

Table 2: Upregulated genes in the mantle when compared to the foot

Transcript	logFC	Description	E Value	SwissProt ID
TRINITY_DN109584_c1_g1_i1	13.74960181	70 kDa neurofilament protein	0	Q01241 (NF70_DORPE)
TRINITY_DN110634_c4_g1_i8	13.59450218			
TRINITY_DN149117_c3_g1_i2	13.43637279			
TRINITY_DN139376_c8_g1_i1	13.21674066			
TRINITY_DN106542_c0_g1_i1	12.82891649			
TRINITY_DN94974_c0_g1_i4	12.81801482	Alpha-2-macroglobulin	5.05E-08	Q7SIH1 (A2MG_BOVIN)
TRINITY_DN110014_c3_g1_i12	12.75501436			
TRINITY_DN140482_c6_g1_i5	12.21300209			
TRINITY_DN96497_c1_g1_i1	11.12526516			
TRINITY_DN120503_c3_g1_i2	10.93529026			
TRINITY_DN95173_c0_g1_i5	10.81018923	CD109 antigen	5.74E-12	Q6YHK3 (CD109_HUMAN)
TRINITY_DN130363_c0_g2_i1	10.53671829			
TRINITY_DN110634_c4_g1_i1	10.52523251			
TRINITY_DN108220_c2_g1_i4	10.42053094	Galaxin	4.10E-18	D9IQ16 (GXN_ACRMI)
TRINITY_DN118207_c1_g1_i1	10.40361985	C3 and PZP-like alpha-2-macroglobulin domain	4.54E-07	Q8IZJ3 (CPMD8_HUMAN)
TRINITY_DN94974_c0_g1_i1	10.36764527	Murinoglobulin-2	4.11E-08	Q6IE52 (MUG2_RAT)
TRINITY_DN127647_c9_g1_i1	10.14303943	CD109 antigen	1.59E-09	Q6YHK3 (CD109_HUMAN)
TRINITY_DN127647_c9_g2_i1	10.13802383			
TRINITY_DN148175_c6_g1_i1	9.966865301			
TRINITY_DN127647_c9_g2_i2	9.941489203			
TRINITY_DN117957_c4_g2_i2	9.906102977			
TRINITY_DN94717_c1_g1_i4	9.872076898	CD109 antigen	3.51E-52	Q8R422 (CD109_MOUSE)
TRINITY_DN127647_c9_g4_i1	9.869369442			
TRINITY_DN96894_c8_g1_i1	9.868307845			
TRINITY_DN98415_c2_g1_i6	9.768064494			
TRINITY_DN146621_c3_g1_i1	9.738122379			
TRINITY_DN144329_c1_g2_i7	9.727775165			
TRINITY_DN127647_c9_g4_i3	9.661579082			
TRINITY_DN114604_c2_g3_i2	9.637707126	Adhesion G protein-coupled receptor L2	1.12E-10	O95490 (AGRL2_HUMAN)
TRINITY_DN148473_c9_g1_i4	9.636456085	CD109 antigen	2.71E-13	Q6YHK3 (CD109_HUMAN)
TRINITY_DN148473_c9_g1_i2	9.634757104			
TRINITY_DN136326_c1_g2_i2	9.616827072			
TRINITY_DN96497_c1_g1_i2	9.521803304			
TRINITY_DN96497_c1_g2_i1	9.505495172	Mucin-17	1.03	Q685J3 (MUC17_HUMAN)
TRINITY_DN117957_c4_g2_i1	9.482596683			
TRINITY_DN116710_c2_g1_i1	9.39495305	Endoglucanase 17	0.407	O81416 (GUN17_ARATH)
TRINITY_DN141091_c0_g1_i6	9.331955527			
TRINITY_DN117957_c4_g2_i3	9.328570847	30S ribosomal protein S13	6.69	Q12G80 (RS13_POLSJ)
TRINITY_DN110634_c4_g1_i3	9.306944603			
TRINITY_DN95173_c0_g1_i4	9.155182777	UPF0215 protein TGAM_0348	1.23	C5A3N8 (Y348_THEGJ)
TRINITY_DN132915_c2_g1_i1	9.093852683	Lectin L6	7.31E-27	P82151 (LEC6_TACTR)
TRINITY_DN144329_c1_g2_i5	8.978017498			
TRINITY_DN119459_c4_g2_i1	8.970374291			
TRINITY_DN99400_c3_g2_i1	8.941438438	Latrophilin Cirl	0.00611	B4GD14 (LPHN_DROPE)
TRINITY_DN144329_c1_g2_i3	8.927118041			
TRINITY_DN139376_c8_g2_i1	8.90405173			
TRINITY_DN121323_c0_g1_i2	8.894144656			
TRINITY_DN114604_c2_g3_i1	8.814588137	Adhesion G protein-coupled receptor L2	7.42E-13	O97817 (AGRL2_BOVIN)
TRINITY_DN144329_c1_g1_i1	8.782331786			
TRINITY_DN99400_c3_g1_i4	8.706714651			
TRINITY_DN126041_c2_g1_i1	8.674477338	Cysteine and glycine-rich protein 3	0.00484	P50462 (CSRP3_MOUSE)
