**Sequences of primers for quadruplication structure identification and qPCR primers for copy number confirmation.**

|  |  |  |  |
| --- | --- | --- | --- |
| **Function** | **ID** | **Forward primer** | **Reverse Primer** |
| quadruplication verification by PCR | 1 | CGTAGCCAAAGTGAAAGGGAAGA | CTCTTTCCGTTCAAGTCGGTTTT |
| 2 | CATAGAAGGCAGCACCAGTTAGA | ACAGGTCCTCTGGTAACGGTAAG |
| copy number verification by qPCR | 1 | AACACGATAATGCTGCTAAAGATG | ATTTGCTGCTGATTGGAGTTATG |
| 2 | GGGAAAGCAACCAGGAGAAA | TGTGCCATTGTCAGTGAATAGT |
| 3 | GCCGCTTAAGTACCTGTGATAA | TGCGAGTATGTGCACTAGTTAAA |
| 4 | GCAAGGATACAGCGTGATAAGA | CTTCGGTCTCCTCGGTAGTAT |
| 5 | GGAGACCGAAGTGGTTAAGAAA | CCATTCTTCTTCCCTTTCACTTTG |

**Sequences of primers for *synV* SNVs/indels amplification and Sanger sequencing.**

|  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- |
| **Variant Target Region** | **Amplify\_forward**  **\_primer** | **Amplify\_reverse**  **\_primer** | **Synthetic**  **Amplicon Size (bp)** | **Variant Amplicon Size (bp)** | **Digestion Enzyme** |
| 1 | CCGTTCTATACATCCGTGTAACTTA | AGTGCTGGGTAGTCTGATTATGG | 890 | 4148 | - |
| 2 | TTGAATGGCAACTGTAGTGAGGT | CACTTGGCTCGACTACCTTTACC | 1944 | 2071 | - |
| 3 | CAACCATCGGCTACAAACCAAAT | TGATGTTACTATGCCGCCAATTA | 670 | 636 | *Bsr*GI |
| 4 | ACCATTTCGACGACTTAGTTC | GATAATCTCACCGTTGGGTAGCA | 833 | 833 |  |
| 5 | TCTATCTGGATTATTAAAGGCTGCTC | TAGACTGGTCTGAAGAGGGAGATG | 1253 | 1253 | - |
| 6 | CCAATACTGCCATTACGGATACAA | AGCAGCGTCCAATCAAGCCCTAA | 1048 | 1048 | - |
| 7 | ATGGCTCGTTAATTGCCCTGTCG | TATGTTGTTGTTCGGTCCTCCTG | 1279 | 1245 | *Bsr*GI |
| 8 | GCGTTTCCGTCGCACAGTAAGAG | AGAACCTCCTAAAGAATAGAACTG | 1054 | 1054 | - |
| 9 | AGTTCTTCCTGAGATTTAGCCTTTG | CGTCATCTTTCACTACCCTTTAC | 789 | 789 | *Bsl*I |
| 10 | AGGTCCTTATGATGACAGATTGG | GTTTTGTTCTGTTCTTTGAAGCCA | 822 | 822 | *Bsa*BI |
| 11 | TTGCTATTCCCACTGCCATCTAA | AAGGATGAGACGCAGATACGAAA | 995 | 995 | - |
| 12 | CGAACTGTATTTAGTAGACTCCCTT | AACTCCTTCTCATTTCCGTCTTT | 955 | 955 | - |
| 13 | ACCTGGAGGAGTTGGGCTTGACA | ATCGTTCGGTCTAATGATGAGGA | 1642 | 1642 | *Bsa*AI |
| 14 | CCTATCCCTTATCCAGAACAACC | CTAACCTTTGGAGCACCACTGAC | 620 | 620 | *Tsp*DTI |
| 15 | GCCTTCCCACCGCCTTGGTTGTT | AAACTTATCACAGCCGCTATTCA | 1910 | 1910 | *Rsa*I |
| 16 | AGGAACTGGGACGCTCAAGACGC | TTTAGTCCACATCCACCAACCAC | 822 | 822 | - |
| 17 | TAGATAAGGGACCTGACTGAGCG | GTGCTGGTCTGATCTTCAAACACTACG | 768 | 768 | *Sfi*I |
| 18 | ACCGACTTCGCCAGTTCGTAAGG | ACTTCCACTTGATGTCGCCCAAA | 892 | 892 | *Blp*I |
| AG1 | CGTAGCCAAAGTGAAAGGGAAGA | AGCGGTGATATTATGGAATGTATGG | 883 | 883 | *Alu*I |
| AG2 | AATGAACTAAAGCACGGATCTAACA | AAGCCGTCTACAATAACGTCAGG | 974 | 974 | *Bse*8I |
| AG3 | GCTACTGTTATCACGGCTATGTCTA | GAACTTGATTCTTTGACGGGTTTG | 926 | 926 | *Mae*III |
| AG4 | TGGTGGTGAAGGGAAAGTAGCAT | GCCCGATGACTACGAGGCTAT | 1163 | 1163 | *Spe*I |

