MJ _ Supplementary Data:

Table S1. Mutated genes with high & medium impact variants overlap with genes in FOne.

Sample ID	Gene	Variant Type	Amino acid change
AP20T	ATRX	missense	Asn1860Ser
AP20T	ATRX	missense	Ser1861Thr
AP20T	ATM	missense	Asn1243Ser
AP20T	ROS1	frameshift	His580GlnfsTer26
AP18T	MAGI2	inframe_deletion	Arg1322_Ala1323delinsSer
AP18T	ASXL1	frameshift	Arg397ProfsTer61
AP18T	APC	frameshift	Glu1712GlyfsTer2
AP18T	RBM10	splice_donor	c.2295+2_2296del
AP18T	RBM10	missense	Leu33Arg
AP18T	BRCA2	inframe_deletion	Asp2983del
AP26T	MAGI2	missense	Gly1283Asp
AP11T	FAT1	frameshift	Val2290ProfsTer7
AP11T	KDM6A	missense	Arg559_Pro560delinsHisThr
AP15T	DICER1	missense	Asn157Thr
AP15T	TAF1	stop_gained	Glu1710_Asp1711insAsnLysValTyrIleTer
AP15T	TAF1	stop_gained	Glu1710delinsGlyTer
AP9T	ATM	missense	Phe2799Asn
AP9T	NFKBIA	missense	Gly132Lys
AP19T	ATRX	missense	Ile347Ser
AP19T	GRIN2A	missense	Arg19His
AP19T	MDM4	missense	Pro41Leu
AP19T	CCND2	missense	Tyr261Phe
AP10T	MED12	frameshift	Tyr1797MetfsTer39
AP10T	SLIT2	stop_gained	c.1192+9_1192+10ins

Table S2: Examples of high impact variants identified in each sample

ID	HI variants
AP9T	*NOTCH4*/I360Sfs*12, *LATS2*/H412Pfs*158, *DDX3X*/X288_splice
AP10T	*MED12*/Y1947Mfs*39, *KSR2*/T710Nfs*19
AP11T	*FAT1* V2290Pfs*7, *ATXN2* Q1252Pfs*23
AP15T	*IRAK2*/V54delinsASKHSQVS*, *PCTP/*T36Kfs*12, *ABHD17C* /Y208Afs*6
AP18T	*APC*/E1712Gfs*2, *ASXL1/* R402Pfs*61, *RAD51C*/Leu177Ter
AP19T	*ELP4*/K375_R376insI*, *RTL8C/* A76Rfs*18, *MTRF1L*/R262Yfs*2, *PIM2*/.D258Vfs*77,
AP20T	*MRE11A*/I93Sfs*16, *EGFL7*/T190Sfs*8, *NEK3*/R254delinsLKSK*, *ROS1*/H571Qfs*22,
AP26T	*ANK3*/S3023_S4377delins, *ANKRD17*/I1293Qfs*4, *MMP17*/A46Sfs*34
AP30T	*MAP2K7*/E287Hfs*6, *KIF3B*/T330Vfs*4, *DMD*/K891Nfs*16
AP44T	*XRN1*/A456delins, *H3C11*/K37Mfs*12

Table S3: Examples of medium impact variants identified in each sample

ID	MI variants
AP9T	ATM/F2799N, TRAK1/T900_N911del, PASK/V1129delinsAGVVEL, POLA1/F1337C
AP10T	RASL11A/S138del, COL6A3/T49delinsSA, PISD/V71L
AP11T	OR2M2/S275C, MUC17/R2661S
AP15T	GRK1/A429Q, IL17RA/Y327S
AP18T	BRCA2/D2983del, AKAP4/I742del, MBD6/H332_P334del
AP19T	SPIN2A/V104I, ZNF92/F277S, RAB6D/N162H
AP20T	ATRX/N1822S, ZNF649/R34K, MMP17/E540V, ZNF793/H361H, ZNF589/Q226H
AP26T	FOXK2/G24_G34del, SORBS3/R9P, CSPP1/E323L, MUC4/L1926P
AP30T	TSSK2/Q193_Y216del, NEXMIF/N576S, TOE1/I97V
AP44T	BRD/L615I, TEX45/S90A,

Supplementary Figure S1.

