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SUPPLEMENTARY MATERIAL

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Identification of abnormally high expression of *POGZ* as a new biomarker associated with a poor prognosis in osteosarcoma

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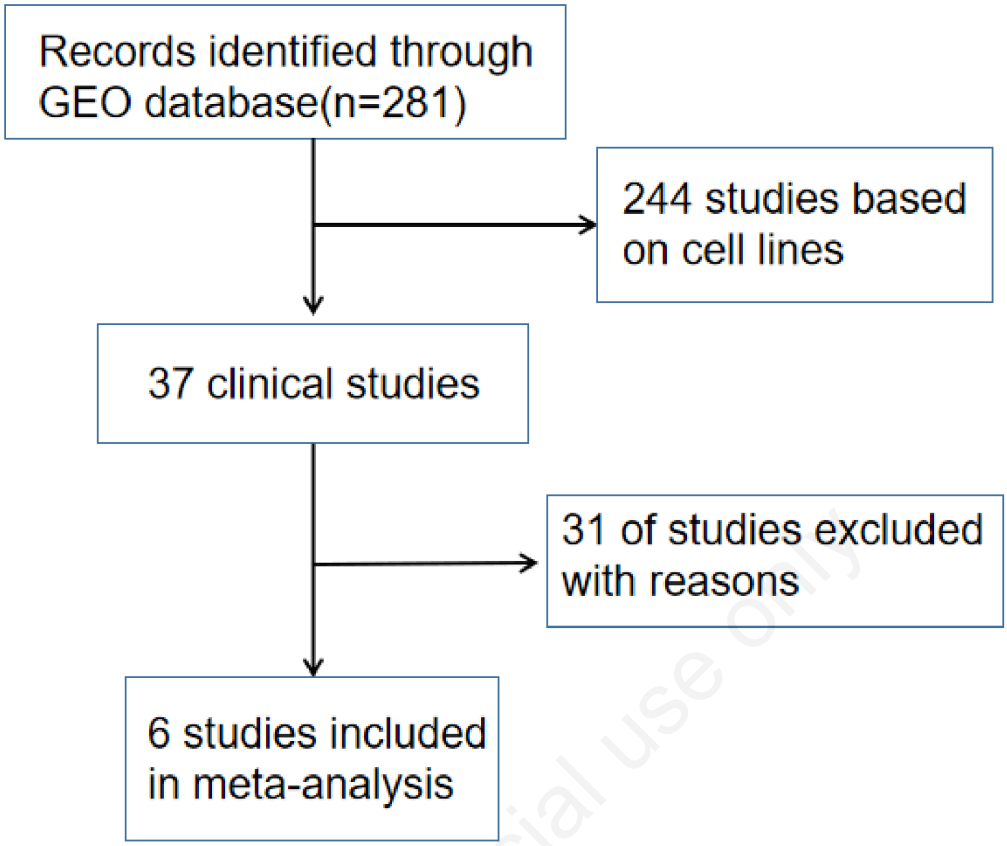
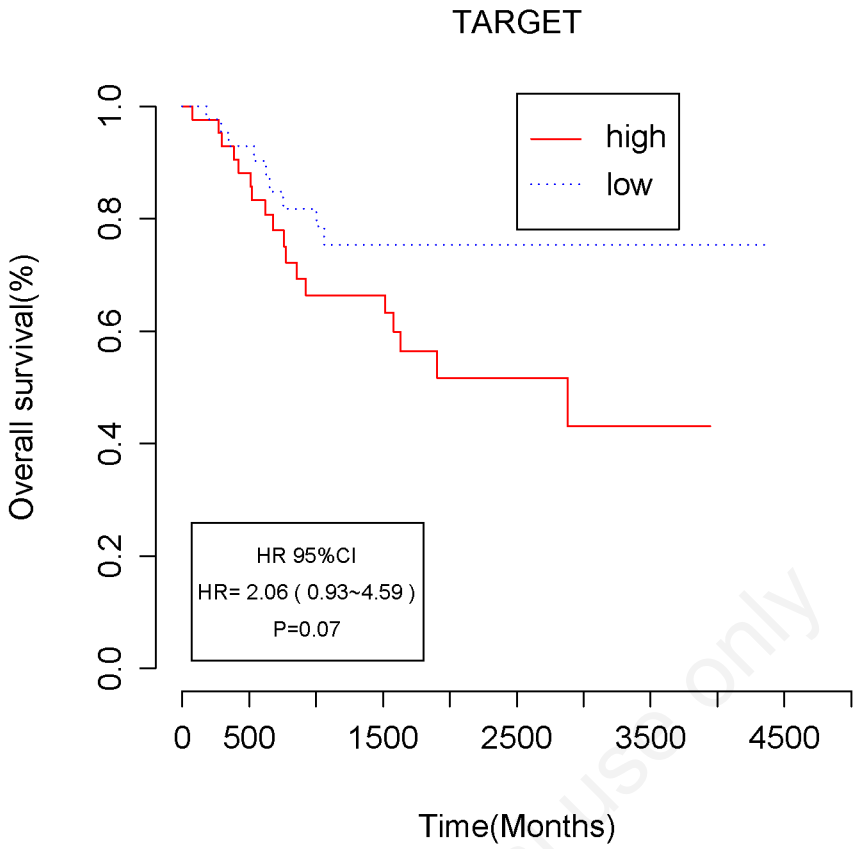
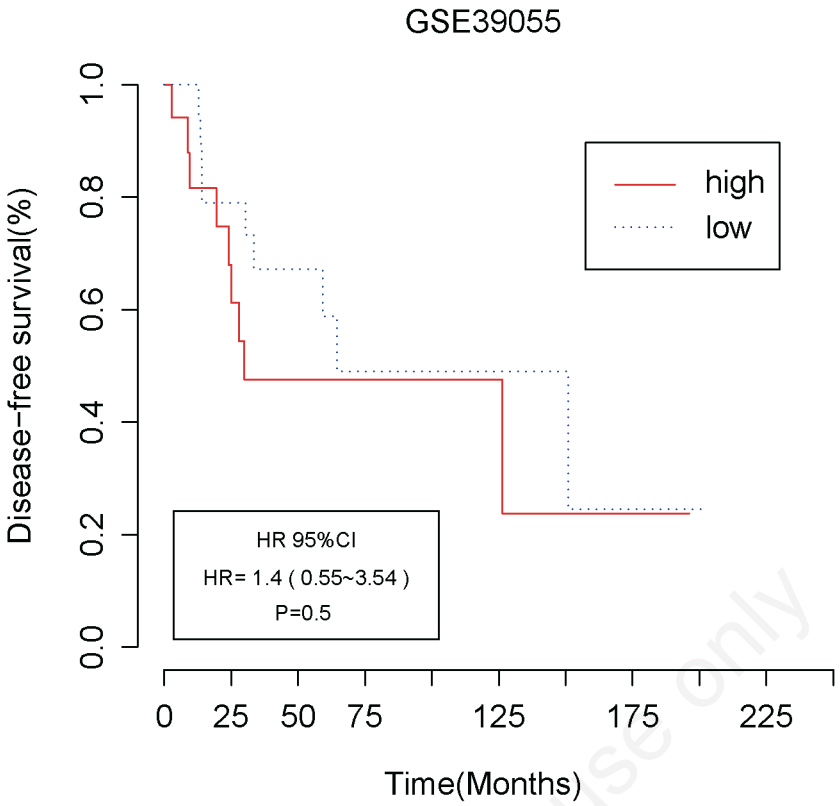
Key words: Prognosis; osteosarcoma; biomarkers; POGZ; cell cycle.



