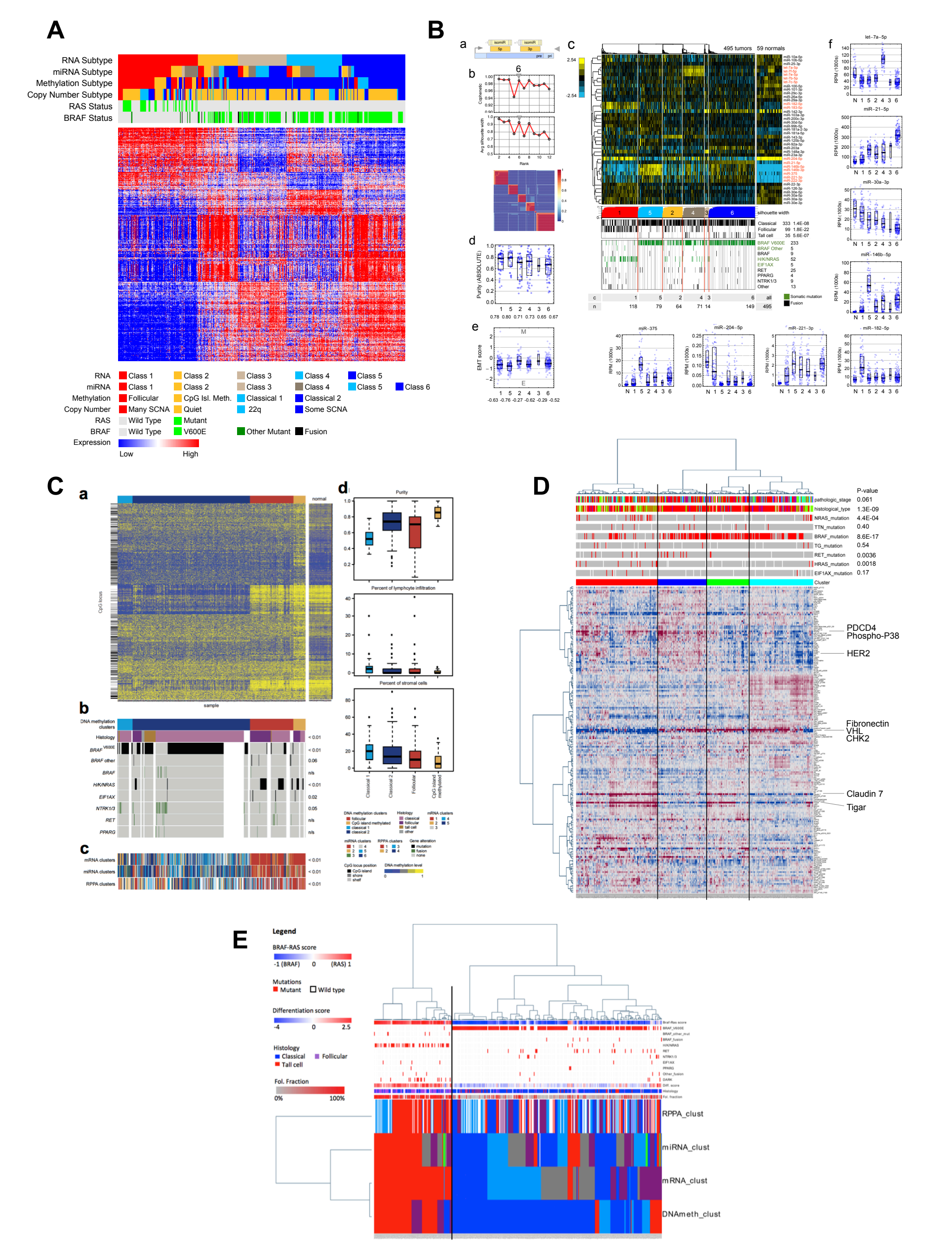
A
RNA Subtype
miRNA Subtype
Methylation Subtype
Copy Number Subtype
RAS Status
BRAF Status
RNA Class 1 Class 2 Class 3 Class 4 Class 5
miRNA Class 1 Class 2 Class 3 Class 4 Class 5 Class 6
Methylation Follicular CpG Isl. Meth. Classical 1 Classical 2
Copy Number Many SCNA Quiet 22q Some SCNA
RAS Wild Type Mutant
BRAF Wild Type V600E Other Mutant Fusion
Expression Low High
B
495 tumors 59 normals
silhouette width
Classical 333 1.4E-08
Follicular 99 1.8E-22
Tall cell 35 5.6E-07
BRAF V600E 233
BRAF Other 5
BRAF 9
H/K/NRAS 52
EIF1AX 5
RET 25
PPARG 4
NTRK1/3 9
Other 13
Somatic mutation
Fusion
let-7a-5p
miR-21-5p
miR-30a-3p
miR-146b-5p
miR-375
miR-204-5p
miR-221-3p
miR-182-5p
C
D
P-value
pathologic_stage 0.061
histological_type 1.3E-09
NRAS_mutation 4.4E-04
TTN_mutation 0.40
BRAF_mutation 8.6E-17
TG_mutation 0.54
RET_mutation 0.0036
HRAS_mutation 0.0018
EIF1AX_mutation 0.17
Cluster
PDCD4
Phospho-P38
HER2
Fibronectin
VHL
CHK2
Claudin 7
Tigar
E
Legend
BRAF-RAS score
-1 (BRAF) 0 (RAS) 1
Mutations
Mutant Wild type
Differentiation score
-4 0 2.5
Histology
Classical Follicular
Tall cell
Fol. Fraction
0% 100%
RPPA_clust
miRNA_clust
mRNA_clust
DNAmeth_clust