

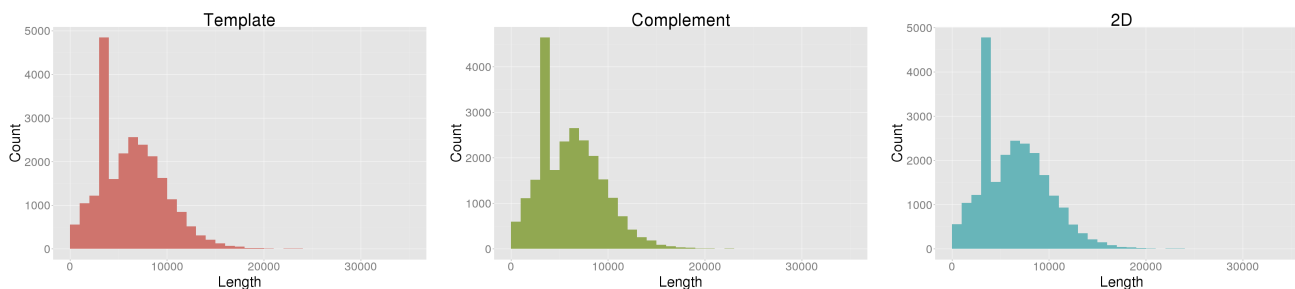
NanoOK report for WTCHG_MARC_Ph1.1

Pass and fail counts

Type	Pass	Fail
Template	23566	0
Complement	23566	0
2D	23566	0

Read lengths

Type	NumReads	TotalBases	Mean	Longest	Shortest	N50	N50Count	N90	N90Count
Template	23566	150956583	6405.69	49028	166	7978	7185	3521	17782
Complement	23566	145929165	6192.36	45561	169	7734	7170	3434	17691
2D	23566	153741579	6523.87	48834	159	8142	7177	3581	17745



Template alignments

Number of reads	23566
Number of reads with alignments	23479 (99.63%)
Number of reads without alignments	87 (0.37%)

ID	Size	Number of Reads	% of Reads	Mean read length	Aligned bases	Mean coverage	Longest Perf Kmer
Control sequence	3560	4167	17.68	3316.43	14544732	4085.60	84
Escherichia coli	4641652	19312	81.95	7095.89	145822256	31.42	88

Complement alignments

Number of reads	23566
Number of reads with alignments	23415 (99.36%)
Number of reads without alignments	151 (0.64%)

ID	Size	Number of Reads	% of Reads	Mean read length	Aligned bases	Mean coverage	Longest Perf Kmer
Control sequence	3560	4151	17.61	3162.70	13110944	3682.85	59
Escherichia coli	4641652	19264	81.74	6885.84	140531595	30.28	72

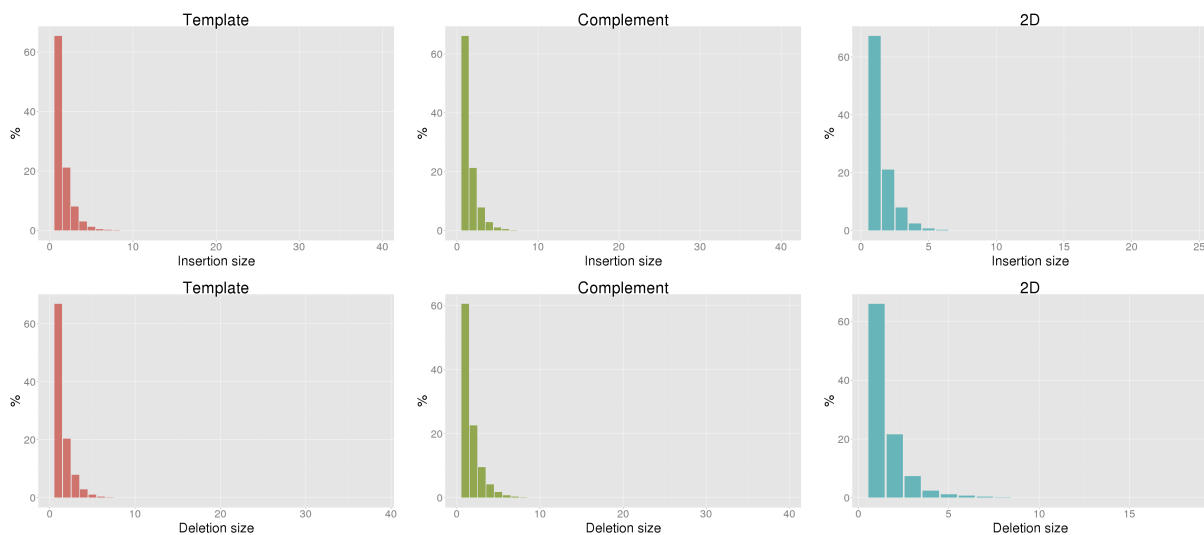
2D alignments

Number of reads	23566
Number of reads with alignments	23563 (99.99%)
Number of reads without alignments	3 (0.01%)

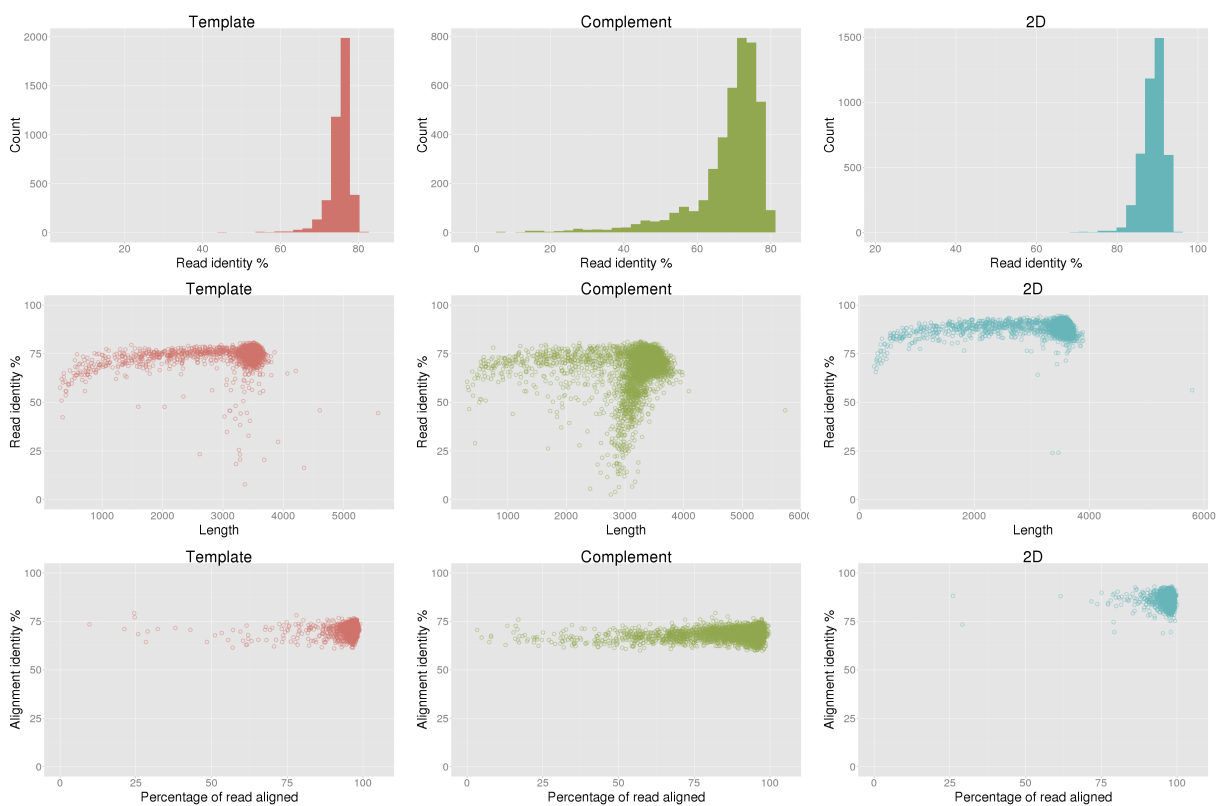
ID	Size	Number of Reads	% of Reads	Mean read length	Aligned bases	Mean coverage	Longest Perf Kmer
Control sequence	3560	4186	17.76	3341.43	14350536	4031.05	222
Escherichia coli	4641652	19377	82.22	7211.11	143686154	30.96	264

