Wang/Xu Figure S2

a

H   M

CD45/Cd45
C1QA/C1qa
HBE1/Hba-x
CD71/Cd71
VEGFR3/Vegfr3
PDGFRA/Pdgfra
PDPN/Pdpn
HNF4A/Hnf4a

Cell lineage family
Endoderm-derived lineages
Erythroid lineages
Non-erythroid hematopoietic lineages
Mesoderm-derived non-hematopoietic lineages

b

R=0.64

log(centralities of mouse genes)
log(centralities of human genes)

c

Hepatoblast/Hepatocyte   Erythroid progenitor

H

M

tSNE 2
tSNE 1

Eigengene

Gene expression
High
Low

d

Hepatoblast/Hepatocyte   Erythroid progenitor

NRN1/Nrn1

ORM1/Orm1

LDHB/Ldhb

Correlation to mouse eigengene
Correlation to human eigengene

e

ORM1   NRN1   LDHB

H

Orm1   Nrn1   Ldhb

M

tSNE 2
tSNE 1

Gene expression
High
Low
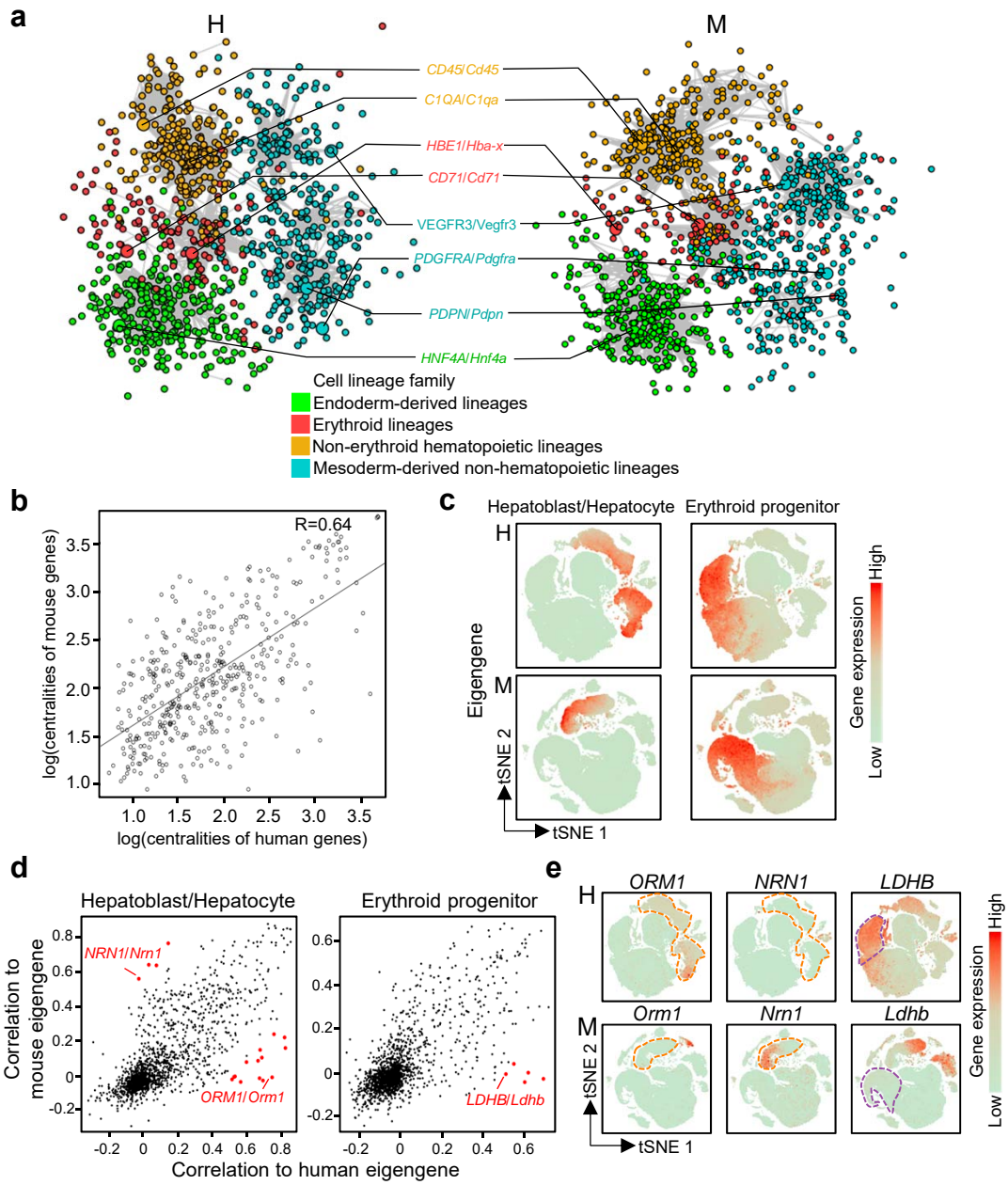
Supplementary information, Fig. S2 Cross-species analysis of weighted gene co-expression networks and gene expression patterns. a Weighted gene co-expression networks (WGCNs) of human (H) and mouse (M) cells. Colored dots indicate differentially expressed genes among the four cell lineage families within the species. Polylines point out the marker genes among the four cell lineage families. **b** Correlation between the centralities of human and mouse WGCNs. **c** Eigengenes of hepatoblasts/hepatocytes and erythroid progenitors in human (H) and mouse (M) samples. **d** Correlations of genes with human or mouse eigengenes associated with hepatoblasts/hepatocytes or erythroid progenitors. Red dots indicate genes for which the correlation to one species was 0.5 higher than the other species and the correlation itself was higher than 0.5. **e** t-SNE plots showing the expression levels of three genes identified in **d**.