

Appendix

Appendix A: Alignment of the VDR sequence covering the *BsmI*-*Apal*-*TaqI* region, amplified and sequenced for all 23 individuals.

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| 4 | 29 | -CTAAGCTCTGC-ITGCAGAGTGTGCAGGCGATTTCGTAGGGGGGATTCTGAGGAAGTAGATAAGC | 92 |
| 9 | 29 | -CTAAGCTCTGC-ITGCAGAGTGTGCAGGCGATTTCGTAGGGGGGATTCTGAGGAAGTAGATAAGC | 92 |
| 2 | 77 | -CCTAGCTCTGCCTTGCAGAGTGTGCAGGCGATTTCGTAGGGGGGATTCTGAGGAAGTAGATAAGC | 140 |
| 1 | 45 | CCCTAGCTCTGCCTTGCAGAGTGTGCAGGCGATTTCGTAGGGGGGATTCTGAGGAAGTAGATAAGC | 109 |
| 10 | 14 | CCCTAGCTCTGCCTTGCAGAGTGTGCAGGCGATTTCGTAGGGGGGATTCTGAGGAAGTAGATAAGC | 78 |
| 8 | 40 | CCCTAGCTCTGCCTTGCAGAGTGTGCAGGCGATTTCGTAGGGGGGATTCTGAGGAAGTAGATAAGC | 104 |
| 6 | 14 | CCCTA-CTCTGCCTTGCAGAGTGTGCAGGCGATTTCGTAGGGGGGATTCTGAGGAAGTAGATAAGC | 77 |
| 11 | 29 | CCCTAGCTCTGCCTTGCAGAGTGTGCAGGCGATTTCGTAGGGGGGATTCTGAGGAAGTAGATAAGC | 93 |
| 5 | 49 | -CCTAGCTCTGCCTTGCAGAGTGTGCAGGCGATTTCGTAGGGGGGATTCTGAGGAAGTAGATAAGC | 112 |
| 17 | 36 | -CTAAGCTCTGCCTTGCAGAGTGTGCAGGCGATTTCGTAGGGGGGATTCTGAGGAAGTAGATAAGC | 100 |
| 16 | 86 | ACTCAACTCTCCCTCAGAGAGAGCAGGCGATTTCGTAGGGGGGATTCTGAGGAAGTAGATAAGC | 150 |
| 23 | 25 | CCCTAGCTCTGCCTTGCAGAGTGTGCAGGCGATTTCGTAGGGGGGATTCTGAGGAAGTAGATAAGC | 89 |
| VDR | 190 | -CCTAGCTCTGCCTTGCAGAGTGTGCAGGCGATTTCGTAGGGGGGATTCTGAGGAAGTAGATAAGC | 253 |
| 21 | 32 | -CCTAGCTCTGCCTTGCAGAGTGTGCAGGCGATTTCGTAGGGGGGATTCTGAGGAAGTAGATAAGC | 95 |
| 14 | 33 | -CCTAGCTCTGCCTTGCAGAGTGTGCAGGCGATTTCGTAGGGGGGATTCTGAGGAAGTAGATAAGC | 96 |
| 15 | 33 | -CCTAGCTCTGCCTTGCAGAGTGTGCAGGCGATTTCGTAGGGGGGATTCTGAGGAAGTAGATAAGC | 96 |
| 13 | 36 | -CCTAGCTCTGCCTTGCAGAGTGTGCAGGCGATTTCGTAGGGGGGATTCTGAGGAAGTAGATAAGC | 99 |
| 22 | 28 | -CCTAGCTCTGCCTTGCAGAGTGTGCAGGCGATTTCGTAGGGGGGATTCTGAGGAAGTAGATAAGC | 91 |
| 19 | 31 | -CCTAGCTCTGCCTTGCAGAGTGTGCAGGCGATTTCGTAGGGGGGATTCTGAGGAAGTAGATAAGC | 94 |
| 20 | 32 | -CCTAGCTCTGCCTTGCAGAGTGTGCAGGCGATTTCGTAGGGGGGATTCTGAGGAAGTAGATAAGC | 95 |
| 7 | 118 | -CT-AGCTCTGC-ITGCAGAGTGTGCAGGCGATTTCGTAGGGGGGATTCTGAGGAAGTAGATAAGC | 179 |
| 12 | 268 | -CT-AGCTCTGC-ITGCAGAGTGTGCAGGCGATTTCGTAGGGGGGATTCTGAGGAAGTAGATAAGC | 329 |
| 3 | 58 | -CT-AGCTCTGCCTTGCAGAGTGTGCAGGCGATTTCGTAGGGGGGATTCTGAGGAAGTAGATAAGC | 120 |
| 18 | 35 | -CCTAGCTCTGCCTTGCAGAGTGTGCAGGCGATTTCGTAGGGGGGATTCTGAGGAAGTAGATAAGC | 98 |
| <i>BsmI</i> | | | |
| 4 | 93 | AGGGTTCCCTGGGGCCACAGACAGGCCTGCACATTCCTCCCAATACTCAGGCTCTGTACTTGC CGGAAT | 158 |
| 9 | 93 | AGGGTTCCCTGGGGCCACAGACAGGCCTGCACATTCCTCCCAATACTCAGGCTCTGTACTTGC CGGAAT | 158 |
| 2 | 141 | AGGGTTCCCTGGGGCCACAGACAGGCCTGCACATTCCTCCCAATACTCAGGCTCTGTACTTGC CGGAAT | 206 |
| 1 | 110 | AGGGTTCCCTGGGGCCACAGACAGGCCTGCACATTCCTCCCAATACTCAGGCTCTGTACTTGC CGGAAT | 175 |
| 10 | 79 | AGGGTTCCCTGGGGCCACAGACAGGCCTGGGCATTCCTCCCAATACTCAGGCTCTGTACTTGC CGGAAT | 144 |
| 8 | 105 | AGGGTTCCCTGGGGCCACAGACAGGCCTGCGCATTCCTCCCAATACTCAGGCTCTGTACTTGC CGGAAT | 170 |
| 6 | 78 | AGGGTTCCCTGGGGCCACAGACAGGCCTGCACATTCCTCCCAATACTCAGGCTCTGTACTTGC CGGAAT | 143 |
| 11 | 94 | AGGGTTCCCTGGGGCCACAGACAGGCCTGCACATTCCTCCCAATACTCAGGCTCTGTACTTGC CGGAAT | 159 |
| 5 | 113 | AGGGTTCCCTGGGGCCACAGACAGGCCTGGGCATTCCTCCCAATACTCAGGCTCTGTACTTGC CGGAAT | 178 |
| 17 | 101 | AGGGTTCCCTGGGGCCACAGACAGGCCTGCACATTCCTCCCAATACTCAGGCTCTGTACTTGC CGGAAT | 166 |
| 16 | 151 | AGGGTTCCCTGGGGCCACAGGCAGGCCTGGGCATTCCTCCCAATACTCAGGCTCTGTACTTGC CGGAAT | 217 |
| 23 | 90 | AGGGTTCCCTGGGGCCACAGACAGGCCTGCACATTCCTCCCAATACTCAGGCTCTGTACTTGC CGGAAT | 155 |
| VDR | 254 | AGGGTTCCCTGGGGCCACAGACAGGCCTGGGCATTCCTCCCAATACTCAGGCTCTGTACTTGC CGGAAT | 319 |
| 21 | 96 | AGGGTTCCCTGGGGCCACAGACAGGCCTGCGCATTCCTCCCAATACTCAGGCTCTGTACTTGC CGGAAT | 161 |
| 14 | 97 | AGGGTTCCCTGGGGCCACAGACAGGCCTGGGCATTCCTCCCAATACTCAGGCTCTGTACTTGC CGGAAT | 162 |
| 15 | 97 | AGGGTTCCCTGGGGCCACAGACAGGCCTGCACATTCCTCCCAATACTCAGGCTCTGTACTTGC CGGAAT | 162 |
| 13 | 100 | AGGGTTCCCTGGGGCCACAGACAGGCCTGGGCATTCCTCCCAATACTCAGGCTCTGTACTTGC CGGAAT | 165 |
| 22 | 92 | AGGGTTCCCTGGGGCCACAGACAGGCCTGCACATTCCTCCCAATACTCAGGCTCTGTACTTGC CGGAAT | 157 |
| 19 | 95 | AGGGTTCCCTGGGGCCACAGACAGGCCTGGGCATTCCTCCCAATACTCAGGCTCTGTACTTGC CGGAAT | 160 |
| 20 | 96 | AGGGTTCCCTGGGGCCACAGACAGGCCTGCGCATTCCTCCCAATACTCAGGCTCTGTACTTGC CGGAAT | 161 |
| 7 | 180 | AGGGTTCCCTGGGGCCACAGACAGGCCTGCACATTCCTCCCAATACTCAGGCTCTGTACTTGC CGGAAT | 245 |
| 12 | 330 | AGGGTTCCCTGGGGCCACAGACAGGCCTGCGCATTCCTCCCAATACTCAGGCTCTGTACTTGC CGGAAT | 395 |
| 3 | 121 | AGGGTTCCCTGGGGCCACAGACAGGCCTGGGCATTCCTCCCAATACTCAGGCTCTGTACTTGC CGGAAT | 186 |
| 18 | 99 | AGGGTTCCCTGGGGCCACAGACAGGCCTGCACATTCCTCCCAATACTCAGGCTCTGTACTTGC CGGAAT | 164 |
| <i>Apal</i> | | | |
| 4 | 159 | GGGCTCAACATTCTGTATTTGAGGTTTTCGCGGCAGGGTACAAAACCTTTGGAGCCTGAGGAGG | 224 |
| 9 | 159 | GGGCTCAACATTCTGTATTTGAGGTTTTCGCGGCAGGGTACAAAACCTTTGGAGCCTGAGGAGG | 224 |
| 2 | 207 | GGGCTCAACATTCTGTATTTGAGGTTTTCGCGGCAGGGTACAAAACCTTTGGAGCCTGAG-AGG | 271 |
| 1 | 176 | GGGCTCAACATTCTGTATTTGAGGTTTTCGCGGCAGGGTACAAAACCTTTGGAGCCTGAG-AGG | 240 |
| 10 | 145 | GGGCTCAACATTCTGTATTTGAGGTTTTCGCGGCAGGGTACAAAACCTTTGGAGCCTGAG-AGG | 209 |
| 8 | 171 | GGGCTCAACATTCTGTATTTGAGGTTTTCGCGGCAGGGTACAAAACCTTTGGAGCCTGAG-AGG | 235 |
| 6 | 144 | GGGCTCAACATTCTGTATTTGAGGTTTTCGCGGCAGGGTACAAAACCTTTGGAGCCTGAG-AGG | 208 |
| 11 | 160 | GGGCTCAACATTCTGTATTTGAGGTTTTCGCGGCAGGGTACAAAACCTTTGGAGCCTGAG-AGG | 224 |
| 5 | 179 | GGGCTCAACATTCTGTATTTGAGGTTTTCGCGGCAGGGTACAAAACCTTTGGAGCCTGAG-AGG | 243 |
| 17 | 167 | GGGCTCAACATTCTGTATTTGAGGTTTTCGCGGCAGGGTACAAAACCTTTGGAGCCTGAG-AGG | 231 |
| 16 | 218 | GGGCTCAACATTCTGTATTTGAGGTTTTCGCGGCAGGGTACAAAACCTTTGGAGCCTGAG-AGG | 283 |
| 23 | 156 | GGGCTCAACATTCTGTATTTGAGGTTTTCGCGGCAGGGTACAAAACCTTTGGAGCCTGAG-AGG | 220 |

