```
                    ┌─────────────────────────────┐
                    │   Publicly-available        │
                    │   DNA microarray datasets   │
                    │   (GEO, ArrayExpress)       │
                    └─────────────────────────────┘
                               │        Selected for
                               │        • Affymetrix platform
                               │        • Accurate sample annotation
                               ▼        • Presence of data from normal tissue  controls
                    ┌─────────────────────────────┐
                    │   Four datasets selected    │
                    │ (Cifola, Gumz, Lenburg, Yusenko) │
                    └─────────────────────────────┘
                               │    • Log₂ transformation
                               │    • Normalization
                               │    • Standardization
                               │      (e.g. removal of probe IDs
                               ▼       not mapped to genes)
                         ┌──────────────┐
                         │  MergeMaid   │
                         └──────────────┘
                               │
                               ▼
                    ┌─────────────────────────────┐
                    │       Meta-analysis         │
                    │   (RankProd method)         │
                    └─────────────────────────────┘
```

- Log$_2$ transformation
- Normalization
- Standardization
  (e.g. removal of probe IDs
   not mapped to genes)

Selected for
- Affymetrix platform
- Accurate sample annotation
- Presence of data from normal tissue controls

Publicly-available
DNA microarray datasets
(GEO, ArrayExpress)

Four datasets selected
(Cifola, Gumz, Lenburg, Yusenko)

MergeMaid

Meta-analysis
(RankProd method)

Curated list
of NF-κB targets

'NF-κB signature'

TCGA data

Survival analysis

Ingenuity
Pathways
Analysis

Correlation with *VHL*
mutational status