1 Supplementary information for

- 2 Melatonin modulates the hypothalamic-pituitary neuroendocrine axis to
- 3 regulate physiological color change in teleost fish

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1 9 1 99 1 99 1 59 1 59 1 79 1 99 99 99 99 99 99 99 99 99	M GTGA V TTTGG F TM GTAG V TACT Y AACT N CAGG Q AACA N S CAGG Q CaGG Q CaGG Q CaGG Q CaGG Q CaGG Q CAGG CAGG V C CAGG V C CAGG CAGA CAGA C	I V AGCCC K F TGGT V V CGAT A I TCCAT F M TCCAT F R ACAC D S ATAA N N N Saac CATAA N N N Saac CATAA SAAC SAAC SAAC SAAC SAAC SAAC SAA	T CCAC CCA	Y IGTG V 263) ACCA P CTAC Y IGAA CCAACC N GGTT V CCAACC N GGTT V CCAACC N GGTT V CCAACA S GGTT V V V V V V V V V V V V V	C CGT R CTC L GAG E TTC F TTC T T C T T C C T C L C C C C L C C C C	TAC Y CCCC P TTT F GTG GTG V AAC N AAC N AAG K GCA A GTG V gac tatat tatat tatat tatat tatat	CTG L L AAAG K GGTG A CGCT A CGCT A CGCT C C C C C C C C C C C C C C C C C	CGCI R CTAI L GTT V V GTT C C ATT GAGI E GAGI E S GAGI S gag gag gag gag gag gag gag gag gag g	ATT I ACCG T C C C C C C C C C C C C C C C C C	W P FGG W W CTC. L AAAT N GTG V CTC. L TGA * aacaa aaccigaatti tagaatti taggacti	I GCAT H GCA A A A A A C A A C A A C A A C A A C A A C A A C A A C A A A C A A A A C A A A A A A A A A A A A A	L GAC D CCG P CCA P CCA P CCA P CCA P CCA P CCA CC P CCA CCG P CCA CCG P CCA CCG P CCA CCG P CCA CCG P CCG CCG P CCG CCG P CCG CCG P CCG CCG	V GTT V GAG E GTG V TGC C AAA K aaaaaatta aatta aatta aatta aatta aatta aatta aatta aatta	I AGA R AACC N TGG W TAT T CCCG P CCCG P CCCG P CCCG CCCG CCCG	Q AAC N TTCC F TTA GGT G GGCA A TCA S O GGCA A S O GGCA A S O GGCA A S O G G C C C C C C C C C C C C C	V TTT F TTT T TTT F TTT F CGTG V CGC R CCA R P aaat aaaa cctg ggt cgca cata aaaacc ctata ctata	R GGTC V GGTG G CTG CTG CTG CTG CTG CTG CTG CTG	R ACC T CTG CTG CTG A CTG A CTG A A CTTC F M Gaa agcc acat atat agt tattat ggt tattat	R ATG M GCT A GCT A AGC S 98) CAG S Q Q TTC F T tgg tga tata aggatata agatata agatata
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Fig. S1. Characteristics of gene structure and the deduced amino acid sequence of *LcMtnr1a1-like*.The phosphorylation sites predicted with NetPhos 3.1 Server are marked by solid dots in three difficult colors (Ser, Tyr and green are in blue, orange and green, respectively); the N-linked glycosylation sites predicted with NetNGlyc 1.0 Server are highlighted by red triangles; Seven-transmembrane (7TM) domains predicted with I-TASSER are labeled in boxes in 7 different colors; the NRY, CYICHS and NAXXY sequences predicted with PROSITE are labeled in brown, pink and gray boxes, respectively. TM: transmembrane.

LcMtnr1a2

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1									JCCC										
57	cccg																		
17	cccc																		
77	gga																		
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97	aaaa	aaa	aaa	aaa	aac	tga	tccr	cgg	actt	tca	aat	taaa	agc	cac	aaa	atg	aco	gtca	atga
357	caca																		
17	ATGO	CTG	AAT	GGA	CCG	ACC	TTC	CGC	GAC	CGC	GAC	CCG	ATG	CGA	CTC	GTC	GAC	CCG	AGG
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.01	A	F	V	V	S	L	A	L	A	D	L	V	V	A	Ι	Y	Ρ	Y	Ρ
		1			•		TN	12	(10)	2~12	24)								
77	GTCC	CTTC	ACT	GCC	שייד	TTC	_	_				GCC	GGC	TAC	ATC	CAC	TGT	CAG	ATC
21	V	L	Т	A	I	F	Н	D	G	W	Ι	A	G	Y	Ι	Н	С	Q	I
21	V	ш	1	A	- L	г	11	D	G	m	1	A	G	1					
															TN			• •	61)
337	GGC	FTC	CTC	ATG	GGT	CTC	AGC	GTC	ATT	GGC		ATC	TTC	AAC	ATC.		-	ATC	GCC
41	G	F	L	М	G	L	S	V	I	G	S	I	F	N	I	Т	G	I	A
											•								
897	AACO	CGC	TAC	TGC	TAC	ATC	TGT	CAC	AGC	CTT	AAG	TAT	GAC	AAA	CTG	TTC	TCC	AAC	AGC
61	N	R	Y	С	Y	I	C	Н	S	L	K	Y	D	K	L	F	S	N	S
		-		-	-	-		100											
957	ACCZ	ame	mee	mac	CIEC	CIEC	CIE	CIE	mcc	ceci	ma	ACC		ame			CIEC	coo	220
181	T	M	C	Y	V	V	L	V	W	A	L	T	I	L	A	I	V	P	N
101	- 1	141	C	1	v	v	Ъ	v	w	A	Ъ	1	1	Ч	A	1	v	P	IN
		TN	<u>14</u>	(18	2~2	02)													
	TTC																		
201	F	V	E	S	L	Q	Y	D	Ρ	R	V	Y	S	С	Т	F	A	Q	S
															٠				
077	AGC	rcg	CTG	TAC	ACT	ATC	ACG	GTA	GTG	GTG	GTT	CAC	TTC	ATC	CTG	CCG	ATC	GCC	ATC
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221	S						-	TN	AF	(22	0 7	=0)							
221		•											-						
	•	PAC	TCT	TAC	CTTC	CGT	אייר						CAC	anc:	ACC	ccc	ACC		220
137	ACCI							TGG	ATC	CTA	STC	ATC						GTC	
137	•	O TAC' Y	TGT C	TAC Y	CTG L	R	ATC						CAG Q	GTG. V	AGG R	CGG R	AGG R		K K
137 241	ACCI T	Y	С	Y	L	R	I	W	I	L	V	I	Q	V	R	R	R	GTC V	K
137 241 197	ACCI T GACI	Y TCG	C CGG	Y	L AAG	R	I	W	I	GAC	V CTC	I CGC	Q AAC	V	R CTC	R ACC	R ATG	GTC V TTC	K
137 241 197	ACCI T	Y	С	Y	L	R	I	W	I	L	V	I	Q	V	R	R ACC T	R ATG M	GTC V TTC F	K
137 241 197 261	ACCI T GACI D	Y TCG S	C CGG R	Y CCA P	L AAG K	R ATC I	I AAG K	W W CCG P	I CAC	GAC D	U V CTC	ATC I CGC. R	Q AAC N	V F	R CTC L	R ACC T	R ATG M 4~2	GTC V TTC F	K GTC V
137 241 197 261 257	ACCI T GACI D TTCC	Y TCG S GTG	C CGG R CTC	Y CCA P TTC	L AAG K	R ATC I GTC	I AAG K TGT	W CCG P TGG	ATCO I CACO H	CTA L GAC D	STC: V CTC L CTG	ATC I CGC. R AAC	Q AAC N CTA	V F TN ATC	R CTC. L 16 GGA	R ACC T (27 CTG	R ATG M 4~2 GCG	GTC V TTC F 96) GTC	K GTC V GCC
137 241 197 261 257	ACCI T GACI D	Y TCG S	C CGG R	Y CCA P	L AAG K	R ATC I	I AAG K	W W CCG P	I CAC	GAC D	U V CTC	ATC I CGC. R	Q AAC N	V F	R CTC L	R ACC T	R ATG M 4~2	GTC V TTC F	K GTC V
1 137 241 1 197 261 1 257 281	GACT D TTCC	Y S S GTG V	C CGG R CTC L	Y CCA P TTC F	L AAG K GCT A	R ATC I GTC V	I K TGT C	TGG W CCG P TGG W	I CACO H GCAO A	CTA L GAC D CCG	STC: V CTC: L CTG: L	ATC I CGC. R AAC	Q AAC N CTAL	V F TN ATC	R L L GGA G	R ACC T (27 CTG L	R ATG M 4~2 GCG A	GTC V TTC F 96 GTG V	K GTC V GCC A
137 241 197 261 257 281 317	ACCI T GACI D TTCC	Y S S GTG V	C CGG R CTC L	Y CCA P TTC F	L AAG K GCT A	R ATC I GTC V	I K TGT C	TGG W CCG P TGG W	I CACO H GCAO A	CTA L GAC D CCG	STC: V CTC: L CTG: L	ATC I CGC. R AAC	Q AAC N CTAL	V F TN ATC I	R L L GGA G	R ACC T (27 CTG L	R ATG M 4~2 GCG A	GTC V TTC F 96 GTG V	K GTC V GCC A
1137 241 1197 261 1257 281 1317	GACT D TTCC	Y S S GTG V	C CGG R CTC L	Y CCA P TTC F	L AAG K GCT A	R ATC I GTC V	I K TGT C	TGG W CCG P TGG W	I CACO H GCAO A	CTA L GAC D CCG	STC: V CTC: L CTG: L	ATC I CGC. R AAC	Q AAC N CTAL	V F TN ATC	R L L GGA G	R ACC T (27 CTG L	R ATG M 4~2 GCG A	GTC V TTC F 96 GTG V	K GTC V GCC A
1137 241 1197 261 1257 281 1317	GACT T GACT D TTCC F GACT	Y TCG S GTG V TCT.	C R CTC L AGG	Y P TTC F	L AAG. K GCT A	R ATC I GTC V	I K TGT C	TGG W CCG P TGG W	I CACO H GCAO A	CTA L GAC D CCG P GAG	STC: V L CTG: L FGG	ATC I CGC R AAC N CTG	Q AAC N CTAI L TTCI F	V F TN ATCO I ACGO	R L L G G G G C C. A	R T CTG L AGC	R ATG M 4~2 GCG A TAC	GTC V F 96 GTC V TTC	K GTC V GCG A
137 241 197 261 1257 281 1317 301	GACT D TTCC F GACT D	Y S GTG V FCT.	C R CTC L AGG R	Y P TTC F CTG L	AAG K GCT A GGCC G	R I GTC V CGG R	I K TGT C GCG A	TGG W TGG W ATA I	ATCO I CACO H GCAO A CCGO P	CTA L GAC D CCG P GAG E	STC: V L CTG: L FGG	ATC I CGC. R AAC N CTG L	Q AAC N CTAI L TTCI F (31	V F TN ATCO I ACGO T	R L G G G G G C C A 33)	R T CTG L AGC S	R M 4~2 GCG A A TAC	GTC V TTC F GTG V TTC F	K GTC V GCG A A SATG
1137 241 1197 261 1257 281 1317 301 1377	GACT D TTCC F GACT D	Y S GTG V FCT.	C R CTC L AGG R	Y P TTC F CTG L	AAG K GCT A GGCC G	R I GTC V CGG R	I K TGT C GCG A	TGG W TGG W ATA I	ATCO I CACO H GCAO A CCGO P	CTA L GAC D CCG P GAG E	STC: V L CTG: L FGG	ATC I CGC. R AAC N CTG L	Q AAC N CTAI L TTCI F (31	V F TN ATCO I ACGO T	R L G G G G G C C A 33)	R T CTG L AGC S	R M 4~2 GCG A A TAC	GTC V TTC F GTG V TTC F	K GTC V GCG A A SATG
241 1197 261 1257 281 1317 301	GACT T GACT D TTCC F GACT	Y S GTG V FCT.	C R CTC L AGG R	Y P TTC F CTG L	L AAG K GCT A GGCC G	R I GTC V CGG R	I K TGT C GCG A	TGG W TGG W ATA I	ATCO I CACO H GCAO A CCGO P	CTA L GAC D CCG P GAG E	STC: V L CTC: L STG: V TAC: TAC:	ATC I CGC. R AAC N CTG L	Q AAC N CTAI L TTC F (31 GTC	V F TN ATCO I ACGO T	R L GGA GCC. A 33)	R T CTG L AGC S	R M 4~2 GCG A A TAC	GTC V TTC F GTG V TTC F	K GTC V GCG A A SATG
1137 241 1197 261 1257 281 1317 301 1377 321	GACT D TTCC F GACT D TTCC TTCC TTCC TTCC TTCC TTCC TTCC	Y S GTG V TCT. S TTC.	C CGG R CTC L AGG R AAC	Y P TTC F CTG L S	L AAG K GCT A GGCC G TGC C	R I GTC V CGG R CCGG L	I K TGT C GCG A A X	TGG W TGG W EATA I SGCT	ATCO I CACO H CCACO P CCCO P CCCO V	CTA L GAC D CCCG P CCCG P GAC E CCCG V	V V CTC L CTG L CTG L V V V T CTG C TGG	ATC I R AACC N CTG L 47 GGC G	Q AAC N CTAI L TTCI F (31 GTC V	V FTC F I ACG T T 1~3 CCG	R L G G G G G G G C C A 33) AAC	R T (27 CTG L AGC S CAC	R M 4~2 GCG A TAC Y N	GTC V F 96) GTG GTG V TTC F	K GCCG A CATG R R
1137 241 1197 261 1257 281 1317 301 1377 321 1437	GACT D TTCC F GACT D TTCC TTCC TTCC TTCC TTCC TTCC TTCC	Y S GTG V TCT. S TTC.	C CGG R CTC L AGG R AAC	Y P TTC F CTG L S	L AAG K GCT A GGCC G TGC C	R I GTC V CGG R CCGG L	I K TGT C GCG A A X	TGG W TGG W EATA I SGCT	ATCO I CACO H CCACO P CCCO P CCCO V	CTA L GAC D CCCG P CCCG P GAC E CCCG V	V V CTC L CTG L CTG L V V V T CTG C TGG	ATC I R AACC N CTG L 47 GGC G	Q AAC N CTAI L TTCI F (31 GTC V	V FTC F I ACG T T 1~3 CCG	R L G G G G G G G C C A 33) AAC	R T (27 CTG L AGC S CAC	R M 4~2 GCG A TAC Y N	GTC V F 96) GTG GTG V TTC F	K GCCG A CATG R R
11137 241 1197 261 1257 281 1317 301 1377 321 1437 341	GACT T GACT D TTCC F GACT D TACT Y GAGT E	Y FCG S GTG V TCT. S TTC. F	C CGG R CTC L AGG R AAG N AAG	Y P TTC F CCTG L S AGC R	L AAG K GGCT A GGCC G TGC C ATCC I	R I I CGCC R CCCC R CCCC L I CCCCC V	I CAAG K C C C C C C C C C C C C C	TGG W P TGG W ZATA I SGCT A A A A C I	I CACC H GCACC H CCCCC P GCCC V V ATC: I	CTA L L D CCCG P CCCG P CCCG P CCCG C CCCG C C CCCG C C CCCG C C C C	V V CTC L CTG L FGG W TN FAC Y K	ATC I CGC: R AAC N CTG I CTG G G CTG F	Q N CTAN F GTCC V CAC	V F F I ACCG T T ACCG P F GCC C	R L GGGA G GGCC. A 33) AAC N TGA *	R ACC T CTG L AGC S CAC H gac	R ATG M 4~2 GCG A A TAC Y A AAC N	GTC V F 96) GTG V TTC F TTC F	K GGCG A SATG M CAGG R R
11137 241 1197 261 1257 281 1317 301 1377 321 1437 341	GACT T GACT D TTCC F GACT D TACT Y GAGT E	Y FCG S GTG V TCT. S TTC. F	C CGG R CTC L AGG R AAG N AAG	Y P TTC F CCTG L S AGC R	L AAG K GGCT A GGCC G TGC C ATCC I	R I I CGCC R CCCC R CCCC L I CCCCC V	I CAAG K C C C C C C C C C C C C C	TGG W P TGG W ZATA I SGCT A A A A C I	I CACC H GCACC H CCCCC P GCCC V V ATC: I	CTA L L D CCCG P CCCG P CCCG P CCCG C CCCG C C CCCG C C CCCG C C C C	V V CTC L CTG L FGG W TN FAC Y K	ATC I CGC: R AAC N CTG I CTG G G CTG F	Q N CTAN F GTCC V CAC	V F F I ACCG T T ACCG P F GCC C	R L GGGA G GGCC. A 33) AAC N TGA *	R ACC T CTG L AGC S CAC H gac	R ATG M 4~2 GCG A A TAC Y A AAC N	GTC V F 96) GTG V TTC F TTC F	K GGCG A SATG M CAGG R R
1137 241 1197 261 1257 281 1317 301 1377 321 1437 341 1497	ACCT T D GACT D TTCC F J GACT D TACT Y GAGT T C tga	Y FCG S GTG V TCT. S F TTC. Y agg	C CGG R CTC L AGG R AAGC N AAGC K cttg	Y P TTC F CCTG L CAGC S AGG R gtga	L AAG K GCCT A GGCC G TGC C L ATCC I I C ATCC	R I I CCCC R CCCC L CCCC L CCCC L CCCCC L	I C C C C C C C C C C C C C C C C C C C	TGG W TGG W TGG W TGG T A A A A A A A A A A A A A A A A A	I CACC H GCACC H CCCCC P GCCC V V ATC I tatti	CTA L L D CCCG P CCCG P CCCG P CCCG P CCCG C C CCCG C C CCCG C C C C	V CTC L CTG L CTG V TAC Y K aag	ATC I CGC. R AACC N CTG G G TTT F tga	Q N CTAN F (31 GTCC V CAC! H ttaa	V FTCC F I ACCG T T CCCG P F C C a a g	R L GGGA G GGCC A 33) AAC N TGA *	R ACC T CTG L AGC S CAC H gac	R ATG M 4~2 GCG A A TAC Y N sgag	GTC V F 96) GTG V TTC F TTC F Ugcg act	K COCC A CATC A CATC R CACC R CACC R CACC R CACC C C C C C
11137 241 1197 261 1257 281 1317 301 1317 321 1437 341 1497 1557	ACCT T GACT D TTCC F GACT D TACT T C GACT D TACT T C GACT T C GACT D	Y TCG S GTG V TCT. S TTC. F TTC. Y agg	C CGG R CTC L AGG R AAGG N AAGG K cttggga	Y P TTC F CTG L AGC S AGG R gtga 999	L AAAG K GGCT A GGCC G TGC C I AATC I I C AATC	R I GTC V CCGG R CCTC L CCTC V agaa	I C C C C C C C C C C C C C C C C C C C	TGG W TGG W TGG W TGG T TGG N TGG T TGG P TGG P TGG P TGG P TGG P TGG P TGG P TGG P TGG P TGG P TGG P TGG P TGG P TGG N TGG P TGG P TGG N TGG T G TGG T T TGG T T TGG T T TGG T T TGG T T TGG T T T TGG T	I CACC H GCACA P GCCG P GCCG V V ATC' I tatta tatta	CTAC L D CCCG P GAG' E GAG' V TTC: F aaaa aaaa	STC: V L CTC L CTG L I GGG W TN I AAG' K aaggaa	ATC I CGC: R AACC N CTG G G TTT F SGC G TTT F Itga taa	Q AAAC' N CTAJ F GTCC V CAC' H taa gaa	V FTCC F ACCG T ACCG T T ACCG P FGC C C aagaat	R L L GGA G G G G G C C A A A A C N N TGA * aaa aaa	R ACC T (277 CTG L AGC S CAC H gac	R ATG M 4~2 GCG GCG A TAC Y N Sgag caaa cac	GTC V F 96) GTG V TTC F TTC F acta	K COCC A CATC A CATC R CACC R CACC R CACC R CACC C C C C C
1137 241 1197 261 1257 281 1317 301 1377 321 1437 341 1497 1557 1617	/ ACCT T J GACT J TTCCC T J TTCCC J J GACT T GACT T C GACT T T C GACT T T C C T T C C T T C C T T C C C T T C C C T T C C C T T C C C C C C T D T T C C C C	Y S GTG V TCT. S TTC. F TTC. Y agg saag	C CGGG R CTC L AGG R AAGC N AAGC K cttggga aga	Y P TTC F CTG L AGC S AGG R gtga 999	L AAAG K GGCT A GGCC G TGC C A TGC C I A A A C A A C A A A A A A A A A A	R J GTC V CCGG R CCTC L SCTC V agaa accagaa	I C C C C C C C C C C C C C C C C C C C	TGG W F TGG W TGG W TGG T T A TGGCT A T A A C C C C C G C T G C C G C C G C C G C C G C C G C C G C C C G C	I CACC H GCAC A CCCGO P GTCC V V ATC' I tatta tatta atgaa	CTA L D GAC P CCG P CCG C C C C C C C C C C C C C	STC: V L CTC L CTG L FGGG W TIAC Y K aaggaa Stggaa	I CGCC R AAAC N CTG G CTG G G TTT F ttga ttaa gag	Q N CTAJ L TTCJ F (31) GTCC V CAC H taa gaa gaagtgt	V FTCC F ACCG T ACCG T T ACCG P FGC C C aaag aat gga	R L L GGA G G G G G C C A A A A C N N TGA * aaaaaaaaaaaaaaaaaaaaaaaaaaaaaaaaaaa	R ACC T 277 CTG L AGC S CAC H gac aga	R ATG M 4~2 GCG GCG A TAC Y N Sgag caaa cac	GTC V F 96) GTG F V TTC F ggcg act aca gggg	K GCCG A CACG M CACG R R CACG R taa ttttt
1137 241 1197 261 1257 281 1317 301 3377 341 497 557 617 677	/ ACC ¹ T J GAC ¹ J TTCC F J GAC ¹ T C GAC ¹ T C C GAC ¹ T C C GAC ¹ J	Y S S TCC S TCC S TTCC Y S S TTCC S S TTCC S S S S S S S S S S S	C CGGG R CTC L AGG R AAGC N AAGC K cttggga agaa	Y P TTCC F CCTG L AGC S CTGG S CTGG S CTGG S S CTGG S S CTGG S S S S S S S S S S S S S S S S S S	L AAAG K GGCT A GGCC G TGC C TGC C TGC C TGC C TGC C TGC C TGC C	R ATC I CGTC V CCGG R CCTC L CTC L CGTC V agaaa aacaa gaaataaa	I C C C C C C C C C C C C C	TGG W P TGG W W ZATA I ZATA I ZATA I ZATA I ZATA ZATC I agc zcta actti atga	ATCC I CACC H GCAC A A CCCG C P C CCCG C P V V ATCC I I tatta tatta atga agaai acgc	CTAC L GAC D CCG P CCG P CCG CCG CCG CCG CC	V V CTC L CTG L FGGG W TAC Y X AAG' K aaggaa ctgggag	I CGCC R AAAC N CTG G CTG G G TTT F ttga ttaa ggt	Q AAC N L TTC: F 31 GTCC V CAC H taa ggaa gtgt tatc	V FTCC F AATCC I AACGC T T C C aaggaaat ggaaat	R L L GGA G G G G CCC. A 333) AAC N TGA * aaaaaaaaaaaaaaaaaaaaaaaaaaaaaaaaaaa	R ACC T CTG L AGC S CAC H gac aga gcc	R ATG M 4~2 GCG GCG A TAC Y N Sgag caa cac ggt tttc	GTC V F 96) GTG F TTC F TTC F actaca gagg	K GCCG A CACG M CACGG R R CACGG R taa ttttt ttgggaa
1137 241 1197 261 1257 281 1317 301 1377 321 1437 1557 1557 1617 1617 1617	/ GACT J GACT D / TTCC F / GACT D / TACT Y / GACT / C / C / C / C / C / C / C / C	Y S GTG V TTCT. S TTCC. Y S TTCC. Y S S S S S S S S S S S S S S S S S S	C CGGG R L AGG R AAGG N AAGG CTC C CTC C C C C C C C C C C C C C C	Y P TTCC F CCTG L AGC S CTGG S CTGG S S CTGG S S CTGG S S CTGG S S S S S S S S S S S S S S S S S S	L AAG GCT A GGCC G TGC C TGC C TGC C TGC C TGC C TGC C TGC C TGC C	R ATC I V CCCC R CCCC L CCCC L CCCC L CCCC L CCCCC L CCCCC L CCCCC L CCCCC L CCCCCC	I C C C C C C C C C C C C C	TGG W P TGG W TGG W A TGG T A A A A A A A A A A A A A A A A	ATCC I CACC H GCAC A CCCG C C C C C C C C C C C C C C	CTA L GAC D CCCG P E GAC P E GAC V V TTC: aaaa aaaataga aataga	V V CTC L CTG L FGGG W TAC Y K aaggaa ctgg gaggcaag	I CGCC R AAAC N CTG G CTG G TTT F ttgag ttgag tagg	Q N CTAN L TTC: F (31 GTC: V CAC! K taa gaa gaa gtgt tatcc	V FTCC F AATCC I T T AACGC P FGC C aaag aat gga aat gga	R L L GGA G G G CC. A 33) AAC N TGA * aaa aaa gga gat	R ACC T CTG CTG L AGC S CAC H gac aga gac aga gcc acac	R M 4~2 GCG A TAC Y A AAAC N Sgag caa cac cac cac cac cac cac cac cac	GTC V F 96) GTG F TTC F TTC F acta aca gagg aac	K GCCC A CATC M CATC R R CATC R R CATC R R CTCC R R CTCCC R
1137 241 1197 261 1257 281 1317 301 1377 321 1437 341 1497 1617 1617 1617 1737	/ ACC ¹ T J GAC ¹ J TTCC F J GAC ¹ T C GAC ¹ T C C GAC ¹ T C C GAC ¹ J	Y S GTG V TCT. S TTC. F TTC. Y agg gtca aca gag	C CGGG R L AGG R AAGG N AAGG S CTC R R AAGG R R AAGG S R R R R R R R R R R R R R R R R R R	Y P F TTC F CTG CTG CTG S CTG S CTG S CTG S S S S S S S S S S S S S S S S S S S	L AAG K GGCT A GGCC C TGCC C A TGCC I a aaaa aaaaa aaaaaaaaaaaaaaaaaaaaa	R I GTC V CCGG R CCTC I CCTC V agaa aacaaaataaataagaataaataagaatga	I C C C C C C C C C C C C C C C C C C C	TGG W P TGG W W ATA A I A CATC I A agco gcta agco gcta agco gcta agco gcta agco gcta	ATCC I GCACC H A GCCACC P CCCCC P CCCCCCC P CCCCCCCCCC	CTA L D CCCG P CCCG P CCCG P C CCCG P C CCCG P C CCCG P C CCCG P C CCCG P C CCCG P C CCCG P C CCCG P C CCCG P C C CCCG P C C C C	V CTC L CTG L TGGG W TAC Y X AAG X S S S S S S S S S S S S S S S S S S	I CGCC R AAAC N CTG G CTG G TTT F ttgag ttgag ttca	Q AAC' N CTAA F GTCC V CAC' H taa gaaa gtgt tatcc ctccg ccac	V FTC F ACCG T T ACCG P F C C C C C C C C C C C C C C C C C C	R L L GGA G G CCC. A 33) AAC N TGA * aaa aaa gga gat agta	R T CTG L AGCC S CTG S CTG S CACC H gac agaa gac agaa gac	R M 4-22 GCGG A TAC Y R AAAC N gag caa cac cac cac cac cac cac cac cac	GTC V F 96) GTG F TTC F acta acag agg aacta agg	K GCCG A CATG M CATG R R CATG R R CATG R R CTCG R R CTCG R R CTCCCCCCCCCCCCC

