

Gyrals Peaks Reveal Brain Function Disparities in Diverse Social Environment

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Supplementary Information

Table S1: Functions of common genes regulating similar pathways in the three datasets in gene enrichment analysis for peaks.

Gene Symbol	Gene Function
CHRNA1	The muscle acetylcholine receptor consists of 5 subunits of 4 different types: 2 alpha subunits and 1 each of the beta, gamma, and delta subunits. This gene encodes an alpha subunit that plays a role in acetylcholine binding/channel gating. Alternatively spliced transcript variants encoding different isoforms have been identified. [provided by RefSeq, Nov 2012]
CHRNA9	This gene is a member of the ligand-gated ionic channel family and nicotinic acetylcholine receptor gene superfamily. It encodes a plasma membrane protein that forms homo- or hetero-oligomeric divalent cation channels. This protein is involved in cochlea hair cell development and is also expressed in the outer hair cells (OHCs) of the adult cochlea. [provided by RefSeq, Feb 2012]
CHRND	The acetylcholine receptor of muscle has 5 subunits of 4 different types: 2 alpha and 1 each of beta, gamma and delta subunits. After acetylcholine binding, the receptor undergoes an extensive conformation change that affects all subunits and leads to opening of an ion-conducting channel across the plasma membrane. Defects in this gene are a cause of multiple pterygium syndrome lethal type (MUPSL), congenital myasthenic syndrome slow-channel type (SCCMS), and congenital myasthenic syndrome fast-channel type (FCCMS). Several transcript variants encoding different isoforms have been found for this gene. [provided by RefSeq, Jul 2015]
CHRNE	Acetylcholine receptors at mature mammalian neuromuscular junctions are pentameric protein complexes composed of four subunits in the ratio of two alpha subunits to one beta, one epsilon, and one delta subunit. The acetylcholine receptor changes subunit composition shortly after birth when the epsilon subunit replaces the gamma subunit seen in embryonic receptors. Mutations in the epsilon subunit are associated with congenital myasthenic syndrome. [provided by RefSeq, Sep 2009]
GABRA4	Gamma-aminobutyric acid (GABA) is the major inhibitory neurotransmitter in the mammalian brain where it acts at GABA-A receptors, which are ligand-gated chloride channels. Chloride conductance of these channels can be modulated by agents such as benzodiazepines that bind to the GABA-A receptor. At least 16 distinct subunits of GABA-A receptors have been identified. This gene encodes subunit alpha-4, which is involved in the etiology of autism and eventually increases autism risk through interaction with another subunit, gamma-aminobutyric acid receptor beta-1 (GABRB1). Alternatively spliced transcript variants encoding different isoforms have been found in this gene. [provided by RefSeq, Feb 2011]
GABRB1	The gamma-aminobutyric acid (GABA) A receptor is a multisubunit chloride channel that mediates the fastest inhibitory synaptic transmission in the central nervous system. This gene encodes GABA A receptor, beta 1 subunit. It is mapped to chromosome 4p12 in a cluster comprised of genes encoding alpha 4, alpha 2 and gamma 1 subunits of the GABA A receptor. Alteration of this gene is implicated in the pathogenetics of schizophrenia. [provided by RefSeq, Jul 2008]
GABRB2	The gamma-aminobutyric acid (GABA) A receptor is a multisubunit chloride channel that mediates the fastest inhibitory synaptic transmission in the central nervous system. This gene encodes GABA A receptor, beta 2 subunit. It is mapped to chromosome 5q34 in a cluster comprised of genes encoding alpha 1 and gamma 2 subunits of the GABA A receptor. Alternative splicing of this gene generates 2 transcript variants, differing by a 114 bp insertion. [provided by RefSeq, Jul 2008]

