|  |
| --- |
| Supplementary Table 1. Distribution by cardiological treatment and age in corresponding groups. |
| **Drug**  | **cohort**  | **Treatment status**  | **n**  | **%** | **Mean age (years)**  | **±SD**  |
| **ACEi**  | **CINRG-DNHS**  | **Untreated**  | 1 | 1.49% | 13.87 | NA  |
| **Treated**  | 66 | 98.51% | 17.23 | 6.63 |
| **Italian cohort**  | **Untreated**  | 91 | 45.05% | 6.6 | 3.48 |
| **Treated**  | 111 | 54.95% | 11.84 | 5.55 |
| **Total**  | **Untreated**  | 92 | 34.20% | 6.68 | 3.54 |
| **Treated**  | 177 | 65.80% | 13.85 | 6.51 |
| **BBs**  | **CINRG-DNHS**  | **Untreated**  | 39 | 60% | 14.61 | 6.1 |
| **Treated**  | 26 | 40% | 20.64 | 5.73 |
| **Italian cohort**  | **Untreated**  | 145 | 72.14% | 7.78 | 4.1 |
| **Treated**  | 56 | 27.86% | 14.11 | 5.8 |
| **Total**  | **Untreated**  | 184 | 69.17% | 9.23 | 5.36 |
| **Treated**  | 82 | 30.83% | 16.18 | 6.51 |
| **ACEi BBs**  | **CINRG-DNHS**  | **Untreated**  | 1 | 1.47% | 19.15 | NA  |
| **Treated**  | 67 | 98.53% | 17.18 | 6.59 |
| **Italian cohort**  | **Untreated**  | 144 | 71.29% | 7.59 | 4.1 |
| **Treated**  | 58 | 28.71% | 14.42 | 5.23 |
| **Total**  | **Untreated**  | 145 | 53.70% | 7.67 | 4.19 |
| **Treated**  | 125 | 46.30% | 15.9 | 6.13 |
| SD: Standard Deviation. ACEi: angiotensin converting enzyme inhibitors. BBs: beta blockers. CINRG-DNHS: Cooperative International Neuromuscular Group Duchenne Natural History Study. |

Supplementary Table 2. Coefficients of Univariate Generalized Estimating Equation (GEE) analyses obtained analyses obtained (whole study)

|  |  |  |  |
| --- | --- | --- | --- |
| **Covariate** | **Ejection Fraction (%)** | **Shortening Fraction (%)** | **End Diastolic Volume indexed (mL/m2)** |
| **Estimate** | **SE** | **p-value** | **Estimate** | **SE** | **p-value** | **Estimate** | **SE** | **p-value** |
| **Intercept** | **68.75** | **0.57** | **0** | **38.96** | **0.65** | **0** | **53.4** | **2.96** | **<0.001** |
| **Age (years)** | **-0.80** | **0.03** | **<0.001** | **-0.41** | **0.039** | **<0.001** | **0.42** | **0.16** | **0.06** |
| **On glucocorticoids** | **1.12** | **0.36** | **0.048** | **1.69** | **0.49** | **0.0009** | **2.03** | **2.63** | **n.s.** |
| **Mutation groups by molecular treatment amenability** | **"skip 8" deletions** | **2.70** | **2.47** | **0.08** | **1.42** | **1.96** | **n.s.** | **2.66** | **11.61** | **n.s.** |
| **"skip 44" deletions** | **2.21** | **1.46** | **0.024** | **0.20** | **1.20** | **n.s.** | **-17.64** | **10.25** | **0.008** |
| **"skip 45" deletions** | **0.60** | **1.29** | **n.s.** | **0.98** | **1.13** | **n.s.** | **14.03** | **18.95** | **0.00016** |
| **"skip 51" deletions** | **0.18** | **1.15** | **n.s.** | **-1.39** | **0.97** | **n.s.** | **-4.041** | **6.20** | **n.s.** |
| **"skip 53" deletions** | **-2.58** | **1.25** | **0.041** | **-0.22** | **1.29** | **n.s.** | **8.58** | **5.73** | **n.s.** |
| **Nonsense**  | **-1.50** | **1.34** | **n.s.** | **0.43** | **1.20** | **n.s.** | **3.79** | **6.14** | **n.s.** |
| **Splice site**  | **1.34** | **2.11** | **n.s.** | **-1.48** | **2.88** | **n.s.** | **-1.17** | **7.81** | **n.s.** |
| **Proximal to Dp140 (5’ intron 44)** | **0.10** | **0.75** | **n.s.** | **0.75** | **0.7** | **n.s.** | **2.07** |  **4.26** | **n.s.** |
| **Proximal to Dp116 (5’ intron 55)** | **-3.52** | **1.93** | **0.019** | **-1.3** | **1.70** | **n.s.** | **11.88** | **8.42** | **0.007** |
| **Proximal to Dp71(5’ intron 62)** | **3.68** | **2.62** | **n.s.** | **1.15** | **2.57** | **n.s.** | **-3.97** | **13.31** | **n.s.** |
| **Modifier genotypes** | **SPP1 rs28357094 (dom)** | **-0.40** | **0.79** | **n.s.** | **0.43** | **0.60** | **n.s.** | **-3.85** | **2.92** | **n.s.** |
| **CD40 rs1883832 (add)** | **-0.50** | **0.59** | **n.s.** | **-0.64** | **0.44** | **n.s.** | **1.78** | **2.66** | **n.s.** |
| **LTBP4 rs10880 (rec)** | **1.61** | **1.10** | **n.s.** | **-0.09** | **0.82** | **n.s.** | **-7.19** | **3.78** | **0.016** |
| **IAAM haplotype (rec)** | **0.70** | **1.28** | **n.s.** | **-0.041** | **0.99** | **n.s.** | **-8.61** | **4.21** | **0.010** |

