

**Supplementary Table 8**

Association results between markers at the *LOXL1* locus on Chromosome 15 at susceptibility to XFS. Shown here are all SNP markers surpassing  $1 \times 10^{-7}$  on primary association testing. Additional analyses conditioning for key *LOXL1* SNPs (rs4886776 and rs3825942) are also appended.

SNP	BP	A1	MAF cases	MAF controls	A2	OR <sup>a</sup>	P <sup>a</sup>	OR <sup>b</sup>	P <sup>b</sup>	OR <sup>c</sup>	P <sup>c</sup>	OR <sup>d</sup>	P <sup>d</sup>
rs4886776	74224996	G	0.1015	0.5008	A	0.12	7.37E-137	-	-	0.13	2.13E-102	-	-
rs2304721	74240354	A	0.0465	0.2329	C	0.16	9.79E-67	0.93	0.61	0.14	4.00E-71	0.77	0.12
rs4461027	74211548	G	0.1115	0.3123	A	0.26	2.65E-62	0.94	0.57	0.25	9.18E-63	0.86	0.21
rs12438872	74177764	G	0.1462	0.3492	A	0.31	3.59E-58	0.85	0.087	0.34	7.53E-46	0.83	0.053
rs4886725	74171006	G	0.1459	0.3338	A	0.33	2.83E-52	0.87	0.12	0.35	6.07E-45	0.84	0.058
rs4886693	74141238	G	0.1349	0.316	A	0.34	1.12E-49	0.83	0.048	0.35	3.27E-42	0.81	0.024
rs8042039	74225518	A	0.02596	0.1532	G	0.14	5.28E-48	0.82	0.22	-	-	-	-
rs1078967	74222987	A	0.02561	0.1529	G	0.14	6.52E-48	0.81	0.19	0.78	0.75	1.19	0.84
rs4445847	74172013	A	0.1267	0.2971	G	0.33	1.20E-47	0.85	0.088	0.31	1.42E-48	0.80	0.023
rs3825942	74219582	A	0.02594	0.1521	G	0.14	1.32E-47	0.82	0.21	-	-	-	-
rs8041685	74225193	A	0.0192	0.1066	G	0.14	7.30E-35	0.85	0.37	1.08	0.79	1.15	0.64
rs999742	74115517	G	0.285	0.4537	A	0.48	3.45E-33	0.98	0.77	0.49	2.18E-29	0.96	0.59
rs12101466	74248388	G	0.1924	0.3527	A	0.45	5.33E-33	1.07	0.44	0.58	5.57E-15	1.09	0.35
rs7179978	74200358	A	0.09048	0.2113	G	0.36	1.09E-32	0.77	0.011	0.35	7.75E-32	0.74	0.0042
rs4886647	74110101	G	0.2844	0.4516	A	0.49	1.17E-32	0.97	0.67	0.49	3.78E-29	0.95	0.49
rs1452389	74138822	A	0.127	0.2614	G	0.41	6.47E-32	0.86	0.11	0.45	4.03E-24	0.86	0.092
rs8029844	74193472	A	0.09299	0.2117	G	0.37	2.48E-31	0.79	0.025	0.36	8.67E-31	0.76	0.010
rs8030745	74133091	G	0.1224	0.2538	A	0.42	9.72E-31	0.84	0.064	0.45	1.46E-23	0.83	0.051
rs4886425	74124543	A	0.124	0.2559	G	0.42	1.11E-30	0.83	0.050	0.45	1.06E-23	0.83	0.040
rs2165241	74222202	A	0.02832	0.1128	G	0.21	1.45E-30	1.30	0.10	0.19	1.43E-32	1.23	0.22
rs750460	74241506	A	0.02898	0.1124	G	0.22	2.23E-30	1.32	0.082	0.20	6.33E-32	1.26	0.18
rs16958445	74176557	A	0.0566	0.1574	G	0.31	2.30E-30	0.83	0.13	0.27	5.25E-34	0.78	0.048
rs2507	74275676	G	0.1863	0.3333	A	0.47	2.67E-29	1.09	0.33	0.61	6.05E-12	1.11	0.24
rs11636934	74275170	G	0.1867	0.3325	A	0.47	5.11E-29	1.09	0.32	0.61	7.70E-12	1.11	0.24
rs1452388	74139078	G	0.1046	0.2241	A	0.40	6.50E-29	0.84	0.076	0.39	3.83E-29	0.81	0.036
rs10519015	74125955	A	0.1012	0.2201	G	0.40	1.14E-28	0.81	0.038	0.38	5.97E-29	0.78	0.017
rs746655	74107677	A	0.1032	0.2222	G	0.40	1.64E-28	0.80	0.028	0.39	6.82E-29	0.78	0.012
rs4886782	74228810	A	0.02561	0.1023	G	0.22	1.15E-27	1.28	0.14	0.20	1.14E-28	1.21	0.27

