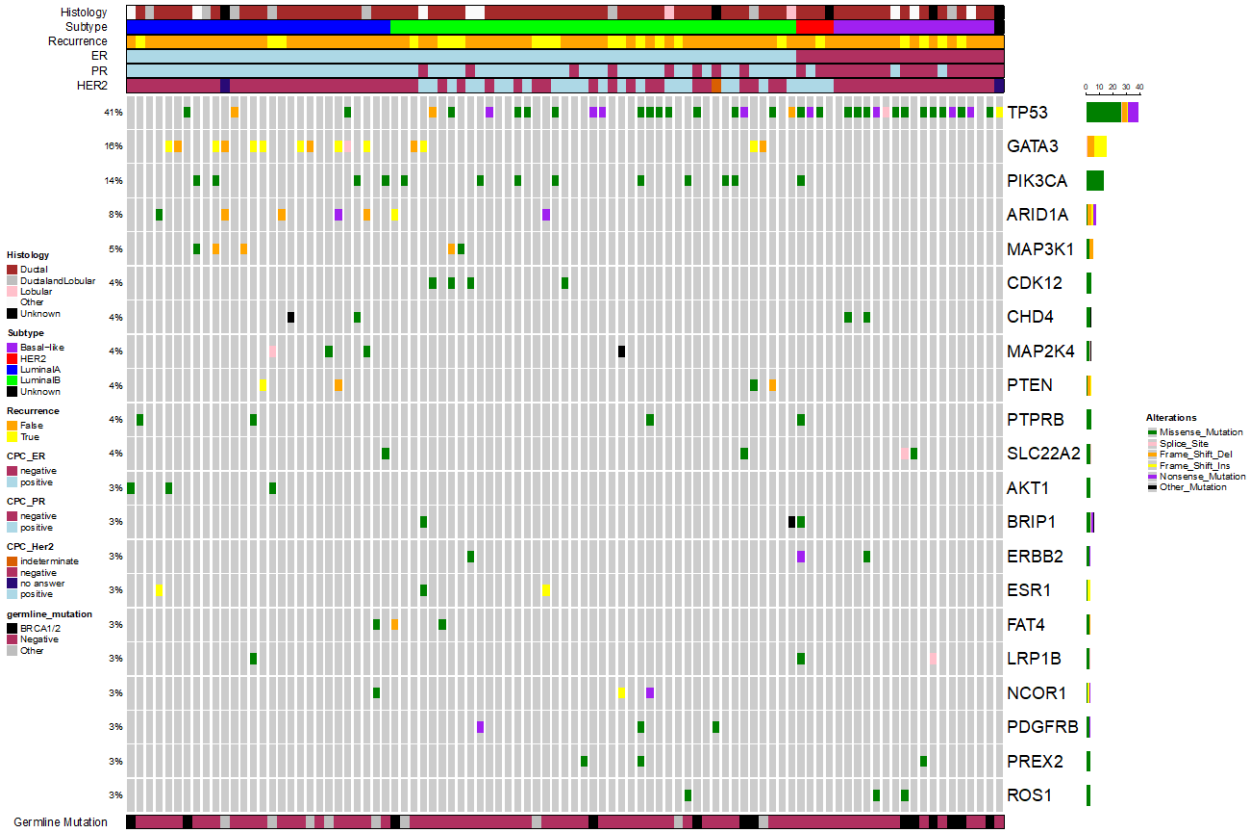
SUPPLEMENTAL FIGURES

Figures: 8

- Supplementary Fig. S1: SNVs/short indels, without significance analysis (just listing)
- Supplementary Fig. S2A: CNV analysis, without significance analysis (just listing)
- Supplementary Fig. S2B: CNV analysis, with significance analysis
- Supplementary Fig. S3: SLC22A2 alteration lollipop plot
- Supplementary Fig. S4: SNVs/short indels in parous vs nulliparous young women
- Supplementary Fig. S5: SNVs/short indels in young women with pregnancy-associated vs non-pregnancy-associated breast cancer

