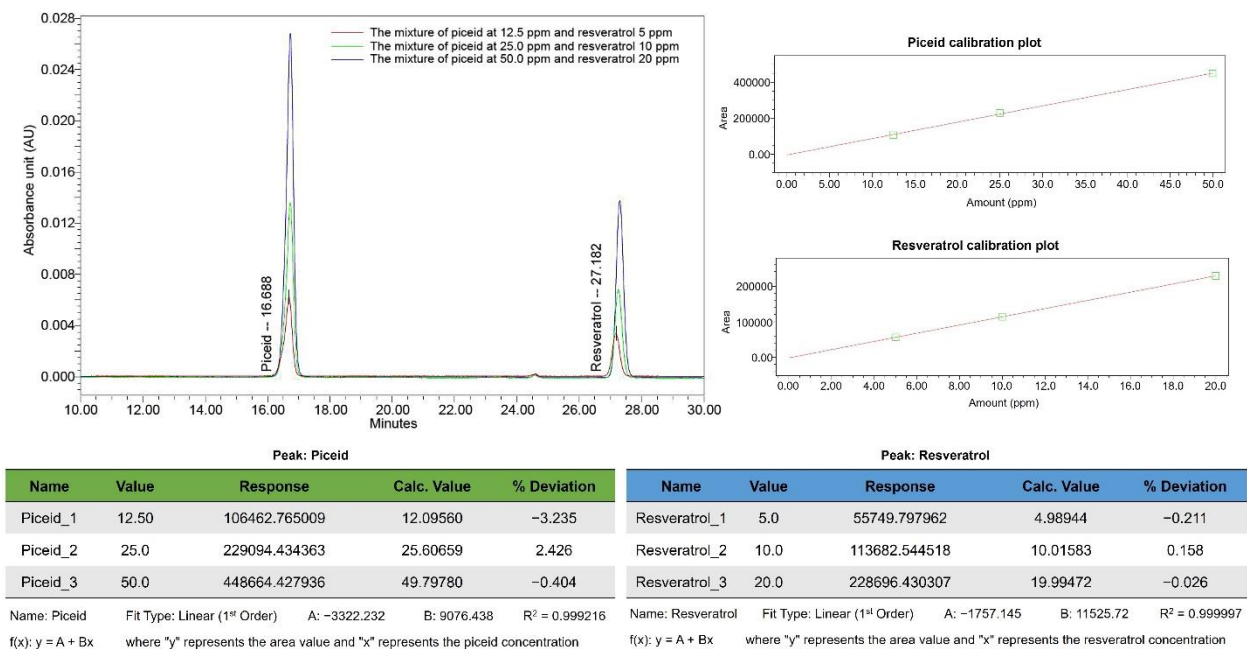
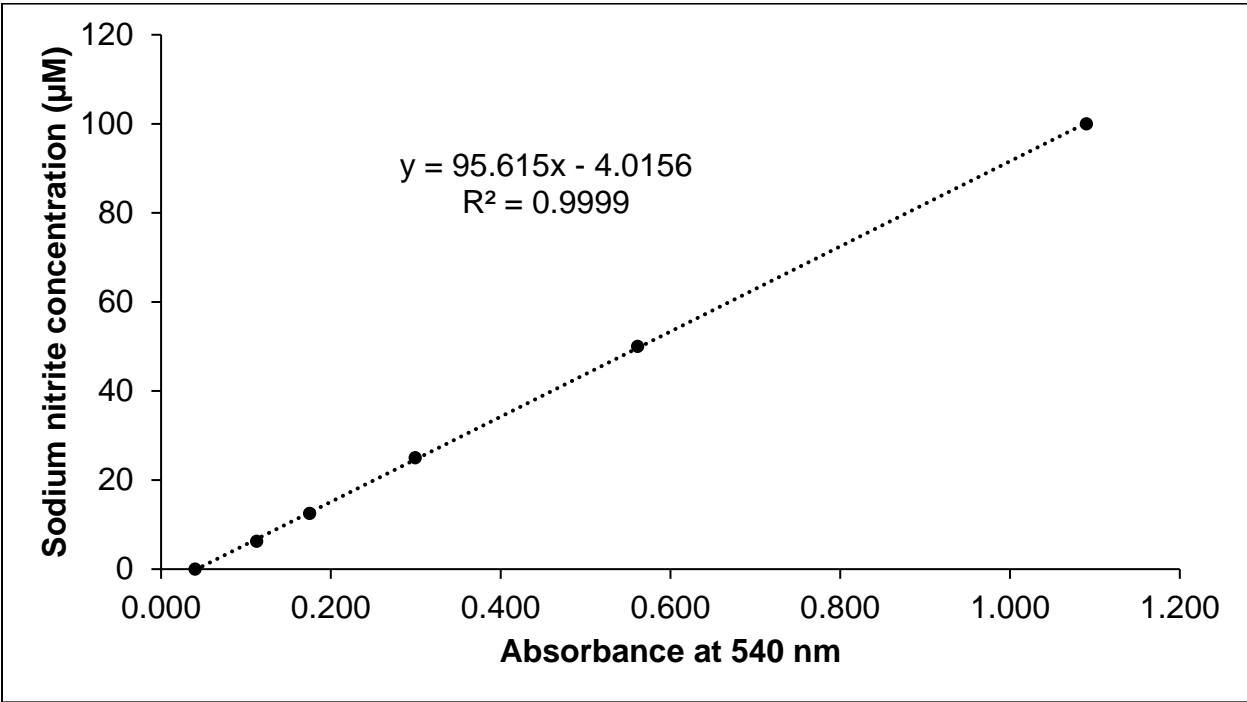


