

APPLICATION OF COMPOSITION IN PREPARATION OF DRUG FOR DIAGNOSING INFANTILE HEMANGIOMA AND/OR MONITORING PROGRESS AND PROGNOSIS THEREOF, AND KIT AND DRUG

TECHNICAL FIELD

The application relates to the use of a composition in the preparation of a drug for diagnosing hemangioma and/or monitoring its progress and prognosis, as well as a kit and a medicament, more specifically, the application relates to a composition for preparing and diagnosing infantile hemangioma and/or the use of drugs to monitor its progress and prognosis, as well as detection kits and drugs for the treatment of infantile hemangioma.

BACKGROUD TECHNIQUE

Infantile hemangioma, IH is the most common benign tumor in infants and young children, commonly known as "Red Birthmark", the incidence rate is as high as 1-10%. It usually appears a few weeks after birth as a dot-shaped red mass, which rapidly proliferates in the following months and becomes a red mass. If not treated in time, 10%-15% will develop complications, leading to appearance damage, large-scale ulcer infection, respiratory tract compression and obstruction, and even life-threatening.

Therefore, early diagnosis and timely therapeutic intervention are crucial to obtain a satisfactory prognosis. Infantile hemangioma is difficult to distinguish from other common skin diseases such as neonatal erythema (Nevus Simplex, NS) in the early stage of disease. At present, there is no effective prediction/early warning and early differential diagnosis technology for infantile hemangioma. However, due to the rapid development of infantile hemangioma, once the timing of treatment is delayed, serious consequences will result. On the contrary, if other common skin diseases are misdiagnosed as infantile hemangioma, resulting in overtreatment, it may also cause unnecessary iatrogenic damage to children.

In addition, the conventional method, which relies on measuring the size of the hemangioma and observing the texture and color changes by the doctor, is still used to

evaluate the treatment effect of drugs against infantile hemangioma. Large measurement errors still exist. Therefore, evaluating the curative effect timely, accurately, and objectively, and correctly judging the end point of the course of the disease are still challenging.

Also, a deep infantile hemangioma may be easily missed or misdiagnosed because there are no obvious symptoms on the body surface or only a bulge on the skin surface. At present, there is a lack of early and accurate differential diagnosis technology. In addition, patients with infantile hemangioma have a high recurrence rate. If surface symptoms disappear or stop developing, the tumor may still recur after withdrawal. How to determine the endpoint of medication is also a challenge that existing technology has not yet overcome.

In summary, there is an urgent need for rapid, accurate, sensitive and quantifiable infantile hemangioma prediction/early warning and early diagnosis technology, technology for monitoring the progress of the disease, and effective prediction technology for the effect of drug treatment and recurrence after stopping treatment.

SUMMARY OF THE INVENTION

The purpose of the present invention is to overcome the existing international lack of predictive and early warning technologies for infantile hemangiomas, as well as the shortcomings of low detection rate, poor detection sensitivity, easy confusion with other skin diseases with similar appearances, large measurement errors in technology for treatment effectiveness and prognosis evaluation, and the inability to quantify detection indicators, in order to provide a detection technology that is fast, accurate sensitivity and quantitative prediction/warning of infantile hemangioma, precise early diagnosis, close monitoring of disease progression, objective evaluation of drug treatment efficacy, and accurate reflection of prognosis.

The present invention provides use of a composition for manufacturing a medicament for diagnosing infantile hemangioma and/or monitoring its progress and prognosis is characterized in that the composition includes at least one of the

following four groups of substances:

(1) Fatty acid, wherein the fatty acid is total fatty acid or total saturated fatty acid or total monounsaturated fatty acid or at least one of the fatty acids selected from the group consisting of C10:0, C11:0, C12:0, C14:0, C15:0, C15:1N5, C16:0, C17:0, C18:0, C18:2N6, C20:0, C20:3N3, C20:5N3, C21:0, C22:1N9, C23:0, C24:0 and C8:0;

(2) Metabolites, wherein the metabolites is at least one of the metabolites selected from the group consisting of (3-carboxypropyl)trimethylammonium cation, α -D-(+)-talose, 1-aminocyclopropanecarboxylic acid, 1-meat Myristoyl-sn-glycero-3-phosphocholine, 1-oleoyl-sn-glycero-3-phosphocholine, 1-palmitoyl-sn-glycero-3-phosphocholine, 1-stearoyl-sn -Glycero-3-phosphocholine, bilirubin, choline, D-2-pipercolic acid, DL-indole-3-lactic acid, glycylglutamate, glycerophosphorylcholine, isomaltose, L - Arginine, L-glutamic acid, L-phenylalanine, L-tryptophan, NG,NG-dimethyl-L-arginine, tyramine, phenylacetic acid, (S)-lime Acid, 1-oleoyl-L-alpha-lysophosphatidic acid, 1-palmitoyl lysophosphatidic acid, alpha-mangostin, arachidonic acid (peroxide free), citramalic acid, cyclamate /salt, D-galactate/salt, D-threitol, D(-)-beta-hydroxybutyric acid, inositol galactoside, glyceric acid, L-aspartic acid, L-carnosine, L - In the group consisting of malic acid, N-acetyl-L-aspartic acid, N-acetylneuraminic acid, norethindrone acetate, phosphorylcholine, sn-glycero-3-phosphoethanolamine and succinate/salt;

(3) Protein, wherein the protein is at least one of the proteins selected from the group consisting of COLEC10, CPQ, LDHB, ACAN, KRT1, ARHGDIB, POSTN, LAMA5, CPN1, PROC, C1S, HPX, SUPT6H, BCAR3, BCHE, SOX30, C1R, PON1, CFHR4, PROZ, IGKV1D-16, APOC-3, COMP, SELENOP, PMFBP1, GSN, SELL, FUCA2, HLA-B, FGFBP2, FKBP1A, HSPE1, SAA1, PGD, CDH1, SOD1, ISLR, CORO1A, ZYX, RLBP1, IDH1, IGKV6-21, SORL1, FAM3C, CST6, COTL1, PIGR, A0A1W6IYJ2, PRDX1, CAT, PROS1, CD5L, HMFT1766, C1QA, KRT2, and APP; and

(4)Lipid subclass substances or lipid molecules, wherein the lipid subclass

substance is at least one of the lipid subclass substances selected from the group consisting of acetylcarnitine, ceramide, monosaccharide ceramide, disaccharide ceramide, glycosyl ceramide series, trisaccharide Ceramide, cholesteryl ester, cardiolipin, ganglioside, lysophosphatidylcholine, lysophosphatidylethanolamine, monogalactosyldiacylglyceride, phosphatidic acid, phosphatidylcholine, phosphatidylethanolamine, phytosphingosine, phosphatidylinositol, phosphatidylserine, sphingomyelin and triglyceride, and wherein the lipid molecule is at least one of the lipid molecules selected from the group consisting of PS(39:4)-H, SM(d45:6)+H, PC(14:0/20:4)+HCOO, SM(d20:0/18:1)+HCOO, PS(49:4)-H, LPC(26:0)+HCOO, SM(d20:0/16: 0)+HCOO, PA(50:4)-H, LPC(20:4)+HCOO, PC(36:5)+H, LPC(20:1)+HCOO, PC(38:8)+H, PC(46:5)+H, PE(18:0p/22:5)-H, SM(d22:0/16:0)+HCOO, PC(15:0/20:4)+HCOO, SM(d18:0/20:4)+HCOO, LPC(22:4)+HCOO, PI(18:0/22:4)-H, PC(16:1/18:2)+HCOO, PS(40:4)-H, Cer(d20:0/24:1)+H, SM(d37:0)+HCOO, PC(17:1/16:0)+HCOO, SM(d20:0/22:5)+HCOO, PC(44:11)+H, SM(d32:0)+HCOO, LPC(22:1)+H, PC(33:0e)+H, SM(d56:2+pO)+H, SM(d42:1)+HCOO, LPC(17:1)+HCOO, SM(d17:0/18:2)+HCOO, Cer(d18:1/24:0)+H, SM(d36:3)+HCOO, AcCa(14:2)+H, Cer(d18:1/24:0 O)+H, PE(20:0p/20:4)-H, LPC(26:1)+HCOO, PC(37:5)+H, SM(d44:1)+HCOO, Cer(d18:1/26:1)+H, PE(40 :6e)+H, TG(18:1/20:2/22:4)+NH₄, SM(d34:3)+H, PE(40:4)-H, SM(d22:0/18:2)+HCOO, Cer(d18:0/22:0)+H, SM(d44:0)+HCOO, PI(16:1/20:4)-H, PC(20:3/20:4)+HCOO, PE(38:1p)-H and SM(d39:0)+HCOO.

The present invention also provides a detection kit, which includes the composition described in the present invention and instructions for using the kit.

The above-mentioned use and detection kit of the present invention can quickly, accurately, sensitively and quantitatively realize the prediction/early warning, early diagnosis, close monitoring of the progress of the disease course, objectively evaluate the therapeutic effect of drugs, and accurately reflect the prognosis of infantile hemangioma .

In addition, the present application also provides a drug for treating infantile

hemangioma including substances that regulate the expression of LDHB, KRT1, BCHE, CFHR4, CPQ, APOC-3, ARHGDIB and LAMA5, thereby providing new effective way.

DESCRIPTION OF DRAWING

Fig. 1 is the lesion photograph at the cubital fossa of the neonate suffering from infantile hemangioma involved in Example 1 of the present invention at the age of 6 weeks;

Fig. 2 is the photograph of the lesion on the back of a newborn with infantile hemangioma involved in Example 2 of the present invention at 6 weeks of birth;

Fig. 3 is the photo of the head lesion of a newborn suffering from neonatal erythema involved in Example 3 of the present invention at 6 weeks after birth;

Fig. 4 is the photo of the head lesion of a newborn suffering from neonatal erythema involved in Example 4 of the present invention at 6 weeks after birth;

Fig. 5 is the photo of the lesion at the cubital fossa of a newborn with infantile hemangioma involved in Example 1 of the present invention at 12 weeks of birth;

Fig.6 is a photo of the back lesion of a newborn with infantile hemangioma involved in Example 2 of the present invention at 12 weeks of birth;

Fig.7 is a photo of the head lesion of a newborn with neonatal erythema involved in Example 3 of the present invention at 12 weeks of birth;

Fig. 8 is a photo of the head lesion of a newborn with neonatal erythema involved in Example 4 of the present invention at 12 weeks of birth;

Fig. 9 is a comparative photo of the lesion at the eyelid of a newborn suffering from an infantile hemangioma related to Example 7 of the present invention before and after treatment and before and after drug withdrawal;

Fig. 10 Statistical results of lipid subclasses (lipid class) and the number of lipid molecules (lipid species) identified in each category;

Fig. 11 control group and IH group total lipid content figure;

Fig. 12 control group and IH group general difference lipid subclass content

graph;

Fig. 13 control group and IH group significant difference lipid subclass content figure;

Fig. 14 High-throughput swissport proteomics detection fitting model ROC curve;

Fig. 15 High-throughput uniport proteomics detection fitting model ROC curve;

Fig. 16 metabolite group fitting model ROC curve;

Fig. 17 The ROC curve of the IH group and the control group fitting model in the fatty acid group;

Fig. 18 ROC curve of the fitting model of the IH group and the NS group in the fatty acid group.

Fig. 19 ROC curve of IH group and control group involving 5 fatty acids in the training set fitting model.

Fig. 20 ROC curve of IH group and control group involving 5 fatty acids.

DETAILED WAYS

The invention provides use of a composition for manufacturing a medicament for diagnosing infantile hemangioma and/or monitoring its progress and prognosis is characterized in that the composition includes at least one of the following four groups of substances:

(1) Fatty acid, wherein the fatty acid is total fatty acid or total saturated fatty acid or total monounsaturated fatty acid or at least one of the fatty acids selected from the group consisting of C10:0, C11:0, C12:0, C14:0, C15:0, C15:1N5, C16:0, C17:0, C18:0, C18:2N6, C20:0, C20:3N3, C20:5N3, C21:0, C22:1N9, C23:0, C24:0 and C8:0;

(2) Metabolites, wherein the metabolites is at least one of the metabolites selected from the group consisting of (3-carboxypropyl)trimethylammonium cation, α -D-(+)-talose, 1-aminocyclopropanecarboxylic acid, 1-meat Myristoyl-sn-glycero-3-phosphocholine, 1-oleoyl-sn-glycero-3-phosphocholine,

1-palmitoyl-sn-glycero-3-phosphocholine, 1-stearoyl-sn -Glycero-3-phosphocholine, bilirubin, choline, D-2-pipercolic acid, DL-indole-3-lactic acid, glycylglutamate, glycerophosphorylcholine, isomaltose, L - Arginine, L-glutamic acid, L-phenylalanine, L-tryptophan, NG,NG-dimethyl-L-arginine, tyramine, phenylacetic acid, (S)-lime Acid, 1-oleoyl-L-alpha-lysophosphatidic acid, 1-palmitoyl lysophosphatidic acid, alpha-mangostin, arachidonic acid (peroxide free), citramalic acid, cyclamate /salt, D-galactate/salt, D-threitol, D(-)-beta-hydroxybutyric acid, inositol galactoside, glyceric acid, L-aspartic acid, L-carnosine, L - In the group consisting of malic acid, N-acetyl-L-aspartic acid, N-acetylneuraminic acid, norethindrone acetate, phosphorylcholine, sn-glycero-3-phosphoethanolamine and succinate/salt;

(3) Protein, wherein the protein is at least one of the proteins selected from the group consisting of COLEC10, CPQ, LDHB, ACAN, KRT1, ARHGDIB, POSTN, LAMA5, CPN1, PROC, C1S, HPX, SUPT6H, BCAR3, BCHE, SOX30, C1R, PON1, CFHR4, PROZ, IGKV1D-16, APOC-3, COMP, SELENOP, PMFBP1, GSN, SELL, FUCA2, HLA-B, FGFBP2, FKBP1A, HSPE1, SAA1, PGD, CDH1, SOD1, ISLR, CORO1A, ZYX, RLBP1, IDH1, IGKV6-21, SORL1, FAM3C, CST6, COTL1, PIGR, A0A1W6IYJ2, PRDX1, CAT, PROS1, CD5L, HMFT1766, C1QA, KRT2, and APP; and

(4)Lipid subclass substances or lipid molecules, wherein the lipid subclass substance is at least one of the lipid subclass substances selected from the group consisting of acetylcarnitine, ceramide, monosaccharide ceramide, disaccharide ceramide, glycosyl ceramide series, trisaccharide Ceramide, cholesteryl ester, cardiolipin, ganglioside, lysophosphatidylcholine, lysophosphatidylethanolamine, monogalactosyldiacylglyceride, phosphatidic acid, phosphatidylcholine, phosphatidylethanolamine, phytosphingosine, phosphatidylinositol, phosphatidylserine, sphingomyelin and triglyceride, and wherein the lipid molecule is at least one of the lipid molecules selected from the group consisting of PS(39:4)-H, SM(d45:6)+H, PC(14:0/20:4)+HCOO, SM(d20:0/18:1)+HCOO, PS(49:4)-H, LPC(26:0)+HCOO, SM(d20:0/16: 0)+HCOO, PA(50:4)-H, LPC(20:4)+HCOO,

PC(36:5)+H, LPC(20:1)+HCOO, PC(38:8)+H, PC(46:5)+H, PE(18:0p/22:5)-H, SM(d22:0/16:0)+HCOO, PC(15:0/20:4)+HCOO, SM(d18:0/20:4)+HCOO, LPC(22:4)+HCOO, PI(18:0/22:4)-H, PC(16:1/18:2)+HCOO, PS(40:4)-H, Cer(d20:0/24:1)+H, SM(d37:0)+HCOO, PC(17:1/16:0)+HCOO, SM(d20:0/22:5)+HCOO, PC(44:11)+H, SM(d32:0)+HCOO, LPC(22:1)+H, PC(33:0e)+H, SM(d56:2+pO)+H, SM(d42:1)+HCOO, LPC(17:1)+HCOO, SM(d17:0/18:2)+HCOO, Cer(d18:1/24:0)+H, SM(d36:3)+HCOO, AcCa(14:2)+H, Cer(d18:1/24:0 O)+H, PE(20:0p/20:4)-H, LPC(26:1)+HCOO, PC(37:5)+H, SM(d44:1)+HCOO, Cer(d18:1/26:1)+H, PE(40 :6e)+H, TG(18:1/20:2/22:4)+NH₄, SM(d34:3)+H, PE(40:4)-H, SM(d22:0/18:2)+HCOO, Cer(d18:0/22:0)+H, SM(d44:0)+HCOO, PI(16:1/20:4)-H, PC(20:3/20:4)+HCOO, PE(38:1p)-H and SM(d39:0)+HCOO.

In the present invention, the C10:0 refers to decanoic acid. The C11:0 refers to undecanoic acid. The C12:0 refers to dodecanoic acid. The C14:0 refers to myristic acid. The C15:0 refers to pentadecanoic acid . The C15:1N5 refers to cis-10-pentadecene acid. The C16:0 refers to palmitic acid. The C17:0 refers to heptadecanoic acid. The C18:0 refers to stearic acid. The C18:2N6 refers to linoleic acid. The C20:0 refers to arachidic acid. The C20:3N3 refers to cis-11,14,17-eicosatrienoic acid. The C20:5N3 refers to cis-5,8,11,14,17-eicosapentaenoic acid. The C21:0 refers to heneicosanic acid . The C22:1N9 refers to erucic acid. The 23:0 refers to tricosanic acid. The C24:0 refers to tetracosanoic acid. The C8:0 refers to octanoic acid. The fatty acid of the invention is preferably selected from at least one of the group consisting of C8:0, C10:0, C11:0, C16:0, C20:5N3, C22:1N9, C23:0 and C24:0. It is further preferably selected from at least one of the group consisting of C8:0, C10-0-C16:0, C20:0-C20:5N3, C22:1N9, C23:0, C24:0; It is preferably selected from at least one of the group consisting of C20:5N3, C22:1N9, C23:0 and C24-0. Preferably, the fatty acid of the invention is selected from the group consisting of C10:0, C14:0, C16:0, C18:0, C18:2N6.C20:0, C20:1N9, C20:5N3-C22:1N9, C24:0, and C8:0.The more preferable fatty acid of the invention is selected from the group consisting of C10:0, C16:0, C20:0, C20:5N3 and

C22:1N9.

