Supplemental Figure 1. Two polyadenylation signals (PAS) in the *HLA-A* 3'UTR. Alignment of 3'UTR sequences of common *HLA-A* alleles are shown. The 3' UTR was amplified by PCR and sequenced using genomic DNA from individuals homozygous for the indicated allele. Identical nucleotides are shown as dots. Proximal and distal PAS are indicated with the blue and red underlines, respectively.

A.

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HLA-A  GACAGCTGCCTTGTGTGGGACTGAGAGGCAAGAGTTGTTCCTGCCCTTCCCTTTGTGACTTGAAGAACC-
HLA-B  ........T......A..........T...G..T..C...AC...-.C.............C....G..T
HLA-C  ..........-.............T...G..T..C...ACA..-.CT............C....G..T

HLA-A  -CTGACTTTGTTTCTGCAAAGGCACCTGCATGTGTCTGTGTTCGTGTAGGCATAATGTGAGGAGGTGGGG
HLA-B  CTG.CA.C.C.................A.........C..C.C...TA...................A.
HLA-C  CTG.CA.C.C.................A.........C....C...TA...................A.

HLA-A  AGACCACCCCACCCCCATGTCCACCATGAC-CCTCTTCCCACGCTGACCTGTGCTCCCTCCCCAATCATC
HLA-B  ....-.........TTG.......TG....C...G......T...........T.T........G.....
HLA-C  ....-...........G........G....C...G.C.....A..........T.........G......

HLA-A  TTTCCTGTTCCAGAGAGGTGGGGCTGAGGTGTCTCCATCTCTGTCTCAACTTCATGGTGCACTGAGCTGT
HLA-B  ....T.....................-.........................T.C.-............C
HLA-C  ..........................-.....................A...................C

HLA-A  AACTTCTTCCTTCCCTATTAAA-ATTAGAACCTGAGTATAAATTTACTTTCTCAAATTCTTGCCATGAGA
HLA-B  ........A........C.G..A..A....TC...A.........GT..........AT....T......
HLA-C  ........A........A.G..GT.A.........A.........GTG.........AT....T....AG

