**Figure S1. Proportion of subjects developing neuropsychiatric symptoms among mTBI and non-mTBI cohorts during the 1-year follow-up period from the index date**



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| **Table S1. The allele frequency of single nucleotide polymorphisms (SNPs) in different ethnic groups** |  |
| **Gene** | **Position** (**GRCh37)** | **SNP** |  | **Allele** |  | **AFR****freq** | **AMR****freq** | **ASN****freq** | **EUR****freq** | **TWB controls** |  | **mTBI patients** |
|  | **Ref** | **Alt** |  | **freq** | **HWE**  |  | **freq** | **HWE** |
| *IGF1* | chr12:102875569 | rs35767 |  | G | A |  | 0.42 | 0.25 | 0.34 | 0.16 | 0.35 | 0.054 |  | 0.35 | 0.806 |
| chr12:102874864 | rs5742612 |  | A | G |  | 0.02 | 0.1 | 0.29 | 0.05 | 0.29 | 0.710 |  | 0.33 | 0.817 |
| chr12:102838515 | rs7136446 |  | T | C |  | 0.3 | 0.23 | 0.19 | 0.39 | 0.17 | 0.774 |  | 0.22 | 0.623 |
| chr12:102824921 | rs972936 |  | C | T |  | 0.4 | 0.26 | 0.44 | 0.25 | 0.44 | 0.740 |  | 0.50 | 0.939 |
| chr12:102813632 | rs2072592 |  | C | T |  | 0 | 0.09 | 0.25 | 0.02 | 0.28 | 0.666 |  | 0.28 | 0.742 |
| *AFR* African American, *AMR*, Americas, *ASN* Asian, *EUR* European, *TWB* Taiwan Biobank, Freq: frequency shows as Alt allele. mTBI: mild traumatic brain injury patients recruited in our study. HWE: *p*-value for Hardy-Weinberg equilibrium. |

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| **Table S2. Basal characteristics of patients with mild traumatic brain injury (mTBI) stratified by sex** |
| **Characteristics** | **Males** | **Females** |
| Number of subjects | 55 | 121 |
| Age (years)a | 37.98 ± 15.46 | 39.17 ± 13.83 |
|  Range | 20-83 | 20-75 |
| Cause of injury, no. (%) |  |  |
|  Transportation accidents | 26 (47.3) | 70 (57.9) |
|  Falls | 18 (32.7) | 35 (28.9) |
|  Other | 11 (20.0) | 16 (13.2) |
| GCSb | 15 [15~15] | 15 [15~15] |
| GOSEb | 7 [6~8] | 7 [6~8] |
| BAIb | 4.5 [2~9] | 7 [2.25~12] |
| BDIb | 6 [2~10.5] | 7 [2~12] |
| DHIb | 12 [2~31] | 26 [10.5~42] |
| PSQIb | 6 [5~8.75] | 7 [5~9] |
| Serum IGF-1 (ng/mL)a | 144.75 ± 64.63 | 175.30± 80.74 |
| amean ± standard deviation. bmedian [interquartile range]. *GCS* Glasgow Coma Scale, *GOSE* Extended Glasgow Outcome Scale, *BAI* Beck Anxiety Inventory, *BDI* Beck Depression Inventory, *DHI* Dizziness Handicap Inventory, *PSQI* Pittsburgh Sleep Quality Index, *IGF-1* Insulin-like growth factor 1 |

