

**Appendix from R. M. Cox et al., “Hormonally Mediated Increases in Sex-Biased Gene Expression Accompany the Breakdown of Between-Sex Genetic Correlations in a Sexually Dimorphic Lizard”
(Am. Nat., vol. 189, no. 3, p. 315)**

Supplemental Tables A1–A7 and Figure A1

Table A1: Quantitative genetics of sexual dimorphism in growth rate

Trait and age	Sample size (N)		Residual variance (V_e)		Additive genetic variance (V_a)		Heritability (h^2)		Between-sex covariance	Between-sex r_{mf}
	Male	Female	Male	Female	Male	Female	Male	Female		
SVL growth:										
1-3	339	355	$3.93 \times 10^{-4} \pm 4.02 \times 10^{-5}$	$3.87 \times 10^{-4} \pm 4.19 \times 10^{-5}$	$2.23 \times 10^{-5} \pm 2.97 \times 10^{-5}$	$3.42 \times 10^{-5} \pm 3.42 \times 10^{-5}$	$.054 \pm .071$	$.081 \pm .080$	2.76×10^{-5}	1
3-6	318	338	$2.71 \times 10^{-4} \pm 2.15 \times 10^{-5}$	$1.82 \times 10^{-4} \pm 2.28 \times 10^{-5}$	0	$2.98 \times 10^{-5} \pm 2.09 \times 10^{-5}$	0	$.141 \pm .096$...	1
6-9	271	291	$4.53 \times 10^{-4} \pm 3.90 \times 10^{-5}$	$1.57 \times 10^{-4} \pm 2.04 \times 10^{-5}$	0	$1.29 \times 10^{-5} \pm 1.72 \times 10^{-5}$	0	$.076 \pm .100$...	1
9-12	283	299	$3.67 \times 10^{-4} \pm 5.63 \times 10^{-5}$	$8.96 \times 10^{-5} \pm 1.18 \times 10^{-5}$	$9.75 \times 10^{-5} \pm 5.67 \times 10^{-5}$	$1.42 \times 10^{-5} \pm 1.06 \times 10^{-5}$	$.210 \pm .171$	$.137 \pm .100$	3.72×10^{-5}	$1 \pm .476$
12-24	269	290	$5.49 \times 10^{-5} \pm 1.05 \times 10^{-5}$	$1.14 \times 10^{-5} \pm 1.41 \times 10^{-6}$	$2.66 \times 10^{-5} \pm 1.19 \times 10^{-5}$	$1.39 \times 10^{-6} \pm 1.16 \times 10^{-6}$	$.326 \pm .134$	$.109 \pm .092$	2.91×10^{-6}	$.479 \pm .435$
Mass growth:										
1-3	356	374	$1.96 \times 10^{-6} \pm 1.90 \times 10^{-7}$	$2.01 \times 10^{-6} \pm 1.81 \times 10^{-7}$	$2.47 \times 10^{-8} \pm 1.24 \times 10^{-7}$	$2.15 \times 10^{-8} \pm 1.08 \times 10^{-7}$	$.012 \pm .063$	$.011 \pm .054$	2.31×10^{-8}	1
3-6	338	355	$3.11 \times 10^{-6} \pm 2.88 \times 10^{-7}$	$1.44 \times 10^{-6} \pm 1.73 \times 10^{-7}$	$1.44 \times 10^{-7} \pm 1.87 \times 10^{-7}$	$2.96 \times 10^{-7} \pm 1.64 \times 10^{-7}$	$.044 \pm .057$	$.171 \pm .091$	2.06×10^{-7}	1
6-9	288	297	$7.13 \times 10^{-6} \pm 5.95 \times 10^{-7}$	$2.69 \times 10^{-6} \pm 3.33 \times 10^{-7}$	0	$1.69 \times 10^{-7} \pm 2.64 \times 10^{-7}$	0	$.059 \pm .092$...	-1
9-12	291	300	$1.64 \times 10^{-5} \pm 1.98 \times 10^{-6}$	$4.80 \times 10^{-6} \pm 3.93 \times 10^{-7}$	$3.08 \times 10^{-7} \pm 1.4 \times 10^{-6}$	0	$.018 \pm .088$	0	...	1
12-24	275	296	$6.46 \times 10^{-6} \pm 1.08 \times 10^{-6}$	$9.19 \times 10^{-7} \pm 1.30 \times 10^{-7}$	$2.13 \times 10^{-6} \pm 1.13 \times 10^{-6}$	$2.09 \times 10^{-7} \pm 1.27 \times 10^{-7}$	$.248 \pm .124$	$.185 \pm .108$	4.30×10^{-7}	$.644 \pm .370$

