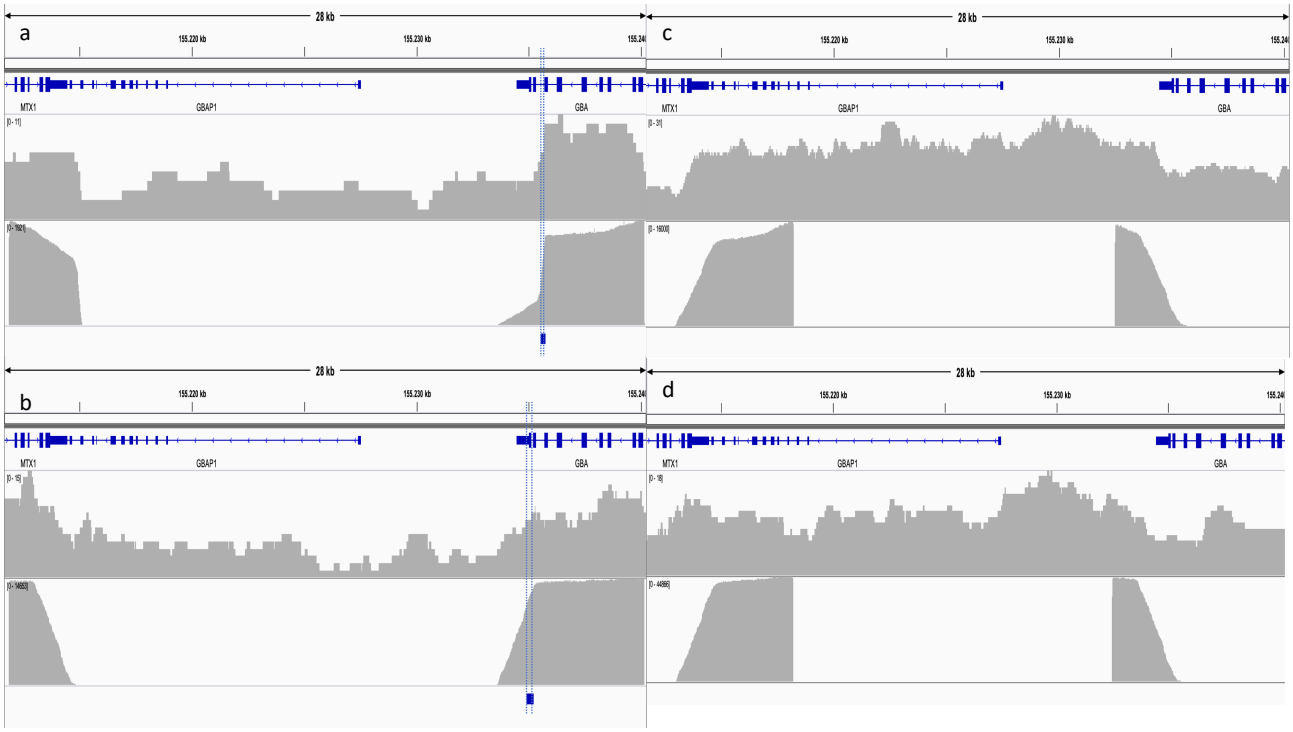
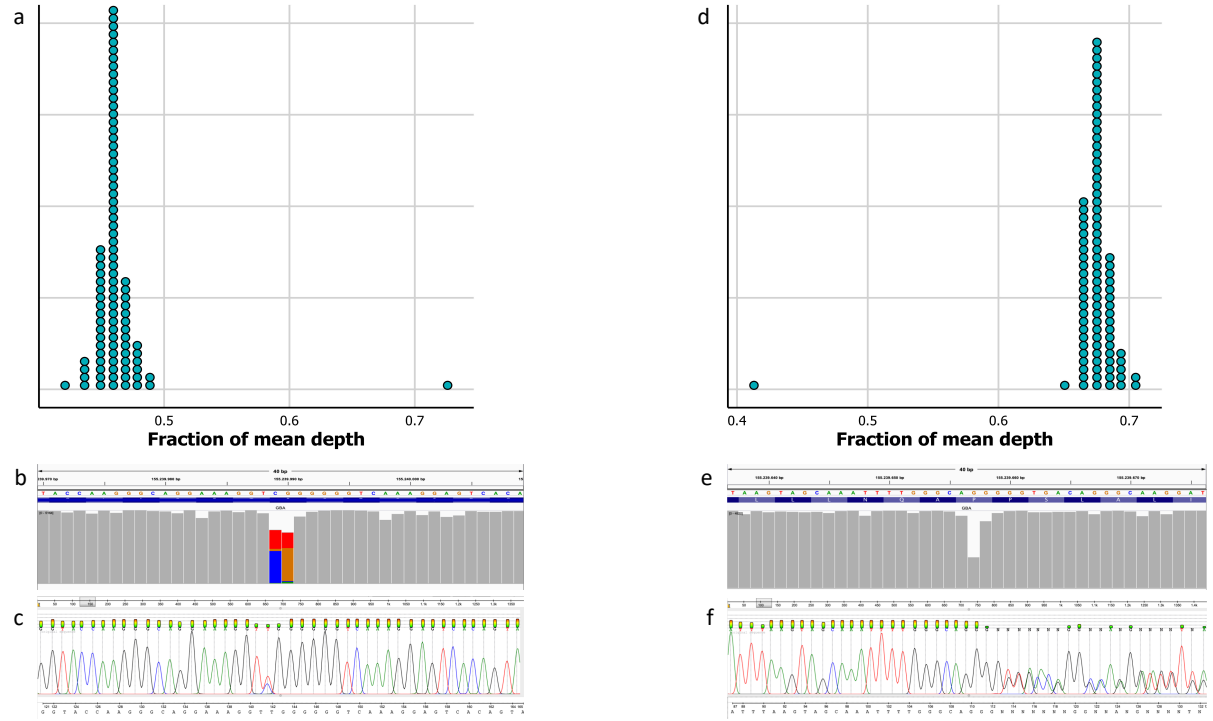
Supplementary figures

