

Supplemental Table S1

Sequences of primers and oligonucleotide probes modified with minor groove binder (MGB) for *OPRK1* and *PDYN* genotype analysis using TaqMan[®] assays; positions in chromosome are assigned according to dbSNP build 132

Position ^a , reference SNP ID # (Gene name)	Position in chromosome ^b	Primer or probe name ^c	Sequence of TaqMan MGB probes and primers for genotype studies (5'→3')
-1205G>A rs3808627 (<i>OPRK1</i>)	54164802 (Chr. 8) (5' end)	-1205 For -1205 Rev -1205C -1205T	CCGTCTGCTCTAACTGGGATG TCCCTGGAGCACCCTGAG AGGGCAAACACTCTCCTTA, FAM labeled AGGGCAAACATTCTCCTTA, VIC labeled
-298G>A rs16918955 (<i>OPRK1</i>)	54163895 (Chr. 8) (Intron 1)	-298 For -298 Rev -298C -298T	GAACCATAGGTAAGCTTTGGGCTT TCGCTCCTTCTCCCCAG AGGCACCGGCCCC, FAM labeled AGGCACTGGCCCC, VIC labeled

Supplemental Table S1 (Continued). Sequences of primers and oligonucleotide probes modified with minor groove binder (MGB) for *OPRK1* and *PDYN* genotype analysis using TaqMan[®] assays; positions in chromosome are assigned according to dbSNP build 132

Position ^a , reference SNP ID # (Gene name)	Position in chromosome ^b	Primer or probe name ^c	Sequence of TaqMan MGB probes and primers for genotype studies (5'→3')
-72C>T	54163669 (Chr. 8)	-72 For	AGCGAGAAGTCCGTTCTCCC
rs9282806 (<i>OPRK1</i>)	(Intron 1)	-72 Rev	AGCAGGAAGGCGAGGACAG
		-72C*	TCCGCGTCCAGCCGG, FAM labeled
		-72T*	TCCGCGTCTAGCCGGT, VIC labeled
36G>T (Pro12Pro)	54163562 (Chr. 8)	36 For	GCAAAGTTTGCCTCTCCGC
rs1051660 (<i>OPRK1</i>)	(Exon 2)	36 Rev	GAAACCAGGCGCTGCTGTT
		36C	AGGGCCCGGCTCG, FAM labeled
		36A	AGGGCCAGGCTCG, VIC labeled
IVS2+2225AG>A	54161116 (Chr. 8)	2225 For	CAGGCCTGATGATCACAACG
rs6985606	(Intron 2)	2225 Rev	TGATAGATGGTTCAAGGATTGAAAA
		2225C	ACCCTCTCTCCGATCTT, FAM labeled
		2225T	ACCCTCTCTCTGATCTTC, VIC labeled

Supplemental Table S1 (Continued). Sequences of primers and oligonucleotide probes modified with minor groove binder (MGB) for *OPRK1* and *PDYN* genotype analysis using TaqMan[®] assays; positions in chromosome are assigned according to dbSNP build 132

Position ^a , reference SNP ID # (Gene name)	Position in chromosome ^b	Primer or probe name ^c	Sequence of TaqMan MGB probes and primers for genotype studies (5'→3')
IVS2+7886A>G rs12548098 (<i>OPRK1</i>)	54155455 (Chr. 8) (Intron 2)	7886 For 7886 Rev 7886C 7886T	CTGGGATTACGGGCCTGAG CACTTGCCTTCTCCATTGGC TTGTCGTCCTCCATTGAA, FAM labeled TTGTCGTCCTCCATTGAAA, VIC labeled
IVS2+10658G>T rs1365098 (<i>OPRK1</i>)	54152683 (Chr. 8) (Intron 2)	10658 For 10658 Rev 10658G* 10658T*	TTAACTCAGTTTCCCCACCCC GAGAAACAGGGCAAGGTCCA TCCATTGAGGGGTAGTATTTA, FAM labeled TCCATTGAGGGTTAGTATTT, VIC labeled
IVS2+10963G>A rs997917 (<i>OPRK1</i>)	54152378 (Chr. 8) (Intron 2)	10963 For 10963 Rev 10963C 10963T	ACATGACTGCTCCTGCTGTTGT TTCCAAGAAGTGA AAAA AACTGAGA AATCCCATAAGATA CCACTGCC, FAM labeled AATCCCATAAGATA TCACTGCCT, VIC labeled

Supplemental Table S1 (Continued). Sequences of primers and oligonucleotide probes modified with minor groove binder (MGB) for *OPRK1* and *PDYN* genotype analysis using TaqMan[®] assays; positions in chromosome are assigned according to dbSNP build 132

Position ^a , reference SNP ID # (Gene name)	Position in chromosome ^b	Primer or probe name ^c	Sequence of TaqMan MGB probes and primers for genotype studies (5'→3')
IVS2+13236T>A	54150105 (Chr. 8)	13236 For	CAGAGAGATGAGTACAGGCAATAATCA
rs7016778 (<i>OPRK1</i>)	(Intron 2)	13236 Rev	AAGGATACCAGTACCTACCACATGAAG
		13236A	AGCTTTGTCTCAATTCATC, FAM labeled
		13236T	AGCTTTGTCTCATTTTCATC, VIC labeled
459C>T (Ser153Ser)	54147470 (Chr. 8)	459 For	CTTCAAGGGTGTGCGGAAGT
rs7815824 (<i>OPRK1</i>)	(Exon 3)	459 Rev	TGATGAATTCCTGGCCTTTTG
		459T*	ATGATGAGTGTGGACCGCTA, FAM labeled
		459C*	ATGATGAGCGTGGACCGC, VIC labeled
IVS3+3773C>G	54143548 (Chr. 8)	3773 For	TGACACTGGAAAAATCTGCTTCA
rs16918884 (<i>OPRK1</i>)	(Intron 3)	3773 Rev	TCCAAGGTTTCATCTGGTATTTC
		3773C	TAGAATATCCAATCTTACTAGAATTT, FAM labeled
		3773G	TAGAATATCCAATGTTACTAGAATTT, VIC labeled

Supplemental Table S1 (Continued). Sequences of primers and oligonucleotide probes modified with minor groove binder (MGB) for *OPRK1* and *PDYN* genotype analysis using TaqMan[®] assays; positions in chromosome are assigned according to dbSNP build 132

Position ^a , reference SNP ID # (Gene name)	Position in chromosome ^b	Primer or probe name ^c	Sequence of TaqMan MGB probes and primers for genotype studies (5'→3')
IVS3+4504C>A rs7817710 (<i>OPRK1</i>)	54142815 (Chr. 8) (Intron 3)	4504 For 4504 Rev 4504G 4504T	ACACTTCTCCCAGACCTAAGGCT GTTGACCCACATAATGATTTCCTG TTGTAATAAATGACTAAATATTTCAAATCT, FAM labeled TTGTAATAAAT T ACTAAATATTTCAAATCT, VIC labeled
843A>G (Ala281Ala) rs702764 (<i>OPRK1</i>)	54142157 (Chr. 8) (Exon 4)	843 For ^d 843 Rev ^d 843C 843T	TCTGGCTCCCGAGAGAAAGA TGTGAATGGGAGTCCAGCAG ACGAA(GA)ACCGCCACC, FAM labeled ACGAA(GA)ACTGCCACC, VIC labeled
846C>T (Val282Val) rs16918875 (<i>OPRK1</i>)	54142154 (Chr. 8) (Exon 4)	843 For ^d 843 Rev ^d 846G 846A	TCTGGCTCCCGAGAGAAAGA TGTGAATGGGAGTCCAGCAG ACGAAGAC(TC)GCCACC, FAM labeled ACGAAAAC(TC)GCCACC, VIC labeled

Supplemental Table S1 (Continued). Sequences of primers and oligonucleotide probes modified with minor groove binder (MGB) for *OPRK1* and *PDYN* genotype analysis using TaqMan[®] assays; positions in chromosome are assigned according to dbSNP build 132

Position ^a , reference SNP ID # (Gene name)	Position in chromosome ^b	Primer or probe name ^c	Sequence of TaqMan MGB probes and primers for genotype studies (5'→3')
1176G>A rs963549 (<i>OPRK1</i>)	54141824 (Chr. 8) (3' UTR)	1176 For 1176 Rev 1176C 1176T	CGTGGTCTGCATCTGATGACTT CTGCTTACCTGAGGGACATCG TCCTCTCTTCCCGAAGAA, FAM TCCTCTCTTCCCTGAAGAAC, VIC labeled
1796C>T rs3802282 (<i>OPRK1</i>)	54141204 (Chr. 8) (3' UTR)	1796 For 1796 Rev 1796A 1796G	TTTCTTGACAATGGGACATGCT GCTTGGACCCACATCTGAGG ACTGTAGTTTTTGAGAAATTA, FAM labeled ACTGTAGTTTTTGGAATA, VIC labeled
1837A>G rs3802281 (<i>OPRK1</i>)	54141163 (Chr. 8) (3' UTR)	1837 Forv 1837 Rev 1837C 1837T	TTTCTTGACAATGGGACATGCT GCTTGGACCCACATCTGAGG AAGACTGTCTACCTGAATAGC, FAM labeled AAGACTGTTTACCTGAATAGC, VIC labeled

Supplemental Table S1 (Continued). Sequences of primers and oligonucleotide probes modified with minor groove binder (MGB) for *OPRK1* and *PDYN* genotype analysis using TaqMan[®] assays; positions in chromosome are assigned according to dbSNP build 132

Position ^a , reference SNP ID # (Gene name)	Position in chromosome ^b	Primer or probe name ^c	Sequence of TaqMan MGB probes and primers for genotype studies (5'→3')
-13718A>G rs6045935 (<i>PDYN</i>)	1977448 (Chr. 20) (5' end)	-13718 For -13718 Rev -13718A -13718G	CCTTCCGCAGCCTCCTTTAC ACAGGGCCAGCACCATGAT CACACACATAGAAGGCC, FAM labeled CACACACGTAGAAGGC, VIC labeled
-13315A>T rs10854244 (<i>PDYN</i>)	1977045 (Chr. 20) (5' end)	-13315 For -13315 Rev -13315T -13315A	ACTTGGCCACATCTCAGGCT AAGAGAGCAGTTGGAGTGAGGC AGCGTCTTCTTCATCCC, VIC labeled AGCGTCTACTTCATCCC, FAM labeled
-12290 (68bp)n rs35286281 (<i>PDYN</i>)	1976020-21(Chr. 20) (5' end)	-12290 For -12290 F-FAM -12290 Rev -12290 R-FAM	CTGCACCAGGCGGTTAGGTA FAM- CTGCACCAGGCGGTTAGGTA ^e AGTGTGGGCAGATTCAAGCC FAM- AGTGTGGGCAGATTCAAGCC ^e

Supplemental Table S1 (Continued). Sequences of primers and oligonucleotide probes modified with minor groove binder (MGB) for *OPRK1* and *PDYN* genotype analysis using TaqMan[®] assays; positions in chromosome are assigned according to dbSNP build 132

Position ^a , reference SNP ID # (Gene name)	Position in chromosome ^b	Primer or probe name ^c	Sequence of TaqMan MGB probes and primers for genotype studies (5'→3')
-11128G>A rs1997794 (<i>PDYN</i>)	1974858 (Chr. 20) (5' end)	-11128 For -11128 Rev -11128T -11128C	GCAGTCAGAGCACAGACCCC GGCCGGATTTC AAGTGACAA TGGGCCTGACACAATA, FAM labeled TGGGCCCGACACAAT, VIC labeled
-3548C>T rs6045868 (<i>PDYN</i>)	1967278 (Chr. 20) (Intron 3)	5952 For 5952 Rev 5952G 5952A	GCCCCTGTGCTCAGAACTCT TCCAATCTGTCTGGGTGCTG ACA ACTCCGTAAGACTGG, FAM labeled ACA ACTCCATAAGACTGGG, VIC labeled
IVS3+189C>T rs6035222 (<i>PDYN</i>) (His200His)	1963413 (Chr. 20) (Intron 4)	189 For 189 Rev 189G 189A	CTGACTGCCGAAGTCAGCAC GTCCTGCCCTATAGATGGCCT TGGCGAGGTCTGGAGTG, FAM labeled TGGCGAAGTCTGGAGTG, VIC labeled

Supplemental Table S1 (Continued). Sequences of primers and oligonucleotide probes modified with minor groove binder (MGB) for *OPRK1* and *PDYN* genotype analysis using TaqMan[®] assays; positions in chromosome are assigned according to dbSNP build 132

Position ^a , reference SNP ID # (Gene name)	Position in chromosome ^b	Primer or probe name ^c	Sequence of TaqMan MGB probes and primers for genotype studies (5'→3')
600T>C (His200His) rs6045819 (<i>PDYN</i>)	1961134 (Chr. 20) (Exon 5)	600 For 600 Rev 600A 600G	CTTGAGCTTGGGACGAATGC AGGACCCCAAGGAGCAGGT AGGTCCTCATGGCCC, FAM labeled AGGTCCTCGTGGCCC, VIC labeled
1421T>C rs10485703 (<i>PDYN</i>)	1960313 (Chr. 20) (3' UTR)	1421 For 1421 Rev 1421A 1421G	TAAGGAGTTAGGCACTGTCCAGG AGAGGGTCCAGTCTTCTAGTGGG AGGACTCAGAGTACACTGAC, FAM labeled AGGACTCAGAGTGCACTGA, VIC labeled
1508T>C rs910080 (<i>PDYN</i>)	1960226 (Chr. 20) (3' UTR)	1508 For 1508 Rev 1508A 1508G	GGTTTGCCTTTCTCCCTCCT CTTCCTGAACTCCCAGTCATGTT AGGAGTTAGGCACTGTCC, FAM labeled AGGAGTTGGGCACTGTC, VIC labeled

Supplemental Table S1 (Continued). Sequences of primers and oligonucleotide probes modified with minor groove binder (MGB) for *OPRK1* and *PDYN* genotype analysis using TaqMan[®] assays; positions in chromosome are assigned according to dbSNP build 132

Position ^a , reference SNP ID # (Gene name)	Position in chromosome ^b	Primer or probe name ^c	Sequence of TaqMan MGB probes and primers for genotype studies (5'→3')
1536T>C	1960198 (Chr. 20)	1536 For	GCTGAGGGAAGTGGTCCACA
rs910079 (<i>PDYN</i>)	(3' UTR)	1536 Rev	CCCTGGACAGTGCCTAACTCC
		1536A	TCCGAAAGAGGTTTTTCAC, FAM labeled
		1536G	TCCGAAAGGGGTTTTTC, VIC labeled
1795C>T	1959939 (Chr. 20)	1795 For	AGCTGCTGCTTCTGGAGTCC
rs2235749 (<i>PDYN</i>)	(3' UTR)	1795 Rev	TCCATGGTGAAGTGAAGCAGAG
		1795G	CCAGTGCATATGTTGGG, FAM labeled
		1795A	CCAGTGCATATGTTGGGC, VIC labeled

