Online Repository Materials

Genome-Wide Association Study of Lung Function Phenotypes in a Founder Population

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Table E1. Air quality data for the 10 Hutterite colonies in South Dakota participating in these studies (from http://www.homefacts.com/airquality/South-Dakota.html). These data are gathered from measuring stations across the country. A higher number (on a scale of 1-10) reflects fewer amounts of pollutants (i.e., a 9.0 means that 90% of the stations around the country are measuring higher amounts than the local station). The six air pollutants reported are carbon monoxide, ozone, particulate matter (PM) 10, PM 2.5, and sulfur dioxide. The range of values for the six pollutants and overall ratings are shown. Values for the individual pollutants can be found at the above website.

Zip Code	Number of colonies at this zip code	Range of air quality values	Overall air quality	Overall Rating
57042	1	5.0-9.9	9.2	Outstanding
57076	1	5.7-9.9	9.2	Outstanding
57301	2	6.8-9.9	9.6	Outstanding
57311	2	6.8-9.9	9.6	Outstanding
57314	1	5.0-9.9	9.2	Outstanding
57334	1	6.8-9.9	9.2	Outstanding
57334	1	6.8-9.9	9.6	Outstanding
57366	1	6.8-9.9	9.6	Outstanding

Table E2. Characteristics of the Non-asthmatic and Asthmatic Sample Subsets.

	Males		Females	
	6-17 years	> 17 years	6-17 years	> 17 years
Asthmatics				
Sample Size	25	48	38	51
Number with atopy (%)	13 (52.0%)	34 (70.8%)	20 (52.6%)	24 (47.1%)
Mean age ± SD (yr)	10.8 ± 3.2	39.4 ± 14.6	12.0 ± 2.9	38.2 ± 15.6
Mean FEV_1 ± SD (L)	2.28 ± 0.92	3.76 ± 0.78	2.56 ± 0.81	2.80 ± 0.53
Mean FVC ± SD (L)	2.75 ± 1.13	5.03 ± 0.90	2.93 ± 0.95	3.64 ± 0.70
Mean FEV_1/FVC ± SD (%)	83.5 ± 7.1	74.9 ± 7.5	87.8 ± 6.7	77.2 ± 8.0
Non-asthmatics				
Sample Size	155	303	157	367
Number with atopy (%)	63 (40.6%)	157 (51.8%)	73 (46.5%)	170 (46.3%)
Mean age ± SD (yr)	11.5 ± 3.2	40.2 ± 15.4	12.2 ± 2.9	39.8 ± 15.6
Mean FEV_1 ± SD (L)	2.65 ± 1.06	3.92 ± 0.77	2.56 ± 0.77	2.96 ± 0.60
Mean FVC ± SD (L)	3.08 ± 1.31	4.89 ± 0.91	2.85 ± 0.90	3.61 ± 0.70
Mean FEV_1/FVC ± SD (%)	87.3 ± 7.5	80.4 ± 7.6	90.0 ± 6.3	82.1 ± 6.8

Table E3. SNPs associated with lung function at $P < 10^{-5}$ in the Hutterites. *P*-values highlighted in bold exceeded the threshold for Bonferroni-corrected genome-wide significance ($P < 2.0 \times 10^{-7}$). MAF, minor allele frequency.

