Fig. S.1 Diagram of the edible and inedible parts of white and green Asparagus.

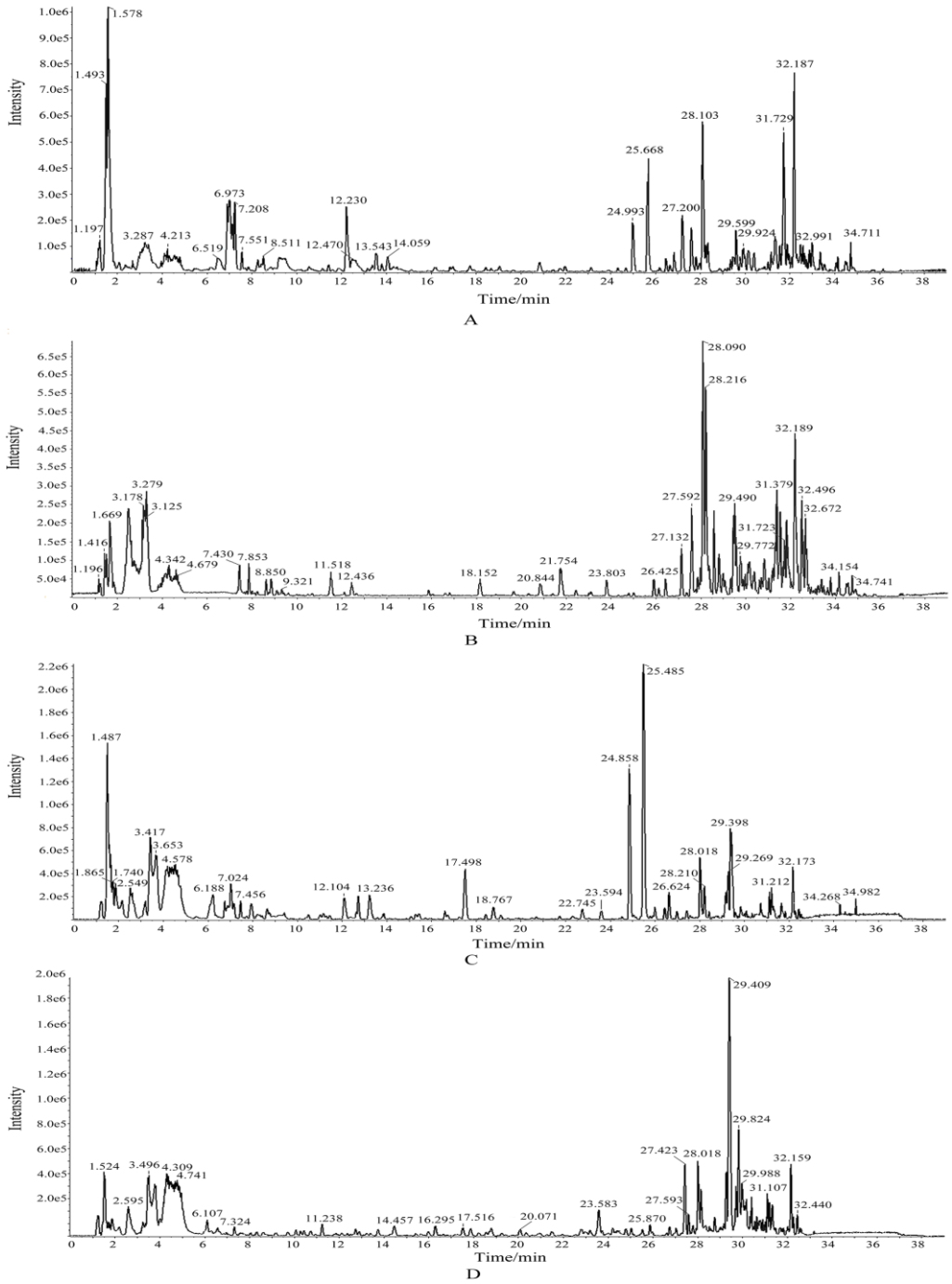

Fig. S.2 Base peak intensity (BPI) chromatograms of the inedible parts of white and green Asparagus by UPLC-Q-TOF MS/MS analysis. A: The inedible parts of green Asparagus in positive ion pattern; B: The inedible parts of white Asparagus in positive ion pattern; C: The inedible parts of green Asparagus in negative ion pattern; D: The inedible parts of white Asparagus in negative ion pattern

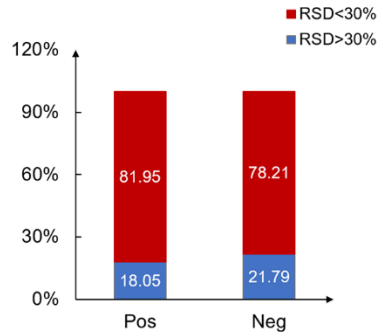

Fig. S.3 RSD distribution of all compounds of QC samples in the metabolomics analysis.

