

| <i>Task</i> | Number of genes common in X% of discovered signatures | | | | | |
|---|---|-----|-----|-----|-----|------|
| | 50% | 60% | 70% | 80% | 90% | 100% |
| <i>Lung Cancer Diagnosis</i> | 4 | 0 | 0 | 0 | 0 | 0 |
| <i>Lung Cancer Subtype Classification</i> | 5 | 0 | 0 | 0 | 0 | 0 |
| <i>Breast Cancer Subtype Classification</i> | 15 | 11 | 4 | 1 | 0 | 0 |
| <i>Breast Cancer 5 Yr. Prognosis</i> | 85 | 85 | 84 | 84 | 84 | 1 |
| <i>Glioma Subtype Classification</i> | 48 | 48 | 48 | 47 | 41 | 0 |
| <i>Leukemia 5 Yr. Prognosis</i> | 23 | 23 | 23 | 20 | 1 | 0 |

Table S5: Number of common genes in 50%, 60%, ..., 100% of signatures discovered by TIE* algorithm for each dataset.