

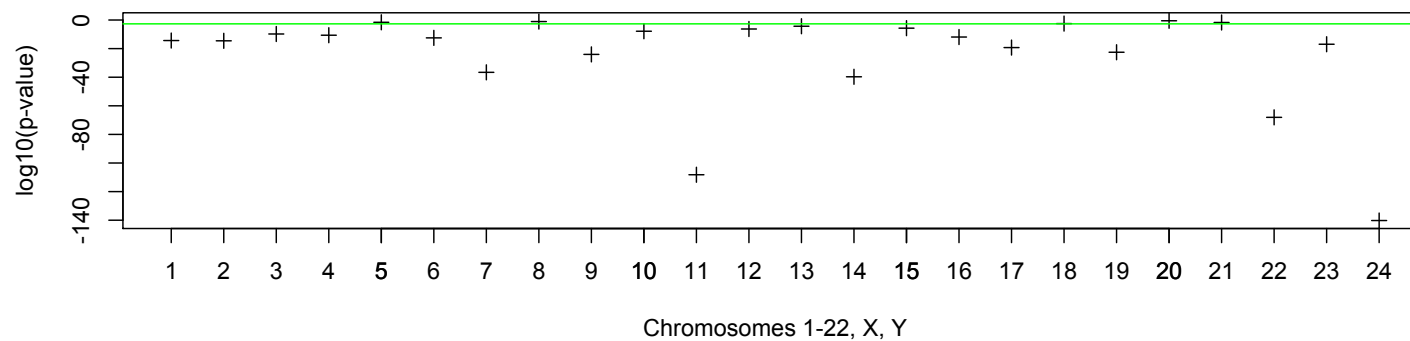
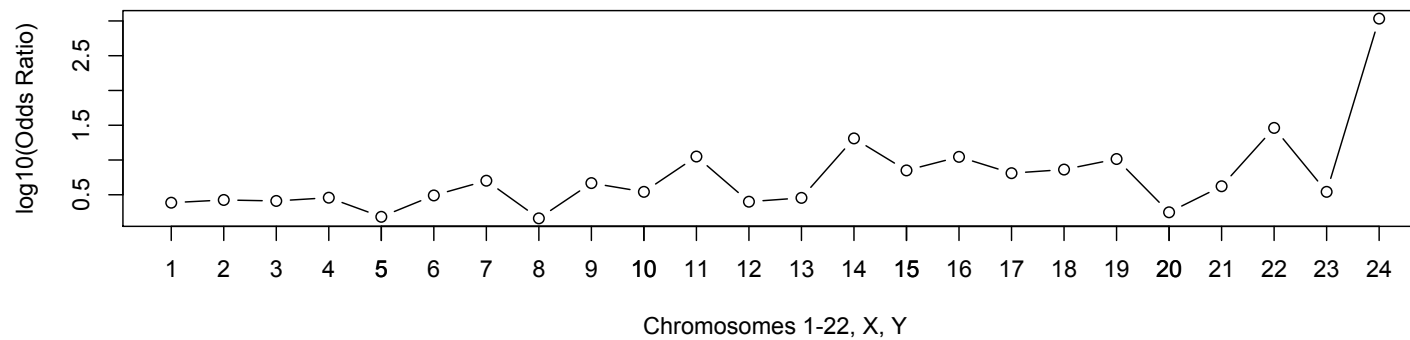
Cross-species Comparison
Pseudogene's Localization Relative
to their Parent Genes (ctd)

Yan Zhang

7/17/2013

Is co-residence random? Human: No.

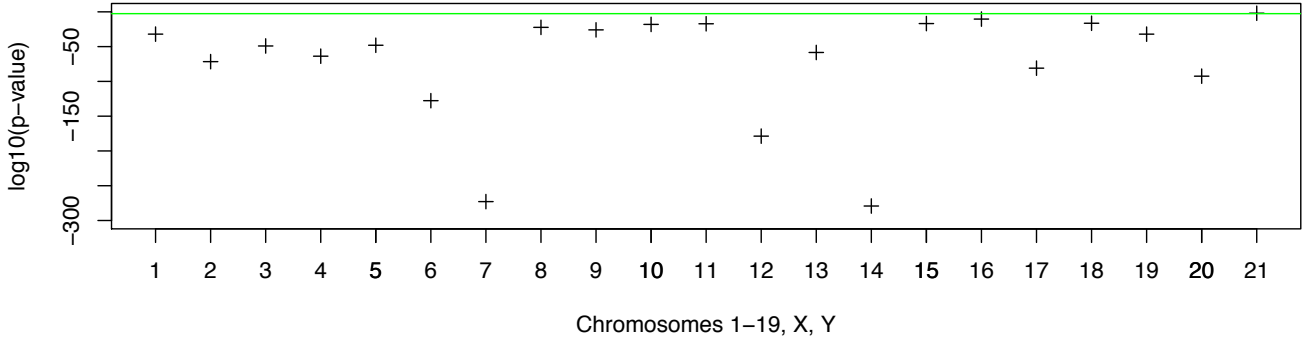
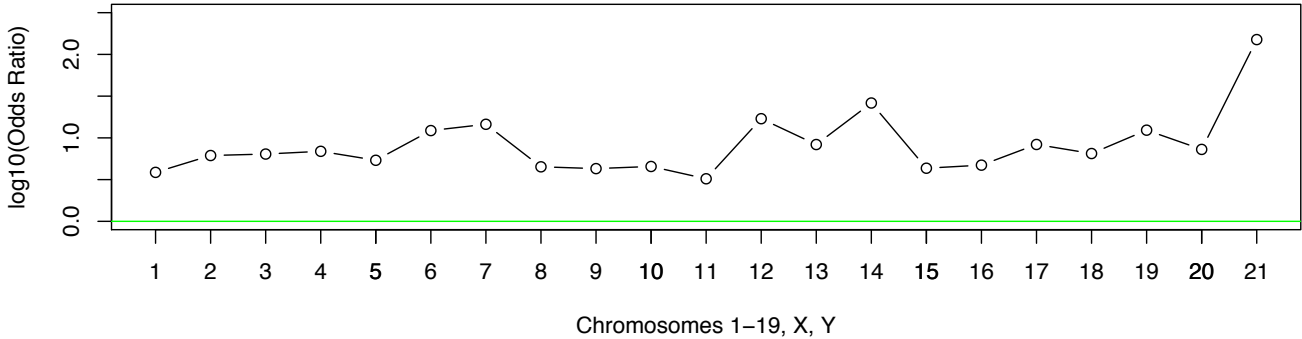
Fisher's Exact Test: Co-residence is Random or Not for Each Chromosome



Worm, Fly: No, too.