TRINITY_DN121323_c0_g1_i1	8.631725492			
TRINITY_DN144175_c3_g2_i1	8.619020961			
TRINITY_DN114604_c2_g2_i2	8.604603987	E3 ubiquitin-protein ligase rnf213-beta	5.9	A0A0R4I9Y1 (R213B_DANRE)
TRINITY_DN117957_c4_g3_i1	8.540243285			
TRINITY_DN121323_c0_g2_i1	8.537072858			
TRINITY_DN109805_c3_g6_i1	8.465464502	Lipase chaperone	2.13	Q05490 (LIFO_BURGL)

TRINITY_DN145134_c2_g1_i3	8.409546038	CD109 antigen	5.82E-25	Q6YHK3 (CD109_HUMAN)
TRINITY_DN109805_c3_g1_i13	8.408591689	General transcription and DNA repair factor III	1.34	Q02870 (ERCC3_DROME)
TRINITY_DN128972_c2_g2_i1	8.405877513	Galaxin	8.76E-37	D9IQ16 (GXN_ACRMI)
TRINITY_DN123635_c6_g5_i2	8.374398616			
TRINITY_DN138006_c5_g1_i7	8.246137972			
TRINITY_DN130572_c0_g2_i1	7.89376657	Arylsulfatase J	1.77E-59	Q8BM89 (ARSL_MOUSE)
TRINITY_DN99688_c2_g1_i3	7.789277315	ATP-dependent 6-phosphofructokinase, platelet	4.32	P47859 (PFKFB3_RABIT)
TRINITY_DN148527_c7_g2_i3	7.776327997	Ethanolamine utilization protein EutN	3.74	P0AEJ9 (EUTN_ECOL6)
TRINITY_DN148527_c7_g2_i4	7.56478481			
TRINITY_DN135656_c2_g2_i2	7.213149754			
TRINITY_DN139376_c8_g1_i2	7.174204111			
TRINITY_DN124813_c1_g1_i1	6.849848663	Peptidase inhibitor 16	6.16E-28	Q9ET66 (PI16_MOUSE)
TRINITY_DN114296_c7_g1_i2	6.843448282	Non-reducing polyketide synthase terA	6.72	Q0D1N9 (TERA_ASPTN)
TRINITY_DN145281_c7_g7_i1	6.409371204			
TRINITY_DN145281_c7_g1_i1	6.189486252			
TRINITY_DN143301_c3_g1_i14	6.043908185			
TRINITY_DN95720_c3_g1_i6	6.038373703	Beta-galactosidase	3.31	B4S2K9 (BGAL_ALTMD)
TRINITY_DN95720_c3_g1_i7	6.021648463	Vasopressin V2 receptor	6.92	O77808 (V2R_CANLF)
TRINITY_DN99688_c2_g1_i7	5.993633436	Lipoprotein signal peptidase	8.78	A9M1J8 (LSPA_NEIM0)
TRINITY_DN145281_c7_g1_i2	5.864406104			
TRINITY_DN114296_c7_g1_i3	5.803198405	Non-reducing polyketide synthase terA	6.5	Q0D1N9 (TERA_ASPTN)
TRINITY_DN145281_c7_g2_i1	5.793852156			
TRINITY_DN114296_c7_g1_i1	5.746231803	Non-reducing polyketide synthase terA	5.85	Q0D1N9 (TERA_ASPTN)
TRINITY_DN104901_c1_g1_i3	5.6522867	Myosin heavy chain, striated muscle	0	P24733 (MYS_ARGIR)
TRINITY_DN96216_c6_g1_i5	5.482918143	Tropomyosin-2	8.12E-83	P43689 (TPM2_BIOGL)
TRINITY_DN145281_c7_g3_i4	5.467127833	PH and SEC7 domain-containing protein 1	0.274	F1MUS9 (PSD1_BOVIN)
TRINITY_DN114296_c7_g3_i1	5.443747923	Myosin heavy chain, muscle	7.63E-21	P05661 (MYSA_DROME)
TRINITY_DN119191_c3_g2_i2	5.342466264	Rac guanine nucleotide exchange factor B	1.83E-06	Q55E26 (GXCB_DICDI)
TRINITY_DN99688_c2_g1_i16	5.326962916			
TRINITY_DN114296_c7_g2_i1	5.280800571			
TRINITY_DN138834_c0_g2_i4	5.212266142	Genetic interactor of prohibitins 3, mitochondrial	0.147	A7TQC5 (GEP3_VANPO)
TRINITY_DN148066_c3_g1_i2	5.200508971			
TRINITY_DN114296_c7_g2_i2	5.192479216			
TRINITY_DN113425_c0_g2_i1	5.140773443	Paramyosin	1.43E-32	O96064 (MYSP_MYTGA)
TRINITY_DN145281_c7_g2_i5	5.120429785			
TRINITY_DN115859_c5_g1_i1	5.075432795			
TRINITY_DN134975_c0_g1_i4	5.058126823			
TRINITY_DN147058_c7_g1_i7	5.037531783			
