

Figure S1. Amino acid alignment of MSTN of medaka (*Oryzias latipes*; [AB520935.1](#)), tilapia (*Oreochromis mossambicus*; [AF197193.3](#)), gilthead seabream (*Sparus aurata*; [AF258448.1](#)), carp (*Cyprinus carpio*; [GQ214770.1](#)), catfish (*Ictalurus punctatus*; [AF396747.1](#)), turbot (*Scophthalmus maximus*; [EF683115.1](#)), zebrafish (*Danio rerio*; [AY258034.1](#)), fugu (*Takifugu rubripes*; [AY445322.1](#)), salmon (*Salmo salar*; [NM_001123549.1](#)) and pejerrey (*Odontesthes bonariensis*; [HM061693.1](#)). Identical amino acids are in black. The proteolytic processing site RXXR is boxed. Asterisks show the 9 conserved cysteines in the bioactive TGF- β 2 domain, which is indicated by a black line over the sequence.

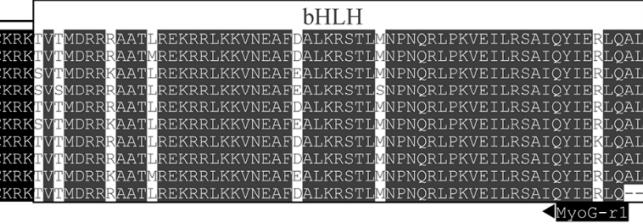
		His / Cys-rich
Tilapia	MELFETNPYFFPDQRFYE GGDSYFSRLP GAYDQAGYQDRN-SM GLCGNLSGGVG VGVTG-TEDKAS PSS -----MSPH SEP -HCPGQCLPWACKL	89
Seabream	MELFETNPYFFPDOR YEGGDSYFSRLP GAYDQAGYQDRN-SM GLGSLSGGV VGVTG-TEDKAS PSS -----ISP HSEP -HCPGQCLPWACKL	89
Carp	MELFETNPYFLADOR YEGGDNF FSRLI GGFD QGYQDRS-SM MGLG -DGRLLS NVG -LEDKPS SSSLGLS LSPHQE QHCP QCLPWACKV	93
Catfish	MELFETNPYFFP DOR Y ESEN FF SRLI GGFD OQGYQDRS -SM MGLG -DGRLLS NVG -LEDKPS SSSL LSLSPNQE QHCP QCLPWACKV	93
Sole	--LFETNPYFFPDQRFYE GGDSYFSRLP G GGYD TGYQDRS-SM GLGSLSGAGV VGVTG-TEDKVS PSS -----MSPH SEP -HCPGQCLPWACKL	87
Zebrafish	MELFETNPYFFND RF Y EADNF FSR RING GF EOAGYQDRN -SM MGLG -DGRMLTTWG-LEDKPS SSSL GLMSLSPHQE QHCP QCLPWACKV	93
Fugu	-ELFETNPYFFPDOR YEGGDTYFSRLP G GSYDQGTYQDRN -TM MGLGSLSGGV DVGVTG-ABDKAS PSS -----ISP HSEP -HCPGQCLPWACKL	88
Pufferfish	-ELFETNPYFFPDOR YEGGDSYFSRLP G GSYDOSTYQDRN -SM MGLGSLSGGV DVGVTG-TEDKAS PSS -----ISP HSEA -HCPGQCLPWACKI	88
Salmon	MELFETNPYFFPDQRFYE GGDNFYQSRLP G GGYDGGYQERGGSM GLGGLS RVGVLGGGM DKATPSG-----ISP HPEP -HCPGQCLPWACKL	91
Pejerrey	-ELFETNPYFFPDQRFYE GGDGYFSRLP GAYDQAGYQDRN-SM MGLGSLSGGV VGVTG-TEDKAS PSS -----ISP HSES -HCPGQCLPWACKL	88
	MyoG-f1▶	
		
