Supplementary Information

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S1 Detailed methods for lipidomic analysis

S1.1 Blood collection and lipid extraction

Peripheral blood from patients was sampled and lipid extraction performed as previously described. Whole blood was collected into 10mL EDTA-containing tubes and two-step centrifugation performed to separate plasma and buffy coat. The centrifugation speed differed between the two cohorts. For the discovery cohort, blood samples were first centrifuged at 1600 x g for 15 minutes and the supernatant transferred to a fresh tube, where it was centrifuged again at 5000 x g for 10 min. For the validation cohort, both centrifugation speeds were 3000 rpm for 10 minutes. Aliquots of the plasma after the second centrifugation were stored at -80^{o}C until required.

10µL of plasma was used to extract lipids using a butanol/methanol extraction method. Internal standards were added to the plasma prior to lipid extraction, in order to calculate the concentration of the lipids [lipid concentration = (area of analyte/area of corresponding internal standard) x concentration of internal standard x response factor]. Internal standards and response factors are listed in Huynh *et al* (2019).

S1.2 Quality control samples

Replicates of two types of quality controls (QC) were extracted and ran together with the study plasma samples:

- Pooled human plasma from healthy individuals (PQC)
- National Institute of Standards and Technology human plasma standard reference material 1950 (NIST1950). This was developed by NIST from a collaboration with the National Institute of Health (NIH), and the National Institute of Diabetes and Digestive and Kidney Disease (NIDDK), to allow comparisons between data sets run within the same laboratory and with other laboratories globally.

The coefficient of variation (%CV) of the lipid levels in these QC samples passed the required threshold of mean %CV <15% and median %CV <10%.

S1.3 Liquid chromatography-mass spectrometry analysis

Liquid chromatography-mass spectrometry (LC-MS) analysis was performed as previously described. Lipid extracts were analysed on an Agilent 6490 QQQ mass spectrometer with an Agilent 1290 series HPLC system. Samples from the validation cohort were analysed with other samples not part of this study as 3 batch runs, where the batch differences were adjusted by median centering with PQC samples. The median concentration of each lipid species of the PQC samples in the 3 batches was first calculated, and then used to derive a median center value for each lipid species (median center value = median of batch 1 / median of batch 1, 2 or 3). The median center value of each batch was then multiplied to the concentration of lipids in the study samples, resulting in the alignment of all batches to the first batch.

S1.4 Data normalisation

Normalisation is a data pre-processing step that is essential for large scale analyses of multi-variable data (e.g. genomic, proteomic). This normalisation step adjusts for biases that can arise from sample preparation (e.g. sample loss, evaporation, irregular extraction efficiency, pipetting errors), biological effects (e.g. differences in water content) or biological variation (e.g. differences in individuals unrelated to disease pathology).

The lipidomic datasets from both cohorts were normalised independently according to the Probabilistic Quotient (PBQ) normalization method as previously described, and adapted from Dieterle *et al* (2006). The reference sample used in PBQ normalization was created from the mean levels of each lipid species across all the plasma samples of each cohort respectively. Final values are logarithm-2 of pmol/mL.

S1.5 Dataset alignment and calculation of the 3-lipid signature

To determine the presence of the circulating 3LS of poor prognosis, the lipidomic data was first aligned to that of the original cohort from which the 3LS was derived using the ComBat algorithm (R package sva, v3.34.0) to remove batch differences, as the lipidomic datasets were produced by different LC-MS instruments and on a different occasion. Next, the 3LS status of each patient was calculated from a logistic regression model consisting of ceramide Cer(d18:1/24:1), sphingomyelin SM(d18:2/16:0) and phosphatidycholine PC(16:0/16:0), derived in Lin et al (2017) as follows:

$$y = (3.1319 \times \text{Cer(d18:1/24:1)}) + (2.1724 \times \text{SM(d18:2/16:0)}) + (1.8593 \times \text{PC(16:0/16:0)}) - 91.217$$

$$p = e^{y}/(1+ e^{y})$$

Patient has the poor prognostic 3LS when $p \geq 0.5$

S2 Detailed methods for targeted cfDNA sequencing

S2.1 Blood collection and cfDNA extraction

Peripheral blood was sampled and cell-free DNA (cfDNA) was isolated as published previously. The process of blood collection was described in S1.1. Samples were then stored at -80^{o}C until required for batch processing. Up to 5mL of plasma was used to extract cfDNA using the QIAamp circulating nucleic acid kit (Qiagen, Hilden, Germany), with large genomic fragments removed with AMPure XP beads (Beckman Coulter, Brea, CA, USA). DNA was quantified (Qubit 2.0 fluorometer, ThermoFisher Scientific, Waltham, Massachusetts, USA) and underwent quality assessment (Bioanalyzer 2100, Agilent Technologies, California, USA).

S2.2 Targeted capture, sequencing and bioinformatics

Library preparation, hybrid-capture and sequencing

Up to 40ng of extracted cfDNA was used for preparation of next-generation sequencing (NGS) libraries, a process which has been described in detail previously. Amplified DNA libraries underwent further quality assessment (Bioanalyzer 2100) and then were subsequently hybridised overnight to a targeted panel capturing exonic regions from 90-120 genes (Table S1.2.1). Captured fragments were further PCR amplified and underwent a final quality assessment (Bioanalyzer 2100), before being sequenced on the Illumina HiSeq X Ten.

Table S2.2.1: Predicine cfDNA assay gene list

Predicine 90-gene cfDNA assay (Discovery cohort)									
AKT1	ALK	APC	AR	ARAF	ARID1A	ATM	BRAF	BRCA1	BRCA2
CCND1	CCNE1	CD274	CDH1	CDK4	CDK6	CDKN2A	CTNNB1	CYP2C19	CYP2D6
CYP3A4	DDR2	DNAJB1	DPYD	EGFR	ERBB2	ERBB3	ESR1	EZH2	FBXW7
FGFR1	FGFR2	FGFR3	GNA11	GNAQ	GNAS	GSTP1	HRAS	IDH1	IDH2
JAK2	JAK3	KIT	KRAS	MAP2K1	MAP2K2	MAPK1	MDM2	MET	MLH1
MPL	MSH2	MTHFR	MTOR	MYC	MYCN	MYD88	NF1	NFE2L2	NPM1
NRAS	NTRK1	NTRK3	PDCD1LG2	PDGFRA	PIK3CA	POLD1	POLE	PPP2R1A	PRKACA
PRKD1	PTEN	PTPN11	RAF1	RB1	RET	RNF43	ROS1	SMAD4	SMO
SPOP	STK11	TERT	TP53	TSC1	TSC2	UGT1A1	VHL	XPC	XRCC1

Predicine 120-gene cfDNA assay (Validation cohort)									
ABRAXAS1	AKT1	ALK	APC	AR	ARAF	ARID1A	ATM	ATR	BAP1
BARD1	BRAF	BRCA1	BRCA2	BRIP1	CCND1	CCNE1	CD274	CDH1	CDK12
CDK4	CDK6	CDKN2A	CHEK1	CHEK2	CTNNB1	DDR2	DNAJB1	EGFR	EPCAM
ERBB2	ERBB3	ERCC1	ERCC2	ERCC4	ESR1	EZH2	FANCA	FANCC	FANCD2
FANCI	FANCL	FANCM	FBXW7	FGFR1	FGFR2	FGFR3	GNA11	GNAQ	GNAS
HDAC2	HRAS	IDH1	IDH2	JAK2	JAK3	KIT	KRAS	MAP2K1	MAP2K2
MAPK1	MDM2	MET	MLH1	MPL	MRE11	MSH2	MSH6	MTOR	MYC
MYCN	MYD88	NBN	NF1	NFE2L2	NPM1	NRAS	NTRK1	NTRK3	PALB2
PDCD1LG2	PDGFRA	PIK3CA	PMS2	POLD1	POLE	PPM1D	PPP2R1A	PPP2R2A	PRKACA
PRKD1	PTEN	PTPN11	RAD50	RAD51	RAD51B	RAD51C	RAD51D	RAD54L	RAF1
RB1	RECQL	RET	RNF43	ROS1	RPA1	SMAD4	SMO	SPOP	STK11
TERT	TMPRSS2	TP53	TP53BP1	TSC1	TSC2	VHL	XRCC2	XRCC3	XRCC4

Somatic mutation identification

Consensus binary alignment map (BAM) files were derived as previously described to reduce sequencing and PCR errors. Candidate somatic variants were identified using an in-house pipeline. A variant was considered a candidate somatic mutation when all 3 criteria were met: 1) presence of at least 4 distinct fragments contained the mutation, 2) variant allelic frequency (AF) was at least 0.25%, or 0.1% for hotspot loci (as defined by COSMIC and http://www.cancerhotspots.org), and 3) variant does not appear in public databases of common germline variants (1000 genomes, ExAC, gnomAD and KAVIAR). Candidate somatic mutations were further filtered to include missense, nonsense, frameshift or splice site alterations, and to exclude benign variants and haematopoietic expansion-related variants.

