

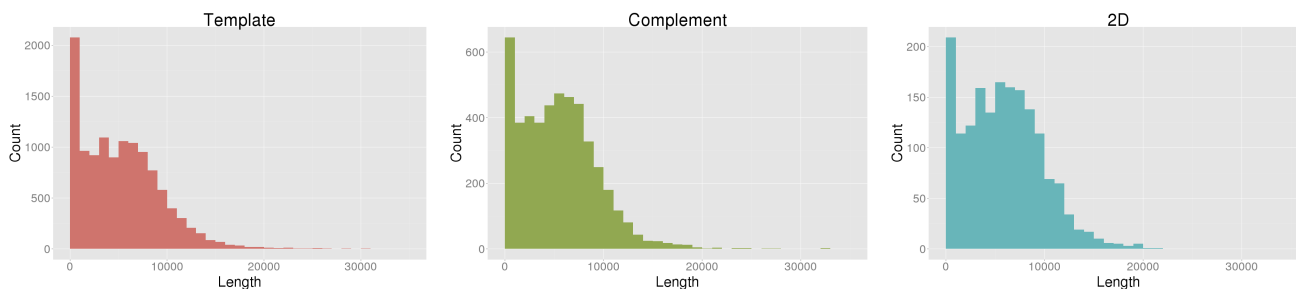
NanoOK report for MARC_ecoli_032615

Pass and fail counts

Type	Pass	Fail
Template	0	11789
Complement	0	4752
2D	0	1708

Read lengths

Type	NumReads	TotalBases	Mean	Longest	Shortest	N50	N50Count	N90	N90Count
Template	11789	64379730	5461.00	310267	7	8009	2775	3481	7261
Complement	4752	26183291	5509.95	32884	10	7700	1248	3534	3097
2D	1708	10063532	5892.00	21912	177	8169	469	3746	1141



Template alignments

Number of reads	11789
Number of reads with alignments	5674 (48.13%)
Number of reads without alignments	6115 (51.87%)

ID	Size	Number of Reads	% of Reads	Mean read length	Aligned bases	Mean coverage	Longest Perf Kmer
Control sequence	3560	448	3.80	2877.08	1284538	360.83	74
Escherichia coli	4641652	5226	44.33	7142.31	32875559	7.08	98

Complement alignments

Number of reads	4752
Number of reads with alignments	2696 (56.73%)
Number of reads without alignments	2056 (43.27%)

ID	Size	Number of Reads	% of Reads	Mean read length	Aligned bases	Mean coverage	Longest Perf Kmer
Control sequence	3560	75	1.58	2572.32	159446	44.79	47
Escherichia coli	4641652	2621	55.16	6703.65	15072351	3.25	66

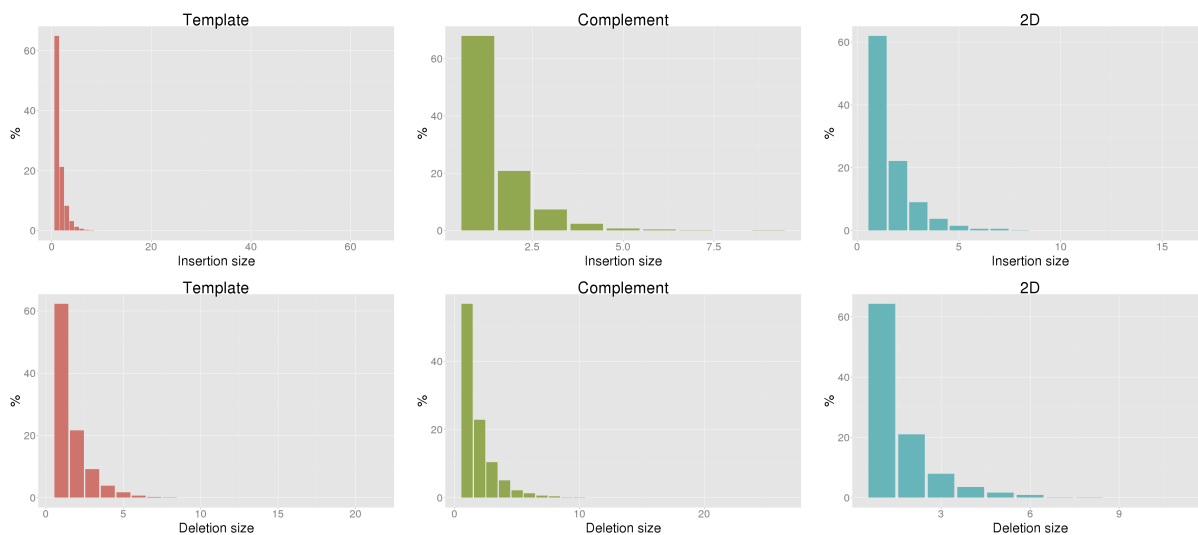
2D alignments

Number of reads	1708
Number of reads with alignments	1350 (79.04%)
Number of reads without alignments	358 (20.96%)

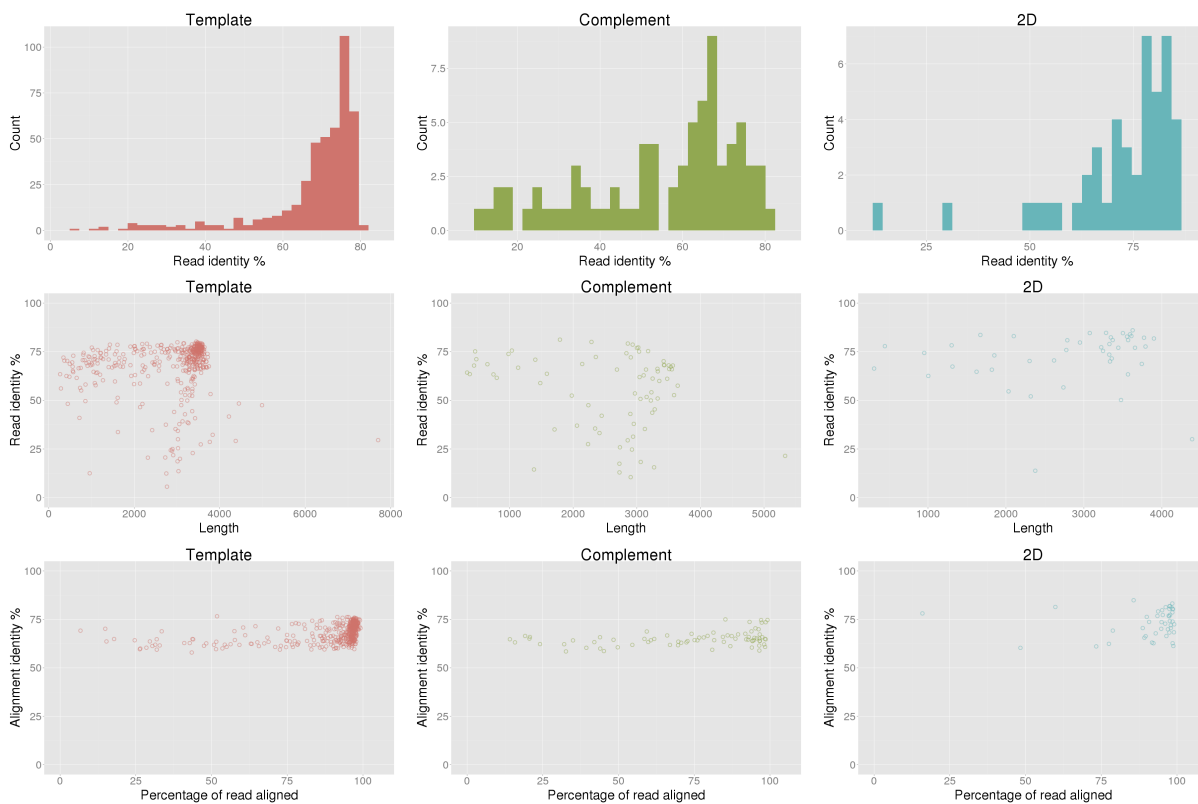
ID	Size	Number of Reads	% of Reads	Mean read length	Aligned bases	Mean coverage	Longest Perf Kmer
Control sequence	3560	45	2.63	2785.38	123293	34.63	89
Escherichia coli	4641652	1305	76.41	6615.68	8571112	1.85	195