Tilapia	CKRKIVTMDRRRAATLREKRLLKVNNEADALKRSTLMNPQNRLPKVEILRS AIQYIERLQALVSSLNQ QDETETGQQGILYR PSPTQF --RVSSSE 184	
Seabream	CKRKIVTMDRRRAATLREKRLLKVNNEADALKRSTLMNPQNRLPKVEILRS AIQYIERLQALVSSLNQ Q ON NTETGQQGILYR PSATQF --RVSSSE 184	
Carp	CKRKIVTMDRRKAATLREKRLLKVNNEA E ALKRSTLMNPQNRLPKVEILRS AIQYIERLQALVSSLNQ QHEQQG--NUHYR STAPQ --AVSSSD 185	
Catfish	CKRKIVSMDRRRAATLREKRLLKVNNEADALKRSTL SNPQNRLPK VEILRS AIQYIERLQALVSSLNQ QHEQT--GHYR SSAAQ --RVSSSE 185	
Sole	CKRKIVTMDRRRAATLREKRLLKVNNEADALKRSTLMNPQNRLPKVEILRS AIQYIERLQALVSSLNQ QDSETGQQGILYR PNTTQF --RVSSSE 182	
Zebrafish	CKRKIVTMDRKRAATLREKRLLKVNNEADALKRSTLMNPQNRLPKVEILRS AIQYIERLQALVSSLNQ QDETETGQQGILYR ATAAPHTQVSSSD 188	
Fugu	CKRKIVTMDRRRAATLREKRLLKVNNEADALKRSTLMNPQNRLPKVEILRS AIQYIERLQALVSSLNQ QDETETGQQGILYR ITSAVQF --RVSSSE 183	
Pufferfish	CKRKIVTMDRRRAATLREKRLLKVNNEADALKRSTLMNPQNRLPKVEILRS AIQYIERLQALVSSLNQ QDETETAQALHFR TSAAQF --RVSSSE 183	
Salmon	CKRKIVTMDRRKAATLREKRLLKVNNEADALKRSTLMNPQNRLPKVEILRS AIQYIERLQALVSSLNQ QENDQGTQGILYRTGPAQF--RVSSSE 186	
Pejerrey	CKRKIVTMDRRRAATLREKRLLKVNNEADALKRSTLMNPQNRLPKVEILRS AIQYIERLQ ----- 149	
	MyoG-rl1	
Tilapia	PSSGSTCCSSPEWS STPECC QSYSS--EDL ISAAD SP E GNM RALTSIVDS ISAADGP-VAF--PV DIPK 250	
Seabream	PSSGSTCCSSPEWS STPECC QSYSS--EDL ISAAT SP E GNM RALTSIVNS ISAADGA-VAF--PM DIPK 250	
Carp	QGSGSTCCSSPEWS SASEQC CAPAY STHED LLN-DDS SEC TNIR SLTISVDS ITGTEVTFV PY --SV DISK 253	
Catfish	QGSGSTCCSSPEWS STPECC QSYSS--EDL ISAAD SP E GS MRLTLSIVD ITGTEGAP VAY --SV DTK 253	
Sole	PSTGSTCCSSPEWS STPECC QSYSS--EDL ISAAD SP E GS MRLTLSIVD ITG TEATVAY --SV DISK 244	
Zebrafish	QGSGSTCCSSPEWS SASDHCPVASSA ED LLN-DDSSECSNLRLTLSIVD ITGTE ATVAY --SV DISK 256	
Fugu	PSSGSTCCSSPEWS STPDQCT QSYSS--EDL ISAAD SP D GS MRLTLSIAIVD IS AADAA -VAF--SM DIP 248	
Pufferfish	PSSGSTCCSSPEWS STPECC QSYSS--EDL ISAAD SP E GS MRLTLSIAIVD IS AADAA -VAF--SM DIP 248	
Salmon	QGSGSTCCSSPEWS NTSDHCTQSYSN -ED LIS-ADSP CTN IRLTLSIVDS ITAAEGAP VAYPVPVDIPK 254	
Pejerrey	----- 149	

Figure S2. Amino acid alignment of MyoG of tilapia (*Oreochromis niloticus*; [GU246717.1](#)), gilthead seabream (*Sparus aurata*; [EF462192.1](#)), carp (*Cyprinus carpio*; [AB012881.1](#)), catfish (*Ictalurus punctatus*; [AY534329.1](#)), sole (*Solea senegalensis*; [EU934044.1](#)), zebrafish (*Danio rerio*; [NM_131006.1](#)), fugu (*Takifugu rubripes*; [AY566282.1](#)), pufferfish (*Tetraodon nigroviridis*; [AY822074.1](#)), salmon (*Salmo salar*; [NM_001123600.1](#)) and pejerrey (*Odontesthes bonariensis*; [HM061694.1](#)). Identical amino acids are in black. The His / Cys-rich domain is indicated by a black line over the sequence and the bHLH domain is boxed.

