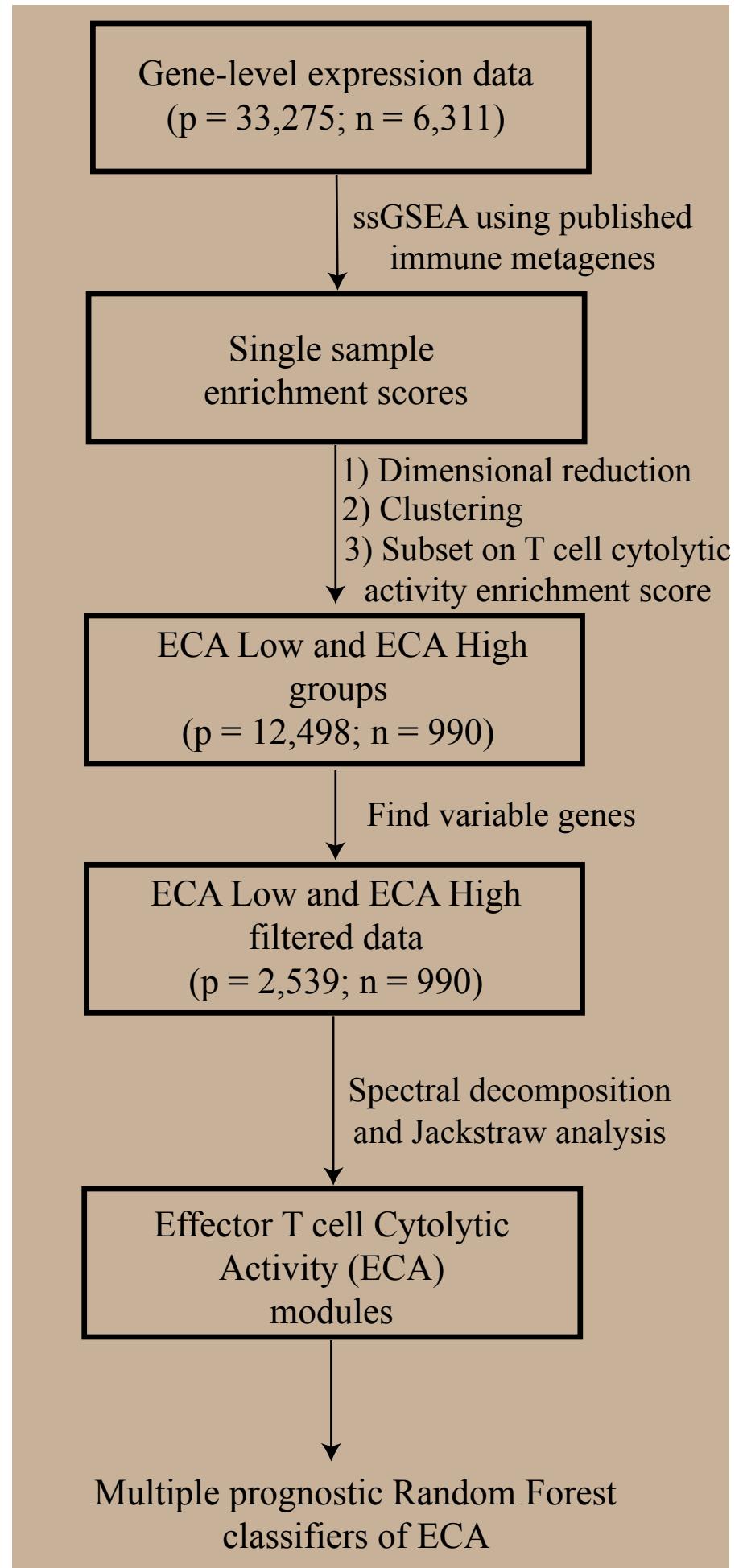
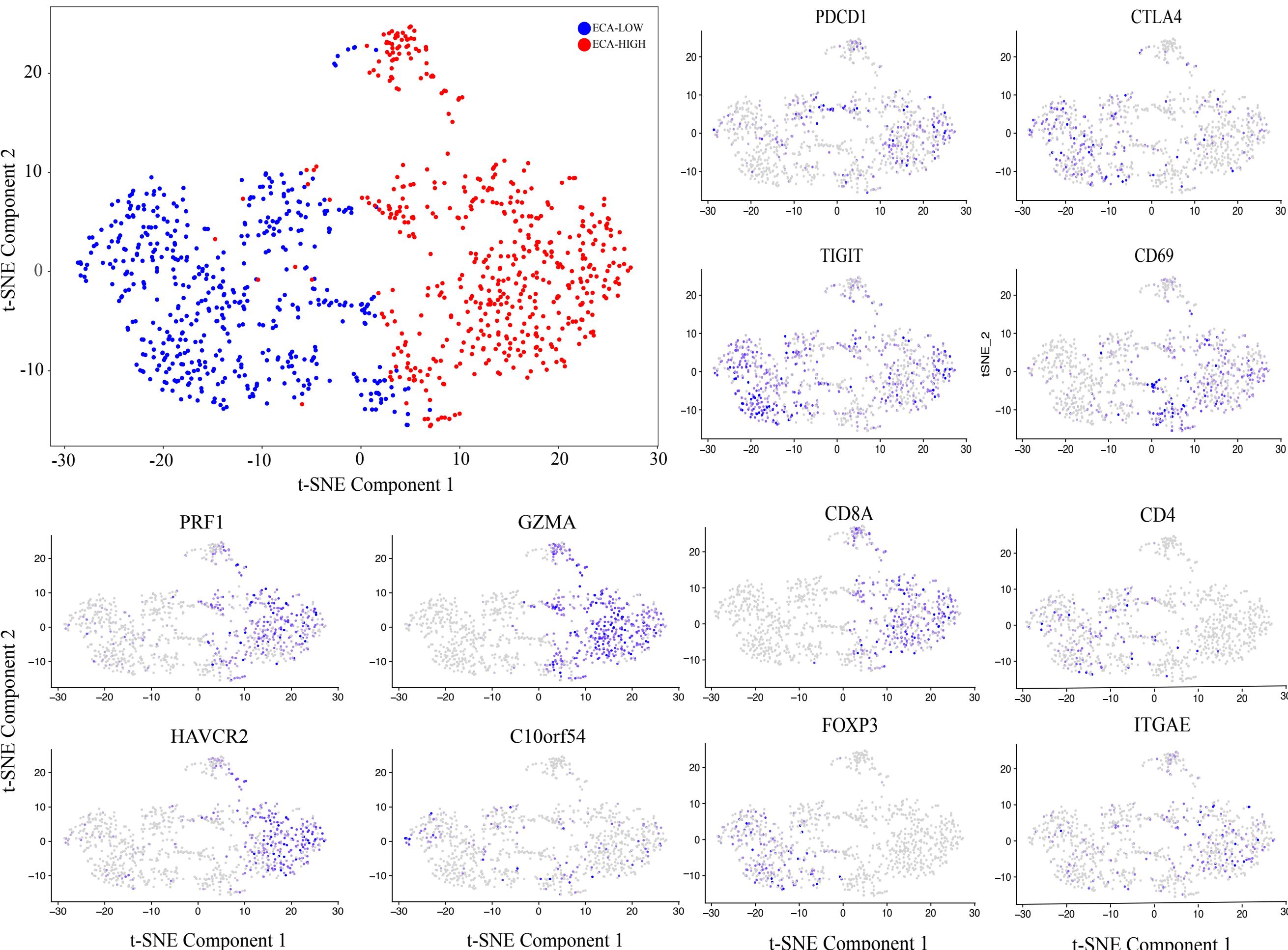


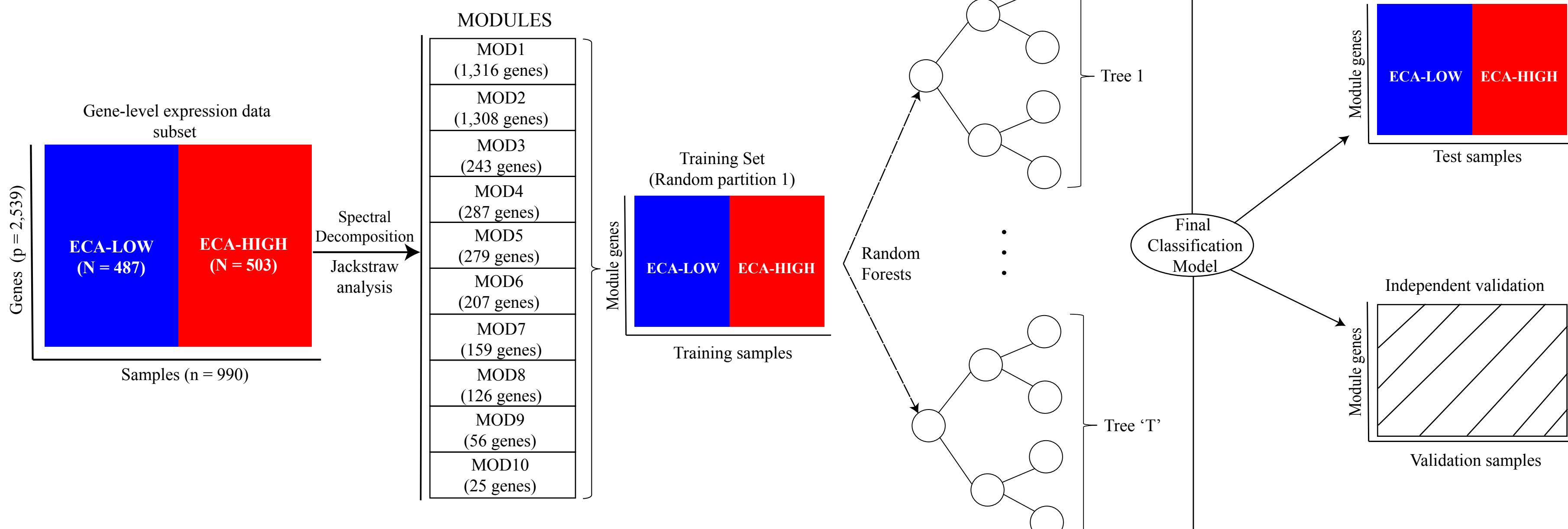
a. CD3+ single T cells from human primary TNBC



