

ajcr0000003 Supplementary data

Supplementary Table 1. Primer sequences used for determination of gene expression by real time RT-PCR

	Name	Primer sequence	Amplicon size (bps)
1	mCldn6-F1-85	5'-agacaaagctgaccgagcac-3'	213
	mCldn6-R1-297	5'-gctctgaaccacacaggaca-3'	
2	mCxcl17-F1-135	5'-tggtgcttcagtgatgctc-3'	169
	mCxcl17-R1-303	5'-gctgtggctttctctttgg-3'	
3	mDdr1-F2-856	5'-gggcagaccatgcagtatc-3'	187
	mDdr1-R2-1042	5'-tgctccatcccacatagtca-3'	
4	mEmp2-F1-354	5'-ctctggagagtgtgcaccaa-3'	198
	mEmp2-R1-551	5'-cgtcaggacgaacctctctc-3'	
5	mEsrrb-F1-809	5'-ggcgttctcaagagaacca-3'	225
	mEsrrb-R1-1033	5'-aggttcaggtaggggctgtt-3'	
6	mFgg-F1-1030	5'-tgggacaacgacaacgataa-3'	155
	mFgg-R1-1184	5'-ccgtcgtcgaaccattagt-3'	
7	mGAPDH-R2-674	5'-ggatgcagggatgatgttct-3'	239
	mGAPDH-F2-436	5'-ttgtgatgggtgtgaaccac-3'	
8	mGrhl2-F1-1858	5'-tgccagtggagaaaatcaca-3'	155
	mGrhl2-R1-2010	5'-ctccatcagcgtgatcttga-3'	
9	mGrhl3-F1-1529	5'-acatactgcccagaaac-3'	174
	mGrhl3-R1-1702	5'-aggctcaaactcctcagcaa-3'	
10	mHnf1b-F2-1201	5'-ctcctccaccaacaaga-3'	203
	mHnf1b-R2-1403	5'-ccgacactgtgatctgcatt-3'	
11	mIl11-F1-400	5'-ctgggacattgggatctttg-3'	236
	mIl11-R1-635	5'-ggggatcacaggttggtct-3'	
12	mIL13ra2-F2-548	5'-cgcatttgcagagcattgt-3'	218
	mIL13ra2-R2-765	5'-atccaagccctcataccaga-3'	
13	mLad1-F1-1737	5'-gcgacacctttgagaagg-3'	187
	mLad1-R1-1923	5'-agccctcttggtgactgatg-3'	
14	mMia1-F1-272	5'-tgattgccgcttcttgacta-3'	155
	mMia1-R1-426	5'-ggacaatgctactgggaaa-3'	
15	mMuc4-F2-8879	5'-ctttgcggctcaatacaaca-3'	176
	mMuc4-R2-9054	5'-cattttgggtcagcagaaca-3'	
16	mNr2f2-F1-566	5'-ttcaccgccaactaaag-3'	181
	mNr2f2-R1-746	5'-caggtacgagtgagcagttga-3'	
17	mOlfm4-F2-241	5'-ggacctgcccagtggtctgtt-3'	188
	mOlfm4-R2-428	5'-gaccttactcggaccgtca-3'	
18	mPcbd1-F1-158	5'-aggccgagatgctatcttca-3'	161
	mPcbd1-R1-318	5'-cacattcatgggtgctcaag-3'	
19	mRfx4-F1-1639	5'-gaccgatgcgtttaaagg-3'	180
	mRfx4-R1-1818	5'-gagcacgtagtctgaaca-3'	
20	mSlc39a4-F1-458	5'-gacgattacctggccacact-3'	226
	mSlc39a4-R1-683	5'-cttgaagcaggaccatta-3'	
21	mShh-F1-533	5'-gaagatcacaagaaactccgaacg-3'	170
	mShh-R1-702	5'-cactccaggccactgggtc-3'	

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Supplementary Table 2. Complete list of genes with altered expression (n=150) in thyroid tumors of *Thrb^{PV/PV}*

