

**Supplementary Table S1 TCF7L2-binding motifs in the 3'-flanking region of *MOSPD1***

JASPAR score	Strand	Sequence (5' to 3')	Name of motif
14.737	-	CAAGATCAAAGTGA	TBE2
14.153	-	CCACATCAAAGACC	TBE1
13.362	-	CCAGTTCAAAGAAG	TBE3
7.626	-	GAATAACAAAGAGT	
5.934	-	AGAGAACAAAATG	
4.817	+	GCAAATCACAGAAA	
4.808	+	AATGAACAAAATAA	
4.212	-	GTTAATCAAAGAT	

**Supplementary Table S2 Sequence of primers for cloning**

Gene	Strand	Restriction enzyme	Sequence* (5' to 3')
<i>MOSPD1</i>	5'-flanking	Forward	<i>Xho</i> I CCG <u>CTCGAG</u> GGGAGAGCAGAACACAAAGG
		Reverse	<i>Bgl</i> II GGA <u>AGATCT</u> ITCCAAACCCAGTCTTCTTGG
	3'-flanking	Forward	<i>Xho</i> I CCG <u>CTCGAG</u> AGTAGTCAGAGACCTGGGGTTT
		Reverse	<i>Bgl</i> II GGA <u>AGATCT</u> IGATTTCGCATTGTTTTCTCTACCC

\*Restriction enzyme sites are underlined.

**Supplementary Table S3 Sequence of primers for mutagenesis**

Mutated region	Strand	Sequence (5' to 3')
TBE1	Forward	AGTTACCACATCAGCGACCCTTTAAGTAAG
	Reverse	CTTACTTAAAGGGTCGCTGATGTGGTAACTGG
TBE2	Forward	TAGTCAACAAGATCAGCGTGACACCTGCCATG
	Reverse	CATGGCAGGTGTCACGCTGATCTTGTTGACTA
TBE3	Forward	ACTGGGTCCAGTTCAGCGAAGATGATGGTGAG
	Reverse	CTCACCATCATCTTCGCTGAACTGGACCCAGT

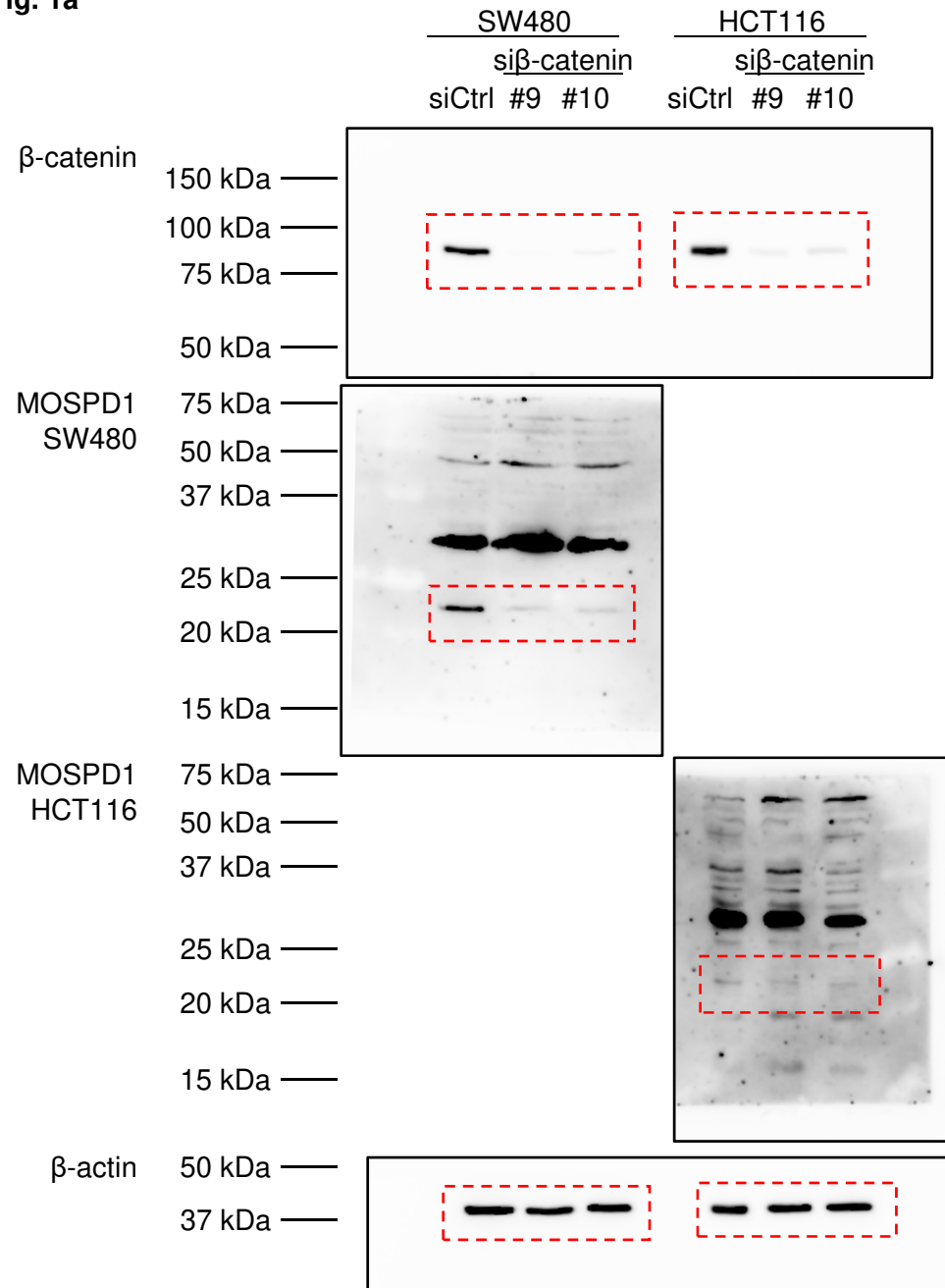
**Supplementary Table S4 Sequence of primers for CHIP-qPCR**

Gene	Strand	Sequence (5' to 3')
<i>MOSPD1</i>	Forward	GGACATTCCTCACCATCATC
	Reverse	ACAAGATCAAAGTGACACCTG
<i>RNF43</i>	Forward	TCAACTCTCTGGATAAGGTGGAATAGC
	Reverse	GACTTTTGGGGTGGGTGGGAAATA
Nagative control	Forward	AGCTCAGGCCTCAAGACCTT
	Reverse	AAGAAGATGCGGCTGACTGT

### Supplementary Figure

We present diagrams of the entire gels of the original Western blots before cutting out the band's parts to produce Figure 1.

**Fig. 1a**



**Fig. 1b**