^aNumbering of the polymorphism position is based upon the previously reported system that gives value +1 to the first nucleotide of AUG initiation codon; bases belonging to the coding region have positive values; bases belonging to the upstream 5' initiation codon have negative values;

^bNumbering according to dbSNP build 129;

^cSince both genes analyzed in this study are located in direction opposite to the counting of nucleotide bases in chromosome, all TaqMan probes except those labeled with * were chosen from the strand opposite to the gene counting strand, not the chromosome coding strand;

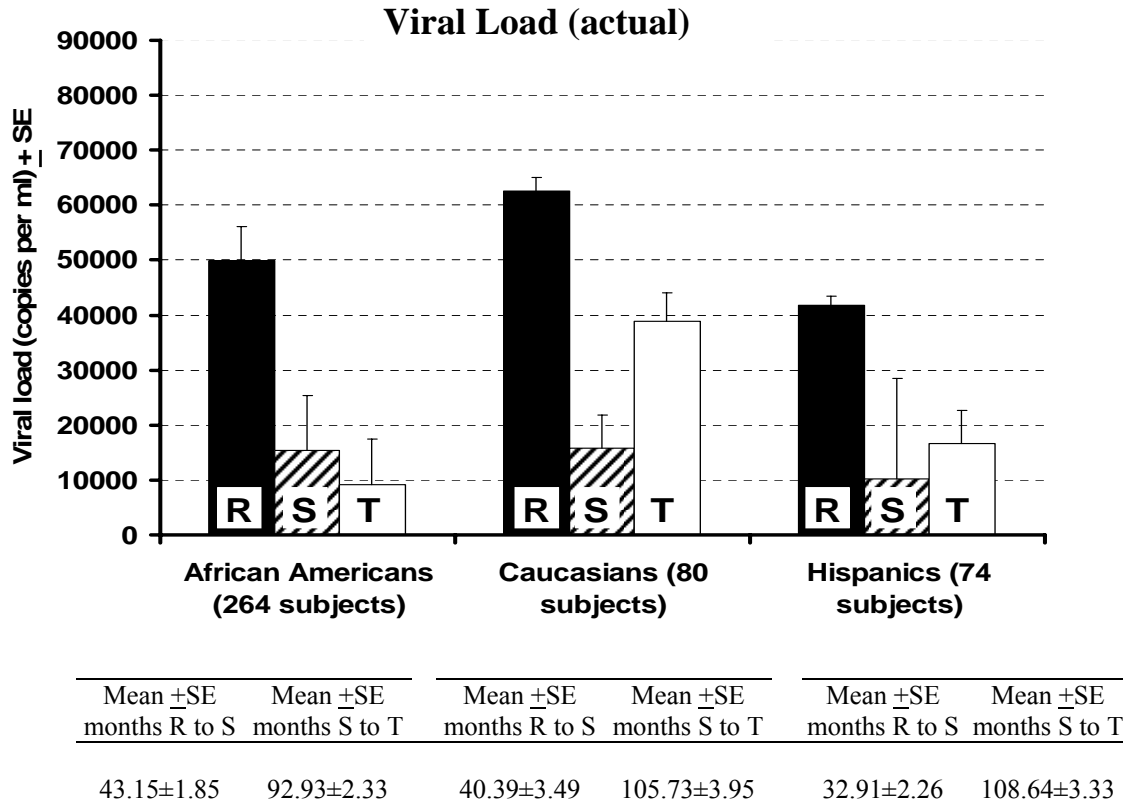
^dThe same set of primers was used for genotyping of 846C>T and 843A>G;

^eNon- MGB probes labeled with 5'-FAM used in regular PCR for generating fluorescently labeled amplicons for fragment analysis (number of repeats)

Supplemental Figure S1A-B. Mean values of equivalent and ln of viral load at different study

points with mean time intervals for subjects of different ethnicities (Data Set 1, Table 1C)

1A

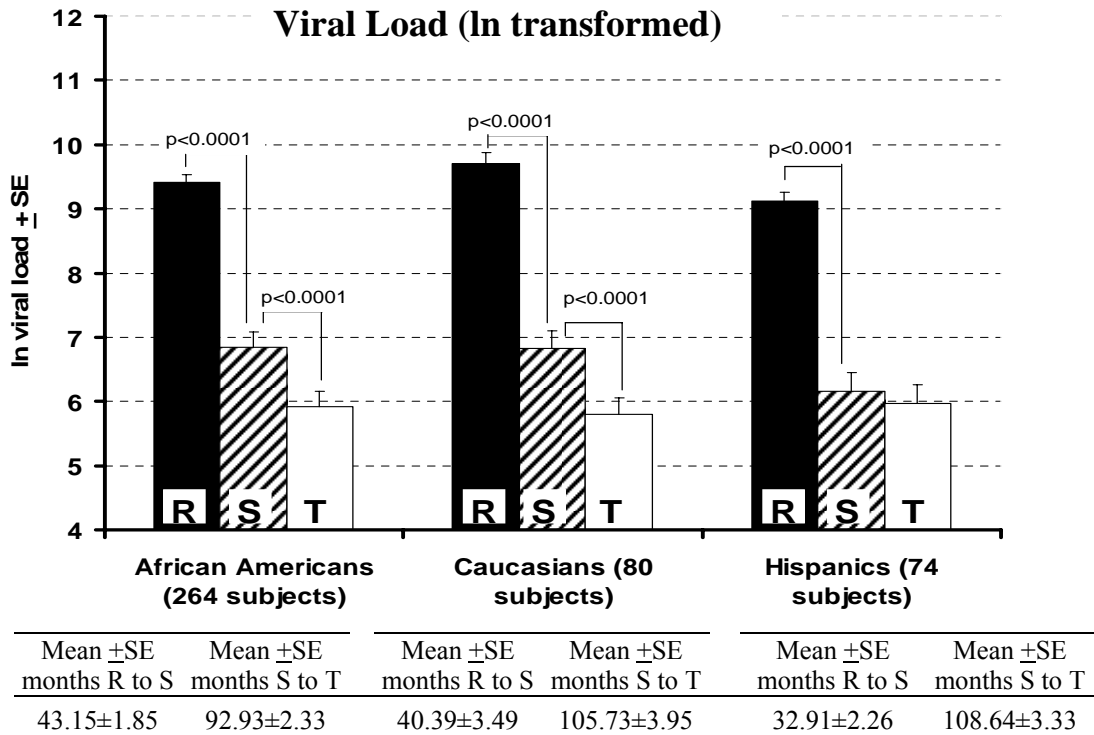


R- defined as time of admission to WIHS

S- defined as initiation of HAART

T- defined as most recent visit for which clinical information was available

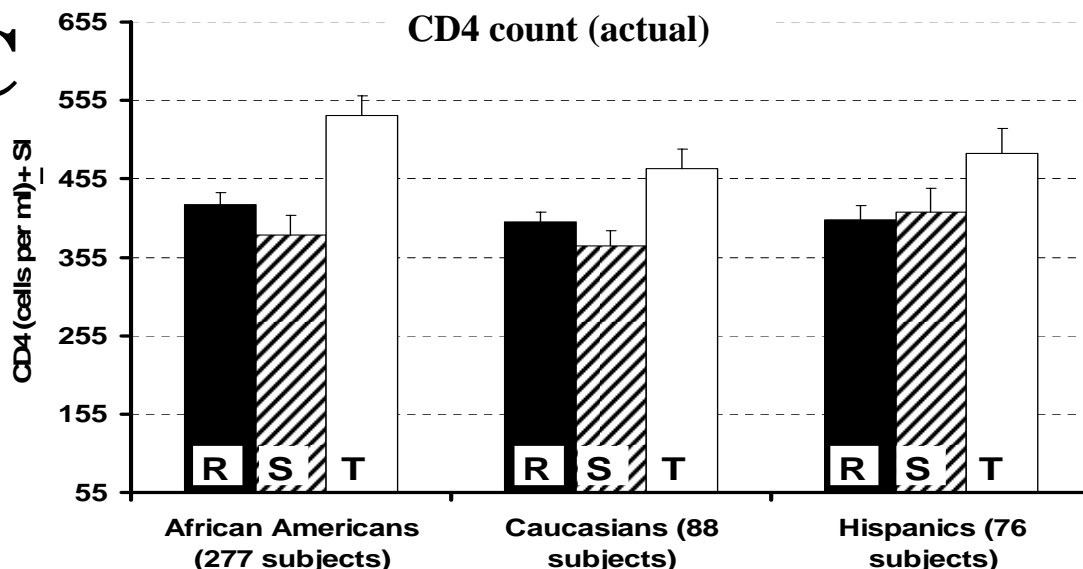
1B



- A. Mean + SE values of viral load in different ethnic groups. Only subjects who had measurements at each of three study points were included in this analysis. The study points are defined as: R- entrance to WIHS study, S- initiation of HAART treatment and T- most recent WIHS visit (Table 1B). Mean + SE time (months) intervals that subjects of different ethnicities spent from the entrance to WIHS study until initiation of HAART treatment (X), and from initiation of HAART treatment until most recent visit (Y).
- B. Transformed data for statistical analysis. Mean + SE values of ln of viral load are plotted and indicated on left Y-axis. The right Y-axis shows the equivalent values of viral load.

Supplemental Figure S1C-D. Mean values of equivalent and ln of CD4 count at different study points with mean time intervals for subjects of different ethnicities (Data Set 1, Table 1C)

1C



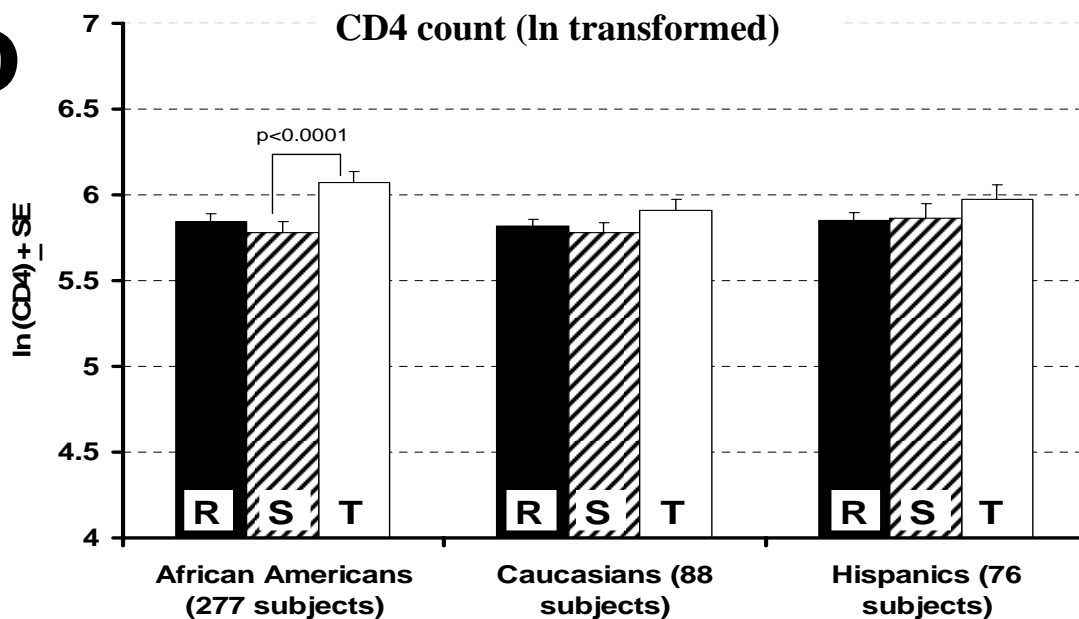
Mean ± SE	Mean ± SE	Mean ± SE	Mean ± SE	Mean ± SE	Mean ± SE
months R to S	months S to T	months R to S	months S to T	months R to S	months S to T
42.77±1.79	93.95±2.25	39.20±3.22	107.15±3.86	32.84±2.20	109.08±3.26

R- defined as time of admission to WIHS

S- defined as initiation of HAART

T- defined as most recent visit for which clinical information was available

1D



Mean ± SE	Mean ± SE	Mean ± SE	Mean ± SE	Mean ± SE	Mean ± SE
months R to S	months S to T	months R to S	months S to T	months R to S	months S to T
42.77±1.79	93.95±2.25	39.20±3.22	107.15±3.86	32.84±2.20	109.08±3.26

C. Mean + SE values of CD4 count in different ethnic groups. Only subjects who had measurements at each of three study points were included in this analysis.. The study points are defined as: R- entrance to WIHS study, S- initiation of HAART treatment and T- most recent WIHS visit (Table 1B). Mean + SE time (months) intervals that subjects of different ethnicity spent from the entrance to WIHS study until initiation of HAART treatment (X), and from initiation of HAART treatment until most recent visit (Y).

D. Transformed data for statistical analysis. Mean + SE values of ln of CD4 count are plotted and indicated on left Y-axis. The right Y-axis shows the equivalent values of CD4 count.