SNP	Chr.	NCBI36 Position	Gene	SNP-Gene Relationship	Major/Minor Allele	MAF	FEV_1/FVC *P*	FEV_1 *P*	FVC *P*
rs10864907	2	113,400,346	*IL37*	7.4k downstream	G/A	0.44	1.5E-01	6.7E-06	3.9E-04
rs2637260	10	77,990,352	*C10orf11*	3.2k downstream	T/C	0.44	7.5E-06	1.4E-01	3.9E-01
rs2637261	10	77,990,599	*C10orf11*	3.5k downstream	G/A	0.44	7.5E-06	1.4E-01	3.9E-01
rs2637266	10	78,001,324	*C10orf11*	14.2k downstream	T/C	0.44	2.0E-06	1.1E-01	4.2E-01
rs10824425	10	78,010,316	*C10orf11*	23.2k downstream	C/G	0.44	8.2E-06	1.1E-01	4.7E-01
rs11856830	15	68,211,555	*TLE3*	34.2k upstream	A/G	0.40	3.2E-06	1.6E-01	8.7E-01
rs2114719	15	68,720,392	*UACA*	13.6k downstream	G/A	0.12	4.2E-07	6.9E-04	2.5E-01
rs2162555	15	68,720,626	*UACA*	13.3k downstream	G/A	0.12	5.7E-07	2.2E-04	1.6E-01
rs6494886	15	68,720,785	*UACA*	13.2k downstream	C/A	0.12	3.9E-07	1.2E-03	2.5E-01
rs2162556	15	68,723,492	*UACA*	10.5k downstream	C/T	0.12	4.2E-07	6.9E-04	2.5E-01
rs1991088	15	68,791,504	*UACA*	intron	C/T	0.18	1.2E-06	3.8E-02	8.6E-01
rs1477439	15	68,821,634	*UACA*	intron	G/C	0.28	5.3E-06	1.3E-01	5.4E-01
rs4777305	15	68,832,522	*UACA*	intron	T/C	0.18	1.5E-06	2.5E-02	8.1E-01
rs11633212	15	69,387,305	*THSD4*	intron	A/G	0.33	3.8E-06	1.6E-01	6.4E-01
rs17786786	15	69,395,673	*THSD4*	intron	A/C	0.27	**4.2E-08**	1.6E-01	4.2E-01
rs6494904	15	69,396,576	*THSD4*	intron	T/C	0.25	**1.4E-08**	5.8E-02	5.9E-01
rs11855326	15	69,397,889	*THSD4*	intron	G/A	0.25	**2.5E-08**	5.4E-02	6.6E-01
rs1837762	15	69,399,357	*THSD4*	intron	C/T	0.11	**5.7E-08**	1.7E-03	4.5E-01
rs11858540	15	69,409,840	*THSD4*	intron	T/G	0.12	3.0E-07	1.5E-02	7.4E-01
rs1441361	15	69,412,176	*THSD4*	intron	A/G	0.12	2.8E-07	1.5E-02	7.3E-01
rs1568010	15	69,455,566	*THSD4*	intron	T/G	0.44	7.6E-06	3.8E-01	5.8E-02
rs11858454	15	69,456,169	*THSD4*	intron	C/T	0.44	5.3E-06	3.8E-01	6.1E-02
rs8033889	15	69,467,134	*THSD4*	intron	G/T	0.25	2.3E-07	4.4E-03	3.3E-01
rs4531689	15	69,476,033	*THSD4*	intron	C/T	0.46	4.8E-06	5.0E-01	5.4E-02
rs4288952	15	69,477,937	*THSD4*	intron	G/A	0.45	4.6E-06	4.6E-01	4.8E-02

rs12441227	15	69,483,940	*THSD4*	intron	T/C	0.22	**3.4E-09**	2.2E-03	3.7E-01
rs712046	17	31,382,410	*CCL23*	13.3k upstream	G/A	0.32	3.2E-07	8.2E-02	5.0E-01
rs854679	17	31,382,952	*CCL23*	13.8k upstream	G/T	0.32	3.4E-07	8.9E-02	5.2E-01
rs854674	17	31,384,085	*CCL23*	15.0k upstream	T/C	0.32	6.8E-07	1.3E-01	4.6E-01
rs2017854	17	62,918,483	*PITPNC1*	intron	G/C	0.41	2.6E-06	5.2E-01	8.5E-04
rs4799710	18	29520739	*ASXL3*	intron	A/G	0.32	2.8E-01	6.4E-04	6.7E-06
rs2835345	21	36,723,304	*CHAF1B*	12.3k downstream	G/T	0.25	8.3E-06	1.1E-01	4.9E-01

Table E4. Results of analyses of FEV_1/FVC in combined sample, in sample excluding asthmatics (non-asthmatics), and in analyses stratified by age. All SNPs with *P*-value < 10^{-5} in the combined sample are shown.

