

Supplementary Table 1A: Overview of cloned zebrafish and fugu rtms

Gene	Transcripts	Exons	Identification	size of identified 5'UTR (bp)	position of upstream stop codon (bp)	Kozak Consensus (gccAccATGG)	ORF (bp)	size of identified 3'UTR (bp)	position of polyA signal (bp)	protein (aa)	pI value of N terminus	ER retention (KRKAE)
(DANRE)rtn1	rtn1-a1	I(a), II, III, IV-IX	5'race, library screen ¹	168	-93 to -91	tccAaaATGT	2304	1055	3341-3346	767	4.6	KRKAE
	rtn1-a2	I(a), IV-IX	RT-PCR			tccAaaATGT	789			263	4.3	KRKAE
	rtn1-c	I(c), IV-IX	5'race, library screen ¹	138	-120 to -118	cctAgtATGC	639	1055	1678-1681	212	6.2	KRKAE
(DANRE)rtn2	rtn2-c	I(c), II-VII	RT-PCR	65	-42 to -40	tccAaaATGA	612	41		203	9.0	KPKAH
(DANRE)rtn3	rtn3-a1	I(a), III-VIII	RT-PCR, ESTs	156	-114 to -112	caaAaaATGG	666	473	1123-1128, 1168-1173	221	5.3	RCKAE
	rtn3-a2	I(a), II, III-VIII	RT-PCR			caaAaaATGG	711			236	4.3	RCKAE
(DANRE)rtn4	rtn4-l	I(l), II-VII	5'race, ESTs, library screen ¹	206	-33 to -31	gcaAcaATGG	969	970	1771-1776, 1796-1801, 1909-1914, 1920-1925	322	4.4	KPKTE
	rtn4-l(-63/188)	I(l)Δ-63/188, II-VII	RT-PCR, ESTs, library screen ¹			tccAcaATGC	765			254	4.7	KPKTE
	rtn4-l(-10/195)	I(l)Δ-10/195, II-VII	RT-PCR			tccAcaATGC	765			254	4.7	KPKTE
	rtn4-m	I(m), II-VII	5'race	89	-6 to -4	tgaCcgATGC	639			212	6.3	KPKTE
	rtn4-n	I(n), II-VII	ESTs, library screen ¹	48	-18 to -16	agcGagATGG	582	970	1514-1519	193	6.0	KPKTE
(DANRE)rtn5	rtn5-a1	I(a), II, III, IV-IX	5'race, library screen ¹	118	-51 to -53	gcaAgcATGT	2457	132		818	4.4	AKKKE
	rtn5-a2	I(a), IV-IX	RT-PCR			gcaAgcATGT	750			249	4.3	AKKKE
	rtn5-a1(265/1584)	I(a), IIΔ, IIIΔ, IV-IX	RT-PCR			gcaAgcATGT	1137			378	4.9	AKKKE
	rtn5-a1(297/2025)	I(a), IIIΔ, IVΔ-IX	RT-PCR			gcaAgcATGT	462			153	4.1	truncated
	rtn5-a1(309/2025)	I(a), IIIΔ, IVΔ-IX	RT-PCR			gcaAgcATGT	474			157	4.1	truncated
	rtn5-a1(558/1048)	I(a), IIΔ, III, IV-IX	RT-PCR			gcaAgcATGT	678			225	4.2	truncated
	rtn5-c	I(c), IV-IX	library screen ¹	175	-75 to -73	acaGacATGG	612	132		203	9.0	AKKKE
(DANRE)rtn6	rtn6-a1	I(a), II, III, IV-IX	ESTs, library screen ¹	284	-102 to -100	ctcCcgATGG	2628	321	2927-2932	875	3.9	KKKSD
	rtn6-a2	I(a), II, IV-IX	RT-PCR			ctcCcgATGG	1569			522	3.8	KKKSD
	rtn6-a3	I(a), III, IV-IX	ESTs			ctcCcgATGG	2583			860	3.8	KKKSD
	rtn6-a1(337/555)	I(a)Δ, II, III, IV-IX	EST			ctcCcgATGG	2409			802	3.9	KKKSD
	rtn6-a1(1576/1860)	I(a), II, IIIΔ, IV-IX	RT-PCR			ctcCcgATGG	2343			780	3.8	KKKSD
	rtn6-a1(1761/2150)	I(a), II, IIIΔ, IVΔ-IX	RT-PCR			ctcCcgATGG	2238			745	3.9	KKKSD
	rtn6-a1(1773/2152)	I(a), II, IIIΔ, IVΔ-IX	RT-PCR			ctcCcgATGG	1926			641	3.9	truncated
	rtn6-a1(1774/2212)	I(a), II, IIIΔ, IVΔ-IX	RT-PCR			ctcCcgATGG	1968			655	3.9	truncated
	rtn6-a1(1775/2140)	I(a), II, IIIΔ, IVΔ-IX	RT-PCR			ctcCcgATGG	2262			753	3.9	KKKSD
	rtn6-a1(1775/2152)	I(a), II, IIIΔ, IVΔ-IX	RT-PCR			ctcCcgATGG	2250			749	3.9	KKKSD
	rtn6-a1(1775/2344)	I(a), II, IIIΔ, VΔ-IX	RT-PCR			ctcCcgATGG	2058			685	3.9	KKKSD
	rtn6-a1(1777/1956)	I(a), II, IIIΔ, IV-IX	RT-PCR			ctcCcgATGG	2448			815	3.9	KKKSD
(DANRE)rtn8	rtn8-a1(2023/2173)	I(a), II, IIIΔ, IVΔ-IX	RT-PCR			ctcCcgATGG	2043			680	3.9	truncated
(DANRE)rtn8	rtn8-c	I(c), II-VII	5'race, RT-PCR, EST	53	-36 to -34	gcaGaaATGG	627	213		208	9.0	KQKTK

Gene	Transcripts	Exons	Identification	size of identified 5'UTR (bp)	position of upstream stop codon (bp)	Kozak Consensus (gccAccATGG)	ORF (bp)	size of identified 3'UTR (bp)	position of polyA signal (bp)	protein (aa)	pI value of N terminus	ER retention (KRKAE)
(FUGRU)rtn1	rtn1-a1	I(a), II, III, IV-IX	RT-PCR	16	-6 to -4	tagAccATGT	2190	32		729	4.3	KRKEE
(FUGRU)rtn2	rtn2-c	I(c), II-VII	genomic, 3'race			actAaaaATGG	612	277		203	9.0	KPKNQ
(FUGRU)rtn3	rtn3-a1	I(c), II-VII	RT-PCR	72	-15 to +13	aatAcaaATGG	663	18		220	5.5	SNKTE
(FUGRU)rtn4	rtn4-l1	I(l), IV-IX	RT-PCR, ESTs	210	-73 to -75	acgAaaaATGG	1029	28		342	4.0	KRKTE
	rtn4-l2	I(l), II, IV-IX	RT-PCR			acgAaaaATGG	1068			355	4.1	KRKTE
	rtn4-l3	I(l), III, IV-IX	RT-PCR			acgAaaaATGG	1083			360	4.0	KRKTE
	rtn4-n	I(n), IV-IX	RT-PCR, ESTs	17		ttcAagATGG	682	44		193	9.0	KRKTE
(FUGRU)rtn7		IIa, IIb, III-VII	genomic									KVKAE
(FUGRU)rtn8	rtn8-c	I(c), II-VII	RT-PCR, ESTs	76	-43 to -45	gctGaaATGG	645	32		214	9.0	KAKAK

¹Library screening was performed at the RZPD (Deutsches Ressourcenzentrum für Genomforschung GmbH, Heidelberg Germany) and for the different zebrafish rtn genes, the following clones were identified:

- rtn1: embryo library:
brain library:

ICRFp524P16147Q8
UCDMp61IH0866Q2, UCDMp61IK0437Q2, UCDMp61IL1236Q2, UCDMp61IC245Q2, UCDMp61IE0247Q2, UCDMp61IH01100Q2, UCDMp61ID2082Q2, UCDMp61IL0217Q2, UCDMp61IM1391Q2, UCDMp61IB10104Q2, UCDMp61IM2385Q2, UCDMp61IF1912Q2, UCDMp61IBF2122Q2, UCDMp61IM1173Q2
- rtn4: embryo library:

ICRFp524H2158Q8, ICRFp524N0372Q8, ICRFp524M15145Q8, ICRFp524E1950Q8, ICRFp524J2089Q8, ICRFp524M03107Q8, ICRFp524N1146Q8, ICRFp524O2163Q1, ICRFp524G20163Q8, ICRFp524N15110Q8, ICRFp524O0124Q8, ICRFp524K10135Q8
- retina library:

UWS_p760C0818Q2, UWS_p760F0665Q2, UWS_p760G2345Q2, UWS_p760N0712Q2
- rtn5: retina library:

UWS_p760O115Q2
- rtn6: embryo library:

ICRFp524L08126Q8, ICRFp524L08126Q8, ICRFp524A0107Q8
- brain library:

UCDMp61IB22132Q2

Supplementary Table 1B: Primer used for RT-PCR and RDH mapping

(DANRE)rtn1		
No	Sequence	Project
1	GTC TAA ATA AAC TGG AAG TTG CTG AGA C	RDH mapping sense primer
2	CAT GGG ACA GTG ACA TCT CCA CAT CC	RDH mapping antisense primer
3	GAA AAG ATG TCC ACC ATG	RT-PCR sense primer (-a1 splice form)
4	ATA AGA GCT CCA ACA TAG G	RT-PCR antisense primer (-a1 splice form)
5	ATG CAG GCC AGC ACC ATG	RT-PCR sense primer (-c splice form)
2	CAT GGG ACA GTG ACA TCT CCA CAT CC	RT-PCR antisense primer (-c splice form)

(DANRE)rtn2		
No	Sequence	Project
6	GGG TTT CAG AGA TCA GG	RDH mapping sense primer
7	ACT GCT ATG TGG GAC TTC	RDH mapping antisense primer
8	CGG TCC ATG AAG ACT C	RT-PCR sense primer (c splice form)
9	GAG TGA CAG CGC ATG G	RT-PCR antisense primer (c splice form)

(DANRE)rtn3		
No	Sequence	Project
10	GCT CTT CAG TGT ACC GCC CAT CTA TG	RDH mapping sense primer
11	GCC ATT GAG ACA CCG CGG ACA CC	RDH mapping antisense primer
12	ATG GCA GAC CCA ATG ACC	RT-PCR sense primer (-a1 and -a2 splice forms)
13	GGA TCA TTC TGC TTT ACA GC	RT-PCR antisense primer (-a1 and -a2 splice forms)

(DANRE)rtn4		
No	Sequence	Project
14	ATG GAT GAT CAA ATA AGC TC	RDH mapping sense primer
15	GTT ACA TTT ATA TGG CGC TAC TGT TGG C	RDH mapping antisense primer
14	ATG GAT GAT CAA ATA AGC TC	RT-PCR sense primer (-l splice form)
16	CCT GAC TGG ATA TAT GAC C	RT-PCR sense primer (-m splice form)
17	ATG AGC GAG ATG GAT TCC	RT-PCR sense primer (-n splice form)
18	GAA ATG AAT CCA AAT GGC C	RT-PCR antisense primer (-l, -m and -n splice forms)

(DANRE)rtn5		
No	Sequence	Project
19	GTT TGG CAG TGT GCT GCT GCT C	RDH mapping sense primer
20	GGA ATC GTG ACT ATT CCA GTT TCG CGC	RDH mapping antisense primer
21	TGA GGA TGA AGA TGA CAT CC	RT-PCR sense primer (-a1 splice form)
22	GGT TAA AGA GAA GAG CAG C	RT-PCR antisense primer (-a1 splice form)
23	GGC TGA TCT GTC CTT GC	RT-PCR sense primer (-a1/b splice form)
24	ATG GAT AAA GGG AAG AAA GAG	RT-PCR sense primer (-c splice form)
25	GAA GTG AAG AGT TTA TTC CTT C	RT-PCR antisense primer (-a1/b and -c splice forms)

