### SUPPLEMENTAL MATERIAL

## Montalcino Aortic Consortium (MAC)

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# Supplemental Table 1. Predicted functional impact of 41 ACTA2 mutations and frequency and age at presentation of aortic events or

last follow-up of families and individuals assessed.

	Nucleotide change*	Amino acid substitution <sup>†</sup>		PROVEAN <sup>2</sup> /	Mutation	Mutation			# of	# of	Wi	th aortic event	Wit	hout aortic event
Exon				PolyPhen-2 <sup>1</sup>	SIFT	Taster <sup>3</sup>	Assessor <sup>4</sup>	LRT <sup>5</sup>	FATHMM <sup>6</sup>	families assessed	individuals assessed	n	Median age (min- max)	n
2	c.55T>C	p.C19R	possibly damaging	Deleterious	disease causing	high	Neutral	Damaging	1	1	1	49	0	
2	c.64G>A	p.G22S	possibly damaging	Deleterious	disease causing	high	Deleterious	Damaging	1	2	1	31	1	68
2	c.115C>T	p.R39C <sup>7-9</sup>	benign	Deleterious	disease causing	medium	Deleterious	Damaging	2	2	2	26 (22- 30)	0	
2	c.115C>G	p.R39G	possibly damaging	Deleterious	disease causing	high	Deleterious	Damaging	1	14	4	29.5 (22- 37)	10	35.5 (1-65)
2	c.116G>A	p.R39H <sup>10</sup>	benign	Neutral	disease causing	medium	Deleterious	Damaging	2	12	7	37 (23-76)	5	34 (22- 68)
3	c.143G>T	p.G48V	probably damaging	Deleterious	disease causing	high	Deleterious	Damaging	1	2	1	42	1	49
3	c.145A>G	p.M49V <sup>7, 9</sup>	benign	Neutral	disease causing	medium	Deleterious	Damaging	1	3	1	35	2	11 (8- 14)
3	c.191G>A	p.R64K	benign	Neutral	disease causing	medium	Deleterious	Damaging	1	1	1	49	0	
3	c.206T>A	p.L69Q	probably damaging	Deleterious	disease causing	high	Neutral	Damaging	1	3	3	51 (39- 62)	0	
3	c.215C>A	p.P72Q <sup>10</sup>	probably damaging	Deleterious	disease causing	high	Deleterious	Damaging	1	5	1	47	4	12 (1-27)
4	c.262T>C	p.W88R	probably damaging	Deleterious	disease causing	high	Deleterious	Damaging	1	10	3	37 (12- 51)	7	55 (21- 62)
4	c.350A>C	p.N117T <sup>11</sup>	possibly damaging	Deleterious	disease causing	high	Deleterious	Damaging	1	4	2	41 (29- 53)	2	62.5 (56- 69)
4	c.353G>A	p.R118Q <sup>11</sup>	probably damaging	Deleterious	disease causing	high	Deleterious	Damaging	2	14	8	41 (12- 57)	6	44.5 (24- 80)
5	c.403T>C	p.Y135H <sup>11</sup>	probably damaging	Deleterious	disease causing	medium	Deleterious	Damaging	1	4	1	52	3	48 (35- 53)
5	c.422T>C	p.V141A	possibly damaging	Deleterious	disease causing	medium	Deleterious	Damaging	1	3	1	21	2	34.5 (20- 49)
5	c.442G>A	p.G148R	probably damaging	Deleterious	disease causing	high	Deleterious	Damaging	1	4	4	44.5 (36- 60)	0	
5	c.445C>T	p.R149C <sup>11-13</sup>	probably damaging	Deleterious	disease causing	high	Deleterious	Damaging	10	69	33	29 (13- 56)	36	30 (3- 77)
6	c.461T>C	p.V154A <sup>11</sup>	probably damaging	Deleterious	disease causing	medium	Deleterious	Damaging	1	7	2	33.5 (31- 36)	5	25 (13- 73)
6	c.479G>A	p.G160D <sup>10</sup>	probably damaging	Deleterious	disease causing	medium	Deleterious	Damaging	2	9	4	32 (23- 51)	5	54 (1- 85)

