

Identification of rare sequence variation underlying heritable pulmonary arterial hypertension.

Gräf *et al.*

Supplementary Information

Supplementary Table 1 Patient demographics and clinical characteristics by diagnostic group. Drug and anorexigen group (3 dasatinib exposures, 47 anorexigen exposures, 12 amphetamine exposures); 2 patients had multiple exposures. mPAP - mean pulmonary artery pressure, PCWP - pulmonary capillary wedge pressure, CO - cardiac output, KCO - transfer coefficient for carbon monoxide. Data presented as median [IQR] unless stated.

Group	n	Number with a family history of PAH [%]	Number with a <i>BMPR2</i> mutation [%]	WGS inferred ethnicity [% European]	Age at diagnosis (years)	Gender: number female [%]	mPAP (mmHg)	PCWP (mmHg)	CO (L/min)	Functional class 1/2/3/4 [%]	KCO (% predicted)
IPAH	908	0 [0.0%]	111 [12.2%]	806 [88.8%]	49.7 [37.0 - 64.6]	624 [68.7%]	53 [44.0 - 61.0]	10 [7 - 12]	4.0 [3.2 - 5.0]	18 [2.3%] / 165 [21.1%] / 506 [64.8%] / 92 [11.8%]	72.0 [51.6 - 87.0]
HPAH	58	58 [100.0%]	44 [75.9%]	55 [94.8%]	38.1 [30.4 - 53.5]	34 [58.6%]	54 [48.0 - 64.5]	8 [6 - 11]	3.8 [2.8 - 4.8]	0 [0.0%] / 14 [24.1%] / 37 [63.8%] / 7 [12.1%]	75.5 [69.0 - 85.0]
Drug and anorexigen exposed	60	0 [0.0%]	5 [8.3%]	53 [88.3%]	52.4 [40.6 - 60.6]	52 [86.7%]	53 [43.8 - 60.0]	9 [6.5 - 12]	4.2 [3.5 - 5.2]	0 [0.0%] / 10 [17.5%] / 40 [70.2%] / 7 [12.3%]	79.0 [64.0 - 92.6]
PVOD/PCH	22	2 [9.1%]	0 [0.0%]	20 [90.9%]	52.2 [39.7 - 68.1]	13 [59.1%]	48 [41.0 - 57.0]	10.5 [8 - 12]	3.5 [2.6 - 4.4]	1 [4.8%] / 2 [9.5%] / 14 [66.7%] / 4 [19%]	38.0 [29.6 - 47.0]

Supplementary Table 2 Copy number deletions identified in *BMPR2* (ENST00000374580) in this study. Previously in Girerd *et al.*¹ reported deletions are marked with asterisks.

Combined (quality based)						MANTA		CANVAS	
Chr	start	end	HGVS (genomic)	HGVS (cDNA)	EXON	start	end	start	end
2	201106312	204901853	chr2:g.201106312_204901853del	c.-2135886_*1477184del	1-13/13	201106432	204901548	201106312	204901853
2	201822159	205450144	chr2:g.201822159_205450144del	c.-1420039_*2025475del	1-13/13	201822961	205450144	201822159	205449696
2	202772559	205218660	chr2:g.202772559_205218660del	c.-469639_*1793991del	1-13/13	202772963	205218660	202772559	205218576
2	202999184	203486009	chr2:g.202999184_203486009del	c.-243014_*61340del	1-13/13	202999402	203485750	202999184	203486009
2	203223399	203248850	chr2:g.203223399_203248850del	c.-18799_76+6577del	1/13	203223399	203248060	203223420	203248850
2	203225712	203256467	chr2:g.203225712_203256467del	c.-16486_76+14194del	1/13	203226401	203255921	203225712	203256467 *
2	203228120	203905293	chr2:g.203228120_203905293del	c.-14078_*480624del	1-13/13	203228906	203905293	203228120	203905004
2	203234119	203242446	chr2:g.203234119_203242446del	c.-8079_76+173del	1/13	203235908	203242364	203234119	203242446
2	203325317	203332529	chr2:g.203325317_203332529del	c.77-4215_418+117del	2-3/13	203325958	203332529	203325317	203332065
2	203327217	203331596	chr2:g.203327217_203331596del	c.77-2315_248-646del	2/13	203327217	203331596	203327390	203331395 *
2	203328407	203332511	chr2:g.203328407_203332511del	c.77-1125_418+99del	2-3/13	203329838	203332511	203328407	203332252
2	203329730	203335416	chr2:g.203329730_203335416del	c.247+28_418+3004del	3/13	203330505	203335416	203329730	203334949
2	203339329	203392988	chr2:g.203339329_203392988del	c.418+6917_968-2529del	4-7/13	203339329	203392988	203339531	203391830
2	203341496	203422058	chr2:g.203341496_203422058del	c.418+9084_2866+804del	4-12/13	203342249	203422058	203341496	203421779
2	203372762	203382260	chr2:g.203372762_203382260del	c.419-5680_622-1285del	4-5/13	203373003	203382260	203372762	203381787
2	203379275	203389196	chr2:g.203379275_203389196del	c.530-336_967+4272del	5-7/13	203380130	203388919	203379275	203389196
2	203383741	203388057	chr2:g.203383741_203388057del	c.818_967+3133del	6-7/13	203384088	203387879	203383741	203388057
2	203386133	203445336	chr2:g.203386133_203445336del	c.967+1209_*20667del	8-13/13	203387039	203444732	203386133	203445336
2	203403086	203415133	chr2:g.203403086_203415133del	c.1277-3948_1414-2306del	10/13	203403129	203415088	203403086	203415133
2	203406092	203412701	chr2:g.203406092_203412701del	c.1277-942_1414-4738del	10/13	203406727	203412701	203406092	203412028 *
2	203406461	203414964	chr2:g.203406461_203414964del	c.1277-573_1414-2475del	10/13	203406613	203414964	203406461	203414695 *
2	203411230	203418627	chr2:g.203411230_203418627del	c.1413+4060_1586+1016del	11/13	203411808	203418627	203411230	203418411
2	203421702	203434798	chr2:g.203421702_203434798del	c.2866+448_*10129del	13/13	203422398	203434798	203421702	203434395

Supplementary Table 3 Summary of clinical characteristics in patients with mutations in **(a)** the previously reported PAH genes and **(b)** the novel PAH genes identified in this study. FHx - Family history; mPAP - mean pulmonary artery pressure; PCWP - pulmonary capillary wedge pressure; KCO - transfer coefficient for carbon monoxide.

