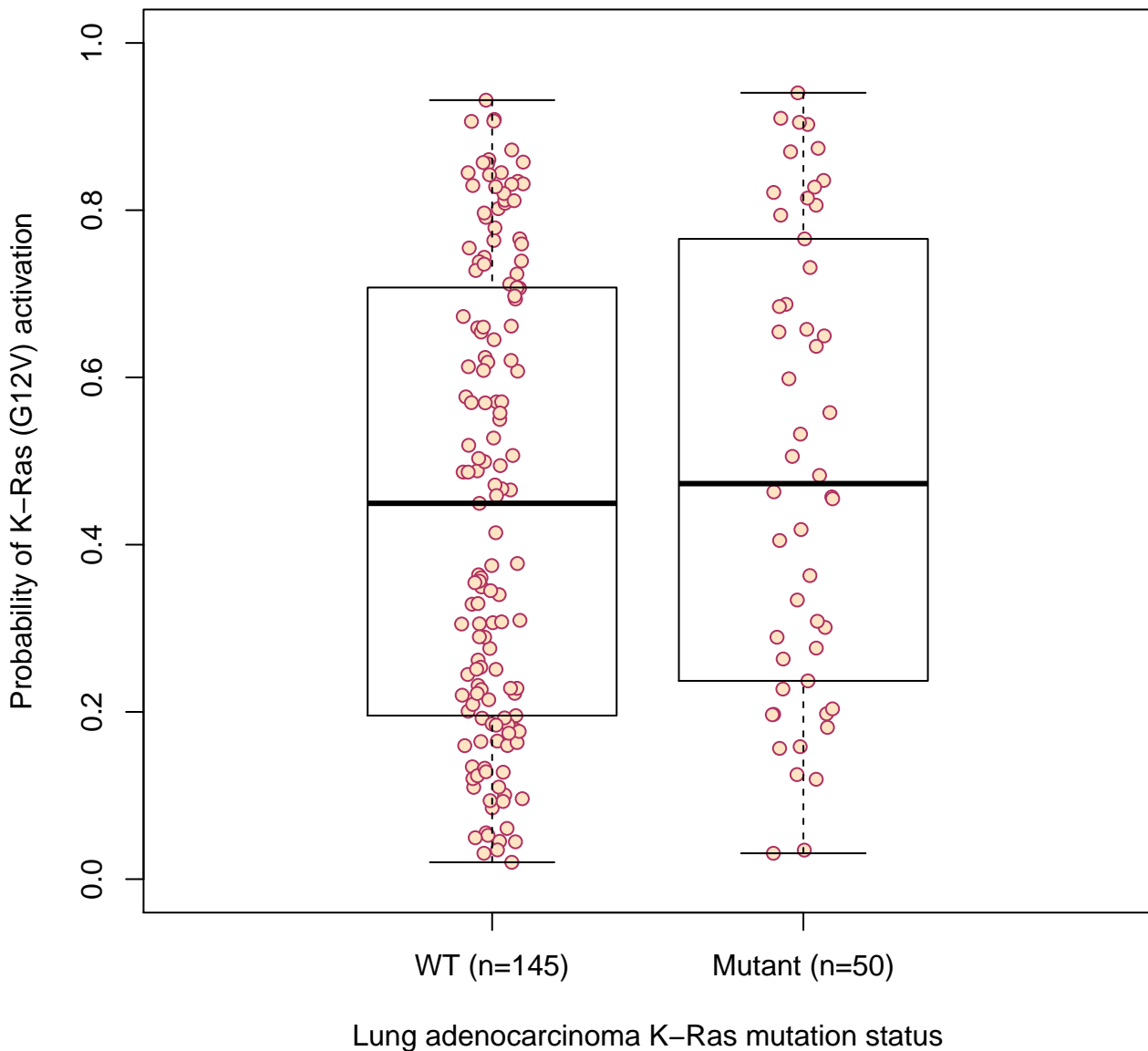
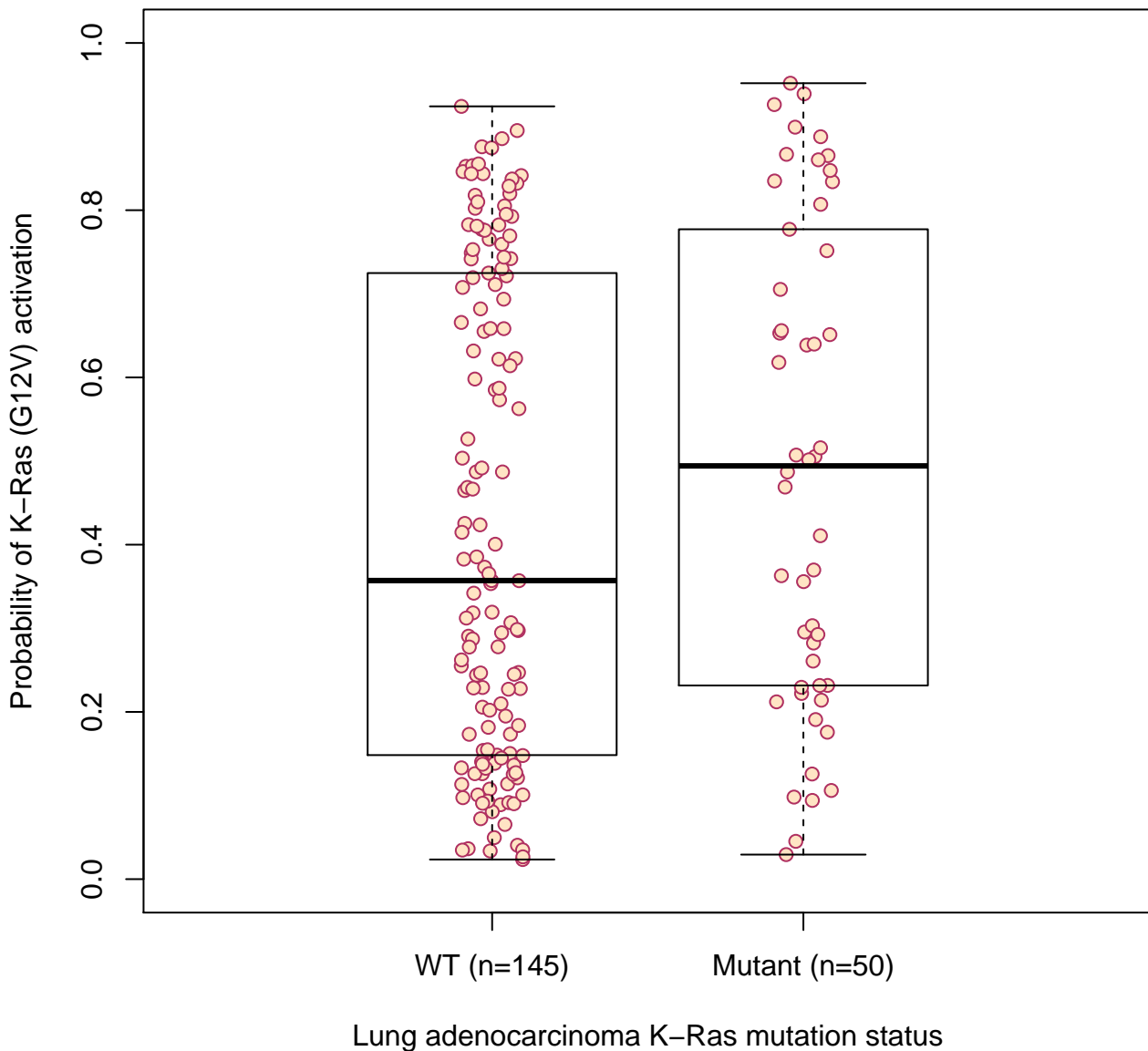