Supplemental Table S2

Genotype and allele frequencies of the polymorphisms studied in *OPRK1* and *PDYN* genes; estimation of difference of genotype frequency between control subjects of different ethnicities (Data set from Table 1A)

OPRK1: rs3808627, -1205G>A

Genotype/ allele	African Americans		African Americans		Caucasians		Caucasians		Hispanics		Hispanics	
	HIV-		HIV+		HIV-		HIV+		HIV-		HIV+	
	N	freq.	N	freq.	N	freq.	N	freq.	N	freq.	N	freq.
GG	182	0.858	423	0.914	31	0.674	70	0.625	50	0.735	78	0.729
GA	27	0.127	37	0.080	14	0.304	40	0.357	14	0.206	23	0.215
AA	3	0.014	3	0.006	1	0.022	2	0.018	4	0.059	6	0.056
Total	212	1.000	463	1.000	46	1.000	112	1.000	68	1.000	107	1.000
G	391	0.922	883	0.954	76	0.826	180	0.804	114	0.838	179	0.836
A	33	0.078	43	0.046	16	0.174	44	0.196	22	0.162	35	0.164
Total	424	1.000	926	1.000	92	1.000	224	1.000	136	1.000	214	1.000

p (HIV-)^a = **0.007**

N- Number of subjects; highlighted are polymorphisms with allele frequency <0.05 in both control and case group and which were not analyzed further; ^ap shows estimation of difference of genotype frequency between control subjects of different ethnicities; significant values (p<0.05) are in bold italic

Supplemental Table S2 (Continued). Genotype and allele frequencies of the polymorphisms studied in *OPRK1* and *PDYN* genes; estimation of difference of genotype frequency between control subjects of different ethnicities (Data set from Table 1A)

OPRK1: rs16918955 , -298G>A

Genotype/ allele	African Americans		African Americans		Caucasians		Caucasians		Hispanics		Hispanics	
	HIV-		HIV+		HIV-		HIV+		HIV-		HIV+	
	N	freq.	N	freq.	N	freq.	N	freq.	N	freq.	N	freq.
GG	184	0.872	396	0.870	41	0.891	104	0.929	61	0.924	98	0.933
GA	26	0.123	57	0.125	5	0.109	8	0.071	5	0.076	7	0.067
AA	1	0.005	2	0.004	0	0.000	0	0.000	0	0.000	0	0.000
Total	211	1.000	455	1.000	46	1.000	112	1.000	66	1.000	105	1.000
G	394	0.934	849	0.933	87	0.946	216	0.964	127	0.962	203	0.967
A	28	0.066	61	0.067	5	0.054	8	0.036	5	0.038	7	0.033
Total	422	1.000	910	1.000	92	1.000	224	1.000	132	1.000	210	1.000

p (HIV-)^a = 0.789

N- Number of subjects; highlighted are polymorphisms with allele frequency <0.05 in both control and case group and which were not analyzed further; ^ap shows estimation of difference of genotype frequency between control subjects of different ethnicities; significant values (p<0.05) are in bold italic

Supplemental Table S2 (Continued). Genotype and allele frequencies of the polymorphisms studied in *OPRK1* and *PDYN* genes; estimation of difference of genotype frequency between control subjects of different ethnicities (Data set from Table 1A)

OPRK1: rs9282806, -72C>T

Genotype/ allele	African Americans		African Americans		Caucasians		Caucasians		Hispanics		Hispanics	
	HIV-		HIV+		HIV-		HIV+		HIV-		HIV+	
	N	freq.	N	freq.	N	freq.	N	freq.	N	freq.	N	freq.
CC	169	0.793	381	0.825	45	0.978	111	0.991	63	0.926	102	0.953
CT	41	0.192	80	0.173	1	0.022	1	0.009	5	0.074	4	0.037
TT	3	0.014	1	0.002	0	0.000	0	0.000	0	0.000	1	0.009
Total	213	1.000	462	1.000	46	1.000	112	1.000	68	1.000	107	1.000
C	379	0.890	842	0.911	91	0.989	223	0.996	131	0.963	208	0.972
T	47	0.110	82	0.089	1	0.011	1	0.004	5	0.037	6	0.028
Total	426	1.000	924	1.000	92	1.000	224	1.000	136	1.000	214	1.000

p (HIV-)^a = **0.006**

N- Number of subjects; highlighted are polymorphisms with allele frequency <0.05 in both control and case group and which were not analyzed further; ^ap shows estimation of difference of genotype frequency between control subjects of different ethnicities; significant values (p<0.05) are in bold italic

Supplemental Table S2 (Continued). Genotype and allele frequencies of the polymorphisms studied in *OPRK1* and *PDYN* genes; estimation of difference of genotype frequency between control subjects of different ethnicities (Data set from Table 1A)

OPRK1: rs1051660, 36G>T (Pro12Pro)

Genotype/ allele	African Americans		African Americans		Caucasians		Caucasians		Hispanics		Hispanics	
	HIV-		HIV+		HIV-		HIV+		HIV-		HIV+	
	N	freq.	N	freq.	N	freq.	N	freq.	N	freq.	N	freq.
GG	175	0.822	368	0.797	38	0.826	92	0.821	55	0.821	94	0.879
GT	37	0.174	89	0.193	8	0.174	20	0.179	12	0.179	12	0.112
TT	1	0.005	5	0.011	0	0.000	0	0.000	0	0.000	1	0.009
Total	213	1.000	462	1.000	46	1.000	112	1.000	67	1.000	107	1.000
G	387	0.908	825	0.893	84	0.913	204	0.911	122	0.910	200	0.935
T	39	0.092	99	0.107	8	0.087	20	0.089	12	0.090	14	0.065
Total	426	1.000	924	1.000	92	1.000	224	1.000	134	1.000	214	1.000
p (HIV-) ^a	=0.969											

N- Number of subjects; highlighted are polymorphisms with allele frequency <0.05 in both control and case group and which were not analyzed further; ^ap shows estimation of difference of genotype frequency between control subjects of different ethnicities; significant values (p<0.05) are in bold italic

Supplemental Table S2 (Continued). Genotype and allele frequencies of the polymorphisms studied in *OPRK1* and *PDYN* genes; estimation of difference of genotype frequency between control subjects of different ethnicities (Data set from Table 1A)

OPRK1: rs6985606, IVS2+2225G>A

Genotype/ allele	African Americans		African Americans		Caucasians		Caucasians		Hispanics		Hispanics	
	HIV-		HIV+		HIV-		HIV+		HIV-		HIV+	
	N	freq.	N	freq.	N	freq.	N	freq.	N	freq.	N	freq.
GG	181	0.858	395	0.859	13	0.283	36	0.324	36	0.529	58	0.547
GA	25	0.118	61	0.133	22	0.478	50	0.450	28	0.412	41	0.387
AA	5	0.024	4	0.009	11	0.239	25	0.225	4	0.059	7	0.066
Total	211	1.000	460	1.000	46	1.000	111	1.000	68	1.000	106	1.000
G	387	0.917	851	0.925	48	0.522	122	0.550	100	0.735	157	0.741
A	35	0.083	69	0.075	44	0.478	100	0.450	36	0.265	55	0.259
Total	422	1.000	920	1.000	92	1.000	222	1.000	136	1.000	212	1.000
p (HIV-) ^a	< 0.001											

N- Number of subjects; highlighted are polymorphisms with allele frequency <0.05 in both control and case group and which were not analyzed further; ^ap shows estimation of difference of genotype frequency between control subjects of different ethnicities; significant values (p<0.05) are in bold italic

Supplemental Table S2 (Continued). Genotype and allele frequencies of the polymorphisms studied in *OPRK1* and *PDYN* genes; estimation of difference of genotype frequency between control subjects of different ethnicities (Data set from Table 1A)

OPRK1: rs12548098, IVS2+7886A>G

Genotype/ allele	African Americans		African Americans		Caucasians		Caucasians		Hispanics		Hispanics	
	HIV-		HIV+		HIV-		HIV+		HIV-		HIV+	
	N	freq.	N	freq.	N	freq.	N	freq.	N	freq.	N	freq.
AA	143	0.675	290	0.630	38	0.826	102	0.911	56	0.824	86	0.804
AG	49	0.231	124	0.270	8	0.174	10	0.089	11	0.162	18	0.168
GG	20	0.094	46	0.100	0	0.000	0	0.000	1	0.015	3	0.028
Total	212	1.000	460	1.000	46	1.000	112	1.000	68	1.000	107	1.000
A	335	0.790	704	0.765	84	0.913	214	0.955	123	0.904	190	0.888
G	89	0.210	216	0.235	8	0.087	10	0.045	13	0.096	24	0.112
Total	424	1.000	920	1.000	92	1.000	224	1.000	136	1.000	214	1.000
p (HIV-) ^a = 0.015												

N- Number of subjects; highlighted are polymorphisms with allele frequency <0.05 in both control and case group and which were not analyzed further; ^ap shows estimation of difference of genotype frequency between control subjects of different ethnicities; significant values (p<0.05) are in bold italic

Supplemental Table S2 (Continued). Genotype and allele frequencies of the polymorphisms studied in *OPRK1* and *PDYN* genes; estimation of difference of genotype frequency between control subjects of different ethnicities (Data set from Table 1A)

OPRK1: rs1365098, IVS2+10658G>T

Genotype/ allele	African Americans		African Americans		Caucasians		Caucasians		Hispanics		Hispanics	
	HIV-		HIV+		HIV-		HIV+		HIV-		HIV+	
	N	freq.	N	freq.	N	freq.	N	freq.	N	freq.	N	freq.
GG	25	0.117	37	0.080	21	0.457	51	0.455	19	0.279	32	0.299
GT	84	0.394	182	0.394	18	0.391	49	0.438	34	0.500	51	0.477
TT	104	0.488	243	0.526	7	0.152	12	0.107	15	0.221	24	0.224
Total	213	1.000	462	1.000	46	1.000	112	1.000	68	1.000	107	1.000
G	134	0.315	256	0.277	60	0.652	151	0.674	72	0.529	115	0.537
T	292	0.685	668	0.723	32	0.348	73	0.326	64	0.471	99	0.463
Total	426	1.000	924	1.000	92	1.000	224	1.000	136	1.000	214	1.000

p (HIV-)^a < **0.001**

N- Number of subjects; highlighted are polymorphisms with allele frequency <0.05 in both control and case group and which were not analyzed further; ^ap shows estimation of difference of genotype frequency between control subjects of different ethnicities; significant values (p<0.05) are in bold italic

Supplemental Table S2 (Continued). Genotype and allele frequencies of the polymorphisms studied in *OPRK1* and *PDYN* genes; estimation of difference of genotype frequency between control subjects of different ethnicities (Data set from Table 1A)

OPRK1: rs997917, IVS2+10963G>A

Genotype/ allele	African Americans		African Americans		Caucasians		Caucasians		Hispanics		Hispanics	
	HIV-		HIV+		HIV-		HIV+		HIV-		HIV+	
	N	freq.	N	freq.	N	freq.	N	freq.	N	freq.	N	freq.
GG	104	0.488	243	0.527	7	0.152	12	0.107	15	0.221	24	0.224
GA	84	0.394	180	0.390	18	0.391	49	0.438	34	0.500	51	0.477
AA	25	0.117	38	0.082	21	0.457	51	0.455	19	0.279	32	0.299
Total	213	1.000	461	1.000	46	1.000	112	1.000	68	1.000	107	1.000
G	292	0.685	666	0.722	32	0.348	73	0.326	64	0.471	99	0.463
A	134	0.315	256	0.278	60	0.652	151	0.674	72	0.529	115	0.537
Total	426	1.000	922	1.000	92	1.000	224	1.000	136	1.000	214	1.000
p (HIV-) ^a	< 0.001											

N- Number of subjects; highlighted are polymorphisms with allele frequency <0.05 in both control and case group and which were not analyzed further; ^ap shows estimation of difference of genotype frequency between control subjects of different ethnicities; significant values (p<0.05) are in bold italic

Supplemental Table S2 (Continued). Genotype and allele frequencies of the polymorphisms studied in *OPRK1* and *PDYN* genes; estimation of difference of genotype frequency between control subjects of different ethnicities (Data set from Table 1A)

OPRK1: rs7016778, IVS2+13236T>A

Genotype/ allele	African Americans		African Americans		Caucasians		Caucasians		Hispanics		Hispanics	
	HIV-		HIV+		HIV-		HIV+		HIV-		HIV+	
	N	freq.	N	freq.	N	freq.	N	freq.	N	freq.	N	freq.
AA	103	0.486	197	0.426	33	0.717	95	0.848	47	0.691	74	0.692
AT	88	0.415	212	0.459	13	0.283	17	0.152	20	0.294	31	0.290
TT	21	0.099	53	0.115	0	0.000	0	0.000	1	0.015	2	0.019
Total	212	1.000	462	1.000	46	1.000	112	1.000	68	1.000	107	1.000
A	294	0.693	606	0.656	79	0.859	207	0.924	114	0.838	179	0.836
T	130	0.307	318	0.344	13	0.141	17	0.076	22	0.162	35	0.164
Total	424	1.000	924	1.000	92	1.000	224	1.000	136	1.000	214	1.000
p (HIV-) ^a	= 0.001											

N- Number of subjects; highlighted are polymorphisms with allele frequency <0.05 in both control and case group and which were not analyzed further; ^ap shows estimation of difference of genotype frequency between control subjects of different ethnicities; significant values (p<0.05) are in bold italic

Supplemental Table S2 (Continued). Genotype and allele frequencies of the polymorphisms studied in *OPRK1* and *PDYN* genes; estimation of difference of genotype frequency between control subjects of different ethnicities (Data set from Table 1A)

OPRK1: rs7815824, 459C>T (Ser153Ser)

Genotype/ allele	African Americans		African Americans		Caucasians		Caucasians		Hispanics		Hispanics	
	HIV-		HIV+		HIV-		HIV+		HIV-		HIV+	
	N	freq.	N	freq.	N	freq.	N	freq.	N	freq.	N	freq.
CC	150	0.704	330	0.713	44	0.957	106	0.946	58	0.853	90	0.841
CT	61	0.286	121	0.261	2	0.043	5	0.045	10	0.147	16	0.150
TT	2	0.009	12	0.026	0	0.000	1	0.009	0	0.000	1	0.009
Total	213	1.000	463	1.000	46	1.000	112	1.000	68	1.000	107	1.000
C	361	0.847	781	0.843	90	0.978	217	0.969	126	0.926	196	0.916
T	65	0.153	145	0.157	2	0.022	7	0.031	10	0.074	18	0.084
Total	426	1.000	926	1.000	92	1.000	224	1.000	136	1.000	214	1.000
p (HIV-) ^a = 0.002												

N- Number of subjects; highlighted are polymorphisms with allele frequency <0.05 in both control and case group and which were not analyzed further; ^ap shows estimation of difference of genotype frequency between control subjects of different ethnicities; significant values (p<0.05) are in bold italic

Supplemental Table S2 (Continued). Genotype and allele frequencies of the polymorphisms studied in *OPRK1* and *PDYN* genes; estimation of difference of genotype frequency between control subjects of different ethnicities (Data set from Table 1A)

OPRK1: rs16918884, IVS3+3773C>G

Genotype/ allele	African Americans		African Americans		Caucasians		Caucasians		Hispanics		Hispanics	
	HIV-		HIV+		HIV-		HIV+		HIV-		HIV+	
	N	freq.	N	freq.	N	freq.	N	freq.	N	freq.	N	freq.
CC	172	0.808	348	0.758	45	0.978	108	0.973	62	0.912	96	0.906
CG	22	0.103	59	0.129	0	0.000	1	0.009	3	0.044	4	0.038
GG	19	0.089	52	0.113	1	0.022	2	0.018	3	0.044	6	0.057
Total	213	1.000	459	1.000	46	1.000	111	1.000	68	1.000	106	1.000
C	366	0.859	755	0.822	90	0.978	217	0.977	127	0.934	196	0.925
G	60	0.141	163	0.178	2	0.022	5	0.023	9	0.066	16	0.075
Total	426	1.000	918	1.000	92	1.000	222	1.000	136	1.000	212	1.000

p (HIV-)^a = **0.023**

N- Number of subjects; highlighted are polymorphisms with allele frequency <0.05 in both control and case group and which were not analyzed further; ^ap shows estimation of difference of genotype frequency between control subjects of different ethnicities; significant values (p<0.05) are in bold italic

Supplemental Table S2 (Continued). Genotype and allele frequencies of the polymorphisms studied in *OPRK1* and *PDYN* genes; estimation of difference of genotype frequency between control subjects of different ethnicities (Data set from Table 1A)