Note: Quantitative-genetic parameter estimates for growth in SVL (in millimeters per day) or body mass (in grams per day) over five age intervals. Parameter estimates (\pm SE) are derived from animal model analysis using a paternal half-sib breeding design. Boldface indicates values of V_a , h^2 , and r_{mf} significantly ($P < .05$) greater than 0.

Table A2: Gene ontology terms significantly enriched for sex-biased genes

Gene ontology category	Sex-biased genes	Adjusted <i>P</i>
Metabolic process	309	.0026
Single-organism metabolic process	305	.0010
Organic substance metabolic process	301	.0006
Primary metabolic process	289	.0021
Regulation of metabolic process	172	.0031
Response to wounding	55	.0016
Hemostasis	31	.0044
Negative regulation of multicellular organismal process	23	.0044
Steroid metabolic process	21	.0037
Digestion	18	<.0001
Protein activation cascade	16	<.0001
Protein maturation	15	.0015
Acute inflammatory response	15	<.0001
Neutral lipid metabolic process	13	.0031
Acylglycerol metabolic process	13	.0031
Triglyceride metabolic process	13	.0022
Protein processing	13	.0044
Platelet degranulation	13	.0002
Humoral immune response	12	.0009
Complement activation	11	<.0001
Regulation of coagulation	10	.0013
Regulation of hemostasis	10	.0009
Regulation of wound healing	10	.0044
Regulation of blood coagulation	10	.0009
Negative regulation of coagulation	9	.0003
Negative regulation of hemostasis	9	.0002
Acute-phase response	9	.0003
Negative regulation of blood coagulation	9	.0002
Regulation of ARF protein signal transduction	8	.0044
Regulation of ARF GTPase activity	8	.0005
Fibrolysis	8	<.0001
Complement activation, alternative pathway	7	<.0001
Regulation of protein processing	7	.0044
Lipid digestion	7	<.0001
Complement activation, classical pathway	6	.0038
Regulation of fibrolysis	6	.0002
Positive regulation of hemostasis	5	.0044
Intestinal cholesterol absorption	4	.0044
Negative regulation of fibrolysis	4	.0032
Multicellular organismal lipid catabolic process	3	.0031

Note: Significance was assessed following correction for multiple comparisons (Benjamini and Hochberg 1995). Gene ontology categories are sorted by the number of sex-biased genes and often represent subsets of larger categories.

