

UCLA INTERNATIONAL HLA DNA EXCHANGE

115TH SUMMARY

SEPTEMBER 19, 2012

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DNA Sample	
#711	#714
#712	#715
#713	#716

DNA #711 CAUCASIAN

	ALLELE		AGREEMENT (n/total)		SBT LABS
	#1	#2	low	high	Allele level
A*	03:01	23:01	209/210	102/105	70/98
B*	27:02		104/104	62/62	44/48
C*	02:02		90/90	59/59	41/46
DRB1*	11:04	16:01	213/214	139/145	97/104
DRB3*	02:02		50/53	22/24	3/5
DRB5*	02:02		50/53	31/32	5/5
DQA1*	01:02	05:05	94/94	35/36	2/4
DQB1*	03:01	05:02	196/196	139/139	83/88
DPB1*	04:01	04:02	90/90	72/72	40/44
DPA1*	01:03		16/16	14/14	1/1

This sample from a Caucasian donor has an agreement greater than 90%.

This sample was first typed in January 1998 as DNA #184, sent in Exchange #27. DQA1*05 has been updated from DQA1*05:01 (100%) to DQA1*05:05 (92%). DQA1*05:05 was formally recognized in April 1998, according to the IMGT/HLA website.

Discrepancies or ambiguities reported:

A*: 03:19/59, 32:04	Not excluded: 03:01N/8, 23:02/13/17/39
B*:	Not excluded: 27:01/53/77
C*:	Not excluded: 02:03/10/29
DRB1*: 11:01/4/37	Not excluded: 11:01/6/88/104, 16:02/9/13N
DRB3*: 01:01/2/12, 03:01	Not excluded: 02:26/28
DRB5*: 01:01/2	Not excluded:
DQA1*:	Not excluded: 01:08
DQB1*:	Not excluded: 03:04/19/21/27/29, 05:01/14
DPB1*:	Not excluded: 105:01, 120:01N, 126:01, 134:01

DNA #712 HISPANIC

	ALLELE		AGREEMENT (n/total)		SBT LABS
	#1	#2	low	high	Allele level
A*	01:01	03:01	209/210	111/112	79/98
B*	39:20	55:01	205/208	125/126	92/96
C*	03:03	12:03	178/180	105/107	74/92
DRB1*	08:04	14:54	216/216	119/128	79/104
DRB3*	02:02		50/53	23/24	3/5
DQA1*	01:04	04:01	94/94	49/50	2/4
DQB1*	03:19	05:03	196/196	126/130	78/88
DPB1*	03:01	17:01	85/88	72/76	36/44
DPA1*	01:03	02:01	33/34	23/23	2/2

This Hispanic sample has an agreement greater than 90%, except at the DRB1 locus.

This sample was first typed in 2006 as DNA #481, sent in Exchange #76. DRB1*14 has been updated from DRB1*14:01 (100%) to DRB1*14:54 (83%) and DQB1*03 has been updated from DQB1*03:01 (100%) to DQB1*03:19 (96%). The agreement for the uncommon B*39:20 increased from 94% in 2006 to 98% in this send-out.

Fifteen labs reported DRB1*14:01/54. DRB1*14:54 is more commonly found than DRB1*14:01 in all populations and differs from DRB1*14:01 in exon 3 at codon 112, resulting in an amino acid change (Tyr->His). DRB1*14:01 usually associates with DRB3*02:01, while DRB1*14:54 almost exclusively associates with DRB3*02:02, as found in this sample. DRB1*14:54-DRB3*02:02-DQB1*05:03 is the most common DRB1*14 association in Hispanics, as noted in ASHI Abstract 97-P, *DRB1*1401/*1454 Associations Vary By Race* (Beduhn, et al. Human Imm 2008; 69(Suppl 1):S55).

Discrepancies or ambiguities reported:

A*: 36:04	Not excluded: 01:01N/4N/100, 03:01N/63/97
B*: 14:XX, 15:XX, 39:10/16, 67:XX	Not excluded: 39:10, 55:03
C*: 03:02/9, 14:XX, 16:XX	Not excluded: 03:04/11/20N, 12:04/23/58
DRB1*: 08:01/2, 14:01/7/26	Not excluded: 14:01
DRB3*: 01:01/2, 03:01	Not excluded: 02:26/28
DQA1*: 01:01	Not excluded: 01:01/5
DQB1*: 03:01/4, 05:01/2	Not excluded: 03:01, 05:06/8/10
DPB1*: 06:01, 35:01	Not excluded: 104:01, 124:01, 131:01
DPA1*: 01:01/2	Not excluded: 02:02

DNA #713 CAUCASIAN

	ALLELE	ALLELE	AGREEMENT (n/total)		SBT LABS
	#1	#2	low	high	Allele level
A*	03:01	30:04	195/196	94/98	57/76
B*	14:01	37:01	194/194	93/94	54/76
C*	06:02	08:02	164/166	87/91	47/72
DRB1*	03:01	15:01	205/206	126/126	86/102
DRB3*	01:01		49/50	27/28	5/5
DRB5*	01:01		49/50	28/30	5/5
DQA1*	01:02	05:01	88/88	54/54	2/4
DQB1*	02:01	06:02	188/188	126/127	78/86
DPB1*	01:01	02:01	84/84	77/77	44/44
DPA1*	01:03	02:01	34/34	23/23	2/2

This sample from a Caucasian donor has an agreement greater than 90%. Fifteen sequencing labs noted that this sample failed to amplify or had weak amplification for one or more of the class I loci in exons 2 and 3. The gel check and optical density of the sample were determined to be within acceptable ranges. At this time, the cause of this amplification failure is unknown.

This sample contains the A*03:01-B*37:01-C*06:02 association, which is common in Caucasians (HF=0.00126), according to the Bioinformatics website. The other probable class I association is A*30:04-B*14:01-C*08:02.

