Table S1. Demographic and clinical data of 28 women with a history of cTMA and pregnancy.

			Pregnancy condition	
Characteristic	All	Before cTMA	With cTMA	After cTMA
Women	28	16	13	10
Pregnancies	74ª	39	13ª	22 ^b
Pregnancies before 2012 ^c	40 (54)	30 (77)	5 (38)	5 (23)
Age at delivery	29 (24, 34)	27 (20, 32)	30 (26, 34)	30 (28, 34)
Age at diagnosis of cTMA	30 (23, 40)	38 (29, 52)	28 (24, 34)	20 (13, 24)
Biopsy confirming TMA	19 (68)	11 (69)	8 (62)	6 (60)
Eculizumab use				
Continuous before-during-				
after pregnancy	2 (7) W/3 (4) P	-	-	2 (20) W/3 (14) P
At pregnancy for postpartum				
P-cTMA	4 (14) W/4 (5) P	-	4 (31) W/4 (31) P	-
Not related to pregnancy	8 (29) W	8 (50) W	-	-
Plasma exchanges or infusions				
Continuous before-during-				
after pregnancy	4 (7) W/7 (10) P	-	1 (8) W/1 (8) P	4 (40) W/6 (27) P
			(switch to ecu)	
At pregnancy for postpartum				
P-cTMA	7 (25) W/7 (10) P	-	7 (54) W/7 (54) P	-
			(2 x switch to ecu)	
Not related to pregnancy	7 (25) W (6 x switch to ecu)	7 (44) W (6 x switch to ecu)	-	-
Impaired kidney function				
before pregnancy	8 (29) W/16 (22) P	-	2 (15) KTR/2 (15) P	7 (70) W/14 (64) P
Dialysis at last follow-up	4 (14)	1 (6)	3 (23)	1 (10)
Kidney transplant at last follow-up		6 (38)	2 (15)	3 (30)
Deaths	4 (14),2 HD, 2 KTR	2 (13) KTR	2 (15) HD	1 (10) HD
Age at death, years	49 (41-55)	44-55	41-54	54

Data are given as n (%) or median (p25, p75)

^a, includes one set of twins; ^b, 3 women received aspirin during 3 pregnancies; ^c, before use of eculizumab in our center cTMA, complement mediated thrombotic microangiopathy; KTR, kidney transplant recipient; HD, hemodialysis

W, women; P, pregnancies; ecu, eculizumab

Table S2. Genetic variants, risk haplotypes, and copy number variations of 28 women with cTMA and a history of pregnancy.