Gene Symbol	Gene Function
GABRQ	The gamma-aminobutyric acid (GABA) A receptor is a multisubunit chloride channel that mediates the fastest inhibitory synaptic transmission in the central nervous system. This gene encodes the theta subunit of the GABA A receptor. The gene is mapped to chromosome Xq28 in a cluster of genes including those that encode the alpha 3 and epsilon subunits of the GABA A receptor. [provided by RefSeq, Jul 2017]
GABRR1	GABA is the major inhibitory neurotransmitter in the mammalian brain where it acts at GABA receptors, which are ligand-gated chloride channels. GABRR1 is a member of the rho subunit family. Several transcript variants encoding different isoforms have been found for this gene. [provided by RefSeq, Feb 2012]
GABRR3	The neurotransmitter gamma-aminobutyric acid (GABA) functions in the central nervous system to regulate synaptic transmission of neurons. This gene encodes one of three related subunits, which combine as homo- or hetero-pentamers to form GABA(C) receptors. In humans, some individuals contain a single-base polymorphism (dbSNP rs832032) that is predicted to inactivate the gene product. [provided by RefSeq, Jan 2012]

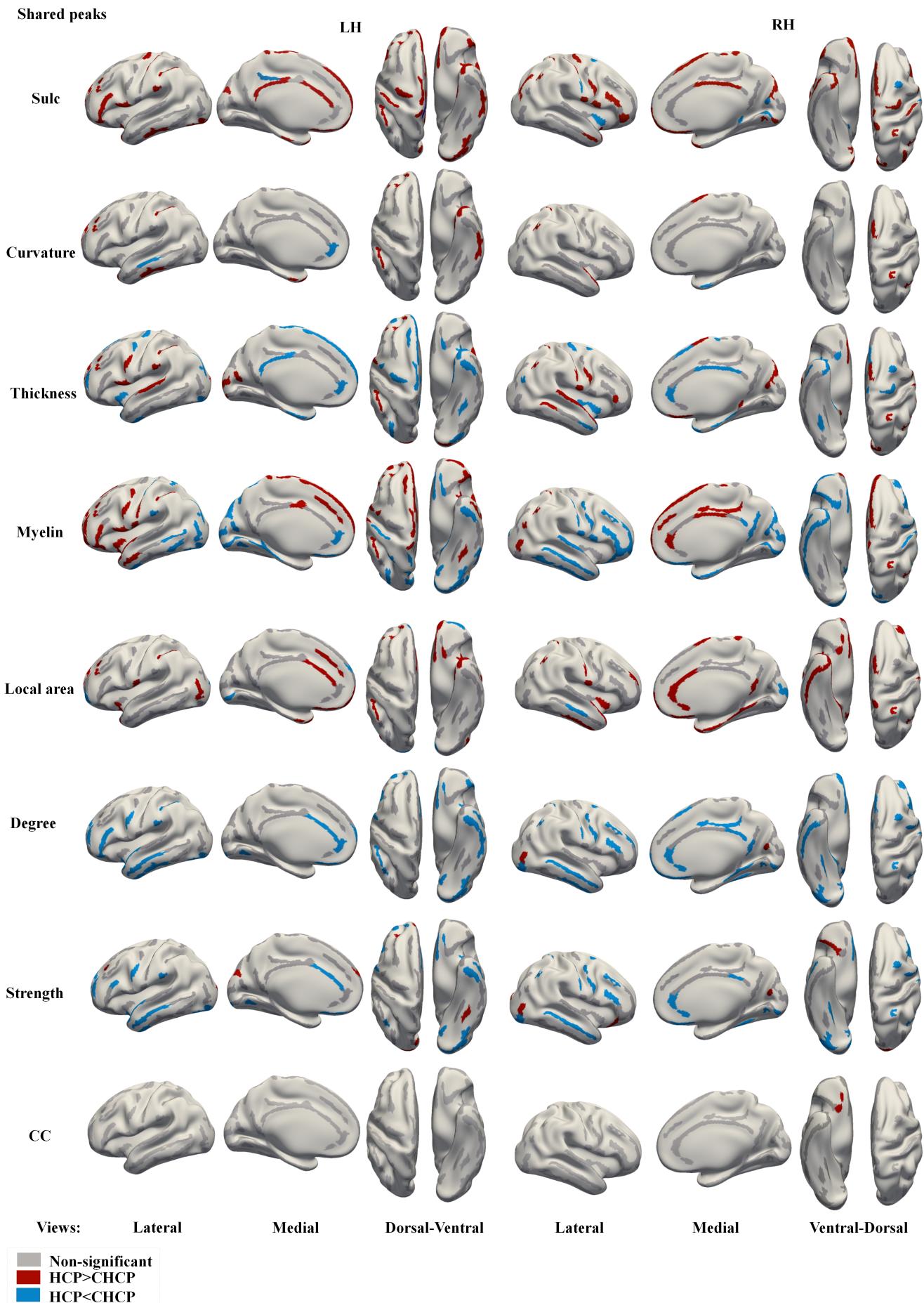
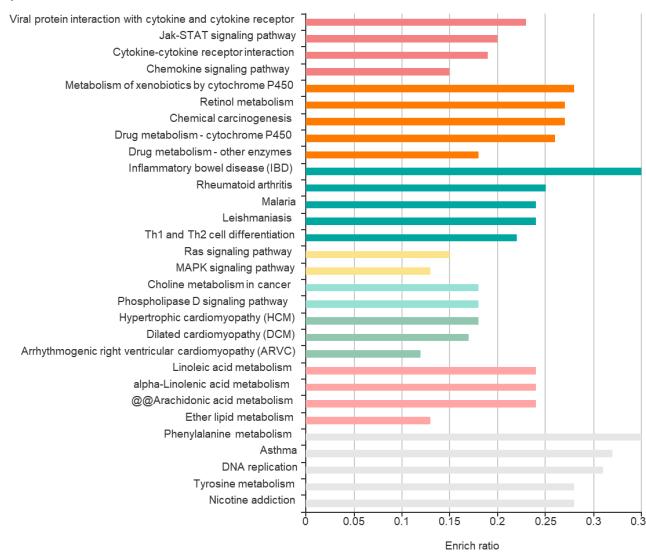


