ENCODEC

DL

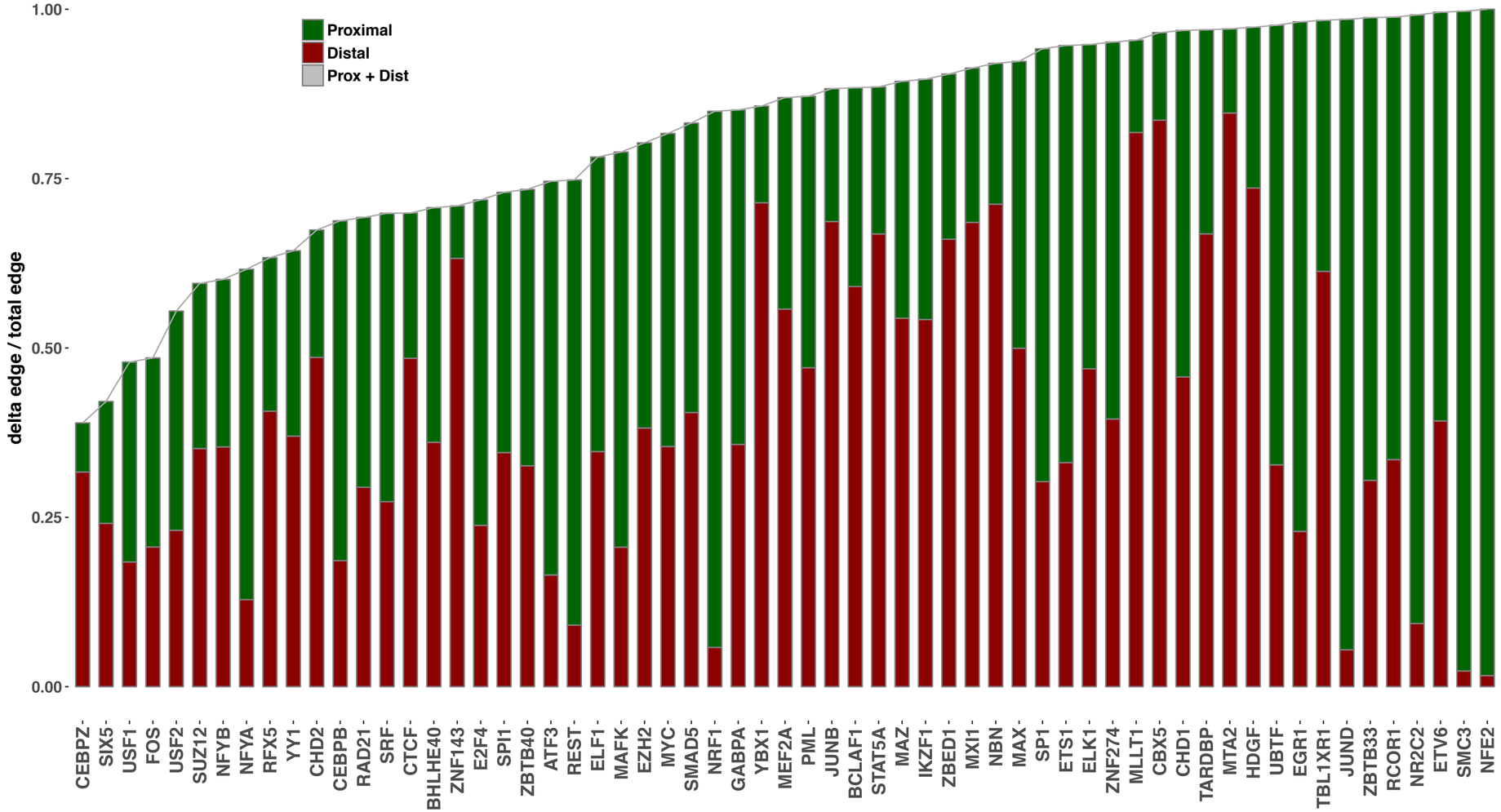
-- Ref 4.5 – Relationship of H1 to other stem cells --

3) One of the conclusions, deriving from the analysis of H1-hESC is the some cancer are “moving away from stemness”. However, while it is true that the cancer cells pattern diverge from the H1 cells, H1 is a human embryonic stem cells: although interesting, H1 may not necessarily be the best cells to compare with tumor phenotype. Authors should discuss/ defend of further elaborate on this approach. I believe that a key analysis should be done against other stem cells (like tissutal stem cells, etc.).

-- Ref 5.21 – Rewiring network --

16. In the tumor-normal network comparison, is the fraction of edge changes related to the total number of edges for a given TF? This analysis should further clearly state its null hypothesis (what changes are expected?). What happens when edges are randomly permuted?

Fraction of edge changes



Previous Analysis:

(G + L) / fullyConnected

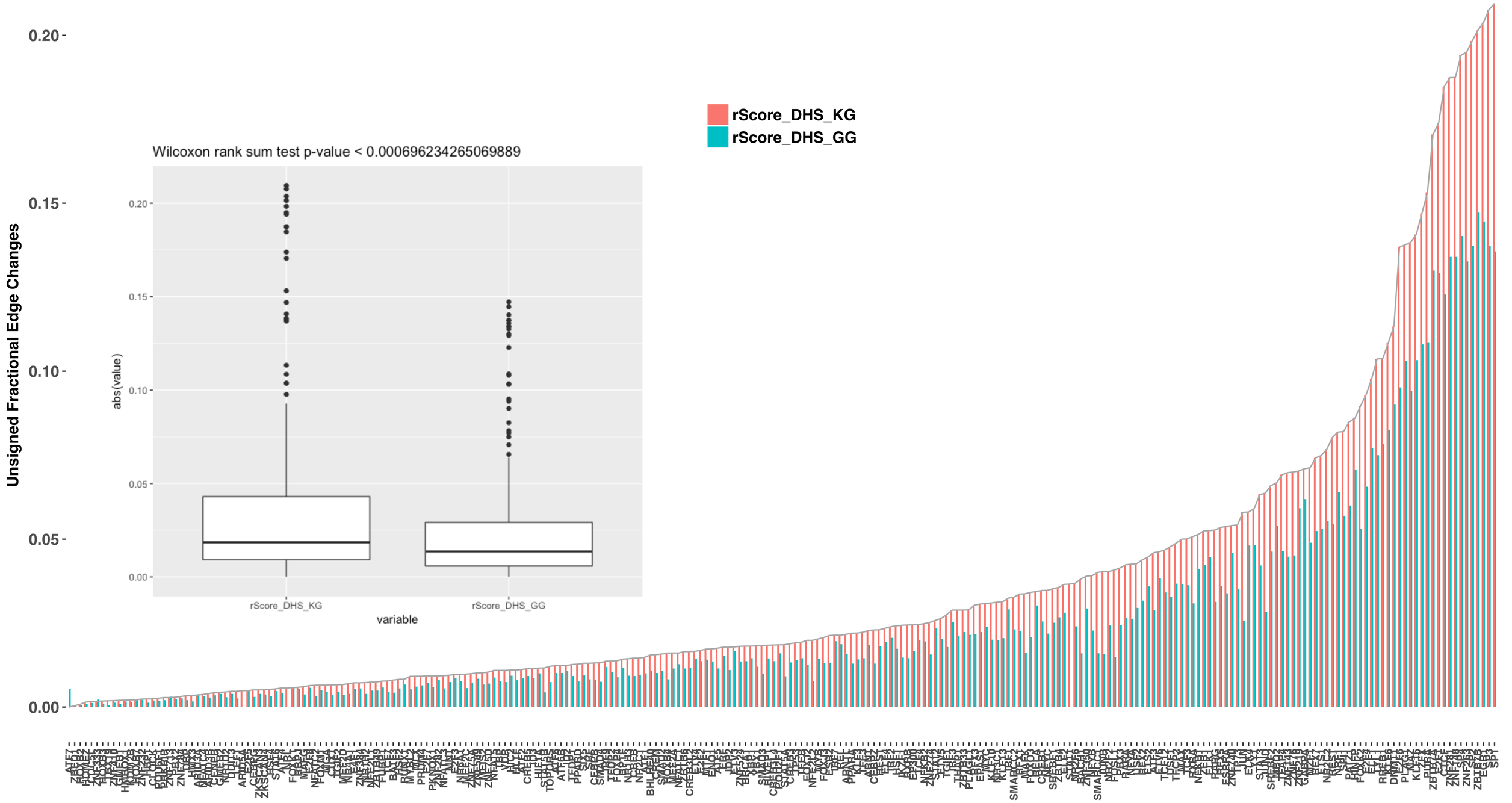
fullyConnected = nTF + nGENE - 1

New Analysis:

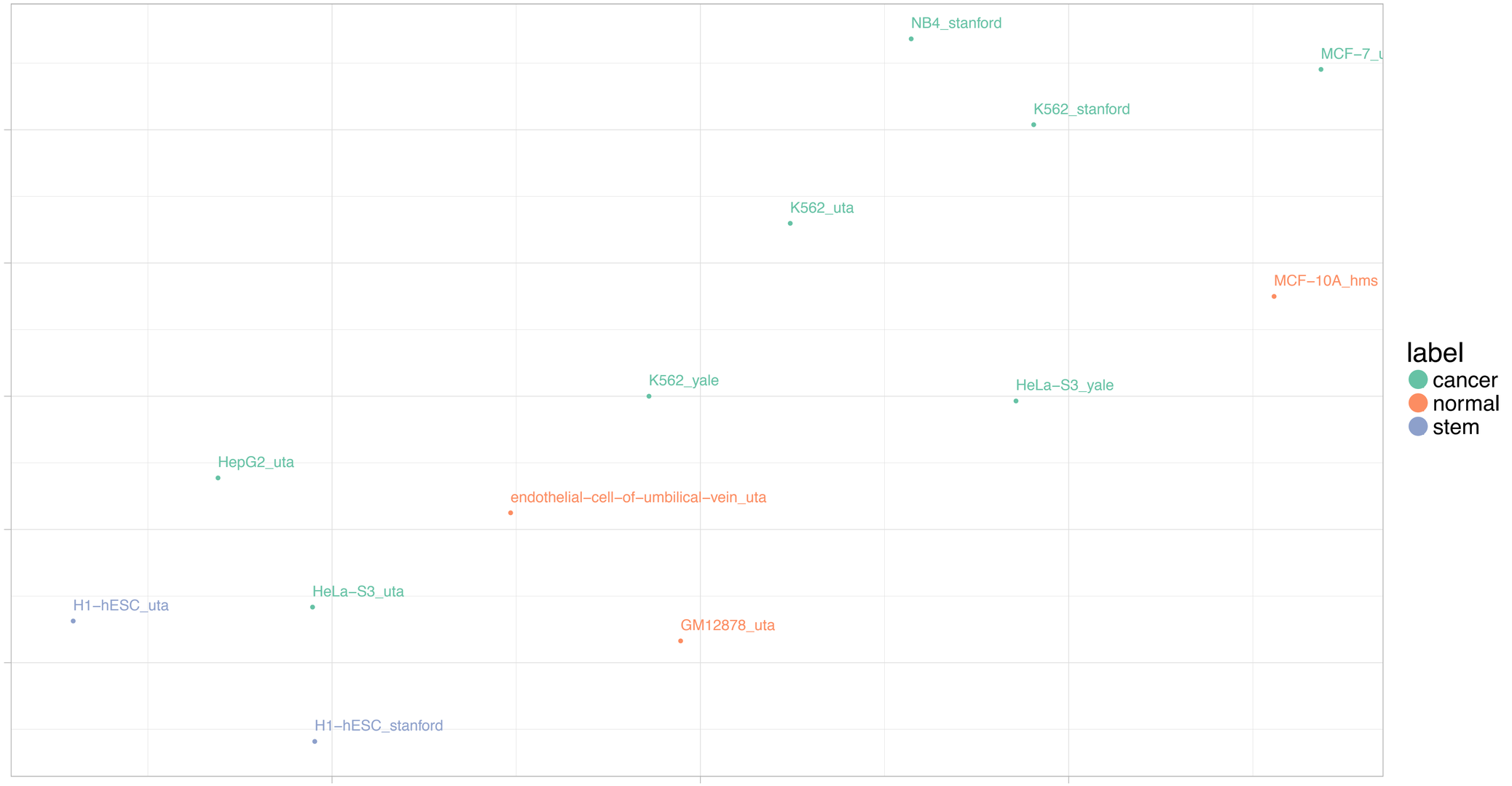
(G + L) / totalEdges

totalEdges varies TF to TF

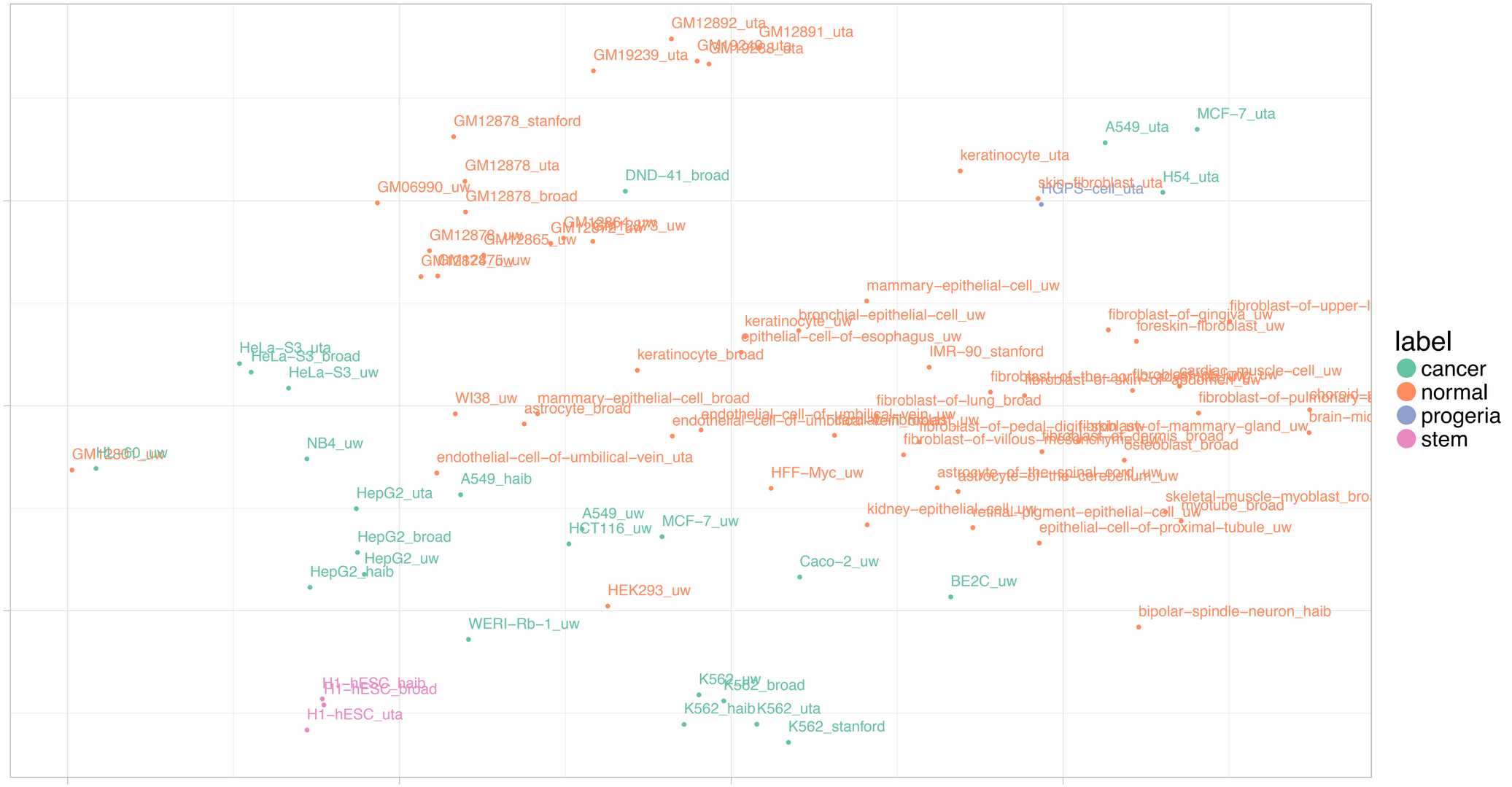
delta edge / total edge
1.0
0.5
0.0
−0.5
FracGain
FracLoss
FracEdgeChg
ZNF143
MTA2
CBX5
MLLT1
CEBPZ
YBX1
JUNB
NBN
HDGF
STAT5A
MXI1
ZBED1
CHD2
CTCF
TARDBP
BCLAF1
MEF2A
RFX5
TBL1XR1
MAZ
IKZF1
SUZ12
NFYB
YY1
SIX5
MAX
PML
BHLHE40
ELK1
SMAD5
EZH2
SPI1
CHD1
ZBTB40
ELF1
MYC
FOS
RAD21
GABPA
USF2
ZNF274
ETV6
SRF
USF1
ETS1
RCOR1
UBTF
E2F4
SP1
ZBTB33
CEBPB
MAFK
EGR1
ATF3
NFYA
REST
NR2C2
NRF1
JUND
SMC3
NFE2