EF: ejection fraction; EDV: end diastolic volume; SF: shortening fraction; SE: Standard Error; skip 8: mutations amenable to treatment with skipping of exon 8 (same for other exon numbers); n.s.: not significant; dom: dominant inheritance model; add: additive inheritance model; rec: recessive inheritance model. Significant p-values (p<0.05) are bold.

Supplementary Table 3 Coefficients of Univariate Generalized Estimating Equation (GEE) analyses obtained from the Italian or the CINRG-DNHS cohort.

|  |  |  |  |
| --- | --- | --- | --- |
| **Covariate** | **Ejection Fraction (%)** | **Shortening Fraction (%)** | **End Diastolic Volume indexed (mL/m2)** |
| **Estimate** | **SE** | **p-value** | **Estimate** | **SE** | **p-value** | **Estimate** | **SE** | **p-value** |
| **Intercept** | **68.12** | **0.64** | **0** | **36.63** | **1.25** | **<0.001** | **53.39** | **2.93** | **<0.001** |
| **Age (years)** | **-0.79** | **0.04** | **<0.001** | **-0.39** | **0.07** | **<0.001** | **0.42** | **0.16** | **0.06** |
| **On glucocorticoids** | **0.22** | **0.22** | **n.s.** | **-0.09** | **0.89** | **n.s.** | **2.03** | **2.63** | **n.s** |
| **"skip44" deletions** | **1.93** | **1.85** | **n.s.** | **0.04** | **2.67** | **n.s.** | **-17.64** | **10.25** | **0.009** |
| **"skip45" deletions** | **0.22** | **1.65** | **n.s.** | **1.28** | **3.31** | **n.s.** | **14.03** | **18.95** | **<0.001** |
| **"skip51" deletions** | **-0.29** | **1.48** | **n.s.** | **-3.55** | **2.58** | **n.s.** | **-4.04** | **6.2** | **n.s.** |
| **"skip53" deletions** | **-3.63** | **1.42** | **0.007** | **-0.97** | **2.27** | **n.s.** | **8.58** | **5.73** | **n.s.** |
| **"skip8" deletions** | **2.7** | **3.31** | **0.059** | **0.86** | **5.34** | **n.s.** | **2.66** | **11.61** | **n.s.** |
| **Nonsense** | **-1.7** | **1.6** | **n.s.** | **-0.18** | **2.13** | **n.s.** | **3.8** | **6.14** | **n.s.** |
| **Splice site mutations** | **1.60** | **2.14** | **n.s.** | **-0.82** | **3.32** | **n.s.** | **-1.74** | **7.81** | **n.s.** |
| **Proximal to Dp140 (5’ intron 44)** | **0.23** | **0.88** | **n.s.** | **1.48** | **1.28** | **n.s.** | **2.08** | **4.26** | **n.s.** |
| **Proximal to Dp116 (5’ intron 55)** | **-5.16** | **2.15** | **0.002** | **-4.44** | **2.6** | **<0.001** | **11.88** | **8.42** | **0.007** |
| **Proximal to Dp71(5’ intron 62)** | **3.69** | **2.96** | **n.s.** | **-2.05** | **4.71** | **n.s.** | **-3.97** | **13.31** | **n.s.** |
| **Modifier genotypes** | **SPP1 rs28357094 (dom)** | **0.67** | **1.02** | **n.s.** | **0.45** | **1.26** | **n.s.** | **-3.85** | **2.93** | **n.s.** |
| **CD40 rs1883832 (add)** | **-0.65** | **0.78** | **n.s.** | **-0.46** | **0.83** | **n.s.** | **1.78** | **2.66** | **n.s.** |
