

**Supplementary Table S4** Genetic variants associated with the level of fatigue at suggestive significance ( $p < 1.0E-05$ ) in patients with primary Sjögren's syndrome in the UK cohort (n=128)

SNP ID	Chr	Position (hg19)	A1	A2	MAF	P-value	Beta (SE) <sup>‡</sup>	Gene symbol	Closest gene
rs12679528	8	15566164	G	A	0.41	1.20E-07	17.95 (3.21)	TUSC3	TUSC3
rs2111755	8	15562357	G	C	0.39	2.50E-07	17.35 (3.20)	TUSC3	TUSC3
rs5889597	8	15562455	TAAA	T	0.39	2.72E-07	17.16 (3.17)	TUSC3	TUSC3
rs1421259	8	15562672	A	G	0.39	2.72E-07	17.16 (3.17)	TUSC3	TUSC3
rs4240180	8	15555541	C	T	0.27	3.45E-07	20.11 (3.75)	TUSC3	TUSC3
rs4379450	8	15555791	A	G	0.27	3.45E-07	20.11 (3.75)	TUSC3	TUSC3
rs4322010	8	15555800	T	C	0.27	3.45E-07	20.11 (3.75)	TUSC3	TUSC3
rs13273264	8	15563463	C	T	0.39	3.57E-07	17.08 (3.19)	TUSC3	TUSC3
rs13275229	8	15563739	A	G	0.39	3.57E-07	17.08 (3.19)	TUSC3	TUSC3
rs4520084	7	147908658	T	C	0.50	3.61E-07	16.98 (3.17)	CNTNAP2	CNTNAP2
rs13275202	8	15563714	A	G	0.40	3.65E-07	17.15 (3.20)	TUSC3	TUSC3
rs13272655	8	15563933	G	T	0.40	3.65E-07	17.15 (3.20)	TUSC3	TUSC3
rs12545813	8	15564321	G	A	0.40	3.65E-07	17.15 (3.20)	TUSC3	TUSC3
rs13265882	8	15565257	T	C	0.40	3.65E-07	17.15 (3.20)	TUSC3	TUSC3
rs13266483	8	15565457	T	A	0.40	3.65E-07	17.15 (3.20)	TUSC3	TUSC3
rs10074116	5	91786204	A	G	0.07	5.85E-07	-35.36 (6.66)	LOC105379080	LOC105379080
rs6861154	5	91787760	C	A	0.07	6.03E-07	-35.07 (6.66)	LOC105379080	LOC105379080
rs72777101	5	91784726	A	G	0.07	6.48E-07	-35.24 (6.68)	LOC105379080	LOC105379080
rs10075974	5	91780657	A	G	0.07	8.99E-07	-34.76 (6.72)	LOC105379080	LOC105379080
rs1018365	22	33679425	G	C	0.09	1.11E-06	-29.54 (5.81)	LARGE1	LARGE1
rs150429125	5	91777642	TA	T	0.07	1.13E-06	-34.16 (6.74)	LOC105379080	LOC105379080
rs2604340	8	15594312	A	G	0.27	1.16E-06	19.27 (3.78)	TUSC3	TUSC3
rs10068591	5	91775806	C	A	0.07	1.22E-06	-34.02 (6.74)	LOC105379080	LOC105379080
rs144557845	5	91775404	T	A	0.07	1.24E-06	-33.99 (6.74)	LOC105379080	LOC105379080
rs13258543	8	15556834	A	T	0.33	1.38E-06	17.82 (3.52)	TUSC3	TUSC3
rs7285350	22	33678629	T	G	0.09	1.67E-06	-28.60 (5.71)	LARGE1	LARGE1
rs145200158	5	91768548	A	AT	0.07	1.68E-06	-33.26 (6.68)	LOC105379080	LOC105379080
rs147272260	22	33678095	C	T	0.09	1.68E-06	-28.60 (5.71)	LARGE1	LARGE1
rs140964403	22	33678112	C	T	0.09	1.68E-06	-28.60 (5.71)	LARGE1	LARGE1
rs370181045	22	33678332	AAAA ACAA ACAA AC	A	0.09	1.68E-06	-28.60 (5.71)	LARGE1	LARGE1
rs7284378	22	33678520	G	C	0.09	1.68E-06	-28.60 (5.71)	LARGE1	LARGE1
rs145710420	22	33672271	TTTT G	T	0.09	1.69E-06	-28.59 (5.71)	LARGE1	LARGE1
rs79710384	22	33673814	G	A	0.09	1.69E-06	-28.60 (5.71)	LARGE1	LARGE1
rs76913609	22	33674479	A	C	0.09	1.69E-06	-28.60 (5.71)	LARGE1	LARGE1
rs78324545	22	33675752	A	G	0.09	1.69E-06	-28.60 (5.71)	LARGE1	LARGE1
rs78317122	22	33675853	A	G	0.09	1.69E-06	-28.60 (5.71)	LARGE1	LARGE1
rs5998839	22	33676283	T	C	0.09	1.69E-06	-28.59 (5.71)	LARGE1	LARGE1
rs17795296	22	33677816	T	G	0.09	1.69E-06	-28.60 (5.71)	LARGE1	LARGE1
rs41282597	22	33670679	G	A	0.09	1.70E-06	-28.59 (5.71)	LARGE1	LARGE1
rs10041199	5	91765897	A	T	0.07	1.72E-06	-33.19 (6.68)	LOC105379080	LOC105379080
rs148762098	22	33668923	G	GA	0.09	1.73E-06	-28.60 (5.71)	LARGE1	LARGE1
rs149577011	22	33668470	GAAC	G	0.09	1.74E-06	-28.45 (5.67)	LARGE1	LARGE1
rs9314231	5	91764149	G	T	0.07	1.76E-06	-33.12 (6.67)	LOC105379080	LOC105379080
rs10052520	5	91760661	T	A	0.07	1.88E-06	-32.93 (6.64)	LOC105379080	LOC105379080
rs10054799	5	91755102	A	T	0.07	2.14E-06	-32.51 (6.55)	LOC105379080	LOC105379080
rs72777081	5	91745264	C	G	0.07	2.15E-06	-32.48 (6.55)	LOC105379080	LOC105379080
rs28669887	5	91748254	C	T	0.07	2.15E-06	-32.48 (6.55)	LOC105379080	LOC105379080

