Supplementary Table S1: PCR protocols used for genotyping

ADRB1 Ser49Gly (rs1801252)	**Forward primer**	**Reverse primer**	**Sensor WT**	**Sensor MUT**
	gTCgCCgCCCgCCTCgTT	CCATgCCCgCTgTCCACTgCT	6-FAM-CCAgCgAA**A**gCCCCgAgCC-DB	YAK-CCAGCgAA**g**gCCCCgAgC-DB
	$MgCl_2$ concentration	**PCR protocol details**		
	10 mM	DEN: 95 °C for 60 s; ANN: 70 °C for 6 s; ELO: 72 °C for 4 s, transition rate of 20 °C/s between plateaus; 50 cycles		
ADRB1 Arg389Gly (rs1801253)	**Forward primer**	**Reverse primer**	**Sensor WT**	**Sensor MUT**
	ggCCTTCAACCCCATCATCTA	CCggTCTCCgTgggTCgCgT	6-FAM-AggCCTTCCAg**C**gACTgCTCTgC-DB	YAK-AggCCTTCCAg**g**gACTgCTCTgCT-DB
	$MgCl_2$ concentration	**PCR protocol details**		
	11 mM	DEN: 95 °C for 60 s; ANN: 69 °C for 6 s; ELO: 72 °C for 5 s, transition rate of 20 °C/s between plateaus; 55 cycles		
ADRB2 Gly16Arg (rs1042713)	**Forward primer**	**Reverse primer**	**Sensor WT**	**Sensor MUT**
	gAACggCAgCgCCTTCT	CAggACgATgAgAgACATgACgAT	6-FAM-CgCATggCTTC**C**ATTgggTgC-DB	YAK-CgCATggCTTC**T**ATTgggTgC-DB
	$MgCl_2$ concentration	**PCR protocol details**		
	9 mM	DEN: 95 °C for 60 s; ANN: 70 °C for 6 s; ELO: 72 °C for 5 s; transition rate of 20 °C/s between plateaus; 45 cycles		
ADRB2 Gln27Glu (rs1042714)	**Forward primer**	**Reverse primer**	**Sensor WT**	**Sensor MUT**
	ggAACggCAgCgCCTTCT	CAggACgATgAgAgACATgACgAT	6-FAM-CTCgTCCCTTT**g**CTgCgTgACgT-DB	YAK-CTCgTCCCTTT**C**CTgCgTgACgT-DB
	$MgCl_2$ concentration	**PCR protocol details**		
	9 mM	DEN: 95 °C for 60 s; ANN: 71 °C for 6 s; ELO: 72 °C for 5 s, transition rate of 20 °C/s between plateaus; 45 cycles		

Polymerase chain reaction Master Mix: LightCycler DNA Master Hybridization Probes mixture (Roche Molecular

Biochemicals, Rotkreuz, Switzerland) containing 0.5 µmol/L (forward primer), 0.5 µmol/L (reverse primer), 0.2 µmol/L of each sensor, and 5 pg/20 µL DNA. The total volume in the LightCycler capillary was 20 µL.

DEN=denaturation; ANN=annealing; ELO=elongation.

Supplementary Figures

Figure S1: Framingham risk assessment of the study population.

