

Table 1: Distribution of *HLA-C* rs9264942, *HCP5* rs2395029, and *RNF39/ZNRD1***rs2074479 genotypes**

SNP	Change	Gene	Chr	MAJ	HZ	MIN	ancestral allele	minor allele
rs9264942	T>C	<i>HLA-C</i>	6	164 (49.0%)	139 (41.5%)	32 (9.6%)	69.7%	30.3%
rs2395029	T>G	<i>HCP5</i>	6	315 (94.0%)	20 (6.0%)		97.0%	3.0%
rs2074479	T>C	<i>RNF39/ZNRD1</i>	6	273 (81.5%)	58 (17.3%)	4 (1.2%)	90.1%	9.9%

Chr, chromosome; MAJ, homozygotes for the major allele; HZ, heterozygotes; MIN, homozygotes for the minor allele.

Table 2: Predictive value of *HLA-C* rs9264942 and *HCP5* rs2395029 genotype for progression to AIDS or AIDS-related death in the Amsterdam Cohort Studies on HIV infection and AIDS.

SNP	Comparison	AIDS					AIDS-related death				
		<i>n</i>	Univariate		Multivariate		<i>n</i>	Univariate		Multivariate	
			<i>P</i> value	RH (95% CI)	<i>P</i> value	RH (95% CI)		<i>P</i> -value	RH (95% CI)	<i>P</i> value	RH (95% CI)
rs9264942	MIN+HZ vs. MAJ	335	6.38×10^{-4}	0.80 (0.70-0.91)	6.48×10^{-3}	0.83 (0.73-0.95)	335	2.66×10^{-3}	0.80 (0.69-0.92)	2.03×10^{-2}	0.84 (0.72-0.97)
rs2395029	HZ vs. MAJ	335	4.54×10^{-3}	0.38 (0.20-0.74)	2.06×10^{-2}	0.45 (0.23-0.88)	335	7.55×10^{-3}	0.26 (0.10-0.70)	2.11×10^{-2}	0.31 (0.11-0.84)

CI, confidence interval; MAJ, homozygotes for the major allele; HZ, heterozygotes; MIN, homozygotes for the minor allele; *n*, number of individuals included in analysis; RH, relative hazard; SNP, single-nucleotide polymorphism. *P* value from uni- and multivariate Cox proportional hazard analyses.

Table 3: Predictive value of *HLA-C* rs9264942, *HCP5* rs2395029, and *CCR5* genotype for progression to AIDS or AIDS-related death in the Amsterdam Cohort Studies on HIV infection and AIDS.

SNP	Comparison	AIDS					AIDS-related death				
		<i>n</i>	Univariate		Multivariate		<i>n</i>	Univariate		Multivariate	
			<i>P</i> value	RH (95% CI)	<i>P</i> value	RH (95% CI)		<i>P</i> value	RH (95% CI)	<i>P</i> value	RH (95% CI)
rs9264942	MIN+HZ vs. MAJ	335	6.38 x 10 ⁻⁴	0.80 (0.70-0.91)	1.47 x 10 ⁻²	0.85 (0.75-0.94)	335	2.66 x 10 ⁻³	0.80 (0.69-0.92)	3.32 x 10 ⁻²	0.85 (0.73-0.99)
rs2395029	HZ vs. MAJ	335	4.54 x 10 ⁻³	0.38 (0.20-0.74)	1.33 x 10 ⁻²	0.42 (0.22-0.84)	335	7.55 x 10 ⁻³	0.26 (0.10-0.70)	1.57 x 10 ⁻²	0.29 (0.11-0.79)
CCR5	Δ32 vs. WT	335	1.95 x 10 ⁻⁴	0.52 (0.36-0.73)	2.30 x 10 ⁻⁴	0.52 (0.37-0.74)	335	2.70 x 10 ⁻⁵	0.38 (0.24-0.60)	2.63 x 10 ⁻⁵	0.38 (0.24-0.60)

CI, confidence interval; MAJ, homozygotes for the major allele; HZ, heterozygotes; MIN, homozygotes for the minor allele; *n*, number of individuals included in analysis; RH, relative hazard; SNP, single-nucleotide polymorphism; WT, wild type. *P* value from uni- and multivariate Cox proportional hazard analyses.