Gene	Number of patients	FHx of PH [%]	WGS inferred ethnicity: European [%]	Age at diagnosis (years)	Gender: female [%]	mPAP (mmHg)	PCWP (mmHg)	Cardiac output (L/min)	Functional class 1 / 2 / 3 / 4 [%]	KCO (% predicted)
(a) Previously reported PAH disease genes.										
No mutation	802	9 [1.1%]	713 [88.9%]	52.6 [39.1 - 66.5]	562 [70.1%]	51 [42.0 - 60.0]	10 [7.0 - 12.0]	4.1 [3.3 - 5.2]	16 [2.3%] / 142 [20.5%] / 459 [66.2%] / 76 [11.0%]	69.0 [47.2 - 84.0]
BMPR2*	160	44 [27.5%]	149 [93.1%]	39.3 [32.0 - 51.2]	106 [66.2%]	57 [51.0 - 68.2]	10 [7.0 - 12.0]	3.3 [2.7 - 4.0]	2 [1.3%] / 33 [21.9%] / 90 [59.6%] / 26 [17.2%]	82.0 [73.5 - 92.5]
EIF2AK4	14	2 [14.3%]	7 [50.0%]	31.2 [23.4 - 38.6]	7 [50.0%]	50.5 [41.8 - 59.2]	10.5 [7.2 - 12.0]	4.5 [3.0 - 4.9]	0 [0.0%] / 2 [14.3%] / 9 [64.3%] / 3 [21.4%]	33.0 [29.1 - 33.0]
TBX4	14	1 [7.1%]	12 [85.7%]	56.4 [39.9 - 71.8]	9 [64.3%]	58 [48.0 - 67.0]	11 [7.5 - 13.5]	3.8 [2.9 - 4.1]	0 [0.0%] / 2 [18.2%] / 7 [63.6%] / 2 [18.2%]	89.7 [83.3 - 91.8]
ACVRL1	9	1 [11.1%]	9 [100.0%]	46.9 [44.8 - 57.7]	8 [88.9%]	54 [42.8 - 58.5]	11.5 [10.2 - 12.8]	4.6 [3.5 - 5.0]	0 [0.0%] / 4 [57.1%] / 3 [42.9%] / 0 [0.0%]	72.1 [60.5 - 77.3]
ENG	5	0 [0.0%]	4 [80.0%]	42.2 [35.7 - 47.2]	4 [80.0%]	55 [52.0 - 58.0]	6.5 [0.8 - 13.5]	3.8 [3.5 - 4.2]	0 [0.0%] / 0 [0.0%] / 3 [75%] / 1 [25%]	47.0 [46.0 - 51.0]
KCNK3	4	0 [0.0%]	4 [100.0%]	26.8 [25.1 - 38.5]	2 [50.0%]	48 [43.5 - 63.0]	7.5 [6.2 - 8.8]	3.8 [2.3 - 5.1]	0 [0.0%] / 1 [33.3%] / 2 [66.7%] / 0 [0.0%]	85.7 [85.7 - 85.7]
SMAD9	3	0 [0.0%]	2 [66.7%]	51.3 [39.8 - 56.2]	2 [66.7%]	46 [43.0 - 55.0]	11 [9.0 - 12.0]	5.0 [4.7 - 5.0]	0 [0.0%] / 0 [0.0%] / 3 [100%] / 0 [0.0%]	92.5 [81.2 - 103.8]
(b) Novel PAH disease genes.										
ATP13A3	11	0 [0.0%]	9 [81.8%]	47.5 [41.5 - 58.4]	10 [90.9%]	57 [49.5 - 62.0]	10.5 [7.5 - 16.0]	3.1 [2.6 - 4.6]	0 [0.0%] / 0 [0.0%] / 8 [88.9%] / 1 [11.1%]	88.5 [82.2 - 91.4]
SOX17	9	0 [0.0%]	9 [100.0%]	27.3 [21.4 - 40.2]	5 [55.6%]	58 [57.0 - 68.0]	10 [7.0 - 11.5]	4.1 [3.8 - 5.1]	1 [14.3%] / 1 [14.3%] / 5 [71.4%] / 0 [0.0%]	80.9 [78.3 - 83.5]
AQP1	9	2 [22.2%]	9 [100.0%]	32.2 [25.3 - 46.2]	4 [44.4%]	61.5 [48.0 - 68.2]	8 [7.5 - 8.0]	4.7 [4.3 - 5.3]	0 [0.0%] / 4 [50%] / 3 [37.5%] / 1 [12.5%]	81 [78.2 - 91.0]
GDF2	8	1 [12.5%]	7 [87.5%]	49.9 [45.0 - 53.8]	4 [50.0%]	46 [43.2 - 50.5]	8 [6.0 - 9.5]	4.8 [3.7 - 4.9]	0 [0.0%] / 2 [28.6%] / 5 [71.4%] / 0 [0.0%]	70.0 [69.0 - 71.1]

* This group includes one case with deleterious variant in *BMPR2* and *SMAD9*.

Supplementary Table 4 Case-control analysis of variants in previously reported PAH genes. Only protein-coding variants were considered after standard filtering and variants shared between cases and controls and variants of uncertain significance in cases have been removed. *P* values have been adjusted for false discovery rate.

Gene	Number of cases	Number of controls	Frequency of cases	Frequency of controls	<i>P</i>	Adj. <i>P</i>
<i>BMPR2</i>	148	20	0.1426	0.0031	7.77E-107	1.01E-105
<i>EIF2AK4</i>	14	0	0.0135	0	1.01E-12	6.59E-12
<i>TBX4</i>	14	15	0.0135	0.0023	9.99E-06	4.33E-05
<i>ACVRL1</i>	9	12	0.0087	0.0019	0.0012	0.0039
<i>ENG</i>	6	16	0.0058	0.0025	0.0759	0.1973
<i>KCNK3</i>	4	13	0.0039	0.0020	0.2057	0.4386
<i>KLF2</i>	3	10	0.0029	0.0016	0.2697	0.4386
<i>SMAD9</i>*	4	15	0.0039	0.0023	0.2699	0.4386
<i>BMPR1B</i>	4	17	0.0039	0.0027	0.3369	0.4867
<i>TOPBP1</i>	5	25	0.0048	0.0039	0.4119	0.5354
<i>CAV1</i>	0	5	0	8.00E-04	1	1
<i>SMAD1</i>	0	10	0	0.0016	1	1
<i>SMAD4</i>	0	8	0	0.0013	1	1

* This group includes one case with deleterious variant in *BMPR2* and *SMAD9*.

Supplementary Table 5 List of top 50 genes from rare protein truncating variant (PTV) case-control analysis, excluding patients carrying variants in previously reported genes. Genes are ranked by *P* value.

Gene	No. of individuals in cases	No. of individuals in controls	Frequency of cases	Frequency of controls	<i>P</i>	adj. <i>P</i>
ATP13A3	6	0	0.00715	0.00000	2.42E-06	0.03505
EVI5	5	1	0.00596	0.00016	0.00011	1
KDR	4	0	0.00477	0.00000	0.00018	1
CAMTA2	7	8	0.00834	0.00125	0.00077	1
RAB36	4	1	0.00477	0.00016	0.00082	1
ERI1	4	1	0.00477	0.00016	0.00082	1
KIF1C	4	1	0.00477	0.00016	0.00082	1
ALG10	4	1	0.00477	0.00016	0.00082	1
PRSS53	4	1	0.00477	0.00016	0.00082	1
ZFP69B	4	1	0.00477	0.00016	0.00082	1
LCAT	4	1	0.00477	0.00016	0.00082	1
COMT	3	0	0.00358	0.00000	0.00156	1
SRM	3	0	0.00358	0.00000	0.00156	1
ZMYM5	3	0	0.00358	0.00000	0.00156	1
FRMD1	3	0	0.00358	0.00000	0.00156	1
CYP3A4	3	0	0.00358	0.00000	0.00156	1
METTL7B	3	0	0.00358	0.00000	0.00156	1
JAG2	3	0	0.00358	0.00000	0.00156	1
FAM151A	5	4	0.00596	0.00063	0.00176	1
TARBP1	6	7	0.00715	0.00110	0.00201	1
HAP1	6	7	0.00715	0.00110	0.00201	1
CDK11A	4	2	0.00477	0.00031	0.00223	1
LILRB5	4	2	0.00477	0.00031	0.00223	1
MYH3	4	2	0.00477	0.00031	0.00223	1
IFIH1	7	12	0.00834	0.00188	0.00397	1
SHC2	4	3	0.00477	0.00047	0.00473	1
ALPPL2	4	3	0.00477	0.00047	0.00473	1
CTSF	4	3	0.00477	0.00047	0.00473	1
SUGCT	4	3	0.00477	0.00047	0.00473	1
ATP6V0A2	4	3	0.00477	0.00047	0.00473	1
EXD3	4	3	0.00477	0.00047	0.00473	1
TFAP2E	3	1	0.00358	0.00016	0.00570	1
PIGT	3	1	0.00358	0.00016	0.00570	1
TMEM62	3	1	0.00358	0.00016	0.00570	1
RHOT2	3	1	0.00358	0.00016	0.00570	1
ENAH	3	1	0.00358	0.00016	0.00570	1
KMT2D	3	1	0.00358	0.00016	0.00570	1
ANTXR1	3	1	0.00358	0.00016	0.00570	1
ZFPM1	3	1	0.00358	0.00016	0.00570	1
RXRΒ	3	1	0.00358	0.00016	0.00570	1
N4BP2L2	3	1	0.00358	0.00016	0.00570	1
SACS	5	8	0.00596	0.00125	0.01208	1
TTC37	5	8	0.00596	0.00125	0.01208	1

<i>COL9A2</i>	3	2	0.00358	0.00031	0.01303	1
<i>UHRF1BP1</i>	3	2	0.00358	0.00031	0.01303	1
<i>PLEKHH3</i>	3	2	0.00358	0.00031	0.01303	1
<i>FMO2</i>	3	2	0.00358	0.00031	0.01303	1
<i>KRT32</i>	3	2	0.00358	0.00031	0.01303	1
<i>CRBN</i>	3	2	0.00358	0.00031	0.01303	1
<i>PCID2</i>	3	2	0.00358	0.00031	0.01303	1

Supplementary Table 6 List of top 50 genes from rare missense variant case-control analysis, excluding patients carrying variants in previously reported genes. Genes are ranked by *P* value.

