

589 **Table Captions**

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592 **Table 2. Intrinsic geometric cortical features and their definitions**

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595 **Ensembl.**

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ADNI Initiative

The National Institute on Aging (NIA), the National Institute of Biomedical Imaging and Bioengineering (NIBIB), the Food and Drug Administration (FDA) initiated the Alzheimer's Disease Neuroimaging Initiative (ADNI) in 2003. ADNI employs magnetic resonance imaging (MRI), positron emission tomography (PET), biological markers, and clinical and neuropsychological measures to detect, track and predict the progression of MCI and early AD. To aid clinical investigators in developing new treatments, assess their effectiveness, and improve efficiency (reduce time and cost of clinical trials), ADNI investigators are studying specific markers of very early AD. Michael W. Weiner, M.D., at the VA Medical Center and University of California San Francisco is the ADNI Principle Investigator. In phase I, ADNI aimed to recruit 800 adults, ages 55 to 90, to participate in the research and followed for 3 years. Details of the ADNI study design, protocols and information is available online at <http://www.adni-info.org>.

615 **Supplementary Table 2** The 140 common genes that appeared commonly in RefSeq, UCSC and
 616 Ensembl.
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ACSS1	COL23A1	INSC	NALCN	SNTB1
ADAM12	CPVL	ISPD	NKAIN2	SNX14
ADAMTS12	CSGALNACT1	ITGA8	NPAS3	SORT1
ADAMTSL1	CUBN	ITPR1	OCA2	STOML1
ADTRP	CYFIP2	KBTBD12	PDE10A	SULF1
AGBL3	DCDC2	KCNC2	PDE4B	SUPT20H
ANKRD44	DEFB129	KCNIP1	PML	SV2C
APBA1	DLC1	KCNK10	POLR3G	SYNPR
APOE	DSCAM	KIF5C	PPP3CA	TBC1D14
ARHGEF10	EGFEM1P	KYNU	PREX2	TLN2
ARL11	EHMT2	LHPP	PRIMA1	TMC7
ATP6V1E1	ERC2	LINC00326	PSMA5	TMEFF2
BCL11A	ETV6	LINC00507	PTGER3	TMEM132C
BRCA2	EXOSC8	LINC00948	PTPRG	TOMM40
C15orf41	FAM188B	LINGO2	PVR	TRAPPC9
C2	FAM65C	LRRC47	PWP2	TRIO
C21orf33	FERMT2	MAD2L2	RAI1	UBASH3B
C3orf55	FHIT	MLLT3	RAP1GAP2	USP34
C6orf10	FOXP2	MOXD1	RCBTB1	VEPH1
CA10	FSD1L	MSRA	RGS6	VIPR1
CADPS2	GABRR1	MTSS1	RHOBTB3	WDR7
CCL11	GADL1	MYLK	RNF150	WFDC12
CCSER1	GALNT10	MYO3B	S100P	XKR6
CDA	GNAI1	MYOF	SDK1	XPO1
CDH18	GPR110	MYT1	SEMA5A	XYLT1
CGNL1	HRASLS5	N4BP2L1	SHD	ZBTB12
CHCHD6	IL2RA	N4BP2L2	SLC25A29	ZNF343
CNTN4	IMPG1	NAALADL2	SNAP25	ZNF560

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620 **Supplementary Table 3.** Gene network analysis (Gene enrichment analysis using the hypergeometric
621 test)

DB	Overlap (Number)	Our genes (Number)	Total genes (Number)	DB (Size)	P-value (hypergeometric test)	References
AlzGene	2	140	60,155	47	0.005427975	ALZGENE (http://www.alzgene.org/)
Beige	4	140	60,155	95	7.59E-05	Top 20 modules relevant to AD pathology [41].
Brown2	5	140	60,155	78	1.17E-06	
Darkcyan	6	140	60,155	110	2.50E-07	
Gold2	6	140	60,155	83	4.65E-08	
Gold3	6	140	60,155	69	1.52E-08	
Gray1	6	140	60,155	52	2.66E-09	
Green4	7	140	60,155	56	6.70E-11	
Greenyellow	13	140	60,155	722	1.72E-08	
Grey60	16	140	60,155	507	8.39E-14	
Honeydew	18	140	60,155	127	0	
Khaki	25	140	60,155	262	0	
Lightyellow	28	140	60,155	382	0	
Pink	33	140	60,155	743	0	
Purple	46	140	60,155	805	0	
Red	55	140	60,155	987	0	
Red2	55	140	60,155	83	0	
Red3	55	140	60,155	67	0	
Seashell	56	140	60,155	278	0	
Tan	62	140	60,155	700	0	
Yellow	69	140	60,155	1108	0	
KEGG	20	140	60,155	168	0	KEGG pathway: hsa05010 (http://www.genome.jp/dbget-bin/www_bget?pathway:map05010)

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Supplementary Table 4 . Summary of the most significant genetics and imaging phenotypes
- 80 derived-bioimaging markers and the 80 SNPs