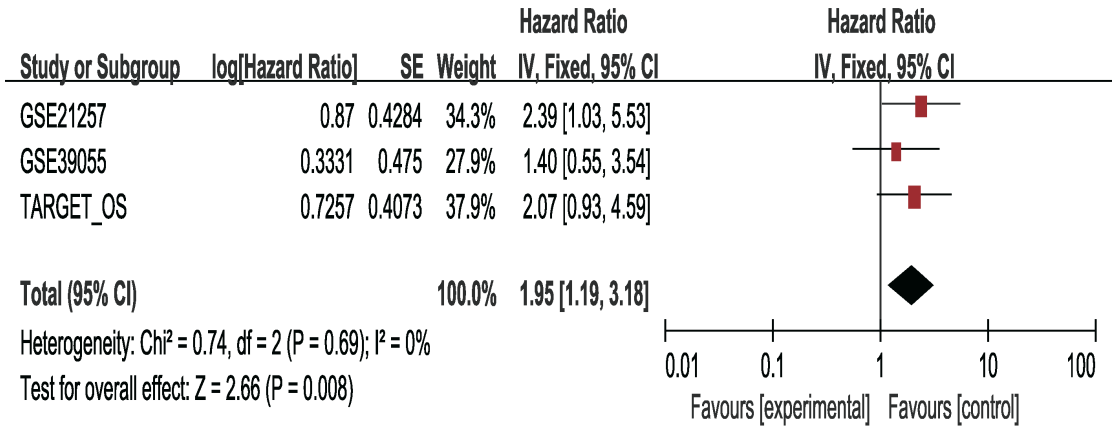
Supplementary Figure 1.
Screening data set flowchart. We screened out 281 data sets by searching keywords in GEO Datasets and eliminated 244 cell line studies and 31 non-conforming studies based on the inclusion and exclusion criteria, and finally included 6 data sets.



