

**COMPREHENSIVE SUPPLEMENTAL INFORMATION:**

**The Hippo transducer TAZ interacts with the SWI/SNF complex to regulate breast epithelial lineage commitment**

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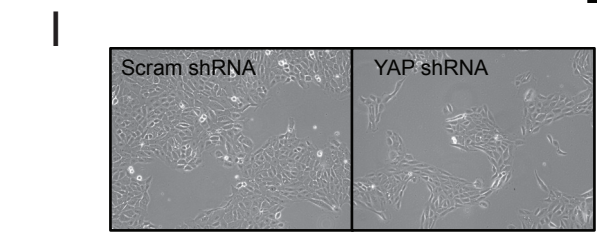
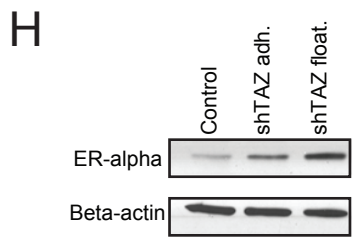
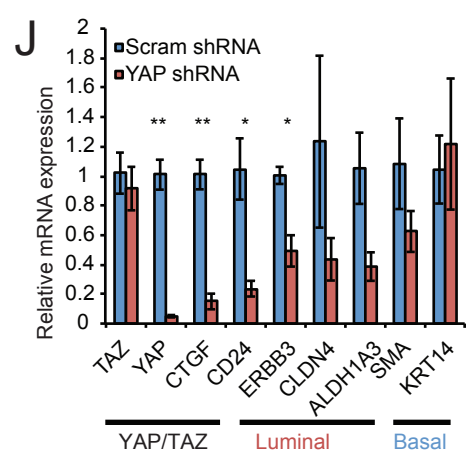
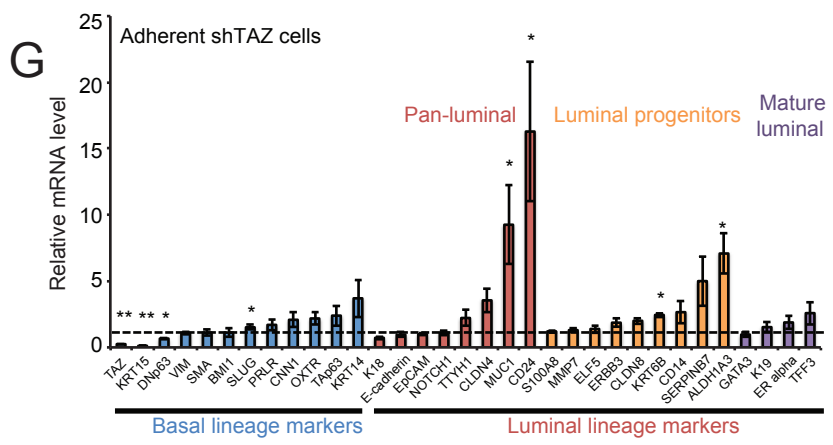
