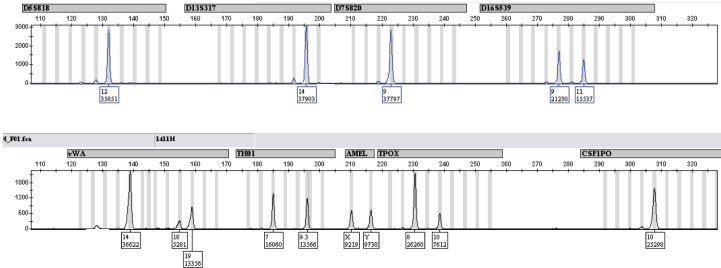
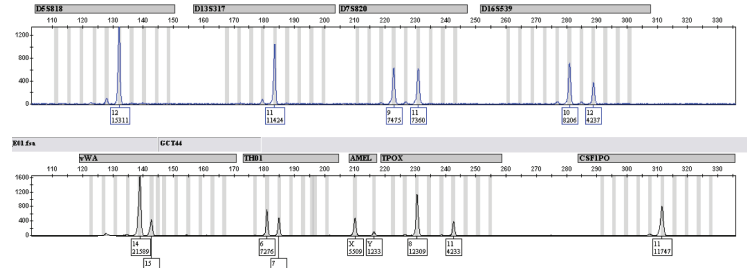


1411H



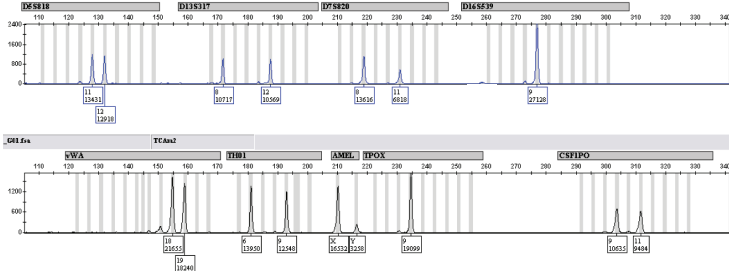
D5S818: 12; D13S317: 14; D7S820: 9;
 D16S539: 9,11; vWA: 14,18,19; TH01: 7,9,3;
 TPOX: 8,10; CSF1PO: 10; Amelogenin: X,Y

GCT44



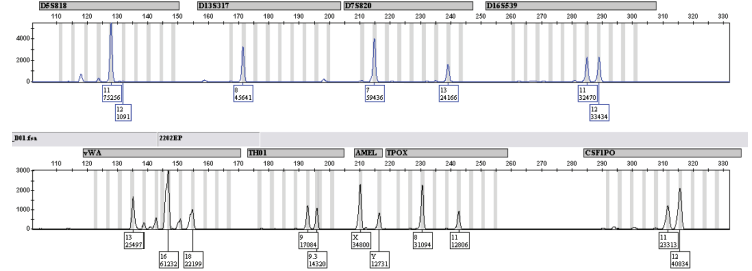
D5S818: 12; D13S317: 11; D7S820: 9,11;
 D16S539: 10,12; vWA: 14,15; TH01: 6,7;
 TPOX: 8,11; CSF1PO: 11; Amelogenin: X,Y

TCam-2



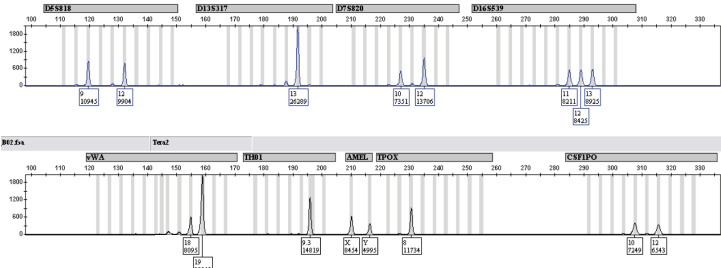
D5S818: 11,12; D13S317: 8,12; D7S820: 8,11;
 D16S539: 9; vWA: 18,19; TH01: 6,9; TPOX: 9;
 CSF1PO: 9,11; Amelogenin: X,Y

2102Ep



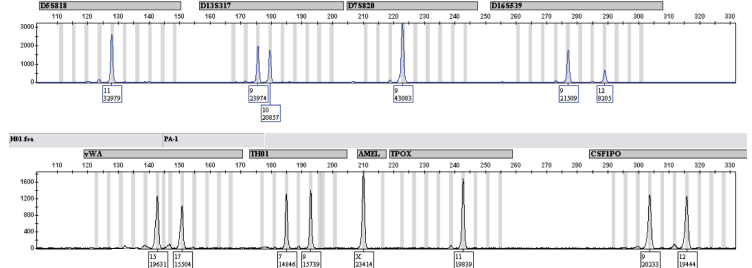
D5S818: 11; D13S317: 8; D7S820: 7,13;
 D16S539: 11,12; vWA: 13,16,18; TH01: 9,9,3;
 TPOX: 8,11; CSF1PO: 11,12; Amelogenin: X,Y

Tera2



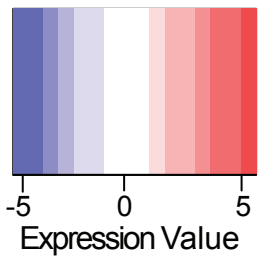
D5S818: 9,12; D13S317: 13; D7S820: 10,12;
 D16S539: 11,12,13; vWA: 18,19; TH01: 9,3;
 TPOX: 8; CSF1PO: 10,12; Amelogenin: X,Y

PA-1

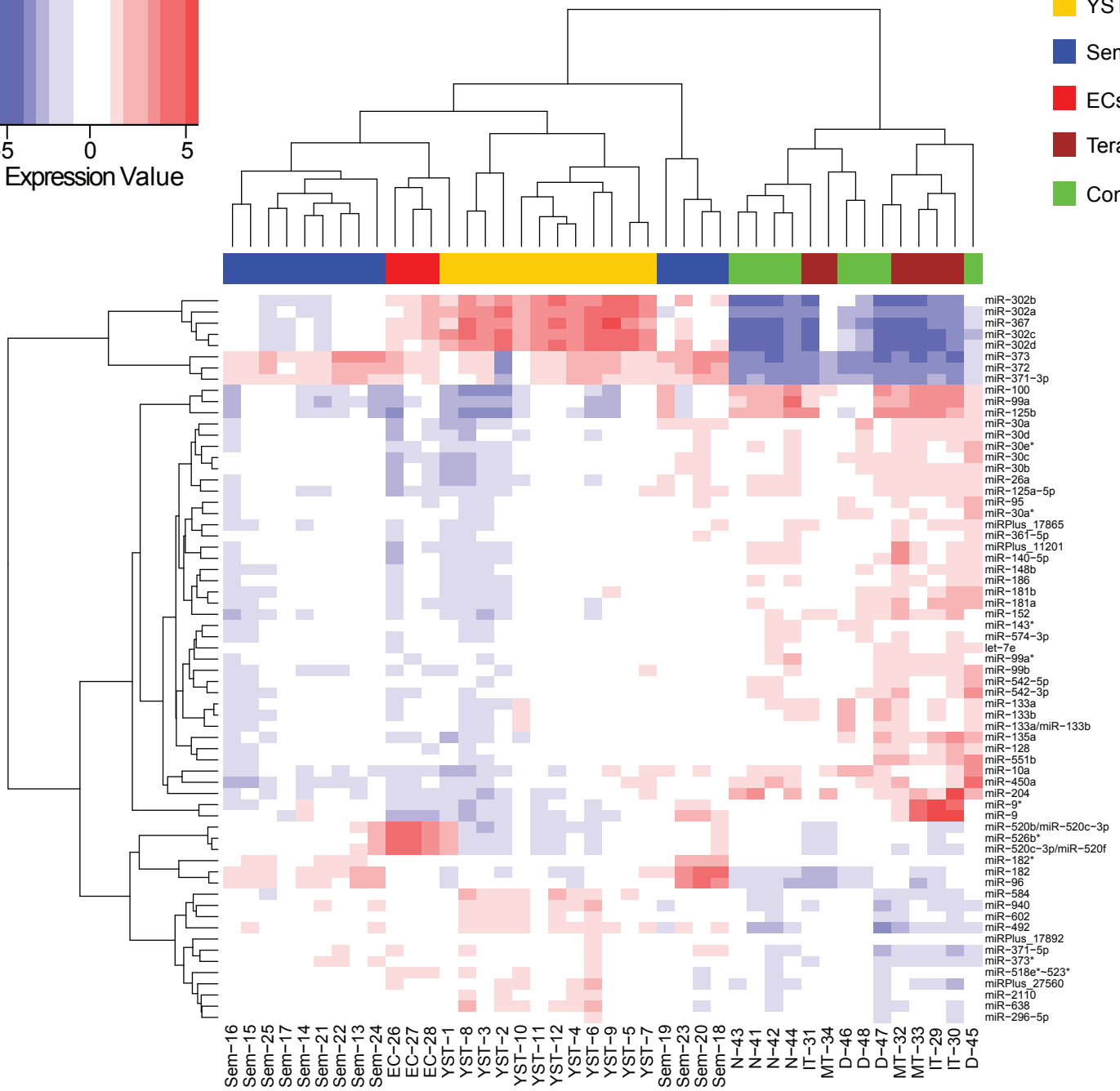


D5S818: 11; D13S317: 9,10; D7S820: 9;
 D16S539: 9,12; vWA: 15,17; TH01: 7,9;
 TPOX: 11; CSF1PO: 9,12; Amelogenin: X

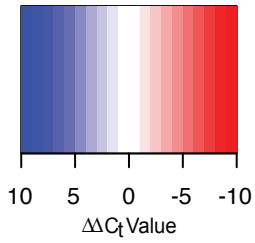
Palmer_Suppl_Fig_S2



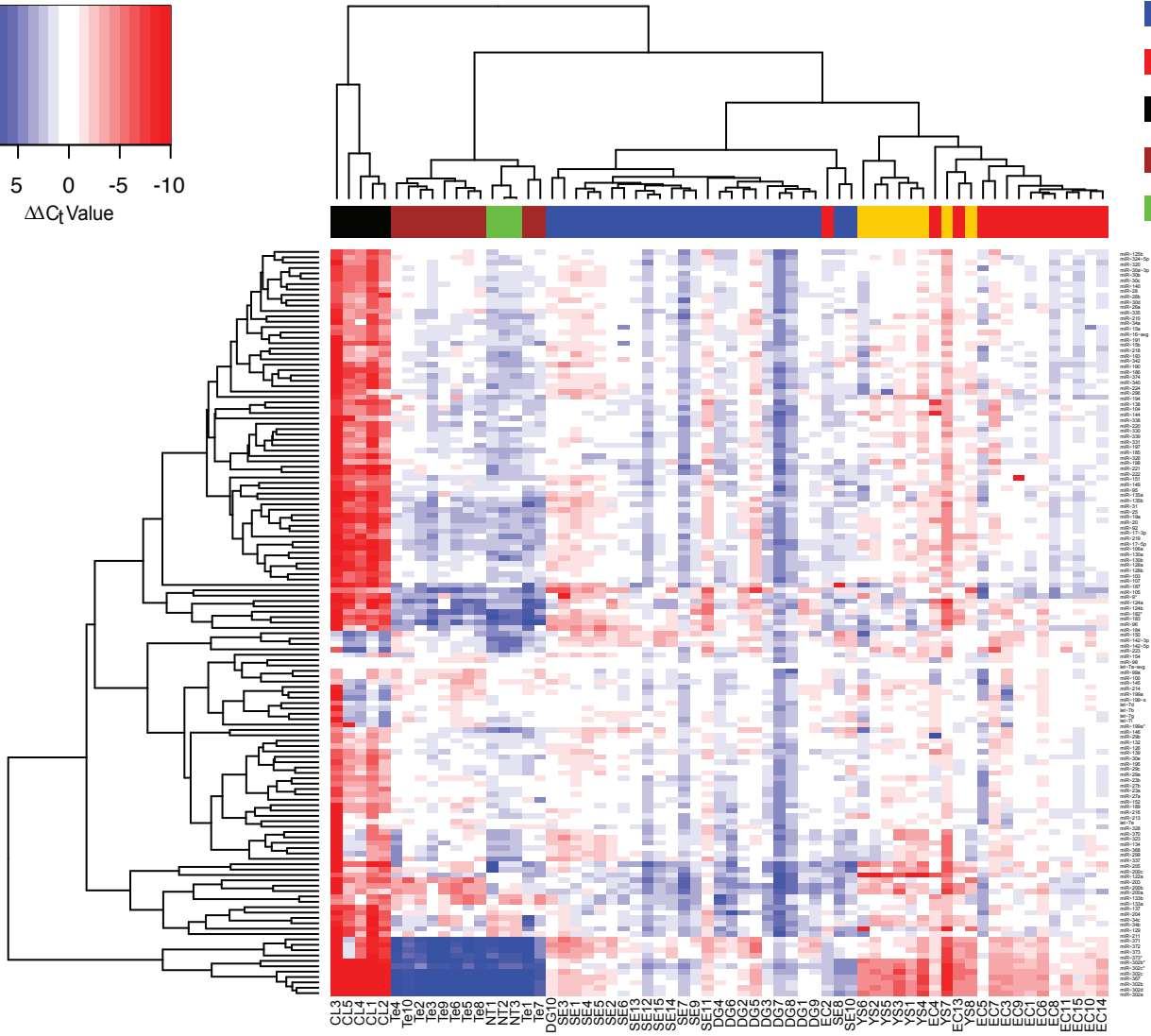
- YSTs
- Seminomas
- ECs
- Teratomas
- Controls



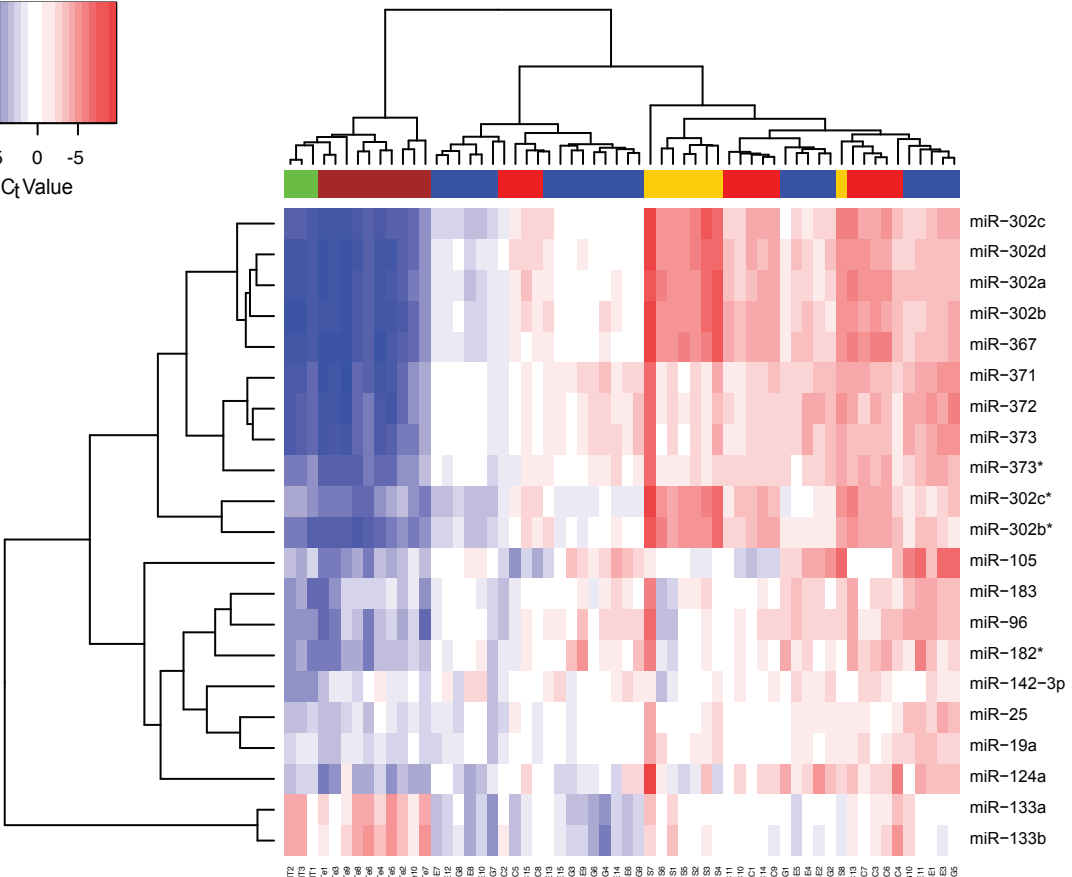
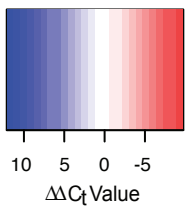
A