Table 4: Predictive value of *HLA-C* rs9264942, *HCP5* rs2395029 genotype, *CCR5* genotype, set point CD4⁺ T-cell count and set point HIV-1 viral load for progression to AIDS or AIDS-related death in the Amsterdam Cohort Studies on HIV infection and AIDS.

SNP	Comparison	AIDS ^a						AIDS-related death ^a					
		Univariate			Multivariate			Univariate			Multivariate		
		<i>n</i>	<i>P</i> value	RH (95% CI)	<i>n</i>	<i>P</i> value	RH (95% CI)	<i>n</i>	<i>P</i> value	RH (95% CI)	<i>n</i>	<i>P</i> value	RH (95% CI)
rs9264942	MIN+HZ vs MAJ	315	1.43 x 10 ⁻³	0.81 (0.71-0.92)	306	2.34 x 10 ⁻¹	0.92 (0.80-1.05)	321	3.29 x 10 ⁻³	0.80 (0.69-0.93)	310	2.95 x 10 ⁻¹	0.92 (0.79-1.07)
rs2395029	HZ vs MAJ	315	5.49 x 10 ⁻³	0.39 (0.20-0.76)	306	1.18 x 10 ⁻¹	0.56 (0.27-1.16)	321	7.79 x 10 ⁻³	0.26 (0.10-0.70)	310	1.87 x 10 ⁻¹	0.51 (0.18-1.39)
CCR5	Δ32 vs WT	315	1.70 x 10 ⁻⁴	0.51 (0.36-0.72)	306	7.08 x 10 ⁻⁴	0.54 (0.38-0.75)	321	2.89 x 10 ⁻⁵	0.38 (0.25-0.60)	310	1.36 x 10 ⁻⁴	0.41 (0.26-0.65)
CD4	>500 cells/μl	307	3.40 x 10 ⁻⁸	0.47 (0.36-0.62)	306	1.75 x 10 ⁻⁵	0.55 (0.42-0.72)	312	4.39 x 10 ⁻⁶	0.49 (0.37-0.67)	310	7.40 x 10 ⁻⁴	0.59 (0.43-0.80)
HIV RNA	<1 x 10 ^{4.5} log cp/ml	312	7.52 x 10 ⁻¹³	0.37 (0.28-0.48)	306	9.06 x 10 ⁻¹⁰	0.41 (0.31-0.55)	318	1.11 x 10 ⁻¹⁶	0.27 (0.19-0.36)	310	3.56 x 10 ⁻¹³	0.30 (0.22-0.42)

CI, confidence interval; MAJ, homozygotes for the major allele; HZ, heterozygotes; MIN, homozygotes for the minor allele; *n*, number of individuals included in analysis; RH, relative hazard; SNP, single-nucleotide polymorphism; WT, wild type. ^a Univariate and multivariate analysis in a model analyzing the time from 2 years after SC until AIDS diagnosis or AIDS-related death. *P* value from uni- and multivariate Cox proportional hazard analyses