Table 52.	Jenetic	variants, risk naprotypes, ar			women with CTMA and a history of pregna	l
Patient ID	Gene	Variant ^a	MAF % ^b (gnomAD global)	MAF % ^c (1000G global)	Risk haplotype	(Variants) Copy number of CFHR-1,2,3,5
1	-	-	-	-	CFH H3, het; CD46ggaac, het	WT
2	THBD	p.E560Q het (LPV)	0.0018%	0.02%	CFH H3, het	WT
3	CFHR5	p.G228A het (VUS)	0.0016%	0	CFH H3, hom	WT
4	-	-	-	-	CFH H3, het; CD46ggaac, hom	WT
5	-	-	-	_	CD46ggaac, hom	WT
6	<i>C3</i>	p.D61N het (VUS)	0.002%	0	CFH H3, het; CD46ggaac, hom	WT
7	CFH	p.C1032* het (PV)	0	0	CD46ggaac, hom; CFH H8, het	het del <i>CFHR1,3</i>
8	_	-	=	-	CFH H3, hom; CD46ggaac, het	WT
9	_	-	-	_	CFH H3, het	WT
10	CD46	p.E142Q het (VUS)	0.008%	0	CFH H3, het	het del <i>CFHR1,3</i>
11	_	-	-	-	-	het del <i>CFHR1,3</i>
12	CFHR5	c.479_480insA het (VUS)	0.2%	0.08%	CD46ggaac, het	WT
13	CFH	p.N516K het (VUS)	0.03%	0.02%	CFH H3 het; CFH H8, het CD46ggaac, hom	WT
14	-	-	-	-	CFH H3, het; CD46ggaac, hom	WT
15	-	-	-	-	CFH H3, het; CD46ggaac, hom	WT
1.0	<i>C3</i>	p.K104E het (VUS)	0	0	CELLUZ hat CD46aaaa hat	WT
16	<i>C3</i>	p.D1457H het (VUS)	0.03%	0.16%	CFH H3, het; CD46ggaac, het	W I
17	CFI	p.I416L het (VUS)	0.03%	0.09%	CD46ggaac, het	het del <i>CFHR1,3</i>
18	<i>C3</i>	p.V1296A het (VUS)	0	0	CFH H3, het; CD46ggaac, het	het del <i>CFHR1,3</i>
19	-	-	-	-	CFH H3, het; CD46ggaac, hom	n.a.
20	-	-	-	-	CFH H3, het	WT
21	-	-	-	-	CFH H3, hom; CD46ggaac, het	WT
22	CFI CD46	p.G342E het (LPV) p.D257Vfs41 het (LPV)	0.0012% 0	0	CFH H3, het; CD46ggaac, het	WT
23	CD46	p.E234K het (VUS)	0.0056%	0.02%	CFH H3, het; CD46ggaac, het	n.a.
24	CFH	p.D748Nfsa10 het (PV)	0	0	CFH H3, het; CD46ggaac, het	WT
25	_	-	-	-	CD46ggaac het	het del <i>CFHR1,3</i>
26	_	-	-	-	-	het del <i>CFHR1,3</i>
27	_	_	-	-	CD46ggaac, het	n.a.
	CFH	p.S1191L het (PV)	0	0	35,	elevated signal of <i>CFHR1</i> exon 6 due to
28	CFH	p.V1197A het (PV)	0.0004%	0	CD46ggaac, het	mutations in <i>CFH</i> (resulting from gene conversion between <i>CFH</i> and <i>CFHR1</i>)

^a, Variant classification according to the American College of Genetics and Genomics in parenthesis

b, Minor allele frequency (MAF) of the variant allele in the overall (global) gnomAD population (https://gnomad.broadinstitute.org/)

c, Minor allele frequency (MAF) of the variant allele in the overall (global) 1000Genomes population (https://www.internationalgenome.org/)

cTMA, complement mediated thrombotic microangiopathy; het, heterozygous; hom, homozygous; PV, pathogenic variant; LPV, likely pathogenic variant; VUS, variant of unknown significance; WT, wild-type; n.a., not analyzed

Table S2, discussion.

Papers reporting on the genetic background of pregnancy-associated aHUS usually list all the identified rare complement gene variants, including those classified as VUS. In our cohort, there were 5 cases, or 17% of total patients, with variations classified as PV or LPV (patient 2, 7, 22, 24 and 28). There were a further 7 patients with variations classified as VUS in the *CFH*, *CFI*, *CD46* or *C3* genes. Altogether, this is 42% of all patients with a rare complement gene variation, which is comparable to previous reports.

A multicenter study (France, United Kingdom, Italy, PMID: 28596415) aimed to identify presentation, outcomes, and frequency of complement alternative pathway gene variants with an international cohort of 87 patients with p-HUS. Novel or rare variants of complement genes were present in 56% (49/87) of women and this list included VUS variations as well (for example the *CFH* p.N516K identified in our cohort as well, or the *CFI* p.I416L which they assessed as pathogenic). In a retrospective study of the Spanish P-aHUS Registry (PMID: 28911789), 9 out of 22 patients (41%) were reported to carry a complement abnormality in the aHUS-associated candidate genes, although not all of the listed variants are pathogenic based on the current ACMG guidelines (e.g. *C3* p.S1619R is likely benign according to the complement database, www.complement-db.org).

