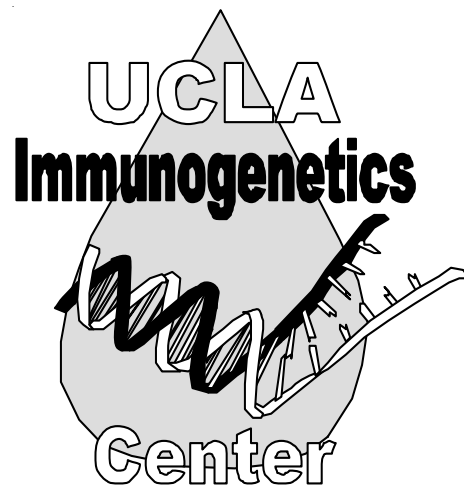


# SUMMARY OF THE 83rd INTERNATIONAL HLA DNA EXCHANGE

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## EXCHANGE #83 CONSENSUS

### DNA #519 HISP

	ALLELE #1	ALLELE #2	AGREEMENT ( n/total)		SBT LABS Allele level
			low	high	
A*	3002	3101	229/230	149/149	90/96
B*	1402	3517	225/228	166/166	91/96
Cw*	0401	0802	195/196	133/133	69/94
DRB1*	0901	1503	232/232	180/181	98/100
DRB3*					
DRB4*	0101		77/77	59/59	13/13
DRB5*		0101	76/77	58/59	13/13
DQA1*	0102	0303	60/60	46/47	7/12
DQB1*	0202	0602	184/186	153/155	53/54
DPB1*	0201	0402	74/74	74/74	38/38
DPA1*	0103		5/5	4/4	1/1

Agreement for this sample was greater than 95%. This sample appears to carry a genetic admixture.

In a study on DR2 alleles (n=248), DRB1\*1503 was only found in African Americans (64%) and Hispanics (3%). (Limited diversity of HLA-DRB1\*02 alleles and DRB1-DRB5 haplotype associations in four US population groups. Baldassarre, LA. et al. Tissue Antigens 2003: 61; 249-252).

DRB1\*1503 was associated with MS in an African American study (OR = 1.5). (Mapping Multiple Sclerosis susceptibility to the HLA-DR locus in African Americans. Oksenberg, J. et al. Am. J. Hum. Genet. 2004: 74;160-167).

The MS susceptibility alleles; DRB1\*1501, \*1503, \*0301 \*0401 and \*0801/3 share an aromatic residue (Tyr) at position 60, whereas the common resistance allele DRB1\*14 carries the basic residue (His). (Heterogeneity at the HLA-DRB1 locus and risk for Multiple Sclerosis. Barcellos, L. et al. Human Molecular Genetics 2006:15; 2813-2824).

M. Fernandez Vina comments that this sample carries a haplotype fragment. A\*310102 - B\*3517 - Cw\*0401 is found exclusively in Native Americans from Mexico and Central America. DRB1\*0901 - DRB4\*0101 - DQB1\*0202 and DRB1\*1503 - DRB5\*0101-DQB1\*0602 have an African origin. The hybrid haplotype probably originated from a crossing over between HLA-B and DRB1 loci involving haplotypes from different ethnic origins.

### DNA #520 HISP

	ALLELE #1	ALLELE #2	AGREEMENT ( n/total)		SBT LABS Allele level
			low	high	
A*	0201	2402	228/230	136/136	84/96
B*	1515	1539	227/228	143/147	92/96
Cw*	0102	0303	194/196	138/140	24/46
DRB1*	0404	BLANK	114/115	88/88	50/50
DRB3*					
DRB4*	0103		77/77	58/59	13/13
DRB5*					
DQA1*	0301	BLANK	30/30	22/22	3/6
DQB1*	0302	BLANK	92/93	76/77	27/27
DPB1*	0402	BLANK	37/37	37/37	29/29
DPA1*	0103	BLANK	5/5	4/5	1/1

Agreement for this sample was greater than 95%.

This is the first B\*1539 (B62) sent in the DNA Exchange. Consensus was 97%.

In a US population study (n=1,296), B\*1515 and Cw\*0303 had frequencies of 0.0043 and 0.0256, respectively, in Hispanics. (Analysis of the frequencies of HLA-A, B, and C alleles and haplotypes in the five major ethnic groups of the US reveals high levels of diversity in these loci and contrasting distribution patterns in these populations. Cao, K. et al. Human Immunology 2001: 62; 1009-1030).

In a Peruvian study (n=148) B\*1539 and DRB1\*0404 have frequencies of 4.8% and 38%, respectively. (HLA Class I and Class II allele distribution in the Peruvian population. de Pablo, R. et al. Tissue Antigens 2000:56: 507-514).

In a rheumatoid arthritis study, patients homozygous for DRB\*0404 recognized a synovial protein identified as calpastatin. RA patients' sera contain autoantibodies to citrullinated proteins (filaggrin, fibrinogen...) which are specific for RA. Synovial calpastatin is not citrullinated. Calpastatin specifically inhibits calpain, a calcium dependent cysteine protease involved in the development of inflammation. Calpain is overexpressed in rheumatoid synovial tissue and calpain/calpastatin imbalance may be associated with cartilage destruction. (HLA-DRB1\*0404 is strongly associated with anti-calpastatin antibodies in rheumatoid arthritis. Auger, I. et al. Annals Rheumatic Dis: online 26 Feb 2007;digital object identifier: 10.1136/ard.2006.067231).

## EXCHANGE #83 CONSENSUS

### DNA #521 ASIAN

	ALLELE #1	ALLELE #2	AGREEMENT ( n/total)		SBT LABS Allele level
			low	high	
A*	2601	2603	220/222	139/139	89/94
B*	0702	1501	219/220	132/132	80/94
Cw*	0702	1502	187/190	127/128	72/92
DRB1*	0901	1502	226/228	169/174	89/100
DRB3*					
DRB4*	0103		74/75	57/58	12/13
DRB5*		0102	72/75	54/55	12/13
DQA1*	0103	0302	58/58	47/48	7/12
DQB1*	0303	0601	184/184	152/153	53/54
DPB1*	0501	0901	71/72	71/72	38/38
DPA1*	0201	0202	8/8	8/8	2/2

Agreement for this sample was greater than 95%.  
 This sample is from a Japanese donor. Consensus at DRB1\*1502 was 95%. 16% of SBT labs could not exclude DRB1\*1519.  
 A\*26 is one of the alleles associated with a slow progression to AIDS. The frequency of A\*2601 and A\*2603 in Japan is 8.1% and 2.4%, respectively. Two HLA-A\*2603-restricted HIV-1 epitopes are Gag169-177 and Env63-72. Gag169-177 is presented by both A\*2601 and A\*2603, whereas only A\*2603 presented Env63-72. Gag169-177 is a relatively conserved epitope and the specific CTLs were frequently detected in chronically HIV-1 infected individuals with either A\*2601 or A\*2603. Therefore, it can be speculated that Gag169-177-specific CTLs play an important role in the suppression of HIV-1 replication in slow progressors. If Gag 169-177- specific CTLs have a strong ability to suppress HIV-1 replication, a vaccine that can include Gag-169-177 epitope might be useful in the areas where A26 is frequently found. (Identification and characterization of HIV-1 epitopes presented by HLA-A\*2603: comparison between HIV-1 epitopes presented by A\*2601 and A\*2603. Kawashima, Y. et al. Human Immunology 2005;66;155-1166).  
 In an aplastic anemia (AA) study (n=140), DRB1\*1502 had the highest frequency (43.6%). The frequency of DRB1\*1502 in AA patients 40 years of age and older (52.4%) was markedly higher than that in those younger than 40 years old (16.2%). (Roles of DRB1\*1501 and DRB1\*1502 in the pathogenesis of aplastic anemia. Sugimori, C. et al. Exp. Hematology: 35; 2007 13-20).

