Details of literature gene lists

HG-U133A

Gene list ID	Probesets number	PMID	Source	Description
hs1a	867	16531451	Provenzani *et al.*, 2006	Probesets differentially expressed in the total RNA sample. Extracted from Supplementary Table I.
hs1b	2018	16531451	Provenzani *et al.*, 2006	Probesets changed in the polysomal RNA sample. Extracted from Supplementary Table II.
hs1c	397	16531451	Provenzani *et al.*, 2006	Probesets common to polysomal and total RNA sample. Extracted from Supplementary Table III.
hs2a	269	15210650	Lee *et al.*, 2004	Transcripts with greater than 3-fold enrichment in every T cell subpopulation compared to TSC. Extracted from Supplementary Table 1.
hs2b	1521	15210650	Lee *et al.*, 2004	Transcripts whose expression changed by more than 3-fold during T cell differentiation. Extracted from Supplementary Table 2.
hs2c	134	15210650	Lee *et al.*, 2004	Transcripts enriched in both ITTP and DP by more than 3-fold. Extracted from Supplementary Table 3-1.
hs2d	76	15210650	Lee *et al.*, 2004	Transcripts enriched in more mature cells (SP4, CB4, and AB4) by more than 3-fold. Extracted from Supplementary Table 3-2.
hs2e	28	15210650	Lee *et al.*, 2004	Transcripts enriched by more than 3-fold in ITTP compared to other lymphocytes. Extracted from Supplementary Table 3-3.
hs2f	28	15210650	Lee *et al.*, 2004	Transcripts enriched by more than 3-fold in DP compared to other lymphocytes. Extracted from Supplementary Table 3-4.
hs2g	16	15210650	Lee *et al.*, 2004	Transcripts enriched by more than 3-fold in SP4 compared to other lymphocytes. Extracted from Supplementary Table 3-5.
hs2h	25	15210650	Lee *et al.*, 2004	Transcripts enriched in naïve CD4 T cells (CB4, and AB4) by more than 3-fold. Extracted from Supplementary Table 3-6.
hs2i	32	15210650	Lee *et al.*, 2004	Transcripts showing SP4>CB4>AB4 pattern. Extracted from Supplementary Table 4-1.
hs2j	240	15210650	Lee *et al.*, 2004	Transcripts showing more than 2 fold higher expression in CB4 than in AB4. Extracted from Supplementary Table 4-2.
hs3a	400	15897907	Farmer *et al.*, 2005	Genes which best discriminate apocrine vs luminal (AL). Extracted from Supplementary Table Sheet 2.
hs3b	400	15897907	Farmer *et al.*, 2005	Genes which best discriminate apocrine vs basal (AB). Extracted from Supplementary Table Sheet 2.
hs3c	400	15897907	Farmer *et al.*, 2005	Genes which best discriminate basal vs luminal (BL). Extracted from Supplementary Table Sheet 2.
hs4a	181	16260967	Radom-Aizik *et al.*, 2005	Genes whose expression increased after training. Extracted from Table S2 in the main paper.
hs4b	216	16260967	Radom-Aizik *et al.*, 2005	Genes whose expression decreased after training. Extracted from Table S3 in the main paper.
hs5a	135	12958056	Gimino *et al.*, Sep 2003	Genes that are up-regulated in gene expression in acute rejection vs. no rejection (False Discovery Rate = 0.94%). Extracted from Supplementary Table E1.
hs5b	858	12958056	Gimino *et al.*, Sep 2003	Genes with significant changes in gene expression in acute rejection vs. no rejection (False Discovery Rate = 4.63 %). Extracted from Supplementary Table E2.
hs6a	181	16319128	Vanharanta *et al.*, 2006	Down-regulated genes in FH mutant relative to FH wild-type fibroids. Extracted from Supplementary Table 1.

Details of literature gene lists (continued)

HG-U133A

Gene list ID	Probesets number	PMID	Source	Description
hs6b	179	16319128	Vanharanta *et al.*, 2006	Up-regulated genes in FH mutant relative to FH wild-type fibroids. Extracted from Supplementary Table 1.
hs6c	228	16319128	Vanharanta *et al.*, 2006	Down-regulated genes in FH mutant relative to normal myometrium. Extracted from Supplementary Table 3.
hs6d	199	16319128	Vanharanta *et al.*, 2006	Up-regulated genes in FH mutant relative to normal myometrium. Extracted from Supplementary Table 3.
hs7	1434	15817885	Barth *et al.*, 2005	Genes differentially expressed in atrial fibrillation. Extracted from Supplementary Table 3.
hs8	412	15971941	Barberi *et al.*, 2005	Genes shared between primary and hESC-derived mesenchymal precursors but significantly different from undifferentiated hESCs. Extracted from Supplementary Table S2.
hs9a	26	15558013	O'Donnell *et al.*, 2005	Genes down-regulated in N+ primary tumours. Extracted from Supplementary Figure 1.
hs9b	93	15558013	O'Donnell *et al.*, 2005	Genes up-regulated in N+ primary tumours. Extracted from Supplementary Figure 1.
hs10	256	16203770	Best *et al.*, 2005	Unabridged list of genes differentially expressed between AD and AI prostate cancer. Extracted from Supplementary Data.
hs11a	113	16049480	Minn *et al.*, 2005	Genes differentially expressed between parental MDA-MB-231 and LM2 cell lines selected to be highly metastatic to lung. Extracted from Supplementary Table 2.
hs11b	65	16049480	Minn *et al.*, 2005	Lung metastasis candidate genes. Extracted from Supplementary Table 4.
hs12a	2707	16089502	Eckfeldt *et al.*, 2005	Probesets differentially expressed between umbilical cord blood derived Rho-lo and Rho-hi cells. Extracted from Supplementary Table S1.
hs12b	4677	16089502	Eckfeldt *et al.*, 2005	Probesets differentially expressed between adult bone marrow derived Rho-lo and Rho-hi cells. Extracted from Supplementary Table S2.
hs12c	304	16089502	Eckfeldt *et al.*, 2005	Probesets differentially expressed between Rho-lo and Rho-hi cells from both umbilical cord blood and adult bone marrow. Extracted from Supplementary Table S3.
hu13	235	16205643	Liu *et al.*, 2006	Genes induced by c-Myb and v-Myb in MCF-7 cells. Extracted from Supplementary Table 1.
hs14a	299	14872006	Hall *et al.*, 2004	Genes differentially expressed in 19 paired human samples comparing pre and post mechanical unloading with a LVAD. Extracted from Supplementary Table S1.
hs14b	144	14872006	Hall *et al.*, 2004	Genes differentially expressed in Non-Ischemic Cohort. Extracted from Supplementary Table S3.
hs14c	97	14872006	Hall *et al.*, 2004	Genes differentially expressed in Ischemic Cohort. Extracted from Supplementary Table 4.
hs14d	22	14872006	Hall *et al.*, 2004	Genes differentially expressed in Acute MI Cohort. Extracted from Supplementary Table 5.
hs15a	104	12756304	Cousins *et al.*, 2003	Group 1 zinc responsive genes. Extracted from Supplementary Table 3.
hs15b	86	12756304	Cousins *et al.*, 2003	Group 4 zinc responsive genes. Extracted from Supplementary Table 4.
hs16	57	16116475	Chow *et al.*, 2006	Genes differentially expressed in C666-1 RASSF1A-transfected clones. Extracted from Table 1 in the original paper.

