

Table S1. Real-time quantitative PCR primers used in this study.

Locus	primer sequence (5'→3')	Annealing temperature	Amplified fragment length
<i>β-actin</i>	F:ACCGAAACAAGAACCCAT	56	133
	R:CCGACACGATAAGACTGC		
<i>CAV1</i>	F:TGCCGAACCAGAGGGAACAC	56	171
	R:GCCCAGATGTGCAGGAATGAC		
<i>IRS2</i>	F:CAGTGGTGGCGCAGAACAT	56	155
	R:GGTAATGGGGTGCCTAGCTG		
<i>LDB3</i>	F:TCGACTTCAGCCTACCCAAC	56	153
	R:TACCAGGAAAGGACCCCGAA		
<i>LDHA</i>	F:TGTCCACAAGGAAGAGCACG	56	149
	R:CTCTCAGCTTGTCTCCACG		
<i>MYL3</i>	F:TGAAACCTTCCTGCCGATGCT	56	174
	R:ACCTCCTCTTCAGTCAGCCTCT		

Table S2. Genome alignment analysis

Samples	total_reads	total_map	unique_map	multi_map	positive_map	negative_map
A1	42100124	38410013	37326929	1083084	18665393	18661536
		(91.23%)	(88.66%)	(2.57%)	(44.34%)	(44.33%)
A2	40232798	36794914	35958629	836285	17978015	17980614
		(91.46%)	(89.38%)	(2.08%)	(44.68%)	(44.69%)
A3	39816432	36314397	35410874	903523	17708823	17702051
		(91.2%)	(88.94%)	(2.27%)	(44.48%)	(44.46%)
A4	40533992	37099191	36229269	869922	18115567	18113702

		(91.53%)	(89.38%)	(2.15%)	(44.69%)	(44.69%)
B1	43250912	39658978	38751589	907389	19380485	19371104
		(91.7%)	(89.6%)	(2.1%)	(44.81%)	(44.79%)
B2	39288900	35745398	34724163	1021235	17375746	17348417
		(90.98%)	(88.38%)	(2.6%)	(44.23%)	(44.16%)
B3	44464890	40724353	39786913	937440	19900966	19885947
		(91.59%)	(89.48%)	(2.11%)	(44.76%)	(44.72%)
B4	44434414	40601311	39580767	1020544	19796629	19784138
		(91.37%)	(89.08%)	(2.3%)	(44.55%)	(44.52%)
C1	44081482	40220568	39015390	1205178	19524369	19491021
		(91.24%)	(88.51%)	(2.73%)	(44.29%)	(44.22%)
C2	44523064	40339249	38980266	1358983	19494937	19485329
		(90.6%)	(87.55%)	(3.05%)	(43.79%)	(43.76%)
C3	44572368	40596027	39430578	1165449	19716378	19714200
		(91.08%)	(88.46%)	(2.61%)	(44.23%)	(44.23%)
C4	44076128	40021520	38718860	1302660	19375700	19343160
		(90.8%)	(87.85%)	(2.96%)	(43.96%)	(43.89%)
D1	44062570	40019621	38723817	1295804	19379380	19344437
		(90.82%)	(87.88%)	(2.94%)	(43.98%)	(43.9%)
D2	43390542	39315419	38055392	1260027	19031787	19023605
		(90.61%)	(87.7%)	(2.9%)	(43.86%)	(43.84%)
D3	44144060	40195997	38848201	1347796	19436840	19411361
		(91.06%)	(88.0%)	(3.05%)	(44.03%)	(43.97%)
D4	45648164	41429101	40142912	1286189	20092699	20050213
		(90.76%)	(87.94%)	(2.82%)	(44.02%)	(43.92%)

total_reads: The number of clean reads of sequencing data after quality control

total_map: Compare the number and percentage of reads on the genome

unique_map: Compare the number and percentage of reads to the unique location of the reference genome

multi_map: The number and percentage of reads to multiple locations of the reference genome were compared

positive_map: Compare the number and percentage of reads on the positive chain of the reference genome

negative_map: Compare the number and percentage of reads on the negative strand of the reference genome