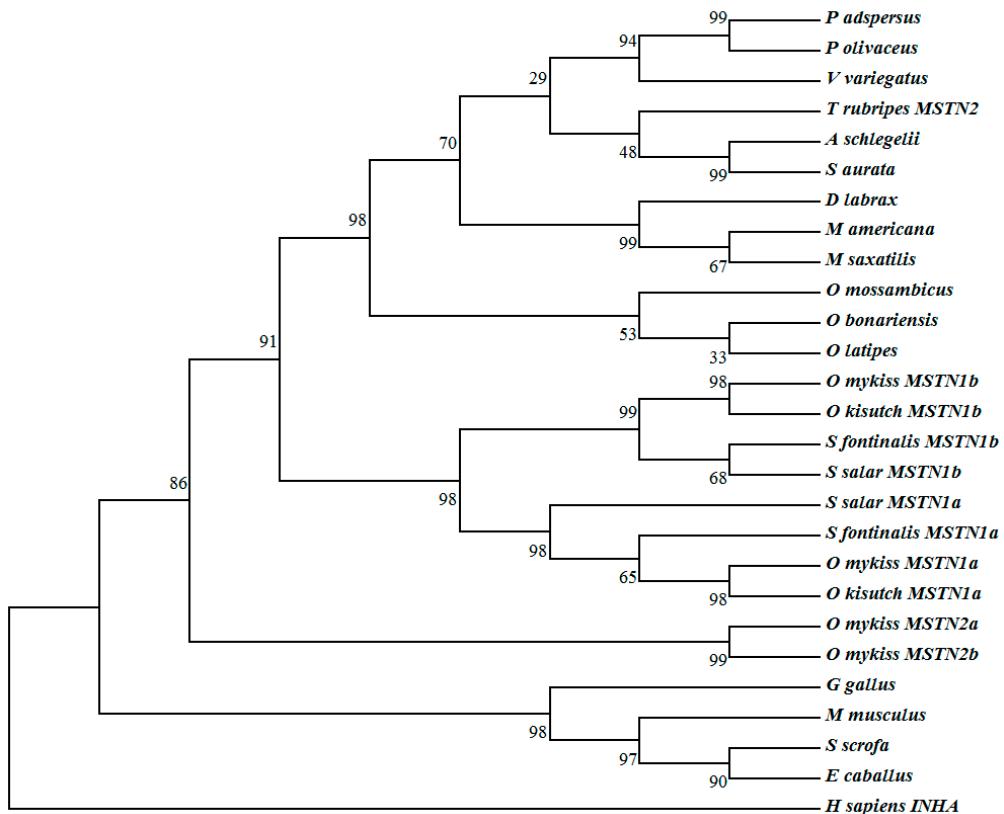


Figure S3. Molecular Phylogenetic analysis by Maximum Likelihood method carried out with the partial nucleotide sequence of MSTN open reading frame (500 bootstrap replicates, nucleotide p-distance and 864 informative sites) with Mega5 program (Tamura et al., 2011). The percentage of replicate trees in which the associated taxa clustered together in the bootstrap test (500 replicates) is shown next to the branches. The human α -inhibin (NM_002191.3) was used as out-group. The accession numbers of the MSTN sequences are as follows: *Acanthopagrus schlegelii* (DQ303480.1), *Dicentrarchus labrax* (AY839106.1), *Equus caballus* (NM_001081817.1), *Gallus gallus* (NM_001001461.1), *Morone americana* (AF290911.1), *Morone saxatilis* (AF290910.1), *Mus musculus* (NM_010834.2), *Odontesthes bonariensis* (HM061693.1), *Oncorhynchus mykiss* (NM_001124282.1), *Oncorhynchus mykiss* MSTN-2 (NM_001124283.2), *Oreochromis mossambicus* (AF197193.3), *Oryzias latipes* (NM_001201499.1), *Paralichthys adspersus* (EU443627.1), *Paralichthys olivaceus* (DQ412048.1), *Salmo salar* MSTN-1a (NM_001123549.1), *Salmo salar* MSTN-1b (NM_001123634.1), *Salvelinus fontinalis* (AF247650.2), *Sparus aurata* (AF258448.1), *Sus scrofa* (NM_214435.2), *Takifugu rubripes* MSTN-2 (NM_001032672.1), *Verasper variegatus* (JN226745.1).