Neuroimaging phenotypes	Shape & Volume Measures	P-value	Index	SNPs	CHR	P-value	Gene
L_hippocampus	Volume	8.38E-12	1	rs2075650	19	2.93E-10	TOMM40
R_hippocampus	Volume	1.68E-11	2	rs11072463	15	1.13E-07	PML
L_inferior_temporal_gyrus	Volume	3.17E-09	3	rs1052242	15	5.72E-07	PML
L_inferior_temporal_gyrus	SurfaceArea	8.24E-09	4	rs793291	3	8.28E-07	ADAMTS9-AS2
R_caudate	Volume	1.05E-08	5	rs12691813	2	9.52E-07	-
L_hippocampus	SurfaceArea	1.89E-08	6	rs17027976	4	1.20E-06	-
R_caudate	SurfaceArea	2.25E-08	7	rs4972310	2	1.73E-06	-
L_hippocampus	ShapeIndex	1.28E-07	8	rs1975545	2	2.55E-06	-
R_hippocampus	SurfaceArea	2.63E-07	9	rs4886844	15	3.39E-06	PML
R_inferior_temporal_gyrus	Volume	4.09E-07	10	rs12822144	12	4.25E-06	-
R_caudate	Curvedness	1.02E-05	11	rs11680332	2	5.34E-06	-
L parahippocampal_gyrus	Volume	2.38E-05	12	rs734854	15	9.38E-06	STOML1
R_hippocampus	ShapeIndex	3.08E-05	13	rs12036909	1	9.54E-06	CDA
L_caudate	SurfaceArea	3.88E-05	14	rs6427160	1	1.02E-05	-
L_caudate	Volume	4.00E-05	15	rs439401	19	1.15E-05	APOE
R parahippocampal_gyrus	Volume	5.23E-05	16	rs11579101	1	1.62E-05	CDA
R parahippocampal_gyrus	ShapeIndex	5.56E-05	17	rs12512622	4	1.86E-05	-
R_inferior_temporal_gyrus	Curvedness	5.99E-05	18	rs4886387	13	1.96E-05	-
R_inferior_temporal_gyrus	SurfaceArea	6.24E-05	19	rs157580	19	2.97E-05	TOMM40
L_superior_temporal_gyrus	Volume	6.82E-05	20	rs9896368	17	3.13E-05	GAS2L2
L parahippocampal_gyrus	SurfaceArea	9.22E-05	21	rs16885921	5	4.09E-05	CDH18
R_inferior_temporal_gyrus	AverageMeanCurvature	1.08E-04	22	rs7985759	13	4.23E-05	-
L_middle_temporal_gyrus	SurfaceArea	1.33E-04	23	rs2883782	2	5.14E-05	MYO3B
L_hippocampus	Curvedness	1.46E-04	24	rs7902368	10	5.29E-05	-
L_fusiform_gyrus	Volume	1.57E-04	25	rs4829605	23	5.28E-05	-
R parahippocampal_gyrus	AverageMeanCurvature	1.60E-04	26	rs11726692	4	6.03E-05	RNF150
L_superior_temporal_gyrus	SurfaceArea	1.65E-04	27	rs17430865	1	6.32E-05	-
R_hippocampus	AverageMeanCurvature	2.91E-04	28	rs259659	1	6.79E-05	-
L_fusiform_gyrus	SurfaceArea	3.11E-04	29	rs1469259	4	6.87E-05	-
R_fusiform_gyrus	Volume	3.70E-04	30	rs7578676	2	7.13E-05	-
R parahippocampal_gyrus	SurfaceArea	4.07E-04	31	rs7903954	10	7.32E-05	LOC100129821
L_caudate	AverageMeanCurvature	4.65E-04	32	rs1701506	18	7.72E-05	-
L_inferior_temporal_gyrus	ShapeIndex	5.15E-04	33	rs1498853	3	7.77E-05	-
R_hippocampus	Curvedness	5.89E-04	34	rs11899232	2	8.43E-05	KIF5C
R_inferior_occipital_gyrus	ShapeIndex	6.08E-04	35	rs17028008	4	8.71E-05	-
R_insular_cortex	Volume	6.26E-04	36	rs17246639	11	8.80E-05	LOC100507145
L_caudate	Curvedness	6.27E-04	37	rs7146951	14	9.12E-05	-
L_lateral_orbitofrontal_gyrus	AverageMeanCurvature	6.43E-04	38	rs1801406	13	9.33E-05	BRCA2
L_insular_cortex	ShapeIndex	6.98E-04	39	rs2799182	1	9.63E-05	LOC388588
R_fusiform_gyrus	SurfaceArea	7.47E-04	40	rs9301386	13	9.69E-05	-
L_putamen	ShapeIndex	8.09E-04	41	rs3846829	6	1.00E-04	DCDC2
L_precentral_gyrus	ShapeIndex	1.11E-03	42	rs8027939	15	1.02E-04	-
R_middle_temporal_gyrus	Volume	1.41E-03	43	rs288496	3	1.02E-04	-
L_middle_temporal_gyrus	Volume	1.53E-03	44	rs2518112	9	1.03E-04	FSD1L
R_caudate	AverageMeanCurvature	2.16E-03	45	rs462074	21	1.05E-04	-

L_lateral_orbitofrontal_gyrus	Volume	2.65E-03	46	rs4899412	14	1.07E-04	RGS6
L_putamen	Curvedness	2.81E-03	47	rs3842979	9	1.08E-04	LINGO2
L_insular_cortex	Volume	3.10E-03	48	rs12018260	13	1.15E-04	-
L_putamen	Volume	3.41E-03	49	rs7494784	15	1.19E-04	-
R_superior_temporal_gyrus	SurfaceArea	3.75E-03	50	rs288503	3	1.19E-04	-
R_superior_temporal_gyrus	Volume	3.90E-03	51	rs1934935	10	1.22E-04	-
L_superior_temporal_gyrus	ShapeIndex	4.92E-03	52	rs11252839	10	1.22E-04	-
R_middle_temporal_gyrus	SurfaceArea	5.08E-03	53	rs2829647	21	1.27E-04	-
R_superior_temporal_gyrus	Curvedness	5.51E-03	54	rs9711441	2	1.26E-04	KIF5C
R_inferior_occipital_gyrus	Volume	6.28E-03	55	rs1788070	18	1.26E-04	-
R_inferior_temporal_gyrus	ShapeIndex	6.84E-03	56	rs2697269	2	1.29E-04	ANKRD44
R_superior_temporal_gyrus	ShapeIndex	7.07E-03	57	rs4807567	19	1.29E-04	SHD
brainstem	ShapeIndex	7.21E-03	58	rs12352272	9	1.29E-04	ADAMTSL1
L_lingual_gyrus	ShapeIndex	7.88E-03	59	rs1334496	23	1.32E-04	-
R_middle_orbitofrontal_gyrus	Curvedness	8.49E-03	60	rs7661978	4	1.37E-04	-
L_putamen	SurfaceArea	8.87E-03	61	rs10820813	9	1.40E-04	FSD1L
L_cingulate_gyrus	ShapeIndex	1.14E-02	62	rs7326137	13	1.42E-04	NALCN
R_superior_temporal_gyrus	AverageMeanCurvature	1.39E-02	63	rs11620374	13	1.44E-04	-
R_fusiform_gyrus	Curvedness	1.42E-02	64	rs1396260	6	1.46E-04	-
L parahippocampal_gyrus	AverageMeanCurvature	1.48E-02	65	rs895792	1	1.47E-04	-
L_caudate	ShapeIndex	1.57E-02	66	rs746947	3	1.48E-04	-
R_middle_frontal_gyrus	ShapeIndex	1.83E-02	67	rs7268938	20	1.48E-04	-
R_fusiform_gyrus	AverageMeanCurvature	1.83E-02	68	rs10464068	5	1.49E-04	COL23A1
R_inferior_occipital_gyrus	SurfaceArea	1.89E-02	69	rs6569792	6	1.55E-04	MOXD1
L_fusiform_gyrus	Curvedness	2.35E-02	70	rs6090754	20	1.57E-04	-
R_insular_cortex	SurfaceArea	2.57E-02	71	rs4972269	2	1.60E-04	KIF5C
R parahippocampal_gyrus	Curvedness	2.62E-02	72	rs1392188	3	1.60E-04	-
R_cingulate_gyrus	Curvedness	2.62E-02	73	rs7839488	8	1.61E-04	SNTB1
R_lateral_orbitofrontal_gyrus	Curvedness	2.76E-02	74	rs11951324	5	1.62E-04	ZNF474
R_postcentral_gyrus	Curvedness	2.88E-02	75	rs645184	11	1.62E-04	-
R_superior_frontal_gyrus	ShapeIndex	2.93E-02	76	rs1981542	4	1.63E-04	-
R_postcentral_gyrus	AverageMeanCurvature	3.15E-02	77	rs2137962	8	1.67E-04	-
R_superior_parietal_gyrus	Volume	3.26E-02	78	rs4075242	11	1.70E-04	-
L_lateral_orbitofrontal_gyrus	SurfaceArea	3.81E-02	79	rs2649734	3	1.71E-04	-
R_superior_occipital_gyrus	Volume	3.89E-02	80	rs1048009	4	1.73E-04	TBC1D14

