

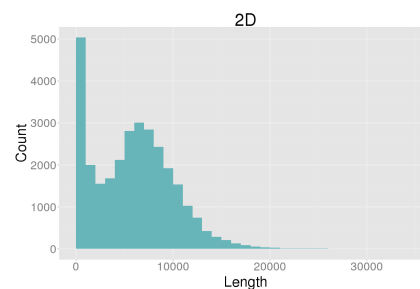
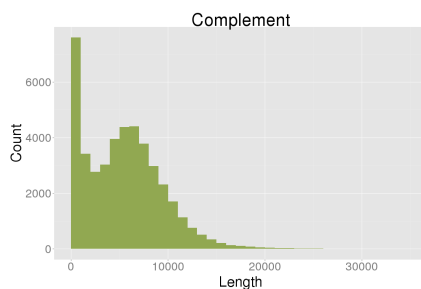
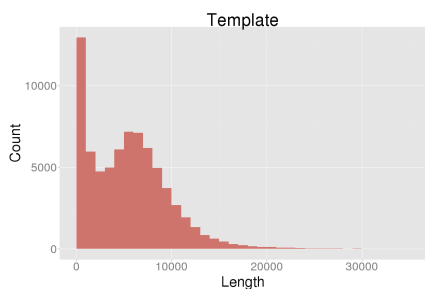
NanoOK report for MARC_1b_050814

Pass and fail counts

| Type | Pass | Fail |
|------------|------|-------|
| Template | 0 | 73271 |
| Complement | 0 | 43937 |
| 2D | 0 | 30044 |

Read lengths

| Type | NumReads | TotalBases | Mean | Longest | Shortest | N50 | N50Count | N90 | N90Count |
|------------|----------|------------|---------|---------|----------|------|----------|------|----------|
| Template | 73271 | 408743673 | 5578.52 | 409201 | 5 | 8015 | 17939 | 3854 | 45402 |
| Complement | 43937 | 240235093 | 5467.72 | 81372 | 12 | 7806 | 11216 | 3821 | 27661 |
| 2D | 30044 | 178256777 | 5933.19 | 45268 | 131 | 8395 | 8014 | 4337 | 19125 |



Template alignments

| | |
|------------------------------------|----------------|
| Number of reads | 73271 |
| Number of reads with alignments | 34403 (46.95%) |
| Number of reads without alignments | 38868 (53.05%) |

| ID | Size | Number of Reads | % of Reads | Mean read length | Aligned bases | Mean coverage | Longest Perf Kmer |
|------------------|---------|-----------------|------------|------------------|---------------|---------------|-------------------|
| Control sequence | 3560 | 45 | 0.06 | 2132.91 | 96061 | 26.98 | 32 |
| Escherichia coli | 4641652 | 34358 | 46.89 | 7132.65 | 204161888 | 43.98 | 75 |

Complement alignments

| | |
|------------------------------------|----------------|
| Number of reads | 43937 |
| Number of reads with alignments | 22925 (52.18%) |
| Number of reads without alignments | 21012 (47.82%) |

| ID | Size | Number of Reads | % of Reads | Mean read length | Aligned bases | Mean coverage | Longest Perf Kmer |
|------------------|---------|-----------------|------------|------------------|---------------|---------------|-------------------|
| Control sequence | 3560 | 4 | 0.01 | 1676.50 | 5702 | 1.60 | 32 |
| Escherichia coli | 4641652 | 22921 | 52.17 | 6905.54 | 130725601 | 28.16 | 52 |

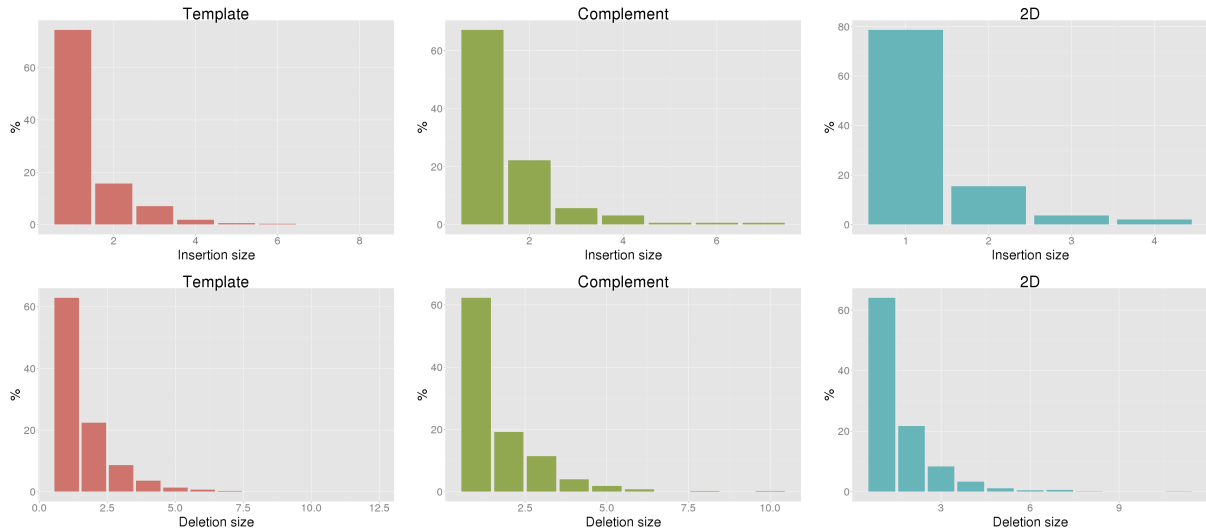
2D alignments

| | |
|------------------------------------|----------------|
| Number of reads | 30044 |
| Number of reads with alignments | 24491 (81.52%) |
| Number of reads without alignments | 5553 (18.48%) |

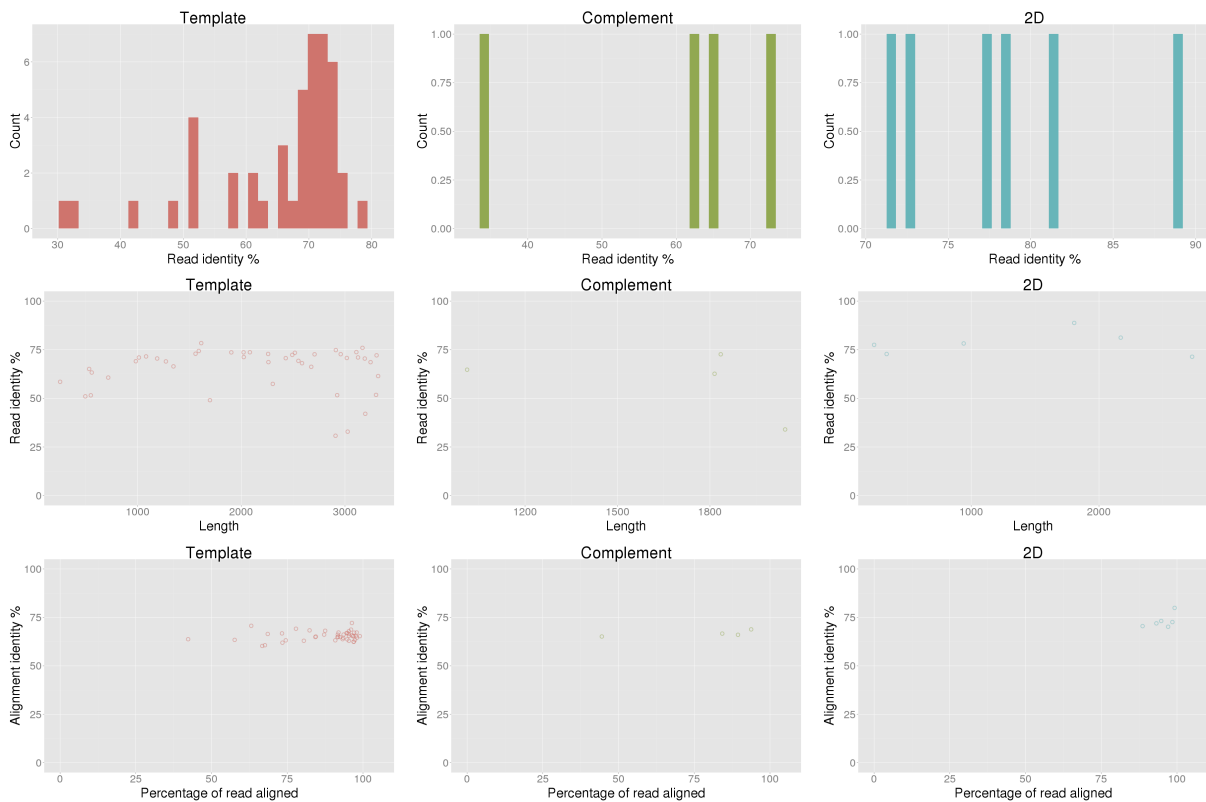
| ID | Size | Number of Reads | % of Reads | Mean read length | Aligned bases | Mean coverage | Longest Perf Kmer |
|------------------|---------|-----------------|------------|------------------|---------------|---------------|-------------------|
| Control sequence | 3560 | 6 | 0.02 | 1370.67 | 8809 | 2.47 | 48 |
| Escherichia coli | 4641652 | 24485 | 81.50 | 6424.84 | 154816987 | 33.35 | 148 |

