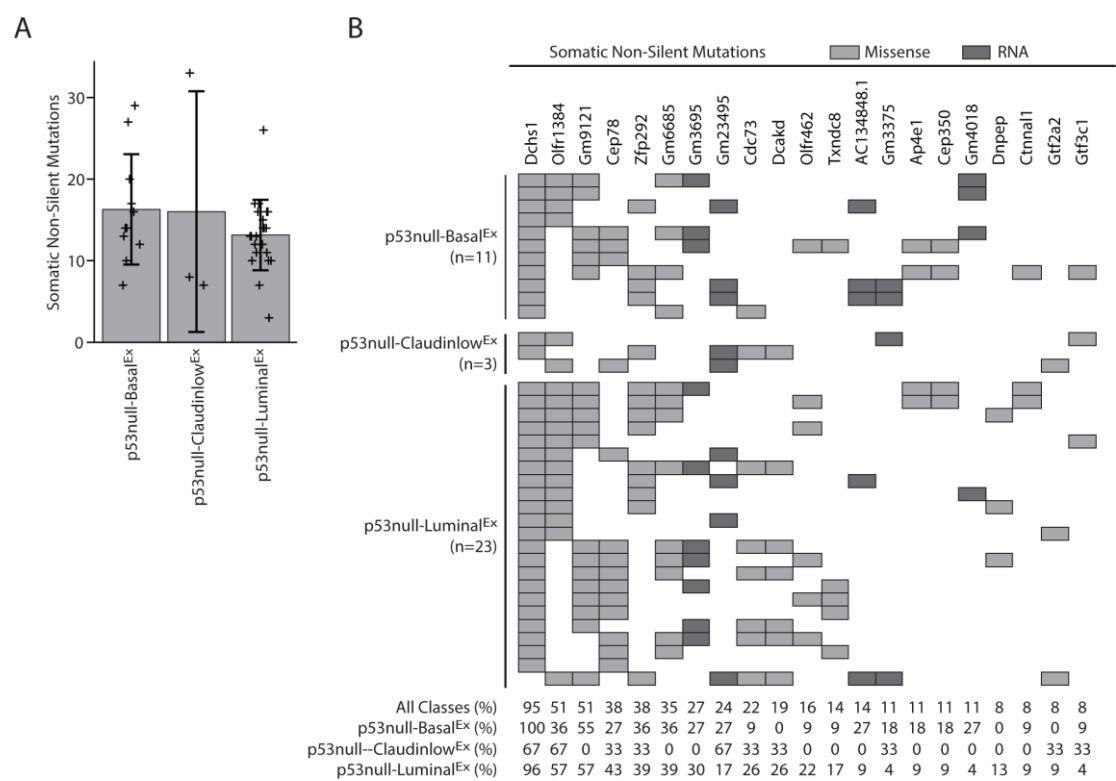


### Supplemental Figure 1: Molecular pathway signatures

Median expression values were calculated for 963 publically available pathway-based gene signatures across our murine and human expression datasets (Pfefferle et al., 2013).

Molecular pathway signatures were identified using a 2-class (class X vs all others) SAM analysis (FDR 0%) across our 385 murine microarray dataset. The standardized average of these pathway signatures was calculated across more than three thousand human tumors and displayed by intrinsic subtype.



**Supplemental Figure 2: Somatic non-silent mutation analysis**

**A.** The total number of somatic non-silent mutations was determined for each sample and plotted by *Trp53*null transplant class. Error bars represent one standard deviation. **B.** All somatic non-silent mutations with a mutational frequency greater than or equal to 8% across all *Trp53*null tumors are displayed by *Trp53*null class. Each row represents an individual tumor, with boxes corresponding to a mutation within the gene on that column.

### **Supplemental Table 1: *Trp53*null mammary transplant tumor sample information**

[Click here to Download Table S1](#)

### **Supplemental Table 2: *Trp53*null mammary transplant tumor SNVs**

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### **Supplemental Table 3: *Trp53*null mammary transplant tumor SVs**

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