Table S1. Calculation of Rare Variant Minor Allele Frequency (MAF) Cutoff

# of ♂ X Chrs (m)	# of ♀ X Chrs (f)	# of X Chrs Total
525	2 x 567	1659

# of mut. alleles in 1000 Genomes (n)	Prob. alleles only in ♀ carriers	Prob. (eq) alleles only in ♀ carriers
1	68.35%	$$\prod_{i=(f-n+1)}^{f} \frac{2i}{2i+m}$$
2	46.70%	
3	31.88%	
4	21.76%	
5	14.84%	
6	10.11%	
7	6.89%	
8	4.69%	
9	3.19%	
10	2.17%	
11	1.48%	
12*	**1.00%**	**12 / 1659 = 0.73%**

* At 12 copies of a mutant allele in the 1000 Genomes dataset, the probability of seeing all 12 alleles in only female carriers is only 1%. At >12 copies of a mutant allele, the probability is less than 1%. 12 mutant allele copies is ~ 0.73% minor allele frequency. We can safely assume that potential pathological variants with a MAF < 0.73% could exist purely in a female carrier state. Therefore, such variants should be removed from dbSNP before implemention of a dbSNP-based filter.