(DANRE)rtn6		
No	Sequence	Project
26	TGC TGC AGC TGC TGT ACT GGC G	RDH mapping sense primer
27	GCA TGG CCT GTA GCA CCG CCG TG	RDH mapping antisense primer
28	AAA AGC AGG TGC AGC AG	RT-PCR sense primer (-a1/a3 splice form)
29	ACT GCC AAC TTC AGC GAG	RT-PCR antisense primer (-a1/a3 splice form)

(DANRE)rtn8		
No	Sequence	Project
30	GGA TCT GAT ATA CTG GCG	RDH mapping sense primer
31	TTC CTG TTG TTA CAG TTA CC	RDH mapping antisense primer
30	GGA TCT GAT ATA CTG GCG	RT-PCR sense primer (RHD)
32	GTG AGC TCC ACA TTT CTC	RT-PCR antisense primer (RHD)

Actin		
No	Sequence	Project
33	GCT CAC CAT GGA TGA TGA TAT CGC	RT-PCR sense primer
34	GGA GGA GCA ATG ATC TTG ATC TTC	RT-PCR antisense primer

Supplementary Table 1C: RT-PCR conditions

(DANRE)rtn1					
Primer sense	Primer antisense	Annealing Temp.	Elongation Time	Number of Cycles	Ampified Splice Form
3	4	51 °C	35 sec	35	(DANRE)rtn1-a1
5	2	59 °C	30 sec	35	(DANRE)rtn1-c

(DANRE)rtn2					
Primer sense	Primer antisense	Annealing Temp.	Elongation Time	Number of Cycles	Ampified Splice Form
8	9	54 °C	45 sec	35	(DANRE)rtn2-c

(DANRE)rtn3					
Primer sense	Primer antisense	Annealing Temp.	Elongation Time	Number of Cycles	Ampified Splice Form
12	13	58 °C	45 sec	35	(DANRE)rtn3-a1 and -a2

(DANRE)rtn4					
Primer sense	Primer antisense	Annealing Temp.	Elongation Time	Number of Cycles	Ampified Splice Form
14	18	56 °C	90 sec	35	(DANRE)rtn4-l
16	18	60 °C	40 sec	35	(DANRE)rtn4-m
17	18	59 °C	70 sec	35	(DANRE)rtn4-n

(DANRE)rtn5					
Primer sense	Primer antisense	Annealing Temp.	Elongation Time	Number of Cycles	Ampified Splice Form
21	22	58 °C	120 sec	35	(DANRE)rtn5-a1
23	25	60 °C	50 sec	35	(DANRE)rtn5-a1/b
24	25	55 °C	45 sec	35	(DANRE)rtn5-c

(DANRE)rtn6					
Primer sense	Primer antisense	Annealing Temp.	Elongation Time	Number of Cycles	Ampified Splice Form
28	29	63 °C	60 sec	35	(DANRE)rtn6-a1

(DANRE)rtn8					
Primer sense	Primer antisense	Annealing Temp.	Elongation Time	Number of Cycles	Ampified Splice Form
30	32	59 °C	20 sec	35	(DANRE)rtn8-RHD

Actin					
Primer sense	Primer antisense	Annealing Temp.	Elongation Time	Number of Cycles	Ampified Splice Form
33	34	50 °C	90 sec	25	(DANRE)Actin

Supplementary Table 1D: GeneBank accession numbers of vertebrate rtn genes

Chordate RTN subfamily						
Urochordate RTN						
Species	Gene	Transcript	GenBank Accession for newly identified RTN Genes	GenBank Accession for previously identified RTN Genes ^a	Published	
Ciona intestinalis	(CIOIN)RTN			BK001680 (AY164660)	24	
				BK001675 (AY164756)	24	
				BK001674 (AY164755)	24	
				BK001678 (AY164757)	24	
				BK001677 (AY164760)	24	
				BK001676 (AY164759)	24	
				BK001679 (AY164758)	24	
Vertebrate RTN						
Species	Gene	Transcript	GenBank Accession for newly identified RTN Genes	GenBank Accession for previously identified RTN Genes	Published	
Homo sapiens	(HUMAN)RTN1			NT_025892, AY164662	1, 2, 24	
				L10333, NM_021136.1	3	
				L10334	3	
	(HUMAN)RTN1-C			L10335, BC003003	3	
		(HUMAN)RTN2			NT_011109, AY164661	4
					BK001687 AF004222, (AY164714)	4, 24
				BK001690 (AY164717)	24	
				BK001688 (AY164715)	4, 24	
				BK001691 (AY164718)	24	
				BK001686 AF004224, (AY164713)	4, 24	
				BK001689 (AY164716)	24	
	(HUMAN)RTN3			NT_033241; NT_009984 (m)	5	
				BK001681 NM_006054, AF059524, (AY164701)	5, 24	
				BK001684 (AY164704)	24	
	(HUMAN)RTN3-A3 (e)			BK001683 (AY164703)	24	
				BK001682 (AY164702)	24	
				BK001685 (AY164705)	24	
		(HUMAN)RTN3-Δ8 (e)			BK001696	
					NT_016606	5
					AY102285	6, 7, 8
		(HUMAN)RTN4			AY102279 , AB020693, AB040462, AF148537	6, 7, 9, 10
				AY123245	6	
				AY123246	6	
				AY102277 , AB015639, AF132047, AF148538	6, 9, 10	
				AY102278	6	
				AY102276 , AF077050, AF087901	6, 9, 10, 11	
				AY123247	6	
				AY123248 , AF333336	6, 12	
				AY123249	6	
				AY123250	6	
	Pan troglodytes	(PANTR)RTN1				
			(PANTR)RTN1w	BK003953		24
		(PANTR)RTN3				
			(PANTR)RTN3-A1	BK003954		24
	(PANTR)RTN4					
		(PANTR)RTN4-C	BK001700		24	
	Ateles belzebuth chamek	(ATEBE)RTN1			BK001692 AF029167, (AY164729)	24
			(ATEBE)RTN1-Aw			
	Macaca mulatta	(MACMU)RTN1				
			(MACMU)RTN1-Cw	BK001697		24
(MACMU)RTN3						
		(MACMU)RTN3w	BK003957		24	
(MACMU)RTN4						
(MACMU)RTN4-Cw (Part1)			BK003948	24		
	(MACMU)RTN4-Cw (Part2)			BK003949	24	
Macaca fascicularis	(MACFA)RTN4					
		(MACFA)RTN4-Aw			13	
		(MACFA)RTN4-C		BK001695 AB049853, (AY164742)	24	
Mus musculus	(MOUSE)Rtn1			NW_000053		
				BK001694 AB074899, BC030455, (AY164731)	24	
				BK001698	24	
				BK001693 , AK002997, AK014358, XM_127007, (AY164730)	24	
	(MOUSE)Rtn1-d			BK001699	24	
					14, 15	
		(MOUSE)Rtn2-b			BK001789 NM_013648, (AY164711)	14, 24
					BK001790 NM_013648, (AY164712)	14, 24
	(MOUSE)Rtn3			NW_000139	16	
				NM_053076, AY164700	24	
				BK001796 (AY164699)	24	
				BK003955	24	
	(MOUSE)Rtn4			AY102286 , NW_000035	6	
				AY102284	6	
				AY102281	6	
				AY102282	6	
			AY102283 , NM_024226	6		
			AY102280	6		
Rattus norvegicus	(RAT)Rtn1					
				NM_053865.1, U17604, AY164728	17, 18, 24	
				U17603, X52817, AY164727	17, 18, 19, 24	
	(RAT)Rtn2			BK001788 (AY164710)	24	
		(RAT)Rtn2-B				
	(RAT)Rtn3			AY164698	24	
		(RAT)Rtn3-a1				
	(RAT)Rtn4			AJ242961	20	
				AJ242962, AF132046, AY164740	20, 24	
				AF132045, AY164741	24	
				AJ242963, AF051335	11, 20	
Bos taurus	(BOVIN)RTN1					
				AY164734	24	
				BK003967	24	
				BK003968	24	
	(BOVIN)RTN2					
				BK001798	24	
	(BOVIN)RTN2-C			BK001791 (AY164719)	24	
		(BOVIN)RTN3			BK001797 (AY164707)	24
(BOVIN)RTN4						
	(BOVIN)RTN4-C			AY164744	21, 24	
Sus scrofa	(PIG)RTN1					
				BK001792 (AY164726)	24	
(PIG)RTN2						
			BK001798 (AY164709)	24		

	(PIG)RTN3	(PIG)RTN2-C		BK001787 (AY164708)	24
		(PIG)RTN3-A1	BK003952		24
	(PIG)RTN4				
		(PIG)RTN4-Aw		AY164739	24
		(PIG)RTN4-Aw (Part1)		BK003964	24
		(PIG)RTN4-Aw (Part2)		BK003965	24
		(PIG)RTN4-Aw (Part3)		BK003966	24
		(PIG)RTN4-C		BK001795 (AY164739)	24
Canis familiaris	(CANFA)RTN1				
		(CANFA)RTN1-Aw		BK001794 (AY164733)	24
		(CANFA)RTN1-C		BK001793 (AY164732)	24
	(CANFA)RTN3				
		(CANFA)RTN3w		AY164706	24
		(CANFA)RTN3w (Part1)		BK003961	24
		(CANFA)RTN3w (Part2)		BK003962	24
		(CANFA)RTN3w (Part3)		BK003963	24
	(CANFA)RTN4				
		(CANFA)RTN4-Cw		AY164743	24
		(CANFA)RTN4-Cw (Part1)		BK003959	24
		(CANFA)RTN4-Cw (Part2)		BK003960	24
Capra hircus	(CAPHI)RTN3				
		(CAPHI)RTN3w (Part1)	BK003950		24
		(CAPHI)RTN3w (Part2)	BK003951		24
Ovis aries	(SHEEP)RTN3				
		(SHEEP)RTN3-A1w	BK003956		24
	(SHEEP)RTN4				
		(SHEEP)RTN4w	BK003958		24
Gallus gallus	(CHICK)RTN1				
		(CHICK)RTN1-A	AY164724	U17606, AY164724	18, 24
		(CHICK)RTN1-C	AY164723	U17605, AY164723	18, 24
	(CHICK)RTN3				
		(CHICK)RTN3w	BK044006	(AY164697)	24
	(CHICK)RTN4				
		(CHICK)RTN4-Aw			22
		(CHICK)RTN4-B1	BK004061		24
		(CHICK)RTN4-B2	BK004062		24
		(CHICK)RTN4-C	AY164737	AY164737	22, 24
Columba livia	(COLLI)RTN1				
		(COLLI)RTN1w		BK004009 (AY164725)	24
Xenopus laevis	(XENLA)RTN1.1				
		(XENLA)RTN1.1-C		BK004007 (AY164721)	24
	(XENLA)RTN1.2				
		(XENLA)RTN1.2-C	BK004058		24
	(XENLA)RTN2				
		(XENLA)RTN2-A	BK004978		24
		(XENLA)RTN2-C	BK004977		24
	(XENLA)RTN3.1				
		(XENLA)RTN3.1		BK004012 (AY164749)	24
	(XENLA)RTN3.2				
		(XENLA)RTN3.2	BK004057		24
	(XENLA)RTN4-1				
		(XENLA)RTN4.1-A1		AY316197	23
		(XENLA)RTN4.1-A2		AY316196	23
		(XENLA)RTN4.1-A3		AY316195	23
		(XENLA)RTN4.1-B1		AY316194	23
		(XENLA)RTN4.1-B2		AY316193	23
		(XENLA)RTN4.1-C		AY316192	23
		(XENLA)RTN4.1-N		AY316191	23
	(XENLA)RTN4-2				
		(XENLA)RTN4.2-A1		AY316190	23
		(XENLA)RTN4.2-A2		AY316189	23
		(XENLA)RTN4.2-A3		AY316188	23
		(XENLA)RTN4.2-B1		AY316187	23
		(XENLA)RTN4.2-B2		AY316186	23
		(XENLA)RTN4.2-B3		AY316185	23
		(XENLA)RTN4.2-C		AY316184	23
		(XENLA)RTN4.2-N		AY316183	23
Silurana tropicalis	(XENTR)RTN1				
		(XENTR)RTN1-Aw		BK004008 (AY164722)	24
	(XENTR)RTN2				
		(XENTR)RTN2-A	BK005003		24
		(XENTR)RTN2-C	BK005002		24
	(XENTR)RTN3				
		(XENTR)RTN3		BK004013 (AY164750)	24
	(XENTR)RTN4				
		(XENTR)RTN4-A1w (Part1)	BK004063		24
		(XENTR)RTN4-A1w (Part2)	BK004064		24
		(XENTR)RTN4-B1		BK004011 (AY164736)	24
		(XENTR)RTN4-B2	BK004059		24
		(XENTR)RTN4-C	BK004060		24
		(XENTR)RTN4-N		BK004010 (AY164735)	24
Carassius auratus	(CARAU)RTN3				
		(CARAU)RTN3w		AY164748	24
	(CARAU)RTN4				
		(CARAU)RTN4-M		AY164754	22, 24
Danio rerio	(DANRE)rtn1				
		(DANRE)rtn1-a1	AY555034		
		(DANRE)rtn1-a2	AY555035		
		(DANRE)rtn1-c	AY555036	BC052753	25
	(DANRE)rtn2				
		(DANRE)rtn2-c	AY576807		
	(DANRE)rtn3				
		(DANRE)rtn3-a1	AY555037	BC049315, BC062828	
		(DANRE)rtn3-a2	AY555038		
	(DANRE)rtn4				
		(DANRE)rtn4-j	AY555039		
		(DANRE)rtn4-l(-10/195)	AY555040		
		(DANRE)rtn4-l(-63/188)	AY555041		
		(DANRE)rtn4-m	AY555042		
		(DANRE)rtn4-n	AY555043		
	(DANRE)rtn5				
		(DANRE)rtn5-a1	AY555044		
		(DANRE)rtn5-a2	AY555049		
		(DANRE)rtn5-a1(265-1584)	AY555046		
		(DANRE)rtn5-a1(297-2025)	AY555045		
		(DANRE)rtn5-a1(309-2025)	AY555047		
		(DANRE)rtn5-a1(558-1048)	AY555048		
		(DANRE)rtn5-c	AY555050	BC059623	25
	(DANRE)rtn6				
		(DANRE)rtn6-a1	AY555051		
		(DANRE)rtn6-a2	AY555062		
		(DANRE)rtn6-a3	AY555063		

