

Supplementary Table 1. Literature-Based Functional Descriptions and References for 46 miRNAs Implicated in Prostate Cancer

miRNAs	Functional Description	Reference
hsa-let-7a-5p	Its decreased expression has been associated with prostate cancer progression and poorer biochemical recurrence-free survival in patients undergoing radical prostatectomy	Giglio et al., 2021 and Rana et al., 2022 ^{37,43}
hsa-let-7d-5p	Disruption of its gene expression pattern has been implicated in prostatic neoplastic progression	Kolenda et al., 2014 and Wagner et al., 2014 ^{98,112}
hsa-let-7i-5p	Its aberrant expression may be implicated in prostatic carcinogenesis. The let-7 family of regulators represents a promising target in prostate cancer. It is a suitable target for diagnosis, prognosis, and therapeutic approaches	Wagner et al., 2014 ⁹⁸
hsa-miR-100-5p	Decreased expression has been observed in prostate cancer, suggesting a role in tumor progression	Ye et al., 2020 ⁹⁹
hsa-miR-101-3p	It serves as a valuable tool for distinguishing between patients with metastatic prostate cancer. Its expression is observed to be elevated in these patients	Duca et al., 2021 and Liu et al., 2022 ^{81,113}
hsa-miR-1185-2-3p	Preliminary studies suggest a potential involvement in the regulation of prostatic tumor processes, functioning as a biomarker for prostate cancer detection	Urabe et al., 2019 ⁵⁶
hsa-miR-125a-5p	Its reduced plasma expression has been associated with prostate cancer progression, rendering it a promising potential biomarker for prostate cancer	Damodaran et al., 2021 and W. Li et al., 2020 ^{49,100}
hsa-miR-125b-5p	It is an androgen receptor-induced microRNA. Its dysregulated expression has been observed in prostate cancer, indicating a potential role in tumorigenesis. Furthermore, it acts as an oncomiR capable of suppressing p14 (ARF) to modulate p53-dependent and p53-independent apoptosis in prostate cancer	Amir et al., 2013, Karadag et al., 2021 and Vanacore et al., 2017 ^{38,114,115}
hsa-miR-1299	Recent evidence suggests that its function is to suppress cellular proliferation and motility in prostate cancer cells	P. Li et al., 2021 ¹⁰¹
hsa-miR-1307-3p	Studies suggest a potential correlation with prostate cancer aggressiveness. Elevated expression levels have been observed to significantly promote prostate cancer progression	Hashimoto et al., 2021 ¹⁰²
hsa-miR-139-5p	It has been observed that treatment of prostate cancer cells with miR-139 induces phenotypic changes characteristic of autophagic cells. It appears that miR-139 elicits the blockade of autophagic flux, leading to apoptosis in prostate cancer cells via mTOR and Beclin-1 proteins	Nam et al., 2020 ¹⁰³
hsa-miR-141-3p	The role of miR-141 in PCa remains ambiguous, but its overexpression following castration has been demonstrated, suggesting its potential involvement in the androgenic mechanism, encompassing both androgen-dependent and castration-resistant metastatic prostate cancer. Consequently, the role of miR-141 in cancer progression warrants	Bergez-Hernández et al., 2022, Cai et al., 2021, Mitchell et al., 2008 and Vancore et al., 2017 ^{40,53,115,116}

