

Genetic Pathways and Networks Interacting with Sports to Modify Learning and Memory in Adolescents



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No SNPs passed the significance threshold (p ≤ 5e-08) for the

Collagen Activated Signaling Pathway

Neuromuscular Junction Development

Calcium Ion Regulated Exocytosis of Neurotransmitter

Modulation of Excitatory Postsynaptic Potential

Positive Regulation of Excitatory Postsynaptic

Vesicle Mediated Transport in Synapse

Odontogenesis of Dentin Containing Tooth

Positive Regulation of Cell Growth

Inhibitory Postsynaptic Potential

Spontaneous Synaptic Transmission

Calcium Ion Regulated Exocytosis

Response to Tumor Necrosis Factor -

Positive Regulation of NIK NF KappaB Signaling

Positive Regulation of Nervous System Process

Cell Surface Receptor Signaling Pathway Involved in

Regulation of DNA Binding Transcription Factor Activity

Regulation of Vesicle Mediated Transport -

Trachea Development

Cell Matrix Adhesion

Synapse Organization -

Dendrite Extension

Figure 1. GOBP Pathways that were enriched for the GWAS SNPs with stronger

SHARED PATHWAYS IN mTBI STUDY AND SPORTS STUDY

associations. 24 pathways showed significant enrichment (FDR < 0.05).

Tube Formation

Salivary Gland Development

Exocrine System Development

interaction term, but 15 SNPs passed a threshold of p \leq 1e-06

MOST PATHWAYS MAPPED BROADLY TO SYNAPTIC FUNCTION,

DEVELOPMENTAL PROCESSES, AND CELLULAR SIGNALING

GOBP Pathways with enrichment for SNPs

Introduction

- Regular physical activity is known to improve learning, memory, and executive function through increased hippocampal volume and enhanced synaptic function especially during adolescence when brain development is most dynamic (Erickson, 2011).
- Large individual variability exists in cognitive gains from exercise → suggests genetic factors modulate these effects but the gene-environment interaction driving this variability remains incompletely understood.
- Using the Adolescent Brain Cognitive Development (ABCD) study, we conducted a genome-wide interaction study (GWIS) to identify gene-by-sports interactions influencing learning- and memory-related pathways. We integrated these results with cell-type-specific regulatory networks to pinpoint key driver genes in cognition-relevant brain regions and assessed the clinical relevance of using polygenic risk scores.

Methods

1. ABCD Cohort Data



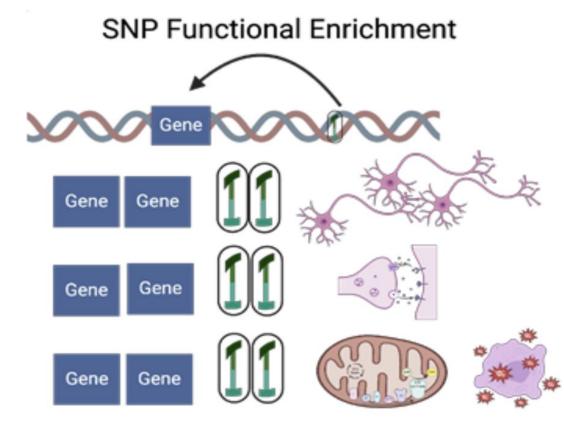
No Sports \rightarrow 1,174 Sports \rightarrow 6,435 To measure learning and memory

performance: - derived 3 PCs that condensed scores from NIH Toolbox Cognitive Battery, Rey Auditory Verbal Learning Test, and Little

