Prostate cancer is a common malignancy in men, with a markedly variable clinical course. Somatic alterations in DNA drive the growth of prostate cancers and may underlie the behavior of aggressive versus indolent tumors. The accelerating application of genomic technologies over the last two decades has identified mutations that drive prostate cancer formation, progression, and therapeutic resistance. Here, we discuss exemplary somatic mutations in prostate cancer, and highlight mutated cellular pathways with biological and possible therapeutic importance. Examples include mutated genes involved in androgen signaling, cell cycle regulation, signal transduction, and development. Some genetic alterations may also predict the clinical course of disease or response to therapy, although the molecular heterogeneity of prostate tumors poses challenges to genomic biomarker identification. The widespread application of massively parallel sequencing technology to the analysis of prostate cancer genomes should continue to advance both discovery-oriented and diagnostic avenues.

Keywords: prostate cancer, genomic, genome sequencing
et al., 2010; Kumar et al., 2011; unpublished data). It remains to be determined whether the high levels of mutation in these tumors are caused by MMR deficiency, and whether hyper-mutated cancers reflect different environmental etiology or biological behavior as well. Activating mutations in KRAS occur in 10–20% of Asian patients but are rare in Caucasian men, perhaps reflecting different environmental etiology or biological behavior of cancers in these populations (Watanabe et al., 1994; Konishi et al., 1997) while the androgen receptor is mutated only in metastatic or treatment-resistant disease (Linja and Visakorpi, 2004; Taylor et al., 2010). Ethnicity may influence mutation prevalence as well. Activating mutations in KRAS and BRAF occur in ~10% of Asian patients but are rare in Caucasian men, perhaps reflecting different environmental etiology or biological behavior of cancers in these populations (Watanabe et al., 1994; Konishi et al., 1997; Cho et al., 2006).

Defects in DNA mismatch repair (MMR) machinery have been reported in prostate cancers and may accelerate progression to castration-independence (Dahiya et al., 1997; Chen et al., 2001). Some tumors display “closed chains” of balanced rearrangements, in which multiple DNA breaks occur throughout the genome and the resulting fragments are shuffled and rejoined to one another. These rearrangements may arise when the affected genetic loci are physically proximal to each other, possibly due to co-regulation by transcriptional machinery or nuclear co-localization in open- or closed-chromatin compartments (Osborne et al., 2004; Berger et al., 2011). Consistent with this hypothesis, androgen stimulation can induce physical co-localization of TMPRSS2 and ERG and permit fusion of these genes de novo via a topoisomerase 2B-mediated mechanism (Haffner et al., 2010).

The diverse categories of genomic aberrations underscore the need for comprehensive genomic analyses both to understand tumor biology and to direct targeted therapies on a genotype-specific basis (Roychowdhury et al., 2011).

**CELLULAR PATHWAYS DYSREGULATED BY RECURRENT PROSTATE CANCER GENOMIC ALTERATIONS**

Genomic alterations in prostate cancer can increasingly be conceptualized in terms of the molecular processes and pathways on which they impinge (Taylor et al., 2010). Mutations in prostate cancer may affect signal transduction pathways that regulate growth and proliferation, as well as genes involved in the normal development of the prostate. Below, we highlight several themes and pathways that provide a framework for understanding genomic alterations in prostate cancer.

**PI3K AND MAPK SIGNALING**

The phosphoinositide 3-kinase (PI3K) pathway is a central mediator of cellular proliferation and growth that is aberrantly activated in prostate cancer. In response to pro-proliferative signals, PI3K catalyzes the formation of phosphatidylinositol (3,4,5)-triphosphate (PIP3), which recruits Akt to the plasma membrane. Upon phospho-activation at the plasma membrane, Akt phosphorylates a wide array of substrates that promote proliferation and cell survival.

Prostate tumors achieve activation of PI3K signaling most frequently via inactivation of the tumor-suppressor gene PTEN (Figure 2). PTEN encodes a lipid–protein phosphatase that counteracts signaling by PI3K via dephosphorylation of PIP3. Loss of heterozygosity at the PTEN locus is found in up to 70% of primary prostate cancers and inactivating mutations occur in 5–10%

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**FIGURE 1 | Genomic alterations in four high-risk prostate cancers.** Cross plots depicting genomic rearrangements and copy number alterations in four prostate tumors analyzed by whole-genome sequencing (unpublished data). Green and pink lines designate intrachromosomal and interchromosomal rearrangements, respectively. Somatic copy number alterations are indicated in red (amplification) and blue (deletion) in the inner rings. Gleason scores indicate the two most prevalent histologic grades in each tumor. Pathological stage is noted as well, where pT3 indicates locally invasive disease.
FIGURE 2 | Somatic alterations in the PI3K pathway in prostate cancer.

