

Group 4

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Power Q1.3

What sample size is needed to detect it with power of 80% at Genome Wide $P=0.05$, in study assessing 500,000 SNPs

P(D) cases: $0.3 = p_1$

P(D) controls: $0.2 = p$

Power 80%

α : $0.05/500,000 = 10^{-7}$

For Z_α : use R, type in: `sqrt(qchisq(1-0.05/500000,1))`

Z_α : 5.33

Z_β : 0.84

Power Q1.3

Formula:

$$N = ((2p(1-p_1) + p_1(2-p_1) - p^2) * (Z_\alpha + Z_\beta)^2) / (4(p_1-p)^2)$$

$$N = ((2*0.2*(1-0.3) + 0.3*(2-0.3) - 0.2^2) * (5.33 + 0.84)^2) / (4*(0.3 - 0.2)^2)$$

$$N = 454.3$$

So you need 455 cases and 455 controls

Power Q2

Power using Genetic Power Calculator
<http://pngu.mgh.harvard.edu/~purcell/gpc/>

T2D locus IGF2BP2

600 cases

1200 controls

From article (Table 1):

Allele frequency risk allele in controls: 0.30

OR: 1.28 (FUSION stage 1)

OR is for allelic test

Input screen

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http://pngu.mgh.harvard.edu/~purcell/gpc/cc2.html

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Genetic Power Calculator

Case - control for discrete traits

High risk allele frequency (A) : (0 - 1)

Prevalence : (0.0001 - 0.9999)

Genotype relative risk Aa : (>1)

Genotype relative risk AA : (>1)

D-prime : (0 - 1)

Marker allele frequency (B) : (0 - 1)

Number of cases : (0 - 10000000)

Control : case ratio : (>0)
(1 = equal number of cases and controls)

Unselected controls? (* see below)

User-defined type I error rate : (0.00000001 - 0.5)

User-defined power: determine N : (0 - 1)
(1 - type II error rate)

Created by [Shaun Purcell](#) 28.Aug.2006

http://pngu.mgh.harvard.edu/~purcell/gpc/qtdt.html

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Output

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http://pngu.mgh.harvard.edu/~purcell/cgi-bin/cc2.cgi

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Genetic Power Calculator

[Case-control for discrete traits](#)

Case-control parameters

Number of cases	600
Number of controls	1200
High risk allele frequency (A)	0.3
Prevalence	0.1
Genotypic relative risk Aa	1.25
Genotypic relative risk AA	1.56
Genotypic risk for aa (baseline)	0.08655

Marker locus B

High risk allele frequency (B)	0.3
Linkage disequilibrium (D')	1
Penetrance at marker genotype bb	0.08655
Penetrance at marker genotype Bb	0.1082
Penetrance at marker genotype BB	0.135
Genotypic odds ratio Bb	1.28
Genotypic odds ratio BB	1.647

Expected allele frequencies

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Power for single test

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Expected allele frequencies

	Case	Control
B	0.3487	0.2946
b	0.6513	0.7054

Expected genotype frequencies

	Case	Control
BB	0.1215	0.0865
Bb	0.4544	0.4162
bb	0.4241	0.4973
H-W test NCP	7.934e-05	0.002237
Power (alpha=0.05)	0.05001	0.05026

Case-control statistics

Sample NCP = 10.91

Alpha	Power	N cases for 80% power
0.1	0.9513	340.1
0.05	0.9103	431.8
0.01	0.7662	642.6
0.001	0.5047	939.5
0.05	0.9103	431.8

Controls are selected (i.e. screened for not being a case)

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Power for GWA 300K

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Genetic Power Calculator

Case - control for discrete traits

High risk allele frequency (A)	: 0.30	(0 - 1)
Prevalence	: 0.1	(0.0001 - 0.9999)
Genotype relative risk Aa	: 1.25	(>1)
Genotype relative risk AA	: 1.56	(>1)
D-prime	: 1	(0 - 1)
Marker allele frequency (B)	: 0.30	(0 - 1)
Number of cases	: 600	(0 - 10000000)
Control : case ratio	: 2	(>0) (1 = equal number of cases and controls)
<input type="checkbox"/> Unselected controls? (* see below)		
User-defined type I error rate	: 0.000000167	(0.00000001 - 0.5)
User-defined power: determine N (1 - type II error rate)	: 0.80	(0 - 1)

Process Reset

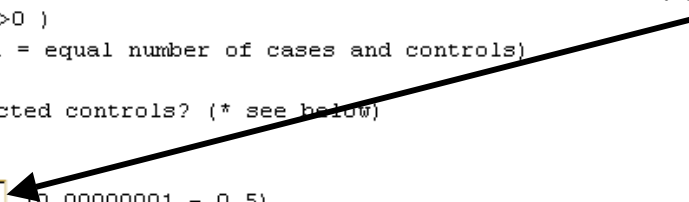
Created by [Shaun Purcell](#) 28.Aug.2006

Meta: unselected controls indicates a true random population sample (e.g. for a 1% disease, 1% of controls would also, by chance, have the disease); if

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GW significance 5%:
 $\alpha = 5/300,000$
 $= 1.67E-07$



Power for GWA 300K

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0.001	0.5047	939.5
1.67e-07	0.02678	2030

Controls are selected (i.e. screened for not being a case)

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