Discrepancies or ambiguities reported:

A*: 03:04/50, 30:01/2, 33:04	Not excluded: 03:01N, 30:02/6/29
B*: 14:08	Not excluded: 14:07N/14/26, 37:02/3N/4/23
C*: 05:01:01G/16, 06:11	Not excluded: 06:03/6, 08:01/29/52N
DRB1*: 13:XX	Not excluded: 03:04/47/50/68N, 15:02/3/20/45
DRB3*: 03:01	Not excluded: 01:02/12
DRB5*: 4*XX:XX, 01:08	Not excluded: 01:02
DQA1*:	Not excluded: 01:08
DQB1*: 02:02	Not excluded: 02:02/5, 06:01/33/47
DPB1*:	Not excluded: 123:01
DPA1*:	Not excluded: 02:02

DNA #714 BLACK

	ALLELE	ALLELE	AGREEMENT (n/total)		SBT LABS
	#1	#2	low	high	Allele level
A*	30:02	34:02	200/200	123/123	91/102
B*	49:01	53:01	194/198	118/118	88/100
C*	04:01	07:01	170/170	100/100	74/94
DRB1*	01:01	04:05	201/202	126/128	91/104
DRB4*	01:03		47/47	18/20	0/3
DQA1*	01:01	03:03	86/86	23/25	2/4
DQB1*	03:02	05:01	184/186	128/128	79/88
DPB1*	01:01	17:01	86/86	78/78	42/44
DPA1*	02:01		16/16	11/11	1/1

This sample from a Black donor has an agreement of 90%, except at the DQA1 locus. DQA1*03:03 was identified with an agreement of 83%. Two labs incorrectly identified the allele as DQA1*03:01 and 3 labs assigned DQA1*03:01/02.

The class II associations, DRB1*01:01-DQB1*05:01 and DRB1*04:05-DQB1*03:02, with respective haplotype frequencies of 0.02732 and 0.01214, are quite common in Black populations. The probable class I associations are: A*34:02-B*53:01-C*04:01 (HF = 0.00230) and A*30:02-B*49:01-C*07:01 (HF=0.00146).

Discrepancies or ambiguities reported:

A*:	Not excluded: 30:01/33, 34:01/4
B*: 35:XX, 44:XX	Not excluded: 49:04/11, 53:02/8/10/18/23
C*:	Not excluded: 04:03/7/9N/82, 07:02/6
DRB1*: 01:31, 03:XX, 04:01/2/77	Not excluded: 01:02/32/36, 04:03/30
DRB4*: 3*01:XX, 01:01/2	Not excluded:
DQA1*: 03:01/2	Not excluded: 01:04
DQB1*: 02:XX, 06:XX	Not excluded: 03:05, 05:02/7/12
DPB1*:	Not excluded: 131:01
DPA1*:	Not excluded: 02:02

DNA #715 HISPANIC

	ALLELE		AGREEMENT (n/total)		SBT LABS
	#1	#2	low	high	Allele level
A*	02:01	68:03	205/206	112/113	84/102
B*	39:05	51:01	193/202	121/127	85/100
C*	02:02	07:02	175/176	102/104	75/96
DRB1*	04:04	04:07	208/210	95/105	73/106
DRB4*	01:03	01:03:01:02N	102/102	53/54	4/10
DQA1*	03:01		44/44	26/26	1/2
DQB1*	03:02		96/96	72/72	44/45
DPB1*	04:02	05:01	90/90	85/85	47/48
DPA1*	01:03		16/16	14/14	1/1

This sample from a Hispanic donor has an agreement greater than 90%.
 The rare DRB1*04-DRB4*01:03:01:02N association has been identified in this sample. This association was initially observed by Voorter et al., as noted in *Presence of the DRB4*0103102N null allele in different DRB1*04-positive individuals* (Tissue Antigens 2000 Jan;55(1):37-43). DRB4*01:03:01:02N almost exclusively associates with the DRB1*07:01-DQB1*03:03 haplotype. However, the investigators noted that the null DRB4 allele was segregating with DRB1*04 and DQB1*03 in four different Caucasian families; as a result of the family studies, three unusual DRB1*04-DRB4*01:03:01:02N-DQB1*03 haplotypes were found. The DRB1*04:04-DRB4*01:03:01:02N-DQB1*03:02 haplotype detected in this sample was found in two different families in the Voorter et al. study.

Discrepancies or ambiguities reported:

A*: 02:90, 68:01/2/5/20, BLANK	Not excluded: 02:01L/2/9/90/95, 68:02/5
B*: 14:XX, 38:01:01, 39:01/1L, 78:02:02	Not excluded: 51:03/11N/96
C*: 01:60, 07:15	Not excluded: 02:03/10/29, 07:01/50
DRB1*: 01:XX, 04:01/2/3/5/6/8	Not excluded: 04:03/8/23/92
DRB4*: 01:01/2	Not excluded:
DQA1*:	Not excluded: 01:02
DQB1*:	Not excluded: 03:05/37
DPB1*:	Not excluded: 105:01

DNA #716 HISPANIC

	ALLELE		AGREEMENT (n/total)		SBT LABS
	#1	#2	low	high	Allele level
A*	02:01	29:02	206/206	110/114	87/102
B*	15:30	44:03	203/204	123/125	89/100
C*	01:02	04:01	177/178	99/101	73/96
DRB1*	01:03	04:03	210/210	147/150	100/106
DRB4*	01:03		50/50	18/19	1/5
DQA1*	01:01	03:01	87/88	27/28	2/4
DQB1*	03:02	05:01	192/192	136/137	85/90
DPB1*	03:01	04:02	90/90	79/79	43/48
DPA1*	01:03		16/16	14/14	1/1

This sample from a Hispanic donor has an agreement greater than 90%.
 This sample contains a strong class I association, A*02:01-B*15:30-C*01:02, which occurs primarily in Hispanic populations (HF = 0.00087). The other probable class I association, A*29:02-B*44:03-C*04:01, is common in all ethnic groups, and carries a haplotype frequency of 0.00076 in Hispanic populations.

