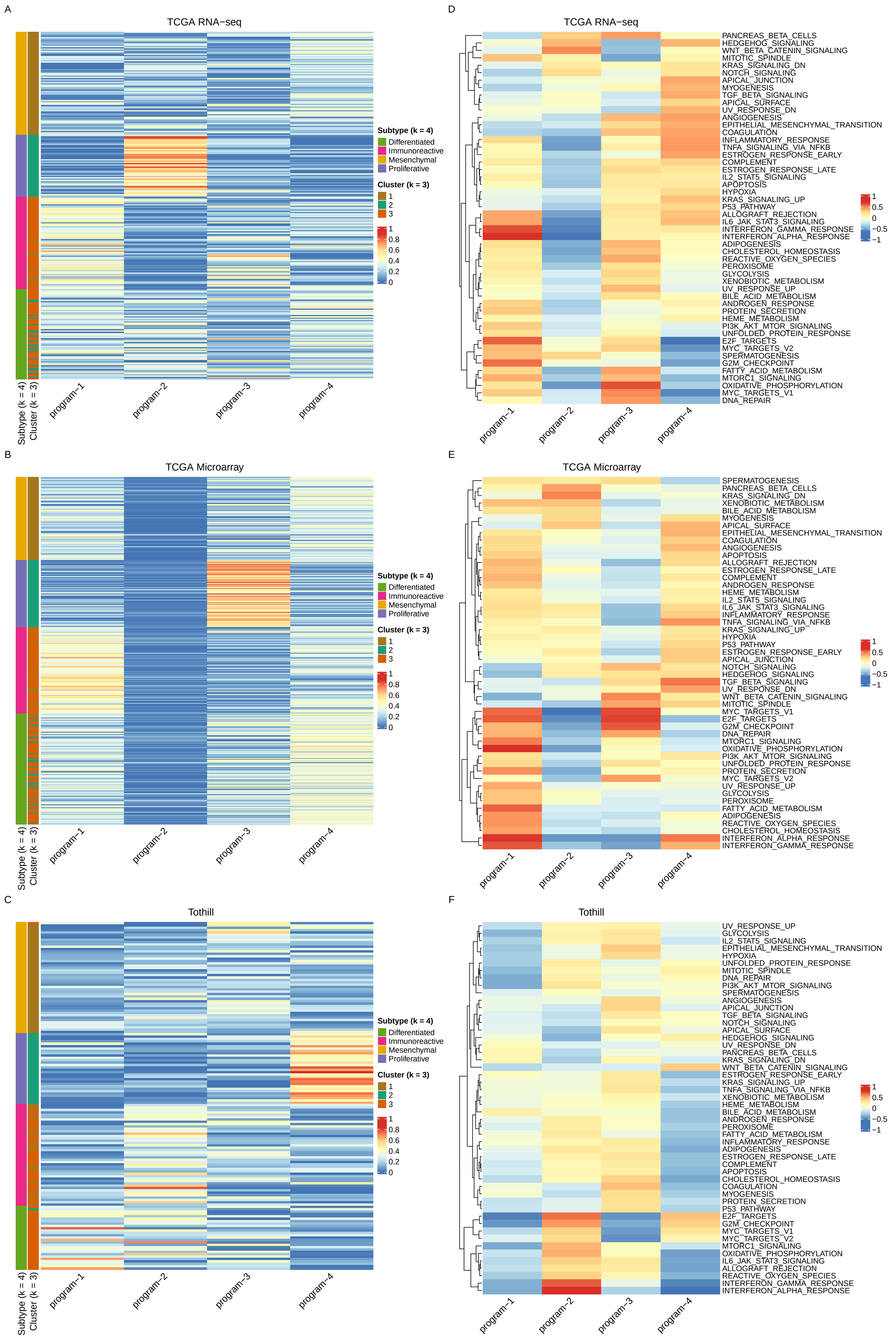
A
TCGA RNA−seq
Subtype (k = 4)
Differentiated
Immunoreactive
Mesenchymal
Proliferative
Cluster (k = 3)
1
2
3
1
0.8
0.6
0.4
0.2
0
Subtype (k = 4)
Cluster (k = 3)
program−1
program−2
program−3
program−4
B
TCGA Microarray
C
Tothill
D
TCGA RNA−seq
PANCREAS_BETA_CELLS
HEDGEHOG_SIGNALING
WNT_BETA_CATENIN_SIGNALING
MITOTIC_SPINDLE
KRAS_SIGNALING_DN
NOTCH_SIGNALING
APICAL_JUNCTION
MYOGENESIS
TGF_BETA_SIGNALING
APICAL_SURFACE
UV_RESPONSE_DN
ANGIOGENESIS
EPITHELIAL_MESENCHYMAL_TRANSITION
COAGULATION
INFLAMMATORY_RESPONSE
TNFA_SIGNALING_VIA_NFKB
ESTROGEN_RESPONSE_EARLY
COMPLEMENT
ESTROGEN_RESPONSE_LATE
IL2_STAT5_SIGNALING
APOPTOSIS
HYPOXIA
KRAS_SIGNALING_UP
P53_PATHWAY
ALLOGRAFT_REJECTION
IL6_JAK_STAT3_SIGNALING
INTERFERON_GAMMA_RESPONSE
INTERFERON_ALPHA_RESPONSE
ADIPOGENESIS
CHOLESTEROL_HOMEOSTASIS
REACTIVE_OXYGEN_SPECIES
PEROXISOME
GLYCOLYSIS
XENOBIOTIC_METABOLISM
UV_RESPONSE_UP
BILE_ACID_METABOLISM
ANDROGEN_RESPONSE
PROTEIN_SECRETION
HEME_METABOLISM
PI3K_AKT_MTOR_SIGNALING
UNFOLDED_PROTEIN_RESPONSE
E2F_TARGETS
MYC_TARGETS_V2
SPERMATOGENESIS
G2M_CHECKPOINT
FATTY_ACID_METABOLISM
MTORC1_SIGNALING
OXIDATIVE_PHOSPHORYLATION
MYC_TARGETS_V1
DNA_REPAIR
1
0.5
0
−0.5
−1
E
TCGA Microarray
F
Tothill