rScore_DHS_KG
rScore_DHS_GG
Unsigned Fractional Edge Changes
0.20
0.15
0.10
0.05
0.00
Wilcoxon rank sum test p-value < 0.000696234265069889
abs(value)
rScore_DHS_KG
rScore_DHS_GG
variable

t−SNE: MYC


NB4_stanford
MCF−7_u
K562_stanford
K562_uta
MCF−10A_hms
K562_yale
HeLa−S3_yale
HepG2_uta
endothelial−cell−of−umbilical−vein_uta
HeLa−S3_uta
H1−hESC_uta
GM12878_uta
H1−hESC_stanford
label
cancer
normal
stem

t–SNE: CTCF

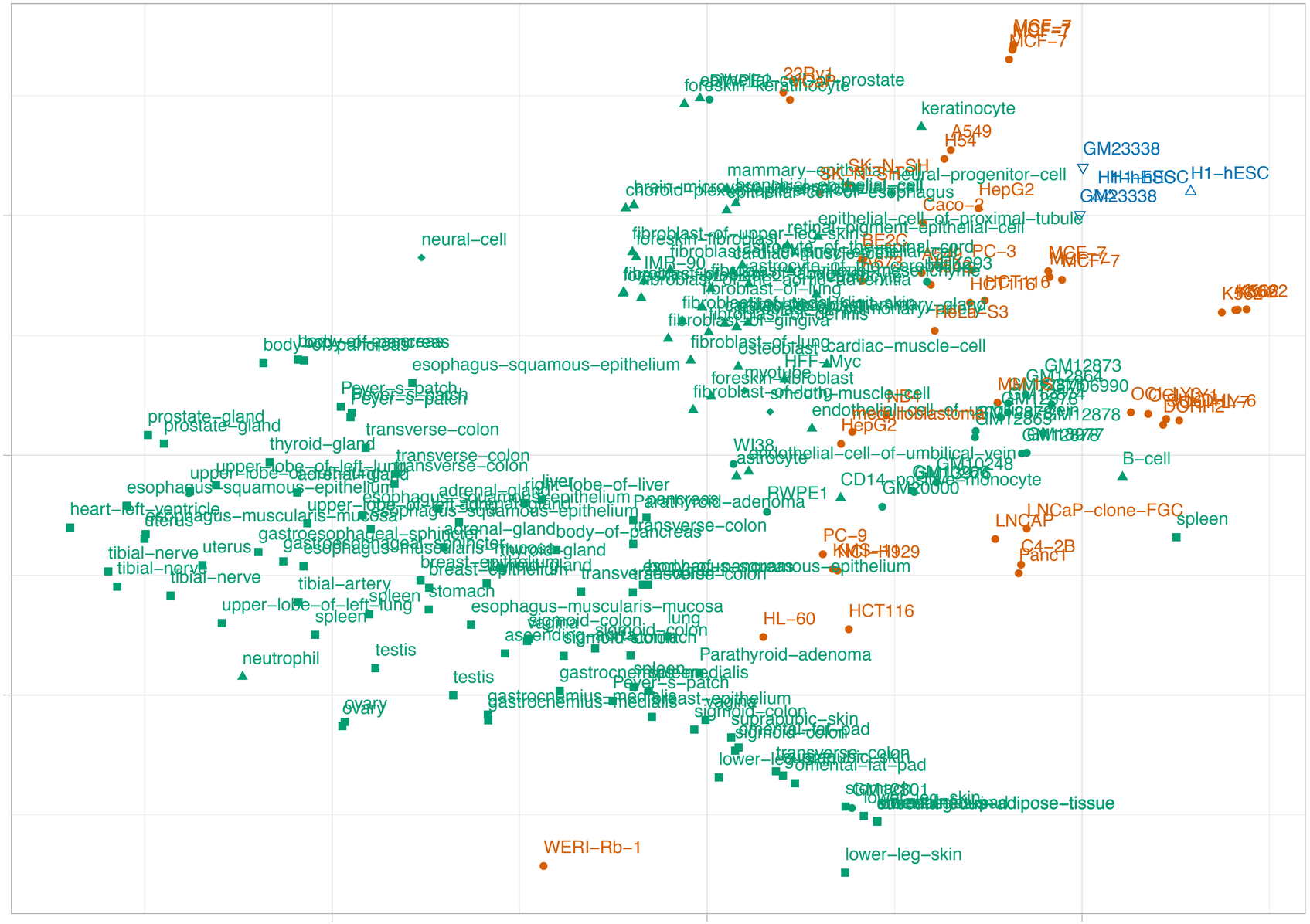

GM12892_uta
GM12891_uta
GM19239_uta
GM12878_stanford
A549_uta
MCF–7_uta
keratinocyte_uta
GM12878_uta
DND–41_broad
skin_fibroblast_uta
H54_uta
GM06990_uw
GM12878_broad
HGPS–cell_uta
GM12865_uw
mammary–epithelial–cell_uw
bronchial–epithelial–cell_uw
fibroblast–of–gingiva_uw
keratinocyte_uw
foreskin–fibroblast_uw
epithelial–cell–of–esophagus_uw
HeLa–S3_uta
HeLa–S3_broad
keratinocyte_broad
IMR–90_stanford
HeLa–S3_uw
cardiac_muscle–cell_uw
WI38_uw
mammary–epithelial–cell_broad
fibroblast–of–lung_broad
astrocyte_broad
fibroblast–of–pulmonary–
endothelial–cell–of–umbilical–vein_uw
brain–mic
fibroblast–of–mammary–gland_uw
NB4_uw
fibroblast–of–villous–mesenchyme_uw
osteoblast_broad
endothelial–cell–of–umbilical–vein_uta
HFF–Myc_uw
astrocyte–of–the–spinal–cord_uw
A549_haib
astrocyte–of–the–cerebellum_uw
HepG2_uta
skeletal–muscle–myoblast_bro
myotube_broad
kidney–epithelial–cell_uw
A549_uw
MCF–7_uw
HCT116_uw
epithelial–cell–of–proximal–tubule_uw
HepG2_broad
HepG2_uw
Caco–2_uw
HepG2_haib
BE2C_uw
HEK293_uw
bipolar–spindle–neuron_haib
WERI–Rb–1_uw
K562_broad
K562_haib
K562_uta
K562_stanford
H1–hESC_broad
H1–hESC_uta
label
cancer
normal
progeria
stem

