

Additional Electronic Supplementary Information uploaded on 27th November 2015.

This version replaces the version uploaded on the 14th November 2014.

Table 1 Chemical structures and concentrations of major components in SMI

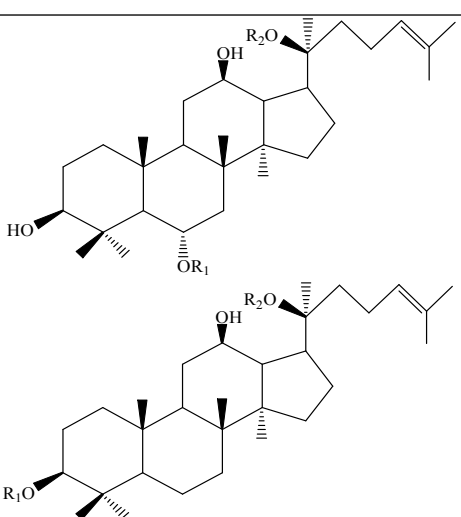
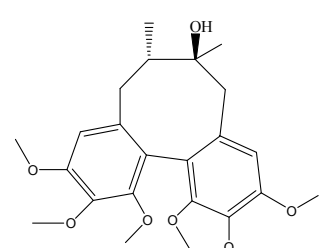
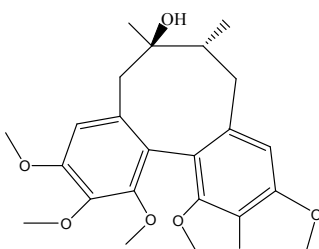
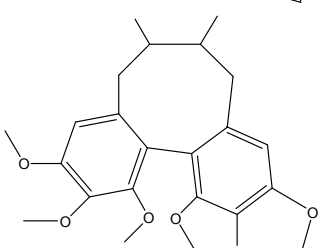
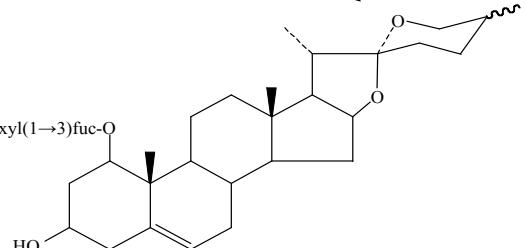
Structure	Component	R ₁	R ₂	Concentration (μg/mL)
	Ginsenoside Rg1	Glc	Glc	129.6
	Ginsenoside Re	Glc ² -Rha	Glc	100.6
	Ginsenoside Rf	Glc ² -Glc	H	38.50
	Ginsenoside Rg2	Glc ² -Rha	H	25.58
	Ginsenoside Rb1	Glc ² -Glc	Glc ⁶ -Glc	221.7
	Ginsenoside Rd	Glc ² -Glc	Glc	45.60
	Ginsenoside Rc	Glc ² -Glc	Glc ⁶ -Ara	145.2
	Schisandrin			13.70
	Schisandrol B			0.6574
	Schizandrin B			0.0327
	Ophiopogonin D			0.0054

Table 2 Characterization of the identified altered proteins and relative spot intensity of their spot volumes

Spot number ^a	Protein identity	NCBI accession number	(Theoretical values)pI/kDa	Peptide count	Sequence coverage (%)	Score	Relative spot intensity % (Sham, 100)	
							IR	IR+SMI
Glucose metabolism proteins								
1	Triosephosphate isomerase	124056485	6.89/27	13	43	80	72±33.9*	123±67.1#
2	Pyruvate dehydrogenase E1 component subunit beta	122065728	6.20/40	4	12	58	58±28.7**	110±62.0#
3	Aldose reductase	6978491	6.26/36	16	36	165	57±39.4*	106±80.8
4	L-lactate dehydrogenase B chain	1170739	5.70/37	11	14	85	63±45.0*	104±21.1#
5	Aldolase A	202837	8.31/39	17	38	463	41±7.2*	102±21.3##
Lipid metabolism proteins								
6	Short-chain specific acyl-CoA dehydrogenase	11968090	8.47/45	17	23	296	160±33.5*	107±29.9
7	3-ketoacyl-CoA thiolase	149027157	8.64/38	14	31	140	166±45.1*	98±39.8#
TCA cycle protein								
8	Malate dehydrogenase	81861572	6.16/36	10	23	124	62±31.6*	106±67.5
Rsp-Chain protein								
9	ATP synthase, H ⁺ transporting	149029483	8.24/55	24	34	267	35±18.9*	70±32.9#
10	ATP synthase subunit beta	114562	5.19/56	7	7	173	67±23.6*	96±32.9#
11	Creatine kinase M-type	6978661	6.58/43	13	29	182	185±44.8*	115±79.1
Other proteins								
12	Cytokeratin-6A	123781839	8.06/59	15	24	87	75±23.5*	104±48.0#
13	Tu translation elongation factor	149067905	7.65/44	17	31	321	79±50.2**	120±102.3
14	rCG27551, isoform CRA_a	149041248	8.45/21	5	15	101	71±28.4*	109±53.0

^a The marked spot number in Fig. 2(A). * $P < 0.05$, ** $P < 0.01$ vs. Sham group, # $P < 0.05$, ## $P < 0.01$ vs. IR group