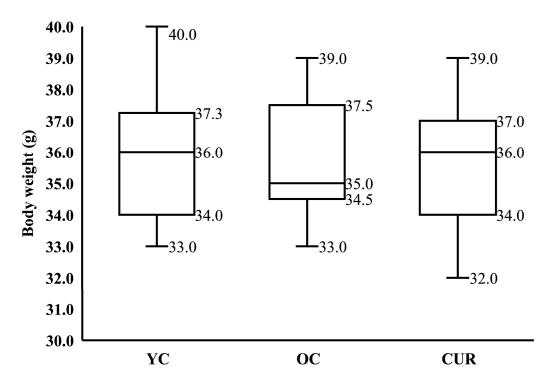
## Uemura et al. Supplementary Table

Supplementary Table 1: Primers used in this study.

Abbreviations: *Actb*, beta-actin; *Tnfα*, tumor necrosis factor alpha; *Defb*, beta-defensin; *Wdr5*, WD40 repeat protein 5; *Traf6*, tumor necrosis factor receptor associated factor 6; *Myd88*, myeloid differentiation factor 88; *IL-1β*, interleukin-1beta.

GENE		sequence (5' to 3')	Tm	Product length	Annealing temperature
Actb	Fw	GATGTGGATCAGCAAGCAGGA	60.41	91	55
NM_001101.5	Rev	AAACGCAGCTCAGTAACAGTCC	61.12		
Defb1	Fw	CCTGGGAGTTTCACATCCTCTC	60.09	124	60
NM_007843.3	Rev	AGAATGCCAACACCTGGCTC	60.61		
Defb2	Fw	TGCTGATATGCTGCCTCCTT	59.16	89	50
NM_010030.2	Rev	GCAGTGGTCAAGTTCTGCTTC	59.73		
Wdr5	Fw	TCCTCCAGTGTCCTTCGTGA	60.18	187	55
NM_080848.2	Rev	AGACACAATCCACTTCCCGC	60.32		
Traf6	Fw	TCCTCATCAGAGAACAGATGCC	59.57	130	55
NM_009424.3	Rev	TCTTGCAAGTGTCGTGCCA	60.15		
Myd88	Fw	CAGTGTCCCACAAACAAAGGAAC	60.43	99	55
NM_010851.3	Rev	GGGCAGTAGCAGATAAAGGCATC	61.36		
Tnfa	Fw	CGTCGTAGCAAACCACCAAG	59.49	149	60
NM_013693.3	Rev	GAGAACCTGGGAGTAGACAAGG	59.50		
IL-1β	Fw	ATGCCACCTTTTGACAGTGATG	59.44	147	55
NM_008361.4	Rev	GCTCTTGTTGATGTGCTGCT	59.12		

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Supplemental Fig. 1. Disclosure of initial mouse weight for group allocation.

Figure shows the weight of mice in each group on the day before the start of treatment (Day 0). The Tukey method was used to ensure that there were no statistically significant differences in allocation in order to homogenize the mean values (p value > 0.05). The median and standard deviation were also disclosed by box-and-whisker plots to show uniformity.

Abbreviations: YC- Young control; OC- Old control; CUR- curcumin administrated.



Supplemental Fig. 2. Distribution and amount of RNA expression in tissues.

The figure shows the number of  $\beta$ -Defensins transcripts per million in salivary gland and small intestine. The data were obtained from the Human Protein Atlas Project (v23.0) (https://www.proteinatlas.org/). These data provide information about the expression levels of  $\beta$ -Defensins transcripts in different organs, aiding in the understanding of the distribution and abundance of these transcripts in various tissues.