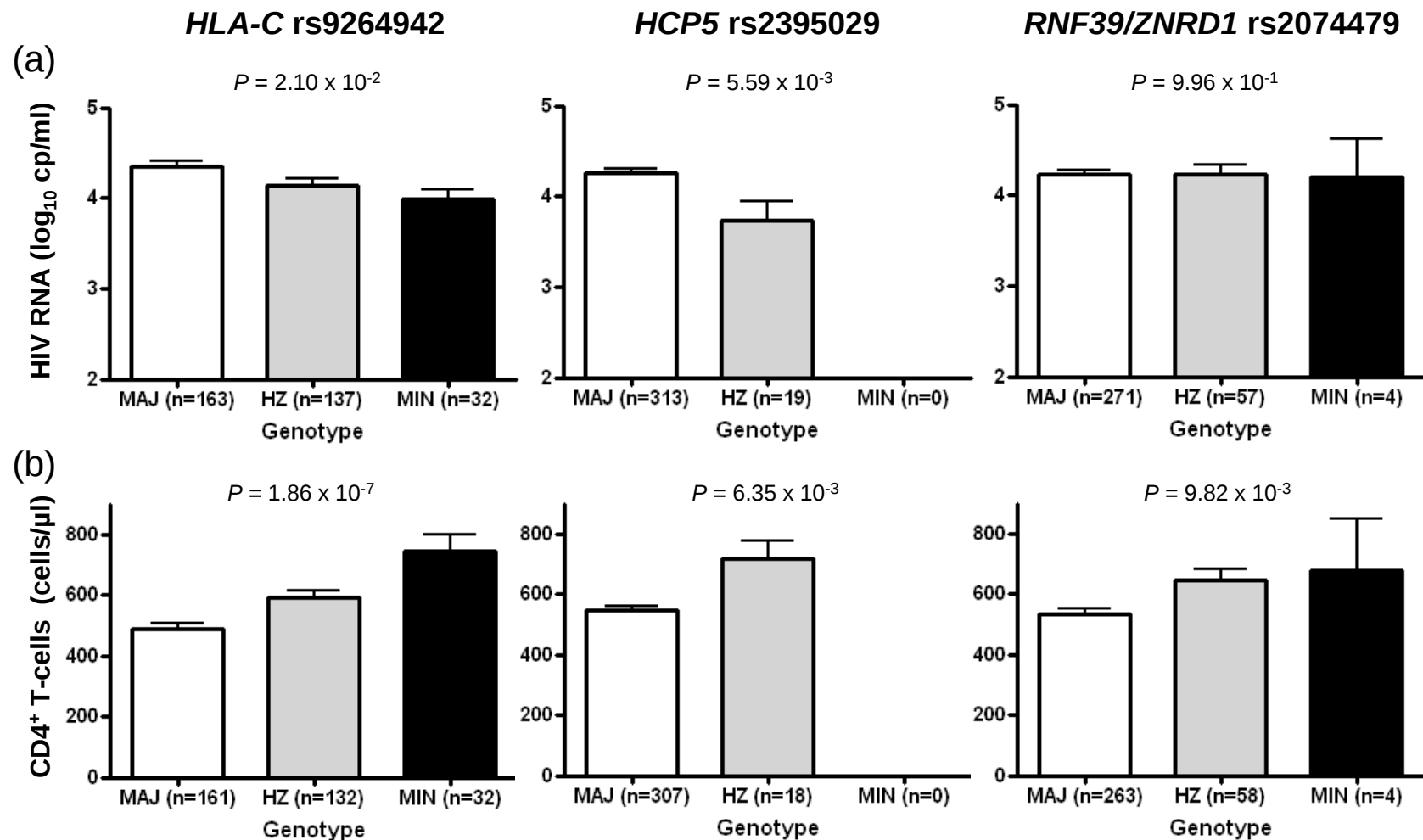


Fig. 1. Set point HIV viral load and set point CD4⁺ T-cell count per genotypic group. (a) HIV viral load at set point is correlated with the HLA-C rs9264942 genotype (left panel), where T is the major allele and C is the minor allele, and with the HCP5 rs2395029 genotype (middle panel), where T is the major allele and G is the minor allele, but not with the RNF39/ZNRD1 rs2074479 genotype (right panel), where T is the major allele and C is the minor allele. (b) CD4⁺ T-cell count at set point is correlated with the HLA-C rs9264942 genotype (left panel), the HCP5 rs2395029 genotype (middle panel), and with the RNF39/ZNRD1 rs2074479 genotype (right panel). Mean and SEM (error bars) are represented for the respective genotypes. Number of participants per genotype is indicated below each bar. MAJ, homozygotes for the major allele; HZ, heterozygotes; MIN, homozygotes for the minor allele. P values for significance are shown above each figure.