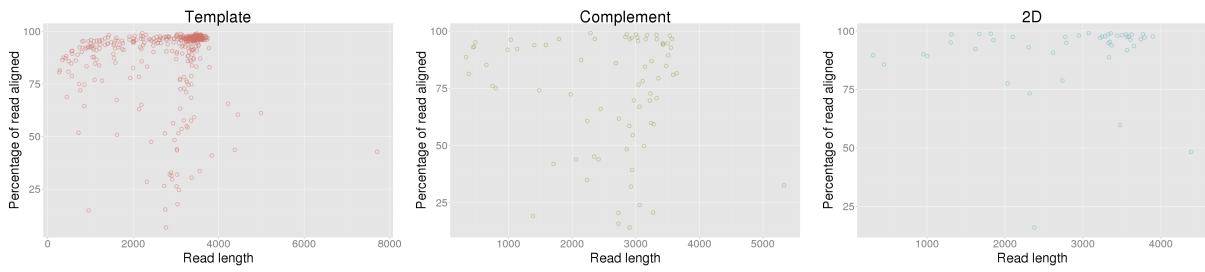
Control sequence error analysis

	Template	Complement	2D
Overall base identity (excluding indels)	68.40%	53.53%	72.61%
Aligned base identity (excluding indels)	81.14%	79.06%	85.66%
Identical bases per 100 aligned bases (including indels)	68.63%	64.77%	73.81%
Inserted bases per 100 aligned bases (including indels)	5.45%	4.62%	6.23%
Deleted bases per 100 aligned bases (including indels)	9.97%	13.45%	7.60%
Substitutions per 100 aligned bases (including indels)	15.95%	17.16%	12.36%
Mean insertion size	1.60	1.50	1.67
Mean deletion size	1.66	1.85	1.63

