Relating tissue specialisation to the differentiation of expression of singleton and duplicate mouse genes

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Supplementary data

Comparison between the main and the additional dataset. Two sources of microarray data were analysed for the work reported here: expression information collected on Affymetrix U74Av2 GeneChip arrays and expression information collected on Novartis GNF1M GeneChip arrays (see text). Of the 4914 proteins mapped to a probe-set from the U74Av2 GeneChip, and 13045 proteins mapped to a probe-set from the GNF1M Genechip, there are 3935 proteins in common. We studied the expression pattern (Absence/Presence calls) of these proteins in 14 tissues reported by the two datasets. The number of proteins expressed in each tissue from both sources of data and from the overlap set is shown in Supplementary Figure 1. Most proteins that are reported as present by the GNF1M GeneChip are also reported as present by the U74Av2 GeneChip, but not vice versa. These differences between the GeneChips may be explained by the differences in their sensitivity due to differences in their probe-sets. In the U74Av2 GeneChip most probe-sets are composed of 16 individual reporters, while in GNF1M GeneChip most probe-sets are composed of only 11 individual reporters. Those design differences affect the sensitivity of the MAS5 Presence/Absence call.

Based on the analysis performed and the design of the reporter sets, we believe that the U74Av2 arrays are more sensitive when only reporting absence or presence of expression. Therefore, we chose to report the results from this data source in the paper (main dataset). We have repeated all analyses with the GNF1M arrays (additional dataset).

Testing the dependence between expression breadth and the number of duplicatepairs in a group of slow-evolving metazoan-specific proteins. In order to verify that the correlation observed in the metazoan-specific protein subset between expression breadth and number of duplicates is not derived from the enrichment of this group in fast-evolving proteins we have repeated the analysis with a group of slow-evolving metazoan-specific proteins. A significant negative correlation between expression breadth and number of duplicate-pairs were found both in a group of 248 metazoan-specific proteins where mouse-rat evolutionary rate (ka/ks) < 0.05 (group 1) and in a group of 49 proteins where rate < 0.005 (group 2). Correlation was also detected in the group of the 248 fastest evolving proteins (group 3, evolutionary rate > 0.23). The values of evolutionary rates between mouse and rat proteins were obtained as described in the method section in the main text. Correlation for group 1: kendall's tau = -0.28, P value = 5.11 x 10⁻¹¹. Correlation for group 2: kendall's tau = -0.39, P value = 3.27 x 10⁻⁵. Correlation for group 3: kendall's tau = -0.29, P value = 6.7 X 10⁻¹².

Figure legends

Supp. Figure 1: Number of proteins expressed in a tissue, out of 3935 proteins common to the main and additional dataset.

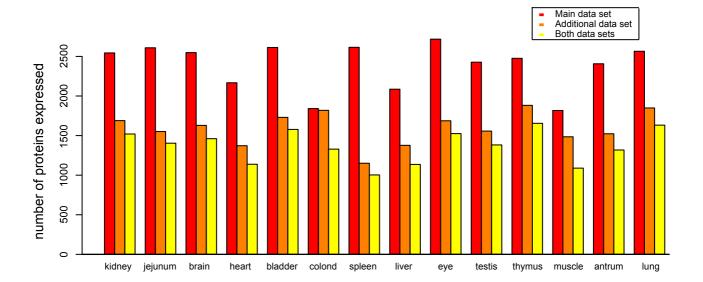
Supp. Figure 2: Analysis based on the additional database. Expression breadth versus the number of duplicate-pairs. Red dots – singleton proteins, black dots – duplicate proteins. The tissues tested are the 20 cluster-representing tissues. (A) The size of the dots represents the number of proteins that have the same number of duplicate-pairs and the same expression breadth. The blue dots represent the average expression breadth of proteins with the same number of duplicate-pairs. Sample size: 7127 proteins; kendall's tau = -0.02; P value = 8.7 x 10^{-4} ; 95% confidence intervals: (-0.04, -0.01). (B) Proteins are ordered according to their number of duplicate-pairs and collected into bins of at least 100 proteins. Each point represents a bin. Error bars indicate the standard deviation from the mean obtained by bootstrapping.

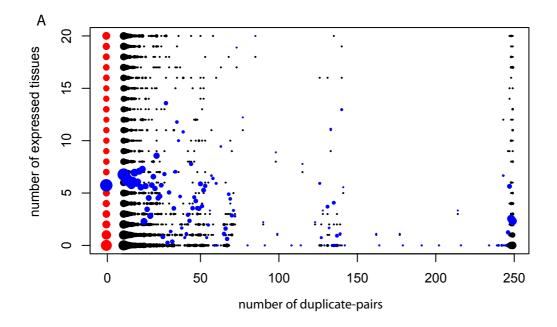
Supp. Figure 3: Analysis based on the additional database. Expression breadth versus the number of duplicate-pairs. Red dots – singleton proteins, black dots – duplicate proteins. The tissues tested are the 20 cluster-representing tissues. (A,C,E) The size of the dots represents the number of proteins that have the same number of duplicate-pairs and the same expression breadth. The blue dots represent the average expression breadth of proteins with the same number of duplicate-pairs. preMD subset (A): 489 proteins, kendall's tau = 0.07, P value = 0.99, 95% confidence intervals: (-0.01, 0.14); postMD subset (C): 875 proteins, kendall's tau = -0.07, P value = 1.5×10^{-3} , 95% confidence intervals: (-0.12, -0.02); Metazoan-specific proteins subset (E): 3281 proteins, kendall's tau = -0.11, P value = 3.7×10^{-22} , 95% confidence intervals: (-0.14, -0.09); (B,D,F) Proteins are ordered according to their number of duplicate-pairs and collected into bins of at least 10 proteins. Each point represents a bin. Error bars indicate the standard deviation from the mean obtained by bootstrapping.