OPRK1: rs7817710, IVS3+4504C>A

Genotype/ allele	African Americans		African Americans		Caucasians		Caucasians		Hispanics		Hispanics	
	HIV-		HIV+		HIV-		HIV+		HIV-		HIV+	
	N	freq.	N	freq.	N	freq.	N	freq.	N	freq.	N	freq.
CC	108	0.509	203	0.439	37	0.804	85	0.759	35	0.515	57	0.533
CA	85	0.401	206	0.446	8	0.174	25	0.223	30	0.441	44	0.411
AA	19	0.090	53	0.115	1	0.022	2	0.018	3	0.044	6	0.056
Total	212	1.000	462	1.000	46	1.000	112	1.000	68	1.000	107	1.000
C	301	0.710	612	0.662	82	0.891	195	0.871	100	0.735	158	0.738
A	123	0.290	312	0.338	10	0.109	29	0.129	36	0.265	56	0.262
Total	424	1.000	924	1.000	92	1.000	224	1.000	136	1.000	214	1.000
p (HIV-) ^a	= 0.004											

N- Number of subjects; highlighted are polymorphisms with allele frequency <0.05 in both control and case group and which were not analyzed further; ^ap shows estimation of difference of genotype frequency between control subjects of different ethnicities; significant values (p<0.05) are in bold italic

Supplemental Table S2 (Continued). Genotype and allele frequencies of the polymorphisms studied in *OPRK1* and *PDYN* genes; estimation of difference of genotype frequency between control subjects of different ethnicities (Data set from Table 1A)

OPRK1: rs702764, 843A>G (Ala281Ala)

Genotype/ allele	African Americans		African Americans		Caucasians		Caucasians		Hispanics		Hispanics	
	HIV-		HIV+		HIV-		HIV+		HIV-		HIV+	
	N	freq.	N	freq.	N	freq.	N	freq.	N	freq.	N	freq.
AA	59	0.284	122	0.266	32	0.696	78	0.696	29	0.433	47	0.448
GA	104	0.500	219	0.478	13	0.283	31	0.277	31	0.463	48	0.457
GG	45	0.216	117	0.255	1	0.022	3	0.027	7	0.104	10	0.095
Total	208	1.000	458	1.000	46	1.000	112	1.000	67	1.000	105	1.000
A	222	0.534	463	0.505	77	0.837	187	0.835	89	0.664	142	0.676
G	194	0.466	453	0.495	15	0.163	37	0.165	45	0.336	68	0.324
Total	416	1.000	916	1.000	92	1.000	224	1.000	134	1.000	210	1.000
p (HIV-) ^a	< 0.001											

N- Number of subjects; highlighted are polymorphisms with allele frequency <0.05 in both control and case group and which were not analyzed further; ^ap shows estimation of difference of genotype frequency between control subjects of different ethnicities; significant values (p<0.05) are in bold italic

Supplemental Table S2 (Continued). Genotype and allele frequencies of the polymorphisms studied in *OPRK1* and *PDYN* genes; estimation of difference of genotype frequency between control subjects of different ethnicities (Data set from Table 1A)

OPRK1: rs16918875, 846C>T (Val282Val)

Genotype/ allele	African Americans		African Americans		Caucasians		Caucasians		Hispanics		Hispanics	
	HIV-		HIV+		HIV-		HIV+		HIV-		HIV+	
	N	freq.	N	freq.	N	freq.	N	freq.	N	freq.	N	freq.
CC	147	0.693	332	0.720	41	0.891	104	0.929	58	0.866	95	0.888
CT	59	0.278	119	0.258	5	0.109	8	0.071	9	0.134	11	0.103
TT	6	0.028	10	0.022	0	0.000	0	0.000	0	0.000	1	0.009
Total	212	1.000	461	1.000	46	1.000	112	1.000	67	1.000	107	1.000
C	353	0.833	783	0.849	87	0.946	216	0.964	125	0.933	201	0.939
T	71	0.167	139	0.151	5	0.054	8	0.036	9	0.067	13	0.061
Total	424	1.000	922	1.000	92	1.000	224	1.000	134	1.000	214	1.000
p (HIV-) ^a = 0.006												

N- Number of subjects; highlighted are polymorphisms with allele frequency <0.05 in both control and case group and which were not analyzed further; ^ap shows estimation of difference of genotype frequency between control subjects of different ethnicities; significant values (p<0.05) are in bold italic

Supplemental Table S2 (Continued). Genotype and allele frequencies of the polymorphisms studied in *OPRK1* and *PDYN* genes; estimation of difference of genotype frequency between control subjects of different ethnicities (Data set from Table 1A)

OPRK1: rs963549, 1176G>A

Genotype/ allele	African Americans		African Americans		Caucasians		Caucasians		Hispanics		Hispanics	
	HIV-		HIV+		HIV-		HIV+		HIV-		HIV+	
	N	freq.	N	freq.	N	freq.	N	freq.	N	freq.	N	freq.
GG	65	0.305	127	0.277	32	0.696	78	0.696	28	0.418	48	0.449
AG	102	0.479	220	0.479	13	0.283	31	0.277	33	0.493	49	0.458
AA	46	0.216	112	0.244	1	0.022	3	0.027	6	0.090	10	0.093
Total	213	1.000	459	1.000	46	1.000	112	1.000	67	1.000	107	1.000
G	232	0.545	474	0.516	77	0.837	187	0.835	89	0.664	145	0.678
A	194	0.455	444	0.484	15	0.163	37	0.165	45	0.336	69	0.322
Total	426	1.000	918	1.000	92	1.000	224	1.000	134	1.000	214	1.000
p (HIV-) ^a	< 0.001											

N- Number of subjects; highlighted are polymorphisms with allele frequency <0.05 in both control and case group and which were not analyzed further; ^ap shows estimation of difference of genotype frequency between control subjects of different ethnicities; significant values (p<0.05) are in bold italic

Supplemental Table S2 (Continued). Genotype and allele frequencies of the polymorphisms studied in *OPRK1* and *PDYN* genes; estimation of difference of genotype frequency between control subjects of different ethnicities (Data set from Table 1A)

OPRK1: rs3802282, 1796C>T

Genotype/ allele	African Americans		African Americans		Caucasians		Caucasians		Hispanics		Hispanics	
	HIV-		HIV+		HIV-		HIV+		HIV-		HIV+	
	N	freq.	N	freq.	N	freq.	N	freq.	N	freq.	N	freq.
CC	68	0.319	124	0.268	33	0.717	75	0.670	26	0.382	48	0.449
TC	99	0.465	221	0.477	12	0.261	34	0.304	36	0.529	47	0.439
TT	46	0.216	118	0.255	1	0.022	3	0.027	6	0.088	12	0.112
Total	213	1.000	463	1.000	46	1.000	112	1.000	68	1.000	107	1.000
C	235	0.552	469	0.506	78	0.848	184	0.821	88	0.647	143	0.668
T	191	0.448	457	0.494	14	0.152	40	0.179	48	0.353	71	0.332
Total	426	1.000	926	1.000	92	1.000	224	1.000	136	1.000	214	1.000
p (HIV-) ^a	< 0.001											

N- Number of subjects; highlighted are polymorphisms with allele frequency <0.05 in both control and case group and which were not analyzed further; ^ap shows estimation of difference of genotype frequency between control subjects of different ethnicities; significant values (p<0.05) are in bold italic

Supplemental Table S2 (Continued). Genotype and allele frequencies of the polymorphisms studied in *OPRK1* and *PDYN* genes; estimation of difference of genotype frequency between control subjects of different ethnicities (Data set from Table 1A)

OPRK1: rs3802281, 1837A>G

Genotype/ allele	African Americans		African Americans		Caucasians		Caucasians		Hispanics		Hispanics	
	HIV-		HIV+		HIV-		HIV+		HIV-		HIV+	
	N	freq.	N	freq.	N	freq.	N	freq.	N	freq.	N	freq.
AA	68	0.319	123	0.267	33	0.717	75	0.670	30	0.441	47	0.439
GA	98	0.460	224	0.486	12	0.261	34	0.304	32	0.471	48	0.449
GG	47	0.221	114	0.247	1	0.022	3	0.027	6	0.088	12	0.112
Total	213	1.000	461	1.000	46	1.000	112	1.000	68	1.000	107	1.000
A	234	0.549	470	0.510	78	0.848	184	0.821	92	0.676	142	0.664
G	192	0.451	452	0.490	14	0.152	40	0.179	44	0.324	72	0.336
Total	426	1.000	922	1.000	92	1.000	224	1.000	136	1.000	214	1.000
p (HIV-) ^a	< 0.001											

N- Number of subjects; highlighted are polymorphisms with allele frequency <0.05 in both control and case group and which were not analyzed further; ^ap shows estimation of difference of genotype frequency between control subjects of different ethnicities; significant values (p<0.05) are in bold italic

Supplemental Table S2 (Continued). Genotype and allele frequencies of the polymorphisms studied in *OPRK1* and *PDYN* genes; estimation of difference of genotype frequency between control subjects of different ethnicities (Data set from Table 1A)

PDYN: rs6045935 (rs79537654), -13718A>G

Genotype/ allele	African Americans		African Americans		Caucasians		Caucasians		Hispanics		Hispanics	
	HIV-		HIV+		HIV-		HIV+		HIV-		HIV+	
	N	freq.	N	freq.	N	freq.	N	freq.	N	freq.	N	freq.
AA	42	0.198	95	0.207	23	0.511	58	0.523	33	0.485	44	0.411
GA	115	0.542	228	0.496	20	0.444	43	0.387	26	0.382	51	0.477
GG	55	0.259	137	0.298	2	0.044	10	0.090	9	0.132	12	0.112
Total	212	1.000	460	1.000	45	1.000	111	1.000	68	1.000	107	1.000
A	199	0.469	418	0.454	66	0.733	159	0.716	92	0.676	139	0.650
G	225	0.531	502	0.546	24	0.267	63	0.284	44	0.324	75	0.350
Total	424	1.000	920	1.000	90	1.000	222	1.000	136	1.000	214	1.000
p (HIV-) ^a	< 0.001											

N- Number of subjects; highlighted are polymorphisms with allele frequency <0.05 in both control and case group and which were not analyzed further; ^ap shows estimation of difference of genotype frequency between control subjects of different ethnicities; significant values (p<0.05) are in bold italic

Supplemental Table S2 (Continued). Genotype and allele frequencies of the polymorphisms studied in *OPRK1* and *PDYN* genes; estimation of difference of genotype frequency between control subjects of different ethnicities (Data set from Table 1A)

PDYN: rs10854244, -13315A>T

Genotype/ allele	African Americans		African Americans		Caucasians		Caucasians		Hispanics		Hispanics	
	HIV-		HIV+		HIV-		HIV+		HIV-		HIV+	
	N	freq.	N	freq.	N	freq.	N	freq.	N	freq.	N	freq.
AA	42	0.197	98	0.212	24	0.522	60	0.536	33	0.485	44	0.411
TA	116	0.545	226	0.489	20	0.435	42	0.375	26	0.382	51	0.477
TT	55	0.258	138	0.299	2	0.043	10	0.089	9	0.132	12	0.112
Total	213	1.000	462	1.000	46	1.000	112	1.000	68	1.000	107	1.000
A	200	0.469	422	0.457	68	0.739	162	0.723	92	0.676	139	0.650
T	226	0.531	502	0.543	24	0.261	62	0.277	44	0.324	75	0.350
Total	426	1.000	924	1.000	92	1.000	224	1.000	136	1.000	214	1.000
p (HIV-) ^a	< 0.001											

N- Number of subjects; highlighted are polymorphisms with allele frequency <0.05 in both control and case group and which were not analyzed further; ^ap shows estimation of difference of genotype frequency between control subjects of different ethnicities; significant values (p<0.05) are in bold italic

Supplemental Table S2 (Continued). Genotype and allele frequencies of the polymorphisms studied in *OPRK1* and *PDYN* genes; estimation of difference of genotype frequency between control subjects of different ethnicities (Data set from Table 1A)

PDYN: rs35286251, -12290 (68bp)n analyzed as short (S, 1 and 2 repeats) vs. long (L, 3 and more repeats)

Genotype/ allele	African Americans		African Americans		Caucasians		Caucasians		Hispanics		Hispanics	
	HIV-		HIV+		HIV-		HIV+		HIV-		HIV+	
	N	freq.	N	freq.	N	freq.	N	freq.	N	freq.	N	freq.
SS	44	0.207	119	0.258	1	0.022	16	0.143	9	0.132	17	0.159
SL	90	0.423	155	0.335	24	0.522	47	0.420	26	0.382	36	0.336
LL	79	0.371	188	0.407	21	0.457	49	0.438	33	0.485	54	0.505
Total	213	1.000	462	1.000	46	1.000	112	1.000	68	1.000	107	1.000
S	178	0.418	393	0.425	26	0.283	79	0.353	44	0.324	70	0.327
L	248	0.582	531	0.575	66	0.717	145	0.647	92	0.676	144	0.673
Total	426	1.000	924	1.000	92	1.000	224	1.000	136	1.000	214	1.000
p (HIV-) ^a	0.020											

N- Number of subjects; highlighted are polymorphisms with allele frequency <0.05 in both control and case group and which were not analyzed further; ^ap shows estimation of difference of genotype frequency between control subjects of different ethnicities; significant values (p<0.05) are in bold italic

Supplemental Table S2 (Continued). Genotype and allele frequencies of the polymorphisms studied in *OPRK1* and *PDYN* genes; estimation of difference of genotype frequency between control subjects of different ethnicities (Data set from Table 1A)

PDYN: rs1997794, -11128G>A

Genotype/ allele	African Americans		African Americans		Caucasians		Caucasians		Hispanics		Hispanics	
	HIV-		HIV+		HIV-		HIV+		HIV-		HIV+	
	N	freq.	N	freq.	N	freq.	N	freq.	N	freq.	N	freq.
GG	98	0.460	265	0.574	2	0.043	17	0.152	17	0.250	27	0.252
GA	98	0.460	164	0.355	28	0.609	52	0.464	26	0.382	54	0.505
AA	17	0.080	33	0.071	16	0.348	43	0.384	25	0.368	26	0.243
Total	213	1.000	462	1.000	46	1.000	112	1.000	68	1.000	107	1.000
G	294	0.690	694	0.751	32	0.348	86	0.384	60	0.441	108	0.505
A	132	0.310	230	0.249	60	0.652	138	0.616	76	0.559	106	0.495
Total	426	1.000	924	1.000	92	1.000	224	1.000	136	1.000	214	1.000
p (HIV-) ^a	< 0.001											

N- Number of subjects; highlighted are polymorphisms with allele frequency <0.05 in both control and case group and which were not analyzed further; ^ap shows estimation of difference of genotype frequency between control subjects of different ethnicities; significant values (p<0.05) are in bold italic

Supplemental Table S2 (Continued). Genotype and allele frequencies of the polymorphisms studied in *OPRK1* and *PDYN* genes; estimation of difference of genotype frequency between control subjects of different ethnicities (Data set from Table 1A)

