

Table 4: Upregulated genes in the mantle when compared to the head

Transcript	logFC	Description	E Value	SwissProt ID
TRINITY_DN109055_c4_g1_i10	15.41109371	Inactive serine protease 54	0.0955	Q6PEW0 (PRSS4_HUMAN)
TRINITY_DN111971_c4_g1_i2	13.94620008			
TRINITY_DN148840_c8_g1_i4	13.29632725	Xylosyltransferase oxt	2.05E-07	Q5QQ53 (XYLT_DROPS)
TRINITY_DN115689_c2_g1_i3	13.14595585			
TRINITY_DN121418_c5_g3_i1	12.8617091	Tolloid-like protein 1	5.42E-09	Q43897 (TLL1_HUMAN)
TRINITY_DN126331_c0_g1_i9	12.7669012			
TRINITY_DN123796_c5_g1_i1	12.72311609	MMS19 nucleotide excision repair protein homolog	3.27	Q96T76 (MMS19_HUMAN)
TRINITY_DN144158_c3_g1_i5	12.71313511			
TRINITY_DN126331_c0_g1_i3	12.69278649			
TRINITY_DN102687_c0_g1_i1	12.63844687	Beta-1,3-glucan-binding protein	3.94E-78	Q8N0N3 (BGBP_PENMO)
TRINITY_DN110933_c4_g1_i3	11.83857306			
TRINITY_DN109584_c1_g1_i1	11.6935748	70 kDa neurofilament protein	0	Q01241 (NF70_DORPE)
TRINITY_DN139924_c3_g1_i1	11.36875957			
TRINITY_DN144158_c3_g1_i4	11.31761619			
TRINITY_DN149128_c14_g3_i2	11.29842683			
TRINITY_DN118212_c5_g1_i1	11.23204653			
TRINITY_DN110351_c9_g5_i2	11.16978967	Serine protease 53	3.15	Q571E5 (PRS53_MOUSE)
TRINITY_DN147542_c5_g1_i2	11.12283598	Acrosin	0.216	P29293 (ACRO_RAT)
TRINITY_DN121315_c3_g1_i1	11.10407265	Peritrophin-48	6.5	P91745 (PE48A_LUCCU)
TRINITY_DN95963_c6_g1_i3	10.94854639	Myeloperoxidase	1.78E-67	P11247 (PERM_MOUSE)
TRINITY_DN109055_c4_g1_i6	10.93334844	Inactive serine protease 54	0.0529	Q6PEW0 (PRSS4_HUMAN)
TRINITY_DN111315_c1_g1_i5	10.9114457	Galectin-3-binding protein	2.84E-14	O70513 (LG3BP_RAT)
TRINITY_DN131457_c3_g1_i3	10.82763606			
TRINITY_DN111315_c1_g1_i7	10.81954835	Galectin-3-binding protein	3.96E-14	Q07797 (LG3BP_MOUSE)
TRINITY_DN121878_c4_g6_i1	10.80993841			
TRINITY_DN95771_c1_g1_i4	10.79209538	Carboxypeptidase B	2.23E-61	P04069 (CBPB_ASTAS)
TRINITY_DN115689_c2_g1_i1	10.77729667			
TRINITY_DN144158_c3_g1_i3	10.77156948	Tenascin-R	7.43	Q00546 (TENR_CHICK)
TRINITY_DN144001_c0_g4_i1	10.75177237	Coagulation factor IX	1.08E-07	P16293 (FA9_PIG)
TRINITY_DN115689_c2_g4_i1	10.74314636			
TRINITY_DN144001_c0_g2_i1	10.73989754			
TRINITY_DN144158_c3_g1_i7	10.72562165	Tenascin-R	5.36	Q00546 (TENR_CHICK)
TRINITY_DN146204_c1_g1_i2	10.67744529	Fibropellin-1	3.42E-34	P10079 (FBP1_STRPU)