ENCODEC

DL

CTCF

t–SNE: CTCF



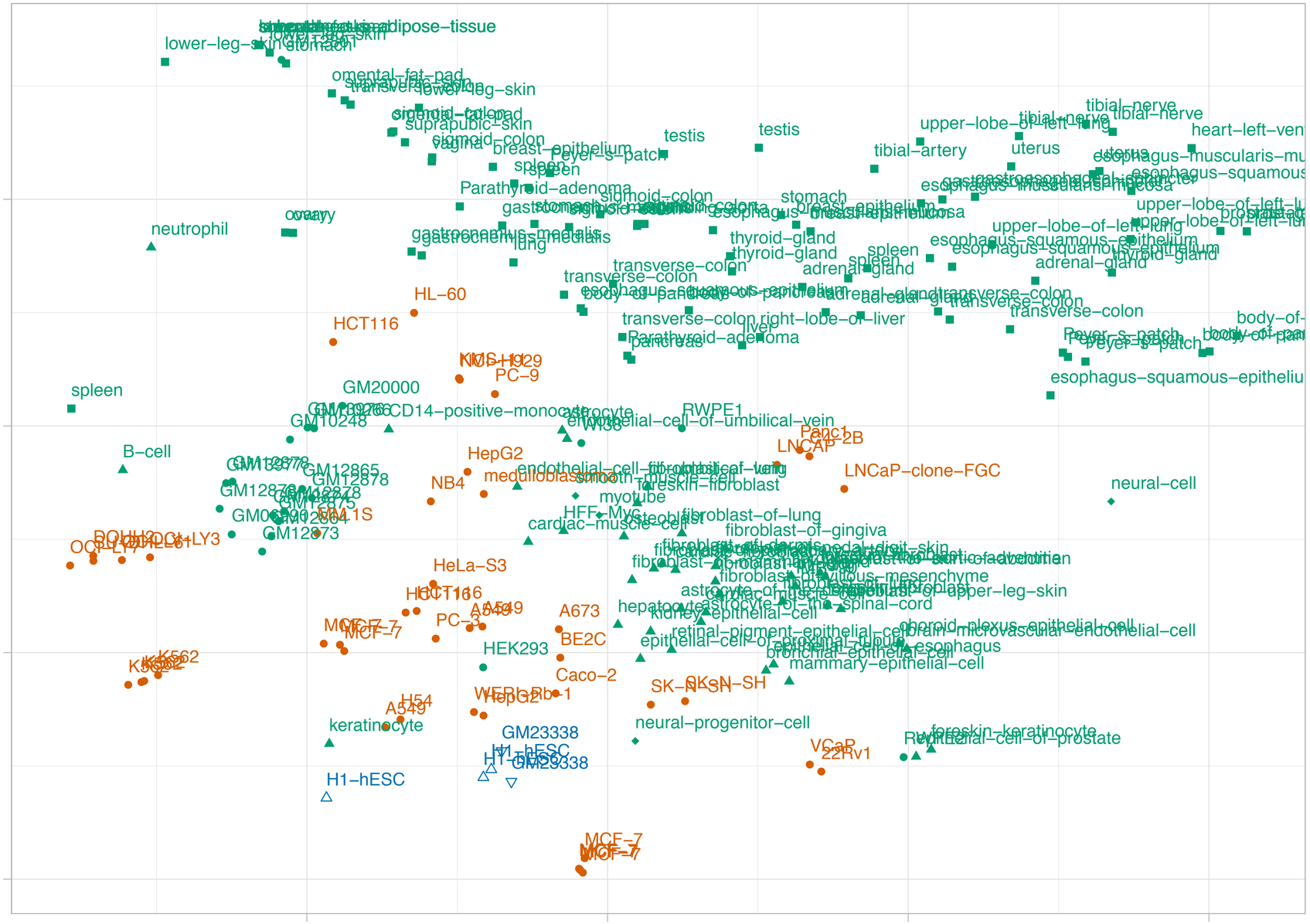
State

- cancer
- normal
- stem

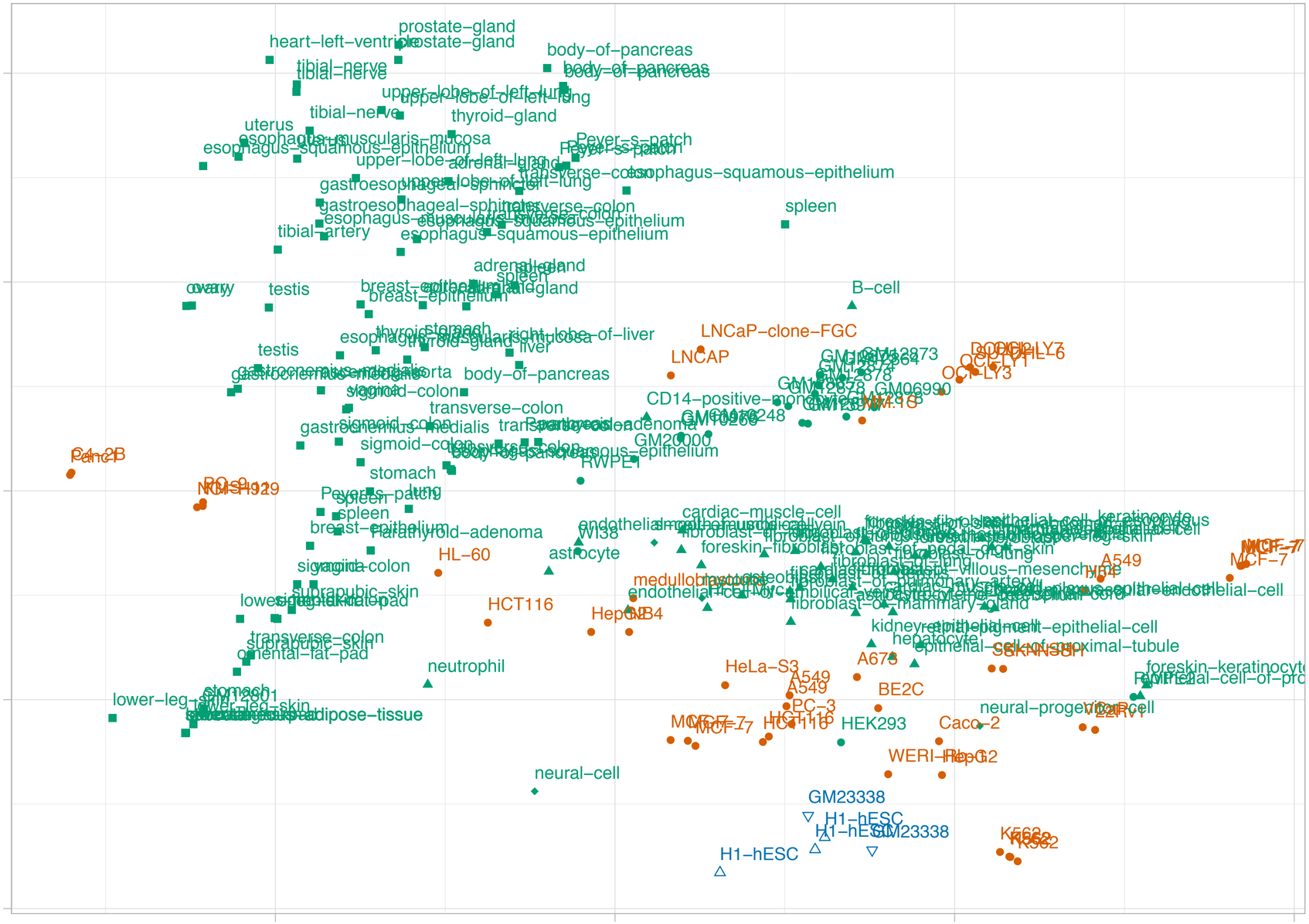
Type

- immortalized–cell–line
- in–vitro–differentiated–cells
- induced–pluripotent–stem–cell–line
- primary–cell
- stem–cell
- tissue