A further study by Rondeau et al. (PMID: 34515154) recorded that pathogenic variants were identified in 20 out of 33 (60.6%) tested aHUS patients who became pregnant. Among them, patients carrying only risk haplotypes/polymorphisms were also listed; there were only 7 patients with (L)PV variations, according to the classification of complement-database.org.

In a recent study by Fakhouri et al. (PMID: 33826112), the proportion of women with pregnancy-associated aHUS carrying pathogenic variant(s) in complement genes and/or anti-CFH antibody was found to be 45.1% (23/51). The detailed list of the identified pathogenic variations was not available for review.

Of note, conflicting interpretations of pathogenicity are available for some of the variations listed as VUS in our paper.

The *CFI* p.I416L variation - classified as pathogenic in PMID: 28596415 - was reported to dramatically decrease the FI level in cell culture supernatants as detected by enzyme-linked immunosorbent assay (ELISA) and western blotting, as well as to reduce the amount of intracellular FI. (PMID: 20016463). It was identified in several aHUS patients, however, based on the study by Osborne et al (PMID: 29500241), the allele frequency in aHUS patients was not found to be higher than the MAF in healthy populations, thus the complement database classified it as of uncertain significance.

The CD46 p.E234K was reported as an aHUS associated mutation in PMID: 26054645. However, as no other appearance of the corresponding variation was described in the literature and its frequency is 0.0056% in gnomAD and 0.02% in 1000Genomes, we classified it as VUS.

In addition, mutations that are absent from (C3 p.V1296A, C3 p.K104E) or have very low frequency in large population studies (C3 p.D61N, gnomAD: 0.002%, 1000Genome: 0), were classified as of uncertain significance, because we did not find records of them in other complement mediated TMA patients and no data is available on their functional role.

References:

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PMID: 28911789, Huerta A, Arjona E, Portoles J, et al. A retrospective study of pregnancy-associated atypical hemolytic uremic syndrome. Kidney Int 2018; 93: 450–459.

PMID: 34515154, Eric Rondeau et al, Pregnancy in Women with Atypical Hemolytic Uremic Syndrome. Nephron. 2022;146(1):1-10.

PMID: 33826112, Fakhouri et al. Pregnancy-triggered atypical hemolytic uremic syndrome (aHUS): a Global aHUS Registry analysis. J Nephrol. 2021 Oct;34(5):1581-1590.

PMID: 20016463, Bienaime et al. Mutations in components of complement influence the outcome of Factor I-associated atypical hemolytic uremic syndrome. Kidney Int. 2010 Feb;77(4):339-349.

PMID: 29500241,Osborne et al. Statistical validation of rare complement variants provides insights into the molecular basis of atypical hemolytic uremic syndrome and C3 glomerulopathy. J Immunol. 2018 Apr;200(7):2464-2478.

Table S3. Maternal risk factors for worse delivery outcomes of 47 live births.

		Pregnancy condition						
Characteristic	All	Before cTMA	With cTMA	After cTMA				
Women with live births, n	26	14	8	9				
Live births, n	47 ^a	22	9 ^a	16				
In vitro fertilization	3 (6)	0	3 (33)	0				
Current smoking	15 (32)	11 (50)	2 (22)	2 (13)				
Hypertension ^b	20 (43)	2 (9)	5 (56)	13 (81)				
Proteinuria ^b	19 (40)	2 (9)	4 (44)	13 (81)				
Impaired kidney function ^c	14 (30)	0	2 (22)	12 (75)				
Pregnancies in KTRs	8 (17) ^d	0	2 (22) ^e	6 (38) ^f				

Data are given as n (%)

^a, includes one set of twins; ^b, during pregnancy; ^c, elevated serum creatinine or proteinuria before pregnancy; ^d, five women; ^e, two women; ^f, three women

cTMA, complement mediated thrombotic microangiopathy; KTR, kidney transplant recipient

Table S4. Individual delivery and neonatal outcomes of 74 pregnancies in 28 women with cTMA.

