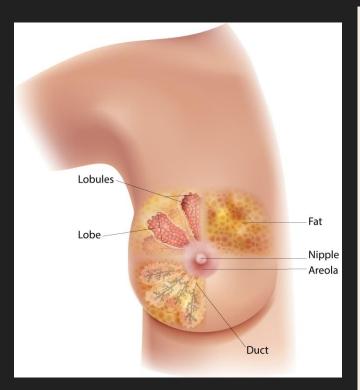
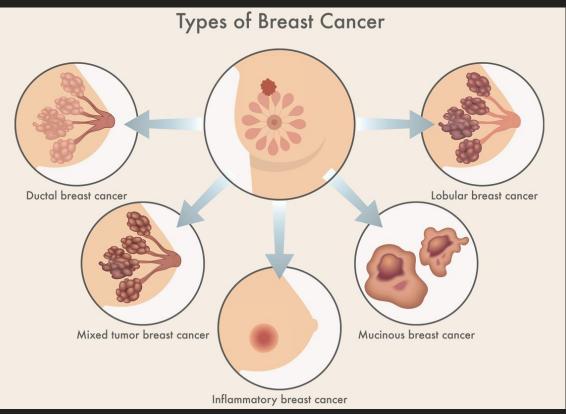
The Role of TP53 Co-Mutations in Breast Cancer Patient Survival

Kailin Liu, Chloe Liu, Colin Yeo

Introduction - Breast Cancer





Introduction - Breast Cancer Statistics

In 2022, an estimated **287,500 new cases** of invasive breast cancer will be diagnosed in women in the U.S. 🞗

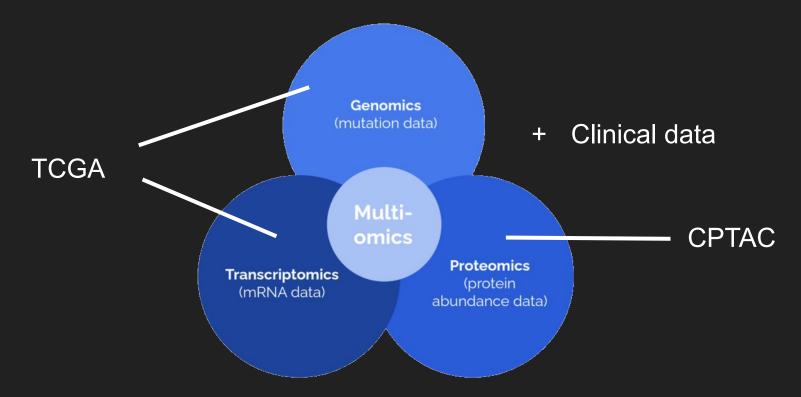


Introduction - Datasets





Introduction - Multi-omic Data Analysis



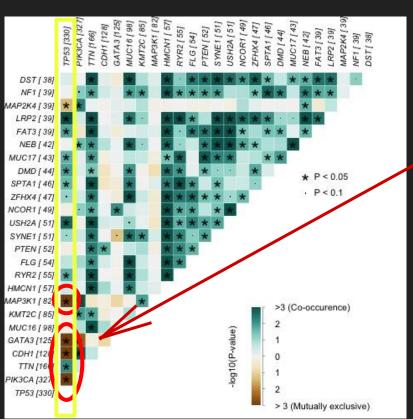
Research Question:

How does TP53 co-mutation influence survival in breast cancer patients and interact with other genes/protein production?

Methods

- R
 - TCGA (~1100 patients)
 - BiocManager, Summarized Experiment
 - Maftools, ggplot2, survival, survminer
- Python
 - CPTAC (122 patients)
 - Numpy, Pandas, Scipy, Matplotlib, Seaborn

4 Genes Show Mutual Exclusivity with TP53 (Fig 1)





Somatic Interaction Plot that highlights 4 mutually exclusive genes with TP53.

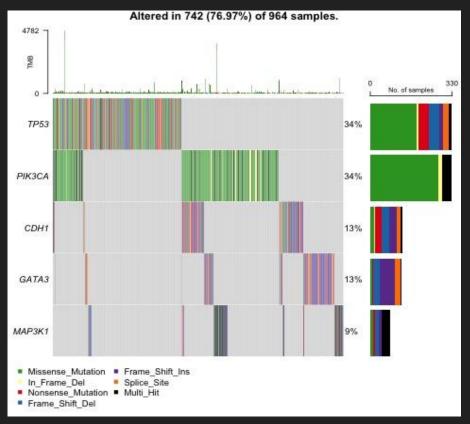
Our 4 Chosen Genes

- MAP3K1 (cell migration/survival), GATA3 (cell development/function), CDH1 (tumor suppression), PIK3CA (cell growth)

