

SUPPLEMENTAL MATERIAL

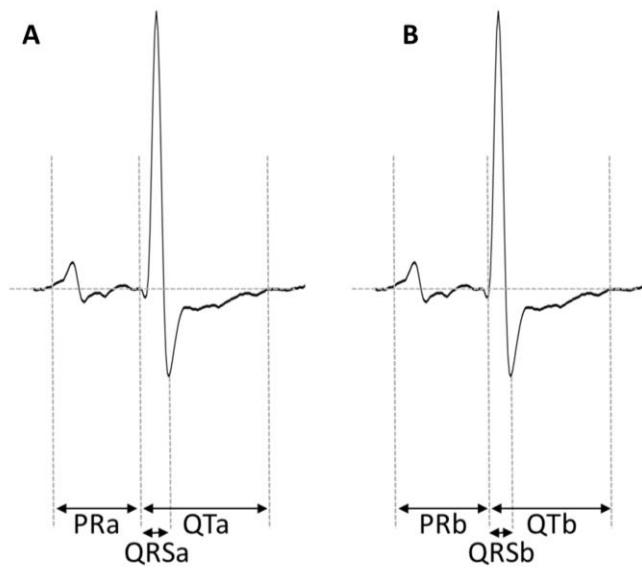
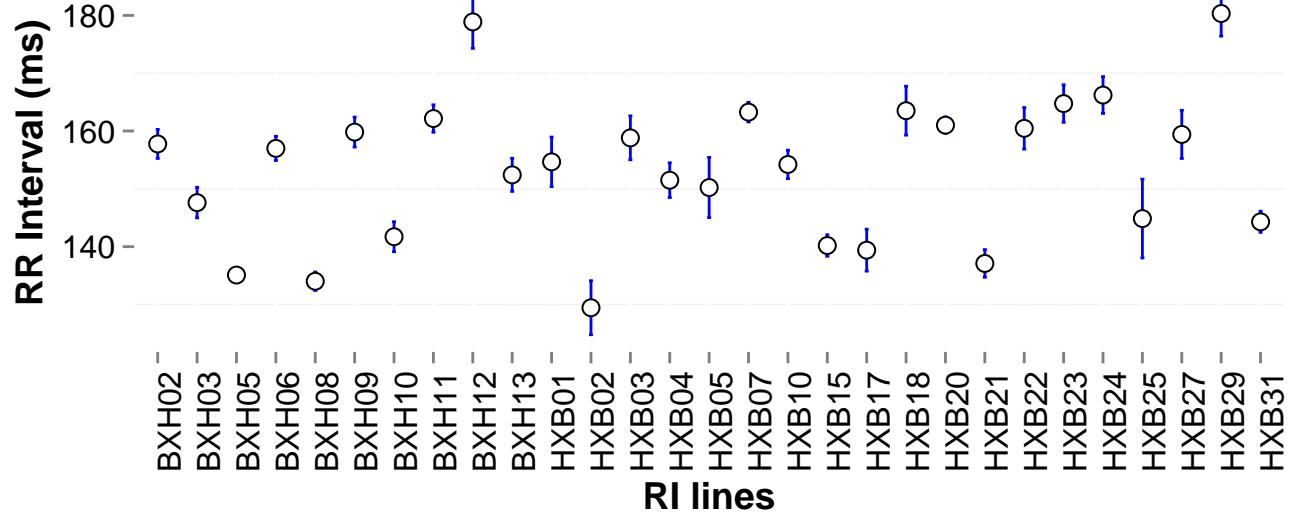
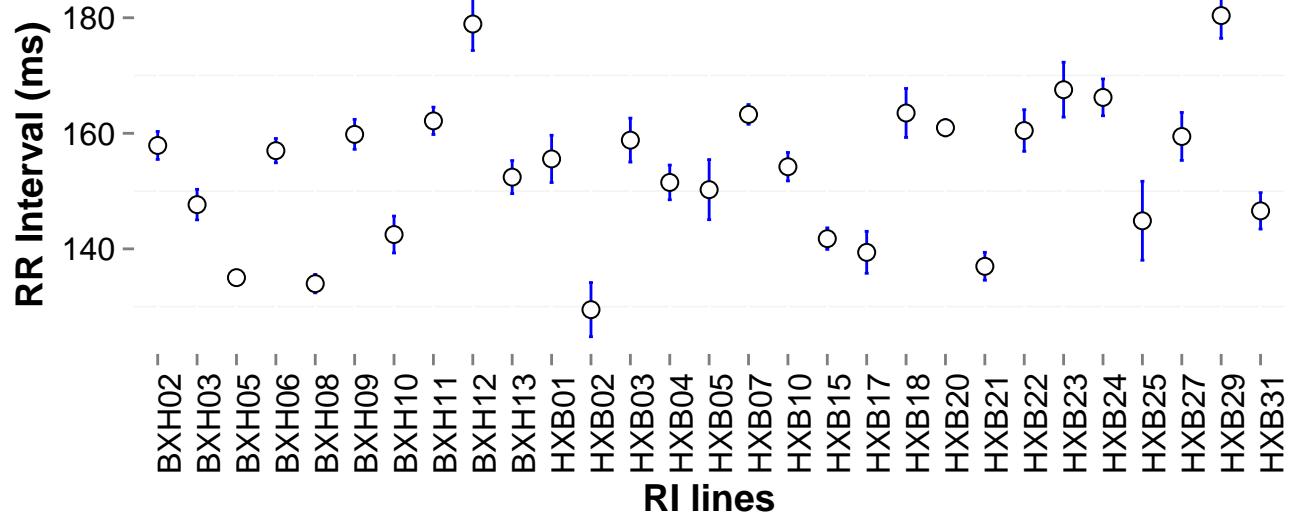


Figure S1. Figure illustrating the principle of determining PR interval in an ECG in two ways: (A) with the start of the QRS complex defined as the very first deflection from the baseline (typically a downward slope), and (B) with the start of the QRS complex defined as the start of its fast upstroke.

