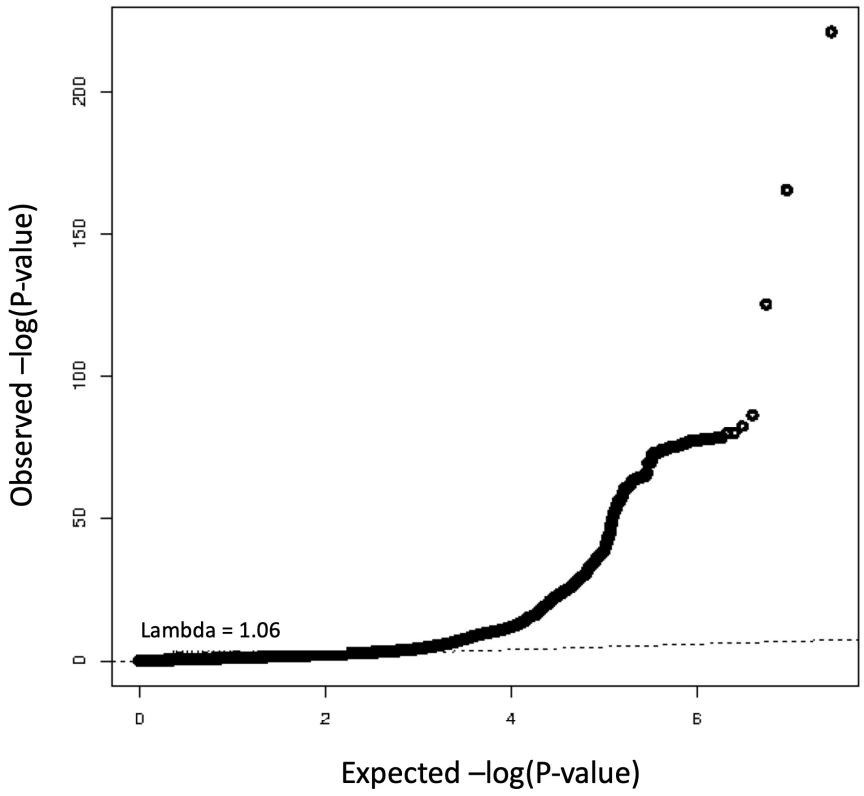
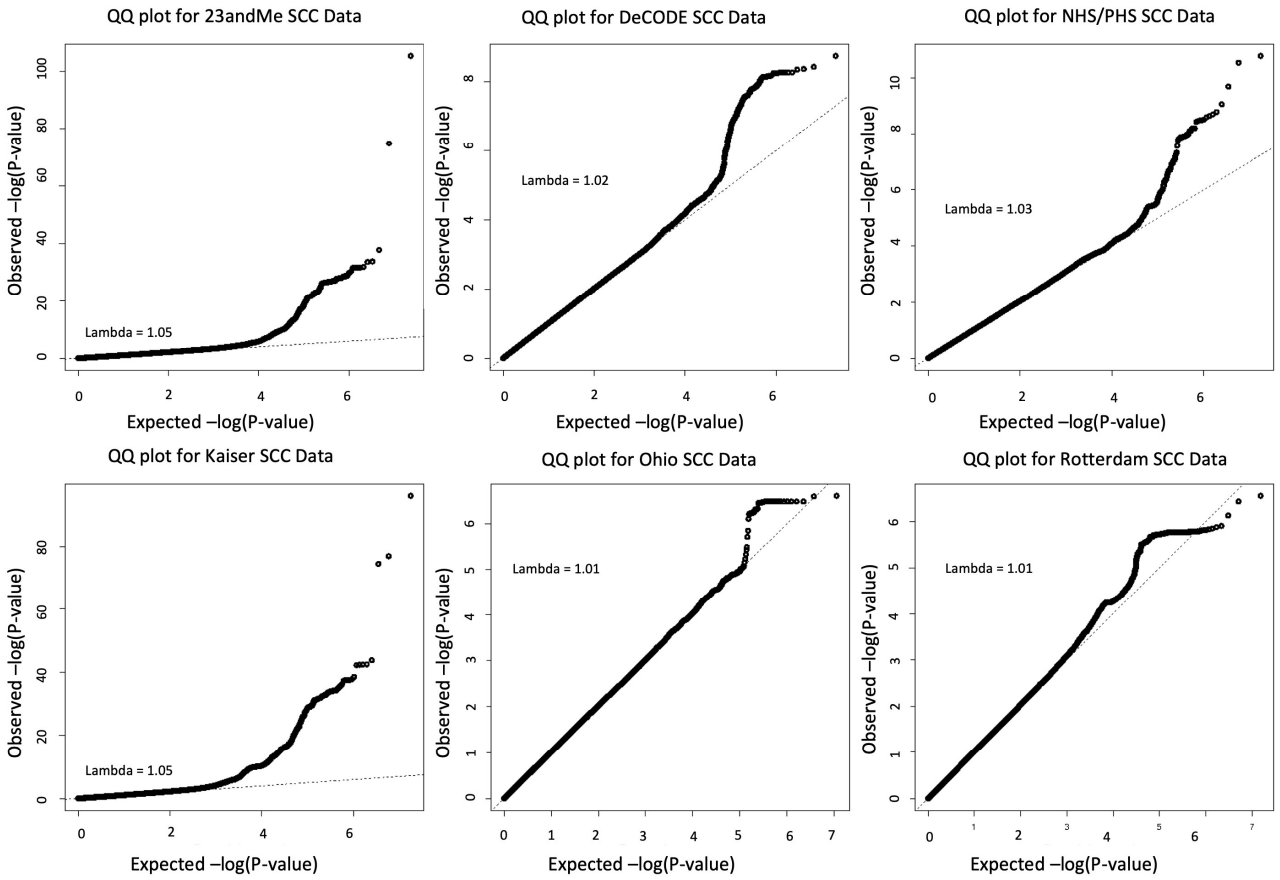
Genome-wide meta-analysis identifies eight new susceptibility loci for cutaneous squamous cell carcinoma

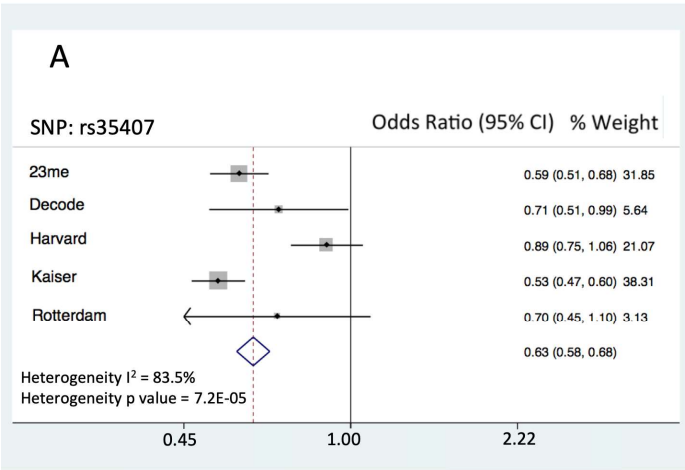
Sarin et al.

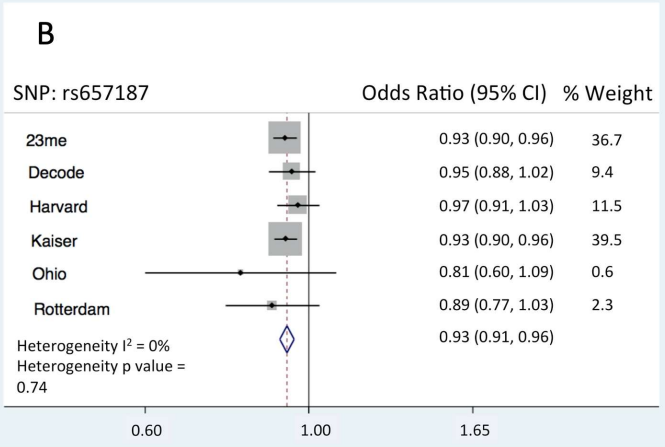


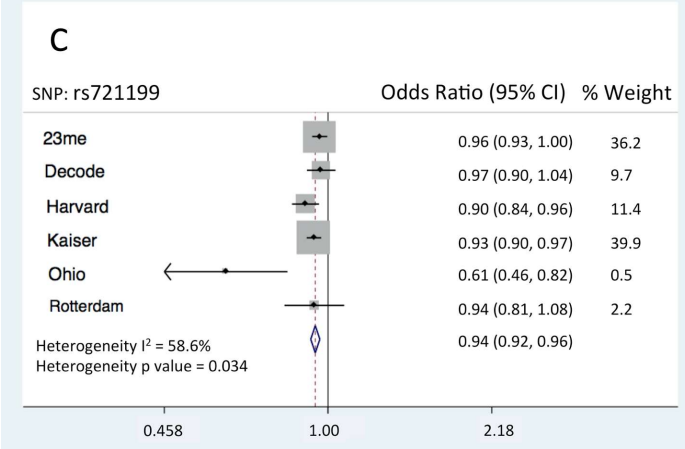
Supplementary Figure 1: QQ plot for SCC Meta-analysis

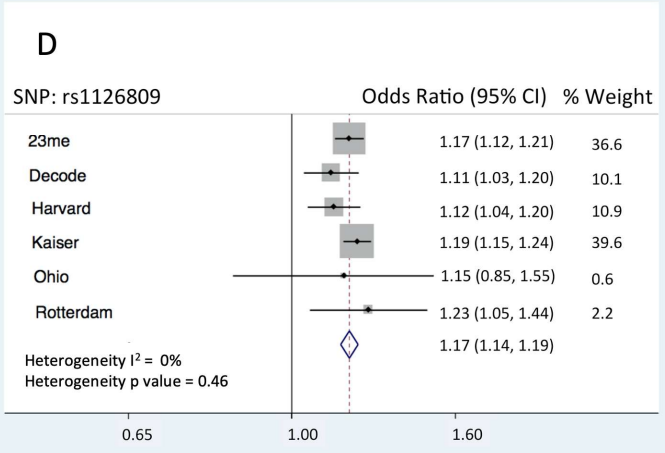


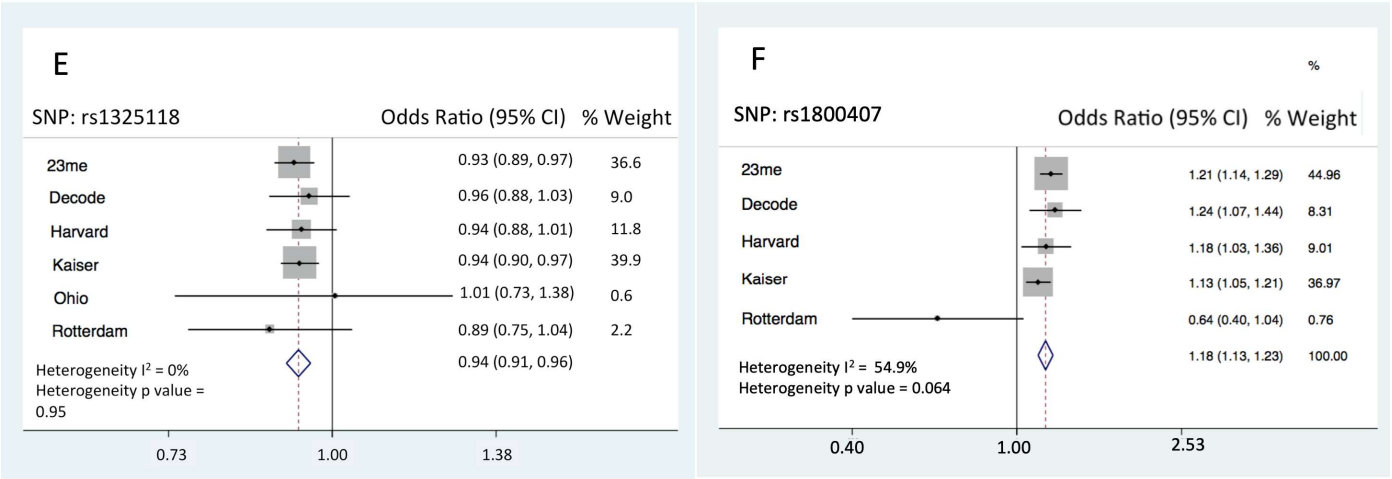
Supplementary Figure 2: QQ plot by individual GWAS study used in meta-analysis