Preferably, the metabolite is at least one selected from the group consisting of choline, 1-aminocyclopropanecarboxylic acid, 1-myristoyl-sn-glycero-3-phosphocholine, D-2-pipecolinic acid, DL-indole-3-lactic acid, glycyl glutamic acid (Gly- Glu), L-Glutamate, L-Phenylalanine, L-Tryptophan, Tyramine, Phenylacetic acid, Glyceric acid, Cyclohexylsulfamate/salt, D-galactate/salt and sn-glycerol-3-phosphoethanolamine. The most preferable metabolites are at least one selected from the group consisting of 1-myristoyl-sn-glycero-3-phosphocholine, glycyl glutamic acid (Gly-Glu), L-phenylalanine, DL-Indole-3-lactic acid, L-Tryptophan, Phenylacetic acid, and Glyceric acid.

Among the proteins involved in the present invention, the COLEC10 refers to collagen lectin-10 (Collectin-10). The CPQ refers to carboxypeptidase Q. The LDHB refers to L-lactate dehydrogenase B chain. The ACAN refers to proteoglycan core protein. The KRT1 refers to keratin, type II cytoskeletal 1. The POSTN refers to periostin. The LAMA5 refers to laminin subunit alpha-5. The CPN1 refers to carboxypeptidase Ncatalytic chain. The PROC refers to vitamin K-dependent protein C. The C1S refers to the complement C1s subcomponent. The HPX refers to hemopexin. The SUPT6H refers to transcription elongation factor SPT6. The BCAR3 refers to breast cancer anti-estrogen resistance protein 3. The BCHE refers to Cholinesterase. The SOX30 refers to the transcription factor SOX-30. The C1R refers to a complement C1r subcomponent. The PON1 refers to serum paraoxonase/arylesterase 1. The CFHR4 refers to complement factor H-related protein 4. The PROZ refers to vitamin K-dependent protein Z. The IGKV1D-16 refers to the immunoglobulin kappa variable 1D-16. The APOC-3 refers to apolipoprotein C-III. The COMP refers to cartilage oligomeric matrix protein. The SELENOP refers to

selenoprotein P. The PMFBP1 refers to polyamine-modulated factor 1-binding protein 1. The GSN refers to gelsolin . The SELL refers to L-selectin. The FUCA2 refers to plasma α -L-fucosidase. The HLA-B refers to human leukocyte antigen B antigen. The FGFBP2 refers to fibroblast growth factor-binding protein 2. The FKBP1A refers to peptidyl-prolyl cis-trans isomerase. The HSPE1 refers to heat shock protein 10 . The SAA1 refers to serum amyloid A-1. The PGD refers to 6-phosphogluconate dehydrogenase . The CDH1 refers to Cadherin-1. The SOD1 refers to superoxide dismutase [Cu-Zn]. The ISLR refers to the immunoglobulin superfamily containing leucine-rich rich in leucine repeat sequence. The CORO1A refers to Coronin-1A. The ZYX refers to Zexin. The RLBP1 refers to retinal binding protein 1. The IDH1 refers to cytoplasmic isocitrate dehydrogenase. The IGKV6-21 refers to immunoglobulin kappa variable region 6-21. The SORL1 refers to a sortin-related receptor . The FAM3C refers to FAM3C protein. The CST6 refers to cysteine protease inhibitor-M . The COTL1 refers to actin-like protein. The PIGR refers to polymeric immunoglobulin receptor. The A0A1W6IYJ2 refers to the N90-VRC38.05 heavy chain variable region. The PRDX1 refers to peroxide reductase-1. The CAT refers to catalase. The PROS1 refers to vitamin K-dependent protein S . The CD5L refers to CD5 antigen-like. The HMFT1766 refers to leucine-rich alpha-2-glycoprotein . The C1QA refers to the complement C1q- α subcomponent . The KRT2 refers to keratin 2. The APP refers to amyloid-beta precursor protein.

Wherein LDHB, KRT1, BCHE, CFHR4 and CPQ are up-regulated proteins, while APOC-3, ARHGDIB and LAMA5 are down-regulated proteins. The protein is further preferably at least one selected from the group consisting of HSPE1, PGD, CDH1, ISLR, CPQ, IDH1, PIGR, POSTN, PROC, PROZ, PMFBP1, SELL, A0A1W6IYJ2, CAT, PROS1, CD5L, C1QA, KRT1 and FGFBP2. The protein is most preferably at least one selected from the group consisting of HSPE1, CDH1, ISLR, IDH1, COTL1 and FGFBP2.

The lipids (Lipids) described in the present invention are a class of hydrophobic or amphiphilic small molecules, including eight categories (named by LIPID MAPS ®

system) (Fahy et al., 2009): fatty acids (such as linoleic acid, arachidic acid, etc.), glycerolipids (such as TG, DG, etc.), glycerophospholipids (such as PC, PE, PG, PA, etc.), sphingolipids (such as Cer, SM, etc.), sterol lipids (such as sterol esters, etc.) , glycolipids (such as MGDG, SQDG, etc.), pregnenolone lipids (such as CoA, etc.) and polyvinyls (antibiotics, etc.). Lipids are the main components of biological membrane structures (such as outer membranes, mitochondria, exosomes, endoplasmic reticulum, exosomes and other subcells), as well as small signaling molecules and energy substances. Specifically, the names of lipid subclasses involved in the present invention and their English abbreviations are shown in Table 1 below:

Table 1 The names and English abbreviations of lipid subclasses

category	subclass	subclass abbreviation	Molecular species	Summary of molecular species
	Acetylcarnitine	AcCa	13	13
	Wax esters	WE	2	2
Glycerophospholipid GP	Cardiolipin	CL	1	379
	Lysophosphatidylcholine	LPC	45	
	Lysophosphatidylethanolamine	LPE	16	
	Lysophosphatidylinositol	LPI	2	
	Phosphatidic acid	Well	1	
	Phosphatidylcholine	PC	208	
	Phosphatidylethanolamine	ON	63	
	Phosphatidylinositol	PI	22	
	Phosphatidylserine	PS	21	
Glycerides GL	diglycerides	DG	18	187
	Triglycerides	TG	169	
Sterol Lipid ST	cholesteryl ester	That	7	7
Sphingolipid SP	Ceramide	Cer	59	211
	Gangliosides	GM3	11	
	Phytosphingosine	phSM	8	
	Sphingomyelin	SM	130	
	Sphingosine	So	3	
Glycolipids	monosaccharide ceramide	CerG1	11	21
	Bisaccharylceramide	CerG2	4	
	Glycosylceramide series	CerG2GNAc1	2	
	Triosylceramide	CerG3	2	
	monogalactose diacylglyceride	MGDG	2	

Pregnenolone Lipid PR	coenzyme	Co	1	1
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The lipid subclass substance of the present invention is further preferably selected from the group consisting of Cer, ChE, LPC, LPE, PA, PC, PE, PI, PS, and SM. Most preferably it is selected from the group consisting of LPC, LPE, PA, PC and PE. Preferably, the lipid molecule is selected from the group of consisting of PS(39:4)-H, SM(d45:6)+H, PC(14:0/20:4)+HCOO, SM(d20:0/18:1)+HCOO, PS(49:4)-H, LPC(26:0)+HCOO, SM(d20:0/16: 0)+HCOO, PA(50:4)-H, LPC(20:4)+HCOO, PC(36:5)+H, LPC(20:1)+HCOO, PC(38:8)+H, PC(46:5)+H, PE(18:0p/22:5)-H, SM(d22:0/16:0)+HCOO, PC(15:0/20:4)+HCOO, SM(d18:0/20:4)+HCOO, LPC(22:4)+HCOO, PI(18:0/22:4)-H, PC(16:1/18:2)+HCOO, PS(40:4)-H, Cer(d20:0/24:1)+H, SM(d37:0)+HCOO, PC(17:1/16:0)+HCOO, SM(d20:0/22:5)+HCOO, PC(44:11)+H, SM(d32:0)+HCOO, LPC(22:1)+H, PC(33:0e)+H, SM(d56:2+pO)+H, SM(d42:1)+HCOO, LPC(17:1)+HCOO, SM(d17:0/18:2)+HCOO, Cer(d18:1/24:0)+H, SM(d36:3)+HCOO, AcCa(14:2)+H, Cer(d18:1/24:0 O)+H, PE(20:0p/20:4)-H, LPC(26:1)+HCOO, PC(37:5)+H, SM(d44:1)+HCOO, Cer(d18:1/26:1)+H, PE(40 :6e)+H, TG(18:1/20:2/22:4)+NH₄, SM(d34:3)+H, PE(40:4)-H, SM(d22:0/18:2)+HCOO, Cer(d18:0/22:0)+H, SM(d44:0)+HCOO, PI(16:1/20:4)-H, PC(20:3/20:4)+HCOO, PE(38:1p)-H and SM(d39:0)+HCOO. Further preferably, the lipid molecule is selected from: PS(39:4)-H, SM(d45:6)+H, PC(14:0/20:4)+HCOO, SM(d20:0/18:1)+HCOO, PS(49:4)-H, LPC(26:0)+HCOO, SM(d20:0/16 :0)+HCOO, PA(50:4)-H and LPC(20:4)+HCOO. Most preferably, the lipid molecule selected from PS(39:4)-H, SM(d45:6)+H, PC(14:0/20:4)+HCOO and SM(d20:0/18:1)+HCOO.

The inventor of the present invention collects umbilical cord blood of 3089 cases of newborns, including 63 cases of positive samples of infantile hemangioma. Thousands of metabolites in healthy newborns, neonatal erythema patients, and infant hemangioma patients were analyzed and compared using high-throughput metabolomics, fatty acid profile targeting quantitative metabolomics, general

metabolomics, proteomics, and lipidomics. Specific fatty acids, metabolites, proteins and lipid subclass substances or lipid molecules listed above have been found to be useful in early warning/prediction, early diagnosis and/or monitoring of the progress and prognosis of infantile-age hemangioma, generating startling specificity and sensitivity.

Any of the fatty acids, metabolites, proteins and lipid subclasses or lipid molecules listed here in this application can be used alone to determine whether infantile hemangioma is present and whether the drug for treating infantile hemangioma is curative. In order to further verify the test results, two or more substances can be used for mutual confirmation. Preferably, the fatty acid is at least 2 of the fatty acids defined in (1); the metabolite is at least 2 of the metabolites defined in (2); the protein is the at least 2 of the proteins defined in (3); or the lipid subtypes or lipid molecules are at least 2 of the lipid subtypes or lipid molecules defined in (4). Further preferably, the fatty acid is at least 3 of the fatty acids defined in (1); the metabolite is at least 3 of the metabolites defined in (2); the protein is the At least 3 of the proteins defined in (3); or the lipid subtypes or lipid molecules are at least 3 of the lipid subtypes or lipid molecules defined in (4). Considering the cost and detection efficiency, the fatty acid is 1 to 6 of the fatty acids defined in (1); the metabolite is 1 to 6 of the metabolites defined in (2). 6 types; or the protein is 1 to 6 of the proteins defined in (3); Or the lipid subclass substance or lipid molecule is one to six of the lipid subclass substance or lipid molecule defined in said (4).

Preferably, the fatty acid in (1) is selected from the group consisting of C8:0, C10:0, C11:0, C16:0, C20:0, C20:5N3, C22:1N9, C23:0 and C24:0; the metabolites in (2) are selected from the group consisting of choline, 1-aminocyclopropanecarboxylic acid, 1-myristoyl-sn-glycero-3-phosphocholine, D-2-pipecolic acid, DL-indole-3-lactic acid, glycyl glutamic acid, L-glutamic acid, L-phenylalanine, L-tryptophan, tyramine, glyceric acid, cyclamate, D - galactate/salt and

sn-glycero-3-phosphoethanolamine; said (3) protein is selected from the group consisting of HSPE1, PGD, CDH1, ISLR, CPQ, IDH1, PIGR, POSTN, PROC, PROZ, PMFBP1, SELL, A0A1W6IYJ2, CAT, PROS1, CD5L, C1QA, KRT1 and FGFBP2; or the (4) Lipid subclass substances selected from the group consisting of Cer, ChE, LPC, LPE, PA, PC, PE, PI, PS and SM, the lipid molecule is selected from PS(39:4)-H, SM(d45:6)+H, PC(14:0/20:4) +HCOO, SM (d20:0/18:1) +HCOO, PS(49:4)-H, LPC(26:0) +HCOO, SM(d20:0/16:0) +HCOO, PA(50:4)-H and LPC (20:4) +HCOO. Further preferably, the fatty acid in (1) is selected from the group consisting of C20:5N3, C22:1N9, C23:0 and C24:0; The metabolites in said (2) are selected from the group consisting of 1-myridamyl-Sn-glycero-3-phosphate choline, glycine glutamic acid, L-phenylalanine, DL-hondole-3-lactic acid, L-tryptophan and glycolic acid. The (3) protein is selected from the group consisting of HSPE1, CDH1, ISLR, IDH1, COTL1 and FGFBP2; or the (4) lipid subclass is selected from the group consisting of LPC, LPE, PA, PC and PE or said lipid molecules are selected from PS(39:4)-H, SM(d45:6)+H, PC(14:0/20:4)+HCOO and SM(d20:0/18:1)+HCOO .

The present application also provides a detection kit, which includes the composition of the present invention and instructions for using the kit. Fatty acids, metabolites and lipid subclasses or lipid molecules of the present application can be determined using conventional methods, for example, spectrophotometry, gas chromatography, liquid chromatography, gas-liquid chromatography, mass spectrometry, gas chromatography Combined use, liquid chromatography-mass spectrometry routine serum total lipid determination, etc. Similarly, the protein can also be determined by conventional methods. Kits may optionally include other reagents, such as buffers, salts, enzymes, enzyme cofactors, substrates, detection reagents, etc., to perform a diagnostic assay or to facilitate quality control assessments. Other components such as buffers and solutions (eg, pretreatment reagents) for isolating and/or processing test samples may also be included in the kit. Optionally, the kit may also contain at least one calibrator or control. Any calibrators or controls can be included in the kit. The kit may additionally include one or more other controls.

One or more of the kit components may be lyophilized, and the kit may further include reagents suitable for reconstituting the lyophilized components.

The various components of the kit are optionally provided in suitable containers. One or more of the containers may be a microtiter plate. Kits may further include containers for holding or storing samples (eg, containers or cartridges for blood or urine samples). Kits may also optionally include reaction vessels, mixing vessels, and other components to facilitate reagent or test sample preparation, as appropriate. Kits can also include one or more instruments, such as syringes, pipettes, forceps, measured spoons, etc., to assist in obtaining test samples.

The instructions for using the kit of the present invention can be provided in paper form or computer-readable form such as disk, CD, DVD, flash memory, online download link, mobile phone APP application and the like. The instructions may include a baseline value data set of normal indicators for comparison.

The samples detected by the kit are selected from the group consisting of whole blood, plasma, serum, lymphocyte suspension, cerebrospinal fluid, bone marrow, pleural effusion, urine, saliva and peritoneal effusion. Samples that do not interfere with the subject are preferred. More preferably, the samples detected by the kit are selected from the group consisting of umbilical cord blood and peripheral blood.

Preferably, the kit is a dry blood patch kit. The dry blood spot is obtained by the dry blood paper method. The principle is that the whole blood drops are added to the filter paper, and the dry blood spot is obtained after drying. After solvent extraction, the information of the components to be detected in the dry blood spot is analyzed by fluorescence reaction method and tandem mass spectrometry to reflect the patient's diagnostic results, such as metabolite content, etc. From the perspective of sample preservation, dry blood stains are more stable than whole blood, and the storage and transportation cost is much lower than whole blood. In addition, dried blood paper can collect a small number of samples, so dried blood paper has specific advantages in the detection that requires multiple samples for diagnosis, especially for neonatal disease

screening.

The present application also provides a medicament for treating infantile hemangioma, the medicament includes a substance that regulates the expression of LDHB, KRT1, BCHE, CFHR4, CPQ, APOC-3, ARHGDIB and LAMA5. The inventors of the present invention are the first to discover that the relevant protein is related to infantile hemangioma, and the treatment of infantile hemangioma can be achieved by regulating the expression of the relevant protein.

EXAMPLE

The present invention will be further described through the following embodiments in conjunction with the accompanying drawings, but the present invention is not limited to the following embodiments.

EXAMPLE OF SAMPLE COLLECTION

The inventor of the present application collected and preserved 3,089 neonatal umbilical cord blood samples, compared multiple factors and dimensions between patients with the disease and normal newborns, and finally found that there are significant statistical differences in indicators among (1) fatty acids, (2) metabolites, (3) protein and (4) lipid subclasses or lipid molecular.

