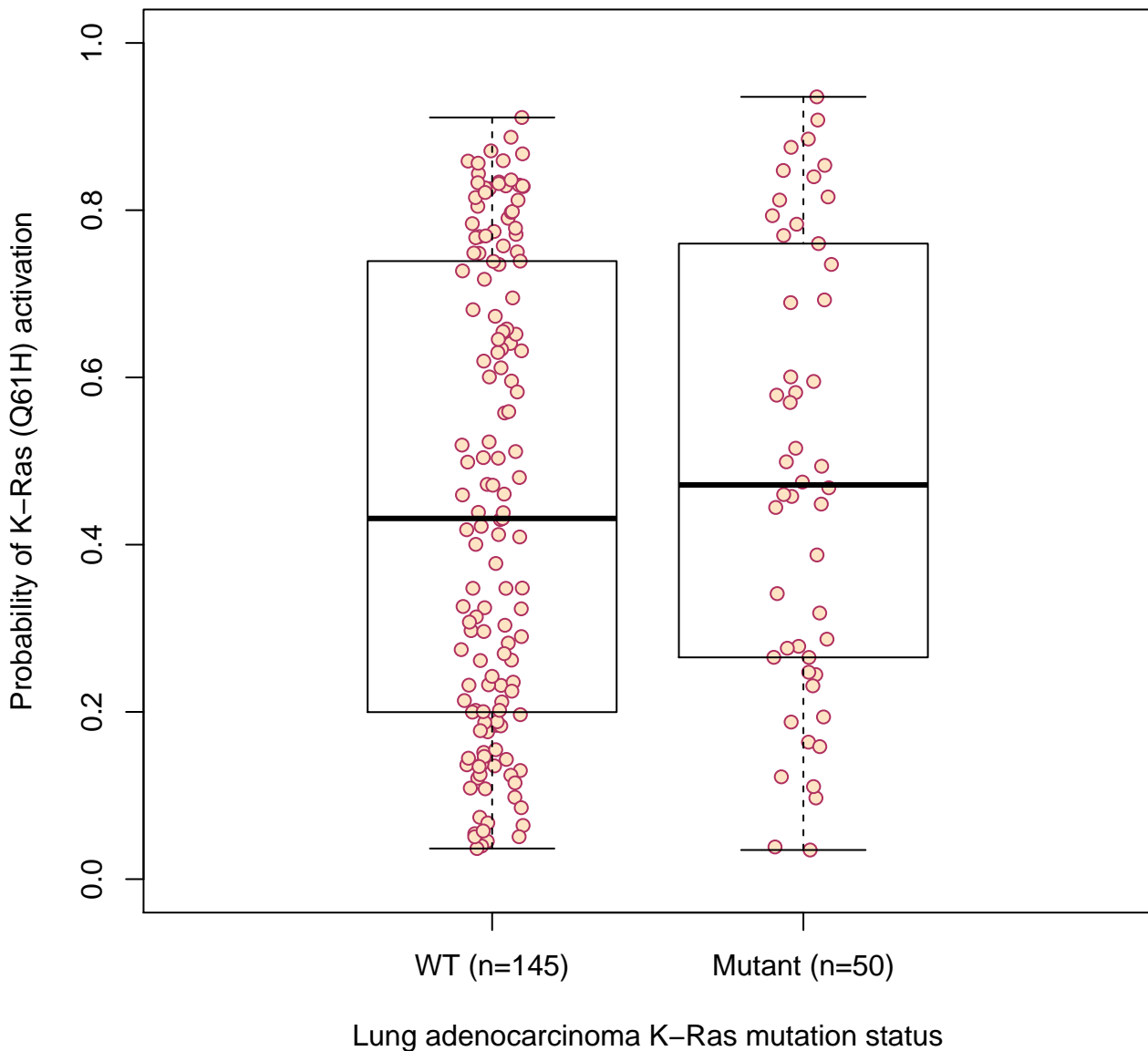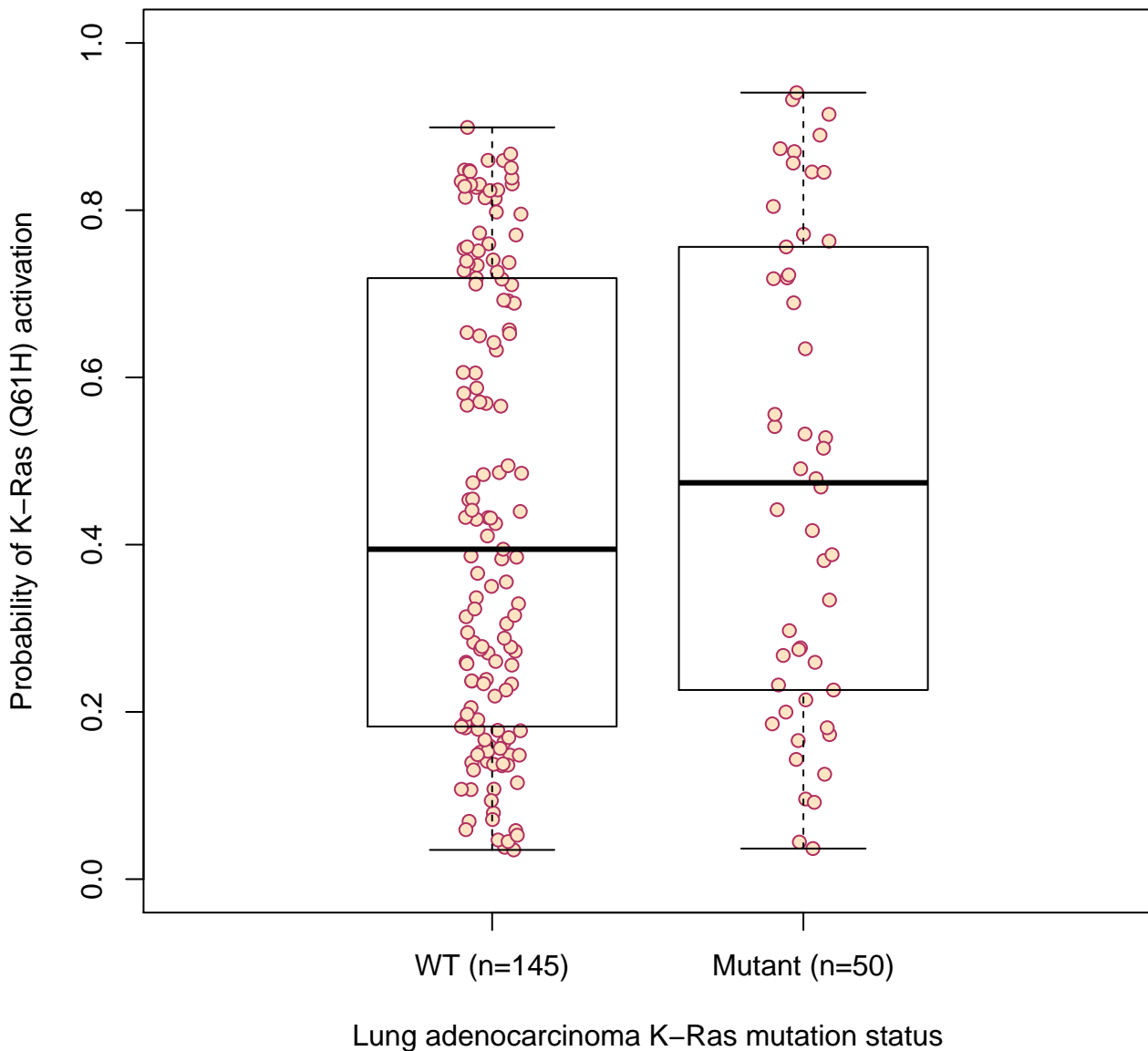**K−Ras Q61H signature validation**
Parameters: −d normalization, 125 genes, 1 metagene(s)
(p=0.450)

K−Ras Q61H signature validation
Parameters: −d normalization, 200 genes, 1 metagene(s)
(p=0.368)

Probability of K−Ras (Q61H) activation

WT (n=145)   Mutant (n=50)

