Decoding breast cancer: unveiling the role of hallmark genes in tumor progression and prognosis

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CancerHallmarks

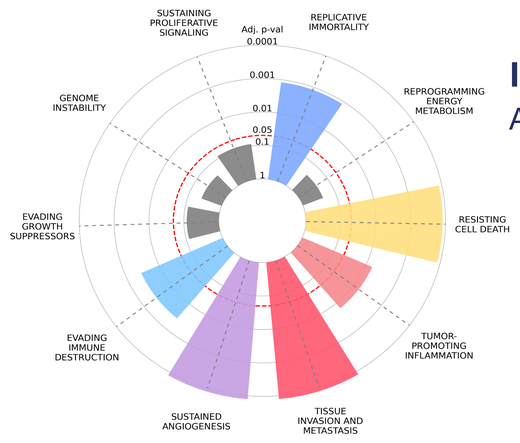
Summary

- we established a consensus gene set of cancer hallmark genes
- developed an online tool (www.cancerhallmarks.com) for enrichment analysis of cancer hallmark genes
- performed a cancer hallmarks enrichment analysis for prognostic genes linked to overall survival in breast cancer
- „evading immune destruction" and „tumor promoting inflammation" are the key cancer hallmarks linked to breast cancer prognosis

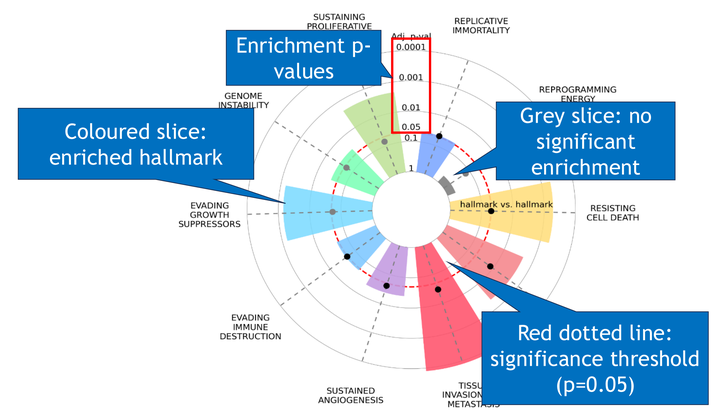
THE CANCER HALLMARK ENRICHMENT PLOT

a tool to identify cancer-associated hallmarks in novel gene sets

Background
Integrated database of 6,763 cancer hallmark genes



Input
Any gene set related to biological processes



Methods

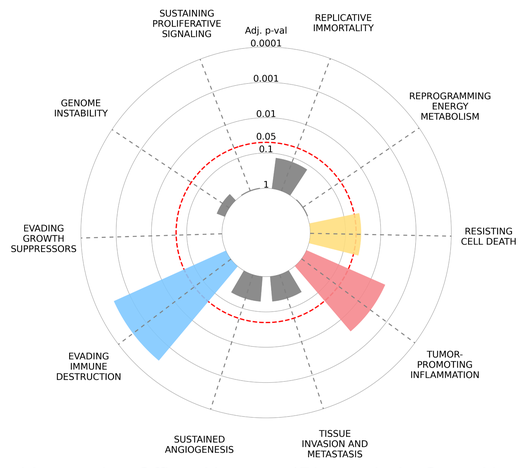
Consolidation of cancer hallmark genes

literature search
↓
7 publications
4 GO
1 KEGG
2 curated
↓
hallmark gene extraction
↓
data consolidation
↓
Cancer hallmark gene set (n=6,763)

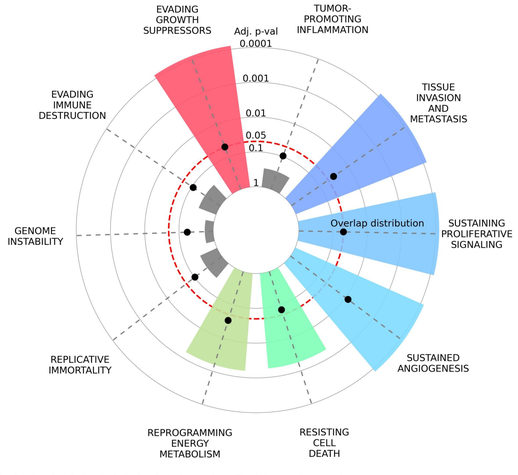
we consolidated data from seven projects and identified 6,763 genes linked to ten cancer hallmarks

Hallmark enrichment in BC

genes linked to lower HR were enriched in
- evading immune destruction (p=3e-05)
- tumor-promoting inflammation (p=7.3e-04)
- resisting cell death (p=0.01)



hallmarks enrichment of differentially expressed genes between normal and tumor samples



Advantages of cancerhallmarks.com over Gene Ontology:

- obvious link to a biological function
- cancer specific genes
- easy interpretation
- facilitates data integration and comparison
- user friendly online tool with downloadable graphical outcome

Reference:

Menyhart,O; Kothalawala, WJ; Győrffy,B
A gene set enrichment analysis for the cancer hallmarks, J Pharmaceutical Analysis,2024,101065

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Acknowledgments
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