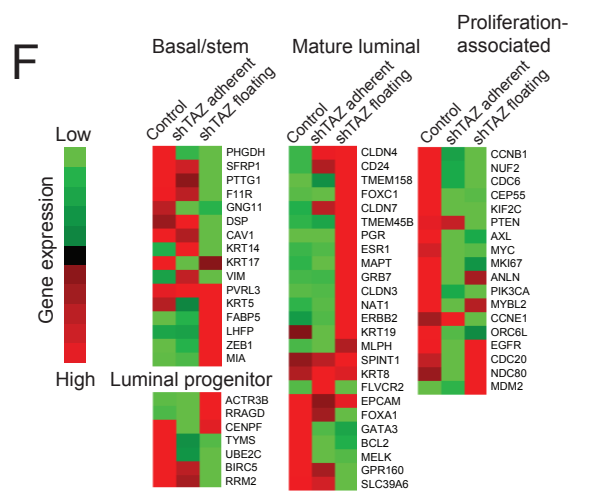
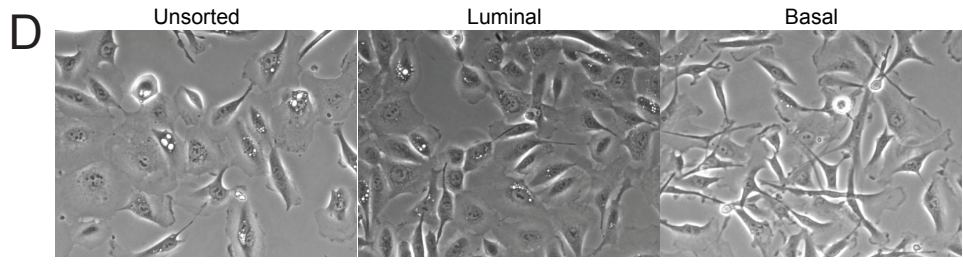
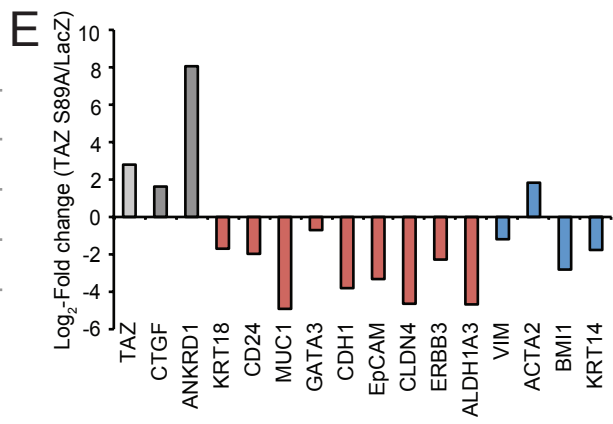
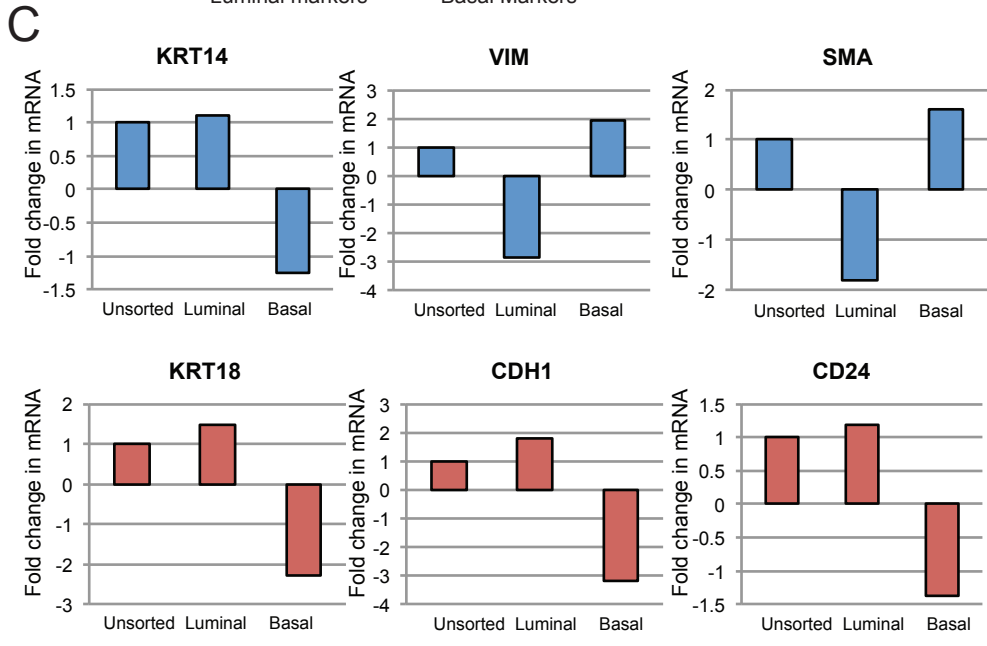
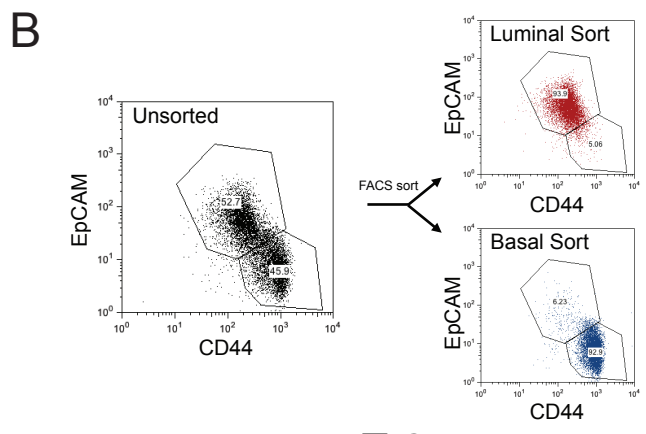
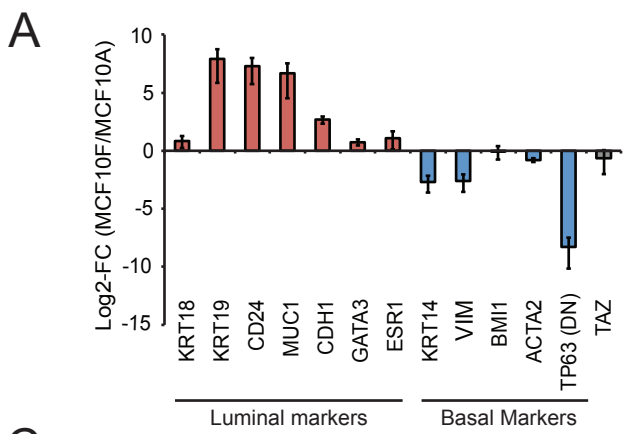
<sup>2</sup> Molecular Oncology Research Institute, Tufts Medical Center, 800 Washington St., Boston, MA 02111