Mother and pregnancy ID	Pregnancy before, with, after cTMA	Pregnancy outcome	Gestational age (week+days)	Time of delivery	Mode of delivery	Infants we sex	ight Birth weigh		Birth weight z-score			Birth length z-score	Birth head circumference (cm)	Birth head circumference centile	Birth head circumferenc e z-score	Apgar score (1 minute)	Apgar score (5 minutes)		Admission to NICU	Malformations*	Weight at follow-up (g)	Weight at follow-up centile	Weight at follow-up z-score	Length at follow-up (cm)	Length at follow-up centile	Length at follow-up z-score	Head circumference at follow-up	Head circumferenc e at follow-up	Head circumferenc e at follow-up	Breastfeedin		Infants age as of December 2020 (years)
1-1	Before	L	35+6	Late PT		m 21	17 Low BW	9,00	-1,35	49		0,81	33,0	62,00	0,30	7	9	9	-		2880	16	-1,00	50,0	52	0,06	(cm) 35,0	centile 66	z-score 0,42		25,0	8,3
1-2	With	S L	33+1 35+0	Moderate PT Late PT	Vaginal Vaginal	f 18	50 Low BW 50 Low BW	49,00	-0,03	41 48	85,00	1,04	29,0 33,0	85,00	1,03	8	10	10			3300	42	-0,21	51,0	57	0,18	34,0	26	-0,64		43,0	1,5
1-4	After With	A (i)	<12 18																													
2-2	After	M	7																												_	
2-3 3-1	After Before	M M	9+6 <12																													
3-2	Before Before	L	40 40	Full term	Vaginal Vaginal	m 26 f 31	50 Normal BV 00 Normal BV		-2,21 -0.88	46 49		-3,04 -1.45	32,5 34,0	1 25	-2,38 -0,69	9	10	na na	- :		5100 4330	15 59	-1,04 0,22	54,0 52,5	0,99	-2,61 -0.63	38,0 38,5	10 95	-1,3 1,64	na na	67,0 36,0	21,0
3-4 4-1	Before With	M	<12	Extremely PT			38 xtremely low		-0.20			-0.08	24.0	39.00	-0.29	5	,	9	Yes		900	0.99	-7.14	34.5	0.99	-7.86	24.5	0.99	-7.92		25.0	19,0
5-1	Before	Ĺ	41+0	Full term	C section	m 32	70 Normal BV	15	-1,04	52	32	-0.48	36,0	53	0,08	na	na na	na	·		na	na	na	na	na	na	na	na	na	Yes	na	39,1
5-2 6-1	Before Before	A (i)	40+5 na	Full term	Vaginal	f 35	00 Normal BV	46	-0,11	50	17	-0,94	34,0	19	-0,86	9	10	10		Yes	4400	39	-0,29	57,0	84	0,98	37,5	58	0,2	-	36,0	31,2
6-2 7-1	Before After	L M	38+3	Full term	C section	m 33	65 Normal BV	48	-0,05	52	59	0,24	36,5	85	1,05	9	10	10		Yes	5150	85	1,05	55,0	54	0,11	39,0	93	1,45	Yes	40,0	15,0
7-2	After	L	37+0	Full term	Vaginal	m 30	82 Normal BV	48	-0,04		47	-0,08	34,0	39	-0,27	8	10	10			4460	68	0,47	56,0	87	1,14	36,0	26	-0,65	Yes	46,0	1,9
8-1 9-1	With Before	L S	31+1 na	very PT na	C section	m 12	10 Very low B1	na	na	na na	na	na	na na	na	na	na	na	na		na	na	na	na	na	na	na	na	na	na	na	na	29,3
10-1	Before Before	M M	- 6 - 7																												-	
10-3	With	L	32+0	Moderate PT	C section	f 12	20 Very low B	V 11,00	-1,25 -0.67		11,00	-1,23	29,0	54,00	0,11	8	9	9	Yes		2300	1	-2,25	42,5	0,99	-3,57	32,5	12 67	-1,16 0.44		49,0 38.0	2,3
12-1	Before With	M M	18+3				90 Normal BV					1110	33,0		1,00		10					39		52,0	36		36,5	-				16,9