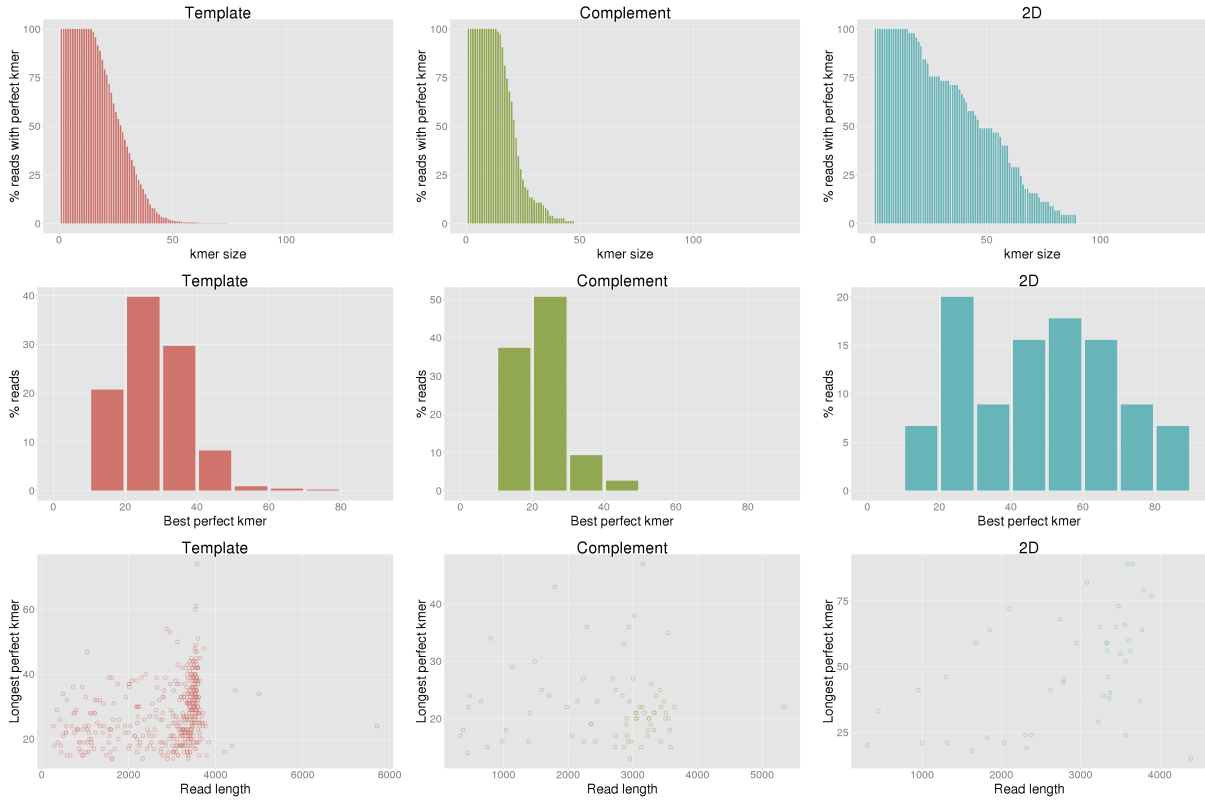


Control sequence read identity

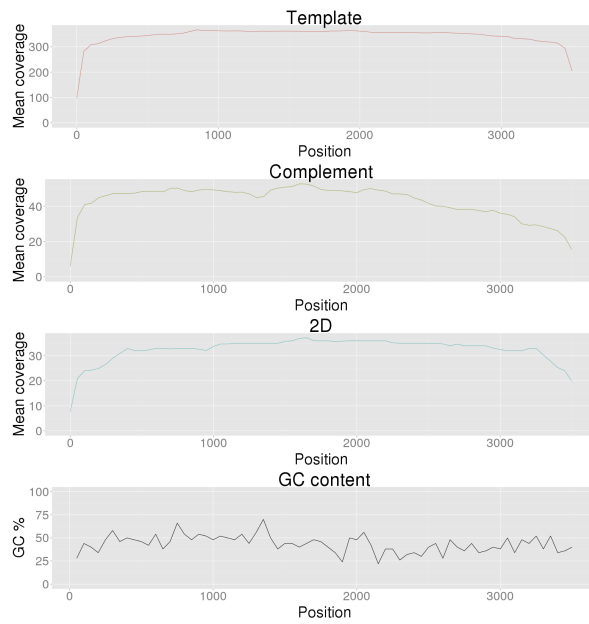




Control sequence perfect kmers



Control sequence coverage



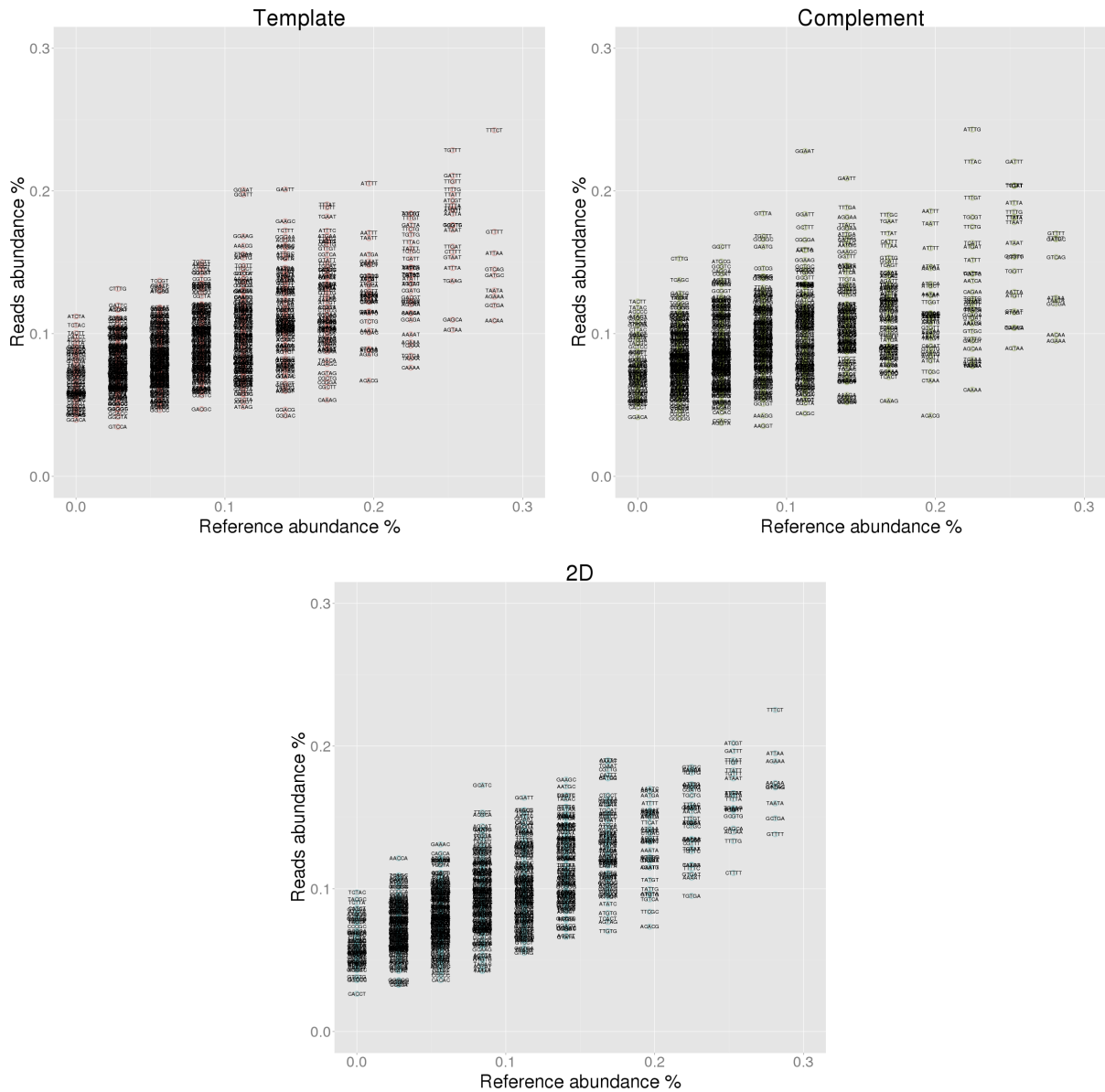
Control sequence 5-mer analysis

Under-represented 5-mers

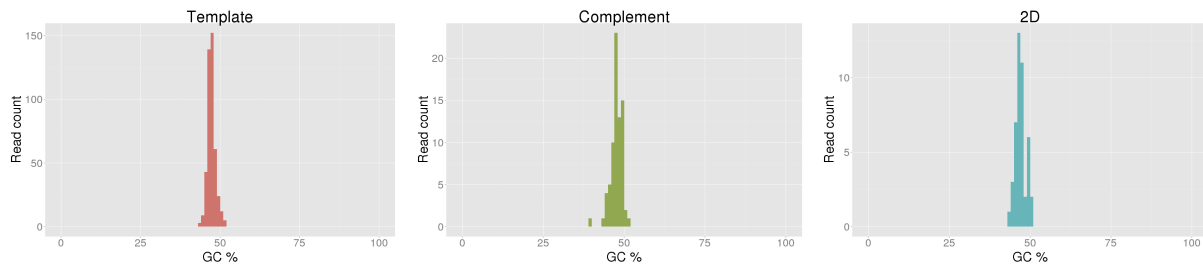
Rank	Template				Complement				2D			
	kmer	Ref %	Read %	Diff %	kmer	Ref %	Read %	Diff %	kmer	Ref %	Read %	Diff %
1	TTTTT	0.759	0.121	-0.638	TTTTT	0.759	0.091	-0.668	TTTTT	0.759	0.039	-0.719
2	AAAAA	0.478	0.069	-0.409	AAAAA	0.478	0.047	-0.431	AAAAA	0.478	0.052	-0.426
3	TGATG	0.393	0.145	-0.249	AA AAC	0.337	0.093	-0.244	TGATG	0.393	0.153	-0.241
4	AAAAC	0.337	0.104	-0.233	TGATG	0.393	0.162	-0.231	GATGT	0.309	0.138	-0.171
5	CTGAT	0.309	0.117	-0.192	GATGT	0.309	0.096	-0.213	AAAAC	0.337	0.171	-0.166
6	GATGT	0.309	0.119	-0.190	GCAAT	0.309	0.123	-0.186	CTGAT	0.309	0.155	-0.154
7	AACAA	0.281	0.109	-0.172	AGAAA	0.281	0.095	-0.186	AATAT	0.309	0.157	-0.152
8	GCTGA	0.281	0.120	-0.161	AACAA	0.281	0.099	-0.182	GTTTT	0.281	0.138	-0.143
9	AATAT	0.309	0.154	-0.155	CTGAT	0.309	0.129	-0.180	CTTTT	0.253	0.111	-0.142
10	AGAAA	0.281	0.126	-0.155	TTATC	0.309	0.138	-0.171	GCAAT	0.309	0.173	-0.136

Over-represented 5-mers

Rank	Template				Complement				2D			
	kmer	Ref %	Read %	Diff %	kmer	Ref %	Read %	Diff %	kmer	Ref %	Read %	Diff %
1	ATCTA	0.000	0.112	0.112	CTTTG	0.028	0.153	0.125	TCTAC	0.000	0.098	0.098
2	TCTAC	0.000	0.106	0.106	TACTT	0.000	0.123	0.123	AACCA	0.028	0.121	0.093
3	CTTTG	0.028	0.131	0.103	TATAC	0.000	0.118	0.118	TACGC	0.000	0.093	0.093
4	TACTT	0.000	0.100	0.100	GGAAT	0.112	0.228	0.116	TCTTA	0.000	0.090	0.090
5	CATCT	0.000	0.098	0.098	ACCCC	0.000	0.115	0.115	GCATC	0.084	0.173	0.088
6	ACCCC	0.000	0.096	0.096	ATACT	0.000	0.112	0.112	CATCT	0.000	0.086	0.086
7	TCTTA	0.000	0.094	0.094	GAGGA	0.000	0.111	0.111	GTCGA	0.000	0.086	0.086
8	GATTC	0.028	0.120	0.092	TCAGC	0.028	0.138	0.110	ATCTA	0.000	0.084	0.084
9	CCCCA	0.000	0.091	0.091	CCCCA	0.000	0.109	0.109	TTAGA	0.000	0.082	0.082
10	GTCTT	0.000	0.091	0.091	TTAGA	0.000	0.107	0.107	AAGGG	0.000	0.082	0.082