PDYN: rs6045868, -3548C>T

Genotype/ allele	African Americans		African Americans		Caucasians		Caucasians		Hispanics		Hispanics	
	HIV-		HIV+		HIV-		HIV+		HIV-		HIV+	
	N	freq.	N	freq.	N	freq.	N	freq.	N	freq.	N	freq.
CC	38	0.178	77	0.167	29	0.630	52	0.464	29	0.426	34	0.318
CT	101	0.474	208	0.450	15	0.326	50	0.446	26	0.382	52	0.486
TT	74	0.347	177	0.383	2	0.043	10	0.089	13	0.191	21	0.196
Total	213	1.000	462	1.000	46	1.000	112	1.000	68	1.000	107	1.000
C	177	0.415	362	0.392	73	0.793	154	0.688	84	0.618	120	0.561
T	249	0.585	562	0.608	19	0.207	70	0.313	52	0.382	94	0.439
Total	426	1.000	924	1.000	92	1.000	224	1.000	136	1.000	214	1.000
p (HIV-) ^a	< 0.001											

N- Number of subjects; highlighted are polymorphisms with allele frequency <0.05 in both control and case group and which were not analyzed further; ^ap shows estimation of difference of genotype frequency between control subjects of different ethnicities; significant values (p<0.05) are in bold italic

Supplemental Table S2 (Continued). Genotype and allele frequencies of the polymorphisms studied in *OPRK1* and *PDYN* genes; estimation of difference of genotype frequency between control subjects of different ethnicities (Data set from Table 1A)

PDYN: rs6035222, IVS3+189C>T

Genotype/ allele	African Americans		African Americans		Caucasians		Caucasians		Hispanics		Hispanics	
	HIV-		HIV+		HIV-		HIV+		HIV-		HIV+	
	N	freq.	N	freq.	N	freq.	N	freq.	N	freq.	N	freq.
CC	101	0.474	221	0.479	37	0.804	84	0.750	53	0.779	70	0.654
CT	85	0.399	196	0.425	9	0.196	28	0.250	13	0.191	30	0.280
TT	27	0.127	44	0.095	0	0.000	0	0.000	2	0.029	7	0.065
Total	213	1.000	461	1.000	46	1.000	112	1.000	68	1.000	107	1.000
C	287	0.674	638	0.692	83	0.902	196	0.875	119	0.875	170	0.794
T	139	0.326	284	0.308	9	0.098	28	0.125	17	0.125	44	0.206
Total	426	1.000	922	1.000	92	1.000	224	1.000	136	1.000	214	1.000
p (HIV-) ^a	< 0.001											

N- Number of subjects; highlighted are polymorphisms with allele frequency <0.05 in both control and case group and which were not analyzed further; ^ap shows estimation of difference of genotype frequency between control subjects of different ethnicities; significant values (p<0.05) are in bold italic

Supplemental Table S2 (Continued). Genotype and allele frequencies of the polymorphisms studied in *OPRK1* and *PDYN* genes; estimation of difference of genotype frequency between control subjects of different ethnicities (Data set from Table 1A)

PDYN: rs6045819, 600T>C (His200His)

Genotype/ allele	African Americans		African Americans		Caucasians		Caucasians		Hispanics		Hispanics	
	HIV-		HIV+		HIV-		HIV+		HIV-		HIV+	
	N	freq.	N	freq.	N	freq.	N	freq.	N	freq.	N	freq.
TT	115	0.540	223	0.484	38	0.826	87	0.777	48	0.706	66	0.617
TC	74	0.347	195	0.423	8	0.174	25	0.223	19	0.279	35	0.327
CC	24	0.113	43	0.093	0	0.000	0	0.000	1	0.015	6	0.056
Total	213	1.000	461	1.000	46	1.000	112	1.000	68	1.000	107	1.000
T	304	0.714	641	0.695	84	0.913	199	0.888	115	0.846	167	0.780
C	122	0.286	281	0.305	8	0.087	25	0.112	21	0.154	47	0.220
Total	426	1.000	922	1.000	92	1.000	224	1.000	136	1.000	214	1.000
p (HIV-) ^a	< 0.001											

N- Number of subjects; highlighted are polymorphisms with allele frequency <0.05 in both control and case group and which were not analyzed further; ^ap shows estimation of difference of genotype frequency between control subjects of different ethnicities; significant values (p<0.05) are in bold italic

Supplemental Table S2 (Continued). Genotype and allele frequencies of the polymorphisms studied in *OPRK1* and *PDYN* genes; estimation of difference of genotype frequency between control subjects of different ethnicities (Data set from Table 1A)

PDYN: rs10485703, 1421T>C

Genotype/ allele	African Americans		African Americans		Caucasians		Caucasians		Hispanics		Hispanics	
	HIV-		HIV+		HIV-		HIV+		HIV-		HIV+	
	N	freq.	N	freq.	N	freq.	N	freq.	N	freq.	N	freq.
TT	151	0.709	318	0.688	36	0.783	90	0.804	53	0.779	78	0.729
TC	52	0.244	128	0.277	10	0.217	22	0.196	15	0.221	23	0.215
CC	10	0.047	16	0.035	0	0.000	0	0.000	0	0.000	6	0.056
Total	213	1.000	462	1.000	46	1.000	112	1.000	68	1.000	107	1.000
T	354	0.831	764	0.827	82	0.891	202	0.902	121	0.890	179	0.836
C	72	0.169	160	0.173	10	0.109	22	0.098	15	0.110	35	0.164
Total	426	1.000	924	1.000	92	1.000	224	1.000	136	1.000	214	1.000
p (HIV-) ^a = 0.194												

N- Number of subjects; highlighted are polymorphisms with allele frequency <0.05 in both control and case group and which were not analyzed further; ^ap shows estimation of difference of genotype frequency between control subjects of different ethnicities; significant values (p<0.05) are in bold italic

Supplemental Table S2 (Continued). Genotype and allele frequencies of the polymorphisms studied in *OPRK1* and *PDYN* genes; estimation of difference of genotype frequency between control subjects of different ethnicities (Data set from Table 1A)

PDYN: rs910080, 1508T>C

Genotype/ allele	African Americans		African Americans		Caucasians		Caucasians		Hispanics		Hispanics	
	HIV-		HIV+		HIV-		HIV+		HIV-		HIV+	
	N	freq.	N	freq.	N	freq.	N	freq.	N	freq.	N	freq.
TT	56	0.265	123	0.267	27	0.587	54	0.482	29	0.433	44	0.411
TC	105	0.498	236	0.512	18	0.391	51	0.455	31	0.463	46	0.430
CC	50	0.237	102	0.221	1	0.022	7	0.063	7	0.104	17	0.159
Total	211	1.000	461	1.000	46	1.000	112	1.000	67	1.000	107	1.000
T	217	0.514	482	0.523	72	0.783	159	0.710	89	0.664	134	0.626
C	205	0.486	440	0.477	20	0.217	65	0.290	45	0.336	80	0.374
Total	422	1.000	922	1.000	92	1.000	224	1.000	134	1.000	214	1.000
p (HIV-) ^a	< 0.001											

N- Number of subjects; highlighted are polymorphisms with allele frequency <0.05 in both control and case group and which were not analyzed further; ^ap shows estimation of difference of genotype frequency between control subjects of different ethnicities; significant values (p<0.05) are in bold italic

Supplemental Table S2 (Continued). Genotype and allele frequencies of the polymorphisms studied in *OPRK1* and *PDYN* genes; estimation of difference of genotype frequency between control subjects of different ethnicities (Data set from Table 1A)

PDYN: rs910079, 1536T>C

Genotype/ allele	African Americans		African Americans		Caucasians		Caucasians		Hispanics		Hispanics	
	HIV-		HIV+		HIV-		HIV+		HIV-		HIV+	
	N	freq.	N	freq.	N	freq.	N	freq.	N	freq.	N	freq.
TT	56	0.263	109	0.236	27	0.587	54	0.482	29	0.426	40	0.374
TC	102	0.479	247	0.535	18	0.391	50	0.446	31	0.456	50	0.467
CC	55	0.258	106	0.229	1	0.022	8	0.071	8	0.118	17	0.159
Total	213	1.000	462	1.000	46	1.000	112	1.000	68	1.000	107	1.000
T	214	0.502	465	0.503	72	0.783	158	0.705	89	0.654	130	0.607
C	212	0.498	459	0.497	20	0.217	66	0.295	47	0.346	84	0.393
Total	426	1.000	924	1.000	92	1.000	224	1.000	136	1.000	214	1.000
p (HIV-) ^a	< 0.001											

N- Number of subjects; highlighted are polymorphisms with allele frequency <0.05 in both control and case group and which were not analyzed further; ^ap shows estimation of difference of genotype frequency between control subjects of different ethnicities; significant values (p<0.05) are in bold italic

Supplemental Table S2 (Continued). Genotype and allele frequencies of the polymorphisms studied in *OPRK1* and *PDYN* genes; estimation of difference of genotype frequency between control subjects of different ethnicities (Data set from Table 1A)

PDYN: rs2235749, 1795C>T

Genotype/ allele	African Americans		African Americans		Caucasians		Caucasians		Hispanics		Hispanics	
	HIV-		HIV+		HIV-		HIV+		HIV-		HIV+	
	N	freq.	N	freq.	N	freq.	N	freq.	N	freq.	N	freq.
CC	56	0.263	109	0.236	27	0.600	54	0.482	29	0.426	40	0.374
CT	102	0.479	247	0.535	17	0.378	50	0.446	31	0.456	50	0.467
TT	55	0.258	106	0.229	1	0.022	8	0.071	8	0.118	17	0.159
Total	213	1.000	462	1.000	45	1.000	112	1.000	68	1.000	107	1.000
C	214	0.502	465	0.503	71	0.789	158	0.705	89	0.654	130	0.607
T	212	0.498	459	0.497	19	0.211	66	0.295	47	0.346	84	0.393
Total	426	1.000	924	1.000	90	1.000	224	1.000	136	1.000	214	1.000
p (HIV-) ^a	< 0.001											

N- Number of subjects; highlighted are polymorphisms with allele frequency <0.05 in both control and case group and which were not analyzed further; ^ap shows estimation of difference of genotype frequency between control subjects of different ethnicities; significant values (p<0.05) are in bold italic

Supplemental Table S2 (Continued). Number of individuals bearing different combinations of -12290 (68bp)n repeat polymorphism in different ethnic groups with different HIV status (Data set from Table 1A)

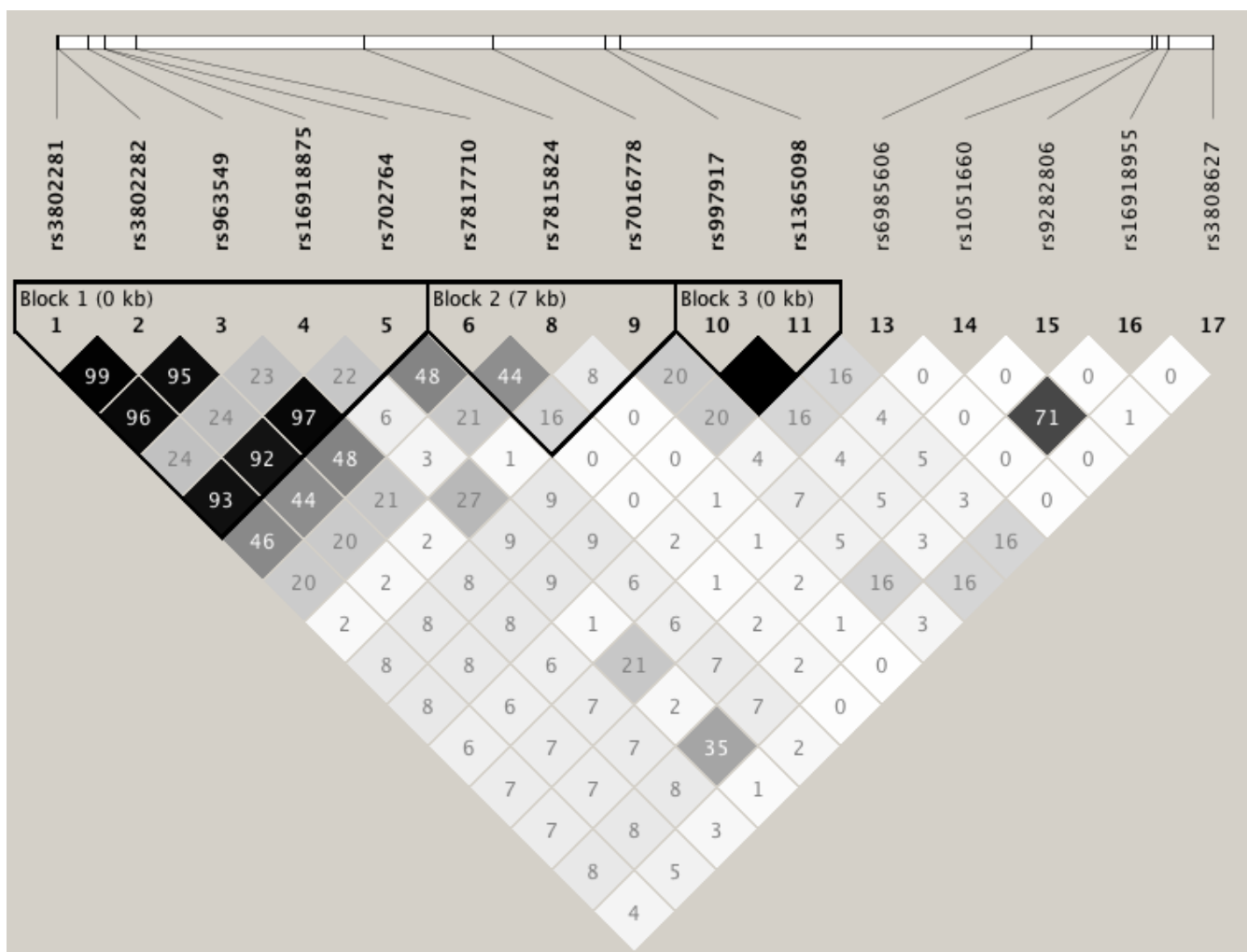
PDYN: rs35286251 -12290 (68bp)n

Sum of repeats in 2 alleles	African Americans		African Americans		Caucasians		Caucasians		Hispanics		Hispanics	
	HIV-		HIV+		HIV-		HIV+		HIV-		HIV+	
	N	Frequency	N	Frequency	N	Frequency	N	Frequency	N	Frequency	N	Frequency
2 repeats	0	0.000	1	0.002	0	0.000	0	0.000	0	0.000	0	0.000
3 repeats	1	0.005	12	0.026	0	0.000	3	0.027	0	0.000	2	0.018
4 repeats	46	0.217	110	0.238	5	0.109	16	0.143	11	0.162	16	0.147
5 repeats	76	0.358	121	0.261	20	0.435	41	0.366	20	0.294	34	0.312
6 repeats	66	0.311	163	0.352	18	0.391	48	0.429	34	0.500	53	0.486
7 repeats	15	0.071	36	0.078	3	0.065	4	0.036	3	0.044	2	0.018
8 repeats	5	0.024	18	0.039	0	0.000	0	0.000	0	0.000	2	0.018
9 repeats	1	0.005	1	0.002	0	0.000	0	0.000	0	0.000	0	0.000
10 repeats	2	0.009	1	0.002	0	0.000	0	0.000	0	0.000	0	0.000
Total	212	1.000	463	1.000	46	1.000	112	1.000	68	1.000	109	1.000

