

Supplementary Files

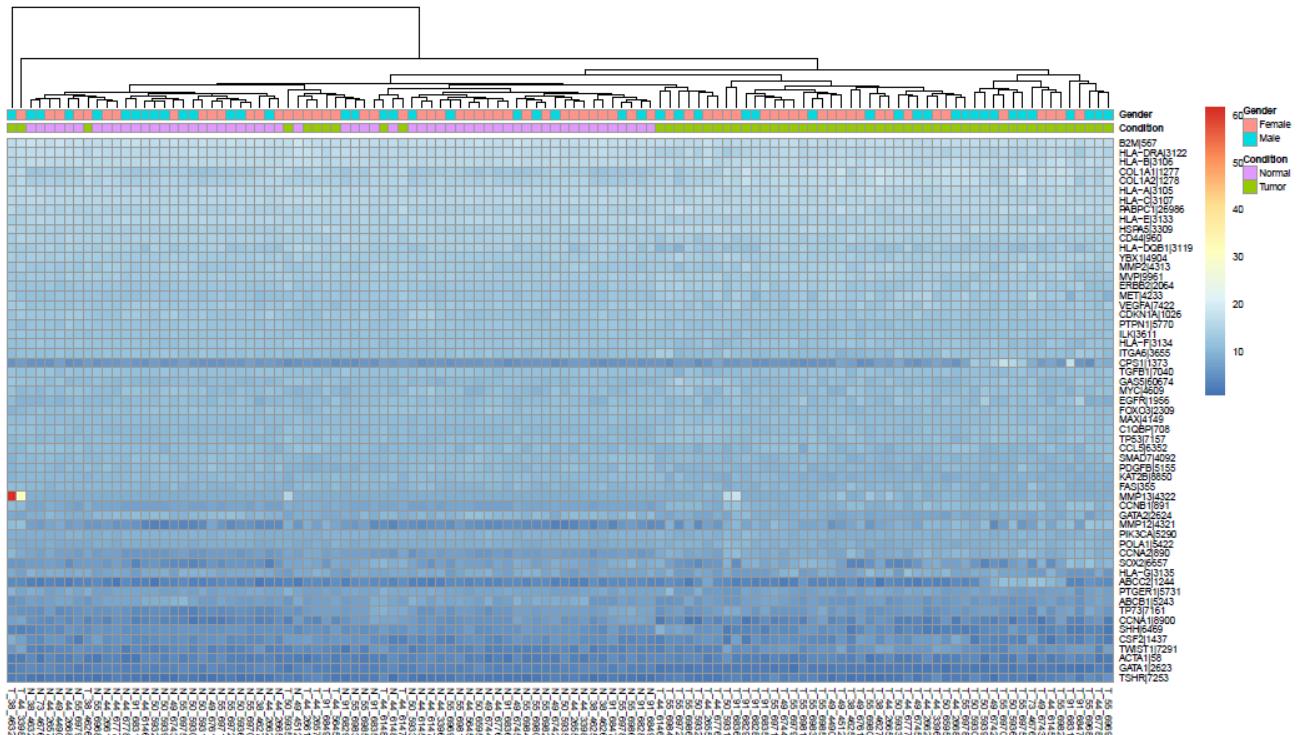
Table S1. Differential Expression Analysis Result. The genes which have p-adjusted value < 0.05 are chosen as differentially expressed. 43 genes are differentially expressed. They are arranged based on the logarithmic fold change in ascending order.