rs1869177	74160556	A	0.09333	0.2041	G	0.40	6.02E-27	0.80	0.027	0.39	1.19E-26	0.77	0.013
rs10851869	74331083	G	0.1951	0.3312	A	0.51	6.98E-25	1.13	0.17	0.65	1.21E-09	1.15	0.12
rs12437465	74243246	A	0.3575	0.5051	G	0.55	1.95E-24	1.00	0.98	0.41	3.14E-43	0.94	0.46
rs3784556	74332188	A	0.1038	0.2125	C	0.44	8.40E-24	1.12	0.30	0.64	5.69E-07	1.15	0.19
rs2289412	74276092	A	0.07918	0.1771	G	0.42	5.35E-22	1.08	0.52	0.57	1.15E-08	1.10	0.43
rs2289413	74276228	G	0.07918	0.1768	A	0.42	6.78E-22	1.08	0.50	0.57	1.34E-08	1.10	0.42
rs1963477	74091872	A	0.1203	0.218	G	0.48	3.05E-20	0.89	0.24	0.50	2.19E-17	0.88	0.19
rs4272992	74172153	G	0.03136	0.08923	A	0.29	4.84E-20	1.05	0.77	0.26	2.26E-22	0.99	0.93
rs4886717	74165128	A	0.03201	0.09007	G	0.30	9.03E-20	1.06	0.70	0.26	3.75E-22	1.00	0.99
rs4886467	74198813	A	0.01887	0.07323	C	0.23	9.05E-20	0.96	0.84	0.20	2.59E-21	0.90	0.57
rs11639300	74176277	A	0.01922	0.0686	G	0.24	8.10E-18	1.04	0.85	0.22	3.93E-19	0.97	0.88
rs17773784	74080674	G	0.1375	0.2281	A	0.53	1.78E-17	0.89	0.21	0.53	1.58E-15	0.88	0.17
rs1823718	74147244	G	0.02796	0.07828	A	0.30	2.67E-17	1.03	0.89	0.27	1.94E-19	0.96	0.83
rs11072447	74166455	G	0.02768	0.07806	A	0.30	2.82E-17	1.02	0.90	0.26	1.35E-19	0.96	0.80
rs4886617	74089793	C	0.4896	0.3683	A	1.64	3.12E-17	1.11	0.14	1.55	7.57E-13	1.11	0.13
rs4886616	74089733	A	0.4906	0.3716	G	1.61	1.73E-16	1.11	0.15	1.53	2.80E-12	1.11	0.15
rs896598	74036629	A	0.4768	0.3586	G	1.61	2.66E-16	1.02	0.82	1.50	3.28E-11	1.02	0.83
rs4886621	74092804	A	0.44	0.3237	G	1.61	5.77E-16	1.12	0.12	1.56	4.94E-13	1.12	0.10
rs4887140	74046663	C	0.4714	0.3552	A	1.60	1.01E-15	1.01	0.84	1.50	6.42E-11	1.01	0.85
rs4886809	74258449	A	0.4468	0.3256	G	1.59	3.15E-15	1.01	0.93	1.53	7.09E-12	1.01	0.85
rs3784563	74290993	A	0.4353	0.319	C	1.58	1.09E-14	1.02	0.75	1.54	7.87E-12	1.03	0.66
rs16958237	74075608	A	0.1584	0.2449	G	0.58	6.04E-14	0.94	0.52	0.64	3.06E-09	0.95	0.54
rs7173049	74244610	G	0.2156	0.3102	A	0.62	1.50E-13	1.03	0.74	0.72	2.13E-06	1.03	0.72
rs723434	74343330	G	0.4067	0.3039	A	1.54	6.20E-13	1.02	0.81	1.40	7.44E-08	1.02	0.81
rs3522	74244344	G	0.4114	0.322	A	1.52	2.29E-12	1.02	0.75	1.26	0.000172	1.01	0.87
rs531019	73598607	A	0.3063	0.4049	G	0.67	2.04E-11	0.89	0.11	0.71	8.05E-08	0.89	0.11
rs12442096	74038773	A	0.4235	0.5181	G	0.69	7.12E-11	0.97	0.68	0.74	4.83E-07	0.97	0.70
rs1478558	74116224	A	0.04144	0.08123	G	0.45	2.07E-10	1.14	0.39	0.41	2.57E-12	1.09	0.57
rs2415231	74116864	A	0.04144	0.08123	G	0.45	2.07E-10	1.14	0.39	0.41	2.57E-12	1.09	0.57
rs7169087	74068380	A	0.5243	0.4356	G	1.43	4.96E-10	1.01	0.93	1.46	5.40E-10	1.02	0.83
rs11072405	73485160	A	0.345	0.4358	G	0.70	6.42E-10	0.91	0.19	0.74	1.53E-06	0.91	0.20
rs2415145	73540362	G	0.3514	0.4423	A	0.70	9.29E-10	0.91	0.20	0.75	2.11E-06	0.91	0.21
rs746654	74107712	A	0.04178	0.08039	G	0.47	1.10E-09	1.09	0.56	0.42	1.28E-11	1.05	0.77
rs13638	74181538	G	0.02123	0.05219	A	0.37	1.17E-09	1.01	0.96	1.00	1.00	1.13	0.55
rs3784807	73631830	G	0.4538	0.545	A	0.71	3.10E-09	0.92	0.24	0.72	3.34E-08	0.92	0.22
rs1979409	73465477	A	0.1375	0.2012	G	0.63	3.30E-09	0.81	0.030	0.64	2.58E-08	0.81	0.025

