

Summary of the curatedPCaData-package

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Contents

1	Summary of all MAE-objects	2
1.1	End-points	2
1.1.1	Gleason grades	2
1.1.2	Overall Survival	2
1.1.3	Recurrence	3
1.1.4	Other end-points	3
2	Individual MAE-summaries	3
2.1	abida	4
2.2	barbieri	5
2.3	chandran	6
2.4	friedrich	8
2.5	hieronymus	9
2.6	icgcca	10
2.7	igc	11
2.8	kim	13
2.9	kunderfranco	14
2.10	ren	15
2.11	sun	17
2.12	taylor	18
2.13	tcga	19
2.14	true	21
2.15	wallace	22
2.16	wang	24
2.17	weiner	25

This is a summary of the MultiAssayExperiment-objects (MAE) offered for curated prostate cancer datasets in the *curatedPCaData*-package version 0.6.0. The following objects are currently available in the package:

```
> utils::data(package="curatedPCaData")$result[,c("Item", "Title")]
```

	Item	Title
[1,]	"mae_abida"	"Abida et al. MAE-object"
[2,]	"mae_barbieri"	"Barbieri MAE-object"
[3,]	"mae_chandran"	"Barwick MAE-object"
[4,]	"mae_friedrich"	"Friedrich et al. MAE-object"
[5,]	"mae_hieronymus"	"Hieronymus et al. MAE-object"

```

[6,] "mae_icgcca"      "ICGC CA MAE-object"
[7,] "mae_igc"        ""
[8,] "mae_kim"        ""
[9,] "mae_kunderfranco" "Kunderfranco et al. MAE-object"
[10,] "mae_ren"       "Ren 2017 MAE-object"
[11,] "mae_sun"       "Sun et al. MAE-object"
[12,] "mae_taylor"    "Taylor et al. MAE-object"
[13,] "mae_tcga"      "TCGA MAE-object"
[14,] "mae_true"      "True et al. MAE-object"
[15,] "mae_wallace"   "Wallace et al. MAE-object"
[16,] "mae_wang"      ""
[17,] "mae_weiner"    "MultiAssayExperiment object containing gene expression (gex),"

```

They can be accessed via syntax `curatedPCaData::mae_name` or by first calling `library("curatedPCaData")` and then calling directly the objects `mae_name` in the workspace environment.

1 Summary of all MAE-objects

Summary table of all MAE-objects and availability of most important variables.

1.1 End-points

1.1.1 Gleason grades

Gleason grade distribution over studies:

	5	6	7	8	9	10	Other	N/A
abida	-	-	-	-	-	-	0 (0%)	444 (100%)
barbieri	-	-	-	-	-	-	112 (100%)	0 (0%)
chandran	6 (1%)	46 (9%)	85 (17%)	21 (4%)	35 (7%)	-	3 (1%)	307 (61%)
friedrich	2 (1%)	47 (18%)	54 (21%)	68 (27%)	43 (17%)	2 (1%)	0 (0%)	39 (15%)
hieronymus	-	16 (15%)	78 (75%)	4 (4%)	6 (6%)	-	0 (0%)	0 (0%)
icgcca	-	12 (6%)	58 (27%)	5 (2%)	-	-	0 (0%)	138 (65%)
igc	-	27 (33%)	40 (48%)	13 (16%)	-	-	0 (0%)	3 (4%)
kim	-	-	-	-	-	-	266 (100%)	0 (0%)
kunderfranco	1 (1%)	9 (13%)	32 (48%)	6 (9%)	5 (7%)	-	0 (0%)	14 (21%)
ren	-	-	-	-	-	-	65 (100%)	0 (0%)
sun	-	-	-	-	-	-	0 (0%)	79 (100%)
taylor	2 (1%)	104 (48%)	77 (35%)	19 (9%)	15 (7%)	-	0 (0%)	1 (0%)
tcga	-	45 (9%)	244 (49%)	64 (13%)	137 (28%)	4 (1%)	0 (0%)	0 (0%)
true	-	4 (14%)	20 (69%)	1 (3%)	4 (14%)	-	0 (0%)	0 (0%)
wallace	2 (2%)	21 (25%)	57 (69%)	1 (1%)	2 (2%)	-	0 (0%)	0 (0%)
wang	-	-	-	-	-	-	0 (0%)	148 (100%)
weiner	-	-	-	-	-	-	0 (0%)	838 (100%)

1.1.2 Overall Survival

Quantiles [min, 25%, median, 75%, max] for follow-up times and 0 (no event) and 1 (event) for survival:

	0 (no event)	1 (event)	N/A (event)	Time (d)	N/A (time)
abida	52 (12%)	84 (19%)	308 (69%)	[50,321,595,883,2070]	308 (69%)
barbieri	-	-	112 (100%)	-	112 (100%)
chandran	-	-	503 (100%)	-	503 (100%)
friedrich	230 (90%)	25 (10%)	0 (0%)	[641,3005,3614,4301,6771]	91 (36%)
hieronymus	96 (92%)	8 (8%)	0 (0%)	[295,1575,2139,2895,3758]	0 (0%)
icgcca	198 (93%)	8 (4%)	7 (3%)	[1460,2190,2920,3650,4745]	1 (0%)
igc	-	-	83 (100%)	-	83 (100%)
kim	-	-	266 (100%)	-	266 (100%)
kunderfranco	-	-	67 (100%)	-	67 (100%)
ren	-	-	65 (100%)	-	65 (100%)
sun	-	-	79 (100%)	-	79 (100%)
taylor	-	-	218 (100%)	-	218 (100%)
tcga	484 (98%)	10 (2%)	0 (0%)	[23,525,926,1466,5034]	0 (0%)
true	-	-	29 (100%)	-	29 (100%)
wallace	-	-	83 (100%)	-	83 (100%)
wang	-	-	148 (100%)	-	148 (100%)
weiner	-	-	838 (100%)	-	838 (100%)

1.1.3 Recurrence

Quantiles [min, 25%, median, 75%, max] for follow-up times and counts for 0 (no event) and 1 (event) for recurrence:

	0 (no event)	1 (event)	N/A (event)	Time (d)	N/A (time)
abida	-	-	444 (100%)	-	444 (100%)
barbieri	-	-	112 (100%)	-	112 (100%)
chandran	-	-	503 (100%)	-	503 (100%)
friedrich	-	-	255 (100%)	-	255 (100%)
hieronymus	-	-	104 (100%)	-	104 (100%)
icgcca	-	-	213 (100%)	-	213 (100%)
igc	-	-	83 (100%)	-	83 (100%)
kim	-	-	266 (100%)	-	266 (100%)
kunderfranco	-	-	67 (100%)	-	67 (100%)
ren	-	-	65 (100%)	-	65 (100%)
sun	40 (51%)	39 (49%)	0 (0%)	-	79 (100%)
taylor	137 (63%)	61 (28%)	20 (9%)	[3,717,1386,1974,4909]	20 (9%)
tcga	397 (80%)	91 (18%)	6 (1%)	[23,427,823,1376,5034]	6 (1%)
true	-	-	29 (100%)	-	29 (100%)
wallace	-	-	83 (100%)	-	83 (100%)
wang	-	-	148 (100%)	-	148 (100%)
weiner	-	-	838 (100%)	-	838 (100%)

1.1.4 Other end-points

TODO, for example the newer grading system available in Weiner et al.

