

Additional File 8

Genes and Gene Expression Modules Associated with Caloric Restriction and Aging in the Laboratory Mouse

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Genes Regulated by Aging in Heart

This file provides information on genes significantly influenced by aging in the heart. The first set of charts displays differential expression results of the 200 genes most strongly up regulated by aging in heart, while the second set of charts displays differential expression results for the 200 genes most strongly down regulated by aging in heart. Each row corresponds to an individual gene and each column corresponds to a separate experiment (see Additional File 1). Symbols are interpreted as follows:

- Gene is significantly up regulated by age ($P_u < 0.05$)
- Gene is significantly down regulated by age ($P_d < 0.05$)
- Gene is marginally up regulated by age ($0.05 < P_u < 0.10$)
- Gene is marginally down regulated by age ($0.05 < P_d < 0.10$)
- Non-significant age effect ($P_u > 0.10$ and $P_d > 0.10$)
- × No data (gene not represented in experiment or array annotation was limiting)
- * Evidence conflicts but favors up regulation by age
- * Evidence conflicts, but favors down regulation by age

The last two categories (* and *) indicate significant effects with conflicting evidence. This can arise if multiple transcripts associated with the same gene symbol yield opposite conclusions. Alternatively, a conflict may arise if $P_u < 0.05$ and also $P_d < 0.05$. Symbols shown in charts are based upon a comparison-wise type I error rate of 0.05. The final column in each chart lists meta-analysis p-values generated using Fisher's method, which have been adjusted using the Benjamini-Hochberg method to control the false discovery rate among all 21,327 genes.

The remainder of the file includes lists of over-represented gene ontology terms, over-represented KEGG pathways, and over-represented KEGG pathways defined based upon IP domain signatures (see Hahne et al. 2008, BMC Bioinformatics 9:3). Genes were also analyzed to determine if there existed an over-abundance of targets for certain microRNAs (see Betel et al. 2008, Nucleic Acids Res. 36: D149-153), and a list of associated microRNAs is provided based upon this analysis. Lastly, tests for over-representation of identified genes with respect to each chromosome were performed, and an idiogram mapping of identified genes to chromosomal locations is shown.

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↑ Age

Genes up regulated by Age

		hrt1	hrt12	hrt13	hrt20	hrt24	hrt29	hrt31a	hrt31b	hrt31c	hrt31d	hrt31e	hrt31f	hrt31g	P _u
4933439C20Rik	C4b	●	●	●	×	●	×	●	●	●	●	●	●	●	5.08e-16
	Pah	●	●	●	×	●	●	●	●	●	●	●	●	●	5.08e-16
	Cxcl14	●	●	●	×	●	—	●	●	●	●	●	●	●	2.57e-12
	Skap2	●	●	—	—	●	—	●	●	●	●	●	●	●	1.13e-11
	Myh7	●	●	●	×	●	×	—	●	●	●	●	●	—	3.28e-11
	Cp	●	—	●	—	●	—	●	●	●	●	●	●	●	1.5e-10
	Cpxm2	●	●	●	×	●	—	●	●	—	●	●	—	●	1.5e-10
	Csprs	●	×	×	×	×	×	●	●	—	●	●	●	●	3.49e-10
	Amy1	●	●	—	×	●	—	●	●	—	●	●	●	●	1.62e-09
	Akr1b8	●	●	●	×	●	—	—	●	—	●	—	●	●	3.28e-09
	Ccl8	●	●	—	×	—	—	●	●	●	●	—	●	●	3.32e-09
	Ccnd1	●	×	×	—	×	×	●	●	●	●	●	●	●	9.77e-09
	Serpina3n	●	●	●	×	●	—	●	●	●	●	●	●	—	3.06e-08
	100040213	●	●	●	×	—	×	—	—	●	●	●	●	●	4.03e-08
	Kcnk1	●	●	●	×	—	×	—	—	●	●	—	—	●	4.27e-08
	Tgfb2	●	—	—	—	—	—	—	—	●	●	●	●	●	1.19e-07
	Klk1b26	●	—	—	—	—	—	—	—	●	●	●	●	●	1.19e-07
	Lect1	●	×	×	×	×	—	●	—	—	●	●	●	●	1.19e-07
	Thbs3	●	●	●	×	—	—	●	●	●	●	—	●	●	1.19e-07
	Fcgr2b	●	—	—	×	—	●	●	—	●	●	●	●	●	1.92e-07
	H19	●	●	●	●	—	—	—	●	●	—	●	—	●	3.43e-07
	Ier3	●	—	—	—	●	—	●	●	—	●	●	—	—	3.77e-07
	Bdh1	●	×	×	×	×	●	●	●	●	●	●	●	●	4.2e-07
	Mmp3	●	—	●	×	●	●	—	—	●	●	●	●	—	9.43e-07
	Prnp	●	●	—	—	●	—	—	●	●	●	●	●	●	1e-06
	Lilrb4	●	●	—	—	—	×	●	●	●	●	—	●	●	1.05e-06
	Amot	●	—	—	●	●	—	●	●	●	—	*	—	●	1.21e-06
	Timp1	●	—	●	×	—	×	●	●	—	●	—	●	●	1.3e-06
	C1qc	—	●	●	—	—	—	●	—	—	●	●	●	—	1.4e-06

↑ Age

Genes up regulated by Age

	hrt1	hrt12	hrt13	hrt20	hrt24	hrt29	hrt31a	hrt31b	hrt31c	hrt31d	hrt31e	hrt31f	hrt31g	P _u
Cyp2b10	●	—	●	×	—	—	●	—	●	●	●	●	●	1.59e-06
Serpine2	—	●	●	—	—	—	—	●	●	●	●	●	●	1.59e-06
Wisp2	—	—	●	×	—	—	●	●	●	●	—	●	—	1.59e-06
Postn	—	●	—	×	—	—	—	●	—	●	●	●	●	2.2e-06
Uchl1	●	●	●	●	—	—	—	●	●	●	—	—	—	2.2e-06
Prkcq	●	×	×	×	×	—	●	—	●	●	—	—	●	2.28e-06
Adamts8	—	×	×	×	×	—	●	●	●	●	—	●	●	2.72e-06
Vsig4	—	×	×	×	×	—	●	●	●	●	●	●	—	2.72e-06
Oas1g	●	×	×	—	×	×	●	●	●	●	●	—	●	5.89e-06
Crlf2	●	×	×	×	×	—	—	●	●	●	—	—	●	6.96e-06
Figf	●	—	●	×	—	—	●	●	●	●	—	●	●	8.91e-06
Nppb	●	—	●	—	●	—	—	●	—	●	●	●	—	1.07e-05
Myot	●	×	×	×	×	—	●	—	—	—	●	●	●	1.12e-05
Lyz2	—	●	●	—	—	×	●	●	●	●	●	●	●	1.15e-05
Ms4a6d	●	×	×	●	×	—	—	—	—	●	*	●	●	1.31e-05
Parp3	●	×	×	×	×	—	●	●	●	●	●	—	—	1.36e-05
Acsl6	●	×	×	×	×	●	●	—	—	●	—	●	—	1.37e-05
Aqp8	●	—	●	×	—	—	●	●	—	●	●	—	—	1.44e-05
Aebp1	—	—	●	—	—	—	—	●	●	●	●	●	●	1.5e-05
Ephx1	●	—	—	●	●	—	—	●	—	●	●	●	—	1.56e-05
Crlf1	—	×	●	×	—	—	●	●	●	●	—	●	—	1.58e-05
Cyp4b1	●	—	●	×	●	×	—	—	●	—	●	●	—	1.58e-05
Trim30	●	●	●	×	—	×	●	—	●	●	—	●	●	1.8e-05
Lman1l	●	×	×	×	×	●	—	—	●	●	●	—	●	2.1e-05
Abat	●	—	●	—	—	●	—	●	—	●	●	—	—	2.31e-05
Ccnd2	*	●	—	—	—	—	●	●	●	—	●	●	●	2.47e-05
Atf5	●	●	●	×	—	●	—	●	—	—	●	—	—	2.89e-05
Ccl6	●	—	●	×	●	—	●	—	●	●	●	●	—	3.64e-05
Grk5	●	—	●	—	●	●	—	—	—	●	●	—	●	3.64e-05
Plscr1	●	—	●	×	●	×	—	—	—	●	●	●	—	3.8e-05