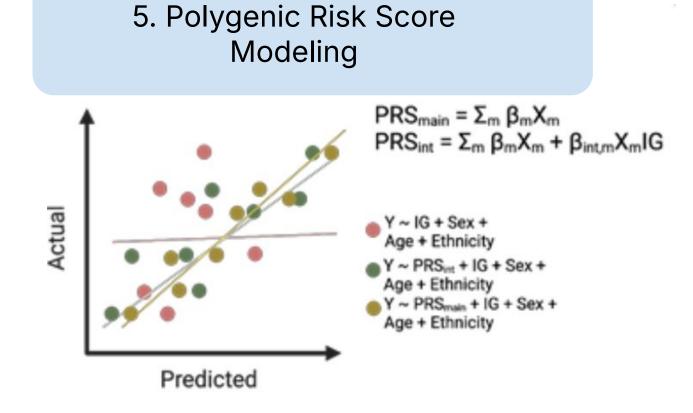
- used NPC3 for analysis

Man Task

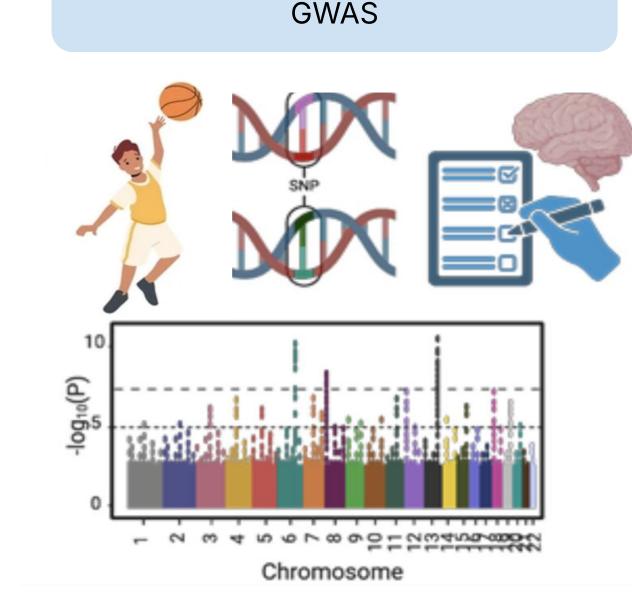
3. Marker Set **Enrichment Analysis**





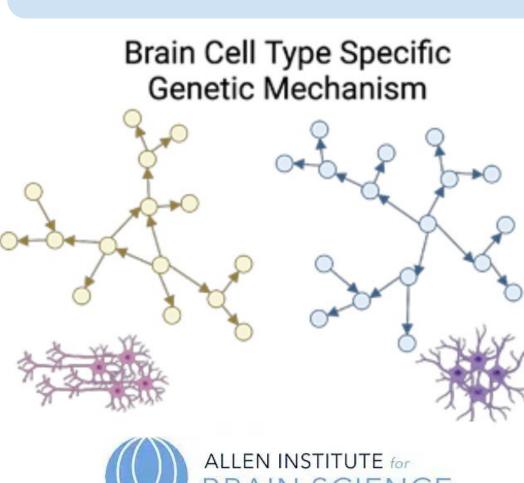


2. Gene-by-Sport Interaction



NPC3 = B0 + B1*SNP +B2*Env + B3*(SNP x Env) + covariates

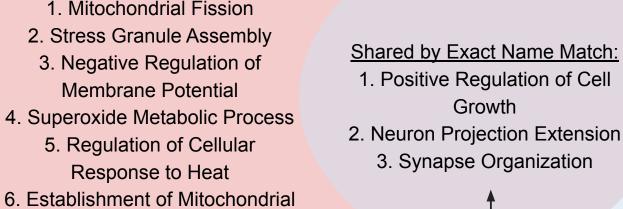
4. Key Driver Analysis

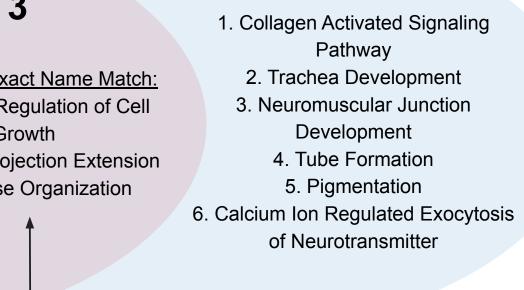


TBI - 57 1. Mitochondrial Fission 2. Stress Granule Assembly 3. Negative Regulation of Membrane Potential 4. Superoxide Metabolic Process

