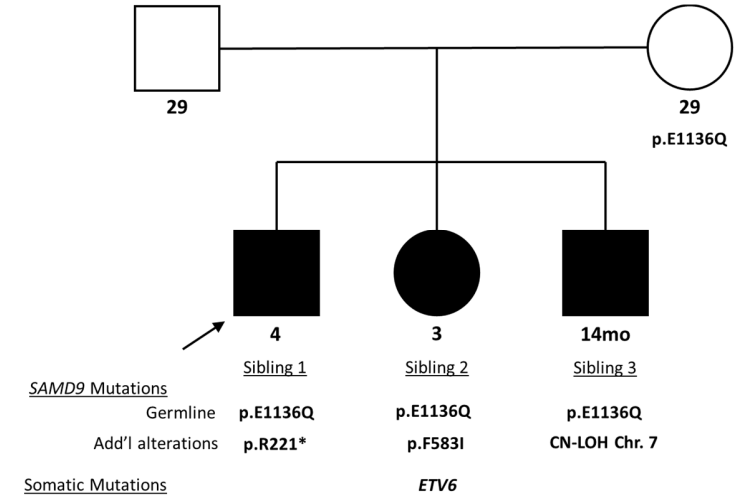
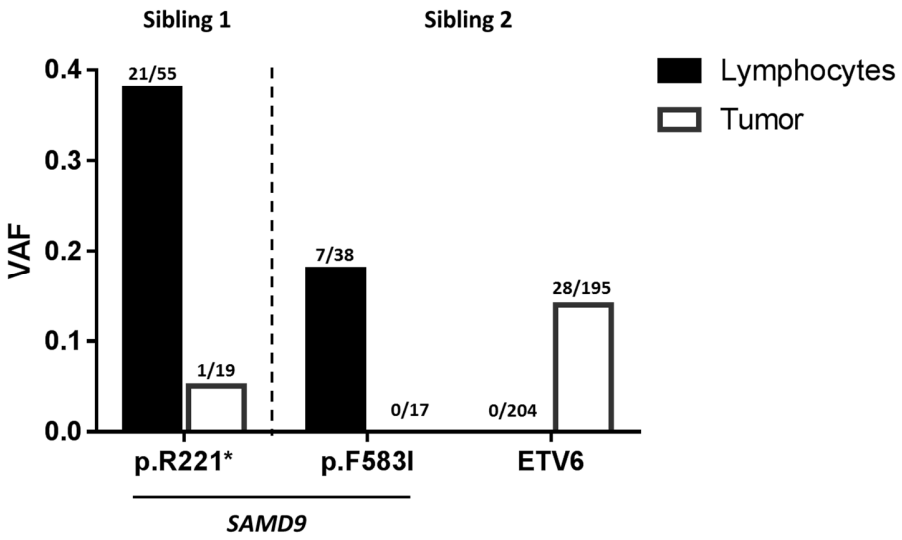
Supplemental Figure 3. A.) Family pedigree identifying those with germline and additional *SAMD9* mutations, as well as relevant somatic mutations. Monosomy 7 status indicated by filled (monosomy 7) or open (untested karyotype) symbols. Ages at diagnosis are below pedigree symbols. B.) Variant allele frequency (VAF) obtained from WES data of additional *SAMD9* and other somatic mutations. Read counts are listed in fractions above each data point. The read counts for the *ETV6* mutation are based on amplicon deep sequencing. C.) Tables depicting results of long range PCR followed by subcloning and Sanger sequencing to determine the relationship (*cis* or *trans*) of additional *SAMD9* variants to p.E1136Q.

A



B



C

patient	clone	R221*	E1136Q
SJ015856	1	mut	mut
SJ015856	2	mut	mut
SJ015856	3	mut	mut
SJ015856	4	mut	mut
SJ015856	5	mut	mut
SJ015856	6	mut	mut
SJ015856	7	ref	ref
SJ015856	8	ref	ref
SJ015856	9	ref	mut
SJ015856	10	ref	ref

patient	clone	F583I	E1136Q
SJ015855	1	ref	ref
SJ015855	2	ref	mut
SJ015855	3	ref	ref
SJ015855	4	ref	mut
SJ015855	5	ref	ref
SJ015855	6	ref	mut
SJ015855	7	ref	ref
SJ015855	8	ref	mut
SJ015855	9	ref	ref
SJ015855	10	ref	mut
SJ015855	11	ref	mut
SJ015855	12	ref	ref
SJ015855	13	ref	ref
SJ015855	14	ref	ref
SJ015855	15	ref	ref
SJ015855	16	ref	mut
SJ015855	17	ref	mut
SJ015855	18	mut	mut
SJ015855	19	mut	mut
SJ015855	20	ref	ref
SJ015855	21	ref	ref
SJ015855	22	ref	mut