	investigation. Furthermore, elevated serum levels of miR-141 have been observed in PCa patients	
hsa-miR-142-3p	Its aberrant expression may influence prostate cancer progression. Indeed, elevated expression levels have been observed in the urine of patients with metastatic prostate cancer	Santo et al., 2022 and Valera et al., 2020 ^{104,105}
hsa-miR-145-5p	Decreased expression of this microRNA has been associated with accelerated prostate cancer progression and diminished survival rates. Furthermore, this microRNA has been evaluated in multiple independent studies, consistently demonstrating a correlative trend with prostate cancer progression	Bergez-Hernández et al., 2022 and Rana et al., 2022 ^{37,40}
hsa-miR-146a-5p	Its aberrant expression has been observed in prostate cancer, suggesting a potential role in tumor progression. In fact, it has been attributed diagnostic properties in liquid biopsies for prostate cancer	Dobrijević et al., 2024 and Vanacore et al., 2017 ^{59,115}
hsa-miR-148b-3p	This miRNA is found to be underexpressed in patients with prostate cancer. Furthermore, a correlation has been observed between miR148b-3p expression and the PSA and PCA3 genes, which are used as prognostic biomarkers for this disease. It is also directly implicated in mechanisms related to the development of this tumor	Bergez-Hernández et al., 2022 ⁴⁰
hsa-miR-150-5p	Its aberrant expression may be implicated in prostatic carcinogenesis. It has been shown to be associated with prostate cancer metastasis and a higher Gleason score	Cruz-Burgos et al., 2023 and Ghamlouche et al., 2023 ^{57,117}
hsa-miR-152-3p	Diminished expression has been associated with prostate cancer progression	Rana et al., 2022 ³⁷
hsa-miR-155-5p	miR-155-5p has been observed to exhibit differential expression between Gleason Grades 2 and 1. Furthermore, miR-155-5p inhibits prostate cancer cell migration and represents a potential target for antitumor therapies	Ramirez-Garrastacho et al., 2022 and Santo et al., 2022 ^{104,106}
hsa-miR-17-3p	miR-17-3p has been observed to serve as a biomarker for the detection of prostate cancer in serum. miR-17-3p has been demonstrated to function as an oncogenic microRNA in prostate cancer, promoting the proliferation and invasion of these tumor cells	Urabe et al., 2019 ⁵⁶
hsa-miR-182-5p	Its overexpression in tissues and plasma has been associated with increased aggressiveness in prostate cancer	Bidarra et al., 2019 ⁴⁶
hsa-miR-183-5p	Its overexpression has been associated with prostate cancer progression, therefore it is proposed as a specific diagnostic biomarker in prostate cancer	Schitcu et al., 2022 ⁴¹

hsa-miR-186-5p	Its diminished expression has been associated with increased cellular proliferation in prostate cancer, rendering it a promising candidate for patient stratification based on ISUP grade (miR-186-5p expression decreases significantly between grades 3 and 2)	Ramirez-Garrastacho et al., 2022 ¹⁰⁶
hsa-miR-195-5p	It has been associated with prostate cancer progression in multiple cohorts and studies	Rana et al., 2022 ³⁷
hsa-miR-210-3p	It is considered one of the most relevant biomarkers for prostate cancer aggressiveness and diagnosis. Its significance has been demonstrated in processes such as cellular proliferation and MET	Martínez-González et al., 2021 ²⁸
hsa-miR-21-3p	It has been observed that inhibition of this miRNA's expression enhances resistance to Doxorubicin treatment. Furthermore, it appears to suppress cellular proliferation in human prostate cancer cells	Zhao et al., 2021 ¹⁰⁷
hsa-miR-21-5p	Alterations in its expression levels have been associated with changes in tumor size and vascular infiltration in patients with prostate cancer	Stafford et al., 2022 and W. T. Zhang et al., 2022 ^{33,34}
hsa-miR-221-3p	The expression levels of miR-221-3p are significantly downregulated in patients with prostate cancer. Furthermore, ectopic expression of miR-221-3p results in significant inhibition of cellular proliferation and altered cellular morphology. This renders it a potential therapeutic target for prostate cancer	Karadag et al., 2021 ³⁸
hsa-miR-224-5p	Alterations in its expression levels have been associated with prostate cancer progression	Rana et al., 2022 ³⁷
hsa-miR-23c	It represents a potential biomarker for prostate cancer risk stratification, which could be incorporated into non-invasive strategies such as liquid biopsy within the framework of precision medicine	Martínez-González et al., 2021 ²⁸
hsa-miR-24-3p	It has been observed to be overexpressed in the serum of patients with prostate cancer	S. Zhang et al., 2021 ⁴²
hsa-miR-26b-5p	Decreased expression of it has been associated with prostate cancer progression. Furthermore, it has been observed to differentiate between patients with low (patients with high miR-26b-5p expression levels) and high Gleason scores	Giglio et al., 2021 ⁴³
hsa-miR-27a-3p	It functions as an oncomiR with the potential to influence the migration, invasion, and proliferation of prostate cancer tumor cells	Koh et al., 2022 ⁴⁴
hsa-miR-29a-3p	Aberrations in its expression have been correlated with the proliferative and metastatic capacity of prostate cancer cells	Liao et al., 2021 ¹⁰⁸
hsa-miR-324-5p	Its underexpression has been associated with metastasis in prostate cancer tissue samples	Lang et al., 2020 ¹⁰⁹
hsa-miR-331-3p	Its diminished expression has been associated with ERBB-2 receptor overexpression in prostate cancer cells, suggesting a role in tumor progression	Epis et al., 2009 and Hu & Yang et al., 2020 ^{110,118}
hsa-miR-375-3p	It has been observed that this miRNA exhibits a statistically significant higher expression in patients with elevated PSA levels. Furthermore, it has been demonstrated to be a robust biomarker for prostate cancer	Abramovic et al., 2021 and Fredsøe et al., 2020 ^{50,119}

