

Developmental genes significantly afflicted by aberrant promoter methylation and somatic mutation predict overall survival of late-stage colorectal cancer

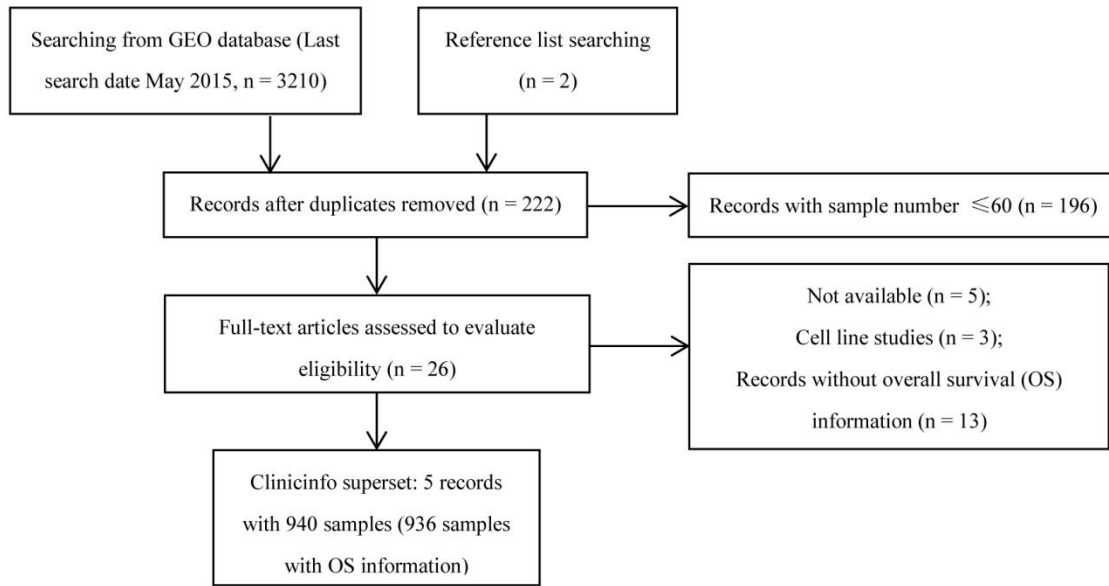
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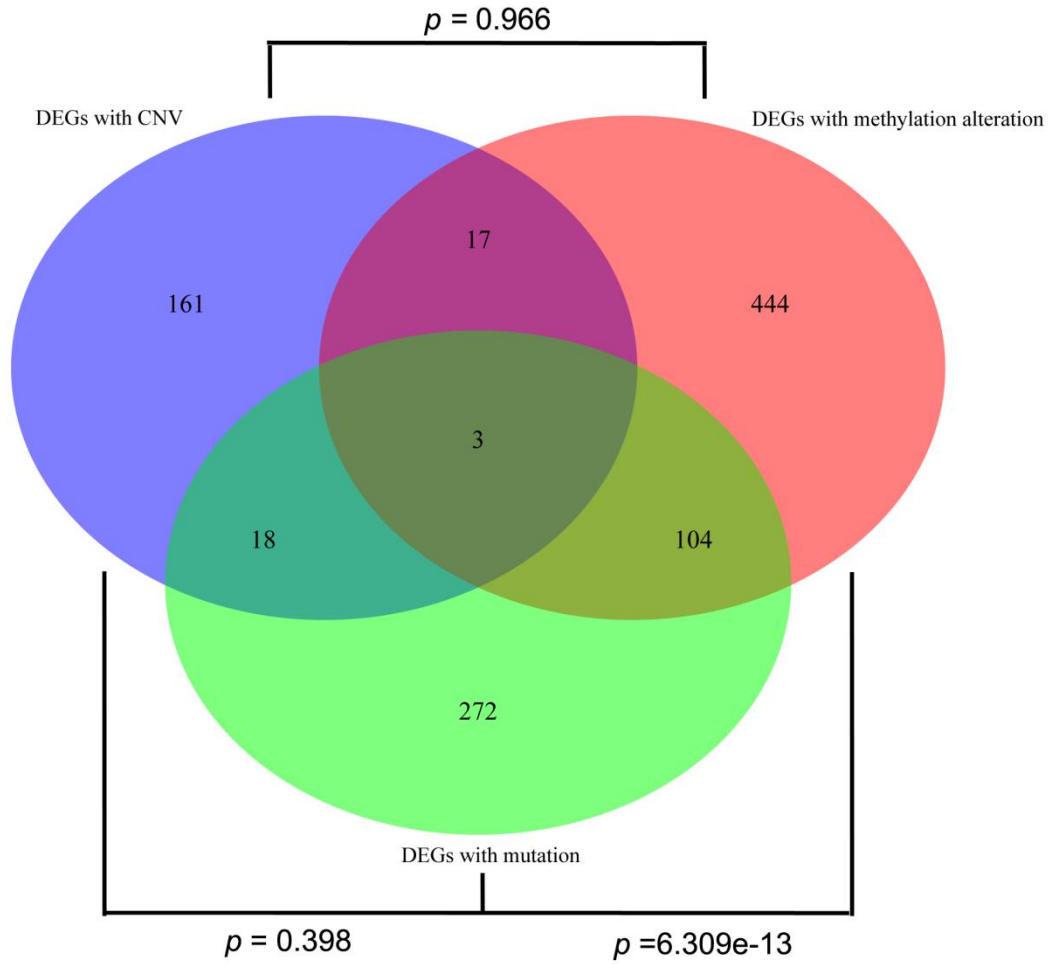
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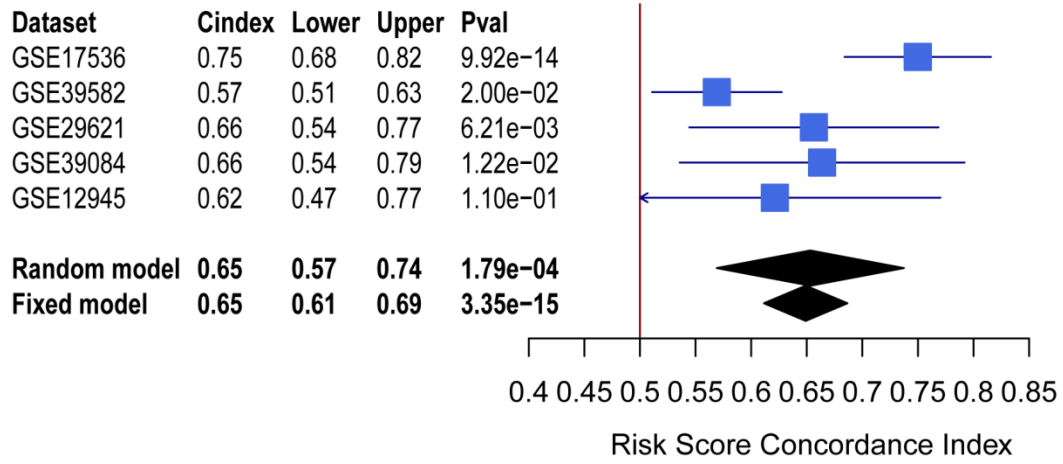


Supplementary Figure S1. Schematic of Clinicoinfo dataset collection.



Supplementary Figure S2. Overlapping among three candidate gene groups. The statistical significance of overlapping was calculated via hypergeometric distribution, and the corresponding p value was presented between each two gene groups.

Overall concordance index analysis



Supplementary Figure S3. Forest plot of overall concordance index analysis to evaluate the predictive ability of the 37-gene signature.