Table A3: Mean expression of genes in the GH/IGF network by sex and age

Ensembl ID	Gene	Ensembl description	Juveniles (cpm)		Subadults (cpm)	
			Male	Female	Male	Female
ENSACAT00000010700	GHR	Growth hormone receptor	171.89	132.75	235.36	172.57
ENSACAT00000006111	GHRRH	Growth hormone releasing hormone receptor	24.74	26.66	22.71	31.81
ENSACAT00000016563	IGF1	Insulin-like growth factor 1 (somatomedin C)	30.11	16.87	230.29	17.29
ENSACAT00000008062	IGF1BP1	Insulin-like growth factor binding protein 1	44.05	30.15	30.97	51.77
ENSACAT00000004558	IGF1BP2	Insulin-like growth factor binding protein 2	30.91	25.17	21.44	17.61
ENSACAT00000008083	IGF1BP3	Insulin-like growth factor binding protein 3	21.31	25.49	13.49	15.55
ENSACAT00000016203	IGF1BP4	Insulin-like growth factor binding protein 4	103.75	60.52	263.98	146.04
ENSACAT00000000083	IGF1BP5	Insulin-like growth factor binding protein 5	1.39	.82	1.38	.70
ENSACAT00000029049	IGF1BP6	Insulin-like growth factor binding protein 6	.35	.12	.00	.00
ENSACAT00000002051	IGF1BP7	Insulin-like growth factor binding protein 7	5.33	6.36	7.61	3.63
ENSACAT00000029347	IGF1R	Insulin-like growth factor 1 receptor	1.45	1.02	.62	1.35
ENSACAT00000009701	IGF2	Insulin-like growth factor 2 (somatomedin A)	89.78	63.29	171.47	64.74
ENSACAT00000006271	IGF2BP1	Insulin-like growth factor 2 mRNA binding protein 1	.31	.34	.07	.00
ENSACAT00000008070	IGF2BP2	Insulin-like growth factor 2 mRNA binding protein 2	22.93	20.32	10.08	13.98
ENSACAT00000013612	IGF2BP3	Insulin-like growth factor 2 mRNA binding protein 3	204.22	224.05	174.28	282.02
ENSACAT00000014553	SHBG	Sex hormone-binding globulin	120.27	101.02	23.26	69.22

Note: This table shows 16 genes whose transcripts were quantified by RNA-seq analysis of *Anolis sagrei* livers and assigned to the growth hormone/insulin-like growth factor (GH/IGF) network based on the annotated cDNA set of the congener *Anolis carolinensis* (AnoCar 2.0; Ensembl release 75; Alföldi et al. 2011), the KEGG database (Kanehisa et al. 2004), and WikiPathways (Kelder et al. 2011).

Table A4: Mean expression of genes in the mTOR network by sex and age

Ensembl ID	Gene	Ensembl description	Juveniles (cpm)		Subadults (cpm)	
			Male	Female	Male	Female
ENSACAT00000011634	AKT1	V-AKT murine thymoma viral oncogene homolog 1	54.50	50.96	42.90	48.72
ENSACAT00000011317	BRAF	B-RAF protooncogene, serine/threonine kinase	.66	.62	.71	.48
ENSACAT00000029358	EIF4EBP1	Eukaryotic translation initiation factor 4E binding protein	255.31	267.55	533.88	207.88
ENSACAT00000011021	HIF1AN	Hypoxia inducible factor 1, α subunit inhibitor	3.73	6.00	4.72	5.02
ENSACAT00000003820	IRS1	Insulin receptor substrate 1	9.74	11.83	5.35	9.79
ENSACAT00000000480	MTOR	Mechanistic target of rapamycin	53.60	48.59	39.75	69.44
ENSACAT00000004979	PIK3CA	Phosphatidylinositol-4,5-bisphosphate 3-kinase, catalytic subunit α	4.57	4.26	2.68	3.95
ENSACAT00000017770	PIK3R5	Phosphoinositide-3-kinase, regulatory subunit 5	.00	.15	.00	.23
ENSACAT00000010286	PRKAA1	Protein kinase, AMP-activated, α 1 catalytic subunit	28.32	32.19	33.64	36.15
ENSACAT00000006834	PRKAA2	Protein kinase, AMP-activated, α 2 catalytic subunit	8.48	6.39	6.57	4.85
ENSACAT00000013230	PRKAB2	Protein kinase, AMP-activated, β 2 noncatalytic subunit	2.06	2.53	1.82	2.14
ENSACAT00000008189	PRKAG1	Protein kinase, AMP-activated, γ 1 noncatalytic subunit	29.95	26.06	33.25	31.72
ENSACAT00000002435	PRKAG2	Protein kinase, AMP-activated, γ 2 noncatalytic subunit	6.09	6.96	7.63	9.61
ENSACAT00000012952	PRKAG3	Protein kinase, AMP-activated, γ 3 noncatalytic subunit	2.70	2.34	1.68	3.83
ENSACAT00000006498	PRKCH	Protein kinase C	21.02	24.38	18.22	17.37
ENSACAT00000015152	PTEN	Phosphatase and tensin homolog	13.46	15.56	14.35	13.75
ENSACAT00000010084	RICTOR	RPTOR independent companion of MTOR, complex 2	39.74	42.68	15.21	22.40
ENSACAT00000015640	RPTOR	Regulatory associated protein of MTOR, complex 1	2.90	2.44	2.55	1.41
ENSACAT00000015594	RPS6KA2	Ribosomal protein S6 kinase	13.80	17.28	14.06	7.56
ENSACAT00000006193	RPS6KC1	Ribosomal protein S6 kinase	41.86	25.62	48.74	21.61
ENSACAT00000012470	STRADA	STE20-related kinase adaptor α	11.18	11.72	15.75	14.92
ENSACAT00000001329	STRADB	STE20-related kinase adaptor β	103.90	103.52	78.71	116.19
ENSACAT00000004260	TSC1	Tuberous sclerosis 1	449.04	298.67	112.80	149.76
ENSACAT00000008992	TSC2	Tuberous sclerosis 2	10.97	14.72	8.24	12.10
ENSACAT00000001649	VEGFA	Vascular endothelial growth factor A	106.00	101.38	72.27	99.97