2 Individual MAE-summaries

Looping over and summarizing the datasets:

2.1 abida

	Instances	Missingness
overall_survival_status	NA: 308 (69%);1: 84 (19%);0: 52 (12%)	n=308 (69%)
days_to_overall_survival	[50.26,321.04,594.78,882.8,2069.65], NA n=308	n=308 (69%)
age_at_initial_diagnosis	[38,56,61,66,89], NA n=51	n=51 (11%)
year_diagnosis	N/A	n=444 (100%)
gleason_grade	N/A	n=444 (100%)
gleason_major	N/A	n=444 (100%)
gleason_minor	N/A	n=444 (100%)
source_of_gleason	N/A	n=444 (100%)
grade_group	N/A	n=444 (100%)
T_pathological	N/A	n=444 (100%)
T_substage_pathological	N/A	n=444 (100%)
T_clinical	N/A	n=444 (100%)
T_substage_clinical	N/A	n=444 (100%)
ERG_fusion_CNA	N/A	n=444 (100%)
ERG_fusion_IHC	N/A	n=444 (100%)
ERG_fusion_GEX	N/A	n=444 (100%)
disease_specific_recurrence_status	N/A	n=444 (100%)
days_to_disease_specific_recurrence	N/A	n=444 (100%)
metastasis_occurrence_status	N/A	n=444 (100%)
days_to_metastatic_occurrence	N/A	n=444 (100%)
psa	[0.2,5.7,14.04,52.84,3118], NA n=91	-
race	N/A	n=444 (100%)
smoking_status	N/A	n=444 (100%)
extraprostatic_extension	N/A	n=444 (100%)
perineural_invasion	N/A	n=444 (100%)
seminal_vesicle_invasion	N/A	n=444 (100%)
angiolymphatic_invasion	N/A	n=444 (100%)
androgen_ablation	N/A	n=444 (100%)
capsule	N/A	n=444 (100%)
M_stage	N/A	n=444 (100%)
M_substage	N/A	n=444 (100%)
other_patient	N/A	n=444 (100%)
sample_type	N/A	n=444 (100%)
genomic_alterations	N/A	n=444 (100%)
tumor_margins_positive	N/A	n=444 (100%)
tissue_source	LN: 167 (38%);Bone: 160 (36%);Liver: 64 (14%); ...	-
metastatic_site	N/A	n=444 (100%)
microdissected	N/A	n=444 (100%)
frozen_ffpe	N/A	n=444 (100%)
other_feature	N/A	n=444 (100%)
batch	N/A	n=444 (100%)
other_sample	N/A	n=444 (100%)
tumor_purity_pathology	N/A	n=444 (100%)
tumor_purity_demix	N/A	n=444 (100%)
tumor_purity_absolute	N/A	n=444 (100%)

zone_of_origin	N/A	n=444 (100%)
zone_of_origin_estimated	N/A	n=444 (100%)
immune_infiltration	N/A	n=444 (100%)
mutational_signatures	N/A	n=444 (100%)
neoantigen_load	N/A	n=444 (100%)
AR_activity	N/A	n=444 (100%)
N_stage	N/A	n=444 (100%)
N_substage	N/A	n=444 (100%)
therapy_radiation_initial	N/A	n=444 (100%)
therapy_radiation_salvage	N/A	n=444 (100%)
therapy_surgery_initial	N/A	n=444 (100%)
therapy_hormonal_initial	N/A	n=444 (100%)
other_treatment	N/A	n=444 (100%)
psa_category	Feature not found in MAE	-
genome_altered	Feature not found in MAE	-

2.2 barbieri

	Instances	Missingness
overall_survival_status	N/A	n=112 (100%)
days_to_overall_survival	N/A	n=112 (100%)
age_at_initial_diagnosis	[34, 58, 62.5, 68, 77]	-
year_diagnosis	N/A	n=112 (100%)
gleason_grade	NA: 112 (100%)	-
gleason_major	3: 71 (63%);4: 41 (37%)	-
gleason_minor	4: 66 (59%);3: 42 (38%);5: 4 (4%)	-
source_of_gleason	N/A	n=112 (100%)
grade_group	3+4: 58 (52%);4+3: 29 (26%);<=6: 13 (12%); ...	-
T_pathological	N/A	n=112 (100%)
T_substage_pathological	N/A	n=112 (100%)
T_clinical	3: 68 (61%);2: 44 (39%)	-
T_substage_clinical	a: 53 (47%);c: 39 (35%);b: 20 (18%)	-
ERG_fusion_CNA	N/A	n=112 (100%)
ERG_fusion_IHC	N/A	n=112 (100%)
ERG_fusion_GEX	N/A	n=112 (100%)
disease_specific_recurrence_status	N/A	n=112 (100%)
days_to_disease_specific_recurrence	N/A	n=112 (100%)
metastasis_occurrence_status	N/A	n=112 (100%)
days_to_metastatic_occurrence	N/A	n=112 (100%)
psa	[2.7,5.55,7.8,10.9,31.5], NA n=1	n=1 (1%)
race	N/A	n=112 (100%)
smoking_status	N/A	n=112 (100%)
extraprostatic_extension	N/A	n=112 (100%)
perineural_invasion	N/A	n=112 (100%)
seminal_vesicle_invasion	N/A	n=112 (100%)
angiolymphatic_invasion	N/A	n=112 (100%)
androgen_ablation	N/A	n=112 (100%)
capsule	N/A	n=112 (100%)

M_stage	N/A	n=112 (100%)
M_substage	N/A	n=112 (100%)
other_patient	N/A	n=112 (100%)
sample_type	N/A	n=112 (100%)
genomic_alterations	N/A	n=112 (100%)
tumor_margins_positive	N/A	n=112 (100%)
tissue_source	N/A	n=112 (100%)
metastatic_site	Feature not found in MAE	-
microdissected	N/A	n=112 (100%)
frozen_ffpe	N/A	n=112 (100%)
other_feature	N/A	n=112 (100%)
batch	N/A	n=112 (100%)
other_sample	N/A	n=112 (100%)
tumor_purity_pathology	N/A	n=112 (100%)
tumor_purity_demix	N/A	n=112 (100%)
tumor_purity_absolute	N/A	n=112 (100%)
zone_of_origin	N/A	n=112 (100%)
zone_of_origin_estimated	N/A	n=112 (100%)
immune_infiltration	N/A	n=112 (100%)
mutational_signatures	N/A	n=112 (100%)
neoantigen_load	N/A	n=112 (100%)
AR_activity	N/A	n=112 (100%)
N_stage	N/A	n=112 (100%)
N_substage	N/A	n=112 (100%)
therapy_radiation_initial	N/A	n=112 (100%)
therapy_radiation_salvage	N/A	n=112 (100%)
therapy_surgery_initial	N/A	n=112 (100%)
therapy_hormonal_initial	N/A	n=112 (100%)
other_treatment	N/A	n=112 (100%)
psa_category	Feature not found in MAE	-
genome_altered	Feature not found in MAE	-

2.3 chandran

	Instances	Missingness
overall_survival_status	N/A	n=503 (100%)
days_to_overall_survival	N/A	n=503 (100%)
age_at_initial_diagnosis	[13,20,24,48,63], NA n=452	n=452 (90%)
year_diagnosis	N/A	n=503 (100%)
gleason_grade	[4,6,7,8,9], NA n=307	n=307 (61%)
gleason_major	N/A	n=503 (100%)
gleason_minor	N/A	n=503 (100%)
source_of_gleason	N/A	n=503 (100%)
grade_group	N/A	n=503 (100%)
T_pathological	[2,2,3,3,4], NA n=307	n=307 (61%)
T_substage_pathological	NA: 310 (62%);b: 102 (20%);a: 91 (18%)	n=310 (62%)
T_clinical	N/A	n=503 (100%)
T_substage_clinical	N/A	n=503 (100%)
ERG_fusion_CNA	N/A	n=503 (100%)

ERG_fusion_IHC	N/A		n=503 (100%)
ERG_fusion_GEX	N/A		n=503 (100%)
disease_specific_recurrence_status	N/A		n=503 (100%)
days_to_disease_specific_recurrence	N/A		n=503 (100%)
metastasis_occurrence_status	N/A		n=503 (100%)
days_to_metastatic_occurrence	N/A		n=503 (100%)
psa	N/A		n=503 (100%)
race	NA: 452 (90%);caucasian: 45 (9%);african_american: 6 (1%)	45	n=452 (90%)
smoking_status	N/A		n=503 (100%)
extraprostatic_extension	N/A		n=503 (100%)
perineural_invasion	N/A		n=503 (100%)
seminal_vesicle_invasion	N/A		n=503 (100%)
angiolympathic_invasion	N/A		n=503 (100%)
androgen_ablation	N/A		n=503 (100%)
capsule	N/A		n=503 (100%)
M_stage	N/A		n=503 (100%)
M_substage	N/A		n=503 (100%)
other_patient	N/A		n=503 (100%)
sample_type	primary: 196 (39%);adjacentnormal: 181 (36%);metastatic: 75 (15%); ...		-
genomic_alterations	N/A		n=503 (100%)
tumor_margins_positive	N/A		n=503 (100%)
tissue_source	N/A		n=503 (100%)
metastatic_site	NA: 428 (85%);lymph_node: 45 (9%);liver: 15 (3%); ...		n=428 (85%)
microdissected	N/A		n=503 (100%)
frozen_ffpe	N/A		n=503 (100%)
other_feature	N/A		n=503 (100%)
batch	N/A		n=503 (100%)
other_sample	N/A		n=503 (100%)
tumor_purity_pathology	N/A		n=503 (100%)
tumor_purity_demix	N/A		n=503 (100%)
tumor_purity_absolute	N/A		n=503 (100%)
zone_of_origin	N/A		n=503 (100%)
zone_of_origin_estimated	N/A		n=503 (100%)
immune_infiltration	N/A		n=503 (100%)
mutational_signatures	N/A		n=503 (100%)
neoantigen_load	N/A		n=503 (100%)
AR_activity	N/A		n=503 (100%)
N_stage	N/A		n=503 (100%)
N_substage	N/A		n=503 (100%)
therapy_radiation_initial	N/A		n=503 (100%)
therapy_radiation_salvage	N/A		n=503 (100%)
therapy_surgery_initial	N/A		n=503 (100%)
therapy_hormonal_initial	N/A		n=503 (100%)
other_treatment	N/A		n=503 (100%)
psa_category	Feature not found in MAE		-
genome_altered	Feature not found in MAE		-