Supplementary Figure 1: Confirmation of the structure of 4 reciprocal recombinant alleles with ONT.



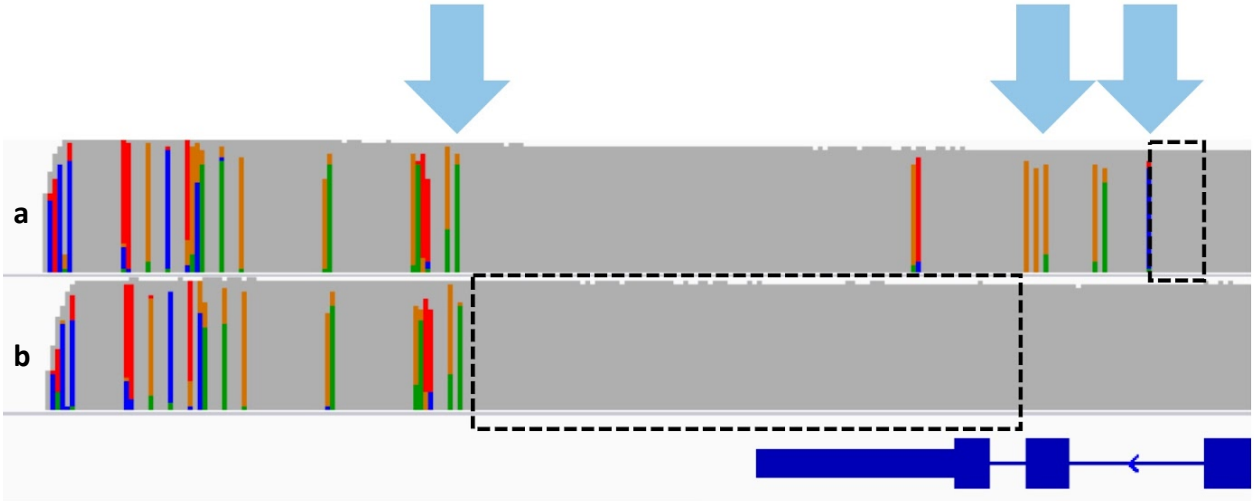
Each panel shows results of one sample: genomic sequencing with adaptive sampling (top), and sequencing of PCR product obtained with primers 2 or 3 (bottom). **a)** Pathogenic CNL allele. **b)** non-pathogenic CNL allele. **c)** CNG allele with a copy number of 5 copies as called by Gauchian 5. **d)** CNG allele with a copy number of 3 copies as predicted by Gauchian.
For the fusion recombinants (A and B), the blue squares and dotted lines at the bottom show the position of the breakpoint predicted with ONT (as described in methods). The breakpoint cannot be refined further as the sequences are identical; see also figure S2. Alignment with LAST.
Genomic region depicted: g.chr1:155,211,770-155,240,380

Supplementary Figure 2: Detection of SNVs in homopolymers with ONT.



