

## Correction: A functional single nucleotide polymorphism of SET8 is prognostic for breast cancer

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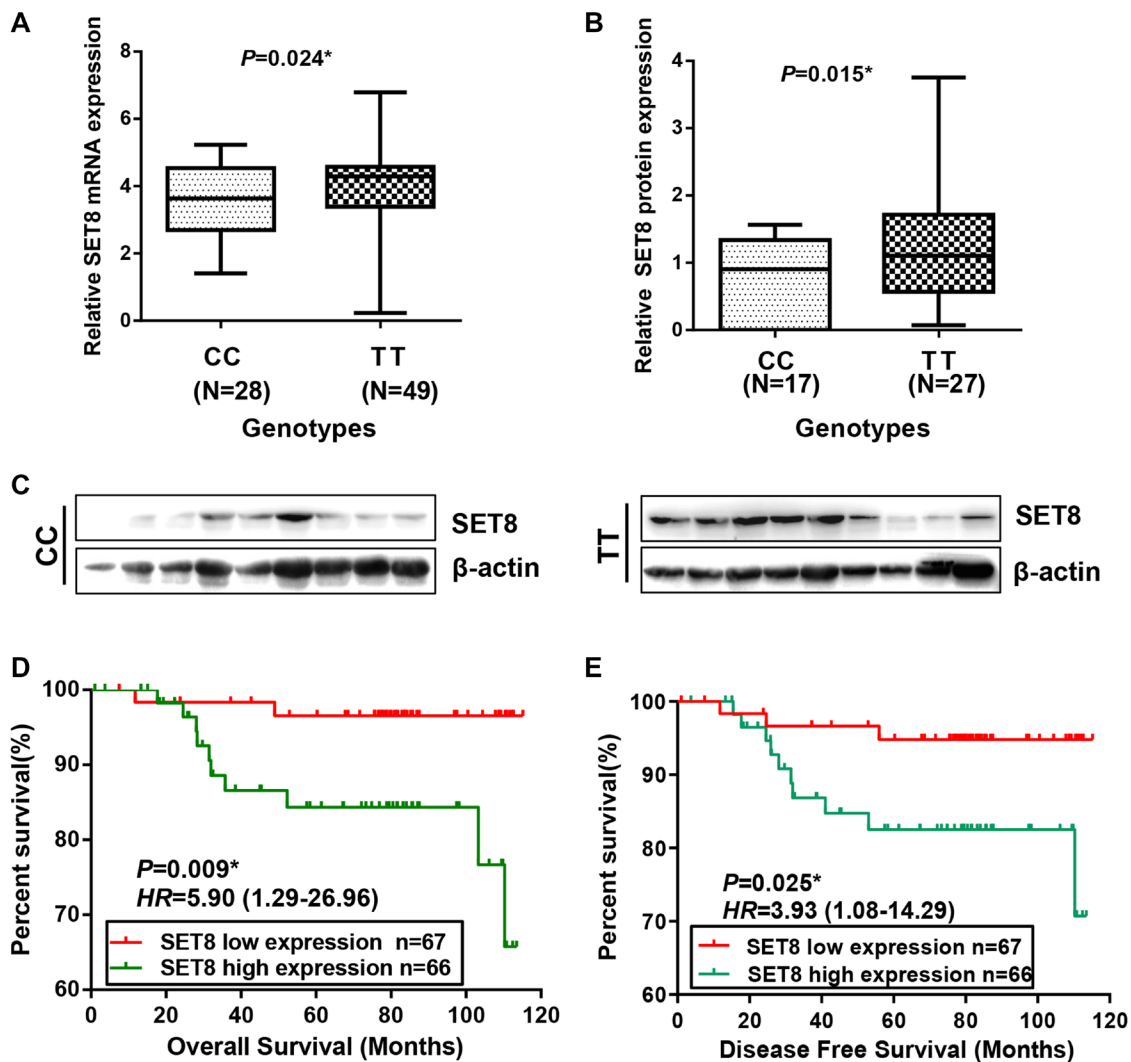
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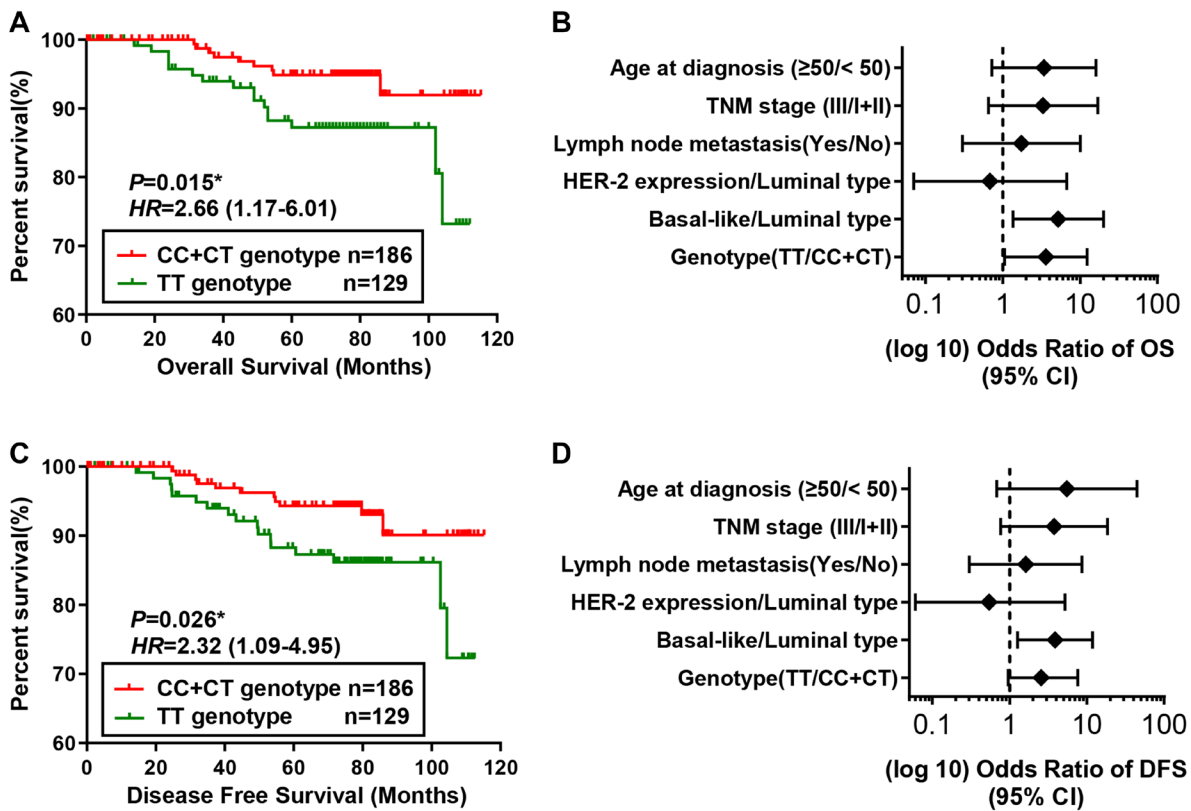
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**This article has been corrected:** In Figures 1E, 4A and 4C, the colors of the KM curves were accidentally reversed. The corrected figures, produced from the original data, are shown below. The authors declare that these corrections do not change the results or conclusions of this paper.