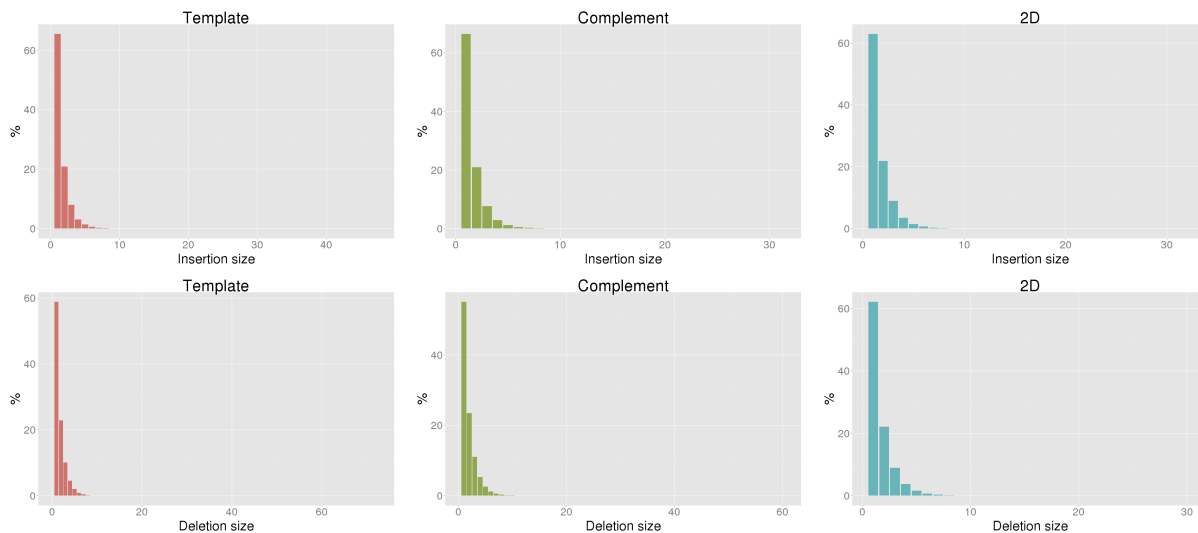


Control sequence GC content

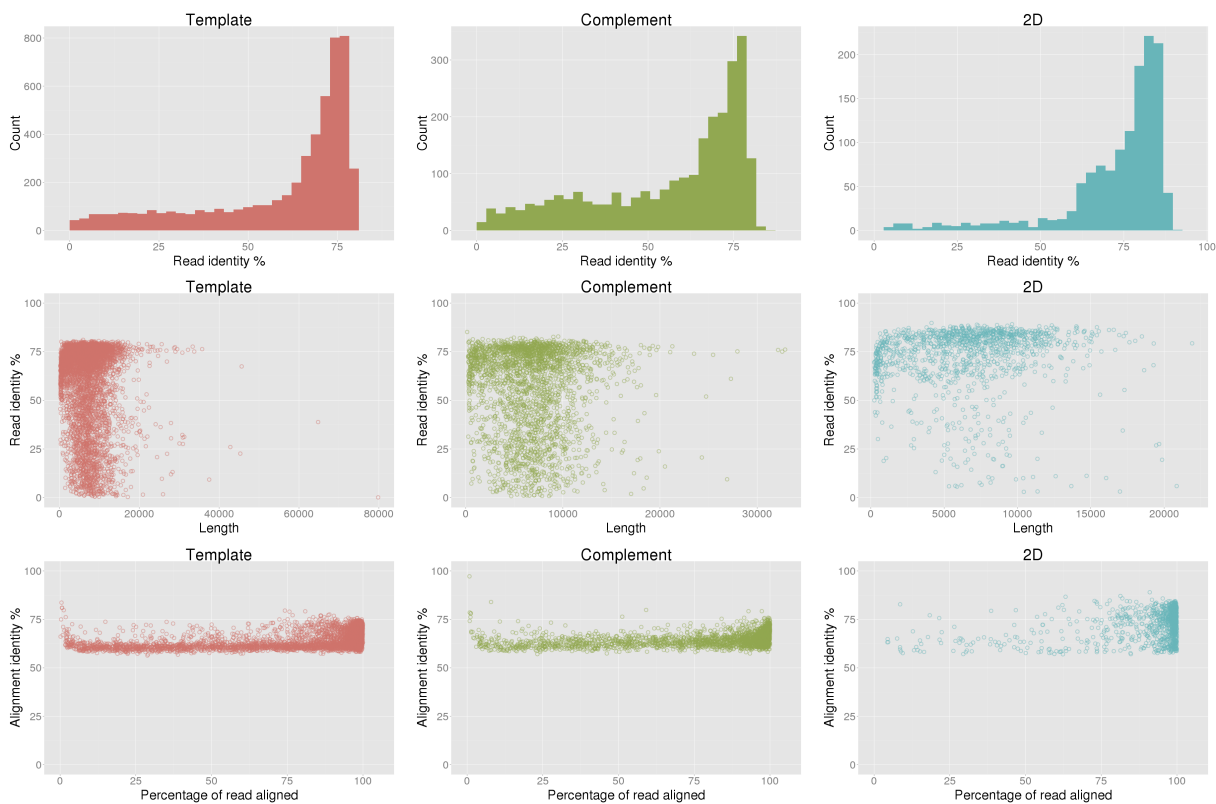


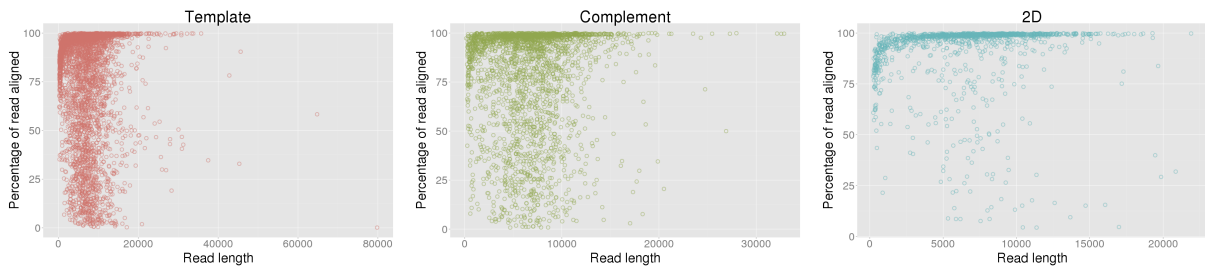
Escherichia coli error analysis

	Template	Complement	2D
Overall base identity (excluding indels)	57.75%	55.63%	73.06%
Aligned base identity (excluding indels)	79.04%	79.92%	85.58%
Identical bases per 100 aligned bases (including indels)	65.57%	64.85%	73.60%
Inserted bases per 100 aligned bases (including indels)	5.36%	4.73%	6.08%
Deleted bases per 100 aligned bases (including indels)	11.68%	14.12%	7.93%
Substitutions per 100 aligned bases (including indels)	17.39%	16.30%	12.40%
Mean insertion size	1.59	1.56	1.64
Mean deletion size	1.75	1.88	1.66