Figure S2. Characteristics of gene structure and the deduced amino acid sequence of *LcMtnr1a2-like*.The phosphorylation sites predicted with NetPhos 3.1 Server are marked by solid dots in three difficult colors (Ser, Tyr and green are in blue, orange and green, respectively); the N-linked glycosylation sites predicted with NetNGlyc 1.0 Server are highlighted by red triangles; 7TM domains predicted with I-TASSER are labeled in boxes in 7 different colors; the NRY, CYICHS and NAXXY sequences predicted with PROSITE are labeled in brown, pink and gray boxes, respectively. TM: transmembrane.

LcMtnr1b1

	LcMtnr1b1
1	agggcatcacagatggttaggg
23	aagacgatttgttcccccgtttgcacagagaatagcaaattacatcggaaggactccggg
83	cggttcagtggtttgatattttagagaggaatgtttttttccctcaatgtgggcgcatgc
143	agacgactgggagttcgagatgccaaccagcaagccagagacacctgacgaggatggaga
203	cgtgaaatctgagtgctctggggattttttaatgacataatttctaaaggactattaaat
263	tacattttctttttcagggaggaggtgtggcaccacagcgtgtccgaccagcttccagtg
323	gcgcatggatttatgacttttgtgcgaagacaaagaaaagacaagaagagtctacgtaac
383	ttatataggtcacacccacgccacataatatcacctaactcatatcgtctttaagtaga
443	actcggggaggcacccaggtgcgctccatgtttcattcaggacgcaccggtaccggcggt
503	acctgcgggacataaacgcacagttggaacgcgagagcagcgttgggctgtgggccagtg
563	ATGCCGGACACATTCACACTCATAAAGAACCGGACAGAGCCACGGCTGGGGCAGCTAGAG
	M P D T F T L I K N R T E P R L G Q L E
1	
623	CGCACACTGGACACAGAGGGAAGCGCCCGCCCGCCTGGGTCATAGGAATCCTGGCCAGC
21	R T L D T E G S A R P A W V I G I L A S
	• • • TM1 (37~59) •
683	GTGTTGATCTTCACCACGGTGGTGGACGTGTTGGGGGAATCTGCTGGTCATCATCTCGGTG
41	V L I F T T V V D V L G N L L V I I S V
11	
743	TTCCGGAACCGTAAGCTGAGGAACTCGGGTAATGTGTTTGTGGTCAGTTTGGCATTTGCT
51	F R N R K L R N S G N V F V V S L A F A
)1	• TM2 (72~94)
0.2	
803	GACCTTGTGGTAGCCTTCTACCCCTACCCCTTGGTTCTCTATGCTCTCTTCCACGATGGA
31	D L V V A F Y P Y P L V L Y A L F H D G
63	TGGGCACTGGGAAACACACAATGCATGGTCAGTGGTTTCCTGATGGGGGCTGAGTGTCATC
01	W A L G N T Q C M V S G F L M G L S V I
	TM3 (109~131)
22	GGCTCCATTTTCAACATCACTGGGATTGCAGTGAACAGATACTGCTACATCTGTCACTCA
23	
21	G S I F N I T G I A V N R Y C Y I C H S
83	TTCTCTTACAGTCGGCTGTACAGCTATCGCAACACTCTGCTGTTTGTT
41	FSYSRLYSYRNTLLFVALIW
	• TM4 (152~174)
1043	GTGCTTACAATTGTGGCCATTATCCCCCAATTTCTTTGTTGGCTCCTTGCGCTACGACCCG
	V L T I V A I I P N F F V G S L R Y D P
161	V D I I V K I I I W I I V O S D K I D I
100	CGGGTATACTCTTGCACCTTTGCCCAGAATGTCAGCAGTTCCTACACAGTGGCAGTAGTA
103	
81	RVYSCTFAQNVSSSYTVAVV
163	GTGGTTCACTTCTTGGTTCCCATTGCAGTGGTTACCTTCTGTTATCTACGCATCTGGGTG
)1	V V H F L V P I A V V T F C Y L R I W V
	TM5 (199~221)
223	CTTGTGATTCAGGTGCGACGCAAAGTGAAGACAGAGGAGAGCCCTCGCCTCAGGCCAAGT
	LVIQVRRKVKTEESPRLRPS
21	
283	GACTTGCGGAATTTCATCACCATGTTCGTGGTCTTTGTGCTGTTTGCCATCTGCTGGGCT
41	D L R N F I T M F V V F V L F A I C W A
	TM6 (248~270)
343	CCACTTAACCTGATCGGCTTGGCGGTGGCCATAGATCCATCC
61	P L N L I G L A V A I D P S H V A P H I
403	CCTGAGTGGCTTTTTGTGGTCAGCTACTTCATGGCCTACTTTAATAGCTGTCTGAATGCC
81	
1	PEWLFVVSYFMAYFNSCLNA
	TM7 (285~307)
163	ATTATATATGGCTTACTCAACAGGAATTTCAGGAATGAGTACAAACGCATTGTCACCTCC
01	IIYGLLNRNFRNEYKRIVTS
	• • • •
523	GTATGGGTGACGCGACTTTTTGTGACAGAGACTTCGCGGGCTGCAACGGACGG
21	V W V T R L F V T E T S R A T D G R S
	• • • •
583	ATGAGGAGCAAGCAGTCACCACCTCCACCGCTCAATAACAACGAGTCAGGAGCAGCACGC
41	M R S K Q S P P P P L N N N E S G A A R
612	ACAAACAAAGAATGA actiggacctagaaactcggaccatttaccattaaggacaaaaat
643	
61	TNKE*
703	
	acactgtaagtctgcgatcacgtcgatttctcatagttaagtgttcactttgactttatg
763	taccgagctgaacatggatctttgagcctggtaaatggtaattcctgtttttatgtgaca
823	ttcagacgctagtgcagctaaagagtatcaattcacaagtgaaactgaaatacatggctc

44

Figure S3. Characteristics of gene structure and the deduced amino acid sequence of *LcMtnr1b1-like*.The phosphorylation sites predicted with NetPhos 3.1 Server are marked by solid dots in three difficult colors (Ser, Tyr and green are in blue, orange and green, respectively); the N-linked glycosylation sites predicted with NetNGlyc 1.0 Server are highlighted by red triangles; 7TM domains predicted with I-TASSER are labeled in boxes in 7 different colors; the NRY, CYICHS and NAXXY sequences predicted with PROSITE are labeled in brown, pink and gray boxes, respectively. TM: transmembrane.

