

Table S5, Roth et al. 2002

Before-ST	After-ST	Ratio	Acc#	Gene
1.715	0.175	0.102	R68106	Fc fragment of IgG, low affinity IIb, receptor for (CD32)
1.303	0.146	0.112	AA443634	ubiquitin-conjugating enzyme E2G 2 (homologous to yeast UBC7)
1.082	0.268	0.248	AA455925	four and a half LIM domains 1
1.646	0.432	0.262	N78927	myosin, light polypeptide 2, regulatory, cardiac, slow
0.987	0.261	0.265	AA455300	cold shock domain protein A
1.798	0.535	0.297	H16958	glyceraldehyde-3-phosphate dehydrogenase
1.912	0.594	0.311	H16958	glyceraldehyde-3-phosphate dehydrogenase
0.885	0.310	0.350	AA481780	carbonic anhydrase III, muscle specific
0.697	0.265	0.380	W58092	tropomyosin 1 (alpha)
0.692	0.280	0.405	AA634006	actin, alpha 2, smooth muscle, aorta
0.230	0.102	0.442	AA192166	myosin, light polypeptide 3, alkali; ventricular, skeletal, slow
0.670	0.299	0.446	R44290	actin, beta
1.537	0.698	0.454	AA196393	Human alkali myosin light chain 3 mRNA, complete cds
0.315	0.144	0.456	AA112660	forkhead box F1
0.210	0.101	0.484	R43973	eukaryotic translation elongation factor 1 gamma
0.425	0.206	0.484	T61948	FBJ murine osteosarcoma viral oncogene homolog B
0.173	0.084	0.489	N62761	fragile X mental retardation, autosomal homolog 1
0.149	0.075	0.503	AA680322	NADH dehydrogenase (ubiquinone) 1 alpha subcomplex, 4 (9kD, MLRQ)
0.234	0.118	0.505	AA708298	ATP synthase, H <sup>+</sup> transporting, mitochondrial F1 complex, beta polypeptide
0.421	0.214	0.508	AA182848	troponin I, skeletal, slow
0.253	0.130	0.513	R40850	ARP1 (actin-related protein 1, yeast) homolog A (centractin alpha)
0.574	0.298	0.520	R44290	actin, beta
0.174	0.091	0.520	R43973	eukaryotic translation elongation factor 1 gamma
0.113	0.059	0.524	AA680244	ribosomal protein L11
0.223	0.118	0.529	AA126265	calnexin
0.732	0.400	0.547	R60160	topoisomerase (DNA) I
0.172	0.094	0.548	AA599175	nuclease sensitive element binding protein 1
0.593	0.328	0.554	R52541	EST
0.140	0.078	0.556	AA045508	adenylyl cyclase-associated protein 2
0.294	0.165	0.559	W93500	potassium voltage-gated channel, KQT-like subfamily, member 1
0.210	0.118	0.562	T67270	EST
0.516	0.291	0.565	AA428058	NADH dehydrogenase (ubiquinone) 1 beta subcomplex, 7 (18kD, B18)
0.406	0.230	0.567	H64325	son of sevenless (Drosophila) homolog 1
0.465	0.264	0.567	AA477400	tropomyosin 2 (beta)
0.203	0.115	0.569	AA634008	ribosomal protein S23
0.283	0.161	0.571	H88599	predicted osteoblast protein
0.573	0.327	0.571	AA868929	troponin T1, skeletal, slow
0.700	0.400	0.571	AA176957	nebulin
15.151	8.733	0.576	AA872001	annexin A6
0.123	0.071	0.579	AA044059	voltage-dependent anion channel 1
0.135	0.078	0.579	H85355	ATPase, Ca <sup>++</sup> transporting, cardiac muscle, slow twitch 2
0.219	0.127	0.579	AA453766	CASP8 and FADD-like apoptosis regulator
3.721	2.163	0.581	R33154	EST
0.223	0.130	0.583	R53942	solute carrier family 25 (mitochondrial carrier; adenine nucleotide translocator), member 4

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1.261	0.736	0.584	T94169	mitogen-activated protein kinase 8
0.422	0.249	0.589	T60048	actin, gamma 2, smooth muscle, enteric
3.666	2.162	0.590	AA176581	myoglobin
0.054	0.092	1.704	N54165	defensin, alpha 1, myeloid-related sequence
0.195	0.333	1.705	AA400474	ESTs, Highly similar to zona-pellucida-binding protein [H.sapiens]
0.055	0.094	1.706	AA083478	stimulated trans-acting factor (50 kDa)
1.410	2.406	1.707	R43325	death associated protein 3
0.042	0.072	1.709	AA219045	microtubule-associated protein 1B
0.100	0.171	1.712	AA126009	FXVD domain-containing ion transport regulator 3
0.071	0.121	1.714	AA418077	GTP-binding protein overexpressed in skeletal muscle
0.117	0.201	1.721	AA620553	flap structure-specific endonuclease 1
0.060	0.103	1.731	H65034	EST
0.048	0.083	1.742	AA678295	BRCA1 associated RING domain 1
3.610	6.440	1.784	AA099394	signal sequence receptor, alpha (translocon-associated protein alpha)
0.046	0.083	1.801	AA464267	Bicaudal D (Drosophila) homolog 1
0.044	0.081	1.852	AA456295	TNF receptor-associated factor 6
0.041	0.076	1.864	AA488366	transcription factor 12 (HTF4, helix-loop-helix transcription factors 4)
0.095	0.182	1.909	AA496359	immediate early protein
0.083	0.160	1.923	AA159359	dystrobrevin, beta
0.040	0.078	1.943	H61188	EST
0.064	0.125	1.950	R32756	Ewing sarcoma breakpoint region 1
0.102	0.206	2.011	R45264	proteolipid protein 1 (Pelizaeus-Merzbacher disease, spastic paraplegia 2, uncomplicated)
0.117	0.249	2.131	AA464601	tetraspan 5
0.171	0.371	2.175	N92901	fatty acid binding protein 4, adipocyte
0.155	0.378	2.438	AA291749	estrogen receptor 1