NanoOK report for sample

Read lengths

Type	NumReads	TotalBases	Mean	Longest	Shortest	N50	N50Count	N90	N90Count
Template	5406	31523281	5831.17	145552	12	7967	1490	3640	3596
Complement	4028	24573708	6100.72	23218	18	7601	1250	3887	2940
2D	3068	20968580	6834.61	23496	192	8127	1018	4497	2336
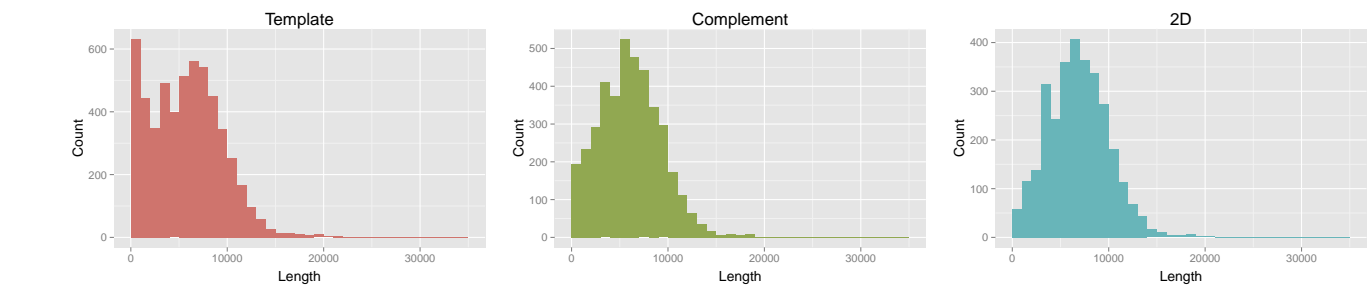
Template alignments

Number of reads	5406	
Number of reads with alignments	4505	(83.33%)
Number of reads without alignments	901	(16.67%)

ID	Size	Number of Reads	% of Reads	Mean read length	Aligned bases	Mean coverage	Longest Perf Kmer
burn-in	48502	4505	83.33	6425.72	29160057	601.21	90

Complement alignments

Number of reads	4028	
Number of reads with alignments	3512	(87.19%)
Number of reads without alignments	516	(12.81%)

ID	Size	Number of Reads	% of Reads	Mean read length	Aligned bases	Mean coverage	Longest Perf Kmer
burn-in	48502	3512	87.19	6450.06	23190925	478.14	61

2D alignments

Number of reads	3068	
Number of reads with alignments	3008	(98.04%)
Number of reads without alignments	60	(1.96%)

ID	Size	Number of Reads	% of Reads	Mean read length	Aligned bases	Mean coverage	Longest Perf Kmer
burn-in	48502	3008	98.04	6887.56	21409279	441.41	232