rs1564239	74073647	A	0.4292	0.5114	G	0.71	3.46E-09	1.00	0.99	0.73	1.46E-07	0.99	0.91
rs2415230	74059081	A	0.5219	0.4373	G	1.40	3.84E-09	0.99	0.85	1.43	3.55E-09	1.00	0.95
rs12917099	74028569	A	0.5296	0.4465	G	1.39	7.16E-09	1.01	0.90	1.31	5.11E-06	1.01	0.90
rs1542544	74020740	G	0.5313	0.4487	A	1.38	8.67E-09	1.02	0.83	1.31	6.03E-06	1.01	0.84
rs2218949	74075536	A	0.4279	0.5076	G	0.72	1.29E-08	1.00	0.97	0.74	4.57E-07	1.00	0.96
rs12905211	73628168	A	0.2224	0.2982	G	0.69	1.68E-08	0.85	0.052	0.66	2.72E-09	0.85	0.043
rs1038094	74012437	G	0.4531	0.5341	A	0.73	1.81E-08	1.00	0.97	0.77	1.90E-05	1.00	0.96
rs6495042	73282726	A	0.5313	0.4532	G	1.36	3.29E-08	1.18	0.014	1.30	6.97E-06	1.18	0.013
rs1900901	73257725	A	0.5337	0.4562	G	1.36	3.63E-08	1.18	0.015	1.30	6.75E-06	1.18	0.014
rs17762600	73488753	A	0.2294	0.3018	C	0.70	5.14E-08	0.89	0.13	0.73	5.25E-06	0.89	0.13
rs11632630	73254545	C	0.0438	0.07955	A	0.51	5.19E-08	0.67	0.0076	0.47	3.31E-09	0.66	0.0049
rs488156	73625895	G	0.3827	0.4693	A	0.73	5.77E-08	0.91	0.20	0.76	7.31E-06	0.91	0.21
rs7164592	73276931	C	0.4431	0.5181	A	0.74	9.15E-08	0.85	0.020	0.77	8.79E-06	0.85	0.018
rs4238458	73250485	G	0.5243	0.4503	A	1.35	9.34E-08	1.17	0.019	1.29	1.21E-05	1.17	0.018

a: Unconditioned OR and P

b: Conditioned for rs4886776

c: Conditioned for rs3825942

d: Conditioned for both rs4886776 and rs3825942

A1: Minor allele; A2: Major allele.