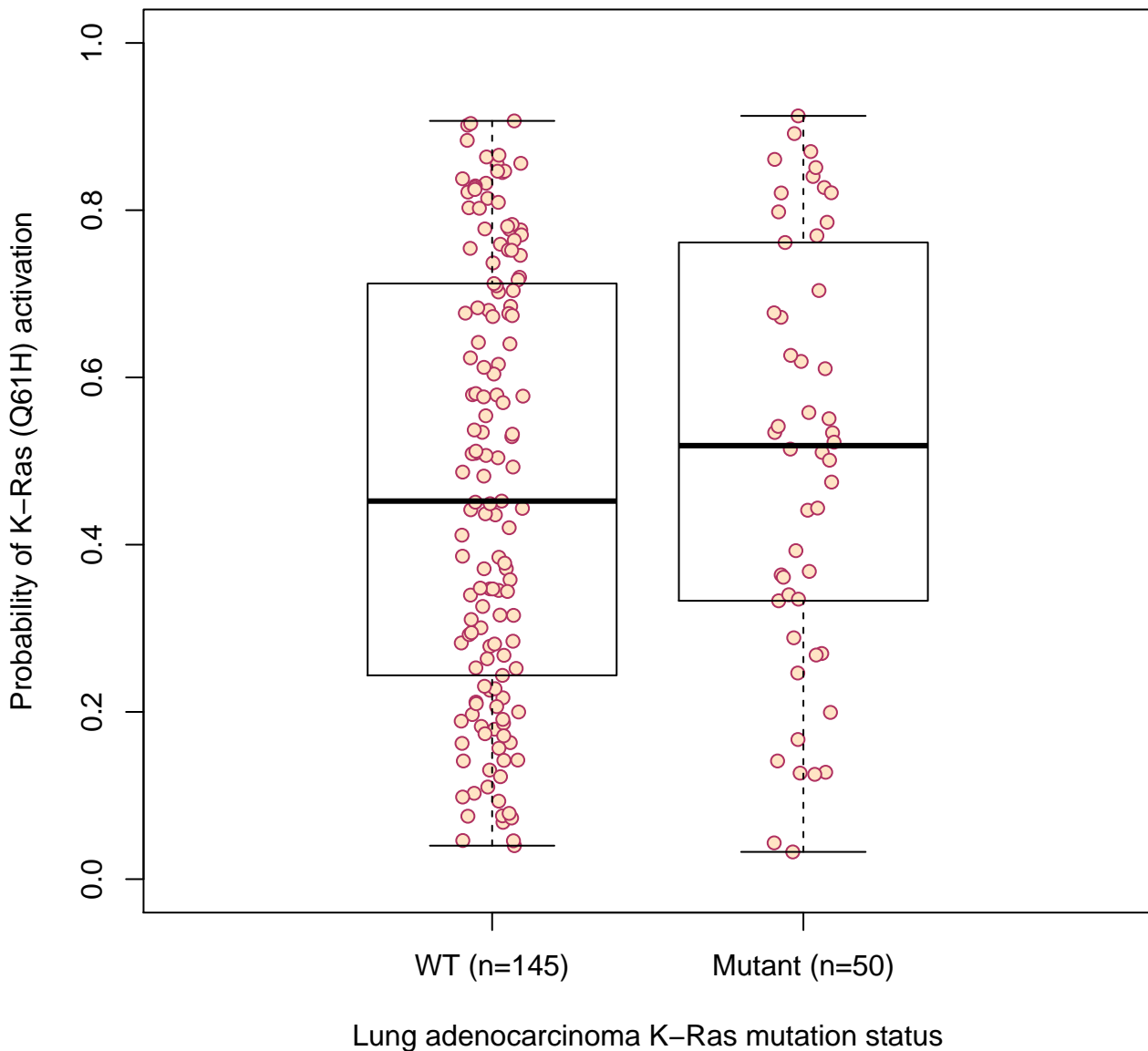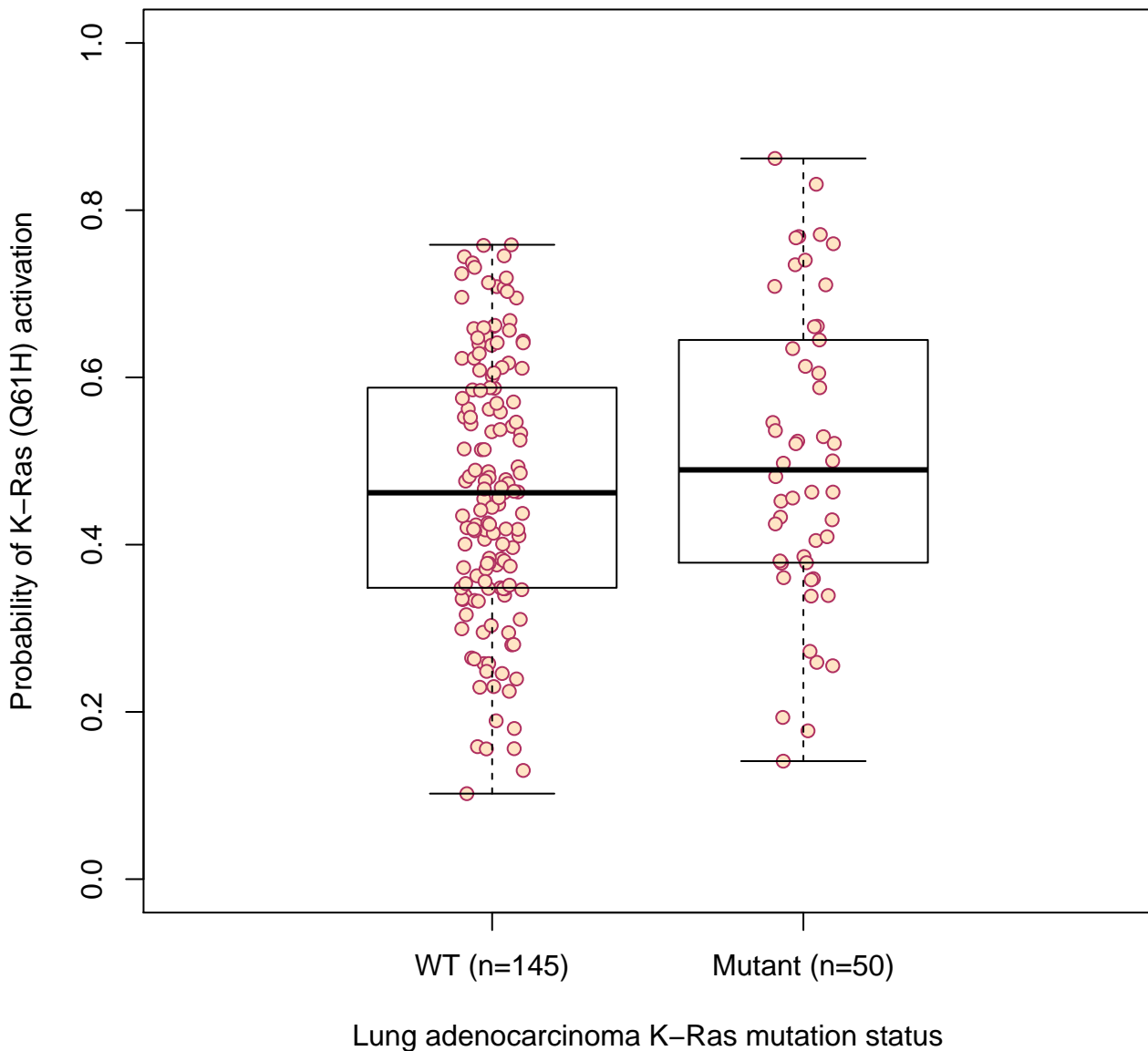Lung adenocarcinoma K−Ras mutation status

K−Ras Q61H signature validation
Parameters: −d normalization, 75 genes, 1 metagene(s)
(p=0.422)

K−Ras Q61H signature validation
Parameters: −d normalization, 125 genes, 2 metagene(s)
(p=0.255)

Probability of K−Ras (Q61H) activation

WT (n=145)   Mutant (n=50)