N- Number of subjects

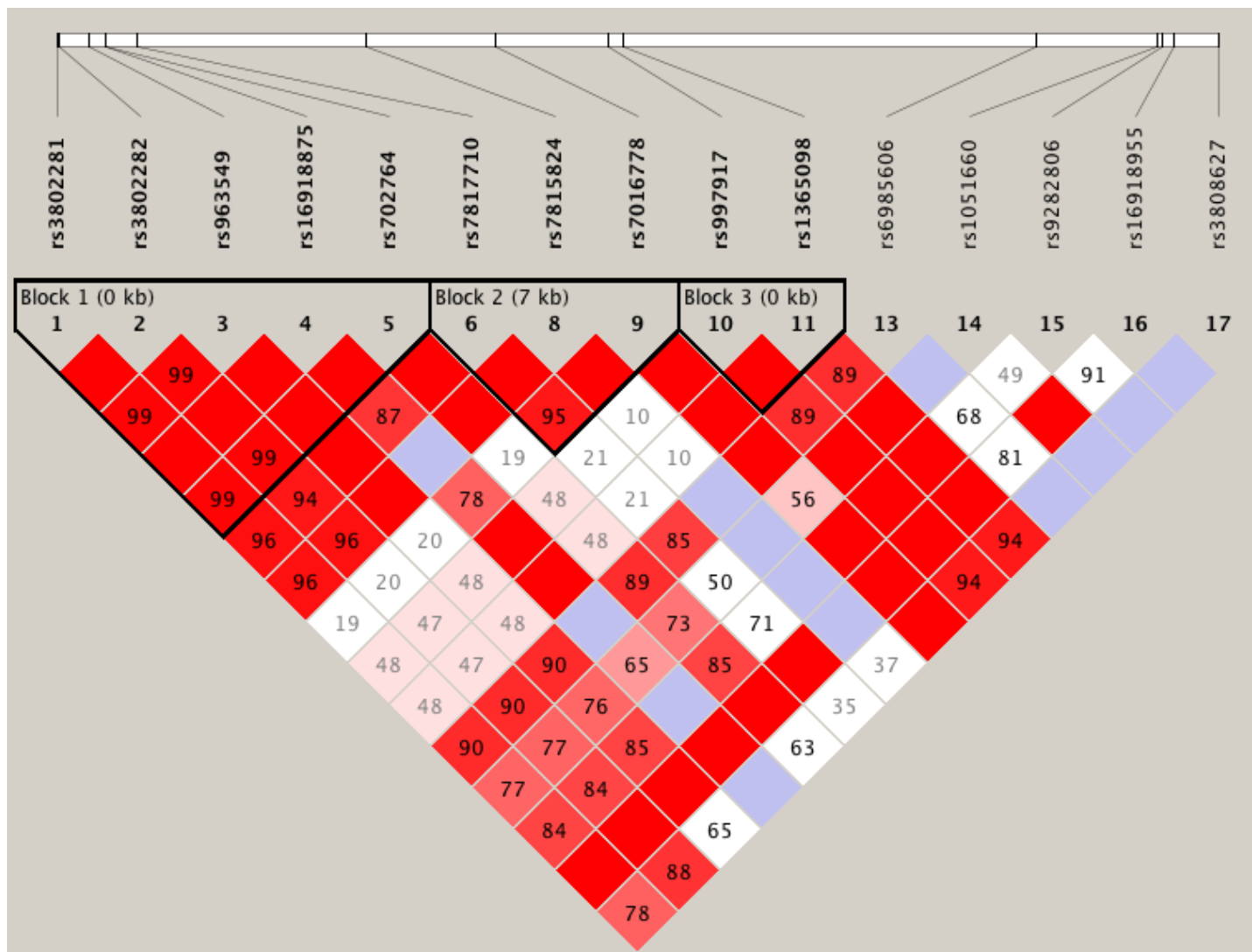
Supplemental Figure S2. Results of linkage disequilibrium analysis (Data set from Table 1A)

A. Linkage disequilibrium analysis of the variants of the *OPRK1* gene in HIV- (control) group of African Americans (r^2)



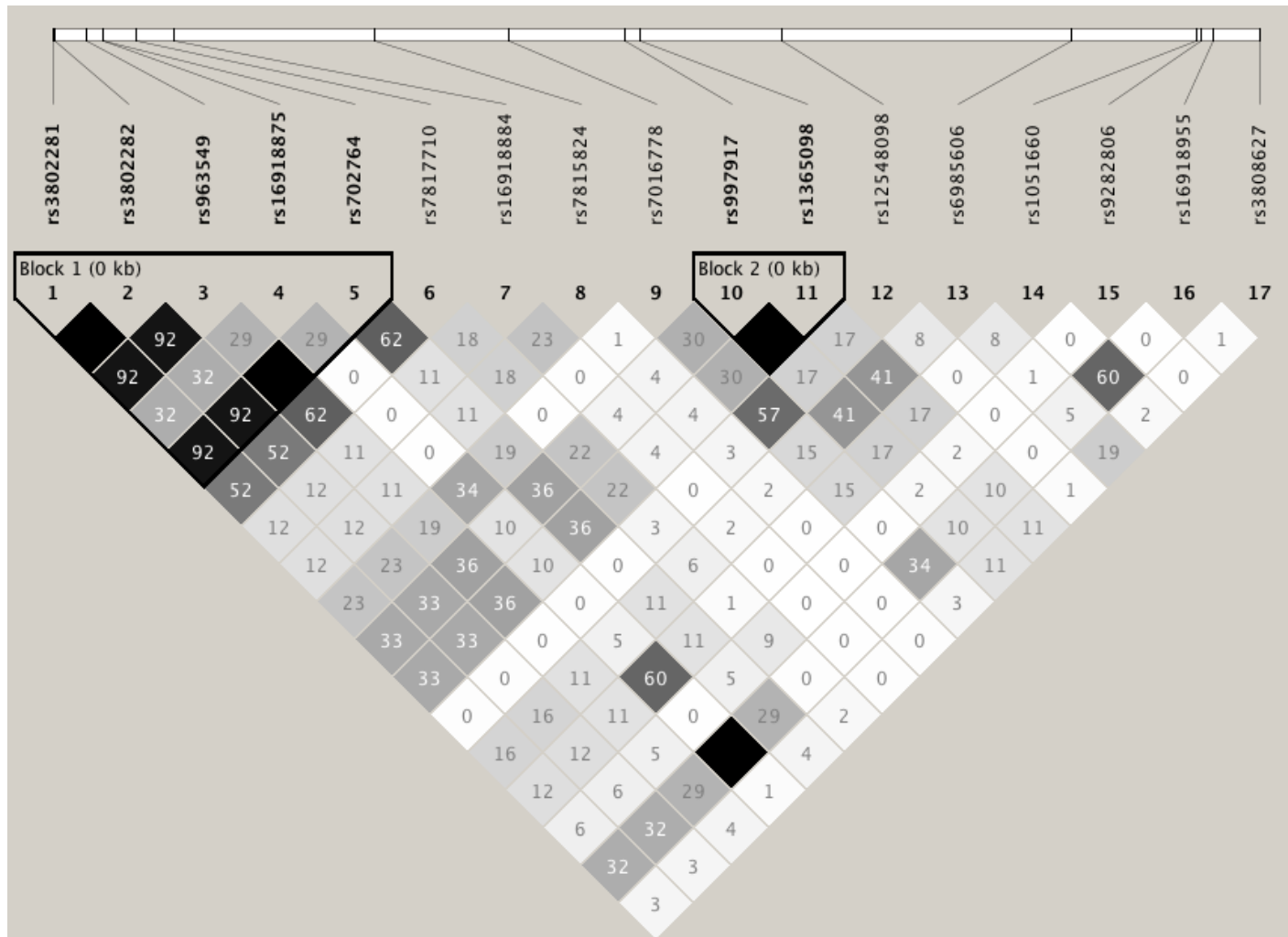
In this map genetic variants are arranged according to their location in chromosome (opposite to orientation in the gene, Fig. 1)

Supplemental Figure S2B. Linkage disequilibrium analysis of the variants of the *OPRK1* gene in HIV- (control) group of African Americans (D')



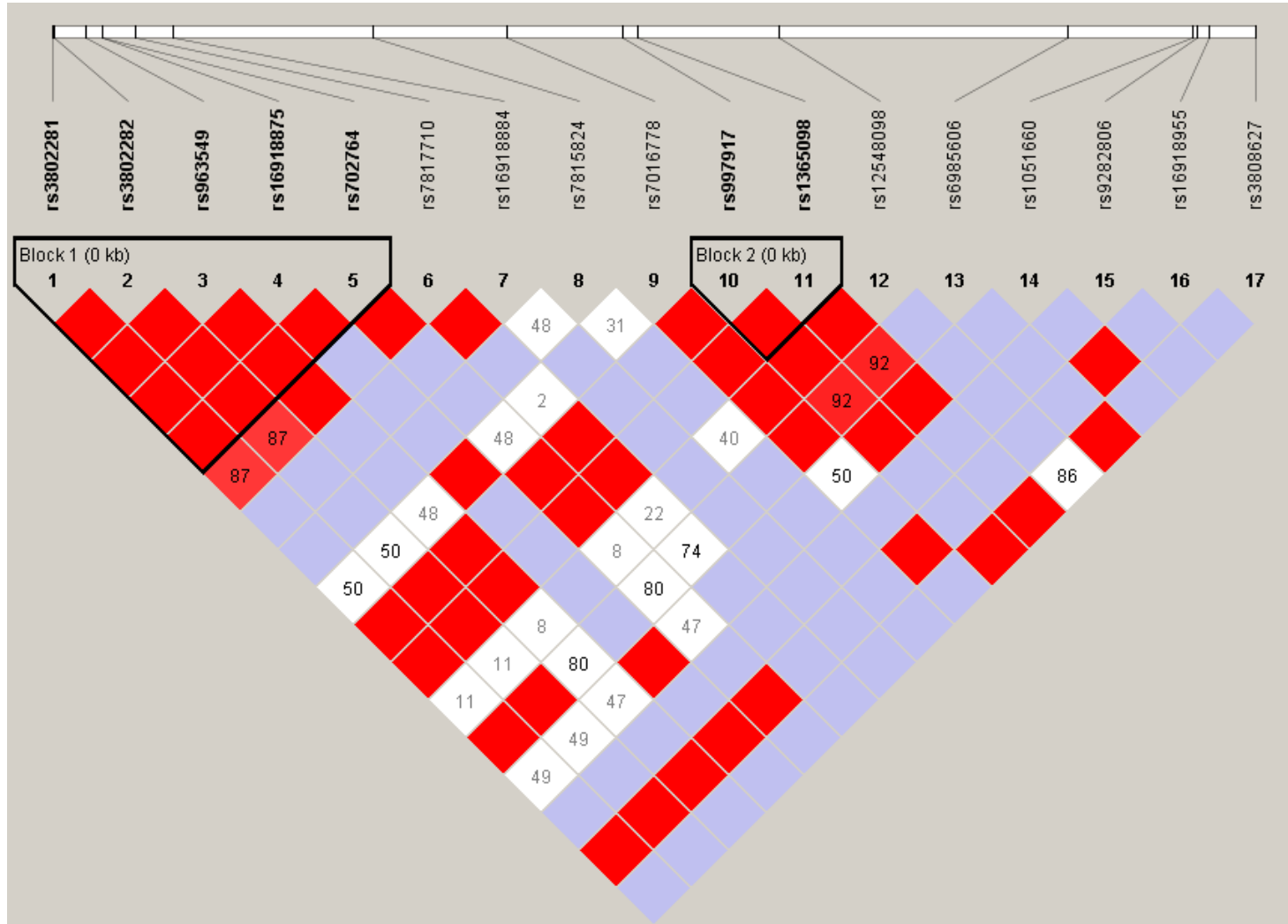
In this map genetic variants are arranged according to their location in chromosome (opposite to orientation in the gene, Fig. 1)

Supplemental Figure S2C. Linkage disequilibrium analysis of the variants of the *OPRK1* gene in HIV- (control) group of Caucasians (r^2)



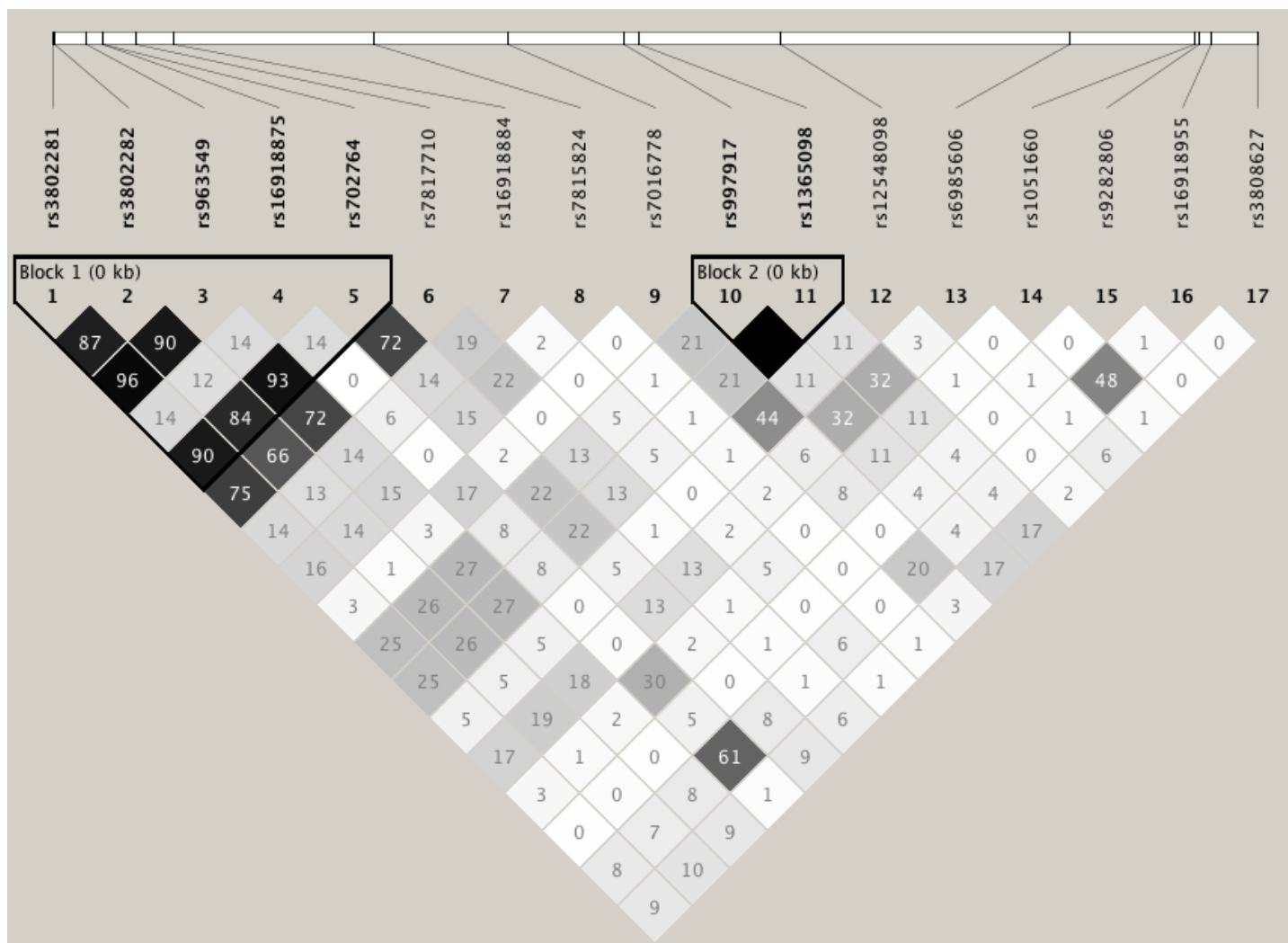
In this map genetic variants are arranged according to their location in chromosome (opposite to orientation in the gene, Fig. 1)