TRINITY_DN144001_c0_g2_i3	10.67581093			
TRINITY_DN144499_c1_g2_i1	10.65477288	Protein PIF	7.29E-05	H2A0N4 (PIF_PINMG)
TRINITY_DN110933_c4_g2_i3	10.65148434	Ovochymase-1	8.02	Q7RTY7 (OVCH1_HUMAN)
TRINITY_DN109055_c4_g1_i8	10.62899479	Inactive serine protease 54	0.102	Q6PEW0 (PRSS4_HUMAN)
TRINITY_DN143860_c2_g2_i2	10.60032537	Protein obstructor-E	0.0108	Q9VMM6 (OBSTE_DROME)
TRINITY_DN141434_c5_g3_i1	10.55678871	Acidic mammalian chitinase	2.72E-96	Q6RY07 (CHIA_RAT)
TRINITY_DN123796_c5_g2_i1	10.50415715			
TRINITY_DN109055_c4_g1_i7	10.36433753	Inactive serine protease 54	0.0698	Q6PEW0 (PRSS4_HUMAN)
TRINITY_DN95963_c6_g2_i2	10.36216788	Peroxidase	6.86E-08	Q01603 (PERO_DROME)
TRINITY_DN110351_c9_g1_i1	10.32663574			
TRINITY_DN110933_c4_g1_i2	10.2706185			
TRINITY_DN116629_c1_g1_i2	10.20176581			
TRINITY_DN137009_c1_g3_i1	10.20106986	Ribulose bisphosphate carboxylase small chain, chloroplastic	7.87	P17537 (RBS_CHLMO)
TRINITY_DN129967_c1_g3_i1	10.0566066			
TRINITY_DN141695_c2_g1_i6	9.923494346	Trypsin I-P1	0.0954	Q90627 (TRY1_CHICK)
TRINITY_DN139924_c3_g3_i2	9.870505194	G-type lectin S-receptor-like serine/threonine-protein kinase LECRK3	0.0326	Q25AG3 (LERK3_ORYSI)
TRINITY_DN115980_c6_g1_i1	9.852350264			
TRINITY_DN137871_c3_g1_i2	9.841444622			
TRINITY_DN137871_c3_g2_i2	9.841409786			
TRINITY_DN109055_c4_g1_i4	9.764617814	Inactive serine protease 54	0.0926	Q6PEW0 (PRSS4_HUMAN)
TRINITY_DN144111_c0_g1_i3	9.760765258			
TRINITY_DN109055_c4_g1_i9	9.741008259	Inactive serine protease 54	0.0992	Q6PEW0 (PRSS4_HUMAN)
TRINITY_DN102308_c5_g1_i2	9.699131954	3-isopropylmalate dehydratase large subunit	2.06	Q7U9J4 (LEUC_SYNPX)
TRINITY_DN134881_c5_g3_i1	9.683145083			
TRINITY_DN139924_c3_g2_i2	9.619159758	Probable metalloprotease ARX1	9.72	Q5AI37 (ARX1_CANAL)
TRINITY_DN144111_c0_g1_i2	9.557429445			
TRINITY_DN109055_c4_g1_i2	9.531241463	Inactive serine protease 54	0.0506	Q6PEW0 (PRSS4_HUMAN)
TRINITY_DN110933_c4_g2_i1	9.451153807	Ovochymase-1	4.99	Q7RTY7 (OVCH1_HUMAN)
TRINITY_DN135341_c4_g1_i1	9.267059769	Chymotrypsinogen B	8.93E-10	Q9CR35 (CTRB1_MOUSE)
TRINITY_DN148840_c8_g2_i1	9.011874169	Cell surface hyaluronidase	2.10E-95	Q5FWI3 (TMEM2_MOUSE)
TRINITY_DN129967_c1_g3_i2	8.984288316	Homeobox-leucine zipper protein HDG11	3.52	Q9FX31 (HDG11_ARATH)
