Supplemental table 1. Sequences of primers used for genotyping in stage II

SNP	Amplification primers(5' to 3')	Allele-specific probes
rs7134069	F GAGCCCAGGAATTCAAGATCAG	TGGGCAACATGGCAA
	R CCATCATACCTGGCTAATTTTTGTATT	TGGGCAACCTGGCAA
rs2859398	F GAACCCAGGAGGCAAAGCTT	AGCCAAGATTGCACC
	R GACGGAGTCTCGCTGGAGTT	AGCCAAGACTGCACC
rs2859394	F TGGAGACAAACAACAAATAGGATAAATAG	AGAAGACGGTGATAAGT
	R TTCTCTTGCTTTGTTTTTCTGCTTAG	AGAAGATGGTGATAAGTG
rs10849833	F TCACTTGAGGCCAGGAGTTCA	AGCTGGACACCTGCAA
	R GGACTAAGCCCTGGAGCACTT	AGCTGGACGCCTGC
rs12315068	F CACGGGTTCAAGCGATTCTC	ACGCCCGGCTAAT
	R CCCCGTCTCTACTAAAAATACAAAAAA	ACGCCCAGCTAATT
rs28360476	F AACAGCTCAGAAACGCCACC	CGTGCCATTCCCGAA
	R CATGGCAGTGGGCCTCAG	CGTGCCATTACCGAA
rs3213546	F CCTACAGAGCCCTGGGTAAGG	CACCCCAGGAGACT
	R GGCCATGAGTAAAGGTGAGACACT	CACCCCAGCAGACT
rs10849829	F TGCAGCATGTAGGTTTTACTTCAAA	CACTGGCCCCTGTT
	R CGCTGGCGTGCTTACTCA	CACTGGTCCCTGTTG
rs7969180	F TCCAGGAGCAGGTCCATCAC	AGTGGTGAAGCCTT
	R ATGGGTACTGAAGAAGACGAGAATTT	AGTGGTGAAACCTT
rs11307154	F TTTTCCCATGCTAGCTCCTACAA	AGCACTGAAATGGT
	R TTGGCCTTCTTGCTCTCTGAA	AGCACTGAATGGTC
rs3861793	F CAGCTTCATCCTGGGTCTGAAG	AGCAGCTGGAATTC
	R TCACTGTCTTGGATGCCATAGATC	AGCAGCTCGAATTC
rs12819210	F GCTGGAAACAGAGCCTCTCCT	TCTTCTTCGAGAGGAT
	R AGGACTGGTTGGGTCTGGG	CTTCTTTGAGAGGATG
rs2259697	F CGCTTGAGCCGAGGAGTTC	TGGGTATCACAGGGAGA
	R ACCACACCCAGTGAATTATTTTTTTA	TGGGTATCATAGGGAGAC
rs7134141	F AGGCACTTTTTCTGTCCCTGAA	CAAACAGAGGTGGGAGA
	R CCTCTGGTCAATTTAGCAATCATAATC	CAAACAGAAGTGGGAGAT

Supplemental table 2. Allele frequency of association analysis of SVR and selected SNPs in stage I