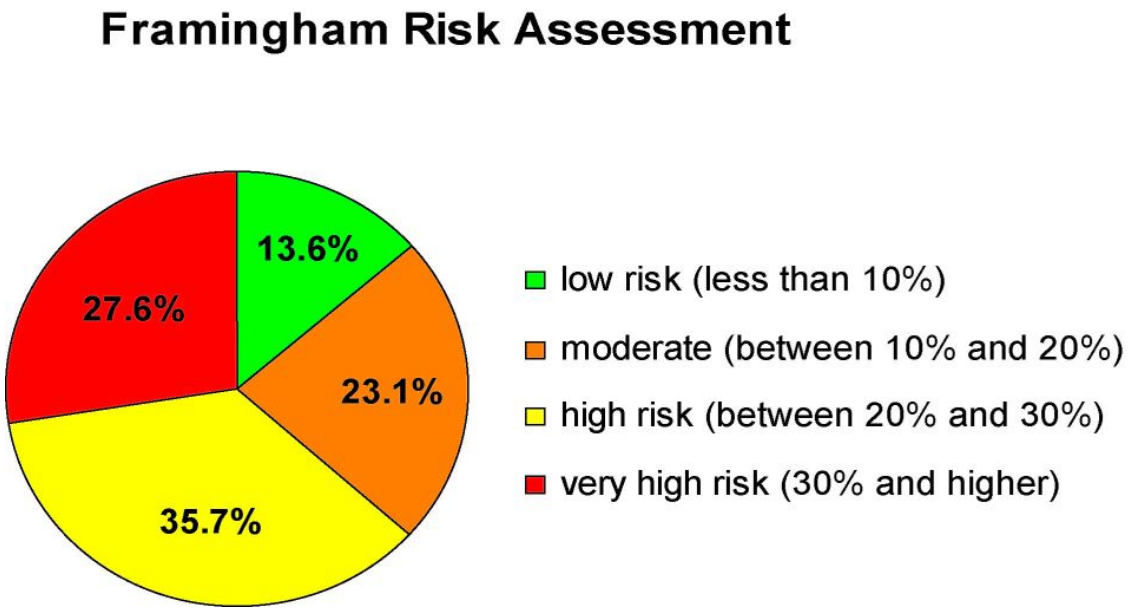

Figure S2: Distribution of β-adrenergic receptor polymorphisms in the study population. WT=wildtype; HET=heterozygous; MUT=mutant; HWE=Hardy-Weinberg Equilibrium. P<0.05 indicates deviation from HWE.

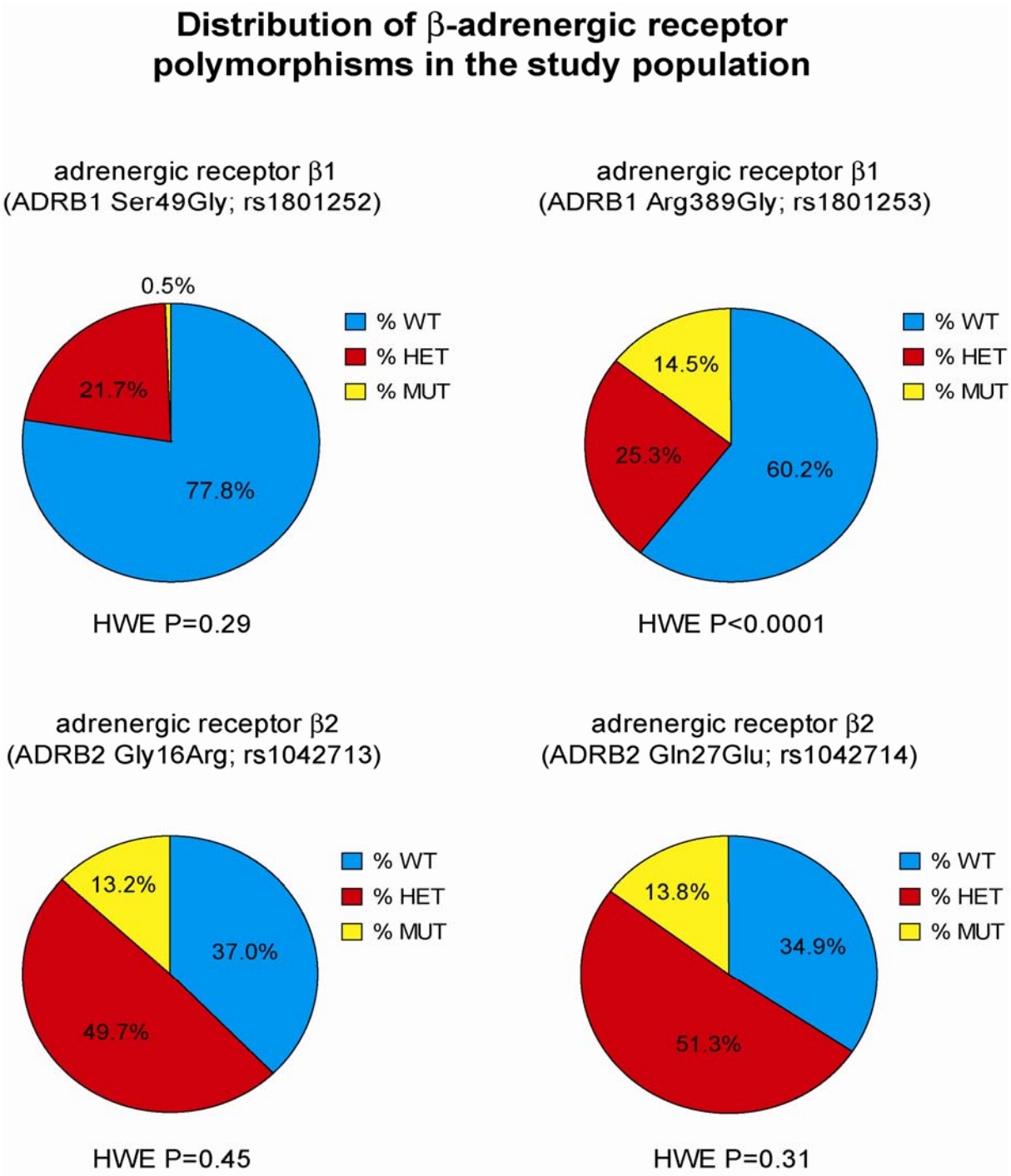

Figure S3: Cardiovascular biomarkers (NT-proBNP = N-terminal brain natriuretic peptide, CKMB = creatine kinase isoform MB, CKtot= creatine kinase total, PAPP-A = pregnancy-associated plasma protein A). Repeated measures analysis-of-variance detected a significant difference in (log-transformed) NT-proBNP values. NS=not significant.