TRINITY_DN102308_c5_g1_i3	8.947364046	ATP-dependent helicase FUN30	0.643	P31380 (FUN30_YEAST)
TRINITY_DN99338_c2_g2_i1	8.920383358	Fibropellin-1	1.17E-37	P10079 (FBP1_STRPU)
TRINITY_DN124269_c0_g1_i1	8.849857331			
TRINITY_DN148840_c8_g1_i1	8.828409136	Xylosyltransferase oxt	1.55E-07	Q5QQ53 (XYLT_DROPS)
TRINITY_DN141319_c0_g1_i6	8.732554418	Proclotting enzyme	3.83E-06	P21902 (PCE_TACTR)

TRINITY_DN106963_c5_g1_i2	8.597747975			
TRINITY_DN133828_c2_g1_i3	8.535266322			
TRINITY_DN109055_c4_g1_i3	8.52509908	Inactive serine protease 54	0.0686	Q6PEW0 (PR554_HUMAN)
TRINITY_DN149304_c12_g3_i1	8.2902468	Collagen alpha-1(XIV) chain	1.98E-13	P32018 (COEA1_CHICK)
TRINITY_DN148767_c4_g3_i2	8.124540135			
TRINITY_DN142871_c2_g1_i4	8.123089967			
TRINITY_DN142570_c2_g1_i1	6.879406363			
TRINITY_DN132386_c0_g3_i4	4.905935034			
TRINITY_DN138139_c1_g3_i3	4.902123277	Poly(3-hydroxyalkanoate) depolymerase C	0.32	P52090 (PHA1_PAULE)
TRINITY_DN102687_c0_g1_i2	4.63896317	Beta-1,3-glucan-binding protein	3.16E-78	Q8N0N3 (BGBP_PENMO)
TRINITY_DN121144_c2_g2_i4	4.09029057	Protein usf	2.28E-17	P46209 (USF_AQUPY)
TRINITY_DN124975_c0_g1_i8	4.083233259	Chorion peroxidase	1.00E-85	Q7QH73 (PERC_ANOGA)
TRINITY_DN148452_c0_g1_i1	3.941317147	von Willebrand factor D and EGF domain-containing protein	1.70E-05	Q8N2E2 (VWDE_HUMAN)
TRINITY_DN124975_c0_g1_i9	3.840691065	Chorion peroxidase	1.37E-85	Q7QH73 (PERC_ANOGA)
TRINITY_DN140777_c2_g2_i1	3.595930313			
TRINITY_DN149221_c8_g1_i1	3.36364244	Fibrillin-1	2.85E-77	P98133 (FBN1_BOVIN)
TRINITY_DN147599_c1_g1_i3	3.149841047	Anti-sigma-I factor RsgI6	1.84E-32	A3DH97 (RSGI6_CLOTH)
TRINITY_DN125814_c1_g1_i4	3.120386124	Dopamine beta-hydroxylase	7.16E-29	P09172 (DOPO_HUMAN)
TRINITY_DN149194_c6_g1_i1	3.086289669	Aminopeptidase Ey	0	O57579 (AMPN_CHICK)
TRINITY_DN140369_c2_g1_i1	3.078412314	Temptin	2.45E-28	Q7Z0T3 (TEMPT_APLCA)
TRINITY_DN110584_c2_g1_i1	2.98931254			
TRINITY_DN148918_c2_g1_i3	2.950434332	Threonylcarbamoyl-AMP synthase	6.02E-17	P39153 (SUA5_BACSU)
TRINITY_DN137670_c6_g1_i2	2.941564439			
TRINITY_DN125814_c1_g1_i6	2.908056815	Dopamine beta-hydroxylase	4.31E-38	P09172 (DOPO_HUMAN)
TRINITY_DN125756_c0_g1_i6	2.408609964	Myosin essential light chain, striated adductor muscle	5.73E-69	P07291 (MLE_ARGIR)
TRINITY_DN149234_c1_g1_i2	2.400826991	Protocadherin Fat 4	0	Q2P2L6 (FAT4_MOUSE)