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| VDR | 320 | GGGCTCAACATTCTGTATTTGAGGTTTTGCGGGCAGGGTACAAAACCTTTGGAGCCTGAG-AGG | 384 |
| 21 | 162 | GGGCTCAACATTCTGTATTTGAGGTTTTGCGGGCAGGGTACAAAACCTTTGGAGCCTGAG-AGG | 226 |
| 14 | 163 | GGGCTCAACATTCTGTATTTGAGGTTTTGCGGGCAGGGTACAAAACCTTTGGAGCCTGAG-AGG | 227 |
| 15 | 163 | GGGCTCAACATTCTGTATTTGAGGTTTTGCGGGCAGGGTACAAAACCTTTGGAGCCTGAG-AGG | 227 |
| 13 | 166 | GGGCTCAACATTCTGTATTTGAGGTTTTGCGGGCAGGGTACAAAACCTTTGGAGCCTGAG-AGG | 230 |
| 22 | 158 | GGGCTCAACATTCTGTATTTGAGGTTTTGCGGGCAGGGTACAAAACCTTTGGAGCCTGAG-AGG | 222 |
| 19 | 161 | GGGCTCAACATTCTGTATTTGAGGTTTTGCGGGCAGGGTACAAAACCTTTGGAGCCTGAG-AGG | 225 |
| 20 | 162 | GGGCTCAACATTCTGTATTTGAGGTTTTGCGGGCAGGGTACAAAACCTTTGGAGCCTGAG-AGG | 226 |
| 7 | 246 | GGGCTCAACATTCTGTATTTGAGGTTTTGCGGGCAGGGTACAAAACCTTTGGAGCCTGAG-AGG | 310 |
| 12 | 396 | GGGCTCAACATTCTGTATTTGAGGTTTTGCGGGCAGGGTACAAAACCTTTGGAGCCTGAG-AGG | 460 |
| 3 | 187 | GGGCTCAACATTCTGTATTTGAGGTTTTGCGGGCAGGGTACAAAACCTTTGGAGCCTGAG-AGG | 251 |
| 18 | 165 | GGGCTCAACATTCTGTATTTGAGGTTTTGCGGGCAGGGTACAAAACCTTTGGAGCCTGAG-AGG | 229 |
| 4 | 225 | -ATGGTCTGCCTATATAGTTTACCTGAT-TGATTTTGGAGGCAATGTGCAGTGACCCTTGACCCT | 289 |
| 9 | 225 | -ATGGTCTGCCTATATAGTTTACCTGAT-TGATTTTGGAGGCAATGTGCAGTGACCCTTGACCCT | 289 |
| 2 | 272 | -ATGGTCTGCCTATATAGTTTACCTGAT-TGATTTTGGAGGCAATGTGCAGTGACCCTTGACCCT | 336 |
| 1 | 241 | -ATGGTCTGCCTATATAGTTTACCTGAT-TGATTTTGGAGGCAATGTGCAGTGACCCTTGACCCT | 305 |
| 10 | 210 | -ATGGTCTGCCTATATAGTTTACCTGAT-TGATTTTGGAGGCAATGTGCAGTGACCCTTGACCCT | 274 |
| 8 | 236 | -ATGGTCTGCCTATATAGTTTACCTGAT-TGATTTTGGAGGCAATGTGCAGTGACCCTTGACCCT | 300 |
| 6 | 209 | -ATGGTCTGCCTATATAGTTTACCTGAT-TGATTTTGGAGGCAATGTGCAGTGACCCTTGACCCT | 273 |
| 11 | 225 | -ATGGTCTGCCTATATAGTTTACCTGAT-TGATTTTGGAGGCAATGTGCAGTGACCCTTGACCCT | 289 |
| 5 | 244 | -ATGGTCTGCCTATATAGTTTACCTGAT-TGATTTTGGAGGCAATGTGCAGTGACCCTTGACCCT | 308 |
| 17 | 232 | -ATGGTCTGCCTATATAGTTTACCTGAT-TGATTTTGGAGGCAATGTGCAGTGACCCTTGACCCT | 297 |
| 16 | 284 | AATGGTCTGCCTATATAGTTTACCTGAT-TGATTTTGGAGGCAATGTGCAGTGACCCTTGACCCT | 349 |
| 23 | 221 | -ATGGTCTGCCTATATAGTTTACCTGAT-TGATTTTGGAGGCAATGTGCAGTGACCCTTGACCCT | 285 |
| VDR | 385 | -ATGGTCTGCCTATATAGTTTACCTGAT-TGATTTTGGAGGCAATGTGCAGTGACCCTTGACCCT | 449 |
| 21 | 227 | -ATGGTCTGCCTATATAGTTTACCTGAT-TGATTTTGGAGGCAATGTGCAGTGACCCTTGACCCT | 291 |
| 14 | 228 | -ATGGTCTGCCTATATAGTTTACCTGAT-TGATTTTGGAGGCAATGTGCAGTGACCCTTGACCCT | 292 |
| 15 | 228 | -ATGGTCTGCCTATATAGTTTACCTGAT-TGATTTTGGAGGCAATGTGCAGTGACCCTTGACCCT | 292 |
| 13 | 231 | -ATGGTCTGCCTATATAGTTTACCTGAT-TGATTTTGGAGGCAATGTGCAGTGACCCTTGACCCT | 295 |
| 22 | 223 | -ATGGTCTGCCTATATAGTTTACCTGAT-TGATTTTGGAGGCAATGTGCAGTGACCCTTGACCCT | 287 |
| 19 | 226 | -ATGGTCTGCCTATATAGTTTACCTGAT-TGATTTTGGAGGCAATGTGCAGTGACCCTTGACCCT | 290 |
| 20 | 227 | -ATGGTCTGCCTATATAGTTTACCTGAT-TGATTTTGGAGGCAATGTGCAGTGACCCTTGACCCT | 291 |
| 7 | 311 | -ATGGTCTGCCTATATAGTTTACCTGAT-TGATTTTGGAGGCAATGTGCAGTGACCCTTGACCCT | 375 |
| 12 | 461 | -ATGGTCTGCCTATATAGTTTACCTGAT-TGATTTTGGAGGCAATGTGCAGTGACCCTTGACCCT | 525 |
| 3 | 252 | -ATGGTCTGCCTATATAGTTTACCTGAT-TGATTTTGGAGGCAATGTGCAGTGACCCTTGACCCT | 316 |
| 18 | 230 | -ATGGTCTGCCTATATAGTTTACCTGAT-TGATTTTGGAGGCAATGTGCAGTGACCCTTGACCCT | 294 |
| 4 | 290 | TCCGCTGGTTAGAGGTGAGAAGAGGGGAGAAAAGGCCGAAGAGGAAGTTATTGTGACTTGGGACAT | 356 |
| 9 | 290 | TCCGCTGGTTAGAGGTGAGAAGAGGGGAGAAAAGGCCGAAGAGGAAGTTATTGTGACTTGGGACAT | 356 |
| 2 | 337 | TCCGCTGGTTAGAGGTGAGAAGAGGGGAGAAAAGGCCGAAGAGGAAGTTATTGTGACTTGGGACAT | 403 |
| 1 | 306 | TCCGCTGGTTAGAGGTGAGAAGAGGGGAGAAAAGGCCGAAGAGGAAGTTATTGTGACTTGGGACAT | 372 |
| 10 | 275 | TCCGCTGGTTAGAGGTGAGAAGAGGGGAGAAAAGGCCGAAGAGGAAGTTATTGTGACTTGGGACAT | 341 |
| 8 | 301 | TCCGCTGGTTAGAGGTGAGAAGAGGGGAGAAAAGGCCGAAGAGGAAGTTATTGTGACTTGGGACAT | 367 |
| 6 | 274 | TCCGCTGGTTAGAGGTGAGAAGAGGGGAGAAAAGGCCGAAGAGGAAGTTATTGTGACTTGGGACAT | 340 |
| 11 | 290 | TCCGCTGGTTAGAGGTGAGAAGAGGGGAGAAAAGGCCGAAGAGGAAGTTATTGTGACTTGGGACAT | 356 |
| 5 | 309 | TCCGCTGGTTAGAGGTGAGAAGAGGGGAGAAAAGGCCGAAGAGGAAGTTATTGTGACTTGGGACAT | 375 |
| 17 | 298 | TCCGCTGGTTAGAGGTGAGAAGAGGGGAGAAAAGGCCGAAGAGGAAGTTATTGTGACTTGGGACAT | 364 |
| 16 | 350 | TCCGCTGGTTAGAGGTGAGAAGAGGGGAGAAAAGGCCGAAGAGGAAGTTATTGTGACTTGGGACAT | 416 |
| 23 | 286 | TCCGCTGGTTAGAGGTGAGAAGAGGGGAGAAAAGGCCGAAGAGGAAGTTATTGTGACTTGGGACAT | 352 |
| VDR | 450 | TCCGCTGGTTAGAGGTGAGAAGAGGGGAGAAAAGGCCGAAGAGGAAGTTATTGTGACTTGGGACAT | 516 |
| 21 | 292 | TCCGCTGGTTAGAGGTGAGAAGAGGGGAGAAAAGGCCGAAGAGGAAGTTATTGTGACTTGGGACAT | 358 |
| 14 | 293 | TCCGCTGGTTAGAGGTGAGAAGAGGGGAGAAAAGGCCGAAGAGGAAGTTATTGTGACTTGGGACAT | 359 |
| 15 | 293 | TCCGCTGGTTAGAGGTGAGAAGAGGGGAGAAAAGGCCGAAGAGGAAGTTATTGTGACTTGGGACAT | 359 |
| 13 | 296 | TCCGCTGGTTAGAGGTGAGAAGAGGGGAGAAAAGGCCGAAGAGGAAGTTATTGTGACTTGGGACAT | 362 |
| 22 | 288 | TCCGCTGGTTAGAGGTGAGAAGAGGGGAGAAAAGGCCGAAGAGGAAGTTATTGTGACTTGGGACAT | 354 |
| 19 | 291 | TCCGCTGGTTAGAGGTGAGAAGAGGGGAGAAAAGGCCGAAGAGGAAGTTATTGTGACTTGGGACAT | 357 |
| 20 | 292 | TCCGCTGGTTAGAGGTGAGAAGAGGGGAGAAAAGGCCGAAGAGGAAGTTATTGTGACTTGGGACAT | 358 |
| 7 | 376 | TCCGCTGGTTAGAGGTGAGAAGAGGGGAGAAAAGGCCGAAGAGGAAGTTATTGTGACTTGGGACAT | 442 |
| 12 | 526 | TCCGCTGGTTAGAGGTGAGAAGAGGGGAGAAAAGGCCGAAGAGGAAGTTATTGTGACTTGGGACAT | 592 |
| 3 | 317 | TCCGCTGGTTAGAGGTGAGAAGAGGGGAGAAAAGGCCGAAGAGGAAGTTATTGTGACTTGGGACAT | 383 |
| 18 | 295 | TCCGCTGGTTAGAGGTGAGAAGAGGGGAGAAAAGGCCGAAGAGGAAGTTATTGTGACTTGGGACAT | 361 |
| 4 | 357 | GATGTCGGTGATAGGTCCAAAGAGGGGGCGGCCCTGCCTCAGCCTGTGCTAGTGCCTGTGCCAG | 422 |
| 9 | 357 | GATGTCGGTGATAGGTCCAAAGAGGGGGCGGCCCTGCCTCAGCCTGTGCTAGTGCCTGTGCCAG | 422 |
| 2 | 404 | GATGTCGGTGATAGGTCCAAAGAGGGGGCGGCCCTGCCTCAGCCTGTGCTAGTGCCTGTGCCAG | 469 |
| 1 | 373 | GATGTCGGTGATAGGTCCAAAGAGGGGGCGGCCCTGCCTCAGCCTGTGCTAGTGCCTGTGCCAG | 438 |
| 10 | 342 | GATGTCGGTGATAGGTCCAAAGAGGGGGCGGCCCTGCCTCAGCCTGTGCTAGTGCCTGTGCCAG | 407 |
| 8 | 368 | GATGTCGGTGATAGGTCCAAAGAGGGGGCGGCCCTGCCTCAGCCTGTGCTAGTGCCTGTGCCAG | 433 |
| 6 | 341 | GATGTCGGTGATAGGTCCAAAGAGGGGGCGGCCCTGCCTCAGCCTGTGCTAGTGCCTGTGCCAG | 406 |
| 11 | 357 | GATGTCGGTGATAGGTCCAAAGAGGGGGCGGCCCTGCCTCAGCCTGTGCTAGTGCCTGTGCCAG | 422 |