### DNA #522 BLACK

	ALLELE #1	ALLELE #2	AGREEMENT ( n/total)		SBT LABS Allele level
			low	high	
A*	0201	3004	216/216	141/141	90/94
B*	0702	5802	212/212	140/140	89/94
Cw*	0602	0702	186/186	130/130	91/92
DRB1*	1303	1501	222/222	167/167	97/100
DRB3*	0101		73/73	55/56	12/13
DRB4*					
DRB5*		0101	70/73	55/57	12/13
DQA1*	0102	0505	60/60	44/46	6/12
DQB1*	0301	0602	180/180	154/154	51/54
DPB1*	0401	0602	66/64	65/68	40/40
DPA1*	0103	0301	8/8	7/7	2/2

Agreement for this sample was greater than 95%.  
 In a US study, A\*0201 and A\*3004 had frequencies of 0.0060 and 0.0020, respectively, in African Americans. B\*0702 and B\*5802 had frequencies of 0.0817 and 0.0339, respectively. (Analysis of the frequencies of HLA-A, B and C alleles and haplotypes in the five major ethnic groups of the US reveals high levels of diversity in these loci and contrasting distribution patterns in these populations. Cao, K. et al. Human Immunology 2001;62; 1009-1030).  
 In an African study, A\*3004 was only found in 4 of 7 African populations studied. The highest frequency is found in the Zulu, 0.0150. (Differentiation between African populations is evidenced by the diversity of alleles and haplotypes of HLA Class I loci. Cao, K. et al. Tissue Antigens 2004;63;293-325).  
 Discrepancies or ambiguities reported:  
 A\*: Not excluded: 3006.  
 B\*: Not excluded: 5801/7.  
 Cw\*: Not excluded: 0610.  
 DRB1\*: Not excluded: 1366, 1506/16/18.

## EXCHANGE #83 CONSENSUS

### DNA #523 CAUC

	ALLELE #1	ALLELE #2	AGREEMENT ( n/total)		SBT LABS
			low	high	Allele level
A*	0201	2902	214/214	128/130	85/92
B*	1801	4403	211/212	130/130	69/92
Cw*	0701	1601	184/184	119/119	72/90
DRB1*	0701	1108	220/220	171/171	95/98
DRB3*	0202		72/73	53/54	12/13
DRB4*		0101	70/73	53/55	12/13
DRB5*					
DQA1*	0201	0505	52/54	40/43	6/12
DQB1*	0202	0301	177/178	145/147	48/52
DPB1*	0201	0402	65/66	65/66	39/40
DPA1*	0103	BLANK	4/4	3/3	1/1

Agreement for this sample was greater than 95%.  
We thank E. Mickelson from Fred Hutchinson Cancer Research Center - Seattle for providing this B-cell line.

This sample was also sent in the UCLA Cell Exchange B-cell line Exchange as Ter-386 (2007). In the Cell Exchange, 69% of participants assigned DRB1\*1108. (Report of the 322nd Cell Exchange, February 7, 2007). In this sample, 80% (88/110) of participants assigned DRB1\*1108.

This sample appears to have a new Cw\* allele. 5 SBT labs reported a polymorphism in exon 4, position 861 C-T (Y).

This sample may also have a new DPB1\* allele. E. Rozemuller (Utrecht - Netherlands) reports that exon 3 did not resolve the ambiguity. The exon 3 sequence shows heterozygosity at position #441 (R) and #619 (M) and did not match any pattern in the IMGT 2.17 database.

Discrepancies or ambiguities reported:

A\*: 2901. Not excluded: 0207/31, 2901.

B\*: Not excluded: 1805/17, 4446.

Cw\*: Not excluded: 0718, 1608.

DRB1\*: Not excluded: 0709/10, 1101/42.

### DNA #524

	ALLELE #1	ALLELE #2	AGREEMENT ( n/total)		SBT LABS
			low	high	Allele level
A*	3001	3002	214/214	136/137	92/92
B*	4201	4403	212/212	149/149	92/92
Cw*	0401	1701	182/184	107/107	55/90
DRB1*	1101	1331	218/220	158/164	92/98
DRB3*	0202	0301	143/146	106/108	24/26
DRB4*					
DRB5*					
DQA1*	0102	0505	54/54	39/40	6/12
DQB1*	0301	0502	177/178	142/151	43/52
DPB1*	0101	0602	66/66	66/66	40/40
DPA1*	0103	0201	8/8	7/8	2/2

Agreement for this sample was greater than 95%, except at DRB1\*13 and DQB1\*03. This is the first DRB1\*1331 sent in the DNA Exchange. The DRB1\*1331 high resolution consensus was 93%.

We thank H. Bass and C. Darke, Welsh Blood Service, Pontyclun for providing this B-cell line.

This sample was also sent in the UCLA Cell Exchange as Ter-381 (2006). In the Cell Exchange, 66% of participants assigned DRB1\*1331. (Report of the 320th Cell Exchange, October 4, 2006). In this sample, 70% (77/110) of participants assigned DRB1\*1331. 5% of labs reported DRB1\*1302.

At DQB1\*03; 35% (9/26) of SBT reported DQB1\*0319, 54% (14/26) of SBT reported DQB1\*0301. Labs using SSP or SSOP reported DQB1\*0301. At this time, the consensus is DQB1\*0301 (88%). DQB1\*0319 was assigned in September 2006 and last modified in October 2006. For DQB1\*0319, the polymorphism occurs in exon 3, position #650 (C-T). (IMGT database). This sample was graded as DQB1\*0301g. This is based on the use of alternative names for groups of alleles with identical sequences in exon 2 and includes DRB1\*0309\*19. Refer to: (Common and Well-Documented HLA alleles. Report of the Ad-hoc committee of the American Society for Histocompatibility and Immunogenetics. Cano, P. et al. Human Immunology 2007: 68; 392-417).

In Cell Exchange sample Ter-381, there were no reports of DQB1\*0309. At that time, DQB1\*0319 was not yet identified in the database.

