

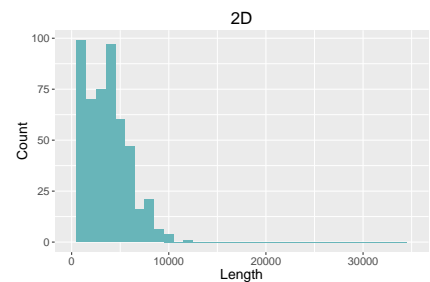
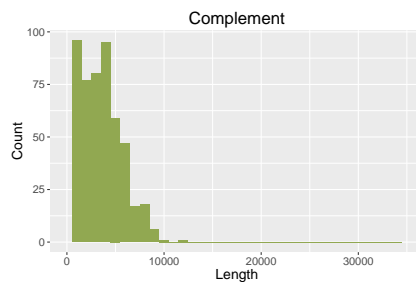
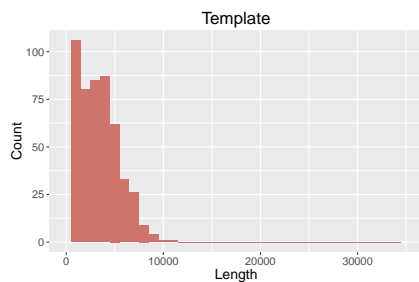
NanoOK report for main

Pass and fail counts

Type	Pass	Fail
Template	500	0
Complement	500	0
2D	500	0

Read lengths

Type	NumReads	TotalBases	Mean	Longest	Shortest	N50	N50Count	N90	N90Count
Template	500	1685124	3370.25	10794	260	4309	144	1969	354
Complement	500	1788780	3577.56	12018	300	4533	146	2014	358
2D	500	1824129	3648.26	12165	297	4672	145	2117	355



Template alignments

Number of reads	500
Number of reads with alignments	45 (9.00%)
Number of reads without alignments	455 (91.00%)

ID	Size	Number of Reads	% of Reads	Mean read length	Aligned bases	Mean coverage	Longest Perf Kmer
NC 005128	48508	0	0.00	0.00	0	0.00	0
NC 005139	3354505	43	8.60	5129.23	53616	0.02	0
NC 005140	1857073	2	0.40	3070.00	1199	0.00	0

Complement alignments

Number of reads	500
Number of reads with alignments	40 (8.00%)
Number of reads without alignments	460 (92.00%)

ID	Size	Number of Reads	% of Reads	Mean read length	Aligned bases	Mean coverage	Longest Perf Kmer
NC 005128	48508	0	0.00	0.00	0	0.00	0
NC 005139	3354505	35	7.00	5237.51	54614	0.02	0
NC 005140	1857073	5	1.00	3464.00	3889	0.00	0

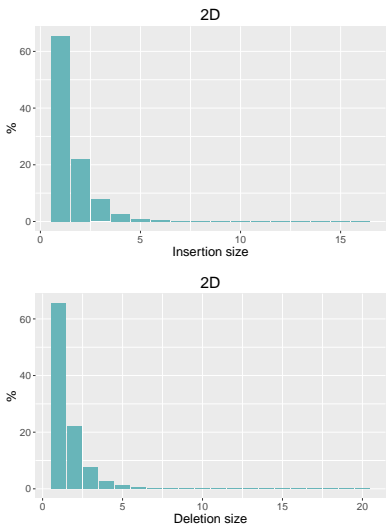
2D alignments

Number of reads	500
Number of reads with alignments	250 (50.00%)
Number of reads without alignments	250 (50.00%)

