

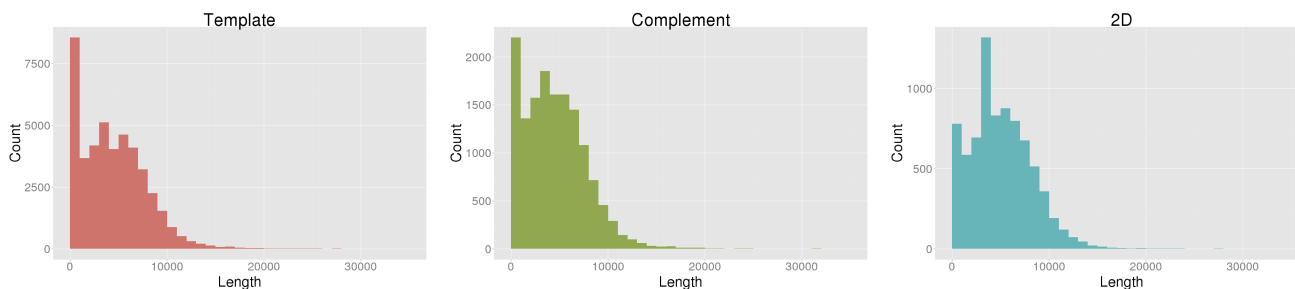
NanoOK report for MA_286_R7.3_MARC_K12_03_27_15

Pass and fail counts

| Type | Pass | Fail |
|------------|------|-------|
| Template | 0 | 43915 |
| Complement | 0 | 14679 |
| 2D | 0 | 7951 |

Read lengths

| Type | NumReads | TotalBases | Mean | Longest | Shortest | N50 | N50Count | N90 | N90Count |
|------------|----------|------------|---------|---------|----------|------|----------|------|----------|
| Template | 43915 | 202050231 | 4600.94 | 227038 | 7 | 6755 | 10573 | 3034 | 27315 |
| Complement | 14679 | 67300239 | 4584.80 | 43287 | 5 | 6441 | 3805 | 2945 | 9649 |
| 2D | 7951 | 40755577 | 5125.84 | 38555 | 123 | 6808 | 2206 | 3268 | 5562 |



Template alignments

| | |
|------------------------------------|----------------|
| Number of reads | 43915 |
| Number of reads with alignments | 20100 (45.77%) |
| Number of reads without alignments | 23815 (54.23%) |

| ID | Size | Number of Reads | % of Reads | Mean read length | Aligned bases | Mean coverage | Longest Perf Kmer |
|------------------|---------|-----------------|------------|------------------|---------------|---------------|-------------------|
| Control sequence | 3560 | 2340 | 5.33 | 3028.16 | 6651007 | 1868.26 | 58 |
| Escherichia coli | 4641652 | 17760 | 40.44 | 6321.36 | 97493278 | 21.00 | 71 |

Complement alignments

| | |
|------------------------------------|---------------|
| Number of reads | 14679 |
| Number of reads with alignments | 7251 (49.40%) |
| Number of reads without alignments | 7428 (50.60%) |

| ID | Size | Number of Reads | % of Reads | Mean read length | Aligned bases | Mean coverage | Longest Perf Kmer |
|------------------|---------|-----------------|------------|------------------|---------------|---------------|-------------------|
| Control sequence | 3560 | 882 | 6.01 | 2739.22 | 2086340 | 586.05 | 49 |
| Escherichia coli | 4641652 | 6369 | 43.39 | 5859.53 | 31299717 | 6.74 | 59 |

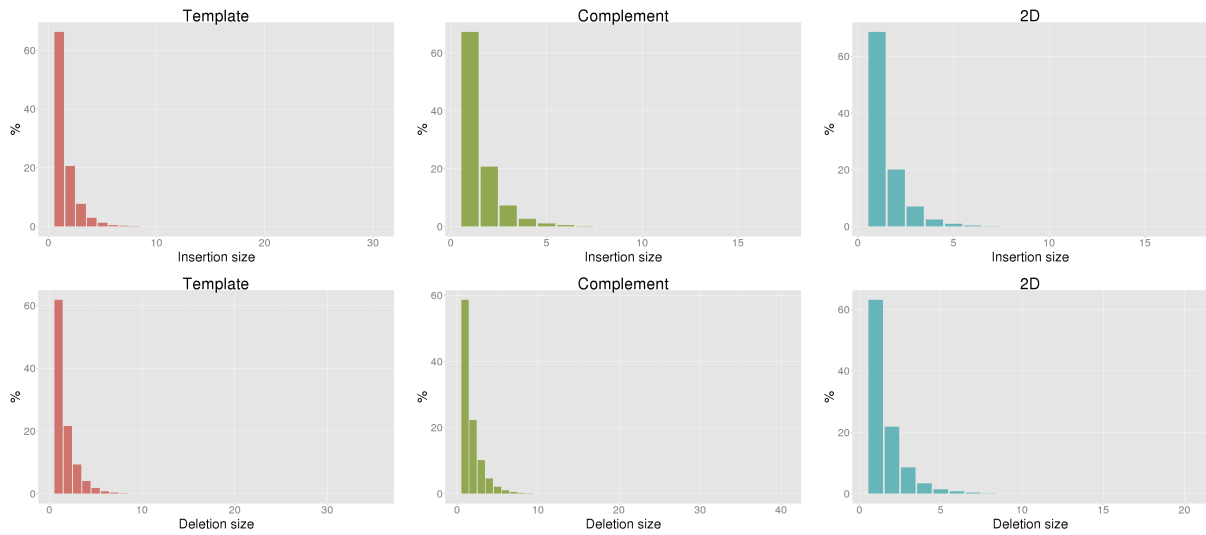
2D alignments

| | |
|------------------------------------|---------------|
| Number of reads | 7951 |
| Number of reads with alignments | 6038 (75.94%) |
| Number of reads without alignments | 1913 (24.06%) |