LcMtnr1b2

aat		tgg									cac	tgg						ga
		gta aaa																
ATG	TCČ	ATG	CAA	GAA	GĂĂ		CAA	CTG	CTG	GAG	ATC	GCA	AAT	GAC	GGC	GCC	AGT	GT
Μ	S	М	Q	Е	E	D	Q	L	L	Е	Ι	A	Ν	D	G	A	S	V
~~~	220	AAC	mam	~~~	com	cimm	acc	C 3 0		CIEC	2.00	~~~		mee	~~~	-		
D	N	N	S	D	GGT	V	R	D	K	V	M	A	V	W	O	Y	Q	R
D	À	14	5	D	0	v	K	D	11	v	11	п		n	×	+	×	IX
CTA	ACA	CAG	CGC	GTG	AAA	AAC	CCT	GTT	GCC	ATT	GCC	AAC	ATC	CTA	TCT	GTG	GAA	GCC
L	Т	Q	R	V	K	N	Ρ	V	A	Ι	Α	Ν	I	L	S	V	Е	A
	•					-	01020	13000	1.000		TM		52-			Sera		was
V	F	C		D									F	N	GAC D	N	CTG	TTT:
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CTC	CTT	CTG	TCC	TTT	ACA	GGA	AAT	GTG	TTT	GTG	GTG	AGT	CTG	GCC	TTC	GCT	GAC	TTC
L	L	L	S	F	Т	G	Ν	v	F	V	V	S	L	A	F	A	D	L
			•		•					TN	12	(91/	-11	2)				
		TTC															TGG	
V	Α	F	Y	Ρ	Y	Ρ	L	V	L	Y	A	Ι	F	Н	D	G	W	S
~~~		GCC		mee		CIEC	a cim	cca	mmc	ama	2.00	~~~~		a cm	CIE	2 000	cca	ma
G	D	A	O	C	K	V	S	G	F	L		GGC	L	S	V	T	GGGC	S
9	2		×	0	10	1	2	0	TN	_		1-1		5		-	0	-
TTC	AAC	ATA	ACA	GGC	ATT	GCT	ATC	AAC						TGC	CAC	AGC	TTC	AG
F	Ν	I	Т	G	Ι	A	I	Ν	R	Y	С	Y	I	С	Н	S	F	S
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D	K	L	Y	S	Y	R	Ν	Т	L	L	L	V	A	L	I	W	L	L
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V	V	A	T	V	P	N	F	F	V	G	S	L	Q	Y	D	P	R	V
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TCA	TGC	ACA	TTT	GCA	CAG	ACA	GTC	AGC	ACC	TCA	TAC	ACC	ATT	ACA	GTG	GTG	GTT	ATC
S	С	т	F	A	Q	Т	V	S	Т	S	Y	Т	Ι	Т	V	V	V	I
•		•						•	•	•				•	TN		(21	
	mmm	GTT																GTO
			P	I	A	V	V	Т	F	С	Y	L	R	I	W	I	L	V
F	F	V									TCA	CGC	ATC	AAG	ccc	AGT	CAC	CIM7
F	F	V	CGG	AAG	GTA	AAG	TCA	GAG	GTC	CGT								C17
F	F		CGG R	AAG K	GTA V	AAG K	TCA	GAG	GTC	CGT R	S	R	I	K	Ρ	S	D	L
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F CAG Q AAC	F GTG V	R	R	K ATG	V	K GTG	S	E	V GTG	R	• TTT	GCC		TGT	TGG	GCA	D	L
F Q AAC	F GTG V TTT	R R R R TATC I	R ACC T	K ATG M	v	K	s	Е	V	R	•				5	õ	D	L
F Q AAC N	F GTG V TTT F	R R TATC I	R ACC T 4~2	к Атс М 85)	V TTT F	K GTG V	S GTG V	E TTT F	V GTG V	R CTA L	• TTT F	GCC	ATT I	TGT C	TGG W	GCA A	D CCA P	L CTC
F Q AAC N TTT	F V TTTT F 16	AGG R ATC I (26- CGGG	R ACC T 4~2 CTT	K ATG M 85) GCT	V TTT F GTG	K GTG V GCT	S GTG V	E TTT F	V GTG V CCT	R CTA L GAA	TTT F GCA	GCC A GTG	ATT I GTA	C C C	TGG W CGC	GCA A	D CCA P	L
F Q AAC N	F GTG V TTT F	R R TATC I	R ACC T 4~2	к Атс М 85)	V TTT F	K GTG V	S GTG V	E TTT F	V GTG V	R CTA L	• TTT F	GCC	ATT I	TGT C	TGG W	GCA A	D CCA P	L CTC
F Q AAC N TTT F	F V TTT F 16 ATT I	R R I (26- GGGG G	R ACC T 4~2 CTT L	K ATG M 85) GCT A	V TTT F GTG V	K GTG V GCT A	S GTG V ATT	E TTT F AAC N	V GTG V CCT	R CTA L GAA E	F GCA A	GCC A GTG V	ATT I GTA V	C C C C C C C C C	TGG W CGC R	A A A A T A T C	D P CCA P	L CTC L GAC
F Q AAC N TN FTT	F V TTT F 16 ATT I	AGG R ATC I (26- CGGG	R ACC T 4~2 CTT L	K ATG M 85) GCT A	V TTT F GTG V	K GTG V GCT A	S GTG V ATT	E TTT F AAC N	V GTG V CCT	R CTA L GAA E	F GCA A	GCC A GTG V	ATT I GTA V	C C C C C C C C C	TGG W CGC R	A A A A T A T C	D P CCA P	L CT L GA E
F Q AAAC N TN TTT F CTC L	F GTG V TTT F A16 PATT I TTT F	R R I (26- G G G G G G G G G G G G G G G G G G G	R T 4~2 CTT L GTC V 1~3	K ATG M 85) GCT A A CT S 19)	V TTT F GTG V TAC	K GTG V GCT A TTC F	S GTG V ATT I ATG M	E TTT F AAC N GCT A	V GTG V CCT P TAC	R L GAA E TTC F	GCA A A A A A A A A A	GCC A GTG V AGT S	ATT I GTA V TGC	C C C C C C C C C C C C C C C C C C C	TGG W CGC R AAT	GCA A A CATC I GCC A	D P CCA P SATC I	L CTC L GAC E SATC
F CAG Q AACON TTTT F CTC L TN GGC	F CTTT F A16 CTTT F CTTT F CTG	R R I (26- G G G G C T G C T G C T G C T G	R ACC T 4~2 CTT L GTC V 1~3 AAC	K ATG M 85) GCT A CAGC	V TTT F GTG V TAC Y	K GTG V GCT A TTC F	S GTG V ATT I ATG M	E TTT F N GCT A	V GTG V CCT P TAC Y GAG	R CTA L GAA E TTC F	GCA A AAC N	GCC A GTG V AGT S CGC	ATT I GTA V TGC C ATC	CCT CCT CTT L	TGG W CGC R AAT	GCA A A CATC I GCC A	D CCA P CCA P SATC	L L L GAC E E CAT(I I TG(
F CAG Q AAC N TN TTT F CTC L	F GTG V TTT F A16 PATT I TTT F	R R I (26- G G G G G G G G G G G G G G G G G G G	R T 4~2 CTT L GTC V 1~3	K ATG M 85) GCT A A CT S 19)	V TTT F GTG V TAC	K GTG V GCT A TTC F	S GTG V ATT I ATG M	E TTT F AAC N GCT A	V GTG V CCT P TAC	R L GAA E TTC F	GCA A A A A A A A A A	GCC A GTG V AGT S	ATT I GTA V TGC	C C C C C C C C C C C C C C C C C C C	TGG W CGC R AAT	GCA A A CATC I GCC A	D P CCA P SATC I	L CTC L GAC E SATC
F CAG Q AAC N TT F CTC L TT GGC G	F V TTTT F 16 TTTT F V 77 CTG L	AGG R ZATC I COGG G G C C G C C G C C G C C G C C G C	R T 4~2 CTT L GTC V 1~3 AAC	K M 85) GCT A S 19) CAG	V TTT F GTG V TAC Y N	K GTG V GCT A TTC F TTC F	S GTG V ATT I ATG M CGC R	E TTTT F AACC N GCCT A R	V GTG V CCT P TAC Y GAG	R CTA L GAA E TTC F TTC F Y	GCA A A AAC N AAAC K	GCC A GTG V AGT S CGC R	ATT I GTA V TGC C ATC I	TGT C C C C C T L C C T L	TGG W CGC R AAT	A A A A A C A C C C C C C C C C A C C C A C C A C C A C C A C C A C C A C C A C C A C C A C C A C C A C C C C A C	D P P P P P P P T T CCA P P T T CCA P P P P P P P P P P P P P P P P P P	L GACIC L CATC I STGC W
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F CAG Q AACON TTT F CTC L TN GGC G G CCA	F V TTT F A16 PATT I F TTT F U 7 CTG L CAC H	AGG R I (26- G G G G C G C C G C C C G C C C C C C	R T 4~2 CTT L GTC V 1~3 AAC N TTC F	K M 85) GCT A A A CAG S 19) CAG Q TTC F	V TTT F STG V TAC Y AAC N CAG Q	K GTG V GCT A TTC F TTC F GAG E	S GGTG V ATT I ATG M CCGC R ACA T	E TTTT F PAAC N SGCT A A CAGG R TCG S	V GTG V CCT P TAC Y GAG E CGG R	R L GAA E TTC F TAC Y GGGG G	GCA F A A A A A A A A A C K G G G G	GCC A GTG V AGT S CGC R ACT T	ATT I GTA V TGC C ATC I GAG E	TGT C C C C T P C T T L A T C C T C P C T T C P C C T C P C C T C P C C C C	TGG W CGC R AAT N ATG M ATG	A A A A CATCC A A CTCT S A A GCCC A K	D CCA P CCCA S CCCA P CCCA S CCCCA S CCCA S CCCA S CCCA S CCCA S CCCA S CCCA S CCCA S CCCCA S CCCA S CCCA S CCCA S CCCA S CCCA S CCCA S CCCA S CCCA S CCCA S CCCA S CCCA S CCCA S CCCA S CCCA S CCCA S CCCCCA S CCCCA S C C C C	L AGAO E E TGO W K
F CAG Q AACON TTT F CTC L TN GGC G G CCA	F V TTT F A16 PATT I F TTT F U 7 CTG L CAC H	AGG R ZATC I CGGG G G CGGG C CGGG C CGGG C C CGGG C	R T 4~2 CTT L GTC V 1~3 AAC N TTC F	K M 85) GCT A A A CAG S 19) CAG Q TTC F	V TTT F STG V TAC Y AAC N CAG Q	K GTG V GCT A TTC F TTC F GAG E	S GGTG V ATT I ATG M CCGC R ACA T	E TTTT F PAAC N SGCT A A CAGG R TCG S	V GTG V CCT P TAC Y GAG E CGG R	R L GAA E TTC F TAC Y GGGG G	GCA F A A A A A A A A A C K G G G G	GCC A GTG V AGT S CGC R ACT T	ATT I GTA V TGC C ATC I GAG E	TGT C C C C T P C T T L A T C C T C P C T T C P C C T C P C C T C P C C C C	TGG W CGC R AAT N ATG M ATG	A A A A CATCC A A CTCT S A A GCCC A K	D CCA P CCCA S CCCA P CCCA S CCCCA S CCCA S CCCA S CCCA S CCCA S CCCA S CCCA S CCCA S CCCCA S CCCA S CCCA S CCCA S CCCA S CCCA S CCCA S CCCA S CCCA S CCCA S CCCA S CCCA S CCCA S CCCA S CCCA S CCCA S CCCCCA S CCCCA S C C C C	L AGAO E E TGO W K
F CAG Q AAAC N TTT F CTC C C C C C C C C C C C C C C C	F V TTTT F CTTT F TTTT F TTTT F CTTG L CCCC H	R R I C C C C C C C C C C C C C C C C C	R ACC T 4~2 CTT L GTC V 1~3 AAC N TTC F CTC L	K ATG M 85) GCT A S S 19) CAG Q TTC F AAT N	V TTT F GTG V TAC Y AAAC N CAG Q AAAT N	K GTG V GCT A TTC F TTC F GAG E AAT N	S GTG V ATT I ATG M CCGC R R CCGC R T GAG E	E TTTT F AACC N GGCT A CAGG R TCG S CCAA	V GTG V CCT P TAC Y GAG E CGG R R GTA V	R CTA L GAA E TTC F TTC Y GGGG G AAA K	TTT F GCA A AAC N AAG K GGT G GCA A	GCC A GTG V AGT S CGC R ACT T GAG E	ATT I GTA V TGC C ATC I GAG E ACT T	TGT C C C C C C C C C C C C C C C C C C	TGG W CGC R AAT N ATG M ATG M TGA	A A A CATC I CAC A CACC A CACC K	D CCA P CCCA CCCA P CCCA P CCCA CCCCA CCCCCA CCCCA CCCA	L L GAC E SATC I W W K AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA
F Q AAC N TTT F CTC G G G G G CCA P CCA S O CCA S O O	F GGTG V TTT F A16 TTT F I TTT F I TTT F I I TTT F C TG L C C C C C C C C C C C C C C C C C C	AGG R ZATC I CGGG G G CGGG C CGGG C CGGG C CGGG C CGGG C CGGG C CGGGG C CGGGG C CGGGGGG	R ACC T 4~2 CTT L GTC V 1~3 AAC N TTC F CTC L aaaa	K ATG M 85) GCT A S S 19) CAG Q TTC F AAT N gta	V TTT F GTG V TAC Y AAAC N CAG Q AAAT N gaa	K GTG V GCT A TTC F GAG E AAT N 999	S GTG V ATT I ATG M CCGC R R CCGC R T GAG GAG E	E TTTT F PAACC N GCCT A A CCAA Q A 3993	V GTG V CCT P TAC Y GAG E CGG R GTA V	R L GAA E TTC F TTC GGGG G G AAA K aga	CA A A A A A A A A A G G C A A a g a	GCCC A GTG V AGT S CCCC R ACT T GAG E CCCC	ATT I GTA V TGC C ATC I GAG E ACT T aat	TGT C C C C C T P C T T C C C C C C C C C	TGG W CGC R AAT N ATG M ATG M TGA *	GCA A A A A A C C C A A C C C A A C C C A C C C A C C A C C A C A C C A C C A C C A C C A C C A C C A C C A C C C C A C C C C C C A C	D P P P CCCA P P CCCA P P CCCA P P CCCA P P CCCA P P CCCA P P P CCCA P P P CCCA P P P CCCA P P CCCA P P CCCA P P P CCCA P P CCCA P P CCCA P P CCCA P P CCCA P P CCCA P P CCCA CCCA P P CCCA CCCA P P CCCA CCCA P P CCCCA CCCCA CCCCA CCCCA CCCCA CCCA	L GAGA E STG W W CAAS K Atg ggt

Figure S4. Characteristics of gene structure and the deduced amino acid sequence of *LcMtnr1b2-like*.The phosphorylation sites predicted with NetPhos 3.1 Server are marked by solid dots in three difficult colors (Ser, Tyr and green are in blue, orange and green, respectively); the N-linked glycosylation sites predicted with NetNGlyc 1.0 Server are highlighted by red triangles; 7TM domains predicted with I-TASSER are labeled in the boxes in 7 different colors; the NRY, CYICHS and NAXXY sequences predicted with PROSITE are labeled in brown, pink and gray boxes, respectively. TM: transmembrane.

LcMtnr1c

LSRNH	AGAGT E S
• •	•
L A S V I	TGATC
33~55)	<u> </u>
CTGTCCGTGTACA	GGAAC
LSVYH	R N
TCCGTGGCAGACC	TGGTG
	LV
•	
CACAGTGACTGGA	
H S D W T	г м
AGCGTCATCGGCT	CCATC
SVIGS	S I
•	
C H S L H	
СНЫЦИ	1 I
CTCACCTGGCTGC	FCACC
LTWLI	L T
0	•
Y D P R	TTTAC
IDPK.	1 1
TCAGTGGTGGTTA	TCAC
SVVV	I H
	~212)
ATATGGGTGCTGG	TGATI
I W V L	/ 1
AAACCTAGTGATG	TAAGG
KPSDV	V R
TGCTGGGCTCCAC	
	I. N
	-
CCCAATATACCTG	
	E W
	00 2
TM7 (2 CTCAACGCCATCA	
TM7 (2 CTCAACGCCATCA L N A I	TATAC I Y
TM7 (2 CTCAACGCCATCAT L N A I C	TATAC I Y GCATC
TM7 (2 CTCAACGCCATCAT L N A I C	TATAC I Y
TM7 (2 CTCAACGCCATCAT L N A I C	TATAC I Y GCATC C I
TM7 (2 CTCAACGCCATCAT L N A I C CTTCTTGCTCTTTC L L A L (GGACTGAAGAGTAJ	TATAC I Y GCATC C I
TM7 (2 CTCAACGCCATCAT L N A I CTTCTTGCTCTTTC L L A L (GGACTGAAGAGTAI G L K S I	TATAC I Y GCATC C I AACCI K P
TM7 (2 CTCAACGCCATCAT L N A I C CTTCTTGCTCTTTC L L A L (GGACTGAAGAGGTAJ G L K S I TAA accggtgcttg	TATAC I Y GCATC C I AACCI K P
TM7 (2 CTCAACGCCATCAT L N A I CTTCTTGCTCTTTC L L A L (GGACTGAAGAGTAI G L K S I	GCATC C I AACCI K P gactg
TM7 (2 CTCAACGCCATCAT L N A I C CTTCTTGCTCTTTC L L A L (GGACTGAAGAGGTAJ G L K S I TAA accggtgcttg * gtgacatgattca aatcatgttcgga	TATAC I Y GCATC C I AACCI K P gactg gactg
TTAA accgdtgatta ggaaaatgttcag ggaaaatgttcag ggaaaatgttcag	TATAC IY GCATC CI AACCT KP gactg actg acct agag ttgtg
TM7 (2 CTCAACGCCATCAT L N A I C CTTCTTGCTCTTTC L L A L (GGACTGAAGAGGTAJ G L K S I TAA accggtgcttg * gtgacatgattca aatcatgttcgga	TATAC I Y GCATC C I AACCI K P gactg acct tagag ttgtg acac

Figure S5. Characteristics of gene structure and the deduced amino acid sequence of *LcMtnr1c-like*. The phosphorylation sites predicted with NetPhos 3.1 Server are marked by solid dots in three difficult colors (Ser, Tyr and green are in blue, orange and green, respectively); the N-linked glycosylation sites predicted with NetNGlyc 1.0 Server are highlighted by red triangles; 7TM domains predicted with I-TASSER are labeled in the boxes in 7 different colors; the NRY, CYICHS and NAXXY sequences predicted with PROSITE are labeled in brown, pink and gray boxes, respectively. TM: transmembrane.