TRINITY_DN149234_c1_g1_i1	2.30501455	Fat-like cadherin-related tumor suppressor homolog	7.91E-14	Q9VW71 (FAT2_DROME)
TRINITY_DN126569_c1_g2_i5	2.253841989	Collagen alpha-5(VI) chain	1.10E-15	A6H584 (CO6A5_MOUSE)
TRINITY_DN113425_c0_g2_i1	2.250892524	Paramyosin	1.43E-32	O96064 (MYSP_MYTGA)
TRINITY_DN117352_c3_g2_i2	2.132516023			
TRINITY_DN125756_c0_g1_i8	2.118681196	Myosin essential light chain, striated adductor muscle	2.84E-66	P07291 (MLE_ARGIR)
TRINITY_DN96216_c6_g1_i6	2.050045628	Tropomyosin-2	4.93E-82	P43689 (TPM2_BIOGL)
TRINITY_DN95237_c0_g1_i1	1.915267462	Myosin heavy chain, striated muscle	0	P24733 (MYS_ARGIR)
TRINITY_DN147918_c10_g2_i1	1.884505991	Putative uncharacterized protein ART2	3.25E-18	Q8TGM7 (ART2_YEAST)
TRINITY_DN137316_c1_g1_i2	1.852622466			
TRINITY_DN129891_c2_g1_i4	1.840403141	Non-neuronal cytoplasmic intermediate filament protein	8.00E-175	P22488 (IFEA_HELAS)
TRINITY_DN108975_c5_g1_i1	1.837038134	Troponin I	1.45E-11	Q7M3Y3 (TNNI_CHLNI)
TRINITY_DN141996_c0_g2_i2	1.791745928	Cubilin	4.35E-58	O70244 (CUBN_RAT)
TRINITY_DN147918_c10_g1_i4	1.747534573	Protein TAR1	2.05E-15	Q6CQE5 (TAR1_KLULA)
TRINITY_DN114296_c7_g3_i1	1.744293009	Myosin heavy chain, muscle	7.63E-21	P05661 (MYS_A_DROME)
TRINITY_DN104901_c1_g1_i1	1.717023765	Myosin heavy chain, striated muscle	0	P24733 (MYS_ARGIR)
TRINITY_DN148060_c1_g1_i2	1.714821319	Calmodulin-2/4	1.22E-07	Q7DMP0 (CALM2_SOLTU)
TRINITY_DN129891_c2_g6_i1	1.687909612			
TRINITY_DN137316_c1_g1_i1	1.687174391			
TRINITY_DN146235_c8_g3_i1	1.682365698			
TRINITY_DN97747_c6_g2_i1	1.627665225	Myosin regulatory light chain LC-2, mantle muscle	1.24E-65	P08052 (MLR_TODPA)
TRINITY_DN147058_c7_g1_i4	1.608586859			
TRINITY_DN114296_c7_g1_i3	1.542926045	Non-reducing polyketide synthase terA	6.5	Q0D1N9 (TERA_ASPTN)
TRINITY_DN130480_c1_g1_i11	1.483700042	Endonuclease MutS2	4.59	Q9ZLL4 (MUTS2_HELPJ)
TRINITY_DN148981_c7_g3_i1	1.459113208			
TRINITY_DN114296_c7_g2_i1	1.414209959			
TRINITY_DN125348_c6_g2_i1	1.373041285	Alanine--tRNA ligase	0.527	A8F866 (SYA_PSELT)
TRINITY_DN138834_c0_g6_i1	1.362327968	Myosin catalytic light chain LC-1, mantle muscle	2.33E-13	P05945 (MLE_TODPA)
TRINITY_DN95720_c3_g1_i7	1.360297998	Vasopressin V2 receptor	6.92	O77808 (V2R_CANLF)
TRINITY_DN111557_c5_g1_i4	1.343058367	Paramyosin	4.40E-11	O96064 (MYSP_MYTGA)