# DNA #519

CENTER	DRB1		DRB3/4/5		DQA1		DQB1		DPB1		DPA1		A-Locus		B-Locus		C-Locus	
7	09	1503	401	501	0102	03	0202	0602					30	31	1402	3517	04	08
16	090102	1503	40101	50101	01	03	02	0602	020102	0402			3002/14	310102	140201	3517	0401/9	0802
61																		
80	09	15	4	5			02	06					30	31	14	35	04	08
124	0901	1503	401	50101			0202	0602	0201	0402			3002	3101	1402	3517	0401/9	0802
134	0901	1503	40101	50101			0202	0602	0201	0402			3002	3101	1402	3517	0401	0802
138	0901	1503					0202	0602					3002	3101	1402	3517	0401	0802
139	09	1503	401	501									30	31	1402/3	35		
142	09	15	401	501			02	06					30	31	1402	35		
144	0901	1503					0202	0602					3002	3101/14	1402	3517	0401/9	0802
145	0901	1503	40101	50101			0202	0602					30	31	14	35	04	08
147	0901	1503	40101	50101	0102	0303	0302	BLANK	0201	0402			3002	3101	1402	3517	0401	0802
148	0901	1503	40101	50101			0202	0602	0201	0402			3002	3101	1402	3517	0401	0802
151	0901	1503	4	5									3002	3101	1402	3517	0401	0802
152	09	15											30	31	14	35		
153	09	15	4	5			02	06					30	31	14	35	04	08
155													3002	3101	1402	3517	0401	0802
156	0901	1503											3002	3101	1402	3517	0401	0802
158	0901	1503	40101	50101									3002	3101	1402	3517	0401	0802
160							0202	0602	0201	0402			3002	3101	1402	3517	0401	0802
161																		
162	090102	1503	4010101	5010101	010201	0303	0202	0602	020102	0402	010301	BLANK	300201	310102	140201	3517	040101	0802
163	0901	1503	NT	NT									30	31	14	35		
164	09	15											30	31	14	35		
166	0901	1503	40101	50101	0102	0303	0202	0602	0201	0402			30	31	14	35	04	08
167	090102	1503											300201	310102	140201	3517	040101	0802
168	09	1503											30	31	14	35		
170	0901	1503	40101	50109	0102	0303	0202	0602					30	31	14	35	04	08
171	0901	1503	40101	50101			0202	0602					30	31	14	35	04	08
173	0901	1503			0102	0301	0201	0602					30	31	1402	3517		
174	09	1503											30	31	1402	3517		
175	0901	1503	401	501			0202	0602					3002	3101	1402	3517	04	08
179	090102	1503	401	BLANK	0102	03	0202	0602					3002	3101	140201	3517	04	0802/5
180	0901	1503	4010101	5010101	0102	0303	0202	0602	0201	0402			3002	3101	1402	3517	0401	0802
185	090102	1503					0202	0602					3002	310102	140201	3517	04	0802
186	0901	1503	40101	50101	0102	0303	0202	0602	0201	0402			3002	3101	1402	3517	0401	0802
187	0901	1503											30	31	1402	3517		
188	0901	1503	40101	50101									3002	3101	1402	3517	0401	0802
189	0901	1503	401	501			0202	0602					3002	3101	1402	3517	0401	0802
190	09	15	4	5			02	06					30	31	14	35	04	08
192	0901	1503	40101	50101			0202	0602					3002	3101	1402	3517	0401	0802
193	09	1503											30	31	1402	3517		
194	09	15	4	5									30	31	BLANK	35		
195	0901	1503	40101	50101			0202	0602					3002	3101	1402	3517	0401	0802
196	090102	1503	4010101	5010101	0102	0303	0202	0602	0201	0402			3002	310102	1402	3517	0401	0802
197	0901	1503	401	501	01	03	0202	0602	0201	0402			3002	3101	1402	3517	0401	0802
199	09	15	4	5			02	06										
200																		
201	0901	1503	40101	50101			0202	0602					30	31	14	35	04	08
202	0901	1503	40101	50101			0202	0602					3002	3101	1402	3517	0401	08
203	0901	1501	4	5			02	06					30	BLANK	42	44	04	17
204	090102	1503											3002	310102	140201	3517	040101	0802
205	0901	1503	401	501			0202	0602					3002	3101	1402	3517	0401	0802
206	09	15											30	31	14	35		
207	0901	1503	40101	50101			0202	0602	0201	0402			3002	3101	1402	3517	0401	0802
208	09	1503											30	31	1402	3517		
210													3002	3101/14	140201	3517	04	0802
216	0901	1503					0202	0602					3002	3101	1402	3517	0401	0802
230	0901	1503	40101	50101	0102	0302/3	0202	0602	0201	0402			3002	3101	1402	3517	0401	0802
239	09	1503	40101	50101	0102	0303	0202	0602					30	31	14	35		
278	0901	1503	40101	50101	0102	03	0202	0602	0201	0402			3002	3101/11	1402	3517	04	0802
291	0901/5	1503	401	50101	0102	0303	0202	0602					30	31	14	3517/51	04	08
401	0901	1503					0202	0602	0201	0402								
452	0901	1503					0202	0602	0201	0402			3002	3101	1402	3517	0401	0802
519	0901	1503					02	0602					3002	3101	1402	3517	0401/9	0802
615	090102	1503	401	5010101	01	03	0202	0602	020102	0402								
615.1	09	15																
635	09	15	4	5			02	06					30	31	14	35	04	08

# DNA #519

CENTER	DRB1		DRB3/4/5		DQA1		DQB1		DPB1		DPA1		A-Locus		B-Locus		C-Locus	
642	090102	1503											300201	310102	140201	3517		
702	0901	1503	40101	50101	0102	0303	0202	0602	0201	0402			3002	3101	1402	3517	0401	0802
714	0901	1503					0202	0602					3002	3101	1402	3517	0401	0802
726	0901	1503					0202	0602					3002	3101	1402	3517	0401	0802
732	090102	1503	4010101	5010101			0202	0602					300201	310102	140201	3517	0401/9	0802
743	09	15	4	5			0202	0602					30	31	14	35	04	08
805	09	1503					0202	0602					30	31	14	35	04	08
1018	0901	1503	4	5			0202	0602					3002	3101	1402	3517	0401	0802
1113	0901	1503	401	50101			0202	0602	0201	0402			3002	3101	1402	3517	0401	0802
1189	0901	1503	40101	50101			0202	0602					3002	3101	1402	3517	0401	0802
1212	0901	1503	40101	50101			0202	0602	0201	0402			3002	3101	1402	3517	0401	0802
1251	0901	1503	401010101	5010101	0102	0303	0202	0602	0201	0402			3002	310102	1402	3517	0401	0802
1260	09	15											30	31	1402	3517	04	0802/5
1498	0901	1503	401	5010101	0102	0303	0202	0602					30	31	1402/3	35	04	08
1647	09	15	4	5			02	06					30	31	14	35	04	08
1686	0901	1503	40101	50101	0102	0303	0202	0602	0201	0402	0103	BLANK	3002	3101	1402	3517	0401	0802
1905	0901	1503	40101	50101			0202	0602	0201	0402			3002	3101	1402	3517	0401	0802
2004	090102	1503											300201	310102	140201	3517	0401/9	0802
2013	0901	1503	4	5			02	06					30	31	1402/3	35	04	08
2015													3002	3101	1402	3517	0401	0802
2019																		
2042																		
2063	09	1503	401	501			02	0602										
2347	09	15	4	5			NT	NT					30	31	14	35	NT	NT
2375																		
2411	09	15											30	31	14	35		
2518	0901	1503					0202	0602					3002	3101	1402	3517	0401	0802
2549	0901	1503	4	5	0102	0303	0202	0602	0201	0402			3002	3101	1402	3517	0401	0802
3248	090102	1503	40101	5010101			0202	0602					3002	310102	140201	3517	0401	0802
3261	0901	1503	4	5			0202	0602	0201	0402			3002	3101	1402	3517	0401	0802
3324	0901	1503	401	501	0102/6	03	0202	0602	0201	0402			3002	3101	1402	3517	0401/9	0802
3325	0901	1503	401	501	0102	0303	0202	0602					3002	3101	1402	3517	04	08
3410	0901	1503					0202	0602					3002	3101	1402	3517	0401	0802
3438	0901	1503	401	501			0202	0602					3002	3101	1402	3517	0401	0802
3522	0901	1503			0102	0303	0202	0602					3002	3101	1402	3517	04	08
3548	0901	1503	40101	50101			0202	0602					3002	3101	1402/5	3501	0401	0802
3582	0901	1503	401	50101			0202	0602	0201	0402			3002	3101/14	1402	3517	04	0802/5
3600	09	15	4	5			02	06					30	31	14	35	04	08
3614	0901	1503					0202	0602					3002	3101/11	1402	3517	0401	0802/5
3625	0901	1503	401	501	0102	03	0202	0602	0201	0402	01	BLANK	30	31	14	35	0401	0802
3631	0901	1503	40101	50101	0102	0303	0202	0602	0201	0402	0103	BLANK	3002	3101	1402	3517	0401	0802
3798	0901	1503	40101	50101	01	03	0202	0602					3002	3101	1402	3517	0401/9	0802
3807	090102	1503	4010101	50101	0102	0303	0202	0602	020102	0402			300201	310102	140201	3517	0401/9	0802
3849	0901	1503	401	50101	0102	0302/3	0202	0602					30	31	1402	3517/51	04	08
4237																		
4281																		
4336	0901	1503					0202	0602					3002	3101	1402	3517	04	0802/5
4349	0901	1503	401	501			0202	0602					3002	3101	1402	3517	0401	0802
4420	0901	1501/3											3002	3101	1402	3517	0401	0802
4545	0901	1503	401	501	0102	0303	0202	0602	0201	0402	0103	BLANK	3002	3101	1402	3517	0401/9	0802
4551	09	15	NT	NT			02	06	NT	NT			30	31	14	35	04	08
4582	0901	1503	401	501			0202	0602					3002	310102	1402	3517	0401	0802
4585	09	1503					0202	06					30	31	1402	35	04	08
4613													3002	3101	1402	3517	0401	0802
4623									020102	0402			300201	310102				
4653	090102	1503					0202	0602					3002	310102	140201	3517	0401/9	0802
4709	0901/4	1503	40101	50101			0202	0602	0201	0402			3002	310102	1402	3517	0401	0802
5204													30	31	14	35	04	08
5231																		
5365	09	15	4	5			02	06					30	31	14	35	04	08
5720	0901	1503	40101	50101			0202	0602	0201	0402			3002	3101	1402	3517	0401	0802
5982	090102	1503					0202	0602	020102	0402			300201	310102	140201	3517	040101	0802
6051	09	1503	401	501			02	0602/19	0201	0402			30	31	1402	35	04	08
6313	0901/5	1503					0202	0602					300201	310102	140201	3517	04	0802/5
9221	09	15	4	5			02	06					30	31	14	35	04	08