LcMtnr1a1	SSPDPTTTVLNHPPWVTT	28
LcMtnr1a2	MLNGPTFRDRDPMRLVDPRHLPQLMSLEDHEPTMVEGTLVPRNSTPAGE- GTPGQQHQSFPWVVT	65
SsMtnr1aaα	MERRKATGEYHGIPVSKM <mark>S</mark> SLDPY <mark>E</mark> EVLN <mark>H</mark> PPWVTT	36
SsMtnr1aaβ	SSLDFYREVLNRPPWVTT	28
SsMtnr1a EcMtnr1a	SSVAPNDTTLNBPPWVAT	29
DIMtnr1a	SSPKPSTVIN PPWVTT MITNGSHLNSSSPDPALAVIN PPWVTT	28 28
TaMtnr1a	SAPDPSCARLYRPPWVTT	28
MmMtnr1a	ATQQAPGGGEGGRPHPSWLAS	31
SgMtnr1a	SAPDPS AVLS PPWVT	28
LcMtnr1a1	TLGCELIETIVVDILGNLLVIFSV <mark>YRNERLE</mark> NAGNIEVVSLAVADLVVAI <mark>Y</mark> FYPLVL <mark>TSIFE</mark> NGWNLGYA	98
LcMtnr1a2	LLAGVLITTIVVOVIGNLLVIVSVFRNERLEKAGNAFVVSLALADLVVAIYPYPLVLTAIFHDGWIAGYI	135
SsMtnr1aaa		106 98
SsMtnr1aaβ SsMtnr1a	TLGCFLIFTIVVDILGNLLVIFSVYRNKKLENAGNIFVVSLAVADLVVAINFYPLVLTSIFHKGWNLGYV TLGCFLIFTIVVDILGNLLVIISVYRNKKLENAGNVFVVSLAVADLVVAFYPYPLVLSSIFNNGWNLGFI	99
EcMtnr1a	TLGCFLIFTIIVDILGNLLVIFSVYRNKKLPNAGNIFVVSLAVADLVVAIYFYPLVLTSIFFNGWNLGYV	98
DIMtnr1a	TLGCFLIFTIVVDILGNLLVIFSVYRNKYLHNAGNIFVVSLAVADLVVAIYFYPLVLTSIFHNGWNLGYV	98
TaMtnr1a	TLGCFLIFTIVVDILGNLLVIFSVYRNKKLENAGNIFVVSLAVADLVVAIYPYPLVLTSIFHNGWNLGSV	98
MmMtnr1a	TLAFILIFTIVVDILGNLLVILSVYRNKKLENSGNIFVVSLAVADLVVAVYFYPLVLTSILNNGWNLGYL	101
SgMtnr1a	TLGCELIETIIV ILGNLLVIFSVYHNKKLMAGNIEVVSLAVALLVVAIYFYPLVLSSIE NGWNLGYV	98
LcMtnr1a1	HCQISGFIMGVSVIGSIFNITGIAINRYCYICHSLKYDYLYS <mark>D</mark> KMSVCYVMLIWALTVVAIVFNLFVGSL	168
LcMtnr1a2	HCOISGFLMGLSVIGSIFNITGIAINRYCYIC SLAYD ALFSNSNTMCYVVLVWALTILAIVPNWFVESL HCOISGFLMGVSVIGSIFNITGIAINRYCYIC SLAYD ALYS MNSVCYVLLIWALTIVAIVPNLFVGSL	205
SsMtnr1aaα SsMtnr1aaβ	eccisgflmgvsvigsifnitgiainbycviceslkydklysdknsvcyvlliwaltivaivpnlfvgsl eccisgflmgisvigsifnitgiainbycviceslkydklysdknsvcyvlliwaltivaivpnlfvgsl	168
SsMtnr1a	HCOVSGPLMGLSVIGSIFNITGIAINBYCYICHSLEVERLYSDKNSLCYVLLIWLLTVVALVPNFFVGSL	169
EcMtnr1a	- COISGFLMGVSVIGSIFNITGIAINFYCYIC'SLKYDKLYSCKNSVCYVMLIWALTVVAIVFNLFVGSL HCOISGFLMGVSVIGSIFNITGIAINFYCYIC'SLKYDKLYSCKNSVCYVMLIWALTVVAIVFNLFVGSL	168
DIMtnr1a	HCQISGFLMGVSVIGSIFNITGIAINFYCYICHSLKYDKLYSDKNSVCYVMLIWALTVVAIVPNLFVGSL	168
TaMtnr1a	COISCFLMCVSVIGSIFNITGIAINBYCYIC SLRYD LYSDRNSVCYVMLIWLLIVVAIVPNLFVGSL COVSAFLMCLSVIGSIFNITGIANNBYCYIC SLRYD IYSN NSLCYVFLIWMLTLIAIMPNLCIGIL	168
MmMtnr1a		171
SgMtnr1a	COISGELMGVSVIGSIFNITGIAINEYCYICESLEYDELYSENSVCYVMLIWALTVVAIVPNLEVGSL	168
LcMtnr1a1	QYPPVYSCTFEQSASSAYTIAVVFFHFILPIMIVTYCYLEIWILVIQVREAVKPDNAPFLTFFQVENFV	238
LcMtnr1a2	QY <mark>I</mark> PHVYSCTEAQSVSSLYTITVVVVHFILPIAIVTYCYLRIWILVIQVRRRVMPDS PFIKPHDLRNFL	275
LcMtnr1a2 SsMtnr1aaα	QY <mark>T</mark> PRVYSCTFAQSVSSLYTITVVVV FILPIAIVTYCYLRIWILVIQVRRVN FPSHPNIKF <mark>D</mark> LRNFL QYTPRVYSCTFEQSASSAYTIAVVFFHFILPIMIVTYCYLRIWILVIQVRRVMPDNHPNLTPNUVRNFV	275 246
LcMtnr1a2 SsMtnr1aaα SsMtnr1aaβ	QY <mark>T</mark> PRVYSCTFAQSVSSLYTITVVVVHFILPIAIVTYCYLRIWILVIQVRRRVAFTSHPXIKFTDLRNFL QYTPRVYSCTFEQSASSAYTIAVVFFHFILPIMIVTYCYLRIWILVIQVRRRVAPDNAPXLTPN QYTPRVYSCTFEQSASSAYTIAVVFFHFILPIMIVTYCYLRIWILVIQVRRRVAPDNAFXLTFDVRNFV	275 246 238
LcMtnr1a2 SsMtnr1aaα	OYDPRVYSCTFAQSVSSLYTITVVVV FILPIAIVTYCYLAIWILVIQVRRVYFLSHPRIKF DLRNFL OYDPRVYSCTFEQSASSAYTIAVVFFHFILPIMIVTYCYLAIWILVIQVRRVXPDNHPRLTFN VRNFV OYDPRVYSCTFEQSASSAYTIAVVFFHFILPIMIVTYCYLAIWILVIQVRRVXPDNHPRLTF DVRNFV OYDPRVYSCTFVQSANSAYTIAVVFFHFILPIMIVTYCYLAIWILVIQVRRVXPEFHFILTF DVRNFV	275 246
LcMtnr1a2 SsMtnr1aaα SsMtnr1aaβ SsMtnr1a	QYDPRVYSCTFAQSVSSLYTITVVVV FFILPIAIVTYCYLEIWILVIQVRRRVAFPS FPRIKFDLRAFI QYDPRVYSCTFEQSASSAYTIAVVFFHFILPIMIVTYCYLEIWILVIQVRRRVAFDAFPRLTFADVRAFV QYDPRVYSCTFEQSASSAYTIAVVFFHFILPIMIVTYCYLEIWILVIQVRRRVAFDAFPRLTFDVRAFV QYDPRVYSCTFVQSANSAYTIAVVFFHFILPIMIVTYCYLEIWILVIQVRRRVAFFFPRLTFDVRAFV QYDPRVYSCTFEQSASSAYTIAVVFFHFILPIMIVTYCYLEIWILVIQVRRRVAFFFPRLTFDVRAFV	275 246 238 239
LcMtnr1a2 SsMtnr1aaα SsMtnr1aaβ SsMtnr1a EcMtnr1a	QYT PRVYSCTFAQSVSSLYTITVVVVHFILPIAIVTYCYL IWILVIQVRRAV PTSPPNIK FOLRAFI QYT PRVYSCTFEQSASSAYTIAVVFFHFILPIMIVTYCYL IWILVIQVRRAVFPNN PRLTPN VNRAV QYT PRVYSCTFEQSASSAYTIAVVFFHFILPIMIVTYCYL IWILVIQVRRAVFPNN PRLTF DVRAFU QYT PRVYSCTFEQSASSAYTIAVVFFHFILPIMIVTYCYL IWILVIQVRRAVFPNN PRLTF DVRAFU QYT PRVYSCTFEQSASSAYTIAVVFFHFILPIMIVTYCYL IWILVIQVRRAVFPNN PRLTF DVRAFU QYT PRVYSCTFEQSASSAYTIAVVFFHFILPIMIVTYCYL IWILVIQVRRAVFPNN PRLTF DVRAFU QYT PRVYSCTFEQSASSAYTIAVVFFHFILPIMIVTYCYL IWILVIQVRRAVFPNN PRLTF DVRAFU	275 246 238 239 238 238 238
LcMtnr1a2 SsMtnr1aaα SsMtnr1aaβ SsMtnr1a EcMtnr1a DIMtnr1a TaMtnr1a MmMtnr1a	QYT PRVYSCTFAQSVSSLYTITVVVVHFILPIAIVTYCYL IWILVI QVRRRVNPTSHPNIKFTDLRNFL QYT PRVYSCTFE QSASSAYTIAVVFFHFILPIMIVTYCYL IWILVI QVRRRVNPDN PRLTPN VNRV QYT PRVYSCTFE QSASSAYTIAVVFFHFILPIMIVTYCYL IWILVI QVRRRVNPDN PRLTF DVRNFV QYT PRVYSCTFE QSASSAYTIAVVFFHFILPIMIVTYCYL IWILVI QVRRRVNPDN PRLTF DVRNFV	275 246 238 239 238 238 238 238 238
LcMtnr1a2 SsMtnr1aaα SsMtnr1aaβ SsMtnr1a EcMtnr1a DIMtnr1a TaMtnr1a	QYT PRVYSCTFAQSVSSLYTITVVVVHFILPIAIVTYCYL IWILVIQVRRAV PTSPPNIK FOLRAFI QYT PRVYSCTFEQSASSAYTIAVVFFHFILPIMIVTYCYL IWILVIQVRRAVFPNN PRLTPN VNRAV QYT PRVYSCTFEQSASSAYTIAVVFFHFILPIMIVTYCYL IWILVIQVRRAVFPNN PRLTF DVRAFU QYT PRVYSCTFEQSASSAYTIAVVFFHFILPIMIVTYCYL IWILVIQVRRAVFPNN PRLTF DVRAFU QYT PRVYSCTFEQSASSAYTIAVVFFHFILPIMIVTYCYL IWILVIQVRRAVFPNN PRLTF DVRAFU QYT PRVYSCTFEQSASSAYTIAVVFFHFILPIMIVTYCYL IWILVIQVRRAVFPNN PRLTF DVRAFU QYT PRVYSCTFEQSASSAYTIAVVFFHFILPIMIVTYCYL IWILVIQVRRAVFPNN PRLTF DVRAFU	275 246 238 239 238 238 238
LcMtnr1a2 SsMtnr1aaα SsMtnr1aaβ SsMtnr1a EcMtnr1a DIMtnr1a TaMtnr1a MmMtnr1a SgMtnr1a LcMttnr1a1	QYT PRVYSCTFAQSVSSLYTITVVVVHFILPIAIVTYCYLAIWILVIQVRRAVAPDS PNIKFADLANFL QYT PRVYSCTFAQSASSAYTIAVVFFHFILPIMIVTYCYLAIWILVIQVRRAVAPDS PNLTPD VRNFV QYT PRVYSCTFAQSASSAYTIAVVFFHFILPIMIVTYCYLAIWILVIQVRRAVAPDS PNLTFD VRNFV QYT PRVYSCTFAQSASSAYTIAVVFFHFILPIMIVTYCYLAIWILVIQVRRAVAPDS PNITFD VRNFV	275 246 238 239 238 238 238 241 238 308
LcMtnr1a2 SsMtnr1aaα SsMtnr1aaβ SsMtnr1a EcMtnr1a DIMtnr1a TaMtnr1a SgMtnr1a LcMttnr1a1 LcMttnr1a2	QYT PRVYSCTFAQSVSSLYTITVVVVHFILPIAIVTYCMLEIWILVIQVRRAVPDSSPNIKFOLENFL QYT PRVYSCTFEQSASSAYTIAVVFFHFILPIMIVTYCMLEIWILVIQVRRAVAPDN PRLTFDVRNFV QYT PRVYSCTFQSASSAYTIAVVFFHFILPIMIVTYCMLEIWILVIQVRRAVAPDN PRLTFDVRNFV QYT PRVYSCTFQSASSAYTIAVVFFHFILPIMITVICMLEIWILVIQVRRAVAPDN PRITFDVRNFV QYT PRVYSCTFQSASSAYTIAVVFFHFILPIMITVICMLEIWILVIQVRRAVAPDN PRITFDVRNFV QYT PRVYSCTFQSASSAYTIAVVFFHFILPIMITVICMLEIWILVIQVRRAVAPDN PRITFDVRNFV QYT PRVYSCTFQSASSAYTIAVVFFHFILPIMITVICMLEIWILVIQVRRAVAPDN PRITFDVRNFV QYT PRVYSCTFQSASSAYTIAVVFFHFILPIMITVICMLEIWILVIQVRRAVAPDN PRITFDVRNFV	275 246 238 239 238 238 238 241 238 308 344
LcMtnr1a2 SsMtnr1aaα SsMtnr1aaβ SsMtnr1a EcMtnr1a DIMtnr1a TaMtnr1a SgMtnr1a LcMttnr1a1 LcMtnr1a2 SsMtnr1aaα	QYT PRVYSCTFAQSVSSLYTITVVVVHFILPIAIVTYCYLAIWILVIQVRRVNPDS PRIKPADLENFL QYT PRVYSCTFEQSASSAYTIAVVFFHFILPIMIVTYCYLAIWILVIQVRRVNPDN PRLTPD VRNFV QYT PRVYSCTFEQSASSAYTIAVVFFHFILPIMIVTYCYLAIWILVIQVRRVNPDN PRLTPD VRNFV QYT PRVYSCTFEQSASSAYTIAVVFFHFILPIMIVTYCYLAIWILVIQVRRVNPDN PRLTPD VRNFV QYT PRVYSCTFEQSASSAYTIAVVFFHFILPIMIVTYCYLAIWILVIQVRRVNPDN PRITFD VRNFV QYT PRVYSCTFEQSASSAYTIAVVFFHFILPIMIVTYCYLAIWILVIQVRRVPDN PRIFFD VRNFV QYT PRVYSCTFEQSASSAYTIAVVFFHFILPIMIVTYCYLAIWILVIQVRRVPDN PRIFFD VRNFV QYT PRVYSCTFEQSASSAYTIAVVFFHFILPIMIVTYCYLAIWILVIQVRRVPDN PRIFFD VRNFV QYT PRVYSCTFEQSASSAYTIAVVFFHFILPIMIVTYCYLAIWILVIQVRRVPDN PRIFFD VRNFV TYPVYNANTATAVANANNFYNNN PRIFFT QYNFY	275 246 238 239 238 238 238 241 238 308 344 316
LcMtnr1a2 SsMtnr1aaα SsMtnr1aaβ SsMtnr1a EcMtnr1a DiMtnr1a TaMtnr1a SgMtnr1a LcMttnr1a1 LcMtnr1a2 SsMtnr1aaα SsMtnr1aaα	QYT PRVYSCTFAQSVSSLYTITVVVVHFILPIAIVTYCYL IWILVIQVRRVNPTS PRIKPEDLENFL QYT PRVYSCTFEQSASSAYTIAVVFFHFILPIMIVTYCYL IWILVIQVRRVNPDN PRLTPD VRNFV QYT PRVYSCTFEQSASSAYTIAVVFFHFILPIMIVTYCYL IWILVIQVRRVNPDN PRLTF DVRNFV QYT PRVYSCTFEQSASSAYTIAVVFFHFILPIMIVTYCYL IWILVIQVRRVNPDN PRLTF DVRNFV QYT PRVYSCTFEQSASSAYTIAVVFFHFILPIMIVTYCYL IWILVIQVRRVNPDN PRLTF DVRNFV QYT PRVYSCTFEQSASSAYTIAVVFFHFILPIMIVTYCYL IWILVIQVRRVNPDN PRITF DVRNFV TYPRVYSCTFEQSASSAYTIAVVFFHFILPIMIVTYCYL IWILVIQVRRVNPDN PRITF DVRNFV QYT PRVYSCTFEQSASSAYTIAVVFFHFILPIMIVTYCYL IWILVIQVRRVNPDN PRITF DVRNFV TYPRVYSCTFEQSASSAYTIAVVFFHFILPIMIVTYCYL IWILVIQVRRVNPDN PRITF DVRNFV QYT PRVYSCTFEQSASSAYTIAVVFFHFILPIMIVTYCYL IWILVIQVRRVNPDN PRITF DVRNFV TYPVFVLFAVCNAPLNFIGLAVAIKPEVVPLIPFWLFVASYFMAYFNSCINAVY SVLNONFFREYF TYPVFVLFAVCNAPLNFIGLAVAINPEVVPLIPFWLFVASYFMAYFNSCINAVY SVLNONFFREYFR TYPVFVLFAVCNAPLNFIGLAVAINPEVVPLIPFWLFVASYFMAYFNSCINAVY SVLNONFFREYFR	275 246 238 239 238 238 241 238 308 344 316 308
LcMtnr1a2 SsMtnr1aaα SsMtnr1aaβ SsMtnr1a EcMtnr1a DIMtnr1a TaMtnr1a SgMtnr1a LcMttnr1a1 LcMtnr1a2 SsMtnr1aaα	QYT PRVYSCTFAQSVSSLYTITVVVVHFILPIAIVTYCYL IWILVIQVRRVNPIS PNIKPID LRNFL QYT PRVYSCTFEQSASSAYTIAVVFFHFILPIMIVTYCYL IWILVIQVRRVNPIN PRLTPD VRNFV QYT PRVYSCTFEQSASSAYTIAVVFFHFILPIMIVTYCYL IWILVIQVRRVNPIN PRLTF DVRNFV QYT PRVYSCTFEQSASSAYTIAVVFFHFILPIMIVTYCYL IWILVIQVRRVNPIN PRITF DVRNFV QYT PRVYSCTFEQSASSAYTIAVVFFHFILPIMIVTYCYL IWILVIQVRRVNPIN PRITF DVRNFV QYT PRVYSCTFEQSASSAYTIAVVFFHFILPIMIVTYCYL IWILVIQVRRVNPIN PRITF DVRNFV QYT PRVYSCTFEQSASSAYTIAVVFFHFILPIMIVTYCYL IWILVIQVRRVNPIN PRITF DVRNFV TYPVFVLFAVCWAPLNFIGLAVAIKPEVVPLIPFWLFVASYFMAYFNSCINAIVY GVLNONFKRYM TMFVVFVLFAVCWAPLNFIGLAVAINFFULPINVTYCYL IWILVIQVRRVNFSCINAIVY GVLNONFKRYM TMFVVFVLFAVCWAPLNFIGLAVAINFEVVPLIPFWLFVASYFMAYFNSCINAIVY GVLNONFKRYM TMFVVFVLFAVCWAPLNFIGLAVAINFEVVPLIPFWLFVASYFMAYFNSCINAIVY GVLNONFRRYM TMFVVFVLFAVCWAPLNFIGLAVAINFEVVPLIPFWLFVASYFMAYFNSCINAIVY GVLNONFRRYM TMFVVFVLFAVCWAPLNFIGLAVAINPEVVPLIPFWLFVASYFMAYFNSCINAIVY GVLNONFRRYM	275 246 238 239 238 238 238 241 238 308 344 316
LcMtnr1a2 SsMtnr1aaα SsMtnr1aaβ SsMtnr1a EcMtnr1a DIMtnr1a TaMtnr1a MmMtnr1a SgMtnr1a LcMttnr1a2 SsMtnr1aaα SsMtnr1aaβ SsMtnr1aaβ	QYT PRVYSCTFAQSVSSLYTITVVVVHFILPIAIVTYCYL IWILVIQVRRVNPIS PNIKPID LRNFL QYT PRVYSCTFEQSASSAYTIAVVFFHFILPIMIVTYCYL IWILVIQVRRVNPIN PRLTPD VRNFV QYT PRVYSCTFEQSASSAYTIAVVFFHFILPIMIVTYCYL IWILVIQVRRVNPIN PRLTF DVRNFV QYT PRVYSCTFEQSASSAYTIAVVFFHFILPIMIVTYCYL IWILVIQVRRVNPIN PRITF DVRNFV QYT PRVYSCTFEQSASSAYTIAVVFFHFILPIMIVTYCYL IWILVIQVRRVNPIN PRITF DVRNFV QYT PRVYSCTFEQSASSAYTIAVVFFHFILPIMIVTYCYL IWILVIQVRRVNPIN PRITF DVRNFV QYT PRVYSCTFEQSASSAYTIAVVFFHFILPIMIVTYCYL IWILVIQVRRVNPIN PRITF DVRNFV TYPVFVLFAVCWAPLNFIGLAVAIKPEVVPLIPFWLFVASYFMAYFNSCINAIVY GVLNONFKRYM TMFVVFVLFAVCWAPLNFIGLAVAINFFULPINVTYCYL IWILVIQVRRVNFSCINAIVY GVLNONFKRYM TMFVVFVLFAVCWAPLNFIGLAVAINFEVVPLIPFWLFVASYFMAYFNSCINAIVY GVLNONFKRYM TMFVVFVLFAVCWAPLNFIGLAVAINFEVVPLIPFWLFVASYFMAYFNSCINAIVY GVLNONFRRYM TMFVVFVLFAVCWAPLNFIGLAVAINFEVVPLIPFWLFVASYFMAYFNSCINAIVY GVLNONFRRYM TMFVVFVLFAVCWAPLNFIGLAVAINPEVVPLIPFWLFVASYFMAYFNSCINAIVY GVLNONFRRYM	275 246 238 239 238 241 238 308 344 316 308 309
LcMtnr1a2 SsMtnr1aaα SsMtnr1aaβ SsMtnr1a EcMtnr1a DIMtnr1a TaMtnr1a MmMtnr1a SgMtnr1a LcMtnr1a2 SsMtnr1aaβ SsMtnr1aaβ SsMtnr1aaβ	QYT PRVYSCTFAQSVSSLYTITVVVVHFILPIAIVTYCYL IWILVIQVRRVNPSSPNIKFOLANFL QYT PRVYSCTFQSASSAYTIAVVFFHFILPIMIVTYCYL IWILVIQVRRVNPDN PRLTPD VRNFV QYT PRVYSCTFQSASSAYTIAVVFFHFILPIMIVTYCYL IWILVIQVRRVNPDN PRLTFD VRNFV QYT PRVYSCTFQSASSAYTIAVVFFHFILPIMIVTYCYL IWILVIQVRRVNPDN PRITFD VRNFV QYT PRVYSCTFQSASSAYTIAVVFFHFILPIMITYCYL IWILVIQVRRVNPDN PRITFD VRNFV QYT PRVYSCTFQSASSAYTIAVVFFHFILPINITYCYL IWILVIQVRRVNPN PNN PRITFD VRNFV TMFVVFVLFAVCWAPLNFIGLAVAINPEVVPLIPEWLFVASYFMAYFNSCINAIVY GVLNQNFRREYK TMFVVFVLFAVCWAPLNFIGLAVAINPEVVPLIPEWLFVASYFMAYFNSCINAIVY GVLNQNFRREYK TMFVVFVLFAVCWAPLNFIGLAVANPAAVIPNIFWLFVSVFNSCINAIVY GVLNQNFRREYK TMFVVFVLFAVCWAPLNFIGLAVAINPAVIPAVIPNIFWLFVSVFNSCINAIVY GVLNQNFRREYK TMFVVFVLFAVCWAPLNFIGLAVAINPAVIPNAVIPNIFWLFVSVFNSCINAIVY GVLNQNFRREYK	275 246 238 239 238 238 241 238 308 344 316 308 309 308