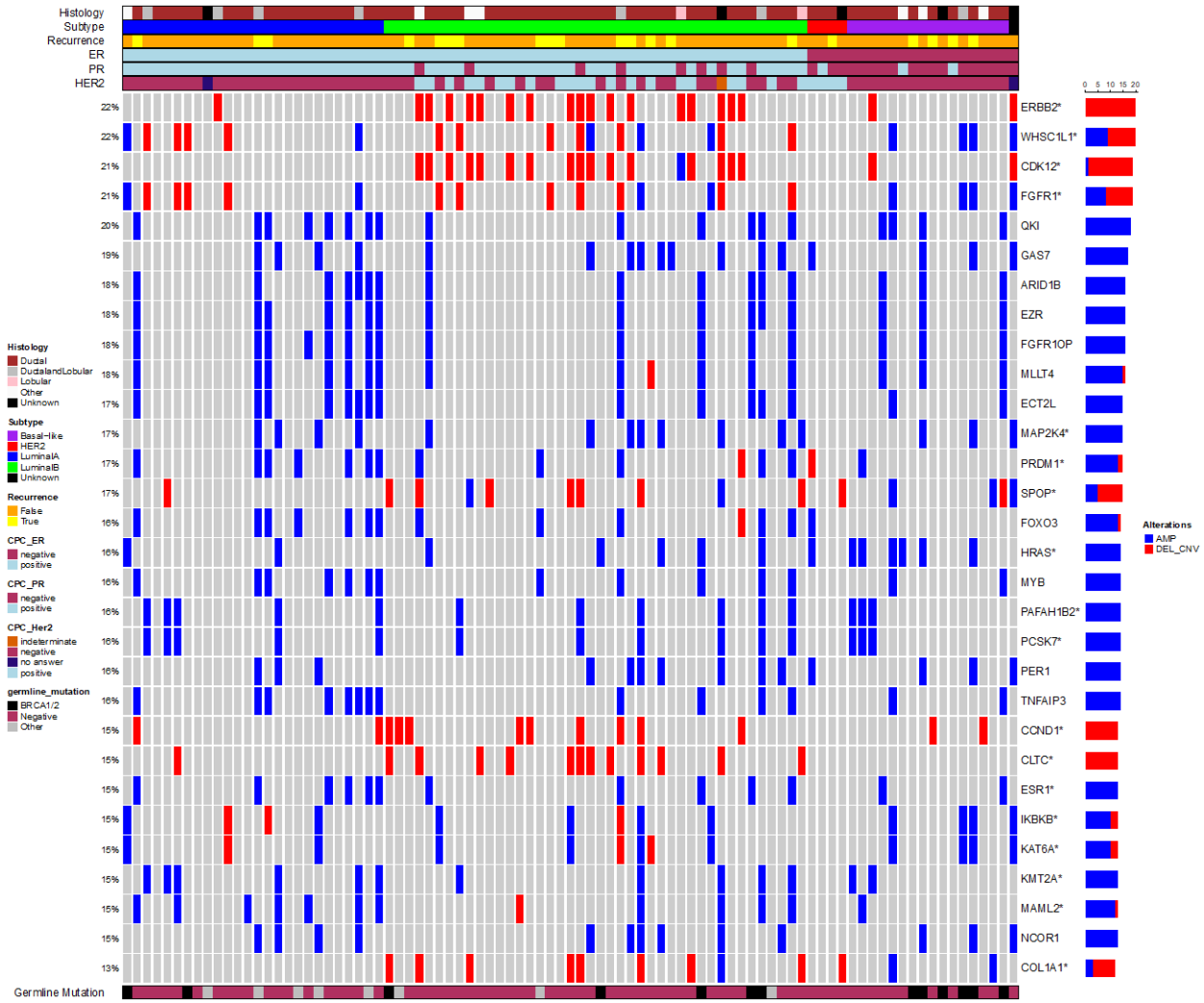
  Supplementary Fig. S6: PIK3CA alteration lollipop plot in young women (A) and older women (B)
- Supplementary Fig. S7: Tumor mutational burden by age
- Supplementary Fig. S8: SNVs/short indels in luminal A + B patients, comparing young women versus older women

Supplementary Fig. S1: SNVs/short indels, without significance analysis (just listing)



