

Table S 1. Post-trimming and mapping results to reference genome for all groups

Total reads	Mapping reads	Mapping >1 time	Mapping 1 time	Mapping 0 time
GBA-PD				
12245034	94.47%	1390912	10177533	676589
12534145	94.15%	1522375	10278974	732796
13364587	96.02%	1616992	11215592	532003
14588079	96.17%	1520881	12507829	559369
22038017	95.96%	2889324	18258227	890466
GBA-carriers				
16815993	94.19%	1868206	13970248	977539
20016766	96.44%	2595136	16708395	713235
11328352	95.71%	1415542	9427273	485537
15042608	95.42%	2338602	12014382	689624
Controls				
13186256	94.77%	1922697	10573358	690201
12888917	94.42%	1349391	10820389	719137
29105091	96.34%	2980649	25060066	1064376
13276643	95.33%	1916805	10740334	619504

GBA-PD - Parkinson's disease associated with mutations in the GBA gene; GBA-carriers - asymptomatic GBA mutation carriers

Table S 2. Differentially expressed genes from L444P/N GBA-PD patients compared to controls in monocyte-derived macrophages

DEGs	padj	log2FoldChange
<i>JUNB</i>	1.56×10^{-8}	-1.273329
<i>HOOK2</i>	2.39×10^{-7}	-1.109320
<i>EGR1</i>	3.17×10^{-6}	-4.187828
<i>DUSP1</i>	3.95×10^{-6}	-3.25103
<i>IL6</i>	3.95×10^{-6}	-3.4155
<i>ARL4C</i>	5.06×10^{-6}	-2.147519
<i>NR4A2</i>	2.94×10^{-4}	-3.001167
<i>CCL3L1</i>	4.026×10^{-4}	-5.2936939
<i>PPBP</i>	0.00123	7.01866736
<i>RPL18</i>	0.00149	-0.724112
<i>IER2</i>	0.003892	-2.148075
<i>TRBV5-1</i>	0.00389	-2.648457

<i>CXCL2</i>	0.00412	-2.436204
<i>MAL</i>	0.00412	-3.526525
<i>MMP7</i>	0.0052	3.5695832
<i>CCL3</i>	0.0052	-2.8581180
<i>DUSP2</i>	0.00665	-2.0777352
<i>ATP2B1-AS1</i>	0.0087	-2.08186683
<i>CCL4</i>	0.0095	-3.10118915
<i>CCL4L2</i>	0.0111	-4.86057595
<i>MIR34AHG</i>	0.0123	1.293966592
<i>KIAA0319</i>	0.0173	2.7304552
<i>JUN</i>	0.0202	-1.8078662
<i>TPTEP1</i>	0.0246	2.2196251
<i>ZFP36</i>	0.03487	-1.5978346
<i>IER3</i>	0.0348	-1.26935
<i>TTLL4</i>	0.0412	0.89197963
<i>COLEC12</i>	0.0412	-2.26691
<i>CXCL5</i>	0.041	2.862093
<i>ENPP2</i>	0.0427	-3.299636
<i>ABHD2</i>	0.0427133	0.90893
<i>HSPA1B</i>	0.042713	0.996150

GBA-PD - Parkinson's disease associated with mutations in the GBA gene; *GBA-carriers* - asymptomatic GBA mutation carriers; *DEGs* - differentially expressed genes

Table S 3. Differentially expressed genes from L444P/N GBA-carriers compared to controls in monocyte-derived macrophages

DEGs	padj	log2FoldChange
<i>IL31RA</i>	9.87×10^{-18}	-19.44049
<i>ACOD1</i>	4.78×10^{-14}	-18.67938
<i>PRSS22</i>	4.94×10^{-6}	-19.411937
<i>LINC01891</i>	4.055×10^{-4}	-18.4905145
<i>ATP1B4</i>	4.70×10^{-4}	-21.902312
<i>TBX3</i>	4.70×10^{-4}	-21.694237

<i>VATIL</i>	0.00100337	-16.8595347
<i>NXPH3</i>	0.0013055	-20.8813694
<i>MTIM</i>	0.0014474	-7.5301355
<i>SHC4</i>	0.002294	-20.309837
<i>HLA-J</i>	0.002965	3.1020326
<i>SPRY4</i>	0.004660	-4.39827985
<i>KCNMB1</i>	0.008565	-2.8714975
<i>JAKMIP2</i>	0.0094078	1.4094559
<i>OSCAR</i>	0.0098210	-1.30014117
<i>KIAA0319</i>	0.016259	3.2499566
<i>FGL2</i>	0.0314813	-2.086525

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Table S 4. Differentially expressed genes from L444P/N GBA-PD patients compared to GBA-carriers in monocyte-derived macrophages

