Data S1

Appendix S1. Inclusion criteria.

Item	Included	Excluded
Population	• Men (aged ≥18 yrs) with known DDR status with: o mCRPC o mPC o CRPC o Any type of PC	• Pediatric or adolescent populations • Upregulated or downregulated wild-type DDR genes
Interventions	Not relevant	Not relevant
Comparator	Not relevant	Not relevant
Outcomes	• Incidence/prevalence rates of DDR+ (germline or somatic mutations) • Incidence/prevalence of DDR (germline or somatic mutations) expressed as a percentage • Incidence/prevalence of DDR (germline or somatic mutations) expressed as a proportion *Note:* The 11 DDR genes of interest are listed below. *Note*: These data may be based on archival and/or fresh tissue samples and/or liquid (eg, blood) samples. Both patient-level and sample-level data will be included, where relevant.	• Incidence/prevalence of individual polymorphisms—unless proven to be
Study design	• Any observational study (retrospective, prospective, cross-sectional) • Database/registry studies • Systematic reviews (these will be checked for primary studies)	• Clinical trials, experimental studies, and interventional studies involving highly selected patient populations • Studies that analyze only cell lines rather than primary patient specimens • Case reports
DDR	• Any of the following individual genes*: ATM, ATR, BRCA1, BRCA2, CHEK2, FANCA, MLH1, MRE11A, NBN, PALB2,* and *RAD51C*. DDR defined as any combination of the listed genes.	• When the prevalence of multiple variants for a given gene were presented (or single nucleotide polymorphisms), only those described as pathogenic were extracted; others were excluded.

ATM, ataxia telangiectasia mutated; *ATR*, ataxia telangiectasia and *Rad3*-related protein; *BRCA*, breast cancer susceptibility gene; *CHEK2*, checkpoint kinase 2; CRPC, castration-resistant PC; DDR, DNA damage repair; *FANCA*, Fanconi anemia complementation group A; m, metastatic; *MLH1*, mutL homolog 1; *MRE11A*, *MRE11* homolog A, double-strand break repair nuclease; *NBN*, nibrin; *PALB2*, partner and localizer of *BRCA2*; PC, prostate cancer; *RAD51C*, *RAD51* paralog C.

Appendix S2. Literature searches.

Searches were carried out to identify studies in the treatment and epidemiology of DDR-positive prostate cancer. All search methods were conducted to follow best practice standards in systematic reviews (1,2).

Search strategies were developed specifically for each database and the key words adapted according to the configuration of each database. Only studies conducted in humans were sought. Searches were not limited by language or publication status (unpublished or published).

The following databases were searched from study inception to December 2017:

- MEDLINE (Ovid): 1946-2017/11/wk 4
- MEDLINE In-Process Citations, Medline Daily Update & Epub Ahead of Print (Ovid): up to 2017/12/05
- Embase (Ovid): 1974-2017/12/04
- Cochrane Database of Systematic Reviews (CDSR) (Wiley): Issue 12/Dec 2017
- Cochrane Central Register of Controlled Trials (CENTRAL) (Wiley): Issue 11/Nov 2017
- Database of Abstracts of Reviews of Effects (DARE) (Wiley): Issue 4/April 2015
- Health Technology Assessment Database (HTA) (Wiley): Issue 4/Oct 2016
- NHS Economic Evaluation Database (NHS EED) (Wiley): Issue 4/April 2015
- PubMed (NLM) (Internet): up to 2017/12/11
- CINAHL (EBSCO): 1981-2017/12/06
- LILACS (BIRME): up to 2017/12/11

Supplementary searches were undertaken in the following trial registers:

- ClinicalTrials.gov (Internet): up to 2017/12/11 http://www.clinicaltrials.gov/
- WHO International Clinical Trials Registry Platform (ICTRP): up to 2017/12/12 http://www.who.int/ictrp/en/

Conference abstracts and proceedings were identified as part of a 3-stage approach:

- The main Ovid Embase search strategy was employed to include conference abstracts and proceedings;
- A second tailored search was conducted using the Northern Light Life Sciences Conference Abstracts database via Ovid (2016-2017/wk 47)
- Limited internet scanning was conducted for any unindexed conference proceedings, selected by Pfizer.

The named conference proceedings were checked against Embase and Northern Light to determine which proceedings were indexed within the databases. The following proceedings were indexed and included in the Embase and Northern Light database searches:

- American Society for Clinical Oncology (ASCO): 2016 & 2017
- ASCO Genitourinary Cancers Symposium: 2016 & 2017

- European Society for Medical Oncology (ESMO): 2016 only
- European CanCer Organisation (ECCO): 2017 only
- American Urological Association (AUA): 2016 & 2017
- European Association of Urology (EAU): 2016 & 2017
- American Association for Cancer Research (AACR): 2016 & 2017

Limited additional scanning of internet conference proceedings was carried for the following unindexed proceedings (2016-2017 only):

- European Society for Medical Oncology (ESMO): 2017 only
- National Comprehensive Cancer Network (NCCN): 2016 & 2017
- Society of Urologic Oncology (SUO): 2016 & 2017

Handling of citations

Identified references were downloaded into Endnote X8 software for further assessment and handling. Individual records within the Endnote reference library were tagged with searching information, such as searcher, date searched, database host, database searched, strategy name and iteration, theme or search question.

Quality assurance within the search process

The main Embase strategy was independently peer reviewed by a second Information specialist. Strategy peer review was informed by items based on the CADTH checklist (3,4).

Search Strategies

Embase (Ovid): 1974-2017/12/04

Searched 5.12.17

1 exp prostate cancer/ (183779)

2 exp prostate tumor/ (208063)

3 (prostat$ adj4 (cancer$ or neoplas$ or carcinoma$ or malignan$ or adenocarcinoma$ or tumo?r$ or adenoma$ or met or mets or metasta$)).ti,ab,ot. (184826)

4 (prostat$ adj3 (castrat$ resist$ or hormone refrac$ or androgen independ$ or androgen insensit$ or androgen in-sensit$ or androgen resist$)).ti,ab,ot. (14783)

5 (mpc or mcrpc or crpc).ti,ab,ot. (11297)

6 or/1-5 (235566)

7 exp DNA damage/ (128563)

8 exp DNA repair/ (82299)

9 (DNA adj2 damag$).ti,ab,ot. (93314)

10 (DNA adj2 repair$).ti,ab,ot. (60659)

11 (DNA adj2 injur$).ti,ab,ot. (753)

12 DDR$.ti,ab,ot. (6742)

13 (base excision repair$ or BER).ti,ab,ot. (7366)

14 (deoxyribonucleic acid adj3 (damag$ or injur$)).ti,ab,ot. (315)

15 (dna adj2 lesion$).ti,ab,ot. (9081)

16 ((photoinduced or photo induced) adj2 dna).ti,ab,ot. (208)

17 (genotoxic adj2 stress$).ti,ab,ot. (3467)

18 (Homologous recombination deficit$ or HRD).ti,ab,ot. (653)

19 (double strand break$ or DSB).ti,ab,ot. (21165)

20 (single strand break$ or SSB).ti,ab,ot. (9297)

21 (H2AX or pH2AX or phosphorylated H2AX or phosphorylated-H2AX or gamma-H2AX or gamma H2AX or yH2AX).ti,ab,ot. (6742)

22 comet assay/ (11267)

23 (comet adj2 assay$).ti,ab,ot. (11305)

24 BRCA1 protein/ (14056)

25 BRCA2 protein/ (10158)

26 (BRCA$ or gBRCA or BRIP1 or BACH1).ti,ab,ot. (24734)

27 Rad51 protein/ (4150)

28 RAD51c$.ti,ab,ot. (506)

29 Fanconi anemia/ (5758)

30 Fanconi anemia protein/ or Fanconi anemia group A protein/ (956)

31 (FANCA or FA-H or FA1 or FAA or FACA or FAH or FANCH or "Fanconi anemia complementation group A" or Fam175a).ti,ab,ot. (3110)

32 ((familial or hereditary) adj3 hypoplastic$ adj3 an?emia).ti,ab,ot. (7)

33 ((familial or hereditary) adj3 aplastic$ adj3 an?emia).ti,ab,ot. (35)

34 (fanconi$ adj3 an?emia).ti,ab,ot. (5138)

35 ((fanconi$ or congenital) adj3 pancytop?enia).ti,ab,ot. (81)

36 mckusick 2276$.ti,ab,ot. (0)

37 checkpoint kinase 2/ (3796)

38 ((Checkpoint adj2 Kinase) or CHEK2 or CHK2 or HuCds or HCds1 or CDS1).ti,ab,ot. (4937)

39 cyclin dependent kinase/ (9776)

40 ((cyclin or cycle) adj3 kinase).ti,ab,ot. (19964)

41 (Cdc2 or CRKRS or CRK7 or KIAA0904 or HCDK12 or CRKR).ti,ab,ot. (5709)

42 (PALB2 or PNCA3).ti,ab,ot. (929)

43 (MRE11$ or Meiotic Recombination or AT-Like Disease$ or HNGS1).ti,ab,ot. or MRE11 protein/ (4761)

44 nibrin/ (1157)

45 (nibrin or NBN or NBS1 or Nijmegen breakage syndrome$).ti,ab,ot. (2271)

46 (KIAA1794 or Protein FACI).ti,ab,ot. (2)

47 ATM protein/ (8350)

48 (ATM or Ataxia Telangiectasia or A-T Mutated or Telomere Maintenance 1 or AT Mutated).ti,ab,ot. (20754)

49 ATR protein/ (3016)

50 (ATR or FRP1 or Mitosis Entry Checkpoint).ti,ab,ot. (10857)

51 (FACD$ or FA-D2 or FAD2 or FA4).ti,ab,ot. (315)

52 MutL protein homolog 1/ (567)

53 (MLH1 or MLH3 or COCA2 or HNPCC7 or (MutL adj3 homolog)).ti,ab,ot. (5322)

54 or/7-53 (304179)

55 exp nicotinamide adenine dinucleotide adenosine diphosphate ribosyltransferase inhibitor/ (8926)

56 ((PARP$ or PARS$) adj3 inhibitor$).ti,ab,ot,rn. (5297)

57 talazoparib/ (292)

58 (talazoparib or BMN-673 or bmn673 or BMN-673ts or bmn673ts or 1207456-01-6 or 1373431-65-2).ti,ab,ot,rn. (348)

59 olaparib/ (2790)

60 (olaparib or Lynparza or AZD-2281 or AZD2281 or ku-0059436 or ku0059436 or ku-59436 or ku59436 or 763113-22-0).ti,ab,ot,rn. (2867)

61 veliparib/ (1334)

62 (Veliparib or ABT-888 or abt888 or 912444-00-9).ti,ab,ot,rn. (1490)

63 rucaparib/ (594)

64 (Rucaparib or rubraca or ag-014699 or ag014699 or ag-14447 or ag14447 or ag14699 or ag-14699 or co-338 or co338 or pf-01367338 or pf1367338 or pf01367338 or pf-1367338 or pf1367338bw or pf-1367338bw or 859053-21-6 or 283173-50-2 or 459868-92-9).ti,ab,ot,rn. (625)

65 niraparib/ (385)

66 (Niraparib or Zejula or MK-4827 or MK4827 or 038915-60-4).ti,ab,ot,rn. (403)

67 or/55-66 (9985)

68 54 or 67 (308401)

69 6 and 68 (6611)

70 animal/ or animal experiment/ (3989568)

71 (rat or rats or mouse or mice or murine or rodent or rodents or hamster or hamsters or pig or pigs or porcine or rabbit or rabbits or animal or animals or dogs or dog or cats or cow or bovine or sheep or ovine or monkey or monkeys).ti,ab,ot,hw. (6682078)

72 70 or 71 (6682078)

73 exp human/ or human experiment/ (19273429)

74 72 not (72 and 73) (5205450)

75 (letter or editorial or note).pt. (2256220)

76 69 not (74 or 75) (5987)

Appendix S3. A. Studies not included in the analysis of prevalence in the unselected population or in subgroup analysis.

Author, year	Country	PC Group	Selected population	Germline or somatic mutation	Mutation Definition	Period of data collection	Gene	% prevalence	No. patients	References
Unselected population										
Liu *et al*, 2016	NR	PC	Unselected	Somatic	Undefined	NR	*ATM*	5.6	36	(5)
							MLH1	5.6	36	
Sonpavde *et al*, 2017	NR	mCRPC	Unselected	Somatic	Undefined	NR	*BRCA1*	5.0	514	(6)
							BRCA2	5.0	514	
Tanaka *et al*, 2009	Japan	PC	Unselected	Somatic	*MLH1* T/A at codon 384 (genotype)	1997 to 2003	*MLH1*	3.4	177	(7)
Dall'Era *et al*, 2017	USA	Primary PC	Unselected	NR/ unclear	85 DDR genes associated with cancer predisposition syndromes (undefined)	NR	DDR	20.1	936	(8)
Dall'Era *et al*, 2017	USA	mPC	Unselected	NR/ unclear	85 DDR genes associated with cancer predisposition syndromes (undefined)	NR	DDR	18.8	936	(8)
Daniel *et al*, 2017	USA	mPC	Unselected	NR/ unclear	≥1 deleterious *BRCA* GA (*BRCA1* or *BRCA2*)	NR	DDR	11.3	1911	(9)
Feldman *et al*, 2014	USA	PC	Unselected	NR/ unclear	*ATM* (undefined)	NR	*ATM*	5	>330	(10)
Dawson *et al*, 2016	USA	PC	Unselected	NR/ unclear	Alterations in ≥1 DNA repair gene (tested using a 592 gene hybrid capture NGS)	NR	DDR	84	31	(11)
	USA	PC	Unselected	NR/ unclear	*BRCA2* (undefined)	NR	*BRCA2*	6	437	

Author, year	Country	PC Group	Selected population	Germline or somatic mutation	Mutation Definition	Period of data collection	Gene	% prevalence	No. patients	References
Uchida *et al*, 1999	Japan	Primary PC	Unselected	NR/ unclear	LOH at ≥1 loci on chr17q (D17S250, D17S1320, D17S855, D17S1322, D17S1323, D17S579, D17S588)	NR	*BRCA1*	16.7	24	(12)
Angele *et al*, 2004	UK	PC	Unselected	Germline	*ATM* 3161C>G	1993 to 2002	*ATM*	7.4	226	(13)
Browning *et al*, 2006	USA	PC	Unselected	Germline	*ATM* heterozygous IVS62+60G/A polymorphism	1997	*ATM*	30.61	98	(14)
					ATM homozygous IVS62+60G/G	1997	*ATM*	18.37	98	
					ATM homozygous IVS62+60A/A	1997	*ATM*	51.02	98	
Nam *et al*, 2005	Canada	PC	Unselected	Germline	All *CHEK2* (1100delC)	Jun 1998 to Jan 2003	*CHEK 2*	0.2	996	(15)
Naslund Koch *et al*, 2016	Denmark	PC	Unselected	Germline	All *CHEK2**1100delC	2003-2010	*CHEK 2*	0.74	39014	(16)
Gambhira *et al*, 2016	USA	mCRPC	Unselected	Somatic	*BRCA1*, *BRCA2*, *ATM*, *CDK12*, *MLH1* and/or *MSH2*	NR	DDR	54	13	(17)
Xia *et al*, 2015	USA	PC	Unselected	Somatic	All *ATM* (c.8012T>G (p.V2671G))	NR	*ATM*	5.0	20	(18)
					All *ATR* (c.7762G>A (p.A2588T))		*ATR*	5.0	20	
					All (*CHEK2* c.721G>A (p.V241I))		*CHEK 2*	5.0	20	

Author, year	Country	PC Group	Selected population	Germline or somatic mutation	Mutation Definition	Period of data collection	Gene	% prevalence	No. patients	References
					FANCA c.1626G>T (pE542D)		*FANCA*	5.0	20	
					FANCA c.4009delA (p.S1337fs)		*FANCA*	5.0	20	
					All *FANCA* (c.4009delA (p.S1337fs); c.1626G>T (pE542D))		*FANCA*	10.0	20	
					All *MLH1* (c.547T>A (p.Y183N))		*MLH1*	5.0	20	
					All *NBN* (c.2186T>A (p.V729E))		*NBN*	5.0	20	
					DDR mutations		DDR	25	20	
Beltran *et al*, 2015	USA	mPC	Unselected	Somatic	*FANCA* deletion	Feb 2013 to Sep 2014	*FANCA*	14	29	(19)
Palapattu *et al*, 2015	USA	PC	Unselected	Somatic	All (K2524fs)	NR	*BRCA2*	11.1	9	(20)
Robbins *et al*, 2011	USA	mPC	Unselected	Somatic	All. 7840C>T likely damaging	NR	*BRCA2*	12.5	8	(21)
Beltran *et al*, 2013	USA	CRPC	Unselected	Somatic	DNA alterations in *ATM* in CRPC	NR	*ATM*	8	25	(22)
		CRPC			DNA alterations in *BRCA2* in CRPC	NR	*BRCA2*	12	25	
		mPC			DNA alterations in *ATM* in metastatic hormone-naïve PC	NR	*ATM*	0	4	
		mPC			DNA alterations in *BRCA2* in metastatic hormone-naïve PC	NR	*BRCA2*	25	4	

Author, year	Country	PC Group	Selected population	Germline or somatic mutation	Mutation Definition	Period of data collection	Gene	% prevalence	No. patients	References
		Primary PC			DNA alterations in *ATM* in clinically localized PC	NR	*ATM*	0	16	
		Primary PC			DNA alterations in *BRCA2* in clinically localized PC	NR	*BRCA2*	6.25	16	
		CRPC			Total mutations across 182 cancer-related genes (3230 exons) and 14 commonly rearranged genes (37 introns) in CRPC	NR	DDR	100	25	
		mPC				NR	DDR	100	4	
		Primary PC				NR	DDR	56.25	16	
Subgroups										
Cheng *et al*, 2011	Australia	PC	Familial	NR/ unclear	Undefined	NR	*BRCA2*	26.5	147	(23)
Nicolas *et al*, 2015	USA	PC	Familial	Germline	One affected gene; high-value DDR or androgen signalling pathway gene variants that may contribute to familial prostate risk	NR	DDR	91.7	12	(24)
					≥2 or more affected genes: high-value DDR or androgen signalling pathway gene variants that may contribute to familial prostate risk	NR		41.7	12	
Meyer *et al*, 2007	Germany	Primary PC	Treatment	Germline	*ATM* missense variant P1054R	Oct 2000 to Apr 2006	*ATM*	9.6	261	(25)

Author, year	Country	PC Group	Selected population	Germline or somatic mutation	Mutation Definition	Period of data collection	Gene	% prevalence	No. patients	References
Damaraju *et al*, 2006	Canada	Primary PC	Treatment	Germline	*MLH1* C>T,Val219Ile	Sept 1996 to Dec 2000	*MLH1*	11	84	(26)
					NBN G>C, Glu185Gln		*NBN*	83	84	
					BRCA1 G>A,Met1652Ile		*BRCA1*	6	83	
					BRCA1 A>G, Arg356Gln		*BRCA1*	11	83	
					BRCA2 A>G, Lys1132Lys		*BRCA2*	57	83	
					ATM A>G, Asp1853Asn		*ATM*	69	84	
Schweizer *et al*, 2016	USA	Ductal PC	Ductal PC	Somatic	All (c.5946delT+likely LOH)	NR	*BRCA2*	11.1	9	(27) [Linked: True 2017(28)]
					All (c.1100delC+LOH)	NR	*CHEK 2*	11.1	9	
					All (exon 19+ 3'UTR homozygous deletion)	NR	*MLH1*	11.1	9	
					CHEK2, *BRCA2*, *MSH6*, *MSH2*, *MLH1*	NR	DDR	66.7	9	
Stephens *et al*, 2016	NR	Neuroendocrine PC	Neuroendocrine PC	Somatic	Undefined	NR	DDR	14	32	(29)

Red text indicates criteria that led to studies being deemed irrelevant to the analysis. *ATM*, ataxia telangiectasia mutated; *ATR*, ataxia telangiectasia and Rad3-related protein; *BRCA*, breast cancer susceptibility gene; *CHEK2*, checkpoint kinase 2; CRPC, castration-resistant PC; DDR, DNA damage repair; *FANCA*, Fanconi anemia complementation group A; LOH, loss of heterozygosity; m, metastatic; *MLH1*, mutL homolog 1; *MRE11A*, *MRE11* homolog A, double-strand break repair nuclease; MSH, MutS homolog; *NBN*, nibrin; *PALB2*, partner and localizer of *BRCA2*; PC, prostate cancer; *RAD51C*, *RAD51* paralog C.

B. Excluded records at full paper screening.

Reference	Reason for exclusion
[1] Abida W, Brennan R, Armenia J, Curtis KR, Gopalan A, Arcila ME, et al. Genomic characterization of primary and metastatic prostate cancer (PC) using a targeted next-generation sequencing assay. In: American Society of Clinical Oncology Genitourinary Cancers Symposium 2016; 07-Jan-2016, 2016. Available from: American Society of Clinical Oncology (ASCO) https://discovery.northernlight.com/document.php?datasource=PHE&docid=PE20160202020001400&context=WK%40northernlight.com&doctype=abstract&docurl=http%3A%2F%2Fmeetinglibrary.asco.org%2Fcontent%2F158192-172&token=b3e6fad5b65095aa7eeaccfd610b2e1b http://ovidsp.ovid.com/ovidweb.cgi?T=JS&CSC=Y&NEWS=N&PAGE=fulltext&D=dscv6&AN=PE2016020202000 1400	Duplicate
[2] A'Hern R, De Bono J, Sandhu S, Kalaitzaki E, Usdin M, Hall EE. Phase II investigation of a PARP inhibitor (olaparib) in castration resistant prostate cancer (CRPC) which incorporates the possibility that treatment effect may be restricted to biomarker defined subgroups. Trials 2011.	No relevant outcome
[3] A'Hern R, De Bono J, Sandhu S, Kalaitzaki E, Usdin M, Hall E. A two stage phase II design incorporating the possibility that the treatment effect may be restricted to a biomarker defined subgroup: Investigation of a PARP inhibitor (Olaparib) in Castration Resistant Prostate Cancer (CRPC). Clin Trials 2012;9(4):552-553.	No relevant outcome
[4] Allen-Brady K, Farnham JM, Camp NJ, Karlins E, Ostrander EA, Cannon-Albright LA. No evidence of BRCA2 mutations in chromosome 13q-linked Utah high-risk prostate cancer pedigrees. BMC Res Notes 2009;2:94.	Not a relevant population
[5] Annala M, Struss WJ, Warner EW, Beja K, Vandekerkhove G, Wong A, et al. Treatment outcomes and tumor loss of heterozygosity in germline DNA repair-deficient prostate cancer. Eur Urol 2017;72(1):34-42.	Not relevant study design
[6] Anonymous. Repair-Gene Mutations Uncovered in Metastatic Prostate Cancer. Cancer Discovery 2016;6(9):OF3.	Not primary research
[7] Evans JR. (S028) patient-level DNA damage and repair pathway profiles are prognostic after prostatectomy for high-risk prostate cancer. Oncology 2015;29(4 Suppl 1):21.	No DDR mutation/not relevant
[8] Armenia J, Mullane S, Gao J, Chakravarty D, Kundra R, Huang F, et al. The long tail of significantly mutated genes in prostate cancer. Cancer Res 2017.	No data (abstract)
[9] Armenia J, Mullane SA, Gao JJ, Chakravarty D, Kundra R, Huang FW, et al. The long tail of significantly mutated genes in prostate cancer. J Clin Oncol 2017.	No data (abstract)
[10] AstraZeneca. Open label study to assess efficacy and safety of olaparib in confirmed genetic BRCA1 or BRCA2 mutation pats. NCT01078662. In: ClinicalTrials.gov [Internet]. Bethesda (MD): National Library of Medicine (US). 2012 [accessed 11.12.17]. Available from: https://ClinicalTrials.gov/show/NCT01078662.	No relevant outcome

[11] AstraZeneca. Study of Olaparib (Lynparza™) Versus enzalutamide or abiraterone acetate in men with metastatic castration-resistant prostate cancer (PROfound Study). NCT02987543. In: WHO International Clinical Trials Registry Platform (ICTRP) [Internet]. Geneva: World Health Organization (WHO). 2016 [accessed 12.12.17]. Available from: https://clinicaltrials.gov/show/NCT02987543.	No relevant outcome
[12] AstraZeneca. Study of Olaparib (Lynparza™) Versus enzalutamide or abiraterone acetate in men with metastatic castration-resistant prostate cancer (PROfound Study). EUCTR2016-000300-28-SE. In: WHO International Clinical Trials Registry Platform (ICTRP) [Internet]. Geneva: World Health Organization (WHO). 2017 [accessed 12.12.17]. Available from: https://www.clinicaltrialsregister.eu/ctr-search/search?query=eudract_number:2016-000300-28.	No relevant outcome
[13] AstraZeneca. Study of olaparib (Lynparza™) versus enzalutamide or abiraterone acetate in men with metastatic castration-resistant prostate cancer (PROfound Study). NCT02987543. In: ClinicalTrials.gov [Internet]. Bethesda (MD): National Library of Medicine (US). 2020 [accessed 11.12.17]. Available from: https://ClinicalTrials.gov/show/NCT02987543.	Duplicate
[14] Aurelius Omlin. Carboplatin in castration-resistant prostate cancer. NCT02311764. In: WHO International Clinical Trials Registry Platform (ICTRP) [Internet]. Geneva: World Health Organization (WHO). 2014 [accessed 12.12.17]. Available from: https://clinicaltrials.gov/show/NCT02311764.	No relevant outcome
[15] Banks P, San Leong H, Ryland G, Beshay V, Tran B, Toner G, et al. DNA repair gene defects in Australian men with metastatic castration-resistant prostate cancer (mCRPC). BJU Int 2017.	No data (abstract)
[16] Banks P, Leong HS, Ryland G, Beshay V, Tran B, Toner G, et al. DNA repair gene defects in Australian men with metastatic castration-resistant prostate cancer (MCRPC). Asia Pac J Clin Oncol 2017.	No data (abstract)
[17] Barrett A, Schwartz LE. Morphologic and clinical comparison of BRCA+ And BRCA prostate carcinoma. In: United States & Canadian Academy of Pathology Annual Meeting 2017; 04-Mar-2017, 2017. Available from: United States & Canadian Academy of Pathology (USCAP). https://discovery.northernlight.com/document.php?datasource=PHE&docid=PE20170228000002090&context=WK%40northernlight.com http://ovidsp.ovid.com/ovidweb.cgi?T=JS&CSC=Y&NEWS=N&PAGE=fulltext&D=dscv6&AN=PE2017022800002090	Duplicate
[18] Barrett A, Schwartz LE. Morphologic and clinical comparison of BRCA+ and brcaprostate carcinoma. Lab Invest 2017.	No relevant outcome
[19] Basu S, Majumder S, Bhowal A, Ghosh A, Naskar S, Nandy S, et al. A study of molecular signals deregulating mismatch repair genes in prostate cancer compared to benign prostatic hyperplasia. PLoS One 2015;10(5):e0125560.	No relevant outcome
[20] Bednarz N, Eltze E, Semjonow A, Rink M, Andreas A, Mulder L, et al. BRCA1 loss preexisting in small subpopulations of prostate cancer is associated with advanced disease and metastatic spread to lymph nodes and peripheral blood. Clin Cancer Res 2010;16(13):3340-3348.	No relevant outcome

[21] Bednarz N, Semjonow A, Osther PJ, Brandt B. BRCA1 loss in prostate cancer is associated with metastatic spread: Novel predictor of parp-inhibitory therapy? Biochimica Clinica 2013;37:S160.	No relevant outcome
[22] BeiGene Usa Inc, Myriad Genetics Inc, BeiGene. Study to assess safety, tolerability and clinical activity of BGB-290 in combination with temozolomide (TMZ) in subjects with locally advanced or metastatic solid tumors. NCT03150810. In: ClinicalTrials.gov [Internet]. Bethesda (MD): National Library of Medicine (US). 2020 [accessed 11.12.17]. Available from: https://ClinicalTrials.gov/show/NCT03150810.	No relevant outcome
[23] Beltran H, Stephens PJ, Mosquera JM, Cronin MT, Rubin MA, Yelensky R, et al. Massively parallel DNA-sequencing of aggressive prostate cancer reveals disease heterogeneity and identifies targetable mutations. Cancer Res 2012.	Not a relevant population
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Appendix S4.

Table of Contents for Appendix S4.

A1. Summary of *BRCA2* and DDR gene mutation prevalence in familial prostate cancer germline tissues.

% period prevalence, median (range)	Prostate cancer
Specific *BRCA2*	0.5 (0.21, 2.63) 3 studies (n=703) 12 datasets (n=3248)
All *BRCA2*	3.7 (1.3, 7.9) 6 studies (n=945)

DDR[a]	29.3 (7.3, 91.67) 3 studies (n=327) 4 datasets (n=339)

[a]DDR=multiple gene definitions for DNA damage response gene that includes at least one of our genes of interest.
BRCA, breast cancer susceptibility gene; DDR, DNA damage repair; n, sample size.

B1. Reported prevalence for familial *BRCA2* and DNA damage response mutations in germline prostate cancer populations.

Gene	DDR definition	% prevalence	N	Variant described as pathogenic for PC?	Variant described as pathogenic for other cancers?	Variant shown to be associated with PC or risk to PC?	Country	Author, year	Ref-erences
Specific *BRCA2*	*BRCA2* (5531delTT)	2.63	38	Yes	Yes	Yes	UK	Gayther *et al*, 2000	(50)
	BRCA2 (6710delACAA)	2.63	38	Yes	Yes	Yes	UK	Gayther *et al*, 2000	(50)
	BRCA2 (9078 G>T or K2950N)	2.63	38	No	Yes	Yes	UK	Gayther *et al*, 2000	(50)
	BRCA2 (c.1813_14_insA or I605fs) frameshift	0.21	474	Yes	Yes	Yes	Germany	Maier *et al*, 2014	(72)
	BRCA2 (c.3847delGT or V128fs) frameshift	0.21	474	Yes	Yes	Yes	Germany	Maier *et al*, 2014	(72)
	BRCA2 (c.4449delA or T1483fs) frameshift	0.21	474	Yes	Yes	Yes	Germany	Maier *et al*, 2014	(72)
	BRCA2 (c.6037A>T or K2013X) nonsense	0.21	474	Yes	Yes	Yes	Germany	Maier *et al*, 2014	(72)
	BRCA2 (c.7495C>T or Q2499X) nonsense	0.21	474	Yes	Yes	Yes	Germany	Maier *et al*, 2014	(72)
	BRCA2 c.4876_4877del: p.(Asn1626Serfs*12)	0.52	191	Yes	Unclear	Yes	UK	Leongamornlert *et al*, 2014	(70)

	BRCA2 c.4981del:p.(Tyr1661Ilefs*9)	0.52	191	Yes	Unclear	Yes	UK	Leongamornlert *et al*, 2014	(70)
	BRCA2 c.5909C>A: p.(Ser1970*)	0.52	191	Yes	Unclear	Yes	UK	Leongamornlert *et al*, 2014	(70)
	BRCA2 c.9382C>T: p.(Arg3128*)	0.52	191	Yes	Unclear	Yes	UK	Leongamornlert *et al*, 2014	(70)
All *BRCA2*	*BRCA2*	3.23	124	NA	NA	NA	USA	Ledet *et al*, 2017	(67)
	BRCA2 exon sequence variants	1.3	382	NA	NA	NA	Germany	Maier *et al*, 2014	(72)
	Five *BRCA2* variants (L61P, H1458R, G2508S, H3056Y, and R3384X)	4.24	118	NA	NA	NA	Japan	Hayano *et al*, 2016	(57)
	Total undefined *BRCA2* variants	7.9	38	NA	NA	NA	UK	Gayther *et al*, 2000	(50)
	Undefined *BRCA2*	4.35	92	NA	NA	NA	USA	Marshall *et al*, 2017	(74)
	All *BRCA2* (c.9382C>T: p.(Arg3128*); c.4876_4877del: p.(Asn1626Serfs*12); c.4981del:p.(Tyr1661Ilefs*9); *BRCA2* c.5909C>A: p.(Ser1970*))	2.09	191	NA	NA	NA	UK	Leongamornlert *et al*, 2014	(70)
DDR	DDR (25-79 cancer-related genes)	16.9	124	NA	NA	NA	USA	Ledet *et al*, 2017	(67)
	Deleterious LoF mutations	7.3	191	NA	NA	NA	UK	Leongamornlert *et al*, 2014	(70)

	One affected gene; High value DDR or androgen signalling pathway gene variants that may contribute to familial prostate risk	91.67	12	NA	NA	NA	USA	Nicolas *et al*, 2015	(24)
	Two or more affected genes: High value DDR or androgen signalling pathway gene variants that may contribute to familial prostate risk	41.67	12	NA	NA	NA	USA	Nicolas *et al*, 2015	(24)
BRCA, breast cancer susceptibility gene; DDR, DNA damage repair; LoF, loss of function; NA, not available; PC, prostate cancer.									

C1. Reported prevalence for familial *BRCA2* and DDR mutations in germline PC populations (definitions of familial and inclusion criteria).

Gene	DDR definition	% prevalence	N	Definition of familial cancer	Inclusion criteria	Author, year	Ref-erences
Specific *BRCA2*	*BRCA2* (5531delTT)	2.63	38	NR	Clusters with a relative risk of developing prostate cancer of ≥4; clusters of ≥3 prostate cancers at any age or in sibling pairs, preferably where one is <65 years at diagnosis	Gayther *et al*, 2000	(50)
	BRCA2 (6710delACAA)	2.63	38				
	BRCA2 (9078 G>T or K2950N)	2.63	38				
	BRCA2 (c.1813_14_insA or I605fs) frameshift	0.21	474	NR	Patients with familial PC who are members of families with PC clustering; or patients with sporadic early onset PC who underwent radical	Maier *et al*, 2014	(72)
	BRCA2 (c.3847delGT or V128fs) frameshift	0.21	474				

	BRCA2 (c.4449delA or T1483fs) frameshift	0.21	474		prostatectomy and reported a negative family history for prostate cancer		
	BRCA2 (c.6037A>T or K2013X) nonsense	0.21	474				
	BRCA2 (c.7495C>T or Q2499X) nonsense	0.21	474				
	BRCA2 c.4876_4877del: p.(Asn1626Serfs*12)	0.52	191	Two or more relatives affected by PC	Men with PC who had two or more relatives affected by PC	Leongamornlert *et al*, 2014	(70)
	BRCA2 c.4981del:p. (Tyr1661Ilefs*9)	0.52	191				
	BRCA2 c.5909C>A: p.(Ser1970*)	0.52	191				
	BRCA2 c.9382C>T: p.(Arg3128*)	0.52	191				
All *BRCA2*	*BRCA2*	3.23	124	PC patients with a family history that met NCCN guidelines for genetic testing	Patients with prostate cancer who met NCCN guidelines for genetic testing	Ledet *et al*, 2017	(67)
	BRCA2 exon sequence variants	1.3	382	NR	See above	Maier *et al*, 2014	(72)
	Five *BRCA2* variants (L61P, H1458R, G2508S, H3056Y, and R3384X)	4.24	118	Small PC families (2 patients with PC; n=118)	Patients in families with two or more prostate cancer patients	Hayano *et al*, 2016	(57)
	Total undefined *BRCA2* variants	7.9	38	NR	See above	Gayther *et al*, 2000	(50)

	Undefined *BRCA2*	4.35	92	Personal history of PC and ≥1 close blood relative with breast, ovarian, pancreatic or prostate cancer; or a personal history of PC	Men with PC; personal history of PC and ≥1 close blood relative with breast, ovarian, pancreatic or prostate cancer; or a personal history of PC; underwent hereditary panel testing	Marshall *et al*, 2017	(74)
	All *BRCA2* (c.9382C>T: p.(Arg3128*); c.4876_4877del: p.(Asn1626Serfs*12); c.4981del:p.(Tyr1661Ilefs*9); *BRCA2* c.5909C>A: p.(Ser1970*))	2.09	191	Two or more relatives affected by PC	Men with PC who had two or more relatives affected by PC	Leongamornlert *et al*, 2014	(70)
DDR	DDR (25-79 cancer-related genes)	16.9	124	PC patients with a family history that met NCCN guidelines for genetic testing	Patients with prostate cancer who met NCCN guidelines for genetic testing	Ledet *et al*, 2017	(67)
	Deleterious LoF mutations	7.3	191	Two or more relatives affected by PC	Men with PC who had two or more relatives affected by PC	Leongamornlert *et al*, 2014	(70)
	One affected gene; High value DDR or androgen signalling pathway gene variants that may contribute to familial prostate risk	91.67	12	NR	Strong family cancer history with either multiple first-degree or second-degree relatives with prostate cancer or other cancers	Nicolas *et al*, 2015	(24)
	Two or more affected genes: High value DDR or androgen signalling pathway gene variants that may contribute to familial prostate risk	41.67	12				

BRCA, breast cancer susceptibility gene; DDR, DNA damage repair; LoF, loss of function; NCCN, National Comprehensive Cancer Network; NR, not reported; PC, prostate cancer.

