Fig. S6

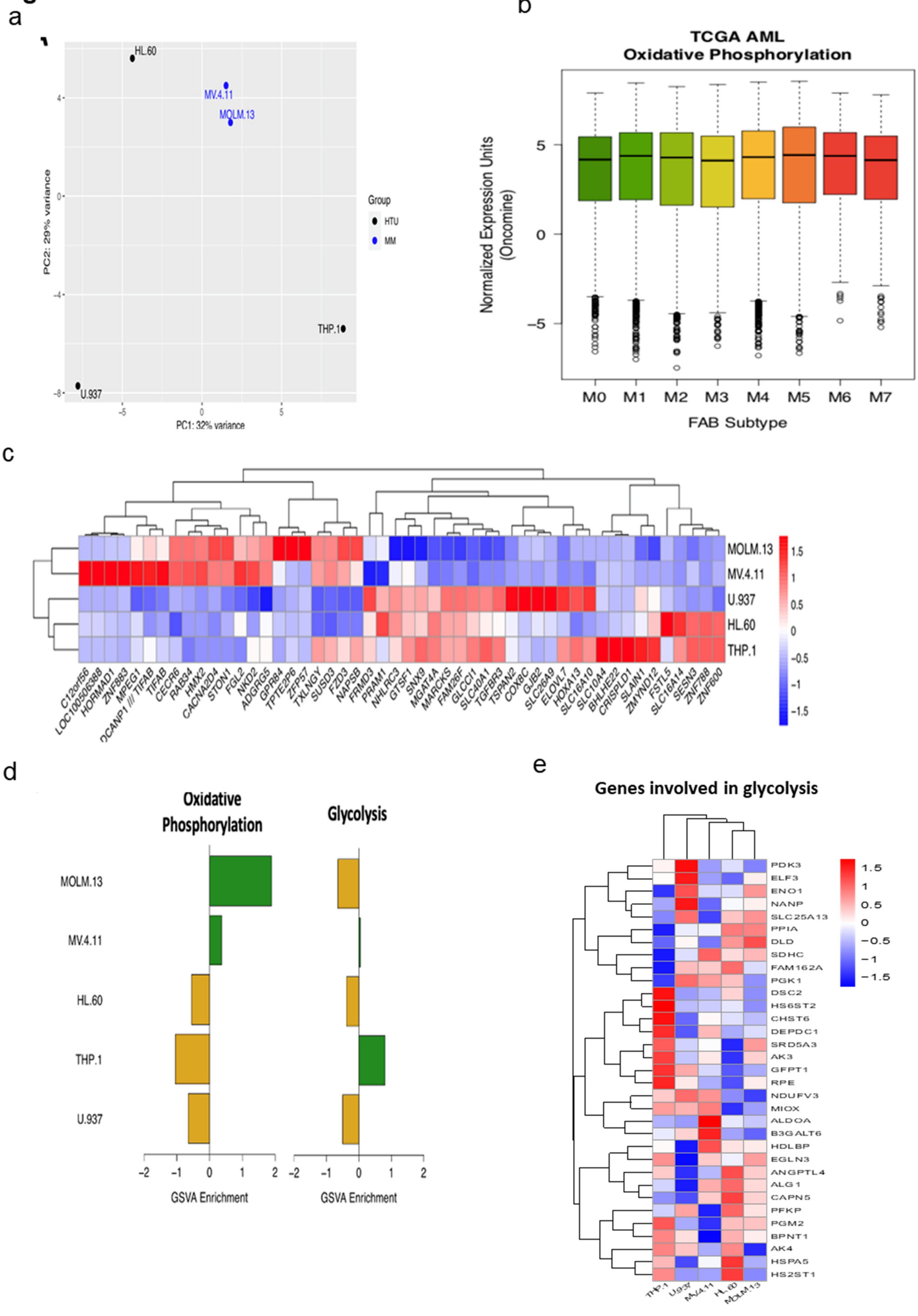
a
HL.60
MV.4.11
MOLM.13
THP.1
U.937
PC2: 29% variance
PC1: 32% variance
4
0
-4
-8
-5
0
5
Group
HTU
MM
b
TCGA AML
Oxidative Phosphorylation
Normalized Expression Units (Oncomine)
5
0
−5
M0
M1
M2
M3
M4
M5
M6
M7
FAB Subtype
c
MOLM.13
MV.4.11
U.937
HL.60
THP.1
C12orf56
LOC100506388
HORMAD1
ZNF883
MPEG1
DCANP1 /// TIFAB
TIFAB
CECR6
RAB34
HMX2
CACNA2D4
STON1
FGL2
NKD2
ADGRG5
GPR84
TPTE2P6
ZFP57
TXLNGY
SUSD3
FZD3
NAPSB
FRMD3
PRAM1
NHLRC3
GTSF1
SNX9
MGAT4A
MARCKS
FAM26F
GLCCI1
SLC40A1
TGFBR3
TSPAN2
COX8C
GJB2
SLC26A9
ELOVL7
HOXA13
SLC16A10
SLC10A4
BHLHE22
CRISPLD1
SLAIN1
ZMYND12
FSTL5
SLC16A14
SESN3
ZNF788
ZNF600
1.5
1
0.5
0
-0.5
-1
-1.5
d
Oxidative Phosphorylation
Glycolysis
MOLM.13
MV.4.11
HL.60
THP.1
U.937
−2
−1
0
1
2
GSVA Enrichment
e
Genes involved in glycolysis
PDK3
ELF3
ENO1
NANP
SLC25A13
PPIA
DLD
SDHC
FAM162A
PGK1
DSC2
HS6ST2
CHST6
DEPDC1
SRD5A3
AK3
GFPT1
RPE
NDUFV3
MIOX
ALDOA
B3GALT6
HDLBP
EGLN3
ANGPTL4
ALG1
CAPN5
PFKP
PGM2
BPNT1
AK4
HSPA5
HS2ST1
THP.1
U.937
MV.4.11
HL.60
MOLM.13
1.5
1
0.5
0
−0.5
−1
−1.5

Fig. S6. Inherent differences in AML cell line OXPHOS gene expression. a, c-e. Gene expression datasets for MOLM-13, MV4-11, THP-1, HL-60, and U937 AML cell lines were recovered from the CCLE database (www.broadinstitute.org/ccle). Expression levels were RMA normalized. Glycolytic and OXPHOS pathways were interrogated. PCA plot is shown in panel a. An unsupervised analysis of the top 50 most variable genes is shown as a heat map in panel c. Glycolysis and OXPHOS z-score–scaled gene set variation analysis enrichment scores are shown in panel d. Panel e shows the heat map of the glycolytic genes. **b**. Gene expression datasets for primary AML cells and TCGA (The Cancer Genome Atlas) data were recovered from the Oncomine database. Levels of the OXPHOS gene set were assessed in different AML FAB subtypes (M0-M7).