- YSTs
- Seminomas
- ECs
- Cell Lines
- Teratomas
- Controls

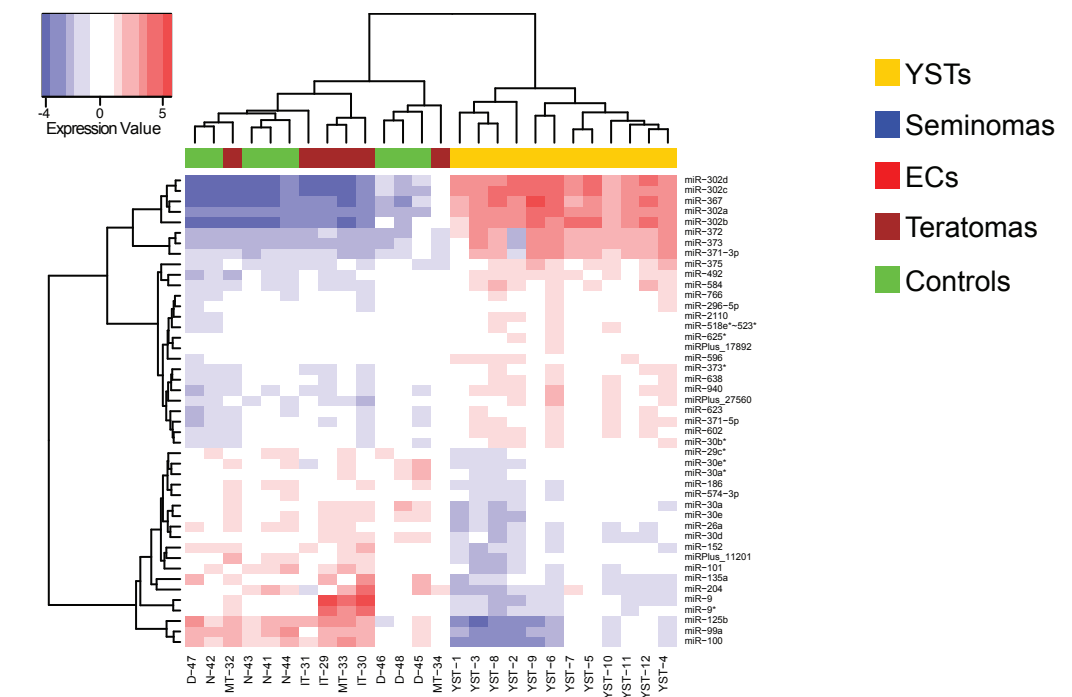


B

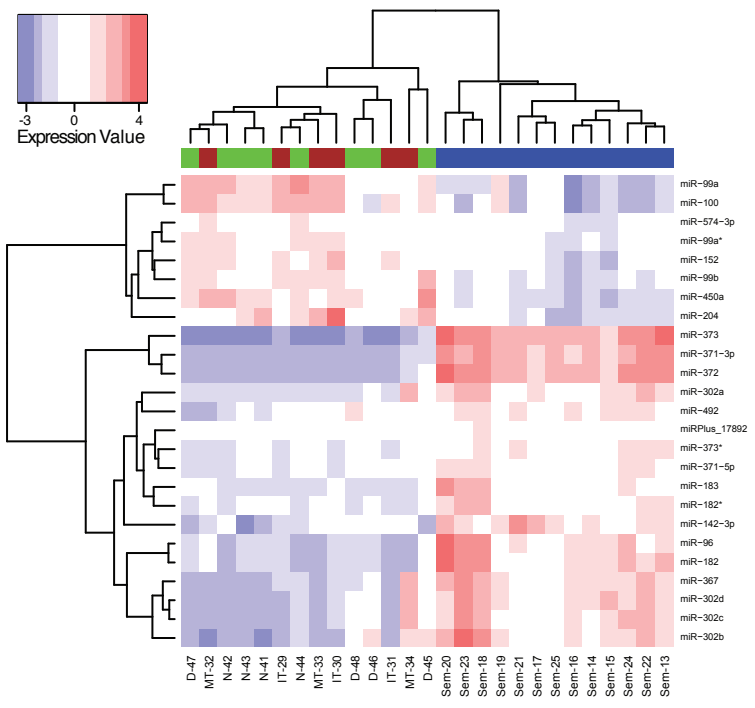


- miR-302c
- miR-302d
- miR-302a
- miR-302b
- miR-367
- miR-371
- miR-372
- miR-373
- miR-373*
- miR-302c*
- miR-302b*
- miR-105
- miR-183
- miR-96
- miR-182*
- miR-142-3p
- miR-25
- miR-19a
- miR-124a
- miR-133a
- miR-133b

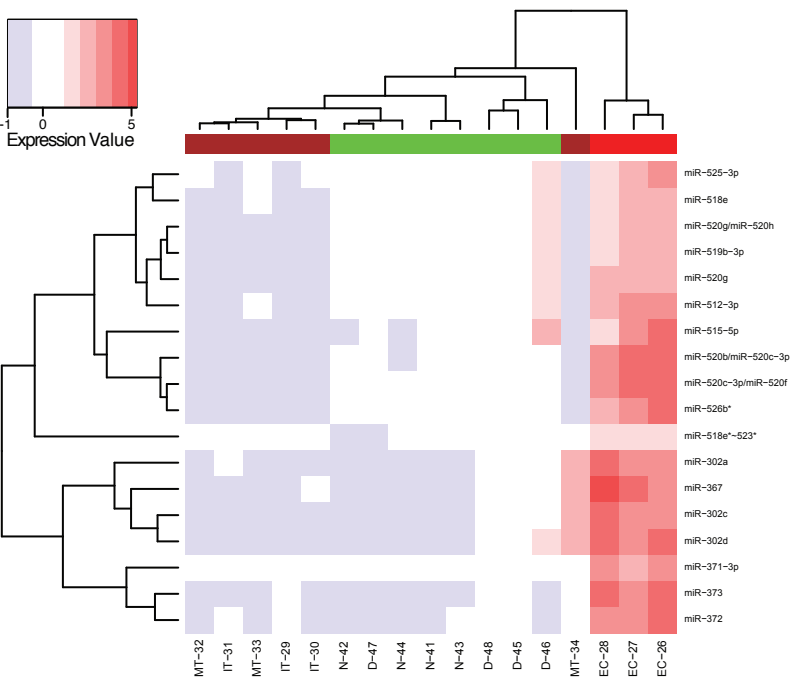
A

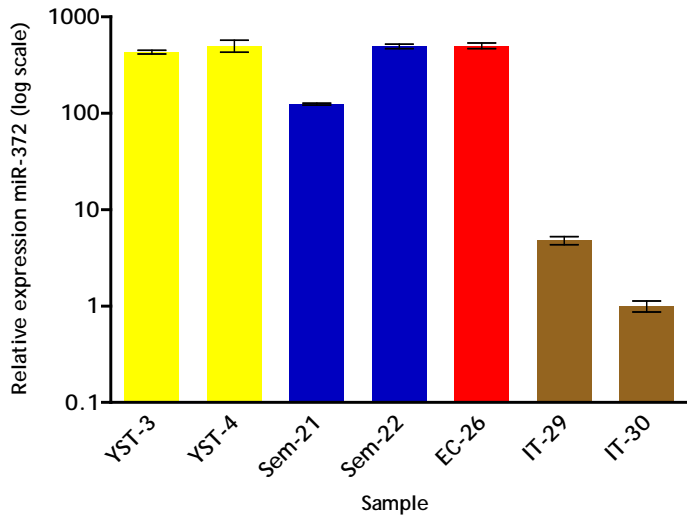
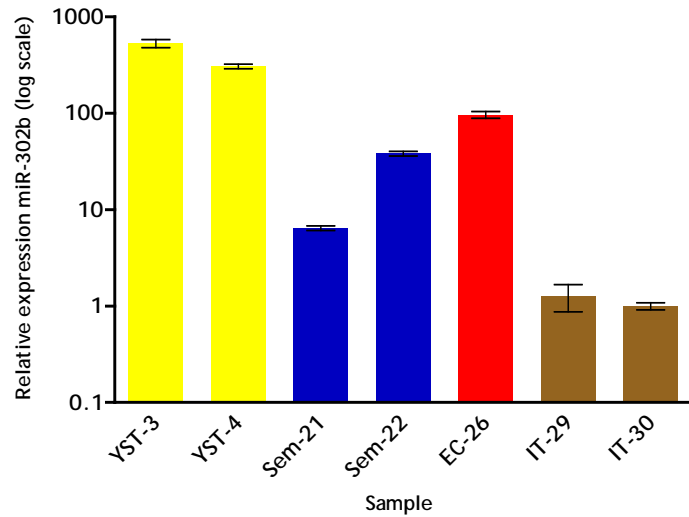
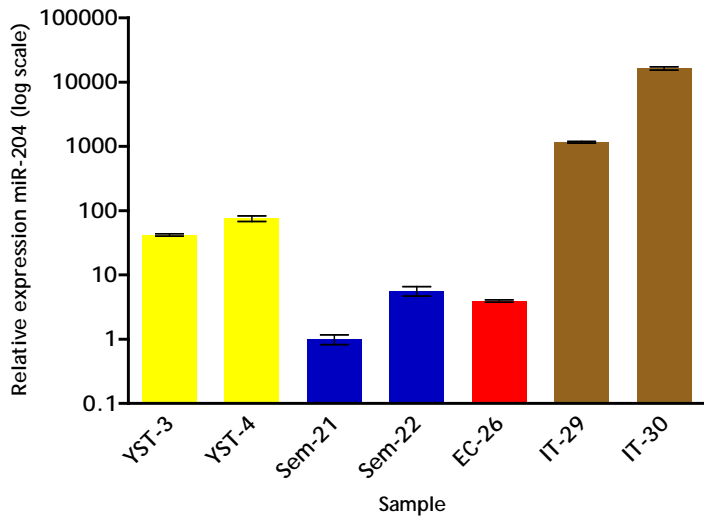
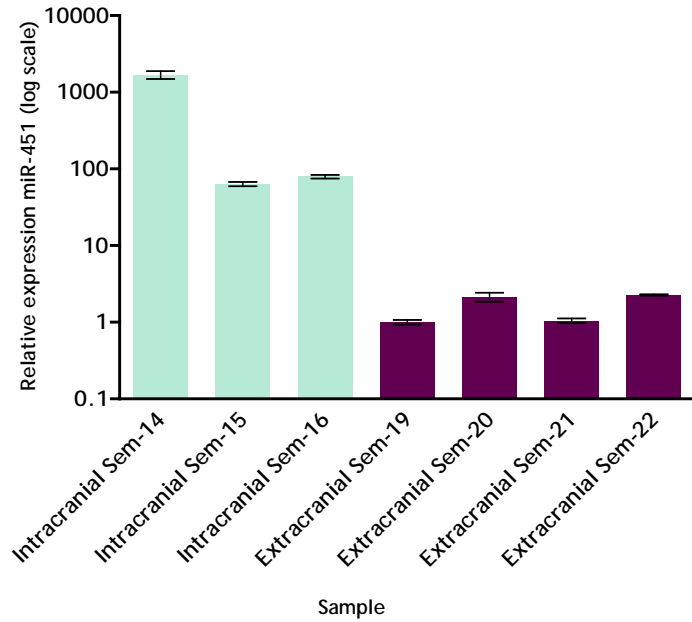