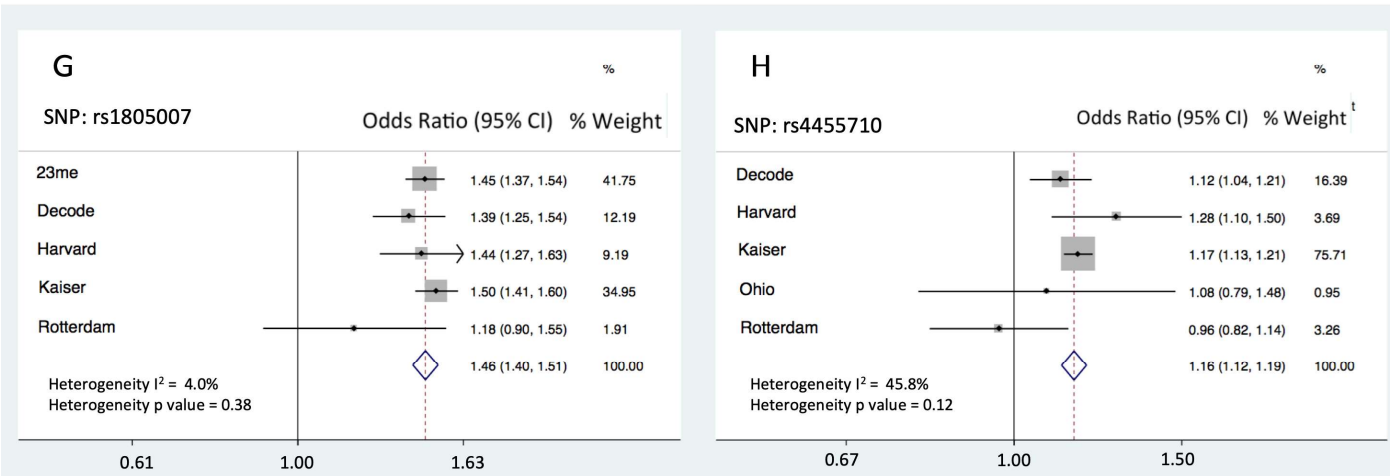

A
SNP: rs35407
Odds Ratio (95% CI) % Weight
23me
Decode
Harvard
Kaiser
Rotterdam
0.59 (0.51, 0.68) 31.85
0.71 (0.51, 0.99) 5.64
0.89 (0.75, 1.06) 21.07
0.53 (0.47, 0.60) 38.31
0.70 (0.45, 1.10) 3.13
0.63 (0.58, 0.68)
Heterogeneity I² = 83.5%
Heterogeneity p value = 7.2E-05
0.45
1.00
2.22

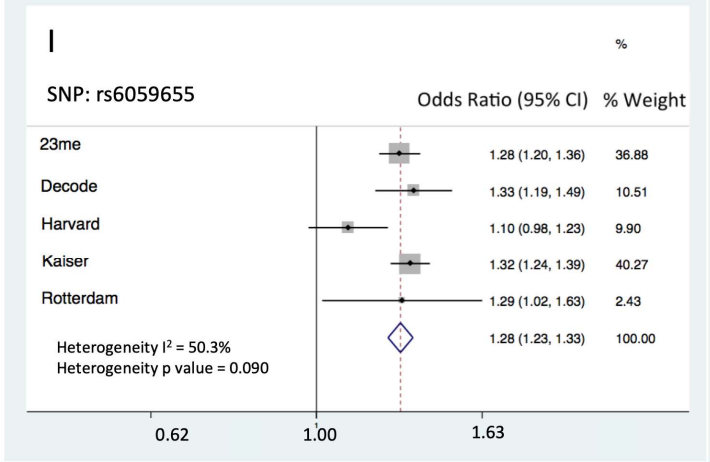

B
SNP: rs657187
Odds Ratio (95% CI) % Weight
23me
Decode
Harvard
Kaiser
Ohio
Rotterdam
0.93 (0.90, 0.96) 36.7
0.95 (0.88, 1.02) 9.4
0.97 (0.91, 1.03) 11.5
0.93 (0.90, 0.96) 39.5
0.81 (0.60, 1.09) 0.6
0.89 (0.77, 1.03) 2.3
0.93 (0.91, 0.96)
Heterogeneity I² = 0%
Heterogeneity p value = 0.74
0.60
1.00
1.65

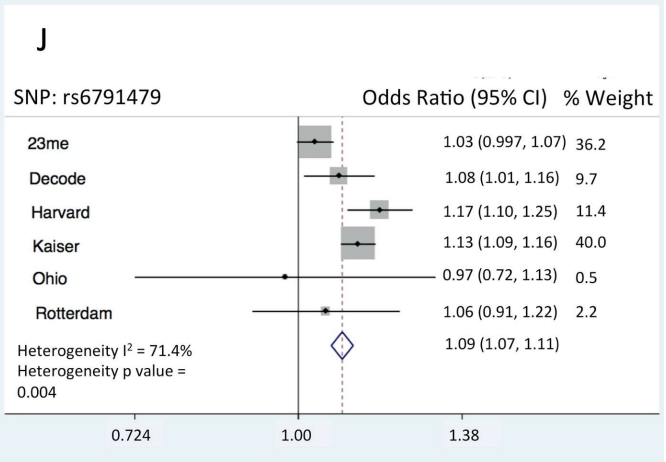

C
SNP: rs721199
Odds Ratio (95% CI) % Weight
23me
Decode
Harvard
Kaiser
Ohio
Rotterdam
0.96 (0.93, 1.00) 36.2
0.97 (0.90, 1.04) 9.7
0.90 (0.84, 0.96) 11.4
0.93 (0.90, 0.97) 39.9
0.61 (0.46, 0.82) 0.5
0.94 (0.81, 1.08) 2.2
0.94 (0.92, 0.96)
Heterogeneity I² = 58.6%
Heterogeneity p value = 0.034
0.458
1.00
2.18

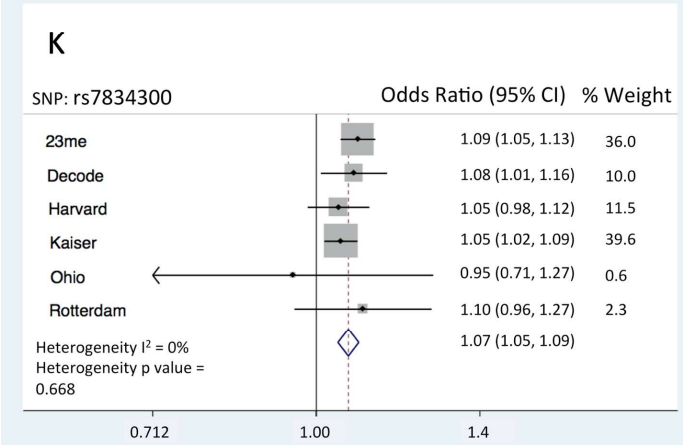

D
SNP: rs1126809
Odds Ratio (95% CI) % Weight
23me
Decode
Harvard
Kaiser
Ohio
Rotterdam
1.17 (1.12, 1.21) 36.6
1.11 (1.03, 1.20) 10.1
1.12 (1.04, 1.20) 10.9
1.19 (1.15, 1.24) 39.6
1.15 (0.85, 1.55) 0.6
1.23 (1.05, 1.44) 2.2
1.17 (1.14, 1.19)
Heterogeneity I² = 0%
Heterogeneity p value = 0.46
0.65
1.00
1.60

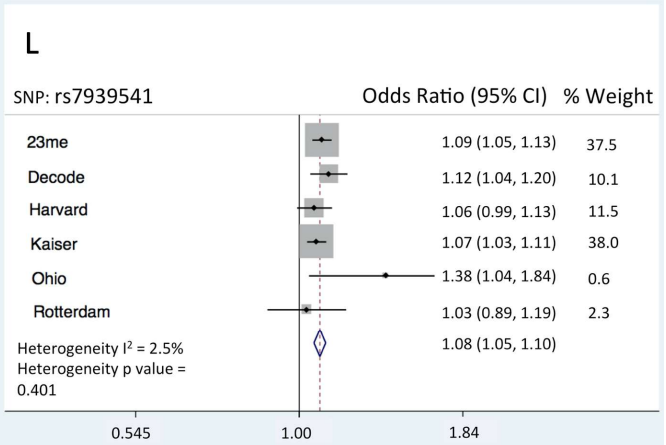

E
SNP: rs1325118
Odds Ratio (95% CI)
% Weight
23me
Decode
Harvard
Kaiser
Ohio
Rotterdam
0.93 (0.89, 0.97)
36.6
0.96 (0.88, 1.03)
9.0
0.94 (0.88, 1.01)
11.8
0.94 (0.90, 0.97)
39.9
1.01 (0.73, 1.38)
0.6
0.89 (0.75, 1.04)
2.2
0.94 (0.91, 0.96)
Heterogeneity I² = 0%
Heterogeneity p value = 0.95
0.73
1.00
1.38
F
%
SNP: rs1800407
Odds Ratio (95% CI)
% Weight
23me
Decode
Harvard
Kaiser
Rotterdam
1.21 (1.14, 1.29)
44.96
1.24 (1.07, 1.44)
8.31
1.18 (1.03, 1.36)
9.01
1.13 (1.05, 1.21)
36.97
0.64 (0.40, 1.04)
0.76
1.18 (1.13, 1.23)
100.00
Heterogeneity I² = 54.9%
Heterogeneity p value = 0.064
0.40
1.00
2.53

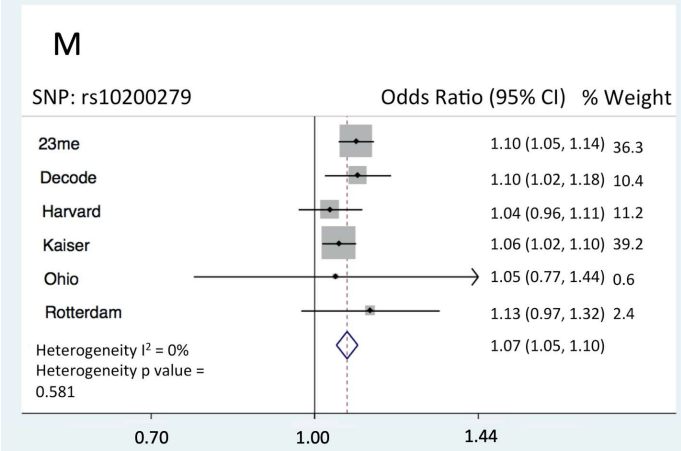

G
%
SNP: rs1805007
Odds Ratio (95% CI)
% Weight
23me
Decode
Harvard
Kaiser
Rotterdam
1.45 (1.37, 1.54)
41.75
1.39 (1.25, 1.54)
12.19
1.44 (1.27, 1.63)
9.19
1.50 (1.41, 1.60)
34.95
1.18 (0.90, 1.55)
1.91
1.46 (1.40, 1.51)
100.00
Heterogeneity I² = 4.0%
Heterogeneity p value = 0.38
0.61
1.00
1.63
H
%
SNP: rs4455710
Odds Ratio (95% CI)
% Weight
Decode
Harvard
Kaiser
Ohio
Rotterdam
1.12 (1.04, 1.21)
16.39
1.28 (1.10, 1.50)
3.69
1.17 (1.13, 1.21)
75.71
1.08 (0.79, 1.48)
0.95
0.96 (0.82, 1.14)
3.26
1.16 (1.12, 1.19)
100.00
Heterogeneity I² = 45.8%
Heterogeneity p value = 0.12
0.67
1.00
1.50

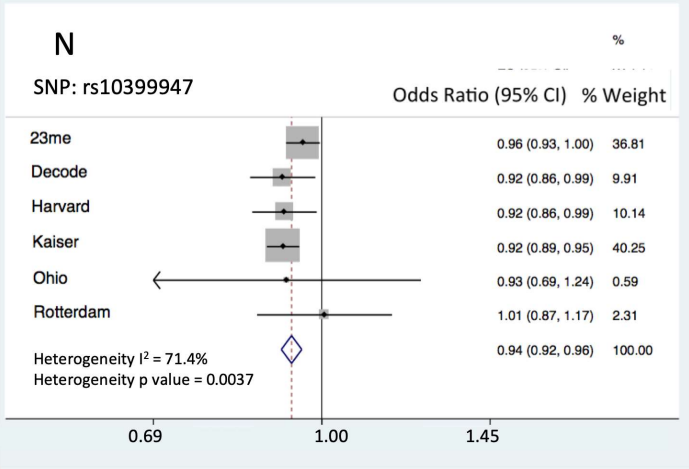

I
SNP: rs6059655
Odds Ratio (95% CI)
% Weight
23me
Decode
Harvard
Kaiser
Rotterdam
1.28 (1.20, 1.36) 36.88
1.33 (1.19, 1.49) 10.51
1.10 (0.98, 1.23) 9.90
1.32 (1.24, 1.39) 40.27
1.29 (1.02, 1.63) 2.43
1.28 (1.23, 1.33) 100.00
Heterogeneity I² = 50.3%
Heterogeneity p value = 0.090
0.62
1.00
1.63