Note: This table shows 25 genes whose transcripts were quantified by RNA-seq analysis of *Anolis sagrei* livers and assigned to the mechanistic target of rapamycin (mTOR) network based on the annotated cDNA set of the congener *Anolis carolinensis* (AnoCar 2.0; Ensembl release 75; Alföldi et al. 2011), the KEGG database (Kanehisa et al. 2004), and WikiPathways (Kelder et al. 2011).

Table A5: Mean expression of genes in the insulin-signaling network by sex and age

Ensembl ID	Gene	Ensembl description	Juveniles (cpm)		Subadults (cpm)	
			Male	Female	Male	Female
ENSACAT00000011634	AKT1	V-AKT murine thymoma viral oncogene homolog 1	54.50	50.96	42.90	48.72
ENSACAT00000004315	CDKN1B	Cyclin-dependent kinase inhibitor 1B	9.33	7.09	10.18	8.91
ENSACAT00000014236	EIF4E	Eukaryotic translation initiation factor 4E	17.09	18.09	24.13	21.31
ENSACAT00000029358	EIF4EBP1	Eukaryotic translation initiation factor 4E binding protein 1	255.31	267.55	533.88	207.88
ENSACAT00000004723	ELK1	ELK1, member of ETS oncogene family	.41	.69	1.36	1.26
ENSACAT00000013303	FBP1	Fructose-1,6-biphosphatase 1	1,277.06	1,218.46	1,412.73	1,602.15
ENSACAT00000017291	FLOT1	Flotillin 1	89.01	87.89	67.43	50.60
ENSACAT00000008015	FLOT2	Flotillin 2	227.34	244.52	217.14	213.97
ENSACAT00000001070	G6PC2	Glucose-6-phosphatase, catalytic 2	.72	1.00	.26	1.07
ENSACAT00000007397	GNL3	Guanine nucleotide binding protein-like 3	5.10	4.18	5.86	6.49
ENSACAT00000006564	GRB2	Growth factor receptor-bound protein 2	77.34	100.82	59.66	64.33
ENSACAT00000004836	GYS1	Glycogen synthase 1 (muscle)	26.10	23.33	23.18	14.30
ENSACAT00000002209	CBL	CBL protooncogene, E3 ubiquitin protein ligase	3.94	3.70	2.47	2.25
ENSACAT00000007957	LIPE	Lipase, hormone sensitive	.04	.40	.50	.29
ENSACAT000000003820	IRS1	Insulin receptor substrate 1	9.74	11.83	5.35	9.79
ENSACAT00000012637	IRS4	Insulin receptor substrate 4	27.22	19.77	13.00	18.16
ENSACAT00000000408	MAP2K2	Mitogen-activated protein kinase 2	29.76	30.62	23.50	28.56
ENSACAT00000001764	MAP2K3	Mitogen-activated protein kinase 3	114.24	65.24	30.77	37.04
ENSACAT00000017532	MAP2K4	Mitogen-activated protein kinase 4	8.02	8.76	7.92	9.24
ENSACAT00000010177	MAP2K5	Mitogen-activated protein kinase 5	11.07	13.02	17.16	16.20
ENSACAT000000030866	MAP2K6	Mitogen-activated protein kinase 6	17.19	18.65	14.87	11.12
ENSACAT00000009956	MAP2K7	Mitogen-activated protein kinase 7	3.10	3.25	5.27	3.44
ENSACAT00000013773	MLST8	MTOR associated protein, LST8 homolog	25.24	10.51	13.88	13.94
ENSACAT00000010374	MYC	V-MYC avian myelocytomatosis viral oncogene homolog	18.26	22.49	47.86	119.55
ENSACAT00000013790	NR3C1	Nuclear receptor subfamily 3, group C, member 1	3.54	5.53	6.18	2.99