# DNA #520

CENTER	DRB1		DRB3/4/5		DQA1		DQB1		DPB1		DPA1		A-Locus		B-Locus		C-Locus	
635	04	BLANK	4	BLANK			03	BLANK					02	24	15	15	01	03
642	0404	BLANK											0201	2402	1515	1539		
702	0404	BLANK	40103	BLANK	0301	BLANK	0302	BLANK	0402	BLANK			0201	2402	1515	1539	0102	0303
714	0404	BLANK					0302	BLANK					0201	2402	1515	1539	0102	0303
726	0404	BLANK					0302	BLANK					0201	2402	1515	1539	0102	0303
732	0404	BLANK	4010301	BLANK			030201	BLANK					020101	240201	1515	1539	010201	030301
743	04	BLANK	4	BLANK			03	BLANK					02	24	15	15	01	03
805	0404	BLANK					0302	BLANK					02	24	15	15	01	03
1018	0404	BLANK	4	BLANK			0302	BLANK					0201	2402	1515	1539	0102	0303
1113	0404	BLANK	40103	BLANK			0302	BLANK	0402	BLANK			0201	2402	1515	1539	0102	0303
1189	0404	BLANK	40103	BLANK			0302	BLANK					0201	2402	1515	1539	0102	0303
1212	0404	BLANK	40103	BLANK			0302	BLANK	0402	BLANK			0201	2402	15	15	0102	0303
1251	0404	BLANK	40103	BLANK	030101	BLANK	0302	BLANK	0402	BLANK			0201	2402	1515	1539	0102	0303
1260	04	BLANK											02	24	15	15	01	03
1498	0404	BLANK	401	BLANK	030101	BLANK	0302/18	BLANK					02	24	1515	15	01	03
1647	04	BLANK	4	BLANK			03	BLANK					02	24	15	15	01	03
1686	0404	BLANK	40103	BLANK	0301	BLANK	0302	BLANK	0402	BLANK	0103	BLANK	0201	2402	1515	1539	0102	0303
1905	0404	BLANK	40103	BLANK			0302	BLANK	0402	BLANK			0201	2402	1515	1539	0102	0303
2004	0404	BLANK											020101	24020101	1515	1539	0102	0303/20
2013	0404	BLANK	4	BLANK			03	BLANK					02	24	15	15	01	03
2015													0201	2402	1515	1539	0102	0303
2019																		
2042																		
2063	0404	BLANK	401	BLANK			03	BLANK										
2347	04	BLANK	4	BLANK			NT	NT					02	24	15	15	NT	NT
2375																		
2411	04	BLANK											02	24	15	15		
2518	0404	BLANK					0302	BLANK					0201	2402	1515	1539	0102	0303
2549	0404	BLANK	4	BLANK	0301	BLANK	0302	BLANK	0402	BLANK			0201	2402	1515	1539	0102	0303
3248	0404	BLANK	40103	BLANK			0302	BLANK					0201	2402	1515	1539	0102	0303
3261	0404	BLANK	4	BLANK			0302	BLANK	0402	BLANK			0201	2402	1515	1539	0102/11	0303
3324	0404	BLANK	401	BLANK	03	BLANK	0302	BLANK	0402	BLANK			0201/90	2402/30	1515	1539	0102/11	0303/20
3325	0404	BLANK	401	BLANK	0301	BLANK	0302	BLANK					0201/7	2402	1502/15	1501/39	01	03
3410	0404	BLANK					0302	BLANK					0201	2402	1515	1539	0102	0303
3438	0404	BLANK	401	BLANK			0302	BLANK					0201	2402	1515	1539	0102	0303
3522	0404	BLANK			0301	BLANK	0302	BLANK					0201	2402	1515	1539	0102	0303
3548	0404	BLANK	40103	BLANK			0302	BLANK					0201	2402	1515	15	0102	0303
3582	0404	BLANK	401	BLANK			0302	BLANK	0402	BLANK			02	24	1515	1539	0102	0303/20
3600	04	BLANK	4	BLANK			03	BLANK					02	24	15	15	01	03
3614	0404/23	BLANK					0302	BLANK					0201	2402/27	1515	1539	01	0303
3625	0404	BLANK	401	BLANK	03	BLANK	0302	BLANK	0402	BLANK	01	BLANK	02	24	15	15	0102	0303
3631	0404	BLANK	40103	BLANK	0301	BLANK	0302	BLANK	0402	BLANK	0103	BLANK	0201	2402	1515	1539	0102	0303
3798	0404	BLANK	40103	BLANK	03	BLANK	0302	BLANK					0201	2402	1515	1539	0102	0303/20
3807	0404	BLANK	4010101	BLANK	030101	BLANK	030201	BLANK	0402	BLANK			0201	24020101	1515	1539	010201	0303/20
3849	0404	BLANK	401	BLANK	0301	BLANK	0302	BLANK					02	24	1515	1539/98	01	0303/20
4237																		
4281																		
4336	0404	BLANK					0302	BLANK					0201	2402	1515	1539	0102	0303/20
4349	0404	BLANK	401	BLANK			0302	BLANK					0201	2402	1515	1539	0102	0303
4420	0404	BLANK											0201	2402	1515	1539	0102	0303
4545	0404	BLANK	401	BLANK	0301	BLANK	0302	BLANK	0402	BLANK	0103	BLANK	0201	2402	1515	1539	0102	0303/20
4551	04	BLANK	NT	NT			03	BLANK	NT	NT			02	24	15	15	01	03
4582	0404	BLANK	401	BLANK			0302	BLANK					0201	2402	1515	1539	0101	0303
4585	NT	NT					03	BLANK					02	24	15	15	01	03
4613													0201	2402	1515	1539	0102	0303
4623									0402	BLANK			02010101	24020101				
4653	0404	BLANK					0302	BLANK					020101	240201	1515	1539	0102	0303/20
4709	0404	BLANK	40103	BLANK			0302	BLANK	0402	BLANK			0201	2402	1515	1539	0102	0303
5204													02	24	15	15	01	03
5231																		
5365	09	15	4	5			03	06					26	26	07	15	07	15
5720	0404	BLANK	40103	BLANK			0302	BLANK	0402	BLANK			0201	2402	1515	1539	0102	0303/20
5982	0404	BLANK					030201	BLANK	0402	BLANK			020101	24020101	1515	1539	010201	030301
6051	0404	BLANK	401	BLANK			03	BLANK	0402	BLANK			02	24	1502	1501	01	03
6313	0404	BLANK					0302	BLANK					0201	2402	1515	1539	0102	0303
9221	04	BLANK	4	BLANK			03	BLANK					02	24	15	15	01	03