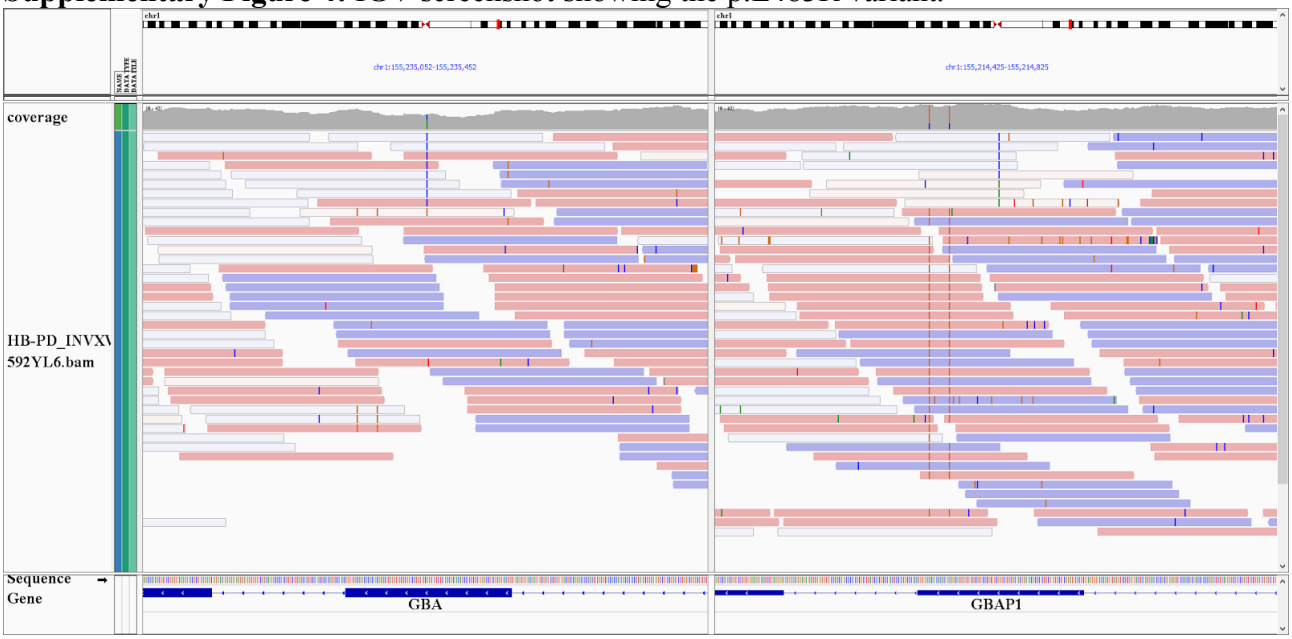
At position chr1:155,239,990 one sample shows an adjusted depth of coverage that is more than 5 median absolute deviations (MAD) higher than the mean of the other samples **(a)**. Inspection of the sequencing data obtained from ONT (primer pair 1) shows that this is probably due to the presence of a single base substitution at position chr1:155,239,989 **(b)**, as confirmed by sanger sequencing **(c)**. Similarly, at position chr1:155,239,657, one sample shows an adjusted depth of coverage that is more than 5 MAD lower than the mean of the other samples, suggesting the deletion of a G in the poly-G. This corresponds to the variant NM_001005742.3:c.413delC **(d)**. Inspection of the sequencing data obtained from ONT (primer pair 1) confirms the drop in depth of coverage **(e)** and Sanger sequencing confirms the presence of a deletion in the poly-G sequence **(f)**.

Supplementary Figure 3: Visual display of two reciprocal fusion recombinant alleles.



The light blue arrows represent the sentinel positions where *GBA* and *GBAP1* are not homologous. The dotted boxes represent the predicted position of the breakpoints. **a)** breakpoint is between exon 9 and intron 9, so this recombinant allele is predicted to be pathogenic. This is a case of GD, where a pathogenic allele is expected, and indeed had been previously reported independently. **b)** Breakpoint does not affect coding sequence. Exon 11 of *GBA* is 100% homologous to *GBAP1*, so recombinations involving this area do not alter the ORF, so this recombinant is non-pathogenic.

Supplementary Figure 4: IGV screenshot showing the p.L483R variant.



Reads carrying the C variant in the middle are aligned to either *GBA* or *GBAP1*. Many of them have a mapping quality of zero. Hence the variant is missed by BWA-GATK.
Genomic region depicted: g.chr1:155,235,052-155,235,452 (left) and g.chr1:155,214,425-155,214,825 (right)

Supplementary tables

Supplementary Table 1: Results of dPCR. The mean dPCR copy number of 2 probes is given.

Sample	Copy number detected by Gauchian	Copy number (dPCR)	ONT CNV detected
NA20756	3	3.18	Duplication
HG01912	5	5.15	Duplication
HG01889	7	6.71	Duplication
HG02284	8	7.86	Duplication
RAP1	not analysed	0.98	Fusion
RAP2	not analysed	2.06	None

Supplementary Table 2: Phenotypes and genotypes of all samples from the RAPSODI cohort.

	Wild type	**Heterozygous carriers***	**Homozygous and compound heterozygous carriers***	**Total**
PD Patients	195	36	0	231
GD Patients	0	0	33	33
Healthy individuals	74	43	0	117
total	269	79	33	381

*Including pathogenic structural variants.

Supplementary Table 3: All variants detected in the RAPSODI and QSBB cohorts.