t–SNE: CTCF


adipose–tissue
lower–leg–skin
stomach
omental–fat–pad
suprapubic–skin
sigmoid–colon
vagina
breast–epithelium
Peyer's–patch
testis
spleen
Parathyroid–adenoma
ovary
neutrophil
gastrocnemius–medialis
lung
thyroid–gland
transverse–colon
adrenal–gland
esophagus–squamous–epithelium
tibial–nerve
tibial–artery
uterus
heart–left–ven
esophagus–muscularis–mu
esophagus–squamous
upper–lobe–of–left–lung
HL–60
HCT116
liver
pancreas
body–of–pancreas
NCI–H929
PC–9
GM20000
CD14–positive–monocyte
GM10248
RWPE1
WI38
endothelial–cell–of–umbilical–vein
Panc1
LNCaP–2B
LNCAP
B–cell
HepG2
NB4
medulloblastoma
smooth–muscle–cell
foreskin–fibroblast
myotube
LNCaP–clone–FGC
neural–cell
GM12865
GM12878
GM12891
GM12892
GM12875
GM12864
GM12873
HFF–Myc
osteoblast
cardiac–muscle–cell
fibroblast–of–lung
fibroblast–of–gingiva
fibroblast–of–dermis
pedal–digit–skin
fibroblast–of–skin–of–abdomen
fibroblast–of–upper–leg–skin
fibroblast–of–breast
fibroblast–of–prostate–gland
fibroblast–of–mammary–gland
fibroblast–of–lung–adventitia
fibroblast–of–esophagus–smooth–muscle
fibroblast–of–dermis–penile–skin
fibroblast–of–dermis–scrotal–skin
fibroblast–of–dermis–lower–leg–skin
fibroblast–of–dermis–upper–leg–skin
fibroblast–of–dermis–umbilical–skin
fibroblast–of–dermis–abdominal–skin
fibroblast–of–dermis–suprapubic–skin
fibroblast–of–dermis–foreskin
fibroblast–of–dermis–sigmoid–colon
fibroblast–of–dermis–vagina
fibroblast–of–dermis–breast
fibroblast–of–dermis–Peyer's–patch
fibroblast–of–dermis–testis
fibroblast–of–dermis–spleen
fibroblast–of–dermis–parathyroid–adenoma
fibroblast–of–dermis–ovary
fibroblast–of–dermis–neutrophil
fibroblast–of–dermis–gastrocnemius–medialis
fibroblast–of–dermis–lung
fibroblast–of–dermis–thyroid–gland
fibroblast–of–dermis–transverse–colon
fibroblast–of–dermis–adrenal–gland
fibroblast–of–dermis–esophagus–squamous–epithelium
fibroblast–of–dermis–tibial–nerve
fibroblast–of–dermis–tibial–artery
fibroblast–of–dermis–uterus
fibroblast–of–dermis–esophagus–muscularis–mucosa
fibroblast–of–dermis–upper–lobe–of–left–lung
fibroblast–of–dermis–heart–left–ventricle
fibroblast–of–dermis–esophagus–squamous
fibroblast–of–dermis–esophagus–gastroesophageal–sphincter
fibroblast–of–dermis–body–of–pancreas
fibroblast–of–dermis–liver
fibroblast–of–dermis–right–lobe–of–liver
fibroblast–of–dermis–Peyer's–patch–lymphoid–follicle
fibroblast–of–dermis–esophagus–squamous–epitheliu
fibroblast–of–dermis–body–of–pan
fibroblast–of–dermis–adipose–tissue
fibroblast–of–dermis–omental–fat–pad
fibroblast–of–dermis–stomach
fibroblast–of–dermis–transverse–colon
fibroblast–of–dermis–suprapubic–skin
fibroblast–of–dermis–sigmoid–colon
fibroblast–of–dermis–lower–leg–skin
fibroblast–of–dermis–adrenal–gland
fibroblast–of–dermis–thyroid–gland
fibroblast–of–dermis–esophagus–squamous–epithelium
fibroblast–of–dermis–upper–lobe–of–left–lung
fibroblast–of–dermis–esophagus–muscularis–mucosa
fibroblast–of–dermis–esophagus–gastroesophageal–sphincter
fibroblast–of–dermis–esophagus–muscularis–mu
fibroblast–of–dermis–esophagus–squamous
fibroblast–of–dermis–tibial–nerve
fibroblast–of–dermis–uterus
fibroblast–of–dermis–tibial–artery
fibroblast–of–dermis–testis
fibroblast–of–dermis–Peyer's–patch

