

## SUPPLEMENTARY MATERIAL

**Supplementary Table 1.** Primer/probe sequences used for real-time PCR.

Target	Forward Primer	Probe	Reverse Primer
MHC IIb	5' TCAACAAGCTGCGGGTAA 3'	AGCCGAGAGGTTACACA	5' TGAGCTATTCTTCGCTTATGACTTIG 3'
MHC IIx	5' GCGAGGTTACACCAAAATCA 3'	AGCGAAGAGTGATCG	5' TGGTCACTTTCCTGCTTTGGA 3'
Homer2	5' GGGCGGAGCCTAGATGGA 3'	AGTGAAAAGCGTGTGTGAG	5' AATGCCCTATGCCCACTTCA 3'

**Supplementary Table 2.** Probe sets with significant atrophy main effects after the Bonferroni adjustment. Probe sets are organized by putative functions in column 1. Column 2 is the accession number, column 3 is an unadjusted p-value where  $4 \times 10^{-6}$  is significant, and column 4 is the fold increase (positive number) or decrease (negative sign) for the 10-day immobilized as compared to the control value, e.g., the -1.69-fold decrease for the EST for human filamin c, gamma, in row 1 means that immobilized soleus muscles were less than control.

Gene Name	ID	p-value	Fold
<b>ACTIN BINDING/CYTOSKELETON</b>			
ESTs similar to human filamin C, gamma (actin binding protein 280)	AA799773	5.772E-07	-1.69
ESTs similar to human synaptopodin 2 (myopodin)	AI171209	1.918E-06	-1.40
ESTs similar to mouse cofilin 2, muscle myozenin 2 (calsarcin-1)	AI010742 AI104354	3.842E-06 3.295E-07	-2.06 -1.56
ESTs similar to mouse ankyrin 1, erythroid	AI137502	7.306E-07	-1.63
<b>AMINO ACID METABOLISM</b>			
ornithine decarboxylase 1	J04791	6.400E-10	-2.95
ornithine decarboxylase 1	X07944	4.887E-09	-2.16
ornithine decarboxylase 1	J04792	4.190E-08	-2.03
glutamic-oxaloacetic transaminase 2, mitochondrial (aspartate aminotransferase 2)	M18467	3.097E-07	-1.60
ESTs similar to mouse glutamate-cysteine ligase, modifier subunit	AI008385	9.011E-08	-1.88
Branched chain alpha-ketoacid dehydrogenase subunit E1 alpha	J02827	2.757E-06	1.65
cytosolic cysteine dioxygenase 1	AA942685	3.696E-06	1.94
ESTs similar to mouse spermine synthase	AI236640	1.592E-06	-1.66
<b>ATP BINDING</b>			
adenylate kinase 2	AA799466	8.682E-07	-1.54
<b>CARBOHYDRATE METABOLISM</b>			
ESTs similar to mouse acid sphingomyelinase-like phosphodiesterase 3a	AI177804	7.782E-08	1.73
ESTs similar to mouse sphingomyelin phosphodiesterase 1, acid lysosomal	AI169302	1.573E-06	-1.29
<b>CELL ADHESION</b>			

ESTs similar to mouse lectin, galactose binding, soluble 7	AI112969	3.282E-07	-1.76
afadin (also known as myeloid/lymphoid or mixed lineage-leukemia translocation to 4 homolog) (Drosophila)	D90401	3.532E-07	-1.74
ESTs weakly similar to mouse putative neuronal cell adhesion molecule	AI175338	8.578E-07	1.81
ESTs similar to mouse transforming growth factor, beta induced, 68 kDa	AI231127	4.611E-09	1.61

### CELL CYCLE

ESTs weakly similar to mouse paneth cell enhanced expression	AI045824	1.551E-09	3.95
ESTs similar to mouse cyclin G2	AI171262	4.599E-07	1.68
ESTs similar to mouse cyclin-dependent kinase 9 (CDC2-related kinase)	AA955926	3.811E-09	1.44
growth arrest specific 5	U77829	1.739E-08	1.95
growth arrest specific 5	AI111599	5.481E-08	2.30

### CELL PROLIFERATION

ESTs similar to mouse interferon-stimulated protein (20 kDa)	AI045075	2.856E-06	1.99
--	----------	-----------	------

### CHAPERONE

ESTs similar to mouse McKusick-Kaufman syndrome protein	AI104266	1.786E-06	-1.69
ESTs similar to mouse DnaJ (Hsp40) homolog, subfamily A, member 4	AA799570	3.570E-09	-3.01
ESTs similar to mouse DnaJ (Hsp40) homolog, subfamily A, member 4	AA848268	3.653E-09	-3.13
ESTs similar to mouse heat shock protein, 105 kDa	AI236601	1.233E-08	-2.80
heat shock protein 60 (liver)	X54793	3.466E-08	-1.76
ESTs similar to human DnaJ (Hsp40) homolog, subfamily B, member 4	AI008643	4.930E-08	-2.46
heat shock 70kD protein 5 (glucose-regulated protein precursor (GRP 78)/immunoglobulin heavy chain binding protein)	S63521	1.433E-07	-2.43
testis-specific heat shock protein-related gene hst70	X15705	1.930E-07	-3.00
heat shock 70 kDa protein 4	AF077354	6.643E-07	-1.77
Heat shock 10 kDa protein 1	AI170613	2.102E-06	-1.41

### COENZYME BIOSYNTHESIS

ESTs similar to mouse pantothenate kinase 1	AA850195	2.945E-06	-3.34
---	----------	-----------	-------

### CYCLIC NUCLEOTIDE METABOLISM

diphosphoinositol polyphosphate phosphohydrolase type II (nudix (nucleoside diphosphate linked moiety X)-type motif 4)	U95001	7.525E-09	-2.48
diphosphoinositol polyphosphate phosphohydrolase type II	AA891107	3.512E-06	-3.15

### DEVELOPMENT

amino-terminal enhancer of split (related to Drosophila groucho gene)	L14462	5.781E-07	-2.00
---	--------	-----------	-------

FAT tumor suppressor (Drosophila) homolog AI103370 2.263E-06 -1.62

## ELECTRON TRANSPORT

ESTs similar to mouse cytochrome P450, AI176856 2.647E-08 2.69  
1b1, benz[a]anthracene inducible

Rieske iron-sulfur polypeptide 1, ubiquinol- M24542 1.837E-07 -1.39  
cytochrome c reductase

cytochrome P450, subfamily 1B, polypeptide U09540 3.621E-07 3.65  
1

ESTs weakly similar to human interleukin 4 AI233687 3.981E-07 2.25  
induced 1

ESTs similar to mouse aspartate-beta- AA799621 2.091E-09 -1.86  
hydroxylase

ESTs similar to human NADH AI171362 7.924E-07 -2.26  
dehydrogenase (ubiquinone) Fe-S protein 1,  
75kDa (NADH-coenzyme Q reductase)

ESTs similar to human NADH AA891171 7.945E-07 -1.48  
dehydrogenase (ubiquinone) 1, subcomplex  
unknown, 2, 14.5kDa

ESTs similar to human NADH AA875107 4.715E-07 -1.68  
dehydrogenase (ubiquinone) 1 alpha  
subcomplex, 3, 9kDa

ESTs weakly similar to mouse NADH AA685112 1.602E-06 -1.67  
dehydrogenase:ubiquinone Fe-S protein 8  
(Ndufs8) gene

## TCA CYCLE

ESTs similar to mouse isocitrate AI105469 5.725E-07 -1.40  
dehydrogenase 3 (NAD+) beta

Malate dehydrogenase-like enzyme AF093773 1.239E-07 -1.56

ESTs weakly similar to mouse pyruvate AI176117 2.037E-06 -1.38  
dehydrogenase (lipoamide) beta

ESTs highly similar to mouse isocitrate AI172491 1.389E-11 -2.24  
dehydrogenase 2 (NADP+), mitochondrial

ESTs similar to human succinate AI172320 2.166E-10 -1.64  
dehydrogenase complex, subunit B, iron  
sulfur (Ip)

malate dehydrogenase mitochondrial AI010480 2.723E-09 -1.69

ESTs similar to mouse succinate AA925554 1.268E-08 -1.65  
dehydrogenase complex, subunit A,  
flavoprotein (Fp)

ESTs similar to mouse succinate AA925554 1.505E-07 -1.87  
dehydrogenase complex, subunit A,  
flavoprotein (Fp)

succinate-CoA ligase, GDP-forming, alpha J03621 6.303E-07 -1.49  
subunit

## ESTS UNKNOWN FUNCTION

ESTs unknown function AI009340 2.669E-11 -3.23

ESTs unknown function AI101500 4.094E-11 -2.29

ESTs unknown function AA858892 2.083E-10 4.68

ESTs unknown function AA996832 2.941E-10 -2.24

ESTs unknown function AI170673 7.303E-10 1.71

ESTs unknown function AA901326 8.863E-10 2.45

ESTs unknown function AA799773 1.722E-09 -1.75

ESTs unknown function AI178272 5.659E-09 -1.99

ESTs unknown function	AA944906	6.077E-09	1.65
ESTs unknown function	AI011920	6.805E-09	2.04
ESTs unknown function	AI145095	8.050E-09	2.82
ESTs unknown function	AI232776	8.823E-09	-2.83
ESTs unknown function	AA817976	1.272E-08	2.15
ESTs unknown function	AI179601	1.467E-08	2.23
ESTs unknown function	AI009467	1.883E-08	-1.79
ESTs unknown function	AI145607	1.889E-08	1.48
ESTs unknown function	AI044120	2.665E-08	-1.89
ESTs unknown function	AA955369	2.686E-08	-1.95
ESTs unknown function	AA997596	2.798E-08	-1.97
ESTs unknown function	AA925708	3.884E-08	1.91
ESTs unknown function	AI104099	3.886E-08	-1.45
ESTs unknown function	AI011634	4.743E-08	-1.86
ESTs unknown function	AI170251	6.613E-08	1.99
ESTs unknown function	AI172007	7.268E-08	-1.69
ESTs unknown function	AA800576	7.383E-08	1.49
ESTs unknown function	AA998013	8.195E-08	-2.11
ESTs unknown function	AA964617	8.237E-08	1.64
ESTs unknown function	AA925049	8.561E-08	2.52
ESTs unknown function	AA801048	9.215E-08	1.84
ESTs unknown function	AA818846	9.227E-08	2.05
ESTs unknown function	AI236778	9.503E-08	1.80
ESTs unknown function	AA892773	1.276E-07	1.54
ESTs unknown function	AA875147	1.502E-07	1.54
ESTs unknown function	AA998222	1.555E-07	2.14
ESTs unknown function	AI175541	1.590E-07	-1.52
ESTs unknown function	AI045056	1.657E-07	2.29
ESTs unknown function	AI043913	1.714E-07	1.79
ESTs unknown function	AI059014	2.174E-07	-2.29
ESTs unknown function	AI228128	2.388E-07	-1.89
ESTs unknown function	AI171982	2.515E-07	-2.02
ESTs unknown function	AI175534	2.843E-07	-1.36
ESTs unknown function	AI234038	3.101E-07	1.42
ESTs unknown function	AA800197	3.236E-07	2.06
ESTs unknown function	AA892010	3.400E-07	-1.70
ESTs unknown function	AA819717	3.428E-07	-1.45
ESTs unknown function	AA957785	3.454E-07	2.01
ESTs unknown function	AI228760	3.463E-07	2.17
ESTs unknown function	AI232724	3.925E-07	-1.65
ESTs unknown function	AI104039	3.981E-07	-1.51
ESTs unknown function	AI177836	4.178E-07	1.98
ESTs unknown function	AA817726	4.780E-07	1.44
ESTs unknown function	AI044874	5.254E-07	-1.67
ESTs unknown function	AI236520	6.622E-07	-1.64
ESTs unknown function	AA925708	6.851E-07	1.58
ESTs unknown function	AI011058	7.062E-07	1.45
ESTs unknown function	AI058524	7.106E-07	-2.12
ESTs unknown function	AA946415	7.363E-07	-1.42
ESTs unknown function	AI103153	8.247E-07	1.44
ESTs unknown function	AI030259	8.261E-07	-1.54
ESTs unknown function	AI639166	8.309E-07	1.97
ESTs unknown function	AA893193	8.876E-07	1.58
ESTs unknown function	AI227902	8.910E-07	1.70
ESTs unknown function	AI112118	9.510E-07	-1.65
ESTs unknown function	AI105465	9.522E-07	-1.34
ESTs unknown function	AI172157	9.763E-07	-1.73
ESTs unknown function	AI231074	1.001E-06	1.68
ESTs unknown function	AI231219	1.073E-06	1.63

ESTs unknown function	AI639167	1.081E-06	2.51
ESTs unknown function	AI009509	1.173E-06	-1.63
ESTs unknown function	AI233812	1.209E-06	-1.67
ESTs unknown function	AI180247	1.220E-06	1.34
ESTs unknown function	AI236307	1.235E-06	1.53
ESTs unknown function	AI229154	1.266E-06	1.56
ESTs unknown function	AI169150	1.432E-06	1.71
ESTs unknown function	AA817708	1.434E-06	1.32
ESTs unknown function	AI232440	1.525E-06	1.95
ESTs unknown function	AI012648	1.530E-06	1.77
ESTs unknown function	AI175776	1.556E-06	2.22
ESTs unknown function	AA996578	1.564E-06	1.90
ESTs unknown function	AA875390	1.606E-06	2.16
ESTs unknown function	AI236528	1.630E-06	1.63
ESTs unknown function	AI231083	1.669E-06	-1.53
ESTs unknown function	AI172246	1.695E-06	2.01
ESTs unknown function	AI172460	1.752E-06	1.53
ESTs unknown function	AI071166	1.754E-06	1.99
ESTs unknown function	AI179865	1.778E-06	1.40
ESTs unknown function	AI044433	1.833E-06	1.54
ESTs unknown function	AI137037	1.837E-06	-1.41
ESTs unknown function	AI045021	1.865E-06	-1.81
ESTs unknown function	AI231797	1.880E-06	1.56
ESTs unknown function	AA893584	1.903E-06	1.55
ESTs unknown function	AA893000	1.989E-06	2.00
ESTs unknown function	AA946032	2.134E-06	-1.93
ESTs unknown function	AA926354	2.136E-06	1.42
ESTs unknown function	AA946509	2.450E-06	1.55
ESTs unknown function	AI232494	2.965E-06	-1.59
ESTs unknown function	AI170609	3.084E-06	1.81
ESTs unknown function	AA849827	3.144E-06	-2.51
ESTs unknown function	AI070107	3.160E-06	-1.78
ESTs unknown function	AI169595	3.407E-06	1.89
ESTs unknown function	AI171759	3.451E-06	-1.88
ESTs unknown function	AI012619	3.470E-06	-1.43
ESTs unknown function	AA955358	3.492E-06	-1.80
ESTs unknown function	AI175619	3.495E-06	1.75
ESTs unknown function	AI235950	3.744E-06	-1.62
ESTs unknown function	AA892310	3.823E-06	1.37
ESTs unknown function	AI013971	3.837E-06	-1.65
ESTs unknown function	AI112074	3.857E-06	1.51

GENES UNCLEAR/UNKNOWN FUNCTIONS
---------------------------------------

ESTs similar to mouse mannose-P-dolichol utilization defect 1	AI169037	1.196E-11	1.77
ESTs similar to human parkin co-regulated gene protein	AI010950	2.393E-11	-9.16
ESTs similar to human chromobox homolog 7	AA997327	5.378E-11	2.32
ESTs similar to mouse ankyrin repeat domain 2 (stretch responsive muscle)	AI170842	1.452E-10	-5.96
ESTs similar to mouse mitsugumin 29 mannosidase, alpha, class 2C, member 1	AI171372 AA946384	1.770E-09 3.296E-09	-3.90 1.72
peroxisomal integral membrane protein 47	AA894090	4.090E-09	1.85

Rat endogenous retroviral sequence, 5' and 3' LTR	AI177033	4.493E-09	1.63
Mk1 protein	AA819834	8.775E-09	1.99
neurolysin (metallopeptidase M3 family)	X87157	9.302E-09	2.04
zinc finger protein Y1 (RLZF-Y)	AF052042	1.073E-08	-1.64
ESTs similar to mouse Rac/Cdc42 guanine nucleotide exchange factor (GEF) 6	AI177431	1.235E-08	-2.20
ESTs similar to mouse glutamate receptor, ionotropic, N-methyl D-aspartate-like 1A	AI171953	1.797E-08	-1.61
ESTs similar to human histidyl-tRNA synthetase 2	AI233365	3.459E-08	1.55
ESTs similar to human Opa-interacting protein 2	AA924460	4.456E-08	1.52
ESTs weakly similar to mouse novel nuclear protein 1	AI172021	5.213E-08	-2.00
ESTs similar to mouse formin binding protein 4	AI176976	5.378E-08	1.89
ESTs similar to human uncharacterized hypothalamus protein HT012	AA819653	8.690E-08	-1.97
ESTs similar to human uncharacterized hematopoietic stem/progenitor cells protein MDS032	AA892132	9.202E-08	1.70
ESTs similar to human mitochondrial ribosomal protein L24	AA892843	9.908E-08	-1.66
ESTs similar to human SR rich protein	AA925771	1.383E-07	2.46
ESTs weakly similar to zebrafish dead eye	AI169375	1.728E-07	1.55
GCIP-interacting protein p29	AI228120	2.366E-07	1.67
glutathione transferase subunit 8	X62660	2.519E-07	-1.91
ESTs similar to mouse LIM domain binding 3 (cypher)	AI175028	2.790E-07	-1.89
ESTs similar to human oxidoreductase UCPA	AI232784	3.071E-07	2.15
ESTs similar to mouse imprinted and ancient (Impact)	AI101901	3.215E-07	2.05
upregulated by 1,25-dihydroxyvitamin D-3 (also known as thioredoxin interacting protein)	AI237654	3.504E-07	2.30
EST similar to rat Hsp70-3 gene	AA875620	3.671E-07	1.60
ESTs similar to human CGI-10 protein	AA956185	3.876E-07	-1.35
ESTs similar to human ubiquinol-cytochrome c reductase complex (7.2 kD)	AI007981	4.094E-07	-1.42
ESTs similar to human slingshot 2	AA924428	4.136E-07	1.28
ESTs similar to human uveal autoantigen with coiled-coil domains and ankyrin repeats	AA684631	4.519E-07	1.75
proline rich protein	U61729	5.141E-07	2.00
ESTs similar to mouse SPRY domain-containing SOCS box protein SSB-4	AI111413	5.897E-07	-1.58
ribosomal DNA external transcribed spacer 1	AI008579	6.794E-07	-2.62
ESTs similar to human cyclin M4	AA860015	8.729E-07	-1.76
ESTs similar to mouse LIM domain binding 3 (cypher)	AA800216	9.527E-07	-2.01
CCA2 protein	AB000199	1.019E-06	-1.66

ESTs similar to mouse BCL2-like 13 (apoptosis facilitator)	AA800808	1.140E-06	2.37
ESTs similar to mouse ALL1-fused gene from chromosome 1q	AI009661	1.264E-06	-3.26
ESTs similar to mouse pM5 protein	AI011709	1.266E-06	1.89
ESTs similar to mouse FN5 protein	AI172530	1.489E-06	-1.54
ESTs similar to mouse ataxin-1 ubiquitin-like interacting protein	AI177410	1.510E-06	-1.80
ESTs similar to mouse sclerostin	AI170797	1.513E-06	1.53
ESTs similar to mouse pleckstrin homology domain containing, family B (evectins) member 2	AI233241	1.587E-06	-1.65
ESTs weakly similar to human thioredoxin-like protein p19	AA925478	1.750E-06	-1.57
RNA, U87 small nucleolar	AI232081	1.938E-06	1.70
ESTs similar to mouse feminization homolog a (C. elegans)	AA900474	1.940E-06	-1.59
ESTs similar to mouse feminization homolog a (C. elegans)	AA848569	2.361E-06	-1.51
ESTs similar to human U6 snRNA-associated Sm-like protein LSm8	AI177016	2.494E-06	1.69
ESTs similar to human CGI-128 protein	AI232613	2.960E-06	-1.63
ESTs similar to mouse GH regulated protein 1	AI070859	2.988E-06	-2.15
ESTs similar to human retinoic acid induced 17	AI230440	3.420E-06	1.60
ESTs similar to human catenin, beta like 1	AI059023	3.591E-06	1.36

## GLUTATHIONE TRANSFERASE

glutathione S-transferase, mu 5	U86635	7.809E-11	2.53
Glutathione-S-transferase, mu type 2 (Yb2)	X04229	8.867E-10	2.03
Glutathione-S-transferase, mu type 2 (Yb2)	J03914	2.279E-09	3.82
Glutathione-S-transferase, mu type 2 (Yb2)	J02592	6.327E-09	3.92
glutathione S-transferase, mu 5	U86635	1.990E-08	2.04
Glutathione-S-transferase, mu type 2 (Yb2)	J02810	2.987E-08	1.54
glutathione S-transferase, mu type 3 (Yb3)	E01415	1.059E-07	1.86
microsomal glutathione S-transferase 1	J03752	2.269E-06	1.91
ESTs similar to human glutathione S-transferase theta 1	AA819192	3.090E-06	-1.43

## G-PROTEIN COUPLED RECEPTOR SIGNALING

corticotrophin releasing hormone receptor 2	U16253	3.848E-08	2.35
ESTs weakly similar to mouse neuropeptide Y receptor Y1	AI231501	2.956E-07	1.43
Calmodulin 1 (phosphorylase kinase, delta)	E02315	1.020E-06	-1.35

## GTP BINDING

ESTs similar to human RAB1B, member RAS oncogene family	AA851765	5.698E-07	-1.46
---	----------	-----------	-------

## HEME BIOSYNTHESIS

aminolevulinatase, delta-, dehydratase	AA800745	8.522E-07	-1.43
--	----------	-----------	-------

## IMMUNE/INFLAMMATORY RESPONSE

MHC class I histocompatibility antigen RT- BM1 alpha chain	AF029240	2.136E-06	1.92
--	----------	-----------	------

ESTs similar to mouse annexin A11	AI232030	1.403E-06	1.89
-----------------------------------	----------	-----------	------

Complement component 4	U42719	1.041E-06	1.86
------------------------	--------	-----------	------

## ION TRANSPORT

Solute carrier family 30 (zinc transporter), member 2	U50927	3.463E-06	1.95
---	--------	-----------	------

voltage-dependent anion channel 1	AI176266	1.007E-08	-1.28
-----------------------------------	----------	-----------	-------

voltage-dependent anion channel 1	AA848348	5.339E-07	-1.46
-----------------------------------	----------	-----------	-------

ATPase, Na <sup>+</sup> /K <sup>+</sup> transporting, alpha 1	AI072060	8.844E-07	-1.83
---	----------	-----------	-------

ATPase Na <sup>+</sup> /K <sup>+</sup> transporting beta 1 polypeptide	AI112173	3.599E-06	-2.05
--	----------	-----------	-------

## IRON/COPPER HOMEOSTASIS

ceruloplasmin	AI010470	8.536E-09	3.66
---------------	----------	-----------	------

ceruloplasmin	L33869	1.333E-06	4.34
---------------	--------	-----------	------

## LECTIN

ESTs similar to mouse osteoclast inhibitory lectin	AI012222	1.390E-06	2.11
--	----------	-----------	------

## LIPID METABOLISM

ESTs similar to mouse acetyl-Coenzyme A synthetase 2	AA848492	9.745E-07	-1.94
--	----------	-----------	-------

L-3-hydroxyacyl-Coenzyme A dehydrogenase, short chain	A AA848758	9.880E-07	-1.80
---	------------	-----------	-------

carnitine O-octanoyltransferase	U26033	1.248E-06	1.66
---------------------------------	--------	-----------	------

Uncoupling protein 3, mitochondrial	AF035943	2.788E-06	2.95
-------------------------------------	----------	-----------	------

apolipoprotein D	X55572	7.238E-08	2.29
------------------	--------	-----------	------

apolipoprotein E	X04979	1.657E-07	1.56
------------------	--------	-----------	------

apolipoprotein E	S76779	9.591E-10	2.79
------------------	--------	-----------	------

phosphatidylinositol transfer protein, beta	D21132	6.316E-08	1.46
---	--------	-----------	------

brain acyl-CoA hydrolase	Y09332	1.715E-07	-2.07
--------------------------	--------	-----------	-------

brain acyl-CoA hydrolase	D88890	3.825E-07	-1.70
--------------------------	--------	-----------	-------

## LYSOSOME

ESTs similar to human glucosamine (N-acetyl)-6-sulfatase (Sanfilippo disease IIID)	AA892086	2.132E-08	1.38
--	----------	-----------	------

Lysosomal-associated membrane protein 2	M32016	5.227E-07	1.92
---	--------	-----------	------

Lysosomal-associated membrane protein 2	D90211	1.373E-06	2.42
---	--------	-----------	------

## MUSCLE DEVELOPMENT

ESTs similar to mouse kyphoscoliosis	AI070590	5.105E-07	5.96
--------------------------------------	----------	-----------	------

cysteine-rich protein 3	X81193	5.814E-07	-3.09
-------------------------	--------	-----------	-------

## MUSCLE CONTRACTION

myosin, light polypeptide 2, alkali; ventricular, skeletal, slow	M11851	7.887E-12	-4.69
--	--------	-----------	-------



nonmuscle tropomyosin 5 (Tpm5) isoforms NM 5 and NM 6 mRNA, partial cds	AI170847	9.089E-08	-2.28
tropomyosin isoform 6	S82383	3.365E-07	-2.01
ESTs similar to mouse tropomyosin 3, gamma	AI071098	3.202E-06	-2.19
creatine kinase, mitochondrial 2, sarcomeric	X59736	1.040E-12	-2.57
ESTs similar to mouse troponin T3, skeletal, fast	AI136540	3.130E-08	2.75
ESTs weakly similar to human titin immunoglobulin domain protein (myotilin)	AI235512	2.279E-08	1.78
ESTs similar to rat myosin heavy chain, polypeptide 7 (cardiac muscle, beta)	AA998374	5.347E-07	-1.83

### NUCLEIC ACID BINDING

breakpoint cluster region protein, leiomyoma, 1; barrier to autointegration factor	AA848386	3.800E-09	-1.86
ESTs similar to human SON DNA binding protein	AA996621	4.897E-07	1.71
ESTs similar to mouse Son cell proliferation protein	AI103377	1.268E-06	1.42
nucleophosmin 1	J03969	1.879E-06	1.51
ESTs similar to human ataxin 2-binding protein 1	AI102057	2.125E-06	1.66
ESTs similar to human PR domain containing 2, with ZNF domain	AA899723	1.488E-06	1.67

### OSMOREGULATION/EXCRETION

ESTs similar to mouse nephronophthisis 1 (juvenile) homolog (human)	AI176028	1.175E-11	1.83
---	----------	-----------	------

### PROTEIN GLYCOSYLATION

UDP-GalNAc:polypeptide acetylgalactosaminyltransferase T5	N- AF049344	4.245E-08	-1.45
ESTs similar to mouse sirtuin 2 (silent mating type information regulation 2, homolog) 2 (S. cerevisiae)	AA799614	3.286E-07	1.40
ESTs similar to mouse ADP-ribosyltransferase 5	AI070764	3.553E-08	2.94

### PROTEIN PHOSPHORYLATION

ESTs similar to mouse protein kinase, cAMP dependent regulatory, type I, alpha	AA946421	1.017E-08	-1.48
ESTs similar to mouse serine/threonine kinase 23	AI072058	4.547E-07	-1.67
serine/threonine kinase 6	AI146058	6.371E-09	2.68

### PROTEIN BINDING

ESTs similar to mouse enigma homolog (R. norvegicus)	AA997341	7.486E-11	-2.35
ESTs similar to human enigma (LIM domain protein)	AI104117	4.209E-09	-2.74
ESTs similar to mouse PTPRF interacting protein, binding protein 1 (liprin beta 1)	AI012434	1.492E-08	1.59

ESTs similar to human myosin regulatory light chain interacting protein	AA818380	3.496E-07	1.90
ESTs similar to mouse integrin beta 1 binding protein 2 (melusin)	AA849578	5.671E-07	-2.02

### PROTEIN DEGRADATION

ESTs similar to mouse autophagy 12-like (S. cerevisiae)	AI178979	1.320E-06	1.24
for proteasomal ATPase (SUG1) (also known as protease (prosome, macropain) 26S subunit, ATPase 5)	AB000491	9.077E-07	1.77
ESTs similar to mouse proteasome (prosome, macropain) 26S subunit, non-ATPase, 2	AI172107	1.168E-06	1.46
proteasome (prosome, macropain) 26S subunit, non-ATPase, 9	AI175576	1.886E-06	2.00
proteasome (prosome, macropain) subunit, alpha type 7	AI179950	2.441E-06	1.41
ESTs similar to mouse proteasome (prosome, macropain) subunit, beta type 4	AI172162	2.759E-06	1.73

cathepsin L	S85184	4.372E-11	4.66
calpain 3	J05121	2.215E-09	-1.81
calpain 3	AF052540	2.729E-09	-1.85
membrane-bound transcription factor protease, site 1	AI101111	9.134E-09	1.64
calpain 3	AF061726	1.148E-07	-1.95
cathepsin L	S85184	1.762E-07	2.11
ESTs similar to mouse f-box and leucine-rich repeat protein 3a	AI145387	3.803E-09	2.10
ubiquitin C	D17296	7.469E-07	1.48

### PROTEIN SYNTHESIS

ESTs similar to mouse alanyl-tRNA synthetase	AI180068	2.298E-06	-1.37
ESTs similar to human translation initiation factor IF2	AA945769	1.630E-06	1.59
eukaryotic translation initiation factor binding protein 1	4E U05014	2.536E-07	1.93

### PROTON TRANSPORT

ATPase, H+ transporting, lysosomal noncatalytic accessory protein 1a	M58758	2.469E-07	1.76
ESTs similar to mouse ATP synthase, H+ transporting, mitochondrial F0 complex, subunit g	AA849619	2.755E-06	-1.43
ESTs highly similar to rat ATP synthase, H+ transporting, mitochondrial F0 complex, subunit c (subunit 9) isoform 3	AI180425	8.982E-08	-1.58
ATP synthase, H+ transporting, mitochondrial F1 complex, epsilon subunit	AI171844	1.428E-06	-1.34

### REGULATION OF TRANSCRIPTION

ESTs similar to mouse activating transcription factor 5	AI233425	2.104E-07	-2.05
Kruppel-like factor 15	AI103584	1.119E-06	1.87
ESTs similar to mouse CD8 beta opposite strand	AI010736	4.916E-09	-2.03

ESTs similar to mouse mini chromosome AA858636 maintenance deficient 7 ( <i>S. cerevisiae</i> )	2.319E-06	1.52
ESTs similar to human sirtuin silent mating type information regulation 2 homolog 5 ( <i>S. cerevisiae</i> )	2.524E-06	1.55
ESTs similar to mouse signal transducer and activator of transcription 1	1.146E-07	-2.18
ESTs similar to mouse transcription factor-like 4	4.907E-07	1.44
ESTs highly similar to mouse estrogen related receptor, alpha	1.925E-06	-1.70
ESTs similar to mouse tripartite motif protein 10 (also known as ring finger protein 9)	1.229E-06	-1.29
ESTs similar to mouse polymerase (RNA) II (DNA directed) polypeptide E (25kDa)	3.531E-06	2.44
ESTs similar to mouse RNA polymerase 1-3 (16 kDa subunit)	1.231E-06	1.48
ESTs similar to mouse leucine rich repeat (in FLII) interacting protein 1	2.494E-10	-1.95
ESTs similar to mouse SWI/SNF related, matrix associated, actin dependent regulator of chromatin, subfamily e, member 1	1.888E-06	1.56
ESTs similar to mouse serum response factor	3.342E-06	-1.56
ESTs similar to mouse ash2 (absent, small, or homeotic)-like ( <i>Drosophila</i> )	6.209E-07	1.46
ESTs weakly similar to human SWI/SNF related, matrix associated, actin dependent regulator of chromatin, subfamily a, member 2	9.975E-07	2.29

## RNA PROCESSING

ESTs similar to human decapping enzyme hDcp1b	AA819177	2.334E-06	1.41
ESTs similar to human splicing factor, arginine/serine-rich 7, 35kDa	AI171267	9.419E-07	1.58
splicing factor, arginine/serine-rich 5	L13635	7.078E-08	1.62
ESTs similar to mouse heterogeneous nuclear ribonucleoprotein C	AA799995	1.949E-08	-1.61
ESTs similar to mouse fragile X mental retardation gene 2, autosomal homolog	AI232174	2.200E-08	1.46
transporter protein; system N1 Na <sup>+</sup> and H <sup>+</sup> - coupled glutamine transporter (heterogeneous nuclear ribonucleoprotein U)	D14048	7.503E-07	1.63
ESTs very weakly similar to human dual specificity phosphatase 11 (RNA/RNP complex 1-interacting)	AI232489	2.994E-06	-1.30
ESTs similar to mouse apolipoprotein B editing complex 2	AA945951	3.459E-06	-1.89

## SELENIUM BINDING

ESTs similar to mouse selenoprotein R	AI011843	1.760E-08	1.73
---------------------------------------	----------	-----------	------

## SIGNAL TRANSDUCTION

ESTs similar to mouse and rat gamma-aminobutyric acid (GABA) B receptor, 1	AI227854	7.062E-07	1.63
--	----------	-----------	------

ESTs similar to mouse IK cytokine	AI070067	3.678E-08	1.65
ESTs similar to human microtubule-associated protein, RP/EB family, member 2	AI176863	7.394E-08	-1.71
ESTs similar to mouse casein kinase II, alpha 2, polypeptide	AI169125	1.211E-07	1.95
HGF-regulated tyrosine kinase substrate	AI007857	2.989E-07	1.82
synaptotagmin 2 binding protein	AI172060	3.375E-07	-1.55
guanine nucleotide binding protein, beta polypeptide 2	AA817892	5.019E-07	1.31
ADP-ribosylation factor related protein 1	X78603	2.589E-06	-1.44
vascular endothelial growth factor	AA924335	3.295E-06	-1.97
adenylyl cyclase-associated protein 2	AI145367	3.324E-06	-1.54
afadin (also known as myeloid/lymphoid or mixed lineage-leukemia translocation to 4 homolog) (Drosophila)	D90401	3.775E-06	-1.57
calcitonin gene-related peptide-receptor component protein	AA799418	1.645E-07	1.74

### SMALL MOLECULE TRANSPORT

ESTs similar to mouse endosulfine alpha	AI169421	1.259E-12	3.04
ESTs similar to mouse ATP-binding cassette, sub-family A (ABC1), member 1	AA848829	2.764E-09	3.87
ESTs similar to mouse ATP-binding cassette, sub-family A (ABC1), member 1	AA848829	6.483E-09	3.30
solute carrier family 25 (mitochondrial adenine nucleotide translocator) member 4	D12770	6.636E-09	-1.34
ESTs similar to mouse endosulfine alpha	AI070829	1.704E-08	2.96
ESTs similar to human ATP-binding cassette, sub-family C (CFTR/MRP), member 3	AI009814	1.530E-07	-1.80
ATP-binding cassette, sub-family C (CFTR/MRP), member 1a	X96394	5.983E-07	2.31
chloride intracellular channel 5	AA850229	8.547E-07	-2.48
mRNA highly similar to rat ATP-binding cassette, sub-family C (CFTR/MRP), member 1a	X90642	8.777E-07	2.64
2-oxoglutarate carrier (also known as solute carrier family 25 (mitochondrial carrier; oxoglutarate carrier), member 11)	U84727	1.054E-06	-1.43
ESTs similar to human endosulfine alpha	AI145627	1.139E-06	1.45
ESTs similar to mouse solute carrier family 7 (cationic amino acid transporter, y+ system), member 8	AA899235	1.223E-06	2.28
solute carrier family 12, member 2	AF051561	2.713E-06	2.24

### STEROID METABOLISM

farnesyl diphosphate farnesyl transferase 1 (squalene synthase)	M95591	3.133E-06	1.70
sulfotransferase family 1A, phenol-preferring, member 1	L19998	2.414E-06	2.11

### STRESS RESPONSE

ESTs similar to mouse stress-induced phosphoprotein 1	AA900247	1.211E-06	-1.89
---	----------	-----------	-------

## STRUCTURAL CONSTITUENT OF CYTOSKELTON

ESTs similar to mouse tubulin, alpha 4 AA800948 6.502E-07 -2.74

## STRUCTURAL CONSTITUENT OF RIBOSOME

ESTs similar to mouse ribosomal protein S6 AA955039 1.282E-07 -1.87  
kinase, 90kD, polypeptide 2

ribosomal protein L10 AA945611 1.589E-07 1.57

ESTs similar to mouse mitochondrial ribosomal protein L16 AI175221 1.642E-07 -1.46

ESTs similar to mouse ribosomal protein S6 AA858705 3.881E-07 -1.99  
kinase, 90kD, polypeptide 2

ribosomal protein L3 X62166 5.361E-07 1.48

ESTs highly similar to mouse ribosomal protein L21 AI070653 1.085E-06 -1.63

ribosomal protein L3 AA892367 1.198E-06 1.78

ESTs similar to mouse mitochondrial ribosomal protein S14 AA850451 2.904E-06 -1.34

ESTs similar to mouse mitochondrial ribosomal protein S18B AI011970 6.762E-08 -1.88

ribosomal protein L32 X06483 1.284E-07 1.34

ribosomal protein L12 X53504 3.593E-06 1.46

## TRANSPORT

ESTs weakly similar to mouse neuronal pentraxin 2 AI105049 1.051E-09 -2.31

ESTs highly similar to mouse ubiquitin-like 4 AI232649 8.570E-07 -1.83

## TUMOR ANTIGEN

ESTs weakly similar to mouse next to the Brca1 AA956140 2.198E-08 1.83

squamous cell carcinoma antigen AB014722 3.122E-08 1.75  
recognised by T cells

squamous cell carcinoma antigen AB014722 3.716E-06 1.91  
recognized by T-cells 1

## VESICLE TRANSPORT

ESTs similar to mouse kinesin family member 3c AI013107 3.489E-06 1.39

ESTs similar to mouse actin-related protein 1 homolog A (yeast) AA926303 2.370E-07 1.39

ESTs similar to mouse RAB6, member RAS oncogene family AI103834 3.486E-10 -1.85

ESTs similar to mouse golgi SNAP receptor complex member 2 AA964687 1.134E-06 1.25

ESTs similar to mouse adaptor-related protein complex AP-3, beta 1 subunit AI170332 3.198E-06 1.41

## VISION

crystallin, mu AI233209 2.287E-08 -5.96

**Supplementary Table 3.** All significant Bonferroni-adjusted probe sets with age-atrophy interactions are shown. Column 1 of the table shows the GenBank accession number of each probe set significant after the Bonferroni adjustment. The group identification (columns 2 and 3) is given by O = old; Y = Young; C = control; and T + treatment of hindlimb immobilization). Presence of the probe set on the microarray is indicated in columns 4 and 5 by: P/M = present or marginal calls, Abs = absent calls, the blue shading indicates >60% P/M calls for a given group. Mean Signal values for a treatment group and SEM for each treatment group are shown in columns 6 and 7. The p-values for each individual comparison between groups (columns 10-13 where  $p < 4.0 \times 10^{-6}$  is significant), and the relative-fold differences between groups (columns 14-17). The fold differences are listed as absolute differences by using the lower signal intensity in the denominator. Yellow shading shows fold differences >1.80. The corresponding gene names and putative functions for the following probe sets can be found in Supplementary Table 4.