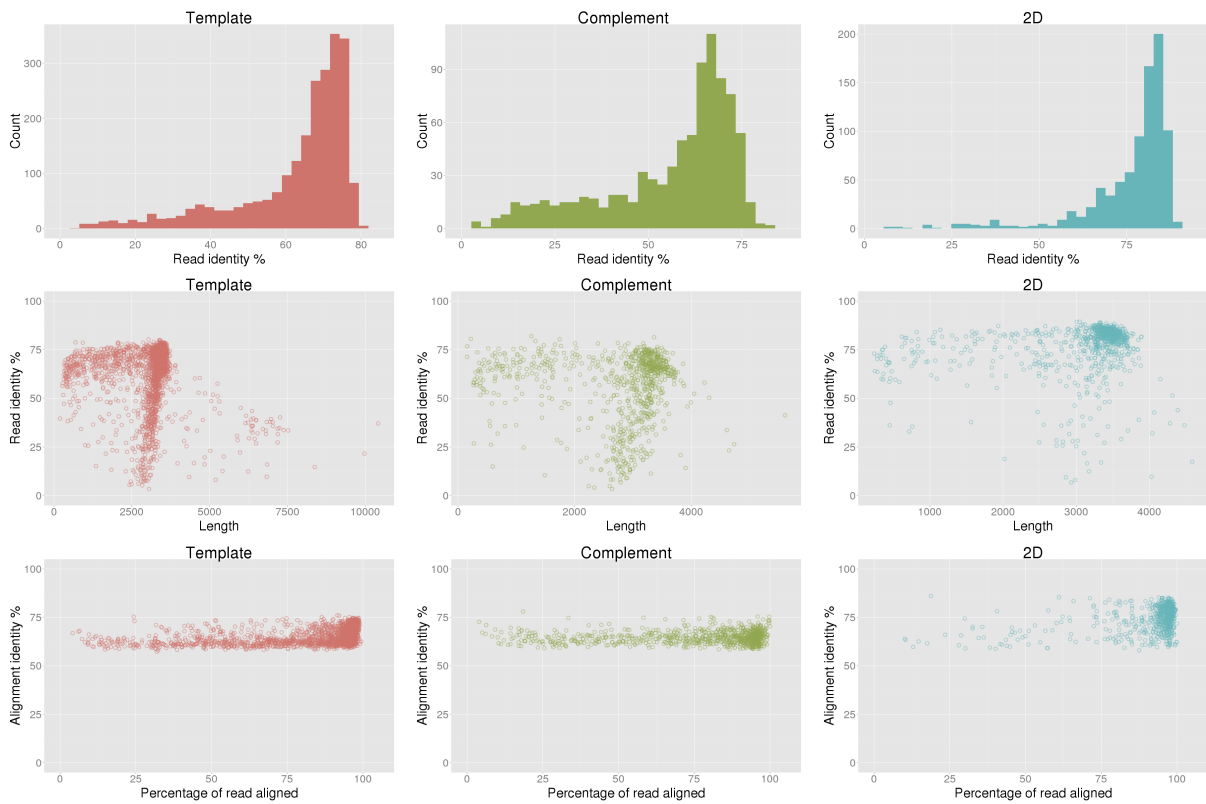
| ID | Size | Number of Reads | % of Reads | Mean read length | Aligned bases | Mean coverage | Longest Perf Kmer |
|------------------|---------|-----------------|------------|------------------|---------------|---------------|-------------------|
| Control sequence | 3560 | 868 | 10.92 | 3055.63 | 2683165 | 753.70 | 160 |
| Escherichia coli | 4641652 | 5170 | 65.02 | 5854.97 | 30090593 | 6.48 | 171 |

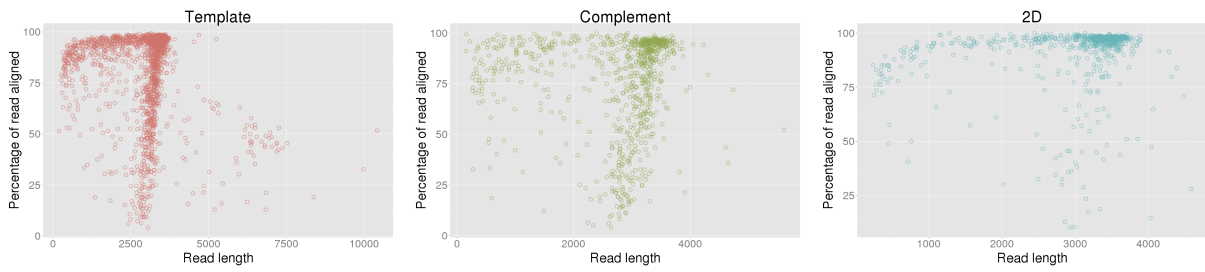
Control sequence error analysis

| | Template | Complement | 2D |
|--|----------|------------|--------|
| Overall base identity (excluding indels) | 62.01% | 55.55% | 76.64% |
| Aligned base identity (excluding indels) | 78.97% | 78.22% | 87.00% |
| Identical bases per 100 aligned bases (including indels) | 66.07% | 64.33% | 75.76% |
| Inserted bases per 100 aligned bases (including indels) | 5.11% | 4.79% | 4.43% |
| Deleted bases per 100 aligned bases (including indels) | 11.23% | 12.97% | 8.48% |
| Substitutions per 100 aligned bases (including indels) | 17.60% | 17.91% | 11.32% |
| Mean insertion size | 1.58 | 1.54 | 1.50 |
| Mean deletion size | 1.68 | 1.79 | 1.64 |

