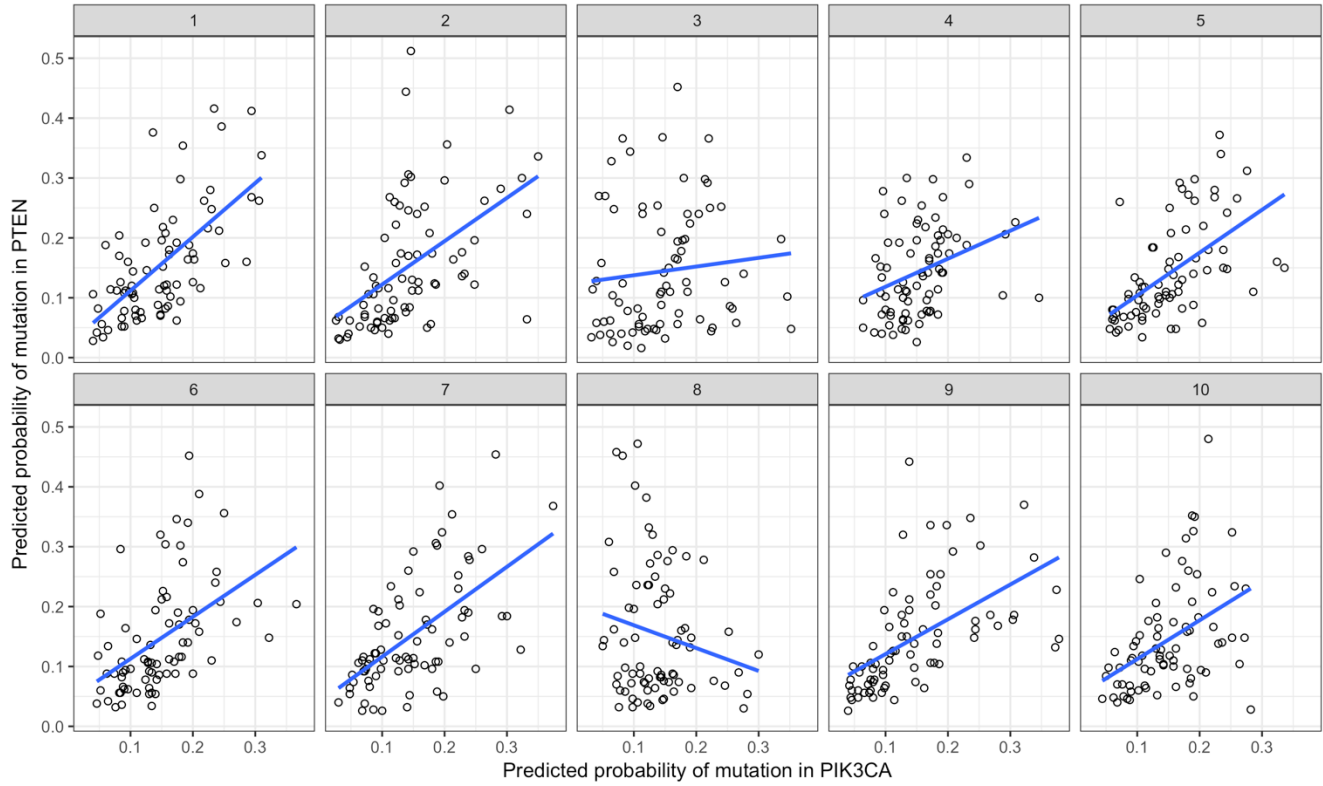


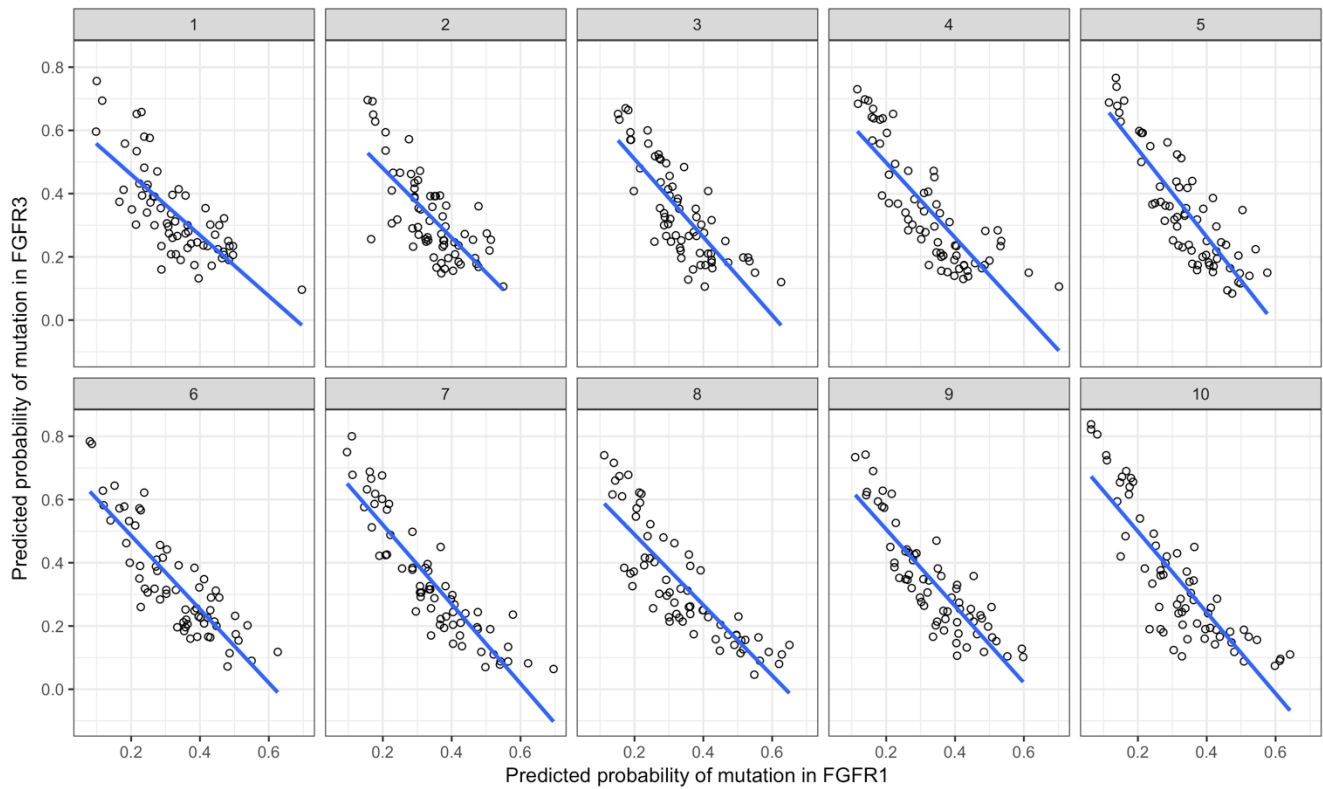
# Supplementary Material

Classifying cancer genome aberrations by their mutually exclusive effects on transcription