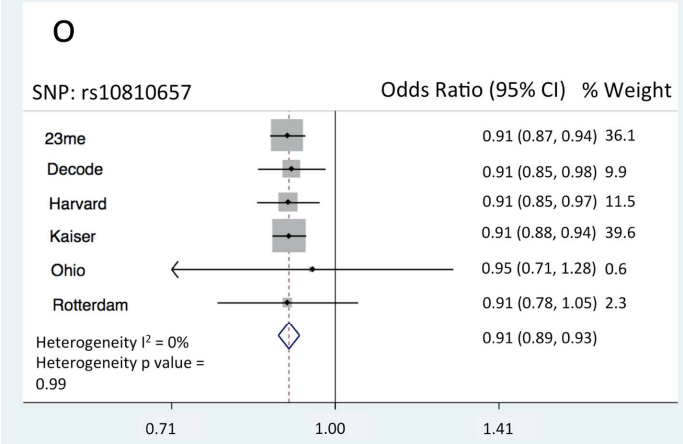

J
SNP: rs6791479
Odds Ratio (95% CI)
% Weight
23me
Decode
Harvard
Kaiser
Ohio
Rotterdam
1.03 (0.997, 1.07) 36.2
1.08 (1.01, 1.16) 9.7
1.17 (1.10, 1.25) 11.4
1.13 (1.09, 1.16) 40.0
0.97 (0.72, 1.13) 0.5
1.06 (0.91, 1.22) 2.2
1.09 (1.07, 1.11)
Heterogeneity I² = 71.4%
Heterogeneity p value = 0.004
0.724
1.00
1.38

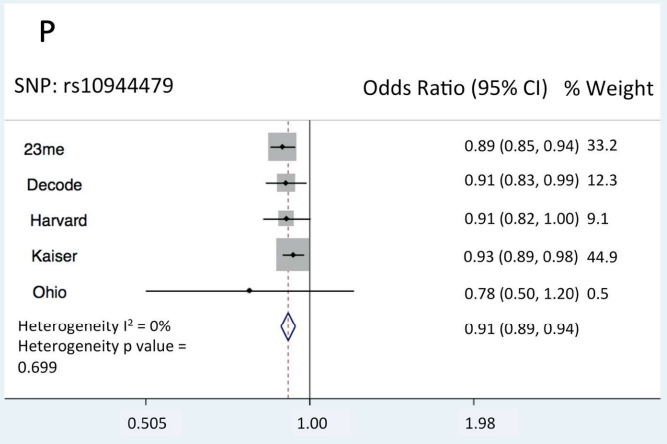

K
SNP: rs7834300
Odds Ratio (95% CI)
% Weight
23me
Decode
Harvard
Kaiser
Ohio
Rotterdam
1.09 (1.05, 1.13) 36.0
1.08 (1.01, 1.16) 10.0
1.05 (0.98, 1.12) 11.5
1.05 (1.02, 1.09) 39.6
0.95 (0.71, 1.27) 0.6
1.10 (0.96, 1.27) 2.3
1.07 (1.05, 1.09)
Heterogeneity I² = 0%
Heterogeneity p value = 0.668
0.712
1.00
1.4

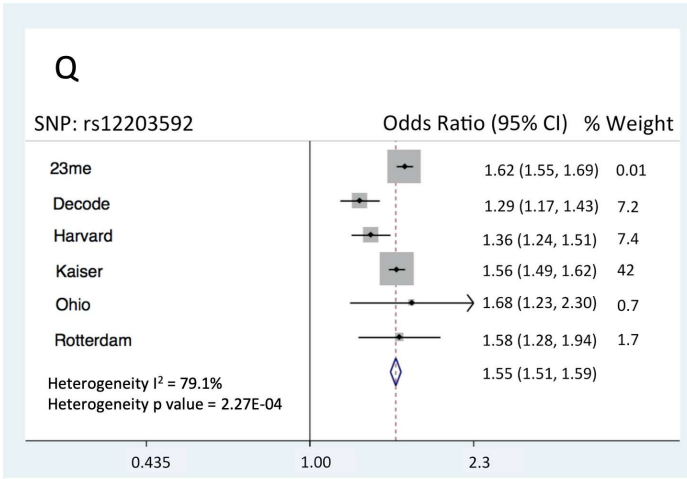

L
SNP: rs7939541
Odds Ratio (95% CI)
% Weight
23me
Decode
Harvard
Kaiser
Ohio
Rotterdam
1.09 (1.05, 1.13) 37.5
1.12 (1.04, 1.20) 10.1
1.06 (0.99, 1.13) 11.5
1.07 (1.03, 1.11) 38.0
1.38 (1.04, 1.84) 0.6
1.03 (0.89, 1.19) 2.3
1.08 (1.05, 1.10)
Heterogeneity I² = 2.5%
Heterogeneity p value = 0.401
0.545
1.00
1.84

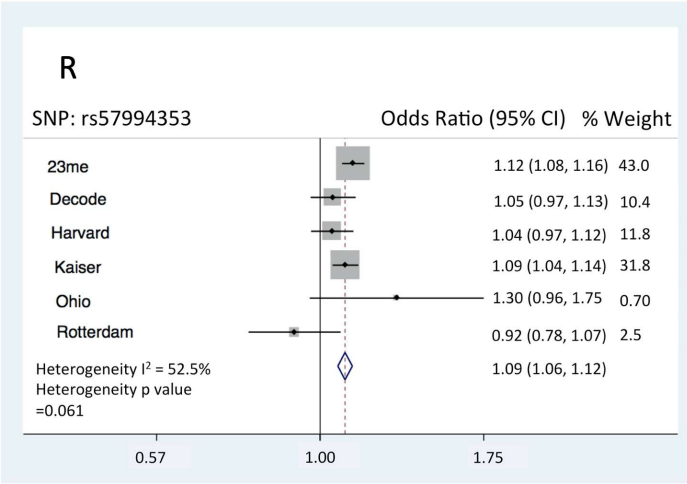

M
SNP: rs10200279
Odds Ratio (95% CI)
% Weight
23me
1.10 (1.05, 1.14) 36.3
Decode
1.10 (1.02, 1.18) 10.4
Harvard
1.04 (0.96, 1.11) 11.2
Kaiser
1.06 (1.02, 1.10) 39.2
Ohio
1.05 (0.77, 1.44) 0.6
Rotterdam
1.13 (0.97, 1.32) 2.4
1.07 (1.05, 1.10)
Heterogeneity I² = 0%
Heterogeneity p value = 0.581
0.70
1.00
1.44

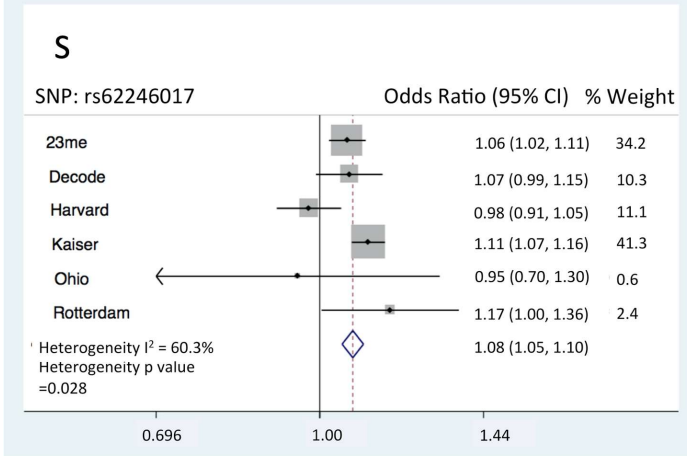

N
%
SNP: rs10399947
Odds Ratio (95% CI)
% Weight
23me
0.96 (0.93, 1.00) 36.81
Decode
0.92 (0.86, 0.99) 9.91
Harvard
0.92 (0.86, 0.99) 10.14
Kaiser
0.92 (0.89, 0.95) 40.25
Ohio
0.93 (0.69, 1.24) 0.59
Rotterdam
1.01 (0.87, 1.17) 2.31
0.94 (0.92, 0.96) 100.00
Heterogeneity I² = 71.4%
Heterogeneity p value = 0.0037
0.69
1.00
1.45

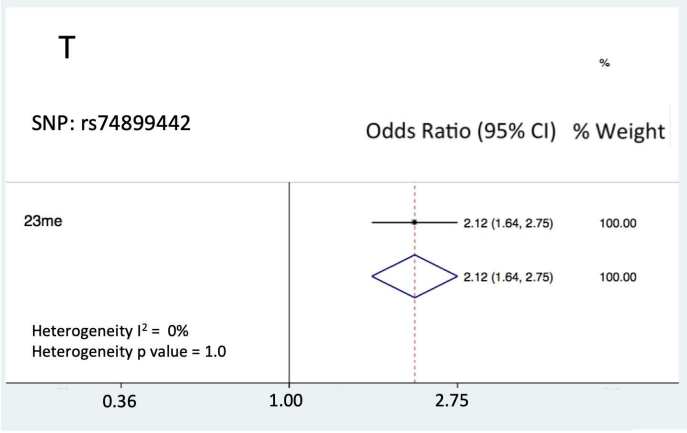

O
SNP: rs10810657
Odds Ratio (95% CI)
% Weight
23me
0.91 (0.87, 0.94) 36.1
Decode
0.91 (0.85, 0.98) 9.9
Harvard
0.91 (0.85, 0.97) 11.5
Kaiser
0.91 (0.88, 0.94) 39.6
Ohio
0.95 (0.71, 1.28) 0.6
Rotterdam
0.91 (0.78, 1.05) 2.3
0.91 (0.89, 0.93)
Heterogeneity I² = 0%
Heterogeneity p value = 0.99
0.71
1.00
1.41

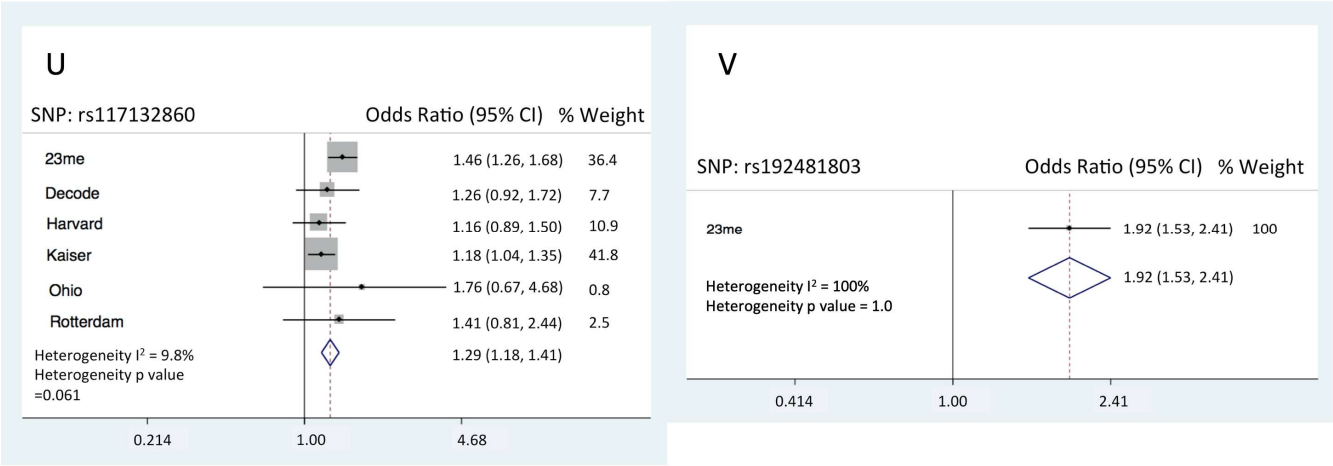

P
SNP: rs10944479
Odds Ratio (95% CI)
% Weight
23me
0.89 (0.85, 0.94) 33.2
Decode
0.91 (0.83, 0.99) 12.3
Harvard
0.91 (0.82, 1.00) 9.1
Kaiser
0.93 (0.89, 0.98) 44.9
Ohio
0.78 (0.50, 1.20) 0.5
0.91 (0.89, 0.94)
Heterogeneity I² = 0%
Heterogeneity p value = 0.699
0.505
1.00
1.98


Q
SNP: rs12203592
Odds Ratio (95% CI)
% Weight
23me
1.62 (1.55, 1.69)
0.01
Decode
1.29 (1.17, 1.43)
7.2
Harvard
1.36 (1.24, 1.51)
7.4
Kaiser
1.56 (1.49, 1.62)
42
Ohio
1.68 (1.23, 2.30)
0.7
Rotterdam
1.58 (1.28, 1.94)
1.7
1.55 (1.51, 1.59)
Heterogeneity I² = 79.1%
Heterogeneity p value = 2.27E-04
0.435
1.00
2.3