burn-in error analysis

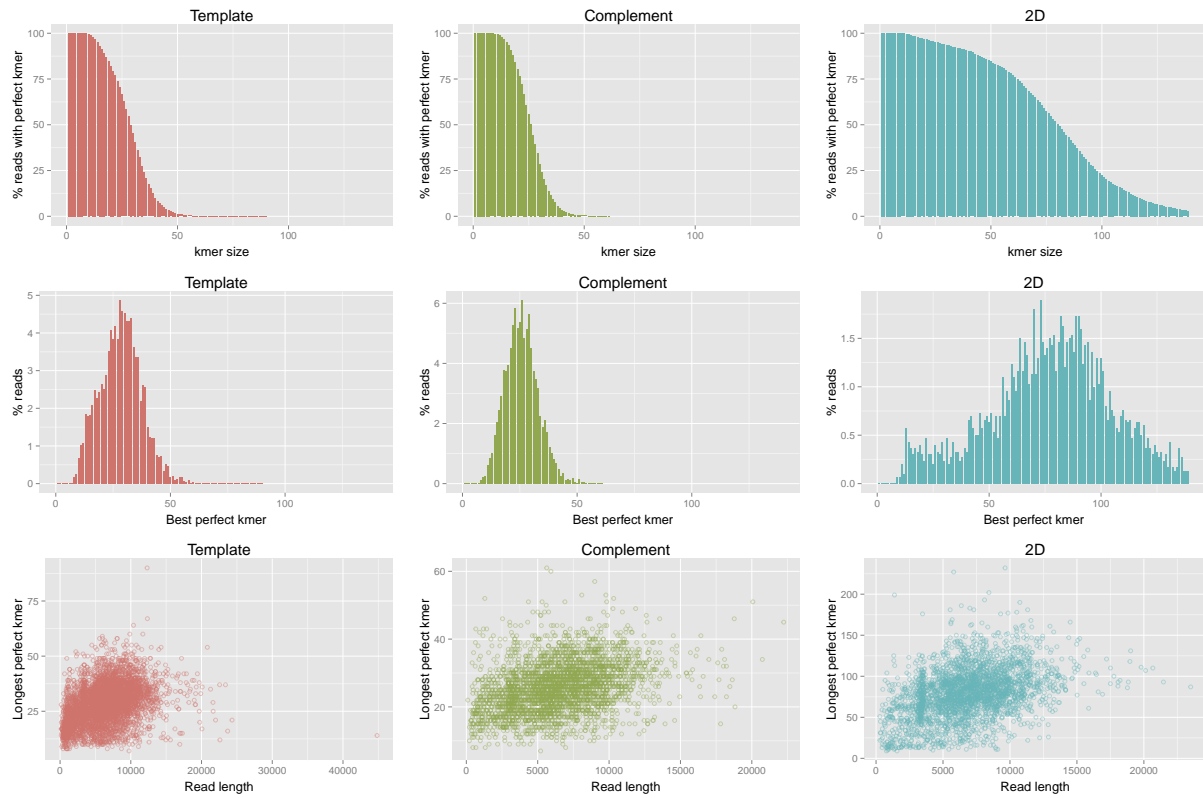|	Template	Complement	2D
Overall base identity (excluding indels)	67.50%	68.16%	84.55%
Aligned base identity (excluding indels)	79.44%	80.71%	91.39%
Identical bases per 100 aligned bases (including indels)	67.01%	66.58%	81.81%
Inserted bases per 100 aligned bases (including indels)	5.04%	4.49%	2.90%
Deleted bases per 100 aligned bases (including indels)	10.61%	13.02%	7.58%
Substitutions per 100 aligned bases (including indels)	17.34%	15.91%	7.71%
Mean insertion size	1.56	1.54	1.45
Mean deletion size	1.64	1.78	1.65
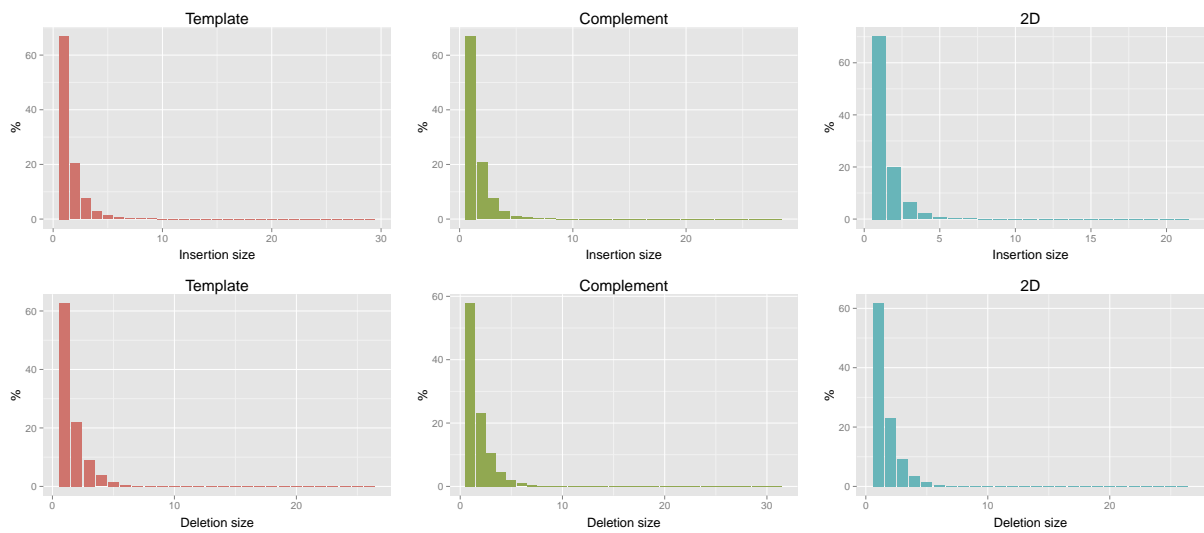
burn-in read identity
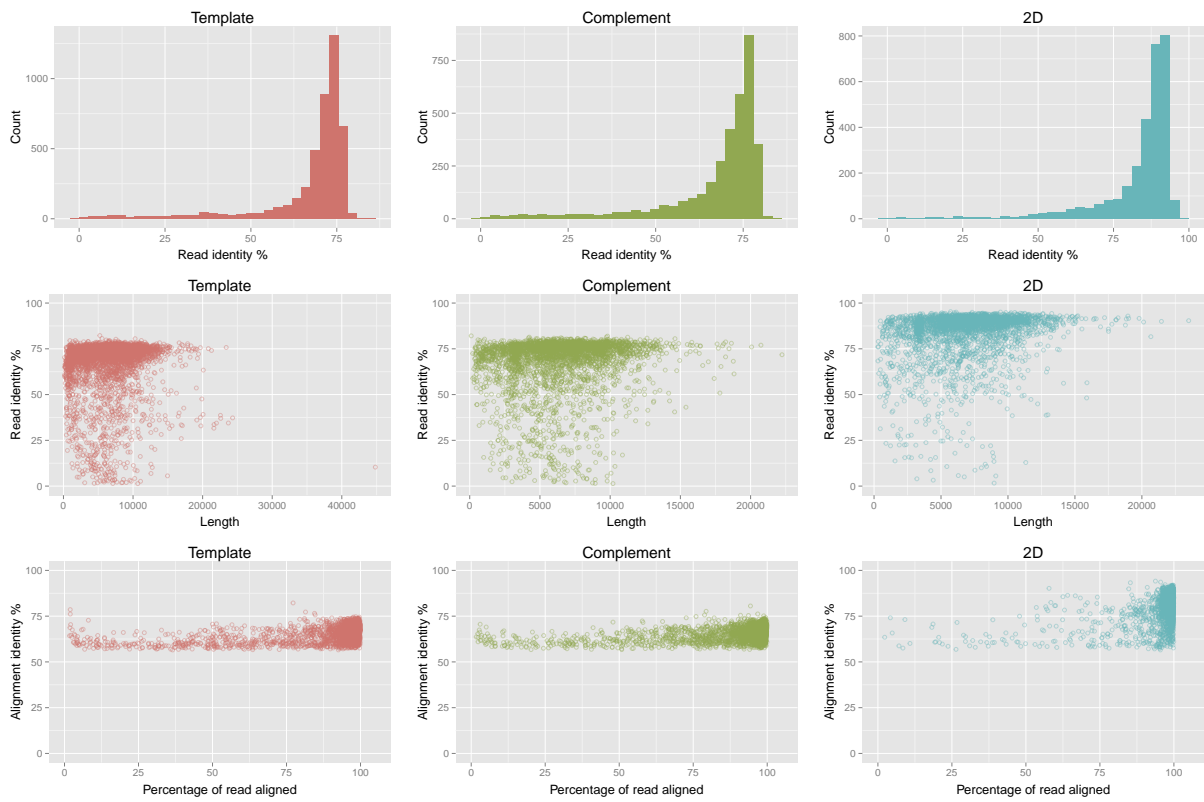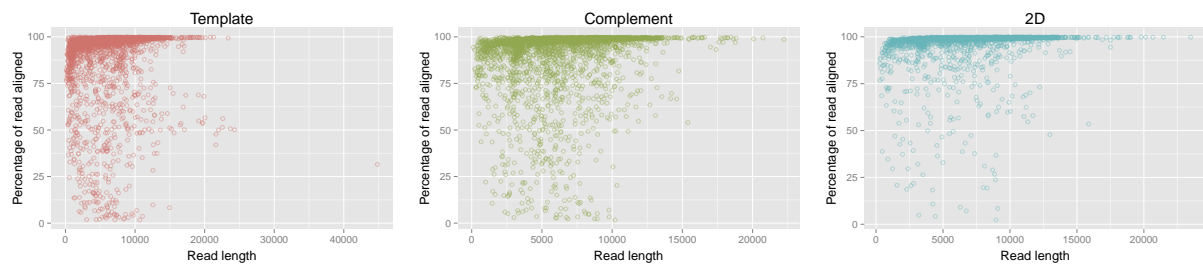
burn-in perfect kmers