Supplementary Figure 2.
The Kaplan-Meier survival curve of TARGET_OS dataset shows that HR=2.06(0.93~4.59) and p=0.07. The result indicates that high expression of POGZ is a risk factor for OS.

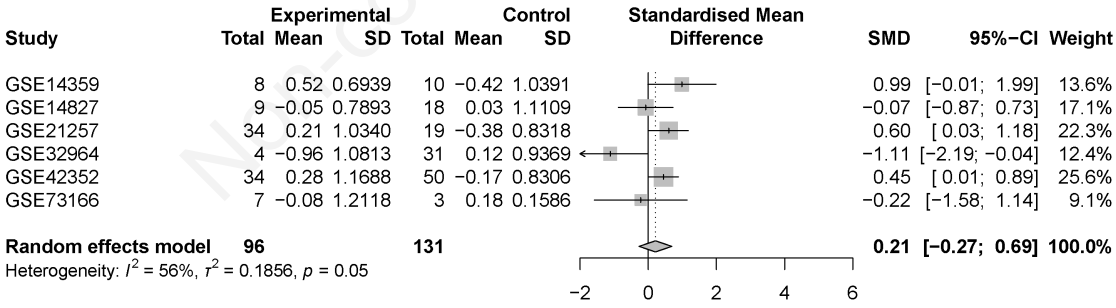


Supplementary Figure 3.
The Kaplan-Meier survival curve of GSE39055 dataset shows that HR=1.4(0.55~3.54) and p=0.5. The result indicates that high expression of POGZ is a risk factor for OS.



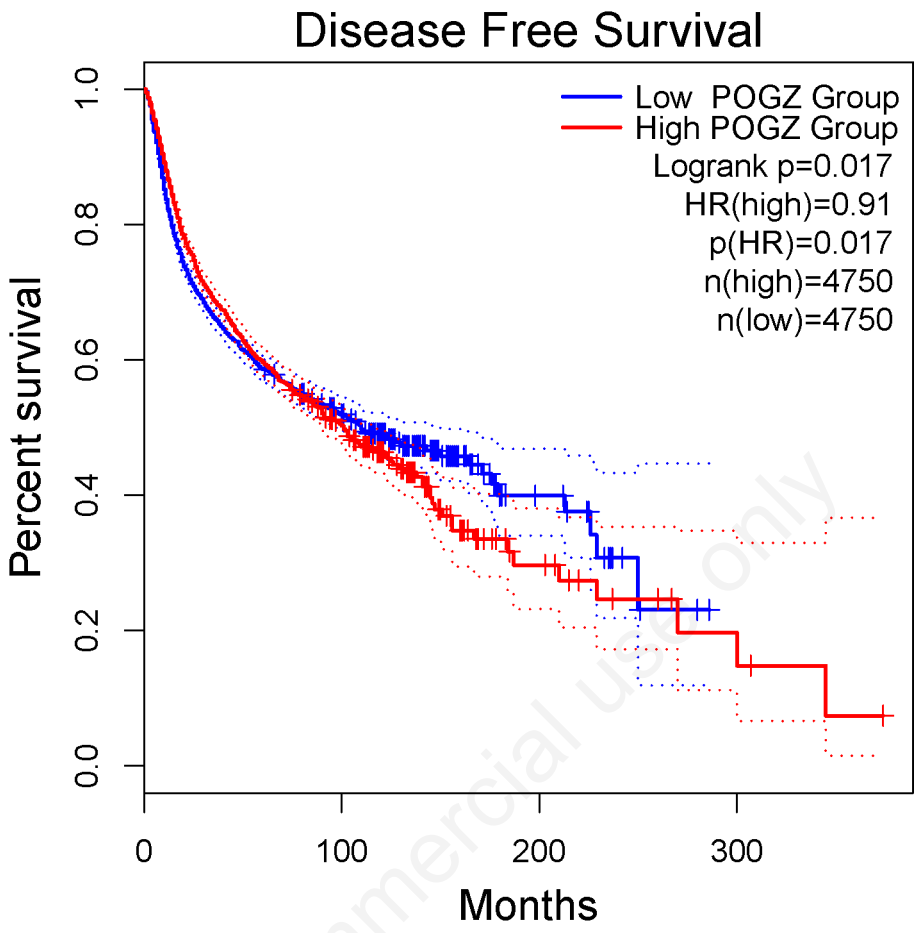
Supplementary Figure 4.