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| **Table S3. Sex-stratified analyses for Beck Anxiety Inventory (BAI) score** |
| **Sex** | **SNP** | **Genotype** | **BAI score** | **OR (95% CI)** | **Additive modela** |
| **BAI ≤7** | **BA I>7** | ***p-*value** | **Bonferroni** |
| **Males** | rs35767 | GG | 15 (39.5) | 5 (31.2) | 1.38 (0.58-3.29) | 0.468  | 1.000 |
|  |  | GA | 18 (47.4) | 8 (50.0) |  |  |  |
|  |  | AA | 5 (13.2) | 3 (18.8) |  |  |  |
|  | rs5742612 | AA | 16 (42.1) | 4 (26.7) | 1.96 (0.75-5.06) | 0.160  | 1.000 |
|  |  | AG | 19 (50.0) | 8 (53.3) |  |  |  |
|  |  | GG | 3 (7.9) | 3 (20.0) |  |  |  |
|  | rs7136446 | TT | 24 (63.2) | 10 (62.5) | 1.10 (0.39-3.12) | 0.853 | 1.000 |
|  |  | TC | 13 (34.2) | 5 (31.2) |  |  |  |
|  |  | CC | 1 (2.6) | 1 (6.2) |  |  |  |
|  | rs972936 | CC | 12 (31.6) | 2 (12.5) | 1.79 (0.74-4.33) | 0.187 | 1.000 |
|  |  | CT | 18 (47.4) | 9 (56.2) |  |  |  |
|  |  | TT | 8 (21.1) | 5 (31.2) |  |  |  |
|  | rs2072592 | CC | 19 (51.4) | 7 (43.8) | 1.57 (0.63-3.86) | 0.331 | 1.000 |
|  |  | CT | 16 (43.2) | 6 (37.5) |  |  |  |
|  |  | TT | 2 (5.4) | 3 (18.8) |  |  |  |
| **Females** | rs35767 | GG | 29 (46.0) | 23 (42.6) | 1.04 (0.61-1.78) | 0.892  | 1.000 |
|  |  | GA | 26 (41.3) | 25 (46.3) |  |  |  |
|  |  | AA | 8 (12.7) | 6 (11.1) |  |  |  |
|  | rs5742612 | AA | 31 (48.4) | 24 (45.3) | 1.04 (0.60-1.80) | 0.890  | 1.000 |
|  |  | AG | 26 (40.6) | 24 (45.3) |  |  |  |
|  |  | GG | 7 (10.9) | 5 (9.4) |  |  |  |
|  | rs7136446 | TT | 43 (67.2) | 27 (50.0) | 1.61 (0.89-2.93) | 0.112  | 1.000 |
|  |  | TC | 17 (26.6) | 23 (42.6) |  |  |  |
|  |  | CC | 4 (6.2) | 4 (7.4) |  |  |  |
|  | rs972936 | CC | 13 (20.6) | 17 (31.5) | 0.68 (0.41-1.15) | 0.152 | 1.000 |
|  |  | CT | 32 (50.8) | 26 (48.1) |  |  |  |
|  |  | TT | 18 (28.6) | 11 (20.4) |  |  |  |
|  | rs2072592 | CC | 33 (52.4) | 27 (50.9) | 1.07 (0.59-1.93) | 0.820  | 1.000 |
|  |  | CT | 26 (41.3) | 22 (41.5) |  |  |  |
|  |  | TT | 4 (6.3) | 4 (7.5) |  |  |  |
| aAdjusted for age. *OR* odds ratio, *CI* confidence interval |

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| **Table S4. Sex-stratified analyses for Beck Depression Inventory (BDI) score** |
| **Sex** | **SNP** | **Genotype** | **BDI score** | **OR (95% CI)** | **Additive modela** |
| **BDI ≤9** | **BDI >9** | ***p-*value** | **Bonferroni** |
| **Males** | rs35767 | GG | 16 (41.0) | 5 (31.2) | 1.73 (0.72-4.16) | 0.212  | 1.000 |
|  |  | GA | 19 (48.7) | 7 (43.8) |  |  |  |
|  |  | AA | 4 (10.3) | 4 (25.0) |  |  |  |
|  | rs5742612 | AA | 16 (42.1) | 5 (31.2) | 2.13 (0.83-5.46) | 0.107  | 1.000 |
|  |  | AG | 20 (52.6) | 7 (43.8) |  |  |  |
|  |  | GG | 2 (5.3) | 4 (25.0) |  |  |  |
|  | rs7136446 | TT | 23 (59.0)  | 12 (75) | 0.45 (0.13-1.51) | 0.169  | 1.000 |
|  |  | TC | 14 (35.9) | 4 (25) |  |  |  |
|  |  | CC | 2 (5.1) | 0 (0) |  |  |  |
|  | rs972936 | CC | 10 (25.6)  | 5 (31.2) | 1.08 (0.47-2.50) | 0.855 | 1.000 |
|  |  | CT | 21 (53.8) | 6 (37.5) |  |  |  |
|  |  | TT | 8 (20.5) | 5 (31.2) |  |  |  |
|  | rs2072592 | CC | 19 (48.7)  | 8 (53.3) | 1.57 (0.63-3.88) | 0.333 | 1.000 |
|  |  | CT | 19 (48.7) | 3 (20.0) |  |  |  |
|  |  | TT | 1 (2.6) | 4 (26.7) |  |  |  |
| **Females** | rs35767 | GG | 34 (44.2) | 18 (45) | 0.92 (0.52-1.63) | 0.778 | 1.000 |
|  |  | GA | 33 (42.9) | 18 (45) |  |  |  |
|  |  | AA | 10 (13.0) | 4 (10) |  |  |  |
|  | rs5742612 | AA | 35 (44.9) | 20 (51.3) | 0.80 (0.44-1.44) | 0.448 | 1.000 |
|  |  | AG | 34 (43.6) | 16 (41.0) |  |  |  |
|  |  | GG | 9 (11.5) | 3 (7.7) |  |  |  |
|  | rs7136446 | TT | 50 (64.1) | 20 (50.0) | 1.49 (0.81-2.73) | 0.201 | 1.000 |
|  |  | TC | 23 (29.5) | 17 (42.5) |  |  |  |
|  |  | CC | 5 (6.4) | 3 (7.5) |  |  |  |
|  | rs972936 | CC | 19 (24.7) | 11 (27.5) | 1.10 (0.64-1.89) | 0.723 | 1.000 |
|  |  | CT | 41 (53.2) | 17 (42.5) |  |  |  |
|  |  | TT | 17 (22.1) | 12 (30.0) |  |  |  |
|  | rs2072592 | CC | 35 (45.5) | 25 (64.1) | 0.62 (0.32-1.20) | 0.144 | 1.000 |
|  |  | CT | 37 (48.1) | 11 (28.2) |  |  |  |
|  |  | TT | 5 (6.5) | 3 (7.7) |  |  |  |
| aAdjusted for age. *OR* odds ratio, *CI* confidence interval |

