

DATASET S1 Nef and Vpu amino acid alignment of viruses phenotyped in this study.

The alignment demonstrates substantial sequence variation. Numbering is based on the subtype C LANL consensus (shown as "C"), which is similar to HXB2 numbering. Amino acids that differ from the subtype C consensus are shown in color throughout the alignment, while dots are positions that match the consensus sequence. Dashes represent the absence of an amino acid at that position. Arrows point to significant positions found from Sequence Harmony analysis shown in Table 1, some of which are displayed in Figure 5.

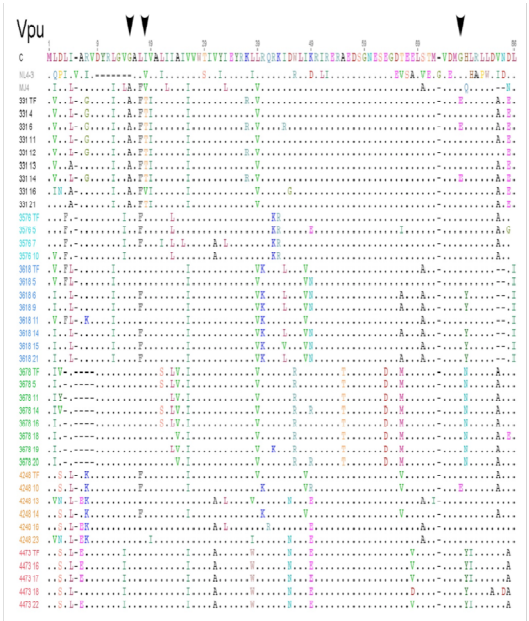
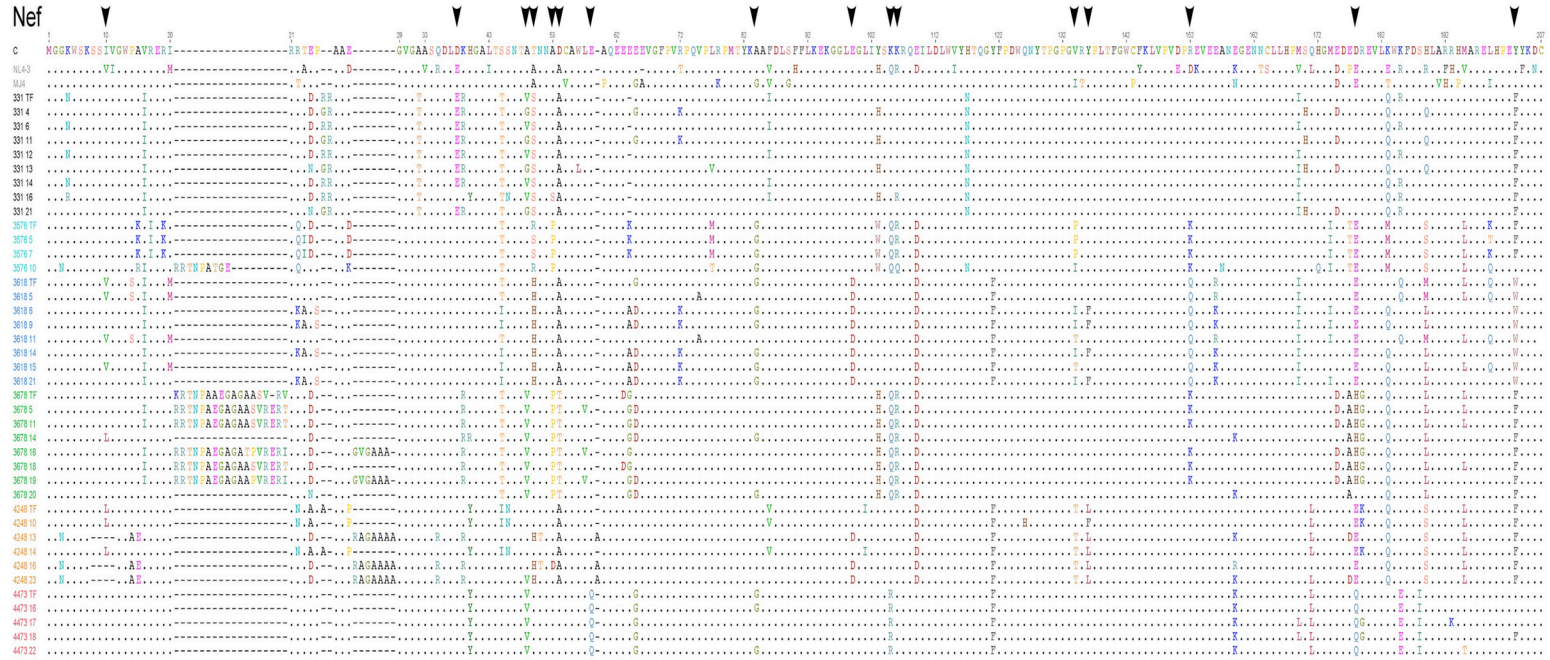


Figure S1

Correcting for replicative capacity score did not alter the correlation between HLA-C downregulation and NK suppression.