TRINITY_DN97751_c4_g3_i6	5.029607436	Myosin heavy chain, striated muscle	9.56E-39	P24733 (MYS_ARGIR)
TRINITY_DN94893_c4_g1_i1	4.958464474	Paramyosin	5.19E-38	O96064 (MYSP_MYTGA)
TRINITY_DN137587_c4_g2_i2	4.932370825	Actin, adductor muscle	6.21E-178	Q26065 (ACT_PLAMG)
TRINITY_DN100883_c3_g1_i3	4.89742475	50S ribosomal protein L28	4.67	Q74IN6 (RL28_LACJO)
TRINITY_DN111557_c5_g1_i4	4.897309314	Paramyosin	2.26E-11	O96064 (MYSP_MYTGA)
TRINITY_DN114296_c7_g4_i1	4.774990378			
TRINITY_DN98201_c3_g4_i1	4.715010785			
TRINITY_DN101698_c5_g1_i5	4.694930788	Serine--tRNA ligase	4.52	A5CVL9 (SYS_VESOH)
TRINITY_DN97751_c4_g2_i1	4.668331736	Uncharacterized protein At4g14342	9.24	P58728 (SF3BB_ARATH)
TRINITY_DN148981_c7_g3_i1	4.592717475			
TRINITY_DN138834_c0_g6_i1	4.583057429	Myosin catalytic light chain LC-1, mantle muscle	2.33E-13	P05945 (MLE_TODPA)
TRINITY_DN148981_c7_g2_i3	4.568644472			
TRINITY_DN113473_c3_g2_i7	4.554675479	Calponin-2	2.44E-14	Q08094 (CNN2_PIG)
TRINITY_DN125734_c6_g2_i6	4.547945862	Zinc finger protein Rlf	3.94	Q13129 (RLF_HUMAN)
TRINITY_DN138834_c0_g2_i2	4.544577041			
TRINITY_DN94893_c3_g2_i1	4.532706084	Paramyosin	8.29E-116	O96064 (MYSP_MYTGA)
TRINITY_DN95372_c0_g1_i2	4.527833558	Myosin heavy chain, striated muscle	1.10E-55	P24733 (MYS_ARGIR)
TRINITY_DN132357_c3_g3_i1	4.513965503	Mediator of RNA polymerase II transcription	0.00357	Q6BQ63 (MED21_DEBHA)
TRINITY_DN95372_c0_g2_i1	4.479907197	Myosin heavy chain, striated muscle	8.41E-56	P24733 (MYS_ARGIR)
TRINITY_DN98201_c3_g3_i1	4.466001101			
TRINITY_DN94893_c3_g1_i1	4.462635	Paramyosin	0	O96064 (MYSP_MYTGA)

TRINITY_DN132357_c3_g1_i14	4.319213303			
TRINITY_DN148981_c6_g3_i1	4.223987438	Four and a half LIM domains protein 2	1.29E-58	O35115 (FHL2_RAT)
TRINITY_DN125734_c6_g2_i3	4.223007348	Ribosome production factor 2 homolog	2.93	Q9LUG5 (RPF2_ARATH)
TRINITY_DN138834_c0_g2_i1	4.176659566			
TRINITY_DN148285_c15_g1_i2	4.129339856	Myosin heavy chain, striated muscle	1.11E-67	P24733 (MYS_ARGIR)
TRINITY_DN148793_c1_g2_i2	4.097957277	Filamin-C	6.82E-43	Q14315 (FLNC_HUMAN)
TRINITY_DN148285_c15_g3_i1	4.095772245			
TRINITY_DN141356_c1_g2_i2	4.087051191			
TRINITY_DN125734_c6_g2_i9	4.061248112	Ribosome production factor 2 homolog	5.09	Q9LUG5 (RPF2_ARATH)
TRINITY_DN146235_c8_g3_i1	4.055847426			
TRINITY_DN125457_c2_g1_i1	4.049983569			
TRINITY_DN98201_c3_g1_i3	4.036737766	Actin, muscle	3.84E-29	Q25381 (ACTM_LYTPI)
TRINITY_DN125348_c6_g1_i6	3.999875873			
TRINITY_DN138834_c0_g3_i1	3.95130181			
TRINITY_DN148793_c1_g4_i3	3.937355323			
TRINITY_DN149258_c19_g1_i2	3.93529102			
TRINITY_DN146551_c3_g3_i1	3.88341308			
TRINITY_DN95990_c5_g1_i9	3.871954385	Tubulin alpha-8 chain	4.08E-133	P09645 (TBA8_CHICK)
TRINITY_DN130348_c1_g1_i2	3.821326849			
TRINITY_DN105350_c0_g1_i1	3.796830415	UDP-glucuronosyltransferase 2C1	1.71E-55	P36514 (UD2C1_RABIT)
TRINITY_DN148660_c8_g1_i1	3.791783056	Calponin-1	6.41E-23	P26932 (CNN1_CHICK)
TRINITY_DN146586_c3_g1_i1	3.76327881			
TRINITY_DN147058_c7_g2_i1	3.762501917			
TRINITY_DN148285_c15_g4_i1	3.760287736			