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| **Table S5. Sex-stratified analyses for Dizziness Handicap Inventory (DHI) score** |
| **Sex** | **SNP** | **Genotype** | **DHI score** | **OR (95% CI)** | **Additive modela** |
| **DHI ≤30** | **DHI >30** | ***p-*value** | **Bonferroni** |
| **Males** | rs35767 | GG | 17 (42.5) | 3 (21.4) | 1.87 (0.75-4.64) | 0.169  | 1.000 |
|  |  | GA | 18 (45.0) | 8 (57.1) |  |  |  |
|  |  | AA | 5 (12.5) | 3 (21.4) |  |  |  |
|  | rs5742612 | AA | 18 (45) | 3 (21.4) | 1.91 (0.74-4.93) | 0.176  | 1.000 |
|  |  | AG | 18 (45) | 9 (64.3) |  |  |  |
|  |  | GG | 4 (10) | 2 (14.3) |  |  |  |
|  | rs7136446 | TT | 28 (70.0) | 7 (50.0) | 2.18 (0.75-6.31) | 0.150  | 1.000 |
|  |  | TC | 11 (27.5) | 6 (42.9) |  |  |  |
|  |  | CC | 1 (2.5) | 1 (7.1) |  |  |  |
|  | rs972936 | CC | 13 (32.5) | 2 (14.3) | 2.58 (1.02-6.55) | 0.037\* | 0.740 |
|  |  | CT | 20 (50.0) | 6 (42.9) |  |  |  |
|  |  | TT | 7 (17.5) | 6 (42.9) |  |  |  |
|  | rs2072592 | CC | 21 (53.8) | 5 (35.7) | 1.46 (0.58-3.71) | 0.424  | 1.000 |
|  |  | CT | 14 (35.9) | 8 (57.1) |  |  |  |
|  |  | TT | 4 (10.3) | 1 (7.1) |  |  |  |
| **Females** | rs35767 | GG | 30 (42.3) | 23 (50.0) | 0.65 (0.36-1.17) | 0.146  | 1.000 |
|  |  | GA | 31 (43.7) | 21 (45.7) |  |  |  |
|  |  | AA | 10 (14.1) | 2 (4.3) |  |  |  |
|  | rs5742612 | AA | 33 (46.5) | 23 (50.0) | 0.68 (0.38-1.23) | 0.195  | 1.000 |
|  |  | AG | 28 (39.4) | 22 (47.8) |  |  |  |
|  |  | GG | 10 (14.1) | 1 (2.2) |  |  |  |
|  | rs7136446 | TT | 49 (69.0) | 21 (44.7) | 2.73 (1.44-5.18) | 0.001\*\*  | 0.020\* |
|  |  | TC | 21 (29.6) | 19 (40.4) |  |  |  |
|  |  | CC | 1 (1.4) | 7 (14.9) |  |  |  |
|  | rs972936 | CC | 13 (18.3) | 16 (34.8) | 0.60 (0.35-1.04) | 0.062 | 1.000 |
|  |  | CT | 38 (53.5) | 21 (45.7) |  |  |  |
|  |  | TT | 20 (28.2) | 9 (19.6) |  |  |  |
|  | rs2072592 | CC | 34 (48.6)  | 26 (56.5) | 0.74 (0.40-1.39) | 0.344  | 1.000 |
|  |  | CT | 31 (44.3) | 18 (39.1) |  |  |  |
|  |  | TT | 5 (7.1) | 2 (4.3) |  |  |  |
| aAdjusted for age. \*indicates *p*<0.05, \*\*indicates *p*<0.01. *OR* odds ratio, *CI* confidence interval |