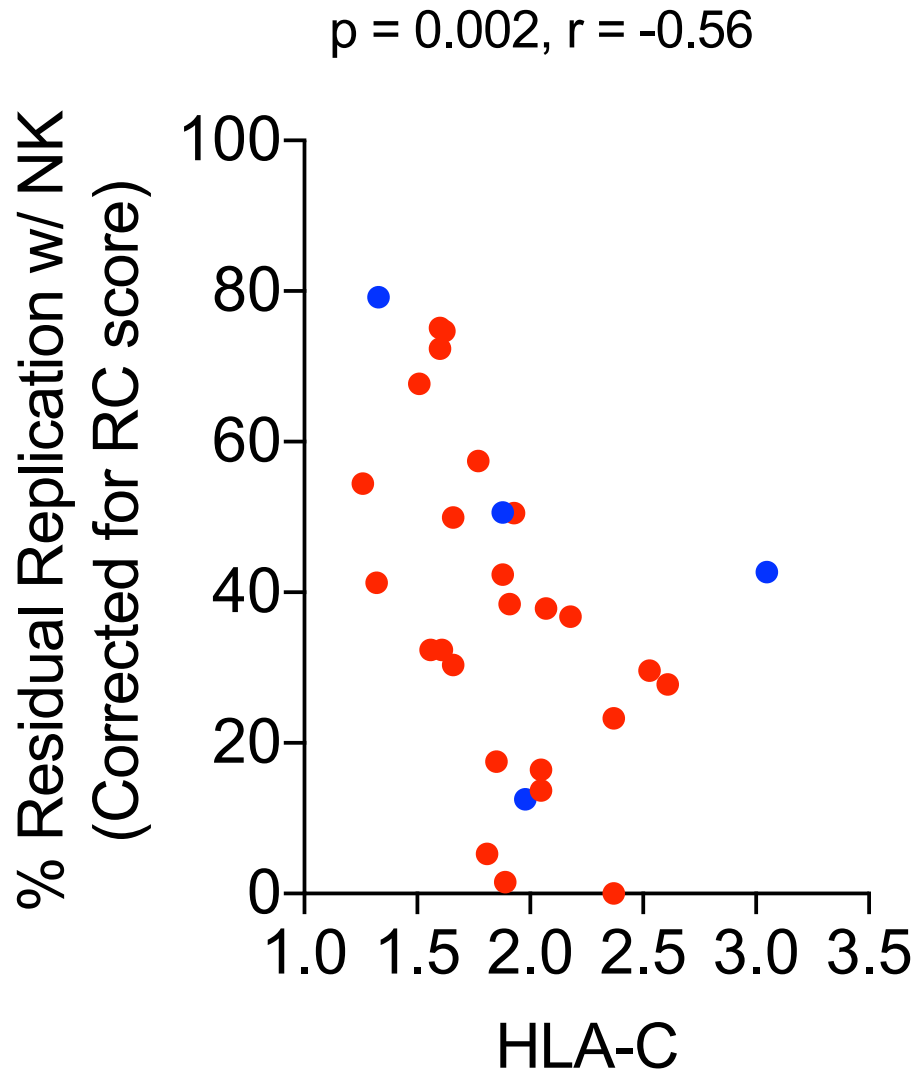


Table S1 Genbank accession numbers prviously published and listed here for ease of access

Variant ID	Genbank accession numbers
331 4	KR820308
331 6	KR820310
331 11	KR820294
331 12	KR820295
331 13	KR820296
331 14	KR820297
331 16	KR820299
331 21	KR820303
331 TF	KR820323
3576 5	KR820336
3576 7	KR820338
3576 10	KR820326
3576 TF	KR820325
3618 5	KR820354
3618 6	KR820355
3618 9	KR820357
3618 11	KR820342
3618 14	KR820344
3618 15	KR820345
3618 21	KR820351
3618 TF	KR820366
3678 5	KR820384
3678 11	KR820369
3678 14	KR820371
3678 16	KR820373
3678 18	KR820375
3678 19	KR820376
3678 20	KR820377
3678 TF	KR820393
4248 10	KR820395
4248 13	KR820398
4248 14	KR820399
4248 16	KR820401
4248 23	KR820407
4248 TF	KR820421
4473 16	KR820428
4473 17	KR820429
4473 18	KR820430
4473 22	KR820434
4473 TF	KR820449