Supplemental Figure S2D. Linkage disequilibrium analysis of the variants of the *OPRK1* gene in HIV- (control) group of Caucasians (D')



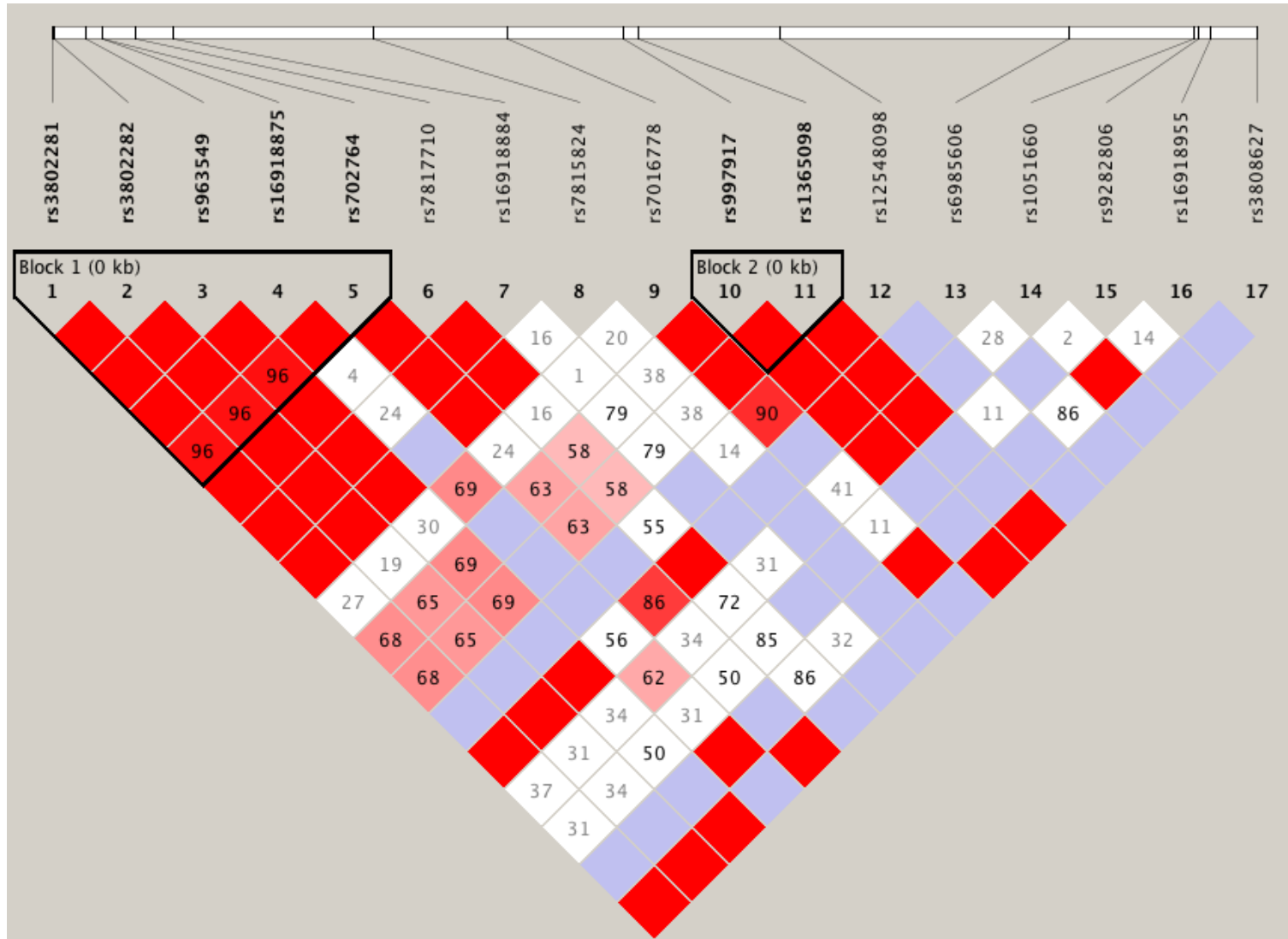
In this map genetic variants are arranged according to their location in chromosome (opposite to orientation in the gene, Fig. 1)

Supplemental Figure S2E. Linkage disequilibrium analysis of the variants of the *OPRK1* gene in HIV- (control) group of Hispanics (r^2)



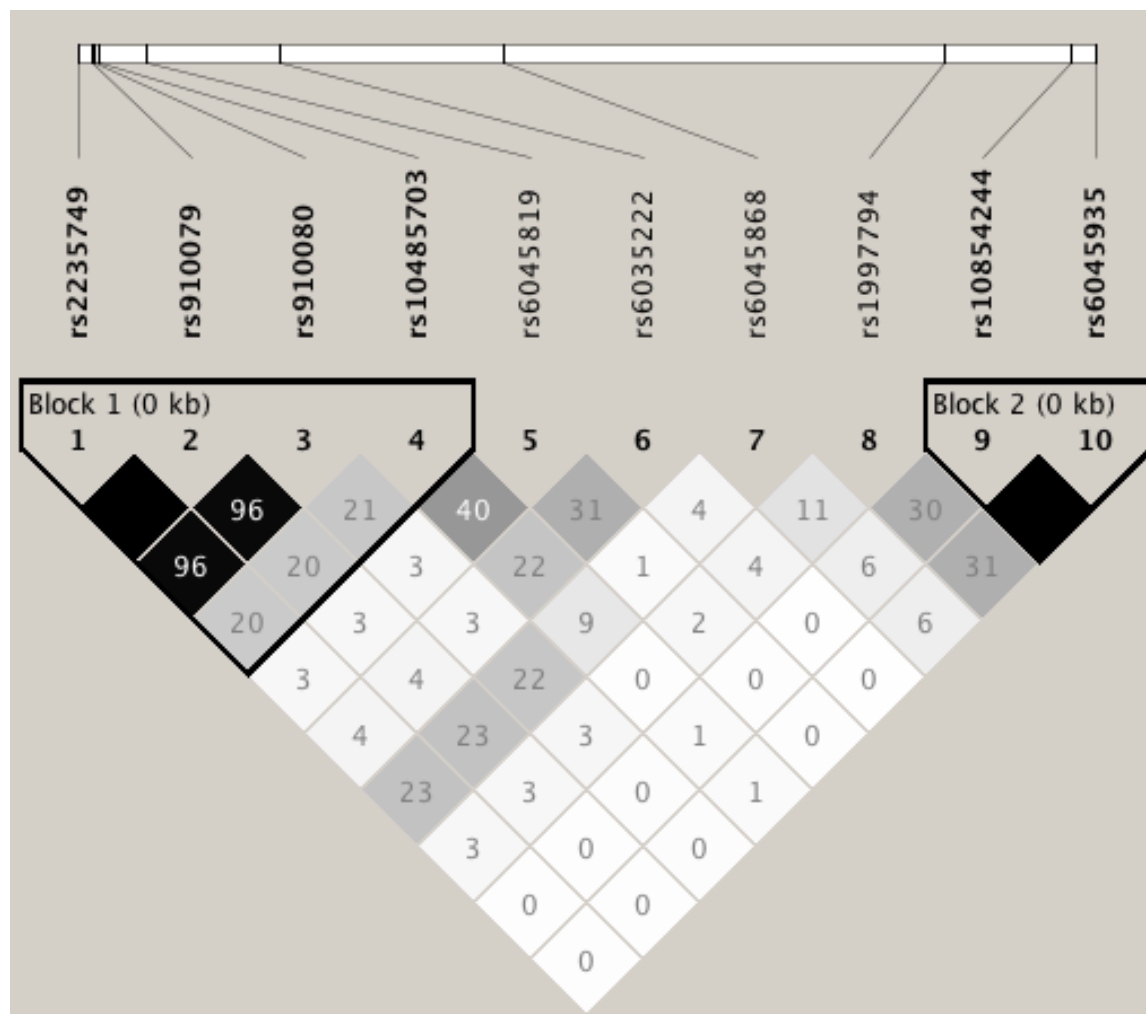
In this map genetic variants are arranged according to their location in chromosome (opposite to orientation in the gene, Fig. 1)

Supplemental Figure S2F. Linkage disequilibrium analysis of the variants of the *OPRK1* gene in HIV- (control) group of Hispanics (D')



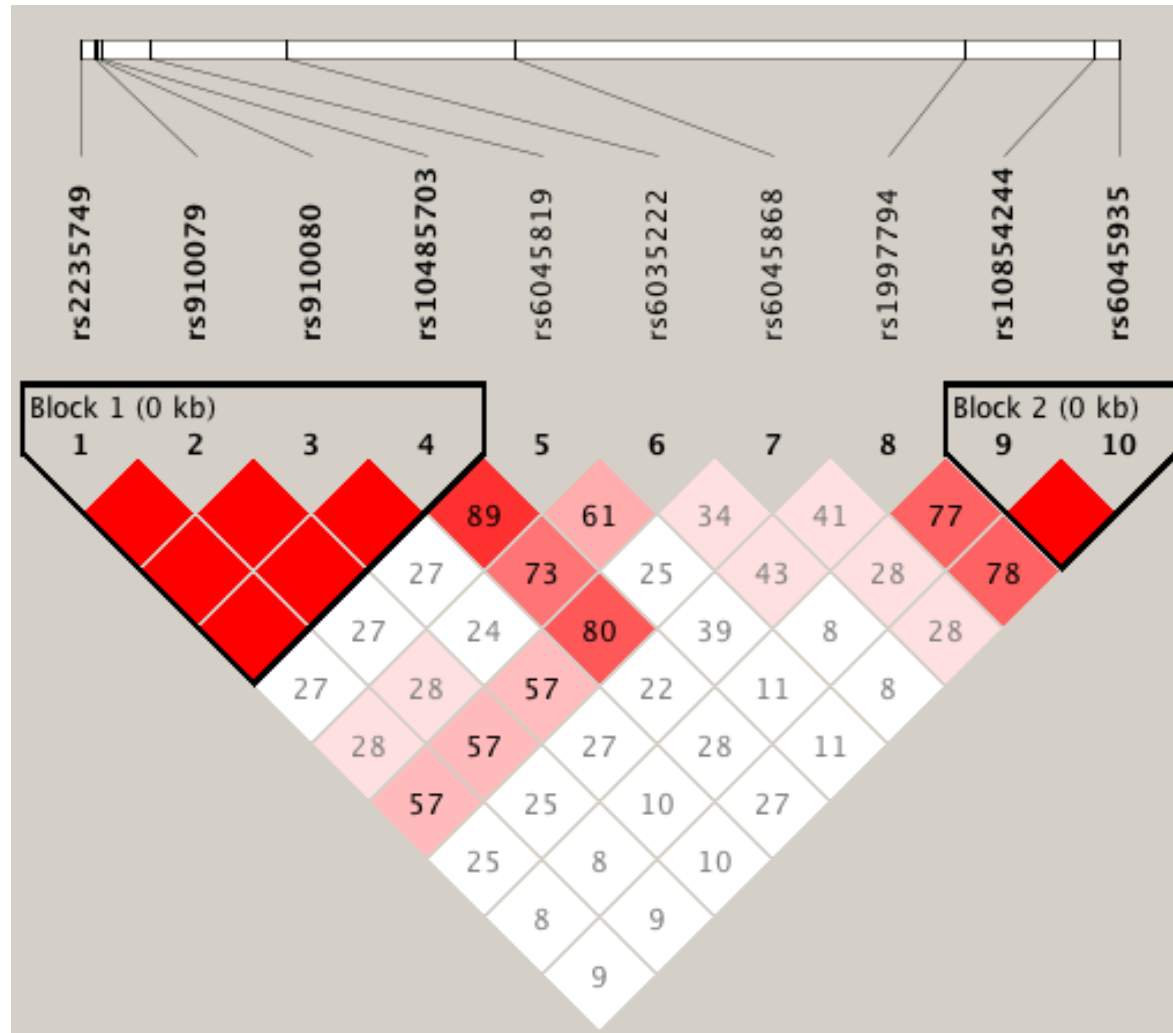
In this map genetic variants are arranged according to their location in chromosome (opposite to orientation in the gene, Fig. 1)

Supplemental Figure S2G. Linkage disequilibrium analysis of the variants of the *PDYN* gene in HIV- (control) group of African Americans (r^2)