DEGs	padj	log2FoldChange
<i>IL31RA</i>	3.42×10^{-28}	22.81419
<i>ACOD1</i>	4.92×10^{-24}	22.49465
<i>VATIL</i>	1.62×10^{-7}	21.26457
<i>ATP1B4</i>	1.77×10^{-7}	26.877062
<i>PRSS22</i>	3.74×10^{-7}	20.0742
<i>MTIM</i>	5.64×10^{-7}	9.60953
<i>SHC4</i>	1.52×10^{-5}	23.66668
<i>UTS2R</i>	4.197×10^{-5}	18.4369
<i>NXPH3</i>	4.62×10^{-5}	22.674242
<i>KCNMB1</i>	7.34×10^{-5}	3.408771
<i>FGD5</i>	7.34×10^{-5}	3.005397
<i>TBX3</i>	1.57×10^{-4}	21.40274
<i>MTIF</i>	1.87×10^{-4}	3.56241
<i>HSPH1</i>	2.75×10^{-4}	0.75877
<i>SPRY4</i>	3.032×10^{-4}	4.830094
<i>KCNJ2</i>	4.24×10^{-4}	2.810203

<i>MTIL</i>	5.049×10^{-4}	6.71591
<i>LINC01891</i>	0.0010437551433765133	16.980
<i>ARL4C</i>	0.0011152363202132764	-1.954802
<i>DUSP1</i>	0.002709	-2.793141
<i>OSCAR</i>	0.004080	1.2904701
<i>TGM2</i>	0.007633753	2.083364
<i>SRSF5</i>	0.008446	-0.616122
<i>UNC5B</i>	0.010984	2.2372
<i>BATF2</i>	0.0218465	2.8215
<i>MTIX</i>	0.027678	3.16545
<i>SLC39A8</i>	0.0284	2.780923830
<i>ZNF704</i>	0.03119	-2.44145
<i>CALHM6</i>	0.03119	4.1001527
<i>STON2</i>	0.0320245	-5.194386
<i>SERPINH1</i>	0.035644	0.92875318
<i>LIPM</i>	0.036739	9.097984
<i>RNF144B</i>	0.03789	1.6824349
<i>NT5C3B</i>	0.0378908	-1.271271
<i>SNHG3</i>	0.04101556	-0.962452

GBA-PD - Parkinson's disease associated with mutations in the GBA gene; *GBA-carriers* - asymptomatic GBA mutation carriers; *DEGs* - differentially expressed genes

Table S 5. Differentially expressed genes from GBA-PD (L444P/N+N370S/N) patients compared to controls in monocyte-derived macrophages

DEGs	padj	log2FoldChange
<i>JUNB</i>	2.37×10^{-12}	-1.253670176
<i>HOOK2</i>	2.88×10^{-9}	-1.071183696
<i>EGR1</i>	4.68×10^{-6}	-4.119209619
<i>ARL4C</i>	1.07×10^{-5}	-2.025843567
<i>NR4A2</i>	3.91×10^{-5}	-2.986036049
<i>IL6</i>	6.95×10^{-5}	-3.866493754
<i>DUSP1</i>	0.000139485	-3.369818756

<i>MMP7</i>	0.000489067	3.915533725
<i>CCL3L1</i>	0.000770649	-5.74901087
<i>PPBP</i>	0.000821926	6.654290865
<i>TRBV5-1</i>	0.001747096	-2.531049969
<i>RPL18</i>	0.001949174	-0.703837045
<i>IER2</i>	0.00485697	-2.103641578
<i>TPTEP1</i>	0.005948528	2.203616802
<i>ZFP36</i>	0.007195823	-1.668224122
<i>TRIM13</i>	0.00850527	0.725108438
<i>ENPP2</i>	0.009314153	-3.404150223
<i>VMP1</i>	0.012172779	0.624239627
<i>CCL4L2</i>	0.01305784	-5.208863091
<i>BCL6</i>	0.0210965	0.756069963
<i>CCL3</i>	0.021273736	-2.691408178
<i>COLEC12</i>	0.02135696	-2.182528256
<i>MAL</i>	0.02135696	-3.03596868
<i>CXCL2</i>	0.027199467	-2.713284496
<i>SLC4A8</i>	0.03342678	1.181900735
<i>CYP4V2</i>	0.035836308	0.789161862
<i>SKIL</i>	0.039183179	0.637145847
<i>DOCK5</i>	0.045685169	1.06312728

Table S 6. Differentially expressed genes from GBA-carriers (L444P/N+N370S/N) compared to controls in monocyte-derived macrophages

DEGs	padj	log2FoldChange
<i>IL31RA</i>	2.36×10^{-18}	-17.683476
<i>ACOD1</i>	2.88×10^{-18}	-18.210591
<i>NXPH3</i>	1.77×10^{-16}	-29.984238
<i>LINC01891</i>	3.37×10^{-16}	-29.999458
<i>VAT1L</i>	0.00032722	-14.087655
<i>ATP5PDP3</i>	0.00045205	18.7100791

<i>JUNB</i>	0.00046733	-0.8331051
<i>HOOK2</i>	0.00632252	-0.7218695

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Table S 7. Differentially expressed genes from GBA-PD (L444P/N+N370S/N) patients compared to GBA-carriers (L444P/N+N370S/N) in monocyte-derived macrophages