LcMtnr1a2 SsMtnr1aaα SsMtnr1aaβ SsMtnr1a EcMtnr1a DIMtnr1a TaMtnr1a SgMtnr1a LcMttnr1a1 LcMtnr1a2 SsMtnr1aaβ SsMtnr1aaβ SsMtnr1a DIMtnr1a TaMtnr1a	QYT PRVYSCTEAQSVSSLYTITVVVV FILPIAIVTYCYL IWILVIQVRRVNPTS SPNIKP DLENFL QYT PRVYSCTEQSASSAYTIAVVFFFFILPIMIVTYCYL IWILVIQVRRVNPDN PRLTPN VNPV QYT PRVYSCTEQSASSAYTIAVVFFFFILPIMIVTYCYL IWILVIQVRRVNPDN PRLTF DVRNFV QYT PRVYSCTFQSASSAYTIAVVFFFFILPIMIVTYCYL IWILVIQVRRVNPDN PRLTF DVRNFV QYT PRVYSCTFQSASSAYTIAVVFFFFILPIMIVTYCYL IWILVIQVRRVNPDN PRLTF DVRNFV TYPVFVLFAVCNAPLNFIGLAVAINPFVVPLIPEWLFVASYFMAYFNSCINAIVY SVLNONFFRFYR TMFVVFVLFAVCNAPLNFIGLAVAINPFVVPLIPEWLFVASYFMAYFNSCINAIVY SVLNONFFRFYR TMFVVFVLFAVCNAPLNFIGLAVAINPFVVPLIPEWLFVASYFMAYFNSCINAIVY SULNONFFRFYR TMFVVFVLFAVCNAPLNFIGLAVAINPAVIPNIPEWLFVASYFMAYFNSCINAIVY SULNONFFRFYR TMFVVFVLFAVCNAPLNFIGLAVAINPAVIPNIPEWLFVASYFMAYFNSCINAIVY SULNONFFRFYR TMFVVFVLFAVCNAPLNFIGLAVAINPAVIPLIPEWLFVASYFMAYFNSCINAIVY SULNONFFRFYR TMFVVFVLFAVCNAPLNFIGLAVAINPAVIPLIPEWLFVASYFMAYFNSCINAIVY SULNONFFRFYR TMFVVFVLFAVCNAPLNFIGLAVAINPAVIPLIPEWLFVASYFMAYFNSCINAIVY SULNONFFRFYR TMFVVFVLFAVCNAPLNFIGLAVAINPAVIPLIPEWLFVASYFMAYFNSCINAIVY SULNONFFRFYR TMFVVFVLFAVCNAPLNFIGLAVAINPAVIPLIPEWLFVASYFMAYFNSCINAIVY SULNONFFRFYR TMFVVFVLFAVCNAPLNFIGLAVAIRFEVVVPLIPEWLFVASYFMAYFNSCINAIVY SULNONFFRFYR TMFVVFVLFAVCNAPLNFIGLAVAIRFEVVPLIPEWLFVASYFMAYFNSCINAIVY SULNONFFRFYR TMFVVFVLFAVCNAPLNFIGLAVAIRFEVVPLIPEWLFVASYFMAYFNSCINAIVY SULNONFFRFYR TMFVVFVLFAVCNAPLNFIGLAVAIRFEVVVPLIPEWLFVASYFMAYFNSCINAIVY SULNONFFRFYR TMFVVFVLFAVCNA	275 246 238 239 238 238 241 238 308 344 316 308 308 308 308 308 308
LcMtnr1a2 SsMtnr1aaα SsMtnr1aaβ SsMtnr1a EcMtnr1a TaMtnr1a TaMtnr1a SgMtnr1a LcMtnr1a1 LcMtnr1a2 SsMtnr1aaα SsMtnr1aaα SsMtnr1aaα SsMtnr1a EcMtnr1a	QYT PRVYSCTFAQSVSSLYTITVVVV FILPIAIVTYCNLE IWILVIQVRRAV PDS PNIKF DLENFL QYT PRVYSCTFE QSASSAYTIAVVFFFFILPIMIVTYCYLE IWILVIQVRRAVAPDN PNLTPN VNFV QYT PRVYSCTFU QSASSAYTIAVVFFFFILPIMIVTYCYLE IWILVIQVRRAVAPDN PNLTF DVRNFV QYT PRVYSCTFU QSASSAYTIAVVFFHFILPIMIVTYCYLE IWILVIQVRRAVAPDN PNLTF DVRNFV TMFVVFVLFAVCWAPLNEIGLAVAIKPEVVVPLIPEWLFVASYFMAYFNSCINAIVY SVLNQNFFREYK IMFVVFVLFAVCWAPLNEIGLAVAINPEVVVPLIPEWLFVASYFMAYFNSCINAIVY SVLNQNFFREYK IMFVVFVLFAVCWAPLNEIGLAVAINPEVVVPLIPEWLFVASYFMAYFNSCINAIVY SVLNQNFFREYK IMFVVFVLFAVCWAPLNEIGLAVAINPEVVVPLIPEWLFVASYFMAYFNSCINAIVY SVLNQNFFREYK IMFVVFVLFAVCWAPLNEIGLAVAINPEVVVPLIPEWLFVASYFMAYFNSCINAIVY SVLNQNFFREYK IMFVVFVLFAVCWAPLNEIGLAVAINPEVVVPLIPEWLFVASYFMAYFNSCINAIVY SVLNQNFFREYK IMFVVFVLFAVCWAPLNEIGLAVAINPEVVVPLIPEWLFVASYFMAYFNSCINAIVY SVLNQNFFREYK IMFVVFVLFAVCWAPLNEIGLAVAINPEVVVPLIPEWLFVASYFMAYFNSCINAIVY SVLNQNFFREYK IMFVVFVLFAVCWAPLNFIGLAVAINPEVVVPLIPEWLFVASYFMAYFNSCINAIVY SVLNQNFFREYK IMFVVFVLFAVCWAPLNFIGLAVAIKPEVVVPLIPEWLFVASYFMAYFNSCINAIVY SVLNQNFFREYK IMFVVFVLFAVCWAPLNFIGLAVAIKPEVVVPLIPEWLFVASYFMAYFNSCINAIVY SVLNQNFFREYK IMFVVFVLFAVCWAPLNFIGLAVAIKPEVVVPLIPEWLFVASYFMAYFNSCINAIVY SVLNQNFFREYK IMFVVFVLFAVCWAPLNFIGLAVAIKPEVVVPLIPEWLFVASYFMAYFNSCINAIVY SVLNQNFFREYK IMFVVFVLFAVCWAPLNFIGLAVAIKPEVVPLIPEWLFVASYFMAYFNSCINAIVY SVLNQNFFREYK	275 246 238 239 238 238 241 238 308 344 316 308 308 308 308 308
LcMtnr1a2 SsMtnr1aaα SsMtnr1aaβ SsMtnr1a EcMtnr1a TaMtnr1a TaMtnr1a SgMtnr1a LcMttnr1a1 LcMtnr1a2 SsMtnr1aaα SsMtnr1aaα SsMtnr1aaα SsMtnr1a EcMtnr1a DiMtnr1a TaMtnr1a SgMtnr1a	QYL PRVYSCTEAQSVSSLYTITVVVVHFILPIAIVTYCYL IWILVIQVRRVVPLS PNIKPID LRNFL QYL PRVYSCTEQSASSAYTIAVVFFHFILPIMIVTYCYL IWILVIQVRRVVPDN PNLTPN VNRV QYL PRVYSCTEQSASSAYTIAVVFFHFILPIMIVTYCYL IWILVIQVRRVVPDN PNLTPN VNRV QYL PRVYSCTEQSASSAYTIAVVFFHFILPIMIVTYCYL IWILVIQVRRVVPDN PNLTF DVRNFV QYL PRVYSCTEQSASSAYTIAVVFFHFILPIMIVTYCYL IWILVIQVRRVNPDN PNLTF DVRNFV QYL PRVYSCTEQSASSAYTIAVVFFHFILPIMIVYCYL IWILVIQVRRVNPDN PNLTFE VRPV TMFVVFVLFAVCNAPLNEIGLAVAKKPEVVPLIFWIYKYK QYL PRVYSCTEQSASSAYTIAVVFFHFILPINIVYKYK QYL PRVYSCTEQSASSAYTIAVVFFHFILPINIVYKYK QYL PRVYSCTEQSASSAYTIAVVFFHFILPINIVYKYK QYL PRVYSCTEQSASSAYTIAVVFFHFILPINIYKYK QYL PRVYSCTEQSASSAYTIAVVFHFILPINITYKYK QYL PRVYSCTEQS	2755 246238 239238 238238 241238 308344 316308 308309 308308 308311 308311
LcMtnr1a2 SsMtnr1aag SsMtnr1aag SsMtnr1a EcMtnr1a DIMtnr1a TaMtnr1a SgMtnr1a LcMtnr1a1 TaMtnr1a SgMtnr1a SgMtnr1a LcMttnr1a1 LcMttnr1a2 SsMtnr1aag SsMtnr1aag SsMtnr1a EcMtnr1a JIMtnr1a TaMtnr1a SgMtnr1a EcMtnr1a SgMtnr1a LcMtnr1a1 TaMtnr1a SgMtnr1a LcMtnr1a1 LcMtnr1a1 LcMtnr1a1 LcMtnr1a1 LcMtnr1a1	QYL PRVYSCTEAQSVSSLYTITVVVVFILPIAIVTYCXLE IWILVIQVRRVVPDS SPNIKPID LENFL QYL PRVYSCTEQSASSAYTIAVVFFFILPINIVTYCXLE IWILVIQVRRVVPDS PRLTPD VRNFV QYL PRVYSCTEQSASSAYTIAVVFFFFILPINIVTYCXLE IWILVIQVRRVPDS VPDN PRLTPD VRNFV QYL PRVYSCTEQSASSAYTIAVVFFFFILPINIVTYCXLE IWILVIQVRRVPDS VPDN PRLTPD VRNFV QYL PRVYSCTEQSASSAYTIAVVFFFFFILPINIVTYCXLE IWILVIQVRRVPDN PRLTPD VRNFV QYL PRVYSCTEQSASSAYTIAVVFFFFILPINITY QYL PRVYSCTEQSASSAYTIAVVFFFFILPINITY QYL PRVYSCTEQSASSAYTIAVVFFFFILPINITY QYL PRVYSCTEQSASSAYTIAVVFFFFILPINITY QYL PRVYSCTEQSASSAYTIAVVFFFFILPINITY QYL PRVYSCTEQSASSAYTAX	2755 246238 239238 238238 241238 308344 316308 308309 308308 308311 308311
LcMtnr1a2 SsMtnr1aaα SsMtnr1aaβ SsMtnr1a EcMtnr1a DIMtnr1a TaMtnr1a SgMtnr1a LcMtnr1a1 LcMtnr1a2 SsMtnr1aaα SsMtnr1a LcMttnr1a1 LcMtnr1a2 SsMtnr1aa DiMtnr1a SsMtnr1aaβ SsMtnr1a DiMtnr1a SgMtnr1a LcMtnr1a1 LcMtnr1a2 SgMtnr1a SgMtnr1a SgMtnr1a SgMtnr1a SgMtnr1a SgMtnr1a SgMtnr1a SgMtnr1a SgMtnr1a LcMtnr1a1 SgMtnr1a2 SsMtnr1a3	QYL PRVISCTEAQSVSSLYTITVVVVFILPIAIVTYCXLE IWILVIQVRRVVPDS PRIKPED LENFL QYL PRVISCTEQSASSAYTIAVVFFFILPINIVTYCXLE IWILVIQVRRVVPDS PRIFPED VRNFV QYL PRVISCTEQSASSAYTIAVVFFFFILPINIVTYCXLE IWILVIQVRRVVPDS PRIFPED VRNFV QYL PRVISCTEQSASSAYTIAVVFFFFILPINIVTYCXLE IWILVIQVRRVVPDS PRIFPED VRNFV QYL PRVISCTEQSASSAYTIAVVFFFFILPINIVTYCXLE IWILVIQVRRVPDS PRIFPED VRNFV QYL PRVISCTEQSASSAYTIAVVFFFFILPINIVTYCXLE IWILVIQVRRVPDS PRIFPED VRNFV QYL PRVISCTEQSASSAYTIAVVFFFFILPINIVTYCXLE IWILVIQVRRVPDS PRIFPET VRNFV QYL PRVSCTEQSASSAYTIAVVFFFFILPINIVTYCXLE IWILVIQVRRVPDS PRIFPET VRNFV QYL PRVSCTEQSASSAYTIAVVFFFFILPINIVTYCXLE IWILVIQVRRVPDS PRIFPET VRNFV QYL PRVSCTEQSASSAYTIAVVFFFFILPINITYCXLE IWILVIQVRRVPDS PRIFPET VRNFV QYL PRVSCTEQSASSAYTIAVVFFFFILPINITYCXLE IWILVIQVRRVPDS PRIFPET VRNFV QYL PRVSCTEQSASSAYTIAVVFFFFILPINITYCXLE IWILVIQVRRVPSCINATVSVFNFF QYL PRVSCTEQSASSAYTIAVVFFFFILPINITYCXLE IWILVIQVRRVPSCINATVSVFFFFILPON VRNFV QYL PRVSCTEQSASSAYTIAVVFFFFILPINITYCXLE IWILVIQVRRVPSCINATVSVFNFFILPON PRIFFET VRNFV QYL PRVS	2755 246238 239238 238238 241238 308344 316308 308309 308308 308311 308311
LcMtnr1a2 SsMtnr1aaα SsMtnr1aaβ SsMtnr1a EcMtnr1a DIMtnr1a TaMtnr1a SgMtnr1a LcMtnr1a1 LcMtnr1a2 SsMtnr1aaβ SsMtnr1a DIMtnr1a DIMtnr1a SgMtnr1a LcMtnr1a1 LcMtnr1a1 LcMtnr1a2 SsMtnr1aaα SsMtnr1aaα	QYL PRVNSCTFAQSVSSLYTITVVVVFFLPIAIVTYCXL.IWILVIQVRRVVPCSSPNIKF_DLENFL QYL PRVNSCTFQ SASSAYTIAVVFFFFLPINIVTYCXL.IWILVIQVRRVVPDN PRLTPN VNFV QYL PRVNSCTFQ SASSAYTIAVVFFFFLPINIVTYCXL.IWILVIQVRRVVPDN PRLTP DVRNFV QYL PRVNSCTFQ SASSAYTIAVVFFFFLPINIVTYCXL.IWILVIQVRRVVPDN PRLTF DVRNFV QYL PRVNSCTFQ SASSAYTIAVVFFFFLPINIVTYCXL.IWILVIQVRRVVPDN PRLTF DVRNFV QYL PRVNSCTFQ SASSAYTIAVVFFFFLPINIVTYCXL.IWILVIQVRRVVPDN PRLTF DVRNFV QYL PRVNSCTFQ SASSAYTIAVVFFFFLPINIVTYCXL.IWILVIQVRRVPDN PNIFFLFYDVRPN QYL PRVNSCTFQ SASSAYTIAVVFFFFILPINIVTYCXL.IWILVIQVRRVPDN PNIFFLFYDVRPN QYL PRVNSCTFQ SASSAYTIAVVFFFFILPINIVTYCXL.IWILVIQVRRVPN PNIFFLPINFYDVRPN QYL PRVNSCTFQ SASSAYTIAVVFFFFILPINIVTYCXL.IWILVIQVRRVPN PNIFFLFYDVRPN QYL PRVNSCTFQ SASSAYTIAVVFFFFILPINIVTYCXL.IWILVIQVRRVPN PNIFFLFYDVRPN TMEVYFVLFAVCMAPLNFIGLAVAIKPEVVPLIPENLTYXXX TMEVVFVLFAVCMAPLNFIGLAVAIKPEVVPLIPENLTYXX	2755 246238 239238 238238 241238 308344 316308 308309 308308 308311 308311
LcMtnr1a2 SsMtnr1aaα SsMtnr1aaβ SsMtnr1a EcMtnr1a TaMtnr1a TaMtnr1a SgMtnr1a LcMtnr1a1 LcMtnr1a2 SsMtnr1aaβ SsMtnr1a EcMtnr1a DIMtnr1a TaMtnr1a SgMtnr1a LcMtnr1a1 LcMtnr1a2 SsMtnr1aa SsMtnr1aaβ SsMtnr1aaβ SsMtnr1aaβ SsMtnr1aaβ SsMtnr1aaβ SsMtnr1aaβ SsMtnr1aaβ SsMtnr1aaβ	QY PRVMSCTEAQSVSSLYTITVVVVHFILPIAIVTYCALSIWILVIQVRRVNPDSSPNIKPIDENELT QY PRVMSCTEQSASSATIAVVFFHFILPIMIVTYCALSIWILVIQVRRVNPDSPNIPLTFNVNFV QY PRVMSCTFQSASSATIAVVFFHFILPIMIVTYCALSIWILVIQVRRVNPDSPNIPLTFNVNFV QY PRVMSCTFQSASSATIAVVFFHFILPIMIVTYCALSIWILVIQVRRVNPDSPNIPLTFNVNFV QY PRVMSCTFQSASSATIAVVFFHFILPIMIVTYCALSIWILVIQVRRVNPDSPNIPLTFNVNFV QY PRVMSCTFQSASSATIAVVFFHFILPIMIVTYCALSIWILVIQVRRVNPDSPNFNFT QY PRVMSCTFQSASSATIAVVFFHFILPIMIVTYCALSIWILVIQVRRVNPDSPNFPLTFNVNFV QY PRVMSCTFQSASSATIAVVFFHFILPIMIVTYCALSIWILVIQVRRVNPDSPNFPNFPLTFNVNFV QY PRVMSCTFQSASSATIAVVFFHFILPIMIVTYCALSIWILVIQVRRVNPDSPNFPNFPNFPNFPNFPNFPNFPNFPNFPNFPNFPNFPNFP	2755 246238 239238 238238 241238 308344 316308 308309 308308 308311 308311
LcMtnr1a2 SsMtnr1aaα SsMtnr1aaβ SsMtnr1a EcMtnr1a TaMtnr1a TaMtnr1a SgMtnr1a LcMtnr1a1 LcMtnr1a2 SsMtnr1aaβ SsMtnr1a BiMtnr1a TaMtnr1a SgMtnr1a LcMtnr1a1 LcMtnr1a1 LcMtnr1a2 SsMtnr1aaβ SsMtnr1aaβ SsMtnr1aaβ SsMtnr1aaβ SsMtnr1aaβ SsMtnr1aaβ SsMtnr1aaβ SsMtnr1aaβ SsMtnr1aaβ SsMtnr1aaβ	QY PRVMSCTEAQSVSSLYTITVVVVHFILPIAIVTYCALSIWILVIQVRRVNPDSSPNIKPIDENELT QY PRVMSCTEQSASSATIAVVFFHFILPIMIVTYCALSIWILVIQVRRVNPDSPNIPLTFNVNFV QY PRVMSCTFQSASSATIAVVFFHFILPIMIVTYCALSIWILVIQVRRVNPDSPNIPLTFNVNFV QY PRVMSCTFQSASSATIAVVFFHFILPIMIVTYCALSIWILVIQVRRVNPDSPNIPLTFNVNFV QY PRVMSCTFQSASSATIAVVFFHFILPIMIVTYCALSIWILVIQVRRVNPDSPNIPLTFNVNFV QY PRVMSCTFQSASSATIAVVFFHFILPIMIVTYCALSIWILVIQVRRVNPDSPNFNFT QY PRVMSCTFQSASSATIAVVFFHFILPIMIVTYCALSIWILVIQVRRVNPDSPNFPLTFNVNFV QY PRVMSCTFQSASSATIAVVFFHFILPIMIVTYCALSIWILVIQVRRVNPDSPNFPNFPLTFNVNFV QY PRVMSCTFQSASSATIAVVFFHFILPIMIVTYCALSIWILVIQVRRVNPDSPNFPNFPNFPNFPNFPNFPNFPNFPNFPNFPNFPNFPNFP	2755 246238 239238 238238 241238 308344 316308 308309 308308 308311 308311
LcMtnr1a2 SsMtnr1aaα SsMtnr1aaβ SsMtnr1a EcMtnr1a TaMtnr1a TaMtnr1a SgMtnr1a LcMtnr1a1 LcMtnr1a2 SsMtnr1aaβ SsMtnr1a BiMtnr1a TaMtnr1a SgMtnr1a LcMtnr1a1 LcMtnr1a1 LcMtnr1a2 SsMtnr1aaβ SsMtnr1aaβ SsMtnr1aaβ SsMtnr1aaβ SsMtnr1aaβ SsMtnr1aaβ SsMtnr1aaβ SsMtnr1aaβ SsMtnr1aaβ SsMtnr1aaβ	QY PRVMSCTEAQSVSSLYTITVVVVHFILPIAIVTYCALSIWILVIQVRRVNPDSSPNIKPIDENELT QY PRVMSCTEQSASSATIAVVFFHFILPIMIVTYCALSIWILVIQVRRVNPDSPNIPLTFNVNFV QY PRVMSCTFQSASSATIAVVFFHFILPIMIVTYCALSIWILVIQVRRVNPDSPNIPLTFNVNFV QY PRVMSCTFQSASSATIAVVFFHFILPIMIVTYCALSIWILVIQVRRVNPDSPNIPLTFNVNFV QY PRVMSCTFQSASSATIAVVFFHFILPIMIVTYCALSIWILVIQVRRVNPDSPNIPLTFNVNFV QY PRVMSCTFQSASSATIAVVFFHFILPIMIVTYCALSIWILVIQVRRVNPDSPNFNFT QY PRVMSCTFQSASSATIAVVFFHFILPIMIVTYCALSIWILVIQVRRVNPDSPNFPLTFNVNFV QY PRVMSCTFQSASSATIAVVFFHFILPIMIVTYCALSIWILVIQVRRVNPDSPNFPNFPLTFNVNFV QY PRVMSCTFQSASSATIAVVFFHFILPIMIVTYCALSIWILVIQVRRVNPDSPNFPNFPNFPNFPNFPNFPNFPNFPNFPNFPNFPNFPNFP	2755246 238239238 238238 238241 2383241 308344 316308 308309 308308 308311 308
LcMtnr1a2 SsMtnr1aaα SsMtnr1aaβ SsMtnr1a EcMtnr1a TaMtnr1a TaMtnr1a SgMtnr1a LcMttnr1a1 LcMtnr1a2 SsMtnr1aaβ SsMtnr1a EcMtnr1a DIMtnr1a TaMtnr1a SgMtnr1a LcMtnr1a1 LcMtnr1a2 SsMtnr1aa SsMtnr1aaβ SsMtnr1aaβ SsMtnr1aaβ SsMtnr1aaβ SsMtnr1aaβ SsMtnr1aaβ SsMtnr1aaβ SsMtnr1aaβ SsMtnr1aaβ	QYD PRVISCTEAD SVSSLYT ITVVVV FILPIAIVTYCYLS IWILVI QVRRUVPES PIKPED LENEL QYD PRVISCTEE SASSAYTIAVVFFFFILPIMIVTYCYLS IWILVI QVRRUVPES PIKPED VENEV QYD PRVISCTEE SASSAYTIAVVFFFILPIMIVTYCYLS IWILVI QVRRUVPES PIKPED VENEV QYD PRVISCTEE SASSAYTIAVVFFFILPIMIVTYCYLS IWILVI QVRRUVPES PIKPE PILTPED VENEV QYD PRVISCTEE SASSAYTIAVVFFFILPIMIVTYCYLS IWILVI QVRRUVPES PITPED VENEV QYD PRVISCTEE SASSAYTIAVVFFFILPIMIVTYCYLS IWILVI QVRRUVPES PITPED VENEV QYD PRVISCTEE SASSAYTIAVVFFFILPIMIVTYCYLS IWILVI QVRRUVPES PITPED VENEV QYD PRVISCTEE SASSAYTIAVVFFFILPIMIVTYCYLS IWILVI QVRRUVPES PINPI PITPED VENEV QYD PRVISCTEE SASSAYTIAVVFFFILPIMIVTYCYLS IWILVI QVRRUVPES PINPI PITPED VENEV QYD PRVISCTEE SASSAYTAVVFFFILPIMIVTYCYLS IWILVI QVRRUVPES PINPI PITPED VENEV QYD PRVISCTEE SASSAYTAVVFFFILPINIVTYCYLS IWILVI QVRRUVPES PINPI PITPED VENEV QYD PRVISCTEE SASSAYTAVVFFFILPINIVTYCYLS IWILVI QVRRUVPES PINPI PITPED VENEV QYD PRVISCTEE SASAYTAVVFFFILPINITY YD PRVISCTEE SASAYTAVVFFFILPINIVTYCYLS IWILVI QVRRUVFTSUNAVSTAVESTAVY </th <th>2755246 238239238 238238 238241 2383241 308344 316308 308309 308308 308311 308</th>	2755246 238239238 238238 238241 2383241 308344 316308 308309 308308 308311 308