Gene	No. of individuals in cases	No. of individuals in controls	Frequency of cases	Frequency of controls	<i>P</i>	adj. <i>P</i>
<i>GDF2</i>	11	5	0.01311	0.00078	1.23E-07	0.00233
<i>AQP1</i>	8	4	0.00954	0.00063	1.03E-05	0.19641
<i>OR8U1</i>	14	28	0.01669	0.00439	0.00017	1
<i>CACNB2</i>	12	21	0.01430	0.00329	0.00019	1
<i>ATP13A5</i>	13	25	0.01549	0.00392	0.00021	1
<i>C5orf42</i>	20	55	0.02384	0.00861	0.00025	1
<i>FMO4</i>	9	12	0.01073	0.00188	0.00030	1
<i>C5AR1</i>	6	4	0.00715	0.00063	0.00033	1
<i>FLNA</i>	15	35	0.01788	0.00548	0.00037	1
<i>PIWIL1</i>	8	10	0.00954	0.00157	0.00048	1
<i>MICU3</i>	8	10	0.00954	0.00157	0.00048	1
<i>ALPPL2</i>	8	10	0.00954	0.00157	0.00048	1
<i>LGR4</i>	8	10	0.00954	0.00157	0.00048	1
<i>DOCK8</i>	19	54	0.02265	0.00846	0.00049	1
<i>UNC13D</i>	15	37	0.01788	0.00579	0.00059	1
<i>C3orf20</i>	9	14	0.01073	0.00219	0.00066	1
<i>THNSL2</i>	7	8	0.00834	0.00125	0.00077	1
<i>CDCA7</i>	7	8	0.00834	0.00125	0.00077	1
<i>BTNL8</i>	4	1	0.00477	0.00016	0.00082	1
<i>CRYZ</i>	4	1	0.00477	0.00016	0.00082	1
<i>COL5A2</i>	16	43	0.01907	0.00673	0.00083	1
<i>MYO5A</i>	12	26	0.01430	0.00407	0.00085	1
<i>MYZAP</i>	5	3	0.00596	0.00047	0.00087	1
<i>TBC1D2</i>	9	15	0.01073	0.00235	0.00095	1
<i>ZNF48</i>	10	19	0.01192	0.00298	0.00107	1
<i>CYP4Z1</i>	6	6	0.00715	0.00094	0.00120	1
<i>ZXDB</i>	6	6	0.00715	0.00094	0.00120	1
<i>KRTAP4-11</i>	6	6	0.00715	0.00094	0.00120	1
<i>ZC3H6</i>	9	16	0.01073	0.00251	0.00134	1
<i>MFRP</i>	10	20	0.01192	0.00313	0.00144	1
<i>CACNA1C</i>	11	24	0.01311	0.00376	0.00145	1
<i>SPTBN1</i>	14	37	0.01669	0.00579	0.00152	1
<i>HIST1H3I</i>	3	0	0.00358	0.00000	0.00156	1
<i>NBPF12</i>	3	0	0.00358	0.00000	0.00156	1
<i>CLEC2A</i>	3	0	0.00358	0.00000	0.00156	1
<i>PADI4</i>	8	13	0.00954	0.00204	0.00163	1
<i>DEAF1</i>	8	13	0.00954	0.00204	0.00163	1
<i>NUP43</i>	5	4	0.00596	0.00063	0.00176	1
<i>MAP7D3</i>	5	4	0.00596	0.00063	0.00176	1
<i>CD3E</i>	5	4	0.00596	0.00063	0.00176	1
<i>PTPRC</i>	9	17	0.01073	0.00266	0.00184	1
<i>CD248</i>	9	17	0.01073	0.00266	0.00184	1
<i>ABCF1</i>	9	17	0.01073	0.00266	0.00184	1

<i>ZNF292</i>	14	38	0.01669	0.00595	0.00186	1
<i>KLC3</i>	11	25	0.01311	0.00392	0.00188	1
<i>ZNF343</i>	7	10	0.00834	0.00157	0.00189	1
<i>DLL4</i>	7	10	0.00834	0.00157	0.00189	1
<i>ADC</i>	7	10	0.00834	0.00157	0.00189	1
<i>DENND2D</i>	7	10	0.00834	0.00157	0.00189	1
<i>HOMEZ</i>	7	10	0.00834	0.00157	0.00189	1

Supplementary Table 7 List of top 50 genes from combined rare PTV and missense variant case-control analysis, excluding patients carrying variants in previously reported genes. Genes are ranked by *P* value.

Gene	No. of individuals in cases	No. of individuals in controls	Frequency of cases	Frequency of controls	<i>P</i>	adj. <i>P</i>
<i>GDF2</i>	12	6	0.01430	0.00094	5.33E-08	0.00103
<i>AQP1</i>	9	5	0.01073	0.00078	4.30E-06	0.08294
<i>ALPPL2</i>	12	13	0.01430	0.00204	6.86E-06	0.13246
<i>ATP13A3</i>	11	14	0.01311	0.00219	4.64E-05	0.89511
<i>OR8U1</i>	15	30	0.01788	0.00470	9.92E-05	1
<i>IFT74</i>	11	17	0.01311	0.00266	0.00016	1
<i>FLNA</i>	16	36	0.01907	0.00564	0.00017	1
<i>SOX17</i>	8	9	0.00954	0.00141	0.00030	1
<i>ATP13A5</i>	13	27	0.01549	0.00423	0.00038	1
<i>C3orf20</i>	10	16	0.01192	0.00251	0.00039	1
<i>PIWIL1</i>	8	10	0.00954	0.00157	0.00048	1
<i>DOCK8</i>	20	60	0.02384	0.00940	0.00062	1
<i>C5orf42</i>	21	65	0.02503	0.01018	0.00064	1
<i>RABL3</i>	6	5	0.00715	0.00078	0.00066	1
<i>C5AR1</i>	6	5	0.00715	0.00078	0.00066	1
<i>SPTBN1</i>	15	38	0.01788	0.00595	0.00074	1
<i>SLC9A3R1</i>	8	11	0.00954	0.00172	0.00075	1
<i>CD248</i>	10	18	0.01192	0.00282	0.00078	1
<i>BTNL8</i>	4	1	0.00477	0.00016	0.00082	1
<i>UNC13D</i>	16	43	0.01907	0.00673	0.00083	1
<i>CRTAM</i>	5	3	0.00596	0.00047	0.00087	1
<i>OR13C2</i>	5	3	0.00596	0.00047	0.00087	1
<i>ZNF292</i>	15	39	0.01788	0.00611	0.00091	1
<i>FMO4</i>	9	15	0.01073	0.00235	0.00095	1
<i>CACNB2</i>	14	35	0.01669	0.00548	0.00099	1
<i>MAMDC4</i>	19	58	0.02265	0.00908	0.00100	1
<i>COL5A2</i>	16	44	0.01907	0.00689	0.00101	1
<i>MICU3</i>	8	12	0.00954	0.00188	0.00112	1
<i>IRAK4</i>	8	12	0.00954	0.00188	0.00112	1
<i>LGR4</i>	8	12	0.00954	0.00188	0.00112	1
<i>KRTAP4-11</i>	6	6	0.00715	0.00094	0.00120	1
<i>ICK</i>	7	9	0.00834	0.00141	0.00123	1
<i>HES4</i>	7	9	0.00834	0.00141	0.00123	1
<i>ERMP1</i>	13	32	0.01549	0.00501	0.00133	1
<i>MYO5A</i>	12	28	0.01430	0.00439	0.00141	1
<i>CACNA1C</i>	11	24	0.01311	0.00376	0.00145	1
<i>CACNA1A</i>	24	86	0.02861	0.01347	0.00153	1
<i>OTUB1</i>	3	0	0.00358	0.00000	0.00156	1
<i>NBPF12</i>	3	0	0.00358	0.00000	0.00156	1
<i>ZNF343</i>	8	13	0.00954	0.00204	0.00163	1
<i>NUP43</i>	5	4	0.00596	0.00063	0.00176	1
<i>ZNF561</i>	5	4	0.00596	0.00063	0.00176	1
<i>P2RY14</i>	5	4	0.00596	0.00063	0.00176	1

<i>GALT</i>	5	4	0.00596	0.00063	0.00176	1
<i>DEPDC1</i>	9	17	0.01073	0.00266	0.00184	1
<i>INPP4A</i>	9	17	0.01073	0.00266	0.00184	1
<i>ITIH4</i>	9	17	0.01073	0.00266	0.00184	1
<i>SLC1A7</i>	9	17	0.01073	0.00266	0.00184	1
<i>ZC3H6</i>	9	17	0.01073	0.00266	0.00184	1
<i>TBC1D9B</i>	14	38	0.01669	0.00595	0.00186	1

Supplementary Table 8 List of top 50 genes and *P* values identified by case-control comparison using SKAT-O, excluding carriers of deleterious variants in previously reported genes. Genes are ranked by *P* value.