R
SNP: rs57994353
Odds Ratio (95% CI)
% Weight
23me
1.12 (1.08, 1.16)
43.0
Decode
1.05 (0.97, 1.13)
10.4
Harvard
1.04 (0.97, 1.12)
11.8
Kaiser
1.09 (1.04, 1.14)
31.8
Ohio
1.30 (0.96, 1.75
0.70
Rotterdam
0.92 (0.78, 1.07)
2.5
1.09 (1.06, 1.12)
Heterogeneity I² = 52.5%
Heterogeneity p value
=0.061
0.57
1.00
1.75

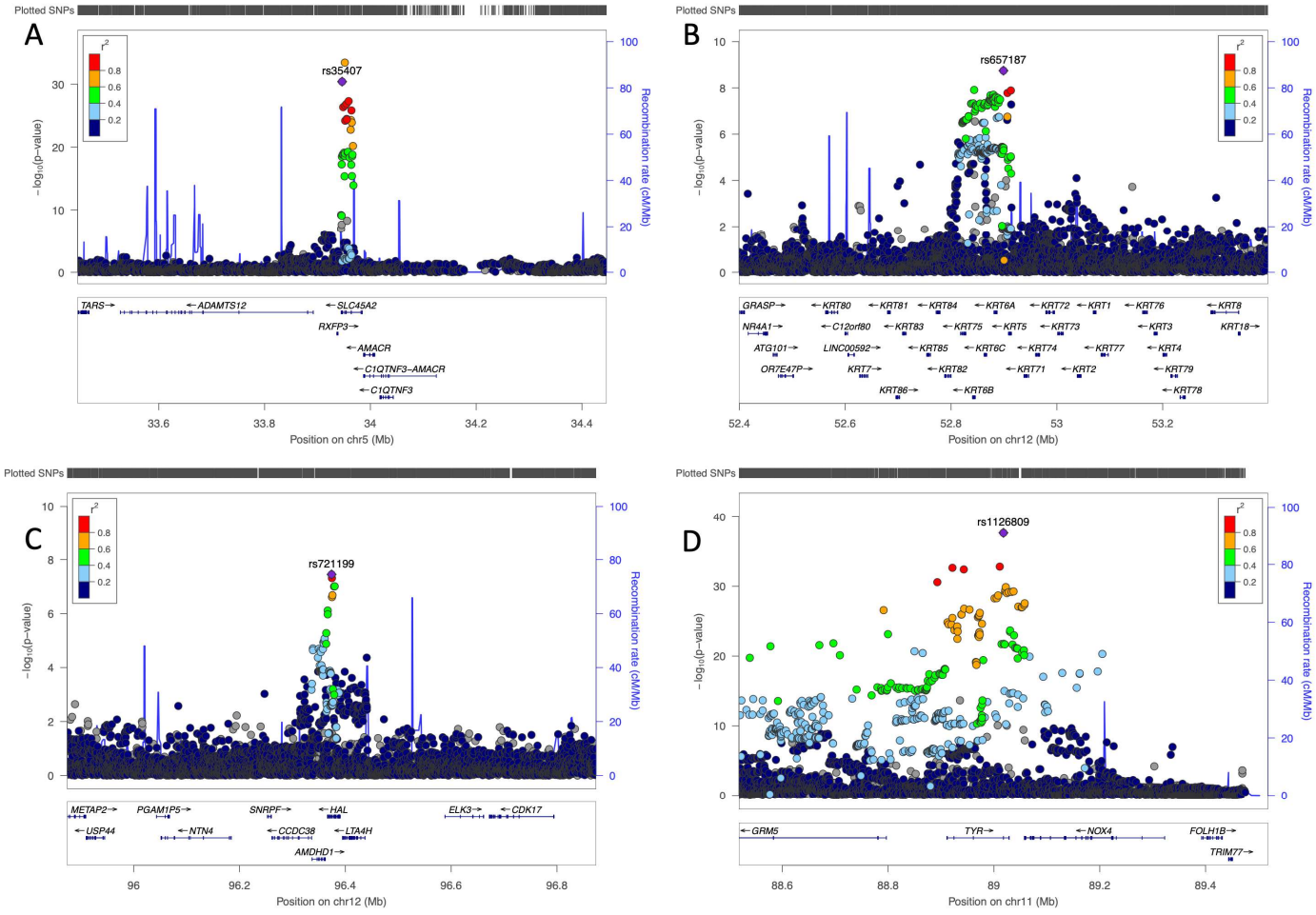

S
SNP: rs62246017
Odds Ratio (95% CI)
% Weight
23me
1.06 (1.02, 1.11)
34.2
Decode
1.07 (0.99, 1.15)
10.3
Harvard
0.98 (0.91, 1.05)
11.1
Kaiser
1.11 (1.07, 1.16)
41.3
Ohio
0.95 (0.70, 1.30)
0.6
Rotterdam
1.17 (1.00, 1.36)
2.4
1.08 (1.05, 1.10)
Heterogeneity I² = 60.3%
Heterogeneity p value
=0.028
0.696
1.00
1.44

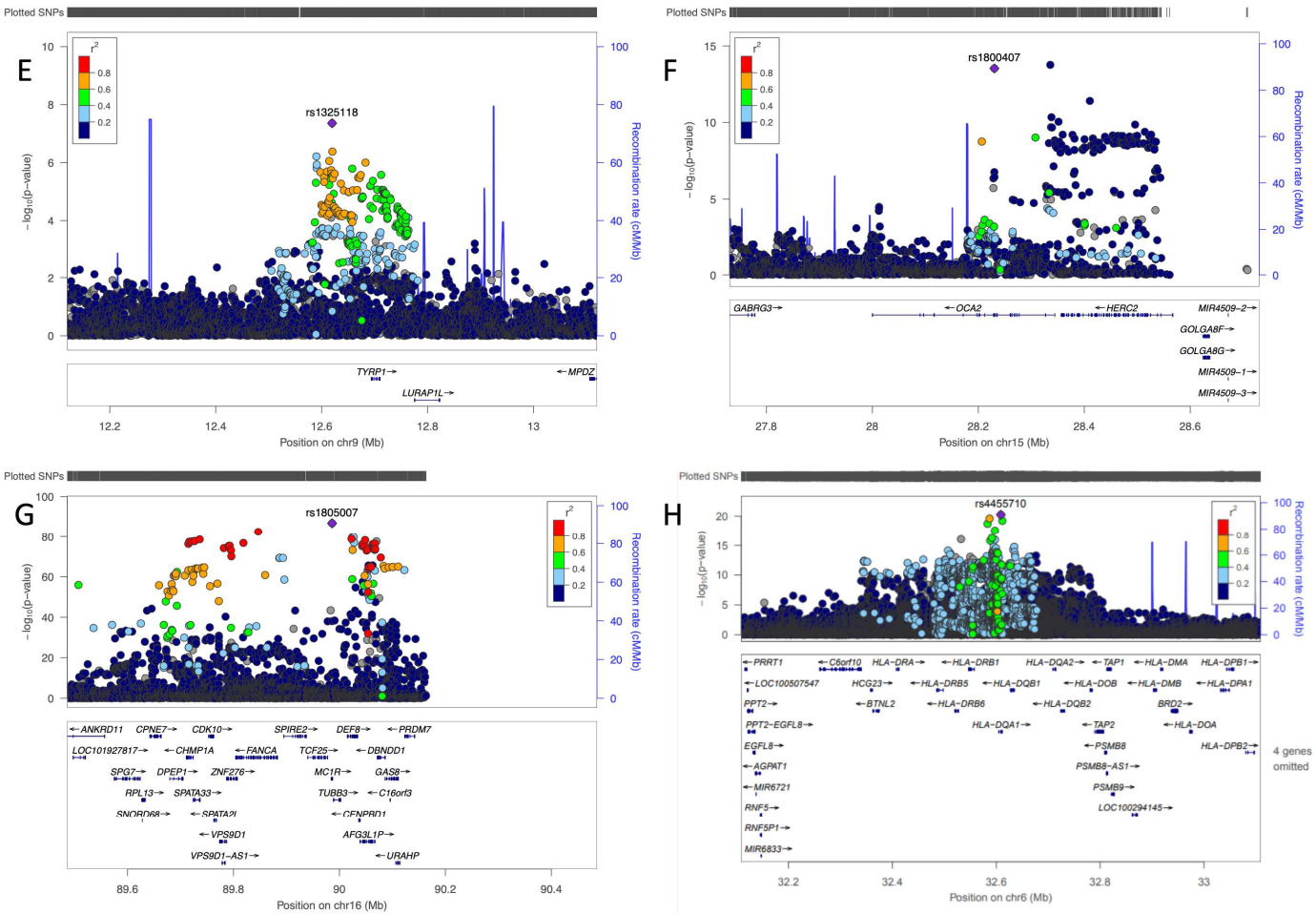

T
%
SNP: rs74899442
Odds Ratio (95% CI)
% Weight
23me
2.12 (1.64, 2.75)
100.00
2.12 (1.64, 2.75)
100.00
Heterogeneity I² = 0%
Heterogeneity p value = 1.0
0.36
1.00
2.75