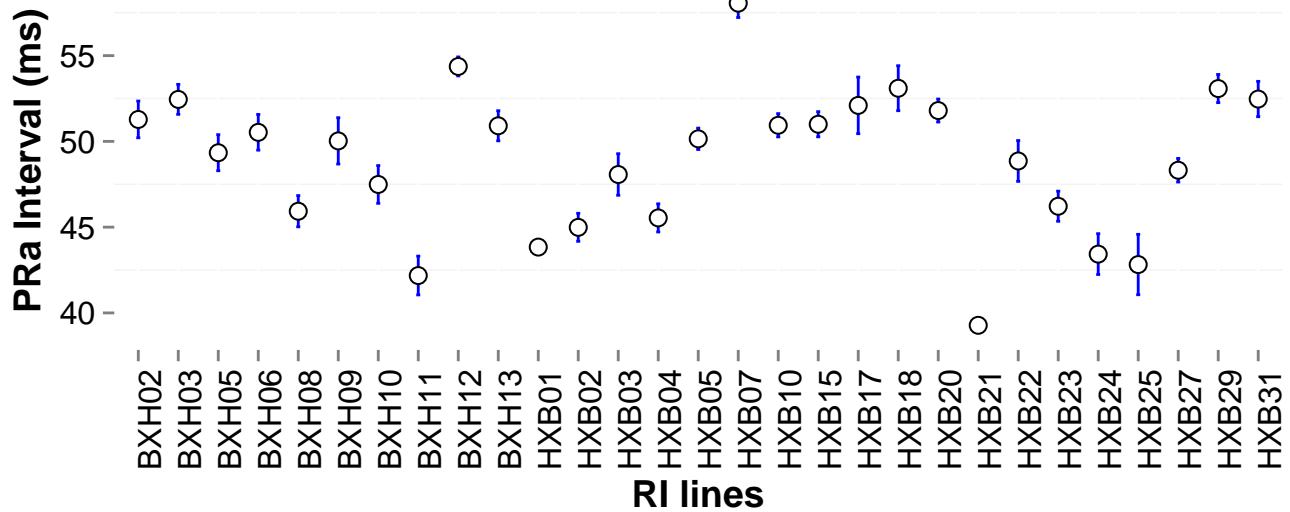
RR Interval (ms) (Channel 1)



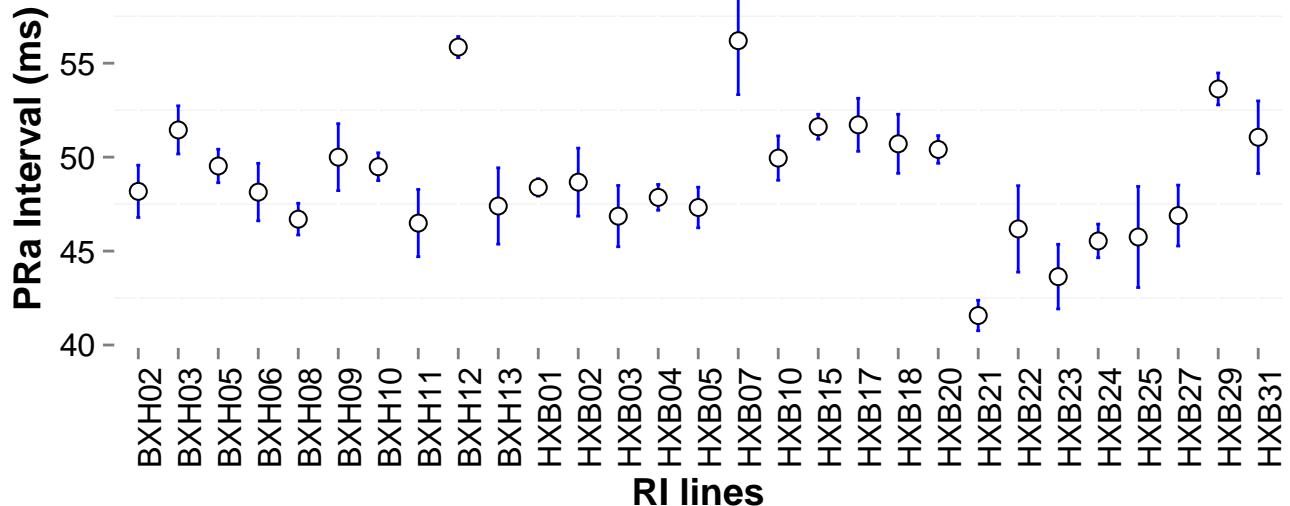
RR Interval (ms) (Channel 2)



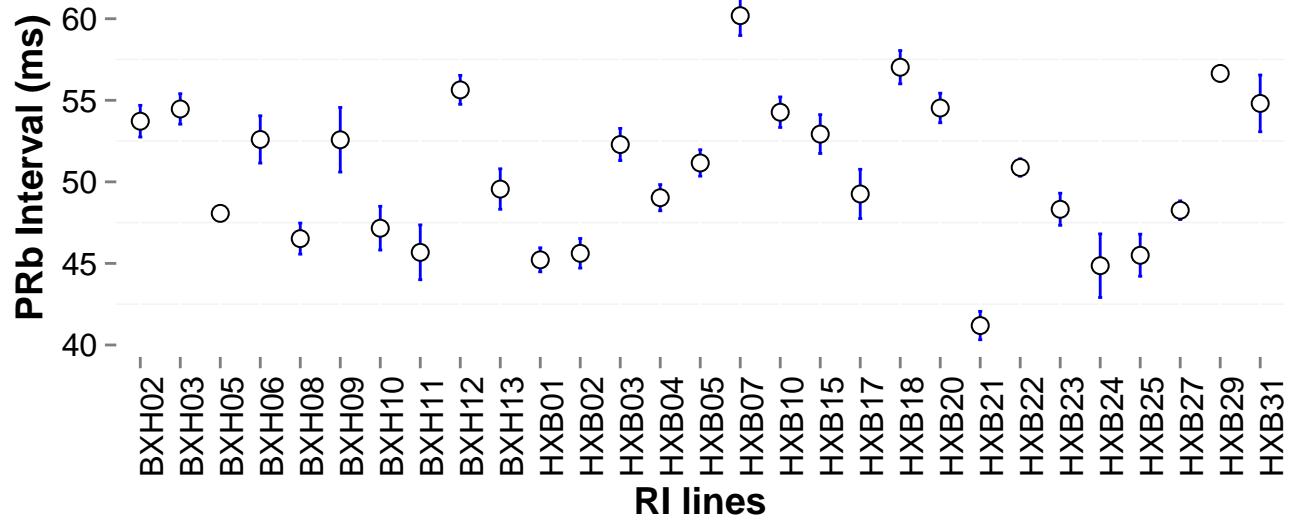
PRA Interval (ms) (Channel 1)