# DNA #521

CENTER	DRB1		DRB3/4/5		DQA1		DQB1		DPB1		DPA1		A-Locus		B-Locus		C-Locus	
635	09	15	4	5			03	06					26	26	07	15	07	15
642	090102	150201											260101	2603	070201	150101		
702	0901	1501	40103	50102	0103	0302	0303	0601	0501	0901			2601	2603	0702	1501	0702	1502
714	0901	1502					0303	0601					2601	2603	0702	1501	0702	1502
726	0901	1502					0303	0601					2601	2603	0702	1501	0702	1502
732	090102	150201	4010302	50102			030302	0601					260101	2603	070201	150101	070201	150201
743	09	15	4	5			0303	0601					NT	NT	NT	NT	NT	NT
805	09	1502					0303	0601					26	26	07	15	07	15
1018	0901	1502	4	5			0303	0601					2601	2603	0702	1501	0702	1502
1113	0901	1502	40103	50102			0303	0601	0501	0901			2601	2603	0702	1501	0702	1502
1189	0901	1502	40103	50102			0303	0601					2601/9	2603	0702	1501	0702	1502
1212	0901	1502	40103	50102			0303	0601	0501	0901			2601	2603	0702	1501	0702	1502
1251	0901	1502	40103	50102	0103	0302	0303	0601	0501	0901			2601	2603	0702	1501	0702	1502
1260	09	15											26	26	07	15	07	15
1498	0901	150201	401	501	0103	0302	0303	0601					26	26	07	15	07	15
1647	09	15	4	5			03	06					26	26	07	15	07	15
1686	0901	1502	40103	50102	0103	0302	0303	0601	0501	0901	0201	0202	2601	2603	0702	1501	0702	1502
1905	0901	1502	40103	50102			0303	0601	0501	0901			2601	2603	0702	1501	0702	1502
2004	090102	1502/19											260101	2603	070201	150101	070201	1502/13
2013	0901	1502	4	5			03	06					26	26	07	15	07	15
2015													2601	2603	0702	1501	0702	1502
2019																		
2042																		
2063	09	1502	401	501			03	0601										
2347	09	15	4	5			NT	NT					26	26	07	15	NT	NT
2375																		
2411	09	15											26	26	07	15		
2518	0901	1502					0303	0601					2601	2603	0702	1501	0702	1502
2549	0901	1502/19	4	5	0103	0302	0303	0601	0501	0901			2601	2603	0702	1501	0702	1502
3248	090102	1502	40103	50102			0303	0601					2601	2603	0702	1501	0702	1502
3261	0901	1502/19	4	5			0303	0601	0501	0901			2601	2603	0702	1501	0702	1502
3324	0901	1502	401	50102	0103	03	0303	0601	0501	0901			2601	2603	0702	1501	0702	1502/13
3325	0901	1515	401	501	0103	0302	0303	0601					2601/2	2603	0702	1501	07	15
3410	0901	1502					0303	0601					2601	2603	0702	1501	0702	1502
3438	0901	1502	401	501			030302	0601					NT	NT	NT	NT	NT	NT
3522	0901	1502			0103	0302	0303/15	0601					2601	2603	0702	1501	0702	15
3548	0901	1502/19	40103	50102			0303	0601					2601	2603/21	0702	1501/78	0702	1502
3582	0901	1502	401	501			0303	0601	0501	0901			26	2603	07	15	07	15
3600	09	15	4	5			03	06					26	26	07	15	07	15
3614	0901	1502					0303	0601					2601	2603	0702	1501	0702/10	1502/8
3625	0901	1502	401	501	0103	03	0303	0601	0501	0901	0201	0202	26	26	07	15	0702	1502/14
3631	NT	NT	NT	NT	NT	NT	NT	NT	NT	NT	NT	NT	NT	NT	NT	NT	NT	NT
3798	0901	1502	40103	50102	0103	03	0303	0601					2601	2603	0702	1501	0702	1502
3807	090102	1502/19	30212	4010101	0103	0302	030302	060101	0501	0901			260101	2603	0702/24	150101	070201	150201
3849	0901	1502	401	501	0103	0302/3	0303	0601					26	26	07	15	07	15
4237																		
4281																		
4336	0901	1502					0303	0601					2601	2603	0702	1501	07	15
4349	0901	1502	401	501			0303	0601					2601	2603	0702	1501	0702	1502
4420	0901	1502											2601	2603	0702	1501	0702	1502
4545	0901	1502	401	50102	0103	0302	0303	0601	0501	0901	0201	0202	2601	2603	0702	1501	0702	1502
4551	09	15	NT	NT			03	06	NT	NT			26	26	07	15	07	15
4582	0901	1502	401	501			0303	0601					2601	2603	0702	1501	0702	1502
4585	09	15					03	0601					26	26	07	15	07	15
4613													2601	2603	0702	1501	0702	1502
4623									0501	0901			260101	2603				
4653	090201	150201					0303	0601					260101	2603	070201	150101	070201	150201
4709	0901/4	1502	40103	50102			0303	0601	0501	0901			2601	2603	0702	1501	0702	1502
5204													26	26	07	15	07	15
5231																		
5365	04	BLANK	4	BLANK			03	BLANK					02	24	15	15	01	03
5720	0901	1502	40103	50102			0303	0601	0501	0901			2601	2603	0702	1501	0702	1502
5982	090102	1502/19					030302	060101	0501	0901			260101	2603	070201	15010101	070201	150201
6051	09	15	401	501			03	06	0501	0901			26	26	07	1501/7	07	15
6313	0901/5	1502					0303	0601					260101	2603	07	15	07	15
9221	0901	1502	4	5			03	06					26	26	07	15	07	15



# DNA #522

CENTER	DRB1		DRB3/4/5		DQA1		DQB1		DPB1		DPA1		A-Locus		B-Locus		C-Locus	
635	13	15	3	5			03	06					02	30	07	58	06	07
642	130301	150101											020101	3004	070201	5802		
702	1303	1501	30101	50101	0102	0505	0301	0602	0401	0602			0201	3004	0702	5802	0602	0702
714	1303	1501					0301	0602					0201	3004	0702	5802	0602	0702
726	1303	1501					0301	0602					0201	3004	0702	5802	0602	0702
732	130301	150101	30101	5010101			030101	0602					020101	3004	070201	5802	060201	070201
743	13	15	3	5			0301	0602					NT	NT	NT	NT	NT	NT
805	1303	1501					0301/19	0602					02	30	07	58	06	07
1018	1303	1501	3	5			0301	0602					0201	3004	0702	5802	0602	0702
1113	1303	1501/18	30101	50101			0301	0602	0401	0602			0201	3004	0702	5802	06	0702
1189	1303	1501	30101	50101			0301/19	0602					0201	3004/6	0702	5802	0602	0702
1212	NT	NT	NT	NT			NT	NT	NT	NT			NT	NT	NT	NT	NT	NT
1251	NT	NT	NT	NT	NT	NT	NT	NT	NT	NT			NT	NT	NT	NT	NT	NT
1260	13	15											02	3004/6	07	5802	06	07
1498	1303	1501	30101	5010101	0102	0505/8	0301	0602					02	30	07	58	06	07
1647	13	15	3	BLANK			03	06					02	30	07	58	06	07
1686	1303	1501	30101	50101	0102	0505	0301	0602	0401	0602	0103	0301	0201	3004	0702	5802	0602	0702
1905	1303	1501	30101	50101			0301	0602	0401	0602			0201	3004	0702	5802	0602	0702
2004	130301	150101											020101	3004	070201	5802	060201	070201
2013	1303	1501	3	5			03	06					02	30	07	5802/7	06	07
2015													0201	3004	0702	5802	0602	0702
2019																		
2042																		
2063	1303	15	301	501			03	0602										
2347	1303	1501	3	5			0301	0602					02	30	07	58	06	07
2375																		
2411	13	15											02	30	07	58		
2518	1303	1501					0301	0602					0201	3004	0702	5802	0602	0702
2549	1303	1501	3	5	0102	05	0301/16	0602	0401	0602			0201	3004	0702	5802	0602	0702
3248	1303	1501	30101	50101			0301	0602					0201	3004	0702	5802	0602	0702
3261	1303	1501	301	5			0301	0602	0401	0602			0201	3004/6	0702	5802	0602	0702
3324	1303	1501	301	501	0102/6	05	0301	0602	0401	0602			0201	3004	0702	5802	0602	0702
3325	1303	1501	301	501	0102	0505/8	0301	0602					02	3004/6	0702	5801/2	06	07
3410	1303	1501					0301	0602					0201	3004	0702	5802	0602	0702
3438	1303	1501	301	501			030101	0602					NT	NT	NT	NT	NT	NT
3522	1303	1501			0103	0505/8	0301/13	0602					0201	3004	0702	5802	0602	0702
3548	1303	15	30101	50101			0301	0602					0201	3004/6	0702	5802	0602	0702
3582	1303	1501	301	50101			0301/19	0602	0401	0602			02	3004	07	5802	0602	0702
3600	13	15	3	5			03	06					02	30	07	58	06	07
3614	1303	1501					0301	0602					0201	3004/6	0702	5802	0602/10	0702
3625	1303	1501	301	501	0102	05	0301	0602	0401	0602	01	0301	02	30	07	58	0602	0702
3631	NT	NT	NT	NT	NT	NT	NT	NT	NT	NT	NT	NT	NT	NT	NT	NT	NT	NT
3798	1303	1501	30101	50101	01	05	0301	0602					0201	3004	0702	5802	0602	0702
3807	130301	150101	3020201	30301	0102	0505	030101	0602	0401	0602			0201	3004	070201	5802	060201	070201
3849	1303	1501	301	50101	0102	0505/8	0301	0602					02	3004/6	07	5802	06	07
4237																		
4281																		
4336	1303	1501					0301	0602					0201	3004	0702	5802	0602	0702
4349	1303	1501	301	501			0301	0602					0201	3004	0702	5802	0602	0702
4420	1303	1501/3											0201	3004	0702	5802	0602	0702
4545	1303	1501	301	501	0102	0505	0301	0602	0401	0602	0103	0301	0201	3004	0702	5802	0602	0702
4551	1303	1501	30101	50101			0301	0602	0401	0602			0201	3004	0702	5802	0602	0702
4582	1303	1501	30101	501			0301	0602					0201	3004	0702	5802	0602	0702
4585	13	15					03	06					02	30	07	58	06	07
4613													0201	3004	0702	5802	0602	0702
4623									040101	0602			02010101	3004				
4653	130301	150101					0301	0602					020101	3004	070201	5802	060201	070201
4709	130301	1501/16	30101	50101			0301	0602	0401	0602			0201	3004	0702	5802	0602	0702
5204													02	30	07	58	06	07
5231																		
5365	13	15	3	5			03	06					02	30	07	58	06	07
5720	1303	1501	30101	50101			0301	0602	0401	0602			0201	3004	0702	5802	0602	0702
5982	1303	150101					030101	0602	040101	0602			020101	3004	070201	5802	060201	070201
6051	13	15	301	501			0301/9	0602/19	0402	0602			02	3004/6	07	5802	06	07
6313	1303	1501					0301	0602					0201	3004	070201	5802	0602	0702
9221	1303	1501	3	5			03	06					02	30	07	58	06	07