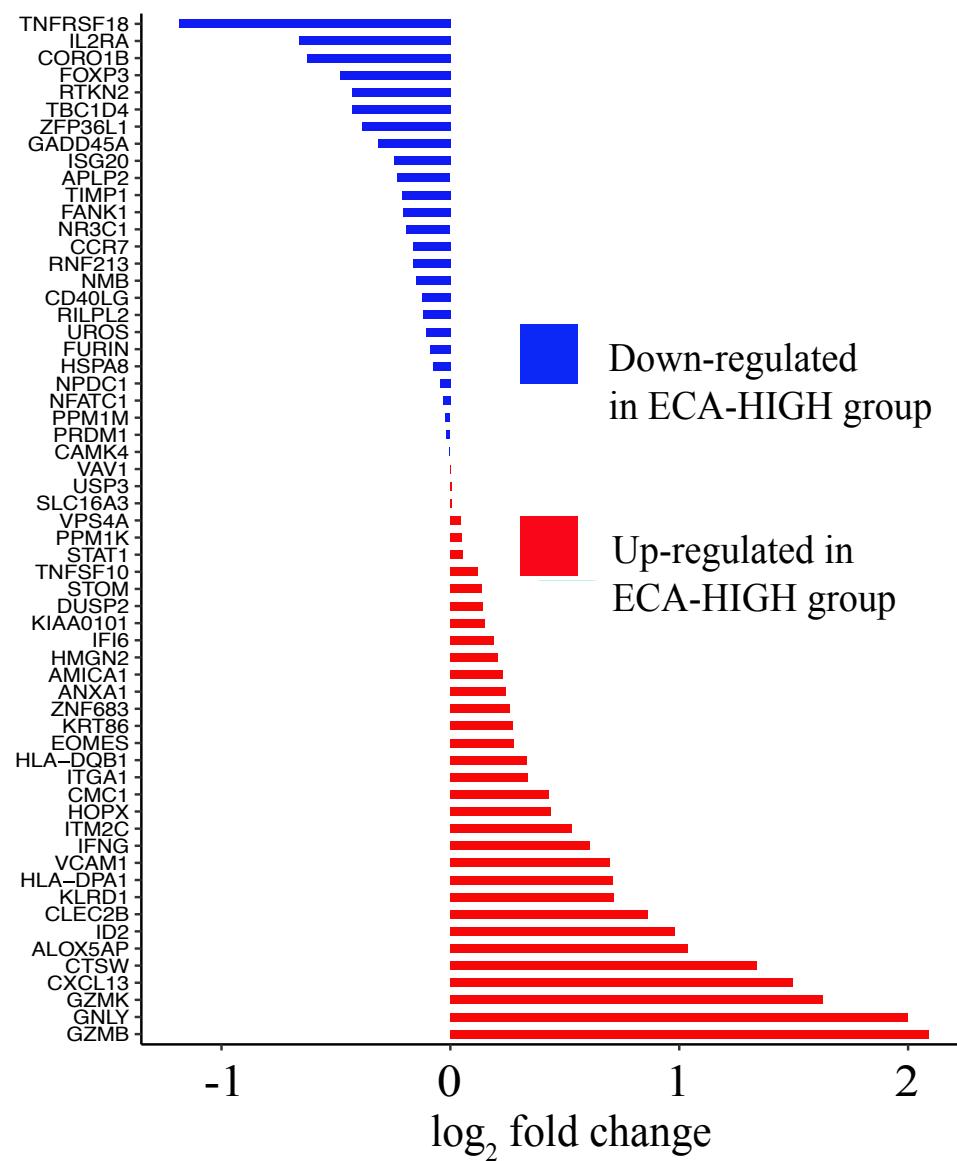
b.



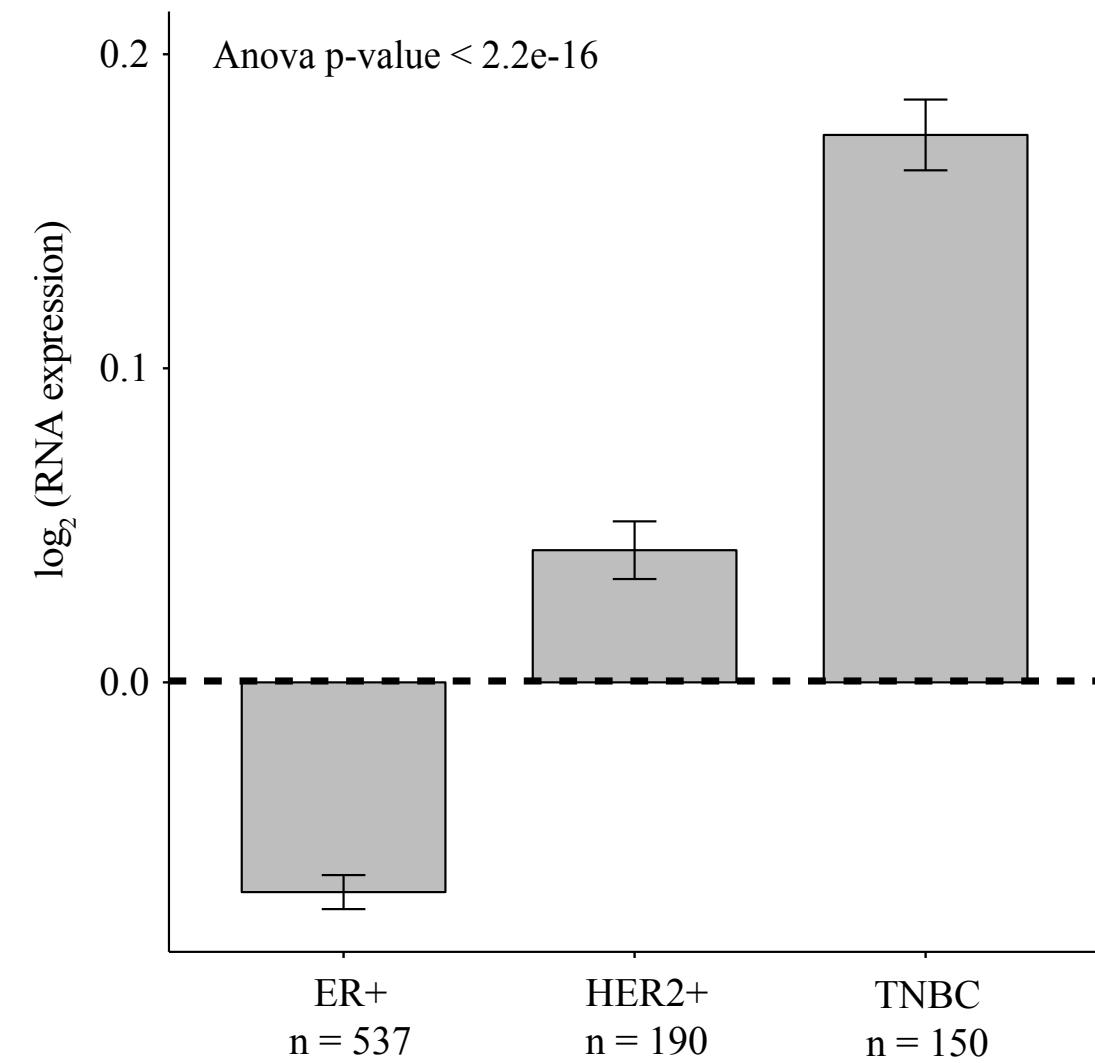
c.



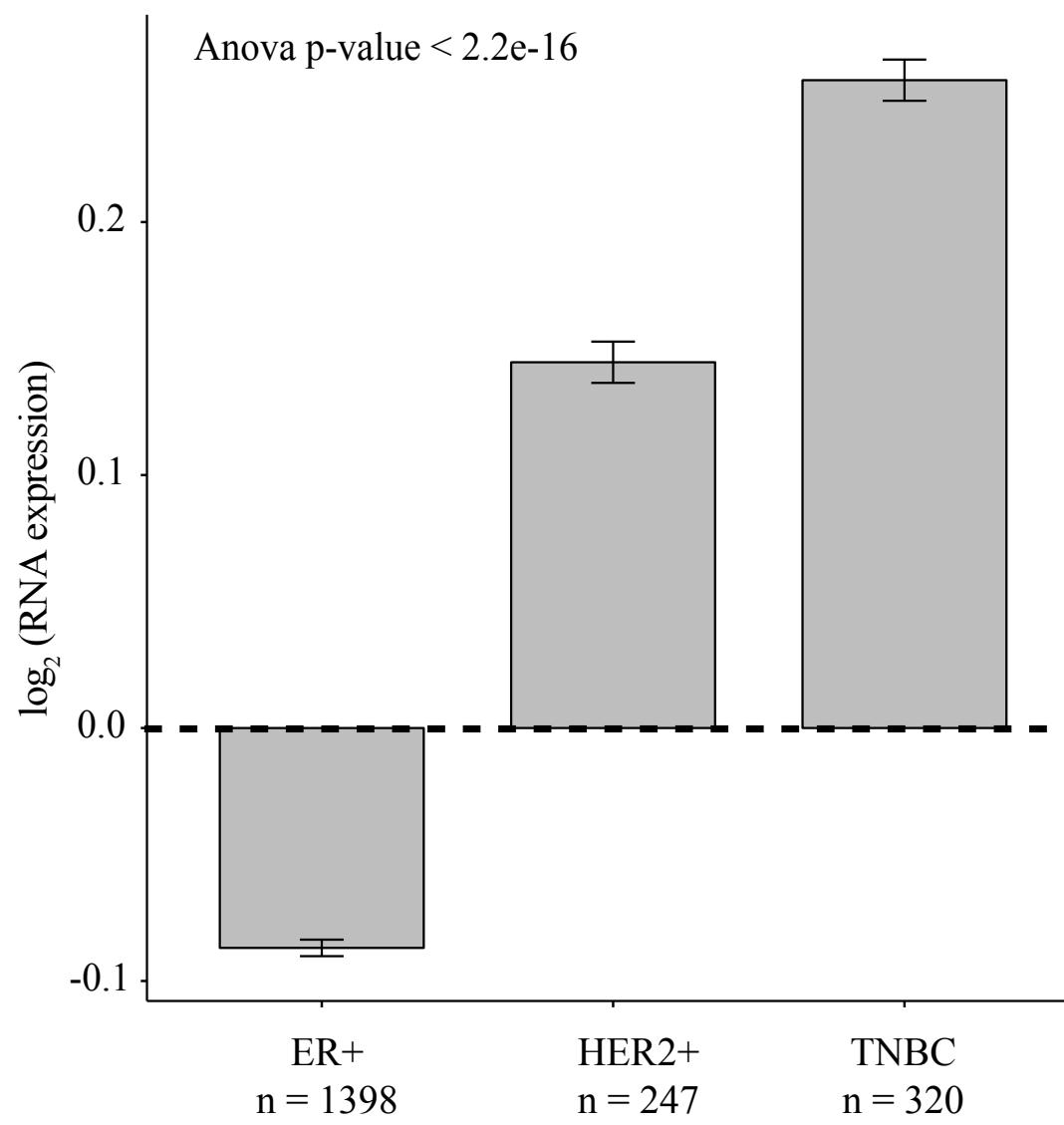
a. 60 genes from the Random Forest model from MOD5