Gene symbol	Accession no.	Adjusted P value	Fold change	Gene name
Upregulated genes				
Fgg	NM_133862	0.025	10.868	fibrinogen gamma chain
Slc39a4	BC023498	0.034	9.088	solute carrier family 39 (zinc transporter), member 4
Car4	NM_007607	0.025	6.695	carbonic anhydrase 4
Slc5a5	AF380353	0.024	5.979	solute carrier family 5 (sodium iodide symporter), member 5
Shh	AV304616	0	5.804	sonic hedgehog
Got1	AA792094	0.037	5.784	glutamate oxaloacetate transaminase 1, soluble
Fam163a	BB183509	0.005	5.626	family with sequence similarity 163, member A
Olfm4	AV290148	0.025	5.517	olfactomedin 4
Bcat1	X17502	0.035	5.22	branched chain aminotransferase 1, cytosolic
Gm266	BB829749	0.008	5.032	predicted gene 266
Ppp2r3a	AI642021	0.016	4.636	protein phosphatase 2 (formerly 2A), regulatory subunit B", alpha
Sbf1	AV121839	0.035	4.389	SET binding factor 1
Esrrb	AV333667	0.024	4.003	estrogen related receptor, beta
Muc4	AF218265	0.033	3.853	mucin 4
B4galnt2	AI593864	0.017	3.548	beta-1,4-N-acetyl-galactosaminyl transferase 2
8430419L09Rik	NM_028982	0.022	3.541	RIKEN cDNA 8430419L09 gene
Lad1	NM_133664	0.024	3.354	ladinin
Slc22a23	BM234253	0.019	3.278	solute carrier family 22, member 23
Ankrd40	BB213578	0.016	3.229	ankyrin repeat domain 40
Cldn6	BC005718	0.03	3.215	claudin 6
Fxyd4	NM_033648	0.025	3.112	FXD domain-containing ion transport regulator 4
Tmed6	NM_025458	0.013	2.969	transmembrane emp24 protein transport domain containing 6
Kif5c	AI844677	0.039	2.936	kinesin family member 5C
Rbm20	AK003783	0.024	2.906	RNA binding motif protein 20
Kdm6b	BB494168	0.03	2.876	KDM1 lysine (K)-specific demethylase 6B
Pcbd1	NM_025273	0.015	2.864	pterin 4 alpha carbinolamine dehydratase/dimerization cofactor of hepatocyte nuclear factor 1 alpha (TCF1) 1
BC017612	NM_133214	0.045	2.848	cDNA sequence BC017612
AI314604	BE991175	0.016	2.819	expressed sequence AI314604
C4bp	NM_007576	0.01	2.815	complement component 4 binding protein
Dusp14	AK009744	0.034	2.793	dual specificity phosphatase 14
Suc1g2	BF608645	0.017	2.778	succinate-Coenzyme A ligase, GDP-forming, beta subunit
Slmo1	BB835597	0.017	2.766	slowmo homolog 1 (Drosophila)
Mtm1	NM_019926	0.039	2.732	X-linked myotubular myopathy gene 1
B3gnt1	AV032053	0.043	2.654	UDP-GlcNAc:betaGal beta-1,3-N-acetylglucosaminyltransferase 1
Tcea1	BC011290	0.037	2.65	transcription elongation factor A (SII)-like 1
Rsh12a	AA544511	0.037	2.643	radial spokehead-like 2A; radial spoke 3A homolog (Chlamydomonas)
Mapk6	BC024684	0.033	2.588	mitogen-activated protein kinase 6 (Extracellular signal-regulated kinase 3) (ERK-3)
Thy1	AV028402	0.03	2.574	thymus cell antigen 1, theta
Grhl3	AV231424	0.013	2.53	grainyhead-like 3 (Drosophila)
Trpm3	BB125842	0.037	2.53	transient receptor potential cation channel, subfamily M, member 3
Ddr1	BF225985	0.049	2.497	discoidin domain receptor family, member 1
Rcor1	AW543416	0.028	2.493	REST corepressor 1
LOC100045988	BM199323	0.039	2.49	similar to OPR
Socs1	AB000710	0.015	2.474	suppressor of cytokine signaling 1
Lsm2	AF204156	0.025	2.466	LSM2 homolog, U6 small nuclear RNA associated (S. cerevisiae)
Emp2	AF083876	0.032	2.427	epithelial membrane protein 2
Gm941	BB479096	0.032	2.4	predicted gene 941
Dync1i1	NM_010063	0.046	2.351	dynein cytoplasmic 1 intermediate chain 1
Fut9	AU067636	0.013	2.317	fucosyltransferase 9
Rtn4ip1	NM_130892	0.01	2.299	reticulin 4 interacting protein 1
Lamc2	NM_008485	0.018	2.259	laminin, gamma 2
Rfx4	AV255458	0.024	2.253	regulatory factor X, 4 (influences HLA class II expression)
Mt3	NM_013603	0.022	2.208	metallothionein 3