hsa-miR-423-3p	Elevated levels of plasma miR-423-3p have been reported in patients with metastatic castration-resistant prostate cancer	Guo et al., 2020 ¹¹¹
hsa-miR-4732-3p	It has been observed that miR-4732-3p levels are significantly elevated in patients with prostate cancer, demonstrating enhanced diagnostic accuracy in high-grade prostate cancer	Giglio et al., 2021 ⁴³
hsa-miR-494-3p	It is one of the miRNAs that commonly exhibit differential expression in urine, plasma, and tissue samples from patients with prostate cancer. Furthermore, it has been observed to function as a suppressor of specific gene expression in this tumor	Koh et al., 2022 ⁴⁴
hsa-miR-199a-5p	A miRNA signature (miR-511-5p, miR-598-3p, and miR-199a-5p) associated with improved disease outcome demonstrated to provide risk refinement beyond standard clinicopathological features. This signature is downregulated in clinical samples from prostate cancer patients. Additionally, miR-199a-5p has been shown to function as a tumor suppressor, as its reconstitution in PCa models diminishes cell proliferation, motility, and tumor angiogenesis, while enhancing apoptosis	Gandellini et al., 2021 ³⁹
hsa-miR-511-5p		
hsa-miR-598-3p		
hsa-miR-93-5p	It is suggested that miRNA miR-93-5p represents a potential biomarker for prostate cancer risk stratification, suitable for integration into non-invasive strategies such as liquid biopsy within precision medicine for the management of this neoplasm	Martínez-González et al., 2021 ²⁸
hsa-miR-96-5p	Its overexpression has been associated with prostate cancer progression, demonstrating that liquid biopsy is a potential detection tool for this biomarker in prostate cancer	Schitcu et al., 2022 ⁴¹
hsa-miR-98-5p	Its diminished expression has been observed in prostate cancer, suggesting a role in tumor progression. Furthermore, it allows for the differentiation between patients with low and high Gleason grade	Azani et al., 2023, Ghamlouche et al., 2023 and Giglio et al., 2021 ^{19,43,117}

Notes:

- miRNA: The microRNA identifier.
- Functional Description: A summary of the reported roles, expression patterns, or mechanistic insights of the miRNA in prostate cancer.

Supplementary Table 2: Differential expression of 46 miRNAs selected from the literature (2020–2024) between cases and controls

