**Supplementary material 1.** VP1 mutation analysis.

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| **JCV VP1 primers set** | **Published mutations** |
| BC loop | 5’ ACCCCGTGCAAGTTCCAAAA 3’5’ TTAAGGTCACAGCCTCCCAC 3’ | L55F, K60E/N/M, S61P/T,D66H/N | not present |
| HI loop | 5’ TTTGGTGTTGGGCCACTTTG 3’5’ ATGCCATACATAGGCTGCCC 3’ | N265S/D/T, S267F/L/T, S269F/Y/C, Q271H | not present |
| C - terminus | Set 1:5’ CTCCTAGAGTTGATGGGCAGC 3’5’ CTGCAAATGTTAAGTAAAGCTGGT 3’Confirming Set 2:5’ GACTCCTAGAGTTGATGGGCAG 3’5’ CAAAGACCCCTCCCCCAAAATA 3’ | In-frame and out-of-frame deletions, duplications, mutations termed JCVGCN1-8 | not present |
| **New mutation (JCVGCN9)** |
| 7th position after VP1 C-terminus(ATA Isoleucine/I to AAA Lysine/K) |

To amplify the fragments around mutations L55 (BC loop) and S267/S269 (HI loop) in JCV VP1 region, we have designed two pairs of primers flanking size of 291 bp and 230 bp respectively. For BC loop, forward primer: 5’ ACCCCGTGCAAGTTCCAAAA 3’, reverse primer: 5’ TTAAGGTCACAGCCTCCCAC 3’. For HI loop, forward primer: 5’ TTTGGTGTTGGGCCACTTTG 3’, reverse primer: 5’ ATGCCATACATAGGCTGCCC 3’. Two sets of primers were used for PCR VP1 C-terminus: Set 1 forward primer: 5’ CTCCTAGAGTTGATGGGCAGC 3’; set 1 reverse primer: 5’ CTGCAAATGTTAAGTAAAGCTGGTT 3’; set 2 forward primer: 5’ GACTCCTAGAGTTGATGGGCAG 3’; set 2 reverse primer: 5’ CAAAGACCCCTCCCCCAAAATA 3’. Viral genome DNA was extracted from the patient’s frozen plasma and CSF using QIAamp MiniElute Virus Spin Kit (Qiagen GmbH, Hilden, Germany) and PCR products were amplified with GoTag Green [Promega (Madison, WI)] with 5-10 µl of JCV virus. PCR program was as follows: 94 oC 2’, then 50 cycles at 94 oC 20 second, 56 oC 30 second, 68 oC 1’ due to low yield of JCV virus DNA from patient’s plasma and CSF. After amplifying both BC loop and HI loop fragments of JCV VP1 region, we detected 291 bp and 230 bp PCR products respectively from both plasma and CSF. For the C-terminus PCR, we detected 243 bp and 218 bp PCR products respectively using the two different sets of primers in plasma and CSF. The sequencing was done on these purified PCR fragments. Sequencing was repeated twice with fresh PCR fragments to eliminate any PCR errors during PCR or sequencing.