(1) Subject recruitment

Make a brochure for the popularization of infantile hemangioma, provide it to the delivery room of the cooperative hospital, distribute the brochure to the expectant mothers and their families, introduce the incidence and treatment of infantile hemangioma to the mothers and their families, and inform the rights and benefits of participating researchers; The purpose of this study and the follow-up time were explained to all patients, ensuring that patients know the importance of adhering to designated follow-up times for early intervention in IH. With the full knowledge of the puerpera and her family members, fully respect her will, whether she agrees or not, will not affect any of her treatment and rights. Under the condition that the parturients and their family members agree to participate in the research, they will sign relevant

informed consent forms for the collection of cord blood, placental tissue, maternal and neonatal medical history, and data.

(2) Collect specimens and record maternal and neonatal information

After the fetus and placenta were delivered and the umbilical cord was severed, and the health of the fetus and the mother was ensured, 30 mL of the discarded umbilical vein and umbilical cord blood in the placenta were collected aseptically, and injected into a coagulation blood collection tube (purchased from Fuzhou Chang Gung Medical Instrument Co., Ltd. (CHANGGENG)), containing diatomaceous earth), shake slowly. After standing at room temperature for half an hour, the neonatal cord blood was centrifuged at 3000g/min for 15 minutes, and the supernatant was taken and stored at -80°C. A total of 3089 neonatal umbilical cord blood samples were collected.

The clinical diagnosis and treatment data will be established under the guidance of statistical professionals for data entry; the specimens and personal information will be marked with research numbers rather than names.

(3) Follow-up

Telephone follow-up was conducted at the 6th and 12th week after birth to track the occurrence of IH. The telephone follow-up personnel consisted of two postgraduates. After strict training, the follow-up time avoided the rest time of the newborn's family members. During the follow-up, no newborn was missed. The reason for the newborn who quits midway will be registered. During the follow-up, if the symptom description is consistent with infantile hemangioma, the follow-up staff will ask the parents of the infant to send pictures of the lesion to help the diagnosis, and notify all children who are initially diagnosed as infantile hemangioma to the outpatient clinic for diagnosis.

(4) Match grouping and control confounding factors

After the follow-up, all the cord blood samples of infantile hemangioma diagnosed through outpatient service were selected as the case group. Then, according to the baby's sex, birth weight, gestational weeks and other relevant information as

matching conditions, children without infantile hemangioma were matched as the control group.

(5) Obtaining sample information

A total of 63 cases with positive IH samples were collected during follow-up, and 28 cases were randomly selected as the IH group. And according to the infant gender, birth weight, gestational weeks and other relevant information of the IH group, the matching conditions were used as matching conditions, and 32 samples of the control group with the same conditions were screened out. In addition, cord blood from 37 children with neonatal erythema (Nevus Simplex, NS) was collected (NS group), a total of 97 samples. Each umbilical cord blood specimen of the IH group and the control group was divided into 100 μ L/tube in a 1.5ml centrifuge tube, and stored at -80°C until testing.

Table 2

Sample grouping	Sample group name	quantity
1	IH group	28
2	control group	32
3	NS group	37

(6) Introduction to statistical methods and indicators used in the present invention

Table 3 below shows the results of a specific disease diagnosis using a specific diagnostic method.

table 3

diagnostic test	gold standard		total
	patient	normal person	
Positive	a(true negative)	b(false positive)	a+ b
Negative	c (false negative)	d (true negative)	c+ d
total	a +c	b +d	a+ b+ c +d

Sppecificity: $Sp=d/(bd) \times 100\%$ indicates the ability of the diagnostic test to identify non-patients (that is, the probability that a person who is actually not sick is diagnosed as negative), that is, the true negative rate. The larger the value, the higher the diagnostic test is. (method) is more precise.

Sensitivity: $Se = a/(a+c) \times 100\%$ indicates the ability to diagnose patients, that is, the true positive rate. The larger the value, the more sensitive the diagnostic method is.

Receiver operating characteristic curve: ROC curve also known as the sensitivity curve: a coordinate diagram composed of the false positive rate (1-specificity) as the horizontal axis and the true positive rate (sensitivity) as the vertical axis, and the subjects in a specific Curves drawn for different results obtained by using different judgment criteria under stimulus conditions. The horizontal and vertical coordinates can be calculated by software (SPSS\Origin\Graphpad Prism), and the area under the ROC curve can be obtained from the results obtained in the software to compare the diagnostic value of the diagnostic test.

The role of the ROC curve:

- 1) Find the "best" diagnostic cutoff for a diagnostic test.
- 2) The area under the ROC curve (AUC) was calculated to evaluate the discriminative power of a diagnostic test.
- 3) Compare the area under the ROC curve of multiple tests to screen out the best diagnostic scheme.

Area Under the Curve (AUC):

The ROC curve AUC can reflect the value of the diagnostic test, usually in the range of 0.5-1. In the case of $AUC > 0.5$, the closer the AUC is to 1, the better the diagnostic effect. 0.5 for a completely worthless diagnosis and 1 for a completely ideal diagnosis.

It is generally believed that: AUC:

Between 0.5-0.7: indicates low diagnostic value and low accuracy;

Between 0.7-0.9: it means that the diagnostic value is medium and has a certain accuracy;

> 0.9 : indicates high diagnostic value and high accuracy.

The larger the area under the curve (AUC), the higher the overall diagnostic rate:

Significant: Statistical significance, also known as statistical significance, refers to the risk level to be borne if the null hypothesis is true and we rejected it, also known as probability level, or significance level. The ability to distinguish groups from one another. In statistical hypothesis testing, the recognized probability value of a small probability event is called the significance level of statistical hypothesis testing. The same quantity is measured several times, and then the average value is calculated.

Examples of fatty acid group indicators:

(1) Experimental method

1. Preparation of standard products

Forty kinds of fatty acid methyl ester mixed standard solution were used, each of which produced ten standard concentration gradients of 0.5mg/L, 1mg/L, 5mg/L, 10mg/L, 25mg/L, 50mg/L, 100mg/L, 250mg/L, 500mg/L and 1000mg/L.

Take 500 μ L of 40 fatty acid methyl ester mixed standards at the same concentration, add 25 μ L of 500 ppm methyl n-nonadecanoate as an internal standard, mix well and add to the injection bottle, enter the GC-MS detection, the injection volume is 1 μ L, split ratio 10:1, split injection.

2. Extraction of metabolites from samples to be tested

The sample was thawed on ice, and 60 μ L of the sample was taken in a 2 mL glass centrifuge tube. Add 1 mL of chloroform-methanol solution, sonicate for 30 min, take the supernatant, add 2 mL of 1% sulfuric acid-methanol solution, place it on a water bath at 80 °C, methylate for half an hour, add 1 mL of n-hexane for extraction, wash with 5 mL pure water, absorb 500 μ L of the supernatant, add 25 μ L of methyl salicylate as an internal standard, mix well and add to the injection bottle, and enter the GC-MS detection. The injection volume is 1 μ L, the split ratio is 10:1, and split injection.

3. Chromatography-mass spectrometry analysis

(1) Gas chromatography conditions: The samples were separated by Agilent DB-WAX capillary column (30 m $\times$ 0.25 mm ID $\times$ 0.25 μ m) gas chromatography system.

Temperature program: initial temperature 50°C; hold for 3 minutes, then raise the temperature to 220°C at 10°C/min; and maintain for 5 minutes. The carrier gas was helium at a flow rate of 1.0 mL/min. A quality control (QC) sample was set for every 7 experimental samples in the sample queue to detect and evaluate the stability and repeatability of the system.

(2) Mass spectrometry: Agilent 7890/5975C gas-mass spectrometer was used for mass spectrometry. The inlet temperature was 280°C; the ion source temperature was 230°C; the transfer line temperature was 250°C. Electron impact ionization (EI) source, SIM scan mode, electron energy 70eV.

(3) Data processing: MSD ChemStation software was used to extract the chromatographic peak area and retention time. Draw a calibration curve and calculate the content of medium and long-chain fatty acids in the sample.

(4) Statistics: Data analysis was carried out using SPSS software (version 25.0; IBM, Armonk NY, USA). Analysis of variance (ANOVA) was used to analyze the differences among the three groups, and the SNK-q test was further used for multiple comparisons. ROC (receiver operating characteristic curve) analysis was used to judge the diagnostic value of difference variables. Binary logistic regression analysis is used to build a logistic regression model to further improve the predictive sensitivity and specificity, and improve the diagnostic value

(3) Results

(1) Test results

A total of 39 medium- and long-chain fatty acids were detected this time, and the sum of fatty acid amounts of five medium- and long-chain fatty acid subclasses was calculated: total_SFA (saturated fatty acid), total_MUFA (monounsaturated fatty acid), total_PUFA (polyunsaturated fatty acids), total N3 (omega-3 cluster fatty acids, the first unsaturated bond in unsaturated fatty acids appears at the third position of the methyl end of the carbon chain) and total N6 (omega-6 cluster fatty acids, in unsaturated fatty acids The first unsaturated bond occurs at the sixth position of the methyl end of the carbon chain).

(2) Analysis of variance: ANOVA was used to compare whether there were differences among the three groups of medium and long-chain fatty acids, and the SNK-q test was further used to make pairwise comparisons among the three groups. The results of variance analysis showed that there were 18 medium and long-chain fatty acids among the 39 medium- and long-chain fatty acids with significant differences among the three groups ($P<0.05$), namely: C10:0, C11:0, C12:0, and C14:0, C15:0, C15:1N5, C16:0, C17:0, C18:0, C18:2N6, C20:0, C20:3N3, C20:5N3, C21:0, C22:1N9, C23:0, C24 :0 and C8:0. Moreover, there were also significant differences ($P<0.05$) in total saturated fatty acids (SFA) and total monounsaturated fatty acids (MUFA) among the five medium and long-chain fatty acid subcategories (see Table 4, unit: $\mu\text{g/ml}$).

Table 4

fatty acid	average value (THEM)	median (THEM)	average value (NS)	median (NS)	average value (comparison)	median (comparison)	F	P value
C10:0	0.033	0.026	0.019	0.018	0.016	0.014	6.876	0.002
C11:0	0.020	0.018	0.013	0.012	0.010	0.011	8.735	<0.001
C12:0	0.355	0.201	0.169	0.170	0.203	0.160	4.351	0.016
C13:0	0.272	0.100	0.107	0.106	0.107	0.098	2.598	0.080
C14:0	3.677	3.265	3.111	2.874	2.616	2.677	4.551	0.013
C14:1N5	1.947	1.226	1.283	0.971	1.299	1.215	2.539	0.085
C15:0	0.736	0.659	0.668	0.660	0.534	0.543	4.633	0.012
C15:1N5	32.961	29.701	23.354	23.955	23.096	24.300	7.170	0.001
C16:0	107.953	109.688	96.440	92.488	84.327	89.819	4.910	0.010
C16:1N7	13.516	11.342	13.932	13.158	12.273	11.446	0.532	0.589
C17:0	0.714	0.689	0.641	0.628	0.577	0.564	3.273	0.043
C17:1N7	1.062	0.939	0.807	0.814	0.873	0.843	2.038	0.137
C18:0	56.347	47.203	47.645	45.315	40.140	41.039	6.244	0.003
C18:1N9	62.658	41.994	47.061	43.025	42.914	42.835	2.747	0.070
C18:1TN9	0.408	0.286	0.237	0.201	0.308	0.201	2.578	0.082
C18:2N6	137.475	100.765	103.635	97.846	94.803	86.513	3.883	0.024
C18:2TTN6	0.238	0.174	0.179	0.150	0.184	0.152	1.070	0.348
C18:3N3	1.246	1.030	1.183	1.027	0.954	0.916	1.716	0.186
C18:3N6	1.197	1.103	1.037	0.903	1.085	0.872	0.532	0.589
C20:0	1.127	0.571	0.351	0.290	0.278	0.234	9.337	<0.001
C20:1N9	2.015	0.939	1.220	0.614	0.993	0.734	1.897	0.156
C20:2N6	3.566	3.574	3.646	3.531	3.669	3.725	0.058	0.944
C20:3N3	0.395	0.337	0.566	0.540	0.371	0.347	12.852	<0.001

C20:3N6	26.394	24.024	23.545	21.967	24.392	24.075	0.835	0.438
C20:4N6	86.394	80.404	89.092	90.703	88.562	86.514	0.076	0.927
C20:5N3	0.614	0.369	0.215	0.188	0.151	0.134	12.955	<0.001
C21:0	0.142	0.116	0.076	0.073	0.074	0.077	8.440	<0.001
C22:0	1.971	1.485	1.756	1.389	1.998	1.300	0.271	0.764
C22:1N9	9.569	6.997	7.392	6.903	4.582	4.076	10.379	<0.001
C22:2N6	3.750	3.511	3.430	3.184	3.060	2.880	0.861	0.426
C22:4N6	3.571	3.325	3.658	3.605	3.707	3.581	0.097	0.908
C22:5N3	2.323	1.862	2.067	1.813	2.134	1.560	0.311	0.734
C22:5N6	3.560	3.487	3.819	3.828	4.100	3.522	0.897	0.412
C22:6N3	6.370	6.034	6.090	5.329	6.246	6.023	0.100	0.905
C23:0	0.171	0.107	0.081	0.070	0.051	0.040	12.731	<0.001
C24:0	0.804	0.491	0.299	0.254	0.208	0.180	11.609	<0.001
C24:1N9	27.289	25.613	27.672	25.543	28.701	25.588	0.151	0.860
C6:0	1.268	1.033	1.084	1.060	1.402	1.300	2.277	0.109
C8:0	0.088	0.037	0.057	0.053	0.028	0.022	4.760	0.011
Total MUFA	151.426	127.730	122.957	117.964	115.040	121.479	4.040	0.021
Total_N3	10.948	9.555	10.122	9.088	9.856	9.007	0.505	0.605
Total_N6	266.145	233.985	232.042	234.020	223.562	215.155	2.223	0.115
Total_PUFA	277.093	241.162	242.164	241.044	233.418	223.316	2.195	0.118
Total_SFA	175.678	172.089	152.517	146.986	132.569	139.578	5.916	0.004

(3) SNK-q test: For the medium and long-chain fatty acids with significant differences among the three groups by variance analysis, the SNK-q test was used to make pairwise comparisons among the three groups. The results showed that compared with the control group, the IH group had significant differences ($P<0.05$) in 17 medium and long-chain fatty acids, namely: C10:0, C11:0, C12:0, C14:0, C15:0, C15:1N5, C16:0, C17:0, C18:0, C18:2N6, C20:0, C20:5N3, C21:0, C22:1N9, C23:0, C24:0, and C8:0, And there are also significant differences in total saturated fatty acids (SFA) and total monounsaturated fatty acids (MUFA) ($P<0.05$); IH group compared with the NS group, there were 13 medium and long-chain fatty acids with significant differences ($P<0.05$), respectively: C10:0, C11:0, C12:0, C15:1N5, C18:0, C18:2N6, C20:0, C20:3N3, C20:5N3, C21:0, C22:1N9, C23:0 and C24:0, And there were also significant differences in total monounsaturated fatty acids (MUFA) ($P<0.05$); compared with the control group, there were significant differences in 3 medium and long-chain fatty acids ($P<0.05$), respectively: C15:0, C20:3N3 and C22:1N9 (see Table 5).

(4) ROC curve analysis: draw the ROC curves of the above 44 differential metabolites, and calculate the AUC value. Compared with the control group, the AUC values of 12 medium and long-chain fatty acids in the IH group were greater than 0.7, namely: C10:0, C11:0, C15:1N5, C18:0, C20:0, C20:5N3, and C21:0 , C22:1N9, C23:0, C24:0, C6:0 and C8:0; compared with the IH group and the NS group, there were 9 medium and long-chain fatty acids with AUC values greater than 0.7, which were: C10:0, C12:0, C15:1N5, C20:0, C20:3N3, C20:5N3, C21:0, C23:0, and C24:0. (See Table 5)

Table 5

fatty acid	F	P value	SNK-qtest (IH vs control)	SNK-qtest (IH vs NS)	SNK-qtest (NS vs control)	AUC (IH vs control)	AUC (IH vs NS)
C10:0	6.876	0.002	P<0.05	P<0.05		0.785	0.707
C11:0	8.735	0.000	P<0.05	P<0.05		0.774	0.690
C12:0	4.351	0.016	P<0.05	P<0.05		0.691	0.731
C13:0	2.598	0.080				0.548	0.543
C14:0	4.551	0.013	P<0.05			0.686	0.580
C14:1N5	2.539	0.085				0.596	0.663
C15:0	4.633	0.012	P<0.05		P<0.05	0.697	0.539
C15:1N5	7.170	0.001	P<0.05	P<0.05		0.744	0.711
C16:0	4.910	0.010	P<0.05			0.673	0.572
C16:1N7	0.532	0.589				0.473	0.401
C17:0	3.273	0.043	P<0.05			0.662	0.575
C17:1N7	2.038	0.137				0.558	0.641
C18:0	6.244	0.003	P<0.05	P<0.05		0.704	0.569
C18:1N9	2.747	0.070				0.532	0.457
C18:1TN9	2.578	0.082				0.638	0.652
C18:2N6	3.883	0.024	P<0.05	P<0.05		0.670	0.582
C18:2TTN6	1.070	0.348				0.591	0.588
C18:3N3	1.716	0.186				0.623	0.495
C18:3N6	0.532	0.589				0.601	0.607
C20:0	9.337	0.000	P<0.05	P<0.05		0.808	0.705
C20:1N9	1.897	0.156				0.633	0.662
C20:2N6	0.058	0.944				0.455	0.482
C20:3N3	12.852	0.000		P<0.05	P<0.05	0.471	0.146
C20:3N6	0.835	0.438				0.532	0.584
C20:4N6	0.076	0.927				0.436	0.387
C20:5N3	12.955	0.000	P<0.05	P<0.05		0.849	0.718

C21:0	8.440	0.000	P<0.05	P<0.05		0.747	0.736
C22:0	0.271	0.764				0.572	0.553
C22:1N9	10.379	0.000	P<0.05	P<0.05	P<0.05	0.827	0.546
C22:2N6	0.861	0.426				0.601	0.552
C22:4N6	0.097	0.908				0.455	0.430
C22:5N3	0.311	0.734				0.591	0.527
C22:5N6	0.897	0.412				0.428	0.426
C22:6N3	0.100	0.905				0.529	0.529
C23:0	12.731	0.000	P<0.05	P<0.05		0.849	0.705
C24:0	11.609	0.000	P<0.05	P<0.05		0.821	0.702
C24:1N9	0.151	0.860				0.486	0.472
C6:0	2.277	0.109				0.295	0.437
C8:0	4.760	0.011	P<0.05			0.713	0.418
Total_MUF A	4.040	0.021	P<0.05	P<0.05		0.622	0.580
Total_N3	0.505	0.605				0.593	0.538
Total_N6	2.223	0.115				0.611	0.537
Total_PUFA	2.195	0.118				0.607	0.541
Total_SFA	5.916	0.004	P<0.05			0.684	0.583

(5) Binary logistic regression analysis of IH group VS control group: screening IH group and control group Different even-numbered carbon medium and long-chain fatty acids: C10:0, C12:0, C14:0, C16:0, C18:0, C18:2N6, C20:0, C20:5N3, C22:1N9, C24:0 and C8: 0, a total of 11, binary logistic regression analysis was carried out, and the optimal model was obtained by using the step-by-step method, and the optimal model constructed with 6 variables was established (Table 6 below). To calculate the new predicted value (Y): $Y = \text{logit}(P) = \ln(P/(1-P)) = 126.02 \times C10:0 - 0.16 \times C16:0 + 5.38 \times C20:0 + 23.28 \times C20:5N3 + 0.78 \times C22:1N9 - 67.68 \times C8:0 + 1.79$

Table 6: Binary logistic regression of IH group VS control group

fatty acid	B	standard error	p-value
C10:0	126.02	74.24	0.090
C16:0	-0.16	0.06	0.008
C20:0	5.38	4.25	0.205
C20:5N3	23.28	12.78	0.069
C22:1N9	0.78	0.4	0.047
C8:0	-67.68	63.92	0.290
constant	1.79	2.28	0.432

(6) ROC curve analysis of the fitting model: use this model to generate the predicted value Y value, and draw the ROC curve with the Y value (as shown in

Figure 17), and calculate the AUC up to 0.960. At this time, the sensitivity of the model is 0.917 and the speciality is 0.923.

