TABLE 26.2. How replicable are association studies?			
Associated Gene, Phenotype	Number of Studies (Total)	Number of Studies ( $p < 0.05$ ) Same Direction as Original Report	Number of Studies ( $p < 0.05$ ) Opposite Direction as Original Report
ABCC8, type 2 diabetes <sup>a</sup>	9	1	1
ABCC8, type 2 diabetes <sup>a</sup>	4	2	0
ADD1, hypertension	18	5	2
APOE, schizophrenia	12	0	1
BLMH, Alzheimer's disease	5	0	0
COL1A1, osteoporotic fracture	12	5	0
COMT, bipolar disorder	12	0	0
COMT, schizophrenia	9	0	1
CTLA4, type 1 diabetes	20	8	0
DRD2, schizophrenia	8	2	1
DRD3, schizophrenia	48	5	2
GSTM1, breast cancer	15	0	0
GSTM1, head/neck cancer	25	3	1
GYS1, type 2 diabetes	3	0	1
HTR2A, schizophrenia	28	3	1
INSR, type 2 diabetes	4	1	0
INSR, type 2 diabetes	4	0	0
KCNJ11, type 2 diabetes	6	0	0
NTF3, schizophrenia	7	0	0
PON1, coronary artery disease	14	5	0
PPARG, type 2 diabetes	14	4	1
SERPINE1, myocardial infarction	13	1	0
SLCA1, type 2 diabetes	3	2	0
SLCA2, type 2 diabetes	3	0	0
TPH, bipolar disorder	5	0	0
Total	301	47	12

From Table 1 of Lohmueller K.E. et al. 2003.  $\it Nat. Genet.$  33: 177–182 ( $^{\odot}$  Macmillan Publishers, www.nature.com).

A survey of 25 associations between markers and complex diseases found a total of 301 follow-up studies. Of these, 59 were significant at the 5% level, far higher than the number expected if the initial reports had been "false positives" ( $301 \times 0.05 \sim 15$ ), but still a minority. Moreover, many of the subsequent significant findings were in the opposite direction. The significant replications were concentrated among 11 of the associations (in bold type), which suggests that about one-half of these associations actually exist.

<sup>&</sup>lt;sup>a</sup>The two entries for *ABCC8* in the first and second rows are for variants in the intron and exon, respectively.