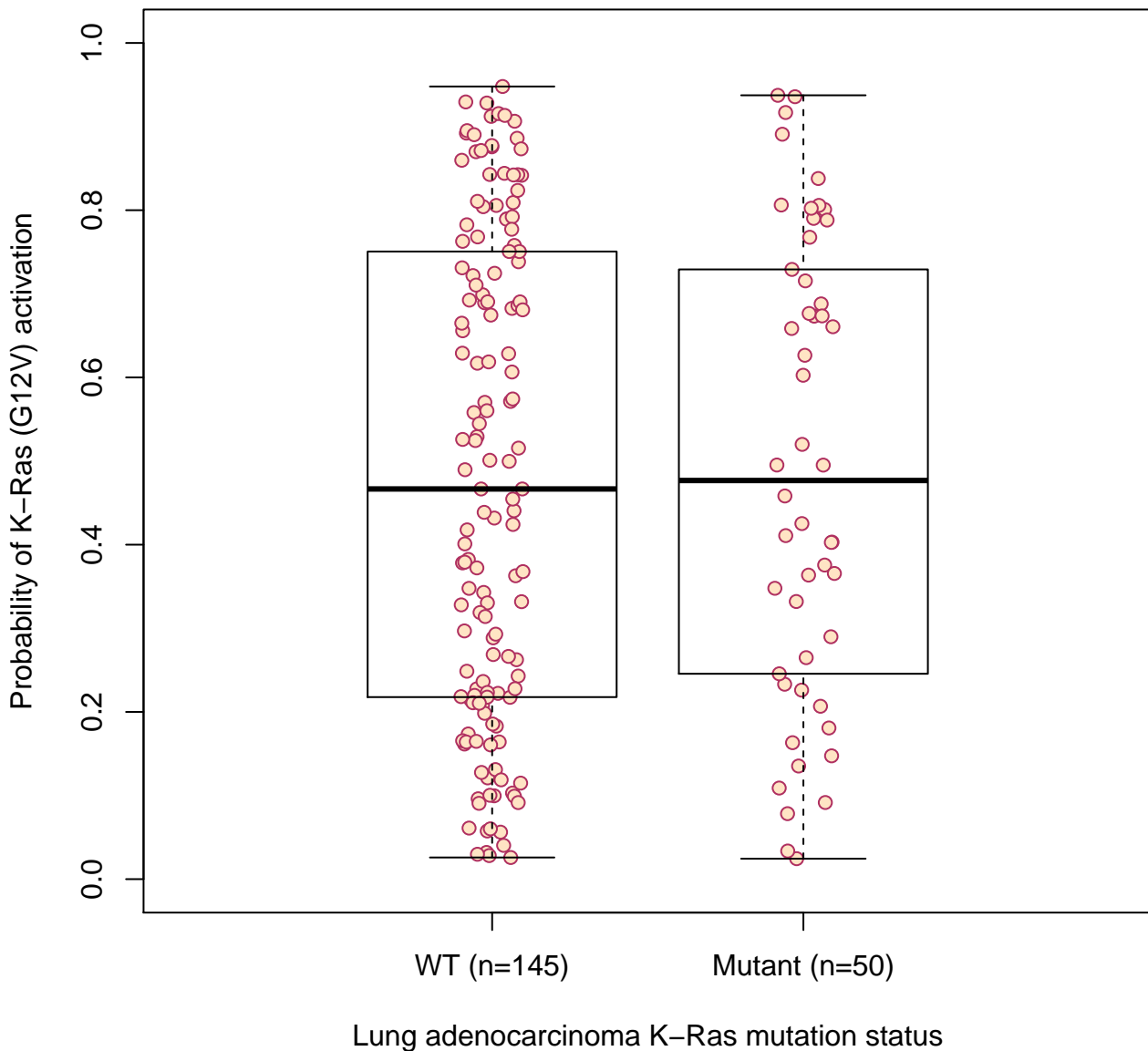
K-Ras G12V signature validation
Parameters: -d normalization, 125 genes, 1 metagene(s)
(p=0.289)



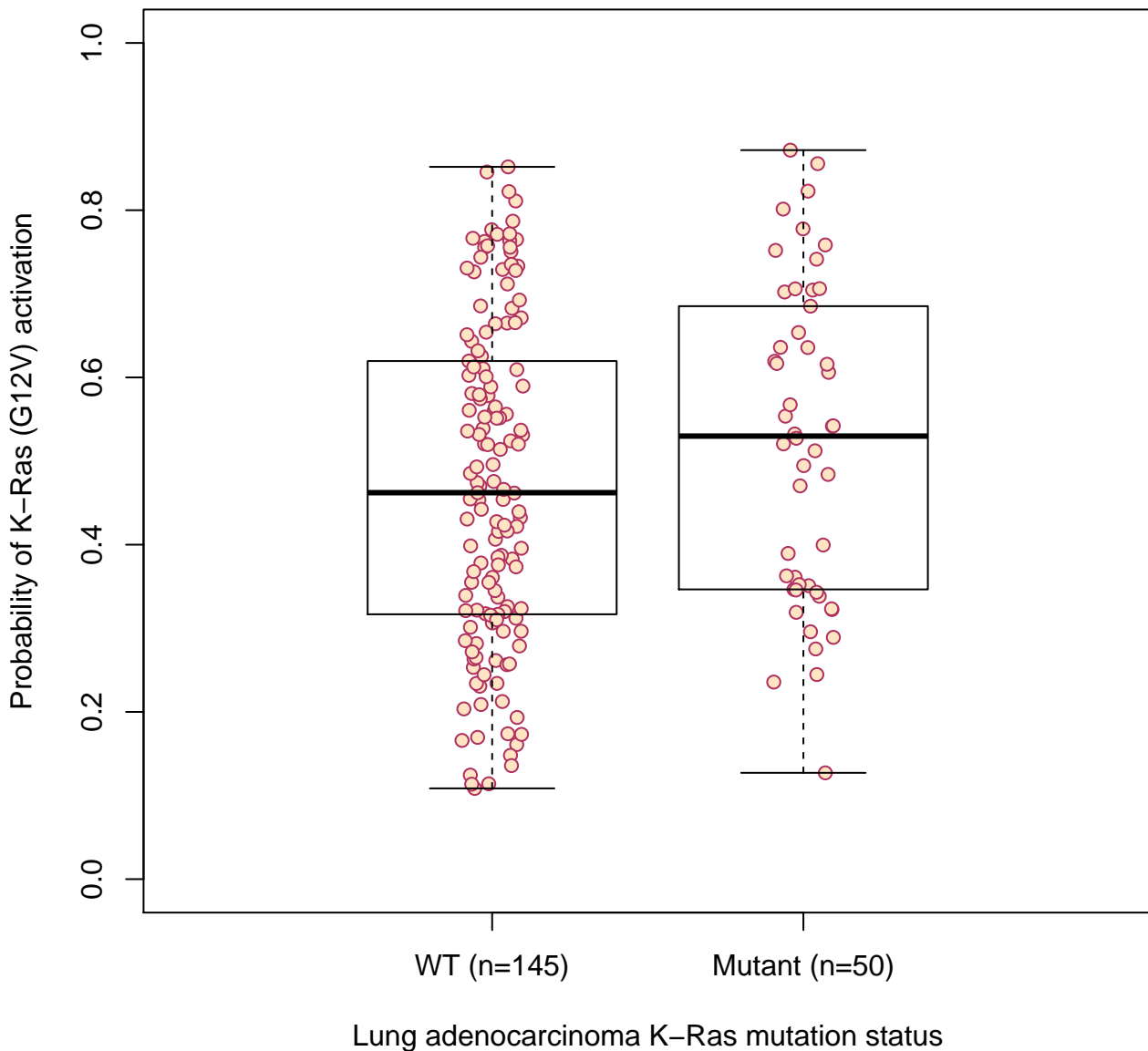
K-Ras G12V signature validation
Parameters: -d normalization, 200 genes, 1 metagene(s)
(p=0.155)