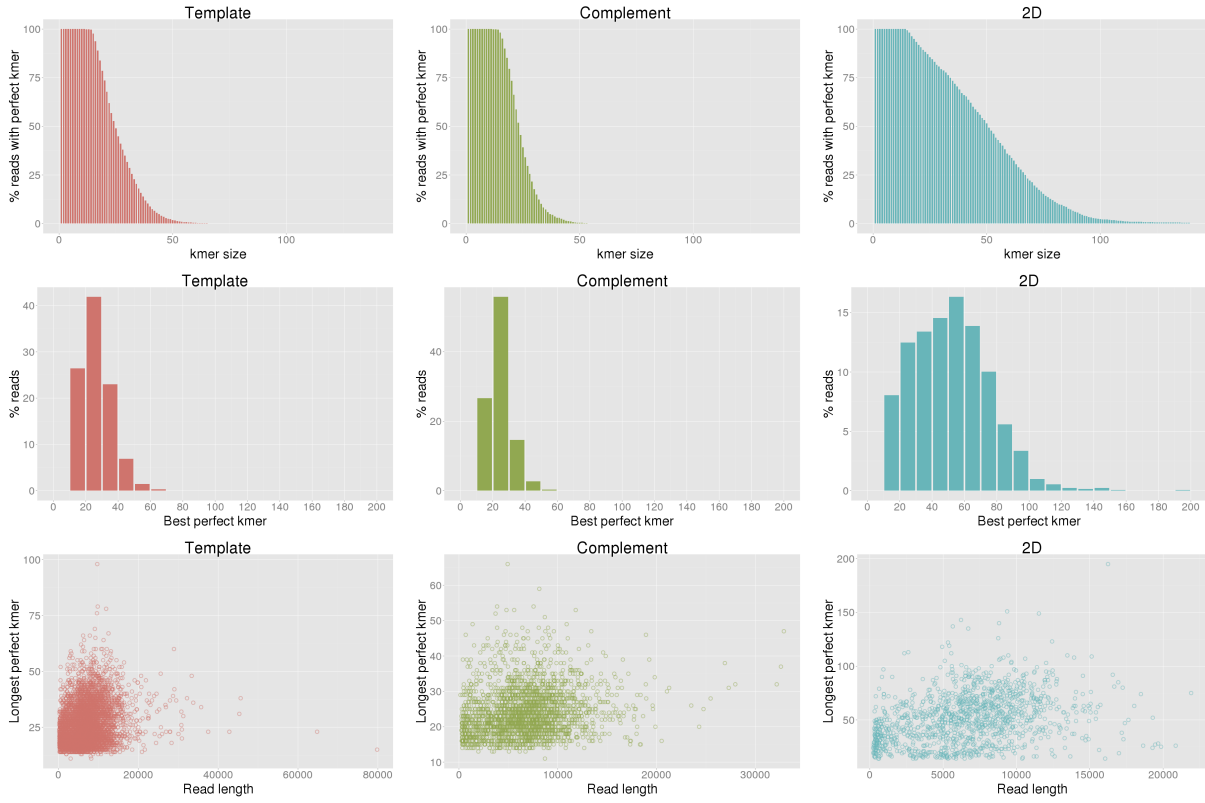


Escherichia coli read identity

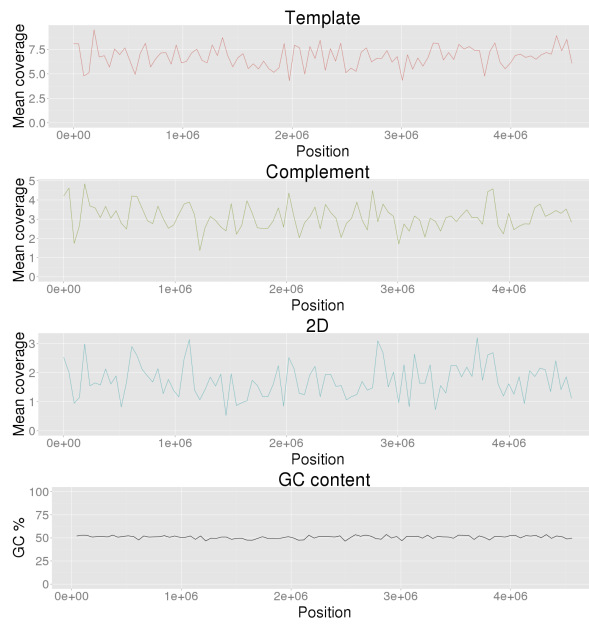




Escherichia coli perfect kmers



Escherichia coli coverage



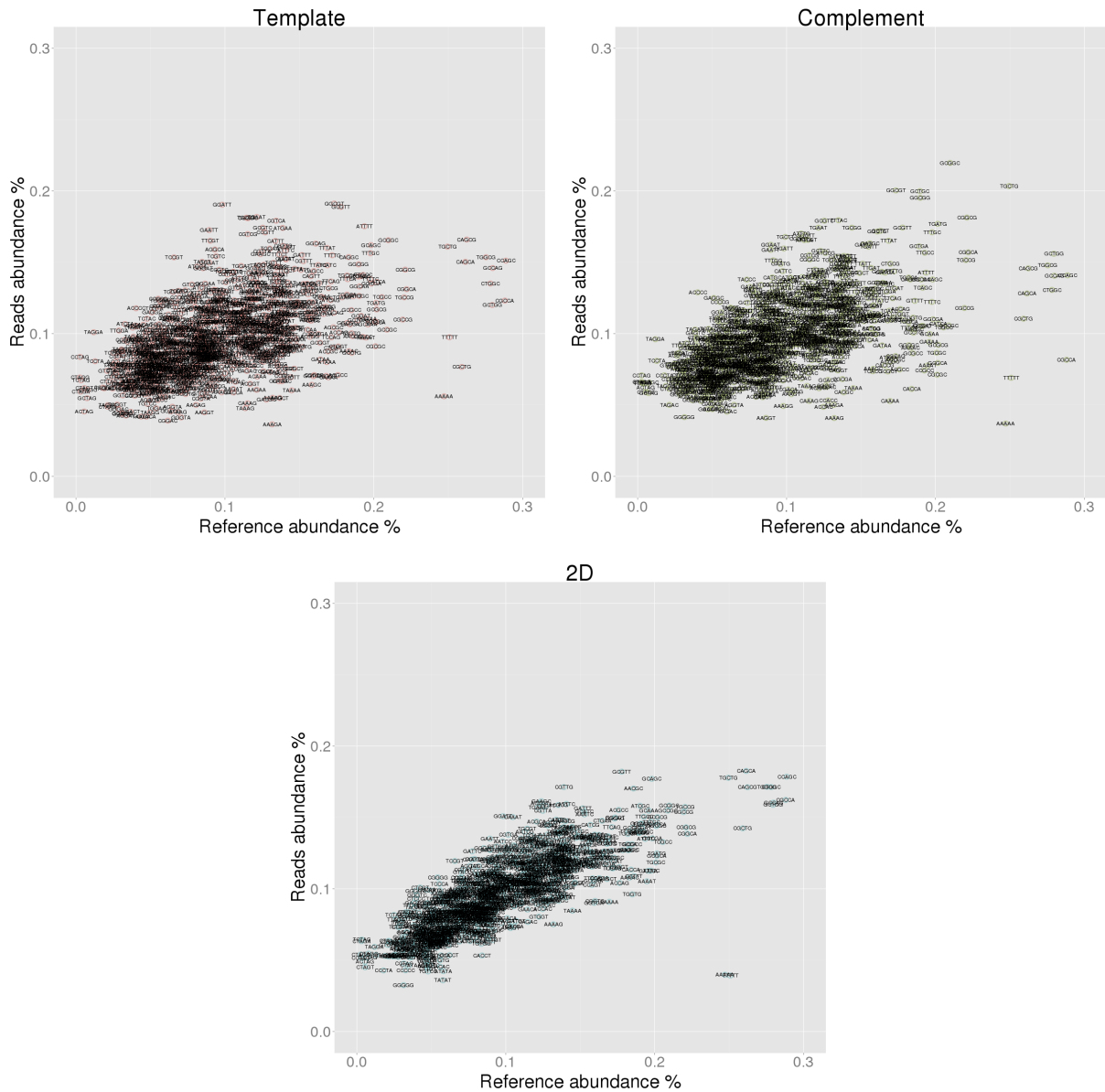
Escherichia coli 5-mer analysis

Under-represented 5-mers

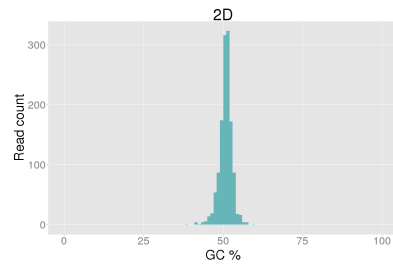
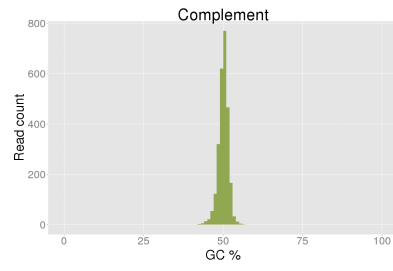
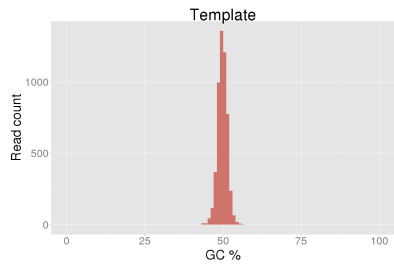
Rank	Template				Complement				2D			
	kmer	Ref %	Read %	Diff %	kmer	Ref %	Read %	Diff %	kmer	Ref %	Read %	Diff %
1	AAAAA	0.247	0.056	-0.191	AAAAA	0.247	0.037	-0.210	TTTTT	0.251	0.039	-0.212
2	CGCTG	0.259	0.077	-0.182	CGCCA	0.288	0.082	-0.206	AAAAA	0.247	0.040	-0.207
3	CGCCA	0.288	0.123	-0.165	TTTTT	0.251	0.069	-0.182	CGCCA	0.288	0.162	-0.126
4	GCTGG	0.279	0.120	-0.159	CGCTG	0.259	0.111	-0.149	GCTGG	0.279	0.159	-0.121
5	TTTTT	0.251	0.098	-0.153	CCAGC	0.289	0.141	-0.148	GCCAG	0.280	0.160	-0.119
6	CTGGC	0.278	0.135	-0.143	CTGGC	0.278	0.131	-0.148	CGCTG	0.259	0.142	-0.117
7	CCAGC	0.289	0.151	-0.137	GCCAG	0.280	0.141	-0.139	CCAGC	0.289	0.179	-0.110
8	GCCAG	0.280	0.146	-0.134	CAGCA	0.261	0.128	-0.133	CTGGC	0.278	0.171	-0.107