TRINITY_DN113473_c3_g2_i5	1.341740697	Calponin-3	1.98E-09	P37397 (CNN3_RAT)
TRINITY_DN149057_c3_g1_i1	1.33935054	Microtubule-associated tumor suppressor 1 homolog A	5.22E-23	A0JMQ7 (MTS1A_DANRE)
TRINITY_DN115859_c5_g1_i1	1.321661517			
TRINITY_DN145537_c3_g2_i3	1.317963044			
TRINITY_DN148660_c8_g1_i1	1.315165935	Calponin-1	6.41E-23	P26932 (CNN1_CHICK)
TRINITY_DN149258_c19_g1_i2	1.267308389	Twitchin	0	Q23551 (UNC22_CAEEL)
TRINITY_DN148300_c8_g3_i1	1.227327289	Microtubule cross-linking factor 1	8.51E-17	Q3UHU5 (MTCL1_MOUSE)
TRINITY_DN121689_c0_g2_i1	1.187282691	LIM domain-containing protein WLM2a	2.75E-07	O04193 (WLI2A_ARATH)
TRINITY_DN145537_c3_g4_i1	1.18328923	LHFPL tetraspan subfamily member 3 protein	2.83E-07	Q86UP9 (LHPL3_HUMAN)
TRINITY_DN125736_c1_g1_i2	1.157195493	Protein disulfide-isomerase	1.32E-164	P07237 (PDIA1_HUMAN)
TRINITY_DN145281_c7_g2_i1	1.132692458			
TRINITY_DN148066_c3_g1_i3	1.132457357	Filamin-B	0	Q80X90 (FLNB_MOUSE)
TRINITY_DN94893_c3_g1_i1	1.127770703	Paramyosin	0	O96064 (MYSP_MYTGA)
TRINITY_DN129397_c5_g4_i1	1.127003695	Myophilin	5.36E-36	Q24799 (MYPH_ECHGR)
TRINITY_DN104901_c1_g1_i3	1.099959482	Myosin heavy chain, striated muscle	1.50E-152	P24733 (MYS_ARGIR)
TRINITY_DN144740_c4_g3_i2	1.092553897	Troponin C	2.35E-64	Q9BLG0 (TNNC_TODPA)

TRINITY_DN96216_c6_g1_i10	1.038260022	Tropomyosin-2	4.79E-72	P43689 (TPM2_BIOGL)
TRINITY_DN97751_c4_g3_i6	1.03577725	Myosin heavy chain, striated muscle	3.86E-38	P24733 (MYS_ARGIR)
TRINITY_DN121683_c1_g3_i1	1.023570601	S-adenosylmethionine synthase isoform type-2	0	P18298 (METK2_RAT)
TRINITY_DN149308_c23_g1_i1	1.007144853	Ryanodine receptor	0	Q24498 (RYR_DROME)
TRINITY_DN94893_c3_g2_i1	1.003460226	Paramyosin	2.38E-95	O96064 (MYS_PMYTGA)
TRINITY_DN147945_c2_g3_i3	0.985904743	Cadherin-87A	1.25E-113	Q9VGG5 (CAD87_DROME)
TRINITY_DN148285_c15_g2_i2	0.977214147	Myosin heavy chain, striated muscle	0	P24733 (MYS_ARGIR)
TRINITY_DN148285_c15_g4_i1	0.939319771	Myosin heavy chain, striated muscle	0	P24733 (MYS_ARGIR)
TRINITY_DN142849_c4_g2_i1	0.912937462	Cysteine and glycine-rich protein 2	3.77E-33	Q16527 (CSRP2_HUMAN)
TRINITY_DN148285_c15_g3_i1	0.899670601	Myosin heavy chain, striated muscle	2.24E-157	P24733 (MYS_ARGIR)
TRINITY_DN121683_c1_g1_i5	0.881782954			

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