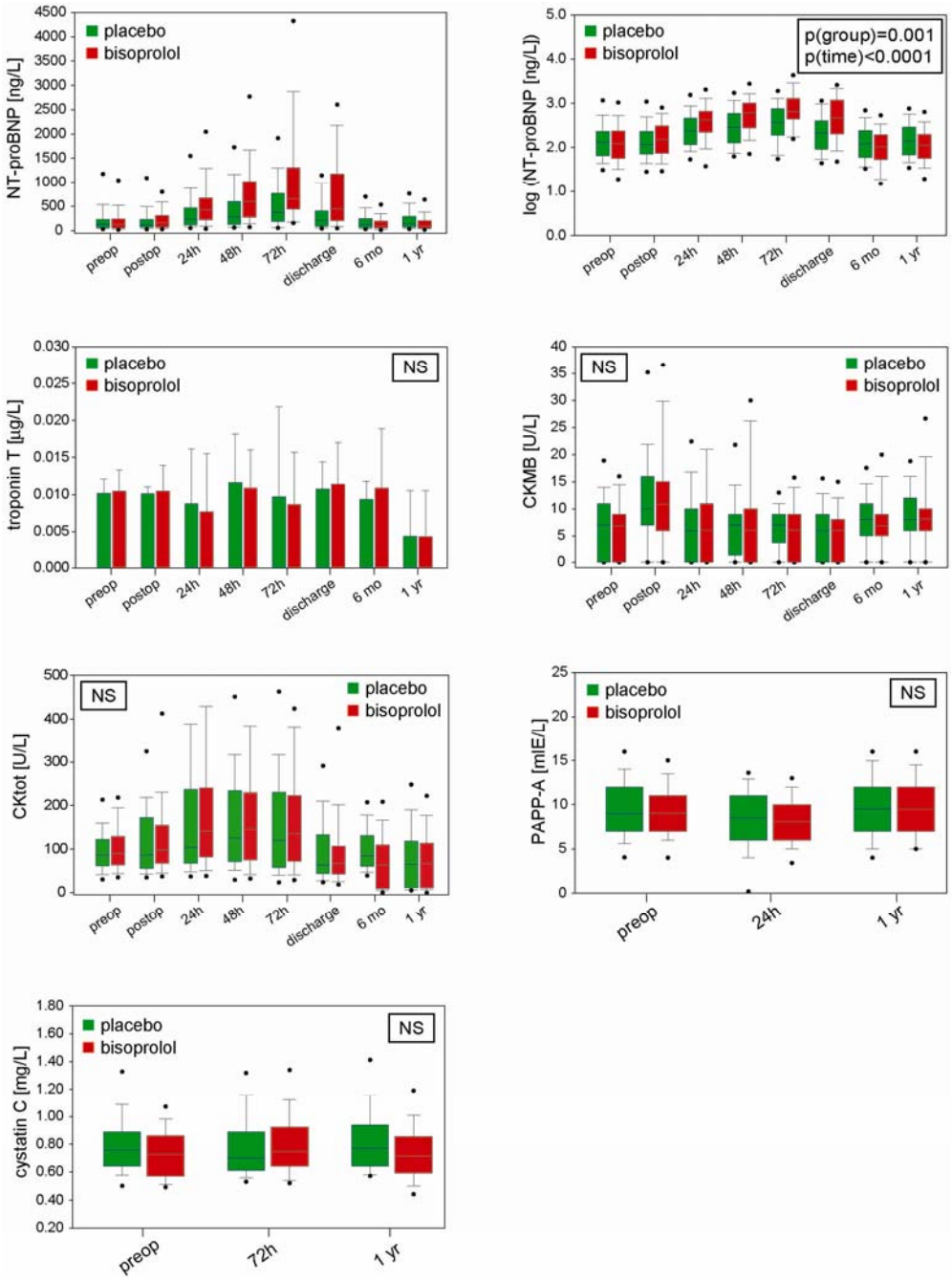

Figure S4: Analysis of Holter electrocardiography recordings in the preoperative period. HR=heart rate; bpm=beats per minute. NS=not significant.