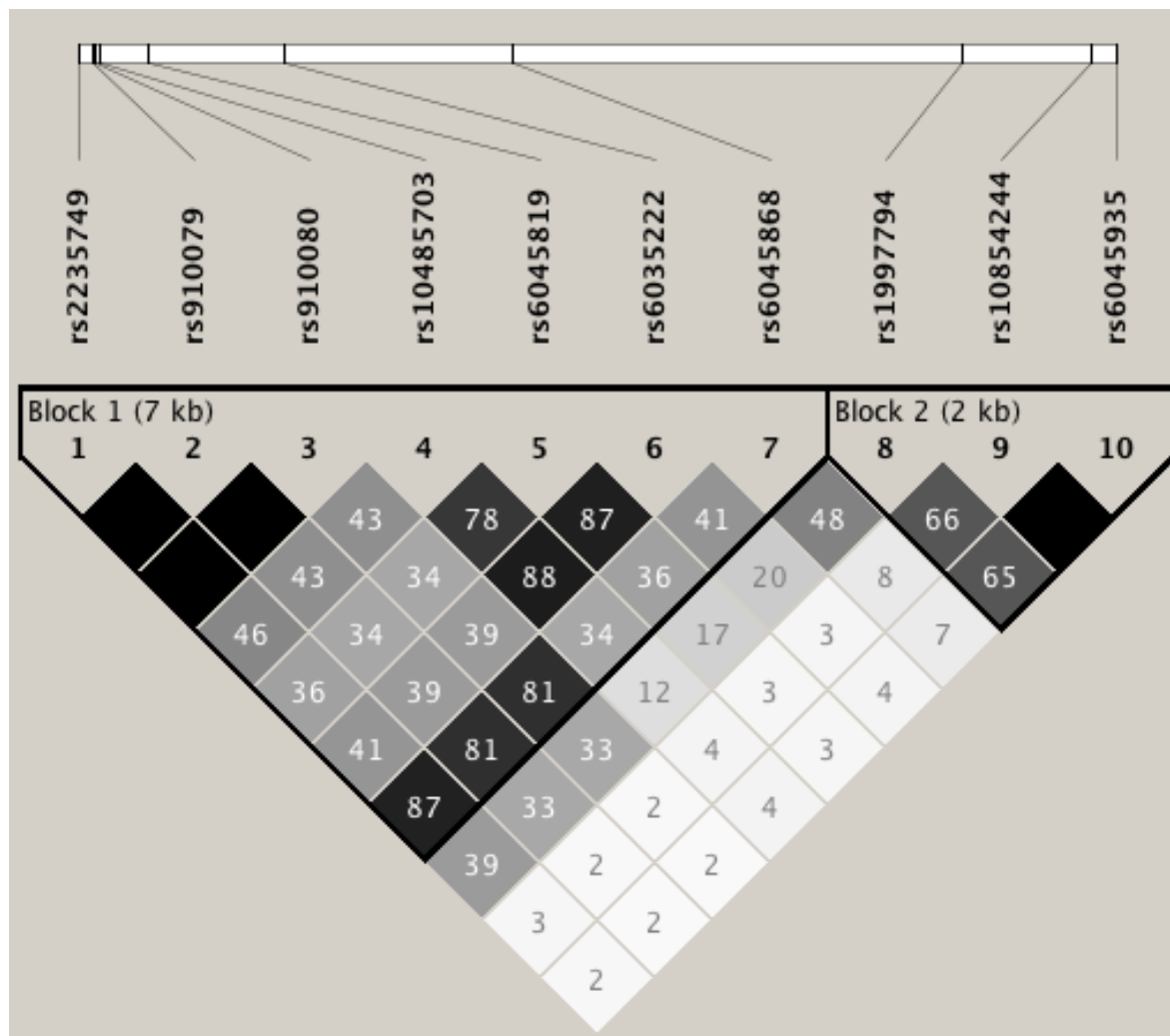
In this map genetic variants are arranged according to their location in chromosome (opposite to orientation in the gene, Fig. 2)

Supplemental Figure S2H. Linkage disequilibrium analysis of the variants of the *PDYN* gene in HIV- (control) group of African Americans (D')



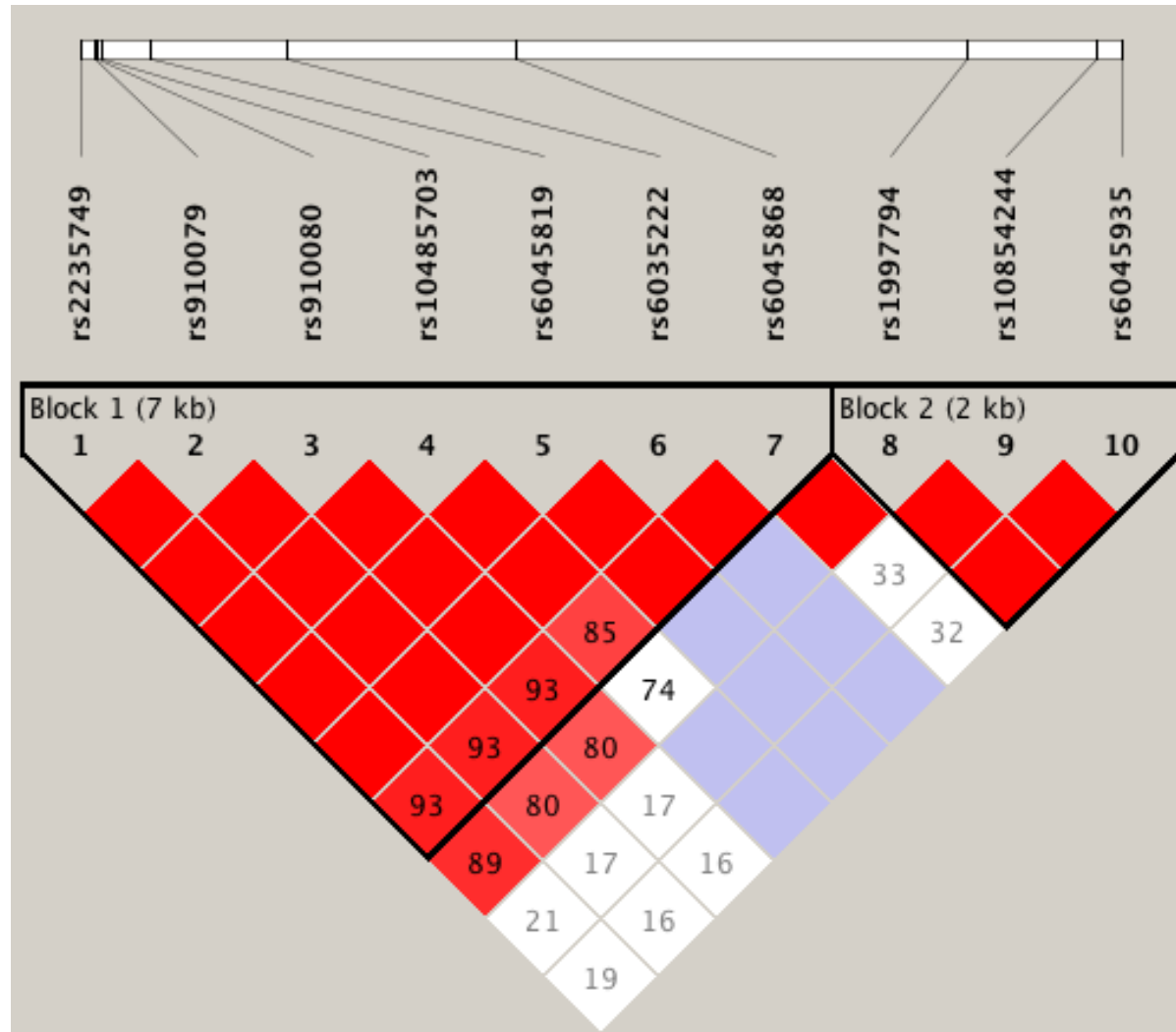
In this map genetic variants are arranged according to their location in chromosome (opposite to orientation in the gene, Fig. 2)

Supplemental Figure S2I. Linkage disequilibrium analysis of the variants of the *PDYN* gene in HIV- (control) group of Caucasians (r^2)



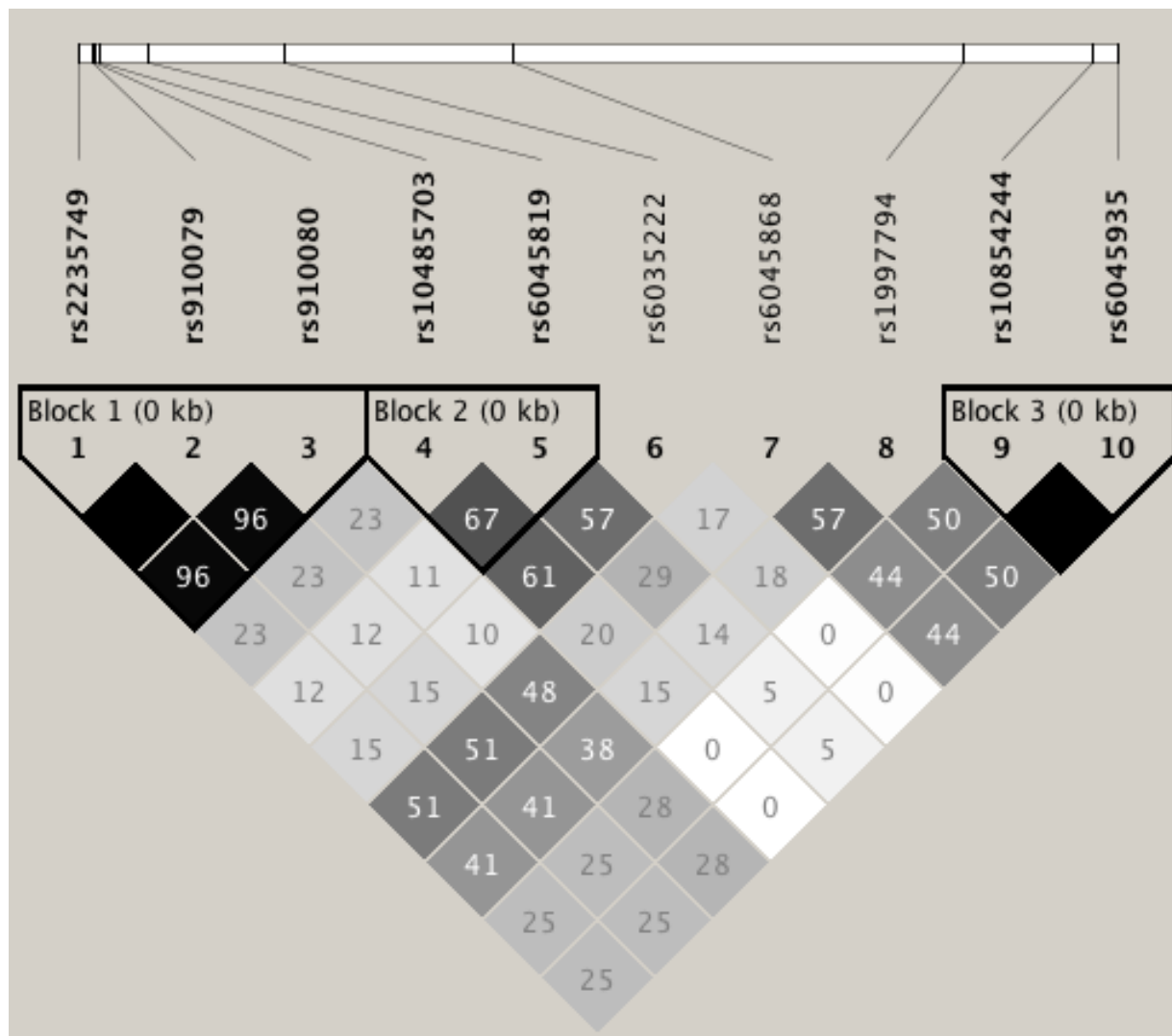
In this map genetic variants are arranged according to their location in chromosome (opposite to orientation in the gene, Fig. 2)

Supplemental Figure S2J. Linkage disequilibrium analysis of the variants of the *PDYN* gene in HIV- (control) group of Caucasians (D')



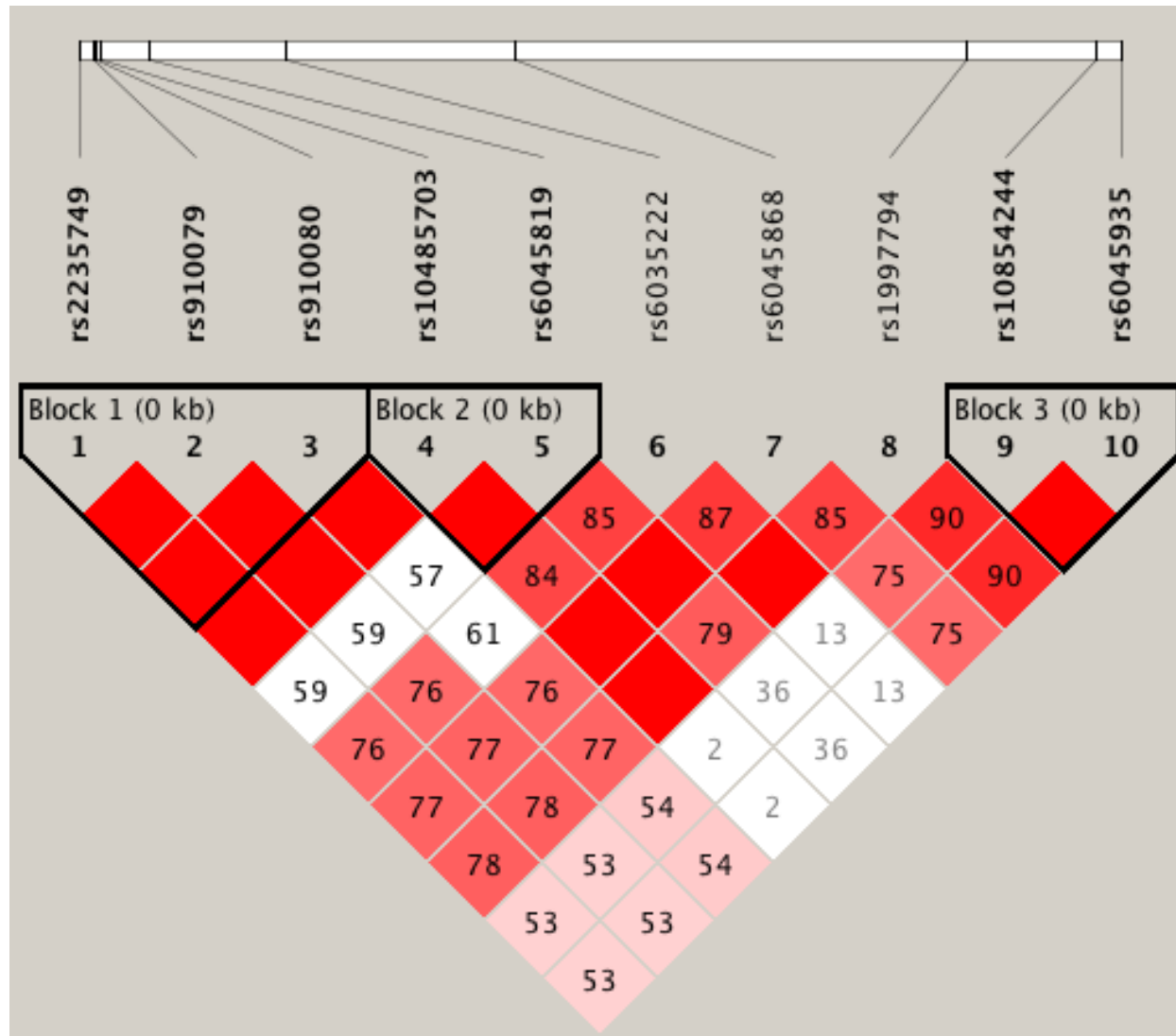
In this map genetic variants are arranged according to their location in chromosome (opposite to orientation in the gene, Fig. 2)

Supplemental Figure S2K. Linkage disequilibrium analysis of the variants of the *PDYN* gene in HIV- (control) group of Hispanics (r^2)



In this map genetic variants are arranged according to their location in chromosome (opposite to orientation in the gene, Fig. 2)

Supplemental Figure S2L. Linkage disequilibrium analysis of the variants of the *PDYN* gene in HIV- (control) group of Hispanics (D')



In this map genetic variants are arranged according to their location in chromosome (opposite to orientation in the gene, Fig. 2)