

Additional file 5. Overlapping SNPs between the HapMap Project and three genotyping platforms within the extended MHC region¹.

Overlap	HapMap²	Affy 5.0	Affy 6.0	Illumina 550K
HapMap	1 ³	0.792319	0.822969	0.887571
	(6,749) ⁴	(1,114)	(1,813)	(1,721)
Affy 5.0	0.165061	1	0.595098	0.139247
		(1,406)	(1,311)	(270)
Affy 6.0	0.268632	0.932432	1	0.232078
			(2,203)	(450)
Illumina 550K	0.255001	0.192034	0.204267	1
				(1,939)

¹The range of the extended MHC region is chr6 28,799,220–34,204,868 [31].

²HapMap SNPs from the Chinese Han Beijing population.

³The proportion of the overlapping SNPs between the two genotyping platforms.

⁴The number of SNPs in each genotyping platform.