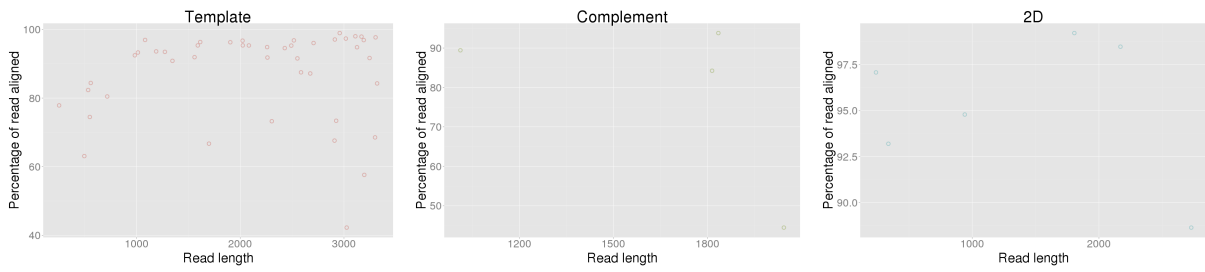
Control sequence error analysis

| | Template | Complement | 2D |
|--|----------|------------|--------|
| Overall base identity (excluding indels) | 65.40% | 56.96% | 78.81% |
| Aligned base identity (excluding indels) | 78.36% | 79.20% | 85.89% |
| Identical bases per 100 aligned bases (including indels) | 65.34% | 66.99% | 73.57% |
| Inserted bases per 100 aligned bases (including indels) | 3.17% | 4.23% | 2.75% |
| Deleted bases per 100 aligned bases (including indels) | 13.44% | 11.19% | 11.59% |
| Substitutions per 100 aligned bases (including indels) | 18.04% | 17.59% | 12.09% |
| Mean insertion size | 1.40 | 1.53 | 1.29 |
| Mean deletion size | 1.63 | 1.70 | 1.62 |