Table S3. The significantly enriched GO molecular function and cellular component terms

	modules	GO ID	Description	pvalue
Cellular Component	Blue	GO:0043292	contractile fiber	0.000000
		GO:0016529	sarcoplasmic reticulum	0.000000
		GO:0042383	sarcolemma	0.000000
		GO:0032982	myosin filament	0.000097
		GO:1902495	transmembrane transporter complex	0.000754
		GO:0031143	pseudopodium	0.000772
		GO:1990351	transporter complex	0.001308
		GO:1904813	ficolin-1-rich granule lumen	0.009059
		GO:0062023	collagen-containing extracellular matrix	0.010735
	Green	GO:0043209	myelin sheath	0.000000
		GO:0097386	glial cell projection	0.000015
		GO:0016323	basolateral plasma membrane	0.000209
		GO:0005922	connexin complex	0.000326
		GO:0098574	cytoplasmic side of lysosomal membrane	0.017790
		GO:1990531	phospholipid-translocating ATPase complex	0.017790
		GO:0031092	platelet alpha granule membrane	0.021562
		GO:0043025	neuronal cell body	0.025296

	GO:0008305	integrin complexBlue	0.038983
	GO:0098636	protein complex involved in cell adhesion	0.070549
Grey	GO:0030672	synaptic vesicle membrane	0.000313
	GO:0099501	exocytic vesicle membrane	0.000313
	GO:0048786	presynaptic active zone	0.003477
	GO:0071546	pi-body	0.010710
	GO:0033391	chromatoid body	0.012839
	GO:0043194	axon initial segment	0.022364
	GO:0008076	voltage-gated potassium channel complex	0.080692
Turquoise	GO:0062023	collagen-containing extracellular matrix	0.000000
	GO:0097060	synaptic membrane	0.000000
	GO:0098982	GABA-ergic synapse	0.000000
	GO:0005871	kinesin complex	0.000005
	GO:0071162	CMG complex	0.000006
	GO:0043198	dendritic shaft	0.000008
	GO:0016342	catenin complex	0.000018
	GO:0005581	collagen trimer	0.000118
	GO:0000307	cyclin-dependent protein kinase holoenzyme complex	0.000425
	GO:0034702	ion channel complex	0.000708
	GO:0043025	neuronal cell body	0.000784
	GO:0030496	midbody	0.001611
	GO:1902711	GABA-A receptor complex	0.014671
	GO:0030672	synaptic vesicle membrane	0.022955

molecular function		GO:0099501	exocytic vesicle membrane	0.022955
		GO:0005912	adherens junction	0.033473
		GO:0030118	clathrin coat	0.040547
		GO:0042627	chylomicron	0.041973
		GO:0042622	photoreceptor outer segment membrane	0.071001
		GO:0005903	brush border	0.071336
	Blue	GO:0043292	contractile fiber	0.000000
		GO:0016529	sarcoplasmic reticulum	0.000000
		GO:0042383	sarcolemma	0.000000
		GO:0032982	myosin filament	0.000097
		GO:1902495	transmembrane transporter complex	0.000754
		GO:0031143	pseudopodium	0.000772
		GO:1990351	transporter complex	0.001308
		GO:1904813	ficolin-1-rich granule lumen	0.009059
		GO:0062023	collagen-containing extracellular matrix	0.010735
	Green	GO:0019911	structural constituent of myelin sheath	0.000097
		GO:0005243	gap junction channel activity	0.000116
		GO:0005506	iron ion binding	0.001118
		GO:0098632	cell-cell adhesion mediator activity	0.002177
		GO:0043208	glycosphingolipid binding	0.013530
		GO:0016725	oxidoreductase activity, acting on CH or CH2 groups	0.014873
		GO:0140333	glycerophospholipid flippase activity	0.017555
		GO:0140327	flippase activity	0.021564
		GO:0008525	phosphatidylcholine transporter activity	0.022896

