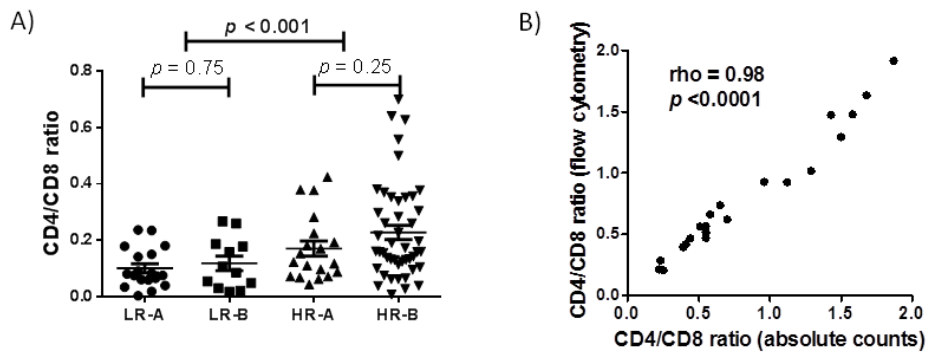


1 Supplementary Table 1. Clinical data of HIV-subjects from the case:control study.

Characteristics	LR-subjects (n=19)	HR-subjects (n=19)	<i>p</i>
Male sex, n/n (%)	19/19 (100)	19/19 (100)	1
Age (years)	39 [33-54]	40 [34-49]	0.8
CD4 counts (cells/ μ L)	70 [56-140]	126 [46-165]	0.28
CD4/CD8 ratio ^A	0.08 [0.04-0.15]	0.12 [0.07-0.22]	0.026
VL (log HIV RNA copies/mL)	4.8 [4.2-5.2]	5.0 [4.6-5.7]	0.23
Time to diagnosis (months)	1.0 [0-2.2]	1.0 [0-4.0]	0.26
IDU transmission, n/n (%)	2/19 (10%)	3/19 (16%)	0.6
Previous C event, n/n (%)	5/19 (26)	6/19 (32)	0.7
Anti-HVC ^B , n/n (%)	3/17 (18)	1/18 (6)	0.26
X4-viral tropism ^C , n/n (%)	5/16 (31)	2/17 (12)	0.17

2 Continuous variables are expressed as median values (IQR) and categorical variables
3 are expressed as number of cases (%). VL, Viral Load; IDU, Intravenous Drug User.
4 Mann-Whitney U and Chi-squared tests were used to analyze continuous and
5 categorical variables, respectively. ^ACalculated using frequencies from flow-cytometry.
6 ^BData only available from 17 LR-subjects and 18 HR-subjects. ^CData only available
7 from 16 LR-subjects and 17 HR-subjects.



Supplementary Figure 1

8

9 Supplementary Figure 1. Comparison between the CD4/CD8 ratio in the two different
 10 groups of LR- and HR-subjects. In the case:control study (LR-A and HR-A), CD4 and
 11 CD8 T-cell frequency determined by flow-cytometry were used to calculate the
 12 CD4/CD8 ratio, whereas in additional subjects from the Virgen del Rocío Hospital (LR-
 13 B and HR-B), clinical data of CD4 and CD8 T-cell absolute counts were used to
 14 calculate CD4/CD8 ratio (A). Mann-Whitney U-test was used for comparison. An
 15 additional group of HIV subjects, also from the Virgen del Rocío Hospital, had
 16 available CD4 and CD8 data from both, absolute values and cytometry values, and the
 17 correlation between such paired data of CD4/CD8 ratios was performed (B). Spearman
 18 rank test was used for the correlation.

19 SUPPLEMENTAL MATERIAL

20 *Supplemental information about subjects and the study design*

21 LR- and HR-subjects from the case:control study were selected from the Spanish AIDS
22 Research Network (RIS) cohort CoRIS (1) and associated samples were obtained from
23 the RIS-BB (2). Additional LR- and HR-subjects were HIV-infected subjects visiting
24 the Infectious Diseases Service of the University Hospital Virgen del Rocío between
25 2003 and 2013. The supplementary group of HIV-infected subjects used for the
26 correlation between paired data of CD4/CD8 ratios, calculated by both absolute counts
27 and cytometry frequencies, was also from the Infectious Diseases Service of the
28 University Hospital Virgen del Rocío.

29 *Laboratory measurements*

30 For the case:control study, clinical and demographic data from HIV-infected individuals
31 were obtained from CoRIS (1). For subjects from the Virgen del Rocío Hospital, the
32 absolute numbers of CD4 and CD8 T-cells were determined in fresh blood with an
33 Epics XL-MCL flow cytometer (Beckman Coulter) and plasma HIV-1 RNA levels were
34 measured by quantitative PCR (COBAS Ampliprep/COBAS Taqman HIV-1 test, Roche
35 Molecular Systems), according to the manufacturer's instructions. The detection limit
36 for this assay was 40 HIV RNA copies/mL. Plasma samples were also tested for
37 Hepatitis C virus antibodies using an HCV ELISA (Siemens Healthcare Diagnosis).

38 *Flow-Cytometry*

39 Briefly, thawed PBMCs were incubated at 4°C with surface marker antibodies for 20
40 minutes, followed by fixation and permeabilization according to the manufacturer's
41 instructions (FoxP3/Transcription Factor Staining Buffer, Ebioscience), and

42 subsequently incubated with intracellular FoxP3 for 30 minutes. Viable cells were
43 identified using LIVE/DEAD fixable Aqua Blue Dead Cell Stain (Life Technologies,
44 USA). Antibodies used were: anti-CD3, anti-CD4, anti-FoxP3, anti-ki67, anti-CD95
45 (BD Biosciences, USA) and anti-CD45RA (Life Technologies, CA, USA). Isotype
46 controls for FoxP3, Ki67 and CD95 were included in each experiment. Flow cytometry
47 was performed on LSR Fortessa (BD, USA), and a minimum of 1×10^6 total events was
48 collected. Analysis was performed using FlowJo version 9.2 (Tree Star) and data is
49 expressed as frequencies and MFI (Mean Fluorescence Intensity). Regulatory T-cells
50 (Treg) were defined using Miyara's phenotype for activated/effector Treg
51 ($CD4+CD45RA-FoxP3^{high}$) (3).

52 *Determination of viral tropism*

53 V3 loop amplification and sequencing were performed as previously described (4). The
54 V3 sequences were interpreted using the bioinformatics genotypic tropism predictor
55 geno2pheno (G2P), which is freely available online ([http://coreceptor.bioinf.mpi-
57 inf.mpg.de/index.php](http://coreceptor.bioinf.mpi-
56 inf.mpg.de/index.php)). A clonal version of G2P with false-positive rates (FPR) of 5%
58 (G2P5%clo) was used. HIV-1 variants were classified as R5 or X4, with the latter
59 classification including pure X4 and dual-tropic viruses.

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