

Supplementary Table S1. Associations of rs2736100 *TERT* and rs1278769 *ATP11A* with the RA subsets.

<i>TERT</i>	Dominant model for C				Recessive model for C				Codominant model	
rs2736100	<i>P</i>	OR	95%CI	<i>P<sub>c</sub></i>	<i>P</i>	OR	95%CI	<i>P<sub>c</sub></i>	<i>P</i>	<i>P<sub>c</sub></i>
UIP(+)RA, n (%)	0.1091	0.69	(0.44-1.07)	0.3273	0.8641	1.04	(0.53-2.03)	NS	0.1892	0.5675
NSIP(+)RA, n (%)	1.0000	1.02	(0.67-1.55)	NS	0.6378	1.14	(0.63-2.09)	NS	0.8117	NS
AD(+)RA, n (%)	0.0382	1.46	(1.03-2.06)	0.1146	0.0074	1.84	(1.18-2.86)	0.0222	0.0042	0.0127
CLD(-)RA, n (%)										

  

<i>ATP11A</i>	Dominant model for G				Recessive model for G				Codominant model	
rs1278769	<i>P</i>	OR	95%CI		<i>P</i>	OR	95%CI	<i>P<sub>c</sub></i>	<i>P</i>	<i>P<sub>c</sub></i>
UIP(+)RA, n (%)	1.0000	1.06	(0.53-2.13)	NS	0.4330	0.83	(0.53-1.28)	NS	0.5035	NS
NSIP(+)RA, n (%)	0.6297	1.21	(0.62-2.35)	NS	0.0229	1.62	(1.07-2.46)	0.0687	0.0347	0.1042
AD(+)RA, n (%)	0.0572	1.77	(0.98-3.19)	0.1716	0.8694	1.03	(0.75-1.43)	NS	0.4682	NS
CLD(-)RA, n (%)										

RA: rheumatoid arthritis, UIP: usual interstitial pneumonia, NSIP: nonspecific interstitial pneumonia, AD: airway disease, CLD: chronic lung disease, OR: odds ratio, CI: confidence interval. Associations were tested by Fisher's exact test using  $2 \times 2$  contingency tables for dominant or recessive models or Cochran-Armitage test for codominant model.