SNPs	Imaging biomarkers	P-values
rs2137962 (Chr 8)	L parahippocampal_gyrus (SurfaceArea)	0.0000222
rs2137962 (Chr 8)	L_hippocampus (SurfaceArea)	0.0000432
rs4829605 (Chr23)	R_inferior_temporal_gyrus (Curvedness)	0.0000729
rs17430865 (Chr 1)	R_cingulate_gyrus (Curvedness)	0.000081
rs259659 (Chr 1)	L_lateral_orbitofrontal_gyrus (AverageMeanCurvature)	0.000112
rs2137962 (Chr 8)	L_hippocampus (Volume)	0.000106
rs2137962 (Chr 8)	L parahippocampal_gyrus (Volume)	0.000204
rs2137962 (Chr 8)	R parahippocampal_gyrus (SurfaceArea)	0.000223
rs2137962 (Chr 8)	R_hippocampus (SurfaceArea)	0.000213
rs2137962 (Chr 8)	R_hippocampus (Curvedness)	0.000246
rs2137962 (Chr 8)	R parahippocampal_gyrus (Curvedness)	0.000285
rs2137962 (Chr 8)	R_hippocampus (Volume)	0.000353
rs2137962 (Chr 8)	L_insular_cortex (Volume)	0.000417
rs259659 (Chr 1)	L_lateral_orbitofrontal_gyrus (Volume)	0.000483
rs2137962 (Chr 8)	R_hippocampus (AverageMeanCurvature)	0.000576
rs645184 (Chr 11)	R_hippocampus (SurfaceArea)	0.000616
rs2137962 (Chr 8)	R parahippocampal_gyrus (Volume)	0.000997
rs2137962 (Chr 8)	R_superior_temporal_gyrus (AverageMeanCurvature)	0.001118
rs2137962 (Chr 8)	L_hippocampus (Curvedness)	0.001186
rs1981542 (Chr 4)	L_caudate (ShapeIndex)	0.001202
rs2137962 (Chr 8)	L_fusiform_gyrus (Curvedness)	0.001366

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Supplementary Table 5 (B). MCI ranked association results

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SNPs	Imaging biomarkers	P-values
rs1334496 (Chr 23)	R_inferior_temporal_gyrus (Curvedness)	937e-10
rs1334496 (Chr 23)	R_inferior_temporal_gyrus (AverageMeanCurvature)	0.0000182
rs4829605 (Chr 23)	R_inferior_temporal_gyrus (Curvedness)	0.000358
rs1801406 (Chr 13)	R_superior_occipital_gyrus (Volume)	0.000381
rs1788070 (Chr 18)	R_lateral_orbitofrontal_gyrus (Curvedness)	0.000413
rs2697269 (Chr 2)	R_cingulate_gyrus (Curvedness)	0.000539
rs12822214 (Chr 12)	R_cingulate_gyrus(Curvedness)	0.000534
rs17028008 (Chr 4)	R_fusiform_gyrus (AverageMeanCurvature)	0.000741
rs1702797 (Chr 4)	R_fusiform_gyrus (AverageMeanCurvature)	0.000933
rs1788070 (Chr 18)	L_fusiform_gyrus (Curvedness)	0.001057
rs7146951 (Chr 14)	R_middle_orbitofrontal_gyrus (Curvedness)	0.001091
rs1125283 (Chr 10)	R_superior_occipital_gyrus (Volume)	0.001178
rs6090754 (Chr 20)	R_lateral_orbitofrontal_gyrus (Curvedness)	0.001341
rs2829647 (Chr 21)	R_inferior_occipital_gyrus (ShapeIndex)	0.001617
rs2829647 (Chr 21)	L_putamen (Curvedness)	0.001617
rs2075650 (Chr 19)	R_caudate (Curvedness)	0.001713
rs1788070 (Chr 18)	L_hippocampus (ShapeIndex)	0.001732
rs2075650 (Chr 19)	R_caudate (volume)	0.002271
rs1251262 (Chr 4)	R_fusiform_gyrus (AverageMeanCurvature)	0.002574
rs8027939 (Chr 15)	L_putamen (ShapeIndex)	0.003718

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Supplementary Table 5 (C). NC ranked association results

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SNPs	Imaging biomarkers	P-values
rs1469259 (Chr 4)	R_hippocampus (Curvedness)	0.000986
rs6569792 (Chr 6)	R_inferior_occipital_gyrus (SurfaceArea)	0.001042
rs7902368 (Chr 10)	L_caudate (AverageMeanCurvature)	0.001047
rs11620374 (Chr 13)	L_fusiform_gyrus (Volume)	0.001055
rs11899232 (Chr 2)	R_middle_orbitofrontal_gyrus (Curvedness)	0.001071
rs4972269 (Chr 2)	R_middle_orbitofrontal_gyrus (Curvedness)	0.001358
rs1469259 (Chr 4)	R_hippocampus (AverageMeanCurvature)	0.001448
rs4886844 (Chr 15)	R_hippocampus (Volume)	0.001482
rs11680332 (Chr 2)	L_putamen (ShapeIndex)	0.002418
rs1052242 (Chr 15)	R_insular_cortex (Volume)	0.002407
rs9301386 (Chr 13)	L_cingulate_gyrus (ShapeIndex)	0.002552
rs4899412 (Chr 14)	L_caudate (SurfaceArea)	0.002992
rs17430865 (Chr 1)	brainstem (ShapeIndex)	0.002983
rs6569792 (Chr 6)	L_middle_temporal_gyrus (Volume)	0.002966
rs4886844 (Chr 15)	R_hippocampus (SurfaceArea)	0.003117
rs4886844 (Chr 15)	R_insular_cortex (Volume)	0.003176
rs1052242 (Chr 15)	R_hippocampus (Volume)	0.003103
rs7902368 (Chr 10)	L_lateral_orbitofrontal_gyrus (Volume)	0.003162
rs11072463 (Chr 15)	R_insular_cortex (Volume)	0.003349
rs11620374 (Chr 13)	L_fusiform_gyrus (SurfaceArea)	0.003401

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Genes	Summary for the genes
TOMM40	The gene is for the channel-forming subunit of a translocase of the mitochondrial outer membrane (TOM) that is essential for protein transport into mitochondria.
PML	The gene codes for 'promyelocytic leukemia' protein that prevents cells from growing and dividing too rapidly or in an uncontrolled manner and interacts with other proteins that are involved in cell growth and division (proliferation) as well as in self-destruction (apoptosis). This gene is often involved in the translocation with the retinoic acid receptor alpha gene implicated in acute promyelocytic leukemia.
ADAMTS9-AS2	The gene is for ADAMTS9 antisense RNA 2 (link RNA). ADAMTS9 is expressed in spinal cord and brain along with other tissues and is a susceptibility gene for type-2 diabetes, also for LOAD.
STOML1	The gene codes for stomatin (EPB72)-like 1.
APOE	The gene provides instructions for making a protein called apolipoprotein E which combines with fats (lipids) in the body to form molecules called lipoproteins.
CDA	The gene is for 'cytidine deaminase' which is associated with decreased sensitivity to the cytosine nucleoside analogue cytosine arabinoside used in the treatment.
GAS2L2	The gene codes for 'growth arrest-specific 2 like 2' that appears to crosslink microtubules and microfilaments and may be part of the cytoskeleton.
CDH18	The gene codes a type II classical cadherin from the cadherin superfamily of integral membrane proteins.
MYO3B	The gene is associated with probable actin-based motor with a protein kinase activity.
RNF150	The gene is for 'ring finger protein 150' which is a protein-coding gene.
LOC100129821	The gene has sufficient evidence that the predicted model represents a distinct locus.
KIF5C	The gene mediates dendritic trafficking of mRNAs.
LOC100507145	The gene is mir-100-let-7a-2 cluster host gene (non-protein coding).
BRCA2	The gene is involved in double-strand break repair and/or homologous recombination.
LOC388588	The gene is small integral membrane protein 1 (SMIMI1).
DCDC2	The gene may be involved in neuronal migration during development of the cerebral neocortex.

