

Additional file 4: Comparison of predictions of solo LTR and provirus from *f indsoloLTR* and *findprovirus* pipelines to PCR based genotypes for solo LTR (S) and provirus (P) polymorphisms

18q21.1_W2 (Ref. allele: Solo LTR)	Individuals <i>findprovirus</i> PCR	S_Mala-2 S/S	S_Mala-3 P S/P	S_Kapu-1 P S/P	S_Kapu-2 P S/P	S_Yadava-1 P S/P	S_Yadava-2 P P/P	S_Relli-1 P S/P
4q22.1_H8 (Ref. allele: Solo LTR)	Individuals <i>findprovirus</i> PCR	S_Madiga-2 P P/P	S_Kapu-1 P S/P	S_Kapu-2 P S/P	S_Brahmin-2 P S/P	S_Mala-2 P P/P	S_Yadava-1 P S/P	
5p15.31_H2 (Ref. allele: Solo LTR)	Individuals <i>findprovirus</i> PCR	S_Madiga-2 P* P	S_Yadava-1 P* P	S_Brahmin-1 P	S_Brahmin-2 P	S_Mala-2 P* P	S_Kapu-1 P	
5p13.3_K2 (Ref. allele: Provirus)	Individuals <i>findsoloLTR</i> PCR	S_Brahmin-1 S\$ S/P	S_Brahmin-2 S\$ S/P	S_Relli-1 S\$ S/S	S_Irula-2 S\$ S/P	S_Yadava-1 S/P	S_Yadava-2 S\$ S/P	S_Luhya-2 S\$ S/P
2q34_H4 (Ref. allele: Provirus)	Individuals <i>findsoloLTR</i> PCR	S_Madiga-2 S S/P	S_Kapu-1 P/P	S_Kapu-2 P/P	S_Mala-2 P/P	S_Mala-3 P/P		
3p14.3_H1 (Ref. allele: Provirus)	Individuals <i>findsoloLTR</i> PCR	S_Luhya-2 S S/P	S_Madiga-2 P/P	S_Mala-2 P/P	S_Mala-3 P/P	S_Yadava-1 P/P	S_Brahmin-1 P/P	S_Kapu-1 P/P

Footnotes: 'S' denotes solo LTR and 'P' denotes Provirus. *no of discordant reads identified were less than 4. \$ The Percentage Read Depth criteria in those individuals are between 51-60.