HLA-A  GGTTGATGAGTTAATTAAAGGAGAAGATTCCTAAAATTTGAGAGACAAAATAAATGGAAGACATGAGAAC
HLA-B  ...................TA..TCA......GG..........GC.......GACCT....ACCTTC---
HLA-C  C.................TA..TCA.......G..G........GC.......GACCT..G.ACCTTC-
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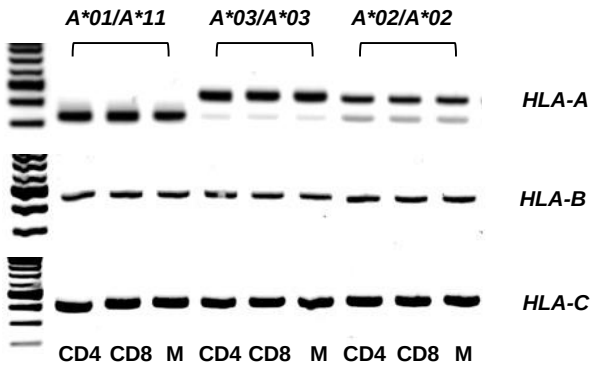
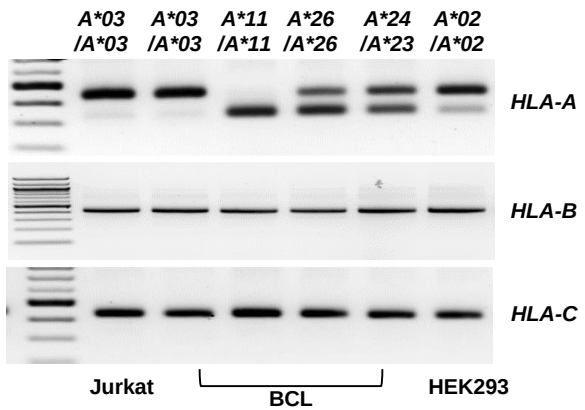
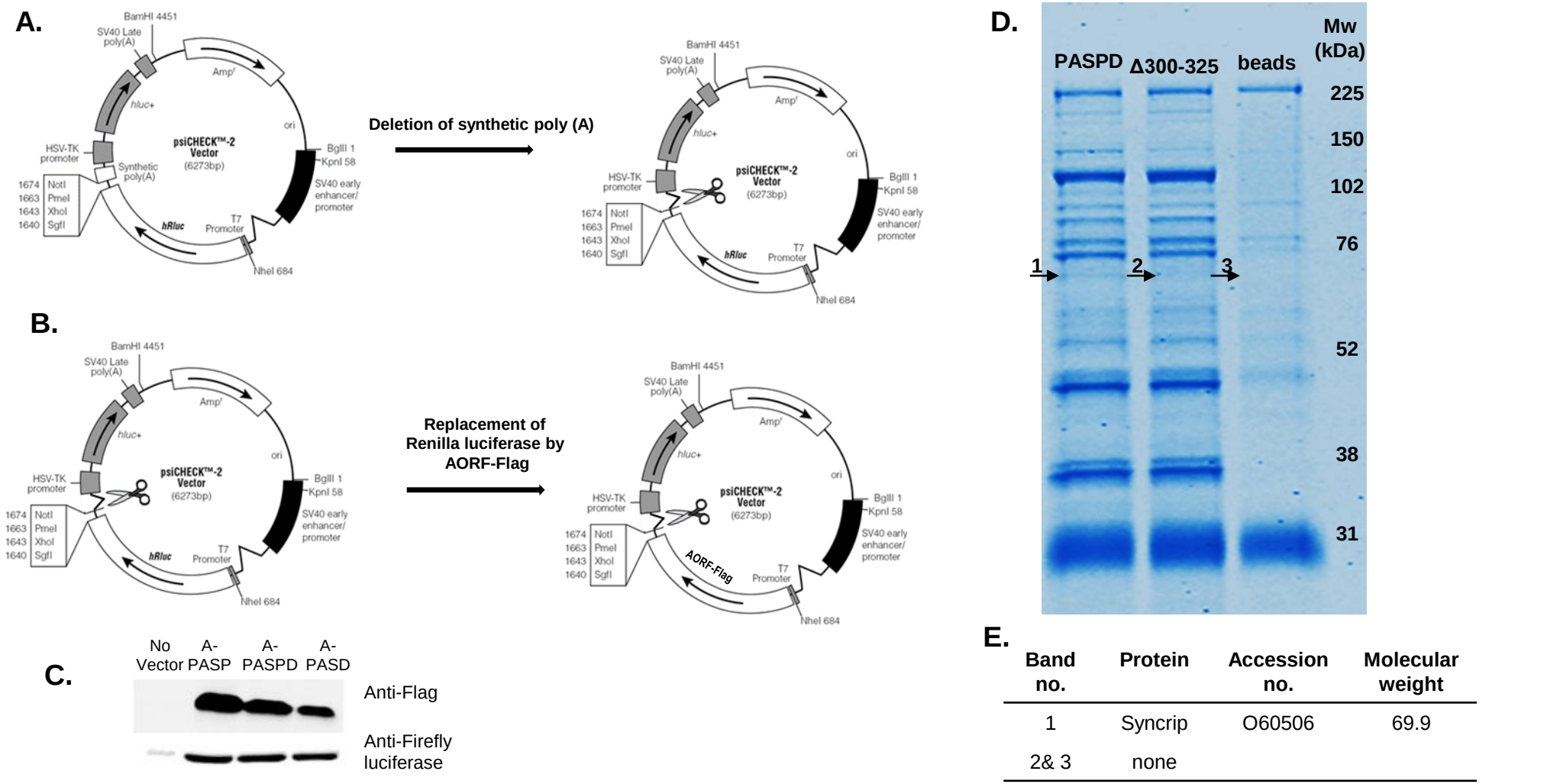
B.



C.