TRINITY_DN113473_c3_g2_i5	3.744270256	Calponin-3	1.98E-09	P37397 (CNN3_RAT)
TRINITY_DN107026_c2_g3_i1	3.72766943	Tubulin alpha-1 chain	5.16E-96	P06603 (TBA1_DROME)
TRINITY_DN95372_c0_g3_i1	3.726166976	Myosin heavy chain, striated muscle	6.45E-36	P24733 (MYS_ARGIR)
TRINITY_DN98201_c4_g2_i4	3.716092896	Nuclear cap-binding protein subunit 2	9.71	COH859 (NCBP2_SALSA)
TRINITY_DN145652_c2_g1_i1	3.704932053			
TRINITY_DN108975_c5_g1_i1	3.585070427	Troponin I	1.43E-11	Q7M3Y3 (TNNI_CHLNI)
TRINITY_DN148793_c0_g2_i1	3.574554103	Filamin-A	1.25E-71	Q9VEN1 (FLNA_DROME)
TRINITY_DN95974_c2_g3_i1	3.542064441	Collagen alpha-1(XX) chain	6.82E-10	Q923P0 (COKA1_MOUSE)
TRINITY_DN148285_c15_g2_i2	3.537166532			
TRINITY_DN147058_c7_g3_i1	3.522563675			
TRINITY_DN143753_c1_g3_i2	3.51250856	von Willebrand factor A domain-containing pr	1.73E-22	Q70UZ7 (VWA2_MOUSE)
TRINITY_DN97394_c0_g1_i1	3.468399025	Calponin-3	7.21E-49	Q32L92 (CNN3_BOVIN)
TRINITY_DN101139_c2_g1_i1	3.442185263	Actin, adductor muscle	1.33E-92	Q26065 (ACT_PLAMG)
TRINITY_DN126193_c0_g2_i3	3.424300476	Troponin T, skeletal muscle	0.175	P19351 (TNNT_DROME)
TRINITY_DN147058_c7_g1_i4	3.37021466			
TRINITY_DN123144_c3_g4_i1	3.346666339			
TRINITY_DN126193_c0_g1_i1	3.341930208	Troponin T, skeletal muscle	3.06E-21	P19351 (TNNT_DROME)
TRINITY_DN146235_c8_g2_i2	3.332690161			
TRINITY_DN96341_c6_g2_i2	3.308068027	Myosin regulatory light chain, smooth muscle	2.02E-68	P08051 (MLR_SPISA)
TRINITY_DN115794_c1_g4_i1	3.18474527	Actin-1	1.18E-47	P0DM41 (ACT1_CAEEL)
TRINITY_DN142849_c4_g1_i1	3.177300219			
TRINITY_DN115959_c4_g1_i2	3.17166806	Actin	3.84E-72	Q11212 (ACT_SPOLI)
TRINITY_DN107026_c2_g4_i2	3.161549798	Tubulin alpha chain	5.59E-19	Q8WQ47 (TBA_LEPDS)
TRINITY_DN138099_c4_g1_i1	3.130675546			
TRINITY_DN145652_c2_g5_i1	3.125000594	Transgelin-3	3.59E-09	Q5R6R2 (TAGL3_PONAB)
TRINITY_DN147377_c4_g1_i1	3.09701888			
TRINITY_DN148328_c9_g2_i1	3.029806268			
TRINITY_DN132357_c3_g1_i4	3.013385267			
TRINITY_DN147910_c6_g3_i1	3.00278577			
TRINITY_DN144740_c4_g3_i2	2.993432602	Troponin C	2.35E-64	Q9BLG0 (TNNC_TODPA)
TRINITY_DN132357_c3_g1_i1	2.978824958			
TRINITY_DN143097_c8_g6_i1	2.949377379			
TRINITY_DN129669_c0_g2_i2	2.936914127			
TRINITY_DN126193_c0_g2_i2	2.905202808	Troponin T, skeletal muscle	0.118	P19351 (TNNT_DROME)
TRINITY_DN149308_c23_g1_i1	2.809001514			

TRINITY_DN149288_c8_g1_i1	2.784870632			
TRINITY_DN132800_c5_g1_i1	2.768366701			
TRINITY_DN96216_c6_g3_i2	2.76724786	DNA ligase	1.77	Q89FV8 (DNLJ_BRADU)
TRINITY_DN135031_c13_g1_i1	2.758204997			
TRINITY_DN142849_c4_g2_i1	2.751437855			
TRINITY_DN127119_c2_g1_i2	2.657409036	Tubulin beta chain	3.28E-18	P02556 (TBB_LYTPI)
TRINITY_DN148300_c8_g3_i1	2.65559905			
TRINITY_DN96216_c6_g1_i10	2.639654816	Tropomyosin-2	5.87E-83	P43689 (TPM2_BIOGL)
TRINITY_DN143097_c8_g1_i1	2.621618437			
TRINITY_DN149057_c3_g1_i1	2.617147151			
TRINITY_DN125348_c6_g2_i1	2.5820959	Alanine--tRNA ligase	0.527	A8F866 (SYA_PSELT)
TRINITY_DN96216_c6_g1_i6	2.574518347	Tropomyosin-2	4.53E-101	P43689 (TPM2_BIOGL)