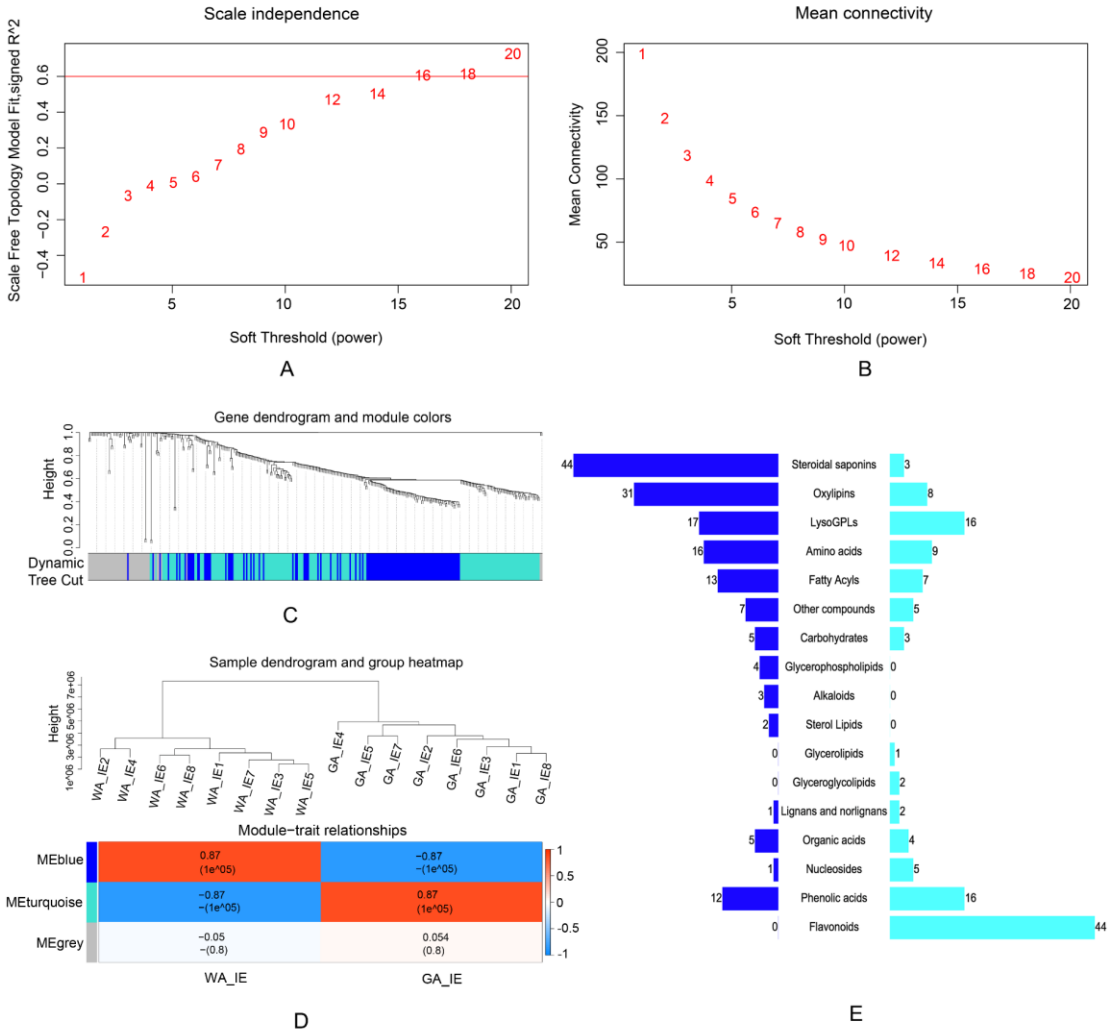

Fig. S.4 Correlation of metabolites with the inedible part of white and green Asparagus based on WGCNA. (A) R^2 corresponding to different soft thresholds; (B) the gene adjacency coefficients corresponding to different soft thresholds; (C) Clustering dendrogram of the average network adjacency for the identification of metabolite co-expression modules; (D) Sample cluster dendrogram and module-group relationships. Each row corresponded to a module eigengene, column to a variety. Each cell contained the corresponding correlation and value of p. The table was color-coded by correlation according to the color legend; (E) Distribution of different types of metabolites in blue and turquoise modules.