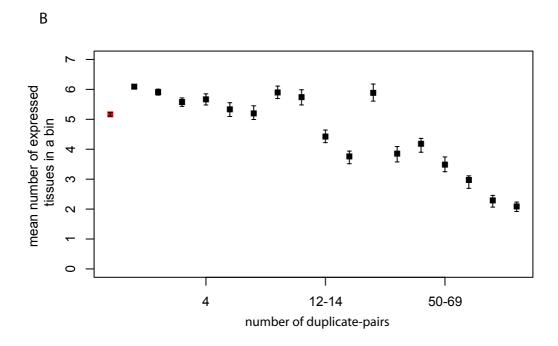
Supp. Figure 4: Analysis based on the additional database. Average cumulative expression coverage in bins of protein families, ordered by size of family. Protein families where

expression information is available for at least a single member (black) are grouped into bins of at least 35 proteins (total number of families: 2054). Protein families where expression information is available or at least 75% of the family members (green) are grouped into bins of at least 10 proteins (total number of families: 761). Each point represents a bin. Values on the X-axis describe the size of a family with any expression information (black dots). The size of families with 75% expression information (green dots) is the value on top of each green dot. The tissues tested are the 20 cluster-representing tissues.

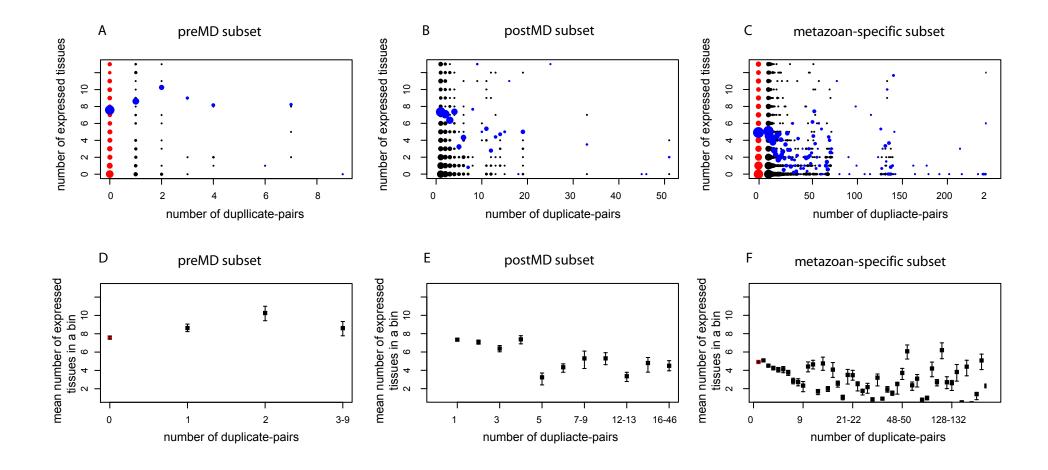
Supplement Figure 1

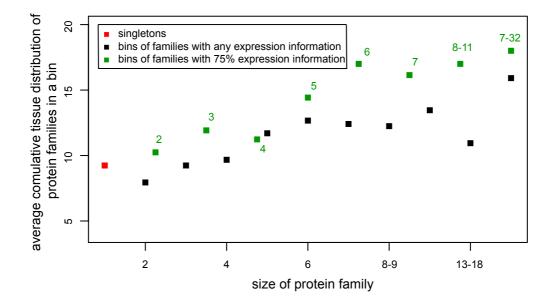






Supplement Figure 3





Supplementary Table 1. The total number of proteins in the different groups of phyletic age/time of duplication analysed. The numbers in brackets are the numbers of proteins in the group for which expression data was available in the additional dataset.

	Complete dataset	PreMD subset	PostMD subset	Metazoan-specific subset
Number of proteins in the mouse proteome	31535 (13045)	2231 (1317)	3699 (1335)	15394 (5908)
Number of proteins that are either singleton or duplicate proteins	18075 (7127)	811 (489)	2495 (875)	9390 (3281)
Number of singleton proteins	3691 (2054)	667 (396)	0 (0)	1960 (1041)
Number of duplicate proteins	14384 (5073)	144 (93)	2495 (875)	7430 (2240)

Supplementary Table 2. Annotations of specifically expressed singleton proteins (expressed in at most 3 tissues).

	ENSEMBL id	SWISSPROT	GO Molecular Function	GO Biological	GO Cellular
	(phyletic group*)	accession and name		Process	Component
antrum	ENSMUSP000000 23510 (PM)	PYR5_MOUSE Uridine 5'- monophosphate synthase	nucleobase, nucleoside, nucleotide and nucleic acid metabolism,'de novo' pyrimidine base biosynthesis,aromatic compound metabolism,biosynthesis,nuc leobase metabolism,heterocycle metabolism,	transferase activity,lyase activity,	
antrum	ENSMUSP000000 47720 (PM)				
appendix	ENSMUSP000000 43369 (MS)	IL5_MOUSE Interleukin-5 [Precursor]	phosphorus metabolism,phosphate metabolism,immune response,response to biotic stimulus,positive regulation of metabolism,peptidyl- tyrosine phosphorylation,peptidyl- tyrosine modification,regulation of phosphate metabolism,regulation of metabolism,macromolecule metabolism,positive regulation of phosphate metabolism,positive regulation of peptidyl- tyrosine phosphorylation,	receptor binding,	
bladder	ENSMUSP000000 06692 (PM)	ER19_MOUSE Diphosphomevalon ate decarboxylase	alcohol metabolism,lipid metabolism,cholesterol biosynthesis,phosphorus metabolism,phosphate metabolism,biosynthesis,ma cromolecule metabolism,	nucleotide binding,kinase activity,lyase activity,	
bladder	ENSMUSP000000 21130 (MS)		eromorecure incurronsin,		
bladder	ENSMUSP000000 25773 (PM)	DPD4_MOUSE DNA polymerase delta subunit 4	nucleobase, nucleoside, nucleotide and nucleic acid metabolism,cell cycle,cell growth and/or maintenance,	transferase activity,	nucleus,
bladder	ENSMUSP000000 47720 (PM)				
bladder	ENSMUSP000000 71235 (MS)	PHX4_MOUSE Putative per- hexamer repeat protein 4			integral to membrane,
brain	ENSMUSP000000 18595 (MS)				
brain	ENSMUSP000000 26466 (MS)	TKNK_MOUSE Neurokinin B [Precursor]	signal transduction,cell surface receptor linked signal transduction,tachykinin signaling pathway,neuropeptide signaling pathway,cell-cell signaling,transmission of nerve impulse,neurophysiological process,organismal movement,neuromuscular	receptor binding,	

