

Table S2. Association between 28 DNA variants in miRNA biogenesis genes and ccRCC in Volga-Ural populations.

Gene name	Chromosome	Position, (GRCh37)	rsID	Risk Allele/ Non-risk allele	Effect allele frequency cases/controls	OR (95%CI)	P-value
<i>AGO1</i>	1	36,380,133	rs595055	T/C	0.26/0.30	1.20 (0.71-0.99)	0.04
<i>FAM212B</i>	1	112,296,374	rs11584657	C/T	0.20/0.20	1.02 (0.80-1.19)	0.82
<i>DDX20</i>	1	112,308,953	rs197412	T/C	0.47/0.49	1.11 (0.77-1.06)	0.21
<i>DROSHA</i>	5	31,401,003	rs642321	T/C	0.26/0.25	1.05 (0.88-1.26)	0.57
<i>DROSHA</i>	5	31,401,447	rs10719	A/G	0.31/0.30	1.06 (0.90-1.25)	0.51
<i>DROSHA</i>	5	31,435,627	rs4867329	A/C	0.46/0.49	1.11 (0.77-1.05)	0.19
<i>C5orf22</i>	5	31,532,789	rs17409893	A/G	0.31/0.32	1.08 (0.78-1.10)	0.37
<i>XPO5</i>	6	43,492,578	rs2257082	G/A	0.33/0.33	1.00 (0.84-1.18)	0.98
<i>AGO2</i>	8	141,555,862	rs3864659	A/C	0.12/0.14	1.15 (0.69-1.10)	0.24
<i>AGO2</i>	8	141,594,460	rs7005286	T/C	0.23/0.21	1.11 (0.93-1.33)	0.26
<i>MIR196A2</i>	12	54,385,599	rs11614913	T/C	0.38/0.37	1.06 (0.91-1.25)	0.45
<i>PIWIL1</i>	12	130,852,174	rs11060845	G/T	0.07/0.11	1.69 (0.44-0.79)	4.32×10⁻⁴
<i>PIWIL1</i>	12	130,856,316	rs10773771	T/C	0.40/0.43	1.14 (0.74-1.03)	0.11
<i>RAN</i>	12	131,355,546	rs3809142	C/T	0.11/0.16	1.57 (0.50-0.81)	3.05×10⁻⁴
<i>DICER1</i>	14	95,554,142	rs1057035	C/T	0.44/0.29	1.85 (1.58-2.18)	4.05×10⁻¹⁴
<i>DICER1</i>	14	95,556,747	rs13078	T/A	0.13/0.17	1.28 (0.62-0.98)	0.03
<i>FAM57A (GEMIN4)</i>	17	643,426	rs2740351	G/A	0.41/0.40	1.06 (0.91-1.24)	0.47
<i>GEMIN4</i>	17	648,186	rs7813	G/A	0.41/0.39	1.04 (0.89-1.22)	0.59
<i>GEMIN4</i>	17	649,232	rs3744741	C/T	0.15/0.18	1.19 (0.68-1.04)	0.11
<i>GEMIN4</i>	17	649,505	rs4968104	T/A	0.21/0.22	1.06 (0.78-1.14)	0.55
<i>GEMIN4</i>	17	649,935	rs2740348	G/C	0.19/0.17	1.20 (0.98-1.47)	0.07
microRNA-423 (<i>NSRP1</i>)	17	28,444,183	rs6505162	A/C	0.50/0.46	1.17 (1.00-1.37)	0.04
<i>DDX5</i>	17	62,502,435	rs1991401	G/A	0.44/0.38	1.25 (1.07-1.47)	4.99×10⁻³
<i>MIR27A</i>	19	13,947,292	rs895819	T/C	0.34/0.35	1.06 (0.80-1.11)	0.45
<i>DGCR8*</i>	22	20,098,359	rs1640299	G/T	0.39/0.38	1.06 (0.90-1.25)	0.51
<i>DGCR8*</i>	22	20,098,544	rs417309	G/A	0.08/0.10	1.17 (0.65-1.12)	0.26
<i>DGCR8*</i>	22	20,098,582	rs720012	A/G	0.24/0.20	1.24 (1.03-1.49)	0.02
<i>DGCR8*</i>	22	20,098,882	rs720014	C/T	0.24/0.21	1.15 (0.95-1.40)	0.14

Weighted PRS analysis demonstrated $OR(95\%CI)=1.60(1.42-1.80)$ of the ccRCC risk with a statistical significance $P\text{-value}=4.20\times10^{-15}$. The microRNA biogenesis pathway weighted PRS predicted the risk of developing ccRCC with $AUC=0.637$ ($95\%CI[0.61-0.67]$), sensitivity of 0.58 and a specificity of 0.66 (Figure S2).

