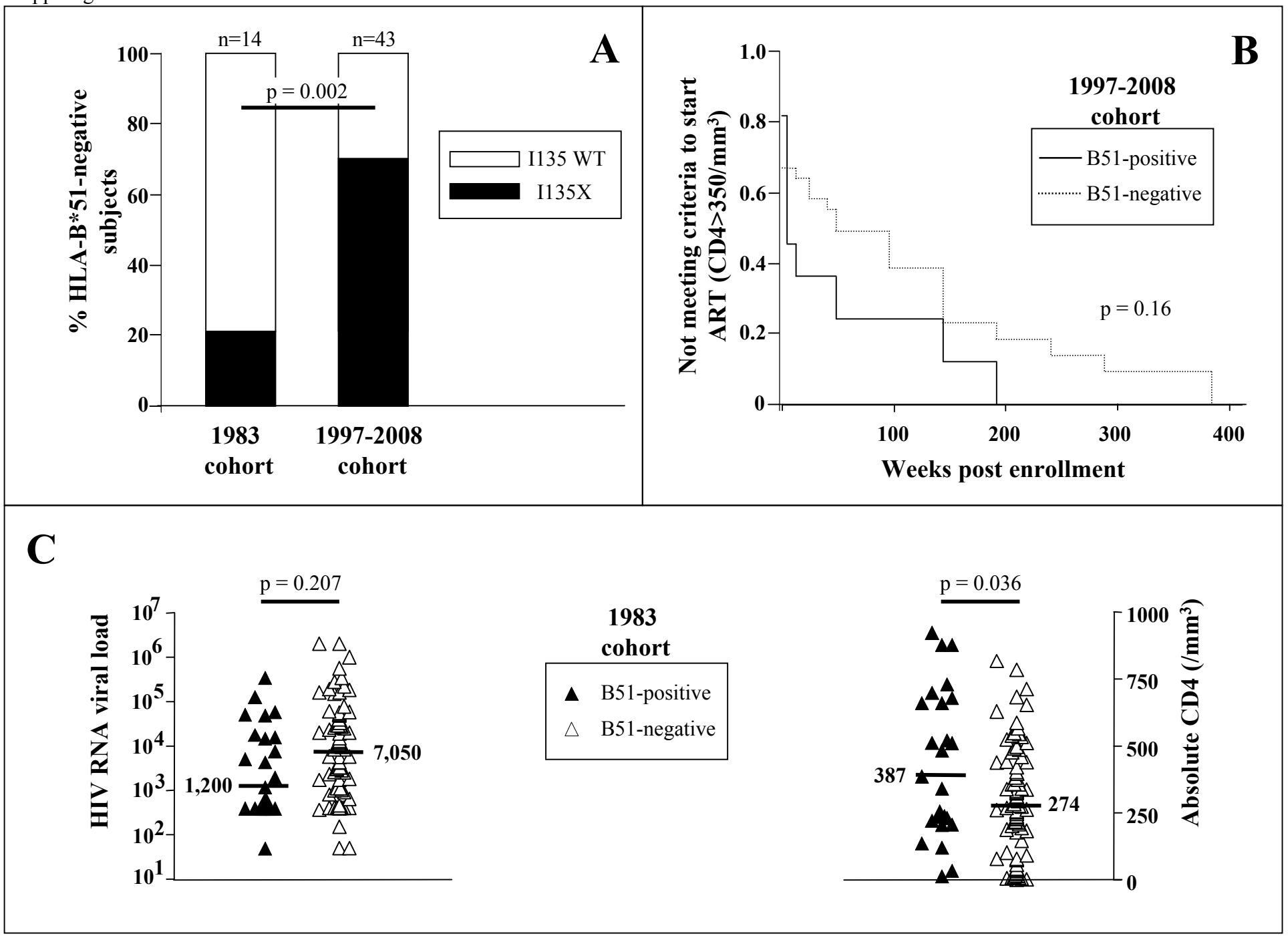
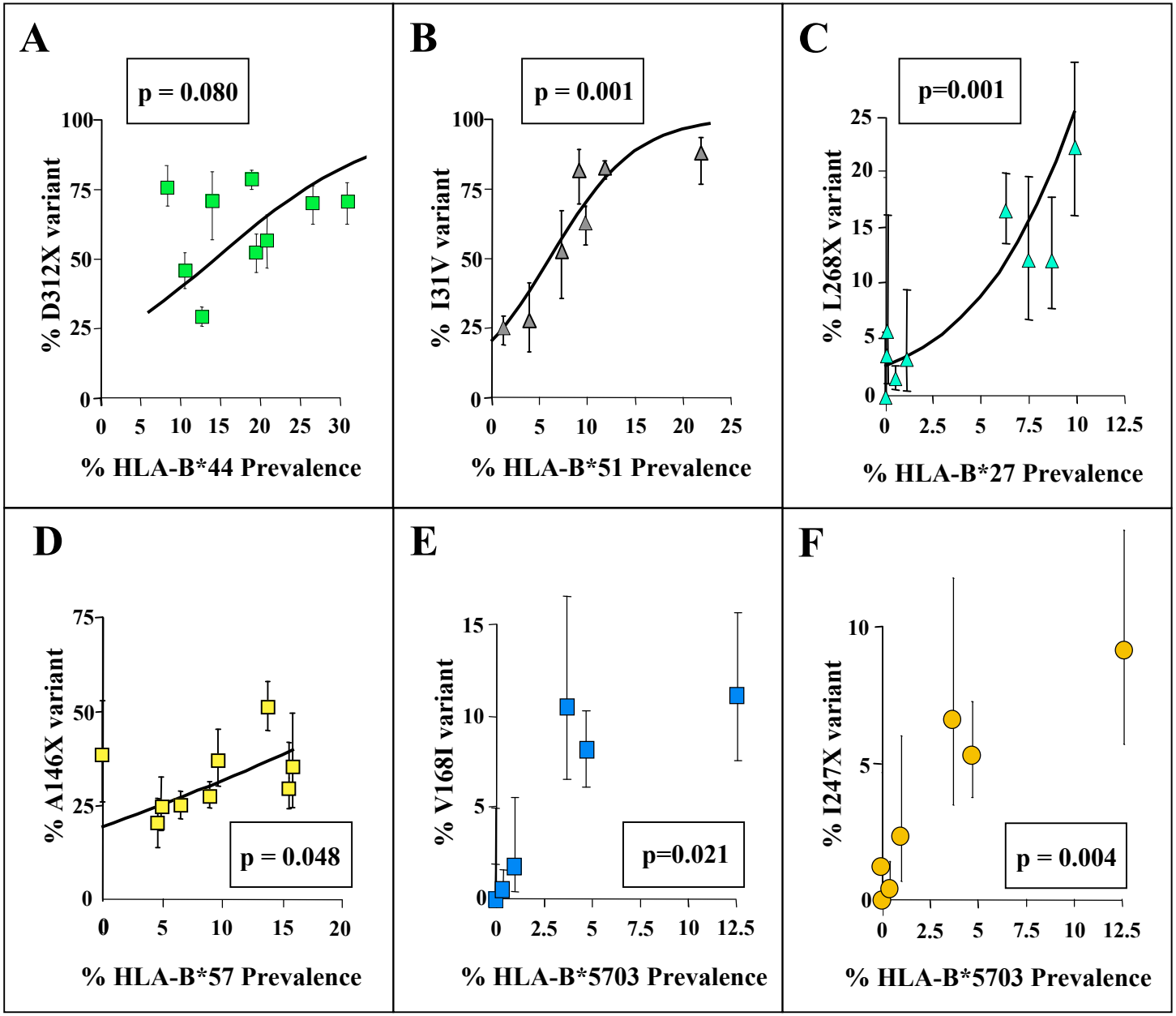
Suppl Fig 1