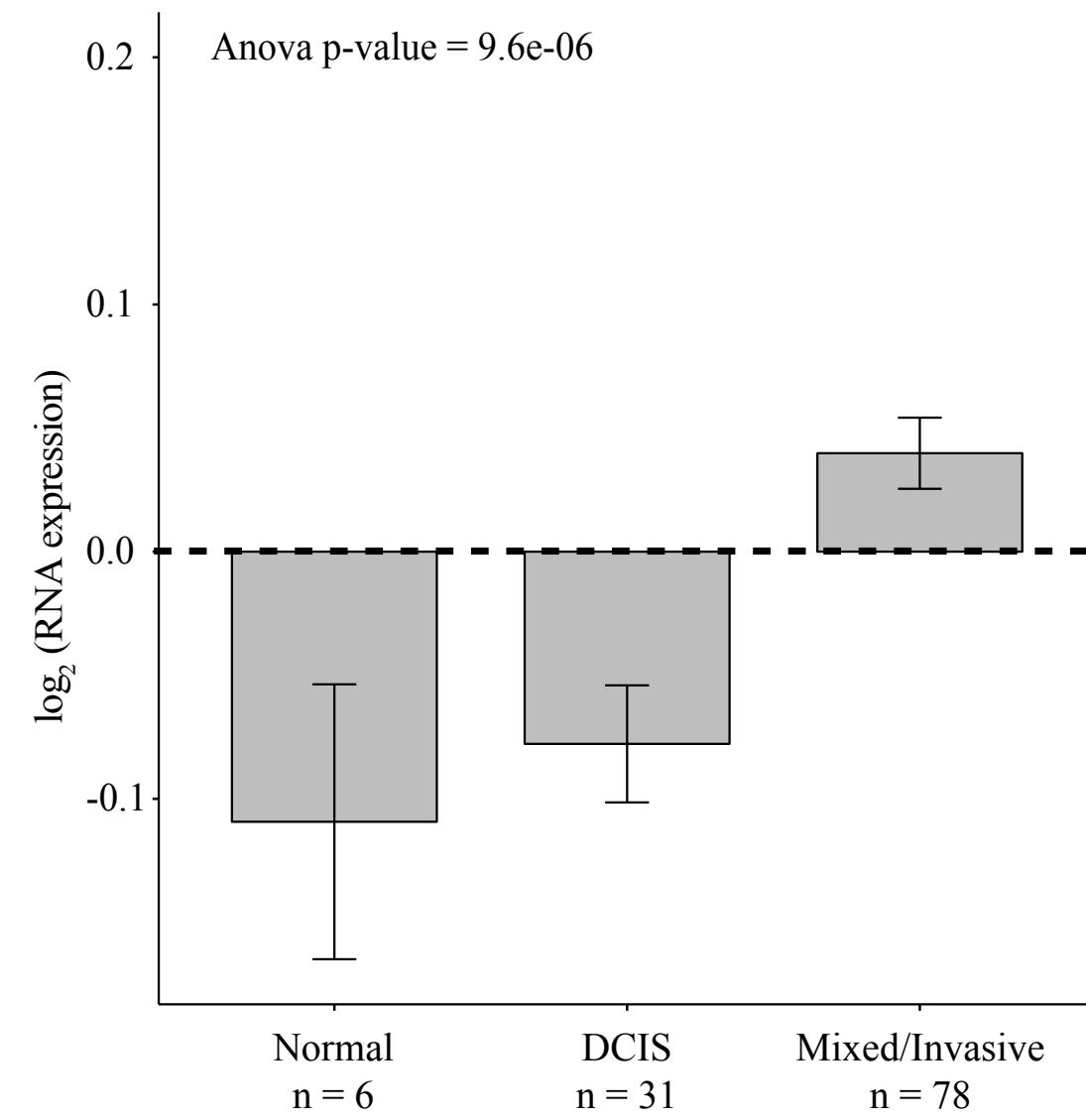
b. TCGA breast dataset (N = 877)



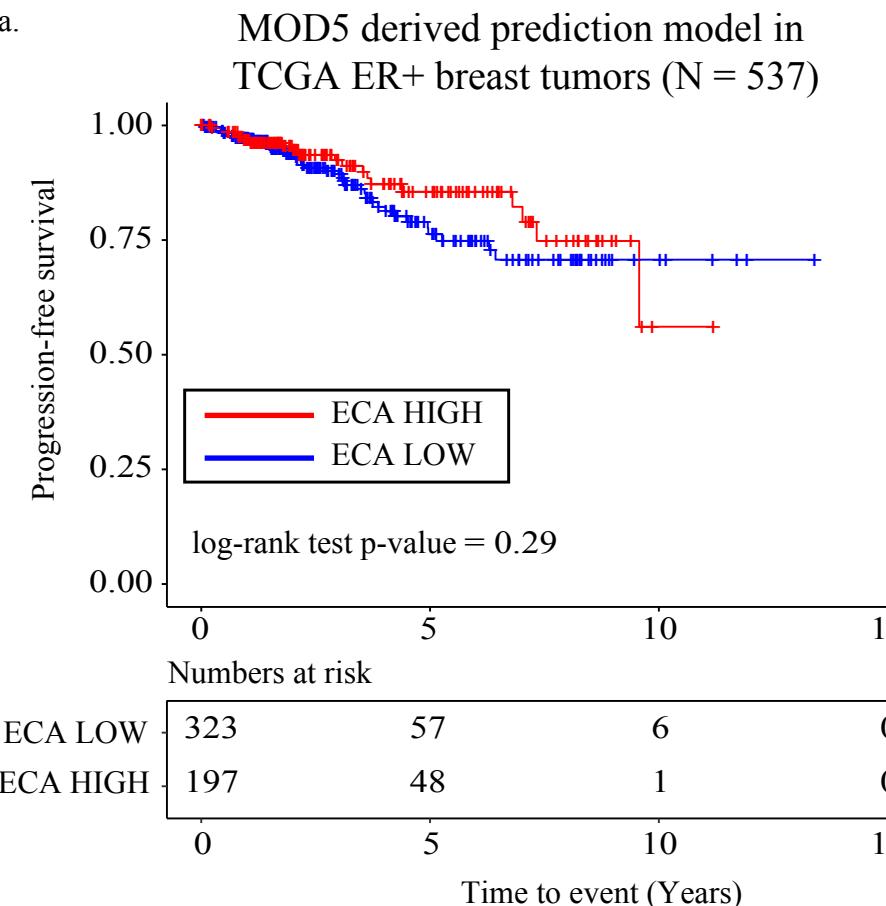
c. METABRIC dataset (N = 1965)



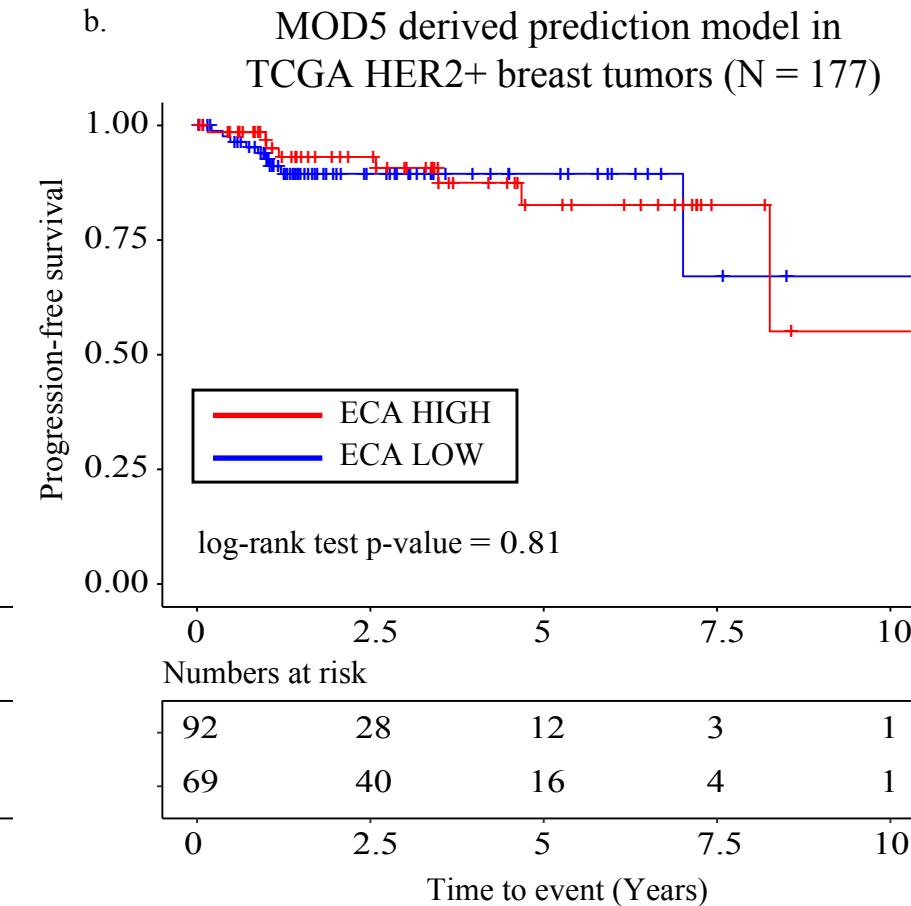
d. GSE26304 (N = 115)