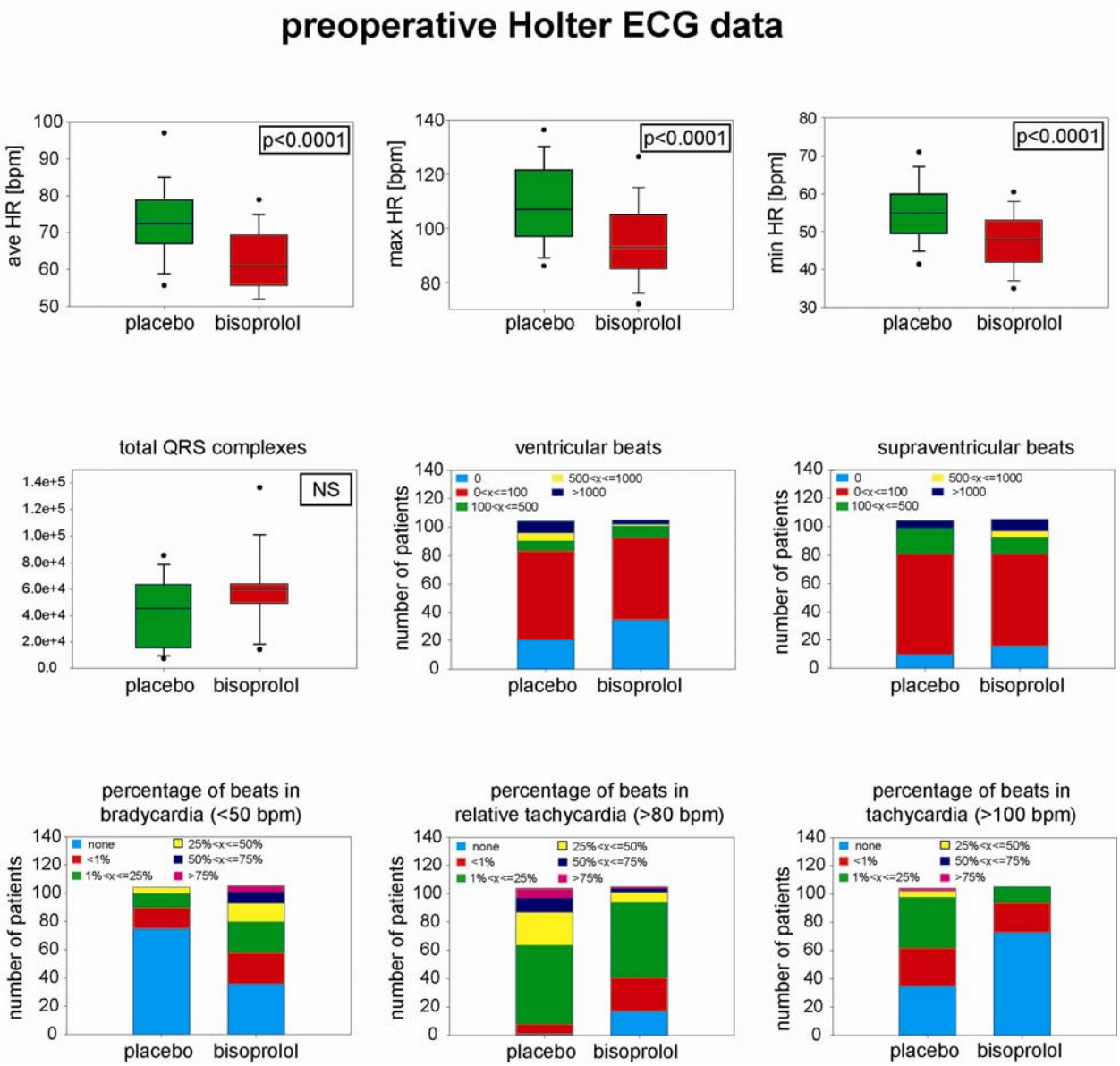

Figure S5: Analysis of Holter electrocardiography recordings in the intraoperative period. HR=heart rate; bpm=beats per minute. NS=not significant.