Subject	Timepoint	TAFTIPSI
Subject-1	Baseline	-------T
	12 months	-------T
Subject-2	Baseline	-------T
Subject-3	Baseline	-------R
	12 months	-------R
Subject-4	Baseline	--------
	12 months	--------
	18 months	--------
	24 months	-------T
Subject-5	Baseline	-------R
	Baseline	-------R
	Baseline	-------R
Subject-6	Baseline	-------R
	12 months	-------R
	24 months	-------R
	36 months	-------R
Subject-7	Baseline	-------T
	10 months	-------T
	12 months	-------T
	24 months	-------T
	36 months	-------T
Subject-8	Baseline	--------
	12 months	-------R
	24 months	-------T
Subject-9	Baseline	-------T
	7 months	-------T
	12 months	-------T
Subject-10	Baseline	--------
	12 months	-------T
	24 months	-------T
Subject-11	Baseline	-------T
	12 months	-------T
	24 months	-------T
Subject-12	Baseline	-------T
Subject-13	Baseline	--------
	6 months	-------T
	12 months	-------T

Suppl Fig 2

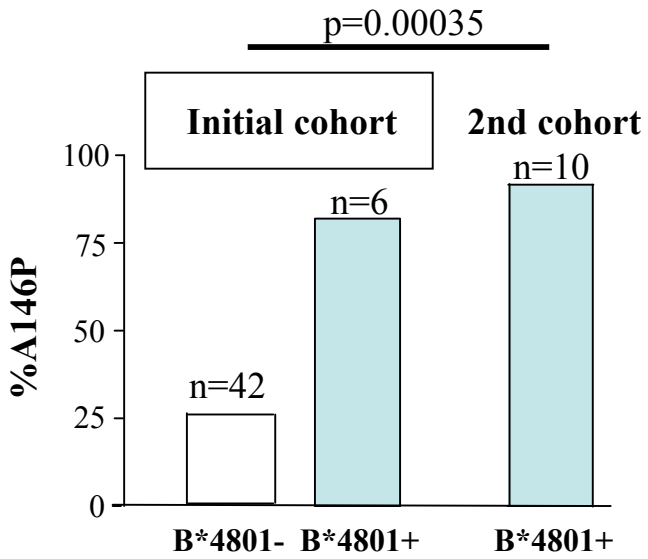

A
n=14
n=43
p = 0.002
% HLA-B*51-negative subjects
I135 WT
I135X
1983 cohort
1997-2008 cohort
B
1997-2008 cohort
B51-positive
B51-negative
p = 0.16
Not meeting criteria to start ART (CD4>350/mm3)
Weeks post enrollment
C
p = 0.207
HIV RNA viral load
1,200
7,050
1983 cohort
B51-positive
B51-negative
p = 0.036
387
274
Absolute CD4 (/mm3)

Suppl Fig 3


A
p = 0.080
% D312X variant
% HLA-B*44 Prevalence
B
p = 0.001
% I31V variant
% HLA-B*51 Prevalence
C
p=0.001
% L268X variant
% HLA-B*27 Prevalence
D
p = 0.048
% A146X variant
% HLA-B*57 Prevalence
E
p=0.021
% V168I variant
% HLA-B*5703 Prevalence
F
p = 0.004
% I247X variant
% HLA-B*5703 Prevalence

