	0.096	-0.105	CAGCA	0.261	0.128	-0.133	AAAAT	0.195	0.103	-0.091

Over-represented 5-mers

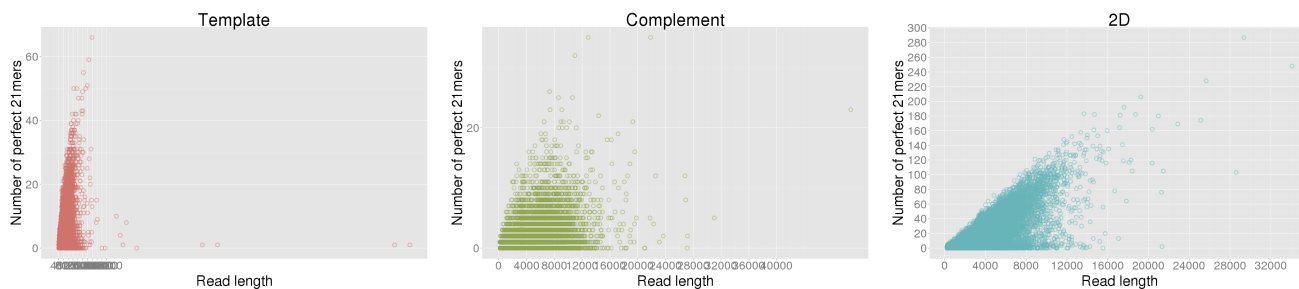
Rank	Template				Complement				2D			
	kmer	Ref %	Read %	Diff %	kmer	Ref %	Read %	Diff %	kmer	Ref %	Read %	Diff %
1	TAGGA	0.012	0.096	0.085	ACCCC	0.040	0.130	0.090	CTAGA	0.003	0.062	0.059
2	ACCCC	0.040	0.124	0.083	TAGGA	0.012	0.098	0.086	TCTAG	0.003	0.062	0.059
3	GGATT	0.098	0.177	0.079	GGAAT	0.089	0.163	0.074	CTCGT	0.042	0.099	0.056
4	TCCGT	0.066	0.145	0.079	TGCTT	0.099	0.172	0.073	TCTAA	0.025	0.081	0.056
5	CCTAG	0.003	0.081	0.078	TCCTA	0.013	0.081	0.068	GGGTC	0.040	0.095	0.055
6	ATCTA	0.033	0.107	0.074	CCTAG	0.003	0.069	0.066	CCTCC	0.033	0.087	0.054
7	CCCCG	0.055	0.126	0.071	ATTTA	0.112	0.177	0.065	GCCTC	0.050	0.103	0.053
8	AGCCA	0.134	0.204	0.070	GAGGC	0.051	0.116	0.065	TAGAT	0.035	0.087	0.052
9	GAATT	0.089	0.158	0.069	GAACC	0.075	0.140	0.064	GGGGT	0.039	0.092	0.052
10	CCCCC	0.033	0.101	0.069	CCTAT	0.028	0.092	0.064	TTAGA	0.026	0.078	0.052