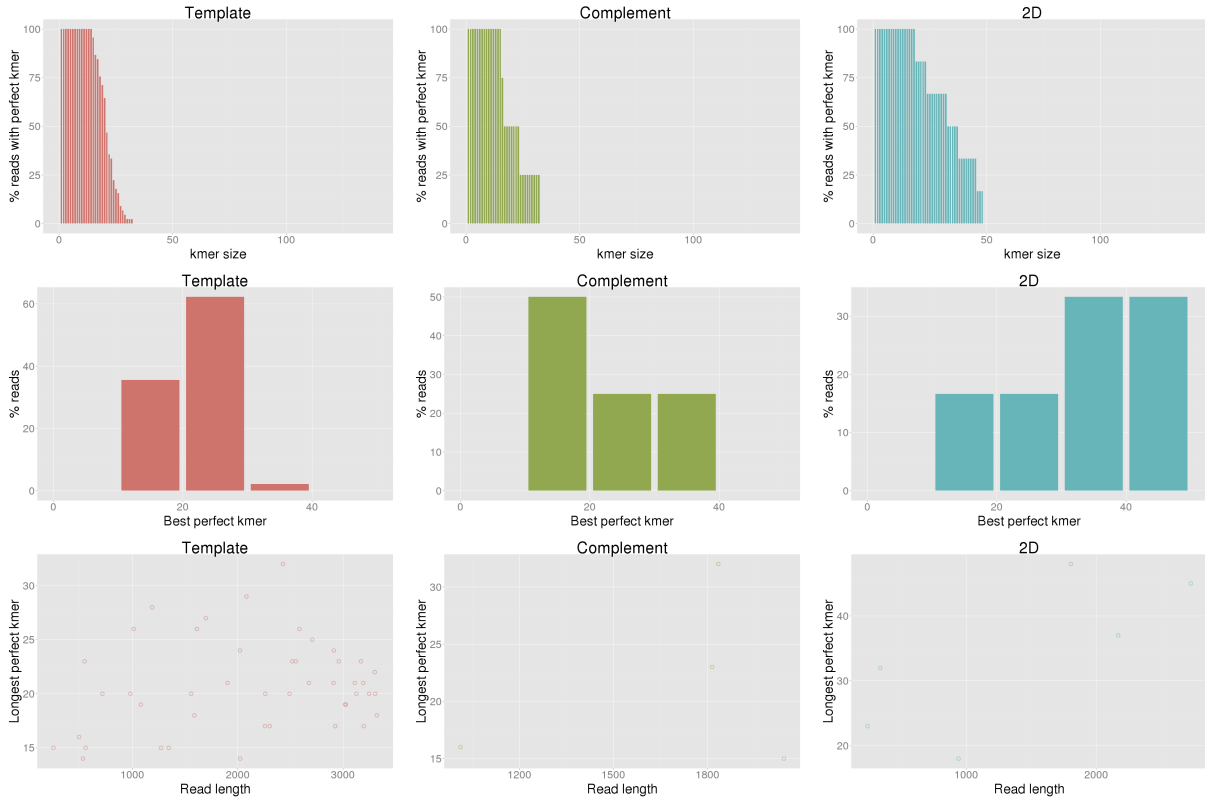


Control sequence read identity

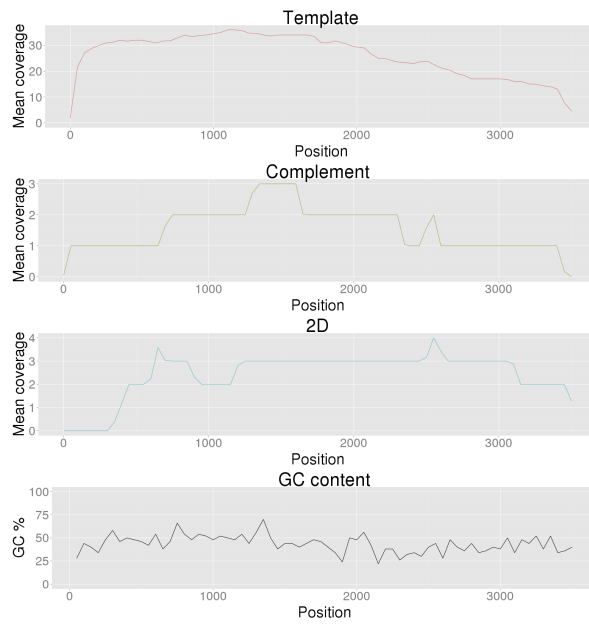




Control sequence perfect kmers



Control sequence coverage



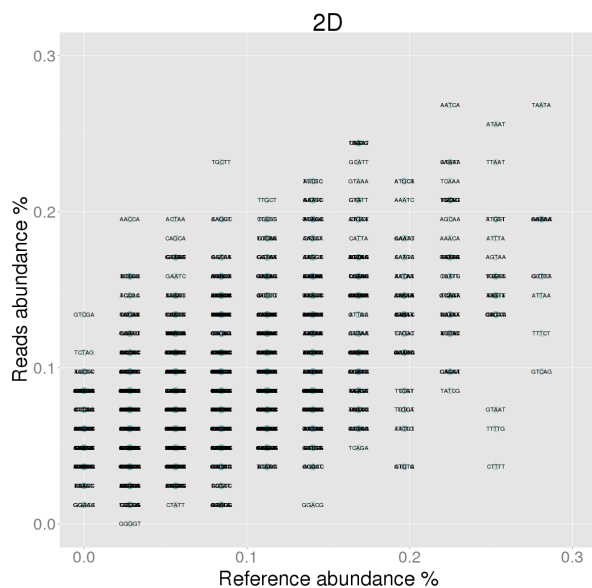
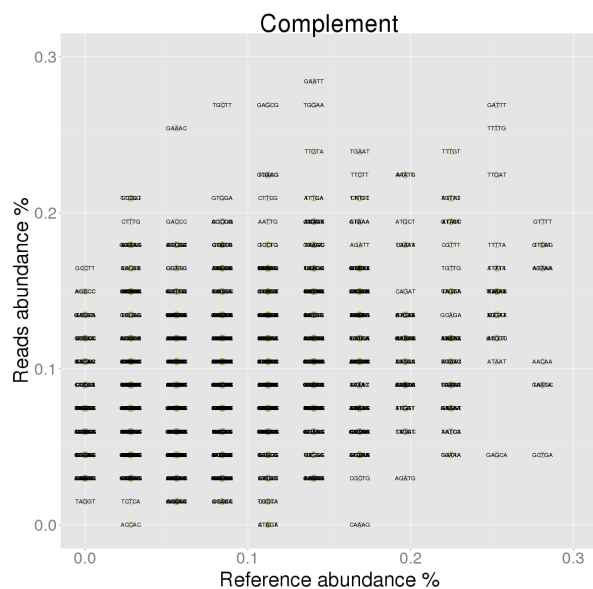
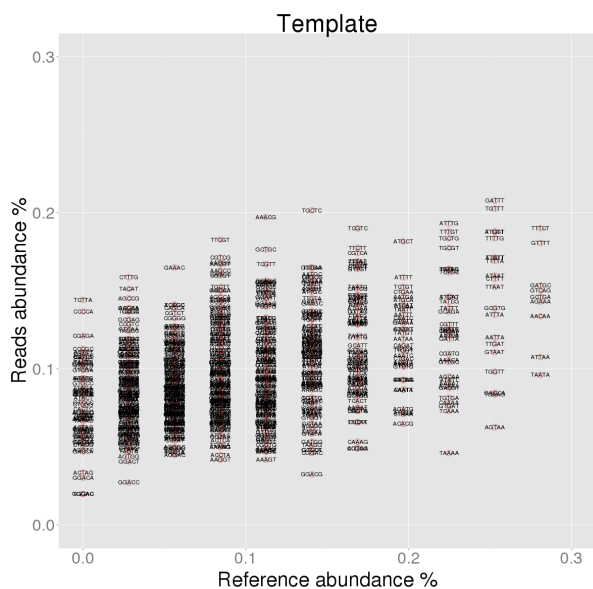
Control sequence 5-mer analysis

Under-represented 5-mers

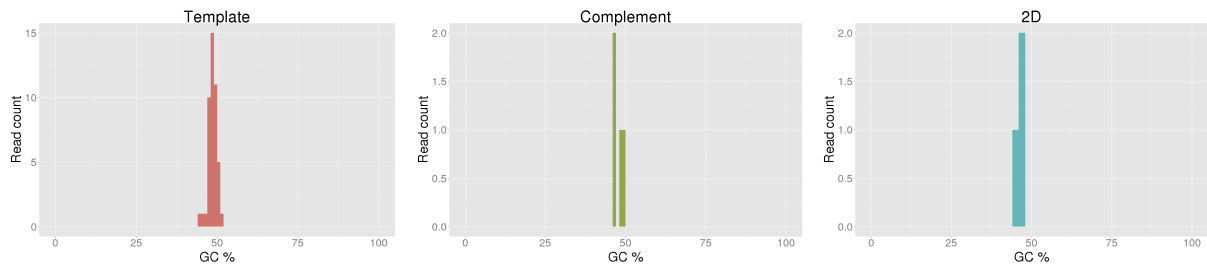
| Rank | Template | | | | Complement | | | | 2D | | | |
|------|----------|-------|--------|--------|------------|-------|--------|--------|-------|-------|--------|--------|
| | kmer | Ref % | Read % | Diff % | kmer | Ref % | Read % | Diff % | kmer | Ref % | Read % | Diff % |
| 1 | TTTTT | 0.759 | 0.126 | -0.632 | TTTTT | 0.759 | 0.120 | -0.639 | TTTTT | 0.759 | 0.037 | -0.722 |
| 2 | AAAAA | 0.478 | 0.067 | -0.411 | AAAAA | 0.478 | 0.060 | -0.418 | AAAAA | 0.478 | 0.085 | -0.392 |
| 3 | TGATG | 0.393 | 0.139 | -0.254 | TGATG | 0.393 | 0.090 | -0.304 | TGATG | 0.393 | 0.159 | -0.235 |
| 4 | AAAAC | 0.337 | 0.102 | -0.235 | GATGT | 0.309 | 0.060 | -0.249 | CTTTT | 0.253 | 0.037 | -0.216 |
| 5 | GATGT | 0.309 | 0.091 | -0.218 | TTATC | 0.309 | 0.060 | -0.249 | AAAAC | 0.337 | 0.134 | -0.203 |
| 6 | AATAT | 0.309 | 0.098 | -0.211 | AAAAC | 0.337 | 0.090 | -0.247 | TTTTG | 0.253 | 0.061 | -0.192 |
| 7 | GCAAT | 0.309 | 0.112 | -0.197 | GCTGA | 0.281 | 0.045 | -0.236 | TGATT | 0.309 | 0.122 | -0.187 |
| 8 | AGTAA | 0.253 | 0.063 | -0.190 | CTGAT | 0.309 | 0.090 | -0.219 | GTCAG | 0.281 | 0.098 | -0.183 |
| 9 | CTGAT | 0.309 | 0.119 | -0.190 | GAGCA | 0.253 | 0.045 | -0.208 | GTAAT | 0.253 | 0.073 | -0.180 |
| 10 | TAATA | 0.281 | 0.096 | -0.185 | AATAT | 0.309 | 0.105 | -0.204 | ATTAT | 0.309 | 0.146 | -0.163 |

Over-represented 5-mers

| Rank | Template | | | | Complement | | | | 2D | | | |
|------|----------|-------|--------|--------|------------|-------|--------|--------|-------|-------|--------|--------|
| | kmer | Ref % | Read % | Diff % | kmer | Ref % | Read % | Diff % | kmer | Ref % | Read % | Diff % |
| 1 | TCTTA | 0.000 | 0.144 | 0.144 | GAAAC | 0.056 | 0.254 | 0.198 | AACCA | 0.028 | 0.195 | 0.167 |
| 2 | CCCCA | 0.000 | 0.137 | 0.137 | TGCTT | 0.084 | 0.269 | 0.185 | TGCTT | 0.084 | 0.232 | 0.148 |
| 3 | CTTTG | 0.028 | 0.159 | 0.131 | GCCGT | 0.028 | 0.209 | 0.181 | ACTAA | 0.056 | 0.195 | 0.139 |
| 4 | TACAT | 0.028 | 0.151 | 0.123 | TTCCG | 0.028 | 0.209 | 0.181 | GTCGA | 0.000 | 0.134 | 0.134 |
| 5 | CGAGA | 0.000 | 0.121 | 0.121 | CTTTG | 0.028 | 0.194 | 0.166 | ATTAG | 0.028 | 0.159 | 0.131 |
| 6 | AGCCG | 0.028 | 0.145 | 0.117 | GCCTT | 0.000 | 0.165 | 0.165 | CTCC | 0.028 | 0.159 | 0.131 |
| 7 | CCCGC | 0.000 | 0.113 | 0.113 | GAGCG | 0.112 | 0.269 | 0.157 | TCACA | 0.028 | 0.159 | 0.131 |
| 8 | GCGAA | 0.028 | 0.139 | 0.111 | ACATA | 0.028 | 0.179 | 0.151 | TGTGC | 0.028 | 0.159 | 0.131 |
| 9 | AACCA | 0.028 | 0.139 | 0.111 | CATAC | 0.028 | 0.179 | 0.151 | CAGCA | 0.056 | 0.183 | 0.127 |
| 10 | ACTCT | 0.000 | 0.111 | 0.111 | CGGCG | 0.028 | 0.179 | 0.151 | ACCAA | 0.028 | 0.146 | 0.118 |