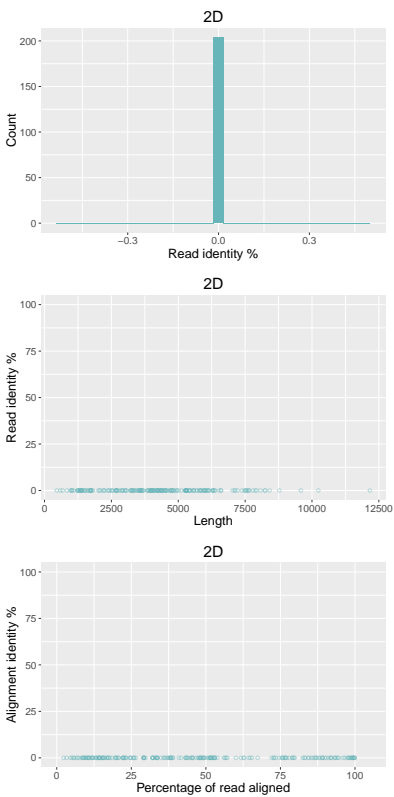
ID	Size	Number of Reads	% of Reads	Mean read length	Aligned bases	Mean coverage	Longest Perf Kmer
NC 005128	48508	0	0.00	0.00	0	0.00	0
NC 005139	3354505	204	40.80	4231.70	367518	0.11	0
NC 005140	1857073	46	9.20	3830.28	48951	0.03	0

NC 005139 error analysis

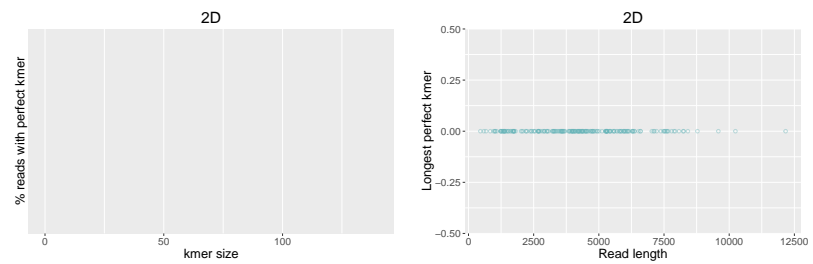
	Template	Complement	2D
Overall base identity (excluding indels)	0.00%	0.00%	0.00%
Aligned base identity (excluding indels)	0.00%	0.00%	0.00%
Identical bases per 100 aligned bases (including indels)	0.00%	0.00%	0.00%
Inserted bases per 100 aligned bases (including indels)	4.89%	5.33%	5.70%
Deleted bases per 100 aligned bases (including indels)	11.30%	11.13%	6.97%
Substitutions per 100 aligned bases (including indels)	83.82%	83.55%	87.32%
Mean insertion size	1.54	1.54	1.55
Mean deletion size	1.69	1.64	1.56



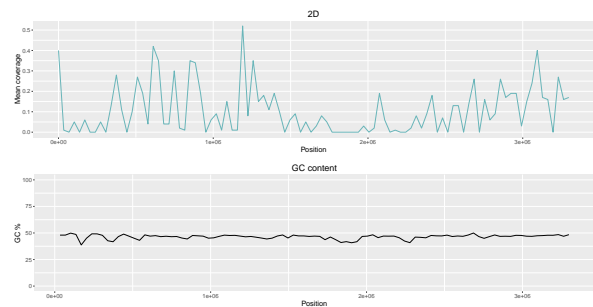
NC 005139 read identity



NC 005139 perfect kmers



NC 005139 coverage



NC 005139 5-mer analysis

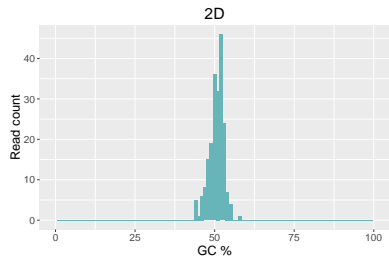
Under-represented 5-mers

Rank	Template				Complement				2D			
	kmer	Ref %	Read %	Diff %	kmer	Ref %	Read %	Diff %	kmer	Ref %	Read %	Diff %
1	ttttt	0.279	0.000	-0.279	ttttt	0.279	0.000	-0.279	ttttt	0.279	0.000	-0.279
2	aaaaa	0.278	0.000	-0.278	aaaaa	0.278	0.000	-0.278	aaaaa	0.278	0.000	-0.278
3	caaaa	0.243	0.000	-0.243	caaaa	0.243	0.000	-0.243	caaaa	0.243	0.000	-0.243
4	ttttg	0.237	0.000	-0.237	ttttg	0.237	0.000	-0.237	ttttg	0.237	0.000	-0.237
5	ttgat	0.232	0.000	-0.232	ttgat	0.232	0.000	-0.232	ttgat	0.232	0.000	-0.232
6	atcaa	0.227	0.000	-0.227	atcaa	0.227	0.000	-0.227	atcaa	0.227	0.000	-0.227
7	accaa	0.226	0.000	-0.226	accaa	0.226	0.000	-0.226	accaa	0.226	0.000	-0.226
8	gccaa	0.222	0.000	-0.222	gccaa	0.222	0.000	-0.222	gccaa	0.222	0.000	-0.222
9	ttggc	0.215	0.000	-0.215	ttggc	0.215	0.000	-0.215	ttggc	0.215	0.000	-0.215
10	aaaac	0.214	0.000	-0.214	aaaac	0.214	0.000	-0.214	aaaac	0.214	0.000	-0.214

