

Figure S1. Analysis of mortality rate in Chile. A. Map with regional mortality rates due to COPD in Chile (2011); B. Mortality rate due to COPD in Maule region from 2001-2011.

Table S1. Eighty-nine common SNPs included in the study from previous GWAS in populations of diverse ethnic background.

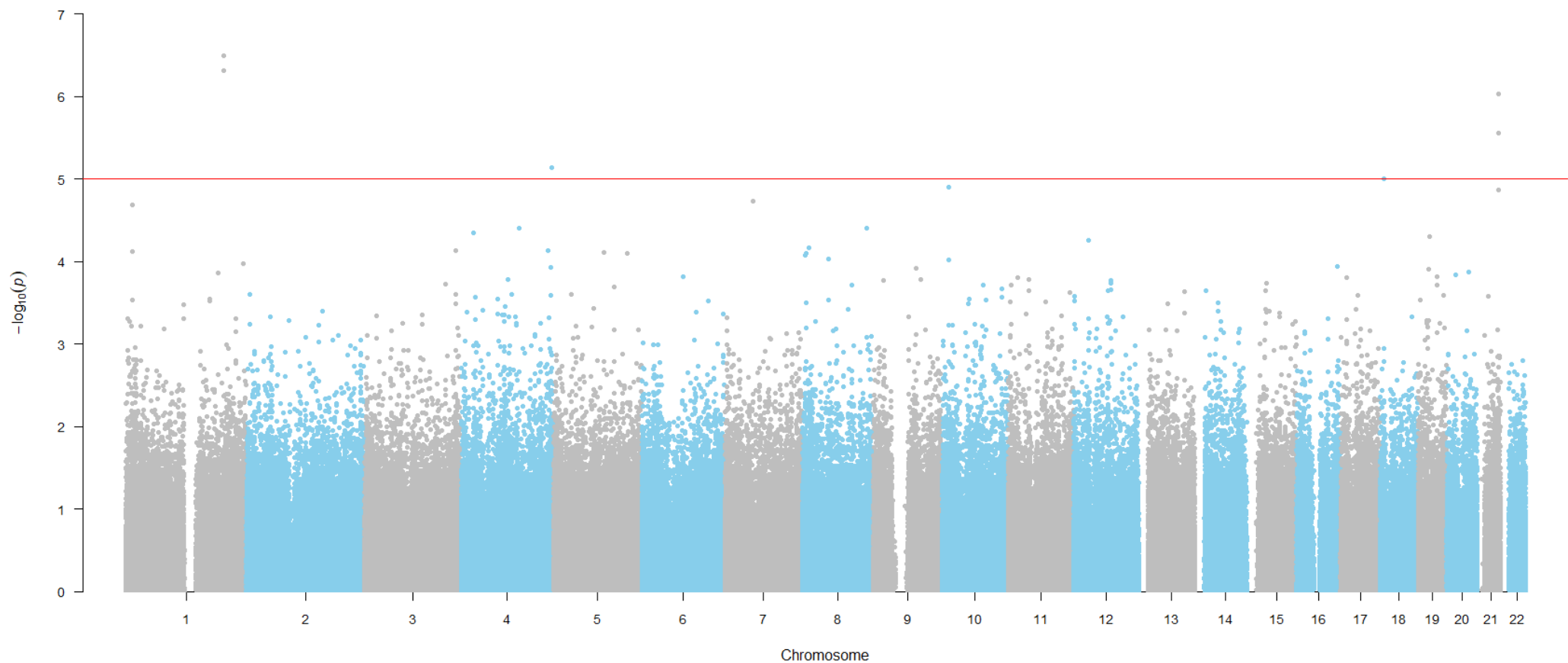
ID	SNP	Position**	Region	Gene/nearest gene(s)	Quality Control
1	rs114216682*	53871085	1p32.3	FLJ40434	pass
2	rs17111652*	55590465	1p32.3	USP24	pass
3	rs4846480	218598469	1q41	TGFB2	pass
4	rs10429950*	218624533	1q41	TGFB2	pass
5	rs1737890*	31042595	20q11.21	NOL4L	pass
6	rs12692398	10200316	2p25.1	CYS1	pass
7	rs16825267*	229569919	2q36.3	PID1	pass
8	rs1529672	25520582	3p24.2	RARB	pass
9	rs41526344*	2985142	3p26.2	CNTN4	pass
10	rs2955083*	127961178	3q21.3	EEFSEC	pass
11	rs546764*	138294336	3q22.3	CEP70	pass