9	TGGCG	0.275	0.154	-0.122	CGCGC	0.201	0.071	-0.130	TGGCG	0.275	0.171	-0.104
10	CAGCA	0.261	0.150	-0.111	TGGCG	0.275	0.148	-0.127	CAGCG	0.262	0.171	-0.091

Over-represented 5-mers

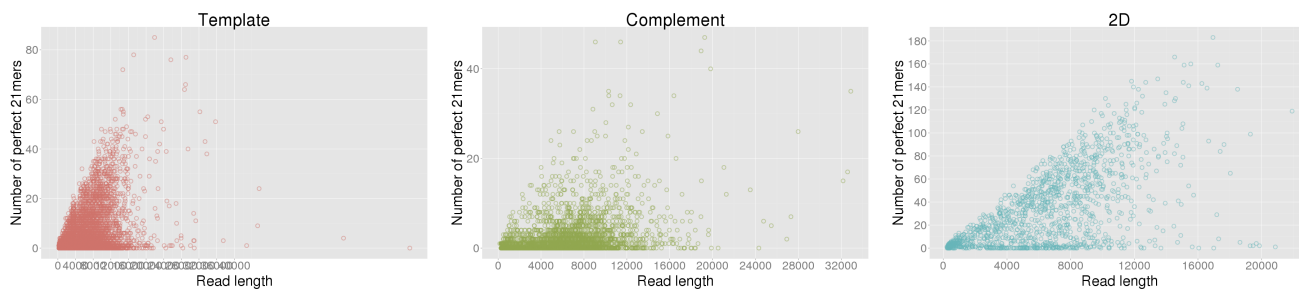
Rank	Template				Complement				2D			
	kmer	Ref %	Read %	Diff %	kmer	Ref %	Read %	Diff %	kmer	Ref %	Read %	Diff %
1	GGATT	0.098	0.190	0.092	ACCCC	0.040	0.129	0.089	TCTAG	0.003	0.064	0.061
2	TAGGA	0.012	0.101	0.089	TAGGA	0.012	0.096	0.084	CTAGA	0.003	0.063	0.060
3	TCCGT	0.066	0.153	0.088	GAGGC	0.051	0.125	0.074	GGGGT	0.039	0.099	0.059
4	GAATT	0.089	0.173	0.083	GGAAT	0.089	0.162	0.073	CTCGT	0.042	0.101	0.058
5	CCTAG	0.003	0.084	0.081	GAATT	0.089	0.159	0.069	TCTAA	0.025	0.082	0.057
6	ACCCC	0.040	0.118	0.077	TGCTT	0.099	0.168	0.069	GGGTC	0.040	0.095	0.055
7	TTCGT	0.090	0.165	0.075	TCCTA	0.013	0.081	0.068	TCCGT	0.066	0.120	0.054
8	ATCTA	0.033	0.107	0.074	CCTAG	0.003	0.071	0.068	CGGGG	0.054	0.108	0.054
9	TTGGA	0.029	0.102	0.073	CCCCG	0.055	0.122	0.067	CTCCC	0.040	0.093	0.053
10	CCCCG	0.055	0.125	0.069	TACCC	0.073	0.138	0.065	GGATT	0.098	0.151	0.053



