

Supporting Information

Supplementary Tables

Supplementary Table S1. ROC analysis on the differential fecal metabolites of AMD detected in positive and negative ion mode.

Supplementary Table S2. ROC analysis on the differential serum metabolites detected in positive and negative ion mode.

Supplementary Figures

Supplementary Figure S1. Permutation test of the PLS-DA model in the (A) positive and (B) negative ion modes based on the fecal metabolomics data of the study cohort. The R²Y value represents the goodness of fit of the model. The Q² value represents the predictability of the models. All R²Y and Q² values to the left were lower than the original points to the right of the blue regression line of the Q² points, which intersects the vertical axis (on the left) at or below zero, showing that the PLS-DA model was valid. Permutation test plot for the PLS-DA model (number of permutations, 200; intercepts R²=0.0, 0.708, Q²=0.0, -0.209 in ESI+; R²=0.0, 0.677, Q²=0.0, -0.15 in ESI-). ESI, electrospray ionization; PLS-DA, partial least squares-discriminant analysis.

Supplementary Figure S2. Permutation test of the PLS-DA model in the (A) positive and (B) negative ion modes based on the serum metabolomics data of the study cohort. The R²Y value represents the goodness of fit of the model. The Q² value represents the predictability of the models. All R²Y and Q² values to the left were lower than the original points to the right of the blue regression line of the Q² points, which intersects the vertical axis (on the left) at or below zero, showing that the PLS-DA model was valid. Permutation test plot for the PLS-DA model (number of permutations, 200; intercepts R²=0.0, 0.64, Q²=0.0, -0.159 in ESI+; R²=0.0, 0.829, Q²=0.0, -0.162 in ESI-). ESI, electrospray ionization; PLS-DA, partial least squares-discriminant analysis.

Supplementary Tables

Supplementary Table S1. ROC analysis on the differential fecal metabolites of AMD detected in positive and negative ion mode calculated.

Ion mode	Metabolites	AUC	SE	p-value	95% CI
Positive ion mode	Palmitoyl ethanolamide	0.838	0.072	0.001	0.697-0.979
	Stearoyl ethanolamide	0.79	0.078	0.004	0.638-0.943
	Sphingosine	0.765	0.09	0.009	0.588-0.941
	Oleoyl ethanolamide	0.746	0.085	0.016	0.579-0.913
	N-Acetylputrescine	0.735	0.088	0.021	0.564-0.907
	2-(14,15-Epoxyeicosatrienoyl) glycerol	0.482	0.103	0.857	0.28-0.683
	5-Hydroxyindoleacetic acid	0.415	0.102	0.407	0.216-0.615
	N6,N6,N6-Trimethyl-L-lysine	0.375	0.101	0.221	0.177-0.573
	Creatinine	0.467	0.104	0.746	0.264-0.67
	Benzamide	0.463	0.103	0.719	0.262-0.664
	Dimethylbenzimidazole	0.456	0.103	0.666	0.255-0.657
	Uridine	0.768	0.082	0.009	0.608-0.929
	Nicotinic acid	0.761	0.086	0.011	0.593-0.929
	p-Anisic acid	0.741	0.086	0.019	0.572-0.91
Negative ion mode	D-Xylose	0.746	0.085	0.016	0.579-0.914
	Glyceric acid	0.746	0.088	0.016	0.574-0.918
	2-Methylbenzoic acid	0.305	0.091	0.056	0.126-0.484
	Chenodeoxycholic Acid	0.316	0.096	0.072	0.129-0.503

Notes: AMD, age-related macular degeneration; ROC, receiver operating characteristic; AUC, area under the curve; CI, confidence interval;

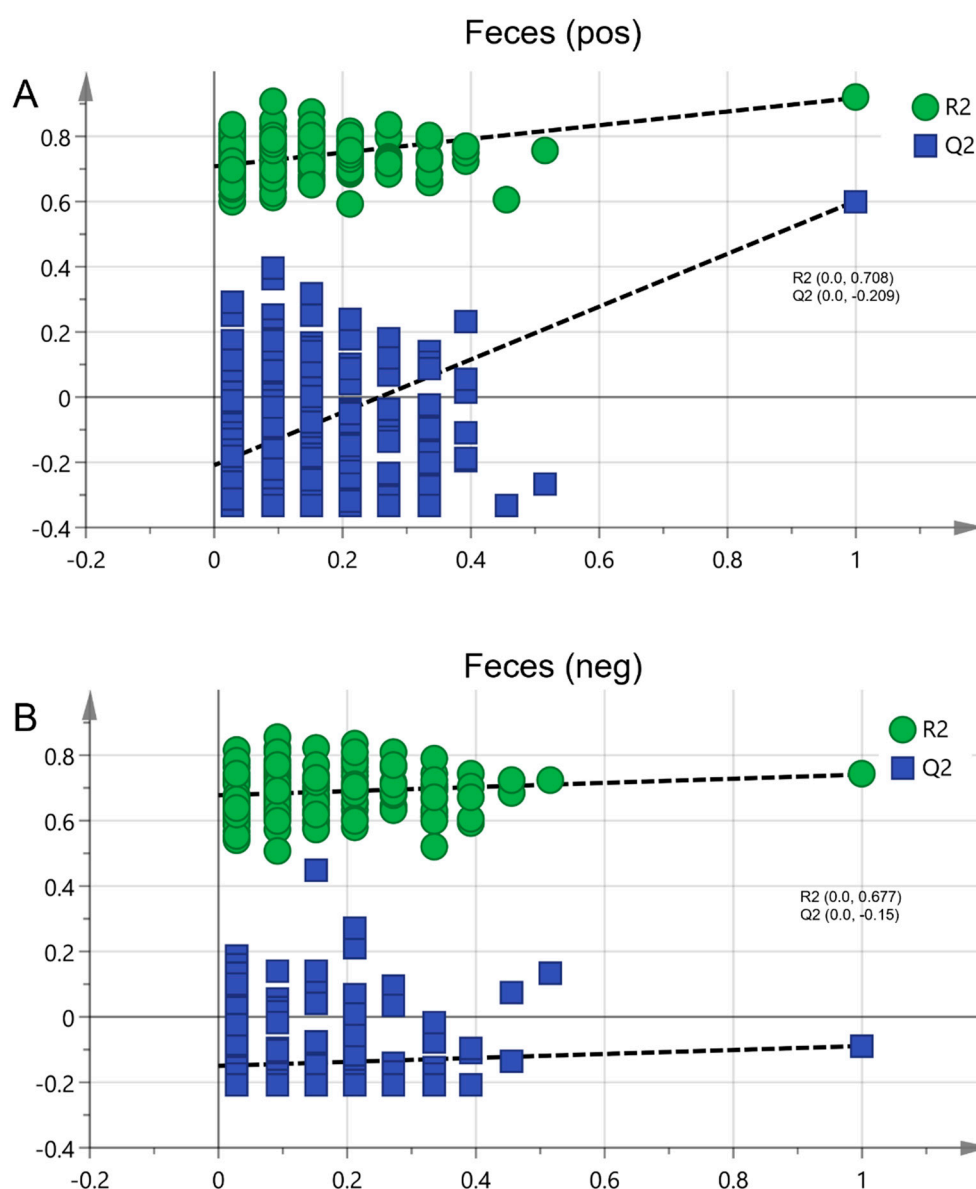
Supplementary Table S2. ROC on the differential serum metabolites detected in positive and negative ion mode.

