Supplemental Figure 1 Structural Alignment of HIV-1, ASV, and MPMV IN

A structural alignment of HIV-1, ASV and MPMV integrases (Snasel, Krejcik et al. 2005) was used to identify amino acid residues near the LTR DNA ends in the structural model that were unique at structurally conserved positions. The residues from this analysis are in addition to those that were previously studied (Chen, Weber et al. 2006). Residues highlighted in blue and green were analyzed by Aiping Chen while those highlighted in yellow were analyzed by James Dolan. HIV-1 IN chimeras were assembled by substitution of the ASV amino acid residue into the structurally related position of HIV-1 IN and assayed for 3' processing as described in the Materials and Methods.

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             1        10        20        30        40
                      |         |         |         |
hivin      --FLDGIDKAQEEHEKYHSNWRAMASDFNLPPVVAKEIVASCDKCQLKG
asvin      -----PLREAKDLHTALHIGPRALSKACNISMQQAREVVQTCPHCNSAP
mpmvin     SNINTNLESAQNAHTLHHLNAQTLRLMFNIPREQARQIVKQCPICVTYL

             50
             |
hivin      EAMH-GQV--DCSP-
asvin      ALEA-GVNPRGLGPL        N-TERMINAL DOMAIN
mpmvin     PVPHLGVNPRGLFPN

            60          70          80        90       100
            |           |           |         |         |
hivin      GIWQLDCTHLE--G--KVILVAVHVASGYIEAEVIPAETGQETAYFLLKLAGRW
asvin      QIWQTDFTLEPRMAPRSWVAVTVDTASSAIVVTQHGRVTSVAAQHHWATAIAVL
mpmvin     MIWQMDVTHYSEFGNLKYIHVSIDTFSGFLLATLQTGETTKHVITHLLHCFSII

            110       120       130       140       150       160
             |         |         |         |         |         |
hivin      -PVKTVHTDNGSNFTSTTVKAACWWAGIKQEFGIPYNPQSQGVIESMNKELKKI
asvin      GRPKAIKTDNGSCFTSKSTREWLARWGIAHTTGIPGNSQGQAMVERANRLLKDR
mpmvin     GLPKQIKTDNGPGYTSKNFQEFCSTLQIKHITGIPYNPQGQGIVERAHLSLKTT

                    170             180       190
                     |               |         |
hivin      IGQVR--DQAE------HLKTAVQMAVFIHNFKRKGGIGGY
asvin      IRVLAEGDGFMKRIPTSKQGELLAKAMYALNHFERGENTK-   CATALYTIC
mpmvin     IEKIKKGEWYPRK---GTPRNILNHALFILNFLNLDDQNK-   CORE DOMAIN

               200       210       220
                |         |         |
hivin      SAGERIVDIIATDIQTKELQKQITKI
asvin      TPIQKHWRPTVLT-------------
mpmvin     SAADRFWHNNPKK-------------

                   230       240       250         260       270
                    |         |         |           |         |
hivin      QNFRVYYRDSRDPVWKGPAKLLWKGEGAVVIQD-N-SDIKVVPRRKAKIIRD
asvin      EGPPVKIRIET-GEWEKGWNVLVWGRGYAAVKNRDTDKVIWVPSRKVKPDIT
mpmvin     QFAMVKWKDPLDNTWHGPDPVLIWGRGSVCVYSQTYDAARWLPERLVRQVSN

hivin      YGKQMAGDD-----CVASR-----QDED      C-TERMINAL DOMAIN
asvin      QKDEVTKKDEASPLFAGSSDWIPWGDEQEGLQEEAASNKQEGPGEDTLAANES
mpmvin     NN---QSRE
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