**Table S1:** The table reports the GRIK4 genetic variants (start Kb 120150- End Kb 12030) in CEU population with MAF>0.1. Investigated SNPs are marked in red and those found significant in our study are in red bold. For each variant we reported the position, the location and the Regulome score (http://www.regulomedb.org/). All the investigated SNPs are intronic and are not in linkage disequilibrium (LD) with functional variants or regulatory elements in non coding region. Blocks have been generated using Haploviewer 4.2.

|  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- |
|  | | **N** | | **Name** | | **Position** | | **ObsHET** | **PredHET** | | **HWpval** | | **MAF** | | **Alleles** | | **Location** | | | **Regulome Score** | |
|  | | 9 | | rs879602 | | 120161782 | | 0.234 | 0.221 | | 0.6751 | | 0.127 | | T:C | | intron | | | 5 | |
|  | | 10 | | rs7105258 | | 120162254 | | 0.395 | 0.361 | | 0.2609 | | 0.237 | | C:T | | intron | | | 5 | |
| Block2 | | 11 | | rs2155258 | | 120162654 | | 0.517 | 0.464 | | 0.1445 | | 0.366 | | A:G | | intron | | | 5 | |
|  | | 12 | | rs3133861 | | 120164695 | | 0.234 | 0.221 | | 0.6751 | | 0.127 | | G:T | | intron | | | 5 | |
|  | | 13 | | **rs1954787\*** | | 120168573 | | 0.546 | 0.499 | | 0.2306 | | 0.473 | | C:T | | intron | | | 5 | |
|  | | 28 | | rs7121527 | | 120192530 | | 0.502 | 0.492 | | 0.8986 | | 0.437 | | T:C | | intron | | | 5 | |
|  | | 29 | | rs4936553 | | 120193809 | | 0.424 | 0.442 | | 0.6573 | | 0.329 | | G:A | | intron | | | 5 | |
|  | | 30 | | rs4935752 | | 120194329 | | 0.434 | 0.468 | | 0.3584 | | 0.373 | | A:C | | intron | | | 4 | |
|  | | 32 | | rs7940347 | | 120195501 | | 0.488 | 0.485 | | 1 | | 0.415 | | G:T | | intron | | | 5 | |
| Block3 | | 33 | | rs4936554 | | 120196495 | | 0.366 | 0.334 | | 0.2641 | | 0.212 | | C:T | | intron | | | 2b | |
|  | | 35 | | rs7952068 | | 120198343 | | 0.429 | 0.453 | | 0.53 | | 0.346 | | C:G | | intron | | | // | |
|  | | 37 | | rs11218016 | | 120199964 | | 0.444 | 0.399 | | 0.1596 | | 0.276 | | C:T | | intron | | | 5 | |
|  | | 38 | | rs4573685 | | 120201507 | | 0.229 | 0.225 | | 1 | | 0.129 | | G:A | | intron | | | 5 | |
|  | **N** | | **Name** | | **Position** | | **ObsHET** | | **PredHET** | **HWpval** | | **MAF** | | **Alleles** | | **Location** | | | **Regulome Score** | |
|  | 44 | | rs7114615 | | 120209869 | | 0.259 | | 0.253 | 1 | | 0.149 | | G:T | | intron | | | 6 | |
|  | 45 | | rs12226536 | | 120211969 | | 0.424 | | 0.485 | 0.0948 | | 0.412 | | C:G | | intron | | | 4 | |
|  | 46 | | rs3934628 | | 120212854 | | 0.454 | | 0.499 | 0.233 | | 0.476 | | C:T | | intron | | | 5 | |
|  | 48 | | rs7949440 | | 120215525 | | 0.259 | | 0.253 | 1 | | 0.149 | | G:A | | intron | | | 5 | |