Lung adenocarcinoma K−Ras mutation status
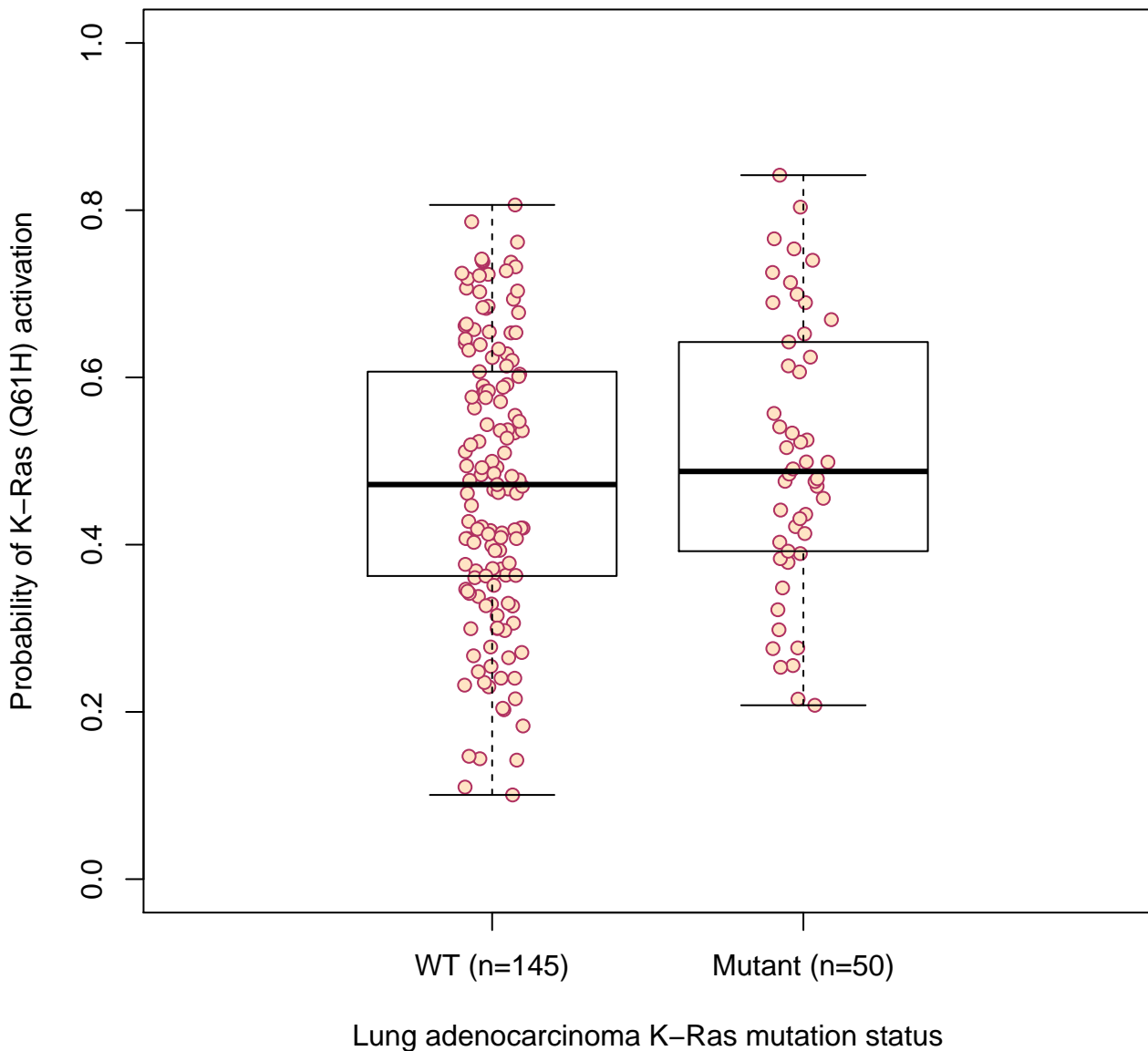
K−Ras Q61H signature validation
Parameters: −d normalization, 200 genes, 2 metagene(s)
(p=0.180)