Estimation of ctDNA fraction

Circulating tumour DNA (ctDNA) was estimated based on the allele fractions of autosomal somatic mutations, using a method described previously. ctDNA fraction was dichotomized to above or below 2% for multivariable analyses, an approach that has been used in other studies involving patients with advanced prostate cancer due to challenges in accurately calculating ctDNA fraction in samples with low ctDNA abundance.

Targeted copy number analysis

Estimation of panel-based copy number variation (CNV) has been described in greater detail previously. Briefly, in-house algorithms calculated the on-target unique fragment coverage using the consensus BAM file. The fragment was corrected for GC bias, then compared against corresponding coverage from a group of normal reference samples to estimate the significance of the copy number variant. Gains or deletions with an absolute z-score >3 and absolute CNV change above minimum gain/deletion thresholds were considered true events.

S2.3 Analytical validation of cfDNA assay CNV detection

Details of analytical validation of sensitivity, specificity and precision of the CNV detection assay in cfDNA has been described in a previous study.

S3 Principal components analysis (PCA) of baseline plasma lipidomic profiles in the discovery cohort

Fig S3.1: PCA of baseline plasma lipidomic profiles in the discovery cohort, samples labelled by treatment type

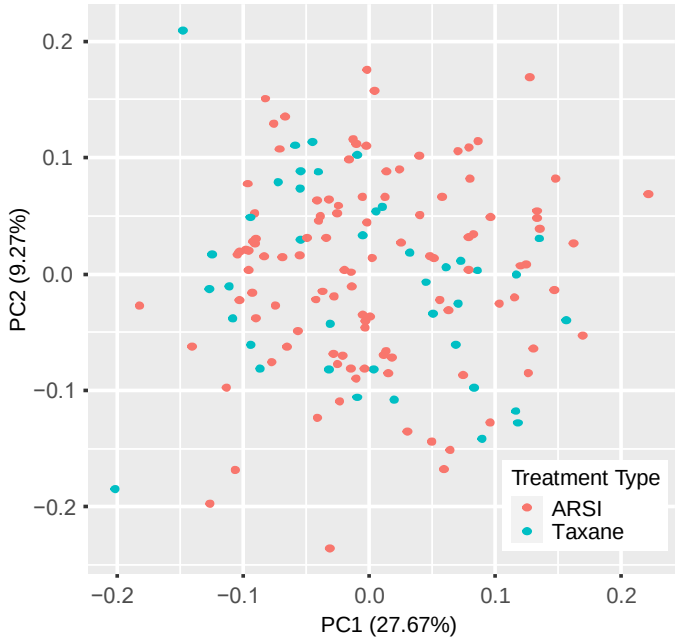


Fig S3.2: PCA of baseline plasma lipidomic profiles in the discovery cohort, samples labelled by treatment line

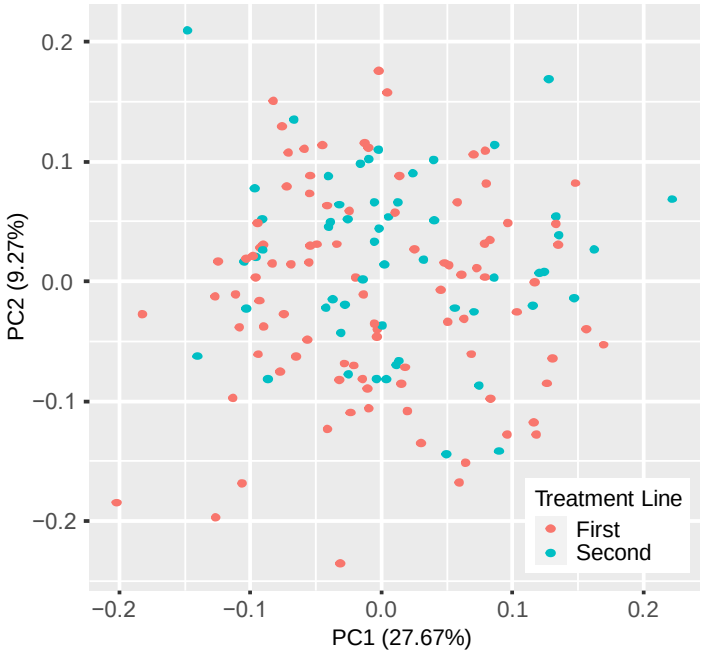


Fig S4: CONSORT diagram

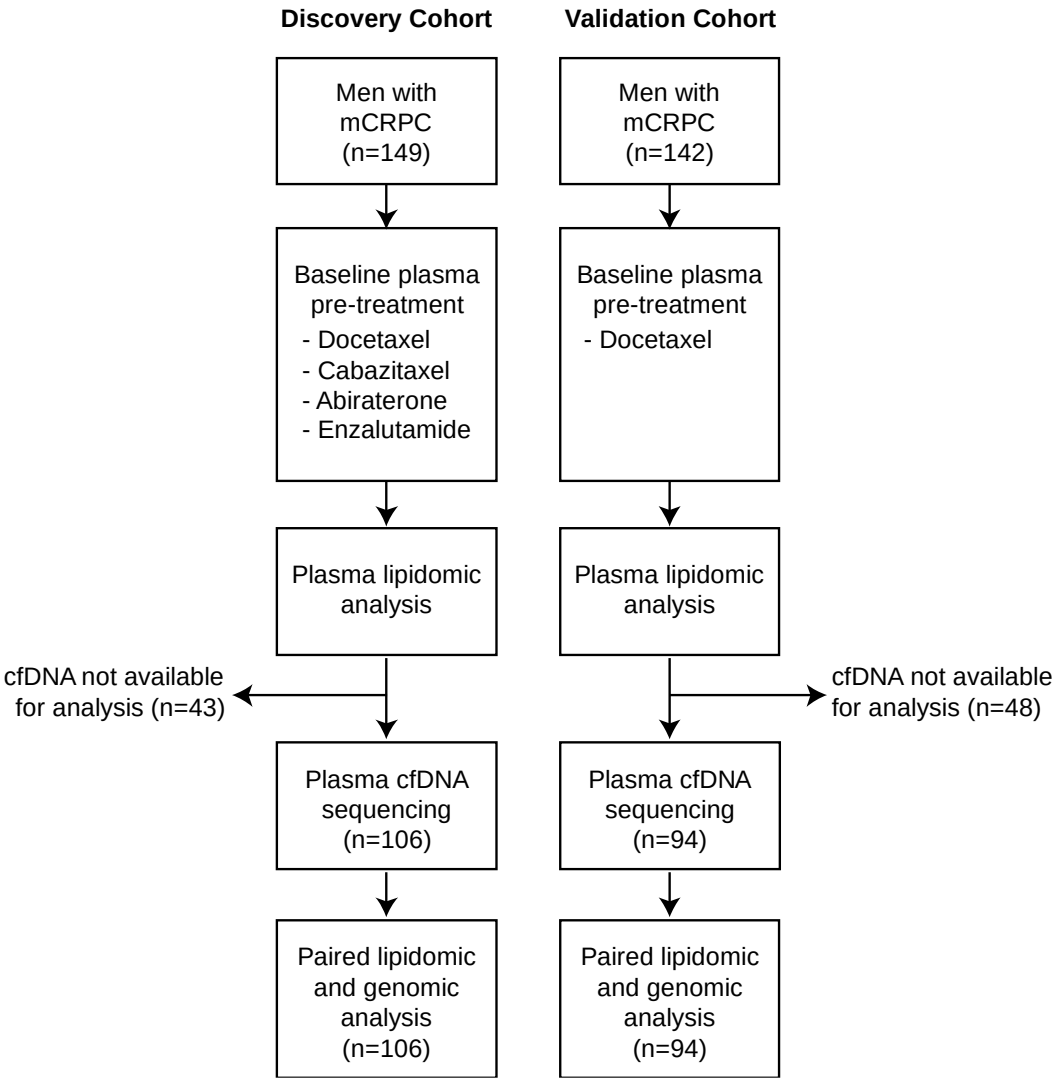


Table S5: Patient characteristics of the discovery and validation cohorts

	Discovery cohort With lipidomic data	Discovery cohort With lipidomic and cfDNA data	Validation cohort With lipidomic data	Validation cohort With lipidomic and cfDNA data
Number of men	149	106	142	94
Median age, years [Q1,Q3]	73 [67,81]	73 [66, 79]	72 [66, 77]	73 [66, 77]
Median follow-up time, months [Q1,Q3]	20 [13, 28]	18 [12,25]	26 [14, 47]	24 [13, 45]
Prostate specific antigen at time of sample collection, ng/mL [Q1, Q3]	30 [11, 72]	31 [9, 94]	14 [3, 52]	12 [4, 52]
Deceased	87 [58%]	61 [58%]	125 [88%]	83 [88%]
Gleason grade				
≤6	7 [5%]	5 [5%]	15 [11%]	10 [11%]
7	26 [17%]	16 [15%]	49 [34%]	28 [30%]
8	19 [13%]	13 [12%]	24 [17%]	16 [17%]
≥9	73 [49%]	56 [53%]	45 [32%]	32 [34%]
unknown	24 [16%]	16 [15%]	9 [6%]	8 [8%]
Type of metastasis				
Bone	131 [88%]	93 [88%]	124 [87%]	81 [86%]
Visceral	15 [10%]	13 [12%]	10 [7%]	7 [7%]
unknown	0 [0%]	0 [0%]	15 [11%]	11 [12%]
Treatment at enrolment				
Docetaxel	39 [26%]	36 [34%]	72 [51%]	50 [53%]
Cabazitaxel	1 [1%]	0 [0%]	0 [0%]	0 [0%]
Enzalutamide	78 [52%]	49 [46%]	0 [0%]	0 [0%]
Abiraterone	31 [21%]	21 [20%]	1 [1%]	1 [1%]
Cis/carboplatin	0 [0%]	0 [0%]	2 [1%]	2 [2%]
Unknown	0 [0%]	0 [0%]	67 [47%]	41 [44%]
Line of systemic treatment at enrolment				
First line	94 [63%]	65 [61%]	142 [100%]	94 [100%]
Second line	55 [37%]	41 [39%]	0 [0%]	0 [0%]
3-Lipid Signature				
Yes	54 [36%]	43 [41%]	56 [39%]	39 [41%]
No	95 [64%]	63 [59%]	86 [61%]	55 [59%]