Is co-residence random? Mouse: No.

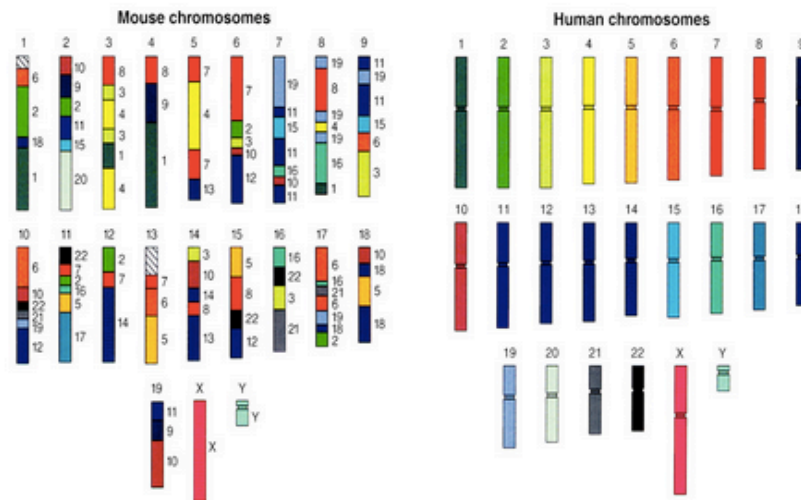
Fisher's Exact Test: Co-residence is Random or Not for Each Chromosome



Reference slide (1 slide)

Human-Mouse Chromosome Homologies

Mouse and Human Genetic Similarities



Courtesy Lisa Stubbs
Oak Ridge National Laboratory

Human: Exchange among X, Y and Autosomes (Hyp6)

As seen before:

		Parent (source)		
		Autochromosomes	X	Y
Pseudogene (destination)	Autochromosomes	7729	306	4
	X	549	81	1
	Y	105	33	87

- 3by3: Pearson's Chi-squared test & Fisher's Exact Test: p-value < 2.2e-16.
- 2by2 (X, Y only): Fisher's Exact Test: p-value < 2.2e-16.
Sample estimat: odds ratio \approx 208.
- Y chromosome very seldom exports to other chromosomes.

Y as source

- All of parent genes on Y

14 Unique Human Parent Transcript IDs on Y

	ParentTranscriptID	Freq.ParentT	ParentGeneN	ParentStart	ParentEnd	ParentLength
1	ENST00000250784	1	RPS4Y1	2709527	2734997	25470
2	ENST00000288666	1	RPS4Y2	22918050	22942918	24868
3	ENST00000303728	4	PRY	24636544	24660784	24240
4	ENST00000304790	1	HSFY1	20933700	20935621	1921
5	ENST00000306609	11	CDY1	27768309	27771049	2740
6	ENST00000307393	3	HSFY1	20708557	20710478	1921
7	ENST00000331070	1	BPY2	25130410	25151606	21196
8	ENST00000336079	1	DDX3Y	15016742	15032390	15648
9	ENST00000338981	29	USP9Y	14813160	14972764	159604
10	ENST00000361963	9	CDY1	27768264	27770483	2219
11	ENST00000382707	21	RBMX1A1	23696765	23711212	14447
12	ENST00000421178	2	FAM197Y1	9374241	9384693	10452
13	ENST00000426950	1	TSPY4, 8, 10	9175073	9177887	2814
14	ENST00000451548	7	TSPY1	9304564	9307357	2793

Question: Are these high freq parent genes highly expressed, in specific tissues?

High Freq Parent Genes

- **CDY1**: “Members of the CDY family have different expression patterns: CDY1 transcripts have the best correlation with complete spermatogenesis”.
 - Hum Genet. 2003 Nov;113(6):486-92. Epub 2003 Sep 3.
 - <http://www.genecards.org/cgi-bin/carddisp.pl?gene=CDY1&search=CDY1>
- **USP9Y**
- **RBMY1A1**
- **TSPY1**

High Freq Parent Genes (ctd)