Allele detected	Number of alleles
p.N409S (NC_000001.11:g.155235843T>G)	35
p.L483P (NC_000001.11:g.155235252A>G)	19
p.E365K (NC_000001.11:g.155236376C>T)	15
p.T408M (NC_000001.11:g.155236246G>A)	4
p.R502C (NC_000001.11:g.155235196G>A)	3
IVS6-2 (NC_000001.11:155238308T>C)	2
p.R301H (NC_000001.11:g.155237438C>T)	2
p.84GG (NC_000001.11:g.155240661dup)	1
p.D419N (NC_000001.11:g.155235814C>T)	1
IVS9+1 (NC_000001.11:g.155235680C>T)	1
p.K13R (NC_000001.11:g.155240707T>C)	1
p.R301G (NC_000001.11:g.155237439G>C)	1
p.T270I (NC_000001.11:g.155237531G>C)	1
p.T408M + L104= (NC_000001.11:g.155236246G>A + 155239758C>T)	1
p.A357D (NC_000001.11:g.155236399G>T)	1
p.D354H (NC_000001.11:g.155236409C>G)	1
p.G241R (NC_000001.11:g.155238174C>T)	1
p.L519P (NC_000001.11:g.155235050A>G)	1
p.P211T (NC_000001.11:g.155238234G>T)	1
c.413delC (NC_000001.11:g.155239661del)	1
RecNciI(p.A495P + p.Val499= + p.L483P) / reciprocal	5
RecNciI(p.A495P + p.Val499= + p.L483P) / non-reciprocal	1
RecTL (p.A495P + p.Val499= + p.L483P + p.D448H) + c.1263del / non-reciprocal	2
Non-pathogenic reciprocal CN loss recombinants	4*
Non-pathogenic reciprocal CN gain recombinants	7**

These do not include the variants found in the 95 samples previously reported (Salazar et al, 2019)
*In two alleles, a non-pathogenic CNL was detected in cis with p.L444P
**In two samples, a CNG was detected together with c.1263del+RecTL (gene conversion). In two other samples, a duplication recombinant was detected together with the p.L483P variant. These were not phased.

Supplementary Table 4: List of *GBAP1*-like variant calls in Exon 9-11 homology region in 1kGP and AMP-PD cohorts.

sampleID	IsBiallelic	IsCarrier	CN(GBA+GBAP1)	Deletion breakpoint in *GBA*	Recombinant variant allele1	Recombinant variant allele2
HG00422	FALSE	TRUE	3	TRUE	RecNciI	
LB-00540	FALSE	TRUE	3	TRUE	RecNciI	
LB-00542	FALSE	TRUE	3	TRUE	RecNciI	
LB-00599	FALSE	TRUE	3	TRUE	RecNciI	
LB-00695	FALSE	TRUE	3	TRUE	RecNciI	
LB-01632	FALSE	TRUE	3	TRUE	c.1263del+RecTL	
LB-01652	FALSE	TRUE	3	FALSE	L483P	
LB-01755	FALSE	TRUE	3	TRUE	RecNciI	
LB-01782	FALSE	TRUE	3	TRUE	RecNciI	
LB-01788	FALSE	TRUE	3	TRUE	RecNciI	
LB-02286	FALSE	TRUE	3	TRUE	RecNciI	
LB-02338	FALSE	TRUE	3	TRUE	RecNciI	

LB-02662	FALSE	TRUE	3	TRUE	c.1263del+RecTL	
LB-02817	FALSE	TRUE	3	TRUE	RecNciI	
HB-PD_INVDX373MWV	FALSE	TRUE	3	FALSE	L483P	
HB-PD_INVWN635UXR	FALSE	TRUE	3	TRUE	RecNciI	
PD-PDEK306DBC	FALSE	TRUE	3	FALSE	L483P	
PD-PDLR687WTH	FALSE	TRUE	3	TRUE	c.1263del+RecTL	
HG00119	FALSE	TRUE	4	None	c.1263del+RecTL	
NA20815	FALSE	TRUE	4	None	L483P	
NA18991	FALSE	TRUE	4	None	L483P	
HG02613	FALSE	TRUE	4	None	A495P	
HG00115	FALSE	TRUE	4	None	c.1263del+RecTL	
HG02439	FALSE	TRUE	4	None	c.1263del	
NA20513	FALSE	TRUE	4	None	L483P	
HG00310	FALSE	TRUE	4	None	L483P	
HG02151	FALSE	TRUE	4	None	c.1263del	
HG03967	FALSE	TRUE	4	None	L483P	
LB-00009	FALSE	TRUE	4	None	RecNciI	
LB-00092	FALSE	TRUE	4	None	L483P	
LB-00483	FALSE	TRUE	4	None	RecNciI	
LB-00490	FALSE	TRUE	4	None	L483P	
LB-00575	FALSE	TRUE	4	None	c.1263del	
LB-00668	FALSE	TRUE	4	None	L483P	
LB-00734	FALSE	TRUE	4	None	L483P	
LB-00760	FALSE	TRUE	4	None	L483P	
LB-00906	FALSE	TRUE	4	None	A495P	
LB-01188	FALSE	TRUE	4	None	L483P	
LB-01223	FALSE	TRUE	4	None	c.1263del	
LB-01297	FALSE	TRUE	4	None	L483P	
LB-01339	FALSE	TRUE	4	None	A495P	
LB-01351	FALSE	TRUE	4	None	L483P	
LB-01363	FALSE	TRUE	4	None	L483P	
LB-01388	FALSE	TRUE	4	None	L483P	
LB-01391	FALSE	TRUE	4	None	L483P	
LB-01403	FALSE	TRUE	4	None	L483P	
LB-01440	FALSE	TRUE	4	None	A495P	
LB-01477	FALSE	TRUE	4	None	c.1263del	
LB-01540	FALSE	TRUE	4	None	D448H	
LB-01599	FALSE	TRUE	4	None	L483P	
LB-01613	FALSE	TRUE	4	None	D448H	
LB-01631	FALSE	TRUE	4	None	RecNciI	
LB-01696	FALSE	TRUE	4	None	L483P	
LB-01752	FALSE	TRUE	4	None	L483P	

