

Supporting Information

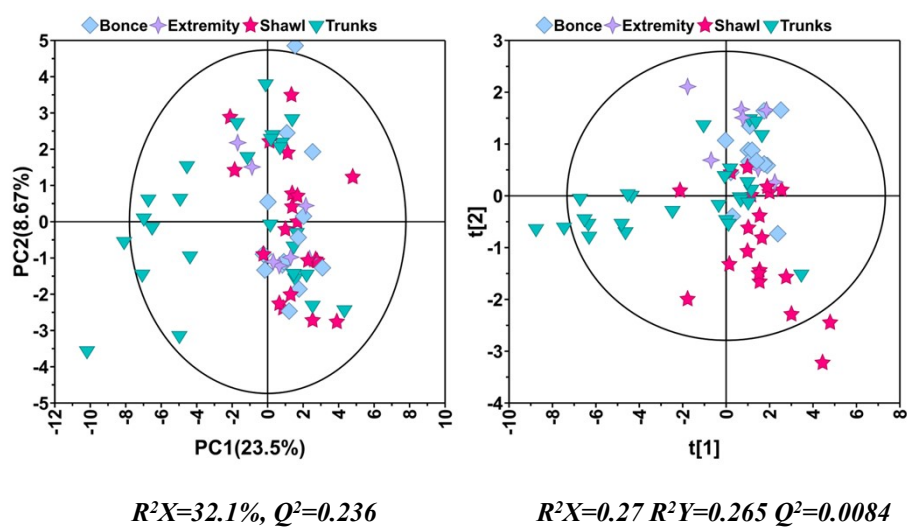


Figure S1. PCA (left panel) and PLS-DA (right panel) score plots based on ¹H NMR data of four subtypes of LGCMN tissues according to the BEST classification system.

Table S1 The identified metabolites from ¹H-NMR spectra of tissue samples

No.	Metabolites	Abbr.	Chemical shift (multiplicity ^a)
1	Isoleucine	Ile	0.94(t); 1.01(d); 1.27(m); 3.68(d)
2	Leucine	Leu	0.97(dd)
3	Valine	Val	0.99(d); 1.05(d); 2.28(m)
4	α -Ketoisovalerate	α -KIV	1.15(d)
5	3-Hydroxybutyrate	3-HB	1.21(d); 2.31(dd); 4.14(m)
6	Methylmalonate	MM	1.25(d)
7	Lactate	Lac	1.33(d); 4.11(q)
8	Lysine	Lys	1.42(m); 1.73(m); 1.92(m); 3.03(t); 3.76(t)
9	Alanine	Ala	1.48(d)
10	Citrulline	Cit	1.52(m); 1.84(m); 3.15(m)
11	Arginine	Arg	1.69(m); 1.95(m)
12	Pyroglutamate	PG	2.01(m); 2.41(m); 2.51(m); 4.18(m)
13	Glutamate	Glu	2.06(m); 2.12(m); 2.35(m)
14	Glutamine	Gln	2.14(m); 2.45(m); 3.78(t)
15	Methionine	Met	2.19(m); 2.65(t)
16	N-Acetylglutamate	NAcGlu	2.23(t)
17	Pyruvate	PA	2.37(s)
18	Aspartate	Asp	2.69(dd); 2.81(dd); 3.88(dd)
19	Sarcosine	Sar	2.76(s); 3.57(s)
20	Trimethylamine	TMA	2.85(s)
21	Asparagine	Asn	2.87(dd); 2.96(dd); 4.00(dd)
22	N,N-Dimethylglycine	DMG	2.93(s)
23	Phosphocreatine	PC	3.04(s); 3.93(s)
24	Tyrosine	Tyr	3.06(dd); 3.95(dd); 6.91(d); 7.2(d)
25	Cysteine	Cys	3.11(m)
26	Malonate	Mal	3.12(s)
27	Choline	Cho	3.20(s)