Supplementary Materials

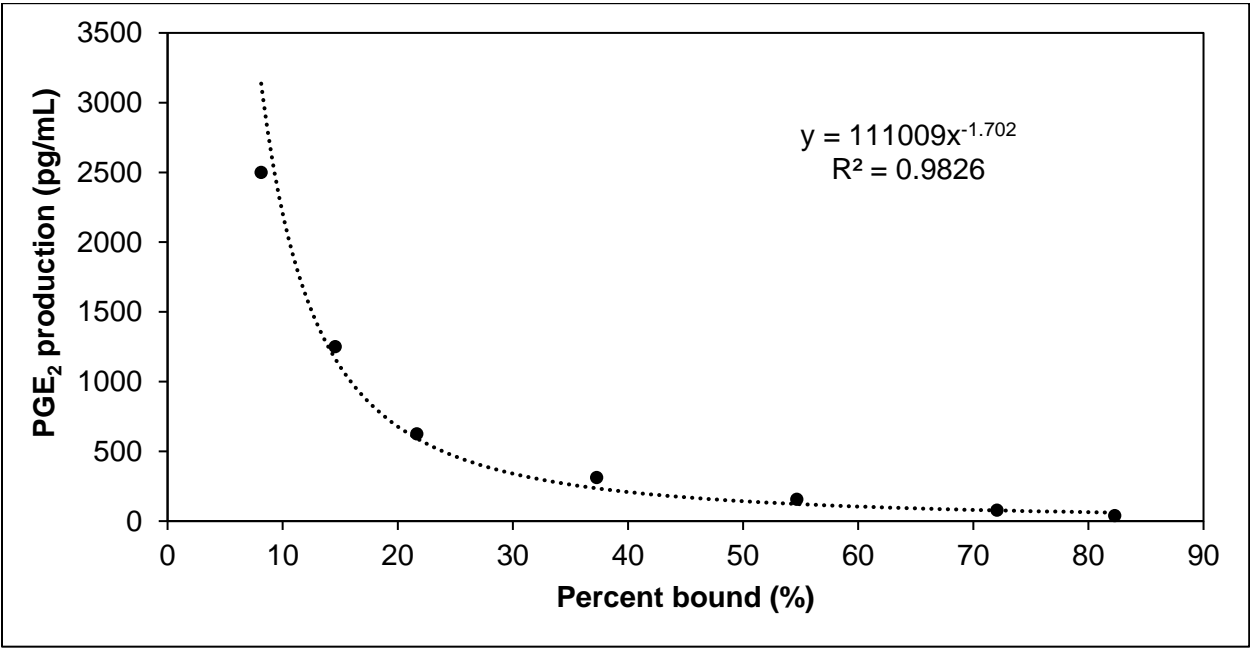
**Figure S1.** Sample chromatographs (left panel) and calibration standard curves for piceid (right upper panel) and resveratrol (right lower panel).