TRINITY_DN148066_c3_g1_i3	2.560580459			
TRINITY_DN148328_c9_g1_i2	2.529167793			
TRINITY_DN148897_c1_g1_i3	2.473286684			
TRINITY_DN144529_c5_g2_i1	2.460185013			
TRINITY_DN140616_c7_g1_i1	2.442220047			
TRINITY_DN109584_c1_g2_i3	2.381014112			
TRINITY_DN113497_c5_g3_i2	2.298869552			
TRINITY_DN148891_c4_g1_i2	2.28001834			
TRINITY_DN117900_c4_g1_i1	2.26462188			
TRINITY_DN148462_c1_g2_i1	2.250678368			
TRINITY_DN148843_c0_g1_i3	2.23926354			
TRINITY_DN112180_c2_g1_i7	2.185359741	Tubulin beta chain	7.94E-55	P18700 (TBB_STRPU)
TRINITY_DN125756_c0_g1_i8	2.140416824	Myosin essential light chain, striated adductor	2.84E-66	P07291 (MLE_ARGIR)
TRINITY_DN135670_c1_g1_i6	2.137652003			
TRINITY_DN147058_c7_g1_i1	2.135320019			
TRINITY_DN127119_c2_g1_i4	2.124832866	Tubulin beta chain	1.11E-18	P02556 (TBB_LYTPI)
TRINITY_DN148843_c3_g1_i6	2.101579031	Tubulin beta chain	7.63E-65	P02556 (TBB_LYTPI)
TRINITY_DN102049_c2_g1_i1	2.080768109	Tubulin beta chain	2.50E-144	P41386 (TBB_HALDI)
TRINITY_DN140411_c4_g2_i1	2.004189758			
TRINITY_DN148595_c5_g1_i1	1.997714753			
TRINITY_DN113017_c0_g1_i1	1.981017107			
TRINITY_DN118324_c4_g3_i1	1.977156638			
TRINITY_DN135061_c1_g1_i7	1.974550296			
TRINITY_DN138446_c4_g3_i1	1.972504175			
TRINITY_DN102992_c7_g4_i1	1.965915687			
TRINITY_DN137587_c4_g2_i4	1.945411046	Actin, cytoplasmic	0	Q93129 (ACTC_BRABE)
TRINITY_DN110232_c6_g1_i1	1.929798946	Olfactory receptor 51J1	7.36	Q9H342 (O51J1_HUMAN)
TRINITY_DN148843_c2_g1_i5	1.908583851	Tubulin beta chain	8.08E-140	P41386 (TBB_HALDI)
TRINITY_DN104559_c1_g5_i1	1.903201496	Tubulin beta-4B chain	1.27E-104	P86221 (TBB4B_MESAU)
TRINITY_DN149257_c10_g1_i1	1.889067132			
TRINITY_DN135670_c1_g1_i2	1.878543179			
TRINITY_DN97747_c6_g2_i1	1.875032318	Myosin regulatory light chain LC-2, mantle mu	1.92E-65	P08052 (MLR_TODPA)
TRINITY_DN148462_c1_g1_i4	1.842960385			
TRINITY_DN142485_c1_g1_i1	1.838632698			
TRINITY_DN122375_c10_g1_i1	1.823794582			
TRINITY_DN140411_c4_g4_i1	1.809312421	Structural maintenance of chromosomes protein	0.592	G5EG17 (SMC6_CAEEL)
TRINITY_DN142538_c2_g1_i6	1.784161365	Cytochrome b	3.80E-40	P34864 (CYB_SARCH)
TRINITY_DN127253_c5_g3_i2	1.774424481			
TRINITY_DN148119_c2_g2_i1	1.769191903			
TRINITY_DN129828_c3_g1_i1	1.761764069			
TRINITY_DN126917_c0_g1_i1	1.751347582	Fibrillin-1	3.33E-14	P98133 (FBN1_BOVIN)
TRINITY_DN148843_c3_g1_i4	1.751312634	Tubulin beta chain	1.34E-86	P02556 (TBB_LYTPI)
TRINITY_DN136970_c0_g1_i4	1.732498504	NADH dehydrogenase [ubiquinone] iron-sulfur	2.31E-108	P42028 (NDUS8_BOVIN)
TRINITY_DN102049_c2_g4_i1	1.725826613	Tubulin beta-4B chain	6.08E-15	P86221 (TBB4B_MESAU)
TRINITY_DN125736_c1_g1_i2	1.713912293	Protein disulfide-isomerase	2.51E-174	P07237 (PDIA1_HUMAN)
TRINITY_DN140739_c2_g1_i1	1.699443868			
TRINITY_DN136157_c3_g2_i1	1.673944933			

TRINITY_DN123957_c0_g1_i1	1.667104824		
TRINITY_DN127203_c3_g1_i1	1.666367805		
TRINITY_DN122984_c6_g1_i5	1.654510304	Protein-L-isoaspartate(D-aspartate) O-methyl	5.91E-103 Q5F3N1 (PIMT_CHICK)