28	Phosphorylcholine	PCr	3.21(s)
29	Glycerophosphorylcholine	GPC	3.22(s); 4.33(m)
30	Betaine	Bet	3.23(s); 3.90(m)
31	Trimethylamine N-oxide	TMAO	3.25(s)
32	Taurine	Tau	3.27(t); 3.42(t)
33	myo-Inositol	m-I	3.29(t); 3.54(dd); 3.63(t); 4.07(t)
34	α -Glucose	α -Glc	3.40(t); 3.53(dd); 3.84(m); 5.24(d)
35	β -Glucose	β -Glc	3.41(t); 3.47(m); 3.49(t); 3.73(dd); 3.90(dd); 4.65(d)
36	Glycine	Gly	3.56(s)
37	Glycerol	Gro	3.60(dd); 3.66(dd); 3.78(m)
38	Serine	Ser	3.85(m)
39	Uridine	Urd	4.23(t); 4.36(dd); 5.91(d); 5.92(d); 7.88(d)
40	Threonine	Thr	4.26(m)
41	Inosine	Ino	4.30(dd); 4.44(dd); 6.1(d); 8.24(s); 8.35(s)
42	N-Acetylaspartate	NAA	4.37(t)
43	Nicotinamide adenine dinucleotide	NAD	4.42(m); 4.50(m); 6.09(d); 6.14(d); 8.43(s); 8.84(d); 9.14(d); 9.34(s)
44	β -Galactose	β -Gal	4.52(d)
45	Trehalose	Tre	5.21(d)
46	Polyunsaturated Fatty Acid	PUFA	5.33(br)
47	Glycogen	Glyc	5.42(m)
48	Uracil	Ura	5.81(d); 7.55(d)
49	Cytidine	Cyd	5.85(d); 6.07(d)
50	Uridine diphosphate glucose	UDG	5.99(m); 7.96(d)
51	Urocanate	Uroc	6.4(d); 7.31(d); 7.40(s); 7.85(s)
52	Fumarate	Fum	6.52(s)
53	Histidine	His	7.10(s); 7.90(s)
54	Unknown-1	U1	7.22(d); 7.8(d)

55	Tryptophan	Trp	7.29(m); 7.74(d)
56	Phenylalanine	Phe	7.33(d); 7.38(m); 7.43(m)
57	Nicotinamide	NA	7.60(dd); 8.25(d); 8.72(dd); 8.94(d)
58	1-Methylhistidine	1-MH	7.68(s)
59	Adenine	Ade	8.01(s)
60	Hypoxanthine	HX	8.20(s); 8.22(s)
61	Pterin	Pr	8.38(s)
62	Formate	For	8.46(s)

^a Multiplicity: s, singlet; d, doublet; t, triplet; q, quartet; dd, doublet of doublets; m, multiplet

Table S2. Detailed information on the differential metabolites between the different subtypes of LGCMN tissues and the corresponding control skins

Groups	Differential Metabolites	VIP	FC	r	p-value
LGCMN vs. Control	3-Hydroxybutyrate	1.756	0.456	0.824	1.02E-18
	Alanine	6.867	1.629	0.748	6.46E-14
	Asparagine	4.271	0.814	0.795	1.54E-05
	Aspartate	1.756	1.322	0.683	8.36E-08
	Choline	1.724	1.291	0.623	3.01E-08
	Citrulline	2.892	1.794	0.834	1.26E-19
	Glutamate	2.540	1.202	0.814	3.7E-06
	Glycerophosphorylcholine	2.802	1.358	0.626	4.99E-03
	Glycine	6.968	1.697	0.654	3.32E-11
	Hypoxanthine	1.526	1.532	0.694	3.03E-11
	Isoleucine	3.635	1.268	0.786	0.000268
	Leucine	3.889	1.444	0.601	1.27E-05
	Lysine	3.161	1.280	0.762	7.01E-06
	Methionine	1.329	0.849	0.864	0.008192
	Methylmalonate	2.022	0.512	0.769	7.43E-16
	N-Acetylglutamate	1.625	0.574	0.894	8.38E-19
	Phenylalanine	1.954	1.822	0.603	1.76E-09
	Phosphorylcholine	6.259	1.326	0.684	9.48E-09
	Phosphocreatine	4.121	1.872	0.696	1.11E-06
	Pyruvate	1.133	0.878	0.642	0.00044
	Serine	2.891	1.490	0.657	2.25E-11
	Trimethylamine N-oxide	2.230	1.420	0.629	1.18E-07
	Tyrosine	3.624	1.622	0.717	4.34E-10
	Valine	3.999	1.466	0.826	6.11E-07
	α -Ketoisovalerate	1.437	0.474	0.843	2.09E-13
LGCMN-B vs. Control- B	Alanine	8.860	1.578	0.817	1.94E-05
	Citrulline	3.026	1.923	0.796	2.37E-06
	Glutamate	3.936	1.231	0.812	6.41E-04
	Glycine	9.444	1.690	0.792	4.46E-05
	Hypoxanthine	2.455	1.829	0.866	1.87E-05
	Phenylalanine	2.417	1.511	0.722	5.15E-05
	Phosphocreatine	3.866	1.554	0.719	1.70E-04
	Phosphorylcholine	8.304	1.810	0.697	7.52E-05
	Serine	3.348	1.479	0.726	1.78E-04
	Taurine	5.236	1.708	0.735	2.13E-05
	Trimethylamine N-oxide	2.551	1.570	0.626	3.72E-04
	Uridine	1.198	2.851	0.685	2.93E-04
	Valine	5.197	1.258	0.697	1.21E-03