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	9.16	9.18	5.17	0.00	9.09	8.87	5.39	0.00	9.38	8.99	4.84
C	8.35	0.00	8.60	9.43	8.87	0.00	8.32	9.18	8.45	0.00	9.64	8.36
G	9.16	8.78	0.00	8.13	8.58	8.63	0.00	8.79	8.47	9.96	0.00	8.20
T	5.58	9.51	8.95	0.00	5.77	9.30	9.21	0.00	5.08	9.24	9.39	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 (3.24%)	TTC (3.52%)	AAA (4.46%)	AAA (2.92%)	AAA (2.98%)	AAA (4.35%)	AAA (3.19%)	AAA (2.89%)	AAA (4.17%)	Most common
2	AAA (2.98%)	TGC (3.00%)	TTC (3.58%)	TTC (2.89%)	TGC (2.90%)	GCA (3.41%)	GCA (3.05%)	TGC (2.72%)	GCA (3.52%)	
3	GCA (2.75%)	AAA (2.98%)	GCA (3.22%)	TGC (2.82%)	TTC (2.70%)	GAA (3.37%)	TTC (2.84%)	GCA (2.58%)	GAA (3.20%)	
4	TGC (2.69%)	GCA (2.80%)	GAA (3.13%)	GCA (2.75%)	GCA (2.67%)	TTC (3.10%)	GAA (2.59%)	TTC (2.48%)	TTC (2.91%)	
5	ATC (2.55%)	TCA (2.41%)	TTT (2.76%)	GAA (2.53%)	GAA (2.56%)	TTT (2.67%)	TCA (2.54%)	TCA (2.46%)	TTT (2.87%)	
6	TCA (2.50%)	GAA (2.38%)	AAT (2.75%)	AAT (2.39%)	GGC (2.56%)	AAT (2.50%)	AAT (2.52%)	GAA (2.46%)	AAT (2.81%)	
7	TTT (2.50%)	AAT (2.36%)	TGC (2.46%)	TCA (2.36%)	AAT (2.39%)	TGC (2.49%)	TGC (2.41%)	GCG (2.27%)	GTT (2.56%)	
8	GAA (2.39%)	ATC (2.26%)	TCA (2.36%)	ATC (2.31%)	TCA (2.34%)	TCA (2.43%)	ATC (2.28%)	CAG (2.23%)	TCA (2.31%)	
9	AAT (2.35%)	GCC (2.21%)	CAA (2.35%)	TTT (2.30%)	CAG (2.22%)	CAA (2.26%)	TTT (2.27%)	GCC (2.22%)	TGC (2.15%)	
10	GCC (2.07%)	AAC (2.15%)	ATC (2.15%)	CAG (2.25%)	ATC (2.13%)	ATC (2.19%)	GCG (2.13%)	ATC (2.10%)	GCC (2.14%)	
										Least common
-10	CTC (0.97%)	GGG (0.94%)	CGA (0.91%)	AGT (0.98%)	CCC (0.94%)	CCC (0.91%)	CTT (1.03%)	GGG (1.02%)	AGG (0.97%)	
-9	CGA (0.96%)	AGG (0.94%)	AGA (0.88%)	AGA (0.97%)	CCT (0.93%)	CTT (0.89%)	CTC (1.00%)	GTA (1.01%)	CCC (0.94%)	
-8	AGA (0.87%)	AGT (0.91%)	GGT (0.86%)	CTC (0.86%)	CGA (0.93%)	CTC (0.86%)	GAG (0.90%)	CCT (0.95%)	ACT (0.90%)	
-7	CCC (0.86%)	GAG (0.87%)	GGG (0.84%)	GGA (0.85%)	AGG (0.90%)	CCT (0.86%)	AGA (0.86%)	AGA (0.88%)	GAG (0.84%)	
-6	GGA (0.84%)	CTT (0.84%)	AGG (0.84%)	CCC (0.79%)	CTC (0.89%)	ACT (0.78%)	GGA (0.84%)	CGA (0.88%)	CTT (0.82%)	
-5	GAG (0.82%)	CGA (0.77%)	AGT (0.81%)	GAG (0.79%)	ACT (0.89%)	AGG (0.78%)	CCC (0.79%)	CTT (0.86%)	CGA (0.74%)	
-4	AGG (0.70%)	AGA (0.75%)	CTT (0.76%)	AGG (0.73%)	GAG (0.88%)	GGG (0.73%)	AGG (0.77%)	ACT (0.86%)	GGA (0.73%)	
-3	GGG (0.68%)	GGA (0.72%)	GAG (0.72%)	GGG (0.57%)	GGG (0.75%)	GAG (0.64%)	GGG (0.67%)	GGA (0.77%)	AGA (0.68%)	
-2	CTA (0.53%)	TAG (0.60%)	TAG (0.42%)	CTA (0.56%)	TAG (0.57%)	CTA (0.43%)	CTA (0.59%)	TAG (0.69%)	TAG (0.52%)	