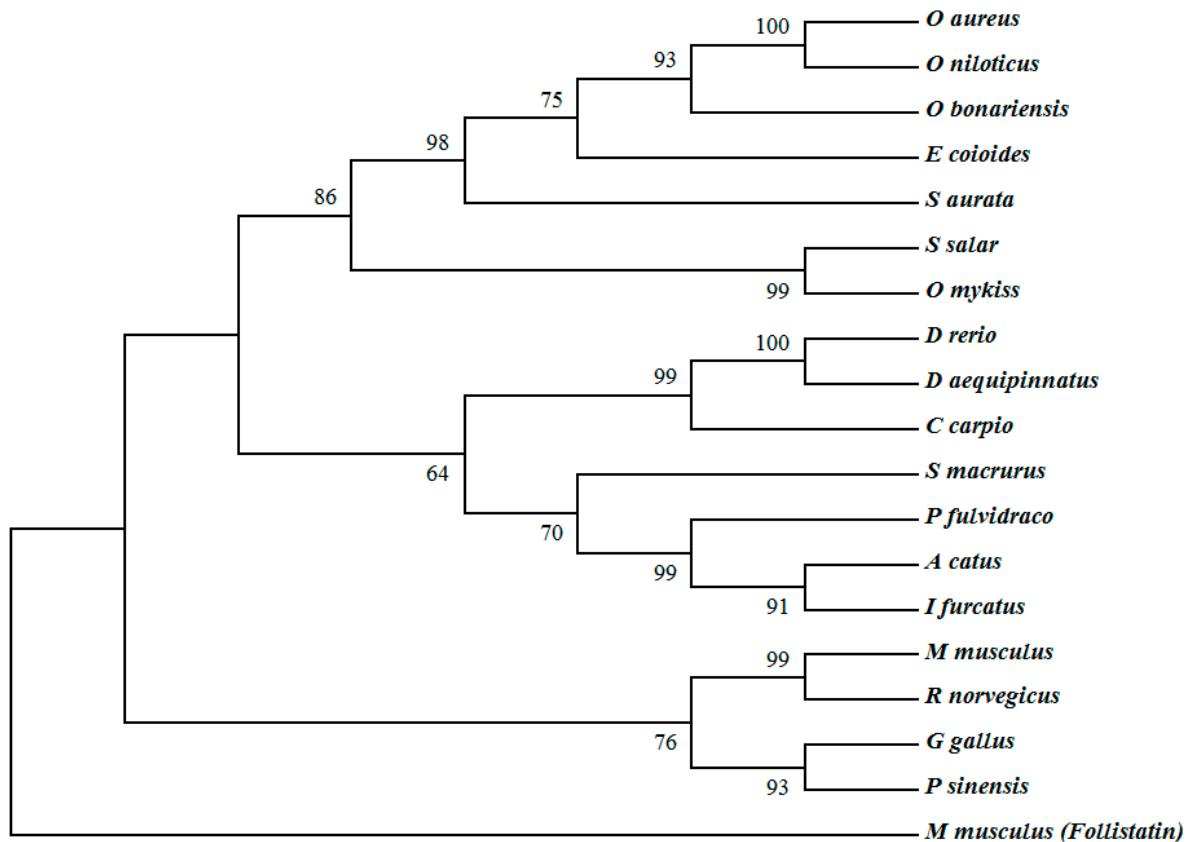


Figure S4. Molecular Phylogenetic analysis by Maximum Likelihood method carried out with the partial nucleotide sequence of MyoG open reading frame (500 bootstrap replicates, nucleotide p-distance and 394 informative sites) with Mega5 program (Tamura et al. 2011). The percentage of replicate trees in which the associated taxa clustered together in the bootstrap test (500 replicates) is shown next to the branches. The mouse follistatin (NM_008046.2) was used as out-group. The accession numbers of the MSTN sequences are as follows: *Ameiurus catus* ([AY562557.1](#)), *Cyprinus carpio* ([AB012881.1](#)), *Danio aequipinnatus* ([DQ219849.1](#)), *Danio rerio* ([NM_131006.1](#)), *Epinephelus coioides* ([HM190251.1](#)), *Gallus gallus* ([NM_204184.1](#)), *Ictalurus furcatus* ([AY540993.1](#)), *Mus musculus* ([NM_031189.2](#)), *Odontesthes bonariensis* ([HM061694.1](#)), *Oncorhynchus mykiss* ([Z46912.1](#)), *Oreochromis aureus* ([GU246726.1](#)), *Oreochromis niloticus* ([GU246725.1](#)), *Pelodiscus sinensis* ([AB480162.1](#)), *Pelteobagrus fulvidraco* ([HQ246723.1](#)), *Rattus norvegicus* ([NM_017115.2](#)), *Salmo salar* ([DQ294029.2](#)), *Sparus aurata* ([EF462191.1](#)), *Sternopygus macrurus* ([AY396565.1](#)).

