

MicroRNA-31 regulates expression of *Wntless* in both *Drosophila melanogaster* and human oral cancer cells

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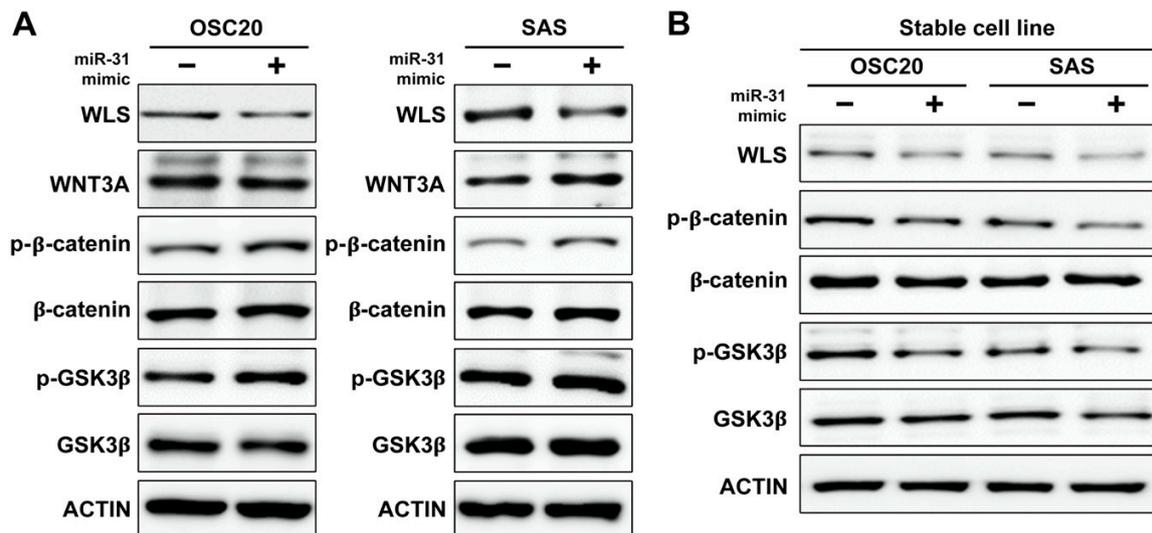
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box. (B) The relative luciferase activity is compared among OSC20 cells transfected with 1) a construct containing *WLS* 3'UTR sequence (blue box in A) fused with luciferase domain (Luc-*WLS* target), 2) a *WLS* 3'UTR-containing construct as well as a miR-31 mimic (Luc-*WLS* target+miR-31), or 3) a *WLS* 3'UTR-containing construct, a miR-31 mimic and a synthetic single-stranded miR-31-inhibitor oligonucleotide complementary to mature miR-31 (Luc-*WLS* target+miR-31+miR-31-inhibitor). Mean± SEM indicated. **, $P<0.01$ and ***, $P<0.001$.



Supplementary Figure S3. Expression of Wnt pathway components in OSCC cells following transient transfection of miR-31.

(A and B) The protein levels of Wnt pathway components are shown in a western blot analysis 1) before and after transfection of miR-31 mimics in SAS and OSC20 cells (A) or 2) in a stable miR-31-expressing SAS and OSC20 cell lines (B).

