

Meditative Movement (MM) associated with positive BDNF Gene Expression changes and improved cognitive performance in Breast Cancer Survivors (BCSs).

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Introduction: BCSs report decrements in cognitive performance.

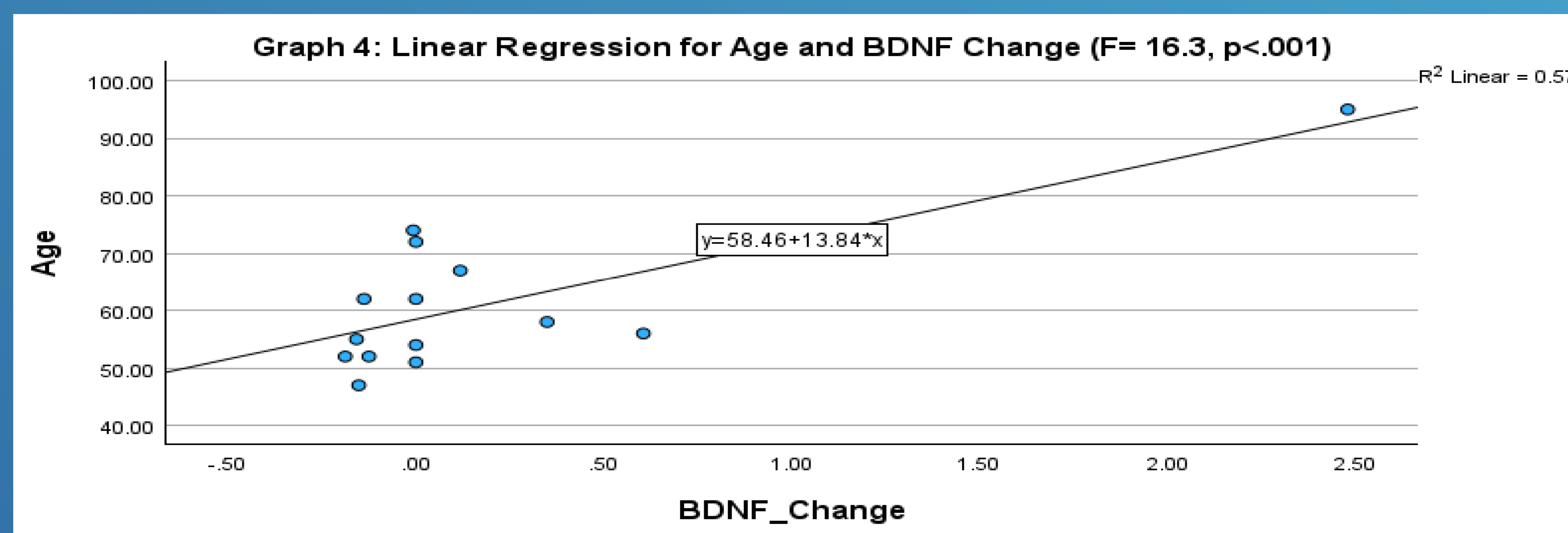
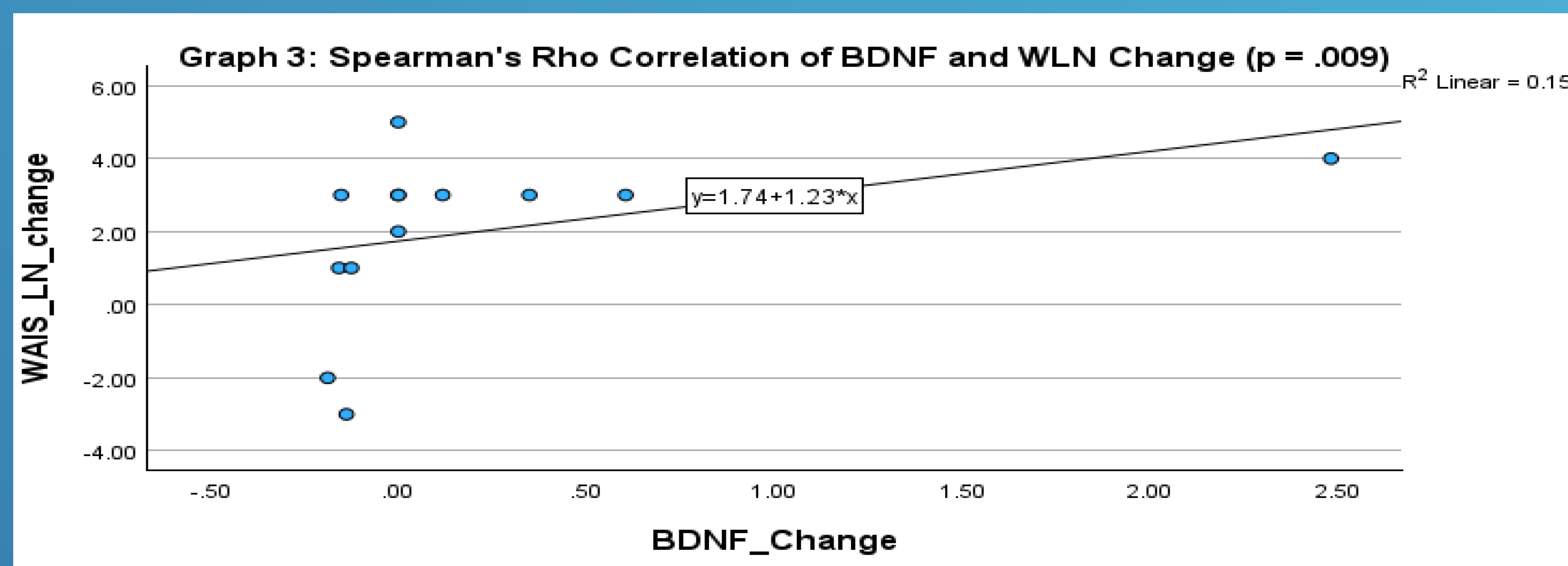
