

1. BIP

Grey shade - Identical amino acid sequences

Yellow shade - Nucleotide-binding domain

Hm BIP 1	MKLSLVAAMLLLSAARAEEDKEDV	GTVVGIDLGTTCYSCVGFNKRVEI	IANDQGNR	60	
Ms BIP 2	MKLSLVAAMLLLSAARAEEDKEDV	GTVVGIDLGTTCYSCVGFNKRVEI	IANDQGNR	61	
Hm BIP 61	ITPSYVAFTEPEGERLIGDAAKNQLT	SNPENTVFDAKRLIGRTWNPDSVQ	QDQIKLPPFKVV	120	
Ms BIP 122	ITPSYVAFTEPEGERLIGDAAKNQLT	SNPENTVFDAKRLIGRTWNPDSVQ	QDQIKLPPFKVV	121	
Hm BIP 121	EKKTKPYIQVDIGGGQTKTFAP	EIISAMVLRKMKETAAYLGKVKTHAV	VTVPAIFNDQA	180	
Ms BIP 182	EKKTKPYIQVDIGGGQTKTFAP	EIISAMVLRKMKETAAYLGKVKTHAV	VTVPAIFNDQA	181	
Hm BIP 181	ROATKDAGTIAGLNMVRIINEP	TAAAYGLDKRREGEKNI	LVFDLGGGTFVDSLLTIDNG	240	
Ms BIP 242	ROATKDAGTIAGLNMVRIINEP	TAAAYGLDKRREGEKNI	LVFDLGGGTFVDSLLTIDNG	241	
Hm BIP 241	VFEVATNGDTHLGGEDFDQR	VMHEPFIKLYKTKTKGDKV	RKDNRAVQKLRREVEKAKRAL	300	
Ms BIP 242	VFEVATNGDTHLGGEDFDQR	VMHEPFIKLYKTKTKGDKV	RKDNRAVQKLRREVEKAKRAL	301	
Hm BIP 301	SOHOARIEIESFEGEDFSETL	TRAKFEELNMDLFRSTMKPVQK	VLSDKSKSDIDEIV	360	
Ms BIP 302	SOHOARIEIESFEGEDFSETL	TRAKFEELNMDLFRSTMKPVQK	VLSDKSKSDIDEIV	361	
Hm BIP 361	LVGGSTRIPKIQQLVKEFNG	KPEFRSGINPDEAVYGA	VAQVQVLSGDDQDGLVLLDVC	420	
Ms BIP 362	LVGGSTRIPKIQQLVKEFNG	KPEFRSGINPDEAVYGA	VAQVQVLSGDDQDGLVLLDVC	421	
Hm BIP 421	PLTGLIEVGGVMTKILPR	NTVPTKKSQIFSTADSNQ	PVTIKVYGERPLTKDNHLLG	480	
Ms BIP 422	PLTGLIEVGGVMTKILPR	NTVPTKKSQIFSTADSNQ	PVTIKVYGERPLTKDNHLLG	481	
Hm BIP 441	TFDLTGIPAPRGVQIEV	TFEIDVNGILRVTAEDK	TGNKNIITINDQNR	LTPEEIER	540
Ms BIP 442	TFDLTGIPAPRGVQIEV	TFEIDVNGILRVTAEDK	TGNKNIITINDQNR	LTPEEIER	541
Hm BIP 541	MVNDAEKFAEDKLLKER	IDTRNELESYAYSLK	QIDGKELGKLSSEDKETMEKAVEE	600	
Ms BIP 542	MVNDAEKFAEDKLLKER	IDTRNELESYAYSLK	QIDGKELGKLSSEDKETMEKAVEE	601	
Hm BIP 601	KIEWLESHQDADIEDPK	KAKKLEEEIQPIISK	LYSAGPPPTGEEDTARKDEL	654	
Ms BIP 602	KIEWLESHQDADIEDPK	KAKKLEEEIQPIISK	LYSAGPPPTGEEDTARKDEL	655	