ENSACAT00000017591	PDE3A	Phosphodiesterase 3A, cGMP-inhibited	5.87	7.01	5.34	5.22
ENSACAT00000003554	PDPK1	3-phosphoinositide dependent protein kinase 1	34.56	33.05	34.22	36.69
ENSACAT00000016391	PCK1	Phosphoenolpyruvate carboxykinase 1	2.02	2.38	3.65	1.69
ENSACAT00000001275	PCK2	Phosphoenolpyruvate carboxykinase 2	1,552.15	1,160.37	1,196.04	1,167.98
ENSACAT00000004827	PPARA	Peroxisome proliferator-activated receptor α	1.98	2.58	4.01	4.55
ENSACAT00000011918	PHKA2	Phosphorylase kinase, α 2	18.44	20.48	11.11	18.49
ENSACAT00000004979	PIK3CA	Phosphatidylinositol-4,5-bisphosphate 3-kinase, catalytic subunit α	4.57	4.26	2.68	3.95
ENSACAT00000017770	PIK3R5	Phosphoinositide-3-kinase, regulatory subunit 5	.00	.15	.00	.23
ENSACAT00000010286	PRKAA1	Protein kinase, AMP-activated, α 1 catalytic subunit	28.32	32.19	33.64	36.15
ENSACAT00000006834	PRKAA2	Protein kinase, AMP-activated, α 2 catalytic subunit	8.48	6.39	6.57	4.85
ENSACAT00000013230	PRKAB2	Protein kinase, AMP-activated, β 2 noncatalytic subunit	2.06	2.53	1.82	2.14
ENSACAT00000008189	PRKAG1	Protein kinase, AMP-activated, γ 1 noncatalytic subunit	29.95	26.06	33.25	31.72
ENSACAT00000002435	PRKAG2	Protein kinase, AMP-activated, γ 2 noncatalytic subunit	6.09	6.96	7.63	9.61
ENSACAT00000012952	PRKAG3	Protein kinase, AMP-activated, γ 3 noncatalytic subunit	2.70	2.34	1.68	3.83
ENSACAT00000006498	PRKCH	Protein kinase C	21.02	24.38	18.22	17.37
ENSACAT00000015152	PTEN	Phosphatase and tensin homolog	13.46	15.56	14.35	13.75
ENSACAT00000012973	RAC1	RAS-related C3 botulinum toxin substrate 1	33.66	29.72	33.38	30.59
ENSACAT00000016135	RAC2	RAS-related C3 botulinum toxin substrate 2	6.03	7.80	4.68	8.06
ENSACAT000000029270	RAF1	RAF-1 protooncogene, serine/threonine kinase	.88	1.46	1.68	2.21
ENSACAT00000013894	RAPGEF1	RAP guanine nucleotide exchange factor (GEF) 1	1.85	2.04	1.61	2.74
ENSACAT00000004483	RASD1	RAS, dexamethasone-induced 1	3.32	2.94	2.17	11.12
ENSACAT00000002273	RHEB	RAS homolog enriched in brain	16.96	17.81	23.28	11.01
ENSACAT00000014310	RHO	Anolis carolinensis rhodopsin (rho), mRNA	.09	.16	.14	.00
ENSACAT00000010084	RICTOR	RPTOR independent companion of MTOR, complex 2	39.74	42.68	15.21	22.40
ENSACAT00000013049	RPS6KB1	Ribosomal protein S6 kinase, 70kDa, polypeptide 1	6.84	4.63	5.82	4.23
ENSACAT00000016838	RPS6L1	Ribosomal protein S6 kinase-like 1	7.91	9.09	6.01	9.99
ENSACAT00000015640	RPTOR	Regulatory associated protein of MTOR	2.90	2.44	2.55	1.41
ENSACAT00000015879	SHC1	SHC (SRC homology 2 domain containing) transforming protein 1	29.40	40.61	22.13	34.72
ENSACAT00000012679	SHC2	SHC (SRC homology 2 domain containing) transforming protein 2	22.22	23.86	24.69	19.66

