

		MNGT-1	MNGT-2
Age (years)		6	9
Gender		M	F
Location		Temporal	Parietal
Symptoms		New onset seizures	Lifelong seizures, resolved after first surgery 5 years prior
Imaging Characteristics		Cortical based, small cystic areas, T2 hyperintense	T1 and T2 signal alteration extending from surgical cavity
Primary vs. Recurrent		Primary	Recurrent (after 5 years)
Glial-Neuronal element (GNE)		No	No
Pools of Mucin		No	No
Oligodendroglial-like cells		Yes	Yes
Neurons		Yes	Yes
Floating Neurons		No	No
Astrocytes		Yes	Yes
Calcification		Yes (sparse)	Yes (abundant)
Microvascular changes		No	No
Rosenthal Fibers		No	No
Eosinophilic Granular Bodies		No	No
Necrosis		No	No
CD34 Immunohistochemistry		Positive	Obscured by calcification
Ki-67		1-2%	<1%
Gene Fusion	5' Partner	FGFR2 (NM_000141.4) exon 17	FGFR2 (NM_000141.4) exon 17
	3' Partner	INA (NM_032727.3) exon 2	INA (NM_032727.3) exon 2

Supplemental Table 1. Summary of the clinical, radiographic, histopathologic, and *FGFR2-INA* fusion in MNGT.

MNGT #	Chromosome	Position^	TranscriptID	Nucleotide change	Gene	Expected Protein change	Classification*	VAF	Exonic Function	ExaC Frequency	dbSNP	SIFT (v6.2.0)	MutationTaster (v2013)	Nucleotide/Amino Acid Conservation	COSMIC Entry	Notes
1	chr 9	139410051	NM_017617.4	c.1787C>T	NOTCH1	p.Thr596Met	Tier 3	0.46	nonsynonymous SNV	0.0002	rs61755997	deleterious	disease causing	high/high	CM061876	
1	chr19	37866098	NM_004448.3	c.607C>T	ERBB2	p.Arg203Cys	Tier 3	0.44	nonsynonymous SNV	N/A	N/A	tolerated	polymorphism	none/weak	COSM3970014	
1	chr19	30308110	NM_001238.3	c.247G>C	CCNE1	p.Asp83His	Tier 3	0.44	nonsynonymous SNV	0.0003	rs147120845	tolerated	N/A	weak/moderate	No	
2	chr11	108155009	NM_000051.3	c.3802delG	ATM	p.V1268*	Pathogenic	0.53	stopgain	0.00003	rs587779834	N/A	N/A	N/A	COSM1315821	Confirmed germline on follow-up testing
2	chr1	118166196	NM_017709.3	c.706C>A	FAM46C	p.P236T	Tier 3	0.48	nonsynonymous SNV	N/A	N/A	deleterious	disease causing	high/high	No	
2	Chr1	120458982	NM_024408.3	c.6363G>C	NOTCH2	p.K2121N	Tier 3	0.46	nonsynonymous SNV	0.0004	rs144047610	tolerated	disease causing	weak/high	No	
2	chr1	161298206	NM_003001.3	c.98C>T	SDHC	p.T33M	Tier 3	0.40	nonsynonymous SNV	0.000057	rs148566767	tolerated	disease causing	moderate/moderate	No	

Supplemental Table 2. Single nucleotide variants identified in two MNGT tumors.

Abbreviation: VAF = Variant allele fraction, N/A = not applicable, SNV = single nucleotide variant

^Genomic position based on genome build hg19.

*Based on Li et al. 2017 JMD [7] except for ATM variant which was confirmed germline and is classified based on ACMG Criteria (Richards et al. 2015 PMID: 25741868)

Chromosome	Abnormality	Copies	Notes
X WC	Gain	4	
2 WC	cnLOH	2	
3 WC	Gain	3	
5 WC	Gain	3	
6 WC	Gain	3	
7 WC	Gain	4	includes BRAF
8 WC	Gain	3	includes FGFR1
9 WC	Gain	4	
10 WC	cnLOH	2	
11 WC	Gain	3	
12 WC	Gain	3	
13 WC	cnLOH	2	
14 WC	Gain	3	
15 WC	Gain	3	
16 WC	cnLOH	2	
19 WC	Gain	4	
20 WC	Gain	3	
22 WC	Gain	3	

Supplemental Table 3. Copy number variants identified in MNGT-2.

