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Supplemental Information

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Supplementary information

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Short title: Correction of *TGM1* mutation using ABE system

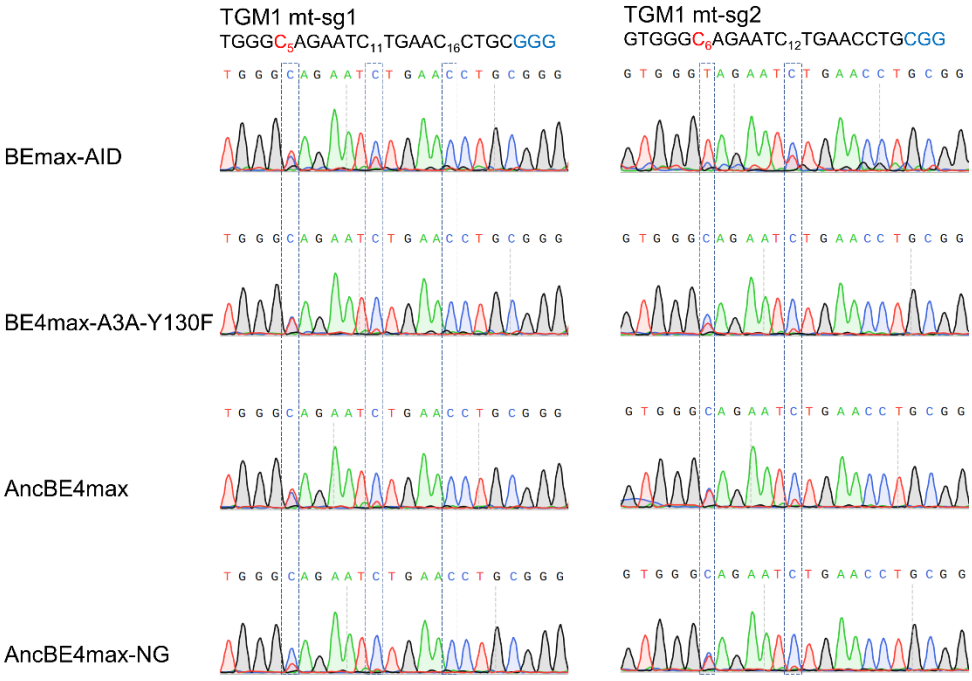

Figure S1. Sanger sequencing chromatogram for the edited HEK293T cell. The target site highlighted in red and with a numeric subscript. The non-target sites are highlighted with a numeric subscript.

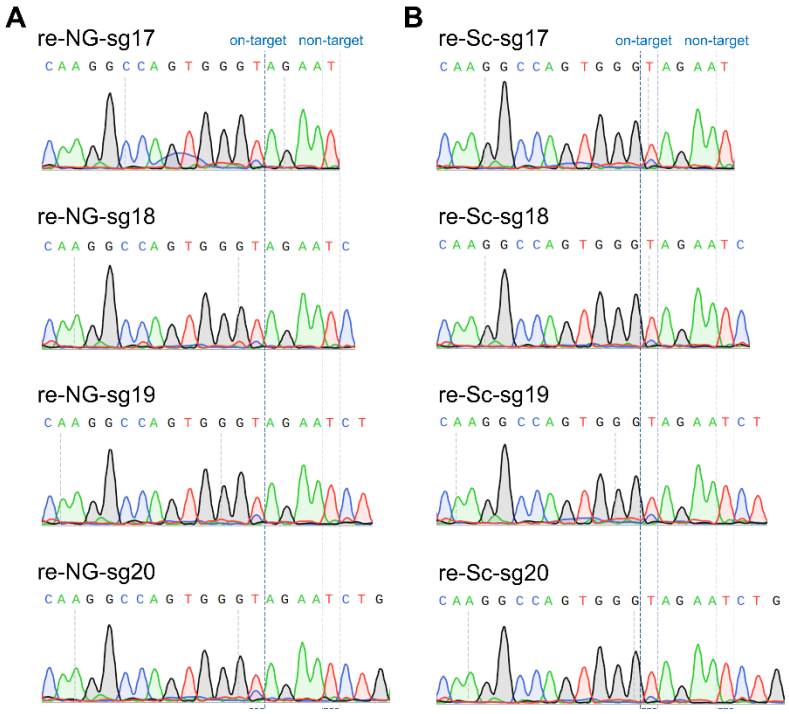

Figure S2. Sanger sequencing chromatogram for the correction of the pathogenic mutation by ABEmax-NG (A) and Sc-ABEmax (B) combined with truncated sgRNA.