12-2	After Before	L		Late PT Full term				19,00	-0,87 0.64	44 53	36,00 68		31,0 33,0	44,00	-0,16 -1.77	9	9	10	- :	Yes	2482 4410	4 75	-1,77 0,69	48,0 56.0	27 92,0	-0,62	33,0 37,5	23 82	-0,74 0,92	Yes	28,0 26,0	3,4 18,2
13-2	After With	Ĺ	38+3	Full term	C section	m 30	30 Normal BV	21	-0,82 0,15	51		-0,19	33,0 34,0	6 41	-1,53 -0,23	9	10	10		Yes	4860 4540	63	0,32	56,0	63	0,34	na 36,5	na 59	na 0,24		45,0 40,0	7,2 5,1
14-1	Before	M M	<12	Full term																											40,0	
14-2	Before Before	L	40+0 43+1	Full term	Vaginal Vaginal	m 39 f 35			0,74 -0,15	53 49	50 7	0,00	na 34,0	na 15	na -1,05	na 10	na 10	na na	-		na 3900	na 9	na -1,33	na 53,0	na 12	na -1.19	na na	na na	na na	Yes Yes	29,0	43,9 42,2
14-4	Before	M	<12 41+0						0.75	50	16	-11.1	35.0	44	-0.15	-	10	10			4900		0.57								34.0	36.5
14-6	Before Before	L		Full term	Vaginal Vaginal				0,75	51	37		34,0	17	-0,15	9	10	10			4260	72 49	-0,03	na 54,0	na 48	na -0,05	na 38,0	na 82	na 0,92	Yes	33,0	36,5 27,2
15:1 15:2a	Before With	M	<12 31+5	Very PT	C section	f 13	40 Very low B1	V 22,00	-0.78	38	14.00	-1.08	28.0	35.00	-0.38	7	9	9	Yes	Yes	2790	16	-1.01	49.5	58	0.19	33.9	51	0.02		42.0	2.5
15-2b	With	Ĺ	31+5	Very PT	C section	f 14	95 Very low B	V 36,00	-0,35	40	31,00	-0,51	29,5	74,00	0,64	8	9	9	Yes		2920	24	-0,7	52,0	94	1,53	34,4	67	0,44		42,0	2,5
16-1 16-2	With After	L		Full term		f 31	30 Normal BV	56	2,07 0,16	53 49	35		38,0 35,0	99 75	2,19 0,68	8 7	10 7	10 9	Yes		6150 5350	85 93	1,04	63,0 60,0	99 100	2,42	42,0 39,5	100 99	2,7 2,2	Yes	63,0 53,0	9,1 6,6
16-3 16-4	After After	L		Full term					-0,06 -0.12	51 53	60 89	0,26	33,5 34.0	27 44	-0,62 -0.14	6	8 10	9	- :	- :	na 4610	na 63	na 0.33	na 56	na 78	na 0.78	na 39	na 96	na 1.72	Yes Yes	na 52.0	5,5 0.1
17-1	After	Ĺ	37+3 40+3	Full term Full term	Vaginal	m 31	10 Normal BV	1 42	-0,19	51		0,17	33,0 36,0	13	-1,11 0,21	9 9	10	10			4100	66 93	0,40	54,5 55,0	81 29	0,89	37,5 39.0	88 81	1,16		36,0 37,0	10,9
17-3	After	S	33+3	Moderate PT	Vaginal	m 22	30 Low BW		0,64	46		9100	35,0			g			•		5900											
17-4 17-5	After After	L	36+0 38+2	Late PT Full term	Vaginal Vaginal	m 34 m 39	 Normal BV Normal BV 	94,00	1,54 1,36	49 52	77,00 61	0,74	36,0 35.0	99,00 50	2,25	7 9	8 10	9 10	Yes	- :	5180 4970	99 92	2,38 1,43	55,0 57,5	92 98	1,39 2,06	40,0 38,5	100 95	3,54 1,63	- :	41,0 33,0	4,6 1.4
18-1	With Before	L	39+1	Full term	Vaginal	m 26	85 Normal BV		-1,89	50	19	-0,86	33,0 na	4 na	-1,80 na	na na	na na	10 na	Yes		3930 na	35 na	-0,38 na	53,0 na	37 na	-0,34 na	38,0 na	87 na	1,13 na	Yes	31,0 na	2,9 31.0
19-2	Before	Ĺ	40+0	Full term	Vaginal	m 32	00 Normal BV		-0,96	na			na	na	na	na	na	na			na	na	na	na	na	na	na	na	na	Yes	na	29,5
20·1 20·2	After After	M L	<12 38+2	Full term	Vaginal	m 31	70 Normal BV	33	-0,44	52	61	0,29	34,0	23	-0,74	9	10	10			4490	32	-0,46	57,0	75	0,66	38,0	57	0,18	Yes	49,0	0,3
