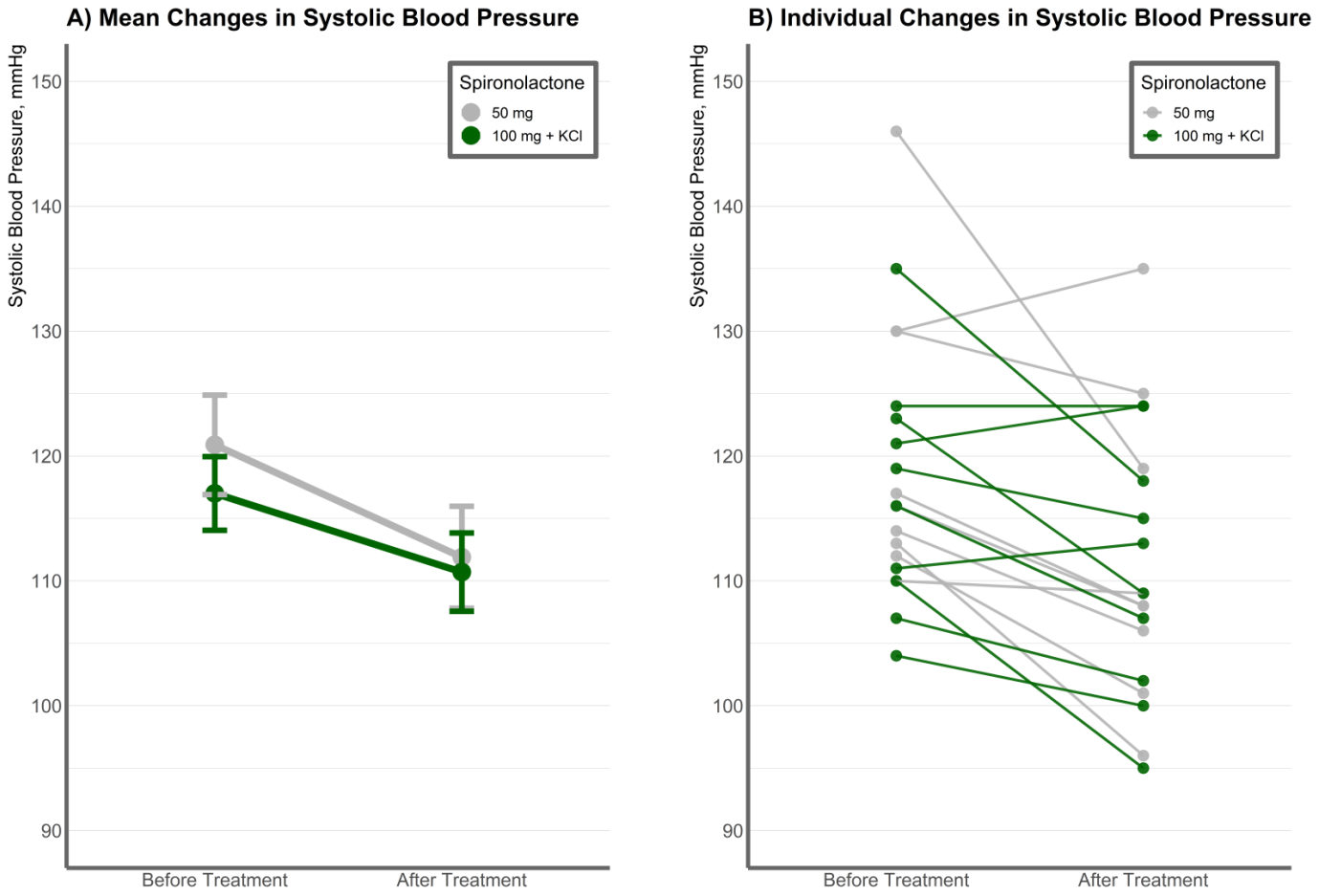
Supplemental Table 1 – List of Unique Genetic Variants Found in Participants

