Table S1. Amino acid pairwise distances among nine *SLA-1* alleles.

	SLA-1*04:01	SLA-1*05:01	SLA-1*08:04	SLA-1*08:05	SLA-1*10:02	SLA-1*11:04	SLA-1*12:01	SLA-1*13:01	SLA-1*15:02
SLA-1*04:01									
SLA-1*05:01	0.1606								
SLA-1*08:04	0.2455	0.2469							
SLA-1*08:05	0.2205	0.2452	0.1203						
SLA-1*10:02	0.2183	0.2156	0.2382	0.2463					
SLA-1*11:04	0.1796	0.1980	0.2722	0.2446	0.1620				
SLA-1*12:01	0.1458	0.1898	0.2438	0.2487	0.2027	0.1819			
SLA-1*13:01	0.0480	0.1489	0.2932	0.2557	0.2367	0.1869	0.1440		
SLA-1*15:02	0.1022	0.1430	0.2599	0.2325	0.2278	0.1818	0.1307	0.0798	

Amino acid pairwise distances among nine *SLA-1* alleles were indicated as the number of amino acid substitutions per site from the SLA-1 amino acid sequences that were analyzed by MEGA X program using the JTT matrix-based model with a gamma distribution [23,24]. Over all mean distance was 0.1972. 181 amino acids from α1 to a part of α2 domains of *SLA-1* alleles were referred from those registered in the DDBJ/EMBL/GenBank databases (*SLA-1*04:01*; AF464002: *SLA-1*05:01*; AF464044: *SLA-1*08:04*; AK396218: *SLA-1*08:05*; AF484015: *SLA-1*10:02*; DQ303230: *SLA-1*11:04*; EU440338: *SLA-1*12:01*; EU440335: *SLA-1*13:01*; EU440336 and *SLA-1*15:02*; AK232719).

Table S2. Amino acid pairwise distances among eight *SLA-3* alleles.

	SLA-3*01:01	SLA-3*03:05	SLA-3*04:01	SLA-3*05:02	SLA-3*06:01	SLA-3*06:02	SLA-3*07:01:02	SLA-3*08:01
SLA-3*01:01								
SLA-3*03:05	0.1603							
SLA-3*04:01	0.0596	0.1569						
SLA-3*05:02	0.0925	0.0946	0.0988					
SLA-3*06:01	0.0452	0.1435	0.0652	0.1014				
SLA-3*06:02	0.0518	0.1657	0.0794	0.1165	0.0384			
SLA-3*07:01:02	0.0385	0.1428	0.0584	0.0872	0.0188	0.0318		
SLA-3*08:01	0.1966	0.2061	0.2148	0.2142	0.1975	0.2184	0.2038	

Amino acid pairwise distances among eight *SLA-3* alleles were indicated as the number of amino acid substitutions per site from the SLA-3 amino acid sequences that were analyzed by MEGA X program using the JTT matrix-based model with a gamma distribution [23,24]. Over all mean distance was 0.1178. 188 amino acids from α1 to a part of α2 domains of *SLA-3* alleles were referred from those registered in the DDBJ/EMBL/GenBank databases databases (*SLA-3*01:01*; DQ303224: *SLA-3*03:05*; AB828067: *SLA-3*04:01*; AF464011: *SLA-3*05:02*; AF464041: *SLA-3*06:01*; AF464010: *SLA-3*06:02*; DQ303227: *SLA-3*07:01:02*; AK232238 and *SLA-3*08:01*; AK234307).

Table S3. Amino acid pairwise distances among eight *SLA-2* alleles.

