Table S3. Research Progress on Risk Stratification and Treatment Outcome Assessment Models for Prostate Cancer

Model Name	Time and Institution	Contents	Detection Efficacy	Purpose	Existing Issues
Decipher Gene Classifier (GC) [1]	Genome Dx Biosciences, Vancouver, Canada, 2015.	Evaluation of RNA expression levels of 22 biomarkers in prostate cancer tissue samples, risk assessment scored from 0-1.	AUC: 0.64-0.72; C-index: 0.71 for predicting risk of distant metastasis 5 years after biopsy [2-4].	Recommended by NCCN guidelines for risk stratification of prostate cancer following radical prostatectomy, predicting 10-year risk of distant metastasis, and guiding postoperative radiation dosage based on latest research as of 2022.	Multiple biomarkers are involved and High testing thro ughput.
Prolaris (CCP Score) [5-7]	Research on breast cancer started in 2002; Prostate cancer-related research conducted by Myriad Genetics, Salt Lake City in 2014.	Tests 31 cell cycle-related genes and 15 housekeeping genes in prostate tissue to evaluate related risks using a scoring system from 1.3 to 4.7.	For every one point increase in CCP score after surgery, there is a 1.89-fold increase in the risk of biochemical recurrence [8,9].	Recommended by NCCN guidelines for predicting distant metastasis rate and mortality in patients post-prostatectomy. Also being evaluated for assessing the efficacy of radiotherapy.	The efficacy of this model has not yet been validated by prospective randomized controlled trials.
OncotypeDX® Genomic Prostate Score (GPS) [10]	Developed by Genomic Health, Redwood City, USA in 2013 [11].	Tests the expression of 17 genes in prostate cancer tissue samples that are involved in 4 pathways: androgen receptor, cell proliferation, cellular and extracellular matrix.	For every 20-point increase in GPS score, there is a 1.9-fold increase in the risk of distant metastasis.	Recommended by NCCN guidelines to help assess patient prognosis and risk stratification.	-

Contimued Table S3. Research Progress on Risk Stratification and Treatment Outcome Assessment Models for Prostate Cancer

Model Name	Time and Institution	Contents	Detection Efficacy	Purposes	Existing Issues
ProMark [12]	2014, Metamark Genetics, USA.	Used immunofluorescence to detect expression of 8 protein molecules in prostate cancer tissues, scored from 0-1.	Predictive value of 95%	Recommended in the NCCN guidelines for prognostic risk stratification	No relevant prospective randomized controlled trials have yet validated the predictive power of this model.
ADT-RS [13]	2018, Mayo Clinic, USA.	Selected 49 relevant genes from the Decipher GRID database to predict response to ADT treatment.	Single-center study	Patients with higher ADT-RS scores can benefit from ADT treatment; these patients experience a decrease in distant metastasis rates after receiving ADT.	Lacks multicenter, prospective data to confirm.
PAM50 [14,15]	Started in breast cancer research in 2009, and transitioned to prostate cancer by the University of Michigan research team in 2017	Using the expression of 50 PAM50 genes and 5 control genes in surgical specimens, prostate cancer is classified into Lum A, Lum B, and Basal subtypes for molecular typing.	Single-center study	Luminal B subtype can benefit from postoperative ADT, while the benefits for other subtypes are not significant.	Recent studies have shown that molecular typing can be performed in patients with mCRPC.
RSI [16]	Conducted by the National Cancer Institute (NCI) in the US in 2012	11 relevant genes were screened from the molecular expression profiles of over 60 irradiated cells.	-	It can predict the sensitivity of prostate cancer patients to radiotherapy.	It cannot predict the outcome of radiotherapy for prostate cancer patients; the lack of validation by clinical trials.

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