SUPPLEMENTAL TABLE 1a.

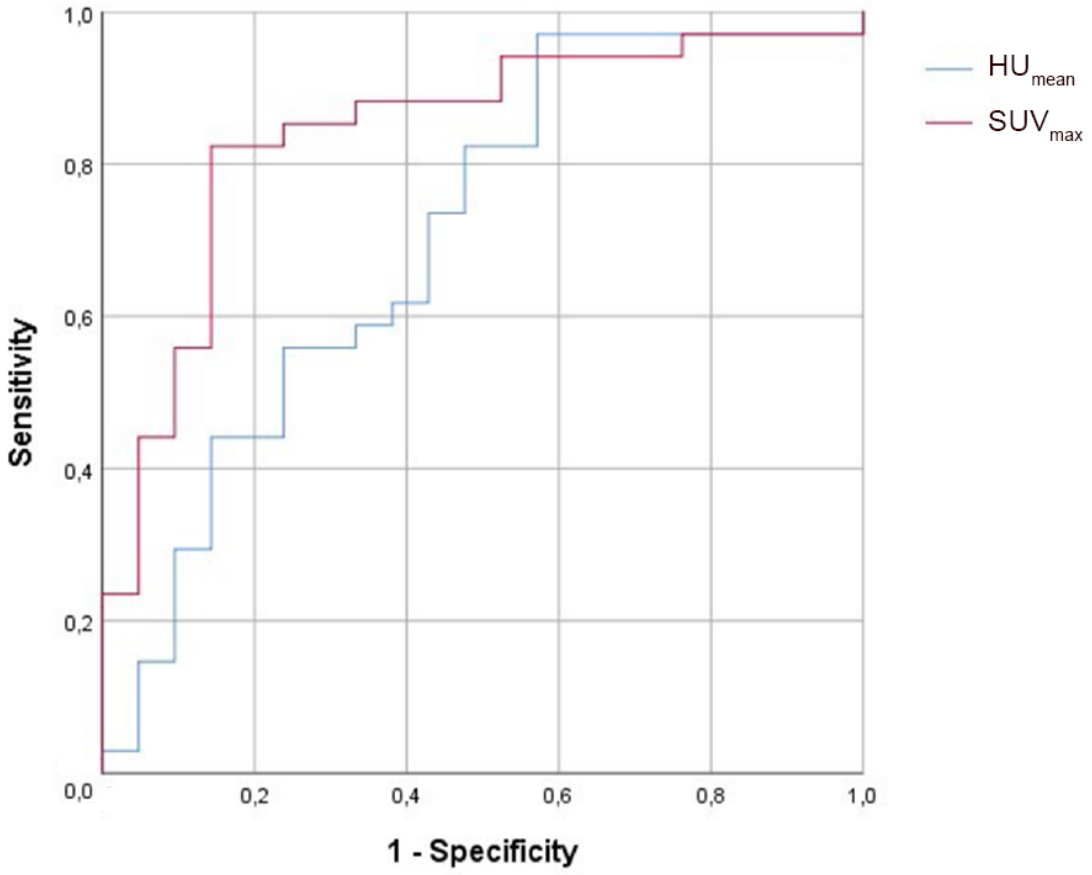
Univariate logistic regression analysis of biopsy outcome and significant continuous variables. N=55 biopsies.

Variable	p	Odds ratio	95% CI
SUV_{mean}	0.016	4.509	1.324-15,355
SUV_{max}	0.008	6.889	1.646-28.834
HU_{mean}	0.006	0.996	0.993-0.999
HU_{max}	0.037	0.998	0.995-1.000

SUPPLEMENTAL TABLE 1b.

