Supplementary Materials

Supplemental Table S1: Multi-organ dysfunction syndrome (MODS) diagnosis and resolution

Organ	MODS diagnosis*	MODS resolution
Renal	≥50% reduction of Cystatin C GFR from pre-HSCT value. Document the lowest value till completion of TA-TMA targeted therapy	Cyst C GFR of 70 mg/ml or ≥50% increase of Cystatin C GFR from the lowest value during diagnosis of TMA
Pulmonary	Any need for positive pressure ventilation (non-invasive or invasive) for ≥24 hours with a PF ratio <300 or SF ratio <264	Resolution of positive pressure ventilation (non-invasive or invasive), resolution of oxygen requirements
Cardio-vascular	Pulmonary hypertension (PH) diagnosed by cardiologist using cardiac catheterization or PH criteria on echo (RV pressure ≥50% of systemic pressure, ventricular septal flattening, right ventricular dysfunction)	Resolution of pulmonary hypertension (may receive anti-PH medications if still on maintenance therapy)
Serositis	Clinically significant serositis requiring medical therapy (like diuretics) or drainage	No evidence of clinically serositis requiring medical therapy or drainage
Hypertension (severe)	Hypertension requiring continuous antihypertensive medication infusion for ≥12 hours.	Hypertension control at <99% for age on no more than 2 medications (not including diuretics)
Central nervous system	Seizures attributable to posterior reversible encephalopathy syndrome (PRES)	No uncontrolled seizures (may be on Tx), no active PRES (residual radiologic signs are acceptable without clinical symptomatology)
Gasto-intestinal	GI Bleeding and/or intestinal strictures requiring medical or surgical interventions	No active GI bleeding, no evidence of unresolved intestinal strictures (hx of surgical stricture correction is acceptable)

**MODS is diagnosed if subject has hematologic evidence of TA-TMA and at least another one of the listed organ systems affected*

Supplemental table S2: Complement variants identified in tested subjects with TA-TMA[#]

	GENE NAME (w/ Reference Sequence)	VARIANT (predicted effect)	INTERPRETATION	Status
1	*C3*	c.2203C>T(p.Arg735Trp)	Likely pathogenic	alive
	CFHR3	c.839_840del(p.Ile280fs)	Associated with aHUS when it occurs in the homozygous or compound heterozygous state with another CFHR3 mutation	
2	*CFB* (NM_001710.5)	c.95G>A(p.R32Q),heterozygous	VUCS unable to predict	alive
	CFHR3 (NM_021023.5)	c.786A>T(p.P262P),heterozygous	VUCS unable to predict	
3	*CFB* (NM_001710.5)	c.95G>A(p.R32Q),heterozygous	VUCS unable to predict	alive
4	*CFHR5*	c.486_487insAA(p.E163fs)	Frameshift mutations associated with aHUS	alive
	CFHR3/CFHR1	heterozygous deletion	Unknown if in heterozygous state confers any additional risk for aHUS	
5	*CFHR3/CFHR1*	heterozygous deletion	Unknown if in heterozygous state confers any additional risk for aHUS	deceased
	CFB (NM_001710.5)	c.95G>A(p.R32Q),heterozygous	VUCS unable to predict	
	CFH (NM_000186.3)	c.2850G>T(p.Q950H),heterozygous	VUCS unable to predict	
6	*THBD*	c.1502C>T(p.P501L)	Increases the risk of developing aHUS	deceased
	CFHR3/CFHR1	Heterozygous deletion	Unknown if in heterozygous state confers any additional risk for aHUS	
	DGKE	c.966G>A(p.W322*), heterozygous	Associated with atypical hemolytic uremic syndrome (aHUS) in the homozygous or compound heterozygous state.	
7	*CFHR3* (NM_021023.5)	c.786A>T(p.P262P), heterozygous	VUCS unable to predict	deceased
	CFHR5 (NM_030787.3)	c.1067G>A(p.R356H), heterozygous	Likely benign	
8	*CFHR3/CFHR1*	Homozygous deletion	Associated with Factor H auto Ab and an increased risk of aHUS	alive
	CFB (NM_001710.5)	c.95G>A (p.R32Q),heterozygous	VUCS unable to predict	
9	*CFHR3/CFHR1*	Heterozygous deletion	Unknown if in heterozygous state confers any additional risk for aHUS	deceased
10	*CFHR3/CFHR1*	Heterozygous deletion	Unknown if in heterozygous state confers any additional risk for aHUS	alive
11	*CFB* (NM_001710.5)	c.559G>A(p.V187I), heterozygous	VUCS unable to predict	deceased
	MCP/CD46 (NM_002389.4)	c.1058C>T(p.A353V), heterozygous	VUCS unable to predict	
12	*CFHR3/CFHR1*	Heterozygous deletion	Unknown if in heterozygous state confers any additional risk for aHUS	alive
13	*CFB* (NM_001710.5)	c.1697A>C (p.E566A), heterozygous	VUCS unable topredict	alive
14	*CFB* (NM_001710.5)	c.1697A>C(p.E566A), heterozygous	VUCS, unable to predict	alive

	CFHR1 (NM_002113.2)	c.310C>T(p.H104Y), heterozygous	VUCS, unable to predict	
	CFHR3	Heterozygous deletion	The clinical significance of this deletion is unknown.	
15	*CFHR3/CFHR1*	Heterozygous deletion	Unknown if in heterozygous state confers any additional risk for aHUS	alive
16	*CFHR3/CFHR1*	Heterozygous deletion	Unknown if in heterozygous state confers any additional risk for aHUS	deceased
17	*CFHR3/CFHR1*	Heterozygous deletion	Unknown if in heterozygous state confers any additional risk for aHUS	deceased
18	*CFB* (NM_001710.5) Inheritance: AD	c.1697A>C (p.E566A),heterozygous	VUCS-unable to predict	deceased
	CFH (NM_000186.3) Inheritance: AD	c.3506T>C (p.I1169T),heterozygous	VUCS-unable to predict	deceased
19	*CFHR3/CFHR1*	Homozygous deletion	Associated with Factor H auto Ab and an increased risk of aHUS	deceased
20	*CFHR3/CFHR1*	Homozygous deletion	Associated with Factor H auto Ab and an increased risk of aHUS	deceased
21	*CFHR3/CFHR1*	Homozygous deletion	Associated with Factor H auto Ab and an increased risk of aHUS	alive

#Genes sequenced: *C3, CFB, CFH, CFHR1, CFHR3, CFHR5, CFI, DGKE, MCP, THBD.*
CFHR3/CFHR1 deletion analysis performed by MLPA.