2.4 friedrich

	Instances	Missingness
overall_survival_status	0: 230 (90%);1: 25 (10%)	-
days_to_overall_survival	[641,3004.75,3614.5,4301,6771], NA n=91	n=91 (36%)
age_at_initial_diagnosis	N/A	n=255 (100%)
year_diagnosis	N/A	n=255 (100%)
gleason_grade	[5,7,8,8,10], NA n=39	n=39 (15%)
gleason_major	N/A	n=255 (100%)
gleason_minor	N/A	n=255 (100%)
source_of_gleason	N/A	n=255 (100%)
grade_group	N/A	n=255 (100%)
T_pathological	N/A	n=255 (100%)
T_substage_pathological	N/A	n=255 (100%)
T_clinical	N/A	n=255 (100%)
T_substage_clinical	N/A	n=255 (100%)
ERG_fusion_CNA	N/A	n=255 (100%)
ERG_fusion_IHC	N/A	n=255 (100%)
ERG_fusion_GEX	N/A	n=255 (100%)
disease_specific_recurrence_status	N/A	n=255 (100%)
days_to_disease_specific_recurrence	N/A	n=255 (100%)
metastasis_occurrence_status	N/A	n=255 (100%)
days_to_metastatic_occurrence	N/A	n=255 (100%)
psa	N/A	n=255 (100%)
race	caucasian: 255 (100%)	-
smoking_status	N/A	n=255 (100%)
extraprostatic_extension	N/A	n=255 (100%)
perineural_invasion	N/A	n=255 (100%)
seminal_vesicle_invasion	N/A	n=255 (100%)
angiolymphatic_invasion	N/A	n=255 (100%)
androgen_ablation	N/A	n=255 (100%)
capsule	N/A	n=255 (100%)
M_stage	N/A	n=255 (100%)
M_substage	N/A	n=255 (100%)
other_patient	N/A	n=255 (100%)
sample_type	primary: 164 (64%);adjacentnormal: 52 (20%);BPH: 39 (15%)	-
genomic_alterations	N/A	n=255 (100%)
tumor_margins_positive	N/A	n=255 (100%)
tissue_source	prostatectomy: 216 (85%);cystoprostatectomy: 28 (11%);TURP: 11 (4%)	-
metastatic_site	Feature not found in MAE	-
microdissected	1: 255 (100%)	-
frozen_ffpe	frozen: 255 (100%)	-
other_feature	N/A	n=255 (100%)
batch	N/A	n=255 (100%)
other_sample	N/A	n=255 (100%)
tumor_purity_pathology	N/A	n=255 (100%)
tumor_purity_demix	N/A	n=255 (100%)
tumor_purity_absolute	N/A	n=255 (100%)

zone_of_origin	N/A	n=255 (100%)
zone_of_origin_estimated	N/A	n=255 (100%)
immune_infiltration	N/A	n=255 (100%)
mutational_signatures	N/A	n=255 (100%)
neoantigen_load	N/A	n=255 (100%)
AR_activity	N/A	n=255 (100%)
N_stage	N/A	n=255 (100%)
N_substage	N/A	n=255 (100%)
therapy_radiation_initial	N/A	n=255 (100%)
therapy_radiation_salvage	N/A	n=255 (100%)
therapy_surgery_initial	N/A	n=255 (100%)
therapy_hormonal_initial	N/A	n=255 (100%)
other_treatment	N/A	n=255 (100%)
psa_category	Feature not found in MAE	-
genome_altered	Feature not found in MAE	-

2.5 hieronymus

	Instances	Missingness
overall_survival_status	0: 96 (92%);1: 8 (8%)	-
days_to_overall_survival	[294.83, 1575.33, 2139.07, 2895.21, 3757.6]	-
age_at_initial_diagnosis	[41.07, 53.25, 58.19, 63.06, 75.63]	-
year_diagnosis	N/A	n=104 (100%)
gleason_grade	[6, 7, 7, 7, 9]	-
gleason_major	3: 72 (69%);4: 30 (29%);5: 2 (2%)	-
gleason_minor	4: 60 (58%);3: 39 (38%);5: 5 (5%)	-
source_of_gleason	prostatectomy: 104 (100%)	-
grade_group	3+4: 56 (54%);4+3: 22 (21%);<=6: 16 (15%); ...	n=4 (4%)
T_pathological	2: 54 (52%);3: 49 (47%);4: 1 (1%)	-
T_substage_pathological	b: 54 (52%);a: 44 (42%);c: 4 (4%); ...	n=2 (2%)
T_clinical	1: 61 (59%);2: 41 (39%);3: 2 (2%)	-
T_substage_clinical	c: 67 (64%);a: 18 (17%);b: 18 (17%); ...	n=1 (1%)
ERG_fusion_CNA	N/A	n=104 (100%)
ERG_fusion_IHC	N/A	n=104 (100%)
ERG_fusion_GEX	N/A	n=104 (100%)
disease_specific_recurrence_status	N/A	n=104 (100%)
days_to_disease_specific_recurrence	N/A	n=104 (100%)
metastasis_occurrence_status	0: 101 (97%);1: 3 (3%)	-
days_to_metastatic_occurrence	[121.25, 1455.26, 1989.62, 2752.45, 3694.65]	-
psa	[1,4.35,5.3,8,56.24], NA n=1	n=1 (1%)
race	N/A	n=104 (100%)
smoking_status	N/A	n=104 (100%)
extraprostatic_extension	0: 52 (50%);1: 52 (50%)	-
perineural_invasion	N/A	n=104 (100%)
seminal_vesicle_invasion	0: 90 (87%);1: 14 (13%)	-
angiolymphatic_invasion	N/A	n=104 (100%)
androgen_ablation	N/A	n=104 (100%)
capsule	N/A	n=104 (100%)

M_stage	N/A	n=104 (100%)
M_substage	N/A	n=104 (100%)
other_patient	N/A	n=104 (100%)
sample_type	N/A	n=104 (100%)
genomic_alterations	N/A	n=104 (100%)
tumor_margins_positive	N/A	n=104 (100%)
tissue_source	N/A	n=104 (100%)
metastatic_site	Feature not found in MAE	-
microdissected	N/A	n=104 (100%)
frozen_ffpe	N/A	n=104 (100%)
other_feature	N/A	n=104 (100%)
batch	N/A	n=104 (100%)
other_sample	N/A	n=104 (100%)
tumor_purity_pathology	N/A	n=104 (100%)
tumor_purity_demix	N/A	n=104 (100%)
tumor_purity_absolute	N/A	n=104 (100%)
zone_of_origin	N/A	n=104 (100%)
zone_of_origin_estimated	N/A	n=104 (100%)
immune_infiltration	N/A	n=104 (100%)
mutational_signatures	N/A	n=104 (100%)
neoantigen_load	N/A	n=104 (100%)
AR_activity	N/A	n=104 (100%)
N_stage	N/A	n=104 (100%)
N_substage	N/A	n=104 (100%)
therapy_radiation_initial	N/A	n=104 (100%)
therapy_radiation_salvage	N/A	n=104 (100%)
therapy_surgery_initial	N/A	n=104 (100%)
therapy_hormonal_initial	N/A	n=104 (100%)
other_treatment	N/A	n=104 (100%)
psa_category	Feature not found in MAE	-
genome_altered	Feature not found in MAE	-