No. of patients	Treatment Group	Gene	Protein and Coding Region	Mutation type	Functional analysis*		Ref
					Polyphen-2	Mutation Assessor	
3	**3***High+*	*KCNQ1*	p.Arg366Trp , R366W (c.1096C>T)	Missense	2	2	A
2	**2***Low*	*KCNQ1*	p.His363Asn, H363N (c.1087C>A)	Missense	1	2	B,C
1	**1***Low,*	*KCNQ1*	p.Val254Met, V254M *(c.760G>A)*	Missense	2	2	D,E
1	**1***Low*	*KCNQ1*	p.Arg190Trp, R190W *(c.568C>T)*	Missense			B
1	**1***High+*	*KCNQ1*	*p.Ala344=, A344sp (c.1032G>A)*	Splice-site			F
1	**1***High+*	KCNQ1	*p. Gly572Arg G572R (c.1714G>C)* *rs9333649*	Missense	2	2	G
4	**2***Low*, **2***High+*	KCNH2	*p.Lys101Glu , K101E (c.301A>G)*	Missense	0	3	G
2	**2***Low*	*KCNH2*	p.Arg366Stop, R366X (c.1096C>T)	Nonsense	2	2	G
2	**2***Low*	*KCNH2*	p.Ser428fs, S428fs (c.1286delC)	Frameshift	0	2	
1	**1***Low*	*KCNH2*	p.Ser428Leu, S428L (c.1283C>T)	*Missense*			
1	**1***High+*	*KCNH2*	p.Gly584Ser, G584S (c. 1750G>A)	*Missense*	1	0	
1	**1***High+*	*KCNH2*	p.Leu109Pro, L109P(c.326T>C)	Missense	1	2	
1	**1***High+*	*KCNH2*	p. Ile571Phe (c.1711A>T)	Missense			

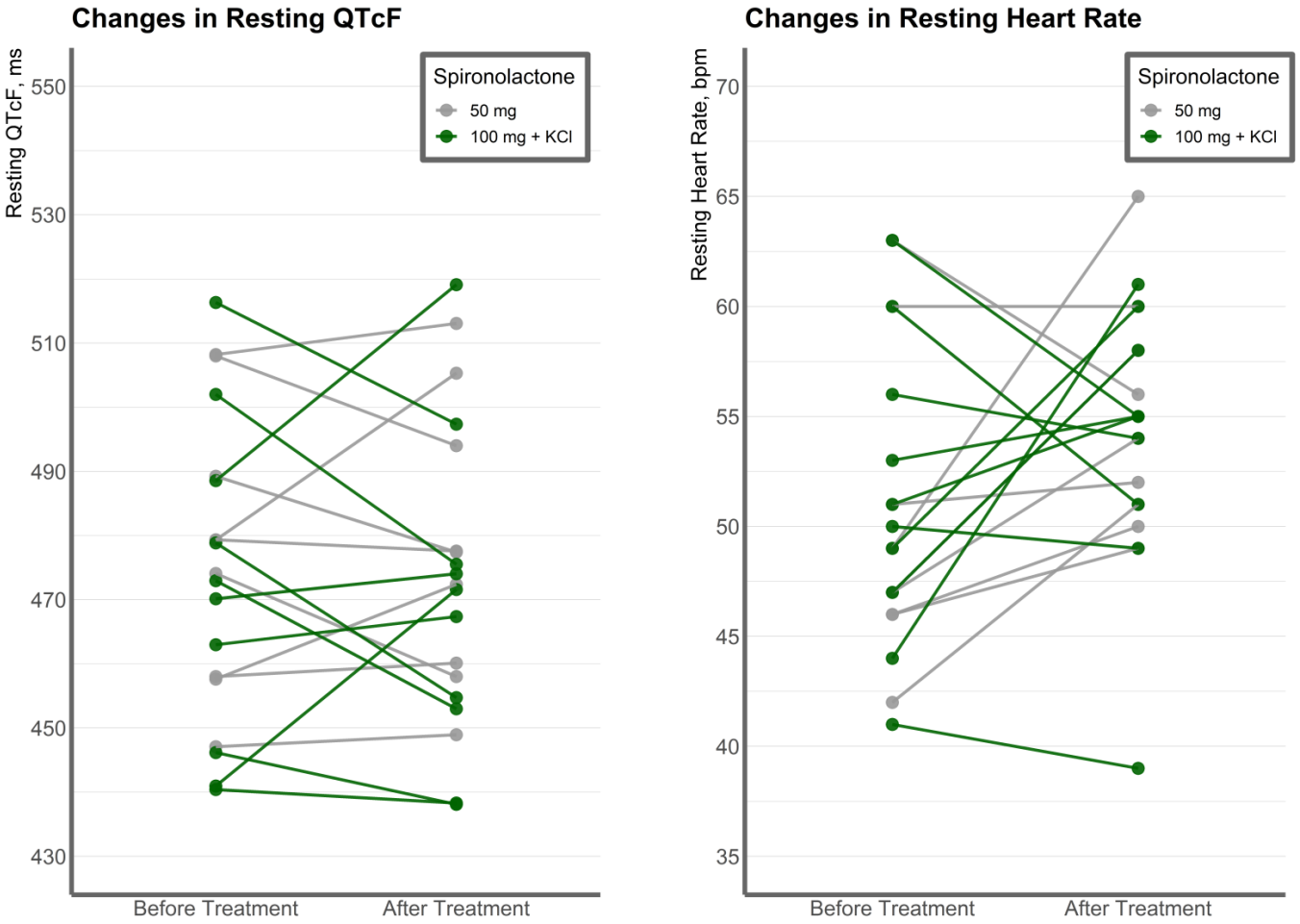
*Polyphen-2 scores: 0: benign, 1 possibly damaging for function; 2: Probably damaging for function.