Jonathan B. Dayton, Stephen R. Piccolo

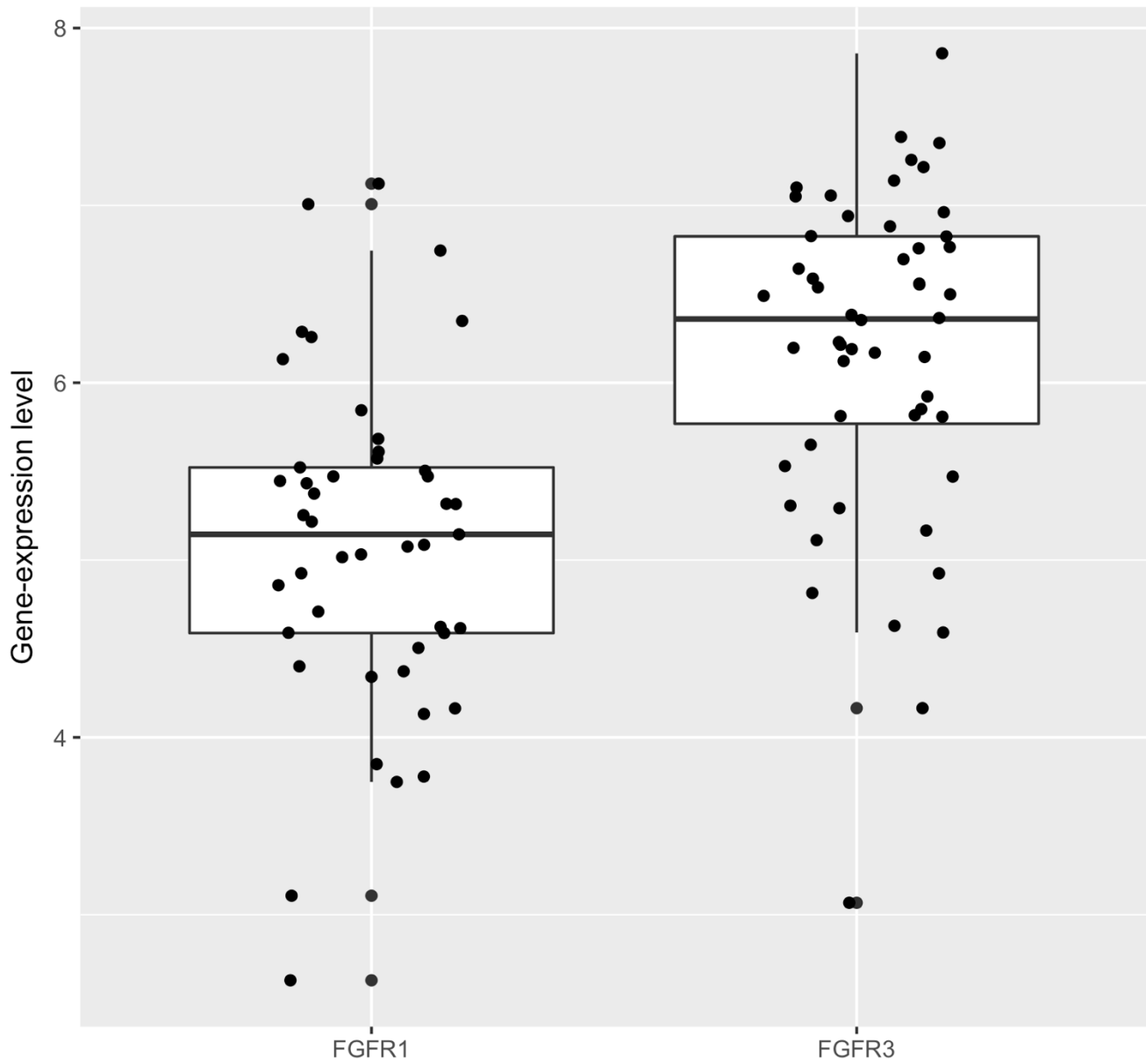


**Figure S1:** Scatterplots depicting correlations between predicted probabilities for breast-carcinoma samples with a mutation in *PIK3CA* or *PTEN*. Each scatterplot represents probabilistic predictions for a single iteration of cross validation.