Suppl Fig 4

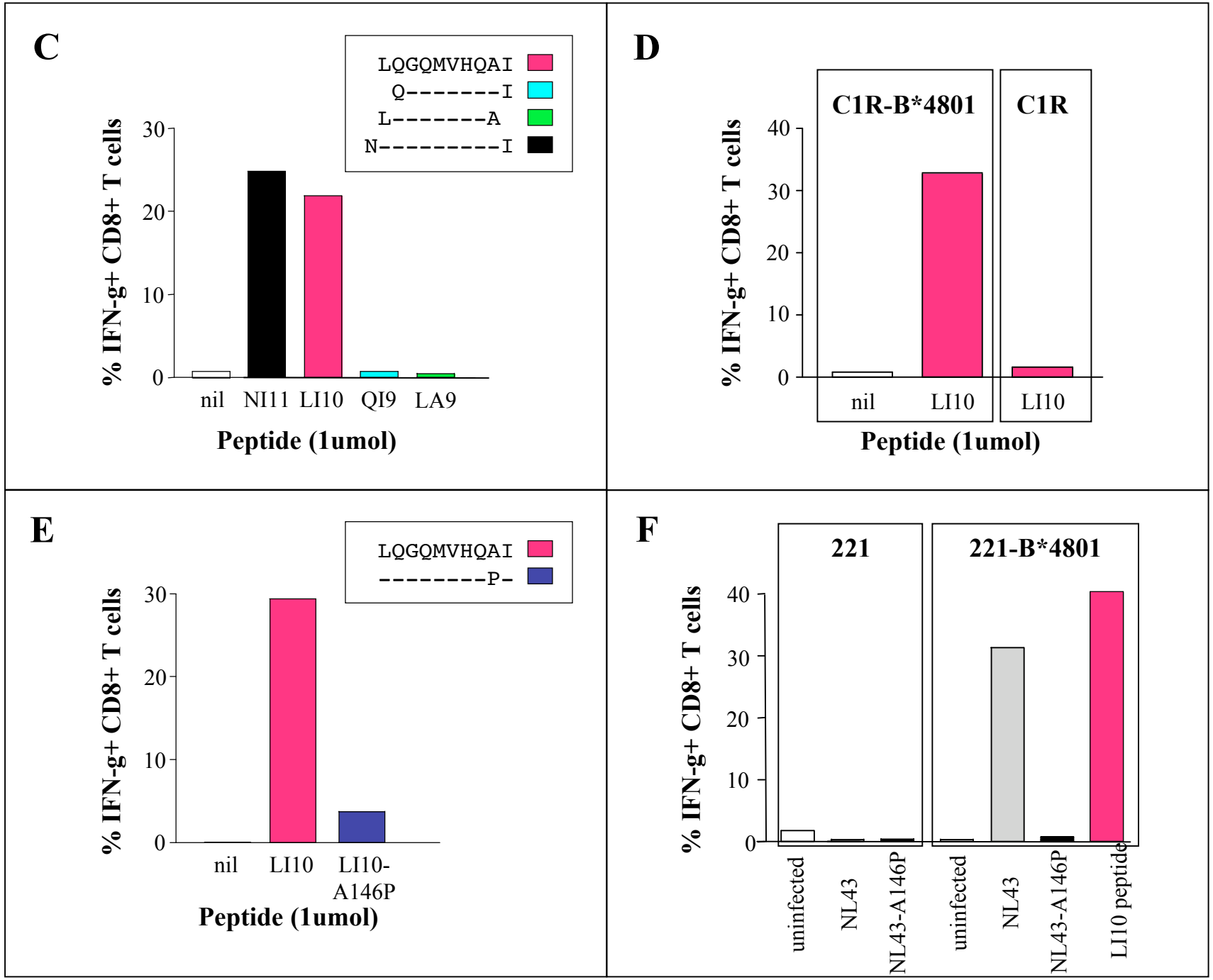
A



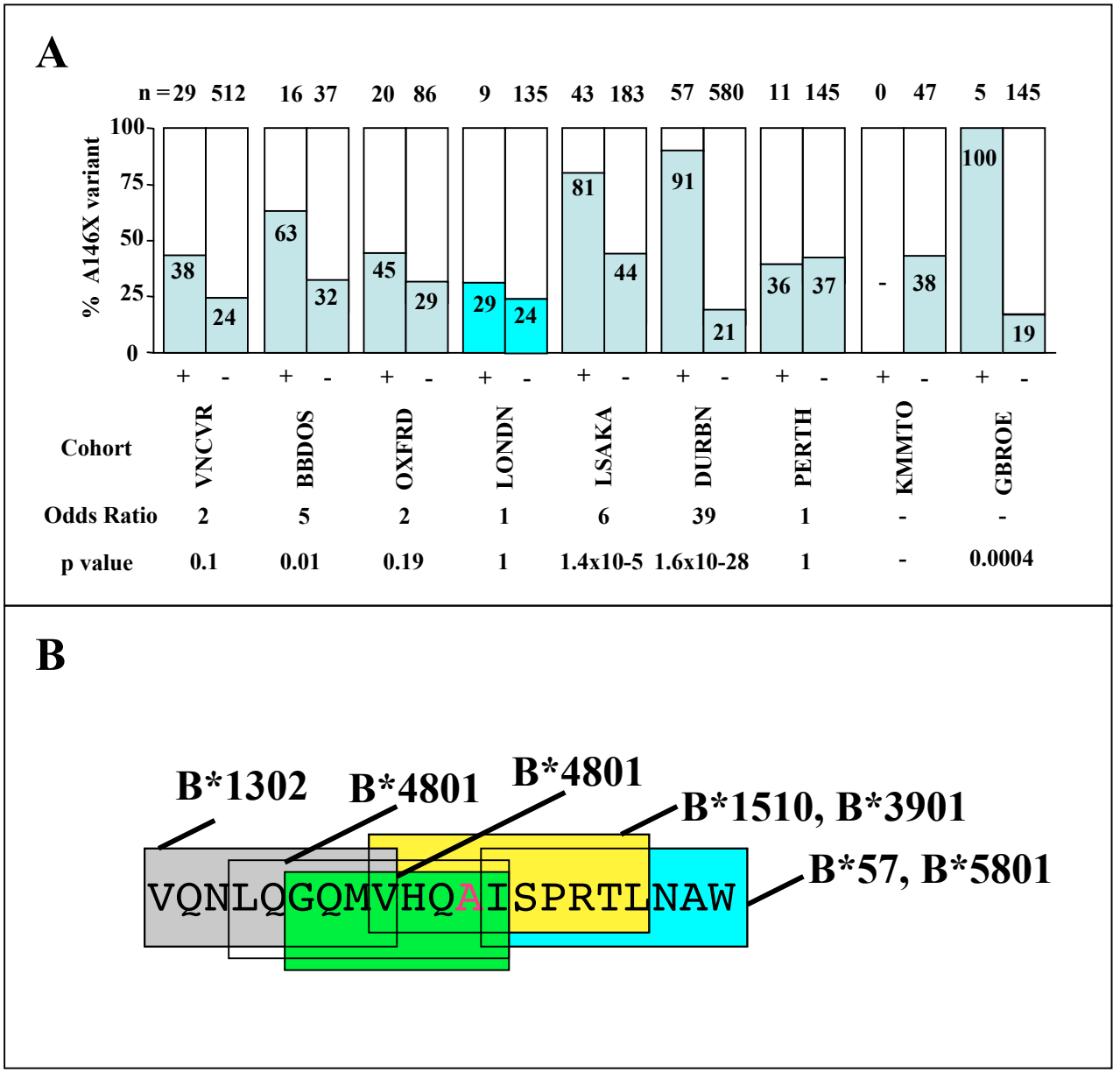
B

Date	Gag sequence	Population sequence/Clones
01/22/2001	LQGQMVHQAI	Population sequence
	----------	10/10 clones
04/05/2004	----------	10/10 clones
14/12/2004	--------P-	Population sequence
20/12/2005	--------P-	Population sequence
	--------P-	10/10 clones

