

Table S1. The real-time PCR primers of DEGs and DERs

Symbol	Sequence ID	Primer name	Sequence (5'-3')
bta-miR-369-5p	MI0005020	RT-Primer	CTCAACTGGTGTCGTGGAGTCGGCAATTCAGTTGAGAAAGATCA
		F-Primer	ACACTCCAGCTGGGAATAATACATGGTTG
		R-Primer	TGGTGTCGTGGAGTCG
bta-miR-376e	MI0022290	RT-Primer	CTCAACTGGTGTCGTGGAGTCGGCAATTCAGTTGAGAATGTGGA
		F-Primer	ACACTCCAGCTGGGAACATAGAGGAAAATC
		R-Primer	TGGTGTCGTGGAGTCG
bta-miR-382	MI0009822	RT-Primer	CTCAACTGGTGTCGTGGAGTCGGCAATTCAGTTGAG CGAATCCA
		F-Primer	ACACTCCAGCTGGGGAAGTTGTTCGTGGTG
		R-Primer	TGGTGTCGTGGAGTCG
bta-miR-3578	MI0015945	RT-Primer	CTCAACTGGTGTCGTGGAGTCGGCAATTCAGTTGAG GAAGTTGT
		F-Primer	ACACTCCAGCTGGGGAATCCACCACGAAC
		R-Primer	TGGTGTCGTGGAGTCG
bta-miR-432	MI0009831	RT-Primer	CTCAACTGGTGTCGTGGAGTCGGCAATTCAGTTGAG CCACCCTT
		F-Primer	ACACTCCAGCTGGGTCTTGGAGTAGGTCATT
		R-Primer	TGGTGTCGTGGAGTCG
bta-miR-411c-5p	MI0022292	RT-Primer	CTCAACTGGTGTCGTGGAGTCGGCAATTCAGTTGAGAATGTATG
		F-Primer	ACACTCCAGCTGGGGGTTGATCAGAGAACA
		R-Primer	TGGTGTCGTGGAGTCG
bta-miR-433	MI0009832	RT-Primer	CTCAACTGGTGTCGTGGAGTCGGCAATTCAGTTGAG ACACCGAG
		F-Primer	ACACTCCAGCTGGGATCATGATGGGCTCCT
		R-Primer	TGGTGTCGTGGAGTCG

bta-miR-485	MI0009842	RT-Primer F-Primer R-Primer	CTCAACTGGTGTCGTGGAGTCGGCAATTCAGTTGAG CGAATTCA ACACTCCAGCTGGGAGAGGCTGGCCGTGATG TGGTGTCGTGGAGTCG
bta-miR-487b	MI0005060	RT-Primer F-Primer R-Primer	CTCAACTGGTGTCGTGGAGTCGGCAATTCAGTTGAGAAGTGGAT ACACTCCAGCTGGGAATCGTACAGGGTCAT-3 TGGTGTCGTGGAGTCG
bta-miR-493	MI0009847	RT-Primer F-Primer R-Primer	CTCAACTGGTGTCGTGGAGTCGGCAATTCAGTTGAGCCTGGCAC ACACTCCAGCTGGGTGAAGGTCTACTGTGT TGGTGTCGTGGAGTCG
bta-miR-495	MI0009849	RT-Primer F-Primer R-Primer	CTCAACTGGTGTCGTGGAGTCGGCAATTCAGTTGAGAAGAAGTG ACACTCCAGCTGGGAAACAAACATGGTGCA TGGTGTCGTGGAGTCG
bta-miR-665	MI0009882	RT-Primer F-Primer R-Primer	CTCAACTGGTGTCGTGGAGTCGGCAATTCAGTTGAG AGGGGCCT ACACTCCAGCTGGGACCAGTAGGCCGAG TGGTGTCGTGGAGTCG
bta-miR-151-5p	MI0004738	RT-Primer F-Primer R-Primer	CTCAACTGGTGTCGTGGAGTCGGCAATTCAGTTGAGACTAGACT ACACTCCAGCTGGGTCGAGGAGCTCACAG TGGTGTCGTGGAGTCG
U6	NR_004394.1	RT-Primer F-Primer R-Primer	AACGCTTCACGAATTTGCGT CTCGCTTCGGCAGCACA AACGCTTCACGAATTTGCGT
CELF3	NM_001076845.1	F-Primer R -Primer	CAACAGCAGCAGCAGCAA ACATCTGGAGGATCTCTGAGTC