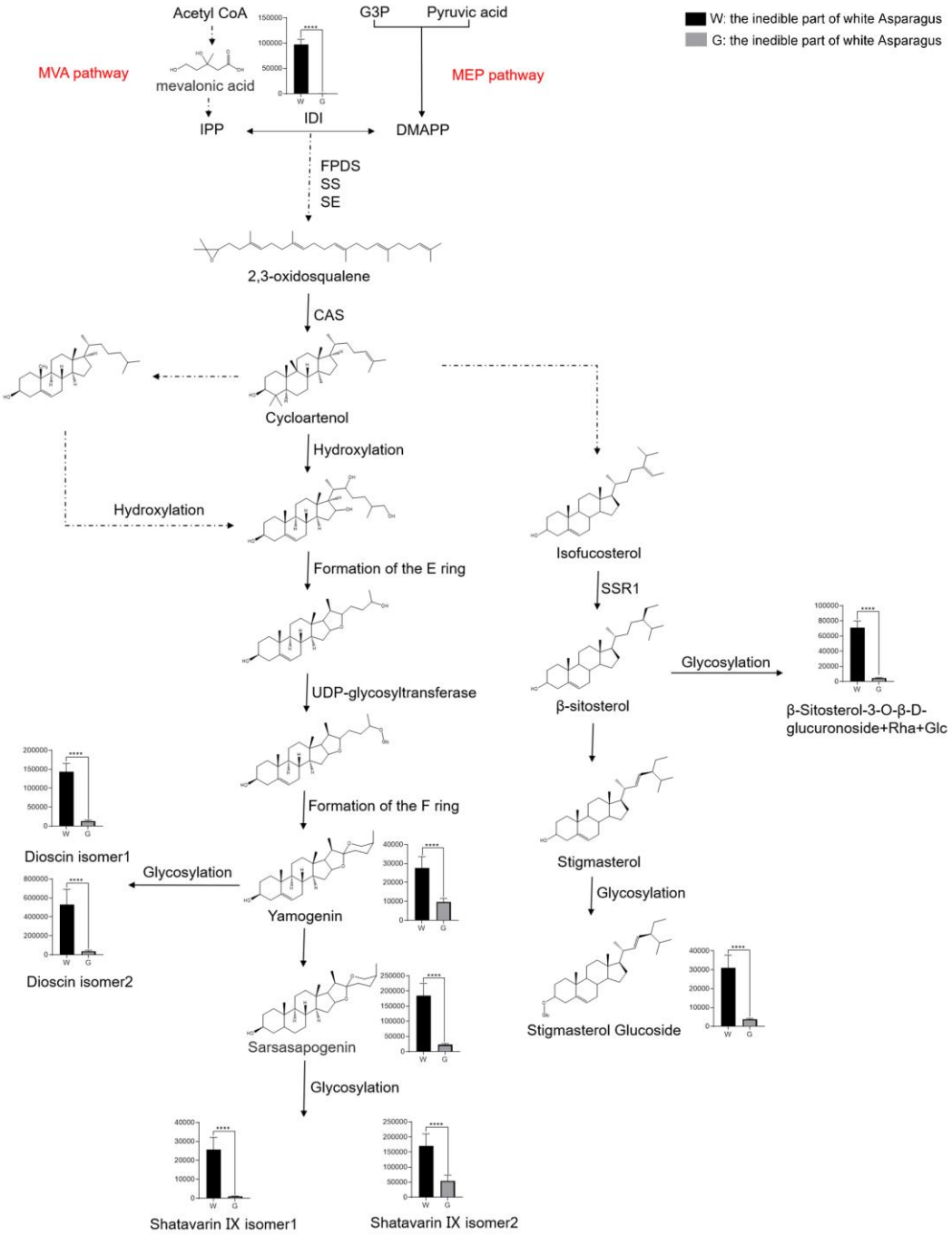

Fig. S.5 Biosynthetic pathway of the steroid saponins.