			African American(n=180)				Caucasian American(n=194)		
SNP	**location in Chr.**	**Variant allele**	**SVR(n=49)%$^{\#}$**	**NR(n=131)%$^{\#}$**	**p-value***	**Variant allele**	**SVR(n=104)%$^{\#}$**	**NR(n=90)%$^{\#}$**	**p-value***
Chr. 1: *G1P2*									
rs1921	3229102	A	40.8	42.8	0.74	A	37.4	40.6	0.52
rs9331223	3230171	C	32.3	30	0.6	T	41.3	43.9	0.6
Chr. 1: *G1P3*									
rs11247653	27594308	G	7.1	11.8	0.2	G	43.2	46.7	0.57
rs1141746	27677011								
rs1316896	27680244								
Chr. 2: *STAT1*									
rs3088307	1.92E+08	C	24.5	26	0.78	C	44.2	51.1	0.17
rs1400657	1.92E+08	C	26.5	20.2	0.2	C	11.7	7.2	0.14
rs1914408	1.92E+08	A	14.3	17.6	0.46	A	20.6	19.4	0.78
rs2280234	1.92E+08	C	36.7	38.6	0.75	T	40.3	29.4	0.03
rs2066797	1.92E+08	G	13.3	19.1	0.2	G	7.8	5.1	0.28
rs12693590	1.92E+08	C	18.4	9.9	0.03	C	7.3	7.8	0.85
rs2066802	1.92E+08	C	7.1	7.6	0.88	C	6.3	6.7	0.89
rs1467199	1.92E+08	G	31.6	31.7	0.99	G	20.4	19.4	0.82
Chr.2: *PKR*									
rs2254958	37350826	T	15.3	14.7	0.89	T	42.7	41.3	0.78
rs2287350	37342987	G	18.4	13.7	0.27	G	39.3	41.7	0.64
rs2307478	37327999	C	3.1	4.6	0.52				
rs2307479	37337090	C	11.2	11.5	0.93	C	1	3.9	0.06
rs2372443	37310594	C	0	2.7	0.1	C	6.3	2.8	0.11
Chr. 4: *IP10*									
rs4859584	77401532	G	35.7	33.2	0.65	G	43.7	46.1	0.63
rs4859587	77401691	A	35.4	33.2	0.7	A	43.7	46.1	0.63
rs4257674	77404080	A	35.7	33.2	0.65	A	43.7	46.1	0.63
rs4309862	77404376	A	35.1	33.2	0.74	A	43.7	46.1	0.64
rs4859591	77406973	G	35.7	33.2	0.65	G	43.7	46.1	0.63
Chr. 11: *IRF7*									

rs12421158	600140	T	36.5	44.3	0.19	C	35	33.3	0.74
rs7932167	610857	C	34.7	36.3	0.78	C	21.8	23.9	0.63
Chr. 12: *STAT2*									
rs2066808	55024240	T	41.8	49.2	0.21	C	7.8	9.4	0.56
rs2066807	55026949	C	0	0.8	0.39	C	6.8	9.4	0.34
rs2066811	55029264	G	24.5	14.2	0.02	G	1	0	0.35
rs2228259	55034562	C	1	0	0.1				
rs2066816	55036270								
rs2066819	55036471	A	0	0.8	0.39	A	7.3	9.4	0.44
rs11171812	55038129	G	43.9	50.8	0.25	A	1	0	0.19
rs4301822	55041325	T	40.6	46.2	0.35	C	1	0	0.19
Chr. 12: *OAS1*									
rs4766662	1.12E+08	A	35.7	38.2	0.67	A	22.3	20	0.58
rs3741981	1.12E+08	T	24.5	27.1	0.62	C	42.2	38.9	0.52
rs2285934	1.12E+08	A	48	42.4	0.34	A	34.5	31.7	0.56
rs12298890	1.12E+08	T	0	0.4	0.54				
rs2660	1.12E+08	G	41	8.8	0.13	G	34	31.1	0.55
rs6489865	1.12E+08	A	4.1	5.7	0.54	A	33.5	30.6	0.54
Chr. 12: *OAS3*									
rs1981557	1.12E+08	C	9.4	6.2	0.29	C	35.9	30	0.22
rs6489879	1.12E+08	G	4.1	5.7	0.54	G	35.9	29.4	0.18
rs2269899	1.12E+08	G	26.5	26.7	0.97	G	35	28.3	0.16
rs2285933	1.12E+08	C	40.8	37	0.51	C	28.6	25.6	0.5
rs2107418	1.12E+08	G	43.9	40.5	0.56	G	44.2	45	0.87
rs2240189	1.12E+08	T	16.3	17.9	0.72	T	28.6	25	0.42
rs757404	1.12E+08	T	40.8	36.6	0.47	T	29.1	25.6	0.43
Chr. 12: *OAS2*									
rs2010604	1.12E+08	C	8.2	11.8	0.32	C	31.1	22.8	0.07
rs2072138	1.12E+08	C	22.9	24.3	0.77	C	28.4	27.5	0.84
rs1293762	1.12E+08	A	7.1	16.8	0.02	A	44.7	44.4	0.97
rs1293739	1.12E+08	A	29.6	23.7	0.25	A	23.8	23.9	0.98
Chr. 12: *OASL*									
rs1169279	1.2E+08	A	34.7	32.8	0.74	A	40.8	31.1	0.05