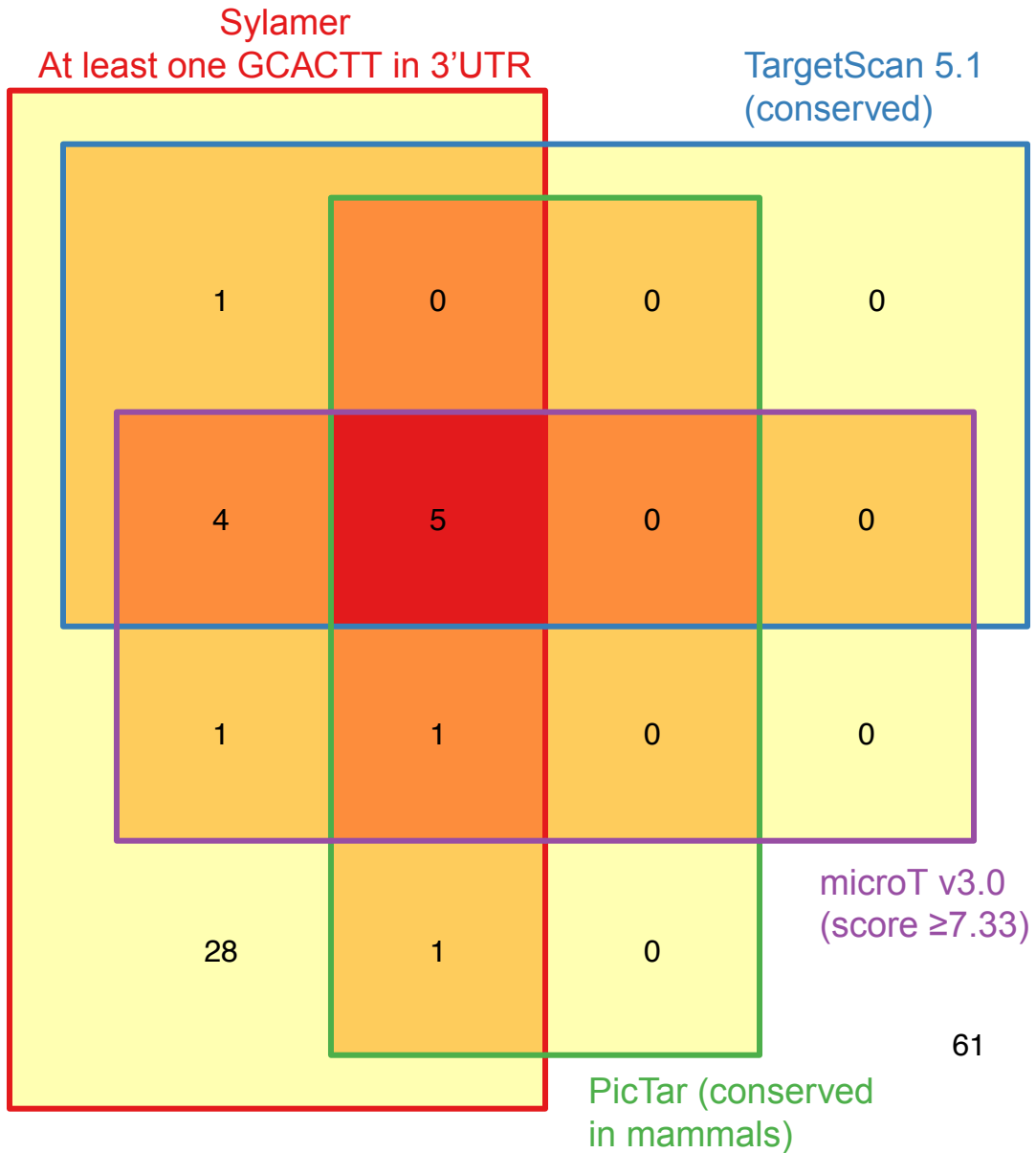
B

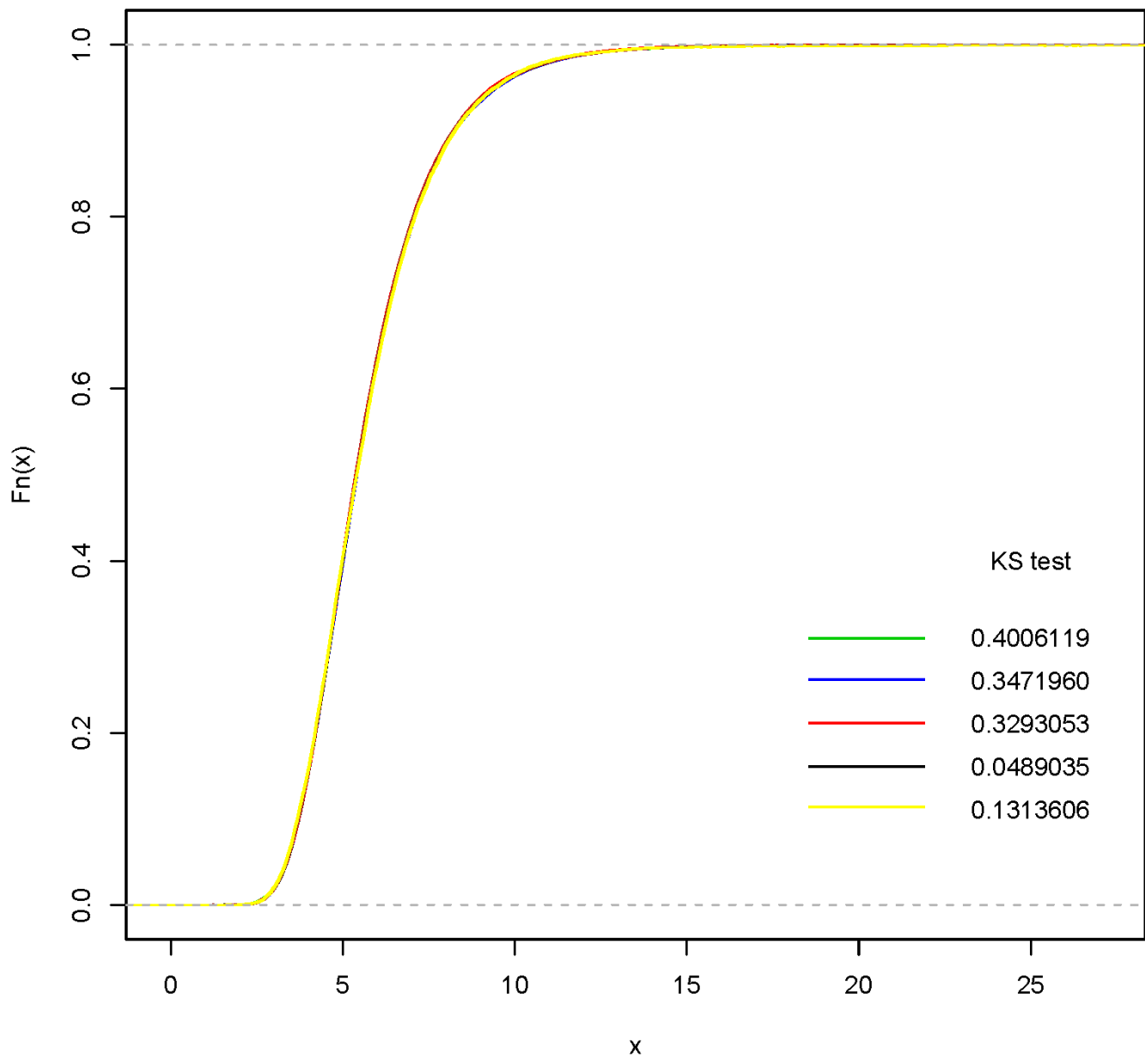


C



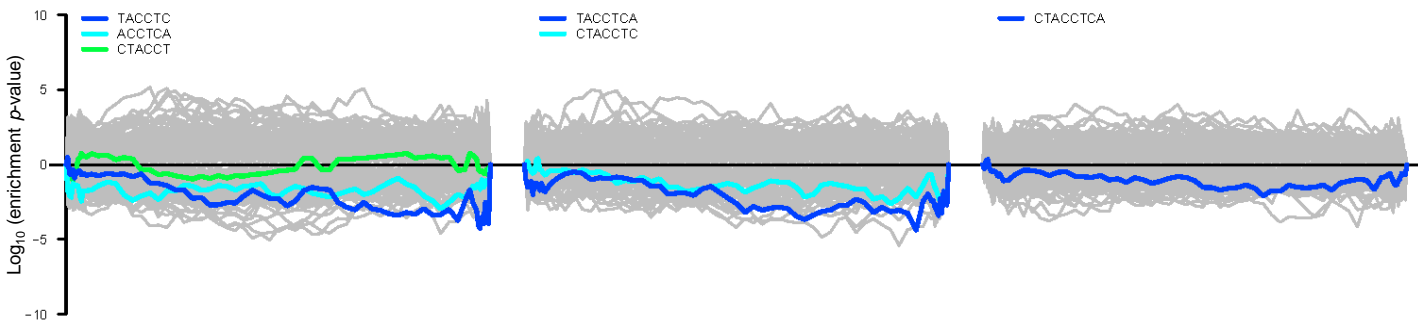
A miR-372 expression referenced to IT-30 sample**B** miR-302b expression referenced to IT-30 sample**C** miR-204 expression referenced to Sem-21 sample**D** miR-451 expression referenced to Sem-19 sample





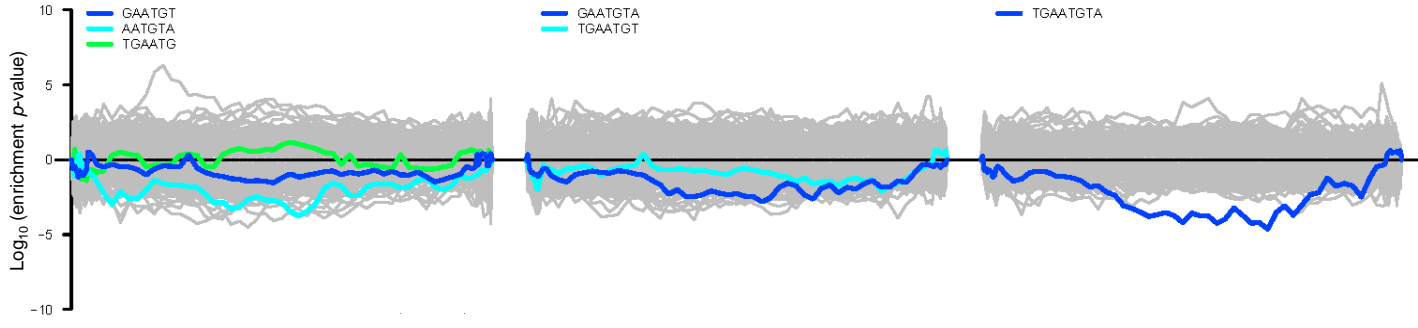
A

Pediatric YST versus Controls; SCR for let-7 family seed; score: -13.132; p -value 1.18×10^{-3}



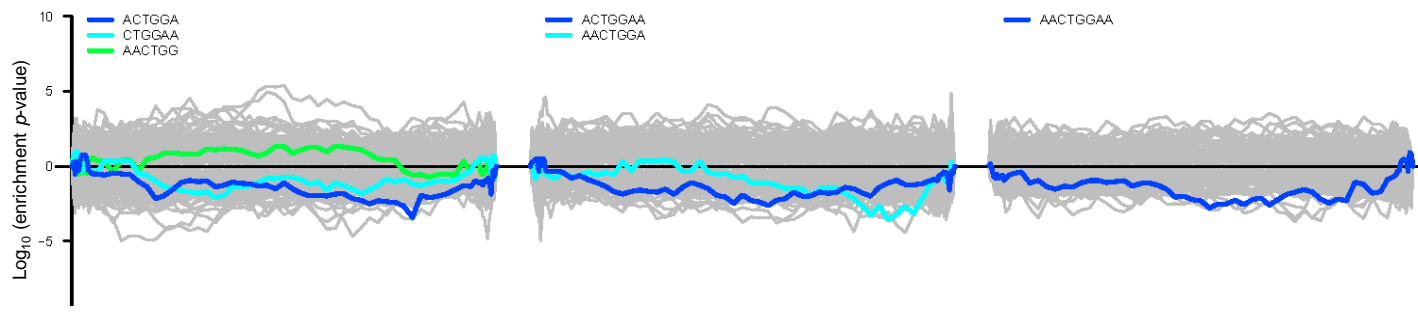
B

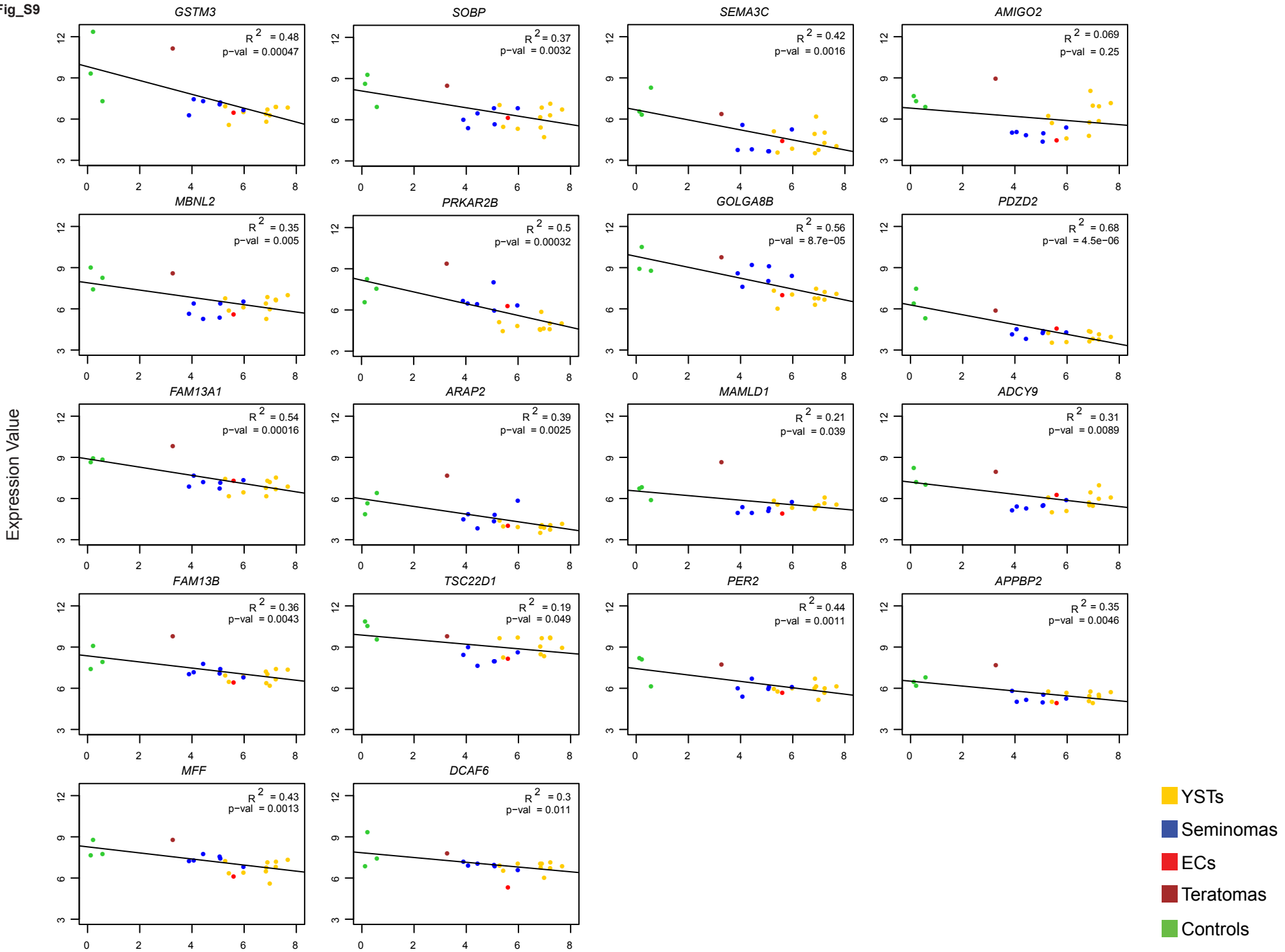
Pediatric Seminoma versus Controls; SCR for miR-181 family seed; score: -11.227; p -value 2.45×10^{-3}



C

Adult malignant TGCT versus Controls; SCR for miR-145 seed; score: -12.013; p -value 4.56×10^{-4}