12	rs10023464*	69659738	4q13.2	UGT2B10	pass
13	rs4416442	89866713	4q22.1	FAM13A	pass
14	rs2869966	89869078	4q22.1	FAM13A	pass
15	rs2869967	89869332	4q22.1	FAM13A	pass
16	rs7674369	89872176	4q22.1	FAM13A	pass
17	rs7671167	89883979	4q22.1	FAM13A	pass
18	rs6837671*	89873092	4q22.1	FAM13A	pass
19	rs1964516*	89875909	4q22.1	FAM13A	pass
20	rs2047409*	106137033	4q24	TET2	HWE p<0.05
21	rs17035917*	106520742	4q24	ARHGEF38	pass
22	rs11727735*	106631870	4q24	NPNT, GSTCD	pass
23	rs13141641	145506456	4q31.21	HHIP	pass
24	rs13105210*	145262927	4q31.21	GYPA	pass
25	rs138641402*	145445779	4q31.21	HHIP-AS1	pass
26	rs9990514*	188842148	4q35.2	Intergenic	pass
27	rs7733088	147856333	5q32	HTR4	pass
28	rs10056066*	155861626	5q33.3	SGCD	MAF<0.01
29	rs2070600*	32151443	6p21.32	AGER	MAF<0.01
30	rs9394152*	33465482	6p21.32	ZBTB9	pass