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| 5 | 376 | GATGTCGGTGATAGGTCCAAAGAGGGGCGGCCCTGCCTCAGCCTGTGCTAGTGGCCTGTGCCAG | 441 |
| 17 | 365 | GATGTCGGTGATAGGTCCAAAGAGGGGCGGCCCTGCCTCAGCCTGTGCTAGTGGCCTGTGCCAG | 430 |
| 16 | 417 | GATGTCGGTGATAGGTCCAAAGAGGGGCGGCCCTGCCTCAGCCTGTGCTAGTGGCCTGTGCCAG | 483 |
| 23 | 353 | GATGTCGGTGATAGGTCCAAAGAGGGGCGGCCCTGCCTCAGCCTGTGCTAGTGGCCTGTGCCAG | 418 |
| VDR | 517 | GATGTCGGTGATAGGTCCAAAGAGGGGCGGCCCTGCCTCAGCCTGTGCTAGTGGCCTGTGCCAG | 582 |
| 21 | 359 | GATGTCGGTGATAGGTCCAAAGAGGGGCGGCCCTGCCTCAGCCTGTGCTAGTGGCCTGTGCCAG | 424 |
| 14 | 360 | GATGTCGGTGATAGGTCCAAAGAGGGGCGGCCCTGCCTCAGCCTGTGCTAGTGGCCTGTGCCAG | 425 |
| 15 | 360 | GATGTCGGTGATAGGTCCAAAGAGGGGCGGCCCTGCCTCAGCCTGTGCTAGTGGCCTGTGCCAG | 425 |
| 13 | 363 | GATGTCGGTGATAGGTCCAAAGAGGGGCGGCCCTGCCTCAGCCTGTGCTAGTGGCCTGTGCCAG | 428 |
| 22 | 355 | GATGTCGGTGATAGGTCCAAAGAGGGGCGGCCCTGCCTCAGCCTGTGCTAGTGGCCTGTGCCAG | 420 |
| 19 | 358 | GATGTCGGTGATAGGTCCAAAGAGGGGCGGCCCTGCCTCAGCCTGTGCTAGTGGCCTGTGCCAG | 423 |
| 20 | 359 | GATGTCGGTGATAGGTCCAAAGAGGGGCGGCCCTGCCTCAGCCTGTGCTAGTGGCCTGTGCCAG | 424 |
| 7 | 443 | GATGTCGGTGATAGGTCCAAAGAGGGGCGGCCCTGCCTCAGCCTGTGCTAGTGGCCTGTGCCAG | 508 |
| 12 | 593 | GATGTCGGTGATAGGTCCAAAGAGGGGCGGCCCTGCCTCAGCCTGTGCTAGTGGCCTGTGCCAG | 658 |
| 3 | 384 | GATGTCGGTGATAGGTCCAAAGAGGGGCGGCCCTGCCTCAGCCTGTGCTAGTGGCCTGTGCCAG | 449 |
| 18 | 362 | GATGTCGGTGATAGGTCCAAAGAGGGGCGGCCCTGCCTCAGCCTGTGCTAGTGGCCTGTGCCAG | 427 |
| | | | |
| 4 | 423 | GGATGCTTTCCTGGACTGAGGCTCAAGGAATGGAGATGGGCTCCTCTGACCCCTGCCAGCCAGC | 488 |
| 9 | 423 | GGATGCTTTCCTGGACTGAGGCTCAAGGAATGGAGATGGGCTCCTCTTACCCCTGCCAGCCAGC | 488 |
| 2 | 470 | GGATGCTTTCCTGGACTGAGGCTCAAGGAATGGAGATGGGCTCCTCT-ACCCCTGCCAGCCAGC | 534 |
| 1 | 439 | GGATGCTTTCCTGGACTGAGGCTCAAGGAATGGAGATGGGCTCCTCT-TACCCCTGCCAGCCAGC | 503 |
| 10 | 408 | GGATGCTTTCCTGGACTGAGGCTCAAGGAATGGAGATGGGCTCCTCT-TACCCCTGCCAGCCAGC | 472 |
| 8 | 434 | GGATGCTTTCCTGGACTGAGGCTCAAGGAATGGAGATGGGCTCCTCT-TACCCCTGCCAGCCAGC | 498 |
| 6 | 407 | GGATGCTTTCCTGGACTGAGGCTCAAGGAATGGAGATGGGCTCCTCT-TACCCCTGCCAGCCAGC | 471 |
| 11 | 423 | GGATGCTTTCCTGGACTGAGGCTCAAGGAATGGAGATGGGCTCCTCT-TACCCCTGCCAGCCAGC | 487 |
| 5 | 442 | GGATGCTTTCCTGGACTGAGGCTCAAGGAATGGAGATGGGCTCCTCT-TACCC-TGCCAGCCAGC | 504 |
| 17 | 431 | GGATGCTTTCCTGGACTGAGGCTCAAGGAATGGAGATGGGCTCCTCTGACCCCTGCCAGCCAGC | 497 |
| 16 | 484 | GGATGCTTTCCTGGACTGAGGCTCAAGGAATGGAGATGGGCTCCTCT-TACCCCTGCCAGCCAGC | 548 |
| 23 | 419 | GGATGCTTTCCTGGACTGAGGCTCAAGGAATGGAGATGGGCTCCTCT-TACCCCTGCCAGCCAGC | 483 |
| VDR | 583 | GGATGCTTTCCTGGACTGAGGCTCAAGGAATGGAGATGGGCTCCTCT-TACCCCTGCCAGCCAGC | 647 |
| 21 | 425 | GGATGCTTTCCTGGACTGAGGCTCAAGGAATGGAGATGGGCTCCTCT-TACCCCTGCCAGCCAGC | 489 |
| 14 | 426 | GGATGCTTTCCTGGACTGAGGCTCAAGGAATGGAGATGGGCTCCTCT-TACCCCTGCCAGCCAGC | 490 |
| 15 | 426 | GGATGCTTTCCTGGACTGAGGCTCAAGGAATGGAGATGGGCTCCTCT-TACCC-TGCCAGCCAGC | 489 |
| 13 | 429 | GGATGCTTTCCTGGACTGAGGCTCAAGGAATGGAGATGGGCTCCTCT-TACCCCTGCCAGCCAGC | 493 |
| 22 | 421 | GGATGCTTTCCTGGACTGAGGCTCAAGGAATGGAGATGGGCTCCTCT-TACCCCTGCCAGCCAGC | 485 |
| 19 | 424 | GGATGCTTTCCTGGACTGAGGCTCAAGGAATGGAGATGGGCTCCTCT-TACCCCTGCCAGCCAGC | 488 |
| 20 | 425 | GGATGCTTTCCTGGACTGAGGCTCAAGGAATGGAGATGGGCTCCTCT-TACCCCTGCCAGCCAGC | 489 |
| 7 | 509 | GGATGCTTTCCTGGACTGAGGCTCAAGGAATGGAGATGGGCTCCTCT-TACCCCTGCCAGCCAGC | 573 |
| 12 | 659 | GGATGCTTTCCTGGACTGAGGCTCAAGGAATGGAGATGGGCTCCTCT-TACCCCTGCCAGCCAGC | 723 |
| 3 | 450 | GGATGCTTTCCTGGACTGAGGCTCAAGGAATGGAGATGGGCTCCTCT-TACCCCTGCCAGCCAGC | 514 |
| 18 | 428 | GGATGCTTTCCTGGACTGAGGCTCAAGGAATGGAGATGGGCTCCTCT-TACCCCTGCCAGCCAGC | 492 |
| | | | |
| 4 | 489 | CTTCTCTCATTTCATCCACTCTAGCAACAATTTATTGAGCACCTATTAGGTACCAGGCACTA | 553 |
| 9 | 489 | CTTCTCTCATTTCATCCACTCTAGCAACAATTTATTGAGCACCTATTAGGTACCAGGCACTA | 553 |
| 2 | 535 | CTTCTCTCATTTCATCCACTCTAGCAACAATTTATTGAGCACCTATTAGGTACCAGGCACTA | 599 |
| 1 | 504 | CTTCTCTCATTTCATCCACTCTAGCAACAATTTATTGAGCACCTATTAGGTACCAGGCACTA | 568 |
| 10 | 473 | CTTCTCTCATTTCATCCACTCTAGCAACAATTTATTGAGCACCTATTAGGTACCAGGCACTA | 537 |
| 8 | 499 | CTTCTCTCATTTCATCCACTCTAGCAACAATTTATTGAGCACCTATTAGGTACCAGGCACTA | 563 |
| 6 | 472 | CTTCTCTCATTTCATCCACTCTAGCAACAATTTATTGAGCACCTATTAGGTACCAGGCACTA | 536 |
| 11 | 488 | CTTCTCTCATTTCATCCACTCTAGCAACAATTTATTGAGCACCTATTAGGTACCAGGCACTA | 552 |
| 5 | 505 | CTTCTCTCATTTCATCCACTCTAGCAACAATTTATTGAGCACCTATTAGGTACCAGGCACTA | 569 |
| 17 | 498 | CTTCTCTCATTTCATCCACTCTAGCAACAATTTATTGAGCACCTATTAGGTACCAGGCACTA | 562 |
| 16 | 549 | CTTCTGTCAATTTCATCCACTCTAGCAACAATTTATTGAGCACCTATTAGGTACCAGGCACTA | 615 |
| 23 | 484 | CTTCTCTCATTTCATCCACTCTAGCAACAATTTATTGAGCACCTATTAGGTACCAGGCACTA | 548 |
| VDR | 648 | CTTCTCTCATTTCATCCACTCTAGCAACAATTTATTGAGCACCTATTAGGTACCAGGCACTA | 712 |
| 21 | 490 | CTTCTCTCATTTCATCCACTCTAGCAACAATTTATTGAGCACCTATTAGGTACCAGGCACTA | 554 |
| 14 | 491 | CTTCTCTCATTTCATCCACTCTAGCAACAATTTATTGAGCACCTATTAGGTACCAGGCACTA | 555 |
| 15 | 490 | CTTCTCTCATTTCATCCACTCTAGCAACAATTTATTGAGCACCTATTAGGTACCAGGCACTA | 554 |
| 13 | 494 | CTTCTCTCATTTCATCCACTCTAGCAACAATTTATTGAGCACCTATTAGGTACCAGGCACTA | 558 |
| 22 | 486 | CTTCTCTCATTTCATCCACTCTAGCAACAATTTATTGAGCACCTATTAGGTACCAGGCACTA | 550 |
| 19 | 489 | CTTCTCTCATTTCATCCACTCTAGCAACAATTTATTGAGCACCTATTAGGTACCAGGCACTA | 553 |
| 20 | 490 | CTTCTCTCATTTCATCCACTCTAGCAACAATTTATTGAGCACCTATTAGGTACCAGGCACTA | 554 |
| 7 | 574 | CTTCTCTCATTTCATCCACTCTAGCAACAATTTATTGAGCACCTATTAGGTACCAGGCACTA | 638 |
| 12 | 724 | CTTCTCTCATTTCATCCACTCTAGCAACAATTTATTGAGCACCTATTAGGTACCAGGCACTA | 788 |
| 3 | 515 | CTTCTCTCATTTCATCCACTCTAGCAACAATTTATTGAGCACCTATTAGGTACCAGGCACTA | 579 |
| 18 | 493 | CTTCTCTCATTTCATCCACTCTAGCAACAATTTATTGAGCACCTATTAGGTACCAGGCACTA | 557 |
| | | | |
| 4 | 554 | GCTAGGTACTGGGGTTCAGCAGCAAATGGGACACAGGCTCCTCCTCCCATGAAGC-TTAGGAGGA | 616 |
| 9 | 554 | GCTAGGTACTGGGGTTCAGCAGCAAATGGGACACAGGCTCCTCCTCCCATGAAGC-TTAGGAGGA | 616 |
| 2 | 600 | GCTAGGTACTGGGGTTCAGCAGCAAATGGGACACAGGCTCCTCCTCCCATGAAGC-TTAGGAGGA | 662 |
| 1 | 569 | GCTAGGTACTGGGGTTCAGCAGCAAATGGGACACAGGCTCCTCCTCCCATGAAGC-TTAGGAGGA | 631 |