Palmer_Suppl_ Table_S1

Sample	Histology	Code	Tumor composition	Site	Gender	Age (y)	Stage	mRNA profiling
1	YST	YST-1	Mixed, with MT	CNS	M	12	1	✓
2	YST	YST-2	Mixed, with MT	SCT	F	3	4	✓
3	YST	YST-3	Pure	Testis	M	2	1	✓
4	YST	YST-4	Pure	Ovary	F	13	3	✓
5	YST	YST-5	Pure	Ovary	F	12	1	✓
6	YST	YST-6	Pure	Testis	M	4	1	✓
7	YST	YST-7	Pure	Testis	M	0	1	✓
8	YST	YST-8	Mixed, with MT	SCT	F	2	4	✓
9	YST	YST-9	Pure	Ovary	F	4	4	
10	YST	YST-10	Pure	Ovary	F	0	2	✓
11	YST	YST-11	Pure	Ovary	F	14	1	✓
12	YST	YST-12	Pure	Vagina	F	1	1	
13	Seminoma	Sem-13	Pure	Ovary	F	12	1	✓
14	Seminoma	Sem-14	Pure	CNS	F	10	1	✓
15	Seminoma	Sem-15	Pure	CNS	M	16	1	✓
16	Seminoma	Sem-16	Pure	CNS	M	12	1	
17	Seminoma	Sem-17	Pure	Testis	M	25	1	
18	Seminoma	Sem-18	Pure	Testis	M	35	1	
19	Seminoma	Sem-19	Pure	Ovary	F	8	N/A	
20	Seminoma	Sem-20	Pure	Ovary	F	9	3	
21	Seminoma	Sem-21	Pure	Metastasis #	F	11	4	
22	Seminoma	Sem-22	Pure	Ovary	F	14	3	
23	Seminoma	Sem-23	Pure	Ovary	F	13	3	✓
24	Seminoma	Sem-24	Pure	Ovary	F	12	1	✓
25	Seminoma	Sem-25	Pure	Ovary	F	13	1	✓
26	EC	EC-26	Pure	Metastasis #	M	15	4	✓*
27	EC	EC-27	Pure	Testis	M	15	N/A	
28	EC	EC-28	Pure	Testis	M	13	4	
29	IT	IT-29	Pure	Ovary	F	0	-	
30	IT	IT-30	Pure	Ovary	F	15	-	
31	IT	IT-31	Pure	Abdominal	M	0	-	
32	MT	MT-32	Pure	SCT	F	0	-	
33	MT	MT-33	Pure	Ovary	F	3	-	
34	MT	MT-34	Mixed, with YST	Ovary	F	12	-	✓*
35	Tera-2 (EC)	CL-35	-	Cell Line	-	-	-	
36	GCT44 (YST)	CL-36	-	Cell Line	-	-	-	
37	PA-1 (IT)	CL-37	-	Cell Line	-	-	-	
38	1411H (YST)	CL-38	-	Cell Line	-	-	-	
39	TCam-2 (seminoma)	CL-39	-	Cell Line	-	-	-	
40	2102Ep (EC)	CL-40	-	Cell Line	-	-	-	
41	Normal (pre-pubertal)	N-41	-	Testis	M	9	-	✓*
42	Normal (pre-pubertal)	N-42	-	Ovary	F	7	-	
43	Normal (post-pubertal)	N-43	-	Testis	M	27	-	✓*
44	Normal (post-pubertal)	N-44	-	Ovary	F	43	-	✓*
45	Developmental (fetal)	D-45	-	Yolk sac	N/A	-	-	
46	Developmental (fetal)	D-46	-	Yolk sac	F	-	-	
47	Developmental (fetal)	D-47	-	Ovary	F	-	-	
48	Developmental (fetal)	D-48	-	Ovary	F	-	-	

Key

YST – yolk sac tumor

EC – embryonal carcinoma

IT – immature teratoma

MT – mature teratoma

SCT – sacrococcygeal teratoma

CNS - central nervous system

Staging – according to tumor-node metastasis system

from gonadal primary

* mRNA profiles previously unpublished

Palmer_Suppl_Table_S2A

(A) List of differentiating miRNAs for pediatric GCTs versus non-malignant tissues, ranked by adjusted <i>p</i> -value					
Over-expressed	Log2 fold change	Adjusted <i>p</i> -value	Under-expressed	Log2 fold change	Adjusted <i>p</i> -value
hsa-miR-302a	4.40881897	6.28E-15	hsa-miR-152	-2.063914854	5.09E-09
hsa-miR-373	5.391576539	2.55E-14	hsa-miR-204	-2.955600047	2.32E-08
hsa-miR-367	5.095098475	2.55E-14	hsa-miR-30d	-1.811160594	6.14E-08
hsa-miR-302c	5.071235772	2.55E-14	hsa-miR-99a	-3.470265793	9.25E-08
hsa-miR-371-3p	4.309924554	2.55E-14	hsa-miR-100	-3.385412435	1.23E-07
hsa-miR-372	4.907600543	4.09E-14	hsa-miR-574-3p	-1.311926777	1.74E-07
hsa-miR-302d	5.080151319	6.85E-14	hsa-miR-186	-1.462022893	2.09E-07
hsa-miR-302b	4.803575667	4.65E-11	hsa-miR-30a*	-1.287810497	2.16E-07
hsa-miR-373*	1.653141211	5.26E-11	hsa-miR-99a*	-1.417079846	2.16E-07
miRPlus_17892	1.074655904	1.38E-10	hsa-miR-99b	-1.79882643	3.24E-07
hsa-miR-371-5p	1.773515888	9.48E-10	hsa-let-7e	-1.147428812	4.45E-07
hsa-miR-940	1.577103167	2.42E-08	miRPlus_11201	-1.765197447	5.25E-07
hsa-miR-492	2.005593571	1.25E-07	hsa-miR-135a	-2.131835153	6.03E-07
hsa-miR-520c-3p	1.850361383	2.58E-07	hsa-miR-133a	-1.791180842	7.96E-07
hsa-miR-584	1.432324394	2.75E-07	hsa-miR-125b	-3.446981685	9.59E-07
hsa-miR-518e*	1.033306037	4.57E-07	hsa-miR-30a	-1.823260641	1.18E-06
hsa-miR-96	2.09974333	4.70E-07	hsa-miR-133a/b	-1.313869601	1.20E-06
hsa-miR-526b*	1.718536991	5.37E-07	hsa-miR-181a	-1.836798349	1.28E-06
hsa-miR-520b	1.817371691	1.79E-06	hsa-miR-26a	-1.903180281	1.30E-06
hsa-miR-2110	0.897221	2.45E-06	hsa-miR-125a-5p	-1.917003854	1.30E-06
hsa-miR-182	1.99707157	3.27E-06	hsa-miR-148b	-1.311449669	1.34E-06
miRPlus_27560	1.340802693	3.53E-06	hsa-miR-133b	-1.670182579	1.52E-06
hsa-miR-182*	0.98155748	4.68E-06	hsa-miR-542-3p	-1.499261794	1.54E-06
hsa-miR-638	1.04881876	5.35E-06	hsa-miR-30e*	-1.478334142	1.75E-06
hsa-miR-602	1.079267913	9.41E-06	hsa-miR-30b	-1.73375691	2.21E-06
hsa-miR-296-5p	0.881107622	9.41E-06	hsa-miR-140-5p	-1.771429989	2.43E-06
hsa-miR-766	0.886323657	1.38E-05	hsa-miR-9*	-2.220975697	2.45E-06
hsa-miR-596	1.141276129	1.71E-05	hsa-miR-9	-2.511761527	2.45E-06
hsa-miR-623	1.094251422	2.09E-05	hsa-miR-181b	-1.646891224	2.48E-06
hsa-miR-625*	0.766591601	2.36E-05	hsa-miR-95	-1.309531872	2.50E-06
hsa-miR-30b*	0.988246337	2.92E-05	hsa-miR-450a	-2.05887218	2.52E-06
hsa-miR-611	1.091602535	6.66E-05	hsa-miR-128	-1.437029713	3.24E-06
hsa-miR-183	1.220534751	0.00016252	hsa-miR-30c	-1.687900166	3.85E-06
hsa-miR-512-3p	1.166899818	0.000250435	hsa-miR-551b	-1.70540519	4.02E-06
hsa-miR-483-3p	0.771478606	0.000359432	hsa-miR-10a	-2.151435903	4.02E-06
hsa-miR-515-5p	1.297819857	0.001558432	hsa-miR-143*	-1.103866914	5.05E-06
hsa-miR-518a-5p	0.670414831	0.001744319	hsa-miR-361-5p	-1.113381931	6.96E-06
hsa-miR-520g/h	0.933230179	0.003021334	hsa-miR-542-5p	-1.274237523	8.17E-06
hsa-miR-525-3p	0.759966545	0.003076572	miRPlus_17865	-1.237994138	8.99E-06
hsa-miR-520g	0.996606474	0.003630444	hsa-miR-499-5p	-1.070551543	1.18E-05
hsa-miR-518e	0.812909702	0.003630444	hsa-miR-24	-1.649940986	1.18E-05
hsa-miR-326	0.793083538	0.004367093	hsa-miR-27b	-1.579214896	1.19E-05
hsa-miR-519b-3p	0.871038614	0.00479448	hsa-miR-98	-1.820927515	1.21E-05
hsa-miR-515-3p	0.7864083	0.006735831	hsa-miR-320a	-1.35002557	1.22E-05
			hsa-miR-455-5p	-1.314181524	1.36E-05
			hsa-miR-29c*	-1.030552205	1.39E-05
			hsa-miR-424	-1.977222963	1.41E-05
			hsa-miR-101	-1.540210246	1.77E-05

hsa-miR-338-3p	-1.55551537	1.82E-05
hsa-miR-23a	-1.539590735	2.12E-05
hsa-miR-30e	-1.481373131	2.21E-05
hsa-miR-132	-0.904051467	2.31E-05
hsa-miR-214	-1.859451157	2.64E-05
hsa-miR-23b	-1.545640208	2.70E-05
hsa-miR-1	-1.319762454	3.55E-05
hsa-miR-15a	-1.078058994	3.76E-05
hsa-miR-218	-1.762104908	3.76E-05
hsa-let-7d	-1.702406219	4.01E-05
hsa-miR-199a-5p	-2.546090217	4.59E-05
hsa-miR-28-5p	-1.034416571	5.05E-05
hsa-miR-199b-5p	-2.237105202	6.75E-05
hsa-miR-191	-0.943114027	6.82E-05
hsa-miR-126*	-1.320284881	6.82E-05
hsa-miR-532-5p	-1.171268046	7.76E-05
hsa-miR-365	-1.242695944	7.90E-05
hsa-miR-449a	-2.191490569	7.97E-05
hsa-miR-660	-1.297398959	8.43E-05
hsa-miR-151-3p	-1.00968863	9.11E-05
hsa-let-7a	-1.879555586	9.19E-05
hsa-miR-199a-3p/-199b-3p	-2.300256702	0.00010053
hsa-let-7c	-1.827521304	0.000118464
hsa-miR-127-3p	-1.505641636	0.000121666
hsa-miR-145*	-1.16571029	0.000125045
hsa-miR-33a	-0.932242702	0.00013193
hsa-miR-148a	-1.194592506	0.00013193
hsa-miR-151-5p	-1.094302081	0.000191731
hsa-miR-19b	-1.125266381	0.000192559
hsa-miR-345	-0.789931824	0.000212641
hsa-miR-362-3p	-1.18482227	0.000214283
hsa-miR-374b	-1.081480092	0.000216848
hsa-let-7g	-1.302735394	0.000233943
hsa-miR-429	-1.416366498	0.000250435
hsa-miR-335	-1.807198014	0.000272893
hsa-miR-487b	-1.180439247	0.00028982
hsa-miR-455-3p	-1.288005301	0.000292364
hsa-miR-107	-0.971983533	0.000293809
hsa-miR-136	-2.079709911	0.000321307
hsa-miR-154	-0.988978824	0.000323668
hsa-miR-145	-1.583851305	0.000340837
hsa-let-7b	-1.782463537	0.000340837
hsa-miR-126	-1.505971686	0.000401173
hsa-miR-411	-1.275501147	0.000423169
hsa-miR-193b	-1.022616906	0.00051578
hsa-miR-301a	-1.370578911	0.00055519
hsa-miR-143	-1.72724441	0.000608804
hsa-miR-27a	-1.117647227	0.000621183
hsa-let-7f	-1.241234002	0.000855845
hsa-miR-432	-1.124149987	0.001081931
hsa-miR-337-5p	-1.457002426	0.001081931
hsa-miR-34b*	-1.709729258	0.001081931

hsa-miR-19a	-0.88626336	0.001182033
hsa-miR-497	-0.99366573	0.001271971
hsa-miR-410	-1.207216001	0.001520246
hsa-miR-10b	-2.05884951	0.001610488
hsa-miR-374a	-0.82472481	0.001744319
hsa-miR-376c	-1.38391637	0.001968038
hsa-miR-377	-1.553765795	0.002034384
hsa-miR-92a	-0.77149936	0.002234204
hsa-miR-369-3p	-1.309403021	0.002488963
hsa-let-7i	-1.163348137	0.002625098
hsa-miR-130a	-1.176215016	0.002768451
hsa-miR-34c-5p	-1.371229301	0.002768451
hsa-miR-886-3p	-1.532314964	0.003005048
hsa-miR-329	-0.830841521	0.003630444
hsa-miR-379	-1.100975445	0.003793949
hsa-miR-376a	-1.40644061	0.003804157
hsa-miR-654-3p	-1.125581978	0.00427844
hsa-miR-363	-1.246808481	0.004561884
hsa-miR-32	-0.997293616	0.005379974
miRPlus_17848	-1.133760683	0.005379974
hsa-miR-16	-0.732855914	0.00571899
hsa-miR-708	-1.32108352	0.006735831
hsa-miR-886-5p	-1.15989741	0.007095961
hsa-miR-22	-0.946951307	0.007701659
hsa-miR-514	-1.529529309	0.008091386
hsa-miR-491-3p	-0.857364737	0.008432708

Palmer_Suppl_Table_S2B

(B) List of differentiating miRNAs for adult malignant GCTs versus non-malignant tissues, ranked by adjusted p-value					
Over-expressed	ΔΔ Ct	Adjusted p-value	Under-expressed	ΔΔ Ct	Adjusted p-value
hsa-miR-371	-11.18	1.18E-24	hsa-miR-133a	4.00	4.67E-07
hsa-miR-373	-10.26	1.66E-22	hsa-miR-133b	3.88	4.28E-06
hsa-miR-372	-10.79	4.87E-22	hsa-miR-100	2.20	2.65E-05
hsa-miR-302b	-12.45	1.65E-20	hsa-miR-203	4.03	3.71E-05
hsa-miR-302d	-12.41	1.65E-20	hsa-miR-99a	2.14	1.94E-04
hsa-miR-373*	-8.72	2.85E-20	hsa-miR-211	2.48	4.42E-04
hsa-miR-367	-12.38	8.08E-20	hsa-miR-145	1.89	1.12E-03
hsa-miR-302a	-12.14	1.30E-19	hsa-miR-328	1.47	7.20E-03
hsa-miR-302c	-11.41	5.62E-17	hsa-miR-200b	2.95	9.21E-03
hsa-miR-302b*	-9.61	8.97E-16	hsa-miR-200a	2.95	9.69E-03
hsa-miR-182*	-6.08	2.36E-12			
hsa-miR-96	-6.31	7.14E-12			
hsa-miR-302c*	-7.18	2.55E-09			
hsa-miR-183	-5.01	2.63E-09			
hsa-miR-25	-3.12	6.61E-07			
hsa-miR-124a	-4.92	1.53E-06			
hsa-miR-142-3p	-3.13	1.53E-06			
hsa-miR-105	-5.38	1.97E-06			
hsa-miR-19a	-2.71	2.74E-06			
hsa-miR-124b	-3.78	1.32E-05			
hsa-miR-92	-2.47	2.52E-05			
hsa-miR-17-3p	-2.33	2.69E-05			
hsa-miR-142-5p	-2.65	3.23E-05			
hsa-miR-9	-3.50	3.51E-05			
hsa-miR-20	-2.70	3.71E-05			
hsa-miR-17-5p	-2.61	7.33E-05			
hsa-miR-146	-2.66	1.47E-04			
hsa-miR-219	-2.48	3.24E-04			
hsa-miR-135b	-2.44	3.85E-04			
hsa-miR-185	-1.97	3.85E-04			
hsa-miR-31	-2.61	3.88E-04			
hsa-miR-130a	-1.95	8.03E-04			
hsa-miR-106a	-2.25	8.60E-04			
hsa-miR-184	-2.91	1.12E-03			
hsa-miR-368	-1.99	2.65E-03			
hsa-miR-374	-1.59	3.49E-03			
hsa-miR-340	-1.47	3.49E-03			
hsa-miR-210	-1.90	3.51E-03			
hsa-miR-223	-2.29	3.67E-03			
hsa-miR-130b	-1.83	8.04E-03			
hsa-miR-150	-2.09	8.13E-03			
hsa-miR-15b	-1.60	8.39E-03			
hsa-miR-151	-1.93	9.13E-03			
hsa-miR-34a	-1.38	9.13E-03			
hsa-miR-330	-1.36	9.13E-03			
hsa-miR-342	-1.30	9.13E-03			