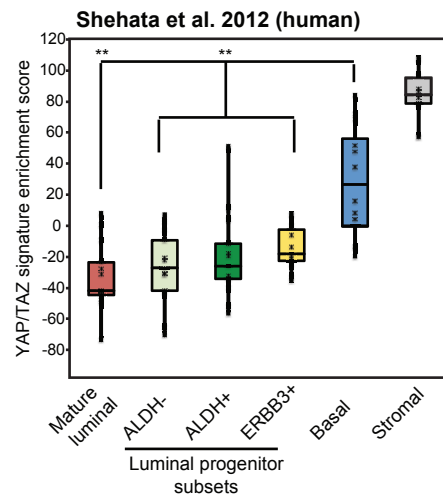
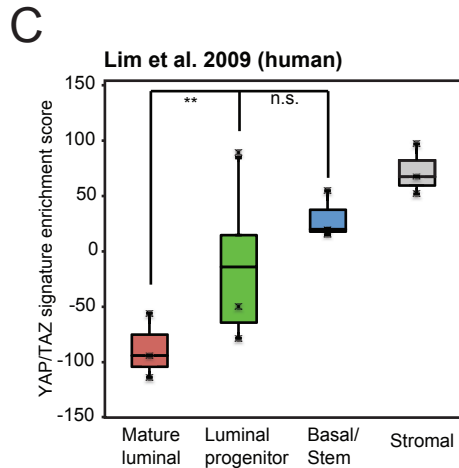
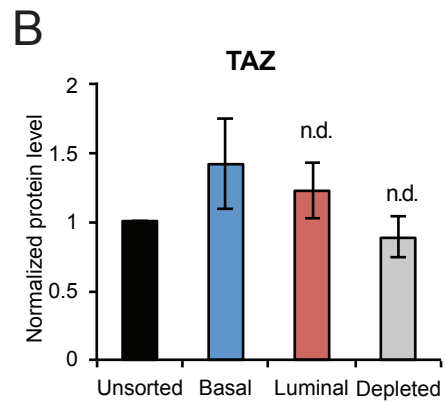
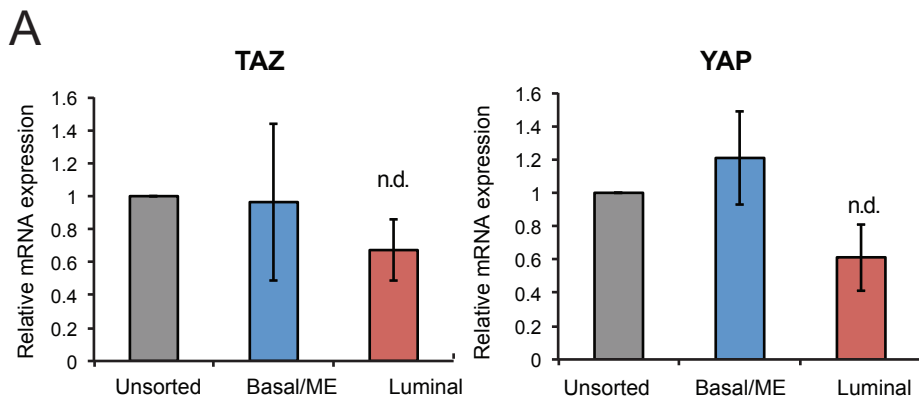
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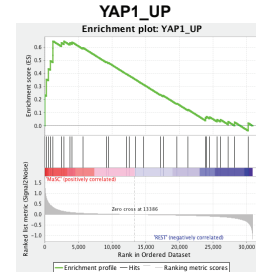
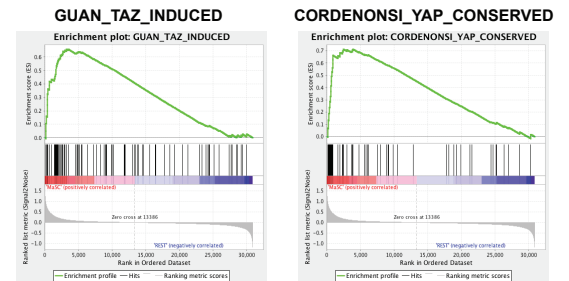
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**D**

