

# Identifying metabolic shift gene signature pattern in the Wnt-associated epithelial-mesenchymal plasticity of the PMC42 breast cancer model system

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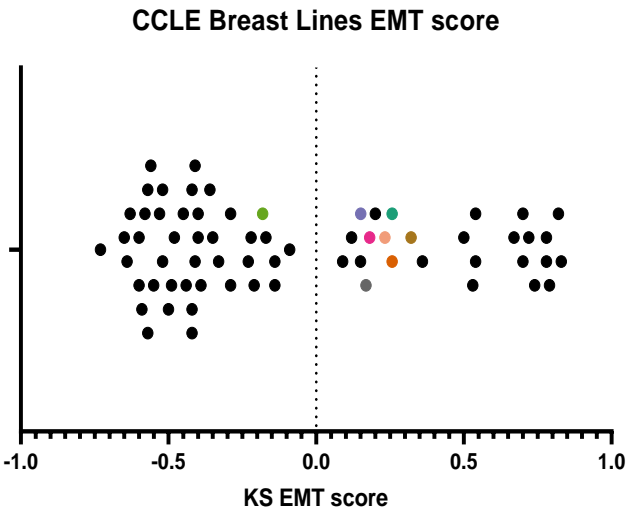
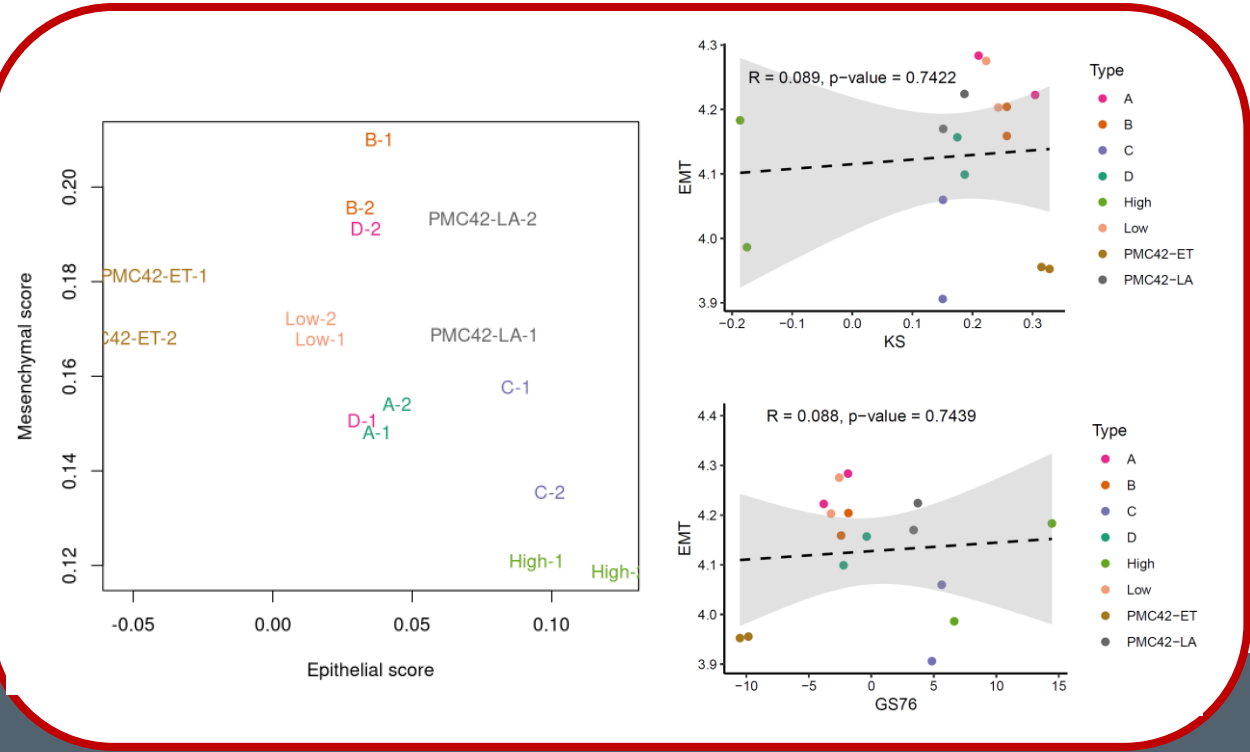
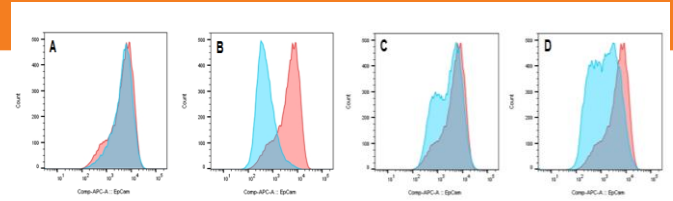
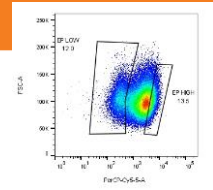
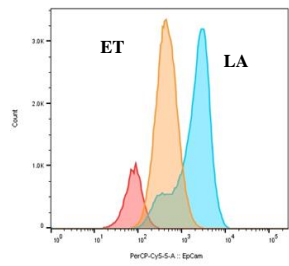
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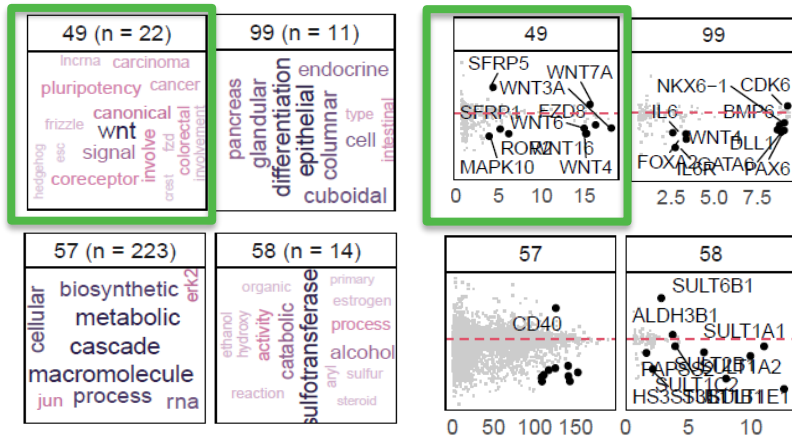
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# EMT scoring using KS, 76-GS (gene signature) and Singscore method