<i>SIDT2</i>	NM_001024530.3	F-Primer R-Primer	GCTCTGTGGAGGAAGATGACTA AGGTATTGCTTGGTGCGAATG
<i>GRIN2A</i>	XM_024985455.1	F-Primer R-Primer	GCCTTCTTCGCCGTCATCT GGAATAGTCGTGAGGTCTCTGAA
<i>ASCC2</i>	NM_001015524.1	F-Primer R-Primer	TGAGTACGACGACACATACGA TAGCCTCCTCCTCCTCTTCC
<i>DYNLL2</i>	NM_001113303.1	F-Primer R-Primer	CACGCAGGCTATGGAGAAGTA TCTTGATGTAGGCAGCAATGTC
<i>FAM83F</i>	XM_002687938.6	F-Primer R-Primer	AACCTCCTCCTCCTCCTGAC GCTGGTACAAGTTCACCTCCT
<i>SLC1A4</i>	NM_001081577.1	F-Primer R-Primer	CTGGCTGTGGACTGGATTGT TGATTCAAGGTGGTGGAGGATG
<i>TAL1</i>	NM_001192495.2	F-Primer R-Primer	GCGGCAGCAGAATGTGAAC CCTCCTCCTCCTGGTCATTG
<i>ATOH8</i>	NM_001193104.3	F-Primer R-Primer	CAGGTGCCGTGTTACTCATAC GCCAGGGACAGGATGTAGTT
<i>HNF4A</i>	NM_001015557.1	F-Primer R-Primer	CCTCAGCAACGGACAGATGT CTTGACGATGGTGGCAATAGC
<i>NIPAL4</i>	XM_015472345.2	F-Primer R-Primer	ATCAGCACTCAGGTCAACTTC TGGAGGAGGTCATCACTGTC
<i>SEMA4G</i>	NM_001101117.2	F-Primer R-Primer	GTGACCAGCCATCCAACCT TTCAGCATAGCAGCCGTAGT
<i>BSN</i>	XM_024983183.1	F-Primer R-Primer	ACAGCGACAGCGACTACAG CCAGGTCTGACTCCACATCC
<i>PDE10A</i>	XM_024997131.1	F-Primer R-Primer	TTGATGATGACCGCCTGTGA

			CCTCGTCCTTCTTGTCTCTGT
<i>ZMIZ2</i>	NM_001205533.1	F-Primer	GCCATCCACCGACTTCACT
		R-Primer	GCTCCTGACTCTGCTTCTCC
<i>UBN1</i>	NM_001205922.1	F-Primer	TGAGCAGCGTGACATCGT
		R-Primer	GAAGACAGCAGGTTCAAGGAT
<i>GAPDH</i>	NM_001034034.2	F-Primer	GTTTGTGATGGGCGTGAAC
		R-Primer	ATGGACCTGGGTCATGAGT
<i>SMAD1</i>	NM_001076223.2	F-Primer	CCATTGGAATGCTGCGAGTT
		R-Primer	AGGCTGTGCTGAGGATTGTAT
<i>WNT9A</i>	XM_024995391.1	F-Primer	GCGAGGCTTCAAGGAGACA
		R-Primer	TTGACGAACTTGCTGCTGTAC
<i>β-actin</i>	NM_173979.3	F-Primer	AGAGCAAGAGAGGCATCC
		R-Primer	TCGTTGTAGAAGGTGTGGT

Table S2. Details of sequencing data by RNA-seq

Samples	Total Reads	Clean Reads	UniqueMapped	ReadsFilter%	UniqueMappedRat%
I1	52,246,126	51,617,112	44,214,723	0.988	85.7
I2	54,526,368	53,850,456	46,284,731	0.988	86.0
I3	54,526,368	53,857,862	46,081,945	0.988	85.6
M1	54,259,542	53,610,616	46,624,308	0.988	87.0
M2	53,161,792	52,538,338	45,130,866	0.988	85.9
M3	52,817,552	52,281,870	45,131,041	0.989	86.3

Samples: samples name; I1, I2, I3: immature testicular tissues of Chinese Red Steppes; M1, M2, M3: mature testicular tissues of Chinese Red Steppes.

Table S3. Details of sequencing data by Solexa

Samples	Total Reads	Clean Reads	UniqueMapped	ReadsFilter%	UniqueMappedRat%
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I	6,000,000	5,354,600	97.2	0.892	35.5
M	6,000,000	5,737,270	98.5	0.956	83.1

Note: UniqueMapped: Unique mapped reads of the genome; UniqueMappedRat%: Unique mapped ratio of the genome.