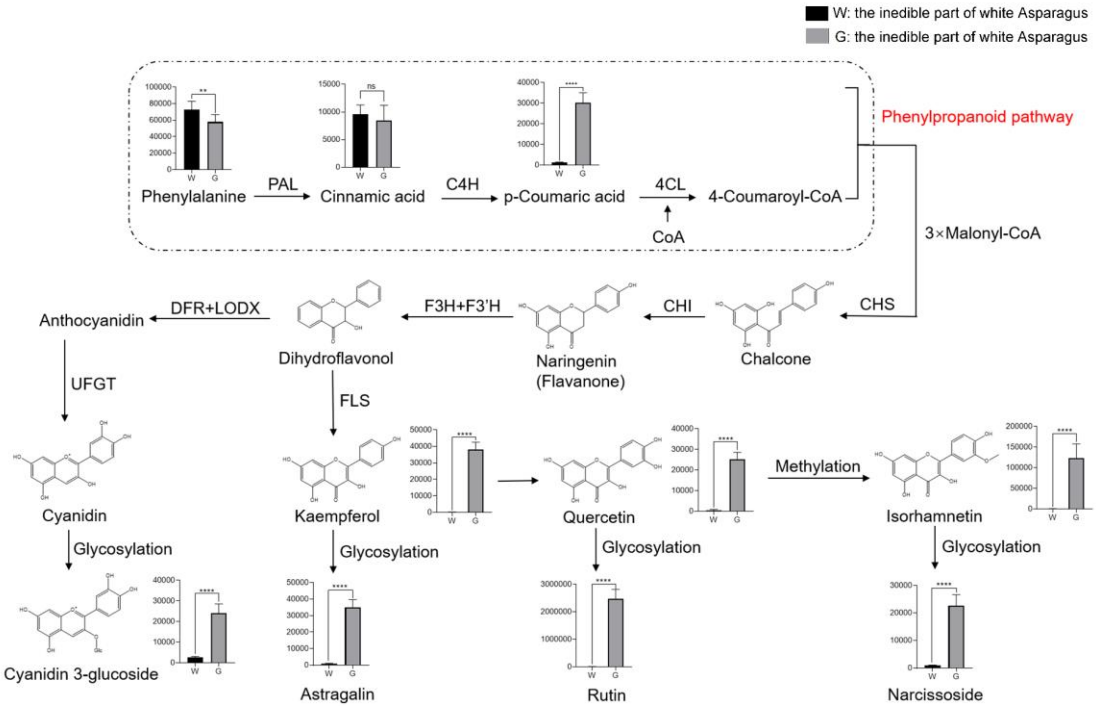

Fig. S.6 Biosynthetic pathway of the flavonoids.

Table S6 The model parameters of OPLS-DA

Group	Positive ion mode	Negative ion mode
WA_E vs WA_IE	R^2X=0.683, Q^2=0.988	R^2X=0.741, Q^2=0.990
GA_E vs GA_IE	R^2X=0.700, Q^2=0.976	R^2X=0.728, Q^2=0.978
WA_IE vs GA_IE	R^2X=0.733, Q^2=0.987	R^2X=0.755, Q^2=0.992

Table S7 Molecular docking results of sarsasapogenin and yamogenin with the related key targets

Compound	Target	PDB ID	Binding energy (kcal·mol^{-1})	Hydrogen-binding sites	Hydrophobic sites
Sarsasapogenin	MTOR	4DRI	-10.50	ILE87	PHE77, ILE87, PHE130, LEU2031, PHE2039, TRP2101, PHE2108
	ALK	6MX8	-10.18	TRP1320, PRO1398	LEU1325, TYR1327, PRO1331, ASP1349, PRO1351, LYS1352, PRO1398, GLU1400
	CDK4	2W96	-9.23	TRP238, HIS281	LEU186, GLN188, LEU223, TRP238, PHE278, PRO280
	MDM2	1RV1	-9.02		LYS51, LEU54, PHE55, LEU57, ILE61, PHE91, VAL93, ILE99
	PIK3CA	4JPS	-8.17	TRP424, PRO447, GLN478	TRP446, PRO447, GLN478, HIS676, LYS678
	VEGFA	4KZN	-7.97	CYS61	GLU67
	PTGS2	5F19	-7.96	TYR385, GLY526, GLY533, LEU534	PHE205, VAL344, TYR348
	HSP90AA1	4BQG	-7.37	LYS204, TYR216	VAL207, LYS208, GLN212
Yamogenin	ALK	6MX8	-9.74	LYS1352, PRO1398	LEU1325, TYR1327, PRO1331, ASP1349, PRO1351, LYS1352, PRO1398, GLU1400
	MDM2	1RV1	-8.67	HIS96	LEU54, LEU57, ILE61, VAL93, ILE99, TYR100
	IL2	1M47	-7.89	LYS32, LYS35	ASN30, TYR31, LYS32, LYS35
	CDK4	2W96	-7.85		LEU65, LYS72, GLU75, PHE78
	SRC	2BDF	-7.20	LYS316	LYS316, ASN381, LEU410