Table S1. Preprocessing statistics and quality control of the raw data.

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<th>Q30%</th>
<th>GC%</th>
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Supplemental Figure Captions

Figure S1. Representative elution profiles of tea catechins, gallic acid, caffeine, theobromine and theophylline from oolong tea (1, gallic acid; 2, (-)-gallocatechin (GC); 3, theobromine; 4, EGC; 5, (-)-catechin (C); 6, theophylline; 7, EGCG; 8, caffeine; 9, EC; 10, (-)-gallocatechin-3-gallate (GCG); 11, EGCG3”Me; 12, ECG; 13, (-)-catechin gallate (CG)).

Figure S2. Effect of OTP on body weight in mice fed with HFD for four weeks.
* Indicates significant body weight differences ($P < 0.05$) between different treatments.

Figure S3. LEfSe identified the most differentially abundant taxa in the faecal microbiota of the HFD-induced obesity mouse model. Taxonomic cladogram obtained from LEfSe analysis of 16S rRNA sequencing. (Red) HFD-0 enriched taxa; (Green) HFD-4 enriched taxa; (Blue) HFD-OTP0 enriched taxa; (Purple) HFD-OTP4 enriched taxa (A). The brightness of each dot is proportional to its effect size.

Figure S4. Principal coordinate analysis plot of the faecal microbiota based on the unweighted UniFrac metric.

Figure S5. KEGG analysis of differentially expressed genes between HFD-OTP0 and HFD-OTP4.
Fig. S4
Fig. S5