Details of literature gene lists (continued)

HG-U133A

Gene list ID	**Probesets number**	**PMID**	**Source**	**Description**
hs17a	73	16804116	Chng *et al.*, 2006	Genes that displayed distinct expression profile in WM compared to CLL and MM. Extracted from Supplementary Table S1: WM Unique Genes.
hs17b	1247	16804116	Chng *et al.*, 2006	Genes that displayed distinct expression profile in MM compared to CLL and WM. Extracted from Supplementary Table S1: MM Unique Genes
hs17c	396	16804116	Chng *et al.*, 2006	Genes that displayed distinct expression profile in CLL compared to WM and MM. Extracted from Supplementary Table S1: CLL Unique Genes.
hs17d	314	16804116	Chng *et al.*, 2006	A cluster of genes that were over-expressed in B-cell, WM and CLL. Extracted from Supplementary Table S1: WM CLL B-cell cluster.
hs18a	46	16836768	Pfoertner *et al.*, 2006	Up-regulated genes comparing CD4+CD25+ T cells vs CD4+CD25- T cells. Extracted from Additional file 1.
hs18b	21	16836768	Pfoertner *et al.*, 2006	Down-regulated genes comparing CD4+CD25+ T cells vs CD4+CD25- T cells. Extracted from Additional file 1.
hs18c	313	16836768	Pfoertner *et al.*, 2006	Genes differentially expressed in Foxp3 over-expressing CD4+ Th cell lines cells relative to the GFP transduced CD4+ Th controls. Extracted from Additional file 4.
hs19a	262	15869706	Rosty *et al.*, 2005	Up-regulated genes in FGFR3 mutated tumours relative to FGFR3 wild type tumours. Extracted from Additional file 2: Positive Significant Genes.
hs19b	552	15869706	Rosty *et al.*, 2005	Down-regulated genes in FGFR3 mutated tumours relative to FGFR3 wild type tumours. Extracted from Additional file 2: Negative Significant Genes
hs20	1207	15604246	Berger *et al.*, 2004	Genes differentially expressed between LHSR and LHS. Extracted from Supplementary Table 1.

Details of literature gene lists (continued)

HG-U133 Plus 2.0

Gene list ID	Probesets number	PMID	Source	Description
hu1	1191	15361855	Donninger *et al.*, 2004	Differentially regulated genes identified in advanced papillary serous tumor specimens. Extracted from Supplementary Table S1.
hu2	1527	16205643	Liu *et al.*, 2006	Genes induced by c-Myb and v-Myb in human monocytes. Extracted from Supplementary Table 3.
hu3a	81	16982809	Szatmari et al, 2006	Genes regulated by PPAR-gamma agonist, RAR-alpha agonists and the RAR-alpha antagonist (referred to as cluster 3 in the main text). Extracted from Supplementary Table S1.
hu3b	72	16982809	Szatmari et al, 2006	Genes down-regulated by PPAR-gamma ligand (referred to as cluster 6 in the main text). Extracted from Supplementary Table S2.
hu4a	195	16926187	Vendelin *et al.*, 2006	Genes differentially expressed in contrasts 1 and 2 (NPS stimulated versus unstimulated NPSR1-A cells, and NPS stimulated NPSR1-A versus NPS stimulated HEK-293H, respectively). Extracted from Supplementary Table S1.
hu4b	43	16926187	Vendelin *et al.*, 2006	Co-regulated genes. Extracted from Supplementary Table 3.
hu5a	690	16210406	Jaatinen *et al.*, 2006	Differentially expressed genes in CD133+ relative to CD133–. Extracted from Supplementary Table 2.
hu5b	257	16210406	Jaatinen *et al.*, 2006	Genes expressed only in CD133+ and absent in CD133- samples. Extracted from Supplementary Table 3.
hu6	225	16242812	Dunckley *et al.*, 2006	Genes whose expression differed significantly when comparing ND non-NFT neurons to AD non-NFT neurons and then to AD NFT neurons. Data downloaded from http://www.tgen.org/research/index.cfm?pageid=502.
hu7	50	16949412	Hassan *et al.*, 2006	Top 50 probesets that displayed differential expression between TL samples and TNL samples. Extracted from Table II in the main paper.
hu8a	724	16772347	Lampron *et al.*, 2006	Complete list of probesets statistically related to GIP-dependent AIMAH. Extracted from Supplementary Table 2.
hu8b	94	16772347	Lampron *et al.*, 2006	Probesets with intensity levels linked to the presence of a GIP-dependent nodule. Extracted from Supplementary Table 4.
hu9a	51	16728703	Zhan *et al.*, 2006	Top 50 over-expressed genes unique to PR subgroup. Extracted from Supplementary Table S2.
hu9b	56	16728703	Zhan *et al.*, 2006	Top 50 over-expressed genes unique to LB subgroup. Extracted from Supplementary Table S2.
hu9c	52	16728703	Zhan *et al.*, 2006	Top 50 over-expressed genes unique to MS subgroup. Extracted from Supplementary Table S2.
hu9d	53	16728703	Zhan *et al.*, 2006	Top 50 over-expressed genes unique to HY subgroup. Extracted from Supplementary Table S2.
hu9e	53	16728703	Zhan *et al.*, 2006	Top 50 over-expressed genes unique to CD-1 subgroup. Extracted from Supplementary Table S2.
hu9f	57	16728703	Zhan *et al.*, 2006	Top 50 over-expressed genes unique to CD-2 subgroup. Extracted from Supplementary Table S2.
hu9g	52	16728703	Zhan *et al.*, 2006	Top 50 over-expressed genes unique to MF subgroup. Extracted from Supplementary Table S2.

Details of literature gene lists (continued)

HG-U133 Plus 2.0

Gene list ID	Probesets number	PMID	Source	Description
hu9h	52	16728703	Zhan *et al.*, 2006	Top 50 under-expressed genes unique to PR subgroup. Extracted from Supplementary Table S3.
hu9i	58	16728703	Zhan *et al.*, 2006	Top 50 under-expressed genes unique to LB subgroup. Extracted from Supplementary Table S3.
hu9j	55	16728703	Zhan *et al.*, 2006	Top 50 under-expressed genes unique to MS subgroup. Extracted from Supplementary Table S3.
hu9k	54	16728703	Zhan *et al.*, 2006	Top 50 under-expressed genes unique to HY subgroup. Extracted from Supplementary Table S3.
hu9l	55	16728703	Zhan *et al.*, 2006	Top 50 under-expressed genes unique to CD-1 subgroup. Extracted from Supplementary Table S3.
hu9m	54	16728703	Zhan *et al.*, 2006	Top 50 under-expressed genes unique to CD-2 subgroup. Extracted from Supplementary Table S3.
hu9n	58	16728703	Zhan *et al.*, 2006	Top 50 under-expressed genes unique to MF subgroup. Extracted from Supplementary Table S3.
hu9o	172	16728703	Zhan *et al.*, 2006	Genes commonly dysregulated in CD-1 and CD-2 groups. Extracted from Supplementary Table S5.
hu9p	131	16728703	Zhan *et al.*, 2006	Genes that were differentially expression between CD-1 and CD-2 subgroups. Extracted from Supplementary Table S6.
hu10	157	16670265	Radmacher *et al.*, 2006	Bullinger Validation Signature that separated AML from normal karyotype. Extracted from Supplementary Table S1.
hu11	70	16953664	Maier *et al.*, 2006	Genes differentially expressed in response to retrovirally mediated MDR1 over-expression. Extracted from Table 1 in the original paper.
hu12a	4176	16638148	Oudes *et al.*, 2006	Genes detected in sorted cells but not in the whole tissue. Extracted from Supplementary Table 2.
hu12b	239	16638148	Oudes *et al.*, 2006	Genes detected in whole prostate but not in sorted cells. Extracted from Supplementary Table 4.
hu12c	197	16638148	Oudes *et al.*, 2006	Genes detected only in prostate luminal cells. Extracted from Supplementary Table 5.
hu12d	150	16638148	Oudes *et al.*, 2006	Genes detected only in prostate basal cells. Extracted from Supplementary Table 6.
hu12e	632	16638148	Oudes *et al.*, 2006	Genes detected only in prostate stromal cells. Extracted from Supplementary Table 7.
hu13	123	16863911	Fruehauf *et al.*, 2006	Genes differentially expressed in AMD3100 + G-CSF-mobilized PBPC compared to G-CSF-mobilized cells. Extracted from Table 1 in the original paper.
hu14	361	16474848	Hooi *et al.*, 2006	Genes present 2 fold expression changes by ST7-1a expression in PC-3 cells. Extracted from Supplementary table.
hu15a	183	16682435	Peddada *et al.*, 2006	Genes significantly increased upon differentiation. Extracted from Supplementary Table 1.
hu15b	12	16682435	Peddada *et al.*, 2006	Genes significantly increased upon differentiation and significantly increased in D-UT vs. D-MT comparison. Extracted from Supplementary Table 2.
hu15c	8	16682435	Peddada *et al.*, 2006	Genes significantly increased upon differentiation and significantly decreased in D-UT vs. D-MT comparison. Extracted from Supplementary Table 3.
hu15d	45	16682435	Peddada *et al.*, 2006	Genes significantly decreased upon differentiation. Extracted from Supplementary Table 4.