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|-----|-----|--|-----------|-----|
| 10 | 538 | GCTAGGTTACTGGGGTTCAGCAGCAAATGGGACACAGGCTCCTCCTCCCATGAAGC | TTAGGAGGA | 600 |
| 8 | 564 | GCTAGGTTACTGGGGTTCAGCAGCAAATGGGACACAGGCTCCTCCTCCCATGAAGC | TTAGGAGGA | 626 |
| 6 | 537 | GCTAGGTTACTGGGGTTCAGCAGCAAATGGGACACAGGCTCCTCCTCCCATGAAGC | TTAGGAGGA | 599 |
| 11 | 553 | GCTAGGTTACTGGGGTTCAGCAGCAAATGGGACACAGGCTCCTCCTCCCATGAAGC | TTAGGAGGA | 615 |
| 5 | 570 | GCTAGGTTACTGGGGTTCAGCAGCAAATGGGACACAGGCTCCTCCTCCCATGAAGC | TTAGGAGGA | 632 |
| 17 | 563 | GCTAGGTTACTGGGGTTCAGCAGCAAATGGGACACAGGCTCCTCCTCCCATGAAGC | TTAGGAGGA | 627 |
| 16 | 616 | GCTAGGTTACTGGGGTTCAGCAGCAAATGGGACACAGGCTCCTCCTCCCATGAAGC | TTAGGAGGA | 680 |
| 23 | 549 | GCTAGGTTACTGGGGTTCAGCAGCAAATGGGACACAGGCTCCTCCTCCCATGAAGC | TTAGGAGGA | 611 |
| VDR | 713 | GCTAGGTTACTGGGGTTCAGCAGCAAATGGGACACAGGCTCCTCCTCCCATGAAGC | TTAGGAGGA | 775 |
| 21 | 555 | GCTAGGTTACTGGGGTTCAGCAGCAAATGGGACACAGGCTCCTCCTCCCATGAAGC | TTAGGAGGA | 617 |
| 14 | 556 | GCTAGGTTACTGGGGTTCAGCAGCAAATGGGACACAGGCTCCTCCTCCCATGAAGC | TTAGGAGGA | 618 |
| 15 | 555 | GCTAGGTTACTGGGGTTCAGCAGCAAATGGGACACAGGCTCCTCCTCCCATGAAGC | TTAGGAGGA | 617 |
| 13 | 559 | GCTAGGTTACTGGGGTTCAGCAGCAAATGGGACACAGGCTCCTCCTCCCATGAAGC | TTAGGAGGA | 621 |
| 22 | 551 | GCTAGGTTACTGGGGTTCAGCAGCAAATGGGACACAGGCTCCTCCTCCCATGAAGC | TTAGGAGGA | 613 |
| 19 | 554 | GCTAGGTTACTGGGGTTCAGCAGCAAATGGGACACAGGCTCCTCCTCCCATGAAGC | TTAGGAGGA | 616 |
| 20 | 555 | GCTAGGTTACTGGGGTTCAGCAGCAAATGGGACACAGGCTCCTCCTCCCATGAAGC | TTAGGAGGA | 617 |
| 7 | 639 | GCTAGGTTACTGGGGTTCAGCAGCAAATGGGACACAGGCTCCTCCTCCCATGAAGC | TTAGGAGGA | 701 |
| 12 | 789 | GCTAGGTTACTGGGGTTCAGCAGCAAATGGGACACAGGCTCCTCCTCCCATGAAGC | TTAGGAGGA | 851 |
| 3 | 580 | GCTAGGTTACTGGGGTTCAGCAGCAAATGGGACACAGGCTCCTCCTCCCATGAAGC | TTAGGAGGA | 642 |
| 18 | 558 | GCTAGGTTACTGGGGTTCAGCAGCAAATGGGACACAGGCTCCTCCTCCCATGAAGC | TTAGGAGGA | 598 |
| | | | | |
| 4 | 617 | AACATTTAAACAAATGTTATTTAATTATTAATTCCTAACAAAGGCAAGGGTTTTCGAAATAAAGCTA | 681 | |
| 9 | 617 | AACATTTAAACAAATGTTATTTAATTATTAATTCCTAACAAAGGCAAGGGTTTTCGAAATAAAGCTA | 681 | |
| 2 | 663 | AACATTTAAACAAATGTTATTTAATTATTAATTCCTAACAAAGGCAAGGGTTTTAAAAATAAAG-TA | 726 | |
| 1 | 632 | AACATTTAAACAAATGTTATTTAATTATTAATTCCTAACAAAGGCAAGGGTTTTAAAAATAA-AGTA | 695 | |
| 10 | 601 | AACATTTAAACAAATGTTATTTAATTATTAATTCCTAACAAAGGCAAGGGTTTTAAAAATAA-AGTA | 664 | |
| 8 | 627 | AACATTTAAACAAATGTTATTTAATTATTAATTCCTAACAAAGGCAAGGGTTTTAAAAATAA-AGTA | 690 | |
| 6 | 600 | AACATTTAAACAAATGTTATTTAATTATTAATTCCTAACAAAGGCAAGGGTTTTAAAAATAA-AGTA | 663 | |
| 11 | 616 | AACATTTAAACAAATGTTATTTAATTATTAATTCCTAACAAAGGCAAGGGTTTTAAAAATAA-AGTA | 679 | |
| 5 | 633 | AACATTTAAACAAATGTTATTTAATTATTAATTCCTAACAAAGGCAAGGGTTTTAAAAATAA-AGTA | 696 | |
| 17 | 628 | AACATTTAAACAAATGTTATTTAATTATTAATTCCTAACAAAGGCAAGGGTTTTAAAAATAA-AGTA | 692 | |
| 16 | 681 | AACATTTAAACAAATGTTATTTAATTATTAATTCCTAACAAAGGCAAGGGTTTTAAAAATAAAGTA | 746 | |
| 23 | 612 | AACATTTAAACAAATGTTATTTAATTATTAATTCCTAACAAAGGCAAGGGTTTTAAAAATAA-AGTA | 675 | |
| VDR | 776 | AACATTTAAACAAATGTTATTTAATTATTAATTCCTAACAAAGGCAAGGGTTTTAAAAATAA-AGTA | 839 | |
| 21 | 618 | AACATTTAAACAAATGTTATTTAATTATTAATTCCTAACAAAGGCAAGGGTTTTAAAAATAA-AGTA | 681 | |
| 14 | 619 | AACATTTAAACAAATGTTATTTAATTATTAATTCCTAACAAAGGCAAGGGTTTTAAAAATAA-AGTA | 682 | |
| 15 | 618 | AACATTTAAACAAATGTTATTTAATTATTAATTCCTAACAAAGGCAAGGGTTTTAAAAATAA-AGTA | 681 | |
| 13 | 622 | AACATTTAAACAAATGTTATTTAATTATTAATTCCTAACAAAGGCAAGGGTTTTAAAAATAA-AGTA | 685 | |
| 22 | 614 | AACATTTAAACAAATGTTATTTAATTATTAATTCCTAACAAAGGCAAGGGTTTTAAAAATAA-AGTA | 677 | |
| 19 | 617 | AACATTTAAACAAATGTTATTTAATTATTAATTCCTAACAAAGGCAAGGGTTTTAAAAATAA-AGTA | 680 | |
| 20 | 618 | AACATTTAAACAAATGTTATTTAATTATTAATTCCTAACAAAGGCAAGGGTTTTAAAAATAA-AGTA | 681 | |
| 7 | 702 | AACATTTAAACAAATGTTATTTAATTATTAATTCCTAACAAAGGCAAGGGTTTTAAAAATAA-AGTA | 764 | |
| 12 | 852 | AACATTTAAACAAATGTTATTTAATTATTAATTCCTAACAAAGGCAAGGGTTTTAAAAATAA-AGTA | 914 | |
| 3 | 643 | AACATTTAAACAAATGTTATTTAATTATTAATTCCTAACAAAGGCAAGGGTTTTAAAAATAA-AGTA | 706 | |
| 18 | 599 | AACATTTAAACAAATGTTATTTAATTATTAATTCCTAACAAAGGCAAGGGTTTTAAAAATAA-AGTA | 660 | |
| | | | | |
| 4 | 682 | AGGTGATGCTACAGAA---CGGTTAGAAATACGAGAGAG---ACG-GGTAACGCTGT---GGCCTA | 736 | |
| 9 | 682 | AGGTGATGCTACAGAA---CGGTTAGAAATACGAGAGAG---ACG-GGTAACGCTGT---GGCCTA | 736 | |
| 2 | 727 | AGG-GATGCTACAGAA---CGGTTAGAAATAGAAAGGACGGGAACG-CTGAGCGCTGTCTTGGTCTA | 786 | |
| 1 | 696 | -AGTGATGCTACAGAA---GGTTAGAAATAGAAAG-GAGGGAAG--CTGA-CGTGT-CTG-GGC-A | 748 | |
| 10 | 665 | -AGTGATGCTACAGAA---GGTTAGAAATAGAAAG-GAGGGAAG--CTGA-CGTGTCTG-GGCTA | 719 | |
| 8 | 691 | -AGTGATGCTACAGAA---GGTTAGAAATAGAAAGAGAGGGGAAG--CTGAACGTGTGCTG-GGCA | 747 | |
| 6 | 664 | -AGTGATGCTACAGAA---GGTTAGAAATAGAAAGGAGGGAAG--CTGA-CGTGTGCTG-GGCTA | 718 | |
| 11 | 680 | -AGTGATGCTACAGAA---GGTTAGAAATAGAAAGGAGGGAAG--CTGA-CGTGTCTG-GGCTA | 735 | |
| 5 | 697 | -AGTGATGCTACAG---AAGGG-TAGAAATAGAAATAGAAAGGAGGAGCTGA-CGTGGTCTG-GGCTA | 756 | |
| 17 | 693 | AAGTGATGCTACAG---CCCCGCTAGAAATAGAAAGAGTATGTG---TGA---TAGGCTG-AGCTA | 746 | |
| 16 | 747 | AGCTGATGCTACAGGACACCCGGCTAGAAATAGAAAGGATTCGAGGA--CGA-CGTGGGTTG-AGCTA | 807 | |
| 23 | 676 | AG-TGATGCTACAG-AA---GGTTAGAAATAGAAAGGAGGGAAG--TGA-CGTGTCTG-GGCTA | 730 | |
| VDR | 840 | -AGTGATGCTACAGAA---GGTTAGAAATAGAAAGGAGGG-AAG--CTGA-CGTGGTCTG-GGCTA | 894 | |
| 21 | 682 | -AGTGATGCTACAGAA---GGTTAGAAATAGAAAGGAGGG-AAG--CTGA-CGTGGTCTG-GGC-A | 735 | |
| 14 | 683 | -AGTGATGCTACAGAA---GGTTAGAAATAGAAAGGAGGG-AAG--CTGA-CGTGGTCTG-GGCTA | 737 | |
| 15 | 682 | -AGTGATGCTACAGAA---CCCTAGAAATAGAAAGGAAG--AAG--CTGT-CGTGGTCTCGGTTTC | 736 | |
| 13 | 686 | -AGTGATGCTACAGAA---GGTTAGAAATAGAAAGGAGGG-AAG--TGA-CGTGGTCTG-GGCTA | 739 | |
| 22 | 678 | -AGTGATGCTACAGAA---GGTTAGAAATAGAAAGGAGGG-AAG--CTGA-CGTGGTCTC-CGCA | 730 | |
| 19 | 681 | -AGTGATGCTACAGAA---GGTTAGAAATAGAAAGGAGGG-AAG--CTGA-CGTGGTCTG-GGCTA | 735 | |
| 20 | 682 | -AGTGATGCTACAGAA---GGTTAGAAATAGAAAGGAGGG-AAG--CTGC-CGAGTTTTC-AGCTC | 736 | |
| 7 | 765 | -AGTGATGCTACAGAA---GGTTAGAAATAGAAAGGAGGG-AAG--CTGA-CGTGGTCTG-GGCTA | 818 | |
| 12 | 915 | -AGTGATGCTACAGAA---GGTTAGAAATAGAAAGGAGGGGAAG--CTGA-CGTGGTCTG-GGCTA | 969 | |
| 3 | 707 | -AGTGATGCTACAGAA---GGTTAGAAATAGAAAGGAGGG-AAG--CTGA-CGTG-TCTG-GGC-A | 759 | |
| 18 | 661 | -ACTGATGCTACAGAA---GGTTAGAAATAGAAAGGAGGG-AAG--CTGA-----C---A | 702 | |