miRNA	TMM cases	TMM controls	log2(FC)	Fold Change (FC)	P-value	adjusted P-value	Reference
hsa-let-7a-5p	0.705	0.673	0.032	1.022	0.582	0.705	Giglio et al. 2021 and Rana et al. 2022 ^{37,43}
hsa-let-7d-5p	-1.051	-1.236	0.185	1.137	0.002	0.010	Kolenda et al. 2014; Wagner et al. 2014)
hsa-let-7i-5p	1.051	1.236	-0.185	0.880	0.002	0.009	Kolenda et al. 2014; Wagner et al. 2014)
hsa-miR-100-5p	-4.564	-4.678	0.114	1.082	0.558	0.694	Ye, Li, and Wang 2020 ⁹⁹
hsa-miR-101-3p	1.261	1.501	-0.240	0.847	0.044	0.112	Duca et al. 2021 ⁸¹
hsa-miR-1185-2-3p	-5.507	-5.461	-0.046	0.969	0.444	0.659	Urabe et al. 2019 ⁵⁶
hsa-miR-125a-5p	-2.406	-2.645	0.239	1.180	0.047	0.114	Damodaran et al. 2021 and Li et al. 2020 ^{49,100}
hsa-miR-125b-5p	-4.145	-4.248	0.103	1.074	0.523	0.729	Karadag et al. 2021 ³⁸
hsa-miR-1299	-6.056	-6.143	0.087	1.062	0.545	0.716	Li et al. 2021 ¹⁰¹
hsa-miR-1307-3p	-5.014	-5.371	0.357	1.281	0.019	0.067	Hashimoto et al. 2021 ¹⁰²
hsa-miR-139-5p	-3.970	-4.154	0.184	1.136	0.247	0.406	Nam et al. 2020 ¹⁰³
hsa-miR-141-3p	-5.716	-5.408	-0.308	0.808	0.108	0.226	Bergez-Hernández et al. 2022 and Cai et al. 2020 ^{40,53}
hsa-miR-142-3p	2.600	2.295	0.305	1.235	0.001	0.008	Santo et al. 2022 and Valera et al. 2020 ^{104,105}
hsa-miR-145-5p	-1.700	-2.306	0.606	1.522	0.001	0.007	Bergez-Hernández et al. 2022 ⁴⁰
hsa-miR-146a-5p	-0.164	-0.087	-0.077	0.948	0.492	0.707	Drobijevic et al. 2024 and Kookli et al. 2024 ^{58,59}
hsa-miR-148b-3p	-1.744	-1.863	0.119	1.086	0.177	0.339	Bergez-Hernández et al. 2022 ⁴⁰
hsa-miR-150-5p	-0.258	0.316	-0.574	0.672	0.001	0.012	Cruz-Burgos et al. 2023 ⁵⁷
hsa-miR-152-3p	-4.015	-4.034	0.019	1.013	0.833	0.912	Rana et al. 2022 ³⁷
hsa-miR-155-5p	-5.991	-5.920	-0.071	0.952	0.668	0.768	Ramirez-Garrastacho et al. 2022 and Santo et al. 2022 ^{104,106}
hsa-miR-17-3p	-5.127	-5.306	0.179	1.132	0.246	0.419	Urabe et al. 2019 ⁵⁶
hsa-miR-182-5p	-6.085	-5.728	-0.357	0.781	0.033	0.089	Bidarra et al. 2019 and Souza et al. 2022 ^{46,90}
hsa-miR-183-5p	-6.468	-6.371	-0.097	0.935	0.612	0.722	Schitcu et al. 2022 ⁴¹
hsa-miR-186-5p	-3.440	-3.597	0.157	1.115	0.170	0.340	Ramirez-Garrastacho et al. 2022 ¹⁰⁶
hsa-miR-195-5p	-6.837	-6.827	-0.010	0.993	0.961	0.982	Rana et al. 2022 ³⁷
hsa-miR-199a-5p	-3.465	-4.267	0.802	1.744	0.001	0.023	Gandellini et al. 2021 ³⁹
hsa-miR-210-3p	-3.462	-3.491	0.029	1.020	0.839	0.898	Martínez-González et al. 2021 ²⁸
hsa-miR-21-3p	-4.514	-4.674	0.160	1.117	0.289	0.458	Zhao et al. 2021 ¹⁰⁷
hsa-miR-21-5p	3.534	3.653	-0.119	0.921	0.202	0.357	Stafford et al. 2022 and Zhang et al. 2022 ^{33,34}
hsa-miR-221-3p	0.187	-0.203	0.390	1.310	0.001	0.006	Karadag et al. 2021 ³⁸
hsa-miR-224-5p	-5.652	-5.959	0.307	1.237	0.088	0.193	Rana et al. 2022 ³⁷
hsa-miR-23c	-6.120	-6.116	-0.004	0.997	0.981	0.981	Maartínez-González et al. 2021 ²⁸
hsa-miR-24-3p	2.253	1.805	0.448	1.364	0.001	0.015	Zhang et al. 2021 ⁴²
hsa-miR-26b-5p	0.038	-0.128	0.166	1.122	0.023	0.071	Giglio et al. 2021 ⁴³
hsa-miR-27a-3p	1.832	1.485	0.347	1.272	0.001	0.046	Koh et al. 2022 ⁴⁴
hsa-miR-29a-3p	-0.274	0.033	-0.307	0.808	0.022	0.072	Liao et al. 2021 ¹⁰⁸
hsa-miR-324-5p	-3.540	-3.745	0.205	1.153	0.069	0.159	Lang et al. 2020 ¹⁰⁹
hsa-miR-331-3p	-4.050	-4.362	0.312	1.241	0.006	0.025	Hu and Yang 2020 ¹¹⁰
hsa-miR-375-3p	-4.615	-4.803	0.188	1.139	0.384	0.589	Abramovic et al. 2021 and Fredsøe et al. 2020 ^{50,54}
hsa-miR-423-3p	-1.143	-1.517	0.374	1.296	0.001	0.009	Guo et al. 2020 ¹¹¹
hsa-miR-4732-3p	-5.517	-5.412	-0.105	0.930	0.539	0.729	Giglio et al. 2021 ⁴³
hsa-miR-494-3p	-6.833	-7.227	0.394	1.314	0.029	0.083	Koh et al. 2022 ⁴⁴
hsa-miR-511-5p	-5.516	-5.534	0.018	1.013	0.915	0.957	Gandellini et al. 2021 ³⁹
hsa-miR-598-3p	-5.423	-5.507	0.084	1.060	0.555	0.709	Gandellini et al. 2021 ³⁹