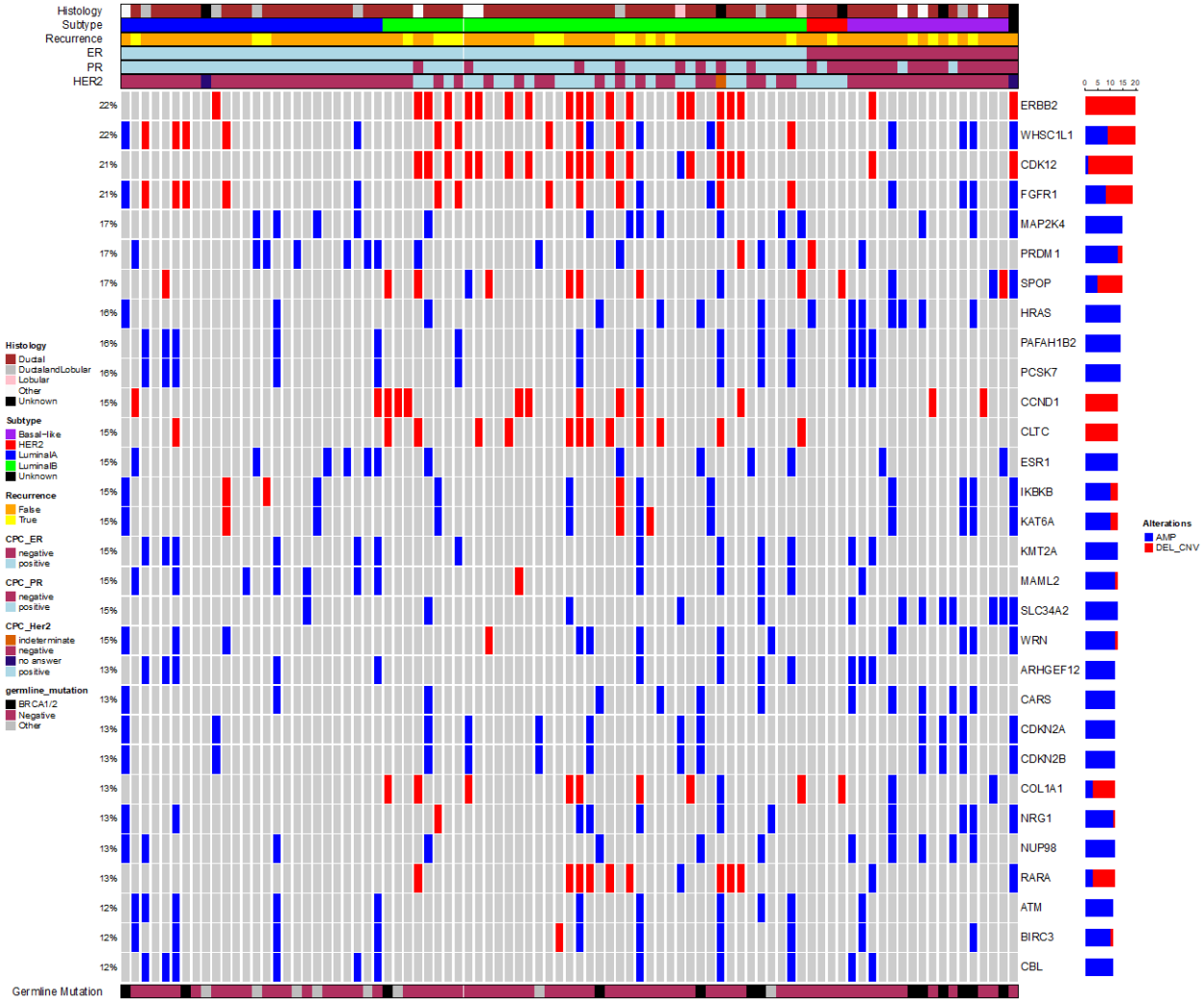
Supplemental Figure 1. Somatic alterations (key to the right) in frequently altered cancer-associated genes across the cohort of 93 tumor samples from 92 patients. Genes were selected from the Cancer Gene Census (CGC), in addition to genes found to be significant by MutSig2CV. Information for each tumor sample is shown in the upper panels, including tumor histology, disease subtype, disease recurrence and ER, PR and HER2 receptor status. Bottom panel annotations shows cancer-specific pathogenic germline variants for each of the tumor samples (key to the left).