-1	TAG (0.48%)	CTA (0.50%)	CTA (0.37%)	TAG (0.50%)	CTA (0.50%)	TAG (0.42%)	TAG (0.58%)	CTA (0.64%)	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 (1.00%)	TTTC (1.18%)	AAAA (1.56%)	CAAA (0.91%)	CAAA (0.94%)	CAAA (1.26%)	CAAA (0.95%)	CAAA (0.86%)	AAAA (1.22%)
2	GAAA (0.97%)	TTCA (0.92%)	TTTC (1.25%)	ATCA (0.88%)	TGGC (0.92%)	AAAA (1.20%)	GAAA (0.87%)	TTCA (0.85%)	GAAA (1.13%)
3	AAAA (0.92%)	GAAA (0.90%)	GAAA (1.24%)	CTGC (0.84%)	TTGC (0.92%)	TGAA (1.02%)	AACA (0.83%)	GGAA (0.82%)	GGCA (1.01%)
4	TTTT (0.92%)	TTGC (0.90%)	TTTT (0.98%)	TTGC (0.84%)	CAGC (0.91%)	GAAA (1.01%)	AAAA (0.81%)	TGGC (0.81%)	TGCA (0.97%)
5	TTCA (0.88%)	AAAA (0.88%)	GCAA (0.98%)	CAGC (0.82%)	CGGC (0.90%)	AGAA (0.94%)	TGCA (0.81%)	CAGC (0.79%)	CAAA (0.97%)
6	TTGC (0.83%)	TTCC (0.87%)	CAAA (0.95%)	AAAA (0.80%)	CTGC (0.88%)	AGCA (0.90%)	TTCA (0.80%)	ATCA (0.78%)	GGAA (0.96%)
7	ATCA (0.82%)	TGCC (0.86%)	TGAA (0.91%)	TGGC (0.76%)	TTCC (0.82%)	TAAA (0.89%)	ATCA (0.80%)	ATGC (0.78%)	TTTC (0.91%)
8	AACG (0.79%)	CTGC (0.82%)	TGCA (0.88%)	ATTC (0.76%)	ATCA (0.81%)	TTTC (0.89%)	GGCA (0.79%)	GAAA (0.77%)	TGAA (0.88%)
9	TGCC (0.78%)	GTTC (0.81%)	AACG (0.86%)	GAAA (0.75%)	TTCA (0.80%)	ATCA (0.87%)	TGAA (0.78%)	CTGC (0.76%)	TGTT (0.87%)
10	AATC (0.77%)	ATTC (0.81%)	AAAT (0.86%)	TTTC (0.74%)	AGCA (0.78%)	TGCA (0.87%)	TTTC (0.75%)	AGCA (0.73%)	CGTT (0.86%)
-10	TAGT (0.13%)	CGAG (0.12%)	GGGT (0.11%)	GGGG (0.12%)	CTAT (0.12%)	ACCT (0.11%)	GGAC (0.14%)	CTAA (0.15%)	CCGA (0.13%)
-9	GAGG (0.13%)	TAGT (0.11%)	CTAT (0.11%)	TAGA (0.12%)	GGAC (0.12%)	GTGT (0.11%)	AGGG (0.14%)	CCCT (0.14%)	CGGA (0.12%)
-8	TTAG (0.13%)	CTAA (0.11%)	TAGT (0.11%)	CGAG (0.11%)	CGAG (0.12%)	CTAT (0.10%)	GAGG (0.14%)	ACCT (0.14%)	CTTG (0.12%)
-7	TCTA (0.12%)	TCTA (0.11%)	CGAG (0.09%)	AGGG (0.11%)	ACCT (0.11%)	ACTA (0.10%)	CTTG (0.13%)	CCGA (0.13%)	ACTA (0.11%)
-6	AGGG (0.12%)	CTAT (0.11%)	ACTA (0.09%)	GAGG (0.11%)	ACTA (0.11%)	GGAC (0.09%)	CCCC (0.13%)	CCCC (0.13%)	CTAT (0.10%)
-5	GGAC (0.09%)	TAGG (0.10%)	TCTA (0.08%)	GGAC (0.10%)	TAGA (0.11%)	CGAG (0.08%)	TCTA (0.13%)	CTAT (0.13%)	TCTA (0.10%)
-4	CCTA (0.08%)	GGAC (0.10%)	GGAC (0.08%)	CCCT (0.10%)	CCCC (0.11%)	CCCT (0.08%)	TAGA (0.09%)	TAGG (0.12%)	TAGA (0.07%)
-3	TAGA (0.08%)	CCTA (0.07%)	TAGG (0.06%)	CCTA (0.09%)	TAGG (0.09%)	CCTA (0.06%)	CCTA (0.08%)	CCTA (0.11%)	TAGG (0.06%)
-2	TAGG (0.05%)	TAGA (0.06%)	CCTA (0.05%)	TAGG (0.07%)	CCTA (0.06%)	TAGG (0.06%)	TAGG (0.06%)	TAGA (0.09%)	CCTA (0.05%)
-1	CTAG (0.01%)	CTAG (0.01%)	CTAG (0.01%)	CTAG (0.02%)	CTAG (0.01%)	CTAG (0.01%)	CTAG (0.03%)	CTAG (0.02%)	CTAG (0.02%)