t–SNE: CTCF



State

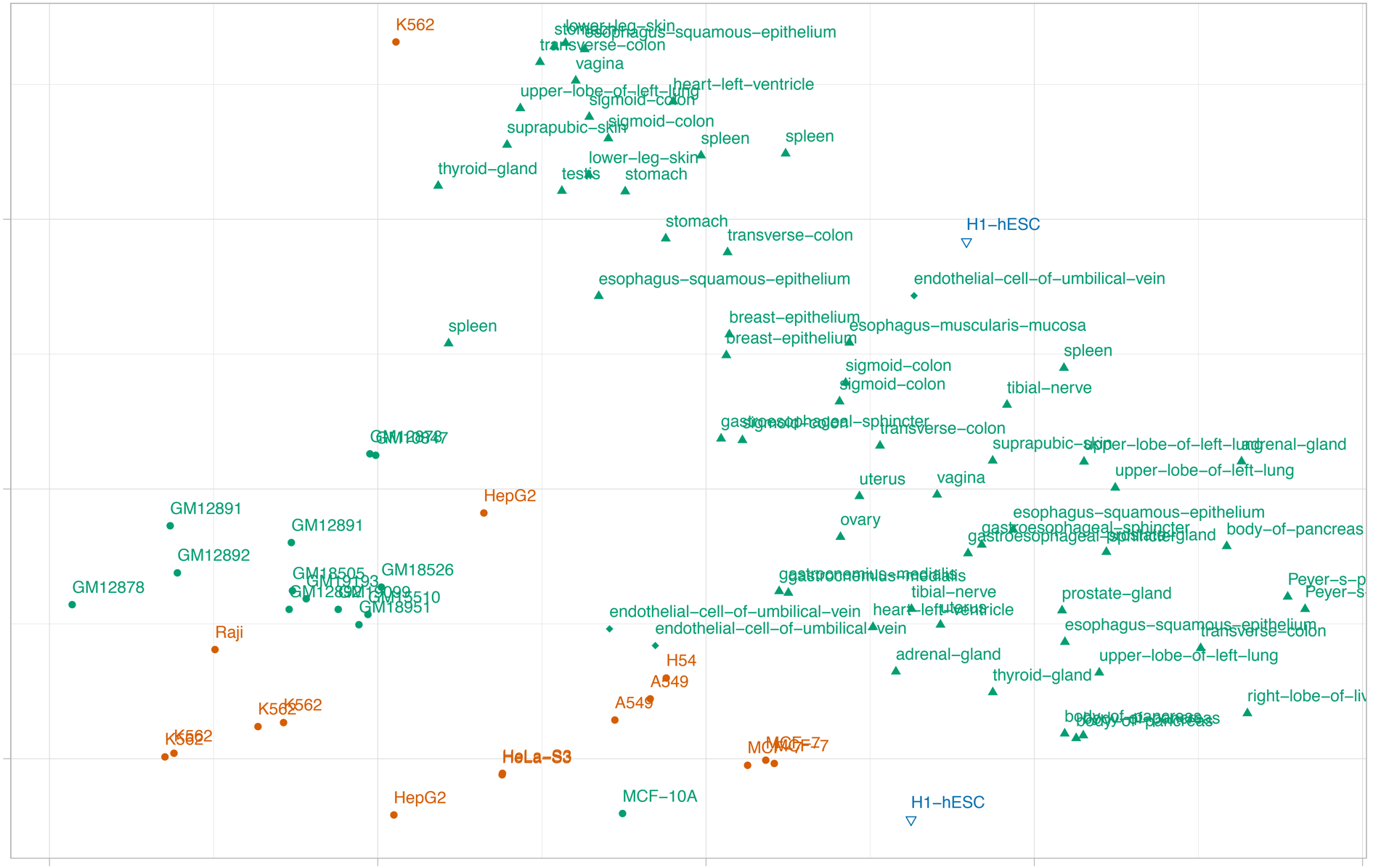
- cancer
- normal
- stem

Type

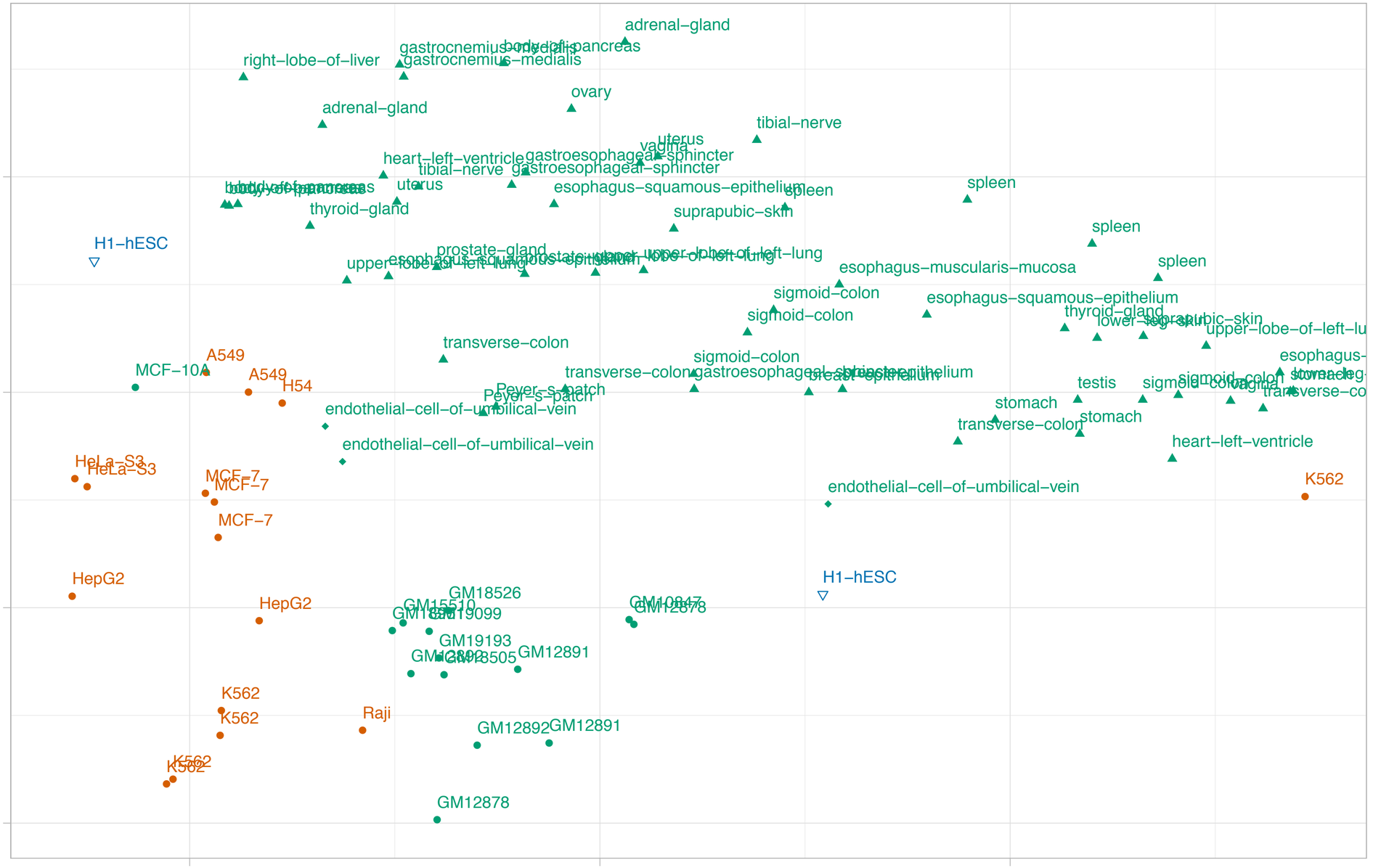
- immortalized–cell–line
- in–vitro–differentiated–cells
- induced–pluripotent–stem–cell–line
- primary–cell
- stem–cell
- tissue

POLR2A

t–SNE: POLR2A


K562
lower–leg–skin
stomach
esophagus–squamous–epithelium
transverse–colon
vagina
heart–left–ventricle
upper–lobe–of–left–lung
sigmoid–colon
sigmoid–colon
suprapubic–skin
spleen
spleen
lower–leg–skin
thyroid–gland
testis
stomach
stomach
transverse–colon
H1–hESC
esophagus–squamous–epithelium
endothelial–cell–of–umbilical–vein
breast–epithelium
esophagus–muscularis–mucosa
spleen
breast–epithelium
spleen
sigmoid–colon
sigmoid–colon
tibial–nerve
gastroesophageal–sphincter
transverse–colon
suprapubic–skin
upper–lobe–of–left–lung
adrenal–gland
upper–lobe–of–left–lung
uterus
vagina
HepG2
GM12891
GM12891
esophagus–squamous–epithelium
ovary
gastroesophageal–sphincter
body–of–pancreas
GM12892
GM12878
GM18505
GM18526
GM19193
GM18510
GM18951
tibial–nerve
prostate–gland
Peyer–s–p
Peyer–s
endothelial–cell–of–umbilical–vein
heart–left–ventricle
uterus
esophagus–squamous–epithelium
transverse–colon
Raji
endothelial–cell–of–umbilical–vein
adrenal–gland
upper–lobe–of–left–lung
H54
A549
thyroid–gland
A549
K562
K562
right–lobe–of–liv
K562
K562
MCF–7
HeLa–S3
HepG2
MCF–10A
H1–hESC
State
cancer
normal
stem
Type
immortalized–cell–line
primary–cell
stem–cell
tissue