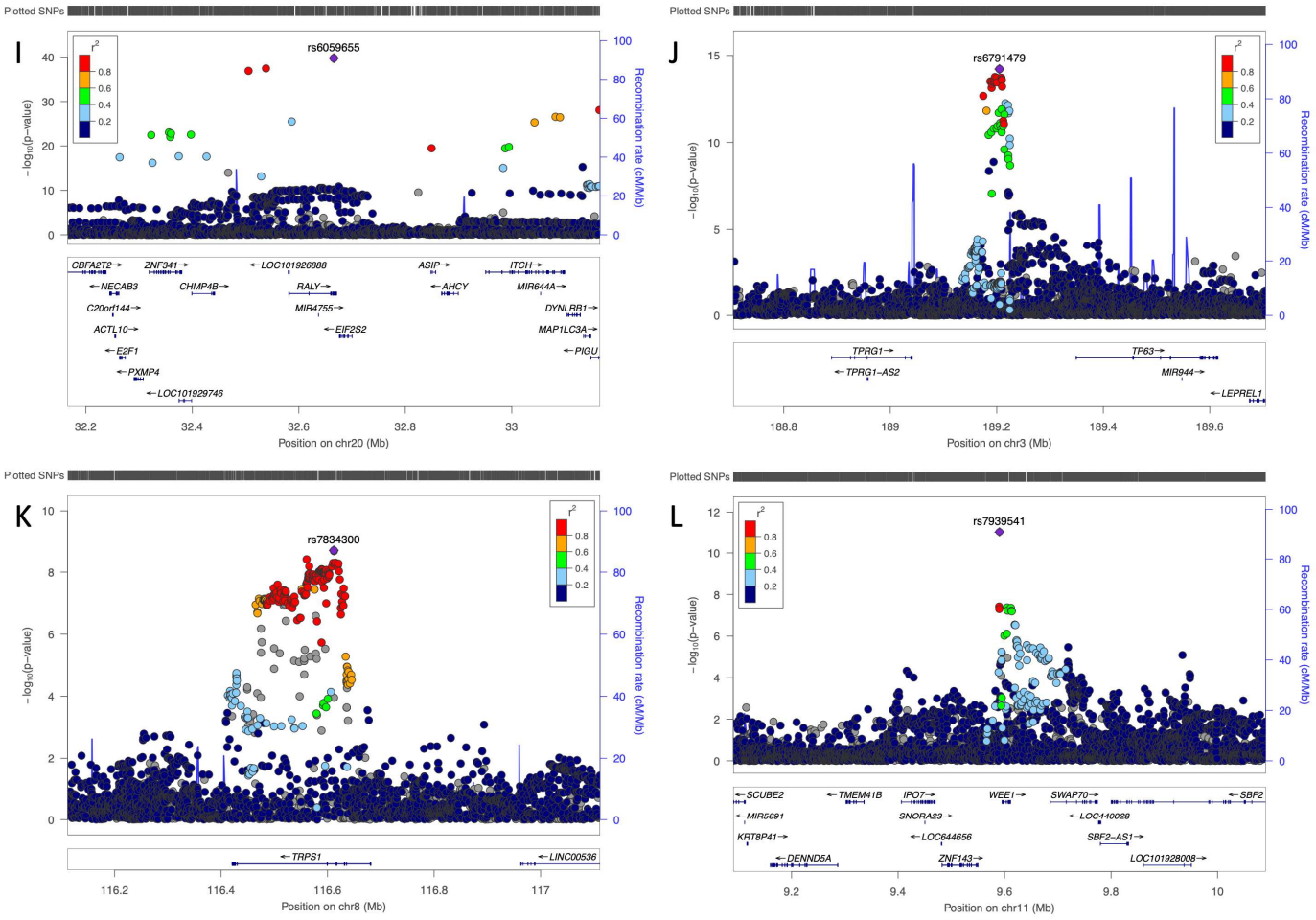


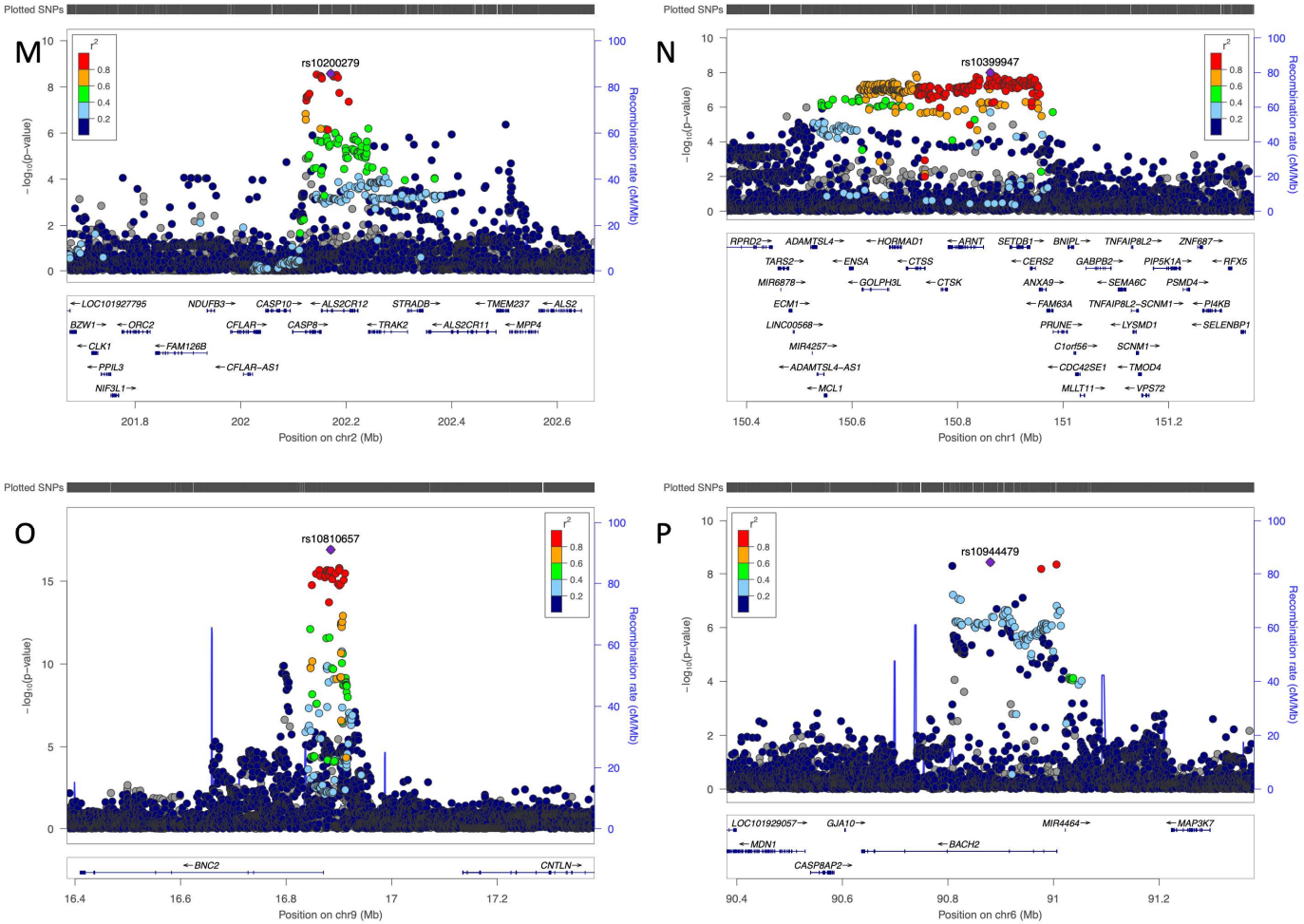
Supplementary Figure 3A-V: Forest plots of odds ratios for each SNP associated with SCC by individual study in the meta-analysis. The error bars represent the 95% confidence interval for the odds ratios for each study.

Supplementary Figure 4A-V:Regional association plots for novel SNP hits (Locus Zoom)




E
Plotted SNPs
rs1325118
r²
0.8
0.6
0.4
0.2
−log10(p−value)
Recombination rate (cM/Mb)
TYRP1
MPDZ
LURAP1L
12.2
12.4
12.6
12.8
13
Position on chr9 (Mb)
F
Plotted SNPs
rs1800407
GABRG3
OCA2
HERC2
MIR4509−2
GOLGA8F
GOLGA8G
MIR4509−1
MIR4509−3
27.8
28
28.2
28.4
28.6
Position on chr15 (Mb)
G
Plotted SNPs
rs1805007
ANKRD11
CPNE7
CDK10
SPIRE2
DEF8
PRDM7
LOC101927817
CHMP1A
FANCA
TCF25
DBNDD1
SPG7
DPEP1
ZNF276
MC1R
GAS8
RPL13
SPATA33
TUBB3
C16orf3
SNORD68
SPATA2l
CFNPRD1
VPS9D1
AFG3L1P
VPS9D1−AS1
URAHP
89.6
89.8
90
90.2
90.4
Position on chr16 (Mb)
H
Plotted SNPs
rs4455710
PRRT1
C6orf10
HLA−DRA
HLA−DRB1
HLA−DQA2
TAP1
HLA−DMA
HLA−DPB1
LOC100507547
HCG23
HLA−DRB5
HLA−DQB1
HLA−DOB
HLA−DMB
HLA−DPA1
PPT2
BTNL2
HLA−DRB6
HLA−DQB2
BRD2
PPT2−EGFL8
HLA−DQA1
TAP2
HLA−DOA
EGFL8
PSMB8
HLA−DPB2
AGPAT1
PSMB8−AS1
MIR6721
PSMB9
RNF5
LOC100294145
RNF5P1
MIR6833
4 genes omitted
32.2
32.4
32.6
32.8
33
Position on chr6 (Mb)


I
Plotted SNPs
rs6059655
r²
0.8
0.6
0.4
0.2
−log10(p−value)
Recombination rate (cM/Mb)
CBFA2T2→
ZNF341→
←LOC101926888
ASIP→
ITCH→
←NECAB3
CHMP4B→
RALY→
←AHCY
MIR644A→
C20orf144→
MIR4755→
DYNLRB1→
ACTL10→
←EIF2S2
MAP1LC3A→
←E2F1
←PIGU
←PXMP4
←LOC101929746
Position on chr20 (Mb)
J
Plotted SNPs
rs6791479
TPRG1→
TP63→
←TPRG1−AS2
MIR944→
←LEPREL1
Position on chr3 (Mb)
K
Plotted SNPs
rs7834300
←TRPS1
←LINC00536
Position on chr8 (Mb)
L
Plotted SNPs
rs7939541
←SCUBE2
←TMEM41B
IPO7→
WEE1→
SWAP70→
←SBF2
←MIR5691
SNORA23→
←LOC440028
KRT8P41→
←LOC644656
SBF2−AS1→
←DENND5A
ZNF143→
LOC101928008→
Position on chr11 (Mb)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r^2
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0.6
0.4
0.2
$-\log_{10}$(p-value)
Recombination rate (cM/Mb)
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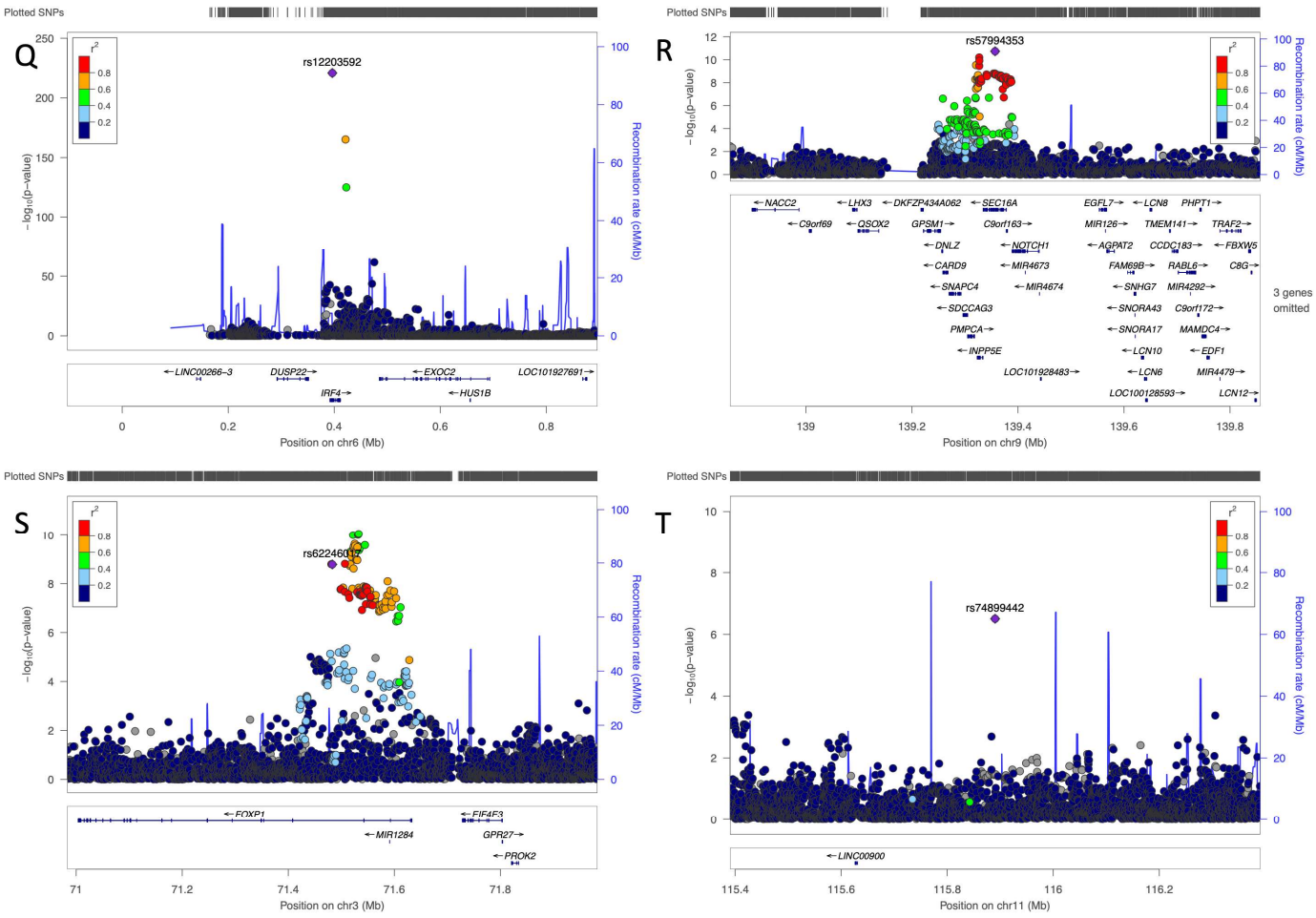
NDUFB3
CASP10
ALS2CR12
STRADB
TMEM237
ALS2
BZW1
ORC2
CFLAR
CASP8
TRAK2
ALS2CR11
MPP4
CLK1
FAM126B
PPIL3
CFLAR-AS1
NIF3L1
201.8
202
202.2
202.4
202.6
Position on chr2 (Mb)
N
Plotted SNPs
rs10399947
RPRD2
ADAMTSL4
HORMAD1
ARNT
SETDB1
BNIPL
TNFAIP8L2
ZNF687
TARS2
ENSA
CTSS
CERS2
GABPB2
PIP5K1A
RFX5
MIR6878
GOLPH3L
CTSK
ANXA9
SEMA6C
PSMD4
ECM1
FAM63A
TNFAIP8L2-SCNM1
PI4KB
LINC00568
PRUNE
LYSMD1
SELENBP1
MIR4257
C1orf56
SCNM1
ADAMTSL4-AS1
CDC42SE1
TMOD4
MCL1
MLLT11
VPS72
150.4
150.6
150.8
151
151.2
Position on chr1 (Mb)
O
Plotted SNPs
rs10810657
BNC2
CNTLN
16.4
16.6
16.8
17
17.2
Position on chr9 (Mb)
P
Plotted SNPs
rs10944479
LOC101929057
GJA10
MIR4464
MAP3K7
MDN1
BACH2
CASP8AP2
90.4
90.6
90.8
91
91.2
Position on chr6 (Mb)