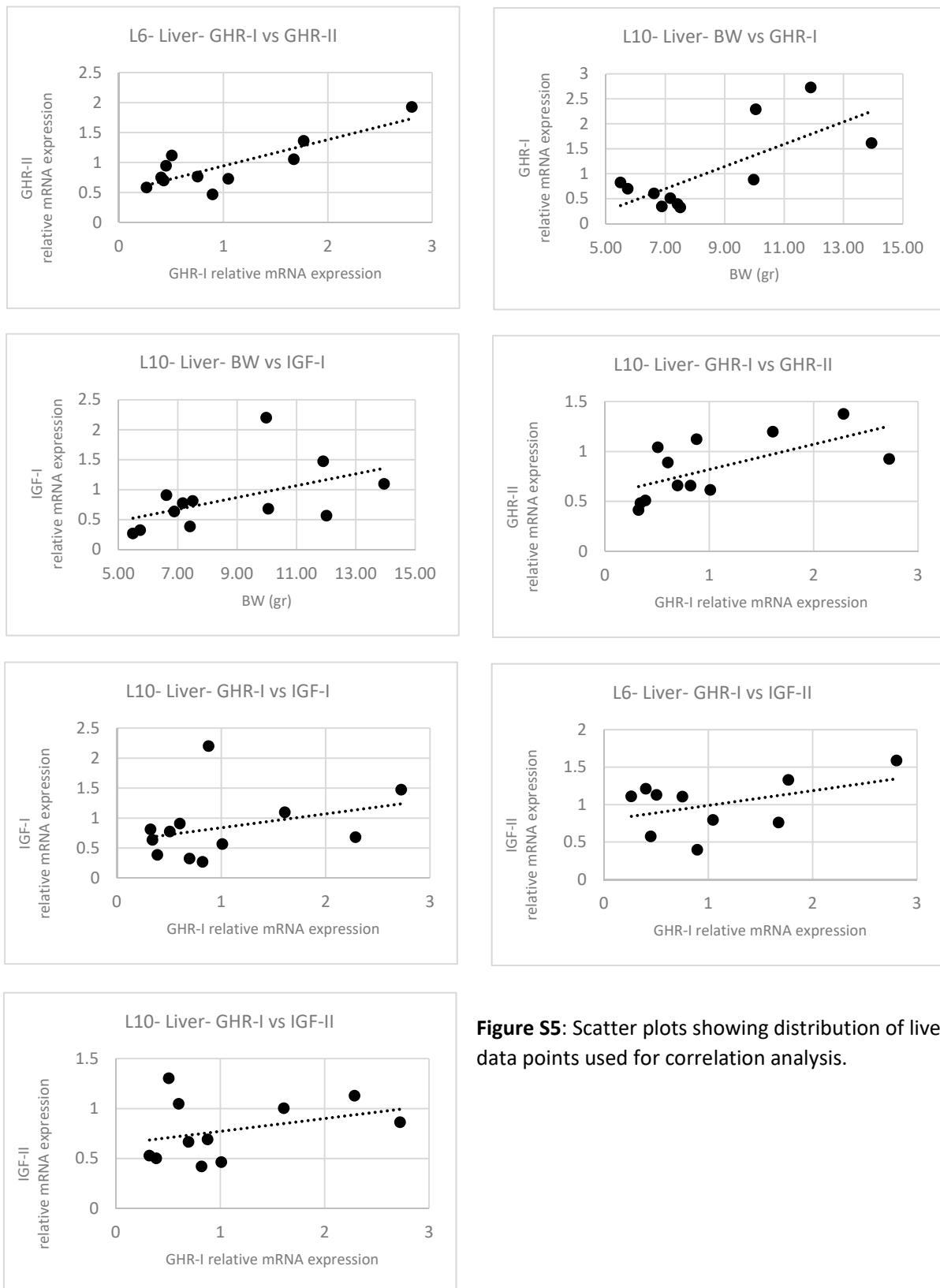


Figure S5: Scatter plots showing distribution of liver data points used for correlation analysis.