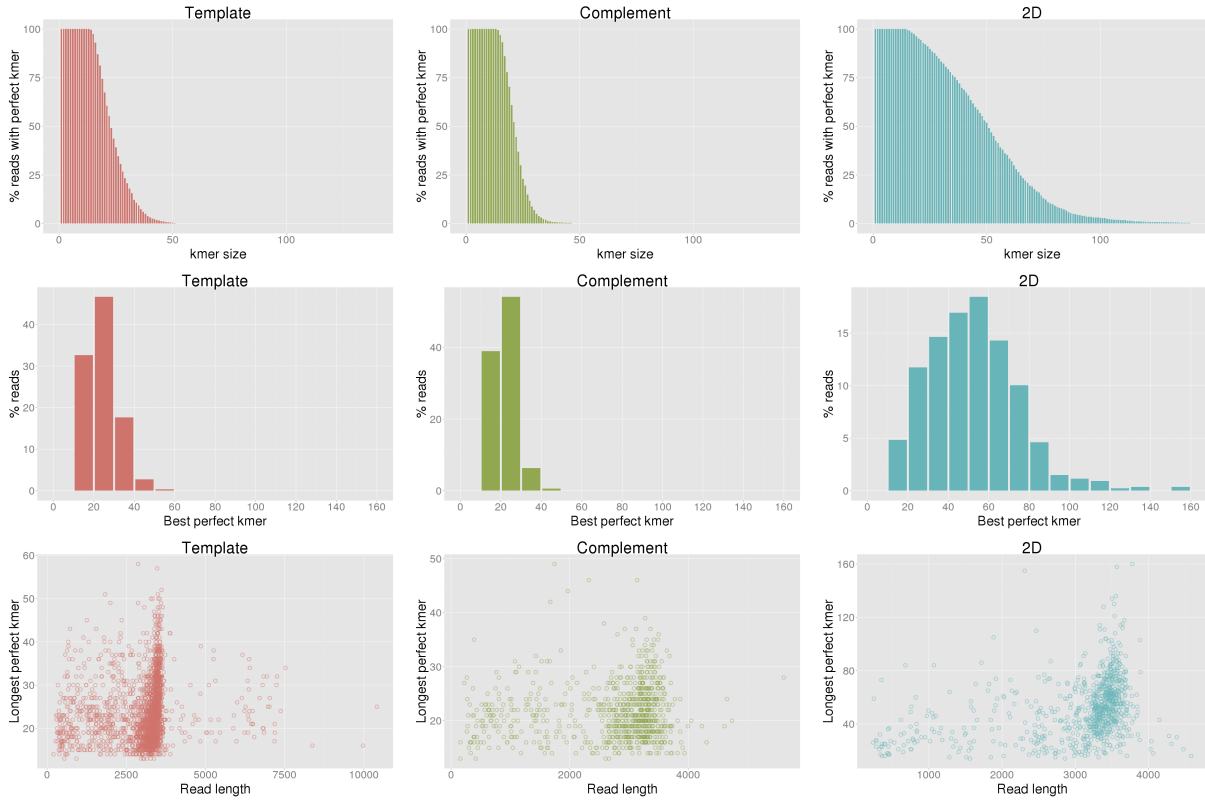


Control sequence read identity

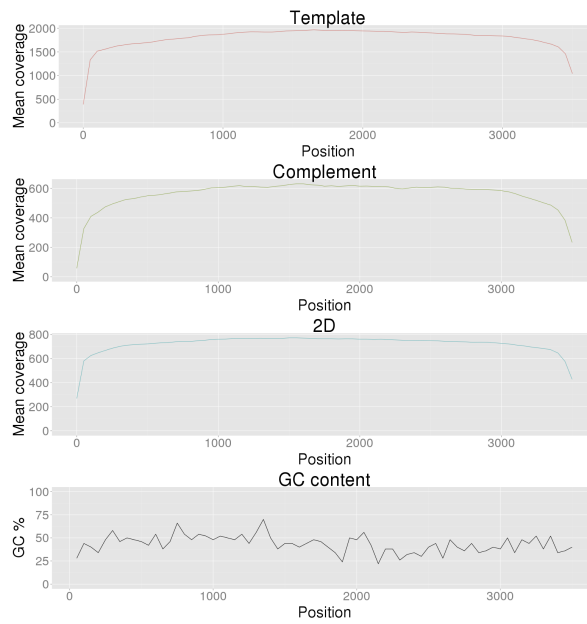




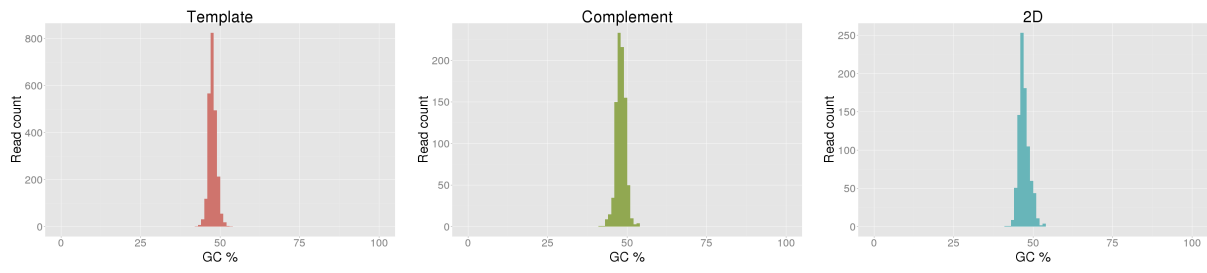
Control sequence perfect kmers



Control sequence coverage

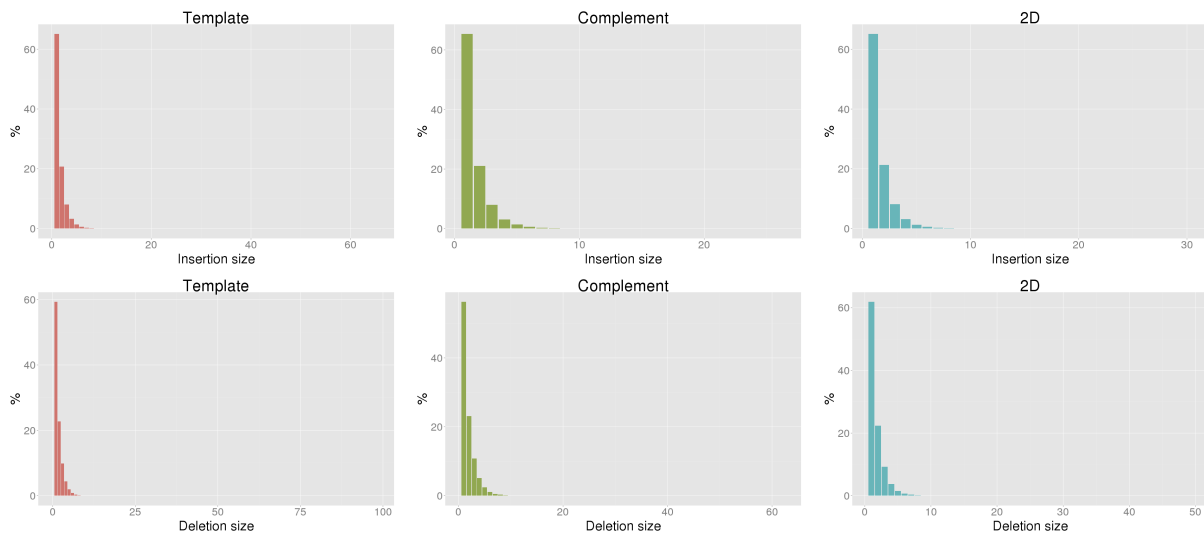


Control sequence GC content

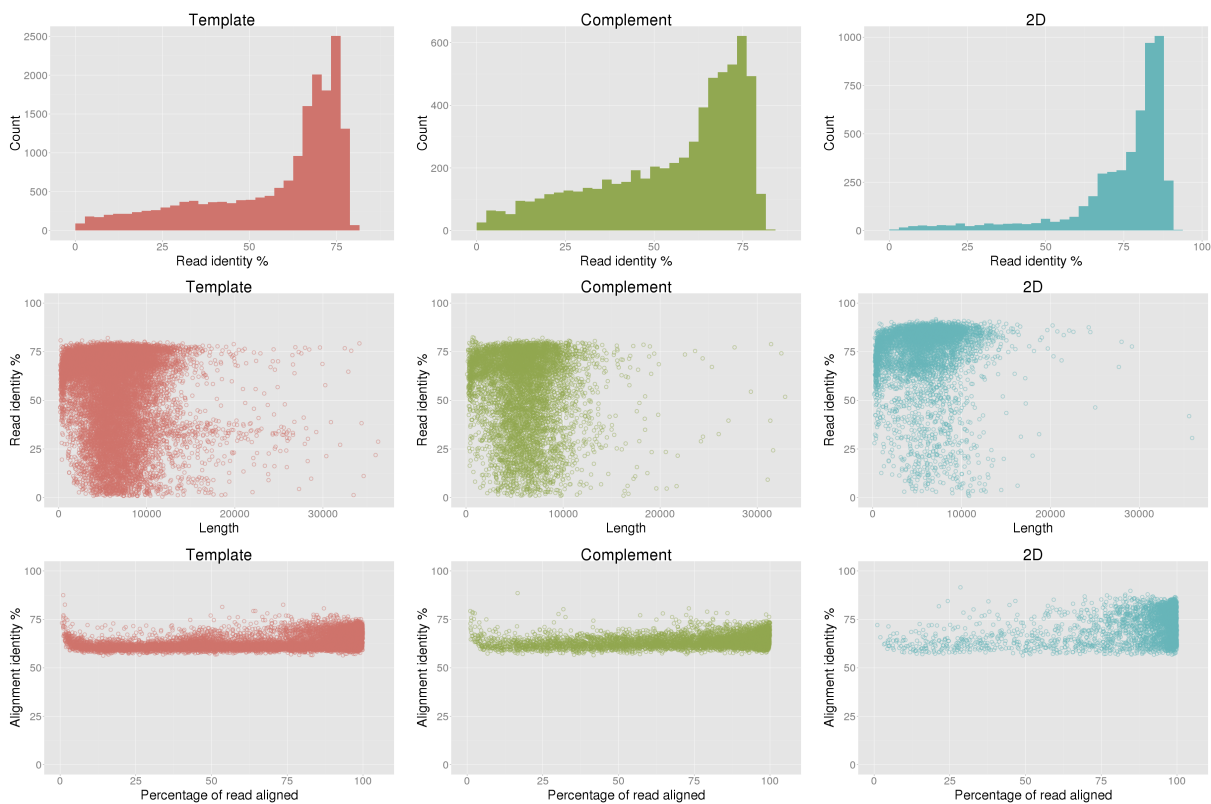


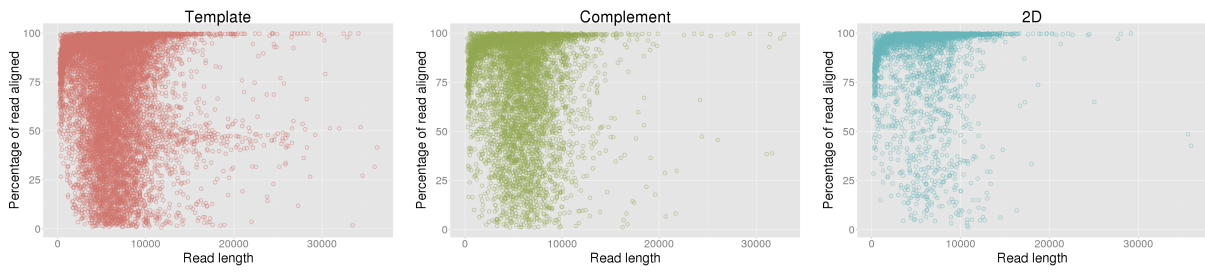
Escherichia coli error analysis

| | Template | Complement | 2D |
|--|----------|------------|--------|
| Overall base identity (excluding indels) | 55.71% | 53.72% | 74.17% |
| Aligned base identity (excluding indels) | 77.77% | 78.90% | 86.32% |
| Identical bases per 100 aligned bases (including indels) | 64.15% | 64.06% | 74.62% |
| Inserted bases per 100 aligned bases (including indels) | 5.50% | 5.08% | 5.14% |
| Deleted bases per 100 aligned bases (including indels) | 12.01% | 13.74% | 8.42% |
| Substitutions per 100 aligned bases (including indels) | 18.34% | 17.13% | 11.82% |
| Mean insertion size | 1.61 | 1.59 | 1.59 |
| Mean deletion size | 1.73 | 1.85 | 1.66 |