A2. Familial germline mutations in patients with prostate cancer.

Country	Gene	DDR definition	% prevalence	n	Period of data collection	Author, year	Ref-erences
Australia	*BRCA1*	Undefined (unclear germline or somatic)	7.5	147	NR	Cheng *et al*, 2011	(23)
	BRCA2	Undefined (unclear germline or somatic)	26.5	147	NR		
Germany	*BRCA2*	*BRCA2* (c.1813_14_insA or I605fs) frameshift [a]	0.2[c]	474	1998-2007	Maier *et al*, 2014 (Linked: Maier *et al*, 2010)	(72) (107)
		BRCA2 (c.3847delGT or V128fs) frameshift [a]	0.2[c]	474	1998-2007		
		BRCA2 (c.4449delA or T1483fs) frameshift [a]	0.2[c]	474	1998-2007		
		BRCA2 (c.6037A>T or K2013X) nonsense [a]	0.2[c]	474	1998-2007		
		BRCA2 (c.7495C>T or Q2499X) nonsense [a]	0.2[c]	474	1998-2007		
		BRCA2 exon sequence variants	1.3[c]	382	1998-2007		
	NBN	*NBN* 657del5 [a]	0.0	299	NR	Hebbring *et al*, 2006	(58)
Japan	*BRCA2*	Five *BRCA2* variants (L61P, H1458R, G2508S, H3056Y, and R3384X)	4.2[b]	118	NR	Hayano *et al*, 2016	(57)
Multi-national	*NBN*	*NBN* 657del5 [a]	0.2	1819	NR	Hebbring *et al*, 2006	(58)
UK	*ATM*	*ATM* c.7327C>T:p.(Arg2443*) [a]	0.5	191	NR	Leongamornlert *et al*, 2014	(70)
		ATM c.7777C>T: p.(Gln2593*) [a]	0.5	191	NR		
		All *ATM* (c.7777C>T: p.(Gln2593*); c.7327C>T:p.(Arg2443*))	1.0	191	NR		
	BRCA1	Total undefined *BRCA1* variants	0.0	38	NR	Gayther *et al*, 2000	(50)

		All *BRCA1* (c.4065_4068del: p.(Asn1355Lysfsa10))	0.5	191	NR	Leongamornlert *et al*, 2014	(70)
	BRCA2	*BRCA2* (5531delTT) [a]	2.6	38	NR	Gayther *et al*, 2000	(50)
		BRCA2 (6710delACAA) [a]	2.6	38	NR		
		BRCA2 (9078 G>T or K2950N) [a]	2.6	38	NR		
		BRCA2 c.4876_4877del: p.(Asn1626Serfs*12) [a]	0.5	191	NR	Leongamornlert *et al*, 2014	(70)
		BRCA2 c.4981del:p.(Tyr1661Ilefs*9) [a]	0.5	191	NR		
		BRCA2 c.5909C>A: p.(Ser1970*) [a]	0.5	191	NR		
		BRCA2 c.9382C>T: p.(Arg3128*) [a]	0.5	191	NR		
		Total undefined *BRCA2* variants	7.9	38	NR	Gayther *et al*, 2000	(50)
		All *BRCA2* (c.9382C>T: p.(Arg3128*); c.4876_4877del: p.(Asn1626Serfs*12); c.4981del:p.(Tyr1661Ilefs*9); *BRCA2* c.5909C>A: p.(Ser1970*))	2.1	191	NR	Leongamornlert *et al*, 2014	(70)
	CHEK2	*CHEK2* c.1263del:p.(Ser422Valfs*15) [a]	0.5	191	NR		
		CHEK2 c.869del:p.(Asn290Thrfs*14) [a]	0.5	191	NR		
		All (*CHEK2* c.869del:p.(Asn290Thrfs*14); c.1263del:p.(Ser422Valfs*15))	1.0	191	NR		
	MLH1	NA (no mutations identified)	0.0	191	NR		
	MRE11A	NA (no mutations identified)	0.0	191	NR		
	NBN	NA (no mutations identified)	0.0	191	NR		
	PALB2	All *PALB2* (c.3507_3508del:p.(His1170Phefs*19))	0.5	191	NR		
	RAD51C	NA (no mutations identified)	0.0	191	NR		
	DDR	Deleterious LoF mutations	7.3	191	NR		

USA	*ATM*	Undefined *ATM*	1.6[c]	124	2015 to 2016	Ledet *et al*, 2017 (linked: Lin *et al*, 2017)	(67) (108)
			2.1[b]	NR	NR	LaDuca *et al*, 2017	(65)
			3.3	92	NR	Marshall *et al*, 2017	(74)
	BRCA1	Undefined *BRCA1*	2.4[c]	124	2015 to 2016	Ledet *et al*, 2017 (linked: Lin *et al*, 2017)	(67) (108)
			1.1	92	NR	Marshall *et al*, 2017	(74)
	BRCA2	Undefined *BRCA2*	3.2[c]	124	2015 to 2016	Ledet *et al*, 2017 (linked: Lin *et al*, 2017)	(67) (108)
			4.3	92	NR	Marshall *et al*, 2017	(74)
	CHEK2	Undefined *CHEK2*	2.4[c]	124	2015 to 2016	Ledet *et al*, 2017 (linked: Lin *et al*, 2017)	(67) (108)
			2.2	92	NR	Marshall *et al*, 2017	(74)
	NBN	*NBN*	0.8[c]	124	2015 to 2016	Ledet *et al*, 2017 (linked: Lin *et al*, 2017)	(67) (108)
		NBN 657del5[a]	0.3	1520	NR	Hebbring *et al*, 2006	(58)
		novel S706* G>C	1.2	85	NR	Zuhlke *et al*, 2012	
		rs1805794 C>G E185Q	54.1	85	NR		(102)

	DDR	DDR (25-79 cancer-related genes)	16.9	124	2015 to 2016	Ledet *et al*, 2017 (linked: Lin *et al*, 2017)	(67) (108)

[a]Analysis for a specific mutation (not all mutations for a given gene), these studies were not highlighted in grey; [b]high risk of bias for country representation and statistical analysis; [c]high risk of bias for country representation.
Note all patients are designated 'PC' and all mutations are germline (except Cheng 2011 which has unclear germline or somatic designation).
ATM, ataxia telangiectasia mutated; *BRCA*, breast cancer susceptibility gene; *CHEK2*, checkpoint kinase 2; DDR, DNA damage repair; LoF, loss of function; *MLH1*, mutL homolog 1; *MRE11A*, *MRE11* homolog A, double-strand break repair nuclease; NA, not applicable; *NBN*, nibrin; NR, not reported; *PALB2*, partner and localizer of *BRCA2*; PC, prostate cancer; RAD, DNA repair protein.

B2. DDR mutations in Ashkenazi Jewish patients with prostate cancer.

Country	Germline or somatic mutation	Prostate cancer group	Gene	DDR definition	% prevalence	n	Period of data collection	Author, yearr	Ref-erences
Canada	Germline	PC	*BRCA1*	*BRCA1* (185delAG)* [a]	0.0[c]	146	1991 to 2002	Hamel *et al*, 2003	(55)
			BRCA2	*BRCA1* (5382insC)* [a]	0.0[c]	146	1991 to 2002		
				BRCA2 (6174delT)* [a]	1.4[c]	146	1991 to 2002		
			CHEK2	*CHEK2* exon 10 1180G>A E394F	0.0[c]	136	NR	Tischkowitz *et al*, 2008	(97)
				CHEK2 exon 11 1270T>C Y424H	0.0[c]	136	NR		
				CHEK2 exon 11 1283C>T S428F	2.8[c]	141	NR		
				CHEK2 exon 11 1312G>T D438Y	0.7[c]	143	NR		
Israel	Germline	PC	*BRCA1*	*BRCA1* (185delAG) [a]	2.3[c]	87	Jan 1991 to Jul 1997	Hubert *et al*, 1999	(59)
					2.3[c]	87	1998	Vazina *et al*, 2000	
				BRCA1 (5382insC) [a]	3.3[c]	60	1998		(98)

			BRCA2	*BRCA2* (6174delT) [a]	1.1[c]	86	1998		
					1.1[c]	87	Jan 1991 to Jul 1997	Hubert *et al*, 1999	(59)
			DDR	*BRCA1* (185delAG) or *BRCA2* (6174delT)	3.4[c]	87	Jan 1991 to Jul 1997		
	Somatic		*BRCA1*	*BRCA1* (185delAG) [a]	1.5	940	1994 to 1995	Giusti *et al*, 2003	(51)
				BRCA1 (5382insC) [a]	0.2	940	1994 to 1995		
				Total *BRCA1* [185delAG or 5382insC] [a]	1.7	940	1994 to 1995		
			BRCA2	*BRCA2* (6174delT) [a]	1.5	940	1994 to 1995		
USA	Germline	CRPC	DDR	*BRCA1**185delAG and *BRCA2**6174delT *	8.0	88	Jun 1998 to Dec 2007	Gallagher *et al*, 2011 (Linked: Gallagher *et al*, 2010)	(48) (49)
			BRCA1	*BRCA1**185delAG[a]	3.4[c]	88	Jun 1998 to Dec 2007		
			BRCA2	*BRCA2**6174delT[a]	4.5[c]	88	Jun 1998 to Dec 2007		
		PC	*BRCA1*	185delAG*[a]	0.0[c]	60	NR	Lehrer *et al*, 1998	(68)
					1.1	965	1998 to 2005	Agalliu *et al*, 2009	(32)
					1.2 [b,c]	83	1991 to 1996	Nastiuk *et al*, 1999	(78)
				185delAG *and 5382incC*[a]	2.0[c]	251	Apr 2000 to Sep 2002	Kirchoff *et al*, 2004	(63)
				5382incC*[a]	0.1	975	1998 to 2005	Agalliu *et al*, 2009	(32)
			BRCA2	6174deIT*[a]	0.0[c]	60	NR	Lehrer *et al*, 1998	(68)

					1.9	951	1998 to 2005	Agalliu *et al*, 2009	(32)
					2.4[b,c]	82	1991 to 1996	Nastiuk *et al*, 1999	(78)
					3.2[c]	251	Apr 2000 to Sep 2002	Kirchoff *et al*, 2004	(63)
		Other (localized)	DDR	*BRCA1**185delAG and *BRCA2**6174delT	3.1[c]	832	Jun 1998 to Dec 2007	Gallagher *et al*, 2011 (Linked: Gallagher *et al*, 2010)	(48) (49)
			BRCA1	*BRCA1**185delAG	0.7[c]	832	Jun 1998 to Dec 2007		
			BRCA2	*BRCA2**6174delT	2.4[c]	832	Jun 1998 to Dec 2007		

[a]Analysis for a specific mutation (not all mutations for a given gene); [b]high risk of bias for country representation and statistical analysis; [c]high risk of bias for country representation.
Note only Tischkowitz 2008(97) analyzed all mutations for a given gene.
Agalliu 2009 (32) most representative of USA; Giusti 2003(51) most representative of Israel.
All mutations were reported as founder mutations (except Tishkowitz 2008).
BRCA, breast cancer susceptibility gene; CHEK2, checkpoint kinase 2; CRPC, castration-resistant PC; DDR, DNA damage repair; NR, not reported; PC, prostate cancer.

C2. DDR mutations in patients receiving a pre-specified treatment regimen.

Country	Germline or somatic mutation	Prostate cancer group	Gene	DDR definition	% prevalence	n	Period of data collection	Author, yearr	Ref-erences
Germany	Somatic	mCRPC	*BRCA1*	Undefined	0.0	53	1998 and 2016	Nientiedt *et al*, 2017	(82)
			BRCA2	Deleterious, otherwise undefined	15.1	53	1998 and 2016		
USA	Germline		*ATM*	All *ATM* mutations (c.C4106A; c.5707dupA; c.6227delT)	1.7	172	Oct 2011 to Dec 2015	Antonarakis *et al*, 2018	(34)

				ATM (c.5707dupA) [a]	0.6	172	Oct 2011 to Dec 2015		
				ATM (c.6227delT) [a]	0.6	172	Oct 2011 to Dec 2015		
				ATM (c.C4106A) [a]	0.6	172	Oct 2011 to Dec 2015		
				All pathogenic (c.7271T>G; p.Val2424Gly missense; c.3245_3247delinsTGAT; p.His1082LeufsX14 framshift)	2.9	69	Jun 2013 to Aug 2014	Hart *et al*, 2016 (Linked: NCT01953640)	(56) (109)
				c.3245_3247delinsTGAT; p.His1082LeufsX14 framshift [a]	1.4	69	Jun 2013 to Aug 2014		
				c.7271T>G; p.Val2424Gly missense [a]	1.4	141	Jun 2013 to Aug 2014		
				All *ATM* c.A>8266>T; p.K>2756>X	0.7[c]	69	2001 to 2015	Pomerantz *et al*, 2017	(85)
			ATR	All *ATR* c.4957C>T; p.Arg1653X Stop gained	1.4	141	Jun 2013 to Aug 2014	Hart *et al*, 2016 (Linked: NCT01953640)	(56) (109)
				All *ATR* (c.2634-1G>A)	0.6	69	Oct 2011 to Dec 2015	Antonarakis *et al*, 2018	(34)
			BRCA1	Undefined pathogenic	0.0	172	Jun 2013 to Aug 2014	Hart *et al*, 2016 (Linked: NCT01953640)	(56) (109)
				All *BRCA1* (c.C3893A)	0.6	69	Oct 2011 to Dec 2015	Antonarakis *et al*, 2018	(34)
			BRCA2	All *BRCA2* mutations (c.5946delT; c.C9076T; c.5946delT; c.C9285T; c.5946delT)	2.9	69	Oct 2011 to Dec 2015	Antonarakis *et al*, 2018	(34)

				BRCA2 (c.5946delT) [a]	0.6	172	Oct 2011 to Dec 2015		
				BRCA2 (c.C9076T) [a]	0.6	172	Oct 2011 to Dec 2015		
				BRCA2 (c.C9285T) [a]	0.6	141	Oct 2011 to Dec 2015		
				All *BRCA2* variants	5.7	172	2001 to 2015	Pomerantz *et al*, 2017	(85)
				c.1189_1190insTTAG; p.Q>397>fs [a]	0.7	172	2001 to 2015		
				c.2330dupA; p.D>777>fs [a]	0.7	172	2001 to 2015		
				c.3545_3546del; p.F>1182>fs [a]	0.7	141	2001 to 2015		
				c.5946delIT; p.S>1982>fs [a]	2.1	141	2001 to 2015		
				c.6275_6276del; p.L>2092>fs [a]	0.7	141	2001 to 2015		
				c.8537_8538del p.E>2846>fs [a]	0.7	69	2001 to 2015		
				All pathogenic (c.469_470delAA; p.Lys157ValfsX25 (frameshift); c.6444dupT; p.Ile2149TyrfsX2 frameshift; c.9513_9516delACTT; p.Leu3172AlafsX44 frameshift)	4.3	141	Jun 2013 to Aug 2014	Hart *et al*, 2016 (Linked: NCT01953640)	(56) (109)
				c.469_470delAA; p.Lys157ValfsX25 (frameshift) [a]	1.4	141	Jun 2013 to Aug 2014		

				c.6444dupT; p.Ile2149TyrfsX2 frameshift ǂ	1.4	69	Jun 2013 to Aug 2014		
				c.9513_9516delACTT; p.Leu3172AlafsX44 frameshift[a]	1.4	141	Jun 2013 to Aug 2014		
			CHEK2	All *CHEK2* (c.A349G)	0.6	69	Oct 2011 to Dec 2015	Antonarakis *et al*, 2018	(34)
			DDR	50 defined DDR genes, including: *ATM*, *ATR*, *BRCA1*, *BRCA2*, *CHEK2*, *FANCA*, *FANCD2*, *MLH1*, *MRE11A*, *NBN*, *PALB2*, *RAD51C*; *BAP1*, *BARD1*, *BLM*, *BRAP*, *BRIP1*, *CDH1*, *CDK12*, *CENPQ*, *CHEK1*, *EPCAM1*, *ERCC1*, *ERCC2*, *ERCC3*, *ERCC4*, *ERCC6*, *FAM175A*, *FAM175B*, *FANCC*, *FANCD2*, *FANCE*, *FANCF*, *FANCG*, *FANCI*, *FANCL*, *GEN1*, *HDAC2*, MLH3, *MSH2*, *MSH6*, *MUTYH*, *PIF1*, *PMS2*, *RAD51*, RAD51B, *RAD51D*, *RAD54L*, *RDM1*, *TP53*, and *XRCC2*.	12.8	172	Oct 2011 to Dec 2015		
			FANCA	NR	0.0	69	Oct 2011 to Dec 2015		
				All *FANCA* c.A>100>T; p.K>34>X	0.7[c]	172	2001 to 2015	Pomerantz *et al*, 2017	(85)
			MLH1	NR	0.0	141	Oct 2011 to Dec 2015	Antonarakis *et al*, 2018	(34)
			MRE11A	NR	0.0	172	Oct 2011 to Dec 2015		

			NBN	NR	0.0	141	Oct 2011 to Dec 2015		
			PALB2	NR	0.0	172	Oct 2011 to Dec 2015		
			RAD51 C	NR	0.0	172	Oct 2011 to Dec 2015		
		PC	*ATM*	25 *ATM* genetic variants	44.0[c]	172	Jun 1990 to Mar 2006	Cesaretti *et al*, 2007 (Linked: Cesaretti *et al*, 2005)	(41); (110)
				ATM 5557G>A [a]	9.0[b]	172	NR	Zhu *et al*, 2010	(101)

[a]Analysis for a specific mutation (not all mutations for a given gene), these studies were not highlighted in grey; [b]high risk of bias for country representation and statistical analysis; [c]high risk of bias for country representation.

Treatments were as follows: Nientiedt 2017 (docetaxel); Antonarakis 2018 (enzalutamide or abiraterone); Hart 2016 (androgen deprivation therapy); Pomerantz 2017 (carboplatin-based chemotherapy); Cesaretti 2007 (brachytherapy).

ATM, ataxia telangiectasia mutated; *ATR*, ataxia telangiectasia and Rad3-related protein; *BAP1*, *BRCA1*-associated protein 1; *BLM*, Bloom syndrome RecQ like helicase; *BRCA*, breast cancer susceptibility gene; *BRAP*, *BRCA1*-associated binding protein; *BRIP1*, *BRCA1* interacting protein C-terminal helicase 1; *CDH1*, cadherin 1; CDK, cyclin-dependent kinase; *CENPQ*, centromere protein Q; *CHEK2*, checkpoint kinase 2; CRPC, castration-resistant PC; DDR, DNA damage repair; EPCAM, epithelial cell adhesion molecule; ERCC, excision repair cross-complementation group; FAM175, family with sequence similarity 175,member; FANC, Fanconi anemia complementation group; *GEN1*, GEN1, Holliday junction 5' flap endonuclease; HDAC, histone deacetylase; m, metastatic; *MLH1*, mutL homolog 1; *MRE11A*, *MRE11* homolog A, double-strand break repair nuclease; MSH, muS homolog; *MUTYH*, mutY DNA glycosylase; *NBN*, nibrin; *PALB2*, partner and localizer of *BRCA2*; PC, prostate cancer; *PIF1*, PIF1 5'-to-3' DNA helicase; *PMS2*, *PMS1* homolog 2, mismatch repair system component; RAD, DNA repair protein; *RDM1*, *RAD52* motif containing 1XRCC, x-ray repair cross complementing.

D2. DDR mutations in patients with young-onset PC.

Country	PC Group	Selected population	Germline or somatic mutation	Definition	Period of data collection	Gene	% prevalence	n	Author, year	Ref-rences
UK	Young-onset PC (≤65 years)	Young-onset PC (≤65 years)	Germline	All *BRCA2* (protein-truncating mutations - 16 frameshift and 3 nonsense)	NR	*BRCA2*	1.2	1589	Kote-Jarai *et al*, 2011 (Linked: Kote-Jarai *et al*, 2011)	(104); (64)
	Young-onset PC (≤55 years)	Young-onset PC (≤55 years)		All *BRCA2* (deleterious; 5 frameshift, 1 splice site)	1992 to 1999		2.3	263	Edwards *et al*, 2010 (Linked: Edwards *et al*, 2003)	(105); (44)
USA				All protein truncating and SNPs in *BRCA2*	Jan 1993 to Dec 2005		0.69	290	Agalliu *et al*, 2007	(31)

E2. DDR mutations in African-American patients.

Country	PC Group	Selected population	Germline or somatic	Definition	Period of data collection	Gene	% prevalence	n	Author, year	Ref-rences

			mutation							
USA	African American	African American	Somatic	Pathogenic and variant of unknown significance (VUS) mutations	NR	*BRCA2*	3.5	857	Petrovics *et al*, 2016	(84)
			Germline	DDR (*BRCA1* or *BRCA2*)	NR	DDR	3.7	857		

F. DDR mutations in patients with lethal PC.

Country	PC Group	Selected population	Germline or somatic mutation	Definition	Period of data collection	Gene	% prevalence	n	Author, yr	Ref-rences
Multinational	Lethal PC	Lethal PC	Germline	DNA repair gene mutation (no further definition)	NR	DDR	21.4	313	Na *et al*, 2017 (Linked: Na *et al*, 2017; Zheng *et al*, 2017; Na *et al*, 2016; Na *et al*, 2017	(106); (111); (112); (113); (77))

Appendix S5. Baseline characteristics.

Abida *et al*, 2017 (30)
USA
PC; mPC; mCRPC. Diagnosis: Histology Other details (Mixed population of locoregional (n=50); biochemically recurrent (n=53); metastatic (n=348))
Population (further details): unselected (NR)
Treatment (further details): NR (NR)
Total (n=451)
Mean age (SD): NR (NR) Median age (range): 61 (41, 84)
Ethnicity: White non-Hispanic (23.7); White Hispanic (0.7); White unknown (61.6); Black (5.3); Asian (1.6); Unknown (6.9); Other (0.2)
Gleason score: 6 (5.5); 7 (31.0); 8-10 (57.2); unknown (6.2)
AJCC stage: NR
TNM stage: M0 (75); M1 (24); Unknown MX (1)
ECOG score 0: NR 1: NR 0-1: NR ≥2: NR
Previous treatments: Surgery (57); ADT (23); Radiation +/- ADT (16); Other/Unknown (4)
Familial history of PC: NR

Mean years since diagnosis (SD): NR (NR) Median years since diagnosis (range): NR (NR)
Mean PSA ng/ml (SD): 9.1 (NR) Median PSA ng/ml (range): NR) (0.9, 11330)
Comments: Age and PSA are mean levels at diagnosis; 451 patients were included for somatic mutation analysis; 221 patients were included for germline mutation analysis
ADT, androgen deprivation therapy; AJCC, American Joint Committee on Cancer; CRPC, castration-resistant PC; ECOG, Eastern Cooperative Oncology Group; m, metastatic; NR, not reported; PC, prostate cancer; PSA, prostate-specific antigen; SD, standard deviation; TNM, Tumor Nodes Metastasis classification of malignant tumors.

Agalliu *et al*, 2007 (31)
USA
Other. Diagnosis: Histology Other details (early onset, <55 years)
Population (further details): unselected (NR)
Treatment (further details): NR (NR)
Total (n=290)
Mean age (SD): NR (NR) Median age (range): NR (NR)
Ethnicity: Caucasian (86.8); African American (11.4); Jewish (1.7)
Gleason score: 2-4 (6.6); 5-6 (52.1); 3+4 (27.2); 4+3 (6.9); 8-10 (5.5); Missing (1.7)
AJCC stage: NR
TNM stage: NR

ECOG score 0: NR 1: NR 0-1: NR ≥2: NR
Previous treatments: NR
Familial history of PC: 108 (37.3)
Mean years since diagnosis (SD): NR (NR) Median years since diagnosis (range): NR (NR)
Mean PSA ng/ml (SD): NR (NR) Median PSA ng/ml (range): NR) (NR)
Comments: 35-49 years (33.4%); 50-54 years (66.6%). PSA ng/ml: 0-3.9 (19); 4.0-9.9 (48.3); 10-19.9 (12.4); ≥20 (10.3); missing (10)
AJCC, American Joint Committee on Cancer; ECOG, Eastern Cooperative Oncology Group; NR, not reported; PC, prostate cancer; PSA, prostate-specific antigen; SD, standard deviation; TNM, Tumor Nodes Metastasis classification of malignant tumors.

Agalliu *et al*, 2009 (32)
USA
PC. Diagnosis: Reason for prostate cancer diagnosis: Abnormal PSA 741 (73.1), Abnormal DRE 123 (12.1), Symptoms 25 (2.5), TURP for BPH 15 (1.5), Other procedures 57 (5.6), Unknown 18 (1.8) Other details (NR)
Population (further details): Ashkenazi (NR)
Treatment (further details): NR (NR)
Total (n=979)

Mean age (SD): 69.4 (NR) Median age (range): NR (NR)
Ethnicity: Ashkenazi Jewish men (100)
Gleason score: 2-6 (63); 7 (25); 8-10 (12); unknown (8)
AJCC stage: NR
TNM stage: NR
ECOG score 0: NR 1: NR 0-1: NR ≥2: NR
Previous treatments: NR
Familial history of PC: 276 (28.2)
Mean years since diagnosis (SD): NR (NR) Median years since diagnosis (range): NR (NR)
Mean PSA ng/ml (SD): NR (NR) Median PSA ng/ml (range): NR) (NR)
Comments: familial history in column AO is only data on first-degree family history
AJCC, American Joint Committee on Cancer; ECOG, Eastern Cooperative Oncology Group; m, metastatic; NR, not reported; PC, prostate cancer; PSA, prostate-specific antigen; SD, standard deviation; TNM, Tumor Nodes Metastasis classification of malignant tumors.

Angele *et al*, 2004 (13)
UK

PC. Diagnosis: NR Other details (NR)
Population (further details): unselected (NR)
Treatment (further details): NR (NR)
Total (n=637)
Mean age (SD): NR (NR) Median age (range): NR (43, 86)
Ethnicity: Caucasian (100)
Gleason score: NR
AJCC stage: NR
TNM stage: NR
ECOG score 0: NR 1: NR 0-1: NR ≥2: NR
Previous treatments: NR
Familial history of PC: NR
Mean years since diagnosis (SD): NR (NR) Median years since diagnosis (range): NR (NR)
Mean PSA ng/ml (SD): NR (NR) Median PSA ng/ml (range): NR) (NR)

AJCC, American Joint Committee on Cancer; ECOG, Eastern Cooperative Oncology Group; NR, not reported; PC, prostate cancer; PSA, prostate-specific antigen; SD, standard deviation; TNM, Tumor Nodes Metastasis classification of malignant tumors.

Annala *et al*, 2017 (33)	
Canada	
PC. Diagnosis: NR Other details (NR)	
Population (further details): unselected (NR)	
Treatment (further details): Mixed (AR-directed therapies, including prostatectomy 7 (32%); external beam radiation 5 (23%); androgen deprivation 8 (36%); brachytherapy 2 (9%); docetaxel/cabazitaxel 9 (41%); enzalutamide 5 (23%); abiraterone 8 (36%); Other 0 (0%))	
DDR+ (n=22)	DDR- (n=113)
Mean age (SD): 63 (NR) Median age (range): NR (NR)	Mean age (SD): 64 (NR) Median age (range): NR (NR)
Ethnicity: NR	Ethnicity: NR
Gleason score: 6 (9); 7 (23); 8-10 (59); unknown (9)	Gleason score: 6 (5); 7 (19); 8-10 (68); unknown (8)
AJCC stage: NR	AJCC stage: NR
TNM stage: NR	TNM stage: NR
ECOG score 0: NR 1: NR 0-1: NR ≥2: NR	ECOG score 0: NR 1: NR 0-1: NR ≥2: NR
Previous treatments: NR	Previous treatments: NR

Familial history of PC: NR	Familial history of PC: NR
Mean years since diagnosis (SD): NR (NR) Median years since diagnosis (range): NR (NR)	Mean years since diagnosis (SD): NR (NR) Median years since diagnosis (range): NR (NR)
Mean PSA ng/ml (SD): 10.3 (NR) Median PSA ng/ml (range): NR) (NR)	Mean PSA ng/ml (SD): 27.2 (NR) Median PSA ng/ml (range): NR) (NR)
AJCC, American Joint Committee on Cancer; ECOG, AR, androgen receptor; Eastern Cooperative Oncology Group; NR, not reported; PC, prostate cancer; PSA, prostate-specific antigen; SD, standard deviation; TNM, Tumor Nodes Metastasis classification of malignant tumors.	

Antonarakis *et al*, 2018 (34)	
USA	
mCRPC. Diagnosis: Histologically confirmed prostate adenocarcinoma, progressive disease despite "castration levels" of serum testosterone (<50 ng/dl), and radiographic metastases on computed tomography (CT) or technetium-99 bone scans. Patients had to have three or more rising serum prostate-specific antigen (PSA) values measured ≥ 2 weeks apart. Other details (NR)	
Population (further details): treatment (enzalutamide or abiraterone)	
Treatment (further details): Enzalutamide was given at 160 mg daily, and abiraterone was given at 1000 mg daily (with prednisone 5 mg twice daily). (NR)	
DDR+ (n=22)	DDR- (n=150)
Mean age (SD): NR (NR) Median age (range): 64 (NR)	Mean age (SD): NR (NR) Median age (range): 70 (NR)
Ethnicity: White (86.4); non-white (13.6)	Ethnicity: White (87.3); non-white (12.7)
Gleason score: ≥8 (68.2)	Gleason score: ≥8 (65.2)
AJCC stage: NR	AJCC stage: NR
TNM stage: T1/T2 (21.1); T3/T4 (78.9); M1 (19.0)	TNM stage: T1/T2 (55.8); T3/T4 (44.2); M1 (26.1)

ECOG score 0: NR 1: NR 0-1: NR ≥2: NR	ECOG score 0: NR 1: NR 0-1: NR ≥2: NR
Previous treatments: chemotherapy (22.7)	Previous treatments: chemotherapy (23.3)
Familial history of PC: NR	Familial history of PC: NR
Mean years since diagnosis (SD): 6.3 (NR) Median years since diagnosis (range): NR (NR)	Mean years since diagnosis (SD): 7.4 (NR) Median years since diagnosis (range): NR (NR)
Mean PSA ng/ml (SD): NR (NR) Median PSA ng/ml (range): 22.9) (NR)	Mean PSA ng/ml (SD): NR (NR) Median PSA ng/ml (range): 22.6) (NR)
Comments: ECOG ≥1 (5.3)	Comments: ECOG ≥1 (32.1)
AJCC, American Joint Committee on Cancer; CRPC, castration-resistant PC; DDR, DNA damage repair; ECOG, Eastern Cooperative Oncology Group; m, metastatic; NR, not reported; PC, prostate cancer; PSA, prostate-specific antigen; SD, standard deviation; TNM, Tumor Nodes Metastasis classification of malignant tumors.	

Beltran *et al*, 2013 (22)
USA
Primary PC; mPC; CRPC. Diagnosis: Histology Other details (Localized PC, hormone-naïve mPC, and mCRPC)
Population (further details): unselected (NR)
Treatment (further details): NR (NR)
Total (n=45)

Mean age (SD): 63 (NR) Median age (range): NR (NR)
Ethnicity: NR
Gleason score: NR
AJCC stage: NR
TNM stage: NR
ECOG score 0: NR 1: NR 0-1: NR ≥2: NR
Previous treatments: NR
Familial history of PC: NR
Mean years since diagnosis (SD): NR (NR) Median years since diagnosis (range): NR (NR)
Mean PSA ng/ml (SD): NR (NR) Median PSA ng/ml (range): NR) (NR)
Comments: Mean age calculated based on 20 out of 45 patients in supplementary table 3
AJCC, American Joint Committee on Cancer; CRPC, castration-resistant PC; ECOG, Eastern Cooperative Oncology Group; m, metastatic; NR, not reported; PC, prostate cancer; PSA, prostate-specific antigen; SD, standard deviation; TNM, Tumor Nodes Metastasis classification of malignant tumors.

Beltran *et al*, 2015 (35)
USA
Primary PC; mPC. Diagnosis: Histology Other details (Mixed population of localized PC (n=69) and advanced mPC (n=29))
Population (further details): unselected (NR)
Treatment (further details): NR (NR)
Total (n=97)
Mean age (SD): NR (NR) Median age (range): NR (NR)
Ethnicity: NR
Gleason score: NR
AJCC stage: NR
TNM stage: NR
ECOG score 0: NR 1: NR 0-1: NR ≥2: NR
Previous treatments: NR
Familial history of PC: NR
Mean years since diagnosis (SD): NR (NR) Median years since diagnosis (range): ()

Mean PSA ng/ml (SD): NR (NR) Median PSA ng/ml (range): NR) (NR)
Comments: For a full text study with a comprehensive supplementary appendix, there was very little information on population (age, cancer scores, previous treatments, etc)
AJCC, American Joint Committee on Cancer; ECOG, Eastern Cooperative Oncology Group; m, metastatic; NR, not reported; PC, prostate cancer; PSA, prostate-specific antigen; SD, standard deviation; TNM, Tumor Nodes Metastasis classification of malignant tumors.

Boudadi *et al*, 2017 (36)
USA
Other. Diagnosis: Histologically or cytologically confirmed adenocarcinoma of the prostate; Metastatic disease as defined by 2 or more bone metastases confirmed by bone scintigraphy or radiographic soft tissue metastasis; detectable circulating tumor cells (CTCs) with detectable AR-V7 splice-variant by reverse transcriptase (RT)-polymerase chain reaction (PCR). Other details (androgen receptor-variant-7 positive mCRPC)
Population (further details): unselected (NR)
Treatment (further details): Nivolumab and ipilimumab (Nivolumab 3 mg/kg IV over 60 minutes and ipilimumab 1 mg/kg IV over 90 minutes every 3 weeks for 12 weeks. Patients then receive maintenance nivolumab 3 mg/kg IV over 60 minutes every 2 weeks for 36 weeks in the absence of disease progression or unacceptable)
Total (n=15)
Mean age (SD): NR (NR) Median age (range): 65 (NR)
Ethnicity: NR
Gleason score: NR
AJCC stage: NR
TNM stage: NR

ECOG score 0: NR 1: NR 0-1: NR ≥2: NR
Previous treatments: ≥4 prior treatment for mCRPC (60)
Familial history of PC: NR
Mean years since diagnosis (SD): NR (NR) Median years since diagnosis (range): NR (NR)
Mean PSA ng/ml (SD): NR (NR) Median PSA ng/ml (range): 115) (NR)
Comments: Median follow-up 8.4 months (range: 1.9, 10.5 months)
AJCC, American Joint Committee on Cancer; CRPC, castration-resistant PC; ECOG, Eastern Cooperative Oncology Group; m, metastatic; IV, intravenous; NR, not reported; PC, prostate cancer; PSA, prostate-specific antigen; SD, standard deviation; TNM, Tumor Nodes Metastasis classification of malignant tumors.

Browning *et al*, 2006 (14)
USA
PC. Diagnosis: Histology Other details (NR)
Population (further details): unselected (NR)
Treatment (further details): NR (NR)
Total (n=98)

Mean age (SD): NR (NR) Median age (range): 63 (40, 81)
Ethnicity: White (100)
Gleason score: ≤6 (63.3); >6 (36.7)
AJCC stage: I (9.2); II (68.4); III (22.4)
TNM stage: NR
ECOG score 0: NR 1: NR 0-1: NR ≥2: NR
Previous treatments: radical prostatectomy (100)
Familial history of PC: NR
Mean years since diagnosis (SD): NR (NR) Median years since diagnosis (range): NR (NR)
Mean PSA ng/ml (SD): ≤4 ng/ml (17.3%); 4-10 ng/ml (53.1); ≥10 ng/ml (29.6) (NR) Median PSA ng/ml (range): NR) (NR)
AJCC, American Joint Committee on Cancer; ECOG, Eastern Cooperative Oncology Group; NR, not reported; PC, prostate cancer; PSA, prostate-specific antigen; SD, standard deviation; TNM, Tumor Nodes Metastasis classification of malignant tumors.

The Cancer Genome Atlas, 2015 (37)
Multinational

PC. Diagnosis: Histology Other details (NR)
Population (further details): unselected (NR)
Treatment (further details): radical prostatectomy (NR)
Total (n=333)
Mean age (SD): NR (NR) Median age (range): 61 (43, 76)
Ethnicity: Caucasian (81.1); African descent (12.9); Asian (2.4); NR (3.6)
Gleason score: 3+3 (19.5); 3+4 (30.6); 4+3 (23.4); ≥8 (26.4)
AJCC stage: NR
TNM stage: NR
ECOG score 0: NR 1: NR 0-1: NR ≥2: NR
Previous treatments: radical prostatectomy
Familial history of PC: NR
Mean years since diagnosis (SD): NR (NR) Median years since diagnosis (range): NR (NR)
Mean PSA ng/ml (SD): 7.4 (NR) Median PSA ng/ml (range): NR) (1.6, 87)

AJCC, American Joint Committee on Cancer; ECOG, Eastern Cooperative Oncology Group; NR, not reported; PC, prostate cancer; PSA, prostate-specific antigen; SD, standard deviation; TNM, Tumor Nodes Metastasis classification of malignant tumors.