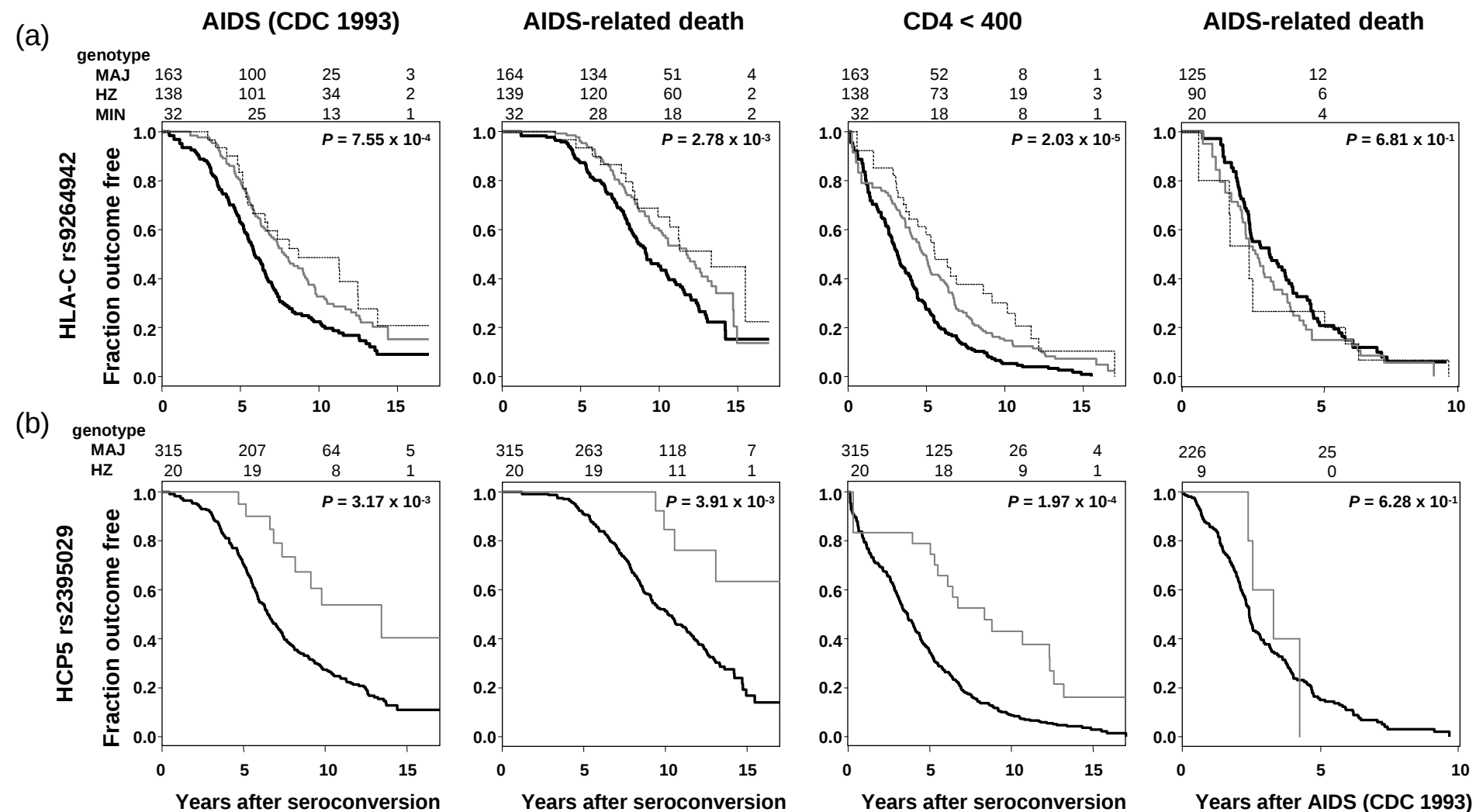


Fig. 2. Kaplan–Meier survival analysis for the HLA-C rs9264942 and HCP5 rs2395029 genotype. Kaplan–Meier survival analysis for time from seroconversion to AIDS (left panel), to AIDS-related death (middle left panel), to CD4⁺ T-cell count below 400 cells/ml blood (middle right panel), and for time from AIDS diagnosis to AIDS-related death (right panel) for HLA-C rs9264942 genotype groups (a) and for HCP5 rs2395029 genotype groups (b). Black lines indicate homozygotes for the major allele (MAJ); gray lines indicate individuals with the heterozygous genotype (HZ); black dashed lines indicate individuals homozygous for the minor allele (MIN). Numbers at the top of each figure represent the number of participants at risk per genotype, per time point. P value from log rank test, as implemented in S-PLUS software, is denoted above each figure.