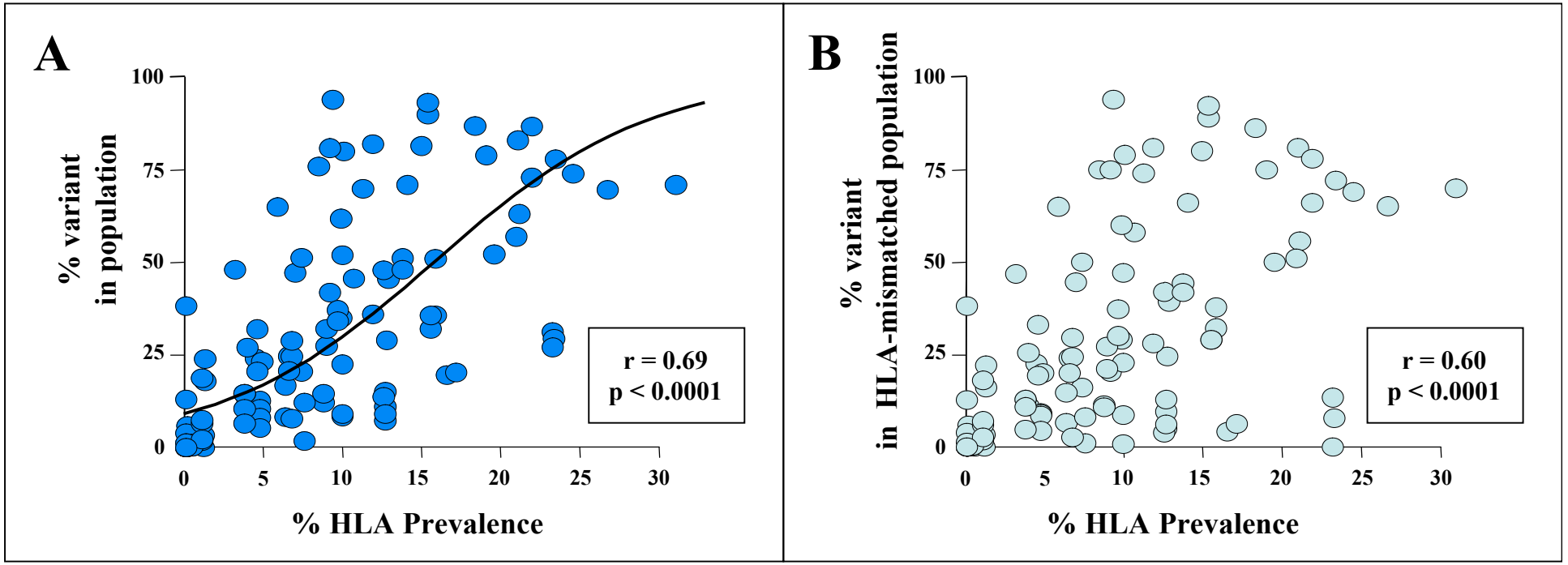
Suppl
Fig 4


C
LQGQMVHQAI
Q-------I
L-------A
N---------I
% IFN-g+ CD8+ T cells
0
10
20
30
nil
NI11
LI10
QI9
LA9
Peptide (1umol)
D
C1R-B*4801
C1R
% IFN-g+ CD8+ T cells
0
10
20
30
40
nil
LI10
LI10
Peptide (1umol)
E
LQGQMVHQAI
--------P-
% IFN-g+ CD8+ T cells
0
10
20
30
nil
LI10
LI10-
A146P
Peptide (1umol)
F
221
221-B*4801
% IFN-g+ CD8+ T cells
0
10
20
30
40
uninfected
NL43
NL43-A146P
uninfected
NL43
NL43-A146P
LI10 peptide