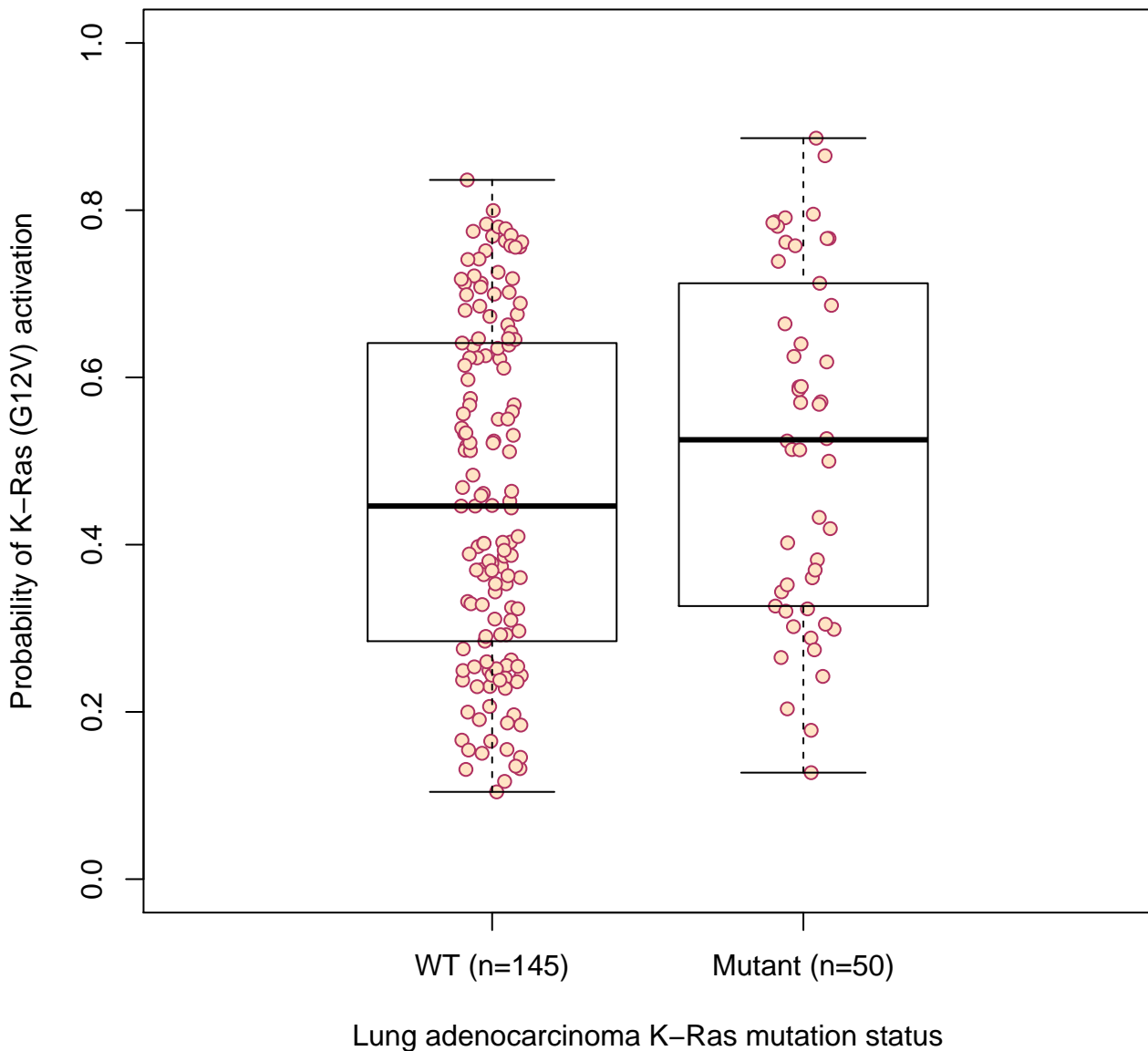
K-Ras G12V signature validation
Parameters: -d normalization, 75 genes, 1 metagene(s)
(p=0.761)



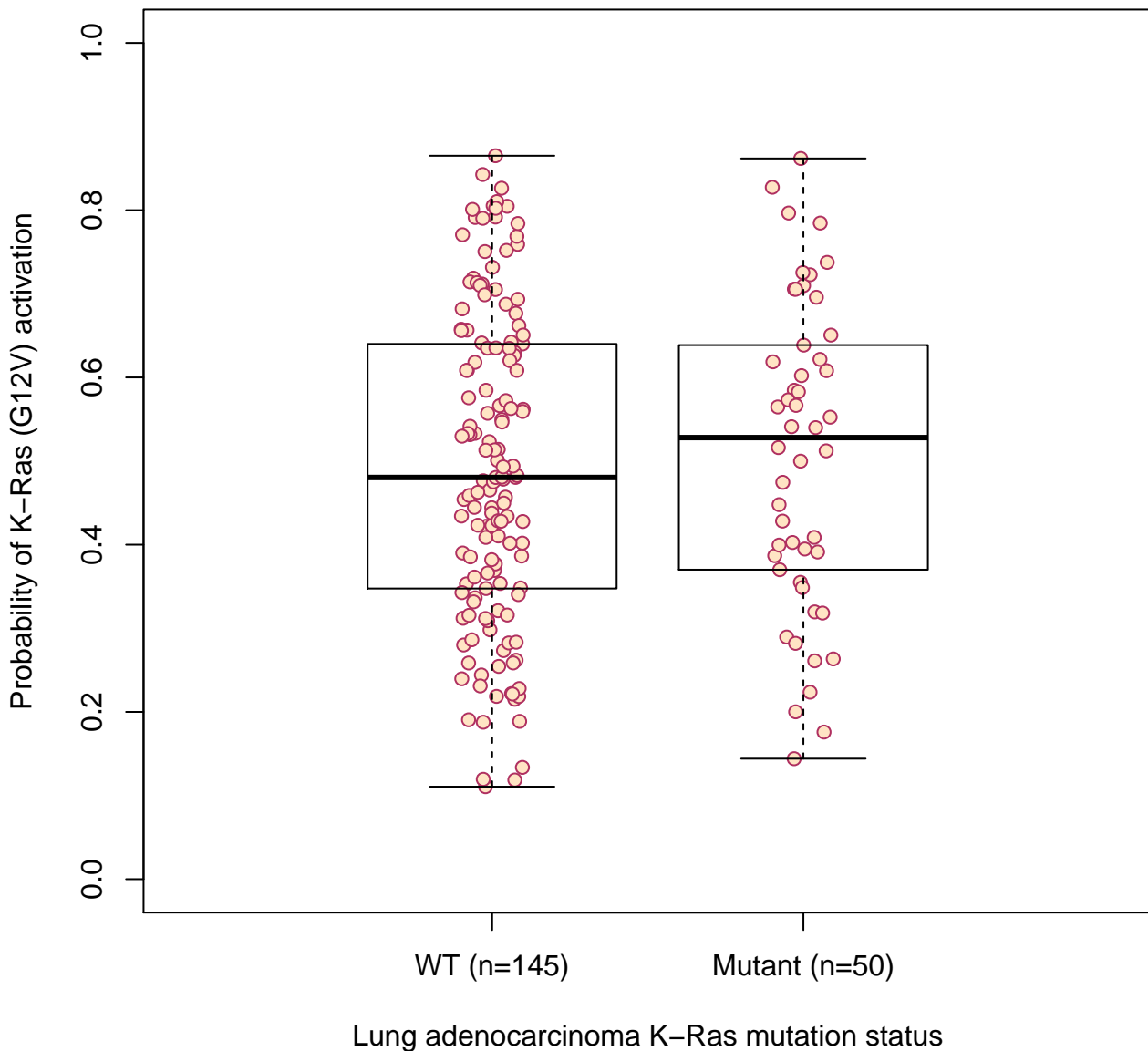
K-Ras G12V signature validation
Parameters: -d normalization, 125 genes, 2 metagene(s)
(p=0.122)