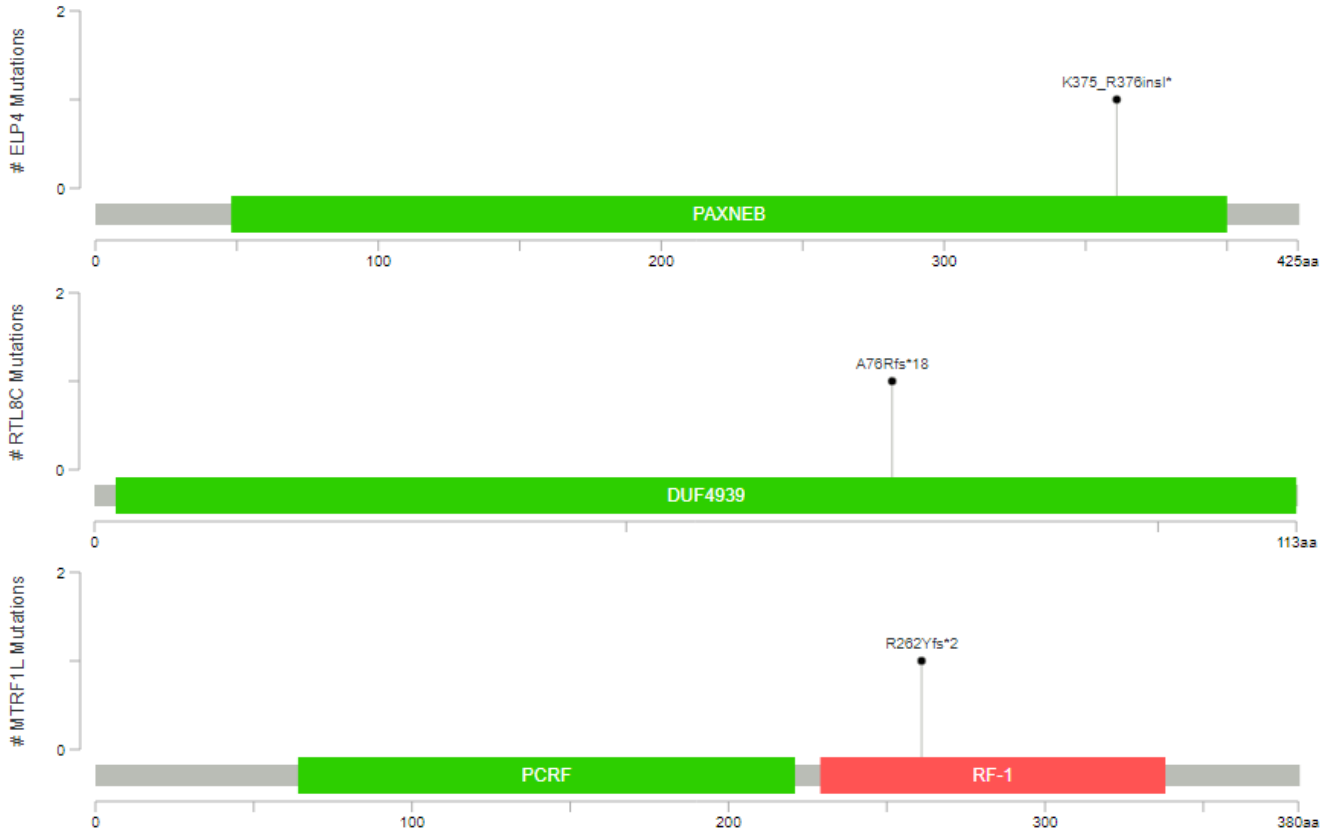

Figure S1. Three mutated genes with truncating variants unique in AP19T. Nonsense mutation (ELP4/K375_R376insl*, RTL8C/ A76Rfs*18, and MTRF1L/R262Yfs*2) locations were visualized using Mutation Mapper tool. The annotation tracks examined included reference to the databases Cancer Hotspots and OncoKB. Missense, in-frame, and truncating mutations were indicated with green, brown or black “lollipops”, respectively.

Supplementary Figure S2.