21-1	Before Before	L	41+3 40+2	Full term					1,12	52		-0,15 -1.16	35,0 36,0	41 59	-0,22 0.24	9	10	10			4900 3950	63 14	0,32	57,0 55.0	77 49	0,75	37,0 37,0	34 35	-0,41 -0.38	Yes	35,0 31,0	17,2
22-1	After	Ĺ	39+1	Full term	Vaginal	f 30	10 Normal BV	20	-0,84	53	79	0,82	33,0	10	-1,26	9	10	10	-		4000	46	-0,10	56,0	92	1,42	36,0	40	-0,25		33,0	11,3
22-2 22-3	After After	L	38+2 40+3	Full term Full term	Vaginal Vaginal				-0,05 0,11	50 52		-0,58 -0,33	33,0 35,0	7 29	-1,47 -0,56	9 9	10 10	10		Yes	4830 4850	64 33	0,35 -0,45	55,0 57,5	46 61	-0,1 0,28	38,5 39.5	80 82	0,83	Yes	45,0 44,0	8,2 2,3
23-1	Before Before	L	na na	na na	C section C section	m n		na na	na na	na na	na na	na na	na na	na na	na na	na na	na na	na na	na na	na na	na na	na na	na na	na na	na na	na na	na na	na na	na na	na na	na na	19,6 15.0
24-1	Before With	L	40+3 35	Full term Late PT	Vaginal	m n	a na	na na	na na	na na	na na	na na	na na	na na	na	na na	na na	na na		na na	na na	na na	na na	na na	na na	na na	na na	na na	na na	na na	na na	18,7
24-2 25-1	After	L	39+2	Full term	Vaginal	m 31	30 Normal BV	18	-0,91	51	32	-0,47	35,0	38	na -0,30	9	10	10	÷	na Yes	4910	96	1,81	58	100	2,8	38	95	1,67	Yes	20,0	0,4
26-1 27-1	With Before	L M	41+2 na	Full term	Vaginal	m 34	20 Normal BV	23	-0,74	51	17	-0,94	35,0	24	-0,72	9	10	10			4215	19	-0,87	55,5	48	-0,04	39,5	94	1,52		29,0	0,9
27-2 27-3	Before Before	M A (i)	na 6																												4	
27-4	Before	L M	38+2	Full term	C section	m 34	85 Normal BV	61	0,29	49	16	-1,01	34,5	35	-0,38	9	10	10	-		4820	95	1,67	54,3	81	0,87	36,0	48	-0,04	Yes	27,0	6,9
27-5 27-6	Before Before	M	na na																													
27-7 27-8	Before Before	M A (i)	na 9+1																												+	
27-9	With Before	A (i)	20 40+0	Full term	Vagina'	m 44	00 Nomal BV	/ 86	1,08	55	96	1.09	na	na	na	9	10	10			na	na	na	na	na	na	na	na	na	Yes	na	47.7
28-2	Before	A (i)	6	Zustein	vaginal	41	oo reumal BV	00	1,00	99	00	1,09	Hd	114	Hd		10	10			IId.	na	11d	114	Ind	IId.	lid.	The .	IId	162		71,1
28-3 Life birth	Before	A (i)	6																													
missing data	L .	•	3	3	0	1 !	5 5	5	5	7	7	7	9	9	9	10	10	12	2	5	11	11	11	12	12	12	14	14	14	7	10	0
	Miscarriages, ab	ortions and still:	births marked gr	ry						H	-1	=																1			+	
	cTMA, compleme M, miscarriage; A	ent mediated the	rombotic microar	ngiopathy h: S. stillbirth																											=	=
	PT, preterm; na, m. male: f, femal	, not available		. ,,																											=	
	BW, birth weight																														$\pm \pm$	
	NICU, neonatal i																														$\pm \pm$	
	Malformations in	clude: hemangio	oma, hip dyspla	sia (2 infants),	patent forame	en ovale & atric	oseptal defect 2, p	igmeted mole, pi	geon toes, pig	eon toes &	frenulum of	f tongue							1				1	1	1			1	1			