LGCMN-E vs. Control- E	α -Glucose	2.283	0.480	0.624	6.47E-03
	Alanine	5.600	1.344	0.758	5.36E-03
	Citrulline	2.242	1.611	0.807	4.90E-03
	Cysteine	1.767	1.775	0.758	4.78E-03
	Malonate	1.778	1.620	0.785	4.01E-03
	Methylmalonate	2.164	0.583	0.861	4.46E-03
LGCMN-S vs. Control- S	3-Hydroxybutyrate	1.572	0.561	0.836	3.38E-04
	Alanine	6.964	1.632	0.780	2.30E-05
	Aspartate	1.767	1.293	0.721	5.89E-03
	Betaine	4.013	1.884	0.680	2.91E-04
	Citrulline	3.546	2.066	0.847	2.90E-06
	Glutamate	2.580	1.188	0.855	9.54E-03
	Glycine	7.785	1.751	0.727	3.16E-05
	Hypoxanthine	1.528	1.520	0.672	8.64E-04
	Isoleucine	2.753	1.232	0.821	7.68E-03
	N-Acetylaspartate	1.004	0.720	0.763	6.79E-04
	N-Acetylglutamate	1.667	0.605	0.890	1.86E-04
	Phenylalanine	1.612	1.579	0.724	8.18E-05
	Phosphocreatine	3.560	1.255	0.610	7.17E-03
	Serine	2.934	1.476	0.608	1.34E-03
	Taurine	3.890	1.554	0.618	1.88E-05
	Trimethylamine N-oxide	2.730	1.466	0.647	1.91E-03
	Tyrosine	3.676	1.547	0.790	1.19E-04
	Valine	3.783	1.369	0.857	1.77E-04
LGCMN-T vs. Control- T	Phosphorylcholine	7.084	1.976	0.640	1.88E-04
	Alanine	6.729	1.718	0.708	2.31E-05
	Leucine	4.911	1.762	0.617	1.53E-03
	Valine	4.637	1.714	0.916	7.90E-04
	Isoleucine	4.580	1.436	0.876	6.70E-03
	Asparagine	3.903	0.717	0.803	2.21E-05
	Tyrosine	3.324	1.928	0.711	1.70E-05
	Lysine	3.309	1.411	0.774	1.88E-03
	Serine	2.745	1.557	0.654	7.12E-05
	Citrulline	2.543	1.605	0.928	6.11E-08
	Phenylalanine	2.329	2.310	0.601	6.92E-05
	3-Hydroxybutyrate	2.030	0.316	0.896	1.89E-13
	Methylmalonate	1.933	0.435	0.841	5.38E-10
	Choline	1.868	1.293	0.646	1.02E-03
	Aspartate	1.861	1.431	0.739	4.00E-04
	N-Acetylglutamate	1.745	0.475	0.946	3.11E-12
	α -Ketoisovalerate	1.422	0.374	0.899	9.84E-10
	Hypoxanthine	1.298	1.466	0.671	1.79E-04

Uridine	1.092	2.770	0.741	4.23E-04
Pyruvate	1.083	0.768	0.847	8.72E-06

B: bonce phenotype of LGCMN; E: extremity phenotype of LGCMN; S: shawl phenotype of LGCMN;

T: trunks phenotype of LGCMN

Table S3. Analysis of significant metabolic pathways in different phenotypes of LGCMN

