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| **Supplemental Table 1:** HWE equilibrium for the eleven KLOTHO SNPs analyzed |
|  | **Homozygote Reference** | **Heterozygote** | **Homozygote variant** | **p value** |
| **Observed** | **Expected** | **Observed** | **Expected** | **Observed** | **Expected** |
| **rs9536254** | 1846 | 1848 | 326 | 322 | 12 | 14 | 0.557 |
| **rs567170** | 869 | 870.5 | 1019 | 1016 | 296 | 296.5 | 0.891 |
| **rs577912** | 1426 | 1426.2 | 677 | 676.5 | 80 | 80.2 | 0.974 |
| **rs580332** | 900 | 886.8 | 984 | 1010.4 | 301 | 287.8 | 0.222 |
| **rs495392** | 1194 | 1185.9 | 830 | 846.1 | 159 | 150.9 | 0.372 |
| **rs2320762** | 829 | 831.4 | 1037 | 1032.2 | 318 | 320.4 | 0.828 |
| **rs562020** | 980 | 978.2 | 964 | 967.5 | 241 | 239.2 | 0.864 |
| **rs576404** | 863 | 854.8 | 1006 | 1022.5 | 314 | 305.8 | 0.451 |
| **rs385564** | 1089 | 1091.7 | 906 | 900.6 | 183 | 185.7 | 0.778 |
| **rs9536282** | 1220 | 1221.8 | 410 | 406.4 | 32 | 33.8 | 0.718 |
| **rs2283368** | 801 | 800 | 202 | 204 | 14 | 13 | 0.755 |
| Comparison between groups by means of a Chi-squared test  |

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| **Supplemental Table 2:**  Klotho polymorphisms and its relation to CVD, Non CVD, and Any Death |
| **SNP(n)** | **CV Death** | **Non CV Death** | **Any Death** |
| **Hom.Dom** | **Heterz** | **Hom.Rec** | **Total** | **p value** | **Hom.Dom** | **Heterz** | **Hom.Rec** | **Total** | **p value** | **Hom.Dom** | **Heterz** | **Hom.Rec** | **Total** | **p value** |
| **rs9536254**(2184) | 55(3%) | 7(2.1%) | 0(0%) | 62(2.8%) | 0.592 | 1(8.3%) | 18(5.5%) | 89(4.8%) | 108(4.9%) | 0.747 | 144(7.8%) | 25(7.7%) | 1(8.3%) | 170(7.8%) | 0.994 |
| **rs567170**(2183) | 26(3%) | 27(2.6%) | 9(3.1%) | 62(2.8%) | 0.881 | 49(5.6%) | 47(4.6%) | 12(4.1%) | 108(4.9%) | 0.447 | 75(8.6%) | 74(7.3%) | 21(7.1%) | 170(7.8%) | 0.488 |
| **rs577912**(2183) | 42(2.9%) | 20(3%) | 0(0%) | 62(2.8%) | 0.297 | 76(5.3%) | 31(4.6%) | 1(1.3%) | 108(4.9%) | 0.227 | 118(8.3%) | 51(7.5%) | 1 (1.3%) | 170(7.8%) | 0.071 |
| **rs580332**(2185) | 26(2.9%) | 28(2.8%) | 8(2.7%) | 62(2.8%) | 0.978 | 53(5.9%) | 42(4.3%) | 13(4.3%) | 108(4.9%) | 0.233 | 79(8.8%) | 70(7.1%) | 21(7%) | 170(7.8%) | 0.345 |
| **rs495392**(2183) | 40(3.4%) | 19(2.3%) | 3(1.9%) | 62(2.8%) | 0.278 | 60(5%) | 40(4.8%) | 8(5%) | 108(4.9%) | 0.977 | 100(8.4%) | 59(7.1%) | 11(6.9%) | 170(7.8%) | 0.529 |
| **rs2320762**(2184) | 24(2.9%) | 27(2.6%) | 11(3.5%) | 62(2.8%) | 0.719 | 27(3.3%) | 55(5.3%) | 26(8.2%) | 108(4.9%) | **0.002** | 51(6.2%) | 82(7.9%%) | 37(11.6%) | 170(7.8%) | **0.008** |
| **rs562020**(2185) | 28(2.9%) | 31(3.2%) | 3(1.2%) | 62(2.8%) | 0.257 | 52(5.3%) | 49(5.1%) | 7(2.9%) | 108(4.9%) | 0.294 | 80(8.2%) | 80(8.3%) | 10(4.1%) | 170(7.8%) | 0.083 |
| **rs576404**(2183) | 25(2.9%) | 27(2.7%) | 10(3.2%) | 62(2.8%) | 0.890 | 49(5.7%) | 45(4.5%) | 14(4.5%) | 108(4.9%) | 0.445 | 74(8.6%) | 72(7.2%) | 24(7.6%) | 170(7.8%) | 0.519 |
| **rs385564**(2178) | 26(2.4%) | 28(3.1%) | 8(4.4%) | 62(2.8%) | 0.278 | 49(4.5%) | 51(5.6%) | 7(3.8%) | 107(4.9%) | 0.395 | 75(6.9%) | 79(8.7%) | 15(8.2%) | 169(7.8%) | 0.305 |
| **rs9536282**(1662) | 29(2.4%) | 8(2%) | 0(0%) | 37(2.2%) | 0.607 | 51(4.2%) | 16(3.9%) | 1(3.1%) | 68(4.1%) | 0.933 | 8 (6.6%) | 24(5.9%) | 1(3.1%) | 105(6.3%) | 0.664 |
| **rs2283368**(1017) | 27(3.4%) | 7(3.5%) | 0(0%) | 34(3.3%) | 0.781 | 33(4.1%) | 19(9.4%) | 3(21.4%) | 55(5.4%) | **0.000** | 60(7.5%) | 26(12.9%) | 3(21.4%) | 89(8.8%) | **0.013** |

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| **Supplemental Table 3:** Allele frequency in the cohort |
| **rs562020** | GG | 980 | **G** | 0,669 |
| GA | 964 | **A** | 0,33 |
| AA | 241 |   |   |
| **rs2283368** | CC | 14 | **C** | 0,113 |
| CG | 202 | **T** | 0,886 |
| GG | 801 |   |   |
| **rs2320762** | GG | 318 | **G** | 0,383 |
| GT | 1037 | **T** | 0,616 |
| TT | 829 |   |   |

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| **Supplemental Table 4:** Linkage disequilibrium (r2) for the three proposed SNPs ( Control Patients Excluded) |
| **rs562020-rs2283368** | 0.0091 |
| **rs562020-rs2320762** | 0.1078 |
| **rs2283368- rs2320762** | 0.1838 |

Supplemental Figure 1

 

Supplemental Figure 1: Flow diagram of experiment design. From the initial 3,004 volunters, 2,185 were considered for current study. 2184 were genotyped for both, rs562020 and rs2320762 genotypes, and 1,016 were genotyped for the three SNPs.