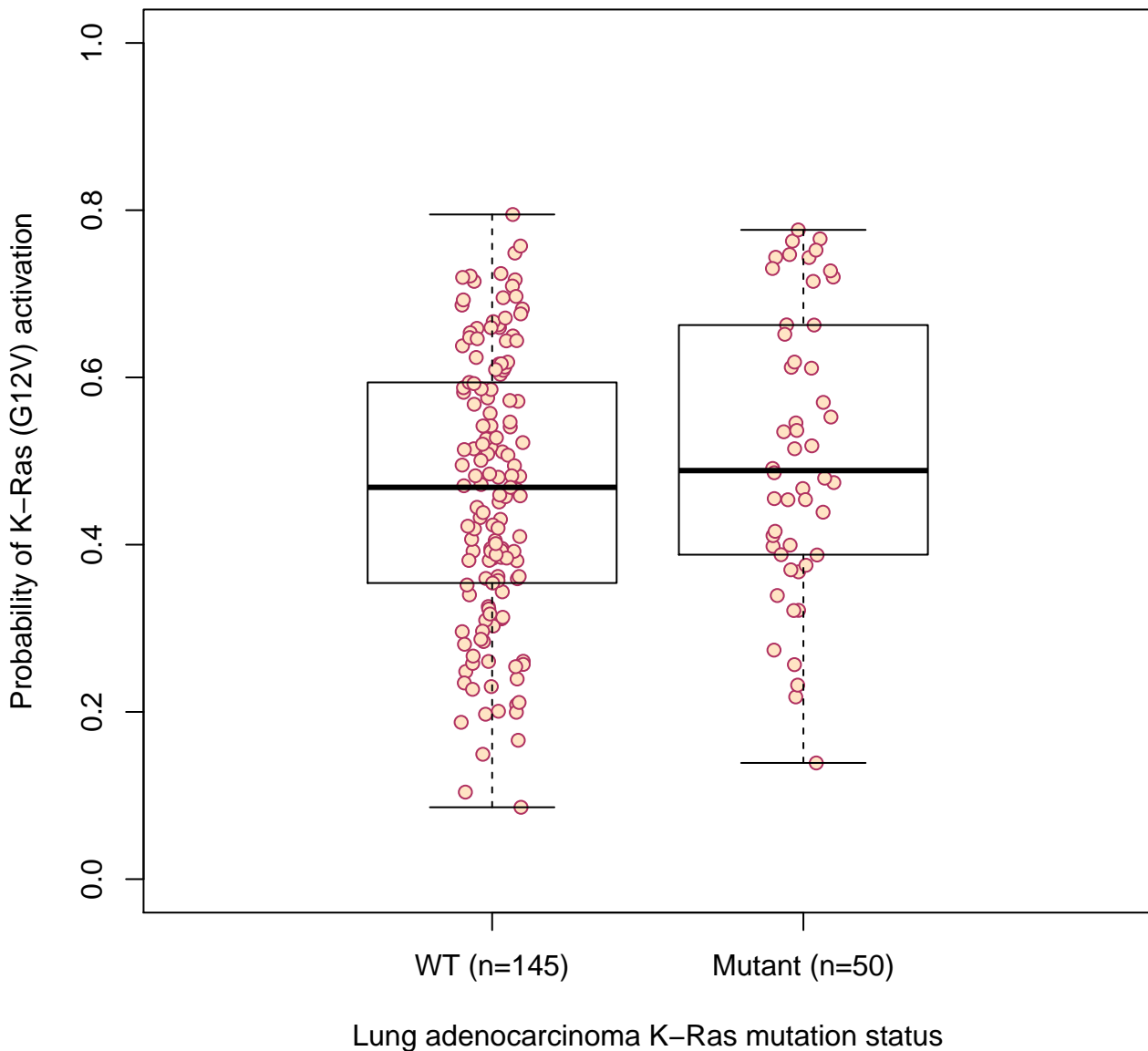
K-Ras G12V signature validation
Parameters: -d normalization, 200 genes, 2 metagene(s)
(p=0.078)



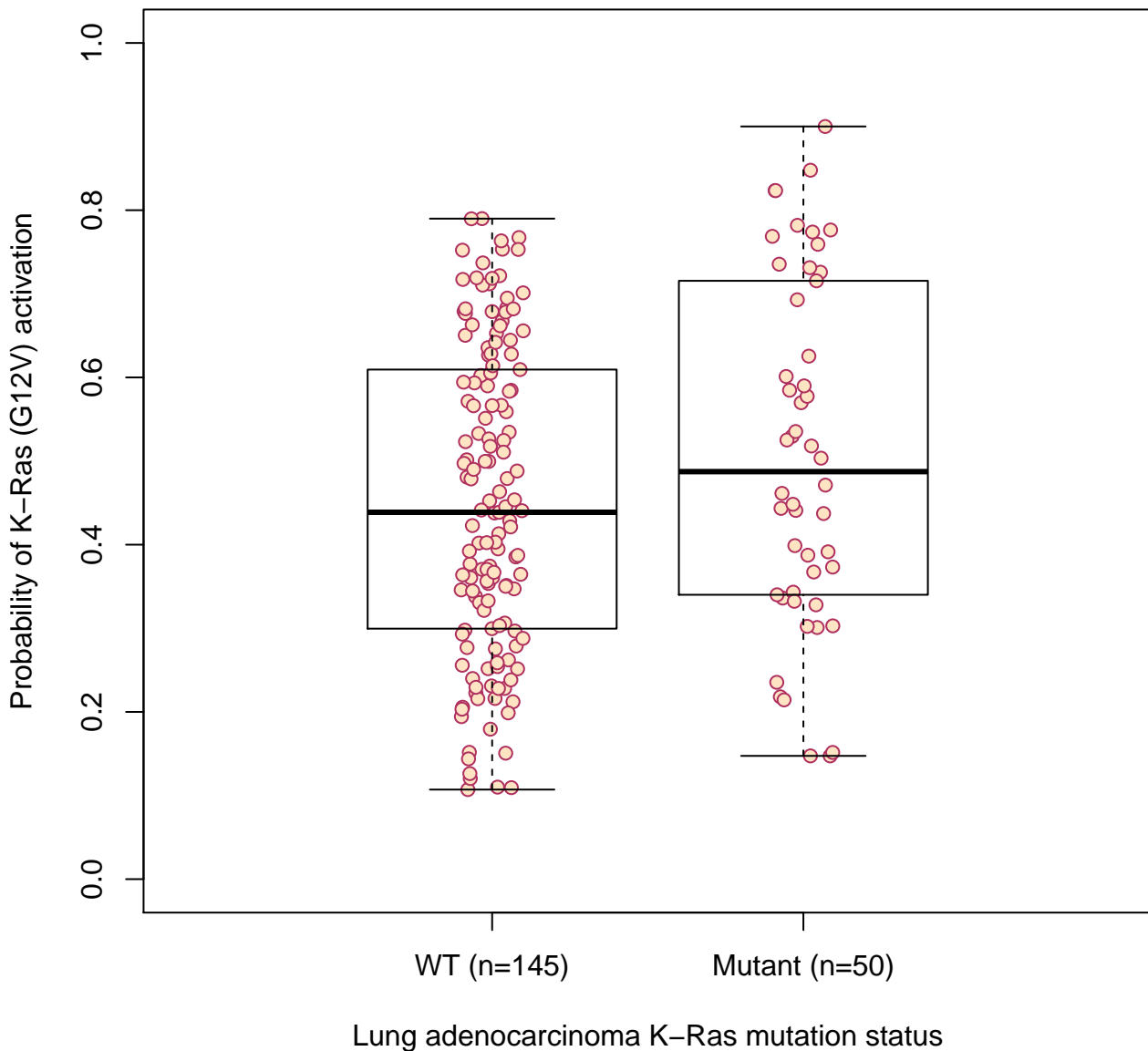
K-Ras G12V signature validation
Parameters: -d normalization, 75 genes, 2 metagene(s)
(p=0.608)



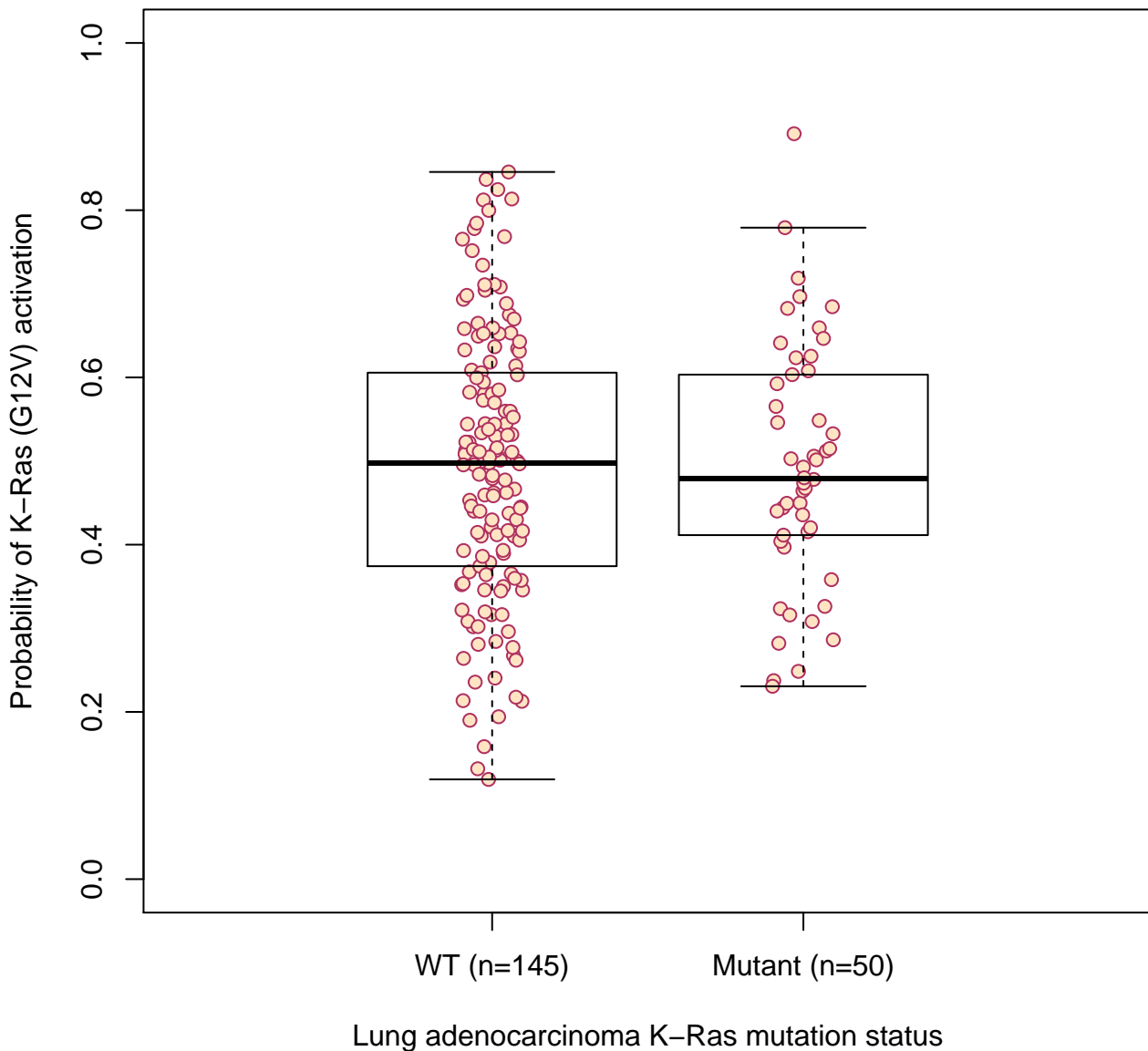
K-Ras G12V signature validation
Parameters: -d normalization, 125 genes, 3 metagene(s)
(p=0.088)



