

SUPPLEMENTARY MATERIALS

Expression of human endogenous retrovirus group K (HERV-K) HML-2 correlates with immune activation of macrophages and type I interferon response

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List of supplementary tables (Excel files)

Supplementary Table S1. Log₂(fold-change) and false-discovery rate adjusted p-value following macrophage M1 (LPS + IFN γ), M2 (IL10), and M2 (IL4) polarization for retroelements and HML-2 loci.

Supplementary Table S2. Comparison of FGL1 and HML2_8p22 expression in primary MDMs and TDMs.

Supplementary Table S3. Log₂(fold-change) and false-discovery rate adjusted p-value following TLR agonist (top) or IFN (bottom) treatment for retroelements and HML-2 loci.

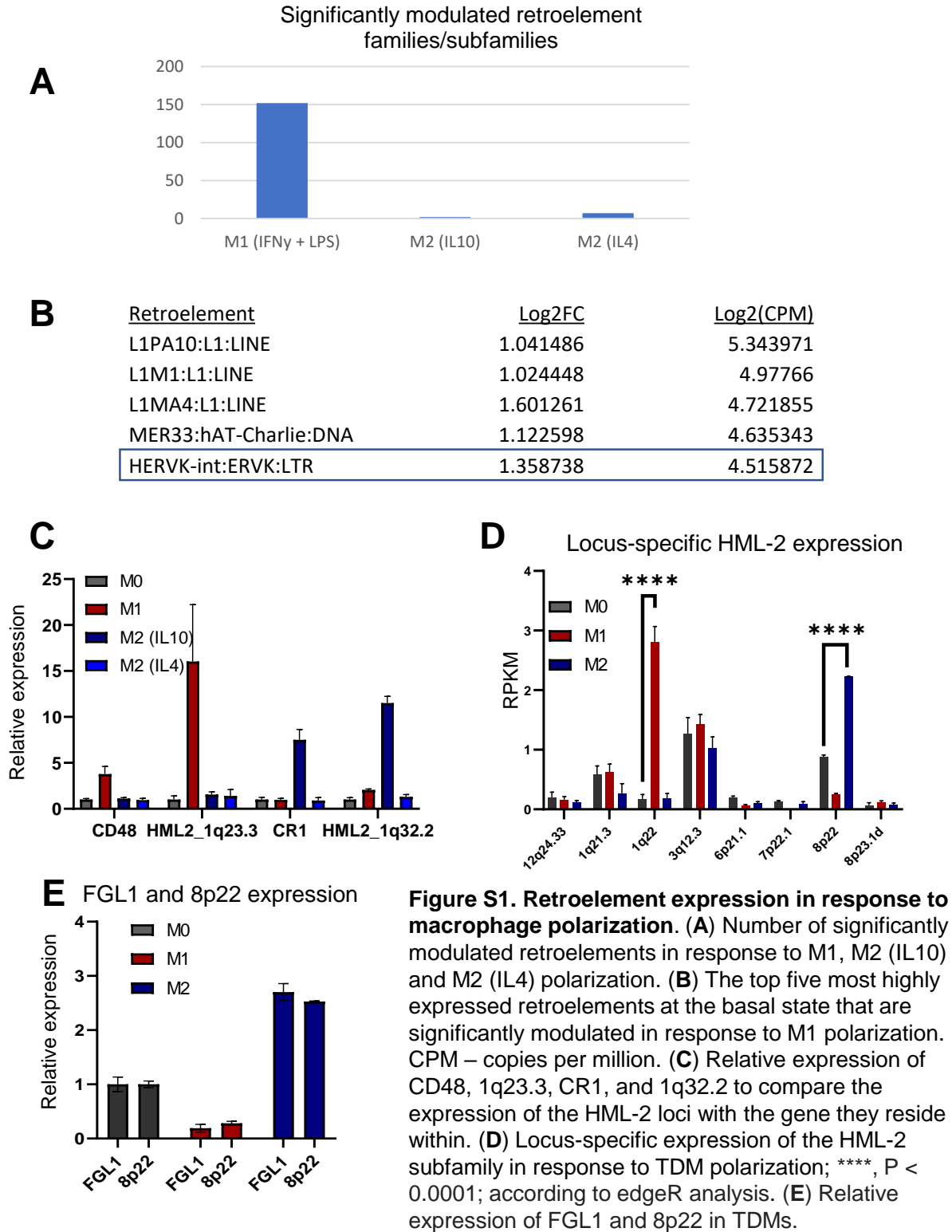
Supplementary Table S4. CPM values and relative expression of genes which 1) contain a GAS but not an ISRE site, 2) contain an ISRE but not a GAS site or 3) contain both GAS/ISRE sites.

Supplementary Table S5. Predicted transcription factors binding sites (TFBSs) by the PROMO software algorithm in LTR12F, the 5'LTR of 1q22, and the 5'LTR of 3q12.3.

Supplementary Table S6. Predicted targets of the HML-2-shRNA; Genome analysis data.

Supplementary Table S7. Reagents and resources.