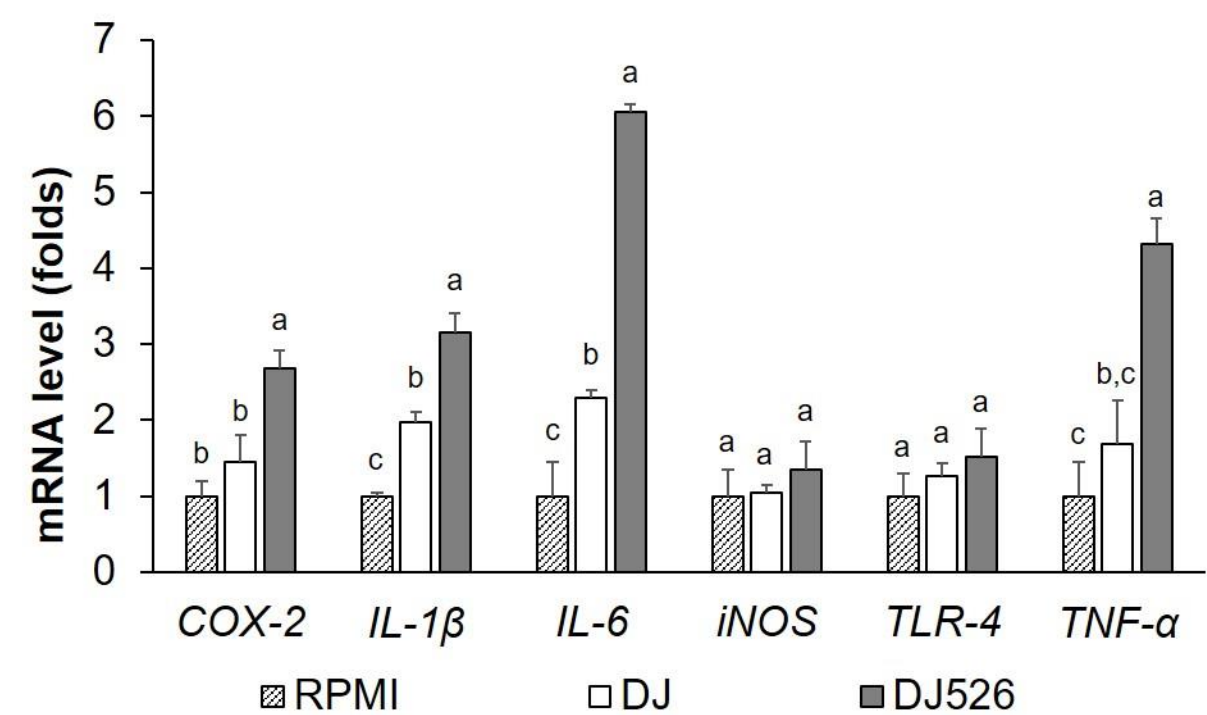
**Figure S2.** The standard curve of sodium nitrite