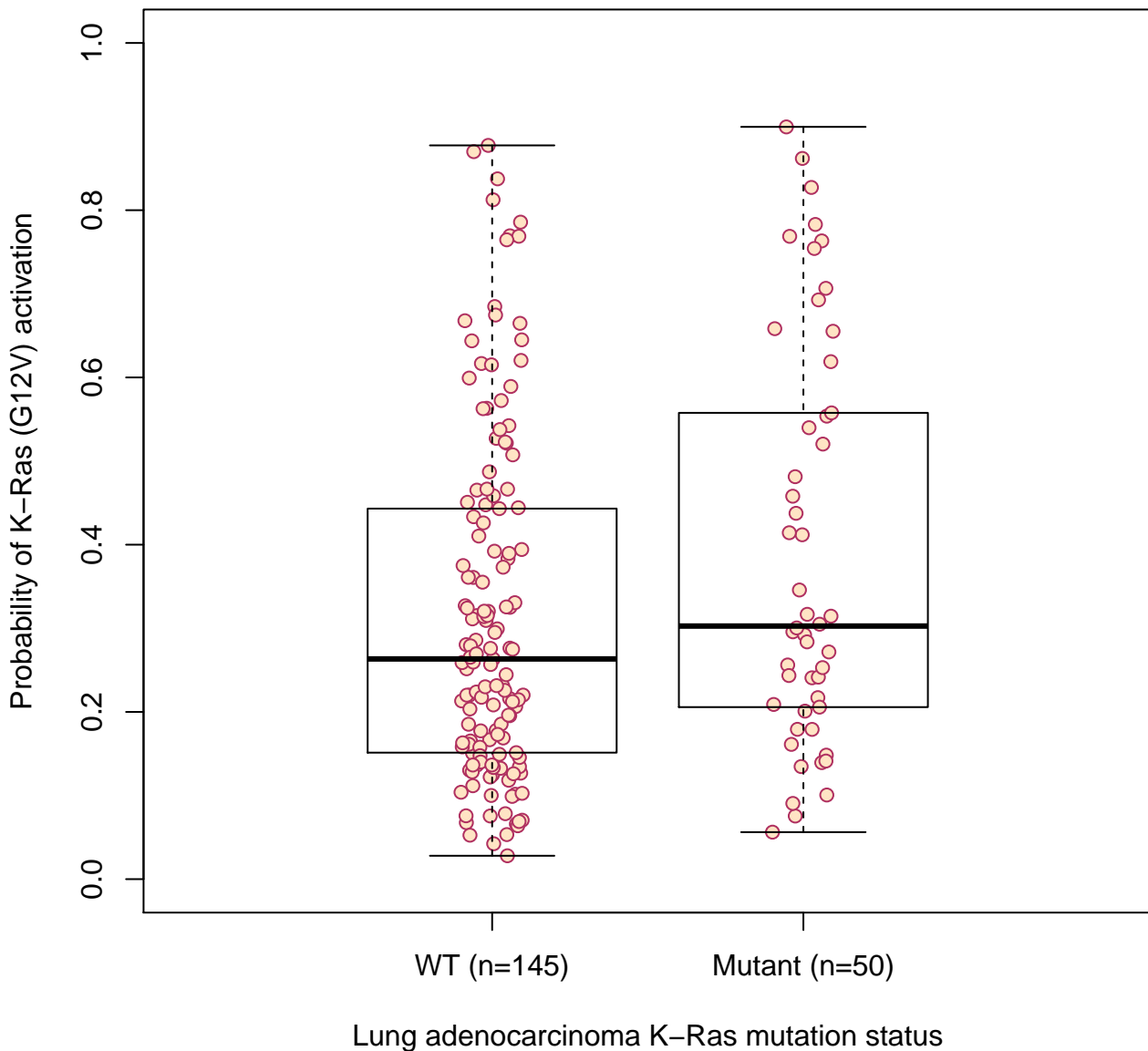
K-Ras G12V signature validation
Parameters: -d normalization, 200 genes, 3 metagene(s)
(p=0.093)



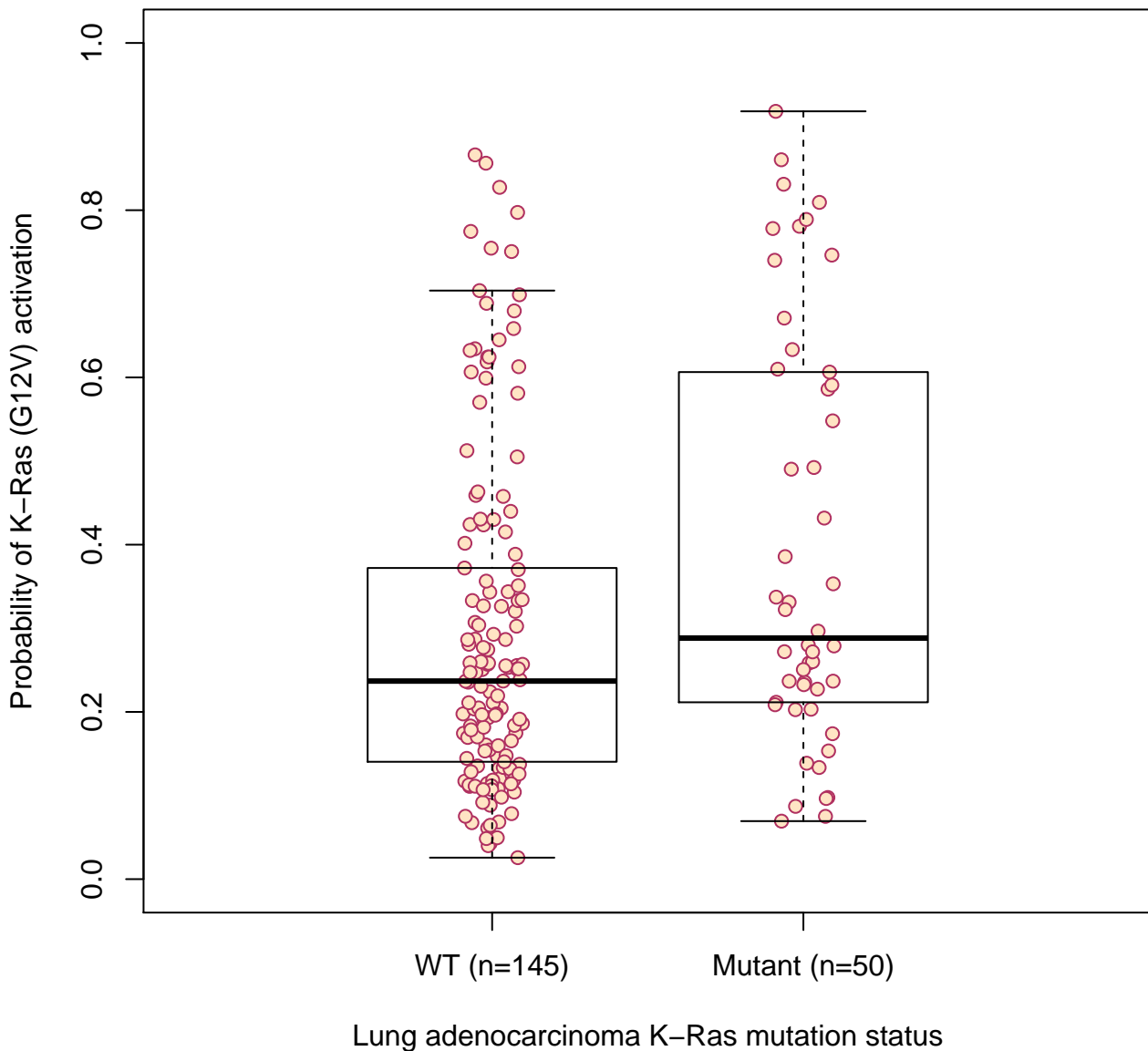
K-Ras G12V signature validation
Parameters: -d normalization, 75 genes, 3 metagene(s)
(p=0.977)