| Gene Set Name            | Normalized Enrichment Score | p-value | FDR q-value | Rank at Max |
|--------------------------|-----------------------------|---------|-------------|-------------|
| GUAN_TAZ_INDUCED         | 1.98                        | 0       | 0           | 3260        |
| CORDENONSI_YAP_CONSERVED | 1.95                        | 0       | 0           | 3889        |
| YAP1_UP                  | 1.63                        | 0.019   | 0.0054      | 1235        |

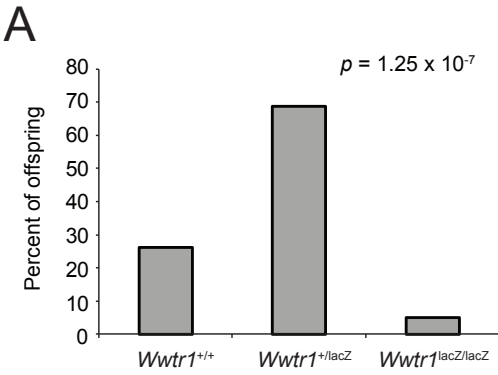


**E** Gene sets used for enrichment analysis

| Gene Set                 | Description   | Source Publication                      | PMID     |
|--------------------------|---|---|----------|
| GUAN_TAZ_INDUCED         | Top 100 genes upregulated in MCF10A cells upon TAZ overexpression | Guan et al., <i>J Biol Chem.</i> , 2009 | 19324877 |
| CORDENONSI_YAP_CONSERVED | 57 genes positively regulated by YAP/TAZ                          | Cordenonsi et al., <i>Cell</i> , 2011   | 22078877 |
| YAP1_UP                  | 50 upregulated genes in MCF10A cells upon YAP overexpression      | Zhang et al., <i>Cancer Res.</i> , 2008 | 18413746 |

**Microarray datasets used for enrichment analysis**

| Dataset   | Lineage depletion  | Subpopulations isolated in dataset  | Purification method | Species | GEO Accession |
|---|--------------------|---|---------------------|---------|---------------|
| Lim et al., <i>Nat Med.</i> , 2009                | CD31, CD45, TER119 | Mature luminal (CD49f-/EpCAM+), luminal progenitor (CD49+/EpCAM+), basal/stem (CD49f+/EpCAM-), stromal (CD49f-/EpCAM-)                              | FACS                | human   | GSE16997      |
| Lim et al. 2010, <i>Breast Cancer Res.</i> , 2010 | CD31, CD45, TER119 | Mature luminal (CD29lo/CD24+/CD61-), luminal progenitor (CD29lo/CD24+/CD61+), basal/MaSC-enriched (CD29hi/CD24+/CD61+), stromal (CD29low/CD24-)     | FACS                | mouse   | GSE19446      |
| Shehata et al., <i>Breast Cancer Res.</i> , 2012  | CD45, CD31         | Mature luminal (CD49f-/EpCAM+), luminal progenitor (CD49+/EpCAM+, with three subsets), basal/MaSC-enriched (CD49f+/EpCAM-), stromal (CD49f-/EpCAM-) | FACS                | human   | GSE35399      |
| Nagarajan et al., <i>Stem Cell Reports</i> , 2013 | CD45, CD31         | Mature luminal (CD49f-/EpCAM+), luminal progenitor (CD49f+/EpCAM+), basal/MaSC-enriched (CD49f+/EpCAM- or low)                                      | FACS                | human   | GSE37223      |



**B**

|              | Expected number | Actual Number |
|--------------|-----------------|---------------|
| Wild-type    | 34.5            | 36            |
| Heterozygous | 69              | 95            |
| Homozygous   | 34.5            | 7             |