K−Ras Q61H signature validation
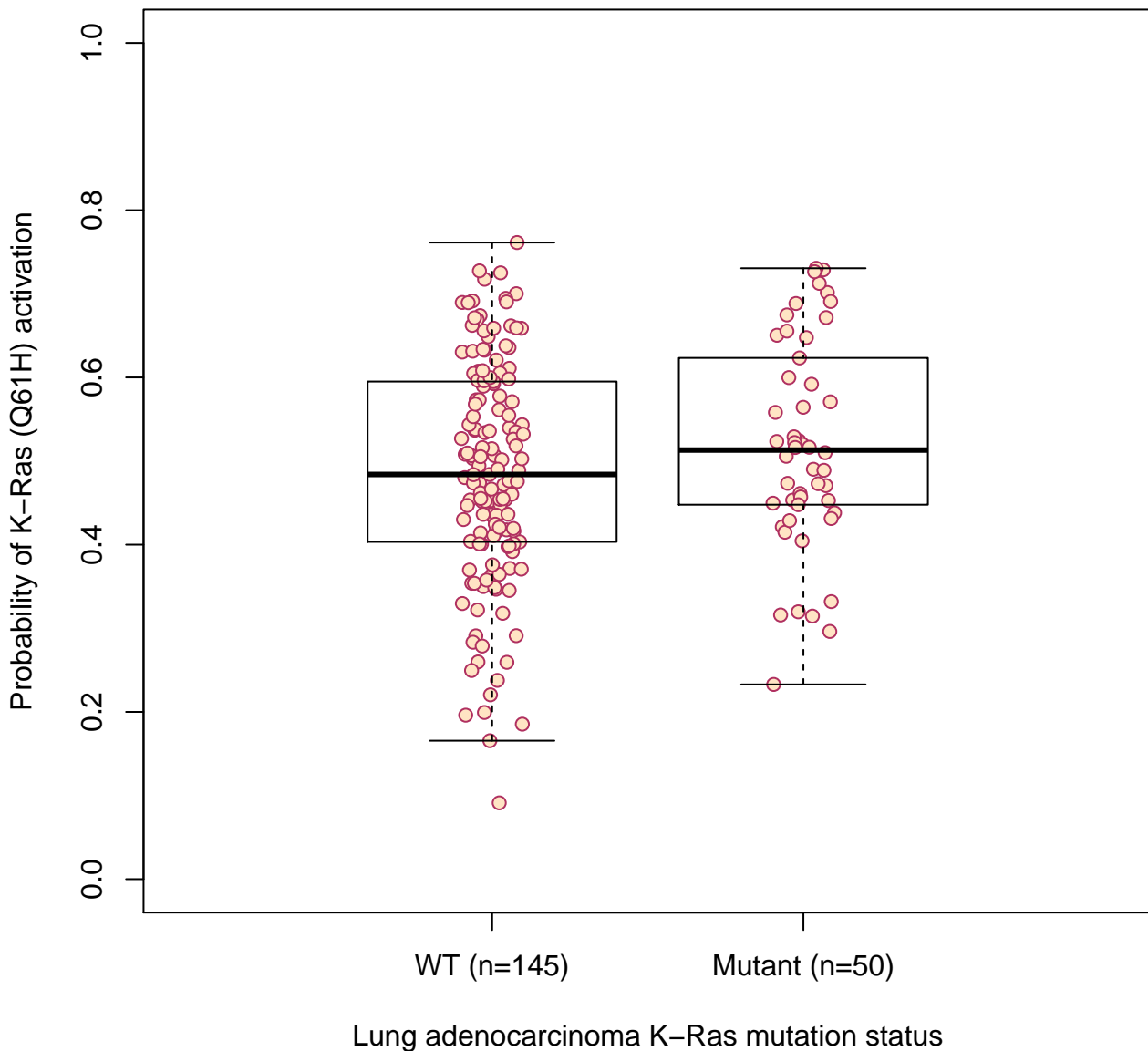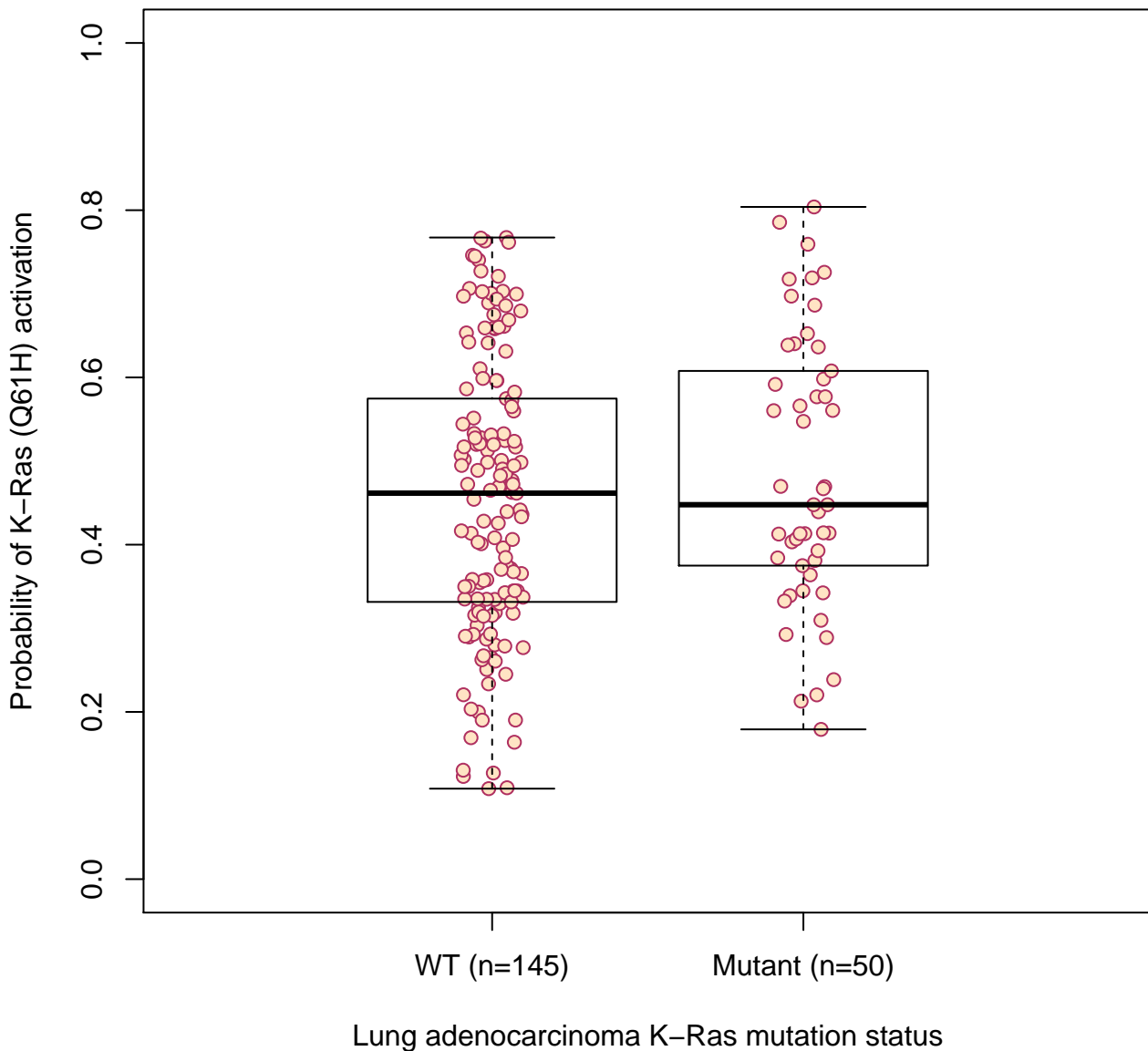