		(DANRE)rtm6-a1(337/555)	AY555052		
		(DANRE)rtm6-a1(1576/1860)	AY555053		
		(DANRE)rtm6-a1(1761/2150)	AY555054		
		(DANRE)rtm6-a1(1773/2152)	AY555055		
		(DANRE)rtm6-a1(1774/2212)	AY555056		
		(DANRE)rtm6-a1(1775/2140)	AY555057		
		(DANRE)rtm6-a1(1775/2152)	AY555058		
		(DANRE)rtm6-a1(1775/2344)	AY555059		
		(DANRE)rtm6-a1(1777/1956)	AY555060		
		(DANRE)rtm6-a1(2023/2173)	AY555061		
	(DANRE)rtm8				
		(DANRE)rtm8-c	AY555064		
Takifugu rubripes	(FUGRU)RTN1			CAAB01001184	
		(FUGRU)rtm1-a1	AY555026		
	(FUGRU)RTN2				
		(FUGRU)rtm2c	AY555027		
	(FUGRU)RTN3			CAAB01002936	
		(FUGRU)rtm3-a1	AY555028	BK005087 (AY164745)	24
	(FUGRU)RTN4			CAAB01004137	
		(FUGRU)rtm4-i1	AY555029		
		(FUGRU)rtm4-i2	AY555030		
		(FUGRU)rtm4-i3	AY555031		
		(FUGRU)rtm4-n	AY555032	BK005090 (AY164753)	24
	(FUGRU)RTN7				
		(FUGRU)rtm7w	BK005143		
	(FUGRU)RTN8				
		(FUGRU)rtm8c	AY555033		
Ictalurus punctatus	(ICTPU)RTN1				
		(ICTPU)RTN1-C		BK005086 (AY164720)	24
	(ICTPU)RTN2				
		(ICTPU)RTN2w	BK004979		24
	(ICTPU)RTN5				
		(ICTPU)RTN5-Aw		BK005089 (AY164752)	24
		(ICTPU)RTN5-Bw		BK005102 (AY164751)	24
Paralichthys olivaceus	(PAROL)RTN3				
		(PAROL)RTN3	BK005088	(AY164746)	24
Oncorhynchus mykiss	(ONCMY)RTN1				
		(ONCMY)RTN1-C		BK005100 (AY262105)	24
	(ONCMY)RTN2*1				
		(ONCMY)RTN2*1	BK004983		24
	(ONCMY)RTN2*2				
		(ONCMY)RTN2*2	BK004982		24
	(ONCMY)RTN3				
		(ONCMY)RTN3-A1		BK004987 (AY262104)	24
		(ONCMY)RTN3-A2		BK005101 (AY262103)	24
	(ONCMY)RTN4				
		(ONCMY)RTN4-L	BK004986		24
		(ONCMY)RTN4-Mw		BK005093 AY262101	24
		(ONCMY)RTN4-N	BK004985		24
	(ONCMY)RTN7				
		(ONCMY)RTN7		BK005092 (AY262100)	24
	(ONCMY)RTN8				
		(ONCMY)RTN8w	BK004981		24
	(ONCMY)RTN9				
		(ONCMY)RTN9-A1	BK005094		24
		(ONCMY)RTN9-A2		BK005095 (AY262102)	24
	(ONCMY)RTN10				
		(ONCMY)RTN10-N	BK004984		24
	(ONCMY)RTN11				
		(ONCMY)RTN11	BK004980		24
Oncorhynchus tshawytsch	(ONCTS)RTN1				
		(ONCTS)RTN1w	BK004991		24
Salmo salar	(SALSA)RTN1				
		(SALSA)RTN1w (part1)	BK004997		24
		(SALSA)RTN1w (part2)	BK004996		24
	(SALSA)RTN3				
		(SALSA)RTN3w	BK004995		24
	(SALSA)RTN4				
		(SALSA)RTN4-M	BK004993		24
	(SALSA)RTN7				
		(SALSA)RTN7w	BK004994		24
	(SALSA)RTN10				
		(SALSA)RTN10W	BK004992		24
Coregonus clupeaformis	(CORCL)RTN1				
		(CORCL)RTN1w	BK005001		24
Cyprinus carpio	(CYPCA)RTN1				
		(CYPCA)RTN1-C		BK005091 (AY262099)	24
	(CYPCA)RTN3				
		(CYPCA)RTN3w	BK004976		24
	(CYPCA)RTN4				
		(CYPCA)RTN4-N		BK005098 (AY262098)	24
	(CYPCA)RTN5				
		(CYPCA)RTN5w	BK004975		24
	(CYPCA)RTN6				
		(CYPCA)RTN6		BK005097 (AY262097)	24
Gasterosteus aculeatus	(GASAC)RTN1				
		(GASAC)RTN1w	BK004990		24
	(GASAC)RTN3				
		(GASAC)RTN3-A1	BK004989		24
		(GASAC)RTN3-A2	BK004988		24
Oryzias latipes	(ORYLA)RTN1				
		(ORYLA)RTN1-C		BK005096 (AY262096)	24
	(ORYLA)RTN2				
		(ORYLA)RTN2	BK005000		24
	(ORYLA)RTN3				
		(ORYLA)RTN3w		BK005099 (AY164747)	24
	(ORYLA)RTN4				
		(ORYLA)RTN4w (part1)	BK004999		24
		(ORYLA)RTN4w (part2)	BK004998		24

(1) Roebroek et al., 1996
(2) Kools et al., 1994
(3) Roebroek et al., 1993
(4) Roebroek et al., 1998
(5) Moreira et al., 1999
(6) Oertle et al., 2003

(7) Yang et al., 2000
(8) Nagase et al., 1998
(9) GrandPré et al., 2000
(10) Prinjha et al., 2000
(11) Morris et al., 1999
(12) Zhang et al., 2002

(13) Barske et al., unpublished
(14) Geisler et al., 1992
(15) Stubbs et al., 1996
(16) Hamada et al., 2002
(17) Baka et al., 1996
(18) Ninkina et al., 1997

(19) Wiczorek and Hughes, 1992
(20) Chen et al., 2000
(21) Spillmann et al., 1998
(22) Simonen, M.; Lecoq, E.; Leiteritz, D., unpublished
(23) Klinger et al., 2004
(24) Oertle et al., 2003
(25) Strausberg et al., direct submission

^a older accession numbers (in brackets) have been replaced by new third party annoation numbers (blue, bold)

Supplementary Table 1E: Rates of nonsynonymous substitutions per nonsynonymous site (d_N) and rates of synonymous substitutions per synonymous site (d_S) calculated for the RHD

	(DANRE)rtn1 versus (DANRE)rtn5	(DANRE)rtn1 versus (HUMAN)RTN1	(DANRE)rtn5 versus (HUMAN)RTN1
mean $d_N \pm SE$	13.39 \pm 1.66	11.94 \pm 1.58	14.14 \pm 1.70
mean $d_S \pm SE$	57.55 \pm 4.18	68.48 \pm 3.91	71.18 \pm 3.81
d_N/d_S	0.23	0.17	0.20

	(DANRE)rtn2 versus (DANRE)rtn8	(DANRE)rtn2 versus (HUMAN)RTN2	(DANRE)rtn8 versus (HUMAN)RTN2
mean $d_N \pm SE$	39.10 \pm 2.31	37.49 \pm 2.31	45.17 \pm 2.36
mean $d_S \pm SE$	63.82 \pm 3.90	69.23 \pm 3.67	68.99 \pm 3.68
d_N/d_S	0.61	0.54	0.65

	(DANRE)rtn4 versus (DANRE)rtn6	(DANRE)rtn4 versus (HUMAN)RTN4	(DANRE)rtn6 versus (HUMAN)RTN4
mean $d_N \pm SE$	27.81 \pm 2.19	18.21 \pm 1.87	32.79 \pm 2.29
mean $d_S \pm SE$	57.29 \pm 4.09	70.66 \pm 3.85	69.40 \pm 3.83
d_N/d_S	0.49	0.26	0.47

	(FUGRU)RTN2 versus (FUGRU)RTN8	(FUGRU)RTN2 versus (HUMAN)RTN2	(FUGRU)RTN8 versus (HUMAN)RTN2
mean $d_N \pm SE$	39.45 \pm 2.32	38.81 \pm 2.35	41.76 \pm 2.35
mean $d_S \pm SE$	65.68 \pm 3.82	62.25 \pm 3.91	67.16 \pm 3.69
d_N/d_S	0.60	0.62	0.62

	(FUGRU)RTN3 versus (FUGRU)RTN7	(FUGRU)RTN3 versus (HUMAN)RTN3	(FUGRU)RTN7 versus (HUMAN)RTN3
mean $d_N \pm SE$	29.80 \pm 2.20	22.58 \pm 2.02	32.75 \pm 2.27
mean $d_S \pm SE$	76.20 \pm 3.59	71.31 \pm 3.83	68.69 \pm 3.92
d_N/d_S	0.39	0.31	0.48