Details of literature gene lists (continued)

HG-U133 Plus 2.0

Gene list ID	Probesets number	PMID	Source	Description
hu15e	4	16682435	Peddada *et al.*, 2006	Genes significantly decreased upon differentiation and significantly increased in D-UT vs. D-MT comparison. Extracted from Supplementary Table 5.
hu15f	26	16682435	Peddada *et al.*, 2006	Genes significantly changed upon differentiation in D-MD vs. D-CD comparison. Extracted from Supplementary Table 6.
hu16	133	16507782	Mense *et al.*, 2006	Hypoxia-induced/suppressed genes in both astrocytes and HeLa cells. Extracted from Table S1.
hu17	1521	16785517	Fulcher *et al.*, 2006	Genes differentially expressed between LPS and galectin-1-treated MDDCs. Extracted from Supplementary Table 1.
hu18	859	16379004	DeFilippis *et al.*, 2006	Differentially regulated genes between HCMV-infected versus uninfected human fibroblasts treated with control siRNA at both 4h and 8h post-infection. Extracted from Supplementary Table 1.
hu19a	1233	16288205	Charafe-Jauffret *et al.*, 2006	Probesets significantly differentially expressed between luminal cell lines and basal cell lines. Supplementary. Extracted from Supplementary Table 2.
hu19b	1309	16288205	Charafe-Jauffret *et al.*, 2006	Probesets significantly differentially expressed between luminal cell lines and mesenchymal cell lines. Extracted from Supplementary Table 3.
hu19c	227	16288205	Charafe-Jauffret *et al.*, 2006	Probesets significantly differentially expressed between basal cell lines and mesenchymal cell lines. Extracted from Supplementary Table 4.
hu20a	205	16644866	Armstrong *et al.*, 2006	hESC-specific transcripts. Extracted from Supplementary Table S1.
hu20b	84	16644866	Armstrong *et al.*, 2006	Highly expressed transcripts in both hES-NCL1 and H1 cell lines. Extracted from Supplementary Table S2.
hu20c	61	16644866	Armstrong *et al.*, 2006	Genes which were unique to hES-NCL1. Extracted from Supplementary Table S3.
hu20d	49	16644866	Armstrong *et al.*, 2006	Genes which were unique to H1. Extracted from Supplementary Table S3.
hu20e	110	16644866	Armstrong *et al.*, 2006	New hESC markers. Extracted from Supplementary Table S4.

Details of literature gene lists (continued)

Mouse 430 2.0

Gene list ID	Probesets number	PMID	Source	Description
ms1	294	16949565	Yu *et al.*, 2006	Significantly differentially expressed genes in Get-1-/- back skin relative to wild-type. Extracted from Supplementary Table 4.
ms2a	490	16860309	Potireddy *et al.*, 2006	List of transcripts enriched at MII stage. Extracted from Supplementary Table 2.
ms2b	1808	16860309	Potireddy *et al.*, 2006	Genes enhanced in the late one-cell embryos. Extracted from Supplementary Table 3.
ms3a	185	16368875	Mitchell *et al.*, 2006	Genes differentially expressed in HRas-v12 hearts (RAS-regulated). Extracted from Supplementary Table 2.
ms3b	251	16368875	Mitchell *et al.*, 2006	Genes differentially expressed in MKK3bE hearts (p38-regulated). Extracted from Supplementary Table 2.
ms3c	257	16368875	Mitchell *et al.*, 2006	Genes differentially expressed in MKK7D hearts (JNK-regulated). Extracted from Supplementary Table 2.
ms4a	98	16940520	Kunz *et al.*, 2006	Genes whose expression is consistently changed between LCMV-cgPi and mock infected animals. Extracted from Supplementary Table S1.
ms4b	77	16940520	Kunz *et al.*, 2006	Genes whose expression is significantly changed between the two mock animals. Extracted from Supplementary Table S2.
ms5	1583	16943279	Lindsley *et al.*, 2006	Genes whose expression is Wnt dependent during ES cell differentiation. Extracted from Supplementary Table 1.
ms6a	123	16926388	Reece *et al.*, 2006	Up-regulated genes in both WT and SCID mice by DPI. Extracted from Supplementary Table S2.
ms6b	220	16926388	Reece *et al.*, 2006	Genes that were differentially expressed in the lungs of WT and SCID mice at days 2, 4, and 12 post-Nippostrongylus brasiliensis infection. Extracted from Supplementary Table S3.
ms7a	1138	16926395	He *et al.*, 2006	Significantly down-regulated probesets at 4h post B. melitensis infection. Extracted from Supplementary Table 1.
ms7b	288	16926395	He *et al.*, 2006	Significantly up-regulated probesets at 4h post B. melitensis infection. Extracted from Supplementary Table 2.
ms8	1528	16772024	Korostynski *et al.*, 2006	Probesets differentially expressed among the four inbred strains of mice. Extracted from Supplementary Table S2.
ms9a	75	16945109	Heinitz *et al.*, 2006	Differentially expressed genes in differentiated SN56.B5.G4 cells after treatment with Abeta(1-42). Extracted from Table 1 in the original paper.
ms9b	14	16945109	Heinitz *et al.*, 2006	Differentially expressed genes in differentiated SN56.B5.G4 cells after treatment with H2O2. Extracted from Table 2 in the original paper
ms9c	15	16945109	Heinitz *et al.*, 2006	Differentially expressed genes in differentiated SN56.B5.G4 cells after treatment with Abeta(1-42) and H2O2. Extracted from Table 3 in the original paper
ms10a	36	16105979	Kawagoe *et al.*, 2005	Genes up-regulated (>5-fold) in MN1-TEL+/HOXA9+ AML cells in mice. Extracted from Supplementary Table S1.
ms10b	32	16105979	Kawagoe *et al.*, 2005	Genes down-regulated (>5-fold) in MN1-TEL+/HOXA9+ AML cells in mice. Extracted from Supplementary Table S2.