		NCBI36	Combined sample		Non-asthmatics		Asthmatics		Adults (>17 years)		Children (≤17 years)	
SNP	Chr.	Position	N	*P*	N	*P*	N	*P*	N	*P*	N	*P*
rs2637260	10	77,990,352	1106	7.50E-06	949	6.34E-07	157	9.82E-01	760	2.70E-04	346	2.69E-02
rs2637261	10	77,990,599	1106	7.50E-06	949	6.34E-07	157	9.82E-01	760	2.70E-04	346	2.69E-02
rs2637266	10	78,001,324	1065	2.00E-06	916	2.43E-07	149	8.31E-01	722	4.22E-05	343	3.38E-02
rs10824425	10	78,010,316	1099	8.23E-06	943	8.98E-07	156	9.99E-01	753	3.34E-04	346	2.58E-02
rs11856830	15	68,211,555	1055	3.17E-06	905	2.41E-04	150	1.42E-01	713	1.87E-03	342	1.40E-03
rs2114719	15	68,720,392	1106	4.15E-07	949	2.97E-05	157	1.93E-02	760	5.56E-05	346	1.98E-02
rs2162555	15	68,720,626	1095	5.68E-07	940	3.74E-05	155	2.38E-02	750	4.62E-05	345	2.38E-02
rs6494886	15	68,720,785	1092	3.87E-07	938	1.50E-05	154	4.28E-02	750	6.07E-05	342	2.58E-02
rs2162556	15	68,723,492	1106	4.15E-07	949	2.97E-05	157	1.93E-02	760	5.56E-05	346	1.98E-02
rs1991088	15	68,791,504	1097	1.18E-06	941	1.72E-04	156	1.64E-03	753	3.87E-04	344	5.35E-03
rs1477439	15	68,821,634	1101	5.34E-06	945	1.18E-03	156	9.70E-03	757	4.63E-03	344	5.08E-04
rs4777305	15	68,832,522	1100	1.47E-06	944	1.60E-04	156	3.22E-03	754	6.59E-04	346	4.03E-03
rs11633212	15	69,387,305	1103	3.80E-06	946	5.33E-04	157	7.29E-05	757	1.22E-04	346	2.31E-02
rs17786786	15	69,395,673	1100	4.23E-08	944	1.28E-05	156	7.28E-05	757	1.08E-05	343	1.09E-02
rs6494904	15	69,396,576	1105	1.43E-08	948	3.64E-06	157	1.57E-04	759	3.23E-06	346	9.91E-03
rs11855326	15	69,397,889	1104	2.47E-08	947	6.12E-06	157	1.57E-04	758	6.08E-06	346	9.91E-03
rs1837762	15	69,399,357	1104	5.65E-08	947	5.42E-06	157	2.36E-02	758	4.17E-05	346	1.59E-02
rs11858540	15	69,409,840	1106	2.98E-07	949	3.44E-05	157	1.26E-02	760	2.05E-04	346	2.12E-02
rs1441361	15	69,412,176	1105	2.76E-07	948	3.06E-05	157	1.26E-02	759	1.95E-04	346	2.12E-02
rs1568010	15	69,455,566	1102	7.56E-06	946	3.10E-04	156	1.45E-01	757	3.08E-05	345	1.15E-01
rs11858454	15	69,456,169	1106	5.26E-06	949	2.26E-04	157	1.38E-01	760	2.87E-05	346	1.04E-01
rs8033889	15	69,467,134	1103	2.31E-07	946	3.56E-05	157	1.08E-03	757	1.89E-05	346	2.07E-03
rs4531689	15	69,476,033	1104	4.77E-06	947	3.87E-04	157	1.05E-01	759	5.60E-05	345	4.50E-02
rs4288952	15	69,477,937	1099	4.58E-06	942	2.60E-04	157	1.03E-01	755	3.51E-05	344	8.37E-02

rs12441227	15	69,483,940	1091	3.38E-09	36	2.79E-06	155	2.05E-03	746	4.70E-06	345	5.86E-04
rs712046	17	31,382,410	1104	3.20E-07	947	7.23E-05	157	4.37E-02	759	6.73E-05	345	6.27E-03
rs854679	17	31,382,952	1097	3.40E-07	941	5.66E-05	156	6.64E-02	751	6.21E-05	346	7.38E-03
rs854674	17	31,384,085	1098	6.77E-07	941	9.55E-05	157	5.44E-02	752	1.39E-04	346	6.92E-03
rs2017854	17	62,918,483	1105	2.58E-06	948	3.87E-05	157	1.48E-03	759	1.63E-05	346	1.19E-02
rs2835345	21	36,723,304	1103	8.29E-06	947	1.92E-04	156	3.39E-03	758	2.45E-03	345	5.70E-03

Table E5. Evidence for associations with lung function in the Hutterites for the 27 previously reported lung function associated loci. If the reported SNP was not genotyped in the Hutterites, a surrogate SNP with the strongest LD to the reported SNP and the amount of LD in HapMap (r^2) are shown. One SNP, rs12447804, did not have any surrogate SNPs in the Hutterites. Other SNPs at the same locus with $P < 0.01$ in the Hutterites are shown in the last column. SNPs replicated at $P < 0.05$ are shown in bold font.