LB-01803	FALSE	TRUE	4	None	L483P	
LB-01894	FALSE	TRUE	4	None	L483P	
LB-01922	FALSE	TRUE	4	None	L483P	
LB-02197	FALSE	TRUE	4	None	L483P	
LB-02483	FALSE	TRUE	4	None	A495P	
LB-02676	FALSE	TRUE	4	None	c.1263del	
LB-02760	FALSE	TRUE	4	None	c.1263del	
LB-02784	FALSE	TRUE	4	None	L483P	
LB-02815	FALSE	TRUE	4	None	c.1263del+RecTL	
LB-08162	FALSE	TRUE	4	None	c.1263del	
LB-06559	FALSE	TRUE	4	None	A495P	
LB-07084	FALSE	TRUE	4	None	D448H	
LB-07658	FALSE	TRUE	4	None	A495P	
BF-1080	FALSE	TRUE	4	None	A495P	
HB-PD_INVHN100ZHK	FALSE	TRUE	4	None	A495P	
HB-PD_INVKJ120VLF	FALSE	TRUE	4	None	L483P	
HB-PD_INVWU757PGL	FALSE	TRUE	4	None	RecNciI	
PD-PDCH154ZHF	FALSE	TRUE	4	None	D448H	
PD-PDDJ206TP0	FALSE	TRUE	4	None	RecNciI	
PD-PDEW749KZU	FALSE	TRUE	4	None	L483P	
PD-PDMD724EA9	FALSE	TRUE	4	None	L483P	
PD-PDXU108EDQ	FALSE	TRUE	4	None	L483P	
PD-PDXU630RLV	FALSE	TRUE	4	None	L483P	
PP-3420	FALSE	TRUE	4	None	L483P	
PP-3429	FALSE	TRUE	4	None	A495P	
PP-3700	FALSE	TRUE	4	None	L483P	
PP-41342	FALSE	TRUE	4	None	L483P	
PP-60060	FALSE	TRUE	4	None	L483P	
HB-PD_INVAV028JED	FALSE	TRUE	4	None	L483P	
HB-PD_INVLR599UE9	FALSE	TRUE	4	None	D448H	
HB-PD_INVLU007ANL	FALSE	TRUE	4	None	L483P	
PD-PDGF687UAV	FALSE	TRUE	4	None	L483P	
PP-57787	FALSE	TRUE	4	None	L483P	

PP-59343	FALSE	TRUE	4	None	L483P	
PP-59926	FALSE	TRUE	4	None	L483P	
LB-00239	FALSE	TRUE	5	None	L483P	
BF-1016	FALSE	TRUE	5	None	L483P	
HB-PD_INVRH572AT6	FALSE	TRUE	5	None	L483P	
PP-3307	FALSE	TRUE	5	None	L483P	
LB-00823	FALSE	TRUE	6	None	D448H	
LB-02672	TRUE	FALSE	7	None	D448H	L483P
LB-01354	FALSE	TRUE	8	None	c.1263del+RecTL	

Supplementary Table 5: Complete list of the number of samples carrying *GBA* variants in population samples.

	1kGP	PD		LBD		
Variant	N=2405	case N=2325	control N=1255	case N=2598	control N=1941	mild/severe
c.115+1G>A	2	3	1	3	0	severe
c.1263del	2	0	0	6	0	severe
c.1263del+RecTL	2	1	0	4	0	severe
p.A348V	0	0	0	1	0	mild
p.A495P	1	3	0	4	2	mild
p.D438N	0	0	0	1	0	severe
p.D448H	0	1	1	4	1	severe
p.E365K	25	91	21	145	30	non-pathogenic (PD risk)
p.F252I	0	1	0	0	0	severe
p.F298L	0	0	0	1	0	severe
p.G241R	0	1	0	4	0	severe
p.G364R	0	0	0	1	0	severe
p.G416S	0	0	0	1	0	mild
p.H350R	0	0	0	1	0	severe
p.K118N	0	0	0	1	0	mild
p.L29fs	0	3	0	0	1	severe
p.L483P	5	14	6	23	0	severe
p.L483R	0	1	0	0	0	severe
p.N227S	1	0	0	1	0	mild
p.N409S	3	128	158	59	19	mild
p.P305fs	0	0	0	1	0	severe
p.R159W	0	3	0	3	0	severe
p.R170C	0	0	0	1	0	severe
p.R296Q	0	3	1	3	0	severe
p.R398X	0	0	0	1	0	severe
p.R502C	2	2	0	8	0	severe
p.R535C	0	0	0	1	0	mild
p.R535H	0	6	3	4	1	mild
p.R87W	0	0	0	1	0	mild
p.S235P	0	1	0	0	0	severe
p.T408M	9	38	10	65	32	non-pathogenic (PD risk)
p.V433L	0	1	0	1	0	severe
p.V499L	0	0	0	1	0	mild
p.W223R	0	0	0	1	0	severe
p.W420X	0	0	0	1	0	unknown
RecNciI	1	3	0	13	0	severe