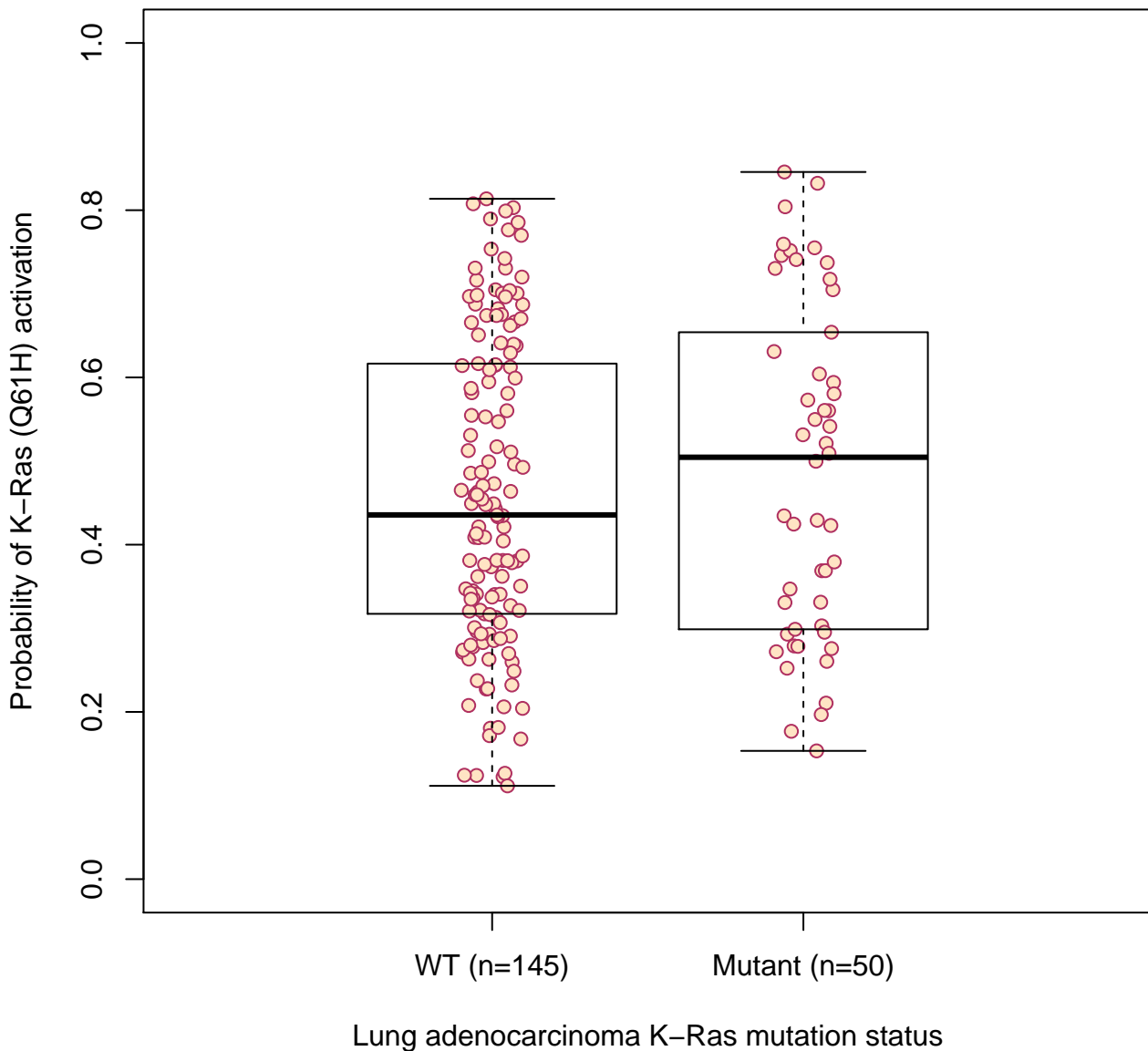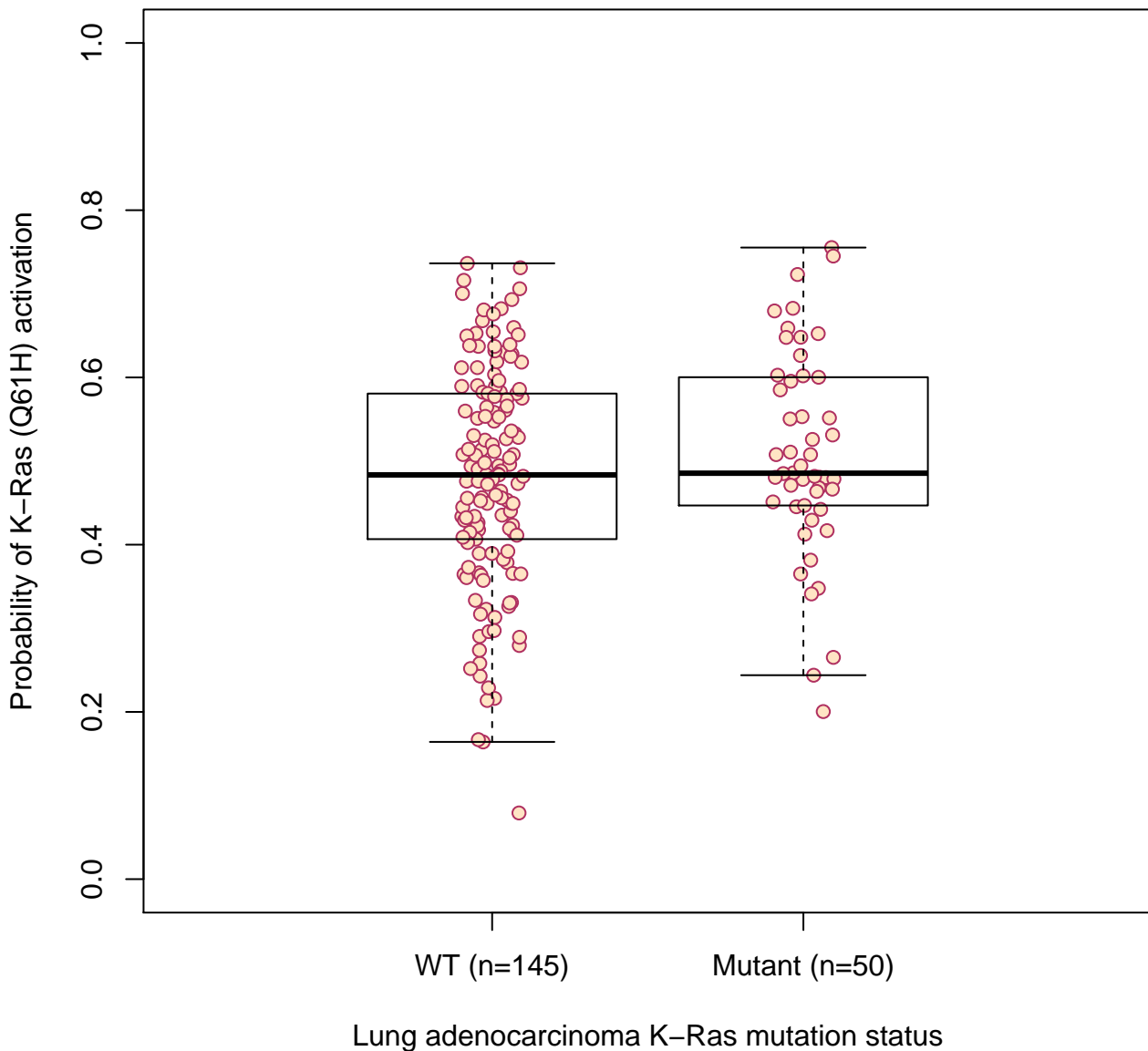**Parameters: −d normalization, 75 genes, 2 metagene(s)**
(p=0.131)

