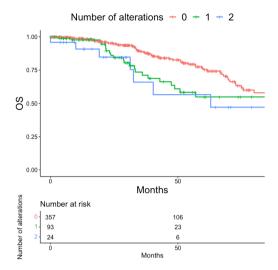
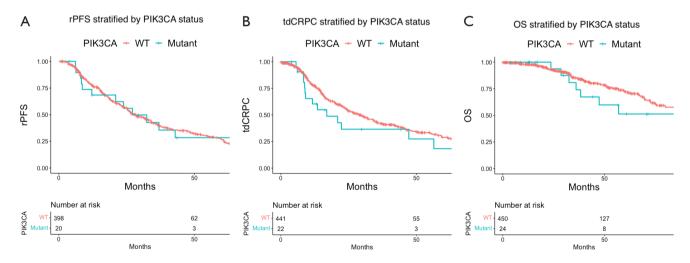
## OS stratified by number of oncogene alterations



**Figure S1** OS stratified by number of oncogene mutations. Compound mutations were also associated with worse median OS (none: 94.2 months, one: 96.1 months, two: 62.8 months, P=0.02).



**Figure S2** RPFS (A), tdCRPC (B), and OS stratified by *PIK3CA* mutational status. *PIK3CA* mutations were not associated with rPFS (27.1 vs. 28.2 months, P=0.59), tdCRPC (16.9 vs. 29.1 months, P=0.26), or OS (NR vs. 96.1 months, P=0.44).

Table S1 Oncogene mutation frequency

Mutation	Frequency
AKT1	8 (4.7%)
AKT2	2 (1.2%)
AKT3	1 (0.58%)
ALK	2 (1.2%)
BRAF	10 (5.8%)
CCND1	10 (5.8%)
CCND2	2 (1.2%)
CCND3	2 (1.2%)
CTNNB1	22 (12.8%)
EGFR	3 (1.7%)
ERBB2	1 (0.58%)
FGFR1	9 (5.2%)
FGFR2	1 (0.58%)
HRAS	6 (3.5%)
KRAS	6 (3.5%)
MDM2	2 (1.2%)
MET	2 (1.2%)
MITF	1 (0.58%)
MYC	29 (16.9%)
NOTCH1	2 (1.2%)
NOTCH2	3 (1.7%)
NOTCH3	5 (2.9%)
NRAS	3 (1.7%)
PIK3CA	24 (14%)
PIK3CB	5 (2.9%)
PIK3R1	8 (4.7%)
RET	3 (1.7%)

 $\begin{tabular}{ll} \textbf{Table S2} & \textbf{Univariate factors associated with rPFS, tdCRPC, and OS \end{tabular}$ 

03		
Characteristic	HR (95% CI)	P value
rPFS		
Oncogene mutation	1.35 (1.03–1.77)	0.03
Gleason group	1.07 (0.95–1.20)	0.24
Met location (vs. bone)		
Node	0.95 (0.71–1.27)	0.72
Visceral	1.23 (0.86–1.76)	0.25
De novo metastasis	1.26 (0.99–1.61)	0.06
Low volume (vs. high)	0.71 (0.55–0.91)	0.01
Age	1.03 (1.02–1.05)	0.0001
tdCRPC		
Oncogene mutation	1.81 (1.37–2.40)	<0.0001
Gleason group	1.39 (1.21–1.60)	<0.0001
Met location (vs. bone)		
Node	0.50 (0.36-0.70)	<0.0001
Visceral	1.58 (1.11–2.25)	0.01
De novo metastasis	2.17 (1.67–2.82)	<0.0001
Low volume (vs. high)	0.35 (0.27-0.45)	<0.0001
Age	1.04 (1.02–1.06)	<0.0001
OS		
Oncogene mutation	1.78 (1.16–2.73)	0.01
Gleason group	1.51 (1.18–1.94)	0.0003
Met location (vs. bone)		
Node	0.53 (0.30-0.93)	0.03
Visceral	1.92 (1.14–3.24)	0.01
De novo metastasis	2.22 (1.67–2.82)	0.0001
Low volume (vs. high)	0.39 (0.26–0.59)	<0.0001
Age	1.04 (1.02–1.07)	0.0004