Jump to Section... ▾

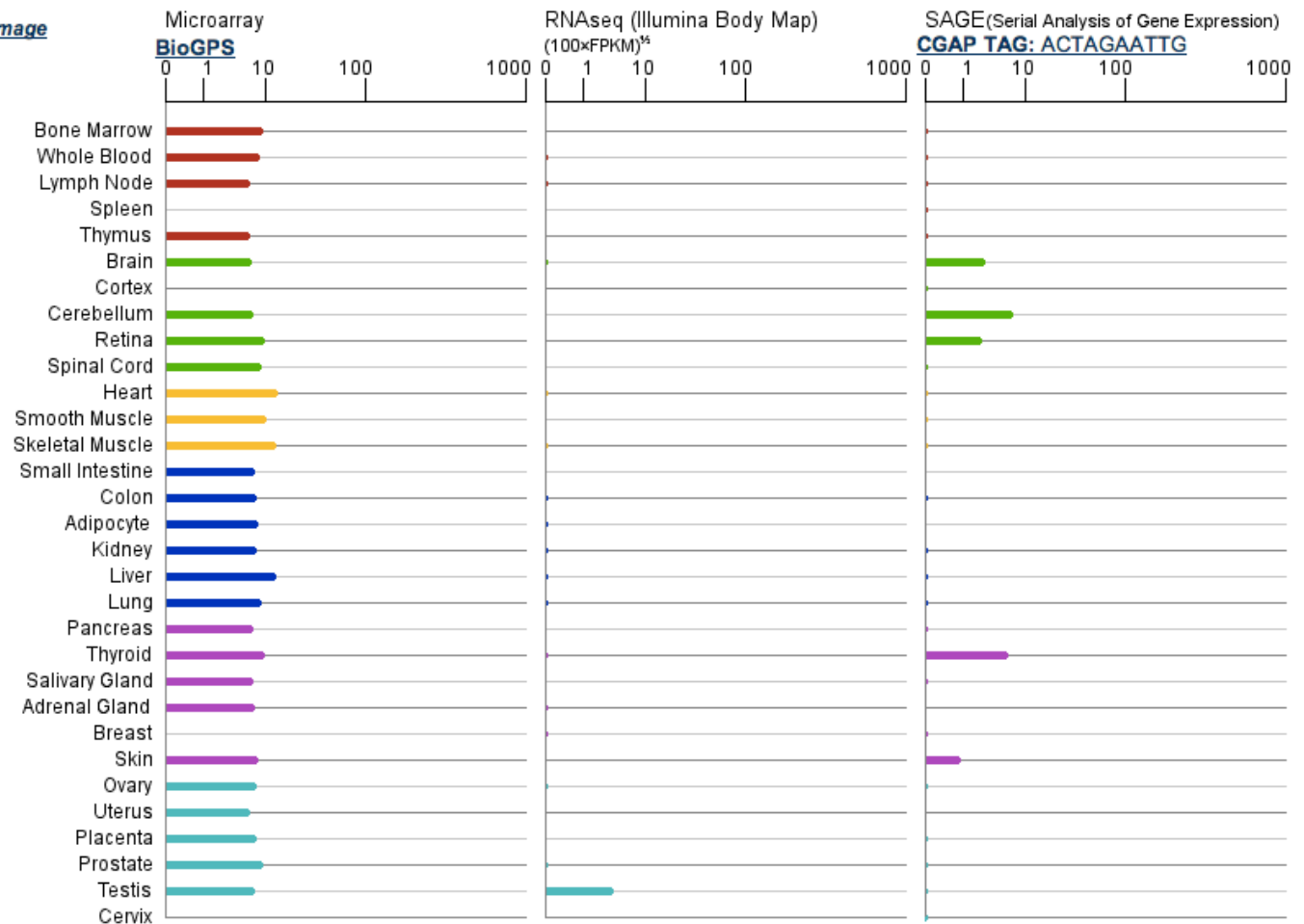
Expression for CDY1 gene

(RNA expression data according to [H-InvDB](#), [NONCODE](#), [miRBase](#), and [RNAdb](#), Expression images according to data from [BioGPS](#), [Illumina Human BodyMap](#), and [CGAP SAGE](#), Sets of similar genes according to [GeneDecks](#), *in vivo* and *in vitro* expression data from [LifeMap Discovery™](#), plus additional links to [Genevestigator](#), and/or [SOURCE](#), and/or [BioGPS](#), and/or [UniProtKB](#), PCR Arrays from [SABiosciences](#), Primers from [OriGene](#), [SABiosciences](#), and/or [QIAGEN](#), *In Situ* Hybridization Assays from [Advanced Cell Diagnostics](#))
[About This Section](#)

Major Tissues

CDY1 expression in normal human tissues (normalized intensities)
 See [probesets specificity/sensitivity at GeneAnnot](#)

[About this image](#)



High Freq Parent Genes (ctd)

- USP9Y: expressed in a wide range of adult and embryonic tissues, including testis, in which it is highly expressed.
 - http://www.proteinlounge.com/cpcscientific/view_datasheet.asp?pname=USP9Y&pfrom=plist
 - USP9Y siRNA (m): sc-154947. SANTA CRUZ BIOTECHNOLOGY, INC.
<http://datasheets.scbt.com/sc-154947.pdf>

High Freq Parent Genes (ctd)

Jump to Section... ▾

Expression for USP9Y gene

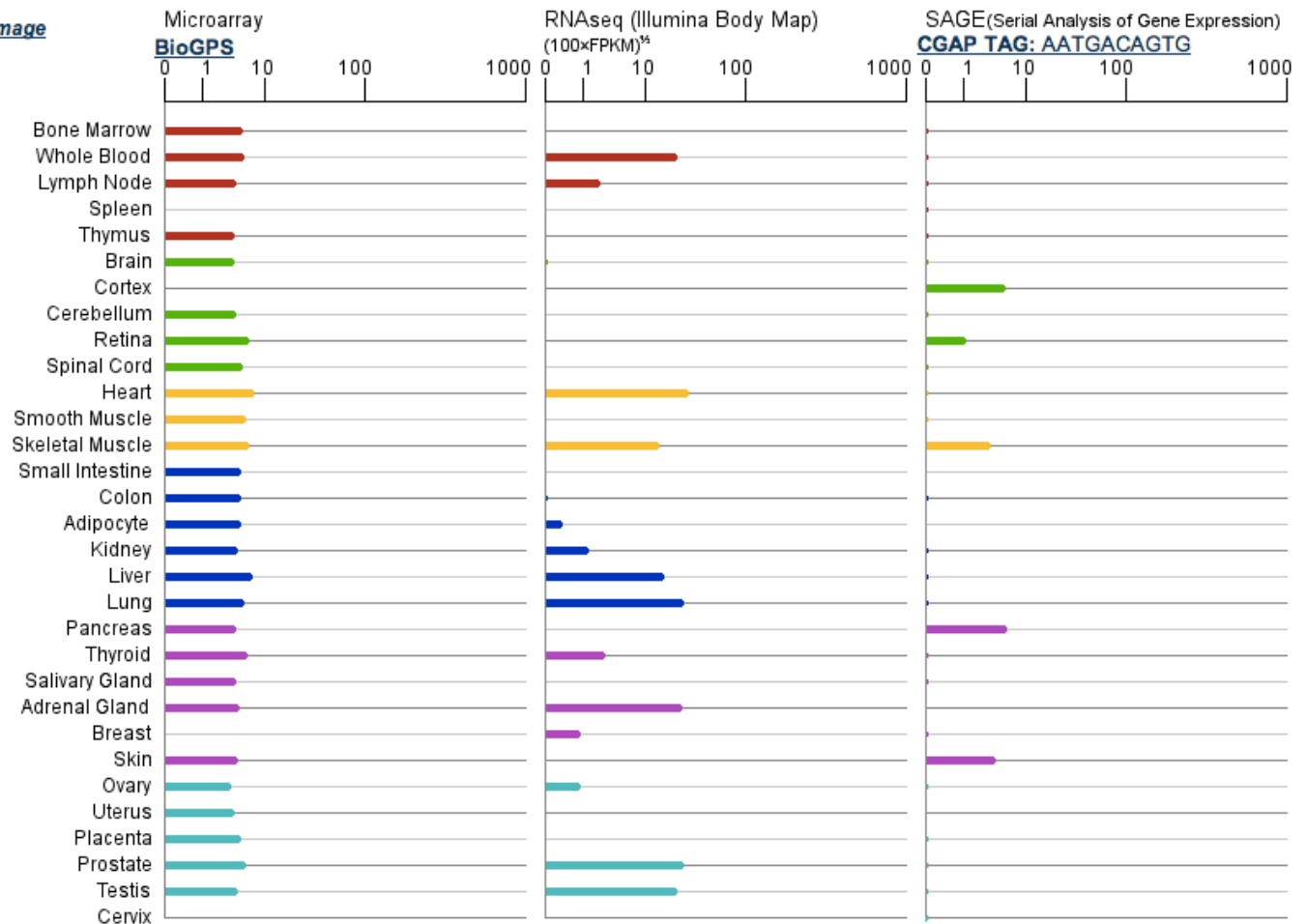
(RNA expression data according to [H-InvDB](#), [NONCODE](#), [miRBase](#), and [RNAdb](#), Expression images according to data from [BioGPS](#), [Illumina Human BodyMap](#), and [CGAP SAGE](#), Sets of similar genes according to [GeneDecks](#), *in vivo* and *in vitro* expression data from [LifeMap Discovery™](#), plus additional links to [Genevestigator](#), and/or [SOURCE](#), and/or [BioGPS](#), and/or [UniProtKB](#), PCR Arrays from [SABiosciences](#), Primers from [OriGene](#), [SABiosciences](#), and/or [QIAGEN](#), *In Situ* Hybridization Assays from [Advanced Cell Diagnostics](#))
[About This Section](#)