Q1 = first quartile, Q3 = third quartile

S6 Fold difference in lipid levels between men with and without genetic aberrations, as assessed with t-tests

The tables below show the fold differences of the sphingolipid levels and P-values from the t-test comparisons. The different sphingolipid isoforms have varying concentration ranges, which are displayed in Section S10.

Table S6.1: Sphingolipids with significantly elevated levels in men with any *AR* aberration in the discovery cohort compared to men without, and their fold-change in the validation cohort.

Lipid	**Discovery cohort** Any *AR* aberration vs none		**Validation cohort** Any *AR* aberration vs none	
	Fold	**P-value**	**Fold**	**P-value**
Cer(d18:1/21:0)	1.25	<0.001	1.19	0.002
Hex3Cer(d18:1/20:0)	1.24	0.029	1.20	0.017
Cer(d17:1/18:0)	1.18	0.004	1.05	0.474
Cer(d18:1/16:0)	1.13	0.009	1.07	0.058
Cer(d18:1/18:0)	1.22	0.007	1.11	0.126
Cer(d18:1/19:0)	1.16	0.010	1.05	0.622
Cer(d18:1/20:0)	1.17	0.005	1.09	0.108
Cer(d18:1/24:1)	1.15	0.013	1.08	0.124
Cer(d18:2/18:0)	1.16	0.024	1.05	0.519
Cer(d18:2/20:0)	1.14	0.010	1.02	0.756
Cer(d18:2/21:0)	1.21	0.010	1.25	0.121
Cer(d19:1/16:0)	1.18	0.032	1.20	0.103
Cer(d19:1/18:0)	1.31	0.021	1.16	0.295
Cer(d19:1/20:0)	1.24	0.004	1.18	0.137
HexCer(d18:1/16:0)	1.14	0.028	1.14	0.057
HexCer(d18:1/20:0)	1.16	0.033	1.06	0.359
SM(38:3) (b)	1.06	0.045	1.17	0.056
SM(d18:1/17:0)/SM(d17:1/18:0)	1.13	0.028	1.03	0.663
Sph(d16:1)	1.10	0.016	1.04	0.345
Sph(d18:1)	1.14	0.026	1.01	0.891
Cer(d20:1/26:0)	1.11	0.041	0.93	0.845
GM3(d18:1/20:0)	1.19	0.020	0.97	0.646

Cer = ceramide; GM3 = GM3 ganglioside; HexCer = monohexosylceramide; Hex3Cer = trihexosylceramide; SM = sphingomyelin; Sph = sphingosine.
Cer(d18:1/24:1), which is a component of the 3-lipid signature, is bolded.

Table S6.2: Sphingolipids with significantly elevated levels in men with any *TP53* aberration in the discovery cohort compared to men without, and their fold-change in the validation cohort.

Lipid	**Discovery cohort** Any *TP53* aberration vs none		**Validation cohort** Any *TP53* aberration vs none	
	Fold	**P-value**	**Fold**	**P-value**
HexCer(d18:1/20:0)	1.16	0.036	1.17	0.011
Cer(d17:1/18:0)	1.13	0.041	1.03	0.709
Cer(d18:1/16:0)	1.10	0.047	1.04	0.265
Cer(d18:1/18:0)	1.25	0.002	1.05	0.506
Cer(d18:1/19:0)	1.19	0.003	1.01	0.917
Cer(d18:1/20:0)	1.22	0.000	1.03	0.567
Cer(d18:1/21:0)	1.19	0.007	1.08	0.176
Cer(d18:2/21:0)	1.23	0.007	1.11	0.484
GM3(d18:1/20:0)	1.19	0.019	1.03	0.647
HexCer(d18:1/18:0)	1.16	0.030	1.13	0.082
Hex2Cer(d18:1/20:0)	1.21	0.026	1.15	0.052
Cer(d16:1/18:0)	1.15	0.040	0.90	0.223
Cer(d16:1/20:0)	1.13	0.041	0.90	0.150
Cer(d17:1/20:0)	1.15	0.008	0.96	0.629
Cer(d18:1/22:0)	1.11	0.014	0.99	0.907
Cer(d18:1/24:1)	1.17	0.004	0.97	0.555
Cer(d18:2/18:0)	1.19	0.009	0.98	0.838
Cer(d18:2/20:0)	1.18	0.001	0.99	0.825
Cer(d18:2/24:1)	1.12	0.042	0.94	0.253
Cer(d19:1/18:0)	1.46	0.001	0.95	0.709
Cer(d19:1/20:0)	1.27	0.002	0.99	0.920
Cer(d19:1/22:0)	1.23	0.018	0.93	0.407
Cer(d19:1/24:1)	1.23	0.029	0.89	0.138
Cer(d20:1/22:0)	1.16	0.011	0.97	0.717
Cer(d20:1/24:1)	1.21	0.013	0.96	0.648

Cer = ceramide; GM3 = GM3 ganglioside; HexCer = monohexosylceramide; Hex2Cer = dihexosylceramide.
Cer(d18:1/24:1), which is a component of the 3-lipid signature, is bolded.

Table S6.3: Sphingolipids with significantly elevated levels in men with *RB1* deletion in the discovery cohort compared to men without, and their fold-change in the validation cohort.

Lipid	**Discovery cohort** *RB1* deletion vs none		**Validation cohort** *RB1* deletion vs none	
	Fold	**P-value**	**Fold**	**P-value**
Cer(d18:1/16:0)	1.13	0.027	1.10	0.014
GM3(d18:1/16:0)	1.23	0.005	1.19	0.003
HexCer(d18:1/16:0)	1.16	0.035	1.21	0.013
Cer(d17:1/18:0)	1.20	0.007	1.00	0.967
Cer(d18:1/14:0)	1.17	0.010	1.09	0.191
Cer(d18:1/18:0)	1.27	0.004	1.07	0.409
Cer(d18:1/20:0)	1.24	0.001	1.08	0.183
Cer(d18:1/24:1)	1.18	0.007	1.09	0.102
Cer(d19:1/16:0)	1.20	0.040	1.19	0.168
GM3(d18:1/20:0)	1.39	0.000	1.09	0.235
GM3(d18:1/24:1)	1.27	0.014	1.06	0.365
Hex2Cer(d18:1/18:0)	1.24	0.035	1.05	0.502
Hex2Cer(d18:1/20:0)	1.29	0.010	1.13	0.125
S1P(d18:1)	1.28	0.002	1.02	0.728
SM(38:3) (a)	1.24	0.014	1.06	0.406
SM(38:3) (b)	1.09	0.023	1.07	0.419
SM(40:3) (a)	1.16	0.041	1.10	0.103
SM(43:2) (b)	1.19	0.004	1.09	0.061
SM(44:2)	1.20	0.009	1.05	0.433
SM(44:3)	1.25	0.007	1.08	0.144
SM(d18:1/17:0)/SM(d17:1/18:0)	1.21	0.003	1.06	0.411
SM(d18:1/18:0)/SM(d16:1/20:0)	1.17	0.031	1.02	0.669
SM(d18:1/24:1)	1.25	0.004	1.10	0.069
SM(d19:1/24:1)	1.23	0.046	1.04	0.591
Sph(d16:1)	1.16	0.002	1.04	0.374
Sph(d18:1)	1.34	0.000	1.11	0.094
Sph(d18:2)	1.20	0.001	1.05	0.358
Cer(d20:1/24:1)	1.31	0.002	0.94	0.533
S1P(d18:0)	1.32	0.019	0.97	0.676
S1P(d18:2)	1.24	0.003	0.98	0.674
SM(d18:2/18:0)	1.15	0.038	1.00	0.958

Cer = ceramide; GM3 = GM3 ganglioside; HexCer = monohexosylceramide; Hex2Cer = dihexosylceramide; SM = sphingomyelin; Sph = sphingosine; S1P = sphingosine-1-phosphate. Cer(d18:1/24:1), which is a component of the 3-lipid signature, is bolded.

Table S6.4: Sphingolipids with significantly elevated levels in men with any PI3K pathway aberration in the discovery cohort compared to men without, and their fold-change in the validation cohort.