Supplementary Table 1F: Mapping data for the analysis of conserved syntenies between rtn1 in zebrafish and RTN1 in human

Accession 5'EST Accession 3'EST ¹	Zebrafish LN54 LG	Zebrafish LN54 Marker Symbol	Human Chromosome	Human Position	Human Accession	Description
AW127896	20	tf04e05	6	6q15 / ???	BAA91551	C6orf166 chromosome 6 open reading frame 166
AW115873	20				no significant resul	
AI437041	20	fb37b08	14	14q24.3 / 78,190 K	NP_036377	SNW1 SKI-interacting protein
AI415949	20		14		NP_036377	SNW1 SKI-interacting protein
NM_131081	20	cdh2	18	18q11.2 / 25,530 K	AAB22854	CDH2 cadherin 2, type 1, N-cadherin (neuronal)
AI626515	20	fc11b08	8	8p23.1 / ???	NP_689779	TDH L-threonine dehydrogenase
AI601430	20				no significant resul	
AW174194	20	tf40c10	14	14q / 103,700 K	NP_001510	BRF1 BRF1 homolog, subunit of RNA polymerase III transcription initiation factor IIIB (S. cerevisiae)
AW171259	20				no significant resul	
NM_180966	20	esr2a	14	14q / 62,740 K	AAD32580	ESR2 estrogen receptor 2 (ER beta)
	20	rtn1 ²	14	14q21-q22 / 58,180 K		RTN1 reticulon 1
AI584923	20	fb93a10	15	15q14 / 38,826 K	NP_077016	MGC4504 hypothetical protein MGC4504
AI584393	20				no significant resul	
AI584766	20	fb83b05*	14	14q23.3-31 / 75,920 K	NP_036243	AHSA1 AHA1, activator of heat shock 90kDa protein ATPase homolog 1 (yeast)
AI584258	20				no significant resul	
BF718073	20	fd56a12	15	15q13 / 25,930 K	NP_004658	HERC2 hect domain and RLD 2
AW019715	20				no significant resul	
AI959375	20	fd08q07	14	14q32.13 / 91,760 K	BAA96049	FLJ10648 function unknown protein 1
AI957952	20				no significant resul	
AI830333	20	fd14e12	14	14q31-q32 / 92,410 K	NP_057234	ASB2 ankyrin repeat and SOCS box-containing 2
AI687222	20	fb08c11	6	6q24.1 / ???	CAB66619	C6orf55 chromosome 6 open reading frame 55
AI397003	20				no significant resul	
AI384710	20				no significant resul	
AI626529	20	fc11c10	1	1q23.1 / 156,529 K	NP_060293	FLJ20442 hypothetical protein FLJ20442
AI601442	20				no significant resul	
AI437173	20	fb38e12	15	15q15.1 / 38,585 K	NP_002866	RAD51 RAD51 homolog (RecA homolog, E. coli) (S. cerevisiae)
AI444341	20				no significant resul	
AI584886	20	fb92f04	6	6q14.1 / ???	XP_029179	FILIP1 filamin A interacting protein 1
AI584886	20				no significant resul	
AI396883	20	fb14g10	2	2p23 / 26,450 K	NP_000174	HADHB hydroxyacyl-Coenzyme A dehydrogenase/3-ketoacyl-Coenzyme A thiolase/enoyl-Coenzyme A hydratase (trifunctional protein), beta subunit
AI384463	20				no significant resul	
AF072456	20	bmp2b*	20	20p12 / 6,702 K	NP_001191	BMP2 bone morphogenetic protein 2
AI588714	20	fb98e10	14	14q24.3 / 73,610 K	NP_006818	TMP21 transmembrane trafficking protein
AI588267	20				no significant resul	
BE201200	20	fk87c02	14	14q24.3 / 73,900 K	NP_569736	JDP2 jun dimerization protein 2
BE200559	20		14		NP_569736	JDP2 jun dimerization protein 2

Accession 5'EST Accession 3'EST ¹	Zebrafish T51 LG	Zebrafish T51 Marker Symbol	Human Chromosome	Human Position	Human Accession	Description
AW077677	20	tf36b10	14	14q31.1 / 79,650 K	NP_056943	GTF2A1 general transcription factor IIA, 1,19/37kDa
AW077677	20		14	14q31.1 / 79,650 K	NP_056943	GTF2A1 general transcription factor IIA, 1,19/37kDa
NM_131459	20	pdgfra*	4	4q11-q13 / 54,980 K	NP_006197	PDGFRA platelet-derived growth factor receptor, alpha polypeptide
AI722747	20	fc31a09	4	4q12 / 56,127 K	NP_060945	TPARL TPA regulated locus
AI721687	20				no significant resul	
AI964923	20	fc83b10	14	14q23.1 / 57,730 K	NP_055807	DAAM1 dishevelled associated activator of morphogenesis 1
AI943021	20				no significant resul	
AI584766	20	fb83b05*	14	14q23.3-31 / 75,920 K	NP_036243	AHSA1 AHA1, activator of heat shock 90kDa protein ATPase homolog 1 (yeast)
AI584258	20				no significant resul	
AI58934	20	fb78b08	14	14q32.33 / 103,453 K	NP_060425	CDC4A cell division cycle associated 4
AI58282	20				no significant resul	
AW305563	20				no significant resul	
AW281997	20	tf60e07	14	14q24.3-q31 / 79,960 K	NP_005056	SEL1L sel-1 suppressor of lin-12-like (C. elegans)
AW184521	20	tf15d08	14	14q31 / 91,480 K	AAH03622	ITPK1 inositol 1,3,4-triphosphate 5/6 kinase
AW232178	20				no significant resul	
AI545336	20	fb74a06	14	14q32.13 / 91,675 K	NP_786924	C14orf130 chromosome 14 open reading frame 130
AI545120	20				no significant resul	
AW174563	20	tfj05f09	14	14q32 / 91,385 K	P10645	CHGA chromogranin A (parathyroid secretory protein 1)
AW203029	20				no significant resul	
NM_131337	20	sox11b*	2	2p25 / 5,842 K	NM_003108	SOX11 SRY (sex determining region Y)-box 11
NM_131370	20	acat2*	6	6q25.3-q26 / 160,025 K	AAH00408	ACAT2 acetyl-Coenzyme A acetyltransferase 2 (acetoacetyl Coenzyme A thiolase)
AI584923	20	fb93a10	15	15q14 / 38,826 K	NP_077016	MGC4504 hypothetical protein MGC4504
AI584393	20				no significant resul	
AI585238	20	fb95h11	14	14q23 / 63,540K	AAH25685	MAX MAX protein
AI584586	20				no significant resul	
AI722866	20	fc32f10	2	2p25.2 / 9,590K	AAH11654	CPSF3 cleavage and polyadenylation specific factor 3, 73kDa
AI722326	20				no significant resul	
AI931020	20	fc76b10	15	15q13.2 / 32,050K	NP_078989	FLJ22557 hypothetical protein FLJ22557
AI884253	20				no significant resul	
AW077569	20	tfj35h03	2	2p24 / 8,920K	T43458	KIDINS220 likely homolog of rat kinase D-interacting substance of 220 kDa
AW077331	20				no significant resul	
NM_173245	20	vps18	15	15q14-q15 / 38,770K	NP_536672	VPS18 vacuolar protein sorting protein 18
NM_131450	20	rm2	2	2p25-p24 / 10,283K	NP_001025	RRM2 ribonucleotide reductase M2 polypeptide
NM_131228	20	elr	14	14q24.1 / 67,846K	NP_004441	ERH enhancer of rudimentary homolog (Drosophila)
AI477869	20	fb57a02	2	2p24.1 / 16,089K	CAA68678	MYCN v-myc myelocytomatosis viral related oncogene, neuroblastoma derived (avian)
AI477486	20				no significant resul	
BM736060	20	TSubC_2E1	6	6q24.3 / ???	NP_056093	SASH1 SAM and SH3 domain containing 1
BM736061	20		6	6q24.3 / ???	NP_056093	SASH1 SAM and SH3 domain containing 1
	20	wz11823	2	2p24-p23 / 21,200K	CAA28420	APOB apolipoprotein B (including Aq(x) antigen)
AI497503	20	fb60h05	4	4q28 / 155,966K	P02679	FGG fibrinogen, gamma polypeptide
AI522694	20				no significant resul	
AI877943	20	fc55e01	8	8q22-q23 / 108,910K	NP_001559.1	EIF3S6 eukaryotic translation initiation factor 3, subunit 6 48kDa
AI793875	20				no significant resul	
not available						
AW077587	20	tf65a12	6	6q21 / 108,840K	NP_001446	FOXO3A forkhead box O3A
AW077358	20	fb34b10	2	2p23.1 / 26,690K	AAG12992	OTOF otoferlin
AW077137	20				no significant resul	
	20	wz12780	1	1q23.3 / 166,540K	AAN23123	PACE-1 ezrin-binding partner PACE-1
AI794465	20	fc44g01	1	1q23.3 / 166,490K	NP_060656	FLJ10706 hypothetical protein FLJ10706
AI883270	20				no significant resul	
AF506208	20	mcm3	6	6p12 / 52,140K	NP_002379	MCM3 MCM3 minichromosome maintenance deficient 3 (S. cerevisiae)

¹ only one accession number for cloned gene

² RTN1 radiation hybrid PCR result: 000000100000000001010001000010100000210000000100100000000000100000020000100012000001001 LOD score = 13.4

* Woods et. al., 2000

Supplementary Table 1G: Mapping data for the analysis of conserved syntenies between *rtn2* in zebrafish and RTN2 in human

Accession 5'EST Accession 3'EST ¹	Zebrafish LN54 LG	Zebrafish LN54 Marker Symbol	Human Chromosome	Human Position	Human Accession	Description
BE016623	15	fb66c02	3	3q25.32 / 159,708K	AAF82807	LXN latexin protein
BE016156	15		3	3q25.32 / 159,708K	AAF82807	LXN latexin protein
AW827061	15	fb57h10	3	3q22.1 / 134,853 K	AAH63001	SRPRB signal recognition particle receptor, B subunit
AW826781	15		3		AAH63001	SRPRB signal recognition particle receptor, B subunit
NM_131670	15	atp1b3b (fb13c07)	3	3q22-q23 / 142,940 K	NP_001670	ATP1B3 ATPase, Na ⁺ /K ⁺ transporting, beta 3 polypeptide
AI496976	15	fb53f10	19	19q13.2 / 44,025K	BAB18649	HNRPL heterogeneous nuclear ribonucleoprotein L
AI497448	15		19		no significant result	
AI477906	15	fb57d05	19	19q13 / 44,072 K	NP_036369	SIRT2 sirtuin (silent mating type information regulation 2 homolog) 2 (S. cerevisiae)
AI477520	15		19		no significant result	
AI522601	15	fb60b03	19	19q13.3 / 52,943 K	AAH07248	GLTSCR2 glioma tumor suppressor candidate region gene 2
AI497098	15		19	19q13.3 / 52,943 K	AAH07248	GLTSCR2 glioma tumor suppressor candidate region gene 2
		rtn 2 ²	19	19q13.32 / 50,686 K		RTN2 reticulin 2
AI331148	15	fb05d08	17	17q23.2 / 60,300K	CAB66646	VMP1 likely ortholog of rat vacuole membrane protein 1
AI330892	15				no significant result	