Major Tissues

USP9Y expression in normal human tissues (normalized intensities)

[See probesets specificity/sensitivity at GeneAnnot](#)

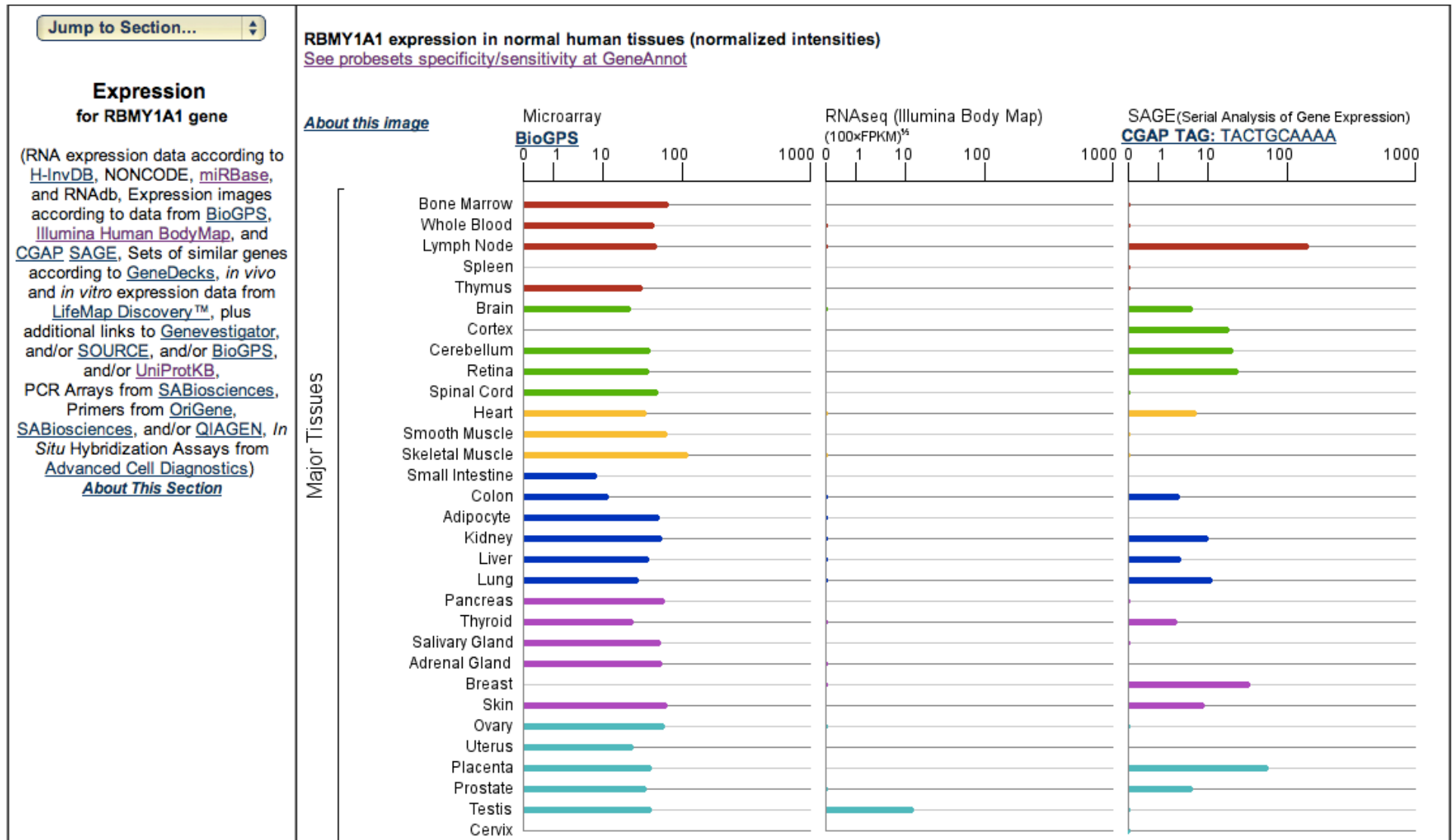
[About this image](#)



High Freq Parent Genes (ctd)

- RBMY1A1: “Expressed in all of the transcriptionally active stages of germ cell development from spermatogonia through spermatocytes to round spermatids.”
 - <http://www.genecards.org/cgi-bin/carddisp.pl?gene=RBMY1A1>

High Freq Parent Genes (ctd)



High Freq Parent Genes (ctd)

- TSPY1: “Note=TSPY is located in the gonadoblastoma critical region and is preferentially expressed in tumor germ cells of gonadoblastoma specimens. Expression also correlates with testicular seminoma and tumorigenesis of the prostate gland.”
 - <http://www.genecards.org/cgi-bin/carddisp.pl?gene=TSPY1&search=TSPY1>

High Freq Parent Genes (ctd)

Jump to Section...

