

TATA box

CCTTCAGAACGAGCGGGAAATGTAACAACACTAACAACGCACTCGTTCCAAATCCAGTGCAATGAATATAATTCAAT
GAATTGGTCAGTTTTAGAGGAAAGTTTTCCCGTTCAGTACAAGGTACCATTGGAGTTATTTATGCCAGACTTCACGA
GTGAACGATTAACCTGTACAACAGTCTGTTGCAATAAGTGGATCAGACTGGGGAGGGTCCACGGGAGGTCAATATT
CAGCAGCCAACCTCTGTCTTACTTTTTCAGTTGAGCCACTGAACCACTCGGAGGCAACCAAATGCCTCTCAGTCATCTCA
AACAGGCCTAAGATCCAAAGCTAATTACAGATTGCCATTTGCGAAGAATTTGCCGAGAGCTCAAAGAATGTGGCAA

5' UTR M W Q

GTTCTGTTCTTGCTCGCTGCCCTTGCAAGT --> 1841bp AGGCCCTTTGACAGCTGA
V L F L L A A L A G P L T A D

TGACTCTCTATATCTCGCCATATCTCTGAGTCGCTGGGAAAATGAAACAGTGACGTTGAATTGTTTCACCTCCA
D T L Y I S P I S L S R W E N E T V T L N C F T S

GGACTGTGGATAATTATTACCTCATCTGGGGATCCGCCAAGCCGGGAGATCTCATGATCTCGTGGATTCTTTACTGG
R T V D N Y Y L I W G S A K P G D L M I S W I L Y W

ATGCCGGGATCGAGTGTCTCTTTACCCGTCCTGGTTCAGCGATCGCTTCATTGGCTCAAAGGACTGGACCAGCAA
M P G S S A A L Y P S V V S D R F I G S K D W T S K

GAAGTTCTCACTGACAATAAAAGGTCTCCGACAAGAAGATTCAGCCAGATATTATTGTGGCAGCTCAAACACTTACT
K F S L T I K G L R Q E D S A R Y Y C G S S N T Y

TCCCATTGACGACAGACTGGAGCGGATGTGGAGTCACGCTCACTGTTAAAGCAGGT --> 2625bp
F P F S T D W S G C G V T L T V K A

ATCAGTGTGAGCCGTAATTAACCTTGTGGCCACTTAGTAACAGATTCATTTCCATTTTCAGCTCCCTCAGTGTCTCC
A P S V S P

TCCGTTGGTTTTATTTCCAAAACCCACACCCTGAGGATGTCTTTCTCCGGAAGAACATCTCGCTGCTCTGTGCGGCAG
P L V Y F Q N P H P E D V F L R K N I S L L C A A

AAAGCTTTTACCCGGACGACCTCTCATTTTCTGGCGTGTGATGGTGAGCAGGTCCACAGAGGGGTCTCGCATTCT
E S F Y P D D L S F S W R V D G E Q V H R G V S H S

GCCTCACTTTTGGGAGACAACGGCACCTACACAGCGATCAGTAAGCTGGTATCAATACATCCCAGTGGATCAAAGG
A S L L G D N G T Y T A I S K L V I N T S Q W I K G

ATCTATTATCAGCTGCCAAGTATCACATGGGGCACTGCCTTCTCCCATCATCAAGCACATAAGTAACACTGGT
S I I S C Q V S H G A L P S P I I K H I S N T

--> 2287bp GACAGACTCAGTTGTGATTGTTACACAGAGCGGTACCCCATGGAGCCAAAGCTGTAT
E R Y P M E P K L Y

CTCCTGTCACCGACTTTAGAAGAGCTCGTCACAATGGAAAAAGCAACCCTGGTCTGCCTAGCAACTGGCTTCTACCC
L L S P T L E E L V T M E K A T G L V C L A T G C F Y P

AGCGGAGATCTCTTTCCATTGGTTCATCAATGGCAATCCGGTGGTGCAGCAGCATCAAGATCTACCCACCAATTCTCA
A E I S F H W F I N G N P V V D S I K I Y P P I L

ATATCAACGGCACCTACTCTCCAGAGTGAAGTACCACATCTGATCAAATGTGGAACCGGGGTACAGAATACACT
N I N G T Y S S Q S E L T T S D Q M W N R G T E Y T

TGTGAGATTGAGCAGTGTGAGTCCAGACAGCATCATTCAAACCATCAATAAAACCCGGGT --> 1837bp
C E I Q H M S V P D S I I Q T I N K T R

TTAAGGGAAAATGTCTGTTGATTGAAATGTTTTATCTCTGCCTGTAACAGAATTTATTTTCCCAACCGACGATAA
E F I F L Q P T I

CCCCCATCAAGGTTGAGTACGTCGACTCCCGTCCGCCACAAGCTGTGACGTTGGCGTGTGTTTGTTCGGGGTCTAT
T P I K V Q S R D S R R P Q A V T L A C F V S G F Y

CCCGCCGGGATCTATGTGAAGTGGAGAACGGAGAGGGATTTGCAAGTTCGGGCAGTGTGACCAACTTCCAGTGGT
P A G I Y V N W R T E R D L Q V P G S V T N F P V V

GAGGGACGTGAGTGGGACCTACAGTACAGTCAGTCAGATGACCATTGCCTTTGTGGATGTGGACCCCACTCAGACGT
R D V S G T Y S T V S Q M T I A F V D V D P T Q T