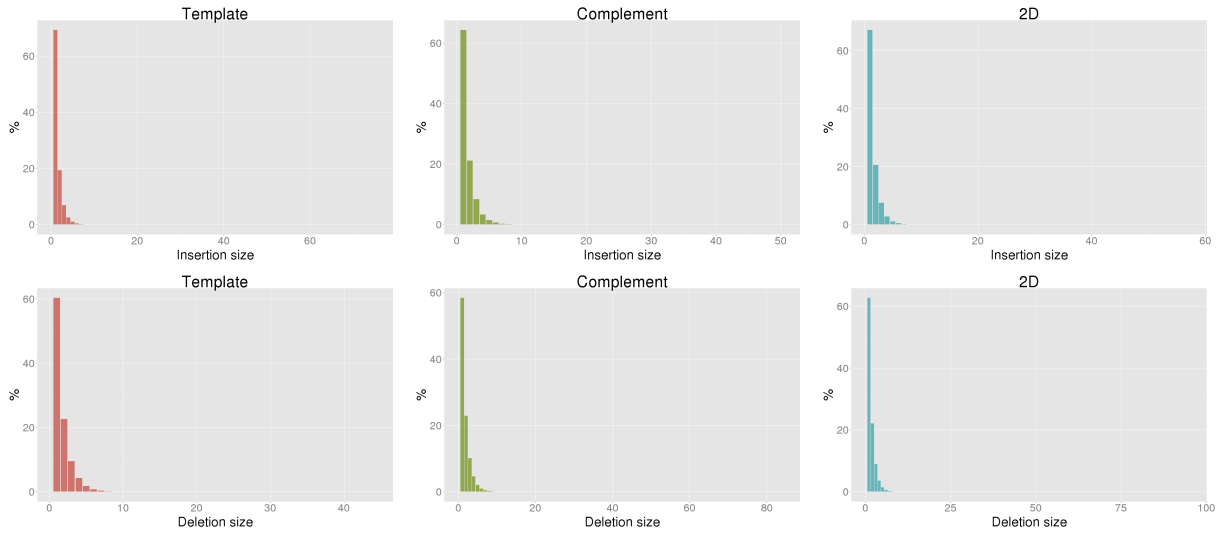


Control sequence GC content

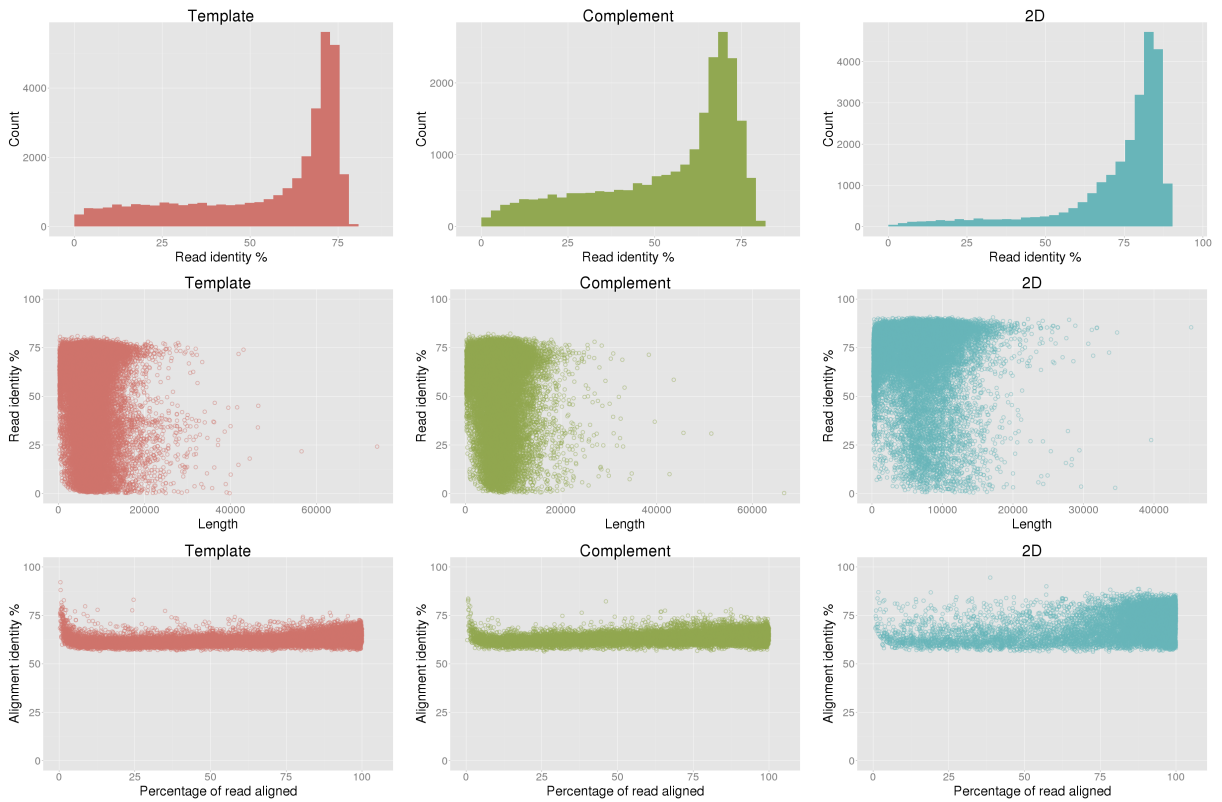


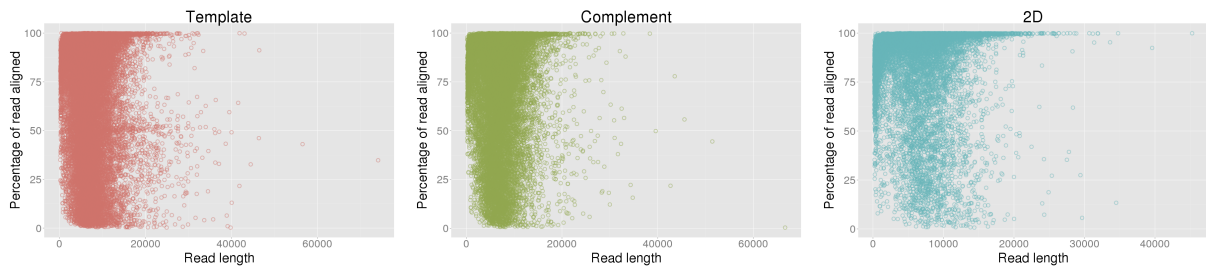
Escherichia coli error analysis

| | Template | Complement | 2D |
|--|----------|------------|--------|
| Overall base identity (excluding indels) | 52.78% | 52.51% | 72.11% |
| Aligned base identity (excluding indels) | 76.86% | 77.93% | 85.32% |
| Identical bases per 100 aligned bases (including indels) | 63.35% | 63.58% | 73.28% |
| Inserted bases per 100 aligned bases (including indels) | 4.35% | 5.80% | 4.64% |
| Deleted bases per 100 aligned bases (including indels) | 13.22% | 12.62% | 9.48% |
| Substitutions per 100 aligned bases (including indels) | 19.08% | 18.00% | 12.60% |
| Mean insertion size | 1.51 | 1.62 | 1.54 |
| Mean deletion size | 1.71 | 1.76 | 1.63 |

