Supplementary Tables and Supplementary Table Legends

Supplementary Table 1
Microarray experiments and hybridizations downloaded from ArrayExpress which were used to reverse-engineer the human and mouse gene networks.

Supplementary Table 2
List of the genes associated to multiple probe-sets.

Supplementary Table 3
List of genes associated to multiple probe-sets that are consistent.

Supplementary Table 4
The top 1000 connections with the highest MI in the human network. Connections are sorted according with their Mutual Information. For each connection, we reported the *Probe ID* and *Gene Symbol* of the gene pair, along with the corresponding Mutual Information.

Supplementary Table 5
Protein-protein interactions that have been tested via Yeast two Hybrid assays. Red highlights pairs of proteins whose physical interaction was already known from literature. Green highlights pairs of proteins whose physical interaction has been confirmed via Yeast two Hybrid assay.

Supplementary Table 6
Human and mouse communities of genes obtained by applying a hierarchical clustering algorithm. For each community we report the list of genes composing it.

Supplementary Table 7
Gene Ontology enriched for each of the communities. We report the significant Gene Ontology terms ($P < 0.05$ after Bonferroni correction) along with their p-values computed as described in the Supplementary Experimental Procedures.

Cellular Component: Lysosome

P	Probeset ID	Gene Symbol	Gene Info
7.89E-41	200701_at	NPC2	Niemann-Pick disease, type C2
1.88E-36	211284_s_at	GRN	granulin
2.41E-34	200743_s_at	TPP1	tripeptidyl peptidase I
7.74E-33	212663_at	FKBP15	FK506 binding protein 15, 133kDa
3.76E-32	201212_at	LGMN	legumain
7.10E-31	201494_at	PRCP	prolylcarboxypeptidase (angiotensinase C)
8.76E-31	218217_at	SCPEP1	serine carboxypeptidase 1
5.99E-30	202944_at	NAGA	N-acetylgalactosaminidase, alpha-
8.99E-30	217118_s_at	C22ORF9	chromosome 22 open reading frame 9
9.02E-30	204204_at	SLC31A2	solute carrier family 31 (copper transporters), member 2
2.31E-29	200871_s_at	PSAP	prosaposin
9.49E-29	201944_at	HEXB	hexosaminidase B (beta polypeptide)
2.73E-28	35820_at	GM2A	GM2 ganglioside activator
3.67E-28	200839_s_at	CTSB	cathepsin B
7.29E-28	202295_s_at	CTSH	cathepsin H
7.29E-28	202838_at	FUCA1	fucosidase, alpha-L- 1, tissue
8.89E-28	200748_s_at	FTH1	ferritin, heavy polypeptide 1
5.39E-27	202545_at	PRKCD	protein kinase C, delta
7.00E-27	202087_s_at	CTSL1	cathepsin L1
8.61E-27	208704_x_at	APLP2	amyloid beta (A4) precursor-like protein 2

Biological process: Lysosome Organization

P	Probeset ID	Gene Symbol	Gene Info
1.58E-09	200661_at	CTSA	cathepsin A
7.17E-06	200742_s_at	TPP1	tripeptidyl peptidase I
3.20E-05	207809_s_at	ATP6AP1	ATPase, H+ transporting, lysosomal accessory protein 1
3.48E-05	211284_s_at	GRN	granulin
2.10E-04	202545_at	PRKCD	protein kinase C, delta
2.25E-04	201050_at	PLD3	phospholipase D family, member 3
2.90E-04	200766_at	CTSD	cathepsin D
3.73E-04	217118_s_at	C22ORF9	chromosome 22 open reading frame 9
3.74E-04	219952_s_at	MCOLN1	mucolipin 1
4.58E-04	202812_at	GAA	glucosidase, alpha;
2.54E-03	208926_at	NEU1	sialidase 1 (lysosomal sialidase)
3.54E-03	205090_s_at	NAGPA	N-acetylglucosamine-1-phosphodiester alpha-N-acetylglucosaminidase
3.81E-03	200649_at	NUCB1	nucleobindin 1
4.56E-03	218282_at	EDEM2	ER degradation enhancer, mannosidase alpha-like 2
4.56E-03	219020_at	HS1BP3	HCLS1 binding protein 3
4.56E-03	203045_at	NINJ1	ninjurin 1
4.56E-03	201494_at	PRCP	prolylcarboxypeptidase (angiotensinase C)
4.56E-03	212647_at	RRAS	related RAS viral (r-ras) oncogene homolog
4.56E-03	218217_at	SCPEP1	serine carboxypeptidase 1
4.56E-03	203167_at	TIMP2	TIMP metallopeptidase inhibitor 2

Supplementary Table 8
The top 20 genes significantly associated to *Lysosome* (Cellular Component gene ontology class) or *Lysosome Organization* (Biological Process gene ontology class) resulting from the application of the guilty-by-association analysis, sorted according to the associated p-values.