31	rs3130559	31097301	6p21.33	PSORS1C1	pass
32	rs1265093	31107187	6p21.33	PSORS1C1, CCHCR1	pass
33	rs2074488	31240431	6p21.33	HLA-C	pass
34	rs9266629	31346822	6p21.33	FGFR3P	genotyped <80% samples
35	rs2076295	7563232	6p24.3	DSP	pass
36	rs2806356*	109266255	6q21	ARMC2	pass
37	rs9399401*	142668901	6q24.2	ADGRG6, GPR126	pass
38	rs858249	23220639	7p15.3	KLHL7, NUPL2	pass
39	rs78060357*	132056248	7q32.3	PLXNA4	pass
40	rs10491678	29568686	9p21.1	intergenic	pass
41	rs12245299*	55913700	10q21.1	PCDH15	pass
42	rs1923539	81694950	10q22.3	RP11-479O17.4	pass
43	rs7078012	81705433	10q22.3	SFTPD	pass
44	rs3923564	81735981	10q22.3	SFTPD	pass
45	rs12220777	81788104	10q22.3	RP11-369J21.6, RP11-369J21.5	pass
46	rs728616	81847914	10q22.3	RP11-369J21.2	pass
47	rs3851050	81882370	10q22.3	RP11-369J21.4	pass
48	rs207675*	79154537	10q22.3	KCNMA1	pass
49	rs721917*	81706324	10q22.3	SFTPD	pass
50	rs6585424*	81933748	10q22.3	ANXA11	pass
51	rs7079679*	102055546	10q24.31	PKD2L1	pass
52	rs4751240*	129136409	10q26.2	DOCK1	pass
53	rs7929679	34805849	11p13	APIP, EHF	pass
54	rs34391416	831818	11p15.5	EFCAB4A, CHID1, AP2A2	pass
55	rs2463822	62103420	11q12.3	ASRGL1	pass
56	rs3741240	62186542	11q12.3	SCGB1A1	pass
57	rs2077224	62197427	11q12.3	AHNAK	pass
58	rs17157266	62199817	11q12.3	AHNAK	pass
59	rs286499*	85193869	11q14.1	DLG2	pass
60	rs626750	102720945	11q22.2	MMP12	pass
61	rs16906714*	30860557	12p11.21	intergenic	Monomorphic
62	rs9599114*	66987131	13q21.32	PCDH9	pass
63	rs6576132	28728111	14q12	FOGX1	pass
64	rs140706189*	61151425	14q23.1	SIX1, SIX4, SIX6, MNAT1	pass
65	rs7140285	88462988	14q31.3	GALC	pass
66	rs754388	93115410	14q32.12	RIN3	pass
67	rs76677753*	34898066	15q14	GOLGA8B	Monomorphic
68	rs1441358*	71612514	15q23	THSD4	pass
69	rs7181486	78741618	15q25.1	IREB2, AGPHD1	pass
70	rs8042238	78774271	15q25.1	IREB2	pass
71	rs11858836	78783277	15q25.1	IREB2	pass
72	rs13180	78789488	15q25.1	CHRNA5, IREB2, CHRNA3	pass
73	rs8034191	78806023	15q25.1	CHRNA5, CHRNA3, CHRNA4, LOC123688	pass
74	rs17486278	78867482	15q25.1	CHRNA5, PSMA4, IREB2, AGPHD1, CHRNA3	pass
75	rs12914385	78898723	15q25.1	CHRNA3	pass
76	rs8192482*	78886198	15q25.1	CHRNA3	pass
77	rs8038108*	90089276	15q26.1	LINC00928, TICRR	pass
78	rs17707300*	28593347	16p11.2	CCDC101, IL27	pass
79	rs8050136	53816275	16q12.2	FTO	pass
80	rs7186831*	75473155	16q23.1	CFDP1	pass
81	rs114132812*	83817888	16q23.3	CDH13	Monomorphic
82	rs115067260*	83822302	16q23.3	CDH13	pass
83	rs145442019*	83844678	16q23.3	HSBP1	Monomorphic
84	rs8048576	84423034	16q24.1	ATP2C2	pass
85	rs2286351*	13928401	17p12	CDRT15P1	pass
86	rs140948272*	1460896	17p13.3	PITPNA	Monomorphic
87	rs647097*	8808464	18p11.22	MTCL1	pass
88	rs7937	41302706	19q13.2	RAB4B	pass
89	rs12459249*	41339896	19q13.2	CYP2A6	pass