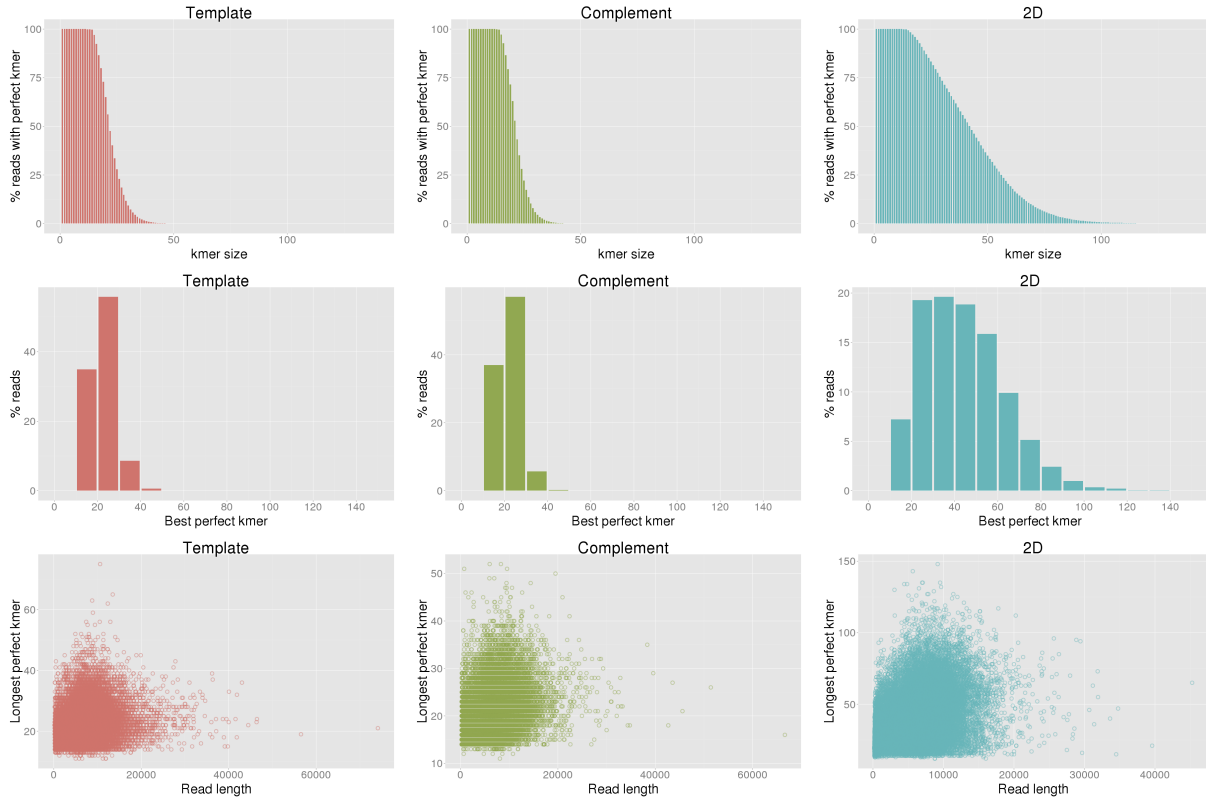


Escherichia coli read identity

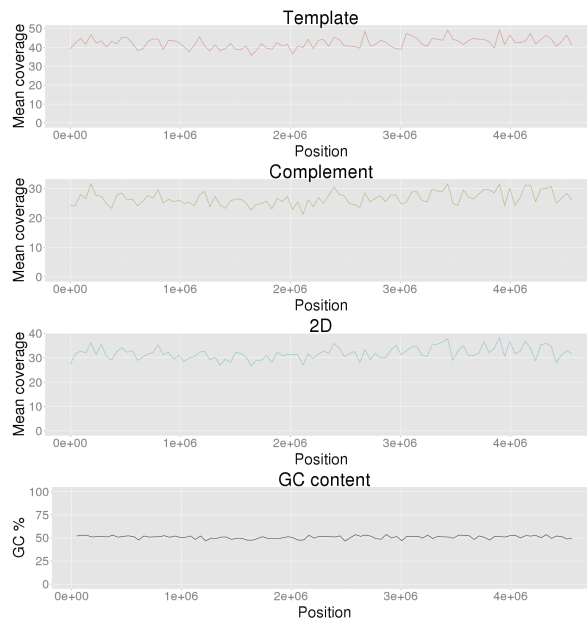




Escherichia coli perfect kmers



Escherichia coli coverage



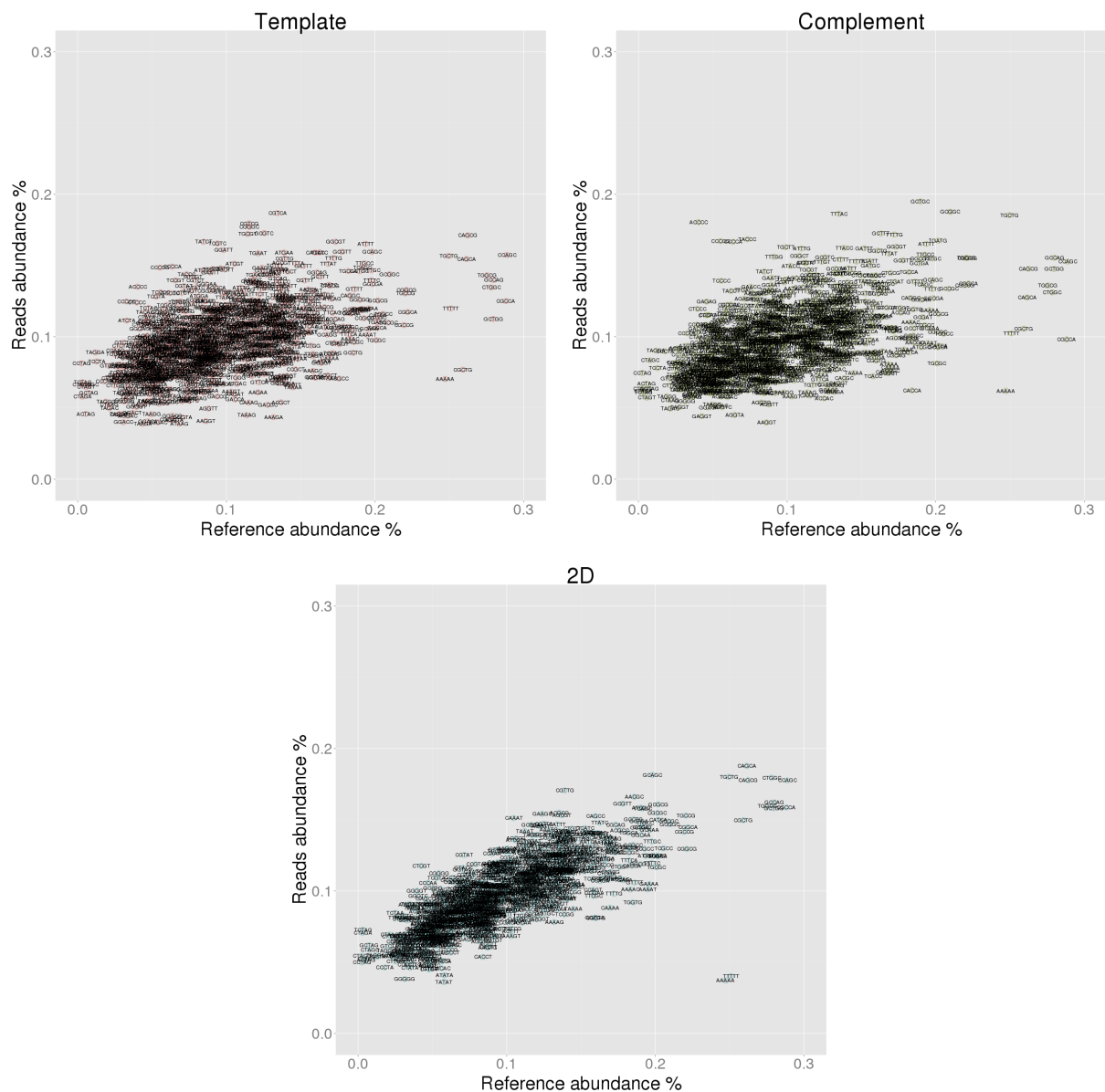
Escherichia coli 5-mer analysis

Under-represented 5-mers

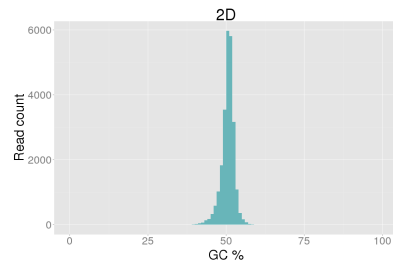
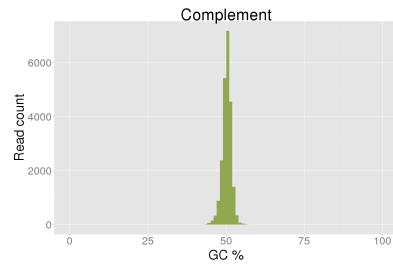
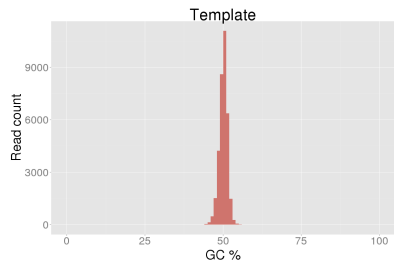
| Rank | Template | | | | Complement | | | | 2D | | | |
|------|----------|-------|--------|--------|------------|-------|--------|--------|-------|-------|--------|--------|
| | kmer | Ref % | Read % | Diff % | kmer | Ref % | Read % | Diff % | kmer | Ref % | Read % | Diff % |
| 1 | CGCTG | 0.259 | 0.077 | -0.182 | CGCCA | 0.288 | 0.098 | -0.190 | TTTTT | 0.251 | 0.040 | -0.211 |
| 2 | AAAAA | 0.247 | 0.070 | -0.177 | AAAAA | 0.247 | 0.062 | -0.185 | AAAAA | 0.247 | 0.037 | -0.210 |
| 3 | GCTGG | 0.279 | 0.113 | -0.167 | CGCTG | 0.259 | 0.106 | -0.153 | CGCCA | 0.288 | 0.159 | -0.129 |
| 4 | CGCCA | 0.288 | 0.125 | -0.163 | TTTTT | 0.251 | 0.102 | -0.148 | GCTGG | 0.279 | 0.158 | -0.121 |
| 5 | CTGGC | 0.278 | 0.135 | -0.144 | CTGGC | 0.278 | 0.131 | -0.147 | GCCAG | 0.280 | 0.162 | -0.118 |
| 6 | GCCAG | 0.280 | 0.140 | -0.140 | TGGCG | 0.275 | 0.136 | -0.139 | TGGCG | 0.275 | 0.160 | -0.116 |
| 7 | TGGCG | 0.275 | 0.143 | -0.132 | CCAGC | 0.289 | 0.153 | -0.136 | CCAGC | 0.289 | 0.178 | -0.111 |
| 8 | CCAGC | 0.289 | 0.158 | -0.131 | CAGCA | 0.261 | 0.128 | -0.134 | CGCTG | 0.259 | 0.150 | -0.109 |
