

Table SI. Primers for qRT-PCR validation of the candidate circRNAs.

circRNA	Sense primer	Antisense primer
chr5: 161330882-161336769-	CACAATCAACACCCACCTCC	TATCATCGCCACGCCAGTA
chr12: 129699809-129700698-	CCAAAGACCGTGAGGAAAG	GAGGTAGGTGGGCAGCAAG
chr9: 22046750-22097364+	TCAGTAGAGGAAGTGGCAGGA	GCTGTTGAATCAGAATGAGGCTTA
chr20: 17456347-17465553+	TCACGACGAGGTCCATCAG	TCCAGAGCCAGTGCAAACA
chr7: 116699070-116700284+	CGATCTGCCATGTGTGCATT	CTCGGACTTTGCTAGTGCCT
chr8: 18765448-18804898-	CTGTCAGGAGTTCATTGCAAATC	TGCTGCTGGTACCATTACTGAG
chr7: 22308338-22318037-	TCAAACAGTGGACCAGCATC	CTGGGAAGGCGTATGTTCAAG
chr5: 38523418-38530666-	CTGCTGATTTCTCAACCTC	CTTTTATTGTCCACCATCC

Table SII. Characteristics of the 53 differentially expressed circRNAs of papillary thyroid carcinoma (PTC) with RNA sequencing.

ID	circRNA	log ₂ FC	padj	Regulation	circBase ID	Gene name	Catalogue	Feature	Length
1	chr5:161330882-161336769-	7.3422	4.08E-08	Up		GABRB2	Antisense	exon:161329433-161331127, intron:161334904-161336631, exon:161334751-161334904, intron:161331127-161334751;	5,887
2	chr5:122692596-122693767+	6.2613	1.32E-03	Up		FRMD3	Intergenic	intron:83311975-83313659,	1,171
3	chr9:83290602-83335639-	6.0441	0.002365	Up			Antisense	intron:83298816-83299111, intron:83299186-83309535, intron:83310548-83311886, intron:83313747-83335515, intron:83290727-83298747, intron:83309624-83310484	4,4314
4	chr12:94169152-94209704+	6.0396	0.0027538	Up		PLXNC1	Annot intron	intron:94181580-94186372, intron:94169293-94181445, intron:94186473-94209589	40,060
5	chr12:129699809-129700698-	5.9252	0.015753	Up		TMEM132D	Antisense	exon:129699809-129700698;	889
6	chrX:38072046-38110482+	5.7452	0.0084421	Up		RP5-972B16.2	One intron	intron:37426000-38666120;	3,8436
7	chr21:31245487-31266983-	5.7067	0.0079758	Up		TIAM1	Antisense	intron:31245660-31251741, intron:31252189-31339242, exon:31251741-31252189	21,496
8	chr5:161410974-161459844-	5.6354	0.012143	Up		GABRB2	One intron	intron:161411057-161545226	48,870
9	chr7:3606251-3642105+	5.5858	0.012143	Up		SDK1	Exon intron	intron:3619239-3639003, exon:3619079-3619239,	22,771
10	chr9:22046750-22097364+	5.509	0.018117	Up	hsa_circ_0008796	CDKN2B-AS1	One intron	intron:3639110-3641957	1,719
11	chr8:140864311-140925749-	5.4249	0.021704	Up	hsa_circ_0008778	PTK2	Antisense	intron:22049228-22120503; intron:140846678-140890542, intron:140890603-140925561, exon:140890315-140890769, intron:140890769-141001124;	571
12	chr11:46894588-46895291-	5.4161	0.02071	Up		LRP4	Antisense	intron:46894819-46895165, exon:46894588-46894819	577
13	chr15:27326808-27328888+	5.405	0.00012486	Up	hsa_circ_0034186	GABRG3	One exonic	exon:27326807-27327029;	304
14	chr1:45700069-45729769-	5.4019	0.023363	Up		IPP	Antisense	exon:45714245-45714466, intron:45717017-45719202, exon:45727630-45727798, intron:45700190-45714245, intron:45714466-45716894, intron:45719340-45727630, intron:45727798-45729613, exon:45729613-45729769;	2,9318

Table SII. Continued.