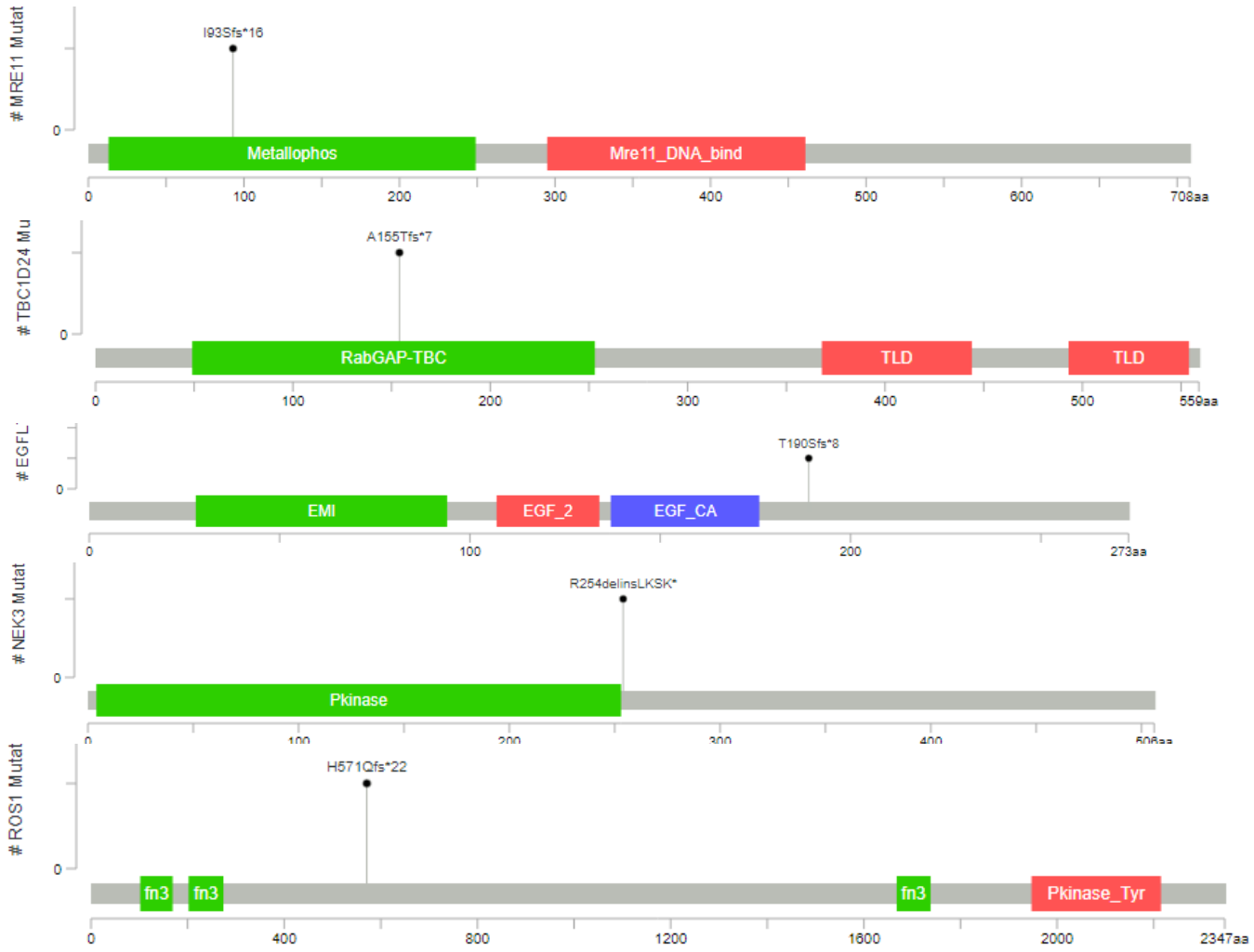

Figure S2. Five mutated genes with truncated variant types unique in AP20T. Variants include *MRE11*/ I93Sfs*16 fs del, *TBC1D24*/A155Tfs*7 nonsense, *EGFL7*/T190Sfs*8 nonsense, *NEK3*/ R254delinsLKSK* and *ROS1*/H571Qfs*22 del. Mutation locations were visualized using Mutation Mapper tool. The annotation tracks examined included reference to the databases Cancer Hotspots and OncoKB. Missense, in-frame, and truncating mutations were indicated with green, brown or black “lollipops”, respectively.

Supplementary Figure S3.

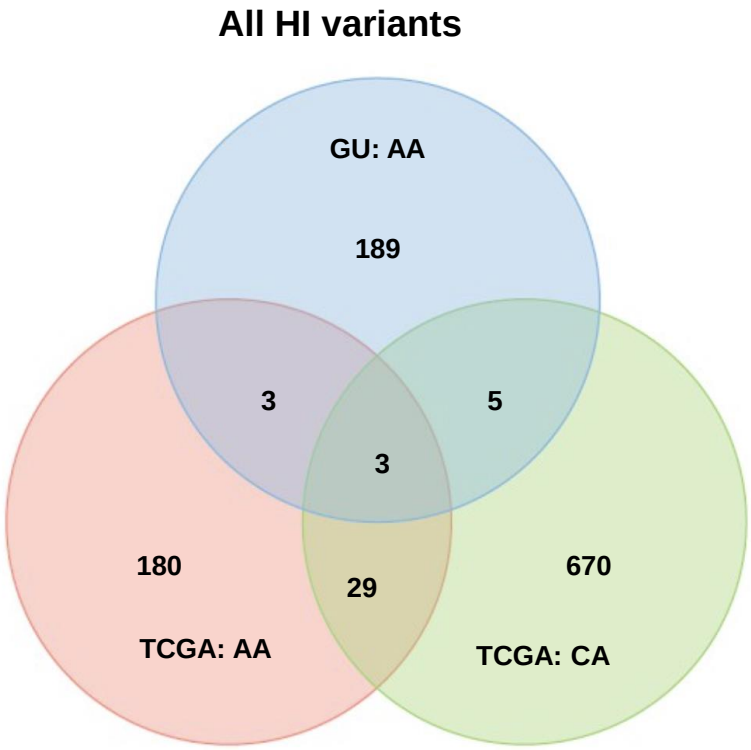

Figure S3. High impact genes shared among TCGA: AA and CA and GU: AA data sets. High impact variants were obtained from TCGA mutation datasets under the clinical parameters, including gender (male), race (black/African American or White/CA), tissue or organ of origin (prostate gland), prostate gland, locoregional primary tumor type, disease type (adenoma and adenocarcinoma), primary Gleason grade (pattern 3 and pattern 4), secondary Gleason grade (pattern 3 and pattern 4), and VEP impact genes. MyVenn was used to generate a Venn diagram.