



**Supplementary Figure 1. Pedigree of families 1 and 2**

(A) Pedigree of family 1 with black fill denoting siblings with azoospermia. The two brothers underwent WES. (B) Pedigree of family 2 with black fill denoting azoospermia in male and infertile female patient. The male patient underwent WES. The arrowheads indicate the probands in families 1 and 2.

**Supplementary table 1. Primer sequences used for Sanger sequencing.**

<i>SHOC1</i> locus	Forward primers (5'-3')	Reverse primers (5'-3')
<i>SHOC1</i> -528 in family 1	GACCAAGAACCAGTAAACAGAATAA	GAGACAGGACTGACAGCTAAA
<i>SHOC1</i> -78 in family 1	CTTCTCTGTGTCTGTTGGAATTG	CTTAGAGTTATGCAGGTGGATCTT
<i>SHOC1</i> -400 in family 2	CCAGTGTGGTTCTGTTTATTGTG	ATGGGACCTAGAGAAATCCAAAG
<i>SHOC1</i> -489 in Individual case	CACTCGTTTAGGTTGGAAGT	AGTCTTTGAGGTGCAAGTCTTAT

**Supplementary table 2. Clinical Characteristics of the Chinese Study Subjects at the Clinical Assessment.**

Parameters	Proband in family 1	Brother in family 1	Proband in family 2	Individual case
Age (years)	29	32	30	25
Testicular Volume (Left)	10	10	15	10
Testicular Volume (Right)	10	10	20	10
FSH (IU/L)	12.44	11.26	3.9	4.83
LH (IU/L)	5.76	3.03	5.33	4.47
Testosterone (nmol/L)	13.67	13.74	8.5	27.24
Semen Volume (mL)	3	2	4	2.5
Total Sperm Count	0	0	0	0
Karyotype	N	N	N	N
Y Chromosome Microdeletions	N	N	N	N

Abbreviations: AZF, azoospermia factor; FSH, follicle-stimulating hormone; LH, luteinizing hormone; N indicates normal phenotype

**Supplementary table 3: Biallelic SHOC1 LoF mutations identified in the subjects with meiotic defects**

Position	ID	Gene	cDNA mutation	Protein alteration	gnomAD Dataset		Case(s)	Genotype	
					MAF	Carriers		Father	Mother
Variant identified in two NOA-affected patients in family 1 using WES									
chr9:114489973	rs1004968910	<i>SHOC1</i>	c.C1582T	p.R528X	1.8×10 <sup>-5</sup>	Het:5;Hom:0	G/A	G/A	G/G
chr9:114538089	rs777595871	<i>SHOC1</i>	c.231_232del	p.L78Sfs*9	2.8 ×10 <sup>-5</sup>	Het:7;Hom:0	AGT/A	AGT/AGT	AGT/A
Variant identified in NOA-affected proband in family 2 using WES									
chr9:114500590	rs1432616103	<i>SHOC1</i>	c.1194delA	p.L400Cfs*7	8.0×10 <sup>-6</sup>	Het:2;Hom:0	AT/A	AT/A	AT/A
Variant identified in NOA-affected Chinses sporadic case subject using WES									
chr9:114490090	NA	<i>SHOC1</i>	c.1464delT	p.D489Tfs*13	NA	NA	CA/C	NA	NA