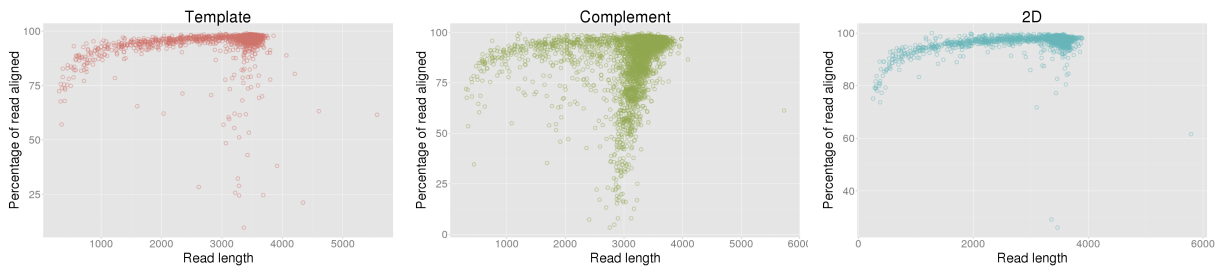
Control sequence error analysis

	Template	Complement	2D
Overall base identity (excluding indels)	75.10%	68.54%	88.90%
Aligned base identity (excluding indels)	82.66%	81.68%	94.39%
Identical bases per 100 aligned bases (including indels)	71.35%	68.63%	86.65%
Inserted bases per 100 aligned bases (including indels)	5.14%	4.78%	3.31%
Deleted bases per 100 aligned bases (including indels)	8.54%	11.21%	4.90%
Substitutions per 100 aligned bases (including indels)	14.97%	15.39%	5.15%
Mean insertion size	1.59	1.55	1.50
Mean deletion size	1.54	1.70	1.56