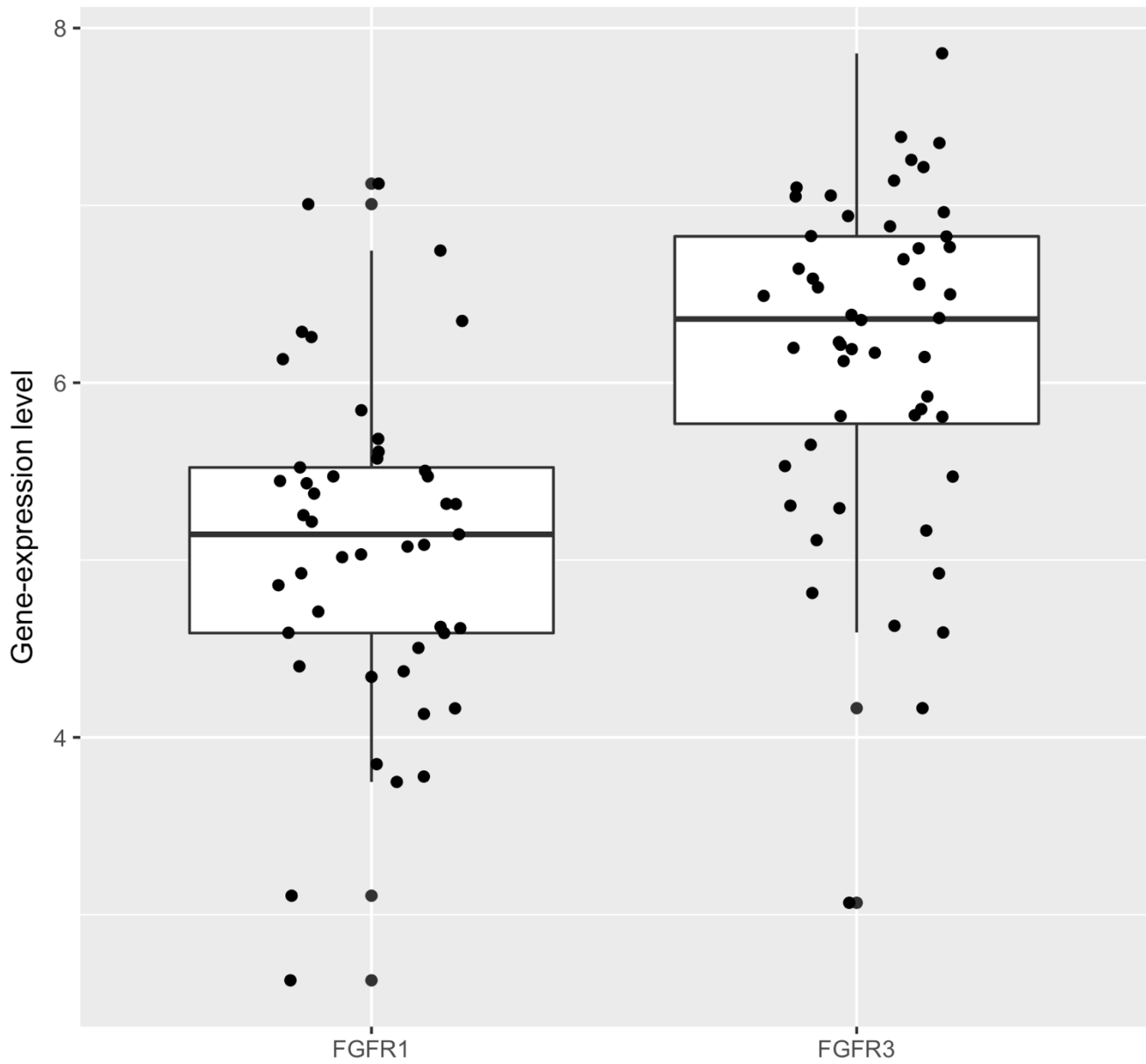
**Figure S2:** Scatterplots depicting correlations between predicted probabilities for bladder-carcinoma samples with a mutation in *PIK3CA* or *PTEN*. Each scatterplot represents probabilistic predictions for a single iteration of cross validation.