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| **Table S6. Sex-stratified analyses for Pittsburgh Sleep Quality Index (PSQI) score** |
| **Sex** | **SNP** | **Genotype** | **PSQI score** | **OR (95% CI)** | **Additive modela** |
| **PSQI ≤8** | **PSQI >8** | ***p-*value** | **Bonferroni** |
| **Males** | rs35767 | GG | 12 (32.4) | 7 (53.8) | 0.67 (0.24-1.81) | 0.421  | 1.000 |
|  |  | GA | 21 (56.8) | 4 (30.8) |  |  |  |
|  |  | AA | 4 (10.8) | 2 (15.4) |  |  |  |
|  | rs5742612 | AA | 13 (35.1) | 6 (50.0) | 0.84 (0.30-2.36) | 0.744  | 1.000 |
|  |  | AG | 21 (56.8) | 4 (33.3) |  |  |  |
|  |  | GG | 3 (8.1) | 2 (16.7) |  |  |  |
|  | rs7136446 | TT | 22 (59.5) | 9 (69.2) | 0.59 (0.17-2.03) | 0.388  | 1.000 |
|  |  | TC | 13 (35.1) | 4 (30.8) |  |  |  |
|  |  | CC | 2 (5.4) | 0 (0) |  |  |  |
|  | rs972936 | CC | 8 (21.6) | 5 (38.5) | 0.71 (0.27-1.85) | 0.475 | 1.000 |
|  |  | CT | 21 (56.8) | 5 (38.5) |  |  |  |
|  |  | TT | 8 (21.6) | 3 (23.1) |  |  |  |
|  | rs2072592 | CC | 17 (47.2) | 8 (61.5) | 0.89 (0.32-2.45) | 0.815 | 1.000 |
|  |  | CT | 17 (47.2) | 3 (23.1) |  |  |  |
|  |  | TT | 2 (5.6) | 2 (15.4) |  |  |  |
| **Females** | rs35767 | GG | 32 (44.4) | 17 (47.2) | 0.93 (0.51-1.70) | 0.814 | 1.000 |
|  |  | GA | 32 (44.4) | 15 (41.7) |  |  |  |
|  |  | AA | 8 (11.1) | 4 (11.1) |  |  |  |
|  | rs5742612 | AA | 35 (48.6) | 17 (47.2) | 0.98 (0.53-1.83) | 0.958 | 1.000 |
|  |  | AG | 30 (41.7) | 16 (44.4) |  |  |  |
|  |  | GG | 7 (9.7) | 3 (8.3) |  |  |  |
|  | rs7136446 | TT | 48 (66.7) | 16 (43.2) | 1.97 (1.04-3.74) | 0.035\* | 0.700 |
|  |  | TC | 20 (27.8) | 17 (45.9) |  |  |  |
|  |  | CC | 4 (5.6) | 4 (10.8) |  |  |  |
|  | rs972936 | CC | 14 (19.4) | 13 (36.1) | 0.57 (0.31-1.03) | 0.058 | 1.000 |
|  |  | CT | 38 (52.8) | 17 (47.2) |  |  |  |
|  |  | TT | 20 (27.8) | 6 (16.7) |  |  |  |
|  | rs2072592 | CC | 36 (50.7) | 19 (52.8) | 0.96 (0.49-1.88) | 0.896 | 1.000 |
|  |  | CT | 31 (43.7) | 15 (41.7) |  |  |  |
|  |  | TT | 4 (5.6) | 2 (5.6) |  |  |  |
| aAdjusted for age. \*indicates *p*<0.05. *OR* odds ratio, *CI* confidence interval |