FSD1L	The gene is for 'fibronectin type III and SPRY domain containing 1-like' which is a protein-coding gene (related to molecular function).
RGS6	The gene is for 'regulator of G-protein signaling 6' which inhibits signal transduction by increasing the GTPase activity of G protein alpha subunits thereby driving them into their inactive GDP-bound form.
LINGO2	The gene is for 'leucine rich repeat and Ig domain containing 2' which is a protein-coding gene. Diseases associated with LINGO2 include neuronitis and essential tremor.
KIF5C	The gene is for kinesin heavy chain isoform 5C which mediates dendritic trafficking of mRNAs. Kinesin is a microtubule-associated force-producing protein that may play a role in organelle transport.
ANKRD44	The gene is for 'ankyrin repeat domain 44' which is putative regulatory subunit of protein phosphatase 6 (PP6) that may be involved in the recognition of phosphoprotein substrates.
SHD	The gene may function as an adapter protein.
ADAMTSL1	The gene codes a secreted protein and member of the ADAMTS (a disintegrin and metalloproteinase with thrombospondin motif) family.
NALCN	The gene is responsible for the background sodium ion leak current in neurons and controls neuronal excitability.
COL23A1	The gene is for 'collagen type 23, alpha 1' which is a member of the transmembrane collagens, a subfamily of the nonfibrillar collagens that contain a single pass hydrophobic transmembrane domain.
MOXD1	The gene is for 'monooxygenase DBH-like 1' which maintains many of the structural features of dopamine beta-monooxygenase DBH; the SNTB1 gene may link various receptors to the actin cytoskeleton and the dystrophin glycoprotein complex.
SNTB1	The gene encodes a DNA binding protein that specifically binds nuclear matrix attachment regions. The encoded protein is involved in transcription regulation and chromatin remodeling. Defects in this gene are associated with isolated cleft palate and mental retardation.
ZNF474	The gene is for 'zinc finger protein 474' which is a protein coding gene (zinc ion binding).
TBC1D14	The gene is for 'TBC1 Domain Family, Member 14' which is a negative regulator of starvation-induced autophagosome formation.

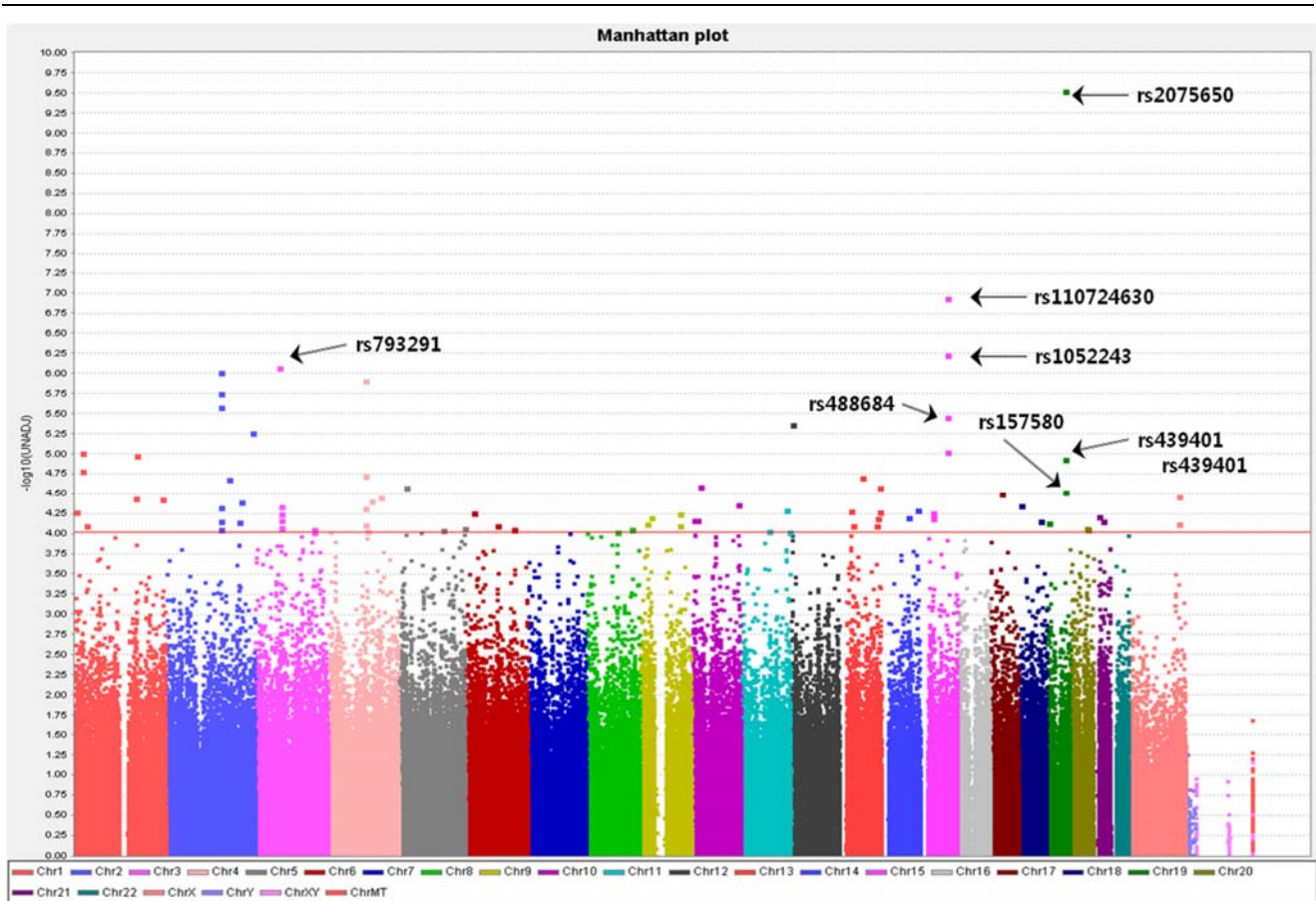
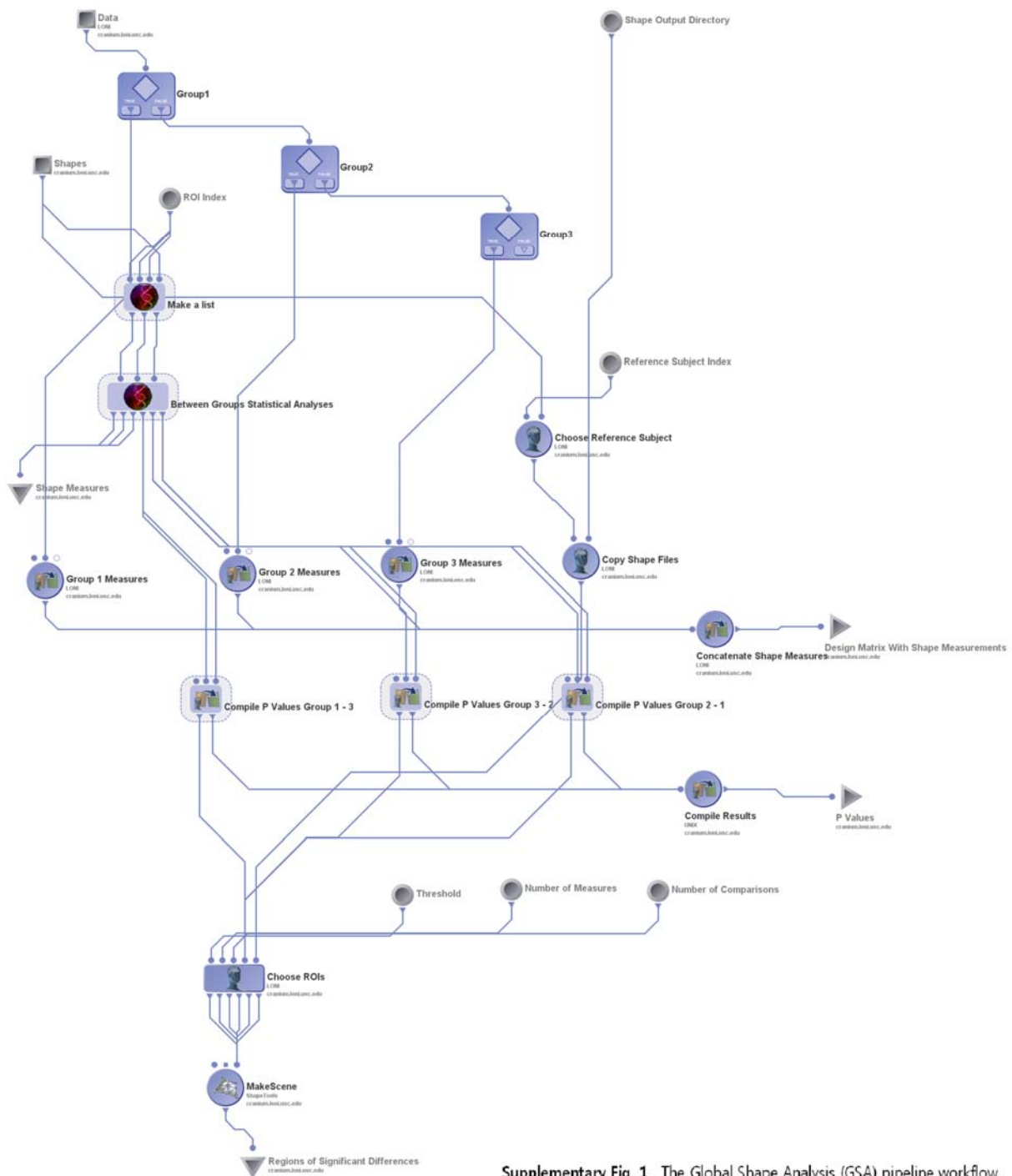