burn-in coverage
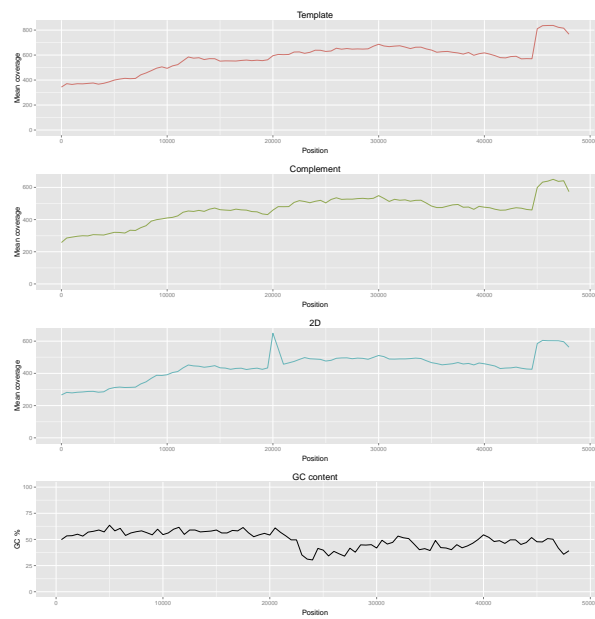
burn-in 5-mer analysis

Under-represented 5-mers

	Template				Complement				2D		
Rank	kmer	Ref %	Read %	Diff %	kmer	Ref %	Read %	Diff %	kmer	Ref %	Read %	Diff %
1	AAAAA	0.303	0.095	-0.208	AAAAA	0.303	0.059	-0.245	AAAAA	0.303	0.048	-0.255
2	GCAGA	0.291	0.119	-0.172	TTTTT	0.274	0.078	-0.196	TTTTT	0.274	0.043	-0.232
3	CCGGA	0.231	0.064	-0.167	GCAGA	0.291	0.129	-0.162	CGGTG	0.223	0.095	-0.127
4	TTTTT	0.274	0.119	-0.155	AAAAC	0.260	0.116	-0.144	AAAAC	0.260	0.134	-0.126
5	CGCTG	0.233	0.079	-0.155	CGGTG	0.223	0.089	-0.133	TGATG	0.274	0.160	-0.115
6	TGATG	0.274	0.122	-0.152	CCGGA	0.231	0.099	-0.132	GAAAA	0.256	0.142	-0.114
7	CGGTG	0.223	0.076	-0.147	CGCTG	0.233	0.106	-0.127	GCAGA	0.291	0.178	-0.113
8	GCTGG	0.262	0.115	-0.147	GAAAA	0.256	0.133	-0.123	GGTGA	0.206	0.096	-0.110
9	AAAAC	0.260	0.114	-0.146	CGCAG	0.198	0.076	-0.122	GCTGG	0.262	0.152	-0.109
10	GCCGG	0.235	0.093	-0.142	GGTGA	0.206	0.088	-0.118	CCGGA	0.231	0.125	-0.106