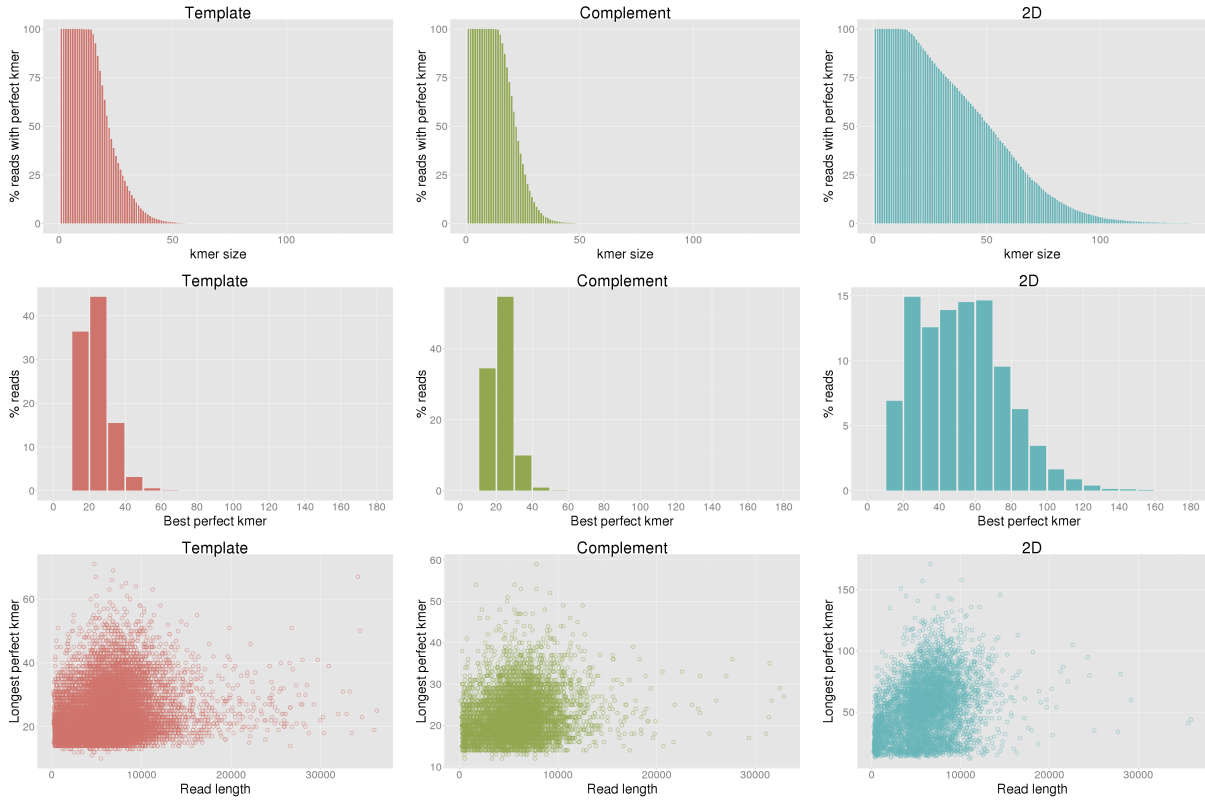


Escherichia coli read identity

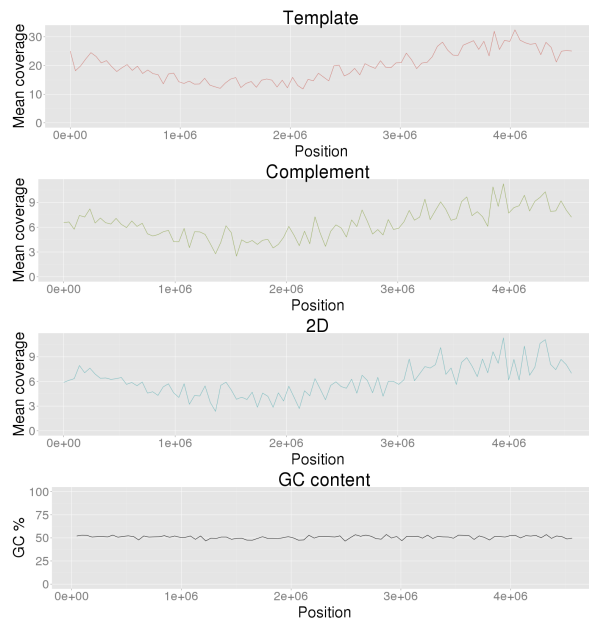




Escherichia coli perfect kmers



Escherichia coli coverage



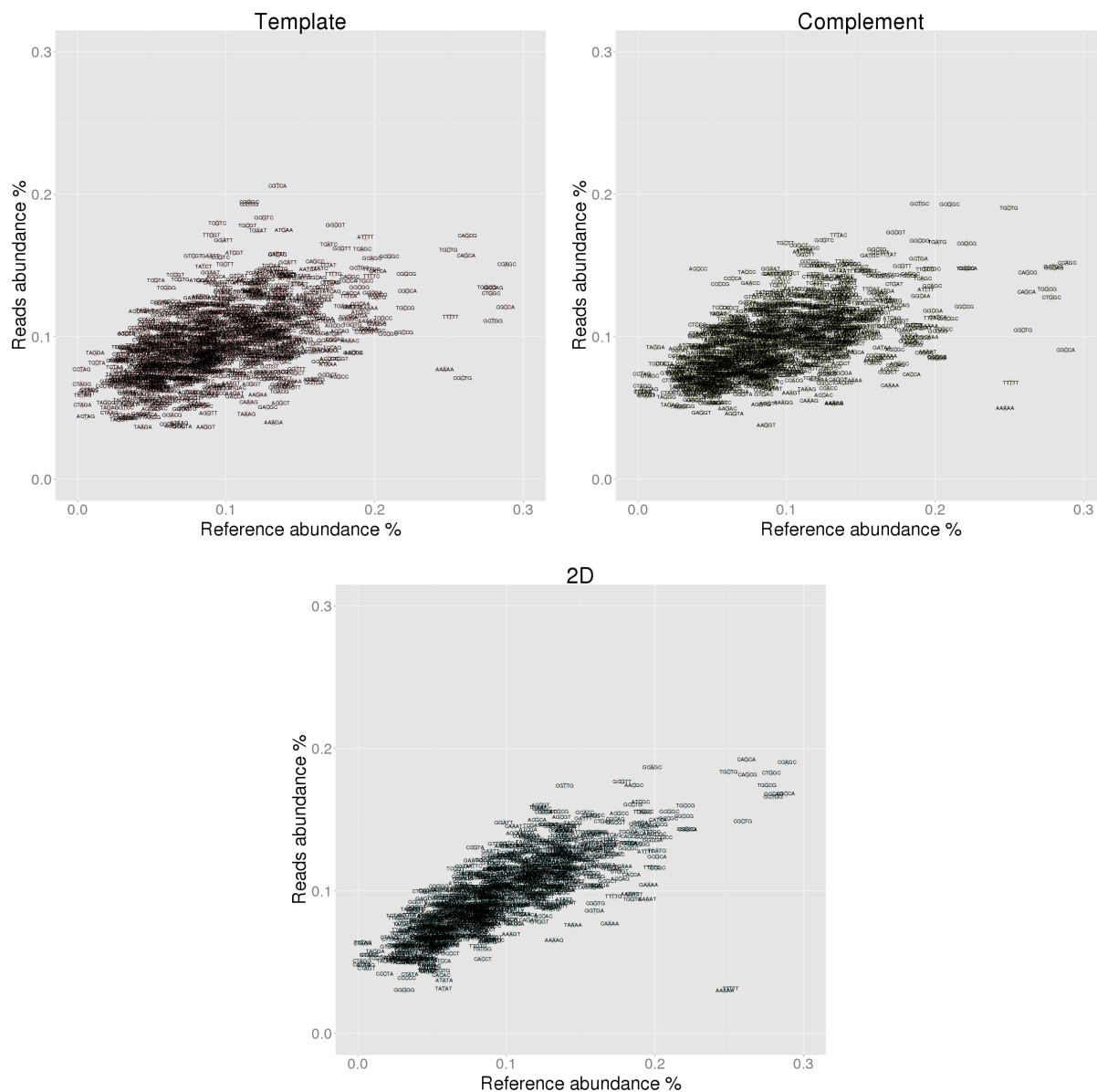
Escherichia coli 5-mer analysis

Under-represented 5-mers

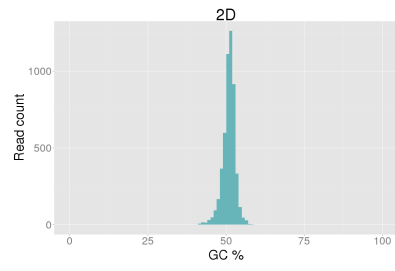
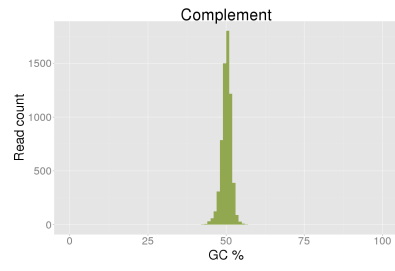
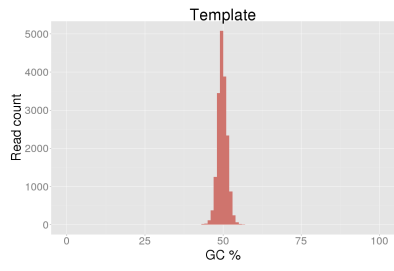
| Rank | Template | | | | Complement | | | | 2D | | | |
|------|----------|-------|--------|--------|------------|-------|--------|--------|-------|-------|--------|--------|
| | kmer | Ref % | Read % | Diff % | kmer | Ref % | Read % | Diff % | kmer | Ref % | Read % | Diff % |
| 1 | CGCTG | 0.259 | 0.071 | -0.188 | CGCCA | 0.288 | 0.091 | -0.197 | TTTTT | 0.251 | 0.031 | -0.219 |
| 2 | AAAAA | 0.247 | 0.077 | -0.170 | AAAAA | 0.247 | 0.050 | -0.197 | AAAAA | 0.247 | 0.030 | -0.217 |
| 3 | GCTGG | 0.279 | 0.111 | -0.168 | TTTTT | 0.251 | 0.068 | -0.183 | CGCCA | 0.288 | 0.168 | -0.120 |
| 4 | CGCCA | 0.288 | 0.121 | -0.167 | CGCTG | 0.259 | 0.105 | -0.154 | GCTGG | 0.279 | 0.166 | -0.113 |
| 5 | CTGGC | 0.278 | 0.131 | -0.148 | CTGGC | 0.278 | 0.128 | -0.151 | GCCAG | 0.280 | 0.168 | -0.112 |
| 6 | GCCAG | 0.280 | 0.135 | -0.145 | TGGCG | 0.275 | 0.134 | -0.142 | CGCTG | 0.259 | 0.149 | -0.110 |
| 7 | TGGCG | 0.275 | 0.135 | -0.141 | CCAGC | 0.289 | 0.152 | -0.137 | TGGCG | 0.275 | 0.174 | -0.101 |
| 8 | CCAGC | 0.289 | 0.151 | -0.138 | GCCAG | 0.280 | 0.148 | -0.131 | AAAAT | 0.195 | 0.094 | -0.101 |
| 9 | TTTTT | 0.251 | 0.114 | -0.137 | CAGCA | 0.261 | 0.131 | -0.130 | CCAGC | 0.289 | 0.190 | -0.098 |
| 10 | CGCCG | 0.219 | 0.103 | -0.116 | GCTGG | 0.279 | 0.149 | -0.130 | CTGGC | 0.278 | 0.183 | -0.095 |

