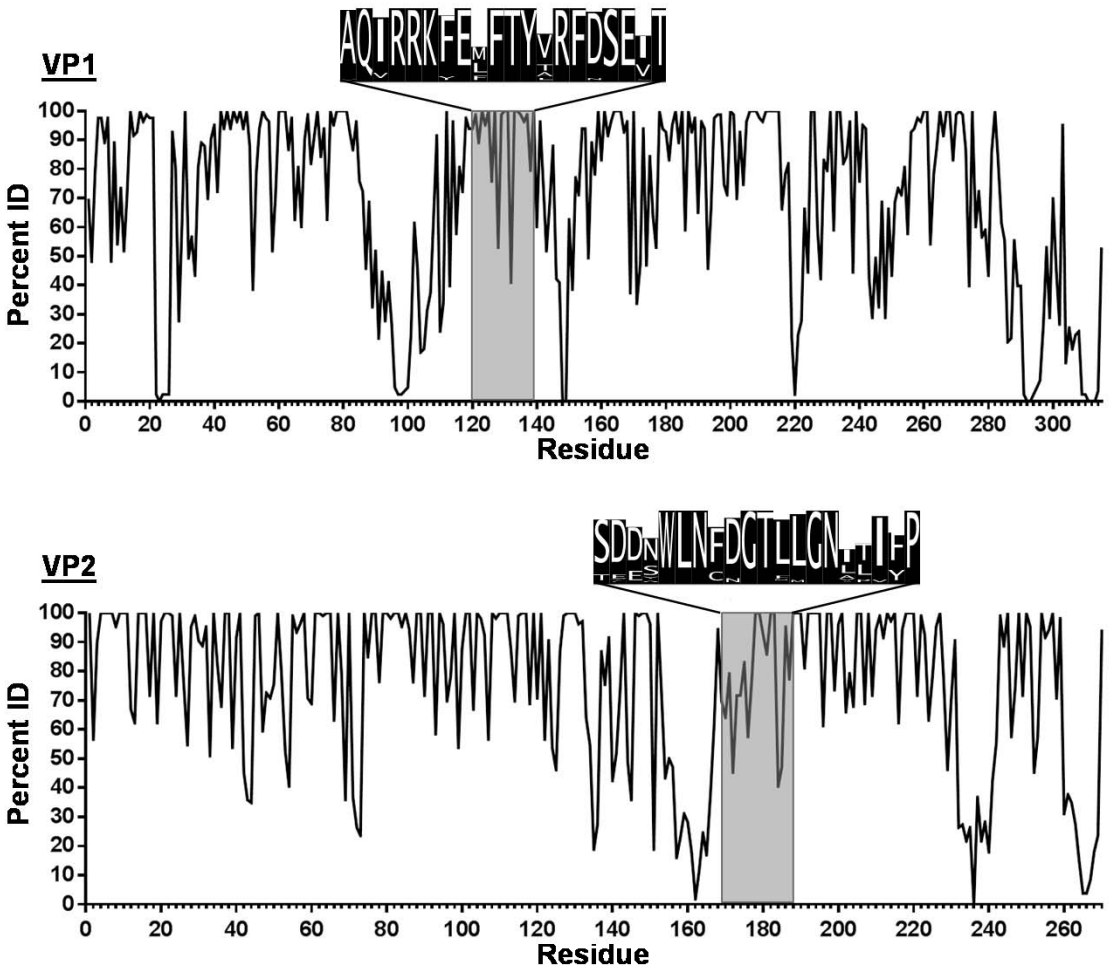
A



B

Epitope	Prevalence of Amino Acid Sequence Identity Among Strains of Each Rhinovirus Species								
	RV A					RV B		RV C	
	100%	99-95%	94-90%	89-85%	Total	Total	Range (% identity)	Total	Range (% identity)
$VP1_{P14}$ AQVRRKFEMFTYVRFDSEIT	1/77 (1.3%)	10/77 (13.0%)	24/77 (31.2%)	27/77 (35.1%)	62/77 (80.5%)	8/29 (27.6%)	80-75%	5/51 (9.8%)	90-80%
$VP2_{P60}$ SDDNWLNFDGTLLGNLLIFP	5/77 (6.5%)	13/77 (16.9%)	20/77 (26.0%)	17/77 (22.1%)	55/77 (71.4%)	24/29 (82.8%)	70-50%	6/51 (11.8%)	60-50%

Supplementary Figure 2. Peptide Epitopes of RV-A39 Displayed on HLA-DR4 Tetramers. Two epitopes were identified by tetramer-guided epitope mapping of RV-A39 capsid proteins VP1 and VP2 in the context of HLA-DRB1*0401. **(A)** Location of RV-A39 peptides within VP1 and VP2. Amino acid sequence identity for RV-A, -B, and –C strains and consensus sequences are depicted. **(B)** Sequence similarity between RV-A39 epitopes and RV-A, -B, and -C species. Values denote the prevalence of strains within each RV species sharing amino acid identity with RV-A39 epitopes, with percentages in parentheses. For RV-B and –C species, only the total prevalence within the top 5,000 hits with a corresponding range of amino acid identities are shown. Underlines denote the predicted minimal MHCII binding cores for each peptide epitope.