Castro *et al*, 2011 (38)			
UK			
PC. Diagnosis: NR Other details (NR)			
Population (further details): unselected (NR)			
Treatment (further details): NR (NR)			
Total (n=2181)	*BRCA1*+ (n=5)	*BRCA2*+ (n=34)	DDR- (n=2142)
Mean age (SD): NR (NR) Median age (range): 57 (32, 89)	Mean age (SD): NR (NR) Median age (range): NR (NR)	Mean age (SD): NR (NR) Median age (range): NR (NR)	Mean age (SD): NR (NR) Median age (range): NR (NR)
Ethnicity: NR	Ethnicity: NR	Ethnicity: NR	Ethnicity: NR
Gleason score: NR	Gleason score: ≥8 (20)	Gleason score: ≥8 (50)	Gleason score: ≥8 (21)
AJCC stage: NR	AJCC stage: NR	AJCC stage: NR	AJCC stage: NR
TNM stage: NR	TNM stage: N1 (50); M1 (20)	TNM stage: N1 (35); M1 (21)	TNM stage: N1 (11); M1 (9)
ECOG score 0: NR 1: NR 0-1: NR ≥2: NR	ECOG score 0: NR 1: NR 0-1: NR ≥2: NR	ECOG score 0: NR 1: NR 0-1: NR ≥2: NR	ECOG score 0: NR 1: NR 0-1: NR ≥2: NR
Previous treatments: NR	Previous treatments: NR	Previous treatments: NR	Previous treatments: NR
Familial history of PC: NR	Familial history of PC: NR	Familial history of PC: NR	Familial history of PC: NR

Mean years since diagnosis (SD): NR (NR) Median years since diagnosis (range): NR (NR)	Mean years since diagnosis (SD): NR (NR) Median years since diagnosis (range): NR (NR)	Mean years since diagnosis (SD): NR (NR) Median years since diagnosis (range): NR (NR)	Mean years since diagnosis (SD): NR (NR) Median years since diagnosis (range): NR (NR)
Mean PSA ng/ml (SD): NR (NR) Median PSA ng/ml (range): NR) (NR)	Mean PSA ng/ml (SD): NR (NR) Median PSA ng/ml (range): NR) (NR)	Mean PSA ng/ml (SD): NR (NR) Median PSA ng/ml (range): NR) (NR)	Mean PSA ng/ml (SD): NR (NR) Median PSA ng/ml (range): NR) (NR)
Comments: details for *BRCA1*, *BRCA2*, and non-carriers	Comments: details for *BRCA1*, *BRCA2*, and non-carriers	Comments: details for *BRCA1*, *BRCA2*, and non-carriers	Comments: details for *BRCA1*, *BRCA2*, and non-carriers
AJCC, American Joint Committee on Cancer; *BRCA*, breast cancer susceptibility gene; ECOG, Eastern Cooperative Oncology Group; IV, intravenous; NR, not reported; PC, prostate cancer; PSA, prostate-specific antigen; SD, standard deviation; TNM, Tumor Nodes Metastasis classification of malignant tumors.			

Castro *et al*, 2013 (39)			
UK			
PC. Diagnosis: Histology Other details (NR)			
Population (further details): unselected (NR)			
Treatment (further details): Mixed treatment Primary radical treatment in non-metastatic disease: External-beam radiotherapy (35.4%), Radical prostatectomy (33.8%), Brachytherapy (3.1%), Any local radical treatment (72.3%). Primary hormone treatment indication for early disease: Neoadjuvant-adjuvant (35.9%), Single therapy (6.3%). Primary hormone treatment indication for advanced disease: Palliative (55.4%). Other treatments for metastatic disease: chemotherapy (17.1%).			
DDR+ (n=79)	*BRCA1*+ (n=18)	*BRCA2*+ (n=61)	DDR- (n=1940)

Mean age (SD): NR (NR) Median age (range): 58.3 (41.7, 88)	Mean age (SD): NR (NR) Median age (range): 60.8 (48.3, 73.5)	Mean age (SD): NR (NR) Median age (range): 57.6 (41.7, 88)	Mean age (SD): NR (NR) Median age (range): 57.2 (32.3, 88.9)
Ethnicity: NR	Ethnicity: NR	Ethnicity: NR	Ethnicity: NR
Gleason score: ≤6 (25.3); 7 (24.1); 8-10 (35.4); unknown=(15.2)	Gleason score: ≤6 (33.3); 7 (22.2); 8-10 (27.8); unknown=(16.7)	Gleason score: ≤6 (23.0); 7 (24.6); 8-10 (37.7); unknown=(14.8)	Gleason score: ≤6 (37.8); 7 (26.3); 8-10 (15.4); unknown=(20.5)
AJCC stage: I (10.1); IIa (11.4); IIb (16.5); III (16.5); IV (27.8); not assessed (17.7)	AJCC stage: I (11.1); IIa (5.6); IIb (16.7); III (22.2); IV (16.7); not assessed (27.8)	AJCC stage: I (9.8); IIa (13.1); IIb (16.4); III (18.1); IV (31.1); not assessed (11.5)	AJCC stage: I (19.2); IIa (16.8); IIb (11.0); III (18.9); IV (12.8); not assessed (21.3)
TNM stage: NR	TNM stage: NR	TNM stage: NR	TNM stage: NR
ECOG score 0: NR 1: NR 0-1: NR ≥2: NR	ECOG score 0: NR 1: NR 0-1: NR ≥2: NR	ECOG score 0: NR 1: NR 0-1: NR ≥2: NR	ECOG score 0: NR 1: NR 0-1: NR ≥2: NR
Previous treatments: NR	Previous treatments: NR	Previous treatments: NR	Previous treatments: NR
Familial history of PC: NR	Familial history of PC: NR	Familial history of PC: NR	Familial history of PC: NR
Mean years since diagnosis (SD): NR (NR) Median years since diagnosis (range): NR (NR)	Mean years since diagnosis (SD): NR (NR) Median years since diagnosis (range): NR (NR)	Mean years since diagnosis (SD): NR (NR) Median years since diagnosis (range): NR (NR)	Mean years since diagnosis (SD): NR (NR) Median years since diagnosis (range): NR (NR)
Mean PSA ng/ml (SD): NR (NR) Median PSA ng/ml (range): 11.5) (0.5, 3000)	Mean PSA ng/ml (SD): NR (NR) Median PSA ng/ml (range): 8.9) (0.7, 3000)	Mean PSA ng/ml (SD): NR (NR) Median PSA ng/ml (range): 15.1) (0.5, 761)	Mean PSA ng/ml (SD): NR (NR) Median PSA ng/ml (range): 11.3) (0.2, 7800)

Comments: TNM reported separately	Comments: TNM reported separately	Comments: TNM reported separately	Comments: TNM reported separately
AJCC, American Joint Committee on Cancer; DDR, DNA damage repair; ECOG, Eastern Cooperative Oncology Group; m, metastatic; NR, not reported; PC, prostate cancer; PSA, prostate-specific antigen; SD, standard deviation; TNM, Tumor Nodes Metastasis classification of malignant tumors.			

Castro *et al*, 2015 (40)	
UK	
Primary PC. Diagnosis: Histology Other details (NR)	
Population (further details): unselected (NR)	
Treatment (further details): radical prostatectomy (NR)	
DDR+ (n=35)	DDR- (n=500)
Mean age (SD): NR (NR) Median age (range): 58.7 (47.1, 65.3)	Mean age (SD): NR (NR) Median age (range): 56.9 (36.9, 85.8)
Ethnicity: NR	Ethnicity: NR
Gleason score: ≤6 (42.9); 7 (28.6); 8-10 (25.7); unknown=(2.9)	Gleason score: ≤6 (56.8); 7 (32.2); 8-10 (8.8); unknown (2.2)
AJCC stage: I (11.4); IIa (22.9); IIb (42.9); III (17.1); IV (5.7)	AJCC stage: I (34.2); IIa (35.4); IIb (12.6); III (15.8); IV (2.0)
TNM stage: NR	TNM stage: NR

ECOG score 0: NR 1: NR 0-1: NR ≥2: NR	ECOG score 0: NR 1: NR 0-1: NR ≥2: NR
Previous treatments: ADT (14.3)	Previous treatments: ADT (8.8)
Familial history of PC: NR	Familial history of PC: NR
Mean years since diagnosis (SD): NR (NR) Median years since diagnosis (range): NR (NR)	Mean years since diagnosis (SD): NR (NR) Median years since diagnosis (range): NR (NR)
Mean PSA ng/ml (SD): NR (NR) Median PSA ng/ml (range): 6) (0.5, 29.1)	Mean PSA ng/ml (SD): NR (NR) Median PSA ng/ml (range): 7.6) (0.7, 138.9)
ADT, androgen deprivation therapy; AJCC, American Joint Committee on Cancer; DDR, DNA damage repair; ECOG, Eastern Cooperative Oncology Group; NR, not reported; PC, prostate cancer; PSA, prostate-specific antigen; SD, standard deviation; TNM, Tumor Nodes Metastasis classification of malignant tumors; UK, United Kingdom.	

Castro *et al*, 2015 (40)	
UK	
Primary PC. Diagnosis: Histology Other details (NR)	
Population (further details): unselected (NR)	
Treatment (further details): external-beam radiotherapy (NR)	
DDR+ (n=32)	DDR- (n=735)

Mean age (SD): NR (NR) Median age (range): 59.3 (46.0, 77.5)	Mean age (SD): NR (NR) Median age (range): 57.3 (36.0, 79.0)
Ethnicity: NR	Ethnicity: NR
Gleason score: ≤6 (21.9); 7 (34.4); 8-10 (43.8); unknown (0)	Gleason score: ≤6 (44.1); 7 (35.1); 8-10 (18.5); unknown (2.3)
AJCC stage: I (12.5); IIa (6.3); IIb (18.8); III (37.5); IV (25.0)	AJCC stage: I (19.7); IIa (19.3); IIb (22.0); III (33.5); IV (5.4)
TNM stage: NR	TNM stage: NR
ECOG score 0: NR 1: NR 0-1: NR ≥2: NR	ECOG score 0: NR 1: NR 0-1: NR ≥2: NR
Previous treatments: ADT (84.4)	Previous treatments: ADT (77.7)
Familial history of PC: NR	Familial history of PC: NR
Mean years since diagnosis (SD): NR (NR) Median years since diagnosis (range): NR (NR)	Mean years since diagnosis (SD): NR (NR) Median years since diagnosis (range): NR (NR)
Mean PSA ng/ml (SD): NR (NR) Median PSA ng/ml (range): 19.4) (2.1, 68.5)	Mean PSA ng/ml (SD): NR (NR) Median PSA ng/ml (range): 13.9) (1.2, 143.0)
ADT, androgen deprivation therapy; AJCC, American Joint Committee on Cancer; DDR, DNA damage repair; ECOG, Eastern Cooperative Oncology Group; NR, not reported; PC, prostate cancer; PSA, prostate-specific antigen; SD, standard deviation; TNM, Tumor Nodes Metastasis classification of malignant tumors.	

Cesaretti *et al*, 2007 (41)
USA

PC. Diagnosis: Biopsy and Histology Other details (Patients were staged according to the 1992 American Joint Committee on Cancer standard and had biopsy-proven prostatic adenocarcinoma)
Population (further details): treatment (Brachytherapy)
Treatment (further details): Brachytherapy (125I implant, a 103Pd implant, or the combination of external beam radiotherapy with a 103Pd implant)
Total (n=108)
Mean age (SD): NR (NR) Median age (range): 64 (46, 79)
Ethnicity: NR
Gleason score: 5 (5); 6 (81); 7 (12); 8-10 (3)
AJCC stage: NR
TNM stage: T1b (1); T1c (59); T2a (20); T2b (15); T2c (4); T recurrent after 70 Gy in 1996 (1)
ECOG score 0: NR 1: NR 0-1: NR ≥2: NR
Previous treatments: NR
Familial history of PC: NR
Mean years since diagnosis (SD): NR (NR) Median years since diagnosis (range): NR (NR)

Mean PSA ng/ml (SD): NR (NR) Median PSA ng/ml (range): 6.1) (0.8, 41)
AJCC, American Joint Committee on Cancer; ECOG, Eastern Cooperative Oncology Group; NR, not reported; PC, prostate cancer; PSA, prostate-specific antigen; SD, standard deviation; TNM, Tumor Nodes Metastasis classification of malignant tumors.

Cheng *et al*, 2011 (23)
Australia
PC. Diagnosis: Histology Other details (NR)
Population (further details): familial (PC patients from familial breast cancer families)
Treatment (further details): NR (NR)
Total (n=147)
Mean age (SD): NR (NR) Median age (range): NR (NR)
Ethnicity: NR
Gleason score: NR
AJCC stage: NR
TNM stage: NR
ECOG score 0: NR 1: NR 0-1: NR ≥2: NR

Previous treatments: NR
Familial history of PC: NR
Mean years since diagnosis (SD): NR (NR) Median years since diagnosis (range): NR (NR)
Mean PSA ng/ml (SD): NR (NR) Median PSA ng/ml (range): NR) (NR)
Comments: Data apparently recorded but not presented in abstract
AJCC, American Joint Committee on Cancer; ECOG, Eastern Cooperative Oncology Group; NR, not reported; PC, prostate cancer; PSA, prostate-specific antigen; SD, standard deviation; TNM, Tumor Nodes Metastasis classification of malignant tumors.

Chi *et al*, 2017 (42)
Canada
mCRPC. Diagnosis: Biopsy histology; PSA; bone or CT scan Other details (NR)
Population (further details): unselected (NR)
Treatment (further details): Mixed (Abiraterone [Abi] acetate 1000 mg PO OD with prednisone 5 mg PO BID or 10 mg OD as per standard of care, or until PSA progression then cross-over to ENZ; enzalutamide 160 mg PO OD as per standard of care, or until PSA progression then cross-over to Abi)
Total (n=NR)
Mean age (SD): NR (NR) Median age (range): 75 (49, 74)
Ethnicity: NR
Gleason score: NR

AJCC stage: NR
TNM stage: NR
ECOG score 0: NR 1: NR 0-1: NR (83) ≥2: NR
Previous treatments: None
Familial history of PC: NR
Mean years since diagnosis (SD): NR (NR) Median years since diagnosis (range): NR (NR)
Mean PSA ng/ml (SD): 36.1 (NR) Median PSA ng/ml (range): NR) (1.7, 2817)
AJCC, American Joint Committee on Cancer; BID, twice daily; CRPC, castration-resistant PC; CT, computed tomography; ECOG, Eastern Cooperative Oncology Group; NR, not reported; OD, once daily; PC, prostate cancer; PO, per oral; PSA, prostate-specific antigen; SD, standard deviation; TNM, Tumor Nodes Metastasis classification of malignant tumors.

Dall'Era *et al*, 2017 (8)
USA
Primary PC; mPC. Diagnosis: NR Other details (NR)
Population (further details): treatment (NR)
Treatment (further details): NR (NR)

Total (n=936)
Mean age (SD): NR (NR) Median age (range): NR (NR)
Ethnicity: NR
Gleason score: NR
AJCC stage: NR
TNM stage: NR
ECOG score 0: NR 1: NR 0-1: NR ≥2: NR
Previous treatments: NR
Familial history of PC: NR
Mean years since diagnosis (SD): NR (NR) Median years since diagnosis (range): NR (NR)
Mean PSA ng/ml (SD): NR (NR) Median PSA ng/ml (range): NR) (NR)
Comments: Very limited patient characteristics provided
AJCC, American Joint Committee on Cancer; ECOG, Eastern Cooperative Oncology Group; m, metastatic; NR, not reported; PC, prostate cancer; PSA, prostate-specific antigen; SD, standard deviation; TNM, Tumor Nodes Metastasis classification of malignant tumors; USA, United States of America.

Damaraju *et al*, 2006 (26)
Canada
Primary PC. Diagnosis: Biopsy with T classification, staging bone scan and CT scan Other details (NR)
Population (further details): treatment (3-DCRT)
Treatment (further details): 3-DCRT (The clinical target volume (prostatic tissue containing biopsy-proven adenocarcinoma or its suspected microscopic extensions) received a mean dose of 77.1 Gy (range, 68.3-82.1 Gy) in five daily fractions per week. The number of fractions ranged from 35 to to 44, and in all patients, the planning target volume received a minimum dose per fraction of 1.8 to 2 Gy. Pelvic lymph nodes were not treated by intention in any patient).
Total (n=83)
Mean age (SD): 67 (NR) Median age (range): NR (45, 78)
Ethnicity: Caucasian (86%); Caucasian French-Canadian (7%); Aboriginal (4%); Pacific Asian (2%); Afro-Caribbean (1%)
Gleason score: NR
AJCC stage: NR
TNM stage: T1 (22); T2 (53); T3 (24); Tx (1)
ECOG score 0: NR 1: NR 0-1: NR ≥2: NR
Previous treatments: Abdominopelvic surgery (n=30; 36%); neoadjuvant hormone therapy (n=35; 42%; adjuvant hormone therapy (n=6; 7%).
Familial history of PC: NR

Mean years since diagnosis (SD): NR (NR) Median years since diagnosis (range): NR (NR)
Mean PSA ng/ml (SD): 11.8 (NR) Median PSA ng/ml (range): NR) (0.2, 74.0)
AJCC, American Joint Committee on Cancer; CT, computed tomography; ECOG, Eastern Cooperative Oncology Group; NR, not reported; PC, prostate cancer; PSA, prostate-specific antigen; SD, standard deviation; TNM, Tumor Nodes Metastasis classification of malignant tumors; 3-DCRT, three dimensional conformational radiation therapy.

Daniel *et al*, 2017 (9)
USA
mCRPC. Diagnosis: NR Other details (predominantly relapsed, refractory or metastatic prostate carcinoma (mPC + CRPC + mCRPC))
Population (further details): unselected (NR)
Treatment (further details): NR (NR)
Total (n=1911)
Mean age (SD): NR (NR) Median age (range): NR (NR)
Ethnicity: NR
Gleason score: NR
AJCC stage: NR
TNM stage: NR

ECOG score 0: NR 1: NR 0-1: NR ≥2: NR
Previous treatments: NR
Familial history of PC: NR
Mean years since diagnosis (SD): NR (NR) Median years since diagnosis (range): NR (NR)
Mean PSA ng/ml (SD): NR (NR) Median PSA ng/ml (range): NR) (NR)
Comments: no details
AJCC, American Joint Committee on Cancer; CRPC, castration-resistant PC; ECOG, Eastern Cooperative Oncology Group; m, metastatic; NR, not reported; PC, prostate cancer; PSA, prostate-specific antigen; SD, standard deviation; TNM, Tumor Nodes Metastasis classification of malignant tumors; USA, United States of America.

Dawson *et al*, 2016 (11)
USA
PC. Diagnosis: NR Other details (NR)
Population (further details): unselected (NR)
Treatment (further details): NR (NR)
Total (n=437)

Mean age (SD): NR (NR) Median age (range): 67 (NR)
Ethnicity: NR
Gleason score: NR
AJCC stage: NR
TNM stage: NR
ECOG score 0: NR 1: NR 0-1: NR ≥2: NR
Previous treatments: NR
Familial history of PC: NR
Mean years since diagnosis (SD): NR (NR) Median years since diagnosis (range): NR (NR)
Mean PSA ng/ml (SD): NR (NR) Median PSA ng/ml (range): NR) (NR)
AJCC, American Joint Committee on Cancer; ECOG, Eastern Cooperative Oncology Group; NR, not reported; PC, prostate cancer; PSA, prostate-specific antigen; SD, standard deviation; TNM, Tumor Nodes Metastasis classification of malignant tumors; USA, United States of America.

Decker *et al*, 2016 (43)
Multinational

PC and mCRPC. Diagnosis: Histology Other details (NR)		
Population (further details): unselected (NR)		
Treatment (further details): radical prostatectomy or NR (NR)		
PC USA (n=10)	PC Multinational (Australia; USA) (n=50)	mCRPC Multinational (USA, UK, Israel) (n=150)
Mean age (SD): 63.6 (NR) Median age (range): NR (54, 77)	Mean age (SD): NR (NR) Median age (range): NR (NR)	Mean age (SD): NR (NR) Median age (range): NR (NR)
Ethnicity: European descent (100)	Ethnicity: NR	Ethnicity: NR
Gleason score: 7 (10); 8 (20); 9 (60); 10 (10)	Gleason score: <7 (70); 8-10 (22); NR (8)	Gleason score: NR
AJCC stage: NR	AJCC stage: NR	AJCC stage: NR
TNM stage: NR	TNM stage: NR	TNM stage: NR
ECOG score 0: NR 1: NR 0-1: NR ≥2: NR	ECOG score 0: NR 1: NR 0-1: NR ≥2: NR	ECOG score 0: NR 1: NR 0-1: NR ≥2: NR
Previous treatments: radical prostatectomy (100)	Previous treatments: treatment naïve (100)	Previous treatments: NR
Familial history of PC: 2 (20)	Familial history of PC: NR	Familial history of PC: NR
Mean years since diagnosis (SD): NR (NR) Median years since diagnosis (range): NR (NR)	Mean years since diagnosis (SD): NR (NR) Median years since diagnosis (range): NR (NR)	Mean years since diagnosis (SD): NR (NR) Median years since diagnosis (range): NR (NR)

Mean PSA ng/ml (SD): 11.6 (NR) Median PSA ng/ml (range): NR) (4.4, 22.3)	Mean PSA ng/ml (SD): NR (NR) Median PSA ng/ml (range): NR) (NR)	Mean PSA ng/ml (SD): NR (NR) Median PSA ng/ml (range): NR) (NR)
Comments: Original study cohort of ten patients from the Mayo clinic	Comments: Reference study of 50 patients from Baca et al	Comments: Second reference study of 150 patients from Robinson et al
AJCC, American Joint Committee on Cancer; CRPC, castration-resistant PC; ECOG, Eastern Cooperative Oncology Group; m, metastatic; IV, intravenous; NR, not reported; PC, prostate cancer; PSA, prostate-specific antigen; SD, standard deviation; TNM, Tumor Nodes Metastasis classification of malignant tumors; UK, United Kingdom; USA, United States of America.		

Edwards *et al*, 2003 (44)
UK
Other. Diagnosis: <55, no further details Other details (Young onset)
Population (further details): unselected (NR)
Treatment (further details): NR (NR)
Total (n=263)
Mean age (SD): 51 (NR) Median age (range): NR (32, 55)
Ethnicity: White (96); Black African/Caribbean (4)
Gleason score: NR
AJCC stage: NR
TNM stage: NR

ECOG score 0: NR 1: NR 0-1: NR ≥2: NR
Previous treatments: NR
Familial history of PC: NR
Mean years since diagnosis (SD): NR (NR) Median years since diagnosis (range): NR (NR)
Mean PSA ng/ml (SD): NR (NR) Median PSA ng/ml (range): NR) (NR)
AJCC, American Joint Committee on Cancer; ECOG, Eastern Cooperative Oncology Group; NR, not reported; PC, prostate cancer; PSA, prostate-specific antigen; SD, standard deviation; TNM, Tumor Nodes Metastasis classification of malignant tumors; UK, United Kingdom.

Evans *et al*, 2016 (45)			
USA			
PC. Diagnosis: NR Other details (high risk)			
Population (further details): unselected (NR)			
Treatment (further details): radical prostatectomy (NR)			
Mayo discovery (n=545)	Mayo validation (n=232)	Cleveland clinic (n=130)	Thomas Jefferson University (n=183)

Mean age (SD): 65.3 (6.4) Median age (range): NR (NR)	Mean age (SD): 63.1 (7.4) Median age (range): NR (NR)	Mean age (SD): 61.6 (6.3) Median age (range): NR (NR)	Mean age (SD): 60 (7) Median age (range): NR (NR)
Ethnicity: NR	Ethnicity: NR	Ethnicity: NR	Ethnicity: NR
Gleason score: 6 (11); 7 (49); 8 (13); 9 (24); 10 (2); NA (1)	Gleason score: 6 (7); 7 (50); 8 (17); 9 (25); 10 (1); NA (1)	Gleason score: 6 (17); 7 (62); 8 (13); 9 (12); 10 (0); NA (0)	Gleason score: 6 (13); 7 (57); 8 (17); 9 (10); 10 (1.5); NA (1.5)
AJCC stage: I (0); II (40): III (46); IV (0); NA (13)	AJCC stage: I (0); II (42); III (44); IV (0); NA (14)	AJCC stage: NA (100)	AJCC stage: I (0); II (8); III (87); IV (5); NA (0)
TNM stage: NR	TNM stage: NR	TNM stage: NR	TNM stage: NR
ECOG score 0: NR 1: NR 0-1: NR ≥2: NR	ECOG score 0: NR 1: NR 0-1: NR ≥2: NR	ECOG score 0: NR 1: NR 0-1: NR ≥2: NR	ECOG score 0: NR 1: NR 0-1: NR ≥2: NR
Previous treatments: NR	Previous treatments: NR	Previous treatments: NR	Previous treatments: NR
Familial history of PC: NR	Familial history of PC: NR	Familial history of PC: NR	Familial history of PC: NR
Mean years since diagnosis (SD): NR (NR) Median years since diagnosis (range): NR (NR)	Mean years since diagnosis (SD): NR (NR) Median years since diagnosis (range): NR (NR)	Mean years since diagnosis (SD): NR (NR) Median years since diagnosis (range): NR (NR)	Mean years since diagnosis (SD): NR (NR) Median years since diagnosis (range): NR (NR)
Mean PSA ng/ml (SD): NR (NR) Median PSA ng/ml (range): NR) (<10 (52); 10-20 (22); >20 (24); NA (3))	Mean PSA ng/ml (SD): NR (NR) Median PSA ng/ml (range): NR) (<10 (54); 10-20 (27); >20 (19); NA (0))	Mean PSA ng/ml (SD): NR (NR) Median PSA ng/ml (range): NR) (<10 (69); 10-20 (23); >20 (7); NA (1))	Mean PSA ng/ml (SD): NR (NR) Median PSA ng/ml (range): NR) (<10 (64); 10-20 (19); >20 (11); NA (5))

AJCC, American Joint Committee on Cancer; ECOG, Eastern Cooperative Oncology Group; NA, not available; NR, not reported; PC, prostate cancer; PSA, prostate-specific antigen; SD, standard deviation; TNM, Tumor Nodes Metastasis classification of malignant tumors; USA, United States of America.

Fachal *et al*, 2012 (46)
Spain
PC. Diagnosis: NR Other details (NR)
Population (further details): treatment (Three-dimensional conformational radiotherapy (3D-CRT))
Treatment (further details): Three-dimensional conformational radiotherapy (3D-CRT) (1.8-2 Gy/fraction)
Total (n=698)
Mean age (SD): 71 (NR) Median age (range): NR (47, 86)
Ethnicity: NR
Gleason score: 2-4 (10.03); 5-6 (51.58); 7 (26.65); 8-10 (10.17); missing (1.58)
AJCC stage: NR
TNM stage: ≤cT2a (33.1); cT2b (22.4); cT2c (15.5); cT3 (8.3); cT4 (1); recurrent (18.9); Missing (0.9)
ECOG score 0: NR 1: NR 0-1: NR ≥2: NR
Previous treatments: radiotherapy; prostatectomy (15.9%)

Familial history of PC: NR
Mean years since diagnosis (SD): NR (NR) Median years since diagnosis (range): NR (NR)
Mean PSA ng/ml (SD): 15.95 (NR) Median PSA ng/ml (range): NR) (0.63, 236)
Comments: patients with radical radiotherapy received a total dose for the PTV I that ranged from 70 to 76 Gy, as well as 56 Gy for the PTV II and 46 Gy for PTV III
AJCC, American Joint Committee on Cancer; ECOG, Eastern Cooperative Oncology Group; NR, not reported; PC, prostate cancer; PSA, prostate-specific antigen; SD, standard deviation; PTV, planning target volume; TNM, Tumor Nodes Metastasis classification of malignant tumors.

Feldman *et al*, 2014 (10)
USA
PC. Diagnosis: Histology Other details (NR)
Population (further details): unselected (NR)
Treatment (further details): NR (NR)
Total (n=330)
Mean age (SD): NR (NR) Median age (range): NR (NR)
Ethnicity: NR
Gleason score: NR
AJCC stage: NR

TNM stage: NR
ECOG score 0: NR 1: NR 0-1: NR ≥2: NR
Previous treatments: NR
Familial history of PC: NR
Mean years since diagnosis (SD): NR (NR) Median years since diagnosis (range): NR (NR)
Mean PSA ng/ml (SD): NR (NR) Median PSA ng/ml (range): NR) (NR)
Comments: no details
AJCC, American Joint Committee on Cancer; ECOG, Eastern Cooperative Oncology Group; NR, not reported; PC, prostate cancer; PSA, prostate-specific antigen; SD, standard deviation; TNM, Tumor Nodes Metastasis classification of malignant tumors.

Fontugne *et al*, 2015 (47)
Multinational
PC. Diagnosis: NR Other details (Mixed population of patients with a spectrum of localized and advanced PC)
Population (further details): unselected (NR)
Treatment (further details): NR (NR)
Total (n=51)

Mean age (SD): NR (NR) Median age (range): NR (NR)
Ethnicity: NR
Gleason score: NR
AJCC stage: NR
TNM stage: NR
ECOG score 0: NR 1: NR 0-1: NR ≥2: NR
Previous treatments: NR
Familial history of PC: NR
Mean years since diagnosis (SD): NR (NR) Median years since diagnosis (range): NR (NR)
Mean PSA ng/ml (SD): NR (NR) Median PSA ng/ml (range): NR) (NR)
Comments: 69 tumors from 51 patients analyzed
AJCC, American Joint Committee on Cancer; ECOG, Eastern Cooperative Oncology Group; NR, not reported; PC, prostate cancer; PSA, prostate-specific antigen; SD, standard deviation; TNM, Tumor Nodes Metastasis classification of malignant tumors.

Gallagher *et al*, 2012 (48)
USA

CRPC. Diagnosis: Pathology Other details (NR)	
Population (further details): Ashkenazi (NR)	
Treatment (further details): Mixed treatment (For the total population, treatment was reported for 76 taxanes based therapies: single-agent docetaxel (n=33 patients), docetaxel + estramustine (17 patients), docetaxel + samarium (five patients), docetaxel + bevacizumab (four patients), docetaxel + 17AAG (two patients), docetaxel + DN-101 (two patients), docetaxel + carboplatin (one patient), docetaxel + traztusumab (one patient), docetaxel + cyclophosphamide (one patient), paclitaxel (three patients), paclitaxel + carboplatin + estramustine (six patients) and paclitaxel + estramustine (one patient).	
DDR+ (n=7)	DDR- (n=81)
Mean age (SD): NR (NR) Median age (range): 72 (59, 82)	Mean age (SD): NR (NR) Median age (range): 75 (69, 79)
Ethnicity: Jewish (100)	Ethnicity: Jewish (100)
Gleason score: ≤ 6 (14); 7 (43); 8 (0); 9 (44); unknown (0)	Gleason score: ≤ 6 (16); 7 (35); 8 (23); 9 (23); unknown (2)
AJCC stage: NR	AJCC stage: NR
TNM stage: T1 (14); T2 (43); T3 (29); T4 (0); unknown (14)	TNM stage: T1 (14); T2 (26); T3 (27); T4 (4); unknown (30)
ECOG score 0: NR 1: NR 0-1: NR ≥2: NR	ECOG score 0: NR 1: NR 0-1: NR ≥2: NR
Previous treatments: Prostatectomy (43); Radiotherapy alone (14); Radiotherapy + ADT (29); Hormones alone (14); Watchful waiting (0); Chemotherapy (0)	Previous treatments: Prostatectomy (48); Radiotherapy alone (27); Radiotherapy + ADT (15); Hormones alone (9); Watchful waiting (4); Chemotherapy (1)
Familial history of PC: NR	Familial history of PC: NR

Mean years since diagnosis (SD): NR (NR) Median years since diagnosis (range): NR (NR)	Mean years since diagnosis (SD): NR (NR) Median years since diagnosis (range): NR (NR)
Mean PSA ng/ml (SD): NR (NR) Median PSA ng/ml (range): 199 (3, 811)	Mean PSA ng/ml (SD): NR (NR) Median PSA ng/ml (range): 73 (18, 262)
ADT, androgen deprivation therapy; AJCC, American Joint Committee on Cancer; CRPC, castration-resistant PC: ECOG, Eastern Cooperative Oncology Group; NR, not reported; PC, prostate cancer; PSA, prostate-specific antigen; SD, standard deviation; TNM, Tumor Nodes Metastasis classification of malignant tumors; USA, United States of America.	

Gallagher *et al*, 2012 (49)		
USA		
Primary PC. Diagnosis: Pathology Other details (localized)		
Population (further details): Ashkenazi (Ashkenazi Jewish background)		
Treatment (further details): radical prostatectomy; radiation therapy; radiation therapy + hormones; Hormone therapy alone; Chemotherapy alone; Watchful waiting; (NR)		
BRCA1+ (n=6)	BRCA2+ (n=20)	DDR- (n=806)
Mean age (SD): NR (NR) Median age (range): 67.1 (NR)	Mean age (SD): NR (NR) Median age (range): 62 (NR)	Mean age (SD): NR (NR) Median age (range): 68.2 (NR)
Ethnicity: Jewish (100)	Ethnicity: Jewish (100)	Ethnicity: Jewish (100)
Gleason score: <7 (50); ≥7 (50); NA (0)	Gleason score: <7 (10); ≥7 (85); NA (5)	Gleason score: <7 (40.2); ≥7 (54.2); NA (5.6)
AJCC stage: NR	AJCC stage: NR	AJCC stage: NR
TNM stage: NR	TNM stage: NR	TNM stage: NR

ECOG score 0: NR 1: NR 0-1: NR ≥2: NR	ECOG score 0: NR 1: NR 0-1: NR ≥2: NR	ECOG score 0: NR 1: NR 0-1: NR ≥2: NR
Previous treatments: Prostatectomy (0); Radiotherapy (17); Radiotherapy + Hormones (50); Hormones alone (34)	Previous treatments: Prostatectomy (50); Radiotherapy alone (20); Radiotherapy + Hormones alone (30)	Previous treatments: Prostatectomy (30); Radiotherapy alone (34); Radiotherapy + Hormones (27); Hormones alone (4); Watchful waiting (4); Chemotherapy (0.1)
Familial history of PC: NR	Familial history of PC: NR	Familial history of PC: NR
Mean years since diagnosis (SD): NR (NR) Median years since diagnosis (range): NR (NR)	Mean years since diagnosis (SD): NR (NR) Median years since diagnosis (range): NR (NR)	Mean years since diagnosis (SD): NR (NR) Median years since diagnosis (range): NR (NR)
Mean PSA ng/ml (SD): NR (NR) Median PSA ng/ml (range): 6.5 (5, 8)	Mean PSA ng/ml (SD): NR (NR) Median PSA ng/ml (range): 7 (6, 9)	Mean PSA ng/ml (SD): NR (NR) Median PSA ng/ml (range): 7 (2, 10)
AJCC, American Joint Committee on Cancer; BRCA, breast cancer susceptibility gene; CRPC, castration-resistant PC; DDR, DNA damage repair; ECOG, Eastern Cooperative Oncology Group; NA, not available; NR, not reported; PC, prostate cancer; PSA, prostate-specific antigen; SD, standard deviation; TNM, Tumor Nodes Metastasis classification of malignant tumors; USA, United States of America.		

Gambhira *et al*, 2016 (17)
USA
mCRPC. Diagnosis: Other details (NR)
Population (further details): unselected (NR)

Treatment (further details): NR (NR)
Total (n=13)
Mean age (SD): NR (NR) Median age (range): NR (NR)
Ethnicity: NR
Gleason score: NR
AJCC stage: NR
TNM stage: NR
ECOG score 0: NR 1: NR 0-1: NR ≥2: NR
Previous treatments: NR
Familial history of PC: NR
Mean years since diagnosis (SD): NR (NR) Median years since diagnosis (range): NR (NR)
Mean PSA ng/ml (SD): NR (NR) Median PSA ng/ml (range): NR) (NR)
Comments: No patient characteristics provided
AJCC, American Joint Committee on Cancer; CRPC, castration-resistant PC; ECOG, Eastern Cooperative Oncology Group; m, metastatic; NR, not reported; PC, prostate cancer; PSA, prostate-specific antigen; SD, standard deviation; TNM, Tumor Nodes Metastasis classification of malignant tumors; USA, United States of America.