Over-represented 5-mers

	Template				Complement				2D		
Rank	kmer	Ref %	Read %	Diff %	kmer	Ref %	Read %	Diff %	kmer	Ref %	Read %	Diff %
1	CCCCC	0.021	0.136	0.116	CCCCA	0.031	0.135	0.104	TTCCT	0.074	0.138	0.064
2	CCCCA	0.031	0.145	0.114	ACCCC	0.039	0.142	0.103	GCATC	0.118	0.175	0.057
3	CCCCG	0.045	0.149	0.104	CCCCG	0.045	0.134	0.089	TAGAA	0.023	0.078	0.055
4	GCCCC	0.029	0.132	0.104	TCCCC	0.049	0.127	0.077	ATAGA	0.031	0.082	0.051
5	ACCCC	0.039	0.137	0.098	GCCCC	0.029	0.102	0.073	ATCCA	0.066	0.117	0.051
6	TCTAC	0.029	0.118	0.089	TCTAC	0.029	0.102	0.073	GTTGG	0.047	0.098	0.051
7	ACTCT	0.043	0.129	0.086	GGAAT	0.099	0.171	0.072	CCTCC	0.045	0.096	0.050
8	TCCCC	0.049	0.135	0.085	CCCAG	0.037	0.109	0.072	TAAAC	0.072	0.122	0.050
9	CTCCC	0.037	0.116	0.079	TAGGA	0.025	0.096	0.071	CGACT	0.039	0.088	0.049
10	CCTAG	0.010	0.086	0.076	TACCC	0.060	0.130	0.070	TAGAT	0.033	0.082	0.049
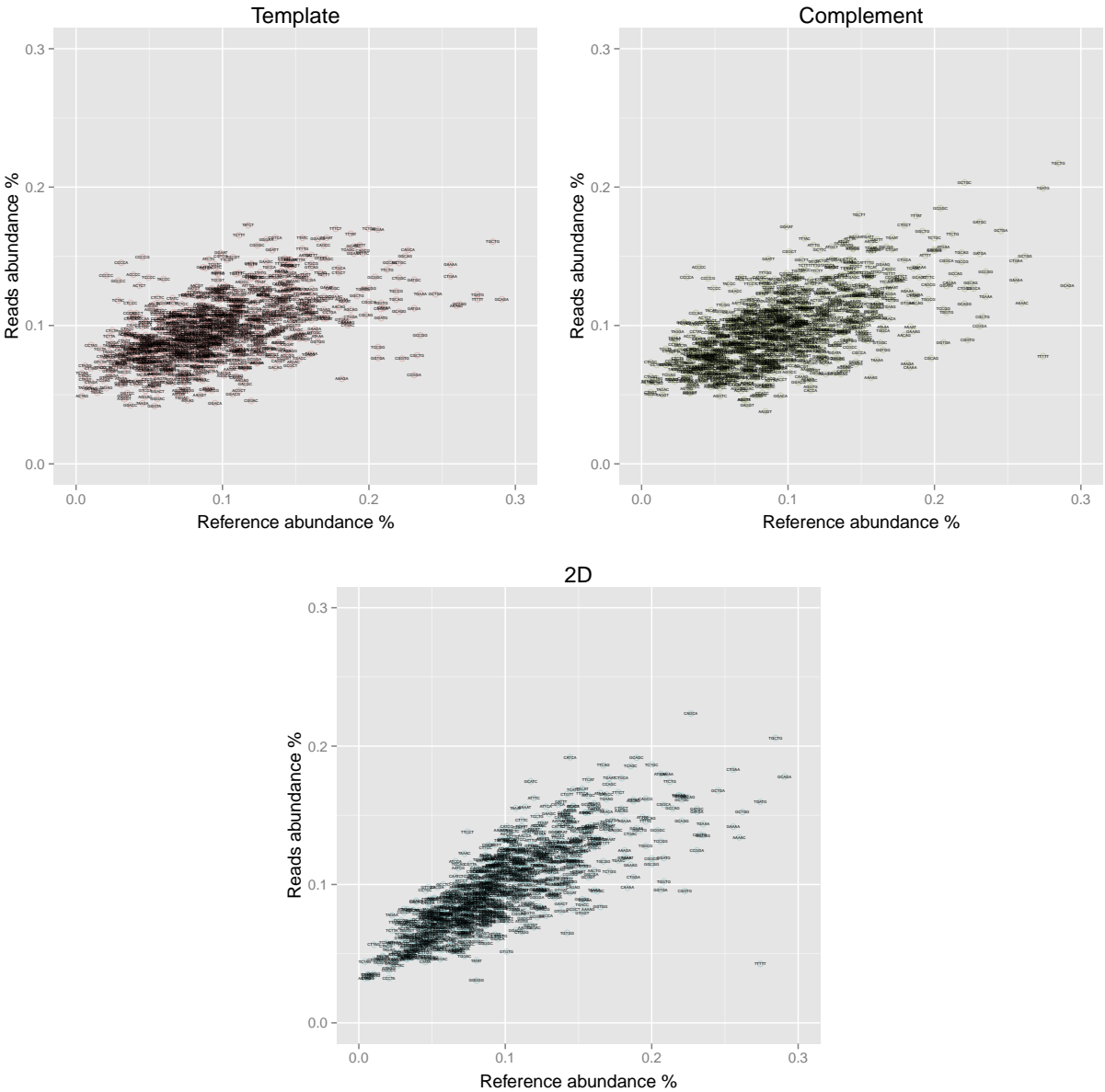
All reference 21mer analysis