2. ATP6

Grey shade - Identical amino acid sequences

Yellow shade - Transcription activation domain

Green shade - B-zip domain

Hm ATP6 1	MESPPSPGLFHRLED	WDSALFAELGYFTD	TDELEAENFIYENNFD	NLDLDDLMPWE	70		
Ms ATP6 1	MESPPSPGLFHRLED	WDSALFAELGYFTD	TDELEAENFIYENNFD	NLDLDDLMPWE	60		
Hm ATP6 71	SDIWINNOICTVK	IKAEQPLSPASSSV	SSPRSDSSTQHV	PEELDLSSSQS	130		
Ms ATP6 61	SDIWINNOICTVK	IKAEQPLSPASSSV	SSPRSDSSTQHV	PEELDLSSSQS	118		
Hm ATP6 131	PLSYGNSNSLSA	EAPLKEKDPVTPGR	NKTEENGLTPKKIQV	NSKPSIQPKLLPAA	190		
Ms ATP6 119	PLSYGNSNSLSA	EAPLKEKDPVTPGR	NKTEENGLTPKKIQV	NSKPSIQPKLLPAA	177		
Hm ATP6 191	KTQTNSSVPAK	IIQTPTLPA	MLAKQOPIISLQ	PAPTRGQTVLLSQ	PTVQLQAVLP	250	
Ms ATP6 178	KTQTNSSVPAK	IIQTPTLPA	MLAKQOPIISLQ	PAPTRGQTVLLSQ	PTVQLQAVLP	237	
Hm ATP6 251	SAQPLVAVAGG	VTVLPHVNVV	PAPSANVPGKLS	VTKPVQLSTMR	NVGSIAVLR	310	
Ms ATP6 238	SAQPLVAVAGG	VTVLPHVNVV	PAPSANVPGKLS	VTKPVQLSTMR	NVGSIAVLR	297	
Hm ATP6 311	QRMIKRESAC	QRKKEVYMLGL	EARLKAALSEN	BOLKKEGNIKRL	EVVSENQRKL	370	
Ms ATP6 298	QRMIKRESAC	QRKKEVYMLGL	EARLKAALSEN	BOLKKEGNIKRL	EVVSENQRKL	357	
Hm ATP6 371	VSPKRRVVC	MIVLAFIIL	INYPGMSMLE	QDSRRMNP	SVSPANORHLLG	FSKAEQDTS	430
Ms ATP6 358	VSPKRRVVC	MIVLAFIIL	INYPGMSMLE	QDSRRMNP	SVSPANORHLLG	FSKAEQDTS	417
Hm ATP6 431	DGIIQKNSY	RYDHSVNDK	ALMVLTEPELLY	IPPPCQPLINT	TESLRNLH	ELRGVHRH	490
Ms ATP6 418	DGIIQKNSY	RYDHSVNDK	ALMVLTEPELLY	IPPPCQPLINT	TESLRNLH	ELRGVHRH	477
Hm ATP6 491	EVERTKSR	RMNTNQQKTR	ILQALQEG	QNSQLMAVQY	TETTSSISR	NSGSELQVYASR	550
Ms ATP6 478	EVERTKSR	RMNTNQQKTR	ILQALQEG	QNSQLMAVQY	TETTSSISR	NSGSELQVYASR	536
Hm ATP6 551	SYQDFE	AIRRRGDTF	YVVSFRD	HLLPATTHNKT	TRPKMSIVL	PAININ	510
Ms ATP6 498	SYQDFE	AIRRRGDTF	YVVSFRD	HLLPATTHNKT	TRPKMSIVL	PAININ	510
Hm ATP6 611	EVMMQIDC	QVMDTRILH	IKSSVPPYLR	DQQRQNTFF	GGPPAATE	THVSTIPESLQ	670
Ms ATP6 598	EVMMQIDC	QVMDTRILH	IKSSVPPYLR	DQQRQNTFF	GGPPAATE	THVSTIPESLQ	656

3. IRE1r

Grey shade - Identical amino acid sequences

Yellow shade - Luminal dimerization domain

Green shade - Catalytic domain

Hm IRE1a 20	FGSTSTVTL	PETLLEFVSLD	SGSLHVA	SRRTGSKRWL	KEDPVLQV	PTHVEEPAFLDPD	79
Ms IRE1a 22	FGSTSTVTL	PETLLEFVSLD	SGSLHVA	SRRTGSKRWL	KEDPVLQV	PTHVEEPAFLDPD	81
Hm IRE1a 80	GSYTLGK	KNKNGLTKL	PFTTPEL	VQASPCRS	DGILYMK	QKDIWYV	139
Ms IRE1a 82	GSYTLGK	KNKNGLTKL	PFTTPEL	VQASPCRS	DGILYMK	QKDIWYV	141