Palmer_Suppl_Table_S3

List of differentiating miRNAs for pediatric YSTs versus non-malignant tissues, ranked by adjusted <i>p</i> -value					
Over-expressed	Log2 fold change	Adjusted <i>p</i> -value	Under-expressed	Log2 fold change	Adjusted <i>p</i> -value
hsa-miR-302a	6.54289778	2.91E-19	hsa-miR-152	-2.042773501	4.57E-08
hsa-miR-302c	7.329122262	4.80E-18	hsa-miR-100	-3.697534908	1.26E-07
hsa-miR-367	7.055124727	2.34E-17	hsa-miR-186	-1.628549732	1.49E-07
hsa-miR-302d	7.239796082	3.10E-17	hsa-miR-30d	-1.83008469	2.72E-07
hsa-miR-302b	6.639856943	9.49E-14	hsa-miR-99a	-3.511735467	3.94E-07
hsa-miR-375	2.404779015	2.99E-12	hsa-miR-125b	-3.885864347	7.35E-07
hsa-miR-371-3p	3.911797082	5.20E-12	hsa-miR-30a	-2.061930414	8.46E-07
hsa-miR-372	4.451957649	1.24E-11	miRPlus_11201	-1.891356016	9.47E-07
hsa-miR-584	2.413254974	1.61E-11	hsa-miR-204	-2.629968516	1.15E-06
hsa-miR-373	4.619133965	2.84E-11	hsa-miR-30e	-2.015923227	1.18E-06
hsa-miR-940	2.223217936	5.35E-11	hsa-miR-101	-2.016937316	1.67E-06
hsa-miR-373*	1.719490873	2.16E-10	hsa-miR-30a*	-1.253519869	1.77E-06
hsa-miR-371-5p	1.867418793	2.88E-09	hsa-miR-9	-2.785484937	2.82E-06
miRPlus_17892	1.007872913	7.56E-09	hsa-miR-135a	-2.138093612	3.29E-06
hsa-miR-2110	1.347598745	9.26E-09	hsa-miR-26a	-1.991105185	3.54E-06
hsa-miR-638	1.639756406	1.22E-08	hsa-miR-30e*	-1.538694007	5.44E-06
hsa-miR-30b*	1.687242424	2.48E-08	hsa-miR-9*	-2.367416328	5.44E-06
hsa-miR-602	1.666387577	3.45E-08	hsa-miR-574-3p	-1.163703421	6.65E-06
hsa-miR-492	2.331535447	3.73E-08	hsa-miR-29c*	-1.202502789	8.85E-06
miRPlus_27560	1.884488502	5.99E-08	hsa-miR-133a	-1.689636125	1.16E-05
hsa-miR-766	1.317204265	1.26E-07	hsa-miR-181a	-1.767083461	1.34E-05
hsa-miR-296-5p	1.246464399	1.87E-07	hsa-miR-551b	-1.770630015	1.46E-05
hsa-miR-625*	1.10816539	4.58E-07	hsa-miR-133a/b	-1.233367964	1.78E-05
hsa-miR-623	1.490438744	1.11E-06	hsa-miR-99a*	-1.184592823	2.13E-05
hsa-miR-518e*	1.068543336	1.41E-06	hsa-miR-95	-1.283341165	2.13E-05
hsa-miR-596	1.499826217	1.51E-06	hsa-miR-30b	-1.672858026	2.16E-05
hsa-miR-302c*	0.979840025	1.51E-05	hsa-miR-148b	-1.223245185	2.19E-05
hsa-miR-483-3p	1.066965655	3.06E-05	hsa-miR-140-5p	-1.71470017	2.19E-05
hsa-miR-720	0.870590887	0.00092982	hsa-miR-133b	-1.562680865	2.30E-05
hsa-miR-611	0.943225386	0.001291452	hsa-miR-132	-1.01890924	2.40E-05
hsa-miR-552	0.80761441	0.001538917	hsa-miR-361-5p	-1.141177719	2.67E-05
hsa-miR-210	0.722910245	0.003322521	hsa-miR-128	-1.400002708	2.67E-05
hsa-miR-326	0.869302164	0.005507403	hsa-miR-30c	-1.646953249	3.08E-05
			hsa-let-7e	-0.949139491	4.15E-05
			hsa-miR-33a	-1.136917234	5.30E-05
			hsa-miR-125a-5p	-1.664078183	5.55E-05
			hsa-miR-181b	-1.492073476	5.87E-05
			miRPlus_17865	-1.215975233	6.07E-05
			hsa-miR-320a	-1.332969568	7.93E-05
			hsa-miR-98	-1.784848917	8.56E-05
			hsa-let-7d	-1.815635273	8.97E-05
			hsa-miR-99b	-1.357701166	0.000115202
			hsa-miR-542-3p	-1.241520852	0.000124621
			hsa-miR-151-3p	-1.117732211	0.000125965
			hsa-miR-499-5p	-1.013422768	0.000126322
			hsa-let-7g	-1.533397916	0.000155338
			hsa-miR-191	-0.99917938	0.000159627
			hsa-miR-23a	-1.490384603	0.000167087
			hsa-miR-24	-1.512052083	0.000189176
			hsa-miR-10a	-1.835411359	0.000193376
			hsa-miR-143*	-0.948525776	0.00021073
			hsa-miR-199a-5p	-2.533483607	0.000237846
			hsa-miR-27b	-1.377099294	0.000359275
			hsa-miR-1	-1.240369808	0.000375119

hsa-miR-29b	-1.828941729	0.000375119
hsa-miR-449a	-2.191076924	0.000375119
hsa-miR-532-5p	-1.163323063	0.000384719
hsa-miR-23b	-1.411781638	0.00041269
hsa-miR-886-3p	-2.132770109	0.000419329
hsa-miR-19b	-1.182803297	0.000465795
hsa-miR-335	-1.959267225	0.000465795
hsa-let-7i	-1.556266054	0.000542047
hsa-miR-136	-2.245006771	0.000575497
hsa-let-7c	-1.779524281	0.000694315
miRPlus_17848	-1.619889951	0.000711299
hsa-miR-199b-5p	-2.068227229	0.000724578
hsa-miR-660	-1.220602416	0.000738834
miRPlus_28302	-1.113342034	0.000766186
hsa-miR-345	-0.79546022	0.000783791
hsa-miR-338-3p	-1.288984933	0.000821937
hsa-miR-199a-3p/- 199b-3p	-2.16717826	0.000824985
hsa-miR-193b	-1.108847701	0.000830953
hsa-miR-214	-1.568054995	0.00089293
hsa-miR-886-5p	-1.668972643	0.00092155
hsa-let-7a	-1.735816875	0.000922488
hsa-miR-542-5p	-0.979309003	0.000927843
hsa-miR-362-3p	-1.169396902	0.000927843
hsa-miR-450a	-1.465157518	0.00092982
hsa-miR-15a	-0.905639851	0.001153568
hsa-miR-19a	-1.002547282	0.001153568
hsa-miR-218	-1.476569864	0.001181555
hsa-let-7b	-1.77909911	0.001264325
hsa-miR-28-5p	-0.864810558	0.00148738
hsa-miR-424	-1.495908684	0.001584961
hsa-miR-590-5p	-0.80484525	0.00167917
hsa-miR-146b-5p	-1.208258436	0.001701829
hsa-miR-340	-0.688751086	0.001796447
hsa-miR-374b	-0.989874262	0.001889252
hsa-miR-342-3p	-1.162189618	0.001902944
hsa-miR-127-3p	-1.286392935	0.002285889
hsa-miR-107	-0.886473263	0.002532382
hsa-miR-27a	-1.080272397	0.002780355
hsa-miR-145	-1.446903684	0.0028197
hsa-miR-148a	-0.987827839	0.003280936
hsa-miR-151-5p	-0.926967911	0.003373061
hsa-miR-146a	-1.236954176	0.003624457
hsa-miR-491-3p	-1.079166163	0.003737097
hsa-miR-145*	-0.932698925	0.004081324
hsa-miR-378	-0.835109105	0.004540026
hsa-miR-29a	-1.64489676	0.004540026
hsa-miR-337-5p	-1.387273562	0.004767784
hsa-miR-497	-0.960039865	0.004819097
hsa-miR-487b	-0.982434688	0.005223749
hsa-miR-517a/b	-0.872016249	0.005968
hsa-miR-135b	-1.277783209	0.006003971
hsa-miR-365	-0.906920347	0.006107536
hsa-miR-92a	-0.766120094	0.00614097
hsa-miR-221	-1.229234436	0.006642956
hsa-miR-374a	-0.784316113	0.006912661
hsa-miR-154	-0.77976878	0.008471443
hsa-miR-155	-0.808155629	0.008702465
hsa-miR-222	-1.193983066	0.009445671

Palmer_Suppl_Table_S3

List of differentiating miRNAs for pediatric Seminomas versus non-malignant tissues, ranked by adjusted <i>p</i> -value					
Over-expressed	Log2 fold change	Adjusted <i>p</i> -value	Under-expressed	Log2 fold change	Adjusted <i>p</i> -value
hsa-miR-371-3p	4.812651609	1.58E-14	hsa-miR-152	-2.048470712	5.80E-08
hsa-miR-373	6.181135608	1.58E-14	hsa-miR-204	-2.667766407	1.15E-06
hsa-miR-372	5.341612201	6.98E-14	hsa-miR-99b	-1.844563552	1.51E-06
hsa-miR-182*	2.004639184	1.61E-11	hsa-miR-574-3p	-1.225010433	3.38E-06
hsa-miR-96	3.420477575	1.04E-10	hsa-miR-450a	-2.303235628	3.38E-06
miRPlus_17892	1.137471681	3.69E-10	hsa-miR-99a	-3.127576351	3.38E-06
hsa-miR-182	3.499939066	3.69E-10	hsa-miR-99a*	-1.341880557	3.39E-06
hsa-miR-373*	1.658642598	4.89E-10	hsa-miR-100	-3.067268703	3.76E-06
hsa-miR-302c	3.085156462	7.59E-08	hsa-let-7e	-1.057632482	1.04E-05
hsa-miR-371-5p	1.606952793	8.14E-08	hsa-miR-542-5p	-1.396534445	1.46E-05
hsa-miR-302a	2.369168826	1.84E-07	hsa-miR-205	-2.732884508	1.57E-05
hsa-miR-302d	3.132865228	1.84E-07	hsa-miR-542-3p	-1.448943017	1.77E-05
hsa-miR-183	2.149688931	1.98E-07	hsa-miR-455-5p	-1.466023403	1.87E-05
hsa-miR-367	2.936587781	2.49E-07	hsa-miR-133a	-1.604395096	2.85E-05
hsa-miR-492	1.858653465	3.38E-06	hsa-miR-199b-5p	-2.701987914	3.37E-05
hsa-miR-302b	3.151989378	3.38E-06	hsa-miR-338-3p	-1.693580668	3.77E-05
hsa-miR-142-3p	2.426748466	5.29E-06	hsa-miR-181b	-1.537735498	4.74E-05
hsa-miR-940	1.246281077	1.04E-05	hsa-miR-135a	-1.812083436	4.74E-05
hsa-miR-142-5p	1.866418651	7.33E-05	hsa-miR-133a/b	-1.144655826	5.85E-05
hsa-miR-146a	1.699379039	0.000161206	hsa-miR-148b	-1.150111799	6.11E-05
hsa-miR-520c-3p	1.151204166	0.000962554	hsa-miR-30a*	-1.000788792	6.56E-05
hsa-miR-602	0.840171452	0.001046457	hsa-miR-181a	-1.585653358	6.75E-05
hsa-miR-155	1.029810549	0.001354791	hsa-miR-133b	-1.45201128	7.18E-05
hsa-miR-625*	0.6079268	0.001628409	hsa-miR-455-3p	-1.659797221	7.18E-05
hsa-miR-520b	1.195237648	0.001719475	hsa-miR-551b	-1.572599091	7.97E-05
hsa-miR-584	0.776966644	0.00330463	hsa-miR-186	-1.089041879	0.000101117
hsa-miR-526b*	0.969588038	0.003313879	hsa-miR-429	-1.745150849	0.000101117
hsa-miR-623	0.74494365	0.005322775	hsa-miR-214	-1.917030004	0.000101117
hsa-miR-146b-5p	1.05233817	0.005780377	hsa-miR-143*	-1.001533111	0.000117601
hsa-miR-296-5p	0.557091708	0.005807573	hsa-miR-125b	-2.779427618	0.000118621
hsa-miR-596	0.749883196	0.005893477	hsa-miR-424	-1.907483989	0.000130625
			hsa-miR-127-3p	-1.68734885	0.000153363
			hsa-miR-410	-1.697534992	0.000159198
			hsa-miR-199a-5p	-2.628628341	0.000159463
			hsa-miR-199a-3p/-199b-3p	-2.46565386	0.000217831
			hsa-miR-30d	-1.151266545	0.000302545
			hsa-miR-200b	-2.386516073	0.000302545
			hsa-miR-10a	-1.770428694	0.00031443
			hsa-miR-126*	-1.322724673	0.000325711
			hsa-miR-218	-1.646719729	0.000449096
			hsa-miR-301a	-1.560869668	0.000629098
			hsa-miR-23b	-1.355016166	0.00072299
			hsa-miR-409-3p	-1.374385295	0.00072299
			hsa-miR-24	-1.337462579	0.000843443
			hsa-miR-23a	-1.303549077	0.00084515
			hsa-miR-654-3p	-1.534907475	0.000942938
			hsa-miR-128	-1.043223461	0.001046457
			hsa-miR-27b	-1.25242071	0.001046457
			hsa-miR-375	-0.820020886	0.001048175
			hsa-miR-140-5p	-1.254635913	0.001048175
			hsa-miR-145*	-1.09120171	0.001145851
			hsa-miR-148a	-1.123442638	0.001145851
			hsa-miR-329	-1.055924236	0.001453137

hsa-miR-335	-1.749677387	0.001581921
hsa-miR-95	-0.892619451	0.001586418
hsa-miR-98	-1.379870694	0.001586418
hsa-miR-126	-1.501297084	0.001629855
hsa-miR-1	-1.0644425	0.001784349
hsa-miR-34b*	-1.845686342	0.001792107
miRPlus_11201	-1.062084315	0.001834639
hsa-miR-449a	-1.84808712	0.002075124
hsa-miR-411	-1.236501797	0.002165425
hsa-miR-432	-1.180625344	0.002265375
hsa-miR-196b	-1.193801041	0.002680785
hsa-miR-125a-5p	-1.16301812	0.002848386
hsa-miR-26a	-1.138124042	0.003296905
hsa-miR-154	-0.891241461	0.003311939
hsa-miR-499-5p	-0.729553113	0.003746489
hsa-miR-200a	-1.922154761	0.003746489
miRPlus_17865	-0.823319508	0.003897375
hsa-miR-193b	-0.928129047	0.004346682
hsa-miR-369-3p	-1.393425788	0.004346682
hsa-miR-320a	-0.891537527	0.005024825
hsa-miR-379	-1.212326696	0.005024825
hsa-miR-363	-1.388251512	0.005532212
hsa-miR-130b	-0.944121924	0.005570205
hsa-miR-487b	-0.98126021	0.005633421
hsa-miR-34c-5p	-1.420265208	0.005780377
hsa-miR-365	-0.915293098	0.005893477
hsa-miR-9*	-1.278515417	0.005893477
hsa-miR-30b	-0.983708896	0.006032736
hsa-miR-144	-1.96768362	0.006042656
hsa-miR-143	-1.503578992	0.00631759
hsa-miR-451	-2.037506033	0.006708779
hsa-miR-145	-1.290404729	0.007026436
hsa-let-7d	-1.158184405	0.007158717
hsa-miR-337-5p	-1.305452036	0.007555411
hsa-miR-28-5p	-0.708630697	0.00762575
hsa-miR-301b	-1.039720251	0.007806272
hsa-miR-200c	-1.664543232	0.008013761
hsa-miR-132	-0.573033412	0.008742367
hsa-miR-30e*	-0.782510803	0.008742367
hsa-miR-660	-0.901608161	0.009076216