| **LTBP4 rs10880 (rec)** | **1.26** | **1.38** | **n.s.** | **-0.28** | **1.48** | **n.s.** | **-7.2** | **3.78** | **0.016** |
| **IAAM haplotype (rec)** | **0.37** | **1.58** | **n.s.** | **1.13** | **1.86** | **n.s.** | **-8.62** | **4.21** | **0.01** |
| **Intercept** | **70.89** | **1.2** | **0** | **38.49** | **0.76** | **0** | **NA** | **NA** | **NA** |
| **Age (years)** | **-0.87** | **0.07** | **<0.001** | **-0.41** | **0.05** | **<0.001** | **NA** | **NA** | **NA** |
| **On glucocorticoids** | **1.53** | **0.91** | **0.088** | **1.64** | **0.56** | **0.006** | **NA** | **NA** | **NA** |
| **"skip44" deletions** | **2.58** | **2.03** | **0.075** | **0.07** | **1.26** | **n.s.** | **NA** | **NA** | **NA** |
| **"skip45" deletions** | **0.99** | **1.73** | **n.s.** | **0.78** | **1.13** | **n.s.** | **NA** | **NA** | **NA** |
| **"skip51" deletions** | **0.22** | **1.58** | **n.s.** | **-1.20** | **1.00** | **n.s.** | **NA** | **NA** | **NA** |
| **"skip53" deletions** | **2.00** | **2.30** | **n.s.** | **0.39** | **1.53** | **n.s.** | **NA** | **NA** | **NA** |
| **"skip8" deletions** | **1.93** | **3.19** | **n.s.** | **1.12** | **1.97** | **n.s.** | **NA** | **NA** | **NA** |
| **Nonsense** | **-0.37** | **2.23** | **n.s.** | **1.05** | **1.41** | **n.s.** | **NA** | **NA** | **NA** |
| **Splice site mutations** | **NA** | **NA** | **NA** | **NA** | **NA** | **NA** | **NA** | **NA** | **NA** |
| **Proximal to Dp140 (5’ intron 44)** | **0.55** | **1.22** | **n.s.** | **0.84** | **0.80** | **n.s.** | **NA** | **NA** | **NA** |
| **Proximal to Dp116 (5’ intron 55)** | **2.07** | **3.63** | **n.s.** | **1.19** | **2.17** | **n.s.** | **NA** | **NA** | **NA** |
| **Proximal to Dp71(5’ intron 62)** | **3.12** | **4.67** | **n.s.** | **1.42** | **2.97** | **n.s.** | **NA** | **NA** | **NA** |
| **Modifier genotypes** | **SPP1 rs28357094 (dom)** | **-1.00** | **1.11** | **n.s.** | **0.62** | **0.70** | **n.s.** | **NA** | **NA** | **NA** |
| **CD40 rs1883832 (add)** | **0.01** | **0.84** | **n.s.** | **-0.67** | **0.51** | **n.s.** | **NA** | **NA** | **NA** |
| **LTBP4 rs10880 (rec)** |  |  | **n.s.** | **0.16** | **0.97** | **n.s.** | **NA** | **NA** | **NA** |
| **IAAM haplotype (rec)** | **2.01** | **1.98** | **n.s.** | **-0.35** | **1.15** | **n.s.** | **NA** | **NA** | **NA** |

EF: ejection fraction; EDV: end diastolic volume; SF: shortening fraction; SE: Standard Error; skip 8: mutations amenable to treatment with skipping of exon 8 (same for other exon numbers); n.s.: not significant; dom: dominant inheritance model; add: additive inheritance model; rec: recessive inheritance model. Significant p-values (p<0.05) are bold.