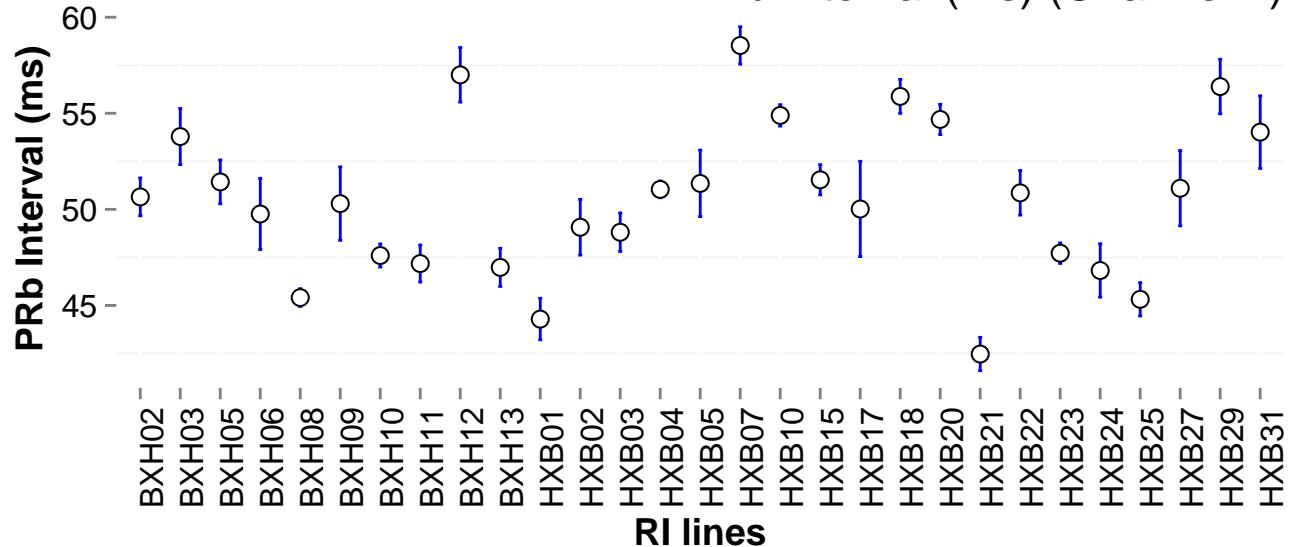
PRA Interval (ms) (Channel 2)



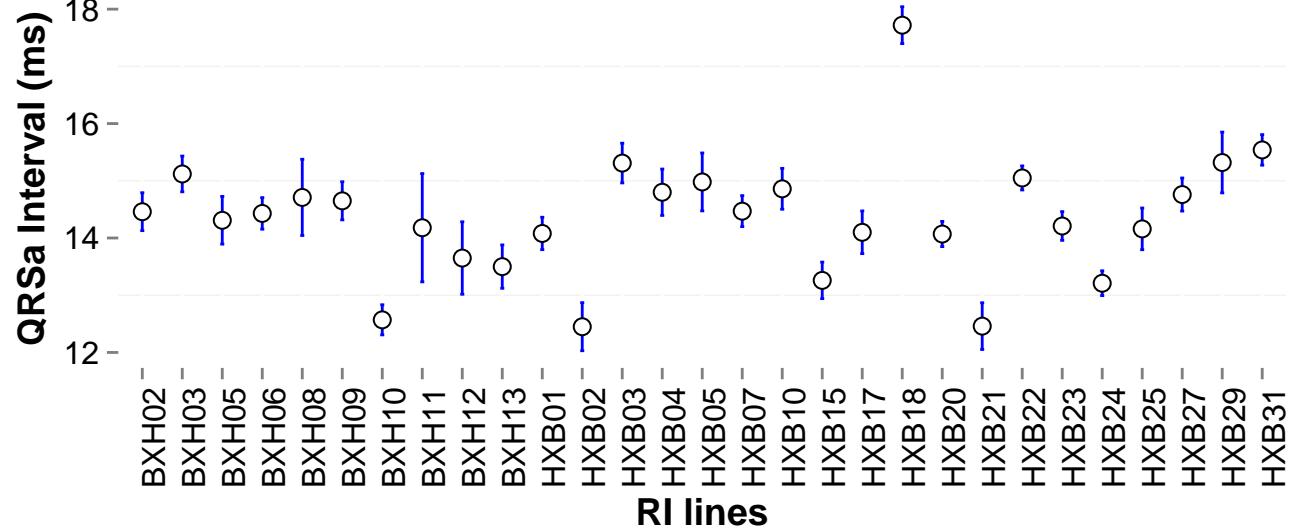
PRb Interval (ms) (Channel 1)