(7) Binary logistic regression analysis of IH group VS NS group:

Screening the difference between IH group and NS group even-numbered carbon long-chain fatty acids: C10:0, C12:0, C18:0, C18:2N6, C20:0, C20:3N3, C20:5N3, C22:1N9 and C24:0, A total of 9, binary logistic regression analysis was carried out, and the optimal model was obtained by stepwise method, and the optimal model constructed with 4 variables was established (Table 7 below).

Thus calculating the new predicted value (Y):

$$Y = \text{logit}(P) = \ln(P/(1-P)) = 12.41 \times C12:0 - 19.42 \times C20:3N3 + 14.10 \times C20:5N3 - 0.44 \times C22:1N9 + 5.56$$

Table 7: Binary logistic regression for IH group VS NS group

fatty acid	B	standard error	p-value
C12:0	12.41	4.92	0.012
C20:3N3	-19.42	5.70	0.001
C20:5N3	14.10	8.05	0.080
C22:1N9	-0.44	0.33	0.180
constant	5.56	2.48	0.025

(8) ROC curve analysis of the fitted model: the model was used to generate the predicted value Y, and the ROC curve was drawn with the Y value (Figure 18), and the calculated AUC was 0.966. At this time, the sensitivity of the model was 0.917, and the specificity was 0.946.

In conclusion, there are significant differences between the fatty acid indexes of infantile hemangioma and neonatal erythema with similar clinical appearance symptoms. The inventors of the present invention have found that there are not only significant differences between the fatty acid indexes of infantile hemangioma children and normal children, but also significant differences between the fatty acid indexes of neonatal erythema with similar clinical appearance symptoms, which is beneficial to clinically distinguish other diseases with symptoms similar to infantile hemangiomas, so as to avoid overtreatment or delayed treatment timing caused by misdiagnosis.

Fatty acid group indicator Embodiment 2:

According to the above fatty acid group index embodiment 1 method, further screening and verification of the IH detection effect by detecting a small amount of fatty acids. The differences from the above fatty acid group index embodiment 1 are highlighted below.

Obtaining sample information

A total of 63 patients with IH positive specimens were collected during follow-up, and 24 patients were randomly selected as the training set of the IH group. In addition, according to the infant gender, birth weight, gestational weeks and other relevant information of the children in the IH group, matching was conducted, and 26 sample control group training sets with the same conditions were screened. The test set is randomly selected with 28 cases as the IH group test set. In addition, according to the infant gender, birth weight, gestational weeks and other relevant information of the children in group IH, the matching conditions were used as matching conditions, and 32 samples of the control group with the same conditions were selected as the test set of the control group.

Fatty acid test data were obtained

The fatty acid data of the training set and the test set samples were measured by the above-mentioned fatty acid detection method.

In the training set and the test set, the total number of even carbon differential fatty acids ($p < 0.05$) was 11, including cis-5, 8, 11, 14, 17-eicosapentaenoic acid, erucic acid, linoleic acid, stearic acid, cis-11-eicosapentaenoic acid, arachacid, capric acid, myristic acid, palmitic acid, decanoate, Myristate, palmitate, octanoate, tetracosanoate) (C20:5 n3, C22:1 the n9, C18:2 n6, C18:0, C20:1 n9, C20:0, C10:0, C14:0, C16:0, C8:0, C24: 0) as shown in **Table 8**.

Table 8

EVEN-NUMBERED CARBON FATTY ACIDS WERE	TRAINING SET DATA			
	Multiple	p- value (T	AUC	P(AUC)

DIFFERENT IN BOTH BATCHES		change	test)		
zfs0001	C10:0	2.05680931	0.00712709	0.7852564	0.0005473
zfs0005	C14:0	1.405472314	0.013531497	0.6858974	0.0242886
zfs0009	C16:0	1.280179	0.008605967	0.6730769	0.0359771
zfs0013	C18:0	1.403749634	0.003917408	0.7035256	0.013658
zfs0016	C18:2N6	1.450114664	0.03296498	0.6698718	0.0395566
zfs0020	C20:0	4.052589244	0.004999897	0.8076923	0.0001928
zfs0021	C20:1N9	2.028896504	0.034341765	0.6330128	0.1070215
zfs0026	C20:5N3	4.063899911	0.000820796	0.849359	2.304E-05
zfs0029	C22:1N9	2.088188606	0.000528246	0.8269231	7.453E-05
zfs0036	C24:0	3.861035025	0.001321701	0.8205128	0.0001029
zfs0039	C8:0	3.160951336	0.019706952	0.713141	0.0098046

Continuation of Table 8

TEST SET DATA		
Multiple change	p-value (T test)	AUC (A over B plus D)
14.37978226	3.83076E-09	0.938
2.969710454	5.17568E-09	0.911
2.472324809	7.56839E-10	0.882
2.105599798	2.51299E-07	0.951
2.378743233	1.36996E-06	0.958
63.45552674	1.49574E-10	0.987
15.81861152	4.8717E-09	0.931
2.646920437	0.000140038	0.856
16.89111097	1.8511E-06	0.946
4.240622636	1.23929E-05	0.942
3.192145091	1.3846E-05	0.8

The above 11 even-carbon differential fatty acids are analyzed by binary logistics regression, and the optimal model is obtained by stepwise method. The optimal model is constructed with 5 variables, as shown in **Table 9**.

Variable in an equation							
		B	Standard error	Wald	Degree of freedom	significance	Exp(B)

Step 1	C10:0	66.062	49.852	1.756	1	0.185	4902892411507649 00 00000000000.000
	C16:0	-0.158	0.062	6.443	1	0.011	0.854
	C20:0	4.560	4.418	1.065	1	0.302	95.562
	C20:5N3	24.205	13.250	3.337	1	0.068	32517540987.178
	C20:5N3	0.814	0.410	3.930	1	0.047	2.256
	constant	1.189	2.093	0.322	1	0.057	3.283

a. Enter variables in Step 1: zfs0001, zfs0009, zfs0020, zfs0026, zfs0029.

Thus, the new predicted value (Y) is calculated:

$$\text{logit}(P) = \ln(P/(1-P)) = 66.062 \times C10:0 - 0.158 \times C16:0 + 4.560 \times C20:0 + 24.205 \\ \times C20:5N3 + 0.814 \times C22:1N9 + 1.189$$

ROC curve analysis of fitted model:

The predicted Y value was generated by this model, and the ROC curve was drawn with the Y value (as shown in FIG. 19 and FIG. 20), and the AUC of the training set and the test set were calculated to be 0.955 and 0.951.

From the above results, it can be seen that even if only 5 kinds of fatty acids are detected, good detection effect can be obtained.

Metabolome Examples of indicators:

(1) Experimental method

1. Sample treatment: Take out the samples (all samples shown in Table 2) at -80°C, slowly dissolve at 4°C, take 100ul of samples from each group, add 400ul of pre-cooled methanol-acetonitrile solution (1:1, v/v), Vortex for 60s, place at -20°C for 1h to precipitate protein, centrifuge at 14000rcf, 4°C for 20min, take the supernatant and freeze-dry, store the sample at -80°C.

2. Sample detection: The sample was separated by Agilent 1290 Infinity LC ultra-high performance liquid chromatography (UHPLC) HILIC column. After the

sample detection, the AB Triple TOF 6600 mass spectrometer was used to collect the first-order and second-order spectra of the sample.

3. Data processing: Metabolome detection data was converted into .mzXML format by ProteoWizard, and then XCMS program was used for peak alignment, retention time correction and peak area extraction. The identification of metabolite structure was carried out by accurate mass matching (<25 ppm) and secondary spectrum matching, and the self-built database of the laboratory was searched. XCMS software was used to extract metabolite ion peaks, and 10733 and 9688 peaks were detected in positive and negative ion modes, respectively. And through the laboratory self-built database for qualitative, positive ion mode, negative ion mode (positive ion mode, negative ion mode) qualitative metabolites 228,189 metabolites respectively.

Table 10

model	Number of peaks	qualitative metabolites
Positive ions	10733	228
negative ions	9688	189

4. Statistics:

Data analysis was performed using SPSS software (version 25.0; IBM, Armonk NY, USA) and SIMCA-P software (version 14.1; Umetrics, Umeå, Sweden). Two independent samples T-test (Student's t-test) was used to analyze whether the variables were different, and the two-tailed test P value less than 0.05 was considered significant. Orthogonal partial least squares discriminant analysis (OPLS-DA) is used to establish a relationship model between the expression of metabolites and the sample category to realize the prediction of the sample category, and at the same time calculate the variable importance for the projection (Variable Importance for the Projection, VIP) to measure the effect of the expression pattern of each metabolite on The impact strength and explanatory power of the classification and discrimination of samples in each group can assist in the screening of marker metabolites (with VIP >1.0 as the screening standard). ROC (receiver operating characteristic curve) analysis was used

to judge the diagnostic value of difference variables. Binary logistic regression analysis was used to construct a logistic regression model to further improve the predictive sensitivity and specificity, and improve the diagnostic value.

(2) Results:

(1) Analysis of differential metabolites: Metabolites with both orthogonal partial least squares discriminant analysis VIP >1 and T-test analysis $P < 0.05$ were selected as metabolites with significant differences. There were 21 metabolites with significant difference in positive ion mode, and 21 metabolites with significant difference in negative ion mode.

(2) ROC curve analysis: draw the ROC curves of the above 42 differential metabolites, and calculate the AUC value. Among them, the AUC values of 12 differential metabolites were greater than 0.7, and the AUC values of 7 differential metabolites were greater than 0.75. See Table 11 below for details.

Table 11: Differential metabolites

describe	median (THEM)	average value (THEM)	S.D. (THEM)	median (compar ison)	average value (compar ison)	S.D. (compar ison)	VI P	T-test (P value)	AUC
positive ion mode									
(3-carboxypropyl)trimethylammonium cation	318829	337322	94154	268980	290309	75926	1.809	0.037	0.671
α -D-(+)-talose	16412	23794	21161	14509	15218	4831	1.266	0.030	0.641
1-Aminocyclopropanecarboxylic acid	78140	85632	33244	62309	63625	13650	1.212	0.001	0.723
1-myristoyl-sn-glycero-3-phosphocholine	204125	243120	122191	152627	176533	86010	2.129	0.017	0.756
1-oleoyl-sn-glycero-3-phosphocholine	51623	72145	48799	47835	52639	21808	1.671	0.046	0.606
1-palmitoyl-sn-glycero-3-phosphocholine	5485501	7466180	6888066	4577518	4507420	2206886	10.600	0.025	0.682
1-Stearoyl-sn-gl	98217	131318	111441	73130	87696	38256	2.721	0.042	0.634

ycero-3-phospho									
choline									
Bilirubin	121286	182944	184129	103975	108052	32347	4.064	0.027	0.670
choline	155944	161306	55092	117173	123514	33338	1.681	0.002	0.729
D-2-piperidicolic									
acid	393813	366494	154802	313629	289746	109651	2.554	0.029	0.720
DL-indole-3-lact									
ic acid	774455	807224	258688	584886	601723	201018	3.230	0.001	0.789
Glycyl									
glutamate	12840	17494	13646	6743	8584	7216	1.033	0.002	0.763
Glycerophospho									
rylcholine	1251462	1341116	614631	830505	961891	399832	5.393	0.006	0.694
Isomaltose	164450	232645	218406	140273	144117	46350	4.162	0.029	0.646
L-Arginine	4486781	4189379	1382270	4224622	3248590	1864913	6.779	0.032	0.634
L-glutamic acid	92028	108588	72200	43835	54623	34453	1.933	<0.001	0.738
L-phenylalanine	460866	491808	140133	409709	396129	73837	2.144	0.001	0.762
L-tryptophan	154242	163224	50570	119779	120672	41031	1.460	0.001	0.794
NG,NG-Dimeth									
yl-L-arginine	1578923	1720633	1051204	1200899	1226584	592838	4.751	0.026	0.669
Tyramine	1113942	1179400	290829	984725	962736	174741	3.366	0.001	0.750
Phenylacetic									
acid	22391	22557	5796	27750	28846	7451	1.033	0.001	0.756
Anion mode									
(S)-Citromalic									
acid	6167	11667	14554	5327	5643	2312	1.266	0.024	0.643
1-Oleoyl-L- α -lys									
ophosphatidic	82402	112027	125362	58520	62618	36811	3.639	0.037	0.621
acid									
1-palmitoyl									
lysophosphatidi	8580	17111	25773	4819	5915	4018	1.647	0.018	0.679
c acid									
α -mangostin	359331	376257	148392	316713	315394	79561	2.760	0.049	0.624
Arachidonic									
Acid (peroxide	368849	449317	252387	306437	345335	138980	3.686	0.049	0.604
free)									
citric acid	1575	10750	20950	1182	1744	2849	1.597	0.019	0.657
cyclamate	26712	53820	65089	23137	25270	13771	1.070	0.019	0.617
D-galactate	18570	30921	26563	47558	55103	42388	2.099	0.012	0.695
D-threitol	210466	309909	297672	181664	194584	59441	4.225	0.036	0.605
D(-)-beta-Hydro									
xybutyrate	90708	109747	75725	124524	168560	135681	2.688	0.047	0.602
Inositol									
galactoside	1042995	1544553	1349174	935864	1029118	395909	10.115	0.043	0.594
glyceric acid	64867	69975	33257	37110	39662	17540	2.351	<0.001	0.809

L-Aspartic Acid	41762	62595	52823	29016	31032	14768	2.672	0.002	0.679
L-Carnosine	35521	41278	33837	56855	66084	40918	2.463	0.014	0.683
L-malic acid	16062	32591	38103	12548	15798	10828	2.077	0.020	0.648
N-acetyl-L-aspartic acid	27000	29910	13185	20684	21624	7228	1.238	0.003	0.694
N-acetylneuraminic acid	33713	48444	36969	29165	32899	17857	1.920	0.039	0.679
norethindrone acetate	111580	132137	76908	89852	89933	41677	2.548	0.009	0.677
Phosphocholine	38592	46442	26464	27420	32016	15580	1.586	0.011	0.675
sn-glycero-3-phosphoethanolamine	121230	153725	107756	78483	91679	44298	2.831	0.004	0.683
Succinate	28332	38221	23498	23040	26354	11530	1.921	0.014	0.627

(3) Binary logistic regression: Perform binary logistic regression analysis on the above 42 differential metabolites, and use a step-by-step algorithm to obtain the optimal model, and establish the optimal model constructed with 6 variables (see Table 10), so as to calculate New predicted value (Y): $Y = \text{logit}(P) = \ln(P/(1-P)) = -5.55 \times 10^{-5} \times \text{DL-indole-3-lactic acid} + 3.17 \times 10^{-4} \times \text{L-Tryptophan} + 3.50 \times 10^{-5} \times \text{cyclohexyl sulfamate} - 4.15 \times 10^{-5} \times \text{D-galactate} + 4.13 \times 10^{-5} \times \text{glyceric acid} + 1.45 \times 10^{-5} \times \text{sn-glycero-3-phosphoethanolamine} - 9.32$

Table 12: Logistic regression analysis to establish a predictive model.

describe	B	standard error	significance
DL-indole-3-lactic acid	-5.55×10^{-5}	2.68×10^{-5}	0.038
L-Tryptophan	3.17×10^{-4}	1.39×10^{-4}	0.022
Cyclohexylsulfamate	3.50×10^{-5}	1.77×10^{-5}	0.048
D-galactate	-4.15×10^{-5}	2.60×10^{-5}	0.111
glyceric acid	4.13×10^{-5}	2.77×10^{-5}	0.136
sn-glycero-3-phosphoethanolamine	1.45×10^{-5}	8.59×10^{-6}	0.091
constant	-9.32	2.90	0.001

(4) Fitting model ROC curve analysis: use this model to generate the predicted value Y value, and draw the ROC curve with the Y value (as shown in Figure 16), and calculate the AUC up to 0.952. At this time, the sensitivity is 0.893 and the specificity is 0.906.

