Supplementary Tables

Supplementary Table-S1

Sample	Subtype	Tumor site	Age	Sex	Stage	Follow-up	microRNA data	mRNA data
1	YST	Ovary	14	F	4	NED		
2	YST	Vagina	1	F	1	NED	✓	
3	YST	Testis	1	M	2	NED	✓	✓
4	YST	Ovary	4	F	4	NED	✓	
5	YST	Ovary	2	F	1	REL	✓	✓
6	YST	Ovary	13	F	3	NED	✓	✓
7	YST	Ovary	14	F	1	NED	✓	✓
8	YST	Ovary	12	F	2	NED		
9	YST	Sacrococcygeal	1	M	4	NED		
10	Germinoma	Central nervous system	12	M	N/A	DOD		
11	Germinoma	Ovary	8	F	N/A	NED	✓	
12	Germinoma	Ovary	14	F	3	NED	✓	
13	Germinoma	Lymph node metastasis from ovary	11	F	4	REL	✓	
14	Germinoma	Ovary	13	F	1	REL	✓	✓
15	Germinoma	Testis	25	M	1	NED	✓	
16	Germinoma	Testis	35	M	1	NED	✓	
17	Germinoma	Ovary	12	F	N/A	NED		
18	Germinoma	Ovary	9	F	3	NED	✓	
19	Embryonal ca	Testis	Adult; N/A	M	N/A	N/A		
20	Embryonal ca	Testis	15	M	N/A	N/A	✓	
21	Embryonal ca	Lung metastasis from testis	15	M	4	REL	✓	✓
22	Cell Line	N/A	N/A	N/A	N/A	N/A	✓	
23	Cell Line	N/A	N/A	N/A	N/A	N/A	✓	
24	Cell Line	N/A	N/A	N/A	N/A	N/A	✓	
25	Cell Line	N/A	N/A	N/A	N/A	N/A	✓	
26	Cell Line	N/A	N/A	N/A	N/A	N/A	✓	
27	Cell Line	N/A	N/A	N/A	N/A	N/A	✓	
28	Teratoma	Mediastinum	2	F	Mature	NED		
29	Teratoma	Ovary	11	F	Immature	NED		
30	Teratoma	Ovary	15	F	Immature	NED	✓	
31	Teratoma	Abdominal	0	M	Immature	NED	✓	
32	Teratoma	Ovary	3	F	Mature	NED	✓	

Key

YST = yolk sac tumor; Embryonal ca = embryonal carcinoma; NED = no evidence of disease; REL = relapsed; DOD = died of disease; N/A not available; ✓= data available

Supplementary Table-S2

Gene	**5’ to 3’ forward primer sequence**	**5’ to 3’ reverse primer sequence**	**Product size (bp)**
LIN28	**GAAGCGCAGATCAAAAGGAG**	**CTGATGCTCTGGCAGAAGTG**	**114**
LIN28B	**GGAGCCCCTGTTTAGGAAGT**	**TCAAGGCCACCACAGTTGTA**	**97**
ZCCHC11	**TGCTTCAGGAATTGAAGACG**	**TCATCTATCACAGTGGCATTTTC**	**114**
MYCN	**ACACCCTGAGCGATTCAGAT**	**CTTGGTGTTGGAGGAGGAAC**	**104**
CCNF	**CAGCTGCAGAGGACTCACAA**	**CCTCCTCAAACAGGTCATGG**	**109**
RRM2	**GCTGGAACTGGGTTTTAGCA**	**CCATCCTCTGATACTCGCCTA**	**104**
AURKB	**GTCACCCCATCTGCACTTGT**	**ACGCCCAATCTCAAAGTCAT**	**144**
MKI67	**AGCCCCAACCAAAAGAAAGT**	**TTTGTGCCTTCACTTCCACA**	**131**
C12orf5	**CTCGCTTCGCTCTGACTGTT**	**AGCTGCTGCTTGTTTAAATCC**	**119**
FZD5	**GCTTCTCAGCGGAGTGACC**	**GCTGGGGAGAGACGGTTAG**	**123**
SMAGP	**AGAAGATGGAGCCAGCACAG**	**GGTGACGTAGCTGCCTTTGT**	**121**
PGK1	**AAGCTGGACGTTAAAGGGAAG**	**AATTTGATGCTTGGGACAGC**	**116**
RAB25	**CGAATGTTCGCTGAAAACAA**	**GTCCGGATGCTGTTCTGTCT**	**140**
MRS2	**CGTGAGCTTAGGGTGCTGAT**	**GAGAAGGTTCCCATGGTCAG**	**113**
KRAS	**GCAAGAGTGCCTTGACGATA**	**TCCAAGAGACAGGTTTCTCCA**	**118**
SLC2A3	**GACTCTTCGTCAACCGCTTT**	**CATAAAGCAGCCACCAGTGA**	**80**
LASP1	**GTATCCCACGGAGAAGGTGA**	**GTGTCATCTTGCAGGTCTCG**	**80**
RAB15	**GGCTGATGAGGAGCAGAAAC**	**TCAGACGCGTGAATGACTCT**	**131**
AGL	**CCCGGAGACTACTGCAAAGA**	**ACTGGGCATTCTCATTGGTC**	**119**
HMGA2	**AGCGCCTCAGAAGAGAGGAC**	**CTTCCCCTGGGTCTCTTAGG**	**87**
YWHAZ	**ACTTTTGGTACATTGTGGCTTCAA**	**CCGCCAGGACAAACCAGTAT**	**95**
RPL13A	**CCTGGAGGAGAAGAGGAAAGAGA**	**TTGAGGACCTCTGTGTATTTGTCAA**	**126**
HMBS	**GGCAATGCGGCTGCAA**	**GGGTACCCACGCGAATCAC**	**64**
ACTB	**Qiagen Hs_ACTB_2_SG**	**Qiagen Hs_ACTB_2_SG**	**N/A**