Note: No copy number changes were detected in MNGT-1

Abbreviations: WC- whole chromosome; cnLOH- copy neutral loss of heterozygosity

RNA-seq panel included at least 1 or more targets in the following genes:	DNA-based NGS sequencing panel included the coding region and 5 base pairs flanking intronic sequences of the following 237 genes:
<p><i>ABL1, ABL2, AKT3, ALK, ARHGAP26, AXL, BCL2, BCL6, BCR, BRAF, BRD3, BRD4, CAMTA1, CFBF, CCNB3, CCND1, CIC, CRFL2, CSF1R, DUSP22, EGFR, EPC1, EPOR, ERG, ESR1, ESRRA, ETV1, ETV4, ETV5, ETV6, EWSR1, FGFR1, FGFR2, FGFR3, FGR, FOXO1, FUS, GLI1, GLIS2, HMGA2, IL2RB, INSR, JAK2, JAZF1, KMT2A, MALT1, MAML2, MAST1, MAST2, MEAF6, MECOM, MET, MKL1, MKL2, MSMB, MUSK, MTB, NCOA2, NOTCH1, NOTCH2, NRG1, NTRK1, NTRK2, NTRK3, NUMBL, NUP214, NUP98, NUT, PAX5, PDGFB, PDGFRA, PDGFRB, PICALM, PIK3CA, PKN1, PLAG1, PPARG, PRKCA, PRKCB, PTK2B, RAF1, RARA, RBM15, RELA, RET, ROS1, RSPO2, RSPO3, RUNX1, RUNX1T1, SS18, STAT6, TAF15, TAL1, TCF12, TCF3, TERT, TFE3, TFEB, TFG, THADA, TMPRSS2, TSLP, TYK2, USP6, YWHAE</i></p>	<p><i>ABL1, ACVR1, AKT1, AKT2, AKT3, ALK, APC, AR, ARAF, ARID1A, ARID1B, ARID2, ASXL1, ATM, ATR, ATRX, AURKA, AURKB, AXIN1, AXL, B2M, BAP1, BARD1, BCL2, BCL6, BCOR, BCORL1, BLM, BRAF, BRCA1, BCRA2, BRD4, BRIP1, CARD11, CFBF, CBL, CCND1, CCND2, CCND3, CCNE1, CD274, CD79B, CDC73, CDH1, CDK12, CDK4, CDK6, CDK8, CDKN1B, CDKN2A, CDKN2B, CDKN2C, CHEK1, CHEK2, CIC, CREBBP, CRKL, CRLF2, CSF1R, CTCF, CTNNB1, DAXX, DDR2, DNMT3A, DOT1L, EED, EGFR, EP300, EPHA3, EPHA5, EPHB1, ERBB2, ERBB3, ERBB4, ERG, ESR1, ETV6, EZH2, FAM46C, FANCA, FANCC, FBXW7, FGF19, FGF3, FGF4, FGFR1, FGFR2, FGFR3, FGFR4, FLCN, FLT1, FLT3, FLT4, FOXL2, FOXP1, FUBP1, GATA1, GATA2, GATA3, GNA11, GNAQ, GNAS, GRIN2A, GSK3B, H3F3A, HGF, HIST1H1C, HIST1H3B, HNF1A, HRAS, IDH1, IDH2, IGF1R, IKBKE, IKZF1, IL7R, INPP4B, IRF4, IRS2, JAK1, JAK2, JAK3, JMJD1C, JUN, KDM5A, KDM5C, KDM6A, KDR, KEAP1, KIT, KMT2A, KMT2C, KRAS, MAP2K1, MAP2K2, MAP2K4, MAP3K1, MAPK1, MCL1, MDM2, MDM4, MED12, MEF2B, MEN1, MET, MITF, MLH1, MPL, MRE11A, MSH2, MSH6, MTOR, MUTYH, MYB, MYC, MYCN, MYD88, MYOD1, NF1, NF2, NFE2L2, NKX2-1, NOTCH1, NOTCH2, NPM1, NRAS, NTRK1, NTRK2, NTRK3, PALB2, PAX5, PBRM1, PDCD1, PDGFRA, PDGFRB, PHOX2B, PIK3CA, PIK3CG, PIK3R1, PIK3R2, PIM1, PPM1D, PPP2R1A, PRDM1, PRKAR1A, PTCH1, PTEN, PTPN11, RAD50, RAD51, RAF1, RARA, RB1, RET, RHOA, RICTOR, RNF43, ROS1, RPTOR, RUNX1, SDHA, SDHB, SDHC, SDHD, SETD2, SF3B1, SMAD2, SMAD4, SMARCA4, SMARCB1, SMO, SOCS1, SOX2, SPEN, SPOP, SRC, STAG2, STK11, SUFU, SUZ12, TERT, TET2, TGFB2, TNFAIP3, TNFRSF14, TOP1, TP53, TP63, TSC1, TSC2, TSHR, U2AF1, VHL, WHSC1, WT1, AMER1, XPO1</i></p>

Supplemental Table 4. Targeted RNA-seq fusion panel genes and 237 cancer related genes sequenced by NGS

		<i>FGFR2 e17 - INA e2</i>
Primer Sequence	Inner left	CGAATTCTCACTCTCACAACCA
	Inner right	GGTGTTCCTCAGATCATCTCC
	Outer left	GAAGGAAGGACACAGAATGGAT
	Outer right	TTTGACATTGAGCAAGTCCTG

Supplemental Table 5. PCR Primers for *FGFR-INA* fusion confirmation