Over-represented 5-mers

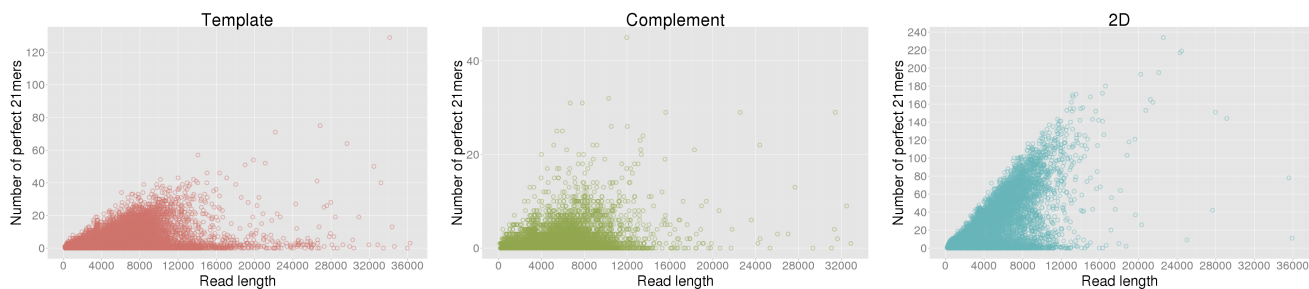
| Rank | Template | | | | Complement | | | | 2D | | | |
|------|----------|-------|--------|--------|------------|-------|--------|--------|-------|-------|--------|--------|
| | kmer | Ref % | Read % | Diff % | kmer | Ref % | Read % | Diff % | kmer | Ref % | Read % | Diff % |
| 1 | TCGTA | 0.053 | 0.140 | 0.087 | ACCCC | 0.040 | 0.148 | 0.107 | TCTAG | 0.003 | 0.064 | 0.061 |
| 2 | TCGTC | 0.094 | 0.180 | 0.086 | CCCCG | 0.055 | 0.137 | 0.082 | CTAGA | 0.003 | 0.063 | 0.060 |
| 3 | TTCGT | 0.090 | 0.171 | 0.081 | TAGGA | 0.012 | 0.093 | 0.081 | TCTAA | 0.025 | 0.083 | 0.058 |
| 4 | CGGGC | 0.116 | 0.195 | 0.079 | CCCCA | 0.064 | 0.141 | 0.077 | CTCGT | 0.042 | 0.100 | 0.057 |
| 5 | GTCGT | 0.078 | 0.157 | 0.079 | TACCC | 0.073 | 0.146 | 0.072 | TTAGA | 0.026 | 0.081 | 0.055 |
| 6 | CGTCG | 0.115 | 0.193 | 0.078 | CCTAG | 0.003 | 0.074 | 0.071 | CCCAA | 0.047 | 0.101 | 0.054 |
| 7 | TCCGT | 0.066 | 0.144 | 0.078 | CTCCC | 0.040 | 0.109 | 0.069 | TAGAT | 0.035 | 0.087 | 0.052 |
| 8 | ACCCC | 0.040 | 0.118 | 0.078 | TCCTA | 0.013 | 0.081 | 0.068 | GGGTC | 0.040 | 0.093 | 0.052 |
| 9 | TAGGA | 0.012 | 0.089 | 0.077 | TGCTT | 0.099 | 0.166 | 0.067 | CCGTA | 0.079 | 0.130 | 0.052 |
| 10 | TCGGG | 0.060 | 0.135 | 0.075 | ACCTA | 0.027 | 0.092 | 0.065 | ATCTA | 0.033 | 0.083 | 0.050 |



