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Table 1. Significant associations in the replication series and/or final joint meta-analysis

SNP	HGVS Nomenclature (GRCh37)	Nearest gene	Reference Allele##	Alternate Allele	Effect Allele#	Discovery				Replication				Combined					
						Female (N=5,087)		Male (N=8,143)		Female (N=2,974)		Male (N=8,113)		Female (N=8,061)			Male (16,256)		
						OR[95%CI]	P	OR[95%CI]	P	OR[95%CI]	P	OR[95%CI]	P	OR [95%CI]	Meta P-value	Het Pvalue	OR [95%CI]	Meta P-value	Het Pvalue
rs4903064	NC_000014.8:g.73279420T>C	DPF3**	T	C	C	1.47 [1.33-1.62]	$9.0x10^{-14}$	1.09 [1.01-1.19]	0.02	1.24 [1.07-1.42]	0.003	1.09 [0.98-1.21]	0.10	1.38 [1.27-1.50]	$1.5x10^{-14}$	0.10	1.09 [1.03-1.16]	0.005	0.54
rs2121266	NC_000002.11:g.46535924C>A	EPAS1**	C	A	C	1.06 [0.97-1.15]	0.20	1.2 [1.12-1.28]	$2.5x10^{-7}$	1.14 [1.00-1.30]	0.03	1.15 [1.05-1.26]	0.002	1.09 [1.01-1.17]	0.02	0.001	1.18 [1.12-1.25]	$1.8x10^{-9}$	0.62
rs147304092	NC_000007.13:g.33442937A>G	BBS9*	A	G	G	0.62 [0.52-0.76]	$2.0x10^{-6}$	1.05 [0.91-1.22]	0.49	0.97 [0.76-1.24]	0.82	1.20 [1.00-1.43]	0.05	0.72 [0.63-0.84]	$1.0x10^{-5}$	0.03	1.11 [0.99-1.24]	0.08	0.54
rs13027293	NC_000002.11:g.120001118G>T	STEAP3*	G	T	T	1.23 [1.12-1.35]	$8.0x10^{-6}$	0.96 [0.89-1.03]	0.28	0.87 [0.77-1.00]	0.04	1.00 [0.91-1.10]	0.95	1.10 [1.02-1.19]	0.01	$1.6x10^{-4}$	0.97 [0.92-1.03]	0.37	0.52
rs6554676	NC_000005.9:g.1233350A>T	SLC6A18*	A	T	A	0.62 [0.51-0.77]	$6.0x10^{-6}$	0.81 [0.69-0.95]	0.008	0.80 [0.61-1.05]	0.11	0.81 [0.67-0.99]	0.04	0.68 [0.58-0.81]	$6.1x10^{-6}$	0.07	0.81 [0.72-92]	0.001	0.67
rs10484683	NC_000006.11:g.148152077A>G	SAMD5**	A	G	G	0.96 [0.87-1.07]	0.48	0.8 [0.74-0.88]	$4.7x10^{-7}$	1.04 [0.89-1.21]	0.63	0.93 [0.82-1.04]	0.20	0.98 [0.90-1.07]	0.68	$2.9x10^{-4}$	0.83 [0.78-0.89]	$1.7x10^{-8}$	0.20
rs78971134	NC_000012.11:g.107652531A>G	BTBD11**	A	G	G	0.91 [0.78-1.06]	0.23	0.69 [0.61-0.79]	$4.5x10^{-8}$	0.97 [0.78-1.20]	0.78	0.87 [0.74-1.03]	0.10	0.93 [0.82-1.06]	0.26	0.21	0.75 [0.68-0.83]	$1.6x10^{-8}$	0.15

** indicates association identified at <5% FDR and * indicates association identified at <30% FDR in the discovery series;

OR[95%CI]= Odds Ratio [95% confidence interval]; Meta P-Value= Meta-analysis P-value; Het P-value= heterogeneity P-value among studies , HGVS=Human Genome Variation Society

Reference and alternate alleles as given by dbSNP, # Allele for which the effect size was calculated