

Supplementary Table 1. Primer design and genomic coordinates for long-range PCR amplification of ADAMTS13

Family	PCR	Target region (chr9, GRCh38)	Product size (bp)	Forward primer	Reverse primer
USS-S	PCR1	133423438_133433779	10,342	GGCCTCTGCTGAGCTGGCTGATTTTC	CACAGATGGTCACTTTGGCTCCCCCA
	PCR2	133429050_133438489	9,440	CTCCTTCTGTCTACCTCTCCATC	CATCCAGGGCTGAGTGAGTGTG
	PCR3	133434246_133443653	9,408	GGAGAACCTCCCCACTAGGAATACA	GAGGAGGGGATTCTCAGAAGGATGG
	PCR4	133437122_133447240	10,119	TAGATCAGGCACTGACATCCCATCT	AGCAAGTGGTCAGGGTTTTCGTTTA
	PCR5	133439369_133449197	9,829	ATGTCACGTTTCTGACAGTTACCCC	GCATCCCAGATCCTGTGCAATGTA
	PCR6	133445616_133455878	10,263	CTGCTGCCTGAGAAGATCGAGAC	CTGCTACCAGATGATCCAGCAAGAG
USS-2M	PCR1	133413819_133428272	14,454	CTACTGCACTTGACAATAAGCCTCAAGA	GTTTACATGGATGTGTTGAGCGTGAAAT
	PCR2	133423438_133433779	10,342	GGCCTCTGCTGAGCTGGCTGATTTTC	CACAGATGGTCACTTTGGCTCCCCCA
	PCR8†	133431163_133437140	5,978	CTTTGTTACCCAGGCTTGCTAGGA	GATGTCACTGCCTGATCTACCAGC
	PCR3	133432655_133441927	9,273	TTCCTCTCCTGGATGGGACAGAATGT	GGCTGGGTAGAGGATAAAGTGCAGTG
	PCR4	133433570_133448537	14,968	ATACCATAGTCCCTAGTTGAAGGCAGTG	AGGCTCACTGGACACCTCTAGCACATA
	PCR5	133443713_133458626	14,914	TAAGTGTGCTGTCAGAGTTCCCTACTA	TAGCTGTCAGTCTACATCAGAAAGGTCT
	PCR6	133449169_133464250	15,082	TAAAGTACATTGCACAGGATCTGGGATG	GACCTGAATCTCGTCTAGCTCTGTACC
	PCR7	133453726_133468456	14,731	CAAATCAGCATCCAGTTGCTCATGCCAG	ATTCTGATTCCCCAGAGACAACCTGCTG

This table lists the PCR amplicons used for targeted long-read sequencing of the ADAMTS13 gene in patients USS-S and USS-2M.

Each row includes the chromosomal coordinates (hg38, chromosome 9), product size, and primer sequences where available.

PCR8† for USS-2M was specifically designed to bridge two haplotype blocks (see Extended Data Fig. 6).

Supplementary Table 2. Summary of sequencing quality metrics for PCR-based LRS

Subject	Total bases (bp)	Number of reads	Read length N50 (bp)	Reads above quality cutoffs Q15
USS-S	261,363,575	27,170	9,832	100%
USS-2M	209,243,271	17,107	13,910	100%
USS-2M (reanalysis)	210,651,377	17,344	13,871	100%

Basic statistics for Nanopore sequencing of long-range PCR products for patients USS-S and USS-2M.

"Total bases" indicates the cumulative base count across all reads.

"N50" represents the read length at which 50% of the total bases are contained in reads of that length or longer.

"Reads above quality cutoffs Q15" shows the percentage of reads with a minimum average quality score of 15, filtered using Filtlong.