	SLA-2*03:02	SLA-2*04:02:02	SLA-2*05:04	SLA-2*06:03	SLA-2*09:01	SLA-2*10:01	SLA-2*11:01:02	SLA-2*16:01
SLA-2*03:02								
SLA-2*04:02:02	0.2413							
SLA-2*05:04	0.3206	0.2170						
SLA-2*06:03	0.2412	0.2282	0.3217					
SLA-2*09:01	0.2529	0.2665	0.2680	0.2351				
SLA-2*10:01	0.1932	0.2614	0.3158	0.1570	0.2429			
SLA-2*11:01:02	0.2557	0.1818	0.2440	0.2157	0.2517	0.2571		
SLA-2*16:01	0.2087	0.2583	0.3304	0.1207	0.1340	0.1363	0.1726	

Amino acid pairwise distances among eight *SLA-2* alleles were indicated as the number of amino acid substitutions per site from the SLA-2 amino acid sequences that were analyzed by MEGA X program using the JTT matrix-based model with a gamma distribution [23,24]. Over all mean distance was 0.2330. 188 amino acids from α1 to a part of α2 domains of *SLA-2* alleles were referred from those registered in the DDBJ/EMBL/GenBank databases (*SLA-2*03:02*; DQ104338: *SLA-2*04:02:02*; EU432087: *SLA-2*05:04*; AF464005: *SLA-2*06:03*; AB828064: *SLA-2*09:01*; AB828065: *SLA-2*10:01*; EU432084: *SLA-2*11:01:02*; DQ303222 and *SLA-2*16:01*; AK233069).

Table S4. Amino acid pairwise distances among eight *DRB1* alleles.

	DRB1*04:03	DRB1*06:01	DRB1*07:01	DRB1*08:01	DRB1*09:01	DRB1*10:01	DRB1*11:03	DRB1*14:01
DRB1*04:03								
DRB1*06:01	0.2215							
DRB1*07:01	0.1921	0.2186						
DRB1*08:01	0.1894	0.1994	0.1047					
DRB1*09:01	0.1966	0.1728	0.1225	0.0545				
DRB1*10:01	0.2218	0.1771	0.1505	0.1053	0.1196			
DRB1*11:03	0.1480	0.1786	0.1853	0.2046	0.2001	0.2287		
DRB1*14:01	0.0705	0.2039	0.1623	0.1825	0.1850	0.2149	0.1344	

Amino acid pairwise distances among eight *DRB1* alleles were indicated as the number of amino acid substitutions per site from the DRB1 amino acid sequences that were analyzed by MEGA X program using the JTT matrix-based model with a gamma distribution [23,24]. Over all mean distance was 0.1695. 144 amino acids from β1 to a part of β2 domains of *DRB1* alleles were referred from data registered in the DDBJ/EMBL/GenBank databases (*DRB1*04:03*; AF464037: *DRB1*06:01*; AF464033: *DRB1*07:01*; AY102481: *DRB1*08:01*; AF464034: *DRB1*09:01*; AF464050: *DRB1*10:01*; CJ030292: *DRB1*11:03*; AB828137 and *DRB1*14:01*; DQ303220).

Table S5. Amino acid pairwise distances among six *DQB1* alleles.

	DQB1*03:03	DQB1*04:01:02	DQB1*04:02	DQB1*05:01	DQB1*05:02	DQB1*06:01
DQB1*03:03						
DQB1*04:01:02	0.0794					
DQB1*04:02	0.0867	0.0057				
DQB1*05:01	0.0673	0.0686	0.0759			
DQB1*05:02	0.0791	0.0748	0.0678	0.0235		
DQB1*06:01	0.0667	0.0837	0.0826	0.0677	0.0469	

Amino acid pairwise distances among six *DQB1* alleles were indicated as the number of amino acid substitutions per site from the DQB1 amino acid sequences that were analyzed by MEGA X program using the JTT matrix-based model with a gamma distribution [23,24]. Over all mean distance was 0.0651. 144 amino acids from β1 to a part of β2 domains of *DQB1* alleles were referred from data registered in the DDBJ/EMBL/GenBank databases (*DQB1*03:03*; AF464047: *DQ1B*04:01:02*; DQ303218: *DQB1*04:02*; AK397263: *DQB1*05:01*; AY133574: *DQB1*05:02*; *AY102477* and *DQB1*06:01*; AF464029).