Phenotype	Pathway Name	Pathway Classification	Hits	Total	p-value	Impact
Bonce	Glyoxylate and dicarboxylate metabolism	Carbohydrate metabolism	3	32	1.48E-03	1.48E-01
	Arginine biosynthesis	Amino acid metabolism	2	14	4.60E-03	3.45E-01
	Glutathione metabolism	Metabolism of other amino acids	2	28	1.80E-02	1.08E-01
	Porphyrin metabolism	Metabolism of cofactors and vitamins	2	31	2.19E-02	0.00E+00
	Glycine, serine and threonine metabolism	Amino acid metabolism	2	33	2.46E-02	4.74E-01
	Arginine and proline metabolism	Amino acid metabolism	2	36	2.90E-02	0.00E+00
	Phenylalanine, tyrosine and tryptophan biosynthesis	Amino acid metabolism	1	4	3.02E-02	5.00E-01
	Nitrogen metabolism	Energy metabolism	1	6	4.49E-02	0.00E+00
	Primary bile acid biosynthesis	Lipid metabolism	2	46	4.57E-02	1.52E-02
	Phenylalanine metabolism	Amino acid metabolism	1	8	5.95E-02	3.57E-01
	Taurine and hypotaurine metabolism	Metabolism of other amino acids	1	8	5.95E-02	4.29E-01
Extremity	Thiamine metabolism	Metabolism of cofactors and vitamins	1	7	1.77E-02	0.00E+00
	Taurine and hypotaurine metabolism	Metabolism of other amino acids	1	8	2.02E-02	0.00E+00
	Arginine biosynthesis	Amino acid metabolism	1	14	3.51E-02	2.28E-01
	Pantothenate and CoA biosynthesis	Metabolism of cofactors and vitamins	1	20	4.99E-02	0.00E+00
	Glutathione metabolism	Metabolism of other amino acids	1	28	6.93E-02	3.43E-03
	Glycine, serine and threonine metabolism	Amino acid metabolism	1	33	8.13E-02	0.00E+00
Shawl	Cysteine and methionine metabolism	Amino acid metabolism	1	33	8.13E-02	9.59E-02
	Arginine biosynthesis	Amino acid metabolism	4	14	6.71E-06	5.37E-04
	Phenylalanine, tyrosine and tryptophan biosynthesis	Amino acid metabolism	2	4	5.74E-04	4.53E-02
	Alanine, aspartate and glutamate metabolism	Amino acid metabolism	3	28	2.42E-03	1.88E-01
	Phenylalanine metabolism	Amino acid metabolism	2	8	2.62E-03	2.01E-01
	Glyoxylate and dicarboxylate metabolism	Carbohydrate metabolism	3	32	3.57E-03	2.68E-01

	Glycine, serine and threonine metabolism	Amino acid metabolism	3	33	3.90E-03	2.89E-01
	Butanoate metabolism	Carbohydrate metabolism	2	15	9.41E-03	6.87E-01
	Histidine metabolism	Amino acid metabolism	2	16	1.07E-02	7.70E-01
	Pantothenate and CoA biosynthesis	Metabolism of cofactors and vitamins	2	20	1.65E-02	1.00E+00
	Glutathione metabolism	Metabolism of other amino acids	2	28	3.14E-02	1.00E+00
Trunks	Valine, leucine and isoleucine degradation	Amino acid metabolism	5	40	7.33E-05	3.35E-02
	Arginine biosynthesis	Amino acid metabolism	3	14	4.99E-04	2.28E-01
	Phenylalanine, tyrosine and tryptophan biosynthesis	Amino acid metabolism	2	4	8.16E-04	1.00E+00
	Pantothenate and CoA biosynthesis	Metabolism of cofactors and vitamins	3	20	1.49E-03	0.00E+00
	Phenylalanine metabolism	Amino acid metabolism	2	8	3.70E-03	3.57E-01
	Alanine, aspartate and glutamate metabolism	Amino acid metabolism	3	28	4.03E-03	2.24E-01
	Glycine, serine and threonine metabolism	Amino acid metabolism	3	33	6.46E-03	2.15E-01
	Glyoxylate and dicarboxylate metabolism	Carbohydrate metabolism	2	32	5.52E-02	4.23E-02
	Cysteine and methionine metabolism	Amino acid metabolism	2	33	5.83E-02	2.18E-02
	Glycerophospholipid metabolism	Lipid metabolism	2	36	6.81E-02	3.52E-02
	Tyrosine metabolism	Amino acid metabolism	2	42	8.92E-02	1.40E-01