Table S5. Characteristics of 46 live births according to infant sex^a.

Characteristic	Female infants	Male infants
Women, n	14	19
Infants, n	19^{b}	27
Gestational age (weeks)	38 (35, 41)	39 (38, 40)
Term vs. preterm		
Full term	12 (63)	23 (85)
Late preterm	2 (11)	3 (11)
Moderate preterm	1 (5)	0
Very preterm	2 (11)	0
Extremely preterm	1 (5)	0
Mode of delivery,		
Caesarean section	12 (63) ^b	8 (30)
Vaginal delivery	7 (37)	19 (70)
Induction of labor	2 (29)	7 (37)
Weight at birth		
Grams	3085 (2043, 3435)	3353 (3120, 3643)
Centile	45 (22, 56)	45 (18, 68)
Birth weight categories		
Normal birth weight	12 (63)	23 (85)
Low birth weight	2 (11)	1 (4)
Very low birth weight	3 (16)	0
Extremely low birth weight	1 (5)	0
Size for gestational age		
Small	0	3 (11)
Appropriate	17 (90)	19 (70)
Large	1 (5)	2 (7)
Length at birth		
Centimeter	49 (44, 51)	51 (50, 52)
Centile	33 (14, 60)	40 (28, 61)
Head circumference at birth	• • •	• • •
Centimeter	34 (31, 34)	34 (33, 36)
Centile	41 (25, 54)	32 (10, 56)
Apgar score		• • •