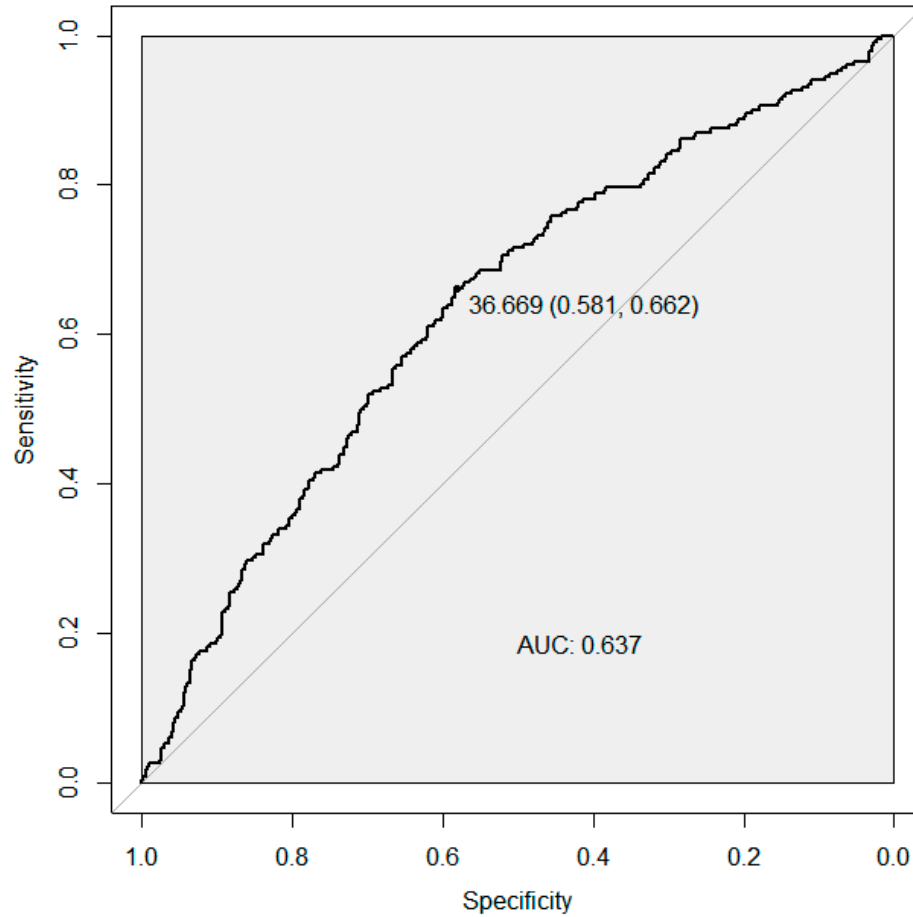


Figure S2. ROC curves assessing the discriminative power of the weighted PRS model for the ccRCC risk. The best predictive point is shown with the ideal cut-off for the PRS and with estimates for specificity and sensitivity at that point. AUC, area under the curve.

Unweighted PRS analysis demonstrated $OR(95\%CI)=1.50(1.34-1.69)$ of the ccRCC risk with a statistical significance $P\text{-value}=4.15\times10^{-12}$. The microRNA biogenesis pathway unweighted PRS predicted the risk of developing ccRCC with $AUC=0.622$ ($95\%CI[0.59-0.65]$), sensitivity of 0.55 and a specificity of 0.69 (Figure S3).

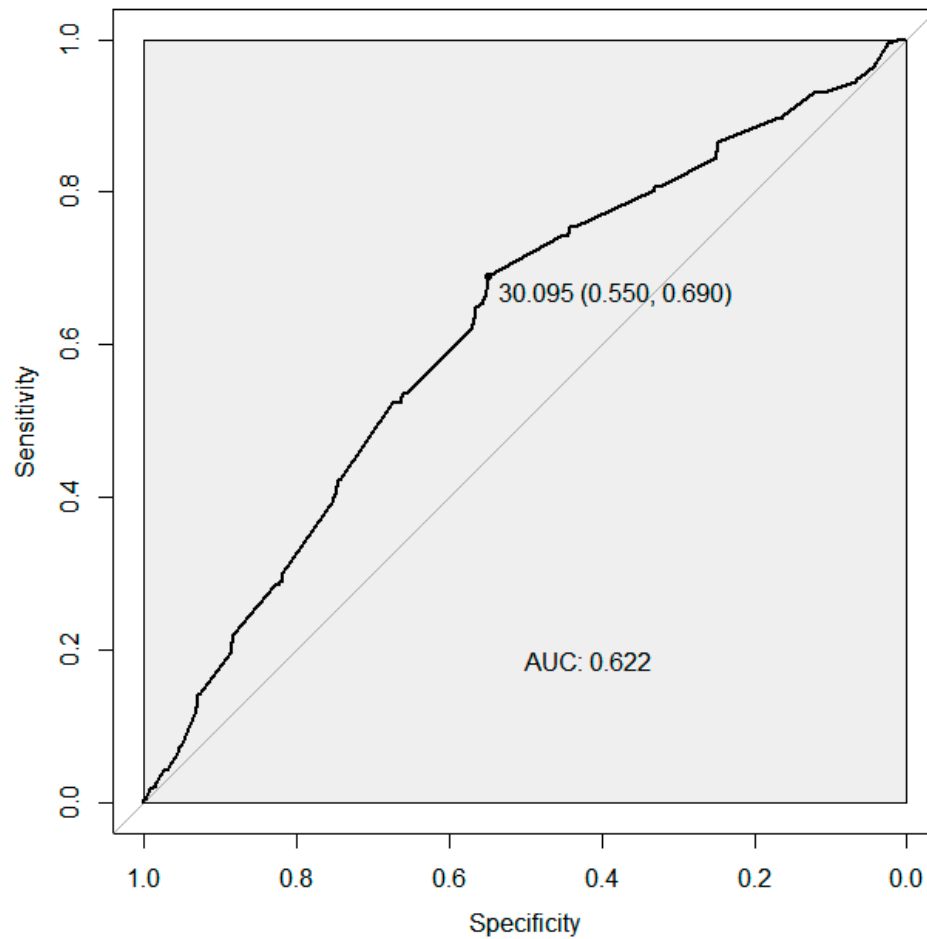


Figure S3. ROC curves assessing the discriminative power of the unweighted PRS model for the ccRCC risk. The best predictive point is shown with the ideal cut-off for the PRS and with estimates for specificity and sensitivity at that point. AUC, area under the curve.