Over-represented 5-mers

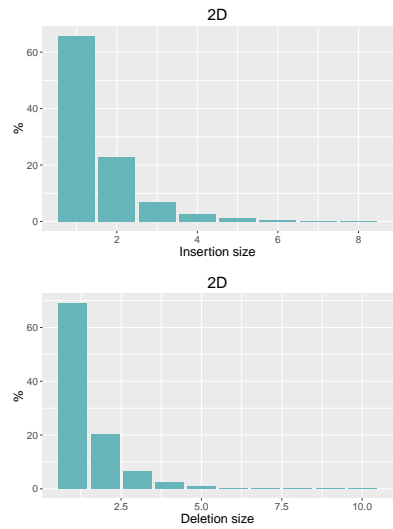
Rank	Template				Complement				2D			
	kmer	Ref %	Read %	Diff %	kmer	Ref %	Read %	Diff %	kmer	Ref %	Read %	Diff %
1	GCGGC	0.000	0.231	0.231	GAGAG	0.000	0.219	0.219	CAGCA	0.000	0.236	0.236
2	TGCTG	0.000	0.223	0.223	GCTGC	0.000	0.214	0.214	TGCTG	0.000	0.229	0.229
3	GGCGG	0.000	0.220	0.220	AGAGA	0.000	0.213	0.213	CCAGC	0.000	0.221	0.221
4	CAGCA	0.000	0.198	0.198	TGCTG	0.000	0.212	0.212	GCTGG	0.000	0.218	0.218
5	CGGCG	0.000	0.195	0.195	GCGGC	0.000	0.207	0.207	CAGCG	0.000	0.216	0.216
6	CAGCG	0.000	0.193	0.193	TGATG	0.000	0.207	0.207	CGCTG	0.000	0.207	0.207
7	CGTCG	0.000	0.191	0.191	CGGCG	0.000	0.199	0.199	GCAGC	0.000	0.206	0.206
8	GCAGC	0.000	0.188	0.188	GGCGG	0.000	0.198	0.198	CTGGC	0.000	0.206	0.206
9	GCTGC	0.000	0.187	0.187	GGCTG	0.000	0.194	0.194	CATCA	0.000	0.198	0.198
10	GGCGT	0.000	0.183	0.183	GCTGA	0.000	0.189	0.189	TGCCG	0.000	0.192	0.192

