# TAG SNPs Identification Papers

PMID: <u>35970579</u>

# From the paper

The subsequent meta-analysis of COURAGE-PD and IPDGC datasets (Ntotal = 25,950) led to the identification of 2 genome-wide significant association signals on Chr 4, including the previously reported *SNCA* locus (rs983361) and a novel *BST1* locus (rs4698412).

riskAllele	pValue	riskFrequency	mappedGenes	tra
rs983361- T	3E-09	0.204	SNCA-AS1	Age ons par dise
rs4698412- A	4E-08	0.562	BST1	Age ons par disc

ref: rs4698412

LD information hg19 LD R-squared

4 15737101	rs117	24635 4
15737348	rs4698412	0.999308
4 15737348	rs46	<b>98412</b> 4
15730146	rs34559912	0.966445
4 15737348	rs46	<b>98412</b> 4
15730398	rs4389574	0.963118
4 15737348	rs46	<b>98412</b> 4
15737101	rs11724635	0.999308
4 15737348	rs46	<b>98412</b> 4
15737348	rs4698412	1
4 15737348	rs46	<b>98412</b> 4
15737882	rs4698413	0.993086
ref: rs983361		
hg19 LD R-squared		
4 90753180	rs273	37002 4
90761944	rs983361	0.817636
4 90757294	rs13	72518 4
90761944	rs983361	0.836286
4 90757505	rs13	72520 4
90761944	rs983361	0.8542
4 90761944	rs98	<b>33361</b> 4
90750326	rs2583978	0.800937

-	90761944		<b>33361</b> 4
90750	588	rs2583979	0.803922
4	90761944	rs98	<b>33361</b> 4
90753	180	rs2737002	0.817636
4	90761944	rs98	<b>33361</b> 4
90754	313	rs1471484	0.825711
4	90761944	rs98	<b>33361</b> 4
90754	771	rs990085	0.819515
4	90761944	rs98	<b>3361</b> 4
90757	294	rs1372518	0.836286
4	90761944	rs98	<b>3361</b> 4
90757	309	rs1372519	0.838199
4	90761944	rs98	<b>3361</b> 4
90757	505	rs1372520	0.8542
4	90761944	rs98	<b>33361</b> 4
90761	944	rs983361	1
4	90761944	rs98	<b>33361</b> 4
90771	499	rs2583990	0.842982
4	90761944	rs98	<b>33361</b> 4
90775	649	rs1442152	0.851479
4	90761944	rs98	<b>33361</b> 4
90776	257	rs2736989	0.842982

4	90761944	rsS	<b>983361</b> 4
90779	9758	rs2583961	0.838894
4	90761944	rsS	<b>983361</b> 4
90779	9823	rs2737026	0.838894

PDID: <u>30957308</u>

# From the paper

We found two genome-wide significant association signals, one at SNCA and the other a protein-coding variant in TMEM175, both of which are known PD risk loci and a Bonferroni corrected significant effect at other known PD risk loci, GBA, INPP5F/BAG3, FAM47E/SCARB2, and MCCC1. Notably, SNCA, TMEM175.

riskAllele	pValue	mappedGenes	traitName	efoTr
rs356203-?	2E-12	SNCA	Parkinson's disease (age of onset)	age a onset disea
rs34311866- C	1E-08	TMEM175	Parkinson's disease (age of onset)	age a onset disea

rs356203

4 90637601	rs356219 4
90666041	<b>rs356203</b> 0.962572
4 90641340	rs356220 4
90666041	<b>rs356203</b> 0.985644
4 90666041	rs356203 4
90635606	rs356209 0.845618
4 90666041	rs356203 4
90636561	rs356215 0.844504
4 90666041	rs356203 4
90637601	rs356219 0.962572
4 90666041	<b>rs356203</b> 4
90641340	rs356220 0.985644
4 90666041	rs356203 4
90646886	rs356165 0.994704
4 90666041	rs356203 4
90666041	<b>rs356203</b> 1
rs34311866	
4 951947	rs34311866 4
951947	<b>rs34311866</b> 1