Results for Interaction Atrophy genes - Age x Group 2-way interaction effect																	
probe_set	age	group	indicates $\geq 60\%$ P/M calls				SEM	age	group	OC	OA	YC	YA	indicates $\geq 1.8$ fold			
			P/M	Abs	Mean Signal	OC								OA	YC	YA	
rc_AA900746_at	O	C		5	12.7	2.069	OC		6.98E-02	2.98E-05	5.05E-01		2.53	2.72	1.25		
rc_AA900746_at	O	T		4	5.0	1.489	OT		6.98E-02		1.88E-06	2.11E-01	2.53		6.89	2.03	
rc_AA900746_at	Y	C	3	2	34.6	3.413	YC		2.98E-05	1.88E-06		8.86E-06	2.72	6.89		3.40	
rc_AA900746_at	Y	T		5	10.2	2.937	YT		5.05E-01	2.11E-01	8.86E-06		1.25	2.03	3.40		
AB007689_g_at	O	C		5	140.4	8.296	OC			1.60E-05	3.26E-02	2.40E-08		1.73	1.16	3.35	
AB007689_g_at	O	T		5	81.1	9.059	OT		1.60E-05		2.86E-07	9.85E-04	1.73		2.01	1.94	
AB007689_g_at	Y	C	4	1	163.2	5.800	YC		3.26E-02	2.86E-07		1.22E-09	1.16	2.01		3.90	
AB007689_g_at	Y	T		5	41.9	2.417	YT		2.40E-08	9.85E-04	1.22E-09		3.35	1.94	3.90		
rc_AI171813_at	O	C		5	80.3	6.398	OC			8.26E-01	3.85E-06	7.98E-01		1.04	2.10	1.04	
rc_AI171813_at	O	T		5	83.2	12.521	OT		8.26E-01		5.75E-06	9.71E-01	1.04		2.03	1.01	
rc_AI171813_at	Y	C	4	1	168.7	11.231	YC		3.85E-06	5.75E-06		6.15E-06	2.10	2.03		2.02	
rc_AI171813_at	Y	T		5	83.7	2.871	YT		7.98E-01	9.71E-01	6.15E-06		1.04	1.01	2.02		
rc_AI176067_s_at	O	C		5	69.1	8.220	OC			6.18E-03	1.23E-04	1.21E-02		2.31	1.90	2.04	
rc_AI176067_s_at	O	T		5	29.9	5.870	OT		6.18E-03		4.14E-07	7.52E-01	2.31		4.40	1.13	
rc_AI176067_s_at	Y	C	5		131.6	11.775	YC		1.23E-04	4.14E-07		6.98E-07	1.90	4.40		3.88	
rc_AI176067_s_at	Y	T		5	33.9	8.263	YT		1.21E-02	7.52E-01	6.98E-07		2.04	1.13	3.88		
rc_AI639088_s_at	O	C		5	21.2	5.611	OC			2.08E-01	6.27E-07	7.09E-01		1.87	3.82	1.16	
rc_AI639088_s_at	O	T		5	11.3	3.585	OT		2.08E-01		8.19E-08	3.65E-01	1.87		7.15	1.62	
rc_AI639088_s_at	Y	C	5		80.8	7.877	YC		6.27E-07	8.19E-08		3.40E-07	3.82	7.15		4.41	
rc_AI639088_s_at	Y	T		5	18.3	2.627	YT		7.09E-01	3.65E-01	3.40E-07		1.16	1.62	4.41		
AA686870_f_at	O	C		5	31.0	4.232	OC			6.66E-01	5.70E-06	3.82E-01		1.15	3.01	1.27	
AA686870_f_at	O	T		5	26.9	3.695	OT		6.66E-01		2.61E-06	1.99E-01	1.15		3.48	1.47	
AA686870_f_at	Y	C	3	2	93.5	9.169	YC		5.70E-06	2.61E-06		3.05E-05	3.01	3.48		2.37	
AA686870_f_at	Y	T	1	4	39.5	7.838	YT		3.82E-01	1.99E-01	3.05E-05		1.27	1.47	2.37		
rc_AA818372_at	O	C		5	56.7	5.458	OC			5.71E-01	2.46E-08	1.72E-02		1.19	4.33	1.88	
rc_AA818372_at	O	T		5	67.5	6.286	OT		5.71E-01		5.57E-08	5.42E-02	1.19		3.64	1.58	
rc_AA818372_at	Y	C	3	2	245.5	23.175	YC		2.46E-08	5.57E-08		1.44E-06	4.33	3.64		2.31	
rc_AA818372_at	Y	T	1	4	106.4	9.762	YT		1.72E-02	5.42E-02	1.44E-06		1.88	1.58	2.31		

rc_AI029021_at	O	C		5	47.9	2.116	OC		1.65E-01	1.25E-06	2.23E-03		1.28	2.38	1.65
rc_AI029021_at	O	T		4	61.1	7.532	OT	1.65E-01		3.17E-05	6.30E-02	1.28		1.86	1.30
rc_AI029021_at	Y	C	3	2	113.9	8.918	YC	1.25E-06	3.17E-05		9.88E-04	2.38	1.86		1.44
rc_AI029021_at	Y	T	1	4	79.2	4.202	YT	2.23E-03	6.30E-02	9.88E-04		1.65	1.30	1.44	
U68417_at	O	C		5	95.6	23.824	OC		5.48E-03	1.40E-01	5.72E-09		2.30	1.63	5.52
U68417_at	O	T		5	219.5	14.235	OT	5.48E-03		1.18E-01	5.84E-07	2.30		1.41	2.40
U68417_at	Y	C		5	155.6	32.357	YC	1.40E-01	1.18E-01		4.68E-08	1.63	1.41		3.39
U68417_at	Y	T	3	2	527.2	34.137	YT	5.72E-09	5.84E-07	4.68E-08		5.52	2.40	3.39	
rc_AA926262_s_at	O	C		5	144.9	9.369	OC		3.60E-01	2.01E-06	3.25E-01		1.30	2.71	1.23
rc_AA926262_s_at	O	T		4	111.6	12.788	OT	3.60E-01		8.90E-07	7.61E-02	1.30		3.52	1.60
rc_AA926262_s_at	Y	C	5		392.7	39.548	YC	2.01E-06	8.90E-07		1.11E-05	2.71	3.52		2.20
rc_AA926262_s_at	Y	T	3	2	178.7	17.861	YT	3.25E-01	7.61E-02	1.11E-05		1.23	1.60	2.20	
rc_AA891950_at	O	C		5	62.9	4.621	OC		7.88E-03	5.44E-02	1.03E-05		1.36	1.33	1.76
rc_AA891950_at	O	T		5	85.8	2.260	OT	7.88E-03		1.05E-04	4.75E-03	1.36		1.82	1.29
rc_AA891950_at	Y	C		5	47.3	6.732	YC	5.44E-02	1.05E-04		2.99E-07	1.33	1.82		2.34
rc_AA891950_at	Y	T	5		110.5	6.485	YT	1.03E-05	4.75E-03	2.99E-07		1.76	1.29	2.34	
rc_AI070446_at	O	C		5	9.7	4.124	OC		2.10E-02	5.53E-01	4.97E-08		2.23	1.29	5.61
rc_AI070446_at	O	T		5	21.7	3.782	OT	2.10E-02		6.87E-02	2.88E-06	2.23		1.73	2.51
rc_AI070446_at	Y	C		5	12.6	2.893	YC	5.53E-01	6.87E-02		1.21E-07	1.29	1.73		4.34
rc_AI070446_at	Y	T	5		54.6	2.042	YT	4.97E-08	2.88E-06	1.21E-07		5.61	2.51	4.34	
U32314_g_at	O	C		5	20.1	1.737	OC		2.84E-01	1.16E-01	3.27E-06		1.20	1.30	2.26
U32314_g_at	O	T		5	24.1	2.268	OT	2.84E-01		5.89E-01	2.50E-05	1.20		1.08	1.88
U32314_g_at	Y	C		5	26.1	1.567	YC	1.16E-01	5.89E-01		7.32E-05	1.30	1.08		1.74
U32314_g_at	Y	T	5		45.3	3.959	YT	3.27E-06	2.50E-05	7.32E-05		2.26	1.88	1.74	
rc_AI232103_at	O	C		5	144.9	10.041	OC		3.72E-01	6.59E-06	5.52E-01		1.14	1.89	1.08
rc_AI232103_at	O	T		5	126.9	12.250	OT	3.72E-01		1.32E-06	1.46E-01	1.14		2.16	1.24
rc_AI232103_at	Y	C	5		273.4	17.371	YC	6.59E-06	1.32E-06		2.04E-05	1.89	2.16		1.74
rc_AI232103_at	Y	T	5		156.8	14.693	YT	5.52E-01	1.46E-01	2.04E-05		1.08	1.24	1.74	
rc_AA943010_at	O	C	1	4	259.6	25.763	OC		1.57E-01	1.39E-05	4.27E-01		1.63	2.55	1.25
rc_AA943010_at	O	T		4	159.1	8.700	OT	1.57E-01		2.07E-06	4.83E-01	1.63		4.16	1.31
rc_AA943010_at	Y	C	5		661.3	82.211	YC	1.39E-05	2.07E-06		3.45E-06	2.55	4.16		3.18
rc_AA943010_at	Y	T		5	207.7	11.154	YT	4.27E-01	4.83E-01	3.45E-06		1.25	1.31	3.18	
AA848563_s_at	O	C	5		228.8	21.825	OC		2.47E-07	6.97E-06	1.34E-07		###	3.49	###
AA848563_s_at	O	T		5	16.1	6.448	OT	2.47E-07		6.49E-02	6.96E-01	###		4.09	2.62
AA848563_s_at	Y	C		5	65.6	27.047	YC	6.97E-06	6.49E-02		3.01E-02	3.49	4.09		###
AA848563_s_at	Y	T		5	6.1	1.040	YT	1.34E-07	6.96E-01	3.01E-02		###	2.62	###	
S66024_at	O	C	5		52.8	4.068	OC		1.56E-08	1.76E-06	5.03E-09		5.47	2.34	8.69
S66024_at	O	T		5	9.7	1.155	OT	1.56E-08		6.77E-03	4.00E-01	5.47		2.33	1.59
S66024_at	Y	C	1	4	22.5	3.212	YC	1.76E-06	6.77E-03		1.10E-03	2.34	2.33		3.71
S66024_at	Y	T		5	6.1	2.481	YT	5.03E-09	4.00E-01	1.10E-03		8.69	1.59	3.71	
rc_AI639060_at	O	C	5		510.8	58.485	OC		7.41E-08	2.48E-05	1.69E-08		7.43	2.19	###
rc_AI639060_at	O	T		5	68.8	20.819	OT	7.41E-08		3.23E-03	3.10E-01	7.43		3.39	3.63
rc_AI639060_at	Y	C	5		233.1	25.033	YC	2.48E-05	3.23E-03		3.57E-04	2.19	3.39		12.31
rc_AI639060_at	Y	T		5	18.9	5.704	YT	1.69E-08	3.10E-01	3.57E-04		###	3.63	12.31	

X77209_at	O	C	4	1	41.3	3.270	OC		9.24E-04	3.75E-04	9.76E-05		1.55	1.39	1.82
X77209_at	O	T	1	4	26.7	2.121	OT	9.24E-04		2.36E-07	2.90E-01	1.55		2.15	1.17
X77209_at	Y	C	5		57.4	1.966	YC	3.75E-04	2.36E-07		4.62E-08	1.39	2.15		2.53
X77209_at	Y	T	2	3	22.7	2.627	YT	9.76E-05	2.90E-01	4.62E-08		1.82	1.17	2.53	
rc_AA996896_at	O	C	5		123.1	4.259	OC		1.58E-05	8.94E-08	1.23E-07		1.60	2.18	2.12
rc_AA996896_at	O	T	1	3	77.0	5.464	OT	1.58E-05		1.41E-02	2.18E-02	1.60		1.36	1.33
rc_AA996896_at	Y	C	1	4	56.5	5.306	YC	8.94E-08	1.41E-02		8.19E-01	2.18	1.36		1.03
rc_AA996896_at	Y	T		5	58.1	5.171	YT	1.23E-07	2.18E-02	8.19E-01		2.12	1.33	1.03	
rc_AI171466_at	O	C	5		1378.5	118.054	OC		4.26E-06	1.29E-07	1.37E-07		3.40	1.93	###
rc_AI171466_at	O	T	1	4	405.0	52.295	OT	4.26E-06		3.72E-11	5.29E-02	3.40		6.56	3.83
rc_AI171466_at	Y	C	5		2657.4	153.417	YC	1.29E-07	3.72E-11		5.60E-12	1.93	6.56		###
rc_AI171466_at	Y	T		5	105.8	27.854	YT	1.37E-07	5.29E-02	5.60E-12		###	3.83	###	
rc_AA946449_at	O	C		5	72.6	4.949	OC		1.60E-03	7.95E-02	3.17E-09		1.44	1.20	2.32
rc_AA946449_at	O	T	2	2	104.4	2.703	OT	1.60E-03		5.62E-02	1.31E-06	1.44		1.20	1.61
rc_AA946449_at	Y	C		5	87.3	4.177	YC	7.95E-02	5.62E-02		3.00E-08	1.20	1.20		1.93
rc_AA946449_at	Y	T	5		168.4	8.237	YT	3.17E-09	1.31E-06	3.00E-08		2.32	1.61	1.93	
rc_AA942906_s_at	O	C		5	66.5	13.636	OC		1.57E-01	4.69E-08	4.65E-04		1.53	4.39	2.50
rc_AA942906_s_at	O	T	2	2	101.9	7.156	OT	1.57E-01		8.85E-07	1.62E-02	1.53		2.86	1.63
rc_AA942906_s_at	Y	C	5		291.5	13.990	YC	4.69E-08	8.85E-07		5.11E-05	4.39	2.86		1.75
rc_AA942906_s_at	Y	T	5		166.2	22.977	YT	4.65E-04	1.62E-02	5.11E-05		2.50	1.63	1.75	
U17697_s_at	O	C	2	3	50.0	2.336	OC		1.30E-03	5.30E-07	6.63E-01		1.31	1.48	1.03
U17697_s_at	O	T	2	3	38.3	1.786	OT	1.30E-03		2.27E-09	3.31E-03	1.31		1.94	1.27
U17697_s_at	Y	C	4	1	74.2	1.948	YC	5.30E-07	2.27E-09		2.61E-07	1.48	1.94		1.53
U17697_s_at	Y	T	4	1	48.7	2.400	YT	6.63E-01	3.31E-03	2.61E-07		1.03	1.27	1.53	
rc_AI180353_at	O	C	4	1	44.3	3.090	OC		1.11E-02	7.13E-09	3.84E-01		1.55	2.36	1.12
rc_AI180353_at	O	T	2	3	28.6	0.614	OT	1.11E-02		2.45E-10	6.57E-02	1.55		3.66	1.38
rc_AI180353_at	Y	C	5		104.6	6.238	YC	7.13E-09	2.45E-10		2.32E-09	2.36	3.66		2.65
rc_AI180353_at	Y	T	4	1	39.4	3.341	YT	3.84E-01	6.57E-02	2.32E-09		1.12	1.38	2.65	
rc_AI172334_at	O	C	5		436.8	18.098	OC		2.23E-06	2.47E-07	1.58E-08		1.99	2.43	3.58
rc_AI172334_at	O	T	2	3	220.0	22.516	OT	2.23E-06		1.99E-01	5.20E-03	1.99		1.23	1.80
rc_AI172334_at	Y	C	1	4	179.4	23.764	YC	2.47E-07	1.99E-01		7.65E-02	2.43	1.23		1.47
rc_AI172334_at	Y	T		5	122.1	20.774	YT	1.58E-08	5.20E-03	7.65E-02		3.58	1.80	1.47	
rc_AA943734_at	O	C	5		107.2	2.472	OC		5.58E-03	5.75E-05	8.35E-04		1.54	1.57	1.74
rc_AA943734_at	O	T	2	2	69.6	10.442	OT	5.58E-03		4.37E-07	5.00E-01	1.54		2.41	1.13
rc_AA943734_at	Y	C	5		167.9	10.648	YC	5.75E-05	4.37E-07		7.51E-08	1.57	2.41		2.73
rc_AA943734_at	Y	T		5	61.5	6.399	YT	8.35E-04	5.00E-01	7.51E-08		1.74	1.13	2.73	
rc_AI229412_at	O	C	5		268.4	18.774	OC		6.27E-10	8.49E-07	2.42E-10		6.61	2.02	###
rc_AI229412_at	O	T	2	3	40.6	3.652	OT	6.27E-10		7.50E-05	3.99E-01	6.61		3.28	1.60
rc_AI229412_at	Y	C	5		132.9	15.285	YC	8.49E-07	7.50E-05		1.41E-05	2.02	3.28		5.23
rc_AI229412_at	Y	T		5	25.4	3.612	YT	2.42E-10	3.99E-01	1.41E-05		###	1.60	5.23	
rc_AI071855_at	O	C		5	47.7	5.532	OC		4.85E-01	4.28E-01	1.63E-05		1.09	1.12	1.80
rc_AI071855_at	O	T	3	2	52.2	3.117	OT	4.85E-01		1.46E-01	6.46E-05	1.09		1.23	1.65
rc_AI071855_at	Y	C		5	42.6	3.705	YC	4.28E-01	1.46E-01		3.69E-06	1.12	1.23		2.02
rc_AI071855_at	Y	T	4	1	86.1	5.094	YT	1.63E-05	6.46E-05	3.69E-06		1.80	1.65	2.02	



rc_AA859543_at	O	C		5	23.8	2.219	OC		6.55E-04	6.07E-03	1.47E-05		2.01	4.09	2.46
rc_AA859543_at	O	T	3	2	47.8	4.805	OT	6.55E-04		1.56E-06	7.50E-02	2.01		8.21	1.23
rc_AA859543_at	Y	C		5	5.8	1.970	YC	6.07E-03	1.56E-06		7.67E-08	4.09	8.21		###
rc_AA859543_at	Y	T	5		58.6	5.734	YT	1.47E-05	7.50E-02	7.67E-08		2.46	1.23	###	
M31837_at	O	C		5	24.8	4.609	OC		8.88E-02	2.33E-02	1.26E-07		1.62	1.85	4.05
M31837_at	O	T	3	2	40.1	4.026	OT	8.88E-02		4.96E-01	2.36E-06	1.62		1.15	2.50
M31837_at	Y	C	4	1	46.0	3.398	YC	2.33E-02	4.96E-01		8.18E-06	1.85	1.15		2.18
M31837_at	Y	T	5		100.3	9.676	YT	1.26E-07	2.36E-06	8.18E-06		4.05	2.50	2.18	
rc_AI228132_i_at	O	C		5	34.2	1.582	OC		9.59E-01	1.99E-06	2.42E-02		1.01	2.55	1.53
rc_AI228132_i_at	O	T	3	2	33.8	1.562	OT	9.59E-01		1.82E-06	2.18E-02	1.01		2.58	1.55
rc_AI228132_i_at	Y	C	5		87.1	8.614	YC	1.99E-06	1.82E-06		2.20E-04	2.55	2.58		1.66
rc_AI228132_i_at	Y	T	5		52.4	5.286	YT	2.42E-02	2.18E-02	2.20E-04		1.53	1.55	1.66	
AJ005396_at	O	C	1	4	7.7	0.946	OC		8.50E-01	2.94E-06	1.25E-02		1.10	4.77	2.51
AJ005396_at	O	T	3	2	8.5	1.086	OT	8.50E-01		4.14E-06	1.85E-02	1.10		4.32	2.28
AJ005396_at	Y	C	5		36.8	4.764	YC	2.94E-06	4.14E-06		6.84E-04	4.77	4.32		1.90
AJ005396_at	Y	T	4	1	19.4	3.113	YT	1.25E-02	1.85E-02	6.84E-04		2.51	2.28	1.90	
AF080568_at	O	C	2	3	149.8	4.444	OC		1.15E-02	1.97E-04	1.19E-02		1.25	1.34	1.25
AF080568_at	O	T	3	2	119.9	6.632	OT	1.15E-02		9.86E-07	9.88E-01	1.25		1.67	1.00
AF080568_at	Y	C	5		200.2	5.610	YC	1.97E-04	9.86E-07		1.01E-06	1.34	1.67		1.67
AF080568_at	Y	T	4	1	120.1	11.192	YT	1.19E-02	9.88E-01	1.01E-06		1.25	1.00	1.67	
AB000507_at	O	C	3	2	159.8	16.140	OC		1.77E-01	3.80E-07	8.88E-02		1.22	2.04	1.30
AB000507_at	O	T	3	2	131.3	6.754	OT	1.77E-01		4.51E-08	6.94E-01	1.22		2.48	1.07
AB000507_at	Y	C	5		326.1	21.667	YC	3.80E-07	4.51E-08		2.57E-08	2.04	2.48		2.65
AB000507_at	Y	T		5	123.2	6.295	YT	8.88E-02	6.94E-01	2.57E-08		1.30	1.07	2.65	
AB007690_s_at	O	C	5		255.4	14.281	OC		1.05E-06	5.52E-06	2.95E-08		2.52	1.53	4.72
AB007690_s_at	O	T	3	2	101.3	7.871	OT	1.05E-06		1.61E-10	3.30E-02	2.52		3.85	1.87
AB007690_s_at	Y	C	5		390.1	21.307	YC	5.52E-06	1.61E-10		1.65E-11	1.53	3.85		7.22
AB007690_s_at	Y	T		5	54.1	9.970	YT	2.95E-08	3.30E-02	1.65E-11		4.72	1.87	7.22	
rc_AA946124_at	O	C	5		209.4	5.641	OC		9.22E-07	1.01E-01	4.00E-02		1.94	1.11	1.15
rc_AA946124_at	O	T	3	1	107.9	11.873	OT	9.22E-07		1.40E-05	3.28E-05	1.94		1.75	1.69
rc_AA946124_at	Y	C	5		188.4	9.790	YC	1.01E-01	1.40E-05		6.22E-01	1.11	1.75		1.03
rc_AA946124_at	Y	T	4	1	182.4	7.698	YT	4.00E-02	3.28E-05	6.22E-01		1.15	1.69	1.03	
rc_AI228284_at	O	C	5		242.4	15.646	OC		7.07E-03	8.83E-04	4.87E-03		1.59	1.49	1.65
rc_AI228284_at	O	T	3	2	152.1	14.193	OT	7.07E-03		2.26E-06	8.62E-01	1.59		2.38	1.04
rc_AI228284_at	Y	C	5		361.6	34.068	YC	8.83E-04	2.26E-06		1.67E-06	1.49	2.38		2.46
rc_AI228284_at	Y	T	4	1	146.9	10.187	YT	4.87E-03	8.62E-01	1.67E-06		1.65	1.04	2.46	
Z12152_at	O	C		5	29.3	3.608	OC		3.43E-04	4.99E-04	5.67E-04		1.65	2.68	2.61
Z12152_at	O	T	4	1	48.4	2.679	OT	3.43E-04		1.41E-07	1.54E-07	1.65		4.42	4.32
Z12152_at	Y	C		5	11.0	3.130	YC	4.99E-04	1.41E-07		9.52E-01	2.68	4.42		1.02
Z12152_at	Y	T		5	11.2	2.383	YT	5.67E-04	1.54E-07	9.52E-01		2.61	4.32	1.02	
rc_AA925744_g_at	O	C		5	236.2	11.234	OC		6.90E-04	9.08E-02	7.07E-07		1.61	1.32	2.10
rc_AA925744_g_at	O	T	4		380.5	39.590	OT	6.90E-04		2.61E-05	3.89E-03	1.61		2.13	1.30
rc_AA925744_g_at	Y	C		5	178.5	20.905	YC	9.08E-02	2.61E-05		5.44E-08	1.32	2.13		2.78
rc_AA925744_g_at	Y	T	5		496.0	20.287	YT	7.07E-07	3.89E-03	5.44E-08		2.10	1.30	2.78	

rc_AA926200_at	O	C		5	80.3	7.712	OC		1.43E-05	7.33E-01	4.04E-10		4.08	1.19	7.56
rc_AA926200_at	O	T	4		327.2	23.276	OT	1.43E-05		8.08E-06	3.47E-06	4.08		4.85	1.85
rc_AA926200_at	Y	C		5	67.4	11.423	YC	7.33E-01	8.08E-06		2.88E-10	1.19	4.85		9.00
rc_AA926200_at	Y	T	5		606.6	45.248	YT	4.04E-10	3.47E-06	2.88E-10		7.56	1.85	9.00	
rc_AA849720_at	O	C	1	4	274.2	9.823	OC		2.87E-03	7.33E-01	1.06E-06		1.31	1.03	1.64
rc_AA849720_at	O	T	4		358.8	23.120	OT	2.87E-03		1.46E-03	1.55E-03	1.31		1.35	1.26
rc_AA849720_at	Y	C		5	266.4	6.999	YC	7.33E-01	1.46E-03		6.21E-07	1.03	1.35		1.69
rc_AA849720_at	Y	T	5		450.5	21.803	YT	1.06E-06	1.55E-03	6.21E-07		1.64	1.26	1.69	
X65948_at	O	C	2	3	47.8	2.219	OC		2.07E-03	5.25E-01	1.74E-07		1.45	1.08	2.06
X65948_at	O	T	4	1	69.2	3.987	OT	2.07E-03		8.11E-03	1.15E-04	1.45		1.34	1.43
X65948_at	Y	C		5	51.6	4.123	YC	5.25E-01	8.11E-03		4.81E-07	1.08	1.34		1.91
X65948_at	Y	T	5		98.7	5.468	YT	1.74E-07	1.15E-04	4.81E-07		2.06	1.43	1.91	
rc_AA964962_at	O	C	3	2	73.1	8.997	OC		1.71E-10	3.22E-01	7.19E-08		3.49	1.19	2.51
rc_AA964962_at	O	T	4		255.3	4.576	OT	1.71E-10		7.11E-11	2.58E-05	3.49		4.16	1.39
rc_AA964962_at	Y	C		5	61.4	5.677	YC	3.22E-01	7.11E-11		1.91E-08	1.19	4.16		2.99
rc_AA964962_at	Y	T	5		183.5	10.763	YT	7.19E-08	2.58E-05	1.91E-08		2.51	1.39	2.99	
rc_AA963167_at	O	C	3	2	249.9	21.103	OC		2.45E-02	3.58E-02	1.00E-04		1.27	1.30	1.53
rc_AA963167_at	O	T	4		316.9	20.336	OT	2.45E-02		3.00E-04	2.77E-02	1.27		1.65	1.21
rc_AA963167_at	Y	C	2	3	191.6	14.036	YC	3.58E-02	3.00E-04		1.76E-06	1.30	1.65		1.99
rc_AA963167_at	Y	T	5		382.2	17.515	YT	1.00E-04	2.77E-02	1.76E-06		1.53	1.21	1.99	
rc_AI009996_at	O	C	4	1	64.6	6.961	OC		7.89E-05	6.76E-03	6.10E-02		1.80	1.79	1.40
rc_AI009996_at	O	T	4		116.3	7.107	OT	7.89E-05		5.27E-07	2.73E-06	1.80		3.23	2.52
rc_AI009996_at	Y	C		5	36.0	8.558	YC	6.76E-03	5.27E-07		2.83E-01	1.79	3.23		1.28
rc_AI009996_at	Y	T	3	2	46.2	1.672	YT	6.10E-02	2.73E-06	2.83E-01		1.40	2.52	1.28	
rc_AI230130_g_at	O	C	4	1	91.4	4.819	OC		6.86E-01	2.51E-06	1.54E-01		1.04	1.62	1.13
rc_AI230130_g_at	O	T	4	1	88.1	3.579	OT	6.86E-01		1.24E-06	7.42E-02	1.04		1.68	1.17
rc_AI230130_g_at	Y	C	5		148.3	7.221	YC	2.51E-06	1.24E-06		3.97E-05	1.62	1.68		1.43
rc_AI230130_g_at	Y	T	3	2	103.4	6.336	YT	1.54E-01	7.42E-02	3.97E-05		1.13	1.17	1.43	
rc_AA850672_at	O	C	4	1	62.7	3.811	OC		2.57E-04	5.10E-02	9.73E-07		1.55	1.30	1.86
rc_AA850672_at	O	T	4		97.0	5.147	OT	2.57E-04		6.51E-06	1.59E-02	1.55		2.01	1.20
rc_AA850672_at	Y	C	1	4	48.3	3.759	YC	5.10E-02	6.51E-06		4.73E-08	1.30	2.01		2.41
rc_AA850672_at	Y	T	5		116.5	6.492	YT	9.73E-07	1.59E-02	4.73E-08		1.86	1.20	2.41	
rc_AA946411_at	O	C	5		525.1	30.361	OC		2.84E-02	3.03E-01	8.11E-06		1.22	1.07	1.85
rc_AA946411_at	O	T	4		431.8	27.641	OT	2.84E-02		3.73E-03	1.67E-03	1.22		1.31	1.52
rc_AA946411_at	Y	C	5		563.8	21.868	YC	3.03E-01	3.73E-03		1.40E-06	1.07	1.31		1.98
rc_AA946411_at	Y	T	1	4	284.6	24.793	YT	8.11E-06	1.67E-03	1.40E-06		1.85	1.52	1.98	
rc_AI232409_at	O	C	5		125.2	5.422	OC		2.04E-03	4.37E-04	6.80E-06		1.46	1.38	2.25
rc_AI232409_at	O	T	4	1	86.0	6.861	OT	2.04E-03		4.81E-07	1.13E-02	1.46		2.00	1.55
rc_AI232409_at	Y	C	5		172.2	7.960	YC	4.37E-04	4.81E-07		7.65E-09	1.38	2.00		3.10
rc_AI232409_at	Y	T	2	3	55.5	9.329	YT	6.80E-06	1.13E-02	7.65E-09		2.25	1.55	3.10	
AB007689_at	O	C	5		381.0	24.431	OC		1.27E-06	1.39E-05	5.77E-08		2.03	1.42	2.78
AB007689_at	O	T	4	1	187.8	8.786	OT	1.27E-06		3.10E-10	6.57E-02	2.03		2.87	1.37
AB007689_at	Y	C	5		539.5	24.399	YC	1.39E-05	3.10E-10		4.12E-11	1.42	2.87		3.94
AB007689_at	Y	T	3	2	137.0	7.575	YT	5.77E-08	6.57E-02	4.12E-11		2.78	1.37	3.94	