↑ Age

Genes up regulated by Age

		hrt1	hrt12	hrt13	hrt20	hrt24	hrt29	hrt31a	hrt31b	hrt31c	hrt31d	hrt31e	hrt31f	hrt31g	P _u
2810474O19Rik	Pcdhb20	●	×	×	×	×	—	●	●	—	—	●	●	—	3.8e-05
	Hey1	●	—	●	×	—	●	—	—	—	●	—	—	●	4.12e-05
	Osmr	●	●	—	×	—	—	●	—	●	●	●	—	—	4.77e-05
	Tmem176a	●	—	●	×	—	—	●	—	●	●	—	●	●	4.77e-05
	Lyz1	—	×	×	×	×	×	●	—	●	●	●	—	—	5.06e-05
	Apod	●	●	—	×	●	—	—	—	●	●	—	●	—	5.12e-05
	Emr1	—	—	●	×	—	—	●	●	●	—	●	—	—	5.63e-05
	Pgam1	●	×	●	—	●	—	●	—	—	●	—	●	—	5.63e-05
	Cd209g	●	×	×	×	×	—	●	●	—	—	—	●	●	6.61e-05
	Cdh22	●	×	×	—	×	●	●	—	●	●	●	●	—	6.61e-05
	Srxn1	●	—	●	—	—	—	—	●	●	●	●	●	●	6.66e-05
	Maoa	●	—	●	●	—	—	●	—	—	—	●	●	●	6.87e-05
	Ms4a7	●	×	×	×	×	×	●	—	●	●	—	●	—	6.87e-05
	Ccl12	●	—	●	×	—	×	●	—	—	●	●	—	—	6.87e-05
	Ifi27	—	●	●	×	—	●	●	—	—	●	●	●	—	6.89e-05
	Fez2	—	●	—	—	●	—	●	●	●	—	—	●	—	6.97e-05
	Enah	●	—	●	×	●	—	—	●	—	●	●	●	—	7.17e-05
	Il33	—	×	×	×	×	—	●	—	●	●	●	—	—	7.17e-05
	Tac1	●	●	—	×	—	×	—	—	—	●	●	—	●	7.22e-05
	Serpina1b	●	●	●	×	—	—	●	●	—	—	●	—	●	8.34e-05
	Itgbl1	●	×	×	×	×	—	●	—	●	●	●	—	—	9.45e-05
	Stab1	—	●	●	—	—	—	●	●	—	—	—	—	—	9.52e-05
	Pdxk	●	—	●	●	●	—	—	●	●	●	●	—	—	0.000106
	Phf20l1	●	●	●	—	—	—	●	—	●	*	●	●	—	0.000106
	Tyrobp	—	●	●	×	●	—	●	—	●	●	—	●	—	0.000106
	Asah3l	—	×	×	×	×	●	—	—	●	●	●	●	—	0.000108
	Tgm2	●	—	—	—	●	—	—	●	●	●	●	●	—	0.000112
	Usp18	—	—	●	×	—	—	●	—	●	●	—	—	—	0.000112
	Dab2	●	●	●	●	●	—	●	●	—	●	●	—	—	0.000118

Genes up regulated by Age

1200016E24Rik

↑ Age

Genes up regulated by Age

		hrt1	hrt12	hrt13	hrt20	hrt24	hrt29	hrt31a	hrt31b	hrt31c	hrt31d	hrt31e	hrt31f	hrt31g	P _u
C130026I21Rik	Rps6ka2	●	●	●	●	●	×	—	●	●	—	●	—	—	0.000383
	C1qb	—	—	●	—	●	—	●	—	●	●	●	—	—	0.000399
	Cdkn1a	●	●	●	×	—	●	●	●	●	●	●	—	—	0.000399
	Rhou	●	—	●	●	—	●	●	●	●	●	●	●	●	0.000399
	Slc25a5	●	—	●	●	●	×	●	—	*	—	●	●	—	5e−04
	Pfkip	●	—	—	—	●	—	●	●	—	●	—	●	—	0.000521
	C130026I21Rik	●	×	×	×	×	×	●	—	—	●	—	—	●	0.000531
	Ntn1	●	—	●	—	●	—	—	●	●	—	—	—	—	0.000543
	C1s	—	×	×	—	×	×	—	—	—	●	●	●	●	0.000543
	Fxyd6	●	×	×	—	×	—	●	●	—	●	—	—	●	0.000558
	Parp14	●	×	×	×	×	●	●	—	—	●	—	—	—	0.00057
	Tspo	●	●	●	●	—	—	—	●	●	●	●	—	—	0.000581
	Adcy4	●	●	—	×	—	●	—	●	—	●	●	—	—	0.000594
	Comtd1	—	×	●	●	—	—	●	●	—	●	—	—	—	0.000641
	Gdf15	—	—	●	×	—	—	—	●	—	●	—	●	—	0.000643
	Pdpn	●	—	●	×	—	—	—	●	—	—	—	—	—	0.000649
	Golga4	●	—	●	●	●	●	—	●	●	—	●	—	—	0.000657
	Slit3	●	×	×	×	×	×	—	●	●	●	●	—	●	0.000665
	Mvp	●	—	●	—	●	●	—	●	—	—	—	—	●	0.000693
	Bgn	—	—	●	—	—	—	—	●	●	●	●	—	—	0.000713
	Ugp2	●	—	●	—	●	—	●	●	●	—	●	●	—	0.000716
	Egfbp2	●	●	●	×	—	—	—	—	—	●	—	●	—	0.00072
	Casp12	●	—	—	—	—	—	●	●	●	●	●	—	—	0.000776
	Ctla2a	●	●	—	—	—	●	—	—	●	—	●	●	●	0.000776
	Cd209f	●	×	×	×	×	—	—	—	●	—	—	—	●	0.000776
	Lnx1	●	●	—	×	—	●	●	●	●	—	—	—	—	0.000782
	Nes	●	●	—	—	—	—	●	*	—	—	●	—	●	0.000832
	Ank1	●	●	●	×	●	—	—	●	●	●	—	—	—	0.000868
	Pla1a	—	×	×	×	×	—	●	●	—	●	—	—	●	0.000892
	Gsta4	●	—	●	●	●	×	●	—	—	—	●	—	—	0.00101

↑ Age

Genes up regulated by Age

		hrt1	hrt12	hrt13	hrt20	hrt24	hrt29	hrt31a	hrt31b	hrt31c	hrt31d	hrt31e	hrt31f	hrt31g	P _u
0610010010	Asns	●	—	●	—	●	●	—	—	●	—	●	—	—	0.00106
	Ccr2	●	—	●	×	—	—	●	●	●	●	—	—	—	0.00108
	Ndel1	●	●	●	—	●	●	—	—	—	●	—	—	—	0.0011
	Psmb10	—	—	●	×	—	—	●	●	—	●	—	●	—	0.0011
	Tgfb1	●	—	—	●	—	×	—	—	●	●	*	●	●	0.00112
	Arhgap9	●	—	●	—	—	●	●	—	●	●	●	●	—	0.00113
	Adh1	—	●	●	×	●	●	●	●	●	●	●	●	—	0.00119
	Gpnmb	●	×	×	×	×	—	●	—	●	—	●	—	—	0.0012
	Ctss	—	—	—	×	—	—	●	—	●	●	●	—	—	0.0012
	Oas2	●	×	×	×	×	●	●	●	●	—	—	—	—	0.0012
D930014E17	H2-Q7	●	●	—	×	—	×	●	—	—	●	—	—	—	0.00121
	Rhd	●	—	●	—	●	—	—	—	●	—	—	—	●	0.00126
	Ch25h	—	—	●	×	—	—	—	—	—	●	—	●	—	0.0013
	Nars	*	—	●	—	●	●	—	●	—	●	—	●	—	0.00133
	Capg	—	×	●	—	●	×	—	●	—	—	●	—	—	0.0014
	Jmjd6	●	—	●	●	●	●	—	—	●	—	—	—	—	0.00148
	Npdc1	●	●	●	×	—	—	—	●	●	●	—	—	—	0.00149
	Arrb1	—	—	●	×	—	—	—	●	●	●	●	—	—	0.0015
	Ly6a	●	●	—	—	—	—	—	—	—	●	—	●	●	0.0015
	Ckap4	●	—	●	—	—	—	—	●	—	—	●	●	—	0.00158
A930034L06	Akr1c13	●	×	×	●	×	×	●	—	●	●	—	—	—	0.00163
	1426074_at	●	×	×	×	×	×	—	—	—	●	—	●	—	0.00165
	Ptgds	●	●	●	×	—	—	—	—	●	—	●	●	—	0.00171
	Abca7	●	×	×	×	×	●	●	●	—	—	—	—	—	0.00178
	Pira6	—	—	●	×	●	×	●	—	—	—	—	●	—	0.00181
	Plekho1	●	—	●	×	●	—	—	●	—	—	—	—	—	0.00185
		●	—	●	×	●	—	—	●	—	—	—	—	—	0.00185
		●	—	●	×	●	—	—	●	—	—	—	—	—	0.00185
		●	—	●	×	●	—	—	●	—	—	—	—	—	0.00185
		●	—	●	×	●	—	—	●	—	—	—	—	—	0.00185