Ensembl Gene	Gene	Genomic Region	<i>P</i>	adj. <i>P</i>
ENSG00000240583	<i>AQP1</i>	7:30951525-30963244	2.15E-10	4.28E-06
ENSG00000235718	<i>MFRP</i>	11:119212258-119217223	6.52E-10	1.30E-05
ENSG00000164736	<i>SOX17</i>	8:55370699-55372555	3.36E-09	6.69E-05
ENSG00000110881	<i>ASIC1</i>	12:50452550-50475432	5.81E-09	0.00012
ENSG00000187801	<i>ZFP69B</i>	1:40916634-40929261	1.17E-08	0.00023
ENSG00000163286	<i>ALPPL2</i>	2:233271605-233274582	1.53E-08	0.00031
ENSG00000172199	<i>OR8U1</i>	11:56143100-56144029	2.05E-08	0.00041
ENSG00000159377	<i>PSMB4</i>	1:151372064-151374305	2.56E-08	0.00051
ENSG00000128802	<i>GDF2</i>	10:48413578-48416693	3.99E-08	0.00079
ENSG00000168404	<i>MLKL</i>	16:74706402-74729655	4.28E-08	0.00085
ENSG00000110324	<i>IL10RA</i>	11:117857183-117870356	6.14E-08	0.00122
ENSG00000177398	<i>UMODL1</i>	21:43491426-43557730	6.56E-08	0.00131
ENSG00000197405	<i>C5AR1</i>	19:47813153-47824087	1.11E-07	0.00220
ENSG00000141837	<i>CACNA1A</i>	19:13318127-13617038	1.21E-07	0.00240
ENSG00000068366	<i>ACSL4</i>	X:108887258-108926715	1.27E-07	0.00252
ENSG00000257019	<i>OR13C2</i>	9:107366952-107367908	1.34E-07	0.00267
ENSG00000174807	<i>CD248</i>	11:66082225-66084498	1.84E-07	0.00366
ENSG00000113758	<i>DBN1</i>	5:176884434-176899211	2.41E-07	0.00479
ENSG00000004766	<i>CCDC132</i>	7:92861781-92987748	2.83E-07	0.00563
ENSG00000132746	<i>ALDH3B2</i>	11:67430686-67434406	2.97E-07	0.00590
ENSG00000128254	<i>C22orf24</i>	22:32330104-32334052	3.16E-07	0.00628
ENSG00000198755	<i>RPL10A</i>	6:35436212-35438527	3.33E-07	0.00661
ENSG00000101384	<i>JAG1</i>	20:10620146-10654178	3.51E-07	0.00699
ENSG00000138073	<i>PREB</i>	2:27354282-27357289	4.45E-07	0.00885
ENSG00000066056	<i>TIE1</i>	1:43766743-43788393	5.00E-07	0.00995
ENSG00000157240	<i>FZD1</i>	7:90894196-90896139	5.16E-07	0.01025
ENSG00000115705	<i>TPO</i>	2:1418181-1546246	5.49E-07	0.01091
ENSG00000184451	<i>CCR10</i>	17:40831571-40833841	5.71E-07	0.01136
ENSG00000125207	<i>PIWIL1</i>	12:130827137-130856143	6.11E-07	0.01214
ENSG00000183690	<i>EFHC2</i>	X:44008041-44202834	6.13E-07	0.01219
ENSG00000144354	<i>CDCA7</i>	2:174219692-174232392	7.30E-07	0.01451
ENSG00000053501	<i>USE1</i>	19:17326215-17330622	7.44E-07	0.01480
ENSG00000126773	<i>PCNXL4</i>	14:60581431-60600939	7.74E-07	0.01538
ENSG00000188177	<i>ZC3H6</i>	2:113033572-113090065	7.74E-07	0.01539
ENSG00000175785	<i>PRIMA1</i>	14:94187790-94254064	1.02E-06	0.02027
ENSG00000156414	<i>TDRD9</i>	14:104394847-104518419	1.13E-06	0.02249
ENSG00000144895	<i>EIF2A</i>	3:150264590-150301698	1.20E-06	0.02394
ENSG00000076258	<i>FMO4</i>	1:171288965-171310978	1.30E-06	0.02580
ENSG00000092929	<i>UNC13D</i>	17:73824046-73840418	1.45E-06	0.02892
ENSG00000166033	<i>HTRA1</i>	10:124221169-124273875	1.64E-06	0.03266
ENSG00000143862	<i>ARL8A</i>	1:202103595-202113700	1.69E-06	0.03365
ENSG00000005379	<i>BZRAP1</i>	17:56381731-56405281	1.80E-06	0.03576
ENSG00000108950	<i>FAM20A</i>	17:66533618-66596807	1.91E-06	0.03805
ENSG00000131126	<i>TEX101</i>	19:43910657-43922549	2.17E-06	0.04321

ENSG00000140853	<i>NLRC5</i>	16:57054625-57116440	2.31E-06	0.04599
ENSG00000268552	<i>AL109927.1</i>	1:28177085-28177255	2.43E-06	0.04825
ENSG00000163216	<i>SPRR2D</i>	1:153012604-153012822	2.53E-06	0.05039
ENSG00000130382	<i>MLL1</i>	19:6213053-6279795	2.53E-06	0.05040
ENSG00000196782	<i>MAML3</i>	4:140640477-141074481	2.65E-06	0.05268
ENSG00000196911	<i>KPNA5</i>	6:117002498-117053486	2.70E-06	0.05373

Supplementary Table 9 PCR primers for human.

Target	Forward	Reverse
Quantitative RT-PCR		
<i>ACTB</i>	GCACCACACCTTCTACAATGA	GTCATCTTCTCGCGGTTGGC
<i>AQP1</i>	CCAGGTGGAGGAGTATGACCT	GACCCCTTCTATTTGGGCTTCA
<i>ATP13A3</i>	GAAAATAGGCACAGGATCAG	ATTTTACACTATGGTGGGTG
<i>B2M</i>	CTCGCGCTACTCTCTCTTTCT	CATTCTCTGCTGGATGACGTG
<i>HPRT</i>	GCTATAAATTCTTTGCTGACCTGCTG	AATTACTTTTATGTCCCCTGTTGACTGG
<i>SOX17</i>	GGACCGCACGGAATTTGAAC	GGACACCACCGAGGAAATGG
Familial segregation analysis		
<i>Family II (Figure 4a)</i>		
BMPR2ex1	GTGATACGGGCAGGATCAGT	ATTAAGGCGATTTCCTGG
BMPR2ex2	GTCATTCGGATAAGACAAAG	TTAACATACTCCCATGTCC
BMPR2ex3	TAGCTTACACGTA CTCTCAC	CCTGGCTTCAACCTTGAATG
BMPR2ex4	GGGTACAGCCTTTCTAAAGG	GATACTATTGAGGCTGGGTG
BMPR2ex5	GCTGCTAATCTTTCTGCAGC	GAATGAAGTCACTGTTCCAG
BMPR2ex6	CAGAGAGCTGTAGCATTCTG	AAGTGATCCACCTGCCTTAG
BMPR2ex7	TTTGCAAATTCTTTATAAGGATGC	AAAATTTCTGTTGTGAATTTTGA
BMPR2ex8	TGTTCAATAGTCCCTTTTATTCATTG	CACCTGGCCAGTAGATGTTTT
BMPR2ex9	TGTTCTTCAGAAATATGCTACGTTCTC	CTAATTTGCATCCTGCTGCT
BMPR2ex10	GCCTGAAGGGGATGAAAAA	TTGTGGCATTAGGCAACTCC
BMPR2ex11	CATGTGGTAAACTGAAAAGCTCA	TTCTTTGTTGGGTCTCAGTTTCT
BMPR2ex12a	TCAGAGGTGTTAAATTTGGAGAGA	TGAGTGGGTAAAGCAAGCTAGA
BMPR2ex12b	TGAAACCAACAAGCTAGACC	TCTACCTGCCACACCATTCA
BMPR2ex12c	CTTGAACAAGTCGAAACTGGA	TAAATGGCCCCAAAAGACAC
BMPR2ex13	CACCCTCCTGAGACATTGGT	GGGTGCTGACAGGAGGATAA
ACVRL1ex2	CTCTGTGATTTCTCTGGGCA	TACATTCTCCCCAGCTTCTCAA
ACVRL1ex3	AGCTGGGACCACAGTGGCTGA	AGGGCAGGGGCCAAGAAGAT
ACVRL1ex4	AGCTGACCTAGTGGAAAGCTGA	CTGATTCTGCAGTTCCTATCTG
ACVRL1ex5	AGGAGCTTGCAGTGACCCAGCA	ATGAGAGCCCTTGGTCCTCATCCA
ACVRL1ex6	AGGCAGCGCAGCATCAAGAT	AAACTTGAGCCCTGAGTGCAG
ACVRL1ex7	TGACGACTCCAGCCTCCCTTAG	CAAGCTCCGCCACCTGTGAA
ACVRL1ex8	AGGTTTGGGAGAGGGGCAGGAGT	GGCTCCACAGGCTGATTCCCCTT
ACVRL1ex9	TCCTCTGGGTGGTATTGGGCCTC	CAGAAATCCCAGCCATGAGCCAC
ACVRL1ex10	TCTCCTCTGCACCTCTCTCCCAA	CTGCAGGCAGAAAGGAATCAGGTGCT