Discrepancies or ambiguities reported:

A*: 02:152, 29:01/1N/22	Not excluded: 02:01L/9, 29:26
B*: 15:01/4, 44:02/2S/65, 45:XX	Not excluded: 15:58/150/233, 44:77/114
C*: 01:37N, 02:01	Not excluded: 01:03/14/17/25, 04:03/7/9N/82/90N
DRB1*: 01:17	Not excluded: 01:39N
DRB4*: 01:01/2	Not excluded: 01:08
DQA1*: 01:03, BLANK	Not excluded: 01:04, 03:02
DQB1*: 05:07	Not excluded: 03:05, 05:02/12
DPB1*:	Not excluded: 104:01, 105:01

ACKNOWLEDGMENT:

The UCLA Immunogenetics Center expresses its thanks to the following for contributing to this Exchange: One Legacy and all organ and tissue donors and families for giving the gift of life and the gift of knowledge by their generous donation to the education and advancement of the study of HLA.

DNA #711

CENTER	DRB1		DRB3/4/5		DQA1		DQB1		DPB1		DPA1		A-Locus		B-Locus		C-Locus	
260																		
262																		
263																		
264	110401	160101					030101G	050201G	040101G	040201G	010301G	BLANK	030101G	230101G	270201	BLANK	020202G	BLANK
265	1101/4	1601/2	30101/2	50101/2	0102	0510	0301/4	0501/2					0301/1N	2301/2	2701/2	BLANK	0202/3	BLANK
266	11	16	3	5			03	05					03	23	27	BLANK	02	BLANK
267	1101	1601/13N	30212	50202	0102	0505/9	0301	0502					0301	2301	2702/53	BLANK	0202	BLANK
268	1101	16			01	05	03	05					03	23	27	BLANK	02	BLANK
278	1104	1601	30202	50202	0102/8	0505/9	0301	0502	0401/12601	0402/10501	0103	BLANK	0301	2301/39	2702/77	BLANK	0202	BLANK
401	1104	1601			01	05	0301/29	0502	0401	0402								
452	1104	1601	3020201G	50202			0301	0502	040101G	040201G			0301	2301	2702	BLANK	0202	BLANK
519	1104	1601	302	502	0102	0505	0301	0502	0401/12001N	0402	0103	BLANK	0301	2301/17	2702	BLANK	0202	BLANK
615	1104	1601	3020201G	50202			0301	050201G	040101G	040201G								
616	11	16											03	23	27	BLANK	02	BLANK
635	11	16	3	5			03	05					03	23	27	BLANK	02	BLANK
702	1104	1601	30202	50202	0102	0505	0301	0502	0401	0402			0301	2301	2702	BLANK	0202	BLANK
714	1104	1601	NT	NT	NT	NT	0301	0502	NT	NT	NT	NT	0301	2301	2702	BLANK	0202	BLANK
726	1104	1601	302	502	0102	0505	0301	0502	0401	0402	0103	BLANK	0301	2301	2702	BLANK	0202P	BLANK
732	110401	160101	30202/28	50202	01	05	0301/19	050201					030101	2301/17	270201	BLANK	020202	BLANK
769	1104	1601	30202	50202			0301	0502	040101G	040201G			0301	2301	2702	BLANK	0202	BLANK
805	1104	1601					0301	0502					0301	2301	2702	BLANK	0202	BLANK
1113	11	16					03	05	0401	0402			03	23	27	BLANK	02	BLANK
1189	1104	1601	30202	50202			0301	0502	0401	0402			0301	2301/17	2702	BLANK	0202	BLANK
1212	11	16					03	05					03	23	27	BLANK		
1251	NT	NT	NT	NT	NT	NT	NT	NT	NT	NT	NT	NT	NT	NT	NT	NT	NT	NT
1498	1104	1601	3020201G	50202	0102	0505/11	030101G	0502	0401/12001N	0402			0301/1N	2301/17	2702	BLANK	0202	BLANK
1647	1104	1601					0301	0502	040101G	040201G			0301	230101G	2702	BLANK	0202	BLANK
1686	1104	1601	30202	50202	0102	0505	0301	0502	0401P	0402P	0103	BLANK	0301	2301	2702	BLANK	0202	BLANK
1905	1104	1601	302	50202			0301	0502	0401P	0402P	0103	BLANK	0301	2301	2702	BLANK	0202	BLANK
2004																		
2013	1104	1601					0301	0502					0301	2301	2702	BLANK	0202	BLANK
2015																		
2063																		
2347	1104	1601	3	5	01	05	0301	0502	040101G	040201G	0103	BLANK	0301	2301	2702	BLANK	0202	BLANK
2411	1104	1601					0301	0502					0301	2301	2702	BLANK	0202	BLANK
2518	1104	1601					0301	0502					0301	230101G	2702	BLANK	0202	BLANK
2549	1104	1601	30202	50202	010201G	0505	030101G	05	040101G	040201G			0301	2301	2702	BLANK	0202	BLANK
3248																		
3261	1104	1601					0301	0502	0401	0402								
3264	11	16	NT	NT	NT	NT	03	05	NT	NT			03	23	27	BLANK	02	BLANK
3324																		
3325	1104	1601	30202	50202	0102	0505	0301	0502					03	23	27	BLANK		
3410	1104	1601					0301	0502					0301	2301	2702	BLANK	0202	BLANK
3438	1104	1601					0301	0502					0301	2301/17	2702	BLANK	0202	BLANK
3522																		
3582	11	16	302	502	01	05	03	05	NT	NT			03	23	27	BLANK	02	BLANK
3614	1104	1601			01	05	0301	0502					0301	2301	2702	BLANK	0202	BLANK
3625	1104	1601	3	5			0301	0502	0401/12601	0402/10501			03	23	27	BLANK	0202	BLANK
3807	1104/104	1601					0301	0502	0401	0402			0301	2301/17	2702	BLANK	0202	BLANK
3849	1104	1601	302	50202	0102	0505	0301	0502					03	23	27	BLANK	02	BLANK
4237																		
4281																		
4420	1104	1601											0301	2301/17	2702	BLANK	0202/10	BLANK
4545	1104	1601	302	50202	0102	05	0301	0502	040101G	040201G			0301	2301/17	2702	BLANK	0202	BLANK
4551	1104	1601	NT	NT	0102/8	0505/9	0301	0502	NT	NT			03	23	27	BLANK	02	BLANK
4585	11	16			01	0505/9	03	0502					03	23	27	BLANK	02	BLANK
4613																		
4653	11	16			0102	0505/9	0301	0502					03	23	27	BLANK	02	BLANK
4709	1104	1601	30202	50202	0102	0505	0301	0502	0401	0402			0301	2301	2702	BLANK	0202	BLANK
5204																		
5982	1104	1104					0301	0502	0401	0402			0319	3204	270201	BLANK	020202	BLANK
6051	1104	1601	302	502	01	0505/9	0301	0502	040101G	040201G	0103	BLANK	03	23	27	BLANK	02	BLANK
6313	1104	1601					0301	0502					0301	2301	2702	BLANK	0202	BLANK
9221	11	16	3	5	01	05	03	05	NT	NT			03	23	27	BLANK	02	BLANK
197H	1104	1601					0301	0502	0401	0402			0301	2301P	2702	BLANK	0202	BLANK
197L	11	16	302	50202	01	05	03	0502			0103	BLANK	03	23	27	BLANK	02	BLANK
271	11	16	301	501			03	05					03	23	27	BLANK		
4582H	1104	1601	30202	50202	01	0505	0301	0502	0401/10501	0402/12601	0103	BLANK	0301	2301	2702	BLANK	0202	BLANK
4582L	11	16	302	502	01	05	03	05	04	04	01	BLANK	03	23	27	BLANK	02	BLANK