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	TTATC (0.36%)	GATGC (0.37%)	GAAAA (0.51%)	CAGCA (0.36%)	CAGCA (0.39%)	CAGCA (0.46%)	CAGCA (0.33%)	GATGC (0.39%)	GAAAA (0.40%)
2	CGTTT (0.35%)	CTGGC (0.35%)	AGAAA (0.44%)	AATCA (0.30%)	CTGGC (0.36%)	ACAAA (0.42%)	GCAAT (0.31%)	ACAAA (0.36%)	TGGCA (0.39%)
3	AGAAA (0.33%)	CAGCA (0.35%)	CAAAA (0.41%)	GCTGC (0.30%)	ACAAA (0.35%)	GAAAA (0.39%)	CGTCA (0.31%)	CTGGC (0.35%)	AGAAA (0.39%)
4	CAAAA (0.31%)	ATTTT (0.34%)	CAGCA (0.35%)	CATCA (0.29%)	GATGC (0.34%)	AAGAA (0.39%)	TCAAA (0.30%)	TATCG (0.34%)	CAAAA (0.37%)
5	GTTTC (0.31%)	GTTC (0.32%)	ATTTT (0.35%)	TTATC (0.29%)	GCGGC (0.32%)	GCAAA (0.37%)	GCAAA (0.30%)	TTATT (0.31%)	CAGCA (0.36%)
6	ATTTT (0.30%)	TGTTT (0.32%)	TAAAA (0.35%)	GATGC (0.29%)	AATCA (0.32%)	CAGAA (0.36%)	CGCCA (0.30%)	GCCAG (0.30%)	GCAAT (0.36%)
7	CTGGC (0.29%)	TTTCA (0.31%)	CGTTT (0.33%)	ACAAA (0.29%)	GCAGC (0.29%)	ATGAA (0.34%)	CAAAA (0.28%)	TTTCA (0.30%)	CGGCA (0.34%)
8	CAGCA (0.29%)	CGAC (0.31%)	TGTTT (0.31%)	TTTGC (0.28%)	TTTGC (0.29%)	AATCA (0.34%)	CTGGC (0.28%)	TGGAA (0.29%)	TAAAA (0.33%)
9	TTTCT (0.29%)	TTTGC (0.31%)	TTTTT (0.31%)	CGTTT (0.28%)	CCAGC (0.29%)	CGGCA (0.34%)	CGGCA (0.28%)	CATCA (0.29%)	AAGAA (0.32%)
10	TGTTT (0.29%)	TATCG (0.30%)	CTGAA (0.31%)	CCAGC (0.27%)	TGATG (0.29%)	AGAAA (0.32%)	TTGCC (0.27%)	CAGCA (0.29%)	GCAAA (0.31%)
-10	CTTAG (0.01%)	GGACC (0.01%)	CTTAG (0.01%)	CTAGA (0.01%)	ACCTA (0.01%)	TAGGG (0.01%)	CTTGG (0.01%)	TAGGA (0.01%)	CCCTA (0.01%)
-9	CTAGT (0.00%)	CCCTA (0.01%)	CCCTA (0.01%)	TAGGG (0.01%)	GCTAG (0.01%)	CCCTA (0.01%)	GGACC (0.01%)	CCCTA (0.01%)	TCCTA (0.01%)
-8	GGACC (0.00%)	GCTAG (0.00%)	GCTAG (0.00%)	GGACC (0.01%)	CCCTA (0.01%)	GCTAG (0.01%)	CTAGA (0.01%)	GCTAG (0.01%)	TTAGA (0.01%)
-7	GCTAG (0.00%)	ACTAG (0.00%)	CTAGC (0.00%)	CTAGC (0.01%)	CTAGA (0.00%)	CTAGA (0.01%)	GCTAG (0.01%)	CTAGA (0.01%)	CTAGT (0.00%)
-6	CCTAG (0.00%)	CTAGA (0.00%)	ACTAG (0.00%)	CTAGT (0.01%)	CTAGC (0.00%)	CTAGT (0.00%)	CCCTA (0.01%)	CTAGC (0.00%)	CCTAG (0.00%)
-5	CTAGA (0.00%)	CTAGC (0.00%)	CTAGT (0.00%)	CCCTA (0.00%)	CTAGT (0.00%)	CTAGC (0.00%)	CTAGT (0.01%)	ACTAG (0.00%)	CTAGA (0.00%)
-4	CTAGC (0.00%)	CTAGT (0.00%)	CTAGA (0.00%)	CCTAG (0.00%)	ACTAG (0.00%)	CTAGG (0.00%)	ACTAG (0.00%)	CTAGT (0.00%)	CTAGC (0.00%)
-3	CTAGG (0.00%)	CCTAG (0.00%)	CCTAG (0.00%)	TCTAG (0.00%)	CCTAG (0.00%)	CCTAG (0.00%)	CTAGC (0.00%)	TCTAG (0.00%)	ACTAG (0.00%)
-2	ACTAG (0.00%)	TCTAG (0.00%)	TCTAG (0.00%)	ACTAG (0.00%)	TCTAG (0.00%)	TCTAG (0.00%)	CTAGG (0.00%)	CCTAG (0.00%)	CTAGG (0.00%)
-1	TCTAG (0.00%)	CTAGG (0.00%)	CTAGG (0.00%)	CTAGG (0.00%)	CTAGG (0.00%)	ACTAG (0.00%)	TCTAG (0.00%)	CTAGG (0.00%)	TCTAG (0.00%)

Most common

Least common

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