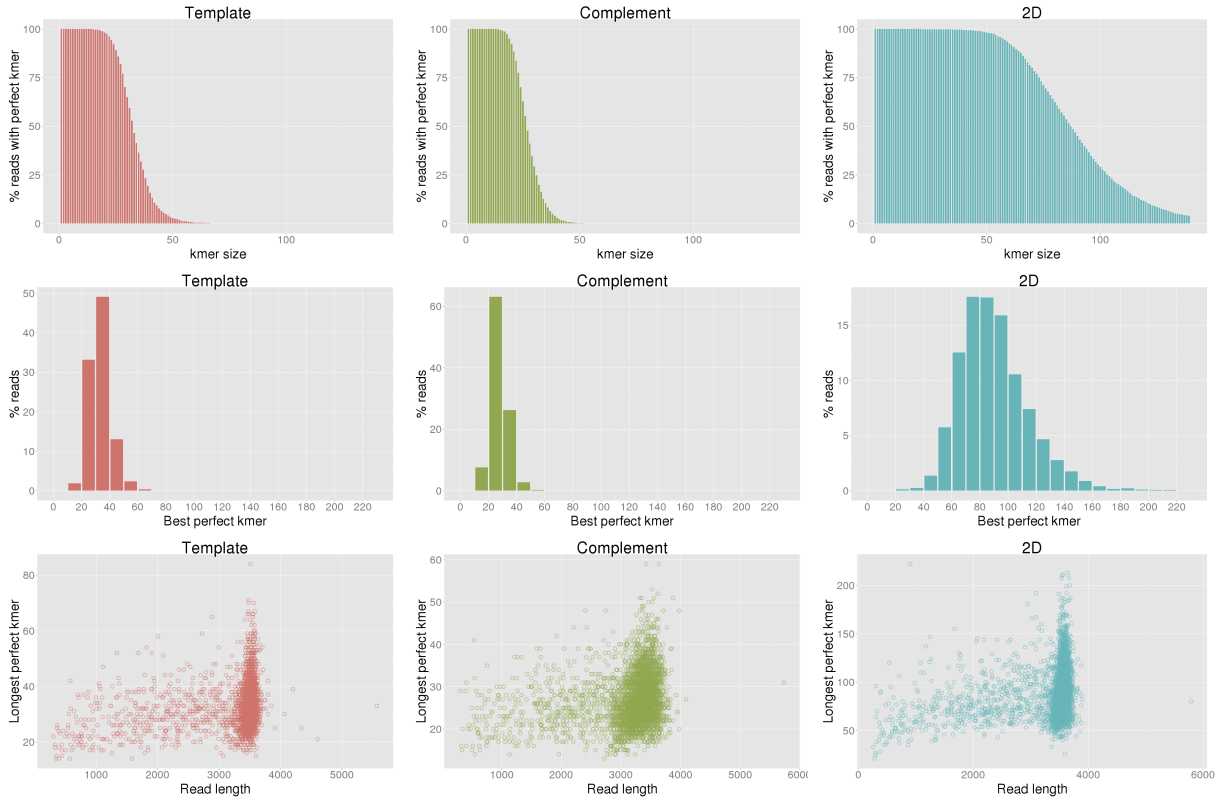


Control sequence read identity

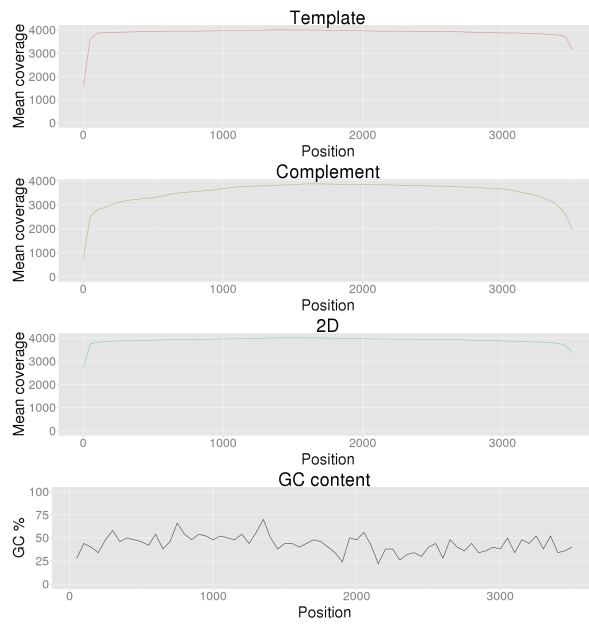




Control sequence perfect kmers



Control sequence coverage



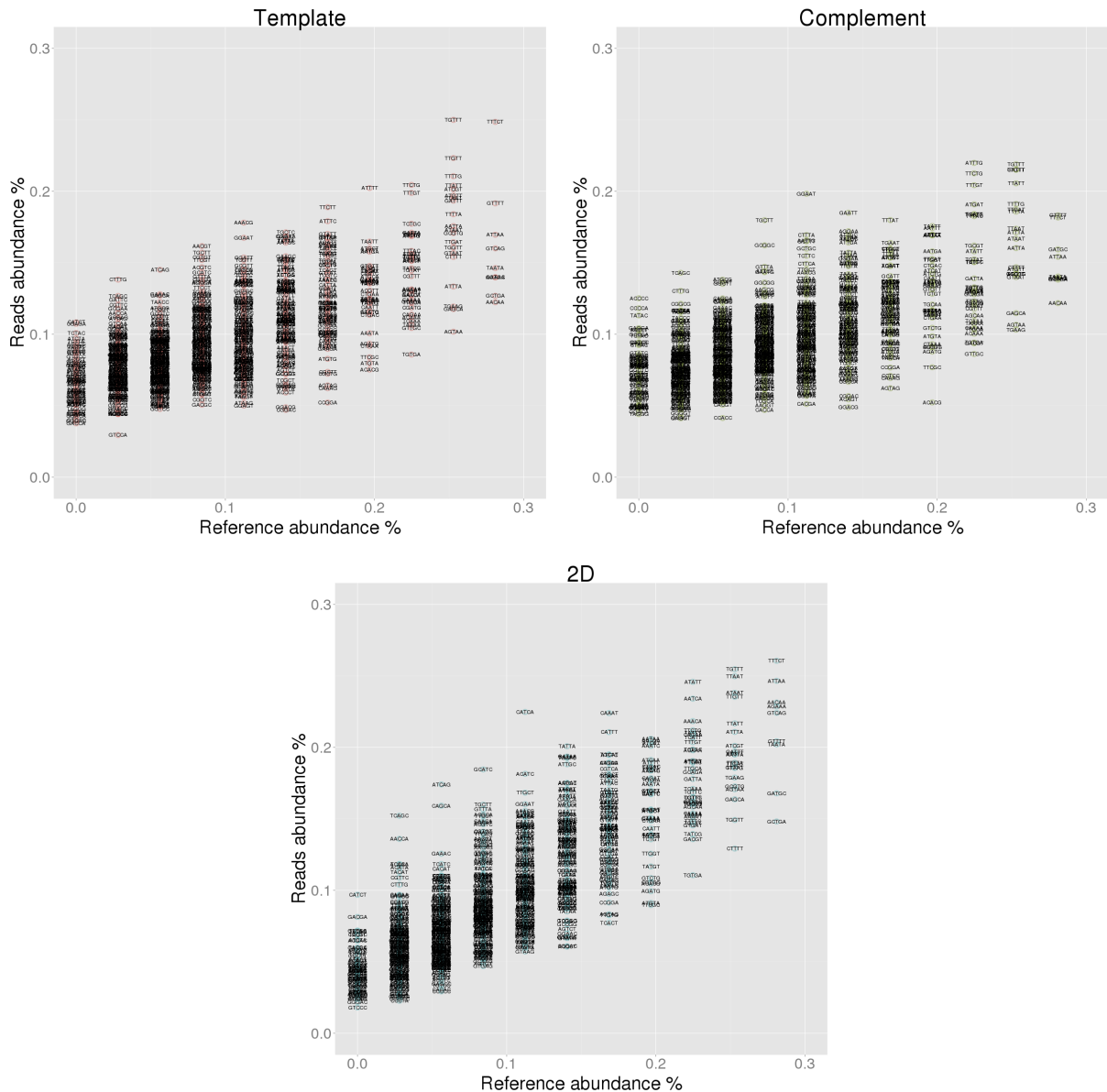
Control sequence 5-mer analysis

Under-represented 5-mers

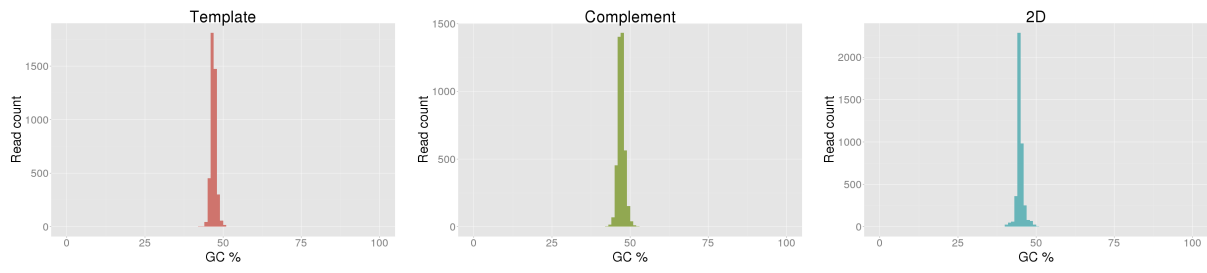
Rank	Template				Complement				2D			
	kmer	Ref %	Read %	Diff %	kmer	Ref %	Read %	Diff %	kmer	Ref %	Read %	Diff %
1	TTTTT	0.759	0.159	-0.600	TTTTT	0.759	0.108	-0.651	TTTTT	0.759	0.068	-0.691
2	AAAAA	0.478	0.123	-0.355	AAAAA	0.478	0.077	-0.401	AAAAA	0.478	0.085	-0.393
3	TGATG	0.393	0.154	-0.239	AA AAC	0.337	0.134	-0.204	TGATG	0.393	0.202	-0.191
4	AAAAC	0.337	0.133	-0.204	TGATG	0.393	0.203	-0.191	CTGAT	0.309	0.158	-0.151
5	GATGT	0.309	0.113	-0.196	GATGT	0.309	0.123	-0.186	GATGT	0.309	0.165	-0.144
6	CTGAT	0.309	0.134	-0.175	GCAAT	0.309	0.137	-0.172	GCTGA	0.281	0.148	-0.133
7	AACAA	0.281	0.122	-0.159	AACAA	0.281	0.122	-0.159	CTTTT	0.253	0.129	-0.124
8	GCTGA	0.281	0.127	-0.154	TTATC	0.309	0.154	-0.155	AAAAC	0.337	0.216	-0.121
9	GCAAT	0.309	0.156	-0.153	TGAAG	0.253	0.103	-0.150	TGTGA	0.225	0.111	-0.114
10	AGTAA	0.253	0.102	-0.151	AGTAA	0.253	0.107	-0.146	GATGC	0.281	0.168	-0.113

Over-represented 5-mers

Rank	Template				Complement				2D			
	kmer	Ref %	Read %	Diff %	kmer	Ref %	Read %	Diff %	kmer	Ref %	Read %	Diff %
1	CTTTG	0.028	0.138	0.110	ACCCC	0.000	0.125	0.125	TCAGC	0.028	0.152	0.124
2	CATCT	0.000	0.108	0.108	CCCCA	0.000	0.118	0.118	ATCAG	0.056	0.174	0.118
3	CGAGA	0.000	0.107	0.107	TCAGC	0.028	0.143	0.115	CATCA	0.112	0.225	0.112
4	TCTAC	0.000	0.101	0.101	TATAC	0.000	0.113	0.113	AACCA	0.028	0.136	0.108
5	TCAGC	0.028	0.127	0.099	GAGGA	0.000	0.104	0.104	CAGCA	0.056	0.159	0.103
6	ATCTA	0.000	0.097	0.097	TACTT	0.000	0.103	0.103	GCATC	0.084	0.185	0.100
7	GATTC	0.028	0.124	0.096	ACTCT	0.000	0.103	0.103	CATCT	0.000	0.097	0.097
8	TCTTA	0.000	0.095	0.095	CTTTG	0.028	0.130	0.102	TCACA	0.028	0.118	0.090
9	ACCCC	0.000	0.093	0.093	GCCGA	0.000	0.100	0.100	ACCAA	0.028	0.118	0.090
10	CGTTC	0.028	0.120	0.092	TCTAC	0.000	0.099	0.099	ACATA	0.028	0.116	0.088

