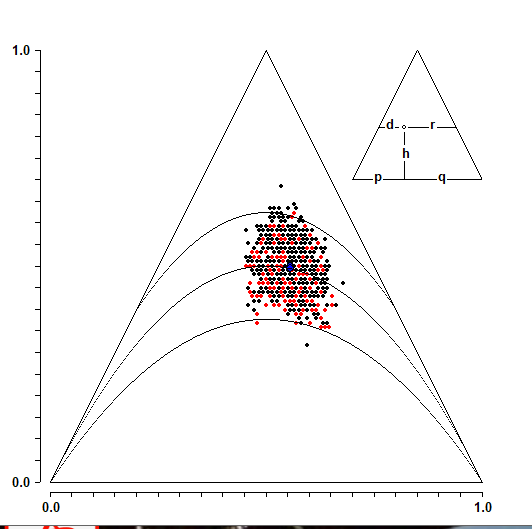
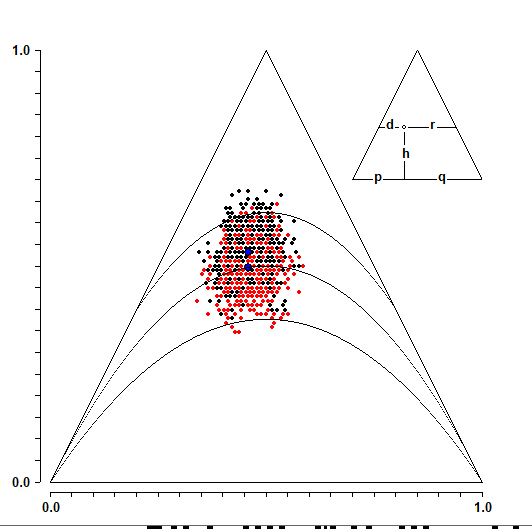
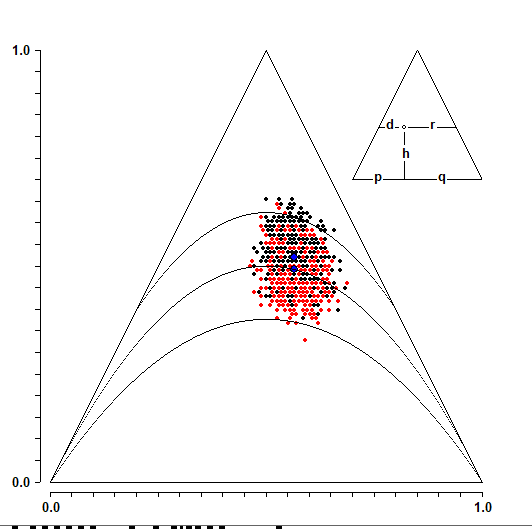
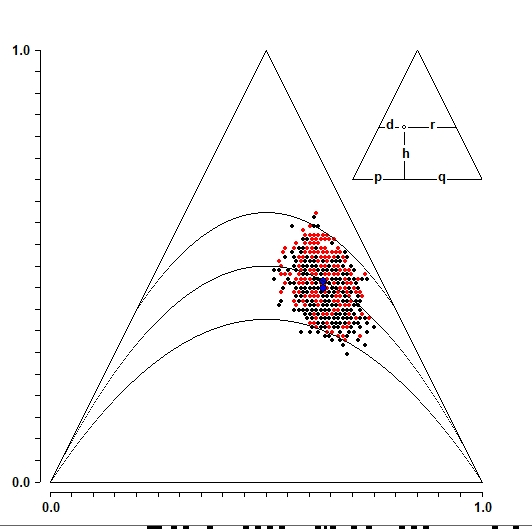
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| --- | --- | --- |
| Supplementary table 1: Primers used for genotype assessment using PCR-HRM | | |
| SNP | Primer Sequences (5’-3’) | Fragment size (bp) |
| *ApaI* | Forward GGGATAGAGAAGAAGGCACAGG  Reverse CTGCCGTTGAGTGTCTGTGTG | 89 |
| *BsmI* | Forward GGAACTAGATAAGCAGGGTTCC  Reverse TAACAGGAATGTTGAGCCCAGT | 99 |
| *FokI* | Forward CTGGCACTGACTCTGGCTCT  Reverse GTCAGGCAGGGAAGTGCTG | 86 |
| *TaqI* | Forward GTGCCCACAGATCGTCCT  Reverse GGATGTACGTCTGCAGTGTGTT | 88 |

|  |  |  |  |  |
| --- | --- | --- | --- | --- |
| Supplementary table 2: PCR-HRM Thermal Cycling Conditions | | | | |
| SNP | *ApaI* | *BsmI* | *FokI* | *TaqI* |
| Holding (temperature/time) | 95oC / 10 min | 95oC / 10 min | 95oC / 10 min | 95oC / 5 min |
| Cycle | 1 | 1 | 1 | 1 |
| PCR amplification (temperature/time) | 95oC / 15 sec  64oC / 15 sec | 95oC / 10 sec  60oC / 30 sec | 95oC / 15 sec  60oC / 30 sec | 95oC / 10 sec  60oC / 30 sec  72oC / 3 sec |
| Cycles | 40 | 35 | 40 | 35 |
| HRM (temperature/time) | 78-88oC   * 1. oC increments   2 sec per step | 77-87oC  0.1 oC increments  2 sec per step | * 1. oC   0.1 oC increments  2 sec per step | * 1. oC   0.1 oC increments  2 sec per step |
| Cycle | 1 | 1 | 1 | 1 |

|  |  |  |
| --- | --- | --- |
| Supplementary table 3: Primers used for Sanger sequencing | | |
| SNP | Primer Sequences (5’-3’) | Fragment size (bp) |
| ApaI / TaqI | Forward AGCAGAGCAGAGTTCCAAGC  Reverse TCGGCTAGCTTCTGGATCAT | 490 |
| BsmI | Forward ACCTGAAGGGAGACGTAGCA  Reverse TCACCTCTAACCAGCGGAAG | 383 |
| FokI | Forward AGCTATGTAGGGCGAATCATGT  Reverse TGCAGCCTTCACAGGTCATAG | 340 |

|  |  |  |  |  |
| --- | --- | --- | --- | --- |
| Supplementary table 4: Hardy-Weinberg calculation of Vitamin D receptor (VDR) polymorphisms based on the Study Participants (N=98). | | | | |
| Variables | p | q | HWE(a) | P (x2 test with Yates' correction) |
| VDR genotypes |  |  |  |  |
| *TaqI* (rs731236) | 0.5533 | 0.4165 | 0.9698 | 0.7017 |
| *Apal* (rs7975232) | 0.5533 | 0.4403 | 0.9936 | 0.9376 |
| *Bsml* (rs1544410) | 0.4403 | 0.5249 | 0.9652 | 0.6361 |
| *FokI* (rs2228570) | 0.6389 | 0.3780 | 1.0168 | 0.9047 |
| a HWE values are expressed as p+q  Analysis was performed with HW\_TEST, Santos, F. A. B., Lemes, R. B., & Otto, P. A. (2020). HW\_TEST, a program for comprehensive HARDY-WEINBERG equilibrium testing. Genetics and Molecular Biology, 43(2). | | | | |



HWE Analysis ApaI

HWE Analysis BsmI

HWE Analysis FokI

HWE Analysis TaqI