Electronic Supplementary Material (ESI) for Food & Function.

Table S1. Basic characteristics in the four libraries with and without EGCG

Sample	Control	SAH	EGCG (1 µM)	EGCG (50µM)
Raw reads	7847243	7800374	7261096	8412576
Q20	98.61%	98.23%	98.48%	98.53%
Q30	95.90%	95.11%	95.57%	95.65%
GC content (%)	47.44%	46.73%	48.20%	48.10%

Q20, Q30, GC content were used to evaluate the quality

Table S2. Statistical summary of the data generated by high-throughput small-RNA sequencing after EGCG pre-treatment

Read type	sRNA libraries			
	~~Control~~	~~SAH~~	~~EGCG (1µM)~~	~~EGCG (50µM)~~
Low quality reads	8195 (0.1%)	10406 (0.13%)	7519 (0.1%)	10612 (0.13%)
N% > 10%	652 (0.01%)	1005 (0.01%)	617 (0.01%)	674 (0.01%)
5’ adapter contaminants	277 (0.00%)	310 (0.00%)	3056 (0.04%)	3308 (0.04%)
3’ adapter null	166663 (2.12%)	152129 (1.95%)	255655 (3.52%)	232659 (2.77%)
Poly (A/T/G/C)	4851 (0.06%)	4433 (0.06%)	8066 (0.11%)	7842 (0.09%)
Clean reads	7666605(97.70%)	7632091(97.84%)	6986183(96.21%)	8157481(96.97%)

N% means undetectable gaps at base calling

Table S3. Statistics of mapped sRNA reads in the four libraries after EGCG pre-treatment

Category	Total sRNAs	Mapped sRNA	‘+’ Mapped sRNA	‘-’ Mapped sRNA
Con	7433820 (100%)	4911847 (66.07%)	4548254 (61.18%)	363593 (4.89%)
SAH	7524170 (100%)	4242974 (56.39%)	4033673 (53.61%)	209301 (2.78%)
EGCG 1 µM	6714013 (100%)	3638355 (54.19%)	3298998 (49.14%)	339457 (5.06%)
EGCG 50 µM	7875625 (100%)	4283201(54.39%)	3879588 (49.26%)	403613 (5.12%)

‘+’ means that the reads align to genome with the same direction, whereas ‘-’ means that the reads reversely aligne to genome.

Table S4. The detail of identified mapped small RNA after EGCG pre-treatment

Read type	Control	SAH	EGCG	EGCG50
total	4911847	4242974	3638455	4283201
mapped sRNAs	4445953	3965322	3284218	3963937
Novel sRNAs	1209	695	864	984
rRNAs	2852	1932	8554	3076
tRNAs	2	0	2	3
snRNAs	1978	1527	3955	2666
snoRNAs	65522	24222	28803	29941
repeat associated RNAs	45142	31982	50640	52919
Other	111135	90566	83086	88018

Table S5. The summary of down-regulated and up-regulated miRNAs targeting p38 MAPK after EGCG pre-treatment

Group	Downregulated miRNA expression	Upregulated miRNA expression
SAH	rno-miR-378a-3p, rno-miR-204-3p, rno-miR-152-5p, rno-miR-3557-5p	rno-miR-16-5p, rno-miR-93-5p, rno-miR-125b-5p, rno-miR-195-5p
EGCG (1 µM)	rno-miR-22-3p, rno-miR-24-3p, rno-miR-193b-3p, rno-miR-192-5p, rno-miR-22-5p	rno-miR-125a-5p, rno-miR-125b-5p, rno-miR-93-5p, rno-miR-195-5p, rno-miR-20a-5p, rno-miR-17-5p, rno-miR-107-3p, rno-miR-106b-5p, rno-miR-15b-5p, rno-miR-497-5p, rno-miR-505-3p, rno-miR-674-5p, rno-miR-200a-3p, rno-miR-19b-3p, rno-miR-324-3p, rno-miR-204-3p, rno-miR-465-3p, rno-miR-883-3p,
EGCG (50 µM)	rno-miR-204-5p, rno-miR-192-5p	rno-miR-26b-3p rno-miR-19b-3p, rno-miR-26b-3p, rno-miR-204-3p, rno-miR-20a-5p, rno-miR-195-5p, rno-miR-125a-5p, rno-miR-125b-5p, rno-miR-324-3p, rno-miR-497-5p, rno-miR-106b-5p, rno-miR-93-5p, rno-miR-17-5p, rno-miR-465-3p, rno-miR-16-5p, rno-miR-15b-5p, rno-miR-505-3p, rno-miR-883-3p, rno-miR-674-5p