Chr.	NCBI36 Position	Reported SNP	Reported Locus	Reported phenotype	Tested SNP	NCBI36 Position	HapMap r^2	FEV_1/FVC *P*	FEV_1 *P*	FVC *P*	Other SNPs at Locus with *P* < 0.01
1	17,051,981	rs2284746	*MFAP2*	FEV_1/FVC	rs7545518	17,374,742	0.574	8.25E-01	9.74E-01	6.60E-01	
1	215,248,463	rs993925	*TGFB2*	FEV_1/FVC	rs642836	219,023,654	0.203	5.54E-01	4.65E-01	1.78E-01	rs1018040 (9.29E-03, FVC)
2	218,508,660	rs2571445	*TNS1*	FEV_1	rs3796028	218,695,102	0.530	7.22E-01	1.13E-01	9.09E-02	
2	229,336,434	rs1435867	*PID1*	FEV_1/FVC	rs373 2192	229,592,304	1	5.18E-02	1.33E-01	5.11E-01	
	229,328,008	rs10498230	*PID1*	FEV_1/FVC	rs10498230	229,328,008	1	5.51E-01	5.01E-01	6.96E-01	
2	**239,613,402**	**rs12477314**	***HDAC4***	**FEV_1/FVC**	**rs12712295**	**239,914,718**	**0.281**	**3.04E-02**	**4.59E-01**	**7.20E-01**	**rs10186131 (5.27E-03, FEV_1/FVC)**
3	**25,495,586**	**rs1529672**	***RARB***	**FEV_1/FVC**	**rs1153582**	**25,543,275**	**0.928**	**1.37E-02**	**7.66E-01**	**3.31E-01**	**rs2116703 (2.23E-03, FEV_1)**
3	**170,782,921**	**rs1344555**	***MECOM***	**FEV_1**	**rs10513678**	**169,312,833**	**0.504**	**5.77E-03**	**5.57E-01**	**3.76E-02**	**rs6444855 (3.68E-04, FVC)**
4	90,226,510	rs2869967	*FAM13A*	FEV_1/FVC	rs6849143	89,928,489	0.743	4.91E-01	6.75E-01	7.72E-01	
	90,134,259	rs6830970	*FAM13A*	FEV_1/FVC	rs6852928	89,926,193	0.468	5.87E-01	8.17E-01	6.36E-01	
4	**107,046,508**	**rs10516526**	***FLJ20184-INTS12-GSTCD-NPNT***	**FEV_1**	**rs11726124**	**106,766,496**	**1**	**6.52E-01**	**1.23E-02**	**7.62E-02**	
	107,165,711	**rs17331332**	***FLJ20184-INTS12-GSTCD-NPNT***	**FEV_1**	**rs7693333**	**107,047,594**	**0.004**	**7.30E-01**	**3.85E-02**	**2.85E-01**	
	107,154,433	rs17036341	*FLJ20184-INTS12-GSTCD-NPNT*	FEV_1	rs10021819	106,895,614	0.118	1.05E-01	9.86E-02	5.15E-01	
	106,976,744	**rs11727189**	***FLJ20184-INTS12-***	**FEV_1**	**rs11097903**	**106,866,077**	**0.004**	**5.79E-01**	**1.56E-01**	**1.53E-02**	