	GO:0046624	sphingolipid transporter activity	0.022896
	GO:0097001	ceramide binding	0.025557
	GO:0005452	solute:inorganic anion antiporter activity	0.026884
	GO:0043027	cysteine-type endopeptidase inhibitor activity involved in apoptotic process	0.028210
	GO:0033691	sialic acid binding	0.029534
	GO:0004435	phosphatidylinositol phospholipase C activity	0.032177
	GO:0051537	2 iron, 2 sulfur cluster binding	0.033496
	GO:0070840	dynein complex binding	0.033496
	GO:0004629	phospholipase C activity	0.036129
	GO:0140326	ATPase-coupled intramembrane lipid transporter activity	0.036129
	GO:0035250	UDP-galactosyltransferase activity	0.037443
	GO:0046625	sphingolipid binding	0.037443
	GO:0071949	FAD binding	0.051781
	GO:0004860	protein kinase inhibitor activity	0.053074
	GO:0043014	alpha-tubulin binding	0.055656
	GO:0048156	tau protein binding	0.056944
	GO:0019210	kinase inhibitor activity	0.058230
	GO:0019894	kinesin binding	0.059515
	GO:0005044	scavenger receptor activity	0.063360
	GO:0030544	Hsp70 protein binding	0.065914
	GO:0051219	phosphoprotein binding	0.118039
	GO:0015297	antiporter activity	0.132412
Grey	GO:0000149	SNARE binding	0.005964
	GO:0005221	intracellular cyclic nucleotide activated monoatomic	0.011915

	cation channel activity	
GO:0043855	cyclic nucleotide-gated monoatomic ion channel activity	0.011915
GO:0099528	G protein-coupled neurotransmitter receptor activity	0.011915
GO:0045028	G protein-coupled purinergic nucleotide receptor activity	0.014067
GO:0015926	glucosidase activity	0.015141
GO:0019992	diacylglycerol binding	0.015141
GO:0016812	hydrolase activity, acting on carbon-nitrogen (but not peptide) bonds, in cyclic amides	0.016214
GO:0005248	voltage-gated sodium channel activity	0.020496
GO:0030552	cAMP binding	0.020496
GO:0001614	purinergic nucleotide receptor activity	0.021563
GO:0016502	nucleotide receptor activity	0.021563
GO:0017075	syntaxin-1 binding	0.021563
GO:0015464	acetylcholine receptor activity	0.022630
GO:0004993	G protein-coupled serotonin receptor activity	0.023695
GO:0005085	guanyl-nucleotide exchange factor activity	0.024956
	oxidoreductase activity, acting on single donors with incorporation of molecular oxygen, incorporation of two atoms of oxygen	0.025822
GO:0016702	oxidoreductase activity, acting on single donors with incorporation of molecular oxygen	0.026884
GO:0016411	acylglycerol O-acyltransferase activity	0.033234
GO:0020037	heme binding	0.139120

Turquoise	GO:0005201	extracellular matrix structural constituent	0.000000
	GO:0005539	glycosaminoglycan binding	0.000000
	GO:0008017	microtubule binding	0.000000
	GO:0017116	single-stranded DNA helicase activity	0.000002
	GO:0003777	microtubule motor activity	0.000005
	GO:0003688	DNA replication origin binding	0.000054
		ligand-gated monoatomic ion channel activity	
	GO:0099507	involved in regulation of presynaptic membrane potential	0.000075
	GO:0005518	collagen binding	0.000082
	GO:0005178	integrin binding	0.000301
	GO:0017147	Wnt-protein binding	0.001737
	GO:0008376	acetylgalactosaminyltransferase activity	0.002294
	GO:0016538	cyclin-dependent protein serine/threonine kinase regulator activity	0.002485
	GO:0008046	axon guidance receptor activity	0.002956
	GO:0004713	protein tyrosine kinase activity	0.004872
	GO:0030547	signaling receptor inhibitor activity	0.005852
	GO:0003697	single-stranded DNA binding	0.005885
	GO:0071837	HMG box domain binding	0.006130
	GO:0004222	metalloendopeptidase activity	0.006904
	GO:0045499	chemorepellent activity	0.007037
	GO:0016918	retinal binding	0.014729
	GO:0031406	carboxylic acid binding	0.023961