Template | Complement | 2D scatter plots of Number of perfect 21mers vs Read length
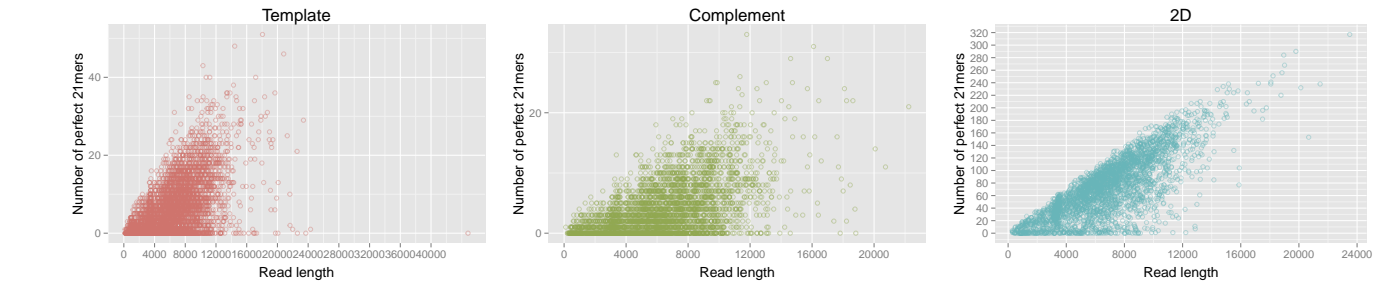
All reference substitutions

		Template substituted %				Complement substituted %				2D substituted %			
		a	c	g	t	a	c	g	t	a	c	g	t
Reference	A	0.00	9.78	9.13	5.14	0.00	9.79	8.77	5.33	0.00	9.35	8.43	4.61
	C	7.55	0.00	8.14	8.62	8.05	0.00	7.81	8.37	8.11	0.00	9.27	8.28
	G	9.62	9.55	0.00	8.49	9.30	9.09	0.00	9.12	9.27	11.00	0.00	9.29
	T	5.09	9.45	9.43	0.00	5.30	9.36	9.72	0.00	4.58	8.73	9.09	0.00

Kmer motifs before errors

3-mer error motif analysis

	Template			Complement			2D			
Rank	Insertion	Deletion	Substitution	Insertion	Deletion	Substitution	Insertion	Deletion	Substitution	
1	AAA (3.39%)	AAA (4.01%)	AAA (4.43%)	AAA (3.16%)	AAA (3.97%)	AAA (4.52%)	AAA (3.19%)	AAA (5.60%)	AAA (4.16%)	Most common
2	TTC (2.89%)	TTC (3.36%)	GCA (3.49%)	TGC (3.05%)	GAA (3.32%)	GAA (3.85%)	GCA (3.18%)	TTT (4.45%)	GAA (3.81%)	
3	TGC (2.82%)	GCA (3.06%)	GAA (3.37%)	GAA (2.88%)	TGC (3.01%)	GCA (3.49%)	GAA (3.15%)	GAA (3.20%)	GCA (3.67%)	
4	GCA (2.74%)	TGC (3.00%)	TTC (3.29%)	GCA (2.76%)	TTT (2.76%)	TTC (2.94%)	TTC (2.59%)	GCA (2.58%)	TTC (2.82%)	
5	GAA (2.63%)	TTT (2.75%)	TTT (2.62%)	TTC (2.59%)	GCA (2.66%)	TGC (2.61%)	TGC (2.59%)	TGC (2.34%)	TTT (2.78%)	
6	TTT (2.56%)	GAA (2.65%)	TGC (2.61%)	CAG (2.55%)	TTC (2.58%)	TTT (2.60%)	TCA (2.46%)	TTC (2.25%)	TCA (2.51%)	
7	TCA (2.46%)	TCA (2.27%)	TCA (2.53%)	TTT (2.40%)	CAG (2.31%)	TCA (2.52%)	CAG (2.40%)	TCA (2.15%)	AAT (2.40%)	
8	CAG (2.25%)	CAG (2.26%)	AAT (2.39%)	TCA (2.28%)	GGC (2.30%)	AAT (2.18%)	TTT (2.25%)	CAG (2.13%)	GTT (2.18%)	
9	TCT (2.23%)	AAC (2.07%)	CAG (2.09%)	GGC (2.15%)	TCA (2.13%)	ATC (2.06%)	GCC (2.12%)	GCC (2.02%)	TGC (2.15%)	
10	ATC (2.22%)	GCC (2.04%)	GCT (2.06%)	TGA (2.09%)	TGA (2.01%)	CAG (2.04%)	AAT (2.05%)	GTT (1.91%)	GCT (2.09%)	