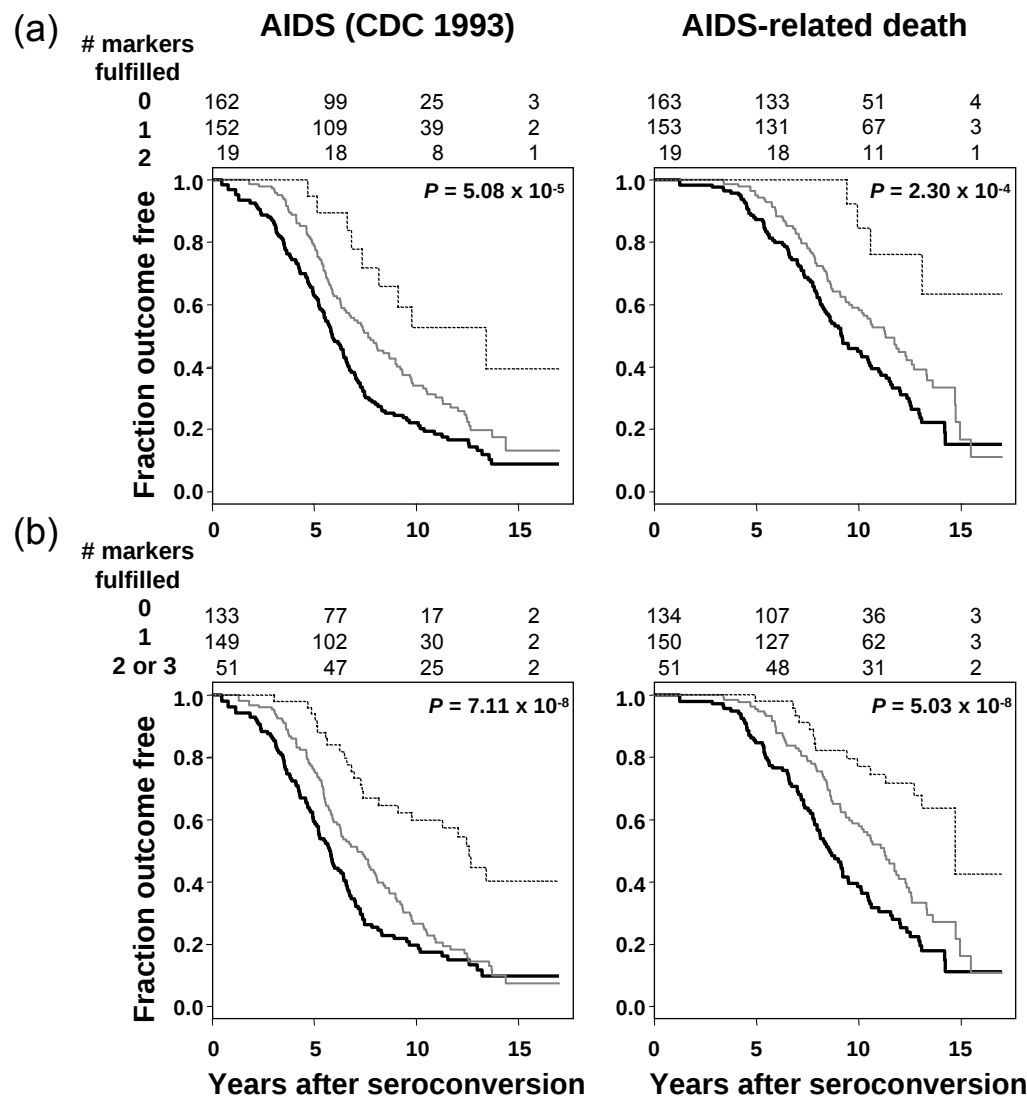


Fig. 3. Cumulative effect of single-nucleotide polymorphism genotypes on time to AIDS or AIDS-related death in the Amsterdam Cohort Studies on HIV infection and AIDS of homosexual men. Kaplan–Meier survival analysis for progression to AIDS (left panel) or AIDS-related death (right panel) with an accumulating number of independent SNP genotypes fulfilled. (a) Absence or presence of any of the protection SNP genotypes: the minor allele of rs9264942 (homozygous and heterozygous genotype) and heterozygous genotype of rs2395029. Three hundred and thirty-five individuals were included in the analysis. Black line indicates 0 progression genotypes fulfilled; gray line indicates one progression genotype fulfilled; black dashed line: two progression genotypes fulfilled. (b) Same as panel (a) but now including the CCR5 Δ 32 heterozygous genotype (relative to a homozygous CCR5 wild-type genotype). Black line indicates 0 progression genotypes fulfilled; gray line indicates one progression genotype fulfilled; black dashed line indicates two or three progression genotypes fulfilled. Numbers at the top of each figure represent the number of participants at risk per group, for different time points. P value from log rank test, as implemented in S-PLUS software, is denoted above each figure.