| 9 | TTTTT | 0.251 | 0.120 | -0.131 | GCTGG | 0.279 | 0.148 | -0.132 | CTGGC | 0.278 | 0.180 | -0.099 |
| 10 | CGCCG | 0.219 | 0.108 | -0.111 | GCCAG | 0.280 | 0.156 | -0.124 | AAAAT | 0.195 | 0.101 | -0.094 |

Over-represented 5-mers

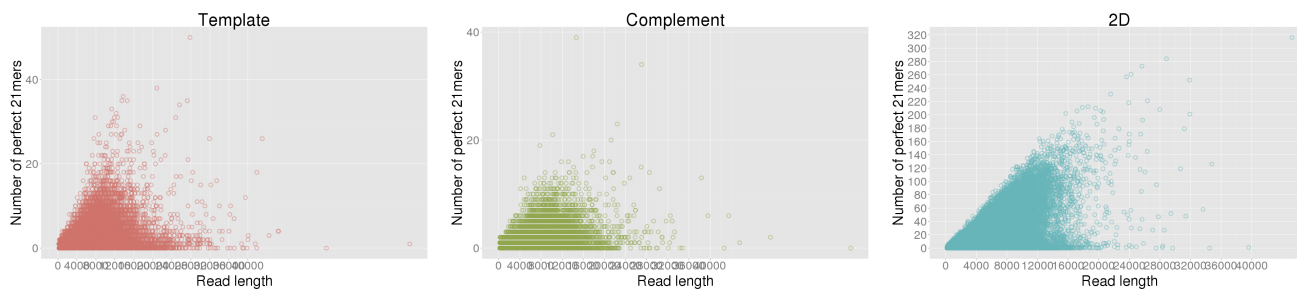
| Rank | Template | | | | Complement | | | | 2D | | | |
|------|----------|-------|--------|--------|------------|-------|--------|--------|-------|-------|--------|--------|
| | kmer | Ref % | Read % | Diff % | kmer | Ref % | Read % | Diff % | kmer | Ref % | Read % | Diff % |
| 1 | ACCCC | 0.040 | 0.135 | 0.095 | ACCCC | 0.040 | 0.181 | 0.140 | CTCGT | 0.042 | 0.118 | 0.075 |
| 2 | CCCCG | 0.055 | 0.149 | 0.093 | CCCCG | 0.055 | 0.167 | 0.112 | TCTAG | 0.003 | 0.073 | 0.069 |
| 3 | CCCCC | 0.033 | 0.125 | 0.092 | CCCCA | 0.064 | 0.167 | 0.103 | CTAGA | 0.003 | 0.071 | 0.068 |
| 4 | CCCCA | 0.064 | 0.149 | 0.086 | TACCC | 0.073 | 0.168 | 0.095 | GGGGT | 0.039 | 0.100 | 0.061 |
| 5 | CTCCC | 0.040 | 0.124 | 0.084 | TCCCC | 0.056 | 0.139 | 0.084 | TCTAA | 0.025 | 0.085 | 0.060 |
| 6 | TATCT | 0.085 | 0.167 | 0.082 | CTCCC | 0.040 | 0.120 | 0.080 | CCCAA | 0.047 | 0.106 | 0.059 |
| 7 | CCTAG | 0.003 | 0.081 | 0.079 | GAGAG | 0.046 | 0.125 | 0.079 | CGGGG | 0.054 | 0.112 | 0.058 |
| 8 | ATCTA | 0.033 | 0.111 | 0.078 | TAGGA | 0.012 | 0.090 | 0.078 | ATCTA | 0.033 | 0.090 | 0.057 |
| 9 | TAGGA | 0.012 | 0.089 | 0.077 | CTAGC | 0.008 | 0.083 | 0.076 | TCGTA | 0.053 | 0.109 | 0.056 |
| 10 | TCCCC | 0.056 | 0.131 | 0.075 | CCCTA | 0.018 | 0.090 | 0.072 | TAGAT | 0.035 | 0.091 | 0.056 |