ENGex1	TCCCTGTGTCCACTTCTCCT	GAATACTTGGGGCCTGGTC
ENGex2	CAGGAAAGCCGTTAGCTCAT	ATCTGCCTTGGAGCTTCCTC
ENGex3	TGGGTGGCACAACTATAACA	TGACCCACAGAGATGGACAG
ENGex4	AATGGGCTGACTCCACAAAT	GGAGCTCAGATTCTCCTGA
ENGex5	GGGGCTCTGTTAGGTGCAG	GCTTTATAAGGGACCGGAGA
ENGex6	ATCCCATAAACCCACACCTG	CTTCCCTGATCCAGAGGTTG
ENGex7	GTGGGGACACAGCAGGAC	GGTGCTTCACCAACAGTGTG
ENGex8	GGGCACACAGTGATCACACA	GGGCTAGGACCCCAAGAGT
ENGex9	GGTTGTGGTCAGTCCTTGGT	CTGCTCTCCCAAACACACCT
ENGex10	ATCTGCAAAAATGGGCGTAT	TTCCAGACACACATGGCTTG
ENGex11	GAGTCAGGCAACTCCACAGG	AGAAAGGCGGAGAGGAAGTT
ENGex12	CCGATATTTGAAGGCAGCAG	TTCCTGCAAACCCACAGACCT
ENGex13	GCCAGGGAGTAAACCTGGA	CCCTTGCCATGTGCTATGT
ENGex14	CAGAGAAGTCGAGGGTCCAT	CAATCCCTCAGAGGCTTCAC
ENGex15	GTGAAGCCTCTGAGGGATTG	GGTGAGTTCACACCAGTGCT
SOX17ex1	ACAGGCCAGAACACGGG	CCTGGTTTTGGGCGTCAG
SOX17ex2a	GTTGCGCAATTCAAAGTC	TAGTACACGTGAAGGGCGC
SOX17ex2b	GACCCGGCTTTCTTCGC	TGTTCAAGTGGCAGACAAAA
Family E011942 (Figure 4b)		
AQP1_ex3a	TATGACTCTCTGCCTTCGC	CCCGTGGGTCTCCTAC
Family E012415 (Figure 4c)		
AQP1_ex2a	GAGGCCTGGGTATCCTTGG	CGCCATCCTCCACCCAAT
Family E010634 (Figure 4d)		
AQP1_ex3b	CCCCACCCTGATTGTTCTCT	CCAGAACAGGAAGGGACACT

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NIHR BioResource Collaborators

NIHR BioResource – Rare Disease Consortium¹, Julian Adlard², Munaza Ahmed³, Tim Aitman^{4,5}, Hana Alachkar⁶, David Allsup⁷, Jeff Almeida-King⁸, Philip Ancliff⁹, Richard Antrobus¹⁰, Ruth Armstrong^{11,12,13}, Gavin Arno^{14,15}, Sofie Ashford^{1,16}, William Astle^{1,16,17}, Anthony Attwood^{1,16}, Chris Babbs^{18,19}, Tamam Bakchoul²⁰, Tadbir Bariana^{21,22}, Julian Barwell^{23,24}, David Bennett²⁵, David Bentley²⁶, Agnieszka Bierzynska²⁷, Tina Biss²⁸, Marta Bleda²⁹, Harm Bogaard³⁰, Christian Bourne²⁶, Sara Boyce³¹, John Bradley¹, Gerome Breen^{32,33}, Paul Brennan^{34,35}, Carole Brewer³⁶, Matthew Brown^{1,16}, Michael Browning³⁷, Rachel Buchan^{38,39}, Matthew Buckland⁴⁰, Teofila Bueser^{41,42,43}, Siobhan Burns⁴⁰, Oliver Burren²⁹, Paul Calleja⁴⁴, Gerald Carr-White⁴², Keren Carss^{1,16}, Ruth Casey^{11,12,13}, Mark Caulfield⁴⁵, John Chambers^{46,47}, Jennifer Chambers^{48,49}, Floria Cheng⁴⁹, Patrick F Chinnery^{1,50,51}, Martin Christian⁵², Colin Church⁵³, Naomi Clements Brod^{1,16}, Gerry Coghlan⁴⁰, Elizabeth Colby²⁷, Trevor Cole⁵⁴, Janine Collins⁵⁵, Peter Collins⁵⁶, Camilla Colombo²⁶, Robin Condliffe⁵⁷, Stuart Cook^{38,58,59,60}, Terry Cook⁶¹, Nichola Cooper⁶², Paul Corris^{63,64}, Abigail Crisp-Hihn^{1,16}, Nicola Curry⁶⁵, Cesare Danesino⁶⁶, Matthew Daniels^{67,68}, Louise Daugherty^{1,16}, John Davis^{1,16}, Sri V V Deevi^{1,16}, Timothy Dent⁶⁸, Eleanor Dewhurst^{1,16}, Peter Dixon⁴⁸, Kate Downes^{1,16}, Anna Drazyk⁶⁹, Elizabeth Drewe⁷⁰, Tina Dutt⁷¹, David Edgar⁷², Karen Edwards^{1,16}, William Egnor⁷³, Wendy Erber⁷⁴, Marie Erwood^{1,16}, Maria C Estiu⁷⁵, Gillian Evans⁷⁶, Dafydd Gareth Evans⁷⁷, Tamara Everington⁷⁸, Mélanie Eyries⁷⁹, Remi Favier^{80,81,82}, Debra Fletcher^{1,16}, James Fox^{1,16}, Amy Fray^{1,16}, Courtney French⁸³, Kathleen Freson⁸⁴, Mattia Frontini^{1,16}, Daniel Gale⁸⁵, Henning Gall⁸⁶, Claire Geoghegan²⁶, Terry Gerighty²⁶, Stefano Ghio⁸⁷, Hossein-Ardeschir Ghofrani^{62,86}, Simon Gibbs³⁸, Kimberley Gilmour⁸⁸, Barbara Girerd^{89,90,91}, Sarah Goddard⁹², Keith Gomez^{21,22}, Pavels Gordins⁹³, David Gosal⁶, Stefan Graf^{1,16,29}, Luigi Grassi^{1,16}, Daniel Greene^{1,16,17}, Lynn Greenhalgh⁹⁴, Andreas Greinacher⁹⁵, Paolo Gresele⁹⁶, Philip Griffiths^{97,98}, Sofia Grigoriadou⁹⁹, Russell Grocock²⁶, Detelina Grozeva¹¹, Scott Hackett¹⁰⁰, Charaka Hadinnapola²⁹, William Hague¹⁰¹, Matthias Haimel^{1,16,29}, Matthew Hall⁷⁰, Helen Hanson⁹⁴, Kirsty Harkness¹⁰², Andrew Harper^{38,67,103}, Claire Harris⁶⁴, Daniel Hart⁵⁵, Ahamad Hassan¹⁰⁴, Grant Hayman¹⁰⁵, Alex Henderson¹⁰⁶, Jonathan Hoffmann⁵⁴, Rita Horvath^{107,108}, Arjan Houweling³⁰, Luke Howard³⁸, Fengyuan Hu^{1,16}, Gavin Hudson¹⁰⁷, Joseph Hughes²⁶, Aarnoud Huissoon¹⁰⁰, Marc Humbert^{89,90,91}, Sean Humphray²⁶, Sarah Hunter²⁶, Matthew Hurles¹⁰⁹, Louise Izatt¹¹⁰, Roger James^{1,16}, Sally Johnson¹¹¹, Stephen Jolles^{112,113}, Jennifer Jolley^{1,16}, Neringa Jurkute^{14,22}, Mary Kasanicki¹¹⁴, Hanadi Kazkaz¹¹⁵, Rashid Kazmi³¹, Peter Kelleher³⁹, David Kiely⁵⁷, Nathalie Kingston¹, Robert Klima⁴⁴, Myrto Kostadima^{1,16}, Gabor Kovacs^{116,117}, Ania Koziell^{118,119}, Roman Kreuzhuber^{1,16}, Taco Kuijpers^{120,121}, Ajith Kumar³, Dinakantha Kumararatne¹¹⁴, Manju Kurian^{122,123}, Michael Laffan^{124,125}, Fiona Laloo⁷⁷, Michele Lambert^{126,127}, Hana Lango Allen^{1,16}, Allan Lawrie¹²⁸, Mark Layton¹²⁴, Claire Lentaigne^{124,125}, Adam Levine⁸⁵, Rachel Linger^{1,16}, Hilary Longhurst⁹⁹, Eleni Louka^{18,19}, Robert MacKenzie Ross¹²⁹, Bella Madan¹³⁰, Eamonn Maher^{11,131}, Jesmeen Maimaris⁸⁸, Sarah Mangles¹³², Rutendo Mapeta^{1,16}, Kevin Marchbank⁶⁴, Stephen Marks⁹, Hugh S Markus⁶⁹, Hanns-Ulrich Marschall¹³³, Andrew Marshall^{134,135,136}, Jennifer Martin^{1,16,29}, Mary Mathias¹³⁷, Emma Matthews^{22,138}, Heather Maxwell¹³⁹, Paul McAlinden⁶⁴, Mark McCarthy^{19,103,140}, Stuart Meacham^{1,16}, Adam Mead¹⁴¹, Karyn Megy^{1,16}, Sarju Mehta¹⁴², Michel Michaelides¹⁴, Carolyn Millar^{124,125}, Shahin Moledina⁹, David Montani^{89,90,91}, Tony Moore^{14,15}, Nicholas Morrell^{1,29}, Monika Mozere⁸⁵, MPGN/C3 Glomerulopathy Rare Renal Disease group¹⁴³, Keith Muir¹⁴⁴, Andrew Mumford^{145,146}, Michael Newnham²⁹, Jennifer O'Sullivan¹³⁰, Samya Obaji⁵⁶, Steven Okoli^{18,19}, Andrea Olschewski¹¹⁶, Horst Olschewski^{116,117}, Kai Ren Ong⁵⁴, Elizabeth

