Supplementary information, Fig. S8

a NSC2(G1/S) trajectory

T0　T1　T2　End　EndSVZ

Temporal patterns

HMGA1
IDH2
SFRP1
MAP2
STMN2
SOX9
NFIA
PTPRZ1
FABP7
JUN
CST3
EGFR
PDGFRA
SOX10
C1QL1
OLIG2
FOS
ASCL1

Z−score
2
0
−2

b NSC-like cells

T0_NSC　T1_Neuron　T1_AC　T2_AC　End_OC

IDH2
ID3
SFRP1
HMGA1
NHLH1
NFIA
STMN2
PTN
PTPRZ1
SOX2
MAP2
FABP7
VIM
EGFR
SPARCL1
CST3
OLIG1
C1QL1
PDGFRA
FOS
OLIG2

Standardized expression
−2　0　2

c

GBM GSC core TF　　GBM stemness score　　Oligodendroglioma stemness score　　IDH-mut glioma stemness score

Meta-module score

Pseudotime

T0　T1　T2　End　End SVZ

d

Pediatric human GBM (Neftel et al.)

Cluster　0　1　2*　3　4　5　6　7*

Expression module
G2/M
G1/S
NSC_cc
NSC_ncc
NSC_adult
AC
OPC/OC
NB/Neuron

Adult human GBM (Neftel et al.)

Cluster　0　1　2　3　4*　5　6*　7　8　9　10

Expression module
G2/M
G1/S
NSC_cc
NSC_ncc
NSC_adult
AC
OPC/OC
NB/Neuron

Meta-module score
2
0
−2

e

Adult human GBM (Wang et al.)

Cluster　0　1　2　3　4*　5　6　7-12

Expression module
G2/M
G1/S
NSC_cc
NSC_ncc
NSC_adult
AC
OPC/OC
NB/Neuron

Adult human GBM (Baduhri et al.)

Cluster　0　1　2　3　4*　5*　6-11

Expression module
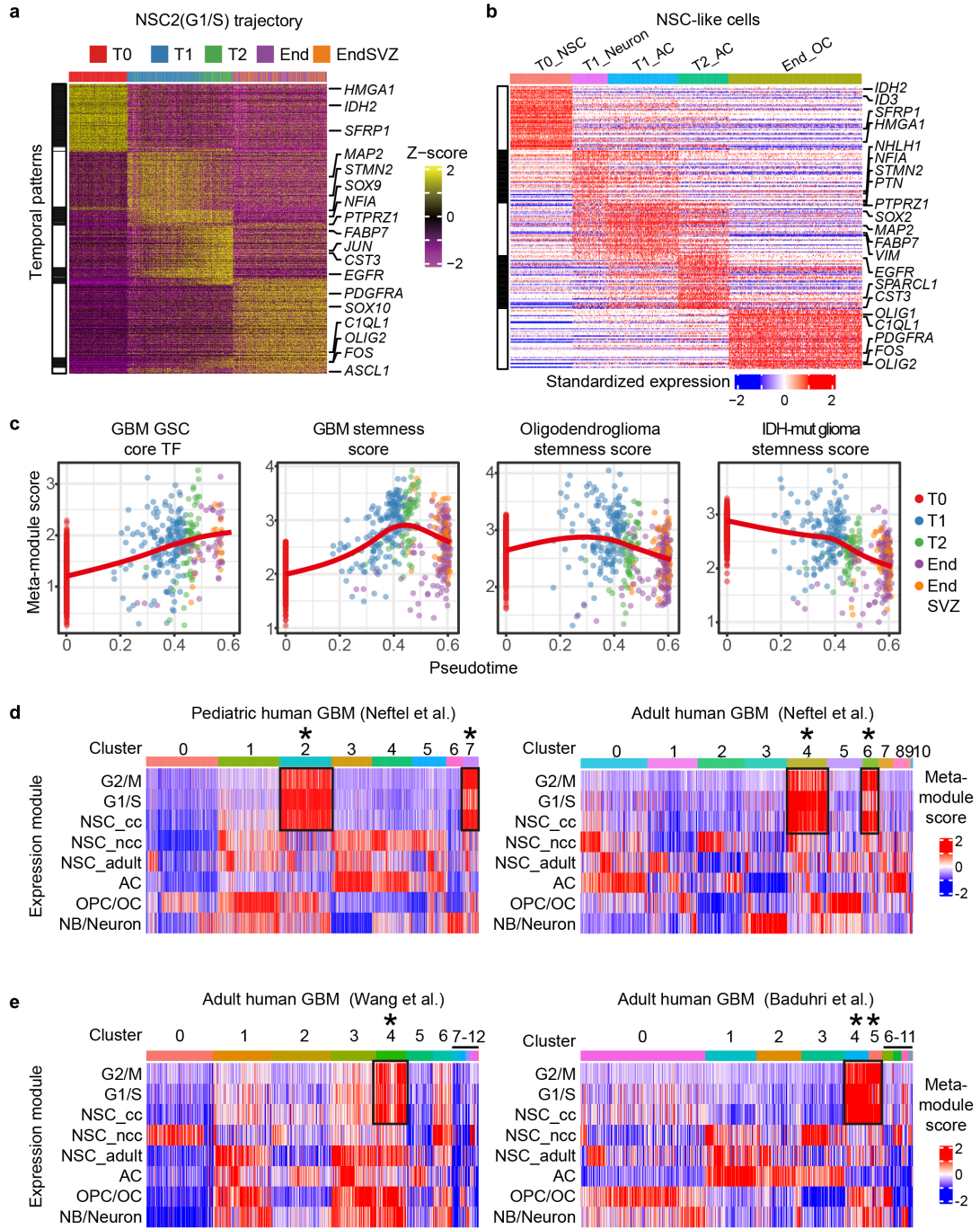G2/M
G1/S
NSC_cc
NSC_ncc
NSC_adult
AC
OPC/OC
NB/Neuron

Meta-module score
2
0
−2

Supplementary information, Fig. S8. Cell-type- and stage-specific signatures of NSC-like cells and their presence in human pediatric and adult GBM samples.

(**a**) Heatmap of gene expression cascades along the pseudotime of NSC2. Columns, pseudotime-ordered cells. Rows, genes. Colors in the top row indicate the actual sample time of each cell. Genes were clustered by their temporal expression patterns (left bars).

(**b**) The heatmap of DE genes in NSC-like cells located in different branches of the gliomagenesis tree (Figure **5a, c**).

(**c**) Trajectory plots of the meta-module score of published glioma stemness gene sets along the pseudotime of NSC1.

(**d, e**) Heatmap of the meta-module scores for single tumor cells of pediatric and adult GBMs from Neftel et al. (**d**), Wang et al. and Baduhri et al. (**e**) studies. The cells clusters were defined by unsupervised clustering in UMAP. Asterisks, NSC-like subpopulations.