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 | 9.04 | 8.78 | 4.92 | 0.00 | 9.25 | 8.58 | 5.25 | 0.00 | 9.09 | 8.70 | 4.51 |
| C | 8.56 | 0.00 | 9.18 | 9.83 | 8.97 | 0.00 | 8.95 | 9.32 | 8.80 | 0.00 | 10.45 | 8.80 |
| G | 9.39 | 9.19 | 0.00 | 8.38 | 9.01 | 9.07 | 0.00 | 8.64 | 8.67 | 10.61 | 0.00 | 8.48 |
| T | 5.21 | 8.69 | 8.82 | 0.00 | 5.40 | 8.54 | 9.03 | 0.00 | 4.55 | 8.45 | 8.89 | 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 (3.06%) | TTC (3.32%) | AAA (4.08%) | AAA (2.86%) | AAA (3.05%) | AAA (4.25%) | GCA (3.06%) | AAA (2.80%) | AAA (3.64%) |
| 2 | GCA (2.85%) | TGC (3.04%) | TTC (3.59%) | TTC (2.70%) | TGC (2.84%) | GCA (3.36%) | TTC (2.82%) | GCA (2.72%) | GCA (3.50%) |
| 3 | AAA (2.79%) | AAA (3.01%) | GCA (3.25%) | GCA (2.67%) | GGC (2.80%) | TTC (3.14%) | AAA (2.76%) | TGC (2.57%) | GAA (2.96%) |
| 4 | TGC (2.52%) | GCA (2.89%) | GAA (2.91%) | TGC (2.60%) | GCA (2.74%) | GAA (3.09%) | TCA (2.47%) | GGC (2.52%) | TTC (2.94%) |
| 5 | ATC (2.48%) | GCC (2.47%) | TTT (2.84%) | TTT (2.39%) | TTC (2.69%) | TTT (3.03%) | GAA (2.36%) | GCG (2.47%) | TTT (2.90%) |
| 6 | TCA (2.24%) | GGC (2.30%) | TGC (2.61%) | CAG (2.37%) | GAA (2.48%) | TGC (2.43%) | ATC (2.34%) | TCA (2.45%) | GTT (2.67%) |
| 7 | GCC (2.23%) | GAA (2.29%) | AAT (2.40%) | GGC (2.28%) | GCC (2.35%) | TCA (2.20%) | TGC (2.27%) | TTC (2.44%) | AAT (2.41%) |
| 8 | TTT (2.22%) | TCA (2.23%) | GCC (2.14%) | GAA (2.27%) | CAG (2.26%) | GCC (2.18%) | TTT (2.25%) | GAA (2.38%) | GCC (2.25%) |
| 9 | GAA (2.20%) | AAC (2.13%) | CAA (2.13%) | GCC (2.24%) | TCA (2.23%) | AAT (2.17%) | GCG (2.21%) | CAG (2.28%) | TGC (2.21%) |
| 10 | GGC (2.14%) | AAT (2.11%) | GTT (2.09%) | ATC (2.20%) | AAT (2.17%) | CAA (2.10%) | CAG (2.20%) | GCC (2.18%) | TCA (2.19%) |
| | | | | | | | | | |
| -10 | AGT (0.96%) | CTT (0.90%) | CCT (0.95%) | GTG (1.06%) | CTT (0.93%) | CTT (0.96%) | AGT (1.07%) | CTC (0.98%) | ATG (0.96%) |
| -9 | AGA (0.96%) | GGG (0.89%) | GTA (0.93%) | AGT (0.96%) | CCC (0.93%) | CTC (0.92%) | CTC (1.04%) | ACT (0.94%) | TGA (0.94%) |
| -8 | CTC (0.93%) | AGT (0.88%) | GGT (0.91%) | CTC (0.90%) | GGA (0.91%) | CCT (0.87%) | AGA (0.91%) | CGA (0.93%) | CCC (0.92%) |
| -7 | GGA (0.85%) | CGA (0.88%) | CTT (0.90%) | GGA (0.88%) | AGT (0.90%) | AGT (0.85%) | GAG (0.86%) | CTT (0.91%) | CCT (0.87%) |
| -6 | CCC (0.83%) | CCT (0.88%) | GGG (0.87%) | CCC (0.87%) | CCT (0.87%) | GGG (0.84%) | GGA (0.78%) | CCC (0.87%) | GAG (0.83%) |
| -5 | GAG (0.76%) | GAG (0.86%) | AGG (0.87%) | GAG (0.83%) | GAG (0.85%) | AGG (0.82%) | AGG (0.78%) | AGA (0.85%) | CGA (0.80%) |
| -4 | AGG (0.72%) | AGA (0.75%) | AGT (0.79%) | AGG (0.72%) | CTC (0.85%) | ACT (0.81%) | CCC (0.75%) | CCT (0.79%) | AGA (0.72%) |
| -3 | GGG (0.66%) | GGA (0.68%) | GAG (0.67%) | GGG (0.61%) | GGG (0.82%) | GAG (0.67%) | GGG (0.67%) | GGA (0.69%) | GGA (0.60%) |
| -2 | CTA (0.49%) | TAG (0.51%) | TAG (0.39%) | CTA (0.53%) | TAG (0.51%) | TAG (0.39%) | CTA (0.58%) | CTA (0.64%) | TAG (0.47%) |
| -1 | TAG (0.41%) | CTA (0.48%) | CTA (0.33%) | TAG (0.43%) | CTA (0.49%) | CTA (0.39%) | TAG (0.47%) | TAG (0.61%) | CTA (0.40%) |
| | | | | | | | | | |

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 (1.02%) | TTTC (1.12%) | AAAA (1.40%) | AAAA (0.95%) | TGGC (1.07%) | AAAA (1.38%) | GGCA (0.86%) | TGGC (0.97%) | GGCA (1.09%) |
| 2 | AAAA (0.94%) | AAAA (0.99%) | TTTC (1.32%) | CAGC (0.93%) | CAGC (0.99%) | TTTT (1.06%) | ATCA (0.85%) | CAGC (0.89%) | AAAA (1.02%) |
| 3 | GAAA (0.86%) | TTGC (0.94%) | GAAA (1.11%) | TGGC (0.85%) | CGGC (0.98%) | TTTC (1.05%) | AACA (0.83%) | TTCA (0.85%) | GAAA (0.97%) |
| 4 | CAGC (0.80%) | TGCG (0.94%) | TTTT (1.04%) | TTTT (0.81%) | AAAA (0.92%) | GAAA (1.04%) | GCCA (0.81%) | CTGC (0.80%) | CGTT (0.94%) |
| 5 | TGGC (0.80%) | TGGC (0.91%) | GGCA (0.94%) | TTTC (0.81%) | CTGC (0.91%) | CAAA (1.00%) | TTTT (0.80%) | CAAA (0.78%) | TTTC (0.93%) |
| 6 | AACG (0.79%) | TTCC (0.90%) | AAAT (0.92%) | ATCA (0.79%) | TTGC (0.88%) | GGCA (0.91%) | GAAA (0.77%) | CGGC (0.77%) | GGAA (0.87%) |
| 7 | TTTT (0.78%) | CTGC (0.89%) | CAAA (0.90%) | TTGC (0.79%) | CAAA (0.85%) | GGAA (0.85%) | TTCA (0.77%) | ATCA (0.76%) | TTTT (0.86%) |
| 8 | ATCA (0.78%) | CAGC (0.88%) | GGAA (0.88%) | CTAG (0.78%) | TTTC (0.84%) | ATCA (0.82%) | CTTC (0.77%) | TGCC (0.75%) | CAAA (0.84%) |
| 9 | GGCA (0.78%) | GAAA (0.87%) | GCAA (0.88%) | CTGC (0.78%) | TTCC (0.82%) | TGAA (0.81%) | CAGC (0.75%) | GCCA (0.74%) | TGTT (0.82%) |
| 10 | TGCC (0.77%) | TTCA (0.84%) | TTGC (0.83%) | CAAA (0.77%) | TGCC (0.81%) | AGCA (0.81%) | CAAA (0.75%) | GAAA (0.74%) | TGAA (0.82%) |
| | | | | | | | | | |
| -10 | TCTA (0.12%) | TCTA (0.12%) | CGAG (0.10%) | TAGT (0.12%) | CCTC (0.11%) | CTAT (0.10%) | AGGG (0.13%) | ACTT (0.14%) | TCGA (0.12%) |
| -9 | ACTA (0.12%) | TAGT (0.12%) | TTAG (0.10%) | TTAG (0.11%) | GGAC (0.11%) | TCTA (0.10%) | TAGT (0.13%) | CCCC (0.14%) | CTAA (0.11%) |
| -8 | TAGT (0.12%) | GGAC (0.11%) | TAGT (0.09%) | CCCT (0.11%) | ACCT (0.11%) | CGAG (0.10%) | TTAG (0.13%) | CGGA (0.13%) | CCCT (0.11%) |
| -7 | CTAA (0.11%) | CCCT (0.11%) | ACTA (0.08%) | GAGG (0.10%) | TAGT (0.11%) | TAGA (0.10%) | CCCT (0.13%) | ACCT (0.13%) | CGGA (0.10%) |
| -6 | TTAG (0.10%) | CGGA (0.11%) | TAGA (0.08%) | CTAA (0.09%) | CTAA (0.10%) | ACTA (0.10%) | GGAC (0.12%) | CTAA (0.12%) | TCTA (0.10%) |
| -5 | GGAC (0.09%) | CTAA (0.10%) | GGAC (0.08%) | TAGA (0.09%) | TAGA (0.09%) | GGAC (0.09%) | CTAA (0.11%) | CCCT (0.09%) | ACTA (0.09%) |
| -4 | TAGA (0.07%) | TAGG (0.07%) | TCTA (0.07%) | GGAC (0.08%) | CCCT (0.08%) | CCCT (0.08%) | TAGA (0.08%) | TAGG (0.09%) | TAGG (0.07%) |
| -3 | CCTA (0.05%) | TAGA (0.06%) | TAGG (0.07%) | CCTA (0.06%) | TAGG (0.07%) | TAGG (0.07%) | CCTA (0.07%) | TAGA (0.09%) | TAGA (0.05%) |
| -2 | TAGG (0.05%) | CCTA (0.05%) | CCTA (0.04%) | TAGG (0.05%) | CCTA (0.06%) | CCTA (0.05%) | TAGG (0.05%) | CCTA (0.07%) | CCTA (0.05%) |
| -1 | CTAG (0.01%) | CTAG (0.01%) | CTAG (0.01%) | CTAG (0.01%) | CTAG (0.01%) | CTAG (0.01%) | CTAG (0.01%) | CTAG (0.02%) | CTAG (0.01%) |
| | | | | | | | | | |