Cancer Type: BLCA; Gene: SMAD3



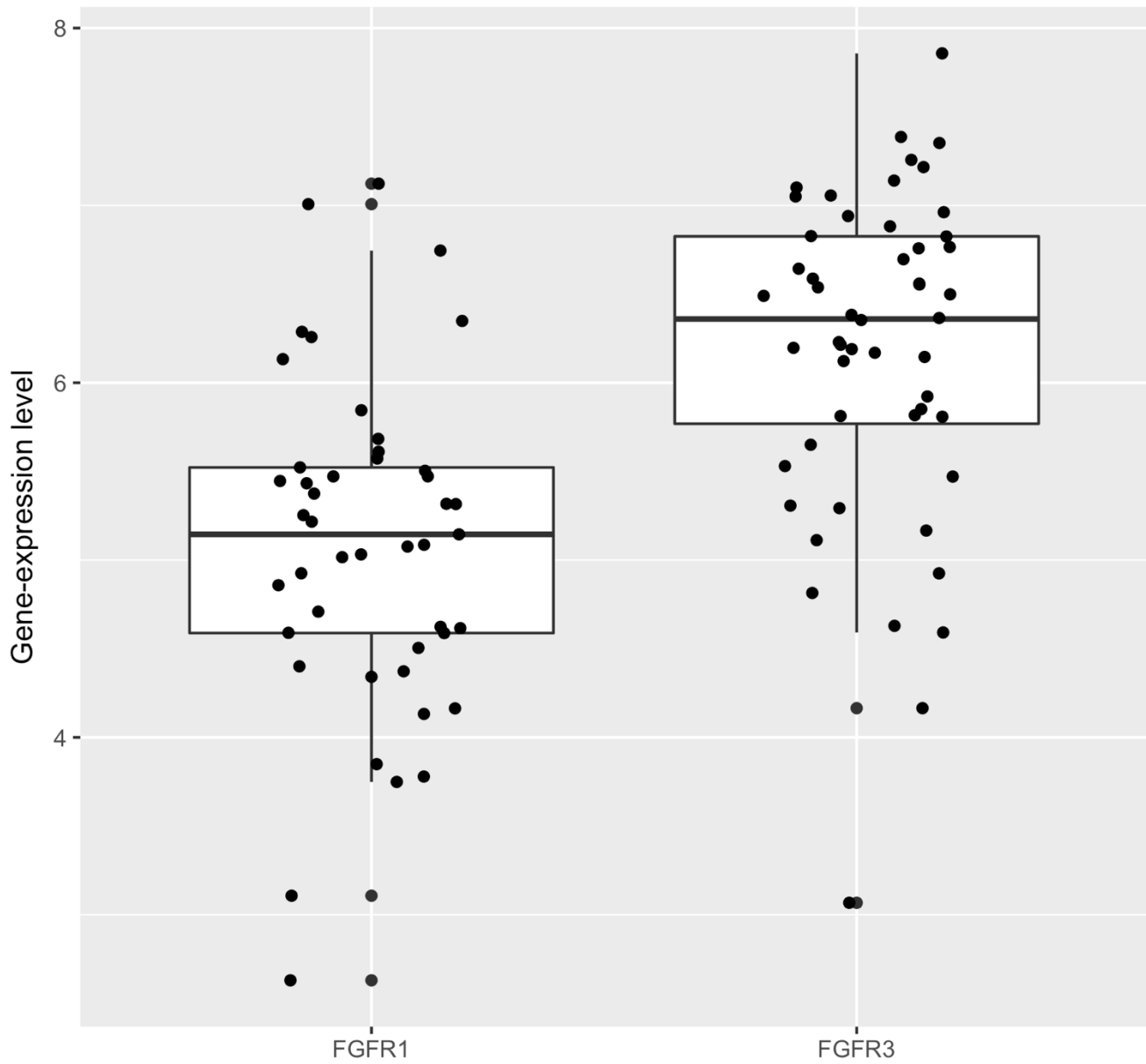
**Figure S3:** Expression levels of the *SMAD3* gene for bladder-carcinoma samples that possessed a somatic mutation in either *FGFR1* or *FGFR3*.