Lipid	**Discovery cohort** Any PI3K aberration vs none		**Validation cohort** Any PI3K aberration vs none	
	Fold	**P-value**	**Fold**	**P-value**
Cer(d18:1/16:0)	1.11	0.023	1.10	0.012
Cer(d17:1/18:0)	1.21	0.001	1.08	0.333
Cer(d18:1/18:0)	1.27	0.001	1.14	0.082
Cer(d18:1/20:0)	1.17	0.004	1.11	0.060
Cer(d18:1/24:1)	1.14	0.016	1.07	0.201
Cer(d18:2/18:0)	1.19	0.008	1.13	0.157
Cer(d19:1/18:0)	1.33	0.016	1.23	0.176
Cer(d19:1/20:0)	1.19	0.026	1.15	0.211
GM3(d18:1/20:0)	1.25	0.003	1.08	0.268
HexCer(d18:1/16:0)	1.21	0.002	1.08	0.267
HexCer(d18:1/18:0)	1.17	0.024	1.01	0.836
HexCer(d18:1/20:0)	1.19	0.015	1.03	0.712
HexCer(d18:1/24:1)	1.17	0.047	1.09	0.186
S1P(d18:0)	1.35	0.003	1.01	0.859
SM(d18:1/17:0)/SM(d17:1/18:0)	1.15	0.015	1.09	0.231
Sph(d18:1)	1.13	0.030	1.02	0.791
Sph(d18:2)	1.13	0.010	1.04	0.440

Cer = ceramide; GM3 = GM3 ganglioside; HexCer = monohexosylceramide; SM = sphingomyelin; Sph = sphingosine; S1P = sphingosine-1-phosphate.
Cer(d18:1/24:1), which is a component of the 3-lipid signature, is bolded.

Table S6.5: Sphingolipids with significantly elevated levels in men with any DNA repair aberration (*BRCA1/2, ATM, CHEK2*) in the discovery cohort compared to men without, and their fold-change in the validation cohort.

Lipid	**Discovery cohort** Any DNA repair aberration vs none		**Validation cohort** Any DNA repair aberration vs none	
	Fold	**P-value**	**Fold**	**P-value**
Cer(d17:1/18:0)	1.14	0.024	1.05	0.543
Cer(d18:1/18:0)	1.17	0.039	1.07	0.357
GM3(d18:1/20:0)	1.19	0.024	1.02	0.748
Hex2Cer(d18:1/20:0)	1.28	0.005	1.10	0.221
Sph(d18:2)	1.12	0.022	1.08	0.162
Cer(d20:1/22:0)	1.18	0.006	0.81	0.008
Cer(d20:1/23:0)	1.12	0.047	0.85	0.026
Cer(d20:1/24:1)	1.20	0.024	0.92	0.336

Cer = ceramide; GM3 = GM3 ganglioside; Hex2Cer = dihexosylceramide; Sph = sphingosine.

Table S6.6: Sphingolipids with significantly elevated levels in men with any mismatch repair (MMR) aberration (MLH1, MSH2, MSH6) in the discovery cohort compared to men without, and their fold-change in the validation cohort.

Lipid	**Discovery cohort** Any MMR aberration vs none		**Validation cohort** Any MMR aberration vs none	
	Fold	**P-value**	**Fold**	**P-value**
Sph(d18:1)	1.22	0.025	1.19	0.147

Sph = sphingosine.

Table S6.7: Sphingolipids with significantly elevated levels in men with any WNT pathway aberration (*APC, CTNNB1*) in the discovery cohort compared to men without, and their fold-change in the validation cohort.

Lipid	**Discovery cohort** Any WNT pathway aberration vs none		**Validation cohort** Any WNT pathway aberration vs none	
	Fold	**P-value**	**Fold**	**P-value**
Cer(d18:1/18:0)	1.34	0.001	1.10	0.282
Cer(d18:1/20:0)	1.25	0.001	1.08	0.268
Cer(d18:1/24:1)	1.18	0.017	1.10	0.126
Cer(d18:2/18:0)	1.22	0.019	1.01	0.888
Cer(d20:1/22:0)	1.21	0.009	1.04	0.711
Cer(d20:1/24:1)	1.33	0.004	1.16	0.17
GM3(d18:1/16:0)	1.18	0.042	1.08	0.296
GM3(d18:1/20:0)	1.34	0.002	1.14	0.14
GM3(d18:1/22:0)	1.20	0.022	1.08	0.262
Hex2Cer(d18:1/20:0)	1.34	0.006	1.03	0.756
Cer(d18:2/20:0)	1.15	0.037	1.00	0.998

Cer = ceramide; GM3 = GM3 ganglioside; Hex2Cer = dihexosylceramide.
Cer(d18:1/24:1), which is a component of the 3-lipid signature, is bolded.

S7 Kaplan Meier analysis of overall survival by aberration and 3-lipid signature in the discovery and validation cohorts.

The Kaplan Meier analyses below are the same as those in Figures 4-5 of the main article, but with Group 1 (3-lipid signature or aberration) displayed separately as Group 1A (3-lipid signature only) and Group 1B (aberration only).

Fig S7.1: Kaplan Meier analysis of overall survival by *AR* aberration and 3-lipid signature in (A) the discovery cohort and (B) the validation cohort.

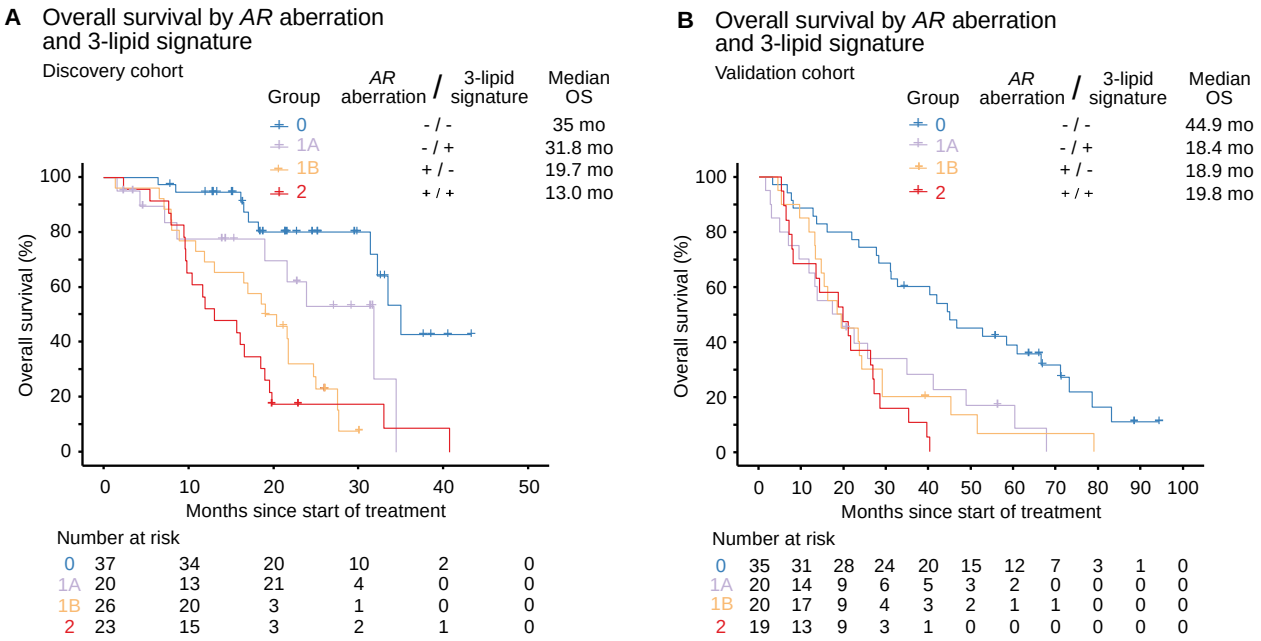


Fig S7.2: Kaplan Meier analysis of overall survival by *TP53* aberration and 3-lipid signature in (A) the discovery cohort and (B) the validation cohort.