* SNPs imputed

** Based on hg19 coordinates

Figure S2. Single-marker allelic association results.



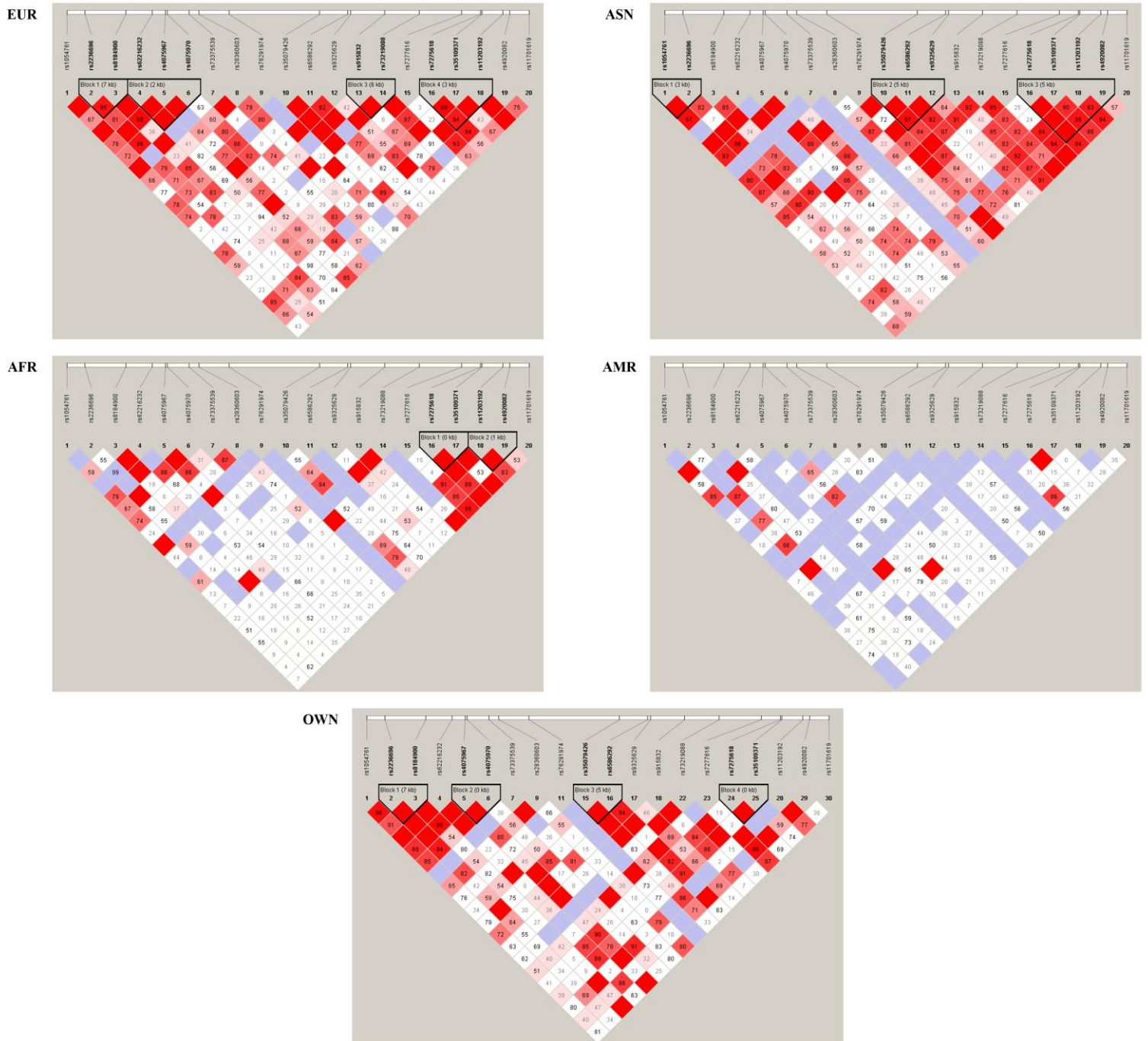
The Manhattan plot graphically represents the $-\log_{10}$ of the p value associated with COPD risk plotted across each chromosome based on 455,564 SNPs, after controlling for age, sex, the first two principal components of a PCA based on genetic data and the proportion of Mapuche ancestry (PMA)

Table S2. Single-SNP allelic association analysis (p-value<10⁻⁵).

CHR	SNP	BP	Gene	Location	A1	OR	P
1	rs12741415	202474774	PPP1R12B	Non Coding Transcript Variant	A	3.01	3.18x10 ⁻⁷
1	rs116062217	202431443	PPP1R12B	Intron	T	2.92	4.89 x10 ⁻⁷
21	rs1054761	43218520	PRDM15	Non Coding Transcript Variant	T	0.44	9.42 x10 ⁻⁷
21	rs4075967	43236176	PRDM15	Synonymous Variant	A	0.45	2.75 x10 ⁻⁶
4	rs4862451	185789995	Intergenic	-	G	2.47	7.21 x10 ⁻⁶

CHR: chromosome; SNP: single nucleotide polymorphism; BP: base pair; A1: minor allele frequency;
OR: odds ratio; P: p-value.

Figure S3. Linkage disequilibrium plots around the *PRDM15* gene.



Squares represent the LD (r^2) value between every 2 single-nucleotide polymorphisms: the more reddish the square, the higher the r^2 pairwise value. Definition of abbreviations: AFR: Africans; AMR: admixed Americans; EAS: East Asians; EUR: Europeans; OWN: Our control population.