Palmer_Suppl_Table_S3

List of differentiating miRNAs for pediatric EC versus non-malignant tissues, ranked by adjusted p-value					
Over-expressed	Log2 fold change	Adjusted p-value	Under-expressed	Log2 fold change	Adjusted p-value
hsa-miR-520c-3p	4.601981788	9.54E-10	hsa-miR-30d	-2.452130546	1.44E-05
hsa-miR-526b*	4.442361265	9.54E-10	hsa-miR-125a-5p	-2.923915259	3.49E-05
hsa-miR-520b	4.707288223	4.78E-09	hsa-miR-204	-3.569065216	3.51E-05
hsa-miR-302a	4.314390304	5.58E-08	hsa-miR-30a	-2.568452724	9.01E-05
hsa-miR-367	5.293582919	9.23E-08	hsa-miR-9	-3.738983611	9.01E-05
hsa-miR-373	5.374460042	2.00E-07	hsa-miR-30b	-2.544703808	9.25E-05
hsa-miR-372	4.92923178	2.00E-07	miRPlus_11201	-2.34215201	0.000100668
hsa-miR-371-3p	4.205324971	2.00E-07	hsa-miR-30e*	-2.113797617	0.000101589
hsa-miR-512-3p	3.605187445	2.00E-07	hsa-miR-30a*	-1.609122829	0.000103331
hsa-miR-302c	4.799428592	2.81E-07	hsa-miR-30c	-2.537528565	0.000104491
hsa-miR-302d	4.867792646	7.48E-07	hsa-miR-152	-2.100500351	0.000138101
hsa-miR-525-3p	2.746318157	1.04E-06	hsa-miR-99a*	-1.724766157	0.000140531
hsa-miR-518e*	1.810520638	1.37E-06	hsa-miR-26a	-2.580311617	0.000143768
hsa-miR-518e	2.878014654	2.08E-06	hsa-let-7e	-1.435514463	0.000163543
hsa-miR-515-5p	4.122415879	2.37E-06	hsa-miR-574-3p	-1.547066476	0.00016414
hsa-miR-520g/h	3.105956021	3.99E-06	hsa-miR-361-5p	-1.663843127	0.000170642
hsa-miR-520g	3.363555531	4.48E-06	hsa-miR-99b	-2.19421457	0.000173342
hsa-miR-519b-3p	3.017863282	5.13E-06	hsa-miR-9*	-3.016995346	0.000237148
hsa-miR-515-3p	2.718006208	1.19E-05	hsa-miR-186	-1.66847707	0.00027996
hsa-miR-302b	4.618880681	2.73E-05	hsa-miR-99a	-3.771485562	0.000285319
hsa-miR-518a-5p/-527	1.862423888	2.73E-05	hsa-miR-95	-1.752635001	0.000288659
miRPlus_17892	1.078623117	2.79E-05	hsa-miR-140-5p	-2.344953885	0.000298769
hsa-miR-373*	1.581290161	3.18E-05	hsa-miR-10a	-2.848467658	0.000495793
hsa-miR-521	2.400851383	3.51E-05	hsa-miR-128	-1.867862969	0.000498942
hsa-miR-371-5p	1.846176078	4.42E-05	hsa-miR-29c*	-1.471473643	0.000533295
hsa-miR-519e	1.843377741	4.90E-05	hsa-miR-15a	-1.648919475	0.000545362
hsa-miR-519c-3p	1.735710428	0.000100668	hsa-miR-126*	-2.101773583	0.000558802
hsa-miR-517a/b	2.16754604	0.000140531	hsa-miR-135a	-2.445328412	0.000558802
hsa-miR-611	1.602844004	0.001034727	hsa-miR-133a/b	-1.563585012	0.00055956
hsa-miR-492	1.826591801	0.001772042	hsa-miR-133a	-2.079511305	0.00055956
hsa-miR-940	1.261810489	0.002618068	hsa-miR-542-3p	-1.807321513	0.000602986
hsa-miR-2110	0.940397471	0.002618068	hsa-miR-148b	-1.560992024	0.000608464
miRPlus_27560	1.430721173	0.002709334	miRPlus_17865	-1.674687672	0.000608464
hsa-miR-96	1.886214985	0.003512085	hsa-miR-499-5p	-1.468678748	0.000608788
hsa-miR-638	1.072181534	0.004685988	hsa-miR-455-5p	-1.826701359	0.000608788
hsa-miR-483-3p	1.021193471	0.007660459	hsa-miR-133b	-1.995855592	0.000608788
hsa-miR-596	1.174118974	0.007893235	hsa-miR-30e	-2.130205122	0.000608788
hsa-miR-584	1.106751565	0.008601295	hsa-miR-181a	-2.157658229	0.000613512
hsa-miR-766	0.879245028	0.009145943	hsa-miR-151-3p	-1.590365204	0.000717021
hsa-miR-296-5p	0.839766757	0.009681867	hsa-miR-100	-3.391433694	0.000717021
hsa-miR-637	1.110470588	0.009811004	hsa-miR-320a	-1.825569616	0.000718965
			hsa-miR-27b	-2.108124683	0.000799365
			hsa-miR-365	-1.905874389	0.000810529
			hsa-miR-28-5p	-1.529808456	0.000820345
			hsa-miR-101	-2.087518574	0.000914769
			hsa-miR-143*	-1.361541855	0.00099094
			hsa-miR-151-5p	-1.761275001	0.001008923
			hsa-miR-19b	-1.812638705	0.001008923
			hsa-miR-450a	-2.408223394	0.001034727
			hsa-miR-374b	-1.745281169	0.001067987
			hsa-miR-181b	-1.910864698	0.001067987
			hsa-miR-24	-2.100308295	0.001185378
			hsa-miR-125b	-3.675653091	0.0012594
			hsa-miR-98	-2.298062933	0.001314047

hsa-miR-424	-2.528276217	0.001314047
hsa-miR-191	-1.320833016	0.001680729
hsa-miR-16	-1.564474736	0.001990848
hsa-miR-107	-1.511974646	0.001991363
hsa-miR-126	-2.401420998	0.002049022
hsa-let-7a	-2.637660922	0.002049022
hsa-miR-374a	-1.492411351	0.0023492
hsa-miR-132	-1.12021175	0.002454758
hsa-miR-660	-1.7699863	0.002464979
hsa-miR-15b	-1.384843218	0.002578303
hsa-miR-542-5p	-1.44686912	0.002618068
hsa-miR-19a	-1.505346537	0.002709334
hsa-miR-532-5p	-1.561651284	0.002709334
hsa-miR-1	-1.654475056	0.002709334
hsa-let-7c	-2.510166888	0.002745395
hsa-miR-345	-1.13711738	0.002754222
hsa-let-7d	-2.133398979	0.002914768
hsa-miR-23b	-1.870122819	0.003077262
hsa-miR-23a	-1.824838526	0.003078422
hsa-let-7f	-2.001385911	0.003078422
hsa-miR-455-3p	-1.873960593	0.003170218
hsa-miR-362-3p	-1.668898002	0.003231837
hsa-miR-218	-2.163025132	0.003231837
hsa-miR-190	-1.905111239	0.003446059
hsa-miR-551b	-1.772986464	0.003449592
hsa-let-7g	-1.802176135	0.003991877
hsa-miR-214	-2.093268472	0.005346026
hsa-miR-145*	-1.473230235	0.005495812
hsa-miR-338-3p	-1.68398051	0.005833623
hsa-miR-487b	-1.577622845	0.006186215
hsa-miR-130a	-1.945675746	0.006768078
hsa-miR-148a	-1.472507041	0.006892439
hsa-let-7b	-2.381182367	0.006978842
hsa-miR-363*	-1.227925818	0.007332839
hsa-miR-154	-1.29592623	0.007660459
hsa-miR-497	-1.47590353	0.007745528
hsa-miR-449a	-2.535307664	0.007837204
hsa-miR-33a	-1.118507104	0.008051681
hsa-miR-25	-1.127454825	0.009428618
hsa-miR-145	-2.014245503	0.009474912
hsa-miR-143	-2.315442168	0.009474912
hsa-miR-27a	-1.497857392	0.00953171

Palmer_Suppl_Table_S3

List of differentiating miRNAs for GCT cell lines versus non-malignant tissues, ranked by adjusted <i>p</i> -value					
Over-expressed	Log2 fold change	Adjusted <i>p</i> -value	Under-expressed	Log2 fold change	Adjusted <i>p</i> -value
hsa-miR-302a	8.11584103	4.45E-21	hsa-let-7a	-4.085370292	2.64E-08
hsa-miR-302c	9.035969901	5.90E-20	hsa-miR-143	-4.256262205	5.18E-08
hsa-miR-367	9.217500658	8.96E-20	hsa-miR-126	-3.582017984	6.86E-08
hsa-miR-302d	9.06251183	3.61E-19	hsa-miR-199a-5p	-4.905425586	9.17E-08
hsa-miR-302b	8.61411598	5.14E-16	hsa-miR-199a-3p/-199b-3p	-4.686788424	9.98E-08
hsa-miR-302c*	2.277740031	5.36E-11	hsa-miR-125b	-5.02581113	9.98E-08
hsa-miR-183	3.103702958	1.61E-08	hsa-let-7i	-3.073871201	3.42E-07
hsa-miR-20b	2.430159752	4.02E-06	hsa-miR-214	-3.186767293	3.71E-07
hsa-miR-20a	2.266088676	1.48E-05	hsa-miR-100	-4.074029553	4.06E-07
hsa-miR-96	2.693696425	1.92E-05	hsa-let-7c	-3.14581953	3.89E-06
hsa-miR-17	2.118966428	1.92E-05	hsa-let-7d	-2.639049588	7.12E-06
hsa-miR-584	1.755662968	1.92E-05	hsa-miR-451	-4.323754127	1.54E-05
hsa-miR-106a	2.099632021	2.50E-05	hsa-miR-152	-1.770841731	1.92E-05
hsa-miR-18b	2.232586084	6.19E-05	hsa-miR-99a	-3.330764063	1.92E-05
hsa-miR-18a	2.319764883	7.95E-05	hsa-miR-98	-2.348140339	3.01E-05
hsa-miR-371-3p	3.303391052	9.84E-05	hsa-miR-142-3p	-2.503284003	5.40E-05
hsa-miR-93	1.957224932	9.84E-05	hsa-let-7b	-2.756240875	8.53E-05
hsa-miR-182	2.53172056	0.000101219	hsa-let-7g	-1.918582301	0.000113875
miRPlus_17892	1.061487453	0.000101219	hsa-miR-199b-5p	-2.765912621	0.000288238
hsa-miR-372	3.828309677	0.000113875	hsa-miR-127-3p	-1.908285796	0.00051277
hsa-miR-373	4.009090296	0.000133712	hsa-let-7f	-1.785526485	0.000729142
hsa-miR-15b	1.356757313	0.000198761	hsa-miR-136	-2.722513588	0.001063525
hsa-miR-373*	1.290434634	0.000308489	hsa-miR-377	-2.485281834	0.001088813
hsa-miR-130b	1.856607745	0.000465668	hsa-miR-23a	-1.547227804	0.001099141
hsa-miR-525-3p	1.492813681	0.000635339	hsa-miR-223	-1.832147472	0.001183554
hsa-miR-34a	1.496886411	0.000666869	hsa-miR-154	-1.186714009	0.001661563
hsa-miR-106b	1.424832129	0.001029536	hsa-miR-574-3p	-0.906540085	0.001668398
hsa-miR-521	1.492239323	0.001652654	hsa-miR-145	-1.906763823	0.001668398
hsa-miR-371-5p	1.202832929	0.001652654	hsa-miR-450a	-1.70548986	0.001682577
hsa-miR-492	1.554398978	0.001668398	hsa-miR-542-5p	-1.120898735	0.001729514
hsa-miR-7	1.607298609	0.001729514	hsa-miR-376c	-2.006031262	0.001729514
hsa-miR-340	0.880786945	0.002016214	hsa-miR-30d	-1.247254398	0.001840809
hsa-miR-425	1.048307057	0.002242697	hsa-miR-369-3p	-1.946531015	0.001840809
hsa-miR-512-3p	1.655806207	0.002631054	hsa-miR-23b	-1.470286429	0.001978904
hsa-miR-520b	1.865058018	0.003713109	hsa-miR-10a	-1.87082478	0.001986289
hsa-miR-526b*	1.673732651	0.003890001	hsa-miR-125a-5p	-1.494384992	0.002000193
hsa-miR-363	1.864913592	0.004289998	hsa-miR-144	-2.729129676	0.002081154
hsa-miR-590-5p	0.949773264	0.004322556	hsa-miR-24	-1.434694724	0.002588963
hsa-miR-519b-3p	1.552321849	0.004407237	hsa-miR-26a	-1.434528174	0.002631054
hsa-miR-92b	1.104193826	0.004407742	hsa-miR-337-5p	-1.844469596	0.003114913
hsa-miR-519c-3p	1.09105812	0.004442193	hsa-miR-376a	-2.116853372	0.003890001
hsa-miR-519e	1.074347727	0.004663793	hsa-miR-326	-1.099471551	0.004370398
hsa-miR-744	1.000165187	0.004707045	hsa-miR-126*	-1.242971176	0.004407237
hsa-miR-520c-3p	1.661314999	0.005053441	hsa-miR-411	-1.323037351	0.006562223
hsa-miR-520g/h	1.517759238	0.005053441	hsa-miR-886-3p	-2.369838959	0.006562223
hsa-miR-520g	1.639565072	0.005459524	hsa-miR-886-5p	-2.057490187	0.006563482
hsa-miR-301b	1.936337359	0.005708586	miRPlus_11201	-1.093166446	0.006883881
hsa-miR-517a/b	1.30054696	0.007591869	hsa-miR-204	-1.506478819	0.008003587
hsa-miR-515-3p	1.26872186	0.008130181	hsa-miR-410	-1.385926934	0.008420275
hsa-miR-92a	0.925833052	0.009205973	hsa-miR-572	-0.923388374	0.008748737
hsa-miR-375	1.498749671	0.009553896	hsa-miR-32*	-0.818863638	0.008905946
			hsa-miR-27b	-1.140252427	0.009891562

