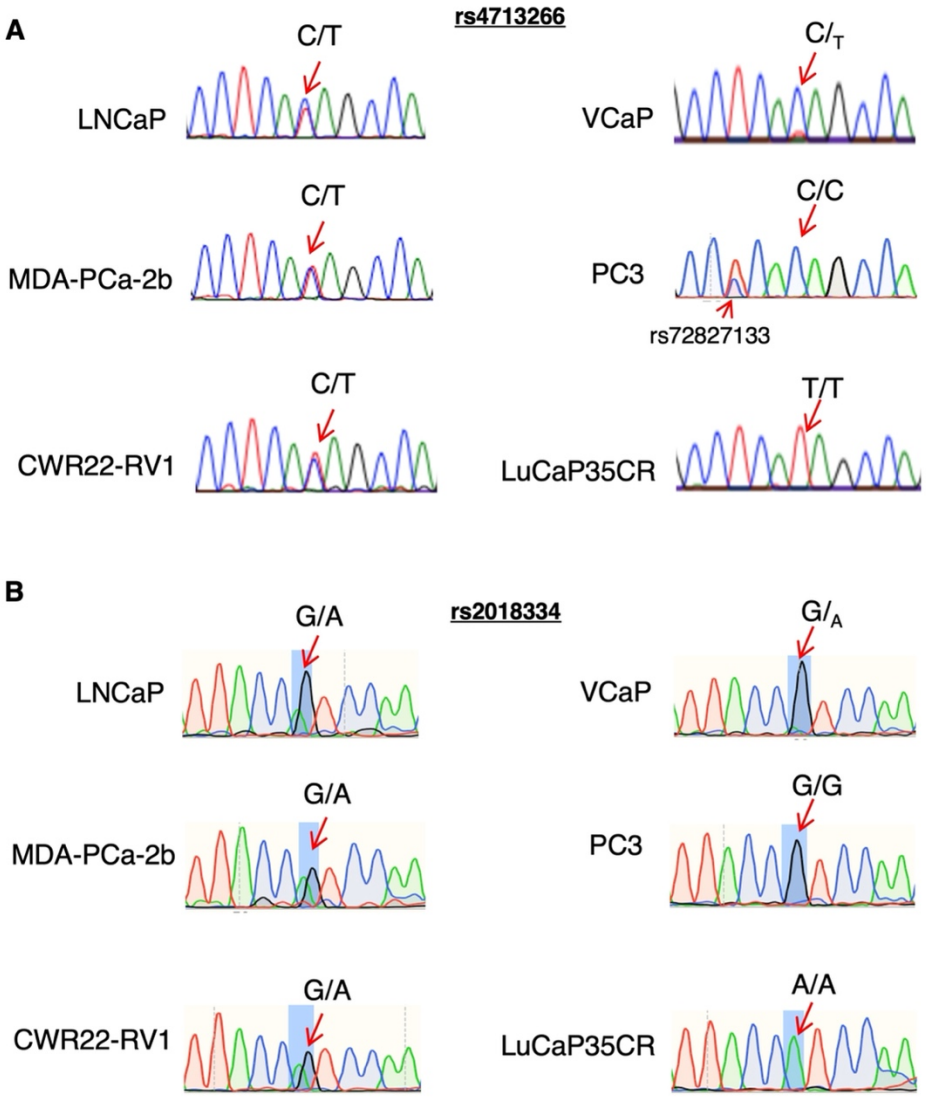
SNP ID	Position (GRCh37/hg19)	Nearby Genes
rs9623117	Chr22:40452119	TNRC6B
rs6983267	Chr8:128413305	CASC8, CCAT2
rs10896449	Chr11:68994667	LOC338694*
rs10993994	Chr10:51549496	MSMB
rs817826	Chr9:110156300	LINC01509*
rs4242382	Chr8:128517573	CASC8*
rs103294	Chr19:54797848	LILRB2, LILRA5
rs4749884	Chr10:9644800	LINC02663
rs1512268	Chr8:23526463	LOC107986930
rs10934853	Chr3:128038373	EEFSEC
rs6062509	Chr20:62362563	ZGPAT
rs7584330	Chr2:238387228	MLPH
rs11902236	Chr2:10117868	GRHL1
rs8102476	Chr19:38735613	PPP1R14A
rs12621278	Chr2:173311553	ITGA6
rs4713266	**Chr6:11219030**	**NEDD9**
rs10486567	Chr7:27976563	JAZF1
rs5759167	Chr22:43500212	BIK
rs6763931	Chr3:141102833	ZBTB38
rs1938781	Chr11:58915110	FAM111A
rs2273669	Chr6:109285189	ARMC2
rs7127900	Chr11:2233574	ASCL2*, IGF2*, TH*
rs339331	Chr6:117210052	RFX6
rs7210100	Chr17:47436749	ZNF652, LOC102724596
rs684232	Chr17:618965	VPS53
rs7611694	Chr3:113275624	SIDT1
rs6465657	Chr7:97816327	LMTK2
rs2121875	Chr5:44365545	FGF10
rs17632542	Chr19:51361757	KLK3
rs1983891	Chr6:41536427	FOXP4
rs1894292	Chr4:74349158	AFM
rs1933488	Chr6:153441079	RGS17
rs17694493	Chr9:22041998	CDKN2B-AS1
rs10875943	Chr12:49676010	TUBA1C, PRPH
rs17021918	Chr4:95562877	PDLIM5
rs11214775	Chr11:113807181	HTR3B
rs1016343	Chr8:128093297	PCAT2

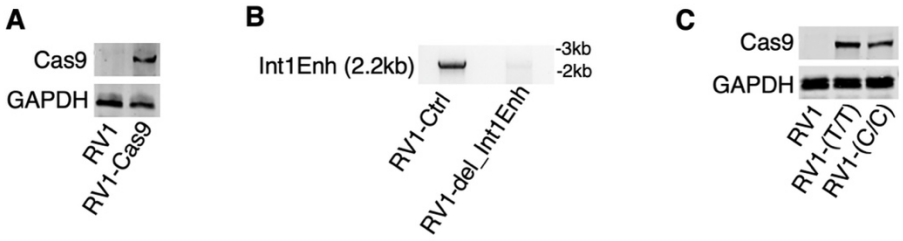
(* distance > 20kb)

Supplementary Figure 1. Candidate PCa susceptibility SNPs that are associated with men of African descent Previous analysis using GWAS database revealed a list of SNPs that are associated with PCa risk and enriched in men of African descent.