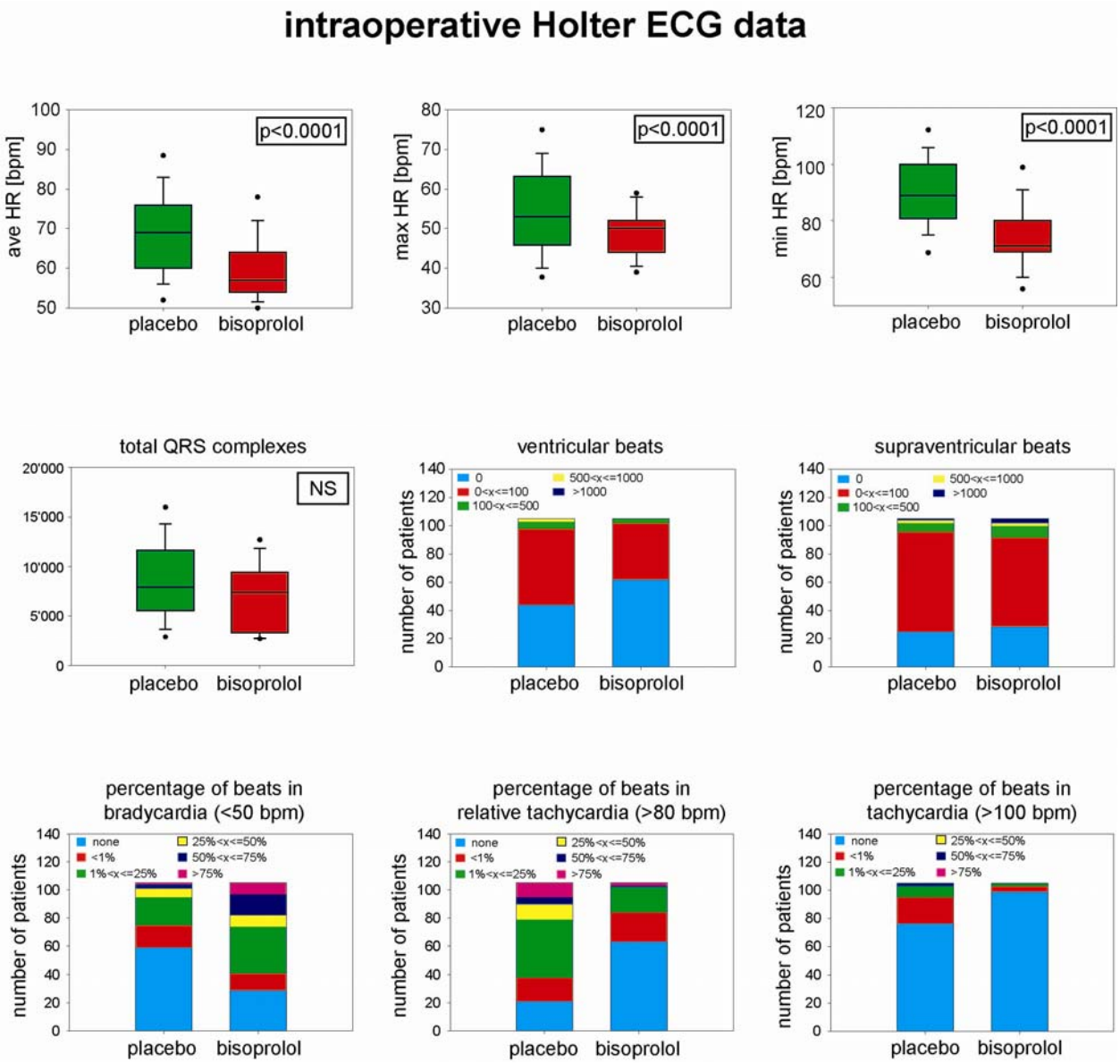

Figure S6: Analysis of Holter electrocardiography recordings in the postoperative period. HR=heart rate; bpm=beats per minute.