Expression for TSPY1 gene

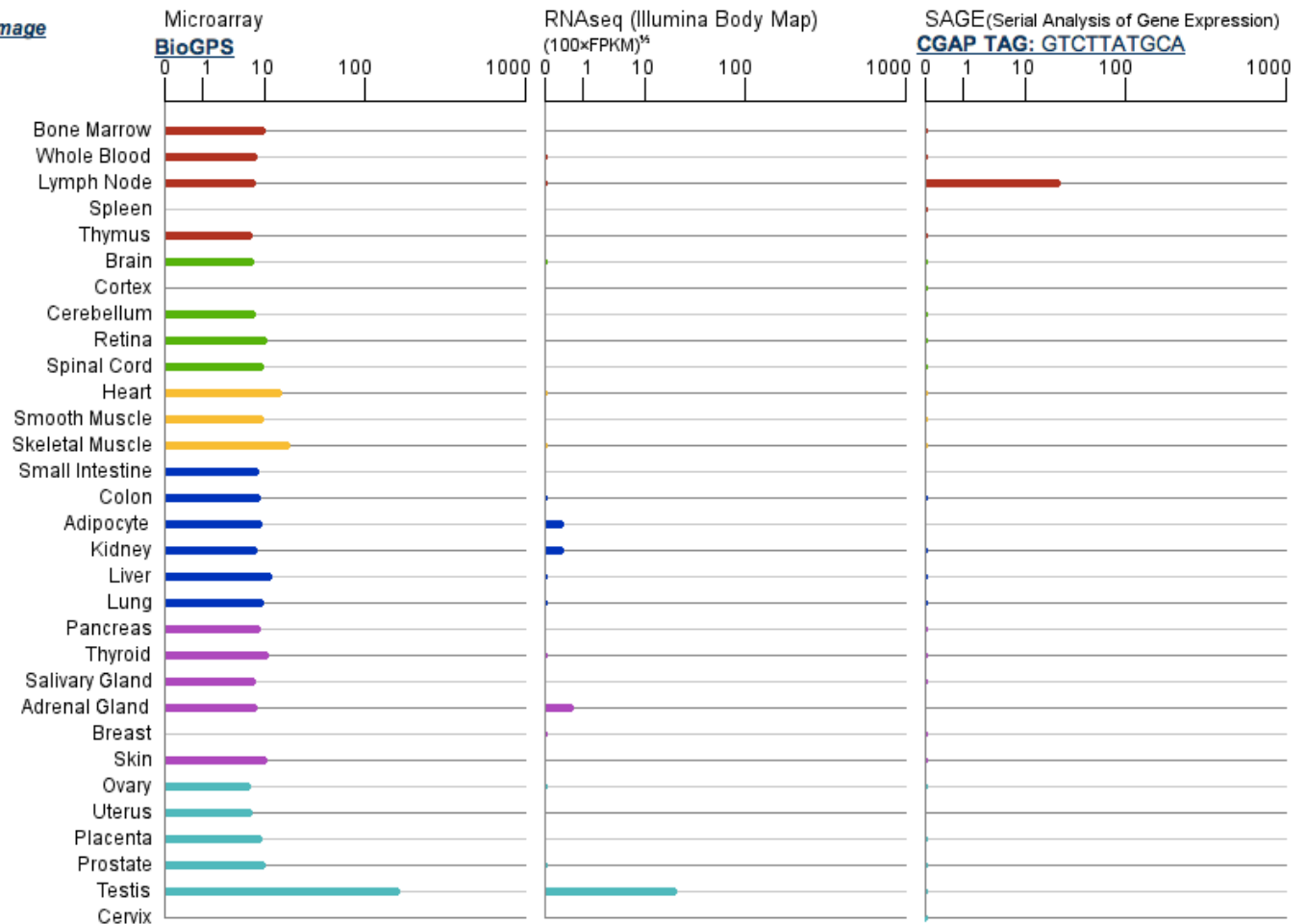
(RNA expression data according to [H-InvDB](#), [NONCODE](#), [miRBase](#), and [RNAdb](#), Expression images according to data from [BioGPS](#), [Illumina Human BodyMap](#), and [CGAP SAGE](#), Sets of similar genes according to [GeneDecks](#), *in vivo* and *in vitro* expression data from [LifeMap Discovery™](#), plus additional links to [Genevestigator](#), and/or [SOURCE](#), and/or [BioGPS](#), and/or [UniProtKB](#), PCR Arrays from [SABiosciences](#), Primers from [OriGene](#), [SABiosciences](#), and/or [QIAGEN](#), *In Situ* Hybridization Assays from [Advanced Cell Diagnostics](#))
[About This Section](#)

TSPY1 expression in normal human tissues (normalized intensities)

See [probesets specificity/sensitivity at GeneAnnot](#)

About this image

Major Tissues



14 Unique Human Parent Genes on Y

No surprise. These genes are “Y-linked”.

The screenshot shows the DAVID Bioinformatics Resources 6.7 Gene Name Batch Viewer interface. The main content area displays a Gene List Report for 14 Y-linked genes in Homo sapiens. The report includes a table with columns for Official Gene Symbol, Gene Name, Related Genes, and Species. The genes listed are: BPY2, CDY1, DDX3Y, FAM197Y1, HSFY1, PRY, RBMY1A1, RPS4Y1, RPS4Y2, TSPY1, TSPY10, TSPY4, TSPY8, and USP9Y. The gene names in the table are underlined in red. The interface also includes a sidebar for Gene List Manager and a navigation menu at the top.