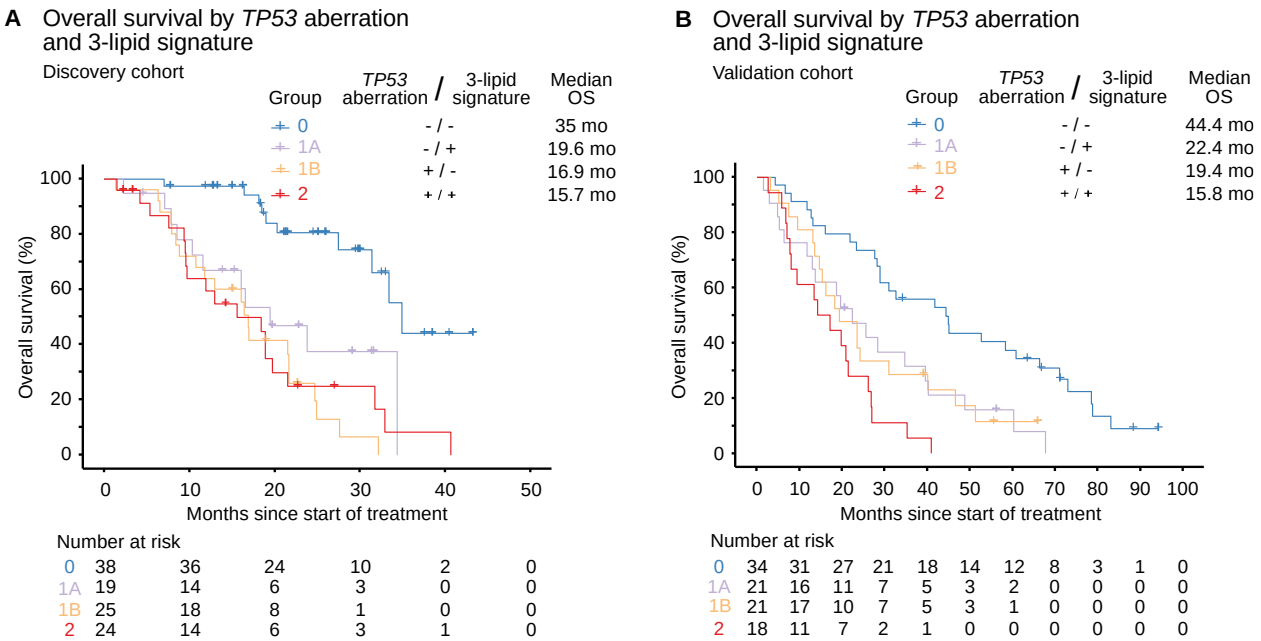
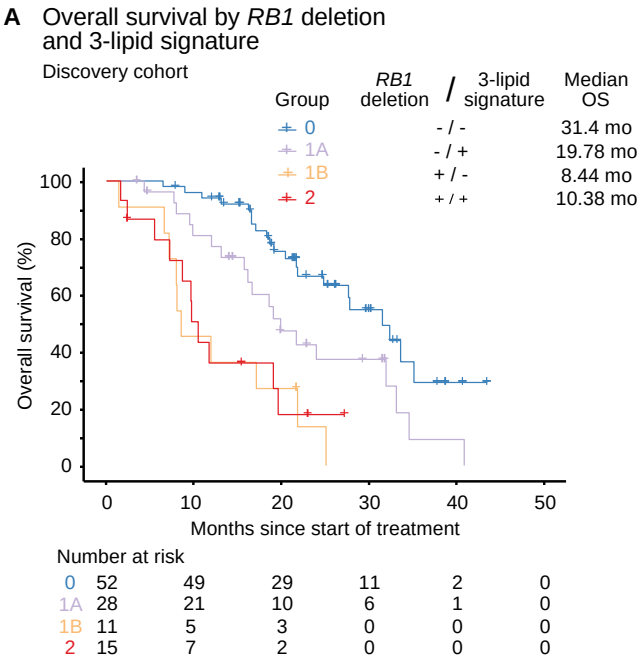


Fig S7.3: Kaplan Meier analysis of overall survival by *RB1* deletion and 3-lipid signature in (A) the discovery cohort and (B) the validation cohort.



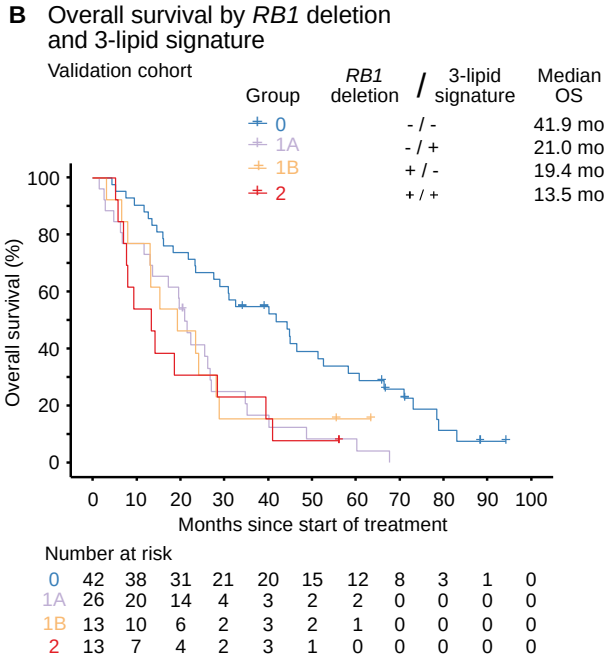
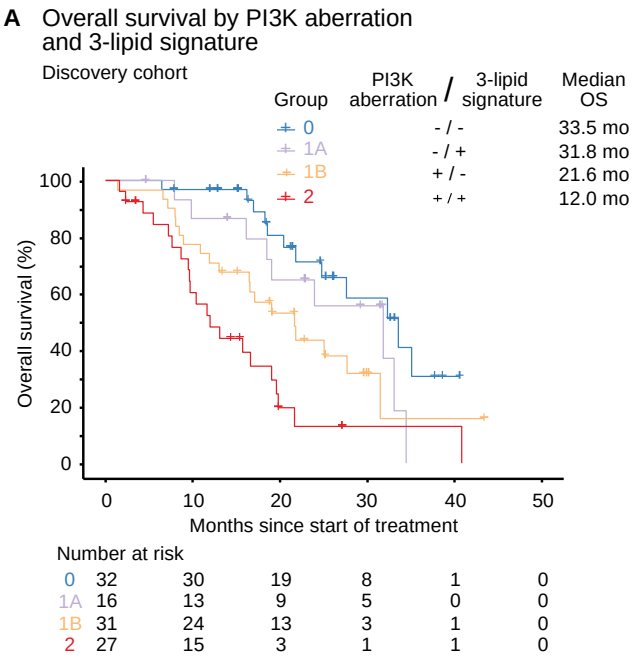


Fig S7.4: Kaplan Meier analysis of overall survival by *PI3K* aberration and 3-lipid signature in (A) the discovery cohort and (B) the validation cohort.



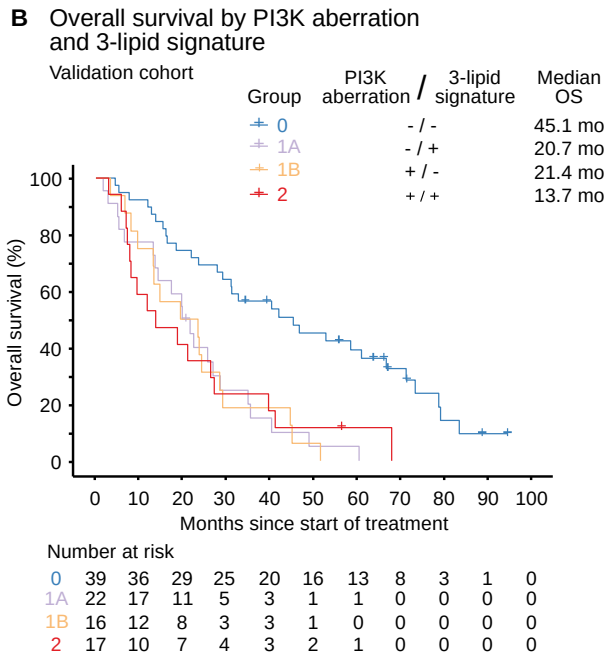
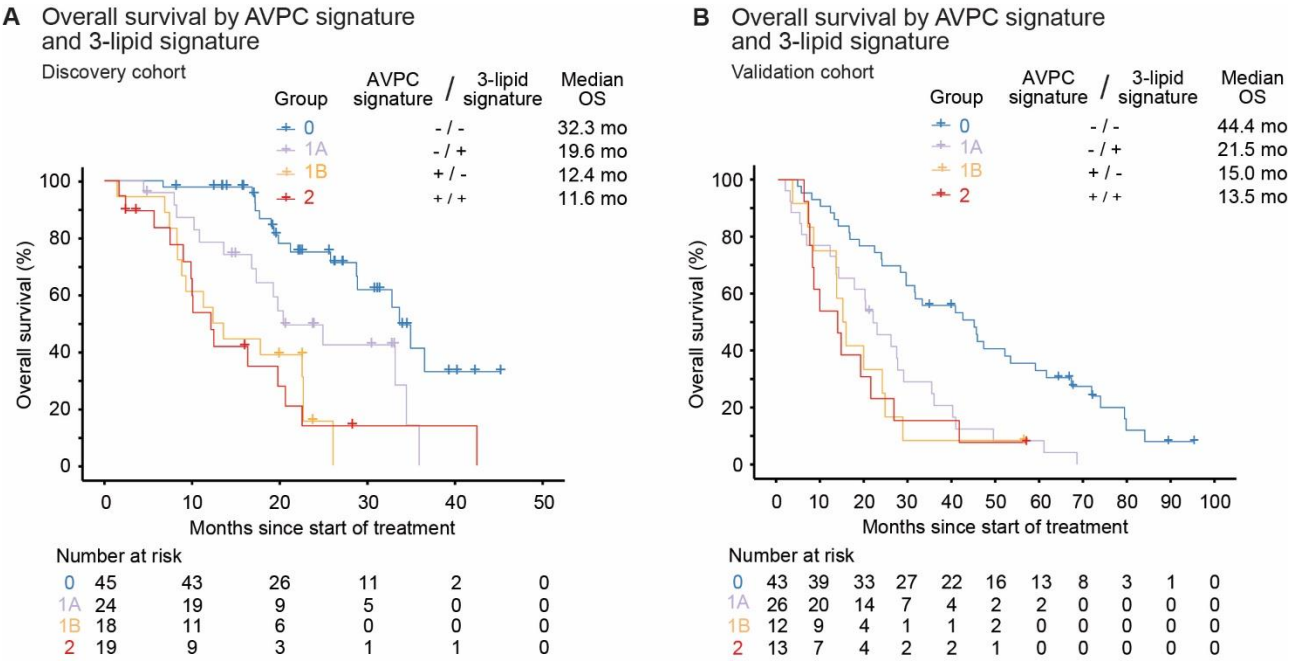


Fig S7.5: Kaplan Meier analysis of overall survival by AVPC signature and 3-lipid signature in (A) the discovery cohort and (B) the validation cohort.