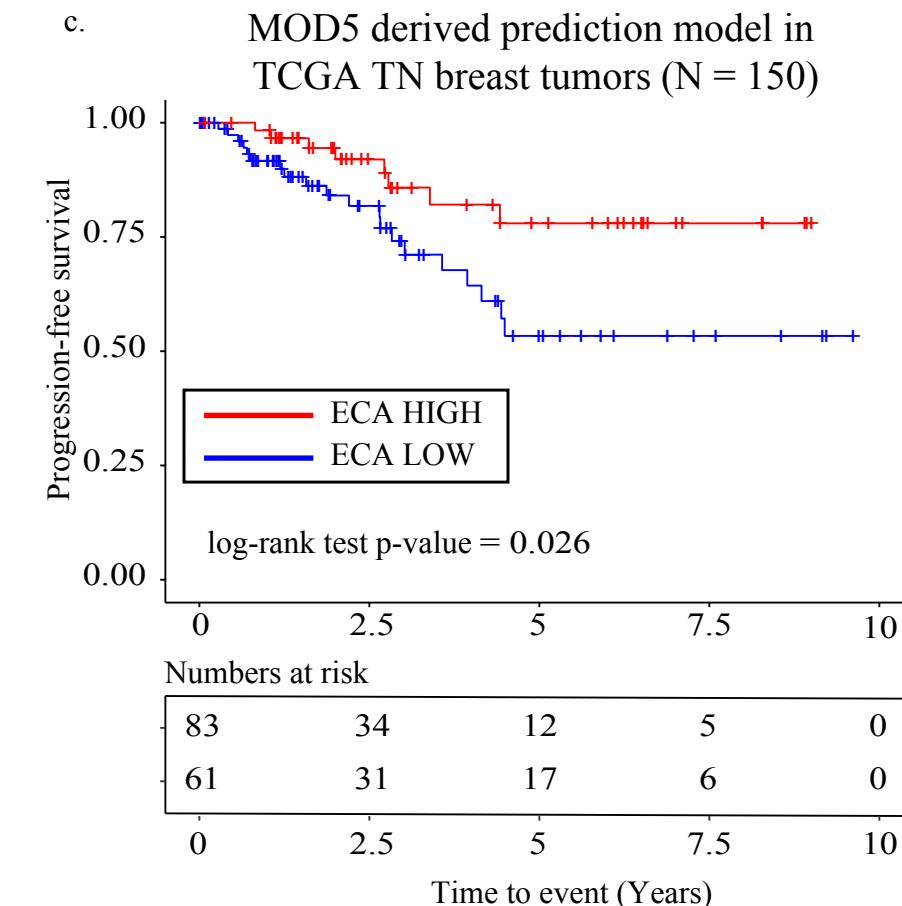
a.



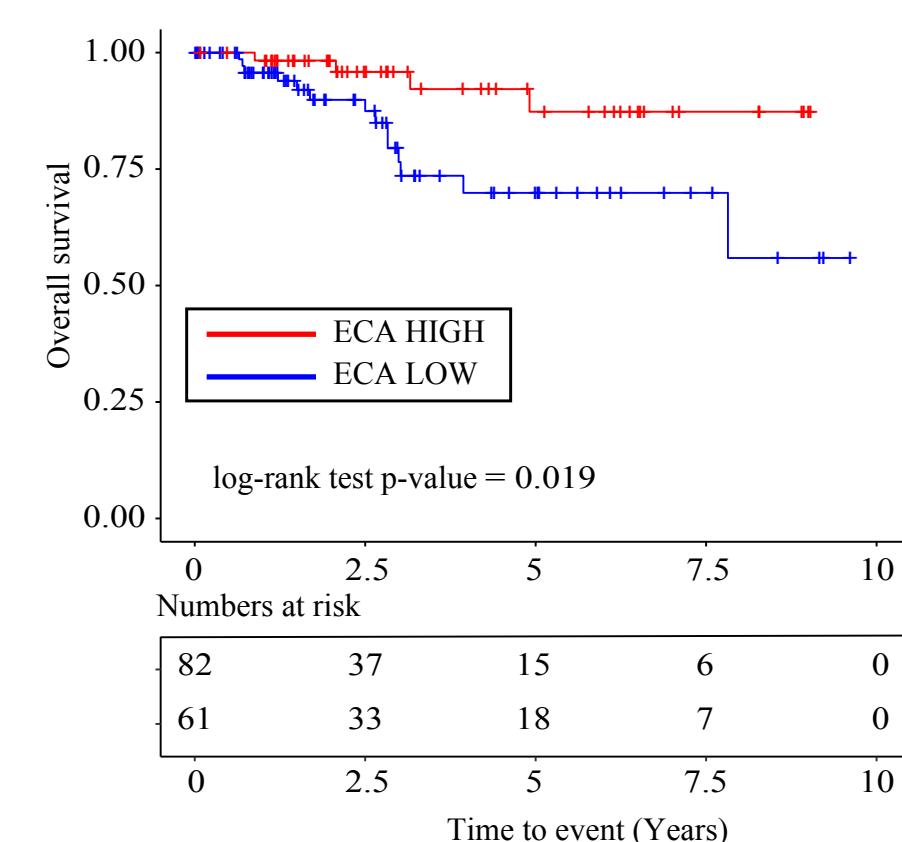
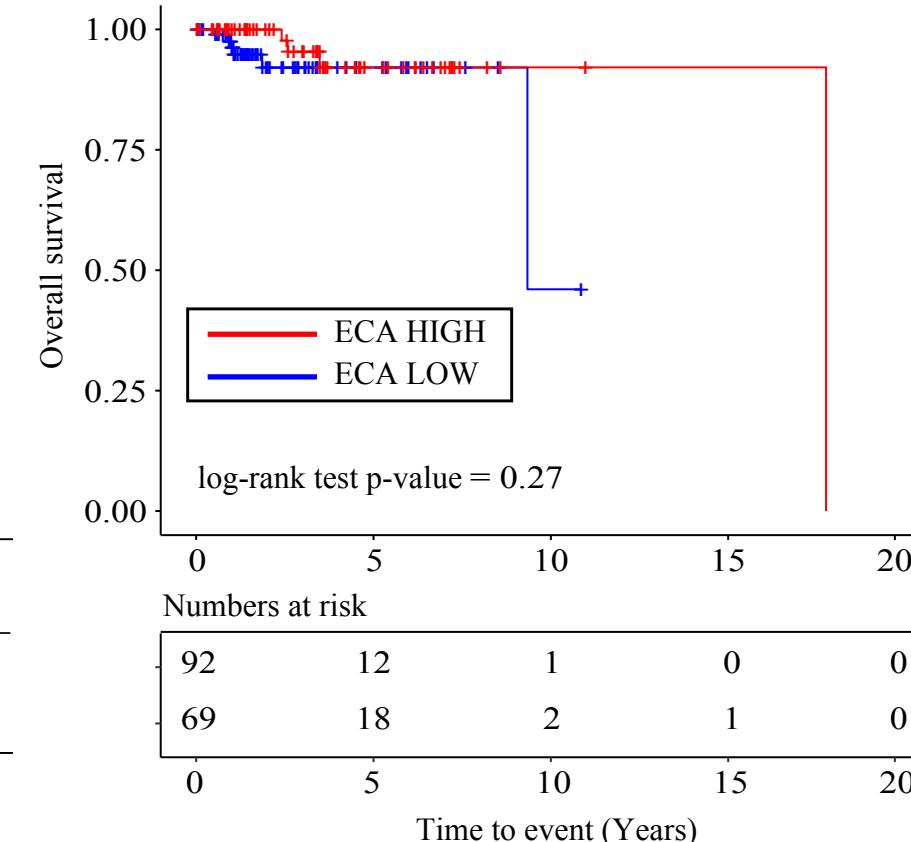
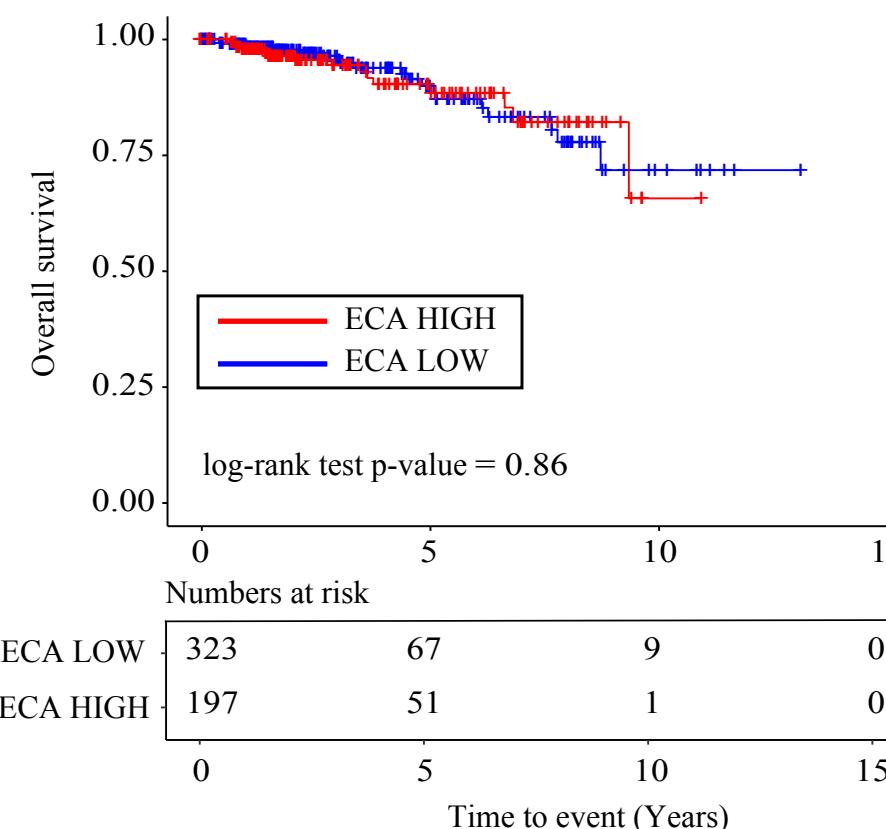
b.



c.

