

Table S2. Allele frequencies and statistical results in the NSDTR population including all ANA-positive cases, ANA^S, ANA^H and controls. Five different DRB1, four DQA1 and five DQB1 alleles were identified.

Allele	ANA % (2n=118)	ANA ^H % (2n=52)	ANA ^S % (2n=54)	Controls % (2n=126)	Total population % (2n=244)	OR	P-value
DRB1*00401	0.0	0.0	0.0	0.8	0.4	-	-
DRB1*00601	46.6	11.5	85.2	37.3	41.8	9.7	<0.0001
DRB1*01501	16.9	32.7	3.7	19.8	18.4	2.0	0.10
DRB1*01502	33.1	53.8	7.4	35.7	34.4	2.1	0.039
DRB1*02301	3.4	1.9	3.7	6.3	4.9	-	-
DQA1*00601	50.0	86.5	11.1	55.6	52.9	5.1	0.00017
DQA1*05011	46.6	11.5	85.2	37.3	41.8	9.7	<0.0001
DQA1*00201	0.0	0.0	0.0	0.8	0.4	-	-
DQA1*00301	3.4	1.9	3.7	6.3	4.9	-	-
DQB1*02301	33.1	53.8	7.4	35.7	34.4	2.1	0.039
DQB1*02001	46.6	11.5	85.2	37.3	41.8	9.7	<0.0001
DQB1*00301	16.9	32.7	3.7	19.8	18.4	2.0	0.1
DQB1*01501	0.0	0.0	0.0	0.8	0.4	-	-
DQB1*00501	3.4	1.9	3.7	6.3	4.9	-	-

S= Speckled, H=Homogeneous

Bold indicate between what groups the largest difference in allele frequencies occurred and where statistics were performed (OR and P-values).