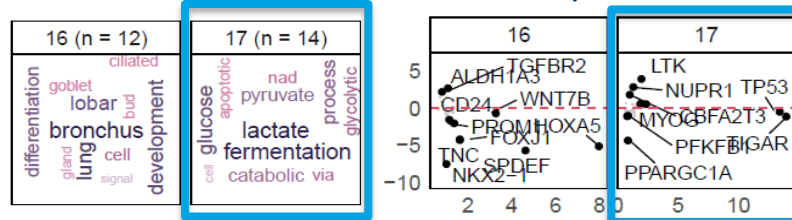




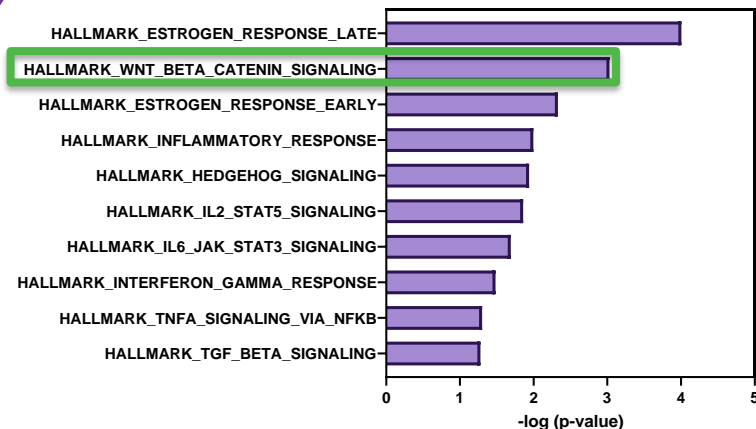
### PMC42-ET (mesenchymal) vs PMC42-LA (epithelial)



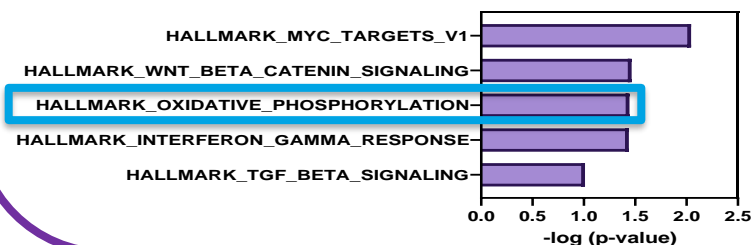
### Clone B (mesenchymal) vs Clone A (epithelial)



### PMC42-ET vs PMC42-LA



### Clone B vs Clone A



vissE: A versatile tool to identify and visualise higher-order molecular phenotypes from functional enrichment analysis

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<https://www.biorxiv.org/content/10.1101/2022.03.06.483195v1>