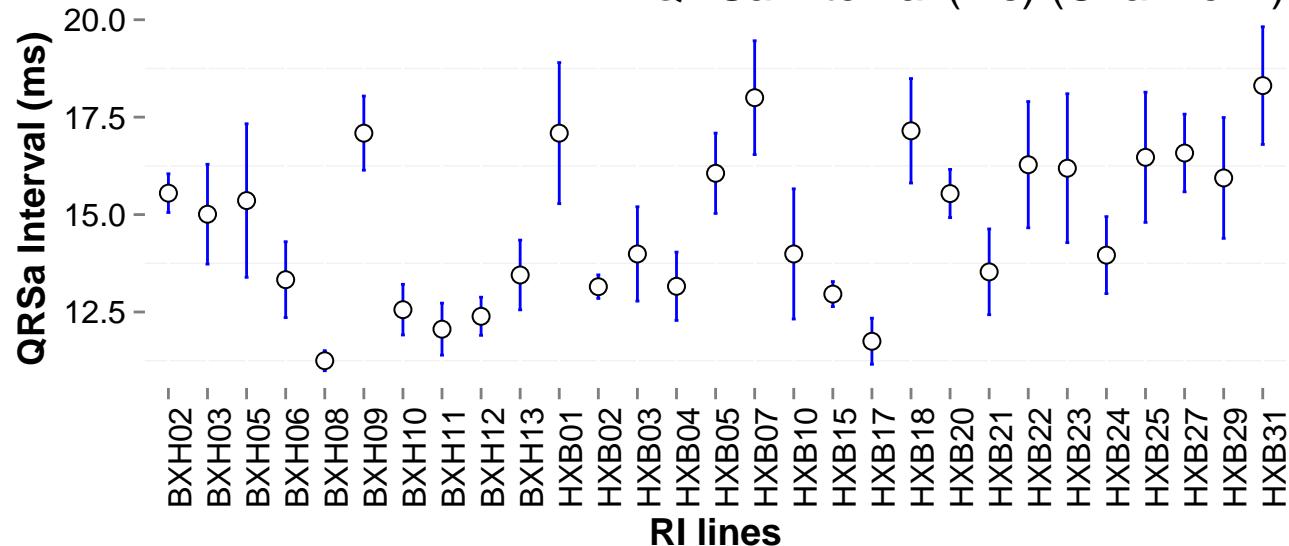
PRb Interval (ms) (Channel 2)



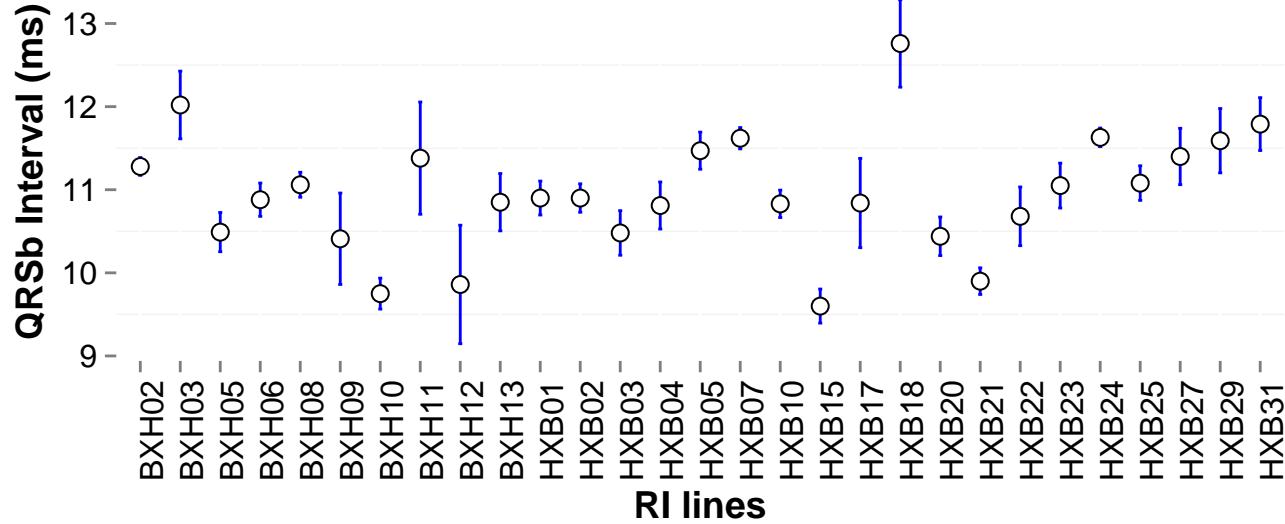
QRSa Interval (ms) (Channel 1)



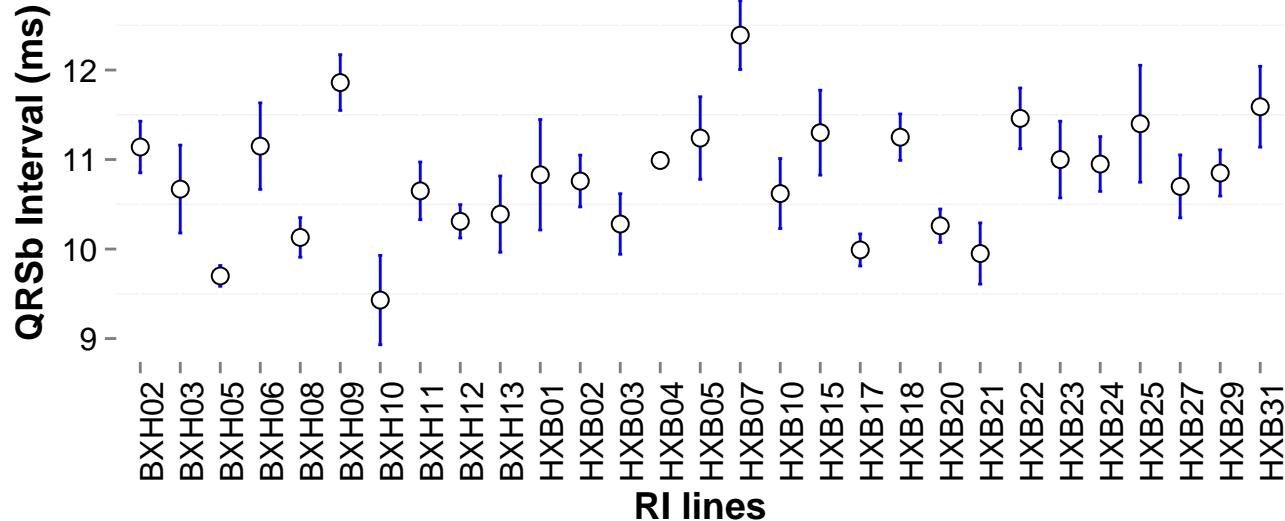
QRSa Interval (ms) (Channel 2)