Figure S1: The result of the attribute comparison of shared peaks. Red represents HCP higher than CHCP, Blue represents HCP lower than CHCP, and gray represents no significant difference between groups. Abbreviations: LH: Left Hemisphere, RH: Right Hemisphere, CC: clustering Coefficient

(a)



(b)



(c)

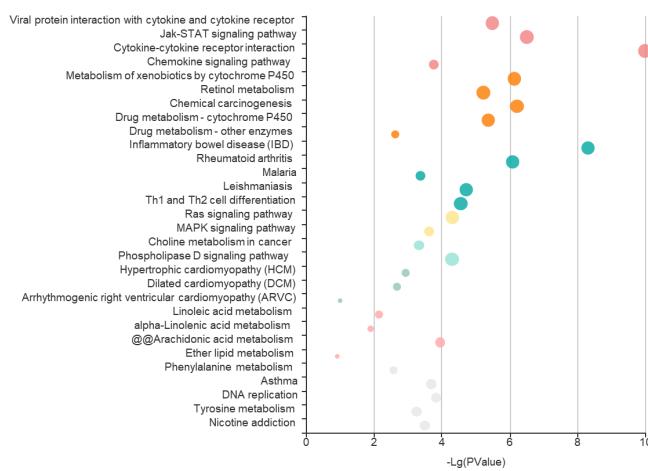


Figure S2: (a) Enriched terms visualized in cirFunMap: Each node represents an enriched term, and the node color represents different clusters; the node size represents 6 levels of enriched p-value, node size from small to large: [0.05,1], [0.01,0.05], [0.001,0.01], [0.0001,0.001], [1e-10,0.0001], [0,1e-10]; the edge represents correlations larger than the user-defined threshold. (b) Enriched terms visualized in barplot: Each row represents an enriched function, and the length of the bar represents the enrich ratio which is calculated as "input gene number" / "background gene number". The color of the bar is the same as the color in the circular network in above, which represents different clusters. For each cluster, if there are more than 5 terms, top 5 with the highest enrich ratio will be displayed. (c) Enriched terms visualized in bubble plot: Each bubble represents an enriched function, and the size of the bubble from small to large: [0.05,1], [0.01,0.05], [0.001,0.01], [0.0001,0.001], [1e-10,0.0001], [0,1e-10]. The color of the bar is the same as the color in the circular network, which represents different clusters. For each cluster, if there are more than 5 terms, top 5 with the highest enrich ratio will be displayed.