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**Figure 1: Functional relevance of SET8 3'-UTR SNP on SET8 expression and the association of SET8 expression with the prognosis of breast cancer patients.** (A) The relative expression level of SET8 mRNA in breast cancer tumor tissues measured by taqman qRT-PCR in 77 breast cancer patients. Housekeeping gene GADPH was used as the reference. (B) The graph represents the relative quantitation of protein expression of SET8 in tumor tissues by Western blot in 44 breast cancer cases. (C) The image shows the representative Western blot result of SET8 expression between two genotypes from panel B. (D) Kaplan–Meier curves of overall survival of breast cancer patients with high or low SET8 expression level. (E) Kaplan–Meier curves of disease free survival of breast cancer patients with high or low SET8 expression level. *P* values are from the log-rank test. HR with 95% CI was from Univariate analysis of OS and DFS.



**Figure 4: Association between the SNP in SET8 3'-UTR and breast cancer survival.** (A, C) Kaplan-Meier analysis of overall survival (OS) (A) and disease free survival (DFS) (C) of patients with the CC + CT phenotypes vs. the TT genotype in 315 cases. Red line represents CC and CT genotypes, and the green line represents TT genotypes. *P* values are from the log-rank test. HR with 95% CI was from Univariate analysis of OS and DFS. (B, D) Forest plot of the association of breast cancer prognosis factors with OS (B) and DFS (D) of 315 breast cancer patients. The results were from Cox regression analysis. The confounding factors include age, TMN stage, lymph node metastasis, and molecular subtype.