

Appendix Table 10. Quality information from included studies																										
Author, year	Randomized?	Genotyping selection bias?	Loss to follow up described?	Loss to follow up quantified?	Differential loss to follow up?	Adherence described?	Missing data >10%?	Method for handling missing data?	Selective reporting -- associations prespecified?	Population stratification for race	Addressed Multiple Comparisons?	Methods for genotyping reported?	Genotyping method	Genotyping method detail	Allele-calling algorithm	GWAS call rate	SNP-specific call rate	Concordance	Concordance detail	HWE	HWE methods	Other genotyping QC	Masking	Plates	Industry support?	Case-control selection described?
Metformin																										
Zhou 2009	No	NR	No	NR	NR	Yes	NR		Yes	NR	NR	Yes	PCR	Taqman allelic-discrimination assay	No	Not GWAS	Yes	≥90%		HWE	In HWE		NR	NR	No	N/A
Moore 2009	No	Yes	No	NR	No	No	NR		Yes	Adjusted for self-reported race/ethnicity	Holm procedure	Yes	allele-specific primer ext of multiplex amplified, mass spec w/ Sequenom	N/A	Not GWAS	Yes	NR		HWE	In HWE		NR	NR	Yes	N/A	
Moore 2008	No	Yes	No	NR	NR	No	NR		Yes	Adjusted for self-reported race/ethnicity	Holm procedure	Yes	allele-specific primer ext of multiplex amplified, mass spec w/ Sequenom	N/A	Not GWAS	Yes	NR		HWE	In HWE		NR	NR	Yes	N/A	
Florez 2008	No	Yes	No	NR	NR	No	NR		Yes	Conducted analyses in all ppts and then in only white ppts	Explained and used P<0.05	Yes	Sequenom		N/A	Not GWAS	Yes	NR		HWE	Genotypes manually corrected and used computerized clustering to achieve HWE		NR	NR	Yes	N/A
Florez 2007	No	Yes	Partial	NR	NR	No	NR		Yes	Stratified and adjusted for race	Modified alpha level	Yes	Sequenom		N/A	Not GWAS	Yes	NR		HWE	In HWE		NR	NR	Yes	N/A
Florez 2006	No	Yes	No	NR	NR	No	NR		Yes	Stratified analysis	Holm procedure	Yes	Sequenom		N/A	Not GWAS	Yes	≥80%		HWE	In HWE		NR	NR	Yes	N/A
Zhou 2011	No	Yes	No	NR	NR	Yes	NR		No	No method, genomic inflation lambda was low	NR	Yes	Referenced, Array	Affy Genome-Wide Human SNP Array 6.0.	Yes	≥95%	N/A	≥90%		HWE	P-value	Relatedness (inclu	NR	NR	No	N/A
Jablonski 2010	No	Yes	No	NR	NR	No	NR		NR	Adjusted for individual admixture	Permutation P	Yes	Array	custom 1,536-SNP oligonucleotide pool array for the Illumina BeadArray platform	N/A	Not GWAS	Yes	NR		NR	NR		NR	NR	Yes	n/a
Pearson 2007	No	NR	No	NR	NR	Yes	NR		Yes	NR	NR	Yes	Referenced	PCR Taqman allelic-discrimination assay	N/A	Not GWAS	Yes	≥90%		HWE	In HWE		NR	n/a	No	N/A
Florez, 2012	No	Yes	No	NR	NR	No	NR		Yes	Adjusted for self-reported race/ethnicity	Explained and used P<0.05	Yes	Sequenom	ILEX platform	n/a	Not GWAS	Yes	NR		NR	NR		NR	NR	Yes	N/A
Florez, 2012	No	Yes	No	NR	NR	No	NR		Yes	showed pooled and stratified analyses	Did not discuss (used P<0.05)	Yes	Sequenom	ILEX platform	n/a	Not GWAS	Yes	NR		NR	NR		NR	NR	Yes	N/A
Dong, 2011	No	Yes	No	NR	NR	No	NR		Yes	Single race/ethnicity studied	N/A (single SNP)	Yes	PCR	ABI 3700 sequencing	n/a	Not GWAS	NR	NR		HWE	In HWE		NR	NR	No	N/A
Tkac, 2013	No	Yes	No	NR	NR	No	NR	NR	Yes	Single race/ethnicity studied	Did not discuss (used P<0.05)	Yes	PCR	Followed by melting analysis	n/a	n/a	NR	NR		HWE	In HWE		NR	NR	No	N/A
Choi, 2011	No	Yes	No	NR	NR	No	NR	Excluded	Yes	race-stratified and race-combined w/out adjustment for race	Did not discuss (used P<0.05)	No	PCR	TaqMan	n/a	n/a	NR	≥90%		HWE	In HWE		NR	NR	No	N/A
Sulfonylureas																										
Becker 2008	No	NR	No	NR	NR	No	NR		Yes	Single race/ethnicity studied	Did not discuss (used P<0.05)	Yes	Referenced	PCR	N/A	Not GWAS	NR	≥90%		HWE	In HWE		NR	NR	NR	N/A
Pearson 2007 (see above)																										