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| **Table S7. Single nucleotide polymorphisms (SNPs)-sex interaction analyses for neuropsychiatric symptoms following mild traumatic brain injury (mTBI)** |
| **SNP** | **BAI** |  | **BDI** |  | **DHI** |  | **PSQI** |
| **OR (95% CI)** | ***p-*valuea** |  | **OR (95% CI)** | ***p-*valuea** |  | **OR (95% CI)** | ***p-*valuea** |  | **OR (95% CI)** | ***p-*valuea** |
| rs35767 | 0.95 (0.75-1.20) | 0.665 |  | 0.88 (0.71-1.10) | 0.261 |  | 0.80 (0.64-1.01) | 0.059 |  | 1.07 (0.85-1.36) | 0.563 |
| rs5742612 | 0.88 (0.69-1.13) | 0.322 |  | 0.82 (0.65-1.03) | 0.088 |  | 0.81 (0.64-1.02) | 0.076 |  | 1.03 (0.81-1.32) | 0.787 |
| rs7136446 | 1.10 (0.83-1.44) | 0.506 |  | 1.27 (0.97-1.65) | 0.079 |  | 1.08 (0.83-1.40) | 0.561 |  | 1.27 (0.97-1.65) | 0.080 |
| rs972936 | 0.97 (0.78-1.21) | 0.794 |  | 0.96 (0.78-1.19) | 0.724 |  | 0.95 (0.77-1.18) | 0.636 |  | 1.19 (0.95-1.49) | 0.128 |
| rs2072592 | 0.92 (0.72-1.18) | 0.510 |  | 0.83 (0.65-1.05) | 0.117 |  | 0.86 (0.68-1.11) | 0.248 |  | 1.00 (0.78- 1.29) | 0.982 |
| aThe *p*-value for interaction term was adjusted for age under additive model. *BAI* Beck Anxiety Inventory, *BDI* Beck Depression Inventory, *DHI* Dizziness Handicap Inventory, *PSQI* Pittsburgh Sleep Quality Index, *OR* odds ratio, *CI* confidence interval |

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| **Table S8. Expression quantitative trail loci (eQTL) results from Genotype-tissue expression (GTEx)** |
| **SNP** | **Gene symbol** | ***p-*value** | **NES** | **Tissue** | **Actiona** |
| **rs7136446** | *WASHC3* | 4.6E-9 | 0.25 | Esophagus-Mucosa | CC<CT<TT |
|  | *WASHC3* | 2.3E-6 | 0.09 | Whole Blood | CC<CT<TT |
|  | *WASHC3* | 8.7E-5 | 0.13 | Skin-Sun Exposed (Lower leg) | CC<CT<TT |
|  | *RP11-210L7.3* | 7.2E-5 | 0.19 | Testis | CC<CT<TT |
|  | *HELLPAR* | 4.4E-5 | 0.11 | Muscle-Skeletal | CT<CC<TT |
|  |  |  |  |  |  |
| **rs972936** | *PARPBP* | 1.1E-4 | -0.20 | Testis | TT>TC>CC |
|  | *PARPBP* | 1.3E-6 | -0.23 | Adipose-Subcutaneous | TT>TC>CC |
|  | *PARPBP* | 1.4E-6 | -0.10 | Cells-Cultured fibroblasts | TT>TC>CC |
|  | *RP11-210L7.3* | 7.5E-14 | 0.40 | Testis | TT<TC<CC |
|  | *WASHC3* | 5.7E-26 | 0.47 | Esophagus-Mucosa | TT<TC<CC |
|  | *WASHC3* | 1.5E-15 | 0.32 | Skin-Not Sun Exposed (Suprapubic) | TT<TC<CC |
|  | *WASHC3* | 1.0E-14 | 0.27 | Skin-Sun Exposed (Lower leg) | TT<TC<CC |
|  | *WASHC3* | 3.6E-10 | 0.20 | Nerve-Tibial | TT<TC<CC |
|  | *WASHC3* | 1.5E-10 | 0.26 | Heart-Left Ventricle | TT<TC<CC |
|  | *WASHC3* | 9.4E-12 | 0.14 | Whole Blood | TT<TC<CC |
|  | *WASHC3* | 3.0E-10 | 0.18 | Muscle-Skeletal | TT<TC<CC |
|  | *WASHC3* | 6.6E-9 | 0.17 | Breast-Mammary Tissue | TT<TC<CC |
|  | *WASHC3* | 1.2E-8 | 0.20 | Colon-Transverse | TT<TC<CC |
|  | *WASHC3* | 8.6E-8 | 0.15 | Esophagus-Muscularis | TT<TC<CC |
|  | *WASHC3* | 7.1E-9 | 0.31 | Stomach | TT<TC<CC |
|  | *WASHC3* | 1.3E-7 | 0.21 | Adipose-Visceral (Omentum) | TT<TC<CC |
|  | *WASHC3* | 8.9E-7 | 0.18 | Adipose-Subcutaneous | TT<TC<CC |
|  | *WASHC3* | 1.0E-7 | 0.14 | Artery-Tibial | TT<TC<CC |
|  | *WASHC3* | 1.0E-6 | 0.25 | Heart-Atrial Appendage | TT<TC<CC |
|  | *WASHC3* | 1.3E-6 | 0.27 | Adrenal Gland | TT<TC<CC |
|  | *WASHC3* | 1.1E-7 | 0.34 | Pancreas | TT<TC<CC |
|  | *WASHC3* | 1.0E-8 | 0.18 | Thyroid | TT<TC<CC |
|  | *WASHC3* | 1.4E-6 | 0.20 | Artery-Aorta | TT<TC<CC |
|  | *WASHC3* | 4.4E-6 | 0.16 | Cells-Cultured fibroblasts | TT<TC<CC |
|  | *WASHC3* | 4.6E-6 | 0.12 | Lung | TT<TC<CC |
|  | *WASHC3* | 2.4E-5 | 0.24 | Spleen | TT<TC<CC |
| aThe median expression level of each genotype. *NES* normalized effect size, *WASHC3* WASH complex subunit 3, *RP11-210L7.3* long intergenic non-protein coding RNA 2456, *HELLPAR* HELLP associated long non-coding RNA, *PARPBP* PARP1 binding protein. Data Source: GTEx Analysis Release V8. |