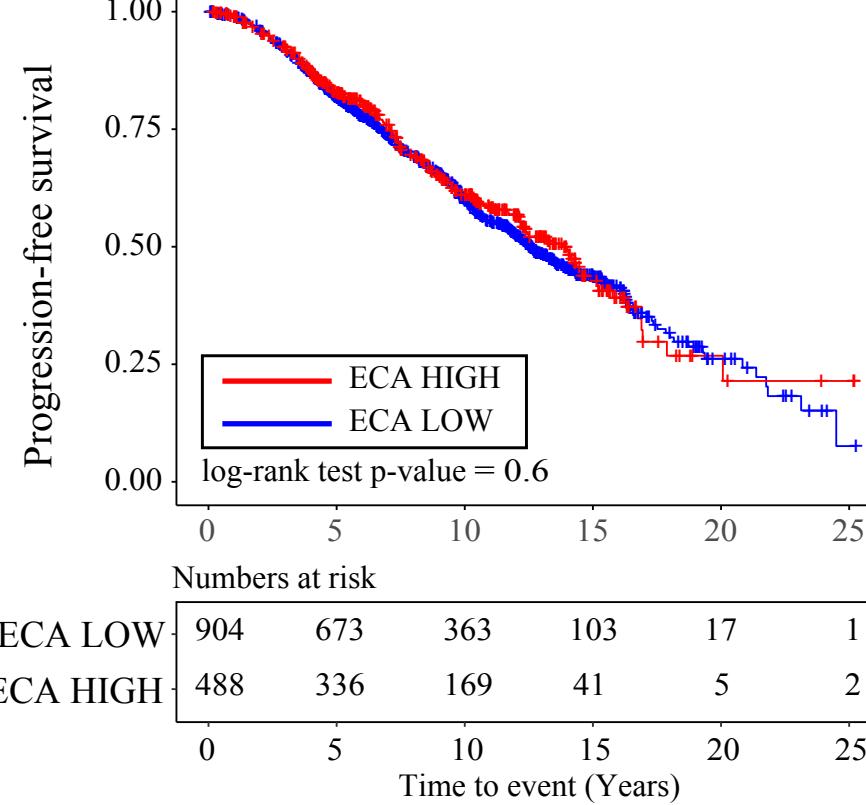


d.



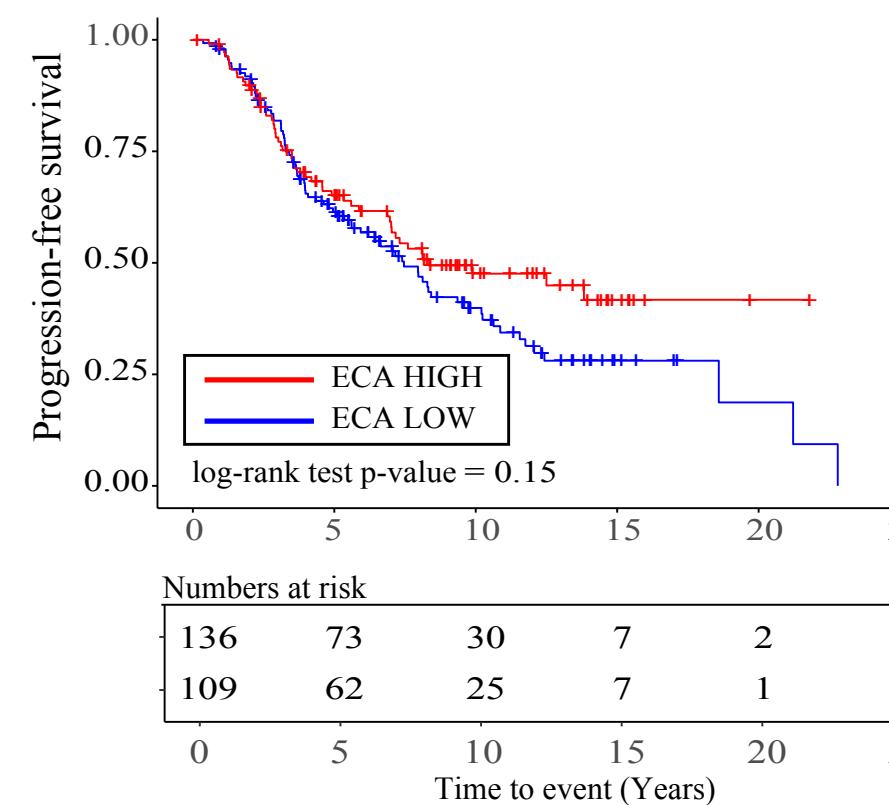
a.

MOD5 derived prediction model in
METABRIC ER+ breast tumors (N = 1,398)



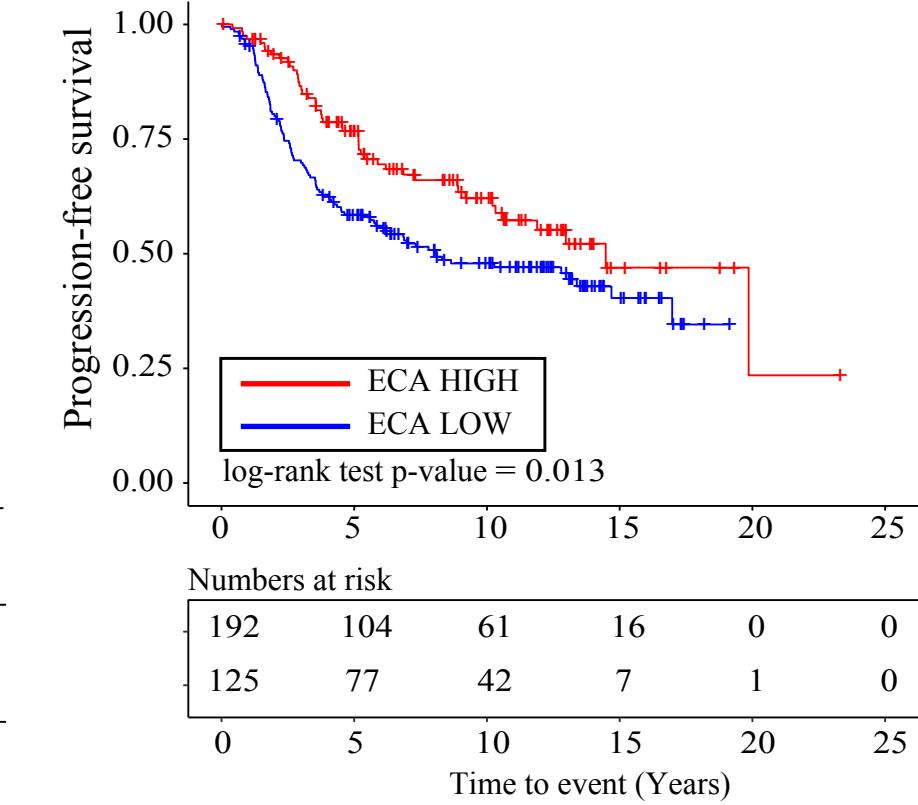
b.

MOD5 derived prediction model in
METABRIC HER2+ breast tumors (N = 247)

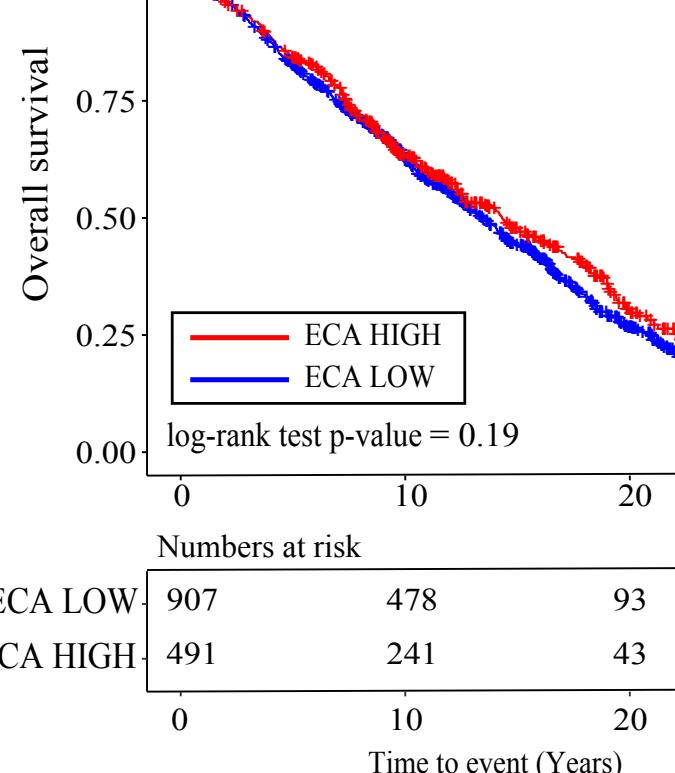


c.