Hm IRE1a140	SSAFADSLCPSTSLYLGR	TEXTITMDYDKTR	RELNRNATYFD	YASLPEDD	VDYKMSHV	199
Ms IRE1a 142	SSAFADSLCPSTSLYLGR	TEXTITMDYDKTR	RELNRNATYFD	YASLPEDD	VDYKMSHV	201
Hm IRE1a200	SNDDGLVVT	YDSESDGLV	QIYQYASV	VVAVYV	WQGVSR	259
Ms IRE1a 202	SNDDGLVVT	YDSESDGLV	QIYQYASV	VVAVYV	WQGVSR	261
Hm IRE1a260	VGRITKWKY	FPFPEAKSKL	TPFLVYK	YKTSYLS	VASV	319
Ms IRE1a 262	VGRITKWKY	FPFPEAKSKL	TPFLVYK	YKTSYLS	VASV	321
Hm IRE1a320	QTDGVTG	DGKGCVITP	STDPVDF	PKSKNKL	NLYRNYLL	379
Ms IRE1a 322	QTDGVTG	DGKGCVITP	STDPVDF	PKSKNKL	NLYRNYLL	381
Hm IRE1a380	PNNLKH	RENVIPADSEK	SFEV	INLVQ	TSNAPT	439
Ms IRE1a 382	PNNLKH	RENVIPADSEK	SFEV	INLVQ	TSNAPT	441
Hm IRE1a440	MLKMATI	ITLSTFL	LGVAFIT	ITP	SLM	499
Ms IRE1a 442	MLKMATI	ITLSTFL	LGVAFIT	ITP	SLM	499
Hm IRE1a500	PGD	TADQ	GLLDT	SGP	YSESS	559
Ms IRE1a 500	PGD	TADQ	GLLDT	SGP	YSESS	559
Hm IRE1a560	ETS	VIVG	KIS	CPK	VDL	619
Ms IRE1a 560	ETS	VIVG	KIS	CPK	VDL	619
Hm IRE1a620	DEHNV	RYE	CTE	KRQ	FOY	679
Ms IRE1a 620	DEHNV	RYE	CTE	KRQ	FOY	679
Hm IRE1a680	HSLN	VHRD	KPHN	IL	SM	739
Ms IRE1a 680	HSLN	VHRD	KPHN	IL	SM	739
Hm IRE1a740	FEH	SEK	NET	YV	IP	799
Ms IRE1a 740	FEH	SEK	NET	YV	IP	799
Hm IRE1a800	HEV	IARE	LE	TK	AM	859
Ms IRE1a 800	HEV	IARE	LE	TK	AM	859
Hm IRE1a860	QL	REG	RAV	V	K	919
Ms IRE1a 860	QL	REG	RAV	V	K	919
Hm IRE1a920	ETL	GS	L	P	D	977
Ms IRE1a 920	ETL	GS	L	P	D	977