Details of literature gene lists (continued)

Mouse 430 2.0

Gene list ID	Probesets number	PMID	Source	Description
ms11a	388	17227850	Jankovic *et al.*, 2007	CMP-associated transcript. Extracted from Supplementary Dataset 1.
ms11b	2038	17227850	Jankovic *et al.*, 2007	HSC-associated transcript. Extracted from Supplementary Dataset 2.
ms12a	1674	17183314	Niedernhofer *et al.*, 2006	Genes differentially expressed in Ercc1-/- compared with wild-type liver. Extracted from Supplementary Table III.
ms12b	1665	17183314	Niedernhofer *et al.*, 2006	Genes differentially expressed in aged (130-wk-old) wt mouse liver compared to young (2-mo-old) controls. Extracted from Supplementary Table V.
ms12c	1773	17183314	Niedernhofer *et al.*, 2006	Genes differentially expressed in adult (4-mo-old) wt mouse livers compared to young (2-mo-old) controls. Extracted from Supplementary Table VI.
ms13a	595	15967997	Rossi *et al.*, 2005	Age-up-regulated genes in LT-HSC. Extracted from Supplementary Table 4.
ms13b	383	15967997	Rossi *et al.*, 2005	Age-down-regulated genes in LT-HSC. Extracted from Supplementary Table 4.
ms14a	252	16110338	Corbo *et al.*, 2005	Genes up-regulated in rd7 mutant retina at P21. Extracted from Supplementary Table S4.
ms14b	138	16110338	Corbo *et al.*, 2005	Genes down-regulated in rd7 mutant retina at P21. Extracted from Supplementary Table S5.
ms15a	767	16373508	Shiina *et al.*, 2005	Down-regulated genes in 8-week-old AR-/- ovaries. Extracted from Supplementary Table 1.
ms15b	346	16373508	Shiina *et al.*, 2005	Up-regulated genes in 8-week-old AR-/- ovaries. Extracted from Supplementary Table 2.
ms15c	323	16373508	Shiina *et al.*, 2005	Down-regulated genes in 3-week-old AR-/- ovaries. Extracted from Supplementary Table 3.
ms15d	516	16373508	Shiina *et al.*, 2005	Up-regulated genes in 3-week-old AR-/- ovaries. Extracted from Supplementary Table 4.
ms16a	266	16399799	Beverdam *et al.*, 2006	Genes specifically up-regulated in 11.5 dpc male somatic cells. Extracted from Supplementary Table S1.
ms16b	50	16399799	Beverdam *et al.*, 2006	Genes specifically down-regulated in 11.5 dpc male somatic gonad cells. Extracted from Supplementary Table S3.
ms16c	243	16399799	Beverdam *et al.*, 2006	Genes specifically up-regulated in 11.5 dpc female somatic cells. Extracted from Supplementary Table S5.
ms17a	509	16166195	Denolet *et al.*, 2005	Transcripts down-regulated in SCARKO as compared to control mice at day 10. Extracted from Supplementary Table 1.
ms17b	342	16166195	Denolet *et al.*, 2005	Transcripts up-regulated in SCARKO as compared to control mice at day 10. Extracted from Supplementary Table 1.
ms18	492	16423883	Jeong *et al.*, 2006	Genes differentially expressed in the liver of SRC-2-/- mice as compared to wild type mice. Extracted from Supplementary Table 2.
ms19	429	16641092	Costinean *et al.*, 2006	Genes differentially expressed in transgenic relative to wild-type mice. Extracted from Supplementary Table 3.
ms20	248	16847333	Sun *et al.*, 2006	Genes differentially expressed in day 5 postpartum Mkl1 KO versus wild type mammary glands. Extracted from Supplementary Table S1.

Details of literature gene lists (continued)

Rat 230 2.0

Gene list ID	**Probesets number**	**PMID**	**Source**	**Description**
rat1a	1215	16854511	Mainwaring *et al.*, 2006	Genes with altered expression post paraquat dosing compared to control lung. Extracted from Supplementary Table 2.
rat1b	543	16854511	Mainwaring *et al.*, 2006	This is a subset of genes in rat1a, selected based on a more stringent statistical test. Extracted from Supplementary Table 3.
rat2	95	16770850	Bardag-Gorce *et al.*, 2006	Differentially expressed genes between the peaks of UAL (group 3) and controls (group 1). Extracted from Table 2 in the main paper.
rat3	257	16574311	Chen *et al.*, 2006	Genes regulated by PPARγ in RIE cells. Extracted from Supplementary data.
rat4a	22	16202214	Jaster *et al.*, 2005	Genes up-regulated in PPARγ1-overexpressing LTC cells. Extracted from Table 1A in the main paper.
rat4b	19	16202214	Jaster *et al.*, 2005	Genes down-regulated in PPARγ1-overexpressing LTC cells. Extracted from Table 1B in the main paper.
rat5a	18	16715494	Ko *et al.*, 2006	Genes up-regulated by haloperidol and clozapine. Extracted from Table IA in the main paper.
rat5b	14	16715494	Ko *et al.*, 2006	Genes down-regulated by haloperidol and clozapine. Extracted from Table IB in the main paper.
rat5c	17	16715494	Ko *et al.*, 2006	Genes up-regulated by amphetamine. Extracted from Table IIA in the main paper.
rat5d	5	16715494	Ko *et al.*, 2006	Genes down-regulated by amphetamine. Extracted from Table IIB in the main paper.
rat5e	15	16715494	Ko *et al.*, 2006	Genes up-regulated by amphetamine, but down-regulated by haloperidol and clozapine. Extracted from Table IIIA in the main paper.
rat5f	6	16715494	Ko *et al.*, 2006	Genes down-regulated by amphetamine, but up-regulated by haloperidol and clozapine. Extracted from Table IIIB in the main paper.
rat5g	23	16715494	Ko *et al.*, 2006	Genes up-regulated by haloperidol, clozapine, and amphetamine. Extracted from Table IVA in the main paper.
rat5h	12	16715494	Ko *et al.*, 2006	Genes down-regulated by haloperidol, clozapine, and amphetamine. Extracted from Table IVB in the main paper.
rat6a	1777	16809437	Lahousse *et al.*, 2006	Genes that displayed a significant expression change within 12h of MEHP exposure. Extracted from Supplementary Table 1.
rat6b	536	16809437	Lahousse *et al.*, 2006	Genes altered significantly at 1, 3, 6, or 12h following fetal DBP exposure. Extracted from Supplementary Table 2.
rat6c	176	16809437	Lahousse *et al.*, 2006	Genes showed altered expression at fetal and prepubertal ages. Extracted from Supplementary Table 3.
rat7a	2410	17082646	Geoffrey *et al.*, 2006	Genes over-represented in DRlyp/lyp. Extracted from Supplementary Table A.
rat7b	2660	17082646	Geoffrey *et al.*, 2006	Gene over-represented in DR+/+ . Extracted from Supplementary Table B.
rat8a	315	16401727	Luyendyk *et al.*, 2006	Genes differentially expressed in LPS/Veh/RAN-treated rats relative to LPS/Veh/FAM-treated rats. Extracted from Supplementary Table 1.
rat8b	145	16401727	Luyendyk *et al.*, 2006	Heparin-responsive probesets in LPS/RAN-treated rats. Extracted from Supplementary Table 2.

Details of literature gene lists (continued)

Rat 230 2.0

Gene list ID	Probesets number	PMID	Source	Description
rat8c	29	16401727	Luyendyk *et al.*, 2006	Subset AB: Genes differentially expressed in LPS/Veh/RAN-treated rats relative to LPS/Veh/FAM-treated rats, and also by heparin. Extracted from Supplementary Table 3.
rat9a	113	17069981	Coyle *et al.*, 2007	Genes up-regulated in Allodynic animals. Extracted from Supplementary Table 3.
rat9b	20	17069981	Coyle *et al.*, 2007	Genes down-regulated in Allodynic animals. Extracted from Supplementary Table 3.
rat10	30	17187413	Yovchev *et al.*, 2007	Genes up-regulated in the oval cell enriched fractions. Extracted from Table 1 in the main paper.
rat11a	436	17332525	Xia *et al.*, 2007	Transcripts with >2-fold changes in their expression by day 4 after Adjudin treatment. Extracted from Supplementary Table 1.
rat11b	1466	17332525	Xia *et al.*, 2007	Transcripts that were significantly altered following Adjudin treatment ($P < 0.05$ by ANOVA). Extracted from Supplementary Table 2.