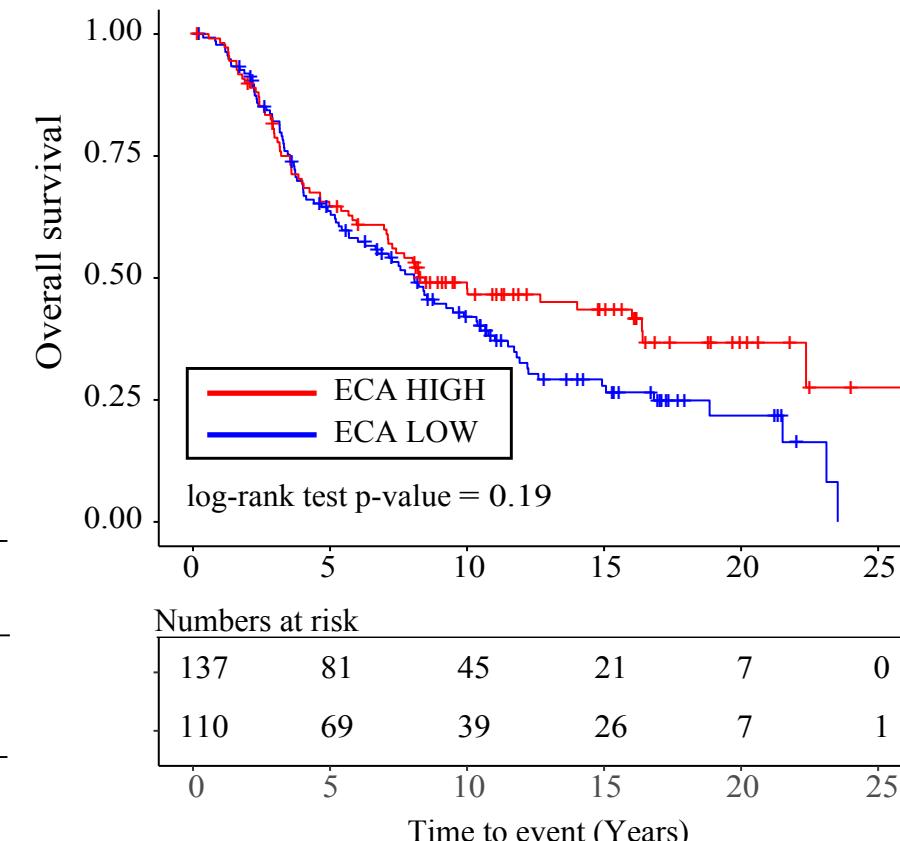
MOD5 derived prediction models in
METABRIC TN breast tumors (N = 320)



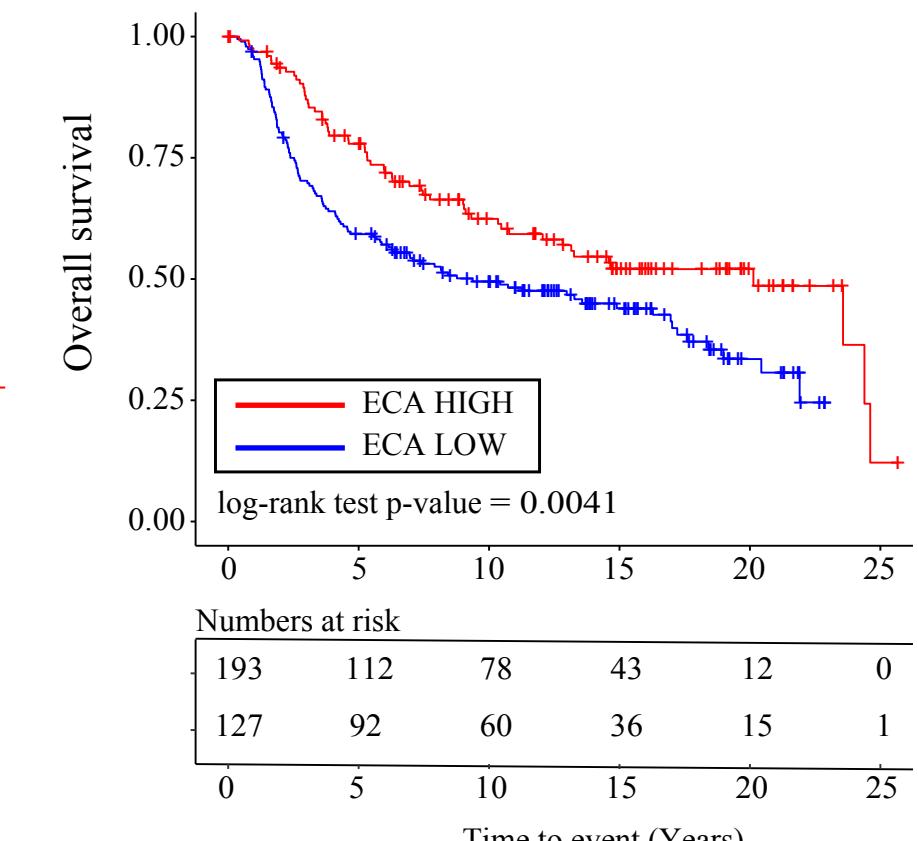
d.