Figure S6. Alignment of the deduced *Lc*Mtnr1a amino-acid sequences with vertebrate

70 Mtnr1a from other species. All sequences were obtained from GenBank and their accession

71 numbers are listed in Table S1. The NRY, CYICHS and NAXXY sequences are marked with pink,

72 dark blue and green boxes, respectively. The percentage of sequences that must agree for identity

73 or similarity coloring was set as 80%.

LcMtnr1b1 MPDTFTLIKNRTEPRLGQLERTLDTEGSARPAWVIGILASVL LcMtnr1b2 MSMQEEDQLLEIANDGASVRDNNSDGVRDKVMAVWQYQRSLTQRVKNPVAIAN MmMtnr1b MPENSSIPNCCEASGLAARPSWSGSAGARPVTARAPWVAPMLSTVV SgMtnr1bb MTRTGRTYVGSPKVFDMPENVSFSRNRTVLDARLGT HsMtnr1b MSENGSFANCCEAGGWAVRFGWSGAGSARPSRTPRPWVAPMLSAVL DrMtnr1b MSENGSFANCCEAGGWAVRFGWSGAGSARPSRTPRPWVAPMLSAVL DrMtnr1b MPENIAFLTNSTDLGHVGRALG-SSARPAWAIAVLASVL TaMtnr1b MPTTFLLKNRTELRLGQLERAVGREGSARPAWVIGILASVL DIMtnr1b MPTTFLLKNRTEPRLGQLERTLATEGSARPAWVIGILASVL	IL <mark>SVEAGVFCSDS 66</mark> VVTTAVFFVG 57 IFTTVVVVLG 59 IVTTAVFVVG 57 IFTTVVVVLG 48 IFTTVVVVLG 52
LcMtnr1b1 NLLVIISVF NEY LENSGNVFVVSLAFAD LVVAFYPYPLVLYALFUD GWALGNT LcMtnr1b2 HQNKFHHFNDNLFPLLIFFTGNVFVVSLAFAD LVVAFYPYPLVLYALFUD GWSLGDA MmMtnr1b NLLVILSVLNKKLENAGNLFVVSLAFAD LVVAFYPYPLVLYAIFUD GWSLGET SgMtnr1bb NLLVILSVLNKKLENAGNVFLVSLAFAD LVVAFYPYPLVLYAIFUD GWSLGET HsMtnr1b NLLVILSVLNKKLENAGNVFLVSLAFAD LVVAFYPYPLVLYAIFUD GWSLGET DrMtnr1b NLLVILSVLNKKLENAGNVFLVSLAFAD LVVAFYPYPLVLYAIFUD GWSLGET TaMtnr1b NLLVIISVFNKKLENAGNVFVVSLAFAD LVVAFYPYPLVLYAIFUD GWALGNT DIMtnr1b NLLVIISVFNKKLENAGNVFVVSLAFAD LVVAFYPYPLVLYAIFUD GWALGNT DIMtnr1b NLLVIISVFNKKLENAGNVFVVSLAFAD LVVAFYPYPLVLYAIFUD GWALGNT	CCKVSCFLMGLSV 136 HCKASAFVMGLSV 124 CCKVSCFLMGLSV 126 HCKASAFVMGLSV 124 CCKISCFLMGLSV 124 CCKISCFLMGLSV 115
LcMtnr1b1IGSIFNITGIAVNRYCYICHSFSYSRLYSYRNTLLFVALIWVLTIVAIIFNFFVGSLLcMtnr1b2IGSIFNITGIAINRYCYICHSFSYDRLYSYRNTLLIVALIWLLTVVAIVPNFFVGSLMmMtnr1bIGSVFNITAIAINRYCYICHSFAYDRLYSYRNTLLIVALWLLTVVAIVPNFFVGSLSgMtnr1bbIGSIFNITGIAINRYCYICHSFAYDRLYSYRNTLLIVGLIWLLTIVAILFNFFVGSLHsMtnr1bIGSVFNITAIAINRYCYICHSFAYDRLYSYRNTLLIVGLIWLLTVVAILFNFFVGSLDrMtnr1bIGSVFNITGIAINRYCYICHSFAYGRLYSFRNTLLIVGLIWLLTVVAILFNFFVGSLDrMtnr1bIGSVFNITGIAINRYCYICHSFAYGRLYSFRNTLLIVALIWLTVVAILFNFFVGSLDlMtnr1bIGSIFNITGIAVNRYCYICHSFSYSLLYNYRNTLLFVALIWVLTVVAIIFNFFVGSLDIMtnr1bIGSIFNITGIAVNRYCYICHSFSYSLYNYRNTLLFVALIWVLTVVAIIFNFFVGSL	QUPPRVYSCTFAQ 206 EYPPRIYSCTFIQ 194 QUPPRVYSCTFAQ 196 EYPPRIYSCTFIQ 194 SYPPRVYSCTFIQ 194 SYPPRVYSCTFIQ 185 RYPPRVYSCTFAQ 189
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LcMtnr1b1ETSRAATDGRSMRSKQSPPPPLNNNESGAARTNKE	G, A, V, L, I F, Y, W C, M S, T K, R, R D, E N, Q F

Figure S7. Alignment of the deduced LcMtnr1b amino-acid sequences with vertebrate Mtnr1a from other species. All sequences were obtained from GenBank and their accession 76

77 numbers are listed in Table S1. The NRY, CYICHS and NAXXY sequences are marked with pink,

dark blue and green boxes, respectively. The percentage of sequences that must agree for identity 78

79 or similarity coloring was set as 80%.

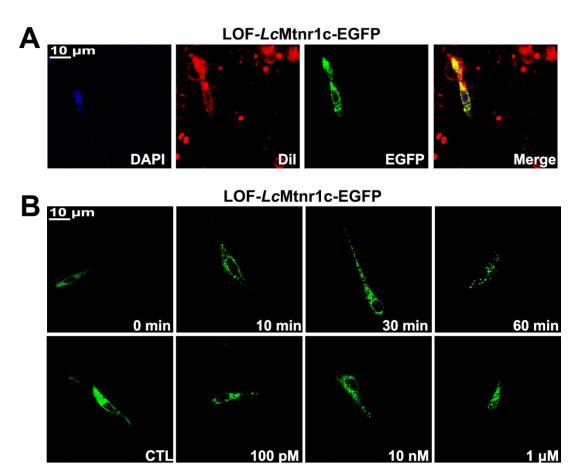
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LcMtnr1c SgMtnr1c DrMtnr1c TaMtnr1c CaMtnr1c DIMtnr1c EcMtnr1c	IFVVSLSVADLVVALYPYPLVLTAIFINDWTMGDLECQASGFIMGLSVIGSIFNITAIAINFYCNICHSL IFVVSLSVADLVVALYPYPLVLTAIFINDWTMGDLNCQASGFIMGLSVIGSIFNITAIAINFYCNICHSL IFVVSLSVADLVVALYPYPLALIAIFINDWTMGSLHCQLSGFIMGLSVIGSVFNITAIAINFYCVICHSL IFVVSLSVADLVVALYPYPLVLTAIFINDWTMGDLHCQASGFIMGLSVIGSVFNITAIAINFYCVICHSL IFVVSLSVADLVVALYPYPLVLTAIFINDWTMGDLHCQASGFIMGLSVIGSVFNITAIAINFYCVICHSL IFVVSLSVADLVVALYPYPLVLTAIFINDWTMGDLHCQASGFIMGLSVIGSVFNITAIAINFYCVICHSL IFVVSLSVADLVVALYPYPLVLTAIFINDWTMGDLHCQASGFIMGLSVIGSVFNITAIAINFYCVICHSL IFVVSLSVADLVVALYPYPLVLTAIFINDWTMGDLHCQASGFIMGLSVIGSIFNITAIAINFYCVICHSL IFVVSLSVADLVVALYPYPLVLTAIFINDWTMGDLHCQASGFIMGLSVIGSIFNITAIAINFYCVICHSL IFVVSLSVADLVVALYPYPLVLTAIFINDWTMGDLHCQASGFIMGLSVIGSIFNITAIAINFYCVICHSL IFVVSLSVADLVVALYPYPLVLTAIFINDWTMGDLHCQASGFIMGISVIGSIFNITAIAINFYCVICHSL ISFV
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LcMtnr1c SgMtnr1c DrMtnr1c TaMtnr1c CaMtnr1c DIMtnr1c EcMtnr1c	353 353 361 356 361 356 353 353 353 353 353 353 353 353 353 354 354 354 354 354 354 354 354 354 354 355 354 355 354 355 354 355 354 355

80 81 Figure S8. Alignment of the deduced LcMtnr1c amino-acid sequences with vertebrate

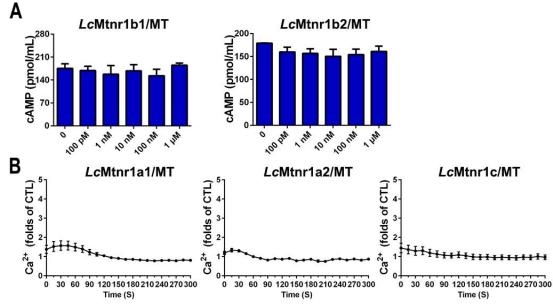
Mtnr1a from other species. All sequences were obtained from GenBank and their accession 82 numbers are listed in Table S1. The NRY, CYICHS and NAXXY sequences are marked with pink,

83 84 dark blue and green boxes, respectively. The percentage of sequences that must agree for identity

85 or similarity coloring was set as 80%.



