

Figure S1

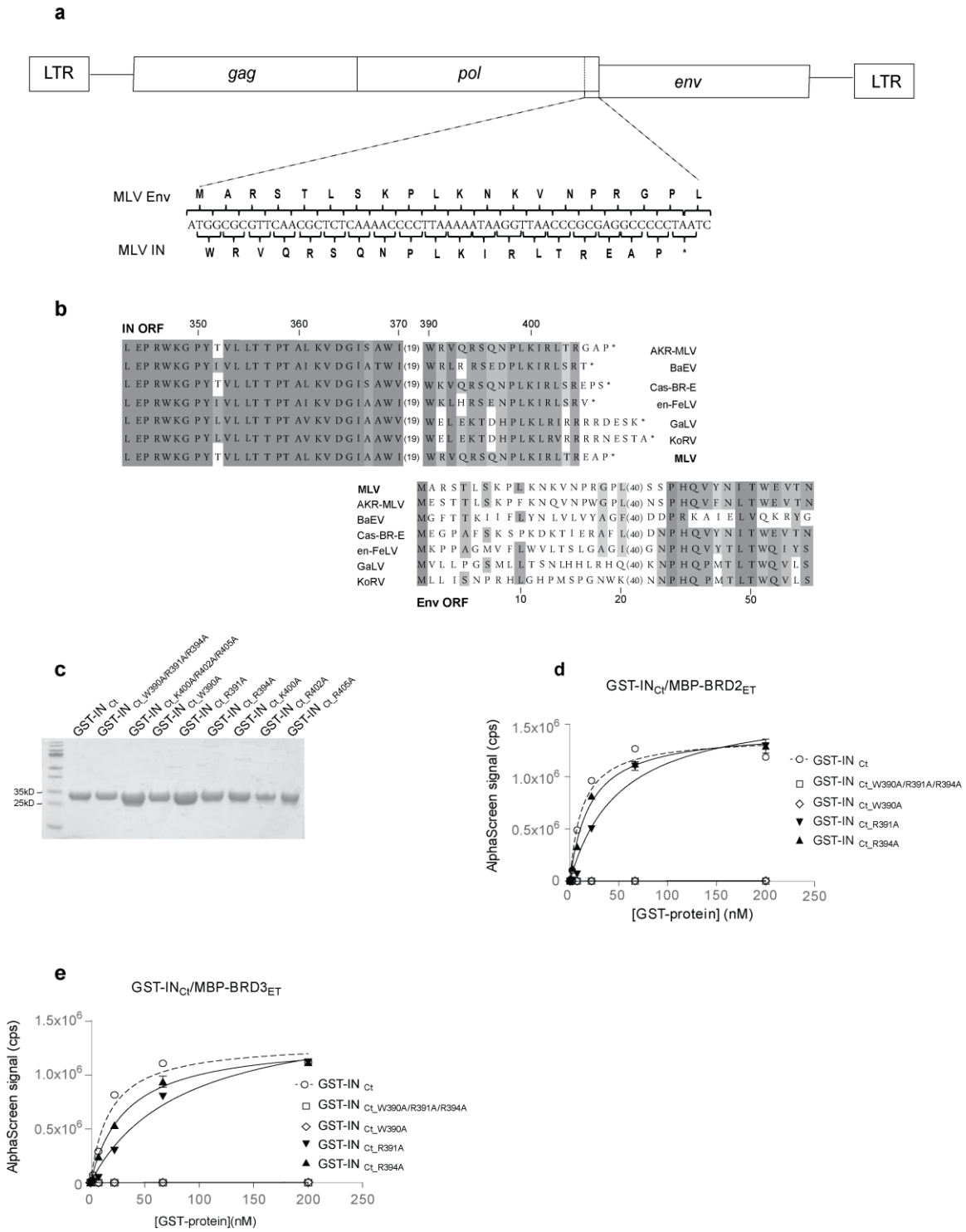


Figure S1: Characterization of the MLV-BET interface

(a) Schematic representation of the MLV genome encoding *gag*, *pol*, and *env* flanked by the long term repeats (LTRs). The C-terminal IN and N-terminal Env open reading frames are shown.

(b) Sequence alignment of the overlapping motifs in the IN open reading frame (upper panel) and Env open reading frame (lower panel) for different gammaretroviruses. MLV; murine leukemia virus (P03355), AKR-MLV; AKR murine leukemia virus (P03356), BaEV; Baboon endogenous virus (P10272), Cas-BR-E; Cas-Br-E murine leukemia virus (P08361), en-FeLV; endogenous feline leukemia (P10273) virus, GaLV; Gibbon ape leukemia virus (P21414), KoRV; Koala retrovirus (Q9TTC1). Protein sequences were downloaded from the UniProt database, aligned with t-coffee software and manually refined. ORF; open reading frame.

(c) Coomassie-stained SDS-PAGE of recombinant GST-tagged MLV mutant peptides. Expected protein size is ca. 31 kDa.

(d-e) Interaction of 2nM of the MBP-fused ET domain of BRD2 (d) and BRD3 (e) with increasing amounts of the GST-fused MLV integrase C-terminal tail (amino acids 381-408) (GST-IN_{Ct}) or its derived mutants as measure by AlphaScreen. Representative experiments are shown. Error bars indicate the standard deviations of triplicate data points.