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2 **Supplementary Figure 1.** The volcano plot was constructed using the fold change values and P-adjust.

3 P < 0.05 was set as the cut-off criterion of significant difference. Red dots indicate upregulated genes;

4 blue dots indicate downregulated genes; grey dots indicate not significant.

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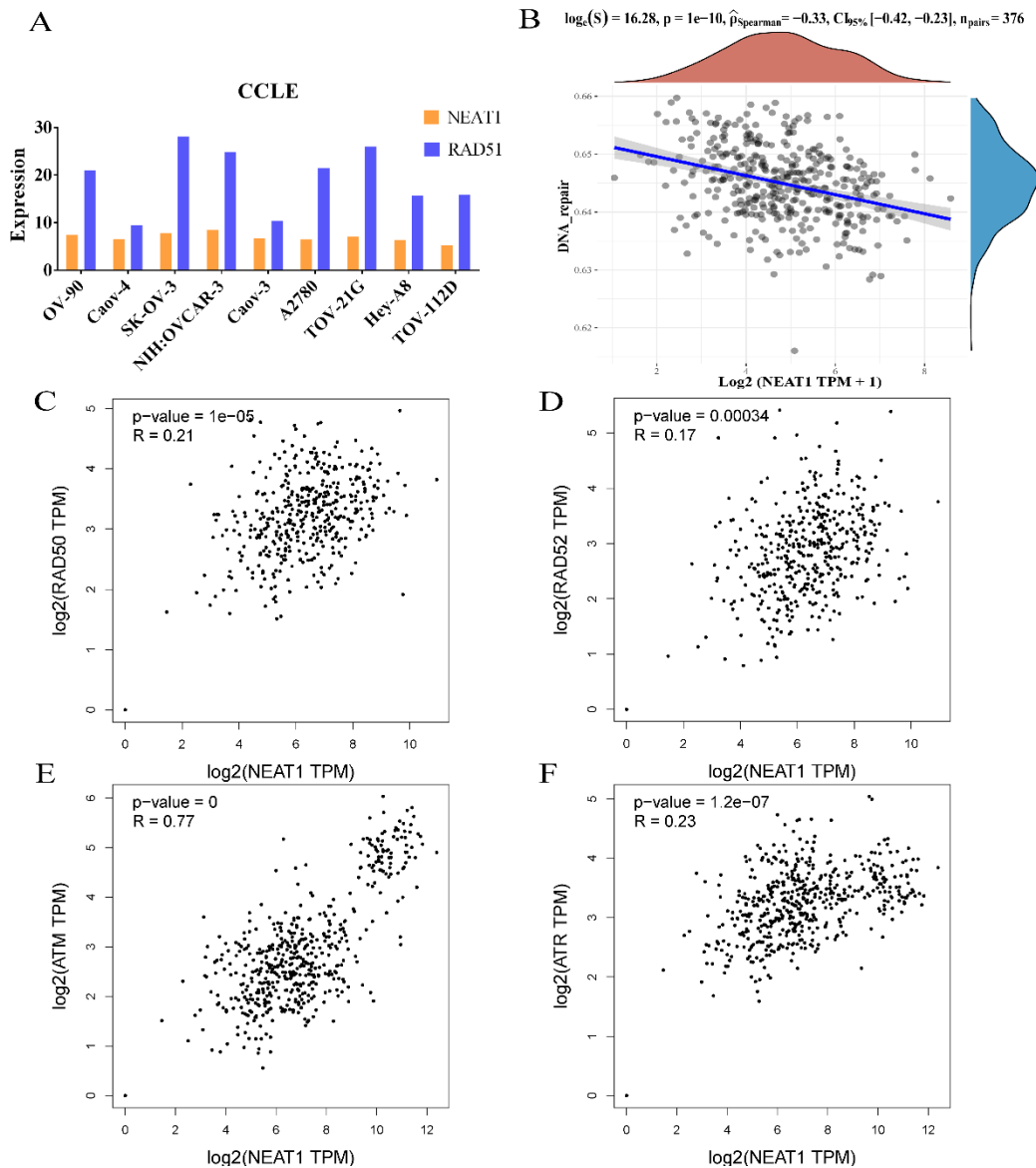
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13 **Supplementary Figure 2.** The relationship between NEAT1 and HR repair pathway.