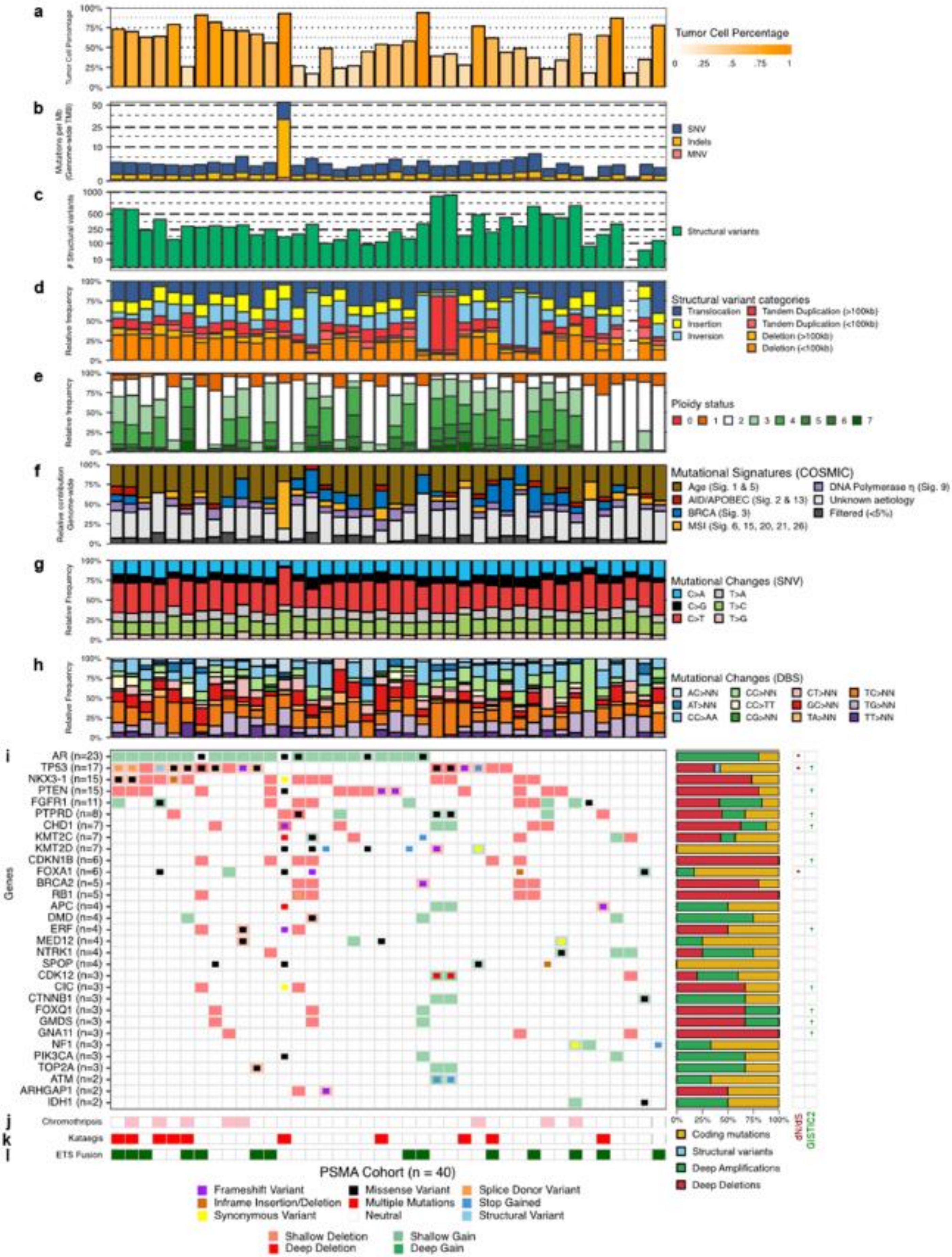
Multivariate logistic regression analysis of biopsy outcome and significant continuous variables. N=55 biopsies.

Variable	p	Odds ratio	95% CI
SUV_{max}	0.003	11.737	2.258-60.996
HU_{mean}	0.003	0.995	0.992-0.998



SUPPLEMENTAL FIGURE 1.

