

Whole-exome sequencing reveals genetic variants in **ERC1** and **KCNG4** associated with complete hydatidiform mole in Chinese Han women

SUPPLEMENTARY MATERIALS

Supplementary Table 1: The primers for PCR amplification of candidate SNPs

Sites		Sequence	
ERC1	c.G48C(p.Q16H)	up	AGATACTTCTTCAAGATTGGACAGC
		down	GCAGTCATCCGAACACCGTAAGG
KCNG4	c.G1114A(p.G372S)	up	AGGTAGGAGTGGGAGAAGGTGT
		down	TCGCTGGCGGTGTCTGAGGAG

The PCR condition: annealing temperature is 50°C and amplification with 25 cycles.

Supplementary Table 2: Summary of the exome sequencing data for 98 samples

See Supplementary File 1

Supplementary Table 3: List of potentially significant SNVs between CHM patients and healthy controls

See Supplementary File 2

Supplementary Table 4: The distribution of SNVs identified using MassARRAY technology

See Supplementary File 3

Supplementary Table 5: Possible genes that influence the risk of CHM

See Supplementary File 4

Supplementary Table 6: Comparison between WES, mass spectrometry, and Sanger sequencing

See Supplementary File 5