Mutation Assessor scores; 0-1: no functional effect, 2-3: functional effect on protein function.

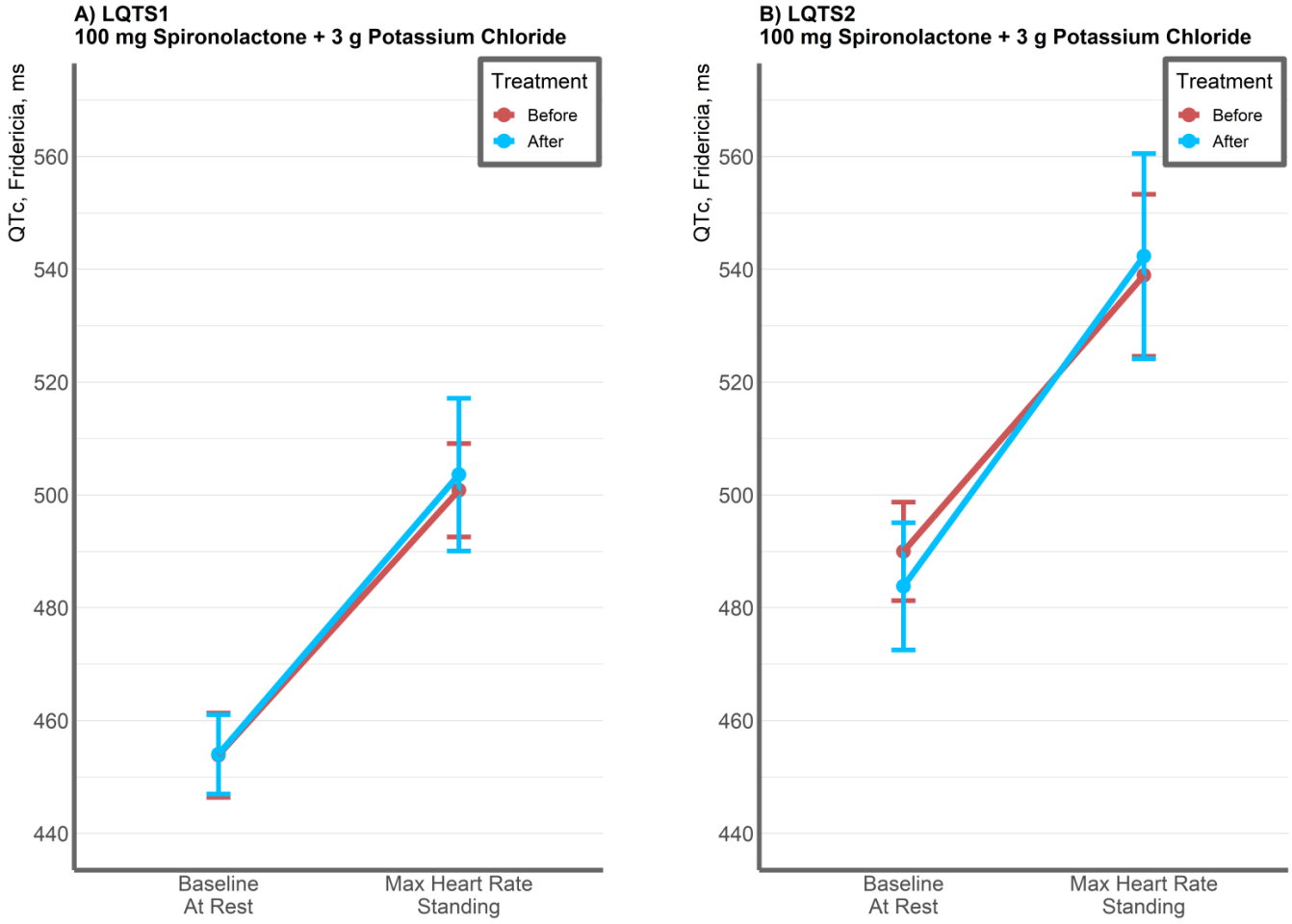
Supplemental Figure 1 – Mean (A) and Individual (B) Changes of Systolic Blood Pressure in Response to Potassium-Elevating Treatment.