Supplementary Table 4. Coefficients of Multivariate Generalized Estimating Equation (GEE) analyses obtained from the Italian or the CINRG-DNHS cohort

|  |  |  |  |
| --- | --- | --- | --- |
| **Covariate** | **Ejection Fraction (%)** | **Shortening Fraction (%)** | **End Diastolic Volume indexed (mL/m2)** |
| **Estimate** | **SE** | **p-value** | **Estimate** | **SE** | **p-value** | **Estimate** | **SE** | **p-value** |
| **Intercept** | 69.08 | 1.73 | <0.001 | 38.11 | 2.48 | <0.001 | 42.45 | 5.15 | <0.001 |
| **Age (years)** | -0.93 | 0.06 | <0.001 | -0.41 | 0.1 | <0.001 | 0.54 | 0.18 | n.s. |
| **On glucocorticoids** | -0.05 | 0.83 | n.s. | 0.89 | 1.44 | n.s. | 2.51 | 2.58 | n.s. |
| **Mutation groups by molecular treatment amenability** | **"skip 8" deletions** | 5.09 | 5.25 | 0.04 | NA | NA | NA | 6.39 | 11.2 | n.s. |
| **"skip 44" deletions** | 1.58 | 3.12 | n.s. | 3.74 | 5.25 | n.s. | -15.24 | 9.49 | 0.005 |
| **"skip 45" deletions** | 1.75 | 2.97 | n.s. | 6.39 | 4.36 | 0.007 | 18.48 | 17.22 | <0.001 |
| **"skip 51" deletions** | 0.61 | 2.03 | n.s. | 2.2 | 2.27 | n.s. | -2.62 | 6.59 | n.s. |
| **"skip 53" deletions** | 0.76 | 2.43 | n.s. | -0.04 | 2.12 | n.s. | 6.57 | 6.57 | n.s. |
| **Nonsense**  | 0.24 | 2.43 | n.s. | -1.79 | 1.63 | n.s. | 5.41 | 6.23 | n.s. |
| **Splice site**  | 1.28 | 4.03 | n.s. | -5.02 | 4.05 | <0.001 | 0.52 | 7.65 | n.s. |
| **Modifier genotypes** | ***SPP1* rs28357094 (dom)** | 0.43 | 1.42 | n.s. | -1.06 | 1.34 | n.s. | 6.5 | 4.26 | 0.04 |
| ***CD40* rs1883832 (add)** | -1.53 | 1.1 | 0.09 | -1.26 | 1.04 | n.s. | 2.06 | 3.86 | n.s. |
| ***LTBP4* rs10880 (rec)** | 3.47 | 1.92 | 0.02 | 2.94 | 2.14 | n.s. | -9.2 | 6.05 | 0.007 |
| **IAAM haplotype (rec)\*** |  3.42 |  2.21 |  0.06 |  6.82 | 2.14  |  <0.001 | -10.60  | 6.17  |  0.0011 |
| **Intercept** | 69.47 | 1.98 | <0.001 | 37.65 | 1.28 | <0.001 | NA | NA | NA |
| **Age (years)** | -0.8 | 0.09 | <0.001 | -0.43 | 0.06 | <0.001 | NA | NA | NA |
| **On glucocorticoids** | 0.35 | 1.12 | n.s. | 1.68 | 0.7 | 0.03 | NA | NA | NA |
| **Mutation groups by molecular treatment amenability** | **"skip 8" deletions** | 2.06 | 3.49 | n.s. | 0.94 | 2.22 | n.s. | NA | NA | NA |
| **"skip 44" deletions** | 1.74 | 2.04 | n.s. | -0.44 | 1.28 | n.s. | NA | NA | NA |
| **"skip 45" deletions** | 0.39 | 1.82 | n.s. | -0.25 | 1.2 | n.s. | NA | NA | NA |
| **"skip 51" deletions** | -0.84 | 1.67 | n.s. | -1.35 | 1.07 | n.s. | NA | NA | NA |
| **"skip 53" deletions** | 1.05 | 2.43 | n.s. | -0.25 | 1.65 | n.s. | NA | NA | NA |
| **Nonsense**  | -0.23 | 2.28 | n.s. | 0.95 | 1.41 | n.s. | NA | NA | NA |
| **Splice site**  | NA | NA | NA | NA | NA | NA | NA | NA | NA |
| **Modifier genotypes** | ***SPP1* rs28357094 (dom)** | -1.86 | 1.25 | n.s. | -0.01 | 0.81 | n.s. | NA | NA | NA |
| ***CD40* rs1883832 (add)** | 0.97 | 0.91 | n.s. | -0.28 | 0.6 | n.s. | NA | NA | NA |
| ***LTBP4* rs10880 (rec)** | 3.46 | 1.83 | 0.01 | 0.56 | 1.2 | n.s. | NA | NA | NA |
| **IAAM haplotype (rec)\*** | 3.20 | 2.19 | 0.038  |  -0.23 |  1.41 |  n.s. | NA | NA | NA |