↑ Age

Genes up regulated by Age

		hrt1	hrt12	hrt13	hrt20	hrt24	hrt29	hrt31a	hrt31b	hrt31c	hrt31d	hrt31e	hrt31f	hrt31g	P _u
1190002N15Rik	Plk2	—	●	—	—	●	—	●	●	●	—	—	—	—	0.00188
	Os9	*	●	●	—	—	—	—	—	●	●	—	—	—	0.00191
	Ptgis	—	—	●	—	●	—	—	●	—	●	—	●	—	0.00194
	S100a8	●	—	●	X	—	—	—	●	—	—	—	—	●	0.00196
	Pros1	—	—	●	—	—	●	—	—	—	●	—	●	●	0.00198
	Plp2	—	—	●	—	●	X	●	—	—	●	●	●	—	0.002
	Iigp1	●	●	●	X	—	—	—	—	●	●	●	—	●	0.00205
	Smad7	●	●	—	X	—	—	—	●	—	—	●	—	—	0.00205
	Hexa	●	—	●	—	●	—	—	—	—	—	●	—	—	0.00205
	Lmna	●	—	*	X	●	—	—	●	—	●	●	—	—	0.00207
	Stx3	●	—	*	●	—	—	●	●	●	●	—	—	●	0.00224
	Fstl3	●	X	X	X	X	—	—	●	●	—	—	●	—	0.00226
	Ifi205	—	—	●	X	●	X	●	●	●	●	●	—	—	0.00229
	Ncoa2	*	—	●	●	—	—	—	—	—	—	—	—	—	0.00234
	Efemp1	—	X	X	X	X	—	●	●	●	—	●	—	—	0.00244
	H2-BI	●	●	●	X	—	—	●	—	—	—	—	—	—	0.00245
	Frzb	●	—	●	—	—	—	●	—	—	—	●	—	●	0.00258
	Myoc	—	—	●	X	—	X	—	●	●	●	●	—	—	0.00274
	Mal	—	—	—	X	●	—	—	—	—	—	●	●	●	0.00287

↓ Age

Genes down regulated by Age

		hrt1	hrt12	hrt13	hrt20	hrt24	hrt29	hrt31a	hrt31b	hrt31c	hrt31d	hrt31e	hrt31f	hrt31g	P _d
2310051E17Rik	Kcnd2	●	—	●	—	—	—	●	—	●	●	●	●	●	9.07e-07
	Casq1	●	—	—	—	—	×	●	—	●	●	●	●	—	9.53e-06
	Tnfaip8	●	×	●	×	—	●	—	●	●	●	—	●	—	1.22e-05
	Ucp3	●	●	—	×	—	—	●	●	—	—	●	—	—	0.00013
	Itm2a	●	—	●	—	—	—	—	●	●	—	●	—	●	0.000282
	Sesn1	●	●	●	—	—	—	—	●	*	—	●	—	—	0.000432
	Slc38a4	—	●	—	●	—	—	—	—	●	●	—	●	—	0.000432
	Mm.392176	—	●	●	×	●	×	—	●	—	●	●	●	●	0.000432
	Pdk4	—	●	●	×	●	—	●	●	—	●	—	—	—	0.000432
	Peci	●	●	●	—	●	—	—	●	—	—	—	—	—	0.000432
D0H4S114	Acaa2	●	●	●	—	●	—	—	●	●	—	—	—	—	0.000494
	Ephx2	—	●	●	●	—	—	●	●	—	—	—	—	—	0.000494
	Kcnj8	●	—	●	×	—	●	—	●	●	●	●	●	—	0.000494
	Ilf1	●	●	●	×	●	●	—	—	●	●	●	●	—	0.000503
	Rit1	●	●	●	×	●	—	—	—	●	—	—	—	—	0.000571
	Gpam	●	×	—	●	—	●	—	●	●	—	—	●	—	0.000604
	Riok1	●	●	●	●	●	—	—	—	●	—	●	—	—	0.000638
	Sf3b1	●	—	●	●	●	—	—	●	●	—	●	—	—	0.000638
	Angptl4	●	●	—	×	—	—	●	●	—	●	—	—	●	0.000707
	Cnot2	*	—	●	—	—	●	—	●	●	—	●	—	—	0.000908
Gadd45b	Col4a1	●	●	—	—	●	—	●	—	●	●	—	●	—	0.000962
	Top2b	●	—	●	●	—	●	—	●	—	—	●	—	—	0.000962
	Fbxo3	●	—	●	●	—	—	—	●	—	—	●	●	●	0.000962
	Emg1	●	×	●	—	—	●	●	—	●	—	—	—	—	0.00101
	Ngfrap1	●	×	×	—	×	—	●	●	●	—	—	—	●	0.00101
	Kcne1	●	—	●	×	—	—	—	—	—	●	—	●	●	0.00102
	Dci	—	●	—	—	●	—	●	●	●	●	—	—	—	0.00104
	Gadd45b	●	×	●	×	—	●	●	●	●	●	●	—	●	0.00106
		●	×	●	×	—	●	●	●	●	●	●	—	●	0.00115

↓ Age

Genes down regulated by Age

	hrt1	hrt12	hrt13	hrt20	hrt24	hrt29	hrt31a	hrt31b	hrt31c	hrt31d	hrt31e	hrt31f	hrt31g	P _d
Isoc1	●	—	●	—	—	●	●	●	●	●	●	●	●	0.00115
Ramp1	●	●	—	×	●	●	—	●	●	—	—	—	●	0.00115
Rbm12	●	—	●	—	●	—	—	●	●	—	—	—	—	0.00115
Rmnd5a	●	●	●	—	—	—	—	●	●	—	—	—	●	0.00115
Snord22	●	—	●	×	●	×	●	●	●	●	●	—	—	0.00115
Synj2	*	—	●	×	—	—	●	●	—	●	●	—	●	0.00115
Asxl1	●	●	●	—	●	×	●	—	●	—	—	●	—	0.00145
Phkg1	—	—	●	×	●	●	●	●	—	●	●	—	●	0.00145
Fbp2	●	●	●	—	●	—	●	●	—	—	—	●	—	0.00145
Ndufs4	*	—	●	—	—	—	●	—	●	●	●	—	—	0.00146
D14Ertd436e	●	×	●	—	—	—	—	—	—	—	—	●	●	0.00154
Bcl2l11	●	—	●	×	—	—	●	●	●	●	●	●	●	0.00157
Nrip1	*	—	●	×	—	—	●	—	—	—	●	●	—	0.00162
Hspd1	●	—	●	●	●	×	—	—	●	—	—	—	—	0.00176
Decr1	—	×	●	×	—	—	●	●	●	●	●	●	—	0.00191
Gtl3	●	●	●	—	●	●	—	—	●	—	●	—	—	0.00197
Rab11b	●	●	●	—	●	×	●	●	—	—	—	—	—	0.00197
Stag1	*	—	●	—	—	—	—	●	—	—	—	●	—	0.00199
Nfkbia	●	●	—	—	●	×	●	●	●	—	●	—	●	0.002
Aqp4	●	—	—	×	—	●	●	●	—	●	●	—	—	0.002
Car4	●	●	●	—	●	—	●	●	—	—	●	—	—	0.002
Commd6	●	●	●	●	●	●	—	—	●	—	—	—	—	0.002
Acot1	●	●	—	×	—	—	●	●	—	—	●	—	—	0.00201
Lgals4	●	×	●	●	●	—	●	●	—	—	●	—	—	0.00213
Mrgprh	●	×	×	×	×	—	—	—	●	●	●	●	—	0.00236
Cpt2	●	●	●	—	—	×	—	●	●	—	●	—	—	0.00247
Aplnr	●	×	×	—	×	●	●	●	—	●	●	●	—	0.00259
Slc41a1	●	—	●	×	—	●	●	●	●	●	●	—	—	0.00263
Sfrs6	●	×	●	●	●	—	●	—	●	—	—	—	—	0.00276
Asph	*	×	×	●	×	—	—	—	●	●	*	●	●	0.0028