rs2260399	1.2E+08	T	38.8	34.4	0.44	C	48.5	51.7	0.54
rs3213545	1.2E+08	T	19.4	14.9	0.3	T	35.4	26.4	0.06
rs10849832	1.2E+08	C	22.5	21.4	0.83	C	14.6	10.6	0.24
Chr. 14: *IRF9*									
rs4981494	22620219	G	34.7	29	0.3	G	29.6	30	0.93
rs2236350	22621138	T	5.1	2.3	0.17	T	8.3	9.4	0.68
rs12432194	22626153	T	10.2	9.5	0.85	T	17.5	15	0.51
Chr. 17: *IFI35*									
rs8076790	41527765	C	33.7	34.4	0.9	C	18	19.4	0.71
rs692692	41528451	A	28.6	26.7	0.73	A	18	18.8	0.96
rs10840	41539582	A	18.4	22.5	0.39	A	8.7	8.3	0.89
rs455055	41541122	T	36.5	30.2	0.26	G	25.3	27.2	0.66
Chr. 21: *IFNAR2*									
rs1476415	33518781	C	46.9	44.3	0.65	A	47.1	46.1	0.85
rs9636866	33520288	C	32.7	32.8	0.98	C	22.8	19.4	0.42
rs2300370	33524953	A	23.5	21.8	0.73	A	30.1	33.9	0.43
rs2248420	33526174	T	15.3	14.5	0.85	T	26.7	32	0.25
rs4986956	33534646	C	4.1	6.9	0.33	C	5.3	7.2	0.45
rs2252650	33538346	A	27.6	26	0.76	A	29.6	33.9	0.37
rs2834165	33542932	G	48	48.9	0.88	A	48.1	46.7	0.79
rs2834166	33547050	A	18.4	20.2	0.69	A	39.3	28.9	0.03
rs2250226	33552712	A	41.8	45.4	0.54	G	30.6	33.3	0.56
rs2834167	33561184	G	18.4	14.9	0.42	G	24.3	22.8	0.73
Chr. 21: *IFNAR1*									
rs2834190	33613407	T	11.5	10	0.69	T	26.7	31.1	0.34
rs2856968	33618377	G	42.9	36.3	0.25	G	40.3	36.1	0.4
rs2252930	33624597	G	11.2	1.3	0.8	G	26.7	31.1	0.34
rs2243592	33628204	G	42.9	36.3	0.25	G	40.3	36.1	0.4
rs2253923	33632815	T	42.9	35.9	0.22	T	39.3	35.6	0.45
rs2257167	33636095	C	16.3	21	0.32	C	14.6	10.7	0.26
rs2834195	33640709	A	6.1	3.8	0.35	A	0.5	0	0.35
rs2243599	33643890	T	29.6	33.6	0.47	G	40.3	36.7	0.47
rs1041868	33647726	A	22.5	22.7	0.96	A	18.5	13.9	0.23

rs2834202	33651350	G	26.5	16.8	0.04	G	24.8	24.4	0.94
Chr. 21: *MX2*									
rs757368	41649987	G	39.8	47	0.23	G	13.6	16.1	0.49
rs2838029	41656115	A	45.9	45.4	0.93	A	12.1	15	0.41
rs443099	41663723	T	23.5	18.3	0.28	G	39.3	38.3	0.84
rs9305739	41679106	C	15.3	22.5	0.13	C	4.9	3.3	0.46
rs369908	41687529	A	23.5	24.2	0.88	G	21.4	17.2	0.31
rs8126663	41703444	T	44.9	43.1	0.76	T	21.8	15	0.09
Chr. 21: *MX1*									
rs17000900	41718426	A	23.4	23.1	0.95	A	10.8	10.6	0.94
rs455816	41725429	G	16.3	17.2	0.85	G	46.6	50.6	0.44
rs456298	41757147	T	37.5	37.8	0.96	T	14.4	12.2	0.53
rs462903	41718002	G	14.3	14.5	0.96	G	41.8	43.9	0.68
rs469390	41738326	A	42.9	47.7	0.41	G	38.5	41.1	0.6