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| **Table S9. Functional annotation by HaploReg V4.1 and RegulomeDB** |
| **SNP** | **Risk allele** | **dbSNP** |  | **HaploReg V4.1** |  | **RegulomeDB** |
| **Promoter****histone marks** | **Enhancer****histone marks** | **DNAse** | **Proteins****bound** | **Motifs****changed** |
| **rs7136446** | C | intronic |  | ― | ― | ― | ― | HDAC2, NRSF, Sin3Ak-20 |  | TF binding + DNase peak |
| **rs972936** | T | intronic |  | ― | 4 tissues | BLD | ― | NF-κB, STAT |  | TF binding or DNase peak |
| *HDAC2* histone deacetylase 2, *NRSF* neuron-restrictive silencer factor, *NF-κB* nuclear factor-κB, *STAT* signal transducer and activator of transcription, *TF* transcription factor |

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| **Table S10.** **Expression quantitative trait loci (eQTL) results of rs7136446 and rs972936 with insulin-like growth factor 1 *(IGF-1*) expressions in brain tissues from Genotype-tissue expression (GTEx)** |
| **Gene** | **SNP** | **Risk allele** | **Brain tissue** | ***p*-value** | **NES** | **Actiona** |
| *IGF-1* | rs7136446 | C | Brain\_Hippocampus | 0.013 | 0.21 | CC<CT<TT |
| rs972936 | T | Brain-Frontal Cortex (BA9) | 0.036 | 0.20 | TT<TC<CC |
| rs972936 | T | Brain\_Hippocampus | 0.047 | 0.22 | TT<TC<CC |
| aThe median expression level of each genotype. *NES* mormalized effect size. Data Source: GTEx Analysis Release V8. |

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| **Table S11.** **Association between insulin-like growth factor 1 (*IGF-1*) expression levels and Alzheimer’s disease (AD) in brain donors with no history of traumatic brain injury (TBI)** |
| **Brain region** | **Alzheimer’s disease** |  | **No Dementia** | ***p*-value** |
| **Samples** | **Mean** | **SD** |  | **Samples** | **Mean** | **SD** |
| Parietal white matter (FWM) | 15 | 0.883 | 0.310 |  | 27 | 0.752 | 0.246  | 0.174 |
| Parietal cortex (PCx) | 15 | 1.012 | 0.239 |  | 27 | 1.005 | 0.181  | 0.926 |
| Temporal cortex (TCx) | 15 | 1.078 | 0.225 |  | 28 | 1.043 | 0.205  | 0.623 |
| Hippocampus (HIP) | 13 | 1.343 | 0.338 |  | 29 | 1.366 | 0.284  | 0.830 |
| *SD* standard deviation. |