

APPENDICES

Appendix 1: Frequencies of Significant Heptamers at the level $\alpha = 10^{-5}$

| Heptamer | DMR-CGIs | Control CGIs | LOD | <i>p</i> -value |
|----------|-----------|--------------|-------|-----------------|
| ACACACA | 0.0002339 | 0.0006223 | -1.41 | 2.80E-06 |
| AGGCGGC | 0.0000439 | 0.0003064 | -2.80 | 1.39E-06 |
| CACACAC | 0.0003070 | 0.0007220 | -1.23 | 4.30E-06 |
| CCGCCGC | 0.0002485 | 0.0009788 | -1.98 | 3.28E-13 |
| CGCCGCC | 0.0002485 | 0.0009383 | -1.92 | 2.60E-12 |
| CGCCGCG | 0.0001316 | 0.0004528 | -1.78 | 3.52E-06 |
| CGCGGCG | 0.0001316 | 0.0004528 | -1.78 | 3.52E-06 |
| CGGCGGC | 0.0001900 | 0.0008085 | -2.09 | 8.78E-12 |
| GCCGCCG | 0.0001900 | 0.0008085 | -2.09 | 8.78E-12 |
| GCCGCCT | 0.0000439 | 0.0003064 | -2.80 | 1.39E-06 |
| GCGCCGC | 0.0001754 | 0.0005408 | -1.62 | 1.69E-06 |
| GCGGCGC | 0.0001754 | 0.0005408 | -1.62 | 1.69E-06 |
| GCGGCGG | 0.0002485 | 0.0009788 | -1.98 | 3.28E-13 |
| GGCGGCG | 0.0002485 | 0.0009383 | -1.92 | 2.60E-12 |
| GTGTGTG | 0.0003070 | 0.0007220 | -1.23 | 4.30E-06 |
| TGTGTGT | 0.0002339 | 0.0006223 | -1.41 | 2.80E-06 |
| AAAATTT | 0.0001462 | 0.0000230 | 2.67 | 8.81E-07 |
| AAATTTG | 0.0001608 | 0.0000168 | 3.26 | 3.73E-09 |
| AAATTTT | 0.0001462 | 0.0000230 | 2.67 | 8.81E-07 |
| AAGCCCT | 0.0002631 | 0.0000728 | 1.85 | 1.33E-06 |
| ACAACTC | 0.0001754 | 0.0000408 | 2.10 | 7.64E-06 |
| ACAATGC | 0.0001462 | 0.0000293 | 2.32 | 8.45E-06 |
| ACTAATG | 0.0001169 | 0.0000091 | 3.68 | 2.25E-08 |
| AGCAGGG | 0.0003801 | 0.0001454 | 1.39 | 5.81E-06 |
| AGCCGAG | 0.0008332 | 0.0001789 | 2.22 | 3.12E-21 |
| AGGGCTT | 0.0002631 | 0.0000728 | 1.85 | 1.33E-06 |
| ATGAGCA | 0.0001900 | 0.0000381 | 2.32 | 6.86E-07 |
| ATGTGAC | 0.0002339 | 0.0000246 | 3.25 | 3.90E-12 |
| ATTAGTA | 0.0001023 | 0.0000064 | 4.00 | 2.22E-08 |
| ATTGCAA | 0.0001169 | 0.0000172 | 2.77 | 4.06E-06 |
| ATTTAGG | 0.0001316 | 0.0000216 | 2.61 | 3.59E-06 |
| CAAATTT | 0.0001608 | 0.0000168 | 3.26 | 3.73E-09 |
| CAACACG | 0.0001608 | 0.0000327 | 2.30 | 4.23E-06 |
| CAGCCGA | 0.0003070 | 0.0000959 | 1.68 | 1.64E-06 |
| CATGTGA | 0.0001900 | 0.0000249 | 2.93 | 4.08E-09 |
| CATTAGT | 0.0001169 | 0.0000091 | 3.68 | 2.25E-08 |
| CCCCCAA | 0.0003655 | 0.0001157 | 1.66 | 2.90E-07 |
| CCCCCCC | 0.0012133 | 0.0003368 | 1.85 | 1.07E-22 |
| CCCTGCT | 0.0003801 | 0.0001454 | 1.39 | 5.81E-06 |