# DNA #523

CENTER	DRB1		DRB3/4/5		DQA1		DQB1		DPB1		DPA1		A-Locus		B-Locus		C-Locus	
635	07	11	3	4			02	03					02	29	18	44	07	16
642	0701	110801											020101	290201	180101	440301		
702	0701	1108	30202	40101	0201	0505	0202	0301	0201	0602			0201	2902	1801	4403	0701	1601
714	0701	1108					0202	0301					0201	2902	1801	4403	0701	1601
726	0701	1108					0202	0301					0201	2902	1801	4403	0701	1601
732	070101	110801	3020201	4010101			0202	030101					020101	290201	1801/17	440301	07	160101
743	07	11	3	4			02	03					NT	NT	NT	NT	NT	NT
805	0701/9	1108					0202	0301/19					02	29	18	44	07	16
1018	0701	1108	3	4			0202	0301					0201	2902	1801	4403	0701	1601
1113	0701	1108	30202	40101			0202	0301	0201	0402			0201	2902	18	4403	0701	1601
1189	0701	1108	30202	40101			0202	0301/19					0201	2902	1801	4403	0701	1601
1212	NT	NT	NT	NT			NT	NT	NT	NT			NT	NT	NT	NT	NT	NT
1251	NT	NT	NT	NT	NT	NT	NT	NT	NT	NT			NT	NT	NT	NT	NT	NT
1260	07	1108											02	29	18	44	07	1601/8
1498	070101	1108	3	401	0201	0505/8	0202	0301					02	29	18	44	07	16
1647	07	11	3	4			02	03					02	29	18	44	07	16
1686	0701	1108	30202	40101	0201	0505	0202	0301	0201	0402	0103	BLANK	0201	2902	1801	4403	0701	1601
1905	0701	1108	302	40101			0202	0301	0201	0402			0201	2902	1801	4403	0701	1601
2004	0701	110801											020101	290201	1801/17	440301	0701/18	160101
2013	0701	1108	3	4			02	03					02	29	18	44	07	16
2015													0201	2902	1801	4403	0701	1601
2019																		
2042																		
2063	07	1108	302	401			02	03										
2347	0701	1108	3	4			0202	0301					02	29	18	44	07	16
2375																		
2411	07	11											02	29	18	44		
2518	0701	1108					0202	0301					0201	2902	1801	4403	0701	1601
2549	0701	1108	3	4	0201	05	0202	0301/16	0201	0402			0201	2902	1801	4403	0701	1601
3248	0701	1108	30202	40101			0202	0301					0201	2902	1801	4403	0701	1601
3261	0701	1108	3	4			0202	0301	0201	0402			0201	2902	1801	4403	0701	1601/8
3324	0701	1108	302	401	0201	05	0202	0301	0201	0402			0201	2902	18	4403/46	07	1601
3325	0701	1108	302	401	0201	0505/8	0202	0301					0201/7	2901/2	1801	4403	07	16
3410	0701	1108					0202	0301					0201	2902	1801	4403	0701	1601
3438	0701	1108	302	401			0202	030101					NT	NT	NT	NT	NT	NT
3522	0701	1108			0202	0301/13	0201	0505/8					0201	2902	1801	4403	07	1601
3548	0701/10	1108	30202	40101			0202	0301					0201	2911	1801	4403	0701	1601
3582	0701	1108	302	401			0202	0301/19	0201	0402			02	2902	1801/17	4403	07	1601
3600	07	11	3	4			02	03					02	29	18	44	07	16
3614	0701	1108					0202	0301					0201	2902	1801/5	4403	0701	1601
3625	0701/9	11	302	401	0201	05	0202	0301	0201	0402	01	BLANK	02	29	18	44	0701	1601
3631	NT	NT	NT	NT	NT	NT	NT	NT	NT	NT	NT	NT	NT	NT	NT	NT	NT	NT
3798	0701	1108	30202	40101	0201	05	0202	0301					0201	2902	1801/17	4403	0701	1601
3807	0701	110801	401030101	50102	0201	0505	0202/3	0301/4	020102	0402			0201	290201	1801/17	440301	07	160101
3849	0701	1108	302	401	0201	0505/8	0202	0301					02	29	18	44	07	1601/8
4237																		
4281																		
4336	0701	1108					0202	0301					0201	2902	1801/17	4403	07	1601
4349	0701	1108	302	401			0202	0301					0201	2902	1801	4403	0701	1601
4420	0701	1108											0201	2902	1801	4403	0701	1601
4545	0701	1108	302	40101	0201	0505	0202	0301	0201	0402	0103	BLANK	0201	2902	1801/17	4403	07	1601
4551	0701	1108	30202	40101			0202	0301	0201	0402			0201	2902	1801	4403	0701	1601
4582	0701	1108	30202	401			0202	0301					0201	2902	1801	4403	0701	1601
4585	07	11					0202	03					02	29	18	44	07	16
4613													0201	2902	1801	4403	0701	1601
4623									020102	0402			02010101	290201				
4653	070101	110801					0202	0301					020101	290201	1801/17	440301	070101	160101
4709	0701	1108	30202	40101			0202	0301	0201	0402			0201	2902	1801	4403	0701	1601
5204													02	29	18	44	07	16
5231																		
5365	07	11	3	4			02	03					02	29	18	44	07	16
5720	0701	1108	30202	40101			0202	0301	0201	0402			0201	2902	1801/17	4403	0701	1601
5982	0701	1108					0202	030101	020102	0402			020101	290201	1801/17	440301	070101	160101
6051	07	1108	302	401			02	0301/9	0201	0402			02	29	18	4403	07	1601/8
6313	0701	110801					0202	0301					0201	290201	180101	440301	07	1601
9221	07	11	3	4			02	03					02	29	18	44	07	16