4. IRE1t

Grey shade - Identical amino acid sequences

Yellow shade - Luminal dimerization domain

Green shade - Catalytic domain

Hm IRE1t49	MASV	RGS	R	W	P	R	L	Q	L	Q	F	A	L	L	G	T	S	P	O	V	H	T	L	R	108	
Ms IRE1t 1	MAR	V	P	Q	L	S	P	L	F	L	Q	L	L	L	L	L	L	L	L	L	L	L	L	L	59	
Hm IRE1t109	K	W	T	L	D	D	D	D	D	D	D	D	D	D	D	D	D	D	D	D	D	D	D	D	168	
Ms IRE1t160	K	W	T	L	D	D	D	D	D	D	D	D	D	D	D	D	D	D	D	D	D	D	D	D	119	
Hm IRE1t169	D	G	V	F	T	G	R	O	D	A	N	F	V	D	P	E	S	G	T	O	M	L	T	T	E	228
Ms IRE1t120	D	G	V	F	T	G	R	O	D	A	N	F	V	D	P	E	S	G	T	O	M	L	T	T	E	179
Hm IRE1t229	T	Y	R	S	A	F	M	D	G	S	P	G	K	Y	M	L	S	H	L	S	C	M	G	L	L	239
Ms IRE1t180	T	Y	R	S	A	F	M	D	G	S	P	G	K	Y	M	L	S	H	L	S	C	M	G	L	L	239
Hm IRE1t289	R	Q	L	P	H	L	T	A	R	D	T	L	H	L	R	W	H	I	L	P	A	S	G	P	R	348
Ms IRE1t240	R	Q	L	P	H	L	T	A	R	D	T	L	H	L	R	W	H	I	L	P	A	S	G	P	R	299
Hm IRE1t349	K	A	L	V	H	G	V	A	L	P	R	G	L	T	A	D	G	P	T	D	E	V	L	O	S	408
Ms IRE1t300	K	A	L	V	H	G	V	A	L	P	R	G	L	T	A	D	G	P	T	D	E	V	L	O	S	359
Hm IRE1t409	G	H	E	L	P	V	L	H	T	T	L	R	V	H	T	L	S	G	O	A	T	R	P	P	T	416
Ms IRE1t360	G	H	E	L	P	V	L	H	T	T	L	R	V	H	T	L	S	G	O	A	T	R	P	P	T	416
Hm IRE1t469	T	P	S	Y	L	G	L	G	P	D	L	A	S	L	T	A	V	L	L	G	W	I	F	V	M	528
Ms IRE1t417	T	P	S	Y	L	G	L	G	P	D	L	A	S	L	T	A	V	L	L	G	W	I	F	V	M	468
Hm IRE1t529	S	L	H	S	A	R	R	S	R	K	L	S	L	S	P	K	A	Q	P	L	D	D	E	A	L	588
Ms IRE1t469	Q	L	S	R	I	L	D	Q	R	R	F	S	P	E	A	P	H	D	E	A	Q	P	T	V	V	528
Hm IRE1t589	G	R	A	V	A	V	K	R	L	E	C	F	G	V	R	R	V	L	Q	S	D	R	H	N	V	648
Ms IRE1t529	G	R	A	V	A	V	K	R	L	E	C	F	G	V	R	V	L	Q	S	D	R	H	N	V	588	
Hm IRE1t649	V	H	N	P	H	L	R	E	P	V	L	Q	S	L	H	S	H	I	R	H	L	R	K	N	I	708
Ms IRE1t589	V	H	N	P	H	L	R	E	P	V	L	Q	S	L	H	S	H	I	R	H	L	R	K	N	I	648
Hm IRE1t709	G	L	C	K	L	P	A	G	R	C	S	F	S	L	H	S	C	P	T	G	M	A	P	L	L	768
Ms IRE1t649	G	L	C	K	L	P	A	G	R	C	S	F	S	L	H	S	C	P	T	G	M	A	P	L	L	707
Hm IRE1t769	S	H	F	P	E	S	L	S	L	S	L	S	L	S	L	S	L	S	L	S	L	S	L	S	L	828
Ms IRE1t708	S	H	F	P	E	S	L	S	L	S	L	S	L	S	L	S	L	S	L	S	L	S	L	S	L	767
Hm IRE1t829	W	S	R	A	K	L	P	O	F	D	D	S	D	L	E	K	S	E	S	P	L	V	R	A	L	888
Ms IRE1t768	W	S	R	A	K	L	P	O	F	D	D	S	D	L	E	K	S	E	S	P	L	V	R	A	L	827
Hm IRE1t889	Y	K	T	S	V	R	L	R	A	V	N	K	K	H	H	Y	E	L	P	V	E	R	V	Q	A	948
Ms IRE1t828	Y	K	T	S	V	R	L	R	A	V	N	K	K	H	H	Y	E	L	P	V						

Supplementary Table 1: The full matrix of the unfolded protein response gene expression profiles in 26 tissues or organs of human and mouse species. Fold changes of gene expression levels in human or mouse tissues were determined by normalization to expression levels of the genes in cerebellum. The expression levels of individual genes in cerebellum were defined as 1