4 737 CAG---AGT----AGA-GTGGTGGCCAGAAATCGCTCCCTTTTGGACGAAGACT-TTTTAAGCTGT 793
9 737 CAG---AGT----AGA-GTGGTGGCCAGAAATCGCTCCCTTTTGGACGAAGACT-TTTTAAGCTGT 793
2 787 CAGG--AGT----AGA-GTGGTGGCCAGGAAT--GTCCCTTTTGGAGAAGACCTTTTAAGCTGT 843
1 749 CAG--ACGT----AGA-GTGGTGGCCAGAAAT--CG-TCCCTTTTGGCAGGA--GACC-TTTTA--GCTGT 801
10 720 CAG--TAGT----AGA-GTGGTGGCCAGGAAT--GG-CCTTTTGGAGAAAGACC-TTTTAAGCTGT 774
8 748 CAG--AAGT----AGAA-GTGGTGGCCAGGAAC--TT-GCCTTTTGGAGAAAGACC-TTTTAAGCTGT 803
6 719 CAG--A-GT----AGAAGTGGTGGCCAGGAA--TG-GCCTTTTGGAGAAAGACC-TTTTAAGCTGT 772
11 736 CAG--AAGT----AGA-GTGGTGGCCAGGA---TG-GCCTTTTGGAGAAAGACC-TTTTAAGCTGT 788
5 757 CAG--TAGT----AGA-GTGGTGGCCAGTAAT--GG-CCTTTTGGAGAA--GACC-TTTTAAGCTGT 811
17 747 CAG--TAGT----AGA-GTGGTGGCCAGGAAT--GG-CCTTTTGGAGAAAGACC-TTTTAAGCTGT 801
16 808 CAG--TAGT----AGA-GTGGTGGCCAGTAAT--GG-CCTTTTGGAGAA--GACC-TTTTAAGCTGT 862
23 731 C-G--AGT----AGAAGTGGTGGCCAGAACT--TG-CCTTTTGGAGAAAGACC-TTTTAAGCTGT 785
VDR 895 CAG--AGGT----AGA-GTGGTGGCCAGGAAT--GG--CCTTTTGGAGGAAGACC-TTTTAAGCTGT 948
21 736 CAGGTAGGT----AGC-GTGGTGGCCAGGAAT--GG--CCTTTTGGAGGAAGACC-TTTTAAGCTGT 791
14 738 CAG--AGGT----AGA-GTGGTGGCCAGGAAT--GG--CCTTTTGGAGGAAGACC-TTTTAAGCTGT 791
15 737 CAG--AGCT----AGA-GTGGTGGCCAGGAAT--GG--CCTTTTGGAGGAAGACC-TTTTAAGCTGT 790
13 740 CAG--AGGT----AGA-GTGGTGGCCAGGAAT--GG--CCTTTTGGAGGAAGACC-TTTTAAGCTGT 793
22 731 CAG--ACGT----AGA-GTGGTGGCCAGGAAT--GG--CCTTTTGGAGGAAGACC-TTTTAAGCTGT 784
19 736 CAG--AGGT----AGA-GTGGTGGCCAGGAAT--GG--CCTTTTGGAGGAAGACC-TTTTAAGCTGT 789
20 737 CCG--AGT----AGA-GTGGTGGCCAGGAAT--GG--CCTTTTGGAGGAAGACC-TTTTAAGCTGT 790
7 819 CAG--AGGT----AGA-GTGGTGGCCAGATAT--AGGTCTTTTGCAGCA--GACC-TTTTA--GCTGT 872
12 970 CAG--AGGT----AGA-GTGGTGGCCAGATAT--AGGTCTTTTGCAGCA--GACC-TTTTA--GCTGT 1023
3 760 CAG--ACGTGGTGAGA--GTGGTGGCCAGGTAA--TGGCCCTTTTGGAGAAAGACC-TTTTAAGCTGT 820
18 703 -----GT-----GTGGTGGCCAGCAATCGTCTCCCTTTTGGACGAAGACTTTTAAGCTGT 752