Q
Plotted SNPs
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r²
0.8
0.6
0.4
0.2
−log10(p-value)
Recombination rate (cM/Mb)
LINC00266-3
DUSP22
EXOC2
LOC101927691
IRF4
HUS1B
Position on chr6 (Mb)
R
Plotted SNPs
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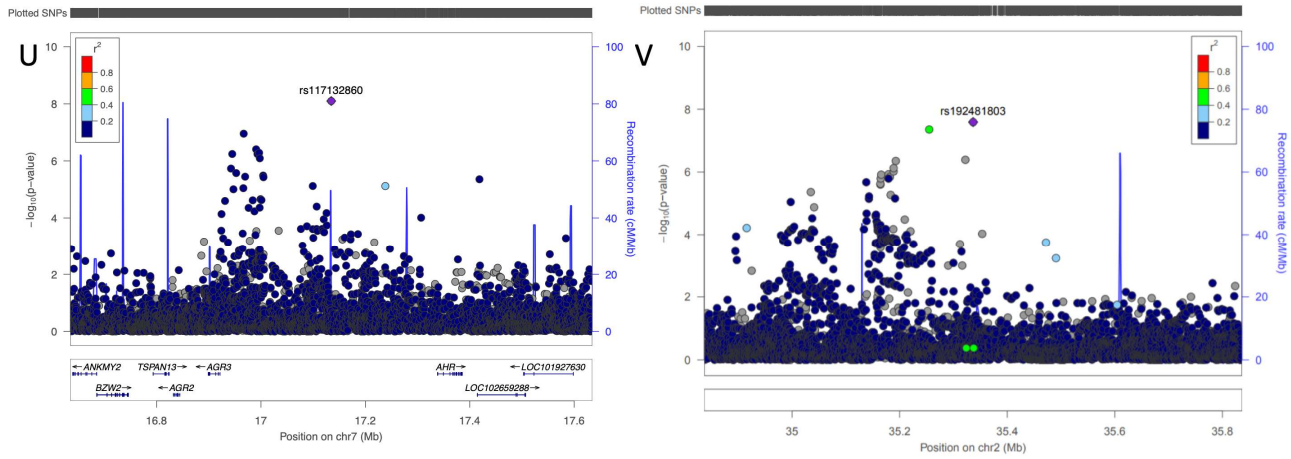
NACC2
LHX3
DKFZP434A062
SEC16A
EGFL7
LCN8
PHPT1
C9orf69
QSOX2
GPSM1
C9orf163
MIR126
TMEM141
TRAF2
DNLZ
NOTCH1
AGPAT2
CCDC183
FBXW5
CARD9
MIR4673
FAM69B
RABL6
C8G
SNAPC4
MIR4674
SNHG7
MIR4292
SDCCAG3
SNORA43
C9orf172
PMPCA
SNORA17
MAMDC4
INPP5E
LCN10
EDF1
LOC101928483
LCN6
MIR4479
LOC100128593
LCN12
3 genes omitted
Position on chr9 (Mb)
S
Plotted SNPs
rs62246017
FOXP1
FIP4F3
MIR1284
GPR27
PROK2
Position on chr3 (Mb)
T
Plotted SNPs
rs74899442
LINC00900
Position on chr11 (Mb)



Supplementary Figures 4A-V: Regional association plots for novel SNP hits in GWAS meta-analysis.

Supplementary Table 1: Summary data for individual datasets by study.

Cohort	Cases	Controls	Genomic inflation (λ)	Number of SNPs	GWAS data Published:
Rotterdam	398	10,629	1.01	7,615,191	partially published (Siiskonen et al)
23&Me	6,579	280,558	1.05	11,468,464	published (Chahal et al)
NHS/PHS	2,287	30,966	1.03	8,316,372	partially published (Chahal et al)
Kaiser	7,701	60,166	1.05	8,723,724	partially published (Asgari et al)
deCODE	2,081	296,015	1.02	10,146,978	Unpublished
Ohio	103	1,715	1.01	9,289,320	Unpublished
Total:	19,149	680,049	1.06	13,607,369	

Supplementary Table 2: Demographic information for each cohort

Study	N	Male (%)	Age <30 yr	Age 30-45 yr	Age 46-60 yr	Age > 60 yr
Rotterdam						
Cases	398	192(48.2%)	0	0	69 (17.3%)	329 (82.7%)
Controls	10,629	4,451(41.9%)	0	0	3,770 (35.5%)	6,859(64.5%)
23&Me						
Cases	6,579	3510 (53.4%)	12 (0.2%)	199 (3.0%) 83,780	1,263 (19.2%)	5,105 (77.6%)
Controls	280,558	151,588 (54.0%)	39,838 (14.2%)	(29.9%)	76,833 (27.4%)	80,107 (28.6%)
NHS/PHS						
Cases	2,287	868 (37.9%)	10(0.4%)	918(40.0%)	1,098 (47.9%)	267 (11.6%)
Controls	30,966	8,687 (26.3%)	885 (2.7%)	17,602 (53.3%)	10,042 (30.4%)	2,491 (7.5%)
Kaiser						
Cases	7,701	4,420 (57.4%)	0 (0%)	45 (0.6%)	899 (11.7%)	6,757 (87.7%)
Controls	60,166	24,324 (40.4%)	918 (1.5%)	5,546 (9.2%)	21,090 (35.1%)	32,612 (54.2%)
deCODE						
Cases	2,081	935 (44.9%)	12 (0.6%)	74 (3.6%)	242 (11.6%)	1,753 (84.2%)
Controls	296,015	151,761(51.3%)	40,708 (13.8%)	64,323 (21.7%)	68,550 (23.2%)	122,434 (41.4%)
Ohio						
Cases	103	61 (59.2%)	0 (0%)	8 (7.7%)	28 (27.2%)	67 (65.0%)
Controls	1,715	499 (29.1%)	281 (16.4%)	516 (30.1%)	603 (35.2%)	315 (18.3%)
Total:						
Cases	19,149	9,986 (52.1%)	34 (0.2%)	1,244 (6.5%)	3,599 (18.8%)	14,278 (74.5%)
Controls	680,049	343,290 (50.3%)	82,630 (12.1%)	171,767 (25.2%)	180,888 (26.5%)	244,818 (35.9%)

Supplementary Table 3: Significant SNPs from previous cutaneous SCC GWAS.

SNP	Chr	Position	Cytoband	Gene	Major allele	Minor allele	MAF	Effect	Direction	p value	StdErr	Het I^2	Het Chi^2	Het	Het p value
rs192481803	2	35336564	2p22.3	[]	C	T	0.007	0.65	+, N, N, N, N, N	2.32E-07	0.12	NA	NA	NA	NA
rs62246017	3	71483084	3p13	FOXP1---[]---EIF4E3	G	A	0.325	0.07	+, +, -, +, -, +	1.65E-09	0.01	60.3%	12.58	5	0.03
rs6791479	3	189205032	3q28	TPRG1---[]---TP63	A	T	0.427	0.09	+, +, +, +, -, +	6.09E-15	0.01	71.4%	17.47	5	0.0037
rs35407	5	33946571	5p13.2	[SLC45A2]	G	A	0.042	-0.47	-, -, -, -, N, -	5.81E-31	0.04	83.5%	24.23	4	0.000072
rs4455710	6	32608858	6p21.32	[HLA-DQA1]	C	T	0.368	0.14	N, +, +, +, +, -	5.57E-21	0.02	45.8%	7.38	4	0.12
rs12203592	6	396321	6p25.3	[IRF4]	C	T	0.166	0.44	+, +, +, +, +, +	1.33E-221	0.01	79.1%	23.90	5	0.00023
rs117132860	7	17134708	7p21.1	AGR3---[]---AHR	G	A	0.021	0.25	+, +, +, +, +, +	7.97E-09	0.04	9.8%	5.54	5	0.35
rs10810657	9	16884586	9p22.2	BNC2--[]---CNTLN	A	T	0.404	-0.10	-, -, -, -, -, -	1.26E-17	0.01	0%	0.16	5	1.00
rs57994353	9	139356987	9q34.3	[SEC16A]	T	C	0.284	0.09	+, +, +, +, +, -	1.84E-11	0.01	52.5%	10.54	5	0.06
rs1126809	11	89017961	11q14.3	[TYR]	G	A	0.279	0.15	+, +, +, +, +, +	2.21E-38	0.01	0%	4.63	5	0.46
rs74899442*	11	115890279	11q23.3	CADM1---[]---BUD13	T	C	0.004	0.75	+, N, N, N, N, +, N	1.52E-07	0.13	NA	NA	NA	NA
rs1800407	15	28230318	15q13.1	[OCA2]	C	T	0.070	0.16	+, +, +, +, N, -	5.12E-14	0.02	54.9%	8.88	4	0.06
rs1805007	16	89986117	16q24.3	TCF25-[]-TUBB3	C	T	0.078	0.38	+, +, +, +, N, +	5.55E-87	0.02	4.0%	4.17	4	0.38
rs6059655	20	32665748	20q11.22	[RALY]	G	A	0.077	0.25	+, +, +, +, N, +	8.42E-40	0.02	50.3%	8.04	4	0.09

[o] degrees of freedom The minor allele is effect allele. MAF represents the minor allele frequency in the pooled meta-analysis.*rs74899442 MAF only met the MAF cutoff in the original dataset in which it was discovered; it did not meet the cutoff in the other cohorts used in this meta-analysis. However, we report these results in our supplementary to further support the significant association. Direction is listed in order for 23me, deCODE, NHS/HPFS, Kaiser, Ohio and Rotterdam. N means not included in analysis.

Supplementary Table 4: Novel SNPs reaching genome-wide significance in the SCC meta-analysis

SNP	Chr	Position	Locus	Gene	Major allele	Minor allele	MAF	Effect	Direction	p value	StdErr	Het I^2	Het Chi squared	Het º	Het p value
rs10399947	1	150861960	1q21.3	ARNT--[]--SETDB1	G	A	0.36	-0.07	-, -, -, -, -, +	6.65E-09	0.01	0%	4.26	5	0.51
rs10200279	2	202170655	2q33.1	[ALS2CR12]	C	T	0.287	0.07	+, +, +, +, +, +	2.67E-09	0.01	0%	3.79	5	0.58
rs10944479	6	90880393	6q15	[BACH2]	G	A	0.189	-0.09	-, -, -, -, -, N	3.75E-09	0.02	0%	2.20	4	0.70
rs7834300	8	116611632	8q23.3	[TRPS1]	C	G	0.438	0.07	+, +, +, +, -, +	2.01E-09	0.01	0%	3.21	5	0.67
rs1325118	9	12619616	9p23	[]--TYRP1	T	C	0.304	-0.07	-, -, -, -, +, -	4.38E-08	0.01	0%	1.15	5	0.95
rs7939541	11	9590389	11p15.4	ZNF143--[]-WEE1	T	C	0.410	0.08	+, +, +, +, +, +	9.23E-12	0.01	2.5%	5.13	5	0.40
rs657187	12	52898985	12q13.13	KRT6A--[]-KRT5	A	G	0.420	-0.07	-, -, -, -, -, -	1.80E-09	0.01	0.0%	2.72	5	0.74
rs721199	12	96374057	12q23.1	[HAL]	C	T	0.463	-0.06	-, -, -, -, -, -	3.55E-08	0.01	58.9%	12.16	5	0.03

º degrees of freedom. Minor allele is effect allele. Minor allele frequency (MAF) is based on the pooled meta-analysis. Direction is listed in order for 23me, deCODE, NHS/HPFS, Kaiser, Ohio and Rotterdam. N means not included in analysis.