↓ Age

Genes down regulated by Age

	hrt1	hrt12	hrt13	hrt20	hrt24	hrt29	hrt31a	hrt31b	hrt31c	hrt31d	hrt31e	hrt31f	hrt31g	P _d
Slc25a20	●	●	●	—	●	—	●	●	—	—	—	●	—	0.0028
Zfp36	●	●	—	×	—	×	●	●	—	—	—	—	—	0.0028
Meg3	●	×	●	—	●	—	●	—	●	●	●	—	—	0.00305
Hdac2	●	×	●	●	●	●	—	—	●	—	—	—	—	0.00315
Peg3	●	●	—	—	●	—	●	●	—	—	●	—	●	0.00315
Rnf166	●	●	●	—	●	—	—	●	—	●	—	—	—	0.00315
Ubl5	●	●	●	—	●	—	—	●	●	—	●	—	—	0.00315
Wasf2	●	×	×	—	×	—	●	●	●	—	—	—	—	0.00315
Mrps33	●	—	●	×	●	●	●	—	●	—	—	—	—	0.00317
Ccng2	●	—	●	×	●	—	—	●	—	—	●	—	●	0.00351
Epha4	●	—	●	×	—	—	—	—	●	●	●	—	—	0.00351
Mlycd	●	●	●	×	●	—	●	●	—	—	●	—	—	0.00351
Ak1	●	●	●	×	●	●	—	●	●	—	—	—	—	0.00361
Ramp2	●	—	●	—	●	●	●	—	—	—	●	—	—	0.00377
Rora	●	●	●	×	—	—	●	—	—	●	●	—	—	0.00377
Pdcd4	●	—	●	●	●	—	—	●	●	—	—	—	—	0.00383
Tmem16k	●	×	×	×	×	—	—	—	●	●	—	—	●	0.00391
Ap1m1	●	●	●	—	●	×	—	—	●	—	●	—	—	0.00408
Errfi1	●	●	—	●	●	—	●	●	—	—	—	—	—	0.00408
Gas5	—	●	●	●	●	—	●	●	●	●	—	—	●	0.00408
Jarid2	—	—	—	●	—	—	—	●	●	●	—	●	—	0.00408
Ireb2	●	—	●	—	—	×	—	●	●	—	—	—	—	0.00408
Cdk2	●	—	●	—	●	—	—	●	—	—	●	—	—	0.00414
Eif4b	●	●	●	●	●	●	●	●	●	—	●	—	—	0.00428
Lpin1	●	●	●	×	●	—	—	●	●	●	—	—	—	0.00428
Pim3	●	●	●	—	—	●	●	●	—	—	—	—	—	0.00428
Hadh	●	—	●	—	●	●	—	—	*	—	●	●	—	0.00459
LOC100045629	—	—	●	●	●	×	●	●	—	—	●	—	—	0.00459
Armxcx3	●	×	×	—	×	●	—	●	—	—	—	●	—	0.0046
Npm3	●	—	●	—	●	×	—	●	●	●	—	—	—	0.00478

↓ Age

Genes down regulated by Age

		hrt1	hrt12	hrt13	hrt20	hrt24	hrt29	hrt31a	hrt31b	hrt31c	hrt31d	hrt31e	hrt31f	hrt31g	P _d
1810015C04Rik	Eif4ebp1	●	●	●	—	●	—	●	—	—	—	●	—	—	0.00481
	Hmgcs2	●	●	●	●	●	—	●	●	—	—	—	—	—	0.00481
	Abcd3	—	—	●	—	●	●	—	—	—	—	—	—	—	0.00497
	Klf15	●	×	×	×	×	—	●	●	—	—	●	—	—	0.00497
	Rpl22l1	—	—	●	—	●	●	—	●	—	●	●	—	—	0.00499
	Cdc37l1	●	×	×	—	×	—	●	●	—	●	—	●	—	0.00502
	Pcna	●	—	●	—	●	●	—	—	●	—	—	—	—	0.00502
	Tmem14c	●	●	●	—	●	●	—	—	●	—	—	—	—	0.00502
	Ddc	●	×	—	×	—	×	●	—	—	—	—	—	●	0.00515
	Mbtps1	●	●	●	—	●	—	●	●	●	—	—	—	—	0.00521
	Rabgap1l	●	—	●	×	●	●	●	●	—	—	—	—	—	0.00522
	Emp2	●	—	●	×	—	—	●	●	●	—	—	—	—	0.0057
	Celsr1	●	—	●	×	—	●	—	—	—	●	—	—	●	0.0057
	Tmem86a	●	×	×	×	×	●	×	×	×	×	×	×	×	0.0057
	Ypel3	—	●	●	—	●	—	●	—	—	●	●	—	—	0.0057
	Ncor1	●	●	●	—	●	●	—	●	●	—	●	●	●	0.0059
	H2afz	●	—	●	—	●	×	—	●	●	—	●	●	—	0.00591
	Chrac1	●	—	●	—	●	—	—	—	●	—	—	—	—	0.00593
	Smc3	●	—	●	—	—	×	—	—	●	—	●	—	—	0.00593
	Tmpo	●	—	●	—	—	—	●	●	—	●	●	—	●	0.00616
	Nr1d1	●	×	×	×	×	●	—	—	●	●	—	—	—	0.00638
	Fdft1	●	—	●	×	—	×	●	●	●	—	●	●	—	0.00675
	Chchd5	●	—	—	×	—	—	●	●	●	●	●	—	—	0.00675
	Psmg1	●	●	●	●	—	●	—	—	●	—	—	—	—	0.00675
	Rom1	●	●	●	×	●	×	—	—	●	●	—	—	—	0.00675
	Gas1	●	—	●	—	●	—	●	—	●	—	●	●	—	0.00685
	Arid1a	●	—	●	●	—	—	●	—	—	●	—	—	—	0.00702
		●	—	●	●	—	●	—	●	●	—	●	●	—	0.00712
		●	—	●	●	—	●	—	●	●	—	●	●	—	0.00734