# rs6532192

4 90743331	rs100052	233 4
90764131	rs6532192	0.803553
4 90750025		28271 4
90764131	rs6532192	0.807909
4 90757272	rs375	6059 4
90764131	rs6532192	0.845287
4 90757394	rs375	66063 4
90764131	rs6532192	0.852115
4 90759556	rs380	06789 4
90764131	rs6532192	0.988154
4 90763360	rs768	30557 4
90764131	rs6532192	0.992393

PMID: <u>27402877</u>

# From the paper

CHR	Gene	SNP	MAF	Discov (NGRC
GWAS Test Cox regression		Effect on AAO Linear regression		

CHR	Gene	SNP	MAF	Discov (NGRC
HR	Р	Beta	95% CI	Р
5	LHFPL2	rs10035651	0.016	4.76
5	LHFPL2	rs344650	0.016	4.77
5	LHFPL2	rs344657	0.016	4.77
8	TRPS1	rs74335301	0.014	4.46
14	KLHDC1	rs79503702	0.012	6.95
14	KLHDC1_ARF6	rs192855008	0.012	7.12
15	TPM1	rs117267308	0.012	6.47

CHR	Gene	SNP	MAF	Discov (NGRC
15	TPM1	rs141049631	0.012	6.47
15	TPM1	rs116860970	0.013	6.52
15	TPM1	rs77362326	0.012	6.47
15	TPM1	rs201411148	0.012	6.47
15	TPM1	rs142383316	0.012	6.47
15	TPM1	rs117484764	0.012	6.46

## rs10035651

5 77860608 rs344650 5 77837737 **rs10035651** 0.926268

#### rs344650

 5
 77860608
 rs344650
 5

 77837737
 rs10035651
 0.926268

 5
 77860608
 rs344650
 5

 77860608
 rs344650
 1

5 77860608 **rs344650** 5 77871164 rs394521 0.901537

rs344657

None

rs74335301

8 116638637 rs**74335301** 8 116638637 rs**74335301** 1

rs79503702

14 50206170 rs**79503702** 14 50206170 rs**79503702** 1

rs192855008

None

rs141049631

None

rs116860970

15 63346376 rs117267308 15 63351500 rs116860970 0.929039

rs77362326

15 63346376 rs117267308 15 63353865 rs**77362326** 0.913295

#### rs201411148

15 63346376 rs117267308 15 63356439 rs201411148 0.964033

#### rs142383316

15 63346376 rs117267308 15 63364309 rs142383316 0.929039

#### rs117484764

15 63346376 rs117267308 15 63365502 **rs117484764** 0.929039

PMID: 33884653

# From the paper

One novel significant intergenic locus rs9783733 (NDN; PWRN4) was identified (P = 3.14E-09, beta = 2.30, SE = 0.39).

riskAllele	pValue	riskFrequency	beta	ci	n
rs9783733-?	3E-09	NR	2.3 unit increase	<b>-</b>	P

#### rs9783733

15 24168950 rs9783733 15 24168950 rs9783733 1

15 24168950 **rs9783733** 15 24177901 rs28671452 0.947717

PMID: <u>19772629</u>

### From the paper

riskAllele	pValue	mappedGenes	traitName	efoTra
rs7577851- T	9E-06	AAK1	Parkinson's disease (age of onset)	age at onset, diseas

#### rs7577851

2 69723710 rs7577851 2 rs71840259 0.996326 69723494 2 69723710 rs7577851 69723710 rs**7577851** 1 2 69723710 rs**7577851** 2 69724366 rs202069720 0.997797 2 69723710 rs**7577851** 2 rs201872917 0.997797 69724371

2 6972371069724649

**rs7577851** 2 rs111258456 0.997798