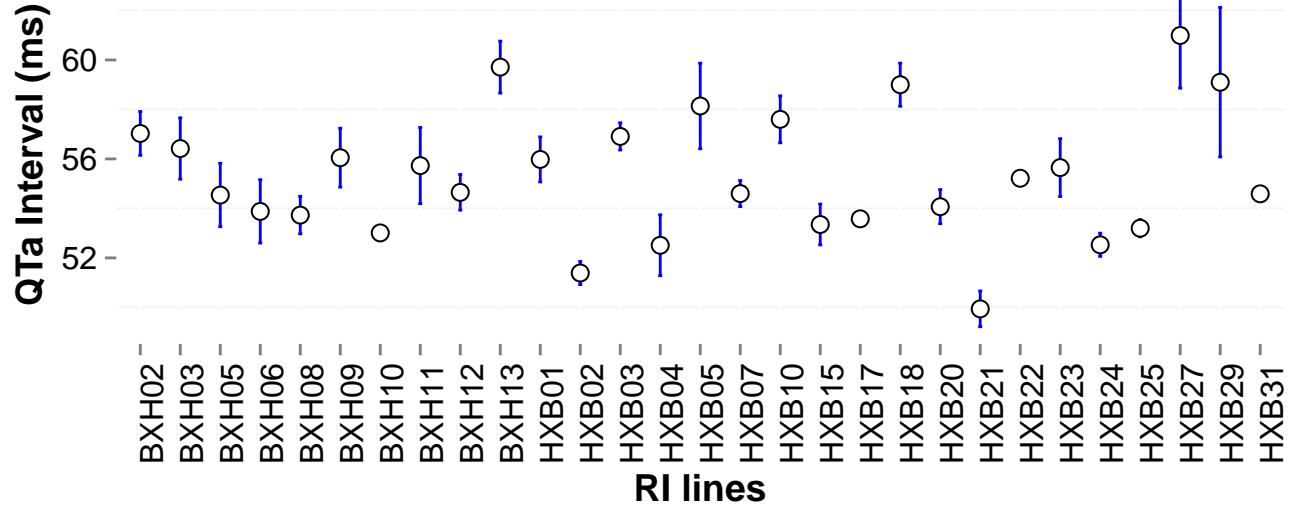
QRSb Interval (ms) (Channel 1)



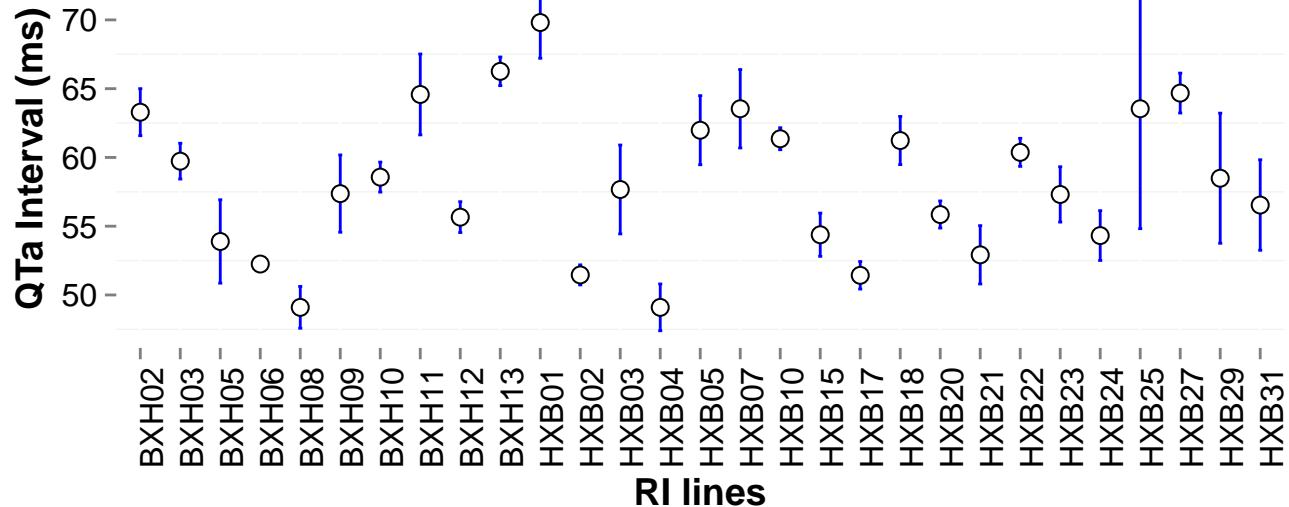
QRSb Interval (ms) (Channel 2)