↓ Age

Genes down regulated by Age

1110057K04Rik

2310028O11Rik

	hrt1	hrt12	hrt13	hrt20	hrt24	hrt29	hrt31a	hrt31b	hrt31c	hrt31d	hrt31e	hrt31f	hrt31g	P _d
Grcc10	●	●	●	×	●	—	—	—	●	—	●	—	—	0.00744
Rnf138	●	—	●	×	—	—	—	—	—	—	●	●	●	0.00744
Tnrc6a	●	●	●	—	●	—	●	●	*	●	●	—	●	0.00744
Syf2	●	●	●	●	●	—	—	—	—	—	—	—	—	0.00804
Col3a1	●	●	—	●	●	●	●	●	—	—	●	●	—	0.00828
Hdlbp	*	—	●	—	●	—	●	●	—	●	●	●	—	0.00877
Armxc4	●	×	×	—	×	●	—	●	●	—	—	—	—	0.00877
Wdr45	●	●	—	×	—	—	●	●	●	—	●	—	—	0.00879
Art1	●	—	●	×	●	●	—	—	*	—	—	—	—	0.00901
Dhx36	●	—	—	●	●	—	—	●	—	—	●	—	—	0.00912
Myo10	●	—	●	—	●	—	—	●	—	●	●	●	●	0.00912
Sfrs2	*	●	●	●	●	—	—	—	●	—	●	●	—	0.00912
Klf10	—	●	●	×	—	—	—	—	●	—	—	—	●	0.00912
Slc27a1	●	●	●	×	—	—	●	—	—	●	●	—	—	0.00913
Dhrs4	●	●	●	×	●	—	—	—	●	—	—	—	—	0.00925
Pias1	—	—	●	×	—	—	●	●	—	—	●	—	●	0.00925
Tbc1d15	●	●	●	●	—	—	—	—	●	●	●	●	—	0.00929
Apbb1	—	●	●	×	—	—	●	●	—	●	●	—	—	0.00939
Smc4	●	—	●	—	●	×	—	●	—	—	●	—	—	0.00963
Tceal8	●	×	×	×	×	—	●	—	—	—	●	—	—	0.00963
Rnf207	●	×	×	×	×	×	—	—	●	●	—	●	—	0.00968
S3-12	●	●	—	×	—	●	●	●	—	—	●	—	—	0.00968
Camk1d	●	×	×	●	×	—	●	—	●	—	—	—	●	0.00977
Mapk6	●	—	●	—	●	—	—	—	●	●	—	—	—	0.0098
Ard1a	●	—	●	—	—	—	●	●	●	—	—	—	—	0.0098
H3f3b	●	—	●	—	●	—	—	—	●	—	●	—	—	0.00989
Slbp	*	×	●	●	—	×	●	—	●	—	—	—	—	0.01
Slc25a26	●	—	—	—	●	—	●	—	●	●	—	●	—	0.0101
	●	—	●	●	●	—	—	—	●	—	—	—	—	0.0105

↓ Age

Genes down regulated by Age

		hrt1	hrt12	hrt13	hrt20	hrt24	hrt29	hrt31a	hrt31b	hrt31c	hrt31d	hrt31e	hrt31f	hrt31g	P _d
BC043118	Eral1	●	—	●	—	—	—	●	—	●	●	●	●	●	0.0105
	BC043118	●	×	×	●	×	●	—	—	—	●	—	●	—	0.0105
	Hsdl2	●	●	●	—	—	—	—	●	—	—	—	—	—	0.0105
	Tfrc	●	●	●	●	—	—	●	●	●	●	—	●	—	0.0107
	Chkb	●	●	—	×	●	—	—	—	●	—	—	—	—	0.0107
	Fbxo9	●	—	●	×	●	●	—	—	—	—	—	●	—	0.0107
	Ift81	●	●	●	—	—	—	—	●	●	●	—	●	—	0.0107
	Matr3	●	—	●	—	—	×	—	●	—	—	●	●	●	0.0107
	Nsmce1	—	—	●	●	●	×	●	—	●	—	—	●	—	0.0107
	Nsun3	●	×	×	●	×	—	×	×	×	×	×	×	×	0.0107
	Lgi1	●	×	×	×	×	●	—	—	—	—	●	●	—	0.0107
	Sfrs10	●	×	●	—	●	×	—	—	●	—	—	—	—	0.0108
	Slc35b4	●	×	×	●	×	—	—	●	●	—	●	—	—	0.0113
	Erh	●	●	●	×	●	×	—	—	●	—	—	—	—	0.0113
	Frat2	●	—	●	—	—	—	—	●	—	●	●	●	—	0.0113
	Rere	●	●	●	—	—	—	●	—	—	—	●	—	—	0.0113
	Zfpm2	●	—	—	×	—	—	●	—	●	—	●	●	—	0.0113
	Rgs4	●	—	—	×	—	—	—	—	●	—	●	—	●	0.0116
	Btg1	●	—	●	—	—	×	—	—	●	—	—	—	—	0.0116
	Rfc4	●	—	—	×	—	●	—	—	—	—	●	—	—	0.0117
	Trp53inp1	●	×	×	—	×	—	●	●	—	●	—	—	—	0.0117
	Nit1	●	×	●	—	●	●	—	—	—	—	●	●	—	0.0118
	Tmem35	●	×	×	×	×	●	●	—	●	—	●	—	●	0.0118
1190002H23Rik	1190002H23Rik	●	×	—	×	●	●	●	●	●	●	●	—	—	0.0118
	Atp1a2	●	—	—	×	—	—	●	●	●	●	—	●	—	0.0118
	Bub1b	●	×	×	●	×	×	—	●	—	—	—	—	●	0.0118
	Dsg2	●	●	●	—	—	●	●	—	●	—	●	●	—	0.0118
	Pex11a	●	●	●	—	●	—	●	●	—	—	●	—	—	0.0118
	Slc25a17	●	—	●	●	●	—	●	●	—	—	●	—	—	0.0118
	Ttll1	●	×	×	×	×	—	●	—	●	●	—	●	—	0.0118

↓ Age

Genes down regulated by Age

	hrt1	hrt12	hrt13	hrt20	hrt24	hrt29	hrt31a	hrt31b	hrt31c	hrt31d	hrt31e	hrt31f	hrt31g	P _d
Usp3	●	●	*	—	—	—	●	●	—	—	—	—	—	0.0118
Vldlr	●	●	●	—	—	●	●	●	●	●	●	●	●	0.0118
Zscan21	●	—	●	—	●	×	—	●	●	●	●	●	—	0.0118
Cirh1a	—	—	●	—	—	●	●	—	—	—	●	●	—	0.0118
Acs1	*	●	●	—	—	—	—	●	—	●	—	—	—	0.0123
Slc25a33	●	×	×	—	×	—	—	●	●	—	—	—	—	0.0123
RP23–136K12.4	●	●	—	●	—	—	●	●	—	—	●	—	—	0.0124
Zfand6	*	●	●	●	●	●	●	—	●	—	—	●	—	0.0124
Csrp2	●	●	—	—	●	●	—	—	●	—	—	—	—	0.0124
Abca1	●	●	●	—	—	—	—	—	—	●	—	—	—	0.0124
Fbxo25	●	×	×	×	×	—	—	—	●	—	●	—	—	0.0124
Ppp1r14a	●	×	×	×	×	—	●	—	—	●	—	—	—	0.0124
Ubb	●	●	●	×	—	×	●	●	●	—	—	—	—	0.0128
Hat1	●	—	●	●	—	●	—	●	●	—	—	—	—	0.0129
Mrfap1	●	×	●	—	●	×	—	—	●	—	—	—	—	0.0131
Agk	●	×	×	×	×	×	—	—	●	—	●	—	●	0.0131
Cdkn1b	●	—	●	×	●	—	—	●	—	—	—	●	●	0.0133
Nfatc3	●	—	●	—	—	—	—	—	—	—	●	—	●	0.0133
Rad21	●	—	●	—	●	—	—	—	●	—	●	—	—	0.0133
Myh14	●	●	●	×	●	—	●	—	●	—	●	—	—	0.0134

Overrepresented Biological Processes

GO Term	P-Value
humoral immune response	5.93e-06
inflammatory response	2.04e-05
activation of plasma proteins during acute inflammatory response	3.65e-05
response to external stimulus	0.000123
positive regulation of phagocytosis	0.000149
complement activation, classical pathway	0.000198
positive regulation of leukocyte activation	0.000341
regulation of lymphocyte proliferation	0.000402
regulation of B cell activation	0.000463
positive regulation of transport	0.000824
activation of immune response	0.000855
regulation of cell activation	0.00123
ISG15-protein conjugation	0.00147
positive regulation of mononuclear cell proliferation	0.00209
prostanoid metabolic process	0.0021
phagocytosis, engulfment	0.0021
erythrocyte development	0.0021
regulation of immune response	0.00261
long-chain fatty acid biosynthetic process	0.0029
defense response to Gram-negative bacterium	0.0029
regulation of cell migration	0.003
leukocyte mediated immunity	0.00349
cell adhesion	0.00372
positive regulation of response to stimulus	0.00382
fibroblast growth factor receptor signaling pathway	0.00413
regulation of endocytosis	0.00479
negative regulation of angiogenesis	0.005
microtubule-based movement	0.00576
positive regulation of cellular component organization and biogenesis	0.00595
positive regulation of B cell proliferation	0.00597

