

Primers used for PCR and Sanger sequencing of SHANK3 (for numbers of exons, see Durand et al Nat. Genet. 2007)

| EXONS | PRIMER F (TAG) | Distance between the primer and the exon (bp) | PRIMER R (TAG) | Distance between the primer and the exon (bp) | SIZE PCR |
|-------|---------------------------------------------|-----------------------------------------------|-----------------------------------------------|-----------------------------------------------|----------|
| 1B | TGTA AACGACGGCCAGTGCCTCCGTTCCCGGCGCGA | 50 | GGATAACAATTCACACAGGCCTCCGCGAACCGGGCCGAA | 210 | 323 |
| 2 | TGTA AACGACGGCCAGTGACCTGAGCTCACGAGCCCGCT | 31 | GGATAACAATTCACACAGGCCTGCCGTGCCCTTCACTGGTC | 85 | 320 |
| 3 | TGTA AACGACGGCCAGTTGCCGTTGGCCAGCATGAG | 98 | GGATAACAATTCACACAGGTCAGCCACACCCAGTACAGGCTCTG | 156 | 326 |
| 4/5 | TGTA AACGACGGCCAGTTGGAGTGCAGGACCGTGGTTGAC | 168 | GGATAACAATTCACACAGGTGAGCAGCTCAGTATCCACACCAG | 318 | 595 |
| 6/7 | TGTA AACGACGGCCAGTTCTGCCTGGTGTATGGGGCTGG | 66 | GGATAACAATTCACACAGGGCACACATGCAATCACCGTACAGG | 117 | 593 |
| 8 | TGTA AACGACGGCCAGTTGTGAGTCCGTGTGTGTGAGCCTG | 126 | GGATAACAATTCACACAGGGTGTCCCTTAGGGCTTCCAGGGA | 114 | 318 |
| 9 | TGTA AACGACGGCCAGTACGAAC TGAGAAGGAGCAG | 101 | GGATAACAATTCACACAGGCACCACTGACCCACATCT | 84 | 252 |
| 10 | TGTA AACGACGGCCAGTTTGCCTGGAACCAAGGCAGTTCC | 129 | GGATAACAATTCACACAGGTAGGCACCACCAGGCCTCTC | 106 | 509 |
| 11 | TGTA AACGACGGCCAGTGGCATCGCTCCGTACCTACGT | 35 | GGATAACAATTCACACAGGGAGGAGACCCAGGCCACTG | 104 | 332 |
| 12 | TGTA AACGACGGCCAGTTGGCAGAACCTGCTCCTGAGGTG | 79 | GGATAACAATTCACACAGGAAC TGAAGGGTGGTCCCCTTGG | 55 | 248 |
| 13/14 | TGTA AACGACGGCCAGTTGTGTGGCAGAGACTGGTGACC | 97 | GGATAACAATTCACACAGGGACATCCCTGAGCGGTGTGCA | 62 | 548 |
| 15/16 | TGTA AACGACGGCCAGTCCACCCGAACCTAGCTGGTGAAGC | 47 | GGATAACAATTCACACAGGTCTAGCACCAGGGATCGGGA | 178 | 584 |
| 17 | TGTA AACGACGGCCAGTTGGAGCGCAAGTGGCACCTGCA | 84 | GGATAACAATTCACACAGGCTGTCTTCTACCCTCTGGCTGGA | 122 | 287 |
| 18 | TGTA AACGACGGCCAGTGGCAGATTTGCTATTCACGG | 176 | GGATAACAATTCACACAGGGCTGGAACCTCCTCACACAC | 84 | 284 |
| 19 | TGTA AACGACGGCCAGTTGTTGGGAGGACATGGCAGTG | 71 | GGATAACAATTCACACAGGCATGGGGTGCACACACCCCTCTGGA | 128 | 330 |
| 20 | TGTA AACGACGGCCAGTCTAGTGCCATTGGAGTGGAGCGGTG | 109 | GGATAACAATTCACACAGGCTGGAACCCAGTTATGGGCAGAG | 113 | 307 |
| 21A | TGTA AACGACGGCCAGTTTGTGTCGGACGGTGGCTTCC | 151 | GGATAACAATTCACACAGGACGGAGCGAAGAGGCTGGCGCTGAA | - | 634 |
| 21B | TGTA AACGACGGCCAGTGCCTCCATGATCATCTGCA | - | GGATAACAATTCACACAGGTTTGCCGGTGAGTGGGTGGA | - | 634 |
| 21C | TGTA AACGACGGCCAGTGCCTCCATGCCATCCCTACAGC | - | GGATAACAATTCACACAGGCACAGCCGCTGACTGCATGG | - | 618 |
| 21D | TGTA AACGACGGCCAGTGTGGCCTCATCGTTGTGCACGCCA | - | GGATAACAATTCACACAGGTTGGGAGGCACTGGTGGCTTCTCGA | - | 626 |
| 21E | TGTA AACGACGGCCAGTAGGCTGACACACGACGCTCC | - | GGATAACAATTCACACAGGAGGCCAAGCAAGCCGATTCAG | 169 | 698 |
| 22A | TGTA AACGACGGCCAGTTTCTCTGGCCGGCTACTC | 131 | GGATAACAATTCACACAGGCATGGTCTCGAAGCGGTGCG | - | 604 |
| 22B | TGTA AACGACGGCCAGTTTCTGTGTGCGCAGCGTGTGAG | - | GGATAACAATTCACACAGGCCTCCGAGCAACAGCAAACAGGACGA | 144 | 468 |