TRINITY_DN149250_c4_g1_i1	1.650244638		
TRINITY_DN112033_c7_g1_i1	1.62266584	Vesicle transport protein SEC20	1.65E-57 Q12981 (SEC20_HUMAN)
TRINITY_DN126458_c1_g4_i1	1.620854628	Peroxisome biogenesis factor 1	7.34 O43933 (PEX1_HUMAN)
TRINITY_DN133784_c1_g2_i1	1.617266142	Mitochondrial import inner membrane translo	1.48E-46 Q9VF08 (TIM16_DROME)
TRINITY_DN146586_c3_g1_i3	1.604460502		
TRINITY_DN138873_c1_g2_i2	1.599176289	FAST kinase domain-containing protein 3, mit	3.17 Q14CZ7 (FAKD3_HUMAN)
TRINITY_DN141403_c3_g2_i5	1.595715117		
TRINITY_DN135734_c0_g1_i3	1.562783552		
TRINITY_DN102031_c2_g1_i1	1.536098524	Cytochrome b	1.03E-59 Q9MDZ9 (CYB_DROSI)
TRINITY_DN148101_c0_g1_i1	1.5107623		
TRINITY_DN148462_c1_g1_i3	1.490339264		
TRINITY_DN141403_c3_g2_i4	1.484586427		
TRINITY_DN121689_c0_g2_i1	1.480416275	LIM domain-containing protein WLIM2a	1.26E-13 O04193 (WLI2A_ARATH)
TRINITY_DN149210_c3_g2_i1	1.48024028		
TRINITY_DN75965_c0_g1_i1	1.471579668	Nucleolar protein 11	0.0132 Q6INI5 (NOL11_XENLA)
TRINITY_DN148773_c11_g1_i3	1.457930346		
TRINITY_DN122156_c3_g1_i1	1.453740796		
TRINITY_DN125593_c57_g1_i3	1.447182195		
TRINITY_DN140815_c0_g1_i11	1.417837596		
TRINITY_DN121195_c4_g2_i3	1.405923763		
TRINITY_DN136231_c5_g3_i1	1.394990177		
TRINITY_DN143656_c1_g1_i3	1.385872206		
TRINITY_DN93287_c0_g1_i1	1.378088429	Cytochrome c oxidase subunit 5B, mitochondri	1.50E-19 Q5REG2 (COX5B_PONAB)
TRINITY_DN138873_c1_g1_i1	1.371080466		
TRINITY_DN142125_c0_g2_i1	1.363355927		
TRINITY_DN118689_c0_g1_i1	1.354496049	Zinc finger protein 765	2.09 Q7L2R6 (ZN765_HUMAN)
TRINITY_DN146972_c1_g1_i2	1.348012445		
TRINITY_DN136239_c3_g1_i2	1.301581487		
TRINITY_DN107664_c6_g1_i3	1.298080481	Hexokinase type 2	3.84E-146 Q9NFT7 (HXK2_DROME)
TRINITY_DN124921_c0_g1_i1	1.296464072		
TRINITY_DN147875_c1_g1_i1	1.292730476		
TRINITY_DN110702_c0_g1_i1	1.29006276	Cytochrome c oxidase subunit 2	2.24E-51 P33505 (COX2_ANOQU)
TRINITY_DN149203_c8_g1_i4	1.279248792		
TRINITY_DN95471_c4_g1_i4	1.275481575		
TRINITY_DN127582_c0_g2_i6	1.273001674		
TRINITY_DN142723_c2_g1_i1	1.262295008		
TRINITY_DN146931_c8_g2_i4	1.250751644	Cytochrome c oxidase subunit 1	2.52E-69 O03539 (COX1_NOTPE)
TRINITY_DN148060_c5_g1_i2	1.234866806		
TRINITY_DN113015_c3_g1_i4	1.214310503	Heat shock cognate 71 kDa protein	0 P11142 (HSP7C_HUMAN)
TRINITY_DN120971_c3_g1_i1	1.209360766		
TRINITY_DN132444_c5_g1_i2	1.200075893	Cytochrome c oxidase subunit 6C	7.84E-18 Q7YRK2 (COX6C_MACSL)
TRINITY_DN149037_c2_g1_i1	1.185931953		
TRINITY_DN131324_c3_g2_i7	1.180190533		
TRINITY_DN130629_c5_g1_i1	1.158641459	Aminoacyl tRNA synthase complex-interacting	3.32E-102 Q12904 (AIMP1_HUMAN)
TRINITY_DN144740_c2_g2_i2	1.158151921		
TRINITY_DN147118_c3_g2_i2	1.151303314		
TRINITY_DN139025_c5_g1_i7	1.141316595	Tubulin alpha-1 chain	5.05E-171 Q8T6A5 (TBA1_APLCA)
TRINITY_DN149107_c4_g1_i1	1.13701996		
TRINITY_DN148290_c4_g1_i2	1.13578517		
TRINITY_DN149288_c8_g1_i2	1.113063787		
TRINITY_DN144662_c1_g2_i1	1.111131576		
TRINITY_DN138859_c0_g1_i1	1.105492902	Cytochrome c oxidase subunit 3	1.28E-28 O47475 (COX3_HETBL)