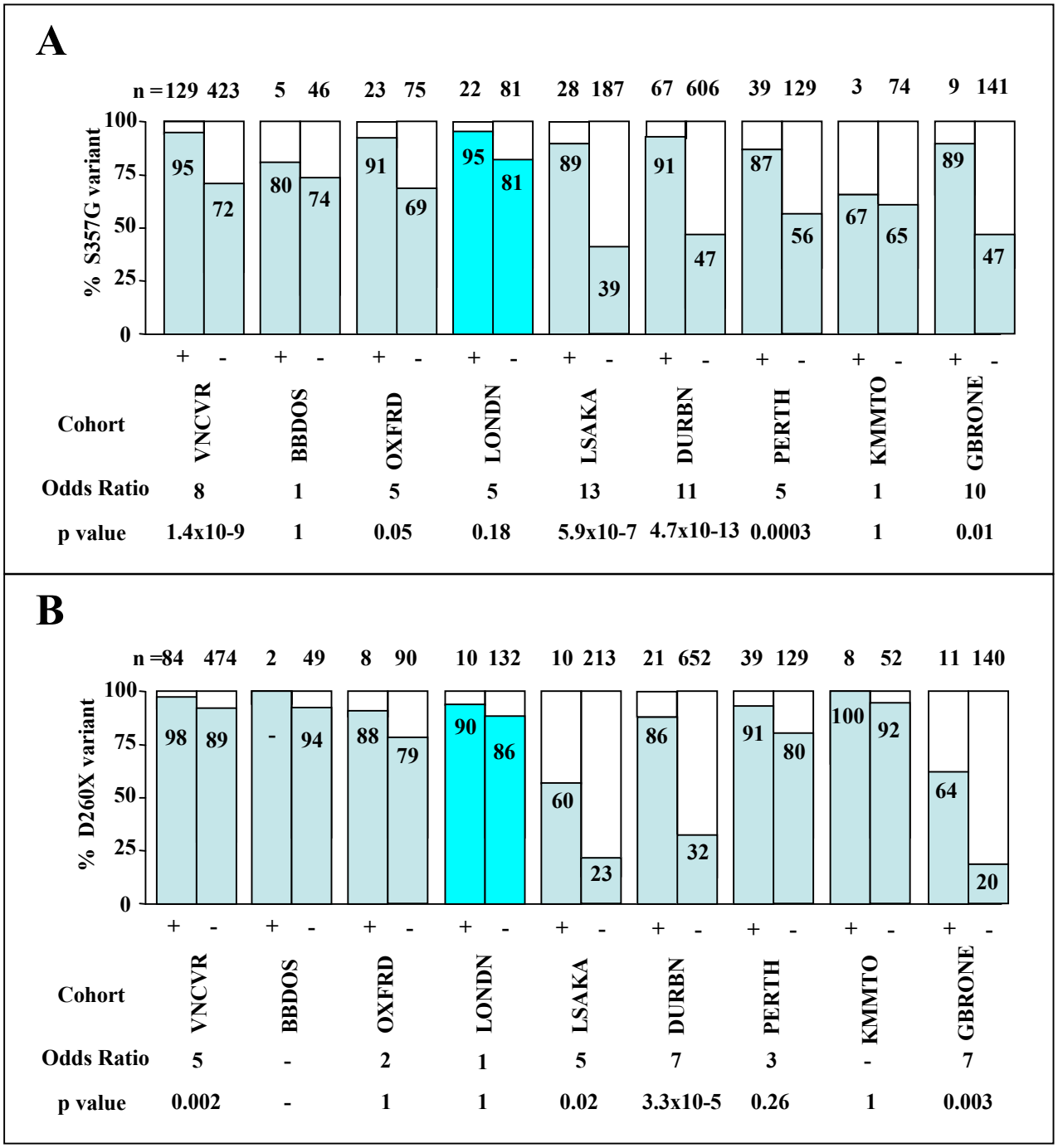
Suppl Fig 5


A
n = 29 512 16 37 20 86 9 135 43 183 57 580 11 145 0 47 5 145
% A146X variant
100
75
50
25
0
38
24
63
32
45
29
29
24
81
44
91
21
36
37
-
38
100
19
+ - + - + - + - + - + - + - + - + -
Cohort
VNCVR BBDOS OXFRD LONDN LSAKA DURBN PERTH KMMTO GBROE
Odds Ratio
2 5 2 1 6 39 1 - -
p value
0.1 0.01 0.19 1 1.4x10-5 1.6x10-28 1 - 0.0004
B
B*1302
B*4801
B*4801
B*1510, B*3901
B*57, B*5801
VQNLQGQMVHQAISPRTLNAW