Gayther *et al*, 2000 (50)
UK
PC. Diagnosis: NR Other details (NR)
Population (further details): familial (NR)
Treatment (further details): NR (NR)
Total (n=38)
Mean age (SD): 60.3 (NR) Median age (range): NR (43, 76)
Ethnicity: NR
Gleason score: NR
AJCC stage: NR
TNM stage: NR
ECOG score 0: NR 1: NR 0-1: NR ≥2: NR
Previous treatments: NR
Familial history of PC: NR
Mean years since diagnosis (SD): NR (NR) Median years since diagnosis (range): NR (NR)

Mean PSA ng/ml (SD): NR (NR) Median PSA ng/ml (range): NR) (NR)
AJCC, American Joint Committee on Cancer; ECOG, Eastern Cooperative Oncology Group; NR, not reported; PC, prostate cancer; PSA, prostate-specific antigen; SD, standard deviation; TNM, Tumor Nodes Metastasis classification of malignant tumors; UK, United Kingdom.

Giusti *et al*, 2003 (51)			
Israel			
PC. Diagnosis: Histology Other details (NR)			
Population (further details): Ashkenazi (Newly diagnosed Ashkenazi Israelis)			
Treatment (further details): NR (NR)			
Total (n=940)	BRCA1+ (n=15)	BRCA2+ (n=14)	DDR- (n=145)
Mean age (SD): NR (NR) Median age (range): NR (NR)	Mean age (SD): 74.2 (NR) Median age (range): NR (NR)	Mean age (SD): 71.6 (NR) Median age (range): NR (NR)	Mean age (SD): 73.6 (NR) Median age (range): NR (NR)
Ethnicity: NR	Ethnicity: NR	Ethnicity: NR	Ethnicity: NR
Gleason score: NR	Gleason score: NR	Gleason score: NR	Gleason score: NR
AJCC stage: NR	AJCC stage: NR	AJCC stage: NR	AJCC stage: NR
TNM stage: NR	TNM stage: NR	TNM stage: NR	TNM stage: NR
ECOG score 0: NR 1: NR 0-1: NR ≥2: NR	ECOG score 0: NR 1: NR 0-1: NR ≥2: NR	ECOG score 0: NR 1: NR 0-1: NR ≥2: NR	ECOG score 0: NR 1: NR 0-1: NR ≥2: NR

Previous treatments: NR	Previous treatments: NR	Previous treatments: NR	Previous treatments: NR
Familial history of PC: NR	Familial history of PC: NR	Familial history of PC: NR	Familial history of PC: NR
Mean years since diagnosis (SD): NR (NR) Median years since diagnosis (range): NR (NR)	Mean years since diagnosis (SD): NR (NR) Median years since diagnosis (range): NR (NR)	Mean years since diagnosis (SD): NR (NR) Median years since diagnosis (range): NR (NR)	Mean years since diagnosis (SD): NR (NR) Median years since diagnosis (range): NR (NR)
Mean PSA ng/ml (SD): NR (NR) Median PSA ng/ml (range): NR) (NR)	Mean PSA ng/ml (SD): NR (NR) Median PSA ng/ml (range): NR) (NR)	Mean PSA ng/ml (SD): NR (NR) Median PSA ng/ml (range): NR) (NR)	Mean PSA ng/ml (SD): NR (NR) Median PSA ng/ml (range): NR) (NR)
AJCC, American Joint Committee on Cancer; BRCA, breast cancer susceptibility gene; DDR, DNA damage repair; ECOG, Eastern Cooperative Oncology Group; m, metastatic; IV, intravenous; NR, not reported; PC, prostate cancer; PSA, prostate-specific antigen; SD, standard deviation; TNM, Tumor Nodes Metastasis classification of malignant tumors.			

Gourdin *et al*, 2016 (52)
USA
mPC. Diagnosis: 82% had CRPC Other details (NR)
Population (further details): unselected (NR)
Treatment (further details): NR (NR)
Total (n=55)
Mean age (SD): NR (NR) Median age (range): NR (NR)
Ethnicity: Caucasian (49%); African-American (49%); Asian (2%)

Gleason score: NR
AJCC stage: NR
TNM stage: NR
ECOG score 0: NR 1: NR 0-1: NR ≥2: NR
Previous treatments: NR
Familial history of PC: NR
Mean years since diagnosis (SD): NR (NR) Median years since diagnosis (range): NR (NR)
Mean PSA ng/ml (SD): NR (NR) Median PSA ng/ml (range): NR) (NR)
Comments: No patient characteristics provided other than ethnicity
AJCC, American Joint Committee on Cancer; CRPC, castration-resistant PC; DDR, DNA damage repair; ECOG, Eastern Cooperative Oncology Group; m, metastatic; NR, not reported; PC, prostate cancer; PSA, prostate-specific antigen; SD, standard deviation; TNM, Tumor Nodes Metastasis classification of malignant tumors; USA, United States of America.

Grasso *et al*, 2012 (53)
USA
mCRPC and primary PC. Diagnosis: NR Other details (NR)

Population (further details): unselected (NR)	
Treatment (further details): NR (NR)	
mCRPC (n=50)	Primary PC (n=11)
Mean age (SD): 71 (7.5) Median age (range): 71 (52, 85)	Mean age (SD): 60.9 (5.8) Median age (range): 60 (54, 71)
Ethnicity: NR	Ethnicity: NR
Gleason score: NR	Gleason score: 7 (18.2); 8 (36.4); 9 (45.4)
AJCC stage: NR	AJCC stage: NR
TNM stage: NR	TNM stage: NR
ECOG score 0: NR 1: NR 0-1: NR ≥2: NR	ECOG score 0: NR 1: NR 0-1: NR ≥2: NR
Previous treatments: NR	Previous treatments: NR
Familial history of PC: NR	Familial history of PC: NR
Mean years since diagnosis (SD): NR (NR) Median years since diagnosis (range): NR (NR)	Mean years since diagnosis (SD): NR (NR) Median years since diagnosis (range): NR (NR)
Mean PSA ng/ml (SD): 1142 (1818) Median PSA ng/ml (range): 324) (0, 8083)	Mean PSA ng/ml (SD): 10.9 (7.6) Median PSA ng/ml (range): 6.5) (4.2, 27.1)
AJCC, American Joint Committee on Cancer; CRPC, castration-resistant PC; ECOG, Eastern Cooperative Oncology Group; m, metastatic; NR, not reported; PC, prostate cancer; PSA, prostate-specific antigen; SD, standard deviation; TNM, Tumor Nodes Metastasis classification of malignant tumors; USA, United States of America.	

Hall *et al*, 1998 (54)
USA
PC. Diagnosis: NR Other details (NR)
Population (further details): treatment (External-beam conformal radiotherapy)
Treatment (further details): External-beam conformal radiotherapy (High-dose external-beam conformal radiotherapy)
Total (n=17)
Mean age (SD): NR (NR) Median age (range): NR (NR)
Ethnicity: NR
Gleason score: NR
AJCC stage: NR
TNM stage: NR
ECOG score 0: NR 1: NR 0-1: NR ≥2: NR
Previous treatments: NR
Familial history of PC: NR
Mean years since diagnosis (SD): NR (NR) Median years since diagnosis (range): NR (NR)

Mean PSA ng/ml (SD): NR (NR) Median PSA ng/ml (range): NR) (NR)
AJCC, American Joint Committee on Cancer; ECOG, Eastern Cooperative Oncology Group; NR, not reported; PC, prostate cancer; PSA, prostate-specific antigen; SD, standard deviation; TNM, Tumor Nodes Metastasis classification of malignant tumors; USA, United States of America.

Hamel *et al*, 2003 (55)
Canada
PC. Diagnosis: Pathology reports from patients' medical charts Other details (NR)
Population (further details): Ashkenazi (Both parents were reported as Ashkenazi Jewish, with no Sephardic heritage.)
Treatment (further details): NR (NR)
Total (n=146)
Mean age (SD): NR (NR) Median age (range): 67.9 (48.6, 84.2)
Ethnicity: NR
Gleason score: ≤5 (36.35%); ≥6 (51.4%)
AJCC stage: NR
TNM stage: NR

ECOG score 0: NR 1: NR 0-1: NR ≥2: NR
Previous treatments: NR
Familial history of PC: 13 (8.9%)
Mean years since diagnosis (SD): NR (NR) Median years since diagnosis (range): 5.7 (0.3, 23.7)
Mean PSA ng/ml (SD): NR (NR) Median PSA ng/ml (range): NR) (NR)
Comments: 5 cases had missing information for the median time since diagnosis
AJCC, American Joint Committee on Cancer; ECOG, Eastern Cooperative Oncology Group; NR, not reported; PC, prostate cancer; PSA, prostate-specific antigen; SD, standard deviation; TNM, Tumor Nodes Metastasis classification of malignant tumors.

Hart *et al*, 2016 (56)	
USA	
mCRPC. Diagnosis: Histology Other details (NR)	
Population (further details): treatment (Adenocarcinoma, Poorly differentiated, carcinoma NOS, Small-cell carcinoma, and Unknown)	
Treatment (further details): androgen deprivation therapy (NR)	
DDR+ (n=13)	DDR- (n=56)

Mean age (SD): NR (NR) Median age (range): NR (NR)	Mean age (SD): NR (NR) Median age (range): NR (NR)
Ethnicity: NR	Ethnicity: NR
Gleason score: 7 (0); 8 (0); 9 (15); 10 (31); no data (54)	Gleason score: 7 (4); 8 (27); 9 (11); 10 (23); no data (38)
AJCC stage: NR	AJCC stage: NR
TNM stage: NR	TNM stage: NR
ECOG score 0: NR 1: NR 0-1: NR ≥2: NR	ECOG score 0: NR 1: NR 0-1: NR ≥2: NR
Previous treatments: NR	Previous treatments: NR
Familial history of PC: 10 (77)	Familial history of PC: 45 (80)
Mean years since diagnosis (SD): NR (NR) Median years since diagnosis (range): NR (NR)	Mean years since diagnosis (SD): NR (NR) Median years since diagnosis (range): NR (NR)
Mean PSA ng/ml (SD): NR (NR) Median PSA ng/ml (range): NR) (NR)	Mean PSA ng/ml (SD): NR (NR) Median PSA ng/ml (range): NR) (NR)
AJCC, American Joint Committee on Cancer; CRPC, castration-resistant PC; DDR, DNA damage repair; ECOG, Eastern Cooperative Oncology Group; m, metastatic; NOS, not otherwise specified; NR, not reported; PC, prostate cancer; PSA, prostate-specific antigen; SD, standard deviation; TNM, Tumor Nodes Metastasis classification of malignant tumors; USA, United States of America.	

Hayano *et al*, 2016 (57)
Japan

PC. Diagnosis: Histology Other details (NR)
Population (further details): familial (Large PC families (with 3 or 4 patients with PC; n=22) or small PC families (2 patients with PC; n=118))
Treatment (further details): NR (NR)
Total (n=140)
Mean age (SD): 69 (NR) Median age (range): NR (40, 88)
Ethnicity: NR
Gleason score: <7 (30); ≥7 (69); unknown (1)
AJCC stage: NR
TNM stage: NR
ECOG score 0: NR 1: NR 0-1: NR ≥2: NR
Previous treatments: NR
Familial history of PC: NR
Mean years since diagnosis (SD): NR (NR) Median years since diagnosis (range): NR (NR)
Mean PSA ng/ml (SD): NR (NR) Median PSA ng/ml (range): NR (NR)

AJCC, American Joint Committee on Cancer; ECOG, Eastern Cooperative Oncology Group; NR, not reported; PC, prostate cancer; PSA, prostate-specific antigen; SD, standard deviation; TNM, Tumor Nodes Metastasis classification of malignant tumors.

Hebbring *et al*, 2006 (58)		
Multinational		
PC. Diagnosis: NR Other details (NR)		
Population (further details): familial (NR)		
Treatment (further details): NR (NR)		
Multinational (n=1819)	USA (Mayo Clinic) (n=428)	Germany (Ulm) (n=299)
Mean age (SD): NR (NR) Median age (range): NR (NR)	Mean age (SD): 66 (NR) Median age (range): NR (45, 84)	Mean age (SD): 64.6 (NR) Median age (range): NR (47, 89)
Ethnicity: NR	Ethnicity: NR	Ethnicity: NR
Gleason score: NR	Gleason score: NR	Gleason score: NR
AJCC stage: NR	AJCC stage: NR	AJCC stage: NR
TNM stage: NR	TNM stage: NR	TNM stage: NR
ECOG score 0: NR 1: NR 0-1: NR ≥2: NR	ECOG score 0: NR 1: NR 0-1: NR ≥2: NR	ECOG score 0: NR 1: NR 0-1: NR ≥2: NR
Previous treatments: NR	Previous treatments: NR	Previous treatments: NR

Familial history of PC: 1819 (100)	Familial history of PC: 428 (100)	Familial history of PC: 299 (100)
Mean years since diagnosis (SD): NR (NR) Median years since diagnosis (range): NR (NR)	Mean years since diagnosis (SD): NR (NR) Median years since diagnosis (range): NR (NR)	Mean years since diagnosis (SD): NR (NR) Median years since diagnosis (range): NR (NR)
Mean PSA ng/ml (SD): NR (NR) Median PSA ng/ml (range): NR) (NR)	Mean PSA ng/ml (SD): NR (NR) Median PSA ng/ml (range): NR) (NR)	Mean PSA ng/ml (SD): NR (NR) Median PSA ng/ml (range): NR) (NR)
Comments: Limited population data presented	Comments: Mean age at diagnosis extracted	Comments: Mean age at diagnosis extracted

Hebbring *et al*, 2006 (58)		
Multinational		
PC. Diagnosis: NR Other details (NR)		
Population (further details): unselected (NR)		
Treatment (further details): NR (NR)		
Multinational (n=1218)	USA (Mayo Clinic) (n=492)	Germany (Ulm) (n=338)
Mean age (SD): NR (NR) Median age (range): NR (NR)	Mean age (SD): 64 (NR) Median age (range): NR (46, 79)	Mean age (SD): 63.7 (NR) Median age (range): NR (42, 84)
Ethnicity: NR	Ethnicity: NR	Ethnicity: NR
Gleason score: NR	Gleason score: NR	Gleason score: NR
AJCC stage: NR	AJCC stage: NR	AJCC stage: NR
TNM stage: NR	TNM stage: NR	TNM stage: NR

ECOG score 0: NR 1: NR 0-1: NR ≥2: NR	ECOG score 0: NR 1: NR 0-1: NR ≥2: NR	ECOG score 0: NR 1: NR 0-1: NR ≥2: NR
Previous treatments: NR	Previous treatments: NR	Previous treatments: NR
Familial history of PC: 0 (0)	Familial history of PC: 0 (0)	Familial history of PC: 0 (0)
Mean years since diagnosis (SD): NR (NR) Median years since diagnosis (range): NR (NR)	Mean years since diagnosis (SD): NR (NR) Median years since diagnosis (range): NR (NR)	Mean years since diagnosis (SD): NR (NR) Median years since diagnosis (range): NR (NR)
Mean PSA ng/ml (SD): NR (NR) Median PSA ng/ml (range): NR) (NR)	Mean PSA ng/ml (SD): NR (NR) Median PSA ng/ml (range): NR) (NR)	Mean PSA ng/ml (SD): NR (NR) Median PSA ng/ml (range): NR) (NR)
Comments: Limited population data presented	Comments: Mean age at diagnosis extracted	Comments: Mean age at diagnosis extracted
AJCC, American Joint Committee on Cancer; ECOG, Eastern Cooperative Oncology Group; NR, not reported; PC, prostate cancer; PSA, prostate-specific antigen; SD, standard deviation; TNM, Tumor Nodes Metastasis classification of malignant tumors; USA, United States of America.		

Hubert *et al*, 1999 (59)
Israel
PC. Diagnosis: Histology and PSA Other details (NR)
Population (further details): Ashkenazi (NR)

Treatment (further details): NR (NR)		
Total (n=87)	DDR+ (n=3)	DDR- (n=84)
Mean age (SD): NR (NR) Median age (range): 71 (NR)	Mean age (SD): 64 (NR) Median age (range): NR (57, 73)	Mean age (SD): NR (NR) Median age (range): NR (NR)
Ethnicity: NR	Ethnicity: NR	Ethnicity: NR
Gleason score: NR	Gleason score: 7 (33.3); ≥8 (66.6)	Gleason score: Average: 5.9
AJCC stage: NR	AJCC stage: NR	AJCC stage: NR
TNM stage: NR	TNM stage: NR	TNM stage: NR
ECOG score 0: NR 1: NR 0-1: NR ≥2: NR	ECOG score 0: NR 1: NR 0-1: NR ≥2: NR	ECOG score 0: NR 1: NR 0-1: NR ≥2: NR
Previous treatments: NR	Previous treatments: NR	Previous treatments: NR
Familial history of PC: 5 (5.7)	Familial history of PC: NR	Familial history of PC: NR
Mean years since diagnosis (SD): NR (NR) Median years since diagnosis (range): NR (NR)	Mean years since diagnosis (SD): NR (NR) Median years since diagnosis (range): NR (NR)	Mean years since diagnosis (SD): NR (NR) Median years since diagnosis (range): NR (NR)
Mean PSA ng/ml (SD): NR (NR) Median PSA ng/ml (range): NR (NR)	Mean PSA ng/ml (SD): 55.8 (NR) Median PSA ng/ml (range): NR (47, 60)	Mean PSA ng/ml (SD): 23.6 (NR) Median PSA ng/ml (range): NR (NR)
Comments: 71 years at diagnosis		
AJCC, American Joint Committee on Cancer; DDR, DNA damage repair; ECOG, Eastern Cooperative Oncology Group; NR, not reported; PC, prostate cancer; PSA, prostate-specific antigen; SD, standard deviation; TNM, Tumor Nodes Metastasis classification of malignant tumors.		

Hussain *et al*, 2017 (60)	
USA	
mCRPC. Diagnosis: Histology or cytology Other details (NR)	
Population (further details): unselected (NR)	
Treatment (further details): Abiraterone (1000 mg per day plus prednisone 5 mg twice per day (arm A) or AAP plus veliparib 300 mg twice per day (arm B), for days 1 to 28. Treatment was continued until radiographic/clinical disease progression, inter-current illness, unacceptable adverse events (A). Abiraterone + veliparib (AAP plus veliparib 300 mg twice per day (arm B), for days 1 to 28. Arm B patients underwent lead-in treatment with AAP, followed on day 8 by veliparib, in cycle 1 only. Treatment was continued until radiographic/clinical disease progression, inter-current)	
A (n=72)	A+V (n=76)
Mean age (SD): NR (NR) Median age (range): 69 (50, 90)	Mean age (SD): NR (NR) Median age (range): 68 (47, 85)
Ethnicity: Caucasian (83); African American (12); other (3)	Ethnicity: Caucasian (94); African American (4); other (3)
Gleason score: NR	Gleason score: NR
AJCC stage: NR	AJCC stage: NR
TNM stage: NR	TNM stage: NR
ECOG score 0: 46 (62) 1: 28 (38) 0-1: NR ≥2: 0	ECOG score 0: 50 (63) 1: 28 (35) 0-1: NR ≥2: 1 (1)

Previous treatments: Docetaxel/cabazitaxel (15); other chemotherapy (7); Enzalutamide (3); Sipuleucel-T (30); Experimental agent (26)	Previous treatments: Docetaxel/cabazitaxel (22); other chemotherapy (8); Enzalutamide (3); Sipuleucel-T (17); Experimental agent (19)
Familial history of PC: NR	Familial history of PC: NR
Mean years since diagnosis (SD): NR (NR) Median years since diagnosis (range): NR (NR)	Mean years since diagnosis (SD): NR (NR) Median years since diagnosis (range): NR (NR)
Mean PSA ng/ml (SD): NR (NR) Median PSA ng/ml (range): 32.7 (0.8, 1557.6)	Mean PSA ng/ml (SD): NR (NR) Median PSA ng/ml (range): 36.4 (0.04, 1074.4)
AJCC, American Joint Committee on Cancer; CRPC, castration-resistant PC; ECOG, Eastern Cooperative Oncology Group; NR, not reported; PC, prostate cancer; PSA, prostate-specific antigen; SD, standard deviation; TNM, Tumor Nodes Metastasis classification of malignant tumors; USA, United States of America.	

Jefferies *et al*, 2017 (61)
UK
Primary PC. Diagnosis: Histology Other details (NR)
Population (further details): unselected (NR)
Treatment (further details): NR (NR)
Total (n=61)
Mean age (SD): NR (NR) Median age (range): NR (NR)
Ethnicity: NR
Gleason score: NR
AJCC stage: NR

TNM stage: NR
ECOG score 0: NR 1: NR 0-1: NR ≥2: NR
Previous treatments: NR
Familial history of PC: NR
Mean years since diagnosis (SD): NR (NR) Median years since diagnosis (range): NR (NR)
Mean PSA ng/ml (SD): NR (NR) Median PSA ng/ml (range): NR) (NR)
Comments: no details
AJCC, American Joint Committee on Cancer; ECOG, Eastern Cooperative Oncology Group; NR, not reported; PC, prostate cancer; PSA, prostate-specific antigen; SD, standard deviation; TNM, Tumor Nodes Metastasis classification of malignant tumors; UK, United Kingdom.

Kaufman *et al*, 2015 (62)
Multi-national
mCRPC. Diagnosis: NR Other details (NR)
Population (further details): unselected (NR)
Treatment (further details): Olaparib (400 mg capsule twice daily)
Total (n=8)

Mean age (SD): 66.6 (9.86) Median age (range): 71 (51, 77)
Ethnicity: Caucasian (100)
Gleason score: NR
AJCC stage: NR
TNM stage: NR
ECOG score 0: 1 (12.5) 1: 4 (50) 0-1: NR ≥2: 3 (37.5)
Previous treatments: Docetaxel (75); platinum carboplatin or cisplatin (50)
Familial history of PC: NR
Mean years since diagnosis (SD): NR (NR) Median years since diagnosis (range): NR (NR)
Mean PSA ng/ml (SD): NR (NR) Median PSA ng/ml (range): NR) (NR)
Comments: No PSA details were presented
AJCC, American Joint Committee on Cancer; CRPC, castration-resistant PC; ECOG, Eastern Cooperative Oncology Group; m, metastatic; NR, not reported; PC, prostate cancer; PSA, prostate-specific antigen; SD, standard deviation; TNM, Tumor Nodes Metastasis classification of malignant tumors.

Kirchoff *et al*, 2004 (63)

USA
PC. Diagnosis: NR Other details (NR)
Population (further details): Ashkenazi (NR)
Treatment (further details): NR (NR)
Total (n=251)
Mean age (SD): 65.7 (NR) Median age (range): NR (NR)
Ethnicity: Ashkenazi Jewish men (100)
Gleason score: NR
AJCC stage: NR
TNM stage: NR
ECOG score 0: NR 1: NR 0-1: NR ≥2: NR
Previous treatments: NR
Familial history of PC: NR
Mean years since diagnosis (SD): NR (NR) Median years since diagnosis (range): NR (NR)
Mean PSA ng/ml (SD): NR (NR) Median PSA ng/ml (range): NR) (NR)

Comments: mean age for DDR+ PC cases, for controls (still DDR+ but no PC) mean age was 51.0, calculations age adjusted, see table 2
AJCC, American Joint Committee on Cancer; DDR, DNA damage repair; ECOG, Eastern Cooperative Oncology Group; NR, not reported; PC, prostate cancer; PSA, prostate-specific antigen; SD, standard deviation; TNM, Tumor Nodes Metastasis classification of malignant tumors; USA, United States of America.

Kote-Jarai *et al*, 2011 (64)
UK
Other. Diagnosis: <65 years; NR Other details (Young-onset PC (onset ≤65 years))
Population (further details): unselected (NR)
Treatment (further details): NR (NR)
Total (n=1589)
Mean age (SD): NR (NR) Median age (range): NR (36, 65)
Ethnicity: NR
Gleason score: NR
AJCC stage: NR
TNM stage: NR
ECOG score 0: NR 1: NR 0-1: NR ≥2: NR

Previous treatments: NR
Familial history of PC: 85.1
Mean years since diagnosis (SD): NR (NR) Median years since diagnosis (range): NR (NR)
Mean PSA ng/ml (SD): NR (NR) Median PSA ng/ml (range): NR) (NR)
AJCC, American Joint Committee on Cancer; ECOG, Eastern Cooperative Oncology Group; NR, not reported; PC, prostate cancer; PSA, prostate-specific antigen; SD, standard deviation; TNM, Tumor Nodes Metastasis classification of malignant tumors; UK, United Kingdom.

LaDuca *et al*, 2017 (65)
USA
PC. Diagnosis: NR Other details (NR)
Population (further details): familial (Patients referred for hereditary cancer multi-gene panel testing)
Treatment (further details): NR (NR)
Total (n=NR)
Mean age (SD): NR (NR) Median age (range): NR (NR)
Ethnicity: NR
Gleason score: NR
AJCC stage: NR
TNM stage: NR

ECOG score 0: NR 1: NR 0-1: NR ≥2: NR
Previous treatments: NR
Familial history of PC: NR
Mean years since diagnosis (SD): NR (NR) Median years since diagnosis (range): NR (NR)
Mean PSA ng/ml (SD): NR (NR) Median PSA ng/ml (range): NR) (NR)
Comments: No details provided regarding patient characteristics (nor even the number of patients)
AJCC, American Joint Committee on Cancer; ECOG, Eastern Cooperative Oncology Group; NR, not reported; PC, prostate cancer; PSA, prostate-specific antigen; SD, standard deviation; TNM, Tumor Nodes Metastasis classification of malignant tumors; USA, United States of America.

Lara *et al*, 2017 (66)
USA
PC. Diagnosis: NR Other details (NR)
Population (further details): unselected (NR)
Treatment (further details): NR (NR)
Total (n=207; 936)

Mean age (SD): NR (NR) Median age (range): NR (NR)
Ethnicity: NR
Gleason score: NR
AJCC stage: NR
TNM stage: NR
ECOG score 0: NR 1: NR 0-1: NR ≥2: NR
Previous treatments: NR
Familial history of PC: NR
Mean years since diagnosis (SD): NR (NR) Median years since diagnosis (range): NR (NR)
Mean PSA ng/ml (SD): NR (NR) Median PSA ng/ml (range): NR) (NR)
AJCC, American Joint Committee on Cancer; ECOG, Eastern Cooperative Oncology Group; NR, not reported; PC, prostate cancer; PSA, prostate-specific antigen; SD, standard deviation; TNM, Tumor Nodes Metastasis classification of malignant tumors; USA, United States of America.

Ledet *et al*, 2017 (67)
USA

PC. Diagnosis: NR Other details (NR)
Population (further details): familial (PC patients with a family history that met NCCN guidelines for genetic testing)
Treatment (further details): NR (NR)
Total (n=124)
Mean age (SD): NR (NR) Median age (range): NR (NR)
Ethnicity: NR
Gleason score: NR
AJCC stage: NR
TNM stage: NR
ECOG score 0: NR 1: NR 0-1: NR ≥2: NR
Previous treatments: NR
Familial history of PC: 124 (100)
Mean years since diagnosis (SD): NR (NR) Median years since diagnosis (range): NR (NR)
Mean PSA ng/ml (SD): NR (NR) Median PSA ng/ml (range): NR) (NR)

Comments: Limited description of population characteristics provided. Ethnicity described for the larger cohort of n=535 patients, but not for the finally selected study cohort of n=124
AJCC, American Joint Committee on Cancer; ECOG, Eastern Cooperative Oncology Group; NCCN, National Comprehensive Cancer Network; NR, not reported; PC, prostate cancer; PSA, prostate-specific antigen; SD, standard deviation; TNM, Tumor Nodes Metastasis classification of malignant tumors; USA, United States of America.

Lehrer *et al*, 1998 (68)
USA
PC. Diagnosis: Histology Other details (NR)
Population (further details): Ashkenazi (Ethnic background was confirmed for all subjects by self-report or interview.)
Treatment (further details): NR (NR)
Total (n=60)
Mean age (SD): 70 (5.25) Median age (range): NR (55, 80)
Ethnicity: Ashkenazi Jewish men (100)
Gleason score: NR
AJCC stage: NR
TNM stage: NR
ECOG score 0: NR 1: NR 0-1: NR ≥2: NR

Previous treatments: NR
Familial history of PC: 6 (10)
Mean years since diagnosis (SD): NR (NR) Median years since diagnosis (range): NR (NR)
Mean PSA ng/ml (SD): NR (NR) Median PSA ng/ml (range): NR) (NR)
Comments: Only looking at PC, no controls but using two earlier papers for control cohort: "Following the finding of a 185delAG frameshift mutation of BRCAJ in several Ashkenazi Jewish breast/ovarian cancer families, the frequency of this mutation was found to be 0"
AJCC, American Joint Committee on Cancer; BRCA, breast cancer susceptibility gene; ECOG, Eastern Cooperative Oncology Group; NR, not reported; PC, prostate cancer; PSA, prostate-specific antigen; SD, standard deviation; TNM, Tumor Nodes Metastasis classification of malignant tumors; USA, United States of America.

Leongamornlert *et al*, 2012 (69)
UK
PC. Diagnosis: NR Other details (NR)
Population (further details): unselected (NR)
Treatment (further details): NR (NR)
Total (n=886)
Mean age (SD): NR (NR) Median age (range): NR (36, 88)
Ethnicity: NR
Gleason score: NR

AJCC stage: NR
TNM stage: NR
ECOG score 0: NR 1: NR 0-1: NR ≥2: NR
Previous treatments: NR
Familial history of PC: NR
Mean years since diagnosis (SD): NR (NR) Median years since diagnosis (range): NR (NR)
Mean PSA ng/ml (SD): NR (NR) Median PSA ng/ml (range): NR) (NR)
Comments: Has data on BRCA1 prevalence stratified by age (36-55, 56-65, 66-88)
AJCC, American Joint Committee on Cancer; BRCA, breast cancer susceptibility gene; ECOG, Eastern Cooperative Oncology Group; NR, not reported; PC, prostate cancer; PSA, prostate-specific antigen; SD, standard deviation; TNM, Tumor Nodes Metastasis classification of malignant tumors; UK, United Kingdom.

Leongamornlert *et al*, 2014 (70)
UK
PC. Diagnosis: Clinical detection or PSA screening Other details (NR)
Population (further details): familial (Two or more relatives affected by PC)

Treatment (further details): NR (NR)		
Total (n=191)	DDR+ (n=14)	DDR- (n=140)
Mean age (SD): NR (NR) Median age (range): NR (NR)	Mean age (SD): NR (NR) Median age (range): 58.5 (41, 71)	Mean age (SD): NR (NR) Median age (range): 59 (47, 82)
Ethnicity: White (68.6); Black African/Caribbean (2.6); Ashkenazi Jew (0.5); unknown (28.3)	Ethnicity: NR	Ethnicity: NR
Gleason score: NR	Gleason score: ≤6 (35.71); 7 (14.29); ≥8 (21.43); unknown (28.57)	Gleason score: ≤6 (44.29); 7 (19.29); ≥8 (10.71); unknown (25.71)
AJCC stage: NR	AJCC stage: I-III (21.43); IV (35.71); unknown (42.86)	AJCC stage: I-III (48.57); IV (5.00); unknown (46.43)
TNM stage: NR	TNM stage: T1 (21.43); T2 (28.57); T3 (14.29); T4 (7.14); TX (28.57); N0 (28.57); N1 (21.43); NX (50.00); M0 (50.00) M1 (21.43); MX (28.57)	TNM stage: T1 (27.14); T2 (32.14); T3 (17.14); T4 (1.43); TX (22.14); N0 (54.29); N1 (0.71); NX (45.00); M0 (52.86) M1 (3.57); MX (43.57)
ECOG score 0: NR 1: NR 0-1: NR ≥2: NR	ECOG score 0: NR 1: NR 0-1: NR ≥2: NR	ECOG score 0: NR 1: NR 0-1: NR ≥2: NR
Previous treatments: NR	Previous treatments: NR	Previous treatments: NR
Familial history of PC: NR	Familial history of PC: NR	Familial history of PC: NR
Mean years since diagnosis (SD): NR (NR) Median years since diagnosis (range): NR (NR)	Mean years since diagnosis (SD): NR (NR) Median years since diagnosis (range): NR (NR)	Mean years since diagnosis (SD): NR (NR) Median years since diagnosis (range): NR (NR)

Mean PSA ng/ml (SD): NR (NR) Median PSA ng/ml (range): NR) (NR)	Mean PSA ng/ml (SD): NR (NR) Median PSA ng/ml (range): 11.1) (3.09, 91.12)	Mean PSA ng/ml (SD): NR (NR) Median PSA ng/ml (range): 8.25) (0.04, 259)
	Comments: PSA given at diagnosis	Comments: PSA given at diagnosis
AJCC, American Joint Committee on Cancer; CRPC, castration-resistant PC; ECOG, Eastern Cooperative Oncology Group; NR, not reported; PC, prostate cancer; PSA, prostate-specific antigen; SD, standard deviation; TNM, Tumor Nodes Metastasis classification of malignant tumors; UK, United Kingdom.		

Liu *et al*, 2016 (5)
NR
PC. Diagnosis: Histology Other details (NR)
Population (further details): unselected (NR)
Treatment (further details): NR (NR)
Total (n=36)
Mean age (SD): NR (NR) Median age (range): NR (NR)
Ethnicity: NR
Gleason score: 7 (100)
AJCC stage: NR
TNM stage: NR

ECOG score 0: NR 1: NR 0-1: NR ≥2: NR
Previous treatments: NR
Familial history of PC: NR
Mean years since diagnosis (SD): NR (NR) Median years since diagnosis (range): NR (NR)
Mean PSA ng/ml (SD): NR (NR) Median PSA ng/ml (range): NR) (NR)
AJCC, American Joint Committee on Cancer; DDR, DNA damage repair; ECOG, Eastern Cooperative Oncology Group; NR, not reported; PC, prostate cancer; PSA, prostate-specific antigen; SD, standard deviation; TNM, Tumor Nodes Metastasis classification of malignant tumors.

Lu *et al*, 2015 (71)
Multi-national
PC. Diagnosis: NR Other details (NR)
Population (further details): unselected (NR)
Treatment (further details): NR (NR)
Total (n=178)
Mean age (SD): 60.4 (6.9) Median age (range): NR (NR)

Ethnicity: Caucasian (73.03); Asian (1.12); African American (3.37); NR (5.62)
Gleason score: NR
AJCC stage: NR
TNM stage: NR
ECOG score 0: NR 1: NR 0-1: NR ≥2: NR
Previous treatments: NR
Familial history of PC: NR
Mean years since diagnosis (SD): NR (NR) Median years since diagnosis (range): NR (NR)
Mean PSA ng/ml (SD): NR (NR) Median PSA ng/ml (range): NR (NR)
Comments: Very limited PC data available
AJCC, American Joint Committee on Cancer; ECOG, Eastern Cooperative Oncology Group; NR, not reported; PC, prostate cancer; PSA, prostate-specific antigen; SD, standard deviation; TNM, Tumor Nodes Metastasis classification of malignant tumors.

Maier *et al*, 2014 (72)
Germany
PC. Diagnosis: NR Other details (NR)

Population (further details): familial and unselected (NR)	
Treatment (further details): NR (NR)	
Familial (n=382)	Unselected (n=92)
Mean age (SD): 61.1 (NR) Median age (range): NR (42, 80)	Mean age (SD): 55.8 (NR) Median age (range): NR (29, 60)
Ethnicity: NR	Ethnicity: NR
Gleason score: Gleason ≤7 and <GIII (71.5); Gleason >7 or GIII (18.3); unknown Gleason and grading (10.2)	Gleason score: Gleason ≤7 and <GIII (82.6); Gleason >7 or GIII (15.2); unknown Gleason and grading (2.2)
AJCC stage: NR	AJCC stage: NR
TNM stage: T1 (2.1); T2 (55.2); T3 (27.2); T4 (5.2); Tx or not recorded (10.2)	TNM stage: T1 (1.1); T2 (56.5); T3 (35.9); T4 (4.3): Tx or not recorded (2.2)
ECOG score 0: NR 1: NR 0-1: NR ≥2: NR	ECOG score 0: NR 1: NR 0-1: NR ≥2: NR
Previous treatments: NR	Previous treatments: Radical prostatectomy
Familial history of PC: 382 (100)	Familial history of PC: 0 (0)
Mean years since diagnosis (SD): NR (NR) Median years since diagnosis (range): NR (NR)	Mean years since diagnosis (SD): NR (NR) Median years since diagnosis (range): NR (NR)
Mean PSA ng/ml (SD): NR (NR) Median PSA ng/ml (range): 9.6 (0.2, 1300)	Mean PSA ng/ml (SD): NR (NR) Median PSA ng/ml (range): 8.2 (0.5, 94)
Comments: Lymph node involvement also reported (pN0, pN1, Nx); PSA level unknown in n=84	Comments: Lymph node involvement also reported (pN0, pN1, Nx); PSA level unknown in n=6

AJCC, American Joint Committee on Cancer; ECOG, Eastern Cooperative Oncology Group; NR, not reported; PC, prostate cancer; PSA, prostate-specific antigen; SD, standard deviation; TNM, Tumor Nodes Metastasis classification of malignant tumors.