Gene Name Batch Viewer
DAVID Bioinformatics Resources 6.7, NIAID/NIH

Home Start Analysis Shortcut to DAVID Tools Technical Center Downloads & APIs Term of Service Why DAVID? About Us

Upload List Background

Gene List Manager

Select to limit annotations by one or more species [Help](#)

- Use All Species -
Homo sapiens(14)
Bos taurus(5)
Macaca mulatta(5)

Select Species

List Manager [Help](#)

List_1

Select List to:

Use Rename
Remove Combine
Show Gene List

Gene List Report

Current Gene List: List_1
Current Background: Homo sapiens
14 DAVID IDs

[Download File](#)

OFFICIAL_GENE_SYMBOL	Gene Name	Related Genes	Species
BPY2	basic charge, Y-linked, 2C; basic charge, Y-linked, 2B; basic charge, Y-linked, 2	RG	Homo sapiens
CDY1	chromodomain protein, Y-linked, 1B; chromodomain protein, Y-linked, 1	RG	Homo sapiens
DDX3Y	DEAD (Asp-Glu-Ala-Asp) box polypeptide 3, Y-linked	RG	Homo sapiens
FAM197Y1	similar to CYorf16 protein	RG	Homo sapiens
HSFY1	heat shock transcription factor, Y-linked 1; heat shock transcription factor, Y linked 2	RG	Homo sapiens
PRY	PTPN13-like, Y-linked pseudogene 4; PTPN13-like, Y-linked pseudogene 3; PTPN13-like, Y-linked; PTPN13-like, Y-linked 2	RG	Homo sapiens
RBMY1A1	RNA binding motif protein, Y-linked, family 1, member A1	RG	Homo sapiens
RPS4Y1	ribosomal protein S4, Y-linked 1	RG	Homo sapiens
RPS4Y2	ribosomal protein S4, Y-linked 2	RG	Homo sapiens
TSPY1	testis specific protein, Y-linked 3; testis specific protein, Y-linked 2; testis specific protein, Y-linked 1; testis specific protein, Y-linked pseudogene 7	RG	Homo sapiens
TSPY10	hypothetical protein LOC100289087	RG	Homo sapiens
TSPY4	similar to testis specific protein, Y-linked 1	RG	Homo sapiens
TSPY8	similar to Testis-specific Y-encoded protein 1	RG	Homo sapiens
USP9Y	ubiquitin specific peptidase 9, Y-linked	RG	Homo sapiens

Functional Annotation Clustering

Parent Genes Only on Y

Functional Annotation Clustering

Current Gene List: List_1

Current Background: Homo sapiens

14 DAVID IDs

Options Classification Stringency Medium

Rerun using options

Create Sublist

[Help and Manual](#)

3 Cluster(s)

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Annotation Cluster 1		Enrichment Score: 3.53		G		Count	P_Value	Benjamini
<input type="checkbox"/>	GOTERM_BP_FAT	spermatogenesis	RT			6	6.9E-7	3.8E-5
<input type="checkbox"/>	GOTERM_BP_FAT	male gamete generation	RT			6	6.9E-7	3.8E-5
<input type="checkbox"/>	GOTERM_BP_FAT	gamete generation	RT			6	2.4E-6	6.5E-5
<input type="checkbox"/>	GOTERM_BP_FAT	sexual reproduction	RT			6	4.9E-6	9.0E-5
<input type="checkbox"/>	GOTERM_BP_FAT	multicellular organism reproduction	RT			6	6.6E-6	9.1E-5
<input type="checkbox"/>	GOTERM_BP_FAT	reproductive process in a multicellular organism	RT			6	6.6E-6	9.1E-5
<input type="checkbox"/>	SP_PIR_KEYWORDS	alternative splicing	RT			7	1.5E-1	7.0E-1
<input type="checkbox"/>	UP_SEQ_FEATURE	splice variant	RT			7	1.5E-1	9.7E-1
<input type="checkbox"/>	SP_PIR_KEYWORDS	polymorphism	RT			3	1.0E0	1.0E0
<input type="checkbox"/>	UP_SEQ_FEATURE	sequence variant	RT			3	1.0E0	1.0E0
Annotation Cluster 2		Enrichment Score: 2.58		G		Count	P_Value	Benjamini
<input type="checkbox"/>	INTERPRO	Nucleosome assembly protein (NAP)	RT			3	3.1E-5	7.4E-4
<input type="checkbox"/>	GOTERM_BP_FAT	chromatin assembly or disassembly	RT			4	6.5E-5	7.2E-4
<input type="checkbox"/>	GOTERM_BP_FAT	nucleosome assembly	RT			3	1.3E-3	1.2E-2
<input type="checkbox"/>	GOTERM_BP_FAT	chromatin assembly	RT			3	1.4E-3	1.1E-2
<input type="checkbox"/>	GOTERM_BP_FAT	protein-DNA complex assembly	RT			3	1.6E-3	1.1E-2
<input type="checkbox"/>	GOTERM_BP_FAT	chromatin organization	RT			4	1.6E-3	9.8E-3
<input type="checkbox"/>	GOTERM_BP_FAT	nucleosome organization	RT			3	1.6E-3	8.9E-3
<input type="checkbox"/>	GOTERM_BP_FAT	DNA packaging	RT			3	2.6E-3	1.3E-2
<input type="checkbox"/>	GOTERM_BP_FAT	chromosome organization	RT			4	3.3E-3	1.5E-2
<input type="checkbox"/>	GOTERM_BP_FAT	cellular macromolecular complex assembly	RT			3	1.8E-2	7.3E-2
<input type="checkbox"/>	GOTERM_BP_FAT	cellular macromolecular complex subunit organization	RT			3	2.2E-2	8.4E-2
<input type="checkbox"/>	GOTERM_BP_FAT	macromolecular complex assembly	RT			3	6.9E-2	2.3E-1
<input type="checkbox"/>	GOTERM_BP_FAT	macromolecular complex subunit organization	RT			3	7.7E-2	2.4E-1
Annotation Cluster 3		Enrichment Score: 0.81		G		Count	P_Value	Benjamini
<input type="checkbox"/>	SP_PIR_KEYWORDS	nucleus	RT			6	5.0E-2	5.4E-1
<input type="checkbox"/>	SP_PIR_KEYWORDS	cytoplasm	RT			5	7.9E-2	5.6E-1
<input type="checkbox"/>	SP_PIR_KEYWORDS	phosphoprotein	RT			3	9.4E-1	1.0E0

Sexual reproduction

Chromatin organization,
DNA packaging

4 terms were not clustered.

Functional Annotation Clustering

(Same as previous slide. Showing genes in each cluster.)