S8 Cox proportional hazards analysis of overall survival based on the aggressive-variant prostate cancer and 3-lipid signature combination

Table S8.1: Cox proportional hazards analysis of overall survival based on the aggressive-variant prostate cancer and 3-lipid signature combination, clinicopathologic factors and ctDNA fraction in the discovery cohort

	Variable	Univariable Cox regression		Multivariable Cox regression using AVPC signature and 3-lipid signature	
		HR (95% CI)	P-value	HR (95% CI)	P-value
	AVPC signature and/or 3-lipid signature (Groups 1 and 2 vs 0)	3.66 (2.05-6.54)	**<0.001**	2.24 (1.21-4.15)	**0.01**
CLINCOPATHOLOGIC FACTORS	Albumin, g/L*	0.86 (0.82-0.91)	**<0.001**	0.89 (0.84-0.95)	**<0.001**
	ECOG performance status (≥2 vs 0-1)	3.94 (1.75-8.87)	**<0.001**	1.71 (0.72-4.06)	0.227
	Pain at baseline (present vs absent)	1.89 (1.12-3.19)	**0.018**	1.65 (0.94-2.89)	0.08
	Haemoglobin (<90 g/L vs ≥90 g/L)	2.70 (0.84-8.73)	0.096	-	-
	PSA, ng/mL*	1.00 (1.00-1.00)	0.081	-	-
	ALP, IU/L*	1.00 (1.00-1.00)	0.197	-	-
	Treatment type (taxane vs ARSI)	1.05 (0.62-1.79)	0.844	-	-
	Treatment line (second line vs first line)	0.87 (0.51-1.48)	0.597	-	-
	Visceral metastases (present vs absent)	1.59 (0.75-3.37)	0.225	-	-
	ctDNA fraction > 2%	1.97 (1.06-3.66)	**0.032**	2.04 (1.08-3.85)	**0.029**

Group 0 = absence of both 3LS and the genetic aberration; Group 1 = presence of one abnormality (either 3LS or the genetic aberration); Group 2 = presence of both 3LS and the genetic aberration.
ALP = alkaline phosphatase; ARSI = androgen receptor signalling inhibitor; AVPC = aggressive-variant prostate cancer; CI = confidence interval; ctDNA = circulating tumour DNA; ECOG = Eastern Cooperative Oncology Group; HR = hazard ratio; PSA = prostate-specific antigen.
All p-values <0.05 are highlighted in bold. Only variables with p<0.05 in univariable analysis were included in multivariable analysis.
*Continuous variable

Table S8.2: Cox proportional hazards analysis of overall survival based on the aggressive-variant prostate cancer and 3-lipid signature combination, clinicopathologic factors and ctDNA fraction in the validation cohort

	Variable	Univariable Cox regression		Multivariable Cox regression using AVPC signature and 3-lipid signature	
		HR (95% CI)	P-value	HR (95% CI)	P-value
	AVPC signature and/or 3-lipid signature (Group 1 and 2 vs 0)	2.94 (1.83-4.74)	**<0.001**	2.62 (1.59-4.34)	**<0.001**
CLINCOPATHOLOGIC FACTORS	PSA, ng/mL*	1.00 (1.00-1.00)	**<0.001**	1.00 (1.00-1.00)	**<0.001**
	ALP, IU/L*	1.00 (1.00-1.00)	**0.002**	1.00 (1.00-1.00)	0.074
	ctDNA fraction > 2%	1.91 (1.18-3.08)	**0.008**	1.47 (0.88-2.44)	0.144

Group 0 = absence of both 3LS and the genetic aberration; Group 1 = presence of one abnormality (either 3LS or the genetic aberration); Group 2 = presence of both 3LS and the genetic aberration.
ALP = alkaline phosphatase; AVPC = aggressive-variant prostate cancer; CI = confidence interval; ctDNA = circulating tumour DNA; HR = hazard ratio; PSA = prostate-specific antigen.
All p-values <0.05 are highlighted in bold. Only variables with p<0.05 in univariable analysis were included in multivariable analysis.
*Continuous variable

S9 Bivariable Cox proportional hazard analyses

Table S9.1: Bivariable Cox proportional hazards analysis of overall survival based on 3-lipid signature and *AR* aberration

Variable	Univariable Cox regression		Bivariable Cox regression	
	HR (95% CI)	**P-value**	**HR (95% CI)**	**P-value**
DISCOVERY COHORT				
3-lipid signature	1.95 (1.18-3.22)	0.01	1.58 (0.94-2.64)	0.085
AR aberration	3.87 (2.21-6.77)	<0.001	3.54 (2.01-6.21)	<0.001
VALIDATION COHORT				
3-lipid signature	2.23 (1.41-3.52)	<0.001	2.00 (1.26-3.19)	0.003
AR aberration	2.26 (1.43-3.58)	<0.001	2.04 (1.28-3.26)	0.003

Table S9.2: Bivariable Cox proportional hazards analysis of overall survival based on 3-lipid signature and *TP53* aberration

Variable	Univariable Cox regression		Bivariable Cox regression	
	HR (95% CI)	**P-value**	**HR (95% CI)**	**P-value**
DISCOVERY COHORT				
3-lipid signature	1.95 (1.18-3.22)	0.01	1.40 (0.83-2.37)	0.209
TP53 aberration	3.55 (2.07-6.08)	<0.001	3.21 (1.84-5.62)	<0.001
VALIDATION COHORT				
3-lipid signature	2.23 (1.41-3.52)	<0.001	2.17 (1.37-3.44)	<0.001
TP53 aberration	2.18 (1.37-3.47)	0.001	2.12 (1.32-3.39)	0.002

Table S9.3: Bivariable Cox proportional hazards analysis of overall survival based on 3-lipid signature and *RB1* deletion

Variable	Univariable Cox regression		Bivariable Cox regression	
	HR (95% CI)	**P-value**	**HR (95% CI)**	**P-value**
DISCOVERY COHORT				
3-lipid signature	1.95 (1.18-3.22)	0.01	1.58 (0.94-2.66)	0.083
RB1 deletion	4.10 (2.33-7.22)	<0.001	3.66 (2.05-6.54)	<0.001
VALIDATION COHORT				
3-lipid signature	2.23 (1.41-3.52)	<0.001	2.09 (1.32-3.32)	0.002
RB1 deletion	1.79 (1.09-2.94)	0.021	1.57 (0.95-2.59)	0.079

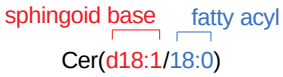
Table S9.4: Bivariable Cox proportional hazards analysis of overall survival based on 3-lipid signature and PI3K aberration

Variable	Univariable Cox regression		Bivariable Cox regression	
	HR (95% CI)	**P-value**	**HR (95% CI)**	**P-value**
DISCOVERY COHORT				
3-lipid signature	1.95 (1.18-3.22)	0.01	1.89 (1.14-3.14)	0.014
PI3K aberration	2.66 (1.55-4.58)	<0.001	2.61 (1.52-4.49)	<0.001
VALIDATION COHORT				
3-lipid signature	2.23 (1.41-3.52)	<0.001	1.91 (1.19-3.07)	0.007
PI3K aberration	2.11 (1.33-3.34)	0.002	1.75 (1.08-2.82)	0.022

PI3K = phosphatidylinositol-3-kinase.

S10 Plasma concentrations of sphingolipids in the discovery and validation cohorts.

Sphingolipids are lipids with a sphingoid base of which the d18:1 isoform is the major isoform present in plasma.



The most abundant ceramide species measured in the plasma of our cohorts were Cer(d18:1/24:0), Cer(d18:1/24:1), Cer(d18:1/22:0) and Cer(d18:1/23:0) (Figure S10.1), of which Cer(d18:1/24:1) is the ceramide in the 3LS. This ceramide is one of the ceramides with significantly elevated levels among patients with genetic aberrations in AR, TP53 or RBI compared to those without the respective aberration. The plasma concentration ranges (pre-treatment) of each individual sphingolipid species are displayed in Table S10.1.

Fig S10.1: Abundance of ceramides in the plasma (pre-treatment) of the Discovery and Validation cohorts.