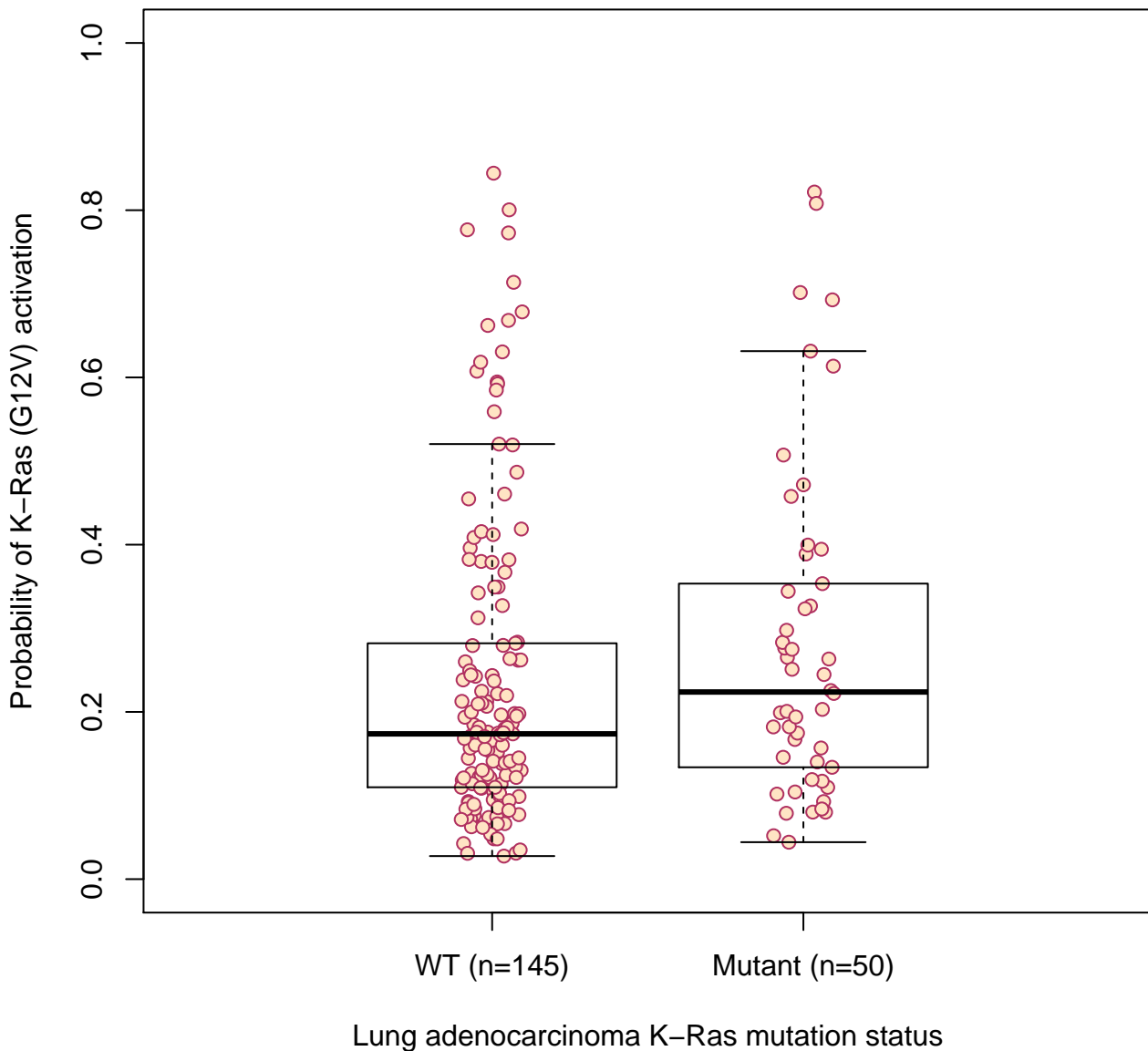
K-Ras G12V signature validation
Parameters: -q normalization, 125 genes, 1 metagene(s)
(p=0.045)



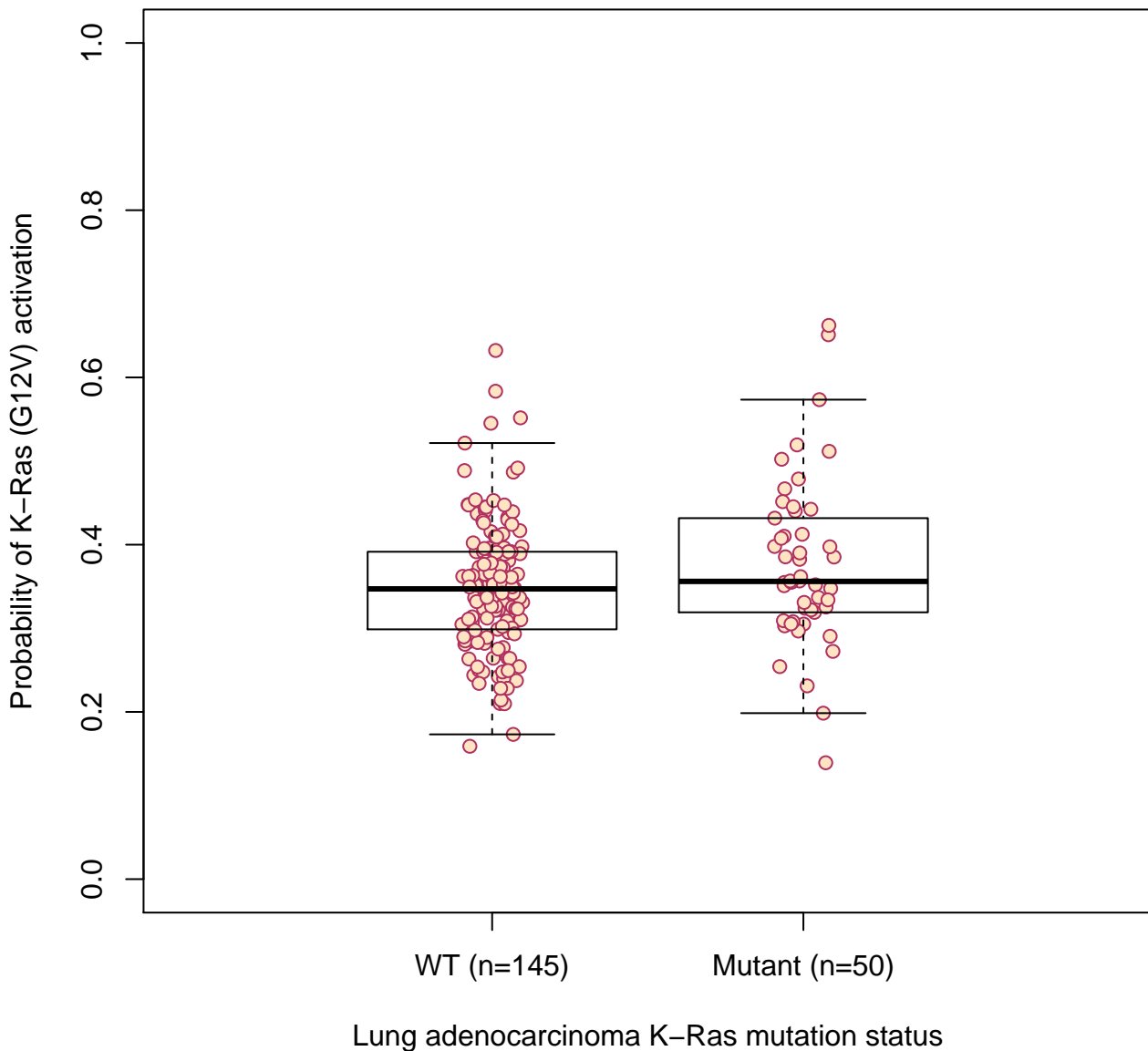
K-Ras G12V signature validation
Parameters: -q normalization, 200 genes, 1 metagene(s)
(p=0.010)