DEGs	padj	log2FoldChange
<i>ACOD1</i>	1.43×10^{-30}	21.1020452
<i>IL31RA</i>	2.00×10^{-28}	19.8053162
<i>IFNB1</i>	1.40×10^{-12}	-30.807576
<i>ARL4C</i>	0.00087384	-1.6917533
<i>TGM2</i>	0.00087384	2.14653337
<i>BCL6</i>	0.00664798	0.82786078
<i>DEPP1</i>	0.00664798	1.83107981
<i>RPL18</i>	0.00795303	-0.6557988
<i>STON2</i>	0.00996956	-4.4615928
<i>KCNE1</i>	0.01102564	2.05763841
<i>YPEL4</i>	0.01374026	1.92204556
<i>LOC100507642</i>	0.01643034	1.07536814
<i>TPTEP1</i>	0.02159264	2.03424689
<i>KLF2</i>	0.02159264	-1.8023782
<i>CXCL5</i>	0.03068743	2.88289408
<i>DUSP1</i>	0.03965958	-2.4511962
<i>COLEC12</i>	0.03965958	-2.0787807
<i>CHST15</i>	0.03965958	0.77291653
<i>TRIM13</i>	0.03965958	0.65318516
<i>BTBD19</i>	0.03965958	1.89239807
<i>HDGFL3</i>	0.04210421	1.05565628
<i>RPL6P19</i>	0.04210421	-1.2254401
<i>ABCC6</i>	0.04819162	1.71221141

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Table S 8. Functional clusters selected according to the results of GO analysis between GBA-PD (L444P/N+N370S/N) patients. GBA-carriers (L444P/N+N370S/N) and controls

	[GO ID] GO term	padjusted	DEGs
GBA-PD (L444P/N+N370S/N) vs controls			
GBA-	[GO:0010941] regulation of cell death	0.039	<i>BCL6. CCL3. DUSP1. EGR1. IL6. MAL. NR4A2. SKIL. TRIM13. ZFP36</i>
	[GO:0010942] positive regulation of cell death	0.0023	<i>BCL6. CCL3. DUSP1. EGR1. IL6. MAL. SKIL. TRIM13</i>
	[GO:0006935] chemotaxis	0.0015	<i>CCL3. CCL3L1. CCL4L1. CXCL2. DUSP1. ENPP2. IL6. PPBP</i>
	[GO:0006954] inflammatory response	0.0041	<i>BCL6. CCL3. CCL3L1. CCL4L1. CXCL2. IL6. PPBP. ZFP36</i>
	[GO:0034097] response to cytokine	2.11×10^{-6}	<i>BCL6. CCL3. CCL3L1. CCL4L1. CXCL2. DUSP1. EGR1. HOOK2. IL6. JUNB. PPBP. SKIL. ZFP36</i>
	[GO:0030595] leukocyte chemotaxis	1.77×10^{-5}	<i>CCL3. CCL3L1. CCL4L1. CXCL2. DUSP1. IL6. PPBP</i>
	[GO:0097529] myeloid leukocyte migration	1.31×10^{-5}	<i>CCL3. CCL3L1. CCL4L1. CXCL2. DUSP1. IL6. PPBP</i>
	[GO:0019221] cytokine-mediated signaling pathway	0.00054	<i>BCL6. CCL3. CCL3L1. CCL4L1. CXCL2. EGR1. IL6. JUNB. PPBP</i>
	[GO:0005125] cytokine activity	0.00046	<i>CCL3. CCL3L1. CCL4L1. CXCL2. IL6. PPBP</i>
	[GO:0002548] monocyte chemotaxis	1.67×10^{-5}	<i>CCL3. CCL3L1. CCL4L1. DUSP1. IL6</i>
PD -	[GO:0048247] lymphocyte chemotaxis	0.033	<i>CCL3. CCL3L1. CCL4L1</i>
	[GO:1990869] cellular response to chemokine	1.85×10^{-6}	<i>CCL3. CCL3L1. CCL4L1. CXCL2. DUSP1. PPBP</i>
	GBA-PD (L444P/N+N370S/N) vs GBA-carriers (L444P/N+N370S/N)		
	[GO:0042092] type 2 immune response	0.00093	<i>BCL6. IFNB1. IL31RA</i>
	[GO:0002520] immune system development	0.047	<i>ACOD1. BCL6. IFNB1. IL31RA. KLF2. STON2</i>
	[GO:0002367] cytokine production involved in immune response	0.025	<i>BCL6. IFNB1. IL31RA</i>
	[GO:0001818] negative regulation of cytokine production	0.019	<i>ACOD1. BCL6. IFNB1. KLF2</i>
	[GO:0071345] cellular response to cytokine stimulus	0.0095	<i>ACOD1. BCL6. CXCL5. DUSP1. IFNB1. IL31RA. KLF2</i>
	[GO:0006952] defense response	0.022	<i>ACOD1. BCL6. COLEC12. CXCL5. IFNB1. IL31RA. TGM2. TRIM13</i>
	GBA-carriers (L444P/N+N370S/N) vs controls		
	[GO:0071345] cellular response to cytokine stimulus	0.0032	<i>ACOD1. HOOK2. IL31RA. JUNB</i>

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