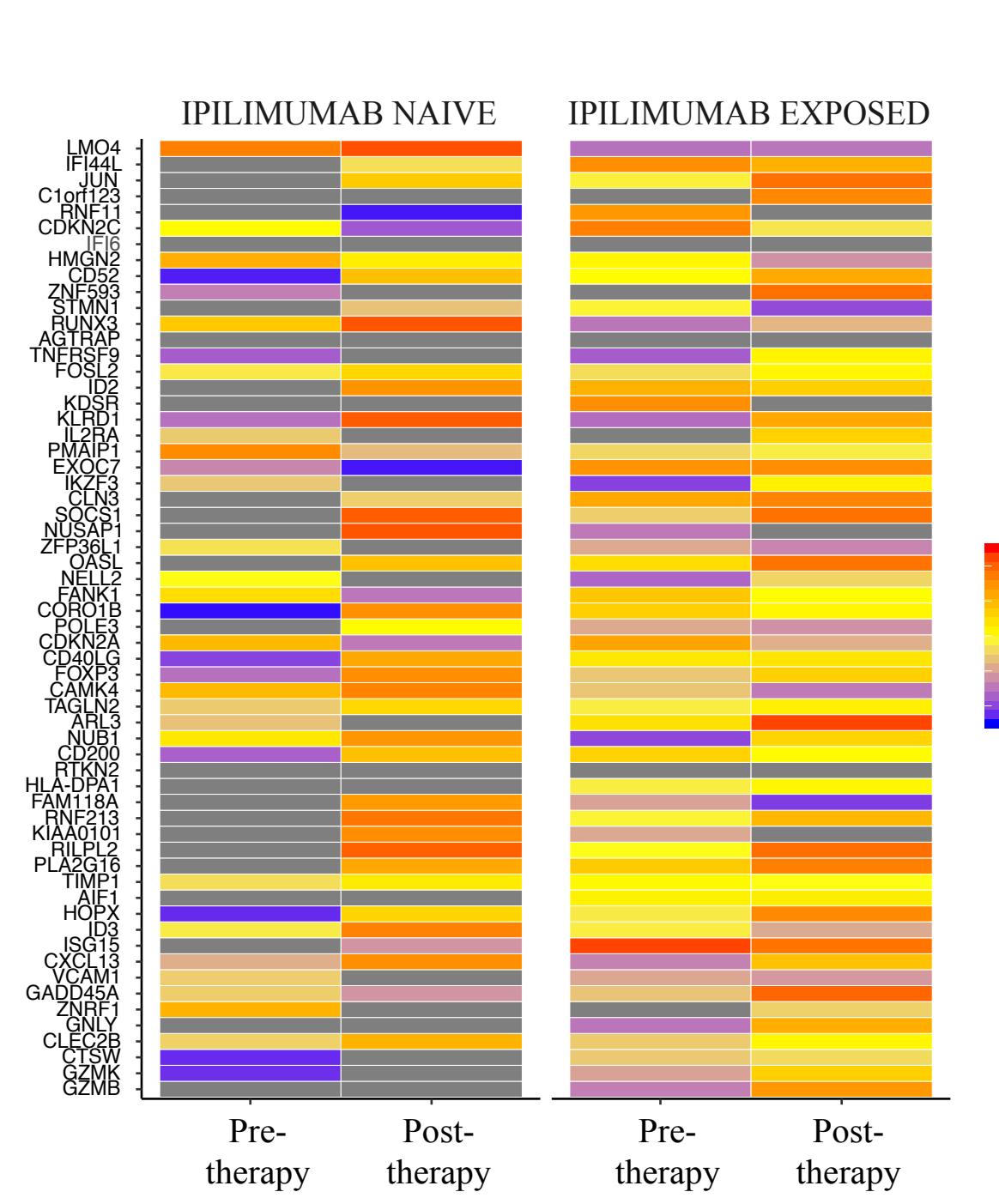
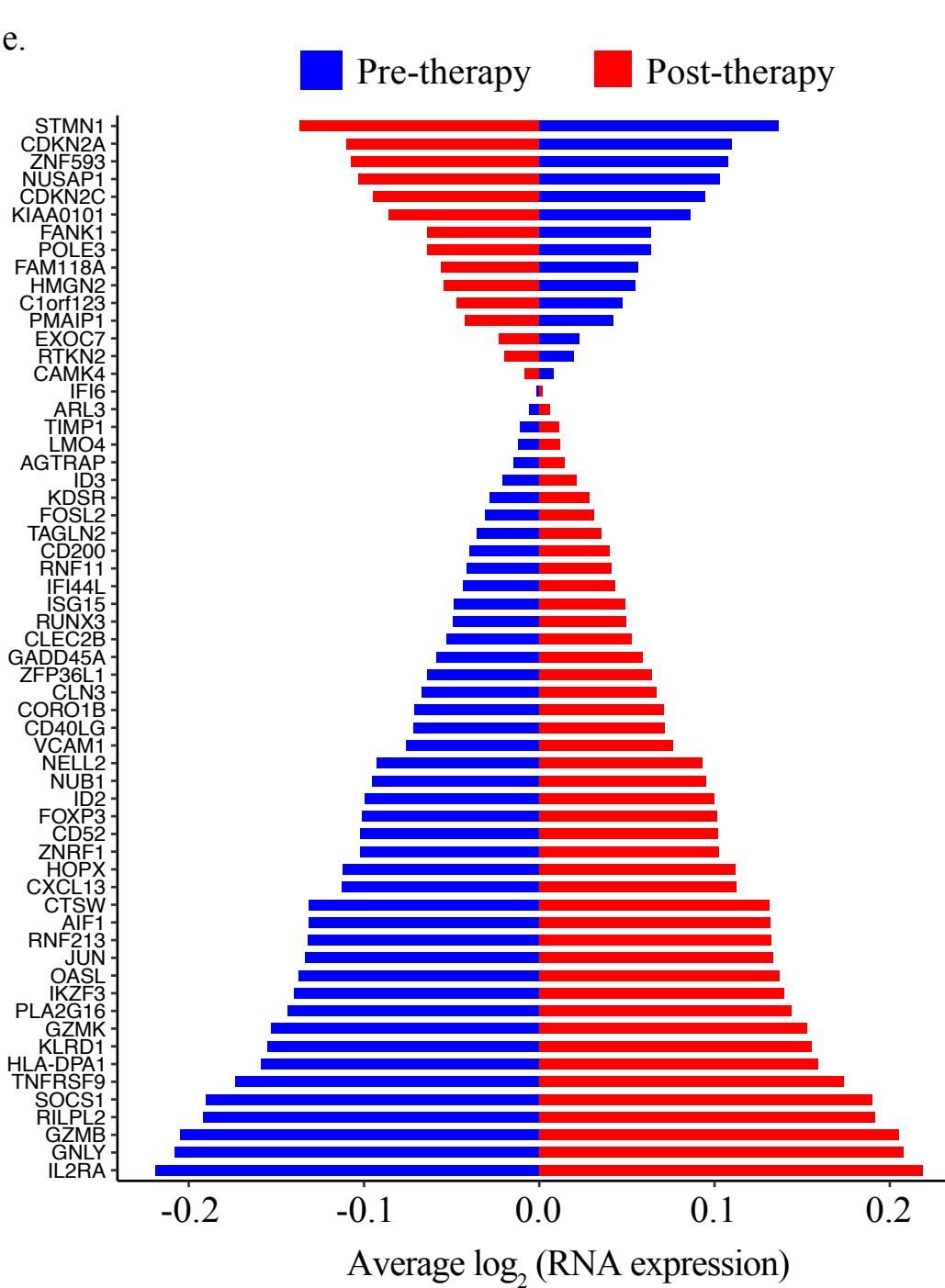
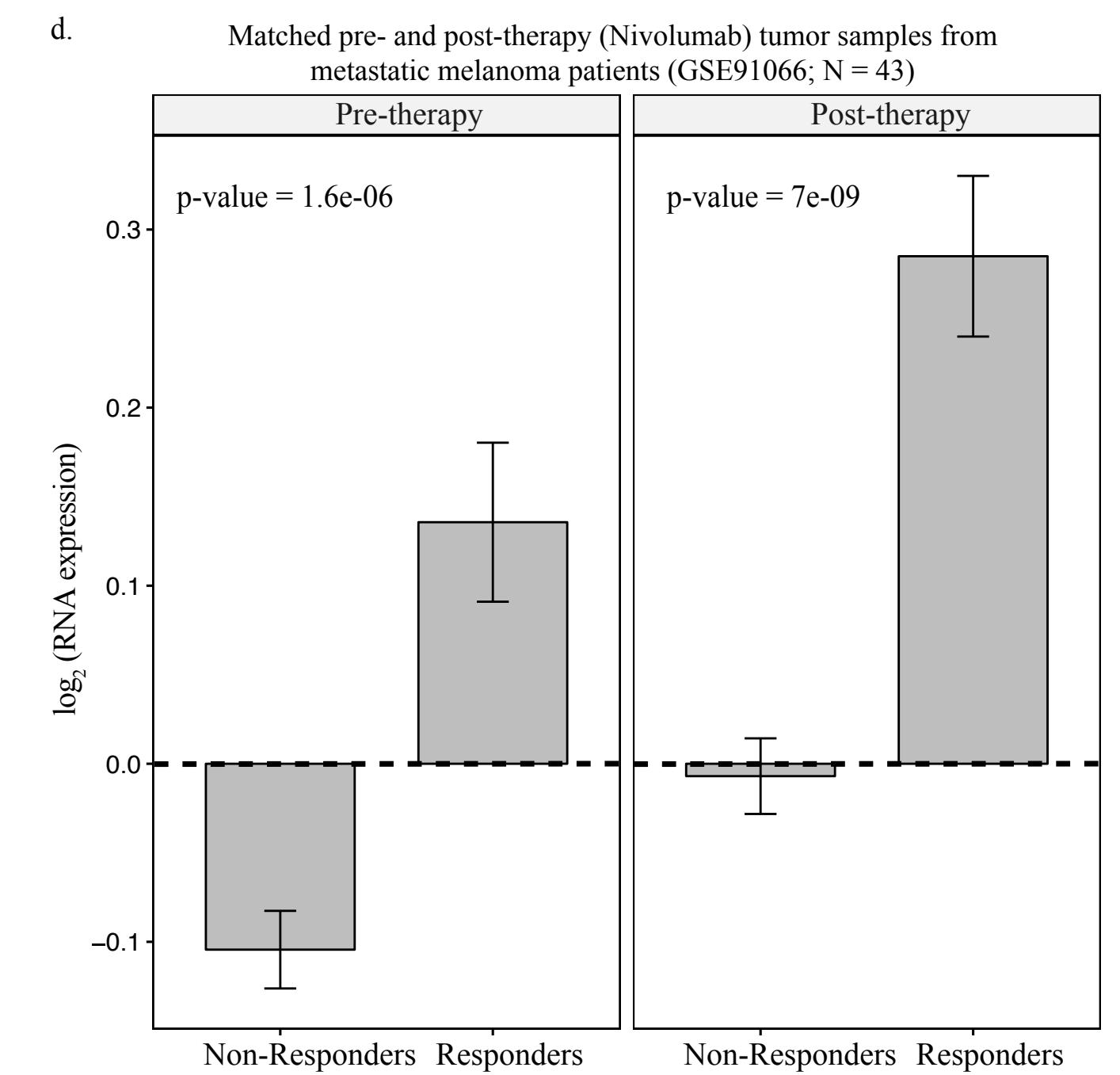
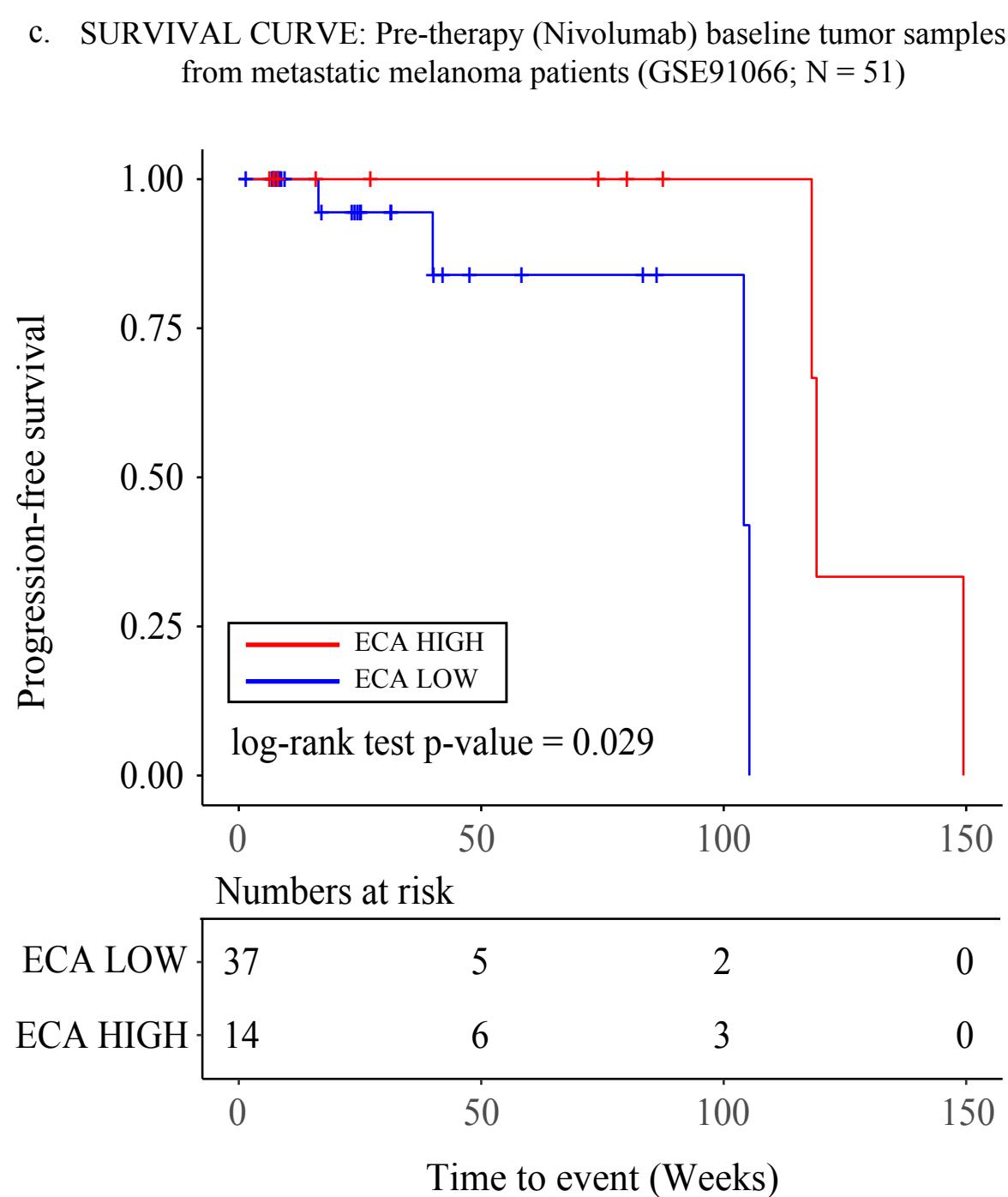
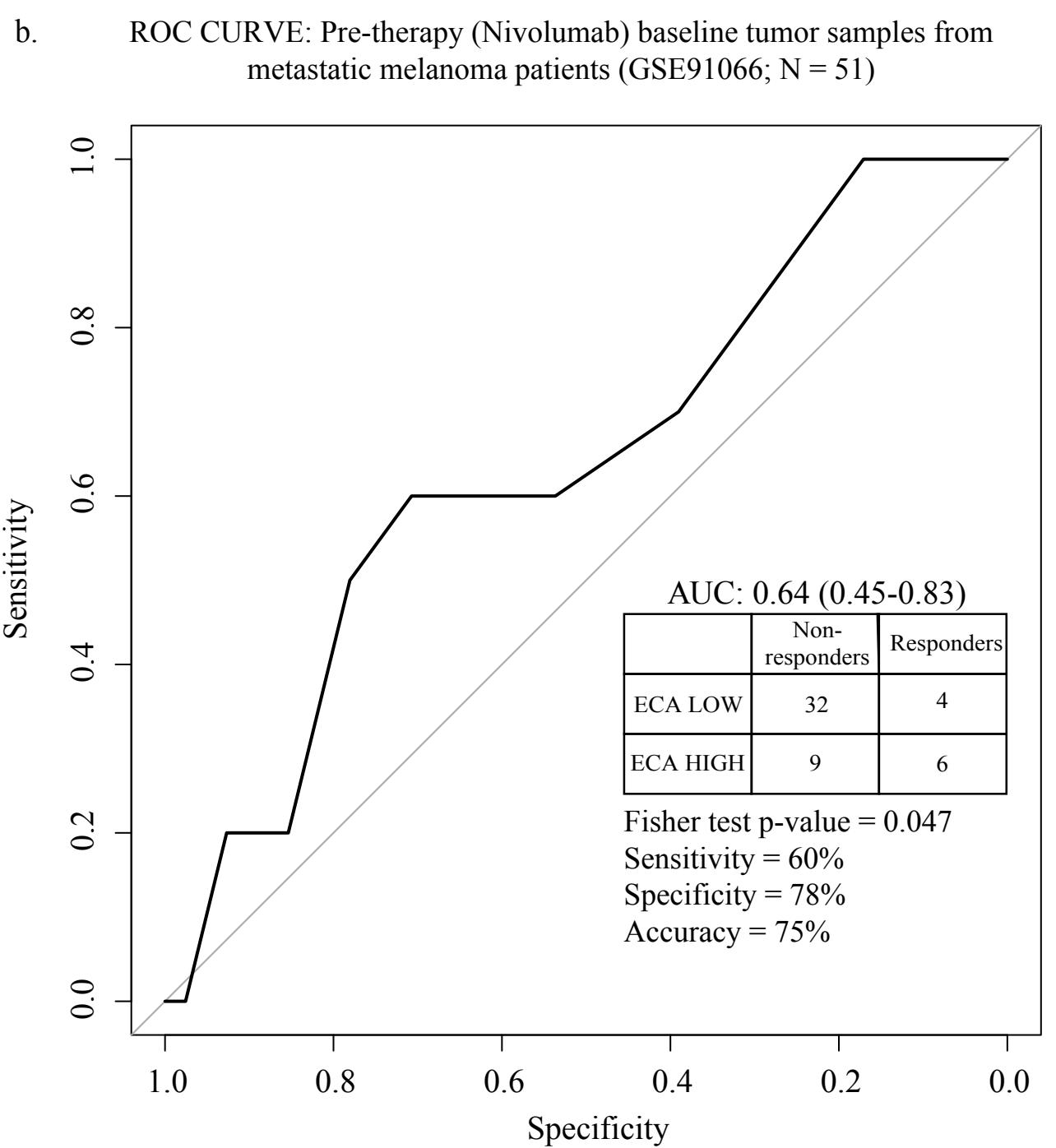
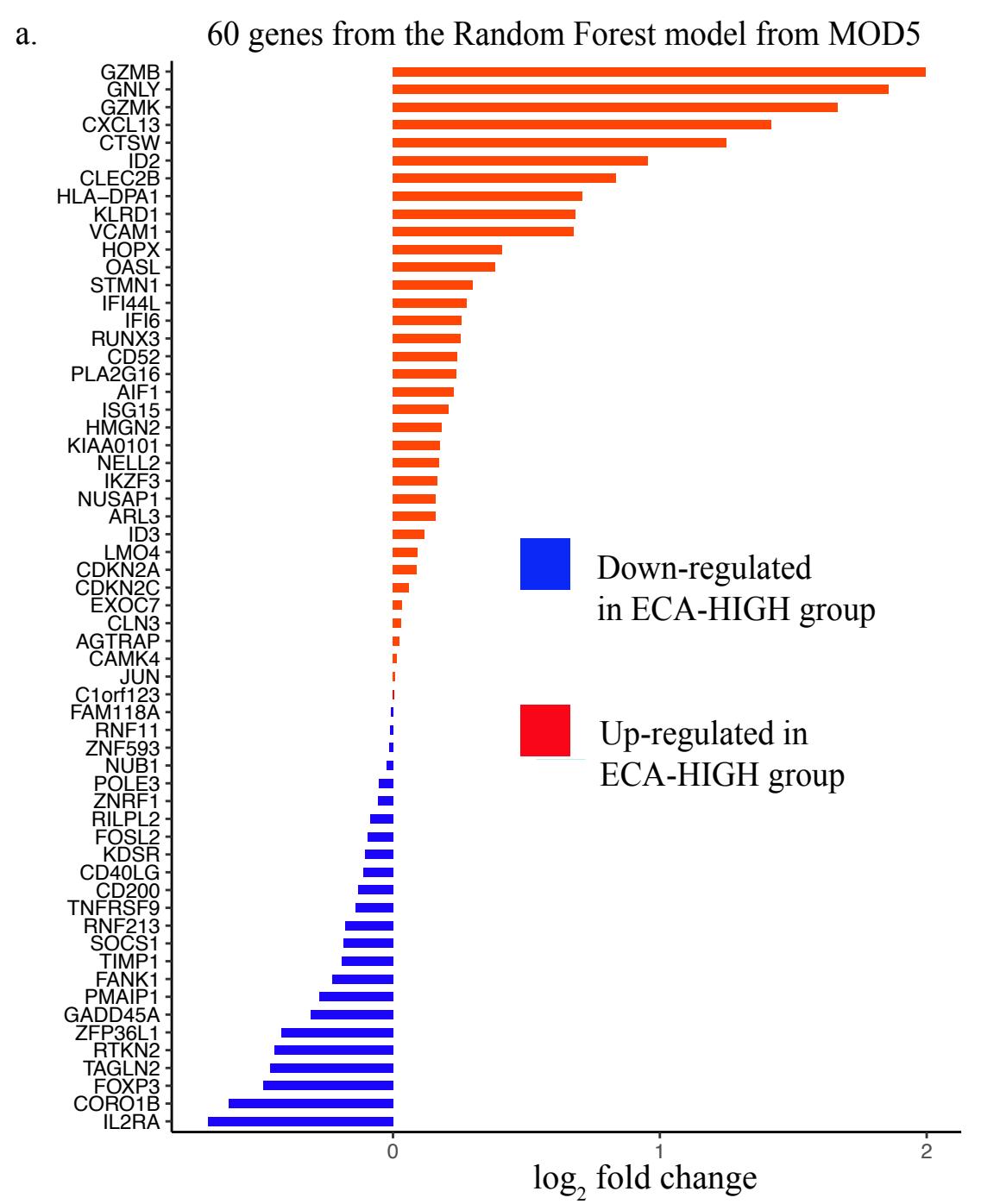