-10	AGT (1.03%)	ACC (0.99%)	GGT (0.94%)	GGG (1.00%)	TCG (1.01%)	TCG (0.93%)	CTT (1.06%)	CTT (1.01%)	CAC (0.96%)	Least common
-9	CAC (1.03%)	ACT (0.97%)	CCT (0.93%)	CTC (0.99%)	CAC (0.95%)	GAG (0.91%)	TAC (1.05%)	CCC (0.95%)	CCT (0.95%)	
-8	TCG (1.01%)	CCT (0.97%)	AGT (0.91%)	TAC (0.97%)	CTC (0.94%)	CGA (0.90%)	GTA (1.04%)	GGA (0.92%)	GTA (0.89%)	
-7	AGG (1.01%)	CTT (0.92%)	GAG (0.90%)	TCG (0.97%)	GTA (0.90%)	CTT (0.88%)	CAC (1.03%)	AGA (0.88%)	CTT (0.84%)	
-6	TAC (1.01%)	CCC (0.89%)	CCC (0.88%)	CGA (0.94%)	CCT (0.89%)	CAC (0.84%)	CCC (1.03%)	CCT (0.76%)	GGA (0.76%)	
-5	CCC (0.99%)	GTA (0.86%)	GTA (0.87%)	AGG (0.93%)	CCC (0.87%)	ACT (0.81%)	GGA (0.91%)	GTA (0.74%)	CCC (0.76%)	
-4	CGA (0.95%)	AGA (0.85%)	CGA (0.82%)	CCC (0.87%)	ACT (0.86%)	CCT (0.80%)	CGA (0.85%)	ACT (0.66%)	AGA (0.66%)	
-3	AGA (0.94%)	CGA (0.77%)	CTT (0.78%)	CAC (0.87%)	CGA (0.76%)	CCC (0.79%)	AGA (0.82%)	CGA (0.59%)	CGA (0.64%)	
-2	CTA (0.53%)	CTA (0.46%)	CTA (0.39%)	CTA (0.55%)	CTA (0.47%)	CTA (0.45%)	CTA (0.57%)	CTA (0.52%)	CTA (0.40%)	
-1	TAG (0.35%)	TAG (0.41%)	TAG (0.29%)	TAG (0.39%)	TAG (0.40%)	TAG (0.30%)	TAG (0.47%)	TAG (0.45%)	TAG (0.37%)	