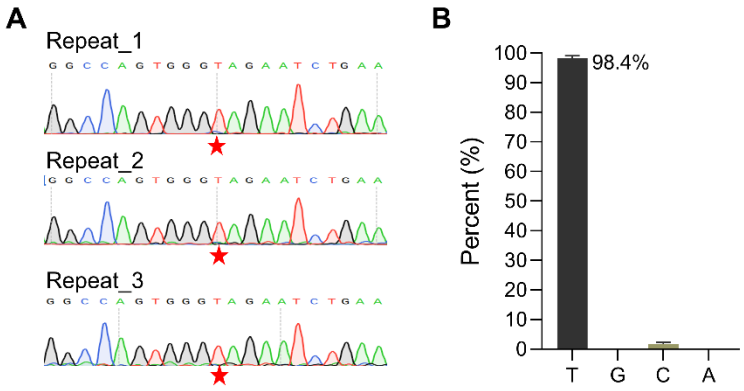

Figure S3. Analysis of the patient sperm. (A) The sequence chromatogram of the sperm from the patient. The red star indicated the pathogenic point mutation. (B) The genotype analysis of sperm sample by deep sequencing.

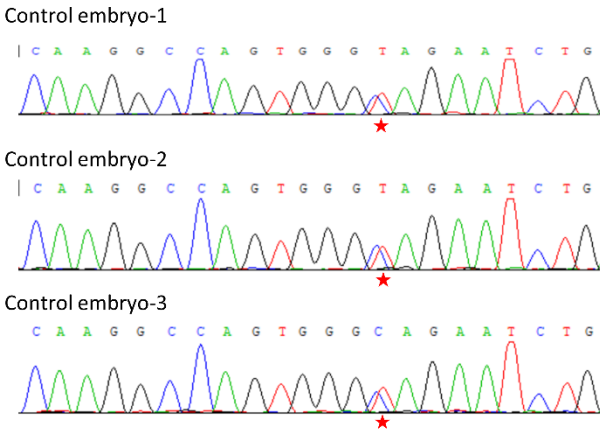

Figure S4. The sequence chromatogram for control embryos. The red star shows the pathogenic mutations.