Supplementary Table 6: Analysis of Trios in the 1kGP cohort.

Proband	variant	father	variant	mother	variant
HG01053	T408M	HG01051	T408M	HG01052	None
HG01096	E365K	HG01094	None	HG01095	E365K
HG01258	N409S	HG01256	None	HG01257	N409S
HG02514	c.115+1G>A	HG02512	c.115+1G>A	HG02513	None
NA07348	E365K	NA07357	None	NA07345	E365K
HG03909	T408M	HG03908	T408M	HG03907	None
NA12335	T408M	NA12340	None	NA12341	T408M
HG02615	A495P	HG02613	A495P	HG02614	None
HG03669	None	HG03667	E365K	HG03668	None
NA10860	None	NA11992	E365K	NA11993	None
NA12386	None	NA12399	E365K	NA12400	None
NA12818	None	NA12829	E365K	NA12830	None
NA12877	None	NA12889	N409S	NA12890	None
NA10865	None	NA11891	None	NA11892	c.115+1G>A
NA12767	None	NA12777	None	NA12778	E365K
NA19151	None	NA19150	None	NA19149	N227S
HG00423	None	HG00421	None	HG00422	RecNciI
HG01062	None	HG01060	None	HG01061	T408M
HG01505	None	HG01503	None	HG01504	T408M
HG01508	None	HG01506	None	HG01507	T408M
No variant detected in the remaining 582 trios					

Supplementary Table 7: Cost of ONT analysis of the *GBA* gene per sample (in GBP_

ONT as performed		Multiplexing at 12x96	Flongle
Longamp polymerase*	4.7		
AmpureXP magnetic beads	1.0		
flow-cell	7.7	0.7	0.8
SQK-LSK109	0.9		
Barcoding kit	1.5	2	
NEBNext companion	0.4		
Electrophoresis	1-2		
Qubit analysis	1-2		
Other consumables**	1		
Total***	18.2	11.7	11.3

*This is the cost per sample for 4 PCR reactions: primer pairs 1-3, and the barcoding PCR for primer pair 1 product. If one of the other PCRs also yields a product, indicating reciprocal recombination, this will also require barcoding and sequencing at additional cost for this sample.
**Estimate of costs for nuclease free water, filtered tips, ethanol, agarose electrophoresis, etc.
***This is an estimate at the time of writing (March 2022) and UK list prices, based on using one full MinION flow-cell for 94 samples (plus 2 controls). Assuming 90% of reads are on target, to reach a coverage of 550x for 94 samples requires 512Mb. The theoretical maximum flow cell yield as per Nanopore website is 50Gb. This suggests that costs could be lowered by further optimising the pipeline, for example higher level barcoding by additionally using the ONT kit SQK-PBK004, or using Flongle flow cells (maximum output 2.8 Gb). Finally, re-using MinION flow-cells after flushing is possible. We do not expect the small amount of DNA carried over to confound analysis, but we have not verified this.

Supplementary Table 8: *GBA*/*GBAP1* differentiating sites. Coordinates are in hg38.

chr	*GBA* position (chr1)	*GBA* base	*GBAP1* position	*GBAP1* base
chr1	155231496	c	155210868	g
chr1	155231522	a	155210894	g
chr1	155231557	t	155210929	c
chr1	155231692	g	155211064	a
chr1	155231693	c	155211065	t
chr1	155231701	t	155211073	c
chr1	155231818	aca	155211190	a
chr1	155231834	g	155211204	a
chr1	155231848	a	155211218	c
chr1	155231857	t	155211227	c
chr1	155231870	a	155211240	g
chr1	155231923	t	155211295	a
chr1	155231936	a	155211308	g
chr1	155231937	g	155211309	a
chr1	155231941	a	155211313	g
chr1	155231942	g	155211314	a
chr1	155231989	g	155211363	a
chr1	155232135	t	155211509	a
chr1	155232231	g	155211605	a
chr1	155232340	c	155211714	t
chr1	155232418	a	155211792	g
chr1	155232440	t	155211814	c
chr1	155232447	a	155211821	g
chr1	155232451	a	155211825	g
chr1	155232540	g	155211914	c
chr1	155232549	c	155211923	g