Table S4. General information of cases selected for transcriptomic analysis

ID	Sex	Age (y)	Location	Pathological type	Krengel Classification
1	Male	2.0	Trunks	Compound nevus	G1 C0 R1 N1 H0 S1
2	Male	2.5	Bonce	Compound nevus	G1 C0 R0 N0 H1 S0
3	Female	5.4	Extremity	Intradermal nevus	G1 C1 R0 N0 H1 S0
4	Female	4.8	Extremity	Compound nevus	G1 C0 R1 N0 H1 S1
5	Female	1.5	Bonce	Intradermal nevus	G2 C2 R1 N0 H0 S1
6	Female	2.0	Trunks	Intradermal nevus	G2 C2 R0 N1 H1 S1
7	Male	7.0	Shawl	Intradermal nevus	G1 C0 R1 N0 H1 S1
8	Male	4.0	Bonce	Compound nevus	G2 C0 R1 N0 H2 S0
10	Male	5.5	Extremity	Compound nevus	G1 C1 R1 N1 H1 S1
12	Male	3.4	Trunks	Compound nevus	G1 C2 R2 N1 H1 S1

Table S5. Ranking of the top 30 nodes according to different topology analysis methods in the CytoHubba plugin

Rank	Closeness		Betweenness		Stress		Radiality		BottleNeck	
	Gene	Score	Gene	Score	Gene	Score	Gene	Score	Gene	Score
1	EGF	171.279	EGF	46639.259	EGF	182864.000	EGF	10.162	EGF	150.000
2	MAPK3	160.804	MAPK3	23748.678	MAPK3	112146.000	MAPK3	10.045	ANK3	45.000
3	TYR	158.246	ANK3	22294.603	TYR	79912.000	TYR	9.980	MAPK3	35.000
4	POU5F1	155.120	TYR	17302.477	POU5F1	64550.000	POU5F1	9.946	NRXN1	30.000
5	SOX10	150.946	RACK1	16393.321	ANK3	63970.000	UBE2I	9.902	SOX10	24.000
6	UBE2I	150.870	NRXN1	15843.901	RACK1	57534.000	SOX10	9.870	CEACAM5	22.000
7	MITF	147.589	POU5F1	14423.848	UBE2I	54170.000	ANK3	9.822	RACK1	21.000
8	ANK3	146.702	UBE2I	13268.149	NRXN1	47550.000	RACK1	9.798	POU5F1	21.000
9	RACK1	145.462	NME8	12152.696	SPP1	46684.000	MITF	9.781	UBE2I	20.000
10	NRXN1	143.702	GAPDHS	11594.264	GAPDHS	46348.000	NRXN1	9.770	FLT3	19.000
11	PAX6	142.523	TUFM	10881.561	SOX10	46100.000	S100B	9.755	EDNRB	19.000
12	SPP1	141.221	CEACAM5	10698.803	NME8	44962.000	PAX6	9.723	PAX6	18.000
13	IL18	139.814	SLC4A4	10432.016	EDNRB	43744.000	SPP1	9.714	MSRA	18.000

14	SLC45A2	139.185	BEST1	10420.322	BEST1	43550.000	IL18	9.692	IFT122	16.000
15	CEACAM5	138.931	SOX10	9708.934	MITF	40268.000	BDKRB1	9.690	TUFM	16.000
16	S100B	138.827	MSRA	9688.657	TUFM	40094.000	CEACAM5	9.660	SLC4A4	16.000
17	PMEL	138.426	SPP1	8865.987	MSRA	38100.000	FBXW7	9.655	BEST1	16.000
18	FBXW7	137.749	EDNRB	8618.809	CEACAM5	37810.000	SLC45A2	9.621	SPP1	14.000
19	CD63	136.799	DSG1	7888.815	GPX3	37530.000	PMEL	9.612	ELMO3	14.000
20	NME8	136.556	STUB1	7588.252	DSG1	37128.000	WNT3	9.606	GAPDHS	13.000
21	BDKRB1	135.654	PAX6	7444.386	STUB1	35818.000	CSPG4	9.593	S100B	13.000
22	WNT3	135.456	S100B	7327.236	GPX2	35228.000	CD63	9.590	FBXW7	13.000
23	GAPDHS	133.967	MITF	7295.542	IL18	31484.000	NME8	9.586	NME8	13.000
24	CSPG4	133.663	SPTBN2	6897.955	PAX6	31168.000	TUBB4A	9.575	IL18	12.000
25	FLT3	132.748	FLT3	6833.273	FLT3	26932.000	GAPDHS	9.556	CLDN16	11.000
26	STUB1	132.036	GPX3	6542.228	SLC4A4	26642.000	FLT3	9.549	COL11A2	11.000
27	GPX3	131.993	IL18	6423.023	SELENOI	24700.000	EDNRB	9.517	TYR	11.000
28	EDNRB	131.754	GPX2	6261.110	FBXW7	24588.000	BCAN	9.515	CNP	11.000
29	TUBB4A	130.931	BDKRB1	6150.225	S100B	22758.000	GPX3	9.497	WNT3	11.000
30	PAX3	130.827	FBXW7	5781.578	CNP	22698.000	PAX3	9.484	DSG1	10.000