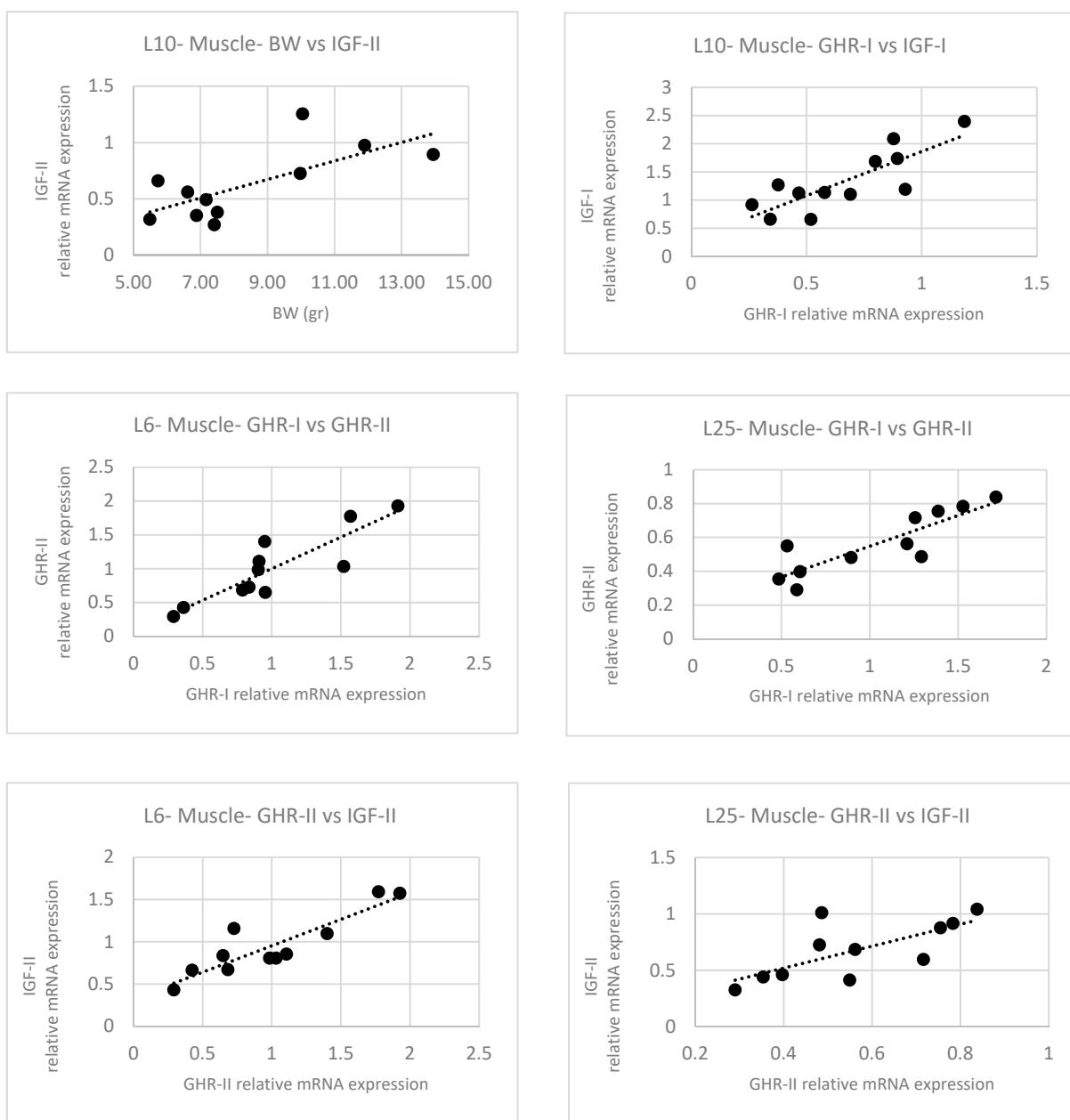


Figure S6: Scatter plots showing distribution of muscle data points used for correlation analysis.

