|  |
| --- |
| **Table S6. Summary table of metastatic tumor mRNA expression signature analysis in TCGA non-small cell lung cancer in human patients** |
|  |  |  |  |
| **Lung metastases genes from genome-wide and minipool CRISPR screens with multiple sgRNA validation** (12 genes from Figures 4G, 5D, and 7D ) | **LUAD** | **LUSC** | *See heatmap in Fig S5D* |
| Upregulated in metastatic tumor vs non metastatic tumor | 3 | 3 |
| Downregulated in metastatic tumor vs non metastatic tumor | 9 | 9 |
| Percent of genes downregulated in metastatic tumor vs non metastatic tumor | 75.0% | 75.0% |
|  |  |  |  |
|  |  |  |  |
| **Lung metastasis CRISPR screen top hits in minipool validation** (all 43 genes in Validation Minipool with human orthologs) | **LUAD** | **LUSC** |  |
| Upregulated in metastatic tumor vs non metastatic tumor | 14 | 17 |  |
| Downregulated in metastatic tumor vs non metastatic tumor | 29 | 26 |  |
| Percent of genes downregulated in metastatic tumor vs non metastatic tumor | 67.4% | 60.5% |  |
|  |  |  |  |
|  |  |  |  |
|  |  |  |  |
| **Lung metastasis CRISPR screen top hits by MPR** (67 genes with MPR > 1 in at least 2 mice) | **LUAD** | **LUSC** | *See heatmap in Fig S5E* |
| Upregulated in metastatic tumor vs non metastatic tumor | 24 | 24 |
| Downregulated in metastatic tumor vs non metastatic tumor | 38 | 38 |
| Percent of genes downregulated in metastatic tumor vs non metastatic tumor | 61.3% | 61.3% |