Supplementary Fig. S2A: CNV analysis, without significance analysis (just listing)



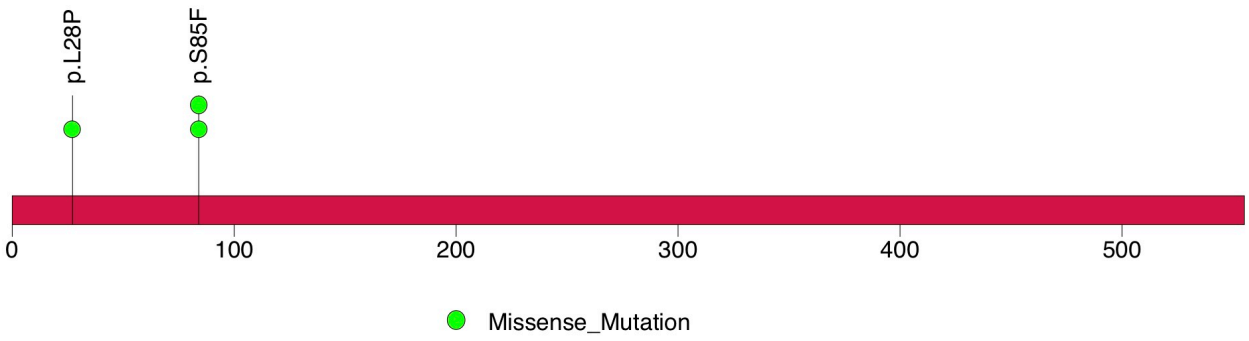
Supplemental Figure 2A. Copy number alterations (key to the right) in the most-frequently altered cancer-associated genes (as specified by CGC) in the cohort of 93 tumor samples from 92 patients. Genes that are significant as per GISTIC are marked by an asterisk. Information for each tumor sample is shown in the upper panels, including tumor histology, disease subtype, disease recurrence and ER, PR and HER2 receptor status. Bottom panel annotations shows cancer-specific pathogenic germline variants for each of the tumor samples (key to the left).

Supplementary Fig. S2B: CNV analysis, with significance analysis



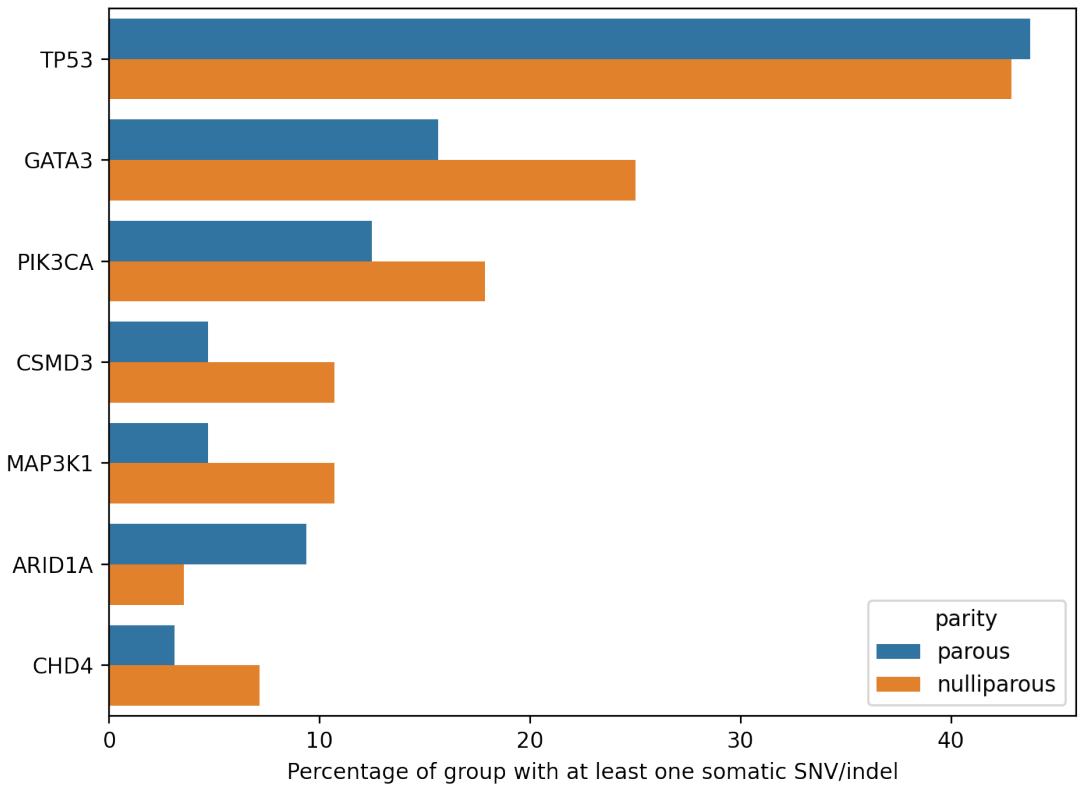
Supplemental Figure 2B. Copy number alterations (key to the right) in genes that are significant as per GISTIC, across the cohort of 93 tumor samples from 92 patients, sorted by alteration frequency in the cohort. Information for each tumor sample is shown in the upper panels, including tumor histology, disease subtype, disease recurrence and ER, PR and HER2 receptor status. Bottom panel annotations shows cancer-specific pathogenic germline variants for each of the tumor samples (key to the left).