			GSTCD-NPNT								
	106,951,178	rs17036090	*FLJ20184-INTS12-GSTCD-NPNT*	FEV_1	rs10470990	106,821,578	0.159	7.16E-01	3.81E-01	7.08E-02	
	106,920,983	rs17036052	*FLJ20184-INTS12-GSTCD-NPNT*	FEV_1	rs17036076	106,575,269	0.702	2.43E-01	1.67E-02	1.96E-01	
	106,889,450	**rs17035960**	***FLJ20184-INTS12-GSTCD-NPNT***	**FEV_1**	**rs17036090**	**106,593,574**	**1**	**2.43E-01**	**1.60E-02**	**1.89E-01**	
	107,087,537	rs11097901	*FLJ20184-INTS12-GSTCD-NPNT*	FEV_1	rs11728716	106,755,996	1	6.12E-01	6.00E-02	2.49E-01	
	107,113,600	**rs11728716**	***FLJ20184-INTS12-GSTCD-NPNT***	**FEV_1**	**rs11726124**	**106,766,496**	**1**	**6.52E-01**	**1.23E-02**	**7.62E-02**	
4	**145,793,929**	**rs12504628**	***HHIP***	**FEV_1/FVC, FEV_1**	**rs13147758**	**145,460,230**	**0.965**	**2.46E-02**	**7.28E-01**	**5.27E-01**	
	145,843,343	**rs1980057**	***HHIP***	**FEV_1/FVC**	**rs1980057**	**145,843,343**	**1**	**2.46E-02**	**7.28E-01**	**5.27E-01**	
	145,792,189	**rs1032295**	***HHIP***	**FEV_1/FVC**	**rs13147758**	**145,460,230**	**0.743**	**2.46E-02**	**7.28E-01**	**5.27E-01**	
5	95,062,456	rs153916	*SPATA9*	FEV_1/FVC	rs153916	95,062,456	1	2.50E-01	6.47E-01	3.19E-01	
5	147,822,546	rs11168048	*HTR4*	FEV_1/FVC	rs7735184	147,822,546	0.930	5.20E-01	2.55E-01	3.36E-01	rs6861078 (2.94E-03, FEV_1)
	147,824,585	rs7735184	*HTR4*	FEV_1/FVC	rs7735184	147,824,585	1	5.20E-01	2.55E-01	3.36E-01	
	147,826,008	rs3995090	*HTR4*	FEV_1	rs3995090	147,826,008	1	9.3E-01	1.38E-01	2.50E-01	
	147,826,900	rs6889822	*HTR4*	FEV_1	rs6889822	147,826,900	1	4.36E-01	3.3E-01	4.33E-01	
5	156,864,954	rs2277027	*ADAM19*	FEV_1/FVC	rs1422795	156,936,364	1	7.83E-01	4.06E-01	2.02E-01	rs9313633 (3.07E-03, FVC)
	156,868,942	rs1422795	*ADAM19*	FEV_1/FVC	rs1422795	156,868,942	1	7.83E-01	4.06E-01	2.02E-01	
6	28,430,275	rs6903823	*ZKSCAN3/ZNF323*	FEV_1	rs6922111	28,325,308	0.945	7.46E-01	4.97E-01	2.98E-01	
6	31,676,448	rs2857595	*NCR3*	FEV_1/FVC	rs2857595	31,676,448	1	6.17E-01	9.31E-01	7.84E-01	
6	32,259,421	rs2070600	*PPT2-AGER-NOTCH4*	FEV_1/FVC	rs206015	32,182,759	0.649	8.48E-01	2.31E-01	1.87E-01	
	32,232,402	**rs10947233**	***PPT2-AGER-NOTCH4***	**FEV_1/FVC**	**rs10947233**	**32,232,402**	**1**	**2.42E-01**	**1.45E-01**	**8.64E-03**	
6	**109,374,743**	**rs2798641**	***ARMC2***	**FEV_1/FVC**	**rs2798641**	**109,374,743**		**2.22E-03**	**8.37E-01**	**2.15E-01**	**rs6904998 (3.25E-03, FVC)**
6	142,792,209	rs3817928	*GPR126*	FEV_1/FVC	rs6906468	142,769,386	1	1.59E-01	6.80E-01	8.07E-01	
	142,818,757	rs7776375	*GPR126*	FEV_1/FVC	rs595184	143,012,314	0.147	4.47E-01	7.77E-01	8.55E-01	
	142,748,826	rs6937121	*GPR126*	FEV_1/FVC	rs6937121	142,748,826	1	1.60E-01	6.47E-01	2.88E-01	