			physiological process,		
brain	ENSMUSP000000 31268 (PM)			hydrolase activity,	
brain	ENSMUSP000000 33198 (PM)	CRYM_MOUSE Mu-crystallin homolog	morphogenesis,organogenes is,	structural constituent of eye lens,	cytoplasm,
brain	ENSMUSP000000 34023 (MS)	SRG1_MOUSE Scrapie-responsive protein 1 [Precursor]			
brain	ENSMUSP000000 39418 (MS)	VHL_MOUSE Von Hippel-Lindau disease tumor suppressor	cell cycle,cell growth and/or maintenance,protein ubiquitination,macromolecul e metabolism,	protein binding,	nucleus,
brain	ENSMUSP000000 40342 (MS)		peptide hormone processing,hormone metabolism,macromolecule metabolism,	enzyme inhibitor activity,	cytoplasm,
brain	ENSMUSP000000 46012 (MS)	APEL_MOUSE Apelin [Precursor]	signal transduction,cell surface receptor linked signal transduction,	receptor binding,	
brain	ENSMUSP000000 65423 (PM)			carbohydrate binding,	
brain	ENSMUSP000000 67770 (MS)				
brain	ENSMUSP000000 75395 (PM)	ER19_MOUSE	nucleobase, nucleoside, nucleotide and nucleic acid metabolism,regulation of transcription, DNA- dependent,regulation of transcription from Pol II promoter,transcription from Pol II promoter,positive regulation of metabolism,regulation of nucleobase,regulation of metabolism,positive regulation of transcription,positive regulation of nucleobase,positive regulation of nucleobase,positive regulation of nucleobase,positive regulation of nucleobase,positive regulation of transcription from Pol II promoter, alcohol metabolism,lipid	transcription cofactor activity,protein binding,	nucleus,
	06692 (PM)	Diphosphomevalon ate decarboxylase	metabolism,cholesterol biosynthesis,phosphorus metabolism,phosphate metabolism,biosynthesis,ma cromolecule metabolism,	binding,kinase activity,lyase activity,	
cecum	ENSMUSP000000 25773 (PM)	DPD4_MOUSE DNA polymerase delta subunit 4	nucleobase, nucleoside, nucleotide and nucleic acid metabolism,cell cycle,cell growth and/or maintenance,	transferase activity,	nucleus,
cecum	ENSMUSP000000 31146 (MS)	NEUU_MOUSE Neuromedin U-23 [Precursor]	cell motility,signal transduction,cell surface receptor linked signal transduction,neuropeptide signaling pathway,		
cecum	ENSMUSP000000 31268 (PM)			hydrolase activity,	
cecum	ENSMUSP000000 45737 (PM)	CND2_MOUSE Condensin complex subunit 2	M phase of mitotic cell cycle,nuclear division,cytokinesis,cell cycle,cell growth and/or maintenance,		nucleus,
cecum	ENSMUSP000000 71235 (MS)	PHX4_MOUSE Putative per- hexamer repeat protein 4			integral to membrane,

cecum	ENSMUSP000000 71936 (PM)	YV03_MOUSE Hypothetical protein PP2447 homolog			
distal colon	ENSMUSP000000 31146 (MS)	NEUU_MOUSE Neuromedin U-23 [Precursor]	cell motility,signal transduction,cell surface receptor linked signal transduction,neuropeptide signaling pathway,		
proximal colon	ENSMUSP000000 31146 (MS)	NEUU_MOUSE Neuromedin U-23 [Precursor]	cell motility,signal transduction,cell surface receptor linked signal transduction,neuropeptide signaling pathway,		
duodenum	ENSMUSP000000 25704 (MS)		cytokinesis,cell growth and/or maintenance,		
duodenum	ENSMUSP000000 31268 (PM)			hydrolase activity,	
duodenum	ENSMUSP000000 39418 (MS)	VHL_MOUSE Von Hippel-Lindau disease tumor suppressor	cell cycle,cell growth and/or maintenance,protein ubiquitination,macromolecul e metabolism,	protein binding,	nucleus,
duodenum	ENSMUSP000000 45737 (PM)	CND2_MOUSE Condensin complex subunit 2	M phase of mitotic cell cycle,nuclear division,cytokinesis,cell cycle,cell growth and/or maintenance,		nucleus,
duodenum	ENSMUSP000000 46012 (MS)	APEL_MOUSE Apelin [Precursor]	signal transduction,cell surface receptor linked signal transduction,	receptor binding,	
duodenum	ENSMUSP000000 56752-D				
eye	ENSMUSP000000 18595 (MS)				
eye	ENSMUSP000000 26466 (MS)	TKNK_MOUSE Neurokinin B [Precursor]	signal transduction,cell surface receptor linked signal transduction,tachykinin signaling pathway,neuropeptide signaling pathway,cell-cell signaling,transmission of nerve impulse,neurophysiological process,organismal movement,neuromuscular physiological process,	receptor binding,	
eye	ENSMUSP000000 31268 (PM)			hydrolase activity,	
eye	ENSMUSP000000 33198 (PM)	CRYM_MOUSE Mu-crystallin homolog	morphogenesis,organogenes is,	structural constituent of eye lens,	cytoplasm,
eye	ENSMUSP000000 36541 (PM)			•	
eye	ENSMUSP000000 40342 (MS)		peptide hormone processing,hormone metabolism,macromolecule metabolism,	enzyme inhibitor activity,	cytoplasm,
eye	ENSMUSP000000 63590 (PM)	N107_MOUSE Nuclear pore complex protein Nup107	cell growth and/or maintenance,		nucleus,end omembrane system,inte gral to membrane,
eye	ENSMUSP000000 65836 (PM)				
eye	ENSMUSP000000 67770 (MS)				
gall bladder	ENSMUSP000000 16031 (PM)	HUTH_MOUSE Histidine	organic acid metabolism,amino acid and	lyase activity,ligase	cytoplasm,