Manson-Bahr *et al*, 2015 (73)
UK
PC. Diagnosis: Histology Other details (NR)
Population (further details): unselected (NR)
Treatment (further details): NR (NR)
Total (n=63)
Mean age (SD): NR (NR) Median age (range): NR (56, 85)
Ethnicity: NR
Gleason score: 6 (13); 7 (60); 8 (13); 9 (14)
AJCC stage: NR
TNM stage: NR
ECOG score 0: NR 1: NR 0-1: NR ≥2: NR
Previous treatments: Hormone Therapy (27); Active Surveillance (8); Radiotherapy (40); Brachytherapy (6); Surgery (19)
Familial history of PC: NR

Mean years since diagnosis (SD): NR (NR) Median years since diagnosis (range): NR (NR)
Mean PSA ng/ml (SD): NR (NR) Median PSA ng/ml (range): NR (5.5, 136)
Comments: Baseline details per individual data.
AJCC, American Joint Committee on Cancer; ECOG, Eastern Cooperative Oncology Group; NR, not reported; PC, prostate cancer; PSA, prostate-specific antigen; SD, standard deviation; TNM, Tumor Nodes Metastasis classification of malignant tumors; UK, United Kingdom.

Marshall *et al*, 2017 (74)
USA
PC. Diagnosis: NR Other details (>=≥7 Gleason score)
Population (further details): familial (personal history of PC and ≥1 close blood relative with breast, ovarian, pancreatic or prostate cancer; or a personal history of PC)
Treatment (further details): NR (NR)
Total (n=92)
Mean age (SD): NR (NR) Median age (range): NR (NR)
Ethnicity: NR
Gleason score: NR
AJCC stage: NR
TNM stage: NR

ECOG score 0: NR 1: NR 0-1: NR ≥2: NR
Previous treatments: NR
Familial history of PC: 2 (1.4)
Mean years since diagnosis (SD): NR (NR) Median years since diagnosis (range): NR (NR)
Mean PSA ng/ml (SD): NR (NR) Median PSA ng/ml (range): NR (NR)
AJCC, American Joint Committee on Cancer; ECOG, Eastern Cooperative Oncology Group; NR, not reported; PC, prostate cancer; PSA, prostate-specific antigen; SD, standard deviation; TNM, Tumor Nodes Metastasis classification of malignant tumors; USA, United States of America.

Mateo *et al*, 2015 (75)
UK
mCRPC. Diagnosis: Histology Other details (NR)
Population (further details): unselected (NR)
Treatment (further details): Olaparib (400 mg tablet twice daily)
Total (n=50)

Mean age (SD): NR (NR) Median age (range): 67.5 (40.8, 79.3)
Ethnicity: NR
Gleason score: NR
AJCC stage: NR
TNM stage: NR
ECOG score 0: 9 (18) 1: 35 (70) 0-1: NR ≥2: 6 (12)
Previous treatments: Docetaxel (100); abiraterone acetate (96); cabazitaxel (58); radical prostatectomy or radiotherapy (50); castration (chemical or surgical) (100); enzalutamide (28); radium-223 (2).
Familial history of PC: NR
Mean years since diagnosis (SD): NR (NR) Median years since diagnosis (range): 5 (NR)
Mean PSA ng/ml (SD): NR (NR) Median PSA ng/ml (range): 349.5 (NR)
Comments: Circulating tumor-cell count (cells/7.5ml blood) was median 37 (IQR 14-110)
AJCC, American Joint Committee on Cancer; CRPC, castration-resistant PC; ECOG, Eastern Cooperative Oncology Group; m, metastatic; NR, not reported; PC, prostate cancer; PSA, prostate-specific antigen; SD, standard deviation; TNM, Tumor Nodes Metastasis classification of malignant tumors; UK, United Kingdom.

Meyer *et al*, 2007 (25)

Germany	
Primary PC. Diagnosis: Histology Other details (Clinically localized low risk early PC)	
Population (further details): treatment (Brachytherapy I 125)	
Treatment (further details): Brachytherapy I 125 (160 Gy)	
DDR+ (n=25)	DDR- (n=236)
Mean age (SD): 63.8 (NR) Median age (range): NR (NR)	Mean age (SD): 65.5 (NR) Median age (range): NR (NR)
Ethnicity: NR	Ethnicity: NR
Gleason score: 3 (0); 4 (12); 5 (8); 6 (605); 7 (20); 8 (0)	Gleason score: 3 (1.5); 4 (5.9); 5 (19.9); 6 (69.5); 7 (2.5); 8 (0.3)
AJCC stage: NR	AJCC stage: NR
TNM stage: cT1c (0); cT2a (80); cT2b (12); cT2c (8); unknown (0)	TNM stage: cT1c (2); cT2a (73.7); cT2b (19); cT2c (1.7); unknown (3.4)
ECOG score 0: NR 1: NR 0-1: NR ≥2: NR	ECOG score 0: NR 1: NR 0-1: NR ≥2: NR
Previous treatments: neoadjuvant hormone therapy (7)	Previous treatments: neoadjuvant hormone therapy (67)
Familial history of PC: NR	Familial history of PC: NR
Mean years since diagnosis (SD): NR (NR) Median years since diagnosis (range): NR (NR)	Mean years since diagnosis (SD): NR (NR) Median years since diagnosis (range): NR (NR)

Mean PSA ng/ml (SD): 6.6 (NR) Median PSA ng/ml (range): NR) (NR)	Mean PSA ng/ml (SD): 7 (NR) Median PSA ng/ml (range): NR) (NR)
Comments: Mean PSA, Gleason and age are for carriers of P1054R variant	Comments:
AJCC, American Joint Committee on Cancer; DDR, DNA damage repair; ECOG, Eastern Cooperative Oncology Group; NR, not reported; PC, prostate cancer; PSA, prostate-specific antigen; SD, standard deviation; TNM, Tumor Nodes Metastasis classification of malignant tumors.	

Myers *et al*, 2016 (76)	
USA	
PC. Diagnosis: NR Other details (NR)	
Population (further details): unselected (NR)	
Treatment (further details): NR (NR)	
DDR+ (n=12)	DDR- (n=73)
Mean age (SD): 58 (NR) Median age (range): NR (NR)	Mean age (SD): 62 (NR) Median age (range): NR (NR)
Ethnicity: NR	Ethnicity: NR
Gleason score: NR	Gleason score: NR
AJCC stage: NR	AJCC stage: NR
TNM stage: NR	TNM stage: NR

ECOG score 0: NR 1: NR 0-1: NR ≥2: NR	ECOG score 0: NR 1: NR 0-1: NR ≥2: NR
Previous treatments: NR	Previous treatments: NR
Familial history of PC: NR	Familial history of PC: NR
Mean years since diagnosis (SD): NR (NR) Median years since diagnosis (range): NR (NR)	Mean years since diagnosis (SD): NR (NR) Median years since diagnosis (range): NR (NR)
Mean PSA ng/ml (SD): NR (NR) Median PSA ng/ml (range): NR (NR)	Mean PSA ng/ml (SD): NR (NR) Median PSA ng/ml (range): NR (NR)
AJCC, American Joint Committee on Cancer; DDR, DNA damage repair; ECOG, Eastern Cooperative Oncology Group; NR, not reported; PC, prostate cancer; PSA, prostate-specific antigen; SD, standard deviation; TNM, Tumor Nodes Metastasis classification of malignant tumors; USA, United States of America.	

Na *et al*, 2017 (77)	
Multi-national	
Other and Primary PC. Diagnosis: NR Other details (Lethal PC)	
Population (further details): unselected (NR)	
Treatment (further details): NR (NR)	
lethal (n=313)	Primary PC (n=486)

Mean age (SD): NR (NR) Median age (range): 62 (NR)	Mean age (SD): NR (NR) Median age (range): 65 (NR)
Ethnicity: European American (83.4); African American (9.6); Chinese (7.0)	Ethnicity: European American (72.4); African American (18.3); Chinese (9.3)
Gleason score: NR	Gleason score: NR
AJCC stage: NR	AJCC stage: NR
TNM stage: NR	TNM stage: NR
ECOG score 0: NR 1: NR 0-1: NR ≥2: NR	ECOG score 0: NR 1: NR 0-1: NR ≥2: NR
Previous treatments: NR	Previous treatments: NR
Familial history of PC: NR	Familial history of PC: NR
Mean years since diagnosis (SD): NR (NR) Median years since diagnosis (range): NR (NR)	Mean years since diagnosis (SD): NR (NR) Median years since diagnosis (range): NR (NR)
Mean PSA ng/ml (SD): NR (NR) Median PSA ng/ml (range): 13.1 (NR)	Mean PSA ng/ml (SD): NR (NR) Median PSA ng/ml (range): 5.3 (NR)
Comments: Outcomes based on ethnicity in lethal vs localized PC are also available but not extracted (European American, African American, Chinese)	Comments: Outcomes based on ethnicity in lethal vs localized PC are also available but not extracted (European American, African American, Chinese)
AJCC, American Joint Committee on Cancer; ECOG, Eastern Cooperative Oncology Group; NR, not reported; PC, prostate cancer; PSA, prostate-specific antigen; SD, standard deviation; TNM, Tumor Nodes Metastasis classification of malignant tumors.	

Nam *et al*, 2005 (15)
Canada
PC. Diagnosis: Histology Other details (NR)
Population (further details): unselected (NR)
Treatment (further details): NR (NR)
Total (n=996)
Mean age (SD): 66.2 (NR) Median age (range): NR (NR)
Ethnicity: White (84.1); Black (11.0); Asian (2.9); Other (1.8)
Gleason score: NR
AJCC stage: NR
TNM stage: NR
ECOG score 0: NR 1: NR 0-1: NR ≥2: NR
Previous treatments: NR
Familial history of PC: 163 (16.3)
Mean years since diagnosis (SD): NR (NR) Median years since diagnosis (range): NR (NR)

Mean PSA ng/ml (SD): NR (NR) Median PSA ng/ml (range): NR) (NR)
Comments: PSA levels (ng/ml) ≤ 4.0 (5.7%); 4.1-10.0 (56.8%); 10.1-20.0 (26.2%); >20.0 (11.2%)
AJCC, American Joint Committee on Cancer; ECOG, Eastern Cooperative Oncology Group; NR, not reported; PC, prostate cancer; PSA, prostate-specific antigen; SD, standard deviation; TNM, Tumor Nodes Metastasis classification of malignant tumors.

Naslund Koch *et al*, 2016 (16)
Denmark
PC. Diagnosis: NR Other details (NR)
Population (further details): unselected (NR)
Treatment (further details): NR (NR)
Total (n=39014)
Mean age (SD): NR (NR) Median age (range): NR (NR)
Ethnicity: NR
Gleason score: NR
AJCC stage: NR
TNM stage: NR

ECOG score 0: NR 1: NR 0-1: NR ≥2: NR
Previous treatments: NR
Familial history of PC: NR
Mean years since diagnosis (SD): NR (NR) Median years since diagnosis (range): NR (NR)
Mean PSA ng/ml (SD): NR (NR) Median PSA ng/ml (range): NR (NR)
Comments: Although age and family history were specified, this was only presented for the full cohort of 86,922 subjects (no details were provided regarding the male cohort).
AJCC, American Joint Committee on Cancer; ECOG, Eastern Cooperative Oncology Group; NR, not reported; PC, prostate cancer; PSA, prostate-specific antigen; SD, standard deviation; TNM, Tumor Nodes Metastasis classification of malignant tumors.

Nastiuk *et al*, 1999 (78)
USA
PC. Diagnosis: NR Other details (Archival records from New York University and Columbia Presbyterian medical centers for stage B PC)
Population (further details): Ashkenazi (NR)
Treatment (further details): NR (NR)
Total (n=83)

Mean age (SD): NR (NR) Median age (range): NR (NR)
Ethnicity: Ashkenazi Jewish men (100)
Gleason score: NR
AJCC stage: NR
TNM stage: NR
ECOG score 0: NR 1: NR 0-1: NR ≥2: NR
Previous treatments: NR
Familial history of PC: NR
Mean years since diagnosis (SD): NR (NR) Median years since diagnosis (range): NR (NR)
Mean PSA ng/ml (SD): NR (NR) Median PSA ng/ml (range): NR) (NR)
Comments: Only looking at PC, no controls, using earlier paper for cohort control (Roa BB, Boyd AA, Volcik K, Richards CS. Ashkenazi Jewish population frequencies for common mutations in BRCA1 and BRCA2. Nat. Genet. 1996; 14:185-187. [PubMed: 8841191].
AJCC, American Joint Committee on Cancer; ECOG, Eastern Cooperative Oncology Group; NR, not reported; PC, prostate cancer; PSA, prostate-specific antigen; SD, standard deviation; TNM, Tumor Nodes Metastasis classification of malignant tumors; USA, United States of America.

Nelson *et al*, 2016 (79)

Multi-national
mPC. Diagnosis: NR Other details (NR)
Population (further details): unselected (NR)
Treatment (further details): NR (NR)
Total (n=569)
Mean age (SD): NR (NR) Median age (range): NR (NR)
Ethnicity: NR
Gleason score: NR
AJCC stage: NR
TNM stage: NR
ECOG score 0: NR 1: NR 0-1: NR ≥2: NR
Previous treatments: NR
Familial history of PC: NR
Mean years since diagnosis (SD): NR (NR) Median years since diagnosis (range): NR (NR)
Mean PSA ng/ml (SD): NR (NR) Median PSA ng/ml (range): NR (NR)

Comments: No patient characteristics provided
AJCC, American Joint Committee on Cancer; ECOG, Eastern Cooperative Oncology Group; NR, not reported; PC, prostate cancer; PSA, prostate-specific antigen; SD, standard deviation; TNM, Tumor Nodes Metastasis classification of malignant tumors.

Nguyen *et al*, 2011 (80)
USA
Primary PC. Diagnosis: NR Other details (NR)
Population (further details): treatment (external radiation or brachytherapy)
Treatment (further details): external radiation or brachytherapy (NR)
Total (n=612)
Mean age (SD): NR (NR) Median age (range): NR (NR)
Ethnicity: NR
Gleason score: NR
AJCC stage: NR
TNM stage: NR
ECOG score 0: NR 1: NR 0-1: NR ≥2: NR
Previous treatments: NR

Familial history of PC: NR
Mean years since diagnosis (SD): NR (NR) Median years since diagnosis (range): NR (NR)
Mean PSA ng/ml (SD): NR (NR) Median PSA ng/ml (range): NR (NR)
AJCC, American Joint Committee on Cancer; ECOG, Eastern Cooperative Oncology Group; NR, not reported; PC, prostate cancer; PSA, prostate-specific antigen; SD, standard deviation; TNM, Tumor Nodes Metastasis classification of malignant tumors; USA, United States of America.

Nicolas *et al*, 2015 (24)
USA
PC. Diagnosis: Histology Other details (NR)
Population (further details): familial (NR)
Treatment (further details): NR (NR)
Total (n=12)
Mean age (SD): 57.8 (NR) Median age (range): NR (41, 68)
Ethnicity: Caucasian (100), Hispanic (0)
Gleason score: 6 (41.7); 7 (50); 8 (8.3)
AJCC stage: NR
TNM stage: T2cN0MX (41.7); T2aN0MX (8.3); T3bN0MX (8.3): T2cN0MX (8.3); T3aN0MX (8.3); T1c (8.3); T3bN1M0 (8.3); T2cNO (8.3)
ECOG score 0: NR 1: NR 0-1: NR ≥2: NR
Previous treatments: NR
Familial history of PC: 12 (100)
Mean years since diagnosis (SD): NR (NR) Median years since diagnosis (range): NR (NR)

Mean PSA ng/ml (SD): NR (NR) Median PSA ng/ml (range): NR) (NR)
AJCC, American Joint Committee on Cancer; ECOG, Eastern Cooperative Oncology Group; NR, not reported; PC, prostate cancer; PSA, prostate-specific antigen; SD, standard deviation; TNM, Tumor Nodes Metastasis classification of malignant tumors; USA, United States of America.

Nicolosi *et al*, 2017 (81)
USA
PC. Diagnosis: NR Other details (NR)
Population (further details): unselected (NR)
Treatment (further details): NR (NR)
Total (n=1158)
Mean age (SD): NR (NR) Median age (range): NR (NR)
Ethnicity: NR
Gleason score: NR
AJCC stage: NR
TNM stage: NR

ECOG score 0: NR 1: NR 0-1: NR ≥2: NR
Previous treatments: NR
Familial history of PC: NR
Mean years since diagnosis (SD): NR (NR) Median years since diagnosis (range): NR (NR)
Mean PSA ng/ml (SD): NR (NR) Median PSA ng/ml (range): NR) (NR)
Comments: No patient characteristics provided
AJCC, American Joint Committee on Cancer; ECOG, Eastern Cooperative Oncology Group; NR, not reported; PC, prostate cancer; PSA, prostate-specific antigen; SD, standard deviation; TNM, Tumor Nodes Metastasis classification of malignant tumors; USA, United States of America.

Nientiedt *et al*, 2017 (82)
Germany
mCRPC. Diagnosis: Histology Other details (NR)
Population (further details): treatment (docetaxel)
Treatment (further details): docetaxel (NR)
Total (n=53)

Mean age (SD): NR (NR) Median age (range): 63 (40, 78)
Ethnicity: NR
Gleason score: 3+4 (9.4); 4+3 (9.4); 8 (9.4); 9-10 (69.8); unknown (1.9)
AJCC stage: NR
TNM stage: T2 (7.5); T3 (69.8); T4 (13.2); Tx (9.4); N0 (35.8); N1 (52.8); Nx (11.3); M0 (54.7); M1 (41.5); Mx (3.8)
ECOG score 0: 30 (56.6) 1: 21 (39.6) 0-1: 2 (3.8) ≥2: 0
Previous treatments: Radical prostatectomy (77.4) Primary radiotherapy (1.9) Androgen deprivation therapy (100) Adjuvant radiotherapy (24.5) Salvage radiotherapy (13.2) Enzalutamide and/or Abiraterone (15.1)
Familial history of PC: NR
Mean years since diagnosis (SD): NR (NR) Median years since diagnosis (range): NR (NR)
Mean PSA ng/ml (SD): NR (NR) Median PSA ng/ml (range): 30) (0.6, 6782)
Comments: Population also included primary metastatic PC; Treatment prior to docetaxel is reported
AJCC, American Joint Committee on Cancer; CRPC, castration-resistant PC; ECOG, Eastern Cooperative Oncology Group; NR, not reported; PC, prostate cancer; PSA, prostate-specific antigen; SD, standard deviation; TNM, Tumor Nodes Metastasis classification of malignant tumors.

Palapattu *et al*, 2015 (20)

USA
PC. Diagnosis: NR Other details (NR)
Population (further details): unselected (NR)
Treatment (further details): NR (NR)
Total (n=9)
Mean age (SD): NR (NR) Median age (range): NR (NR)
Ethnicity: NR
Gleason score: 7 (56)
AJCC stage: NR
TNM stage: NR
ECOG score 0: NR 1: NR 0-1: NR ≥2: NR
Previous treatments: NR
Familial history of PC: NR
Mean years since diagnosis (SD): NR (NR) Median years since diagnosis (range): NR (NR)
Mean PSA ng/ml (SD): NR (NR) Median PSA ng/ml (range): NR) (NR)

Comments: Gleason score all start at 6, after 1 year 5 of 9 are at GS7
AJCC, American Joint Committee on Cancer; ECOG, Eastern Cooperative Oncology Group; NR, not reported; PC, prostate cancer; PSA, prostate-specific antigen; SD, standard deviation; TNM, Tumor Nodes Metastasis classification of malignant tumors; USA, United States of America.

Patel *et al*, 2016 (83)
USA
PC. Diagnosis: NR Other details (NR)
Population (further details): unselected (NR)
Treatment (further details): NR (NR)
Total (n=327)
Mean age (SD): NR (NR) Median age (range): NR (NR)
Ethnicity: NR
Gleason score: NR
AJCC stage: NR
TNM stage: NR
ECOG score 0: NR 1: NR 0-1: NR ≥2: NR

Previous treatments: NR
Familial history of PC: NR
Mean years since diagnosis (SD): NR (NR) Median years since diagnosis (range): NR (NR)
Mean PSA ng/ml (SD): NR (NR) Median PSA ng/ml (range): NR (NR)
AJCC, American Joint Committee on Cancer; DDR, DNA damage repair; ECOG, Eastern Cooperative Oncology Group; NR, not reported; PC, prostate cancer; PSA, prostate-specific antigen; SD, standard deviation; TNM, Tumor Nodes Metastasis classification of malignant tumors; USA, United States of America.

Petrovics *et al*, 2016 (84)
USA
PC. Diagnosis: NR Other details (NR)
Population (further details): unselected (NR)
Treatment (further details): NR (NR)
Total (n=857)
Mean age (SD): NR (NR) Median age (range): NR (NR)
Ethnicity: African American (NR); Caucasian American (NR)
Gleason score:
AJCC stage: NR
TNM stage: NR

ECOG score 0: NR 1: NR 0-1: NR ≥2: NR
Previous treatments: NR
Familial history of PC: NR
Mean years since diagnosis (SD): NR (NR) Median years since diagnosis (range): NR (NR)
Mean PSA ng/ml (SD): NR (NR) Median PSA ng/ml (range): NR (NR)
AJCC, American Joint Committee on Cancer; ECOG, Eastern Cooperative Oncology Group; NR, not reported; PC, prostate cancer; PSA, prostate-specific antigen; SD, standard deviation; TNM, Tumor Nodes Metastasis classification of malignant tumors; USA, United States of America.

Pomerantz *et al*, 2017 (85)		
USA		
mCRPC. Diagnosis: NR Other details (NR)		
Population (further details): treatment (Carboplatin-based chemotherapy)		
Treatment (further details): Carboplatin/docetaxel-based chemotherapy (At least two doses of carboplatin and docetaxel)		
Total (n=141)	DDR+ (n=8)	DDR- (n=133)

Mean age (SD): NR (NR) Median age (range): 59 (40, 80)	Mean age (SD): NR (NR) Median age (range): 53 (40, 62)	Mean age (SD): NR (NR) Median age (range): 60 (40, 80)
Ethnicity: European American (87.2); African American (2.8); Hispanic (1.4); Unknown (8.5)	Ethnicity: European American (100); African American (0); Hispanic (0); Unknown (0)	Ethnicity: European American (86.5); African American (3); Hispanic (1.5); Unknown (9)
Gleason score: 6 (6.4); 7 (22); 8-10 (62.4); unknown (9.2)	Gleason score: 6 (0); 7 (12.5); 8-10 (75); unknown (12.5)	Gleason score: 6 (6.8); 7 (22.6); 8-10 (61.7); unknown (9)
AJCC stage: NR	AJCC stage: NR	AJCC stage: NR
TNM stage: NR	TNM stage: NR	TNM stage: NR
ECOG score 0: NR 1: NR 0-1: NR ≥2: NR	ECOG score 0: NR 1: NR 0-1: NR ≥2: NR	ECOG score 0: NR 1: NR 0-1: NR ≥2: NR
Previous treatments: NR	Previous treatments: NR	Previous treatments: NR
Familial history of PC: 26 (18.4)	Familial history of PC: 2 (25)	Familial history of PC: 24 (18)
Mean years since diagnosis (SD): 6.3 (NR) Median years since diagnosis (range): NR (0.5, 20.7)	Mean years since diagnosis (SD): 4.5 (NR) Median years since diagnosis (range): NR (1.1, 13.7)	Mean years since diagnosis (SD): 6.3 (NR) Median years since diagnosis (range): NR (0.5, 20.7)
Mean PSA ng/ml (SD): 170 (NR) Median PSA ng/ml (range): NR) (0, 9145)	Mean PSA ng/ml (SD): 49 (NR) Median PSA ng/ml (range): NR) (1, 515)	Mean PSA ng/ml (SD): 204 (NR) Median PSA ng/ml (range): NR) (0, 9145)
Comments: PSA at diagnosis also available; PSA presented here is at start of chemo	Comments: PSA at diagnosis also available; PSA presented here is at start of chemo	Comments: PSA at diagnosis also available; PSA presented here is at start of chemo

AJCC, American Joint Committee on Cancer; DDR, DNA damage repair; ECOG, Eastern Cooperative Oncology Group; NR, not reported; PC, prostate cancer; PSA, prostate-specific antigen; SD, standard deviation; TNM, Tumor Nodes Metastasis classification of malignant tumors; USA, United States of America.

Pritchard *et al*, 2014 (86)
USA
mPC. Diagnosis: autopsy Other details (primary and metastatic prostate cancer)
Population (further details): unselected (NR)
Treatment (further details): NR (NR)
Total (n=60)
Mean age (SD): NR (NR) Median age (range): NR (NR)
Ethnicity: NR
Gleason score: NR
AJCC stage: NR
TNM stage: NR
ECOG score 0: NR 1: NR 0-1: NR ≥2: NR
Previous treatments: NR

Familial history of PC: NR
Mean years since diagnosis (SD): NR (NR) Median years since diagnosis (range): NR (NR)
Mean PSA ng/ml (SD): NR (NR) Median PSA ng/ml (range): NR (NR)
AJCC, American Joint Committee on Cancer; ECOG, Eastern Cooperative Oncology Group; m, metastatic; NR, not reported; PC, prostate cancer; PSA, prostate-specific antigen; SD, standard deviation; TNM, Tumor Nodes Metastasis classification of malignant tumors; USA, United States of America.

Pritchard *et al*, 2016 (87)	
Multi-national	
mPC and Primary PC. Diagnosis: Histology Other details (mPC cohort)	
Population (further details): unselected (NR)	
Treatment (further details): NR (NR)	
mPC (n=692)	Primary PC (n=499)
Mean age (SD): <50 (7.2); 50-59 (31.7); 60-69 (43.5); 70-79 (13.6); ≥80 (1.9); unknown (2.2) (NR) Median age (range): NR (NR)	Mean age (SD): <50 (5.4); 50-59 (35.4); 60-69 (48.7); 70-79 (10.4); ≥80 (0); unknown (0) (NR) Median age (range): NR (NR)
Ethnicity: Non-Hispanic white (83.2); Hispanic (1.6); non-Hispanic black (5.8); Asian or Pacific Islander (1.7); other or unknown (7.7)	Ethnicity: Non-Hispanic white (81.4); Hispanic (1.4); non-Hispanic black (11.6); Asian or Pacific Islander (2.4); other or unknown (3.2)
Gleason score: ≤6 (6.07); 3+4 (9.4); 4+3 (13.3); 8-10 (55.2); unknown (16.0)	Gleason score: ≤6 (9.0); 3+4 (29.7); 4+3 (20.2); 8-10 (41.1); unknown (0)

AJCC stage: NR	AJCC stage: NR
TNM stage: NR	TNM stage: NR
ECOG score 0: NR 1: NR 0-1: NR ≥2: NR	ECOG score 0: NR 1: NR 0-1: NR ≥2: NR
Previous treatments: NR	Previous treatments: NR
Familial history of PC: 133 (19.2)	Familial history of PC: NR
Mean years since diagnosis (SD): NR (NR) Median years since diagnosis (range): NR (NR)	Mean years since diagnosis (SD): NR (NR) Median years since diagnosis (range): NR (NR)
Mean PSA ng/ml (SD): NR (NR) Median PSA ng/ml (range): NR) (NR)	Mean PSA ng/ml (SD): NR (NR) Median PSA ng/ml (range): NR) (NR)
AJCC, American Joint Committee on Cancer; ECOG, Eastern Cooperative Oncology Group; m, metastatic; NR, not reported; PC, prostate cancer; PSA, prostate-specific antigen; SD, standard deviation; TNM, Tumor Nodes Metastasis classification of malignant tumors.	

Pugh *et al*, 2009 (88)
Canada
PC. Diagnosis: Histology and PSA Other details (NR)
Population (further details): treatment (Brachytherapy)
Treatment (further details): Brachytherapy (Near-ideal rectal and prostate post-implant dosimetry: prostate D90 <175 Gy (dose covering 90% of the prostate <175 Gy), prostate V100 >85% (volume of the prostate covered by >85% of the radiation dose), and rectal VR100 <1.0 cm^3 (volume of the rectum rec)
Total (n=41)
Mean age (SD): NR (NR) Median age (range): NR (NR)
Ethnicity: NR
Gleason score: NR
AJCC stage: 1C (58); 2A (32); 2B (10)
TNM stage: NR
ECOG score 0: NR 1: NR 0-1: NR ≥2: NR
Previous treatments: NR
Familial history of PC: NR

Mean years since diagnosis (SD): NR (NR) Median years since diagnosis (range): NR (NR)
Mean PSA ng/ml (SD): NR (NR) Median PSA ng/ml (range): NR (NR)
AJCC, American Joint Committee on Cancer; ECOG, Eastern Cooperative Oncology Group; NR, not reported; PC, prostate cancer; PSA, prostate-specific antigen; SD, standard deviation; TNM, Tumor Nodes Metastasis classification of malignant tumors.

Robbins *et al*, 2011 (21)
USA
mPC. Diagnosis: Histology Other details (NR)
Population (further details): unselected (NR)
Treatment (further details): NR (NR)
Total (n=8)
Mean age (SD): NR (NR) Median age (range): NR (NR)
Ethnicity: NR
Gleason score: NR
AJCC stage: NR
TNM stage: NR

ECOG score 0: NR 1: NR 0-1: NR ≥2: NR
Previous treatments: NR
Familial history of PC: NR
Mean years since diagnosis (SD): NR (NR) Median years since diagnosis (range): NR (NR)
Mean PSA ng/ml (SD): NR (NR) Median PSA ng/ml (range): NR (NR)
Comments: Extremely limited patient characteristics presented
AJCC, American Joint Committee on Cancer; ECOG, Eastern Cooperative Oncology Group; m, metastatic; NR, not reported; PC, prostate cancer; PSA, prostate-specific antigen; SD, standard deviation; TNM, Tumor Nodes Metastasis classification of malignant tumors; USA, United States of America.

Robinson *et al*, 2015 (89)
Multi-national
mCRPC. Diagnosis: Histology Other details (NR)
Population (further details): unselected (NR)
Treatment (further details): NR (NR)
Total (n=150)

Mean age (SD): NR (NR) Median age (range): 68 (43, 84)
Ethnicity: NR
Gleason score: NR
AJCC stage: NR
TNM stage: NR
ECOG score 0: NR 1: NR 0-1: NR ≥2: NR
Previous treatments: Abiraterone acetate or enzalutamide (48); taxane chemotherapy (41)
Familial history of PC: NR
Mean years since diagnosis (SD): NR (NR) Median years since diagnosis (range): NR (NR)
Mean PSA ng/ml (SD): 55.78 () Median PSA ng/ml (range): NR (0.04, 4654.92)
AJCC, American Joint Committee on Cancer; CRPC, castration-resistant prostate cancer; ECOG, Eastern Cooperative Oncology Group; m, metastatic; NR, not reported; PC, prostate cancer; PSA, prostate-specific antigen; SD, standard deviation; TNM, Tumor Nodes Metastasis classification of malignant tumors.

Romero *et al*, 2017 (90)
Spain
mCRPC. Diagnosis: Histology Other details (NR)
Population (further details): unselected (NR)
Treatment (further details): NR (NR)
Total (n=419)
Mean age (SD): NR (NR) Median age (range): 73 (43, 94)
Ethnicity: NR
Gleason score: NR
AJCC stage: NR
TNM stage: NR
ECOG score 0: NR 1: NR 0-1: NR (91) ≥2: NR (9)
Previous treatments: NR
Familial history of PC: NR
Mean years since diagnosis (SD): NR (NR) Median years since diagnosis (range): NR (NR)

Mean PSA ng/ml (SD): NR (NR) Median PSA ng/ml (range): 26.95) (<0.02, 5198)
Comments: Population data included for 'at diagnosis of mCRPC' rather than diagnosis of PC (more relevant to the study)
AJCC, American Joint Committee on Cancer; CRPC, castration-resistant prostate cancer; ECOG, Eastern Cooperative Oncology Group; m, metastatic; NR, not reported; PC, prostate cancer; PSA, prostate-specific antigen; SD, standard deviation; TNM, Tumor Nodes Metastasis classification of malignant tumors.

Sanchez *et al*, 2016 (91)	
USA	
Primary PC. Diagnosis: Initially through self-reporting that was confirmed by medical records and pathology reports Other details (NR)	
Population (further details): treatment (Radiotherapy or radical prostatectomy)	
Treatment (further details): Radiotherapy (NR) Radical prostatectomy (NR)	
Radiotherapy (n=802)	Radical prostatectomy (n=1111)
Mean age (SD): 72.1 (5.9) Median age (range): NR (NR)	Mean age (SD): 65.6 (6.1) Median age (range): NR (NR)
Ethnicity: European descent	Ethnicity: European descent
Gleason score: ≤6 (64); 7 (25); ≥8 (11)	Gleason score: ≤6 (43); 7 (45); ≥8 (11)
AJCC stage: NR	AJCC stage: NR
TNM stage: T1/T2 (95); T3 (5)	TNM stage: T1/T2 (98); T3 (2)

ECOG score 0: NR 1: NR 0-1: NR ≥2: NR	ECOG score 0: NR 1: NR 0-1: NR ≥2: NR
Previous treatments: Neoadjuvant/adjuvant ADT (33)	Previous treatments: Neoadjuvant/adjuvant ADT (9)
Familial history of PC: NR	Familial history of PC: NR
Mean years since diagnosis (SD): NR (NR) Median years since diagnosis (range): NR (NR)	Mean years since diagnosis (SD): NR (NR) Median years since diagnosis (range): NR (NR)
Mean PSA ng/ml (SD): NR (NR) Median PSA ng/ml (range): NR (NR)	Mean PSA ng/ml (SD): NR (NR) Median PSA ng/ml (range): NR (NR)
ADT, androgen deprivation therapy; AJCC, American Joint Committee on Cancer; ECOG, Eastern Cooperative Oncology Group; NR, not reported; PC, prostate cancer; PSA, prostate-specific antigen; SD, standard deviation; TNM, Tumor Nodes Metastasis classification of malignant tumors; USA, United States of America.	

Sandhu *et al*, 2013 (92)	
UK and Multi-national	
mCRPC (UK) CRPC (Multi-national). Diagnosis: NR Other details (NR)	
Population (further details): unselected (NR)	
Treatment (further details): Mixed treatment (Olaparib 200 mg (50%); Olaparib 300 mg (25%); Niraparib (MK-4827) (25%))	
mCRPC (n=4)	CRPC (n=23)

Mean age (SD): 55.4 (6.4) Median age (range): NR (54.6, 58)	Mean age (SD): NR (NR) Median age (range): NR (NR)
Ethnicity: NR	Ethnicity: NR
Gleason score: 6 (25); 7 (25); 8 (25); NR (25)	Gleason score: NR
AJCC stage: NR	AJCC stage: NR
TNM stage: T3N0M1 (50); T1cN1M0 (25); TxNXM1 (25)	TNM stage: NR
ECOG score 0: NR 1: NR 0-1: NR ≥2: NR	ECOG score 0: NR 1: NR 0-1: NR ≥2: NR
Previous treatments: Androgen blockade (bicalutamide) (100); carboplatin AUC6 (25); docetaxel (50); docetaxel + figitumumab (25); abiraterone (25); radical radiotherapy (25), radiotherapy to inguinal lymph nodes (25)	Previous treatments: NR
Familial history of PC: NR	Familial history of PC: 0 (0)
Mean years since diagnosis (SD): NR (NR) Median years since diagnosis (range): NR (NR)	Mean years since diagnosis (SD): NR (NR) Median years since diagnosis (range): NR (NR)
Mean PSA ng/ml (SD): NR (NR) Median PSA ng/ml (range): NR (NR)	Mean PSA ng/ml (SD): NR (NR) Median PSA ng/ml (range): NR (NR)
Comments: Sandhu 2013(92)	Comments: ECOG scores were provided for the full cohort but not separated by sub-group
AJCC, American Joint Committee on Cancer; AUC, area under the curve; CRPC, castration-resistant prostate cancer; ECOG, Eastern Cooperative Oncology Group; m, metastatic; NR, not reported; PC, prostate cancer; PSA, prostate-specific antigen; SD, standard deviation; TNM, Tumor Nodes Metastasis classification of malignant tumors; UK, United Kingdom.	