K−Ras Q61H signature validation
Parameters: −d normalization, 125 genes, 3 metagene(s)
(p=0.253)

Probability of K−Ras (Q61H) activation

WT (n=145)   Mutant (n=50)

Lung adenocarcinoma K−Ras mutation status

K−Ras Q61H signature validation
Parameters: −d normalization, 200 genes, 3 metagene(s)
(p=0.381)

Probability of K−Ras (Q61H) activation

WT (n=145)   Mutant (n=50)

Lung adenocarcinoma K−Ras mutation status

K−Ras Q61H signature validation
Parameters: −d normalization, 75 genes, 3 metagene(s)
(p=0.170)

K−Ras Q61H signature validation
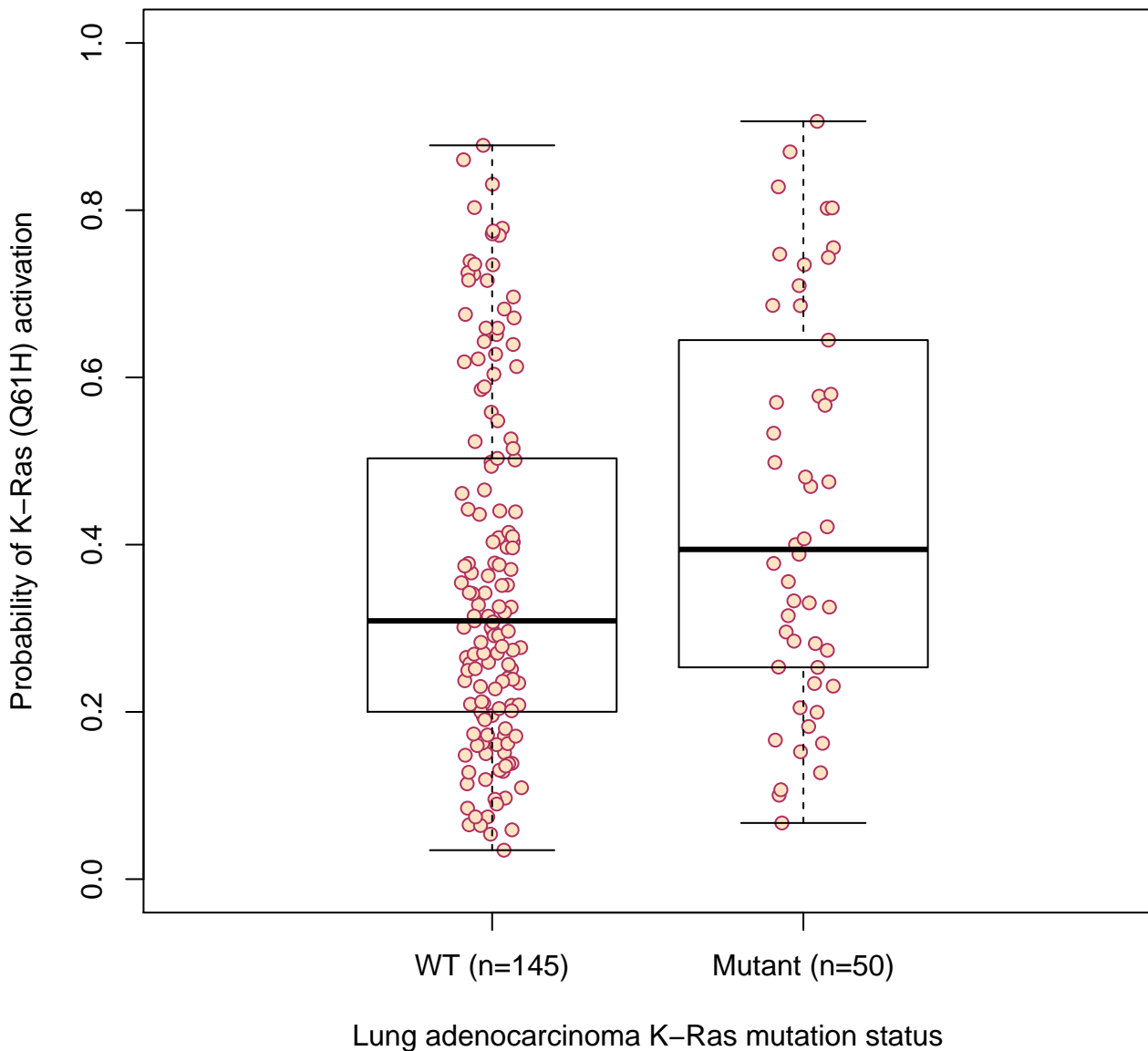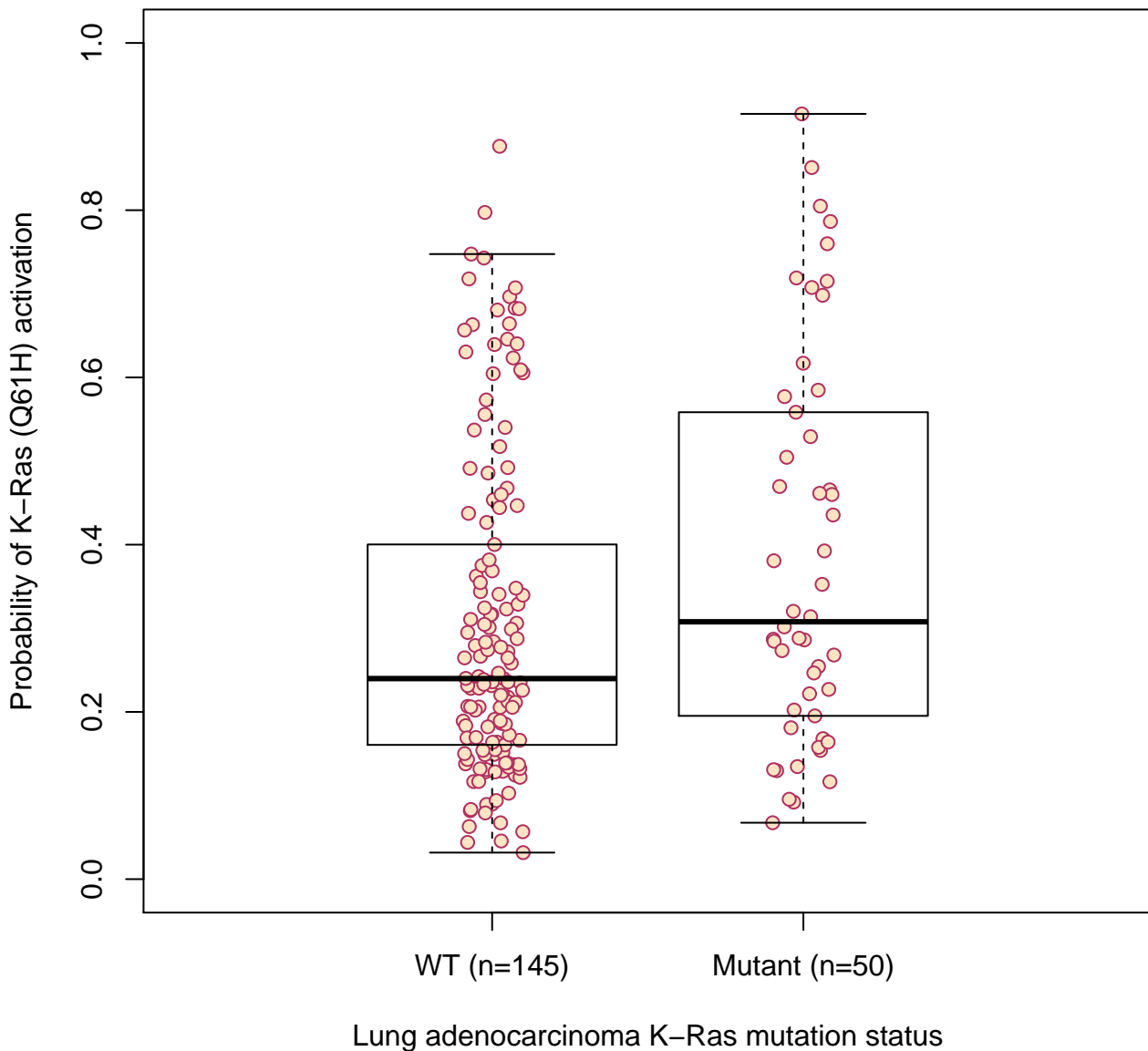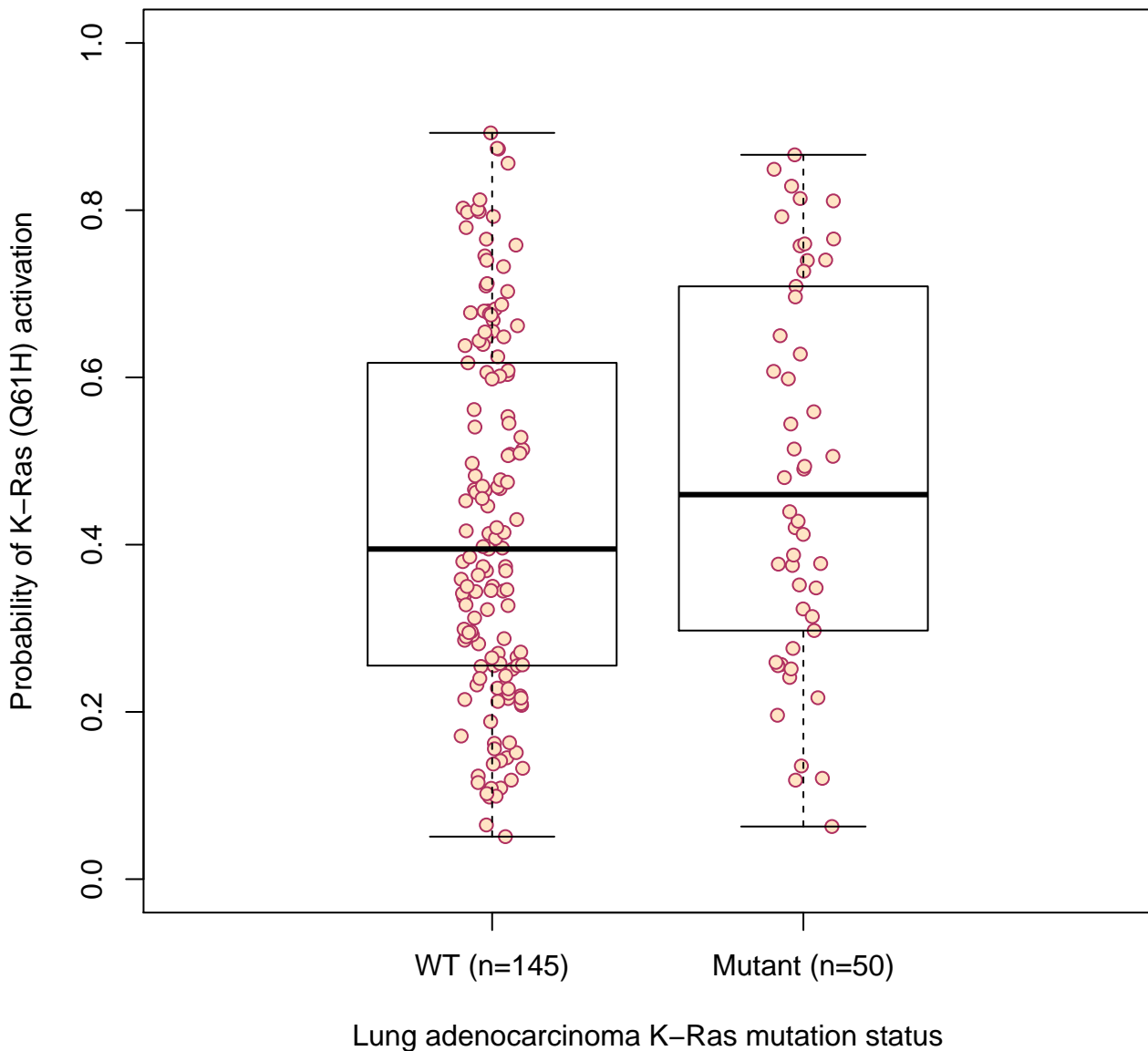**Parameters: −q normalization, 125 genes, 1 metagene(s)**
(p=0.050)

