Outcome:		Disease		
Design:		Matched case-control		
Hypothesis:		Gene only		
Desired power:		0.800000		
Significance:		5.00000e-008, 2-sided		

Gene

 Mode of inheritance: Log-additive

 Allele frequency: 0.1000 to 0.5000 by 0.1000

Disease model   Summary parameters

 P_0 0.010000 $*k_P$ 0.010199

 R_G: 1.1000   (*indicates calculated value)

Parameter	Null	Full	Reduced
Gene	$\beta_G=0$	β_G	——

Frequency	R_G	N Gene	k_P
0.100000	1.1000	46693	0.010199
	1.2000	12355	0.010399
	1.3000	5799	0.010601
0.200000	1.1000	26524	0.010399
	1.2000	7088	0.010806
	1.3000	3359	0.011219
0.300000	1.1000	20405	0.010602
	1.2000	5504	0.011220
	1.3000	2632	0.011854
0.400000	1.1000	18025	0.010807
	1.2000	4906	0.011642
	1.3000	2366	0.012507
0.500000	1.1000	17467	0.011013
	1.2000	4795	0.012072
	1.3000	2331	0.013177

N is the number of case-control pairs required for the desired power