	142,733,242	rs11155242	*GPR126*	FEV_1/FVC	rs6906468	142,769,386	1	1.59E-01	6.80E-01	8.07E-01	
9	95,310,563	rs16909898	*PTCH1*	FEV_1/FVC	rs10512249	98,256,309	1	3.00E-01	4.54E-01	3.29E-01	
	95,335,864	rs10512249	*PTCH1*	FEV_1/FVC	rs10512249	95,335,864	1	3.00E-01	4.54E-01	3.29E-01	
10	12,317,998	rs7068966	*CDC123*	FEV_1/FVC, FEV_1	rs7068966	12,317,998	1	5.98E-01	8.57E-01	7.36E-01	
10	**77,985,230**	**rs11001819**	***C10orf11***	**FEV_1**	**rs2256413**	**78,315,334**	**0.755**	**4.67E-04**	**3.62E-01**	**5.40E-01**	**rs2637266 (2.00E-06, FEV_1/FVC)**
12	55,813,550	rs11172113	*LRP1*	FEV_1/FVC	rs1466535	57,534,470	0.721	5.31E-01	5.70E-02	5.26E-02	
12	94,773,896	rs1036429	*CCDC38*	FEV_1/FVC	rs4762637	96,282,655	0.691	4.79E-01	9.81E-01	3.41E-01	
15	**69,432,174**	**rs12899618**	***THSD4***	**FEV_1/FVC**	**rs12102112**	**71,655,735**	**1**	**3.54E-04**	**8.39E-01**	**1.37E-01**	**rs12441227 (3.38E-09, FEV_1/FVC; 2.99E-04, FEV_1)**
16	56,632,783	rs12447804*	*MMP15*	FEV_1/FVC	- *			- *	- *	- *	
16	73,947,817	rs2865531	*CFDP1*	FEV_1/FVC	rs12444589	75,454,404	1	1.96E-01	7.80E-02	3.13E-01	rs10871308 (5.07E-03, FEV_1)
21	34,574,109	rs9978142	*KCNE2*	FEV_1/FVC	rs10470171	35,652,644	0.857	5.26E-01	8.64E-01	9.41E-01	rs2834455 (8.53E-03, FEV_1/FVC)

*HapMap linkage disequilibrium data is not available for rs12447804, and therefore, no surrogate marker has been selected for rs12447804.

Table E6. 80 SNPs that best predicted FEV_1/FVC in the Hutterites, sorted by the chromosome location. P_{GWAS} is the *P*-value from the FEV_1/FVC GWAS in the Hutterites; Beta (SE) is that of the predictive SNP in the regression model for the 865 Hutterites; and P_{GRAIL} is the region's *P*-value given by GRAIL.

SNP	Chr	NCBI36 Position	P_{GWAS}	Beta (SE)	P_{GRAIL}	Implicated Gene
rs6694986	1p13.3	107631201	4.0E-04	0.090 (0.049)	0.340	*NTNG1*
rs17509160	1p13.3	107656536	6.7E-05	0.074 (0.077)	0.340	*NTNG1*
rs1277216	1p13.3	109160754	4.7E-04	0.105 (0.048)	0.961	*STXBP3*
rs6689641	1p13.3	110521923	7.1E-04	0.090 (0.051)	0.756	*SLC6A17*
rs6662186	1q23.3	163531357	1.2E-04	0.092 (0.077)	0.250	*LMX1A*
rs11887626	2p16.3	47709832	1.4E-04	0.137 (0.062)	0.737	*MSH2*
rs702891	2p14	65611954	4.6E-04	-0.015 (0.049)	0.242	*SPRED2*
rs6733029	2p14	68287661	3.7E-04	0.057 (0.046)	0.516	*PNO1*
rs2707549	2q14.3	124120027	2.3E-04	0.040 (0.047)	N/A	
rs6720935	2q21.2	132882030	6.9E-04	0.067 (0.050)	0.758	*LOC339742*
rs16823807	2q23.3	153146906	9.2E-05	0.044 (0.088)	0.489	*FMNL2*
rs4342060	3q22.3	138698510	7.6E-04	0.050 (0.059)	0.363	*SOX14*
rs3851374	3q26.2	170184342	7.0E-04	-0.102 (0.048)	0.089	*EVI1*
rs11922608	3q27.3	188719180	5.4E-04	0.090 (0.069)	0.482	*SST*
rs10517456	4p14	37631127	9.0E-04	0.046 (0.051)	0.971	*PTTG2*
rs1984960	4p14	37644419	3.0E-04	0.175 (0.080)	0.971	*PTTG2*
rs12512633	4q28.1	124506365	5.2E-04	-0.115 (0.052)	0.149	*SPRY1*
rs6858195	4q31.21	144909047	3.1E-04	0.076 (0.046)	0.978	*GYPE*
rs10045757	5p14.2	23306226	1.0E-03	0.094 (0.059)	0.423	*LOC391771*
rs12659895	5p14.1	27801997	6.4E-04	-0.022 (0.057)	N/A	
rs245610	5q34	162032345	8.9E-04	-0.134 (0.083)	N/A	
rs9460984	6p22.2	24355227	5.6E-05	0.144 (0.059)	0.412	*DCDC2*
rs9368881	6p21.31	35742266	3.5E-04	-0.061 (0.047)	0.641	*C6orf81*
rs4839801	6q16.3	102353321	9.6E-04	0.004 (0.052)	0.777	*GRIK2*
rs1149309	6q21	105856616	4.9E-05	0.031 (0.067)	0.574	*PREP*
rs10872028	6q21	109420421	2.7E-04	-0.055 (0.060)	0.256	*ARMC2*