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Atrn	AW558010	0.043	2.181	attractin
Grhl2	AK005410	0.049	2.099	grainyhead-like 2 (Drosophila)
Rnasek	BI156989	0.047	2.094	ribonuclease, RNase K
Psd3	NM_030263	0.027	2.088	pleckstrin and Sec7 domain containing 3
Lonp1	AK004820	0.026	2.083	lon peptidase 1, mitochondrial
Rfx5	BB392192	0.013	2.076	regulatory factor X, 5 (influences HLA class II expression)
A330068G13Rik	BB246530	0.045	2.062	RIKEN cDNA A330068G13 gene
3110043021Rik	AK014175	0.034	2.02	RIKEN cDNA 3110043021 gene
Map6d1	BB762333	0.045	1.951	MAP6 domain containing 1
Hnf1b	AI987804	0.024	1.949	HNF1 homeobox B
Hira	AW537496	0.017	1.94	histone cell cycle regulation defective homolog A (S. cerevisiae)
C030005G22Rik	BB355326	0.024	1.935	RIKEN cDNA C030005G22 gene
Gfra1	BE534815	0.025	1.904	glial cell line derived neurotrophic factor family receptor alpha 1
Ppif	NM_134084	0.043	1.883	peptidylprolyl isomerase F (cyclophilin F)
Arl13b	AV225959	0.017	1.856	ADP-ribosylation factor-like 13B
2210409E12Rik	NM_028218	0.008	1.835	RIKEN cDNA 2210409E12 gene; coilin
Hmga1	NM_016660	0.048	1.826	high mobility group AT-hook 1, related sequence 1
Rrn3	AA866997	0.028	1.815	RRN3 RNA polymerase I transcription factor homolog (yeast)
Idh2	NM_008322	0.032	1.81	isocitrate dehydrogenase 2 (NADP+), mitochondrial
Ccnj	BB051001	0.024	1.764	cyclin J
Med20	NM_020048	0.032	1.759	mediator complex subunit 20
Fastkd3	AK009264	0.043	1.739	FAST kinase domains 3
4930420K17Rik	BB323696	0.024	1.727	RIKEN cDNA 4930420K17 gene
Cyb5b	NM_025558	0.024	1.697	cytochrome b5 type B
BC037704	BM938208	0.045	1.691	cDNA sequence BC037704
Tomm40	AF109918	0.033	1.654	translocase of outer mitochondrial membrane 40 homolog (yeast)
Egln3	BB284358	0.043	1.646	EGL nine homolog 3 (C. elegans)
Flrt1	BQ173985	0.03	1.638	fibronectin leucine rich transmembrane protein 1
Il11	NM_008350	0.028	1.637	interleukin 11
Usp3	BM206593	0.04	1.56	ubiquitin specific peptidase 3
Hspa4l	NM_011020	0.048	1.535	heat shock protein 4 like
Lrrc47	AK013512	0.016	1.523	leucine rich repeat containing 47
Dph2	AK011199	0.024	1.51	DPH2 homolog (S. cerevisiae)
Gbf1	BM948896	0.013	1.506	golgi-specific brefeldin A-resistance factor 1
Downregulated genes				
Krt8	M21836	0.05	0.667	keratin 8
Otud7a	NM_130880	0.043	0.647	OTU domain containing 7A
Rnf130	BE948550	0.037	0.644	ring finger protein 130
BC063263	BM211194	0.048	0.625	cDNA sequence BC063263
Ttc13	BB492914	0.043	0.605	tetratricopeptide repeat domain 13
Sp3	AK004607	0.044	0.602	trans-acting transcription factor 3
C430049A07Rik	AK021261	0.015	0.595	RIKEN cDNA C430049A07 gene
Rpl11	AK014593	0.009	0.594	ribosomal protein L11
2900010M23Rik	AV046927	0.024	0.584	RIKEN cDNA 2900010M23 gene
N6amt2	BF730076	0.049	0.584	N-6 adenine-specific DNA methyltransferase 2 (putative)
Sra1	BG074964	0.028	0.576	steroid receptor RNA activator 1
Gfod1	AV220135	0.028	0.576	glucose-fructose oxidoreductase domain containing 1
Foxn3	BM196962	0.049	0.572	forkhead box N3
Mbd5	BB086698	0.048	0.57	methyl-CpG binding domain protein 5
2810404F17Rik	AK012982	0.048	0.567	RIKEN cDNA 2810404F17 gene
Pnlipr2	AV060116	0.037	0.563	pancreatic lipase-related protein 2
Samd12	AV347618	0.034	0.548	sterile alpha motif domain containing 12
Tacr3	BB498416	0.048	0.543	tachykinin receptor 3
Rpl37a	AV066985	0.048	0.535	ribosomal protein L37a
Il13ra2	BC003723	0.043	0.533	interleukin 13 receptor, alpha 2
Elf2	BC027739	0.048	0.518	E74-like factor 2
Agr2	AV066597	0.007	0.511	anterior gradient 2 (Xenopus laevis)
Thap4	BB130418	0.024	0.505	THAP domain containing 4
BB187676	BB313560	0.01	0.501	expressed sequence BB187676
Rock1	BI662863	0.024	0.5	Rho-associated coiled-coil containing protein kinase 1
Rnf166	BB870298	0.03	0.5	ring finger protein 166
Trove2	BQ176653	0.043	0.499	TROVE domain family, member 2