4 794 TATCCACAAGGATCAGTACAGAGTCTGGCATAAGATAGCAGAGCAGAGTTCCAAGCCGAGGGAGC 856
9 794 TATCCACAAGGATCAGTA--AGAGTCTGGCATAAGATAGCAGAGCAGAGTTCCAAGCCGAGGGAGC 856
2 844 TATCCACAAGGATCAGTA--AGAGTCTGGCATAAGATAGCAGAGCAGAGTTCCAAGCCGAGGGAGC 905
1 802 TATCCACAAGCATCAGTA--ATAGTCTGGCATAAGATAGCAGAGCAGAGTTCCAAGCCGAGGGAGC 863
10 775 TATCCACAAGGATCAGTA--AGAGTCTGGCATAAGATAGCAGAGCAGAGTTCCAAGCCGAGGGAGC 836
8 804 TATCCACAAGGATCAGTACAGAGTCTGGCATAAGATAGCAGAGCAGAGTTCCAAGCCGAGGGAGC 866
6 773 TATCCACAAGGATCAGTA--AGAGTCTGGCATAAGATAGCAGAGCAGAGTTCCAAGCCGAGGGAGC 834
11 789 TATCCACAAGGATCAGTA--AGAGTCTGGCATAAGATAGCAGAGCAGAGTTCCAAGCCGAGGGAGC 850
5 812 TATCCACAAGGATCAGTA--AGAGTCTGGCATAAGATAGCAGAGCAGAGTTCCAAGCCGAGGGAGC 873
17 802 TATCCACAAGGATCAGTA--AGAGTCTGGCATAAGATAGCAGAGCAGAGTTCCAAGCCGAGGGAGC 863
16 863 TATCCACAAGGATCAGTA--AGAGTCTGGCATAAGATAGCAGAGCAGAGTTCCAAGCCGAGGGAGC 924
23 786 TATCCACAAGGATCAGTACAGAGTCTGGCATAAGATAGCAGAGCAGAGTTCCAAGCCGAGGGAGC 848
VDR 949 TATCCACAAGGATCAGTA--AGAGTCTGGCATAAGATAGCAGAGCAGAGTTCCAAGCCGAGGGAGC 1010
21 792 TATCCACAAGGATCAGTACAGAGTCTGGCATAAGATAGCAGAGCAGAGTTCCAAGCCGAGGGAGC 853
14 792 TATCCACAAGGATCAGTA--AGAGTCTGGCATAAGATAGCAGAGCAGAGTTCCAAGCCGAGGGAGC 853
15 791 TATCCACAAGGATCAGTA--AGAGTCTGGCATAAGATAGCAGAGCAGAGTTCCAAGCCGAGGGAGC 852
13 794 TATCCACAAGGATCAGTA--AGAGTCTGGCATAAGATAGCAGAGCAGAGTTCCAAGCCGAGGGAGC 855
22 785 TATCCACAAGGATCAGTA--AGAGTCTGGCATAAGATAGCAGAGCAGAGTTCCAAGCCGAGGGAGC 846
19 790 TATCCACAAGGATCAGTA--AGAGTCTGGCATAAGATAGCAGAGCAGAGTTCCAAGCCGAGGGAGC 851
20 791 TATCCACAAGGATCAGTA--AGAGTCTGGCATAAGATAGCAGAGCAGAGTTCCAAGCCGAGGGAGC 852
7 873 TATCCACAAGGATCAGTA--ACAGTCTGGCATAAGATAGCAGAGCAGAGTTCCAAGCCGAGGGAGC 934
12 1024 TATCCACAAGGATCAGTA--ACAGTCTGGCATAAGATAGCAGAGCAGAGTTCCAAGCCGAGGGAGC 1085
3 821 TATCCACAAGGATCAGTA--AGAGTCTGGCATAAGATAGCAGAGCAGAGTTCCAAGCCGAGGGAGC 882
18 753 TATCCACAAGGATCAGTA--AGAGTCTGGCATAAGATAGCAGAGCAGAGTTCCAAGCCGAGGGAGC 818

4 857 ACAGATGTGAAGGCTGGTGGCCAGAGAGCATGGCGCATCGGGACGTGAGGGATGGACAGAGCATGG 923
9 857 ACAGATGTGAAGGCTGGTGGCCAGAGAGCATGGCGCATCGGGACGTGAGGGATGGACAGAGCATGG 923
2 906 ACAGATGTGAAGGCTGGTGGCCAGAGAGCATGGCGCATCGGGACGTGAGGGATGGACAGAGCATGG 972
1 864 ACAGATGTGAAGGCTGGTGGCCAGAGAGCATGGCGCATCGGGACGTGAGGGATGGACAGAGCATGG 930
10 837 ACAGATGTGAAGGCTGGTGGCCAGAGAGCATGGCGCATCGGGACGTGAGGGATGGACAGAGCATGG 903
8 867 ACAGATGTGAAGGCTGGTGGCCAGAGAGCATGGCGCATCGGGACGTGAGGGATGGACAGAGCATGG 933
6 835 ACAGATGTGAAGGCTGGTGGCCAGAGAGCATGGCGCATCGGGACGTGAGGGATGGACAGAGCATGG 901
11 851 ACAGATGTGAAGGCTGGTGGCCAGAGAGCATGGCGCATCGGGACGTGAGGGATGGACAGAGCATGG 917
5 874 ACAGATGTGAAGGCTGGTGGCCAGAGAGCATGGCGCATCGGGACGTGAGGGATGGACAGAGCATGG 940
17 864 ACAGATGTGAAGGCTGGTGGCCAGAGAGCATGGCGCATCGGGACGTGAGGGATGGACAGAGCATGG 930
16 925 ACAGATGTGAAGGCTGGTGGCCAGAGAGCATGGCGCATCGGGACGTGAGGGATGGACAGAGCATGG 991
23 849 ACAGATGTGAAGGCTGGTGGCCAGAGAGCATGGCGCATCGGGACGTGAGGGATGGACAGAGCATGG 915
VDR 1011 ACAGATGTGAAGGCTGGTGGCCAGAGAGCATGGCGCATCGGGACGTGAGGGATGGACAGAGCATGG 1077
21 854 ACAGATGTGAAGGCTGGTGGCCAGAGAGCATGGCGCATCGGGACGTGAGGGATGGACAGAGCATGG 920
14 854 ACAGATGTGAAGGCTGGTGGCCAGAGAGCATGGCGCATCGGGACGTGAGGGATGGACAGAGCATGG 920
15 853 ACAGATGTGAAGGCTGGTGGCCAGAGAGCATGGCGCATCGGGACGTGAGGGATGGACAGAGCATGG 919
13 856 ACAGATGTGAAGGCTGGTGGCCAGAGAGCATGGCGCATCGGGACGTGAGGGATGGACAGAGCATGG 922
22 847 ACAGATGTGAAGGCTGGTGGCCAGAGAGCATGGCGCATCGGGACGTGAGGGATGGACAGAGCATGG 913
19 852 ACAGATGTGAAGGCTGGTGGCCAGAGAGCATGGCGCATCGGGACGTGAGGGATGGACAGAGCATGG 918
20 853 ACAGATGTGAAGGCTGGTGGCCAGAGAGCATGGCGCATCGGGACGTGAGGGATGGACAGAGCATGG 919
7 935 ACAGATGTGAAGGCTGGTGGCCAGAGAGCATGGCGCATCGGGACGTGAGGGATGGACAGAGCATGG 1001