ID	circRNA	log ₂ FC	padj	Regulation	circBase ID	Gene name	Catalogue	Feature	Length
15	chr21:31245487-31252189-	5.3133	0.028921	Up		TIAM1	Antisense	exon:31245487-31245660, exon:31251741-31252189, intron:31245660-31251741;	6,702
16	chr2:151841902-151860820-	5.3018	0.028921	Up	hsa_circ_0056731	CTD-2021K4.1	Antisense	intron:151815199-151853447;	544
17	chr21:31164961-31203012-	5.2706	0.033947	Up	hsa_circ_0061405	TIAM1	Antisense	intron:31195305-31210044, exon:31182420-31182645, intron:31182645-31187000, intron:31187087-31195223, intron:31165065-31182420;	603
18	chrX:22090428-22133624+	5.1516	0.049577	Up	hsa_circ_0090071	PHEX	Annot intron	intron:22111560-22114457, intron:22099151-22111466, intron:22094099-22096954, intron:22090497-22093982, intron:22097038-22099005, intron:22114586-22133522;	741
19	chr3:185533570-185535132-	4.6995	0.0027538	Up		LIPH	Antisense	exon:185534764-185535132, intron:185533679-185534764;	1,453
20	chr21:31182420-31203012-	4.3229	4.87E-06	Up	hsa_circ_0061407	TIAM1	Antisense	exon:31182420-31182645, intron:31182645-31187000, intron:31187087-31195223, intron:31195305-31210044;	499
21	chr8:15650696-15673836+	4.1088	0.016397	Up	hsa_circ_0006410	TUSC3	One intron	intron:15659647-15662155;	490
22	chr1:45716894-45729769-	3.8623	0.0027538	Up		IPP	Antisense	exon:45727630-45727798, exon:45729613-45729769, intron:45719340-45727630, intron:45727798-45729613, intron:45717017-45719202;	12,614
23	chr12:40257247-40274993+	3.7022	0.00020619	Up		LRRK2	Annot intron	intron:40259604-40263788, intron:40253016-40259479, intron:40263901-40274582;	17,746
24	chr20:17456347-17465553+	3.4493	0.0076649	Up		PCSK2	Exon intron	intron:17456448-17465325, exon:17463432-17465553;	9,206
25	chr3:64594257-64596991-	3.4414	3.64E-06	Up	hsa_circ_0066444	ADAMTS9	Antisense	exon:64594257-64594434, intron:64594434-64596829;	339

Table SII. Continued.

ID	circRNA	log ₂ FC	padj	Regulation	circBase ID	Gene name	Catalogue	Feature	Length
26	chr12:40310430-40323306+	3.3979	0.0011336	Up	LRRK2	LRRK2	Exon intron	intron:40315300-40319987, intron:40320175-40321033, intron:40314173-40315211, exon:40310430-40310649, intron:40310649-40313971, intron:40322510-40323159, intron:40321188-40322034, exon:40313971-40314173, exon:40322318-40322510, exon:40319987-40320175; exon:50602632-50602813, intron:50596964-50598265, intron:50598535-50602632, intron:50602813-50607380, exon:50607380-50608184, exon:50598265-50598535, exon:50591646-50596964; exon:116699070-116700284; intron:18765538-18799294, exon:18804703-18804898, intron:18801382-18804521; exon:48008633-48009114; intron:31187087-31195223, intron:31182645-31187000, exon:31182420-31182645; exon:3619079-3619239, intron:3639110-3641957, intron:3619239-3639003; intron:40302882-40303947, exon:40303947-40304976; intron:50598535-50602632, exon:50602632-50602813, exon:50607380-50608184, intron:50602813-50607380, exon:50598265-50598535; intron:94181580-94186372, intron:94169293-94181445;	12,201
27	chrX:50595697-50608184-	3.2019	0.0027538	Up	SHROOM4	SHROOM4	Antisense		12,487
28	chr7:116699070-116700284+	3.1895	7.90E-06	Up	hsa_circ_0082002	MET	One exonic		1,214
29	chr8:18765448-18804898-	3.1644	2.06E-10	Up	hsa_circ_0002111	PSD3	Antisense		538
30	chr6:48008633-48009114-	3.1172	0.020919	Up	hsa_circ_0076710	PTCHD4	One exonic		481
31	chr9:21476898-21477292-	3.0822	0.038702	Up	hsa_circ_0008599		Antisense		261
32	chr21:31182420-31195305-	3.0463	0.00020619	Up	hsa_circ_0061406	TIAM1	Antisense		394
33	chr7:3619079-3642105+	2.9826	5.20E-07	Up	SDK1	SDK1	Exon intron		22,771
34	chr12:40302788-40304134+	2.8124	0.00020619	Up	hsa_circ_0025887	LRRK2	Exon intron		281
35	chrX:50598265-50608184-	2.567	0.012143	Up	hsa_circ_0090585	SHROOM4	Antisense		1,255
36	chr12:94169152-94186473+	2.5662	3.64E-06	Up	PLXNC1	PLXNC1	Annot intron		16,944

Table SII. Continued.