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Dnm3os	BB542096	0.008	0.491	dynamins 3, opposite strand
Impact	BB524087	0.015	0.481	imprinted and ancient
Oxtr	BB551848	0.044	0.475	oxytocin receptor
Tgs1	BM233196	0.045	0.465	trimethylguanosine synthase homolog (S. cerevisiae)
Usp37	BB398605	0.037	0.461	ubiquitin specific peptidase 37
D1Ert75e	BG066069	0.016	0.459	DNA segment, Chr 1, ERATO Doi 75, expressed
Tbc1d20	BC002196	0.044	0.452	TBC1 domain family, member 20
Rpl37	BF578245	0.027	0.45	ribosomal protein L37
1700029I01Rik	BQ033755	0.037	0.445	RIKEN cDNA 1700029I01 gene
AI481207	AI481207	0.048	0.439	expressed sequence AI481207
Alcam	AV315205	0.047	0.437	activated leukocyte cell adhesion molecule
Fjx1	AV230815	0.017	0.436	four jointed box 1 (Drosophila)
Spnb2	BM213516	0.044	0.435	spectrin beta 2
Sec14l2	BC005759	0.028	0.426	SEC14-like 2 (S. cerevisiae)
Lman1	BG071597	0.044	0.425	lectin, mannose-binding, 1
Zcchc14	BB223737	0.015	0.413	zinc finger, CCHC domain containing 14
Golim4	BM942873	0.014	0.41	golgi integral membrane protein 4
Fstl1	BI452727	0.037	0.404	folliculin-like 1
Olfm1	BB549310	0.025	0.366	olfactomedin 1
Afp	NM_007423	0.045	0.363	alpha fetoprotein
Taok1	BB151477	0.044	0.349	TAO kinase 1
Tmod3	BB224629	0.017	0.347	tropomodulin 3
Cacna2d1	BB559910	0.03	0.347	calcium channel, voltage-dependent, alpha2/delta subunit 1
Cldnd1	AK012260	0.039	0.347	claudin domain containing 1
Pdlim4	NM_019417	0.005	0.335	PDZ and LIM domain 4
Mia1	NM_019394	0.016	0.332	melanoma inhibitory activity 1
Slc12a2	BG069505	0.024	0.331	solute carrier family 12, member 2
Ggps1	NM_010282	0.045	0.306	geranylgeranyl diphosphate synthase 1
Nr2f2	BB053811	0.044	0.301	nuclear receptor subfamily 2, group F, member 2
Rc3h2	BB527789	0.035	0.299	ring finger and CCCH-type zinc finger domains 2
Atxn2	BE953583	0.009	0.286	ataxin 2
Tor1b	BB004887	0.03	0.276	torsin family 1, member B
Zfp871	BB008634	0.008	0.254	zinc finger protein 871
Cxcl17	BC024561	0.015	0.227	chemokine (C-X-C motif) ligand 17
Map3k2	AV381143	0.028	0.192	mitogen-activated protein kinase kinase kinase 2
Prdm6	AV303905	0.031	0.102	PR domain containing 6