chr 1	155232550	g	155211924	a
chr 1	155232572	t	155211946	c
chr 1	155232721	c	155212095	t
chr 1	155232724	c	155212098	t
chr 1	155232784	a	155212158	g
chr 1	155232834	a	155212208	c
chr 1	155232892	g	155212266	t
chr 1	155232893	a	155212267	t
chr 1	155232916	g	155212290	c
chr 1	155232919	a	155212293	g
chr 1	155232927	g	155212301	a
chr 1	155232935	a	155212309	g
chr 1	155232982	g	155212356	a
chr 1	155233046	a	155212420	g
chr 1	155233268	c	155212642	g
chr 1	155233287	g	155212661	a
chr 1	155233514	a	155212888	g
chr 1	155233517	c	155212891	t
chr 1	155233521	t	155212895	a
chr 1	155233531	g	155212905	a
chr 1	155233612	a	155212985	g
chr 1	155233639	g	155213012	a
chr 1	155234903	c	155214276	t
chr 1	155235203	c	155214576	g
chr 1	155235217	c	155214590	g
chr 1	155235252	a	155214625	g
chr 1	155235379	a	155214752	g
chr 1	155235412	g	155214785	a

chr 1	155235727	c	155215100	g
chr 1	155235749	GGGACTGTCGACAAAGTTACGCACCCAATTGGGTCCT CCTTCGGGGTTCAGGGCAA	155215122	g
chr 1	155235918	a	155215236	g
chr 1	155236097	g	155215415	c
chr 1	155236102	t	155215420	c
chr 1	155236129	t	155215447	c
chr 1	155236145	g	155215463	c
chr 1	155236175	g	155215493	a
chr 1	155236190	a	155215508	g
chr 1	155237982	t	155216705	c
chr 1	155237989	g	155216712	a
chr 1	155237990	c	155216713	t
chr 1	155237996	g	155216719	t
chr 1	155237997	c	155216720	t
chr 1	155238055	t	155216778	c
chr 1	155238088	t	155216811	c
chr 1	155238092	t	155216815	g
chr 1	155238141	a	155216864	t
chr 1	155238174	c	155216897	t
chr 1	155238192	a	155216915	g
chr 1	155238206	a	155216929	c
chr 1	155238214	a	155216937	c
chr 1	155238630	g	155217353	a
chr 1	155238754	g	155217477	a
chr 1	155238872	ag	155217595	t
chr 1	155238882	a	155217604	g
chr 1	155238929	a	155217651	t
chr 1	155238930	g	155217652	t

Supplementary Table 9: *GBA* variants targeted by Gauchian. Coordinates are in hg38.

chr	position	ref	alt	variant_name
chr1	155235002	C	T	p.R535H
chr1	155235003	G	A	p.R535C
chr1	155235007	C	T	p.W533X
chr1	155235057	C	T	p.G517S
chr1	155235101	C	T	c.1506-1G>A
chr1	155235196	G	A	p.R502C
chr1	155235197	G	C	p.N501K
chr1	155235205	C	G	p.V499L
chr1	155235217	C	G	p.A495P
chr1	155235241	C	T	p.A487T
chr1	155235252	A	C	p.L483R
chr1	155235252	A	G	p.L483P
chr1	155235303	A	C	p.I466S
chr1	155235679	A	G	c.1388+2T>C
chr1	155235708	G	C	p.P454R
chr1	155235712	G	A	p.Q453X
chr1	155235721	A	T	p.F450I
chr1	155235726	T	A	p.D448V
chr1	155235727	C	G	p.D448H
chr1	155235749	GGGACTGTCGACAAAGTTACGCACCCAATTGGGTCCTCCTTCGGGGTTCAGGGCAA	G	p.L422fs/c.1263del
chr1	155235750	G	A	p.P440L
chr1	155235757	C	T	p.D438N
chr1	155235760	C	A	p.V437F
chr1	155235772	C	A	p.V433L
chr1	155235780	G	A	p.P430L
chr1	155235790	C	A	p.E427X
chr1	155235798	A	G	p.L424P
chr1	155235810	C	T	p.W420X
chr1	155235819	C	T	p.W417X
chr1	155235823	C	T	p.G416S
chr1	155235829	C	A	p.V414L
chr1	155235831	T	G	p.H413P
chr1	155235841	G	C	p.L410V

chr1	155235843	T	C	p.N409S
chr1	155235843	T	G	p.N409T
chr1	155236255	C	G	p.S405T
chr1	155236261	C	G	p.S403T
chr1	155236277	G	A	p.R398X
chr1	155236285	G	A	p.S395F
chr1	155236292	G	C	p.L393V
chr1	155236295	G	A	p.R392W
chr1	155236295	G	C	p.R392G
chr1	155236298	C	G	p.V391L
chr1	155236318	G	A	p.S384F
chr1	155236328	A	C	p.C381G
chr1	155236379	C	T	p.G364R
chr1	155236384	G	A	p.T362I
chr1	155236416	C	A	p.W351C
chr1	155236417	C	G	p.W351S
chr1	155236420	T	C	p.H350R
chr1	155236426	G	A	p.A348V
chr1	155236439	CA	C	p.K342_Y343insX
chr1	155237099	G	T	c.999+242C>A
chr1	155237357	G	A	p.P328L
chr1	155237370	G	A	p.R324C
chr1	155237394	G	A	p.R316C
chr1	155237411	C	T	p.S310N
chr1	155237412	T	C	p.S310G
chr1	155237425	AG	A	p.P305fs
chr1	155237427	G	C	p.P305A
chr1	155237444	A	G	p.I299T
chr1	155237446	G	T	p.F298L
chr1	155237453	C	T	p.R296Q
chr1	155237454	G	A	p.R296X
chr1	155237470	G	T	p.F290L
chr1	155237474	C	G	p.G289A
chr1	155237480	C	A	p.C287F