6	c.489C>A	p.H163Q	possibly damaging	Deleterious	disease causing	medium	Deleterious	Damaging	1	1	1	41	0	
6	c.496C>A	p.P166T	possibly damaging	Deleterious	disease causing	high	Deleterious	Damaging	1	2	2	39.5 (19- 60)	0	
6	c.535C>T	p.R179C14	probably damaging	Deleterious	disease causing	high	Deleterious	Damaging	4	4	1	14	3	4 (2-4)
6	c.536G>A	p.R179H <sup>15-19</sup>	benign	Deleterious	disease causing	medium	Deleterious	Damaging	15	15	6	13 (11- 25)	9	8 (1- 14)
6	c.536G>T	p.R179L <sup>20</sup>	possibly damaging	Deleterious	disease causing	high	Deleterious	Damaging	1	1	0		1	5
6	c.554G>A	p.R185Q <sup>10</sup>	probably damaging	Deleterious	disease causing	high	Deleterious	Damaging	2	9	2	54 (41- 67)	7	54 (15- 77)
6	c.592C>T	p.R198C	probably damaging	Deleterious	disease causing	medium	Deleterious	Damaging	2	2	2	22 (12- 32)	0	
6	c.593G>A	p.R198H	benign	Deleterious	disease causing	medium	Deleterious	Damaging	1	3	2	43 (41- 45)	1	33
7	c.635G>A	p.R212Q <sup>10, 12</sup>	probably damaging	Deleterious	disease causing	medium	Deleterious	Damaging	3	16	6	31 (16- 53)	10	17.5 (2-76)
7	c.732G>T	p.L244F	possibly damaging	Deleterious	disease causing	high	Deleterious	Damaging	1	2	1	14	1	46
7	c.734C>T	p.P245L <sup>10</sup>	possibly damaging	Deleterious	disease causing	high	Deleterious	Damaging	1	1	1	27	0	
7	c.748A>C	p.I250L <sup>10</sup>	possibly damaging	Neutral	disease causing	medium	Deleterious	Damaging	1	1	1	37	0	
7	c.772C>T	p.R258C <sup>11</sup>	probably damaging	Deleterious	disease causing	high	Deleterious	Damaging	5	12	6	26 (15- 52)	6	18.5 (5-63)
7	c.773G>A	p.R258H <sup>11</sup>	probably damaging	Deleterious	disease causing	high	Deleterious	Damaging	3	11	9	35 (16- 57)	2	21 (16- 26)
7	c.808G>A	p.G270R	probably damaging	Deleterious	disease causing	high	Deleterious	Damaging	1	1	1	69	0	
8	c.824G>C	p.G275A	probably damaging	Deleterious	disease causing	high	Deleterious	Damaging	1	1	1	43	0	
8	c.874A>G	p.R292G <sup>11</sup>	probably damaging	Deleterious	disease causing	high	Deleterious	Damaging	1	5	3	36 (26- 48)	2	62.5 (53-72)
8	c.904T>G	p.S302A	possibly damaging	Neutral	disease causing	medium	Deleterious	Damaging	1	4	2	41 (37-45)	2	18 (1- 35)
8	c.977C>A	p.T326N <sup>10</sup>	benign	Neutral	disease causing	low	Deleterious	Damaging	1	4	0		4	55.5 (35-75)
8	c.984G>T	p.K328N	possibly damaging	Deleterious	disease causing	medium	Deleterious	Damaging	1	2	2	17	0	
8	c.990+1G>C		NA	NA	disease causing	NA	NA	NA	1	1	1	48	0	
9	c.1058C>A	p.T353N <sup>11</sup>	possibly damaging	Deleterious	disease causing	medium	Deleterious	Damaging	1	10	2	33 (17- 49)	8	31 (9-72)

\*Annotation of cDNA and protein changes are based on the *ACTA2* reference sequence NM\_001613.2; <sup>†</sup>references are cited if the mutation has been previously reported; "n" indicates number of individuals with or without an aortic event; "min- max" means minimum to maximum age at aortic event; NA means not available.

Supplemental Table 2. Medical histories, aortic disease characteristics and in-hospital treatment and outcomes of 70 *ACTA2* patients who presented for surgical repair due to aneurysm or dissection.