gall bladder	ENSMUSP000000	ammonia-lyase	derivative metabolism,amino acid metabolism,histidine metabolism,catabolism,bios ynthesis,histidine family amino acid catabolism,amine metabolism,amine catabolism,	activity,	
	22722 (PM)	Immune- responsive protein 1 [Fragment]			
gall bladder	ENSMUSP000000 23519 (PM)	HGD_MOUSE Homogentisate 1,2-dioxygenase	organic acid metabolism,amino acid and derivative metabolism,amino acid metabolism,aromatic compound metabolism,catabolism,arom atic amino acid family catabolism,amine metabolism,amine catabolism,aromatic compound catabolism,	oxidoreductase activity,	
gall bladder	ENSMUSP000000 23832 (PM)	SM30_MOUSE Regucalcin		ion binding,	nucleus,cyt oplasm,
gall bladder	ENSMUSP000000 25249 (MS)	APOM_MOUSE Apolipoprotein M	cell growth and/or maintenance,	lipid transporter activity,	, , , , , , , , , , , , , , , , , , ,
gall bladder	ENSMUSP000000 25773 (PM)	DPD4_MOUSE DNA polymerase delta subunit 4	nucleobase, nucleoside, nucleotide and nucleic acid metabolism,cell cycle,cell growth and/or maintenance,	transferase activity,	nucleus,
gall bladder	ENSMUSP000000 29645 (PM)	T230_MOUSE Tryptophan 2,3- dioxygenase	organic acid metabolism,amino acid and derivative metabolism,amino acid metabolism,tryptophan metabolism,biogenic amine metabolism,aromatic compound metabolism,amine metabolism,indole and derivative metabolism,heterocycle metabolism,	oxidoreductase activity,	
gall bladder	ENSMUSP000000 32141 (PM)				
gall bladder	ENSMUSP000000 34539 (PM)		nucleobase, nucleoside, nucleotide and nucleic acid metabolism,catabolism,macr omolecule catabolism,macromolecule metabolism,	hydrolase activity,	nucleus,
gall bladder	ENSMUSP000000 47720 (PM)				
gall bladder	ENSMUSP000000 71235 (MS)	PHX4_MOUSE Putative per- hexamer repeat protein 4			integral to membrane,
gall bladder	ENSMUSP000000 77192 (PM)		lipid metabolism,phospholipid metabolism,phosphatidylcho line biosynthesis,phospholipid biosynthesis,biosynthesis,m acromolecule metabolism,membrane lipid biosynthesis,phosphatidylch	transferase activity,	cytoplasm, mitochondri al membrane,e ndomembra ne system,inte gral to membrane,

			oline metabolism,glycerophosphol ipid biosynthesis,		
heart	ENSMUSP000000 25554 (MS)	UTER_MOUSE Uteroglobin [Precursor]		enzyme inhibitor activity,steroid binding,	
ileum	ENSMUSP000000 01667 (MS)	CASK_MOUSE Kappa-casein [Precursor]			
ileum	ENSMUSP000000 06692 (PM)	ER19_MOUSE Kappa-casein [Precursor]	alcohol metabolism,lipid metabolism,cholesterol biosynthesis,phosphorus metabolism,phosphate metabolism,biosynthesis,ma cromolecule metabolism,	nucleotide binding,kinase activity,lyase activity,	
ileum	ENSMUSP000000 25704 (MS)		cytokinesis,cell growth and/or maintenance,		
ileum	ENSMUSP000000 25773 (PM)	DPD4_MOUSE DNA polymerase delta subunit 4	nucleobase, nucleoside, nucleotide and nucleic acid metabolism,cell cycle,cell growth and/or maintenance,	transferase activity,	nucleus,
ileum	ENSMUSP000000 31268 (PM)			hydrolase activity,	
ileum	ENSMUSP000000 34359 (MS)				
ileum	ENSMUSP000000 34539 (PM)		nucleobase, nucleoside, nucleotide and nucleic acid metabolism,catabolism,macr omolecule catabolism,macromolecule metabolism,	hydrolase activity,	nucleus,
ileum	ENSMUSP000000 37484 (MS)			ion binding,	
ileum	ENSMUSP000000 45737 (PM)	CND2_MOUSE Condensin complex subunit 2	M phase of mitotic cell cycle,nuclear division,cytokinesis,cell cycle,cell growth and/or maintenance,		nucleus,
ileum	ENSMUSP000000 46012 (MS)	APEL_MOUSE Apelin [Precursor]	signal transduction,cell surface receptor linked signal transduction,	receptor binding,	
ileum	ENSMUSP000000 71936 (PM)	YV03_MOUSE Hypothetical protein PP2447 homolog			
jejunum	ENSMUSP000000 25704 (MS)		cytokinesis,cell growth and/or maintenance,		
jejunum	ENSMUSP000000 31268 (PM)			hydrolase activity,	
jejunum	ENSMUSP000000 34359 (MS)				
jejunum	ENSMUSP000000 45737 (PM)	CND2_MOUSE Condensin complex subunit 2	M phase of mitotic cell cycle,nuclear division,cytokinesis,cell cycle,cell growth and/or maintenance,		nucleus,
jejunum	ENSMUSP000000 46012 (MS)	APEL_MOUSE Apelin [Precursor]	signal transduction,cell surface receptor linked signal transduction,	receptor binding,	
kidney	ENSMUSP000000 06692 (PM)	ER19_MOUSE Kappa-casein [Precursor]	alcohol metabolism,lipid metabolism,cholesterol biosynthesis,phosphorus metabolism,phosphate metabolism,biosynthesis,ma cromolecule metabolism,	nucleotide binding,kinase activity,lyase activity,	
kidney	ENSMUSP000000 23282 (PM)	MIOX_MOUSE Inositol oxygenase	monosaccharide metabolism,alcohol metabolism,regulation of cell volume,signal	oxidoreductase activity,	cytoplasm,i nclusion body,