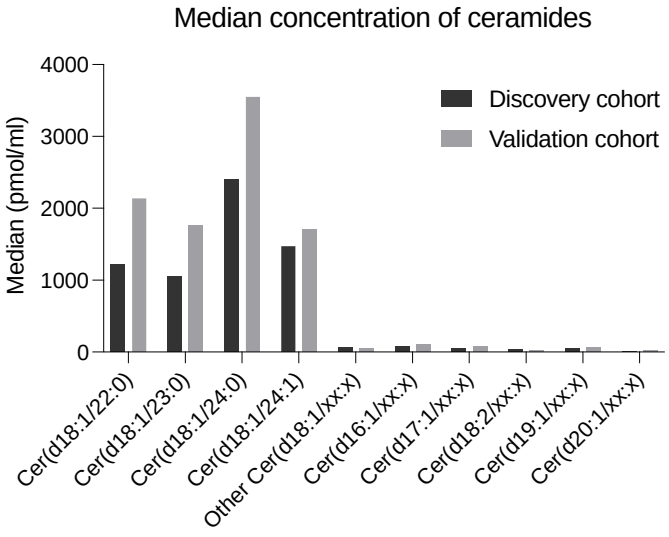


Table S10.1: Concentration range of sphingolipids in plasma (baseline) of the Discovery and Validation cohorts.

	Sphingolipid in plasma	Discovery cohort (pmol/ml)			Validation cohort (pmol/ml)		
		Median	Min	Max	Median	Min	Max
1	Cer(d16:1/16:0)	33.5	13.2	77.3	25.6	4.2	85.6
2	Cer(d16:1/18:0)	46.8	14.7	89.0	30.8	6.1	117.7
3	Cer(d16:1/20:0)	47.8	19.6	98.5	29.4	7.9	149.7
4	Cer(d16:1/22:0)	96.1	32.9	232.8	161.4	43.9	1424.3
5	Cer(d16:1/23:0)	84.0	21.9	232.8	133.1	39.6	830.8
6	Cer(d16:1/24:0)	286.2	89.4	753.8	391.9	60.0	2938.3
7	Cer(d16:1/24:1)	82.4	25.0	179.4	101.5	33.3	550.1
8	Cer(d17:1/16:0)	16.7	6.0	32.5	17.4	6.8	70.2
9	Cer(d17:1/18:0)	10.9	4.4	21.5	12.5	6.3	30.1
10	Cer(d17:1/20:0)	9.2	3.7	18.4	5.2	2.1	18.4
11	Cer(d17:1/22:0)	52.7	14.5	111.9	85.1	25.8	473.3
12	Cer(d17:1/23:0)	60.0	15.6	156.1	70.0	21.7	405.6
13	Cer(d17:1/24:0)	167.3	45.6	376.4	215.6	49.0	855.8
14	Cer(d17:1/24:1)	96.7	25.7	177.6	109.3	47.8	444.4
15	Cer(d18:0/16:0)	N/A	N/A	N/A	29.9	13.8	71.4
16	Cer(d18:0/18:0)	N/A	N/A	N/A	9.7	3.0	29.5
17	Cer(d18:0/20:0)	N/A	N/A	N/A	46.7	21.2	201.3
18	Cer(d18:0/22:0)	N/A	N/A	N/A	252.7	70.4	1224.8
19	Cer(d18:0/24:0)	N/A	N/A	N/A	179.9	46.3	890.5
20	Cer(d18:0/24:1)	N/A	N/A	N/A	141.7	42.7	1014.1
21	Cer(d18:1/14:0)	9.3	4.2	22.0	8.3	2.4	23.5
22	Cer(d18:1/16:0)	306.8	176.6	506.3	257.5	129.0	821.3
23	Cer(d18:1/17:0)	N/A	N/A	N/A	14.4	7.2	29.2
24	Cer(d18:1/18:0)	110.1	42.9	325.8	88.4	32.7	304.2
25	Cer(d18:1/19:0)	7.2	3.8	14.3	3.3	0.7	11.0
26	Cer(d18:1/20:0)	123.1	66.6	254.7	169.6	72.0	780.1
27	Cer(d18:1/21:0)	28.5	11.7	57.9	48.9	23.1	223.1
28	Cer(d18:1/22:0)	1220.0	585.0	2178.5	2136.8	668.8	13258.6
29	Cer(d18:1/23:0)	1049.8	409.8	2103.9	1763.2	584.6	7590.7
30	Cer(d18:1/24:0)	2405.1	971.5	4160.9	3553.1	799.5	16744.0
31	Cer(d18:1/24:1)	1471.4	570.9	2994.7	1700.5	789.4	5881.2
32	Cer(d18:1/26:0)	49.4	22.1	87.4	46.0	12.1	106.2
33	Cer(d18:2/14:0)	2.4	0.4	6.0	2.6	0.5	8.1
34	Cer(d18:2/16:0)	36.6	16.0	72.2	37.0	13.9	94.5
35	Cer(d18:2/17:0)	1.3	0.1	3.5	0.5	0.0	1.7
36	Cer(d18:2/18:0)	32.4	12.0	76.1	18.6	4.9	72.9
37	Cer(d18:2/20:0)	24.4	12.8	45.6	18.4	6.7	89.1
38	Cer(d18:2/21:0)	4.0	1.2	11.3	3.3	1.4	15.9
39	Cer(d18:2/22:0)	179.1	76.3	366.8	339.2	88.9	2423.7
40	Cer(d18:2/23:0)	194.6	53.7	479.0	326.0	93.2	1789.1
41	Cer(d18:2/24:0)	555.2	222.2	1274.2	889.7	139.7	4484.8
42	Cer(d18:2/24:1)	232.0	84.8	567.0	270.1	131.5	1175.6

43	Cer(d18:2/26:0)	9.1	3.1	22.9	8.9	1.3	25.2
44	Cer(d19:1/16:0)	1.3	0.3	2.9	2.6	0.3	7.0
45	Cer(d19:1/18:0)	6.4	1.0	23.8	5.1	0.6	23.4
46	Cer(d19:1/20:0)	8.7	2.5	24.8	9.7	3.2	31.4
47	Cer(d19:1/22:0)	94.5	12.6	248.0	109.5	23.1	422.9
48	Cer(d19:1/23:0)	92.7	13.6	312.4	113.9	25.8	370.6
49	Cer(d19:1/24:0)	217.9	39.0	525.4	268.6	33.6	1301.3
50	Cer(d19:1/24:1)	192.3	21.1	540.8	156.7	53.6	463.9
51	Cer(d19:1/26:0)	7.4	4.2	14.2	4.5	1.8	11.0
52	Cer(d20:1/22:0)	12.9	5.9	24.7	27.2	6.0	84.9
53	Cer(d20:1/23:0)	8.1	3.2	16.6	16.3	1.9	39.8
54	Cer(d20:1/24:0)	20.7	9.8	40.6	33.6	5.2	103.7
55	Cer(d20:1/24:1)	15.6	6.9	51.9	24.0	5.2	70.9
56	Cer(d20:1/26:0)	6.1	3.5	11.0	4.2	2.0	8.6
57	Cer(m18:0/20:0)	8.1	2.3	32.3	27.4	10.0	179.8
58	Cer(m18:0/22:0)	22.1	6.9	77.8	74.3	23.6	455.9
59	Cer(m18:0/23:0)	11.1	2.0	44.7	34.1	8.7	186.3
60	Cer(m18:0/24:0)	27.3	4.9	95.8	77.1	20.0	379.9
61	Cer(m18:0/24:1)	21.1	4.9	74.1	54.1	14.0	214.1
62	Cer(m18:1/18:0)	4.5	1.1	14.5	12.4	2.4	44.6
63	Cer(m18:1/20:0)	24.5	8.5	86.9	93.8	23.4	437.2
64	Cer(m18:1/22:0)	48.3	12.3	163.2	193.1	39.4	1023.0
65	Cer(m18:1/23:0)	20.8	4.7	85.6	80.0	18.1	336.0
66	Cer(m18:1/24:0)	67.8	19.2	247.5	209.9	38.8	894.9
67	Cer(m18:1/24:1)	38.9	8.7	203.2	133.3	25.3	615.4
68	Cer1P(d18:1/16:0)	2.9	1.1	7.0	5.4	2.3	10.8
69	dhCer(d18:0/16:0)	7.8	4.3	13.1	N/A	N/A	N/A
70	dhCer(d18:0/18:0)	2.6	1.0	5.6	N/A	N/A	N/A
71	dhCer(d18:0/20:0)	9.0	4.9	18.9	N/A	N/A	N/A
72	dhCer(d18:0/22:0)	32.0	14.9	75.7	N/A	N/A	N/A
73	dhCer(d18:0/24:0)	28.2	9.6	79.6	N/A	N/A	N/A
74	dhCer(d18:0/24:1)	24.1	9.7	76.4	N/A	N/A	N/A
75	GM1(d18:1/16:0)	44.1	21.9	154.5	46.7	23.2	91.5
76	GM3(d18:1/16:0)	343.4	148.6	703.3	312.1	171.3	1051.4
77	GM3(d18:1/18:0)	116.0	38.6	218.9	136.2	46.4	767.4
78	GM3(d18:1/20:0)	363.6	142.0	1035.4	136.7	58.8	315.3
79	GM3(d18:1/22:0)	355.9	141.4	964.5	387.1	143.1	829.4
80	GM3(d18:1/24:0)	119.6	37.6	290.7	118.5	42.8	314.7
81	GM3(d18:1/24:1)	277.7	45.0	801.2	262.1	108.1	677.4
82	HexCer(d16:1/18:0)	34.4	4.5	112.2	17.6	5.5	51.4
83	HexCer(d16:1/20:0)	40.2	9.8	94.3	23.5	8.6	62.0
84	HexCer(d16:1/22:0)	56.2	17.2	173.8	47.6	19.6	197.4
85	HexCer(d16:1/24:0)	78.5	21.7	279.5	46.7	17.9	193.6
86	HexCer(d18:1/16:0)	826.3	350.4	1614.7	506.6	246.7	1287.4
87	HexCer(d18:1/18:0)	112.0	40.6	254.2	77.2	29.1	341.6
88	HexCer(d18:1/20:0)	106.4	42.6	230.7	73.6	28.3	243.8