Variable*	Ascending	Acute Tho	Chronic			
	aortic aneurysm	Туре А	Туре В	All	Type B dissection	
n	10	41	10	51	9	
Age, years	36.5 (25-44)	36 (29- 46)	28.5 (21- 41)	36 (27- 46)	21 (16- 26)	
Maximum aortic diameter, cm	5.2 (5-5.5)	5.75 (4.7- 6.75)	4.8		6 (4.1- 6.5)	
Aortic disease at other locations						
Ascending aorta	NA	NA	3 (30)		1 (11)	
Descending aorta	2 (2)	2 (5)	NA		NA	
Abdominal aorta	1 (10)	0	0		0	
Presenting symptoms						
Any symptom	4 (40)	38 (97)	10 (100)	48 (98)	8 (100)	
Any pain	4 (40)	31 (80)	10 (100)	41 (84)	6 (75)	
Chest pain	4 (40)	23 (60)	8 (80)	31 (65)	4 (50)	
Back pain	1 (10)	4 (10)	8 (80)	12 (25)	3 (38)	
Abdominal pain	0	6 (15)	4 (40)	10 (20)	0	
Neck/jaw pain	0	8 (20)	0	8 (16)	0	
Upper extremity pain	0	2 (5)	2 (20)	4 (8)	0	
Lower extremity pain	0	2 (5)	1 (10)	3 (6)	0	
Hypotension	0	5 (13)	0	5 (10)	0	
Hypertension	0	3 (8)	4 (40)	7 (14)	0	
Congestive heart failure	0	2 (5)	0	2 (4)	0	
Dyspnea	3 (30)	8 (20)	1 (10)	9 (18)	1 (12)	
Pulse deficit	0	7 (20)	2 (20)	9 (18)	0	

Syncope	0	7 (18)	0	7 (14)	0
Vomiting	0	6 (15)	2 (20)	8 (16)	1 (12)
Extremity numbness/weakness	0	3 (8)	4 (40)	7 (14)	0
Edema	0	2 (5)	1 (10)	3 (6)	0
Diarrhea	0	0	1 (10)	1 (2)	1 (12)
Malaise/fatigue	1 (10)	2 (5)	0	2 (4)	0
Neurologic	0	9 (23)	1 (10)	10 (20)	1 (12)
Medical histories					
Bicuspid aortic valve	1 (10)	1 (2)	0	1 (2)	0
Hypertension	1 (10)	9 (23)	3 (30)	12 (24)	3 (33)
Hypercholesterolemia	2 (20)	2 (5)	0	2 (4)	0
Recent pregnancy	0	5 (33)	1 (17)	6 (29)	0
Stroke	1 (10)	2 (5)	0	2 (4)	0
Myocardial infarction	0	2 (5)	0	2 (4)	0
Patent ductus arteriosus	3 (30)	2 (5)	0	2 (4)	0
Mitral valve prolapse	0	1 (3)	0	1 (2)	0
Family history of TAAD	6 (67)	17 (55)	5 (62)	22 (56)	4 (57)
In-hospital treatment					
Composite valve graft root	4 (40)	18 (44)	0		0
replacement	4 (40)	18 (44)	0		0
Valve-sparing root replacement	5 (50)	2 (5)	0		0
Ascending aortic replacement	1 (10)	17 (42)	0		0
Aortic arch replacement (partial)	1 (10)	8 (20)	0		0
Aortic arch replacement (total)	2 (20)	4 (10)	0		0
Descending aorta replacement	0	0	2 (20)		1 (11)
Extent I TAAA repair	0	0	0		7 (78)
Extent II TAAA repair	0	0	0		1 (11)
Aorto-bifemoral bypass	0	0	1 (10)		0

Endovascular repair	0	0	3 (30)		0
Medical therapy	0	0	4 (40)		0
Peri-operative complications					
Tamponade	1 (10)	7 (34)	0	7 (16)	0
Myocardial infarction	0	3 (9)	0	3 (7)	0
Neurological deficit	0	3 (34)	0	3 (7)	1 (17)
Limb ischemia	0	2 (6)	1 (11)	3 (7)	1 (17)
Renal failure	0	6 (18)	1 (11)	7 (16)	0
Mesenteric ischemia	0	0	0	0	3 (33)
Atrial fibrillation	1 (11)	5 (15)	0	5 (12)	1 (17)
# days hospitalized	6 (5-9)	10 (8- 18)	12 (9-23)	11 (8- 18)	19 (14- 38)
In-hospital deaths	0	6 (15)	1 (10)	7 (14)	0

\*Categorical variables are presented as # of individuals and percentage in parenthesis (missing values were excluded in calculations) and continuous variables are presented as median (interquartile range); NA- not applicable.