Schweizer *et al*, 2016 (27)
USA
Ductal PC. Diagnosis: NR Other details (NR)
Population (further details): unselected (NR)
Treatment (further details): NR (NR)
Total (n=10)
Mean age (SD): 59 (NR) Median age (range): NR (40, 73)
Ethnicity: NR
Gleason score: 7 (20); 8 (20); 9 (60)
AJCC stage: NR
TNM stage: NR
ECOG score 0: NR 1: NR 0-1: NR ≥2: NR
Previous treatments: NR
Familial history of PC: NR
Mean years since diagnosis (SD): NR (NR) Median years since diagnosis (range): NR (NR)

Mean PSA ng/ml (SD): NR (NR) Median PSA ng/ml (range): NR (NR)
AJCC, American Joint Committee on Cancer; ECOG, Eastern Cooperative Oncology Group; NR, not reported; PC, prostate cancer; PSA, prostate-specific antigen; SD, standard deviation; TNM, Tumor Nodes Metastasis classification of malignant tumors; USA, United States of America.

Shapiro *et al*, 2017 (93)
Multi-national
mCRPC. Diagnosis: Histologically or cytologically confirmed adenocarcinoma or poorly differentiated carcinoma of the prostate; and has undergone surgical or medical castration with serum testosterone levels of ≤ 50 ng/dL (1.73 nM) Other details (NR)
Population (further details): unselected (NR)
Treatment (further details): Rucaparib (600 mg oral rucaparib administered twice daily)
DDR+ (n=NR)
Mean age (SD): NR (NR) Median age (range): NR (NR)
Ethnicity: NR
Gleason score: NR
AJCC stage: NR
TNM stage: NR

ECOG score 0: NR 1: NR 0-1: NR ≥2: NR
Previous treatments: NR
Familial history of PC: NR
Mean years since diagnosis (SD): NR (NR) Median years since diagnosis (range): NR (NR)
Mean PSA ng/ml (SD): NR (NR) Median PSA ng/ml (range): NR) (NR)
Comments: Ongoing trial with no reported details.
AJCC, American Joint Committee on Cancer; CRPC, castration-resistant prostate cancer; DDR, DNA damage repair; ECOG, Eastern Cooperative Oncology Group; m, metastatic; NR, not reported; PC, prostate cancer; PSA, prostate-specific antigen; SD, standard deviation; TNM, Tumor Nodes Metastasis classification of malignant tumors.

Sofronescu *et al*, 2012 (94)
USA
PC. Diagnosis: NR Other details (NR)
Population (further details): treatment (radiotherapy)
Treatment (further details): radiotherapy (NR)
Total (n=87)

Mean age (SD): NR (NR) Median age (range): NR (NR)
Ethnicity: NR
Gleason score: NR
AJCC stage: NR
TNM stage: NR
ECOG score 0: NR 1: NR 0-1: NR ≥2: NR
Previous treatments: NR
Familial history of PC: NR
Mean years since diagnosis (SD): NR (NR) Median years since diagnosis (range): NR (NR)
Mean PSA ng/ml (SD): NR (NR) Median PSA ng/ml (range): NR (NR)
AJCC, American Joint Committee on Cancer; ECOG, Eastern Cooperative Oncology Group; NR, not reported; PC, prostate cancer; PSA, prostate-specific antigen; SD, standard deviation; TNM, Tumor Nodes Metastasis classification of malignant tumors; UK, United Kingdom.

Sonpavde *et al*, 2017 (6)
NR
mCRPC. Diagnosis: NR Other details (NR)
Population (further details): unselected (NR)
Treatment (further details): NR (NR)
Total (n=514)
Mean age (SD): NR (NR) Median age (range): 70 (39, 91)
Ethnicity: NR
Gleason score: NR
AJCC stage: NR
TNM stage: NR
ECOG score 0: NR 1: NR 0-1: NR ≥2: NR
Previous treatments: NR
Familial history of PC: NR
Mean years since diagnosis (SD): NR (NR) Median years since diagnosis (range): NR (NR)

Mean PSA ng/ml (SD): NR (NR) Median PSA ng/ml (range): NR (NR)
AJCC, American Joint Committee on Cancer; CRPC, castration-resistant prostate cancer; ECOG, Eastern Cooperative Oncology Group; m, metastatic; NR, not reported; PC, prostate cancer; PSA, prostate-specific antigen; SD, standard deviation; TNM, Tumor Nodes Metastasis classification of malignant tumors.

Stephens *et al*, 2016 (29)
NR
Other. Diagnosis: Histology Other details (Relapsed/metastatic neuroendocrine carcinoma of the prostate (NCAP))
Population (further details): unselected (NR)
Treatment (further details): NR (NR)
Total (n=37)
Mean age (SD): 65.1 (NR) Median age (range): NR (43, 83)
Ethnicity: NR
Gleason score: NR
AJCC stage: IV (100)
TNM stage: NR

ECOG score 0: NR 1: NR 0-1: NR ≥2: NR
Previous treatments: NR
Familial history of PC: NR
Mean years since diagnosis (SD): NR (NR) Median years since diagnosis (range): NR (NR)
Mean PSA ng/ml (SD): NR (NR) Median PSA ng/ml (range): NR (NR)
AJCC, American Joint Committee on Cancer; ECOG, Eastern Cooperative Oncology Group; NR, not reported; PC, prostate cancer; PSA, prostate-specific antigen; SD, standard deviation; TNM, Tumor Nodes Metastasis classification of malignant tumors.

Struss *et al*, 2017 (95)
Canada
mCRPC. Diagnosis: NR Other details (NR)
Population (further details): unselected (NR)
Treatment (further details): chemotherapy; androgen deprivation therapy (NR)
Total (n=319)
Mean age (SD): NR (NR) Median age (range): NR (NR)

Ethnicity: NR
Gleason score: NR
AJCC stage: NR
TNM stage: NR
ECOG score 0: NR 1: NR 0-1: NR ≥2: NR
Previous treatments: NR
Familial history of PC: NR
Mean years since diagnosis (SD): NR (NR) Median years since diagnosis (range): NR (NR)
Mean PSA ng/ml (SD): NR (NR) Median PSA ng/ml (range): NR (NR)
AJCC, American Joint Committee on Cancer; CRPC, castration-resistant prostate cancer; ECOG, Eastern Cooperative Oncology Group; m, metastatic; NR, not reported; PC, prostate cancer; PSA, prostate-specific antigen; SD, standard deviation; TNM, Tumor Nodes Metastasis classification of malignant tumors.

Tanaka *et al*, 2009 (7)
Japan
PC. Diagnosis: Pathology (TNM and Grade) Other details (NR)

Population (further details): unselected (NR)
Treatment (further details): NR (NR)
Total (n=177)
Mean age (SD): 68.6 (0.4) Median age (range): NR (NR)
Ethnicity: NR
Gleason score: NR
AJCC stage: NR
TNM stage: NR
ECOG score 0: NR 1: NR 0-1: NR ≥2: NR
Previous treatments: NR
Familial history of PC: NR
Mean years since diagnosis (SD): NR (NR) Median years since diagnosis (range): NR (NR)
Mean PSA ng/ml (SD): 11.6 (0.8) Median PSA ng/ml (range): NR) (NR)
Comments: Age and PSA levels in BPH patients also available

AJCC, American Joint Committee on Cancer; BPH, benign prostatic hyperplasia; ECOG, Eastern Cooperative Oncology Group; NR, not reported; PC, prostate cancer; PSA, prostate-specific antigen; SD, standard deviation; TNM, Tumor Nodes Metastasis classification of malignant tumors.

Timms *et al*, 2016 (96)	
NR	
PC. Diagnosis: Histology Other details (NR)	
Population (further details): unselected (commercial biobank), unselected (Transatlantic Prostate Group Cohort)	
Treatment (further details): NR (NR)	
Biobank (n=39)	Transatlantic Prostate Group Cohort (n=45)
Mean age (SD): NR (NR) Median age (range): NR (NR)	Mean age (SD): NR (NR) Median age (range): NR (NR)
Ethnicity: NR	Ethnicity: NR
Gleason score: <7 (21); 3+4 (64); 4+3 (15); >7 (0)	Gleason score: <7 (2); 3+4 and 4+3 (82); >7 (18)
AJCC stage: NR	AJCC stage: NR
TNM stage: NR	TNM stage: NR
ECOG score 0: NR 1: NR 0-1: NR ≥2: NR	ECOG score 0: NR 1: NR 0-1: NR ≥2: NR
Previous treatments: NR	Previous treatments: NR

Familial history of PC: NR	Familial history of PC: NR
Mean years since diagnosis (SD): NR (NR) Median years since diagnosis (range): NR (NR)	Mean years since diagnosis (SD): NR (NR) Median years since diagnosis (range): NR (NR)
Mean PSA ng/ml (SD): NR (NR) Median PSA ng/ml (range): NR (NR)	Mean PSA ng/ml (SD): NR (NR) Median PSA ng/ml (range): NR (NR)
AJCC, American Joint Committee on Cancer; ECOG, Eastern Cooperative Oncology Group; NR, not reported; PC, prostate cancer; PSA, prostate-specific antigen; SD, standard deviation; TNM, Tumor Nodes Metastasis classification of malignant tumors.	

Tischkowitz *et al*, 2008 (97)	
Canada	
PC. Diagnosis: NR Other details (NR)	
Population (further details): Ashkenazi (chosen based on the presence of a family history and/or a high Gleason score)	
Treatment (further details): NR (NR)	
family history and/or a high Gleason score (n=25)	Total (n=125)
Mean age (SD): NR (NR) Median age (range): NR (NR)	Mean age (SD): NR (NR) Median age (range): NR (NR)
Ethnicity: NR	Ethnicity: NR
Gleason score: mean Gleason score: 7.4	Gleason score: mean Gleason score: 5.6
AJCC stage: NR	AJCC stage: NR
TNM stage: NR	TNM stage: NR

ECOG score 0: NR 1: NR 0-1: NR ≥2: NR	ECOG score 0: NR 1: NR 0-1: NR ≥2: NR
Previous treatments: NR	Previous treatments: NR
Familial history of PC: NR	Familial history of PC: NR
Mean years since diagnosis (SD): NR (NR) Median years since diagnosis (range): NR (NR)	Mean years since diagnosis (SD): NR (NR) Median years since diagnosis (range): NR (NR)
Mean PSA ng/ml (SD): NR (NR) Median PSA ng/ml (range): NR (NR)	Mean PSA ng/ml (SD): NR (NR) Median PSA ng/ml (range): NR (NR)
Comments: mean age at diagnosis: 67.5 years	Comments: mean age at diagnosis: 68.2 years
AJCC, American Joint Committee on Cancer; ECOG, Eastern Cooperative Oncology Group; NR, not reported; PC, prostate cancer; PSA, prostate-specific antigen; SD, standard deviation; TNM, Tumor Nodes Metastasis classification of malignant tumors.	

Uchida *et al*, 1999 (12)
Japan
Primary PC. Diagnosis: Pathology (Stage and Grade) Other details (NR)
Population (further details): unselected (NR)
Treatment (further details): NR (NR)
Total (n=24)

Mean age (SD): NR (NR) Median age (range): NR (NR)
Ethnicity: NR
Gleason score: NR
AJCC stage: NR
TNM stage: NR
ECOG score 0: NR 1: NR 0-1: NR ≥2: NR
Previous treatments: NR
Familial history of PC: NR
Mean years since diagnosis (SD): NR (NR) Median years since diagnosis (range): NR (NR)
Mean PSA ng/ml (SD): NR (NR) Median PSA ng/ml (range): NR (NR)
Comments: Staged as A2 in 1 patient, B in 3, C in 5, and D in 15 patients. 4 patients had well-differentiated, 9 had moderately differentiated, and 11 had poorly differentiated tumors.
AJCC, American Joint Committee on Cancer; ECOG, Eastern Cooperative Oncology Group; NR, not reported; PC, prostate cancer; PSA, prostate-specific antigen; SD, standard deviation; TNM, Tumor Nodes Metastasis classification of malignant tumors.

Vazina *et al*, 2000 (98)
Israel
PC. Diagnosis: Clinical and histopathological diagnosis Other details (NR)
Population (further details): Unselected or Ashkenazi (Unselected prostate cancer patients (95 out of 174 of Ashkenazi origin))
Treatment (further details): NR (NR)
Total (n=174)
Mean age (SD): NR (NR) Median age (range): 66 (45, 81)
Ethnicity: Ashkenazi (54.6); non-Ashkenazis (45.4)
Gleason score: 5-7 (48.3); 8-10 (6.9)
AJCC stage: NR
TNM stage: T2 (60%); T3 (26.4%)
ECOG score 0: NR 1: NR 0-1: NR ≥2: NR
Previous treatments: NR
Familial history of PC: 19 (10.9)
Mean years since diagnosis (SD): NR (NR) Median years since diagnosis (range): NR (NR)

Mean PSA ng/ml (SD): NR (NR) Median PSA ng/ml (range): NR (NR)
AJCC, American Joint Committee on Cancer; ECOG, Eastern Cooperative Oncology Group; NR, not reported; PC, prostate cancer; PSA, prostate-specific antigen; SD, standard deviation; TNM, Tumor Nodes Metastasis classification of malignant tumors.

Williams *et al*, 1996 (99)
USA
Primary PC. Diagnosis: NR Other details (stage B)
Population (further details): unselected (NR)
Treatment (further details): radical prostatectomy (NR)
Total (n=23)
Mean age (SD): NR (NR) Median age (range): NR (NR)
Ethnicity: NR
Gleason score: NR
AJCC stage: NR
TNM stage: NR
ECOG score 0: NR 1: NR 0-1: NR ≥2: NR

Previous treatments: radical prostatectomy (100)
Familial history of PC: NR
Mean years since diagnosis (SD): NR (NR) Median years since diagnosis (range): NR (NR)
Mean PSA ng/ml (SD): NR (NR) Median PSA ng/ml (range): NR (NR)
Comments: Very limited patient characteristics presented
AJCC, American Joint Committee on Cancer; ECOG, Eastern Cooperative Oncology Group; NR, not reported; PC, prostate cancer; PSA, prostate-specific antigen; SD, standard deviation; TNM, Tumor Nodes Metastasis classification of malignant tumors ; USA, United States of America.

Wu *et al*, 2006 (100)
USA
Primary PC. Diagnosis: NR Other details (NR)
Population (further details): unselected (NR)
Treatment (further details): NR (NR)
Total (n=84)
Mean age (SD): NR (NR) Median age (range): NR (48, 75)
Ethnicity: NR
Gleason score: NR
AJCC stage: NR

TNM stage: NR
ECOG score 0: NR 1: NR 0-1: NR ≥2: NR
Previous treatments: NR
Familial history of PC: NR
Mean years since diagnosis (SD): NR (NR) Median years since diagnosis (range): NR (NR)
Mean PSA ng/ml (SD): NR (NR) Median PSA ng/ml (range): NR) (NR)
Comments: Very limited baseline characteristics presented
AJCC, American Joint Committee on Cancer; ECOG, Eastern Cooperative Oncology Group; NR, not reported; PC, prostate cancer; PSA, prostate-specific antigen; SD, standard deviation; TNM, Tumor Nodes Metastasis classification of malignant tumors ; USA, United States of America.

Xia *et al*, 2015 (18)
USA
PC. Diagnosis: NR Other details (NR)
Population (further details): unselected (NR)
Treatment (further details): NR (NR)

Total (n=20)
Mean age (SD): 65.5 (NR) Median age (range): NR (49, 81)
Ethnicity: NR
Gleason score: 5 (5); 6 (5); 7 (35); 8 (10); 9 (45)
AJCC stage: NR
TNM stage: T1 (0); T2 (451); T3 (45); T4 (5); TX (5); N0 (20); N1 (35); N2(5); Nx(40); M0(65); M1 (35).
ECOG score 0: NR 1: NR 0-1: NR ≥2: NR
Previous treatments: NR
Familial history of PC: NR
Mean years since diagnosis (SD): NR (NR) Median years since diagnosis (range): NR (NR)
Mean PSA ng/ml (SD): 18.9 (NR) Median PSA ng/ml (range): NR (0.33, 126)
Comments: PSA levels reported at the time of the first sample collection
AJCC, American Joint Committee on Cancer; ECOG, Eastern Cooperative Oncology Group; NR, not reported; PC, prostate cancer; PSA, prostate-specific antigen; SD, standard deviation; TNM, Tumor Nodes Metastasis classification of malignant tumors ; USA, United States of America.

Zhu *et al*, 2010 (101)
USA
PC. Diagnosis: NR Other details (NR)
Population (further details): treatment (External beam radiotherapy)
Treatment (further details): External beam radiotherapy (NR)
Total (n=31)
Mean age (SD): NR (NR) Median age (range): NR (NR)
Ethnicity: NR
Gleason score: NR
AJCC stage: NR
TNM stage: NR
ECOG score 0: NR 1: NR 0-1: NR ≥2: NR
Previous treatments: NR
Familial history of PC: NR
Mean years since diagnosis (SD): NR (NR) Median years since diagnosis (range): NR (NR)

Mean PSA ng/ml (SD): NR (NR) Median PSA ng/ml (range): NR (NR)
AJCC, American Joint Committee on Cancer; ECOG, Eastern Cooperative Oncology Group; NR, not reported; PC, prostate cancer; PSA, prostate-specific antigen; SD, standard deviation; TNM, Tumor Nodes Metastasis classification of malignant tumors ; USA, United States of America.

Zuhlke *et al*, 2012 (102)
USA
PC. Diagnosis: medical record review whenever possible Other details (NR)
Population (further details): familial (hereditary prostate cancer)
Treatment (further details): NR (NR)
Total (n=94)
Mean age (SD): NR (NR) Median age (range): NR (NR)
Ethnicity: Seven families were of African descent, 2 were of Asian descent, and the remaining 85 were of European descent
Gleason score: NR
AJCC stage: NR
TNM stage: NR

ECOG score 0: NR 1: NR 0-1: NR ≥2: NR
Previous treatments: radical prostatectomy
Familial history of PC: NR
Mean years since diagnosis (SD): NR (NR) Median years since diagnosis (range): NR (NR)
Mean PSA ng/ml (SD): NR (NR) Median PSA ng/ml (range): NR) (NR)
AJCC, American Joint Committee on Cancer; ECOG, Eastern Cooperative Oncology Group; NR, not reported; PC, prostate cancer; PSA, prostate-specific antigen; SD, standard deviation; TNM, Tumor Nodes Metastasis classification of malignant tumors ; USA, United States of America.

Appendix S6. Methods for DDR gene mutational analysis.

Germline or somatic mutation	Source of DNA	Methods	Details of methods	DDR definition	Author, year	References
Australia						
NR/ unclear	NR	NR	NR	*BRCA1* and *BRCA2* (undefined)	Cheng *et al,* 2011	(23)
Canada						
Germline	Blood sample	other	Sequencing using an ABI 3730XL DNA Sequencer. Sequences were analysed using Chromas 2.3. Long-range PCR to confirm all variants were located within functional copy of *CHEK2* (chromosome 22q12)	*CHEK2* variants (exon 11 1270T>CY424H; exon 11 1283C>T S428F; exon 11 1312G>T D438Y; exon 13 1525C>T P509S)	Tischkowitz *et al,* 2008	(97)
		PCR	PCR and pyrosequencing	*ATM*; *BCL2*; *BRCA1*; *BRCA2*; *CYP1A1*; *CYP2C9*; *CYP2C19*; *CYP3A5*, *CYP2D6*; *CYP11B2*; *CYP17A1*; *ERCC2*; *ESR1*; *LIG4*; *MSH6*; *NBN*; *NR3C1*; *RAD51*; *RAD52*; *TGFB1*; *XPF*; *XRCC1*, *XRCC2*, *XRCC3*	Damaraju *et al,* 2006	(26)
			Multiplex sizing assay. Samples demonstrating a band shift were run again for confirmation	*BRCA1* (185delAG); *BRCA1* (5382insC); *BRCA2* (6174delT)	Hamel *et al,* 2003	(55)
			RFLP	CHK2 (1100delC)	Nam *et al,* 2005	(15)

		Sanger sequencing	Sanger sequencing method for all 26 coding exons of *BRCA2* (NM_000059.3)	Undefined *BRCA2* mutations	Akbari *et al,* 2014	(103)
	plasma ctDNA	PCR	Targeted germline sequencing	22 undefined DDR genes (including *BRCA2*, *PALB2*, and *CDK12*)	Struss *et al,* 2017	(95)
Denmark						
Germline	Blood sample	PCR	Presence of *CHEK2**1100delC was determined by Taqman PCR and sequencing	*CHEK2**1100delC	Naslund Koch *et al,* 2016	(16)
Germany						
Germline	Blood sample	PCR	Allele frequencies assessed using RFLP analysis with AlwI after PCR amplification of a genomic DNA fragment spanning the exons 23 and 24	*ATM* missense variant P1054R	Meyer *et al,* 2007	(25)
		Sanger sequencing	25 target regions spanning all 26 coding exons of the *BRCA2* gene were amplified by PCR and sequenced by Sanger sequencing. Sequence variants with no codon change and alleles with observed frequencies of >2% were omitted	*BRCA2* exon sequence variants	Maier *et al,* 2014	(72)
Somatic	Tumor biopsy	PCR	Limited details. Ion Torrent AmpliSeq™ technology	*BRCA1* or *BRCA2*	Nientiedt *et al,* 2017	(82)
Israel						
Germline	Blood sample	NR/unclear	NR	*BRCA1* (185delAG, 5382insC); *BRCA2* (6174delT)	Hubert *et al,* 1999	(59)

	Peripheral blood and matched paraffin embedded tumor	PCR	PCR with chr17 markers (D17S250, D17S579 (both localise centromeric to the *BRCA1* locus), D17S855, D17S1322, D17S1325 (all internal to the *BRCA1* locus) and D17S1323, D17S1327 (both telomeric to the *BRCA1* locus)) to measure allelic loss; PCR and restriction enzyme digest to identify three predominant mutations across *BRCA1* and *BRCA2*	Founder mutations in *BRCA1* [185delAG; 5382insC] and *BRCA2* [6174delT]	Vazina *et al,* 2000	(98)
Somatic	Tumor sample from paraffin fixed sections	PCR	Multiplex PCR	Founder mutations in *BRCA1* [185delAG; 5382insC] and *BRCA2* [6174delT]	Giusti *et al,* 2003	(51)

Japan						
Germline	Blood sample	NGS	Performed using a SureSelectHuman. All exon V5+lncRNA (Agilent) for preparing capture libraries. Sequencing reads were mapped to a reference genome (hg19) using BWA-mem and SAMtools. Focused on exonic and splicing variants. Synonymous variants were filtered out. Variants in the genomic super duplicated regions were removed. Database-registered single nucleotide polymorphisms (SNPs) were removed, except for clinically reported variants. Rare variants with minor allele frequency (MAF) of <0.001 were filtered in from information from the NHLBI GO Exome Sequencing Project and the 1000 Genomes Project (1KGP). Allele frequency data from more than 60,000 individuals of Exome Aggregation Consortium (ExAC) was used as reference. For allele frequencies in Japanese, we referred to two databases of the integrative Japanese Genome Variation Database (iJGVD) and the Human Genetic Variation Database (HGVD). To further extract cancer-related genes, information from the CGC database was used	Looked for any germline variants in PC, reported for five *BRCA2* variants (L61P, H1458R, G2508S, H3056Y, and R3384X)	Hayano *et al,* 2016	(57)

NR/unclear	Tumor sample	NGS	DNA was amplified by PCR using primers for the four polymorphic sites. PCR products were subjected to direct DNA sequencing. Sequence analysis of purified products was determined using the same primers with ABI 377 sequencer and dye terminator cycle sequencing kit	*MLH1* polymorphisms that lead to amino acid changes at codons 132, 219, 384, and 723	Tanaka *et al,* 2009	(7)
	Tumor and matched peripheral blood	PCR	DNA was amplified by PCR. LOH was determined using 7 highly polymorphic tandem repeat markers: D17S250, D17S1320, D17S855, D17S1322, D17S1323, D17S579 and D17S588. All coding regions from exons 1 to 24 of the *BRCA1* gene were analyzed	Mutations in *BRCA1* coding regions or LOH on chromosome 17q21	Uchida *et al,* 1999	(12)

Spain						
Germline	Blood sample	Sanger sequencing	Validation of pathogenic mutations by Sanger, MLPA or additional NGS performed for 24 genes on the BROCA panel	Aberrations in 24 undefined DNA-repair genes (reported primarily *BRCA1*, *BRCA2*, *ATM*, and *PALB2* genes)	Romero *et al,* 2017	(90)
UK						
Germline	Blood sample	Other	UKGPCS: The coding region of the *BRCA1* and *BRCA2* genes were screened using multiplex fluorescent heteroduplex detection, Sanger sequencing, and multiplex ligation-dependent probe amplification	Undefined *BRCA1* and *BRCA2*	Castro *et al,* 2011	(38)
		PCR	PCR followed by high-performance liquid chromatography or RFLP	Five *ATM* single-nucleotide polymorphisms: 5557G>A, 5558A>T, 3161C>G, ivs38-8t>c, ivs38-15g>c	Angele *et al,* 2004	(13)
			High-throughput multiplex fluorescent heteroduplex analysis method. Multiplexed, dye-tagged PCR fragments were run on an ABI3130xl Genetic Analyzer. Genetic alterations were confirmed by sequencing	germline mutations in *BRCA2*	Kote-Jarai *et al,* 2011	(104)

			Mutations detected by multiplex PCR, sequenced to identify variants, and deleterious mutations were confirmed by Sanger sequencing	*BRCA1* (4 variants: c.68_69delAG; c.212+1G>T; c.1954dupA; c.2475delC)	Leongamo -rnlert *et al,* 2012	(69)
			PCR and fluorescent mutation detection. Sequencing to characterise mutations	*BRCA2* germline mutations	Edwards *et al,* 2003	(105)
Germline		Capture sequencing	Sequenced for 22 tumor suppressor genes using Agilent target enrichment and Illumina technology	22 tumor suppressor genes including *ATM*, *BRCA1*, *BRCA2*, *CHEK2*, *MLH1*, *MRE11A*, *NBN*, *PALB2*, *RAD51C*, *BARD1*, *BRIP1*, *MSH2*, *MSH6*, *MUTYH*, *PMS2*, and *RAD50*	Leongamo -rnlert *et al,* 2014	(70)
Germline	Peripheral blood and tumor tissue	PCR	*BRCA1* and *BRCA2* were both screened for germline mutations using a combination of the protein truncation test (PTT) and a non-radioactive heteroduplex analysis (HA) to identify variants in the sample set. PTT was used to analyse exon 11 of *BRCA1* (representing approximately 60% of the coding sequence), and exons 10 and 11 *BRCA2* (60% of the coding sequence). Direct sequence analysis was used for confirmation	Undefined *BRCA1* and *BRCA2*	Gayther *et al,* 2000	(50)

Somatic	Tumor biopsy	NGS	The Sanger CGP Cancer Genes V3 panel of 365 genes was screened. Eight samples were sequenced to a median depth of 962 reads (IQR, 896-983X) in the target regions, with a median of 93% (IQR, 92.5%-93%) of the target regions being covered at a depth >100×	365 target genes, which included all our genes of interest (except *RAD51C*) and *CDK12*	Manson-Bahr *et al,* 2015	(73)
	Formalin-fixed paraffin embedded (FFPE)	NGS	Targeted-NGS was performed using the Life Technologies Ion Torrent: Ion AmpliSeq Cancer Hotspot Panel v2 and the Ion Personal Genome Machine sequencer. The hotspot panel covers ~2800 COSMIC mutations of 50 oncogenes and tumor suppressor genes	DNA repair genes such as *ATM* (no further definition)	Jefferies *et al,* 2017	(61)
USA						
Germline	Blood sample	NGS	Next-generation targeted sequencing using the Illumina TruSight Cancer Sequencing panel that includes 94 genes (35 have been identified as being involved in human DNA repair)	35 undefined DDR genes. Results were presented for *BRCA2*, *ATM*, *BLM*, *FANCA*, *MSH2* only	Pomerantz *et al,* 2017	(85)
		Other	TaqMan SNP genotyping assay	5557G>A	Zhu *et al,* 2010	(101)

		PCR	PCR was used to amplify each of the 62 exons, and short intronic regions flanking each exon, that constitute the coding region of the *ATM* gene	Fifty-nine *ATM* genetic alterations, representing 25 different variants, were found in the expressed portions (exons) of the *ATM* gene, or within 10 nucleotides of each exon encompassing potential splice sites.	Cesaretti *et al,* 2007	(41)
			The TaqMan (fluorogenic 5′ nuclease) assay was used for SNP genotyping	*BRCA1**185delAG and *BRCA2**6174delT	Gallagher *et al,* 2012	(48)
Germline	Blood sample	PCR	PCR products were analysed by RFLP, using modified sites (ACRES) for restriction enzymes TaqI (185delAG), DdeI (538insC), and BstXI [6174delT (15)]. Carriers were recognized by the comparison of test digest with digests of PCR analyses of previously verified *BRCA1/2* carriers	*BRCA1* (185delAG, 5382insC) and *BRCA2* (6174delT)	Kirchoff *et al,* 2004	(63)
			Aliquots of amplified DNA were transferred to membranes (Hybond) using a standard protocol (Sambrook et al, 1989)	*BRCA1* (185delAG) and *BRCA2* (6174delT)	Lehrer *et al,* 1998	(68)
			Genomic DNA was purified and amplified using 47 primer pairs and sequenced using BigDye Terminator v3.1 sequencing kit	Protein truncating or SNP *BRCA2* mutations. (4625_4629delACATT and 4074_4075delGT; both in exon 11).	Agalliu *et al,* 2007	(31)

		WES	Variants were restricted to a subset of 157 target genes associated with hereditary cancer risk	157 target genes associated with hereditary cancer risk (ST1). Results reported for *ATM*, *ATR*, *BRCA2*, *FANCL*, *MSR1*, *MUTYH*, *RB1*, *TSHR*, and *WRN*.	Hart *et al,* 2016	(56)
			Exome sequencing of germline DNA was performed at 30x coverage using a VCRome kit for library preparation, and 100bp paired end processing using the HiSeq platform. Human hg19 reference-guided alignment and variant calling were performed using Illumina CASAVA	High value DDR or androgen signalling pathway gene variants that may contribute to familial prostate risk. 826 genes analysed including all DDR genes of interest.	Nicolas *et al,* 2015	(24)

			WES focused on the exonic regions of 50 known DDR genes. The final exome library was sequenced using an Illumina HiSeq 3000 for 75 bp paired-end sequencing with a target sequencing coverage of 30x. Only protein-truncating alterations (nonsense/stop-gains, frameshift insertions and deletions, and donor and acceptor splice-site mutations) were coded as pathogenic or likely pathogenic for the current analysis, while missense and other variants of undetermined significance or alterations with lower levels of evidence were excluded, unless specifically designated as pathogenic in ClinVar	50 defined DDR genes including *ATM*, *ATR*, *BRCA1*, *BRCA2*, *CDK12*, *CHEK2*, *FANCA*, *MLH1*, *MRE11A*, *NBN*, *PALB2*, *RAD51C*	Antonarakis *et al,* 2018	(34)
Germline	NR	NR/unclear	Hereditary cancer multi-gene panel test (MGPT) was used to identify pathogenic or likely pathogenic variant frequencies for 34 genes known to predispose to at least one of the six included cancers	Undefined 34-gene hereditary cancer multi-gene panel test (MGPT). Included *ATM*, *BRCA1*, *BRCA2*, *CHEK2*, *FANCA*, and *PALB2*; unclear for others.	LaDuca *et al,* 2017	(65)
			Genetic testing using a commercially available panel (Invitae) consisting of 25-79 cancer-related genes to identify mutations and selected exonic deletions/duplications	Undefined 25-79 cancer-related genes. Included *ATM*, *BRCA1*, *BRCA2*, *CHEK2*, and *NBN*; unclear for others.	Ledet *et al,* 2017	(67)

			NR	Multi-gene hereditary panel testing (32 undefined cancer genes). Results reported for *ATM*, *BRCA1*, *BRCA2*, *CHEK2*, and *MSH6*	Marshall *et al,* 2017	(74)
			DNA sequencing and exon-level copy number analysis	DDR (included 14 undefined genes on a hereditary PCa panel, most of which were DNA repair genes, results reported for *BRCA* and *BRCA2*)	Nicolosi *et al,* 2017	(81)
	Buccal cells and/or a blood sample	PCR	Genomic DNA from blood /buccal swabs using Puregene DNA Isolation kit (Gentra Systems). DNA content quantified using PicoGreen dsDNA quantitation kit using a Perkin-Elmer HTS7000 BioAssay Reader	*BRCA1* (185delAG, 5382insC) and *BRCA2* (6174delT)	Agalliu *et al,* 2009	(32)
	Archived blood DNA specimens	Other	Ion AmpliSeq targeted sequencing	*BRCA1*, *BRCA2* (undefined)	Petrovics *et al,* 2016	(84)
	Tumor sample	PCR	ABI Prism 7900 HT sequence detection system using Taqman probes	*ATM* (homozygous IVS62+60G/G, heterozygous IVS62+60G/A, and homozygous IVS62+60A/A)	Browning *et al,* 2006	(14)

Germline	Tumor sample	Microarray	Purified total RNA was whole-transcriptome amplified using the WT-Ovation FFPE system, fragmented and labelled using the Encore Biotin Module, and hybridized to Affymetrix Human Exon 1.0 ST GeneChips. Profiling of 9 DDR pathways using 17 gene sets for GSEA (Gene Set Enrichment Analysis) of high-density microarray gene expression data	17 gene sets involving 9 DDR gene pathways (over 200 genes analysed including all DDR genes of interest).	Evans *et al,* 2016	(45)
Germline and somatic (mixed)	Tumor and matched blood	NGS	MSK-IMPACT sequencing assay. Germline variants were identified in matched blood samples and filtered out in the somatic analysis process. Mutation clonality was estimated as a cancer cell fraction, and implemented in the FACETS algorithm. Germline analysis of 76 known cancer predisposing genes was performed as previously described (ref 16a - Schrader 2016 (not in library)	Memorial Sloan Kettering-Integrated Mutation Profiling of Actionable Cancer Targets (MSK-IMPACT) gene oncopanel that targets 410 cancer-associated genes plus germline analysis of 76 known cancer-predisposing genes (germline). This included *ATM*, *BRCA1*, *BRCA2*, *CHEK2*, *FANCA*, *MLH1*, and *NBN*, but was unclear for others	Abida *et al,* 2017	(30)

	Tumor with matched adjacent normal tissue biopsy or peripheral blood or buccal swab	IHC/ ISH/ FISH	*FANCA* gene specific probe (BAC clone RP11-79A1) and a reference probe located at 16p12 (BAC clone RP11-450G5) were used for this approach. Five-μm thick tissue sections were used for FISH analysis. Deletion was defined as presence of only copy of *FANCA* specific probe in the presence of two reference signals, per nucleus. At least 100 nuclei were evaluated per tissue section or 50 nuclei per tissue core in tissue microarrays (TMAs), using a fluorescence microscope (Olympus BX51; Olympus Optical, Tokyo, Japan)	*FANCA* deletions	Beltran *et al,* 2015	(19)
	Tumor sample	PCR	DNA isolated from tumor tissues was paired with primers targeting exons 10-14. Products were subject to direct sequencing	*CHEK2*	Wu *et al,* 2006	(100)
NR/ unclear	Genomic DNA	NGS	Targeted sequencing	*NBN*	Zuhlke *et al,* 2012	(102)
	NR	Other	sequencing (NGS, Sanger, pyrosequencing)	*ATM*	Feldman *et al,* 2014	(10)

NR/ unclear	Non-tumor tissue (principally lymph Nodes), formalin fixed and embedded in paraffin	PCR	Genomic DNA from sections from paraffin blocks then processing using a tissue DNA isolation kit (Qiagen). Mutant alleles detected by heteroduplex analysis (HDA) of the PCR products. Amplification products of primer pair A sequenced from nested primer for each on an ABI 373A sequencer at the Columbia University Cancer Center	*BRCA1* (185delAG) and *BRCA2* (6174delT)	Nastiuk *et al,* 1999	(78)
	Tumor tissue or blood sample	NGS	NR	*BRCA1*, *BRCA2*	Daniel *et al,* 2017	(9)
	Tumor biopsy	Other	DNA underwent hybrid capture for all coding exons of 395 cancer-related genes. Utilized two described lists of genes involved in DNA repair: our own in-house list of 74 (UCD) and a list of 20 DNA repair genes associated with cancer predisposition syndromes utilized in a recent publication by Pritchard et al	Genes involved in DNA repair, associated with cancer predisposition syndromes. Undefined but included *ATM*, *ATR*, *BRCA1*, *BRCA2*, and *MLH1*	Dall'Era *et al,* 2017	(8)