Ion mode	Metabolites	AUC	SE	p-value	95% CI
Positive ion mode	4-Hydroxybenzoic acid	0.819	0.082	0.003	0.658 - 0.98
	1-Methylhistidine	0.762	0.092	0.016	0.581 - 0.942
	Creatine	0.743	0.096	0.026	0.555 – 0.93
	Inosine	0.724	0.096	0.04	0.536 – 0.911
	Caffeine	0.724	0.095	0.04	0.538-0.910
	Hypoxanthine	0.719	0.099	0.045	0.526 – 0.912
	DL-Acetylcarnitine	0.71	0.11	0.055	0.493 – 0.926
	1-Monolinolein	0.319	0.109	0.097	0.106 – 0.532
	Adrenic acid	0.981	0.02	<0.0001	0.943-1.0
	Palmitic acid	0.938	0.06	<0.0001	0.82-1.0
	Arachidic acid	0.838	0.079	0.002	0.683-0.993
	2-Hydroxymyristic acid	0.757	0.095	0.018	0.571- 0.943
	1,3,7-Trimethyluric acid	0.748	0.096	0.023	0.56-0.936
	D-(+)-Glucose	0.738	0.101	0.029	0.541-0.935
	Lactic Acid	0.69	0.103	0.081	0.489-0.892
Negative ion mode	5alpha-Dihydrotestosterone glucuronide	0.686	0.103	0.089	0.483-0.888
	1-Methylxanthine	0.667	0.104	0.127	0.464-0.87
	3-Methylglutaric acid	0.605	0.107	0.337	0.396-0.814
	2-Deoxyribose 5-phosphate	0.581	0.109	0.458	0.368-0.794
	Prolylglycine	0.581	0.109	0.458	0.368-0.792
	Ornithine	0.51	0.113	0.93	0.287-0.7732
	Citric acid	0.481	0.113	0.861	0.259-0.703
	Nervonic acid	0.486	0.112	0.896	0.266-0.705
	D-(+)-Tryptophan	0.419	0.109	0.458	0.205-0.633
	Uric acid	0.39	0.107	0.315	0.181-0.6
	Xanthine	0.352	0.112	0.176	0.133-0.572
	L-Histidine	0.343	0.107	0.15	0.134-0.552
	L-Tyrosine	0.319	0.102	0.097	0.120-0.518

Notes: AMD, age-related macular degeneration; ROC, receiver operating characteristic; SVM, support vector machine; AUC, area under the curve; CI, confidence interval.

Supplementary Figures

Supplementary Figure S1. Permutation test of the PLS-DA model in the (A) positive and (B) negative ion modes based on the fecal metabolomics data of the study cohort. The R²Y value represents the goodness of fit of the model. The Q² value represents the predictability of the models. All R²Y and Q² values to the left were lower than the original points to the right of the blue regression line of the Q² points, which intersects the vertical axis (on the left) at or below zero, showing that the PLS-DA model was valid. Permutation test plot for the PLS-DA model (number of permutations, 200; intercepts R²=0.0, 0.708, Q²=0.0, -0.209 in ESI+; R²=0.0, 0.677, Q²=0.0, -0.15 in ESI-). ESI, electrospray ionization; PLS-DA, partial least squares-discriminant analysis.



Supplementary Figure S2. Permutation test of the PLS-DA model in the (A) positive and (B) negative ion modes based on the serum metabolomics data of the study cohort. The R²Y value represents the goodness of fit of the model. The Q² value represents the predictability of the models. All R²Y and Q² values to the left were lower than the original points to the right of the blue regression line of the Q² points, which intersects the vertical axis (on the left) at or below zero, showing that the PLS-DA model was valid. Permutation test plot for the PLS-DA model (number of permutations, 200; intercepts R²=0.0, 0.64, Q²=0.0, -0.159 in ESI+; R²=0.0, 0.829, Q²=0.0, -0.162 in ESI-). ESI, electrospray ionization; PLS-DA, partial least squares-discriminant analysis.