hsa-miR-93-5p	1.524	1.421	0.103	1.074	0.202	0.372	Martínez-González et al. 2021 and Zhanf et al. 2021 (Martínez-González et al. 2021; Zhang et al. 2021)
hsa-miR-96-5p	-6.235	-5.761	-0.474	0.720	0.010	0.038	Schitcu et al. 2022 ⁴¹
hsa-miR-98-5p	-6.449	-6.392	-0.057	0.961	0.687	0.771	Azani et al. 2023 and Giglio et al. 2021 ^{19,43}

Footnotes:

1. Trimmed Mean of M-values (TMM) was used to normalize miRNA expression, accounting for sequencing depth and RNA composition differences.
2. log₂(Fold Change) represents the log₂-transformed ratio of average miRNA expression between cases and controls. Positive values indicate higher expression in cases, while negative values indicate higher expression in controls.
3. Fold Change (FC) is the untransformed ratio of expression levels between cases and controls.
4. P-values reflect statistical comparisons of miRNA expression between cases and controls.
5. Adjusted P-values were computed using the Benjamini-Hochberg method to correct for multiple comparisons. An adjusted P-value < 0.05 was considered statistically significant.
6. References indicate prior studies reporting on specific miRNAs.

Supplementary Table 3. Baseline characteristics of the study population.

Variable	Category	Cases	Controls	p
		203	54	
<i>Recruitment area, n(%)</i>	<i>Asturias</i>	8(3.94)	6(11.11)	<0.001
	<i>Barcelona</i>	96(47.29)	6(11.11)	
	<i>Cantabria</i>	32(15.76)	21(38.89)	
	<i>Huelva</i>	5(2.46)	0(0.00)	
	<i>Madrid</i>	51(25.12)	17(31.48)	
	<i>Valencia</i>	11(5.42)	4(7.41)	
<i>Age (years), mean (SD)</i>		65.18(6.65)	67.39(9.23)	0.048
<i>Ethnicity, n(%)</i>	<i>White/caucasian</i>	200(98.52)	54(100.00)	0.668
	<i>Arabic</i>	2(0.99)	0(0.00)	
	<i>Other African</i>	1(0.49)	0(0.00)	
<i>Marital status, n(%)</i>	<i>Single</i>	12(5.91)	1(1.85)	0.495
	<i>Married</i>	165(81.28)	48(88.89)	
	<i>Divorced</i>	12(5.91)	3(5.56)	
	<i>Widowed</i>	14(6.90)	2(3.70)	
<i>Education, n(%)</i>	<i>Less than primary school</i>	48(23.65)	8(14.81)	0.150
	<i>Primary school</i>	80(39.41)	17(31.48)	
	<i>Secondary school</i>	44(21.67)	16(29.63)	
	<i>University</i>	31(15.27)	13(24.07)	
<i>Socioeconomic level, n(%)</i>	<i>Low</i>	12(5.91)	3(5.56)	0.006
	<i>Medium</i>	129(63.55)	22(40.74)	
	<i>High</i>	62(30.54)	29(53.70)	
<i>Family history, n(%)</i>	<i>No</i>	150(76.53)	46(88.46)	0.060
	<i>Yes</i>	46(23.47)	6(11.54)	
<i>Family history of prostate cancer, n(%)</i>	<i>None</i>	150(76.53)	46(88.46)	0.178
	<i>First degree</i>	33(16.84)	6(11.54)	
	<i>Second degree</i>	4(2.04)	0(0.00)	
	<i>Others</i>	9(4.59)	0(0.00)	
<i>Body Mass Index (kg/m2), n(%)</i>	<i>Underweight</i>	1(0.49)	0(0.00)	0.803
	<i>Normal</i>	55(27.09)	17(31.48)	
	<i>Overweight</i>	104(51.23)	28(51.85)	
	<i>Obese</i>	43(21.18)	9(16.67)	
<i>Energy intake (kcal/day), mean (SD)</i>		2056.75(554.64)	2064.09(667.78)	0.937
<i>Processed meat (g/day), mean (SD)</i>		21.13(25.73)	14.56(15.70)	0.091
<i>All red meat (g/day), mean (SD)</i>		81.85(50.55)	68.92(37.47)	0.096
<i>All meat (g/day), mean (SD)</i>		106.52(57.52)	97.22(51.34)	0.306
<i>Fruits (g/day), mean (SD)</i>		299.72(171.86)	356.54(291.26)	0.084
<i>Vegetables (g/day), mean (SD)</i>		175.16(129.33)	164.62(120.80)	0.609
<i>Physical activity (1-5 years before diagnosis), n(%)</i>	<i>Inactive</i>	37(23.87)	9(24.32)	0.936
	<i>< 500 min/week</i>	18(11.61)	4(10.81)	
	<i>500-1000 min/week</i>	23(14.84)	7(18.92)	
	<i>> 1000 min/week</i>	77(49.68)	17(45.95)	
<i>Smoking status, n(%)</i>	<i>Never smoker</i>	57(28.08)	14(25.93)	0.259
	<i>Former smoker</i>	113(55.67)	26(48.15)	
	<i>Current smoker</i>	33(16.26)	14(25.93)	
<i>Packs per year, mean (SD)</i>		40.32(35.12)	38.95(34.60)	0.839
<i>Alcohol consumption, n(%)</i>	<i>>30 g/day</i>	35(19.44)	7(14.29)	0.568
	<i>20-30 g/day</i>	31(17.22)	11(22.45)	
	<i>≤20 g/day</i>	114(63.33)	31(63.27)	
<i>Work shift , n(%)</i>	<i>Day</i>	130(64.36)	37(68.52)	0.570
	<i>Rotating no night</i>	12(5.94)	5(9.26)	
	<i>Rotating night</i>	34(16.83)	8(14.81)	
	<i>Ever night</i>	26(12.87)	4(7.41)	
<i>International Society of Urological Pathology (ISUP), n(%)</i>	<i>3+3</i>	42(20.69)		
	<i>3+4</i>	55(27.09)		
	<i>4+3</i>	55(27.09)		
	<i>(4+4) (3+5) (5+3)</i>	31(15.27)		
	<i>(4+5) (5+4) (5+5)</i>	20(9.85)		