Fig. 5. Manhattan plot (80 SNPs)

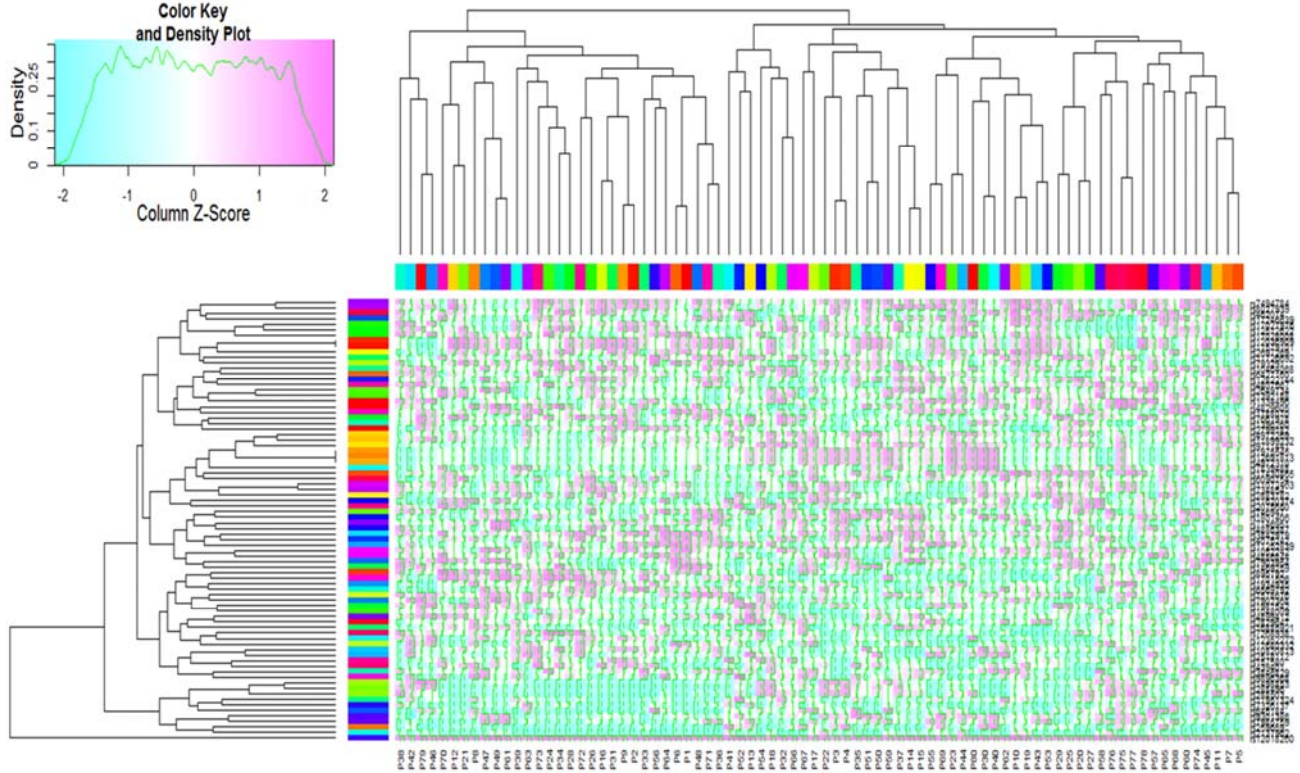
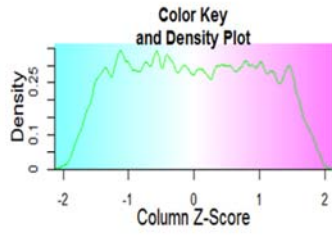
Supplementary Fig. 1



Supplementary Fig. 1. The Global Shape Analysis (GSA) pipeline workflow

Supplementary Fig. 2(A). GWAS association between 80 SNPs and 80 neuroimaging markers (AD)

