

**Table S4** Results from the statistical analysis for identification of CTL-escape mutations performed over genes *pol* and *vpu*

		<i>p</i> -value	OR	Epitope analysis		<i>p</i> -value for association with viral subtype	Prevalence on viral subtype	
				Sequence	Known/predicted		B	F
<i>pol</i>								
P067	B49	0,001	64,50		?	0,352		
P503	B62	0,002	12,14		?	0,513		
P273	B35	0,002	8,24	<u>Q</u> NPDIVIQY	known	<b>0,013</b>	8,9%	100,0%
P016	B57	0,003	31,13		-	1,000		
P324	B44	0,003	28,00		-	1,000		
P310	B62	0,003	7,40		?	0,497		
<i>vpu</i>								
P71	B44	0,001	28,46	G <u>E</u> M <u>G</u> H <u>L</u> A <u>P</u> G <u>N</u> I / A <u>E</u> E <u>L</u> A <u>A</u> L <u>G</u> E <u>M</u>	CBS	0,502		
P48	B39	0,001	15,63		-	1,000		
P71	B40	0,011	4,19	G <u>E</u> M <u>G</u> H <u>L</u> A <u>P</u> G <u>N</u> I / A <u>E</u> E <u>L</u> A <u>A</u> L <u>G</u> E <u>M</u>	CBS	0,502		
P78	B39	0,013	0,27		-	<b>0,000</b>	88,5%	15,8%
P43	B57	0,018	11,85		-	0,180		
P70	B40	0,020	3,67	G <u>E</u> M <u>G</u> H <u>L</u> A <u>P</u> G <u>N</u> I / A <u>E</u> E <u>L</u> A <u>A</u> L <u>G</u> E <u>M</u>	CBS	<b>0,007</b>	15,4%	50,0%
P3	B07	0,020	0,27	Q <u>P</u> L <u>V</u> I <u>L</u> A <u>I</u> V <u>A</u> L	CBS	1,000		
P10	B44	0,021	9,88		-	0,208		
P64	B48	0,021	19,11		?	0,161		
P40	B44	0,026	8,78		-	0,180		
P2	B44	0,026	7,67		-	0,440		
P61	B39	0,029	0,33		-	<b>0,000</b>	100,0%	13,2%
P38	B44	0,033	7,80		-	<b>0,018</b>	11,3%	100,0%

Detailed are the *p*-values and ORs of the 19 sites across *pol* and *vpu* genes where evidence of CTL-escape mutations were found. Correction for multiple comparisons where performed and only associations with a *q*-value lower than 0.2 are shown. For those positions located within known or predicted epitopes, the aminoacidic sequence is detailed. For those significantly associated with viral subtype, *p*-values for association and prevalence on both B and F subtypes are provided.