2.6 icgcca

	Instances	Missingness
overall_survival_status	0: 198 (93%);1: 8 (4%);NA: 7 (3%)	n=7 (3%)
days_to_overall_survival	[1460,2190,2920,3650,4745], NA n=1	n=1 (0%)
age_at_initial_diagnosis	[42, 58, 62, 66, 74]	-
year_diagnosis	N/A	n=213 (100%)
gleason_grade	[6,7,7,7,8], NA n=138	n=138 (65%)
gleason_major	NA: 138 (65%);3: 49 (23%);4: 26 (12%)	n=138 (65%)
gleason_minor	NA: 138 (65%);4: 42 (20%);3: 33 (15%)	n=138 (65%)
source_of_gleason	N/A	n=213 (100%)
grade_group	NA: 138 (65%);3+4: 37 (17%);4+3: 21 (10%); ...	n=138 (65%)
T_pathological	N/A	n=213 (100%)
T_substage_pathological	N/A	n=213 (100%)
T_clinical	NA: 104 (49%);1: 56 (26%);2: 53 (25%)	n=104 (49%)
T_substage_clinical	NA: 104 (49%);c: 55 (26%);a: 30 (14%); ...	n=104 (49%)

ERG_fusion_CNA	N/A	n=213 (100%)
ERG_fusion_IHC	N/A	n=213 (100%)
ERG_fusion_GEX	N/A	n=213 (100%)
disease_specific_recurrence_status	N/A	n=213 (100%)
days_to_disease_specific_recurrence	N/A	n=213 (100%)
metastasis_occurrence_status	N/A	n=213 (100%)
days_to_metastatic_occurrence	N/A	n=213 (100%)
psa	N/A	n=213 (100%)
race	N/A	n=213 (100%)
smoking_status	N/A	n=213 (100%)
extraprostatic_extension	N/A	n=213 (100%)
perineural_invasion	N/A	n=213 (100%)
seminal_vesicle_invasion	N/A	n=213 (100%)
angiolymphatic_invasion	N/A	n=213 (100%)
androgen_ablation	N/A	n=213 (100%)
capsule	N/A	n=213 (100%)
M_stage	N/A	n=213 (100%)
M_substage	N/A	n=213 (100%)
other_patient	N/A	n=213 (100%)
sample_type	N/A	n=213 (100%)
genomic_alterations	N/A	n=213 (100%)
tumor_margins_positive	N/A	n=213 (100%)
tissue_source	N/A	n=213 (100%)
metastatic_site	Feature not found in MAE	-
microdissected	N/A	n=213 (100%)
frozen_ffpe	N/A	n=213 (100%)
other_feature	N/A	n=213 (100%)
batch	N/A	n=213 (100%)
other_sample	N/A	n=213 (100%)
tumor_purity_pathology	N/A	n=213 (100%)
tumor_purity_demix	N/A	n=213 (100%)
tumor_purity_absolute	N/A	n=213 (100%)
zone_of_origin	N/A	n=213 (100%)
zone_of_origin_estimated	N/A	n=213 (100%)
immune_infiltration	N/A	n=213 (100%)
mutational_signatures	N/A	n=213 (100%)
neoantigen_load	N/A	n=213 (100%)
AR_activity	N/A	n=213 (100%)
N_stage	N/A	n=213 (100%)
N_substage	N/A	n=213 (100%)
therapy_radiation_initial	N/A	n=213 (100%)
therapy_radiation_salvage	N/A	n=213 (100%)
therapy_surgery_initial	N/A	n=213 (100%)
therapy_hormonal_initial	N/A	n=213 (100%)
other_treatment	N/A	n=213 (100%)
psa_category	Feature not found in MAE	-
genome_altered	Feature not found in MAE	-

2.7 igc

	Instances	Missingness
overall_survival_status	N/A	n=83 (100%)
days_to_overall_survival	N/A	n=83 (100%)
age_at_initial_diagnosis	NA: 83 (100%)	-
year_diagnosis	N/A	n=83 (100%)
gleason_grade	[6,6,7,7,8], NA n=3	n=3 (4%)
gleason_major	N/A	n=83 (100%)
gleason_minor	N/A	n=83 (100%)
source_of_gleason	N/A	n=83 (100%)
grade_group	N/A	n=83 (100%)
T_pathological	[2,2,2,3,4], NA n=26	n=26 (31%)
T_substage_pathological	c: 33 (40%);NA: 29 (35%);a: 11 (13%); ...	n=29 (35%)
T_clinical	NA: 59 (71%);2: 20 (24%);3: 4 (5%)	n=59 (71%)
T_substage_clinical	NA: 59 (71%);c: 15 (18%);a: 6 (7%); ...	n=59 (71%)
ERG_fusion_CNA	N/A	n=83 (100%)
ERG_fusion_IHC	N/A	n=83 (100%)
ERG_fusion_GEX	N/A	n=83 (100%)
disease_specific_recurrence_status	N/A	n=83 (100%)
days_to_disease_specific_recurrence	N/A	n=83 (100%)
metastasis_occurrence_status	N/A	n=83 (100%)
days_to_metastatic_occurrence	N/A	n=83 (100%)
psa	N/A	n=83 (100%)
race	Caucasian: 74 (89%); African-American: 7 (8%); American Indian: 1 (1%); ...	-
smoking_status	1: 42 (51%);0: 41 (49%)	-
extraprostatic_extension	N/A	n=83 (100%)
perineural_invasion	N/A	n=83 (100%)
seminal_vesicle_invasion	N/A	n=83 (100%)
angiolymphatic_invasion	N/A	n=83 (100%)
androgen_ablation	N/A	n=83 (100%)
capsule	N/A	n=83 (100%)
M_stage	N/A	n=83 (100%)
M_substage	N/A	n=83 (100%)
other_patient	N/A	n=83 (100%)
sample_type	N/A	n=83 (100%)
genomic_alterations	N/A	n=83 (100%)
tumor_margins_positive	N/A	n=83 (100%)
tissue_source	N/A	n=83 (100%)
metastatic_site	N/A	n=83 (100%)
microdissected	N/A	n=83 (100%)
frozen_ffpe	N/A	n=83 (100%)
other_feature	N/A	n=83 (100%)
batch	N/A	n=83 (100%)
other_sample	N/A	n=83 (100%)
tumor_purity_pathology	N/A	n=83 (100%)
tumor_purity_demix	N/A	n=83 (100%)
tumor_purity_absolute	N/A	n=83 (100%)
zone_of_origin	N/A	n=83 (100%)
zone_of_origin_estimated	N/A	n=83 (100%)

immune_infiltration	N/A	n=83 (100%)
mutational_signatures	N/A	n=83 (100%)
neoantigen_load	N/A	n=83 (100%)
AR_activity	N/A	n=83 (100%)
N_stage	N/A	n=83 (100%)
N_substage	N/A	n=83 (100%)
therapy_radiation_initial	N/A	n=83 (100%)
therapy_radiation_salvage	N/A	n=83 (100%)
therapy_surgery_initial	N/A	n=83 (100%)
therapy_hormonal_initial	N/A	n=83 (100%)
other_treatment	N/A	n=83 (100%)
psa_category	Elevated: 74 (89%);Normal: 6 (7%);NA: 3 (4%)	n=3 (4%)
genome_altered	Feature not found in MAE	-

2.8 kim

	Instances	Missingness
overall_survival_status	N/A	n=266 (100%)
days_to_overall_survival	N/A	n=266 (100%)
age_at_initial_diagnosis	[43.41, 57.59, 61.53, 66.91, 76]	-
year_diagnosis	N/A	n=266 (100%)
gleason_grade	NA: 266 (100%)	-
gleason_major	3: 264 (99%);NA: 2 (1%)	-
gleason_minor	[2,3,3,3,4], NA n=2	-
source_of_gleason	N/A	n=266 (100%)
grade_group	<=6: 198 (74%);3+4: 65 (24%);NA: 3 (1%)	n=3 (1%)
T_pathological	N/A	n=266 (100%)
T_substage_pathological	N/A	n=266 (100%)
T_clinical	1: 225 (85%);2: 41 (15%)	-
T_substage_clinical	c: 266 (100%)	-
ERG_fusion_CNA	N/A	n=266 (100%)
ERG_fusion_IHC	N/A	n=266 (100%)
ERG_fusion_GEX	N/A	n=266 (100%)
disease_specific_recurrence_status	N/A	n=266 (100%)
days_to_disease_specific_recurrence	N/A	n=266 (100%)
metastasis_occurrence_status	N/A	n=266 (100%)
days_to_metastatic_occurrence	N/A	n=266 (100%)
psa	[0, 4.16, 5.4, 7.19, 20]	-
race	N/A	n=266 (100%)
smoking_status	N/A	n=266 (100%)
extraprostatic_extension	N/A	n=266 (100%)
perineural_invasion	N/A	n=266 (100%)
seminal_vesicle_invasion	N/A	n=266 (100%)
angiolymphatic_invasion	N/A	n=266 (100%)
androgen_ablation	N/A	n=266 (100%)
capsule	N/A	n=266 (100%)
M_stage	N/A	n=266 (100%)
M_substage	N/A	n=266 (100%)