Overrepresented Biological Processes

GO Term	P-Value
response to stress	0.00671
somatic stem cell division	0.00705
defense response to Gram-positive bacterium	0.00705
blood vessel morphogenesis	0.00732
regulation of leukocyte mediated immunity	0.00743
regulation of cell proliferation	0.00802
regulation of T cell differentiation	0.00822
positive regulation of immune system process	0.00828
immune response	0.00844
positive regulation of B cell differentiation	0.00972
innate immune response	0.00973
fatty acid metabolic process	0.0102
hemopoiesis	0.0106
catabolic process	0.011
phagocytosis, recognition	0.0127
prostaglandin biosynthetic process	0.0128
regulation of acute inflammatory response	0.0128
regulation of hypersensitivity	0.0128
negative regulation of axon extension	0.0128
skeletal development	0.0128
icosanoid biosynthetic process	0.0141
sphingolipid metabolic process	0.0165
cytokine and chemokine mediated signaling pathway	0.0165
ceramide metabolic process	0.0177
chemotaxis	0.0179
negative regulation of lymphocyte mediated immunity	0.0199
oligopeptide transport	0.0199
complement activation, alternative pathway	0.0199
endoplasmic reticulum unfolded protein response	0.0199
neurotransmitter catabolic process	0.0199

Overrepresented Biological Processes

GO Term	P-Value
positive regulation of T cell activation	0.0213
cellular macromolecule catabolic process	0.0235
regulation of immunoglobulin mediated immune response	0.024
positive regulation of immune effector process	0.024
regulation of adaptive immune response based on somatic recombination of immunoglobulin genes	0.024
carboxylic acid biosynthetic process	0.0249
lymphocyte activation	0.0251
cellular developmental process	0.0257
glucose catabolic process	0.0269
monosaccharide catabolic process	0.0269
anatomical structure formation	0.027
negative regulation of immune effector process	0.0284
regulation of inflammatory response to antigenic stimulus	0.0284
water transport	0.0284
regulation of defense response	0.0287
response to unfolded protein	0.0288
blood vessel development	0.0289
immune system development	0.0307
alcohol metabolic process	0.0314
vasculogenesis	0.0314
oxidation reduction	0.032
negative regulation of inflammatory response	0.0331
positive regulation of T cell proliferation	0.0341
antigen processing and presentation of peptide antigen	0.0341
cell death	0.0355
myeloid leukocyte mediated immunity	0.038
cell wall organization and biogenesis	0.038
cell wall catabolic process	0.038
aromatic compound catabolic process	0.038
mast cell activation	0.038

Overrepresented Biological Processes

GO Term	P-Value
immunoglobulin mediated immune response	0.0397
adaptive immune response based on somatic recombination of immune receptors built from immunoglobulin	0.0414
cytoskeleton organization and biogenesis	0.0417
positive regulation of developmental process	0.0424
positive regulation of alpha-beta T cell differentiation	0.0432
regulation of apoptosis	0.0447
cell motility	0.0448
carbohydrate metabolic process	0.0452
anatomical structure development	0.0455
negative regulation of cell activation	0.046
negative regulation of lymphocyte activation	0.046
nervous system development	0.0462
membrane organization and biogenesis	0.0467
tube morphogenesis	0.0485
cartilage condensation	0.0487
organic anion transport	0.0487
negative regulation of response to stimulus	0.0492
negative regulation of cellular component organization and biogenesis	0.0498

Overrepresented Cell Components

GO Term	P-Value
extracellular region	1.05e-06
extracellular space	0.000261
6-phosphofructokinase complex	0.00128
cell surface	0.00405
cytosol	0.00567
external side of plasma membrane	0.00636
proteinaceous extracellular matrix	0.0068
cyclin-dependent protein kinase holoenzyme complex	0.00846
extracellular region part	0.00977
plasma membrane	0.0113
intrinsic to endoplasmic reticulum membrane	0.0146
axon	0.0232
filopodium	0.0248
vacuolar membrane	0.0379
proton-transporting two-sector ATPase complex	0.0412
microtubule	0.0466
cytoplasm	0.0478

Overrepresented Molecular Functions

GO Term	P-Value
heparin binding	0.000233
polysaccharide binding	0.000349
protease inhibitor activity	0.000573
integrin binding	0.000679
chemokine activity	0.000727
6-phosphofructokinase activity	0.00127
folic acid transporter activity	0.00413
G-protein-coupled receptor binding	0.00437
O-methyltransferase activity	0.00611
glutathione transferase activity	0.0102
metalloendopeptidase inhibitor activity	0.0111
lysozyme activity	0.0141
immunoglobulin binding	0.0141
catalytic activity	0.0149
carbohydrate binding	0.0164
aldo-keto reductase activity	0.0173
oligopeptide transporter activity	0.0173
serine-type endopeptidase inhibitor activity	0.0198
water channel activity	0.0209
protein binding	0.0222
protein homodimerization activity	0.0241
GTPase activity	0.0271
hydrogen ion transporting ATP synthase activity, rotational mechanism	0.0282
hydrogen ion transporting ATPase activity, rotational mechanism	0.0282
cyclin-dependent protein kinase regulator activity	0.0288
monooxygenase activity	0.0293
phosphotransferase activity, nitrogenous group as acceptor	0.0306
hydrogen-exporting ATPase activity, phosphorylative mechanism	0.0332
NADP binding	0.0332
hormone receptor binding	0.0332



Overrepresented Biological Processes

GO Term	P-Value
lipid metabolic process	4.25e-05
negative regulation of S phase of mitotic cell cycle	0.000271
fatty acid metabolic process	0.000485
carboxylic acid metabolic process	0.000486
cell cycle arrest	0.000953
regulation of S phase	0.00133
response to exogenous dsRNA	0.00245
sterol metabolic process	0.00602
mitotic cell cycle	0.00655
long-chain fatty acid metabolic process	0.00662
isoprenoid biosynthetic process	0.0088
spleen development	0.0088
actin filament-based movement	0.00999
regulation of G-protein coupled receptor protein signaling pathway	0.0113
posttranscriptional regulation of gene expression	0.0117
thymus development	0.0126
cerebellum morphogenesis	0.014
negative regulation of myeloid cell differentiation	0.014
response to lipopolysaccharide	0.0154
cholesterol biosynthetic process	0.0202
chromosome organization and biogenesis	0.0213
mitosis	0.0216
response to toxin	0.0332
metencephalon development	0.0332
intracellular transport	0.0338
DNA packaging	0.0426
potassium ion transport	0.0444
ear development	0.0466
negative regulation of cell cycle	0.0494