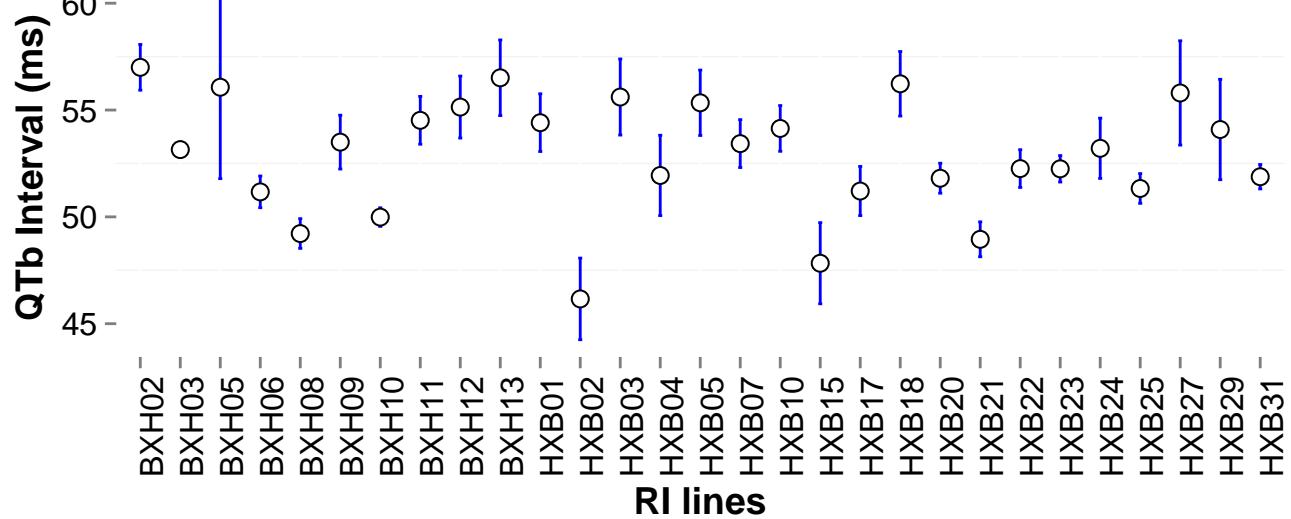
QTa Interval (ms) (Channel 1)



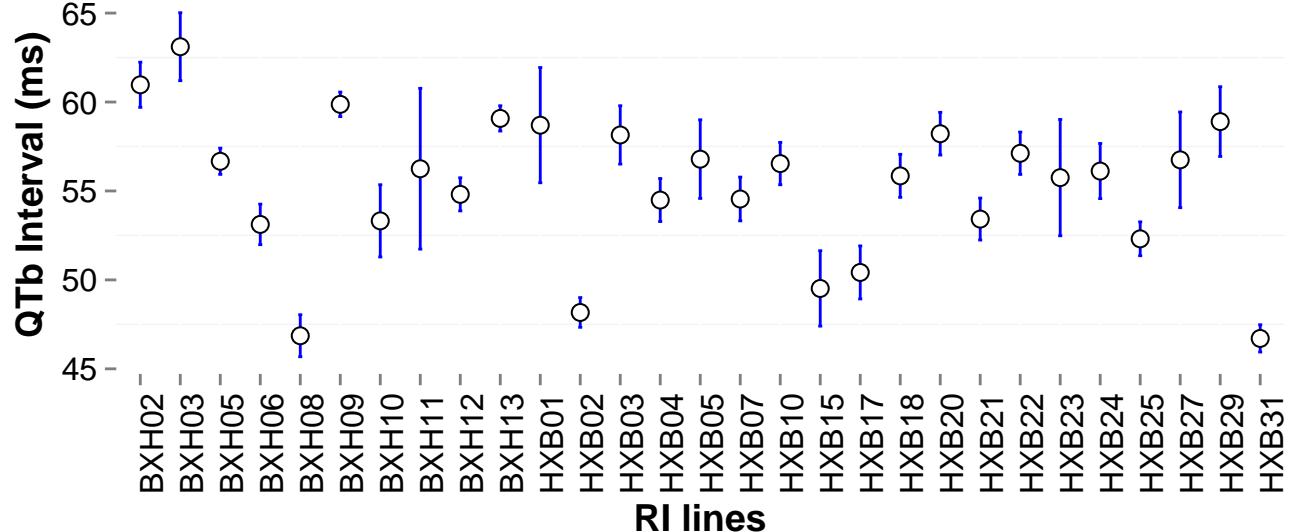
QTa Interval (ms) (Channel 2)



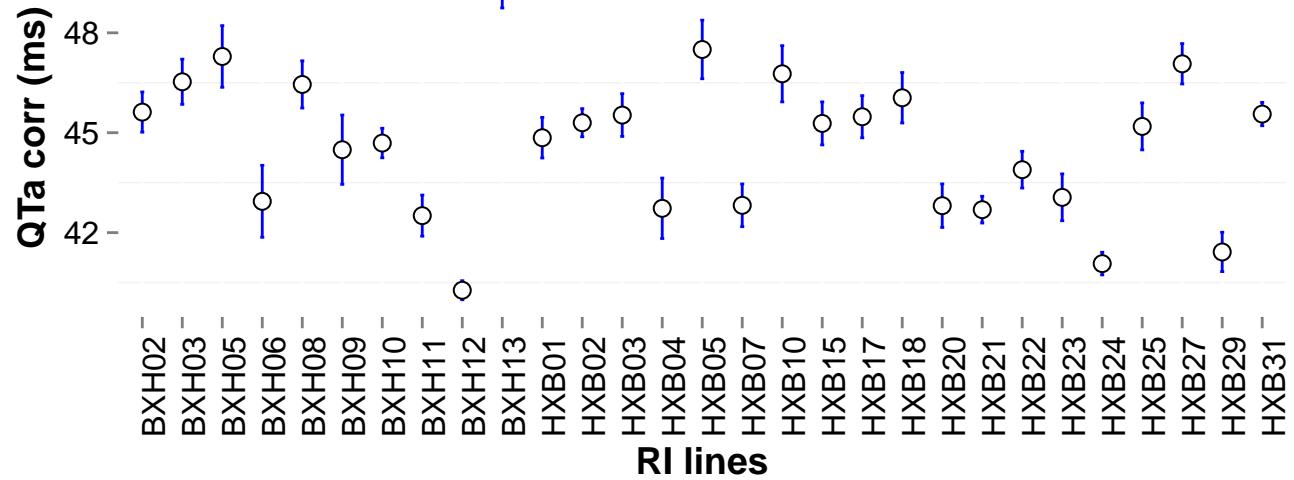
QTb Interval (ms) (Channel 1)