Forest plot of *POGZ* expression across three datasets (GSE21257, GSE39055 and TARGET_OS). The results showed that *POGZ* was steadily upregulated without heterogeneity (I2 = 0%, Z = 2.66, p=0.008).

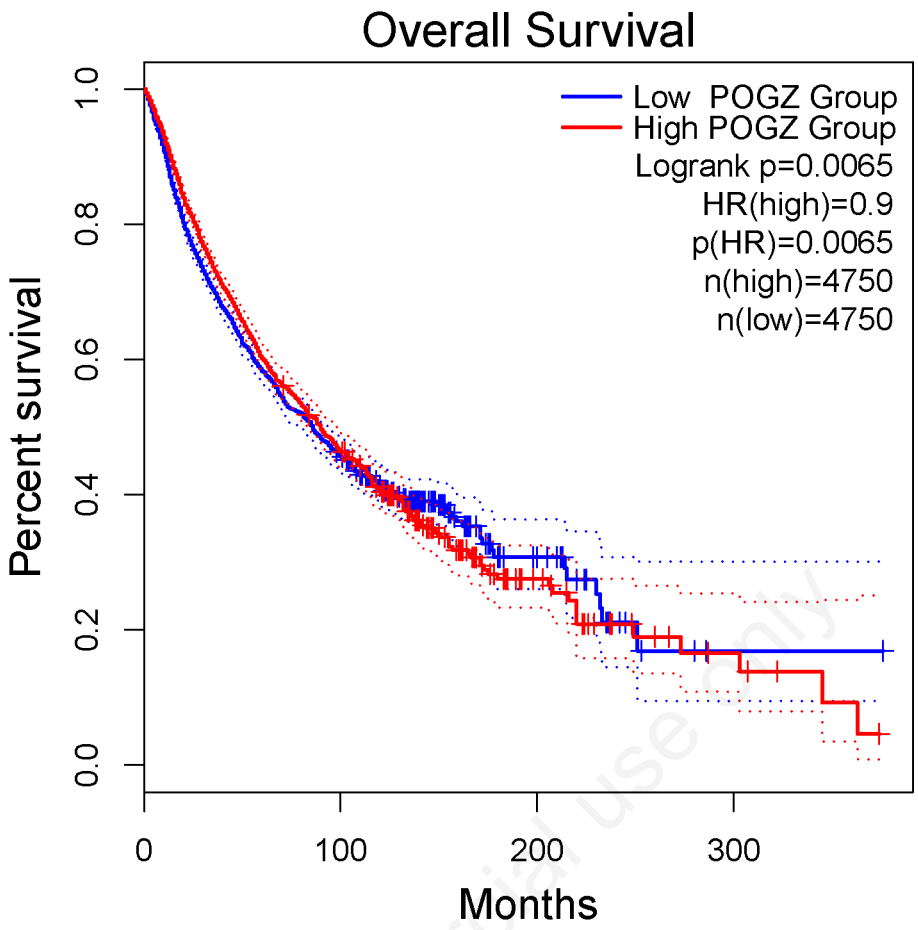


Supplementary Figure 5.

The forest map of *POGZ* expression level analysis for the metastatic and non-metastatic group of six data sets. The results have big heterogeneity.



Supplementary Figure 6.
The relationship between *POGZ* expression and the prognosis of multiple tumors. Compared with the *POGZ* low expression group, the POGZ high expression group had a shorter disease-free survival time and a poor prognosis (disease-free survival rate HR = 0.91, p=0.017).



Supplementary Figure 7.
The relationship between *POGZ* expression and the prognosis of multiple tumors. The results indicate that high expression of *POGZ* is a specific risk factor for overall survival (OS rate HR = 0.9, p=0.0065).