Table S6. Intersection of Gene Interaction Results from Three Network Analysis Methods

No.	A: MCODE	B: cytoNCA	C: cytoHubba	Intersection (A $\cap$ B $\cap$ C)	Intersection (A $\cap$ B)	Intersection (A $\cap$ C)	Intersection (B $\cap$ C)
1	PAX3	TYR	EGF	EDNRB	MITF	NRXN1	MAPK3
2	MITF	BEST1	MAPK3	TYR	PMEL	-	POU5F1
3	MLANA	MAPK3	TYR	SOX10	SLC24A5	-	FBXW7
4	PMEL	RAD23A	POU5F1	EGF	SLC45A2	-	GAPDHS
5	EDNRB	MYO5A	SOX10	RACK1	WNT3	-	S100B
6	GPR143	EDNRB	UBE2I	-	GPX2	-	SPP1
7	SLC24A5	POU5F1	ANK3	-	GPX3	-	IL18
8	SLC45A2	FBXW7	RACK1	-	RAD23A	-	PAX6
9	TYR	SLC24A5	NRXN1	-	BEST1	-	-
10	SOX10	CSPG4	PAX6	-	-	-	-
11	COL7A1	RACK1	SPP1	-	-	-	-
12	COL4A5	GAPDHS	IL18	-	-	-	-
13	COL6A5	SOX10	CEACAM5	-	-	-	-
14	COL11A2	S100B	S100B	-	-	-	-
15	COL28A1	SLC45A2	FBXW7	-	-	-	-
16	COL17A1	SPP1	NME8	-	-	-	-
17	COL23A1	CD63	GAPDHS	-	-	-	-
18	COL13A1	IL18	FLT3	-	-	-	-
19	COLGALT2	GPX3	EDNRB	-	-	-	-
20	NLGN1	GPX2	-	-	-	-	-
21	WNT2B	IRF4	-	-	-	-	-
22	NRXN1	WNT3	-	-	-	-	-
23	WNT7A	GPNMB	-	-	-	-	-
24	EGF	PMEL	-	-	-	-	-
25	WNT16	EGF	-	-	-	-	-
26	LRRTM4	PAX6	-	-	-	-	-
27	PTPRS	MITF	-	-	-	-	-
28	WNT3	-	-	-	-	-	-
29	RSPO1	-	-	-	-	-	-
30	NTNG1	-	-	-	-	-	-
31	WNT4	-	-	-	-	-	-
32	DUOX1	-	-	-	-	-	-
33	GPX2	-	-	-	-	-	-
34	DUOX2	-	-	-	-	-	-
35	ALB	-	-	-	-	-	-
36	GPX3	-	-	-	-	-	-
37	RPLP2	-	-	-	-	-	-
38	RPS20	-	-	-	-	-	-
39	RACK1	-	-	-	-	-	-
40	EIF3G	-	-	-	-	-	-

41	RAD23A	-	-	-	-	-	-
42	PDE6G	-	-	-	-	-	-
43	ROM1	-	-	-	-	-	-
44	PRPF6	-	-	-	-	-	-
45	PRCD	-	-	-	-	-	-
46	BEST1	-	-	-	-	-	-

