**S2 Table.** Univariate analysis of associations between *CASR* SNP genotypes and aortic and coronary artery calcification in patients without hyperparathyroidism.

|  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- |
|  | **rs115759455** | | | **rs7652589** | | | **rs1501899** | | | **A986S** | | | **R990G** | | | **Q1011E** | | |
|  | **Genotype** | **N** | **Value** | **Genotype** | **N** | **Value** | **Genotype** | **N** | **Value** | **Genotype** | **N** | **Value** | **Genotype** | **N** | **Value** | **Genotype** | **N** | **Value** |
| **Aortic** | **CC** | 182 | 2716 ± 6518 | **GG** | 83 | 2638 ± 7416 | **GG** | 83 | 2731 ± 7420 | **AA** | 150 | 2384 ± 5746 | **RR** | 172 | 2623 ± 6283 | **QQ** | 183 | 2661 ± 6434 |
| **calcification** | **CT** | 13 | 1545 ± 2162 | **GA** | 77 | 3039 ± 5428 | **GA** | 82 | 3170 ± 5904 | **AS** | 42 | 3688 ± 8849 | **RG** | 23 | 2750 ± 6781 | **QE** | 14 | 1992 ± 4236 |
| **(AgS)** | **TT** | 2 | - | **AA** | 37 | 1675 ± 5215 | **AA** | 32 | 884 ± 3179 | **SS** | 5 | 495 ± 524 | **GG** | 2 | - | **EE** | 0 | - |
| **Coronary artery** | **CC** | 181 | 704 ± 1327 | **GG** | 83 | 600 ± 1249 | **GG** | 83 | 642 ± 1287 | **AA** | 149 | 720 ± 1302 | **RR** | 171 | 701 ± 1311 | **QQ** | 182 | 683 ± 1282 |
| **calcification** | **CT** | 13 | 879 ± 1382 | **GA** | 76 | 861 ± 1414 | **GA** | 81 | 866 ± 1424 | **AS** | 42 | 646 ± 1451 | **RG** | 23 | 827 ± 1467 | **QE** | 14 | 1046 ± 1791 |
| **(AgS)** | **TT** | 2 | - | **AA** | 37 | 641 ± 1294 | **AA** | 32 | 486 ± 1118 | **SS** | 5 | 887 ± 919 | **GG** | 2 | - | **EE** | 0 | - |
| **Change in AoC** | **CC** | 134 | 280 ± 1557 | **GG** | 67 | 121 ± 981 | **GG** | 67 | 96 ± 989 | **AA** | 108 | 298 ± 1675 | **RR** | 126 | 227 ± 1487 | **QQ** | 136 | 276 ± 1548 |
| **(AgS)** | **CT** | 11 | 535 ± 1312 | **GA** | 51 | 459 ± 2094 | **GA** | 53 | 625 ± 2245 | **AS** | 34 | 315 ± 1093 | **RG** | 17 | 883 ± 1885 | **QE** | 9 | 650 ± 1386 |
|  | **TT** | 0 | - | **AA** | 27 | 439 ± 1432 | **AA** | 25 | 154 ± 442 | **SS** | 3 | 177 ± 386 | **GG** | 2 | - | **EE** | 0 | - |
| **Change in CAC** | **CC** | 134 | 243 ± 731 | **GG** | 67 | 146 ± 362 | **GG** | 67 | 145 ± 363 | **AA** | 108 | 221 ± 543 | **RR** | 126 | 210 ± 544 | **QQ** | 136 | 236 ± 717 |
| **(AgS)** | **CT** | 11 | 432 ± 823 | **GA** | 51 | 458 ± 1121 | **GA** | 53 | 477 ± 1115 | **AS** | 34 | 294 ± 1071 | **RG** | 17 | 638 ± 1545 | **QE** | 9 | 566 ± 982 |
|  | **TT** | 0 | - | **AA** | 27 | 151 ± 365 | **AA** | 25 | 88 ± 162 | **SS** | 3 | 1117 ± 1781 | **GG** | 2 | - | **EE** | 0 | - |

Patients that had serum PTH concentrations > 6.5 pmol/L (N = 70 patients) were excluded from an analysis of *CASR* SNP genotypes and aortic calcification (AoC) and coronary artery calcification (CAC) scores. AoC and CAC scores are provided at baseline in Agatston units (AgS), and the incremental change in calcification scores observed at the follow-up visit (after a mean period of 4.4 ± 0.3 years) are also provided. Results are shown as mean ± SD; -, indicates values not provided. Individual SNP genotypes that were present in N ≤ 3 individuals were excluded from analysis. The genotypic alleles of the A986S, R990G and Q1011E coding region SNPs are represented by amino acids.