DNA #712

CENTER	DRB1	DRB3/4/5	DQA1	DQB1	DPB1	DPA1	A-Locus	B-Locus	C-Locus			
260												
262												
263												
264	080401	140101G					010101G	030101G	3920	550101G	030301G	120301G
265	0801/2	1401/7	30101/2	BLANK	0101/4	0401	0301/4	0501/2	030101G	170101G	010301G	020101
266	08	14	3	BLANK			03	05				
267	0804	1401/26	30202	BLANK	0101/4	0401	0319	0503/8				
268	08	1401			01	04	03	05				
278	0804	1454	30202	BLANK	0101/4	0401	0319	0503	0301	1701	0103	0201
401	0804	1401/54			01	0401	0319	0503/10	0301/10401	1701		
452	0804	1454	30202G	BLANK			0319	0503	030101G	170101G		
519	0804	1401/54	302	BLANK	0104/5	0401	0319	0503	0301/12401	1701	0103	0201
615	0804	1454	3020201G	BLANK			0301/19	050301G	030101G	170101G		
616	08	14										
635	08	14	3	BLANK			03	05				
702	0804	1454	30202	BLANK	0104	0401	0319	0503	0301	1701		
714	0804	1454	NT	NT	NT	NT	0319	0503	NT	NT	NT	NT
726	0804	1454	302	BLANK	0104	0401	0319	0503	0301	1701	0103	0201
732	080401	1454	30202/28	BLANK	01	04	0301/19	0503/10				
769	0804	1454	30202	BLANK			0319	0503	030101G	170101G		
805	0804	1454					0319	0503				
1113	08	14					03	05	0301/12401	1701/13101		
1189	0804	14	30202	BLANK			0319	0503	0301	1701		
1212	08	14					03	05				
1251	NT	NT	NT	NT	NT	NT	NT	NT	NT	NT	NT	NT
1498	080401	1454	3020201G	BLANK	0104	040101G	0319	050301G	030101G	1701		
1647	0804	1401					0319	0503	0301	1701		
1686	0804	1454	30202	BLANK	0104	0401	0319	0502	0301P	1701P	0103	0201
1905	0804	1454	302	BLANK			0319	0503	0301P	1701P	0103	0201/2
2004												
2013	0804	1454					0319	0503				
2015												
2063												
2347	0804	140101G	3	BLANK	01	04	0319	0503	030101G	170101G	0103	0201
2411	0804	1401					0319	0503				
2518	0804	140101G					030101G	0503				
2549	0804	1454	30202	BLANK	0104	0401	0319	0503	0301	170101G		
3248												
3261	0804	1454					0319	0503	0301	1701		
3264	08	14	NT	NT	NT	NT	03	05	NT	NT		
3324												
3325	0804	1401	30202	BLANK	0104	0401	0319	0503				
3410	0804	1454					0319	0503				
3438	0804	1454					0319	0503				
3522												
3582	08	14	302	BLANK	01	04	03	05	NT	NT		
3614	0804	1454			01	0401	0319	0503				
3625	0804	1401/54	3	BLANK			03	05	03	1701		
3807	0804	14					0319	0503	0601	3501		
3849	0804	1401/54	302	BLANK	0104	0401	0319	0503				
4237												
4281												
4420	0804	1401/54										
4545	0804	140101G	30202	BLANK	0104	0401	0319	0503	030101G	170101G		
4551	0804	1454	NT	NT	0101/4	0401	0319	0503	NT	NT		
4585	0804	14			01	0401	0319	05				
4613												
4653	0804	14			01	0401	0301	05				
4709	0804	1454	30202	BLANK	0104	0401	0319	0503	0301	1701		
5204												
5982	0804	1401					0319	0503	0601	0601		
6051	0804	1454	302	BLANK	01	0401	0319	0503/8	030101G	170101G	0103	0101/2
6313	0804	1401/54					0319	0503				
9221	0804	14	3	BLANK	01	04	0319	05	NT	NT		
197H	0804	1401P					0319	0503	0301P	1701		
197L	0804	14	302	BLANK	01	0401	0319	05			0103	02
271	08	14	301	BLANK			03	05				
4582H	0804	1454	30202	BLANK	01	0401	0319	0503	0301	1701	0103	0201/2
4582L	08	14	302	BLANK	01	04	03	05	03	17	01	02