Gene	log2FoldChange	p- adjusted value
GATA1 2623	-1.914759614	1.86E-19
ABCB1 5243	-1.705109849	4.54E-14
GATA2 2624	-1.667103551	7.16E-21
CCNA1 8900	-1.337269496	0.000364571
HLA-E 3133	-0.980943696	3.17E-38
PDGFB 5155	-0.963030858	3.98E-10
KAT2B 8850	-0.937627985	9.12E-18
SMAD7 4092	-0.874579571	1.32E-19
HLA-DRA 3122	-0.852962031	1.96E-08
PTPN1 5770	-0.714748149	2.69E-14
B2M 567	-0.688225643	1.33E-12
CD44 960	-0.63673483	4.31E-10
HLA-DQB1 3119	-0.561264766	0.014170305
CDKN1A 1026	-0.479333565	0.001535024
FOXO3 2309	-0.349793768	0.000882473
TGFB1 7040	-0.294813372	0.001741765
ILK 3611	-0.232509057	0.00316254
MAX 4149	0.211283538	2.34E-05
YBX1 4904	0.224609272	0.030314272
HLA-A 3105	0.238804317	0.018468197
MVP 9961	0.284497267	0.007806657
POLA1 5422	0.793678394	2.27E-13
CSF2 1437	0.846481653	0.006851407
C1QBP 708	0.855811847	8.97E-14
TP53 7157	0.888494843	4.53E-16
MMP2 4313	0.906829078	2.26E-09
ERBB2 2064	0.966997199	4.12E-12
EGFR 1956	1.088296524	3.16E-07
GAS5 60674	1.189383453	1.09E-10
PABPC1 26986	1.259791354	2.56E-31
HSPA5 3309	1.311099146	2.28E-43
MET 4233	1.361412158	2.26E-12
SOX2 6657	1.517231518	0.000108096
COL1A2 1278	2.176929069	1.35E-26

TSHR 7253	2.363801545	2.21E-14
TWIST1 7291	2.711740907	2.39E-21
CCNA2 890	3.29639404	1.43E-67
CCNB1 891	3.396819171	8.27E-82
COL1A1 1277	3.485635594	1.65E-45
CPS1 1373	4.413652361	2.54E-29
MMP12 4321	4.816105537	4.63E-38
ABCC2 1244	5.656440824	3.99E-41
MMP13 4322	5.817902101	2.46E-36

Figure S1.

A. Unsupervised hierarchical clustering between LUAD samples before filtering



B. PCA Plot LUAD sample before filtering

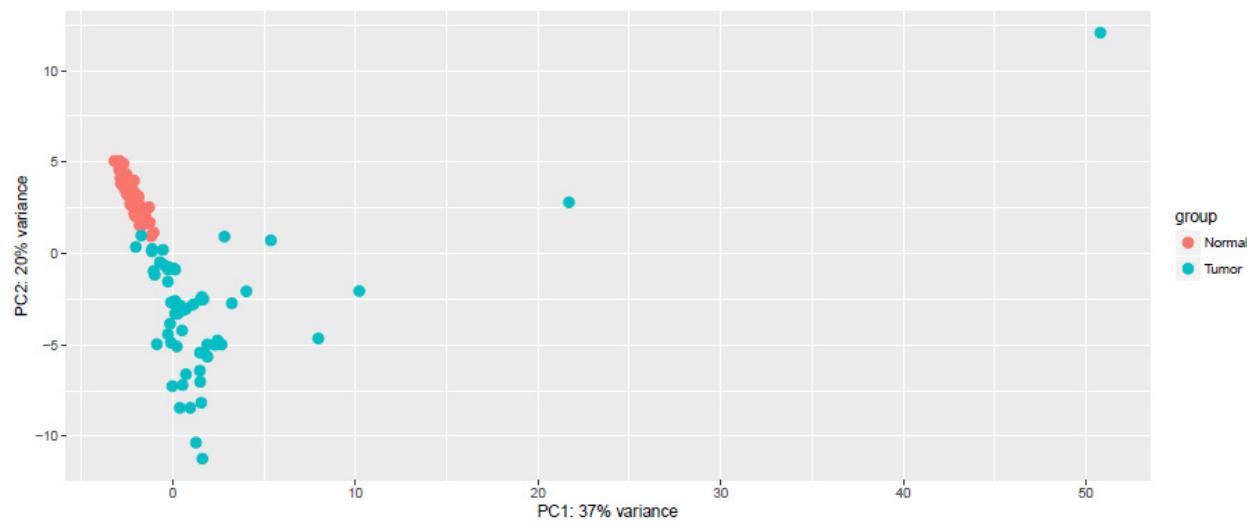


Figure S1. A. Unsupervised clustering for the LUAD samples. Column represents the sample and row represents the gene. It shows the samples are not clustered based on their group, as overlap

among the tumor and normal samples are seen. B. PCA plot shows that the principle components cannot distinguish the normal and tumor samples.