Accession 5'EST Accession 3'EST ¹	Zebrafish T51 LG	Zebrafish T51 Marker Symbol	Human Chromosome	Human Position	Human Accession	Description
AI585206	15	fb95e09	17	17q23.2 / 57,800 K	NP_872375	FLJ37451 hypothetical protein FLJ37451
AI584556	15				no significant result	
AI545363	15	fb74d01	7	7q11.22 / 65,990 K	AAH15591	FLJ10900 hypothetical protein FLJ10900
AI545141	15				no significant result	
AW280776	15	fj45g03	17	17p13.3 / 659 K	NP_057164	CGI-150 CGI-150 protein
AW279847	15		17	17p13.3 / 659 K	NP_057164	CGI-150 CGI-150 protein
	15	tcf2	17	17cen-q21.3 / 36,270 K	NP_000449	TCF2 transcription factor 2, hepatic; LF-B3; variant hepatic nuclear factor
AW281708	15	fj53g11	17	17q11.2 / 27,103 K	XP_371036	KIAA0100 KIAA0100 gene product
AW281348	15				no significant result	
AI522601	15	fb60b03	19	19q13.3 / 52,943 K	AAH07248	GLTSCR2 glioma tumor suppressor candidate region gene 2
AI497098	15		19	19q13.3 / 52,943 K	AAH07248	GLTSCR2 glioma tumor suppressor candidate region gene 2
AI477906	15	fb57d05	19	19q13 / 44,072 K	NP_036369	SIRT2 sirtuin (silent mating type information regulation 2 homolog) 2 (S. cerevisiae)
AI477520	15				no significant result	
AI331661	15	fa99f01	19	19q13.3-q13.4 / 55,090	AAH64378	IL4I1 interleukin 4 induced 1
AI331619	15				no significant result	
AI444403	15	fb38a08	19	19q13.41 / 57,403 K	NP_055040	PPP2R1A protein phosphatase 2 (formerly 2A), regulatory subunit A (PR 65), alpha isoform
AI437123	15				no significant result	
AI546048	15	fb77e08	17	17p13.3 / 2,810 K	AAH63786	KIAA0664 KIAA0664 protein
AI544670	15				no significant result	
AW133613	15	fi09d09	17	17p13.3 / 2,570 K	AAH50603	MGC3329 hypothetical protein MGC3329
AW116121	15		17	17p13.3 / 2,570 K	AAH50603	MGC3329 hypothetical protein MGC3329
AI546041	15	fb77d11	17	17p13.3 / 500 K	AAK27973	FLJ10979 hypothetical protein FLJ10979
AI544668	15				no significant result	

¹ only one accession number for cloned genes

² RTN2 radiation hybrid PCR result: 1010010000000000000000212020001000000000100000011000000000000101100001020010001010010021011

LOD score = 13.4

Supplementary Table 1H: Mapping data for the analysis of conserved syntenies between rtn3 in zebrafish and RTN3 human

Accession 5'EST Accession 3'EST ¹	Zebrafish LN54 LG	Zebrafish LN54 Marker Symbol	Human Chromosome	Human Position	Human Accession	Description
AI496942	7	fb53c07	11	11q13.1 / 66,078 K	AAH00401	SF3B2 splicing factor 3b, subunit 2, 145kDa
AI497263	7		11	11q13.1 / 66,078 K	AAH00401	SF3B2 splicing factor 3b, subunit 2, 145kDa
AI558347	7	fb72a06	2	2p13.2-p13.3 / ???	NP_653183	TEX261 testis expressed gene 261
AI544537	7				no significant result	
AI722947	7	fc27g06	5	5q35.3 / ???	AAF67007	RNF130 ring finger protein 130
AI722468	7				no significant result	
AI657668	7	fc16a03	15	15q26.3 / 99,407 K	AAK15708	LOC55829 AD-015 protein
AI641466	7				no significant result	
AA497354	7	fa04g07	16	16p11.2 / 31,113 K	NP_005872	BCKDK branched chain alpha-ketoacid dehydrogenase kinase
AA497274	7				no significant result	
AI959182	7	fd07h02	15	15q21-q22 / 62,848 K	NP_057714	ACP33 acid cluster protein 33
AI957903	7				no significant result	
AI397205	7	fb06g09 ²	11	11q13 / 61,964 K	NP_002023	FTH1 ferritin, heavy polypeptide 1
AI385072	7				NP_002023	FTH1 ferritin, heavy polypeptide 1
AF212919	7	men1**	11	11q13 / 64,825 K	NP_570711	MEN1 multiple endocrine neoplasia I
AW174010	7	fl38c09	11	11p13 / 31,700 K	NP_061913	ELP4 elongation protein 4 homolog (S. cerevisiae)
AW171173	7				no significant result	
AI882683	7	fb15b04	11	11p15.1 / 20,434 K	NP_006401	HTATIP2 HIV-1 Tat interactive protein 2, 30kDa
AI396618	7		11	11p15.1 / 20,434 K	NP_006401	HTATIP2 HIV-1 Tat interactive protein 2, 30kDa
	7	rtm3 ³	11	11q13 / 63,740 K		RTN3 reticulin 3
AI657572	7	fc15c04	11	11p15.1 / 20,219 K	XP_061930	similar to Homeobox protein DBX1
AI641452	7		11	11p15.1 / 20,219 K	XP_061930	similar to Homeobox protein DBX1
AI722072	7	fd19a03	4	4p16.3 / 2,200 K	NP_078787	MGC4701 hypothetical protein MGC4701
AI722486	7		4	4p16.3 / 2,200 K	NP_078787	MGC4701 hypothetical protein MGC4701
AI332008	7	fa96d04	11	11q13.1 / 64,295 K	NP_004313	BAD BCL2-antagonist of cell death
AI330583	7				no significant result	
AI584984	7	fb93g04	X	Xq28 / 147,770 K	AAL86617	CD99L2 CD99 antigen-like 2
AI584442	7				no significant result	
AI657704	7	fc16d12	17	17p13.2 / ???	AAH32510	MGC49942 hypothetical protein MGC49942
AI641499	7		17	17p13.2 / ???	AAH32510	MGC49942 hypothetical protein MGC49942
AI721901	7	fc26h10	2	2p13.2 / 72,234 K	NP_063938	P450RAI-2 cytochrome P450 retinoid metabolizing protein
AI722415	7				no significant result	
AI657750	7	fc17a06 ⁴	13	13q32 / 95,225 K	AAH33823	DNAJC3 DnaJ (Hsp40) homolog, subfamily C, member
AI641576	7				no significant result	
AW165381	7	fe01c06	11	11q12.3 / 62,637 K	NP_036332	B3GAT3 beta-1,3-glucuronyltransferase 3 (glucuronosyltransferase I)
AW165387	7				no significant result	
AW174821	7	fe06a10	14	14q11.2 / 21,536 K	AAD56725	ACINUS apoptotic chromatin condensation inducer in the nucleus
AW165225	7				no significant result	
AI626294	7	fc12g04	1	1p36.13-q31.3 / 147,014 K	AAH08732	APH-1A likely ortholog of C. elegans anterior pharynx defective 1A
AI601857	7				no significant result	
AW128556	7	fe17d05	16	16q22.1 / 70,020 K	NP_478126	MTR3 homolog of yeast mRNA transport regulator 3
AW117040	7		16	16q22.1 / 70,020 K	NP_478126	MTR3 homolog of yeast mRNA transport regulator 3
BF717593	7	fd47d02	11	11p15.3 / 9,016 K	NP_065695	C11orf15 chromosome 11 open reading frame 15
AW018955	7				no significant result	
no sequence available						
AI878766	7	fc66c05	11	11p15.2 / 14,530 K	AI878766	COPB coatomer protein complex, subunit beta
AI626516	7	fc11b09	11	11p15 / 8,860 K	CAC35387	ST5 suppression of tumorigenicity 5
AI601431	7		11	11p15 / 8,860 K	CAC35387	ST5 suppression of tumorigenicity 5

Accession 5'EST Accession 3'EST ¹	Zebrafish T51 LG	Zebrafish T51 Marker Symbol	Human Chromosome	Human Position	Human Accession	Description
AW175082	7	fb32a10	1	1q42.13 / ???	NP_775106	TGS TUDOR gene similar
AW154742	7		1	1q42.13 / ???	NP_775106	TGS TUDOR gene similar
	7	wz12563	4	4q32.3 / 171,510 K	BAA31601	KIAA0626 KIAA0626 gene product
AI558347	7	fb72a06	2	2p13.2-p13.3 / ???	NP_653183	TEX261 testis expressed gene 261
AI544537	7				no significant result	
NM_131585	7	fth1 ⁺⁻²	11	11q13 / 61,984 K	NM_002032	FTH1 ferritin, heavy polypeptide 1
AW233285	7	fj30e04	11	11q12.3 / 61,456 K	NP_060311	FLJ20487 hypothetical protein FLJ20487
AW232790					no significant result	
AI584932	7	fb93b07	15	15q22.2-q22.3 / 63,038	NP_006651	CLPX ClpX caseinolytic protease X homolog (E. coli)
AI584400	7				no significant result	
AI882683	7	fb15b04	11	11p15.1 / 20,434 K	NP_006401	HTATIP2 HIV-1 Tat interactive protein 2, 30kDa
AI396618	7		11	11p15.1 / 20,434 K	NP_006401	HTATIP2 HIV-1 Tat interactive protein 2, 30kDa
AF212919	7	men1 ^{**}	11	11q13 / 64,825 K	NP_570711	MEN1 multiple endocrine neoplasia I
AI722815	7	fc32a02	17	17p11.2 / 17,110 K	NP_003644	COP3 COP9 constitutive photomorphogenic homolog subunit 3 (Arabidopsis)
AI722283	7				no significant result	
AW154045	7	fi29g02	11	11q12-q13.1 / 62,612 K	NP_004730	MTA1L1 metastasis-associated 1-like 1
AW154581	7				no significant result	
AI942769	7	fc75e01	17	17p11-p13 / 7,068 K	NP_000009	ACADVL acyl-Coenzyme A dehydrogenase, very long chain
AI884210	7				no significant result	
NM_131630	7	prkri ⁻⁴	13	13q32 / 95,220 K	NP_006251	DNAJC3 DnaJ (Hsp40) homolog, subfamily C, member
AI878151	7	fc58a11	12	12q14.3 / 69,704 K	NP_006422	CCT2 chaperonin containing TCP1, subunit 2 (beta)
AI878428	7		12	12q14.3 / 69,704 K	NP_006422	CCT2 chaperonin containing TCP1, subunit 2 (beta)
AW305645	7	fj61g07	7	7q22 / 99,902 K	NP_005828	RPP20 POP7 (processing of precursor, S. cerevisiae) homolog
AW282070	7		7	7q22 / 99,902 K	NP_005828	RPP20 POP7 (processing of precursor, S. cerevisiae) homolog
AW419738		fj82g07	14	14q11.1 / 19,963 K	AAB71850	METTL3 methyltransferase like 3
AW420537			14	14q11.1 / 19,963 K	AAB71850	METTL3 methyltransferase like 3
AI626516	7	fc11b09	11	11p15 / 8,860 K	CAC35387	ST5 suppression of tumorigenicity 5
AI601431	7		11	11p15 / 8,860 K	CAC35387	ST5 suppression of tumorigenicity 5

¹ only one accession number for cloned genes ² fb06g09 (LN54) and fth1 (T51) represent the same gene

[illegible]

⁴fc17a06 (LN54) and prkri (T51) represent the same gene.