		NGS	Molecular profiles of PC tumor samples were defined. Protein expression (IHC), gene amplification (ISH), and NGS were performed. Unclassified variants were included for analysis. In a limited cohort of patients tested used a 592-gene hybrid capture NGS	A panel of 30 undefined DNA repair genes was used to define DNA repair intact (DRI) and DNA repair deficient (DRD) subgroups. Unclassified variants were included for analysis. Results reported for *ATM*, *BRCA2*.	Dawson *et al,* 2016	(11)
Somatic	NR	Other	Tests included gene sequencing (Sanger or NGS), protein expression (IHC), and/or gene amplification (C/FISH)	*BRCA1*, *BRCA2* (undefined)	Myers *et al,* 2016	(76)
	Tumor and needle biopsy	NGS	UW-OncoPlex was performed. Microsatellite instability (MSI) testing was performed directly on NGS data using the mSINGS method. Total mutation burden was estimated from targeted NGS data as previously described, with hyper-mutation defined as >12 mutations/megabase	Undefined mismatch repair genes (including *MLH1*) and homologous repair (including *BRCA2*, *CHEK2*)	Schweizer *et al,* 2016	(27)

Somatic	Cell-free DNA (cfDNA) present in the plasma	PCR	cfDNA was isolated from patient plasma samples using the Qiagen circulating nucleic acid kit. 100ng of cfDNA was utilized for library construction; and the libraries were paired-end sequenced on the Illumina HiSeq 2000. Focused analysis on copy number variations related to AR associated and DNA repair genes	DNA repair genes partial/full amplifications (*BRCA1*, *BRCA2*, *ATM*, *CDK12*, *MLH1*, and/or *MSH2*).	Gambhira *et al,* 2016	(17)
	Cell-free DNA (cfDNA) present in the plasma and matched blood lymphocyte DNA	NGS	Plasma DNA was used to prepare DNA libraries using a NEXTflex DNA-Seq kit. The Comprehensive Cancer Panel (Roche NimbleGen, Madison, WI) was used for NGS. The panel covers 4Mb genomic sequences and targets 578 cancer-related genes. Gene mutations were detected by comparing cfDNA to lymphocyte gDNA in the same patient with 2% variant alleles as the cut-off for mutation calls. Allele-specific PCR was used to validate mutations detected by sequencing	Comprehensive Cancer Panel (578 cancer-related genes). Results reported for *ATM*, *ATR*, *CHEK2*, *FANCA*, *MLH1*, and *NBN* (unclear for other genes of interest)	Xia *et al,* 2015	(18)
	Circulating tumor DNA	PCR	A publicly-accessible assay (Guardant Health) was used to analyse 68 known cancer genes for anomalies (missense mutations, amplifications) by a digital PCR technique	DNA repair genes (*BRCA1*, *BRCA2*, or *ATM*)	Gourdin *et al,* 2016	(52)

	Circulating tumor DNA; tumor tissue	NGS	Foundation ACT NGS assay; Foundation One NGS assay	*BRCA1* and *BRCA2* alterations	Lara *et al,* 2017	(66)
	Tumor biopsy and matched normal tissue	Capture sequencing	Sequenced exome to identify mutations using exome libraries of matched pairs of tumor /normal genomic DNAs. All captured DNA libraries were sequences with the Illumina GAII Genome Analyser or the Illumina HiSeq. Considered only mutations called at covered annotated targeted positions. Sanger sequencing used to validate	*ATM*, *BRCA2*	Grasso *et al,* 2012	(53)
	Tumor sample	NGS	PCR-based NGS	*BRCA2* (K2524fs)	Palapattu *et al,* 2015	(20)
Somatic	Tumor sample	NGS	Targeted NGS using the OncoPanel platform (includes point mutations, insertions, and deletions within exons and select introns/enhancers of 300 candidate genes with a role in oncogenesis). The CIMBA database of published germline *BRCA2* mutations was used to determine whether *BRCA2* mutations found in the prostate tumors studied here have also been reported in the germline	300 genes in the OncoPanel platform. Results reported for *ATM*, *BRCA1*, *BRCA2*, and *PALB2* (unclear for other DDR genes of interest).	Patel *et al,* 2016	(83)

	Tumor sample	NGS	Fresh-frozen metastatic prostate lesions. DNA fragment libraries for each of the RainDance-amplified PCR samples were constructed for sequence analysis on the SOLiD next-generation sequencing platform. After PCR, massively parallel sequencing was conducted for 577 candidate genes	Somatic copy number alterations in 577 undefined cancer related genes, result reported for *BRCA2* (unclear if other included in definition)	Robbins *et al,* 2011	(21)
		PCR	Paired end sequencing (49x49 cycles) was performed using the HiSeq 2000 (based on libraries that were hybrid captured with custom biotinylated RNA oligo pools) and mapped to the reference human genome (hg19). All copy number alterations involving *BRCA2* that were identified by NGS were confirmed by FISH	182 cancer-related genes (3230 exons) and 14 commonly rearranged genes (37 introns). Included all DDR genes of interest (except *MRE11A*, *NBN*, and *PALB2*)	Beltran *et al,* 2013	(22)
			Autopsy samples; formalin-fixed paraffin-embedded tissue or from fresh-frozen tissue Microsatellite instability PCR, Exome sequencing, targeted deep sequencing	MMR hyper-mutation (>300 somatic protein altering mutations based on the distribution of total mutation burden in metastatic tumors, which had matched normal tissue available); Undefined list which included *MSH2*, *MSH6*, and *MLH1*	Pritchard *et al,* 2014	(86)

	Single cell suspensions and touch preparations	FISH	P1 phage FISH probes were prepared, LOH experiments were carried out 'as previously described'	*BRCA1*, 3 flanking sites on 17q12-21	Williams *et al,* 1996	(99)

Multi-national						
Germline	Blood sample	WES	WES performed on germline DNA using an Illumina HiSeq 2500 system. The mean sequencing depth of coverage was 71x. In addition, a customized next-generation sequencing panel targeting 222 cancer related genes was used to sequence the germline DNA of the remaining lethal PCa patients and all the indolent PCa patients. The mean sequencing depth of coverage was 135 overall and was 180, 208, and 219 for *ATM*, *BRCA1*, and *BRCA2*, respectively. All the targeted bases in these three genes were successfully sequenced (> 20) in >99% samples. Sanger sequencing was used for confirmation	*ATM*, *BRCA1*, *BRCA2*	Na *et al,* 2017	(106)
	Blood lymphocyte, saliva, or tissue uninvolved with cancer	Other	Multiplex sequencing assays	Undefined 20 DRGs associated with autosomal dominant cancer predisposition syndromes. Included all DDR genes of interest except *FANCA* and *MLH1*	Nelson *et al,* 2016	(79)

	Buccal swabs, buffy coats, whole blood, non-tumor tissue	Other	Case series 1,2,6: whole exome sequencing of germline and tumor DNA; case series 3: libraries for targeted sequencing constructed using customized GeneRead Dnaseq Panel covering 53 genes and run on the Illumina MiSeq Sequencer; case series 4: Targeted deep sequencing performed using BROCA panel of 53 DNA repair pathway genes; case series 5: exome sequencing; case series 7: genomic sequencing performed using MSK-IMPACT hybrid capture-based next-generation sequencing assay	*ATM*, *ATR*, *BAP1*, *BARD1*, *BRCA1*, *BRCA2*, *BRIP1*, *CHEK2*, *FAM175A*, *GEN1*, *MLH1*, *MRE11A*, *MSH2*, *MSH6*, *NBN*, *PALB2*, *PMS2*, *RAD51C*, *RAD51D*, *XRCC2*	Pritchard *et al,* 2016	(87)
Germline and somatic (mixed)	Tumor sample	Other	Searched for candidate germline cancer predisposition variants in the exome sequence data (Cancer Genome Atlas). Sequencing data were aligned to GRCh37-lite version of the human reference using BWA v0.5.9 and de-duplicated using Picard 1.29	Undefined candidate cancer-associated genes (including *ATM*, *ATR*, *BRCA1*, *BRCA2*, *FANCA*, and *PALB2*)	Lu *et al,* 2015	(71)
Germline and somatic (mixed)	Tumor sample	WES	Whole-exome capture libraries constructed using DNA from normal and tumor tissue subjected to hybrid capture using SureSelect Exome v4 baits (Agilent) and aligned to the hg19 human genome build	Somatic mutations, copy number laterations, and oncogenic structural DNA rearrangements. Included *ATM*, *BRCA1*, *BRCA2*, *CHEK2*, *MLH1*, and *PALB2*	Robinson *et al,* 2015	(89)

			DNA sequenced with the Illumina HiSeq 2000 Genome Analyzer. Reads were aligned to the NCBI GRCh37 human reference genome. The authors performed SNV and indel discovery, genotyping and variant quality score recalibration in all tumor and germline samples simultaneously, according to the GATK HaplotypeCaller v.3.2 best practices recommendations	*BRCA2*. Germline and somatic variants, including single nucleotide variants, indels and structural variants	Decker *et al,* 2016	(43)
NR/ unclear	NR	PCR	Samples genotyped for 657del5 alteration using either ABI3100 and fluorescently labelled PCR (Mayo Clinic, University of Michigan and Universitätsklinikum Ulm), direct sequencing using an Amersham Megabase (Johns Hopkins), or by DNA sequencing (Tampere University Hospital). E185Q and D95N genotyped were obtained using minisequencing (Tampere University Hospital). R215W genotypes were determined using ddNTP-primer extension (Universitätsklinikum Ulm)	*NBN* 657del5 mutation	Hebbring *et al,* 2006	(58)

Somatic	Tumor sample	NGS	After hybridisation capture, sequencing was performed (Illumina HiSeq 2500). Raw sequences were aligned to the human genome reference sequence. An in-house tool identified the somatic single nucleotide variants (SNVs) by comparing the tumor to its matched normal.	DDR gene alterations that may be related to prostate cancer progression, including undefined genes related to DDR pathways (n=112), recurrently mutated genes in PC (n=334), and other cancer-related genes (n=77). Reported *BRCA2* and *NBN*; unclear for other genes of interest	Fontugne *et al,* 2015	(47)
			NGS extracted from FFPE tumor tissue. Included sequencing of 45 DDR genes	Sequencing of 45 DDR genes (including *ATR*, *ATM*, *BRCA1*, *BRCA2*, *CDK12*, *CHEK2*, *FANCA*, *NBN*, *PALB2*, *PPP2R2A*, *RAD52*, *RAD50*, and *RPA1MS1*)	Timms *et al,* 2016	(96)
Somatic	Tumor sample	WES	Whole-exome capture was performed using the Agilent SureSelect Human All Exon protocol containing 188,260 exons from ≈18,560 genes. Sequencing was performed on the Illumina HiSeq 2000 platform	DDR included *ATM*, *BRCA1*, *BRCA2*, *FANCD2*, *MLH1*, and *RAD51C0*. Unclear for other DDR genes of interest.	Cancer Genome Atlas 2015	(37)

Germline and somatic (mixed)		Whole-genome sequencing	DNA sequenced with the Illumina HiSeq 2000 Genome Analyser. Reads were aligned to the NCBI GRCh37 human reference genome. The authors performed SNV and indel discovery, genotyping and variant quality score recalibration in all tumor and germline samples simultaneously, according to the GATK HaplotypeCaller v.3.2 best practices recommendations	*BRCA2*. Germline and somatic variants, including single nucleotide variants, indels and structural variants	Decker *et al,* 2016	(43)
			No details provided	DDR (undefined); *BRCA2*, *BRCA1* reported. Germline and somatic variants, including single nucleotide variants, indels and structural variants		
Country not reported						
Somatic	Tumor biopsy	NGS	70-gene cfDNA next generation sequencing panel from a CLIA-licensed, CAP-accredited laboratory (Guardant Health, Inc.)	70 genes including *BRCA1*, *BRCA2*	Sonpavde *et al,* 2017	(6)
	Circulating tumor DNA					

	Formalin-fixed and paraffin embedded tumor	Capture sequencing	Comprehensive genomic profiling was performed on hybridization captured, adaptor ligation-based libraries to a mean coverage depth of 583X for up to 315 cancer related genes plus 37 introns from 14 genes frequently rearranged in cancer. Clinically relevant GA (CRGA) were defined as genomic alterations linked to drugs on the market or under evaluation in mechanism driven clinical trials	Undefined *BRCA2*	Stephens *et al,* 2016	(29)
		NGS	NGS using the commercially available Ion Torrent Hotspot Cancer Panel. This test is for gene mutation, not for copy number changes or translocations	*ATM*, *MLH1*	Liu *et al,* 2016	(5)

ATM, ataxia telangiectasia mutated; *ATR*, ataxia telangiectasia and Rad3-related protein; *BAP1*, *BRCA1*-associated protein 1; *BARD1*, *BRCA1*-associated RING domain 1; *BLM*, Bloom syndrome RecQ like helicase; *BRCA*, breast cancer susceptibility gene; *BRIP1*, *BRCA1*-interacting protein C-terminal helicase 1; CDK, cyclin-dependent kinase; cfDNA, cell-free DNA; *CHEK2*, checkpoint kinase 2; ctDNA, circulating tumor DNA; CYP, cytochrome P450; DDR, DNA damage repair; dsDNA, double-stranded DNA; *ERCC2*, excision repair cross-complementation group 2; ESR, estrogen receptor 1; *FAM175A*, family with sequence similarity 175,member A; *FANCA*, Fanconi anemia complementation group A; FFPE, formalin-fixed paraffin-embedded; FISH, fluorescent in situ hybridization; gDNA, genomic DNA; *GEN1*, GEN1, Holliday junction 5' flap endonuclease; IHC, immunohistochemistry; *LIG4*, DNA ligase 4; LOH, loss of heterozygosity; MGPT, multi-gene panel test; *MLH1*, mutL homolog 1; MLPA, multiplex ligation-dependent probe amplification; MMR, mismatch repair; *MRE11A*, *MRE11* homolog A, double-strand break repair nuclease; MSH, muS homolog; *MUTYH*, mutY DNA glycosylase; *NBN*, nibrin; NCBI, National Center for Biotechnology Information; NGS, next-generation sequencing; NR, not reported; *NR3C1*, nuclear receptor subfamily 3 group c member 1; *PALB2*, partner and localizer of *BRCA2*; PC, prostate cancer; PCR, polymerase chain reaction; *PMS2*, *PMS1* homolog 2, mismatch repair system component; *PPP2R2A*, protein phosphatase 2 regulatory subunit B alpha; RAD, DNA repair protein; *RB1*, RB transcriptional corepressor 1; RFLP, restriction fragment length polymorphism; RING, really interesting new gene; SNP, single nucleotide polymorphism; *TGFB1*, transforming growth factor beta 1; *TSHR*, thyroid stimulating hormone receptor; UKGPCS, UK genetic prostate cancer study; WES, whole-exome sequencing; *WRN*, Werner syndrome RecQ like helicase; *XPF*, xeroderma pigmentosum complementation group F; XRCC, x-ray repair cross complementing

Appendix S7. Summary of risk of bias (Joanna Briggs Institute [JBI] Critical Appraisal Checklist).

Author, year	Publication type	Was the sample representative of the target population?	Were study participants recruited in an appropriate way?	Was the sample size adequate?	Were the study subjects and setting described in detail?	Is the data analysis conducted with sufficient coverage?	Were objective, standard criteria used for measurement of PC?[a]	Was the condition measured reliably?[b]	Was there appropriate statistical analysis?	Are all important confounding factors accounted for?	Were subpopulations identified using objective criteria?	References
Abida *et al,* 2017	Full paper	No	Unclear	Yes	Yes	Yes	Yes	Yes	Yes	Yes	NA	(30)
Agalliu *et al,* 2007	Full paper	Unclear	Unclear	Yes	Yes	Yes	Yes	Unclear	Yes	Unclear	NA	(31)
Agalliu *et al,* 2009	Full paper	Yes	Yes	Yes	Yes	Yes	Unclear	Unclear	Yes	Yes	Unclear	(32)
Akbari *et al,* 2014	Full paper	No	Yes	Yes	No	Yes	Unclear	Unclear	Yes	Unclear	NA	(103)
Angele *et al,* 2004	Full paper	No	Yes	Yes	No	Yes	Unclear	Unclear	Yes	Unclear	NA	(13)
Antonarakis *et al,* 2018	Full paper	Unclear	Unclear	Yes	Unclear	Yes	Yes	Unclear	Yes	Yes	Yes	(34)
Beltran *et al,* 2013	Full paper	No	Unclear	No	No	Yes	Unclear	Unclear	No	Yes	NA	(22)
Beltran *et al,* 2015	Full paper	No	Unclear	Yes	No	Yes	Unclear	Unclear	Yes	Unclear	NA	(19)
Browning *et al,* 2006	Full paper	No	Unclear	Yes	Yes	Yes	Yes	Yes	Yes	Yes	NA	(14)

Cancer Genome Atlas 2015	Full paper	Yes	Unclear	Yes	Yes	Yes	Yes	Unclear	Yes	Unclear	NA	(37)
Castro *et al,* 2011	Abstract	Yes	Yes	Yes	No	Yes	Unclear	Unclear	Yes	Unclear	NA	(38)
Cesaretti *et al,* 2007	Full paper	No	Unclear	Yes	Yes	Yes	Yes	Yes	Yes	Unclear	Yes	(41)
Cheng *et al,* 2011	Abstract	Unclear	Yes	Yes	No	Yes	Unclear	Unclear	Yes	Unclear	Unclear	(23)
Dall'Era *et al,* 2017	Abstract	Unclear	Unclear	Yes	No	Yes	Unclear	Unclear	No	Unclear	Yes	(8)
Damaraju *et al,* 2006	Full paper	No	Unclear	Yes	Yes	Yes	Yes	Unclear	Yes	Yes	Yes	(26)
Daniel *et al,* 2017	Abstract	Unclear	Unclear	Yes	No	Yes	Unclear	Unclear	Yes	Unclear	NA	(9)
Dawson *et al,* 2016	Abstract	Unclear	Unclear	Yes	No	Yes	Unclear	Unclear	Unclear	Unclear	NA	(11)
Decker *et al,* 2016	Full paper	Yes	Unclear	No	Unclear	Yes	Unclear	Unclear	Yes	Unclear	NA	(43)
Edwards *et al,* 2003	Full paper	Yes	Yes	Yes	No	Yes	Unclear	Unclear	Yes	Yes	NA	(105)
Evans *et al,* 2016	Full paper	Yes	Unclear	Yes	No	Yes	Yes	Unclear	No	Yes	NA	(45)
Feldman *et al,* 2014	Abstract	Unclear	Unclear	Yes	No	Unclear	Unclear	Unclear	No	Unclear	NA	(10)
Fontugne *et al,* 2015	Abstract	Unclear	Unclear	Yes	No	Yes	Unclear	Unclear	No	Unclear	NA	(47)

Gallagher *et al,* 2012	Full paper	No	Yes	Yes	Yes	Yes	Unclear	Unclear	Yes	Yes	Unclear	(48)
Gambhira *et al,* 2016	Abstract	Unclear	Unclear	No	No	Yes	Unclear	Unclear	Yes	Unclear	NA	(17)
Gayther *et al,* 2000	Full paper	Unclear	Unclear	No	No	No	Unclear	Unclear	Yes	Unclear	Yes	(50)
Giusti *et al,* 2003	Full paper	Yes	Yes	Yes	No	Yes	Unclear	Yes	Yes	Unclear	Yes	(51)
Gourdin *et al,* 2016	Abstract	Unclear	Unclear	Yes	No	Yes	Unclear	Unclear	Unclear	Unclear	NA	(52)
Grasso *et al,* 2012	Full paper	Unclear	Unclear	No	Yes	Yes	Unclear	Yes	Yes	Unclear	NA	(53)
Hamel *et al,* 2003	Full paper	No	No	Yes	No	Yes	Unclear	Unclear	Yes	Unclear	Yes	(55)
Hart *et al,* 2016	Full paper	Yes	Unclear	Yes	Yes	Yes	Unclear	Unclear	Yes	Yes	Yes	(56)
Hayano *et al,* 2016	Full paper	Unclear	Unclear	Yes	No	Yes	Unclear	Unclear	No	Unclear	Yes	(57)
Hebbring *et al,* 2006	Full paper	Yes	Unclear	Yes	No	Yes	Unclear	Unclear	Yes	Unclear	Unclear	(58)
Hubert *et al,* 1999	Letter	No	Unclear	Yes	No	Yes	Yes	Unclear	Yes	Yes	No	(59)
Jefferies *et al,* 2017	Abstract	No	Unclear	Yes	No	Unclear	Unclear	Unclear	Yes	Unclear	NA	
Kirchoff *et al,* 2004	Full paper	No	Unclear	Yes	No	No	Unclear	Unclear	Yes	Yes	Unclear	(63)
Kote-Jarai	Full paper	Yes	Yes	Yes	No	Yes	Unclear	Unclear	Yes	Yes	NA	(104)

et al, 2011												
LaDuca *et al,* 2017	Abstract	Unclear	Unclear	Unclear	No	Unclear	Unclear	Unclear	No	Unclear	No	(65)
Lara *et al,* 2017	Abstract	Unclear	Unclear	Yes	No	Yes	Unclear	Unclear	Yes	Unclear	NA	(66)
Ledet *et al,* 2017	Abstract	No	Yes	Yes	No	Yes	Unclear	Unclear	Unclear	Unclear	Yes	(67)
Lehrer *et al,* 1998	Full paper	No	Unclear	Yes	No	Yes	Unclear	Unclear	Yes	Yes	Unclear	(68)
Leongamornlert *et al,* 2012	Full paper	Yes	Unclear	Yes	No	Unclear	Unclear	Unclear	Yes	Unclear	NA	(69)
Leongamornlert *et al,* 2014	Full paper	Yes	Unclear	Yes	Yes	Yes	Yes	Unclear	Yes	Yes	Yes	(70)
Liu *et al,* 2016	Abstract	Unclear	Unclear	No	No	Yes	Unclear	Unclear	Unclear	Unclear	NA	(5)
Lu *et al,* 2015	Full paper	Yes	Unclear	Yes	No	Yes	Unclear	Unclear	No	Unclear	NA	(71)
Maier *et al,* 2014	Full paper	No	Unclear	Yes	Yes	Yes	Yes	Unclear	Yes	Yes	Unclear	(72)
Manson-Bahr *et al,* 2015	Full paper	Unclear	Unclear	Yes	Yes	Yes	Unclear	Unclear	Unclear	Unclear	NA	(73)
Marshall *et al,* 2017	Abstract	Unclear	Unclear	Yes	No	Unclear	Yes	Unclear	Yes	Unclear	Yes	(74)
Meyer *et al,*	Full paper	No	Yes	Yes	Yes	Yes	Yes	Yes	Yes	Yes	Yes	(25)

2007												
Myers *et al,* 2016	Abstract	Unclear	Unclear	Yes	No	Yes	Unclear	Unclear	Yes	Unclear	NA	(76)
Na *et al,* 2017	Full paper	Unclear	Unclear	Yes	No	Yes	Yes	Unclear	Yes	Yes	NA	(106)
Nam *et al,* 2005	Full paper	No	Yes	Yes	Yes	Yes	Unclear	Unclear	Yes	Yes	NA	(15)
Naslund Koch *et al,* 2016	Full paper	No	Yes	Yes	No	Yes	Unclear	Unclear	Yes	Unclear	NA	(16)
Nastiuk *et al,* 1999	Full paper	No	Unclear	Yes	No	Unclear	Unclear	Unclear	No	Unclear	Unclear	(78)
Nelson *et al,* 2016	Abstract	Yes	Unclear	Yes	No	Yes	Unclear	Unclear	Yes	Unclear	NA	(79)
Nicolas *et al,* 2015	Full paper	No	Unclear	No	No	Yes	Yes	Unclear	Yes	Unclear	Yes	(24)
Nicolosi *et al,* 2017	Abstract	Unclear	Unclear	Yes	No	Unclear	Unclear	Unclear	Unclear	Unclear	NA	(81)
Nientiedt *et al,* 2017	Full paper	No	Unclear	Unclear	Yes	Unclear	Yes	Unclear	Yes	Unclear	Unclear	(82)
Palapattu *et al,* 2015	Abstract	Unclear	Unclear	No	No	Yes	Unclear	Unclear	Yes	Unclear	NA	(20)
Patel *et al,* 2016	Abstract	No	Unclear	Yes	No	Yes	Unclear	Unclear	Yes	Unclear	NA	(83)
Petrovics *et al,* 2016	Abstract	Unclear	Unclear	Yes	Unclear	Yes	Unclear	Unclear	Yes	Unclear	NA	(84)
Pomerantz	Full paper	No	Yes	Yes	Yes	Yes	Unclear	Unclear	Yes	Yes	Yes	2017

et al, 2017												(85)
Pritchard *et al,* 2014	Full paper	Unclear	Unclear	Yes	No	Yes	Unclear	Unclear	Yes	NA	NA	(86)
Pritchard *et al,* 2016	Full paper	Yes	Unclear	Yes	Yes	Yes	Yes	Unclear	Yes	Yes	NA	(87)
Robbins *et al,* 2011	Full paper	Unclear	Unclear	No	No	Yes	Unclear	Unclear	Yes	Unclear	NA	(21)
Robinson *et al,* 2015	Full paper	Yes	Unclear	Yes	No	Yes	Unclear	Unclear	Unclear	Unclear	NA	(89)
Romero *et al,* 2017	Abstract	Yes	Unclear	Yes	No	Yes	Unclear	Unclear	Yes	Unclear	NA	(90)
Schweizer *et al,* 2016	Full paper	No	Yes	No	No	Yes	Yes	Yes	Yes	Unclear	NA	(27)
Sonpavde *et al,* 2017	Abstract	Unclear	Unclear	Yes	No	Yes	Unclear	Unclear	Yes	Unclear	NA	(6)
Stephens *et al,* 2016	Abstract	Unclear	Unclear	No	No	Yes	Unclear	Unclear	No	Unclear	NA	(29)
Struss *et al,* 2017	Abstract	Unclear	Unclear	Yes	No	Unclear	Unclear	Unclear	Yes	Unclear	NA	(95)
Tanaka *et al,* 2009	Full paper	No	Unclear	Yes	No	No	Yes	Unclear	Yes	Unclear	NA	(7)
Timms *et al,* 2016	Poster	Unclear	Unclear	Yes	No	Unclear	Unclear	Unclear	Unclear	Unclear	NA	(96)
Tischkowitz *et al,* 2008	Full paper	No	Unclear	Yes	No	Yes	Unclear	Unclear	Yes	Unclear	No	(97)
Uchida *et al,* 1999	Full paper	Unclear	Unclear	No	No	Yes	Yes	Unclear	Yes	Unclear	NA	(12)

Vazina *et al,* 2000	Full paper	No	Yes	Yes	No	Yes	Unclear	Unclear	Yes	Unclear	No	(98)
Williams *et al,* 1996	Full paper	Unclear	Unclear	No	No	Yes	Unclear	Unclear	Unclear	Unclear	NA	(99)
Wu *et al,* 2006	Full paper	No	Yes	Yes	No	Yes	Unclear	Unclear	Yes	Unclear	NA	(100)
Xia *et al,* 2015	Full paper	Unclear	Yes	No	Yes	Yes	Yes	Unclear	No	Yes	NA	(18)
Zhu *et al,* 2010	Abstract	Unclear	Unclear	No	No	Yes	Unclear	Unclear	No	Unclear	Unclear	(101)
Zuhlke *et al,* 2012	Full paper	Unclear	Unclear	Yes	No	Yes	Unclear	Unclear	Yes	Unclear	Yes	(102)

NA, not applicable. [a]Was the diagnostic criterion clearly reported? [b]Who performed the diagnosis and were all samples diagnosed in the same way?

Appendix S8. Summary of DDR gene mutation prevalence in germline tissue.

% period prevalence, median (range)	General prostate cancer (PC)	Metastatic prostate cancer (mPC)	Metastatic castration-resistant prostate cancer (mCRPC)	Castration-resistant prostate cancer (CRPC)
ATM	1.5 (0.41, 3.4) 4 studies (n=1384)	1.7 (1.59, 1.8) 2 studies (n=1261)	1.91 (NA) 1 study (n=419)	NR
ATR	0 (NA) 1 study (n=499)	0.3 (0.3, 0.3) 2 studies (n=1261)	NR	NR
BRCA1	0.6 (0.2, 1.0) 7 studies (n=4784)	0.9 (0.9, 0.9) 2 studies (n=1261)	0.8 (0.7, 1.0) 2 studies (n=569)	NR
BRCA2	1.1 (0.0, 0.9) 8 studies (n=5894)	5.2 (5.1, 5.4) 2 studies (n=1261)	5.0 (3.3, 5.3) 3 studies (n=888)	NR
CHEK2	1.8 (0.4, 10.7) 5 studies (n=1769)	1.5 (1.2, 1.9) 2 studies (n=1103)	1.0 (NA) 1 study (n=419)	NR
FANCA	0.56 (NA) 1 study (n=178)	NR	NR	NR
MLH1	0.0 (NA) 1 study (n=499)	0.0 (NA) 1 study (n=692)	NR	NR
MRE11A	0.2 (NA) 1 study (n=499)	0.2 (0.1, 0.2) 2 studies (n=1261)	NR	NR
NBN	0.3 (0.2, 0.5) 2 studies (n=720)	0.2 (0.2, 0.3) 2 studies (n=1261)	NR	NR
PALB2	0.5 (0.4, 0.6) 3 studies (n=898)	0.5 (0.4, 0.5) 2 studies (n=1261)	0.6 (NA) 1 study (n=319)	NR
RAD51C	0.5 (0.4, 0.6) 2 studies (n=677)	0.2 (0.1, 0.2) 2 studies (n=1261)	NR	NR
DDR[a]	18.6 (17.2, 19)	11.6 (11.4, 11.8)	8.3 (7.5, 9.1)	NR

	3 studies (n=1712)	2 studies (n=1261)	2 studies (n=738)	

[a]DDR=multiple gene definitions for DNA damage response gene that includes at least one of our genes of interest. *ATM*, ataxia telangiectasia mutated; *ATR*, ataxia telangiectasia and Rad3-related protein; *BRCA*, breast cancer susceptibility gene; *CHEK2*, checkpoint kinase 2; DDR, DNA damage repair; *FANCA*, Faconi anemia complementation group A; *MLH1*, MutL homolog 1; *MRE11A*, *MRE11* homolog A, double-strand break repair nuclease; n, sample size; NA, not applicable; *NBN*, nibrin; NR, not reported; *PALB2*, partner and localizer of *BRCA2*; *RAD51C*, *RAD51* paralog C. Original study data can be found in "Mutations in *ATM* gene" in Appendix S7.

Summary of DDR gene mutation prevalence in somatic tissue

% period prevalence, median (range)	General prostate cancer (PC)	Metastatic prostate cancer (mPC)	Metastatic castration-resistant prostate cancer (mCRPC)	Castration-resistant prostate cancer (CRPC)
ATM	3.9 (2.4, 8.0) 7 studies (n=2066)	4 (NA) 1 study (n=70)	6 (0.0, 12.0) 2 studies (n=203)	NR
ATR	0.6 (0.0, 1.2) 2 studies (n=714)	NR	NR	NR
BRCA1	1.1 (0.6, 2.4) 5 studies (n=2487); 6 datasets[a]	NR	2.8 (0.7, 5.0) 2 studies (n=664)	NR
BRCA2	4.9 (0, 11.8) 9 studies (n=3266); 10 datasets[a]	NR	5.0 (2.0, 6.0) 3 studies (n=714)	NR
CHEK2	1.2 (0.8, 2.4) 3 studies (n=798)	NR	NR	NR
FANCA	2.1 (0.5, 16.0) 4 studies (n=1234)	NR	NR	NR

MLH1	0.6 (0.2, 1.0) 2 studies (n=1081)	3.3 (NA) 1 study (n=60)	NR	NR
MRE11A	0.0 (NA) 1 study (n=630)	NR	NR	NR
NBN	1.2 (0.3, 65) 3 studies (n=783)	NR	NR	NR
PALB2	1.3 (0.6, 2.0) 2 studies (n=1081)	0.0 (NA) 1 study (n=70)	4.0 (NA) 1 study (n=153)	NR
RAD51C	1.5 (0.0, 3.0) 2 studies (n=963)	NR	NR	NR
DDR[b]	10.7 (4.9, 22) 3 studies (n=680); 4 datasets[c]	13.2 (10, 16.4) 2 studies (n=105)	NR	NR

[a]One study provided 2 data sets, and both were included; [b]DDR=multiple gene definitions for DNA damage response gene that includes at least 1 of our genes of interest; [c]one study provided two definitions, and both were included. *ATM*, ataxia telangiectasia muted; *ATR*, ataxia telangiectasia and Rad3-related protein; *BRCA*, breast cancer susceptibility gene; *CHEK2*, checkpoint kinase 2; DDR, DNA damage repair; *FANCA*, Faconi anemia complementation group A; *MLH1*, MutL homolog 1; *MRE11A*, *MRE11* homolog A, double-strand break repair nuclease; n, sample size; NA, not applicable; *NBN*, nibrin; NR, not reported; *PALB2*, partner and localizer of *BRCA2*; *RAD51C*, *RAD51* paralog C. Original study data can be found in Mutations in *ATM* gene in Appendix S7.

Summary of DDR gene mutation prevalence in unselected populations.

(A) Mutations in the *ATM* gene.

PC group	Germline or somatic	% prevalence	N	DDR definition	Country	Study level inclusion criteria[a]	Baseline Gleason score (% of population)	Author, year	Ref-erences
mCRPC	Germline	1.91	419	Undefined	Spain	Patients ≥18 years of age; histologically confirmed prostate cancer; presence of metastatic disease according to bone, CT, and/or MRI scan; confirmed castration-resistant prostate cancer; due to start or have started first-line treatment with any approved survival-prolonging therapy for mCRPC within a period of 6 months from study entry; ECOG performance status ≤21	NR	Romero *et al,* 2017	(90)
	Somatic	0	50	*ATM* non-synonymous point mutation	USA	Lethal heavily pre-treated CRPCs obtained at rapid autopsy; or high-grade localized prostate cancers	NR	Grasso *et al,* 2012	(53)
		12	153	*ATM* mut/del	USA	PC patients consenting to genomic analysis of their tumor and germline DNA	NR	Abida *et al,* 2017	(30)
mPC	Germline	1.59	692	*ATM*	Multi-national	Diagnosis of metastatic prostate cancer, as determined by histologic evaluation of a tumor biopsy specimen or surgical resection specimen	≤6 (6.07); 3+4 (9.4); 4+3 (13.3); 8-10 (55.2); unknown (16.0)	Pritchard *et al,* 2016	(87)
		1.8	569	*ATM* (undefined)	Multi-national	Men had to have mPC based on a biopsy of a metastatic site	NR	Nelson *et al,* 2016	(79)
	Somatic	4	70	*ATM* mut/del	USA	PC patients consenting to genomic analysis of their tumor and germline DNA	NR	Abida *et al,* 2017	(30)
PC	Germline	2	221	*ATM* undefined	USA		NR	Abida *et al,* 2017	(30)

		3.4	178	*ATM* truncations	Multi-national	Patients with prostate adenocarcinoma and sequence data from germline and tumor DNA; 50% coverage of the targeted exome having at least 20x coverage in both germline and tumor samples	NR	Lu *et al,* 2015	(71)
		0.41	486	*ATM*	Multi-national	NR	NR	Na *et al,* 2017	(106)
		1.00	499	*ATM*	Multi-national	Diagnosis of metastatic prostate cancer, as determined by histologic evaluation of a tumor biopsy specimen or surgical resection specimen	≤6 (9.0); 3+4 (29.7); 4+3 (20.2); 8-10 (41.1); unknown (0)	Pritchard *et al,* 2016	(87)
PC	Somatic	2.38	84	Defective *ATM* genes (one affected allele)	Multi-national	Selection of PC patients from a commercial biobank and the Transatlantic Prostate Group Cohort	NR	Timms *et al,* 2016	(96)
		3	630	Mutation frequency from DNA_REPAIR gene set	USA	Tumor samples were from 4 published retrospective prostatectomy patient cohorts at the Mayo Clinic (MCI and MCII), Cleveland Clinic (CC), and Thomas Jefferson University (TJU)	NR	Evans *et al,* 2016	(45)
		3.17	63	Undefined	UK	Patients diagnosed with PC, whose biopsy contained >5% of cancer	6 (13); 7 (60); 8 (13); 9 (14)	Manson-Bahr *et al,* 2019	(73)
		3.90	333	Truncating and missense mutations	Multi-national	Patients diagnosed with prostate adenocarcinoma, and had not received prior treatment for their disease (chemotherapy, radiotherapy, or hormonal ablation therapy)	3+3 (19.5); 3+4 (30.6); 4+3 (23.4); ≥8 (26.4)	Cancer Genome Atlas 2015	(37)
		5	451	*ATM* undefined	USA	PC patients consenting to genomic analysis of their tumor and germline DNA	6 (5.5); 7 (31.0); 8-10 (57.2); unknown (6.2)	Abida *et al,* 2017	(30)
		5.62	178	*ATM* somatic mutation	Multi-national	Patients with prostate adenocarcinoma and sequence data from germline and tumor	NR	Lu *et al,* 2015	(71)

						DNA; 50% coverage of the targeted exome having at least 20x coverage in both germline and tumor samples			
		8	327	*ATM*	USA	Men with prostate cancer who had undergone treatment at the Dana Farber Cancer Institute; consented to targeted next generation sequencing	NR	Patel *et al,* 2016	(83)

[a]Study level inclusion criteria may not reflect prostate subgroups because multiple groups are included. *ATM*, ataxia telangiectasia mutated; CRPC, castration-resistant PC; CT, computed tomography; DDR, DNA damage repair; ECOG, Eastern Cooperative Oncology Group; m, metastatic; MRI, magnetic resonance imaging; NR, not reported; PC, prostate cancer. More baseline details can be found in Appendix S5.