t–SNE: POLR2A



State

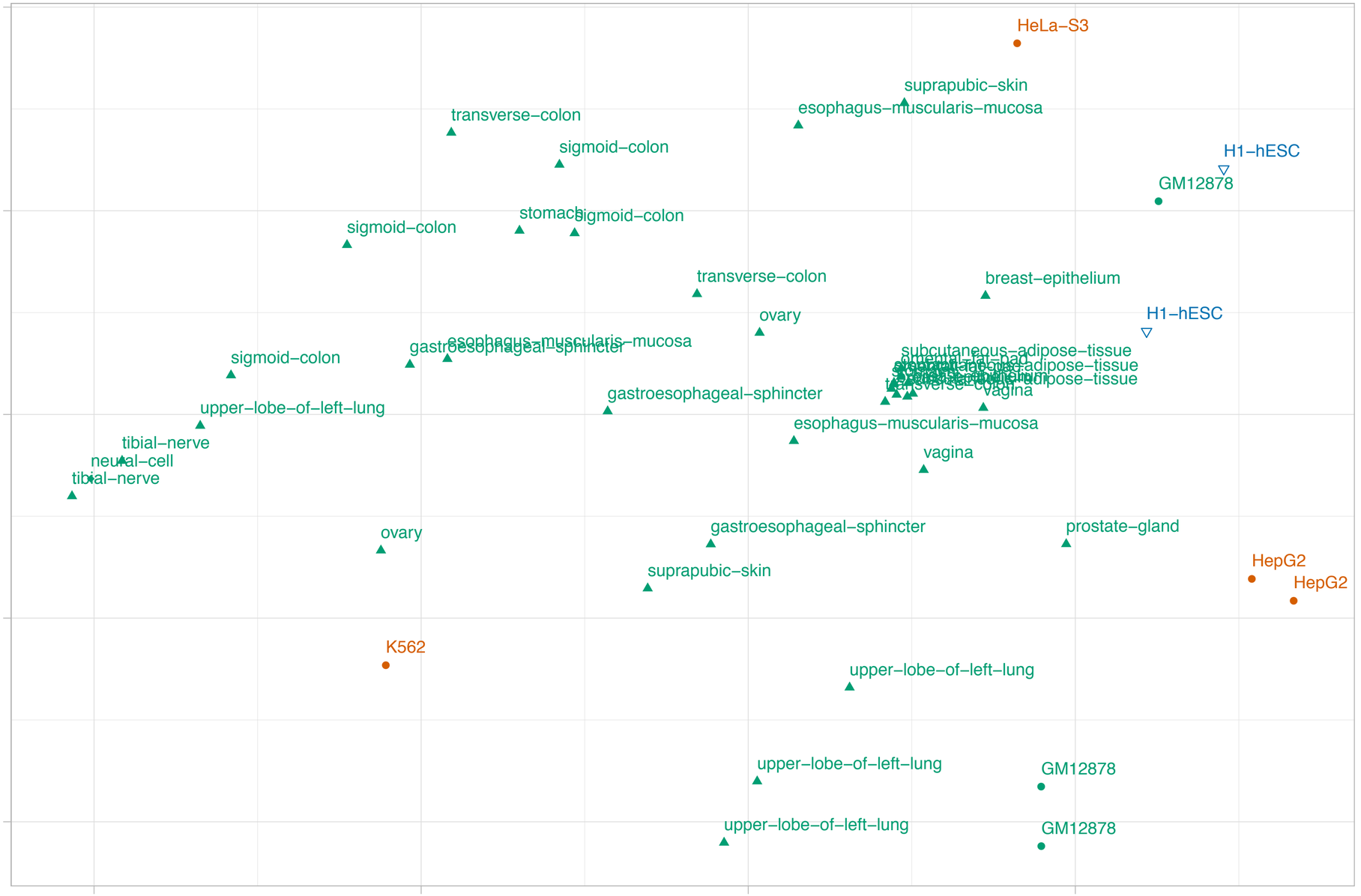
- cancer
- normal
- stem

Type

- immortalized–cell–line
- primary–cell
- stem–cell
- tissue

EP300

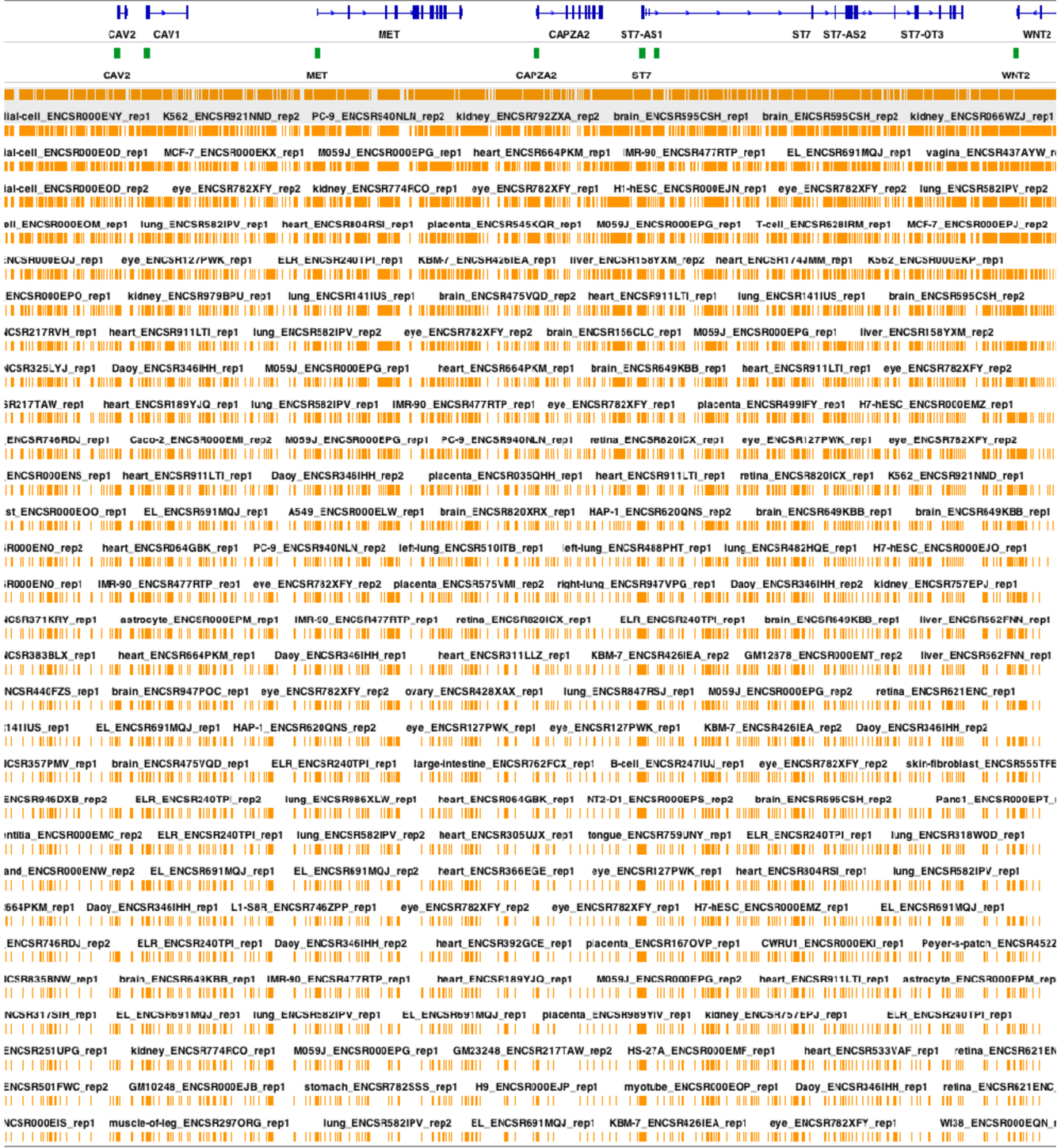
t–SNE: EP300



Type
- immortalized–cell–line
- in–vitro–differentiated–cells
- stem–cell
- tissue