Selected genes in the PI3K pathway are depicted, alongside the mechanisms by which they are altered in prostate cancer. Putative proto-oncogenes are boxed in red and tumor-suppressor genes in blue. PI3K signaling is frequently activated by deletion of PTEN. PHLPP1 encodes a phosphatase that dephosphorylates activated Akt, and is frequently co-deleted with PTEN in metastatic tumors (Chen et al., 2011). Genomic rearrangements disrupt MAGI2, which encodes a scaffolding protein that stabilizes PTEN (Su et al., 2005; Berger et al., 2011). Recurrent deletions inactivate the FND14 gene, which encodes a transcription factor substrate of Akt that mediates PI3K signaling. Although rare, oncogenic mutations in the receptor tyrosine kinase EGFR or AKT1 may activate the pathway upstream or downstream of PI3K (Cai et al., 2006; Boermans et al., 2008). The expression of most pathway members is dysregulated at the transcript level as well.

The PI3K pathway may be activated by genomic alterations at additional pathway nodes and dysregulated expression of constituent genes (Figure 2; Dong et al., 2006; Cai et al., 2008; Taylor et al., 2010). Determining whether these lesions predict sensitivity or resistance to PI3K pathway inhibitors has become an active area of translational research.

The mitogen-activated protein kinase (MAPK) pathway also plays a role in prostate cancer pathogenesis, especially in advanced and castration-resistant tumors. MAPK pathway activation is associated with higher tumor stage and grade and recurrent disease (Giesel et al., 1999). In the setting of castration resistance, PI3K and MAPK signaling are often coordinately dysregulated (Gao et al., 2006; Kinkade et al., 2008). Evidence for collaboration between
these pathways continues to emerge. For instance, PTEN-induced senescence may be overcome by up-regulation of MAPK signaling induced by overexpression of HER2 (Ahmad et al., 2011). Up-regulation of RAS family members, RAF1 and BRAF, or down-regulation of SPRY1 or SPRY2 genes, are common and enriched in prostate cancer metastases (Kwabi-Addo et al., 2004; McKee et al., 2005; Taylor et al., 2010). In some cases, expression of RAS, RAF1, and BRAF is activated by oncogenic fusions with highly expressed promoters (Palaisamy et al., 2011; Wang et al., 2011). Repression of the RAS-GAP gene DARCIP by E2F1 may activate MAPK signaling and drive progression and metastasis (Mian et al., 2010). Defining the relevant mechanisms of pathway activation in greater detail will likely inform strategies for targeting castration-resistant tumors.

CELL CYCLE REGULATORY GENES
Several cell cycle regulatory genes are disrupted in prostate cancer. Inactivation of cell cycle inhibitors appears to be required to avoid senescence induced by oncogenic signaling and possibly to bypass androgen-regulation of growth in metastatic or castration-resistant tumors.

Two critical cell cycle regulatory genes, TP53 and RB1, are commonly deleted or mutated in metastatic tumors (Bookstein et al., 1993; Heidenberg et al., 1995; Tricoli et al., 1996; Hyttinen et al., 1999). p53 activates expression of the p21WAF1 cyclin-dependent kinase inhibitor, and the Rb protein regulates transition from the G1 to S cell cycle phase. Rb1 inactivation is common in castration-resistant tumors (Holcomb et al., 2009; Sharma et al., 2010). Likewise, inactivation of p53 is necessary to bypass cellular senescence mechanisms that are activated upon loss of PTEN (Chen et al., 2005).

Another key cell cycle regulator, CDKN1B, encodes the p27Kip1 cyclin-dependent kinase inhibitor, and resides within the 12p13 chromosomal region that is frequently deleted. Low p27Kip1 expression correlates with poor pathological prognostic markers (Vis et al., 2000; Dreher et al., 2004). Amplification of SKP2, which encodes a ubiquitin ligase that targets p27Kip1 for proteasomal degradation, may also serve to inactivate p27Kip1 (Taylor et al., 2010; Robbins et al., 2011). Downregulation of CDKN1B promotes prostate cancer coordination with hemizygous deletion of chromosome 8p appears to be required for normal development of the prostate and is deleted or down-regulated in up to 90% of prostate cancers (Emmert-Buck et al., 1995; Voeck et al., 1996; Asatiani et al., 2005). Inactivation via hemizygous deletion of chromosome 8p appears to occur early and can be observed in PIN lesions (Emmert-Buck et al., 1995; Asatiani et al., 2003). NKX3-1-deficient mice exhibit defective branching morphogenesis of the prostate gland and develop PIN-like lesions with age (Bhatia-Gaur et al., 1999). In addition, NKX3-1 appears to protect the differentiated prostate epithelium from oxidative DNA damage (Ouyang et al., 2005; Bowen and Gelmann, 2010). Therefore, loss of NKX3-1 may both disrupt terminal differentiation and foster the mutational inactivation of collaborating cancer genes such as PTEN (Kim et al., 2002).