# DNA #524

CENTER	DRB1		DRB3/4/5		DQA1		DQB1		DPB1		DPA1		A-Locus		B-Locus		C-Locus	
635	11	13	3	3			03	BLANK					30	30	42	44	04	17
642	110102	1331											300101	300201	4201	440301		
702	1101	1331	30202	30301	0102	0505	0301	0502	0101	0602			3001	3002	4201	4403	0401	1701
714	1101	1331					0301/19	0502					3001	3002	4201	4403	0401	1701
726	1101	1331					0301	0502					3001	3002	4201	4403	0401	1701
732	110102	1331	3020201	3030101			030101	050201					300101	300201	4201	440301	0401/9	1701
743	11	13	3	3			03	05					NT	NT	NT	NT	NT	NT
805	1101	1331					0301/19	0502/5					30	30	42	44	04	17
1018	1101	1331	3	3			0319	0502					3001	3002	4201	4403	0401	1701
1113	1101	1331	302	303			0301	0502	0101	0602			3001	3002	4201	4403	04	1701/4
1189	1101	1331	30202	30301			0301/19	0502					3001	3002	4201	4403	0401	1701
1212	NT	NT	NT	NT			NT	NT	NT	NT			NT	NT	NT	NT	NT	NT
1251	NT	NT	NT	NT	NT	NT	NT	NT	NT	NT			NT	NT	NT	NT	NT	NT
1260	1101	1331											30	30	4201	44	04	17
1498	1101	1331	3020201	3030101	0102	0505/8	0301	0502					30	30	42	44	04	17
1647	11	13	3	3			03	05					30	30	42	44	04	17
1686	1101	1331	30202	30301	0102	0505	0301	0502	0101	0602	0103	0201	3001	3010	4201	4403	0401	1701
1905	1101	13	302	30301			0319	0502	0101	0602			3001	3002	4201	4403	04	1701
2004	110102	1331											300101	300201	4201	440301	0401/9	1701
2013	1101	1302	3	3			03	05					30	30	4201	44	04	17
2015													3001	3002	4201	4403	0401	1701
2019																		
2042																		
2063	1101	1331	302	303			03	0502										
2347	11	13	3	3			0301	0502					30	30	42	44	04	17
2375																		
2411	11	13											30	30	42	44		
2518	1101	1331					0319	0502					3001	3002	4201	4403	0401	1701
2549	1101	1331	3	3	0102	05	0301/16	0502	0101	0602			3001	3002	4201	4403	0401	1701
3248	110102	1331	30202	30301			0319	0502					3001	3002	4201	4403	0401	1701
3261	1101	1331	3	3			0301	0502	0101	0602			3001	3002	4201	4403	0401	1701/4
3324	1101	1331	302	303	0102/6	05	0301	0502	0101	0602			3001	3002	4201	4403	0401/9	17
3325	1101	13	302	303	0102	0505/8	0301	0502					3001	3002	4201	4402/3	04	17
3410	1101	1331					0301	0502					3001	3002	4201	4403	0401	1701
3438	1101	1302	302	303			030101	050201					NT	NT	NT	NT	NT	NT
3522	1101	1331			0102	0505/8	0301/13	0502					3001	3002	4201	4403	04	17
3548	1101	1331	30202	30301			0301	0502					3001	3002	4201	4403	0401	1701
3582	1101	1331	302	303			0301/19	0502	0101	0602			3001	3002	4201	4403	0401/9	17
3600	11	13	3	3			03	05					30	30	42	44	04	17
3614	1101	1331					0301	0502					3001	3002	4201	4403	0401	1701
3625	11	1331	302	303	0102	05	0301	0502	0101	0602	01	0201	30	30	42	4403/38	04	17
3631	NT	NT	NT	NT	NT	NT	NT	NT	NT	NT	NT	NT	NT	NT	NT	NT	NT	NT
3798	1101	1331	30202	30301	01	05	0301	0502					3001	3002	4201	4403	0401/9	17
3807	110102	1331	40101	50101	0102	0505	0319	050201	010101	0602			300101	300201	4201	440301	0401/9	17
3849	1101	1331	302	303	0102	0505/8	0319	0502					30	30	4201	44	04	17
4237																		
4281																		
4336	1101	1331					0301	0502					3001	3002	4201	4403	0401/9	17
4349	1101	1331	302	303			0301	0502					3001	3002	4201	4403	0401	1701
4420	1101	1120											3001	3002	4201	4403	0401	1701
4545	1101	1331	302	303	0102	0505	0301	0502	0101	0602	0103	0201	3001	3002	4201	4403	0401	17
4551	1101	1331	30202	30301			0301	0502	0101	0602			3001	3002	4201	4403	0401	1701
4582	1101	1331	30202	30301			0301	0502					3001	3002	4201/6	4403	0401	1701
4585	11	13					03	05					30	30	4201	44	04	17
4613													3001	3002	4201	4403	0401	1701
4623									010101	0602			300101	300201				
4653	110102	1331					0301	0502					3001	3002	4201	440301	0401/9	17
4709	110102	1331	30202	30301			0301	0502	0101	0602			3001	3002	4201	4403	0401	1701
5204													30	30	42	44	04	17
5231																		
5365	11	13	3	3			03	05					30	30	42	44	04	17
5720	1101	1331	30202	30301			0319	0502	0101	0602			3001	3002	4201	4403	0401	1701
5982	1101/20	1331/46					0319	050201	010101	0602			300101	300201	4201	440301	040101	1701
6051	11	13	302	303			0301/9	0502	0101	0602			30	30	4201	4403	04	17
6313	11	13					0301	050201					300101	300201	4201	440301	0401/9	17
9221	11	13	3	3			03	05					30	30	42	44	04	17



