TblS1_070817

Table S1. Single nucleotide polymorphisms (SNPs)[a] in the genetic risk score (GRS)

Region	SNP	Nearest Gene(s)	Reference(s)
2p22.3	rs192481803	*AC012593.1*	Chahal et al 2016
3p13	rs62246017	*FOXP1*	Asgari et al 2016
3q28	rs6791479	*TPRG1/TP63*[b]	Asgari et al 2016
5p13.2	rs16891982	*SLC45A2*	Asgari et al 2016
6p25.3	rs12203592	*IRF4*	Asgari et al 2016; Chahal et al 2016
6p21	rs4455710	*HLA-DQA1*	Asgari et al 2016
7p21.1	rs117132860	*AGR3/AHR*[b]	Chahal et al 2016
9p22.2	rs74664507	*BNC2/CNTLN*[b]	Asgari et al 2016
9q34.3	rs57994353	*SEC16A*	Chahal et al 2016
11q23.3	rs74899442	*CADM1/BUD13*[b]	Chahal et al 2016
11q14.3	rs1126809	*TYR*	Asgari et al 2016; Chahal et al 2016
15q13.1	rs12916300	*HERC2*	Asgari et al 2016
15q13.1	rs1800407	*OCA2*	Chahal et al 2016
16q24.3	rs4268748	*DEF8*	Asgari et al 2016
16q24.3	rs1805007	*MC1R*	Chahal et al 2016
20q11.22	rs6059655	*RALY*	Asgari et al 2016; Chahal et al 2016

a) from genome-wide association studies of cSCC risk
b) two flanking genes of an inter-genic SNP