Details of literature gene lists (continued)

Arabidopsis ATH1

Gene list ID	Probesets number	PMID	Source	Description
ath1	685	12920300	Nishimura *et al.*, 2003	Genes response to pathogen attack. Extracted from Supplementary Table S2.
ath2a	3110	16243906	Vanneste *et al.*, 2005	Differentially expressed genes in the wild type versus the slr1 mutant (denoted as the 3110 significant genes in the main text). Extracted from Supplementary Table 1.
ath2b	913	16243906	Vanneste *et al.*, 2005	Lateral root initiation genes (denoted as the 913 LRI genes in the main text). Extracted from Supplementary Table 2.
ath2c	99	16243906	Vanneste *et al.*, 2005	LRI Genes with arf7 arf19–Dependent Auxin Inducibility. Extracted from Supplementary Table 6.
ath3a	222	16299223	Bläsing *et al.*, 2005	3h Glucose-repressed genes. Extracted from Supplementary Table 6.
ath3b	218	16299223	Bläsing *et al.*, 2005	3h Glucose-induced genes. Extracted from Supplementary Table 6.
ath3c	223	16299223	Bläsing *et al.*, 2005	3h Sucrose-repressed genes. Extracted from Supplementary Table 6.
ath3d	224	16299223	Bläsing *et al.*, 2005	3h Sucrose-induced genes. Extracted from Supplementary Table 6.
ath3e	223	16299223	Bläsing *et al.*, 2005	4h Photomorphogenesis repressed genes. Extracted from Supplementary Table 6.
ath3f	219	16299223	Bläsing *et al.*, 2005	4h Photomorphogenesis induced genes. Extracted from Supplementary Table 6.
ath3g	220	16299223	Bläsing *et al.*, 2005	30min NO3 repressed genes. Extracted from Supplementary Table 6.
ath3h	219	16299223	Bläsing *et al.*, 2005	30min NO3 induced genes. Extracted from Supplementary Table 6.
ath3i	235	16299223	Bläsing *et al.*, 2005	3h NO3 repressed genes. Extracted from Supplementary Table 6.
ath3j	209	16299223	Bläsing *et al.*, 2005	3h NO3 induced genes. Extracted from Supplementary Table 6.
ath3k	217	16299223	Bläsing *et al.*, 2005	3h Mannitol repressed genes. Extracted from Supplementary Table 6.
ath3l	228	16299223	Bläsing *et al.*, 2005	3h Mannitol induced genes. Extracted from Supplementary Table 6.
ath3m	232	16299223	Bläsing *et al.*, 2005	4h Carbon fixation repressed genes. Extracted from Supplementary Table 6.
ath3n	218	16299223	Bläsing *et al.*, 2005	4h Carbon fixation induced genes. Extracted from Supplementary Table 6.
ath3o	221	16299223	Bläsing *et al.*, 2005	4h light repressed genes. Extracted from Supplementary Table 6.
ath3p	228	16299223	Bläsing *et al.*, 2005	4h light induced genes. Extracted from Supplementary Table 6.
ath3q	643	16299223	Bläsing *et al.*, 2005	Genes responsive to carbon fixation and glucose. Extracted from Supplementary Table 8.
ath4a	189	17006513	Mouchel *et al.*, 2006	Gene regulated due to residual Uk-1 loci other than brx. Extracted from Supplementary Table 1: root introgression drag bg.
ath4b	4006	17006513	Mouchel *et al.*, 2006	Genes strongly regulated in root of brx. Extracted from Supplementary Table 1: >2x, brx vs. Sav+resc., root.

Details of literature gene lists (continued)

Arabidopsis ATH1

Gene list ID	Probesets number	PMID	Source	Description
ath4c	3072	17006513	Mouchel *et al.*, 2006	Up-regulated genes in root and seedling of brx relative to Sav-0. Extracted from Supplementary Table 1: >2x, vs. Sav+resc., root+seedling.
ath4d	26	17006513	Mouchel *et al.*, 2006	Genes not rescued by BL treatment. Extracted from Supplementary Table 1.
ath5a	19	16805732	Mandaokar *et al.*, 2006	Jasmonate-responsive genes in stamens at 0.5h. Extracted from Supplementary Table S1.
ath5b	198	16805732	Mandaokar *et al.*, 2006	Jasmonate-responsive genes in stamens at 2h. Extracted from Supplementary Table S1.
ath5c	491	16805732	Mandaokar *et al.*, 2006	Jasmonate-responsive genes in stamens at 8h. Extracted from Supplementary Table S1.
ath5d	811	16805732	Mandaokar *et al.*, 2006	Jasmonate-responsive genes in stamens at 22h. Extracted from Supplementary Table S1.
ath6a	911	16107481	Nagpal *et al.*, 2005	Genes whose expression changes during development and peaks at stages 13-14. Extracted from Supplementary Table S1.
ath6b	417	16107481	Nagpal *et al.*, 2005	Genes whose expression changes during development and peaks at stages 11-12. Extracted from Supplementary Table S1.
ath6c	387	16107481	Nagpal *et al.*, 2005	Genes whose expression changes during development and peaks pre-stage 11. Extracted from Supplementary Table S1.
ath6d	79	16107481	Nagpal *et al.*, 2005	Genes whose expression in stage 1-10 flowers is greater in Columbia flowers than in the arf6 arf8 flowers. Extracted from Supplementary Table S2.
ath6e	472	16107481	Nagpal *et al.*, 2005	Genes whose expression in stage 11-12 flowers is greater in Columbia flowers than in the arf6 arf8 flowers. Extracted from Supplementary Table S2.
ath6f	692	16107481	Nagpal *et al.*, 2005	Genes whose expression in stage 13-14 flowers is greater in Columbia flowers than in the arf6 arf8 flowers. Extracted from Supplementary Table S2.
ath6g	35	16107481	Nagpal *et al.*, 2005	Genes induced by auxin-treatment. Extracted from Supplementary Table S3.
ath7a	1592	15908603	Tatematsu *et al.*, 2005	Down-regulated genes in axillary bud. Extracted from Supplementary Table 1b.
ath7b	1184	15908603	Tatematsu *et al.*, 2005	Up-regulated gene in axillary bud. Extracted from Supplementary Table 1c.
ath7c	272	15908603	Tatematsu *et al.*, 2005	SRE-containing down-regulated genes in axillary bud. From Supplementary Table 2a.
ath7d	162	15908603	Tatematsu *et al.*, 2005	Up1-containing up-regulated genes in axillary bud. From Supplementary Table 2b.
ath7e	193	15908603	Tatematsu *et al.*, 2005	Up2-containing up-regulated genes in axillary bud. From Supplementary Table 2c.
ath8a	115	15894741	Tung *et al.*, 2005	Genes regulated in the stigmas relative to wild-type stigmas. Extracted from Supplementary Table 1.
ath8b	33	15894741	Tung *et al.*, 2005	Genes regulated in ablated ovary samples. Extracted from Supplementary Table 2.
ath9	547	15937231	Sibout *et al.*, 2005	Genes with altered expression in the double mutant. Extracted from Supplementary Table 10.
ath10a	104	16021403	Zhang *et al.*, 2005	Genes preferentially expressed in young inflorescences. Extracted from Supplementary Table 6.