Localization

SNP x Sport GWAS:





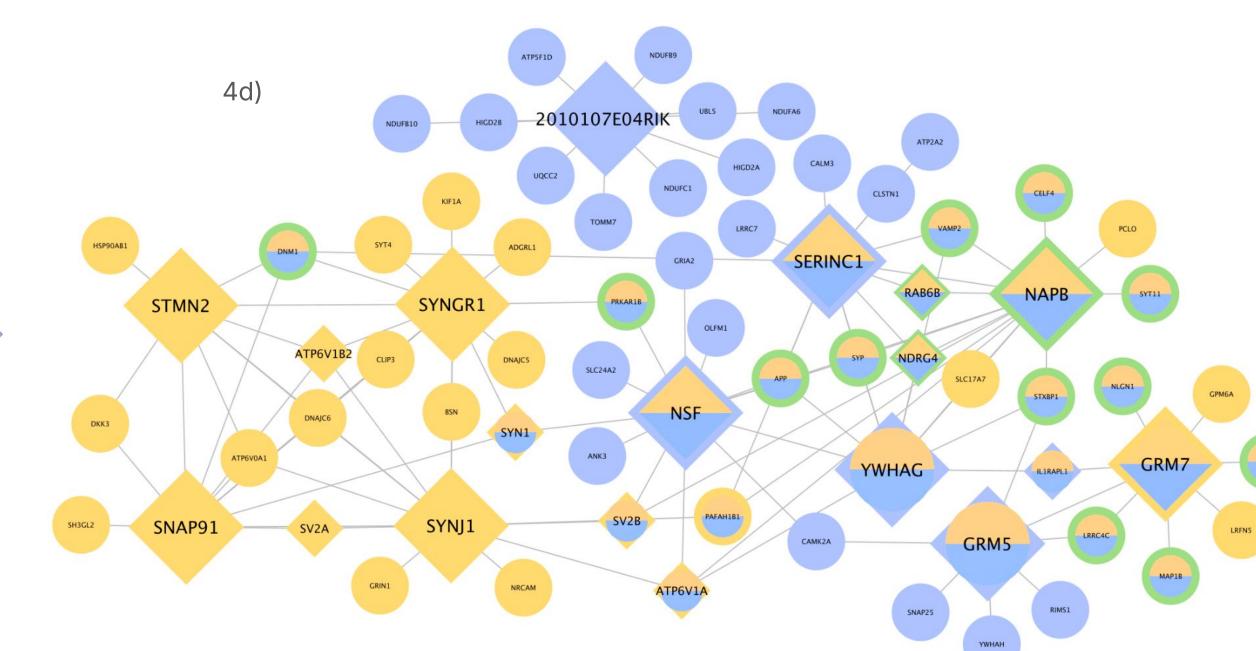
SPORTS - 20

Chi Enrichment

Significant Pathways with 30% gene overlap and the Top Odds Ratio Using Fisher's Exact: 1. Positive Regulation of Cell Growth, Developmental Growth, and Axon Extension

2. Neuron Projection Extension, Axon Extension, and Developmental Growth 3. Dendrite Extension, Developmental Growth, Cell Growth 4. Modulation of Excitatory Postsynaptic Potential, Regulation of Trans Synaptic Signaling 5. Odontogenesis of Dentin Containing Tooth, Amelogenesis

Figure 3. Venn Diagram of Enriched Pathways in the mTBI study (red) and Sports study (Blue)