K−Ras Q61H signature validation
Parameters: −q normalization, 200 genes, 1 metagene(s)
(p=0.031)

Probability of K−Ras (Q61H) activation

WT (n=145)　　　Mutant (n=50)

Lung adenocarcinoma K−Ras mutation status

K−Ras Q61H signature validation
Parameters: −q normalization, 75 genes, 1 metagene(s)
(p=0.132)

K−Ras Q61H signature validation
Parameters: −q normalization, 125 genes, 2 metagene(s)
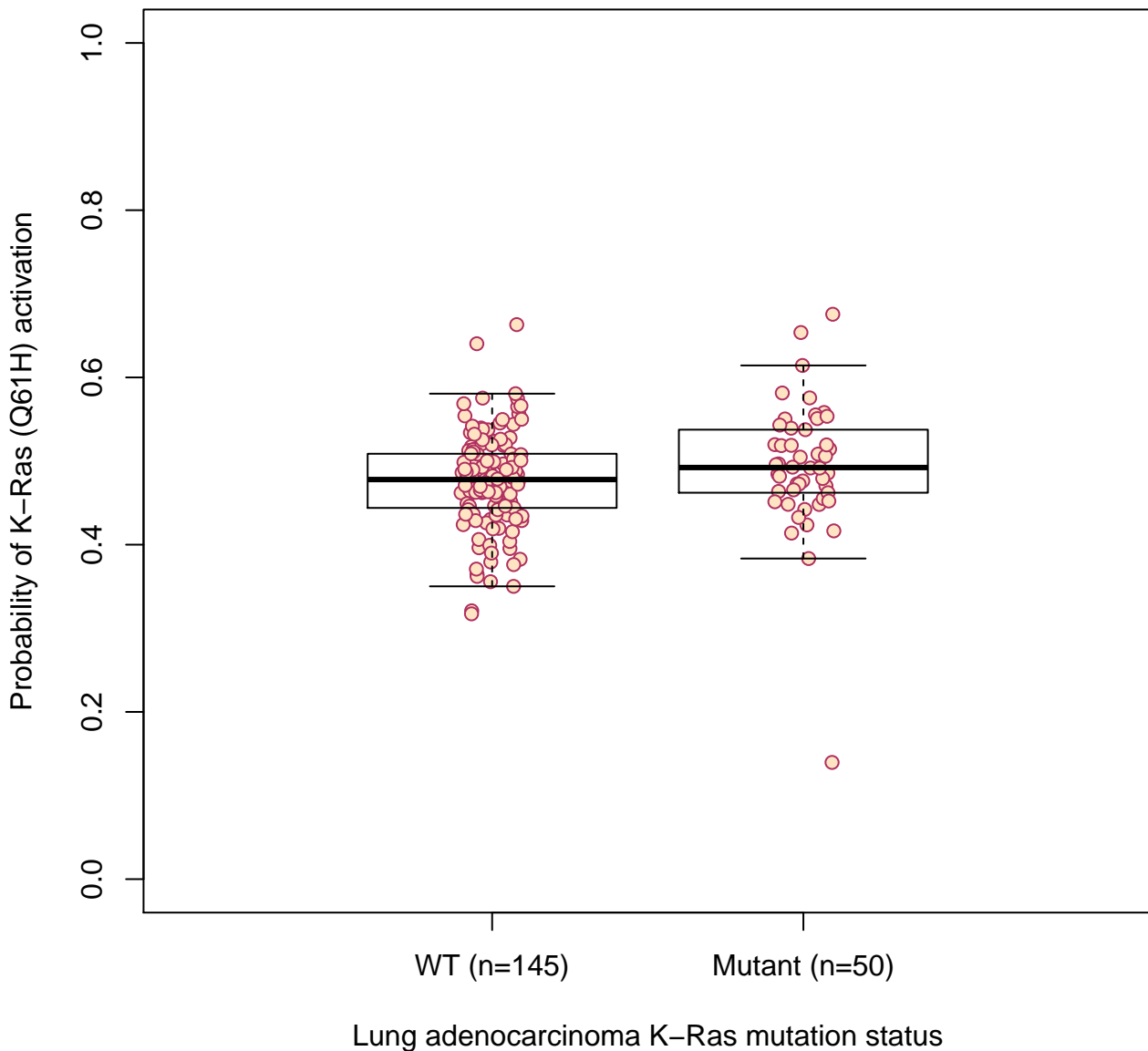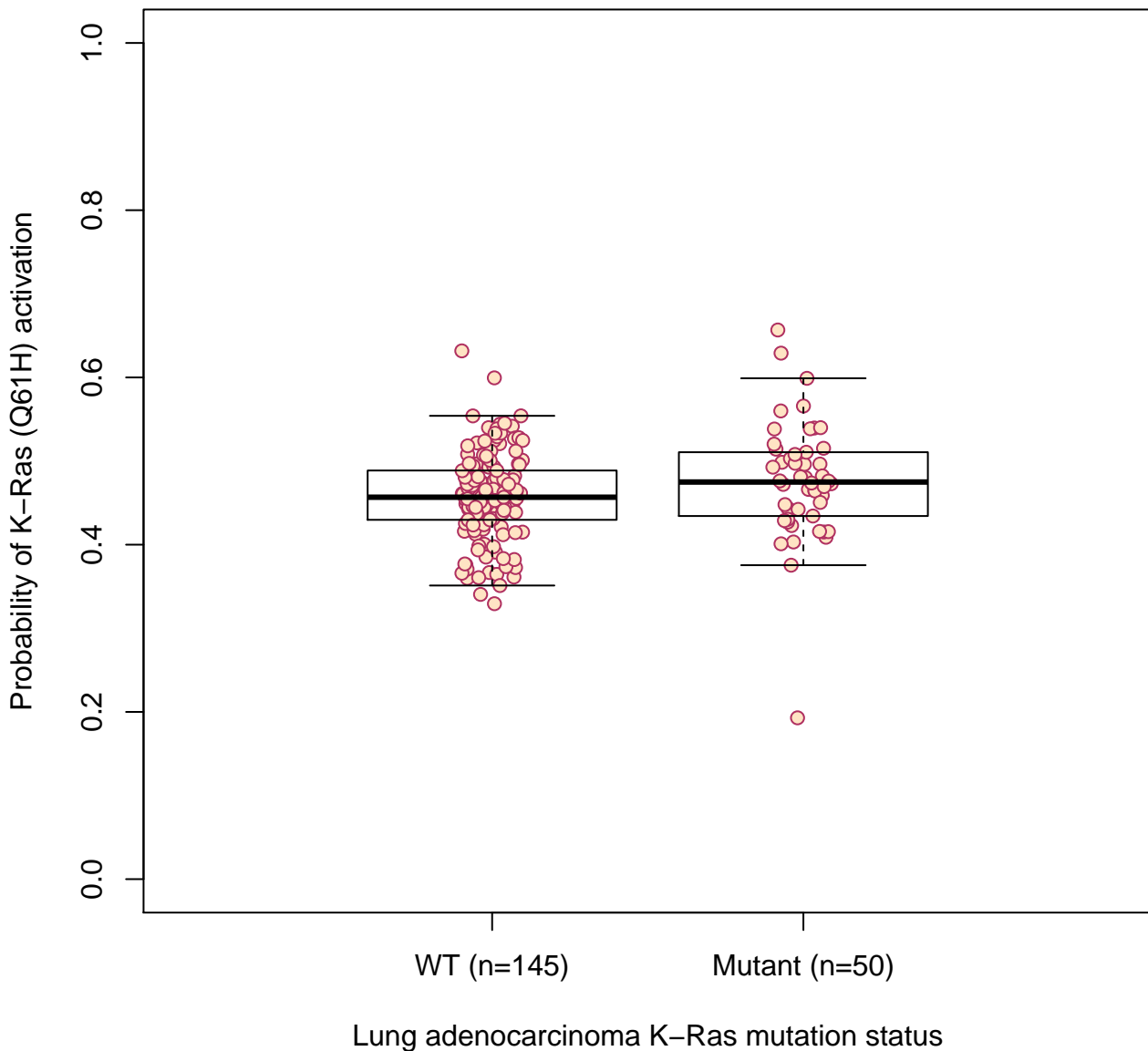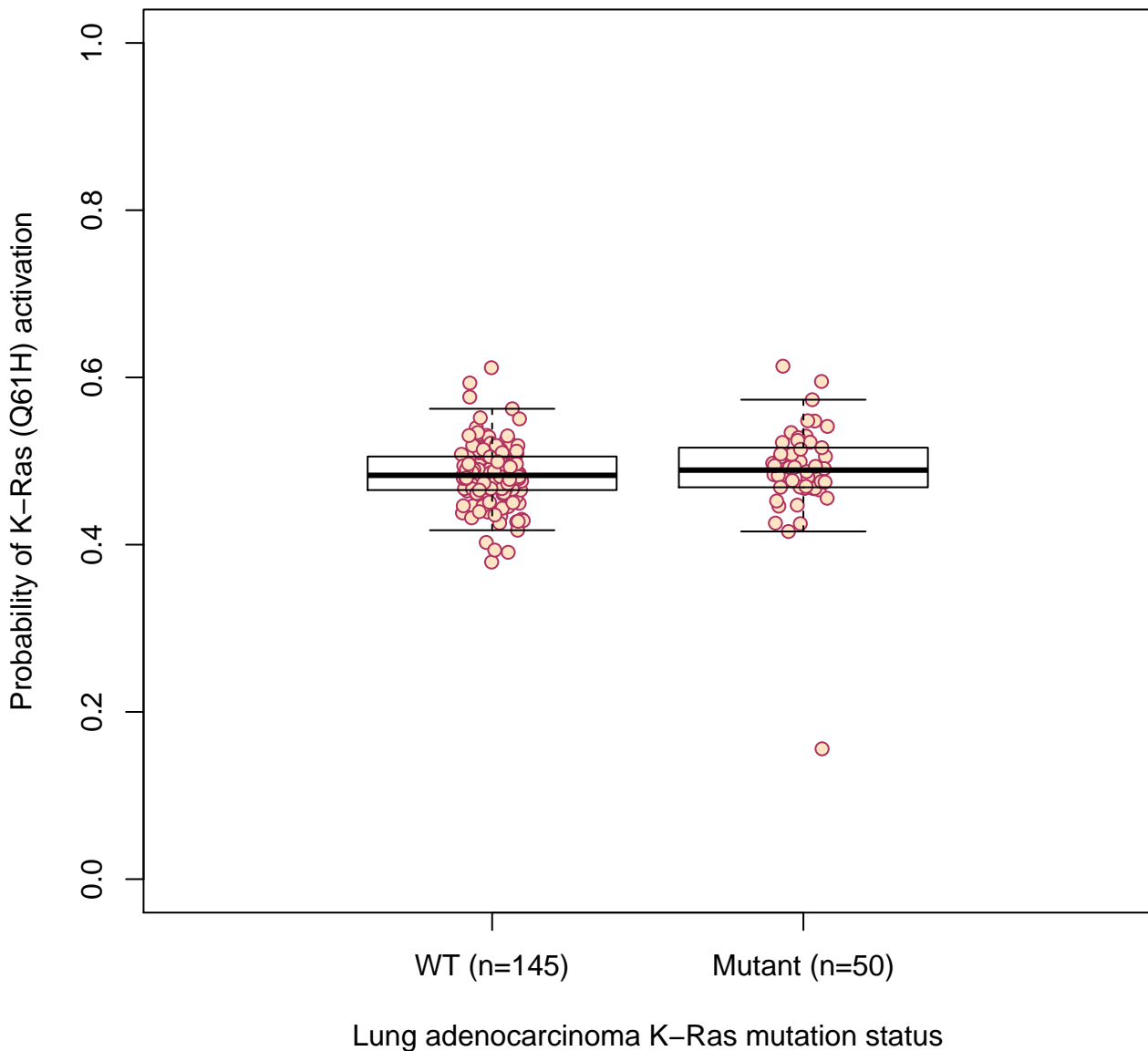**(p=0.160)**
