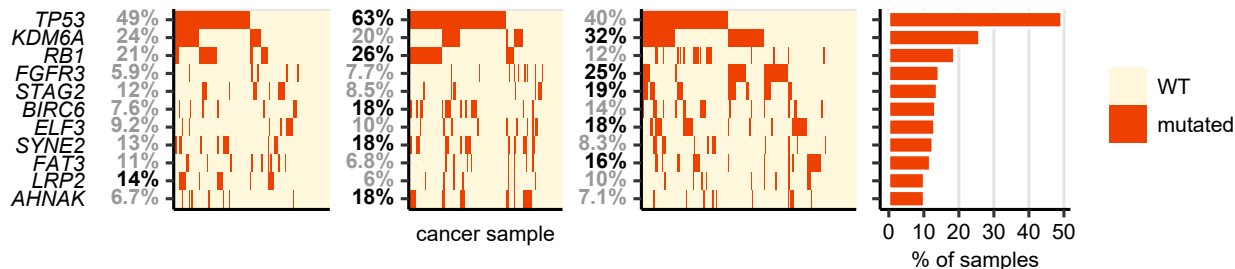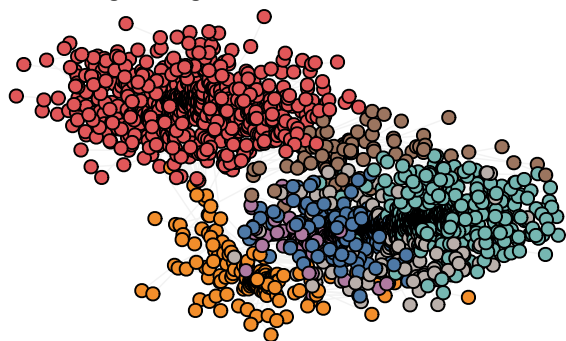**A**

**TCGA BLCA, significant mutations**

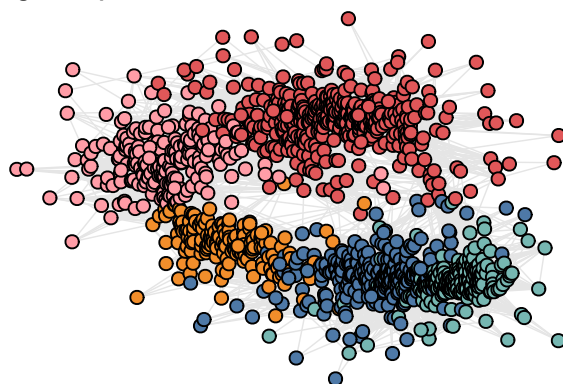#1: n = 119    #2: n = 117    #3: n = 169    cohort: n = 405
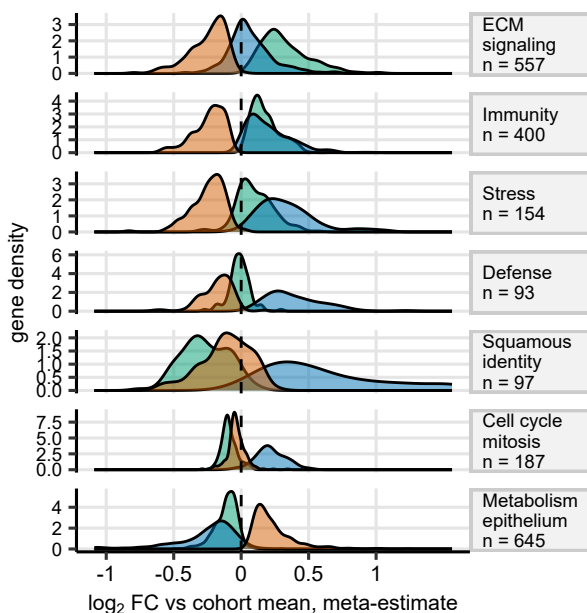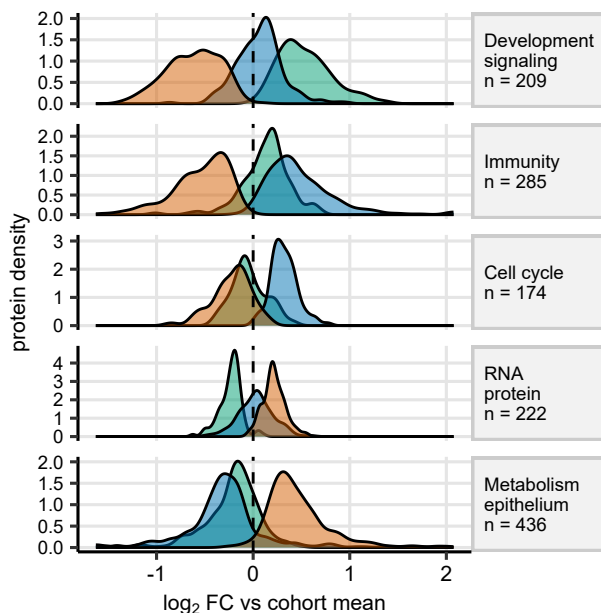
| | #1 | #2 | #3 |
|---|---|---|---|
| TP53 | 49% | 63% | 40% |
| KDM6A | 24% | 20% | 32% |
| RB1 | 21% | 26% | 12% |
| FGFR3 | 5.9% | 7.7% | 25% |
| STAG2 | 12% | 8.5% | 19% |
| BIRC6 | 7.6% | 18% | 14% |
| ELF3 | 9.2% | 10% | 18% |
| SYNE2 | 13% | 18% | 8.3% |
| FAT3 | 11% | 6.8% | 16% |
| LRP2 | 14% | 6% | 10% |
| AHNAK | 6.7% | 18% | 7.1% |

cancer sample

% of samples

WT
mutated

**B**

**Common regulated genes**

gene community
- Immunity
- ECM, signaling
- Stress
- Cell cycle, mitosis
- Metabolism, epithelium
- Squamous identity
- Defense

**Gene communities, differential expression**

ECM signaling n = 557
Immunity n = 400
Stress n = 154
Defense n = 93
Squamous identity n = 97
Cell cycle mitosis n = 187
Metabolism epithelium n = 645

gene density

log$_2$ FC vs cohort mean, meta-estimate

**C**

**Regulated proteins, Groeneveld 2024**

protein community
- RNA, protein
- Development, signaling
- Metabolism, epithelium
- Cell cycle
- Immunity

**Protein communities, differential expression**

Development signaling n = 209
Immunity n = 285
Cell cycle n = 174
RNA protein n = 222
Metabolism epithelium n = 436

protein density

log$_2$ FC vs cohort mean

#1   #2   #3