**Sequences of site-specific primers.**

|  |  |  |  |  |
| --- | --- | --- | --- | --- |
| **Variant Target Region** | **YS-CPCR\_forward**  **\_synthetic\_primer** | **YS-CPCR\_reverse**  **\_synthetic\_primer** | **YS-CPCR\_forward**  **\_variant\_primer** | **YS-CPCR\_reverse**  **\_variant\_primer** |
| 1 | CCGTTCTATACATCCGTGTAACTTA | AGTGCTGGGTAGTCTGATTATGG | --- | --- |
| 2 | TTGAATGGCAACTGTAGTGAGGT | CACTTGGCTCGACTACCTTTACC | --- | --- |
| 3 | ATTAAAGAGTTGGGAAATCATAGATTGTAa | TGGTAGTAAGCACGGTTAGTTATAATT | ATTAAAGAGTTGGGAAATCATAGATTGTAg | --- |
| 4 | TCATTTGAGATTCAAGGCTTAAAGACAG | ACCCTGTGGTACTACTGCCa | --- | ACCCTGTGGTACTACTGCCC |
| 5 | TCTTAAGTTTTGCTGTCGCTATTTc | TAGACTGGTCTGAAGAGGGAGAT | TCTTAAGTTTTGCTGTCGCTATTTt | --- |
| 6 | CCTCCATCCCAGAAGAACAACTA | TTGATTTTTTTGGCTTTGTTTGTTGTc | TTGATTTTTTTGGCTTTGTTTGTTGTg | --- |
| 7--1 | CCTACGACCAGTCATGGATTAGATTAa | CTTCACAATTCGGATCATCAGGT | CCTACGACCAGTCATGGATTAGATTAg | --- |
| 7--2 | CTAAAGACGTTATATCACTTCCTGAATAa | CCAATGGCGACGAAGATGAc | CTAAAGACGTTATATCACTTCCTGAATAg | CCAATGGCGACGAAGATGAT |
| 7--3 | CCGCTGCtgaacttaaactgc | TATGTTGTTGTTCGGTCCTCCTG | CTGCgctggacaaggatga | --- |
| 8 | GTACTCTTCGCGCTCATAGTc | ATACGTGGGATAGTTGGAGAACA | GTACTCTTCGCGCTCATAGTa | --- |
| 9 | CTGGAGGGCCGCAAAATc | TGGCTTGCTAATTTCATCTTATCCT | CTGGAGGGCCGCAAAATg | --- |
| 10 | TCAGCCCCTTTCACTAGATATCAAg | GTAAACGGCTTCTTAGGCTTACAT | TCAGCCCCTTTCACTAGATATCAAt | --- |
| 11 | GCCTGGTGTCAACTCGCc | TTGGTATCGCCATTGGAACAG | GCCTGGTGTCAACTCGCa | --- |
| 12 | CGAACTGTATTTAGTAGACTCCCTTT | TGACCAATGAAACGGTCAAGTTc | TGACCAATGAAACGGTCAAGTTt | --- |
| 13--1 | GTTGGGCTTGACATTATGGAGTAT | TGATAAACCACTCTAGTTCTACAACTACTACc | --- | TGATAAACCACTCTAGTTCTACAACTACTACa |
| 13--2 | GTGGGAGATCCATAAAGGTATAAGA | CGTCGTAGCAGCTTTAATGTTTCAa | --- | CGTCGTAGCAGCTTTAATGTTTCAc |
| 14 | TTGTTTGGATTTCCAAATCATTGGTg | CGTCGTCCTCTTCAGTAGTAGCC | TTGTTTGGATTTCCAAATCATTGGTt |  |
| 15--1 | TTGGTTGTTCTTTGGGAGTGC | CCTAAATCTTTAGTTTTTGATTCACAAGa | --- | CCTAAATCTTTAGTTTTTGATTCACAAGc |
| 15--2 | TTGAGCTGCGAGAGTGTGGg | GCGTAATTCCCTTCTGCTTACACT | TTGAGCTGCGAGAGTGTGGa | --- |
| 16 | AATCCTCGTGCAAGCCATCA | TGATAGTTCAAGAGGTTCTAAGGGg | --- | TGATAGTTCAAGAGGTTCTAAGGGt |
| 17 | TGGCTTGGGCCACAAGg | CAAACGACAACGGTATTAGCAAG | TGGCTTGGGCCACAAGc | --- |
| 18 | CGGTGAACAGTGGTACGAAA | CTGTATTTAGGAACTAAGATTTTgctaagc | --- | CTGTATTTAGGAACTAAGATTTTTgagagt |
| TAG1 | GTGAAAGGGAAGAAGAATGGTTGG | TAGAGCCTTTGTGGAACCAAATTAa | --- | TAGAGCCTTTGTGGAACCAAATTAg |
| TAG2 | GCGAAATCTGGCGACCAATAC | GAACCAAGTATCCAAAGCCTTGTAa | --- | GAACCAAGTATCCAAAGCCTTGTAg |
| TAG3 | GTTATATCCGAGAACAATAGAACTGCTT | CTGTCGAGCGAAAACAACAAGTAa | --- | CTGTCGAGCGAAAACAACAAGTAg |
| TAG4 | AAAAGGTATTACCGATTCAAGTGACTAa | GATAATGGATCTGAAACCGAGCA | AAAAGGTATTACCGATTCAAGTGACTAg |  |