** Yoder et. Litman, 2000

Supplementary Table 1I: Mapping data for the analysis of conserved syntenies between rtn4 in zebrafish and RTN4 human

Accession 5'EST Accession 3'EST ¹	Zebrafish LN54 LG	Zebrafish LN54 Marker Symbol	Human Chromosome	Human Position	Human Accession	Description
not available						
BE017380	6	fk75d08	22	22q13.1 / 33,990 K	Q9UGU5	HMG2L1 high-mobility group protein 2-like 1
AW174737	6	fe02h09	20	20q11.21 / 32,969 K	NP_009169	PXMP4 peroxisomal membrane protein 4, 24kDa
AW165160	6		20	20q11.21 / 32,969 K	NP_009169	PXMP4 peroxisomal membrane protein 4, 24kDa
AI384762	6	fb17a02*	2	2p13-p14 / 55,190 K	NP_008939	RTN4 reticulon 4
AI397219	6				no significant result	
AI588654	6	fb97g10	14	14q11.1 / 19,540 K	BAB84883	FLJ10357 hypothetical protein FLJ10357
AI588215	6				no significant result	
AW019441	6	fe11e12	2	2q31.1 / 172,890 K	BAA09486	TLK1 tousled-like kinase 1
AW059314	6				no significant result	
AI883574	6	fc66d05	13	13q22.1 / 78,860 K	BAB55125	C13orf10 chromosome 13 open reading frame 10
AI878772	6				no significant result	
	6	rtn4 ²	2	2p13-p14 / 55,190 K		RTN4 reticulon 4
AI416175	6	fb19b11	12	12q13 / 56,220 K	NP_006182	PA2G4 proliferation-associated 2G4, 38kDa
AI522470	6				no significant result	
BF717955	6	fd54d02	12	12q13.11 / 49,034 K	NP_057678	FKBP11 FK506 binding protein 11, 19 kDa
AW019545	6				no significant result	
NM_131286	6	sox21*	13	13q31-q32 / 94,210 K	NP_009015	SOX21 SRY (sex determining region Y)-box 21
AI416205	6	fb19f01	19	19p13.2-p13.3 / 11,533K	P13686	ACP5 acid phosphatase 5, tartrate resistant
AI522481	6		19	19p13.2-p13.3 / 11,533K	P13686	ACP5 acid phosphatase 5, tartrate resistant
AW133793	6	fi11h08	19	19p13.1 / 15,385 K	BAB55234	WIZ widely-interspaced zinc finger motifs
AW128209	6				no significant result	
AI437237	6	fb39c08	2	2q32-q33 / 192,668 K	NP_004648	SDPR serum deprivation response (phosphatidylserine binding protein)
AI444529	6				no significant result	
AA494577	6				no significant result	
AA494670	6	fa10c06	2	2q33.3 / 204,100 K	AAG09681	CYP20A1 cytochrome P450, family 20, subfamily A, polypeptide 1
AI883564	6	fc66b09	2	2q31.1 / 174,990 K	NP_037473	PTD004 hypothetical protein PTD004
AI878763	6				NP_037473	
AW174122	6	fi39e04	2	2q33.2 / 203,650 K	NP_612477	LOC130026 hypothetical protein BC000993
AW171348	6				no significant result	
BF717616	6	fd47f07	13	13q33-q34 / 98,210 K	NP_005064	SLC15A1 solute carrier family 15 (oligopeptide transporter), member 1
AW018970	6				no significant result	
AI416096	6	fb33h05	2	2q33-q34 / 206,970 K	AAH22368	NDUFS1 NADH dehydrogenase (ubiquinone) Fe-S protein 1, 75kDa (NADH-coenzyme Q reductase)
AI437455	6		2		AAH22368	NDUFS1 NADH dehydrogenase (ubiquinone) Fe-S protein 1, 75kDa (NADH-coenzyme Q reductase)
AI722248	6	fd20h08	2	2q12 / 106,070 K	O43639	NCK2 NCK adaptor protein 2
AI721455	6				no significant result	

Accession 5'EST Accession 3'EST ¹	Zebrafish T 51 LG	Zebrafish T 51 Marker Symbol	Human Chromosome	Human Position	Human Accession	Description
AW595289	6	fk30b04	22	22q13.1 / 38,160 K	AAH16855	ATF4 activating transcription factor 4 (tax-responsive enhancer element B67)
AW566985	6		22	22q13.1 / 38,160 K	AAH16855	ATF4 activating transcription factor 4 (tax-responsive enhancer element B67)
AI558981	6	fb78g05	4	4q35.1 / 185,190 K	AAH22185	FLJ12716 hypothetical protein FLJ12716
AI558325	6		4	4q35.1 / 185,190 K	AAH22185	FLJ12716 hypothetical protein FLJ12716
AW174737	6	fe02h09	20	20q11.21 / 32,969 K	NP_009169	PXMP4 peroxisomal membrane protein 4, 24kDa
AW165160	6		20	20q11.21 / 32,969 K	NP_009169	PXMP4 peroxisomal membrane protein 4, 24kDa
AI384191	6	fb17f11*	2	2q31.1 / 170,626 K	I37989	SSB Sjogren syndrome antigen B (autoantigen La)
AI397239	6				no significant result	
AW171070	6	fi37a09	2	2q31.1 / 170,430 K	NP_004783	PPIG peptidyl-prolyl isomerase G (cyclophilin G)
AW173843	6				no significant result	
AW019441	6	fe11e12	2	2q31.1 / 172,890 K	BAA09486	TLK1 tousled-like kinase 1
AW059314	6				no significant result	
AW202751	6	fi21g01	2	2q33 / 202,240 K	NP_055864	ALS2CR3 amyotrophic lateral sclerosis 2 (juvenile) chromosome region, candidate 3
AW232545	6		2	2q33 / 202,240 K	NP_055864	ALS2CR3 amyotrophic lateral sclerosis 2 (juvenile) chromosome region, candidate 3
AW567512	6	fk28d02	2	2q31.1 / 172,540 K	NP_001369	DNCI2 dynein, cytoplasmic, intermediate polypeptide 2
AW595038	6				no significant result	
AW153485	6	fi22c04	22	22q13.1 / 35,000 K	NP_002464	MYH9 myosin, heavy polypeptide 9, non-muscle
AW154082	6		22	22q13.1 / 35,000 K	NP_002464	MYH9 myosin, heavy polypeptide 9, non-muscle
NM_131286	6	sox21*	13	13q31-q32 / 94,210 K	NP_009015	SOX21 SRY (sex determining region Y)-box 21
AI497023	6	fb59c03	2	2p14-p16 / 55,438 K	NP_002444	MTIF2 mitochondrial translational initiation factor 2
AI522554	6		2	2p14-p16 / 55,438 K	NP_002444	MTIF2 mitochondrial translational initiation factor 2
AI384762	6	fb17a02*	2	2p13-p14 / 55,190 K	NP_008939	RTN4 reticulon 4
AI397219	6				no significant result	
BM735955	6	tdsubc 1f2	2	2p16 / 55,419 K	AAA36788	RPS27A ribosomal protein S27a
AA494577	6				no significant result	
AA494670	6	fa10c06	2	2q33.3 / 204,100 K	AAG09681	CYP20A1 cytochrome P450, family 20, subfamily A, polypeptide 1
AI416129	6	fb18c11	13	13q12.2-q13.3 / 47,360 K	NP_003841	SUCLA2 succinate-CoA ligase, ADP-forming, beta subunit
AI397474	6				no significant result	
NM_131445	6	chma1	2	2q24-q32 / 175,585 K	NP_000070	CHRNA1 cholinergic receptor, nicotinic, alpha polypeptide 1 (muscle)
AW342883	6	fi80c12	2	2q31 / 176,790 K	BAB21806	KIAA1715 KIAA1715 protein
AW420343	6				no significant result	

¹ only one accession number for cloned genes

² RTN4 radiation hybrid PCR result: 000011000000000000000000110000111000011111011100100000010020000000000010022100000011100*LOD score = 11.6

* Woods et. al., 2000

Supplementary Table 1J: Mapping data for the analysis of conserved syntenies between rtn6 and rtn5 in zebrafish and RTN4 and RNT1 in human