Supplementary Table-S3

Rank	microRNA	5’ to 3’ Sequence	Fold change	Adjusted *p*-value
1	*let-7e*	UGAGGUAGGAGGUUGUAUAGUU	-2.22	4.45×10^{-7}
2	miR-98	UGAGGUAGUAAGUUGUAUUGUU	-3.53	1.21×10^{-5}
3	*let-7d*	UGAGGUAGUAAGUUGUAUUGUU	-3.25	4.01×10^{-5}
4	*let-7a*	UGAGGUAGUAGGUUGUAUAGUU	-3.68	9.19×10^{-5}
5	*let-7c*	UGAGGUAGUAGGUUGUAUGGUU	-3.56	1.18×10^{-4}
6	*let-7g*	UGAGGUAGUAGUUUGUACAGUU	-2.46	2.34×10^{-4}
7	*let-7b*	UGAGGUAGUAGGUUGUGUGGUU	-3.43	3.41×10^{-4}
8	*let-7f*	UGAGGUAGUAGAUUGUAUAGUU	-2.36	8.56×10^{-4}
9	*let-7i*	UGAGGUAGUAGUUUGUGCUGUU	-2.23	2.63×10^{-3}

Supplementary Table-S4

Gene	Accession Number	Chromosomal Location	Pediatric rank (n=50)	Pediatric $\log_2$ fold change	Adult rank (n=106)	Adult $\log_2$ fold change	*Let-7* linear regression *p*-value (microarray)
LIN28	NM_024674	1p36.11	1	4.69	3	3.86	0.000033
FZD5	NM_003468	2q33.3	2	4.48	1	5.27	0.0077
SLC2A3	AB209607	12p13.3	3	3.73	2	5.24	0.016
RRM2	NM_001034	2p24-25	4	3.54	27	2.40	0.00063
ADM	NM_001124	11p15.4	5	3.25	19	2.53	0.011
CDH1	NM_004360	16q22.1	6	2.95	4	3.74	0.027
RAB15	NM_198686	14q23.3	7	2.63	14	2.60	0.008
MRS2	NM_020662	6p22.1-3	8	2.54	36	2.24	0.0046
SMAGP	NM_001031628	12q13.3	10	2.37	60	1.93	0.000022
C12orf5	NM_020375	12p13.3	11	2.29	102	1.57	0.037
MYCN	NM_005378	2p24.3	12	2.29	43	2.11	0.0025
HIC2	NM_015094	22q11.21	13	2.28	96	1.63	0.012
C1orf106	NM_001142569	1q32.1	18	2.17	31	2.31	0.0021
PGK1	NM_000291	Xq13.3	20	2.17	24	2.42	0.0024
AURKB	NM_004217	17p13.1	22	1.99	52	2.01	0.00067
SMC1A	NM_006306	Xp11.21-22	24	1.95	34	2.29	0.0072
DSG2	NM_001943	18q12.1	25	1.90	18	2.53	0.00074
AGL	NM_000028	1p21	28	1.82	48	2.03	0.00028
SPRED2	NM_001128210	2p14	29	1.81	37	2.21	0.0056
MKI67	NM_001145966	10q26.2	32	1.78	78	1.78	0.00025
CCNF	NM_001761	16p13.3	33	1.75	94	1.64	0.0083
RAB25	NM_020387	1q22	34	1.74	15	2.60	0.047
CALU	NM_001130674	7q32.1	35	1.74	81	1.76	0.0033
LRRC59	NM_018509	17q21.33	39	1.66	55	1.97	0.00054
KRAS	NM_004985	12p12.1	43	1.61	64	1.88	0.00016
ANP32E	NM_001136478	1q21.2	47	1.56	29	2.38	0.01
LASP1	NM_006148	17q11-q21.3	50	1.52	22	2.45	0.042

Supplementary Table-S5

Gene	**Accession Number**	***Let-7* linear regression *p*-value (qRT-PCR)**	**Function / Role in Cancer**
RRM2	**NM_001034**	**0.0029**	**Ribonucleotide reductase 2; catalyzes generation of deoxyribonucleotides; regulates cellular proliferation (1)**
C12orf5	**NM_020375**	**0.0246**	**TP53 induced glycolysis and apoptosis regulator (TIGAR); anti-apoptotic (2); depletion radiosensitizes glioma cells (3)**
MYCN	**NM_005378**	**0.0018**	**Transcription factor; known to be up-regulated in malignant GCTs (4); levels in neuroblastoma associated with poor outcome (5)**
AURKB	**NM_004217**	**0.0106**	**Aurora kinase B; high expression associated with unfavorable cytogenetic abnormalities in leukemia (6); AURKB inhibitor cytotoxic to neuroblastoma cells (7)**
MKI67	**NM_001145966**	**0.015**	**Cell proliferation marker (Ki67); high Ki-67 index associated with increased risk of relapse in malignant GCTs (8)**
CCNF	**NM_001761**	**0.0006**	**Cyclin F; regulator of mitosis and genome integrity (9)**