89	HexCer(d18:1/22:0)	583.4	281.9	1225.6	496.4	138.0	1844.2
90	HexCer(d18:1/24:0)	1362.7	560.1	2491.1	1070.3	296.1	2951.8
91	HexCer(d18:1/24:1)	667.7	274.4	1783.6	450.4	150.4	1270.0
92	HexCer(d18:2/18:0)	15.5	1.2	41.3	13.8	5.1	46.5
93	HexCer(d18:2/20:0)	18.3	6.4	46.0	11.5	3.7	44.4
94	HexCer(d18:2/22:0)	73.7	27.6	150.1	59.4	22.4	295.0
95	HexCer(d18:2/24:0)	225.6	94.6	531.4	168.9	58.1	644.9
96	Hex2Cer(d16:1/16:0)	49.1	11.4	129.0	109.2	36.2	288.8
97	Hex2Cer(d16:1/24:1)	31.4	10.9	94.5	22.1	4.5	55.3
98	Hex2Cer(d18:1/16:0)	1213.0	297.6	3630.4	1297.4	492.9	3189.2
99	Hex2Cer(d18:1/18:0)	17.7	3.4	37.2	18.3	5.2	57.6
100	Hex2Cer(d18:1/20:0)	26.6	4.6	80.9	25.4	9.3	70.8
101	Hex2Cer(d18:1/22:0)	131.7	52.4	296.5	116.6	49.1	330.8
102	Hex2Cer(d18:1/24:0)	258.8	107.3	589.8	205.9	89.7	604.4
103	Hex2Cer(d18:1/24:1)	365.9	99.2	858.9	262.9	112.2	715.0
104	Hex2Cer(d18:2/16:0)	61.2	22.5	135.6	77.0	28.7	212.8
105	Hex2Cer(d18:2/24:1)	103.9	21.8	241.4	68.5	24.3	189.2
106	Hex3Cer(d18:1/16:0)	509.0	253.8	1097.6	770.2	432.8	1646.8
107	Hex3Cer(d18:1/18:0)	137.5	50.7	436.8	134.2	38.0	335.8
108	Hex3Cer(d18:1/20:0)	29.8	6.6	83.7	35.2	12.3	118.8
109	Hex3Cer(d18:1/22:0)	107.4	34.4	274.3	132.9	48.6	377.3
110	Hex3Cer(d18:1/24:0)	51.4	21.1	114.9	72.3	27.5	187.8
111	Hex3Cer(d18:1/24:1)	201.4	69.5	485.1	191.8	95.5	616.6
112	SM(34:3)	48.1	22.0	86.8	93.9	41.8	220.4
113	SM(35:2) (b)	28.8	11.0	63.5	140.8	59.3	345.0
114	SM(37:1)	885.2	240.0	1695.5	1025.9	454.3	1796.1
115	SM(37:2)	209.7	77.9	403.1	254.6	126.7	601.6
116	SM(38:3) (a)	233.4	78.3	566.0	376.4	145.1	684.7
117	SM(38:3) (b)	569.4	426.9	743.0	168.8	84.2	315.0
118	SM(40:3) (a)	603.4	257.7	1190.6	1297.4	549.8	3578.5
119	SM(40:3) (b)	649.5	298.2	1483.0	1011.6	528.8	1996.8
120	SM(41:0)	143.3	62.7	441.3	300.9	98.6	1490.9
121	SM(41:1) (a)	791.6	139.1	1672.9	577.7	122.9	1730.6
122	SM(43:1)	863.9	255.4	2108.6	1225.3	285.6	2971.5
123	SM(43:2) (b)	648.1	364.0	1206.3	492.4	237.7	1127.7
124	SM(43:2) (c)	192.7	77.2	325.8	353.4	119.4	646.4
125	SM(44:1)	168.3	75.0	298.3	188.0	59.6	388.3
126	SM(44:2)	270.7	129.7	513.7	353.6	152.5	801.4
127	SM(44:3)	266.4	110.9	569.9	339.4	169.8	687.2
128	SM(d16:1/19:0)	1093.5	227.1	2524.3	1038.6	413.1	2276.8
129	SM(d16:1/23:0)/ SM(d17:1/22:0)	2446.2	752.2	5665.6	4621.5	1761.7	13035.5
130	SM(d16:1/24:1)	3715.1	1866.7	7665.0	4939.9	1688.4	11696.3
131	SM(d17:1/14:0)	169.6	48.9	449.9	210.2	101.8	642.9
132	SM(d17:1/16:0)	8260.4	3605.9	16028.9	6520.6	2605.5	19327.1
133	SM(d17:1/24:1)	2437.6	1162.3	4527.2	3297.7	1417.7	6543.5

134	SM(d18:0/14:0)	127.9	33.9	489.1	204.2	114.7	811.0
135	SM(d18:0/16:0)	5728.4	2787.4	16980.8	5554.8	3059.7	25731.7
136	SM(d18:0/22:0)	304.6	96.2	1120.0	499.6	104.2	2868.6
137	SM(d18:1/14:0)/ SM(d16:1/16:0)	7353.8	3253.9	16495.6	8952.8	4635.8	29381.9
138	SM(d18:1/16:0)	79303.3	32729.1	134579.2	103120.6	55360.8	184453.8
139	SM(d18:1/17:0)/ SM(d17:1/18:0)	2631.2	1103.9	4910.3	1503.0	736.1	3256.4
140	SM(d18:1/18:0)/ SM(d16:1/20:0)	13663.1	6271.0	37707.4	18420.5	8288.9	56466.7
141	SM(d18:1/20:0)/ SM(d16:1/22:0)	6044.3	2832.9	14779.0	11378.9	3906.9	37222.8
142	SM(d18:1/22:0)/ SM(d16:1/24:0)	18981.8	7468.2	35819.2	29834.7	9366.4	90811.9
143	SM(d18:1/23:0)/ SM(d17:1/24:0)	8159.4	2901.0	16405.3	12398.5	3326.1	33077.0
144	SM(d18:1/24:0)	11397.2	5527.6	23784.7	21639.5	6445.1	59810.7
145	SM(d18:1/24:1)	28616.3	12923.4	64957.5	32960.6	16551.9	86692.5
146	SM(d18:2/14:0)	594.3	229.0	1323.6	830.6	440.0	2386.9
147	SM(d18:2/16:0)	8198.6	4018.1	15488.3	14162.4	6320.4	43119.8
148	SM(d18:2/17:0)	271.8	112.5	516.0	383.2	140.0	1014.9
149	SM(d18:2/18:0)	7925.9	3807.9	18444.8	11693.9	5188.3	31823.4
150	SM(d18:2/18:1)	312.0	119.2	638.0	786.9	331.5	1994.0
151	SM(d18:2/20:0)	4278.0	1934.3	6886.8	4623.7	2059.3	10472.9
152	SM(d18:2/22:0)	6826.4	2698.2	13256.2	13650.9	5463.4	39608.1
153	SM(d18:2/23:0)	4190.1	1353.9	7483.4	6249.4	2685.3	16916.2
154	SM(d18:2/24:0)	7349.6	3483.4	15062.8	11618.3	4263.0	26243.3
155	SM(d19:1/24:1)	1637.7	320.1	3961.3	1405.6	384.7	4436.4
156	Sph(d16:1)	45.2	33.4	62.6	18.1	13.0	25.1
157	Sph(d18:1)	46.4	25.6	143.1	61.0	40.4	106.3
158	Sph(d18:2)	18.5	11.8	28.4	17.1	11.3	33.6
159	S1P(d16:1)	156.8	65.4	309.2	115.7	66.0	204.4
160	S1P(d17:1)	42.9	10.1	94.1	N/A	N/A	N/A
161	S1P(d18:0)	46.5	11.7	169.2	71.7	39.2	149.2
162	S1P(d18:1)	773.3	386.7	1822.3	484.4	303.7	885.6
163	S1P(d18:2)	246.7	118.3	570.2	145.2	96.4	258.9

N/A, not measured