Table S7. GO and KEGG pathway analysis results of 23 hub genes in LGCMN

	ID	Description	Hits	Total	p-value	p-adjust
				I		
BP	GO:0043473	pigmentation	8	23	1.98E-13	2.73E-10
BP	GO:0048066	developmental pigmentation	6	23	1.47E-11	1.01E-08
BP	GO:0042438	melanin biosynthetic process	4	23	1.21E-08	4.84E-06
BP	GO:0006582	melanin metabolic process	4	23	1.46E-08	4.84E-06
BP	GO:0044550	secondary metabolite biosynthetic process	4	23	1.75E-08	4.84E-06
BP	GO:0030318	melanocyte differentiation	4	23	2.46E-08	5.67E-06
BP	GO:0050931	pigment cell differentiation	4	23	9.63E-08	1.90E-05
BP	GO:0046189	phenol-containing compound biosynthetic process	4	23	2.42E-07	4.17E-05
BP	GO:0019748	secondary metabolic process	4	23	6.35E-07	8.34E-05
BP	GO:0046148	pigment biosynthetic process	4	23	6.35E-07	8.34E-05
CC	GO:0042470	melanosome	4	23	6.42E-06	2.70E-04
CC	GO:0048770	pigment granule	4	23	6.42E-06	2.70E-04
CC	GO:0033162	melanosome membrane	2	23	1.19E-04	2.00E-03
CC	GO:0045009	chitosome	2	23	1.19E-04	2.00E-03
CC	GO:0090741	pigment granule membrane	2	23	1.19E-04	2.00E-03
CC	GO:1990909	Wnt signalosome	1	23	1.40E-02	1.63E-01
CC	GO:0032585	multivesicular body membrane	1	23	1.52E-02	1.63E-01
CC	GO:0005635	nuclear envelope	3	23	1.74E-02	1.63E-01
CC	GO:0099059	integral component of presynaptic active zone membrane	1	23	1.75E-02	1.63E-01
CC	GO:0031143	pseudopodium	1	23	2.10E-02	1.69E-01
MF	GO:0004602	glutathione peroxidase activity	2	23	3.11E-04	4.20E-02
MF	GO:0030332	cyclin binding	2	23	6.40E-04	4.32E-02
MF	GO:0004601	peroxidase activity	2	23	1.92E-03	5.13E-02
MF	GO:0045309	protein phosphorylated amino acid binding	2	23	1.99E-03	5.13E-02
MF	GO:0016684	oxidoreductase activity, acting on peroxide as acceptor	2	23	2.22E-03	5.13E-02
MF	GO:0048018	receptor ligand activity	4	23	2.90E-03	5.13E-02
MF	GO:0030546	signaling receptor activator activity	4	23	3.01E-03	5.13E-02
MF	GO:0005125	cytokine activity	3	23	3.04E-03	5.13E-02
MF	GO:0043130	ubiquitin binding	2	23	4.05E-03	6.07E-02
MF	GO:0051219	phosphoprotein binding	2	23	5.04E-03	6.32E-02
KEGG	hsa04916	Melanogenesis	5	23	4.22E-09	5.74E-07
KEGG	hsa04550	Signaling pathways regulating pluripotency of stem cells	4	23	1.45E-06	9.89E-05
KEGG	hsa05218	Melanoma	3	23	1.15E-05	4.30E-04
KEGG	hsa05200	Pathways in cancer	5	23	1.27E-05	4.30E-04
KEGG	hsa01521	EGFR tyrosine kinase inhibitor resistance	2	23	1.03E-03	8.43E-03
KEGG	hsa05235	PD-L1 expression and PD-1 checkpoint pathway in cancer	2	23	1.30E-03	8.43E-03
KEGG	hsa05231	Choline metabolism in cancer	2	23	1.60E-03	9.46E-03
KEGG	hsa04014	Ras signaling pathway	2	23	8.24E-03	2.67E-02
KEGG	hsa04010	MAPK signaling pathway	2	23	1.30E-02	4.02E-02

KEGG	hsa04151	PI3K-Akt signaling pathway	2	23	1.83E-02	5.41E-02
KEGG	hsa00480	Glutathione metabolism	2	23	5.32E-04	8.43E-03
KEGG	hsa00590	Arachidonic acid metabolism	2	23	6.67E-04	8.43E-03
KEGG	hsa04918	Thyroid hormone synthesis	2	23	9.11E-04	8.43E-03
KEGG	hsa01100	Metabolic pathways	4	23	9.07E-03	2.87E-02
KEGG	hsa04623	Cytosolic DNA-sensing pathway	1	23	3.68E-02	8.04E-02
KEGG	hsa00350	Tyrosine metabolism	1	23	2.15E-02	5.87E-02
KEGG	hsa03420	Nucleotide excision repair	1	23	2.77E-02	7.12E-02
KEGG	hsa00010	Glycolysis / Gluconeogenesis	1	23	3.97E-02	8.04E-02

BP: biological processes, CC: cellular components, MF: molecular functions. KEGG: Kyoto Encyclopedia of Genes and Genomes