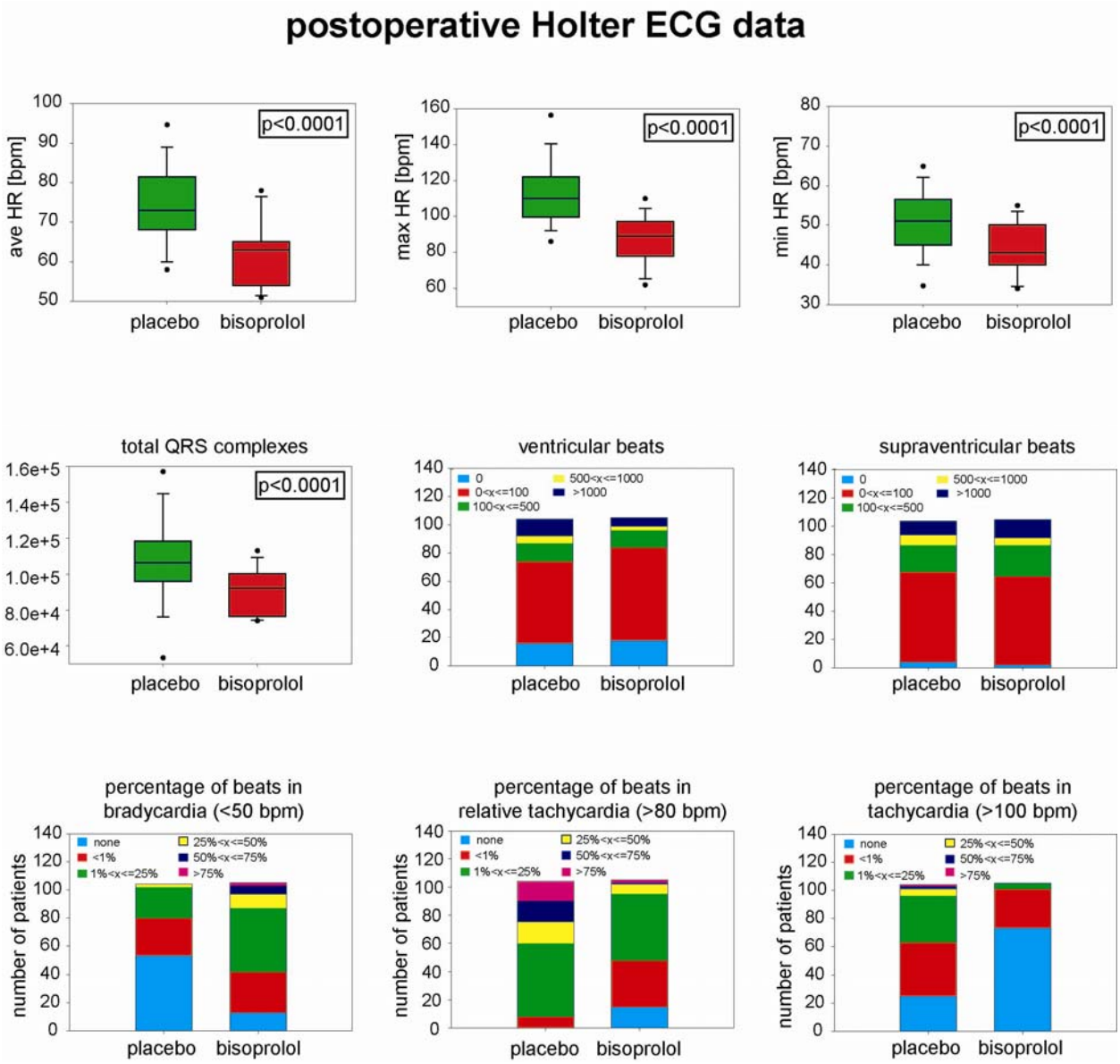

Figure S7: Heart rate and blood pressure after induction of spinal block. Data are presented as mean and standard deviation.