\*The values related to this parameter were calculated by substituting rs10880 in the multivariate model

EF: ejection fraction; EDV: end diastolic volume; SF: shortening fraction; SE: Standard Error; skip 8: mutations amenable to treatment with skipping of exon 8 (same for other exon numbers); n.s.: not significant; dom: dominant inheritance model; add: additive inheritance model; rec: recessive inheritance model. Significant p-values (p<0.05) are bold.

Supplementary Table 4. Coefficients of Multivariate Generalized Estimating Equation (GEE) analyses obtained (whole study)

|  |  |  |  |
| --- | --- | --- | --- |
| **Covariate** | **Ejection Fraction (%)** | **Shortening Fraction (%)** | **End Diastolic Volume indexed (mL/m2)** |
| **Estimate** | **SE** | **p-value** | **Estimate** | **SE** | **p-value** | **Estimate** | **SE** | **p-value** |
| **Intercept** | **69.17** | **3.31** | **<0.001** | **37.22** | **2.69** | **<0.001** | **46.34** | **12.07** | **<0.001** |
| **Age (years)** | **-0.89** | **0.05** | **<0.001** | **-0.38** | **0.06** | **<0.001** | **0.56** | **0.17** | **n.s.** |
| **On glucocorticoids** | **0.91** | **0.69** | **n.s.** | **1.59** | **0.65** | **0.03** | **2.85** | **2.42** | **n.s.** |
| **Proximal to Dp140 (5’ intron 44)** | **-0.03** | **1.06** | **n.s.** | **0.99** | **0.71** | **n.s.** | **2.86** | **4.4** | **n.s.** |
| **Proximal to Dp116 (5’ intron 55)** | **-4.14** | **2.59** | **<0.001** | **-0.29** | **1.76** | **n.s.** | **7.53** | **7.98** | **0.08** |
| **Proximal to Dp71(5’ intron 62)** | **4.03** | **4.04** | **n.s.** | **-0.63** | **3.02** | **n.s.** | **-11.01** | **13.71** | **0.03** |
| **Modifier genotypes** | **SPP1 rs28357094 (dom)** | **-0.55** | **1.03** | **n.s.** | **0.2** | **0.73** | **n.s.** | **4.7** | **4.45** | **n.s.** |
| **CD40 rs1883832 (add)** | **-0.37** | **0.78** | **n.s.** | **-0.46** | **0.53** | **n.s.** | **2.98** | **3.98** | **n.s.** |
| **LTBP4 rs10880 (rec)** | **3.29** | **1.44** | **0.0021** | **1.15** | **1.02** | **n.s.** | **-10.62** | **6.13** | **0.008** |
| **IAAM haplotype (rec)\*** | **2.97** | **1.71** | **0.027** | **1.03** | **1.22** | **n.s.** | **-12.36** | **6.38** | **0.0026** |

\*The values related to this parameter were calculated by substituting rs10880 in the multivariate model

EF: ejection fraction; EDV: end diastolic volume; SF: shortening fraction; SE: Standard Error; n.s.: not significant; dom: dominant inheritance model; add: additive inheritance model; rec: recessive inheritance model. Significant p-values (p<0.05) are bold.