DNA #713

CENTER	DRB1	DRB3/4/5	DQA1	DQB1	DPB1	DPA1	A-Locus	B-Locus	C-Locus									
260																		
262																		
263																		
264	030101G	150101G																
265	0301/4	1501/2	30101/2	50101/2	0102	0501	020101G	060201	010101	020102	010301G	020102	030101G	300401	140101	370101G	0611	050101G
266	03	15	3	5			0201/2	0601/2					0301/1N	3001/2	1401/7N	3701/2	0602/3	0801/2
267	0301	1501	30101	50108	0102	0501	0201	0602	0101	020102	010301G	020102	03	30	14	37	06	08
268	0301	1501			01	05	02	06					0301	3004/6	1401/7N	3701/3N	0602	0802
278	0301	1501	30101	50101	0102/8	0501	0201	0602	0101	0201	0103	0201	0301	3004	1401/26	3701/23	0602	0802
401	0301/68N	1501			01	0501	0201	0602/47	0101	0201								
452	0301	1501	30101	50101			0201	0602	0101	0201			0301	3004	1401	3701	0602	0802
519	0301/68N	1501	301	501	0102	0501	0201	0602	0101	0201/12301	0103	0201	0301	3004	1401	3701	0602	0802
615	030101G	150101G	3010102G	50101			0201	060201G	0101	0201								
616	03	15											03	30	14	37	06	08
635	03	15	3	5			02	06					03	30	14	37	06	08
702	0301	1501	30101	50101	0102	0501	0201	0602	0101	0201			0301	3004	1401	3701	0602	0802
714	0301	1501	NT	NT	NT	NT	0201	0602	NT	NT			0301	3004	1401	3701	0602	0802
726	0301	1501		501	0102	0501	0201	0602	0101	0201	0103	0201	0301	3004	1401	3701	0602	0802
732	030101	1501	3010102	5010101	01	05	020101	060201					03	30	1401/7N	37	0602/6	0802/29
769	0301/68N	1501	30101	50101			0201	0602	0101	0201			0301	3004	1401	3701	0602	0802
805	0301	1501					0201	0602					03	30	14	37	06	08
1113	03	15					02	06	0101	0201			03	30	14	37	06	08
1189	0301	1501	30101	50101			0201	0602	0101	0201			0301	3004	14	37	0602	0802
1212	03	15					02	06					03	30	14	37		
1251	NT	NT	NT	NT	NT	NT	NT	NT	NT	NT			NT	NT	NT	NT	NT	NT
1498	030101/68N	1501	30101/12	50101	0102	0501	0201/5	0602	0101	0201/12301			03	30	14	37	06	08
1647	0301	1501					0202	0602	0101	0201			0301	3004	1401	3701	0602	0802
1686	0301	1501	30101	50101	0102	0501	0201	0602	0101	0201	0103	0201	0301	3004	1401/14	3701	0602	0802
1905	0301	1501	30101	50101			0201	0602	0101	0201	0103	0201/2	NT	NT	NT	NT	0602	0802
2004																		
2013	03	15					02	06					03	30	14	37	06	08
2015																		
2063																		
2347	0301	15	3	5	01	05	02	06	0101	0201	0103	0201	03	30	1401	37	06	08
2411	0301	1501					0201	0602					0301	3004	1401	3701	0602	0802
2518	0301	1501					0201	0602					0301	3004	1401	3701	0602	0802
2549	0301/68N	1501	30101	50101	010201G	0501	0201	0602/47	0101	0201			0301	3002/4	1401	3701	0602	0802
3248																		
3261	0301	1501					0201	0602	0101	0201								
3264	03	15	NT	NT	01	0501	0201	06	NT	NT			03	30	14	37	NT	NT
3324																		
3325	0301	1501	30101	50101	0102	0501	0201	0602					03	30	14	37		
3410	0301	1501					0201	0602					0301	3004	1401	3701	0602	0802
3438	0301	1501					0201	0602					0301	3004	1401	3701	0602	0802
3522																		
3582	0301	1501	30101	50101	NT	NT	0201	0602	0101	0201			0301	3004	1401	3701	0602	0802
3614	0301	1501			01	0501	0201	0602					0301	3004	1401	3701	0602	0802
3625	0301	1501	3	5			0201	0602	0101	0201			03	30	14	37	06	08
3807	03	15					0201	0602	0101	0201			0301	3004	14	37	06	08
3849	0301	1501	301	50101	0102	0501	0201	0602					03	30	1401/7N	37	06	08
4237																		
4281																		
4420	0301	1501/3											0301	3004	1401	3701	0602	0802
4545	0301	1501	30101	50101	0102	0501	0201	0602	0101	0201			030101G	3004	1401	3701	060201G	080201G
4551	0301	1501	NT	NT	0102/8	0501	0201	0602/47	NT	NT			03	30	14	37	06	08
4585	0301	15			01	0501	0201	0602/47					03	30	14	37	06	08
4613																		
4653	03	15			0102	0501	0201	0602					03	30	1401/7N	37	06	08
4709	NT	NT	NT	NT	NT	NT	NT	NT	NT	NT			NT	NT	NT	NT	NT	NT
5204																		
5982	0301	1501					0201	0602	0101	0201			NT	NT	NT	NT	NT	NT
6051	0301/50	1501/20	301	501	01	0501	0201	0602/47	0101	0201	0103	0201/2	03	30	1401/7N	37	06	08
6313	0301	1501					0201	0602					0301	3304	1401	3701	0602	0802
9221	03	15	3	5	01	05	02	06	NT	NT			03	30	14	37	06	08
197H	0301	1501					0201	0602	0101	0201			NT	NT	NT	NT	NT	NT
197L	03	15	30101	50101	01	0501	0201	06			0103	02	03	30	14	3701	06	08
271	03	15	301	501			02	06					03	30	14	37		
4582H	0301	1501	30101	50101	01	0501	0201	0602	0101	0201	0103	0201/2	0301	3004	1401	3701	0602	0802
4582L	03	15	301	501	01	05	02	06	01	02	01	02	03	30	14	37	06	08