iver ENSMUSP000000 ENSMUSP000000 Z3519 (PM) APOM_MOUSE metabolism_armine acid and carbolism_armine catabolism_armine acid and carbolism_armine catabolism_armine acid and carbolism_armine acid and c						
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Total		25249 (MS)	Apolipoprotein M	maintenance,	activity,	
Total	kidney			nucleobase, nucleoside,	transcription	nucleus,
transcription, DNA- dependent, regulation of transcription from Pol II promoter, transcription from Pol II promoter, positive regulation of nucleobase, regulation of franscription, positive regulation of nucleobase, regulation		75395 (PM)			cofactor	
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regulation of metabolism,regulation of nucleobase,regulation of metabolism,positive regulation of transcription of nucleobase,positive regulation of nucleobase,positive regulation of nucleobase,positive regulation of transcription from Pol II promoter, Inver						
liver ENSMUSP000000 HUTH_MOUSE I6031 (PM) Histidine ammonia-lyase ENSMUSP000000 23519 (PM) HGD_MOUSE Iiver ENSMUSP000000 1,2-dioxygenase HGD_MOUSE Iiver ENSMUSP000000 1,2-dioxygenase HGD_MOUSE Iiver ENSMUSP000000 1,2-dioxygenase HGD_MOUSE Iverable immetabolism, regulation of transcription from Pol II promoter, organic acid metabolism, amino acid and derivative metabolism, amino acid metabolism, amino acid catabolism, amine catabolism. ENSMUSP000000 23519 (PM) HGD_MOUSE Homogentisate 1,2-dioxygenase II,2-dioxygenase II,2-dioxygenase II,2-dioxygenase II,2-dioxygenase II,2-dioxygenase II,2-dioxygenase III,2-dioxygenase						
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metabolism,positive regulation of transcription from Pol II promoter, organic acid metabolism,amine catabolism,amine catabolism,amine metabolism,amine catabolism,amine cataboli						
liver ENSMUSP000000 Itiver Itiver ENSMUSP000000 Itiver ENSMUSP000000 Itiver Itiver ENSMUSP000000 Itiver Itiver ENSMUSP000000 Itiver Itiver ENSMUSP000000 Itiver Iti						
transcription,positive regulation of nucleobase,positive regulation of transcription from Pol II promoter, ENSMUSP000000						
liver ENSMUSP000000 HISTORIAN ARTINICATION ENSMUSP000000 TEST AND THE PROPERTY OF THE PROPERTY						
liver ENSMUSP000000 16031 (PM) HUTH_MOUSE Histidine ammonia-lyase Histidine ammonia-lyase Fishistidine metabolism,amino acid and derivative metabolism,catabolism,bios ynthesis,histidine family amino acid catabolism,amine metabolism,amine metabolism,amine catabolism,amine metabolism,amine catabolism,amine catabolism,amine metabolism,amine catabolism,amine catabolism,amine catabolism,amine metabolism,amine catabolism,amine metabolism,amine catabolism,amine metabolism,amine metabolism,amino acid and derivative metabolism.						
liver ENSMUSP00000 HUTH_MOUSE Histidine ammonia-lyase liver ENSMUSP000000 HGD_MOUSE Ammonia-lyase liver ENSMUSP000000 23519 (PM) HGD_MOUSE HOmogentisate 1,2-dioxygenase liver						
liver ENSMUSP000000 HUTH_MOUSE Histidine ammonia-lyase liver ENSMUSP000000 HOTH_MOUSE Histidine ammonia-lyase liver ENSMUSP000000 23519 (PM) HGD_MOUSE Homogentisate 1,2-dioxygenase liver						
liver ENSMUSP000000 16031 (PM) Histidine ammonia-lyase Metabolism,amino acid metabolism,bios ynthesis,histidine family amino acid catabolism,amine metabolism,amine catabolism, Oxidoreductase activity, Axional Activity Diving a civity, Axional Activity Mistidine metabolism,amino acid metabolism,amino derivative metabolism,amino acid and derivative metabolism,amino acid metabolism,amino acid metabolism,aromatic compound metabolism,aromatic compound metabolism,aromatic compound metabolism,aromatic compound metabolism,aromatic compound metabolism,aromatic activity, Oxidoreductase activity,						
Histidine ammonia-lyase ammonia-lyase	liver	ENSMUSP000000	HUTH_MOUSE		lyase	cytoplasm,
derivative metabolism, amino acid metabolism, histidine metabolism, catabolism, bios ynthesis, histidine family amino acid catabolism, amine metabolism, amine catabolism, amine catabolism, amine catabolism, amine catabolism, amine catabolism, amino acid metabolism, amino acid and derivative metabolism, amino acid and derivative metabolism, amino acid metabolism, amino acid metabolism, amino acid metabolism, aromatic compound metabolism, aromatic amino acid family						
liver ENSMUSP000000 HGD_MOUSE 1,2-dioxygenase Homogentisate 1,2-dioxygenase Ensmusposses Homogentisate 1,2-dioxygenase Homogentisate 1,2-dioxygenase Ensmusposses Homogentisate 1,2-dioxygenase Homogentisate 1,2-di						
metabolism,catabolism,bios ynthesis,histidine family amino acid catabolism,amine metabolism,amine catabolism, liver ENSMUSP000000 HGD_MOUSE organic acid metabolism,amino acid and derivative metabolism,amino acid metabolism,amino acid metabolism,amino acid metabolism,amino acid metabolism,amino acid metabolism,amino acid metabolism,aromatic compound metabolism,catabolism,arom atic amino acid family			ammoma-iyasc			
liver ENSMUSP000000 23519 (PM) HGD_MOUSE Homogentisate 1,2-dioxygenase Homogentism, amino acid and derivative metabolism, amino acid metabolism, arom atic amino acid family						
amino acid catabolism,amine metabolism,amine catabolism, liver ENSMUSP000000 23519 (PM) HGD_MOUSE Homogentisate 1,2-dioxygenase Homogentisate Metabolism,amino acid and derivative metabolism,amino acid metabolism,aromatic compound metabolism,arom atic amino acid family						
liver ENSMUSP000000 HGD_MOUSE organic acid metabolism, amino acid and derivative metabolism, aromatic compound metabolism, aromatic amino acid family						
liver ENSMUSP000000 23519 (PM) HGD_MOUSE Homogentisate 1,2-dioxygenase I,2-dioxygenase Homogentisate 1,2-dioxygenase Homogentisate Homogentisat						
liver ENSMUSP000000 23519 (PM) HGD_MOUSE Homogentisate 1,2-dioxygenase 1,2-dioxygenase Homogentisate compound metabolism,aromatic compound metabolism,catabolism,arom atic amino acid family catabolism, oxidoreductase activity, derivative metabolism,aromatic compound metabolism,catabolism,arom atic amino acid family				amino acid		
liver ENSMUSP000000 23519 (PM) HGD_MOUSE Homogentisate 1,2-dioxygenase 1,2-dioxygenase Homogentisate 1,2-dioxygenase derivative metabolism,aromatic compound metabolism,catabolism,arom atic amino acid family oxidoreductase activity, metabolism,aromatic compound metabolism,catabolism,arom atic amino acid family				amino acid catabolism,amine		
23519 (PM) Homogentisate 1,2-dioxygenase metabolism,amino acid and derivative metabolism,aromatic compound metabolism,catabolism,arom atic amino acid family				amino acid catabolism,amine metabolism,amine		
1,2-dioxygenase derivative metabolism,amino acid metabolism,aromatic compound metabolism,catabolism,arom atic amino acid family	Error	ENGMIGROSSOS	HCD MOUSE	amino acid catabolism,amine metabolism,amine catabolism,	quidonolista	
metabolism,amino acid metabolism,aromatic compound metabolism,catabolism,arom atic amino acid family	liver		_	amino acid catabolism,amine metabolism,amine catabolism, organic acid		
metabolism,aromatic compound metabolism,catabolism,arom atic amino acid family	liver		Homogentisate	amino acid catabolism,amine metabolism,amine catabolism, organic acid metabolism,amino acid and		
compound metabolism,catabolism,arom atic amino acid family	liver		Homogentisate	amino acid catabolism,amine metabolism,amine catabolism, organic acid metabolism,amino acid and derivative		
metabolism,catabolism,arom atic amino acid family	liver		Homogentisate	amino acid catabolism,amine metabolism,amine catabolism, organic acid metabolism,amino acid and derivative metabolism,amino acid		
atic amino acid family	liver		Homogentisate	amino acid catabolism,amine metabolism,amine catabolism, organic acid metabolism,amino acid and derivative metabolism,amino acid metabolism,amino acid metabolism,aromatic		
	liver		Homogentisate	amino acid catabolism,amine metabolism,amine catabolism, organic acid metabolism,amino acid and derivative metabolism,amino acid metabolism,aromatic compound		
catabolism,amine	liver		Homogentisate	amino acid catabolism,amine metabolism,amine catabolism, organic acid metabolism,amino acid and derivative metabolism,amino acid metabolism,aromatic compound metabolism,catabolism,arom		