rc_AA963077_at	O	C	5		72.4	8.398	OC		1.65E-06	8.12E-01	1.84E-03		2.87	1.06	1.88
rc_AA963077_at	O	T	4		207.9	24.442	OT	1.65E-06		2.39E-06	1.10E-03	2.87		2.72	1.53
rc_AA963077_at	Y	C	4	1	76.5	6.712	YC	8.12E-01	2.39E-06		3.01E-03	1.06	2.72		1.78
rc_AA963077_at	Y	T	5		136.0	7.609	YT	1.84E-03	1.10E-03	3.01E-03		1.88	1.53	1.78	
rc_AI011087_at	O	C	5		44.5	2.273	OC		9.69E-02	3.02E-01	2.09E-05		1.45	1.35	2.47
rc_AI011087_at	O	T	4		64.6	11.511	OT	9.69E-02		1.40E-02	1.24E-03	1.45		1.96	1.70
rc_AI011087_at	Y	C	4	1	33.0	4.525	YC	3.02E-01	1.40E-02		3.32E-06	1.35	1.96		3.32
rc_AI011087_at	Y	T	5		109.7	10.496	YT	2.09E-05	1.24E-03	3.32E-06		2.47	1.70	3.32	
M69246_at	O	C	5		277.9	25.323	OC		1.39E-03	2.31E-06	2.97E-02		2.75	2.18	1.65
M69246_at	O	T	4	1	101.1	13.822	OT	1.39E-03		7.11E-09	1.60E-01	2.75		5.99	1.67
M69246_at	Y	C	5		605.5	44.311	YC	2.31E-06	7.11E-09		5.30E-08	2.18	5.99		3.59
M69246_at	Y	T	5		168.5	37.457	YT	2.97E-02	1.60E-01	5.30E-08		1.65	1.67	3.59	
rc_AA848948_at	O	C	5		405.9	19.923	OC		2.11E-04	3.44E-02	8.96E-07		1.72	1.48	2.11
rc_AA848948_at	O	T	4		697.3	80.605	OT	2.11E-04		3.96E-06	1.76E-02	1.72		2.54	1.23
rc_AA848948_at	Y	C	5		274.1	23.419	YC	3.44E-02	3.96E-06		3.38E-08	1.48	2.54		3.13
rc_AA848948_at	Y	T	5		857.4	34.181	YT	8.96E-07	1.76E-02	3.38E-08		2.11	1.23	3.13	
rc_AA849312_at	O	C	5		896.7	57.144	OC		9.80E-02	8.48E-01	9.62E-08		1.18	1.02	1.91
rc_AA849312_at	O	T	4		1057.9	58.359	OT	9.80E-02		1.35E-01	3.06E-06	1.18		1.16	1.62
rc_AA849312_at	Y	C	5		913.4	60.884	YC	8.48E-01	1.35E-01		1.26E-07	1.02	1.16		1.88
rc_AA849312_at	Y	T	5		1716.1	70.018	YT	9.62E-08	3.06E-06	1.26E-07		1.91	1.62	1.88	
rc_AA849609_at	O	C	5		1891.3	100.844	OC		2.07E-02	6.13E-03	6.95E-05		1.30	1.27	1.84
rc_AA849609_at	O	T	4		1456.7	148.891	OT	2.07E-02		5.16E-05	2.29E-02	1.30		1.65	1.41
rc_AA849609_at	Y	C	5		2396.4	130.684	YC	6.13E-03	5.16E-05		3.40E-07	1.27	1.65		2.33
rc_AA849609_at	Y	T	5		1030.5	80.943	YT	6.95E-05	2.29E-02	3.40E-07		1.84	1.41	2.33	
rc_AA849754_at	O	C	5		230.3	19.984	OC		9.23E-03	2.00E-04	4.69E-04		1.52	1.53	1.93
rc_AA849754_at	O	T	4		151.3	13.063	OT	9.23E-03		1.64E-06	2.46E-01	1.52		2.33	1.27
rc_AA849754_at	Y	C	5		352.0	24.020	YC	2.00E-04	1.64E-06		1.24E-07	1.53	2.33		2.95
rc_AA849754_at	Y	T	5		119.3	9.336	YT	4.69E-04	2.46E-01	1.24E-07		1.93	1.27	2.95	
rc_AA850130_at	O	C	5		4049.9	97.422	OC		1.24E-02	1.07E-01	3.80E-05		1.29	1.13	1.74
rc_AA850130_at	O	T	4		3145.9	243.947	OT	1.24E-02		4.62E-04	2.06E-02	1.29		1.45	1.35
rc_AA850130_at	Y	C	5		4564.6	273.783	YC	1.07E-01	4.62E-04		1.98E-06	1.13	1.45		1.97
rc_AA850130_at	Y	T	5		2322.1	220.917	YT	3.80E-05	2.06E-02	1.98E-06		1.74	1.35	1.97	
rc_AA850130_g_at	O	C	5		2343.0	29.797	OC		6.32E-02	6.31E-03	6.23E-05		1.14	1.19	1.47
rc_AA850130_g_at	O	T	4		2050.9	109.397	OT	6.32E-02		1.59E-04	6.36E-03	1.14		1.35	1.29
rc_AA850130_g_at	Y	C	5		2778.4	147.557	YC	6.31E-03	1.59E-04		3.19E-07	1.19	1.35		1.75
rc_AA850130_g_at	Y	T	5		1589.7	73.991	YT	6.23E-05	6.36E-03	3.19E-07		1.47	1.29	1.75	
rc_AA851785_at	O	C	5		933.4	26.841	OC		1.07E-01	7.81E-01	4.48E-06		1.10	1.02	1.36
rc_AA851785_at	O	T	4		1022.2	31.302	OT	1.07E-01		6.63E-02	2.08E-04	1.10		1.11	1.25
rc_AA851785_at	Y	C	5		919.5	34.895	YC	7.81E-01	6.63E-02		2.80E-06	1.02	1.11		1.39
rc_AA851785_at	Y	T	5		1274.0	44.142	YT	4.48E-06	2.08E-04	2.80E-06		1.36	1.25	1.39	
rc_AA851926_at	O	C	5		1025.4	52.442	OC		4.18E-03	2.37E-02	2.67E-05		1.32	1.29	1.52
rc_AA851926_at	O	T	4		1348.7	77.797	OT	4.18E-03		3.86E-05	4.10E-02	1.32		1.69	1.16
rc_AA851926_at	Y	C	5		797.9	77.701	YC	2.37E-02	3.86E-05		4.25E-07	1.29	1.69		1.96
rc_AA851926_at	Y	T	5		1563.0	53.781	YT	2.67E-05	4.10E-02	4.25E-07		1.52	1.16	1.96	

rc_AA900580_g_at	O	C	5		2845.2	93.278	OC		4.35E-03	1.48E-01	8.18E-07		1.21	1.07	1.64
rc_AA900580_g_at	O	T	4		2355.3	67.259	OT	4.35E-03		2.37E-04	7.43E-04	1.21		1.30	1.35
rc_AA900580_g_at	Y	C	5		3055.3	105.566	YC	1.48E-01	2.37E-04		9.01E-08	1.07	1.30		1.76
rc_AA900580_g_at	Y	T	5		1739.1	113.954	YT	8.18E-07	7.43E-04	9.01E-08		1.64	1.35	1.76	
rc_AA901343_at	O	C	5		395.8	17.922	OC		2.21E-02	4.71E-01	4.57E-06		1.23	1.07	1.60
rc_AA901343_at	O	T	4		488.8	7.718	OT	2.21E-02		5.37E-03	1.14E-03	1.23		1.32	1.30
rc_AA901343_at	Y	C	5		370.4	38.472	YC	4.71E-01	5.37E-03		1.37E-06	1.07	1.32		1.71
rc_AA901343_at	Y	T	5		634.9	19.346	YT	4.57E-06	1.14E-03	1.37E-06		1.60	1.30	1.71	
rc_AA924075_s_at	O	C	5		337.3	25.963	OC		2.40E-02	4.09E-01	1.87E-07		1.53	1.17	2.80
rc_AA924075_s_at	O	T	4		516.1	32.367	OT	2.40E-02		1.08E-01	2.40E-05	1.53		1.31	1.83
rc_AA924075_s_at	Y	C	5		394.4	41.176	YC	4.09E-01	1.08E-01		6.49E-07	1.17	1.31		2.39
rc_AA924075_s_at	Y	T	5		943.7	73.824	YT	1.87E-07	2.40E-05	6.49E-07		2.80	1.83	2.39	
rc_AA924417_f_at	O	C	5		4393.5	100.628	OC		5.82E-07	5.04E-01	1.27E-09		1.65	1.03	2.44
rc_AA924417_f_at	O	T	4		2662.9	170.031	OT	5.82E-07		2.25E-07	9.34E-04	1.65		1.70	1.48
rc_AA924417_f_at	Y	C	5		4528.8	94.058	YC	5.04E-01	2.25E-07		6.27E-10	1.03	1.70		2.51
rc_AA924417_f_at	Y	T	5		1802.2	192.091	YT	1.27E-09	9.34E-04	6.27E-10		2.44	1.48	2.51	
rc_AA924532_at	O	C	5		729.7	24.726	OC		1.54E-01	1.38E-04	1.57E-03		1.11	1.58	1.28
rc_AA924532_at	O	T	4		813.4	40.226	OT	1.54E-01		1.47E-05	5.01E-02	1.11		1.76	1.15
rc_AA924532_at	Y	C	5		462.7	16.407	YC	1.38E-04	1.47E-05		2.20E-07	1.58	1.76		2.01
rc_AA924532_at	Y	T	5		932.4	57.836	YT	1.57E-03	5.01E-02	2.20E-07		1.28	1.15	2.01	
rc_AA924630_g_at	O	C	5		353.7	13.140	OC		1.43E-02	5.10E-01	5.11E-08		1.31	1.07	2.06
rc_AA924630_g_at	O	T	4		464.2	25.926	OT	1.43E-02		4.99E-02	7.84E-06	1.31		1.22	1.57
rc_AA924630_g_at	Y	C	5		379.1	23.506	YC	5.10E-01	4.99E-02		1.27E-07	1.07	1.22		1.92
rc_AA924630_g_at	Y	T	5		729.3	39.054	YT	5.11E-08	7.84E-06	1.27E-07		2.06	1.57	1.92	
rc_AA924964_g_at	O	C	5		662.7	8.583	OC		9.29E-01	1.18E-02	6.61E-04		1.00	1.13	1.17
rc_AA924964_g_at	O	T	4		665.2	20.490	OT	9.29E-01		1.37E-02	1.30E-03	1.00		1.13	1.16
rc_AA924964_g_at	Y	C	5		588.1	23.017	YC	1.18E-02	1.37E-02		3.38E-06	1.13	1.13		1.32
rc_AA924964_g_at	Y	T	5		774.0	20.368	YT	6.61E-04	1.30E-03	3.38E-06		1.17	1.16	1.32	
rc_AA924985_at	O	C	5		2702.1	65.462	OC		1.62E-09	5.57E-03	5.31E-13		2.16	1.15	9.06
rc_AA924985_at	O	T	4		1248.6	88.365	OT	1.62E-09		6.18E-08	4.52E-07	2.16		1.89	4.19
rc_AA924985_at	Y	C	5		2358.3	102.896	YC	5.57E-03	6.18E-08		5.00E-12	1.15	1.89		7.91
rc_AA924985_at	Y	T	5		298.2	40.555	YT	5.31E-13	4.52E-07	5.00E-12		9.06	4.19	7.91	
rc_AA925045_g_at	O	C	5		425.1	27.463	OC		1.06E-01	2.85E-02	5.33E-05		1.17	1.28	1.50
rc_AA925045_g_at	O	T	4		495.2	44.974	OT	1.06E-01		1.14E-03	3.02E-03	1.17		1.49	1.29
rc_AA925045_g_at	Y	C	5		332.0	22.719	YC	2.85E-02	1.14E-03		8.66E-07	1.28	1.49		1.92
rc_AA925045_g_at	Y	T	5		639.0	16.732	YT	5.33E-05	3.02E-03	8.66E-07		1.50	1.29	1.92	
rc_AA925057_at	O	C	5		1311.6	70.432	OC		3.72E-02	1.81E-05	1.21E-01		1.17	1.38	1.11
rc_AA925057_at	O	T	4		1117.7	59.061	OT	3.72E-02		7.41E-07	4.72E-01	1.17		1.61	1.06
rc_AA925057_at	Y	C	5		1804.7	37.427	YC	1.81E-05	7.41E-07		1.16E-06	1.38	1.61		1.53
rc_AA925057_at	Y	T	5		1180.3	59.503	YT	1.21E-01	4.72E-01	1.16E-06		1.11	1.06	1.53	
rc_AA925814_s_at	O	C	5		6510.7	61.826	OC		9.87E-04	9.97E-04	1.13E-07		1.12	1.10	1.31
rc_AA925814_s_at	O	T	4		5797.0	139.721	OT	9.87E-04		9.73E-07	2.43E-04	1.12		1.24	1.17
rc_AA925814_s_at	Y	C	5		7182.7	97.265	YC	9.97E-04	9.73E-07		8.76E-10	1.10	1.24		1.45
rc_AA925814_s_at	Y	T	5		4960.7	161.279	YT	1.13E-07	2.43E-04	8.76E-10		1.31	1.17	1.45	

rc_AA943110_at	O	C	5		113.0	14.161	OC		5.12E-04	4.34E-01	7.28E-09		1.97	1.17	3.40
rc_AA943110_at	O	T	4		222.8	18.878	OT	5.12E-04		2.38E-03	1.03E-05	1.97		1.69	1.73
rc_AA943110_at	Y	C	5		131.9	15.965	YC	4.34E-01	2.38E-03		1.92E-08	1.17	1.69		2.92
rc_AA943110_at	Y	T	5		384.4	19.141	YT	7.28E-09	1.03E-05	1.92E-08		3.40	1.73	2.92	
rc_AA944212_at	O	C	5		413.4	19.783	OC		1.00E-03	9.69E-03	2.02E-05		1.43	1.42	1.61
rc_AA944212_at	O	T	4		593.1	44.035	OT	1.00E-03		5.38E-06	1.13E-01	1.43		2.04	1.13
rc_AA944212_at	Y	C	5		290.2	27.824	YC	9.69E-03	5.38E-06		1.79E-07	1.42	2.04		2.30
rc_AA944212_at	Y	T	5		667.4	30.281	YT	2.02E-05	1.13E-01	1.79E-07		1.61	1.13	2.30	
rc_AA944335_at	O	C	5		775.2	59.651	OC		1.20E-01	7.25E-01	1.10E-06		1.25	1.05	2.14
rc_AA944335_at	O	T	4		971.5	103.901	OT	1.20E-01		6.57E-02	3.86E-05	1.25		1.32	1.70
rc_AA944335_at	Y	C	5		735.0	46.397	YC	7.25E-01	6.57E-02		6.33E-07	1.05	1.32		2.25
rc_AA944335_at	Y	T	5		1656.0	107.035	YT	1.10E-06	3.86E-05	6.33E-07		2.14	1.70	2.25	
rc_AA944393_at	O	C	5		6793.7	231.179	OC		1.50E-02	3.21E-02	4.76E-06		1.16	1.11	1.50
rc_AA944393_at	O	T	4		5846.0	97.187	OT	1.50E-02		1.67E-04	1.76E-03	1.16		1.29	1.29
rc_AA944393_at	Y	C	5		7562.7	223.017	YC	3.21E-02	1.67E-04		1.29E-07	1.11	1.29		1.67
rc_AA944393_at	Y	T	5		4535.8	299.681	YT	4.76E-06	1.76E-03	1.29E-07		1.50	1.29	1.67	
rc_AA944741_at	O	C	5		681.1	24.147	OC		3.56E-04	9.54E-01	1.40E-08		1.36	1.00	1.81
rc_AA944741_at	O	T	4		925.4	56.748	OT	3.56E-04		3.98E-04	3.59E-05	1.36		1.35	1.33
rc_AA944741_at	Y	C	5		684.0	23.352	YC	9.54E-01	3.98E-04		1.51E-08	1.00	1.35		1.80
rc_AA944741_at	Y	T	5		1233.6	40.847	YT	1.40E-08	3.59E-05	1.51E-08		1.81	1.33	1.80	
rc_AA945149_at	O	C	5		663.4	98.238	OC		1.27E-03	1.79E-01	5.72E-08		2.86	2.68	5.40
rc_AA945149_at	O	T	4		1900.5	347.908	OT	1.27E-03		9.15E-05	7.71E-05	2.86		7.69	1.88
rc_AA945149_at	Y	C	5		247.2	13.514	YC	1.79E-01	9.15E-05		9.68E-09	2.68	7.69		###
rc_AA945149_at	Y	T	5		3582.1	283.908	YT	5.72E-08	7.71E-05	9.68E-09		5.40	1.88	###	
rc_AA946029_at	O	C	5		289.7	17.971	OC		7.49E-06	1.27E-01	6.15E-09		1.81	1.23	2.34
rc_AA946029_at	O	T	4		523.8	42.895	OT	7.49E-06		6.41E-07	5.64E-04	1.81		2.22	1.29
rc_AA946029_at	Y	C	5		236.2	19.549	YC	1.27E-01	6.41E-07		1.04E-09	1.23	2.22		2.86
rc_AA946029_at	Y	T	5		676.7	15.622	YT	6.15E-09	5.64E-04	1.04E-09		2.34	1.29	2.86	
rc_AA955741_at	O	C	5		593.1	13.605	OC		3.64E-03	1.16E-03	5.75E-04		1.25	1.22	1.31
rc_AA955741_at	O	T	4		475.9	11.938	OT	3.64E-03		3.01E-06	5.21E-01	1.25		1.52	1.05
rc_AA955741_at	Y	C	5		721.6	30.621	YC	1.16E-03	3.01E-06		5.07E-07	1.22	1.52		1.59
rc_AA955741_at	Y	T	5		453.5	26.930	YT	5.75E-04	5.21E-01	5.07E-07		1.31	1.05	1.59	
rc_AA956871_at	O	C	5		401.3	20.139	OC		9.80E-03	3.01E-02	2.53E-09		1.21	1.19	1.84
rc_AA956871_at	O	T	4		486.5	20.833	OT	9.80E-03		1.05E-04	2.59E-07	1.21		1.45	1.52
rc_AA956871_at	Y	C	5		336.3	14.579	YC	3.01E-02	1.05E-04		2.19E-10	1.19	1.45		2.20
rc_AA956871_at	Y	T	5		740.0	22.433	YT	2.53E-09	2.59E-07	2.19E-10		1.84	1.52	2.20	
rc_AA957244_i_at	O	C	5		244.5	16.951	OC		1.01E-03	1.37E-02	1.51E-05		1.60	1.24	2.19
rc_AA957244_i_at	O	T	4		153.0	17.956	OT	1.01E-03		7.13E-06	8.57E-02	1.60		1.99	1.37
rc_AA957244_i_at	Y	C	5		303.7	15.276	YC	1.37E-02	7.13E-06		1.81E-07	1.24	1.99		2.72
rc_AA957244_i_at	Y	T	5		111.6	11.403	YT	1.51E-05	8.57E-02	1.81E-07		2.19	1.37	2.72	
rc_AA957501_at	O	C	5		341.9	17.492	OC		5.37E-01	9.01E-05	7.22E-02		1.05	1.39	1.16
rc_AA957501_at	O	T	4		325.2	18.017	OT	5.37E-01		4.85E-05	2.52E-01	1.05		1.46	1.11
rc_AA957501_at	Y	C	5		473.8	24.177	YC	9.01E-05	4.85E-05		2.94E-06	1.39	1.46		1.61
rc_AA957501_at	Y	T	5		293.7	8.919	YT	7.22E-02	2.52E-01	2.94E-06		1.16	1.11	1.61	

rc_AA957596_at	O	C	5		280.0	35.529	OC		4.66E-01	1.26E-07	6.76E-02		1.17	2.97	1.42
rc_AA957596_at	O	T	4		326.9	47.491	OT	4.66E-01		8.17E-07	2.85E-01	1.17		2.54	1.21
rc_AA957596_at	Y	C	5		830.7	55.088	YC	1.26E-07	8.17E-07		2.43E-06	2.97	2.54		2.10
rc_AA957596_at	Y	T	5		396.4	30.046	YT	6.76E-02	2.85E-01	2.43E-06		1.42	1.21	2.10	
rc_AA957653_at	O	C	5		2663.7	201.900	OC		2.34E-09	5.12E-08	1.71E-10		5.67	2.61	###
rc_AA957653_at	O	T	4		470.2	54.022	OT	2.34E-09		6.76E-03	1.06E-01	5.67		2.17	2.78
rc_AA957653_at	Y	C	5		1018.8	90.403	YC	5.12E-08	6.76E-03		1.18E-04	2.61	2.17		6.02
rc_AA957653_at	Y	T	5		169.4	15.052	YT	1.71E-10	1.06E-01	1.18E-04		###	2.78	6.02	
rc_AA957835_at	O	C	5		107.5	7.292	OC		2.67E-03	4.90E-07	3.32E-01		1.98	2.09	1.15
rc_AA957835_at	O	T	4		54.2	6.188	OT	2.67E-03		7.86E-09	1.83E-02	1.98		4.15	1.73
rc_AA957835_at	Y	C	5		224.7	14.510	YC	4.90E-07	7.86E-09		1.16E-07	2.09	4.15		2.40
rc_AA957835_at	Y	T	5		93.5	8.982	YT	3.32E-01	1.83E-02	1.16E-07		1.15	1.73	2.40	
rc_AA963716_at	O	C	5		2490.4	65.965	OC		2.64E-09	2.28E-03	5.57E-09		2.45	1.20	2.12
rc_AA963716_at	O	T	4		1018.0	169.098	OT	2.64E-09		2.02E-07	2.02E-01	2.45		2.04	1.16
rc_AA963716_at	Y	C	5		2081.0	40.748	YC	2.28E-03	2.02E-07		7.26E-07	1.20	2.04		1.77
rc_AA963716_at	Y	T	5		1175.8	13.651	YT	5.57E-09	2.02E-01	7.26E-07		2.12	1.16	1.77	
rc_AA963797_at	O	C	5		219.5	11.342	OC		4.43E-05	3.59E-01	2.85E-02		1.33	1.05	1.15
rc_AA963797_at	O	T	4		292.1	7.552	OT	4.43E-05		2.43E-04	9.20E-07	1.33		1.27	1.54
rc_AA963797_at	Y	C	5		230.9	8.126	YC	3.59E-01	2.43E-04		4.21E-03	1.05	1.27		1.21
rc_AA963797_at	Y	T	5		190.2	6.677	YT	2.85E-02	9.20E-07	4.21E-03		1.15	1.54	1.21	
rc_AA964477_at	O	C	5		345.9	8.714	OC		1.49E-01	1.70E-01	1.02E-05		1.15	1.15	1.60
rc_AA964477_at	O	T	4		397.6	18.285	OT	1.49E-01		1.14E-02	3.49E-04	1.15		1.33	1.39
rc_AA964477_at	Y	C	5		299.8	28.497	YC	1.70E-01	1.14E-02		9.54E-07	1.15	1.33		1.85
rc_AA964477_at	Y	T	5		553.5	28.791	YT	1.02E-05	3.49E-04	9.54E-07		1.60	1.39	1.85	
rc_AA964777_at	O	C	5		375.3	20.001	OC		1.10E-01	9.89E-06	9.34E-01		1.15	1.46	1.01
rc_AA964777_at	O	T	4		327.7	14.328	OT	1.10E-01		1.11E-06	1.27E-01	1.15		1.67	1.14
rc_AA964777_at	Y	C	5		547.5	17.479	YC	9.89E-06	1.11E-06		8.54E-06	1.46	1.67		1.47
rc_AA964777_at	Y	T	5		373.1	21.997	YT	9.34E-01	1.27E-01	8.54E-06		1.01	1.14	1.47	
rc_AA997765_at	O	C	5		264.7	19.272	OC		4.42E-01	2.98E-06	8.23E-01		1.20	2.43	1.05
rc_AA997765_at	O	T	4		220.7	10.598	OT	4.42E-01		1.62E-06	5.74E-01	1.20		2.92	1.15
rc_AA997765_at	Y	C	5		644.4	66.381	YC	2.98E-06	1.62E-06		2.06E-06	2.43	2.92		2.55
rc_AA997765_at	Y	T	5		252.8	18.455	YT	8.23E-01	5.74E-01	2.06E-06		1.05	1.15	2.55	
rc_AA998128_at	O	C	5		222.3	7.871	OC		1.07E-02	5.45E-08	5.88E-05		1.25	1.65	1.57
rc_AA998128_at	O	T	4		177.1	13.522	OT	1.07E-02		3.16E-09	3.67E-02	1.25		2.08	1.25
rc_AA998128_at	Y	C	5		367.5	13.149	YC	5.45E-08	3.16E-09		1.27E-10	1.65	2.08		2.60
rc_AA998128_at	Y	T	5		141.6	7.505	YT	5.88E-05	3.67E-02	1.27E-10		1.57	1.25	2.60	
rc_AA998174_at	O	C	5		576.3	20.543	OC		1.49E-08	9.36E-04	7.94E-01		2.02	1.57	1.02
rc_AA998174_at	O	T	4		1165.6	80.764	OT	1.49E-08		2.30E-10	1.10E-08	2.02		3.17	2.07
rc_AA998174_at	Y	C	5		368.0	18.820	YC	9.36E-04	2.30E-10		1.61E-03	1.57	3.17		1.53
rc_AA998174_at	Y	T	5		562.9	11.647	YT	7.94E-01	1.10E-08	1.61E-03		1.02	2.07	1.53	
rc_AA999183_at	O	C	5		167.2	5.822	OC		4.52E-05	1.39E-01	2.03E-01		1.25	1.07	1.06
rc_AA999183_at	O	T	4		208.5	4.983	OT	4.52E-05		3.42E-06	4.92E-06	1.25		1.33	1.32
rc_AA999183_at	Y	C	5		156.4	3.789	YC	1.39E-01	3.42E-06		8.19E-01	1.07	1.33		1.01
rc_AA999183_at	Y	T	5		158.0	5.065	YT	2.03E-01	4.92E-06	8.19E-01		1.06	1.32	1.01	

rc_AI008066_at	O	C	5		5981.1	125.236	OC		2.33E-04	2.40E-02	2.98E-07		1.27	1.11	1.58
rc_AI008066_at	O	T	4		4692.7	183.573	OT	2.33E-04		3.24E-06	3.88E-03	1.27		1.41	1.24
rc_AI008066_at	Y	C	5		6616.1	164.463	YC	2.40E-02	3.24E-06		1.08E-08	1.11	1.41		1.75
rc_AI008066_at	Y	T	5		3777.7	238.906	YT	2.98E-07	3.88E-03	1.08E-08		1.58	1.24	1.75	
rc_AI008504_at	O	C	5		259.8	9.279	OC		1.60E-03	1.40E-01	4.33E-06		1.20	1.08	1.53
rc_AI008504_at	O	T	4		312.4	7.616	OT	1.60E-03		3.15E-02	2.84E-08	1.20		1.12	1.84
rc_AI008504_at	Y	C	5		279.9	6.147	YC	1.40E-01	3.15E-02		3.75E-07	1.08	1.12		1.65
rc_AI008504_at	Y	T	5		169.7	12.368	YT	4.33E-06	2.84E-08	3.75E-07		1.53	1.84	1.65	
rc_AI009131_at	O	C	5		614.4	23.273	OC		4.10E-01	3.80E-07	7.42E-01		1.08	1.67	1.03
rc_AI009131_at	O	T	4		570.9	44.618	OT	4.10E-01		2.25E-07	6.03E-01	1.08		1.80	1.05
rc_AI009131_at	Y	C	5		1027.5	47.917	YC	3.80E-07	2.25E-07		2.33E-07	1.67	1.80		1.72
rc_AI009131_at	Y	T	5		598.2	18.762	YT	7.42E-01	6.03E-01	2.33E-07		1.03	1.05	1.72	
rc_AI009197_at	O	C	5		548.7	31.673	OC		6.26E-04	1.57E-06	1.68E-04		1.50	1.84	1.55
rc_AI009197_at	O	T	4		825.7	28.482	OT	6.26E-04		1.15E-02	7.09E-01	1.50		1.22	1.03
rc_AI009197_at	Y	C	5		1010.8	65.672	YC	1.57E-06	1.15E-02		1.83E-02	1.84	1.22		1.19
rc_AI009197_at	Y	T	5		850.2	33.135	YT	1.68E-04	7.09E-01	1.83E-02		1.55	1.03	1.19	
rc_AI009490_at	O	C	5		8674.3	353.320	OC		7.67E-02	1.45E-02	4.69E-05		1.10	1.13	1.36
rc_AI009490_at	O	T	4		7852.8	229.368	OT	7.67E-02		4.18E-04	3.82E-03	1.10		1.25	1.23
rc_AI009490_at	Y	C	5		9800.3	220.680	YC	1.45E-02	4.18E-04		4.67E-07	1.13	1.25		1.54
rc_AI009490_at	Y	T	5		6375.6	325.968	YT	4.69E-05	3.82E-03	4.67E-07		1.36	1.23	1.54	
rc_AI010326_at	O	C	5		222.3	3.533	OC		4.41E-03	4.35E-04	1.11E-04		1.55	1.45	2.07
rc_AI010326_at	O	T	4		143.7	8.721	OT	4.41E-03		1.67E-06	1.44E-01	1.55		2.24	1.34
rc_AI010326_at	Y	C	5		321.6	27.856	YC	4.35E-04	1.67E-06		7.75E-08	1.45	2.24		2.99
rc_AI010326_at	Y	T	5		107.5	9.239	YT	1.11E-04	1.44E-01	7.75E-08		2.07	1.34	2.99	
rc_AI010449_at	O	C	5		385.6	15.314	OC		5.86E-03	5.75E-06	3.38E-02		1.53	1.69	1.31
rc_AI010449_at	O	T	4		252.4	22.631	OT	5.86E-03		8.05E-08	3.30E-01	1.53		2.59	1.17
rc_AI010449_at	Y	C	5		652.7	38.679	YC	5.75E-06	8.05E-08		1.57E-07	1.69	2.59		2.22
rc_AI010449_at	Y	T	5		294.2	28.885	YT	3.38E-02	3.30E-01	1.57E-07		1.31	1.17	2.22	
rc_AI011457_at	O	C	5		416.0	22.701	OC		2.64E-04	2.31E-01	5.59E-07		1.77	1.24	2.27
rc_AI011457_at	O	T	4		737.2	75.069	OT	2.64E-04		2.83E-05	7.77E-03	1.77		2.19	1.28
rc_AI011457_at	Y	C	5		336.2	27.737	YC	2.31E-01	2.83E-05		9.35E-08	1.24	2.19		2.81
rc_AI011457_at	Y	T	5		945.3	54.675	YT	5.59E-07	7.77E-03	9.35E-08		2.27	1.28	2.81	
rc_AI011678_at	O	C	5		510.6	11.856	OC		1.93E-01	4.80E-02	1.65E-05		1.09	1.15	1.61
rc_AI011678_at	O	T	4		555.7	16.176	OT	1.93E-01		4.03E-03	2.96E-06	1.09		1.25	1.76
rc_AI011678_at	Y	C	5		443.3	31.990	YC	4.80E-02	4.03E-03		1.02E-03	1.15	1.25		1.40
rc_AI011678_at	Y	T	5		316.3	22.565	YT	1.65E-05	2.96E-06	1.02E-03		1.61	1.76	1.40	
rc_AI011738_at	O	C	5		1952.4	57.491	OC		2.33E-05	1.02E-02	1.23E-06		1.80	1.21	2.19
rc_AI011738_at	O	T	4		1081.7	73.367	OT	2.33E-05		2.64E-07	2.12E-01	1.80		2.18	1.21
rc_AI011738_at	Y	C	5		2352.9	164.035	YC	1.02E-02	2.64E-07		2.01E-08	1.21	2.18		2.63
rc_AI011738_at	Y	T	5		893.1	37.242	YT	1.23E-06	2.12E-01	2.01E-08		2.19	1.21	2.63	
rc_AI012145_s_at	O	C	5		3877.1	173.461	OC		4.98E-02	3.95E-04	8.15E-05		1.17	1.29	1.53
rc_AI012145_s_at	O	T	4		3307.7	290.094	OT	4.98E-02		1.18E-05	1.08E-02	1.17		1.52	1.31
rc_AI012145_s_at	Y	C	5		5018.5	185.204	YC	3.95E-04	1.18E-05		5.84E-08	1.29	1.52		1.98
rc_AI012145_s_at	Y	T	5		2531.6	62.257	YT	8.15E-05	1.08E-02	5.84E-08		1.53	1.31	1.98	

rc_AI013250_s_at	O	C	5		938.3	18.270	OC		9.11E-04	1.38E-02	3.28E-06		1.33	1.16	1.67
rc_AI013250_s_at	O	T	4		707.8	22.327	OT	9.11E-04		6.56E-06	1.89E-02	1.33		1.53	1.26
rc_AI013250_s_at	Y	C	5		1085.4	44.074	YC	1.38E-02	6.56E-06		5.35E-08	1.16	1.53		1.94
rc_AI013250_s_at	Y	T	5		560.5	51.424	YT	3.28E-06	1.89E-02	5.35E-08		1.67	1.26	1.94	
rc_AI014132_at	O	C	5		1271.7	65.452	OC		3.18E-04	8.48E-07	3.86E-04		1.93	1.78	1.80
rc_AI014132_at	O	T	4		660.4	44.831	OT	3.18E-04		3.47E-09	7.26E-01	1.93		3.43	1.07
rc_AI014132_at	Y	C	5		2265.9	137.065	YC	8.48E-07	3.47E-09		2.32E-09	1.78	3.43		3.20
rc_AI014132_at	Y	T	5		707.4	67.881	YT	3.86E-04	7.26E-01	2.32E-09		1.80	1.07	3.20	
rc_AI029702_at	O	C	5		1346.3	51.089	OC		1.97E-06	8.29E-05	2.56E-08		1.87	1.31	2.62
rc_AI029702_at	O	T	4		718.7	47.252	OT	1.97E-06		2.45E-09	2.73E-02	1.87		2.46	1.40
rc_AI029702_at	Y	C	5		1769.0	81.421	YC	8.29E-05	2.45E-09		8.84E-11	1.31	2.46		3.45
rc_AI029702_at	Y	T	5		513.4	34.302	YT	2.56E-08	2.73E-02	8.84E-11		2.62	1.40	3.45	
rc_AI029745_at	O	C	5		198.5	11.584	OC		7.22E-01	2.97E-07	2.66E-02		1.07	2.67	1.47
rc_AI029745_at	O	T	4		213.1	21.735	OT	7.22E-01		1.08E-06	6.95E-02	1.07		2.48	1.37
rc_AI029745_at	Y	C	5		529.3	41.215	YC	2.97E-07	1.08E-06		1.54E-05	2.67	2.48		1.81
rc_AI029745_at	Y	T	5		291.8	24.203	YT	2.66E-02	6.95E-02	1.54E-05		1.47	1.37	1.81	
rc_AI045040_at	O	C	5		450.2	43.808	OC		1.65E-03	1.39E-02	5.74E-09		2.38	1.95	4.99
rc_AI045040_at	O	T	4		1071.4	97.541	OT	1.65E-03		2.48E-01	2.82E-06	2.38		1.22	2.10
rc_AI045040_at	Y	C	5		876.4	136.973	YC	1.39E-02	2.48E-01		2.06E-07	1.95	1.22		2.57
rc_AI045040_at	Y	T	5		2248.5	132.335	YT	5.74E-09	2.82E-06	2.06E-07		4.99	2.10	2.57	
rc_AI045107_at	O	C	5		5641.0	230.297	OC		3.42E-01	1.92E-04	2.30E-04		1.07	1.30	1.42
rc_AI045107_at	O	T	4		5282.4	226.792	OT	3.42E-01		5.03E-05	2.90E-03	1.07		1.39	1.33
rc_AI045107_at	Y	C	5		7328.4	307.954	YC	1.92E-04	5.03E-05		7.34E-08	1.30	1.39		1.84
rc_AI045107_at	Y	T	5		3985.5	208.428	YT	2.30E-04	2.90E-03	7.34E-08		1.42	1.33	1.84	
rc_AI045368_at	O	C	5		948.3	18.927	OC		1.30E-07	9.06E-04	3.25E-08		2.47	1.25	2.66
rc_AI045368_at	O	T	4		383.8	54.017	OT	1.30E-07		1.19E-09	6.60E-01	2.47		3.09	1.08
rc_AI045368_at	Y	C	5		1184.5	55.832	YC	9.06E-04	1.19E-09		3.28E-10	1.25	3.09		3.32
rc_AI045368_at	Y	T	5		356.5	30.468	YT	3.25E-08	6.60E-01	3.28E-10		2.66	1.08	3.32	
rc_AI058656_at	O	C	5		255.6	15.566	OC		5.41E-02	8.87E-01	3.92E-07		1.32	1.02	2.24
rc_AI058656_at	O	T	4		338.3	35.717	OT	5.41E-02		4.18E-02	2.69E-05	1.32		1.35	1.70
rc_AI058656_at	Y	C	5		250.3	13.428	YC	8.87E-01	4.18E-02		3.17E-07	1.02	1.35		2.29
rc_AI058656_at	Y	T	5		573.4	37.666	YT	3.92E-07	2.69E-05	3.17E-07		2.24	1.70	2.29	
rc_AI058957_s_at	O	C	5		163.4	7.327	OC		1.84E-07	4.57E-08	1.04E-08		2.44	1.62	3.26
rc_AI058957_s_at	O	T	4		66.8	6.649	OT	1.84E-07		9.45E-12	1.39E-01	2.44		3.96	1.33
rc_AI058957_s_at	Y	C	5		264.7	8.905	YC	4.57E-08	9.45E-12		1.25E-12	1.62	3.96		5.28
rc_AI058957_s_at	Y	T	5		50.2	5.513	YT	1.04E-08	1.39E-01	1.25E-12		3.26	1.33	5.28	
rc_AI060224_at	O	C	5		202.5	8.108	OC		3.14E-02	1.42E-03	1.44E-03		1.75	1.66	2.97
rc_AI060224_at	O	T	4		115.7	14.692	OT	3.14E-02		2.22E-05	2.14E-01	1.75		2.91	1.70
rc_AI060224_at	Y	C	5		336.9	43.930	YC	1.42E-03	2.22E-05		1.18E-06	1.66	2.91		4.94
rc_AI060224_at	Y	T	5		68.2	10.144	YT	1.44E-03	2.14E-01	1.18E-06		2.97	1.70	4.94	
rc_AI105417_at	O	C	5		67.1	3.656	OC		5.89E-01	5.64E-06	8.13E-01		1.33	3.97	1.11
rc_AI105417_at	O	T	4	1	50.6	4.767	OT	5.89E-01		2.13E-06	4.40E-01	1.33		5.27	1.47
rc_AI105417_at	Y	C	5		266.2	40.826	YC	5.64E-06	2.13E-06		8.74E-06	3.97	5.27		3.58
rc_AI105417_at	Y	T	5		74.3	9.709	YT	8.13E-01	4.40E-01	8.74E-06		1.11	1.47	3.58	