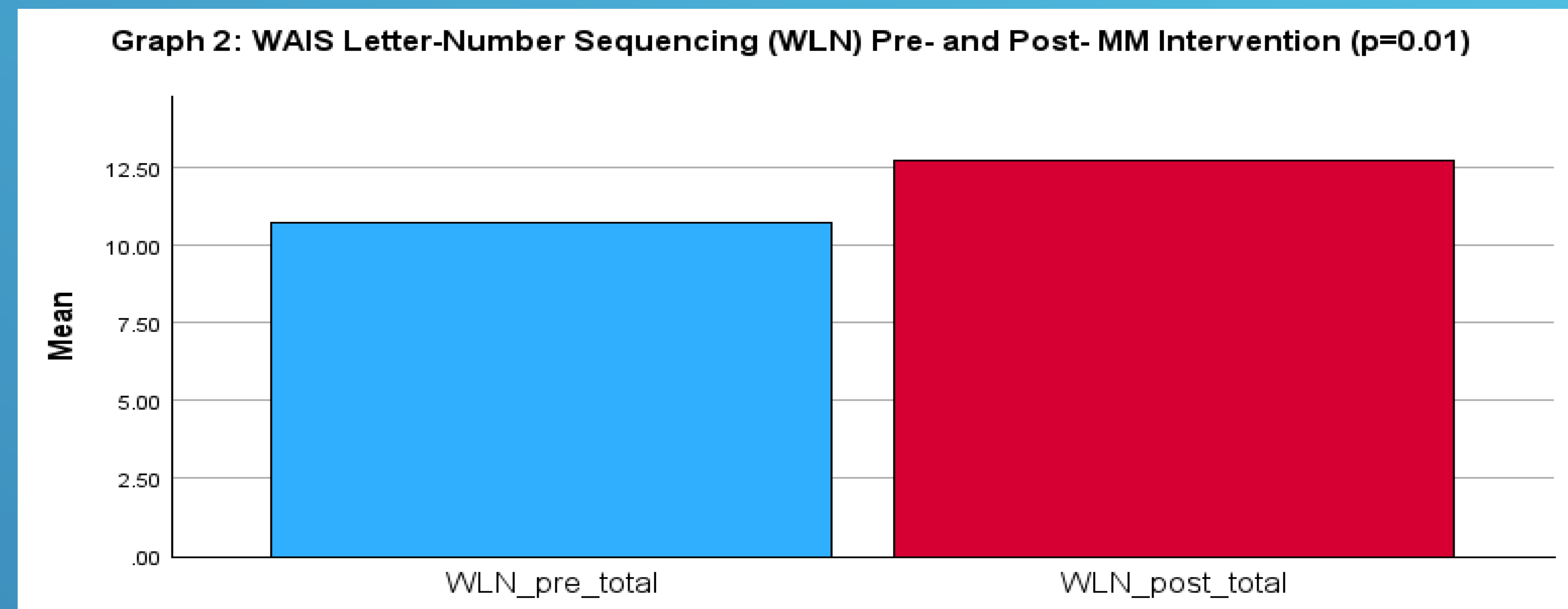
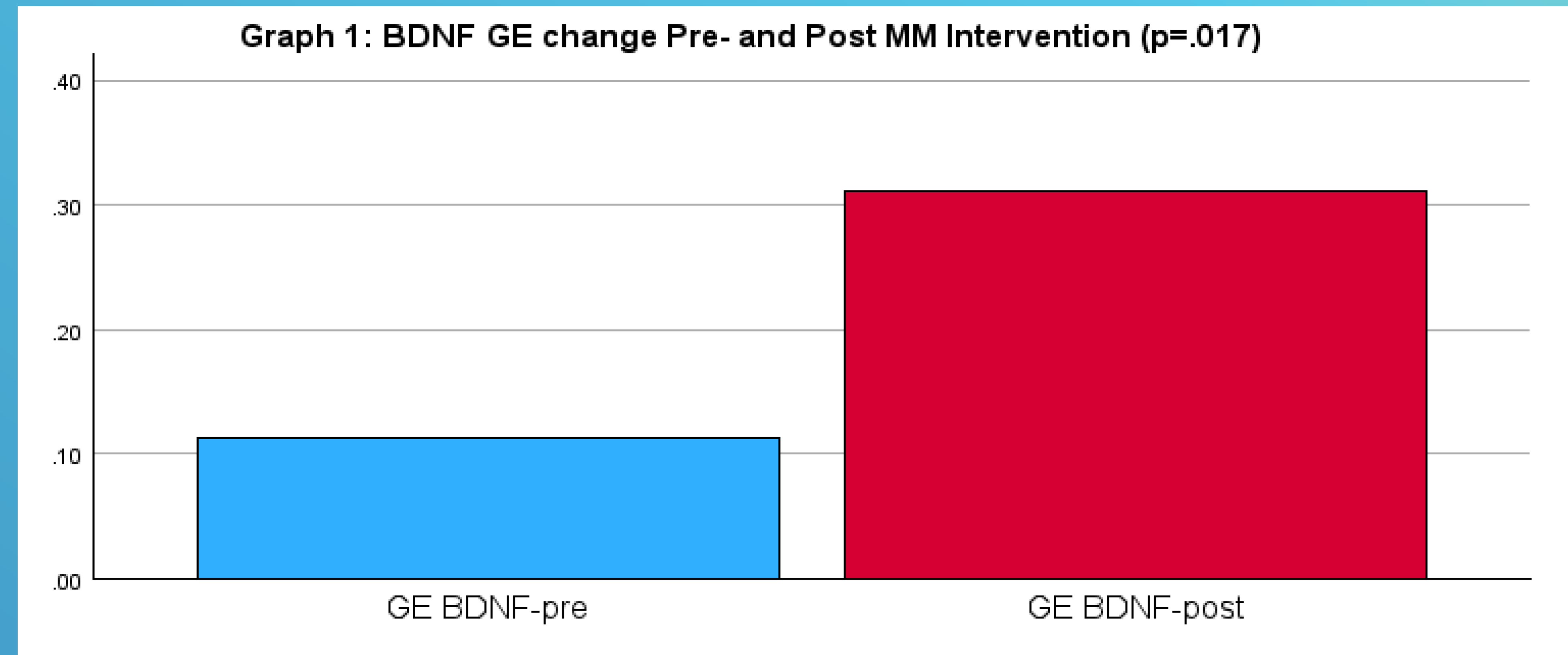
- A MM program, Qigong/Tai Chi Easy, combines meditation and exercise, which are practices known to improve cognitive function.
- The BDNF gene regulates synaptic plasticity associated and positively related with cognitive functioning.