ATATGTGTGAGGTGAGACAGGATCTCTACCAACCCTTTAAGGGAACGGTTTCAGATAAGGTAACGCCTCAATGT
Y M C E V R H E S L T N P L R E R F Q I R

GATGGGACGTGTAAGTGTGTGAGCTGCCCCTTGGCTCAGTATTTACACCTCGATGGGAAGGCAGGTGAGTGTG
-->2779bp CGTTAACGTGCCGTTATGAACCTGCTGTTGAACCAATGTTTCTTTTTCAGATGACATTC
* 3' UTR

CTGCCAAGGACTGATCCAATCATCTGAAATCTTCATATGTCTTCAACAACGAAACACTGGAGTGACATTCCCAGTCG
GACATGGAGCTATTCCATTCTTACCCACTCACGGTGAATTTGAAACTATTAATAATAAAAAGAATATTTTCCCCTTTA
ACTGAATGTTAAACAAAACAGACAATTTTAGGTAATGAATAACTGATCTCTAAGGATTGTGAATTCATCTTAGAGAT
GTTGCAAGCATTAATAAAAAAATTACCTTGGCTTAATTATTTGTTTCAAGTAATATAGTGGCTTTAAGGGGTGAG

Poly(A) signal site

Supplemental Fig 1. Genomic organization of nurse shark UrIg. Introns were shortened with size indicated at the junctions.

A)

	Leader	V domain	
GIWU01140356.1	MWQVLFLLAALAGPLTADDTLYISPIISLRWENETVTLNCFTSRTVDNYYLWGSAPKPGD		60
GIWU01140354.1	MWQVLFLLAALAGPLTADDTLYISPIISLRWENETVTLNCFTSRTVDNYYLWGSAPKPGD		60

GIWU01140356.1	LMISWILYWMPGSSAALYPSVSDRFIGSKDWTSKKFSLTIKGLRQEDSARYYCGSSNTY		120
GIWU01140354.1	LMISWILYWMPGSSAALYPSVSDRFIGSKDWTSKKFSLTIKGLRQEDSARYYCGSSNTY		120

		C1 domain	
GIWU01140356.1	FPFSTDWSGCGVTLTVKAAPSVSPPLVYFQNPHPEDVFLRKNISLLCAAESFYPDDLFSFS		180
GIWU01140354.1	FPFSTDWSGCGVTLTVKAAPSVSPPLVYFQNPHPEDVFLRKNISLLCAAESFYPDDLFSFS		180

GIWU01140356.1	WRVDGEQVHRGVSHSASLLGDNGTYTAISKLVINTSQWIKGSIISCQVSHGALPSPIIKH		240
GIWU01140354.1	WRVDGEQVHRGVSHSASLLGDNGTYTAISKLVINTSQWIKGSIISCQVSHGALPSPIIKH		240

		C2 domain	
GIWU01140356.1	ISNT-----		244
GIWU01140354.1	ISNTERYPMEPKLYLLSPTLEELVTMEKATLVCLATGFYPAEISFHWFINGNPVVDSEIKI		300

		C3 domain	
GIWU01140356.1	-----EFIFLQPTI		253
GIWU01140354.1	YPPILNINGTYSSQSELTTSQMWNRGTEYTCETQHMSVPDSIIQTINKTREFIFLQPTI		360

GIWU01140356.1	TPIKVQSRDSRRPQAVTLACFVSGFYFAGIYVNWRTERDLQVPGSVTNFPVVRDVSGTYS		313
GIWU01140354.1	TPIKVQSRDSRRPQAVTLACFVSGFYFAGIYVNWRTERDLQVPGSVTNFPVVRDVSGTYS		420

GIWU01140356.1	TVSQMTIAFVDVDPTQTYMCEVRHESLTNPLRERFQIR*	351	
GIWU01140354.1	TVSQMTIAFVDVDPTQTYMCEVRHESLTNPLRERFQIR*	458	

B)

C3	EFIFLQPTITPIKVQSRDSRRPQAVTLACFVSG FYP AGIYVNWRTERDLQVPG	53
C2	ERYPMEPKLYLLSPTLEELVTMEKATLV CLATGFYP AEISFHWFINGNP-VVD	52
C1	APSVSPPLVYFQNPHPEDVFLRKNISLL CAAESFYP DDLFSFSWRVDGEQ-VHR	52
	. : .* : : : * * . . ** : . * : : *	
C3	SVTNFPVVRDVSGTYSTVSQMTIAFVDVDPTQTYM CEVR HESLTNPLRERFQIR-	107
C2	SIKIYPPILNINGTYSSQSELTTSQMWNRGTEYTC ETQH MSVPDSIIQTINKTR	107
C1	GVSHSASLLGDNGTYTAISKLVINTSQWIKGSIIS CQV SHGALPSPIIKHISNT-	106
	... : . . ** : : * : : * : : * : : . . : : . .	

% similarity between constant domains (in Amino acid)

	C3	C2	C1
C3	---		
C2	27.27	---	
C1	22.22	29.25	---

Supplemental Fig 2. Additional features of nurse shark UrIg. A. Alternative splicing of C2 domain. **The three constant domains of IgUr are divergent.** The nurse shark UrIg constant domains were aligned using Clustal Omega multiple sequence alignment. Below the matrix shows the % similarity (22-29%), showing that the domains are very divergent. Typical amino acids for C1 IgSF domains are marked in bold letters.