rs10872428	6q23.3	135533565	4.4E-04	0.207 (0.057)	0.324	*MYB*
rs9389370	6q23.3	136472958	5.4E-04	-0.072 (0.044)	0.620	*PDE7B*
rs4092400	8p23.2	2371110	9.9E-04	0.065 (0.048)	0.616	*MYOM2*
rs974120	8p23.2	2634025	3.2E-04	0.038 (0.079)	0.937	*CSMD1*
rs2921026	8p23.1	8384658	6.1E-04	-0.133 (0.046)	0.001	*DEFB107A*
rs10107668	8p12	33643721	8.0E-04	0.038 (0.048)	0.208	*DUSP26*
rs11779911	8p11.21	40301135	7.0E-04	-0.173 (0.049)	0.905	*ZMAT4*
rs7001967	8q21.13	83905913	8.1E-04	0.189 (0.079)	N/A	
rs10955074	8q21.3	87925578	9.6E-04	-0.045 (0.045)	0.680	*CNGB3*
rs1283720	8q23.1	108541504	5.2E-04	-0.099 (0.048)	0.392	*ANGPT1*
rs9886419	8q24.21	129353533	7.1E-04	-0.119 (0.050)	N/A	
rs10810557	9p22.3	16326250	3.4E-04	0.077 (0.044)	0.648	*BNC2*
rs3843935	9p13.3	33777871	9.0E-04	0.029 (0.048)	0.573	*PRSS3*
rs2306183	9q22.31	95092000	9.7E-04	-0.118 (0.045)	0.816	*PHF2*
rs10759765	9q22.33	99347314	4.2E-05	-0.065 (0.048)	0.261	*TMOD1*
rs1570846	10q11.21	43776486	7.1E-04	-0.139 (0.055)	0.037	*CXCL12*
rs2637261	10q22.3	77990599	7.5E-06	0.044 (0.044)	0.766	*KCNMA1*
rs1010006	10q24.2	99562286	4.5E-04	0.051 (0.046)	0.662	*ANKRD2*
rs7963902	12p13.32	4988938	1.9E-04	0.090 (0.043)	0.932	*KCNA6*
rs3925064	12p12.1	23985031	4.2E-04	-0.099 (0.048)	0.271	*SOX5*
rs7968811	12p12.1	24428104	2.8E-04	-0.021 (0.045)	0.271	*SOX5*
rs11050428	12p12.1	29823051	2.2E-04	-0.112 (0.065)	0.818	*TMTC1*
rs1829717	12q21.31	80433224	7.8E-05	0.009 (0.048)	0.899	*PPFIA2*
rs2056218	12q21.31	82056671	4.5E-04	0.147 (0.048)	0.903	*TMTC2*
rs879703	12q22	92946123	2.4E-04	0.049 (0.047)	0.467	*CRADD*
rs7134063	12q23.3	106723461	4.4E-05	0.083 (0.047)	0.167	*PWP1*
rs2329247	13q31.1	82160171	8.0E-04	0.055 (0.077)	N/A	
rs9322855	14q11.2	20223139	7.6E-04	-0.048 (0.046)	0.171	*RNASE4*
rs8016448	14q24.3	72961640	5.9E-04	-0.071 (0.055)	0.316	*C14orf169*
rs2180080	14q32.13	93560454	7.2E-04	-0.132 (0.067)	0.213	*OTUB2*
rs2033785	15q22.33	65228920	2.9E-04	0.044 (0.057)	0.262	*SMAD3*
rs11636597	15q23	68208095	1.5E-05	0.117 (0.059)	0.642	*TLE3*
rs12907875	15q23	68217654	4.6E-04	-0.024 (0.054)	0.642	*TLE3*
rs6494886	15q23	68720785	3.9E-07	-0.018 (0.098)	0.557	*UACA*
rs1477439	15q23	68821634	5.3E-06	0.110 (0.071)	0.557	*UACA*