			metabolism,amine catabolism,aromatic compound catabolism,		
liver	ENSMUSP000000 23832 (PM)	SM30_MOUSE Regucalcin		ion binding,	nucleus,cyt oplasm,
liver	ENSMUSP000000 25249 (MS)	APOM_MOUSE Apolipoprotein M	cell growth and/or maintenance,	lipid transporter activity,	
liver	ENSMUSP000000 29645 (PM)	T230_MOUSE Tryptophan 2,3- dioxygenase	organic acid metabolism,amino acid and derivative metabolism,amino acid metabolism,tryptophan metabolism,biogenic amine metabolism,aromatic compound metabolism,amine metabolism,indole and derivative metabolism,heterocycle metabolism,	oxidoreductase activity,	
liver	ENSMUSP000000 60495 (MS)	LCT2_MOUSE Leukocyte cell- derived chemotaxin 2 [Precursor]	sensory perception,response to external stimulus,neurophysiological process,		
liver	ENSMUSP000000 77192 (PM)		lipid metabolism,phospholipid metabolism,phosphatidylcho line biosynthesis,phospholipid biosynthesis,biosynthesis,m acromolecule metabolism,membrane lipid biosynthesis,phosphatidylch oline metabolism,glycerophosphol ipid biosynthesis,	transferase activity,	cytoplasm, mitochondri al membrane,e ndomembra ne system,inte gral to membrane,
lung	ENSMUSP000000 25554 (MS)	UTER_MOUSE Uteroglobin [Precursor]		enzyme inhibitor activity,steroid binding,	
lung	ENSMUSP000000 44493 (MS)			<i>.</i>	
lung	ENSMUSP000000 44862-D				
lung	ENSMUSP000000 71235 (MS)	PHX4_MOUSE Putative per- hexamer repeat protein 4			integral to membrane,
muscle	ENSMUSP000000 30705 (PM)	RFA2_MOUSE Replication protein A 32 kDa subunit	nucleobase, nucleoside, nucleotide and nucleic acid metabolism,cell cycle,cell growth and/or maintenance,	nucleic acid binding,	nucleus,
muscle	ENSMUSP000000 65423 (PM)			carbohydrate binding,	
spleen	ENSMUSP000000 25773 (PM)	DPD4_MOUSE DNA polymerase delta subunit 4	nucleobase, nucleoside, nucleotide and nucleic acid metabolism,cell cycle,cell growth and/or maintenance,	transferase activity,	nucleus,
spleen	ENSMUSP000000 27162 (MS)		response to biotic stimulus,	antigen binding,receptor binding,peptide binding,	plasma membrane,i ntegral to membrane,
spleen	ENSMUSP000000 30180 (MS)		cell activation,immune response,signal transduction,response to biotic stimulus,T-cell activation,immune cell activation,lymphocyte activation,regulation of T-	receptor signaling protein activity,protein binding,	plasma membrane,i ntegral to membrane,