DNA #714

CENTER	DRB1	DRB3/4/5	DQA1	DQB1	DPB1	DPA1	A-Locus	B-Locus	C-Locus									
260																		
262																		
263																		
264	010102	040501					300201G	340201	490101	530101	040101G	070101G						
265	0101/2	0401/2	40101/2	BLANK	0101/4	0301/2	0302/5	0501/2	010101	170101G	020101	BLANK	3001/2	3401/2	4901/4	5301/2	0401/3	0701/2
266	01	04	4	BLANK			03	05					30	34	49	53	04	07
267	0131	0405/30	40101	BLANK	0101	0301	0302	0501					3002	3402/4	4901	5301	0401	0701
268	01	04					03	05					30	34	49	53	04	07
278	0101	0405	40103	BLANK	0101/4	0301/2	0302	0501/12	0101	1701	0201	BLANK	3002	3402	4901	5301	0401	0701
401	0101	0405			01	03	0302	0501	0101	1701								
452	0101	0405	40103	BLANK			0302	0501	0101	1701			3002	3402	4901	5301	0401	0701
519	0101	0405	401	BLANK	0101	0303	0302	0501	0101	1701	0201	BLANK	3002	3402	4901	5301	0401/9N	0701/6
615	NT	NT	NT	NT			NT	NT	NT	NT								
616	NT	NT					NT	NT					NT	NT	NT	NT	NT	NT
635	01	04	4	BLANK			03	05					30	34	49	53	04	07
702	0101	0405	40103	BLANK	0101	0303	0302	0501	0101	1701			3002	3402	4901	5301	0401	0701
714	0101	0405	NT	NT	NT	NT	0302	0501	NT	NT	NT	NT	3002	3402	4901	5301	0401	0701
726	0101	0405	401	BLANK	0101	0303	0302	0501	0101	1701	0201	BLANK	3002	3402	4901	5301	0401	0701
732	01	04	NT	NT	01	03	03	05					300201	340201	490101	530101	0401/9N	0701/6
769	0101	0405	40103	BLANK			0302	0501	0101	1701			3002	3402	4901	5301	0401	0701
805	0101	0405					0302	0501					3002	3402	4901	5301	040101G	070101G
1113	01	04					03	05	0101	1701			30	34	49	53	04	07
1189	0101	0405	40103	BLANK			0302	0501	0101	1701			3002	3402	4901	5301	0401	0701
1212	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
1498	0101	0405	40103	BLANK	0101	0303	030201G	0501/7	0101	1701			3002	3402	4901	5301	040101G	070101G
1647	0101	0405					0302	0501	0101	1701			3002	3402	4901	5301	0401	0701
1686	0101	0405	40103	BLANK	0101	0303	0302	0501	0101	1701	0201	BLANK	3002	3402	4901	5301/18	0401	0701
1905	0101	0405	40103	BLANK			0302	0501	0101	1701P	0201	BLANK	3002	3402	4901	5301	0401	0701
2004																		
2013	0101	0405					0302	0501					3002	3402	4901	5301	0401	0701
2015																		
2063																		
2347	01	04	4	BLANK	01	03	0302	05	0101	1701	0201	BLANK	30	34	49	53	04	07
2411	0101	0405					0302	0501					3002	3402	4901	5301	0401	0701
2518	0101	0405					0302	0501					3002	3402	4901	5301	0401	070101G
2549	0101	0405	40103	BLANK	0101	0303	030201G	0501	0101	170101G			3002	3402	4901	5301	0401/82	0701
3248																		
3261	0101	0405					0302	0501	0101	1701								
3264	01	04	NT	NT	01	03	0302	05	NT	NT			30	34	49	53	NT	NT
3324																		
3325	0101	0405	40103	BLANK	0101	0303	0302	0501					30	34	49	53		
3410	0101	0405					0302	0501					3002	3402	4901	5301	0401	0701
3438	0101	0405					0302	0501					30	34	49	53	04	07
3522																		
3582	0101	0405	401	BLANK	NT	NT	0302	0501	0101	1701/13101			3002	3402	4901	5301	0401	0701
3614	0101	0405			01	03	0302	0501					3002	3402	4901	5301	0401	0701
3625	0101	0405	4	BLANK			0302	0501	0101	1701			3002	3402	4901	5301	0401	0701
3807	0101	0405					03	0501	0101	1701			3002	3402	4901	5301	04	07
3849	0101	0405	401	BLANK	0101	0303	0302	0501					30	34	49	53	04	07
4237																		
4281																		
4420	0101	0405											3002	3402	4901	5301/10	0401/7	07
4545	0101	0405	NT	NT	NT	NT	0302	0501	0101	170101G			3002	3402	4901	5301	040101G	070101G
4551	0101	0405	40103	BLANK	01	03	0302	0501	0101	1701			3002	3402	4901	5301	0401	070101G
4585	01	04			01	03	0302	0501/12					30	3402/4	49	53	04	07
4613																		
4653	01	04			01	03	0302	0501					30	3402/4	49	53	04	07
4709	0101	0405	NT	NT	01	03	0302	0501	0101	1701			3002	3402	4901	5301	0401	0701
5204																		
5982	0101	0477					0302	0501	0101	1701			3002	3402	4901	5301	0401	0701
6051	0101/36	0405	401	301	01	03	0302	0501/12	0101	1701	0201	BLANK	30	3402/4	49	53	04	07
6313	01	04					03	05					30	34	49	53	04	07
9221	01	04	4	BLANK	01	03	03	05	01	17			30	34	49	53	04	07
197H	0101	0405					0302	0501	0101	1701			3002	3402	4901	5301	0401P	0701P
197L	01	04	401	BLANK	01	03	0302	05			02	BLANK	30	34	49	53	04	07
271	01	04	401	BLANK			03	05					30	34	49	53		
4582H	0101	0405	40103	BLANK	01	03	0302	0501	0101	1701	0201	BLANK	3002	3402	4901	5301	0401	0701
4582L	01	04	401	BLANK	01	03	03	05	01	17	02	BLANK	30	34	49	53	04	07