ID	circRNA	log ₂ FC	padj	Regulation	circBase ID	Gene name	Catalogue	Feature	Length
37	chr5:93553760-93563463-	2.5079	0.0080171	Up	hsa_circ_0007747	NR2F1-AS1	Antisense	intron:93411509-93563363;	325
38	chr12:32327460-32328555+	2.4464	0.0065615	Up	hsa_circ_0025841	BICD1	One exonic	exon:32327460-32328555;	1,095
39	chr7:22308338-22318037-	2.3679	0.0028451	Up		RAPGEF5	Antisense	intron:22308507-22309968, exon:22308338-22308507, intron:22310090-22315369, intron:22315476-22317986;	9,419
40	chr8:18799294-18804898-	2.2327	5.35E-07	Up	hsa_circ_0004458	PSD3	Antisense	intron:18801382-18804521, exon:18804703-18804898;	448
41	chr4:185247293-185267155+	2.0931	0.023363	Up	hsa_circ_0004874	SNX25	Exon intron	intron:185264498-185266968, intron:185247378-185258847, exon:185266968-185267155, intron:185259064-185264437, exon:185264437-185264610, exon:185258847-185259064;	662
42	chr1:232460886-232471528-	1.961	0.00025433	Up		SIPA1L2	Antisense	exon:232460886-232461161, intron:232461161-232464839, exon:232464839-232465416, exon:232471370-232471528, intron:232465416-232471370;	10,642
43	chr15:94356136-94385525+	1.8906	0.035786	Up		MCTP2	Exon intron	intron:94367791-94370086, exon:94367604-94367791, intron:94358612-94367604, intron:94356301-94358546, exon:94355973-94356301, intron:94370180-94384021, intron:94384124-94385422;	29,186
44	chr8:18867673-18872733-	1.8167	0.0028274	Up		PSD3	Antisense	intron:18868069-18871625, exon:18867673-18868069, exon:18871625-18872733;	5,060
45	chr5:124701013-124701269-	1.4807	0.0014106	Up	hsa_circ_0001523	ZNF608	Antisense	exon:124701013-124701269;	256
46	chr5:38523418-38530666-	-1.3171	0.0006677	Down	hsa_circ_0072309	LIFR	Antisense	intron:38527294-38528725, exon:38530505-38530917, intron:38528840-38530505, exon:38523418-38523582, intron:38523582-38527154;	580

Table SII. Continued.

ID	circRNA	log ₂ FC	padj	Regulation	circBase ID	Gene name	Catalogue	Feature	Length
47	chr8:109412264-109427156+	-2.0603	0.039207	Down		PKHD1L1	Exon intron	intron:109419260-109420517, intron:109412414-109413420, intron:109425232-109427001, exon:109420517-109420690, exon:109419096-109419260, exon:109427001-109427156, intron:109413545-109419096; intron:14079354-14140543, exon:14140543-14144785; intron:110144569-110146752, intron:110146835-110147915, exon:110143541-110144569, intron:110148026-110150181; intron:39190502-39204526, intron:39204617-39213399, exon:39229364-39229588, intron:39187709-39190304, intron:39184647-39187626;	10,075
48	chr16:14079289-14140760+	-5.1466	0.049682	Down	hsa_circ_0037936	MKL2	Exon intron		282
49	chr2:110143541-110150256-	-5.3255	0.033947	Down		NPHP1	Antisense		6,446
50	chr2:39179186-39229588-	-5.3702	0.026155	Down		CDKL4	Antisense		28,604
51	chr6:49709144-49714438+	-5.4001	0.023363	Down		VPS50	Intergenic		5,294
52	chr7:93252652-93323732+	-5.4921	0.01831	Down			Exon intron	intron:93257464-93258158, intron:93294636-93296741, intron:93291835-93294544, intron:93253931-93256508, intron:93308942-93311165, intron:93271262-93272634, intron:93259632-93271219, intron:93303550-93305827, intron:93258392-93259549, intron:93239950-93253859, intron:93311272-93340597, intron:93276305-93291702, intron:93306004-93308823, exon:93305827-93306004, intron:93296836-93297144, intron:93272733-93276164, intron:93297243-93303459, intron:93256562-93257393; intron:20412148-20472828, exon:20470932-20472956;	71,080
53	chr20:20425608-20472956-	-5.593	0.012384	Down		RALGAPA2	Antisense		47,348