The Wnt pathway regulates embryological development, and its contribution to prostate cancer is becoming increasingly recognized (Yardy and Brewer, 2003). Key pathway genes including APC, AXIN1 and the β-catenin gene CTNNB1 may be mutated at low frequency (Voeller et al., 1998; Chestire et al., 2000; Yardy et al., 2009). APC undergoes LOH in roughly 20% of primary cancers and promoter CpG methylation in up to 90% (Brewer et al., 1994; Phillips et al., 1994; Yegnasubramanian et al., 2004). β-Catenin may promote proliferation through co-activation of AR-mediated transcription (Truica et al., 2000; Cronauer et al., 2005). Additional mutations in Wnt pathway genes were recently documented in the progression to castration-resistant disease (Kumar et al., 2011). More pairs of pre- and post-release samples should be analyzed to clarify the importance of this pathway in refractory disease.

GENOMIC HETEROGENEITY OF PROSTATE CANCER
Prostate cancer is a clinically and genetically heterogeneous disease. Independent cancerous foci with distinct morphological features often exist in a single prostate. The course of disease also varies widely: some cancers remain indolent for decades while others rapidly progress to lethality. Distinct molecular features appear to underlie the clinical and histological differences. Identifying genomic determinants of aggressive disease might improve experimental modeling and stratification of patients with intermediate-risk prostate cancer.

Prostate cancer may arise in multiple foci from independent precursor cells that are driven to neoplastic transformation by carcinogenic exposures or genetic predisposition (Androusi and Cheng, 2010). The presence of genomic lesions can vary between foci, including TMPRSS2-ERG fusion, MYC amplification, and TP53 mutation (Mirandani et al., 1995; Jenkins et al., 1997; Mehra et al., 2007). Multiple distinct clones can be identified in a single biopsy (Ruíz et al., 2011), but most metastatic prostate cancers appear to originate from a single clone within a primary
tumor (Qian et al., 1995; Holcomb et al., 2009; Liu et al., 2009). Among other lesions, subclonal TP53 mutations may define cells in the primary tumor with metastatic potential (Michaudani et al., 1995; Navone et al., 1999). Intratumoral heterogeneity complicates efforts to define prognostic mutations or expression signatures from primary tumors, because the subtype within a primary tumor that gives rise to metastatic disease must be adequately sampled (Shoemaker et al., 2010).

Despite the challenges posed by tumor heterogeneity, expression signatures have been proposed that delineate histologically aggressive disease or predict outcome independently of clinical variables (Singh et al., 2002; Glinka et al., 2004; True et al., 2006; Fesbø, 2009). However, the overlap between signatures from independent studies is moderate. Some genomic alterations appear to have prognostic value as well. The Tmprss2-ErbC fusion, Mfc amplification, and PTEN or TP53 deletion predict cancer-specific death in at least some patient cohorts (Sato et al., 1999; Demichelis et al., 2007; Siracur et al., 2004). In some cases, a mutational signature may underlie expression-based sub-classifications (Lapointe et al., 2004, 2007).

**PROSTATE CANCER IN THE ERA OF GENOMICS-DRIVEN MEDICINE**

High-throughput genomic profiling has advanced the understanding, prognostication, and treatment of several tumor types. For example, identification of mutations in BAP1 in uveal melanoma (Haboub et al., 2010) or IDH1 in glioblastoma and acute myeloid leukemia (Parsons et al., 2008; Mardis et al., 2009) demonstrated the power of genome sequencing to pinpoint novel cancer-driving mutations. Risk-predictive transcriptional signatures have improved prognostication for patients with breast cancer (Van ’t Veer et al., 2005). Prostate cancer may similarly be ripe for discovery of novel cancer genes and biomarkers as well, since genomic characterization of large cohorts of aggressive tumors has only recently become feasible.

Indeed, whole-exome sequencing of over 100 primary prostate tumor–normal pairs revealed that the ubiquitin ligase complex subunit gene SPOF is among the most frequently mutated genes in primary tumors, though its role in cancer was heretofore unrecognized (Barberi et al., 2012). This study also identified novel recurrent mutations in the fork-head transcription factor gene FOXA1 and mediator complex gene MED12. Experimental study will be required to determine whether these mutations engage known molecular pathways relevant to prostate cancer or reflect novel mechanisms of oncogenesis.

Several hurdles must be overcome for prostate cancer genomics to impact the clinical management of this disease. For instance, biopsies produce scarce material for clinical genotyping and may not fully capture the relevant molecular heterogeneity in a clinical tumor. Expression signatures have not yet demonstrated sufficient prognostic value to merit widespread use. In addition, recurrent genomic lesions identified thus far are largely not considered “druggable.”

These challenges can likely be surmounted by new approaches. For example, genomic characterization may identify opportunities to leverage synthetic lethality by inhibiting targets that are essential in the setting of a particular mutation, such as poly (ADP-ribose) polymerase in ETS-fusion positive prostate cancer (Brenner et al., 2011). The analysis of multiple samples from a primary tumor and perhaps from circulating tumor cells may allow aggressive tumor subclones to be identified. Ultimately, new paradigms for clinical trials may be required that incorporate cancer genomic information. In spite of these challenges, genomic profiling is likely to play an expanding role in the biological study and clinical management of prostate cancer and ultimately in the clinical management of this malignancy.

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