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 | 8.78 | 8.68 | 5.28 | 0.00 | 9.00 | 8.58 | 5.32 | 0.00 | 9.17 | 8.96 | 4.66 |
| C | 8.74 | 0.00 | 8.84 | 9.95 | 9.10 | 0.00 | 8.58 | 9.50 | 8.61 | 0.00 | 9.95 | 8.76 |
| G | 9.58 | 8.91 | 0.00 | 8.49 | 9.04 | 8.82 | 0.00 | 8.87 | 8.75 | 10.11 | 0.00 | 8.31 |
| T | 5.51 | 8.70 | 8.56 | 0.00 | 5.58 | 8.71 | 8.90 | 0.00 | 4.78 | 8.94 | 8.99 | 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 (3.31%) | AAA (4.19%) | TTC (2.87%) | AAA (2.87%) | AAA (4.11%) | GCA (3.06%) | AAA (2.76%) | AAA (3.79%) |
| 2 | AAA (2.84%) | AAA (3.00%) | TTC (3.52%) | AAA (2.79%) | TGC (2.77%) | GCA (3.40%) | AAA (2.92%) | TGC (2.63%) | GCA (3.51%) |
| 3 | GCA (2.75%) | TGC (2.92%) | GCA (3.25%) | GCA (2.72%) | GCA (2.74%) | GAA (3.23%) | TTC (2.80%) | GCA (2.63%) | GAA (3.08%) |
| 4 | TGC (2.66%) | GCA (2.81%) | GAA (2.99%) | TGC (2.71%) | TTC (2.67%) | TTC (3.10%) | GAA (2.48%) | GGC (2.48%) | TTC (2.90%) |
| 5 | ATC (2.54%) | TCA (2.46%) | TTT (2.65%) | GAA (2.42%) | GGC (2.66%) | TTT (2.63%) | TCA (2.47%) | TTC (2.46%) | TTT (2.67%) |
| 6 | TCA (2.39%) | GCC (2.36%) | TGC (2.62%) | CAG (2.34%) | GAA (2.51%) | TGC (2.45%) | TGC (2.41%) | GCC (2.44%) | GTT (2.58%) |
| 7 | TTT (2.26%) | GAA (2.35%) | AAT (2.57%) | TCA (2.29%) | GCC (2.32%) | AAT (2.30%) | AAT (2.34%) | TCA (2.42%) | AAT (2.58%) |
| 8 | GAA (2.22%) | ATC (2.31%) | TCA (2.29%) | ATC (2.25%) | TCA (2.30%) | TCA (2.27%) | ATC (2.28%) | GAA (2.34%) | GCC (2.26%) |
| 9 | GCC (2.18%) | AAT (2.31%) | ATC (2.27%) | GGC (2.24%) | AAT (2.25%) | ATC (2.22%) | GCG (2.28%) | CAG (2.25%) | TGC (2.24%) |
| 10 | AAT (2.18%) | GGC (2.19%) | GCC (2.15%) | TTT (2.22%) | CAG (2.24%) | GCC (2.20%) | TTT (2.14%) | GCC (2.18%) | GCG (2.19%) |
| | | | | | | | | | |
| -10 | AGT (0.98%) | CCT (0.93%) | AGA (0.90%) | AGT (0.99%) | AGT (0.94%) | CTT (0.93%) | CTT (1.06%) | AGT (1.03%) | AGG (0.94%) |
| -9 | CTC (0.94%) | AGG (0.92%) | ACT (0.88%) | AGA (0.98%) | AGG (0.94%) | CTC (0.91%) | CTC (0.98%) | CCC (0.95%) | ACT (0.92%) |
| -8 | AGA (0.85%) | CTT (0.89%) | GGT (0.88%) | CTC (0.88%) | ACT (0.92%) | CCT (0.88%) | GAG (0.86%) | CGA (0.94%) | CCC (0.89%) |
| -7 | CCC (0.84%) | GGG (0.86%) | AGG (0.87%) | GGA (0.87%) | GGA (0.91%) | AGT (0.87%) | AGA (0.85%) | ACT (0.91%) | CGA (0.85%) |
| -6 | GGA (0.83%) | GAG (0.85%) | CTT (0.84%) | CCC (0.82%) | CCT (0.91%) | ACT (0.80%) | GGA (0.85%) | CTT (0.88%) | CTT (0.83%) |
| -5 | GAG (0.80%) | CGA (0.84%) | AGT (0.84%) | GAG (0.82%) | CTC (0.90%) | AGG (0.80%) | AGG (0.77%) | CCT (0.86%) | GAG (0.80%) |
| -4 | AGG (0.76%) | AGA (0.76%) | GGG (0.83%) | AGG (0.73%) | GAG (0.87%) | GGG (0.77%) | CCC (0.76%) | AGA (0.85%) | GGA (0.71%) |
| -3 | GGG (0.69%) | GGA (0.72%) | GAG (0.69%) | GGG (0.63%) | GGG (0.79%) | GAG (0.66%) | GGG (0.73%) | GGA (0.76%) | AGA (0.68%) |
| -2 | CTA (0.50%) | TAG (0.51%) | TAG (0.39%) | CTA (0.53%) | TAG (0.55%) | CTA (0.41%) | CTA (0.56%) | CTA (0.67%) | TAG (0.50%) |
| -1 | TAG (0.43%) | CTA (0.48%) | CTA (0.36%) | TAG (0.45%) | CTA (0.50%) | TAG (0.40%) | TAG (0.48%) | TAG (0.63%) | CTA (0.41%) |
| | | | | | | | | | |