- TP53 & GATA3 implicated in early onset breast cancer (Grote et al., 2021)

TP53 & CDH1 involved in familial breast cancer (Rahim et al., 2022)

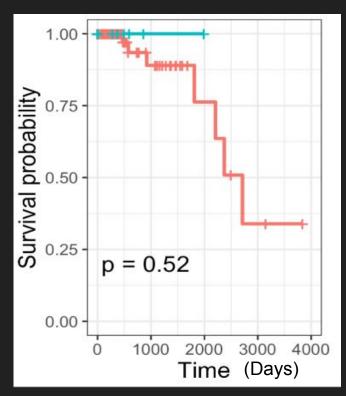
Oncoplot Shows Slight Overlap between Genes (Fig 2)

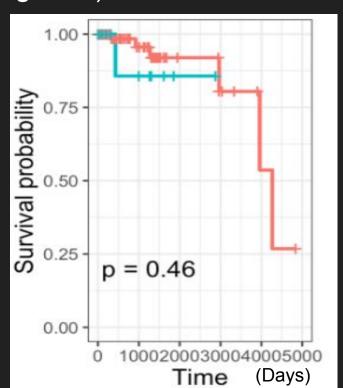


Key Takeaways:

- Certain genetic mutations are caused disproportionately by one type of mutation
- The number of overlaps
 between the gene mutations is
 minor

KM Plot Shows Higher Survival Probability for TP53+/CDH1+ and TP53+/MAP3K1+ Patients (Figs 3-4)





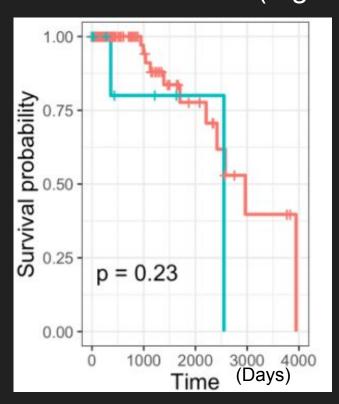
RED = TP53-

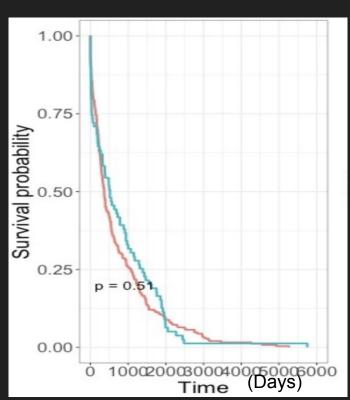
BLUE = TP53+

MAP3K1 (TP53-: 113; TP53+: 9)

CDH1 (TP53-: 123; TP53+: 11)

KM Plot Shows Non-Differential Survival for GATA3+ and PIK3CA+ Patients (Figs 5-6)



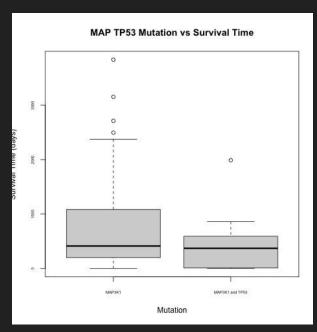


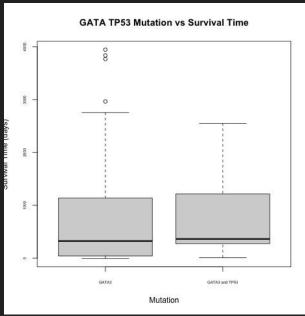
RED = TP53

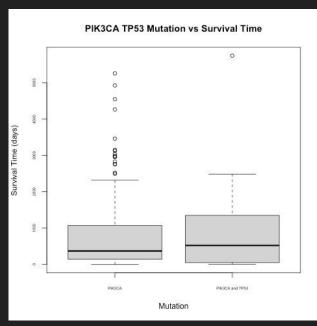
BLUE = TP53+

PIK3CA (TP53-: 289; TP53+: 79)

Survival Time Comparable for 3 Genes (Figures 7, 9, 10)



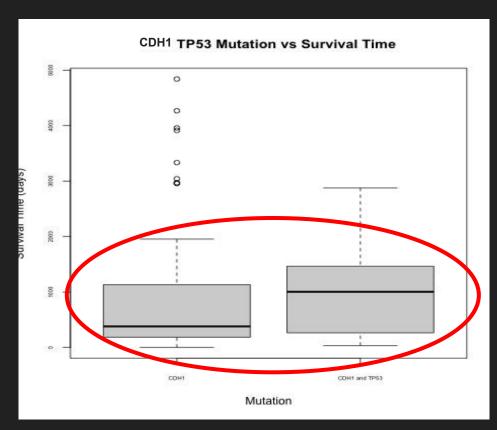




Left = Single Mutation

Right = TP53 Co-mutation

CDH1/TP53 Co-Mutation → Longer Survival (Fig 8)