Results

NPC3 DISTRIBUTIONS FOR SNPS IN ENRICHED PATHWAYS REVEAL SIGNIFICANT DIFFERENCES BETWEEN SPORTS AND NON-SPORTS GROUPS

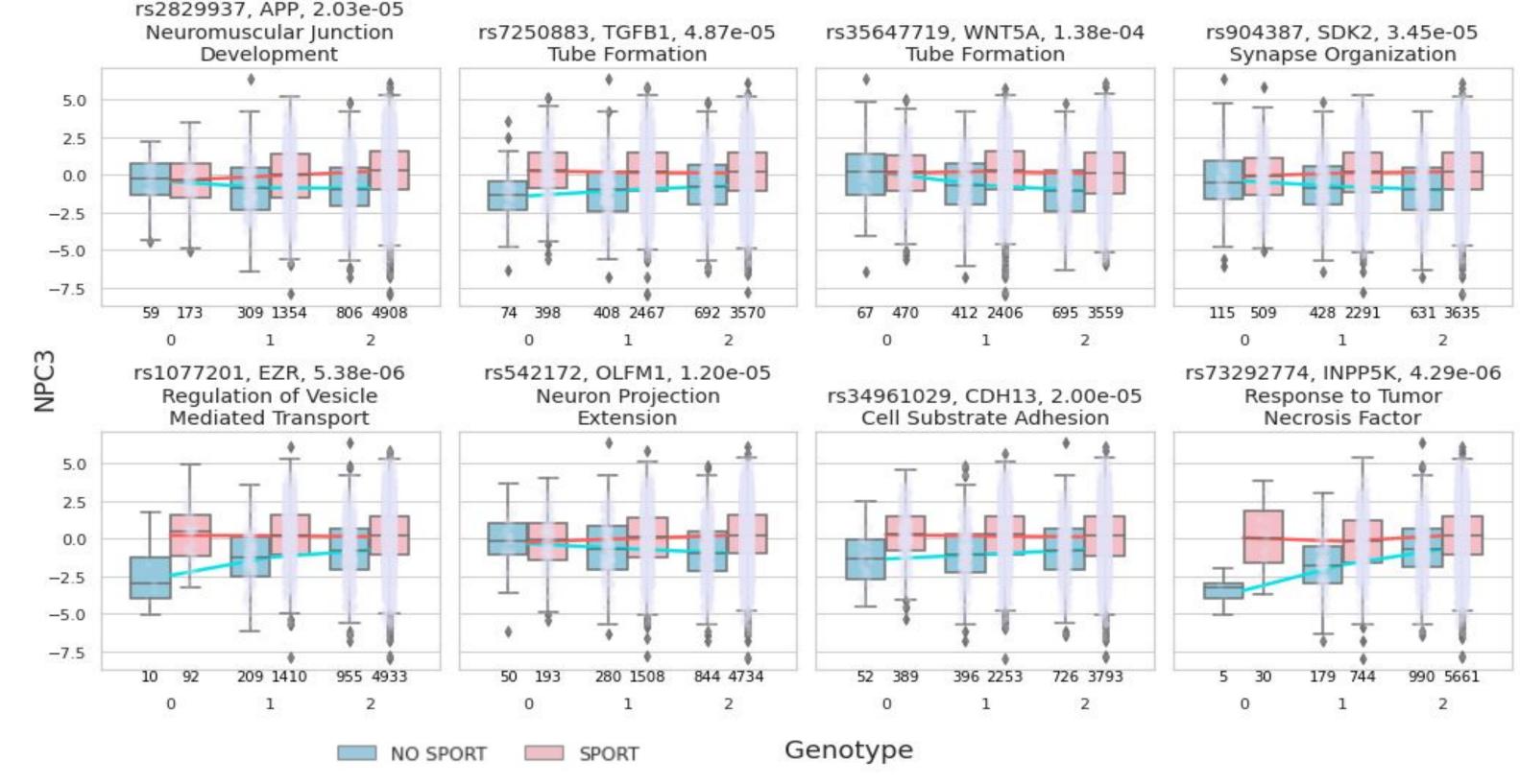


Figure 2. Learning and memory score (NPC3) distributions for SNPs in GO pathways. The count of individuals in each sports group and genotype is shown below each boxplot. Trendlines for each group show significant differences in directionality across genotype for the two groups.