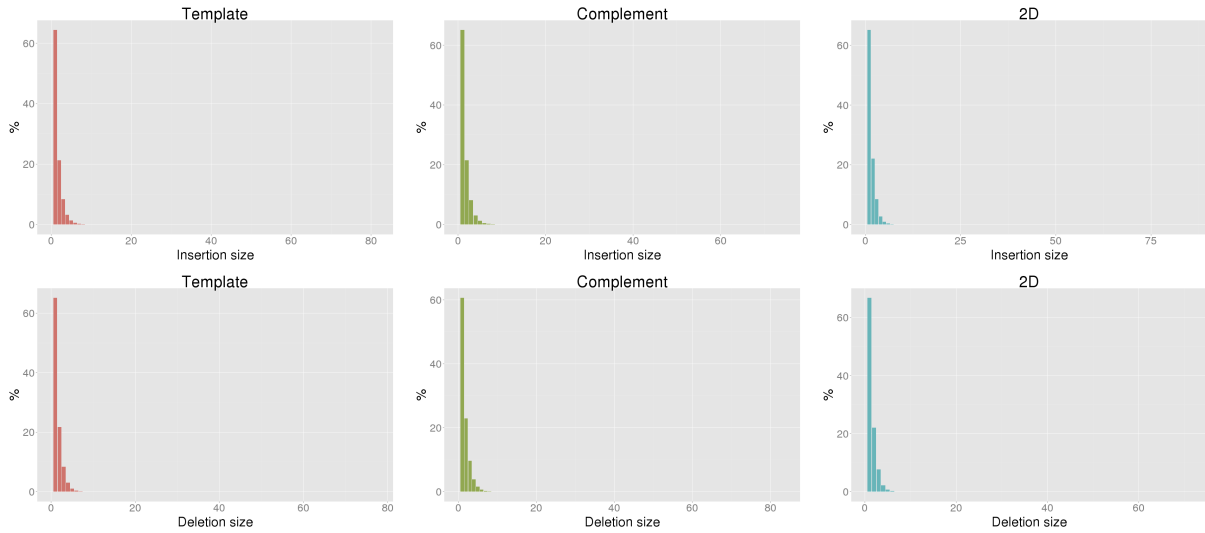


Control sequence GC content

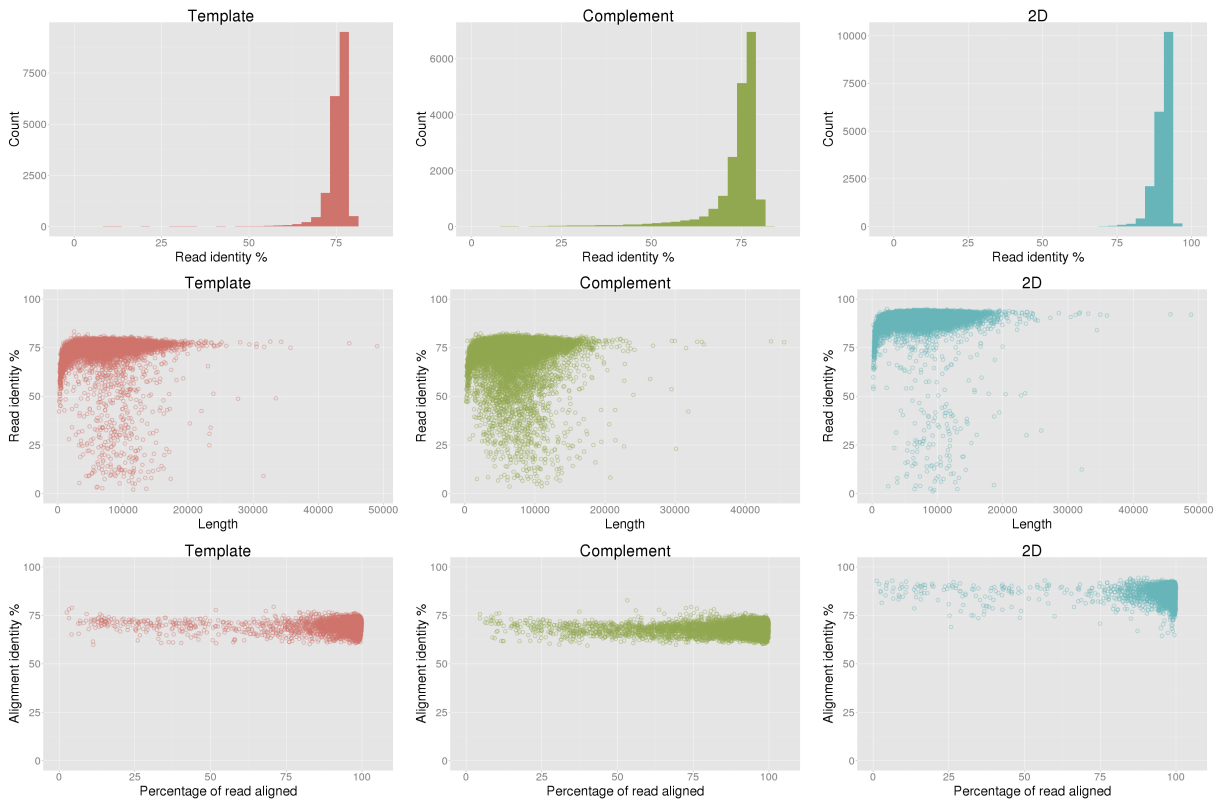


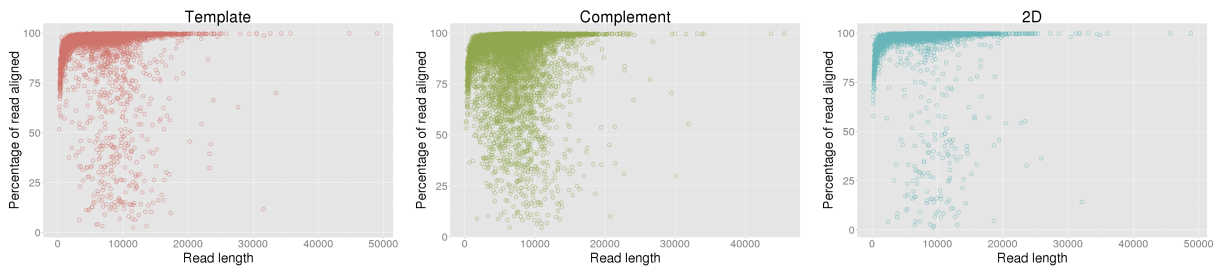
Escherichia coli error analysis

	Template	Complement	2D
Overall base identity (excluding indels)	74.82%	73.08%	89.95%
Aligned base identity (excluding indels)	81.93%	82.12%	94.84%
Identical bases per 100 aligned bases (including indels)	70.32%	68.98%	87.48%
Inserted bases per 100 aligned bases (including indels)	5.54%	5.14%	3.38%
Deleted bases per 100 aligned bases (including indels)	8.63%	10.86%	4.39%
Substitutions per 100 aligned bases (including indels)	15.51%	15.02%	4.76%
Mean insertion size	1.62	1.58	1.55
Mean deletion size	1.56	1.69	1.50