Supplementary Table 5. Coefficients of Multivariate Generalized Estimating Equation (GEE) analyses obtained from the Italian or the CINRG-DNHS cohort

|  |  |  |  |
| --- | --- | --- | --- |
| **Covariate** | **Ejection Fraction (%)** | **Shortening Fraction (%)** | **End Diastolic Volume indexed (mL/m2)** |
| **Estimate** | **SE** | **p-value** | **Estimate** | **SE** | **p-value** | **Estimate** | **SE** | **p-value** |
| **Intercept** | **73.21** | **4.2** | **<0.001** | **35.86** | **5.04** | **<0.001** | **46.34** | **12.07** | **<0.001** |
| **Age (years)** | **-0.93** | **0.06** | **<0.001** | **-0.32** | **0.1** | **0.004** | **0.56** | **0.17** | **n.s.** |
| **On glucocorticoids** | **-0.12** | **0.82** | **n.s.** | **1.21** | **1.53** | **n.s.** | **2.85** | **2.42** | **n.s.** |
| **Proximal to Dp140 (5’ intron 44)** | **-0.79** | **1.43** | **n.s.** | **-0.09** | **1.61** | **n.s.** | **2.86** | **4.4** | **n.s.** |
| **Proximal to Dp116 (5’ intron 55)** | **-5.74** | **3.06** | **<0.001** | **-2.93** | **2.88** | **n.s.** | **7.53** | **7.98** | **0.08** |
| **Proximal to Dp71(5’ intron 62)** | **2.12** | **4.93** | **n.s.** | **2.5** | **4.65** | **n.s.** | **-11.01** | **13.71** | **0.03** |
| **Modifier genotypes** | **SPP1 rs28357094 (dom)** | **0.29** | **1.38** | **n.s.** | **0.13** | **1.64** | **n.s.** | **4.7** | **4.45** | **n.s.** |
| **CD40 rs1883832 (add)** | **-1.42** | **1.07** | **n.s.** | **-0.41** | **1.26** | **n.s.** | **2.98** | **3.98** | **n.s.** |
| **LTBP4 rs10880 (rec)** | **3.08** | **1.88** | **n.s.** | **1.82** | **2.78** | **n.s.** | **-10.62** | **6.13** | **0.008** |
| **IAAM haplotype (rec)** | **3.07** | **2.1** | **n.s.** | **6.44** | **2.78** | **0.0069** | **-12.36** | **6.38** | **0.0026** |
| **Intercept** | **66** | **4.53** | **<0.001** | **37.19** | **3.36** | **<0.001** | **NA** | **NA** | **NA** |
| **Age (years)** | **-0.79** | **0.1** | **<0.001** | **-0.38** | **0.07** | **<0.001** | **NA** | **NA** | **NA** |
| **On glucocorticoids** | **0.6** | **1.23** | **n.s.** | **1.68** | **0.75** | **0.038** | **NA** | **NA** | **NA** |
| **Proximal to Dp140 (5’ intron 44)** | **1.33** | **1.31** | **n.s.** | **1.48** | **0.84** | **0.07** | **NA** | **NA** | **NA** |
| **Proximal to Dp116 (5’ intron 55)** | **0.31** | **4.01** | **n.s.** | **1.74** | **2.46** | **0.062** | **NA** | **NA** | **NA** |
| **Proximal to Dp71(5’ intron 62)** | **2.49** | **5.9** | **n.s.** | **-2.62** | **4.04** | **0.013** | **NA** | **NA** | **NA** |
| **Modifier genotypes** | **SPP1 rs28357094 (dom)** | **-1.38** | **1.31** | **n.s.** | **0.18** | **0.85** | **n.s.** | **NA** | **NA** | **NA** |
| **CD40 rs1883832 (add)** | **0.7** | **0.95** | **n.s.** | **-0.5** | **0.61** | **n.s.** | **NA** | **NA** | **NA** |
| **LTBP4 rs10880 (rec)** | **3.59** | **1.82** | **0.007** | **0.76** | **1.18** | **n.s.** | **NA** | **NA** | **NA** |
| **IAAM haplotype (rec)\*** | **3.27** | **2.22** | **0.027** | **0.11** | **1.39** | **n.s.** | **NA** | **NA** | **NA** |

\*The values related to this parameter were calculated by substituting rs10880 in the multivariate model

EF: ejection fraction; EDV: end diastolic volume; SF: shortening fraction; SE: Standard Error; n.s.: not significant; NA: parameters not included in the analyses; dom: dominant inheritance model; add: additive inheritance model; rec: recessive inheritance model. Significant p-values (p<0.05) are bold.