rc_H31479_at	O	C		5	9.9	0.929	OC		7.64E-06	2.03E-01	9.63E-01		2.37	1.39	1.01
rc_H31479_at	O	T	5		23.6	1.862	OT	7.64E-06		7.64E-07	7.01E-06	2.37		3.31	2.40
rc_H31479_at	Y	C		5	7.1	0.966	YC	2.03E-01	7.64E-07		2.19E-01	1.39	3.31		1.38
rc_H31479_at	Y	T		5	9.8	1.906	YT	9.63E-01	7.01E-06	2.19E-01		1.01	2.40	1.38	
rc_AA819129_at	O	C		5	143.2	11.664	OC		2.65E-02	1.82E-01	2.94E-05		1.95	2.18	3.23
rc_AA819129_at	O	T	5		278.9	38.889	OT	2.65E-02		1.45E-03	4.39E-03	1.95		4.24	1.66
rc_AA819129_at	Y	C		5	65.8	6.850	YC	1.82E-01	1.45E-03		2.30E-06	2.18	4.24		7.03
rc_AA819129_at	Y	T	5		462.9	66.866	YT	2.94E-05	4.39E-03	2.30E-06		3.23	1.66	7.03	
rc_AI171103_at	O	C		5	113.5	9.571	OC		7.03E-02	4.97E-01	2.26E-06		1.31	1.12	2.14
rc_AI171103_at	O	T	5		148.4	12.590	OT	7.03E-02		1.80E-02	8.40E-05	1.31		1.47	1.63
rc_AI171103_at	Y	C	4	1	100.9	9.876	YC	4.97E-01	1.80E-02		7.01E-07	1.12	1.47		2.40
rc_AI171103_at	Y	T	5		242.5	17.360	YT	2.26E-06	8.40E-05	7.01E-07		2.14	1.63	2.40	
rc_AI104675_at	O	C	1	4	125.3	9.109	OC		2.90E-05	1.25E-01	2.15E-01		1.78	1.28	1.21
rc_AI104675_at	O	T	5		223.5	18.493	OT	2.90E-05		1.55E-06	2.72E-06	1.78		2.29	2.16
rc_AI104675_at	Y	C		5	97.7	9.218	YC	1.25E-01	1.55E-06		7.49E-01	1.28	2.29		1.06
rc_AI104675_at	Y	T	2	3	103.3	8.439	YT	2.15E-01	2.72E-06	7.49E-01		1.21	2.16	1.06	
M77694_at	O	C	1	4	30.4	1.649	OC		1.26E-03	7.47E-01	8.81E-07		2.24	1.12	3.46
M77694_at	O	T	5		68.2	5.823	OT	1.26E-03		6.34E-04	1.53E-03	2.24		2.51	1.54
M77694_at	Y	C	1	4	27.2	3.646	YC	7.47E-01	6.34E-04		5.15E-07	1.12	2.51		3.86
M77694_at	Y	T	5		105.2	11.737	YT	8.81E-07	1.53E-03	5.15E-07		3.46	1.54	3.86	
rc_AI169075_at	O	C	1	4	169.2	16.881	OC		1.76E-03	4.31E-01	1.86E-11		2.11	1.24	5.88
rc_AI169075_at	O	T	5		357.2	6.652	OT	1.76E-03		9.60E-03	8.78E-10	2.11		1.70	2.79
rc_AI169075_at	Y	C	3	2	209.7	14.156	YC	4.31E-01	9.60E-03		3.99E-11	1.24	1.70		4.75
rc_AI169075_at	Y	T	5		995.2	67.079	YT	1.86E-11	8.78E-10	3.99E-11		5.88	2.79	4.75	
rc_AI072992_at	O	C	4	1	78.1	5.521	OC		3.02E-02	2.33E-02	2.17E-04		1.23	1.20	1.61
rc_AI072992_at	O	T	5		63.3	3.553	OT	3.02E-02		1.65E-04	3.05E-02	1.23		1.48	1.30
rc_AI072992_at	Y	C	5		93.7	5.478	YC	2.33E-02	1.65E-04		1.91E-06	1.20	1.48		1.93
rc_AI072992_at	Y	T	3	2	48.6	2.070	YT	2.17E-04	3.05E-02	1.91E-06		1.61	1.30	1.93	
rc_AI104483_at	O	C	4	1	155.0	16.230	OC		3.88E-01	2.50E-03	2.15E-03		1.09	1.35	1.55
rc_AI104483_at	O	T	5		141.6	3.075	OT	3.88E-01		3.89E-04	1.38E-02	1.09		1.47	1.41
rc_AI104483_at	Y	C	5		208.7	8.163	YC	2.50E-03	3.89E-04		2.00E-06	1.35	1.47		2.08
rc_AI104483_at	Y	T	4	1	100.1	10.570	YT	2.15E-03	1.38E-02	2.00E-06		1.55	1.41	2.08	
rc_AA800168_at	O	C	4	1	49.8	5.566	OC		4.28E-02	3.62E-01	2.98E-06		1.30	1.15	1.96
rc_AA800168_at	O	T	5		64.8	4.699	OT	4.28E-02		6.36E-03	1.95E-04	1.30		1.50	1.51
rc_AA800168_at	Y	C	3	2	43.4	2.728	YC	3.62E-01	6.36E-03		6.10E-07	1.15	1.50		2.25
rc_AA800168_at	Y	T	5		97.7	5.764	YT	2.98E-06	1.95E-04	6.10E-07		1.96	1.51	2.25	
rc_AA892380_at	O	C	4	1	159.8	6.165	OC		1.38E-02	9.37E-01	1.83E-06		1.25	1.01	1.66
rc_AA892380_at	O	T	5		199.7	11.040	OT	1.38E-02		1.17E-02	3.49E-04	1.25		1.26	1.33
rc_AA892380_at	Y	C	4	1	158.6	7.332	YC	9.37E-01	1.17E-02		1.59E-06	1.01	1.26		1.67
rc_AA892380_at	Y	T	5		265.0	14.274	YT	1.83E-06	3.49E-04	1.59E-06		1.66	1.33	1.67	
rc_AI102083_s_at	O	C	4	1	124.6	3.915	OC		6.88E-06	1.74E-06	1.14E-07		1.63	1.71	1.87
rc_AI102083_s_at	O	T	5		203.2	9.417	OT	6.88E-06		4.47E-01	2.47E-02	1.63		1.05	1.15
rc_AI102083_s_at	Y	C	5		212.6	3.036	YC	1.74E-06	4.47E-01		1.09E-01	1.71	1.05		1.10
rc_AI102083_s_at	Y	T	5		233.1	13.296	YT	1.14E-07	2.47E-02	1.09E-01		1.87	1.15	1.10	

rc_AI171772_at	O	C	4	1	51.3	4.862	OC		2.36E-01	5.27E-01	1.21E-09		1.68	1.36	7.90
rc_AI171772_at	O	T	5		86.3	10.910	OT	2.36E-01		5.67E-01	5.47E-09	1.68		1.24	4.69
rc_AI171772_at	Y	C	5		69.7	4.037	YC	5.27E-01	5.67E-01		2.64E-09	1.36	1.24		5.81
rc_AI171772_at	Y	T	5		404.9	38.159	YT	1.21E-09	5.47E-09	2.64E-09		7.90	4.69	5.81	
rc_AI227690_at	O	C	4	1	179.6	8.087	OC		2.38E-03	8.17E-01	1.17E-09		2.26	1.08	5.36
rc_AI227690_at	O	T	5		405.7	46.947	OT	2.38E-03		3.91E-03	1.42E-07	2.26		2.09	2.37
rc_AI227690_at	Y	C	5		194.3	8.087	YC	8.17E-01	3.91E-03		1.55E-09	1.08	2.09		4.95
rc_AI227690_at	Y	T	5		962.3	74.425	YT	1.17E-09	1.42E-07	1.55E-09		5.36	2.37	4.95	
U75929UTR#1_f_at	O	C	4	1	146.0	12.314	OC		8.64E-01	5.23E-09	2.99E-03		1.05	4.06	1.95
U75929UTR#1_f_at	O	T	5		139.1	14.616	OT	8.64E-01		4.20E-09	2.07E-03	1.05		4.26	2.05
U75929UTR#1_f_at	Y	C	5		593.2	36.274	YC	5.23E-09	4.20E-09		8.33E-07	4.06	4.26		2.08
U75929UTR#1_f_at	Y	T	5		285.0	38.485	YT	2.99E-03	2.07E-03	8.33E-07		1.95	2.05	2.08	
X65747_at	O	C	5		81.6	5.850	OC		9.28E-07	2.75E-08	3.95E-10		2.09	3.11	11.36
X65747_at	O	T	5		39.0	2.610	OT	9.28E-07		3.44E-02	3.00E-05	2.09		1.49	5.43
X65747_at	Y	C	2	3	26.2	3.910	YC	2.75E-08	3.44E-02		3.40E-03	3.11	1.49		3.65
X65747_at	Y	T		5	7.2	2.235	YT	3.95E-10	3.00E-05	3.40E-03		11.36	5.43	3.65	
rc_AA817993_at	O	C	5		1531.0	191.704	OC		2.93E-05	9.48E-07	7.92E-08		2.53	5.17	###
rc_AA817993_at	O	T	5		604.1	114.486	OT	2.93E-05		7.37E-02	2.96E-03	2.53		2.04	###
rc_AA817993_at	Y	C	5		296.1	42.311	YC	9.48E-07	7.37E-02		1.32E-01	5.17	2.04		7.25
rc_AA817993_at	Y	T		5	40.8	12.450	YT	7.92E-08	2.96E-03	1.32E-01		###	###	7.25	
rc_AA818604_s_at	O	C	5		264.8	29.934	OC		5.44E-07	1.80E-05	4.47E-08		4.36	2.37	###
rc_AA818604_s_at	O	T	5		60.7	7.483	OT	5.44E-07		6.31E-02	1.20E-01	4.36		1.84	3.21
rc_AA818604_s_at	Y	C	5		111.6	17.902	YC	1.80E-05	6.31E-02		2.21E-03	2.37	1.84		5.90
rc_AA818604_s_at	Y	T	1	4	18.9	5.032	YT	4.47E-08	1.20E-01	2.21E-03		###	3.21	5.90	
AA684537_at	O	C	5		413.3	25.764	OC		3.79E-05	5.70E-03	7.71E-07		1.79	1.25	2.57
AA684537_at	O	T	5		231.0	14.493	OT	3.79E-05		1.54E-07	4.52E-02	1.79		2.24	1.44
AA684537_at	Y	C	5		516.7	31.724	YC	5.70E-03	1.54E-07		7.29E-09	1.25	2.24		3.22
AA684537_at	Y	T	3	2	160.5	14.875	YT	7.71E-07	4.52E-02	7.29E-09		2.57	1.44	3.22	
AB000362_at	O	C	5		65.1	14.446	OC		4.04E-06	1.16E-01	3.20E-01		2.89	1.85	1.28
AB000362_at	O	T	5		188.2	14.569	OT	4.04E-06		2.54E-07	2.69E-05	2.89		5.35	2.25
AB000362_at	Y	C	5		35.2	3.114	YC	1.16E-01	2.54E-07		1.62E-02	1.85	5.35		2.38
AB000362_at	Y	T	4	1	83.6	14.801	YT	3.20E-01	2.69E-05	1.62E-02		1.28	2.25	2.38	
M22253_at	O	C	5		106.2	10.713	OC		6.40E-07	5.58E-06	3.45E-08		3.48	2.49	8.79
M22253_at	O	T	5		30.5	1.720	OT	6.40E-07		2.25E-01	7.22E-02	3.48		1.40	2.52
M22253_at	Y	C	5		42.6	7.632	YC	5.58E-06	2.25E-01		5.73E-03	2.49	1.40		3.52
M22253_at	Y	T	4	1	12.1	2.684	YT	3.45E-08	7.22E-02	5.73E-03		8.79	2.52	3.52	
rc_AI237589_at	O	C	5		217.5	16.291	OC		9.03E-01	1.66E-05	1.66E-02		1.02	1.73	1.47
rc_AI237589_at	O	T	5		214.3	18.200	OT	9.03E-01		1.32E-05	2.13E-02	1.02		1.75	1.45
rc_AI237589_at	Y	C	5		375.4	26.786	YC	1.66E-05	1.32E-05		1.74E-07	1.73	1.75		2.54
rc_AI237589_at	Y	T	4	1	147.7	6.677	YT	1.66E-02	2.13E-02	1.74E-07		1.47	1.45	2.54	
rc_AI171193_at	O	C	5		81.4	6.204	OC		1.82E-03	3.13E-01	2.92E-06		1.70	1.24	2.32
rc_AI171193_at	O	T	5		138.5	18.550	OT	1.82E-03		2.08E-04	4.66E-03	1.70		2.12	1.36
rc_AI171193_at	Y	C	2	3	65.5	4.075	YC	3.13E-01	2.08E-04		5.05E-07	1.24	2.12		2.89
rc_AI171193_at	Y	T	5		188.9	8.360	YT	2.92E-06	4.66E-03	5.05E-07		2.32	1.36	2.89	

H31125_f_at	O	C	5		254.3	23.152	OC		3.81E-07	3.74E-01	1.09E-02		2.80	1.25	1.63
H31125_f_at	O	T	5		712.4	65.696	OT	3.81E-07		9.35E-08	6.47E-05	2.80		3.50	1.72
H31125_f_at	Y	C	3	2	203.4	29.208	YC	3.74E-01	9.35E-08		1.59E-03	1.25	3.50		2.04
H31125_f_at	Y	T	5		414.5	22.043	YT	1.09E-02	6.47E-05	1.59E-03		1.63	1.72	2.04	
AB002086_at	O	C	5		554.2	40.424	OC		1.03E-04	8.81E-05	1.01E-06		1.36	1.58	1.54
AB002086_at	O	T	5		755.0	22.485	OT	1.03E-04		1.78E-08	2.30E-02	1.36		2.15	1.13
AB002086_at	Y	C	5		350.4	18.927	YC	8.81E-05	1.78E-08		7.75E-10	1.58	2.15		2.44
AB002086_at	Y	T	5		853.5	24.016	YT	1.01E-06	2.30E-02	7.75E-10		1.54	1.13	2.44	
AF034237_s_at	O	C	5		141.8	5.054	OC		2.54E-01	3.21E-06	2.74E-01		1.10	1.59	1.10
AF034237_s_at	O	T	5		156.0	4.264	OT	2.54E-01		2.83E-05	9.61E-01	1.10		1.45	1.00
AF034237_s_at	Y	C	5		225.5	13.363	YC	3.21E-06	2.83E-05		2.57E-05	1.59	1.45		1.45
AF034237_s_at	Y	T	5		155.4	8.182	YT	2.74E-01	9.61E-01	2.57E-05		1.10	1.00	1.45	
D13123_s_at	O	C	5		3494.4	111.153	OC		3.29E-07	3.61E-05	2.24E-09		1.58	1.25	2.11
D13123_s_at	O	T	5		2213.7	102.905	OT	3.29E-07		2.19E-10	2.38E-03	1.58		1.97	1.33
D13123_s_at	Y	C	5		4363.8	140.594	YC	3.61E-05	2.19E-10		6.91E-12	1.25	1.97		2.63
D13123_s_at	Y	T	5		1659.4	67.883	YT	2.24E-09	2.38E-03	6.91E-12		2.11	1.33	2.63	
D14014_at	O	C	5		108.0	7.813	OC		1.49E-01	3.82E-04	2.83E-02		1.22	1.53	1.40
D14014_at	O	T	5		88.5	2.863	OT	1.49E-01		1.88E-05	3.83E-01	1.22		1.87	1.15
D14014_at	Y	C	5		165.5	14.445	YC	3.82E-04	1.88E-05		3.65E-06	1.53	1.87		2.15
D14014_at	Y	T	5		77.0	7.257	YT	2.83E-02	3.83E-01	3.65E-06		1.40	1.15	2.15	
D16478_g_at	O	C	5		1564.4	32.376	OC		9.42E-03	3.45E-03	4.64E-04		1.22	1.21	1.36
D16478_g_at	O	T	5		1286.6	75.035	OT	9.42E-03		9.17E-06	1.71E-01	1.22		1.47	1.12
D16478_g_at	Y	C	5		1887.2	97.377	YC	3.45E-03	9.17E-06		7.56E-07	1.21	1.47		1.64
D16478_g_at	Y	T	5		1151.7	39.727	YT	4.64E-04	1.71E-01	7.56E-07		1.36	1.12	1.64	
D42137exon_s_at	O	C	5		747.7	30.827	OC		3.73E-03	2.79E-04	2.16E-05		1.31	1.32	1.70
D42137exon_s_at	O	T	5		571.5	26.343	OT	3.73E-03		5.38E-07	2.24E-02	1.31		1.73	1.30
D42137exon_s_at	Y	C	5		988.3	58.861	YC	2.79E-04	5.38E-07		1.30E-08	1.32	1.73		2.25
D42137exon_s_at	Y	T	5		440.1	17.138	YT	2.16E-05	2.24E-02	1.30E-08		1.70	1.30	2.25	
D44495_s_at	O	C	5		279.2	13.065	OC		3.05E-07	4.60E-01	1.57E-03		1.77	1.07	1.35
D44495_s_at	O	T	5		494.1	10.536	OT	3.05E-07		1.04E-06	3.14E-04	1.77		1.65	1.31
D44495_s_at	Y	C	5		298.6	22.084	YC	4.60E-01	1.04E-06		7.71E-03	1.07	1.65		1.26
D44495_s_at	Y	T	5		376.8	23.417	YT	1.57E-03	3.14E-04	7.71E-03		1.35	1.31	1.26	
D50694_at	O	C	5		673.7	20.456	OC		4.55E-02	1.36E-01	2.63E-05		1.23	1.20	1.62
D50694_at	O	T	5		828.9	38.195	OT	4.55E-02		1.78E-03	2.18E-03	1.23		1.48	1.31
D50694_at	Y	C	5		561.3	31.181	YC	1.36E-01	1.78E-03		1.53E-06	1.20	1.48		1.94
D50694_at	Y	T	5		1089.7	85.924	YT	2.63E-05	2.18E-03	1.53E-06		1.62	1.31	1.94	
D50695_at	O	C	5		374.0	3.853	OC		5.62E-03	7.52E-02	6.78E-07		1.23	1.16	1.56
D50695_at	O	T	5		459.2	20.503	OT	5.62E-03		1.07E-04	2.51E-04	1.23		1.42	1.27
D50695_at	Y	C	5		323.2	9.230	YC	7.52E-02	1.07E-04		3.74E-08	1.16	1.42		1.81
D50695_at	Y	T	5		584.0	30.022	YT	6.78E-07	2.51E-04	3.74E-08		1.56	1.27	1.81	
D50696_at	O	C	5		650.4	20.260	OC		7.33E-04	6.34E-01	7.05E-07		1.44	1.05	1.82
D50696_at	O	T	5		934.8	41.359	OT	7.33E-04		2.68E-04	1.99E-03	1.44		1.51	1.27
D50696_at	Y	C	5		617.3	38.009	YC	6.34E-01	2.68E-04		3.23E-07	1.05	1.51		1.92
D50696_at	Y	T	5		1186.7	75.922	YT	7.05E-07	1.99E-03	3.23E-07		1.82	1.27	1.92	

D85189_at	O	C	5		44.4	3.139	OC		1.28E-03	1.98E-03	4.92E-04		1.52	1.95	1.58
D85189_at	O	T	5		67.2	5.399	OT	1.28E-03		1.09E-06	6.54E-01	1.52		2.96	1.04
D85189_at	Y	C	5		22.7	1.959	YC	1.98E-03	1.09E-06		5.16E-07	1.95	2.96		3.08
D85189_at	Y	T	5		69.9	5.106	YT	4.92E-04	6.54E-01	5.16E-07		1.58	1.04	3.08	
D86039_at	O	C	5		799.5	61.562	OC		2.96E-02	1.23E-02	7.93E-04		1.20	1.20	1.42
D86039_at	O	T	5		663.6	23.652	OT	2.96E-02		8.60E-05	1.02E-01	1.20		1.45	1.17
D86039_at	Y	C	5		960.1	37.284	YC	1.23E-02	8.60E-05		3.29E-06	1.20	1.45		1.70
D86039_at	Y	T	5		564.8	27.150	YT	7.93E-04	1.02E-01	3.29E-06		1.42	1.17	1.70	
J02773_at	O	C	5		4535.0	204.585	OC		5.24E-03	1.10E-03	4.18E-06		1.36	1.33	2.27
J02773_at	O	T	5		3330.9	370.647	OT	5.24E-03		2.11E-06	2.49E-03	1.36		1.81	1.67
J02773_at	Y	C	5		6015.5	300.342	YC	1.10E-03	2.11E-06		9.53E-09	1.33	1.81		3.01
J02773_at	Y	T	5		1995.4	92.466	YT	4.18E-06	2.49E-03	9.53E-09		2.27	1.67	3.01	
J03190_g_at	O	C	5		142.4	14.393	OC		1.22E-02	6.57E-05	4.33E-03		1.58	1.69	1.75
J03190_g_at	O	T	5		90.4	9.449	OT	1.22E-02		4.21E-07	6.28E-01	1.58		2.67	1.11
J03190_g_at	Y	C	5		240.9	12.893	YC	6.57E-05	4.21E-07		1.94E-07	1.69	2.67		2.96
J03190_g_at	Y	T	5		81.3	14.706	YT	4.33E-03	6.28E-01	1.94E-07		1.75	1.11	2.96	
J05167_at	O	C	5		627.7	28.166	OC		2.31E-05	2.77E-02	1.48E-07		1.63	1.16	2.38
J05167_at	O	T	5		385.9	33.294	OT	2.31E-05		3.40E-07	9.22E-03	1.63		1.88	1.46
J05167_at	Y	C	5		727.3	35.463	YC	2.77E-02	3.40E-07		5.11E-09	1.16	1.88		2.75
J05167_at	Y	T	5		264.3	14.789	YT	1.48E-07	9.22E-03	5.11E-09		2.38	1.46	2.75	
J05592_at	O	C	5		338.7	18.975	OC		8.68E-03	2.39E-07	7.61E-01		1.66	2.14	1.04
J05592_at	O	T	5		203.9	18.202	OT	8.68E-03		3.71E-09	4.53E-03	1.66		3.55	1.73
J05592_at	Y	C	5		723.5	55.594	YC	2.39E-07	3.71E-09		3.89E-07	2.14	3.55		2.05
J05592_at	Y	T	5		352.7	16.961	YT	7.61E-01	4.53E-03	3.89E-07		1.04	1.73	2.05	
J05592_g_at	O	C	5		600.1	37.698	OC		5.19E-02	3.59E-08	3.16E-01		1.27	1.99	1.10
J05592_g_at	O	T	5		472.4	39.110	OT	5.19E-02		2.29E-09	6.37E-03	1.27		2.53	1.40
J05592_g_at	Y	C	5		1196.6	49.973	YC	3.59E-08	2.29E-09		1.64E-07	1.99	2.53		1.80
J05592_g_at	Y	T	5		663.1	44.133	YT	3.16E-01	6.37E-03	1.64E-07		1.10	1.40	1.80	
L01624_at	O	C	5		71.6	15.598	OC		2.48E-02	1.68E-01	3.43E-05		1.68	1.65	2.55
L01624_at	O	T	5		120.2	17.760	OT	2.48E-02		1.22E-03	5.57E-03	1.68		2.77	1.52
L01624_at	Y	C	5		43.3	4.222	YC	1.68E-01	1.22E-03		2.42E-06	1.65	2.77		4.22
L01624_at	Y	T	5		182.9	13.853	YT	3.43E-05	5.57E-03	2.42E-06		2.55	1.52	4.22	
L03294_g_at	O	C	5		1507.0	92.073	OC		5.81E-03	6.61E-04	2.55E-04		1.33	1.33	1.57
L03294_g_at	O	T	5		1136.3	60.885	OT	5.81E-03		1.52E-06	1.55E-01	1.33		1.76	1.18
L03294_g_at	Y	C	5		1997.9	103.325	YC	6.61E-04	1.52E-06		1.39E-07	1.33	1.76		2.08
L03294_g_at	Y	T	5		962.5	65.620	YT	2.55E-04	1.55E-01	1.39E-07		1.57	1.18	2.08	
L24897_s_at	O	C	5		204.5	105.207	OC		3.35E-01	9.63E-01	3.01E-09		2.37	1.07	17.13
L24897_s_at	O	T	5		485.0	158.928	OT	3.35E-01		3.58E-01	1.07E-08	2.37		2.23	7.22
L24897_s_at	Y	C	5		217.9	155.507	YC	9.63E-01	3.58E-01		3.19E-09	1.07	2.23		###
L24897_s_at	Y	T	5		3503.7	314.356	YT	3.01E-09	1.07E-08	3.19E-09		17.13	7.22	###	
L26268_at	O	C	5		268.9	15.265	OC		1.08E-03	3.50E-01	3.95E-07		1.33	1.09	1.68
L26268_at	O	T	5		357.5	9.368	OT	1.08E-03		1.47E-04	6.35E-04	1.33		1.44	1.26
L26268_at	Y	C	5		247.4	17.353	YC	3.50E-01	1.47E-04		8.98E-08	1.09	1.44		1.83
L26268_at	Y	T	5		451.8	19.245	YT	3.95E-07	6.35E-04	8.98E-08		1.68	1.26	1.83	

## SUPPLEMENTARY MATERIAL -CONTINUED

M27207mRNA_s_at	O	C	5		731.4	53.716	OC		2.80E-01	8.66E-13	1.58E-07		1.27	4.86	2.69
M27207mRNA_s_at	O	T	5		574.4	112.480	OT	2.80E-01		3.76E-13	3.08E-08	1.27		6.19	3.42
M27207mRNA_s_at	Y	C	5		3558.1	123.617	YC	8.66E-13	3.76E-13		4.70E-09	4.86	6.19		1.81
M27207mRNA_s_at	Y	T	5		1967.0	92.840	YT	1.58E-07	3.08E-08	4.70E-09		2.69	3.42	1.81	
M38566mRNA_s_at	O	C	5		137.7	7.889	OC		7.57E-02	2.24E-01	2.96E-09		1.51	1.34	4.13
M38566mRNA_s_at	O	T	5		207.6	22.937	OT	7.57E-02		5.35E-01	3.62E-08	1.51		1.13	2.74
M38566mRNA_s_at	Y	C	5		184.3	11.370	YC	2.24E-01	5.35E-01		1.51E-08	1.34	1.13		3.08
M38566mRNA_s_at	Y	T	5		568.4	44.626	YT	2.96E-09	3.62E-08	1.51E-08		4.13	2.74	3.08	
M54926_at	O	C	5		1444.2	45.239	OC		4.37E-02	3.15E-02	3.24E-05		1.17	1.22	1.43
M54926_at	O	T	5		1685.0	50.618	OT	4.37E-02		3.31E-04	2.85E-03	1.17		1.42	1.23
M54926_at	Y	C	5		1185.0	97.708	YC	3.15E-02	3.31E-04		5.00E-07	1.22	1.42		1.75
M54926_at	Y	T	5		2071.9	100.183	YT	3.24E-05	2.85E-03	5.00E-07		1.43	1.23	1.75	
M91597_s_at	O	C	5		3021.6	106.301	OC		1.63E-02	1.10E-01	1.30E-07		1.13	1.08	1.64
M91597_s_at	O	T	5		2667.1	121.421	OT	1.63E-02		3.35E-01	1.18E-05	1.13		1.05	1.45
M91597_s_at	Y	C	5		2798.4	77.428	YC	1.10E-01	3.35E-01		1.99E-06	1.08	1.05		1.52
M91597_s_at	Y	T	5		1843.0	53.194	YT	1.30E-07	1.18E-05	1.99E-06		1.64	1.45	1.52	
M91652complete_seq_at	O	C	5		467.6	50.025	OC		1.77E-03	5.19E-01	6.58E-08		1.95	1.17	3.39
M91652complete_seq_at	O	T	5		914.0	24.994	OT	1.77E-03		7.13E-03	3.66E-05	1.95		1.67	1.74
M91652complete_seq_at	Y	C	5		546.4	52.473	YC	5.19E-01	7.13E-03		1.76E-07	1.17	1.67		2.90
M91652complete_seq_at	Y	T	5		1587.1	150.211	YT	6.58E-08	3.66E-05	1.76E-07		3.39	1.74	2.90	
M91652complete_seq_g_at	O	C	5		805.1	84.827	OC		1.52E-04	7.65E-01	6.97E-09		1.88	1.06	2.97
M91652complete_seq_g_at	O	T	5		1512.6	92.195	OT	1.52E-04		8.26E-05	1.54E-05	1.88		1.99	1.58
M91652complete_seq_g_at	Y	C	5		761.5	44.475	YC	7.65E-01	8.26E-05		4.73E-09	1.06	1.99		3.14
M91652complete_seq_g_at	Y	T	5		2388.3	153.575	YT	6.97E-09	1.54E-05	4.73E-09		2.97	1.58	3.14	
R46953_f_at	O	C	5		267.3	10.531	OC		8.45E-01	6.48E-08	8.48E-02		1.07	4.17	1.62
R46953_f_at	O	T	5		285.2	42.687	OT	8.45E-01		8.67E-08	1.21E-01	1.07		3.91	1.52
R46953_f_at	Y	C	5		1114.7	113.775	YC	6.48E-08	8.67E-08		1.15E-06	4.17	3.91		2.57
R46953_f_at	Y	T	5		433.0	37.256	YT	8.48E-02	1.21E-01	1.15E-06		1.62	1.52	2.57	
R47128_f_at	O	C	5		134.1	17.005	OC		7.34E-01	7.19E-09	1.89E-03		1.17	6.38	2.81
R47128_f_at	O	T	5		156.7	29.047	OT	7.34E-01		1.13E-08	3.93E-03	1.17		5.46	2.41
R47128_f_at	Y	C	5		855.0	53.794	YC	7.19E-09	1.13E-08		1.82E-06	6.38	5.46		2.27
R47128_f_at	Y	T	5		377.4	67.561	YT	1.89E-03	3.93E-03	1.82E-06		2.81	2.41	2.27	
R47150_f_at	O	C	5		179.3	14.394	OC		8.31E-01	9.74E-08	1.42E-01		1.08	4.23	1.55
R47150_f_at	O	T	5		165.5	9.407	OT	8.31E-01		7.07E-08	9.74E-02	1.08		4.59	1.68
R47150_f_at	Y	C	5		758.9	68.667	YC	9.74E-08	7.07E-08		1.11E-06	4.23	4.59		2.74
R47150_f_at	Y	T	5		277.4	55.389	YT	1.42E-01	9.74E-02	1.11E-06		1.55	1.68	2.74	
rc_AA799479_g_at	O	C	5		1070.9	21.159	OC		4.29E-04	1.48E-05	3.29E-05		1.46	1.44	1.68
rc_AA799479_g_at	O	T	5		734.0	33.031	OT	4.29E-04		1.32E-08	2.19E-01	1.46		2.09	1.15
rc_AA799479_g_at	Y	C	5		1537.4	98.419	YC	1.48E-05	1.32E-08		2.57E-09	1.44	2.09		2.42
rc_AA799479_g_at	Y	T	5		636.5	19.941	YT	3.29E-05	2.19E-01	2.57E-09		1.68	1.15	2.42	

rc_AA799518_at	O	C	5		245.9	5.453	OC		2.38E-05	1.18E-05	9.51E-06		1.90	1.50	2.06
rc_AA799518_at	O	T	5		129.3	7.557	OT	2.38E-05		1.81E-09	6.31E-01	1.90		2.86	1.08
rc_AA799518_at	Y	C	5		370.0	25.500	YC	1.18E-05	1.81E-09		1.01E-09	1.50	2.86		3.09
rc_AA799518_at	Y	T	5		119.6	7.303	YT	9.51E-06	6.31E-01	1.01E-09		2.06	1.08	3.09	
rc_AA799518_g_at	O	C	5		666.9	24.526	OC		3.61E-05	1.65E-05	1.25E-05		2.05	1.55	2.29
rc_AA799518_g_at	O	T	5		325.4	31.626	OT	3.61E-05		2.92E-09	5.85E-01	2.05		3.18	1.12
rc_AA799518_g_at	Y	C	5		1033.4	74.769	YC	1.65E-05	2.92E-09		1.49E-09	1.55	3.18		3.54
rc_AA799518_g_at	Y	T	5		291.7	10.633	YT	1.25E-05	5.85E-01	1.49E-09		2.29	1.12	3.54	
rc_AA799539_at	O	C	5		69.2	4.697	OC		3.18E-02	7.28E-04	3.46E-09		1.23	1.40	2.12
rc_AA799539_at	O	T	5		84.9	4.029	OT	3.18E-02		8.85E-02	8.35E-08	1.23		1.14	1.73
rc_AA799539_at	Y	C	5		97.0	3.469	YC	7.28E-04	8.85E-02		1.48E-06	1.40	1.14		1.51
rc_AA799539_at	Y	T	5		146.5	6.243	YT	3.46E-09	8.35E-08	1.48E-06		2.12	1.73	1.51	
rc_AA799645_at	O	C	5		2137.8	82.027	OC		4.16E-06	5.35E-06	1.72E-08		1.48	1.32	1.96
rc_AA799645_at	O	T	5		1449.3	38.847	OT	4.16E-06		3.72E-10	2.80E-03	1.48		1.94	1.33
rc_AA799645_at	Y	C	5		2812.2	83.250	YC	5.35E-06	3.72E-10		1.14E-11	1.32	1.94		2.57
rc_AA799645_at	Y	T	5		1092.8	72.488	YT	1.72E-08	2.80E-03	1.14E-11		1.96	1.33	2.57	
rc_AA799645_g_at	O	C	5		966.8	56.974	OC		7.01E-06	1.46E-05	5.04E-07		1.73	1.40	2.10
rc_AA799645_g_at	O	T	5		557.5	37.938	OT	7.01E-06		9.52E-10	1.44E-01	1.73		2.42	1.21
rc_AA799645_g_at	Y	C	5		1351.2	53.429	YC	1.46E-05	9.52E-10		1.76E-10	1.40	2.42		2.93
rc_AA799645_g_at	Y	T	5		461.2	18.203	YT	5.04E-07	1.44E-01	1.76E-10		2.10	1.21	2.93	
rc_AA799766_at	O	C	5		241.6	11.132	OC		5.02E-01	3.59E-06	1.13E-01		1.04	1.38	1.09
rc_AA799766_at	O	T	5		250.7	9.147	OT	5.02E-01		1.25E-05	3.37E-01	1.04		1.33	1.05
rc_AA799766_at	Y	C	5		333.0	10.063	YC	3.59E-06	1.25E-05		8.40E-05	1.38	1.33		1.26
rc_AA799766_at	Y	T	5		263.8	6.549	YT	1.13E-01	3.37E-01	8.40E-05		1.09	1.05	1.26	
rc_AA800221_at	O	C	5		2113.9	77.263	OC		1.89E-05	7.43E-01	1.41E-08		1.37	1.01	1.89
rc_AA800221_at	O	T	5		1546.9	76.168	OT	1.89E-05		1.01E-05	3.64E-04	1.37		1.39	1.38
rc_AA800221_at	Y	C	5		2145.5	51.490	YC	7.43E-01	1.01E-05		9.05E-09	1.01	1.39		1.91
rc_AA800221_at	Y	T	5		1120.9	59.191	YT	1.41E-08	3.64E-04	9.05E-09		1.89	1.38	1.91	
rc_AA800298_at	O	C	5		53.7	2.307	OC		8.80E-01	9.02E-07	1.03E-02		1.03	2.42	1.53
rc_AA800298_at	O	T	5		52.2	6.321	OT	8.80E-01		7.00E-07	7.44E-03	1.03		2.49	1.58
rc_AA800298_at	Y	C	5		129.7	11.996	YC	9.02E-07	7.00E-07		1.98E-04	2.42	2.49		1.57
rc_AA800298_at	Y	T	5		82.4	2.360	YT	1.03E-02	7.44E-03	1.98E-04		1.53	1.58	1.57	
rc_AA800686_at	O	C	5		288.1	12.705	OC		2.54E-02	2.67E-09	1.80E-03		1.18	1.86	1.27
rc_AA800686_at	O	T	5		339.8	11.301	OT	2.54E-02		7.22E-08	2.22E-01	1.18		1.58	1.08
rc_AA800686_at	Y	C	5		535.3	19.722	YC	2.67E-09	7.22E-08		5.11E-07	1.86	1.58		1.46
rc_AA800686_at	Y	T	5		366.4	14.187	YT	1.80E-03	2.22E-01	5.11E-07		1.27	1.08	1.46	
rc_AA817861_at	O	C	5		154.9	4.760	OC		8.00E-04	3.00E-04	3.07E-04		1.34	1.28	1.39
rc_AA817861_at	O	T	5		115.8	1.963	OT	8.00E-04		1.80E-07	6.51E-01	1.34		1.71	1.04
rc_AA817861_at	Y	C	5		198.4	10.298	YC	3.00E-04	1.80E-07		8.99E-08	1.28	1.71		1.78
rc_AA817861_at	Y	T	5		111.5	6.846	YT	3.07E-04	6.51E-01	8.99E-08		1.39	1.04	1.78	
rc_AA818123_at	O	C	5		257.5	12.297	OC		5.96E-03	7.93E-01	1.85E-07		1.29	1.03	1.80
rc_AA818123_at	O	T	5		332.4	12.630	OT	5.96E-03		3.40E-03	4.60E-05	1.29		1.32	1.39
rc_AA818123_at	Y	C	5		251.2	11.121	YC	7.93E-01	3.40E-03		1.23E-07	1.03	1.32		1.84
rc_AA818123_at	Y	T	5		463.2	26.167	YT	1.85E-07	4.60E-05	1.23E-07		1.80	1.39	1.84	
rc_AA818271_at	O	C	5		109.8	5.197	OC		7.87E-10	1.39E-01	1.23E-13		2.39	1.20	3.48