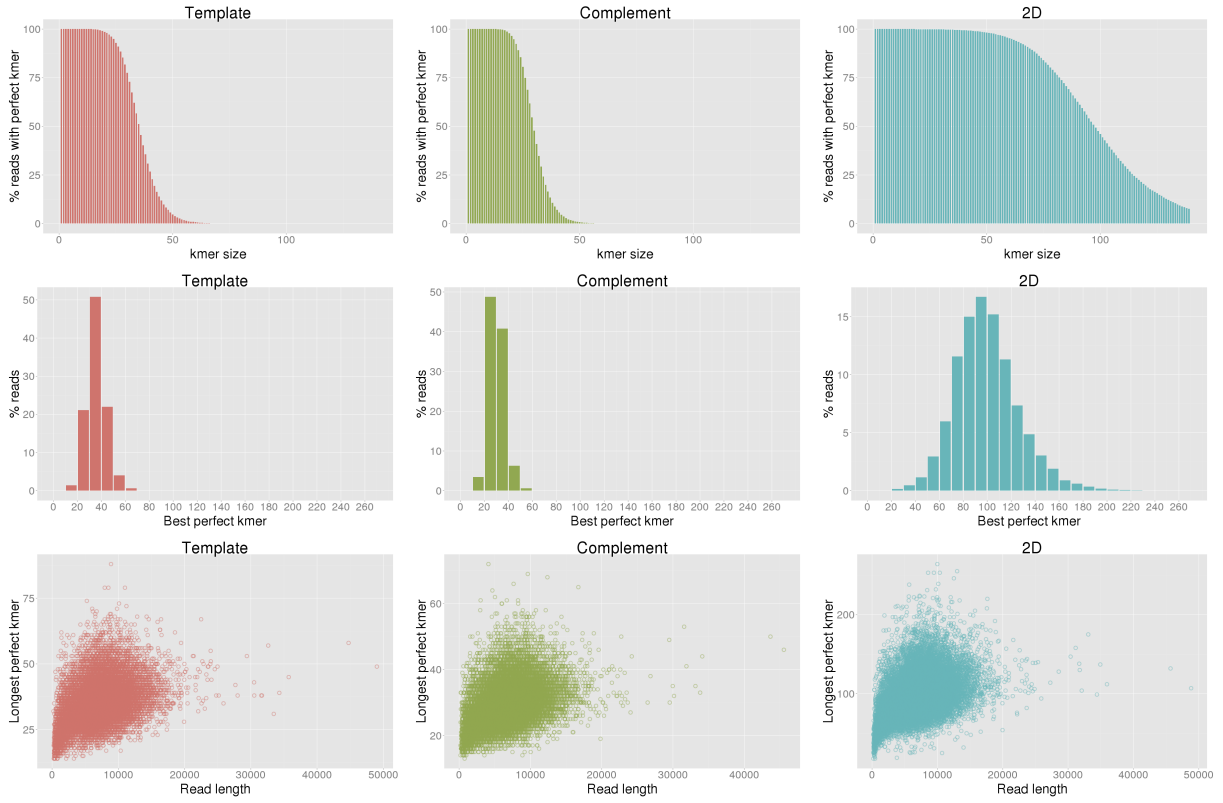


Escherichia coli read identity

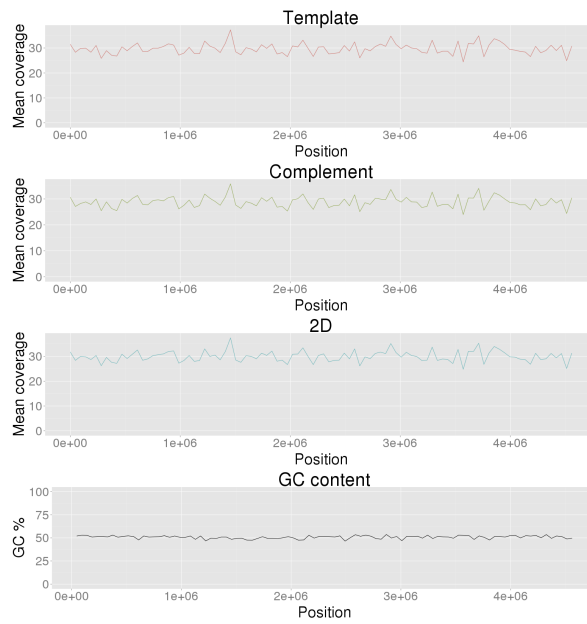




Escherichia coli perfect kmers



Escherichia coli coverage



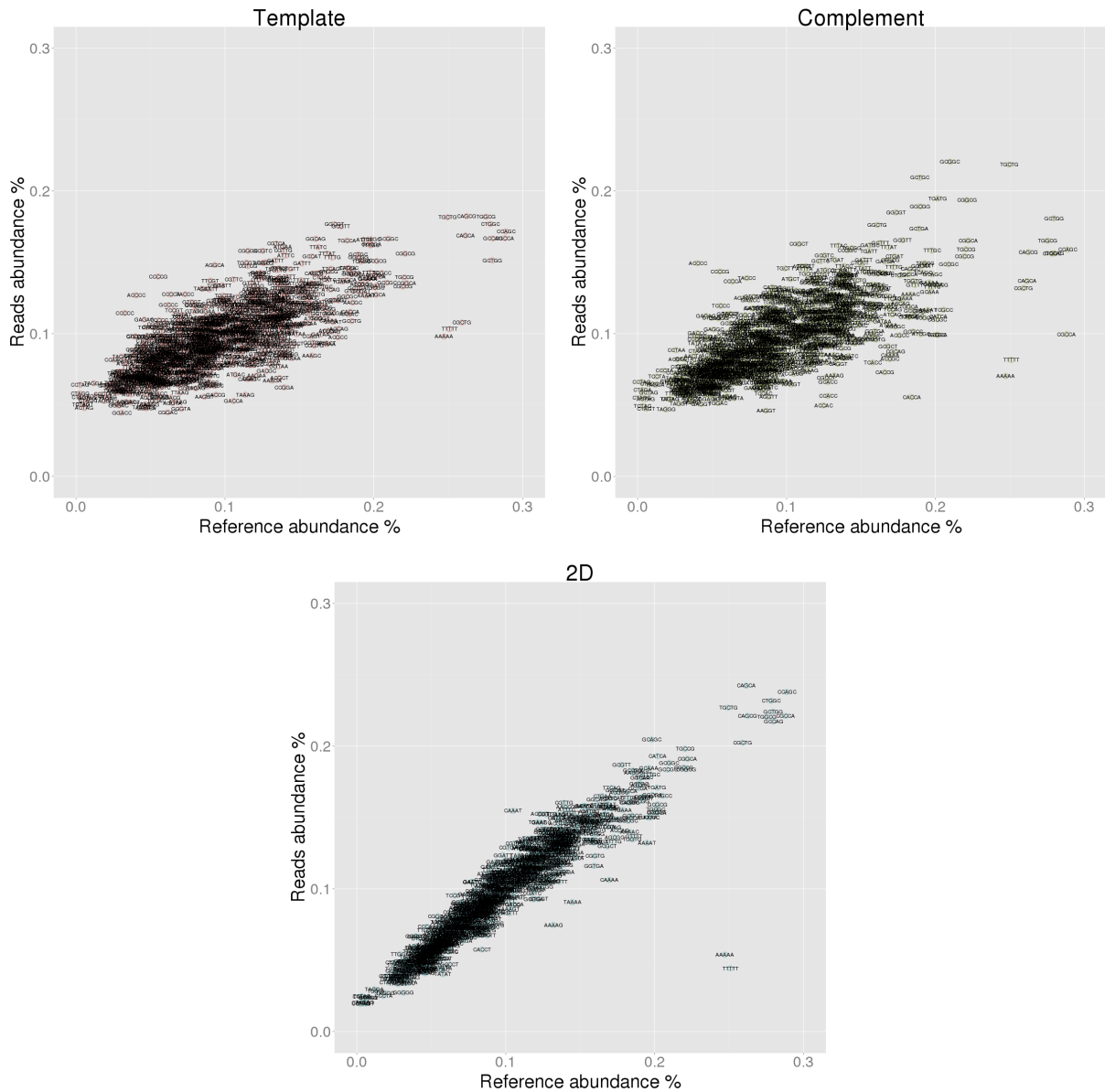
Escherichia coli 5-mer analysis

Under-represented 5-mers

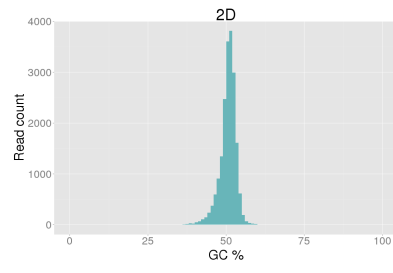
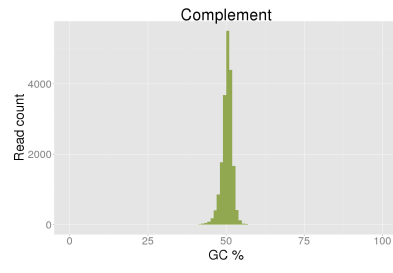
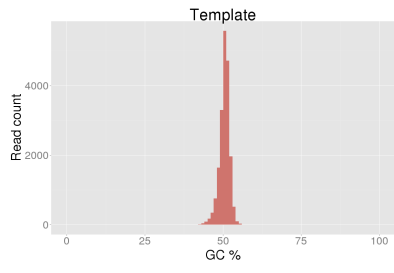
Rank	Template				Complement				2D			
	kmer	Ref %	Read %	Diff %	kmer	Ref %	Read %	Diff %	kmer	Ref %	Read %	Diff %
1	CGCTG	0.259	0.108	-0.151	CGCCA	0.288	0.100	-0.188	TTTTT	0.251	0.044	-0.207
2	AAAAA	0.247	0.098	-0.149	AAAAA	0.247	0.070	-0.177	AAAAA	0.247	0.054	-0.193
3	TTTTT	0.251	0.103	-0.148	TTTTT	0.251	0.082	-0.169	CGCCA	0.288	0.221	-0.067
4	GCTGG	0.279	0.151	-0.128	CCAGC	0.289	0.159	-0.130	CAAAA	0.169	0.106	-0.063
5	CGCCA	0.288	0.167	-0.121	CACCA	0.184	0.055	-0.128	GCCAG	0.280	0.217	-0.063
6	CCAGC	0.289	0.172	-0.117	CGCTG	0.259	0.132	-0.127	AAAAT	0.195	0.132	-0.063
7	GCCAG	0.280	0.167	-0.113	CAGCA	0.261	0.137	-0.125	AAAAG	0.132	0.075	-0.057
8	CTGGC	0.278	0.177	-0.101	GCCAG	0.280	0.156	-0.124	CGCTG	0.259	0.202	-0.057
