Metagenomic approach reveals microbial diversity and predictive microbial metabolic pathways in Yucha, a traditional Li fermented food

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The supplementary information including Table S1 and Figure S1

Table S1 The detailed of sequencing information in present research

Sample Name	Barcode	Sequences	Bases (bp)	Average Length (bp)
QZU1	ACGTCG	26636	11978131	449.7
QZU2	GCGTCT	23834	10721289	449.83
QZU3	ACGTGA	26690	12002644	449.71
QZU4	CCGTGC	27994	12591088	449.78
QZU5	GCGTGT	23676	10606551	447.99
QZU6	ACTACA	24646	11041888	448.02
CJU1	GCTACG	25334	11394688	449.78
CJU2	CCTACT	26319	11841518	449.92
CJU3	GCTAGA	22451	10097414	449.75
CJU4	ACTAGC	25000	11223094	448.92
CJU5	CCTAGT	24663	11088415	449.6
CJU6	GCTATC	25076	11279783	449.82
BTU1	CGAGCA	24982	11238509	449.86
BTU2	AGAGCG	23491	10566724	449.82
BTU3	GGAGCT	23060	10309237	447.06
BTU4	AGAGGA	23500	10552342	449.04
BTU5	GGAGGT	27116	12204493	450.08
BTU6	CGAGTC	23543	10591932	449.9
BSU1	GGAGTG	24550	11046171	449.95
BSU2	GGCTCG	25214	11333031	449.47
BSU3	AGCTCT	23987	10779060	449.37
BSU4	GGCTGA	28068	12557767	447.41
BSU5	AGCTGC	24955	11211338	449.26
BSU6	AGTCCA	27612	12424918	449.98

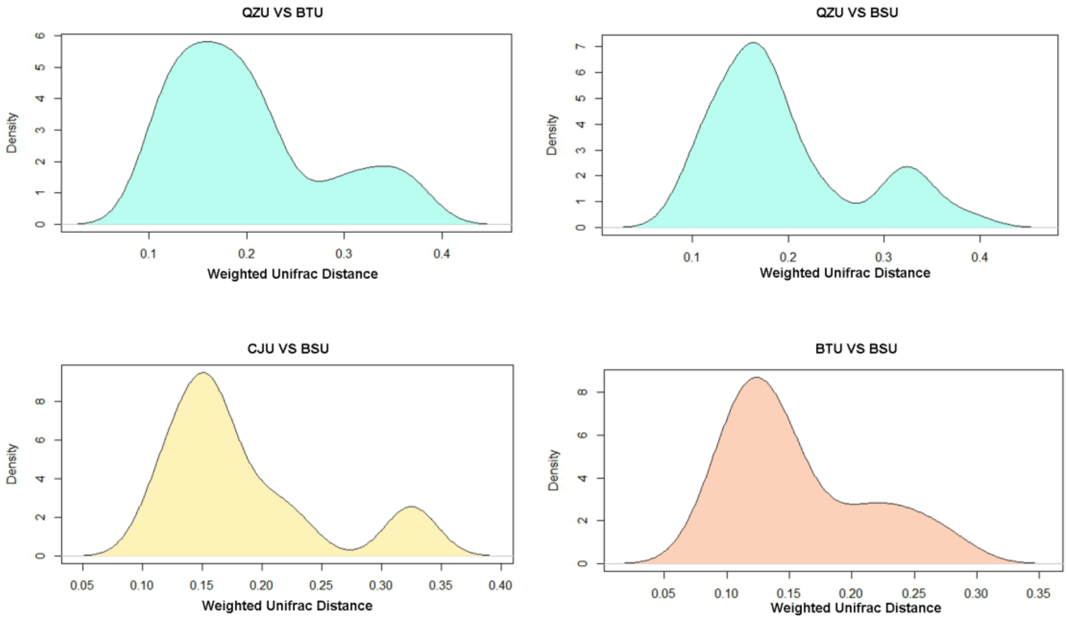

Figure S1 Weighted UniFrac distances between different sample groups.