

Supplementary Table S2 Genetic variants associated with the level of fatigue at suggestive significance ($p < 1.0E-05$) in patients with primary Sjögren's syndrome in the Norwegian cohort (n=225)

SNP ID	Chr	Position (hg19)	A1	A2	MAF	P-value	Beta (SE) [‡]	Gene symbol	Closest gene
rs1969700	20	40147826	G	A	0.37	8.48E-07	12.89 (2.55)	CHD6	CHD6
rs6102453	20	40162911	A	G	0.38	1.13E-06	12.74 (2.55)	CHD6	CHD6
rs1535223	20	40147871	C	G	0.37	2.70E-06	12.33 (2.57)	CHD6	CHD6
rs1535224	20	40147895	C	G	0.37	2.70E-06	12.33 (2.57)	CHD6	CHD6
rs6072406	20	40162781	C	A	0.37	3.05E-06	12.25 (2.56)	CHD6	CHD6
rs6072405	20	40158754	A	G	0.37	3.06E-06	12.25 (2.56)	CHD6	CHD6
rs6102452	20	40158344	G	A	0.37	3.06E-06	12.25 (2.56)	CHD6	CHD6
rs6093492	20	40155005	C	T	0.37	3.07E-06	12.24(2.56)	CHD6	CHD6
rs6065367	20	40155375	C	T	0.37	3.08E-06	12.24 (2.56)	CHD6	CHD6
rs6065366	20	40154517	G	T	0.37	3.09E-06	12.24 (2.56)	CHD6	CHD6
rs6072403	20	40150586	C	T	0.37	3.20E-06	12.23 (2.56)	CHD6	CHD6
rs6072402	20	40150552	A	G	0.37	3.21E-06	12.23 (2.56)	CHD6	CHD6
rs55967559	20	40151029	ACG	A	0.37	3.21E-06	12.23 (2.56)	CHD6	CHD6
rs2547952	5	98051255	T	C	0.09	4.26E-06	19.28 (4.09)	NA	RGMB
rs2547953	5	98051323	T	C	0.09	4.26E-06	19.28 (4.09)	NA	RGMB
rs2547956	5	98052063	T	C	0.09	4.27E-06	19.28 (4.09)	NA	RGMB
rs1828167	5	98057709	T	C	0.09	4.54E-06	19.19 (4.09)	NA	RGMB
rs74512191	3	71383767	C	T	0.23	4.71E-06	14.01 (2.99)	FOXP1	FOXP1
rs6093493	20	40157273	C	T	0.21	5.27E-06	13.55 (2.91)	CHD6	CHD6
rs4603841	20	40169949	G	A	0.21	5.27E-06	13.55 (2.91)	CHD6	CHD6
rs6102461	20	40181975	C	A	0.21	5.27E-06	13.54 (2.91)	CHD6	CHD6
rs6102462	20	40182025	G	A	0.21	5.28E-06	13.54 (2.91)	CHD6	CHD6
rs8115560	20	40152176	T	A	0.21	5.35E-06	13.53 (2.91)	CHD6	CHD6
rs6102448	20	40152483	G	A	0.21	5.35E-06	13.53 (2.91)	CHD6	CHD6
rs6129858	20	40146939	G	A	0.21	5.36E-06	13.53 (2.91)	CHD6	CHD6
rs75175086	3	71394227	T	C	0.23	6.89E-06	13.86 (3.01)	FOXP1	FOXP1
rs766838	7	26030166	T	C	0.48	7.17E-06	-10.92 (2.38)	LOC105375199	MIR148A
rs6461903	7	26033817	A	G	0.48	7.30E-06	-10.93 (2.38)	LOC105375199	MIR148A
rs4719845	7	26034208	G	A	0.48	7.32E-06	-10.93 (2.38)	LOC105375199	MIR148A
rs2893234	7	26034599	T	G	0.48	7.34E-06	-10.93 (2.38)	LOC105375199	MIR148A
rs55792885	8	129165079	G	A	0.15	7.47E-06	16.41 (3.58)	NA	MIR1208
rs80110011	3	71391227	G	A	0.23	7.87E-06	13.74 (3.01)	FOXP1	FOXP1
rs146290797	3	71396926	C	T	0.23	8.37E-06	13.85 (3.04)	FOXP1	FOXP1
rs6978844	7	26026776	G	A	0.48	8.49E-06	-10.86 (2.39)	LOC105375199	MIR148A
rs2866742	20	40163455	G	A	0.36	8.52E-06	11.77 (2.59)	CHD6	CHD6
rs4812521	20	40159872	T	C	0.36	8.52E-06	11.77 (2.59)	CHD6	CHD6
rs4812522	20	40164044	T	C	0.36	8.52E-06	11.77 (2.59)	CHD6	CHD6
rs11481321	20	40155254	G	GA	0.36	8.57E-06	11.76 (2.59)	CHD6	CHD6
rs6964512	7	26026149	G	T	0.48	8.82E-06	-10.85 (2.39)	LOC105375199	MIR148A
rs8056316	16	7681644	G	C	0.13	8.87E-06	-18.03 (3.97)	RBFOX1	RBFOX1
rs78500097	3	71395329	G	A	0.23	8.91E-06	13.75 (3.03)	FOXP1	FOXP1
rs11086806	20	40146737	T	G	0.36	8.93E-06	11.74 (2.59)	CHD6	CHD6
rs4812520	20	40150484	A	C	0.36	9.06E-06	11.78 (2.60)	CHD6	CHD6
rs6461900	7	26024687	A	T	0.48	9.42E-06	-10.82 (2.39)	LOC105375199	MIR148A
rs4719848	7	26035630	T	G	0.48	9.75E-06	-10.87 (2.40)	LOC105375199	MIR148A

[‡] Regression coefficient of the minor allele and standard error.

MAF, minor allele frequency