## Downstream Neighbor of SON (DONSON) Expression is Enhanced in Phenotypically Aggressive Prostate Cancers

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Prostate Cancer TCGA Cohort ( <i>n</i> = 498)		
Clinical-Pathological Parameters	Mean or Sample Size	Range
Age	61.01	41–78
Gleason	7.6	6-10
ISUP	3.2	1–5
Initial PSA	1.74	0.0–323.0
TNM Stage	-	-
≥T3	301	-
N+	79	-
M+	3	-
Survival Endpoints	-	-
OS event	10	-
Overall Survival (months)	35.7	0-165
PFS Events	29	-
Progression-Free Survival (months)	31.7	0-165

Table S1. Clinical-pathological characteristics of the Prostate Cancer TCGA Cohort.

Table S2. Clinical-pathological characteristics of the Bonn Prostate Cancer Tissue Microarray.

Prostate Cancer Tissue Microarray (n = 116)			
Clinical-Pathological Parameters	Mean or Sample Size	Range	
Age	65.25	45-83	
Gleason	6.9	6–10	
ISUP	2.3	1–5	
Initial PSA	10.3	0.7–58.4	
TNM Stage	-	-	
≥T3	38	-	
N+	12	-	
M+	3	-	
Survival Endpoints	-	-	
OS Event	10	-	
Overall Survival (months)	76.5	0-120*	
PFS Events	29	-	
Progression-Free Survival (months)	60.5	0-120*	

\*Endpoints OS and PFS are limited to 120 months follow up.

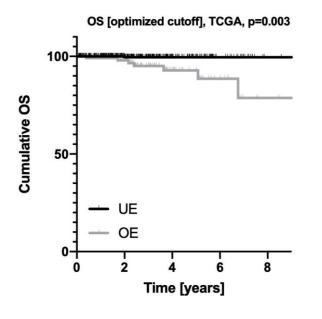
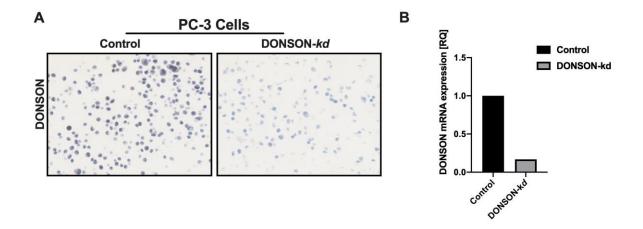
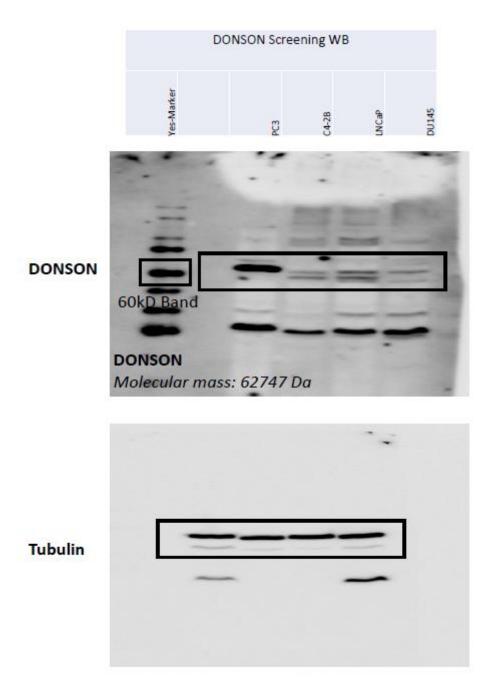
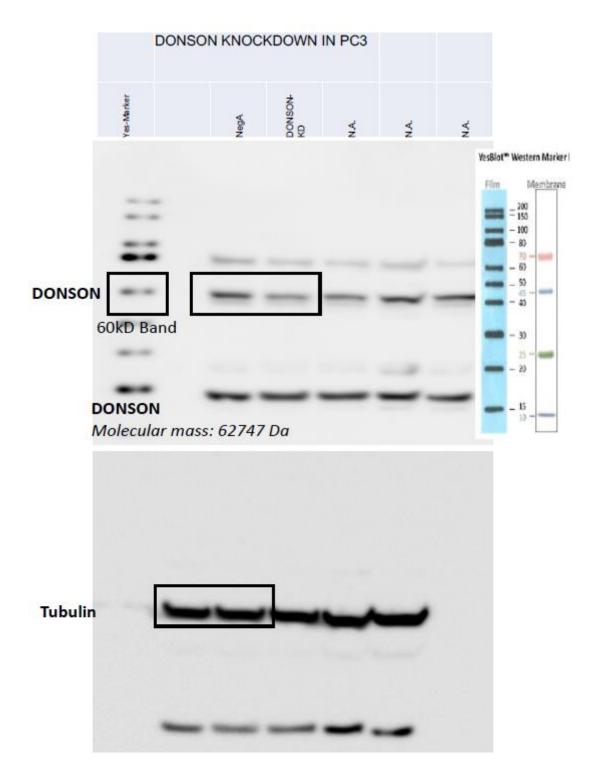


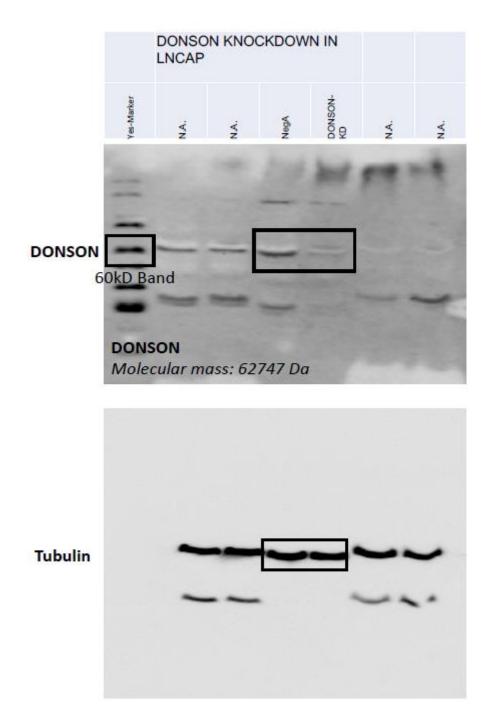
Figure S1. DONSON overexpression is associated with an unfavorable OS in the PCa TCGA cohort.

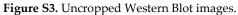


**Figure 2. A**, Immunocytochemical staining of DONSON in PC-3 control cells (NegA) compared to DONSON-knockdown. Images depicted in 10× objective magnification. **B**, The DONSON knockdown efficacy of the respective stained cells was confirmed via qPCR.









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