Supplementary Table 3. Functional analysis of genes (n=150) with aberrant expression in thyroid tumors of *Thrb^{PV/PV}* mice

	Sub-Category	p-value	Molecules
Cell development and differentiation	Reproductive System	1.36E-04	MUC4, OXTR, IL11, AFP, HIRA, SLC12A2, KRT8, ESRRB, DDR1, SOCS1, SP3, SHH
	Development and Function	4.4E-02	
	Embryonic Development	6.01E-04	ARL13B, IL11, HIRA, HNF1B, MAP3K2, KRT8, ESRRB, HMGA1, GRHL3, SHH
		4.4E-02	
	Digestive System Development and Function	1.42E-03	HNF1B, SLC12A2, GFRA1, SPTBN1, SHH
		3.78E-02	
	Hematological System	2.16E-03	IL11, ROCK1, FGG, MAP3K2, ATRN, DDR1, THY1, SOCS1, HMGA1, SP3, SHH
	Development and Function	4.4E-02	
	Renal and Urological System	6.25E-03	IL11, HNF1B, GFRA1, THY1, SHH

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Disease-related	Development and Function	4.4E-02	
	Nervous System Development and Function	4.61E-03-4.4E-02	OLFM1, ROCK1, RFX4, ATRN, GFRA1, SHH, KIF5C, MT3, IL11, HNF1B, FUT9, ALCAM, RTN4, THY1, NR2F2
	Connective Tissue Development and Function	6.14E-03-4.4E-02	MIA, IL11, ROCK1, KRT8, RTN4, THY1, SHH
	Endocrine System Development and Function	6.41E-03-4.4E-02	AFP, KRT8, SLC5A5, SOCS1, HMGA1, SHH
	Cardiovascular System Development and Function	6.41E-03-3.78E-02	HNF1B, DDR1, RTN4, IL13RA2, THY1, NR2F2, SHH
	Gastrointestinal Disease	2.56E-04-2.54E-02	RFX4, TACR3, ESRRB, IL13RA2, SOCS1, LAMC2, GFRA1, TRPM3, SAMD12, SP3, SHH, GFOD1, USP3, IL11, GOT1, SUCLG2, HIRA, DYNC1I1, KRT8, ALCAM, FOXN3
	Genetic Disorder	1.77E-03-4.4E-02	PSD3, TTC13, ATRN, TRPM3, RRN3, SP3, SLC39A4, SHH, USP3, FSTL1, MT3, SUCLG2, HIRA, ALCAM, FOXN3, RTN4, RFX5, SLC22A23, MATR3, LMAN1, MBD5, RNF130, TACR3, PDLIM4, GFRA1, GOT1, DYNC1I1, FUT9, THY1, B3GNT1, GBF1, DDR1, SAMD12, CA4, PCBD1, ATXN2, HNF1B, FGG, CYB5B, GRHL2, OLFM1, RFX4, SLC12A2, TAOK1, ZRANB1, ESRRB, MTM1, SLC5A5, IL13RA2, SOCS1, LAMC2, GFOD1, TOMM40, KRT8, HMGA1, SPTBN1
	Renal and Urological Disease	1.77E-03-1.91E-02	HNF1B, DDR1, SOCS1
	Endocrine System Disorders	3.04E-03-3.16E-02	PSD3, TTC13, GBF1, DDR1, TRPM3, SAMD12, USP3, CA4, HNF1B, ATXN2, LSM2, GRHL2, ALCAM, FOXN3, TROVE2, RFX4, OTUD7A, PDLIM4, SLC5A5, LAMC2, SOCS1, DYNC1I1, FUT9, THY1, SPTBN1
	Auditory Disease	5.57E-03-1.91E-02	SLC12A2, GRHL2, ESRRB
Cell structure and mobility	Inflammatory Disease	3.65E-03-4.4E-02	PSD3, DDR1, RCOR1, SAMD12, TRPM3, SP3, RRN3, SHH, USP3, CA4, HIRA, SUCLG2, FGG, LSM2, CYB5B, ALCAM, FOXN3, PNLIPRP2, GRHL3, RFX4, ZRANB1, ESRRB, IL13RA2, SOCS1, GFRA1, LAMC2, GOT1, DYNC1I1, GOLIM4
	Cell-To-Cell Signaling and Interaction	1.11E-03-4.4E-02	MUC4, ROCK1, ATRN, DDR1, B4GALNT2, SOCS1, GFRA1, LAMC2, SHH, OXTR, IL11, FGG, KRT8, MAP3K2, ALCAM, THY1
	Tissue Morphology	6.01E-04-4.4E-02	MIA, SLC12A2, ESRRB, DDR1, GFRA1, SOCS1, SHH, KIF5C, IL11, HIRA, HNF1B, KRT8, THY1
	Cell Morphology	1.42E-03-4.4E-02	MIA, TMOD3, ROCK1, GBF1, TAOK1, KRT8, ATRN, RTN4, SOCS1, SHH
	Cellular Movement	4.61E-03-	CXCL17, MIA, ROCK1, DDR1, LAMC2, SOCS1, GFRA1, SHH, FSTL1, KIF5C, IL11, TMOD3,