Examples of proteomic indicators:

High-throughput swissport proteomics detection

(1) Experimental method

1. Glossary

DDA: Data Dependent Acquisition, used in this article to establish a library in the DIA analysis process.

DIA: Data Independent Acquisition (Data Independent Acquisition), specifically refers to the data based on Thermo Scientific™ electrostatic field orbitrap Orbitrap in this articlenon-dependent collectionset.

Spectronaut Pulsar X: Proteomics software for the analysis of data independent acquisition (DIA) measurements. The well-known DIA data analysis software from Biognosys.

MaxQuant: The well-known proteomics software from Mann M.'s laboratory, used to build the library and use it when searching.

Direct DIA: The integrated database search engine called Pulsar enables spectral-library free DIA workflow (Integrated database search engine called Pulsar enabling spectral-library free DIA workflow). The algorithm from Biognosys can directly search the library for DIA data, which is used to increase the capacity of the library and increase the number of final qualitative and quantitative results of DIA.

2. Protein detection:

First, the combined samples with the same amount of samples were used as a pool, and Aglient-H14 separated the pool samples. The high-abundance and low-abundance components were respectively enzymolized, and the enzymolized peptides of the low-abundance group were graded by HPRP (10 parts). The above

samples were analyzed by LC-MS/MS (Qe-Hf-dDA mode), and the proteome database was obtained, and the self-built database of APT was combined as the database of DIA. The specific steps are: carry out sample enzymatic hydrolysis and HPRP grading on the mixture of all samples, collect data dependent acquisition (DDA) mass spectrometry data, then use MaxQuant to search and identify, and use Spectronaut pulsar X software to construct a spectral library as a subsequent data independent acquisition (DIA) database for quantification of protein profiles. Download the swissport data package to build a proteome database.

Each sample in the project was independently prepared for sample preparation and protein enzymatic hydrolysis, and then used for DIA (data independent acquisition) analysis on the machine. The obtained DIA original file is imported into Spectronaut Pulsar X for analysis, and the qualitative and quantitative protein expression data of each sample is obtained (the numerical value reflects the area under the peak curve of the protein, and the larger the value, the higher the protein content).

3. Statistics:

Data analysis was performed using SPSS software (version 25.0; IBM, Armonk NY, USA). Two independent samples T-test (Student's t-test) was used to analyze whether the variables were different, and the two-tailed test P value less than 0.05 was considered significant. ROC (receiver operating characteristic curve) was used to analyze the diagnostic value of differential variables. Binary logistic regression analysis was used to construct a logistic regression model to further improve the predictive sensitivity and specificity, and improve the diagnostic value.

(2) Results

(1) Protein screening: A total of 727 proteins were qualitatively quantified, and protein variables with missing values >50% in all samples were filtered to reduce the false positive rate. A total of 603 variables were screened. Missing values are filled with the mean value of variables in the same group to maintain the homogeneity within the data group;

(2) T-test: Two independent sample T-tests are performed on the selected proteins,

and variables with a P value less than 0.05 are selected, a total of 47: PG.Genes:COLEC10, CPQ, LDHB, ACAN, KRT1, ARHGDIB, POSTN, LAMA5, CPN1, PROC, C1S, HPX, SUPT6H, BCAR3, BCHE, SOX30, C1R, PON1, CFHR4, PROZ, IGKV1D-16, APOC3, COMP, SELENOP, PMFBP1, GSN, SELL, FUCA2, HLA-B, FGFBP2, FKBP1A, HSPE1, SAA1, PGD, CDH1, SOD1, ISLR, CORO1A, ZYX, RLBP1, IDH1, IGKV6-21, SORL1, FAM3C, CST6, COTL1, and PIGR.

(3) ROC curve analysis: ROC analysis was performed on the above 47 proteins, and the AUC value was calculated. The results are shown in Table 13 below:

Table 13: Differential proteins.

PG. Gene	Average (IH)	S.D.(IH)	mean (control)	S.D. (control)	multiple of difference	T-test (P value)	AUC
COLLECTION10	489637.08	764638.77	89623.20	164109.90	5.463	0.005	0.661
CPQ	36436.65	28262.77	21563.00	5069.75	1.690	0.005	0.713
LDHB	79562.26	83767.39	46791.54	14756.34	1.700	0.034	0.614
not	345978.53	667176.40	45809.12	26312.64	7.553	0.014	0.657
KRT1	526992.48	490704.26	326165.09	245815.86	1.616	0.046	0.650
ARHGDIB	309369.77	421514.71	806844.88	839090.34	0.383	0.006	0.686
POSTN	77104.52	26098.29	156368.97	182303.19	0.493	0.026	0.656
LAMA5	93517.72	59859.49	325520.40	444572.86	0.287	0.008	0.671
CPN1	228304.42	55973.49	274373.92	64434.35	0.832	0.005	0.705
PROC	87150.44	31495.98	115149.00	47549.83	0.757	0.010	0.680
C1S	996392.59	191222.70	1111291.46	157926.85	0.897	0.013	0.680
HPX	3961113.56	1438689.00	5001838.30	1750057.41	0.792	0.016	0.646
SUPT6H	23247.95	11105.06	16716.20	9491.14	1.391	0.017	0.664
BCAR3	390763.98	94742.67	309680.67	110582.61	1.262	0.004	0.731
bche	234913.11	57678.23	275137.19	68828.44	0.854	0.018	0.652
SOX30	171068.60	68476.92	235378.31	92135.26	0.727	0.004	0.759
C1R	336921.53	59717.26	374292.27	63063.99	0.900	0.022	0.671
MON1	904603.40	233372.19	1060586.34	275769.31	0.853	0.022	0.662
CFHR4	121913.34	51559.66	89199.81	32542.13	1.367	0.004	0.733
PROC	69129.76	18268.32	86769.95	36231.60	0.797	0.023	0.657
IGKV1D-16	315793.03	82607.87	265469.33	85192.65	1.190	0.024	0.670
APOC3	4917626.31	1267527.30	5734103.29	1446015.20	0.858	0.024	0.645
COMP	55980.44	13048.91	47845.23	15039.27	1.170	0.030	0.650
SELENOP	264281.79	111982.72	326773.69	109603.49	0.809	0.033	0.664
PMFBP1	48075.43	9771.30	55789.43	17468.99	0.862	0.043	0.628
GSN	717081.40	125124.78	793469.40	161893.55	0.904	0.048	0.640
SELL	151157.85	36550.70	183022.22	76129.37	0.826	0.048	0.661

FUCA2	52538.48	46157.10	121781.38	149762.35	0.431	0.022	0.683
HLA-B	10646604.77	2221792.49	9556245.15	1871595.86	1.114	0.044	0.688
FGFBP2	59657.01	89861.92	25974.82	9987.49	2.297	0.039	0.667
FKBP1A	26359.98	8534.48	34358.27	8983.43	0.767	0.001	0.769
HSPE1	3387870.63	4905644.02	7279872.42	5294606.09	0.465	0.005	0.756
SAA1	34863.23	14180.22	138707.32	203188.86	0.251	0.009	0.627
PGD	189190.75	136856.42	92360.25	80392.91	2.048	0.001	0.743
CDH1	46609.30	18911.42	79520.77	83116.28	0.586	0.045	0.771
SOD1	68739.73	49231.43	48647.85	23658.30	1.413	0.044	0.645
ISLR	19732.98	8273.89	55587.07	81752.55	0.355	0.025	0.767
CORO1A	50342.75	29586.56	81949.86	56366.82	0.614	0.010	0.693
ZYX	83783.48	32466.72	108730.39	55576.88	0.771	0.042	0.664
RLBP1	293537.94	76649.40	234020.76	70520.16	1.254	0.003	0.771
IDH1	55569.85	55549.76	21911.64	24115.91	2.536	0.003	0.761
IGKV6-21	345471.18	205800.45	245868.70	118661.96	1.405	0.023	0.703
SORL1	4263013.59	2674588.87	3013720.32	2095660.79	1.415	0.047	0.704
FAM3C	11135.84	2445.34	15392.99	7456.62	0.723	0.005	0.747
CST6	36577.08	13747.43	47662.60	20321.70	0.767	0.018	0.720
COTL1	84724.49	55473.51	113931.08	55966.21	0.744	0.047	0.757
PIGR	812006.80	1523374.71	209093.87	345660.72	3.883	0.033	0.749

(4) Binary logistic regression analysis: For the above 47 proteins, binary logistic regression analysis was carried out, and the optimal model was obtained by stepwise algorithm, and the optimal model constructed with 6 variables was established (see Table 12), so as to calculate the new predicted value (Y): $Y = \text{logit}(P) = \ln(P/(1-P)) = 7.02 \times 10^{-6} \times \text{KRT1} - 4.09 \times 10^{-5} \times \text{POSTN} - 1.18 \times 10^{-4} \times \text{PROC} - 1.06 \times 10^{-4} \times \text{PROZ} - 2.30 \times 10^{-4} \times \text{PMFBP1} - 1.12 \times 10^{-4} \times \text{SELL} + 51.03$

Table 14: Logistic regression analysis to establish a predictive model.

PG gene	B	standard error	P value
KRT1	7.02×10^{-6}	3.82×10^{-6}	0.066
POSTN	-4.09×10^{-5}	2.67×10^{-5}	0.126
PROC	-1.18×10^{-4}	5.13×10^{-5}	0.022
PROC	-1.06×10^{-4}	4.39×10^{-5}	0.016
PMFBP1	-2.30×10^{-4}	9.04×10^{-5}	0.011
SELL	-1.12×10^{-4}	4.70×10^{-5}	0.017
constant	-51.03	20.42	0.012

(5) Fitting model ROC curve analysis: Use this model to generate the predicted value Y value, and draw the ROC curve with the Y value (as shown in Figure 14), and calculate the AUC up to 0.965, at this time the sensitivity is 0.929, and the specificity

is 0.906.

High-throughput uniport proteomics detection

The difference from the above-mentioned high-throughput swissport proteomics detection is:

1. Protein detection:

First of all, the combined samples with the same amount of samples to be detected were used as pool, and the pool samples were separated by Aglient-H14. The high-abundance and low-abundance components were respectively enzymolized, and the enzymolized peptides of the low-abundance group were graded by HPRP (10 parts). The above samples were analyzed by LC-MS/MS (Qe-Hf-dDA mode), and the proteome database was obtained, and the self-built database of APT was combined as the database of DIA. The specific steps are: carry out sample enzymatic hydrolysis and HPRP grading on the mixture of all samples, collect data dependent acquisition (DDA) mass spectrometry data, then use MaxQuant to search and identify, and use Spectronaut pulsar X software to construct a spectral library as a subsequent data independent acquisition (DIA) Database for the quantification of protein profiles. Download the uniport package to build a proteome database.

Each sample in the project was independently prepared for sample preparation and protein enzymatic hydrolysis, and then used for DIA (data independent acquisition) analysis on the machine. The obtained DIA original file was imported into Spectronaut Pulsar X for analysis, and the qualitative and quantitative protein quantity of each sample was obtained. (The numerical value reflects the area under the chromatographic peak curve of the protein. The larger the numerical value, the higher the protein content). A total of 2572 proteins were qualitatively quantified, of which 1672 proteins were detected in more than 80% of the samples.

2. Results

(1) Protein screening: A total of 2572 proteins were qualitatively quantified, and protein variables with missing values >20% in all samples were filtered to reduce the

false positive rate. A total of 1672 variables were screened. The missing value is filled with the median value of the variable in the same group to maintain the homogeneity within the data group;

(2) T test: For the selected data, two independent sample T tests were used to select variables with a P value less than 0.05, a total of 71 variables. Immunoglobulins were further removed to obtain 15 differential proteins, PG.Genes: A0A1W6IYJ2, PRDX1, CAT, CPN1, APOC3, HPX, PROS1, CD5L, HMFT1766, C1QA, KRT1, BCHE, KRT2, APP and FGFBP2.

(3) ROC curve analysis: ROC curves were drawn for the above 15 variables, and AUC was calculated, as shown in Table 15:

Table 15

PG gene	median (THEM)	average value (THEM)	S.D. (THEM)	median (control)	average value (control)	S.D. (control)	multiple of difference	T-test (P value)	AUC
A0A1W6IYJ2	614676.563	847905.466	782436.867	267682.690	449783.551	424430.888	1.885	0.016	0.621
PRDX1	234488.560	380525.480	402208.233	195289.940	211431.779	108808.367	1.800	0.026	0.615
CAT	78874.492	228331.400	278356.728	511486.219	541221.860	518190.671	0.422	0.006	0.680
CPN1	257049.453	246976.689	55755.876	292843.563	289185.742	59845.223	0.854	0.007	0.693
APOC3	5772071.500	5645160.777	1421442.818	6292647.750	6559630.852	1679778.529	0.861	0.028	0.638
HPX	2910172.875	2866978.763	921713.682	3162924.125	3476699.133	1092386.498	0.825	0.024	0.643
PROS1	296606.938	286566.921	59902.719	302783.891	341926.284	105979.206	0.838	0.018	0.642
CD5L	173409.594	194614.525	59632.287	220595.852	259493.933	137125.243	0.750	0.024	0.680
HMFT1766	513888.453	525761.571	137879.794	576627.344	661163.935	300058.056	0.795	0.032	0.650
C1QA	1347714.688	1382551.732	297400.801	1138744.750	1178767.666	316600.309	1.173	0.013	0.663
KRT1	392435.797	541165.941	502435.036	270476.336	320891.082	206787.318	1.686	0.027	0.642
bche	199200.516	201879.781	54047.997	218039.750	230290.208	54240.260	0.877	0.047	0.637
KRT2	41263.826	59997.162	60285.469	34441.770	37347.588	16469.441	1.606	0.046	0.617
APP	22074.400	33219.803	33251.508	19111.795	20108.368	9528.227	1.652	0.037	0.641
FGFBP2	29877.820	82835.041	117005.447	26050.620	32308.263	28825.976	2.564	0.021	0.617

(4) Binary logistic regression analysis: Perform binary logistic regression analysis on the above 15 proteins, and use a step-by-step algorithm to obtain the optimal model, and establish the optimal model constructed with 6 variables(See Table 14 below), so as to calculate the new predicted value (Y):

$$Y = \text{logit}(P) = \ln(P/(1-P)) = 3.96 \times 10^{-6} \times A0A1W6IYJ2 - 3.22 \times 10^{-6} \times CAT - 1.92 \times 10^{-5} \times PROS1 - 4.10 \times 10^{-5} \times CD5L + 3.36 \times 10^{-6} \times C1QA + 4.74 \times 10^{-6} \times KRT1 + 6.81$$

Table 16

PG. Gene	B	standard error	P value
A0A1W6IYJ2	3.96×10^{-6}	1.43×10^{-6}	0.00549617
CAT	-3.22×10^{-6}	1.41×10^{-6}	0.02221397
PROS1	-1.92×10^{-5}	8.15×10^{-6}	0.01848923
CD5L	-4.10×10^{-5}	1.54×10^{-5}	0.00786287
C1QA	3.36×10^{-6}	1.79×10^{-6}	0.0602534
KRT1	4.74×10^{-6}	2.12×10^{-6}	0.02552159
constant	6.81	3.57	0.05647654

(5) ROC curve analysis of the fitting model: use this model to generate the predicted value Y value, and draw the ROC curve with the Y value (as shown in Figure 15), and calculate the AUC up to 0.934. At this time, the sensitivity is 0.893 and the specificity is 0.875.

Examples of lipidome indicators:

1. Experimental equipment and reagents

Q-Exactive Plus mass spectrometer (Thermo Scientific)

UHPLC Nexera LC-30A Ultra High Performance Liquid Chromatograph (SHIMADZU)

Low-temperature high-speed centrifuge (Eppendorf 5430R)

Column: Waters, ACQUITY UPLC CSH C18, 1.7 μm , 2.1 mm $\times$ 100 mm column

Acetonitrile (Thermo Fisher), Isopropanol (Thermo Fisher), Methanol (Thermo Fisher)

13 isotopic internal standards (Cer, LPC, PC, LPE, PE, PI, PS, PA, PG, SM, Chol Ester, DG, TG).

2. Experimental method

2.1 Sample information

Preparation of quality control samples (QC): Equal amounts of samples from each group were mixed for QC. QC samples are not only used to test the state of the instrument before sample injection and to balance the chromatography-mass spectrometry system, but also interspersed during the detection of samples to be tested

to evaluate the system stability during the entire experiment.

2.2 Sample preprocessing method

Take 60ul of each sample, add 200 μ L water and 20 μ L internal lipid standard mixture, vortex mix, add 800 μ L methyl tert-butyl ether (MTBE), vortex mix, add 240 μ L pre-cooled Methanol, vortexed, sonicated in a low-temperature water bath for 20 minutes, placed at room temperature for 30 minutes, centrifuged at 14,000 g at 10°C for 15 minutes, took the upper organic phase, dried with nitrogen, and added 200 μ L of 90% isopropanol/acetonitrile solution for mass spectrometry analysis. Vortex well, take 90 μ L of complex solution, centrifuge at 14,000 g at 10°C for 15 min, and take the supernatant for analysis.