Palmer_Suppl_Table_S4

List of differentiating miRNAs for adult YSTs versus non-malignant tissues, ranked by adjusted <i>p</i> -value					
Over-expressed	$\Delta\Delta$ Ct	Adjusted <i>p</i> -value	Under-expressed	$\Delta\Delta$ Ct	Adjusted <i>p</i> -value
hsa-miR-302c	-15.92	8.64E-14	hsa-miR-100	2.00	3.56E-03
hsa-miR-367	-16.22	1.23E-13	hsa-miR-99a	1.90	5.54E-03
hsa-miR-302a	-16.18	1.23E-13			
hsa-miR-302b*	-13.57	1.23E-13			
hsa-miR-302d	-16.42	1.24E-13			
hsa-miR-302b	-16.37	2.14E-13			
hsa-miR-302c*	-11.81	2.62E-13			
hsa-miR-371	-11.85	2.24E-09			
hsa-miR-373*	-9.78	3.34E-09			
hsa-miR-373	-11.13	3.66E-09			
hsa-miR-372	-11.72	4.12E-09			
hsa-miR-17-5p	-4.96	3.01E-08			
hsa-miR-106a	-4.51	3.54E-07			
hsa-miR-92	-4.00	4.79E-07			
hsa-miR-122a	-9.81	5.01E-07			
hsa-miR-19a	-3.94	1.65E-06			
hsa-miR-17-3p	-3.64	3.59E-06			
hsa-miR-339	-3.26	4.25E-06			
hsa-miR-20	-4.04	4.84E-06			
hsa-miR-144	-3.83	1.26E-05			
hsa-miR-25	-3.86	2.26E-05			
hsa-miR-130a	-3.57	4.06E-05			
hsa-miR-128a	-2.08	4.14E-05			
hsa-miR-182*	-5.14	1.02E-04			
hsa-miR-105	-4.97	1.29E-04			
hsa-miR-107	-2.52	1.97E-04			
hsa-miR-128b	-1.76	2.07E-04			
hsa-miR-185	-2.92	2.13E-04			
hsa-miR-210	-3.51	2.31E-04			
hsa-miR-9	-4.81	2.48E-04			
hsa-miR-130b	-3.73	2.48E-04			
hsa-miR-31	-4.29	3.20E-04			
hsa-miR-103	-2.29	3.39E-04			
hsa-miR-15b	-3.11	3.48E-04			
hsa-miR-96	-5.36	6.81E-04			
hsa-miR-220	-2.63	6.81E-04			
hsa-miR-138	-2.31	7.64E-04			
hsa-miR-183	-5.05	7.78E-04			
hsa-miR-340	-2.34	7.82E-04			
hsa-miR-151	-2.40	7.99E-04			
hsa-miR-126	-2.12	7.99E-04			
hsa-miR-219	-3.39	9.48E-04			
hsa-miR-191	-2.29	9.48E-04			
hsa-miR-190	-2.98	9.81E-04			
has-miR-16	-2.16	1.03E-03			
hsa-miR-124b	-4.15	1.61E-03			
hsa-miR-205	-5.36	1.64E-03			
hsa-miR-30c	-1.61	3.03E-03			

hsa-miR-124a	-4.89	3.56E-03
hsa-miR-223	-3.56	3.56E-03
hsa-miR-15a	-1.76	3.65E-03
hsa-miR-9*	-3.53	4.19E-03
hsa-miR-330	-2.09	4.23E-03
hsa-miR-139	-1.34	4.77E-03
hsa-miR-374	-2.29	4.87E-03
hsa-miR-331	-1.89	5.29E-03
hsa-miR-30b	-1.58	5.40E-03
hsa-miR-29b	-1.26	8.96E-03
hsa-miR-320	-1.75	9.11E-03
hsa-miR-338	-2.30	9.67E-03
hsa-miR-186	-1.65	9.80E-03

Palmer_Suppl_Table_S4

List of differentiating miRNAs for adult Seminomas versus non-malignant tissues, ranked by adjusted p-value					
Over-expressed	$\Delta\Delta$ Ct	Adjusted p-value	Under-expressed	$\Delta\Delta$ Ct	Adjusted p-value
hsa-miR-371	-11.04	1.09E-16	hsa-miR-133a	5.06	2.52E-08
hsa-miR-302b	-10.78	1.09E-16	hsa-miR-133b	5.02	1.13E-07
hsa-miR-302d	-10.67	1.09E-16	hsa-miR-203	5.37	9.12E-07
hsa-miR-367	-10.66	1.09E-16	hsa-miR-200a	4.67	6.04E-06
hsa-miR-302a	-10.36	3.65E-16	hsa-miR-200b	4.84	6.36E-06
hsa-miR-373	-10.25	4.19E-16	hsa-miR-100	2.46	1.83E-05
hsa-miR-372	-10.69	3.22E-15	hsa-miR-99a	2.44	1.77E-04
hsa-miR-373*	-8.22	7.65E-15	hsa-miR-211	3.15	1.86E-04
hsa-miR-302c	-9.49	4.02E-14	hsa-miR-145	2.13	3.21E-04
hsa-miR-302b*	-7.82	1.81E-13	hsa-miR-214	1.93	6.78E-04
hsa-miR-96	-6.63	4.05E-11	hsa-miR-204	2.89	1.51E-03
hsa-miR-182*	-6.31	1.75E-10	hsa-miR-199a	1.63	2.68E-03
hsa-miR-105	-7.04	2.92E-09	hsa-miR-23b	1.47	3.61E-03
hsa-miR-302c*	-4.83	2.79E-08	hsa-miR-328	1.86	3.79E-03
hsa-miR-183	-5.13	5.55E-08			
hsa-miR-9	-4.43	2.02E-07			
hsa-miR-184	-4.16	9.33E-06			
hsa-miR-146	-3.33	1.28E-05			
hsa-miR-25	-3.20	1.56E-05			
hsa-miR-142-3p	-3.41	1.79E-05			
hsa-miR-124a	-4.46	5.47E-05			
hsa-miR-135b	-2.96	5.72E-05			
hsa-miR-19a	-2.54	1.09E-04			
hsa-miR-142-5p	-2.80	2.53E-04			
hsa-miR-124b	-3.39	9.32E-04			
hsa-miR-20	-2.24	1.08E-03			
hsa-miR-92	-1.93	1.47E-03			
hsa-miR-17-3p	-2.00	1.94E-03			
hsa-miR-342	-1.72	2.77E-03			
hsa-miR-151	-1.76	5.43E-03			
hsa-miR-9*	-3.52	6.55E-03			
hsa-miR-17-5p	-1.81	6.55E-03			
hsa-miR-374	-1.67	6.55E-03			
hsa-miR-29b	-1.46	6.55E-03			
hsa-miR-130a	-1.79	6.56E-03			

Palmer_Suppl_Table_S4

List of differentiating miRNAs for adult EC versus non-malignant tissues, ranked by adjusted p-value					
Over-expressed	$\Delta\Delta$ Ct	Adjusted p-value	Under-expressed	$\Delta\Delta$ Ct	Adjusted p-value
hsa-miR-302d	-13.21	5.76E-15	hsa-miR-133a	3.06	4.00E-04
hsa-miR-302c	-12.27	1.03E-14	hsa-miR-203	3.55	1.68E-03
hsa-miR-302b	-13.19	1.52E-14	hsa-miR-133b	2.83	4.33E-03
hsa-miR-302a	-13.00	2.10E-14			
hsa-miR-302b*	-10.55	7.81E-14			
hsa-miR-367	-13.26	9.98E-14			
hsa-miR-371	-11.03	7.25E-13			
hsa-miR-373	-9.78	7.25E-13			
hsa-miR-302c*	-8.75	1.64E-12			
hsa-miR-373*	-9.01	4.45E-12			
hsa-miR-372	-10.44	5.30E-12			
hsa-miR-182*	-6.21	1.22E-08			
hsa-miR-96	-6.27	8.07E-08			
hsa-miR-124a	-5.76	3.15E-07			
hsa-miR-17-5p	-2.69	8.69E-07			
hsa-miR-124b	-4.27	3.79E-06			
hsa-miR-92	-2.54	9.15E-06			
hsa-miR-17-3p	-2.19	9.15E-06			
hsa-miR-183	-4.77	1.47E-05			
hsa-miR-25	-2.57	1.96E-05			
hsa-miR-19a	-2.33	2.25E-05			
hsa-miR-106a	-2.42	1.14E-04			
hsa-miR-219	-2.78	2.75E-04			
hsa-miR-20	-2.74	4.64E-04			
hsa-miR-185	-2.17	6.61E-04			
hsa-miR-142-3p	-2.99	7.42E-04			
hsa-miR-368	-2.27	9.63E-04			
hsa-miR-31	-2.56	1.17E-03			
hsa-miR-142-5p	-2.72	1.96E-03			
hsa-miR-223	-3.02	4.56E-03			
hsa-miR-15b	-1.59	5.12E-03			
hsa-miR-150	-2.50	6.09E-03			
hsa-miR-105	-2.64	6.37E-03			
hsa-miR-34a	-1.46	7.57E-03			
hsa-miR-95	-1.45	7.57E-03			
hsa-miR-339	-1.09	7.57E-03			
hsa-miR-299	-1.67	8.79E-03			
hsa-miR-191	-1.17	8.79E-03			

Palmer_Suppl_Table_S5

Accession	Gene Name	Pediatric Rank	Pediatric Log ₂ Fold Change	Function OMIM: http://www.ncbi.nlm.nih.gov/omim/ and GENATLAS: http://genatlas.medecine.univ-paris5.fr/
NM_012082	ZFPM2	2	-3.31	ZFP; TF; modulate GATA proteins
NM_002937	RNASE4	6	-2.48	Ribonuclease; mRNA cleavage
NM_022648	TNS1	13	-2.00	Crosslinks actin, adhesion to ECM
NM_000944	PPP3CA	14	-1.98	Protein phosphatase3; negative regulation CDK4 in cell cycle
NM_001018056	VLDLR	15	-1.97	VLDL receptor; down-regulated in gastric cancer
NM_032199	ARID5B	16	-1.97	TF; AT-rich interactive domain 5B
NM_001128615	ARHGEF3	19	-1.91	Rho guanine nucleotide exchange factor 3; signaling
NM_005324	H3F3B	20	-1.88	Histone H3 member; nucleosome formation
NM_004331	BNIP3L	21	-1.87	TSG; functional homolog of BNIP3; pro-apoptotic, LOH in cancer
NM_003174	SVIL	23	-1.78	Bipartite protein; organizes actin/cytoskeletal proteins
NM_001706	BCL6	28	-1.66	Transcriptional repressor; associated with lymphomas
NM_003927	MBD2	29	-1.65	Methyl-CpG-BP; transcriptional repressor and de-methylase
NM_001018009	SH3BP5	32	-1.61	Negative trans-regulator of BTK signal transduction pathway
NM_015149	RGL1	33	-1.58	Involved in downstream Ras and Ral signaling pathways
NM_031490	LONP2	34	-1.57	Peroxisomal peptidase
NM_016217	HECA	35	-1.57	Regulation of cell differentiation; deleted in pancreatic cancer
NM_012197	RABGAP1	37	-1.56	GTPase activator
NM_153367	ZCCHC24	38	-1.55	ZFP
NM_001001924	MTUS1	39	-1.53	Mitochondrial TSG; growth inhibition, low levels in ovarian ca

Key

TF; transcription factor

BP; binding protein

ZFP; zinc finger protein

MP; membrane protein

TSG; tumor suppressor gene

NR; nuclear receptor

HM; hyper-methylated

ECM extra-cellular matrix

LOH; loss of heterozygosity

Mito/perox; mitochondrial and peroxisomal

A Pediatric YST vs Control, common SCR present

GO Term	GOBPID	Total Genes in GO Term	Gene Count	Expected Gene Count	Adjusted p -value
Regulation of cellular process	GO:0050794	2943	22	12.323	1.30E-03
Regulation of biological process	GO:0050789	3033	22	12.7	2.30E-03
Regulation of S phase of mitotic cell cycle	GO:0007090	6	2	0.025	2.30E-03
Negative regulation of mitotic cell cycle	GO:0045930	8	2	0.033	4.20E-03
Regulation of S phase	GO:0033261	10	2	0.042	6.70E-03
Biological regulation	GO:0065007	3226	22	13.508	6.70E-03
S phase of mitotic cell cycle	GO:0000084	12	2	0.05	9.70E-03

B Pediatric YST vs Control, common SCR absent

GO Term	GOBPID	Total Genes in GO Term	Gene Count	Expected Gene Count	Adjusted p -value
Fat soluble vitamin metabolic process	GO:0006775	6	2	0.043	5.10E-03
Vitamin A metabolic process	GO:0006776	6	2	0.043	5.10E-03

C Adult testicular YST vs Control, common SCR absent

GO Term	GOBPID	Total Genes in GO Term	Gene Count	Expected Gene Count	Adjusted p -value
Spermatogenesis	GO:0007283	106	31	5.75	1.70E-14
Male gamete generation	GO:0048232	106	31	5.75	1.70E-14
Sexual reproduction	GO:0019953	148	36	8.03	5.30E-14
Reproduction	GO:0000003	249	44	13.52	9.70E-12
Gamete generation	GO:0007276	131	31	7.11	9.80E-12
Single fertilization	GO:0007338	18	7	0.98	2.00E-04
Fertilization	GO:0009566	19	7	1.03	3.00E-04
Male gonad development	GO:0008584	11	5	0.6	1.30E-03
Spermatid differentiation	GO:0048515	11	5	0.6	1.30E-03
Steroid biosynthetic process	GO:0006694	44	9	2.39	3.80E-03
Development of primary male sex characteristics	GO:0046546	15	5	0.81	6.90E-03
Reproductive process	GO:0022414	135	17	7.33	7.40E-03
Gonad development	GO:0008406	31	7	1.68	8.70E-03
Reproductive structure development	GO:0048608	31	7	1.68	8.70E-03

A Pediatric Seminoma versus Control, common SCR present

GO Term	GOBPID	Total Genes in GO Term	Gene Count	Expected Gene Count	Adjusted p -value
Multi-cellular process	GO:0032501	1423	22	8.607	2.80E-05
Multi-cellular development	GO:0007275	1097	19	6.635	4.20E-05
Organ morphogenesis	GO:0009887	220	8	1.331	3.60E-04
System development	GO:0048731	833	14	5.038	1.90E-03
Developmental process	GO:0032502	1580	20	9.556	2.40E-03
Blood vessel morphogenesis	GO:0048514	105	5	0.635	3.50E-03
Anatomical structure morphogenesis	GO:0009653	476	10	2.879	3.50E-03
Blood vessel development	GO:0001568	118	5	0.714	5.90E-03
Vasculature development	GO:0001944	119	5	0.72	6.10E-03
Morphogenesis	GO:0016043	1059	15	6.405	6.90E-03
Anatomical structure development	GO:0048856	964	14	5.831	8.80E-03

