mHag	Gene	rsID	Chromosome	position†	SNP	mHag allele	mHag allele frequencies in HapMap				Reporter#
							JPT	CHB	YRI	CEU	
HA-2	*MYO1G*	not registered	7p13-p11.2	44,784,788	G / A	G	-	-	-	~0.776§	den Haan (1995)[1]
HA-1	*HMHA1*	rs1801284	19p13.3	1,019,738	A / G	A	0.367§	-	-	0.443§	den Haan (1998)[2]
HB-1	*HMHB1*	rs161557*	5q31.3	143,180,246	C / T	bidirectional	0.534	0.578	0.717	0.858	Dolstra (1999)[3] Dolstra (2002)[4]
HA-8	*KIAA0020*	rs2173904 *	9p22.3	2,818,765	G / C	G	0.557	0.567	0.558	0.533	Brickner (2001)[5]
HA-3	*AKAP13*	rs2061821 *	15q24-q25	83,923,658	C / T	C	0.602	0.544	0.608	0.667	Spierings (2003)[6]
UGT2B17	*UGT2B17*	NA	4q13	69,262,482‡	deletion	NA	-	-	-	-	Murata (2003)[7]
ACC-1	*BCL2A1*	rs1138357 *	15q25.3	78,050,461	A / G	bidirectional	0.534	0.5	0.217	0.25	Akatsuka (2003)[8] Kawase (2008)[9]
ACC-2	*BCL2A1*	rs3826007 *	15q25.3	78,050,272	A / G	A	0.216	0.189	0.033	0.25	Akatsuka (2003)[8]
LRH-1	*P2RX5*	rs5818907	17p13.3	3,541,026	C / -¶	+C	-	-	-	0.322§	de Rijike (2005)[10]
CTL-7A7	*CEMPM*	rs5758511*	22q13.2	40,660,672	T / C	T	0.398	0.511	0	0.258	Brickner (2006)[11]
ACC-3, -4	*CTSH*	rs2289702	15q24-q25	77,024,348	A / G	A	0.0566§	-	-	-	Torikai (2006)[12]
RDR173	*ECGF1*	not registered	22q13.33	49,254,398	A / G	A	-	-	-	0.0566§	Slager (2006)[13]
DNR-7	*SP110*	rs1365776*	2q37.1	230,898,214	A / G	A	0.911	0.889	0.975	0.625	Warren (2006)[14]
LB-ADIR-1F	*TOR3A*	rs2296377*	1q25.2	175,782,957	T / C	T	0.293	0.233	0	0.213	van Bergen (2007)[15]
ACC-6	*HMSD*	rs9945924*	18q21.33	59,771,746	A / G	A	0.211	0.211	0.467	0.217	Kawase (2007)[16]

† Based on build 35

References are listed in the Supplementary Materials

‡ First base of the epitope

* Included in the Phase II HapMap set

§ Data deduced from the original reports based on Hardy-Weinberg equilibrium.

¶ Frameshift is cauded by a cytosine deletion polymorphism.

NA, not applicable