**Supplementary Table 1: SNP information for 22 SNPs genotyped in both the Western Australian Melanoma Health Study and Genes, Environment and Melanoma Study samples (n=4480)**

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| --- | --- | --- | --- | --- | --- |
| **Chr** | **Gene/Region** | **SNP** | **a/A** | **MAF** | **No. genotyped** |
| **CEUb** | **Sample** |
| 1 | *ARNT* | rs7412746c | C/T | 0.44 | 0.43 | 46 |
| 1 | *NID1* | rs3768080 | G/A | 0.48 | 0.48 | 65 |
| 1 | *PARP1* | rs3219090 | A/G | 0.35 | 0.32 | 84 |
| 5 | *SLC45A2* | rs35391c | T/C | 0.01 | 0.01 | 60 |
| 5 | *TERT;CLPTM1L* | rs4975616 | G/A | 0. 41 | 0.47 | 137 |
| 6 | *IRF4* | rs872071 | A/G | 0.49d | 0.45 | 65 |
| 6 | *IRF4* | rs12203592c | T/C | 0.16 | 0.24 | 37 |
| 9 | *MTAP* | rs7023329 | G/A | 0.49 | 0.46 | 66 |
| 9 | *MTAP* | rs10811629 | G/A | 0.42 | 0.40 | 48 |
| 9 | *TYRP1* | rs1408799c | T/C | 0.33 | 0.30 | 65 |
| 11 | *CCND1* | rs11263498c | T/C | 0.36 | 0.37 | 47 |
| 11 | *TYR* | rs1042602 | A/C | 0.40 | 0.36 | 30 |
| 11 | *TYR* | rs10765198c | C/T | 0.26 | 0.34 | 30 |
| 15 | *OCA2* | rs1800407 | A/G | 0.08 | 0.09 | 33 |
| 15 | *HERC2* | rs1129038 | G/A | 0.23 | 0.22 | 57 |
| 15 | *HERC2* | rs12913832 | A/G | 0.23 | 0.22 | 32 |
| 20 | *ASIP* | rs17305657c | C/T | 0.10 | 0.11 | 58 |
| 20 | *ASIP* | rs4911414c | T/G | 0.33 | 0.38 | 35 |
| 20 | *PIGU* | rs910873 | A/G | 0.09 | 0.12 | 26 |
| 20 | *PIGU* | rs17305573c | C/T | 0.09 | 0.12 | 379 |
| 21 | *MX2* | rs45430 | G/A | 0.34 | 0.36 | 47 |
| 22 | *PLA2G6* | rs132985c | T/C | 0.46 | 0.45 | 40 |
| Abbreviations: Chr: Chromosome; SNP: Single nucleotide polymorphism; a/A: Minor allele/Major allele; MAF: Minor Allele Frequency |
| a Reference allele for each SNP reported using forward strand direction unless otherwise noted (orientation based on dpSNP genome build 150). |
| b MAF calculated from the 1000 Genomes Browser, Phase 3 release. |
| c WAMHS samples genotyped on complementary stand to that reported (i.e. minor allele is the complementary nucleotide base: A=T, G= C). |
| d Opposite allele considered the minor allele in the 1000 Genomes-CEU population for rs872071 (G). |