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Immune response		4.2E-02	MAP3K2, ALCAM, RTN4, THY1, NR2F2
	Cellular Assembly and Organization	6.41E-03-4.4E-02	MIA, ROCK1, TAOK1, MAP6D1, LAMC2, SOCS1, RRN3, SHH, HNF1B, FGG, KRT8, RTN4, RPL11, SPTBN1
	Tumor Morphology	1.28E-02-2.54E-02	GFRA1, HMGA1, SHH
	Infection Mechanism	1.11E-03-1.28E-02	IL11, HMGA1
	Cell-mediated Immune Response	2.16E-03-3.16E-02	MAP3K2, SOCS1, HMGA1, SHH
	Hypersensitivity Response	6.41E-03-4.4E-02	IL11, SOCS1
	Inflammatory Response	6.41E-03-3.23E-02	IL11, KRT8, ATRN, DDR1, ALCAM, SOCS1
	Antimicrobial Response	1.28E-02-2.54E-02	MT3, SOCS1
	Immune Cell Trafficking	1.28E-02-2.52E-02	IL11, ROCK1, FGG, MAP3K2, THY1
	Cell growth or death	Cellular Growth and Proliferation	2.16E-03-4.4E-02
Cell Death		2.74E-03-4.4E-02	PPIF, ROCK1, DDR1, RRN3, SP3, SHH, MT3, FSTL1, IL11, AFP, ATXN2, ALCAM, RTN4, MIA, RPL37, SLC12A2, PDLIM4, SLC5A5, GFRA1, SOCS1, SRA1, KRT8, MAP3K2, EMP2, THY1, HMGA1
Cell Cycle		6.41E-03-3.16E-02	GFRA1, SOCS1, HMGA1, SHH
DNA Replication, Recombination, and Repair		6.41E-03-6.41E-03	HIRA, HMGA1
Metabolism-related	Amino Acid Metabolism	1.24E-02-4.03E-02	GOT1, IL11, SBF1, ROCK1, FUT9, MAPK6, TAOK1, MAP3K2, DDR1, B4GALNT2
	Carbohydrate Metabolism	1.28E-02-4.4E-02	MTM1, B4GALNT2, SOCS1
	Lipid Metabolism	1.28E-02-3.78E-02	HNF1B, MTM1, SEC14L2, PNLIPRP2
	Vitamin and	1.28E-02	SEC14L2

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	Mineral Metabolism	02- 1.28E- 02	
	Nucleic Acid Metabolism	3.16E- 02- 3.16E- 02	B4GALNT2