| | | | |
|-----|------|---|------|
| 12 | 1086 | ACAGATGTGAAGGCTGGTGGCCAGAGAGCATGGCGCATCGGGACGTGAGGGATGGACAGAGCATGT | 1152 |
| 3 | 883 | ACAGATGTGAAGGCTGGTGGCCAGAGAGCATGGCGCATCGGGACGTGAGGGATGGACAGAGCATGG | 949 |
| 18 | 819 | ACAGATGTGAAGGCTGGTGGCCAGAGAGCATGGCGCATCGGGACGTGAGGGATGGACAGAGCATGG | 885 |
| 4 | 924 | ACACGGGAGCAAG-GCCAGGCAGGGACAGGGTCCAGGTGCGCCCATGGAA-GGACCTAGGTCTGGA | 985 |
| 9 | 924 | ACACGGGAGCAAG-GCCAGGCAGGGACAGGGTCCAGGTGCGCCCATGGAA-GGACCTAGGTCTGGA | 985 |
| 2 | 973 | ACACGGGAGCAAG-GCCAGGCAGGGACAGGGTCCAGGTGCGCCCATGGAA-GGACCTAGGTCTGGA | 1034 |
| 1 | 931 | ACACGGCAGCAAG-GCCAGGCAGGTACAGGGTCCAGGTGCGCCCATGGAA-GGACCTAGGTCTGGA | 993 |
| 10 | 904 | ACACGGGAGCAAG-GCCAGGCAGGGACAGGGTCCAGGTGCGCCCATGGAA-GGACCTAGGTCTGGA | 965 |
| 8 | 934 | ACACGGGAGCAAG-GCCAGGCAGGGACAGGGTCCAGGTGCGCCCATGGAA-GGACCTAGGTCTGGA | 995 |
| 6 | 902 | ACACGGGAGCAAG-GCCAGGCAGGGACAGGGTCCAGGTGCGCCCATGGAA-GGACCTAGGTCTGGA | 963 |
| 11 | 918 | ACACGGGAGCAAG-GCCAGGCAGGGACAGGGTCCAGGTGCGCCCATGGAA-GGACCTAGGTCTGGA | 979 |
| 5 | 941 | ACACGGGAGCAAG-GCCAGGCAGGGACAGGGTCCAGGTGCGCCCATGGAA-GGACCTAGGTCTGGA | 1002 |
| 17 | 931 | ACACGGGAGCAAG-GCCAGGCAGGGACAGGGTCCAGGTGCGCCCATGGAA-GGACCTAGGTCTGGA | 992 |
| 16 | 992 | ACACGGGAGCAAG-GCCAGGCAGGGACAGGGTCCAGGTGCGCCCATGGAA-GGACCTAGGTCTGGA | 1053 |
| 23 | 916 | ACACGGGAGCAAG-GCCAGGCAGGGACAGGGTCCAGGTGCGCCCATGGAA-GGACCTAGGTCTGGA | 977 |
| VDR | 1078 | ACACGGGAGCAAG-GCCAGGCAGGGACAGGGTCCAGGTGCGCCCATGGAA-GGACCTAGGTCTGGA | 1139 |
| 21 | 921 | ACACGGGAGCAAG-GCCAGGCAGGGACAGGGTCCAGGTGCGCCCATGGAA-GGACCTAGGTCTGGA | 982 |
| 14 | 921 | ACACGGGAGCAAG-GCCAGGCAGGGACAGGGTCCAGGTGCGCCCATGGAA-GGACCTAGGTCTGGA | 982 |
| 15 | 920 | ACACGGGAGCAAG-GCCAGGCAGGGACAGGGTCCAGGTGCGCCCATGGAA-GGACCTAGGTCTGGA | 981 |
| 13 | 923 | ACACGGGAGCAAG-GCCAGGCAGGGACAGGGTCCAGGTGCGCCCATGGAA-GGACCTAGGTCTGGA | 984 |
| 22 | 914 | ACACGGGAGCAAG-GCCAGGCAGGGACAGGGTCCAGGTGCGCCCATGGAA-GGACCTAGGTCTGGA | 975 |
| 19 | 919 | ACACGGGAGCAAG-GCCAGGCAGGGACAGGGTCCAGGTGCGCCCATGGAA-GGACCTAGGTCTGGA | 980 |
| 20 | 920 | ACACGGGAGCAAG-GCCAGGCAGGGACAGGGTCCAGGTGCGCCCATGGAA-GGACCTAGGTCTGGA | 981 |
| 7 | 1002 | ACACGGGAGCAAG-GCCAGGCAGGGACAGGGTCCAGGTGCGCCCATGGAA-GGACCTAGGTCTGGA | 1063 |
| 12 | 1153 | ACACGGGAGCAAG-GCCAGGCAGGGACAGGGTCCAGGTGCGCCCATGGAA-GGACCTAGGTCTGGA | 1214 |
| 3 | 950 | ACACGGGAGCAAG-GCCAGGCAGGGACAGGGTCCAGGTGCGCCCATGGAAA | 1012 |
| 18 | 886 | ACACGGCAGCAAGT-GCCAGGCAGGGACAGGGTCCAGGTGCGCCCATGGAA-GGACCTAGGTCTGGA | 951 |
| 4 | 986 | TCCTAAATGCACGGAGAAGTCACTGGAGGGCTTTGGGGCCAGGCAGTGGTATCACCGGTCAGCAGT | 1052 |
| 9 | 986 | TCCTAAATGCACGGAGAAGTCACTGGAGGGCTTTGGGGCCAGGCAGTGGTATCACCGGTCAGCAGT | 1052 |
| 2 | 1035 | TCCTAAATGCACGGAGAAGTCACTGGAGGGCTTTGGGGCCAGGCAGTGGTATCACCGGTCAGCAGT | 1101 |
| 1 | 994 | TCCTAAATGCACGGAGAAGTCACTGGAGGGCTTTGGGGCCAGGCAGTGGTATCACCGGTCAGCAGT | 1060 |
| 10 | 966 | TCCTAAATGCACGGAGAAGTCACTGGAGGGCTTTGGGGCCAGGCAGTGGTATCACCGGTCAGCAGT | 1032 |
| 8 | 996 | TCCTAAATGCACGGAGAAGTCACTGGAGGGCTTTGGGGCCAGGCAGTGGTATCACCGGTCAGCAGT | 1062 |
| 6 | 964 | TCCTAAATGCACGGAGAAGTCACTGGAGGGCTTTGGGGCCAGGCAGTGGTATCACCGGTCAGCAGT | 1030 |
| 11 | 980 | TCCTAAATGCACGGAGAAGTCACTGGAGGGCTTTGGGGCCAGGCAGTGGTATCACCGGTCAGCAGT | 1046 |
| 5 | 1003 | TCCTAAATGCACGGAGAAGTCACTGGAGGGCTTTGGGGCCAGGCAGTGGTATCACCGGTCAGCAGT | 1069 |
| 17 | 993 | TCCTAAATGCACGGAGAAGTCACTGGAGGGCTTTGGGGCCAGGCAGTGGTATCACCGGTCAGCAGT | 1059 |
| 16 | 1054 | TCCTAAATGCACGGAGAAGTCACTGGAGGGCTTTGGGGCCAGGCAGTGGTATCACCGGTCAGCAGT | 1120 |
| 23 | 978 | TCCTAAATGCACGGAGAAGTCACTGGAGGGCTTTGGGGCCAGGCAGTGGTATCACCGGTCAGCAGT | 1044 |
| VDR | 1140 | TCCTAAATGCACGGAGAAGTCACTGGAGGGCTTTGGGGCCAGGCAGTGGTATCACCGGTCAGCAGT | 1206 |
| 21 | 983 | TCCTAAATGCACGGAGAAGTCACTGGAGGGCTTTGGGGCCAGGCAGTGGTATCACCGGTCAGCAGT | 1049 |
| 14 | 983 | TCCTAAATGCACGGAGAAGTCACTGGAGGGCTTTGGGGCCAGGCAGTGGTATCACCGGTCAGCAGT | 1049 |
| 15 | 982 | TCCTAAATGCACGGAGAAGTCACTGGAGGGCTTTGGGGCCAGGCAGTGGTATCACCGGTCAGCAGT | 1048 |
| 13 | 985 | TCCTAAATGCACGGAGAAGTCACTGGAGGGCTTTGGGGCCAGGCAGTGGTATCACCGGTCAGCAGT | 1051 |
| 22 | 976 | TCCTAAATGCACGGAGAAGTCACTGGAGGGCTTTGGGGCCAGGCAGTGGTATCACCGGTCAGCAGT | 1042 |
| 19 | 981 | TCCTAAATGCACGGAGAAGTCACTGGAGGGCTTTGGGGCCAGGCAGTGGTATCACCGGTCAGCAGT | 1047 |
| 20 | 982 | TCCTAAATGCACGGAGAAGTCACTGGAGGGCTTTGGGGCCAGGCAGTGGTATCACCGGTCAGCAGT | 1048 |
| 7 | 1064 | TCCTAAATGCACGGAGAAGTCACTGGAGGGCTTTGGGGCCAGGCAGTGGTATCACCGGTCAGCAGT | 1130 |
| 12 | 1215 | TCCTAAATGCACGGAGAAGTCACTGGAGGGCTTTGGGGCCAGGCAGTGGTATCACCGGTCAGCAGT | 1281 |
| 3 | 1013 | TCCTAAATGCACGGAGAAGTCACTGGAGGGCTTTGGGGCCAGGCAGTGGTATCACCGGTCAGCAGT | 1079 |
| 18 | 952 | TCCTAAATGCACGGAGAAGTCACTGGAGGGCTTTGGGGCCAGGCAGTGGTATCACCGGTCAGCAGT | 1018 |
| 4 | 1053 | ATAGAGGGGTGGCCTAGGGGGTGTCTGCCGTTGAGGTCGTGTGGGTGGGGGTGGTGGGATTGAGC | 1119 |
| 9 | 1053 | ATAGAGGGGTGGCCTAGGGGGTGTCTGCCGTTGAGGTCGTGTGGGTGGGGGTGGTGGGATTGAGC | 1119 |
| 2 | 1102 | ATAGAGGGGTGGCCTAGGGGGTGTCTGCCGTTGAGGTCGTGTGGGTGGGGGTGGTGGGATTGAGC | 1168 |
| 1 | 1061 | ATAGAGGGGTGGCCTAGGGGGTGTCTGCCGTTGAGGTCGTGTGGGTGGGGGTGGTGGGATTGAGC | 1127 |
| 10 | 1033 | ATAGAGGGGTGGCCTAGGGGGTGTCTGCCGTTGAGGTCGTGTGGGTGGGGGTGGTGGGATTGAGC | 1099 |
| 8 | 1063 | ATAGAGGGGTGGCCTAGGGGGTGTCTGCCGTTGAGGTCGTGTGGGTGGGGGTGGTGGGATTGAGC | 1129 |
| 6 | 1031 | ATAGAGGGGTGGCCTAGGGGGTGTCTGCCGTTGAGGTCGTGTGGGTGGGGGTGGTGGGATTGAGC | 1097 |
| 11 | 1047 | ATAGAGGGGTGGCCTAGGGGGTGTCTGCCGTTGAGGTCGTGTGGGTGGGGGTGGTGGGATTGAGC | 1113 |
| 5 | 1070 | ATAGAGGGGTGGCCTAGGGGGTGTCTGCCGTTGAGGTCGTGTGGGTGGGGGTGGTGGGATTGAGC | 1136 |
| 17 | 1060 | ATAGAGGGGTGGCCTAGGGGGTGTCTGCCGTTGAGGTCGTGTGGGTGGGGGTGGTGGGATTGAGC | 1126 |
| 16 | 1121 | ATAGAGGGGTGGCCTAGGGGGTGTCTGCCGTTGAGGTCGTGTGGGTGGGGGTGGTGGGATTGAGC | 1187 |
| 23 | 1045 | ATAGAGGGGTGGCCTAGGGGGTGTCTGCCGTTGAGGTCGTGTGGGTGGGGGTGGTGGGATTGAGC | 1111 |
| VDR | 1207 | ATAGAGGGGTGGCCTAGGGGGTGTCTGCCGTTGAGGTCGTGTGGGTGGGGGTGGTGGGATTGAGC | 1273 |
| 21 | 1050 | ATAGAGGGGTGGCCTAGGGGGTGTCTGCCGTTGAGGTCGTGTGGGTGGGGGTGGTGGGATTGAGC | 1116 |
| 14 | 1050 | ATAGAGGGGTGGCCTAGGGGGTGTCTGCCGTTGAGGTCGTGTGGGTGGGGGTGGTGGGATTGAGC | 1116 |
| 15 | 1049 | ATAGAGGGGTGGCCTAGGGGGTGTCTGCCGTTGAGGTCGTGTGGGTGGGGGTGGTGGGATTGAGC | 1115 |
| 13 | 1052 | ATAGAGGGGTGGCCTAGGGGGTGTCTGCCGTTGAGGTCGTGTGGGTGGGGGTGGTGGGATTGAGC | 1118 |

22 1043 ATAGAGGGGTGGCCTAGGGGGTGTGCCGTTGAGGTCGTGTGGGTGGGGGGTGGTGGGATTGAGC 1109
 19 1048 ATAGAGGGGTGGCCTAGGGGGTGTGCCGTTGAGGTCGTGTGGGTGGGGGGTGGTGGGATTGAGC 1114
 20 1049 ATAGAGGGGTGGCCTAGGGGGTGTGCCGTTGAGGTCGTGTGGGTGGGGGGTGGTGGGATTGAGC 1115
 7 1131 ATAGAGGGGTGGCCTAGGGGGTGTGCCGTTGAGGTCGTGTGGGTGGGGGGTGGTGGGATTGAGC 1197
 12 1282 ATAGAGGGGTGGCCTAGGGGGTGTGCCGTTGAGGTCGTGTGGGTGGGGGGTGGTGGGATTGAGC 1348
 3 1080 ATAGAGGGGTGGCCTAGGGGGTGTGCCGTTGAGGTCGTGTGGGTGGGGGGTGGTGGGATTGAGC 1146
 18 1019 ATAGAGGGGTGGCCTAGGGGGTGTGCCGTTGAGGTCGTGTGGGTGGGGGGTGGTGGGATTGAGC 1082