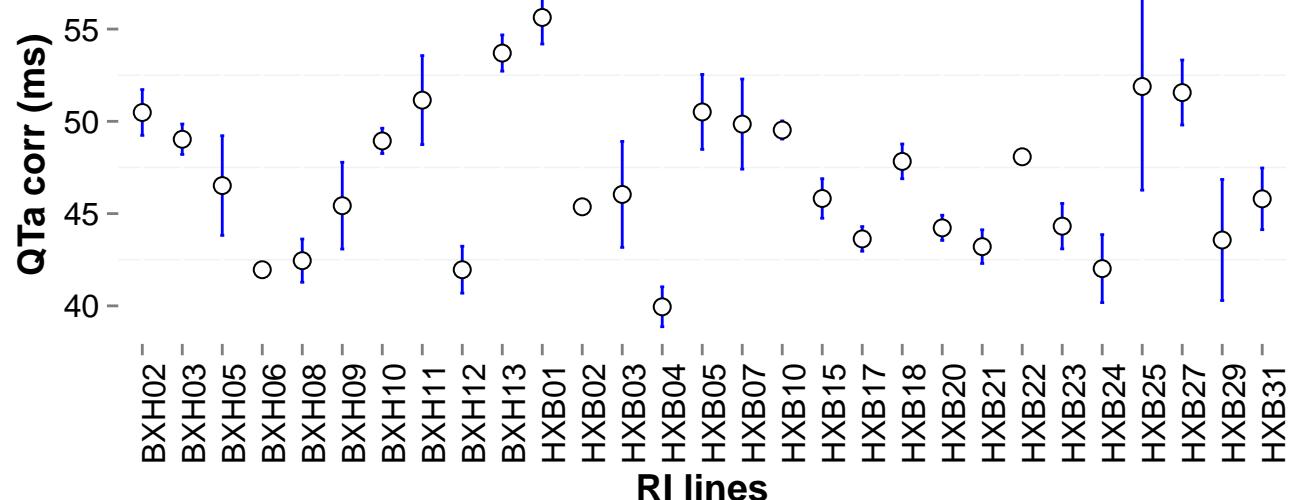
QTb Interval (ms) (Channel 2)



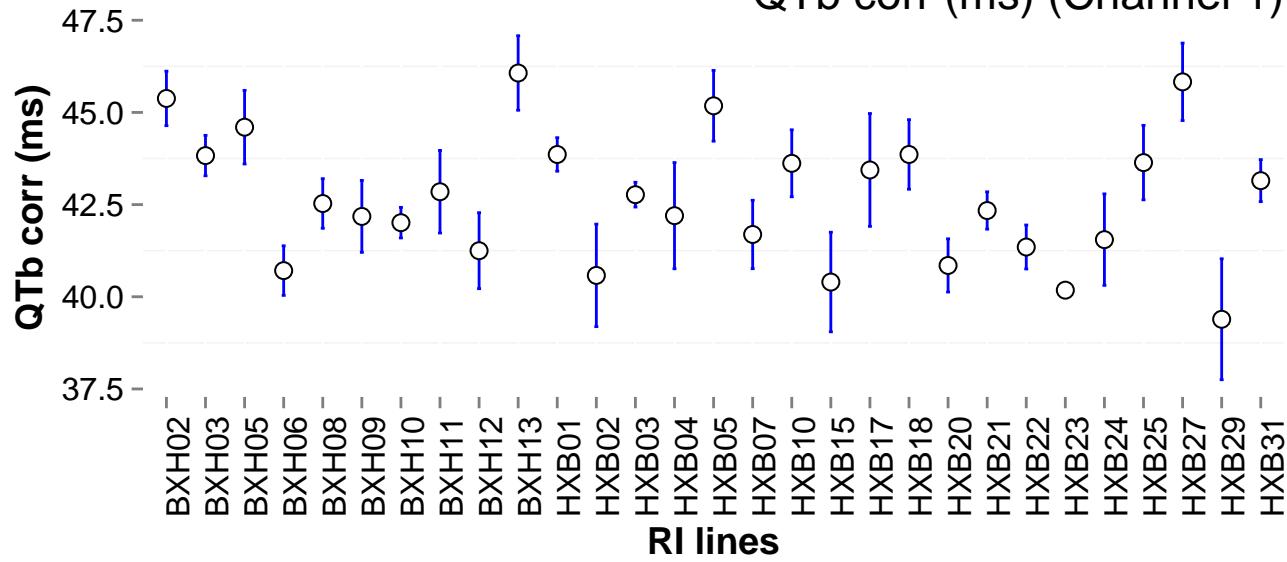
QTa corr (ms) (Channel 1)



QTa corr (ms) (Channel 2)



QTb corr (ms) (Channel 1)



QTb corr (ms) (Channel 2)

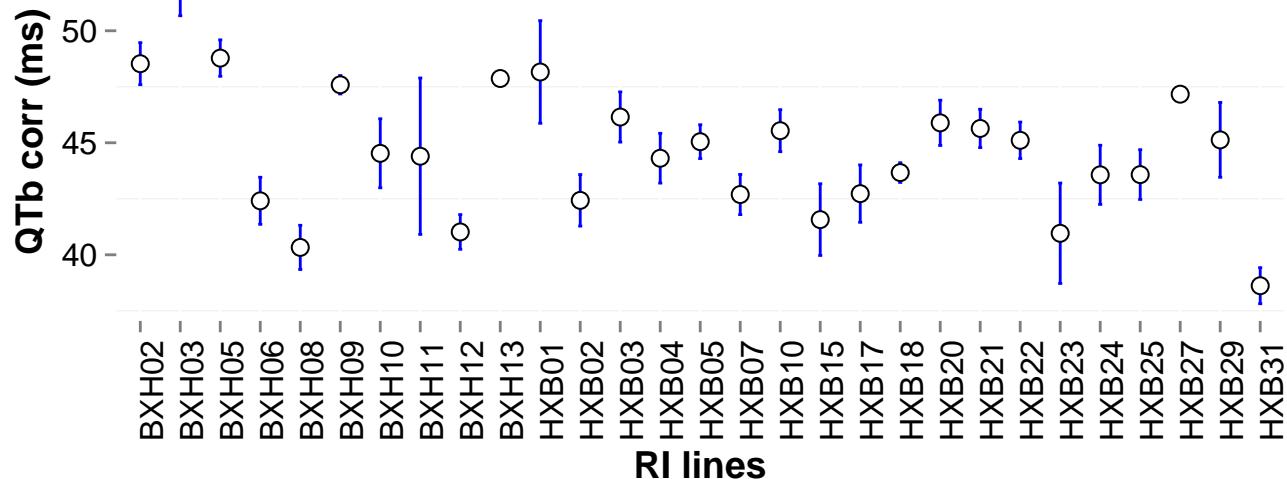


Figure S2 (on previous pages). Variability within and between strains for the different ECG-parameters: RR-interval, PR-interval, QRS-interval and QT-interval with and without correction for heart rate (corr.). Error bars indicate standard error of the mean.