2.3 Chromatography-mass spectrometry

2.3.1 Chromatographic conditions

The samples were separated by UHPLC Nexera LC-30A ultra-high performance liquid chromatography system. C18 chromatographic column;

The column temperature is 45°C; the flow rate is 300 μ L/min. Mobile phase composition A: Acetonitrile aqueous solution (acetonitrile: water = 6:4, v/v), B: acetonitrile isopropanol solution (acetonitrile: isopropanol = 1:9, v/v). The gradient elution program is as follows: 0 --- 2 min, B is maintained at 30%; 2 --- 25 min, B is linearly changed from 30% to 100%; 25 --- 35 min, B is maintained at 30%.

2.3.2 Mass Spectrometry Conditions

Electrospray ionization (ESI) positive and negative ion modes were used for detection. Samples were separated by UHPLC and analyzed by mass spectrometry using a Q Exactive series mass spectrometer (Thermo Scientific™). The ESI source conditions were as follows:

Heater Temp 300°C, Sheath Gas Flow rate 45 arb, Aux Gas Flow Rate 15 arb, Sweep Gas Flow Rate 1 arb, spray voltage (spray voltage) 3.0KV, capillary temperature (Capillary Temp) 350 °C, ion lens voltage frequency level (S-Lens RF Level) 50%, MS 1 scan ranges (scan ranges): 200-1800.

The mass-to-charge ratios of lipid molecules and lipid fragments were collected

as follows: 10 fragment spectra (MS 2 scan, HCD) were collected after each full scan. MS 1 has a resolution of 70,000 at M/Z 200 and MS 2 has a resolution of 17,500 at M/Z 200.

2.4 Data processing and software setting

Use LipidSearch to perform peak identification, peak extraction, and lipid identification (secondary identification) on lipid molecules and internal standard lipid molecules. The main parameters are: precursor tolerance: 5 ppm, product tolerance: 5 ppm, product ion threshold: 5%.

2.5 Statistical analysis

SPSS software (version 25.0; IBM, Armonk NY, USA) was used. Two independent samples T-test (Student's t-test) was used to analyze whether the variables were different, and the two-tailed test P value less than 0.05 was considered significant. The difference was calculated by calculating the Fold change (FC) value, and $FC > 1.5$ or $FC < 0.67$ were considered significant differences. ROC (receiver operating characteristic curve) analysis was used to analyze the diagnostic value of differential variables.

3. Results

3.1 Identification quantity statistics

The International Lipid Classification and Nomenclature Committee divides lipid compounds into 8 major types, each type can be divided into different subclasses (lipid class) according to the difference of the polar head, each subclass Classes are divided into different molecules (lipid species) according to differences such as carbon chain saturation or length, thus forming a three-level classification of lipid compounds: class-subclass-molecule.

The number of lipid compounds in the samples identified by positive and negative ion modes in this experiment.

Table 17: Number of lipid subclasses and molecular identifications

Lipid subclass (Lipid class)	Lipid species
25	821

The statistical results of lipid subclasses (lipid class) identified in positive and negative ion modes and the number of lipid molecules (lipid species) identified in each category are shown in Table 1 and Figure 10.

3.2 Lipid difference analysis

3.2.1 Overall level

The contents of all the quantified lipid molecules in the same sample are summed, that is, the total lipid molecule content of the sample. Then the total content of samples from different groups can be compared, and the T test results showed that the total lipid content of the IH group was lower than that of the control group ($P < 0.01$). (See Figure 11)

3.2.2 Subcategory level

The contents of all the quantified uniform subclasses of lipid molecules in the same sample were summed to compare the expression changes of lipid subclasses in different samples. The results of the T-test show that AcCa, Cer, CerG1, CerG2, CerG2GNAc1, CerG3, ChE, CL, GM3, LPC, LPE, MGDG, PA, PC, PE, phSM, PI, PS, SM, and TG. There was a difference in the content between the two groups ($P < 0.05$), the content of phSM in the IH group was higher than that in the control group, and the rest were lower than that in the control group. The content of Co, DG, LPI, So, WE had no significant difference between the two groups ($P > 0.05$) (see Table 18, Figure 12 and Figure 13).

The diagnostic value of each differential lipid subclass was further analyzed by ROC, and the AUC value was calculated. The results showed that the AUC values of Cer, ChE, LPC, LPE, PA, PC, PE, PI, PS and SM were greater than 0.700, and the AUC value of PA was greater than 0.8, which had good diagnostic value (see Table 18).

Table 18: Differences in the expression of different subclasses of lipids between the two groups

category	average value THEM	average value control	SD THEM	SD control	multiple of differen	P value	AUC
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	ce						
AcCa	0.566	0.730	0.257	0.202	0.776	0.008	0.683
Cer	0.767	1.043	0.347	0.314	0.735	0.002	0.728
CerG1	0.187	0.251	0.101	0.083	0.746	0.010	0.688
CerG2	0.105	0.131	0.052	0.039	0.803	0.031	0.692
CerG2GNAc1	0.245	0.318	0.127	0.120	0.772	0.027	0.662
CerG3	0.014	0.018	0.009	0.006	0.779	0.040	0.655
That	851.707	1148.962	409.562	256.497	0.741	0.001	0.702
CL	0.068	0.084	0.028	0.019	0.807	0.010	0.682
Co	0.171	0.188	0.066	0.053	0.908	0.265	0.573
DG	10.493	12.532	5.347	4.702	0.837	0.121	0.633
GM3	0.621	0.739	0.222	0.197	0.839	0.032	0.642
LPC	51.859	66.396	17.496	12.767	0.781	<0.001	0.752
LPE	4.062	5.539	1.325	1.641	0.733	<0.001	0.758
LPI	0.075	0.078	0.017	0.016	0.968	0.571	0.557
MGDG	0.022	0.028	0.009	0.009	0.808	0.023	0.654
Well	1.845	3.703	1.451	1.791	0.498	<0.001	0.809
PC	399.514	535.430	147.477	106.452	0.746	<0.001	0.752
ON	13.120	16.880	6.148	3.279	0.777	0.004	0.737
phSM	1.958	1.748	0.435	0.317	1.120	0.035	0.623
PI	16.084	18.904	3.639	2.774	0.851	0.001	0.733
PS	610.154	721.305	144.829	134.417	0.846	0.003	0.728
SM	174.300	251.434	90.046	70.220	0.693	<0.001	0.733
So	0.269	0.237	0.091	0.082	1.139	0.145	0.608
TG	164.301	219.492	84.097	84.061	0.749	0.014	0.681
WE	0.072	0.064	0.040	0.032	1.122	0.410	0.542

3.2.3 Lipid molecular level

The qualitative and quantitative 821 lipid molecules between the two groups were subjected to two-sample T-test, and the results showed that there were differences in 567 lipid molecules ($P < 0.05$), and the fold change (FC) was further screened to meet the difference of $FC > 1.5$. There are 6 molecules ($FC > 1.5$) and 130 with $FC < 0.67$. Finally, with the T-test P value < 0.05 , and $FC > 1.5$ or $FC < 0.67$ as the screening conditions, a total of 136 differential molecules were screened.

The diagnostic value of each differential molecule was further analyzed by ROC, and the AUC value was calculated. The results showed: 115 differential molecules with $AUC \geq 0.700$, among which 53 differential molecules with $AUC \geq 0.750$ (see Table 19). Among them, there are 9 differential molecules with $AUC \geq 0.80$, which are

PS(39:4)-H, SM(d45:6)+H, PC(14:0/20:4)+HCOO, SM(d20:0/18:1)+HCOO, PS(49:4)-H, LPC(26:0)+HCOO, SM(d20:0/16:0)+HCOO, PA(50:4)-H, LPC(20:4)+HCOO.

Table 19: There are significant differences between the lipid molecular indexes of children with infantile hemangioma and those of normal children, and the lipid molecules with AUC $\geq$ 0.75.

Classification	lipid molecule	average value_control	Sd_control	Average IH	Sd_THEM	multiple of difference	P-value	AUC
PS	PS(39:4)-H	1.711	0.440	1.075	0.371	0.628	<0.001	0.878
SM	SM(d45:6) H	0.038	0.011	0.022	0.013	0.587	<0.001	0.834
PC	PC(14:0/20:4) HCOO	0.183	0.050	0.111	0.059	0.603	<0.001	0.833
SM	SM(d20:0/18:1) HCOO	0.413	0.155	0.235	0.116	0.570	<0.001	0.831
PS	PS(49:4)-H	0.076	0.021	0.047	0.025	0.617	<0.001	0.823
LPC	LPC(26:0) HCOO	0.062	0.033	0.027	0.017	0.435	<0.001	0.820
SM	SM(d20:0/16:0) HCOO	6.307	2.062	3.844	1.858	0.609	<0.001	0.810
Well	PA(50:4)-H	3.703	1.791	1.845	1.451	0.498	<0.001	0.809
LPC	LPC(20:4) HCOO	6.483	1.589	4.074	2.231	0.628	<0.001	0.800
PC	PC(36:5) H	0.347	0.100	0.229	0.105	0.660	<0.001	0.795
LPC	LPC(20:1) HCOO	0.054	0.018	0.035	0.016	0.639	<0.001	0.787
PC	PC(38:8) H	0.049	0.016	0.031	0.018	0.623	<0.001	0.783
PC	PC(46:5) H	0.013	0.004	0.008	0.005	0.635	<0.001	0.783
ON	FRI (18:0p/22:5)-H	0.068	0.021	0.045	0.021	0.661	<0.001	0.781
SM	SM(d22:0/16:0) HCOO	3.249	1.211	1.946	1.190	0.599	<0.001	0.780
PC	PC(15:0/20:4) HCOO	0.257	0.074	0.162	0.097	0.629	<0.001	0.779
SM	SM(d18:0/20:4) HCOO	0.032	0.015	0.017	0.014	0.538	<0.001	0.778
LPC	LPC(22:4) HCOO	0.084	0.024	0.054	0.031	0.642	<0.001	0.778
PI	PI(18:0/22:4)-H	0.114	0.035	0.075	0.038	0.655	<0.001	0.777
PC	PC(16:1/18:2) HCOO	0.988	0.360	0.613	0.386	0.621	<0.001	0.776
PS	PS(40:4)-H	0.288	0.136	0.168	0.091	0.583	<0.001	0.773
Cer	Cer(d20:0/24:1) H	0.007	0.003	0.004	0.002	0.590	<0.001	0.771
SM	SM(d37:0) HCOO	0.132	0.057	0.077	0.049	0.586	<0.001	0.771
PC	PC(17:1/16:0) HCOO	0.780	0.241	0.521	0.245	0.668	<0.001	0.769
SM	SM(d20:0/22:5) HCOO	0.575	0.200	0.344	0.240	0.599	<0.001	0.769
PC	PC(44:11) H	0.007	0.003	0.004	0.003	0.578	<0.001	0.767
SM	SM(d32:0) HCOO	0.348	0.128	0.215	0.139	0.617	<0.001	0.766
LPC	LPC(22:1) H	0.006	0.004	0.004	0.003	0.604	0.003	0.766
PC	PC(33:0e) H	0.017	0.007	0.010	0.009	0.595	<0.001	0.766
SM	SM(d56:2 pO) H	0.011	0.004	0.006	0.004	0.613	<0.001	0.765
SM	SM(d42:1) HCOO	7.401	3.306	4.429	2.679	0.598	<0.001	0.765
LPC	LPC(17:1) HCOO	0.062	0.023	0.040	0.020	0.651	<0.001	0.763
SM	SM(d17:0/18:2) HCOO	0.153	0.052	0.092	0.063	0.599	<0.001	0.763
Cer	Cer(d18:1/24:0) H	0.093	0.040	0.057	0.032	0.616	<0.001	0.761

SM	SM(d36:3) HCOO	0.166	0.060	0.100	0.072	0.604	<0.001	0.760
AcCa	AcCa(14:2) H	0.020	0.008	0.012	0.008	0.611	<0.001	0.759
Cer	Cer(d18:1/24:0 O) H	0.002	0.001	0.001	0.001	0.634	<0.001	0.759
ON	PE(20:0p/20:4)-H	0.123	0.033	0.082	0.050	0.664	<0.001	0.759
LPC	LPC(26:1) HCOO	0.018	0.005	0.012	0.008	0.634	<0.001	0.757
PC	PC(37:5) H	0.089	0.037	0.058	0.032	0.651	0.001	0.757
SM	SM(d44:1) HCOO	0.072	0.039	0.041	0.028	0.565	<0.001	0.757
Cer	Cer(d18:1/26:1) H	0.005	0.002	0.003	0.002	0.659	<0.001	0.756
ON	PE(40:6e) H	0.124	0.091	0.069	0.050	0.558	0.007	0.754
TG	TG(18:1/20:2/22:4) NH4	0.224	0.105	0.136	0.097	0.607	0.001	0.753
SM	SM(d34:3) H	0.041	0.018	0.026	0.015	0.627	<0.001	0.752
ON	PE(40:4)-H	0.254	0.059	0.169	0.095	0.664	<0.001	0.752
SM	SM(d22:0/18:2) HCOO	0.560	0.225	0.357	0.211	0.638	<0.001	0.752
Cer	Cer(d18:0/22:0) H	0.074	0.029	0.048	0.023	0.659	<0.001	0.752
SM	SM(d44:0) HCOO	0.028	0.012	0.019	0.013	0.669	0.006	0.751
PI	PI(16:1/20:4)-H	0.013	0.004	0.008	0.005	0.669	0.001	0.751
PC	PC(20:3/20:4) HCOO	0.297	0.107	0.191	0.107	0.643	<0.001	0.750
ON	PE(38:1p)-H	0.010	0.003	0.006	0.005	0.637	<0.001	0.750
SM	SM(d39:0) HCOO	0.211	0.087	0.131	0.079	0.617	<0.001	0.750

Fitting model verification example

Substitute the metabolite content detected in the first sample of the positive group and the control group into the above proteomics model, metabolomics model, and fatty acid omics model to obtain the Y value and predict the result. The results showed that among the four models, the Y values of the specimens in the IH group and the control group were significantly different, indicating that the four models all had good predictive effects. (See Table 20 below for details)

Table 20

Model	specimen	Y value	forecast result
swissport proteomics - predictive models	IH Sample-1	3.656	Positive
	Control sample-1	-2.855	Negative
uniport proteomics - prediction model	IH Sample-1	6.371	Positive
	Control sample-1	-0.986	Negative
Metabolomics - Predictive Modeling	IH Sample-1	0.191	Positive
	Control sample-1	-2.809	Negative
Medium and Long Chain Fatty Acids - Prediction Model	IH Sample-1	23238.923	Positive
	Control sample-1	-119.474	Negative

Verification example:

Examples 1-6

This example is used to verify that the significantly different fatty acid index obtained in the present invention can distinguish infantile hemangioma patients, normal children and neonatal erythema patients. The situation of specific embodiments 1-6 is shown in the following table 21.

Table 21

Example	Corresponding detection object	diseased part
Example 1	Infantile hemangioma patient 01	elbow fossa
Example 2	Infantile hemangioma patient 02	the back
Example 3	Neonatal erythema patient 01	head
Example 4	Neonatal erythema patient 02	head
Example 5	Normal Child 01	none
Example 6	Normal Child 02	none

The patients of Examples 1-6 or normal children or patients with neonatal erythema were all tested for relevant indicators of the present invention on their umbilical cord blood samples according to the method described above after birth, and the following table 22 shows the specific test results.

Table 22 Fatty acid detection results of umbilical cord blood samples

fatty acid	Example 1 (IH child 01)	Example 3 (Child with neonatal erythema 01)	Example 5 (normal child 01)	Example 2 (IH child 02)	Example 4 (children with neonatal erythema 02)	Example 6 (normal child 02)	IH compared with normal children	IH compared with neonatal erythema
C10:0	0.028729	0.017742	0.005644	0.050895	0.01759	0.0115453	high	high
C11:0	0.028122	0.010517	0.011587	0.042064	0.022055	0.0146453	high	high
C12:0	0.257488	0.138076	0.055995	0.28728	0.173222	0.1204446	high	high
C14:0	4.351606	2.855441	1.376344	3.941233	2.873807	1.5072576	high	high
C15:0	0.879939	0.770499	0.272857	1.137546	0.637028	0.2611202	high	high
C15:1N5	40.81086	27.47554	8.071184	35.76797	28.15836	19.382075	high	high
C16:0	161.7352	100.2018	52.09138	175.4939	122.9309	56.778036	high	high
C17:0	1.407512	0.720874	0.3251	1.048992	0.701315	0.3122798	high	high
C18:0	84.13666	44.8526	26.16085	105.8078	60.0022	25.229636	high	high
C18:2N6	427.1287	80.70468	80.06693	98.618	72.02917	69.109764	high	high
C20:0	6.136846	0.280865	0.141123	1.110242	0.433811	0.1408695	high	high
C20:3N3	0.463305	0.651841	0.235134	0.342892	0.59305	0.1529013	high	Low
C20:5N3	2.780144	0.286709	0.071016	1.111225	0.338828	0.08811	high	high
C21:0	0.333794	0.073656	0.034127	0.127887	0.11605	0.0527508	high	high
C22:1N9	22.57718	6.348533	3.175789	28.52626	11.03295	2.7116273	high	high
C23:0	0.665975	0.057325	0.023877	0.334212	0.167604	0.0305484	high	high
C24:0	3.583151	0.32263	0.097446	1.345779	0.544029	0.1220033	high	high
C8:0	0.593575	0.042803	0.022378	0.107887	0.084731	0.0217722	high	high

Total MUFA	349.2461	143.8864	64.7684	161.6838	137.6948	69.29005	high	high
Total SFA	267.7383	156.2766	83.08047	292.8814	191.4751	86.04428	high	high

Figures 1 to 8 show the growth of lesions in patients with infantile hemangioma and in patients with neonatal erythema. Figures 1 and 2 show two infantile hemangioma patients with reddish red patches in the cubital fossa and back, respectively, at 6 weeks after birth, which are consistent with the symptoms of neonatal erythema patients in Figures 3 and 4 being not easy to distinguish; Figure 3 and Figure 4 show two patients with neonatal erythema at 6 weeks after birth, and occipital neonatal erythema also showed reddish red patches; Figure 5 and Figure 6 show two infants with blood vessels, at 12 weeks after birth, the infantile hemangiomas in the cubital fossa and back of the patient with hemangioma gradually increased in size and became darker in color. At 12 weeks after birth, the occipital neonatal erythema remained unchanged or faded in color. (Note: Parents of infantile hemangioma patients who agreed to participate in the experiment did not agree to start treatment for IH in advance for children whose umbilical cord blood samples showed abnormalities at the stage of no obvious onset before 12 weeks after birth.)