Cancer Type: BLCA; Gene: SMAD3



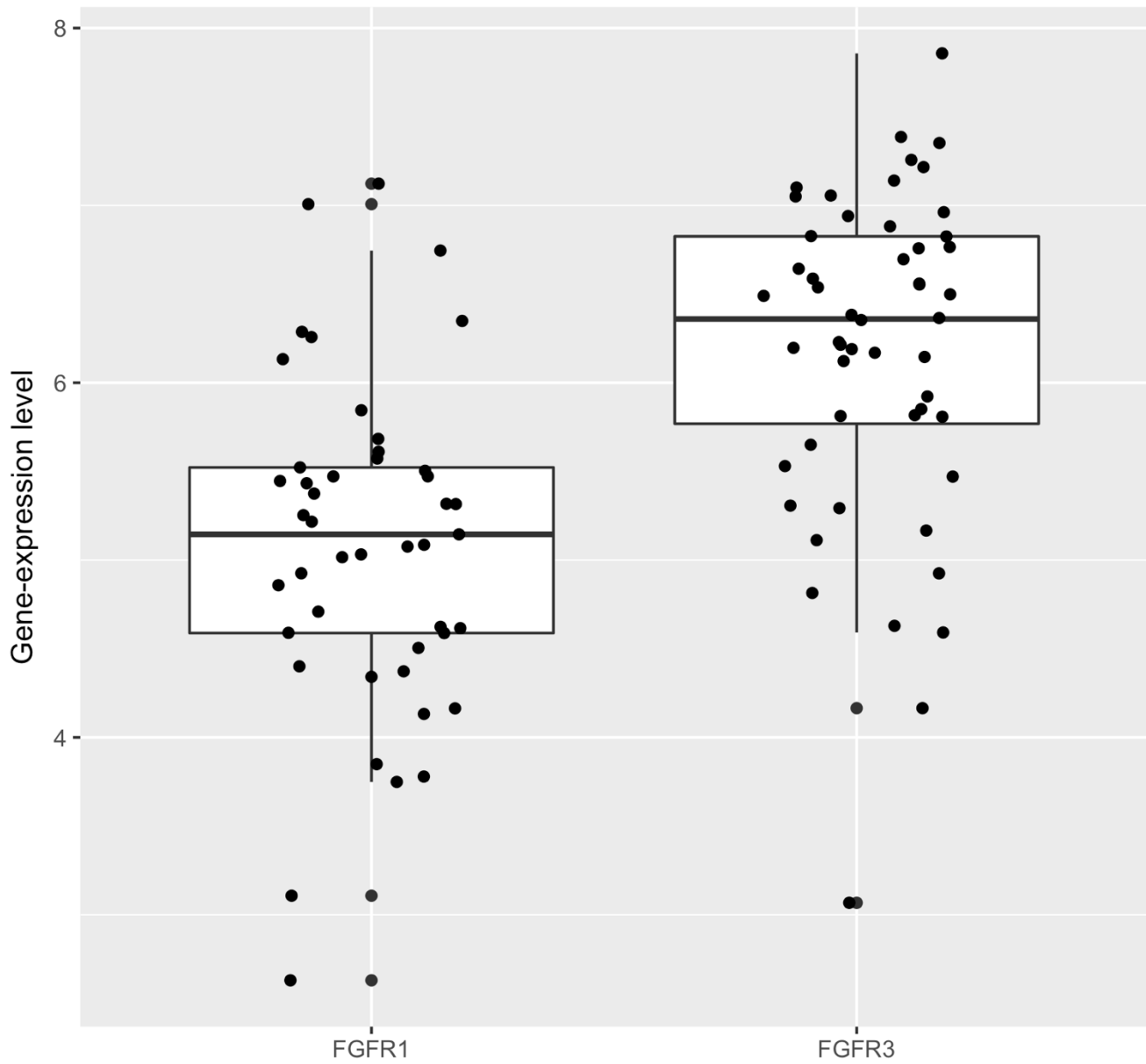
**Figure S4:** Expression levels of the *FGFR3* gene for bladder-carcinoma samples that possessed a somatic mutation in either *FGFR1* or *FGFR3*.