9	TGGCG	0.275	0.182	-0.093	CTGGC	0.278	0.156	-0.122	GCTGG	0.279	0.224	-0.055
10	CAGCA	0.261	0.169	-0.093	TGGCG	0.275	0.165	-0.110	TGGCG	0.275	0.221	-0.055

Over-represented 5-mers

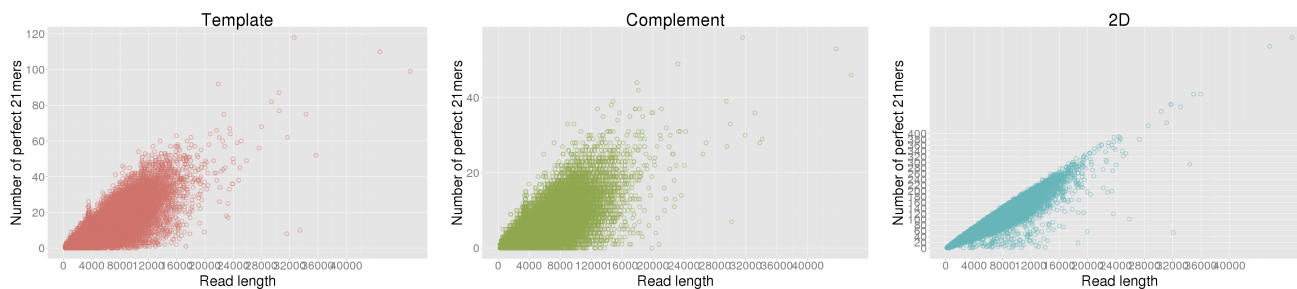
Rank	Template				Complement				2D			
	kmer	Ref %	Read %	Diff %	kmer	Ref %	Read %	Diff %	kmer	Ref %	Read %	Diff %
1	ACCCC	0.040	0.127	0.087	ACCCC	0.040	0.149	0.109	CAAAT	0.105	0.155	0.050
2	CCCCG	0.055	0.140	0.085	CCCCG	0.055	0.144	0.088	TCCGT	0.066	0.095	0.030
3	CCCCC	0.033	0.114	0.082	CCCCC	0.064	0.137	0.073	ACCGT	0.123	0.152	0.029
4	GAGAG	0.046	0.110	0.064	GAGAG	0.046	0.112	0.067	GAATC	0.077	0.105	0.028
5	CCCCA	0.064	0.128	0.064	TACCC	0.073	0.139	0.066	GATTC	0.078	0.105	0.028
6	CCTAG	0.003	0.064	0.061	TCCCC	0.056	0.120	0.064	GGGGT	0.039	0.067	0.027
7	CTCCC	0.040	0.098	0.058	CCTAG	0.003	0.066	0.063	CGTGA	0.102	0.129	0.027
8	GCCCC	0.062	0.120	0.058	CCTAA	0.026	0.088	0.062	CCCAA	0.047	0.073	0.027
9	GGGTC	0.040	0.098	0.057	CTGAG	0.050	0.111	0.061	CGGGG	0.054	0.081	0.026
10	TCTAC	0.048	0.104	0.057	GACCC	0.040	0.100	0.060	CGTTC	0.106	0.132	0.026