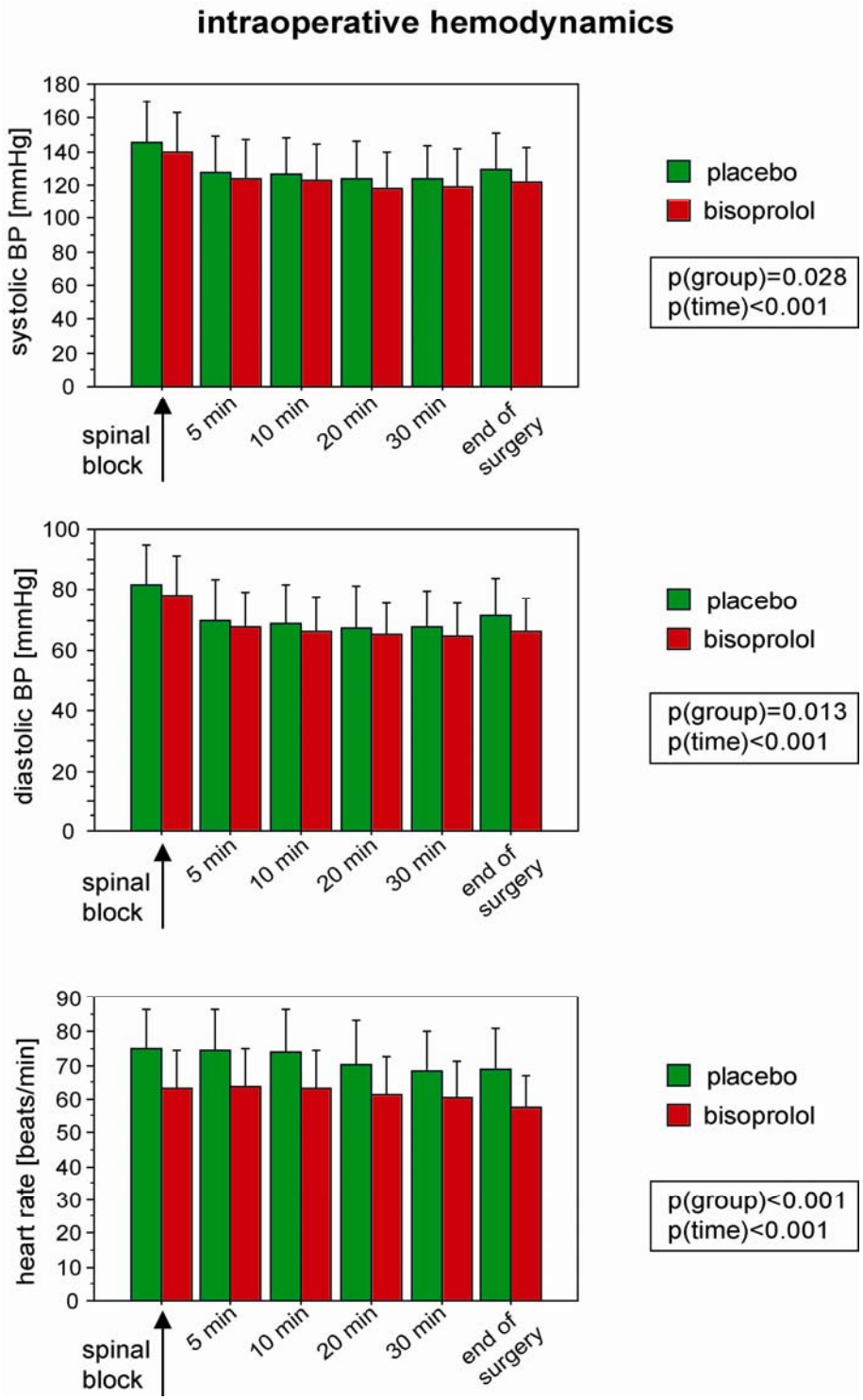

Figure S8: Pulmonary function at baseline related to β_2-adrenergic receptor genotypes. WT=wildtype; HET=heterozygous; MUT=mutant; FEV1=forced expiratory volume in 1 s; peak flow=peak expiratory flow; VC=vital capacity; FVC=forced vital capacity; MEF75=mid-expiratory flow; pred=predicted. No difference between genotypes were found. Dots represent individual patients.

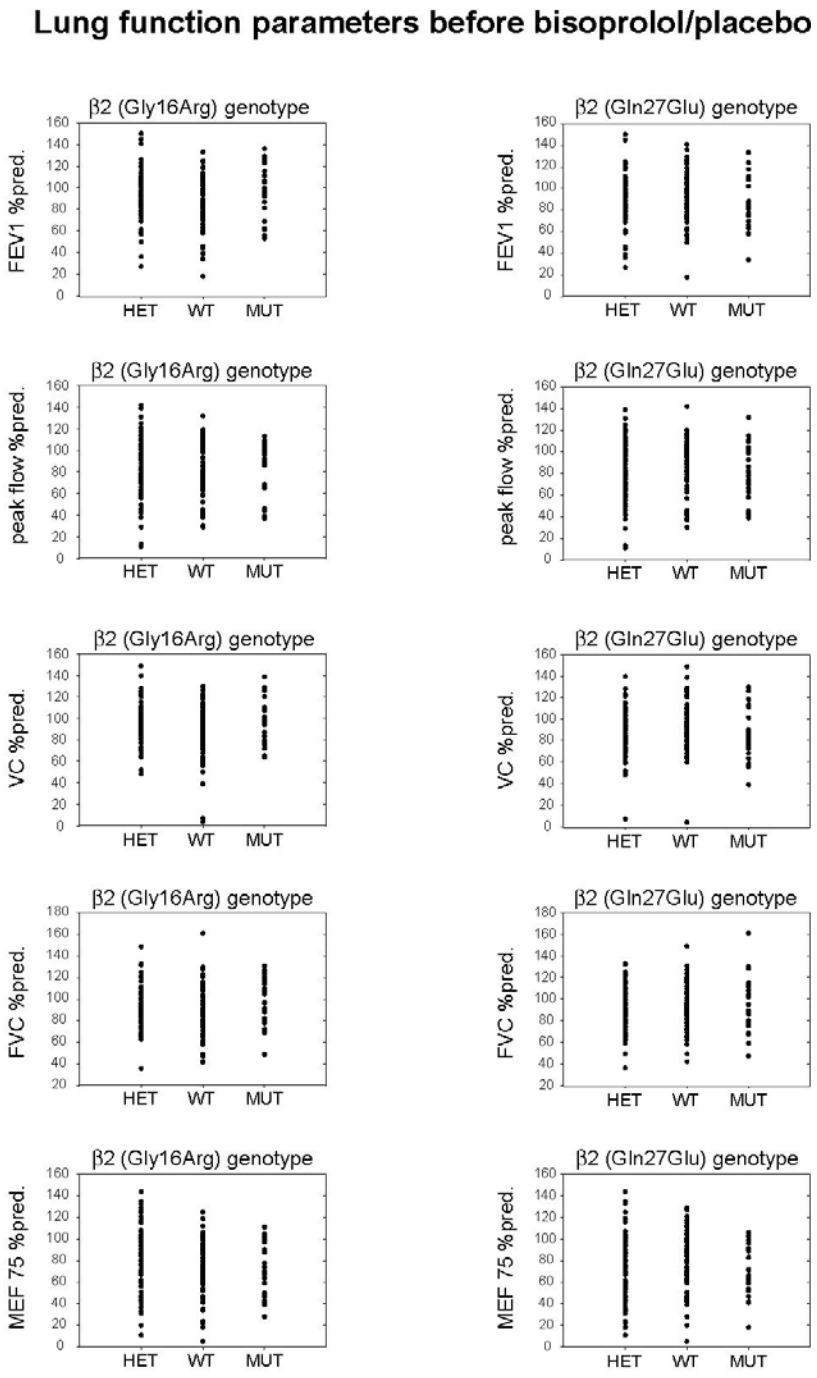

Figure S9: Perioperative changes in pulmonary function and β_2-adrenergic receptor genotypes. WT=wild-type; HET=heterozygous; MUT=mutant; FEV1=forced expiratory volume in 1 s; VC=vital capacity; peak flow=peak expiratory flow; pred=predicted. No difference between genotype and treatment were found. Dots represent individual patients.