1	Annotation Cluster 1	Enrichment Score: 3.526449691908946					
2	Category	Term	Count	%	PValue	Genes	List Total
3	GOTERM_BP_FAT	GO:0007283~spermatogenesis	6	42.8571429	6.92E-07	RBMY1A1, TSPY1, USP9Y, BPY2, CDY1, TSPY10	10
4	GOTERM_BP_FAT	GO:0048232~male gamete generation	6	42.8571429	6.92E-07	RBMY1A1, TSPY1, USP9Y, BPY2, CDY1, TSPY10	10
5	GOTERM_BP_FAT	GO:0007276~gamete generation	6	42.8571429	2.37E-06	RBMY1A1, TSPY1, USP9Y, BPY2, CDY1, TSPY10	10
6	GOTERM_BP_FAT	GO:0019953~sexual reproduction	6	42.8571429	4.90E-06	RBMY1A1, TSPY1, USP9Y, BPY2, CDY1, TSPY10	10
7	GOTERM_BP_FAT	GO:0032504~multicellular organism reproduction	6	42.8571429	6.62E-06	RBMY1A1, TSPY1, USP9Y, BPY2, CDY1, TSPY10	10
8	GOTERM_BP_FAT	GO:0048609~reproductive process in a multicellular organism	6	42.8571429	6.62E-06	RBMY1A1, TSPY1, USP9Y, BPY2, CDY1, TSPY10	10
9	SP_PIR_KEYWORDS	alternative splicing	7	50	0.14883136	RBMY1A1, PRY, HSFY1, TSPY1, USP9Y, CDY1, TSPY10	11
10	UP_SEQ_FEATURE	splice variant	7	50	0.15026933	RBMY1A1, PRY, HSFY1, TSPY1, USP9Y, CDY1, TSPY10	11
11	SP_PIR_KEYWORDS	polymorphism	3	21.4285714	0.99834278	TSPY1, USP9Y, TSPY10	11
12	UP_SEQ_FEATURE	sequence variant	3	21.4285714	0.9990831	TSPY1, USP9Y, TSPY10	11
13							
14	Annotation Cluster 2	Enrichment Score: 2.58122658871902					
15	Category	Term	Count	%	PValue	Genes	List Total
16	INTERPRO	IPR002164:Nucleosome assembly protein (NAP)	3	21.4285714	3.10E-05	TSPY1, TSPY4, TSPY10	10
17	GOTERM_BP_FAT	GO:0006333~chromatin assembly or disassembly	4	28.5714286	6.51E-05	TSPY1, TSPY4, CDY1, TSPY10	10
18	GOTERM_BP_FAT	GO:0006334~nucleosome assembly	3	21.4285714	0.00133331	TSPY1, TSPY4, TSPY10	10
19	GOTERM_BP_FAT	GO:0031497~chromatin assembly	3	21.4285714	0.00142936	TSPY1, TSPY4, TSPY10	10
20	GOTERM_BP_FAT	GO:0065004~protein-DNA complex assembly	3	21.4285714	0.00156245	TSPY1, TSPY4, TSPY10	10
21	GOTERM_BP_FAT	GO:0006325~chromatin organization	4	28.5714286	0.00160371	TSPY1, TSPY4, CDY1, TSPY10	10
22	GOTERM_BP_FAT	GO:0034728~nucleosome organization	3	21.4285714	0.00163115	TSPY1, TSPY4, TSPY10	10
23	GOTERM_BP_FAT	GO:0006323~DNA packaging	3	21.4285714	0.00256605	TSPY1, TSPY4, TSPY10	10
24	GOTERM_BP_FAT	GO:0051276~chromosome organization	4	28.5714286	0.00327291	TSPY1, TSPY4, CDY1, TSPY10	10
25	GOTERM_BP_FAT	GO:0034622~cellular macromolecular complex assembly	3	21.4285714	0.01777917	TSPY1, TSPY4, TSPY10	10
26	GOTERM_BP_FAT	GO:0034621~cellular macromolecular complex subunit organization	3	21.4285714	0.0221145	TSPY1, TSPY4, TSPY10	10
27	GOTERM_BP_FAT	GO:0065003~macromolecular complex assembly	3	21.4285714	0.06904837	TSPY1, TSPY4, TSPY10	10
28	GOTERM_BP_FAT	GO:0043933~macromolecular complex subunit organization	3	21.4285714	0.07749632	TSPY1, TSPY4, TSPY10	10
29							
30	Annotation Cluster 3	Enrichment Score: 0.8107787911112121					
31	Category	Term	Count	%	PValue	Genes	List Total
32	SP_PIR_KEYWORDS	nucleus	6	42.8571429	0.05015272	RBMY1A1, HSFY1, TSPY1, DDX3Y, CDY1, TSPY10	11
33	SP_PIR_KEYWORDS	cytoplasm	5	35.7142857	0.07852065	HSFY1, TSPY1, USP9Y, DDX3Y, TSPY10	11
34	SP_PIR_KEYWORDS	phosphoprotein	3	21.4285714	0.93839402	TSPY1, DDX3Y, TSPY10	11

Y as destination

- Only Pgenes on Y (not all pgenes that are on Y)
 - Functional annotation: 22 clusters
 - broad scope of functions, including cell cycle, membrane, transportation regulation.
 - Seems not sex-specific.

Mouse: Exchange among X, Y and Autosomes (Hyp6)

		Parent (source)		
		Autochromosomes	X	Y
Pseudogene (destination)	Autochromosomes	6798	219	1
	X	622	168	1
	Y	21	0	1

- 3by3: Pearson's Chi-squared test & Fisher's Exact Test: p-value < 2.2e-16.
- Y chromosome very seldom exports to other chromosomes.

Y as source

- All of parent genes on Y

Chrom	Start	End	Strand	Type	LocalID	ParentTranscriptID	SearchEnsemblManually	ParentChrom	ParentStart	ParentEnd	Coreside
1	28046755	28048626	+	PSSD	13943	ENSMUST00000091190	DEAD (Asp-Glu-Ala-Asp) box polypeptide 3, Y-linked [Source:MGI Symbol;Acc:MGI:1349406] [Type: protein coding Ensembl]	Y	1260715	1286613	FALSE
Y	2191651	2195324	+	DUP	7837	ENSMUST00000100360	RNA binding motif protein, Y chromosome [Source:MGI Symbol;Acc:MGI:104732] [Type: protein coding Ensembl]	Y	2830680	2841858	TRUE
X	63278724	63279062	+	PSSD	14681	ENSMUST00000163651	predicted gene 6026 [Source:MGI Symbol;Acc:MGI:3779546] [Type: protein coding Ensembl]	Y	2599099	2599434	FALSE

May be it is also Y-linked? Not known yet.

Y as destination

- Only Pgenes on Y (not all pgenes that are on Y)
 - Functional annotation: 2 clusters
 - Transcription regulation and membrane...
 - Seems not sex-specific. But what about ZFY...