1 minute	9 (8, 9)	9 (9, 9)
5 minutes	10 (9, 10)	10 (10, 10)
10 minutes	10 (9, 10)	10 (10, 10)
Admission to NICU	5 (26)	2 (7)
Malformations	2 (11)	5 (19)
Number of neonates per pregnance	ey condition	
Before cTMA	7 (37)	14 (52)
With cTMA	6 (32)	3 (11)
After cTMA	6 (32)	10 (37)
Breastfeeding	5 (26)	15 (56)

Data are given as n (%) or median (p25, p75)

a, excluding one with unknown sex and mother lost to follow-up
b, including one set of twins

n, number; NICU, neonatal intensive care unit; cTMA; complement mediated thrombotic microangiopathy

Table S6. Neonatal outcomes of 46 infants born **a)** before manifestation of cTMA (n=22), **b)** related to a cTMA onset or recurrence (n=9, including one set of female twins), **c)** after manifestation of cTMA (n=16) according to neonatal sex ^a.

a)

	Female in	fants (n=7)	Male infants (n=14)			
Characteristic	Birth	Follow-up	Birth	Follow-up		
Age at follow-up (days)	-	36 (29-38)	-	31 (25-67)		
Weight (g)	3525 (2890-4090)	4365 (3750-4900)	3425 (2117-4100)	4410 (2880-5150)		
Weight (centile)	45 (19-87)	49 (9-72)	45 (1-86)	49 (14-95)		
Weight gain velocity (g/week)	-	169 (85-239)	-	214 (88-346)		
Length (cm)	50 (47-52)	53(52-57)	52 (46-55)	54 (50-56)		
Length (centile)	12 (7-44)	36 (12-84)	44 (11-86)	53 (<1-92)		
Length gain velocity (cm/week	() -	1.0 (0.8-1.4)	-	0.8 (0.3-1.4)		
Head circumference (cm)	34 (33-35)	37 (37-39)	34 (33-37)	38 (35-39)		
Head circumference (centile)	22 (15-44)	63 (34-95)	44 (1-85)	66 (10-93)		
Head growth (cm/week)	-	0.7 (0.4-0.9)	-	0.6 (0.2-1.2)		
NICU	0	-	0	-		
Breastfeeding	-	2 (29)	-	10 (71)		

b)

	Female in	fants (n=6)	Male infants (n=3)			
Characteristic	Birth	Follow-up	Birth	Follow-up		
Age at follow-up (days)	-	42 (25-63)	-	30 (29-31)		
Weight (g)	1418 (888-4450)	2855 (900-6150)	3053 (2685-3420)	4073 (3930-4215)		
Weight (centile)	39 (11-98)	20 (<1-85)	13 (3-23)	27 (19-35)		
Weight gain velocity (g/week)	-	208 (3.4-242)	-	236 (192-281)		
Length (cm)	39 (35-53)	51 (35-63)	51 (50-51)	54 (53-56)		
Length (centile)	29 (11-66)	71 (<1-99)	18 (17-19)	43 (37-48)		
Length gain velocity (cm/week	-	1.1 (0-2.1)	-	0.9 (0.7-1.1)		
Head circumference (cm)	29 (24-38)	34 (25-42)	34 (33-35)	39 (38-40)		
Head circumference (centile)	48 (35-99)	55 (<1-100)	14 (4-24)	91 (87-94)		
Head growth (cm/week)	-	0.5 (0.1-1.0)	-	1.1 (1.1-1.1)		
NICU	5 (83)	-	1 (33)	-		
Breastfeeding	-	0	<u>-</u>	0		

c)

	Female in	fants (n=6)	Male infants (n=10)			
Characteristic	Birth	Follow-up	Birth	Follow-up		
Age at follow-up (days)	-	43 (28-53)	-	43 (20-49)		
Weight (g)	3040 (1940-3150)	4000 (2482-5350)	3255 (3110-3956)	4855 (4100-5900)		
Weight (centile)	47 (19-56)	46 (4-93)	48 (18-94)	67 (32-99)		
Weight gain velocity (g/week)	-	207 (136-293)	-	224 (180-623)		
Length (cm)	50 (44-53)	56 (48-60)	51 (49-52)	56 (55-58)		
Length (centile)	70 (35-89)	78 (27-100)	45 (28-77)	78 (29-100)		
Length gain velocity (cm/week)	-	0.6 (0.4-1.5)	-	0.8 (0.6-2.5)		
Head circumference (cm)	33 (31-35)	36 (33-40)	35 (33-36)	39 (36-40)		
Head circumference (centile)	44 (10-85)	40 (23-99)	34 (6-99)	82 (26-100)		
Head growth (cm/week)	-	0.6 (0.2-0.7)	-	0.7 (0.3-1.1)		
NICU	0	-	1 (10)	-		
Breastfeeding	-	3 (50)	-	5 (50)		

Data are given as n (%) or median (full range)

NICU, neonatal intensive care unit; cTMA; complement mediated thrombotic microangiopathy

^a, excluding one with unknown sex and mother lost to follow-up