e.

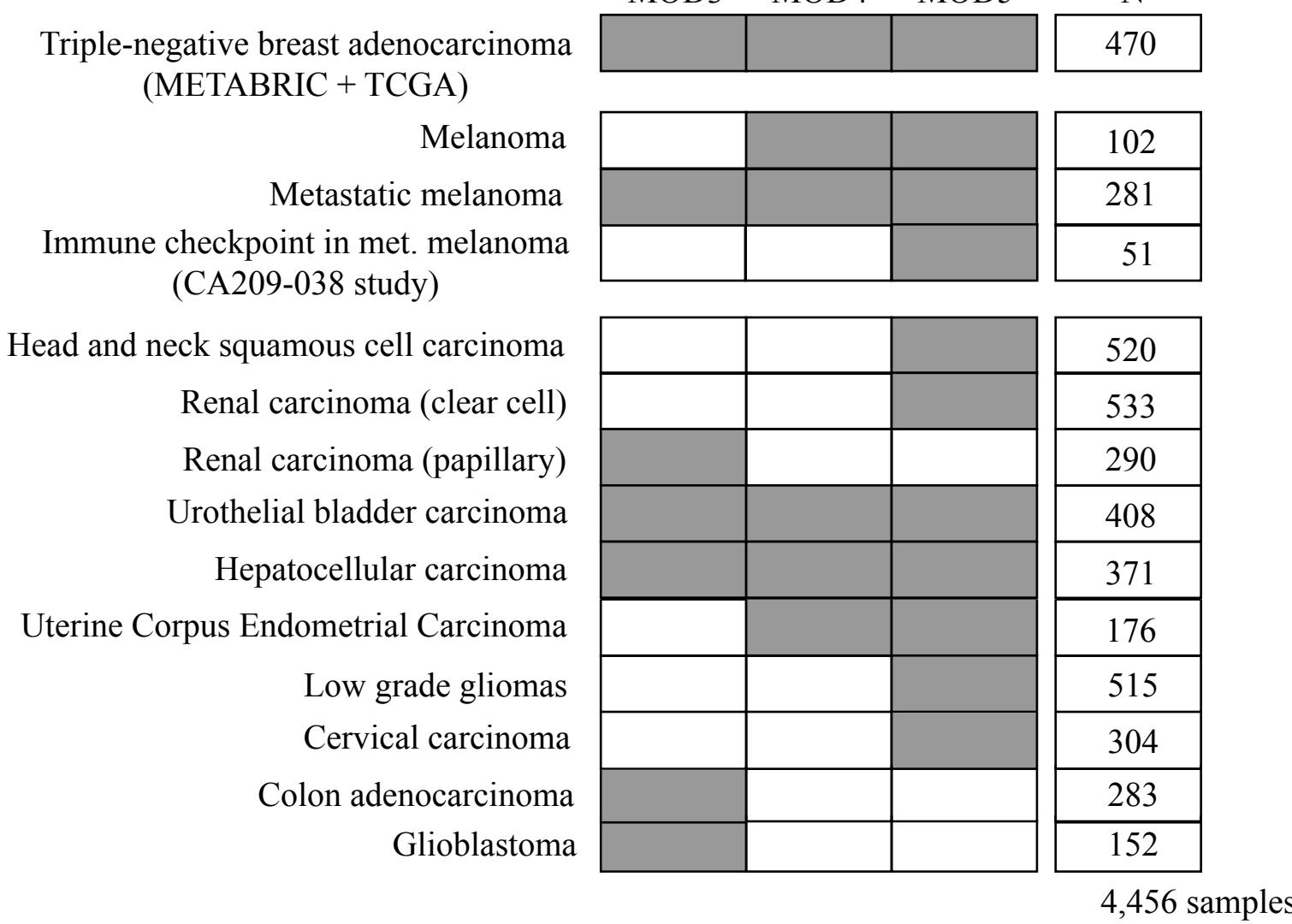


f.





a.



b.