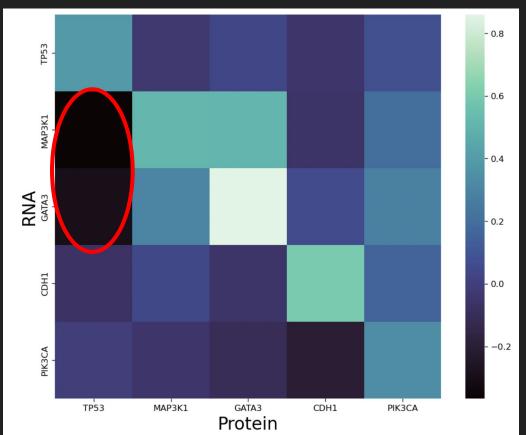


Left = Single Mutation

Right = TP53 Co-mutation

RNA/Protein Expression Heatmap (Fig 11)

Negative Relationship between TP53 Protein & GATA3/MAP3K1 RNA



Notable Takeaways

- TP53+/CDH1+ patients survival time > TP53-/CDH1+ patients in our dataset
 - These mutations are correlated with increase breast cancer risk (Shabnaz et al., 2015)
 - P > 0.05 for this finding, suggests potential statistical weakness

- Low presence of TP53 protein correlated with high expression of GATA3,
 MAP3K1 genes/RNA
 - Recent article (ovarian cancer) suggests GATA3 may cause apoptosis of TP53-producing cells (El-Arabey et al., 2022)

Future areas of study

 Consider the interactions between other genes (outside of the genes chosen for this study)

Repeat this study on a bigger dataset (i.e. TCGA only contained ~1100 patients), might address the statistical significance issues

Why does this matter?

 Clinicians may push for more individualized treatments for patients with various combinations of mutated genes

 Understanding co-mutations' influence on survival may provide families with a loved one's prognosis

Works Cited

Donepudi, M., Kondapalli, K., Amos, S. & Venkanteshan, P. (2014). Breast Cancer Statistics and Markers. J Cancer Res Ther. 10(3): 506-511. DOI: 10.4103/0973-1482.137927.

El-Arabey A., Denizli, M., Kanliklilicer, P., Bayraktar, R., Ivan, C., Rashed, M., Kabil, N., Ozpolat, B., VCalin, G., Salama, S., Abd-Allah, A., Sood, A. & Lopez-Berestein, G. (2020). GATA3 as a master regulator for interactions of tumor-associated macrophages with high-grade serous ovarian carcinoma. Cellular Signaling 68: 109539.

Fuchs, S., Adler, V., Pincus, M. & Ronai, Z. (1998). MEKK1/JNK signaling stabilizes and activates p53. Proc. Natl. Acad. Sci. USA 95: 10541-10546.

Grote, I., Bartels, S., Kandt, L., Bollmann, L., Christgen, H., Gronewold, M., Raap, M., Lehann, U., Gluz, O., Nitz, U., Kuemmel, S., Eulenburg, C., Braun, M., Aktas, B., Grischke, E., Schumacher, C., Luedtke-Heckenkamp, K., Kates, R., Wuerstlein, R., ...Kreipe, H. (2021). TP53

mutations are associated with primary endocrine resistance in luminal early breast cancer. Cancer Medicine 10(23): 8581-8594. DOI: 10.1002/cam4.4376.

Rahim, A., Jan, A., Ali, J., Khuda, F., Muhammad, B., Khan, H., Shah, J. & Akbar, R. (2022). Association of ATM, CDH1 and TP53 genes polymorphisms with familial breast cancer in patients of Khyber Pakhtunkhwa, Pakistan. African Health Sciences 22(3). DOI 10.4314/ahs.v22i3.17

Rosenthal, E., Evans, B., Kidd, J., Brown, K., Gorringe, H., Orman, M. & Manley, S. (2017). Increased Identification of Candidates for High-Risk Breast Cancer Screening Through Expanded Genetic Testing. Journal of the American College of Radiology 14(4): 561-568.

Shabnaz, S., Ahmed, M., Islam, Islam, S., Islam, R., Al-Mamun, A., Islam, M. & Hasnat, A. (2016). Breast cancer risk in relation to TP53 codon 72 and CDH1 gene polymorphisms in the Bangladeshi women. Tumor Biology 37: 7229-7237. DOI: 10.1007/s13277-015-4612-7.

Suravajhala, P., Kogelman, L. & Kadarmideen, H. (2016). Multi-omic data integration and analysis using systems genomics approaches: methods and applications in animal production, health and welfare. Genetics Selection Evolution 48(38).

Questions?