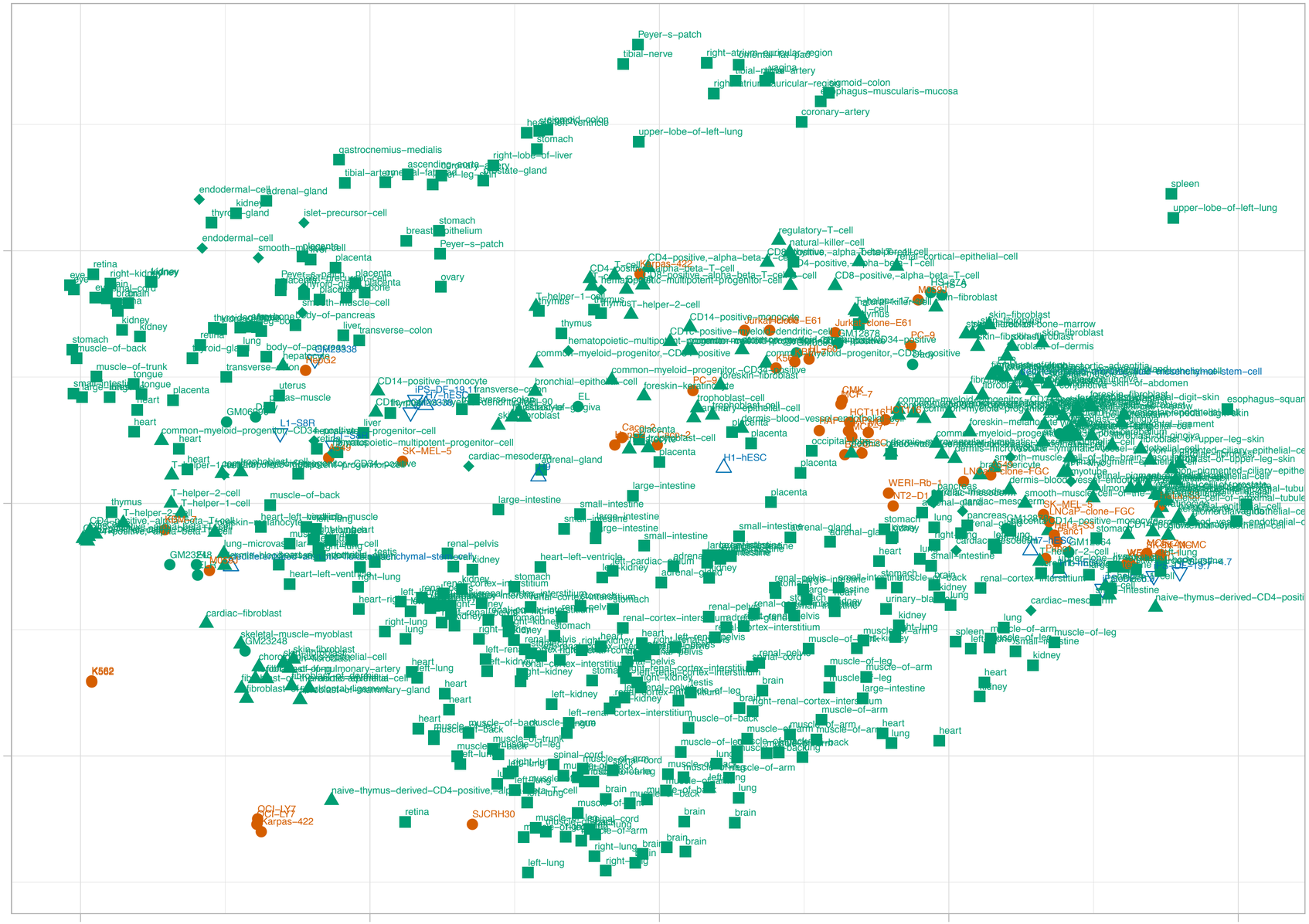
State
- cancer
- normal
- stem

DHS



	MGC4771	MGEA5	MGLL	MGME1	MGMT
HeLa-S3_ENCSR000ENO_rep1	0.06948610	0.03405987	0.00000000	0.05465573	0.04939010
HeLa-S3_ENCSR000ENO_rep2	0.09984670	0.00000000	0.02519497	0.06688660	0.01399720
ıultipotent-progenitor-cell_ENCS...	0.47150600	0.06178760	0.03869225	0.13977187	0.13597300
ıultipotent-progenitor-cell_ENCS...	0.30793850	0.09778040	0.03259350	0.37102600	0.37172600
ıultipotent-progenitor-cell_ENCS...	0.48330300	0.09078180	0.02179565	0.10697847	0.06738643
ıultipotent-progenitor-cell_ENCS...	0.31063750	0.02459510	0.00000000	0.23935200	0.18816200
hepatocyte_ENCSR364MFN_rep1	0.32333550	0.21695700	0.04752383	0.12922422	0.29014200
hepatocyte_ENCSR364MFN_rep2	0.15556883	0.05158970	0.02626143	0.07138577	0.12737450
HepG2_ENCSR000ENP_rep1	0.20862493	0.14697100	0.02789445	0.18556285	0.18416325
HepG2_ENCSR000ENP_rep2	0.10691217	0.04019200	0.01699660	0.19356100	0.09898020
HFF-Myc_ENCSR000ENR_rep1	0.10627850	0.05918820	0.00000000	0.07678470	0.11597700
HFF-Myc_ENCSR000ENR_rep2	0.09628070	0.05458910	0.03919220	0.12737500	0.09498100
dlimb-muscle_ENCSR385AMY_rep1	0.30133950	0.10098000	0.02419520	0.09678071	0.28434300
HL-60_ENCSR000ENU_rep1	0.29604100	0.08398310	0.00000000	0.10584540	0.18576300
HL-60_ENCSR000ENU_rep2	0.29874000	0.10337955	0.00000000	0.11002795	0.18936200
HS-27A_ENCSR000EMF_rep1	0.09408125	0.04939010	0.09778050	0.12557500	0.00000000
HS-5_ENCSR000EMG_rep1	0.09338145	0.13977200	0.00000000	0.09044853	0.05378925
IMR-90_ENCSR477RTP_rep1	0.09518087	0.16656700	0.06438697	0.07598483	0.06212107
iPS-DF-19.11_ENCSR383SNM_rep1	0.22585500	0.05998800	0.04809040	0.06392061	0.15336900
iPS-DF-19.7_ENCSR440QMR_rep1	0.07111927	0.00000000	0.02539490	0.11317700	0.03469305
iPS-DF-4.7_ENCSR014FPY_rep1	0.04639070	0.00000000	0.00000000	0.09398120	0.00000000
iPS-DF-6.9_ENCSR261SMF_rep1	0.07748452	0.00000000	0.02519500	0.10357900	0.04019200
ɔrecursor-cell_ENCSR224FOA_rep1	0.48310300	0.07198560	0.06525350	0.18336340	0.13797200
ɔrecursor-cell_ENCSR224FOA_rep2	0.26754640	0.34293100	0.18306343	0.12910753	0.16560013
ĸat-clone-E61_ENCSR000EOS_rep1	0.09358132	0.08058390	0.03399320	0.06838630	0.14017200
ĸat-clone-E61_ENCSR000EOS_rep2	0.11837600	0.07778440	0.03099380	0.10037975	0.14137200
K562_ENCSR000EPC_rep1	0.12417537	0.24155200	0.00000000	0.10917810	0.00000000
K562_ENCSR000EPC_rep2	0.08438315	0.04019200	0.00000000	0.12537500	0.00000000
K562_ENCSR921NMD_rep1	0.32313500	0.39952000	0.05598880	0.24695050	0.14177200
K562_ENCSR921NMD_rep2	0.31913600	0.49010200	0.00000000	0.23915210	0.08178370
Karpas-422_ENCSR019JDO_rep1	0.21122427	0.07418507	0.05245617	0.30843820	0.12867400
Karpas-422_ENCSR019JDO_rep2	0.14152165	0.05372257	0.03192697	0.18556299	0.07958430

t–SNE: DHS



State
- cancer
- normal
- stem

Type
- immortalized–cell–line
- in–vitro–differentiated–cells
- induced–pluripotent–stem–cell–line
- primary–cell
- stem–cell
- tissue