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	8.74	9.60	4.61	0.00	9.05	8.98	4.88	0.00	8.23	8.89	4.00
C	8.45	0.00	9.16	9.81	9.14	0.00	8.68	9.46	9.12	0.00	11.10	9.03
G	9.25	9.16	0.00	8.06	8.78	8.86	0.00	8.76	8.92	11.23	0.00	8.53
T	4.89	9.85	8.42	0.00	5.15	9.26	8.99	0.00	4.03	8.91	8.01	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 (3.27%)	TTC (3.56%)	AAA (4.13%)	TGC (2.80%)	GGC (2.92%)	AAA (4.13%)	GCA (3.02%)	TGC (2.60%)	AAA (4.12%)
2	AAA (2.81%)	TGC (3.02%)	TTC (3.69%)	TTC (2.72%)	TGC (2.87%)	GCA (3.53%)	TTC (2.80%)	TCA (2.59%)	GCA (3.57%)
3	TGC (2.75%)	GCA (2.81%)	GCA (3.28%)	AAA (2.66%)	AAA (2.79%)	GAA (3.30%)	AAA (2.80%)	GGC (2.56%)	GAA (3.41%)
4	GCA (2.72%)	AAA (2.66%)	GAA (3.05%)	GCA (2.66%)	TTC (2.60%)	TTC (3.11%)	TCA (2.57%)	GCG (2.52%)	TTC (2.94%)
5	ATC (2.57%)	TCA (2.52%)	TGC (2.54%)	CAG (2.45%)	GCA (2.55%)	TTT (2.62%)	TGC (2.52%)	AAA (2.51%)	TTT (2.83%)
6	TCA (2.53%)	GCC (2.40%)	TTT (2.50%)	GGC (2.41%)	TCA (2.29%)	TGC (2.50%)	GAA (2.45%)	TTC (2.49%)	AAT (2.57%)
7	GCC (2.33%)	GGC (2.36%)	AAT (2.42%)	TCA (2.33%)	GCC (2.29%)	TCA (2.42%)	ATC (2.42%)	GCA (2.40%)	GCC (2.44%)
8	GAA (2.25%)	ATC (2.33%)	TCA (2.30%)	ATC (2.33%)	GAA (2.28%)	ATC (2.33%)	CGC (2.32%)	CGC (2.27%)	GCG (2.39%)
9	GGC (2.25%)	AAC (2.21%)	GCC (2.27%)	GAA (2.32%)	CAG (2.24%)	GCC (2.18%)	AAT (2.30%)	ATC (2.27%)	ATC (2.34%)
10	TTT (2.20%)	AAT (2.16%)	CAA (2.21%)	TTT (2.16%)	GCG (2.21%)	GGC (2.13%)	CAG (2.21%)	CAG (2.15%)	TCA (2.27%)
-10	AGT (1.00%)	GTA (0.94%)	CCT (0.93%)	AGA (1.03%)	CGA (0.95%)	CTC (0.97%)	TAC (1.06%)	GAG (0.98%)	GTA (0.86%)
-9	TGT (0.99%)	AGG (0.92%)	GGG (0.89%)	AGT (1.01%)	AGT (0.94%)	CTT (0.90%)	CTC (1.02%)	CCC (0.98%)	ACT (0.86%)
-8	CCC (0.94%)	AGT (0.92%)	AGA (0.85%)	CTC (0.96%)	CCC (0.94%)	AGT (0.87%)	GAG (0.86%)	ACT (0.90%)	TAT (0.85%)
-7	AGA (0.82%)	CTT (0.82%)	AGT (0.83%)	CCC (0.89%)	CTC (0.93%)	CCT (0.82%)	CCC (0.83%)	CGA (0.89%)	CTT (0.73%)
-6	GGA (0.78%)	GAG (0.81%)	AGG (0.78%)	GGA (0.85%)	GGA (0.88%)	AGG (0.81%)	AGA (0.81%)	CCT (0.87%)	GAG (0.69%)
-5	GAG (0.75%)	CGA (0.74%)	TGT (0.76%)	GAG (0.81%)	CCT (0.88%)	GGG (0.78%)	AGG (0.79%)	CTT (0.83%)	CGA (0.69%)
-4	AGG (0.67%)	AGA (0.64%)	CTT (0.73%)	AGG (0.70%)	GAG (0.83%)	ACT (0.73%)	GGA (0.78%)	AGA (0.78%)	AGA (0.52%)
-3	GGG (0.67%)	GGA (0.63%)	GAG (0.62%)	CTA (0.64%)	GGG (0.77%)	GAG (0.62%)	GGG (0.71%)	GGA (0.71%)	GGA (0.50%)
-2	CTA (0.53%)	TAG (0.55%)	CTA (0.39%)	GGG (0.58%)	TAG (0.55%)	CTA (0.48%)	CTA (0.62%)	CTA (0.71%)	TAG (0.48%)
-1	TAG (0.43%)	CTA (0.53%)	TAG (0.39%)	TAG (0.48%)	CTA (0.54%)	TAG (0.39%)	TAG (0.50%)	TAG (0.62%)	CTA (0.42%)

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 (0.97%)	TTTC (1.10%)	AAAA (1.43%)	CAGC (0.94%)	CGGC (1.04%)	AAAA (1.21%)	ATCA (0.90%)	TGGC (0.90%)	AAAA (1.27%)
2	GAAA (0.90%)	TTCA (0.93%)	TTTT (1.19%)	ATCA (0.89%)	TGGC (1.03%)	CAAA (1.07%)	CAAA (0.81%)	ATCA (0.87%)	GGCA (1.09%)
3	AAAA (0.90%)	TGCC (0.92%)	GAAA (1.17%)	CTGC (0.86%)	CAGC (1.02%)	TGAA (0.99%)	GGCA (0.80%)	CAGC (0.87%)	GAAA (1.03%)
4	ATCA (0.89%)	CAGC (0.88%)	GCAA (0.92%)	CGGC (0.83%)	CTGC (0.89%)	GAAA (0.97%)	CAGC (0.79%)	TTCA (0.84%)	TGAA (1.00%)
5	TTCA (0.84%)	TGGC (0.87%)	GTTC (0.91%)	TGGC (0.82%)	TTGC (0.88%)	AGCA (0.94%)	GCCA (0.79%)	CGGC (0.78%)	TTTT (0.95%)
6	CAGC (0.84%)	TTGC (0.86%)	GGCA (0.90%)	TTGC (0.80%)	ATCA (0.82%)	ATCA (0.93%)	CGCA (0.78%)	CAAA (0.74%)	CGCC (0.92%)
7	TGCC (0.83%)	GTTC (0.85%)	TGCC (0.88%)	CCAG (0.80%)	CAAA (0.82%)	AGAA (0.88%)	CGCC (0.77%)	GGCG (0.72%)	GGAA (0.92%)
8	TTGC (0.81%)	CTGC (0.85%)	TTTT (0.87%)	CAAA (0.77%)	AAAA (0.77%)	TTTT (0.88%)	TGAA (0.76%)	CTGC (0.72%)	TTTT (0.87%)
9	CGCC (0.78%)	ATCA (0.84%)	TGAA (0.87%)	AAAA (0.75%)	TTCC (0.76%)	GGCA (0.88%)	AACA (0.76%)	TTGC (0.72%)	CAAA (0.86%)
10	TGCC (0.77%)	AAAA (0.82%)	GGAA (0.83%)	ATGC (0.72%)	TGCC (0.75%)	TTTT (0.84%)	GAAA (0.75%)	CGCC (0.71%)	TGCA (0.85%)
-10	CTAA (0.13%)	GAGA (0.13%)	TTAG (0.11%)	CGAG (0.12%)	CCCC (0.13%)	GTAG (0.11%)	TTAG (0.15%)	CCCC (0.15%)	CTAA (0.11%)
-9	AGGG (0.12%)	CTAT (0.13%)	ACTA (0.11%)	CTAA (0.12%)	GTGT (0.12%)	GAGG (0.11%)	GGGA (0.15%)	ACCT (0.15%)	GAGA (0.11%)
-8	TCTA (0.12%)	TAGT (0.12%)	TAGT (0.11%)	AGGG (0.11%)	CGAG (0.12%)	ACCT (0.11%)	CTAT (0.14%)	CTAT (0.14%)	CGGA (0.10%)
-7	GGAG (0.12%)	TCTA (0.12%)	CGAG (0.10%)	GGAC (0.11%)	ACCT (0.12%)	GGAC (0.10%)	GAGG (0.14%)	GAGA (0.14%)	TCTA (0.10%)
-6	GAGG (0.12%)	CGGA (0.11%)	GGAC (0.10%)	TAGA (0.11%)	CTAA (0.12%)	CTAT (0.09%)	CTAA (0.13%)	CTAA (0.12%)	GGGA (0.10%)
-5	TTAG (0.10%)	CTAA (0.10%)	TAGA (0.08%)	CCCT (0.10%)	TAGA (0.10%)	CGAG (0.09%)	TCTA (0.13%)	CCCT (0.12%)	CTAT (0.09%)
-4	CCTA (0.06%)	TAGG (0.08%)	TCTA (0.08%)	GAGG (0.10%)	CCCT (0.09%)	CCCT (0.07%)	TAGA (0.08%)	TAGG (0.11%)	TAGG (0.07%)
-3	TAGA (0.06%)	CCTA (0.06%)	TAGG (0.06%)	CCTA (0.08%)	TAGG (0.09%)	TAGG (0.06%)	CCTA (0.08%)	CCTA (0.10%)	TAGA (0.05%)
-2	TAGG (0.05%)	TAGA (0.05%)	CCTA (0.05%)	TAGG (0.05%)	CCTA (0.07%)	CCTA (0.06%)	TAGG (0.06%)	TAGA (0.09%)	CCTA (0.04%)
-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%)