ApaI

4 1120 AGTGAGGTGCCAGCTGAGAGCTCCTGTGCCTTCTTCTATCCCCGTGCCACAGATCGTCTCTGG 1185
 9 1120 AGTGAGGGGCCAGCTGAGAGCTCCTGTGCCTTCTTCTATCCCCGTGCCACAGATCGTCTCTGG 1185
 2 1169 AGTGAGGTGCCAGCTGAGAGCTCCTGTGCCTTCTTCTATCCCCGTGCCACAGATCGTCTCTGG 1234
 1 1128 AGTGAGGGGCCAGCTGAGAGCTCCTGTGCCTTCTTCTATCCCCGTGCCACAGATCGTCTCTGG 1193
 10 1100 AGTGAGGGGCCAGCTGAGAGCTCCTGTGCCTTCTTCTATCCCCGTGCCACAGATCGTCTCTGG 1165
 8 1130 AGTGAGGTGCCAGCTGAGAGCTCCTGTGCCTTCTTCTATCCCCGTGCCACAGATCGTCTCTGG 1195
 6 1098 AGTGAGGTGCCAGCTGAGAGCTCCTGTGCCTTCTTCTATCCCCGTGCCACAGATCGTCTCTGG 1163
 11 1114 AGTGAGGGGCCAGCTGAGAGCTCCTGTGCCTTCTTCTATCCCCGTGCCACAGATCGTCTCTGG 1179
 5 1137 AGTGAGGGGCCAGCTGAGAGCTCCTGTGCCTTCTTCTATCCCCGTGCCACAGATCGTCTCTGG 1202
 17 1127 AGTGAGGTGCCAGCTGAGAGCTCCTGTGCCTTCTTCTATCCCCGTGCCACAGATCGTCTCTGG 1192
 16 1188 AGTGAGGGGCCAGCTGAGAGCTCCTGTGCCTTCTTCTATCCCCGTGCCACAGATCGTCTCTGG 1253
 23 1112 AGTGAGGGGCCAGCTGAGAGCTCCTGTGCCTTCTTCTATCCCCGTGCCACAGATCGTCTCTGG 1177
 VDR 1274 AGTGAGGGGCCAGCTGAGAGCTCCTGTGCCTTCTTCTATCCCCGTGCCACAGATCGTCTCTGG 1339
 21 1117 AGTGAGGGGCCAGCTGAGAGCTCCTGTGCCTTCTTCTATCCCCGTGCCACAGATCGTCTCTGG 1182
 14 1117 AGTGAGGGGCCAGCTGAGAGCTCCTGTGCCTTCTTCTATCCCCGTGCCACAGATCGTCTCTGG 1182
 15 1116 AGTGAGGTGCCAGCTGAGAGCTCCTGTGCCTTCTTCTATCCCCGTGCCACAGATCGTCTCTGG 1181
 13 1119 AGTGAGGGGCCAGCTGAGAGCTCCTGTGCCTTCTTCTATCCCCGTGCCACAGATCGTCTCTGG 1184
 22 1110 AGTGAGGGGCCAGCTGAGAGCTCCTGTGCCTTCTTCTATCCCCGTGCCACAGATCGTCTCTGG 1175
 19 1115 AGTGAGGGGCCAGCTGAGAGCTCCTGTGCCTTCTTCTATCCCCGTGCCACAGATCGTCTCTGG 1180
 20 1116 AGTGAGGGGCCAGCTGAGAGCTCCTGTGCCTTCTTCTATCCCCGTGCCACAGATCGTCTCTGG 1181
 7 1198 AGTGAGGTGCCAGCTGAGAGCTCCTGTGCCTTCTTCTATCCCCGTGCCACAGATCGTCTCTGG 1263
 12 1349 AGTGAGGGGCCAGCTGAGAGCTCCTGTGCCTTCTTCTATCCCCGTGCCACAGATCGTCTCTGG 1414
 3 1147 AGTGAGGTGCCAGCTGAGAGCTCCTGTGCCTTCTTCTATCCCCGTGCCACAGATCGTCTCTGG 1212
 18 1083 AGTGAGGGGCCAGCTGAGAGCTCCTGTGCCTTCTTCTATCCCCGTGCCACAGATCGTCTCTGG 1120

TaqI

4 1186 GGTGCAGGACGCCCGCGCTGATCGAGGCCATCCAGGACCGCCTGTCCAACACTGTCAGACGTACATC 1252
 9 1186 GGTGCAGGACGCCCGCGCTGATCGAGGCCATCCAGGACCGCCTGTCCAACACTGTCAGACGTACATC 1252
 2 1235 GGTGCAGGACGCCCGCGCTGATCGAGGCCATCCAGGACCGCCTGTCCAACACTGTCAGACGTACATC 1301
 1 1194 GGTGCAGGACGCCCGCGCTGATCGAGGCCATCCAGGACCGCCTGTCCAACACTGTCAGACGTACATC 1260
 10 1166 GGTGCAGGACGCCCGCGCTGATCGAGGCCATCCAGGACCGCCTGTCCAACACTGTCAGACGTACATC 1232
 8 1196 GGTGCAGGACGCCCGCGCTGATCGAGGCCATCCAGGACCGCCTGTCCAACACTGTCAGACGTACATC 1262
 6 1164 GGTGCAGGACGCCCGCGCTGATCGAGGCCATCCAGGACCGCCTGTCCAACACTGTCAGACGTACATC 1230
 11 1180 GGTGCAGGACGCCCGCGCTGATCGAGGCCATCCAGGACCGCCTGTCCAACACTGTCAGACGTACATC 1246
 5 1203 GGTGCAGGACGCCCGCGCTGATCGAGGCCATCCAGGACCGCCTGTCCAACACTGTCAGACGTACATC 1269
 17 1193 GGTGCAGGACGCCCGCGCTGATCGAGGCCATCCAGGACCGCCTGTCCAACACTGTCAGACGTACATC 1259
 16 1254 GGTGCAGGACGCCCGCGCTGATCGAGGCCATCCAGGACCGCCTGTCCAACACTGTCAGACGTACATC 1320
 23 1178 GGTGCAGGACGCCCGCGCTGATCGAGGCCATCCAGGACCGCCTGTCCAACACTGTCAGACGTACATC 1241
 VDR 1340 GGTGCAGGACGCCCGCGCTGATCGAGGCCATCCAGGACCGCCTGTCCAACACTGTCAGACGTACATC 1403
 21 1183 GGTGCAGGACGCCCGCGCTGATCGAGGCCATCCAGGACCGCCTGTCCAACACTGTCAGACGTACATC 1246
 14 1183 GGTGCAGGACGCCCGCGCTGATCGAGGCCATCCAGGACCGCCTGTCCAACACTGTCAGACGTACATC 1246
 15 1182 GGTGCAGGACGCCCGCGCTGATCGAGGCCATCCAGGACCGCCTGTCCAACACTGTCAGACGTACATC 1245
 13 1185 GGTGCAGGACGCCCGCGCTGATCGAGGCCATCCAGGACCGCCTGTCCAACACTGTCAGACGTACATC 1248
 22 1176 GGTGCAGGACGCCCGCGCTGATCGAGGCCATCCAGGACCGCCTGTCCAACACTGTCAGACGTACATC 1239
 19 1181 GGTGCAGGACGCCCGCGCTGATCGAGGCCATCCAGGACCGCCTGTCCAACACTGTCAGACGTACATC 1244
 20 1182 GGTGCAGGACGCCCGCGCTGATCGAGGCCATCCAGGACCGCCTGTCCAACACTGTCAGACGTACATC 1245
 7 1264 GGTGCAGGACGCCCGCGCTGATCGAGGCCATCCAGGACCGCCTGTCCAACACTGTCAGACGTACATC 1330
 12 1415 GGTGCAGGACGCCCGCGCTGATCGAGGCCATCCAGGACCGCCTGTCCAACACTGTCAGACGTACATC 1481
 3 1213 GGTGCAGGACGCCCGCGCTGATCGAGGCCATCCAGGACCGCCTGTCCAACACTGTCAGACGTACATC 1279
 18 1121 GGTGCAGGACGCCCGCGCTGATCGAGGCCATCCAGGACCGCCTGTCCAACACTGTCAGACGTACATC 1120

4 1253 C-GCTGCCGCCACCCGCCCCCGGGCAGCCACCTGCTCTA-TGCCAAGATGATCCAGA--GCTTAGGC 1315
 9 1253 C-GCTGCCGCCACCCGCCCCCGGGCAGCCACCTGCTCTA-TGCCAAGATGATCCAGA--GCTTAGGC 1315
 2 1302 CCCTGCCGCCACCCGCCCCCGGGCAGCCACCTGCTCTA-TGCCAAGATGATCCAGA--GCCTAACC 1365
 1 1261 C-GCTGCCGCCACCCGCCCCCGGGCAGCCACCTGCTCTA-TGCCAAGATGATCCAGATGGCTTTGCC 1325
 10 1233 C-GCTGCCGCCACCCGCCCCCGGGCAGCCACCTGCTCTA-TGCCAAGATGATCCAGA-GGCTTTGCC 1296
 8 1263 C-GCTGCCGCCACCCGCCCCCGGGCAGCCACCTGCTCTA-TGCCAAGATGATCCAGA-GCCTTAGCC 1326
 6 1231 C-GCTGCCGCCACCCGCCCCCGGGCAGCCACCTGCTCTA-TGCCAAGATGATCCAGA-GCTTTAGCC 1294
 11 1247 C-GCTGCCGCCACCCGCCCCCGGGCAGCCACCTGCTCTA-TGCCAAGATGATCCAGA-GGCTTAGCC 1310
 5 1270 C-GCTGCCGCCACCCGCCCCCGGGCAGCCACCTGCTCTA-TGCCAAGATGATCCAGA-GGCTTTACC 1333
 17 1260 C-GCTGCCGCCACCCGCCCCCGGGCAGCCACCTGCTCTA-TGCCAAGATGATCCAGA-GGCTTTGCC 1323
 16 1321 C-GTGGCCGCCACCCGCCCCCGGGCAGCCACCTGCTCTA-TGCCAAGATGATCCAGA-GGCTTTACC 1384
 23 1242 C-GCTGCCGCCACCCGCCCCCGGGCAGCCACCTGCTCTA-TGCCAAGATGATCC 1293
 VDR 1404 C-GCTGCCGCCACCCGCCCCCGGGCAGCCACCTGCTCTA-TGCCAAGATGATCCAGA--AGCTAGCC 1466

| | | | | |
|----|------|---------------------------------|------------------------------------|------|
| 21 | 1247 | C-GCTGCCGCCACCCGCCCGGGCAGCCACCT | GCTCTA-TGCCAAGATGATCCAGA--AGCTAGCC | 1309 |
| 14 | 1247 | C-GCTGCCGCCACCCGCCCGGGCAGCCACCT | | 1278 |
| 15 | 1246 | C-GTGCCGCCACCCGCCCGGGCAGCCACCT | GCTTTA-TGCCTAGGTGAAACAGT--ACCTAGCC | 1308 |
| 13 | 1249 | C-GTGCCGCCACCCGCCCGGGCAGCCACCT | GCTCTA-TGCCAAGATGA | 1297 |
| 22 | 1240 | C-GTGCCGCCACCCGCCCGGGCAGCCACCT | GCTC---GTCTAT-TGTCCTAA | 1289 |
| 19 | 1245 | C-GTGCCGCCACCCGCCCGGGCAGCCACCT | GCTCTA-TGACAAA-TGCTGTAGA--AGCTAGCC | 1306 |
| 20 | 1246 | C-GTGCCGCCACCCGCCCGGGCAGCCACCT | GCTCTTCTGATAAC-TGCTGTAGA--AG | 1302 |
| 7 | 1331 | C-GTGCCGCCACCCGCCCGGGCAGCCACCT | GCTCTA-TGCCAAGATGATCCAGA--GCTTAGGC | 1393 |
| 12 | 1482 | C-GTGCCGCCACCCGCCCGGGCAGCCACCT | GCTCTA-TGCCAAGATGATCCAGA--GCTTAGGC | 1544 |
| 3 | 1280 | C-GTGCCGCCACCCGCCCGGGCAGCCACCT | GCTCTA-TGCCAAGATGATCCAGA--GCTTAACC | 1342 |
| 18 | 1121 | C-GTGCCGCCACCCGCCCGGGCAGCCACCT | GC-GTATTGAGA | 1120 |