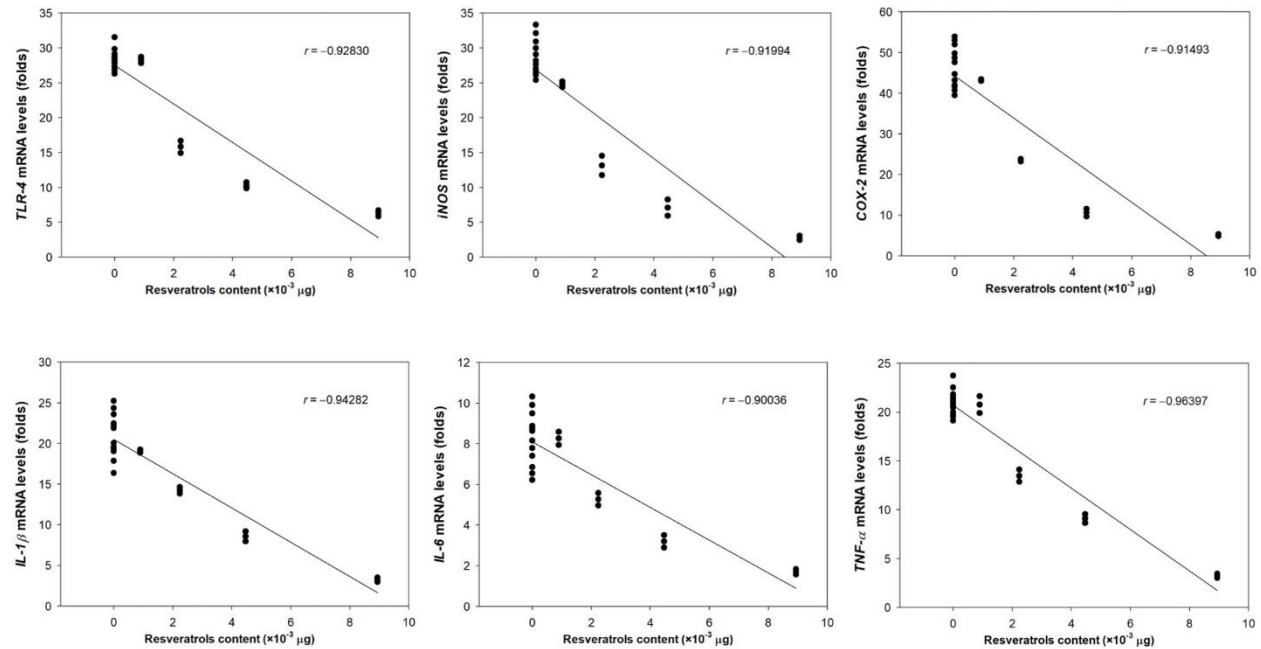
**Figure S3.** Standard curve of PGE<sub>2</sub> production