Cancer Type: BLCA; Gene: SMAD3



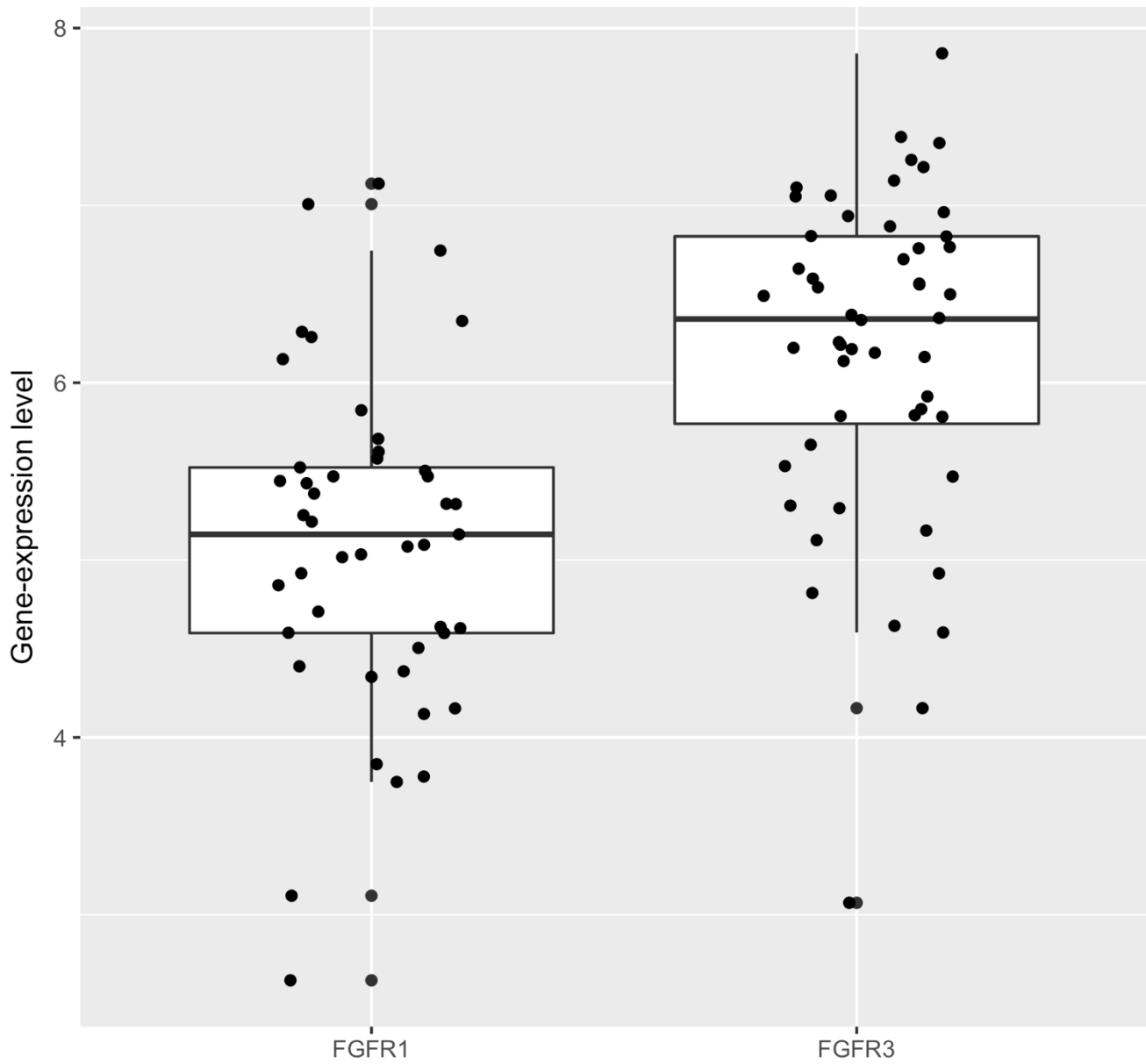
**Figure S5:** Expression levels of the *FNI* gene for bladder-carcinoma samples that possessed a somatic mutation in either FGFR1 or FGFR3.

Cancer Type: BLCA; Gene: SMAD3



**Figure S6:** Expression levels of the *LAMA1* gene for bladder-carcinoma samples that possessed a somatic mutation in either FGFR1 or FGFR3.

Cancer Type: BLCA; Gene: SMAD3



**Figure S7:** Expression levels of the *FGFR1* gene for bladder-carcinoma samples that possessed a somatic mutation in either FGFR1 or FGFR3.