Supplementary Fig. S3: SLC22A2 alteration lollipop plot

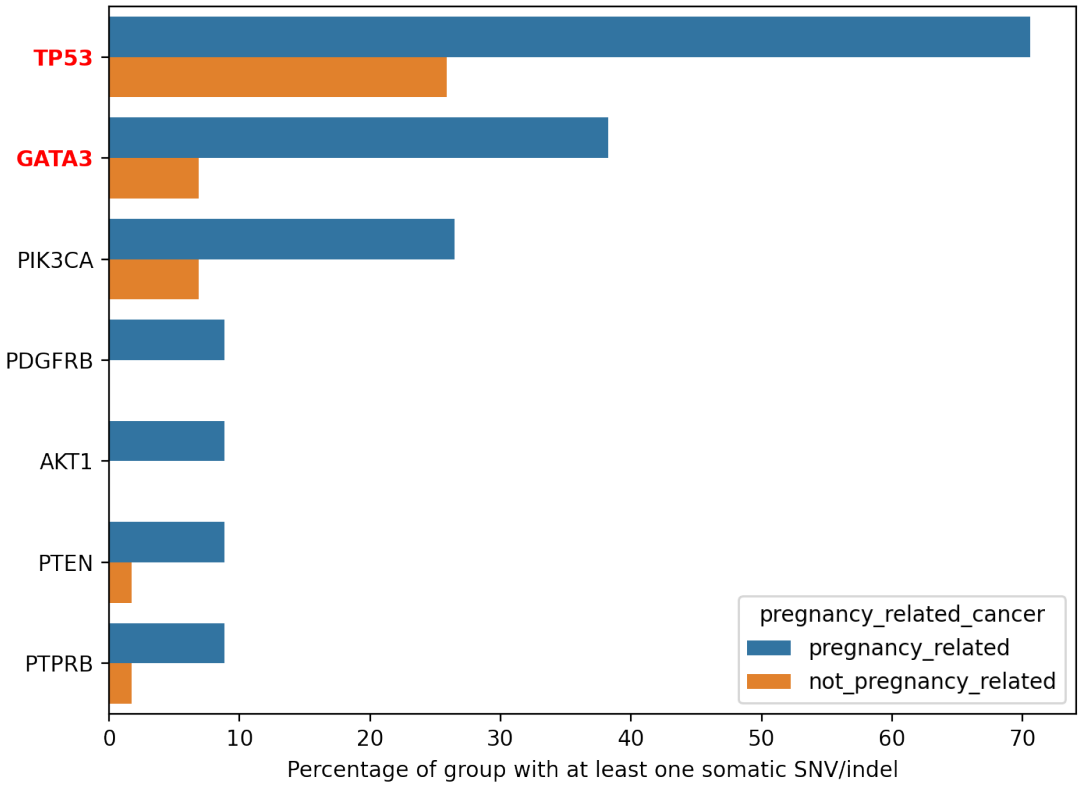


Supplemental Figure 3. Lollipop plot showing the locations of missense mutations identified in the gene *SLC22A2*.