Table A5 (Continued)

Ensembl ID	Gene	Ensembl description	Juveniles (cpm)		Subadults (cpm)	
			Male	Female	Male	Female
ENSACAT0000005997	SHC4	SHC (SRC homology 2 domain containing) family, member 4	.37	.77	.16	.52
ENSACAT00000014599	SOCS1	Suppressor of cytokine signaling 1	3.81	5.46	7.53	7.65
ENSACAT00000012617	SOCS2	Suppressor of cytokine signaling 2	18.95	11.63	17.07	16.71
ENSACAT00000016330	SOCS4	Suppressor of cytokine signaling 4	.99	1.03	.63	.53
ENSACAT00000004217	SOCS5	Suppressor of cytokine signaling 5	7.40	9.72	11.57	11.39
ENSACAT00000011543	SOCS6	Suppressor of cytokine signaling 6	2.55	4.59	4.71	1.51
ENSACAT00000007427	SOCS7	Suppressor of cytokine signaling 7	.74	.29	.52	.23
ENSACAT00000006394	SOS1	Son of sevenless homolog 1	4.83	7.48	6.32	8.10
ENSACAT00000001643	SOS2	Son of sevenless homolog 2	67.37	75.18	58.78	60.00
ENSACAT00000006298	STAT1	Signal transducer and activator of transcription 1	10.58	14.52	12.77	10.59
ENSACAT00000025425	STAT2	Signal transducer and activator of transcription 2	61.21	61.07	59.97	57.71
ENSACAT00000018021	STAT3	Signal transducer and activator of transcription 3	47.95	53.68	33.39	38.34
ENSACAT00000009792	STAT6	Signal transducer and activator of transcription 6	35.54	29.55	27.82	32.07
ENSACAT00000014051	STK11	Serine/threonine kinase 11	22.91	26.03	23.01	31.95
ENSACAT00000001057	TGFB1	Transforming growth factor, β 1	4.14	6.41	6.29	12.76
ENSACAT00000001108	TGFB2	Transforming growth factor, β 2	19.24	10.64	6.40	5.29
ENSACAT00000017101	TGFB3	Transforming growth factor, β 3	14.49	12.67	5.20	6.69
ENSACAT00000025616	TGFBR3L	Transforming growth factor, β receptor 3-like	2.60	2.00	.67	1.18
ENSACAT00000009230	TGFBR1	Transforming growth factor, β receptor 1	5.99	6.42	5.42	4.43
ENSACAT00000014316	TGFBR2	Transforming growth factor, β receptor 2	23.33	29.67	30.08	24.21
ENSACAT00000001424	TGFBR3	Transforming growth factor, β receptor 3	9.30	7.73	9.63	6.30
ENSACAT00000004260	TSC1	Tuberous sclerosis 1	449.04	298.67	112.80	149.76
ENSACAT00000008992	TSC2	Tuberous sclerosis 2	10.97	14.72	8.24	12.10

Note: This table shows 76 genes whose transcripts were quantified by RNA-seq analysis of *Anolis sagrei* livers and assigned to the insulin-signaling network based on the annotated cDNA set of the congener *Anolis carolinensis* (AnoCar 2.0; Ensembl release 75; Alföldi et al. 2011), the KEGG database (Kanehisa et al. 2004), and WikiPathways (Kelder et al. 2011).