Accession 5'EST Accession 3'EST ¹	Zebrafish LN54 LG	Zebrafish LN54 Marker Symbol	Human Chromosom	Human Position	Human Accession	Description
AW078165	13	fe25d09	11	11p13 / 34,140 K	NP_005889	M11S1 membrane component, chromosome 11, surface marker 1
AW059113	13		11	11p13 / 34,140 K	NP_005889	M11S1 membrane component, chromosome 11, surface marker 1
AI477555	13	fb58g07	10	10q21-q22 / 73,490 K	NP_002769	PSAP prosaposin (variant Gaucher disease and variant metachromatic leukodystrophy)
AI477669	13				no significant result	
AI601645	13	fc02e11	2	2p13-p14 / 66,680 K	NP_002389	MEIS1 Meis1, myeloid ecotropic viral integration site 1 homolog (mouse)
AI588472	13		2	2p13-p14 / 66,680 K	NP_002389	MEIS1 Meis1, myeloid ecotropic viral integration site 1 homolog (mouse)
AI601614	13	fc02b11	6	6p21.1 / 43,170 K	AAH02879	PARC p53-associated parkin-like cytoplasmic protein
AI588448	13				no significant result	
AI629244	13	fc10c06	6	6q27 / 167,189 K	NP_003721	RNASE6PL ribonuclease 6 precursor
AI601360	13				no significant result	
AI626149	13	fc06f04	3	3q23 / 143,190 K	NP_689989	MGC40579 hypothetical protein MGC40579
AI626469	13				no significant result	
AI626134	13	fc06e01	2	2p22.3 / 38,520 K	AAM97342	ARL6IP2 ADP-ribosylation-like factor 6 interacting protein 2
AI626460	13		2		no significant result	
AI684783	13	fb83c11	10	10q22 / 71,530 K	NP_542986	COL13A1 collagen, type XIII, alpha 1
AI584271	13				no significant result	
BG985848	13	ibd5135	2	2p21 / 47,190 K	XP_031626	TTC7 tetratricopeptide repeat domain 7
BG985849	13		2	2p21 / 47,190 K	XP_031626	TTC7 tetratricopeptide repeat domain 7
BF171669	13	fd50d08	2	2p21 / 47,094 K	NP_644908	SDNSF multiple coagulation factor deficiency protein 2
AW019194	13		2	2p21 / 47,094 K	NP_644908	SDNSF multiple coagulation factor deficiency protein 2
AW777712	13	fk49e09	10	10q25-q26 / 121,064 K	NP_006784	PRDX3 peroxiredoxin 3
AW778453	13		10	10q25-q26 / 121,064 K	NP_006784	PRDX3 peroxiredoxin 3
AI722119	13	fd19e06	X	Xq26.1 / 127,574 K	BAA90894	HT011 uncharacterized hypothalamus protein HT011
AI722533	13		X	Xq26.1 / 127,574 K	BAA90894	HT011 uncharacterized hypothalamus protein HT011
AW133840	13	fi12d12	1	1q44 / 241,040 K	AAH04485	PNAS-4 CGI-146 protein
AW116199	13				no significant result	
AI476830	13	fb50g11	10	10q22 / 76,873 K	P45880	VDAC2 voltage-dependent anion channel 2
AI477233	13		10	10q22 / 76,873 K	P45880	VDAC2 voltage-dependent anion channel 2
AI497423	13	fb62d04	14	14q32 / 101,980 K	NP_001814	CKB creatine kinase, brain
AI522785	13		14		no significant result	
AI584922	13	fb93a09	2	2q13 / 113,170 K	NP_714923	MGC46235 hypothetical protein MGC46235
AI584392	13				no significant result	
AW116409	13	fi15c03	10	10q26 / 120,950 K	NP_003741	EIF3S10 eukaryotic translation initiation factor 3, subunit 10 theta, 150/170kDa
AW134149	13		10	10q26 / 120,950 K	NP_003741	EIF3S10 eukaryotic translation initiation factor 3, subunit 10 theta, 150/170kDa
AW018508	13	fd58h04	10	10q25.1 / 106,152 K	NP_004823	GSTTLp28 glutathione-S-transferase like; glutathione transferase omega
AW019036	13				no significant result	
not available						
AW116140	13	fi09f10	2	2p16.1 / 60,690 K	NP_075044	BCL11A B-cell CLL/lymphoma 11A (zinc finger protein)
AI658312	13	fc21e02	10	10q22 / 70,990 K	NP_000179	HK1 hexokinase 1
AI641247	13				no significant result	
AW128798	13	fe37e06	10	10q22.1 / 70,847 K	NP_003162	SUPV3L1 suppressor of var1, 3-like 1 (S. cerevisiae)
AW128298	13				no significant result	
not available						
AW019477	13	fd52b02	10	10pter-q25.3 / 69,960 K	NP_071412	MAWBP MAWD binding protein
NM_131621	13	bmpr1a	10	10q22.3 / 88,730 K	AAH28383	BMPRI1A bone morphogenetic protein receptor, type IA
AI722246	13	fd20h06	6	6q27 / 170,548 K	NP_003185	TBP TATA box binding protein
AI721453	13				no significant result	
AI437278	13	fb39g06	10	10q11-q24 / 76,050 K	AAH03568	ADK adenosine kinase
AI444479	13				no significant result	
BE201264	13	fk89a06	10	10q24.3 / 105,950 K	NP_000485	COL17A1 collagen, type XVII, alpha 1
BE200663	13				no significant result	
AI629316	13	fc10e09 ³	6	6q24 / 138,665 K	NP_055135	HEBP2 heme binding protein 2
AI601384	13				no significant result	
NM_131281	13	fgf8	10	10q24 / 103,664 K	NP_006110	FGF8 fibroblast growth factor 8 (androgen-induced)
NM_131184	13	pax2a	10	10q22.1-q24.3 / 102,860 K	NP_000269	PAX2 paired box gene 2
AI385024	13	fb14b12	10	10q22.2 / 71,795 K	AAH16840	MGC34695 hypothetical protein MGC34695
AI396797	13		10	10q22.2 / 71,795 K	AAH16840	MGC34695 hypothetical protein MGC34695
AW173999	13	fi38b10	10	10q22.2 / 73,997 K	NP_060096	DNAJB12 DnaJ (Hsp40) homolog, subfamily B, member 12
AW171164	13				no significant result	
AW174378	13	fi42e02	10	10q24.32 / 104,319 K	CAC08403	MGC2491 hypothetical protein MGC2491
AW171502	13				no significant result	
AI416105	13	fb18a04	14	14q / 33,172 K	NP_068733	CFL2 cofilin 2 (muscle)
AI397450	13		14	14q / 33,172 K	NP_068733	CFL2 cofilin 2 (muscle)
BF717718	13	fd50h11	14	14q32.12-q32.13 / 91,27 K	AAH23021	GOLGA5 golgi autoantigen, golgin subfamily a, 5
AW019226	13		14	14q32.12-q32.13 / 91,27 K	AAH23021	GOLGA5 golgi autoantigen, golgin subfamily a, 5
AI331561	13	fa94c12	14	14q23.1 / 59,490 K	NP_722518	SLC38A6 solute carrier family 38, member 6
AI332252	13				no significant result	
AW127891	13	fi04d12	2	2p23.2 / 32,130 K	NP_057039	CGI-27 C21orf19-like protein
AW115868	13		2		no significant result	
AW115968	13	fi05f05	1	1q32.3-q41 / 206,652 K	NP_055203	DJ434O14.5 novel putative protein similar to YIL091C yeast hypothetical 84 kD protein from SGA1-KTR7
AW127998	13		1	1q32.3-q41 / 206,652 K	NP_055203	DJ434O14.5 novel putative protein similar to YIL091C yeast hypothetical 84 kD protein from SGA1-KTR7
AI416084	13	fb33g03	15	15q14 / 39,320 K	NP_055953	KIAA0252 KIAA0252 protein
AI437443	13				no significant result	
AI658310	13	fc21d12	6	6q21 / 107,361 K	NP_057571	HSPC230 HSPC230 gene
AI641245	13				no significant result	
AI545712	13	fb75d02	20	20p11 / 14,259 K	NP_037413	FLRT3 fibronectin leucine rich transmembrane protein 3
AI544469	13				no significant result	
not available						
AI959634	13	fd12b09	13	13q12.2 / 26,947 K	NP_690876	MTIF3 mitochondrial translational initiation factor 3
AI331318	13	fa98g05	14	14q32.1 / 91,180 K	Q99538	LGMN legumain
AI331432	13				no significant result	
AI331273	13	fa97c03	14	14q22.2 / 52,939 K	NP_004115	GMFB glia maturation factor, beta
AI332203	13				no significant result	
AI558679	13	fb79b10 / btaf1	10	10q22-q23 / 93,870 K	NP_003963	BTA1 BTAF1 RNA polymerase II, B-TFIIID transcription factor-associated, 170kDa (Mot1 homolog, S. cerevisiae)
AI558448	13				no significant result	
AI721792	13	fd16d11	6	6p21 / ???	CAC01626	BTBD9 BTB (POZ) domain containing 9
AI666911	13				no significant result	
AI476860	13	fb51h12	1	1p34.3 / 32,272 K	BAB13825	FLJ10276 hypothetical protein FLJ10276
AI477319	13				no significant result	
Accession 5'EST Accession 3'EST ¹	Zebrafish T 51 LG	Zebrafish T 51 Marker Symbol	Human Chromosom	Human Position	Human Accession	Description
AW174924	13	fi30c07	10	10q21 / 70,622 K	NP_004719	DDX21 DEAD/H (Asp-Glu-Ala-Asp/His) box polypeptide 21
AW174924	13		10	10q21 / 70,622 K	NP_004719	DDX21 DEAD/H (Asp-Glu-Ala-Asp/His) box polypeptide 21
AI331027	13	fb04e08	1	1q42.1 / 220,500 K	NP_005417	TP53BP2 tumor protein p53 binding protein, 2
not available	13	rtn6 ²	2	2p13-p14		RTN4 reticulon 4
BI896341	13	fc45e02	6	6q23.3 / 137,749 K	NP_786923	OLIG3 oligodendrocyte transcription factor 3
AI793378	13				no significant result	

* Woods et. al. 2000

Supplementary Table 1K: Mapping data for the analysis of conserved syntenies between rtn8 in zebrafish and RTN2 in human

Accession 5'EST Accession 3'EST ¹	Zebrafish LN54 LG	Zebrafish LN54 Marker Symbol	Human Chromosome	Human Position	Human Accession	Description
AI416271	21	tb18g12	10	10q11.21 / ???	NP_055568	BMS1L BMS1-like, ribosome assembly protein (yeast)
AI522358	21					no significant result
BE016964	21	tk71g05	4	4q21.22 / 78,441 K	NP_006826	CCN1 cyclin 1
BE018321	21			4q21.22 / 78,441 K	NP_006826	CCN1 cyclin 1
BE556775	21	tk65d02	9	9q34.13 / 125,023 K	BAA11486	KIAA0169
BE201579	21		9	9q34.13 / 125,023 K	BAA11486	KIAA0169
BE016557	21	tk65b10	9	9q34 / 133,834 K	NP_057118	MRPS2 mitochondrial ribosomal protein S2
BE016589	21		9	9q34 / 133,834 K	NP_057118	MRPS2 mitochondrial ribosomal protein S2
BE556816	21	tk91a03	4	4q21.22 / 78,541 K	AAH32518	CNNG2 cyclin G2
BE200769	21		4	4q21.22 / 78,541 K	AAH32518	CNNG2 cyclin G2
not available						
AA658637	21	tk65b05	4	4q21.22 / 78,276 K	XP_233687	hypothetical LOC345079
AF003943	21	celip	9	9q34.3 / 131,218 K	AAB35488	CEL carboxyl ester lipase (bile salt-stimulated lipase)
not available						
AA605859	21	tk20e05	9	9q33-q34 / 126,730 K	AAB41498	SPTAN1 spectrin, alpha, non-erythrocytic 1 (alpha-fodrin)
NM_131112	21	pou5f1/spa	6	6p21.31 / 31,239 K	NM_131112	POU5F1 POU domain, class 5, transcription factor 1
AI588748	21	tk98h11	12	12p24.33 / 130,897 K	AAD21042	PUS1 pseudouridylyl synthase 1
AI588293	21		12	12p24.33 / 130,897 K	AAD21042	PUS1 pseudouridylyl synthase 1
AI524462	21	tk22b05	2	2q21.2 / 131,017 K	BAH32556	FLJ20297 hypothetical protein FLJ20297
AI397441	21					no significant result
AI397201	21	tk06a05	12	12p24 / 109,346 K	NP_057310	VPS29 vacuolar protein sorting 29 (yeast)
AI385089	21		12	12p24 / 109,346 K	NP_057310	VPS29 vacuolar protein sorting 29 (yeast)
NM_131758	21	spb72 *	9	9q34.1 / 119,493 K	NM_004099	STOM stomatin
AI794078	21	tk38b04	9	9q34 / 131,070 K	NP_000359	TSC1 tuberous sclerosis 1
AI697138	21					no significant result
AI657880	21	tk14t10 ³	11	11q23.1 / 111,453 K	NP_001922	DLAT dihydrolipamide S-acetyltransferase (E2 component of pyruvate dehydrogenase complex)
AI641410	21					no significant result
AIW128712	21	tk63e01	11	11q22.2 / 101,312 K	AAO38749	ANGPTL5 angiotensin-like 5
AIW117142	21			11q22.2 / 101,312 K	AAO38749	ANGPTL5 angiotensin-like 5
AA437303	21	tk30h11	11	11q25 / 133,520 K	AAK27221	JAM3 junctional adhesion molecule 3
AI416013	21					no significant result
BE016985	21	rm s ²	19	19q13.32 / 50,686 K		RTN2 reticulon 2
BE016345	21	tk12d03	11	11q13.3 / 73,650 K	NP_057231	PME-1 protein phosphatase methyltransferase-1
BE556794	21	tk6807 **	11	11p15.5 / 4,047 K	AAD37491	RRM1 ribonucleotide reductase M1 polypeptide
BE201598	21		11	11p15.5 / 4,047 K	AAD37491	RRM1 ribonucleotide reductase M1 polypeptide
AA483399	21	tk01c01	11	11q13.1 / 65,546 K	NP_003851	BANF1 barrier to autoneurulation factor 1
AA495322	21					no significant result
NM_131338	21	bf	6	6p21.3 / 32,021 K	AAH04143	BF B-factor, prosperidin
AI386667	21	tk08e11	11	11q13 / 63,862 K	NP_857635	PRDX5 peroxiredoxin 5
AI384806	21		11	11q13 / 63,862 K	NP_857635	PRDX5 peroxiredoxin 5
AIW059432	21	tk14a07	11	11q13 / 62,415 K	P08195	SLC3A2 solute carrier family 3 (activators of dibasic and neutral amino acid transport), member 2
AIW058939	21		11	11q13 / 62,415 K	P08195	SLC3A2 solute carrier family 3 (activators of dibasic and neutral amino acid transport), member 2