other_patient	N/A	n=266 (100%)
sample_type	N/A	n=266 (100%)
genomic_alterations	N/A	n=266 (100%)
tumor_margins_positive	N/A	n=266 (100%)
tissue_source	prostate cancer biopsy: 266 (100%)	-
metastatic_site	Feature not found in MAE	-
microdissected	N/A	n=266 (100%)
frozen_ffpe	N/A	n=266 (100%)
other_feature	N/A	n=266 (100%)
batch	N/A	n=266 (100%)
other_sample	N/A	n=266 (100%)
tumor_purity_pathology	N/A	n=266 (100%)
tumor_purity_demix	N/A	n=266 (100%)
tumor_purity_absolute	N/A	n=266 (100%)
zone_of_origin	N/A	n=266 (100%)
zone_of_origin_estimated	N/A	n=266 (100%)
immune_infiltration	N/A	n=266 (100%)
mutational_signatures	N/A	n=266 (100%)
neoantigen_load	N/A	n=266 (100%)
AR_activity	N/A	n=266 (100%)
N_stage	N/A	n=266 (100%)
N_substage	N/A	n=266 (100%)
therapy_radiation_initial	N/A	n=266 (100%)
therapy_radiation_salvage	N/A	n=266 (100%)
therapy_surgery_initial	N/A	n=266 (100%)
therapy_hormonal_initial	N/A	n=266 (100%)
other_treatment	N/A	n=266 (100%)
psa_category	Feature not found in MAE	-
genome_altered	Feature not found in MAE	-

2.9 kunderfranco

	Instances	Missingness
overall_survival_status	N/A	n=67 (100%)
days_to_overall_survival	N/A	n=67 (100%)
age_at_initial_diagnosis	[50,62,67,70,74], NA n=14	n=14 (21%)
year_diagnosis	N/A	n=67 (100%)
gleason_grade	[5,7,7,7,9], NA n=14	n=14 (21%)
gleason_major	[2,3,3,4,5], NA n=14	n=14 (21%)
gleason_minor	[3,4,4,4,5], NA n=14	n=14 (21%)
source_of_gleason	prostatectomy: 53 (79%);biopsy: 14 (21%)	-
grade_group	3+4: 29 (43%);NA: 14 (21%);>=8: 11 (16%);	-
	...	
T_pathological	N/A	n=67 (100%)
T_substage_pathological	N/A	n=67 (100%)
T_clinical	N/A	n=67 (100%)
T_substage_clinical	N/A	n=67 (100%)
ERG_fusion_CNA	N/A	n=67 (100%)
ERG_fusion_IHC	N/A	n=67 (100%)

ERG_fusion_GEX	N/A	n=67 (100%)
disease_specific_recurrence_status	N/A	n=67 (100%)
days_to_disease_specific_recurrence	N/A	n=67 (100%)
metastasis_occurrence_status	N/A	n=67 (100%)
days_to_metastatic_occurrence	N/A	n=67 (100%)
psa	N/A	n=67 (100%)
race	N/A	n=67 (100%)
smoking_status	N/A	n=67 (100%)
extraprostatic_extension	N/A	n=67 (100%)
perineural_invasion	N/A	n=67 (100%)
seminal_vesicle_invasion	N/A	n=67 (100%)
angiolympathic_invasion	N/A	n=67 (100%)
androgen_ablation	N/A	n=67 (100%)
capsule	N/A	n=67 (100%)
M_stage	N/A	n=67 (100%)
M_substage	N/A	n=67 (100%)
other_patient	N/A	n=67 (100%)
sample_type	primary: 53 (79%);BPH: 14 (21%)	-
genomic_alterations	N/A	n=67 (100%)
tumor_margins_positive	N/A	n=67 (100%)
tissue_source	prostatectomy: 53 (79%);biopsy: 14 (21%)	-
metastatic_site	N/A	n=67 (100%)
microdissected	0: 67 (100%)	-
frozen_ffpe	FFPE: 67 (100%)	-
other_feature	N/A	n=67 (100%)
batch	N/A	n=67 (100%)
other_sample	N/A	n=67 (100%)
tumor_purity_pathology	N/A	n=67 (100%)
tumor_purity_demix	N/A	n=67 (100%)
tumor_purity_absolute	N/A	n=67 (100%)
zone_of_origin	N/A	n=67 (100%)
zone_of_origin_estimated	N/A	n=67 (100%)
immune_infiltration	N/A	n=67 (100%)
mutational_signatures	N/A	n=67 (100%)
neoantigen_load	N/A	n=67 (100%)
AR_activity	N/A	n=67 (100%)
N_stage	N/A	n=67 (100%)
N_substage	N/A	n=67 (100%)
therapy_radiation_initial	N/A	n=67 (100%)
therapy_radiation_salvage	N/A	n=67 (100%)
therapy_surgery_initial	N/A	n=67 (100%)
therapy_hormonal_initial	N/A	n=67 (100%)
other_treatment	N/A	n=67 (100%)
psa_category	Feature not found in MAE	-
genome_altered	Feature not found in MAE	-

2.10 ren

Instances	Missingness
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overall_survival_status	N/A	n=65 (100%)
days_to_overall_survival	N/A	n=65 (100%)
age_at_initial_diagnosis	[49,64.25,69,74,80], NA n=7	n=7 (11%)
year_diagnosis	N/A	n=65 (100%)
gleason_grade	NA: 65 (100%)	-
gleason_major	3: 29 (45%);4: 27 (42%);5: 9 (14%)	-
gleason_minor	4: 39 (60%);3: 18 (28%);5: 8 (12%)	-
source_of_gleason	N/A	n=65 (100%)
grade_group	3+4: 23 (35%);>=8: 14 (22%);4+3: 13 (20%); ...	n=10 (15%)
T_pathological	N/A	n=65 (100%)
T_substage_pathological	N/A	n=65 (100%)
T_clinical	[2,2,2,3,4], NA n=1	n=1 (2%)
T_substage_clinical	c: 38 (58%);b: 11 (17%);a: 10 (15%); ...	n=6 (9%)
ERG_fusion_CNA	N/A	n=65 (100%)
ERG_fusion_IHC	N/A	n=65 (100%)
ERG_fusion_GEX	N/A	n=65 (100%)
disease_specific_recurrence_status	N/A	n=65 (100%)
days_to_disease_specific_recurrence	N/A	n=65 (100%)
metastasis_occurrence_status	N/A	n=65 (100%)
days_to_metastatic_occurrence	N/A	n=65 (100%)
psa	[5.28,10.73,17.3,33.4,271], NA n=2	n=2 (3%)
race	N/A	n=65 (100%)
smoking_status	N/A	n=65 (100%)
extraprostatic_extension	N/A	n=65 (100%)
perineural_invasion	N/A	n=65 (100%)
seminal_vesicle_invasion	N/A	n=65 (100%)
angiolymphatic_invasion	N/A	n=65 (100%)
androgen_ablation	N/A	n=65 (100%)
capsule	N/A	n=65 (100%)
M_stage	N/A	n=65 (100%)
M_substage	N/A	n=65 (100%)
other_patient	N/A	n=65 (100%)
sample_type	N/A	n=65 (100%)
genomic_alterations	N/A	n=65 (100%)
tumor_margins_positive	N/A	n=65 (100%)
tissue_source	N/A	n=65 (100%)
metastatic_site	Feature not found in MAE	-
microdissected	N/A	n=65 (100%)
frozen_ffpe	N/A	n=65 (100%)
other_feature	N/A	n=65 (100%)
batch	N/A	n=65 (100%)
other_sample	N/A	n=65 (100%)
tumor_purity_pathology	N/A	n=65 (100%)
tumor_purity_demix	N/A	n=65 (100%)
tumor_purity_absolute	N/A	n=65 (100%)
zone_of_origin	N/A	n=65 (100%)
zone_of_origin_estimated	N/A	n=65 (100%)
immune_infiltration	N/A	n=65 (100%)

mutational_signatures	N/A	n=65 (100%)
neoantigen_load	N/A	n=65 (100%)
AR_activity	N/A	n=65 (100%)
N_stage	N/A	n=65 (100%)
N_substage	N/A	n=65 (100%)
therapy_radiation_initial	N/A	n=65 (100%)
therapy_radiation_salvage	N/A	n=65 (100%)
therapy_surgery_initial	N/A	n=65 (100%)
therapy_hormonal_initial	N/A	n=65 (100%)
other_treatment	N/A	n=65 (100%)
psa_category	Feature not found in MAE	-
genome_altered	Feature not found in MAE	-