| | | | | |
|----------|-----------|-----------|------|----------|
| CCGAGCC | 0.0008186 | 0.0002751 | 1.57 | 1.08E-12 |
| CCTAAAT | 0.0001316 | 0.0000216 | 2.61 | 3.59E-06 |
| CCTGCTC | 0.0004970 | 0.0001958 | 1.34 | 6.41E-07 |
| CGAATGA | 0.0001169 | 0.0000173 | 2.75 | 4.40E-06 |
| CGAGCCG | 0.0004970 | 0.0001869 | 1.41 | 2.26E-07 |
| CGCCAAC | 0.0002339 | 0.0000656 | 1.83 | 5.07E-06 |
| CGCGGCA | 0.0004532 | 0.0001309 | 1.79 | 1.95E-09 |
| CGGCTCG | 0.0004970 | 0.0001869 | 1.41 | 2.26E-07 |
| CGTGTG | 0.0001608 | 0.0000327 | 2.30 | 4.23E-06 |
| CTCGGCT | 0.0008332 | 0.0001789 | 2.22 | 3.12E-21 |
| GAGCAGG | 0.0004970 | 0.0001958 | 1.34 | 6.41E-07 |
| GAGCCGA | 0.0005409 | 0.0001335 | 2.02 | 8.51E-13 |
| GAGTTGT | 0.0001754 | 0.0000408 | 2.10 | 7.64E-06 |
| GCATTGT | 0.0001462 | 0.0000293 | 2.32 | 8.45E-06 |
| GCCGAGC | 0.0009648 | 0.0002779 | 1.80 | 1.00E-17 |
| GCGCAA | 0.0002777 | 0.0000818 | 1.76 | 1.86E-06 |
| GCGGCAA | 0.0003508 | 0.0000871 | 2.01 | 5.16E-09 |
| GCTCGGC | 0.0009648 | 0.0002779 | 1.80 | 1.00E-17 |
| GGCTCGG | 0.0008186 | 0.0002751 | 1.57 | 1.08E-12 |
| GGGGGGG | 0.0012133 | 0.0003368 | 1.85 | 1.07E-22 |
| GTCACAT | 0.0002339 | 0.0000246 | 3.25 | 3.90E-12 |
| GTGACAA | 0.0002777 | 0.0000349 | 2.99 | 1.56E-12 |
| GTTGGCG | 0.0002339 | 0.0000656 | 1.83 | 5.07E-06 |
| GTTGTCA | 0.0002339 | 0.0000317 | 2.88 | 1.93E-10 |
| TACTAAT | 0.0001023 | 0.0000064 | 4.00 | 2.22E-08 |
| TAGTACA | 0.0000877 | 0.0000100 | 3.13 | 7.81E-06 |
| TCACATG | 0.0001900 | 0.0000249 | 2.93 | 4.08E-09 |
| TCATTGCG | 0.0001169 | 0.0000173 | 2.75 | 4.40E-06 |
| TCGGCTC | 0.0005409 | 0.0001335 | 2.02 | 8.51E-13 |
| TCGGCTG | 0.0003070 | 0.0000959 | 1.68 | 1.64E-06 |
| TGACAAC | 0.0002339 | 0.0000317 | 2.88 | 1.93E-10 |
| TGCCGCA | 0.0003216 | 0.0000868 | 1.89 | 8.35E-08 |
| TGCCGCG | 0.0004532 | 0.0001309 | 1.79 | 1.95E-09 |
| TGCGGCA | 0.0003216 | 0.0000868 | 1.89 | 8.35E-08 |
| TGCTCAT | 0.0001900 | 0.0000381 | 2.32 | 6.86E-07 |
| TGTACTA | 0.0000877 | 0.0000100 | 3.13 | 7.81E-06 |
| TGTCACA | 0.0002193 | 0.0000332 | 2.72 | 2.80E-09 |
| TGTGACA | 0.0002193 | 0.0000332 | 2.72 | 2.80E-09 |
| TTGCAAT | 0.0001169 | 0.0000172 | 2.77 | 4.06E-06 |
| TTGCCGC | 0.0003508 | 0.0000871 | 2.01 | 5.16E-09 |
| TTGGCGC | 0.0002777 | 0.0000818 | 1.76 | 1.86E-06 |
| TTGGGGG | 0.0003655 | 0.0001157 | 1.66 | 2.90E-07 |
| TTGTCAC | 0.0002777 | 0.0000349 | 2.99 | 1.56E-12 |