NC 005139 GC content

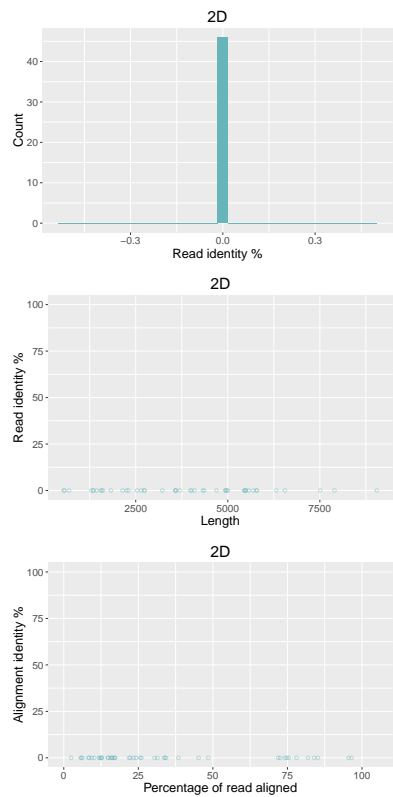


NC 005140 error analysis

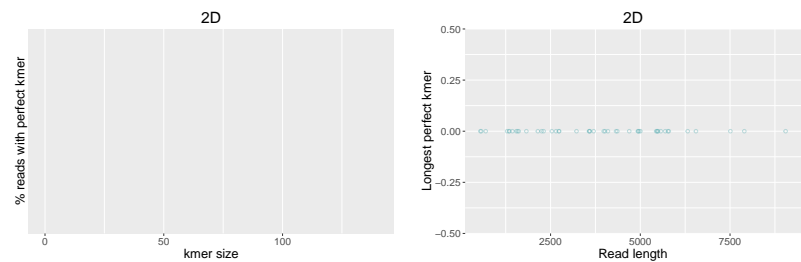
	Template	Complement	2D
Overall base identity (excluding indels)	0.00%	0.00%	0.00%
Aligned base identity (excluding indels)	0.00%	0.00%	0.00%
Identical bases per 100 aligned bases (including indels)	0.00%	0.00%	0.00%
Inserted bases per 100 aligned bases (including indels)	5.00%	5.53%	5.63%
Deleted bases per 100 aligned bases (including indels)	11.09%	8.97%	6.60%
Substitutions per 100 aligned bases (including indels)	83.90%	85.50%	87.77%
Mean insertion size	1.62	1.58	1.53
Mean deletion size	1.66	1.54	1.47



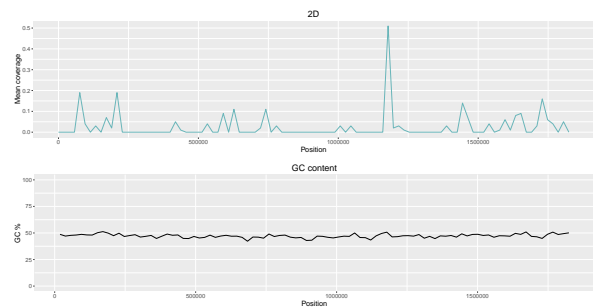
NC 005140 read identity



NC 005140 perfect kmers



NC 005140 coverage



NC 005140 5-mer analysis

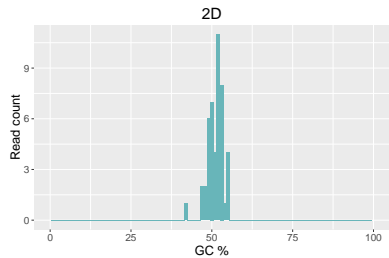
Under-represented 5-mers

Rank	Template				Complement				2D			
	kmer	Ref %	Read %	Diff %	kmer	Ref %	Read %	Diff %	kmer	Ref %	Read %	Diff %
1	ttttt	0.264	0.000	-0.264	ttttt	0.264	0.000	-0.264	ttttt	0.264	0.000	-0.264
2	aaaaa	0.261	0.000	-0.261	aaaaa	0.261	0.000	-0.261	aaaaa	0.261	0.000	-0.261
3	ttggc	0.249	0.000	-0.249	ttggc	0.249	0.000	-0.249	ttggc	0.249	0.000	-0.249
4	gccaa	0.245	0.000	-0.245	gccaa	0.245	0.000	-0.245	gccaa	0.245	0.000	-0.245
5	ttttg	0.241	0.000	-0.241	ttttg	0.241	0.000	-0.241	ttttg	0.241	0.000	-0.241
6	caaaa	0.241	0.000	-0.241	caaaa	0.241	0.000	-0.241	caaaa	0.241	0.000	-0.241
7	ttgat	0.241	0.000	-0.241	ttgat	0.241	0.000	-0.241	ttgat	0.241	0.000	-0.241
8	atcaa	0.237	0.000	-0.237	atcaa	0.237	0.000	-0.237	atcaa	0.237	0.000	-0.237
9	catca	0.228	0.000	-0.228	catca	0.228	0.000	-0.228	catca	0.228	0.000	-0.228
10	cacca	0.221	0.000	-0.221	cacca	0.221	0.000	-0.221	cacca	0.221	0.000	-0.221

