

**A**

	<i>gag</i> plus	<i>gag</i> cdNA	<i>gag</i> minus (rev. compl.)
	GGCCATC-AGAGTCTAAACCACG		GGTCCGAAGAAATAGGGCTGC
c1_A	.....-.....	yes	.....
c1_B	.....-.....T.	yes	.....
c1_C	.....T-.....	yes	.....
c3_A	.....-.....	yes	.....A.....
c3_B	.....-.....	yes	.....
c3_C	.....-.....T.	yes	.....
c3_D	.....-.....	yes	.....T.....
c3_E	.....-.....	yes	.....
c4_A	.....-.....C.....	yes	.....
c5_A	.....-.....	yes	.....
c6_A	.....-.....	yes	.....
c7_A	.....-.....	yes	.....
c7_B	.....-.....	yes	.....
c7_C	.....-.....	yes	.....T.....C.....
c8_A	.....-.....	yes	.....
c10_A	.....-A.....	yes	.....T.....
c10_B	.....-.....G.....	yes	.....
c11_A	.....-.....T.	yes	.....
c11_B	.....-.....	yes	.....
c12_A	.....-.....		.....A.....
c19_A	-----		-----
c21_A	.....C-.....	yes	.....A.....
c22_A	.....-.....	yes	.....
1p36.21	...T.C-...C.....C		..CAT...A...CA...AT
1p36.21	...T.C-...C.....A		..CA...A...CA...AT
3p12.3	.....-.....T.G...T.		..AT.G.A...CA...AT
3q12.3	.....-.....		..A...A...CA...A.
4p16.2	.....-.....T.G.....		..AT...A...CA...A.
4p16.3	-----		..A...A...CA...A.
4p16.1	.....-.....T.G...A.		..AT...A...CA...A.
4q32.2	.....-.....		.....
5p11	.....A-...CA.....T.		.....
5p13.3	.....T-.....T.		.....
5q33.2	..T-.....T.....		..AA.G.A...CA...A.
6p21.1	.....-.....C.....		..A...A...CA...T.A.
6p11.2	.....T-G.G.CTA.....A		-----
6p22.1	...G-.....A		..A...A...A.....
8p22	-----		A.AT.A...A...CC.T....
8p23.1	.A.....-.....T.G.A....		..A...A...CA...A.
8p23.1	.A.....-.....T.G.....		..A...A...CA...A.
8p23.1	.....-.....T.G.....		..A...A...CA...A.
8q11.1	...T.T-G.G.CTA.....		-----
8q24.3	.....-.....		.....
8q24.3	.....-.....T.G.....		..A.G.A...CA...A.
9q34.11	.....T-G.G.CTAC.....A		-----
9q34.3	.....-.....		.....A.....
11p15.4	.....-.....T.G.....		.C.A...A...CA...A.
11q12.1	.....TTG.G.CTA.....G.		-----
11q12.3	.....-.....T.....		...T...T.....
12q24.33	...TG.T-G.G.TA...G...		-----
14q11.2	.T.....-.....T.G.....		..AT.G.A...CA...A.
16p13.3	.....-.....A		-----
17p13.1	-----		A.AT...A...CC.T....
19p12	.....-.....		.....
19p12	.....-.....T.		...A.A.....
19p12	.....-.....		T...T.....
19q12	.....-.....		.....
19q13.12	.....-.....		...A.A.....
19q13.41	...T...A-G.G.CTA.....		-----
20q11.22	.....-.....C.....		.A...C.A...C...
22q11.23	.....-.....C.....		..A...A...CA...A.
Xq28	...G-...G.CTA.....		.....
Yp11.2	.....-.....T.G...G.T.		T...A.AG.A...CA...A.