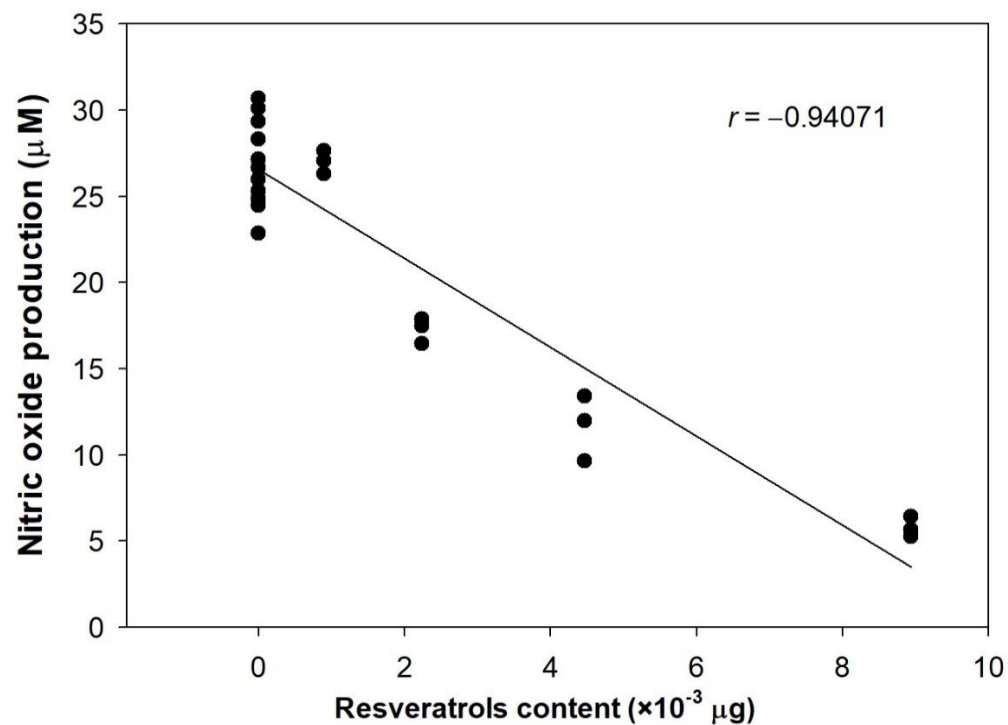
**Figure S4.** The expression levels of pro-inflammatory associated genes in the RPMI-, DJ-, and DJ526-treated cells. Letters (a-c) indicate significant differences ( $p < 0.05$ ) between treatments (where  $a > b > c$ ).



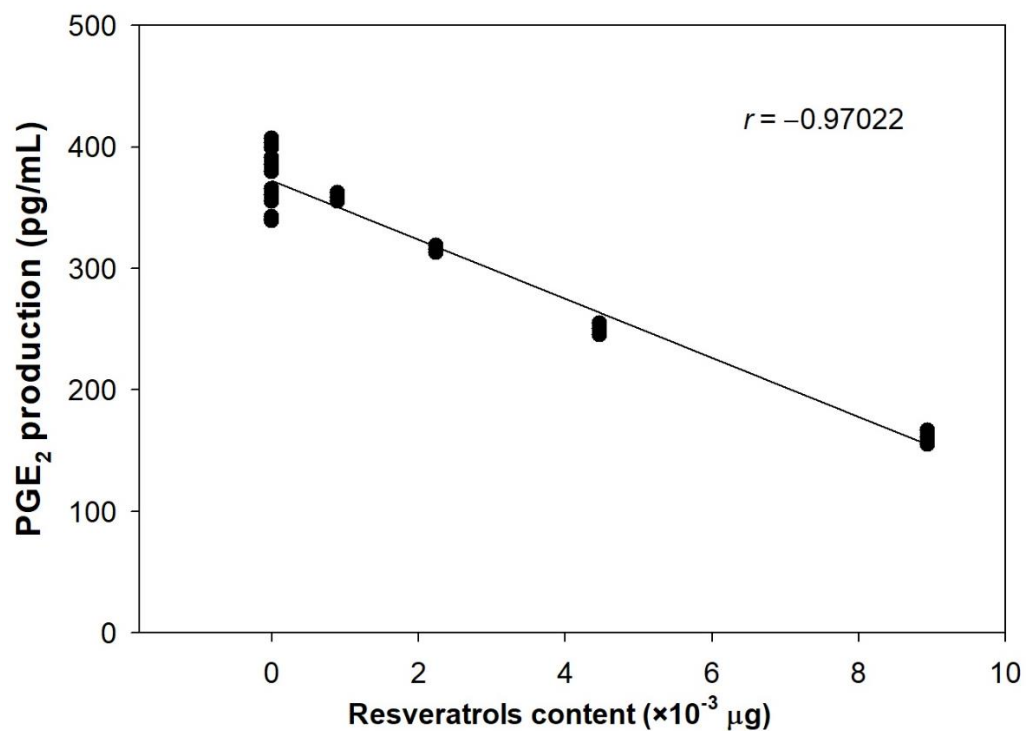
**Figure S5.** Pearson's correlation analyses between the amount of resveratrol (piceid + resveratrol) and mRNA levels (degree of freedom = 22 and  $p = 0.01$ )