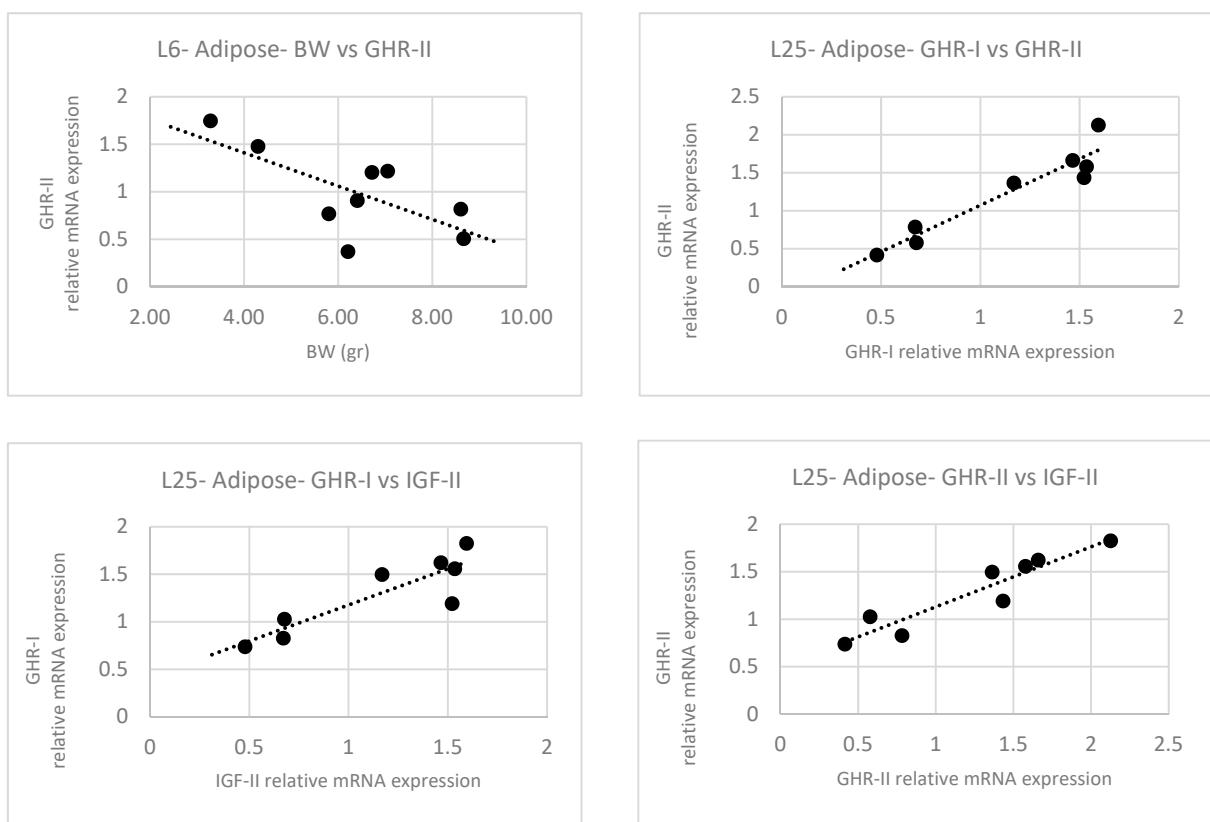


Figure S7: Scatter plots showing distribution of adipose tissue data points used for correlation analysis.