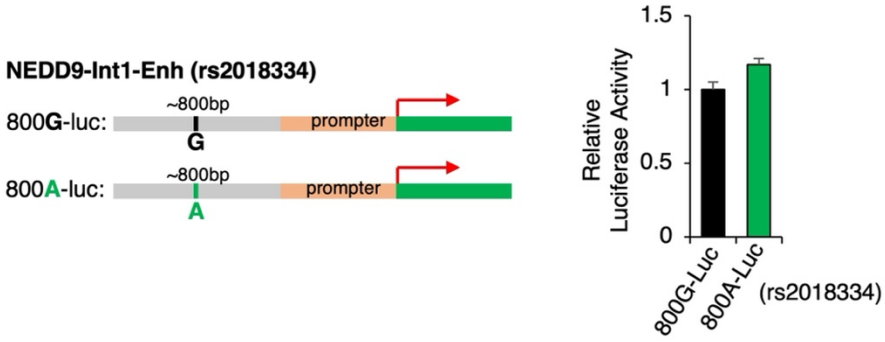
Supplementary Figure 2. Genotypes of rs4713266 and rs2018334 for PCa models

(**A**, **B**) Multiple PCa cell or xenograft lines were genotyped for rs4713266 (A) or rs2018334 (B) using Sanger sequencing on the PCR amplified genomic DNA fragments. LNCaP, MDA-PCa-2b, and CWR22-RV1 lines are heterozygous for both risk and non-risk alleles. VCaP line has gene amplification of the risk allele but may still contain a copy of the non-risk allele. PC-3 line is homozygous for risk alleles but also contains heterozygous T/C for a nonrelevant SNP rs72827133. LuCaP35CR (*TMPRSS2-ERG* positive) is homozygous for non-risk alleles.

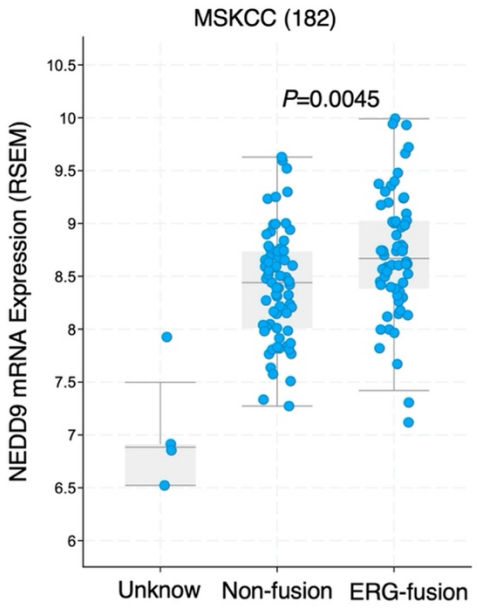


Supplementary Figure 3. CWR22-RV1 cells with CRISPR/Cas9 editing in NEDD9-Int1Enh region

(**A**) Immunoblotting for Cas9 (anti-Cas9, ab210572, Abcam) in the previously established Cas9-expressing CWR22-RV1 stable cells. (**B**) Confirmation of Int1Enh deletion in CWR22-RV1-del_Int1Enh cells by PCR amplifying the enhancer region (~2.2kb) of genomic DNA. The primer sequences are: forward, 5'-TAAATGTCATCAGATTCCAACACAG-3' and reverse, 5'-CTACAAGTCACACCTCTCCGT-3'. (**C**) Immunoblotting for Cas9 in CWR22-RV1-T/T and -C/C isogenic cell lines.

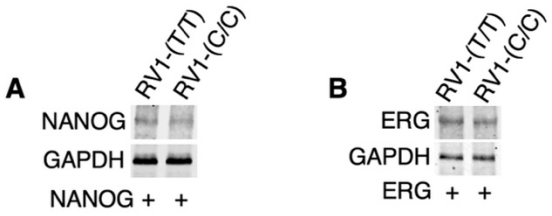


Supplementary Figure 4. The nucleotide variation at rs2018334 does not significantly alter the reporter activity. DNA fragments (~800bp) containing G or A of rs2018334 were cloned into a luciferase reporter system containing a minimum promoter (800C-Luc and 800T-Luc). PC-3 cells were then transfected with 800C-Luc versus 800T-Luc and the luciferase activities were examined.



Supplementary Figure 5. *NEDD9* expression is increased in ERG fusion-positive PCa of MSKCC cohort

Using provided online tools from cBioPortal, *NEDD9* expression was examined in fusion-positive versus fusion negative PCa of MSKCC cohort (Taylor PCa).



Supplementary Figure 6. Transfection of NANOG and ERG in CWR222-RV1 isogenic cell lines

(**A**, **B**) Immunoblotting for NANOG (A) or ERG (B) in the CWR22-RV1 isogenic cell lines transfected by NANOG or ERG expressing plasmids.