Details of literature gene lists (continued)

Arabidopsis ATH1

Gene list ID	Probesets number	PMID	Source	Description
ath10b	105	16021403	Zhang *et al.*, 2005	Genes preferentially expressed in all three reproductive organs (i.e. the young inflorescences, stage-12 floral buds and developing siliques). Extracted from Supplementary Table 7.
ath10c	82	16021403	Zhang *et al.*, 2005	Genes preferentially expressed in young inflorescences and stage 12 floral buds. Extracted from Supplementary Table 8.
ath10d	92	16021403	Zhang *et al.*, 2005	Genes preferentially expressed in stage 12 floral buds and silique. Extracted from Supplementary Table 9.
ath11a	614	16299169	Suh *et al.*, 2005	Genes up-regulated in the epidermis of the base of the stem AND the epidermis of the top of the stem. Extracted from Supplementary Data: Up regulated top and base epid.
ath11b	630	16299169	Suh *et al.*, 2005	Genes up-regulated in the epidermis of the top of the stem only. Extracted from Supplementary Data: Up-regulated top epidermis only.
ath11c	657	16299169	Suh *et al.*, 2005	Genes found to be up regulated in the epidermis of the base of the stem only. Extracted from Supplementary Data: Up-regulated base epidermis only.
ath12	718	16492731	Braybrook *et al.*, 2006	Genes induced by LEC2. Extracted from Supplementary Table 2.
ath13	1122	16299182	Lin *et al.*, 2005	Differentially expressed genes under At5PTase13 deficiency. Extracted from Supplementary Table 1.
ath14	203	16299171	Umbach *et al.*, 2005	Genes differentially expressed in antisense versus wild-type leaves. Extracted from Supplementary Table II.
ath15	72	16330762	Brown *et al.*, 2005	Genes induced by UV-B in wild type but show much reduced UV-B induction in uvr8-1 mutant. Extracted from Supplementary Table 2.
ath16a	104	16372013	Leibfried *et al.*, 2005	Genes up-regulated by WUS but not to STM or LFY induction. Extracted from Supplementary Table S1.
ath16b	44	16372013	Leibfried *et al.*, 2005	Genes down-regulated by WUS but not to STM or LFY induction. Extracted from Supplementary Table S1.
ath17a	668	16183833	Davletova *et al.*, 2005	Transcripts significantly elevated/suppressed (>2-fold) in wild type plants following treatment with hydrogen peroxide. Extracted from Supplementary Table 2.
ath17b	8	16183833	Davletova *et al.*, 2005	Transcripts significantly enhanced in Zat12 over-expressing plants more than in WT plant. Extracted from Supplementary Table 3.
ath17c	90	16183833	Davletova *et al.*, 2005	Transcripts significantly enhanced (>2-fold) in Zat12 over-expressing plants in response to hydrogen peroxide. Extracted from Supplementary Table 4.
ath17d	637	16183833	Davletova *et al.*, 2005	All transcripts significantly elevated in Zat12-overexpressing plants in response to H2O2 stress. Extracted from Supplementary Table 5.
ath18	44	16648214	Kolbe *et al.*, 2006	Genes responsive to short-term DTT treatment. Extracted from Supplementary Table S2.
ath19a	64	15608331	Yang *et al.*, 2005	Genes down-regulated by MSBP1. Extracted from Supplementary Table 1.
ath19b	116	15608331	Yang *et al.*, 2005	Genes up-regulated by MSBP1. Extracted from Supplementary Table 1.
ath20a	579	15505214	Monte *et al.*, 2004	Genes response to 1-h continuous red light (Rc) in wild-type (WT) Arabidopsis seedlings. Extracted from Supplementary Table 3.

Details of literature gene lists (continued)

Arabidopsis ATH1

Gene list ID	Probesets number	PMID	Source	Description
ath20b	370	15505214	Monte *et al.*, 2004	Genes that were induced in the WT by 1-h Rc. Extracted from Supplementary Table 4
ath20c	210	15505214	Monte *et al.*, 2004	Genes that were repressed in the WT by 1-h Rc. Extracted from Supplementary Table 5.

Details of literature gene lists (continued)

DrosGenome1

Gene list ID	Probesets number	PMID	Source	Description
dros1	159	16277749	Wertheim *et al.*, 2005	Probesets differentially expressed between parasitised and control larvae. Extracted from Additional data file 1.
dros2	1456	15345053	Wang *et al.*, 2004	Genes up-regulated in tubule. Extracted from Additional data file 1.
dros3a	150	15777795	Johansson *et al.*, 2005	Genes induced in Drosophila mbn-2 cells 6 h post-challenge with crude LPS. Extracted from Supplementary Table 2.
dros3b	518	15777795	Johansson *et al.*, 2005	Differentially expressed genes in Drosophila mbn-2 cells 6 h post-challenge with crude LPS or E. coli. Extracted from Supplementary Table 3.
dros4a	272	16357214	Goodliffe *et al.*, 2005	Genes up-regulated in response to Myc. Extracted from Supplementary data 1
dros4b	214	16357214	Goodliffe *et al.*, 2005	Genes were elevated upon reduction of Pc. Extracted from Supplementary data 2
dros4c	129	16357214	Goodliffe *et al.*, 2005	Genes that were repressed by a factor of 0.533 or more by the ectopic accumulation of dMyc. Extracted from Supplementary data 3.
dros5	51	12777520	Michalak *et al.*, 2003	Transcripts differed significantly in F1 hybrids from both D. simulans and D. mauritiana. Extracted from Supplementary Table 1.
dros6a	4188	16356271	Beckstead *et al.*, 2005	Genes that change their expression ≥1.5-fold in at least one time point in *EcRi* animals. Extracted from Additional data file 1.
dros6b	743	16356271	Beckstead *et al.*, 2005	20E-regulated and 20E primary-response genes. Extracted from Additional data file 2.
dros7	286	16264191	Badenhorst *et al.*, 2005	Genes differentially expressed in Nurf301 mutants compared with wild-type larvae. The Supplementary data was downloaded from http://home.ccr.cancer.gov/badenhorst.
dros8a	1286	12586708	Asha *et al.*, 2003	Genes that are up-regulated in Ras-act hemocytes. Extracted from Supplementary Table 1.
dros8b	260	12586708	Asha *et al.*, 2003	Genes that are down-regulated in Ras-act hemocytes. Extracted from Supplementary Table 2.
dros9	403	16616121	Terry *et al.*, 2006	Candidate stem cell genes: genes enriched in Os+ bgcn- compared to bgcn-. Extracted from Supplementary Table 1.
dros10a	34	16333985	Sørensen *et al.*, 2005	Genes early up-regulated by stress. Extracted from Table 3A in the original paper.
dros10b	123	16333985	Sørensen *et al.*, 2005	Genes early down-regulated by stress. Extracted from Table 3B in the original paper.
dros10c	34	16333985	Sørensen *et al.*, 2005	Genes late up-regulated by stress. Extracted from Table 3C in the original paper.
dros11a	2308	16204451	Yang *et al.*, 2005	Genes under-represented in fly photoreceptor cells relative to whole head. Extracted from Supplementary Table 1.
dros11b	1499	16204451	Yang *et al.*, 2005	Genes enriched in fly photoreceptor cells relative to whole head. Extracted from Supplementary Table 2.
dros12a	4503	16584578	Girardot *et al.*, 2006	Genes that showed age-dependent expression in body parts. Extracted from Additional file 1.
dros12b	126	16584578	Girardot *et al.*, 2006	Most head- or thorax-enriched genes. Extracted from Additional file 2.