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	CTGGC (0.33%)	CAGCA (0.37%)	GAAA (0.43%)	CAGCA (0.39%)	CAGCA (0.38%)	CAGCA (0.51%)	CAGCA (0.35%)	CTGGC (0.36%)	CAGCA (0.41%)
2	CAGCA (0.32%)	CTGGC (0.36%)	CAGCA (0.40%)	CCAGC (0.31%)	CTGGC (0.38%)	GAAAA (0.35%)	CGCCA (0.33%)	CATCA (0.32%)	GAAAA (0.39%)
3	TTATC (0.31%)	CATCA (0.32%)	CAAAA (0.39%)	CATCA (0.31%)	GCGGC (0.34%)	CGGCA (0.34%)	CGGCA (0.30%)	TATCG (0.30%)	CGGCA (0.39%)
4	CATCA (0.31%)	CGCCA (0.31%)	TGTTT (0.33%)	GCTGC (0.30%)	CCAGC (0.31%)	AAGAA (0.34%)	GCAAA (0.29%)	CGCCA (0.29%)	CAAAA (0.35%)
5	CGCCA (0.30%)	TTTCA (0.31%)	AGAAA (0.32%)	CTGGC (0.30%)	CATCA (0.31%)	CAGAA (0.33%)	CTGGC (0.28%)	CAGCA (0.29%)	TGGCA (0.35%)
6	CAAAA (0.29%)	TTGCC (0.30%)	GCAAA (0.32%)	GCGGC (0.30%)	TCAGC (0.30%)	ATAAA (0.33%)	GCCAG (0.28%)	GCGGC (0.29%)	TAAAA (0.31%)
7	CCAGC (0.28%)	ATTTT (0.30%)	TAAAA (0.31%)	TTATC (0.29%)	GCTGC (0.30%)	CATCA (0.33%)	CAGGC (0.27%)	CCAGC (0.29%)	GCAAA (0.31%)
8	GCAGC (0.28%)	TTTTT (0.30%)	ATTTT (0.31%)	CGGCA (0.27%)	AATCA (0.29%)	GCAAA (0.33%)	CATCA (0.27%)	GCCAG (0.28%)	TTGCC (0.30%)
9	TTGCC (0.27%)	TGTTT (0.30%)	TTGCC (0.31%)	AATCA (0.27%)	TTTTT (0.29%)	AATCA (0.32%)	GCGCA (0.27%)	TGGCG (0.28%)	ATTTT (0.29%)
10	GAAAA (0.27%)	GCAGC (0.30%)	TGAAA (0.30%)	GATGC (0.27%)	TTATC (0.28%)	TTATC (0.32%)	CCAGC (0.26%)	GATGC (0.28%)	CTGAA (0.29%)
-10	GGACC (0.01%)	TAGGA (0.01%)	CTTAG (0.01%)	ACCTA (0.01%)	CCCC (0.01%)	ACCTA (0.01%)	TAGGA (0.01%)	TCCTA (0.01%)	TTAGA (0.01%)
-9	CCCTA (0.01%)	CCCTA (0.01%)	CCCTA (0.01%)	CCCTA (0.01%)	ACCTA (0.01%)	CCCTA (0.01%)	CCCTA (0.01%)	TAGGA (0.01%)	TCCTA (0.01%)
-8	GCTAG (0.00%)	GCTAG (0.01%)	GCTAG (0.00%)	CTAGC (0.01%)	GCTAG (0.01%)	CTAGC (0.01%)	CCTAG (0.01%)	GCTAG (0.01%)	GCTAG (0.01%)
-7	CTAGT (0.00%)	ACTAG (0.00%)	ACTAG (0.00%)	GCTAG (0.01%)	CTAGC (0.01%)	GCTAG (0.01%)	GCTAG (0.01%)	CTAGC (0.01%)	CTAGT (0.00%)
-6	CTAGC (0.00%)	CTAGC (0.00%)	CTAGT (0.00%)	CTAGA (0.01%)	CTAGA (0.00%)	CTAGT (0.00%)	CTAGC (0.01%)	ACTAG (0.01%)	ACTAG (0.00%)
-5	ACTAG (0.00%)	CTAGT (0.00%)	CTAGC (0.00%)	CTAGT (0.01%)	CTAGT (0.00%)	CTAGA (0.00%)	CTAGT (0.00%)	CTAGT (0.00%)	CTAGC (0.00%)
-4	CCTAG (0.00%)	CCTAG (0.00%)	CTAGG (0.00%)	ACTAG (0.00%)	ACTAG (0.00%)	ACTAG (0.00%)	CTAGA (0.00%)	CTAGA (0.00%)	CCTAG (0.00%)
-3	CTAGG (0.00%)	TCTAG (0.00%)	CCTAG (0.00%)	CCTAG (0.00%)	TCTAG (0.00%)	CTAGG (0.00%)	ACTAG (0.00%)	TCTAG (0.00%)	CTAGG (0.00%)
-2	CTAGA (0.00%)	CTAGA (0.00%)	CTAGA (0.00%)	TCTAG (0.00%)	CTAGC (0.00%)	CCTAG (0.00%)	TCTAG (0.00%)	CTAGC (0.00%)	CTAGA (0.00%)
-1	TCTAG (0.00%)	CTAGG (0.00%)	TCTAG (0.00%)	CTAGG (0.00%)	CCTAG (0.00%)	TCTAG (0.00%)	CTAGG (0.00%)	CCTAG (0.00%)	TCTAG (0.00%)

Most common

Least common

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