rc_AA818271_at	O	T	5		262.8	10.023	OT	7.87E-10		1.44E-10	2.67E-08	2.39		2.88	1.46
rc_AA818271_at	Y	C	5		91.2	6.033	YC	1.39E-01	1.44E-10		4.39E-14	1.20	2.88		4.19
rc_AA818271_at	Y	T	5		382.3	11.001	YT	1.23E-13	2.67E-08	4.39E-14		3.48	1.46	4.19	
rc_AA818639_at	O	C	5		352.2	12.401	OC		2.62E-04	2.08E-05	1.25E-03		1.43	1.39	1.34
rc_AA818639_at	O	T	5		245.7	5.588	OT	2.62E-04		1.21E-08	4.65E-01	1.43		1.99	1.07
rc_AA818639_at	Y	C	5		487.9	25.364	YC	2.08E-05	1.21E-08		3.39E-08	1.39	1.99		1.86
rc_AA818639_at	Y	T	5		262.8	14.699	YT	1.25E-03	4.65E-01	3.39E-08		1.34	1.07	1.86	
rc_AA818804_at	O	C	5		747.7	51.190	OC		1.23E-03	3.40E-01	2.79E-08		1.47	1.13	2.20
rc_AA818804_at	O	T	5		1100.5	46.485	OT	1.23E-03		1.61E-04	1.61E-05	1.47		1.67	1.50
rc_AA818804_at	Y	C	5		659.2	54.876	YC	3.40E-01	1.61E-04		7.44E-09	1.13	1.67		2.50
rc_AA818804_at	Y	T	5		1647.6	91.849	YT	2.79E-08	1.61E-05	7.44E-09		2.20	1.50	2.50	
rc_AA818952_at	O	C	5		3662.0	113.715	OC		1.07E-04	1.21E-01	2.21E-07		1.41	1.15	1.69
rc_AA818952_at	O	T	5		5171.3	279.734	OT	1.07E-04		4.78E-06	3.10E-03	1.41		1.63	1.20
rc_AA818952_at	Y	C	5		3178.0	162.894	YC	1.21E-01	4.78E-06		2.04E-08	1.15	1.63		1.95
rc_AA818952_at	Y	T	5		6200.8	239.591	YT	2.21E-07	3.10E-03	2.04E-08		1.69	1.20	1.95	
rc_AA818971_at	O	C	5		2015.5	107.108	OC		2.48E-02	8.09E-03	2.89E-04		1.22	1.22	1.51
rc_AA818971_at	O	T	5		1648.4	140.857	OT	2.48E-02		4.86E-05	4.86E-02	1.22		1.49	1.24
rc_AA818971_at	Y	C	5		2463.7	42.631	YC	8.09E-03	4.86E-05		1.01E-06	1.22	1.49		1.85
rc_AA818971_at	Y	T	5		1331.9	104.155	YT	2.89E-04	4.86E-02	1.01E-06		1.51	1.24	1.85	
rc_AA819207_at	O	C	5		1348.3	171.113	OC		6.51E-01	7.94E-10	1.31E-04		1.22	5.95	2.93
rc_AA819207_at	O	T	5		1108.2	199.762	OT	6.51E-01		4.72E-10	5.24E-05	1.22		7.24	3.57
rc_AA819207_at	Y	C	5		8025.4	486.354	YC	7.94E-10	4.72E-10		7.54E-07	5.95	7.24		2.03
rc_AA819207_at	Y	T	5		3953.9	487.448	YT	1.31E-04	5.24E-05	7.54E-07		2.93	3.57	2.03	
rc_AA819398_at	O	C	5		434.3	20.554	OC		1.69E-02	7.15E-05	2.69E-03		1.20	1.33	1.28
rc_AA819398_at	O	T	5		363.2	13.551	OT	1.69E-02		5.84E-07	3.92E-01	1.20		1.59	1.07
rc_AA819398_at	Y	C	5		575.8	25.620	YC	7.15E-05	5.84E-07		1.47E-07	1.33	1.59		1.69
rc_AA819398_at	Y	T	5		339.8	12.657	YT	2.69E-03	3.92E-01	1.47E-07		1.28	1.07	1.69	
rc_AA819709_at	O	C	5		962.4	52.742	OC		6.40E-03	9.65E-05	1.17E-02		1.21	1.52	1.19
rc_AA819709_at	O	T	5		1163.8	55.908	OT	6.40E-03		3.51E-07	7.76E-01	1.21		1.84	1.02
rc_AA819709_at	Y	C	5		631.3	23.832	YC	9.65E-05	3.51E-07		5.58E-07	1.52	1.84		1.81
rc_AA819709_at	Y	T	5		1145.2	42.237	YT	1.17E-02	7.76E-01	5.58E-07		1.19	1.02	1.81	
rc_AA849769_g_at	O	C	5		462.3	18.046	OC		4.11E-02	1.78E-05	1.01E-01		1.48	1.88	1.34
rc_AA849769_g_at	O	T	5		312.0	25.201	OT	4.11E-02		3.77E-07	6.37E-01	1.48		2.79	1.10
rc_AA849769_g_at	Y	C	5		869.5	76.332	YC	1.78E-05	3.77E-07		8.21E-07	1.88	2.79		2.52
rc_AA849769_g_at	Y	T	5		344.5	48.661	YT	1.01E-01	6.37E-01	8.21E-07		1.34	1.10	2.52	
rc_AA851403_g_at	O	C	5		3202.9	122.242	OC		2.54E-03	2.22E-02	1.74E-05		1.33	1.18	1.72
rc_AA851403_g_at	O	T	5		2407.0	135.196	OT	2.54E-03		1.52E-05	2.56E-02	1.33		1.56	1.29
rc_AA851403_g_at	Y	C	5		3766.8	248.990	YC	2.22E-02	1.52E-05		2.26E-07	1.18	1.56		2.03
rc_AA851403_g_at	Y	T	5		1858.8	63.344	YT	1.74E-05	2.56E-02	2.26E-07		1.72	1.29	2.03	
rc_AA852004_s_at	O	C	5		206.7	13.634	OC		4.66E-03	8.00E-01	2.46E-07		2.11	1.09	3.86
rc_AA852004_s_at	O	T	5		435.3	21.764	OT	4.66E-03		2.71E-03	8.31E-05	2.11		2.31	1.84
rc_AA852004_s_at	Y	C	5		188.8	27.293	YC	8.00E-01	2.71E-03		1.65E-07	1.09	2.31		4.23
rc_AA852004_s_at	Y	T	5		798.8	90.958	YT	2.46E-07	8.31E-05	1.65E-07		3.86	1.84	4.23	
rc_AA858817_at	O	C	5		343.3	32.885	OC		2.29E-01	8.51E-01	1.02E-06		1.88	1.13	6.36
rc_AA858817_at	O	T	5		644.6	136.752	OT	2.29E-01		3.05E-01	9.14E-06	1.88		1.66	3.39

rc_AA858817_at	Y	C	5		389.3	27.961	YC	8.51E-01	3.05E-01		1.41E-06	1.13	1.66		5.61
rc_AA858817_at	Y	T	5		2182.6	309.356	YT	1.02E-06	9.14E-06	1.41E-06		6.36	3.39	5.61	
rc_AA858875_at	O	C	5		761.2	44.866	OC		1.81E-01	3.28E-08	6.50E-03		1.24	2.39	1.78
rc_AA858875_at	O	T	5		611.7	93.978	OT	1.81E-01		5.06E-09	1.03E-01	1.24		2.97	1.43
rc_AA858875_at	Y	C	5		1816.6	108.492	YC	3.28E-08	5.06E-09		6.39E-10	2.39	2.97		4.25
rc_AA858875_at	Y	T	5		427.0	15.299	YT	6.50E-03	1.03E-01	6.39E-10		1.78	1.43	4.25	
rc_AA859284_at	O	C	5		432.6	51.265	OC		8.72E-01	3.99E-10	1.59E-03		1.12	9.50	3.40
rc_AA859284_at	O	T	5		387.6	75.696	OT	8.72E-01		3.34E-10	1.12E-03	1.12		###	3.80
rc_AA859284_at	Y	C	5		4109.3	309.114	YC	3.99E-10	3.34E-10		4.65E-08	9.50	###		2.79
rc_AA859284_at	Y	T	5		1472.2	214.815	YT	1.59E-03	1.12E-03	4.65E-08		3.40	3.80	2.79	
rc_AA859325_at	O	C	5		777.6	26.958	OC		2.39E-04	3.31E-04	1.30E-05		1.32	1.24	1.47
rc_AA859325_at	O	T	5		588.1	37.148	OT	2.39E-04		8.06E-08	1.57E-01	1.32		1.63	1.11
rc_AA859325_at	Y	C	5		960.7	13.528	YC	3.31E-04	8.06E-08		1.02E-08	1.24	1.63		1.82
rc_AA859325_at	Y	T	5		528.2	30.943	YT	1.30E-05	1.57E-01	1.02E-08		1.47	1.11	1.82	
rc_AA859352_at	O	C	5		227.6	18.566	OC		1.75E-07	6.34E-11	4.30E-07		2.45	2.03	2.24
rc_AA859352_at	O	T	5		92.9	7.779	OT	1.75E-07		5.96E-14	5.74E-01	2.45		4.97	1.10
rc_AA859352_at	Y	C	5		461.7	5.009	YC	6.34E-11	5.96E-14		8.72E-14	2.03	4.97		4.54
rc_AA859352_at	Y	T	5		101.8	6.719	YT	4.30E-07	5.74E-01	8.72E-14		2.24	1.10	4.54	
rc_AA859444_at	O	C	5		199.0	23.947	OC		1.17E-01	1.36E-05	2.78E-01		1.27	1.79	1.17
rc_AA859444_at	O	T	5		156.7	5.555	OT	1.17E-01		7.39E-07	5.99E-01	1.27		2.27	1.09
rc_AA859444_at	Y	C	5		355.8	22.122	YC	1.36E-05	7.39E-07		1.82E-06	1.79	2.27		2.09
rc_AA859444_at	Y	T	5		170.4	14.183	YT	2.78E-01	5.99E-01	1.82E-06		1.17	1.09	2.09	
rc_AA859519_g_at	O	C	5		92.7	6.406	OC		1.02E-06	9.52E-02	1.06E-04		1.85	1.20	1.57
rc_AA859519_g_at	O	T	5		171.5	9.739	OT	1.02E-06		2.44E-05	2.27E-02	1.85		1.54	1.18
rc_AA859519_g_at	Y	C	5		111.1	7.458	YC	9.52E-02	2.44E-05		4.21E-03	1.20	1.54		1.31
rc_AA859519_g_at	Y	T	5		145.5	4.688	YT	1.06E-04	2.27E-02	4.21E-03		1.57	1.18	1.31	
rc_AA859885_at	O	C	5		293.0	14.812	OC		6.54E-02	3.72E-06	7.41E-02		1.28	1.77	1.27
rc_AA859885_at	O	T	5		228.1	22.389	OT	6.54E-02		1.45E-07	9.47E-01	1.28		2.27	1.01
rc_AA859885_at	Y	C	5		518.6	27.038	YC	3.72E-06	1.45E-07		1.60E-07	1.77	2.27		2.25
rc_AA859885_at	Y	T	5		230.3	26.451	YT	7.41E-02	9.47E-01	1.60E-07		1.27	1.01	2.25	
rc_AA859942_at	O	C	5		262.8	3.140	OC		3.44E-02	1.24E-01	7.12E-05		1.17	1.14	1.39
rc_AA859942_at	O	T	5		307.9	17.660	OT	3.44E-02		1.18E-03	8.62E-03	1.17		1.33	1.19
rc_AA859942_at	Y	C	5		231.1	15.854	YC	1.24E-01	1.18E-03		3.40E-06	1.14	1.33		1.58
rc_AA859942_at	Y	T	5		366.2	13.702	YT	7.12E-05	8.62E-03	3.40E-06		1.39	1.19	1.58	
rc_AA866452_s_at	O	C	5		2951.1	283.997	OC		1.56E-09	6.51E-07	9.55E-10		9.55	2.37	13.51
rc_AA866452_s_at	O	T	5		309.0	54.631	OT	1.56E-09		5.18E-04	6.81E-01	9.55		4.03	1.41
rc_AA866452_s_at	Y	C	5		1244.3	95.110	YC	6.51E-07	5.18E-04		2.18E-04	2.37	4.03		5.69
rc_AA866452_s_at	Y	T	5		218.5	25.522	YT	9.55E-10	6.81E-01	2.18E-04		13.51	1.41	5.69	
rc_AA866477_at	O	C	5		1734.7	123.517	OC		1.53E-01	2.31E-03	3.73E-03		1.15	1.32	1.43
rc_AA866477_at	O	T	5		1503.7	92.301	OT	1.53E-01		1.03E-04	7.71E-02	1.15		1.52	1.24
rc_AA866477_at	Y	C	5		2291.2	149.110	YC	2.31E-03	1.03E-04		2.96E-06	1.32	1.52		1.89
rc_AA866477_at	Y	T	5		1213.0	36.490	YT	3.73E-03	7.71E-02	2.96E-06		1.43	1.24	1.89	
rc_AA874803_g_at	O	C	5		231.1	20.306	OC		8.04E-01	5.35E-01	6.40E-08		1.04	1.10	2.50
rc_AA874803_g_at	O	T	5		240.3	13.994	OT	8.04E-01		7.08E-01	9.27E-08	1.04		1.06	2.40
rc_AA874803_g_at	Y	C	5		254.4	11.703	YC	5.35E-01	7.08E-01		1.65E-07	1.10	1.06		2.27



rc_AA874803_g_at	Y	T	5		576.9	44.262	YT	6.40E-08	9.27E-08	1.65E-07		2.50	2.40	2.27	
rc_AA875032_at	O	C	5		86.7	7.766	OC		2.20E-01	2.50E-02	2.51E-04		1.13	1.34	1.48
rc_AA875032_at	O	T	5		98.2	6.550	OT	2.20E-01		1.75E-03	3.63E-03	1.13		1.52	1.31
rc_AA875032_at	Y	C	5		64.5	3.669	YC	2.50E-02	1.75E-03		2.29E-06	1.34	1.52		1.99
rc_AA875032_at	Y	T	5		128.7	6.642	YT	2.51E-04	3.63E-03	2.29E-06		1.48	1.31	1.99	
rc_AA875084_at	O	C	5		79.3	9.492	OC		1.08E-01	6.58E-01	5.77E-06		1.68	1.22	3.66
rc_AA875084_at	O	T	5		133.4	12.570	OT	1.08E-01		4.70E-02	1.51E-04	1.68		2.06	2.18
rc_AA875084_at	Y	C	5		64.9	5.372	YC	6.58E-01	4.70E-02		2.60E-06	1.22	2.06		4.47
rc_AA875084_at	Y	T	5		290.3	41.827	YT	5.77E-06	1.51E-04	2.60E-06		3.66	2.18	4.47	
rc_AA875531_s_at	O	C	5		470.4	36.905	OC		8.94E-01	4.16E-09	1.56E-03		1.08	7.41	3.13
rc_AA875531_s_at	O	T	5		434.9	71.595	OT	8.94E-01		3.52E-09	1.17E-03	1.08		8.01	3.39
rc_AA875531_s_at	Y	C	5		3483.6	328.341	YC	4.16E-09	3.52E-09		1.03E-06	7.41	8.01		2.36
rc_AA875531_s_at	Y	T	5		1473.7	157.369	YT	1.56E-03	1.17E-03	1.03E-06		3.13	3.39	2.36	
rc_AA891314_at	O	C	5		584.0	22.062	OC		3.42E-02	1.01E-04	4.55E-02		1.28	1.48	1.25
rc_AA891314_at	O	T	5		457.6	15.562	OT	3.42E-02		1.39E-06	8.85E-01	1.28		1.89	1.02
rc_AA891314_at	Y	C	5		864.0	69.297	YC	1.01E-04	1.39E-06		1.79E-06	1.48	1.89		1.86
rc_AA891314_at	Y	T	5		465.6	20.731	YT	4.55E-02	8.85E-01	1.79E-06		1.25	1.02	1.86	
rc_AA891790_at	O	C	5		71.3	3.318	OC		2.85E-03	7.95E-02	2.99E-08		1.44	1.23	2.24
rc_AA891790_at	O	T	5		102.5	6.089	OT	2.85E-03		1.19E-01	8.45E-06	1.44		1.17	1.56
rc_AA891790_at	Y	C	5		87.9	9.203	YC	7.95E-02	1.19E-01		4.98E-07	1.23	1.17		1.81
rc_AA891790_at	Y	T	5		159.5	4.970	YT	2.99E-08	8.45E-06	4.98E-07		2.24	1.56	1.81	
rc_AA892234_at	O	C	5		2618.0	147.643	OC		1.42E-03	9.55E-04	3.94E-05		1.58	1.39	2.16
rc_AA892234_at	O	T	5		1651.8	184.959	OT	1.42E-03		6.68E-07	9.80E-02	1.58		2.20	1.36
rc_AA892234_at	Y	C	5		3631.4	235.672	YC	9.55E-04	6.68E-07		4.54E-08	1.39	2.20		3.00
rc_AA892234_at	Y	T	5		1210.7	120.374	YT	3.94E-05	9.80E-02	4.54E-08		2.16	1.36	3.00	
rc_AA892314_at	O	C	5		126.1	12.960	OC		1.23E-01	5.59E-01	1.12E-05		1.30	1.12	2.15
rc_AA892314_at	O	T	5		163.8	15.972	OT	1.23E-01		4.10E-02	2.70E-04	1.30		1.46	1.66
rc_AA892314_at	Y	C	5		112.3	11.479	YC	5.59E-01	4.10E-02		3.79E-06	1.12	1.46		2.42
rc_AA892314_at	Y	T	5		271.5	22.809	YT	1.12E-05	2.70E-04	3.79E-06		2.15	1.66	2.42	
rc_AA893185_at	O	C	5		1016.8	26.278	OC		1.78E-06	5.59E-07	4.90E-08		1.57	1.40	1.91
rc_AA893185_at	O	T	5		647.2	24.359	OT	1.78E-06		5.70E-11	3.60E-02	1.57		2.20	1.22
rc_AA893185_at	Y	C	5		1421.6	57.480	YC	5.59E-07	5.70E-11		6.89E-12	1.40	2.20		2.68
rc_AA893185_at	Y	T	5		531.4	23.183	YT	4.90E-08	3.60E-02	6.89E-12		1.91	1.22	2.68	
rc_AA900199_s_at	O	C	5		500.6	43.267	OC		6.97E-01	3.42E-05	1.44E-01		1.03	1.48	1.15
rc_AA900199_s_at	O	T	5		483.9	19.480	OT	6.97E-01		1.61E-05	2.71E-01	1.03		1.53	1.11
rc_AA900199_s_at	Y	C	5		741.2	24.071	YC	3.42E-05	1.61E-05		2.06E-06	1.48	1.53		1.70
rc_AA900199_s_at	Y	T	5		435.6	27.500	YT	1.44E-01	2.71E-01	2.06E-06		1.15	1.11	1.70	
rc_AA924326_s_at	O	C	5		5306.1	160.595	OC		4.69E-01	6.68E-03	1.42E-04		1.06	1.31	1.38
rc_AA924326_s_at	O	T	5		5607.0	178.300	OT	4.69E-01		1.40E-03	6.53E-04	1.06		1.39	1.31
rc_AA924326_s_at	Y	C	5		4042.8	74.103	YC	6.68E-03	1.40E-03		4.92E-07	1.31	1.39		1.81
rc_AA924326_s_at	Y	T	5		7318.2	515.846	YT	1.42E-04	6.53E-04	4.92E-07		1.38	1.31	1.81	
rc_AA946040_at	O	C	5		1187.1	63.384	OC		3.00E-02	8.80E-04	2.61E-05		1.15	1.22	1.46
rc_AA946040_at	O	T	5		1034.8	22.235	OT	3.00E-02		7.91E-06	3.38E-03	1.15		1.40	1.27
rc_AA946040_at	Y	C	5		1447.7	52.445	YC	8.80E-04	7.91E-06		3.18E-08	1.22	1.40		1.78
rc_AA946040_at	Y	T	5		815.1	30.168	YT	2.61E-05	3.38E-03	3.18E-08		1.46	1.27	1.78	

rc_AA946313_s_at	O	C	5		177.5	9.449	OC		8.17E-01	3.68E-07	7.47E-03		1.13	5.56	2.69
rc_AA946313_s_at	O	T	5		200.5	19.825	OT	8.17E-01		5.37E-07	1.22E-02	1.13		4.92	2.38
rc_AA946313_s_at	Y	C	5		986.2	135.012	YC	3.68E-07	5.37E-07		8.86E-05	5.56	4.92		2.07
rc_AA946313_s_at	Y	T	5		477.4	21.976	YT	7.47E-03	1.22E-02	8.86E-05		2.69	2.38	2.07	
rc_AA963839_s_at	O	C	5		300.1	14.734	OC		1.45E-05	1.89E-02	1.44E-01		1.53	1.29	1.15
rc_AA963839_s_at	O	T	5		460.5	21.935	OT	1.45E-05		1.72E-07	9.59E-07	1.53		1.99	1.77
rc_AA963839_s_at	Y	C	5		231.8	22.662	YC	1.89E-02	1.72E-07		2.98E-01	1.29	1.99		1.12
rc_AA963839_s_at	Y	T	5		259.9	12.503	YT	1.44E-01	9.59E-07	2.98E-01		1.15	1.77	1.12	
rc_AA964320_at	O	C	5		6040.2	163.786	OC		3.30E-04	2.38E-01	6.80E-08		1.24	1.05	1.68
rc_AA964320_at	O	T	5		4858.0	227.362	OT	3.30E-04		2.86E-05	1.90E-04	1.24		1.31	1.35
rc_AA964320_at	Y	C	5		6358.6	136.766	YC	2.38E-01	2.86E-05		1.23E-08	1.05	1.31		1.76
rc_AA964320_at	Y	T	5		3605.8	194.822	YT	6.80E-08	1.90E-04	1.23E-08		1.68	1.35	1.76	
rc_AI010581_at	O	C	5		519.7	18.223	OC		1.08E-02	1.96E-01	1.25E-08		1.19	1.08	2.49
rc_AI010581_at	O	T	5		435.1	26.424	OT	1.08E-02		6.34E-04	9.13E-07	1.19		1.29	2.08
rc_AI010581_at	Y	C	5		559.4	24.559	YC	1.96E-01	6.34E-04		2.24E-09	1.08	1.29		2.68
rc_AI010581_at	Y	T	5		209.0	9.573	YT	1.25E-08	9.13E-07	2.24E-09		2.49	2.08	2.68	
rc_AI071578_at	O	C	5		576.8	76.007	OC		3.92E-01	8.12E-09	7.30E-02		1.35	4.18	1.56
rc_AI071578_at	O	T	5		428.6	68.728	OT	3.92E-01		2.67E-09	1.29E-02	1.35		5.63	2.10
rc_AI071578_at	Y	C	5		2413.2	188.835	YC	8.12E-09	2.67E-09		1.19E-07	4.18	5.63		2.68
rc_AI071578_at	Y	T	5		900.0	102.730	YT	7.30E-02	1.29E-02	1.19E-07		1.56	2.10	2.68	
rc_AI071578_g_at	O	C	5		138.3	16.319	OC		4.59E-01	4.20E-07	1.01E-01		1.41	4.15	1.67
rc_AI071578_g_at	O	T	5		97.8	14.800	OT	4.59E-01		1.29E-07	2.36E-02	1.41		5.87	2.36
rc_AI071578_g_at	Y	C	5		574.4	66.495	YC	4.20E-07	1.29E-07		8.33E-06	4.15	5.87		2.48
rc_AI071578_g_at	Y	T	5		231.3	28.089	YT	1.01E-01	2.36E-02	8.33E-06		1.67	2.36	2.48	
rc_AI073178_at	O	C	5		3312.9	120.076	OC		2.79E-03	1.33E-02	1.32E-05		1.24	1.23	1.41
rc_AI073178_at	O	T	5		4092.7	198.692	OT	2.79E-03		1.04E-05	1.74E-02	1.24		1.52	1.14
rc_AI073178_at	Y	C	5		2697.9	117.542	YC	1.33E-02	1.04E-05		1.23E-07	1.23	1.52		1.73
rc_AI073178_at	Y	T	5		4679.0	173.242	YT	1.32E-05	1.74E-02	1.23E-07		1.41	1.14	1.73	
rc_AI101157_at	O	C	5		4217.6	147.846	OC		3.05E-02	2.65E-02	4.08E-04		1.19	1.17	1.44
rc_AI101157_at	O	T	5		3532.8	123.069	OT	3.05E-02		1.90E-04	5.49E-02	1.19		1.39	1.20
rc_AI101157_at	Y	C	5		4922.7	291.902	YC	2.65E-02	1.90E-04		3.65E-06	1.17	1.39		1.68
rc_AI101157_at	Y	T	5		2935.3	210.441	YT	4.08E-04	5.49E-02	3.65E-06		1.44	1.20	1.68	
rc_AI101343_at	O	C	5		180.6	6.468	OC		1.54E-01	6.54E-02	1.01E-04		1.08	1.09	1.32
rc_AI101343_at	O	T	5		168.0	4.996	OT	1.54E-01		3.13E-03	2.24E-03	1.08		1.18	1.22
rc_AI101343_at	Y	C	5		197.4	5.999	YC	6.54E-02	3.13E-03		2.49E-06	1.09	1.18		1.44
rc_AI101343_at	Y	T	5		137.2	6.362	YT	1.01E-04	2.24E-03	2.49E-06		1.32	1.22	1.44	
rc_AI101443_i_at	O	C	5		352.8	16.292	OC		7.64E-01	4.24E-07	2.31E-01		1.33	7.56	2.00
rc_AI101443_i_at	O	T	5		266.2	33.431	OT	7.64E-01		2.62E-07	1.41E-01	1.33		###	2.65
rc_AI101443_i_at	Y	C	5		2667.9	386.911	YC	4.24E-07	2.62E-07		3.44E-06	7.56	###		3.78
rc_AI101443_i_at	Y	T	5		705.6	98.199	YT	2.31E-01	1.41E-01	3.44E-06		2.00	2.65	3.78	
rc_AI101443_r_at	O	C	5		1098.3	68.065	OC		7.57E-01	2.58E-07	6.24E-02		1.23	6.09	2.20
rc_AI101443_r_at	O	T	5		891.0	117.334	OT	7.57E-01		1.59E-07	3.41E-02	1.23		7.50	2.71
rc_AI101443_r_at	Y	C	5		6685.6	867.664	YC	2.58E-07	1.59E-07		7.64E-06	6.09	7.50		2.76
rc_AI101443_r_at	Y	T	5		2418.0	311.550	YT	6.24E-02	3.41E-02	7.64E-06		2.20	2.71	2.76	
rc_AI101443_s_at	O	C	5		2654.5	146.311	OC		2.80E-01	9.05E-10	2.46E-03		1.39	4.17	1.90

rc_AI101443_s_at	O	T	5		1913.9	330.797	OT	2.80E-01		2.61E-10	2.38E-04	1.39		5.78	2.63
rc_AI101443_s_at	Y	C	5		11070.4	733.332	YC	9.05E-10	2.61E-10		9.91E-08	4.17	5.78		2.20
rc_AI101443_s_at	Y	T	5		5032.7	458.498	YT	2.46E-03	2.38E-04	9.91E-08		1.90	2.63	2.20	
rc_AI102715_at	O	C	5		629.4	21.386	OC		4.30E-07	3.29E-03	1.08E-08		1.45	1.13	1.69
rc_AI102715_at	O	T	5		432.7	13.594	OT	4.30E-07		3.32E-09	2.21E-02	1.45		1.65	1.16
rc_AI102715_at	Y	C	5		712.6	20.352	YC	3.29E-03	3.32E-09		1.84E-10	1.13	1.65		1.92
rc_AI102715_at	Y	T	5		371.6	10.323	YT	1.08E-08	2.21E-02	1.84E-10		1.69	1.16	1.92	
rc_AI103500_f_at	O	C	5		963.9	37.328	OC		7.58E-04	4.81E-07	8.01E-06		1.29	1.80	1.55
rc_AI103500_f_at	O	T	5		744.8	54.014	OT	7.58E-04		1.17E-03	3.50E-02	1.29		1.39	1.20
rc_AI103500_f_at	Y	C	5		536.6	29.007	YC	4.81E-07	1.17E-03		1.21E-01	1.80	1.39		1.16
rc_AI103500_f_at	Y	T	5		623.0	20.778	YT	8.01E-06	3.50E-02	1.21E-01		1.55	1.20	1.16	
rc_AI103774_at	O	C	5		288.4	10.840	OC		8.41E-09	4.05E-04	8.63E-09		1.73	1.21	1.73
rc_AI103774_at	O	T	5		166.8	4.391	OT	8.41E-09		8.31E-06	9.85E-01	1.73		1.43	1.00
rc_AI103774_at	Y	C	5		238.7	5.330	YC	4.05E-04	8.31E-06		8.62E-06	1.21	1.43		1.43
rc_AI103774_at	Y	T	5		167.1	9.195	YT	8.63E-09	9.85E-01	8.62E-06		1.73	1.00	1.43	
rc_AI103851_at	O	C	5		2794.0	125.806	OC		3.82E-04	1.33E-03	7.57E-05		1.46	1.27	1.59
rc_AI103851_at	O	T	5		1910.8	98.800	OT	3.82E-04		3.14E-07	4.37E-01	1.46		1.86	1.09
rc_AI103851_at	Y	C	5		3559.7	214.916	YC	1.33E-03	3.14E-07		9.27E-08	1.27	1.86		2.03
rc_AI103851_at	Y	T	5		1753.3	78.192	YT	7.57E-05	4.37E-01	9.27E-08		1.59	1.09	2.03	
rc_AI104035_s_at	O	C	5		4297.4	152.403	OC		5.88E-04	1.03E-02	6.32E-06		1.30	1.16	1.56
rc_AI104035_s_at	O	T	5		3300.2	120.967	OT	5.88E-04		2.20E-06	3.44E-02	1.30		1.51	1.20
rc_AI104035_s_at	Y	C	5		4976.6	190.957	YC	1.03E-02	2.20E-06		5.68E-08	1.16	1.51		1.80
rc_AI104035_s_at	Y	T	5		2760.0	186.600	YT	6.32E-06	3.44E-02	5.68E-08		1.56	1.20	1.80	
rc_AI104244_s_at	O	C	5		2278.6	58.623	OC		1.46E-01	7.51E-07	8.31E-04		1.06	1.30	1.19
rc_AI104244_s_at	O	T	5		2143.6	60.328	OT	1.46E-01		7.01E-08	2.04E-02	1.06		1.39	1.12
rc_AI104244_s_at	Y	C	5		2969.1	76.263	YC	7.51E-07	7.01E-08		2.27E-09	1.30	1.39		1.55
rc_AI104244_s_at	Y	T	5		1916.1	52.157	YT	8.31E-04	2.04E-02	2.27E-09		1.19	1.12	1.55	
rc_AI104393_at	O	C	5		1367.1	81.413	OC		2.71E-04	5.91E-01	2.41E-08		1.69	1.08	2.50
rc_AI104393_at	O	T	5		2308.0	125.833	OT	2.71E-04		8.47E-04	5.31E-05	1.69		1.56	1.48
rc_AI104393_at	Y	C	5		1478.1	120.772	YC	5.91E-01	8.47E-04		5.21E-08	1.08	1.56		2.31
rc_AI104393_at	Y	T	5		3413.5	212.453	YT	2.41E-08	5.31E-05	5.21E-08		2.50	1.48	2.31	
rc_AI104567_g_at	O	C	5		1538.6	89.168	OC		1.27E-10	2.00E-07	5.27E-11		6.27	2.00	9.21
rc_AI104567_g_at	O	T	5		245.2	31.602	OT	1.27E-10		2.44E-05	3.94E-01	6.27		3.13	1.47
rc_AI104567_g_at	Y	C	5		767.5	81.818	YC	2.00E-07	2.44E-05		4.82E-06	2.00	3.13		4.59
rc_AI104567_g_at	Y	T	5		167.1	16.386	YT	5.27E-11	3.94E-01	4.82E-06		9.21	1.47	4.59	
rc_AI104913_at	O	C	5		396.9	39.687	OC		7.40E-02	6.32E-02	6.54E-06		1.23	1.32	1.79
rc_AI104913_at	O	T	5		488.2	41.894	OT	7.40E-02		1.25E-03	2.67E-04	1.23		1.62	1.46
rc_AI104913_at	Y	C	5		301.5	11.295	YC	6.32E-02	1.25E-03		2.29E-07	1.32	1.62		2.36
rc_AI104913_at	Y	T	5		710.4	33.269	YT	6.54E-06	2.67E-04	2.29E-07		1.79	1.46	2.36	
rc_AI104953_s_at	O	C	5		2677.9	96.155	OC		1.03E-03	1.29E-01	6.35E-06		1.50	1.13	2.20
rc_AI104953_s_at	O	T	5		1789.1	104.193	OT	1.03E-03		3.97E-05	2.03E-02	1.50		1.70	1.47
rc_AI104953_s_at	Y	C	5		3033.0	234.490	YC	1.29E-01	3.97E-05		4.17E-07	1.13	1.70		2.49
rc_AI104953_s_at	Y	T	5		1217.2	153.433	YT	6.35E-06	2.03E-02	4.17E-07		2.20	1.47	2.49	
rc_AI105149_at	O	C	5		1314.3	23.903	OC		5.51E-04	2.08E-01	8.34E-07		1.22	1.05	1.48
rc_AI105149_at	O	T	5		1078.4	16.204	OT	5.51E-04		3.90E-05	3.29E-03	1.22		1.29	1.21