<i>Gleason score group</i>	6	42(20.7)
	7	110(54.2)
	≥8	51(25.1)
<i>AJCC 8th edition stage</i>	I	35 (17.2)
	IIA	13 (6.4)
	IIB	48 (23.7)
	IIC	76 (37.4)
	IIIA	6 (3.0)
	IIIB	6 (3.0)
	IIIC	19 (9.4)

Supplementary Table 4. Comparison of AUCs for LASSO-Based Models and Mean AUCs from 10 Repeated Stratified 5-Fold Cross-Validations with Bootstrap Confidence Intervals

Comparison	miRNAs Included	LASSO-Based Model AUC (95% CI)	Repeated 5-Fold CV AUC (95% CI)
General Model (no Gleason-based subset)	hsamir1013p	0.824 (0.756–0.892)	0.774 (0.669–0.844)
	hsamir1395p		
	hsamir1413p		
	hsamir1455p		
	hsamir146a5p		
	hsamir1505p		
	hsamir1825p		
	hsamir199a5p		
	hsamir243p		
	hsamir26b5p		
	hsamir935p		
Low-Risk vs. Controls (Gleason <7 vs. 0)	hsamir1455p	0.930 (0.882–0.979)	0.844 (0.741–0.912)
	hsamir146a5p		
	hsamir1505p		
	hsamir1825p		
	hsamir199a5p		
	hsamir27a3p		
	hsamir3313p		
	hsamir4233p		
Intermediate-Risk vs. Controls (Gleason =7 vs. 0)	hsamir935p	0.806 (0.728–0.883)	0.776 (0.655–0.844)
	hsamir1395p		
	hsamir1413p		
	hsamir1455p		
	hsamir1505p		
	hsamir1825p		
	hsamir199a5p		
	hsamir26b5p		
	hsamir935p		
High-Risk vs. Controls (Gleason >7 vs. 0)	hsamir965p	0.752 (0.658–0.848)	0.767 (0.645–0.850)
	hsamir1505p		
	hsamir199a5p		
	hsamir243p		

- Notes:**
1. The “LASSO-Based Model” AUCs were derived from models using LASSO regression for feature selection on the final miRNA panels.
 2. The “Repeated 5-Fold CV AUC” values represent the mean AUC across 10 repetitions of stratified 5-fold cross-validation, with bootstrap bias-corrected 95% confidence intervals and associated standard deviations. This approach aims to improve the robustness of performance estimates in the context of limited sample size.