ROC curves for biopsy outcome by HU_{mean} and SUV_{max} at biopsy site. N=55 biopsies.


a
Tumor Cell Percentage
b
SNV
Indels
MNV
c
Structural variants
d
Structural variant categories
Translocation
Insertion
Inversion
Tandem Duplication (>100kb)
Tandem Duplication (<100kb)
Deletion (>100kb)
Deletion (<100kb)
e
Ploidy status
f
Mutational Signatures (COSMIC)
Age (Sig. 1 & 5)
AID/APOBEC (Sig. 2 & 13)
BRCA (Sig. 3)
MSI (Sig. 6, 15, 20, 21, 26)
DNA Polymerase η (Sig. 9)
Unknown aetiology
Filtered (<5%)
g
Mutational Changes (SNV)
C>A
C>G
C>T
T>A
T>C
T>G
h
Mutational Changes (DBS)
i
Genes
AR (n=23)
TP53 (n=17)
NKX3-1 (n=15)
PTEN (n=15)
FGFR1 (n=11)
PTPRD (n=8)
CHD1 (n=7)
KMT2C (n=7)
KMT2D (n=7)
CDKN1B (n=6)
FOXA1 (n=6)
BRCA2 (n=5)
RB1 (n=5)
APC (n=4)
DMD (n=4)
ERF (n=4)
MED12 (n=4)
NTRK1 (n=4)
SPOP (n=4)
CDK12 (n=3)
CIC (n=3)
CTNNB1 (n=3)
FOXQ1 (n=3)
GMDS (n=3)
GNA11 (n=3)
NF1 (n=3)
PIK3CA (n=3)
TOP2A (n=3)
ATM (n=2)
ARHGAP1 (n=2)
IDH1 (n=2)
j
Chromothripsis
k
Kataegis
l
ETS Fusion
PSMA Cohort (n = 40)
Frameshift Variant
Inframe Insertion/Deletion
Synonymous Variant
Missense Variant
Multiple Mutations
Neutral
Splice Donor Variant
Stop Gained
Structural Variant
Shallow Deletion
Deep Deletion
Shallow Gain
Deep Gain
Coding mutations
Structural variants
Deep Amplifications
Deep Deletions
dNdS
GISTIC2

SUPPLEMENTAL FIGURE 2.

Mutational landscape of ^{68}Ga-PSMA guided bone biopsies identified by whole-genome sequencing.

A) Estimated tumor cell percentages (*in silico*) obtained from the whole-genome sequencing data. Bars are color-coded based on tumor cell percentage.

B) Number of genomic mutations per Mbp (TMB) of SNV, InDels, and MNV categories. All genome-wide somatic mutations were taken into consideration (square root scale). C) Absolute number of unique structural variants per sample. Cumulative frequency of inversions, tandem duplication, deletions, insertions, and translocations.

D) Relative frequency per structural variant category. Tandem Duplications and Deletions are subdivided into >100 kbp and <100 kbp categories. This track shows whether enrichment for a particular category of (somatic) structural variant can be detected, which in turn, can be indicative for a specific mutational aberration.

E) Relative genome-wide ploidy status, ranging from 0 to ≥7 copies. This track shows the relative percentage of the entire genome which is (partially) deleted (ploidy < 2/diploid) or amplified (> 2/diploid).

F) Relative contribution to mutational signatures (COSMIC) summarized per proposed etiology. This track displays the proposed etiology of each SNV based on their mutational contexts. Signatures with < 5% relative contribution in all samples were summarized in the “Filtered (<5%)” category.

G) Relative frequency of somatic Single Nucleotide Variants (SNV) categories.

H) Relative frequency of somatic Doublet Base Substitution (DBS) categories.

I) Oncoplot showing the somatic mutations per samples for a selection of potential driver genes, as detected by dN/dS and/or GISTIC2 analysis and/or manual selection based on

a list of pan-cancer (CPCT-02) driver genes[1]. Shallow amplifications and deletions are only shown if also accompanied by an additional coding mutation. The right-hand bar-plot depicts the relative frequency of mutational categories (coding mutations, structural variants and deep amplifications/deletions) per gene. Per gene, the inclusion criteria are shown; dN/dS (q≤0.1; *), enriched GISTIC2 focal peak (q ≤ 0.1; †) or if empty, based on the pan-cancer (CPCT-02) driver list.

J) Presence of chromothripsis. Pink color indicates presence of chromothripsis as estimated by ShatterSeek.

K) Presence of kataegis. Red color indicates presence of one or more regions showing kataegis.

L) Presence of a fusion with a member of the ETS transcription factor family. Green color indicates a possible fusion.