A) coding SNVs from the diploid genome in expression-based candidates

candidate status	nsSNVs (miss, nons)	Rn / 10E-03	comparison to NSG by permutation	sSNVs	Rs / 10E-03	comparison to NSG by permutation	Rn / Rs	comparison to NSG
RSG	743 (737,6)	0.365 [0.30-0.38]	P < 1E-5	800	1.31 [1.19-1.41]	P= 0.08418	0.278	P < 1E-05
ISG	571 (568,3)	0.271	P < 1E-5	740	1.199	P= 0.78416	0.226	P= 10E-5
NSG	427 (424,3)	0.177	NA	850	1.179	NA	0.15	NA

B) coding SNVs from the diploid genome in keyword-based candidates

candidate status	nsSNVs (miss, nons)	Rn / 10E-03	comparison to NSG by permutation	sSNVs	Rs / 10-E3	comparison to NSG by permutation	Rn / Rs	comparison to NSG by permutation
ISG	578	0.4803	P < 1E-05	570	1.413	P = 0.02393	0.303	P < 1E-05
NSG	571	0.2258	NA	1078	1.583	NA	0.159	NA

C) coding SNVs from the 200 exomes in expression-based candidates

candidate status	nsSNVs (miss, nons)	Rn / 10E-03	comparison to NSG by permutation	sSNVs	Rs / 10E-03	comparison to NSG by permutation	Rn / Rs	comparison to NSG by permutation
RSG	2324 (2290,34)	1.14 [1.03-1.19]	P < 1E-05	2204	3.62 [3.31-3.77]	P = 0.00073	0.31	P < 1E-05
ISG	2137 (2112,25)	1.01	P < 1E-05	2133	3.458	P = 0.01389	0.29	P = 0.00022
NSG	1807 (1791,16)	0.749	NA	2221	3.08	NA	0.243	NA

D) coding SNVs from the 200 exomes in keyword-based candidates

candidate status	nsSNVs (miss, nons)	Rn / 10E-03	comparison to NSG by permutation	sSNVs	Rs / 10E-03	comparison to NSG by permutation	Rn / Rs	comparison to NSG by permutation
ISG	1708 (1684/24)	1.419	P < 1 E-05	1462	3.89	P = 0.28535	0.349	P < 1 E-05
NSG	2258 (2239/19)	0.8932	NA	2971	4.06	NA	0.229	NA