Details of literature gene lists (continued)

DrosGenome1

Gene list ID	Probesets number	PMID	Source	Description
dros12c	112	16584578	Girardot *et al.*, 2006	Common age-responsive genes. Extracted from Additional file 4.
dros13	539	16798875	Mack *et al.*, 2006	Genes whose expression levels differed significantly in the reproductive tract of unmated vs. mated females at 0, 3, 6, or 24 h postmating. Extracted from Supplementary Table 3.
dros14a	168	15136717	Landis *et al.*, 2004	Genes up-regulated with age. Extracted from Supplementary Table 1: old up.
dros14b	494	15136717	Landis *et al.*, 2004	Genes down-regulated with age. Extracted from Supplementary Table 1: old down.
dros14c	108	15136717	Landis *et al.*, 2004	Genes up-regulated with oxidative stress. Extracted from Supplementary Table 1: O2 up.
dros14d	234	15136717	Landis *et al.*, 2004	Genes down-regulated with oxidative stress. Extracted from Supplementary Table 1: O2 down
dros14e	97	15136717	Landis *et al.*, 2004	Genes up-regulated with age and oxidative stress. Extracted from Supplementary Table 1: old O2 up
dros14f	154	15136717	Landis *et al.*, 2004	Genes down-regulated with age and oxidative stress. Extracted from Supplementary Table 1: old O2 down
dros14g	8	15136717	Landis *et al.*, 2004	Genes down-regulated with age but up-regulated with oxidative stress. Extracted from Supplementary Table 1: old down O2 up
dros14h	6	15136717	Landis *et al.*, 2004	Genes up-regulated with age but down-regulated with oxidative stress. Extracted from Supplementary Table 1: old up O2 down
dros15	353	16754642	Osada *et al.*, 2006	Probesets differentially expressed in MMM and ZZZ. Extracted from Supplementary Table 1.
dros16	321	15090076	Loop *et al.*, 2004	Genes differentially expressed between brat/k06028 and wild type control. Extracted from Additional file 3.
dros17a	552	16938865	Kadener *et al.*, 2006	Genes down-regulated in TIM-MJD fly heads. Extracted from Supporting Table 5.
dros17b	368	16938865	Kadener *et al.*, 2006	Genes up-regulated in TIM-MJD fly heads. Extracted from Supporting Table 6.
dros17c	597	16938865	Kadener *et al.*, 2006	Genes down-regulated in TIM-MJD fly brains. Extracted from Supporting Table 7.
dros17d	739	16938865	Kadener *et al.*, 2006	Genes up-regulated in TIM-MJD fly brains. Extracted from Supporting Table 8.
dros18	427	14749722	Roxstrőm-Lindquist *et al.*, 2004	Genes that were significantly up-regulated following infection with virus, bacteria or fungi in parallel. Extracted from Supplementary Table 2.
dros19a	133	15695583	Apidianakis *et al.*, 2005	Genes up-regulated by P. aeruginosa strain CF5. Extracted from Supplementary Table 1.
dros19b	80	15695583	Apidianakis *et al.*, 2005	Genes down-regulated by P. aeruginosa strain CF5. Extracted from Supplementary Table 1.
dros19c	16	15695583	Apidianakis *et al.*, 2005	Genes up-regulated by P. aeruginosa strain PA14. Extracted from Supplementary Table 2.
dros19d	12	15695583	Apidianakis *et al.*, 2005	Genes down-regulated by P. aeruginosa strain PA14. Extracted from Supplementary Table 2.
dros19e	241	15695583	Apidianakis *et al.*, 2005	Genes differentially expressed in CF5-infected vs. PA14-infected flies. Extracted from Supplementary Table 3.
dros20	1368	15458575	Girardot *et al.*, 2004	Stress responsive genes. Extracted from Supplementary Table S1.

Details of literature gene lists (continued)

Drosophila 2.0

Gene list ID	Probesets number	PMID	Source	Description
dm1	3727	15851659	Mackay *et al.*, 2005	Genes differentially expressed between fast and slow selection lines. Extracted from Supplementary Table 5.
dm2a	16	16269142	Barmina *et al.*, 2005	Genes differentially expressed between Male T1-Male T2. Extracted from Supplementary Table 1.
dm2b	23	16269142	Barmina *et al.*, 2005	Genes differentially expressed between Female T1-Female T2. Extracted from Supplementary Table 2.
dm2c	143	16269142	Barmina *et al.*, 2005	Genes differentially expressed between Male T1-Female T1. Extracted from Supplementary Table 3.
dm2d	35	16269142	Barmina *et al.*, 2005	Genes differentially expressed between Male T2-Female T2. Extracted from Supplementary Table 4.
dm3a	187	16581772	Rehwinkel *et al.*, 2006	Genes regulated in PIWI and AUB knockdowns. Extracted from Supplementary Table I.
dm3b	472	16581772	Rehwinkel *et al.*, 2006	Genes at least 1.5-fold up- or down-regulated in cells depleted of Drosha. Extracted from Supplementary Table II.
dm3c	1081	16581772	Rehwinkel *et al.*, 2006	Genes regulated in AGO1-depleted cells. Extracted from Supplementary Table III.
dm3d	372	16581772	Rehwinkel *et al.*, 2006	Genes regulated in AGO2-depleted cells. Extracted from Supplementary Table IV.
dm3e	137	16581772	Rehwinkel *et al.*, 2006	Genes upregulated in cells depleted of Drosha and AGO1. Extracted from Supplementary Table VI.
dm4	33	16907832	Sun *et al.*, 2006	Genes that were differentially expressed after a 24 h exposure to phenobarbital in the diet of third-instar larvae as compared with larvae reared on control diet. Extracted from Table 1 in the main paper.
dm5	2329	16624921	Hughes *et al.*, 2006	Genes that displayed significant variation among isogenic lines. Extracted from Supplementary Table S1.
dm6a	1593	17044737	Edwards *et al.*, 2006	Probesets differing significantly for the main effect of selection line. Extracted from Supplementary Table S2.
dm6b	1539	17044737	Edwards *et al.*, 2006	Probesets that displayed significant differences in contrast statements. Extracted from Supplementary Table S3.
dm6c	12	17044737	Edwards *et al.*, 2006	Probesets that displayed sexually antagonistic expression. Extracted from Supplementary Table S4.
dm7	582	17054780	Morozova *et al.*, 2006	Probesets differentially expressed following alcohol exposure. Extracted from Additional data file 2.
dm8a	127	16258543	Liu *et al.*, 2005	Genes commonly affected in both males and females after depletion of HP1. Extracted from Supplementary Table 1.
dm8b	203	16258543	Liu *et al.*, 2005	Genes specifically affected in males after depletion of HP1. Extracted from Supplementary Table 2.
dm8c	119	16258543	Liu *et al.*, 2005	Genes specifically affected in females after depletion of HP1. Extracted from Supplementary Table 3.

Details of literature gene lists (continued)