14 (A) CCLE databases showed the expression of NEAT1 and RAD51 in different ovarian cancer cell lines.

15 (B) The correlations between NEAT1 and DNA repair pathway score were analyzed with Spearman. The

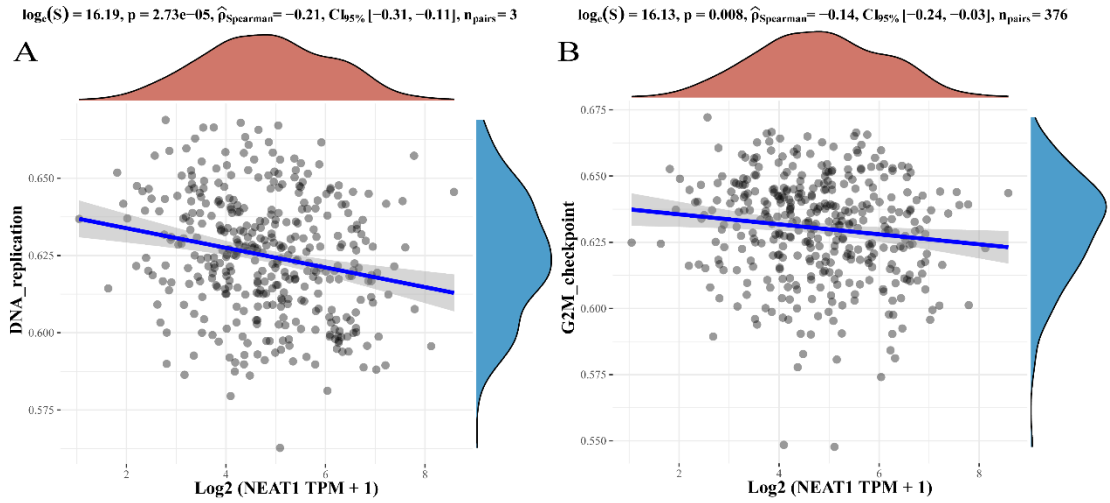
16 abscissa represents the distribution of the gene expression, and the ordinate represents the distribution of

17 the pathway score. The density curve on the right represents the trend in the distribution of pathway

18 immune score, the upper-density curve represents the trend in the distribution of the gene expression.

19 (C-F) The scatter plot showed the correlation between the expression of NEAT1 and HR-associated genes

20 (RAD50, RAD52, ATM, ATR) by EPIC algorithm.



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22 **Supplementary Figure 3.** The relationship between NEAT1 and DNA replication and G2-M checkpoint

23 pathway.

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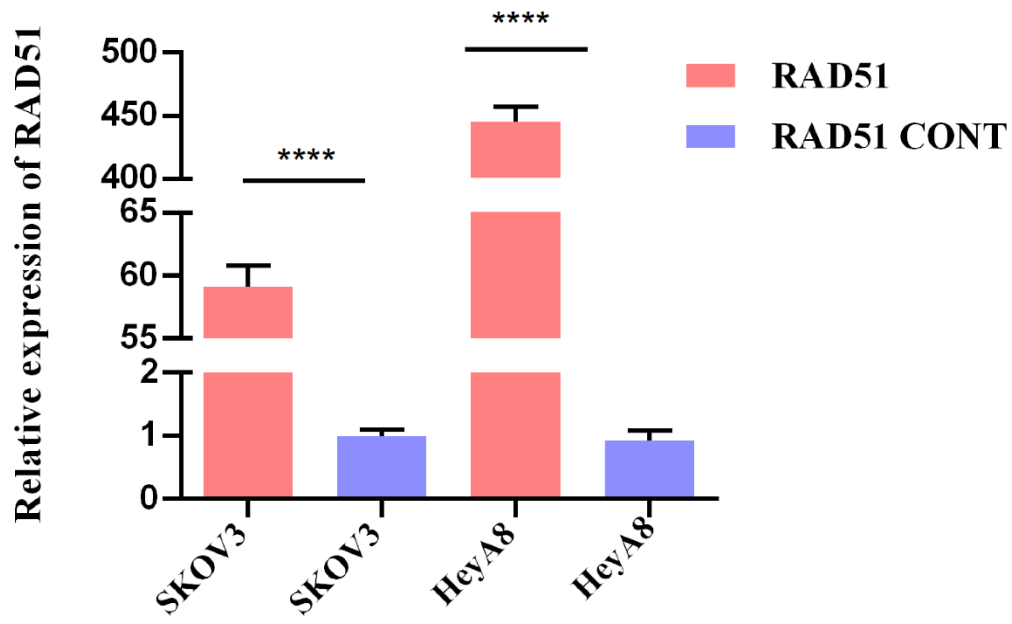
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39 **Supplementary Figure 4.** qRT-PCR analyzed the RAD51 mRNA levels after transfecting the  
 40 overexpression RAD51 plasmid or empty vector into HeyA8 and SKOV3 cells.

