Table 4. Results using pedigree disequilibrium test (PDT) of all polymorphisms used in the fine-mapping of CRF2 region

Marker	PDT (average) χ^2 (df)	PDT (average) *P* value
hCV2443221	0.51	0.476
hCV11354048	0.40	0.526
rs2300370	0.13	0.719
rs2248412	0.33	0.565
rs3153	0.71	0.400
IFNAR2-F8S	**6.63**	**0.010**
IFNAR2-F10V	0.04	0.850
IFNAR2-A285T	0.48	0.487
IL10RB-K47E	**5.55**	**0.019**
IL10RB-CA1	4.05 (1)	0.543
IL10RB-CA2	4.77 (2)	0.190
IL10RB-1165	0.10	0.750
IL10RB-1797	1.36	0.243
IFNAR1-(-408)	0.18	0.675
IFNAR1-GT	10.68 (3)	0.383
IFNAR1-17470	0.04	0.848
IFNAR1-L168V	0.04	0.844
IFNAR1-IVS	1.55 (1)	0.907
IFNAR1-30715	0.29	0.590
IFNGR2-R64Q	2.33	0.127
IFNGR2-2080	2.81	0.094
IFNGR2-2087	0.18	0.671

Degrees of freedom are indicated if > 1. Significant *P* values ($P<0.05$) are shown in bold.

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