rc_AI105149_at	Y	C	5		1386.2	53.469	YC	2.08E-01	3.90E-05		1.06E-07	1.05	1.29		1.56
rc_AI105149_at	Y	T	5		889.0	48.242	YT	8.34E-07	3.29E-03	1.06E-07		1.48	1.21	1.56	
rc_AI105188_at	O	C	5		222.6	6.290	OC		5.08E-02	2.56E-02	6.40E-04		1.18	1.26	1.35
rc_AI105188_at	O	T	5		261.9	20.841	OT	5.08E-02		3.13E-04	5.03E-02	1.18		1.48	1.15
rc_AI105188_at	Y	C	5		176.9	9.289	YC	2.56E-02	3.13E-04		5.21E-06	1.26	1.48		1.70
rc_AI105188_at	Y	T	5		301.3	11.473	YT	6.40E-04	5.03E-02	5.21E-06		1.35	1.15	1.70	
rc_AI105435_at	O	C	5		284.4	5.198	OC		3.11E-01	4.69E-07	8.10E-12		1.06	1.50	2.07
rc_AI105435_at	O	T	5		302.8	18.463	OT	3.11E-01		2.71E-06	2.08E-11	1.06		1.41	1.95
rc_AI105435_at	Y	C	5		426.7	12.560	YC	4.69E-07	2.71E-06		7.52E-08	1.50	1.41		1.38
rc_AI105435_at	Y	T	5		590.0	9.550	YT	8.10E-12	2.08E-11	7.52E-08		2.07	1.95	1.38	
rc_AI105451_at	O	C	5		100.8	5.656	OC		3.70E-04	5.88E-02	7.14E-08		1.67	1.44	2.39
rc_AI105451_at	O	T	5		168.5	10.044	OT	3.70E-04		6.99E-06	1.81E-04	1.67		2.40	1.43
rc_AI105451_at	Y	C	5		70.2	9.207	YC	5.88E-02	6.99E-06		4.50E-09	1.44	2.40		3.44
rc_AI105451_at	Y	T	5		241.4	15.361	YT	7.14E-08	1.81E-04	4.50E-09		2.39	1.43	3.44	
rc_AI137210_at	O	C	5		688.3	33.850	OC		1.26E-03	4.28E-02	4.09E-06		1.25	1.11	1.53
rc_AI137210_at	O	T	5		551.6	25.421	OT	1.26E-03		1.51E-05	1.01E-02	1.25		1.39	1.23
rc_AI137210_at	Y	C	5		765.4	22.045	YC	4.28E-02	1.51E-05		1.12E-07	1.11	1.39		1.70
rc_AI137210_at	Y	T	5		449.5	13.123	YT	4.09E-06	1.01E-02	1.12E-07		1.53	1.23	1.70	
rc_AI137344_at	O	C	5		124.1	16.371	OC		5.05E-04	9.03E-01	8.82E-10		1.92	1.03	3.70
rc_AI137344_at	O	T	5		238.6	21.775	OT	5.05E-04		3.90E-04	3.03E-07	1.92		1.97	1.93
rc_AI137344_at	Y	C	5		120.8	8.153	YC	9.03E-01	3.90E-04		7.64E-10	1.03	1.97		3.80
rc_AI137344_at	Y	T	5		459.5	24.123	YT	8.82E-10	3.03E-07	7.64E-10		3.70	1.93	3.80	
rc_AI137553_at	O	C	5		348.3	24.943	OC		2.77E-10	8.08E-07	2.76E-11		4.78	1.81	###
rc_AI137553_at	O	T	5		72.9	12.540	OT	2.77E-10		1.89E-05	3.59E-02	4.78		2.64	2.69
rc_AI137553_at	Y	C	5		192.8	4.134	YC	8.08E-07	1.89E-05		3.54E-07	1.81	2.64		7.12
rc_AI137553_at	Y	T	5		27.1	2.131	YT	2.76E-11	3.59E-02	3.54E-07		###	2.69	7.12	
rc_AI137579_at	O	C	5		125.1	12.150	OC		3.55E-03	5.22E-02	3.21E-09		1.79	1.49	3.70
rc_AI137579_at	O	T	5		224.1	18.267	OT	3.55E-03		2.06E-01	3.88E-07	1.79		1.21	2.06
rc_AI137579_at	Y	C	5		185.9	10.382	YC	5.22E-02	2.06E-01		5.27E-08	1.49	1.21		2.49
rc_AI137579_at	Y	T	5		462.6	33.063	YT	3.21E-09	3.88E-07	5.27E-08		3.70	2.06	2.49	
rc_AI144692_at	O	C	5		130.0	18.951	OC		5.38E-02	1.50E-01	1.22E-07		1.56	1.41	3.42
rc_AI144692_at	O	T	5		203.1	21.904	OT	5.38E-02		5.78E-01	3.64E-06	1.56		1.11	2.19
rc_AI144692_at	Y	C	5		183.1	26.481	YC	1.50E-01	5.78E-01		1.36E-06	1.41	1.11		2.43
rc_AI144692_at	Y	T	5		444.8	30.357	YT	1.22E-07	3.64E-06	1.36E-06		3.42	2.19	2.43	
rc_AI168941_at	O	C	5		178.5	12.925	OC		3.57E-04	5.33E-07	2.27E-05		1.87	1.83	2.55
rc_AI168941_at	O	T	5		95.4	7.597	OT	3.57E-04		1.09E-09	1.86E-01	1.87		3.42	1.36
rc_AI168941_at	Y	C	5		326.2	18.646	YC	5.33E-07	1.09E-09		2.34E-10	1.83	3.42		4.66
rc_AI168941_at	Y	T	5		70.0	10.275	YT	2.27E-05	1.86E-01	2.34E-10		2.55	1.36	4.66	
rc_AI169053_at	O	C	5		460.0	25.242	OC		2.84E-03	5.22E-02	2.87E-08		1.51	1.30	2.45
rc_AI169053_at	O	T	5		695.4	33.637	OT	2.84E-03		1.74E-01	8.04E-06	1.51		1.16	1.62
rc_AI169053_at	Y	C	5		600.2	32.587	YC	5.22E-02	1.74E-01		6.83E-07	1.30	1.16		1.88
rc_AI169053_at	Y	T	5		1126.5	78.164	YT	2.87E-08	8.04E-06	6.83E-07		2.45	1.62	1.88	
rc_AI169228_at	O	C	5		157.2	6.656	OC		2.98E-02	1.39E-03	1.09E-03		1.13	1.18	1.23
rc_AI169228_at	O	T	5		139.4	5.906	OT	2.98E-02		1.17E-05	1.32E-01	1.13		1.33	1.09
rc_AI169228_at	Y	C	5		185.8	3.365	YC	1.39E-03	1.17E-05		7.30E-07	1.18	1.33		1.46

rc_AI169228_at	Y	T	5		127.6	4.465	YT	1.09E-03	1.32E-01	7.30E-07		1.23	1.09	1.46	
rc_AI169831_at	O	C	5		299.7	13.590	OC		2.78E-06	6.35E-04	2.66E-06		2.92	1.65	2.94
rc_AI169831_at	O	T	5		102.7	11.237	OT	2.78E-06		1.26E-02	9.80E-01	2.92		1.77	1.01
rc_AI169831_at	Y	C	5		181.3	34.572	YC	6.35E-04	1.26E-02		1.19E-02	1.65	1.77		1.78
rc_AI169831_at	Y	T	5		102.0	7.586	YT	2.66E-06	9.80E-01	1.19E-02		2.94	1.01	1.78	
rc_AI170613_g_at	O	C	5		668.0	28.507	OC		4.35E-02	2.63E-03	2.48E-03		1.13	1.18	1.22
rc_AI170613_g_at	O	T	5		593.7	12.995	OT	4.35E-02		2.98E-05	1.83E-01	1.13		1.33	1.09
rc_AI170613_g_at	Y	C	5		788.5	32.180	YC	2.63E-03	2.98E-05		2.34E-06	1.18	1.33		1.44
rc_AI170613_g_at	Y	T	5		546.6	16.636	YT	2.48E-03	1.83E-01	2.34E-06		1.22	1.09	1.44	
rc_AI170709_at	O	C	5		615.3	34.225	OC		3.24E-02	1.30E-02	4.56E-04		1.25	1.43	1.47
rc_AI170709_at	O	T	5		770.6	61.101	OT	3.24E-02		9.93E-05	5.73E-02	1.25		1.79	1.18
rc_AI170709_at	Y	C	5		429.9	33.925	YC	1.30E-02	9.93E-05		2.17E-06	1.43	1.79		2.11
rc_AI170709_at	Y	T	5		906.4	52.354	YT	4.56E-04	5.73E-02	2.17E-06		1.47	1.18	2.11	
rc_AI170770_at	O	C	5		2337.4	65.545	OC		3.03E-05	7.55E-02	3.14E-08		1.30	1.08	1.67
rc_AI170770_at	O	T	5		1793.1	88.447	OT	3.03E-05		9.98E-07	7.36E-04	1.30		1.40	1.28
rc_AI170770_at	Y	C	5		2517.6	67.231	YC	7.55E-02	9.98E-07		2.61E-09	1.08	1.40		1.80
rc_AI170770_at	Y	T	5		1398.7	36.510	YT	3.14E-08	7.36E-04	2.61E-09		1.67	1.28	1.80	
rc_AI170775_at	O	C	5		5380.5	130.385	OC		1.64E-09	3.43E-03	6.86E-12		2.37	1.16	6.00
rc_AI170775_at	O	T	5		2273.8	247.777	OT	1.64E-09		4.16E-11	5.87E-05	2.37		2.75	2.54
rc_AI170775_at	Y	C	5		6254.9	204.384	YC	3.43E-03	4.16E-11		4.44E-13	1.16	2.75		6.97
rc_AI170775_at	Y	T	5		896.8	98.910	YT	6.86E-12	5.87E-05	4.44E-13		6.00	2.54	6.97	
rc_AI170777_at	O	C	5		5434.3	138.750	OC		3.41E-02	4.38E-04	7.34E-03		1.15	1.25	1.21
rc_AI170777_at	O	T	5		4718.5	206.290	OT	3.41E-02		4.87E-06	4.62E-01	1.15		1.44	1.05
rc_AI170777_at	Y	C	5		6797.2	349.369	YC	4.38E-04	4.87E-06		1.31E-06	1.25	1.44		1.52
rc_AI170777_at	Y	T	5		4485.8	84.740	YT	7.34E-03	4.62E-01	1.31E-06		1.21	1.05	1.52	
rc_AI170777_g_at	O	C	5		3411.3	52.832	OC		3.22E-03	3.07E-05	6.73E-03		1.18	1.26	1.16
rc_AI170777_g_at	O	T	5		2885.6	98.367	OT	3.22E-03		8.69E-08	7.30E-01	1.18		1.48	1.02
rc_AI170777_g_at	Y	C	5		4282.5	166.649	YC	3.07E-05	8.69E-08		1.47E-07	1.26	1.48		1.46
rc_AI170777_g_at	Y	T	5		2938.9	76.812	YT	6.73E-03	7.30E-01	1.47E-07		1.16	1.02	1.46	
rc_AI170847_at	O	C	5		5250.2	394.113	OC		5.38E-07	9.10E-02	8.08E-09		3.02	1.15	11.13
rc_AI170847_at	O	T	5		1737.9	415.893	OT	5.38E-07		3.55E-08	1.07E-02	3.02		3.47	3.68
rc_AI170847_at	Y	C	5		6037.8	229.693	YC	9.10E-02	3.55E-08		8.94E-10	1.15	3.47		###
rc_AI170847_at	Y	T	5		471.9	51.888	YT	8.08E-09	1.07E-02	8.94E-10		11.13	3.68	###	
rc_AI170956_at	O	C	5		398.4	35.983	OC		2.15E-03	1.54E-04	4.53E-04		1.79	1.59	2.13
rc_AI170956_at	O	T	5		222.7	21.688	OT	2.15E-03		2.24E-07	4.68E-01	1.79		2.85	1.19
rc_AI170956_at	Y	C	5		635.2	53.086	YC	1.54E-04	2.24E-07		7.32E-08	1.59	2.85		3.40
rc_AI170956_at	Y	T	5		186.9	7.122	YT	4.53E-04	4.68E-01	7.32E-08		2.13	1.19	3.40	
rc_AI171350_at	O	C	5		309.9	22.952	OC		4.26E-02	7.69E-07	2.95E-01		1.19	1.56	1.08
rc_AI171350_at	O	T	5		260.8	9.856	OT	4.26E-02		2.74E-08	2.80E-01	1.19		1.86	1.10
rc_AI171350_at	Y	C	5		483.9	14.704	YC	7.69E-07	2.74E-08		1.39E-07	1.56	1.86		1.69
rc_AI171350_at	Y	T	5		285.7	12.468	YT	2.95E-01	2.80E-01	1.39E-07		1.08	1.10	1.69	
rc_AI171448_at	O	C	5		979.8	69.213	OC		7.25E-04	1.09E-02	4.45E-05		1.50	1.23	1.81
rc_AI171448_at	O	T	5		651.0	30.226	OT	7.25E-04		2.76E-06	1.88E-01	1.50		1.85	1.20
rc_AI171448_at	Y	C	5		1206.9	78.101	YC	1.09E-02	2.76E-06		2.82E-07	1.23	1.85		2.22
rc_AI171448_at	Y	T	5		542.5	25.255	YT	4.45E-05	1.88E-01	2.82E-07		1.81	1.20	2.22	

rc_AI171452_at	O	C	5		1363.7	65.181	OC		2.97E-06	8.28E-05	4.06E-06		2.17	1.40	2.11
rc_AI171452_at	O	T	5		629.1	52.797	OT	2.97E-06		1.55E-09	8.62E-01	2.17		3.04	1.03
rc_AI171452_at	Y	C	5		1912.0	107.994	YC	8.28E-05	1.55E-09		1.92E-09	1.40	3.04		2.95
rc_AI171452_at	Y	T	5		647.7	57.370	YT	4.06E-06	8.62E-01	1.92E-09		2.11	1.03	2.95	
rc_AI171587_at	O	C	5		407.3	15.895	OC		4.88E-05	1.95E-02	1.07E-06		1.55	1.35	1.77
rc_AI171587_at	O	T	5		633.1	35.555	OT	4.88E-05		4.79E-07	5.16E-02	1.55		2.11	1.14
rc_AI171587_at	Y	C	5		300.7	34.367	YC	1.95E-02	4.79E-07		2.10E-08	1.35	2.11		2.39
rc_AI171587_at	Y	T	5		719.5	26.052	YT	1.07E-06	5.16E-02	2.10E-08		1.77	1.14	2.39	
rc_AI171994_at	O	C	5		2083.0	61.055	OC		3.60E-03	8.97E-01	5.33E-07		1.16	1.01	1.49
rc_AI171994_at	O	T	5		1793.7	42.526	OT	3.60E-03		4.74E-03	2.86E-04	1.16		1.16	1.28
rc_AI171994_at	Y	C	5		2071.9	41.217	YC	8.97E-01	4.74E-03		6.60E-07	1.01	1.16		1.48
rc_AI171994_at	Y	T	5		1401.7	84.748	YT	5.33E-07	2.86E-04	6.60E-07		1.49	1.28	1.48	
rc_AI172057_at	O	C	5		477.7	22.942	OC		7.76E-02	8.51E-04	2.05E-10		1.16	1.36	2.23
rc_AI172057_at	O	T	5		556.4	23.634	OT	7.76E-02		4.24E-02	1.70E-09	1.16		1.17	1.91
rc_AI172057_at	Y	C	5		648.4	33.441	YC	8.51E-04	4.24E-02		2.94E-08	1.36	1.17		1.64
rc_AI172057_at	Y	T	5		1063.6	35.745	YT	2.05E-10	1.70E-09	2.94E-08		2.23	1.91	1.64	
rc_AI172308_at	O	C	5		455.4	14.893	OC		1.85E-04	5.99E-01	1.15E-07		1.34	1.04	1.64
rc_AI172308_at	O	T	5		612.3	23.419	OT	1.85E-04		6.30E-05	7.12E-04	1.34		1.40	1.22
rc_AI172308_at	Y	C	5		438.0	27.432	YC	5.99E-01	6.30E-05		5.24E-08	1.04	1.40		1.71
rc_AI172308_at	Y	T	5		748.0	24.252	YT	1.15E-07	7.12E-04	5.24E-08		1.64	1.22	1.71	
rc_AI172335_at	O	C	5		374.8	33.324	OC		7.12E-07	1.42E-09	1.67E-07		2.45	1.93	2.94
rc_AI172335_at	O	T	5		153.2	5.491	OT	7.12E-07		8.47E-13	3.74E-01	2.45		4.71	1.20
rc_AI172335_at	Y	C	5		722.5	18.540	YC	1.42E-09	8.47E-13		4.27E-13	1.93	4.71		5.67
rc_AI172335_at	Y	T	5		127.4	10.515	YT	1.67E-07	3.74E-01	4.27E-13		2.94	1.20	5.67	
rc_AI172411_at	O	C	5		1785.5	80.856	OC		1.99E-07	1.59E-03	5.48E-08		1.81	1.56	1.90
rc_AI172411_at	O	T	5		3238.9	109.785	OT	1.99E-07		1.22E-09	3.99E-01	1.81		2.82	1.04
rc_AI172411_at	Y	C	5		1147.6	113.336	YC	1.59E-03	1.22E-09		4.53E-10	1.56	2.82		2.95
rc_AI172411_at	Y	T	5		3384.5	158.342	YT	5.48E-08	3.99E-01	4.53E-10		1.90	1.04	2.95	
rc_AI172417_at	O	C	5		184.5	6.823	OC		6.77E-01	5.14E-02	8.38E-08		1.06	1.28	2.21
rc_AI172417_at	O	T	5		194.8	20.427	OT	6.77E-01		1.12E-01	1.58E-07	1.06		1.21	2.09
rc_AI172417_at	Y	C	5		235.3	14.633	YC	5.14E-02	1.12E-01		2.45E-06	1.28	1.21		1.73
rc_AI172417_at	Y	T	5		406.9	22.024	YT	8.38E-08	1.58E-07	2.45E-06		2.21	2.09	1.73	
rc_AI172471_at	O	C	5		6111.4	245.599	OC		5.47E-08	9.16E-04	3.79E-08		1.59	1.16	1.62
rc_AI172471_at	O	T	5		3839.2	109.758	OT	5.47E-08		3.40E-10	8.00E-01	1.59		1.84	1.02
rc_AI172471_at	Y	C	5		7080.4	190.128	YC	9.16E-04	3.40E-10		2.57E-10	1.16	1.84		1.87
rc_AI172471_at	Y	T	5		3777.6	74.731	YT	3.79E-08	8.00E-01	2.57E-10		1.62	1.02	1.87	
rc_AI175100_at	O	C	5		626.5	19.985	OC		4.72E-02	1.18E-01	1.87E-05		1.29	1.29	1.81
rc_AI175100_at	O	T	5		809.3	68.269	OT	4.72E-02		1.57E-03	1.43E-03	1.29		1.66	1.40
rc_AI175100_at	Y	C	5		486.1	49.506	YC	1.18E-01	1.57E-03		9.94E-07	1.29	1.66		2.34
rc_AI175100_at	Y	T	5		1136.1	83.361	YT	1.87E-05	1.43E-03	9.94E-07		1.81	1.40	2.34	
rc_AI175474_at	O	C	5		1262.2	54.727	OC		9.36E-02	2.56E-02	3.32E-04		1.17	1.30	1.43
rc_AI175474_at	O	T	5		1474.9	100.339	OT	9.36E-02		6.18E-04	1.39E-02	1.17		1.52	1.22
rc_AI175474_at	Y	C	5		968.5	87.310	YC	2.56E-02	6.18E-04		2.96E-06	1.30	1.52		1.86
rc_AI175474_at	Y	T	5		1804.4	88.258	YT	3.32E-04	1.39E-02	2.96E-06		1.43	1.22	1.86	
rc_AI175529_at	O	C	5		2147.9	89.194	OC		2.08E-06	1.83E-01	3.78E-03		1.89	1.10	1.28

rc_AI175529_at	O	T	5		1136.8	120.485	OT	2.08E-06		2.61E-05	1.49E-03	1.89		1.72	1.47
rc_AI175529_at	Y	C	5		1952.9	73.387	YC	1.83E-01	2.61E-05		6.35E-02	1.10	1.72		1.17
rc_AI175529_at	Y	T	5		1673.3	107.131	YT	3.78E-03	1.49E-03	6.35E-02		1.28	1.47	1.17	
rc_AI175594_at	O	C	5		51.9	2.875	OC		2.32E-03	2.39E-01	1.00E-06		1.39	1.15	1.82
rc_AI175594_at	O	T	5		71.9	4.427	OT	2.32E-03		1.81E-04	9.81E-04	1.39		1.59	1.31
rc_AI175594_at	Y	C	5		45.1	2.890	YC	2.39E-01	1.81E-04		1.43E-07	1.15	1.59		2.09
rc_AI175594_at	Y	T	5		94.2	5.020	YT	1.00E-06	9.81E-04	1.43E-07		1.82	1.31	2.09	
rc_AI175875_s_at	O	C	5		260.1	18.698	OC		2.53E-01	1.30E-06	9.94E-01		1.50	3.10	1.00
rc_AI175875_s_at	O	T	5		173.5	23.583	OT	2.53E-01		1.92E-07	2.50E-01	1.50		4.65	1.50
rc_AI175875_s_at	Y	C	5		806.7	97.075	YC	1.30E-06	1.92E-07		1.32E-06	3.10	4.65		3.09
rc_AI175875_s_at	Y	T	5		260.6	18.277	YT	9.94E-01	2.50E-01	1.32E-06		1.00	1.50	3.09	
rc_AI176362_at	O	C	5		488.1	55.343	OC		2.21E-04	2.98E-02	6.61E-07		1.50	1.34	1.84
rc_AI176362_at	O	T	5		733.2	36.399	OT	2.21E-04		2.40E-06	6.20E-03	1.50		2.01	1.22
rc_AI176362_at	Y	C	5		364.9	21.043	YC	2.98E-02	2.40E-06		1.88E-08	1.34	2.01		2.46
rc_AI176362_at	Y	T	5		896.0	22.615	YT	6.61E-07	6.20E-03	1.88E-08		1.84	1.22	2.46	
rc_AI176393_at	O	C	5		294.7	19.354	OC		3.08E-01	4.79E-08	7.45E-01		1.14	2.10	1.04
rc_AI176393_at	O	T	5		259.2	3.016	OT	3.08E-01		1.12E-08	1.85E-01	1.14		2.39	1.18
rc_AI176393_at	Y	C	5		618.5	34.739	YC	4.79E-08	1.12E-08		7.74E-08	2.10	2.39		2.02
rc_AI176393_at	Y	T	5		305.9	26.116	YT	7.45E-01	1.85E-01	7.74E-08		1.04	1.18	2.02	
rc_AI176500_at	O	C	5		37.3	4.701	OC		7.77E-02	1.63E-06	1.84E-01		1.36	2.03	1.24
rc_AI176500_at	O	T	5		27.4	1.509	OT	7.77E-02		8.18E-08	6.27E-01	1.36		2.77	1.09
rc_AI176500_at	Y	C	5		75.8	4.253	YC	1.63E-06	8.18E-08		1.72E-07	2.03	2.77		2.53
rc_AI176500_at	Y	T	5		30.0	3.533	YT	1.84E-01	6.27E-01	1.72E-07		1.24	1.09	2.53	
rc_AI176540_at	O	C	5		188.2	11.241	OC		2.65E-01	6.85E-08	7.01E-02		1.10	1.76	1.16
rc_AI176540_at	O	T	5		170.4	13.684	OT	2.65E-01		1.36E-08	6.95E-03	1.10		1.95	1.28
rc_AI176540_at	Y	C	5		332.1	9.484	YC	6.85E-08	1.36E-08		1.46E-06	1.76	1.95		1.52
rc_AI176540_at	Y	T	5		218.0	8.318	YT	7.01E-02	6.95E-03	1.46E-06		1.16	1.28	1.52	
rc_AI176595_s_at	O	C	5		579.1	23.208	OC		3.11E-06	7.78E-02	1.78E-08		1.91	1.33	2.35
rc_AI176595_s_at	O	T	5		1106.4	90.955	OT	3.11E-06		1.43E-07	4.18E-03	1.91		2.53	1.23
rc_AI176595_s_at	Y	C	5		436.7	28.314	YC	7.78E-02	1.43E-07		1.62E-09	1.33	2.53		3.11
rc_AI176595_s_at	Y	T	5		1358.6	42.511	YT	1.78E-08	4.18E-03	1.62E-09		2.35	1.23	3.11	
rc_AI176607_at	O	C	5		168.4	14.789	OC		7.19E-01	3.87E-02	1.04E-04		1.03	1.27	1.48
rc_AI176607_at	O	T	5		174.2	9.721	OT	7.19E-01		1.86E-02	2.19E-04	1.03		1.31	1.43
rc_AI176607_at	Y	C	5		132.9	7.824	YC	3.87E-02	1.86E-02		1.59E-06	1.27	1.31		1.87
rc_AI176607_at	Y	T	5		249.0	11.088	YT	1.04E-04	2.19E-04	1.59E-06		1.48	1.43	1.87	
rc_AI176621_at	O	C	5		170.3	8.726	OC		2.66E-04	9.84E-01	8.88E-09		1.42	1.00	1.97
rc_AI176621_at	O	T	5		241.3	9.826	OT	2.66E-04		2.55E-04	1.31E-05	1.42		1.42	1.39
rc_AI176621_at	Y	C	5		170.0	4.344	YC	9.84E-01	2.55E-04		8.64E-09	1.00	1.42		1.98
rc_AI176621_at	Y	T	5		335.7	16.570	YT	8.88E-09	1.31E-05	8.64E-09		1.97	1.39	1.98	
rc_AI176839_at	O	C	5		577.2	41.023	OC		6.10E-06	3.79E-01	2.08E-01		1.84	1.13	1.17
rc_AI176839_at	O	T	5		1063.0	66.190	OT	6.10E-06		1.26E-06	7.33E-05	1.84		2.08	1.58
rc_AI176839_at	Y	C	5		510.7	23.146	YC	3.79E-01	1.26E-06		4.16E-02	1.13	2.08		1.32
rc_AI176839_at	Y	T	5		673.7	65.051	YT	2.08E-01	7.33E-05	4.16E-02		1.17	1.58	1.32	
rc_AI176961_at	O	C	5		763.2	14.212	OC		4.34E-04	1.92E-02	8.61E-06		1.56	1.21	2.08
rc_AI176961_at	O	T	5		490.7	27.849	OT	4.34E-04		2.91E-06	6.32E-02	1.56		1.88	1.34

rc_AI176961_at	Y	C	5		923.9	79.607	YC	1.92E-02	2.91E-06		1.14E-07	1.21	1.88		2.51
rc_AI176961_at	Y	T	5		367.4	17.519	YT	8.61E-06	6.32E-02	1.14E-07		2.08	1.34	2.51	
rc_AI177543_at	O	C	5		528.5	46.016	OC		2.36E-02	1.91E-04	8.52E-02		1.42	1.57	1.28
rc_AI177543_at	O	T	5		372.9	46.486	OT	2.36E-02		1.73E-06	5.14E-01	1.42		2.22	1.11
rc_AI177543_at	Y	C	5		827.8	39.780	YC	1.91E-04	1.73E-06		5.60E-06	1.57	2.22		2.00
rc_AI177543_at	Y	T	5		414.4	43.260	YT	8.52E-02	5.14E-01	5.60E-06		1.28	1.11	2.00	
rc_AI177967_at	O	C	5		398.2	24.415	OC		1.07E-01	5.18E-07	2.74E-01		1.15	1.70	1.10
rc_AI177967_at	O	T	5		457.8	34.004	OT	1.07E-01		9.94E-06	5.73E-01	1.15		1.48	1.05
rc_AI177967_at	Y	C	5		678.6	18.518	YC	5.18E-07	9.94E-06		3.52E-06	1.70	1.48		1.55
rc_AI177967_at	Y	T	5		437.7	18.334	YT	2.74E-01	5.73E-01	3.52E-06		1.10	1.05	1.55	
rc_AI178764_at	O	C	5		351.4	8.444	OC		1.25E-02	6.01E-03	5.54E-04		1.30	1.26	1.55
rc_AI178764_at	O	T	5		270.2	23.207	OT	1.25E-02		1.93E-05	1.58E-01	1.30		1.64	1.19
rc_AI178764_at	Y	C	5		442.8	27.214	YC	6.01E-03	1.93E-05		1.35E-06	1.26	1.64		1.95
rc_AI178764_at	Y	T	5		227.4	17.784	YT	5.54E-04	1.58E-01	1.35E-06		1.55	1.19	1.95	
rc_AI178785_f_at	O	C	5		6551.3	229.046	OC		3.01E-07	5.21E-11	5.57E-12		1.63	3.42	5.55
rc_AI178785_f_at	O	T	5		4027.0	327.438	OT	3.01E-07		2.98E-06	6.01E-08	1.63		2.10	3.41
rc_AI178785_f_at	Y	C	5		1917.8	96.086	YC	5.21E-11	2.98E-06		2.64E-02	3.42	2.10		1.62
rc_AI178785_f_at	Y	T	5		1181.4	111.647	YT	5.57E-12	6.01E-08	2.64E-02		5.55	3.41	1.62	
rc_AI179147_at	O	C	5		1587.8	72.440	OC		2.37E-02	2.21E-03	1.01E-04		1.23	1.27	1.61
rc_AI179147_at	O	T	5		1295.2	99.358	OT	2.37E-02		1.43E-05	1.82E-02	1.23		1.55	1.31
rc_AI179147_at	Y	C	5		2014.0	92.320	YC	2.21E-03	1.43E-05		1.65E-07	1.27	1.55		2.04
rc_AI179147_at	Y	T	5		987.2	61.467	YT	1.01E-04	1.82E-02	1.65E-07		1.61	1.31	2.04	
rc_AI179840_at	O	C	5		402.1	16.692	OC		1.75E-03	4.69E-02	6.69E-06		1.32	1.23	1.56
rc_AI179840_at	O	T	5		530.9	18.475	OT	1.75E-03		2.22E-05	1.29E-02	1.32		1.62	1.18
rc_AI179840_at	Y	C	5		328.1	23.046	YC	4.69E-02	2.22E-05		1.83E-07	1.23	1.62		1.91
rc_AI179840_at	Y	T	5		627.0	34.759	YT	6.69E-06	1.29E-02	1.83E-07		1.56	1.18	1.91	
rc_AI179984_at	O	C	5		559.2	42.031	OC		3.57E-01	1.01E-06	6.61E-03		1.15	2.22	1.50
rc_AI179984_at	O	T	5		643.7	40.573	OT	3.57E-01		5.24E-06	4.53E-02	1.15		1.93	1.30
rc_AI179984_at	Y	C	5		1239.9	89.357	YC	1.01E-06	5.24E-06		3.53E-04	2.22	1.93		1.48
rc_AI179984_at	Y	T	5		837.3	67.159	YT	6.61E-03	4.53E-02	3.53E-04		1.50	1.30	1.48	
rc_AI180187_at	O	C	5		290.2	34.087	OC		7.00E-04	3.00E-01	7.61E-08		1.70	1.22	2.54
rc_AI180187_at	O	T	5		492.2	44.763	OT	7.00E-04		7.83E-05	1.07E-04	1.70		2.06	1.50
rc_AI180187_at	Y	C	5		238.5	10.954	YC	3.00E-01	7.83E-05		1.68E-08	1.22	2.06		3.10
rc_AI180187_at	Y	T	5		738.5	37.068	YT	7.61E-08	1.07E-04	1.68E-08		2.54	1.50	3.10	
rc_AI227672_at	O	C	5		148.6	5.244	OC		4.76E-02	6.92E-01	2.96E-07		1.28	1.05	2.10
rc_AI227672_at	O	T	5		190.2	14.267	OT	4.76E-02		1.01E-01	1.16E-05	1.28		1.22	1.64
rc_AI227672_at	Y	C	5		156.4	12.871	YC	6.92E-01	1.01E-01		5.63E-07	1.05	1.22		1.99
rc_AI227672_at	Y	T	5		311.5	18.872	YT	2.96E-07	1.16E-05	5.63E-07		2.10	1.64	1.99	
rc_AI228301_at	O	C	5		64.4	4.939	OC		6.55E-03	3.27E-05	7.67E-04		1.60	1.68	1.99
rc_AI228301_at	O	T	5		40.2	3.491	OT	6.55E-03		1.51E-07	3.24E-01	1.60		2.69	1.24
rc_AI228301_at	Y	C	5		108.4	8.555	YC	3.27E-05	1.51E-07		3.42E-08	1.68	2.69		3.35
rc_AI228301_at	Y	T	5		32.4	3.082	YT	7.67E-04	3.24E-01	3.42E-08		1.99	1.24	3.35	
rc_AI228484_at	O	C	5		149.1	13.051	OC		1.72E-03	2.05E-01	3.94E-07		1.53	1.23	2.15
rc_AI228484_at	O	T	5		227.7	10.009	OT	1.72E-03		1.12E-04	4.00E-04	1.53		1.88	1.41
rc_AI228484_at	Y	C	5		121.4	7.159	YC	2.05E-01	1.12E-04		5.33E-08	1.23	1.88		2.64