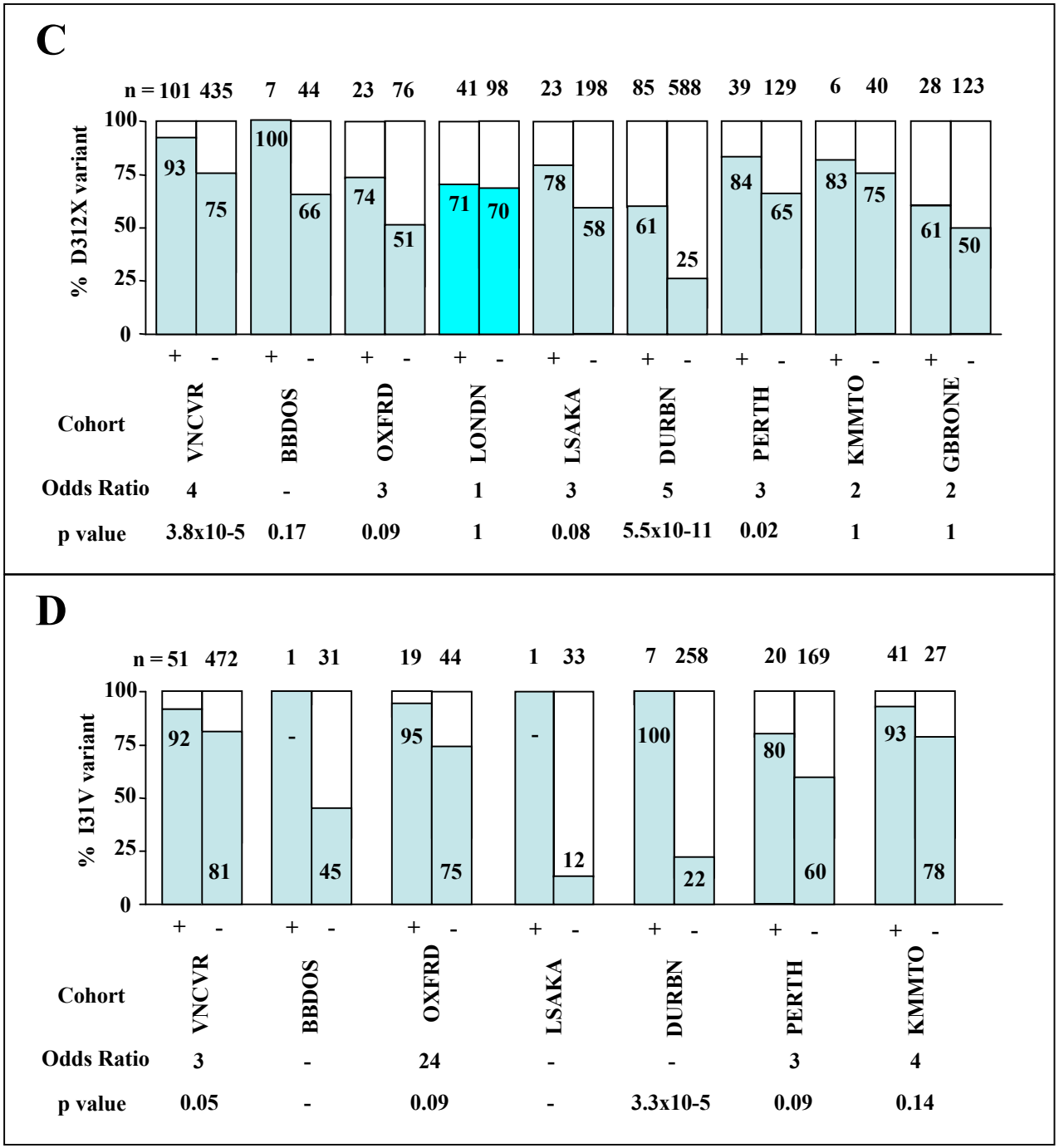
Suppl Fig 6


A
% variant
in population
100
75
50
25
0
0
5
10
15
20
25
30
% HLA Prevalence
r = 0.69
p < 0.0001
B
% variant
in HLA-mismatched population
100
75
50
25
0
0
5
10
15
20
25
30
% HLA Prevalence
r = 0.60
p < 0.0001