chr1	155237576	A	T	p.F255Y
chr1	155237577	A	C	p.F255V
chr1	155237579	C	G	c.762-1G>C
chr1	155238141	A	T	p.F252I
chr1	155238174	C	T	p.G241R
chr1	155238186	T	C	p.K237E
chr1	155238192	A	G	p.S235P
chr1	155238194	C	T	p.G234E
chr1	155238214	A	C	p.N227K
chr1	155238214	AT	CC	p.N227R
chr1	155238215	T	C	p.N227S
chr1	155238228	A	G	p.W223R
chr1	155238234	G	T	p.P221T
chr1	155238242	C	T	p.W218X
chr1	155238264	CG	C	p.V211fs
chr1	155238270	G	A	p.R209C
chr1	155238298	CAG	C	p.L199fs
chr1	155238519	T	G	p.K196Q
chr1	155238525	T	A	p.K194X
chr1	155238547	GA	G	p.F186fs
chr1	155238571	AG	A	p.P178fs
chr1	155238579	C	T	p.D176N
chr1	155238584	T	C	p.Y174C
chr1	155238596	C	A	p.R170L
chr1	155238596	C	T	p.R170H
chr1	155238597	G	A	p.R170C
chr1	155238608	T	A	p.D166V
chr1	155238617	GC	G	p.A163fs
chr1	155238624	G	A	p.P161S
chr1	155238629	C	T	p.R159Q
chr1	155238630	G	A	p.R159W
chr1	155239639	A	C	p.L144R
chr1	155239655	C	G	p.A139P
chr1	155239665	CAG	C	p.L135fs

chr1	155239716	C	G	p.K118N
chr1	155239736	G	A	p.Q112X
chr1	155239934	G	A	p.R87W
chr1	155239939	C	T	p.G85E
chr1	155239968	GGTA	G	p.T75del
chr1	155239989	C	CG	p.T69fs
chr1	155240033	C	A	p.V54L
chr1	155240629	C	T	c.115+1G>A
chr1	155240637	C	T	p.W36X
chr1	155240651	G	GC	p.Q32fs
chr1	155240660	G	GC	p.L29fs
chr1	155240671	AG	A	p.L25fs
p.L483P + p.A495P + p.Val499=				RecNciI
RecNciI + p.D448H				Rec.TL
RecNciI + p.D448H + c.1263del				c.1263del+RecTL

Supplementary Table 10: PCR conditions for primer pair 1.

Reagents	**Volume**		**°C**	**Time**	**cycles**
Template DNA (200ng)	x µL		94	30sec	1
Nuclease free water	19µL - x		94	15sec	35
Mg2+	2µL		65	15sec	
Forward primer	2µL		65	6min	
Reverse primer	2µL		65	10min	1
LongAmp Taq 2x polymerase mix (NEB)	25µL		4	hold	
Primer pair A*	Forward	5′- TTTCTGTTGGTGCTGATATTGCTCCTAAAGTTGTCACCCATACATG -3′			
	Reverse	5′- ACTTGCCTGTCGCTCTATCTTCCCAACCTTTCTTCCTTCTTCTCAA - 3′			

*primers have been edited to contain the ONT barcode adapter sequence.

Supplementary Table 11: PCR conditions for primers pairs 2 and 3.

Reagents	Volume		°C	Time	cycles
Template DNA (100ng)	x µL		95	3min	1
Nuclease free water	24.5µL - x		95	15sec	12
			62	15sec	
Barcode mix	0.5µL		65	10min	
			65	10min	1
LongAmp Taq 2x polymerase mix (NEB)	25µL		4	hold	
Primer pair B*	Forward	5′-TTTCTGTTGGTGCTGATATTGCATGTGTCCATTCTCCATGTCTTCA-3′			
	Reverse	5′-ACTTGCCTGTCGCTCTATCTTCAGCCTTCCTTCCTTCCCTGCAT-3′			
Primer pair C*	Forward	5′-TTTCTGTTGGTGCTGATATTGCGTGTCCGTTCTCCACATCCTTG-3′			
	Reverse	5′-ACTTGCCTGTCGCTCTATCTTCCCAACCTTTCTTCCTTCTTCTCAA-3′			

*primers have been edited to contain the ONT barcode adapter sequence.