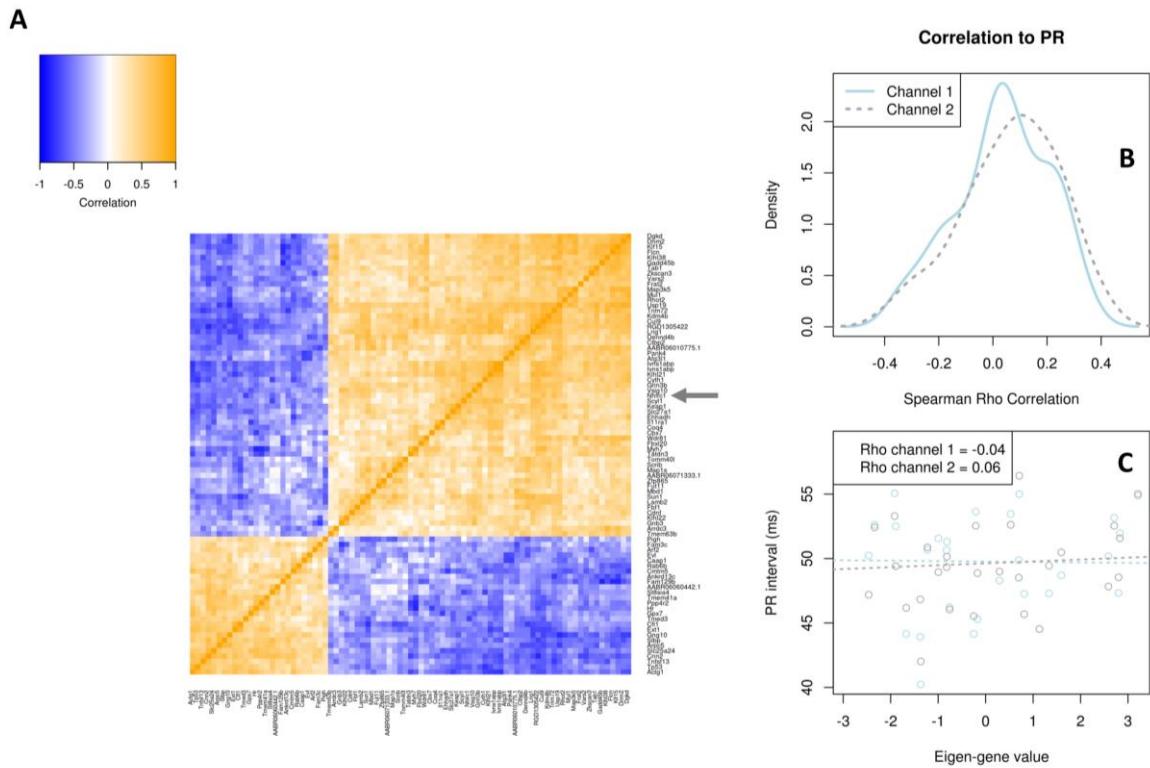


Figure S3. Co-expression network containing the significant eQTL gene *Nhlrc1*. Overview of the co-expression network of 80 genes, containing a candidate gene identified through eQTL analysis. (A) Heatmap showing the Spearman correlation between gene expression patterns of each gene pair. Blue signifies negative correlation, while orange signifies positive correlation. The candidate gene, *Nhlrc1*, is highlighted by grey arrows. (B) Density distribution plot of the Spearman correlation values for each gene in the network with PR interval in channel 1 (solid line) and channel 2 (dashed line). This figure summarizes the correlation of the network to PR interval on gene level. (C) Scatterplot of the network eigengene values versus PR interval. Dotted lines represent the linear least-squares fits for channel 1 (light blue) and channel 2 (grey). Spearman Rho correlation values are given in the legend for each channel. This figure summarizes the correlation of the network to PR on network level.

Supplemental Table Legends (see Excel files):

Table S1. Overview of candidate genes at the identified chromosome 10 and chromosome 17 loci.

Table S2. Overview of all genes that are part of a co-expression network.

Table S3. Correlation of co-expression networks with ECG traits.

Table S4. Gene Ontology Enrichment Analysis results for co-expression network M8.

Table S5. Gene Ontology Enrichment Analysis results for co-expression network M12.

Table S6. Gene Ontology Enrichment Analysis results for co-expression network M24.

Table S7. Gene Ontology Enrichment Analysis results for co-expression network M26.

Table S8. Gene Ontology Enrichment Analysis results for co-expression network M30.

Table S9. Gene Ontology Enrichment Analysis results for co-expression network M37.

Table S10. Overview of all genes that are part of the *Arhgap27* co-expression network.

Table S11. Gene Ontology Enrichment Analysis results for the *Arhgap27* co-expression network.

Table S12. Overview of all genes that are part of the *Acbd4* co-expression network.

Table S13. Gene Ontology Enrichment Analysis results for the *Acbd4* co-expression network.

Table S14. Overview of all genes that are part of the *Nhlrc1* co-expression network.

Table S15. Co-expression network enrichment for cardiac trait GWAS genes.

Table S16. Specification of cardiac trait GWAS genes present in co-expression networks M10 and M22.