|  | 49 | | rs11218025 | | 120215838 | | 0.434 | | 0.483 | 0.1819 | | 0.407 | | T:C | | intron | | | 4 | |
|  | 50 | | rs7110179 | | 120217801 | | 0.288 | | 0.273 | 0.6659 | | 0.163 | | A:G | | intron | | | 5 | |
|  | 52 | | rs9783385 | | 120220884 | | 0.434 | | 0.479 | 0.2182 | | 0.398 | | T:G | | intron | | | // | |
|  | 53 | | rs10892629 | | 120221229 | | 0.356 | | 0.311 | 0.0557 | | 0.193 | | C:T | | intron | | | // | |
|  | 54 | | rs7121233 | | 120222363 | | 0.439 | | 0.482 | 0.2439 | | 0.405 | | T:C | | intron | | | 5 | |
|  | 56 | | **rs11218030\*** | | 120225204 | | 0.278 | | 0.267 | 0.7885 | | 0.159 | | A:G | | intron | | | 5 | |
| Block5 | 57 | | rs11218031 | | 120227667 | | 0.434 | | 0.479 | 0.2182 | | 0.398 | | C:A | | intron | | |  | |
|  | 58 | | rs4430518 | | 120228643 | | 0.356 | | 0.371 | 0.6543 | | 0.246 | | T:G | | intron | | | 5 | |
|  | 59 | | rs6589848 | | 120229228 | | 0.259 | | 0.253 | 1 | | 0.149 | | C:T | | intron | | | 6 | |
|  | 60 | | rs7104543 | | 120229331 | | 0.483 | | 0.492 | 0.8755 | | 0.437 | | A:G | | intron | | | 6 | |
|  | 61 | | rs11218032 | | 120229532 | | 0.439 | | 0.487 | 0.192 | | 0.42 | | T:A | | intron | | | 5 | |
|  | 63 | | rs7342200 | | 120231276 | | 0.434 | | 0.486 | 0.1536 | | 0.417 | | G:A | | intron | | | 4 | |
|  | 64 | | rs7103097 | | 120234037 | | 0.351 | | 0.314 | 0.1387 | | 0.195 | | C:A | | intron | | | 5 | |
|  | 65 | | rs4526780 | | 120235831 | | 0.327 | | 0.293 | 0.1479 | | 0.178 | | G:A | | intron | | | 3a | |
|  | 66 | | rs4414232 | | 120235848 | | 0.488 | | 0.493 | 0.9742 | | 0.439 | | T:C | | intron | | | 4 | |
|  | 67 | | rs3824978 | | 120237718 | | 0.498 | | 0.489 | 0.9326 | | 0.424 | | C:T | | intron | | | 5 | |
|  | 68 | | rs3901285 | | 120238645 | | 0.346 | | 0.371 | 0.4136 | | 0.246 | | C:T | | intron | | | 5 | |
|  | 69 | | rs4569018 | | 120238842 | | 0.493 | | 0.489 | 1 | | 0.427 | | T:C | | intron | | | // | |
|  | 70 | | rs10892631 | | 120239349 | | 0.346 | | 0.366 | 0.5241 | | 0.241 | | G:A | | intron | | | 3a | |
|  | 71 | | rs4344499 | | 120239629 | | 0.346 | | 0.351 | 0.971 | | 0.227 | | T:G | | intron | | | 4 | |
|  | | 90 | | rs2850814 | 120277464 | | 0.293 | | 0.277 | 0.6078 | | 0.166 | | G:A | | intron | | 5 | | |
|  | | 96 | | rs949056 | 120284569 | | 0.376 | | 0.39 | 0.6828 | | 0.266 | | A:G | | intron | | 4 | | |
| Block 7 | | 97 | | rs949055 | 120284730 | | 0.38 | | 0.418 | 0.2485 | | 0.298 | | T:C | | intron | | 4 | | |
|  | | 99 | | rs10892639 | 120285612 | | 0.39 | | 0.422 | 0.3432 | | 0.302 | | A:C | | intron | | 5 | | |
|  | | 101 | | rs2156633 | 120292102 | | 0.371 | | 0.388 | 0.6133 | | 0.263 | | T:C | | intron | | 5 | | |