# References

- 1. Adzhubei IA, Schmidt S, Peshkin L, Ramensky VE, Gerasimova A, Bork P et al. A method and server for predicting damaging missense mutations. *Nat Methods*. 2010;7:248-249.
- 2. Choi Y, Sims GE, Murphy S, Miller JR, Chan AP. Predicting the functional effect of amino acid substitutions and indels. *PLoS ONE*. 2012;7:e46688.
- 3. Schwarz JM, Rodelsperger C, Schuelke M, Seelow D. MutationTaster evaluates diseasecausing potential of sequence alterations. *Nat Methods*. 2010;7:575-576.
- 4. Reva B, Antipin Y, Sander C. Predicting the functional impact of protein mutations: application to cancer genomics. *Nucleic Acids Res.* 2011;39:e118.
- 5. Chun S, Fay JC. Identification of deleterious mutations within three human genomes. *Genome Res.* 2009;19:1553-1561.
- 6. Shihab HA, Gough J, Cooper DN, Stenson PD, Barker GL, Edwards KJ et al. Predicting the functional, molecular, and phenotypic consequences of amino acid substitutions using hidden Markov models. *Hum Mutat.* 2013;34:57-65.
- 7. Hoffjan S, Waldmuller S, Blankenfeldt W, Kotting J, Gehle P, Binner P et al. Three novel mutations in the ACTA2 gene in German patients with thoracic aortic aneurysms and dissections. *Eur J Hum Genet*. 2011;19:520-524.
- 8. Imai T, Horigome H, Shiono J, Hiramatsu Y. Isolated giant ascending aortic aneurysm in a child: a novel mutation of the ACTA2 gene. *Eur J Cardiothorac Surg.* 2011;40:e156-e157.
- 9. Renard M, Callewaert B, Baetens M, Campens L, MacDermot K, Fryns JP et al. Novel MYH11 and ACTA2 mutations reveal a role for enhanced TGFbeta signaling in FTAAD. *Int J Cardiol.* 2013;165:314-321.
- 10. Guo DC, Papke CL, Tran-Fadulu V, Regalado ES, Avidan N, Johnson RJ et al. Mutations in smooth muscle alpha-actin (ACTA2) cause coronary artery disease, stroke, and moyamoya disease, along with thoracic aortic disease. *Am J Hum Genet*. 2009;84:617-627.
- 11. Guo DC, Pannu H, Papke CL, Yu RK, Avidan N, Bourgeois S et al. Mutations in smooth muscle alpha-actin (*ACTA2*) lead to thoracic aortic aneurysms and dissections. *Nat Genet*. 2007;39:1488-1493.
- 12. Morisaki H, Akutsu K, Ogino H, Kondo N, Yamanaka I, Tsutsumi Y et al. Mutation of ACTA2 gene as an important cause of familial and nonfamilial nonsyndromatic thoracic aortic aneurysm and/or dissection (TAAD). *Hum Mutat.* 2009;30:1406-1411.

- 13. Disabella E, Grasso M, Gambarin FI, Narula N, Dore R, Favalli V et al. Risk of dissection in thoracic aneurysms associated with mutations of smooth muscle alpha-actin 2 (ACTA2). *Heart.* 2011;97:321-326.
- 14. Meuwissen ME, Lequin MH, Bindels-de HK, Bruggenwirth HT, Knapen MF, Dalinghaus M et al. ACTA2 mutation with childhood cardiovascular, autonomic and brain anomalies and severe outcome. *Am J Med Genet A*. 2013;161A:1376-1380.
- 15. Milewicz DM, Ostergaard JR, la-Kokko LM, Khan N, Grange DK, Mendoza-Londono R et al. De novo ACTA2 mutation causes a novel syndrome of multisystemic smooth muscle dysfunction. *Am J Med Genet A*. 2010;152A:2437-2443.
- 16. Moosa AN, Traboulsi EI, Reid J, Prieto L, Moran R, Friedman NR. Neonatal stroke and progressive leukoencephalopathy in a child with an ACTA2 mutation. *J Child Neurol.* 2013;28:531-534.
- 17. Richer J, Milewicz DM, Gow R, de NJ, Maharajh G, Miller E et al. R179H mutation in ACTA2 expanding the phenotype to include prune-belly sequence and skin manifestations. *Am J Med Genet A*. 2012;158A:664-668.
- 18. Al-Mohaissen M, Allanson JE, O'Connor MD, Veinot JP, Brandys TM, Maharajh G et al. Brachial artery occlusion in a young adult with an ACTA2 thoracic aortic aneurysm. *Vasc Med.* 2012;17:326-329.
- 19. Roder C, Peters V, Kasuya H, Nishizawa T, Wakita S, Berg D et al. Analysis of ACTA2 in European Moyamoya disease patients. *Eur J Paediatr Neurol*. 2011;15:117-122.
- 20. Munot P, Saunders DE, Milewicz DM, Regalado ES, Ostergaard JR, Braun KP et al. A novel distinctive cerebrovascular phenotype is associated with heterozygous Arg179 ACTA2 mutations. *Brain.* 2012;135:2506-2514.