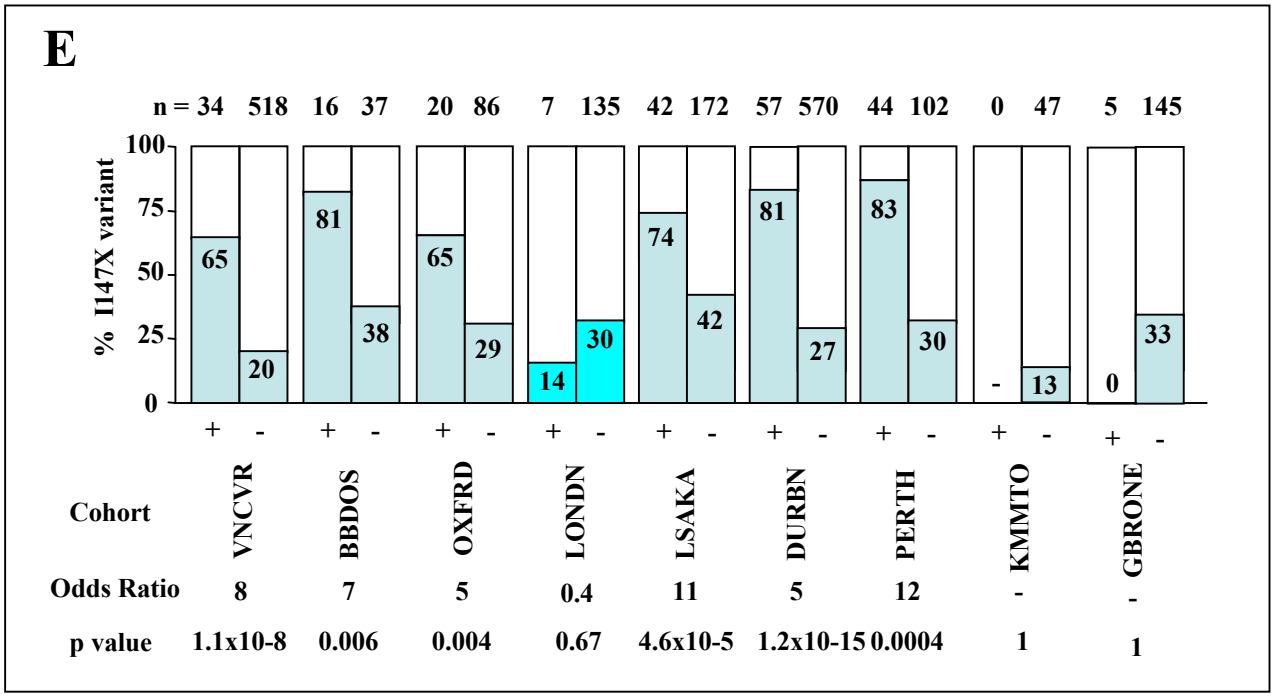
Suppl Fig 7


A
n = 129 423 5 46 23 75 22 81 28 187 67 606 39 129 3 74 9 141
% S357G variant
100
75
50
25
0
95 72 80 74 91 69 95 81 89 39 91 47 87 56 67 65 89 47
+ - + - + - + - + - + - + - + - + -
Cohort VNCVR BBDOS OXFRD LONDN LSAKA DURBN PERTH KMMTO GBRONE
Odds Ratio 8 1 5 5 13 11 5 1 10
p value 1.4x10-9 1 0.05 0.18 5.9x10-7 4.7x10-13 0.0003 1 0.01
B
n = 84 474 2 49 8 90 10 132 10 213 21 652 39 129 8 52 11 140
% D260X variant
100
75
50
25
0
98 89 - 94 88 79 90 86 60 23 86 32 91 80 100 92 64 20
+ - + - + - + - + - + - + - + - + -
Cohort VNCVR BBDOS OXFRD LONDN LSAKA DURBN PERTH KMMTO GBRONE
Odds Ratio 5 - 2 1 5 7 3 - 7
p value 0.002 - 1 1 0.02 3.3x10-5 0.26 1 0.003

Suppl Fig 7


C
n = 101 435 7 44 23 76 41 98 23 198 85 588 39 129 6 40 28 123
% D312X variant
100
75
50
25
0
93
75
100
66
74
51
71
70
78
58
61
25
84
65
83
75
61
50
+ - + - + - + - + - + - + - + - + -
Cohort
VNCVR BBDOS OXFRD LONDN LSAKA DURBN PERTH KMMTO GBRONE
Odds Ratio
4 - 3 1 3 5 3 2 2
p value
3.8x10-5 0.17 0.09 1 0.08 5.5x10-11 0.02 1 1
D
n = 51 472 1 31 19 44 1 33 7 258 20 169 41 27
% I31V variant
100
75
50
25
0
92
81
-
45
95
75
-
12
100
22
80
60
93
78
+ - + - + - + - + - + - + -
Cohort
VNCVR BBDOS OXFRD LSAKA DURBN PERTH KMMTO
Odds Ratio
3 - 24 - - 3 4
p value
0.05 - 0.09 - 3.3x10-5 0.09 0.14

Suppl Fig 7


E
n = 34 518 16 37 20 86 7 135 42 172 57 570 44 102 0 47 5 145
% I147X variant
100
75
50
25
0
65
20
81
38
65
29
14
30
74
42
81
27
83
30
-
13
0
33
+ - + - + - + - + - + - + - + - + -
Cohort
VNCVR
BBDOS
OXFRD
LONDN
LSAKA
DURBN
PERTH
KMMTO
GBRONE
Odds Ratio
8
7
5
0.4
11
5
12
-
-
p value
1.1x10-8
0.006
0.004
0.67
4.6x10-5
1.2x10-15
0.0004
1
1