Kmer space for 3-mers: 64   Random chance for any given 3-mer: 1.56%

4-mer error motif analysis

Rank	Template Insertion	Template Deletion	Template Substitution	Complement Insertion	Complement Deletion	Complement Substitution	2D Insertion	2D Deletion	2D Substitution	
1	GAAA (1.23%)	AAAA (1.65%)	AAAA (1.65%)	GAAA (1.04%)	AAAA (1.38%)	AAAA (1.47%)	GAAA (1.08%)	AAAA (2.18%)	AAAA (1.29%)	Most common
2	AAAA (1.17%)	GAAA (1.24%)	GAAA (1.36%)	CTGC (1.00%)	TGAA (1.10%)	TGAA (1.24%)	TGAA (1.02%)	TTTT (1.82%)	TGAA (1.27%)	
3	TTCT (1.03%)	TTTT (1.19%)	TGCA (1.18%)	AAAA (0.90%)	GAAA (1.07%)	GAAA (1.20%)	GGAA (0.94%)	GAAA (1.33%)	GGAA (1.18%)	
4	TTTT (0.97%)	TTTC (1.16%)	TTTC (1.16%)	TGAA (0.90%)	CAAA (0.99%)	TGCA (1.12%)	GGCA (0.90%)	CAAA (1.26%)	GAAA (1.17%)	
5	TTTC (0.90%)	TGCA (0.95%)	GGAA (1.06%)	ATGC (0.90%)	CTGC (0.97%)	GGAA (1.10%)	TGCA (0.89%)	TGAA (1.09%)	TGCA (1.15%)	
6	TGCT (0.85%)	ATTC (0.88%)	TGAA (1.02%)	GCAG (0.89%)	TTTT (0.93%)	CAAA (0.99%)	GCAG (0.83%)	ATTT (1.06%)	GGCA (1.02%)	
7	CTGC (0.85%)	TTCT (0.86%)	TTTT (1.02%)	GGAA (0.79%)	ATGC (0.85%)	AGAA (0.90%)	TGCC (0.80%)	TAAA (1.06%)	TTTT (0.90%)	
8	TGCA (0.84%)	CTGC (0.85%)	TTCA (0.88%)	TTCT (0.78%)	GGAA (0.84%)	ATCA (0.89%)	AACA (0.80%)	CTTT (0.96%)	TTTC (0.86%)	
9	TTCA (0.83%)	GGAA (0.83%)	GGCA (0.87%)	CAAA (0.77%)	ATTT (0.83%)	CTGC (0.87%)	AAAA (0.79%)	GGAA (0.92%)	TGCT (0.86%)	
10	GCAG (0.79%)	GCAG (0.83%)	CAAA (0.86%)	TGCA (0.77%)	AGAA (0.80%)	TTTC (0.86%)	CAAA (0.78%)	GTTT (0.82%)	CAAA (0.85%)	
	(sequence logo)	*(sequence logo)*	*(sequence logo)*	*(sequence logo)*	*(sequence logo)*	*(sequence logo)*	*(sequence logo)*	*(sequence logo)*	*(sequence logo)*	
-10	TAGT (0.13%)	TTAG (0.13%)	CGAG (0.10%)	TAGT (0.13%)	GGGT (0.12%)	ACTA (0.10%)	GAGA (0.13%)	TCGA (0.12%)	ACTA (0.10%)	Least common
-9	GGAC (0.12%)	ACTT (0.12%)	ACTT (0.10%)	CTAC (0.12%)	CGAG (0.11%)	TAGC (0.09%)	TAGC (0.13%)	TAGC (0.12%)	TCGA (0.09%)	
-8	CTAA (0.12%)	TAGT (0.12%)	ACTA (0.09%)	TTAG (0.10%)	CCTC (0.11%)	TTAG (0.09%)	CTAC (0.13%)	ACTT (0.10%)	TTAG (0.09%)	
-7	TAGC (0.11%)	TAGC (0.11%)	TAGC (0.08%)	CGAG (0.10%)	CCCC (0.11%)	CGAG (0.08%)	TTAG (0.13%)	CACT (0.10%)	TAGC (0.08%)	
-6	GTAG (0.10%)	ACTA (0.10%)	GTAG (0.08%)	CCCT (0.10%)	GTAG (0.10%)	CCCT (0.08%)	GTAG (0.11%)	CCCT (0.09%)	GTAG (0.08%)	
-5	TTAG (0.09%)	GTAG (0.09%)	TTAG (0.07%)	GTAG (0.09%)	CCCT (0.09%)	TAGA (0.07%)	TAGT (0.11%)	TAGG (0.09%)	ACTT (0.08%)	
-4	CCTA (0.07%)	TAGG (0.08%)	TAGA (0.07%)	CCTA (0.08%)	CCTA (0.07%)	GTAG (0.07%)	TAGA (0.07%)	CCTA (0.07%)	CCTA (0.04%)	
-3	TAGA (0.06%)	CCTA (0.06%)	CCTA (0.05%)	TAGA (0.07%)	TAGG (0.06%)	CCTA (0.05%)	CCTA (0.06%)	CCGA (0.07%)	TAGG (0.04%)	
-2	TAGG (0.05%)	TAGA (0.03%)	TAGG (0.05%)	TAGG (0.04%)	TAGA (0.06%)	TAGG (0.04%)	TAGG (0.04%)	TAGA (0.04%)	TAGA (0.03%)	
-1	CTAG (0.01%)	CTAG (0.02%)	CTAG (0.01%)	CTAG (0.03%)	CTAG (0.01%)	CTAG (0.01%)	CTAG (0.03%)	CTAG (0.01%)	CTAG (0.02%)	
	(sequence logo)	*(sequence logo)*	*(sequence logo)*	*(sequence logo)*	*(sequence logo)*	*(sequence logo)*	*(sequence logo)*	*(sequence logo)*	*(sequence logo)*	