As can be seen from Table 22, detecting those indicators discovered by the inventors from their umbilical cord blood samples can screen out the accurate diagnosis of infantile hemangioma patients in advance, so as to timely control the disease incidence and development of infantile hemangioma patients offers possibilities.

Example 7-37

This example is used to verify that the significantly different metabolites, proteins, lipid subclasses and lipid molecular indicators obtained in the present invention can distinguish infantile hemangioma patients from normal children. The specific test results are shown in Table 23-26.

Table 23 Metabolite Detection Results of Cord Blood Samples in Examples 7-16

Metabolites	Example 7 (IH child 03)	Example 8 (normal child 03)	IH compared with normal children
(3-carboxypropyl)trimethylammonium cation	510143.1	227093.9	high
α -D-()-talose	23263.73	15500.56	high

1-Aminocyclopropanecarboxylic acid	188621.6	53239.43	high
1-myristoyl-sn-glycero-3-phosphocholine	639233.5	186504.9	high
1-palmitoyl-sn-glycero-3-phosphocholine	28013391	5866421	high
1-Stearoyl-sn-glycero-3-phosphocholine	373926.7	113154.4	high
choline	227648.3	91692.5	high
DL-indole-3-lactic acid	1300046	461850.9	high
Glycerophosphorylcholine	1688828	671972.8	high
L-Arginine	5502806	1172718	high
L-glutamic acid	240640.1	33478.38	high
L-phenylalanine	785222.5	311896.4	high
L-tryptophan	258068.4	88296.11	high
NG,NG-Dimethyl-L-arginine	2772705	953256.3	high
Tyramine	1792274	781770.9	high
(S)-Citromalic acid	33227.41	4088.282	high
1-Oleoyl-L- α -lysophosphatidic acid	639392.5	63903.35	high
1-palmitoyl lysophosphatidic acid	124968.9	4535.698	high
α -mangostin	670186.4	310314.6	high
Arachidonic Acid (peroxide free)	1260791	284498.3	high
citric acid	94447.07	1097.373	high
cyclamate	24786.94	16467.89	high
D(-)-beta-Hydroxybutyrate	69074.85	34237.41	high
Inositol galactoside	2440690	948031	high
glyceric acid	137497.5	31005.86	high
L-Aspartic Acid	143217.9	21282.67	high
L-Carnosine	4436.155	71437.44	Low
L-malic acid	176454.5	5539.126	high
N-acetyl-L-aspartic acid	69885.77	22113.51	high
N-acetylneuraminic acid	128129.9	16034.11	high
norethindrone acetate	223347.9	51205.17	high
Phosphocholine	89380.63	19148.07	high
sn-glycero-3-phosphoethanolamine	369254.4	48702.83	high
Succinate	101197.9	18696.45	high

Continued Table 23

Metabolites	Example 9 (IH child 04)	Example 10 (normal child 04)	IH compared with normal children
(3-carboxypropyl)trimethylammonium cation	320168.9	232712.5	high
α -D-()-talose	53267.22	7886.056	high
1-Aminocyclopropanecarboxylic acid	97254.68	69077.64	high
1-myristoyl-sn-glycero-3-phosphocholine	345230.1	60107.51	high
1-oleoyl-sn-glycero-3-phosphocholine	225774.6	41495.52	high
1-Stearoyl-sn-glycero-3-phosphocholine	558217.3	109993.2	high
Bilirubin	850090.4	60025.95	high
choline	205465.2	138419.4	high
D-2-piperidic acid	454456.9	258992.6	high
DL-indole-3-lactic acid	868161.1	200081.4	high

Glycyl glutamate	53138.69	19522.78	high
Glycerophosphorylcholine	1915716	865545.9	high
Isomaltose	608459.3	72821.55	high
L-glutamic acid	152540.5	107752	high
L-tryptophan	180972.2	40983.08	high
NG,NG-Dimethyl-L-arginine	1639060	752907.1	high
Phenylacetic acid	22581.97	30875.42	Low
(S)-Citromalic acid	70528.46	2136.355	high
1-Oleoyl-L- α -lysophosphatidic acid	136196.3	22149.72	high
1-palmitoyl lysophosphatidic acid	20645.84	4453.156	high
citric acid	43327.91	1825.697	high
D-threitol	884446.3	103468	high
Inositol galactoside	4131153	482120	high
glyceric acid	66956.89	49771.75	high
L-Aspartic Acid	75412.97	28727.6	high
L-Carnosine	27469.61	59068.78	Low
L-malic acid	73974.38	8678.877	high
N-acetyl-L-aspartic acid	38754.87	20086.51	high
N-acetylneuraminic acid	86250.82	19123.33	high
norethindrone acetate	161323.2	55845.14	high
Phosphocholine	61866.2	28427.71	high
sn-glycero-3-phosphoethanolamine	202229	102070.7	high
Succinate	60314.99	20776.69	high

Continued Table 23

Metabolites	Example 11 (IH child 05)	Example 12 (normal child 05)	IH compared with normal children
(3-carboxypropyl)trimethylammonium cation	477843.8	242084.6	high
α -D-()-talose	90413.87	7239.133	high
1-Aminocyclopropanecarboxylic acid	119348.5	57223.12	high
1-Stearoyl-sn-glycero-3-phosphocholine	220812.3	96530.61	high
Bilirubin	670075.3	113329.1	high
choline	207543.6	73401.95	high
D-2-piperidic acid	500009.2	277428	high
Glycyl glutamate	44759.33	5740.529	high
Glycerophosphorylcholine	1628916	520512.3	high
Isomaltose	888043.1	68745.69	high
L-Arginine	3287753	1150432	high
L-glutamic acid	192515.2	24290.34	high
L-phenylalanine	588987.8	415145.5	high
NG,NG-Dimethyl-L-arginine	1459399	969139.5	high
Tyramine	1408081	998126.4	high
(S)-Citromalic acid	32236.11	2769.362	high
1-palmitoyl lysophosphatidic acid	9578.058	2482.588	high
α -mangostin	444288.8	409402.3	high
citric acid	43895.59	1026.309	high
D-galactate	9160.009	50016.55	Low

D-threitol	1229530	167779.8	high
D(-)-beta-Hydroxybutyrate	105447.8	41209.4	high
Inositol galactoside	5628013	478341.9	high
glyceric acid	143317.8	23650.46	high
L-Aspartic Acid	172437.8	16159.77	high
L-Carnosine	27628.19	81544.39	Low
L-malic acid	84001.01	10688.66	high
N-acetyl-L-aspartic acid	51911.12	14963.55	high
N-acetylneuraminic acid	118212.1	22109.31	high
norethindrone acetate	209976.5	111536.7	high
Phosphocholine	46142.03	15933.69	high
sn-glycero-3-phosphoethanolamine	252622.7	38283.66	high
Succinate	86850.85	17127.58	high

Continued Table 23

Metabolites	Example 13 (IH child 06)	Example 14 (normal child 06)	IH compared with normal children
(3-carboxypropyl)trimethylammonium cation	629036.2	230257.3	high
α -D-()-talose	44115.07	16960.69	high
1-Aminocyclopropanecarboxylic acid	94329.05	49168.4	high
1-myristoyl-sn-glycero-3-phosphocholine	580831.1	179074.7	high
1-oleoyl-sn-glycero-3-phosphocholine	166464.6	59803.85	high
1-palmitoyl-sn-glycero-3-phosphocholine	31923571	5171830	high
choline	307412.2	108971.7	high
DL-indole-3-lactic acid	1837840	521566.6	high
Glycerophosphorylcholine	1355195	692020.8	high
Isomaltose	414269	152420.9	high
L-glutamic acid	140465.1	23508.76	high
L-phenylalanine	996992.2	401872.1	high
L-tryptophan	360420.5	103943	high
Tyramine	2133112	973692.5	high
Phenylacetic acid	20765.4	31707.5	Low
(S)-Citromalic acid	12353.27	4792.731	high
α -mangostin	916127.6	231627.4	high
cyclamate	48629.76	15112.53	high
D-galactate	31600.3	55556.12	Low
Inositol galactoside	3007417	982875.2	high
glyceric acid	79903.29	27278.19	high
L-Aspartic Acid	102114.2	11808.49	high
L-Carnosine	38562.33	112370.8	Low
L-malic acid	102599.6	6392.867	high
N-acetyl-L-aspartic acid	38679.11	13727.85	high
N-acetylneuraminic acid	176493.9	22262.77	high
Phosphocholine	58819.83	20118.58	high
sn-glycero-3-phosphoethanolamine	339402.5	50557.39	high
Succinate	58534.13	13912.63	high

Continued Table 23

Metabolites	Example 15 (IH child 07)	Example 16 (normal child 07)	IH compared with normal children
α -D-()-talose	21646.92	13619.36	high
1-Aminocyclopropanecarboxylic acid	128914.9	53073.99	high
choline	203330	97026.51	high
D-2-piperidic acid	467372	325019.8	high
Glycyl glutamate	36759.24	7489.737	high
Glycerophosphorylcholine	1885700	653829.6	high
L-glutamic acid	224648.1	24824.15	high
NG,NG-Dimethyl-L-arginine	1475795	559897.5	high
(S)-Citromalic acid	16108.88	5697.663	high
1-Oleoyl-L- α -lysophosphatidic acid	139287.4	26931.92	high
1-palmitoyl lysophosphatidic acid	15066.68	3648.164	high
Arachidonic Acid (peroxide free)	428874.9	290231.9	high
citric acid	32548.69	1109.416	high
Inositol galactoside	1459116	865594.7	high
glyceric acid	93033.19	46310.2	high
L-Aspartic Acid	101596.3	19824.56	high
L-Carnosine	15087.77	65887.83	Low
L-malic acid	41259.35	11124.48	high
N-acetyl-L-aspartic acid	44439.19	15711.84	high
N-acetylneuraminic acid	71809.25	27744.24	high
Phosphocholine	62950	20583.36	high
sn-glycero-3-phosphoethanolamine	238898.5	55692.48	high
Succinate	45201.87	17689.08	high

Table 24 The protein detection results of the umbilical cord blood samples of Examples 17-26

protein	Example 17 (IH child 08)	Example 18 (IH child 08)	IH compared with normal children
COLLECTION10	489637.08	37176.48	high
CPQ	50232.41	6951.64	high
LDHB	80543.82	37105.88	high
not	345978.53	34287.12	high
CPN1	174232.73	315119.13	Low
PROC	86069.12	140235.3	Low
SUPT6H	27748.59	10059.42	high
BCAR3	497794	318584.44	high
SOX30	122983.34	250598.77	Low
MON1	884588.38	1645950.4	Low
IGKV1D-16	403878.31	244457.31	high
COMP	56597.46	34517.18	high

FUCA2	31612.46	121781.38	Low
HLA-B	11852718	8710737	high
FKBP1A	26359.98	52192.52	Low
SAA1	17142.71	103461.22	Low
PGD	153134.02	72877.83	high
IGKV6-21	345471.18	243696.84	high
C1QA	1679422	1406025.3	high
APP	27362.17	22903.19	high

Continued Table 24

protein	Example 19 (IH child 09)	Example 20 (IH child 09)	IH compared with normal children
COLLECTION10	1694103.5	30962.67	high
not	2405567.3	22159.97	high
KRT1	1201667.6	338370.22	high
POSTN	38748.93	92234.64	Low
LAMA5	91258.05	325520.4	Low
CPN1	176122.81	312381.63	Low
PROC	59420.95	167681.98	Low
BCAR3	453915.63	322910.13	high
SOX30	46228.37	212304.75	Low
PROC	50152.57	159895.33	Low
IGKV1D-16	423852.69	223151.53	high
PMFBP1	36022	57853.33	Low
FGFBP2	212745.72	26039.64	high
HSPE1	919539	7279872.4	Low
PGD	574242.25	92360.25	high
SOD1	66378.97	48647.85	high
COTL1	36463.08	108060.94	Low
CAT	66668.719	1332205.3	Low
PROS1	232601.3	191883.78	high
CD5L	288586.03	124116.71	high
HMFT1766	703811.06	574892.5	high

Continued Table 24

protein	Example 21 (Children with IH 10)	Example 22 (Children with IH 10)	IH compared with normal children
not	2584658.5	41713.85	high
KRT1	2446204.3	166468.95	high
ARHGDIB	12051.3	872110.06	Low
PROC	75541.1	141050.69	Low
C1S	849727.19	1133271.1	Low
SUPT6H	29087.84	15165.92	high
bche	139511.2	335381.53	Low
C1R	269981.13	395077.63	Low
PROC	51921.99	105892.16	Low
IGKV1D-16	390209.81	248376.56	high

COMP	64995.19	41509.69	high
HSPE1	35990.05	15256183	Low
CDH1	33020.29	57182.13	Low
ISLR	11837.14	34257.99	Low
CORO1A	50342.75	81949.86	Low
ZYX	65370.4	108204.31	Low
A0A1W6IYJ2	153517.8	2168239.5	Low
PRDX1	75655.39	284166.06	Low
CAT	41240.133	743673.63	Low
PROS1	284338.66	197126.7	high
CD5L	248540.08	146032.84	high
HMFT1766	665014.5	493370.72	high
KRT2	317589	32842.34	high

Continued Table 24

protein	Example 23 (Children with IH 11)	Example 24 (Children with IH 11)	IH compared with normal children
COLLECTION10	3388055.3	40016.11	high
POSTN	41532.77	92365.08	Low
PROC	56539.59	149606.16	Low
C1S	742738.81	966209.13	Low
SUPT6H	32310.08	10553.28	high
BCAR3	502538.63	216837.97	high
bche	166995.64	277742.38	Low
SOX30	121270.22	233738.78	Low
C1R	289904.19	359219.97	Low
IGKV1D-16	425436.22	264957.34	high
APOC3	3651022.5	5632990.5	Low
GSN	505719.47	866859.94	Low
SELL	121987.74	159236.16	Low
CDH1	24045.53	90848.18	Low
ZYX	30331.08	128526.67	Low
SORL1	5664647.5	971401.38	high
FAM3C	13536.82	18625.73	Low
CST6	22128.1	88522.59	Low
PRDX1	186841.38	559074.75	Low
C1QA	1726583	1364217.3	high
APP	45928.97	21351.4	high

Continued Table 24

protein	Example 25 (12 children with IH)	Example 26 (12 children with IH)	IH compared with normal children
KRT1	457461.5	223820.53	high
LAMA5	93517.72	1558859.5	Low

HPX	1283580.4	2786933.8	Low
CFHR4	312037.53	48870.82	high
PROC	45383.84	90516.25	Low
IGKV1D-16	384415.78	55965.74	high
SELENOP	221991.19	147792.09	high
PMFBP1	37402.39	46928.19	Low
GSN	726584.06	1053384.4	Low
SELL	106793.16	190474.09	Low
HLA-B	10611360	6585273.5	high
FKBP1A	19399.96	34309.7	Low
PGD	212678.84	31996.6	high
SOD1	71198.32	42425.97	high
ISLR	19732.98	29068.05	Low
RLBP1	475881.03	197928.81	high
IDH1	55569.85	13489.66	high
IGKV6-21	1081120.9	129328.91	high
FAM3C	6287.55	27064.79	Low
CST6	36840.92	47662.6	Low
COTL1	60569.28	113931.08	Low
PIGR	812006.8	209093.87	high
HMFT1766	560376.88	462474.25	high
KRT2	43344.047	16670.71	high

Table 25 The detection results of lipid subclasses in the umbilical cord blood samples of Examples 27-32

lipid subclass	Example 27 (13 children with IH)	Example 28 (normal children 13)	Example 29 (14 children with IH)	Example 30 (normal children 14)	Example 31 (Children with IH 15)	Example 32 (normal children 15)	IH compared with normal children
AcCa	0.321158	1.064138	0.321049	0.896335	0.314356	0.918663	Low
Cer	0.351728	1.533944	0.546616	1.720177	0.379785	1.507481	Low
CerG1	0.07868	0.381009	0.104414	0.370528	0.066404	0.361331	Low
CerG2	0.040803	0.191394	0.05011	0.174356	0.051909	0.191599	Low
CerG2GN Ac1	0.100713	0.455635	0.113086	0.444541	0.11744	0.465601	Low
CerG3	0.004797	0.029168	0.005124	0.022737	0.005923	0.019632	Low
That	380.889	1477.079	353.2145	1357.131	378.9874	1299.011	Low
CL	0.048121	0.115846	0.036232	0.087427	0.028412	0.114302	Low
GM3	0.412922	0.764051	0.536102	0.8271	0.43535	0.839201	Low
LPC	30.01321	76.91753	33.96081	84.09475	31.96249	78.38407	Low
LPE	2.140922	5.229405	2.496672	5.956277	2.860132	5.781476	Low
MGDG	0.010424	0.03236	0.010329	0.032346	0.01034	0.033013	Low
Well	0.683589	3.869103	0.417211	6.172396	0.520085	4.368819	Low
PC	212.0522	629.5946	252.3592	685.9719	214.5748	589.463	Low