Suppl Table 1

% Variant in Population versus Prevalence of HLA Allele in Population

		Linear Regression Model			**Logistic Regression Model**	
Polymorphism	**Epitope**	**r**	**p**	**(Pooled UK, r and p)**	**p**	**(Pooled UK, p)**
I135X	B*51-TAFTIPSI	0.94	0.0002	(0.95 and 0.0004)	0.0001	(<0.0001)
S357X	B*07-GPSHKARVL	0.67	0.051	(0.65 and 0.082)	0.004	(0.005)
D260X	B*35-PPIPVGDIY	0.81	0.008	(0.84 and 0.009)	0.016	(0.003)
D312X	B*44-AEQATQDVKNW	0.30	0.436	(0.26 and 0.539)	0.080	(0.103)
I31V	B*51-LPPIVAKEI	0.84	0.017	(0.84 and 0.017)	0.001	(0.001)
R264X	B*27-KRWIILGLNK	0.85	0.003	(0.92 and 0.001)	0.003	(0.004)
L268X	B*27-KRWIILGLNK	0.93	0.0002	(0.94 and 0.0005)	0.001	(0.003)
A146X	B*57-AISPRTLNAW	0.38	0.317	(0.36 and 0.378)	0.048	(0.068)
I147X	B*57-ISPRTLNAW	0.87	0.002	(0.91 and 0.002)	0.007	(0.007)
A163X	B*5703-KAFSPEVIPMF	0.80	0.031	(0.80 and 0.031)	0.110	(0.110)
S165X	B*5703-KAFSPEVIPMF	0.46	0.303	(0.46 and 0.303)	0.364	(0.364)
I168V	B*5703-KAFSPEVIPMF	0.84	0.019	(0.84 and 0.019)	0.085	(0.085)
T242X	B*57/5801-TSTLQEQIAW	0.99	<0.0001	(0.83 and 0.010)	<0.0001	(0.0003)
I247X	B*5703-TSTLQEQIAW	0.91	0.004	(0.91 and 0.004)	0.041	(0.041)
All polymorphisms		0.69	<0.0001	(0.69 and p<0.0001)	<0.0001	(<0.0001)

Suppl Table 2

% Variant in HLA-Mismatched Population versus Prevalence of HLA Allele in Population

		Linear Regression Model		
Polymorphism	**Epitope**	**r**	**p**	**(Pooled UK, r and p)**
I135X	B*51-TAFTIPSI	0.91	0.0006	(0.93 and 0.001)
S357X	B*07-GPSHKARVL	0.49	0.181	(0.45 and 0.258)
D260X	B*35-PPIPVGDIY	0.81	0.008	(0.84 and 0.009)
D312X	B*44-AEQATQDVKNW	0.19	0.623	(0.12 and 0.783)
I31V	B*51-LPPIVAKEI	0.81	0.027	(0.81 and 0.027)
R264X	B*27-KRWIILGLNK	0.85	0.004	(0.90 and 0.003)
L268X	B*27-KRWIILGLNK	0.87	0.002	(0.91 and 0.002)
A146X	B*57-AISPRTLNAW	0.22	0.562	(0.21 and 0.616)
I147X	B*57-ISPRTLNAW	0.73	0.025	(0.82 and 0.012)
A163X	B*5703-KAFSPEVIPMF	0.66	0.108	(0.66 and 0.108)
S165X	B*5703-KAFSPEVIPMF	0.35	0.439	(0.35 and 0.439)
I168V	B*5703-KAFSPEVIPMF	0.87	0.011	(0.87 and 0.011)
T242X	B*57/5801-TSTLQEQIAW	0.60	0.090	(0.54 and 0.164)
I247X	B*5703-TSTLQEQIAW	0.87	0.012	(0.87 and 0.012)
All polymorphisms		0.60	<0.0001	(0.61 and p<0.0001)

Suppl Table 3

Phylogenetically corrected and uncorrected HLA-HIV amino acid polymorphism associations (Vancouver, Perth, Kumamoto, Durban, Gaborone cohorts)

		Uncorrected Fisher's	Phylogenetically corrected
Polymorphism	**Epitope**	**p**	**p**
I135X	B*51-TAFTIPSI	$1.5x10^{-52}$	$2.9x10^{-45}$
S357X	B*07-GPSHKARVL	$6.7x10^{-24}$	$8.7x10^{-19}$
D260X	B*35-PPIPVGDIY	$3.8x10^{-17}$	$1.8x10^{-9}$
D312X	B*44-AEQATQDVKNW	$4.6x10^{-16}$	$3.1x10^{-12}$
I31V	B*51-LPPIVAKEI	$1.5x10^{-7}$	$9.2x10^{-3}$
R264X	B*27-KRWIILGLNK	$4.0x10^{-10}$	$2.8x10^{-9}$
L268X	B*27-KRWIILGLNK	$7.1x10^{-10}$	$3.4x10^{-10}$
A146X	B*57-AISPRTLNAW	$8.2x10^{-20}$	$1.7x10^{-9}$
I147X	B*57-ISPRTLNAW	$3.6x10^{-23}$	$7.5x10^{-6}$
A163X	B*5703-KAFSPEVIPMF	$1.3x10^{-21}$	$1.8x10^{-18}$
S165X	B*5703-KAFSPEVIPMF	$3.7x10^{-12}$	$5.7x10^{-6}$
I168V	B*5703-KAFSPEVIPMF	ns	ns
T242X	B*57/5801-TSTLQEQIAW	$3.9x10^{-64}$	$2.1x10^{-45}$
I247X	B*5703-TSTLQEQIAW	$5.7x10^{-7}$	$4.9x10^{-6}$

SUPPLEMENTARY INFORMATION

Genbank numbers:

Durban sequences:

Gag:	FJ198407-FJ199088
Pol:	FJ199532-FJ199992

Gaborone Sequences:

Gag p17+p24:	FJ497801-FJ497950
Gag p15:	FJ497951-FJ498243
Pol:	FJ498244-FJ498543
Nef:	FJ498544-FJ498779

London Sequences:

Gag:	FJ473452-FJ474070