

A HAND to TBX5 Explains the Link Between Thalidomide and Cardiac Diseases

Running Title: The HAND2 and TBX5 Pathway in the Heart

**Athar Khalil¹, Rachel Tanos¹, Nehmé El-Hachem^{1,6}, Mazen Kurban^{1,3,4}, Patrice Bouvagnet⁵, Fadi Bitar^{1,2},
and Georges Nemer^{1,*}**

Departments of ¹Biochemistry and Molecular Genetics, ²Pediatrics and Adolescent Medicine, and
³Dermatology, American University of Beirut, Beirut, Lebanon

⁴Department of Dermatology, Columbia University, New York, NY, USA

⁵Laboratoire Cardiogénétique, INMG, CNRS UMR 5310, INSERM U1217 and Université Lyon 1, Lyon,
France

⁶ Integrative systems biology/bioinformatics, IRCM, Montreal, Montreal, Canada

Supplementary Table 1: Phenotype/Genotype of the extended family members for the p.G202V HAND2 variant

Supplementary Figure 1: Differential interaction of Thalidomide with TBX3 versus TBX5

The corresponding protein-ligand interaction diagram shows the most relevant amino acid within 5 Angstroms of thalidomide. Note the different amino acids between TBX3 and TBX5 that get in close proximity to thalidomide. All amino acids that are implicated in the interaction with Thalidomide are listed in yellow.

Supplementary Figure 2: Expression of TBX5 proteins used in EMSA

15 micrograms of nuclear extracts from HEK293 cells overexpressing HA-tagged TBX5 were resolved on a denaturing gel under different conditions (control, DMSO, and Thalidomide). Western blot with HA polyclonal rabbit antibody shows equal amount of proteins under all conditions.

Supplementary Figure 3: MTT assay on HEK293 cells treated with Thalidomide

The data are represented of %cell survival over 24 hours after treatment with Thalidomide (4 μ M) or DMSO. The numbers represent the mean \pm Standard deviation for 3 experiments done in triplicate.

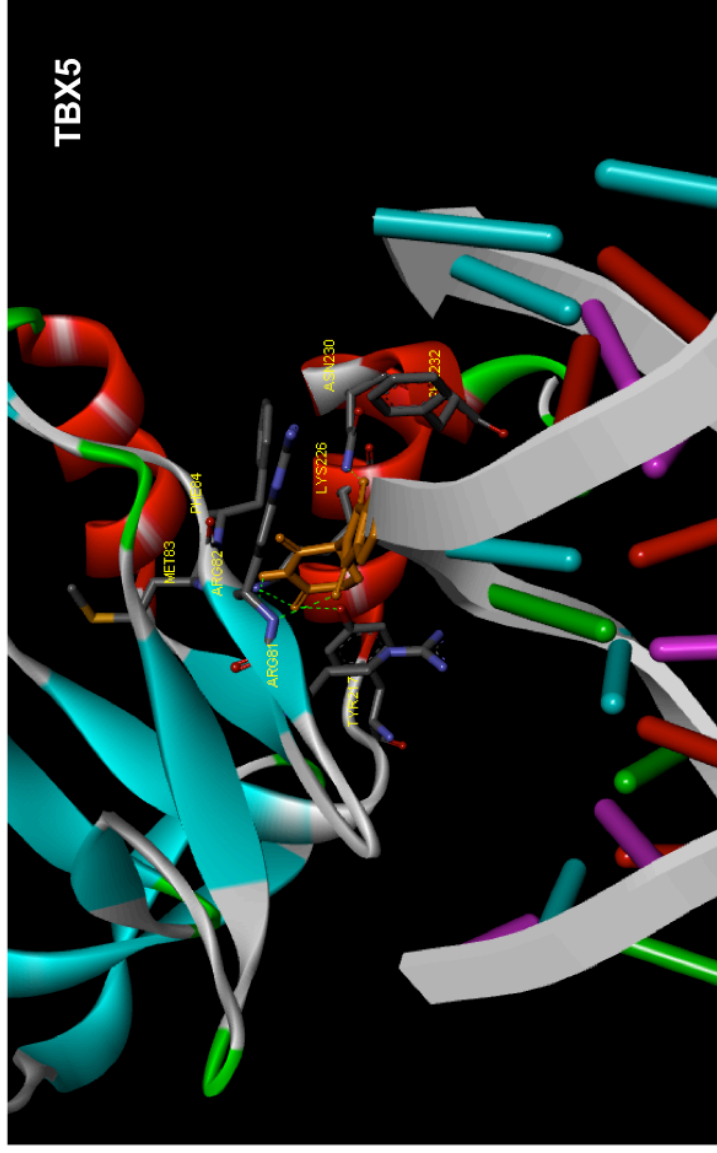
Supplementary Figure 4: Genetic analysis of the p.G202V variant within the large affected family

The pedigree includes all individuals over 6 generations (roman numbers). All coded DNA samples numbers (arabic) are underneath each corresponding individual. Those individuals whom we have a “hear-say” account from family members are given roman numbers. The rest are not numbered.

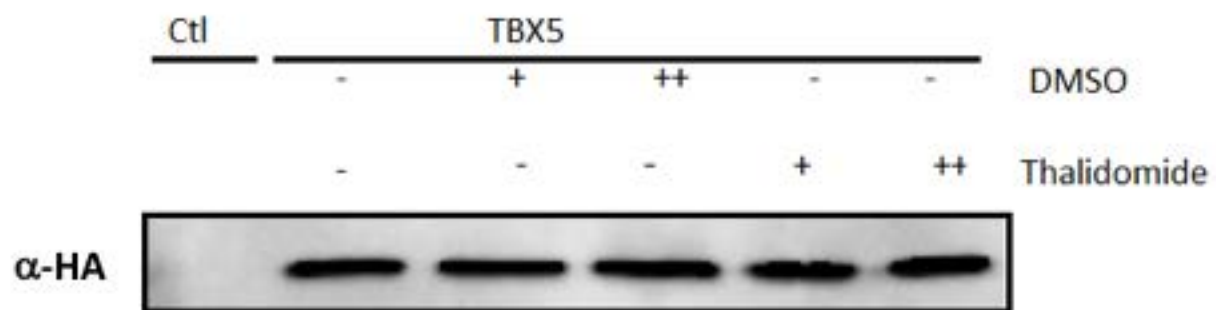
Supplementary Table 1: Phenotype/Genotype of the extended family members for the p.G202V HAND2 variant

Patient ID	Phenotype	HAND2-p.G202V
78		-
79		+
80	TOF	+
81		-
82	TOF	+
890		-
891		-
892		-
894		-
895		-
896		-
897		-
898		-
899		-
900		+
901		-
902		-
903	VSD	-
904	CAD	-
905		-
906		+
907		-
908	TOF like + PA	+
909		-
910		-
911		-
912		-
913		-
914		-
915		-
916		-
917		-
918		+
919		+
920		-
921		-
922		-
923		-
335		+
925		-
926		-
227	AS	+
228		-
229	CoA	+
427		-
429	CAD	+
334		-
55	CAD	+
426	CAD	+
431	CAD	+
57	PDA + VSD	-

TOF: Tetralogy of Fallot
VSD: Ventricular Septal Defect
CAD: Coronary Artery Disease
PA: Pulmonary Atresia
AS: Aortic Stenosis
CoA: Coarctation of the Aorta
PDA: Patent Ductus Arteriosus



Supplementary Figure 1, Khalil A et al



Supp Figure 2, Khalil et al