Functional Annotation Clustering

[Help and Manual](#)

Current Gene List: List_1

Current Background: Mus musculus

21 DAVID IDs

Options Classification Stringency Medium

Rerun using options

Create Sublist

2 Cluster(s)

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Annotation Cluster 1	Enrichment Score: 1.61			Count	P_Value	Benjamini
<input type="checkbox"/> INTERPRO	Transcriptional regulator SCAN	RT		4	7.2E-6	4.7E-4
<input type="checkbox"/> SMART	SCAN	RT		4	7.8E-6	1.3E-4
<input type="checkbox"/> SP_PIR_KEYWORDS	zinc	RT		7	4.3E-3	1.8E-1
<input type="checkbox"/> GOTERM_MF_FAT	zinc ion binding	RT		7	9.8E-3	2.9E-1
<input type="checkbox"/> INTERPRO	Zinc finger, C2H2-type/integrase, DNA-binding	RT		4	1.4E-2	3.7E-1
<input type="checkbox"/> SP_PIR_KEYWORDS	metal-binding	RT		7	2.4E-2	4.2E-1
<input type="checkbox"/> GOTERM_MF_FAT	transition metal ion binding	RT		7	2.7E-2	3.9E-1
<input type="checkbox"/> INTERPRO	Zinc finger, C2H2-like	RT		4	2.9E-2	4.7E-1
<input type="checkbox"/> INTERPRO	Zinc finger, C2H2-type	RT		4	3.0E-2	3.9E-1
<input type="checkbox"/> SMART	ZnF_C2H2	RT		4	3.3E-2	2.5E-1
<input type="checkbox"/> INTERPRO	Zinc finger, RING-type	RT		3	3.3E-2	3.6E-1
<input type="checkbox"/> GOTERM_MF_FAT	transcription factor activity	RT		4	3.7E-2	3.5E-1
<input type="checkbox"/> SP_PIR_KEYWORDS	nucleus	RT		8	3.7E-2	4.4E-1
<input type="checkbox"/> SMART	RING	RT		3	3.7E-2	1.9E-1
<input type="checkbox"/> GOTERM_BP_FAT	regulation of transcription, DNA-dependent	RT		5	4.3E-2	1.0E0
<input type="checkbox"/> GOTERM_BP_FAT	regulation of RNA metabolic process	RT		5	4.6E-2	9.6E-1
<input type="checkbox"/> GOTERM_MF_FAT	metal ion binding	RT		8	5.2E-2	3.8E-1
<input type="checkbox"/> GOTERM_MF_FAT	cation binding	RT		8	5.5E-2	3.3E-1
<input type="checkbox"/> GOTERM_MF_FAT	ion binding	RT		8	5.8E-2	3.0E-1
<input type="checkbox"/> GOTERM_MF_FAT	DNA binding	RT		5	8.5E-2	3.6E-1
<input type="checkbox"/> GOTERM_MF_FAT	transcription regulator activity	RT		4	1.1E-1	3.9E-1
<input type="checkbox"/> GOTERM_BP_FAT	regulation of transcription	RT		5	1.5E-1	1.0E0
<input type="checkbox"/> SP_PIR_KEYWORDS	transcription regulation	RT		4	1.6E-1	8.6E-1
<input type="checkbox"/> SP_PIR_KEYWORDS	Transcription	RT		4	2.1E-1	8.3E-1
<input type="checkbox"/> GOTERM_BP_FAT	transcription	RT		4	2.4E-1	1.0E0
<input type="checkbox"/> SP_PIR_KEYWORDS	zinc-finger	RT		3	2.9E-1	9.0E-1
Annotation Cluster 2	Enrichment Score: 0.33			Count	P_Value	Benjamini
<input type="checkbox"/> GOTERM_CC_FAT	plasma membrane	RT		5	9.1E-2	9.4E-1
<input type="checkbox"/> SP_PIR_KEYWORDS	cell membrane	RT		4	1.9E-1	8.6E-1
<input type="checkbox"/> GOTERM_BP_FAT	cell surface receptor linked signal transduction	RT		4	4.4E-1	1.0E0
<input type="checkbox"/> SP_PIR_KEYWORDS	receptor	RT		3	6.7E-1	9.9E-1
<input type="checkbox"/> SP_PIR_KEYWORDS	membrane	RT		5	7.8E-1	1.0E0
<input type="checkbox"/> GOTERM_CC_FAT	integral to membrane	RT		4	7.9E-1	1.0E0
<input type="checkbox"/> GOTERM_CC_FAT	intrinsic to membrane	RT		4	8.2E-1	1.0E0
<input type="checkbox"/> SP_PIR_KEYWORDS	transmembrane	RT		4	8.9E-1	1.0E0

Transcription regulation

Zinc-finger

Membrane

6 terms were not clustered.

Parent Transcript IDs with high frequencies

ParentTranscriptID	Freq	SearchEnsemblManually					
1 ENSMUST00000002305	1						
2 ENSMUST00000007959	5	ras homolog gene family, member A [Source:MGI Symbol;Acc:MGI:1096342]	Chromosome 9: 108,306,205-108,337,939 forward strand.				
3 ENSMUST00000015486	2						
4 ENSMUST00000033458	2						
5 ENSMUST00000037644	2						
6 ENSMUST00000044200	1						
7 ENSMUST00000049385	1						
8 ENSMUST00000060762	2						
9 ENSMUST00000062609	1						
10 ENSMUST00000076894	1						
11 ENSMUST00000088257	4	tRNA methyltransferase 11-2 [Source:MGI Symbol;Acc:MGI:1914924] [Type: protein coding Ensembl/Havana merge]	19:6909698-6911049:1				
12 ENSMUST00000094863	1						
13 ENSMUST00000096913	1						
14 ENSMUST00000101560	2						
15 ENSMUST00000105001	2						
16 ENSMUST00000106731	1						
17 ENSMUST00000121091	1						
18 ENSMUST00000130870	1						
19 ENSMUST00000147671	5	expressed sequence AU019823 [Source:MGI Symbol;Acc:MGI:2143205] [Type: protein coding Havana]	9:50607701-50617264:-1				
20 ENSMUST00000159611	1						
21 ENSMUST00000164138	3	predicted gene 4868 [Source:MGI Symbol;Acc:MGI:3648712] [Type: protein coding Ensembl]	5:125847949-125848740:-1				
22 ENSMUST00000165611	1						
23 ENSMUST00000168691	1						
24 ENSMUST00000170922	1						