Ormondroyd^{67,68}, Willem Ouwehand^{1,16}, Sofia Papadia^{1,16}, Soo-Mi Park^{12,13,147}, David Parry⁵, Joan Paterson^{11,12,13}, Andrew Peacock⁵³, John Peden²⁶, Kathelijne Peerlinck⁸⁴, Christopher Penkett^{1,16}, Joanna Pepke-Zaba¹⁴⁸, Romina Petersen^{1,16}, Angela Pyle¹⁰⁷, Stuart Rankin⁴⁴, Anupama Rao⁹, F Lucy Raymond^{1,11}, Paula Rayner-Matthews^{1,16}, Christine Rees²⁶, Augusto Rendon⁴⁵, Tara Renton⁴³, Andrew Rice^{149,150}, Sylvia Richardson¹⁷, Alex Richter¹⁰, Irene Roberts^{18,19,151}, Catherine Roughley⁷⁶, Noemi Roy^{18,19,151}, Omid Sadeghi-Alavijeh⁸⁵, Moin Saleem²⁷, Nilesh Samani¹⁵², Alba Sanchis-Juan^{1,16}, Ravishankar Sargur⁷³, Simon Satchell²⁷, Sinisa Savic¹⁵³, Laura Scelsi⁸⁷, Sol Schulman¹⁵⁴, Marie Scully¹¹⁵, Claire Searle¹⁵⁵, Werner Seeger⁸⁶, Carrock Sewell¹⁵⁶, Denis Seyres^{1,16}, Susie Shapiro⁶⁵, Olga Sharmardina^{1,16}, Rakefet Shtoyerman¹⁵⁷, Keith Sibson¹³⁷, Lucy Side³, Ilenia Simeoni^{1,16}, Michael Simpson¹⁵⁸, Suthesh Sivapalaratnam⁵⁵, Anne-Bine Skytte¹⁵⁹, Katherine Smith⁴⁵, Kenneth G C Smith^{29,160}, Katie Snape¹⁶¹, Florent Soubrier⁷⁹, Simon Staines^{1,16}, Emily Staples²⁹, Hannah Stark^{1,16}, Jonathan Stephens^{1,16}, Kathleen Stirrups^{1,16}, Sophie Stock^{1,16}, Jay Suntharalingam¹²⁹, Emilia Swietlik²⁹, R Campbell Tait¹⁶², Kate Talks²⁸, Rhea Tan⁶⁹, James Thaventhiran²⁹, Andreas Themistocleous²⁵, Moira Thomas¹⁶³, Kate Thomson^{67,68}, Adrian Thrasher⁹, Chantal Thys⁸⁴, Marc Tischkowitz¹⁶⁴, Catherine Titterton^{1,16}, Cheng-Hock Toh⁷¹, Mark Toshner²⁹, Matthew Traylor⁶⁹, Carmen Treacy^{29,148}, Richard Trembath⁴¹, Salih Tuna^{1,16}, Wojciech Turek⁴⁴, Ernest Turro^{1,16,17}, Tom Vale²⁵, Chris Van Geet⁸⁴, Natalie Van Zuydam²⁵, Marta Vazquez-Lopez⁴⁹, Julie von Ziegenweidt^{1,16}, Anton Vonk Noordegraaf³⁰, Quintin Waisfisz³⁰, Suellen Walker⁹, James Ware^{38,39,58}, Hugh Watkins^{67,68,103}, Christopher Watt^{1,16}, Andrew Webster^{14,15}, Wei Wei⁵⁰, Steven Welch¹⁰⁰, Julie Wessels⁹², Sarah Westbury^{145,146}, John-Paul Westwood¹¹⁵, John Wharton⁶², Deborah Whitehorn^{1,16}, James Whitworth^{11,12,13}, Martin R Wilkins⁶², Catherine Williamson^{48,165}, Edwin Wong⁹⁸, Nicholas Wood^{166,167}, Yvette Wood^{1,16}, Geoff Woods^{11,114}, Emma Woodward⁷⁷, Stephen Wort^{39,41}, Austen Worth⁹, Katherine Yates^{1,16,29}, Patrick Yong¹⁶⁸, Tim Young^{1,16}, Ping Yu^{1,16}, Patrick Yu-Wai-Man⁵⁰

Affiliations

¹NIHR BioResource, Cambridge University Hospitals NHS Foundation, Cambridge Biomedical Campus, Cambridge, UK. ²Chapel Allerton Hospital, Leeds Teaching Hospitals NHS Trust, Leeds, UK. ³North East Thames Regional Genetics Service, Great Ormond Street Hospital for Children NHS Foundation Trust, London, UK. ⁴MRC Clinical Sciences Centre, Faculty of Medicine, Imperial College London, London, UK. ⁵Institute of Genetics and Molecular Medicine, University of Edinburgh, Edinburgh, UK. ⁶Salford Royal NHS Foundation Trust, Salford, UK. ⁷Queens Centre for Haematology and Oncology, Castle Hill Hospital, Hull and East Yorkshire NHS Trust, Cottingham, UK. ⁸European Molecular Biology Laboratory, European Bioinformatics Institute (EMBL-EBI), Wellcome Genome Campus, Hinxton, Cambridge, UK. ⁹Great Ormond Street Hospital for Children NHS Foundation Trust, London, UK. ¹⁰University Hospitals Birmingham NHS Foundation Trust, Birmingham, UK. ¹¹Department of Medical Genetics, Cambridge Institute for Medical Research, University of Cambridge, Cambridge Biomedical Campus, Cambridge, UK. ¹²Cancer Research UK Cambridge Centre, Cambridge Biomedical Campus, Cambridge, UK. ¹³NIHR Cambridge Biomedical Research Centre, Cambridge Biomedical Campus, Cambridge, UK. ¹⁴Moorfields Eye Hospital NHS Foundation Trust, London, UK. ¹⁵UCL Institute of Ophthalmology, University College London, London, UK. ¹⁶Department of Haematology, University of Cambridge, Cambridge Biomedical Campus, Cambridge, UK. ¹⁷MRC Biostatistics Unit, Cambridge Institute of Public Health, University of Cambridge, Cambridge, UK. ¹⁸MRC Molecular Haematology Unit, Weatherall Institute of Molecular Medicine, University of Oxford, Oxford, UK. ¹⁹NIHR Oxford Biomedical Research Centre, Oxford University