(B) Mutations in the *ATR* gene.

PC group	Germline or somatic	% prevalence	N	DDR definition	Country	Study level inclusion criteria[a]	Baseline Gleason score (% of population)	Author, yr	Ref-erence
mPC	Germline	0.29	692	*ATR*	Multi-national	Diagnosis of metastatic prostate cancer, as determined by histologic evaluation of a tumor biopsy specimen or surgical resection specimen	≤6 (6.07); 3+4 (9.4); 4+3 (13.3); 8-10 (55.2); unknown (16.0)	Pritchard *et al,* 2016	(87)
		0.3	569	*ATR* (undefined)	Multi-national	Men had to have mPC based on a biopsy of a metastatic site	NR	Nelson *et al,* 2016	(79)
PC	Somatic	0	630	Gene frequency from DNA_REPAIR gene set	USA	Tumor samples were from 4 published retrospective prostatectomy patient cohorts at the Mayo Clinic (MCI and MCII), Cleveland Clinic (CC), and Thomas Jefferson University (TJU)	NR	Evans *et al,* 2016	(45)
		1.19	84	Defective *ATR* genes (both alleles affected)	Multi-national	Selection of PC patients from a commercial biobank and the Transatlantic Prostate Group Cohort	NR	Timms *et al* 2016	(96)
PC	Germline	0	499	*ATR*	Multi-national	Diagnosis of metastatic prostate cancer, as determined by histologic evaluation of a tumor biopsy specimen or surgical	≤6 (9.0); 3+4 (29.7); 4+3 (20.2);	Pritchard *et al,* 2016	(87)

						resection specimen	8-10 (41.1); unknown (0)		
[a]Study level inclusion criteria may not reflect prostate subgroups because multiple groups are included. *ATR*, ataxia telanglectasia and Rad3-related protein; DDR, DNA damage repair; m, metastatic; NR, not reported; PC, prostate cancer. More baseline details can be found in Appendix S5.									

(C) Mutations in the *BRCA1* gene.

PC group	Germline or somatic	% prevalence	N	DDR definition	Country	Study level inclusion criteria[a]	Baseline Gleason score (% of population)	Author, year	Ref-erences
mCRPC	Germline	0.66	150	Biallelic loss	Multi-national	Discovery set PC patients were selected based on high Gleason score and availability of both peripheral blood DNA and fresh frozen prostatectomy samples. 150 samples from Robinson 2015 (89)	7 (10); 8 (20); 9 (60); 10 (10)	Decker *et al,* 2016	(43)
		0.95	419	Undefined	Spain	Patients ≥18years of age; histologically confirmed prostate cancer; presence of metastatic disease according to bone, CT, and/or MRI scan; confirmed castration-resistant prostate cancer; due to start or have started first-line treatment with any approved survival-prolonging therapy for mCRPC within a period of 6 months from study entry; ECOG performance status ≤21	NR	Romero *et al,* 2017	(90)
mCRPC	Somatic	0.66	150	Biallelic loss	Multi-national	Discovery set PC patients were selected based on high Gleason score and availability of both peripheral blood DNA and fresh frozen prostatectomy samples. 150 samples from Robinson 2015 (89)	7 (10); 8 (20); 9 (60); 10 (10)	Decker *et al,* 2016	(43)

		5.00	514	Undefined	USA	Patients with mCRPC that underwent baseline ctDNA analysis for potentially actionable alterations using Guardant360 before new systemic therapy were identified	NR	Sonpavde *et al,* 2017	(6)
mPC	Germline	0.87	692	*BRCA1*	Multi-national	Diagnosis of metastatic prostate cancer, as determined by histologic evaluation of a tumor biopsy specimen or surgical resection specimen	≤6 (6.07); 3+4 (9.4); 4+3 (13.3); 8-10 (55.2); unknown (16.0)	Pritchard *et al,* 2016	(87)
		0.90	569	*BRCA1* (undefined)	Multi-national	Men had to have mPC based on a biopsy of a metastatic site	NR	Nelson *et al,* 2016	(79)
PC	Germline	0.23	2181	Undefined *BRCA1*	UK	Patients enrolled in the UKGPCS between1990-2005 with available genomic DNA and clinical and survival data in our prospectively maintained UKGPCS database	NR	Castro *et al,* 2011	(38)
		0.45	886	Total *BRCA1* (4 variants: c.68_69delAG; c.212+1G>T; c.1954dupA; c.2475delC)	UK	Patients enrolled in the UKGPCS. Age at diagnosis of ≤65 years (821 cases; age range 36-65 years); and aged >65 years (92 cases; age range 66-88 years) with a family history of one or more first-degree relatives with PC	NR	Leongamornlert *et al,* 2012	(69)
		0.56	178	*BRCA1* truncation variant	Multi-national	Patients with prostate adenocarcinoma and sequence data from germline and tumor DNA; 50% coverage of the targeted exome having at least 20x coverage in both germline and tumor samples	NR	Lu *et al,* 2015	(71)
		1.00	221	*BRCA1* undefined	USA	PC patients consenting to genomic analysis of their tumor and germline DNA	NR	Abida *et al,* 2017	(30)

		1.00	333	All *BRCA1* mutation	Multi-national	Patients diagnosed with prostate adenocarcinoma, and had not received prior treatment for their disease (chemotherapy, radiotherapy, or hormonal ablation therapy)	3+3 (19.5); 3+4 (30.6); 4+3 (23.4); ≥8 (26.4)	Cancer Genome Atlas 2015	(37)
		0.41	486	*BRCA1*	Multi-national	NR	NR	Na *et al,* 2017	(106)
		0.60	499	*BRCA1*	Multi-national	Diagnosis of metastatic prostate cancer, as determined by histologic evaluation of a tumor biopsy specimen or surgical resection specimen	≤6 (9.0); 3+4 (29.7); 4+3 (20.2); 8-10 (41.1); unknown (0)	Pritchard *et al,* 2016	(87)
PC	Somatic	0.56	178	*BRCA1* somatic mutation	Multi-national	Patients with prostate adenocarcinoma and sequence data from germline and tumor DNA; 50% coverage of the targeted exome having at least 20x coverage in both germline and tumor samples.	NR	Lu *et al,* 2015	(71)
		0.60	630	Gene frequency from DNA_REPAIR gene set	USA	Tumor samples were from 4 published retrospective prostatectomy patient cohorts at the Mayo Clinic (MCI and MCII), Cleveland Clinic (CC), and Thomas Jefferson University (TJU)	NR	Evans *et al,* 2016	(45)
		1.00	451	*BRCA1* undefined	USA	PC patients consenting to genomic analysis of their tumor and germline DNA	6 (5.5); 7 (31.0); 8-10 (57.2); unknown (6.2)	Abida *et al,* 2017	(30)
		1.18	936	Known or likely deleterious mutations in *BRCA1*	USA	Men with PC; No other details	NR	Lara *et al,* 2017	(66)

		1.93	207	Known or likely deleterious mutations in *BRCA1*	USA	Men with PC; No other details	NR	Lara *et al,* 2017	(66)
		2.35	85	Undefined	USA	Advanced prostate cancer patients	NR	Myers *et al,* 2016	(76)
[a]Study level inclusion criteria may not reflect prostate subgroups, because multiple groups are included. *BRCA*, breast cancer susceptibility gene; CRPC, castration-resistant PC; DDR, DNA damage repair; ECOG, Eastern Cooperative Oncology Group; m, metastatic; NR, not reported; PC, prostate cancer; UKGPCS, UK Genetic Prostate Cancer Study. More baseline details can be found in Appendix S5.									

(D) Mutations in the *BRCA2* gene.

PC group	Germline or somatic	% prevalence	N	DDR definition	Country	Study level inclusion criteria[a]	Baseline Gleason score (% of population)	Author, year	Ref-erences
mCRPC	Germline	3.34	419	Undefined	Spain	Patients ≥18years of age; histologically confirmed prostate cancer; presence of metastatic disease according to bone, CT, and/or MRI scan; confirmed castration resistant prostate cancer; due to start or have started first-line treatment with any approved survival-prolonging therapy for mCRPC within a period of 6 months from study entry; ECOG performance status ≤21	NR	Romero *et al,* 2017	(90)
		5.02	319	Undefined deleterious mutation	Canada	Patients with mCRPC	NR	Struss *et al,* 2017	(95)

		5.33	150	Pathogenic germline *BRCA2* mutations	Multi-national	Affected individuals with metastatic disease accessible by image-guided biopsy were eligible for inclusion and who were being considered for abiraterone acetate or enzalutamide as standard of care, or as part of a clinical trial, were considered for enrollment	NR	Robinson *et al,* 2015	(89)
mCRPC	Somatic	2.00	50	*BRCA2* non-synonymous point mutation	USA	Lethal heavily pre-treated CRPCs obtained at rapid autopsy; or high-grade localized prostate cancers	NR	Grasso *et al,* 2012	(53)
		5.00	514	Undefined	USA	Patients with mCRPC that underwent baseline ctDNA analysis for potentially actionable alterations using Guardant360 before new systemic therapy were identified	NR	Sonpavde *et al,* 2017	(6)
		6.00	150	Biallelic mutation	Multi-national	Discovery set PC patients were selected based on high Gleason score and availability of both peripheral blood DNA and fresh frozen prostatectomy samples. 150 samples from Robinson 2015 (89)	7 (10); 8 (20); 9 (60); 10 (10)	Decker *et al,* 2016	(43)
mPC	Germline	5.10	569	*BRCA2* (undefined)	Multi-national	Men had to have mPC based on a biopsy of a metastatic site	NR	Nelson *et al,* 2016	(79)
		5.35	692	*BRCA2*	Multi-national	Diagnosis of metastatic prostate cancer, as determined by histologic evaluation of a tumor biopsy specimen or surgical resection specimen	≤6 (6.07); 3+4 (9.4); 4+3 (13.3); 8-10 (55.2); unknown (16.0)	Pritchard *et al,* 2016	(87)
PC	Germline	0.00	92	*BRCA2* exon sequence variants	Germany	Patients with familial PC who are members of families with PC clustering; or patients with sporadic early onset PC who underwent radical prostatectomy and reported a negative family history for prostate cancer	Gleason ≤7 and <GIII (82.6); Gleason >7 or GIII (15.2); unknown (2.2)	Maier *et al,* 2014	(72)

		0.00	178	*BRCA2* truncation variant	Multi-national	Patients with prostate adenocarcinoma and sequence data from germline and tumor DNA; 50% coverage of the targeted exome having at least 20x coverage in both germline and tumor samples.	NR	Lu *et al,* 2015	(71)
		1.40	1904	Undefined *BRCA2*	Canada	Men diagnosed with prostate cancer at biopsy in a cohort of men who underwent a prostate biopsy because of an elevated prostate-specific antigen (PSA) blood test (>4.0 ng/ml) or an abnormal digital rectal examination	NR	Akbari *et al,* 2014	(103)
		1.56	2181	Undefined *BRCA2*	UK	Patients enrolled in the UKGPCS between1990-2005 with available genomic DNA and clinical and survival data in our prospectively maintained UKGPCS database.	NR	Castro *et al,* 2011	(38)
		1.80	333	*BRCA2*	Multi-national	Patients diagnosed with prostate adenocarcinoma and had not received prior treatment for their disease (chemotherapy, radiotherapy, or hormonal ablation therapy)	3+3 (19.5); 3+4 (30.6); 4+3 (23.4); ≥8 (26.4)	Cancer Genome Atlas 2015	(37)
		9.00	221	*BRCA2* undefined	USA	PC patients consenting to genomic analysis of their tumor and germline DNA	NR	Abida *et al,* 2017	(30)
		0.20	499	*BRCA2*	Multi-national	Diagnosis of metastatic prostate cancer, as determined by histologic evaluation of a tumor biopsy specimen or surgical resection specimen	≤6 (9.0); 3+4 (29.7); 4+3 (20.2); 8-10 (41.1); unknown (0)	Pritchard *et al,* 2016	(87)
		0.82	486	*BRCA2*	Multi-national	NR	NR	Na *et al,* 2017	(106)

PC	Somatic	0.00	50	NR	Multi-national	Discovery set PC patients were selected based on high Gleason score and availability of both peripheral blood DNA and fresh frozen prostatectomy samples. 150 samples from Robinson 2015 (89)	<7 (70); 8-10 (22); NR (8)	Decker *et al,* 2016	(43)
		1.60	630	Gene frequency from DNA_REPAIR gene set	USA	Tumor samples were from 4 published retrospective prostatectomy patient cohorts at the Mayo Clinic (MCI and MCII), Cleveland Clinic (CC), and Thomas Jefferson University (TJU)	NR	Evans *et al,* 2016	(45)
		1.69	178	*BRCA2* somatic mutation	Multi-national	Patients with prostate adenocarcinoma and sequence data from germline and tumor DNA; 50% coverage of the targeted exome having at least 20x coverage in both germline and tumor samples	NR	Lu *et al,* 2015	(71)
		3.00	333	Undefined *BRCA2* mutation	Multi-national	Patients diagnosed with prostate adenocarcinoma, and had not received prior treatment for their disease (chemotherapy, radiotherapy, or hormonal ablation therapy)	3+3 (19.5); 3+4 (30.6); 4+3 (23.4); ≥8 (26.4)	Cancer Genome Atlas 2015	(37)
		4.00	327	*BRCA2*	USA	Men with prostate cancer who had undergone treatment at the Dana Farber Cancer Institute; consented to targeted next generation sequencing	NR	Patel *et al,* 2016	(83)
		5.80	207	Known or likely deleterious mutations in *BRCA2*	USA	Men with PC; no other details	NR	Lara *et al,* 2017	(66)
		6.00	69	*BRCA2* SNVs and indels	Multi-national	NR	NR	Fontugne *et al,* 2015	(47)

		7.00	451	*BRCA2* undefined	USA	PC patients consenting to genomic analysis of their tumor and germline DNA	6 (5.5); 7 (31.0); 8-10 (57.2); unknown (6.2)	Abida *et al,* 2017	(30)
		11.43	936	Known or likely deleterious mutations in *BRCA2*	USA	Men with PC; no other details	NR	Lara *et al,* 2017	(66)
		11.76	85	Undefined	USA	Advanced prostate cancer patients	NR	Myers *et al,* 2016	(76)
[a]Study level inclusion criteria may not reflect prostate subgroups, because multiple groups are included. *BRCA*, breast cancer susceptibility gene; CRPC, castration-resistant PC; CT, computed tomography; DDR, DNA damage repair; ECOG, Eastern Cooperative Oncology Group; m, metastatic; MRI, magnetic resonance imaging; NR, not reported; PC, prostate cancer; SNVs, single nucleotide variations; UKGPCS, UK Genetic Prostate Cancer Study. More baseline details can be found in Appendix S5.									

(E) Mutations in the *CHEK2* gene.

PC group	Germline or somatic	% prevalence	N	DDR definition	Country	Study level inclusion criteria[a]	Baseline Gleason score (% of population)	Author, year	Ref-erences
mCRPC	Germline	0.95	419	Undefined	Spain	Patients ≥18years of age; histologically confirmed prostate cancer; presence of metastatic disease according to bone, CT, and/or MRI scan; confirmed castration resistant prostate cancer; due to start or have started first-line treatment with any approved survival-prolonging therapy for mCRPC within a period of 6 months from study entry; ECOG performance status ≤21	NR	Romero *et al,* 017	(90)
mPC	Germline	1.20	569	*CHEK2* (undefined)	Multi-national	Men had to have mPC based on a biopsy of a metastatic site	NR	Nelson *et al,* 2016	(79)

		1.87	534	*CHEK2*	Multi-national	Diagnosis of metastatic prostate cancer, as determined by histologic evaluation of a tumor biopsy specimen or surgical resection specimen	NR	Pritchard *et al,* 2016	(87)
PC	Germline	1.79	613	*CHEK2* germline pathogenic mutations	Multi-national	NR	NR	Na *et al,* 2017	(106)
		4.00	221	*CHEK2* undefined	USA	PC patients consenting to genomic analysis of their tumor and germline DNA	NR	Abida *et al,* 2017	(30)
		0.40	499	*CHEK2*	Multi-national	Diagnosis of metastatic prostate cancer, as determined by histologic evaluation of a tumor biopsy specimen or surgical resection specimen	≤6 (9.0); 3+4 (29.7); 4+3 (20.2); 8-10 (41.1); unknown (0)	Pritchard *et al,* 2016	(87)
		1.70	352	*CHEK2* germline pathogenic mutations	Multi-national	NR	NR	Na *et al,* 2017	(106)
		10.71	84	all *CHEK2* mutations	USA	Primary prostate tumor tissues	NR	Wu *et al,* 2006	(100)
PC	Somatic	0.80	630	gene frequency from DNA_DAMAGE_CHECKPOINT gene set	USA	Tumor samples were from 4 published retrospective prostatectomy patient cohorts at the Mayo Clinic (MCI and MCII), Cleveland Clinic (CC), and Thomas Jefferson University (TJU)	NR	Evans *et al,* 2016	(45)
		1.19	84	Defective *CHEK2* genes (both alleles affected)	Multi-national	Selection of PC patients from a commercial biobank and the Transatlantic Prostate Group Cohort	NR	Timms *et al,* 2016	(96)

		2.38	84	All *CHEK2* mutations	USA	Primary prostate tumor tissues	NR	Wu *et al,* 2006	(100)

[a]Study level inclusion criteria may not reflect prostate subgroups, because multiple groups are included. *CHEK2*, checkpoint kinase 2; CRPC, castration-resistant PC; CT, computed tomography; ECOG, Eastern Cooperative Oncology Group; m, metastatic; MRI, magnetic resonance imaging; NR, not reported; PC, prostate cancer. More baseline details can be found in Appendix S5.

(F) Mutations in DDR genes

PC group	Germline or somatic	% prevalence	N	DDR definition	Country	Study level inclusion criteria[a]	Baseline Gleason score (% of population)	Author, year	Ref-erences
mCRPC	Germline	7.50	319	Undefined deleterious germline DDR mutations (22 genes including *BRCA2*, *PALB2*, CDK2)	Canada	Patients with mCRPC	NR	Struss *et al,* 2017	(95)
		9.10	419	Aberrations in 24 DNA repair genes	Spain	Patients ≥18years of age; histologically confirmed prostate cancer; presence of metastatic disease according to bone, CT, and/or MRI scan; confirmed castration resistant prostate cancer; due to start or have started first-line treatment with any approved survival-prolonging therapy for mCRPC within a period of 6 months from study entry; ECOG performance status ≤21	NR	Romero *et al,* 2017	(90)

mPC	Germline	11.40	569	20 DNA repair genes associated with autosomal dominant cancer predisposition syndromes (included *BRCA2*, *ATM*, *CHEK2*, *BRCA1*, *PALB2*, *RAD51D*, *ATR*, *FAM175A*, *GEN1*, *MRE11A*, *MSH2*, *MSH6*, *RAD51C*, *NBN*).	Multi-national	Men had to have mPC based on a biopsy of a metastatic site	NR	Nelson *et al,* 2016	(79)
		11.80	692	DDR (20-gene panel: *ATM*, *ATR*, *BAP1*, *BARD1*, *BRCA1*, *BRCA2*, *BRIP1*, *CHEK2*, *FAM175A*, *GEN1*, *MLH1*, *MRE11A*, *MSH2*, *MSH6*, *NBN*, *PALB2*, *PMS2*, *RAD51C*, *RAD51D*, *XRCC2*)	Multi-national	Diagnosis of metastatic prostate cancer, as determined by histologic evaluation of a tumor biopsy specimen or surgical resection specimen	≤6 (6.07); 3+4 (9.4); 4+3 (13.3); 8-10 (55.2); unknown (16.0)	Pritchard *et al,* 2016	(79)
mPC	Somatic	10.00	50	MMR (mismatch repair) genes	USA	Human primary and metastatic prostate cancer tissues were obtained as part of the University of Washington Prostate Cancer Donor Rapid Autopsy Program	NR	Pritchard *et al,* 2014	(86)
		16.40	55	*BRCA1*, *BRCA2*, *ATM*	USA	Patients with metastatic prostate cancer	NR	Gourdin *et al,* 2016	(52)
PC	Germline	18.62	333	*ATM*, *BRCA1*, *BRCA2*, *CDK12*, *FANCD2*, *RAD51C*	Multi-national	Patients diagnosed with prostate adenocarcinoma, and had not received prior treatment for their disease (chemotherapy, radiotherapy, or hormonal ablation therapy)	3+3 (19.5); 3+4 (30.6); 4+3 (23.4); ≥8 (26.4)	Cancer Genome Atlas 2015	(37)
		19.00	221	DDR (including *BRIP1*, *NBN*, *PALB2*, *PMS2*, *MITF*, *RECQL*, *ATM*, *CHEK2*, *BRCA1*, *BRCA2*, *FH*)	USA	PC patients consenting to genomic analysis of their tumor and germline DNA	NR	Abida *et al,* 2017	(30)

		17.2	1158	DDR (included 14 genes on a hereditary PC panel, most of which were DNA repair genes, including *BRCA* and *BRCA2*)	USA	Men with PC	NR	Nicolosi *et al,* 2017	(81)
PC	Somatic	13.10	84	Defective DDR genes (one allele affected); *RAD50*, *ATM*, *NBN*, *ATR*, *PPP2R2A*, *CHEK2*, *FANCA*, *RAD52*	Multi-national	Selection of PC patients from a commercial biobank and the Transatlantic Prostate Group Cohort	NR	Timms *et al,* 2016	(96)
		22.00	451	DDR (including *BRCA2*, *BRCA1*, *ATM*, *FANCA*, *RAD50*, *PALB2*, and *CDK12*)	USA	PC patients consenting to genomic analysis of their tumor and germline DNA	6 (5.5); 7 (31.0); 8-10 (57.2); unknown (6.2)	Abida *et al,* 2017	(30)
		4.90	61	DNA repair genes such as *ATM*	UK	Primary prostate cancer samples for the Welsh Cancer Bank	NR	Jefferies *et al,* 2017	(61)

[a]Study level inclusion criteria may not reflect prostate subgroups, because multiple groups are included. *ATM*, ataxia telangiectasia mutated; *ATR*, ataxia telangiectasia and Rad3-related protein; *BAP1*, *BRCA1*-associated protein 1; *BARD1*, *BRCA1*-associated RING domain 1; *BRCA*, breast cancer susceptibility gene; *BRIP1*, *BRCA1* interacting protein C-terminal helicase 1; *CHEK2*, checkpoint kinase 2; CRPC, castration-resistant PC; CT, computed tomography; DDR, DNA damage repair; ECOG, Eastern Cooperative Oncology Group; *FAM175A*, family with sequence similarity 175,member A; FANC, Fanconi anemia complementation group; *FH*, fumarate hydratase; *GEN1*, GEN1, Holliday junction 5' flap endonuclease; m, metastatic; *MITF*, melanogenesis-associated transcription factor; *MLH1*, mutL homolog 1; MMR, mismatch repair; *MRE11A*, *MRE11* homolog A, double-strand break repair nuclease; MRI, magnetic resonance imaging; MSH, muS homolog; *NBN*, nibrin; *PALB2*, partner and localizer of *BRCA2*; NR, not reported; PC, prostate cancer; *PMS2*, *PMS1* homolog 2, mismatch repair system component; *PPP2R2A*, protein phosphatase 2 regulatory subunit B alpha; RAD, DNA repair protein; *RECQL*, RecQ like helicase; RING, really interesting new gene; XRCC, x-ray repair cross complementing. More baseline details can be found in Appendix S4.

(G) Mutations in *FANCA* gene.

PC group	Germline or somatic	% prevalence	N	DDR definition	Country	Study level inclusion criteria[a]	Baseline Gleason score (% of population)	Author, year	Ref-erences

PC	Germline	0.56	178	*FANCA* truncation variant	Multi-national	Patients with prostate adenocarcinoma and sequence data from germline and tumor DNA; 50% coverage of the targeted exome having at least 20x coverage in both germline and tumor samples	NR	Lu *et al,* 2015	(71)
PC	Somatic	0.50	630	Gene frequency from DNA_REPAIR gene set	USA	Tumor samples were from 4 published retrospective prostatectomy patient cohorts at the Mayo Clinic (MCI and MCII), Cleveland Clinic (CC), and Thomas Jefferson University (TJU)	NR	Evans *et al,* 2016	(45)
		1.19	84	Defective *FANCA* genes (both alleles affected)	Multi-national	Selection of PC patients from a commercial biobank and the Transatlantic Prostate Group Cohort	NR	Timms *et al,* 2016	(96)
		3.00	451	*FANCA* undefined	USA	PC patients consenting to genomic analysis of their tumor and germline DNA	6 (5.5); 7 (31.0); 8-10 (57.2); unknown (6.2)	Abida *et al,* 2017	(30)
		16.00	69	*FANCA* deletion	USA	Mixed population of localized PC (n=69) and advanced mPC (n=29).	NR	Beltran *et al,* 2015	(19)

[a]Study level inclusion criteria may not reflect prostate subgroups, because multiple groups are included. DDR, DNA damage repair; FANC, Fanconi anemia complementation group; m, metastatic; NR, not reported; PC, prostate cancer. More baseline details can be found in Appendix S5.

(H) Mutations in the *MLH1* gene.

PC group	Germline or somatic	% prevalence	N	DDR definition	Country	Study level inclusion criteria[a]	Baseline Gleason score (% of population)	Author, year	References
mPC	Germline	0.00	692	*MLH1*	Multi-national	Diagnosis of metastatic prostate cancer, as determined by histologic evaluation of a tumor biopsy specimen or surgical resection specimen	≤6 (6.07); 3 + 4 (9.4); 4 + 3 (13.3); 8-10 (55.2); unknown (16.0)	Pritchard *et al,* 2016	(87)

mPC	Somatic	3.33	60	All *MLH1* (*MLH1* homozygous copy loss, *MLH1* frameshift (c.1310del)	USA	Human primary and metastatic prostate cancer tissues were obtained as part of the University of Washington Prostate Cancer Donor Rapid Autopsy Program	NR	Pritchard *et al,* 2014	(86)
PC	Somatic	0.20	630	Gene frequency from DNA_REPAIR gene set	USA	Tumor samples were from 4 published retrospective prostatectomy patient cohorts at the Mayo Clinic (MCI and MCII), Cleveland Clinic (CC), and Thomas Jefferson University (TJU)	NR	Evans *et al,* 2016	(45)
		1.00	451	*MLH1* undefined	USA	PC patients consenting to genomic analysis of their tumor and germline DNA	6 (5.5); 7 (31.0); 8-10 (57.2); unknown (6.2)	Abida *et al,* 2017	(30)
PC	Germline	0.00	499	*MLH1*	Multi-national	Diagnosis of metastatic prostate cancer, as determined by histologic evaluation of a tumor biopsy specimen or surgical resection specimen	≤6 (9.0); 3+4 (29.7); 4+3 (20.2); 8-10 (41.1); unknown (0)	Pritchard *et al,* 2016	(87)
[a]Study level inclusion criteria may not reflect prostate subgroups, because multiple groups are included. DDR, DNA damage repair; m, metastatic; *MLH1*, mutL homolog 1; NR, not reported; PC, prostate cancer. More baseline details can be found in Appendix S5.									

(I) Mutations in the *MRE11A* gene.

PC group	Germline or somatic	% prevalence	N	DDR definition	Country	Study level inclusion criteria[a]	Baseline Gleason score (% of population)	Author, year	References
mPC	Germline	0.14	692	*MRE11A*	Multi-national	Diagnosis of metastatic prostate cancer, as determined by histologic evaluation of a tumor biopsy specimen or surgical resection specimen	≤6 (6.07); 3+4 (9.4); 4+3 (13.3); 8-10 (55.2); unknown (16.0)	Pritchard *et al,* 2016	(87)
		0.18	569	*MRE11A* (undefined)	Multi-national	Men had to have mPC based on a biopsy of a metastatic site	NR	Nelson *et al,* 2016	(79)

PC	Somatic	0.00	630	Gene frequency from DNA_REPAIR gene set	USA	Tumor samples were from 4 published retrospective prostatectomy patient cohorts at the Mayo Clinic (MCI and MCII) Cleveland Clinic (CC), and Thomas Jefferson University (TJU)	NR	Evans *et al,* 2016	(45)
PC	Germline	0.20	499	*MRE11A*	Multi-national	Diagnosis of metastatic prostate cancer, as determined by histologic evaluation of a tumor biopsy specimen or surgical resection specimen	≤6 (9.0); 3+4 (29.7); 4+3 (20.2); 8-10 (41.1); unknown (0)	Pritchard *et al,* 2016	(87)
[a]Study level inclusion criteria may not reflect prostate subgroups, because multiple groups are included. DDR, DNA damage repair; m, metastatic; *MRE11A*, *MRE11* homolog A, double-strand break repair nuclease; NR, not reported; PC, prostate cancer. More baseline details can be found in Appendix S5.									

(J) Mutations in the *NBN* gene.

PC group	Germline or somatic	% prevalence	N	DDR definition	Country	Study level inclusion criteria[a]	Baseline Gleason score (% of population)	Author, year	References
mPC	Germline	0.18	569	*NBN* (undefined)	Multi-national	Men had to have mPC based on a biopsy of a metastatic site	NR	Nelson *et al,* 2016	(79)
		0.29	692	*NBN*	Multi-national	Diagnosis of metastatic prostate cancer, as determined by histologic evaluation of a tumor biopsy specimen or surgical resection specimen	≤6 (6.07); 3+4 (9.4); 4+3 (13.3); 8-10 (55.2); unknown (16.0)	Pritchard *et al,* 2016	(87)
PC	Germline	0.45	221	*NBN* undefined	USA	PC patients consenting to genomic analysis of their tumor and germline DNA	NR	Abida *et al,* 2017	(30)
		0.20	499	*NBN*	Multi-national	Diagnosis of metastatic prostate cancer, as determined by histologic evaluation of a tumor biopsy specimen or surgical resection specimen	≤6 (9.0); 3+4 (29.7); 4+3 (20.2); 8-10 (41.1); unknown (0)	Pritchard *et al,* 2016	(87)

PC	Somatic	0.30	630	Gene frequency from DNA_REPAIR gene set	USA	Tumor samples were from 4 published retrospective prostatectomy patient cohorts at the Mayo Clinic (MCI and MCII), Cleveland Clinic (CC), and Thomas Jefferson University (TJU)	NR	Evans *et al,* 2016	(45)
		1.19	84	Defective *NBN* genes (both alleles affected)	Multi-national	Selection of PC patients from a commercial biobank and the Transatlantic Prostate Group Cohort	NR	Timms *et al,* 2016	(96)
		65.00	69	*NBN* amplifications	Multi-national	NR	NR	Fontugne *et al,* 2015	(47)
[a]Study level inclusion criteria may not reflect prostate subgroups, because multiple groups are included.DDR, DNA damage repair; m, metastatic; *NBN*, nibrin; NR, not reported; PC, prostate cancer. More baseline details can be found in Appendix S5.									

(K) Mutations in the *PALB2* gene.

PC group	Germline or somatic	% prevalence	N	DDR definition	Country	Study level inclusion criteria[a]	Baseline Gleason score (% of population)	Author, year	Ref-erences
mCRPC	Germline	0.63	319	Undefined deleterious mutation	Canada	Patients with mCRPC	NR	Struss *et al,* 2017	(95)
mCRPC	Somatic	4.00	153	*PALB2* mut/del in metastatic tumor samples	USA	PC patients consenting to genomic analysis of their tumor and germline DNA	NR	Abida *et al,* 2017	(30)
mPC	Germline	0.43	692	*PALB2*	Multi-national	Diagnosis of metastatic prostate cancer, as determined by histologic evaluation of a tumor biopsy specimen or surgical resection specimen	≤6 (6.07); 3+4 (9.4); 4+3 (13.3); 8-10 (55.2); unknown (16.0)	Pritchard *et al,* 2016	(87)
		0.50	569	*PALB2* (undefined)	Multi-national	Men had to have mPC based on a biopsy of a metastatic site	NR	Nelson *et al,* 2016	(79)
mPC	Somatic	0.00	70	*PALB2* mut/del in metastatic tumor samples	USA	PC patients consenting to genomic analysis of their tumor and germline DNA	NR	Abida *et al,* 2017	(30)

PC	Germline	0.45	221	*PALB2* undefined	USA		NR	Abida *et al,* 2017	(30)
		0.56	178	*PALB2* truncations	Multi-national	Patients with prostate adenocarcinoma and sequence data from germline and tumor DNA; 50% coverage of the targeted exome having at least 20x coverage in both germline and tumor samples	NR	Lu *et al,* 2015	(71)
		0.40	499	*PALB2*	Multi-national	Diagnosis of metastatic prostate cancer, as determined by histologic evaluation of a tumor biopsy specimen or surgical resection specimen	≤6 (9.0); 3+4 (29.7); 4+3 (20.2); 8-10 (41.1); unknown (0)	Pritchard *et al,* 2016	(87)
PC	Somatic	0.60	630	gene frequency from REACTOME_DNA_REPAIR gene set	USA	Tumor samples were from 4 published retrospective prostatectomy patient cohorts at the Mayo Clinic (MCI and MCII), Cleveland Clinic (CC), and Thomas Jefferson University (TJU).	NR	Evans *et al,* 2016	(45)
		2.00	451	*PALB2* undefined	USA	PC patients consenting to genomic analysis of their tumor and germline DNA	6 (5.5); 7 (31.0); 8-10 (57.2); unknown (6.2)	Abida *et al,* 2017	(30)
[a]Study level inclusion criteria may not reflect prostate subgroups, because multiple groups are included. CRPC, castration-resistant PC; m, metastatic; NR, not reported; *PALB2*, partner and localizer of *BRCA2*; PC, prostate cancer. More baseline details can be found in Appendix S5.									

(L) Mutations in the *RAD51C* gene.

PC group	Germline or somatic	% prevalence	N	DDR definition	Country	Study level inclusion criteria[a]	Baseline Gleason score (% of population)	Author, year	Ref-erences

mPC	Germline	0.14	692	*RAD51C*	Multi-national	Diagnosis of metastatic prostate cancer, as determined by histologic evaluation of a tumor biopsy specimen or surgical resection specimen	≤6 (6.07); 3+4 (9.4); 4+3 (13.3); 8-10 (55.2); unknown (16.0)	Pritchard *et al,* 2016	(87)
		0.18	569	*RAD51C* (undefined)	Multi-national	Men had to have mPC based on a biopsy of a metastatic site	NR	Nelson *et al,* 2016	(79)
PC	Germline	0.56	178	*RAD51C* truncation variant	Multi-national	Patients with prostate adenocarcinoma and sequence data from germline and tumor DNA; 50% coverage of the targeted exome having at least 20x coverage in both germline and tumor samples.	NR	Lu *et al,* 2015	(71)
		0.40	499	*RAD51C*	Multi-national	Diagnosis of metastatic prostate cancer, as determined by histologic evaluation of a tumor biopsy specimen or surgical resection specimen	≤6 (9.0); 3+4 (29.7); 4+3 (20.2); 8-10 (41.1); unknown (0)	Pritchard *et al,* 2016	(87)
PC	Somatic	0.00	630	Gene frequency from DNA_REPAIR gene set	USA	Tumor samples were from 4 published retrospective prostatectomy patient cohorts at the Mayo Clinic (MCI and MCII), Cleveland Clinic (CC), and Thomas Jefferson University (TJU)	NR	Evans *et al,* 2016	(45)
		3.00	333	any *RAD51C*	Multi-national	Patients diagnosed with prostate adenocarcinoma, and had not received prior treatment for their disease (chemotherapy, radiotherapy, or hormonal ablation therapy)	3+3 (19.5); 3+4 (30.6); 4+3 (23.4); ≥8 (26.4)	Cancer Genome Atlas 2015	(37)

[a]Study level inclusion criteria may not reflect prostate subgroups, because multiple groups are included. DDR, DNA damage repair; m, metastatic; NR, not reported; PC, prostate cancer; RAD, DNA repair protein. More baseline details can be found in Appendix S5.

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Figure S1. Percentage of studies meeting JBI prevalence quality criteria by question. JBI, Joanna Briggs Institute; NA, not applicable.