

Table S3, Roth et al. 2002

Young Before-ST	Older Before-ST	Before-ST Ratio	Acc#	Gene	Young After-ST	Older After-ST	After-ST Ratio
0.128	0.049	0.380	W72697	cisplatin resistance associated	0.111	0.057	0.514
0.351	0.139	0.395	N90273	ras homolog gene family, member H	0.251	0.123	0.491
0.251	0.100	0.398	AA443634	ubiquitin-conjugating enzyme E2G 2 (homologous to yeast UBC7)	0.223	0.070	0.314
0.089	0.041	0.455	H38839	EST	0.110	0.042	0.379
0.269	0.125	0.464	AA464748	collagen, type VI, alpha 2	0.506	0.154	0.305
0.070	0.033	0.471	H50344	tight junction protein 1 (zona occludens 1)	0.100	0.033	0.326
0.342	0.161	0.471	N55480	HMT1 (hnRNP methyltransferase, S. cerevisiae)-like 2	0.310	0.141	0.454
0.514	0.242	0.471	R60317	dihydrolipoamide dehydrogenase (E3 component of pyruvate dehydrogenase complex, 2-oxo-glutarate complex, branched chain keto acid dehydrogenase complex)	0.432	0.192	0.444
0.095	0.045	0.475	AA670422	ADP-ribosylation factor 3	0.089	0.050	0.559
0.231	0.115	0.496	N62761	fragile X mental retardation, autosomal homolog 1	0.118	0.051	0.433
0.127	0.063	0.499	AA234671	ATP-binding cassette, sub-family D (ALD), member 3	0.119	0.060	0.501
0.085	0.043	0.500	H49592	guanine nucleotide binding protein (G protein), alpha activating activity polypeptide, olfactory type	0.126	0.041	0.322
0.083	0.043	0.513	AA173454	macrophage stimulating 1 receptor (c-met-related tyrosine kinase)	0.111	0.038	0.345
0.065	0.034	0.518	AA447730	pim-1 oncogene	0.067	0.037	0.556
0.078	0.041	0.527	N54794	plasminogen activator inhibitor, type I	0.082	0.043	0.523
0.167	0.089	0.532	N94921	receptor tyrosine kinase-like orphan receptor 2	0.226	0.111	0.492
0.348	0.186	0.533	AA463631	signal recognition particle 72kD	0.328	0.118	0.359
0.268	0.145	0.539	AA045699	transmembrane 4 superfamily member 3	0.233	0.136	0.585
0.110	0.059	0.541	R17676	ubiquinol-cytochrome c reductase hinge protein	0.149	0.070	0.472
0.065	0.036	0.545	H74265	protein tyrosine phosphatase, receptor type, c polypeptide	0.113	0.037	0.325
0.117	0.064	0.545	AA279072	inositol polyphosphate phosphatase-like 1	0.125	0.061	0.489
0.186	0.102	0.547	H48122	breast cancer 2, early onset	0.159	0.093	0.586
0.192	0.105	0.547	AA464544	LIM domain only 2 (rhombotin-like 1)	0.293	0.139	0.475
0.115	0.063	0.554	AA047260	H2A histone family, member O	0.144	0.084	0.584
0.070	0.039	0.555	H90287	ubiquitously transcribed tetratricopeptide repeat gene, X chromosome	0.080	0.038	0.475
0.112	0.062	0.557	H95633	crystallin, alpha A	0.187	0.073	0.388
0.112	0.062	0.557	H41489	adaptor-related protein complex 1, beta 1 subunit	0.133	0.065	0.486
0.076	0.042	0.558	H07899	vascular endothelial growth factor C	0.081	0.041	0.505
0.303	0.169	0.558	AA054321	H.sapiens HCG I mRNA	0.344	0.192	0.559

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0.136	0.076	0.559	H20743	cell division cycle 34	0.249	0.085	0.340
0.220	0.123	0.560	N53351	Ric (Drosophila)-like, expressed in neurons	0.197	0.109	0.552
0.567	0.319	0.562	H54289	Golgi vesicular membrane trafficking protein p18	0.848	0.481	0.567
0.090	0.051	0.565	AA088434	zinc finger protein 38 (KOX 25)	0.105	0.056	0.529
0.094	0.054	0.567	H14359	E74-like factor 4 (ets domain transcription factor)	0.100	0.058	0.578
0.159	0.091	0.569	R48926	hydroxyacyl-Coenzyme A dehydrogenase/3-ketoacyl-Coenzyme A thiolase/enoyl-Coenzyme A hydratase (trifunctional protein), alpha subunit	0.199	0.102	0.512
0.073	0.042	0.570	R89082	A kinase (PRKA) anchor protein 7	0.095	0.040	0.423
0.061	0.035	0.572	AA070358	transketolase (Wernicke-Korsakoff syndrome)	0.093	0.034	0.363
0.074	0.042	0.572	AA019320	adducin 2 (beta)	0.089	0.046	0.514
0.123	0.071	0.573	H05445	growth associated protein 43	0.203	0.073	0.360
0.179	0.103	0.575	AA598759	phosphogluconate dehydrogenase	0.218	0.108	0.496
0.065	0.038	0.577	R67376	pleckstrin homology, Sec7 and coiled/coil domains 3	0.086	0.040	0.467
0.092	0.053	0.578	H99736	chromodomain helicase DNA binding protein 1	0.124	0.051	0.409
0.079	0.046	0.580	AA598401	archain 1	0.103	0.046	0.443
0.507	0.295	0.581	H05820	ribosomal protein, mitochondrial, L3	0.409	0.220	0.539
0.071	0.042	0.584	R70488		0.098	0.043	0.440
0.075	0.044	0.584	AA425853	splicing factor proline/glutamine rich (polypyrimidine tract-binding protein-associated)	0.065	0.037	0.572
0.424	0.732	1.727	AA434144	claudin 3	0.353	0.734	2.076
1.294	2.302	1.779	H16958	glyceraldehyde-3-phosphate dehydrogenase	0.372	0.697	1.873
0.175	0.322	1.836	AA496360	protein kinase C, delta	0.215	0.388	1.805
1.283	2.540	1.979	H16958	glyceraldehyde-3-phosphate dehydrogenase	0.403	0.786	1.952
0.069	0.145	2.115	AA463452	DiGeorge syndrome critical region gene DGS1	0.088	0.164	1.862
0.161	0.378	2.348	R51209	protein phosphatase 2A, regulatory subunit B' (PR 53)	0.236	0.491	2.077
0.528	1.243	2.356	AA481780	carbonic anhydrase III, muscle specific	0.208	0.411	1.977
0.176	0.456	2.601	AA664077	ATPase, vacuolar, 14 kD	0.206	0.368	1.782