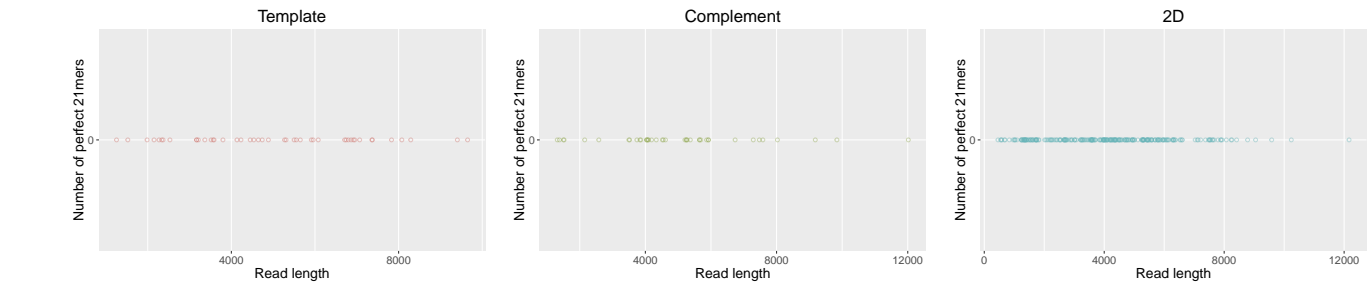
Over-represented 5-mers

Rank	Template				Complement				2D			
	kmer	Ref %	Read %	Diff %	kmer	Ref %	Read %	Diff %	kmer	Ref %	Read %	Diff %
1	CCAGC	0.000	0.359	0.359	TGCTG	0.000	0.312	0.312	CCAGC	0.000	0.280	0.280
2	CAGCG	0.000	0.310	0.310	GCTGG	0.000	0.295	0.295	GCCAG	0.000	0.260	0.260
3	CGGGC	0.000	0.277	0.277	CGGCG	0.000	0.266	0.266	CAGCA	0.000	0.254	0.254
4	TTTCC	0.000	0.277	0.277	GGCTG	0.000	0.260	0.260	CGCCA	0.000	0.246	0.246
5	GGCGT	0.000	0.261	0.261	CTGGC	0.000	0.243	0.243	CAGCG	0.000	0.244	0.244
6	TGATG	0.000	0.261	0.261	GGCGG	0.000	0.243	0.243	TGCTG	0.000	0.237	0.237
7	GATGC	0.000	0.245	0.245	GCGGC	0.000	0.237	0.237	GCAGC	0.000	0.228	0.228
8	CGGCA	0.000	0.245	0.245	CGGCT	0.000	0.220	0.220	CGGCA	0.000	0.207	0.207
9	TTAAC	0.000	0.245	0.245	TGATG	0.000	0.220	0.220	TGCCG	0.000	0.206	0.206
10	TGCTT	0.000	0.245	0.245	GCTGA	0.000	0.208	0.208	TGGCG	0.000	0.202	0.202

NC 005140 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	NaN	NaN	NaN	NaN	NaN	NaN	NaN	NaN	NaN	NaN	NaN	NaN
	C	NaN	NaN	NaN	NaN	NaN	NaN	NaN	NaN	NaN	NaN	NaN	NaN
	G	NaN	NaN	NaN	NaN	NaN	NaN	NaN	NaN	NaN	NaN	NaN	NaN
	T	NaN	NaN	NaN	NaN	NaN	NaN	NaN	NaN	NaN	NaN	NaN	NaN

Kmer motifs before errors

3-mer error motif analysis

Rank	Template			Complement			2D		
	Insertion	Deletion	Substitution	Insertion	Deletion	Substitution	Insertion	Deletion	Substitution
1									
2									
3									
4									
5									
6									
7									
8									
9									
10									
-10									
-9									
-8									
-7									
-6									
-5									
-4									
-3									
-2									
-1									

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										Most common
2										
3										
4										
5										
6										
7										
8										
9										
10										
										Least common
-10										
-9										
-8										
-7										
-6										
-5										
-4										
-3										
-2										
-1										

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										Most common
2										
3										
4										
5										
6										
7										
8										
9										
10										
										Least common
-10										
-9										
-8										
-7										
-6										
-5										
-4										
-3										
-2										
-1										

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