# PARTICIPANTS AND METHODS

CENTER	DRB1	DRB3/4/5	DQA1	DQB1	DPB1	DPA1	A-Locus	B-Locus	C-Locus
635	SSP-OL	SSP-OL		SSP-OL			SSP-OL	SSP-OL	SSP-OL
642	SBT						SBT	SBT	
702	SSOP/SBT	SSP	SSP	SSP/SBT	SBT/SSP		SSOP/SBT	SSOP/SBT	SSP/SSOP/SBT
714	SSP-INVTGN			SSP-INVTGN			SSP-INVTGN	SSP-INVTGN	SSP-INVTGN
726	RSSOP-OL/SSP-GV			RSSOP-OL/SSP-GV			RSSOP-OL/SSP-GV	RSSOP-OL/SSP-GV	RSSOP-OL/SSP-GV
732	SBT/SSP	SBT/SSP		SBT/SSP			SBT	SBT	SBT
743	SSP-INVTGN	SSP-INVTGN		SSP-INVTGN			SSP-INVTGN	SSP-INVTGN	SSP-INVTGN
805	SSOP-TPNL/SSP-PF			SSOP-TPNL/SSP-PF			SSOP-TPNL/SSP-PF	SSOP-TPNL/SSP-PF	SSOP-TPNL/SSP-PF
1018	SSP-PF/SBT-ATRIA	SSP-OL		SSP-PF/SBT-ATRIA			SSP-PF/SBT-ATRIA	SSP-PF/SBT-ATRIA	SSP-PF/SBT-ATRIA
1113	SSOP/SSP/SBT	SSP-DYNL		SSOP/SSP	SSP-DYNL/GV		SSOP/SSP-GV/SBT	SSOP/SSP-GV/SBT	SSOP/SSP-GV/SBT
1189	RSSOP-INGNTCS/SSP-INVTGN	RSSOP-INGNTCS/SSP-INVTGN		RSSOP-INGNTCS/SSP-INVTGN			RSSOP-INGNTCS/SSP-INVTGN	RSSOP-INGNTCS/SSP-INVTGN	RSSOP-INGNTCS/SSP-INVTGN
1212	RSSOP-DYNL/SSP-PF			RSSOP/SSP	SSP		RSSOP-DYNL/SSP-PF	RSSOP/SSP	RSSOP-DYNL/SSP-PF
1251	SSP-OL-BIONBIS	SSP-BIONBIS	SSP-BIONBIS	SSP-OL-BIONBIS	SSP-BIONBIS		SSP-OL-BIONBIS	SSP-OL-BIONBIS	SSP-OL-BIONBIS
1260	SSOP-LMNX			SSOP-LMNX			SSOP-LMNX	SSOP-LMNX	SSOP-LMNX
1498	SSOP	SSOP	SSP-DYNL	SSP-DYNL			SSP	SSP	SSP
1647	SSOP-TPNL	SSOP-TPNL		SSOP-TPNL			SSOP-TPNL	SSOP-TPNL	SSOP-TPNL
1686	SSP	SSP-DYNL	SSP	SSP	SSP	SSP	SSP	SSP	SSP
1905	SSP/SSOP/SBT	SSP/SSOP/SBT		SSP/SSOP/SBT	SSP/SSOP/SBT		SSP/SSOP/SBT	SSP/SSOP/SBT	SSP/SSOP/SBT
2004	SBT-ATRIA						SBT-ATRIA	SBT-ATRIA	SBT
2013									
2015							SBT-ABOT/SSOP-BIOTST	SBT-ABOT/SSOP-BIOTST	SBT-ABOT/SSOP-BIOTST
2019									
2042									
2063									
2347									
2375									
2411	SSOP						SSOP	SSOP	
2518	SSP-OL/SSOP/SBT			SSP-OL/SSOP/SBT			SSP-OL/SSOP/SBT	SSP-OL/SSOP/SBT	SSP-OL/SSOP/SBT
2549	SSO-BIOTST/SSP-PF/SBT-Atria	SSO-Biotest	SSP-Pel-Freez	SSO-Biotest/SSP-PF	SBT-Atria		SSO-BIOTST/SSP-PF/SBT-Atria	SSO-BIOTST/SSP-PF/SBT-Atria	SSO-BIOTST/SSP-PF/SBT-Atria
3248	SBT-ATRIA/SSPGV-PF	SBT-ATRIA/SSPGV-PF		SBT-ATRIA/SSPGV-PF			SBT-ATRIA/SSPGV-PF	SBT-ATRIA/SSPGV-PF	SBT-ATRIA/SSPGV-PF
3261	SSP-PF	SSP-PF		SSP-PF	SSP-OLRUP		SSP-PF	SSP-PF	SSP-PF
3324	SSP/SBT-DYNL	SSP/SBT-DYNL	SSP/SBT-DYNL	SSP/SBT-DYNL	SSP/SBT-DYNL		SSP/SBT-ATRIA	SSP/SBT-ATRIA	SSP/SBT-ATRIA
3325	SSP-INNGNTCS	SSP-INNGNTCS	SSP-INNGNTCS	SSP-INNGNTCS			SSP-INNGNTCS	SSP-INNGNTCS	SSP-INNGNTCS
3410	SBT-Atria/SSP-GV			SBT-Atria/SSP-GV			SBT-Atria/SSP-GV	SBT-Atria/SSP-GV	SBT-Atria/SSP-GV
3438	SBT	SBT		SBT			SBT	SBT	SBT
3522	SBT-ATRIA		SSOP	SSOP			SBT-ATRIA	SBT-ATRIA	SBT-ATRIA
3548									
3582	SBT	SBT		SBT	SBT		SBT	SBT	SBT
3600	InvitrogenSSP	InvitrogenSSP		InvitrogenSSP			InvitrogenSSP	GenoVisionSSP	GenoVisionSSP
3614	SBT			SSP-OL			RSSOP-OL/SSP	RSSOP-OL/SSP	RSSOP-OL/SSP
3625	SSP	SSP	SSP	SSP	SBT	SSP	SSP	SSP	SSP
3631	SSP-OLRUP	SSP-OLRUP	SSP-OLRUP	SSP-OLRUP	SSP-OLRUP	SSP-OLRUP	SSP-OLRUP	SSP-OLRUP	SSP-OLRUP
3798	SBT-PRTRNS/RSSOP-OL	SSP-OL	RSSOP	RSSOP/SSP			SBT-PRTRNS/RSSOP/SSP-OL	SBT-PRTRNS/RSSOP/SSP-OL	SBT-PRTRNS/RSSOP/SSP-OL
3807	SBT-INVTGN	SBT	SBT	SBT-INVTGN	SBT		SBT-INVTGN/SSP-INVT	SBT-INVTGN/SSP-INVT	SBT-INVTGN/SSP-INVT
3849	SSOP/SBT	SSOP	SSOP	SSOP/SBT			SSOP	SSOP	SSOP
4237									
4281									
4336	SBT-Atria			SBT-Atria			SBT-Atria	SBT-Atria	SBT-Atria
4349	SBT-Dynal/SSOP-OL	SSOP-OL		SBT-Dynal/SSOP-OL			SBT-Dynal/SSOP-OL	SBT-Dynal/SSOP-OL	SBT-Dynal/SSOP-OL
4420	WakFlow			WakFlow			WakFlow	WakFlow	WakFlow
4545	SBT/SSOP	SSOP/SSP	SSOP/SSP	SBT/SSOP	SBT/SSP	SSP-OLRUP	SBT/SSOP/SSP	SBT/SSOP/SSP	SBT/SSOP/SSP
4551	SBT-ATRIA/SSP-OLERUP	SSP-OLERUP		SSP-OLRUP/SSO	SBT-ATRIA/SSP-OLERUP		SBT-ATRIA/SSP-DYNAL	SBT-ATRIA/SSP-DYNAL	SBT-ATRIA/SSP-DYNAL
4582	RFLP/SSP-INVTGN	RFLP		RFLP/SSP			SSP-INVTGN	SSP-INVTGN	SSP-INVTGN
4585	RSSOP			RSSOP			RSSOP-DYNL/SSP	RSSOP-DYNL/SSP	RSSOP-DYNL/SSP
4613							SSP-GV/SSP-ATRIA	SSP-GV/SSP-ATRIA	SSP-GV/SSP-ATRIA
4623					SBT		SBT		
4653	SSP/SBT			PCR-SSP/SBT			SSP/SBT	SSP/SBT	SSP/SBT
4709	SSPOneLambda	SSPOneLambda		SSPOneLambda	SSPInvitrogen		SSP-kitsBionobis	SSP-kitsBionobis	SSP-kitsBionobis
5204							SSP-OL-PF	SSP-OL-PF	SSP-OL-PF
5231									
5365	SSP-OL/SSOP-BIOTST	SSP-OL/SSOP-BIOTST		SSP-OL/SSOP-BIOTST			SSP-OL/SSOP-BIOTST	SSP-OL/SSOP-BIOTST	SSP-OL/SSOP-BIOTST
5720	SSOP-BIOTST/SSP-ATRIA	RSSOP-OL-GV		SSOP-BIOTST/SSP-ATRIA	SBT-ATRIA/SSP-PF		RSSOP-DYNL-OL/SSP/SSP	RSSOP-DYNL-OL/SSP/SSP	RSSOP-DYNL-OL/SSP/SSP
5982	SBT-ATRIA			SBT-ATRIA	SBT-ATRIA		SBT-ATRIA	SBT-ATRIA	SBT-ATRIA
6051	RSSOP-OL	RSSOP-OL		RSSOP-OL	RSOP-OL		RSSOP-OL	RSSOP-OL	RSSOP-OL
6313	RDB			RDB			RDB-INGNTCS/SSP-ATRIA	RDB-INGNTCS/SSP-ATRIA	RDB-INGNTCS/SSP-ATRIA
9221	SSP-INVTGN	SSP-INVTGN		SSP-INVTGN			SSP-INVTGN	SSP-INVTGN	SSP-INVTGN