Suzuki 2006	No	NR	No	NR	NR	No	NR		NR	Single race/ethnicity studied	N/A (single SNP)	yes	PCR	TaqMan	N/A	Not GWAS	NR	NR		NR			NR	NR	Yes	N/A
Gloyn 2001	No	NR	No	NR	NR	No	NR		Yes	Single race/ethnicity studied	NR	Yes	RFLP (PCR-based, but not Taqman)		N/A	Not GWAS	NR	NR		HWE not checked			NR	NR	No	N/A
Repaglinide																										
He 2008	No	NR	Complete	<5%	No	No	No		No	Single race/ethnicity studied	Did not discuss (used P<0.05)	Yes	PCR		N/A	Not GWAS	Yes	≥90%		HWE	In HWE		NR	NR	No	N/A
Yu 2011	No	No	Complete	≥5%	No	No	Yes	Excluded	No	Single race/ethnicity studied	No correction	Yes	Referenced	Sequenom; MassARRAY Compact Analyzer	N/A	Not GWAS	NR	NR		HWE	In HWE		NR	NR	No	N/A
Qin 2010	No	NR	Partial	<5%	NR	No	No		No	Single race/ethnicity studied	N/A (single SNP)	Yes	PCR-sequencing		N/A	Not GWAS	NR	NR		HWE	In HWE		NR	NR	No	N/A
Huang 2010	No	NR	NR	NR	NR	No	NR		No	Single race/ethnicity studied	Did not discuss (used P<0.05)	Yes	PCR-RFLP		N/A	Not GWAS	NR	NR		HWE	In HWE		NR	NR	No	N/A
Gong, 2012	No	Yes	No	NR	NR	No	NR	NR	Yes	Single race/ethnicity studied	Did not discuss (used P<0.05)	Yes	PCR	RFLP	N/A	n/a	NR	NR		HWE	In HWE		NR	NR	No	N/A
Jiang 2012	No	Yes	Partial	>=5%	NR	No	Yes	NR	Yes	Single race/ethnicity studied	N/A (single SNP)	Yes	Sequenom	MassARRAY platform	N/A	n/a	Yes	NR		HWE	In HWE		No	NR	No	N/A
Sheng, 2011	No	Yes	No	NR	NR	No	NR	NR	Yes	Single race/ethnicity studied	N/A (single SNP)	Yes	PCR	RFLP	N/A	n/a	NR	NR		HWE	NR		NR	NR	No	N/A
Wang, 2012	No	Yes	No	NR	NR	No	NR	NR	Yes	Single race/ethnicity studied	N/A (single SNP)	Yes	PCR	RFLP	N/A	n/a	NR	NR		NR	NR		NR	NR	NR	N/A
Pioglitazone																										
Blüher 2003	No	NR	Complete	<5%	No	No	No		NR	NR	Did not discuss (used P<0.05)	Yes	PCR	Probe not listed, primers and denaturing gradient gel electrophoresis used to detect PPAR-γ2 gene mutations.	n/a	Not GWAS	NR	NR		HWE	Checked but no change based on P value 0.08		NR	NR	Yes	N/A
Saitou 2010	No	No	Complete	<5%	No	No	NR	NR	No	Single race/ethnicity studied	NR	Yes	Colorimetry-based allele-specific DNA primer probe		N/A	Not GWAS	NR	NR		NR	NR		NR	NR	No	N/A
Pei, 2013	No	No	No	NR	NR	No	NR	NR	Yes	Single race/ethnicity studied	Did not discuss (used P<0.05)	Yes	Sequenom	MassARRAY platform	n/a	n/a	NR	NR		HWE	In HWE		NR	NR	No	N/A
Rosiglitazone																										
Wang 2008	No	NR	Complete	≥5%	NR	No	No		NR	Single race/ethnicity studied	Did not discuss (used P<0.05)	yes	PCR	RFLP	n/a	Not GWAS	NR	≥90%	16 random samples checked	HWE	In HWE		NR	n/a	No	N/A
Yu 2011 (see above)																										
Jiang 2012 (see above)																										
Zhou, 2011	No	Yes	No	NR	NR	No	NR	NR	Yes	single race/ethnicity	Did not discuss (used P<0.05)	Yes	PCR	RFLP	n/a	n/a	NR	≥90%	Stated all repeated ones were concordant	HWE	NR	NR	NR	NR	NR	N/A
Acarbose																										
Andrullonyte 2007	No	Yes	No	NR	NR	No	NR		Yes	Single race/ethnicity studied	Permutation and exact test of nominally significant results [resampled dataset and reanalyzed 1000 times, divided p value by 1000]	Yes	PCR	taqman	N/A	Not GWAS	Yes	≥90%		HWE	In HWE		NR	NR	Yes	N/A
Andrullonyte 2006	No	Yes	No	NR	NR	No	No		Yes	Single race/ethnicity studied	Did not discuss (used P<0.05)	Yes	Referenced	PCR, amplified with GeneAmp PCR, fluoro w/ ABI Prism	N/A	Not GWAS	NR	NR		HWE	+3818247 not in HWE		NR	NR	Yes	N/A
Zacharova 2005	No	Yes	No	NR	NR	No	NR		Yes	Single race/ethnicity studied	N/A (single SNP)	Yes	PCR	taqman	N/A	Not GWAS	NR	NR		HWE	In HWE		NR	NR	Yes	N/A
Andrullonyte 2004	No	Yes	No	NR	NR	No	NR		Yes	Single race/ethnicity studied	Did not discuss (used P<0.05)	Yes	Referenced	PCR-RFLP for gly482 ser using dynazyme and PCR-SSCP used for 12ala with dynazyme	N/A	Not GWAS	NR	NR		HWE	In HWE		NR	NR	Yes	N/A