ON	6.947867	20.06681	6.812983	19.2329	6.519104	18.61558	Low
phSM	2.517173	1.669277	2.425129	1.918006	2.597779	2.024251	high
PI	12.00532	22.26124	13.68311	19.8602	12.94378	19.11935	Low
PS	489.2272	758.3536	480.6222	782.0371	553.1318	734.6101	Low
SM	78.72611	346.3847	71.48079	328.4313	80.3259	316.4796	Low
TG	107.5121	342.3344	117.0316	343.6731	57.17036	407.0348	Low

Table 26 Lipid molecular detection results of umbilical cord blood samples in Examples 33-36

lipid molecule	Example 33 (16 children with IH)	Example 34 (normal children 16)	Example 35 (17 children with IH)	Example 36 (normal children 17)	IH compared with normal children
PS(39:4)-H	0.65898	2.773197	0.505236	1.562799	Low
SM(d45:6) H	0.008445	0.042886	0.003311	0.032579	Low
PC(14:0/20:4) HCOO	0.052594	0.30468	0.060199	0.216308	Low
SM(d20:0/18:1) HCOO	0.154861	0.475846	0.091844	0.605941	Low
PS(49:4)-H	0.010045	0.136636	0.006305	0.057244	Low
LPC(26:0) HCOO	0.006137	0.112732	0.008202	0.083598	Low
SM(d20:0/16:0) HCOO	2.373884	4.600755	2.028368	10.25497	Low
PA(50:4)-H	0.465445	2.706362	0.758617	8.060536	Low
LPC(20:4) HCOO	1.486188	8.882914	2.65547	6.922193	Low
PC(36:5) H	0.135514	0.498213	0.180945	0.419179	Low
LPC(20:1) HCOO	0.020232	0.054994	0.034078	0.069364	Low
PC(38:8) H	0.016202	0.073509	0.022128	0.062792	Low
PC(46:5) H	0.004694	0.021572	0.002089	0.014555	Low
FRI (18:0p/22:5)-H	0.025236	0.103705	0.044721	0.07165	Low
SM(d22:0/16:0) HCOO	0.934436	2.625851	0.705129	5.44385	Low
PC(15:0/20:4) HCOO	0.05268	0.433913	0.042367	0.33059	Low
SM(d18:0/20:4) HCOO	0.002063	0.02705	0.00094	0.068781	Low
LPC(22:4) HCOO	0.035659	0.150585	0.031885	0.082646	Low
PI(18:0/22:4)-H	0.048502	0.15303	0.080136	0.127058	Low
PC(16:1/18:2) HCOO	0.180617	1.099495	0.132978	1.078421	Low
PS(40:4)-H	0.079248	0.523989	0.018216	0.26626	Low
Cer(d20:0/24:1) H	0.002263	0.008674	0.001705	0.006754	Low
SM(d37:0) HCOO	0.032263	0.131899	0.01664	0.215812	Low
PC(17:1/16:0) HCOO	0.316828	1.431112	0.243384	0.90886	Low
SM(d20:0/22:5) HCOO	0.107566	0.60368	0.16029	0.893717	Low
PC(44:11) H	0.001781	0.007933	0.000836	0.008616	Low
SM(d32:0) HCOO	0.074281	0.363346	0.083426	0.671339	Low
LPC(22:1) H	0.001862	0.007073	0.003268	0.006216	Low
PC(33:0e) H	0.001795	0.025562	0.003189	0.021722	Low
SM(d56:2 pO) H	0.003127	0.014044	0.004206	0.013686	Low
SM(d42:1) HCOO	2.109844	9.187529	1.48469	13.52494	Low
LPC(17:1) HCOO	0.016819	0.124613	0.027881	0.061764	Low

SM(d17:0/18:2) HCOO	0.022482	0.205564	0.019586	0.240992	Low
Cer(d18:1/24:0) H	0.034595	0.105274	0.041222	0.097188	Low
SM(d36:3) HCOO	0.021995	0.209217	0.03407	0.234692	Low
AcCa(14:2) H	0.009365	0.017994	0.013856	0.02766	Low
Cer(d18:1/24:0 O) H	0.000219	0.002624	0.001069	0.002788	Low
PE(20:0p/20:4)-H	0.043925	0.117114	0.034398	0.135764	Low
LPC(26:1) HCOO	0.00197	0.028354	0.002493	0.014764	Low
PC(37:5) H	0.018959	0.138687	0.017524	0.108174	Low
SM(d44:1) HCOO	0.015268	0.093548	0.010586	0.124478	Low
Cer(d18:1/26:1) H	0.002071	0.005326	0.002575	0.005759	Low
PE(40:6e) H	0.052156	0.35594	0.037536	0.159764	Low
TG(18:1/20:2/22:4) NH4	0.068634	0.269178	0.029737	0.202736	Low
SM(d34:3) H	0.013771	0.051332	0.014828	0.063531	Low
PE(40:4)-H	0.035489	0.245829	0.025996	0.254869	Low
SM(d22:0/18:2) HCOO	0.137212	0.421372	0.097646	1.111903	Low
Cer(d18:0/22:0) H	0.042999	0.07261	0.041678	0.073546	Low
SM(d44:0) HCOO	0.009909	0.026304	0.001866	0.032173	Low
PI(16:1/20:4)-H	0.001363	0.01667	0.006786	0.011267	Low
PC(20:3/20:4) HCOO	0.108377	0.278518	0.143706	0.503058	Low
PE(38:1p)-H	0.000607	0.014607	0.001942	0.010799	Low
SM(d39:0) HCOO	0.056764	0.245858	0.037246	0.356859	Low

Example 37:

This example is used to illustrate the use of the indicators of the present invention for monitoring the progress of IH and the therapeutic effect of drugs.

As shown in Figure 9: the regression of the left upper eyelid infantile hemangioma after oral administration of propranolol. (A) Before starting to take propranolol, the tumor hyperplasia was obvious; (B) After taking propranolol for 1 month, the tumor gradually subsided; (C) After taking propranolol for 12 months, the IH basically disappeared and stopped (D) After 2 months of drug withdrawal, IH rebounded and grew.

Table 27: Changes of fatty acid C20:0 and C22:6N3 concentrations in peripheral blood before and after oral administration of propranolol in children with IH.

treatment history	C20:0 (μg/ml)	C22:6N3 (μg/ml)
before starting treatment	1.58	12.30
Oral propranolol for 1 month	0.67	9.71

Oral propranolol for 12 months	0.57	7.77
Withdrawal for 2 months	0.99	8.66

It can be seen from Table 27 that the fatty acid index of the present invention can effectively monitor the progress of IH and the therapeutic effect of drugs.

Although the subject matter of this disclosure and its merits have been described in detail, it should be understood that variations, substitutions and alterations may be made without deviating from the spirit and scope of the invention as defined by the attached claims. Furthermore, the scope of this application is not intended to be limited to a specific implementation of the uses, substance compositions, kits, methods and steps described in the specification. The general skilled person in the field will easily understand from the disclosure of the disclosed topic that a use, substance composition, kit, method, or step, existing or to be developed according to this disclosed topic, may be used that performs substantially the same function or achieves substantially the same results as the corresponding implementation described herein. Therefore, the attached claims are intended to include such uses, substance compositions, kits, methods or steps within their scope.

Patents, patent applications, publications, product descriptions and protocols are cited throughout this application, the disclosures of which are hereby incorporated by reference in their entirety for all purposes.

Claims:

1. Use of a composition for manufacturing a medicament for diagnosing infantile hemangioma and/or monitoring its progress and prognosis is characterized in that the composition includes at least one of the following four groups of substances:

(1) Fatty acid, wherein the fatty acid is total fatty acid or total saturated fatty acid or total monounsaturated fatty acid or at least one of the fatty acids selected from the group consisting of C10:0, C11:0, C12:0, C14:0, C15:0, C15:1N5, C16:0, C17:0, C18:0, C18:2N6, C20:0, C20:3N3, C20:5N3, C21:0, C22:1N9, C23:0, C24:0 and C8:0;

(2) Metabolites, wherein the metabolites is at least one of the metabolites selected from the group consisting of (3-carboxypropyl)trimethylammonium cation, α -D-(+)-talose, 1-aminocyclopropanecarboxylic acid, 1-meat Myristoyl-sn-glycero-3-phosphocholine, 1-oleoyl-sn-glycero-3-phosphocholine, 1-palmitoyl-sn-glycero-3-phosphocholine, 1-stearoyl-sn -Glycero-3-phosphocholine, bilirubin, choline, D-2-pipercolic acid, DL-indole-3-lactic acid, glycylglutamate, glycerophosphorylcholine, isomaltose, L - Arginine, L-glutamic acid, L-phenylalanine, L-tryptophan, NG,NG-dimethyl-L-arginine, tyramine, phenylacetic acid, (S)-lime Acid, 1-oleoyl-L-alpha-lysophosphatidic acid, 1-palmitoyl lysophosphatidic acid, alpha-mangostin, arachidonic acid (peroxide free), citramalic acid, cyclamate /salt, D-galactate/salt, D-threitol, D(-)-beta-hydroxybutyric acid, inositol galactoside, glyceric acid, L-aspartic acid, L-carnosine, L - In the group consisting of malic acid,

N-acetyl-L-aspartic acid, N-acetylneuraminic acid, norethindrone acetate, phosphorylcholine, sn-glycero-3-phosphoethanolamine and succinate/salt;

(3) Protein, wherein the protein is at least one of the proteins selected from the group consisting of COLEC10, CPQ, LDHB, ACAN, KRT1, ARHGDIB, POSTN, LAMA5, CPN1, PROC, C1S, HPX, SUPT6H, BCAR3, BCHE, SOX30, C1R, PON1, CFHR4, PROZ, IGKV1D-16, APOC-3, COMP, SELENOP, PMFBP1, GSN, SELL, FUCA2, HLA-B, FGFBP2, FKBP1A, HSPE1, SAA1, PGD, CDH1, SOD1, ISLR, CORO1A, ZYX, RLBP1, IDH1, IGKV6-21, SORL1, FAM3C, CST6, COTL1, PIGR, A0A1W6IYJ2, PRDX1, CAT, PROS1, CD5L, HMFT1766, C1QA, KRT2, and APP; and

(4) Lipid subclass substances or lipid molecules, wherein the lipid subclass substance is at least one of the lipid subclass substances selected from the group consisting of acetylcarnitine, ceramide, monosaccharide ceramide, disaccharide ceramide, glycosyl ceramide series, trisaccharide Ceramide, cholesteryl ester, cardiolipin, ganglioside, lysophosphatidylcholine, lysophosphatidylethanolamine, monogalactosyldiacylglyceride, phosphatidic acid, phosphatidylcholine, phosphatidylethanolamine, phytosphingosine, phosphatidylinositol, phosphatidylserine, sphingomyelin and triglyceride, and wherein the lipid molecule is at least one of the lipid molecules selected from the group consisting of PS(39:4)-H, SM(d45:6)+H, PC(14:0/20:4)+HCOO, SM(d20:0/18:1)+HCOO, PS(49:4)-H, LPC(26:0)+HCOO, SM(d20:0/16: 0)+HCOO, PA(50:4)-H, LPC(20:4)+HCOO, PC(36:5)+H, LPC(20:1)+HCOO, PC(38:8)+H, PC(46:5)+H, PE(18:0p/22:5)-H,

SM(d22:0/16:0)+HCOO, PC(15:0/20:4)+HCOO, SM(d18:0/20:4)+HCOO, LPC(22:4)+HCOO, PI(18:0/22:4)-H, PC(16:1/18:2)+HCOO, PS(40:4)-H, Cer(d20:0/24:1)+H, SM(d37:0)+HCOO, PC(17:1/16:0)+HCOO, SM(d20:0/22:5)+HCOO, PC(44:11)+H, SM(d32:0)+HCOO, LPC(22:1)+H, PC(33:0e)+H, SM(d56:2+pO)+H, SM(d42:1)+HCOO, LPC(17:1)+HCOO, SM(d17:0/18:2)+HCOO, Cer(d18:1/24:0)+H, SM(d36:3)+HCOO, AcCa(14:2)+H, Cer(d18:1/24:0 O)+H, PE(20:0p/20:4)-H, LPC(26:1)+HCOO, PC(37:5)+H, SM(d44:1)+HCOO, Cer(d18:1/26:1)+H, PE(40 :6e)+H, TG(18:1/20:2/22:4)+NH₄, SM(d34:3)+H, PE(40:4)-H, SM(d22:0/18:2)+HCOO, Cer(d18:0/22:0)+H, SM(d44:0)+HCOO, PI(16:1/20:4)-H, PC(20:3/20:4)+HCOO, PE(38:1p)-H and SM(d39:0)+HCOO.

2. The use according to claim 1, wherein the fatty acids are at least 2 of the fatty acids defined in (1); the metabolites are at least 2 of the metabolites defined in (2); the protein are at least 2 of proteins defined in (3); or the lipid subclass substances or lipid molecules are at least 2 of the lipid subclass substances or lipid molecules defined in (4).

3. The use according to claim 1, wherein the fatty acids are at least 3 of the fatty acids defined in (1); the metabolites are at least 3 of the metabolites defined in (2); the protein are at least 3 of proteins defined in (3); or the lipid subclass substances or lipid molecules are at least 3 of the lipid subclass substances or lipid molecules defined in (4).

4. The use according to claim 1, wherein the fatty acids are 1-6 of the fatty acids

defined in (1); the metabolites are 1-6 of the metabolites defined in (2); the protein are 1-6 of proteins defined in (3); or the lipid subclass substances or lipid molecules are 1-6 of the lipid subclass substances or lipid molecules defined in (4).

5. The use according to any one of claims 1-4, wherein the fatty acid(s) in (1) is(are) selected from the group consisting of C8:0, C10:0, C11:0, C16:0, C20:0, C20:5N3, C22:1N9, C23:0 and C24:0; the metabolite(s) in (2) is(are) selected from the group consisting of choline, 1-aminocyclopropanecarboxylic acid, 1-myristoyl-sn-glycerol -3-Phosphocholine, D-2-pipecolic acid, DL-indole-3-lactic acid, glycyl glutamic acid, L-glutamic acid, L-phenylalanine, L-tryptophan, tyramine, glyceric acid, cyclamate, D-galactate/salt and sn-glycero-3-phosphoethanolamine; the protein(s) in (3) is(are) selected from the group consisting of HSPE1, PGD, CDH1, ISLR, CPQ, IDH1, PIGR, POSTN, PROC, PROZ, PMFBP1, SELL, A0A1W6IYJ2, CAT, PROS1, CD5L, C1QA, KRT1 and FGFBP2; or the lipid subclass substance(s) in (4) is(are) selected from the group consisting of Cer, ChE, LPC, LPE, PA, PC, PE, PI, PS and SM, the lipid molecule(s) in (4) is(are) selected from the group consisting of PS(39:4)-H, SM(d45:6)+H, PC(14:0/20:4)+HCOO, SM(d20:0/18:1)+HCOO, PS(49:4)-H, LPC(26:0)+HCOO, SM(d20:0/16:0)+HCOO, PA(50:4)-H and LPC(20:4)+HCOO.

6. The use according to claim 5, wherein the fatty acid(s) in (1) is(are) selected from the group consisting of C20:5N3, C22:1N9, C23:0 and C24:0;

the metabolite(s) in (2) is(are) selected from the group consisting of 1-myristoyl-sn-glycero-3-phosphocholine, glycyl glutamic acid, L-phenylalanine,

DL-indole-3-lactic acid, L-tryptophan and glyceric acid;

the protein(s) in (3) is(are) selected from the group consisting of HSPE1, CDH1, ISLR, IDH1, COTL1 and FGFBP2; or

the lipid subclass substance(s) in (4) is(are) selected from the group consisting of LPC, LPE, PA, PC and PE or the lipid molecule(s) in (4) is(are) selected from the group consisting of PS(39:4)-H, SM(d45:6)+H, PC(14:0/20:4)+HCOO and SM(d20:0/18:1)+HCOO.

7. The use according to any of the claims 1-4, wherein the fatty acid(s) in (1) is(are) selected from the group consisting of C10:0, C14:0, C16:0, C18:2N6, C20:0, C20:1N9, C20:5N3, C22:1N9, C24:0 and C8:0.

8. The use according to Claim 7, the fatty acid(s) in (1) is(are) selected from the group consisting of C10:0, C16:0, C20:0, C20:5N3 and C22:1N9.

9. A test kit comprising the composition described in any of Claims 1-8 and instructions for using the kit.

10. The test kit according to Claim 9, wherein the samples tested by the kit are selected from the group consisting of the subject's whole blood, plasma, serum, lymphocyte suspension, cerebrospinal fluid, bone marrow, pleural effusion, urine, saliva, and abdominal effusion.

11. The test kit according to Claim 9, the samples tested by the kit are selected from

the group consisting of umbilical cord blood and peripheral blood.

12. The test kit according to Claim 9, wherein, said kit is a dry blood spot kit.

13. A drug for treating hemangioma in infants and young children comprises a substance that regulates the expression of selected LDHB, KRT1, BCHE, CFHR4, CPQ, APOC-3, ARHGDIB, and LAMA5.