87 Figure S9. Characterization of LcMtnr1c-EGFP stably expressed in large yellow croaker 88 ovary fibroblast (LOF) cells. (A) Subcellular location of LcMtnr1c-EGFP in large yellow 89 croaker ovary fibroblast (LOF) cells. LOF cells stably expressing LcMtnr1c-EGFP were stained 90 with a membrane plasma probe (Dil, 5 µM) and a nuclei probe (DAPI). (B) Internalization of 91 LcMtnr1c-EGFP stably expressed in LOF cells. LOF-LcMtnr1c cells were incubated with 100 nM 92 MT for the indicated time periods or indicated concentrations of MT at 37 °C for 60 min. Cells 93 were fixed and examined with confocal microscopy as described under "Methods". All pictures 94 shown are representative of at least three independent experiments.



96 Figure S10. The detection of cAMP accumulation and Ca²⁺ mobilization in MT activated

*Lc*Mtnr1b1/2 or *Lc*Mtnr1a1/1a2/1c expressing cells. (A) cAMP accumulation in *Lc*Mtnr1b1/2 expressing HEK293 cells was measured in response to the indicated concentration of MT for 15
 min. (B) Ca²⁺ mobilization in *Lc*Mtnr1a1/1a2/1c-expressing HEK293 cells was measured in
 response to 100 nM MT.

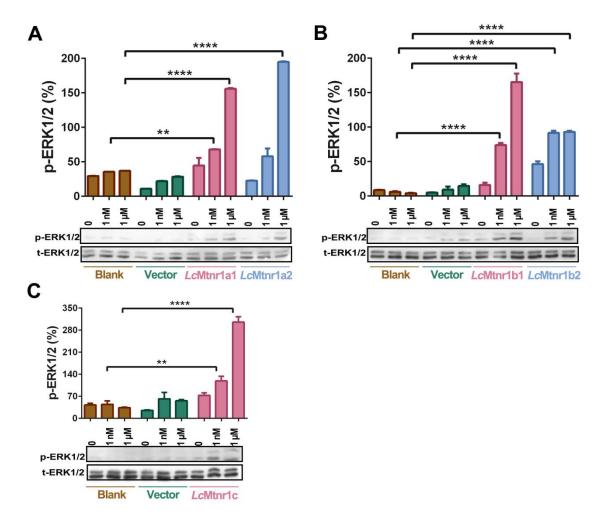
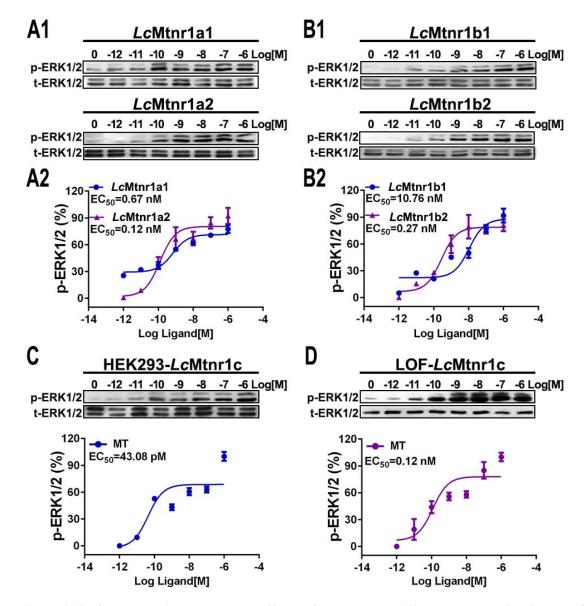


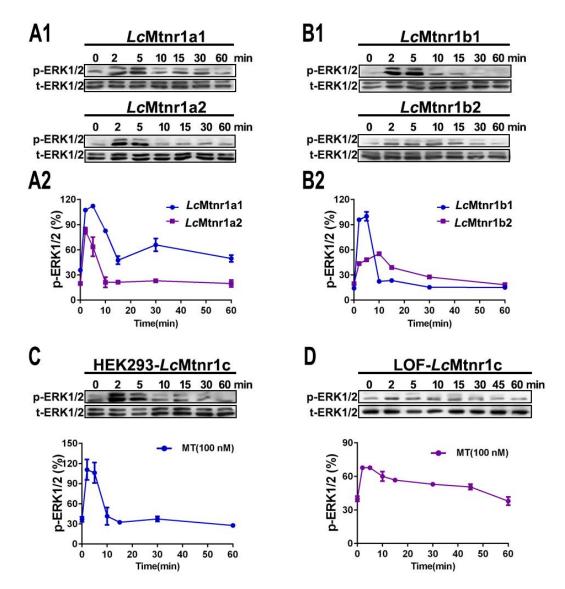
Figure S11. MT-induced ERK1/2 phosphorylation in HEK293 cells. Blank HEK293 cells, HEK293 cells stably expressing pFLAG-CMV-3 empty vector, *Lc*Mtnr1a1/2-FLAG (A), *Lc*Mtnr1b1/2-FLAG (B), and *Lc*Mtnr1c-FLAG (C) were stimulated with or without MT (1 nM and 1 μ M) for 5 min, respectively. Data were analyzed using the one-way ANOVA followed by Tukey's multiple comparison test, ** *P* < 0.01, **** *P* < 0.0001. ERK1/2: extracellular regulated protein kinases 1/2.



109

Figure S12. Concentration-dependent effects of MT on ERK1/2 phosphorylation in FLAG *LcMtnrs expressing cells.* (A-C) and in LOF cells stably expressing FLAG-*LcMtnr1c* (D).
 HEK293-FLAG-*LcMtnrs* and LOF-FLAG-*LcMtnr1c* cells were stimulated with the indicated
 concentrations of MT for 5 min. ERK1/2: extracellular regulated protein kinases 1/2; EC50:

114 concentration for 50% of maximal effect.



115

116 Figure S13. Time-dependent effects of MT on ERK1/2 phosphorylation in FLAG-LcMtnrs

117 expressing HEK293 cells (A-C) and in LOF cells (D). HEK293-FLAG-LcMtnrs and LOF-

118 FLAG-*Lc*Mtnr1c cells were stimulated with the 100 nM MT for the indicated periods of time. MT: 110 maletanin: EPK1/2: autrocallular regulated motoin kineses 1/2

119 melatonin; ERK1/2: extracellular regulated protein kinases 1/2.

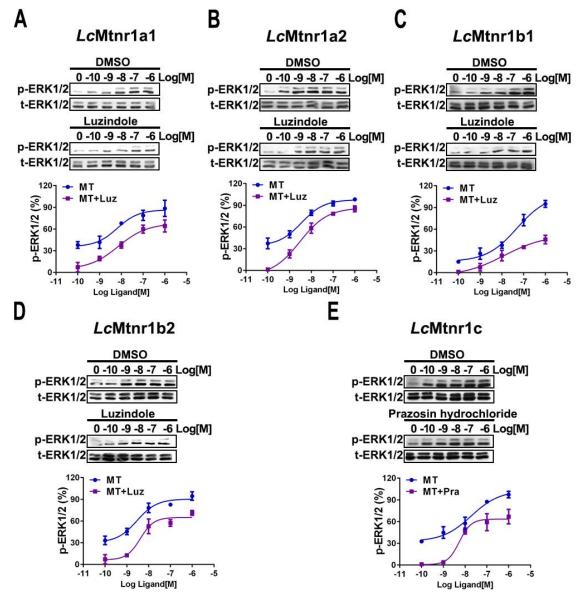


Figure S14. The *Lc*Mtnrs-mediated ERK1/2 phosphorylation activation inhibited by Mtnrs antagonists. HEK293-*Lc*Mtnr1a1/1a2/1b1/1b2 cells were pre-treated with vehicle (DMSO) or Mtnr1a/1b antagonists (10 μ M Luzindole, Luz, 1 h) (A-D), or HEK293-*Lc*Mtnr1c cells were pretreated with Mtnr1c antagonists (0.1 μ M prazosin hydrochloride, Pra, 1 h) (E), and the cells were stimulated with the indicated concentration of MT for 5 min. MT: melatonin; ERK1/2: extracellular regulated protein kinases 1/2.

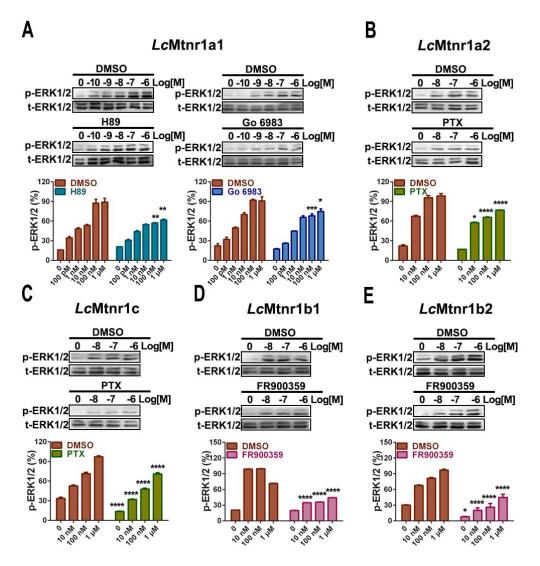
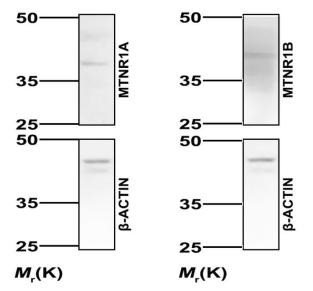




Figure S15. ERK1/2 activation mediated by Larimichthys crocea melatonin receptors. (A) 136 137 ERK1/2 phosphorylation activated by LcMtnr1a1 was blocked by PKA or PKC inhibitors. HEK293-LcMtnr1a1 cells were pre-treated with DMSO, PKA inhibitor (H89, 10 µM), or PKC 138 139 inhibitor (Go 6983, 10 mM) for 1 h prior to MT stimulation. (B-E) MT-induced (10 nM-1 µM, 5 min) ERK1/2 phosphorylation in LcMtnr1a2- expressing (B), LcMtnr1c- expressing (C), 140 LcMtnr1b1-expressing (D), and LcMtnr1b2-expressing (E) cells, in the absence or presence of 141 142 PTX (50 ng/mL, 16 h) or FR900359 (1 μ M, 1 h). Data are presented as means ± SEM. Data were analyzed using one-way ANOVA followed by Tukey's multiple comparison test (*P < 0.05, ** P 143 < 0.01, *** P < 0.001, **** P < 0.0001, all represent the difference between DMSO or inhibitor 144 treated groups). PTX: pertussis toxin; PKA: Protein Kinase A; PKC: Protein Kinase C; H89: a 145 146 PKA inhibitor; Go 6983: a PKC inhibitor; PTX: pertussis toxin; FR900359: an inhibitor of G_{aa} ; 147 ERK1/2: extracellular regulated protein kinases 1/2; DMSO: dimethyl sulfoxide.



149 150 Figure S16. Immunoblot analysis of the antibody specificities of anti-Mtnr1a and anti-

151 Mtnr1b IgG polyclonal antibodies in hypothalamus of large yellow croaker.

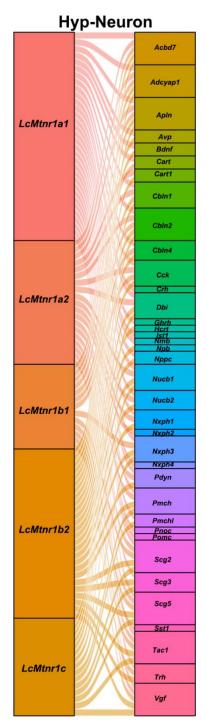


Figure S17. Co-expression of *Lc*Mtnrs and neuropeptides. Co-expression of *Lc*Mtnrs and neuropeptides (*Acbd7*, *Adcyap1*, *Apln*, *Avp*, *Bdnf*, *Cart*, *Cbln1*, *Cbln2*, *Cbln4*, *Cck*, *Crh*, *Dbi*, *Ghrh*, *Ist1*, *Nmb*, *Npb*, *Nppc*, *Nucb1*, *Nucb2*, *Nxph1*, *Nxph3*, *Nxph4*, *Pdyn*, *Pmch*, *Pmchl*, *Pnoc*, *Pmoc*, *Scg2*, *Scg3*, *Scg5*, *Sst1*, *Tac1*, *Trh* and *Vgf*) in hypothalamus neurons of large yellow croaker. The neuropeptide genes, detected with more than four reads per cell (reads \geq 4), are given for further analyses. The diagram was generated by the Xiantao web (https://www.xiantao.love). Source data 1 lists the details. *Acbd7: Acyl-CoA binding domain* 160 containing 7; Adcyap1: adenylate cyclase activating polypeptide 1; Apln: apelin; Avp arginine 161 vasopressin; Bdnf: brain derived neurotrophic factor; Cart: cocaine- and amphetamineregulated transcript; Cbln1: cerebellin 1; Cbln2: cerebellin 2; Cbln4: cerebellin 4; Cck: 162 cholecystokinin; Crh: corticotropin releasing hormone; Dbi: diazepam binding inhibitor, acyl-163 164 CoA binding protein; Gnrh: growth hormone releasing hormone; Hcrt: hypocretin receptor; Ist1: increased sodium tolerance 1 homolog; Nmb: neuromedin B; Npb: neuropeptide B; Nppc: 165 166 natriuretic peptide C; Nucb1: nucleobindin 1; Nucb2: nucleobindin 2; Nxph1: neurexophilin 1; 167 Nxph2: neurexophilin 2; Nxph3: neurexophilin 3; Nxph4: neurexophilin 4; Pdyn: prodynorphin; Pmch: pro-melanin concentrating hormone; Pmchl: pro-melanin-concentrating hormone, like; 168 169 Pnoc: prepronociceptin; Pomc: proopiomelanocortin; Scg2: secretogranin II; Scg3: secretogranin III; Scg5: secretogranin V; Sst1: susceptibility to tuberculosis 1; Tac1: tachykinin 170 171 precursor 1; Trh: thyrotropin releasing hormone; Vgf: VGF nerve growth factor inducible.

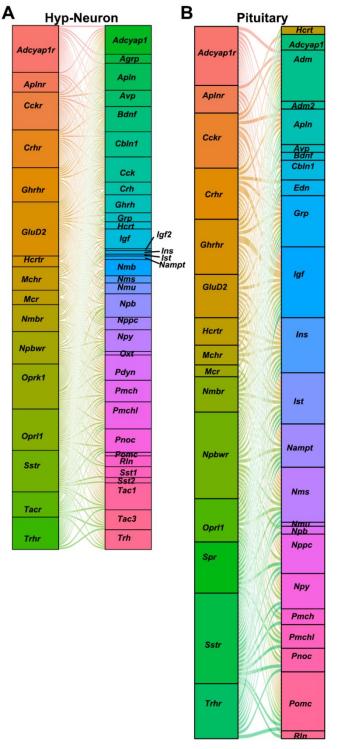


Figure S18. Co-expression of neuropeptides' receptors and other neuropeptides in hypothalamus neurons or pituitary cells. The expression cells of the neuropeptide receptors in hypothalamus neurons (A) or pituitary cells (B) were screened corresponding to the neuropeptides shown in Figure S16. The diagram was generated by the Xiantao web (https://www.xiantao.love). Source data 2 and 3 list the details. *Adcyap1r: pituitary adenylate*

179 cyclase-activating polypeptide type I receptor; Aplnr: apelin receptor; Cckr: cholecystokinin 180 receptor; Crhr: corticotropin-releasing hormone receptor; Gnrhr: gonadotropin releasing hormone receptor; GluD2: glutamate dehydrogenase 2; Hcrtr: hypocretin receptor; Mchr: 181 182 melanin concentrating hormone receptor; Mcr. mast cell regulator; Nmbr: neuromedin B 183 receptor; Npbwr: neuropeptides B and W receptor; Oprk1: opioid receptor kappa 1; Oprl1: opioid related nociceptin receptor 1; Sstr: somatostatin receptor; Tacr: tachykinin peptides 184 185 receptor; Trhr: thyrotropin releasing hormone receptor; Adcyap1: adenylate cyclase activating polypeptide 1; Agrp: agouti related neuropeptide; Apln: apelin; Avp: arginine vasopressin; Bdnf: 186 brain derived neurotrophic factor; Cbln1: cerebellin 1; Cck: cholecvstokinin; Crh: corticotropin 187 188 releasing hormone; Gnrh: growth hormone releasing hormone; Hcrt: hypocretin receptor; Igf: insulin-like growth factor; Igf2: insulin like growth factor 2; Ins: insulin; Ist: IST1 factor 189 associated with ESCRT-III; Nampt: nicotinamide phosphoribosyltransferase; Nmb: neuromedin 190 191 B; Nms: neuromedin S; Nmu: neuromedin U; Npb: neuropeptide B; Nppc: natriuretic peptide C; 192 Npy: neuropeptide Y; Oxt: oxytocin/neurophysin I prepropeptide; Pdyn: prodynorphin; Pmch: 193 pro-melanin concentrating hormone; Pmchl: pro-melanin-concentrating hormone, like; Pnoc: 194 prepronociceptin; Pomc: proopiomelanocortin; Rln: relaxin; Sst1: susceptibility to tuberculosis 1; 195 *Sst2: susceptibility to tuberculosis 2; Tac1: tachykinin precursor 1; Tac3: tachykinin precursor 3;* 196 Trh: thyrotropin releasing hormone; Spr: sepiapterin reductase; Adm: adrenomedullin; Adm2: 197 adrenomedullin 2; Grp: gastrin releasing peptide.