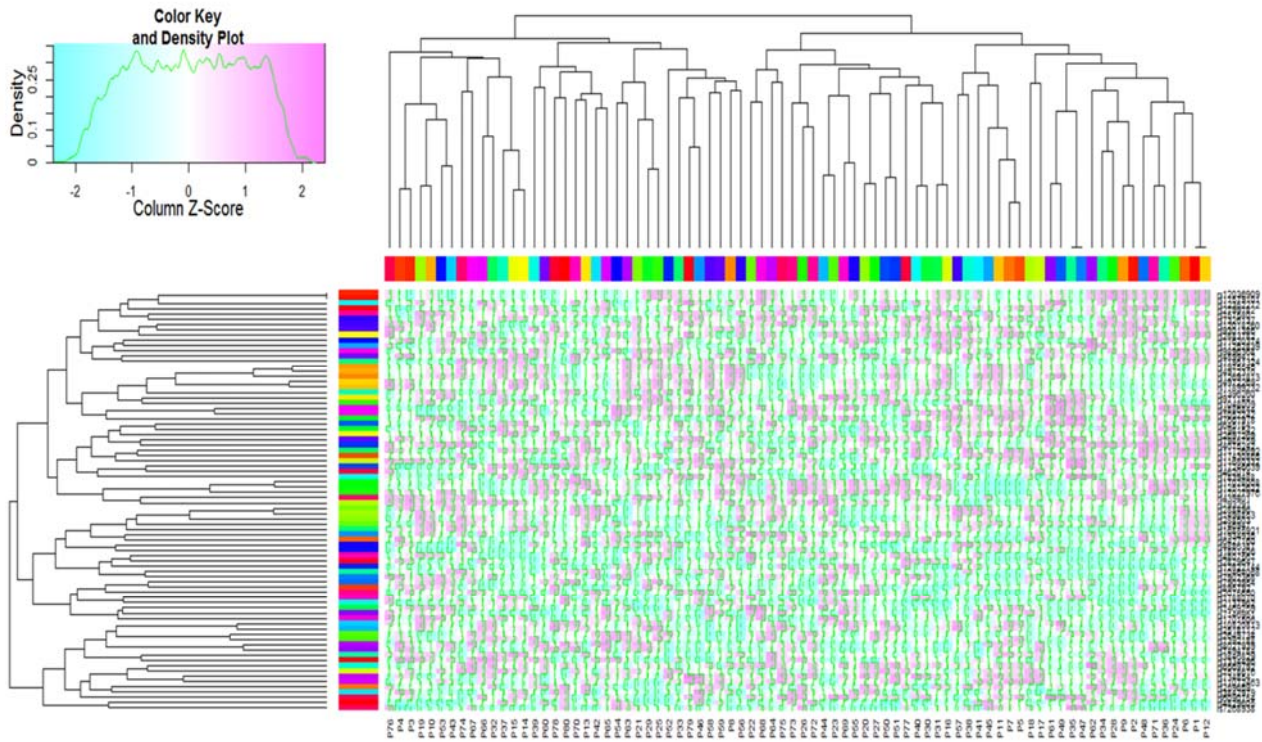
AD_80x80_Assoc_P_values.csv



Supplementary Fig. 2(A). GWAS association between 80 SNPs and 80 neuroimaging markers (AD)

Supplementary Fig. 2(B). GWAS association between 80 SNPs and 80 neuroimaging markers(MCI)

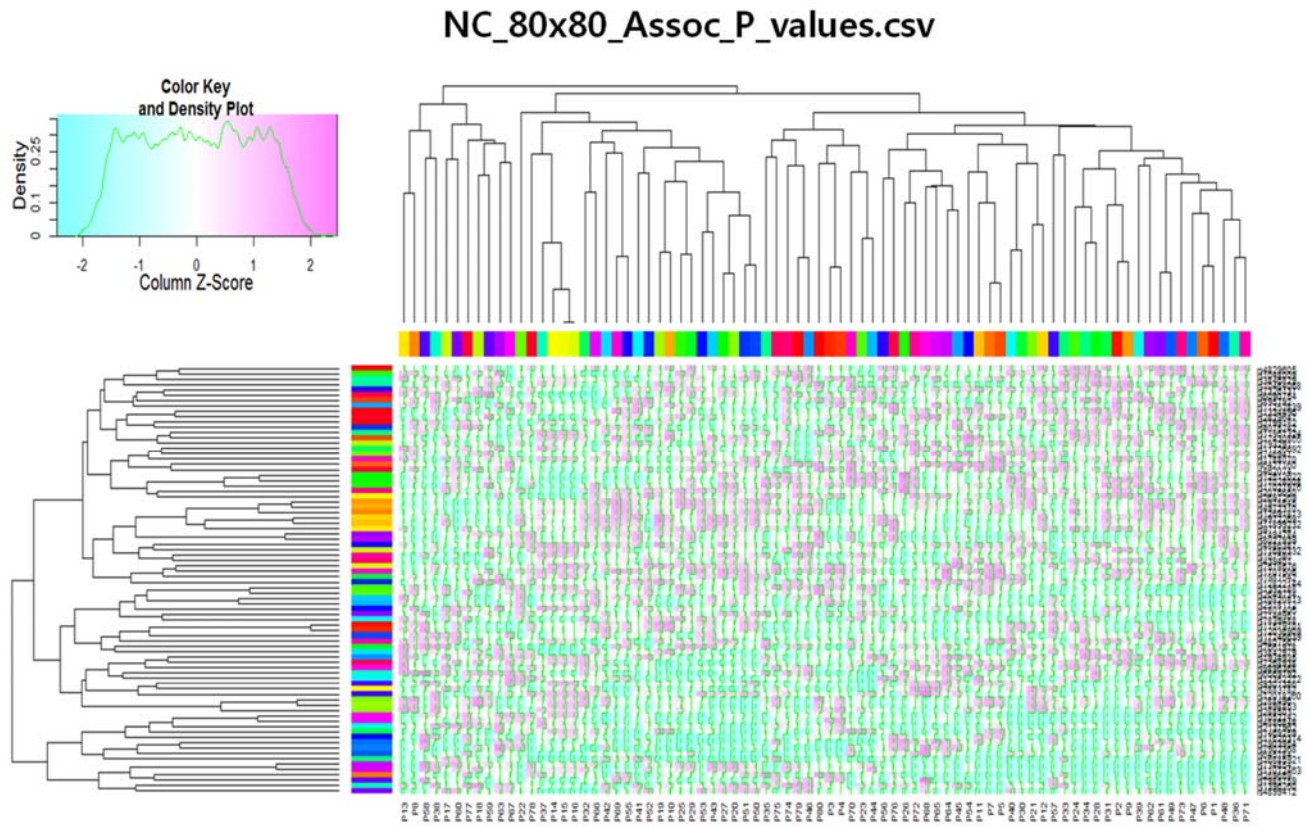
MCI_80x80_Assoc_P_values.csv



Supplementary Fig. 2(B). GWAS association between 80 SNPs and 80 neuroimaging markers (MCI)

Supplementary Fig. 2(C). GWAS association between 80 SNPs and 80 neuroimaging

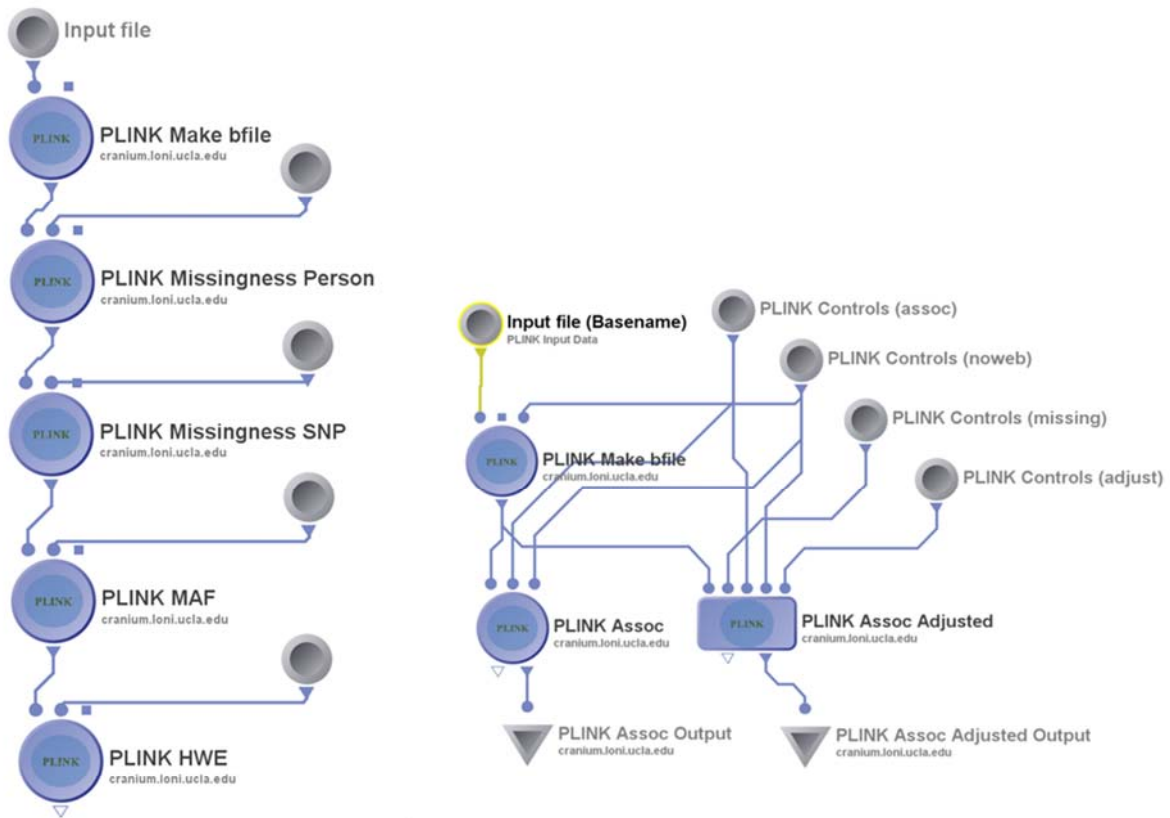
markers (NC)