			cell activation,regulation of cell activation,		
spleen	ENSMUSP000000	RFA2_MOUSE	nucleobase, nucleoside,	nucleic acid	nucleus,
spicen	30705 (PM)	Replication protein A 32 kDa subunit	nucleotide and nucleic acid metabolism,cell cycle,cell	binding,	nucicus,
spleen	ENSMUSP000000		growth and/or maintenance,		
	32141 (PM)				
spleen	ENSMUSP000000 34539 (PM)		nucleobase, nucleoside, nucleotide and nucleic acid metabolism,catabolism,macr omolecule catabolism,macromolecule metabolism,	hydrolase activity,	nucleus,
spleen	ENSMUSP000000 44493 (MS)				
spleen	ENSMUSP000000 47720 (PM)				
spleen	ENSMUSP000000 63590 (PM)	N107_MOUSE Nuclear pore complex protein Nup107	cell growth and/or maintenance,		nucleus,end omembrane system,inte gral to membrane,
spleen	ENSMUSP000000 71235 (MS)	PHX4_MOUSE Putative per- hexamer repeat protein 4			integral to membrane,
spleen	ENSMUSP000000 78413-D	FBS1_MOUSE Fibrosin-1 [Fragment]		receptor binding,	
testis	ENSMUSP000000 20990 (MS)	COLI_MOUSE Corticotropin- lipotropin [Precursor]	signal transduction,cell surface receptor linked signal transduction,neuropeptide signaling pathway,	receptor binding,	
testis	ENSMUSP000000 22019 (MS)	IL9_MOUSE Interleukin-9 [Precursor]	immune response,response to biotic stimulus,	receptor binding,	
testis	ENSMUSP000000 25704 (MS)	-	cytokinesis,cell growth and/or maintenance,		
testis	ENSMUSP000000 31268 (PM)		,	hydrolase activity,	
testis	ENSMUSP000000 31876 (MS)			, J	
testis	ENSMUSP000000 32481 (MS)		reproduction,gametogenesis, spermatid development,sexual reproduction,cell differentiation,	nucleic acid binding,protein binding,enzyme activator activity,	nucleus,cyt oplasm,
testis	ENSMUSP000000 33691 (MS)	TSX_MOUSE Testis-specific protein TSX			
testis	ENSMUSP000000 37484 (MS)			ion binding,	
testis	ENSMUSP000000 39418 (MS)	VHL_MOUSE Von Hippel-Lindau disease tumor suppressor	cell cycle,cell growth and/or maintenance,protein ubiquitination,macromolecul e metabolism,	protein binding,	nucleus,
testis	ENSMUSP000000 44862-D	**			
testis	ENSMUSP000000 45737 (PM)	CND2_MOUSE Condensin complex subunit 2	M phase of mitotic cell cycle,nuclear division,cytokinesis,cell cycle,cell growth and/or maintenance,		nucleus,
testis	ENSMUSP000000 45925 (MS)D		macromolecule metabolism,	protein binding,	ubiquitin ligase complex,cyt