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	8.45	9.03	5.23	0.00	8.61	8.89	5.41	0.00	8.69	8.93	4.90
C	8.93	0.00	8.94	9.77	9.38	0.00	8.67	9.41	8.91	0.00	10.12	8.90
G	9.46	8.94	0.00	8.52	8.86	8.68	0.00	8.98	8.77	10.11	0.00	8.54
T	5.45	8.99	8.30	0.00	5.61	8.93	8.56	0.00	4.88	8.83	8.43	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 (3.38%)	TTC (3.45%)	AAA (4.14%)	TTC (3.00%)	TGC (2.85%)	AAA (4.11%)	TTC (3.00%)	GCA (2.70%)	AAA (3.91%)	Most common
2	AAA (2.92%)	TGC (2.93%)	TTC (3.70%)	TGC (2.88%)	GGC (2.82%)	GCA (3.48%)	AAA (2.99%)	AAA (2.67%)	GCA (3.38%)	
3	TGC (2.78%)	AAA (2.81%)	GCA (3.27%)	AAA (2.84%)	GCA (2.74%)	GAA (3.20%)	GCA (2.99%)	TTC (2.64%)	TTC (3.15%)	
4	GCA (2.73%)	GCA (2.79%)	GAA (3.09%)	GCA (2.60%)	AAA (2.74%)	TTC (3.16%)	TGC (2.58%)	GCG (2.60%)	GAA (3.00%)	
5	ATC (2.51%)	TCA (2.46%)	TTT (2.66%)	GAA (2.50%)	TTC (2.69%)	TTT (2.66%)	GAA (2.42%)	TGC (2.57%)	TTT (2.83%)	
6	TCA (2.43%)	GCC (2.38%)	TGC (2.60%)	CAG (2.35%)	GAA (2.40%)	TGC (2.59%)	TCA (2.40%)	TCA (2.52%)	AAT (2.52%)	
7	GAA (2.32%)	ATC (2.37%)	AAT (2.51%)	TCA (2.33%)	GCC (2.30%)	TCA (2.32%)	ATC (2.35%)	GGC (2.49%)	GTT (2.37%)	
8	TTT (2.31%)	AAT (2.34%)	TCA (2.25%)	ATC (2.26%)	TCA (2.28%)	ATC (2.28%)	CGC (2.32%)	GAA (2.25%)	GCC (2.35%)	
9	GCC (2.30%)	GAA (2.29%)	ATC (2.21%)	TTT (2.26%)	AAT (2.25%)	AAT (2.24%)	TTT (2.27%)	GCC (2.23%)	TGC (2.30%)	
10	AAT (2.23%)	GGC (2.28%)	GCC (2.19%)	GGC (2.25%)	CAG (2.25%)	GCC (2.19%)	GCC (2.25%)	CGC (2.22%)	ATC (2.22%)	
										Least common
-10	TGT (0.99%)	AGG (0.93%)	CCT (0.92%)	GTG (0.96%)	AGT (0.93%)	CCC (0.93%)	CTC (1.03%)	GTA (1.01%)	CCT (0.96%)	
-9	CTC (0.92%)	AGT (0.92%)	AGA (0.86%)	AGA (0.94%)	CCC (0.92%)	CTC (0.91%)	TGT (1.00%)	CCC (0.95%)	AGG (0.94%)	
-8	CCC (0.87%)	CCT (0.89%)	GGG (0.85%)	CTC (0.91%)	AGG (0.91%)	CCT (0.88%)	CCC (0.85%)	ACT (0.93%)	CCC (0.92%)	
-7	GGA (0.78%)	CTT (0.86%)	TGT (0.84%)	GGA (0.88%)	CTC (0.91%)	AGT (0.88%)	GAG (0.81%)	CGA (0.93%)	CGA (0.82%)	
-6	AGA (0.78%)	GAG (0.85%)	AGG (0.83%)	CCC (0.82%)	GGA (0.90%)	ACT (0.81%)	GGA (0.81%)	CTT (0.83%)	CTT (0.81%)	
-5	GAG (0.76%)	CGA (0.83%)	AGT (0.82%)	AGG (0.74%)	CCT (0.85%)	AGG (0.79%)	AGA (0.79%)	CCT (0.82%)	GAG (0.77%)	
-4	AGG (0.69%)	GGA (0.70%)	CTT (0.77%)	GAG (0.72%)	GAG (0.84%)	GGG (0.77%)	AGG (0.73%)	AGA (0.81%)	GGA (0.73%)	
-3	GGG (0.69%)	AGA (0.70%)	GAG (0.63%)	GGG (0.58%)	GGG (0.81%)	GAG (0.59%)	GGG (0.65%)	GGA (0.71%)	AGA (0.68%)	
-2	CTA (0.51%)	TAG (0.51%)	TAG (0.39%)	CTA (0.51%)	TAG (0.53%)	CTA (0.41%)	CTA (0.52%)	CTA (0.61%)	TAG (0.43%)	
-1	TAG (0.42%)	CTA (0.48%)	CTA (0.37%)	TAG (0.42%)	CTA (0.52%)	TAG (0.37%)	TAG (0.46%)	TAG (0.58%)	CTA (0.37%)	

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 (1.07%)	AAAA (1.33%)	TTGC (0.89%)	CGGC (1.01%)	AAAA (1.14%)	TTTC (0.87%)	TTCA (0.95%)	GAAA (1.15%)
2	GAAA (0.98%)	TTCA (0.94%)	TTTT (1.22%)	CAAA (0.88%)	TGGC (1.01%)	CAAA (1.11%)	GAAA (0.87%)	TGGC (0.92%)	AAAA (1.12%)
3	TTCA (0.90%)	TGCC (0.92%)	GAAA (1.20%)	CTGC (0.86%)	CAGC (1.00%)	GAAA (1.01%)	CGCC (0.84%)	CAGC (0.91%)	GGCA (1.00%)
4	AAAA (0.87%)	TTCC (0.92%)	GGCA (0.90%)	ATCA (0.86%)	TTGC (0.94%)	TGAA (0.93%)	ATCA (0.83%)	TTTC (0.78%)	TTTT (0.98%)
5	TTGC (0.85%)	TTGC (0.87%)	CAAA (0.90%)	CAGC (0.85%)	TTCC (0.86%)	TTTT (0.92%)	GGCA (0.81%)	CGCC (0.78%)	TGCC (0.88%)
6	TGCC (0.84%)	AAAA (0.84%)	GTTC (0.90%)	AAAA (0.80%)	CTGC (0.82%)	AGCA (0.88%)	AACA (0.80%)	TGCC (0.78%)	TTTT (0.87%)
7	AACG (0.80%)	CAGC (0.84%)	TTTT (0.89%)	CGGC (0.78%)	TGCC (0.81%)	GGCA (0.88%)	CAAA (0.79%)	GGGC (0.77%)	CGCC (0.85%)
8	TTTC (0.79%)	GAAA (0.83%)	GGAA (0.89%)	ATTC (0.78%)	CAAA (0.81%)	ATCA (0.86%)	TTCA (0.79%)	GGCG (0.75%)	CAAA (0.85%)
9	ATCA (0.79%)	CTGC (0.83%)	TGCC (0.89%)	TTTT (0.77%)	ATCA (0.80%)	TTGC (0.85%)	GCCA (0.78%)	ATCA (0.75%)	CGTT (0.85%)
10	CAGC (0.78%)	GTTC (0.82%)	GCAA (0.88%)	TGCC (0.75%)	TTCA (0.79%)	TGCC (0.85%)	AAAA (0.78%)	CTGC (0.75%)	TGCA (0.83%)
-10	CCCT (0.12%)	CGGA (0.12%)	ACTA (0.11%)	CTAA (0.11%)	GGAC (0.12%)	GGAC (0.11%)	CCCT (0.13%)	CCCC (0.14%)	GCTA (0.11%)
-9	TAGT (0.12%)	TAGT (0.12%)	CTAT (0.11%)	GTGT (0.11%)	CCCC (0.12%)	TAGA (0.10%)	ACTA (0.13%)	CGGA (0.14%)	ACTT (0.11%)
-8	AGGG (0.12%)	CTAT (0.11%)	CGAG (0.10%)	GTAG (0.10%)	GTGT (0.12%)	ACTA (0.10%)	GGGG (0.12%)	CTAT (0.13%)	TCTA (0.10%)
-7	CTAA (0.12%)	GGAC (0.11%)	TAGT (0.10%)	TAGA (0.10%)	ACCT (0.11%)	CGAG (0.09%)	TAGT (0.12%)	ACCT (0.13%)	GTAG (0.10%)
-6	GAGG (0.10%)	CCCT (0.11%)	TAGA (0.09%)	GGAC (0.10%)	CTAA (0.11%)	CTAT (0.09%)	GAGG (0.12%)	CTAA (0.13%)	CTAA (0.10%)
-5	GGAC (0.09%)	CTAA (0.09%)	GGAC (0.09%)	CCCT (0.09%)	TAGA (0.10%)	GAGG (0.09%)	CTAA (0.12%)	CCCT (0.10%)	ACTA (0.09%)
-4	CCTA (0.06%)	TAGG (0.08%)	TCTA (0.08%)	GAGG (0.09%)	CCCT (0.07%)	CCCT (0.08%)	TAGA (0.07%)	TAGG (0.08%)	TAGG (0.07%)
-3	TAGA (0.06%)	TAGA (0.06%)	TAGG (0.07%)	CCTA (0.07%)	TAGG (0.07%)	TAGG (0.07%)	CCTA (0.07%)	TAGA (0.08%)	TAGA (0.05%)
-2	TAGG (0.05%)	CCTA (0.05%)	CCTA (0.05%)	TAGG (0.05%)	CCTA (0.05%)	CCTA (0.05%)	TAGG (0.05%)	CCTA (0.07%)	CCTA (0.04%)
-1	CTAG (0.01%)	CTAG (0.01%)	CTAG (0.01%)	CTAG (0.01%)	CTAG (0.02%)	CTAG (0.01%)	CTAG (0.02%)	CTAG (0.02%)	CTAG (0.01%)

