Gene	log$_2$FC	StdErr	*p*- adj	Direction	Biological function
Activity-dependent signaling					
Egr1	0.554	0.111	1.36×10^{-3}	↑	Immediate early gene, LTP and memory consolidation
Egr2	1.352	0.275	1.72×10^{-3}	↑	Immediate early gene, hindbrain segmentation and development
Nr4a1	0.666	0.147	7.24×10^{-3}	↑	Immediate early gene, synaptic plasticity, dendritic spine regulation
Bdnf	0.27	0.063	1.88×10^{-2}	↑	Neurotrophic factor, synaptic maturation and plasticity
Synaptic modulation					
Chrm3	0.303	0.071	1.88×10^{-2}	↑	Muscarinic M3 receptor, hippocampal GABAergic modulation
Sntb2	0.228	0.057	4.77×10^{-2}	↑	Dystrophin-associated protein complex component, inhibitory postsynaptic organization
ECM and structural					
Emp2	−0.533	0.115	5.60×10^{-3}	↓	Membrane protein, cell surface protein trafficking
Gcnt1	−1.618	0.28	3.26×10^{-5}	↓	Glycosylation, ECM remodeling
Sclt1	−0.801	0.139	3.46×10^{-5}	↓	Ciliogenesis and cellular structure
Vascular, metabolic and stress					
Apold1	0.792	0.194	3.27×10^{-2}	↑	Vascular stress response
Nos3	−0.501	0.122	3.15×10^{-2}	↓	Endothelial nitric oxide synthase (eNOS), vascular tone regulation
Tlcd3b	−0.195	0.046	2.04×10^{-2}	↓	Membrane lipid metabolism
Immune response					
Gbp2b	−5.296	0.695	5.71×10^{-10}	↓	Interferon-induced GTPase, innate immune response
Clec16a	0.418	0.069	8.28×10^{-6}	↑	Autophagy and mitophagy regulation
Adgre5	−0.440	0.103	1.88×10^{-2}	↓	Immune cell adhesion and migration
Transcriptional regulation					
Cbfa2t3	−0.346	0.077	7.31×10^{-3}	↓	Transcriptional corepressor, cell differentiation
Sox13	−0.539	0.13	2.57×10^{-2}	↓	Transcription factor, developmental regulation
Tiparp	0.467	0.088	3.10×10^{-4}	↑	Mono-ADP-ribosyltransferase, transcriptional regulation
Epilepsy / neurodevelopment					
Cdkl5	0.674	0.103	4.89×10^{-7}	↑	CDD causal gene
Other / limited annotation					
Ermardl2	0.619	0.083	7.61×10^{-10}	↑	Poorly characterized
Ermardl1	4.552	0.991	6.04×10^{-3}	↑	Poorly characterized
Ddx4	1.021	0.232	1.21×10^{-2}	↑	RNA helicase; germline expression
Gm5148	−1.478	0.334	1.12×10^{-2}	↓	Predicted gene, unknown function
Gm47204	−0.466	0.11	2.04×10^{-2}	↓	Predicted gene, unknown function
Gm26881	−2.443	0.581	2.16×10^{-2}	↓	Predicted gene, unknown function
F730043M19Rik	−0.477	0.095	1.35×10^{-3}	↓	Uncharacterized gene
E230020A03Rik	−1.257	0.274	6.04×10^{-3}	↓	Uncharacterized gene
Pisd-ps1	−1.329	0.256	5.75×10^{-4}	↓	Poorly characterized
Eno1b	0.516	0.11	4.21×10^{-3}	↑	Predicted gene, putative glycolytic function

Armh4	0.238	0.049	2.69×10^{-3}	↑	Partially characterized; transcriptional context
Prune2	−0.756	0.189	4.63×10^{-2}	↓	Poorly characterized

Table S5. Functional classification of genes showing significant age × genotype interaction in the hippocampus of heterozygous *Cdkl5* +/– female mice. Genes were identified through RNA sequencing of hippocampal tissue from wild-type and heterozygous *Cdkl5* +/– female mice at 3 and 12 months of age, followed by differential expression analysis using DESeq2 with age × genotype interaction term. Log_2 fold change ($\log_2$FC) values and their standard error (StdErr) represent the interaction effect, reflecting differences in $\log_2$ fold changes across age between wild-type and heterozygous mice. A positive $\log_2$FC indicates that expression in heterozygous mice increases relative to wild-type with age (↑); a negative $\log_2$FC indicates that it decreases (↓). Genes are grouped by biological function. All genes with an adjusted *p* -value (*p* -adj) < 0.05 are shown.