	BIP	ATF6	ERN1	ERN2	XBP1	PERK	EIF2a	ATF4	CHOP	GADD34
Human										
Cerebellum	1.00	1.00	1.00	1.00	1.00	1.00	1.00	1.00	1.00	1.00
Hypothalamus	4.74	1.28	1.33	0.79	0.81	1.60	1.36	1.64	1.52	1.26
Pituitary	10.30	1.60	1.43	1.17	3.64	2.59	1.41	1.21	1.49	1.95
Olfactory bulb	13.53	0.96	0.97	0.70	0.74	1.22	1.03	1.65	1.33	3.71
Retina	3.96	1.48	1.48	0.87	1.62	1.89	1.50	1.53	1.87	1.90
Spinal cord	3.44	1.30	1.30	0.85	0.71	1.32	1.33	1.35	1.67	1.60
Dorsa root ganglion	1.41	0.96	0.96	0.68	0.53	1.09	1.04	0.64	0.96	1.01
Bone marrow	2.59	1.26	1.23	0.84	3.79	1.33	1.05	0.91	1.23	3.42
Lymph node	3.72	1.10	1.07	0.76	4.12	3.08	0.87	1.46	1.05	1.46
Amygdala	3.50	1.26	1.26	0.76	0.97	3.89	1.28	0.61	1.19	1.40
Adrenal gland	2.43	1.05	1.04	0.85	2.15	1.61	1.05	1.13	1.22	1.46
Salivary gland	2.57	0.99	0.99	0.71	14.70	3.05	1.08	1.88	1.00	0.98
Adipose tissue	4.71	1.20	1.22	0.77	1.25	1.18	1.63	1.74	1.19	1.44
Pancreas	4.82	1.06	0.99	0.76	7.98	3.14	1.01	1.95	1.05	3.19
Small intestine	6.55	1.36	1.17	0.65	10.39	2.85	1.25	1.16	0.23	1.19
Large intestine	6.42	1.34	1.23	0.91	7.70	4.36	1.17	1.35	0.29	1.34
Liver	6.46	2.02	2.19	0.96	21.41	1.76	1.16	1.24	1.47	3.16
Kidney	1.66	1.06	1.01	0.70	1.30	0.98	0.84	0.45	1.30	1.09
Heart	1.21	1.70	1.58	1.06	2.10	1.75	1.19	0.46	1.43	3.14
Skeletal muscle	0.97	1.58	1.46	1.12	1.09	1.66	1.68	2.74	1.48	1.48
Lung	4.07	1.34	1.35	0.78	9.23	1.34	0.79	2.53	1.00	14.05
Prostate	6.78	1.36	1.43	1.10	27.92	6.15	1.14	2.30	0.63	2.23
Uterus	4.73	1.02	1.00	0.61	3.36	2.18	1.08	1.61	0.61	2.23
Ovary	2.55	0.89	0.81	0.54	1.19	0.90	0.96	0.85	0.76	1.09
Placenta	11.19	1.42	1.35	0.88	13.30	3.29	0.92	2.52	1.16	3.73
Testis	3.67	1.09	1.04	0.70	0.92	0.94	1.10	0.65	1.11	1.15
Mouse										
Cerebellum	1.00	1.00	1.00	1.00	1.00	1.00	1.00	1.00	1.00	1.00
Hypothalamus	1.15	0.45	1.07	1.22	0.78	0.78	1.09	0.80	0.94	0.41
Pituitary	2.15	0.96	6.74	0.98	2.03	1.76	1.32	1.13	1.34	1.58
Olfactory bulb	0.61	0.91	0.92	0.98	0.55	0.85	0.97	0.84	1.23	0.85
Retina	0.94	1.05	1.95	0.98	0.19	0.95	0.60	1.53	0.82	0.22
Spinal cord	0.82	0.70	1.03	0.98	0.38	0.86	0.96	0.86	0.77	0.44
Dorsa root ganglion	0.79	0.87	1.02	0.99	0.52	1.16	1.86	0.93	1.38	1.32
Bone marrow	1.52	1.02	2.24	0.98	0.65	1.26	3.25	1.07	3.10	39.17
Lymph node	1.26	1.15	2.03	0.98	0.90	1.43	2.93	0.71	1.55	1.95
Amygdala	0.59	0.71	0.91	0.98	0.43	0.74	1.29	0.68	0.66	0.29
Adrenal gland	0.88	1.19	12.50	0.99	0.71	0.86	1.15	1.02	5.54	3.49
Salivary gland	2.10	2.36	5.35	1.50	3.83	2.21	1.54	2.09	2.73	1.06
Adipose tissue	1.69	1.38	3.00	0.98	1.31	0.97	1.79	0.81	1.25	0.71
Pancreas	1.64	3.91	6.81	1.69	5.33	3.90	1.63	2.60	1.02	0.65
Small intestine	1.86	1.53	2.26	38.23	1.65	1.37	1.99	1.05	1.66	0.29
Large intestine	1.33	1.51	2.14	304.80	1.24	1.46	1.60	0.80	1.26	0.85
Liver	2.54	3.17	5.14	1.22	1.80	0.85	2.24	0.81	0.50	0.82
Kidney	1.44	1.38	1.49	1.00	0.92	0.99	1.54	0.69	0.82	0.45
Heart	1.34	5.19	1.40	0.98	0.65	0.71	1.66	0.78	1.00	1.39
Skeletal muscle	0.75	1.15	1.17	2.51	0.46	1.00	2.16	1.09	0.81	2.45
Lung	1.53	1.88	1.90	0.98	1.54	1.02	1.28	1.05	1.48	4.62
Prostate	2.73	2.67	5.41	0.98	2.01	2.76	2.04	0.82	1.39	0.76
Uterus	1.00	1.00	2.38	0.98	1.14	0.88	2.23	0.83	1.02	1.69
Ovary	1.42	1.18	3.45	0.98	0.85	0.88	2.40	0.64	1.52	1.31
Placenta	3.66	2.58	4.50	0.98	1.29	1.77	2.86	1.35	3.31	11.83
Testis	0.89	0.34	1.01	0.98	0.10	0.61	4.06	0.70	2.97	0.26