2.11 sun

	Instances	Missingness
overall_survival_status	N/A	n=79 (100%)
days_to_overall_survival	N/A	n=79 (100%)
age_at_initial_diagnosis	N/A	n=79 (100%)
year_diagnosis	N/A	n=79 (100%)
gleason_grade	N/A	n=79 (100%)
gleason_major	N/A	n=79 (100%)
gleason_minor	N/A	n=79 (100%)
source_of_gleason	N/A	n=79 (100%)
grade_group	N/A	n=79 (100%)
T_pathological	N/A	n=79 (100%)
T_substage_pathological	N/A	n=79 (100%)
T_clinical	N/A	n=79 (100%)
T_substage_clinical	N/A	n=79 (100%)
ERG_fusion_CNA	N/A	n=79 (100%)
ERG_fusion_IHC	N/A	n=79 (100%)
ERG_fusion_GEX	N/A	n=79 (100%)
disease_specific_recurrence_status	0: 40 (51%);1: 39 (49%)	-
days_to_disease_specific_recurrence	N/A	n=79 (100%)
metastasis_occurrence_status	N/A	n=79 (100%)
days_to_metastatic_occurrence	N/A	n=79 (100%)
psa	N/A	n=79 (100%)
race	N/A	n=79 (100%)
smoking_status	N/A	n=79 (100%)
extraprostatic_extension	N/A	n=79 (100%)
perineural_invasion	N/A	n=79 (100%)
seminal_vesicle_invasion	N/A	n=79 (100%)
angiolymphatic_invasion	N/A	n=79 (100%)
androgen_ablation	N/A	n=79 (100%)
capsule	N/A	n=79 (100%)
M_stage	N/A	n=79 (100%)
M_substage	N/A	n=79 (100%)
other_patient	N/A	n=79 (100%)
sample_type	primary: 79 (100%)	-

genomic_alterations	N/A	n=79 (100%)
tumor_margins_positive	N/A	n=79 (100%)
tissue_source	N/A	n=79 (100%)
metastatic_site	Feature not found in MAE	-
microdissected	N/A	n=79 (100%)
frozen_ffpe	N/A	n=79 (100%)
other_feature	N/A	n=79 (100%)
batch	N/A	n=79 (100%)
other_sample	N/A	n=79 (100%)
tumor_purity_pathology	N/A	n=79 (100%)
tumor_purity_demix	N/A	n=79 (100%)
tumor_purity_absolute	N/A	n=79 (100%)
zone_of_origin	N/A	n=79 (100%)
zone_of_origin_estimated	N/A	n=79 (100%)
immune_infiltration	N/A	n=79 (100%)
mutational_signatures	N/A	n=79 (100%)
neoantigen_load	N/A	n=79 (100%)
AR_activity	N/A	n=79 (100%)
N_stage	N/A	n=79 (100%)
N_substage	N/A	n=79 (100%)
therapy_radiation_initial	N/A	n=79 (100%)
therapy_radiation_salvage	N/A	n=79 (100%)
therapy_surgery_initial	N/A	n=79 (100%)
therapy_hormonal_initial	N/A	n=79 (100%)
other_treatment	N/A	n=79 (100%)
psa_category	Feature not found in MAE	-
genome_altered	Feature not found in MAE	-

2.12 taylor

	Instances	Missingness
overall_survival_status	N/A	n=218 (100%)
days_to_overall_survival	N/A	n=218 (100%)
age_at_initial_diagnosis	N/A	n=218 (100%)
year_diagnosis	N/A	n=218 (100%)
gleason_grade	[5,6,7,7,9], NA n=1	n=1 (0%)
gleason_major	[3,3,3,4,5], NA n=21	n=21 (10%)
gleason_minor	[3,3,4,4,5], NA n=21	n=21 (10%)
source_of_gleason	N/A	n=218 (100%)
grade_group	<=6: 104 (48%);>=8: 34 (16%);3+4: 34 (16%); ...	n=31 (14%)
T_pathological	[2,2,2,3,4], NA n=18	n=18 (8%)
T_substage_pathological	b: 86 (39%);a: 55 (25%);c: 39 (18%); ...	n=38 (17%)
T_clinical	[1,1,2,2,4], NA n=9	n=9 (4%)
T_substage_clinical	c: 127 (58%);a: 40 (18%);b: 34 (16%); ...	n=17 (8%)
ERG_fusion_CNA	0: 164 (75%);1: 54 (25%)	-
ERG_fusion_IHC	N/A	n=218 (100%)
ERG_fusion_GEX	0: 76 (35%);1: 74 (34%);NA: 68 (31%)	n=68 (31%)
disease_specific_recurrence_status	0: 137 (63%);1: 61 (28%);NA: 20 (9%)	n=20 (9%)

days_to_disease_specific_recurrence	[3,717.25,1386.5,1974.25,4909], NA n=20	n=20 (9%)
metastasis_occurrence_status	N/A	n=218 (100%)
days_to_metastatic_occurrence	N/A	n=218 (100%)
psa	N/A	n=218 (100%)
race	N/A	n=218 (100%)
smoking_status	N/A	n=218 (100%)
extraprostatic_extension	N/A	n=218 (100%)
perineural_invasion	N/A	n=218 (100%)
seminal_vesicle_invasion	N/A	n=218 (100%)
angiolympathic_invasion	N/A	n=218 (100%)
androgen_ablation	N/A	n=218 (100%)
capsule	N/A	n=218 (100%)
M_stage	N/A	n=218 (100%)
M_substage	N/A	n=218 (100%)
other_patient	N/A	n=218 (100%)
sample_type	primary: 181 (83%);metastasis: 37 (17%)	-
genomic_alterations	N/A	n=218 (100%)
tumor_margins_positive	N/A	n=218 (100%)
tissue_source	N/A	n=218 (100%)
metastatic_site	N/A	n=218 (100%)
microdissected	N/A	n=218 (100%)
frozen_ffpe	N/A	n=218 (100%)
other_feature	N/A	n=218 (100%)
batch	N/A	n=218 (100%)
other_sample	N/A	n=218 (100%)
tumor_purity_pathology	N/A	n=218 (100%)
tumor_purity_demix	N/A	n=218 (100%)
tumor_purity_absolute	N/A	n=218 (100%)
zone_of_origin	N/A	n=218 (100%)
zone_of_origin_estimated	N/A	n=218 (100%)
immune_infiltration	N/A	n=218 (100%)
mutational_signatures	N/A	n=218 (100%)
neoantigen_load	N/A	n=218 (100%)
AR_activity	N/A	n=218 (100%)
N_stage	N/A	n=218 (100%)
N_substage	N/A	n=218 (100%)
therapy_radiation_initial	N/A	n=218 (100%)
therapy_radiation_salvage	N/A	n=218 (100%)
therapy_surgery_initial	N/A	n=218 (100%)
therapy_hormonal_initial	N/A	n=218 (100%)
other_treatment	N/A	n=218 (100%)
psa_category	Feature not found in MAE	-
genome_altered	Feature not found in MAE	-

2.13 tcga

	Instances	Missingness
overall_survival_status	0: 484 (98%);1: 10 (2%)	-
days_to_overall_survival	[23.18, 524.9, 925.68, 1466.06, 5034.03]	-