TRINITY_DN109886_c9_g4_i2	1.104037353	Arginine kinase	1.86E-155 O15990 (KARG_LIOJA)
TRINITY_DN96691_c1_g1_i1	1.096681689	Cytochrome c oxidase subunit 2	1.68E-42 P50253 (COX2_DROSI)
TRINITY_DN131102_c2_g1_i3	1.096510439	Cytochrome c oxidase subunit 3	4.07E-60 O03170 (COX3_LATCH)
TRINITY_DN148411_c2_g1_i1	1.094558162		

TRINITY_DN99355_c0_g1_i1	1.084882486	Ribosome biogenesis protein NOP53	1.09E-49	Q8BK35 (NOP53_MOUSE)
TRINITY_DN141432_c0_g2_i1	1.079857058	NADH dehydrogenase [ubiquinone] 1 beta sub	1.82E-18	Q0MQC7 (NDUB2_PONPY)
TRINITY_DN132231_c1_g1_i2	1.074459572	1,3-beta-glucan synthase component FKS3	2.76	Q04952 (FKS3_YEAST)
TRINITY_DN97047_c3_g1_i2	1.073768826	Cytochrome b	4.75E-64	P07704 (CYB_DROYA)
TRINITY_DN128053_c1_g2_i1	1.072442455			
TRINITY_DN137071_c5_g1_i4	1.063353898	Beta-galactosidase 2	6.99	Q2XQU3 (BGAL2_ENTCL)
TRINITY_DN115738_c7_g1_i2	1.058856247	Probable 28S ribosomal protein S10, mitochor	5.21E-06	Q5SPH9 (RT10_DANRE)
TRINITY_DN130139_c7_g2_i1	1.054961321	Cytochrome b	3.22E-20	P51941 (CYB_DROSU)
TRINITY_DN146931_c8_g3_i2	1.046228685			
TRINITY_DN125593_c57_g2_i4	1.046146916			
TRINITY_DN131181_c5_g1_i4	1.043370444			
TRINITY_DN128970_c0_g2_i4	1.040709065			
TRINITY_DN149134_c19_g1_i1	1.040330961			
TRINITY_DN98685_c1_g1_i2	1.038107413	Cytochrome c oxidase subunit 1	5.90E-72	Q9G6J1 (COX1_OCTVU)
TRINITY_DN135161_c1_g2_i2	1.036763318			
TRINITY_DN100201_c0_g1_i3	1.033966728	Cytochrome c	4.86E-60	P81280 (CYC_ALLMI)
TRINITY_DN95471_c4_g1_i2	1.023281281			
TRINITY_DN121042_c2_g1_i1	1.022871556			
TRINITY_DN97715_c0_g1_i3	1.018838638	RWD domain-containing protein 1	7.54E-62	Q9CQK7 (RWDD1_MOUSE)
TRINITY_DN133497_c3_g1_i1	0.998976193	ATP synthase subunit g, mitochondrial	1.74E-24	Q5RFH0 (ATP5L_PONAB)
TRINITY_DN134575_c2_g3_i1	0.985625458			
TRINITY_DN119785_c11_g4_i1	0.980659872	Interferon alpha-inducible protein 27-like prot	0.00103	Q8R412 (IF27A_MOUSE)
TRINITY_DN105746_c3_g1_i5	0.973178836			
TRINITY_DN104380_c4_g1_i1	0.971895939	Cytochrome c oxidase subunit 1	1.19E-33	Q9B229 (COX1_CHRKN)
TRINITY_DN138446_c4_g2_i2	0.970478723			
TRINITY_DN144740_c2_g2_i1	0.970098781			
TRINITY_DN139025_c5_g1_i5	0.951769754	Tubulin alpha-1A chain	0	P68370 (TBA1A_RAT)
TRINITY_DN97047_c3_g1_i3	0.951057608	Cytochrome b	1.55E-54	P07704 (CYB_DROYA)
TRINITY_DN143982_c4_g2_i4	0.946556411			
TRINITY_DN141257_c0_g1_i1	0.945457802			
TRINITY_DN113017_c0_g1_i3	0.944344541			
TRINITY_DN94828_c0_g1_i1	0.943413735	NADH dehydrogenase [ubiquinone] iron-sulfur	2.78E-57	O43181 (NDUS4_HUMAN)
TRINITY_DN142286_c1_g3_i1	0.939582384			
TRINITY_DN148284_c7_g2_i1	0.93921354			
TRINITY_DN98001_c3_g2_i3	0.932978732	ABC transporter G family member 40	0.467	Q8GU85 (AB40G_ORYSJ)
TRINITY_DN105730_c2_g2_i1	0.925923133	Soma ferritin	1.16E-56	P42577 (FRIS_LYMST)
TRINITY_DN97696_c0_g2_i1	0.916760369	Cytochrome c oxidase subunit 6B1	1.10E-33	P14854 (CX6B1_HUMAN)
TRINITY_DN127774_c6_g2_i1	0.908087309	Cytochrome c oxidase subunit 8A, mitochondri	0.014	Q8SPI5 (COX8A_MACFA)