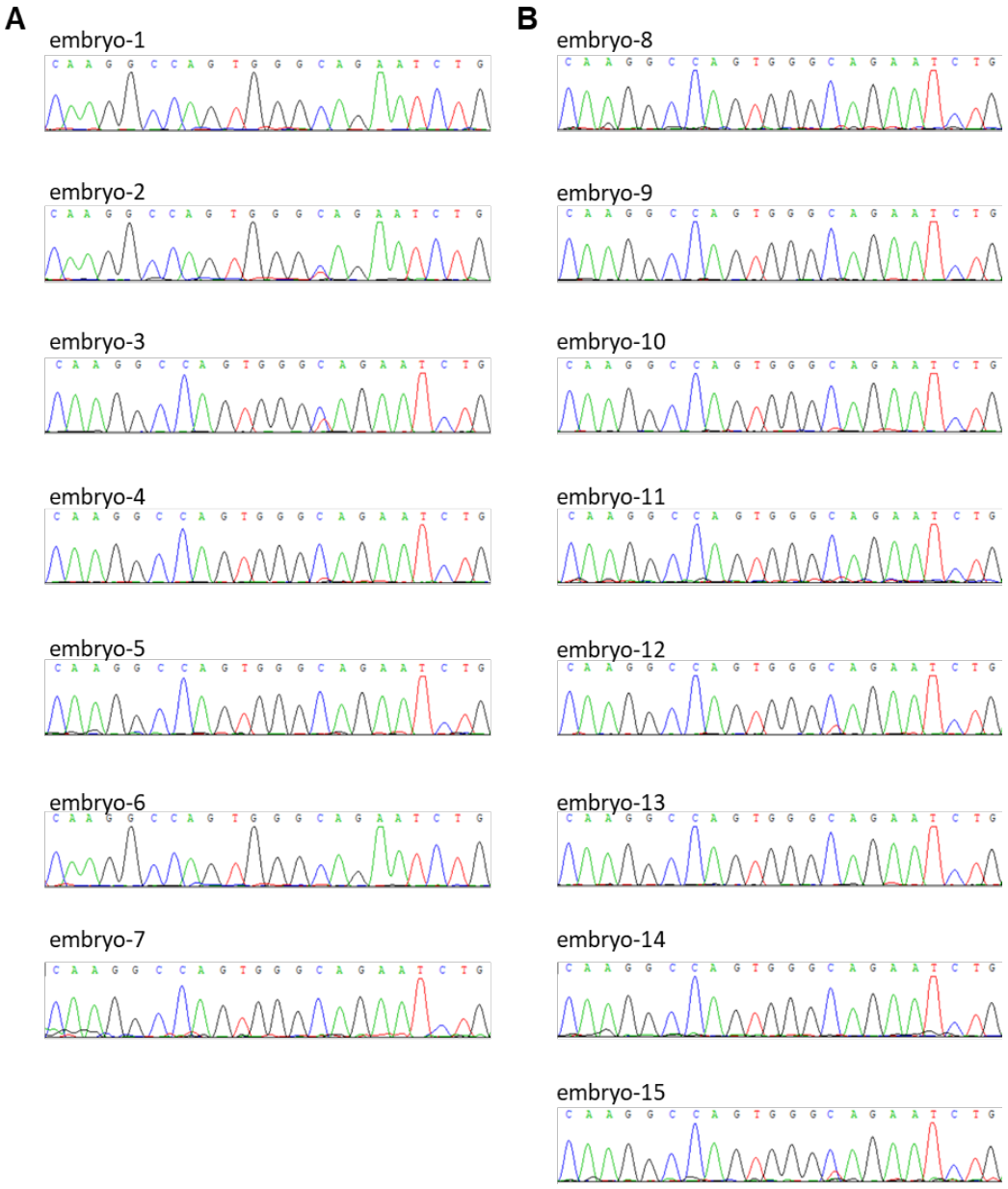

Figure S5. (A, B) The sequence chromatogram for all edited embryos in ABEmax-NG group (A) and Sc-ABEmax group (B).

Table S1 The editing frequency analysis of the corrected embryos.

	Sample name	Percentage of wild genotype on target site (%)	Editing frequency on non-target site (%)
ABEmax-NG group	embryo-1	94.18359	0.206321
	embryo-2	70.01231	0.191813
	embryo-3	71.18183	0.207506
	embryo-4	86.02006	0.219498
	embryo-5	97.86279	0.285806
	embryo-6	91.58933	0.2553
	embryo-7	97.50425	0.206666
Sc-ABEmax group	embryo-8	97.66458	0.285655
	embryo-9	97.16523	0.211075
	embryo-10	81.65478	0.310669
	embryo-11	97.4	0.240646
	embryo-12	67.82205	0.314222
	embryo-13	97.06223	0.346686
	embryo-14	96.45348	0.265436
	embryo-15	79.42178	0.257861

Table S2 The sgRNA sequence used in this study.

sgRNA	Sequence (5'-3')
TGM1 mt-sg1	TGGGCAGAATCTGAACCTGC
TGM1 mt-sg2	GTGGGCAGAATCTGAACCTG
re-NG-sg20	AGGCCAGTGGGTAGAATCTG
re-NG-sg19	AGGCCAGTGGGTAGAATCT
re-NG-sg18	AGGCCAGTGGGTAGAATC
re-NG-sg17	AGGCCAGTGGGTAGAAT
re-Sc-sg20	GGCCAGTGGGTAGAATCTGA
re-Sc-sg19	GGCCAGTGGGTAGAATCTG
re-Sc-sg18	GGCCAGTGGGTAGAATCT
re-Sc-sg17	GGCCAGTGGGTAGAATC

Table S3 The primer used for PCR or deep sequencing.