Supplementary Table 5: Per study results for the significant SNPS in SCC GWAS meta-analysis

SNP	23&Me			deCODE			NHS/PHS			Kaiser			Ohio			Rotterdam		
	Effect	Std Err	p val	Effect	Std Err	p val	Effect	Std Err	p val	Effect	Std Err	p val	Effect	Std Err	p val	Effect	Std Err	p val
rs10399947	-0.04	0.02	2.88E-02	-0.09	0.04	1.83E-02	-0.08	0.04	2.31E-02	-0.08	0.02	2.64E-06	-0.08	0.15	6.1E-01	0.01	0.08	9.36E-01
rs10200279	0.09	0.02	4.69E-06	0.10	0.04	1.04E-02	0.03	0.04	3.34E-01	0.05	0.02	4.77E-03	0.05	0.16	7.70E-01	0.12	0.08	1.17E-01
rs10944479	-0.11	0.03	1.84E-05	-0.10	0.04	2.35E-02	-0.10	0.05	5.99E-02	-0.07	0.02	2.71E-03	-0.25	0.22	2.50E-01	-	-	-
rs7834300	0.09	0.02	2.92E-06	0.08	0.04	2.59E-02	0.05	0.03	1.58E-01	0.05	0.02	3.78E-03	-0.05	0.15	7.45E-01	0.10	0.07	1.82E-01
rs1325118	-0.07	0.02	1.95E-04	-0.04	0.04	2.65E-01	-0.06	0.04	8.60E-02	-0.06	0.02	9.53E-04	0.01	0.16	9.69E-01	-0.12	0.08	1.34E-01
rs7939541	0.08	0.02	4.23E-06	0.11	0.04	1.75E-03	0.06	0.03	8.55E-02	0.06	0.02	3.73E-04	0.32	0.15	2.72E-02	0.03	0.07	7.04E-01
rs657187	-0.07	0.02	7.21E-05	-0.05	0.04	1.57E-01	-0.03	0.03	3.25E-01	-0.07	0.02	6.47E-05	-0.21	0.15	1.58E-01	-0.11	0.07	1.28E-01
rs721199	-0.04	0.02	2.77E-02	-0.03	0.03	3.42E-01	-0.11	0.03	1.08E-03	-0.07	0.02	1.23E-04	-0.49	0.15	9.21E-04	-0.07	0.07	3.65E-01

Supplementary Table 6: Fine mapping of significant loci in SCC GWAS meta-analysis

locus	cytoband	$N_{signals}$	SNP	pos	MAF	p	P_{joint}	C_{99}	C_{80}
1	1q21.3	1	rs10399947	150,861,960	0.368	1e-08	9.3e-09	273	158
2	2q33.1	1	rs10200279	202,170,655	0.287	2.7e-09	2.4e-09	20	9
3	2p22.3	0	(rs192481803)	(35,336,564)	(0.006)	(2.6e-08)			
4	3p13	1	rs62247166	71,532,738	0.479	8.9e-11	8.4e-11	66	17
5	3q28	1	rs9290890	189,196,565	0.427	1.7e-14	1.4e-14	17	9
6	5p13.2	1	rs16891982	33,951,693	0.055	3.7e-34	6.1e-34	1	1
8	6p25.3	2	rs12203592	396,321	0.166	1.3e-221	1.8e-192	1	1
			rs6935510	391,623	0.386	2.8e-43	8.5e-15	1	1
9	6q15	1	rs10944479	90,880,393	0.189	3.8e-09	3.6e-09	82	4
10	7p21.1	1	rs117132860	17,134,708	0.021	8e-09	8.3e-09	12	1
11	8q23.3	1	rs2737206	116,611,902	0.438	2.1e-09	2.3e-09	142	64
12	9p23	1	rs1325118	12,619,616	0.304	4.4e-08	4.9e-08	1990	16
13	9p22.2	2	rs62541919	16,863,364	0.414	2.1e-16	5.1e-16	21	13
			rs10962599	16,795,286	0.251	1.3e-10	3.3e-10	20	12
14	9q34.3	3	rs57994353	139,356,987	0.284	1.8e-11	1.7e-11	37	3
15	11q14.3	1	rs1126809	89,017,961	0.278	2.2e-38	2.8e-38	1	1
16	11q23.3	0	(rs74899442)	(115,890,279)	(0.004)	(1.5e-07)			
17	11p15.4	1	rs7939541	9,590,389	0.41	9.2e-12	8.6e-12	1	1
18	12q13.13	1	rs657187	52,898,985	0.42	1.8e-09	1.9e-09	113	31
19	12q23.1	1	rs721199	96,374,057	0.463	3.6e-08	3.1e-08	59	4
20	15q13.1	2	rs4778138	28,335,820	0.143	1.7e-14	1.9e-13	1	1
			rs1800407	28,230,318	0.070	2.9e-14	3.5e-13	1	1
22	20q11.22	1	rs6059655	32,665,748	0.076	1.7e-40	2.1e-40	1	1

$N_{signals}$: the number of distinct association signals in locus. (i) two loci were excluded: 6p21.32 as it was an HLA region and 16q24.3 as it is the MC1R locus; (ii) two loci have 0 signals as they were excluded from analysis due to being rare variants (iii) most loci have a single signal, as summarized in Table 1 and Supplementary Table 3. **SNP**: index SNP of the association signal from the conditional analysis. **pos**: index SNP position in bp. **MAF**: index SNP minor allele frequency. **P**: index SNP marginal P-value from GWAS meta-analysis. P_{joint}: index SNP P-value in the conditional joint analysis when all signals are included in the model. C_{99}: the size of 99% credible set. C_{80}: the size of 80% credible set. (*): For the two loci 3 and 16 the conditional analysis revealed no signals. The information of the lead SNP from GWAS meta-analysis for these loci is shown in brackets.(**)

Supplementary Table 7: Imputation quality by study for rs117132860

Study	Imputation R^2	Minor allele frequency	p value	Odds Ratio
23me	0.52	0.02	7.19E-07	1.46
Decode	0.99	0.01	1.48E-01	1.26
Harvard	0.65	0.02	2.72E-01	1.16
Kaiser	0.70	0.02	1.31E-02	1.18
Ohio	0.74	0.02	2.84E-01	1.76
Rotterdam	0.69	0.02	2.43E-01	1.41

Supplementary Table 8: Effect of each SNP on SCC on pigmentation traits

Rsid	Chr:Pos (B38)	Minor allele	Major allele	Risk allele	Gene	Variant Effect	Close Genes	Known Associations	p value	Effect	Phenotype
rs1126809	chr11: 89284793	A	G	G	TYR	Missense	TYR NOX4 GRM5 FOLH1B TRIM77 TRIM49	BCC[1] SCC[2,3] Sunburns[4] Tanning[4]	1.80E-28	1.389	Sun sensitivity
									2.31E-28	1.565	Eye color (blue vs green)
									2.75E-06	1.252	Hair color (blond vs brown)
									5.19E-04	1.198	Eye color (blue vs brown)
rs1800407	chr15: 27985172	T	C	C	OCA2	Missense	OCA2 HERC2 LOC645202 GOLGA8F MIR4509-2 GABRG3	SCC[2]	1.39E-71	0.197	Eye color (blue vs brown)
									1.11E-39	0.351	Eye Color (blue vs green)
									5.73E-10	0.522	Hair color (blond vs brown)
									0.00131	0.807	Freckles
rs1805007	chr16: 89919709	T	C	C	MC1R	Missense	MC1R TUBB3 TCF25 DEF8 SPIRE2 CENPBD1	BCC [1,5] SCC[2] Hair color (Blond vs Brown) [6,7] Freckles [6] Hair color [4] Hair color (Red vs not Red) [6,7] Non-melanoma skin cancer[4] Sun sensitivity[6] Sunburns[4] Tanning [4]	8.61E-202	7.726	Hair color (Red vs non-red)
									1.83E-121	3.51	Freckles
									3.45E-91	2.578	Sun sensitivity
									3.94E-16	1.958	Hair (blond vs brown)
									6.68E-05	0.789	Eye color (blue vs green)
rs6059655	chr20: 34077942	A	G	G	RALY	Intronic	RALY EIF2S2 MIR4755 RALY-AS1 ASIP AHCY	BCC[1] SCC[2,3] Facial pigmentation[8] Skin color saturation[9] Sun sensitivity[9]	3.67E-51	2.052	Sun sensitivity
									8.16E-47	2.127	Freckles
									4.27E-19	1.98	Hair color (red vs non-red)
									1.01E-12	1.787	Hair (blond vs brown)
rs35407	chr5: 33946466	A	G	G	SLC45A2	3' UTR	SLC45A2 RXFP3 AMACR C1QTNF3-AMACR	BCC[1] SCC[2]	3.87E-13	0.239	Hair (blond vs brown)
									2.29E-09	0.469	Sun sensitivity

							ADAMTS12 C1QTNF3		3.27E-09	0.448	Eye Color (blue vs green)
									0.000983	0.544	Eye color (blue vs brown)
rs12203592	chr6: 396321	T	C	C	IRF4	Intronic	IRF4 LOC105375104 DUSP22 EXOC2 LOC285766 LOC105374874	Actinic Keratosis[10] BCC[1] SCC[2,3] Non-melanoma skin cancer[4] Hair color (black vs blond, black vs red)[11] Eye color[12] Facial pigmentation[8] Freckling[12] Hair color_(not red)[7] Hair_color [4,7,12,13] Hair (greying) [13] Skin color saturation[9] Tanning [4]	1.26E-149	3.465	Freckles
									2.99E-103	0.177	Hair (blond vs brown)
									9.69E-55	1.91	Sun sensitivity
									1.05E-10	1.699	Eye color (blue vs brown)
rs7834300	chr8: 115599405	G	C	G	TRPS1	Intronic	TRPS1 LINC00536	None	0.000542	1.101	Sun Sensitivity
rs1325118	chr9: 12619616	C	T	T	.	Intergenic	TYRP1 LURAP1L-AS1 LURAP1L,MPDZ LINC01235	None	8.97E-12	0.758	Eye Color (blue vs green)
									4.55E-05	0.802	Eye color (blue vs brown)
rs10810657	chr9: 16884588	T	A	T	.	Intergenic	BNC2 CNTLN C9orf92 SH3GL2 CCDC171	BCC[1] SCC[2]	6.27E-17	0.783	Freckles
									1.18E-11	0.826	Sun sensitivity
									9.49E-06	0.819	Hair (blond vs brown)

Supplementary Table 9: Effect of each SNP on SCC on high vs low photo-distributed sites

SNP	Major/ Minor Allele	High-Photo OR [CI]	p value	Low-Photo OR[CI]	p value	T-Test	T-test p value
rs10200279	C/T	1.10 [1.04-1.16]	2.33E-02	1.03 [0.94-1.12]	5.20E-01	1.19	0.23
rs10399947	G/A	0.94 [0.89-0.99]	2.15E-02	0.94 [0.86-1.02]	1.40E-01	0.05	0.96
rs10810657	A/T	0.91 [0.86-0.96]	4.43E-04	0.93 [0.85-1.01]	6.80E-02	-0.31	0.76
rs10944479	G/A	0.88 [0.85-0.95]	1.07E-03	0.98 [0.87-1.10]	730E-01	-1.01	0.31
rs1126809	G/A	1.14 [1.08-1.21]	7.32E-06	1.09 [0.99-1.19]	6.65E-01	0.87	0.38
rs117132860	G/A	1.28 [1.03-1.60]	2.77E-02	1.10 [0.78-1.15]	6.02E-01	0.84	0.40
rs12203592	C/T	1.39 [1.30-1.51]	5.25E-18	1.33 [1.18-1.50]	3.57E-06	0.80	0.42
rs1325118	T/C	0.96 [091-1.02]	1.71E-01	0.89 [0.82-0.98]	1.41E-02	1.30	0.19
rs1800407	C/T	1.17 [1.04-1.32]	7.30E-03	1.20 [1.01-1.44]	4.30E-02	-0.34	0.73
rs1805007	C/T	1.42 [1.30-1.55]	1.81E-14	1.34 [1.17-1.54]	3.99E-05	0.73	0.47
rs35407	G/A	0.90 [0.76-1.06]	2.06E-01	0.70 [0.53-0.92]	1.15E-02	1.56	0.12
rs4455710	C/T	1.11 [1.03-1.19]	6.56E-03	1.13 [1.00-1.26]	4.37E-02	-0.29	0.77
rs57994353	T/C	1.04 [0.98-1.10]	2.23E-01	1.03 [0.94-1.13]	4.86E-01	0.22	0.83
rs6059655	G/A	1.22 [1.12-1.34]	1.31E-05	1.29 [1.12-1.48]	3.35E-04	-0.52	0.60
rs62246017	G/A	1.02 [0.96-1.08]	5.62E-01	1.08 [0.99-1.18]	7.73E-02	-1.14	0.25
rs657187	A/G	0.96 [0.91-1.01]	9.13E-02	0.94 [0.87-1.03]	1.72E-01	0.26	0.79
rs6791479	A/T	1.11 [1.06-1.17]	5.80E-05	1.15 [1.06-1.25]	8.72E-04	-0.67	0.50
rs721199	C/T	0.96 [0.91-1.01]	8.24E-02	0.86 [0.79-0.93]	1.09E-04	2.22	0.03
rs7834300	C/G	1.07 [1.02-1.13]	6.53E-03	1.06 [0.97-1.15]	1.87E-01	0.21	0.83
rs7939541	T/C	1.11 [1.06-1.17]	3.33E-04	1.03 [0.95-1.12]	5.11E-01	1.46	0.14
rs74899442	T/C	0.99 [049-2.00]	9.79E-01	1.37 [0.43-4.32]	5.93E-01	-0.61	0.54

Minor allele is the effect allele.