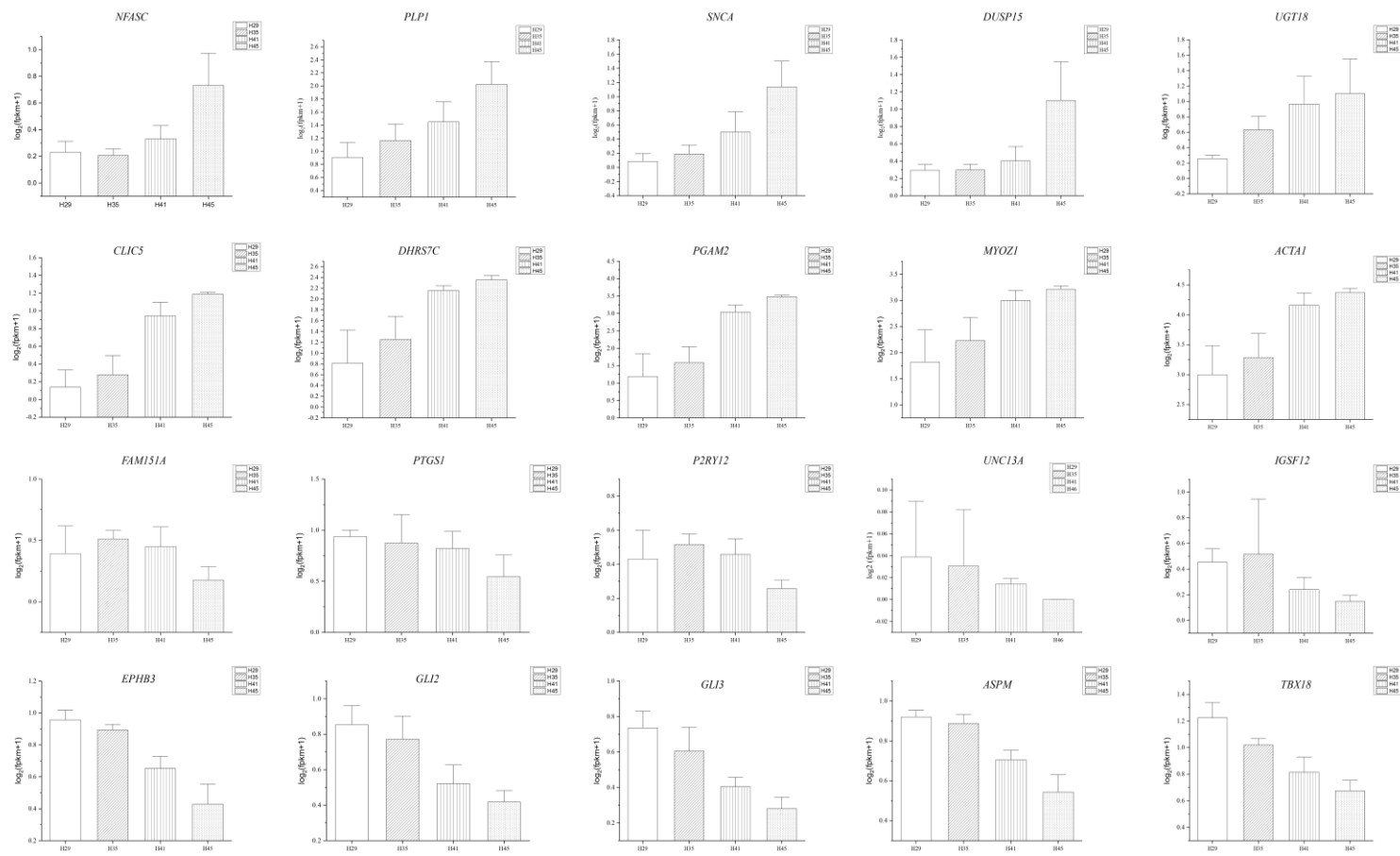


Figure S1. The expression of each hub gene in 4 developmental stages.