Table A6: Sex-biased expression of GH/IGF genes in juveniles and subadults

Gene	Juveniles				Subadults			
	Male (cpm)	Female (cpm)	Sex bias	Uncorrected <i>P</i>	Male (cpm)	Female (cpm)	Sex bias	Uncorrected <i>P</i>
GHR	171.89	132.75	1.30	.1796	235.36	172.57	1.36	.1103
GHRRH	24.74	26.66	-1.07	.7696	22.71	31.81	-1.40	.2435
IGF1	30.11	16.87	1.78	.0553	230.29	17.29	13.14	<.0001
IGFBP1	44.05	30.15	1.47	.1611	30.97	51.77	-1.65	.1691
IGFBP2	30.91	25.17	1.24	.3336	21.44	17.61	1.22	.3401
IGFBP3	21.31	25.49	-1.20	.3482	13.49	15.55	-1.16	.4419
IGFBP4	103.75	60.52	1.71	.0262	263.98	146.04	1.81	.0117
IGFBP5	1.39	.82	1.74	.2623	1.38	.70	1.86	.4791
IGFBP6	.35	.12	2.39	.6358	.00	.00
IGFBP7	5.33	6.36	-1.19	.5580	7.61	3.63	1.98	.0345
IGF1R	1.45	1.02	1.50	.5159	.62	1.35	-2.29	.3469
IGF2	89.78	63.29	1.42	.2735	171.47	64.74	2.63	.0025
IGF2BP1	.31	.34	1.00	.9984	.07	.00
IGF2BP2	22.93	20.32	1.13	.5418	10.08	13.98	-1.38	.1994
IGF2BP3	204.22	224.05	-1.10	.6231	174.28	282.02	-1.62	.0058
SHBG	120.27	101.02	1.19	.4530	23.26	69.22	-2.96	<.0001

Note: Sex bias in gene expression (fold difference in counts per million between males and females; positive values are male biased, and negative values are female biased) is shown for 16 genes assigned to the growth hormone/insulin-like growth factor (GH/IGF) network. Uncorrected *P* values are from pairwise exact tests with a negative binomial distribution. Boldface indicates significant sex-biased expression (uncorrected *P* < .0031 after Bonferroni correction for 16 comparisons). In subadults, two genes (IGFBP6, IGF2BP1) had undetectable expression levels for one or both sexes and therefore could not be assigned a fold difference in expression.

Table A7: IPA pathways significantly enriched for genes responsive to testosterone

Top canonical pathways	<i>P</i>	Overlap	Testosterone-responsive genes in pathway
Factors promoting cardiogenesis in vertebrates	.000049	12/92	BMP4, CER1, PRKCD, TDGF1, ACVR1, PRKCE, DKK1, GSK3B, PRKD3, BMP5, CDK2, PRKCA
Pyridoxal 5'-phosphate salvage pathway	.000237	9/64	PAK1, SGK1, PRKCD, PRKCE, PAK7, G6PC, MAP2K1, CDK2, LIMK1
Growth hormone signaling	.000323	10/81	GHR, IGF1, PRKCD, IRS1, CEBPA, IGFALS, PRKCE, RPS6KA5, PRKD3, PRKCA
LPS/IL-1-mediated inhibition of RXR function	.000404	18/221	CHST4, SLC10A1, GSTM5, HS3ST4, SOD3, IL18, NR0B2, HS3ST2, SULT1A3/SULT1A4, FABP1, CYP2A6, CHST10, FABP5, PLTP, SULT1C3, ALDH16A1, FMO4, ALDH5A1
NRF2-mediated oxidative stress response	.000687	16/193	AKR7A3, GSTM5, PRDX1, DNAJC15, SOD3, DNAJC5G, FTL, PRKCD, IRS1, PRKCE, GSK3B, SQSTM1, MAP2K1, ACTC1, PRKD3, PRKCA

Note: This table shows the top five pathways enriched for genes responsive to testosterone, arranged by increasing *P* values and shown alongside overlap (number of significantly responsive genes/total number of genes in the pathway that were expressed in the liver) and ortholog names for genes responsive to testosterone in juvenile females ($P < .05$ without false discovery rate correction). Analyses were conducted using ingenuity pathway analysis (IPA; Qiagen, Valencia, CA).