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 (1.04%) | TTTC (1.07%) | AAAA (1.42%) | CAGC (0.88%) | CAGC (0.96%) | AAAA (1.16%) | GAAA (0.84%) | TGGC (0.90%) | GAAA (1.05%) |
| 2 | AAAA (0.90%) | TTCA (0.97%) | TTTT (1.21%) | ATCA (0.85%) | CGGC (0.94%) | CAAA (1.10%) | GGCA (0.84%) | CAGC (0.87%) | GGCA (1.04%) |
| 3 | GAAA (0.89%) | AAAA (0.94%) | GAAA (1.14%) | CAAA (0.81%) | TGGC (0.93%) | GAAA (1.00%) | CAAA (0.82%) | TTCA (0.84%) | AAAA (1.04%) |
| 4 | TTCA (0.86%) | TTGC (0.91%) | TTTT (0.96%) | CTGC (0.80%) | TTGC (0.86%) | TTTC (0.94%) | ATCA (0.82%) | CAAA (0.78%) | CGTT (0.91%) |
| 5 | ATCA (0.84%) | TGCC (0.90%) | CAAA (0.95%) | TTGC (0.79%) | CTGC (0.85%) | TGAA (0.92%) | AACA (0.81%) | CTGC (0.77%) | CAAA (0.91%) |
| 6 | TTGC (0.81%) | TTCC (0.89%) | AAAT (0.88%) | TGGC (0.77%) | CAAA (0.84%) | AGCA (0.88%) | TTCA (0.80%) | ATCA (0.75%) | GGAA (0.90%) |
| 7 | AACG (0.80%) | GAAA (0.87%) | TTCA (0.87%) | CGGC (0.77%) | TGCC (0.83%) | GGCA (0.87%) | GCCA (0.76%) | CGGC (0.75%) | TTTC (0.89%) |
| 8 | TTTT (0.80%) | CAGC (0.83%) | GCAA (0.86%) | AAAA (0.77%) | ATCA (0.80%) | ATCA (0.86%) | TGCA (0.76%) | CGCC (0.74%) | TGCA (0.88%) |
| 9 | GTTC (0.79%) | AACG (0.82%) | GGCA (0.86%) | TTTC (0.77%) | TTCC (0.80%) | TAAA (0.83%) | TTTC (0.76%) | GAAA (0.73%) | TGAA (0.84%) |
| 10 | TGCC (0.78%) | CTGC (0.81%) | TGAA (0.85%) | TGCC (0.74%) | TTCA (0.79%) | GGAA (0.83%) | CAGC (0.74%) | TGCC (0.73%) | CGCC (0.83%) |
| | | | | | | | | | |
| -10 | AGGG (0.12%) | TCTA (0.12%) | CCCT (0.11%) | AGGG (0.12%) | ACCT (0.12%) | TAGA (0.11%) | GGAC (0.13%) | ACTT (0.15%) | CTAA (0.12%) |
| -9 | CTAA (0.12%) | TAGT (0.12%) | CGAG (0.10%) | TTAG (0.12%) | TAGT (0.12%) | ACTA (0.11%) | AGGG (0.13%) | ACCT (0.15%) | CGGA (0.12%) |
| -8 | TAGT (0.12%) | CCCT (0.12%) | ACTA (0.10%) | CTAA (0.11%) | GGAC (0.12%) | TTAG (0.10%) | CTAT (0.13%) | CCCC (0.14%) | CCCT (0.11%) |
| -7 | TTAG (0.12%) | CGGA (0.12%) | TAGT (0.10%) | GAGG (0.11%) | ACTA (0.11%) | TCTA (0.10%) | CCCC (0.13%) | CTAT (0.14%) | ACTA (0.11%) |
| -6 | TCTA (0.11%) | GGAC (0.11%) | TAGA (0.08%) | CCCT (0.11%) | CTAA (0.11%) | CGAG (0.10%) | TCTA (0.13%) | CTAA (0.13%) | CTAT (0.11%) |
| -5 | GGAC (0.08%) | CTAA (0.11%) | TCTA (0.08%) | GGAC (0.09%) | TAGA (0.10%) | GGAC (0.09%) | CTAA (0.12%) | CCCT (0.12%) | TCTA (0.10%) |
| -4 | TAGA (0.07%) | TAGG (0.08%) | TAGG (0.07%) | TAGA (0.08%) | CCCT (0.08%) | CCCT (0.08%) | TAGA (0.09%) | TAGG (0.10%) | TAGG (0.07%) |
| -3 | CCTA (0.07%) | TAGA (0.06%) | GGAC (0.07%) | TAGG (0.06%) | TAGG (0.07%) | TAGG (0.06%) | CCTA (0.07%) | CCTA (0.09%) | TAGA (0.06%) |
| -2 | TAGG (0.06%) | CCTA (0.06%) | CCTA (0.04%) | CCTA (0.06%) | CCTA (0.06%) | CCTA (0.05%) | TAGG (0.06%) | TAGA (0.09%) | CCTA (0.05%) |
| -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 | TTATC (0.32%) | CAGCA (0.35%) | GAAAA (0.43%) | CAGCA (0.39%) | CAGCA (0.41%) | CAGCA (0.50%) | CAGCA (0.35%) | CTGGC (0.36%) | CAGCA (0.41%) |
| 2 | CAGCA (0.32%) | TTGCC (0.34%) | CAAAA (0.39%) | CATCA (0.31%) | CTGGC (0.35%) | GAAAA (0.38%) | CGCCA (0.33%) | CAGCA (0.32%) | GAAAA (0.38%) |
| 3 | CAAAA (0.30%) | TTTTG (0.33%) | CAGCA (0.39%) | GCTGC (0.29%) | CGGGC (0.34%) | GCAAA (0.36%) | CTGGC (0.32%) | GCCAG (0.29%) | TGGCA (0.37%) |
| 4 | GAAAA (0.29%) | TTTCA (0.31%) | GCAAA (0.36%) | CTGGC (0.29%) | CCAGC (0.31%) | CGGCA (0.35%) | TGGCA (0.30%) | GCGGC (0.29%) | CGGCA (0.35%) |
| 5 | GCAAA (0.28%) | CTGGC (0.31%) | TTATC (0.32%) | CGGCA (0.29%) | CATCA (0.31%) | ACAAA (0.34%) | CGGCA (0.30%) | TGGCG (0.29%) | GCGTT (0.35%) |
| 6 | ATTTTC (0.28%) | TTTTCC (0.30%) | CGTTTC (0.32%) | CCAGC (0.29%) | AATCA (0.30%) | ATAAA (0.34%) | GCAAAA (0.30%) | GCAGC (0.28%) | GCAAAA (0.33%) |
| 7 | TTGCC (0.28%) | GAAAA (0.30%) | AGAAA (0.31%) | GCGGC (0.28%) | TTGCC (0.30%) | CATCA (0.33%) | CATCA (0.27%) | CGCCA (0.28%) | AGAAA (0.29%) |
| 8 | CGTTC (0.28%) | TTATC (0.30%) | TTGCC (0.31%) | GCAAAA (0.28%) | GCTGC (0.29%) | AAGAA (0.31%) | TGGCG (0.27%) | CCAGC (0.28%) | CAAAA (0.29%) |
| 9 | TTTTTC (0.28%) | ATTTTC (0.29%) | TTTTTC (0.31%) | GCAGC (0.27%) | TTTTGC (0.28%) | AGAAA (0.30%) | TCTTC (0.25%) | TTTCA (0.28%) | TTGCC (0.28%) |
| 10 | CTGGC (0.28%) | CATCA (0.29%) | TGAAA (0.31%) | TTTTGC (0.27%) | ATAAA (0.28%) | ATGAA (0.30%) | CCAGC (0.25%) | CATCA (0.28%) | TGAAA (0.28%) |
| | | | | | | | | | |
| -10 | CCCTA (0.01%) | CCCTA (0.01%) | CTTAG (0.01%) | CCCTA (0.01%) | CCCTC (0.01%) | ACCTA (0.01%) | GGACC (0.01%) | TCCTA (0.01%) | TTAGA (0.01%) |
| -9 | GGACC (0.00%) | GGACC (0.01%) | CCCTA (0.00%) | CTAGT (0.01%) | CCCTA (0.01%) | CTAGT (0.01%) | CCTAG (0.01%) | TAGGA (0.01%) | TAGGA (0.01%) |
| -8 | CTAGC (0.00%) | GCTAG (0.00%) | GCTAG (0.00%) | GGACC (0.01%) | CTAGC (0.01%) | CCCTA (0.01%) | CCCTA (0.01%) | GCTAG (0.01%) | GCTAG (0.00%) |
| -7 | CTAGT (0.00%) | ACTAG (0.00%) | ACTAG (0.00%) | CTAGC (0.00%) | GCTAG (0.00%) | CTAGC (0.00%) | CTAGT (0.00%) | TAGC (0.01%) | CTAGT (0.00%) |
| -6 | ACTAG (0.00%) | CTAGT (0.00%) | CTAGG (0.00%) | GCTAG (0.00%) | CTAGT (0.00%) | GCTAG (0.00%) | GCTAG (0.00%) | ACTAG (0.00%) | CTAGC (0.00%) |
| -5 | TCTAG (0.00%) | CTAGC (0.00%) | CTAGT (0.00%) | CTAGA (0.00%) | ACTAG (0.00%) | ACTAG (0.00%) | ACTAG (0.00%) | CTAGT (0.00%) | CTAGG (0.00%) |
| -4 | GCTAG (0.00%) | CCTAG (0.00%) | CCTAG (0.00%) | CCTAG (0.00%) | CTAGA (0.00%) | CTAGA (0.00%) | CTAGA (0.00%) | TCTAG (0.00%) | CTAGA (0.00%) |
| -3 | CTAGA (0.00%) | CTAGG (0.00%) | CTAGC (0.00%) | TCTAG (0.00%) | TCTAG (0.00%) | CTAGG (0.00%) | CTAGC (0.00%) | CTAGA (0.00%) | TCTAG (0.00%) |
| -2 | CCTAG (0.00%) | CTAGA (0.00%) | CTAGA (0.00%) | CTAGG (0.00%) | CTAGG (0.00%) | TCTAG (0.00%) | TCTAG (0.00%) | CTAGG (0.00%) | ACTAG (0.00%) |
| -1 | CTAGG (0.00%) | TCTAG (0.00%) | TCTAG (0.00%) | ACTAG (0.00%) | CCTAG (0.00%) | CCTAG (0.00%) | CTAGG (0.00%) | CCTAG (0.00%) | CCTAG (0.00%) |
| | | | | | | | | | |

Most common

Least common

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