Supplementary Table 2: The t-statistics of expression of the major unfolded protein response genes in human disease tissues compared to normal control tissues. Data were extracted from the European Molecular Biology Laboratory-European Bioinformatics Institute database (<http://www.ebi.ac.uk/>)

Diseases with UPR genes differentially regulated	t-statistic					
	BIP	PERK	XBP1	ERN2	ERN1	ATF6
Acute HIV-1 infection	-4	-3.6				
Adrenocortical carcinoma	-4	-3.3			-3.8	
Acute malaria-infected	7.4			-3		
Breast carcinoma	6	5.7		-3.6	3.4	8
Breast carcinoma	2.6	4.9		-6.4		3.4
Burkitts lymphoma			-4.8		4.2	
Chronic lymphocytic leukemia	-6.3	-7.1	2.7		-4.8	3.2
Chromophobe renal cell carcinoma		4.3				-3.6
Colon carcinoma	3.5			8.8		
Colorectal cancer				-8.4		6.1
Cryptorchidism	-5.9	3.7		-2.8		
Dermatomyositis		3.4			-4.9	3.1
Down syndrome		3.6		-2.9	-3.9	
Epilepsy		6.2		-3.1		
Esophageal adenocarcinoma	3.8			3.5		
Gastric carcinoma	3.8	-3.9	-4.5			
Glioblastoma	4.3	5.3		-3.4		-4.5
Freidriech's ataxia	3.4	3.4		3.4	3.4	
Huntington's disease		3.5				3
Intrahepatic cholangiocarcinoma			-5.4		-3.6	
Leiomyosarcoma	-5.9	-5.1		3.8		
Liposarcoma	6					8
Lung adenocarcinoma	9.6	3.7	3.9	-3.3	-4.2	3.1
Lung adenocarcinoma	6.7					2.8
Malignant melanoma	8	4.3				3.2
Multiple myeloma	7	6.8				4.5
Muscle invasive carcinoma	4.6				-4.7	
Nasopharyngeal carcinoma				-2.9	-3.5	
Nephrosclerosis		3.3		-3.3		
Non-ischemic cardiomyopathy	3.1			-3.7		
Non-small cell lung cancer	8.4	6.6				-6.4
Oligodendroglioma	-4.2					3.2
Osteosarcoma		6.8		4.5		4.3
Overian serous carcinoma	-3.4	-3.5		3.7	3.8	-4.7
Pancreatic cancer	3.7	-4.4		4.3	-3	
Periodontitis	3.2	7.6			3.5	8.2
Pituitary cancer	-3.5					7.6
Prostate cancer	-3.2					-4.5
Prostate carcinoma	-3	3.6				
Psoriasis	-4.8				2.4	
Rheumatoid arthritis	3.3					-3.6
T-cell acute lymphoblastic leukemia	-3.1	3.1		-3.7	6	4
Testicular agenesis	-3.8			3.3		
Testicular seminoma		10	10			-2.5
X-linked chronic granulomatous	-5.9				2.6	