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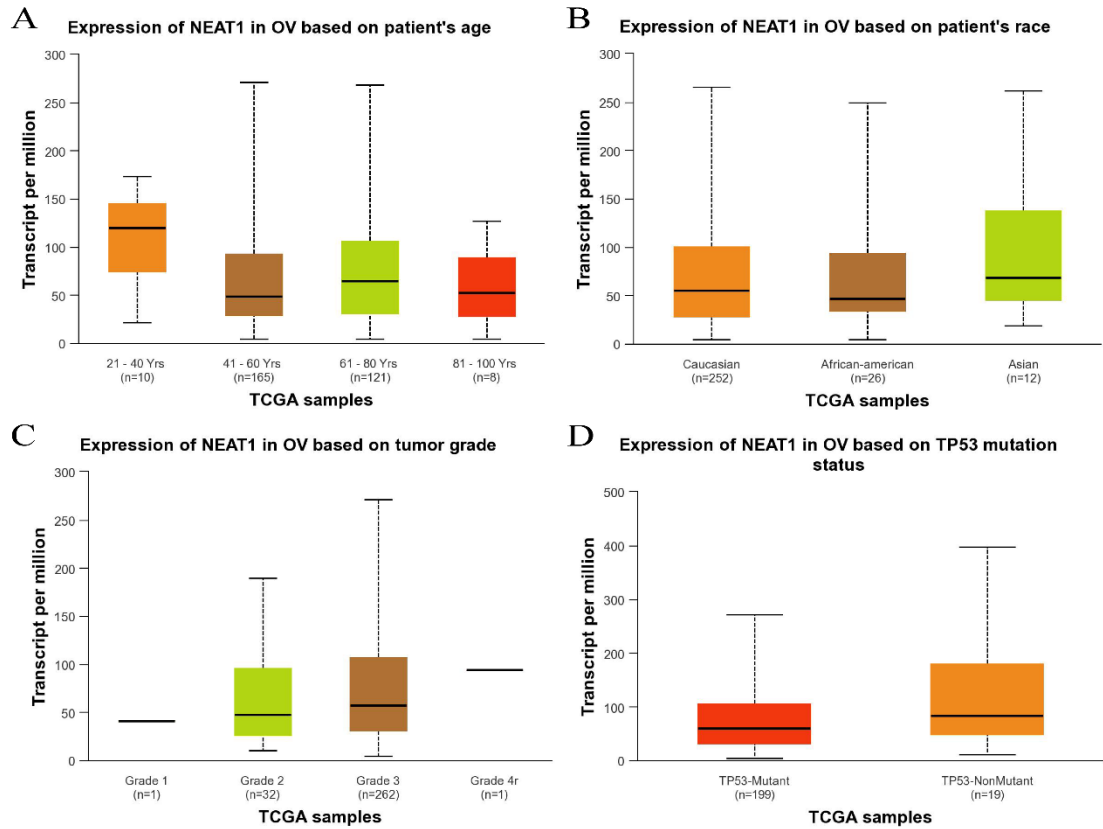
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54 **Supplementary Figure 5.** Relationship between NEAT1 expression and clinicopathological features in

55 OC. The correlation between NEAT1 expression and different clinical features, including age (A), race

56 (B), tumor grade (C), and TP53 mutation status (D). Subtype descriptions: Grade 1: Well differentiated

57 (low grade); Grade 2: Moderately differentiated (intermediate grade); Grade 3: Poorly differentiated

58 (high grade); Grade 4: Undifferentiated (high grade).

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