age_at_initial_diagnosis	[41, 56, 61, 66, 78]	-
year_diagnosis	[2000,2009,2011,2012,2013], NA n=31	n=31 (6%)
gleason_grade	[6, 7, 7, 9, 10]	-
gleason_major	[2, 3, 4, 4, 5]	-
gleason_minor	4: 234 (47%);3: 150 (30%);5: 110 (22%)	-
source_of_gleason	biopsy: 494 (100%)	-
grade_group	>=8: 205 (41%);3+4: 145 (29%);4+3: 99 (20%); ...	-
T_pathological	[2,2,3,3,4], NA n=7	n=7 (1%)
T_substage_pathological	a: 171 (35%);c: 164 (33%);b: 142 (29%); ...	n=17 (3%)
T_clinical	[1,1,2,2,4], NA n=91	n=91 (18%)
T_substage_clinical	c: 224 (45%);NA: 106 (21%);a: 93 (19%); ...	n=106 (21%)
ERG_fusion_CNA	N/A	n=494 (100%)
ERG_fusion_IHC	N/A	n=494 (100%)
ERG_fusion_GEX	N/A	n=494 (100%)
disease_specific_recurrence_status	0: 397 (80%);1: 91 (18%);NA: 6 (1%)	n=6 (1%)
days_to_disease_specific_recurrence	[23.18,427.38,823.04,1375.86,5034.03], NA n=6	n=6 (1%)
metastasis_occurrence_status	N/A	n=494 (100%)
days_to_metastatic_occurrence	N/A	n=494 (100%)
psa	[0,0.03,0.1,0.11,323], NA n=57	n=57 (12%)
race	NA: 338 (68%);caucasian: 147 (30%);african_american: 7 (1%); ...	-
smoking_status	N/A	n=494 (100%)
extraprostatic_extension	N/A	n=494 (100%)
perineural_invasion	N/A	n=494 (100%)
seminal_vesicle_invasion	N/A	n=494 (100%)
angiolymphatic_invasion	N/A	n=494 (100%)
androgen_ablation	N/A	n=494 (100%)
capsule	N/A	n=494 (100%)
M_stage	0: 452 (91%);NA: 39 (8%);1: 3 (1%)	n=39 (8%)
M_substage	: 491 (99%);a: 1 (0%);b: 1 (0%); ...	-
other_patient	N/A	n=494 (100%)
sample_type	Primary: 493 (100%);Metastasis: 1 (0%)	-
genomic_alterations	N/A	n=494 (100%)
tumor_margins_positive	N/A	n=494 (100%)
tissue_source	N/A	n=494 (100%)
metastatic_site	N/A	n=494 (100%)
microdissected	N/A	n=494 (100%)
frozen_ffpe	NA: 493 (100%);: 1 (0%)	-
other_feature	N/A	n=494 (100%)
batch	N/A	n=494 (100%)
other_sample	N/A	n=494 (100%)
tumor_purity_pathology	N/A	n=494 (100%)
tumor_purity_demix	N/A	n=494 (100%)
tumor_purity_absolute	N/A	n=494 (100%)
zone_of_origin	NA: 218 (44%);peripheral: 137 (28%);mixed: 127 (26%); ...	-
zone_of_origin_estimated	N/A	n=494 (100%)
immune_infiltration	N/A	n=494 (100%)

mutational_signatures	N/A	n=494 (100%)
neoantigen_load	N/A	n=494 (100%)
AR_activity	N/A	n=494 (100%)
N_stage	0: 343 (69%);1: 79 (16%);NA: 72 (15%)	n=72 (15%)
N_substage	N/A	n=494 (100%)
therapy_radiation_initial	0: 246 (50%);NA: 208 (42%);1: 40 (8%)	n=208 (42%)
therapy_radiation_salvage	N/A	n=494 (100%)
therapy_surgery_initial	N/A	n=494 (100%)
therapy_hormonal_initial	N/A	n=494 (100%)
other_treatment	0: 244 (49%);NA: 207 (42%);1: 43 (9%)	n=207 (42%)
psa_category	N/A	n=494 (100%)
genome_altered	[0,0.02,0.06,0.12,0.58], NA n=6	n=6 (1%)

2.14 true

	Instances	Missingness
overall_survival_status	N/A	n=29 (100%)
days_to_overall_survival	N/A	n=29 (100%)
age_at_initial_diagnosis	N/A	n=29 (100%)
year_diagnosis	N/A	n=29 (100%)
gleason_grade	[6, 7, 7, 7, 9]	-
gleason_major	3: 15 (52%);4: 12 (41%);5: 2 (7%)	-
gleason_minor	4: 14 (48%);3: 13 (45%);5: 2 (7%)	-
source_of_gleason	N/A	n=29 (100%)
grade_group	4: 11 (38%);3: 10 (34%);5: 6 (21%); ...	n=2 (7%)
T_pathological	N/A	n=29 (100%)
T_substage_pathological	N/A	n=29 (100%)
T_clinical	N/A	n=29 (100%)
T_substage_clinical	N/A	n=29 (100%)
ERG_fusion_CNA	N/A	n=29 (100%)
ERG_fusion_IHC	N/A	n=29 (100%)
ERG_fusion_GEX	N/A	n=29 (100%)
disease_specific_recurrence_status	N/A	n=29 (100%)
days_to_disease_specific_recurrence	N/A	n=29 (100%)
metastasis_occurrence_status	N/A	n=29 (100%)
days_to_metastatic_occurrence	N/A	n=29 (100%)
psa	[1,5,6.35,8.62,15.9], NA n=1	n=1 (3%)
race	N/A	n=29 (100%)
smoking_status	N/A	n=29 (100%)
extraprostatic_extension	N/A	n=29 (100%)
perineural_invasion	N/A	n=29 (100%)
seminal_vesicle_invasion	N/A	n=29 (100%)
angiolymphatic_invasion	N/A	n=29 (100%)
androgen_ablation	N/A	n=29 (100%)
capsule	N/A	n=29 (100%)
M_stage	N/A	n=29 (100%)
M_substage	N/A	n=29 (100%)
other_patient	N/A	n=29 (100%)
sample_type	N/A	n=29 (100%)

genomic_alterations	N/A	n=29 (100%)
tumor_margins_positive	0: 18 (62%);1: 11 (38%)	-
tissue_source	N/A	n=29 (100%)
metastatic_site	N/A	n=29 (100%)
microdissected	1: 29 (100%)	-
frozen_ffpe	N/A	n=29 (100%)
other_feature	Age:60-69 Volume:8 LCM_Gleason_Pattern:5: 2 (7%);Age:40-49 Volume:2.2 LCM_Gleason_Pattern:5: 1 (3%);Age:40-49 Volume:3.5 LCM_Gleason_Pattern:3: 1 (3%); ...	-
batch	N/A	n=29 (100%)
other_sample	N/A	n=29 (100%)
tumor_purity_pathology	N/A	n=29 (100%)
tumor_purity_demix	N/A	n=29 (100%)
tumor_purity_absolute	N/A	n=29 (100%)
zone_of_origin	N/A	n=29 (100%)
zone_of_origin_estimated	N/A	n=29 (100%)
immune_infiltration	N/A	n=29 (100%)
mutational_signatures	N/A	n=29 (100%)
neoantigen_load	N/A	n=29 (100%)
AR_activity	N/A	n=29 (100%)
N_stage	N/A	n=29 (100%)
N_substage	N/A	n=29 (100%)
therapy_radiation_initial	0: 29 (100%)	-
therapy_radiation_salvage	0: 29 (100%)	-
therapy_surgery_initial	N/A	n=29 (100%)
therapy_hormonal_initial	0: 29 (100%)	-
other_treatment	NA: 21 (72%);fish_oil: 2 (7%);selenium: 2 (7%); ...	n=21 (72%)
psa_category	Feature not found in MAE	-
genome_altered	Feature not found in MAE	-

2.15 wallace

	Instances	Missingness
overall_survival_status	N/A	n=83 (100%)
days_to_overall_survival	N/A	n=83 (100%)
age_at_initial_diagnosis	N/A	n=83 (100%)
year_diagnosis	N/A	n=83 (100%)
gleason_grade	[5, 6, 7, 7, 9]	-
gleason_major	N/A	n=83 (100%)
gleason_minor	N/A	n=83 (100%)
source_of_gleason	N/A	n=83 (100%)
grade_group	N/A	n=83 (100%)
T_pathological	N/A	n=83 (100%)
T_substage_pathological	N/A	n=83 (100%)
T_clinical	N/A	n=83 (100%)