rs6494904	15q23	69396576	1.4E-08	-0.016 (0.069)	0.739	*THSD4*
rs12592370	15q24.1	72098742	4.5E-04	-0.027 (0.065)	0.738	*PML*
rs1550434	15q24.1	72118264	2.0E-05	-0.067 (0.057)	0.738	*PML*
rs6495126	15q24.1	72962079	8.0E-04	-0.060 (0.056)	0.976	*RPP25*
rs7171364	15q25.3	83803031	3.4E-04	0.180 (0.064)	0.367	*PDE8A*
rs12919417	16q22.3	70137212	3.2E-04	0.043 (0.068)	0.345	*KIAA0174*
rs707236	16q23.3	82360661	6.3E-04	0.143 (0.045)	0.910	*CDH13*
rs4783102	16q24.1	83535549	1.4E-04	-0.106 (0.054)	0.687	*USP10*
rs7216399	17p11.2	16797303	6.0E-04	-0.065 (0.054)	0.043	*TNFRSF13B*
rs8080953	17p11.2	19381812	1.0E-03	-0.233 (0.100)	0.748	*ZNF179*
rs225207	17q11.2	27918837	4.9E-05	-0.096 (0.065)	0.980	*MYO1D*
rs8064367	17q12	29496973	9.1E-04	-0.018 (0.062)	0.521	*ACCN1*
rs854679	17q12	31382952	3.4E-07	-0.049 (0.059)	0.020	*CCL18*
rs2074158	17q21.2	37510689	8.8E-05	-0.132 (0.083)	0.486	*HSPB9*
rs16950093	17q21.33	46995183	5.6E-04	-0.085 (0.054)	0.205	*UTP18*
rs2017854	17q24.2	62918483	2.6E-06	-0.097 (0.048)	0.828	*PITPNC1*
rs365548	20p13	185618	5.6E-04	0.003 (0.046)	0.001	*DEFB129, RP5-1103G7.6*
rs4815436	20p11.21	25521423	9.4E-04	0.181 (0.069)	0.001	*DEFB115, DEFB116, DEFB123, DEFB124*
rs2835345	21q22.13	36723304	8.3E-06	-0.108 (0.055)	0.900	*CHAF1B*

Figure E1. Measures of lung function in the Hutterites. Distributions of standardized values of **(a)** FEV_1, **(b)** FVC and **(c)** FEV_1/FVC by age and sex (blue, male; orange, female). Correlations between measures of lung function: **(d)** FEV_1 and FVC, **(e)** FEV_1 and FEV_1/FVC and **(f)** FVC and FEV_1/FVC. The linear regression line is shown in red.

Figure E2. Regional association plots for the three most significant associations in the GWAS of FEV_1/FVC in the Hutterites: *THSD4-UACA-TLE3* locus on chromosome 15, *CCL23-CCL18* locus on chromosome 17q12, and *C10orf11* locus on chromosome 10q22.3 in the full sample **(a-c, respectively)** and in sub-analyses excluding asthmatics **(d-f, respectively)**, *THSD4-UACA-TLE3* locus on chromosome 15, *CCL23-CCL18* locus on chromosome 17q12, and *C10orf11* locus on chromosome 10q22.3 in sub-analysis excluding asthmatics **(d-f)**. In each plot the most significantly associated SNP is shown as a large blue diamond. The colors of the other SNPs reflect the linkage disequilibrium with that SNP based on r^2 values in the Hutterites (red, $r^2 \geq 0.8$; orange, $0.5 \leq r^2 < 0.8$; yellow, $0.2 \leq r^2 < 0.5$; white, $r^2 < 0.2$).

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