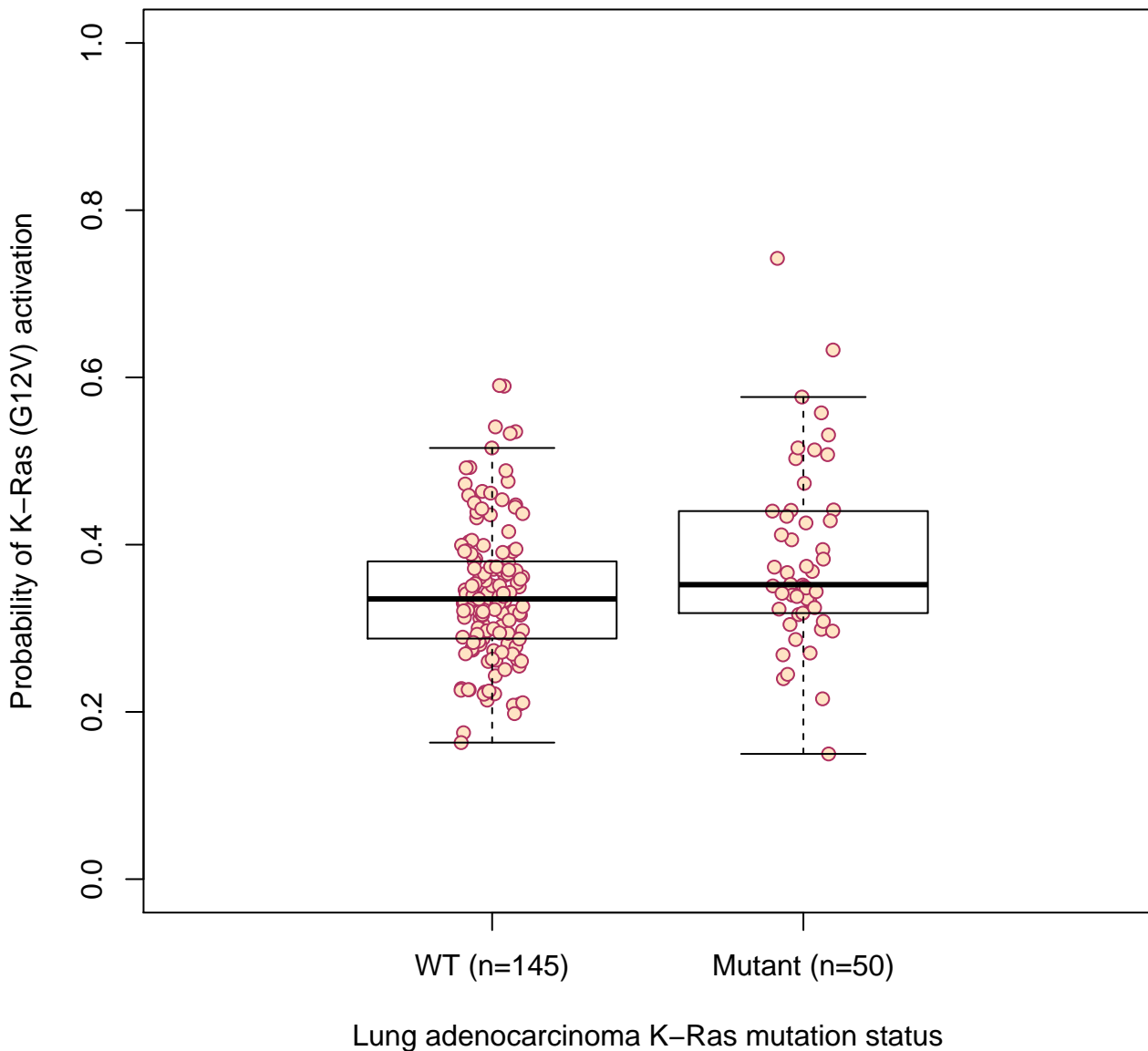
K-Ras G12V signature validation
Parameters: -q normalization, 75 genes, 1 metagene(s)
(p=0.173)



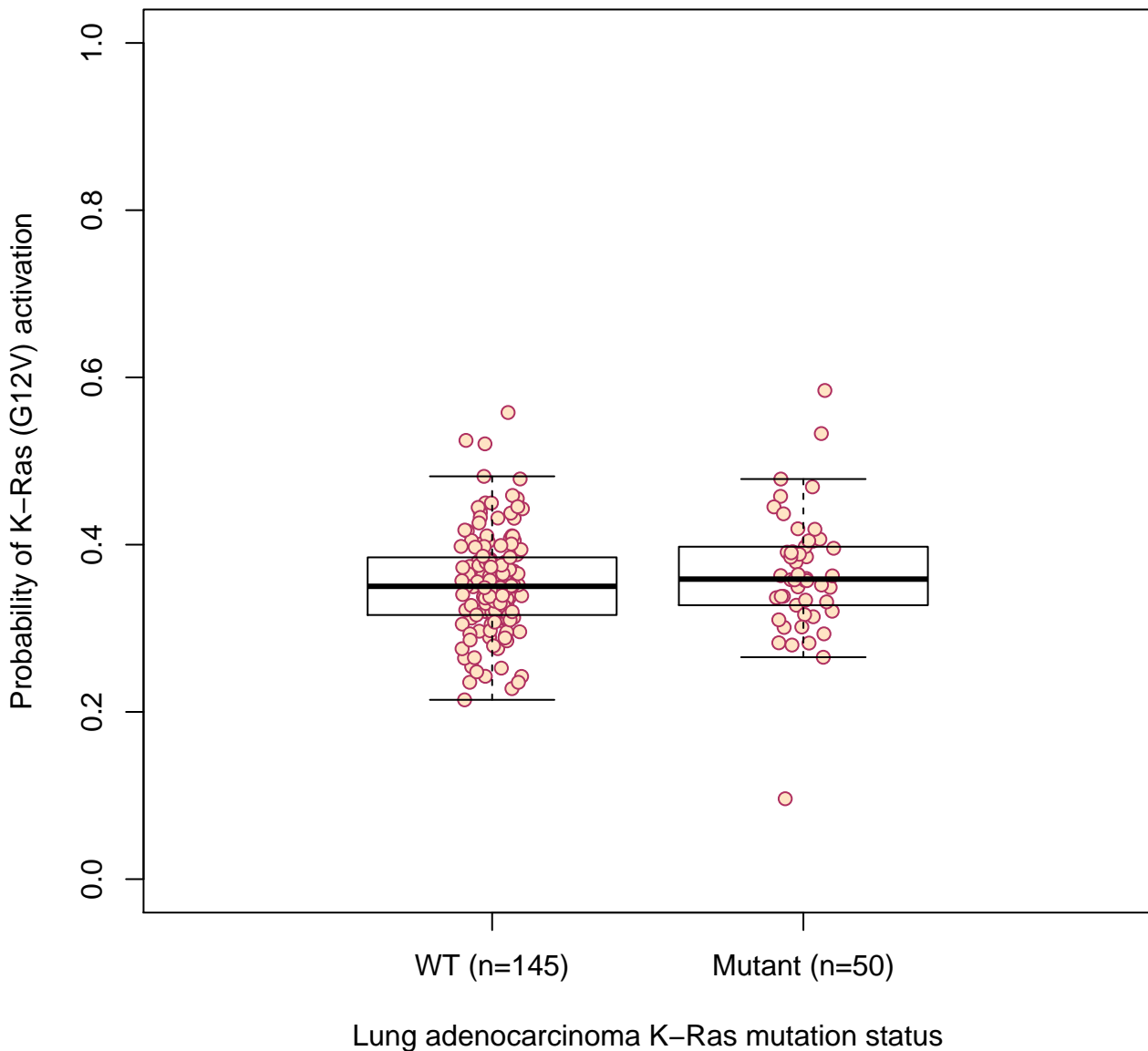
K-Ras G12V signature validation
Parameters: -q normalization, 125 genes, 2 metagene(s)
(p=0.072)