Supplementary Tables

Table S1. Putative targets of dme-miR-31a/b predicted by TargetScanFly

Target Gene ID	Gene symbol	Types of target sites			
		8mer	7mer-m8	7mer-A1	Total
CG11247	<i>CG11247</i>	1	0	1	2
CG6210	<i>wls</i>	0	1	0	1
CG10079	<i>Egfr</i>	1	0	0	1
CG6634	<i>mld</i>	1	0	0	1
CG31240	<i>repo</i>	1	0	0	1
CG13209	<i>sha</i>	1	0	0	1
CG1136	<i>CG1136</i>	1	0	0	1
CG16947	<i>CG16947</i>	1	0	0	1
CG17390	<i>CG17390</i>	0	0	1	1
CG33106	<i>mask</i>	0	0	2	2
CG7852	<i>CG7852</i>	0	0	1	1
CG13287	<i>CG13287</i>	0	0	1	1
CG30429	<i>CG30429</i>	0	1	0	1
CG31243	<i>cpo</i>	0	1	0	1
CG32346	<i>E(bx)</i>	0	1	0	1
CG1864	<i>Hr38</i>	0	1	0	1
CG11770	<i>lin</i>	0	1	0	1
CG4816	<i>qkr54B</i>	0	1	0	1
CG4316	<i>Sb</i>	0	1	0	1
CG14223	<i>CG14223</i>	0	1	0	1
CG14767	<i>CG14767</i>	0	1	0	1
CG14837	<i>CG14837</i>	0	1	0	1
CG18641	<i>CG18641</i>	0	1	0	1
CG32446	<i>CG32446</i>	0	1	0	1

Different sites of each gene putatively targeted by *Drosophila* miR-31 (dme-miR-31a/b) are listed.

The target sites determined by TargetScanFly (ver. 7.2) are categorized into three types: 7mer-A1, 7mer-m8 and 8mer sites (<http://www.targetscan.org/docs/7mer.html>; Supplementary Figure S1).

Table S2. Putative targets of hsa-miR-31 predicted by TargetScanHuman

Target Gene Symbol	Gene name	Types of target sites			
		8mer	7mer-m8	7mer-A1	Total
<i>RNF144B</i>	ring finger protein 144B	0	0	1	1
<i>RSBN1</i>	round spermatid basic protein 1	1	1	0	2
<i>SH2D1A</i>	SH2 domain containing 1A	1	0	0	1
<i>AK4</i>	adenylate kinase 4	1	1	0	2
<i>PAX9</i>	paired box 9	1	0	0	1
<i>LPP</i>	LIM domain containing preferred translocation partner in lipoma	0	0	2	2
<i>PRKCE</i>	protein kinase C, epsilon	1	0	0	1
<i>NR5A2</i>	nuclear receptor subfamily 5, group A, member 2	1	1	0	2
<i>TMEM145</i>	transmembrane protein 145	1	0	0	1
<i>ARHGEF2</i>	ho/Rac guanine nucleotide exchange factor (GEF) 2	0	0	1	1
<i>WDR5</i>	WD repeat domain 5	1	0	0	1
<i>PSMB11</i>	proteasome (prosome, macropain) subunit, beta type, 11	1	0	0	1
<i>PEX5</i>	peroxisomal biogenesis factor 5	1	1	0	2
<i>FGF7</i>	fibroblast growth factor 7	1	0	0	1
<i>SYDE2</i>	synapse defective 1, Rho GTPase, homolog 2 (<i>C. elegans</i>)	2	0	0	2
<i>PDZD2</i>	PDZ domain containing 2	1	0	0	1
<i>SSH1</i>	slingshot protein phosphatase 1	1	0	0	1
<i>TFRC</i>	transferrin receptor	1	0	0	1
<i>IL34</i>	interleukin 34	1	0	0	1
<i>CIAPIN1</i>	cytokine induced apoptosis inhibitor 1	1	0	0	1
<i>PC</i>	pyruvate carboxylase	1	0	0	1
<i>CRYBG3</i>	beta-gamma crystallin domain containing 3	1	0	0	1
<i>EGLN3</i>	egl-9 family hypoxia-inducible factor 3	1	0	0	1
<i>TBXA2R</i>	thromboxane A2 receptor	1	0	0	1

Different sites of each gene putatively targeted by human miR-31 (hsa-miR-31) are listed. The target sites determined by TargetScanHuman (ver. 7.2) are categorized into three types: 7mer-A1, 7mer-m8 and 8mer sites (<http://www.targetscan.org/docs/7mer.html>; Supplementary Figure S1).