C. elegans

Gene list ID	Probesets number	PMID	Source	Description
ce1a	433	16626960	Vartiainen *et al.*, 2006	Up-regulated genes in transgenic C. elegans over-expressing alpha-synuclein. Extracted from Supplementary Table S7.
ce1b	67	16626960	Vartiainen *et al.*, 2006	Down-regulated genes in transgenic C. elegans over-expressing alpha-synuclein. Extracted from Supplementary Table S3.
ce2a	167	16480708	Wang *et al.*, 2006	Genes up-regulated upon over-expression of both CeTwist and CeE/DA. Extracted from Supplementary data S1.
ce2b	34	16480708	Wang *et al.*, 2006	Genes down-regulated upon over-expression of both CeTwist and CeE/DA. Extracted from Supplementary data S2.
ce3	816	16184190	Shen *et al.*, 2005	Genes differentially regulated by ire-1 and xbp-1. Extracted from Supplementary Table S10.
ce4a	1092	15256590	Huffman *et al.*, 2004	Genes that showed significant regulation by Cry5B. Extracted from Supplementary Table 2.
ce4b	1083	15256590	Huffman *et al.*, 2004	Genes that showed significant regulation by cadmium. Extracted from Supplementary Table 3.
ce5a	1348	15308663	McElwee *et al.*, 2004	Genes that were up-regulated in daf-2 compared with daf-16;daf-2. Extracted from Supplementary data <- Final gene lists.xls <- worksheet: Daf-2 final gene list.
ce5b	926	15308663	McElwee *et al.*, 2004	Genes that were down-regulated in daf-2 compared with daf-16;daf-2. Extracted from Supplementary data <- Final gene lists.xls <- worksheet: Daf-2 final gene list.
ce6a	71	16809667	O'Rourke *et al.*, 2006	Genes up-regulated following infection of C. elegans with M. nematophilum. Extracted from Supplementary data S1.
ce6b	22	16809667	O'Rourke *et al.*, 2006	Genes down-regulated following infection of C. elegans with M. nematophilum. Extracted from Supplementary data S1.
ce7a	144	17096597	Troemel *et al.*, 2006	Genes differentially expressed between daf-2 and daf-2;pmk-1. From Supplementary Table S2
ce7b	449	17096597	Troemel *et al.*, 2006	Genes differentially expressed between exposure to E. coli strain OP50 and wild-type P. aeruginosa strain PA14. From Supplementary Table S4.
ce7c	287	17096597	Troemel *et al.*, 2006	Genes differentially expressed between exposure to gacA mutant and wild-type P. aeruginosa strain PA14. From Supplementary Table S5.
ce8a	44	16962739	Towers *et al.*, 2006	Up-regulated genes in the two mutant alleles cx35 and cx18 as compared to the wild-type. From Supplementary Table 1.
ce8b	71	16962739	Towers *et al.*, 2006	Down-regulated genes in the two mutant alleles cx35 and cx18 as compared to the wild-type. From Supplementary Table 2.
ce8c	124	16962739	Towers *et al.*, 2006	Differentially expressed genes between wild-type and dys-1 mutant. These genes were selected based on transcript presence calls and a statistical confidence level of 0.05. From Supplementary Table 3.
ce9	466	17187676	Chen *et al.*, 2006	Genes that show a down regulation of 2.0-fold or higher in daf-19(-) animals compared to the daf-19(+) control animals. Extracted from Additional data file 3.
ce10a	167	15620651	Colosimo *et al.*, 2004	Genes differentially expressed between AFD and AWB. Extracted from Supplementary Table S1.

Details of literature gene lists (continued)

C. elegans

Gene list ID	Probesets number	PMID	Source	Description
ce10b	1513	15620651	Colosimo *et al.*, 2004	Genes differentially expressed between (AFD and AWB) and the unsorted whole embryonic cells. Extracted from Supplementary Table S2.
ce11a	1012	15780142	Fox *et al.*, 2005	unc-4::GFP enriched genes. Extracted from Additional data file 9.
ce11b	1586	15780142	Fox *et al.*, 2005	N2 enriched genes. Extracted from Additional data file 10.

Details of literature gene lists (continued)

Xenopus laevis

Gene list ID	Probesets number	PMID	Source	Description
xp1	463	16872594	Urban *et al.*, 2006	Genes regulated by hedgehog. Extracted from Supplementary material Part I.
xp2	276	16651540	Sinner *et al.*, 2006	Endoderm-enriched genes that were differentially expressed between vegetal and animal cap regions. Extracted from Supplementary Table S1.
xp3a	188	16756679	Hufton *et al.*, 2006	Genes regulated by ectopic organizer signaling. Extracted from Additional file S2.
xp3b	220	16756679	Hufton *et al.*, 2006	Genes that show similar regulation in the full organizer conditions. Extracted from Additional file S3.
xp4a	25	17024524	Malone *et al.*, 2006	Top 25 male biased DEGs in both species. Extracted from Supplementary Table 4.
xp4b	25	17024524	Malone *et al.*, 2006	Top 25 female biased genes in both species. Extracted from Supplementary Table 4.
xp4c	25	17024524	Malone *et al.*, 2006	Top 25 DEGs that show unbiased expression in both species. Extracted from Supplementary Table 4.
xp4d	25	17024524	Malone *et al.*, 2006	Top 25 male biased genes that had no difference in expression between species. Extracted from Supplementary Table 4.
xp4e	25	17024524	Malone *et al.*, 2006	Top 25 female biased genes that had no difference in expression between species. Extracted from Supplementary Table 4.
xp5a	666	15901671	Gurvich *et al.*, 2005	Genes most stimulated by both VPA and TSA in xenopus. Extracted from Supplementary data xenopus.stim key.
xp5b	599	15901671	Gurvich *et al.*, 2005	Genes most inhibited by both VPA and TSA in xenopus. Extracted from Supplementary data xenopus.inhib key.
xp6a	1108	16871633	Grow *et al.*, 2006	Comparison A: St53 1dPA Versus st57 1dPA. Genes differentially expressed between st53 blastemas and st57 pseudoblastemas at day 1 postamputation. Extracted from Supplementary Table using P (Welch's T-test) < 0.05.
xp6b	2428	16871633	Grow *et al.*, 2006	Comparison B: St53 5dPA Versus st57 5dPA. Genes differentially expressed between st53 blastemas and st57 pseudoblastemas during regeneration of the limb (st53) or during spike formation (st57) at 5 days postamputation. Extracted from Supplementary Table using P (Welch's T-test) < 0.05.
xp6c	1677	16871633	Grow *et al.*, 2006	Comparison C: St53 1dPA Versus st53 5dPA. Genes differentially expressed from day 1 to day 5 during the regeneration of the st53 limb. Extracted from Supplementary Table using P (Welch's T-test) < 0.05.
xp6d	115	16871633	Grow *et al.*, 2006	Comparison D: St57 1dPA Versus st57 5dPA. Genes differengtially expressed from day 1 to day 5 during st57 spike formation.Extracted from Supplementary Table using P (Welch's T-test) < 0.05.

Details of literature gene lists (continued)

Zebrafish

Gene list ID	Probesets number	PMID	Source	Description
zf1	295	16631158	Cheng *et al.*, 2006	Liver-enriched genes. Extracted from Supplementary Table 1.
zf2	662	16869712	Lien *et al.*, 2006	Genes that were differentially expressed during heart regeneration process. Extracted from dataset S1.
zf3a	67	16443690	Andreasen *et al.*, 2006	Transcripts enhanced at least 2-fold by TCDD exposure in comparison with their time matched vehicle control. Extracted from Table 2 in original paper.
zf3b	132	16443690	Andreasen *et al.*, 2006	Transcripts repressed at least 2-fold by TCDD exposure in comparison with their time matched vehicle control. Extracted from Table 3 in original paper.
zf4	387	15827125	Weber *et al.*, 2005	Genes differentially regulated between clo and WT siblings. Extracted from Supplementary Table S1.
zf5a	141	16322560	Chen *et al.*, 2005	Transcript down-regulated between def mutant and WT. Extracted from Supplementary material Table 1.
zf5b	23	16322560	Chen *et al.*, 2005	Transcript differentially up-regulated between def mutant and WT. Extracted from Supplementary material Table 2.
zf6	163	16714409	Carney *et al.*, 2006	TCDD-induced genes in the zebrafish heart at 73, 74, 76 and 84 hpf. Extracted from Supplementary data S1.
zf7a	78	17251491	Leung *et al.*, 2007	Over-expressed genes in the RPE Compared with the Retina at 52 hpf. Extracted from Table 2 from the main paper.
zf7b	988	17251491	Leung *et al.*, 2007	Under-expressed genes in the RPE Compared with the Retina at 52 hpf. Extracted from Supplementary Table S3.
zf8	811	16484454	Giraldez *et al.*, 2006	Genes that were up-regulated in MZdicer compared to wild type and MZdicer+miR-430 at 9 hpf. Extracted from Supplementary Table S1.
zf9	220	16638810	Link *et al.*, 2006	Differentially expressed genes between ectodermal and mesendodermal cells. Extracted from Supplementary Table S2.
zf10a	600	15901671	Gurvich *et al.*, 2005	Genes most stimulated by both VPA and TSA in zebrafish. Extracted from Supplementary data zebrafish.stim key.
zf10b	617	15901671	Gurvich *et al.*, 2005	Genes most inhibited by both VPA and TSA in zebrafish. Extracted from Supplementary data zebrafish.inhib key.