

Supplementary Table S1. Function of selected polymorphisms as predicted by SNPinfo (<http://snpinfo.niehs.nih.gov/>) software

miRNA	rs	Chr	Allele	TFBS Splicing (ESE or ESS)		Allele	Asian	CHB
<i>miR-27a</i>	rs895819	19	C/T	Y	Y	T	--	0.711
<i>miR-137</i>	rs1625579	1	T/G	--	--	T	0.947	0.940
<i>miR-146a</i>	rs2910164	5	C/G	Y	Y	G	0.469	0.446
<i>miR-149</i>	rs2292832	2	C/T	Y	Y	C	0.339	0.315
<i>miR-196a2</i>	rs11614913	12	C/T	Y	Y	C	0.427	0.411
<i>miR-218</i>	rs11134527	5	A/G	Y	--	G	0.417	0.367
<i>miR-423</i>	rs6505162	17	A/C	Y	Y	C	0.811	0.833
<i>miR-608</i>	rs4919510	10	C/G	Y	Y	C	0.491	0.488

TFBS, transcription factor binding sites; ESE, exon splicing enhancer; ESS, exon splicing silencer; CHB, Han Chinese in Beijing, China.

Supplementary Table S2. The informed consent and ethics statement.



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Date: Aug.16.2019

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Ethics Reference No: <i>Please quote this ref on all correspondence</i>	LCKY2019-274
Project Title:	Common genetic variants in pre-microRNAs are associated with cervical cancer susceptibility in Southern Chinese women
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Supervisor(s)	Yue Hu

Thank you for your recent application for ethics approval for the above project. This has now been considered at the Second Affiliated Hospital of Wenzhou Medical University Research Ethics Committee meeting, and I am pleased to inform you that ethics approval has been given to your research.

Please note that, if your research should change significantly in any respect, or if risk of harm or breach of confidentiality becomes likely, you will be obliged to submit a new application.

We wish you every success with your research.

Yours sincerely,

Xue-qiong Zhu



Research Ethics Committee of the Second Affiliated Hospital of Wenzhou Medical University



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