DNA #715

CENTER	DRB1	DRB3/4/5	DQA1	DQB1	DPB1	DPA1	A-Locus	B-Locus	C-Locus			
260												
262												
263												
264	040401	040701G					020101G	680301	380101	780202	020202G	070201G
265	0401/2	0401/2	40101/2	40101/2	0301/2	BLANK	0302/5	BLANK	040201G	050101G	010301G	BLANK
266	04	04	4	4			03	BLANK				
267	0403	0405/6	40101	40103N	0301	BLANK	0302	BLANK				
268	04	01			03	BLANK	03	BLANK				
278	0404	0407/92	40103	40103N	0301/2	BLANK	0302	BLANK	0402	0501	0103	BLANK
401	0404	0407/92			03	BLANK	0302	BLANK	0402	0501		
452	0404	040701G	40103	40103N			0302	BLANK	0402	0501		
519	0404	0407/92	401	401	0301	BLANK	0302	BLANK	0402	0501	0103	BLANK
615	0404	040701G	401	40103N			030201G	BLANK	040201G	050101G		
616	04	04										
635	04	04	4				03	BLANK				
702	0404	0407	40103	40103	0301	BLANK	0302	BLANK	0402	0501		
714	0404	0407	NT	NT	NT	NT	0302	BLANK	NT	NT	NT	NT
726	0404	0407	401	401	0301	BLANK	0302	BLANK	0402	0501	0103	BLANK
732	040401	0407/92	40103	4010301N	03	BLANK	030201	BLANK				
769	0404	040701G	40103	401030102N			0302	BLANK	0402	0501		
805	0404	0407					0302	BLANK				
1113	04	04					03	BLANK	0402	0501		
1189	0404	0407/92	40103	40103N			0302	BLANK	0402	0501		
1212	NT	NT					NT	NT				
1251	0404	0407/92	40103	401030102N	0301	BLANK	0302	BLANK	0402	0501		
1498	040401	040701/92	40103	401030102N	030101	BLANK	030201G	BLANK	040201	0501		
1647	0404	0407					0302	BLANK	0402	0501		
1686	0404	0407	40103	401030102N	0301	BLANK	0302	BLANK	0402	0501	0103	BLANK
1905	0404	0407	40101P	401030102N			0302	BLANK	0402P	0501	0103	BLANK
2004												
2013	0404	0407					0302	BLANK				
2015												
2063												
2347	04	04	4	40103N	03	BLANK	0302	BLANK	0402	0501	0103	BLANK
2411	0404	0407					0302	BLANK				
2518	0404	0407					0302	BLANK				
2549	0404	0407/92	40103	4010302N	0301	BLANK	030201G	BLANK	040201G	0501		
3248												
3261	04	04					0302	BLANK	0402	0501		
3264	0404	0407/92	40103	40103N	NT	NT	0302	BLANK	0402	0501		
3324												
3325	0403	0408	40103	40103N	0301	BLANK	0302	BLANK				
3410	0404	0407					0302	BLANK				
3438	0404	0407					0302	BLANK				
3522												
3582	0404	0407/92	401	401	NT	NT	0302	BLANK	040201G	0501		
3614	0404	0407			0301	BLANK	0302	BLANK				
3625	0404	0407/92	4	4			0302	BLANK	0402	0501		
3807	0404	0407/92					0302	BLANK	0402	0501		
3849	0404	0407/92	40103	40103N	0301	BLANK	0302	BLANK				
4237												
4281												
4420	0404	0407										
4545	0404	040701G	40103	40103N	0301	BLANK	0302	BLANK	040201G	0501		
4551	0404	0407	40103	40103N	0301	BLANK	0302	BLANK	0402	0501		
4585	04	04			0301	BLANK	0302	BLANK				
4613												
4653	04	04			03	BLANK	0302	BLANK				
4709	0404	0407	NT	NT	0301	BLANK	0302	BLANK	0402	0501		
5204												
5982	0403	0408	40103	40103N			0302	BLANK	0402	0501		
6051	0404/23	0407/92	401	401	0301	BLANK	0302	BLANK	0402	0501	0103	BLANK
6313	04	04					03	BLANK				
9221	04	04	4	4	03	BLANK	03	BLANK	0402	0501		
197H	0404	0407P					0302	BLANK	0402	0501		
197L	04	04	401	40103N	03	BLANK	03	BLANK			0103	BLANK
271	04	04	401	401			03	BLANK				
4582H	0404	0407	40103	401030102N	0301	BLANK	0302	BLANK	0402	0501	0103	BLANK
4582L	04	04	401	401	03	BLANK	03	BLANK	04	05	01	BLANK