K-Ras G12V signature validation
Parameters: -q normalization, 200 genes, 2 metagene(s)
(p=0.015)

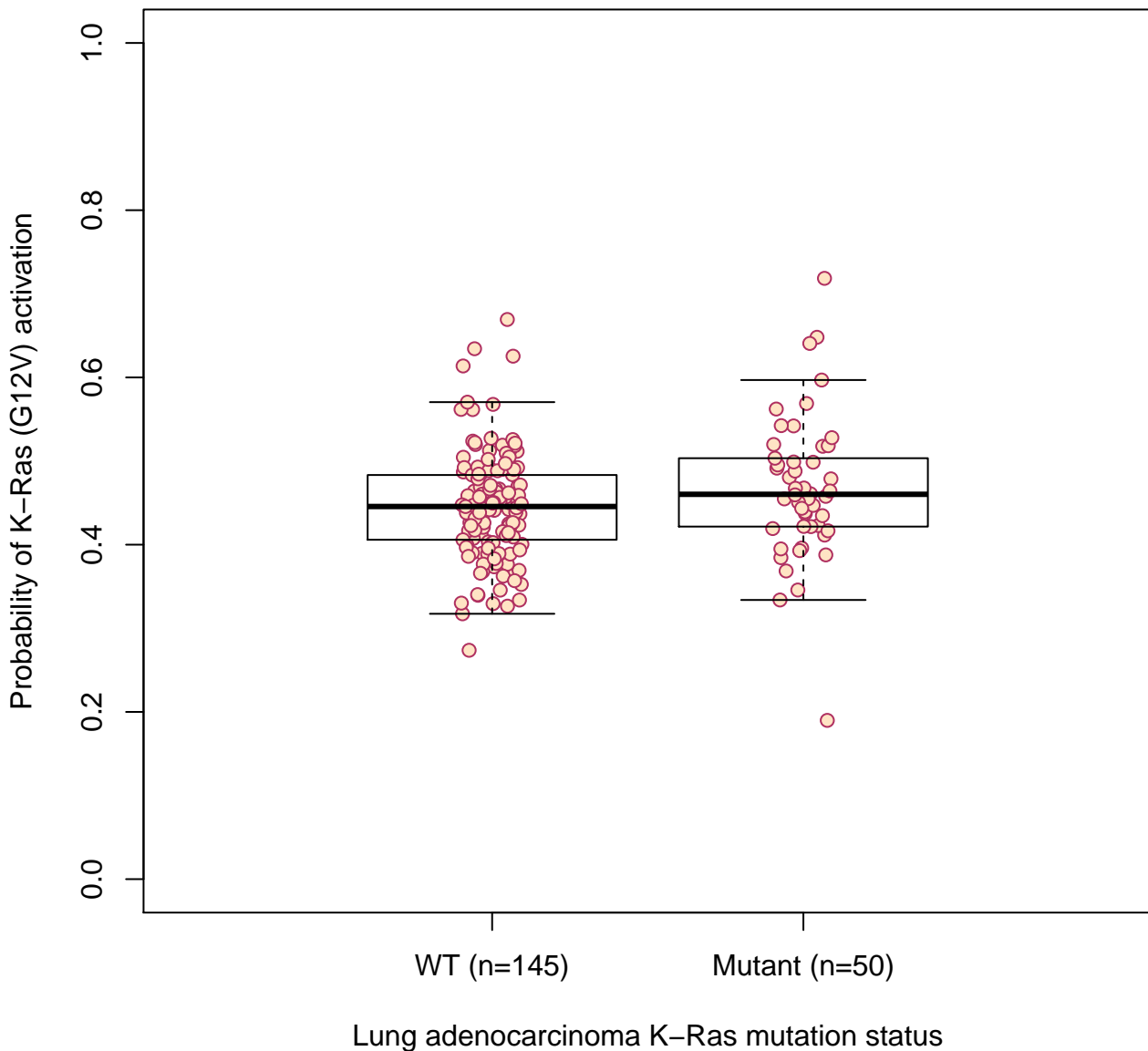


K-Ras G12V signature validation
Parameters: -q normalization, 75 genes, 2 metagene(s)
(p=0.325)

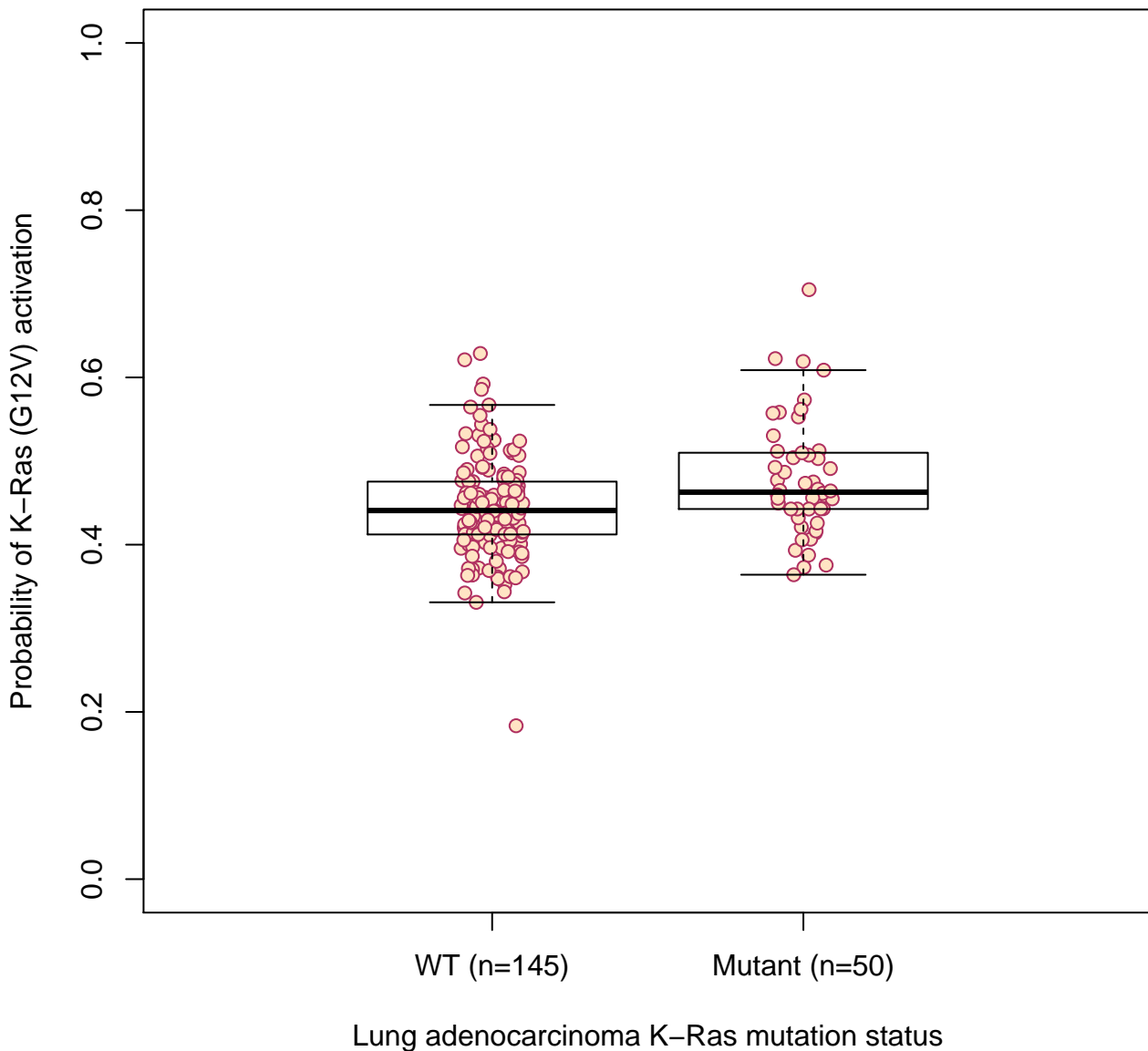


K-Ras G12V signature validation

Parameters: -q normalization, 125 genes, 3 metagene(s)
(p=0.099)



K-Ras G12V signature validation
Parameters: -q normalization, 200 genes, 3 metagene(s)
(p=0.003)



K-Ras G12V signature validation
Parameters: -q normalization, 75 genes, 3 metagene(s)
(p=1.000)