					oplasm,
testis	ENSMUSP000000 47588 (MS)			protein binding,	nucleus,
testis	ENSMUSP000000 59448 (MS)	TUR8_MOUSE Tumor rejection antigen P815A			nucleus,inte gral to membrane,
testis	ENSMUSP000000 59630 (MS)	HSP3_MOUSE Sperm protamine P3	reproduction,M phase of mitotic cell cycle,nuclear division,cell cycle,gametogenesis,cell growth and/or maintenance,sexual reproduction,	nucleic acid binding,	nucleus,chr omosome,
testis	ENSMUSP000000 63590 (PM)	N107_MOUSE Nuclear pore complex protein Nup107	cell growth and/or maintenance,		nucleus,end omembrane system,inte gral to membrane,
testis	ENSMUSP000000 65423 (PM)			carbohydrate binding,	
testis	ENSMUSP000000 65836 (PM)				
testis	ENSMUSP000000 67770 (MS)				
testis	ENSMUSP000000 77192 (PM)		lipid metabolism,phospholipid metabolism,phosphatidylcho line biosynthesis,phospholipid biosynthesis,biosynthesis,m acromolecule metabolism,membrane lipid biosynthesis,phosphatidylch oline metabolism,glycerophosphol ipid biosynthesis,	transferase activity,	cytoplasm, mitochondri al membrane,e ndomembra ne system,inte gral to membrane,
testis	ENSMUSP000000 78413-D	FBS1_MOUSE Fibrosin-1 [Fragment]		receptor binding,	
thymus	ENSMUSP000000 00028 (PM)	CC45_MOUSE CDC45-related protein	nucleobase, nucleoside, nucleotide and nucleic acid metabolism,cell cycle,cell growth and/or maintenance,		nucleus,
thymus	ENSMUSP000000 20765 (PM)	DPD2_MOUSE DNA polymerase delta subunit 2	nucleobase, nucleoside, nucleotide and nucleic acid metabolism,cell cycle,cell growth and/or maintenance,	transferase activity,	nucleus,
thymus	ENSMUSP000000 21130 (MS)				
thymus	ENSMUSP000000 21164 (MS)				
thymus	ENSMUSP000000 25704 (MS)		cytokinesis,cell growth and/or maintenance,		
thymus	ENSMUSP000000 25773 (PM)	DPD4_MOUSE DNA polymerase delta subunit 4	nucleobase, nucleoside, nucleotide and nucleic acid metabolism,cell cycle,cell growth and/or maintenance,	transferase activity,	nucleus,
thymus	ENSMUSP000000 27162 (MS)		response to biotic stimulus,	antigen binding,receptor binding,peptide binding,	plasma membrane,i ntegral to membrane,
thymus	ENSMUSP000000 30180 (MS)		cell activation,immune response,signal transduction,response to biotic stimulus,T-cell activation,immune cell activation,lymphocyte activation,regulation of T- cell activation,regulation of	receptor signaling protein activity,protein binding,	plasma membrane,i ntegral to membrane,

			cell activation,		
thymus	ENSMUSP000000 30705 (PM) ENSMUSP000000	RFA2_MOUSE Replication protein A 32 kDa subunit	nucleobase, nucleoside, nucleotide and nucleic acid metabolism,cell cycle,cell growth and/or maintenance, nucleobase, nucleoside,	nucleic acid binding, hydrolase	nucleus,
	34539 (PM)		nucleotide and nucleic acid metabolism,catabolism,macr omolecule catabolism,macromolecule metabolism,	activity,	
thymus	ENSMUSP000000 38204 (MS)	RAG2_MOUSE V(D)J recombination- activating protein 2	cell activation,nucleobase, nucleoside, nucleotide and nucleic acid metabolism,immune response,response to biotic stimulus,morphogenesis,org anogenesis,lymphocyte differentiation,cell differentiation,immune cell activation,lymphocyte activation,	nucleic acid binding,peroxida se activity,oxidored uctase activity,hydrolas e activity,	nucleus,
thymus	ENSMUSP000000 44493 (MS)				
thymus	ENSMUSP000000 45737 (PM)	CND2_MOUSE Condensin complex subunit 2	M phase of mitotic cell cycle,nuclear division,cytokinesis,cell cycle,cell growth and/or maintenance,		nucleus,
thymus	ENSMUSP000000 47720 (PM)				
thymus	ENSMUSP000000 63590 (PM)	N107_MOUSE Nuclear pore complex protein Nup107	cell growth and/or maintenance,		nucleus,end omembrane system,inte gral to membrane,

 $[*]PM-pre-metazoan\ protein;\ MS-metazoan\text{-specific protein}$

Supplementary Table 3. Tissue list of the main dataset. Cluster representatives are indicated using bold face.

Tissue	Cluster ID
Antrum	1
Appendix	2
Bladder	3
Gall bladder	3 3
Lung	3
Brain	4
Eye	4
Cecum	5
Duodenum	5
Ileum	5
Jejunum	5
Distal colon	6
Proximal colon	6
Heart	7
Kidney	8
Liver	9
Muscle	10
Spleen	11
Thymus	11
Testis	12
Testis	12
Vas deferens	13

Supplementary Table 4. Tissue list of the additional dataset. Cluster representatives are indicated using bold face.

Tissue	Cluster ID
Amygdala	1
Cerebellum	1
Cerebral cortex	1
Dorsal root ganglion	1
Dorsal striatum	1
Frontal cortex	1
	1
Hippocampus	1
Hypothalamus Olfactory bulb	
•	1
Preoptic	1
Retina	1
Lower spinal cord	1
Upper spinal cord	1
Substantianigra	1
Trigeminal	1
b220.bcell	2
cd4.Tcell	2
cd8.Tcell	2 2
Lymph node	2
Thymus	2
Heart	3
Testis	2 3 4 5 5 5 5 5
Adipose tissue	5
Adrenal gland	5
Bladder	5
Lung	5
Prostate	5
Kidney	6
Liver	7
Salivary gland	8
Digits	9
Epidermis	9
Snout epidermis	9
Tongue epidermis	9
Bone	10
Large intestine	11
Small intestine	11
Spleen	12
	13
Pituitary Medial olfactory epithelium (MOE)	13
Vomeral-nasal organ (VMO)	14
Thyroid	15
Stomach	16
Pancreas	17

Brown fat	18
Skeletal muscle	19
Bone marrow	20