DNA #716

CENTER	DRB1	DRB3/4/5	DQA1	DQB1	DPB1	DPA1	A-Locus	B-Locus	C-Locus									
260																		
262																		
263																		
264	0103	040301					020101G	290201G	1530	440301G	010201G	040101G						
265	0103	0401/2	40101/2	BLANK	0101/4	0301/2	030201G	050101G	030101G	040201G	010301G	BLANK	0201/1L	2901/1N	1530/58	4402/2S	0102/3	0401/3
266	01	04	4	BLANK			03	05					02	29	15	44	01	04
267	0103	0403	40101	BLANK	0101/4	0301/2	0302	0501					0201	2901	1530/150	4403	0137N	0401
268	0103	0401			01	03	03	05					02	29	15	44	01	04
278	0103	0403	40103	BLANK	0101/4	0301/2	0302	0501/12	0301/10401	0402	0103	BLANK	0201	2902/26	1530	4403	0102	0401
401	0103	0403			01	03	0302	0501	0301/10401	0402								
452	0103	0403	40103	BLANK			0302	0501	0301	0402			0201	2902	1530	4403	0102	0401
519	0103	0403	401	BLANK	0101	0301	0302	0501	0301	0402	0103	BLANK	0201	2902	1530	4403	0102	0401/82
615	0103	0403	401	BLANK			030201G	050101G	030101G	040201G								
616	01	04											02	29	15	44	01	04
635	01	04	4	BLANK			03	05					02	29	15	44	01	04
702	0103	0403	40103	BLANK	0101	0301	0302	0501	0301	0402			0201	2902	1530	4403	0102	0401
714	0103	0403	NT	NT	NT	NT	0302	0501	NT	NT	NT	NT	0201	2902	1530	4403	0102	0401
726	0103	0403	401	BLANK	0101	0301	0302	0501	0301	0402	0103	BLANK	0201	2902	1530	4403	0102	0401
732	0103	040301	4010301	BLANK	01	03	030201	050101					020101	290201	1530	440301	0102/14	0401/9N
769	0103	0403	40103	BLANK			0302	0501	0301	0402			0201	2902	1530	4403	0102	0401
805	0103	0403					0302	0501					0201	2902	1530	4403	0102	0401
1113	0103/39N	04					03	05	0301	0402			02	29	15	44	01	04
1189	0103	0403	40103	BLANK			0302	0501	0301	0402			0201	2902	1530	4403	0102	0401
1212	NT	NT					NT	NT					NT	NT	NT	NT		
1251	0103	0403	40103	BLANK	0101	0301	0302	0501/12	0301	0402			02	2902	1530	44	01	04
1498	0103	040301	40103	BLANK	0101	030101	030201G	0501	0301	0402			0201/1L	2902	1530	4403	010201G	040101G
1647	0103	0403					0302	0501	0301	0402			0201	2902	1530	4403	0102	0401
1686	0103	0403	40103	BLANK	0101	0301	0302	0501	0301	0402	0103	BLANK	0201	2902	1530	4403	0102	0401
1905	0103	0403	401	BLANK			0302	0501	0301P	0402P	0103	BLANK	0201	2902	1530	4403	0102	0401
2004																		
2013	0103	0403					0302	0501					0201	2902	1530	4403	0102	0401
2015																		
2063																		
2347	0103	04	4	BLANK	01	03	0302	05	0301	0402	0103	BLANK	02	29	1530	44	01	04
2411	0103	0403					0302	0501					0201	2902	1530	4403	0102	0401
2518	0103	0403					0302	0501					0201	2902	1530	4403	0102	0401
2549	0103	0403	40103	BLANK	0101	0301	030201G	0501	030101G	040201G			0201	2902	1530	4403	0102	0401/82
3248																		
3261	0103	0403					0302	0501	0301	0402								
3264	0103	0403	40103	BLANK	NT	NT	0302	0501	0301	0402			0201	2902	1530	4403	0102	0401
3324																		
3325	0103	0403	40103	BLANK	0101	0301	0302	0501					02	29	15	44		
3410	0103	0403					0302	0501					0201	2902	1530	4403	0102	0401
3438	0103	0403					0302	0501					02	29	15	45	01	04
3522																		
3582	0103	0403	401	BLANK	NT	NT	0302	0501	030101G	040201G			0201	2902	1530	4403	0102	0401
3614	0103	0403			01	03	0302	0501					0201	2902	1530	4403	0102	0401
3625	0103	0403	4	BLANK			0302	0501	03	0402			0201	2902	1530	4403	0102	0401
3807	0103/39N	0403					0302	0501	0301	0402			0201	2902	1530	4403	0102	04
3849	0103	0403	401	BLANK	0101	0301	0302	0501					02	29	15	44	01	04
4237																		
4281																		
4420	0117	0402											0201	2902	1530	4403	0102	0401/7
4545	0103	0403	401	BLANK	0101	0301	0302	0501	030101G	040201G			0201	2902	1530	4403	0102	040101G
4551	0103	0403	40103	BLANK	01	03	0302	0501	0301	0402			0201	2902	1530	4403	0102	0401
4585	0103	04			01	03	0302	0501/12					02	29	15	44	01	04
4613																		
4653	0103	04			01	03	0302	0501					02	29	1530/150	44	01	04
4709	0103	0403	NT	NT	01	03	0302	0501	0301	0402			0201	2902	1530	4403	0102	0401
5204																		
5982	0103	0403					0302	0501	0301	0402			02152	2922	1530	4403	0102	0401
6051	0103	0403/52	401	BLANK	0103	BLANK	0302	0501/12	030101G	0402	0103	BLANK	02	29	1530	44	01	04
6313	0103	04					03	05					02	29	15	44	01	04
9221	0103	04	4	BLANK	01	03	03	05	03	0402			02	29	15	44	01	04
197H	0103	0403					0302	0501	0301P	0402			0201	2902	1530	4403	0102	0401P
197L	0103	04	401	BLANK	01	03	0302	0501			0103	BLANK	02	29	15	44	01	04
271	01	04	401	BLANK			03	05					02	29	15	44		
4582H	0103	0403	40103/8	BLANK	01	03	0302	0501	0301	0402	0103	BLANK	0201	2902	1530	4403	0102	0401
4582L	01	04	401	BLANK	01	03	03	05	03	04	01	BLANK	02	29	15	44	01	04