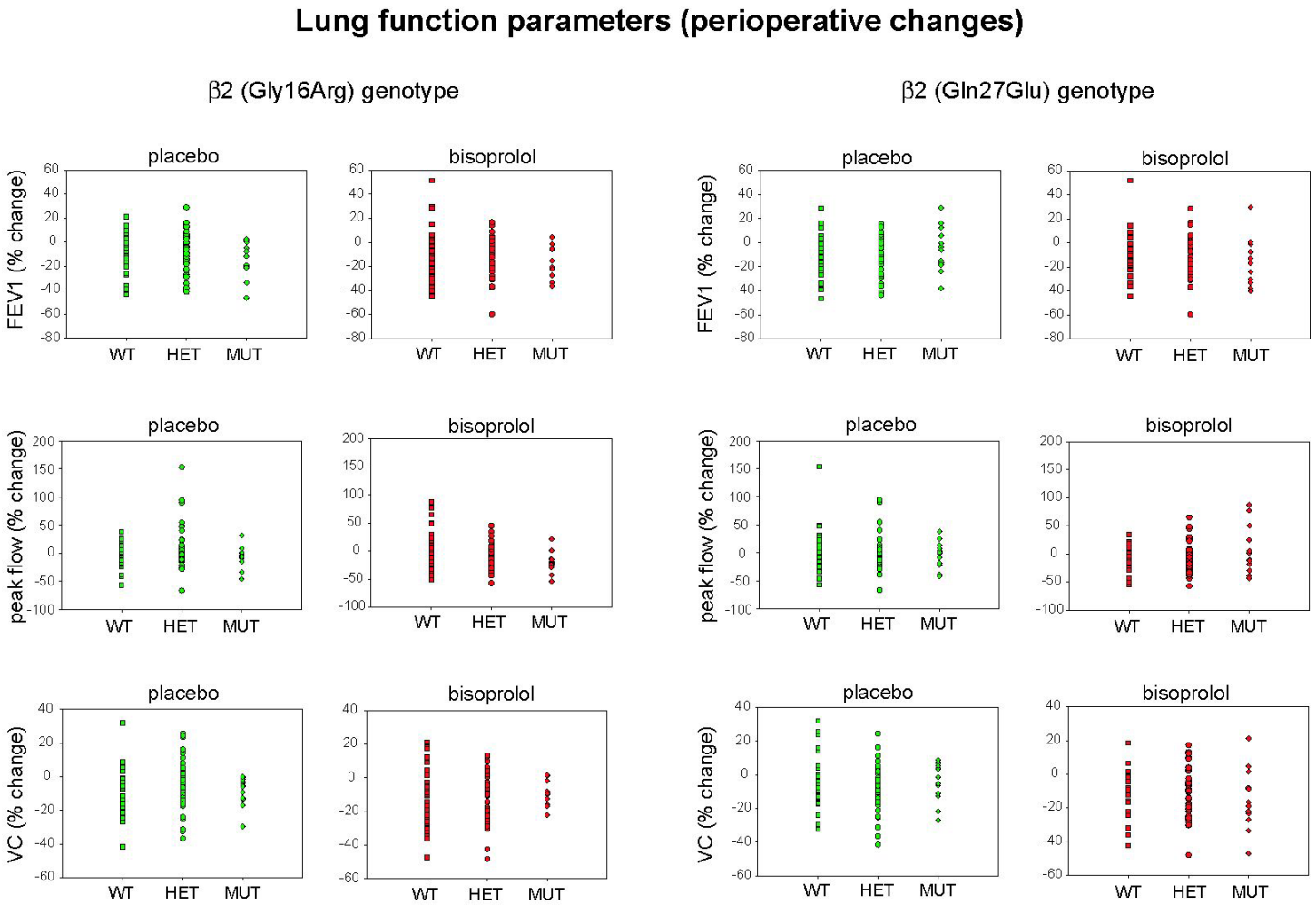

Figure S10: Perioperative changes in pulmonary function and β_2-adrenergic receptor genotypes. WT=wild-type; HET=heterozygous; MUT=mutant; FVC=forced vital capacity; MEF75=mid-expiratory flow; pred=predicted. No difference between genotype and treatment were found. Dots represent individual patients.