**Exploration of molecular mechanism of Traditional Chinese Tuina therapy for insomnia by proteomics analysis**

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**Supplementary information**

**Table S1.** Differentially expressed proteins of BTT *vs* HC , which were filtered by Fold Change > 1.2 for up regulated and Fold Change < 0.83 for down regulated, as well as with a statistical p-value ≤ 0.05.HC, the healthy control group; BTT, before Tuina treatment.

**Table S2.** Differentially expressed proteins of ATT *vs* HC , which were filtered by Fold Change > 1.2 for up regulated and Fold Change < 0.83 for down regulated, as well as with a statistical p-value ≤ 0.05. HC, the healthy control group; ATT, after Tuina treatment.

**Table S3.** Differentially expressed proteins of ATT *vs* BTT , which were filtered by Fold Change > 1.2 for up regulated and Fold Change < 0.83 for down regulated, as well as with a statistical p-value ≤ 0.05. BTT, before Tuina treatment; ATT, after Tuina treatment.

**Table S4.** Gene Ontology enrichment analysis results for differential expressed proteins between BTT and HC.HC, the healthy control; BTT, before Tuina treatment.

**Table S5.** Gene Ontology enrichment analysis results for differential expressed proteins between ATT and HC.HC, the healthy control; ATT, after Tuina treatment.

**Table S6.** Gene Ontology enrichment analysis results for differential expressed proteins between BTT and ATT.BTT, before Tuina treatment; ATT, after Tuina treatment.