**Figure S6.** Pearson's correlation analyses between the amount of resveratrol (piceid + resveratrol) and nitric oxide production (degree of freedom = 22 and  $p = 0.01$ )



**Figure S7.** Pearson`s correlation analyses between the amount of resveratrol (piceid + resveratrol) and PGE<sub>2</sub> production (degree of freedom = 22 and  $p = 0.01$ )



**Table S1.** Cell viability assay results using the EZ-Cytox Cell Viability Assay Kit

Treatment	Absorbance at 450 nm			Mean	StDev	% Mean	% StDev
	1	2	3				
Nontreatment	0.910	0.950	0.949	0.936	0.023	100.00	2.44
DMSO	0.976	1.021	0.995	0.997	0.023	106.51	2.41
Aspirin	0.989	1.008	0.994	0.997	0.010	106.48	1.05
DJ_10 µg/mL	0.991	1.023	0.982	0.999	0.022	106.66	2.30
DJ_25 µg/mL	0.986	0.983	0.988	0.986	0.003	105.27	0.27
DJ_50 µg/mL	0.960	0.978	1.008	0.982	0.024	104.88	2.59
DJ_100 µg/mL	0.959	0.970	1.009	0.979	0.06	104.59	2.81
DJ_125 µg/mL	0.896	0.856	0.854	0.869	0.024	92.77	2.53
DJ_150 µg/mL	0.785	0.794	0.808	0.796	0.012	84.98	1.24
DJ526_10 µg/mL	1.033	0.996	0.998	1.009	0.021	107.76	2.22
DJ526_25 µg/mL	0.969	1.005	1.004	0.993	0.021	106.02	2.19
DJ526_50 µg/mL	0.973	0.962	1.006	0.980	0.023	104.70	2.45
DJ526_100 µg/mL	0.959	0.948	0.994	0.967	0.024	103.28	2.57
DJ526_125 µg/mL	0.905	0.915	0.898	0.906	0.009	96.76	0.91
DJ526_150 µg/mL	0.849	0.803	0.807	0.820	0.025	87.54	2.72

**Table S2.** The mRNA levels of pro-inflammatory associated cytokines.

Treatment	COX-2		IL-1 $\beta$		IL-6		iNOS		TLR-4		TNF- $\alpha$	
	Level (folds)	StDev	Level (folds)	StDev	Level (folds)	StDev	Level (folds)	StDev	Level (folds)	StDev	Level (folds)	StDev
RPMI	1.00	0.19	1.00	0.04	1.00	0.44	1.00	0.34	1.00	0.30	1.00	0.45
LPS	32.54	1.07	20.17	1.67	16.54	2.85	23.75	2.58	14.87	0.83	16.49	2.31
DJ	1.44	0.36	1.97	0.14	2.30	0.10	1.04	0.10	1.26	0.16	1.69	0.57
DJ526	2.69	0.23	3.16	0.24	6.06	0.10	1.35	0.37	1.51	0.38	4.32	0.34

**Note:** RAW264.7 cells were treated with the DJ and DJ526 rice callus extracts at the concentration of 100  $\mu$ g/mL. The cells-treated with 1  $\mu$ g/mL of LPS were assigned as the positive control. After 6 h of treatment, the total RNA was extracted from the cells using Tri reagent. The extracted RNA (1000 ng) was used for cDNA synthesis and the cDNA was prepared at the concentration of 5 ng/ $\mu$ L for the Real-Time PCR. The expression of pro-inflammatory mRNA was increased by the treatment of LPS. This expression concludes that the cells are in the good condition.