[#] allele frequency among SVR or NR

* chi-square test

Supplemental table 3. Selected possible potential functional SNP in the *OASL* gene and allele frequency of association analysis of SVR and selected SNPs

				African American					Caucasian American				
SNP ID	**Location**	**Nucleotide change**	**Potential function**	**N**	**Variant allele**	**Variant allele N(%)**	**p-value**	**RR (95%CI)**	**N**	**Variant allele**	**Variant allele N(%)**	**p-value**	**RR (95%CI)**
rs7134069	promoter region	A-4606C	C/EBPb biding site	358	C	75(20.9)	0.47	1.16(0.78-1.71)	388	C	17(4.4)	0.96	0.99(0.62-1.56)
rs2859398	promoter region	C- 2875T	C/EBPb biding site	360	C	67(18.6)	0.82	1.05(0.69-1.61)	388	C	142(36.6)	0.04	1.22(1.02-1.47)
rs2859394	promoter region	C- 2485T	GATA1 biding site	358	C	39(10.9)	0.61	1.14(0.69-1.89)	386	C	60(15.5)	0.995	0.999 (0.77-1.29)
rs10849833	promoter region	A-1250G	E47 and USF binding site	360	A	77(21.4)	0.76	1.06(0.71-1.59)	388	A	18(4.6)	0.87	1.04(0.68-1.59)
rs12315068	promoter region	A-736G	SP1 binding site	358					388				
rs10849832*	intron 1	C657T		360	C	78(21.7)	0.83	1.05(0.70-1.57)	386	C	49(12.7)	0.24	1.17(0.92-1.50)
rs28360476	extron 2	T5249G	synonymous	356					388				
rs3213545*	extron 2	C5444T	synonymous	360	T	58(16.1)	0.30	1.25(0.83-1.90)	384	T	120(31.3)	0.06	1.21(1.002-1.46)
rs3213546	intron 2	C5565G	Conserved region	360	C	61(16.9)	0.61	0.89(0.55-1.43)	388	C	11(2.8)	0.95	1.02(0.59-1.76)
rs10849829	intron 2	A6525G	Conserved region	360	A	128(35.6)	0.44	1.15(0.81-1.62)	388	G	192(49.5)	0.42	0.93(0.77-1.12)
rs2260399*	intron 2	C7128T		360	T	128(35.6)	0.44	1.15(0.81-1.62)	386	C	193(50.0)	0.54	0.94(0.78-1.14)
rs7969180	extron 4	A11280G	synonymous	360	A	4(1.1)	0.92	0.92(0.17-5.05)	386				
rs11307154	intron 4	-11670A	Conserved region	358	-	177(49.4)	0.40	1.16(0.82,1.63)	388	A	85(21.9)	0.70	0.96(0.76,1.20)
rs3861793	extron 6	C18300G	synonymous	352					388				

rs12819210	extron 6	T18311C	synonymous	360	T	20(5.6)	0.77	1.11(0.56-2.21)	388	T	77(19.8)	0.74	0.96(0.76-1.22)
rs2259697	3-UTR	C18643T	3 end untranslate region	360	C	135(37.5)	0.76	1.06(0.75-1.49)	388	C	79(20.4)	0.55	0.93(0.73-1.18)
rs1169279*	3 end down stream	A18381G		360	A	120(33.3)	0.74	1.06(0.75-1.51)	386	A	140(36.3)	0.049	1.21(1.01-1.46)
rs7134141	3 end down stream	A19708G	Conserved region	358	A	53(14.8)	0.40	0.80(0.47-1.36)	388	A	10(2.6)	0.68	1.12(0.67-1.88)

* SNPs were typed in stage I

Supplemental table 4. Linkage disequilibrium among the 3 SNPs in *OASL*

CA	rs1169279	rs3213545	rs2859398
rs1169279		0.97	0.68
rs3213545	0.75		0.8
rs2859398	0.46	0.5	

AA	rs1169279	rs3213545	rs2859398
rs1169279		0.59	0.5
rs3213545	0.13		0.96
rs2859398	0.12	0.77	

Upper triangle for D'
Lower triangle for r^2