B Pediatric Seminoma versus Control, common SCR absent

GO Term	GOBPID	Total Genes in GO Term	Gene Count	Expected Gene Count	Adjusted p -value
Muscle development	GO:0007517	102	6	1.155	7.80E-03
Multi-cellular process	GO:0032501	1423	28	16.11	9.00E-03
Malate metabolic process	GO:0006108	5	2	0.057	9.90E-03

C Adult testicular Seminoma versus Control, common SCR absent

GO Term	GOBPID	Total Genes in GO Term	Gene Count	Expected Gene Count	Adjusted p -value
Spermatogenesis	GO:0007283	106	27	5.84	6.60E-11
Male gamete generation	GO:0048232	106	27	5.84	6.60E-11
Sexual reproduction	GO:0019953	148	32	8.15	8.60E-11
Reproduction	GO:0000003	249	42	13.71	2.60E-10
Gamete generation	GO:0007276	131	27	7.21	1.20E-08
Single fertilization	GO:0007338	18	7	0.99	2.20E-04
Fertilization	GO:0009566	19	7	1.05	3.30E-04
Spermatid development	GO:0007286	10	5	0.55	7.90E-04
Reproductive process	GO:0022414	135	19	7.43	1.10E-03
Male gonad development	GO:0008584	11	5	0.61	1.40E-03
Spermatid differentiation	GO:0048515	11	5	0.61	1.40E-03
Sex differentiation	GO:0007548	43	9	2.37	3.60E-03
Steroid biosynthetic process	GO:0006694	44	9	2.42	4.30E-03
Reproductive developmental process	GO:0003006	46	9	2.53	6.00E-03
Development of primary male sex characteristics	GO:0046546	15	5	0.83	7.40E-03
Gonad development	GO:0008406	31	7	1.71	9.60E-03
Reproductive structure development	GO:0048608	31	7	1.71	9.60E-03

Palmer_Suppl_Table_S8

A

Adult TGCT Dataset	Number of Down-regulated Genes	Down-regulated Genes with Transcript and 3'UTR information	Common SCR Present in 3'UTR	Common SCR Absent in 3'UTR
Malignant GCT vs Controls	1006	825 (82.0%)	212 (25.7%)	613 (74.3%)
YST vs Controls	1083	895 (82.6%)	247 (27.6%)	648 (72.4%)
Seminoma vs Controls	1061	865 (81.5%)	229 (26.5%)	636 (73.5%)

B

Adult malignant TGCT versus Controls, common SCR absent

GO Term	GOBPID	Total Genes in GO Term	Gene Count	Expected Gene Count	Adjusted p -value
Sexual reproduction	GO:0019953	148	31	7.28	2.20E-11
Spermatogenesis	GO:0007283	106	26	5.22	3.10E-11
Male gamete generation	GO:0048232	106	26	5.22	3.10E-11
Reproduction	GO:0000003	249	39	12.25	4.50E-10
Gamete generation	GO:0007276	131	26	6.45	4.90E-09
Single fertilization	GO:0007338	18	8	0.89	7.00E-06
Fertilization	GO:0009566	19	8	0.94	1.20E-05
Male gonad development	GO:0008584	11	5	0.54	7.90E-04
Reproductive process	GO:0022414	135	17	6.64	2.40E-03
Development of primary male sex characteristics	GO:0046546	15	5	0.74	4.40E-03
Spermatid development	GO:0007286	10	4	0.49	7.50E-03
C-21 steroid hormone process	GO:0006700	5	3	0.25	8.50E-03
Prophase	GO:0051324	5	3	0.25	8.50E-03
Steroid biosynthetic process	GO:0006694	44	8	2.17	9.20E-03

Gene Name	Pediatric Rank	Pediatric Log ₂ Fold Change	Adult Rank	Adult Log ₂ Fold Change	Function OMIM: http://www.ncbi.nlm.nih.gov/omim/ and GENATLAS: http://genatlas.medecine.univ-paris5.fr/
<i>GSTM3</i>	1	-3.56	2	-5.36	Metabolic; mutation in cancer
<i>PRNP</i>	2	-3.32	34	-3.36	Glycosyl-phosphatidyl-inositol-anchored glycoprotein
<i>PRKAR2B</i>	3	-3.07	35	-3.35	cAMP-dependent protein kinase
<i>GOLGA8B</i>	6	-2.62	44	-3.16	Golgi autoantigen, golgin subfamily a, 8B
<i>OSR2</i>	7	-2.52	110	-2.25	ZFP;TF; development and patterning
<i>DIPP3B</i>	8	-2.50	23	-3.68	Phospho-hydrolase
<i>NKX3-1</i>	9	-2.49	25	-3.64	TF; downregulated in TGCTs and prostate cancer
<i>SEMA3C</i>	10	-2.46	144	-2.00	Immunoglobulin domain, short basic domain
<i>NXF3</i>	11	-2.38	18	-3.87	Nuclear RNA export factor
<i>PDZD2</i>	12	-2.33	20	-3.83	Transmembrane receptor-BP
<i>ARAP2</i>	13	-2.19	104	-2.27	ArfGAP protein that regulates focal adhesion
<i>FAM13A1</i>	14	-2.19	154	-1.92	Family with sequence similarity 13, A1. Function unknown
<i>SOBP</i>	15	-2.19	26	-3.58	Nuclear ZFP; cell fate/patterning
<i>HSD17B3</i>	16	-2.18	41	-3.22	17 beta-hydroxysteroid dehydrogenase isoform
<i>MAP3K5</i>	17	-2.15	75	-2.57	Activates MAPK; TSG; pro-apoptotic
<i>ARID5B</i>	18	-2.10	182	-1.74	Modulates leptin/adiposity; allow fat accumulation
<i>HECA</i>	19	-2.08	105	-2.27	Cytoplasmic protein; regulates mitotic cycle re-entry
<i>QKI</i>	22	-2.01	215	-1.60	RNA-BP; RNA export + stability
<i>MBNL2</i>	23	-1.95	128	-2.09	ZFP; regulates alternative splicing in development
<i>CD47</i>	24	-1.94	59	-2.83	MP; cell adhesion to ECM
<i>AHI-1</i>	25	-1.90	172	-1.80	Abelson helper integration site; protein:protein interactions
<i>MBD2</i>	28	-1.84	161	-1.87	Methyl-CpG-BP; transcriptional repressor
<i>ADCY9</i>	29	-1.78	166	-1.82	Adenylate cyclase
<i>SLC7A1</i>	30	-1.76	118	-2.15	Cationic amino acid transporter
<i>DIAPH2</i>	31	-1.74	159	-1.88	Formin homology protein family; actin assembly
<i>CYP26B1</i>	32	-1.73	66	-2.77	Cytochrome P450 enzyme; deveopment
<i>SACS</i>	33	-1.70	198	-1.66	Sacsin protein
<i>FAM13B</i>	34	-1.70	123	-2.13	Family with sequence similarity 13, B. Function unknown
<i>TSPYL2</i>	35	-1.68	102	-2.27	Nucleosome assembly protein; TF
<i>SEPT6</i>	38	-1.62	53	-2.89	Septin GTPase; actin assembly and cell-cycle arrest
<i>BNC2</i>	40	-1.60	188	-1.71	ZFP; TF; downregulated in cancer
<i>ENDOD1</i>	42	-1.59	183	-1.74	Endonuclease, DNase and RNase
<i>PER2</i>	43	-1.58	132	-2.05	Circadian rhythm, HM in cancer
<i>BTG3</i>	45	-1.56	151	-1.93	TSG, transcript regulation, G2/M checkpoint modulator
<i>MFF</i>	47	-1.51	106	-2.27	MP; mito/perox fission, apoptosis

B

Gene Name	Pediatric Rank	Pediatric Log ₂ Fold Change	Function OMIM: http://www.ncbi.nlm.nih.gov/omim/ and GENATLAS: http://genatlas.medecine.univ-paris5.fr/
<i>ZFPM2</i>	4	-2.82	ZFP; TF; modulate GATA proteins
<i>GAS1</i>	5	-2.73	TSG; growth-arrest specific 1; blocks entry to S phase
<i>RNASE4</i>	20	-2.08	Ribonuclease; mRNA cleavage
<i>BNIP3L</i>	21	-2.02	TSG; functional homolog of BNIP3; pro-apoptotic, LOH in cancer
<i>WDR33</i>	26	-1.88	Cell cycle; apoptosis; gene regulation
<i>TNS1</i>	27	-1.86	Crosslinks actin, adhesion to ECM
<i>VLDLR</i>	36	-1.67	VLDL receptor; down-regulated in gastric cancer
<i>RGL1</i>	37	-1.65	Involved in downstream Ras and Ral signaling pathways
<i>LONP2</i>	39	-1.61	Peroxisomal peptidase
<i>CORIN</i>	41	-1.59	Serine protease; embryogenesis
<i>NR3C1</i>	44	-1.57	TF; glucocorticoid nuclear receptor
<i>BCL6</i>	46	-1.54	Transcriptional repressor; associated with lymphomas

Key

TF; transcription factor

BP; binding protein

ZFP; zinc finger protein

MP; membrane protein

TSG; tumor suppressor gene

NR; nuclear receptor

HM; hyper-methylated

ECM extra-cellular matrix

LOH; loss of heterozygosity

Mito/perox; mitochondrial and peroxisomal

A

Gene Name	Pediatric Rank	Pediatric Log ₂ Fold Change	Adult Rank	Adult Log ₂ Fold Change	Function OMIM: http://www.ncbi.nlm.nih.gov/omim/ and GENATLAS: http://genatlas.medecine.univ-paris5.fr/
<i>GJA1</i>	1	-4.24	74	-2.44	Connexin protein in gap junctions; development
<i>GSTM3</i>	4	-3.04	6	-4.70	Metabolic; mutation in cancer
<i>OSR2</i>	5	-2.89	106	-2.14	ZFP; TF; development and patterning
<i>AMIGO2</i>	7	-2.76	120	-2.04	Adhesion molecule
<i>RNASE4</i>	8	-2.74	170	-1.71	Ribonuclease; mRNA cleavage
<i>SEMA3C</i>	10	-2.60	53	-2.83	Immunoglobulin domain, short basic domain
<i>NKX3-1</i>	11	-2.57	22	-3.73	TF; down-regulated in TGCTs and prostate cancer
<i>PPP3CA</i>	14	-2.40	141	-1.89	Protein phosphatase 3; negative regulation CDK4
<i>MBNL2</i>	15	-2.38	115	-2.05	ZFP; regulates alternative splicing
<i>CNN1</i>	19	-2.17	212	-1.57	Calponin; down-regulated in gastric cancer
<i>ADCY9</i>	20	-2.15	208	-1.58	Adenylate cyclase
<i>SOBP</i>	22	-2.12	73	-2.47	Nuclear ZFP; cell fate/patterning
<i>CD99</i>	23	-2.10	122	-2.03	Cell surface glycoprotein; cell adhesion
<i>H3F3B</i>	25	-2.06	229	-1.51	H3 histone, family 3B; nucleosome formation
<i>PDZD2</i>	26	-2.04	50	-2.84	Transmembrane receptor-BP
<i>ERBB4</i>	28	-1.99	87	-2.32	Tyrosine protein kinase (HER4)
<i>TSC22D1</i>	29	-1.93	136	-1.91	TF; early response gene
<i>RBBP7</i>	30	-1.93	138	-1.90	Transcriptional repressor; binds RB and BRCA1 TSG
<i>FAM13A1</i>	31	-1.88	98	-2.24	Family with sequence similarity 13, A1. Function unknown
<i>MAMLD1</i>	33	-1.79	142	-1.88	Transactivates Hes3 promoter
<i>SCCPDH</i>	35	-1.74	14	-3.95	Saccharopine dehydrogenase
<i>CREM</i>	39	-1.62	15	-3.94	TF; cAMP responsive element modulator
<i>DIAPH2</i>	42	-1.59	158	-1.80	Formin homology protein family; actin assembly
<i>MARK4</i>	46	-1.53	176	-1.69	Microtubule affinity regulating kinase 4

B

Gene Name	Pediatric Rank	Pediatric Log ₂ Fold Change	Function OMIM: http://www.ncbi.nlm.nih.gov/omim/ and GENATLAS: http://genatlas.medecine.univ-paris5.fr/
<i>ZFPM2</i>	2	-3.53	ZFP; TF; modulate GATA proteins
<i>PDGFRA</i>	3	-3.10	Platelet derived growth factor receptor A
<i>CAV1</i>	6	-2.86	Caveolin 1; cell growth inhibiting protein; negative regulation of RAS
<i>TMEM47</i>	9	-2.68	Transmembrane protein 47; function unknown
<i>LDLR</i>	12	-2.52	Low density lipoprotein receptor
<i>SVIL</i>	13	-2.50	Bipartite protein; organizes actin/cytoskeletal proteins
<i>VLDLR</i>	16	-2.31	VLDL receptor; down-regulated in gastric cancer
<i>ABLIM1</i>	17	-2.26	Actin-BP
<i>TNS1</i>	18	-2.22	Crosslinks actin, adhesion to ECM
<i>PGRMC1</i>	21	-2.13	Progesterone receptor membrane complex 1
<i>PPAP2B</i>	24	-2.08	Phosphatidic acid phosphatase; germ cell migration
<i>MGAT1</i>	27	-2.04	Mono-acyl-glycerol acyl-transferase; diacyl-glycerol synthesis
<i>F3</i>	32	-1.85	Tissue factor III (thromboplastin)
<i>ZCCHC24</i>	34	-1.77	ZFP
<i>HEG1</i>	36	-1.66	HEG homolog 1; function unknown
<i>EPAS1</i>	37	-1.65	TF; endothelial PAS protein; also called hypoxia inducible factor 2 alpha
<i>PTPRD</i>	38	-1.63	Protein tyrosine phosphatase receptor D; down-regulated in neuroblastoma
<i>MID1</i>	40	-1.62	TF; midline 1 ring finger protein; patterning
<i>SPG20</i>	41	-1.59	Spartin; interacts with microtubules
<i>BCL6</i>	43	-1.58	Transcriptional repressor; associated with lymphomas
<i>MTUS1</i>	44	-1.57	Mitochondrial TSG 1; growth inhibition, low levels in ovarian cancer
<i>SPARC</i>	45	-1.56	Osteonectin; inhibitor of cell proliferation
<i>GNG12</i>	47	-1.53	Guanine nucleotide-BP; signal transducer
<i>BACE1</i>	48	-1.53	Beta-secretase; cleaves amyloid precursor protein
<i>SH3BP5</i>	49	-1.53	Negative trans-regulator of BTK signal transduction pathway
<i>SNED1</i>	50	-1.51	Sushi, nidogen and EGF-like domains protein 1
<i>MCFD2</i>	51	-1.51	Paracrine factor in maintaining stem cell potential

Key

TF; transcription factor

BP; binding protein

ZFP; zinc finger protein

MP; membrane protein

TSG; tumor suppressor gene

NR; nuclear receptor

HM; hyper-methylated

ECM extra-cellular matrix

LOH; loss of heterozygosity

Mito/perox; mitochondrial and peroxisomal