



**Figure S2: Analysis of viral sequences from SFV-infected human LOBAK2.**

Uncultured PBMCs and saliva samples from LOBAK2 hunter accidentally infected by a *Gorilla gorilla* SFV strain were analyzed for the presence of SFV sequences. A total of 18 and 20 different PCR-derived clones are depicted for saliva (red) and PBMCs (blue) samples respectively. Their consensus sequences (PBMC-cons1, SALIVA-cons and PBMC-cons2 respectively) are also depicted. The 8 reference SFV sequences available in GenBank from gorillas of the *Gorilla gorilla* species are aligned (green). 4 G-to-A mutations found in a GG dinucleotide context and absent in the gorilla sequences are highlighted in blue and 4 other mutations between PBMCs and saliva clones also present in some gorilla sequences were highlighted in grey. Sequences are aligned to the consensus sequence of PBMC samples, which served as a reference due to its high similarity with the gorilla strains. The 425bp-fragment of the *pol-in* sequence is shown. Due to the low SFV viral load, LOBAK2 clones of each cluster might derive from one to few *in vivo* SFV copies.