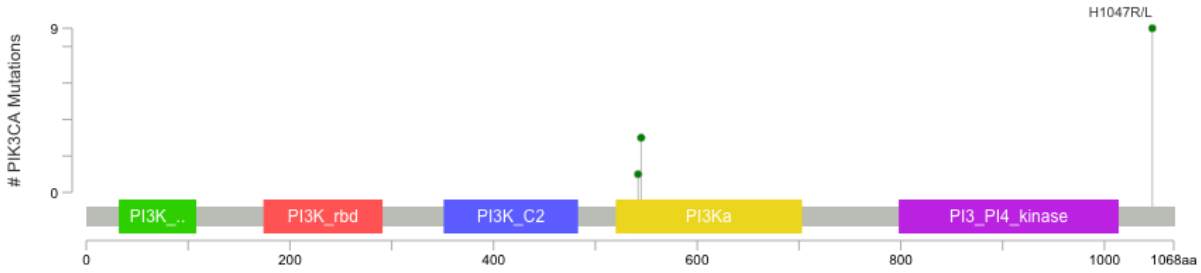
Supplementary Fig. S4: SNVs/short indels in parous vs nulliparous young women

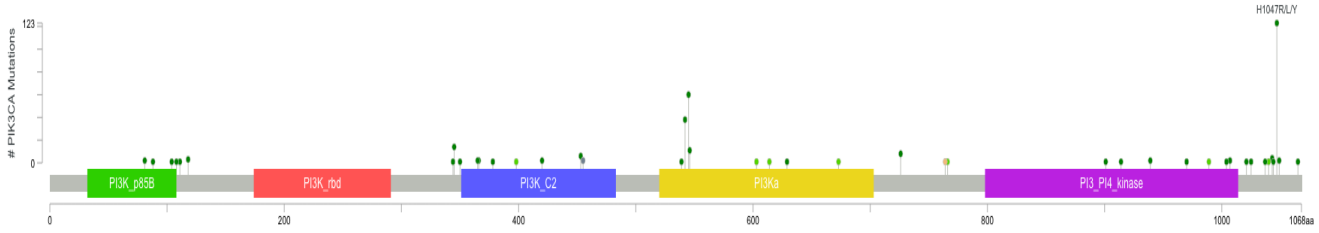


Supplementary Fig. S5: SNVs/short indels in young women with pregnancy-associated vs non-pregnancy-associated breast cancer

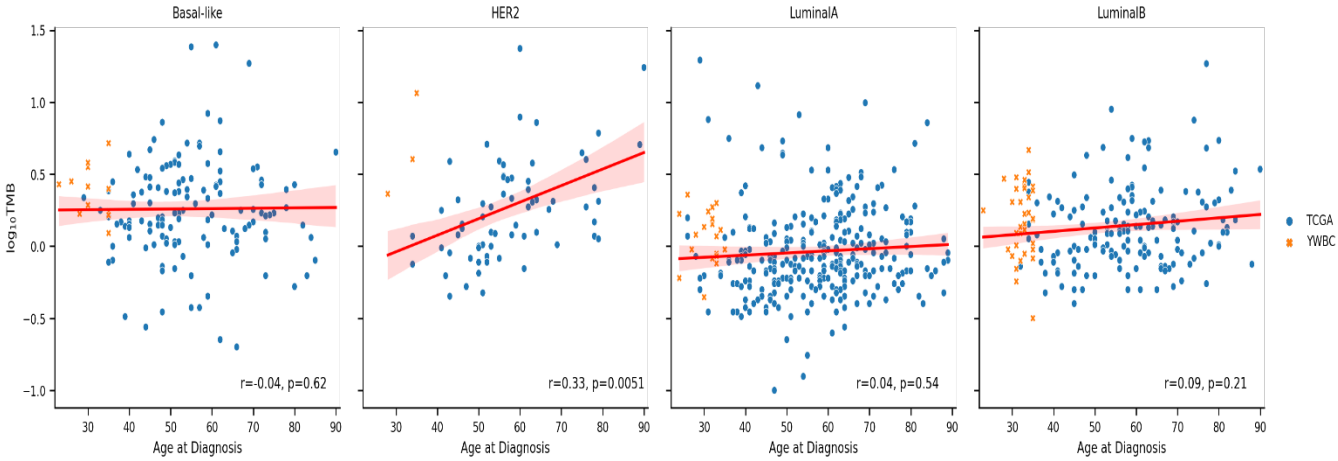


Supplementary Fig. S6: PIK3CA alteration lollipop plot in young women (A) and older women (B)





Supplementary Fig. S7: Tumor mutational burden by age



Supplementary Fig. S8: SNVs/short indels in luminal A + B patients, comparing young women versus older women