Methods: Using a single group, pre- to post-intervention assessment design.

- A pilot study was conducted in BCSs to test the effects of an 8-week MM intervention:
- On cognitive functioning via Wechsler Adult Intelligence Scale subtest on working memory, (WAIS-III Letter-Number Sequencing: WLN)
- On BDNF gene expression factors via blood samples.

Inclusion criteria:

- ≥45 years of age; female breast cancer
- Stage 0–III
- Between six months and five years past primary treatment
- T-test, Spearman's rank correlation and Linear Regression utilized.



Results: Fourteen BCSs (mean age = 61) completed the MM intervention with mean practice time of 729 min (sd=369).

- Analysis indicated a significant increase in BDNF gene expression from pre-intervention [mean (sd), .11 (.9)] to post-intervention, [.30 (.7), $r=.63$, $p=.017$]. (Graph 1)
- Similarly, a significant increase was found between the WLN pre-intervention [10.7 (3.2)] and post-intervention [12.7 (2.8), $p=.01$]. (Graph 2)
- Spearman's correlation found a significant relationship between BDNF gene expression change [0.19 (0.2)] and W memory subtest change [2.0 (0.4), $r=.70$, $p=.009$]. (Graph 3)
- Simple linear regression analysis indicated that BCSs' age explained 57.7% ($R^2=.58$) of variation in BDNF gene expression change ($F=1(12)$, 16.3, $p<.001$). (Graph 4)

Conclusions: There was a significant change in pre- and post-intervention WLN subset, a positive correlation between pre- and post-intervention BDNF gene expression and between BDNF gene expression change and WLN subset change, which was partially explained by age.