Kmer space for 4-mers: 256   Random chance for any given 4-mer: 0.39%

5-mer error motif analysis

Rank	Template Insertion	Template Deletion	Template Substitution	Complement Insertion	Complement Deletion	Complement Substitution	2D Insertion	2D Deletion	2D Substitution	
1	GAAAA (0.41%)	CAAAA (0.50%)	GAAAA (0.56%)	GATGC (0.40%)	GAAAA (0.50%)	CAGAA (0.48%)	TGAAA (0.38%)	ATTTT (0.79%)	CTGAA (0.44%)	Most common
2	AGAAA (0.37%)	GAAAA (0.47%)	CTGAA (0.41%)	GCTGC (0.38%)	GATGC (0.39%)	GAAAA (0.46%)	CTGAA (0.36%)	GAAAA (0.68%)	GAAAA (0.42%)	
3	CAAAA (0.37%)	AAAAA (0.44%)	CAAAA (0.41%)	CAGCA (0.36%)	CAGAA (0.39%)	CTGAA (0.42%)	AGGAA (0.36%)	CAAAA (0.64%)	CAGCA (0.40%)	
4	GATGC (0.32%)	GGAAA (0.40%)	AGAAA (0.40%)	AGAAA (0.33%)	TCTGC (0.38%)	CAGCA (0.42%)	CAGCA (0.36%)	TAAAA (0.58%)	CTGCA (0.39%)	
5	ATTTT (0.32%)	ATTTT (0.37%)	CTGCA (0.37%)	GAAAA (0.32%)	ATAAA (0.37%)	ATGAA (0.41%)	CTGCA (0.32%)	ATAAA (0.53%)	AGGAA (0.38%)	
6	GCTGC (0.31%)	GTTTC (0.37%)	TCTGC (0.36%)	TCTGC (0.32%)	ATTTT (0.37%)	CTGCA (0.40%)	CGGCA (0.31%)	TGAAA (0.43%)	ATGAA (0.37%)	
7	TTTCT (0.30%)	TTTTT (0.36%)	AAAAA (0.36%)	CTGCA (0.31%)	GCTGC (0.37%)	ATAAA (0.39%)	GATGC (0.31%)	CTTTT (0.41%)	CAAAA (0.37%)	
8	CTGCA (0.30%)	TTTCT (0.35%)	CAGCA (0.36%)	ATAAA (0.31%)	CTGAA (0.36%)	CAAAA (0.37%)	ATGAA (0.29%)	GGAAA (0.41%)	TAAAA (0.35%)	
9	GTTCT (0.30%)	GATGC (0.34%)	GGAAA (0.35%)	CAGAA (0.31%)	ATGAA (0.35%)	AGAAA (0.34%)	GAAAA (0.29%)	ACAAA (0.40%)	CAGAA (0.35%)	
10	GTTTT (0.30%)	TCTGC (0.33%)	ATGAA (0.34%)	CTGAA (0.31%)	CAAAA (0.34%)	GATGC (0.34%)	CAGAA (0.27%)	CTGAA (0.38%)	TGGCA (0.35%)	
	(sequence logo)	*(sequence logo)*	*(sequence logo)*	*(sequence logo)*	*(sequence logo)*	*(sequence logo)*	*(sequence logo)*	*(sequence logo)*	*(sequence logo)*	
-10	CTACG (0.01%)	GTCTA (0.01%)	CTAGT (0.00%)	TTAGG (0.01%)	GTAGG (0.01%)	TAGAC (0.01%)	GCTAG (0.01%)	GTCTA (0.01%)	GTCTA (0.01%)	Least common
-9	TAGGG (0.01%)	CTAGT (0.00%)	TAGGG (0.00%)	TACTT (0.01%)	CCCCT (0.01%)	CCTAG (0.00%)	TACTT (0.01%)	ATAGA (0.01%)	CCCTA (0.01%)	
-8	GGACC (0.00%)	CTAGG (0.00%)	TAGGT (0.00%)	CTTAG (0.00%)	CCTAG (0.01%)	GCTAG (0.00%)	CTTAG (0.01%)	TAGGA (0.01%)	TACTT (0.01%)	
-7	CTAGG (0.00%)	ATAGA (0.00%)	CCCTA (0.00%)	CTAGT (0.00%)	CTAGT (0.00%)	CTTAG (0.00%)	TCTAG (0.00%)	TAGGG (0.01%)	GCTAG (0.00%)	
-6	CTTAG (0.00%)	GCTAG (0.00%)	GCTAG (0.00%)	TAGAC (0.00%)	TAGAC (0.00%)	TAGGG (0.00%)	CTAGT (0.00%)	CCTAG (0.01%)	TAGGG (0.00%)	
-5	ACTAG (0.00%)	TAGGG (0.00%)	CTAGG (0.00%)	CTAGG (0.00%)	TAGGG (0.00%)	ACTAG (0.00%)	TAGGG (0.00%)	ACTAG (0.00%)	CTAGA (0.00%)	
-4	CTAGC (0.00%)	CTAGA (0.00%)	CTAGC (0.00%)	TAGGG (0.00%)	ACTAG (0.00%)	CTAGT (0.00%)	CTAGG (0.00%)	GCTAG (0.00%)	CTAGC (0.00%)	
-3	TCTAG (0.00%)	CTAGC (0.00%)	ACTAG (0.00%)	CTAGA (0.00%)	GCTAG (0.00%)	CTAGA (0.00%)	CTAGA (0.00%)	CTAGA (0.00%)	ACTAG (0.00%)	
-2	GCTAG (0.00%)	ACTAG (0.00%)	TCTAG (0.00%)	CTAGC (0.00%)	CTAGG (0.00%)	TAGGG (0.00%)	CTAGC (0.00%)	CTAGG (0.00%)	TCTAG (0.00%)	
-1	CTAGA (0.00%)	TCTAG (0.00%)	CTAGA (0.00%)	TCTAG (0.00%)	TCTAG (0.00%)	TCTAG (0.00%)	ACTAG (0.00%)	TCTAG (0.00%)	CTAGG (0.00%)	
	(sequence logo)	*(sequence logo)*	*(sequence logo)*	*(sequence logo)*	*(sequence logo)*	*(sequence logo)*	*(sequence logo)*	*(sequence logo)*	*(sequence logo)*	

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