Hospitals Trust, Oxford, UK. ²⁰Center for Clinical Transfusion Medicine, University Hospital of Tübingen, Tübingen, Germany. ²¹The Katharine Dormandy Haemophilia Centre and Thrombosis Unit, Royal Free London NHS Foundation Trust, London, UK. ²²University College London, London, UK. ²³Department of Clinical Genetics, Leicester Royal Infirmary, University Hospitals of Leicester, Leicester, UK. ²⁴University of Leicester, Leicester, UK. ²⁵The Nuffield Department of Clinical Neurosciences, University of Oxford, John Radcliffe Hospital, Oxford, UK. ²⁶Illumina Limited, Chesterford Research Park, Little Chesterford, Nr Saffron Walden, UK. ²⁷Bristol Renal, University of Bristol, Bristol, UK. ²⁸Haematology Department, Royal Victoria Infirmary, The Newcastle upon Tyne Hospitals NHS Foundation Trust, Newcastle upon Tyne, UK. ²⁹Department of Medicine, School of Clinical Medicine, University of Cambridge, Cambridge Biomedical Campus, Cambridge, UK. ³⁰Department of Pulmonary Medicine, VU University Medical Centre, Amsterdam, The Netherlands. ³¹Southampton General Hospital, University Hospital Southampton NHS Foundation Trust, Southampton, UK. ³²MRC Social, Genetic & Developmental Psychiatry Centre, Institute of Psychiatry, Psychology & Neuroscience, King's College London, London, UK. ³³NIHR Biomedical Research Centre for Mental Health, Maudsley Hospital, London, UK. ³⁴Newcastle University, Newcastle upon Tyne, UK. ³⁵Newcastle upon Tyne Hospitals NHS Foundation Trust, Newcastle upon Tyne, UK. ³⁶Department of Clinical Genetics, Royal Devon & Exeter Hospital, Royal Devon and Exeter NHS Foundation Trust, Exeter, UK. ³⁷Department of Immunology, Leicester Royal Infirmary, Leicester, UK. ³⁸National Heart and Lung Institute, Imperial College London, Royal Brompton Hospital, London, UK. ³⁹Royal Brompton Hospital, Royal Brompton and Harefield NHS Foundation Trust, London, UK. ⁴⁰Royal Free London NHS Foundation Trust, London, UK. ⁴¹King's College London, London, UK. ⁴²Guy's and St Thomas' Hospital, Guy's and St Thomas' NHS Foundation Trust, London, UK. ⁴³King's College Hospital NHS Foundation Trust, London, UK. ⁴⁴High Performance Computing Service, University of Cambridge, Cambridge, UK. ⁴⁵Genomics England Ltd, London, UK. ⁴⁶Epidemiology and Biostatistics, Imperial College London, London, UK. ⁴⁷Imperial College Healthcare NHS Trust, London, UK. ⁴⁸Division of Women's Health, King's College London, London, UK. ⁴⁹Women's Health Research Centre, Surgery and Cancer, Faculty of Medicine, Hammersmith Hospital, Imperial College Healthcare NHS Trust, London, UK. ⁵⁰Department of Clinical Neurosciences, School of Clinical Medicine, University of Cambridge, Cambridge Biomedical Campus, Cambridge, UK. ⁵¹Medical Research Council Mitochondrial Biology Unit, Cambridge Biomedical Campus, Cambridge, UK. ⁵²Children's Renal and Urology Unit, Nottingham Children's Hospital, QMC, Nottingham University Hospitals NHS Trust, Nottingham, UK. ⁵³Golden Jubilee National Hospital, Glasgow, UK. ⁵⁴West Midlands Regional Genetics Service, Birmingham Women's and Children's NHS Foundation Trust, Birmingham, UK. ⁵⁵The Royal London Hospital, Barts Health NHS Foundation Trust, London, UK. ⁵⁶The Arthur Bloom Haemophilia Centre, University Hospital of Wales, Cardiff, UK. ⁵⁷Sheffield Pulmonary Vascular Disease Unit, Royal Hallamshire Hospital NHS Foundation Trust, Sheffield, UK. ⁵⁸MRC London Institute of Medical Sciences, Imperial College London, London, UK. ⁵⁹National Heart Research Institute Singapore, National Heart Centre Singapore, Singapore, Singapore. ⁶⁰Division of Cardiovascular & Metabolic Disorders, Duke-National University of Singapore, Singapore, Singapore. ⁶¹Imperial College Renal and Transplant Centre, Hammersmith Hospital, Imperial College Healthcare NHS Trust, London, UK. ⁶²Department of Medicine, Imperial College London, London, UK. ⁶³National Pulmonary Hypertension Service (Newcastle), The Newcastle upon Tyne Hospitals NHS Foundation Trust, Newcastle upon Tyne, UK. ⁶⁴Institute of Cellular Medicine, Faculty of Medical Sciences, Newcastle University,

Newcastle upon Tyne, UK. ⁶⁵Oxford Haemophilia and Thrombosis Centre, The Churchill Hospital, Oxford University Hospitals NHS Trust, Oxford, UK. ⁶⁶Department of Molecular Medicine, General Biology, and Medical Genetics Unit, University of Pavia, Pavia, Italy. ⁶⁷Department of Cardiovascular Medicine, Radcliffe Department of Medicine, University of Oxford, Oxford, UK. ⁶⁸Oxford University Hospitals NHS Foundation Trust, Oxford, UK. ⁶⁹Stroke Research Group, Department of Clinical Neurosciences, University of Cambridge, Cambridge Biomedical Campus, Cambridge, UK. ⁷⁰Nottingham University Hospitals NHS Trust, Nottingham, UK. ⁷¹The Roald Dahl Haemostasis and Thrombosis Centre, The Royal Liverpool Hospital, Liverpool, UK. ⁷²Regional Immunology Service, Kelvin Building, Royal Victoria Hospital, Belfast, UK. ⁷³Sheffield Teaching Hospitals NHS Foundation Trust, Sheffield, UK. ⁷⁴Pathology and Laboratory Medicine, University of Western Australia, Crawley, Australia. ⁷⁵Ramón Sardá Mother's and Children's Hospital, Buenos Aires, Argentina. ⁷⁶Haemophilia Centre, Kent & Canterbury Hospital, East Kent Hospitals University Foundation Trust, Canterbury, UK. ⁷⁷Manchester Centre for Genomic Medicine, Saint Mary's Hospital, Manchester, UK. ⁷⁸Salisbury District Hospital, Salisbury NHS Foundation Trust, Salisbury, UK. ⁷⁹Departement de genetique, Hopital Pitie-Salpetriere, Paris, France. ⁸⁰Service d'Hématologie Biologique, Hôpital d'enfants Armand Trousseau, Paris, France, Paris, France. ⁸¹Inserm U1170, Villejuif, France. ⁸²Assistance Publique-Hôpitaux de Paris, Département d'Hématologie, Hôpital Armand Trousseau, Paris, France. ⁸³Department of Paediatrics, School of Clinical Medicine, University of Cambridge, Cambridge Biomedical Campus, Cambridge, UK. ⁸⁴Department of Cardiovascular Sciences, Center for Molecular and Vascular Biology, University of Leuven, Leuven, Belgium. ⁸⁵UCL Centre for Nephrology, University College London, London, UK. ⁸⁶University of Giessen and Marburg Lung Center (UGMLC), Giessen, Germany. ⁸⁷Division of Cardiology, Fondazione IRCCS Policlinico S. Matteo, Pavia, Italy. ⁸⁸UCL Great Ormond Street Institute of Child Health, London, UK. ⁸⁹Universite Paris-Sud, Le Kremlin-Bicêtre, France. ⁹⁰Service de Pneumologie, DHU Thorax Innovation, Hôpital Bicêtre, Le Kremlin-Bicêtre, France. ⁹¹INSERM U999, LabEx LERMIT, Centre Chirurgical Marie Lannelongue, Le Plessis Robinson, France. ⁹²University Hospitals of North Midlands NHS Trust, Stoke-on-Trent, UK. ⁹³East Yorkshire Regional Adult Immunology and Allergy Unit, Hull Royal Infirmary, Hull & East Yorkshire Hospitals NHS Trust, Hull, UK. ⁹⁴Department of Clinical Genetics, Liverpool Women's NHS Foundation, Liverpool, UK. ⁹⁵Institute for Immunology and Transfusion Medicine, University of Greifswald, Greifswald, Germany. ⁹⁶Section of Internal and Cardiovascular Medicine, University of Perugia, Perugia, Italy. ⁹⁷Mitochondrial Research Group, Institute of Genetic Medicine, Newcastle University, Newcastle upon Tyne, UK. ⁹⁸Institute of Genetic Medicine, Newcastle University, Newcastle upon Tyne, UK. ⁹⁹Barts Health NHS Foundation Trust, London, UK. ¹⁰⁰Birmingham Heartlands Hospital, Heart of England NHS Foundation Trust, Birmingham, UK. ¹⁰¹ARCH: Australian Research Centre for Health of Women and Babies, Robinson Research Institute, Discipline of Obstetrics and Gynaecology, The University of Adelaide, Women's and Children's Hospital, Adelaide, Australia. ¹⁰²Department of Neurology, Sheffield Teaching Hospitals NHS Foundation Trust, Sheffield, UK. ¹⁰³Wellcome Trust Centre for Human Genetics, University of Oxford, Oxford, UK. ¹⁰⁴Department of Neurology, Leeds Teaching Hospital NHS Trust, Leeds, UK. ¹⁰⁵Epsom & St Helier University Hospitals NHS Trust, London, UK. ¹⁰⁶Northern Genetics Service, The Newcastle upon Tyne Hospitals NHS Foundation Trust, International Centre for Life, Newcastle upon Tyne, UK. ¹⁰⁷Wellcome Centre for Mitochondrial Research, Institute of Genetic Medicine, Newcastle University, Newcastle upon Tyne, UK. ¹⁰⁸John Walton Muscular Dystrophy Research Centre, Institute of Genetic Medicine, Newcastle University, Newcastle upon Tyne, UK. ¹⁰⁹Wellcome Trust