## B

	env8146f	env cDNA	env8665r (rev. compl.)
	AATGAGTCTGAGCATCACTGGG		CTGTGTC-CACTCAGAGTTGAATGG
c1_A	.....	yes	.....-A.....A.....
c1_B	.....	yes	.....-A.....G.....
c1_C	.....		.....AA.....G.....A.....
c3_A	.....	yes	.....-.....G.....A.....
c3_B	.....	yes	.....-A.....A.....
c3_C	.....A.....	yes	.....-A.....
c3_D	-----		-----
c3_E	.....		..C.....-A.....A.....
c4_A	.....		.....-A.....G.....A.....
c5_A	.....	yes	.....-A.....G.....
c6_A	.....	yes	.....-A.....A.....
c7_A	.....	yes	.....-.....
c7_B	GT..G.CGCC..ATGT.GG..-		-----
c7_C	GG.TG.G.GCCAG..G.AG..-		-----
c8_A	.....C.....		.....-A.....G.....
c10_A	.....	yes	.....-A.....G.....A.....
c10_B	-----		-----
c11_A	.....	yes	.....-A.....
c11_B	.....		.....AA.....G.....A.....
c12_A	.....	yes	.....-A.....A.....
c19_A	.....A.....A.....	yes	.....-.....G.....
c21_A	.....A.....A.....	yes	.....-A.....
c22_A	.....	yes	.....-A.....A.....
1p36.21	.....A.....		T...A.G-G.A...GAG...T.G..
1p34.3	.....		.....-G.....AG...T.....
1q21.2	-----		-----
1q24.1	.....		T...-A.G-G.A...AG...T.G..
1q32.2	.....		.....-A.....G.....A.....
1q43	.....		.....A.G-G.A...AG...T.G..
2q21.1	.....		.....AA.....G.....A.....
2q32.1	.....		.....-.....AGA...T.....
3p12.3	-----		T...A.G-A.A...AG...T.G..
3p12.3	TGATG..TCC...ATGGAAAA		-----
3p12.3	..C..A.....A.....		T...A.A-A.A...AG...T.G..
3q12.3	.....		.....AA.....G.....A.....
3q21.2	-----		T...A.G-A.A...AG...T.G..
4p16.2	.....A.....A.....		-----
4p16.2	-----		T...A.G-A.A...AG...T.GAC
4p16.1	-----		T...A.G-A.A...AG...T.G..
4p16.1	-----		T...A.G-A.A...AG...T.G..
4p16.1	.....A.....A.....		T...A.A-A.A...AG...T.G..
5p11	.....A...T...G..T..		.....-A.....G...AC....
5p13.3	.....		.....-A.....A.....
5q33.2	.....A.A.....A.....		T...CA.G-A.A...AG...T.G..
6p22.1	.....		.....T-G...AG...T.G..
6p21.1	.....		T...A.G-G.A...AG...T.G..
6p11.2	-----		T...A.A-A.A...AG...T.G..
6q25.1	.....C.....C.....		.....A...-A.A...AG...T.....
7q11.21	.....C.....A.....A.....		T...A.G-G.A...AG...T.G..
8p22	.....TTA...A...G....		-----
8p23.1	-----		T...A.G-A.A...AG...T.G.C
8p23.1	-----		T...A.G-A.A...AG...T.G.C
8p23.1	.....A.....A.G.....		T...A.A-A.A...AG...TG.G..
8p23.1	-----		T...A.G-A.A...AG...T.G.C
8p23.1	.....A.....A.G.....		T...A.A-A.A...AG...TG.G..
8p23.1	.....A.....A.G.....		T...A.A-A.A...AG...TG.G..
8q11.1	.....A.....A.....		T...A.G-G.A...AG.C.T.G..
8q24.3	.....		.....-A.....A.....
8q24.3	.....A.....A.....		T...A.G-A.G...AG...T.G..
9q34.11	.....A.....A.....		T...C.G-G.A...AG...T.G..
9q34.3	-----		.....T-A...AG...TG.G..
11p15.4	.....AC...A.....		T...C.A-A.A...AG...T.G..
11q12.1	.....A.....		T...A.G-G.A...AG...T.G..
11q12.3	-----		TC...A.G-A.A...AG...T.G..
11q13.2	-----		TC...A.G-A.A...AG...T.G..
11q13.4	-----		T...A.G-A.A...AG...T.G..
12q24.33	.....A.....A.....		T...A.A-A.A...AT...T.G..
14q11.2	-----		T...A.G-A.A...AG...T.G..
16p11.2	.....		.....-A.....A.....
16p13.3	TCCCC.G...GCTCAGT.A.T-		-----
19p12	.....		.....-A.....
19p12	.....		.....T-G.T...AG...T.....
19p12	.....		.....-A.....G.....A.....
19p12	.....		.....T-G...AG...T.....
19q12	.....		.....-A.....A.....
19q13.12	.....		-----
19q13.41	.....T.....		.....A.T-G.A...AG...T.....
20q11.22	.....		.....A.T-G...AG...T.....
22q11.23	.....		.....-.....AG...T.G..
Yp11.2	.....A...A.A.....		T...A.G-G.A...AG...A.G..

Flockerzi et al. Additional Figure 2: Sequence comparison of PCR primers for amplification of HML-2 *gag* (A) and *env* (B) cDNAs with primer binding regions in HML-2 proviral loci. Proviral loci were included when at least one primer binding region was present. HML-2 loci identified as transcriptionally active are listed first, followed by loci not identified as active in this study. Locations of the latter are given as chromosomal bands. Reverse primer sequences have been reverse-complemented. "yes" indicates that the corresponding HML-2 locus has been found transcriptionally active by detection of its *gag* and/or *env* cDNA. Note that locus c19\_A consists only of *env*-LTR portions, and that loci c3\_D and c10\_B lack relevant *env*-LTR portions (see Additional Fig. 1).