TRINITY_DN146931_c8_g1_i1	0.90606803	NADH-ubiquinone oxidoreductase chain 2	1.00E-16	Q8LX31 (NU2M_LEMCA)
TRINITY_DN138528_c4_g1_i2	0.893537667			
TRINITY_DN146079_c1_g1_i1	0.884783584	Cytochrome b-c1 complex subunit 8	1.43E-23	Q2L897 (QCR8_AILME)
TRINITY_DN108960_c4_g2_i4	0.88295877	60S acidic ribosomal protein P1	2.42E-32	P08570 (RLA1_DROME)
TRINITY_DN103500_c5_g1_i1	0.878054377	Diacylglycerol O-acyltransferase 1-1	5.64	Q51396 (DAT11_ORYSJ)
TRINITY_DN113432_c0_g1_i2	0.875184487	RNA-binding protein NOB1	8.94E-105	Q8BW10 (NOB1_MOUSE)
TRINITY_DN94674_c0_g1_i2	0.86886814	Ubiquitin-fold modifier-conjugating enzyme 1	5.35E-87	A7SM54 (UFC1_NEMVE)
TRINITY_DN106434_c3_g1_i1	0.86391421	Cytochrome c oxidase subunit 5A, mitochondri	3.24E-42	Q94514 (COX5A_DROME)
TRINITY_DN142538_c2_g1_i3	0.863824824	Cytochrome b	2.73E-53	P34864 (CYB_SARCH)
TRINITY_DN119209_c0_g1_i2	0.861036949	Coiled-coil-helix-coiled-coil-helix domain-cont	8.12E-30	Q9D1L0 (CHCH2_MOUSE)
TRINITY_DN109907_c2_g1_i3	0.85986715	GTP-binding nuclear protein Ran	1.67E-139	P79735 (RAN_DANRE)
TRINITY_DN145682_c6_g2_i2	0.85722044			
TRINITY_DN134436_c2_g2_i2	0.856649337			
TRINITY_DN126619_c5_g2_i2	0.851861011	60S ribosomal protein L22	5.64E-15	Q98TF8 (RL22_CHICK)
TRINITY_DN146931_c8_g4_i1	0.84262278			
TRINITY_DN99369_c0_g3_i1	0.841175886	Probable NADH dehydrogenase [ubiquinone]	1.09E-101	Q94360 (NDUS7_CAEEL)
TRINITY_DN111398_c2_g3_i3	0.840281022	60S ribosomal protein L3	3.62E-127	O16797 (RL3_DROME)
TRINITY_DN128688_c5_g1_i2	0.839895529			
TRINITY_DN142385_c1_g2_i2	0.830175382			
TRINITY_DN143360_c2_g3_i1	0.819558288			
TRINITY_DN145682_c6_g3_i2	0.817571896			

TRINITY_DN132227_c3_g2_i2	0.816169958			
TRINITY_DN95538_c0_g1_i1	0.804662357	Cytochrome c oxidase subunit 6A, mitochondri	1.23E-31	O13085 (COX6A_ONCMY)
TRINITY_DN146931_c8_g3_i1	0.789113925	Cytochrome c oxidase subunit 1	1.03E-111	Q34941 (COX1_LUMTE)
TRINITY_DN148712_c9_g2_i3	0.785100555	NADH-ubiquinone oxidoreductase chain 4	6.80E-47	Q34949 (NU4M_LUMTE)
TRINITY_DN149035_c7_g1_i3	0.784862356			
TRINITY_DN99541_c0_g1_i1	0.764394189	T-complex protein 1 subunit delta	0	Q2T9X2 (TCPD_BOVIN)
TRINITY_DN144663_c4_g2_i4	0.763460594			
TRINITY_DN99106_c7_g6_i1	0.762129424	Heat shock protein HSP 90-beta	9.35E-86	Q76LV1 (HS90B_BOVIN)
TRINITY_DN99654_c1_g1_i3	0.752585259	NADH dehydrogenase [ubiquinone]	7.73E-32	O43674 (NDUB5_HUMAN)
TRINITY_DN109715_c7_g1_i4	0.73309365	40S ribosomal protein S25	1.02E-41	Q8ISN9 (RS25_BRABE)
TRINITY_DN130659_c3_g3_i1	0.73178009	Eukaryotic translation initiation factor 1	4.05E-17	P51971 (EIF1_CHICK)
TRINITY_DN97928_c0_g1_i1	0.727505506	Translation machinery-associated protein 7	3.81E-16	Q4SUE2 (TMA7_TETNG)
TRINITY_DN122434_c1_g2_i1	0.720772034			
TRINITY_DN96854_c0_g1_i2	0.714625582	Protein transport protein Sec61 subunit gamm	1.46E-39	Q66KU2 (SC61G_XENLA)
TRINITY_DN108999_c9_g2_i3	0.707356592	60S ribosomal protein L19	7.30E-48	P84100 (RL19_RAT)
TRINITY_DN145719_c7_g4_i1	0.702699835	37S ribosomal protein S9, mitochondrial	4.3	Q7S7R6 (RT09_NEUCR)