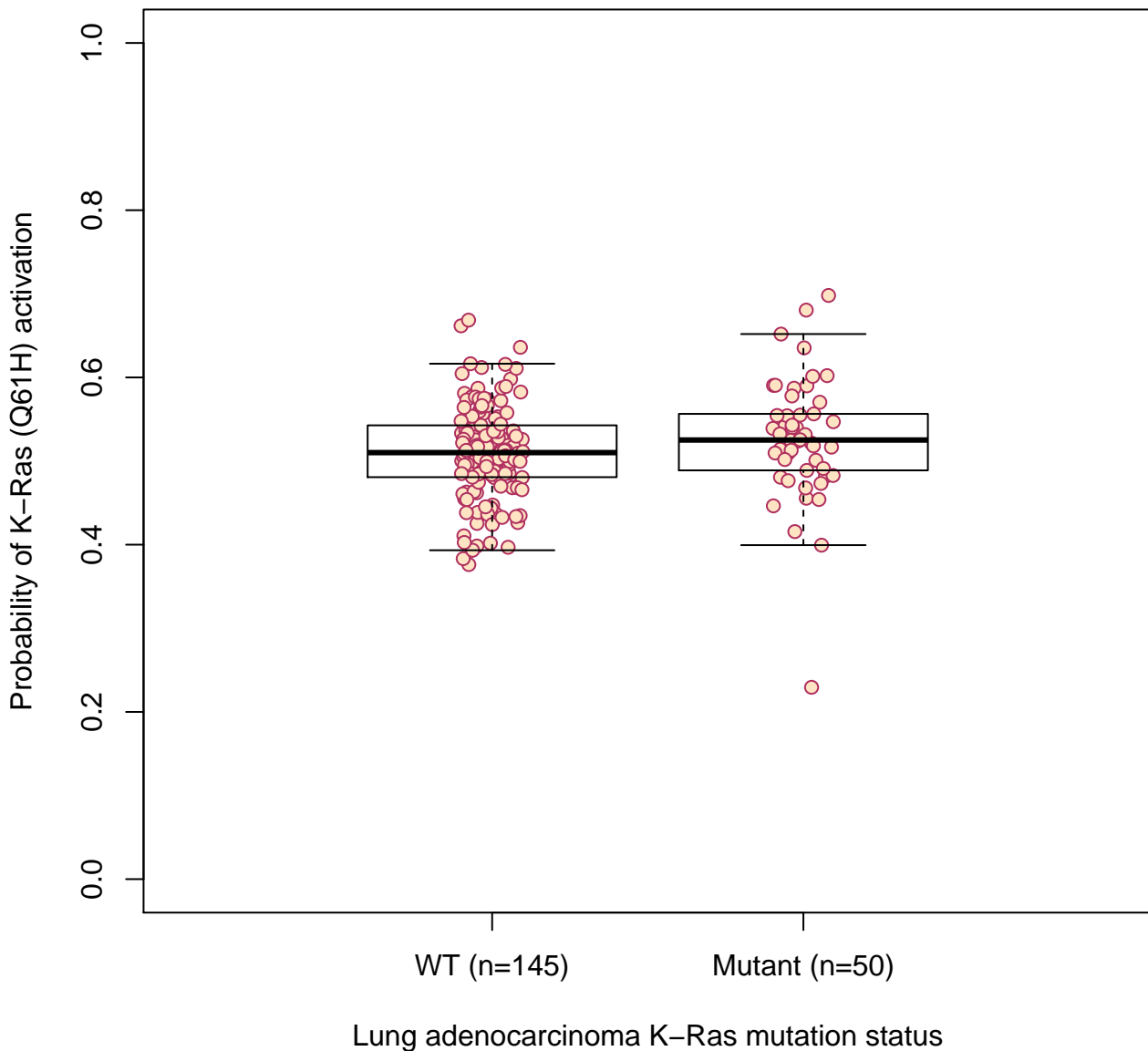
K−Ras Q61H signature validation
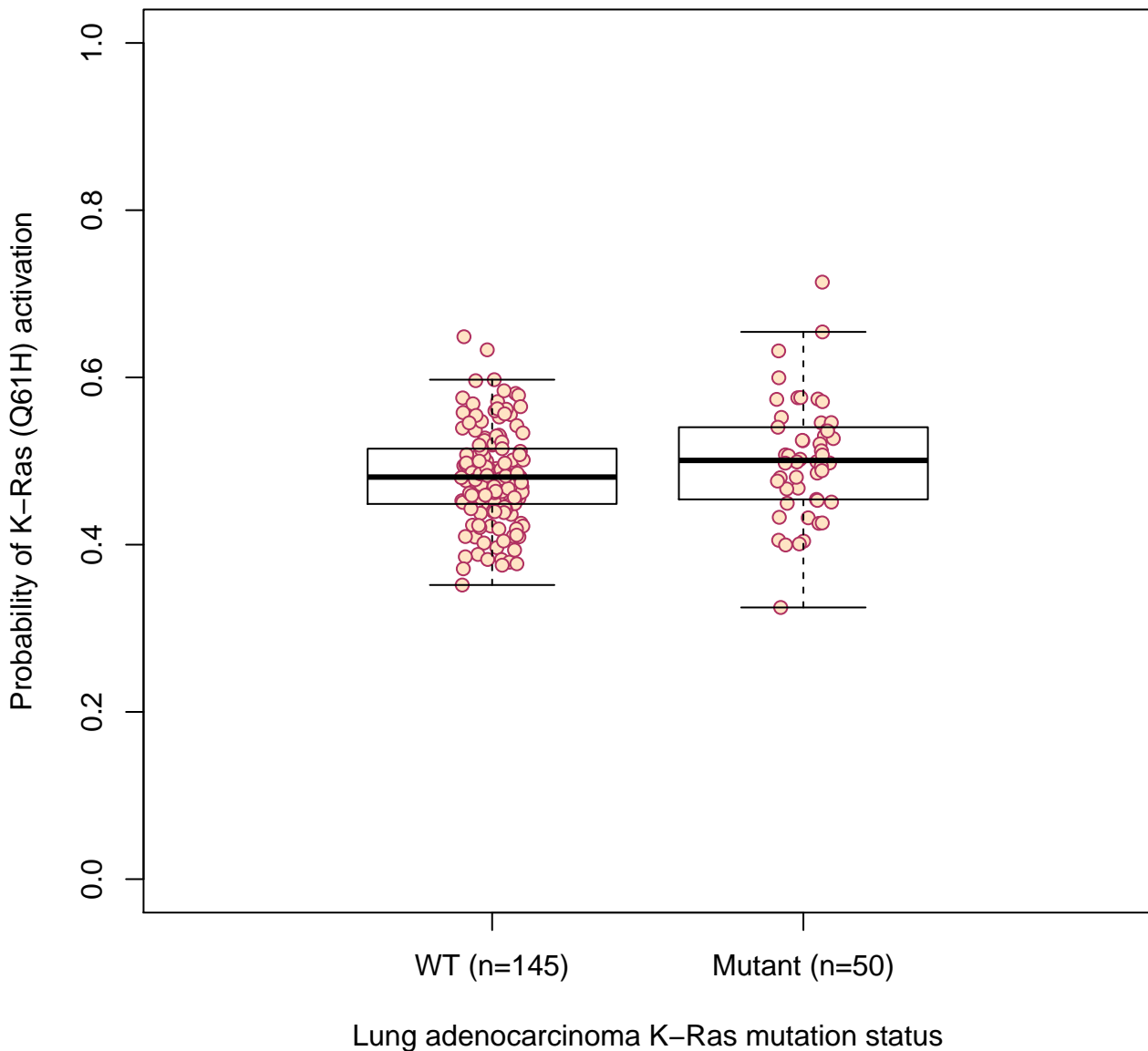Parameters: −q normalization, 200 genes, 2 metagene(s)
(p=0.093)

K−Ras Q61H signature validation
Parameters: −q normalization, 75 genes, 2 metagene(s)
(p=0.607)

K−Ras Q61H signature validation
Parameters: −q normalization, 125 genes, 3 metagene(s)
(p=0.169)

K−Ras Q61H signature validation
Parameters: −q normalization, 200 genes, 3 metagene(s)
(p=0.048)

K−Ras Q61H signature validation
Parameters: −q normalization, 75 genes, 3 metagene(s)
(p=0.648)