rc_AI228484_at	Y	T	5		320.9	23.536	YT	3.94E-07	4.00E-04	5.33E-08		2.15	1.41	2.64	
rc_AI229253_at	O	C	5		258.5	19.064	OC		1.43E-02	3.95E-01	1.24E-07		1.33	1.10	2.06
rc_AI229253_at	O	T	5		342.6	29.944	OT	1.43E-02		7.94E-02	1.24E-05	1.33		1.20	1.56
rc_AI229253_at	Y	C	5		285.2	19.471	YC	3.95E-01	7.94E-02		4.81E-07	1.10	1.20		1.87
rc_AI229253_at	Y	T	5		532.8	15.349	YT	1.24E-07	1.24E-05	4.81E-07		2.06	1.56	1.87	
rc_AI229440_s_at	O	C	5		773.5	30.879	OC		1.34E-05	7.79E-03	1.82E-01		1.37	1.22	1.09
rc_AI229440_s_at	O	T	5		1058.8	31.993	OT	1.34E-05		8.48E-08	1.13E-06	1.37		1.67	1.49
rc_AI229440_s_at	Y	C	5		632.9	42.673	YC	7.79E-03	8.48E-08		1.19E-01	1.22	1.67		1.12
rc_AI229440_s_at	Y	T	5		709.1	21.808	YT	1.82E-01	1.13E-06	1.19E-01		1.09	1.49	1.12	
rc_AI229497_at	O	C	5		1091.2	25.962	OC		4.34E-02	1.38E-01	7.04E-05		1.18	1.11	1.57
rc_AI229497_at	O	T	5		927.6	40.970	OT	4.34E-02		1.72E-03	6.65E-03	1.18		1.30	1.33
rc_AI229497_at	Y	C	5		1207.7	81.694	YC	1.38E-01	1.72E-03		3.75E-06	1.11	1.30		1.74
rc_AI229497_at	Y	T	5		695.2	45.784	YT	7.04E-05	6.65E-03	3.75E-06		1.57	1.33	1.74	
rc_AI229620_s_at	O	C	5		3742.7	181.785	OC		1.93E-03	5.84E-01	1.11E-06		1.26	1.03	1.74
rc_AI229620_s_at	O	T	5		2962.8	135.914	OT	1.93E-03		5.97E-04	1.34E-03	1.26		1.30	1.38
rc_AI229620_s_at	Y	C	5		3860.3	162.275	YC	5.84E-01	5.97E-04		4.43E-07	1.03	1.30		1.80
rc_AI229620_s_at	Y	T	5		2146.2	104.232	YT	1.11E-06	1.34E-03	4.43E-07		1.74	1.38	1.80	
rc_AI229680_at	O	C	5		1466.4	96.445	OC		2.77E-03	3.42E-04	1.22E-04		1.31	1.30	1.50
rc_AI229680_at	O	T	5		1122.6	73.107	OT	2.77E-03		5.02E-07	1.52E-01	1.31		1.70	1.15
rc_AI229680_at	Y	C	5		1907.2	46.733	YC	3.42E-04	5.02E-07		5.08E-08	1.30	1.70		1.95
rc_AI229680_at	Y	T	5		976.2	45.985	YT	1.22E-04	1.52E-01	5.08E-08		1.50	1.15	1.95	
rc_AI229849_at	O	C	5		1115.8	43.136	OC		5.68E-08	8.64E-04	1.25E-08		1.60	1.16	1.72
rc_AI229849_at	O	T	5		697.6	25.330	OT	5.68E-08		3.39E-10	2.92E-01	1.60		1.86	1.07
rc_AI229849_at	Y	C	5		1295.9	32.820	YC	8.64E-04	3.39E-10		1.08E-10	1.16	1.86		1.99
rc_AI229849_at	Y	T	5		649.6	17.506	YT	1.25E-08	2.92E-01	1.08E-10		1.72	1.07	1.99	
rc_AI230199_f_at	O	C	5		153.3	10.197	OC		7.41E-09	5.39E-02	9.12E-01		2.05	1.25	1.01
rc_AI230199_f_at	O	T	5		313.8	12.844	OT	7.41E-09		6.01E-10	6.41E-09	2.05		2.55	2.07
rc_AI230199_f_at	Y	C	5		122.9	8.338	YC	5.39E-02	6.01E-10		6.66E-02	1.25	2.55		1.23
rc_AI230199_f_at	Y	T	5		151.7	9.440	YT	9.12E-01	6.41E-09	6.66E-02		1.01	2.07	1.23	
rc_AI230208_at	O	C	5		351.8	16.317	OC		3.49E-04	2.86E-05	4.69E-03		1.41	1.37	1.27
rc_AI230208_at	O	T	5		248.7	16.284	OT	3.49E-04		1.84E-08	2.34E-01	1.41		1.94	1.11
rc_AI230208_at	Y	C	5		483.4	17.512	YC	2.86E-05	1.84E-08		1.07E-07	1.37	1.94		1.75
rc_AI230208_at	Y	T	5		276.9	14.214	YT	4.69E-03	2.34E-01	1.07E-07		1.27	1.11	1.75	
rc_AI230220_at	O	C	5		4013.3	250.322	OC		3.99E-10	1.42E-06	1.64E-10		8.80	1.49	###
rc_AI230220_at	O	T	5		455.8	39.375	OT	3.99E-10		5.01E-13	4.18E-01	8.80		13.13	1.94
rc_AI230220_at	Y	C	5		5982.7	276.053	YC	1.42E-06	5.01E-13		2.73E-13	1.49	13.13		###
rc_AI230220_at	Y	T	5		235.5	5.535	YT	1.64E-10	4.18E-01	2.73E-13		###	1.94	###	
rc_AI231292_at	O	C	5		2834.6	41.337	OC		7.94E-10	3.36E-04	1.17E-10		1.62	1.28	1.71
rc_AI231292_at	O	T	5		4598.7	82.623	OT	7.94E-10		8.47E-12	9.56E-02	1.62		2.08	1.05
rc_AI231292_at	Y	C	5		2209.6	120.007	YC	3.36E-04	8.47E-12		1.91E-12	1.28	2.08		2.19
rc_AI231292_at	Y	T	5		4842.6	122.453	YT	1.17E-10	9.56E-02	1.91E-12		1.71	1.05	2.19	
rc_AI231472_s_at	O	C	5		440.6	16.575	OC		8.33E-01	1.25E-06	1.17E-01		1.37	10.41	3.08
rc_AI231472_s_at	O	T	5		322.3	59.641	OT	8.33E-01		8.75E-07	7.97E-02	1.37		###	4.21
rc_AI231472_s_at	Y	C	5		4585.1	726.028	YC	1.25E-06	8.75E-07		2.46E-05	10.41	###		3.38
rc_AI231472_s_at	Y	T	5		1355.3	280.325	YT	1.17E-01	7.97E-02	2.46E-05		3.08	4.21	3.38	

rc_AI232313_at	O	C	5		241.8	8.778	OC		4.83E-03	2.55E-01	1.44E-06		1.30	1.12	1.67
rc_AI232313_at	O	T	5		313.5	8.883	OT	4.83E-03		4.05E-04	7.42E-04	1.30		1.45	1.29
rc_AI232313_at	Y	C	5		215.9	14.653	YC	2.55E-01	4.05E-04		2.13E-07	1.12	1.45		1.87
rc_AI232313_at	Y	T	5		404.7	24.331	YT	1.44E-06	7.42E-04	2.13E-07		1.67	1.29	1.87	
rc_AI232783_s_at	O	C	5		1521.5	73.621	OC		2.07E-03	9.59E-01	1.42E-08		1.58	1.01	2.66
rc_AI232783_s_at	O	T	5		2406.9	89.153	OT	2.07E-03		2.31E-03	4.17E-06	1.58		1.57	1.68
rc_AI232783_s_at	Y	C	5		1534.2	123.894	YC	9.59E-01	2.31E-03		1.52E-08	1.01	1.57		2.64
rc_AI232783_s_at	Y	T	5		4050.3	296.070	YT	1.42E-08	4.17E-06	1.52E-08		2.66	1.68	2.64	
rc_AI232900_at	O	C	5		150.1	11.498	OC		5.72E-03	4.74E-07	3.92E-04		1.38	1.96	1.53
rc_AI232900_at	O	T	5		206.7	11.516	OT	5.72E-03		1.57E-04	2.20E-01	1.38		1.42	1.11
rc_AI232900_at	Y	C	5		293.9	14.320	YC	4.74E-07	1.57E-04		2.24E-03	1.96	1.42		1.28
rc_AI232900_at	Y	T	5		229.4	12.685	YT	3.92E-04	2.20E-01	2.24E-03		1.53	1.11	1.28	
rc_AI232903_at	O	C	5		1498.2	60.599	OC		7.86E-02	3.82E-02	5.59E-05		1.12	1.12	1.43
rc_AI232903_at	O	T	5		1343.2	60.964	OT	7.86E-02		7.71E-04	2.68E-03	1.12		1.25	1.28
rc_AI232903_at	Y	C	5		1684.5	44.426	YC	3.82E-02	7.71E-04		9.28E-07	1.12	1.25		1.60
rc_AI232903_at	Y	T	5		1050.6	65.108	YT	5.59E-05	2.68E-03	9.28E-07		1.43	1.28	1.60	
rc_AI232948_at	O	C	5		901.1	26.625	OC		3.33E-01	4.35E-05	1.44E-01		1.06	1.33	1.10
rc_AI232948_at	O	T	5		848.1	21.100	OT	3.33E-01		6.65E-06	5.97E-01	1.06		1.41	1.03
rc_AI232948_at	Y	C	5		1196.1	32.074	YC	4.35E-05	6.65E-06		2.55E-06	1.33	1.41		1.46
rc_AI232948_at	Y	T	5		819.4	58.793	YT	1.44E-01	5.97E-01	2.55E-06		1.10	1.03	1.46	
rc_AI233054_at	O	C	5		4088.2	155.132	OC		1.82E-02	2.86E-04	3.08E-05		1.23	1.33	1.71
rc_AI233054_at	O	T	5		3312.9	267.781	OT	1.82E-02		1.96E-06	6.83E-03	1.23		1.64	1.38
rc_AI233054_at	Y	C	5		5449.6	187.034	YC	2.86E-04	1.96E-06		1.70E-08	1.33	1.64		2.27
rc_AI233054_at	Y	T	5		2397.7	207.784	YT	3.08E-05	6.83E-03	1.70E-08		1.71	1.38	2.27	
rc_AI233787_at	O	C	5		122.5	12.983	OC		2.08E-03	8.08E-01	8.60E-07		1.67	1.05	2.42
rc_AI233787_at	O	T	5		204.9	23.056	OT	2.08E-03		1.23E-03	9.03E-04	1.67		1.75	1.45
rc_AI233787_at	Y	C	5		116.9	8.074	YC	8.08E-01	1.23E-03		5.73E-07	1.05	1.75		2.53
rc_AI233787_at	Y	T	5		296.2	15.627	YT	8.60E-07	9.03E-04	5.73E-07		2.42	1.45	2.53	
rc_AI234218_at	O	C	5		103.5	13.042	OC		7.38E-04	9.71E-01	2.46E-07		1.99	1.01	3.03
rc_AI234218_at	O	T	5		206.4	23.071	OT	7.38E-04		6.83E-04	4.96E-04	1.99		2.01	1.52
rc_AI234218_at	Y	C	5		102.6	2.846	YC	9.71E-01	6.83E-04		2.33E-07	1.01	2.01		3.06
rc_AI234218_at	Y	T	5		313.9	22.621	YT	2.46E-07	4.96E-04	2.33E-07		3.03	1.52	3.06	
rc_AI234712_at	O	C	5		331.1	10.722	OC		2.97E-03	8.13E-01	1.51E-09		1.54	1.04	2.88
rc_AI234712_at	O	T	5		508.4	33.067	OT	2.97E-03		1.79E-03	1.68E-07	1.54		1.59	1.87
rc_AI234712_at	Y	C	5		319.0	29.140	YC	8.13E-01	1.79E-03		1.14E-09	1.04	1.59		2.99
rc_AI234712_at	Y	T	5		952.2	55.472	YT	1.51E-09	1.68E-07	1.14E-09		2.88	1.87	2.99	
rc_AI235250_at	O	C	5		320.2	14.203	OC		4.82E-08	9.70E-09	9.60E-11		2.21	2.59	6.36
rc_AI235250_at	O	T	5		144.8	19.833	OT	4.82E-08		2.60E-01	9.27E-05	2.21		1.17	2.87
rc_AI235250_at	Y	C	5		123.5	6.800	YC	9.70E-09	2.60E-01		1.02E-03	2.59	1.17		2.45
rc_AI235250_at	Y	T	5		50.4	5.085	YT	9.60E-11	9.27E-05	1.02E-03		6.36	2.87	2.45	
rc_AI235481_f_at	O	C	5		298.5	14.538	OC		1.39E-06	2.58E-03	5.80E-01		1.72	1.53	1.06
rc_AI235481_f_at	O	T	5		514.9	25.609	OT	1.39E-06		7.07E-09	5.45E-07	1.72		2.64	1.83
rc_AI235481_f_at	Y	C	5		194.9	27.691	YC	2.58E-03	7.07E-09		8.46E-03	1.53	2.64		1.45
rc_AI235481_f_at	Y	T	5		282.1	7.382	YT	5.80E-01	5.45E-07	8.46E-03		1.06	1.83	1.45	
rc_AI235893_at	O	C	5		572.9	36.181	OC		6.45E-01	6.85E-07	3.01E-02		1.09	2.32	1.40

rc_AI235893_at	O	T	5		527.6	37.702	OT	6.45E-01		3.22E-07	1.16E-02	1.09		2.52	1.52
rc_AI235893_at	Y	C	5		1331.6	105.179	YC	6.85E-07	3.22E-07		4.94E-05	2.32	2.52		1.66
rc_AI235893_at	Y	T	5		802.4	69.218	YT	3.01E-02	1.16E-02	4.94E-05		1.40	1.52	1.66	
rc_AI235948_s_at	O	C	5		212.4	19.471	OC		2.80E-01	2.53E-06	2.66E-01		1.16	1.88	1.17
rc_AI235948_s_at	O	T	5		182.9	14.318	OT	2.80E-01		3.93E-07	9.73E-01	1.16		2.19	1.00
rc_AI235948_s_at	Y	C	5		400.0	27.773	YC	2.53E-06	3.93E-07		3.73E-07	1.88	2.19		2.20
rc_AI235948_s_at	Y	T	5		182.0	6.471	YT	2.66E-01	9.73E-01	3.73E-07		1.17	1.00		2.20
rc_AI236039_f_at	O	C	5		305.2	15.207	OC		3.77E-01	8.73E-06	8.92E-01		1.06	1.41	1.01
rc_AI236039_f_at	O	T	5		287.5	4.466	OT	3.77E-01		1.74E-06	3.11E-01	1.06		1.50	1.07
rc_AI236039_f_at	Y	C	5		430.0	15.800	YC	8.73E-06	1.74E-06		1.12E-05	1.41	1.50		1.40
rc_AI236039_f_at	Y	T	5		307.9	16.084	YT	8.92E-01	3.11E-01	1.12E-05		1.01	1.07	1.40	
rc_AI236726_at	O	C	5		951.4	52.595	OC		6.11E-04	6.76E-05	2.31E-05		1.58	1.46	2.04
rc_AI236726_at	O	T	5		601.7	72.703	OT	6.11E-04		4.97E-08	1.22E-01	1.58		2.31	1.29
rc_AI236726_at	Y	C	5		1390.1	66.531	YC	6.76E-05	4.97E-08		5.45E-09	1.46	2.31		2.98
rc_AI236726_at	Y	T	5		467.2	32.641	YT	2.31E-05	1.22E-01	5.45E-09		2.04	1.29	2.98	
rc_AI237645_at	O	C	5		187.2	22.771	OC		4.75E-01	1.12E-07	8.09E-01		1.44	4.74	1.10
rc_AI237645_at	O	T	5		130.4	16.171	OT	4.75E-01		3.87E-08	3.43E-01	1.44		6.81	1.58
rc_AI237645_at	Y	C	5		887.5	104.471	YC	1.12E-07	3.87E-08		1.63E-07	4.74	6.81		4.30
rc_AI237645_at	Y	T	5		206.3	18.747	YT	8.09E-01	3.43E-01	1.63E-07		1.10	1.58	4.30	
rc_AI639532_at	O	C	5		3093.0	246.193	OC		1.80E-02	2.05E-02	7.06E-05		1.40	1.65	1.81
rc_AI639532_at	O	T	5		4340.7	235.180	OT	1.80E-02		8.66E-05	1.66E-02	1.40		2.31	1.29
rc_AI639532_at	Y	C	5		1875.4	415.378	YC	2.05E-02	8.66E-05		6.75E-07	1.65	2.31		2.99
rc_AI639532_at	Y	T	5		5606.9	400.055	YT	7.06E-05	1.66E-02	6.75E-07		1.81	1.29	2.99	
S68736_at	O	C	5		361.9	72.035	OC		5.88E-04	7.64E-02	7.93E-09		2.76	4.61	5.52
S68736_at	O	T	5		1000.6	82.075	OT	5.88E-04		1.36E-05	5.53E-06	2.76		###	2.00
S68736_at	Y	C	5		78.5	15.995	YC	7.64E-02	1.36E-05		7.87E-10	4.61	###		###
S68736_at	Y	T	5		1996.4	180.535	YT	7.93E-09	5.53E-06	7.87E-10		5.52	2.00	###	
S77858_s_at	O	C	5		536.2	24.559	OC		6.21E-01	4.60E-07	5.19E-03		1.04	1.57	1.23
S77858_s_at	O	T	5		517.1	14.815	OT	6.21E-01		2.08E-07	1.79E-03	1.04		1.63	1.27
S77858_s_at	Y	C	5		843.1	26.544	YC	4.60E-07	2.08E-07		1.66E-04	1.57	1.63		1.28
S77858_s_at	Y	T	5		658.5	36.505	YT	5.19E-03	1.79E-03	1.66E-04		1.23	1.27	1.28	
U05784_s_at	O	C	5		622.4	25.382	OC		1.13E-02	8.39E-01	1.02E-06		1.50	1.04	2.33
U05784_s_at	O	T	5		932.8	43.365	OT	1.13E-02		1.72E-02	2.11E-04	1.50		1.45	1.55
U05784_s_at	Y	C	5		644.8	67.732	YC	8.39E-01	1.72E-02		1.45E-06	1.04	1.45		2.25
U05784_s_at	Y	T	5		1449.2	128.024	YT	1.02E-06	2.11E-04	1.45E-06		2.33	1.55	2.25	
U06099_at	O	C	5		1042.7	18.880	OC		1.66E-04	3.24E-03	1.61E-05		1.43	1.21	1.59
U06099_at	O	T	5		730.4	28.780	OT	1.66E-04		3.22E-07	2.51E-01	1.43		1.73	1.12
U06099_at	Y	C	5		1264.0	77.877	YC	3.24E-03	3.22E-07		5.33E-08	1.21	1.73		1.93
U06099_at	Y	T	5		654.1	30.628	YT	1.61E-05	2.51E-01	5.33E-08		1.59	1.12	1.93	
U23769_at	O	C	5		1206.4	68.190	OC		7.07E-03	7.46E-06	9.53E-05		1.50	1.70	2.24
U23769_at	O	T	5		806.6	68.212	OT	7.07E-03		4.99E-08	5.49E-02	1.50		2.54	1.50
U23769_at	Y	C	5		2046.8	152.769	YC	7.46E-06	4.99E-08		3.16E-09	1.70	2.54		3.80
U23769_at	Y	T	5		538.4	29.913	YT	9.53E-05	5.49E-02	3.16E-09		2.24	1.50	3.80	
U25746_at	O	C	5		99.9	6.401	OC		6.00E-04	1.82E-01	3.08E-07		1.33	1.12	1.65
U25746_at	O	T	5		132.8	5.657	OT	6.00E-04		3.60E-05	8.21E-04	1.33		1.49	1.24

U25746_at	Y	C	5		89.1	3.979	YC	1.82E-01	3.60E-05		3.84E-08	1.12	1.49		1.85
U25746_at	Y	T	5		164.6	5.553	YT	3.08E-07	8.21E-04	3.84E-08		1.65	1.24	1.85	
U38253_at	O	C	5		102.0	4.079	OC		8.56E-04	4.46E-03	2.54E-05		1.25	1.26	1.36
U38253_at	O	T	5		128.0	5.009	OT	8.56E-04		1.51E-06	1.00E-01	1.25		1.58	1.09
U38253_at	Y	C	5		81.0	3.250	YC	4.46E-03	1.51E-06		9.45E-08	1.26	1.58		1.72
U38253_at	Y	T	5		139.1	5.345	YT	2.54E-05	1.00E-01	9.45E-08		1.36	1.09	1.72	
U40836mRNA_s_at	O	C	5		7656.5	403.104	OC		2.16E-04	5.36E-01	1.65E-08		1.43	1.04	2.89
U40836mRNA_s_at	O	T	5		5360.8	348.984	OT	2.16E-04		6.06E-05	3.84E-05	1.43		1.49	2.03
U40836mRNA_s_at	Y	C	5		7962.0	375.608	YC	5.36E-01	6.06E-05		7.13E-09	1.04	1.49		3.01
U40836mRNA_s_at	Y	T	5		2646.9	202.836	YT	1.65E-08	3.84E-05	7.13E-09		2.89	2.03	3.01	
U48828_g_at	O	C	5		233.9	28.760	OC		6.86E-07	1.27E-01	3.02E-01		2.75	1.56	1.24
U48828_g_at	O	T	5		643.4	63.039	OT	6.86E-07		5.76E-08	4.25E-06	2.75		4.29	2.22
U48828_g_at	Y	C	5		150.1	8.044	YC	1.27E-01	5.76E-08		1.65E-02	1.56	4.29		1.93
U48828_g_at	Y	T	5		289.4	23.448	YT	3.02E-01	4.25E-06	1.65E-02		1.24	2.22	1.93	
U57050_g_at	O	C	5		1280.3	55.971	OC		6.98E-03	1.27E-02	3.04E-04		1.27	1.33	1.40
U57050_g_at	O	T	5		1627.3	111.772	OT	6.98E-03		2.24E-05	1.55E-01	1.27		1.69	1.10
U57050_g_at	Y	C	5		965.5	22.941	YC	1.27E-02	2.24E-05		1.52E-06	1.33	1.69		1.86
U57050_g_at	Y	T	5		1794.9	94.958	YT	3.04E-04	1.55E-01	1.52E-06		1.40	1.10	1.86	
U59241_at	O	C	5		261.3	19.643	OC		8.13E-02	8.74E-02	1.31E-05		1.32	1.45	2.05
U59241_at	O	T	5		344.0	34.905	OT	8.13E-02		2.02E-03	5.25E-04	1.32		1.91	1.56
U59241_at	Y	C	5		180.5	9.428	YC	8.74E-02	2.02E-03		5.51E-07	1.45	1.91		2.97
U59241_at	Y	T	5		536.0	47.466	YT	1.31E-05	5.25E-04	5.51E-07		2.05	1.56	2.97	
U69272_at	O	C	5		75.8	5.196	OC		5.49E-03	2.05E-01	1.25E-08		1.94	1.39	4.09
U69272_at	O	T	5		146.6	7.619	OT	5.49E-03		7.77E-02	1.58E-06	1.94		1.40	2.11
U69272_at	Y	C	5		105.0	18.397	YC	2.05E-01	7.77E-02		7.95E-08	1.39	1.40		2.95
U69272_at	Y	T	5		309.5	23.519	YT	1.25E-08	1.58E-06	7.95E-08		4.09	2.11	2.95	
U75405UTR#1_f_at	O	C	5		751.5	78.108	OC		1.90E-01	2.28E-12	1.56E-07		1.41	5.01	2.87
U75405UTR#1_f_at	O	T	5		533.7	102.009	OT	1.90E-01		7.79E-13	2.16E-08	1.41		7.05	4.04
U75405UTR#1_f_at	Y	C	5		3761.4	107.923	YC	2.28E-12	7.79E-13		2.42E-08	5.01	7.05		1.75
U75405UTR#1_f_at	Y	T	5		2154.1	150.232	YT	1.56E-07	2.16E-08	2.42E-08		2.87	4.04	1.75	
U75928UTR#1_s_at	O	C	5		395.4	36.303	OC		5.51E-01	1.19E-08	8.24E-05		1.29	6.01	3.47
U75928UTR#1_s_at	O	T	5		509.1	86.894	OT	5.51E-01		2.72E-08	2.83E-04	1.29		4.67	2.69
U75928UTR#1_s_at	Y	C	5		2374.9	244.148	YC	1.19E-08	2.72E-08		6.06E-05	6.01	4.67		1.73
U75928UTR#1_s_at	Y	T	5		1370.7	32.368	YT	8.24E-05	2.83E-04	6.06E-05		3.47	2.69	1.73	
X06801cds_f_at	O	C	5		665.4	20.425	OC		1.41E-04	9.34E-03	2.11E-06		1.32	1.14	1.54
X06801cds_f_at	O	T	5		505.4	24.172	OT	1.41E-04		6.34E-07	3.98E-02	1.32		1.50	1.17
X06801cds_f_at	Y	C	5		760.6	23.465	YC	9.34E-03	6.34E-07		2.22E-08	1.14	1.50		1.76
X06801cds_f_at	Y	T	5		433.3	22.932	YT	2.11E-06	3.98E-02	2.22E-08		1.54	1.17	1.76	
X07314cds_at	O	C	5		11239.0	278.324	OC		2.89E-07	3.08E-01	6.91E-11		1.81	1.06	5.16
X07314cds_at	O	T	5		6193.9	546.268	OT	2.89E-07		1.62E-06	5.17E-06	1.81		1.71	2.84
X07314cds_at	Y	C	5		####	422.048	YC	3.08E-01	1.62E-06		2.04E-10	1.06	1.71		4.87
X07314cds_at	Y	T	5		2178.2	407.435	YT	6.91E-11	5.17E-06	2.04E-10		5.16	2.84	4.87	
X07314cds_g_at	O	C	5		9403.4	261.330	OC		3.76E-08	6.49E-02	1.65E-11		1.85	1.10	4.52
X07314cds_g_at	O	T	5		5092.4	357.985	OT	3.76E-08		7.77E-07	4.04E-06	1.85		1.67	2.45
X07314cds_g_at	Y	C	5		8529.4	207.267	YC	6.49E-02	7.77E-07		1.12E-10	1.10	1.67		4.10

X07314cds_g_at	Y	T	5		2080.6	386.654	YT	1.65E-11	4.04E-06	1.12E-10		4.52	2.45	4.10	
X07365_s_at	O	C	5		4692.8	264.241	OC		1.19E-04	9.97E-02	5.43E-09		1.44	1.12	3.16
X07365_s_at	O	T	5		3249.4	252.812	OT	1.19E-04		4.50E-03	1.35E-05	1.44		1.29	2.19
X07365_s_at	Y	C	5		4193.3	145.833	YC	9.97E-02	4.50E-03		5.83E-08	1.12	1.29		2.82
X07365_s_at	Y	T	5		1486.0	91.851	YT	5.43E-09	1.35E-05	5.83E-08		3.16	2.19	2.82	
X15030_at	O	C	5		6480.0	237.877	OC		3.86E-04	2.08E-02	1.42E-06		1.23	1.11	1.45
X15030_at	O	T	5		5267.0	224.687	OT	3.86E-04		2.82E-06	9.15E-03	1.23		1.36	1.18
X15030_at	Y	C	5		7175.4	197.745	YC	2.08E-02	2.82E-06		2.76E-08	1.11	1.36		1.61
X15030_at	Y	T	5		4463.1	32.092	YT	1.42E-06	9.15E-03	2.76E-08		1.45	1.18	1.61	
X59736mRNA_at	O	C	5		1819.8	72.342	OC		2.45E-10	1.48E-04	1.89E-10		2.65	1.22	2.73
X59736mRNA_at	O	T	5		687.0	50.156	OT	2.45E-10		2.45E-12	8.11E-01	2.65		3.24	1.03
X59736mRNA_at	Y	C	5		2223.1	65.924	YC	1.48E-04	2.45E-12		2.01E-12	1.22	3.24		3.33
X59736mRNA_at	Y	T	5		667.1	35.208	YT	1.89E-10	8.11E-01	2.01E-12		2.73	1.03	3.33	
X59864mRNA_at	O	C	5		6334.0	261.701	OC		2.65E-06	9.89E-08	5.12E-09		1.89	2.55	4.04
X59864mRNA_at	O	T	5		3343.1	305.688	OT	2.65E-06		5.83E-02	6.88E-04	1.89		1.35	2.13
X59864mRNA_at	Y	C	5		2480.4	259.790	YC	9.89E-08	5.83E-02		4.68E-02	2.55	1.35		1.58
X59864mRNA_at	Y	T	5		1569.1	358.420	YT	5.12E-09	6.88E-04	4.68E-02		4.04	2.13	1.58	
X59864mRNA_g_at	O	C	5		4730.6	292.835	OC		1.02E-06	2.04E-08	1.77E-09		1.80	2.48	3.42
X59864mRNA_g_at	O	T	5		2624.7	160.177	OT	1.02E-06		1.99E-02	3.66E-04	1.80		1.37	1.90
X59864mRNA_g_at	Y	C	5		1910.9	99.207	YC	2.04E-08	1.99E-02		7.42E-02	2.48	1.37		1.38
X59864mRNA_g_at	Y	T	5		1383.7	176.380	YT	1.77E-09	3.66E-04	7.42E-02		3.42	1.90	1.38	
X62660mRNA_g_at	O	C	5		95.7	2.014	OC		1.46E-02	3.14E-01	2.44E-07		1.14	1.05	1.62
X62660mRNA_g_at	O	T	5		83.9	3.985	OT	1.46E-02		1.66E-03	2.82E-05	1.14		1.19	1.42
X62660mRNA_g_at	Y	C	5		100.2	3.023	YC	3.14E-01	1.66E-03		5.16E-08	1.05	1.19		1.70
X62660mRNA_g_at	Y	T	5		59.0	2.849	YT	2.44E-07	2.82E-05	5.16E-08		1.62	1.42	1.70	
X62951mRNA_s_at	O	C	5		149.9	6.885	OC		1.09E-10	2.31E-01	6.16E-05		3.14	1.22	1.79
X62951mRNA_s_at	O	T	5		470.8	28.606	OT	1.09E-10		3.19E-11	7.77E-08	3.14		3.84	1.76
X62951mRNA_s_at	Y	C	5		122.7	6.323	YC	2.31E-01	3.19E-11		5.87E-06	1.22	3.84		2.18
X62951mRNA_s_at	Y	T	5		267.7	7.314	YT	6.16E-05	7.77E-08	5.87E-06		1.79	1.76	2.18	
X64827cds_s_at	O	C	5		6287.8	318.846	OC		4.43E-05	1.27E-02	3.48E-09		1.38	1.14	2.34
X64827cds_s_at	O	T	5		4561.4	112.687	OT	4.43E-05		3.15E-07	1.77E-05	1.38		1.57	1.70
X64827cds_s_at	Y	C	5		7161.6	197.296	YC	1.27E-02	3.15E-07		1.44E-10	1.14	1.57		2.67
X64827cds_s_at	Y	T	5		2685.9	201.208	YT	3.48E-09	1.77E-05	1.44E-10		2.34	1.70	2.67	
X74835cds_at	O	C	5		419.7	30.521	OC		6.72E-07	2.74E-09	3.50E-10		1.82	3.06	4.45
X74835cds_at	O	T	5		230.2	7.471	OT	6.72E-07		1.32E-03	3.55E-05	1.82		1.68	2.44
X74835cds_at	Y	C	5		136.9	9.588	YC	2.74E-09	1.32E-03		9.46E-02	3.06	1.68		1.45
X74835cds_at	Y	T	5		94.2	8.701	YT	3.50E-10	3.55E-05	9.46E-02		4.45	2.44	1.45	
X80130cds_f_at	O	C	5		3234.3	233.160	OC		4.64E-11	2.05E-08	1.83E-11		6.25	2.24	9.38
X80130cds_f_at	O	T	5		517.2	35.759	OT	4.64E-11		7.28E-05	3.40E-01	6.25		2.79	1.50
X80130cds_f_at	Y	C	5		1444.8	72.691	YC	2.05E-08	7.28E-05		1.10E-05	2.24	2.79		4.19
X80130cds_f_at	Y	T	5		344.7	21.855	YT	1.83E-11	3.40E-01	1.10E-05		9.38	1.50	4.19	
X80130cds_i_at	O	C	5		3829.9	411.190	OC		6.45E-09	4.99E-07	3.82E-09		8.43	2.79	11.66
X80130cds_i_at	O	T	5		454.4	25.838	OT	6.45E-09		8.17E-03	6.84E-01	8.43		3.02	1.38
X80130cds_i_at	Y	C	5		1373.5	125.063	YC	4.99E-07	8.17E-03		3.42E-03	2.79	3.02		4.18
X80130cds_i_at	Y	T	5		328.4	11.444	YT	3.82E-09	6.84E-01	3.42E-03		11.66	1.38	4.18	

X96437mRNA_at	O	C	5		194.5	6.599	OC		8.85E-01	9.28E-02	3.25E-05		1.02	1.26	1.66
X96437mRNA_at	O	T	5		197.8	10.500	OT	8.85E-01		7.08E-02	4.33E-05	1.02		1.28	1.63
X96437mRNA_at	Y	C	5		154.5	6.572	YC	9.28E-02	7.08E-02		1.28E-06	1.26	1.28		2.08
X96437mRNA_at	Y	T	5		322.1	28.341	YT	3.25E-05	4.33E-05	1.28E-06		1.66	1.63	2.08	
Z78279_at	O	C	5		237.4	16.372	OC		8.57E-01	4.05E-07	1.30E-01		1.37	###	3.34
Z78279_at	O	T	5		173.4	36.395	OT	8.57E-01		3.03E-07	9.38E-02	1.37		###	4.58
Z78279_at	Y	C	5		3091.4	451.552	YC	4.05E-07	3.03E-07		6.14E-06	###	###		3.89
Z78279_at	Y	T	5		793.9	192.591	YT	1.30E-01	9.38E-02	6.14E-06		3.34	4.58	3.89	
Z78279_g_at	O	C	5		372.7	24.051	OC		6.96E-01	9.51E-08	1.09E-01		1.55	9.17	2.52
Z78279_g_at	O	T	5		240.2	38.791	OT	6.96E-01		5.32E-08	5.23E-02	1.55		###	3.91
Z78279_g_at	Y	C	5		3418.3	439.070	YC	9.51E-08	5.32E-08		1.41E-06	9.17	###		3.64
Z78279_g_at	Y	T	5		939.0	165.484	YT	1.09E-01	5.23E-02	1.41E-06		2.52	3.91	3.64	

**Supplementary Table 4.** Order that probe sets with a significant age-atrophy interaction after Bonferroni adjustment were clustered by SAS 8. Column 1 is the order of appearance of the gene in the hierarchical cluster shown in Figure 1 of Supplementary Material, column 2 is the gene name, column 3 the accession number and column 4 the gene function assigned. Note that when multiple probe sets represent a single mRNA they are clustered together. Likewise, genes of similar expression patterns and functions tend to cluster together.