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	ATTTTC (0.32%)	CAGCA (0.36%)	GAAAA (0.42%)	CAGCA (0.37%)	CAGCA (0.45%)	CAGCA (0.53%)	CAGCA (0.35%)	CTGGC (0.36%)	CAGCA (0.40%)
2	CTGGC (0.31%)	TTGCC (0.32%)	CAAAA (0.38%)	GCTGC (0.35%)	CTGGC (0.36%)	GCAAA (0.40%)	CGCCA (0.32%)	CAGCA (0.32%)	TGGCA (0.37%)
3	TTATC (0.31%)	CTGGC (0.32%)	CAGCA (0.38%)	GCAAA (0.33%)	GCGGC (0.36%)	ATAAA (0.36%)	CGGCA (0.31%)	TGGCG (0.31%)	GAAAA (0.37%)
4	CAGCA (0.31%)	TTTCA (0.31%)	GCAAA (0.36%)	CATCA (0.33%)	CCAGC (0.31%)	CGGCA (0.35%)	CAAAA (0.30%)	CCAGC (0.30%)	CGGCA (0.35%)
5	TTGCC (0.30%)	TTTTG (0.30%)	AGAAA (0.33%)	TTTTG (0.31%)	TTTTG (0.31%)	CAAAA (0.34%)	CTGGC (0.30%)	TTTTCA (0.29%)	TTGCC (0.35%)
6	CAAAA (0.29%)	ATTTTC (0.30%)	ATTTTC (0.33%)	TTGCC (0.29%)	CATCA (0.30%)	CATCA (0.33%)	CATCA (0.29%)	CGCCA (0.28%)	GCAAA (0.34%)
7	CGCCA (0.29%)	CATCA (0.29%)	TGAAA (0.33%)	CCAGC (0.28%)	GCTGC (0.30%)	GAAAA (0.33%)	GCAAA (0.28%)	GCGGC (0.28%)	CAAAA (0.34%)
8	TTTTG (0.28%)	CGCCA (0.29%)	CGTTC (0.32%)	GCGGC (0.28%)	AATCA (0.29%)	TTGCC (0.33%)	TGGCA (0.28%)	GCAGC (0.28%)	GCGTT (0.32%)
9	ATTTT (0.28%)	GCAGC (0.29%)	TGTTT (0.32%)	AACGC (0.27%)	TCAGC (0.29%)	ACGCA (0.32%)	GCTGC (0.27%)	GCAAA (0.27%)	TCTTC (0.31%)
10	GAAAA (0.28%)	TTTTCC (0.29%)	TTGCC (0.31%)	CAAAA (0.27%)	TTGCC (0.29%)	AAGAA (0.30%)	TTGCC (0.27%)	CATCA (0.27%)	CGCCA (0.31%)
-10	GGACC (0.01%)	GGACC (0.01%)	CTTAG (0.01%)	AGTAG (0.01%)	ACCTA (0.01%)	ACCTA (0.01%)	TAGGG (0.01%)	TAGGG (0.01%)	TAGGA (0.01%)
-9	CCCTA (0.01%)	CCCTA (0.01%)	CCCTA (0.01%)	GGGAC (0.01%)	CTAGC (0.01%)	CCCTA (0.01%)	TAGGA (0.01%)	TAGGA (0.01%)	ACTAG (0.01%)
-8	CTAGT (0.00%)	GCTAG (0.00%)	ACTAG (0.00%)	CTTAG (0.01%)	CCCCC (0.01%)	CTAGC (0.00%)	GCTAG (0.01%)	CCCTA (0.01%)	ACCTA (0.00%)
-7	CCTAG (0.00%)	CTAGC (0.00%)	CTAGT (0.00%)	CCCTA (0.01%)	ACTAG (0.01%)	CTAGT (0.00%)	CTAGT (0.01%)	GCTAG (0.01%)	TCCTA (0.00%)
-6	ACTAG (0.00%)	ACTAG (0.00%)	CCTAG (0.00%)	GGGGG (0.01%)	GCTAG (0.01%)	CTAGA (0.00%)	CTAGC (0.00%)	CTAGC (0.01%)	GCTAG (0.00%)
-5	CTAGC (0.00%)	TCTAG (0.00%)	GCTAG (0.00%)	GCTAG (0.00%)	CTAGT (0.00%)	GCTAG (0.00%)	TCTAG (0.00%)	ACTAG (0.01%)	CTAGC (0.00%)
-4	GCTAG (0.00%)	CTAGT (0.00%)	CTAGC (0.00%)	CTAGC (0.00%)	TCTAG (0.00%)	ACTAG (0.00%)	CTAGA (0.00%)	TCTAG (0.00%)	CTAGC (0.00%)
-3	TCTAG (0.00%)	CTAGA (0.00%)	CTAGA (0.00%)	CTAGT (0.00%)	CTAGG (0.00%)	CCTAG (0.00%)	CCTAG (0.00%)	CTAGT (0.00%)	CTAGT (0.00%)
-2	CTAGG (0.00%)	CCTAG (0.00%)	CTAGG (0.00%)	CTAGG (0.00%)	CCTAG (0.00%)	TCTAG (0.00%)	ACTAG (0.00%)	CTAGG (0.00%)	CTAGA (0.00%)
-1	CTAGA (0.00%)	CTAGG (0.00%)	TCTAG (0.00%)	ACTAG (0.00%)	CTAGA (0.00%)	CTAGG (0.00%)	CTAGG (0.00%)	CTAGA (0.00%)	TCTAG (0.00%)

Most common

Least common

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