Supplementary Table 2: Inferred novel *POR* haplotypes in other global superpopulations with core variant(s) alongside *in silico* predictions for each variant. The *POR* variant positions in this table are according to NG\_008930.1 counting from the sequence start, and the protein positions are according to NP\_000932.3.

|  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- |
| Core Variant | Consequence | | | CADD score | Coriell ID |
| [*\*1*+rs145028213~ 75628C>T] | missense (R517C) | | | 29.8 | NA19900 |
| [*\*1*+rs200097755~ 73489C>T] | missense (R301C) | | | 27.3 | HG01530 |
| [*\*28*+rs72557950~ 75950C>T] | missense (R600W) | | | 27.9 | NA19759 |
| [*\*1*+rs545968903~ 75942C>T] | missense (A597V) | | | 26.6 | HG01915 |
| [*\*1*+rs539404456~ 76241C>T] | missense (A635V) | | | 25.2 | HG03851 |
| [*\*28*+rs72557946~ 75493G>C] | missense (V472L) | | | 24.5 | HG01122 |
| [*\*1*+rs562241770~ 73689G>A] | missense (V334I) | | | 24.4 | HG03238, HG03629, HG03767, HG03867, NA21092 |
| [*\*28*+rs200249978~ 74799C>T] | missense (S397L) | | | 23.2 | NA20862 |
| [*\*28*+rs190570042~ 74732A>G] | missense (T375A) | | | 23 | NA19901 |
| [*\*1*+rs148175064~ 76285G>A] | missense (V650M) | | | 23 | HG02307 |
| [*\*28*+rs377159530~ 75592G>A] | missense (E505K) | | | 21.5 | HG03595 |
| [*\*28*+rs72553987~44043\_44045delAAG] | in frame del (KE53K) | | | 21.3 | HG00629 |
| [*\*28*+rs372930296~ 76279G>A] | missense (D648N) | | | 20.2 | HG02307 |
| [*\*28*+rs557324700~ 72142G>A] | missense (V251M) | | | 20.2 | HG03757, HG03937 |
| [*\*1*+rs150949148~ 70385G>A] | missense (A172T) | | | 19.5 | HG00634 |
| [*\*1*+rs370645073~ 75867C>T] | missense (S572L) | | | 19.03 | HG02790, HG03009,HG03781,HG04094 |
| [*\*1*+rs558340290~ 75484C>G] | missense (P469A) | | | 15.34 | NA19795 |
| [*\*1*+rs72557947~ 75532G>A] | missense (A485T) | | | 1.7 | NA18634 |
| [*\*1*+rs574688727~ 76330A>G] | missense (I665V) | | | 0.024 | HG03643 |
| *POR* gene deletion | - | | | - | HG02219 |
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