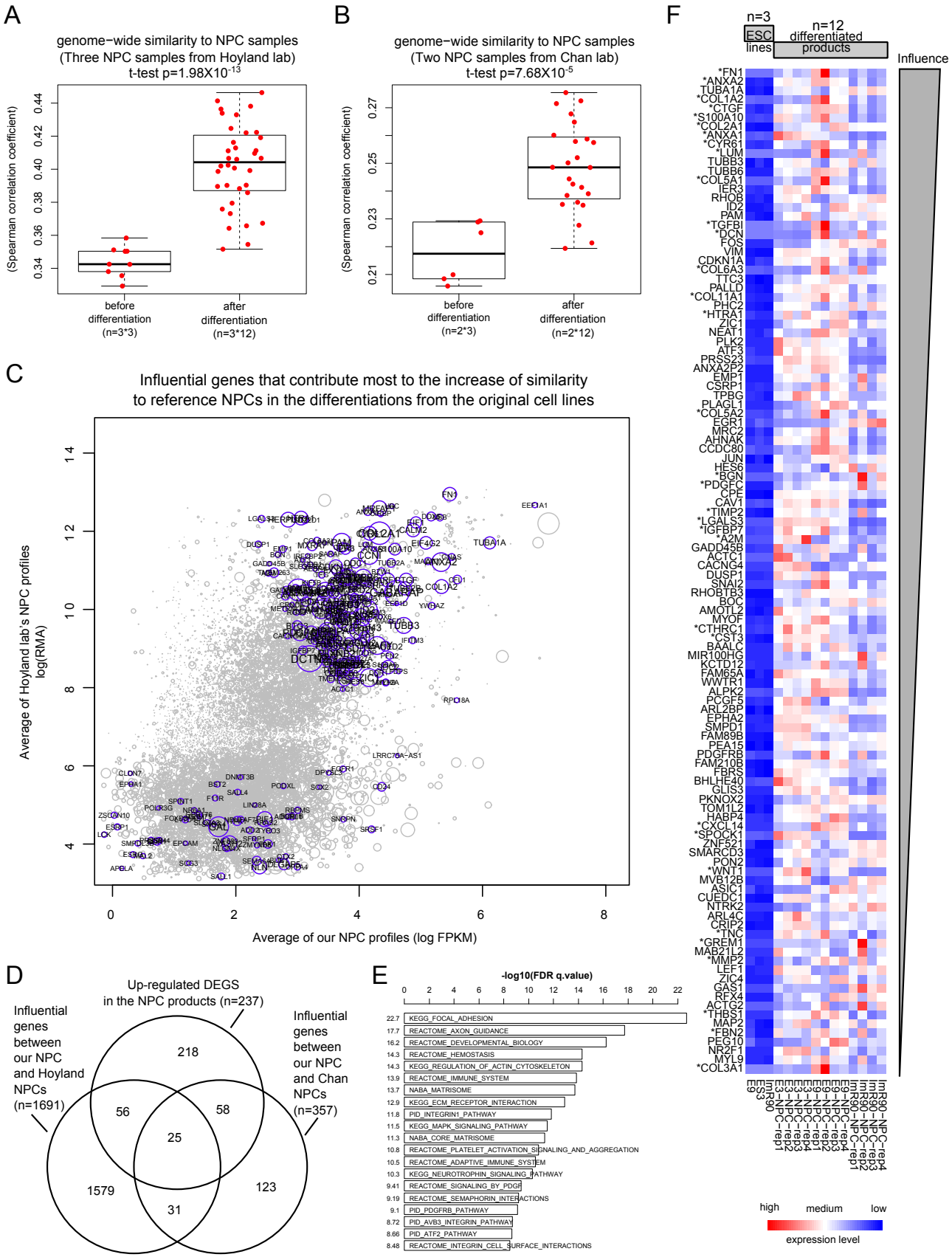
A
genome−wide similarity to NPC samples
(Three NPC samples from Hoyland lab)
t-test p=1.98X10-13
(Spearman correlation coefficient)
before differentiation (n=3*3)
after differentiation (n=3*12)
B
genome−wide similarity to NPC samples
(Two NPC samples from Chan lab)
t-test p=7.68X10-5
(Spearman correlation coefficient)
before differentiation (n=2*3)
after differentiation (n=2*12)
C
Influential genes that contribute most to the increase of similarity
to reference NPCs in the differentiations from the original cell lines
Average of Hoyland lab's NPC profiles log(RMA)
Average of our NPC profiles (log FPKM)
D
Up-regulated DEGS
in the NPC products (n=237)
Influential genes between our NPC and Hoyland NPCs (n=1691)
Influential genes between our NPC and Chan NPCs (n=357)
218
56
58
25
1579
31
123
E
-log10(FDR q.value)
KEGG_FOCAL_ADHESION
REACTOME_AXON_GUIDANCE
REACTOME_DEVELOPMENTAL_BIOLOGY
REACTOME_HEMOSTASIS
KEGG_REGULATION_OF_ACTIN_CYTOSKELETON
REACTOME_IMMUNE_SYSTEM
NABA_MATRISOME
KEGG_ECM_RECEPTOR_INTERACTION
PID_INTEGRIN1_PATHWAY
KEGG_MAPK_SIGNALING_PATHWAY
NABA_CORE_MATRISOME
REACTOME_PLATELET_ACTIVATION_SIGNALING_AND_AGGREGATION
REACTOME_ADAPTIVE_IMMUNE_SYSTEM
KEGG_NEUROTROPHIN_SIGNALING_PATHWAY
REACTOME_SIGNALING_BY_PDGF
REACTOME_SEMAPHORIN_INTERACTIONS
PID_PDGFRB_PATHWAY
PID_AVB3_INTEGRIN_PATHWAY
PID_ATF2_PATHWAY
REACTOME_INTEGRIN_CELL_SURFACE_INTERACTIONS
F
n=3
ESC lines
n=12
differentiated products
Influence
high
medium
low
expression level