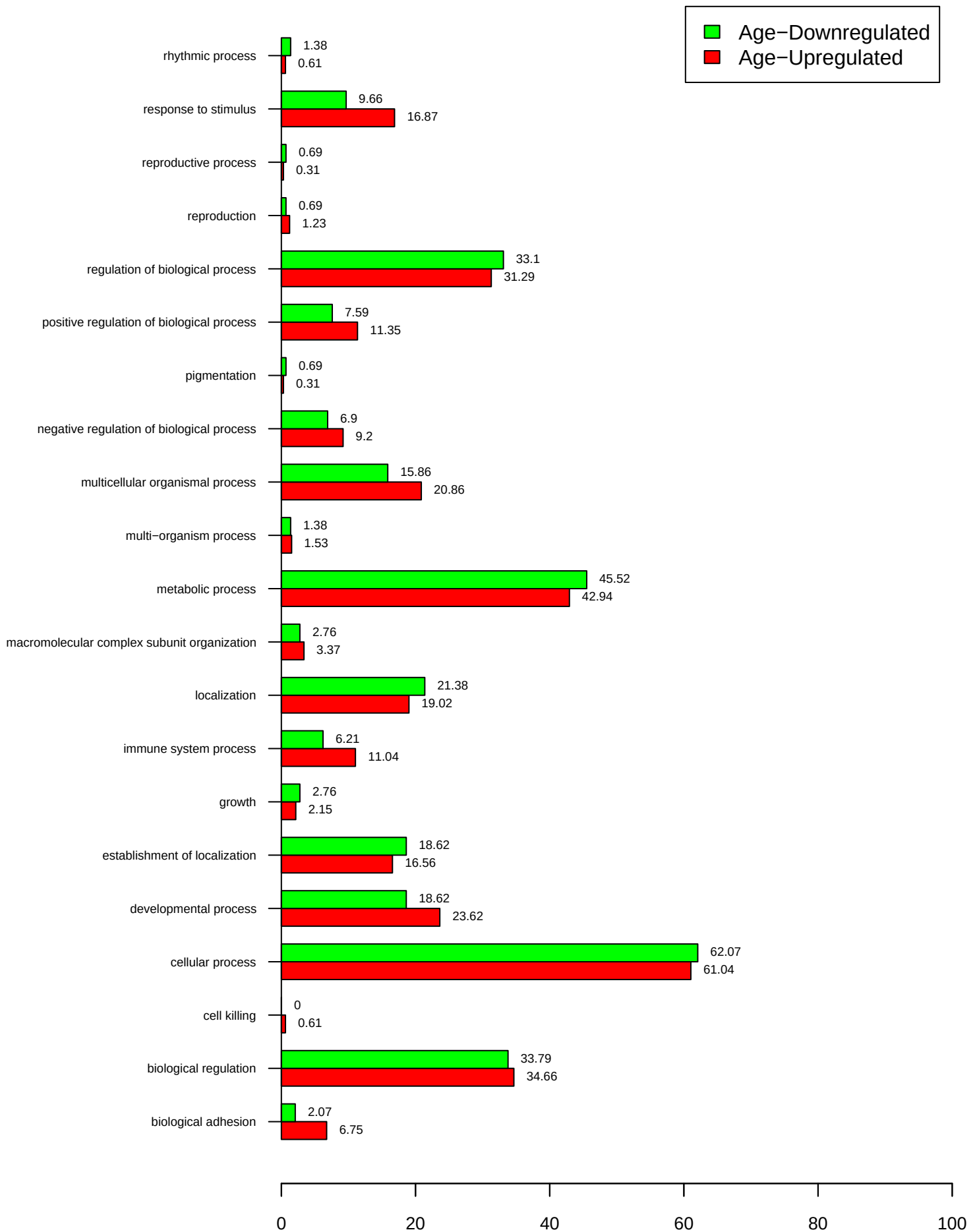
Overrepresented Cell Components

GO Term	P-Value
mitochondrial inner membrane	9.59e-06
intracellular	1.74e-05
mitochondrial envelope	5.22e-05
envelope	6.03e-05
mitochondrion	6.48e-05
peroxisome	0.000244
membrane-bounded organelle	3e-04
intracellular organelle	0.000447
organelle membrane	0.00119
cyclin-dependent protein kinase holoenzyme complex	0.00176
collagen	0.0133
cell part	0.0156
nucleus	0.0183
histone deacetylase complex	0.0192
replication fork	0.0192
early endosome	0.0209
cytoplasm	0.023
sarcoplasm	0.0298
heterochromatin	0.0489
chromosomal part	0.0492

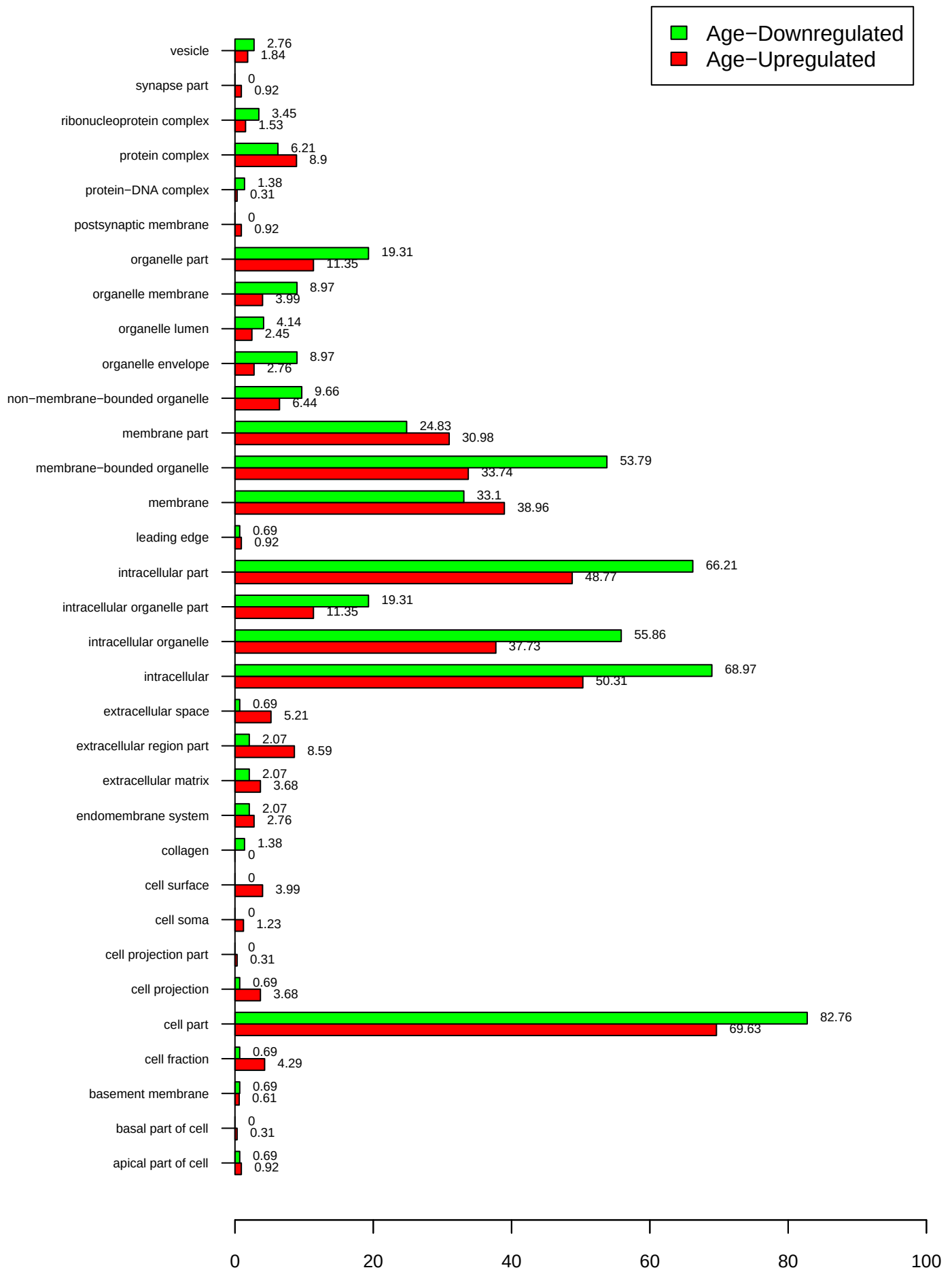
Overrepresented Molecular Functions

GO Term	P-Value
dodecenoyl-CoA delta-isomerase activity	0.000233
coreceptor, soluble ligand activity	0.000233
translation repressor activity	0.000767
extracellular matrix structural constituent	0.019
transferase activity, transferring acyl groups	0.0216
nucleic acid binding	0.037
voltage-gated potassium channel activity	0.0398
Rab GTPase activator activity	0.0404
carbon-carbon lyase activity	0.0404
intramolecular oxidoreductase activity	0.0404