Supplemental Figure 2. ***HLA-B* and *–C* use a single PAS, and *HLA-A* transcripts exhibit allele specific patterns of alternative PAS usage consistently across cell types. (A)** Alignment of 3'UTR sequences of *HLA-A, HLA-B* (IMGT-HLA; http://www.ebi.ac.uk/ipd/imgt/hla/) *and HLA-C* (60) are shown. Identical nucleotides are shown as dots. Proximal and distal PAS are indicated with blue and red underlines, respectively. The proximal PAS is disrupted in *HLA-B* and *HLA-C* alleles. **(B)** RNA was obtained from peripheral blood CD4+T cells (CD4), CD8+ T cells (CD8), and monocytes (M) of 3 healthy donors with distinct *HLA-A* genotypes noted. Rapid amplification of cDNA ends (3' RACE) of 3'UTRs of *HLA-A* alleles from 3 distinct cell types showed a similar pattern of use of either the proximal or distal PAS. *HLA-B* and *HLA-C* 3'UTRs express only a single isoform owing to absence of the proximal PAS. **(C)** RNA was obtained from Jurkat T cells, transformed B cell lines (BCL), and HEK293 cells. Similar to the lymphocytes, the 3'RACE indicated an allele specific pattern of alternative PAS usage for *HLA-A* transcripts; whereas *HLA-B* and *HLA-C* transcript express a single isoform.



Band no.	Protein	Accession no.	Molecular weight
1	Syncrip	O60506	69.9
2& 3	none		

Supplemental Figure 3. **Schematic representation of the modifications to the psicheck2 vector. (A)** Deletion of the synthetic PolyA signal downstream of *Renilla* luciferase is shown. (**B)** *Renilla* luciferase sequence was replaced by c-terminal Flag tagged HLA-A ORF [AORF-Flag]. (**C)** Total cell lysates of HEK293 cells transfected with HLA-AORF-Flag plasmids were used to carry out Western blot analysis with anti-Flag and anti-firefly luciferase antibodies. One of two independent experiments is shown. **Differential binding of Syncrip to the long form of *HLA-A* 3'UTR. (D)** Coomassie blue stained PAGE gel separating the RBPs that were bound to the long form of *HLA-A* 3'UTR (PASPD), the mutant containing a 25bp deletion immediately downstream of proximal PAS (Δ300-325), or avidin beads in the absence of any labeled RNA (beads; lane 3). A distinct protein band, which appeared only in the PASPD lane (Band1) and proteins of corresponding molecular weight in the Δ300-325 lane (Band 2) and the beads only lane (Band 3) were excised and analyzed by MS (**E)** Syncrip was identified by LC-MS/MS in the RBPs bound to the long form of *HLA-A* 3'UTR (PASPD; Band 1), and no RBPs were detected in the Band 2 from the Δ300-325 lane or Band 3 from the beads only control.

Supplemental Table I. Sequences of the morpholino-oligonucleotides and primers

Primer	Sequence
MorpholinoOligonucleotides	
Apro1	ACTCAGGTTCTAATTTTAATAGGGA
Control Morpholino	CCTCTTACCTCAGTTACAATTTATA
HLA-A 3'UTR sequencing	
HLA-A 3'UTRseqFw	TCTGTGGGATCTGACCAGGTT
HLA-A 3'UTRseqRev	AACACGTGGACTCTGGAAGG
3'RACE	
HLA-A 3'UTR 3'RACE Fw	TGAGAGGCAAGAGTTGTTCCT
UAP	5'GGCCACGCGTCGACTAGTACTTTTTTTTTTTTTTT 3'
Cloning	
psicheckAFw	ATCGCTCGAGTGAGAGGCAAGAGTTGTTCCT
psicheckARev	GCCAGCGGCCGCTGGACTCTGGAAGGTT
A03UTR_325_Rev	GCCAGCGGCCGCTTTATTAAGTAAATTTATACTAAG
HLA-AORFFw	GACTCACTATAGGGAGACCCAAGCTGGCTACGCT
HLA-AORFRev	ACCTTGTACGAGTGCGGGTCTCGAGTTATCACTTATCGTC
qPCR	
HLA-A 3'UTR Rev	AAGAGGGTCATGGTGGACAT
Renilla Fw	AAGAGCGAAGAGGGCGAGAA
Renilla Rev	TGCGGACAATCTGGACGAC
Firefly Fw	CGTGCCAGAGTCTTTCGACA
Firefly Rev	ACAGGCGGTGCGATGAGAC
Gapdh Fw	GGTGAAGGTCGGAGTCAACG
Gapdh Rev	GTTGAGGTCAATGAAGGGGTC

Primer and oligonucleotide sequences used in the study are listed.