

**Table S3** Frequencies of the 18 potential CTL-escape mutations

Mutation	Sampling period			Viral subtype
	1987-1997	1998-2002	2003-2006	
<i>Mutations with a significant association to an HLA allele (q-value &lt; 0.02)</i>				
P028	25,0%	35,0%	29,1%	B
P028	9,1%	25,0%	14,3%	F
P030	12,5%	40,0%	43,6%	B
P030	100,0%	66,7%	71,4%	F
P046	6,3%	25,0%	14,5%	B
P046	72,7%	66,7%	71,4%	F
P055	18,8%	25,0%	14,3%	B
P055	0,0%	8,3%	3,3%	F
P065	0,0%	20,0%	7,1%	B
P065	0,0%	16,7%	16,7%	F
P081	0,0%	15,0%	10,7%	B
P081	4,8%	12,1%	11,9%	F
P083	100,0%	95,0%	98,2%	B
P083	52,4%	63,6%	76,1%	F
P118	6,3%	10,0%	8,9%	B
P118	14,3%	18,2%	19,4%	F
P125	25,0%	50,0%	46,4%	B
P125	100,0%	90,9%	100,0%	F
P242	0,0%	5,0%	10,5%	B
P242	14,3%	15,2%	10,1%	F
P357	18,8%	35,0%	40,4%	B
P357	9,5%	18,2%	21,7%	F
<i>Mutations with a significant trend in time (Chi-squared for trend &lt; 0.05)</i>				
P076	14,3%	45,5%	38,8%	F
P076	37,5%	50,0%	66,1%	B
P084	95,2%	97,0%	97,0%	F
P084	18,7%	45,0%	54,4%	B
P095	9,5%	3,0%	22,4%	F
P095	12,5%	30,0%	35,7%	B
P215	28,6%	18,2%	24,6%	F
P215	37,5%	15,0%	12,3%	B
P218	0,0%	18,2%	7,2%	F
P218	0,0%	5,0%	15,8%	B
P223	0,0%	12,1%	23,2%	F
P223	18,8%	40,0%	42,1%	B
P280	0,0%	12,1%	20,3%	F
P280	93,8%	70,0%	82,5%	B

Detail of the frequencies of the 11 polymorphisms identified as potential CTL-escape mutations through statistical analysis (mutation at position 357 was associated with two different HLA alleles) and the 7 additional identified through trend analysis, according to viral subtype.