Supplementary Fig. 2(C). GWAS association between 80 SNPs and 80 neuroimaging markers (NC)

Supplementary Fig. 3. PLINK workflows

Supplementary Fig. 3. PLINK workflows



A: The pipeline workflow for QC

B: Genetic association study

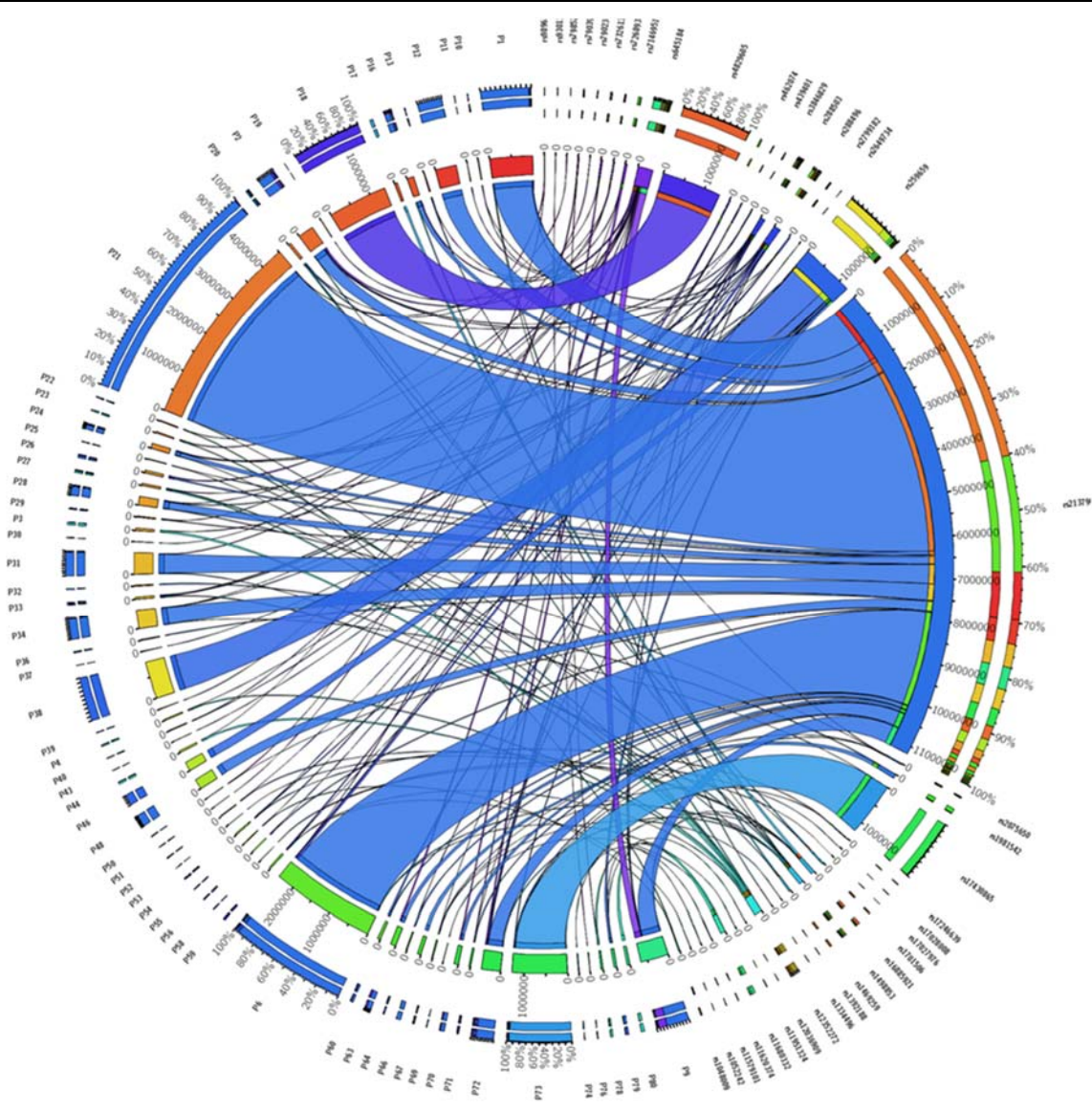
Supplementary Fig. 3. PLINK workflows

Supplementary Fig. 4

Each of the SNPs (represented by unique RS sequence ID) and each shape morphometry measure, corresponding to the most important ROIs, are represented in the connectogram graph by circularly arranged ideograms. Appearance models (style and color) indicate the relative impact of the corresponding SNP (right) and ROI measure (left semicircle). Data tracks comprise the two concentric rings in the outer shell of the graph. Translocations between circular segments are shown as chordal curves that connect regions brought into adjacency by magnitude of the p-value representing the strength of the SNP-ROI association according to the results of the statistical tests. These represent normalized inverse p-values ($1/p$), so large cell values correspond to small p-values and bright/wide ribbons on the circus connectogram graphs.