T_substage_clinical	N/A	n=83 (100%)
ERG_fusion_CNA	N/A	n=83 (100%)
ERG_fusion_IHC	N/A	n=83 (100%)
ERG_fusion_GEX	N/A	n=83 (100%)
disease_specific_recurrence_status	N/A	n=83 (100%)
days_to_disease_specific_recurrence	N/A	n=83 (100%)
metastasis_occurrence_status	N/A	n=83 (100%)
days_to_metastatic_occurrence	N/A	n=83 (100%)
psa	N/A	n=83 (100%)
race	caucasian: 45 (54%);african_american: 38 (46%)	-
smoking_status	1: 37 (45%);NA: 25 (30%);0: 21 (25%)	n=25 (30%)
extraprostatic_extension	0: 54 (65%);1: 27 (33%);NA: 2 (2%)	n=2 (2%)
perineural_invasion	1: 69 (83%);0: 12 (14%);NA: 2 (2%)	n=2 (2%)
seminal_vesicle_invasion	0: 69 (83%);1: 12 (14%);NA: 2 (2%)	n=2 (2%)
angiolymphatic_invasion	0: 76 (92%);1: 5 (6%);NA: 2 (2%)	n=2 (2%)
androgen_ablation	N/A	n=83 (100%)
capsule	N/A	n=83 (100%)
M_stage	N/A	n=83 (100%)
M_substage	N/A	n=83 (100%)
other_patient	N/A	n=83 (100%)
sample_type	primary: 69 (83%);adjacentnormal: 14 (17%)	-
genomic_alterations	N/A	n=83 (100%)
tumor_margins_positive	0: 51 (61%);1: 29 (35%);NA: 3 (4%)	n=3 (4%)
tissue_source	N/A	n=83 (100%)
metastatic_site	N/A	n=83 (100%)
microdissected	0: 83 (100%)	-
frozen_ffpe	frozen: 83 (100%)	-
other_feature	N/A	n=83 (100%)
batch	N/A	n=83 (100%)
other_sample	N/A	n=83 (100%)
tumor_purity_pathology	N/A	n=83 (100%)
tumor_purity_demix	N/A	n=83 (100%)
tumor_purity_absolute	N/A	n=83 (100%)
zone_of_origin	N/A	n=83 (100%)
zone_of_origin_estimated	N/A	n=83 (100%)
immune_infiltration	N/A	n=83 (100%)
mutational_signatures	N/A	n=83 (100%)
neoantigen_load	N/A	n=83 (100%)
AR_activity	N/A	n=83 (100%)
N_stage	N/A	n=83 (100%)
N_substage	N/A	n=83 (100%)
therapy_radiation_initial	0: 83 (100%)	-
therapy_radiation_salvage	0: 83 (100%)	-
therapy_surgery_initial	0: 83 (100%)	-
therapy_hormonal_initial	0: 83 (100%)	-
other_treatment	N/A	n=83 (100%)
psa_category	Feature not found in MAE	-
genome_altered	Feature not found in MAE	-

2.16 wang

	Instances	Missingness
overall_survival_status	N/A	n=148 (100%)
days_to_overall_survival	N/A	n=148 (100%)
age_at_initial_diagnosis	N/A	n=148 (100%)
year_diagnosis	N/A	n=148 (100%)
gleason_grade	N/A	n=148 (100%)
gleason_major	N/A	n=148 (100%)
gleason_minor	N/A	n=148 (100%)
source_of_gleason	N/A	n=148 (100%)
grade_group	N/A	n=148 (100%)
T_pathological	N/A	n=148 (100%)
T_substage_pathological	N/A	n=148 (100%)
T_clinical	N/A	n=148 (100%)
T_substage_clinical	N/A	n=148 (100%)
ERG_fusion_CNA	N/A	n=148 (100%)
ERG_fusion_IHC	N/A	n=148 (100%)
ERG_fusion_GEX	N/A	n=148 (100%)
disease_specific_recurrence_status	N/A	n=148 (100%)
days_to_disease_specific_recurrence	N/A	n=148 (100%)
metastasis_occurrence_status	N/A	n=148 (100%)
days_to_metastatic_occurrence	N/A	n=148 (100%)
psa	N/A	n=148 (100%)
race	N/A	n=148 (100%)
smoking_status	N/A	n=148 (100%)
extraprostatic_extension	N/A	n=148 (100%)
perineural_invasion	N/A	n=148 (100%)
seminal_vesicle_invasion	N/A	n=148 (100%)
angiolymphatic_invasion	N/A	n=148 (100%)
androgen_ablation	N/A	n=148 (100%)
capsule	N/A	n=148 (100%)
M_stage	N/A	n=148 (100%)
M_substage	N/A	n=148 (100%)
other_patient	N/A	n=148 (100%)
sample_type	N/A	n=148 (100%)
genomic_alterations	N/A	n=148 (100%)
tumor_margins_positive	N/A	n=148 (100%)
tissue_source	N/A	n=148 (100%)
metastatic_site	N/A	n=148 (100%)
microdissected	N/A	n=148 (100%)
frozen_ffpe	N/A	n=148 (100%)
other_feature	N/A	n=148 (100%)
batch	N/A	n=148 (100%)
other_sample	N/A	n=148 (100%)
tumor_purity_pathology	N/A	n=148 (100%)
tumor_purity_demix	N/A	n=148 (100%)
tumor_purity_absolute	N/A	n=148 (100%)
zone_of_origin	N/A	n=148 (100%)

zone_of_origin_estimated	N/A	n=148 (100%)
immune_infiltration	N/A	n=148 (100%)
mutational_signatures	N/A	n=148 (100%)
neoantigen_load	N/A	n=148 (100%)
AR_activity	N/A	n=148 (100%)
N_stage	N/A	n=148 (100%)
N_substage	N/A	n=148 (100%)
therapy_radiation_initial	N/A	n=148 (100%)
therapy_radiation_salvage	N/A	n=148 (100%)
therapy_surgery_initial	N/A	n=148 (100%)
therapy_hormonal_initial	N/A	n=148 (100%)
other_treatment	N/A	n=148 (100%)
psa_category	N/A	n=148 (100%)
genome_altered	Feature not found in MAE	-

2.17 weiner

	Instances	Missingness
overall_survival_status	N/A	n=838 (100%)
days_to_overall_survival	N/A	n=838 (100%)
age_at_initial_diagnosis	[39, 57, 61, 65, 76]	-
year_diagnosis	N/A	n=838 (100%)
gleason_grade	N/A	n=838 (100%)
gleason_major	N/A	n=838 (100%)
gleason_minor	N/A	n=838 (100%)
source_of_gleason	N/A	n=838 (100%)
grade_group	3+4: 419 (50%);4+3: 183 (22%);>=8: 171 (20%); ...	-
T_pathological	N/A	n=838 (100%)
T_substage_pathological	N/A	n=838 (100%)
T_clinical	N/A	n=838 (100%)
T_substage_clinical	N/A	n=838 (100%)
ERG_fusion_CNA	N/A	n=838 (100%)
ERG_fusion_IHC	N/A	n=838 (100%)
ERG_fusion_GEX	N/A	n=838 (100%)
disease_specific_recurrence_status	N/A	n=838 (100%)
days_to_disease_specific_recurrence	N/A	n=838 (100%)
metastasis_occurrence_status	N/A	n=838 (100%)
days_to_metastatic_occurrence	N/A	n=838 (100%)
psa	[0,5.2,7.4,11.42,83.44], NA n=18	n=18 (2%)
race	NA: 538 (64%);african_american: 150 (18%);caucasian: 150 (18%)	n=538 (64%)
smoking_status	N/A	n=838 (100%)
extraprostatic_extension	N/A	n=838 (100%)
perineural_invasion	N/A	n=838 (100%)
seminal_vesicle_invasion	N/A	n=838 (100%)
angiolymphatic_invasion	N/A	n=838 (100%)
androgen_ablation	N/A	n=838 (100%)
capsule	N/A	n=838 (100%)

M_stage	N/A	n=838 (100%)
M_substage	N/A	n=838 (100%)
other_patient	N/A	n=838 (100%)
sample_type	primary: 838 (100%)	-
genomic_alterations	N/A	n=838 (100%)
tumor_margins_positive	N/A	n=838 (100%)
tissue_source	prostatectomy: 838 (100%)	-
metastatic_site	N/A	n=838 (100%)
microdissected	0: 838 (100%)	-
frozen_ffpe	FFPE: 838 (100%)	-
other_feature	N/A	n=838 (100%)
batch	Durham Veterans Affairs Hospital: 538 (64%); Johns Hopkins Medical Institute: 300 (36%)	-
other_sample	N/A	n=838 (100%)
tumor_purity_pathology	N/A	n=838 (100%)
tumor_purity_demix	N/A	n=838 (100%)
tumor_purity_absolute	N/A	n=838 (100%)
zone_of_origin	N/A	n=838 (100%)
zone_of_origin_estimated	N/A	n=838 (100%)
immune_infiltration	N/A	n=838 (100%)
mutational_signatures	N/A	n=838 (100%)
neoantigen_load	N/A	n=838 (100%)
AR_activity	N/A	n=838 (100%)
N_stage	N/A	n=838 (100%)
N_substage	N/A	n=838 (100%)
therapy_radiation_initial	0: 838 (100%)	-
therapy_radiation_salvage	0: 838 (100%)	-
therapy_surgery_initial	0: 838 (100%)	-
therapy_hormonal_initial	0: 838 (100%)	-
other_treatment	N/A	n=838 (100%)
psa_category	Feature not found in MAE	-
genome_altered	Feature not found in MAE	-