

Table S1 CCS data volume statistics

Library	Total Bases(bp)	ROI	Mean Length (bp)	Mean quality	Mean Passes
F 0-2K	855,098,963	427,494	2,000	0.97	14
F 2K+	1,154,409,533	337,154	3,423	0.95	7
M 0-2K	754,494,230	400,518	1,883	0.96	13
M 2K+	1,160,635,111	371,683	3,122	0.95	8
Total	3,924,637,837	1,536,849	-	-	-

Table S2 The annotation of gene structure

Type	Number of annotated	Number of Identification
Loci	23,371	30,670
Loci<1k	5,560(23.79%)	2,096(6.83%)
Loci 1-2k	5,909(25.28%)	8,975(29.26%)
Loci 2-3k	4,297(18.39%)	8,628(28.13%)
Loci >3k	7,605(32.54%)	10,971(35.77%)

Table S3 Primers for RT-qPCR

Gene	Primer(5'~3')
<i>Smad4</i>	F:ACCAGCACTGCCAACTTTCCC
	R:GCTGAGGCCCTGATGCTATCTG
<i>Wif1</i>	F:AACCGTCAATGTCCCTCTGCT
	R:CATCCACTTCAAATGCTGCCAC
<i>Nkd2</i>	F:AGGGTGGCTGACAGGAGGTTG
	R:GCGAGGTCCAGGTAGTGGTTTCT
<i>17β-hsd</i>	F:ATGCCACATTGCGGGACCTGA
	R:CACAGCACCCACAGCGTTCAA
<i>CPY2J</i>	F:CCACAACTCTGCGATGGGCTCT
	R:CGCCGTCAAATTGGTCAGGATC
<i>Neur11</i>	F:TGAGGAGTTTGCCAATGAGGG
	R:AGTTGAGTGAGTTCTGCGGGAT
<i>Prp18</i>	F:CGCTCCAAACAACAGAGTCGC
	R:GTCCTCCTCTTCCTCATACTCCACATC
<i>Wdr24</i>	F:GCAGGTGATGCTGTGGAGTCTT
	R:AATGGGCTAGGGCAGGGTTTA