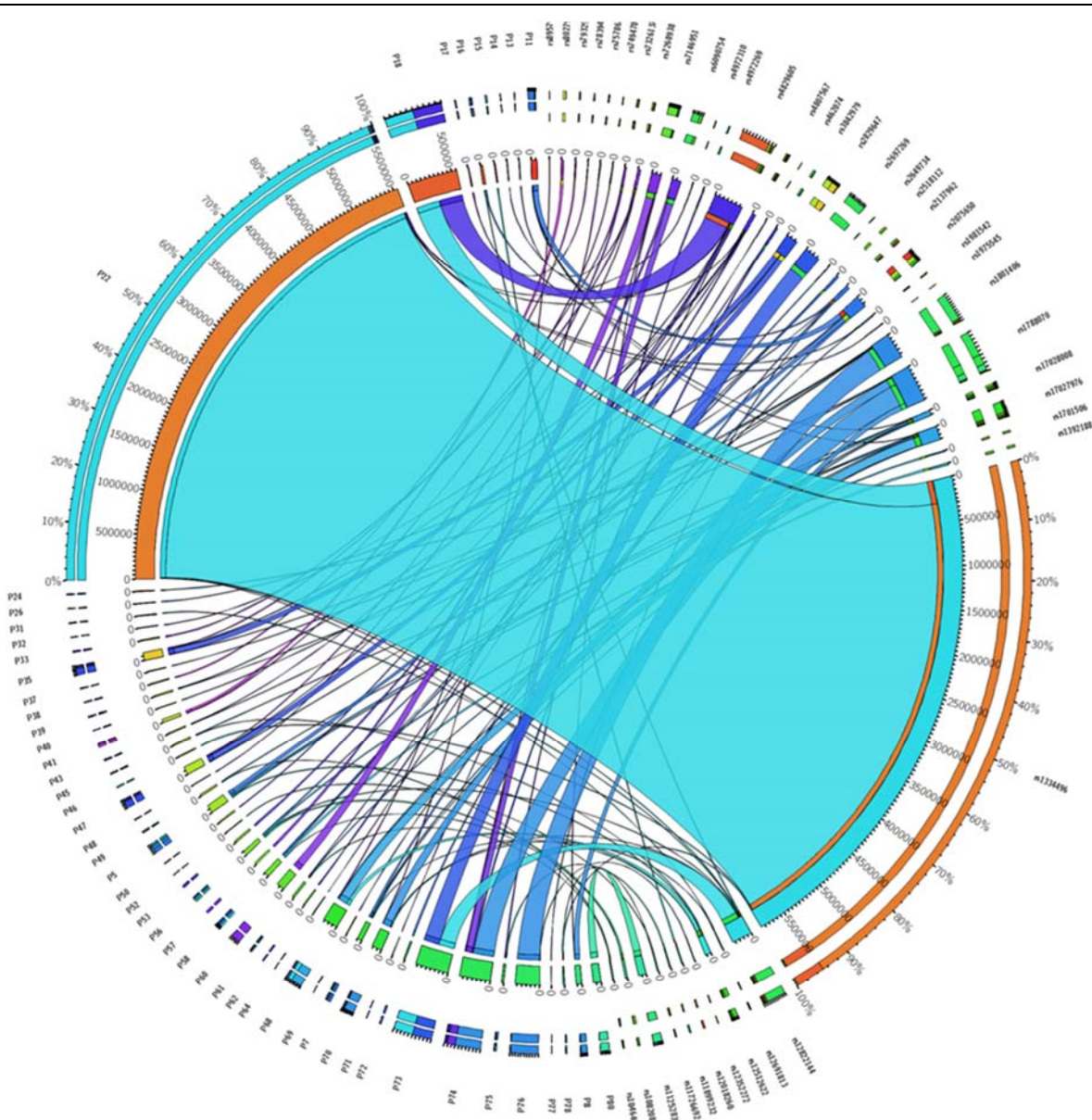
Legend : Neuroimaging biomarkers / SNPs are in the 'Supplementary Table 1' P1-P80 is corresponding with index numbers [Supplementary Table 1]

Supplementary Fig. 4 (A). AD_80*80_Association_P_values_Circos



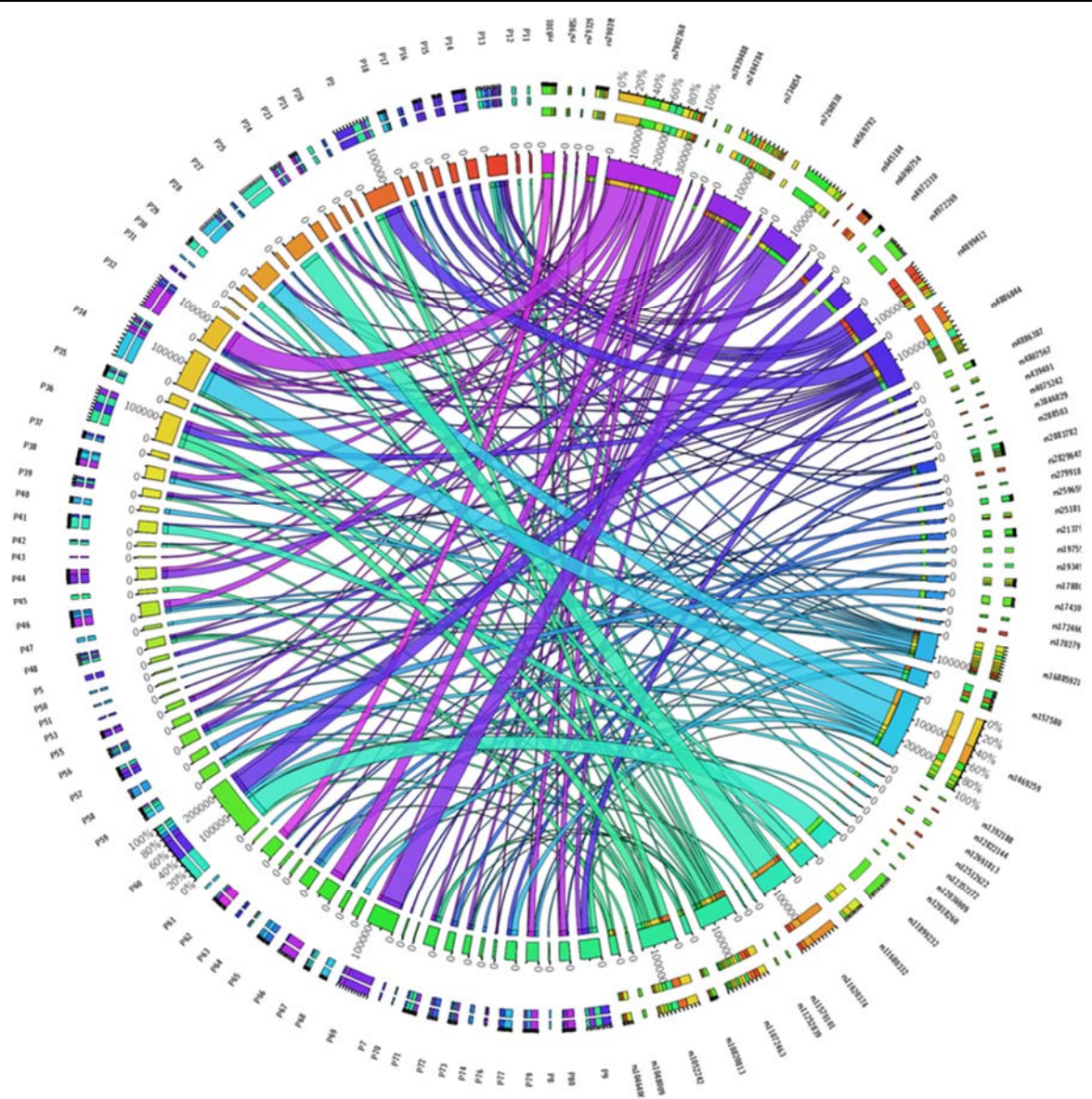
Supplementary Fig. 4(A). AD_80*80_Association_P_values_Circos

Supplementary Fig. 4(B). MCI_80*80_Association_P-values_Circos



Supplementary Fig. 4(B). MCI 80*80_Association_P_values_Circos

Supplementary Fig. 4(C). NC_80*80_Association_P-values_Circos



Supplementary Fig. 4(C). NC 80*80_Association_P_values_Circos



Supplementary pipe. File

Supplementary pipe. file.pipe