Supplementary figures



P value for correlation:
7.60552885105501e-007

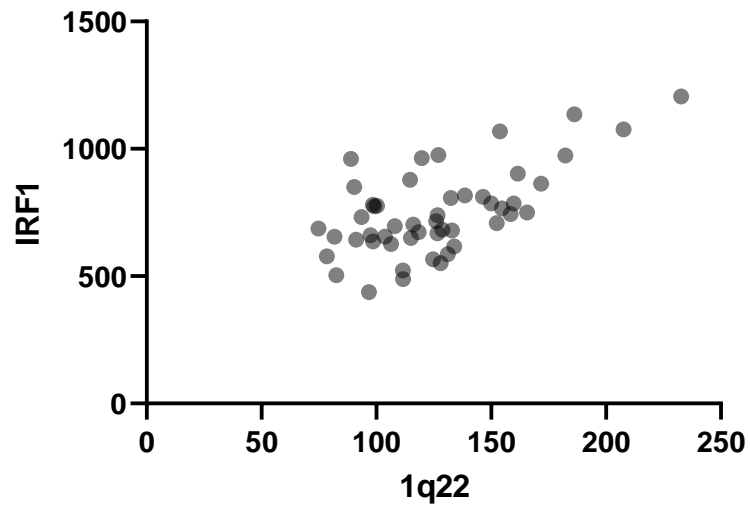


Figure S2. Correlation between IRF1 and HERV-K102 expression in cutaneous leishmaniasis patients. Pearson's *r* correlation between HERV-K102 and IRF1 expression in CL patients.

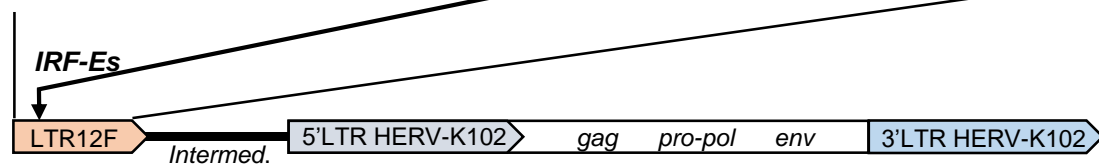
A

| Antibody target (or ATAC) | Chromosome | Beginning of peak | End of peak | Peak length | Peak summit | Fold-enrichment | Adjusted p value | Cell type |
|---------------------------|------------|-------------------|-------------|-------------|-------------|-----------------|------------------|-----------|
| STAT1 | chr1 | 155637480 | 155637773 | 294 | 155637658 | 7.6404 | 3.19963E-55 | MDM |
| IRF1 | chr1 | 155637408 | 155637777 | 370 | 155637618 | 12.0589 | 5.1523E-142 | MDM |
| H3K27ac | chr1 | 155635819 | 155637517 | 1699 | 155637434 | 2.16843 | 9.49511E-19 | MDM |
| ATAC | chr1 | 155637202 | 155637965 | 764 | 155637572 | 3.03479 | 2.66073E-15 | HeLa |
| H3K4me2 | chr1 | 155635765 | 155636040 | 276 | 155635902 | 6.88336 | 2.58941E-13 | HeLa |
| H3K4me2 | chr1 | 155636160 | 155637384 | 1225 | 155636513 | 6.62564 | 1.43648E-22 | HeLa |
| H3K79me2 | chr1 | 155636013 | 155636536 | 524 | 155636280 | 3.8251 | 0.00014639 | HeLa |
| H3K27ac | chr1 | 155635965 | 155637572 | 1608 | 155637302 | 4.08018 | 2.22382E-14 | HeLa |

B

LTR12F_1q22 Solo LTR (chr1:155637452-155637661):

CCGTTGGGAAGACCCAAGGGAAGGTGGTATACCTTCGAAATGAAAGCGAAAGTGAAATGAAAGTGAAAA CGAAATTATTTAGAACG
 GTGGCGTGTGAGAAACCCAGACGTACAAGAGATTACCTCGACATTGTCAGTGGTACTCCAGGTACCGAAGAAAGGAACCTCGGA
 CACTTTGGTGCTTGGGAAGTTAGTTCTTTCTGGAAC



Conserved IRF-E motif: **AANNGAAA** (55)

Sequence motifs in LTR12F that are enriched in IRF-1 binding sites (56):

- 1) **GAAAGCGAAAGT**
- 2) **GAAAGTGAAA**
- 3) **TGAAAGTGAAAA**

Figure S3. ChIP-seq and ATAC-seq analysis of HERV-K102. (A) Peaks identified by MACS2 as significantly enriched within 10kb +/- of HERV-K102. **(B)** Location of three potential IRF-E sites within LTR12F.

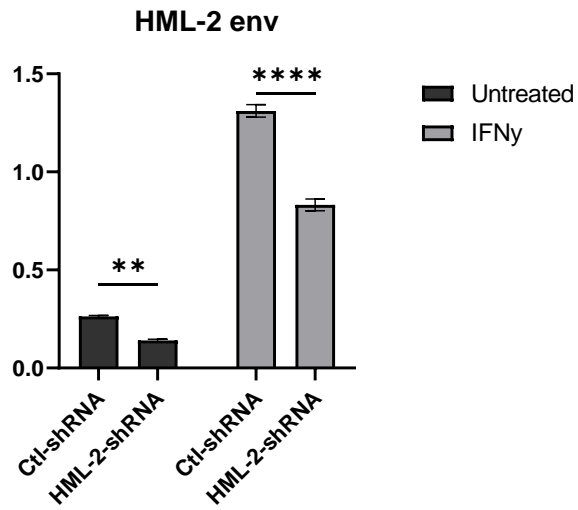


Figure S4. HML-2 env knockdown efficiency. Relative HML-2 env expression in control-shRNA and HML-2-shRNA expressing TDMs following IFN γ treatment. The data are presented as mean values \pm SEM from three biological replicates. ****, $P < 0.0001$ according to two-way Anova.