

Table S1: Summary of data sets used in this study

No	Data set ID	Omics data type	Platform	No. of stage I LUAD patients	Patient ratio (S1/S2)	References
1	FUSCC	Transcriptomic	Illumina HiSeq X	83	1.52	-
2	GSE31210	Transcriptomic	Affymetrix Human Genome U133 Plus 2.0 Array	168	0.89	1,2
3	GSE13213	Transcriptomic	Agilent-014850 Whole Human Genome Microarray 4x44K G4112F	79	1.32	3
4	GSE11969	Transcriptomic	Agilent Homo sapiens 21.6K custom array	47	1.94	4,5
5	GSE50081	Transcriptomic	Affymetrix Human Genome U133 Plus 2.0 Array	92	0.56	6
6	GSE68465	Transcriptomic	Affymetrix Human Genome U133A Array	108	1.16	7
7	GSE42127	Transcriptomic	Illumina HumanWG-6 v3.0 expression beadchip	89	0.68	8,9
8	GSE26939	Transcriptomic	Agilent-UNC-custom-4X44K	62	1.48	10
9	GSE72094	Transcriptomic	Rosetta/Merck Human RSTA Custom Affymetrix 2.0 microarray	265	0.74	11
10	GSE30219	Transcriptomic	Affymetrix Human Genome U133 Plus 2.0 Array	71	0.54	12
11	GSE41271	Transcriptomic	Illumina HumanWG-6 v3.0 expression beadchip	100	0.67	13-16
12	TCGA	Genomic	Illumina HiSeq 2000	232	-	17
12	TCGA	Transcriptomic	Illumina HiSeq 2000	232	1.13	17
13	Gillette et al	Genomic	Illumina HiSeq4000/ HiSeqX	55	-	18
13	Gillette et al	Transcriptomic	Illumina HiSeq4000	55	0.28	18
13	Gillette et al	Proteomics	LC-MS/MS	55	-	18
13	Gillette et al	Phosphorylated proteomics	LC-MS/MS	55	-	18
14	Xu et al	proteomics	LC-MS/MS	51	-	19

References

1. Okayama, H., *et al.* Identification of genes upregulated in ALK-positive and EGFR/KRAS/ALK-negative lung adenocarcinomas. *Cancer research* **72**, 100-111 (2012).
2. Yamauchi, M., *et al.* Epidermal growth factor receptor tyrosine kinase defines critical prognostic genes of stage I lung adenocarcinoma. *PLoS One* **7**, e43923 (2012).
3. Tomida, S., *et al.* Relapse-related molecular signature in lung adenocarcinomas identifies patients with dismal prognosis. *Journal of clinical oncology : official journal of the American Society of Clinical Oncology* **27**, 2793-2799 (2009).
4. Matsuyama, Y., *et al.* Proteasomal non-catalytic subunit PSMD2 as a potential therapeutic target in association with various clinicopathologic features in lung adenocarcinomas. *Molecular carcinogenesis* **50**, 301-309 (2011).
5. Takeuchi, T., *et al.* Expression profile-defined classification of lung adenocarcinoma shows close relationship with underlying major genetic changes and clinicopathologic behaviors. *Journal of clinical oncology : official journal of the American Society of Clinical Oncology* **24**, 1679-1688 (2006).
6. Der, S.D., *et al.* Validation of a histology-independent prognostic gene signature for early-stage, non-small-cell lung cancer including stage IA patients. *Journal of thoracic oncology : official publication of the International Association for the Study of Lung Cancer* **9**, 59-64 (2014).
7. Shedden, K., *et al.* Gene expression-based survival prediction in lung adenocarcinoma: a multi-site, blinded validation study. *Nature medicine* **14**, 822-827 (2008).
8. Tang, H., *et al.* A 12-gene set predicts survival benefits from adjuvant chemotherapy in non-small cell lung cancer patients. *Clinical cancer research : an official journal of the American Association for Cancer Research* **19**, 1577-1586 (2013).
9. Hight, S.K., *et al.* An in vivo functional genomics screen of nuclear receptors and their co-regulators identifies FOXA1 as an essential gene in lung tumorigenesis. *Neoplasia* **22**, 294-310 (2020).
10. Wilkerson, M.D., *et al.* Differential pathogenesis of lung adenocarcinoma subtypes involving sequence mutations, copy number, chromosomal instability, and methylation. *PLoS One* **7**, e36530 (2012).
11. Schabath, M.B., *et al.* Differential association of STK11 and TP53 with KRAS mutation-associated gene expression, proliferation and immune surveillance in lung adenocarcinoma. *Oncogene* **35**, 3209-3216 (2016).
12. Rousseaux, S., *et al.* Ectopic activation of germline and placental genes identifies aggressive metastasis-prone lung cancers. *Science translational medicine* **5**, 186ra166 (2013).
13. Girard, L., *et al.* An Expression Signature as an Aid to the Histologic Classification of Non-Small Cell Lung Cancer. *Clinical cancer research : an official journal of the American Association for Cancer Research* **22**, 4880-4889 (2016).
14. Sato, M., *et al.* Human lung epithelial cells progressed to malignancy through specific oncogenic manipulations. *Mol Cancer Res* **11**, 638-650 (2013).
15. Parra, E.R., *et al.* Image Analysis-based Assessment of PD-L1 and Tumor-Associated Immune Cells Density Supports Distinct Intratumoral Microenvironment Groups in Non-small Cell Lung Carcinoma Patients. *Clinical cancer research : an official journal of the American Association for Cancer Research* **22**, 6278-6289 (2016).
16. Riquelme, E., *et al.* VEGF/VEGFR-2 upregulates EZH2 expression in lung adenocarcinoma cells and EZH2 depletion enhances the response to platinum-based and VEGFR-2-targeted therapy. *Clinical cancer research : an official journal of the American Association for Cancer Research* **20**, 3849-3861 (2014).
17. Comprehensive molecular profiling of lung adenocarcinoma. *Nature* **511**, 543-550 (2014).
18. Gillette, M.A., *et al.* Proteogenomic Characterization Reveals Therapeutic Vulnerabilities in Lung Adenocarcinoma. *Cell* **182**, 200-225.e235 (2020).
19. Xu, J.Y., *et al.* Integrative Proteomic Characterization of Human Lung Adenocarcinoma. *Cell* **182**, 245-261.e217 (2020).