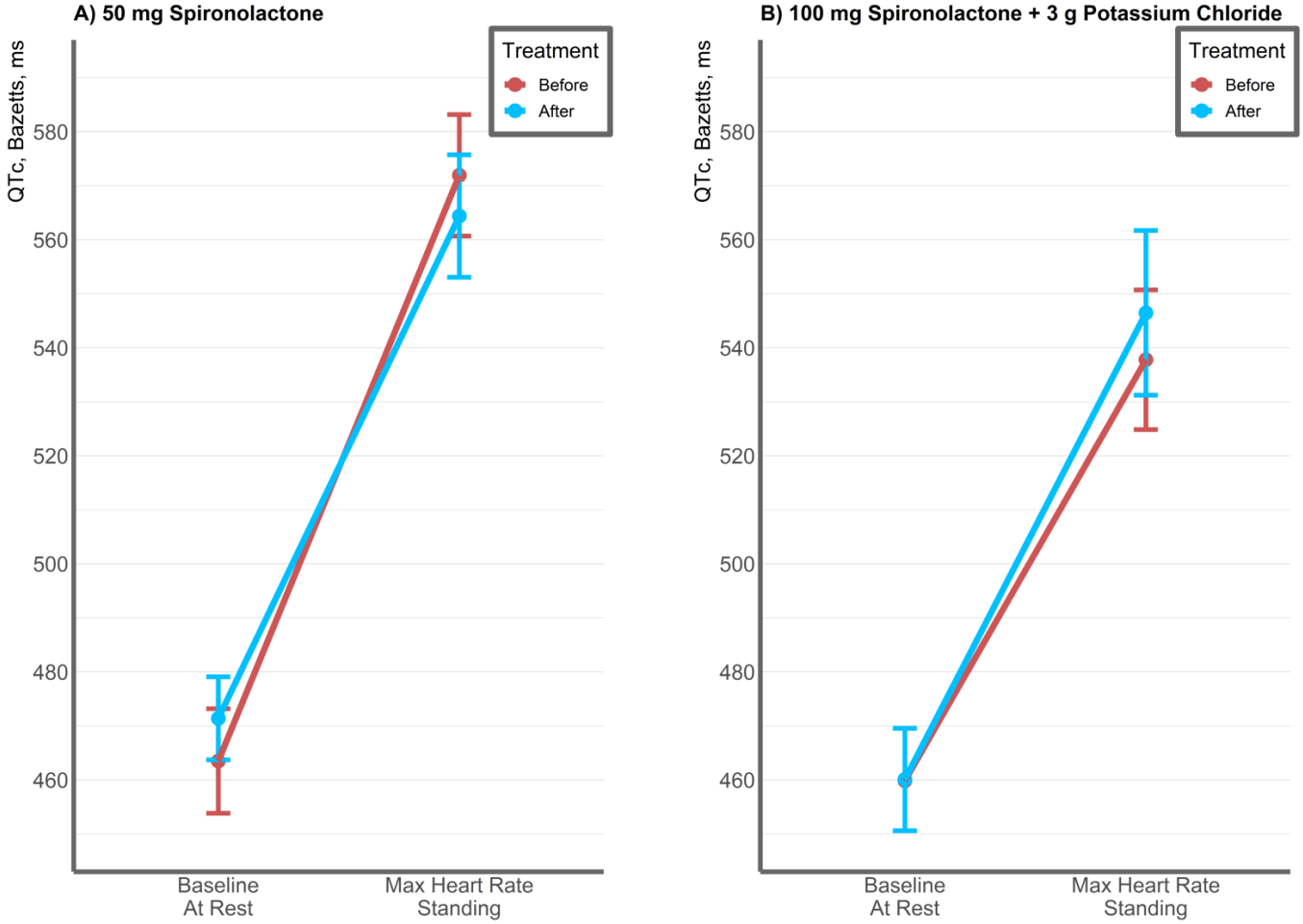
Supplemental Figure 2 – Individual Changes in Resting QTcF and Resting Heart Rate in Response to Potassium-Elevating Treatment.



Supplemental Figure 3 – The Effect of 100 mg spironolactone and 3 g Potassium Chloride on QTcF — Stratified on Genotype.



Supplemental Figure 4 – Bazett's correction



Supplemental references for variants

A) Larsen, L. A. et al. A single strand conformation polymorphism/heteroduplex (SSCP/HD) method for detection of mutations in 15 exons of the KVLQT1 gene, associated with Long QT syndrome. Clinica Chimica Acta 280, 113–125 (1999).

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C) Chen, J., Liu, Z., Creagh, J., Zheng, R. & McDonald, T. V. Physical and functional interaction sites in cytoplasmic domains of KCNQ1 and KCNE1 channel subunits. Am J Physiol Heart Circ Physiol 318, H212–H222 (2020).

D) Kanters, J. K. et al. T(peak)T(end) interval in long QT syndrome. J Electrocardiol 41, 603–608 (2008).

E) Hoefen, R. et al. In Silico Cardiac Risk Assessment in Patients With Long QT Syndrome: Type 1: Clinical Predictability of Cardiac Models. J. Am. Coll. Cardiol 60, 2182–2191 (2012).

F) Kanters, J. K. et al. Novel donor splice site mutation in the KVLQT1 gene is associated with Long QT syndrome. Journal of Cardiovascular Electrophysiology 9, (1998).

G) Larsen, L. A. et al. Screening for mutations and polymorphisms in the genes KCNH2 and KCNE2 encoding the cardiac HERG/MiRP1 ion channel: implications for acquired and congenital long Q-T syndrome. Clinical Chemistry 47, (2001).