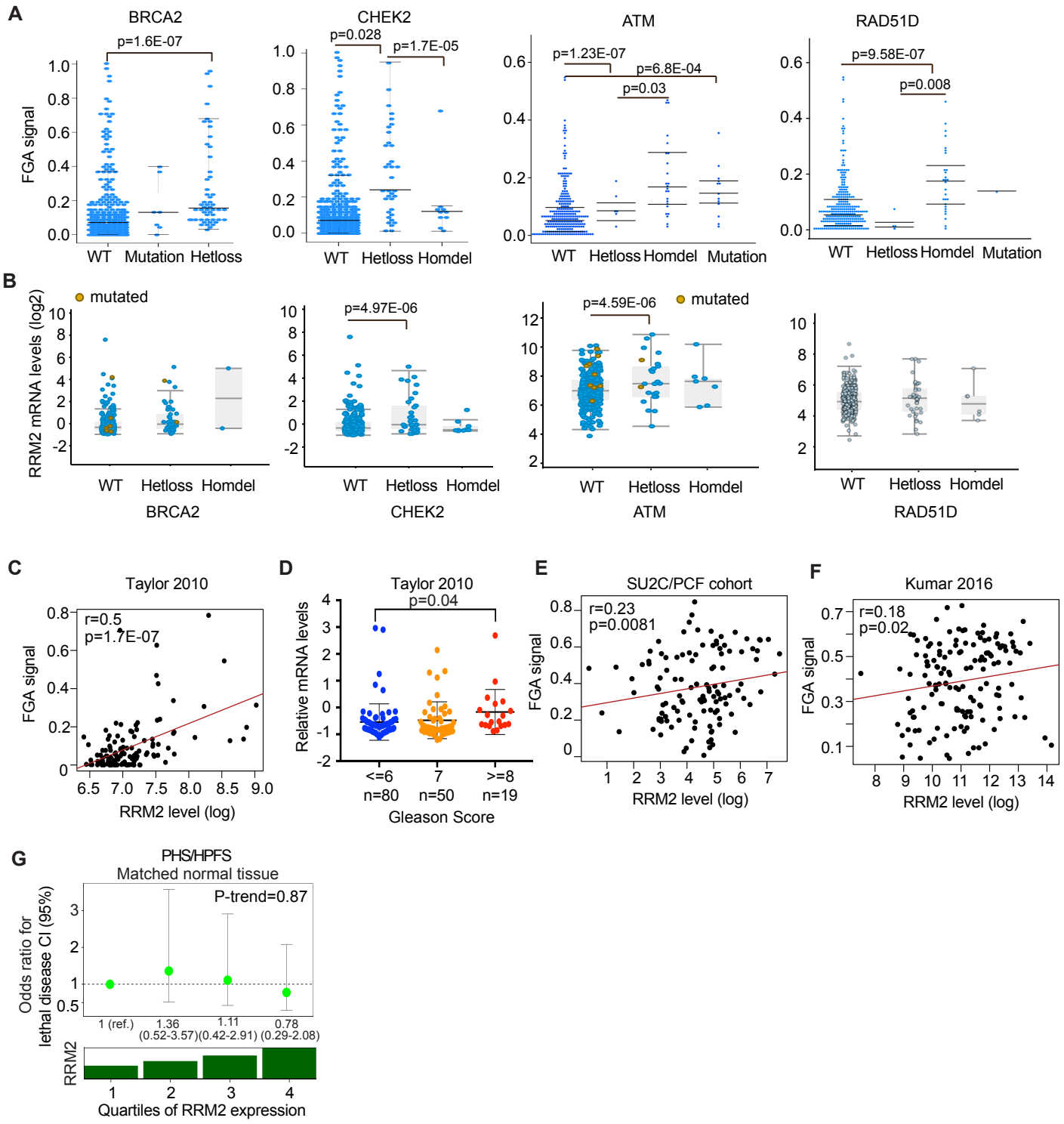
Figure S3


A
BRCA2
p=1.6E-07
FGA signal
WT
Mutation
Hetloss
CHEK2
p=0.028
p=1.7E-05
WT
Hetloss
Homdel
ATM
p=1.23E-07
p=6.8E-04
p=0.03
WT
Hetloss
Homdel
Mutation
RAD51D
p=9.58E-07
p=0.008
WT
Hetloss
Homdel
Mutation
B
mutated
RRM2 mRNA levels (log2)
WT
Hetloss
Homdel
BRCA2
p=4.97E-06
CHEK2
p=4.59E-06
mutated
ATM
RAD51D
C
Taylor 2010
r=0.5
p=1.7E-07
FGA signal
RRM2 level (log)
D
Taylor 2010
p=0.04
Relative mRNA levels
<=6
n=80
7
n=50
>=8
n=19
Gleason Score
E
SU2C/PCF cohort
r=0.23
p=0.0081
FGA signal
RRM2 level (log)
F
Kumar 2016
r=0.18
p=0.02
FGA signal
RRM2 level (log)
G
PHS/HPFS
Matched normal tissue
P-trend=0.87
Odds ratio for lethal disease CI (95%)
1 (ref.)
1.36
(0.52-3.57)
1.11
(0.42-2.91)
0.78
(0.29-2.08)
RRM2
Quartiles of RRM2 expression