rs10053665	5	91752084	G	A	0.07	2.15E-06	-32.49 (6.55)	LOC105379080	LOC105379080
rs10059030	5	91733747	T	G	0.07	2.16E-06	-32.46 (6.55)	LOC105379080	LOC105379080
rs10055515	5	91739393	C	T	0.07	2.16E-06	-32.47 (6.55)	LOC105379080	LOC105379080
rs10055632	5	91739565	C	T	0.07	2.16E-06	-32.47 (6.55)	LOC105379080	LOC105379080
rs10041056	5	91718060	T	C	0.07	2.22E-06	-32.23 (6.52)	LOC105379080	LOC105379080
chr5:91752216	5	91752216	G	A	0.07	2.57E-06	-32 (6.53)	LOC105379080	LOC105379080
rs2543145	8	15593659	T	A	0.27	2.80E-06	18.66 (3.81)	TUSC3	TUSC3
rs1054083	17	908529	A	G	0.12	3.01E-06	23.14 (4.75)	ABR	ABR
rs6993547	8	68973700	G	C	0.19	3.60E-06	-19.27 (4)	PREX2	PREX2
rs13278290	8	15560370	C	T	0.33	3.78E-06	17.17 (3.56)	TUSC3	TUSC3
rs7005752	8	68969350	G	A	0.18	3.96E-06	-19.71 (4.1)	PREX2	PREX2
rs7009725	8	68969463	G	A	0.18	3.96E-06	-19.71 (4.1)	PREX2	PREX2
rs7009954	8	68969814	C	T	0.18	3.96E-06	-19.71 (4.1)	PREX2	PREX2
rs7009963	8	68969882	A	C	0.18	3.96E-06	-19.71 (4.1)	PREX2	PREX2
rs7010514	8	68969951	G	A	0.18	3.96E-06	-19.71 (4.1)	PREX2	PREX2
rs1897874	8	68970343	G	T	0.18	3.96E-06	-19.71 (4.1)	PREX2	PREX2
rs1897875	8	68970492	A	T	0.18	3.96E-06	-19.71 (4.1)	PREX2	PREX2
rs17445951	8	68974103	G	A	0.18	3.96E-06	-19.71 (4.1)	PREX2	PREX2
rs17445916	8	68974008	G	A	0.18	3.97E-06	-19.71 (4.1)	PREX2	PREX2
rs1897876	8	68970772	T	G	0.18	4.00E-06	-19.71 (4.1)	PREX2	PREX2
chr22:33674547	22	33674547	A	T	0.09	4.41E-06	-27.26 (5.71)	LARGE1	LARGE1
rs1477207	8	15557421	A	G	0.33	4.44E-06	17.06 (3.57)	TUSC3	TUSC3
rs6694119	1	90660848	A	G	0.30	4.67E-06	-17.34 (3.63)	NA	LOC105378849
rs7591479	2	159039836	A	T	0.36	5.00E-06	-14.41 (3.03)	CCDC148	CCDC148
rs16992034	22	33669492	G	C	0.09	5.17E-06	-26.93 (5.67)	LARGE1	LARGE1
rs7592105	2	159047406	G	A	0.36	5.51E-06	-14.22 (3)	CCDC148	CCDC148
rs7771959	6	91517533	A	G	0.48	5.68E-06	-15.6 (3.3)	LOC107986623	LOC107986623
rs4075465	16	83148925	G	A	0.45	6.31E-06	16.36 (3.47)	GPC5	GPC5
rs7203162	16	83148282	G	A	0.45	6.86E-06	16.22 (3.47)	GPC5	GPC5
rs17722172	22	33670584	G	A	0.09	7.45E-06	-26.48 (5.68)	LARGE1	LARGE1
rs1190234	14	103398706	G	A	0.15	7.54E-06	-20.4 (4.38)	GPC5	GPC5
rs7750014	6	91513368	A	T	0.48	7.86E-06	-15.31 (3.3)	LOC107986623	LOC107986623
rs35227786	6	91513690	A	AT	0.48	8.39E-06	-15.26 (3.3)	LOC107986623	LOC107986623
rs6492563	13	92607211	T	A	0.37	8.57E-06	16.88 (3.65)	GPC5	GPC5
chr6:26033809	6	26033809	T	TAAG AAG	0.48	8.65E-06	15.96 (3.45)	NA	H2AC4
rs11384857	13	92606807	T	TG	0.37	8.75E-06	16.86 (3.65)	GPC5	GPC5
rs1553484	6	91507934	A	G	0.37	9.04E-06	-16.02 (3.47)	LOC107986623	LOC107986623
rs9301765	13	92614270	C	G	0.37	9.10E-06	16.79 (3.64)	GPC5	GPC5
rs34655502	13	92611601	C	CAAA T	0.37	9.38E-06	16.77 (3.64)	GPC5	GPC5
rs3906157	13	92611379	T	G	0.37	9.87E-06	16.76 (3.64)	GPC5	GPC5
rs437276	20	48233373	C	A	0.25	9.89E-06	-19.53 (4.25)	NA	LOC105372651

‡ Regression coefficient of the minor allele and standard error.

MAF, minor allele frequency