

# The role of gut-microbiota in Sanfilippo Syndrome physiopathology: an approach in two affected siblings

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**Supplementary Table S2.** Sequences of primers used in this study.

Gene	Forward	Reverse
16S rDNA	AGGATTAGATACCCTGGTAGTCCA	AGGCCCGGGAACGTATTCAC
Sus A	CGTAATGAGCCTTTCGCACG	TTCCTGAATCGGGTTGAGCC
Sus B	TTCCGCTTCTGTACGCAACT	TCATATTCTGTACCGCGGGC
Sus E	AGTGTGGAAAGCACCTCCC	GTAGGGAGTTCTGCCTGCTC
Sus G	CAAACGGGCAGACATCTCCT	TACAGGGGTGGATGGGAGAG
BTH	TGGAGTTTACTTTGAATGGAC	CTGCCCTTTTACAATGGG

**Supplementary Table S3.** Bacterial strains isolated and used in this study.

Strain	Specie	Origin
1	<i>Bacteroides fragilis</i>	MPS III sibling 1 stool
2	<i>Bacteroides thetaiotaomicron</i>	MPS III sibling 2 stool
3	<i>Escherichia coli</i>	Healthy volunteer 1 stool
4	<i>Escherichia coli</i>	MPS III sibling 2 stool
5	<i>Enterococcus faecium</i>	Healthy volunteer 1 stool