Sex, ID	Gene:	Nucleotide Variant:	Protein Alteration:	De novo:	Zygosity:	ExAC / gnomAD Allele Frequency
F, 1001	*CDK13*	c.2524A>G	p.N842D	Yes	het	Not present
	No other pathogenic, likely pathogenic or *de novo* variants reported.					
F, 1002	*CDK13*	c.2525A>G	p.N842S	Yes	het	Not present
	No other pathogenic, likely pathogenic or *de novo* variants reported.					
M, 1003	*CDK13*	c.2525A>G	p.N842S	Yes	het	Not present
	No other pathogenic, likely pathogenic or *de novo* variants reported.					
M, 1004	*CDK13*	c.2525A>G	p.N842S	Yes	het	Not present
	No other pathogenic, likely pathogenic or *de novo* variants reported.					
F, 1005	*CDK13*	c.2525A>G	p.N842S	Yes	het	Not present
	No other pathogenic, likely pathogenic or *de novo* variants reported.					
F, 1006	*CDK13*	c.2525A>G	p.N842S	Yes	het	Not present
	No other pathogenic, likely pathogenic or *de novo* variants reported.					
M, 1007	*CDK13*	c.2525A>G	p.N842S	Yes	het	Not present
	No other pathogenic, likely pathogenic or *de novo* variants reported.					
M, 1008	*CDK13*	c.2200A>G	p.K734E	Yes	het	Not present
	No other pathogenic, likely pathogenic or *de novo* variants reported.					

TABLE S1: List of all pathogenic, likely pathogenic or *de novo* variants identified on the clinical genetics laboratory report for Individuals 1001-1008. No additional pathogenic, likely pathogenic or de novo variants were reported on the clinical laboratory exome sequencing reports. None of the *CDK13* variants in this study are listed in ExAC or gnomAD databases (accessed on 6/17/17). Note that ID 1009 was obtained from research sequencing and a paternal sample was not available, thus *de novo* status is unknown. *CDK13* Isoform: NM_003718.