Sanger Institute, Hinxton, Cambridge, UK. ¹¹⁰Department of Clinical Genetics, Guy's and St Thomas' NHS Foundation Trust, London, UK. ¹¹¹Department of Paediatric Nephrology, Great North Children's Hospital, Newcastle upon Tyne Hospitals NHS Foundation Trust, Newcastle upon Tyne, UK. ¹¹²University Hospital of Wales, Cardiff, UK. ¹¹³Cardiff & Vale University LHB, Cardiff, UK. ¹¹⁴Addenbrookes Hospital, Cambridge University Hospitals NHS Foundation Trust, Cambridge, UK. ¹¹⁵University College London Hospitals NHS Foundation Trust, London, UK. ¹¹⁶Ludwig Boltzmann Institute for Lung Vascular Research, Graz, Austria. ¹¹⁷Dept of Internal Medicine, Division of Pulmonology, Medical University of Graz, Graz, Austria. ¹¹⁸Division of Transplantation Immunology and Mucosal Biology, Department of Experimental Immunobiology, Faculty of Life Sciences and Medicine, King's College London, London, UK. ¹¹⁹Department of Paediatric Nephrology, Evelina London Children's Hospital, Guy's & St Thomas' NHS Foundation Trust, London, UK. ¹²⁰Department of Pediatric Hematology, Immunology, Rheumatology and Infectious Diseases, Emma Children's Hospital, Academic Medical Center (AMC), University of Amsterdam, Amsterdam, The Netherlands. ¹²¹Department of Clinical Genetics, Academic Medical Center (AMC), University of Amsterdam, Amsterdam, The Netherlands. ¹²²Molecular Neurosciences, Developmental Neurosciences, UCL Great Ormond Street Institute of Child Health, London, UK. ¹²³Department of Neurology, Great Ormond Street Hospital for Children NHS Foundation Trust, London, UK. ¹²⁴Department of Haematology, Hammersmith Hospital, Imperial College Healthcare NHS Trust, London, UK. ¹²⁵Department of Haematology, Imperial College London, London, UK. ¹²⁶Division of Hematology, The Children's Hospital of Philadelphia, Philadelphia, USA. ¹²⁷Department of Pediatrics, Perelman School of Medicine at the University of Pennsylvania, Philadelphia, USA. ¹²⁸Department of Infection, Immunity & Cardiovascular Disease, University of Sheffield, Sheffield, UK. ¹²⁹Royal United Hospitals Bath NHS Foundation Trust, Bath, UK. ¹³⁰Department of Haematology, Guy's and St Thomas' NHS Foundation Trust, London, UK. ¹³¹Cambridge NIHR Biomedical Research Centre, Cambridge Biomedical Campus, Cambridge, UK. ¹³²Haemophilia, Haemostasis and Thrombosis Centre, Hampshire Hospitals NHS Foundation Trust, Basingstoke, UK. ¹³³Wallenberg Laboratory, Department of Molecular and Clinical Medicine, Sahlgrenska Academy, University of Gothenburg, Gothenburg, Sweden. ¹³⁴Faculty of Medical and Human Sciences, Centre for Endocrinology and Diabetes, Institute of Human Development, University of Manchester, Manchester, UK. ¹³⁵Department of Clinical Neurophysiology, Manchester Royal Infirmary, Central Manchester University Hospitals National Health Service Foundation Trust, Manchester Academic Health Science Centre, Manchester, UK. ¹³⁶National Institute for Health Research/Wellcome Trust Clinical Research Facility, Manchester, UK. ¹³⁷Department of Haematology, Great Ormond Street Hospital for Children NHS Foundation Trust, London, UK. ¹³⁸The National Hospital for Neurology and Neurosurgery, University College London Hospitals NHS Foundation Trust, London, UK. ¹³⁹Royal Hospital for Children, NHS Greater Glasgow and Clyde, Glasgow, UK. ¹⁴⁰Oxford Centre for Diabetes, Endocrinology and Metabolism, University of Oxford, Churchill Hospital, Oxford, UK. ¹⁴¹Centre for Haematology, Department of Medicine, Hammersmith Hospital, Imperial College Healthcare NHS Trust, London, UK. ¹⁴²Department of Clinical Genetics, Addenbrookes Hospital, Cambridge University Hospitals NHS Foundation Trust, Cambridge, UK. ¹⁴³MPGN/C3 Glomerulopathy Rare Renal Disease group, , UK. ¹⁴⁴Institute of Neuroscience and Psychology, University of Glasgow, Glasgow, UK. ¹⁴⁵School of Cellular and Molecular Medicine, University of Bristol, Bristol, UK. ¹⁴⁶University Hospitals Bristol NHS Foundation Trust, Bristol, UK. ¹⁴⁷East Anglian Regional Genetics Service, Cambridge University Hospitals NHS Foundation Trust, Cambridge, UK. ¹⁴⁸Royal Papworth Hospital

NHS Foundation Trust, Cambridge, UK. ¹⁴⁹Pain Research, Department of Surgery and Cancer, Faculty of Medicine, Imperial College London, London, UK. ¹⁵⁰Chelsea and Westminster Hospital NHS Foundation Trust, London, UK. ¹⁵¹Department of Paediatrics, Weatherall Institute of Molecular Medicine, University of Oxford, Oxford, UK. ¹⁵²Departments of Cardiovascular Sciences and NIHR Leicester Cardiovascular Biomedical Research Unit, University of Leicester, Leicester, UK. ¹⁵³The Leeds Teaching Hospitals NHS Trust, Leeds, UK. ¹⁵⁴Beth Israel Deaconess Medical Centre and Harvard Medical School, Boston, USA. ¹⁵⁵Department of Clinical Genetics, Nottingham University Hospitals NHS Trust, Nottingham, UK. ¹⁵⁶Scunthorpe General Hospital, Northern Lincolnshire and Goole NHS Foundation Trust, Scunthorpe, UK. ¹⁵⁷Clinical Genetics Institute, Kaplan Medical Center, Rehovot, Israel. ¹⁵⁸Genetics and Molecular Medicine, King's College London, London, UK. ¹⁵⁹Aarhus University Hospital, Aarhus, Denmark. ¹⁶⁰Cambridge Institute for Medical Research, University of Cambridge, Cambridge Biomedical Campus, Cambridge, UK. ¹⁶¹Department of Clinical Genetics, St George's University Hospitals NHS Foundation Trust, London, UK. ¹⁶²Glasgow Royal Infirmary, NHS Greater Glasgow and Clyde, Glasgow, UK. ¹⁶³Gartnavel General Hospital, NHS Greater Glasgow and Clyde, Glasgow, UK. ¹⁶⁴Addenbrooke's Treatment Centre, Addenbrooke's Hospital, Cambridge University Hospitals NHS Foundation Trust, Cambridge, UK. ¹⁶⁵Institute of Reproductive and Developmental Biology, Surgery and Cancer, Hammersmith Hospital, Imperial College Healthcare NHS Trust, London, UK. ¹⁶⁶Department of Molecular Neuroscience, UCL Institute of Neurology, London, UK. ¹⁶⁷UCL Genetics Institute, London, UK. ¹⁶⁸Frimley Park Hospital, NHS Frimley Health Foundation Trust, Camberley, UK.