Supplementary Table 10: Significant results (FDR < 0.10) of the LDSC regression analysis (baseline model) on 53 publicly available annotations.[1] Annotations with the 500bp windows have "500_0" at the end.
Columns: SNPs, the proportion of SNPs in Annotation; h2, the proportion of heritability explained by SNPs in Annotation (standard error); Enrich., the enrichment computed as ration between the two proportions (standard error); p, p-value for Enrichment computed by the jackknife resampling; p_{adj}, the adjusted p-value by the FDR method (q-value). Rows are ordered by p-values in the column, p.

Annotation	**SNPs**	**h^2**	**Enrich.**	**p**	**p_{adj}**
Coding_UCSC.extend.500_0	0.0646	0.432 (0.1286)	6.691 (1.992)	0.000848	0.032
SuperEnhancer_Hnisz.extend.500_0	0.1716	0.368 (0.0582)	2.147 (0.339)	0.001230	0.032
SuperEnhancer_Hnisz.500_0	0.1684	0.339 (0.1023)	2.010 (0.608)	0.010818	0.094
H3K4me1_Trynka.extend.500_0	0.6092	1.034 (0.1940)	1.697 (0.318)	0.005483	0.071
Repressed_Hoffman.extend.500_0	0.7191	0.390 (0.1149)	0.542 (0.160)	0.003498	0.061

1. Finucane, H.K. *et al.* Partitioning heritability by functional annotation using genome-wide association summary statistics. *Nat Genet* **47**, 1228-35 (2015).

Supplementary Table 11: Top 10 results of the LDSC regression analysis on 220 cell-type-specific publicly available annotations[2], conditioned on the baseline model (53 annotations).

Group	Annotation	SNPs	h^2	Enrich.	Z	p	p_{adj}
Immune	CD19_primary_(BI)	0.0409	0.355	8.68	2.33	0.0196	0.327
Immune	CD19_primary_(UW)	0.0410	0.359	8.75	2.48	0.0130	0.327
Immune	CD4+_CD25-_CD45RA+_naive_primary	0.0131	0.180	13.79	2.30	0.0214	0.327
Immune	CD8_memory_primary	0.0111	0.156	13.97	2.19	0.0288	0.337
Immune	CD19	0.0366	0.340	9.31	2.46	0.0138	0.327
Immune	CD4+_CD25+_CD127-_Treg_primary	0.0142	0.195	13.76	2.35	0.0186	0.327
Immune	CD4_naive_primary	0.0127	0.163	12.87	2.33	0.0198	0.327
Immune	CD3_primary	0.0319	0.190	5.96	1.58	0.1152	0.531
Other	Penis_foreskin_melanocyte_primary	0.0179	0.408	22.81	2.28	0.0227	0.327
Immune	CD4+_CD25+_CD127-_Treg_primary	0.0286	0.309	10.80	2.35	0.0189	0.327

Columns: SNPs, the proportion of SNPs in Annotation; h2, the proportion of heritability explained by SNPs in Annotation; Enrich., the enrichment computed as ration between the two proportions; Z, Z-score computed for each annotation independently by incorporating into the baseline model; p, p-value derived based on Z-score; p_{adj}, the adjusted p-value by the FDR method (q-value). Rows are ordered by p-values computed for Enrichment (column not shown).

Supplementary Table 12: Index SNPs that are eQTLs in skin tissue
The alternate allele in the human genome reference is the eQTL effect allele.[1]

Variant	Gene	Tissue	p value	Normalized Effect Size	Effect allele/Ref allele
rs10399947	*HORMAD1*	Skin - Not Sun Exposed (Suprapubic)	1.3e-75	0.95	A/G
rs10399947	*GOLPH3L*	Skin - Not Sun Exposed (Suprapubic)	2.4e-45	0.55	A/G
rs10399947	*CTSS*	Skin - Not Sun Exposed (Suprapubic)	1.5e-16	0.25	A/G
rs10399947	*SETDB1*	Skin - Not Sun Exposed (Suprapubic)	2.9e-13	-0.22	A/G
rs10399947	*ANXA9*	Skin - Not Sun Exposed (Suprapubic)	1.7e-12	0.19	A/G
rs10399947	*ECM1*	Skin - Not Sun Exposed (Suprapubic)	9.1e-5	-0.11	A/G
rs10399947	*RP11-54A4.2*	Skin - Not Sun Exposed (Suprapubic)	1.5e-4	-0.18	A/G
rs10399947	*HORMAD1*	Skin - Sun Exposed (Lower leg)	6.0e-103	1.0	A/G
rs10399947	*GOLPH3L*	Skin - Sun Exposed (Lower leg)	2.1e-73	0.74	A/G
rs10399947	*CTSS*	Skin - Sun Exposed (Lower leg)	4.6e-24	0.26	A/G
rs10399947	*SETDB1*	Skin - Sun Exposed (Lower leg)	4.7e-10	-0.18	A/G
rs10399947	*ANXA9*	Skin - Sun Exposed (Lower leg)	4.2e-9	0.13	A/G
rs10399947	*CERS2*	Skin - Sun Exposed (Lower leg)	5.1e-7	0.086	A/G
rs10200279	*CASP8*	Skin - Not Sun Exposed (Suprapubic)	1.6e-36	0.56	C/T
rs10200279	*ALS2CR12*	Skin - Not Sun Exposed (Suprapubic)	1.8e-11	-0.38	C/T
rs10200279	*CASP10*	Skin - Not Sun Exposed (Suprapubic)	1.6e-6	-0.19	C/T
rs10200279	*CASP8*	Skin - Sun Exposed (Lower leg)	1.3e-45	0.57	C/T
rs10200279	*ALS2CR12*	Skin - Sun Exposed (Lower leg)	4.3e-14	-0.37	C/T
rs10200279	*PPIL3*	Skin- Sun Exposed (Lower leg)	2.9e-6	-0.22	C/T
rs7939541	*WEE1*	Skin - Not Sun Exposed (Suprapubic)	1.3e-27	0.36	T/C
rs7939541	*snoU13*	Skin - Not Sun Exposed (Suprapubic)	1.6e-11	0.24	T/C
rs7939541	*WEE1*	Skin - Sun Exposed (Lower leg)	3.5e-17	0.28	T/C
rs7939541	*snoU13*	Skin - Sun Exposed (Lower leg)	3.5e-7	0.20	T/C
rs721199	*HAL*	Skin - Not Sun Exposed (Suprapubic)	1.2e-67	-0.47	C/T
rs721199	*RP11-256L6.3*	Skin - Not Sun Exposed (Suprapubic)	1.5e-4	-0.46	C/T
rs721199	*HAL*	Skin - Sun Exposed (Lower leg)	4.1e-79	-0.49	C/T
rs721199	*RP11-256L6.3*	Skin - Sun Exposed (Lower leg)	4.4e-9	-0.22	C/T
rs657187	*KRT6C*	Skin - Not Sun Exposed (Suprapubic)	8.1e-5	0.14	G/A
rs657187	*KRT6C*	Skin - Sun Exposed (Lower leg)	3.6e-19	0.36	G/A

1. The Gtex Consortium, Genetic effects on gene expression across human tissues. *Nature* **550**, 204-213 (2017).

Supplementary Table 13: Characterization of SNPs meeting 0.05 PPA cutoff at locus 2q33.1

SNP	PPA	eQTL in skin tissue	Regulatory motifs altered	Disease associations
rs10200279	0.12	*ALS2CR12* *CASP8* *CASP10* *PPIL3*	CACD_1 Myb_2 Pou2f2_disc2 RREB-1_1, RREB-1_2 Zfp281 Zfp740	
rs10931936	0.11	*ALS2CR12* *CASP8* *CASP10* *PPIL3*	EWSR1-FLI1 PU.1_known2 SPIB TFII-I TFIIA	Esophageal cancer[14] Breast cancer[15]
rs1830298	0.099	*ALS2CR12* *CASP8* *CASP10* *PPIL3*	AIRE_1 Dobox4	Breast cancer[16]
rs3769818	0.094	*ALS2CR12* *CASP8* *CASP10* *PPIL3*	Arid5a Foxj2 Zfp410	_
rs7582362	0.094	*ALS2CR12* *CASP8* *CASP10* *PPIL3*	HNF1 PLZF	_
rs6719014	0.089	*ALS2CR12* *CASP8* *CASP10* *PPIL3*	_	_
rs700635	0.081	*ALS2CR12* *CASP8* *CASP10* *PPIL3*	CCNT2	Prostate cancer[17] Basal cell carcinoma[18]
rs6714430	0.073	*ALS2CR12* *CASP8* *CASP10* *PPIL3*	_	_
rs6743068	0.073	*ALS2CR12* *CASP8* *CASP10* *PPIL3*	Irf Pax-5 RXRA	_
rs9677180	0.071	*ALS2CR12* *CASP8* *CASP10* *PPIL3*	Pax-4	_

Supplementary Table 14: Mutually adjusted analysis for rs657187 and 11170164 at 12q13.13

SNP	Chr	Pos	Maj/Min	M AF	Unadj Effect[Std Error]	Unadj *P* value	Adj Effect [Std Error]	Adj *P* value
rs657187	12	52505201	A/G	0.42.	-0.07 [0.01]	1.803e-09	-0.053 [0.01]	2.28E-06
rs11170164	12	52519884	C/T	0.08	0.11 [0.02]	5.218e-08	0.082 [0.02]	5.67E-05

Minor Allele is Effect Allele. Chr = Chromosome, Pos= Position, Ref = Reference , Maj/Min = Major Allele/Minor Allele AF = Allele Frequency, Unadj = Unadjusted, Adj = Adjusted, Std = Standard

Supplementary References

1. Chahal, H.S. *et al.* Genome-wide association study identifies 14 novel risk alleles associated with basal cell carcinoma. *Nat Commun* **7**, 12510 (2016).
2. Chahal, H.S. *et al.* Genome-wide association study identifies novel susceptibility loci for cutaneous squamous cell carcinoma. *Nat Commun* **7**, 12048 (2016).
3. Asgari, M.M. *et al.* Identification of Susceptibility Loci for Cutaneous Squamous Cell Carcinoma. *J Invest Dermatol* **136**, 930-7 (2016).
4. Zhang, M. *et al.* Genome-wide association studies identify several new loci associated with pigmentation traits and skin cancer risk in European Americans. *Hum Mol Genet* **22**, 2948-59 (2013).
5. Nan, H. *et al.* Genome-wide association study identifies novel alleles associated with risk of cutaneous basal cell carcinoma and squamous cell carcinoma. *Hum Mol Genet* **20**, 3718-24 (2011).
6. Sulem, P. *et al.* Genetic determinants of hair, eye and skin pigmentation in Europeans. *Nat Genet* **39**, 1443-52 (2007).
7. Tung, J.Y. *et al.* Efficient replication of over 180 genetic associations with self-reported medical data. *PLoS One* **6**, e23473 (2011).
8. Jacobs, L.C. *et al.* A Genome-Wide Association Study Identifies the Skin Color Genes IRF4, MC1R, ASIP, and BNC2 Influencing Facial Pigmented Spots. *J Invest Dermatol* **135**, 1735-1742 (2015).
9. Liu, F. *et al.* Genetics of skin color variation in Europeans: genome-wide association studies with functional follow-up. *Hum Genet* **134**, 823-35 (2015).
10. Jacobs, L.C. *et al.* IRF4, MC1R and TYR genes are risk factors for actinic keratosis independent of skin color. *Hum Mol Genet* **24**, 3296-303 (2015).
11. Han, J. *et al.* A genome-wide association study identifies novel alleles associated with hair color and skin pigmentation. *PLoS Genet* **4**, e1000074 (2008).
12. Eriksson, N. *et al.* Web-based, participant-driven studies yield novel genetic associations for common traits. *PLoS Genet* **6**, e1000993 (2010).
13. Adhikari, K. *et al.* A genome-wide association scan in admixed Latin Americans identifies loci influencing facial and scalp hair features. *Nat Commun* **7**, 10815 (2016).
14. Zhao, X.K. *et al.* Shared susceptibility loci at 2q33 region for lung and esophageal cancers in high-incidence areas of esophageal cancer in northern China. *PLoS One* **12**, e0177504 (2017).
15. Sueta, A. *et al.* A genetic risk predictor for breast cancer using a combination of low-penetrance polymorphisms in a Japanese population. *Breast Cancer Res Treat* **132**, 711-21 (2012).
16. Lin, W.Y. *et al.* Identification and characterization of novel associations in the CASP8/ALS2CR12 region on chromosome 2 with breast cancer risk. *Hum Mol Genet* **24**, 285-98 (2015).
17. Stacey, S.N. *et al.* Insertion of an SVA-E retrotransposon into the CASP8 gene is associated with protection against prostate cancer. *Hum Mol Genet* **25**, 1008-18 (2016).
18. Stacey, S.N. *et al.* New basal cell carcinoma susceptibility loci. *Nat Commun* **6**, 6825 (2015).