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 | CAGCA (0.37%) | CAGCA (0.39%) | CAGCA (0.43%) | CAGCA (0.39%) | CAGCA (0.43%) | CAGCA (0.51%) | CAGCA (0.39%) | CTGGC (0.41%) | CAGCA (0.45%) |
| 2 | TTATC (0.34%) | CTGGC (0.37%) | GAAAA (0.41%) | CTGGC (0.34%) | CTGGC (0.41%) | GAAAA (0.39%) | CGCCA (0.33%) | CAGCA (0.36%) | TGGCA (0.41%) |
| 3 | CTGGC (0.33%) | TTTTGC (0.35%) | CAAAA (0.38%) | CATCA (0.32%) | GCGGC (0.35%) | CGGCA (0.36%) | CGGCA (0.33%) | TGGCG (0.29%) | CGGCA (0.40%) |
| 4 | CGCCA (0.31%) | TTGCC (0.35%) | GCAAA (0.35%) | CCAGC (0.31%) | GCTGC (0.34%) | CAAAA (0.35%) | CTGGC (0.31%) | CGCCA (0.29%) | GAAAA (0.37%) |
| 5 | GAAAA (0.29%) | GCTGC (0.34%) | TGGCA (0.35%) | GCTGC (0.29%) | CCAGC (0.33%) | GCAAA (0.34%) | TGGCA (0.31%) | GCGGC (0.29%) | GCGTT (0.35%) |
| 6 | TGGCG (0.29%) | TTTTCC (0.32%) | TTTTTC (0.34%) | GAAAA (0.29%) | TTTTGC (0.32%) | CATCA (0.32%) | CATCA (0.30%) | GCCAG (0.28%) | TCTTC (0.30%) |
| 7 | GCCAG (0.29%) | CGCCA (0.32%) | TCTTC (0.33%) | GCAGC (0.29%) | CATCA (0.31%) | ATAAA (0.32%) | TCTTC (0.28%) | GCTGC (0.28%) | GCAAA (0.29%) |
| 8 | CAAAA (0.29%) | GAAAA (0.31%) | CGTTT (0.33%) | GCGGC (0.29%) | AATCA (0.31%) | AGAAA (0.31%) | GCCAG (0.28%) | ATAAA (0.27%) | AAGAA (0.28%) |
| 9 | CGTTT (0.27%) | CAAAA (0.30%) | TTTTGC (0.32%) | CGGCA (0.28%) | GAAAA (0.30%) | TGGCA (0.31%) | GCAAA (0.27%) | CCAGC (0.27%) | TTGCC (0.28%) |
| 10 | TTTTGC (0.27%) | GCAGC (0.29%) | CGCCA (0.31%) | CGCCA (0.28%) | TTGCC (0.30%) | TTACC (0.30%) | TGGCG (0.26%) | GCAAA (0.27%) | CGCCA (0.28%) |
| | | | | | | | | | |
| -10 | CCCTA (0.01%) | CCCTA (0.01%) | GGACC (0.01%) | ACCTA (0.01%) | TAGGG (0.01%) | CCCTA (0.01%) | GGACC (0.01%) | GGACC (0.01%) | CCCTA (0.01%) |
| -9 | GGACC (0.00%) | GGACC (0.01%) | CCCTA (0.01%) | CCCTA (0.01%) | CCCTA (0.01%) | TAGGT (0.01%) | TAGGA (0.01%) | TAGGA (0.01%) | TAGGA (0.01%) |
| -8 | CTAGC (0.00%) | GCTAG (0.00%) | CTAGC (0.00%) | CTAGC (0.00%) | CTAGC (0.01%) | GCTAG (0.00%) | CTAGC (0.00%) | CTAGC (0.01%) | GCTAG (0.00%) |
| -7 | CTAGA (0.00%) | CTAGC (0.00%) | ACTAG (0.00%) | GCTAG (0.00%) | GCTAG (0.00%) | CTAGC (0.00%) | GCTAG (0.00%) | GCTAG (0.01%) | ACTAG (0.00%) |
| -6 | ACTAG (0.00%) | ACTAG (0.00%) | GCTAG (0.00%) | CTAGT (0.00%) | CTAGT (0.00%) | CTAGT (0.00%) | CTAGT (0.00%) | ACTAG (0.01%) | CTAGT (0.00%) |
| -5 | GCTAG (0.00%) | CTAGT (0.00%) | CTAGG (0.00%) | ACTAG (0.00%) | ACTAG (0.00%) | ACTAG (0.00%) | ACTAG (0.00%) | CTAGT (0.00%) | CTAGC (0.00%) |
| -4 | CTAGT (0.00%) | CTAGG (0.00%) | CTAGT (0.00%) | CCTAG (0.00%) | TCTAG (0.00%) | CTAGG (0.00%) | TCTAG (0.00%) | TCTAG (0.00%) | TCTAG (0.00%) |
| -3 | TCTAG (0.00%) | TCTAG (0.00%) | CTAGA (0.00%) | CTAGG (0.00%) | CTAGA (0.00%) | CTAGA (0.00%) | CTAGG (0.00%) | CTAGG (0.00%) | CTAGG (0.00%) |
| -2 | CCTAG (0.00%) | CCTAG (0.00%) | TCTAG (0.00%) | CTAGA (0.00%) | CCTAG (0.00%) | CCTAG (0.00%) | CCTAG (0.00%) | CCTAG (0.00%) | CCTAG (0.00%) |
| -1 | CTAGG (0.00%) | CTAGA (0.00%) | CCTAG (0.00%) | TCTAG (0.00%) | CTAGG (0.00%) | TCTAG (0.00%) | CTAGA (0.00%) | CTAGA (0.00%) | CTAGA (0.00%) |
| | | | | | | | | | |

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