Accession 5'EST Accession 3'EST ¹	Zebrafish T 51 LG	Zebrafish T 51 Marker Symbol	Human Chromosome	Human Position	Human Accession	Description
not available						
AA603745	21	tk18D04	22	22q11.23 / 23,284 K	NP_004166	SNRPD3 small nuclear ribonucleoprotein D3 polypeptide 18kDa
not available						
AA605859	21	tk20e05	9	9q33-q34 / 126,730 K	AAB41498	SPTAN1 spectrin, alpha, non-erythrocytic 1 (alpha-fodrin)
NM_131112	21	pou5f1/spa	6	6p21.31 / 31,239 K	NM_131112	POU5F1 POU domain, class 5, transcription factor 1
AIW127732	21	tk97b11	5	5p13.1 / 36,213 K	NP_005974	SKP2 S-phase kinase-associated protein 2 (p45)
AIW115560	21		5	5p13.1 / 36,213 K	NP_005974	SKP2 S-phase kinase-associated protein 2 (p45)
AIW174919	21	tk30c01 *	19	19q13.1 / 45,926 K	BAA22524	ITPKC inositol 1,4,5-trisphosphate 3-kinase C 19q13.1
AIW154617	21					no significant result
AIW128712	21	tk63e01	11	11q22.2 / 101,312 K	AAO38749	ANGPTL5 angiotensin-like 5
AIW117142	21			11q22.2 / 101,312 K	AAO38749	ANGPTL5 angiotensin-like 5
not available						
AIW343662	21	tk47e11	11	11q23.3 / 116,169 K	NP_116114	MSG13125 hypothetical protein MGC13125
AI965099	21	tk86g11 ³	11	11q23.1 / 111,453 K	NP_001922	DLAT dihydrolipamide S-acetyltransferase (E2 component of pyruvate dehydrogenase complex)
AI943209	21					no significant result
AIW153341	21	tk19e09	11	11pter-p15.5 / ???	CAA12176	ALG8 asparagine-linked glycosylation 8 homolog (yeast, alpha-1,3-glucosyltransferase)
AIW116759	21		11	11pter-p15.5 / ???	CAA12176	ALG8 asparagine-linked glycosylation 8 homolog (yeast, alpha-1,3-glucosyltransferase)
NM_131338	21	bf	6	6p21.3 / 32,021 K	AAH04143	BF B-factor, prosperidin
AI386667	21	tk08e11	11	11q13 / 63,862 K	NP_857635	PRDX5 peroxiredoxin 5
AI384806	21		11	11q13 / 63,862 K	NP_857635	PRDX5 peroxiredoxin 5
AI497216	21	tk63b04 *	15	15q22-qter / 72,761 K	AAH35738	CYP1A2 cytochrome P450, family 1, subfamily A, polypeptide 2
AI497522	21					no significant result
AI584662	21	tk81g12	11	11q12.3 / 62,362 K	NP_003155	STX5A syntaxin 5A
AI545474	21					no significant result
AI626218	21					no significant result
AI601826	21	tk12d06 *	11	11q12-q13 / 62,431 K	NP_006353	NXF1 nuclear RNA export factor 1
AI722645	21	tk29q12	5	5q31.3 / 139,074 K	NP_067547	HSPC195 hypothetical protein HSPC195
AI721597	21					no significant result
AI722697	21	tk30d10	18	18 B2 / 36,914 K	NP_653324	2610510D14RIKEN cDNA 2610510D14 gene
AI721642	21					no significant result
AIW059432	21	tk14a07	11	11q13 / 62,415 K	P08195	SLC3A2 solute carrier family 3 (activators of dibasic and neutral amino acid transport), member 2
AIW058939	21		11	11q13 / 62,415 K	P08195	SLC3A2 solute carrier family 3 (activators of dibasic and neutral amino acid transport), member 2
AIW059432	21					
NM_131455	21	rm1 *	11	11p15.5 / 4,047 K	AAD37491	RRM1 ribonucleotide reductase M1 polypeptide
	21	w10493	5	5q33.3 / 156,284 K	NP_612388	LOC191937 hypothetical protein BC009868

¹ only one accession number for cloned genes

² RTN8 radiation hybrid PCR result: 0011000000000000010001110000010111010000000000001001001001000000000000000110100010101 LOD score = 11.0

³ tk14t10 (LN54) and tk86g11 (T51) represent the same gene

⁴ tk9507 (LN54) and rm1 (T51) represent the same gene

* Woods et. al., 2000

Supplementary Table 1L: Mapping data for the analysis of conserved syntenies between RTNs in fugu and mammals

(FUGRU)RTN1

Fugu Scaffold	Fugu Position ^a	Ense. Peptide ID	Description	Human Chr	Human Position ^a	Mouse Chr	Mouse Position ^a	Rat Chr	Rat Position ^a
188	3	SINFRUP00000132119.1	AMBIGUOUS	14	58,564	12	67,183	6	94,852
188	16	SINFRUP00000132121.1	ADP RIBOSYLATION STRUCTURE CONTAINING	14	5,843	12	67,113	6	94,772
188	31	SINFRUP00000132124.1	RTN1	14	5,819	12	66,867	6	94,415
188	56	SINFRUP00000132133.1	KNSL7	3	44,809	9	123,275	n.d.r.	
188	63	SINFRUP00000132136.1	TACC3	4	1,696	5	31,927	14	82,754
188	69	SINFRUP00000132138.1	FGFRL1	4	1,002	n.d.r.		n.d.r.	
188	92	SINFRUP00000132142.1	Q9HCC9	4	2,307	5	32,517	14	82,244
188	103	SINFRUP00000132143.1	AMBIGUOUS	n.d.r.		5	32,587	n.d.r.	
188	104	SINFRUP00000132144.1	AMBIGUOUS	n.d.r.		5	32,587	n.d.r.	
188	113	SINFRUP00000132145.1	MRPL35	2	86,407	n.d.r.		4	105,352
188	117	SINFRUP00000132146.1	NM_022912	2	86,477	14	61,006	4	105,306
188	121	SINFRUP00000132147.1	NM_016079	2	86,735	18	6,539	4	105,079
188	126	SINFRUP00000132148.1	OS94_HUMAN	4	129,187	3	40,583	2	127,674
188	132	SINFRUP00000132152.1	STK18	4	129,269	3	40,624	2	127,719
188	144	SINFRUP00000132155.1	ITPK1	14	91,482	12	96,587	6	126,907
188	154	SINFRUP00000132157.1	C14orf130	14	91,674	12	96,782	6	127,044
188	162	SINFRUP00000132160.1	NM_018167	14	91,743	12	96,847	6	127,085
188	186	SINFRUP00000132162.1	AMBIGUOUS	n.d.r.		n.d.r.		6	127,367
188	192	SINFRUP00000132167.1	Q9P2D8	14	92,108	12	97,151	6	127,444
188	212	SINFRUP00000132173.1	NM_138344	14	92,383	12	97,331	6	127,609
188	214	SINFRUP00000132174.1	ASB2	14	92,402	12	97,345	6	127,626
188	225	SINFRUP00000132175.1	C14orf137	14	92,492	12	97,41	6	127,697
188	227	SINFRUP00000132176.1	DDX24	14	92,522	12	97,43	6	127,711
188	231	SINFRUP00000132179.1	SERPINA10	14	92,743	12	97,635	6	127,941
188	235	SINFRUP00000132183.1	MJD	14	90,541	12	95,953	6	126,216
188	244	SINFRUP00000132192.1	UBR1	15	41,033	2	122,547	3	107,609
188	259	SINFRUP00000132195.1	AMBIGUOUS	n.d.r.		n.d.r.		6	137,352

(FUGRU)RTN2

Fugu Scaffold	Fugu Position ^a	Ense. Peptide ID	Description	Human Chr	Human Position ^a	Mouse Chr	Mouse Position ^a	Rat Chr	Rat Position ^a
257	30	SINFRUP00000130858.1	GRLF1	19	52,155	n.d.r.		1	76,842
257	67	SINFRUP00000130860.1	AP2S1	19	52,039	7	11,399	1	77,153
257	106	SINFRUP00000130868.1	RTN2	19	50,686	7	0,013	1	78,731
257	114	SINFRUP00000130872.1	PPM1A	19	50,695	n.d.r.		1	78,721
257	128	SINFRUP00000130879.1	PTGIR	19	51,817	7	11,561	1	77,313
257	141	SINFRUP00000130883.1	AMBIGUOUS	19	51,801	7	11,573	6	124,486
257	141	SINFRUP00000130883.1	CALM2	19	51,801	7	11,573	1	77,325
257	141	SINFRUP00000130883.1	AMBIGUOUS	2	47,37	7	11,573	1	77,325
257	146	SINFRUP00000130886.1	KCNK12	2	47,747	n.d.r.		6	124,178
257	168	SINFRUP00000130889.1	GEMIN7	19	50,28	7	14,009	1	1,51
257	210	SINFRUP00000130898.1	Q8IWK3	19	50,315	7	13,98	1	1,527
257	225	SINFRUP00000130901.1	MRPL28	16	0,358	17	24,815	10	15,396
257	231	SINFRUP00000130904.1	RELB	19	50,214	7	14,06	1	78,998
257	237	SINFRUP00000130907.1	CLPTM1	19	50,169	7	14,092	1	79,033

(FUGRU)RTN3

Fugu Scaffold	Fugu Position ^a	Ense. Peptide ID	Description	Human Chr	Human Position ^a	Mouse Chr	Mouse Position ^a	Rat Chr	Rat Position ^a
346	11	SINFRUP00000140880.1	CD99L2	X	148,641	X	55,663	n.d.r.	
346	57	SINFRUP00000140896.1	Q8N8M0	7	100,378	n.d.r.		n.d.r.	
346	68	SINFRUP00000140901.1	NM_018978	11	124,063	9	37,593	n.d.r.	
346	99	SINFRUP00000140908.1	ING1L	4	185,125	n.d.r.		16	47,789
346	107	SINFRUP00000140913.1	AMBIGUOUS	n.d.r.		7	115,412	1	185,996
346	109	SINFRUP00000140914.1	Q9H3K6	16	29,503	7	115,414	1	185,999
346	124	SINFRUP00000140875.1	SF1 or PYGL	11	64,314	19	4,302	1	209,311
346	119	SINFRUP00000140917.1	PYGM	11	64,296	19	4,281	1	209,332
346	139	SINFRUP00000140921.1	RBM4	11	66,214	19	5,921	1	207,521
346	154	SINFRUP00000140925.1	MAP4K2	11	64,339	19	4,324	1	209,286
346	161	SINFRUP00000140929.1	MEN1	11	64,35	19	4,335	1	209,276
346	166	SINFRUP00000140930.1	RTN3	11	63,263	19	3,642	1	210,296
346	189	SINFRUP00000140937.1	NM_016581	19	11,489	n.d.r.		8	21,184
346	196	SINFRUP00000140938.1	MTA1L1	11	62,14	19	8,09	1	211,781

(FUGRU)RTN4

Fugu Scaffold	Fugu Position ^a	Ense. Peptide ID	Description	Human Chr	Human Position ^a	Mouse Chr	Mouse Position ^a	Rat Chr	Rat Position ^a
2616	3	SINFRUP00000127275.1	RTN4	2	55,213	11	29,875	14	110,775

(FUGRU)RTN7

Fugu Scaffold	Fugu Position ^a	Ense. Peptide ID	Description	Human Chr	Human Position ^a	Mouse Chr	Mouse Position ^a	Rat Chr	Rat Position ^a
3887	1	SINFRUP00000142114.1	RTN7	(11) ^b	63,263	n.d.r.		n.d.r.	
3887	3	SINFRUP00000142116.1	GEMIN6	2	38,981	17	78,861	6	3,128

(FUGRU)RTN8

Fugu Scaffold	Fugu Position ^a	Ense. Peptide ID	Description	Human Chr	Human Position ^a	Mouse Chr	Mouse Position ^a	Rat Chr	Rat Position ^a
2117	12	SINFRUP00000163874.1	CENTD2	11	72,136	n.d.r.		1	158,977
2117	24		RTN8 ^c	(19) ^d	50,686	n.d.r.		n.d.r.	

^a positions are given in kilobasepairs

^b position of RTN3 on human chromosom 11 was not retrieved from ensembl Martview, but from NCBI locuslink

^c RTN8 was not annoated autamically by ensemble peptide prediction and therefore did not recieve an Ense. Peptide ID

^d position of RTN2 on human chromosom 19 was not retrieved from ensembl Martview, but from NCBI locuslink

n.d.r. = no data retrieved with ensembl MartView