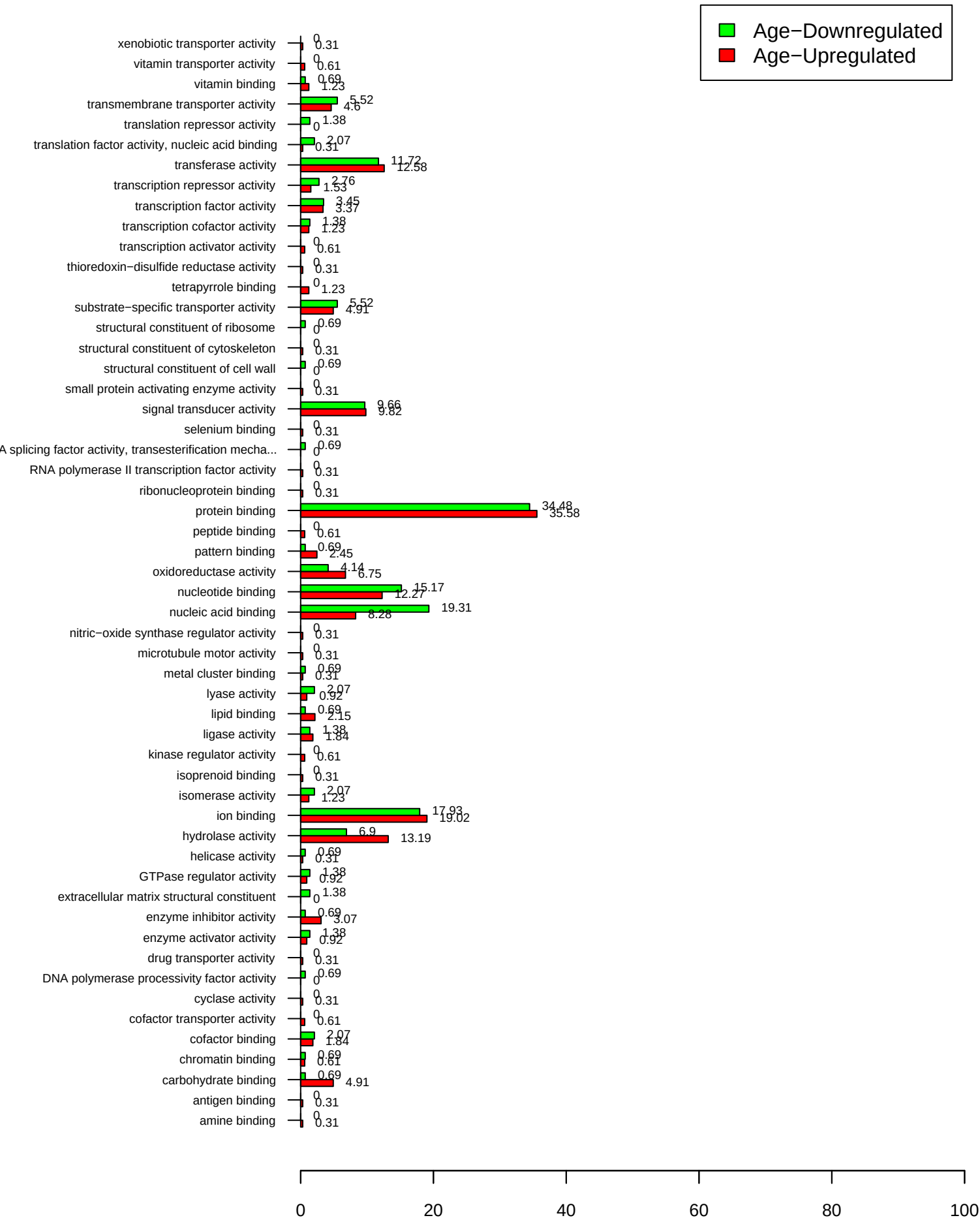
Gene Ontology Profile Comparison (Biological Process Ontology)



Gene Ontology Profile Comparison (Cell Component Ontology)



Gene Ontology Profile Comparison (Molecular Function Ontology)



Overrepresented KEGG Pathways

GO Term	P-Value
Galactose metabolism	0.00191
Glycolysis / Gluconeogenesis	0.00436
Metabolism of xenobiotics by cytochrome P450	0.00804
Type I diabetes mellitus	0.0119
Complement and coagulation cascades	0.0145
Neurodegenerative Diseases	0.0248
Fructose and mannose metabolism	0.0428
Alzheimer's disease	0.0441
Butanoate metabolism	0.0458

↓Age

Overrepresented KEGG Pathways

GO Term	P-Value
Fatty acid metabolism	8.23e-05
Fatty acid elongation in mitochondria	0.00509
p53 signaling pathway	0.00511
PPAR signaling pathway	0.00703
Valine, leucine and isoleucine degradation	0.0101
Small cell lung cancer	0.0143
Cell cycle	0.0304
Phenylalanine metabolism	0.0353

Overrepresented KEGG Pathways

(Based on InterPro Domain Signatures)

GO Term	P-Value
Metabolism of xenobiotics by cytochrome P450	0.0015
Drug metabolism – cytochrome P450	0.0032
Ribosome	0.0065
Glycosphingolipid biosynthesis – globoseries	0.0102
Parkinson's disease	0.0106
Alzheimer's disease	0.0123
Glycosphingolipid biosynthesis – ganglioseries	0.0148
Fructose and mannose metabolism	0.0156
Glycolysis / Gluconeogenesis	0.0158
Starch and sucrose metabolism	0.0296



Overrepresented KEGG Pathways

(Based on InterPro Domain Signatures)

GO Term	P-Value
Butanoate metabolism	0.0016
Fatty acid elongation in mitochondria	0.0047
Terpenoid biosynthesis	0.0049
Lysine degradation	0.0073
Caprolactam degradation	0.0082
Taurine and hypotaurine metabolism	0.0162
Tetrachloroethene degradation	0.0264
PPAR signaling pathway	0.0277
Synthesis and degradation of ketone bodies	0.029
Valine, leucine and isoleucine degradation	0.036
Benzoate degradation via CoA ligation	0.0367
Pentose phosphate pathway	0.0381
C5-Branched dibasic acid metabolism	0.0391
Circadian rhythm	0.0414
Thiamine metabolism	0.043
Nitrogen metabolism	0.0434

↑Age

Abundance of miRNA Targets

miRNA	Freq(Obs)	Freq(Exp)	Obs/Exp	P-value	P-Value(Adj)
miR-293	0.0528	0.0266	1.98	0.00658	1
miR-423-5p	0.175	0.141	1.24	0.0538	1
miR-127	0.0407	0.0272	1.49	0.0748	1
miR-483	0.0854	0.0668	1.28	0.1	1
miR-296-5p	0.065	0.0498	1.31	0.109	1
miR-711	0.0407	0.0303	1.34	0.129	1
miR-762	0.179	0.155	1.15	0.131	1
miR-296-3p	0.146	0.125	1.17	0.133	1
miR-193	0.0935	0.0768	1.22	0.135	1
miR-299	0.0976	0.0809	1.21	0.141	1

Abundance of miRNA Targets

miRNA	Freq(Obs)	Freq(Exp)	Obs/Exp	P-value	P-Value(Adj)
miR-183	0.177	0.106	1.67	0.00542	0.995
miR-148a	0.194	0.126	1.53	0.0116	0.995
miR-148b	0.194	0.129	1.51	0.0143	0.995
miR-715	0.0484	0.0207	2.34	0.0147	0.995
miR-1188	0.137	0.0873	1.57	0.0221	0.995
miR-540-3p	0.129	0.0811	1.59	0.0227	0.995
miR-668	0.113	0.0703	1.61	0.0277	0.995
miR-125b-3p	0.0645	0.036	1.79	0.0356	0.995
miR-152	0.169	0.121	1.4	0.0412	0.995
miR-291b-3p	0.21	0.157	1.33	0.0463	0.995
miR-125a-3p	0.185	0.137	1.35	0.0486	0.995

Tests for Chromosome Over-representation

Chromosome	Age-upregulated Genes	Age-downregulated Genes
1	0.667	0.199
2	0.218	0.642
3	0.202	0.232
4	0.908	0.539
5	0.933	0.985
6	0.567	0.425
7	0.241	0.587
8	0.418	0.328
9	0.513	0.264
10	0.216	0.383
11	0.716	0.881
12	0.709	0.48
13	0.0416*	0.225
14	0.859	0.293
15	0.919	0.139
16	0.377	0.586
17	0.1	0.472
18	0.133	0.113
19	0.184	0.0719
X	0.217	0.117
Y	0.0423*	1.00

The table lists p-values generated from a test that evaluates whether there exists an over-abundance of identified genes with respect to a given chromosome. The null hypothesis assumes that the set of genes has been selected at random from those represented on the Affymetrix 430 2.0 array. A significant test indicates that a chromosome contains more of the identified genes than would be expected if the gene set had been chosen at random.

* = significant p-value, without multiple test adjustment

** = significant p-value, with multiple test adjustment

Chromosome Locations