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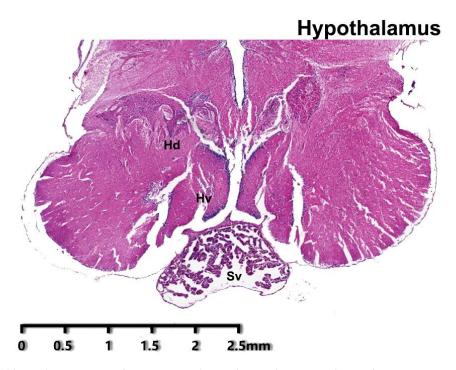


Figure S19. Microscopy of hematoxylin-eosin stained section of large yellow croaker hypothalamus. Hv: the ventral zones of the hypothalamus; Hd: the dorsal zones of the hypothalamus; Sv: Saccus vasulosus. Scale, as indicated.

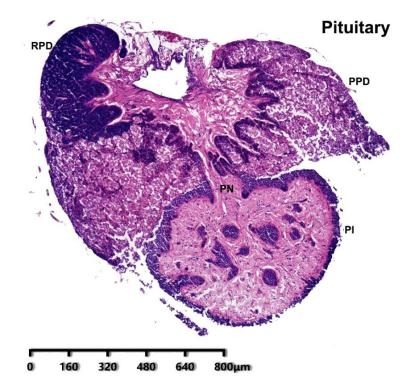


Figure S20. Microscopy of hematoxylin-eosin stained section of large yellow croaker
 pituitary. RPD: rostral pars distalis; PPD: proximal pars distalis; PI: pars intermedia; PN:
 neurohypophysis. Scale, as indicated.

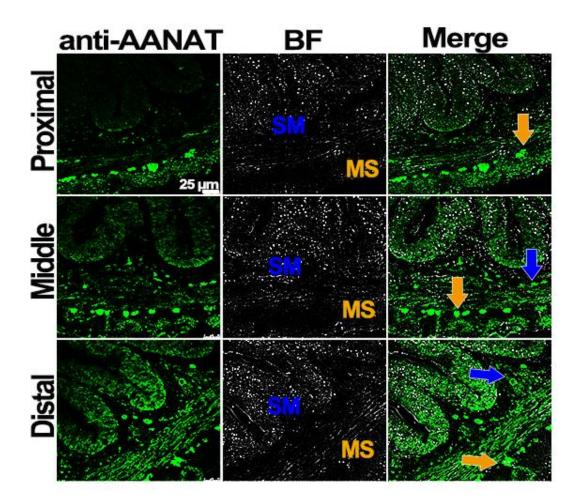




Figure S21. Distribution of AANAT in intestine of large yellow croaker. Immunohistochemical images of presumed MT-synthesizing cells in the intestine of large yellow croaker. The "AANAT" refers to the intestinal sections which were incubated with the anti-AANAT antibody. BF: Bright Field. Arrowheads in merged images indicate AANAT⁺ cells. Ms: muscularis; Sm: submucosa.

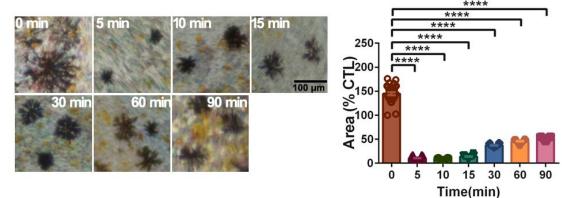


Figure S22. MT-mediated regulation of melanophore mobilization in the large yellow croaker *in vivo*. The bar chart shows the areas of melanophore covered the dorsal skin after indicated times treatment with 5.0 nM MT. The results are expressed as mean (± SEM) and are

one-way ANOVA followed by Tukey's multiple comparison test, **** P < 0.0001. 218

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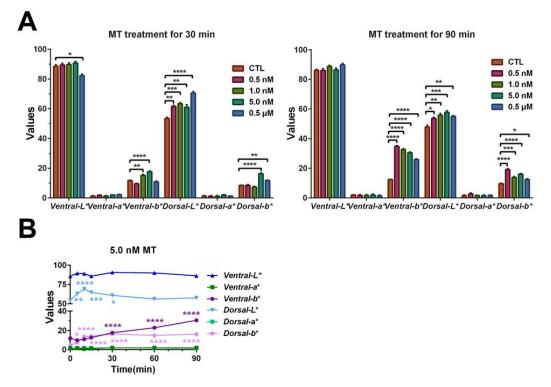
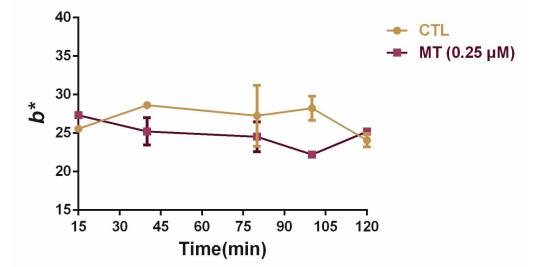




Figure 23. Effects of MT on the skin colors of the adult large yellow croaker. The L*, a*, and 222 b^* values were measured for the ventral and dorsal treated by different concentrations of MT for 223 30 min and 90 min (A) as well as 5.0 nM MT treated within 90 min (B), respectively. Each data 224 represents mean (± SEM) (n=3). Data were analyzed using the one-way ANOVA followed by Tukey's multiple comparison test, *P < 0.05, **P < 0.01, ***P < 0.001, ****P < 0.001. 225 MT: melatonin; CTL: control. 226



228 Figure S24. The b^* values from ventral skin of large yellow croaker with 0.25 μ M MT 229 treatment for indicated times in vitro. Data were analyzed using the two-way ANOVA

- 230 followed by Sidak's multiple comparison test. MT: melatonin.
- 231

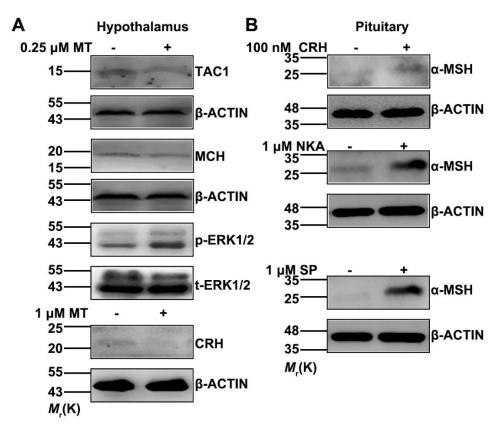


Figure S25. Immunoblot analysis of TAC1, MCH and p-ERK1/2 in hypothalamus and a-233 MSH in pituitary of large yellow croaker. (A) Samples were collected and lysed after 30 min of 234 235 MT (0.25 μ M and 1 μ M) stimulation. (B) Samples were collected and lysed after 30 min of 100 nM CRH, 1 µM neurokinin A (NKA), and 1 µM substance P (SP) stimulation, respectively. The 236 amino 237 acid sequences of CRH, NKA and SP are as follows: CRH, 238 SEDPPISLDLTFHLLREMMEMSRAEQLAQQAQNNRRMMELF-NH₂; NKA, 239 HKVNSFVGLM-NH₂; SP, KPRPHQFIGLM-NH₂. MT: melatonin; TAC1: Tachykinin Precursor 1; MCH: melanin-concentrating hormone; CRH: corticotropin releasing hormone; α -MSH: α -240 melanocyte-stimulating hormone (MSH); ERK1/2: Extracellular signal-Regulated Kinase 1/2. 241

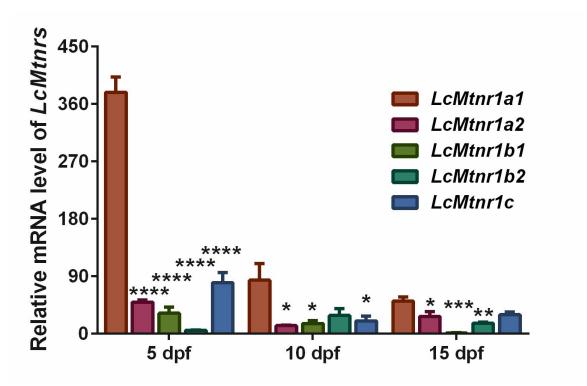
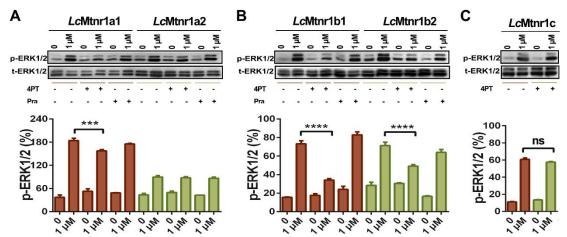




Figure S26. Relative expression of LcMtnrs mRNA at different developmental stages of 243 244 large yellow croaker larvae. Each symbol and vertical bar represent mean \pm SED (n = 6). *P < 0.05, ** P < 0.01, *** P < 0.001, **** P < 0.0001 compared with *Lc*Mtnr1a1, by one-way 245 246 analysis of variance (ANOVA) using Tukey's multiple comparison test. dpf: day post fertilization.





250 251 Figure S27. Effects of 4PT and Pra on the ERK1/2 phosphorylation in HEK293-LcMtnrs 252 cells. Samples were measured after 5 min of 1 µM MT stimulation with or without 1 h of 4-P-PDOT (4PT) (0.1 µM) or , 50 µM prazosin hydrochloride (Pra) (0.1 µM) pre-treatment. Data 253 254 were analyzed using the one-way ANOVA followed by Tukey's multiple comparison test, *** P < 0.001, **** P < 0.0001. ns, not significant. ERK1/2: Extracellular signal-Regulated Kinase 1/2. 255 256

Table S1.

258Accession numbers of melatonin receptor protein sequences of different species were used259for phylogenetic analysis and alignment.

Species	Gene synonym	Accession no.
Homo sapiens		NP 005949.1
Mus musculus		NP_032665.1
Danio rerio		NP_571468.1
Takifugu alboplumbeus		BAI39598.1
Gallus gallus		NP 990693.1
Dicentrarchus labrax		ACB13280.1
Epinephelus coioides		AG003817.1
Esox lucius	Mtnrla	XP 010889900.1
Carassius auratus		BAI65861.1
Lepisosteus oculatus		XP 006631980.2
Salmo salar		XP_014064448.1
Salmo salar		XP 014050730.1
Salmo salar		XP_014068290.1
Salmo salar		XP_014068723.1
Siganus guttatus		ABG77572.1
Homo sapiens		NP 005950.1
Mus musculus		NP_663758.2
Gallus gallus		NP 001280032.1
Danio rerio		NP 571469.1
Takifugu alboplumbeus		BAI39599.1
Dicentrarchus labrax	Mtnr1b	ACB13281.1
Epinephelus coioides		AGO03818.1
Esox lucius		NP 001290778.1
Carassius auratus		BAI65864.1
Lepisosteus oculatus		XP 015196706.1
Salmo salar		XP_014070615.1
Gallus gallus		NP 990692.1
Xenopus laevis		NP 001081388.1
Danio rerio		NP 001154956.1
Carassius auratus		BAI65865.1
Dicentrarchus labrax	Mtnr1c	ACB13282.1
Takifugu alboplumbeus		BAI39600.1
Siganus guttatus		ABG77573.1
Epinephelus coioides		AGO03819.1
Esox lucius		XP_010896763.1
Homo sapiens		BAA94488.1
Homo sapiens		BAA01763.1
Mus musculus		EDL18479.1
Danio rerio		NP 001116793.1
Danio rerio	5-HT1R	NP 001139238.1
Gallus gallus		NP 001163999.1
Xenopus laevis		NP 001079299.1
Salmo salar		XP 013999610.1
Homo sapiens		EAX08770.1
Mus musculus		EDL35846.1
Danio rerio	5-HT2R	ABI18978.1
Gallus gallus		AEV42168.1
Larimichthys crocea		KAE8279357.1

Homo sapiens		CAN84676.1			
Mus musculus	5_UT4D	CAA09598.1			
Larimichthys crocea	5-HT4R	KAE8284925.1			
Salmo salar		XP 014055545.1			
Homo sapiens		EAX04526.1			
Mus musculus		EDL37224.1			
Mus musculus	5-HT5R	EDL39785.1			
Salmo salar		XP 014036159.1			
Homo sapiens		AAA92622.1			
Mus musculus	5-HT6R	AAD46490.1			
Larimichthys crocea		KAE8293148.1			
Homo sapiens		AAC37538.1			
Mus musculus		EDL41763.1			
Danio rerio		XP 690599.7			
Xenopus laevis	— 5-HT7R —	NP 001079253.1			
Larimichthys crocea		KAE8280972.1			
Salmo salar		XP 014026341.1			

Table S2.

263 Sequences of primers used for vector construction, qPCR analysis, and sequence 264 identification for *LcMtnrs*.

Primer	Sequence (5'-3')	Application	Identifier
Lcmtnrlal-seq-F	CCCAAGCTTATGGTTATAAATGGGTC	- vector	NCBI
Lcmtnr1a1-seq-R	CGGGATCCCAGACAGAGTCCACC	construction	BioProject, PRJNA354443
Lcmtnr1a2-seq-F	CCCAAGCTTATGCTGAATGGACCG	_	GenBank:
Lcmtnr1a2-seq-R	GGGGTACCCAGCAGTGAAACTTG	_	OM939679
Lcmtnr1b1-seq-F	CCAAGCTTATGCCGGACACATTC	_	GenBank:
Lcmtnr1b1-seq-R	GGGGTACCCATTCTTTGTTTGTG	Saguanaa	OM939680
Lcmtnr1b2-seq-F	CCAAGCTTATGTCCATGCAAGAAG	- Sequence - identification	NCBI
Lcmtnr1b2-seq-R	CGCGGATCCCACAGAGTCTCTGC		BioProject, PRJNA354443
Lcmtnr1c-seq-F	CCAAGCTTATGGATTTAGAGGTG	_	GenBank:
Lcmtnr1c-seq-R	GGGGTACCGATACATTTATCTCTGC		OM939678
<i>β-actin</i> F	TCGTCGGTCGTCCCAGGCATCAG	Internal	GenBank:
β-actin R	ATGGCGTGGGGGCAGAGCGTAACC	control	EU443733.1
Lcmtnr1a1-q-F	TACAGGTGAGGAGACGAGTGAAG		NCBI
<i>Lcmtnr1a1-</i> q-R	GAAGTAGGCCATGAAGTAGCTGG		BioProject, PRJNA354443
Lcmtnr1a2-q-F	GTGAGCTCGCTGTACACTATCAC	_	GenBank:
Lcmtnr1a2-q-R	CGACGAACATGGTGAGGAAGTTG	-	OM939679
Lcmtnr1b1-q-F	ACACAGTGGCAGTAGTAGTGGT	- qPCR	GenBank:
Lcmtnr1b1-q-R	CAGCACAAAGACCACGAACATG	- qrCK	OM939680
Lcmtnr1b2-q-F	TCAACCGCTACTGTTACATCTGC		NCBI
<i>Lcmtnr1b2</i> -q-R	GTATGAGGTGCTGACTGTCTGTG	_	BioProject, PRJNA354443
<i>Lcmtnr1c</i> -q-F	ACATCTTCGTGGTGAGTTTGTCC		GenBank:
Lcmtnr1c-q-R	GTGATGTTGAAGATGGAGCCGAT		OM939678

Table S3.

268	The sources of Lcmtnrs pro	oes, hairpins,	and	antibodies	used	for	In	situ	HCR	and
269	immunofluorescence detection									

Reagent type	Designation	Source	Identifiers
Probe	<i>Lcmtnr1a1</i> -B4 (RefSeq ID: XP_010727592.1)	Molecular Instruments	LOT.PRH057
Probe	<i>Lcmtnr1a2</i> -B1 (RefSeq ID: XP_010741227.1)	Molecular Instruments	LOT.PRH054
Probe	<i>Lcmtnr1b1</i> -B3 (RefSeq ID: XP 027129075.1)	Molecular Instruments	LOT.PRH056
Probe	<i>Lcmtnr1c</i> -B2 (RefSeq ID: XP 010750373.1)	Molecular Instruments	LOT.PRH055
Hairpin/Fluorophore	B1h1 / Alexa514	Molecular Instruments	LOT.S031921
Hairpin/Fluorophore	B1h2 / Alexa514	Molecular Instruments	LOT.S032021
Hairpin/Fluorophore	B2h1 / Alexa488	Molecular Instruments	LOT.S035322
Hairpin/Fluorophore	B2h2 / Alexa488	Molecular Instruments	LOT.S034422
Hairpin/Fluorophore	B3h1 / Alexa594	Molecular Instruments	LOT.S029722
Hairpin/Fluorophore	B3h2 / Alexa594	Molecular Instruments	LOT.S031822
Hairpin/Fluorophore	B4h1 / Alexa647	Molecular Instruments	LOT.S034722
Hairpin/Fluorophore	B4h2 / Alexa647	Molecular Instruments	LOT.S025122
Antibody	MTNR1A-anti-rabbit IgG (polyclonal)	Abcam	CAT#ab203038
Antibody	MTNR1B-anti-rabbit IgG (polyclonal)	Abcam	CAT#ab203346
Antibody	GAD-65/67-anti-mouse IgG (monoclonal)	Santa Cruz	CAT#sc-365180
Antibody	FITC-conjugated goat anti-mouse IgG (polyclonal, goat)	Beyotime	CAT#A0568
Antibody	Cy3-conjugated goat anti-rabbit IgG (polyclonal, goat)	Beyotime	CAT#A0516
Antibody	TAC1-anti-rabbit IgG (polyclonal)	Proteintech	CAT#28599-1-AP
Antibody	CRF-anti-rabbit IgG (polyclonal)	ThermoFisher	CAT#PA5-102356
Antibody	NPY-anti-rabbit IgG (polyclonal)	ThermoFisher	CAT#PA5-95226
Antibody	ACBD7-anti-rabbit IgG (polyclonal)	Sigma	CAT#HPA062478
Antibody	MCH-anti-rabbit IgG (polyclonal)	Sigma	CAT#M8440

272 273	
274	Source data files:
275	
276	Source data1. The hypothalamus peptidergic neurons co-expressing <i>LcMtnrs</i> .
277	
278	Source data2. The gene expression of neuropeptide receptors in hypothalamus neurons.
279	
280	Source data3. The gene expression of neuropeptide receptors in pituitary cells.