	<b>GENE NAME</b>	<b>ID</b>	<b>GENE FUNCTION</b>
1	ESTs similar to mouse NADH dehydrogenase (ubiquinone) 1 beta subcomplex 5	AA684537	electron transport
2	ESTs unknown function	AI029702	ESTs unknown function
3	ATP synthase, H <sup>+</sup> transporting, mitochondrial F0 complex, subunit c, isoform 1	D13123	proton transport
4	ESTs unknown function	AA957244	ESTs unknown function
5	ESTs similar to mouse mitochondrial ribosomal protein L12	AI176961	structural constituent of ribosome
6	ESTs similar to mouse FXVD domain-containing ion transport regulator 1 (phospholemman)	AA799645	ion transport
7	ESTs unknown function	AI011738	ESTs unknown function
8	solute carrier family 4, member 3, anion exchange protein 3	J05167	small molecule transport
9	fatty acid binding protein 3, heart	J02773	transport
10	ESTs similar to mouse serine hydrolase-like	AI232409	aromatic compound metabolism
11	heat shock protein 70-3	X77209	chaperone
12	ESTs similar to mouse NADH dehydrogenase (ubiquinone) 1 beta subcomplex, 5, 16kDa	AA893185	electron transport
13	ESTs highly similar to mouse estrogen related receptor, alpha	AA799479	regulation of transcription
14	ESTs similar to mouse FXVD domain-containing ion transport regulator 1 (phospholemman)	AA799645	ion transport
15	ESTs similar to mouse microsomal glutathione S-transferase 3	AA892234	glutathione transferase
16	ESTs unknown function	AI010326	ESTs unknown function
17	ESTs unknown function	AI236726	ESTs unknown function
18	ESTs similar to mouse solute carrier family 25 (mitochondrial carrier; adenine nucleotide translocator), member 4	AA849754	small molecule transport
19	ESTs similar to mouse dystroglycan 1 (dystrophin-associated glycoprotein 1)	AA943734	muscle contraction
20	ESTs unknown function	AI228284	ESTs unknown function
21	homer, neuronal immediate early gene, 2	AB007689	signaling
22	creatine kinase, mitochondrial 2, sarcomeric	X59736	muscle contraction
23	ESTs unknown function	AI045368	ESTs unknown function
24	homer, neuronal immediate early gene, 2	AB007689	signaling
25	ESTs similar to mouse protein tyrosine kinase 9-like (A6-related protein)	AI171452	signaling
26	aminolevulinic acid synthase 1	J03190	heme biosynthesis
27	ESTs unknown function	AI228301	ESTs unknown function
28	PDZ and LIM domain 1 (elfin)	U23769	signaling
29	ESTs unknown function	AA799518	ESTs unknown function
30	ESTs unknown function	AA799518	ESTs unknown function
31	ESTs unknown function	AI170956	ESTs unknown function

32	ESTs very weakly similar to human angiomin	AI014132	Genes unknown fxn
33	homer, neuronal immediate early gene, 2	AB007690	signaling
34	homer, neuronal immediate early gene, 2	AI058957	signaling
35	homer, neuronal immediate early gene, 2	AI060224	signaling
36	ESTs unknown function	AI168941	ESTs unknown function
37	serine (or cysteine) proteinase inhibitor, clade H, member 1	M69246	chaperone
38	ESTs weakly similar to human cytidine deaminase	AA859352	nucleic acid metabolism
39	ESTs highly similar to mouse scleraxis	AI172335	Genes unknown fxn
40	ESTs unknown function	AI176067	ESTs unknown function
41	ESTs similar to mouse tropomyosin 2, beta	AA858875	muscle contraction
42	ESTs similar to human NADH:ubiquinone oxidoreductase MLRQ subunit homolog	AA686870	electron transport
43	ESTs similar to mouse P311 mRNA	AA926262	Genes unknown fxn
44	ESTs similar to mouse fibrillin 1	AA997765	extracellular matrix
45	ESTs highly similar to mouse lysyl oxidase-like 2	AI180353	extracellular matrix
46	protein phosphatase 1, regulatory (inhibitor) subunit 1A	J05592	inhibitor
47	ESTs unknown function	AA957835	ESTs unknown function
48	ESTs similar to mouse procollagen, type XV	AA800298	extracellular matrix
49	ESTs similar to mouse procollagen, type VI, alpha 1	AI235893	extracellular matrix
50	ESTs unknown function	AI228132	ESTs unknown function
51	ESTs similar to mouse chondrolectin	AI029745	lectin
52	ESTs similar to mouse kerotocan	AA957596	extracellular matrix
53	collagen type XI, alpha 1	AA942906	extracellular matrix
54	aquaporin 7	AB000507	transport
55	ESTs similar to mouse follistatin like mRNA	AA849769	serine protease inhibitor
56	ESTs similar to mouse nidogen (entactin)	AI176500	extracellular matrix
57	protein phosphatase 1, regulatory (inhibitor) subunit 1A	J05592	inhibitor
58	ESTs similar to mouse procollagen, type IV, alpha 1	AI176393	extracellular matrix
59	ESTs similar to mouse collagen, type XV, alpha 1	AI232103	extracellular matrix
60	ESTs unknown function	AI171813	ESTs unknown function
61	ESTs similar to mouse serum deprivation response	AA859444	phospholipid binding
62	ESTs unknown function	AA859885	ESTs unknown function
63	ESTs similar to mouse nidogen (entactin)	AI235948	extracellular matrix
64	ESTs weakly similar to mouse follistatin like mRNA	AI010449	serine protease inhibitor
65	ESTs similar to mouse protein tyrosine phosphatase-like (proline instead of catalytic arginine), member a	AI177543	signaling
66	cyclin D1	D14014	cell cycle
67	ESTs similar to mouse procollagen, type XIV, alpha 1 (undulin)	AA998128	extracellular matrix
68	ESTs similar to mouse extracellular matrix protein 1	AI237589	extracellular matrix
69	ESTs unknown function	AF034237	ESTs unknown function
70	ESTs similar to human latent transforming growth factor beta binding protein 4	AI177967	extracellular matrix
71	ESTs similar to human growth factor receptor-bound protein 10 (GRB10)	AA800686	signal transduction
72	ectonucleoside triphosphate diphosphohydrolase 2	AI230130	G-protein coupled receptor protein signaling
73	ESTs similar to human myosin, light polypeptide 6, alkali, smooth muscle and non-muscle	S77858	cytoskeleton organization and biogenesis



74	cytochrome P450 lanosterol 14 alpha-demethylase	U17697	electron transport
75	ESTs similar to mouse laminin, gamma 1	AI009131	extracellular matrix
76	ESTs similar to mouse serum deprivation response	AI171350	phospholipid binding
77	ESTs unknown function	AI176540	ESTs unknown function
78	ESTs similar to mouse sialyltransferase 7 ((alpha-N-acetylneuraminy-2,3-beta-galactosyl-1,3)-N-acetyl galactosaminide alpha-2,6-sialyltransferase) D	AA818639	glycosylation
79	ESTs unknown function	AI230208	ESTs unknown function
80	ESTs similar to mouse poly(rC) binding protein 4	AA891314	nucleic acid binding
81	ESTs unknown function	AI029021	ESTs unknown function
82	ESTs similar to mouse serine (or cysteine) proteinase inhibitor, clade F), member 1	AI179984	Inhibitor
83	phosphate cytidyltransferase 2, ethanolamine	AF080568	Genes unknown fxn
84	BCL2/adenovirus E1B 19kD interacting protein 1	AA819398	anti-apoptosis
85	ESTs similar to human NADH dehydrogenase (ubiquinone) 1 beta subcomplex, 6, 17kDa	AA900199	electron transport
86	ESTs similar to human gene overexpressed in astrocytoma	AA957501	Genes unknown fxn
87	ESTs similar to mouse cysteine rich intestinal protein	AA925057	cell proliferation
88	ESTs similar to mouse septin 8	AA964777	Genes unknown fxn
89	ESTs similar to mouse calumenin	AI236039	blood coagulation
90	ATP synthase, H <sup>+</sup> transporting, mitochondrial F1 complex, O subunit (oligomycin sensitivity conferring protein)	AI104244	proton transport
91	ESTs unknown function	AI232948	ESTs unknown function
92	aconitase 2, mitochondrial	AI170777	tricarboxylic acid cycle
93	aconitase 2, mitochondrial	AI170777	tricarboxylic acid cycle
94	ESTs similar to human mitochondrial ribosomal protein L46	AI169228	Genes unknown fxn
95	heat shock 10 kD protein 1 (chaperonin 10)	AI170613	chaperone
96	hydroxyacyl-Coenzyme A dehydrogenase/3-ketoacyl-Coenzyme A hiolase/enoyl-Coenzyme A hydratase (trifunctional protein), alpha subunit	D16478	lipid metabolism
97	potassium inwardly rectifying channel, subfamily J, member 11	D86039	ion transport
98	ESTs unknown function	AA955741	ESTs unknown function
99	ESTs similar to human NADH dehydrogenase (ubiquinone) 1 beta subcomplex, 7, 18kDa	AA850130	electron transport
100	ESTs similar to human cytochrome c oxidase subunit VIb	AA946040	electron transport
101	ESTs similar to mouse ATP synthase, H <sup>+</sup> transporting, mitochondrial F0 complex, subunit f, isoform 2	AI101157	proton transport
102	smooth muscle alpha-actin	X06801	cytoskeleton organization and biogenesis
103	ESTs unknown function	AI104035	ESTs unknown function
104	ESTs unknown function	AA818971	ESTs unknown function
105	ESTs unknown function	AI072992	ESTs unknown function
106	ESTs similar to human NADH dehydrogenase (ubiquinone) 1 beta subcomplex, 8, 19kDa	AA851403	electron transport
107	zinc finger protein Y1 (RLZF-Y) mRNA	AI013250	Genes unknown fxn
108	ESTs similar to human NADH dehydrogenase (ubiquinone) 1 beta subcomplex, 7, 18kDa	AA850130	electron transport
109	ESTs similar to human myofibrillogenesis regulator 1 (MR-1)	AI102715	Genes unknown fxn
110	annexin V	D42137	blood coagulation

111	ESTs similar to human low molecular mass ubiquinone-binding protein (9.5kD)	AI233054	Genes unknown fxn
112	ESTs unknown function	AA849609	ESTs unknown function
113	lipoprotein lipase	L03294	lipid metabolism
114	ESTs similar to human 13kDa differentiation-associated protein (alias: NADH: ubiquinone oxidoreductase subunit B17.2)	AI103851	Genes unknown fxn
115	ESTs unknown function	AI171448	ESTs unknown function
116	peroxiredoxin 2	U06099	selenium binding, oxidoreductase
117	ESTs highly similar to mouse clone similar to ubiquitin-like protein GDX (ubiquitin-like protein 4)	AA817861	protein modification
118	ESTs unknown function	AA859325	ESTs unknown function
119	ESTs unknown function	AI178764	ESTs unknown function
120	ESTs similar to mouse NADH dehydrogenase (ubiquinone) Fe-S protein 3	AI229680	electron transport
121	ESTs similar to mouse cytochrome c oxidase subunit VIIb	AA866477	electron transport
122	ESTs unknown function	AI012145	ESTs unknown function
123	ESTs similar to human electron-transfer-flavoprotein, beta polypeptide	AI179147	electron transport
124	ESTs unknown function	AI104483	ESTs unknown function
125	dapit (known as stretch regulated skeletal muscle protein Usmg5 gene in mouse)	AI045107	Genes unknown fxn
126	ESTs similar to mouse small EDRK-rich factor 2	AI172471	Genes unknown fxn
127	ESTs similar to mouse WD repeat domain 1	AI229849	actin binding
128	nucleoside diphosphate kinase	M91597	ATP binding
129	ESTs unknown function	AI171994	ESTs unknown function
130	cytochrome c oxidase, subunit Va	X15030	electron transport
131	ESTs highly similar to mouse ATP synthase, H <sup>+</sup> transporting, mitochondrial F <sub>0</sub> complex, subunit g	AA944393	proton transport
132	ESTs similar to human NADH dehydrogenase (ubiquinone) 1 beta subcomplex, 10, 22kDa	AI229497	electron transport
133	ESTs similar to human ubiquinol-cytochrome c reductase hinge protein	AI008066	electron transport
134	TBP-interacting protein Tip120B	AI137210	Genes unknown fxn
135	ESTs similar to mouse NADH dehydrogenase (ubiquinone) Fe-S protein 2	AI170770	electron transport
136	ESTs similar to human NADH dehydrogenase (ubiquinone) 1, subcomplex unknown, 2, 14.5kDa	AA900580	electron transport
137	ESTs similar to human NADH dehydrogenase (ubiquinone) 1 beta subcomplex, 8, 19kDa	AA964320	electron transport
138	cytochrome c oxidase subunit Vb	AI229620	electron transport
139	small muscle protein, X-linked	AA800221	muscle contraction
140	ESTs unknown function	AA946411	ESTs unknown function
141	glutathione transferase subunit 8	X62660	Genes unknown fxn
142	ATP synthase subunit d (Atp5jd)	AA925814	proton transport
143	ESTs similar to mouse nuclear transport factor 2	AI101343	transport
144	ESTs similar to mouse cytochrome c oxidase, subunit VIIc	AI009490	electron transport
145	ESTs similar to mouse NADH dehydrogenase (ubiquinone) 1 alpha subcomplex 2	AI232903	electron transport
146	ESTs similar to human GDP dissociation inhibitor 2	AI105149	vesicle transport
147	Cytochrom c oxidase subunit VIII-H (heart/muscle)	U40836	electron transport

148	Cytochrom c oxidase subunit VIII-H (heart/muscle)	X64827	electron transport
149	ATP synthase, H <sup>+</sup> transporting, mitochondrial F1 complex, delta subunit	A1104953	proton transport
150	small muscle protein, X-linked (chisel)	AA924417	muscle contraction
151	diazepam binding inhibitor	A1010581	transport
152	glutathione peroxidase 1	X07365	selenium binding, oxidoreductase
153	ESTs unknown function	AA946124	ESTs unknown function
154	ESTs unknown function	A1175529	ESTs unknown function
155	ESTs unknown function	AA963716	ESTs unknown function
156	dynein light chain-2	A1103774	Genes unknown fxn
157	ESTs similar to human JTV1 gene	AA799766	Genes unknown fxn
158	ESTs unknown function	A1009197	ESTs unknown function
159	peroxiredoxin 4	A1232900	antioxidant
160	ESTs unknown function	A1102083	ESTs unknown function
161	Myosin, light polypeptide 2, alkali; ventricular, skeletal, slow	X07314	muscle contraction
162	Myosin, light polypeptide 2, alkali; ventricular, skeletal, slow	X07314	muscle contraction
163	calsequestrin 2	AA924985	muscle contraction
164	ESTs similar to mouse tropomyosin 3, gamma	A1170775	muscle development
165	ESTs similar to mouse tropomyosin 3, gamma	A1170847	muscle development
166	collagen type XI, alpha 1	AJ005396	extracellular matrix
167	secreted acidic cysteine rich glycoprotein (osteonectin)	U75929	extracellular matrix
168	secreted acidic cysteine rich glycoprotein (osteonectin)	R47128	extracellular matrix
169	secreted acidic cysteine rich glycoprotein (osteonectin)	AA946313	extracellular matrix
170	procollagen, type I, alpha 2	AA819207	extracellular matrix
171	procollagen, type I, alpha 2	A1101443	extracellular matrix
172	procollagen, type I, alpha 1	M27207	extracellular matrix
173	collagen, type 1, alpha 1	U75405	extracellular matrix
174	secreted acidic cysteine rich glycoprotein (osteonectin)	U75928	extracellular matrix
175	secreted acidic cysteine rich glycoprotein (osteonectin)	R46953	extracellular matrix
176	secreted acidic cysteine rich glycoprotein (osteonectin)	R47150	extracellular matrix
177	ESTs similar to mouse P311 mRNA	A1071578	Genes unknown fxn
178	ESTs similar to mouse P311 mRNA	A1071578	Genes unknown fxn
179	ESTs similar to mouse clone similar to human KDEL endoplasmic reticulum protein retention receptor 3	AA818372	Genes unknown fxn
180	collagen, type 1, alpha 1	Z78279	extracellular matrix
181	collagen, type 1, alpha 1	Z78279	extracellular matrix
182	collagen, type 1, alpha 1	A1231472	extracellular matrix
183	procollagen, type I, alpha 2	A1101443	extracellular matrix
184	ESTs similar to human procollagen, type I, alpha 2	AA859284	extracellular matrix
185	ESTs unknown function	AA875531	ESTs unknown function
186	procollagen, type I, alpha 2	A1101443	extracellular matrix
187	ESTs highly similar to rat non-coding RNA expressed in the brain, repeat sequence, clone 12	AA900746	Genes unknown fxn
188	ESTs similar to mouse maternally expressed gene 3	AA943010	Genes unknown fxn
189	ESTs similar to mouse procollagen, type IV, alpha 1	A1175875	extracellular matrix
190	ESTs highly similar to mouse P311 mRNA	A1105417	Genes unknown fxn
191	ESTs similar to mouse transferrin receptor	A1237645	iron homeostasis

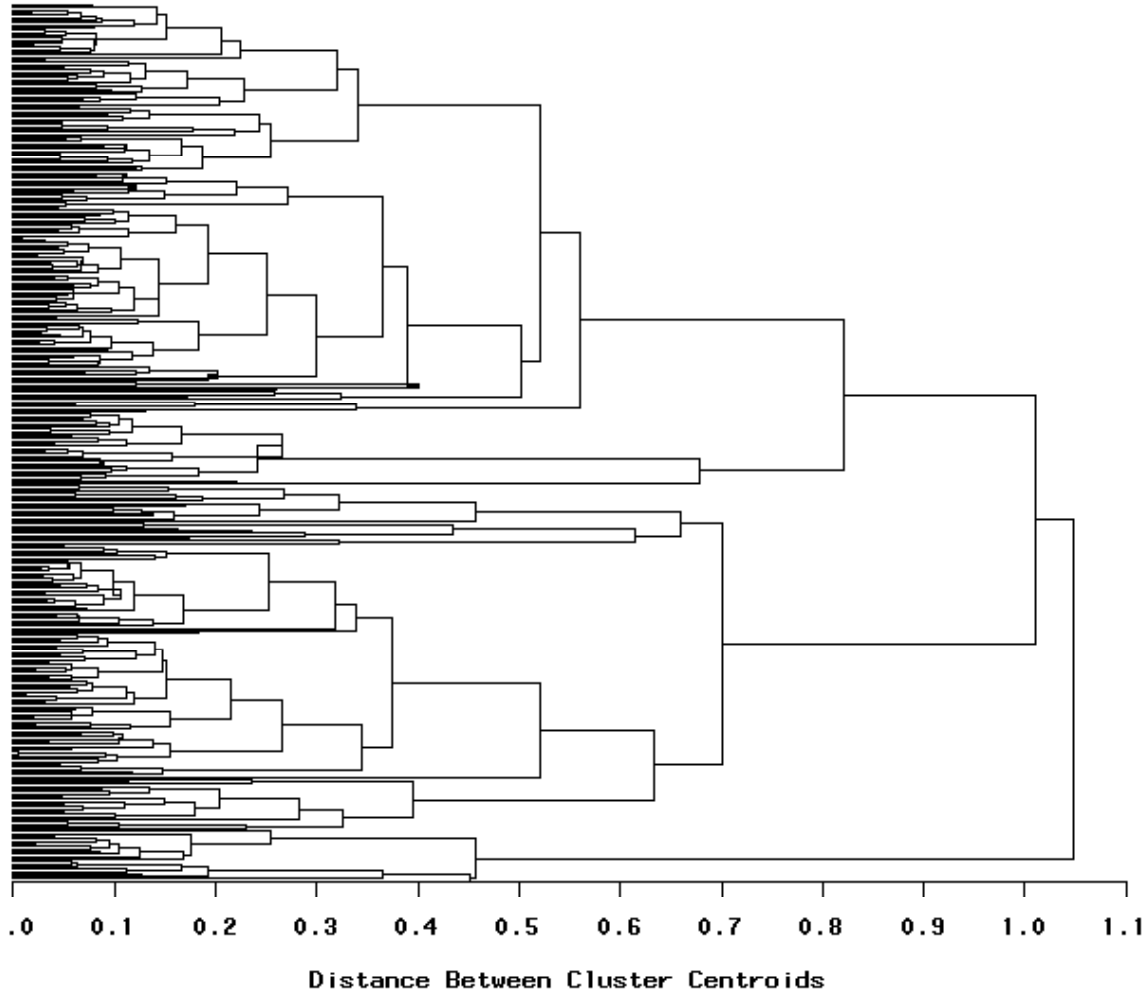
192	ESTs unknown function	AI639088	ESTs unknown function
193	ESTs unknown function	AI171466	ESTs unknown function
194	ESTs similar to human myosin light chain 1 slow a	AI230220	Genes unknown fxn
195	cold inducible RNA binding protein	AB000362	nucleic acid binding
196	retroviral-like ovarian specific transcript 30-1 mRNA	U48828	Genes unknown fxn
197	ESTs similar to mouse immunoglobulin superfamily, member 4	H31479	Genes unknown fxn
198	ESTs similar to rat retroviral-like ovarian specific transcript 30-1 mRNA	H31125	Genes unknown fxn
199	mRNA (pBUS19) with repetitive elements	X62951	Genes unknown fxn
200	ESTs unknown function	AA963077	ESTs unknown function
201	ESTs similar to mouse ATP-binding cassette, subfamily A, member 1	AA964962	small molecule transport
202	diaphorase (NADH) (cytochrome b-5 reductase)	AA963839	iron transport
203	ESTs unknown function	AI176839	ESTs unknown function
204	ESTs unknown function	AA998174	ESTs unknown function
205	VL30 element mRNA	AI230199	Genes unknown fxn
206	ESTs unknown function	AI104675	ESTs unknown function
207	ESTs similar to rat retroviral-like ovarian specific transcript 30-1 mRNA	AI235481	Genes unknown fxn
208	ESTs similar to mouse immunoglobulin superfamily, member 4	AI009996	Genes unknown fxn
209	neurofilament protein, middle polypeptide	Z12152	intermediate filament
210	apurinic/apurimidinic endonuclease 1 (APEX nuclease multifunctional DNA repair enzyme 1)	D44495	DNA repair
211	ESTs similar to mouse RNA binding protein gene with multiple splicing	AA859519	RNA processing
212	ESTs unknown function	AA963797	ESTs unknown function
213	ESTs weakly similar to human PNAS-127 mRNA	AA999183	Genes unknown fxn
214	diaphorase (NADH) (cytochrome b-5 reductase)	AI229440	iron transport
215	ESTs unknown function	AI008504	ESTs unknown function
216	ESTs weakly similar to mouse syndecan 2	AI011678	extracellular matrix
217	ESTs unknown function	AA996896	ESTs unknown function
218	RT1 class Ib gene	AI103500	immune response
219	p47 protein	AB002086	Genes unknown fxn
220	ESTs unknown function	AA944212	ESTs unknown function
221	ESTs unknown function	AI171587	ESTs unknown function
222	cystatin C	AI231292	protease inhibitor
223	fatty acid Coenzyme A ligase, long chain 4	D85189	lipid metabolism
224	ESTs similar to mouse glutathione peroxidase 3	AI172411	selenium binding, oxidoreductase
225	proteasome (prosome, macropain) 26S subunit, ATPase	D50694	Protein degradation
226	proteasome (prosome, macropain) 26S subunit, ATPase, 4	D50695	Protein degradation
227	B-cell translocation gene 1, anti-proliferative	L26268	cell cycle
228	RNA helicase	U25746	Genes unknown fxn
229	ESTs similar to mouse NY-REN-18 antigen	AI232313	Genes unknown fxn
230	ESTs unknown function	AA849720	ESTs unknown function
231	ESTs similar to mouse programmed cell death 5	AI172308	apoptosis
232	ESTs similar to mouse serine palmitoyltransferase, long chain base subunit 1	AA892380	amino acid metabolism

233	ESTs similar to human suppressor of G2 allele of SKP1, <i>S. cerevisiae</i> , homolog of (SGT1)	AA901343	cell cycle
234	lactate dehydrogenase A	M54926	glycolysis
235	ESTs unknown function	AI175474	ESTs unknown function
236	aldolase A, fructose-bisphosphate	AA924326	glycolysis
237	ESTs unknown function	AA875032	ESTs unknown function
238	ESTs similar to mouse next to the Brca1	AA925045	tumor antigen
239	ESTs similar to mouse upregulated skeletal muscle protein Usmg4	AA818952	Genes unknown fxn
240	ESTs similar to mouse DEAD (aspartate-glutamate-alanine-aspartate) box polypeptide 5	AA851926	nucleic acid binding
241	ESTs unknown function	AI179840	ESTs unknown function
242	ESTs similar to mouse neuralized homolog ( <i>Drosophila</i> )	AA963167	neurogenesis
243	ESTs similar to mouse sclerostin	AI170709	Genes unknown fxn
244	ESTs similar to human eukaryotic translation initiation factor 4 gamma, 3	AA964477	protein synthesis
245	ESTs similar to mouse WW domain-containing protein 3	AI176607	Genes unknown fxn
246	eukaryotic translation initiation factor 2B, subunit 3 (gamma, 58kD)	U38253	protein synthesis
247	ESTs similar to mouse partial mRNA for stretch response protein 553 (sr553 gene)	AI073178	Genes unknown fxn
248	ESTs similar to mouse aldehyde dehydrogenase 9, subfamily A1	AI105188	electron transport
249	26S proteasome, subunit p112 (non-ATPase subunit)	U57050	Protein degradation
250	ESTs similar to mouse N-myristoyltransferase 1	AA859942	protein modification
251	purinergic receptor P2X, ligand-gated ion channel 4	AA924532	ion transport
252	Sip30 SNAP25 interacting protein 30	AA819709	Genes unknown fxn
253	ESTs similar to mouse eukaryotic translation initiation factor 3, subunit 8 (110 kDa)	AA851785	protein synthesis
254	ESTs similar to human golgi-specific brefeldin A resistance factor 1	AA924964	Genes unknown fxn
255	protease (prosome, macropain) 26S subunit, ATPase 1	D50696	Protein degradation
256	ESTs unknown function	AI175594	ESTs unknown function
257	ESTs unknown function	AA818123	ESTs unknown function
258	ESTs weakly similar to mouse ribosomal protein L23	AA944741	structural constituent of ribosome
259	general transcription factor IIB	X65948	transcription factor
260	iron-responsive element-binding protein	AI176621	Genes unknown fxn
261	PRG1 gene (immediate early response 3)	X96437	anti-apoptosis
262	ESTs highly similar to mouse lysyl oxidase-like 2	AI071855	extracellular matrix
263	ESTs unknown function	AA800168	ESTs unknown function
264	ESTs unknown function	AA956871	ESTs unknown function
265	ESTs similar to human tropomodulin	AI104913	cytoskeletal
266	ESTs similar to human ataxin 2-binding protein 1	AI175100	nucleic acid binding
267	ESTs unknown function	AA849312	ESTs unknown function
268	ESTs similar to mouse glyoxylate reductase/hydroxypyruvate reductase	AA924630	electron transport
269	zinc finger protein (pMLZ-4) (zinc finger protein 46)	AI229253	nucleic acid binding
270	ESTs unknown function	AI227672	ESTs unknown function
271	ESTs unknown function	AA891790	ESTs unknown function
272	ESTs unknown function	AA946449	ESTs unknown function

273	ESTs unknown function	AI169053	ESTs unknown function
274	microtubule-associated proteins 1A/1B light chain 3 (MPL3)	U05784	Genes unknown fxn
275	ESTs similar to mouse ADP-ribosyltransferase 3	AI104393	glycosylation
276	ESTs similar to human cysteine-rich motor neuron 1	AI233787	neurogenesis
277	ESTs similar to human ataxin 2-binding protein 1	AA818804	nucleic acid binding
278	ESTs unknown function	AI228484	ESTs unknown function
279	isocitrate dehydrogenase 1 (NADP+), soluble	AA892314	tricarboxylic acid cycle
280	ESTs unknown function	AI171103	ESTs unknown function
281	ESTs highly similar to mouse B-cell receptor-associated protein 31	AA944335	immune response
282	ESTs similar to mouse phospholipase C-like 2	AI058656	Genes unknown fxn
283	E-Tropomodulin	U59241	cytoskeletal
284	ESTs unknown function	AA848948	ESTs unknown function
285	cathepsin L	AI176595	Protein degradation
286	ESTs unknown function	AA925744	ESTs unknown function
287	ESTs unknown function	AA946029	ESTs unknown function
288	ESTs weakly similar to mouse follistatin like mRNA	AI011457	serine protease inhibitor
289	ESTs unknown function	AI171193	ESTs unknown function
290	ESTs unknown function	AA850672	ESTs unknown function
291	ESTs unknown function	AI176362	ESTs unknown function
292	ESTs unknown function	AA891950	ESTs unknown function
293	ESTs highly similar to mouse troponin C, fast skeletal	AI639532	muscle contraction
294	serum/glucocorticoid regulated kinase	L01624	protein amino acid phosphorylation
295	ESTs unknown function	AI105451	ESTs unknown function
296	ESTs similar to mouse neuroepithelial cell transforming gene 1	AI180187	signal transduction
297	Glutamine synthetase (glutamate-ammonia ligase)	M91652	amino acid metabolism
298	ESTs similar to mouse RNA polymerase II subunit 5 (RPB5)-mediating protein	AI234218	transcription regulation
299	ESTs similar to mouse ankyrin repeat and SOCS box-containing protein 11	AI011087	Genes unknown fxn
300	fumarylacetoacetate hydrolase	M77694	amino acid metabolism
301	ESTs unknown function	AA818271	ESTs unknown function
302	Glutamine synthetase (glutamate-ammonia ligase)	M91652	amino acid metabolism
303	ESTs similar to mouse RW1 protein	AA943110	Genes unknown fxn
304	ESTs unknown function	AI234712	ESTs unknown function
305	ESTs highly similar to rat myosin light chain kinase 2, skeletal muscle	AA924075	muscle contraction
306	Glutamine synthetase (glutamate-ammonia ligase)	AI232783	amino acid metabolism
307	pyruvate carboxylase	U32314	tricarboxylic acid cycle, gluconeogenesis
308	ESTs unknown function	AI172057	ESTs unknown function
309	ESTs similar to human methylmalonyl CoA epimerase	AI172417	Genes unknown fxn
310	ESTs similar to mouse kelch family protein Nd1	AA799539	Genes unknown fxn
311	ESTs similar to mouse glutaryl-Coenzyme A dehydrogenase	AI105435	Amino-acid metabolism
312	ESTs unknown function	AA859543	ESTs unknown function
313	myosin, heavy polypeptide 4, skeletal muscle (MHC2B)	L24897	muscle contraction
314	ESTs unknown function	AA858817	ESTs unknown function

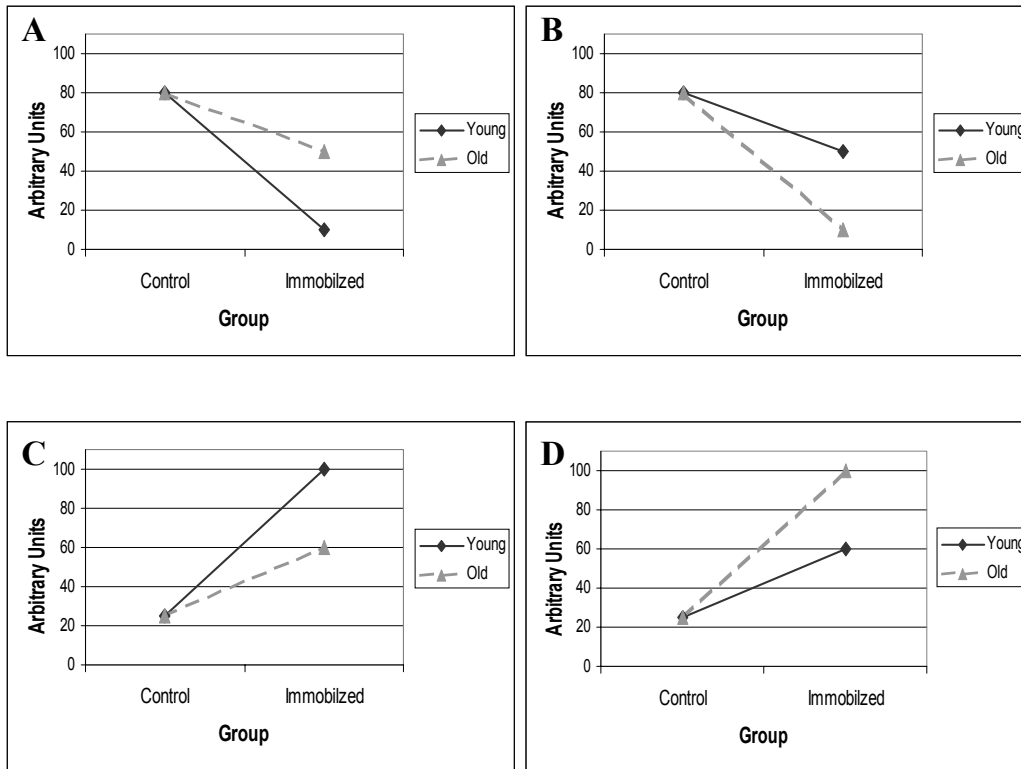
315	ESTs unknown function	AI171772	ESTs unknown function
316	insulin-like growth factor binding protein 3	M31837	signaling
317	interleukin 15	U69272	immune response
318	ESTs similar to mouse diacylglycerol O-acyltransferase 2	AI045040	lipid metabolism
319	ESTs weakly similar to human p53 regulated PA26 nuclear protein	AI137579	cell cycle
320	hypoxia-inducible factor 1-responsive gene, RTP801	AI144692	Genes unknown fxn
321	serine protease inhibitor (spin2b)	M38566	serine protease inhibitor
322	branched chain aminotransferase 2, mitochondrial	U68417	amino acid metabolism
323	ESTs unknown function	AI070446	ESTs unknown function
324	ESTs unknown function	AI227690	ESTs unknown function
325	ESTs similar to mouse glutathione transferase zeta 1 (maleylacetoacetate isomerase)	AI169075	amino acid metabolism
326	Glutamine synthetase (glutamate-ammonia ligase)	AA852004	amino acid metabolism
327	ESTs unknown function	AI137344	ESTs unknown function
328	ESTs weakly similar to human transducin-like enhancer of split 1 (E(sp1) homolog, Drosophila)	AA875084	developmental processes
329	ESTs similar to mouse chemokine (C-X-C motif) ligand 14	AA874803	immune response
330	type 2X myosin heavy chain mRNA, partial cds	S68736	muscle contraction
331	ESTs weakly similar to mouse D-dopachrome tautomerase	AA945149	melanin biosynthesis
332	aldehyde oxidase (female form)	AA926200	inflammatory response
333	ESTs similar to human glutathione S-transferase theta 1	AA819129	glutathione transferase
334	heat shock protein 70-1 (Hspa1a)	AA848563	chaperone
335	sodium channel, voltage-gated, type 1, alpha polypeptide	M22253	ion transport
336	cAMP responsive element modulator	S66024	regulation of transcription
337	actin alpha cardiac 1	X80130	muscle contraction
338	actin, alpha, cardiac	AI104567	muscle contraction
339	ESTs similar to mouse enabled homolog (Drosophila)	AI229412	actin
340	actin, alpha, cardiac	AA866452	muscle contraction
341	ESTs unknown function	AI639060	ESTs unknown function
342	heat shock protein 70-1 (Hspa1a)	AA818604	chaperone
343	ESTs highly similar to mouse enabled homolog (Drosophila)	AA957653	actin
344	actin alpha cardiac 1	X80130	muscle contraction
345	ESTs similar to mouse enabled homolog (Drosophila)	AI137553	actin
346	ASM15 gene	X59864	Genes unknown fxn
347	ESTs unknown function	AI172334	ESTs unknown function
348	ASM15 gene	X59864	Genes unknown fxn
349	cholinergic receptor, nicotinic, delta polypeptide	X74835	muscle contraction
350	ESTs similar to rat tyrosine aminotransferase	AI178785	tyrosine aminotransferase
351	gnat-3 for gustducin	X65747	Genes unknown fxn
352	ESTs weakly similar to human PTH-responsive osteosarcoma B1 protein	AI235250	Genes unknown fxn
353	guanine nucleotide binding protein, beta polypeptide 2	AA817993	signal transduction
354	ESTs similar to mouse ankyrin repeat and SOCs box-containing protein 5	AI169831	Genes unknown fxn

**Supplementary Figure 1.** A condensed view of the hierarchical cluster that resulted from analyzing the 354 significant age-atrophy interactions presented in Table 3 of Supplementary Material are shown. Clusters are based on normalized signal data, by normalizing the maximum value of the four group means, then each of the three remaining means being scaled to the maximal mean. This methodology allowed genes of differing abundances to be normalized to the same percentage scale with a resultant ability to cluster genes of similar expression patterns.



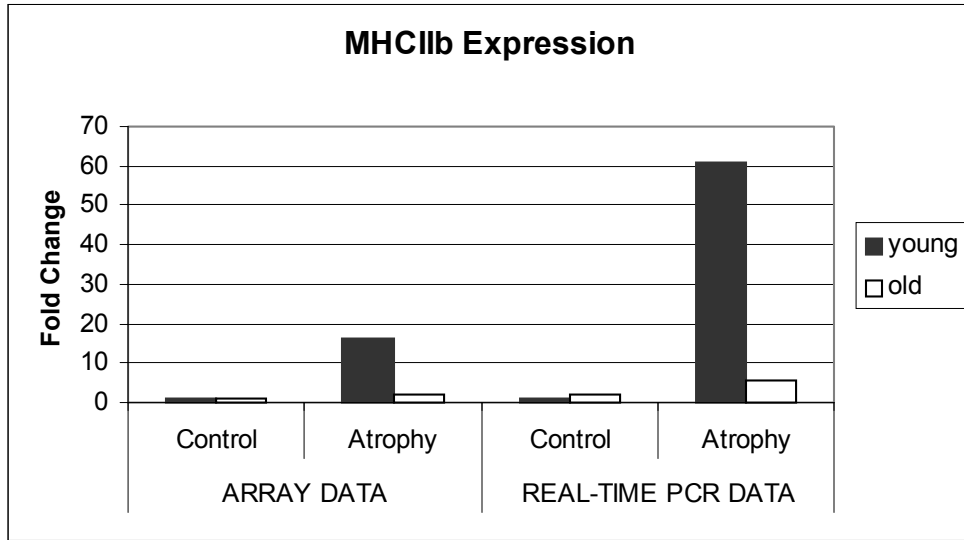


**Supplementary Figure 2.** Age-atrophy interactions consisted of four major graphical patterns illustrated in A-D. A) Illustrates the graphical phenotype when probe sets in the young soleus muscle show a greater decrease in response to immobilization than does the old. B) Shows the pattern of expression when old levels are decreased more than young with atrophy. C) Demonstrates those probe sets where young levels are elevated more so than old. D) Displays the pattern of response when transcript levels are greater in old than young. The y-axis is in arbitrary units, as these graphs are illustrations of the major age-atrophy interactions expression patterns observed, not actual data.



**Supplementary Figure 3.** A) A comparison MHC IIb fold changes in expression with age and atrophy from microarray and real-time PCR analyses. B) Contrasts the fold differences in expression for MHC IIx observed with microarray and real-time PCR analyses.

A.



B.