CELL-TYPE-SPECIFIC NETWORK ANALYSIS REVEALS KEY REGULATORS AND NETWORKS **GOVERNING NEURONAL REPAIR PATHWAYS**

			S	ports Key I	Drivers					
Anterior C Cortex	Anterior Cingulate Cortex		Frontal Pole Secondary Motor Cortex		pus		Prelimbic Infralimbic Cortex	TOTAL		
EXC	INH	EXC	INH	EXC	INH	MICRO	OLIGO	EXC	INH	
1	1	0	1	1	1	0	0	0	1	6
1	1	1	1	0	1	0	0	1	0	6
1	1	1	1	0	0	0	0	1	0	5
1	1	0	1	0	1	0	0	0	1	5
0	1	0	1	1	1	0	0	0	1	5
	Cortex EXC 1 1 1	Cortex EXC INH 1 1 1 1 1 1 1 1	Secondary Cortex Secondary Cortex	Anterior Cingulate Cortex EXC INH EXC INH 1 1 0 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1	Anterior Cingulate Cortex Frontal Pole Secondary Motor Cortex Hippocame EXC INH EXC INH EXC 1 1 0 1 1 1 1 1 1 0 1 1 1 1 0 1 1 1 1 0 1 1 1 0 1 0	Secondary Motor Cortex Hippocampus	Anterior Cingulate Cortex	Anterior Cingulate Cortex Frontal Pole Secondary Motor Cortex Hippocampus EXC INH EXC INH MICRO OLIGO 1 1 0 1 1 0 0 1 1 1 1 0 0 0 1 1 1 1 0 0 0 1 1 1 1 0 0 0 0 1 1 0 1 0 1 0 0	Anterior Cingulate Cortex Cortex Hippocampus Cortex EXC INH EXC INH EXC INH MICRO OLIGO EXC	Anterior Cingulate Cortex

mTBI x Sports Overlapping Key Drivers (Intersection)														
4b)	Anterior Cingulate Cortex			Frontal Pole Secondary Motor Cortex			Hippocampus				Prelimbic Infralimbic Orbital Cortex			тота
	EXC	INH	OLIGO	EXC	INH	OLIGO	EXC	INH	MICRO	OLIGO	EXC	INH	OLIGO	
NSF	1	1	0	1	0	0	0	0	0	0	0	0	0	
NAPB	1	0	0	1	0	0	0	0	0	0	0	0	0	
NDRG4	1	1	0	0	0	0	0	0	0	0	0	0	0	

Figure 4. (a) Table of common key drivers found after overlaying MSEA genes with Allen Institute Brain Networks and (b) shared key drivers found in both the mTBI <u>and</u> sports study (EXC = excitatory, INH = inhibitory, MICRO = microglia, OLIGO = oligodendrocyte) Most key drivers were associated

with the pathways Synapse Organization and Vesicle Mediated Transport in the Synapse across various except for the (c) hippocampal microglia which had key drivers associated with the Tumor Necrosis Factor pathway. Key drivers are shown as diamonds. (d) depicts shared key drivers in mTBI (yellow) and sports (blue) in Anterior Cinqulate Cortex excitatory cells.

Conclusion

- We hypothesize that sports participation interacts with genetic variation to influence learning and memory through pathways like collagen activated signaling, tube formation, and synapse organization.
- Genes known to be involved in learning and memory (eg. APP, TGFB1, WNT5A, CDH13, INPP5K) and novel learning/memory candidates (eg. SDK2, EZR, OLFM1) demonstrated significant differences in NPC3 scores in the two groups
- Hippocampal microglia CCL4/TNF signaling suggests a role in neuroinflammation.
- Overlap with mTBI gene networks highlights shared key drivers (eg. NAPB, NSD, NDRG4) for cognitive resilience and repair.

References & Acknowledgements

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- Erickson KI, Voss MW, Prakash RS, Basak C, Szabo A, Chaddock L, et al. Exercise training increases size of hippocampus and improves memory. Proceedings of the National Academy of Sciences [Internet]. 2011 Jan 31;108(7):3017–22. Available from: https://www.ncbi.nlm.nih.gov/pmc/articles/PMC3041121/