Primer	Sequence Sequence (5'-3')
TGM1-PCR-F	CCTACTCTAGGAAACAACCC
TGM1-PCR-R	GAAGAGGATGTAGATCTCATTG
TGM1-deep seq-F1	atcacgCCTACTCTAGGAAACAACCC
TGM1-deep seq-F2	cgatgttCCTACTCTAGGAAACAACCC
TGM1-deep seq-F3	ttaggcagCCTACTCTAGGAAACAACCC
TGM1-deep seq-F4	tgaccagCCTACTCTAGGAAACAACCC
TGM1-deep seq-F5	acagtgctCCTACTCTAGGAAACAACCC
TGM1-deep seq-F6	gccaatCCTACTCTAGGAAACAACCC
TGM1-deep seq-F7	cagatctCCTACTCTAGGAAACAACCC
TGM1-deep seq-F8	acttgaaaCCTACTCTAGGAAACAACCC
TGM1-deep seq-F9	gatcaggCCTACTCTAGGAAACAACCC
TGM1-deep seq-F10	tagcttccCCTACTCTAGGAAACAACCC
TGM1-deep seq-F11	ggctacCCTACTCTAGGAAACAACCC
TGM1-deep seq-F12	cttgtaCCTACTCTAGGAAACAACCC
OT-F1	ACCTTTCTGTCTTTGGATGT
OT-R1	TCTCCTTGTGTCTGGTGTA
OT-F2	TGAGGACCCATCCAACTC
OT-R2	GCAAGCGTATATGTGAATCC
OT-F3	TGACTAGAAAGTGTGTGCTT
OT-R3	CATGTGTACCTGGTCCATT
OT-F4	TTGGATACCGCCATTGATG
OT-R4	CCTCCTATAAATAACACCCTGA
OT-F5	TATGATGATCCTTCCTTTGC
OT-R5	TATAGTTGTTGGACTCAGGA
OT-F6	TGCTGCCTGTGATTTATGA
OT-R6	GGTCAACTGTGGTGTCTC
OT-F7	TCTTCACTGATCCTATTGACC
OT-R7	CTTAGAGATGATGCTGGAGT
OT-F8	AGTCCCATCTTGTCCACATCA
OT-R8	TAGAGGTGCAGCATGGCCTC
OT-F9	CTGACCTTCGCTGAGATAG
OT-R9	TCACACCAATTCTGATTCCA
OT-F10	GAATCATTCCACAACTCTAGG
OT-R10	TGATGAACAGCAGGAAGG
OT-F11	CATCGGTCATACTGTATTAGG
OT-R11	GTTGGAATGTGGTGAATGTA
OT-F12	CCCTCAACTTTAGAAAGAACTG
OT-R12	TGTAGAAGAGAGATCAGATGTG
OT-F13	CTAATCAGTGTTTACTGGAGAG
OT-R13	GCTCCTCTAACTCTAATGTATG
OT-F14	ACTGAGGTGATTAACAAAGC
OT-R14	TTGGTTAGAGGTTAGGTGTG

OT-F15	TCAGAACCCAGAGCAATCA
OT-R15	AGAGATGGAGTCCGTGTG
OT-F16	CACATGGATGCTCTTCAATC
OT-R16	CATGGTAAGACATACTCATTGG
OT-F17	CGACTGAACATCTCTGTGT
OT-R17	CCTCTAAGTCCTCCACCTT

Table S4 The information of predicted off-target sites.

Name	DNA	Chr	Position	Direction	Mismatches
OT1	GGCCAGTGGGTAGAATagGAGGG	chr15	94,745,816	-	2
OT2	GGCCcaTGGGTAGAATCTGAAGG	chr5	8,503,050	-	2
OT3	GGCCAGTGGGcAGAAgCTGACAG	chr5	135,355,669	+	2
OT4	GGCCAGTGGGTAGAAaCTtAAGG	chr4	73,013,365	-	2
OT5	GGCCAGTGGGctGAATCaGAGAG	chr8	13,409,077	-	3
OT6	GGCCAGgGGGTgGAATCTGtGAG	chr8	28,250,565	+	3
OT7	GGCCAGaGGGTAGAcTCTtACAG	chr5	24,402,175	-	3
OT8	GGCCtGTGGGTAGcATgTGACGG	chr5	180,112,311	+	3
OT9	GGgCAGTGGGgAGAcTCTGATGG	chr20	63,027,610	-	3
OT10	GGCCtGTGGGgAGAtTCTGAGGG	chr1	160,135,818	-	3
OT11	GGCCAGaGGGTAGAATgTtAGGG	chr1	160,810,629	-	3
OT12	GaCCAGTGGGTAGAAaCTGtAGG	chr1	173,804,224	-	3
OT13	atCCAGTGGGTAaAATCTGAAAG	chr1	223,358,725	-	3
OT14	GGCCAGTtGGTgGAATCTGcAAG	chr7	110,235,678	-	3
OT15	GaCCAtTGGGTAGAATCTaACAG	chr7	158,652,020	+	3
OT16	GGCCAGTtGGaAGAATCTtACAG	chr12	10,679,571	-	3
OT17	GGCCAGaaGGTAGAAgCTGAAAG	chr4	25,043,394	+	3