Outcome: Disease Design: Unmatch

Unmatched case-control (1:19)

Gene only 0.800000

Ν

Significance: 5.00000e-008, 2-sided

Gene

Hypothesis:

Desired power:

Mode of inheritance: Log-additive

Allele frequency: 0.1000 to 0.5000 by 0.1000

Disease model Summary parameters

 $P_0$  0.050000  $*k_P$  0.050949

R<sub>G</sub>: 1.1000 (\*indicates calculated value)

Parameter	Null	Full	Reduced
Gene	$\beta_G=0$	$\beta_{G}$	

Frequency	$R_{G}$	Gene	$k_P$
0.100000	1.1000	24366	0.050949
	1.2000	6396	0.051898
	1.3000	2979	0.052844
0.200000	1.1000	13868	0.051907
	1.2000	3682	0.053828
	1.3000	1734	0.055760
0.300000	1.1000	10690	0.052873
	1.2000	2870	0.055791
	1.3000	1365	0.058748
0.400000	1.1000	9462	0.053848
	1.2000	2567	0.057787
	1.3000	1234	0.061808
0.500000	1.1000	9188	0.054831
	1.2000	2518	0.059815
	1.3000	1221	0.064940
		16 11 1 1	

N is the number of cases required for the desired power The required number of controls is 19xN