

Table S1: primer sequences (mouse mRNA and bacterial DNA)

Gene/product	Forward	Reverse	Amplicon length (bp)	Intron skipping ?	Splicing variants ?
Bcr-Abl	TCCGCTGACCATCAATAAGGA	CACTCAGACCCTGAGGCTCAA	74	no intron	1/1
Cathepsin L	GTGGACTGTTCTCACGCTCAAG	TCCGTCCTTCGCTTCATAGG	129	yes	1/1
CD11b	GTCAGAGTCTGCCTCCGTGT	CCTGCGTGTGTTGTTCTTTG	150	yes	2/2
CD11c	ACGTCAGTACAAGGAGATGTTGGA	ATCCTATTGCAGAATGCTTCTTTACC	190	no	1/1
CD3g	TCTCTACTGGGCTCTCTCAA	CCATCTCCAAGGAAACCAAC	116	yes	1/1
CD68	CTTCCCACAGGCAGCACAG	AATGATGAGAGGCAGCAAGAGG	235	yes	½ (the other is non coding RNA)
Ebi3	AGCAGCCTCCTAGCCTTTGT	GGTAGCGGAGTCGGTACTTG	160	yes	1/1
F4/80	TGACAACCAGACGGCTTGTG	CAGGCGAGGAAAAGATAGTGT	60	yes	1/1
Foxp3	TCCTTCCCAGAGTTCTTCCA	CGAACATGCGAGTAAACCAA	157	yes	3/3
IFN γ	AGCGGCTGACTGAACTCAGATTGTAG	GTCACAGTTTTTCAGCTGTATAGGG	247	no	1/1
IL10	GGACAACATACTGCTAACCGAC	AAAATCACTCTTCACCTGCTCG	256	yes	1/1
IL1b	TCGCTCAGGGTCACAAGAAA	CATCAGAGGCAAGGAGGAAAAC	73	no	1/1
IL6	ACAAGTCGGAGGCTTAATTACACAT	TTGCCATTGCACAACCTTTTTTC	72	yes	1/1
IL17A	AGGCCCTCAGACTACCTCAAC	AGCTCTCAGGCTCCCTCTTC	202	yes	1/1
LC3	CACTGCTCTGTCTTGTGTAGTTG	TCGTTGTGCCTTTATTAGTGCATC	171	no	1/1
Lysozyme 1	GCCAAGGTCTACAATCGTTGTGAGTTG	CAGTCAGCCAGCTTGACACCACG	86	yes	1/1
Muc2	ATGCCACCTCCTCAAAGAC	GTAGTTTCCGTTGGAACAGTGAA	101	no intron	1/1
Occludin	ATGTCCGGCCGATGCTCTC	TTTGCTGCTCTTGGGTCTGTAT	177	yes	1/1
Proglucagon	TGGCAGCACGCCCTTC	GCGCTTCTGTCTGGGA	67	yes	1/1
Reg3g	TTCCTGTCCTCCATGATCAAA	CATCCACCTCTGTTGGGTTC	101	yes	1/1
RPL19	GAAGGTCAAAGGGAATGTGTTCA	CCTTGTCTGCCTTCAGCTTGT	74	no	2/2
Pla2g2a	AAGGATCCCCCAAGGATGCCAC	CAGCCGTTTCTGACAGGAGTTCTGG	167	yes	1/1
Tbet/Tbx21	CAGTGTGGAAAGGCAGAAGG	GGGCTGGTACTTGTGGAGAG	189	yes	1/1
TCF-4	ATGGCAAACAGAGGAACTGG	GCCTGCTGAGAGTGAAGGAG	156	yes	2/2
TNF α	AGCCCCCAGTCTGTATCCTT	GGTCACTGTCCCAGCATCTT	113	no	2/2
ZO-1	TTTTTGACAGGGGGAGTGG	TGCTGCAGAGGTCAAAGTTCAAG	227	no	2/2
Defa (α -defensins)	GGTGATCATCAGACCCCAGCATCAGT	AAGAGACTAAAAGTGGAGCAGC	272/273	These primers recognize several α -defensins. (Gulati et al, 2012)	

Intron skipping: the location of the primers is not indicated as it will be different from one splice variant to another.

Splicing variants: number of splicing variants recognized vs number of splicing variants in the NCBI database (does not take into account the predicted sequences).

Bacteria	Forward	Reverse	References	Tan	Amplicon length (bp)
Bacteria Universal P338F and P518r	ACTCCTACGGGAGGCAGCAG	ATTACCGCGGCTGCTGG	(Ovreas et al, 1997)	60	195
<i>Lactobacillus</i> spp.	GAGGCAGCAGTAGGGAATCTTC	GGCCAGTTACTACCTCTATCCTTCTTC	(Delroisse et al, 2008)	60	125
<i>Lactobacillus reuteri</i>	ACCGAGAACACCGCGTTATTT	ACCTAAACAATCAAAGATTGTCT	(Haarman and Knol, 2006)	59	304
<i>Enterobacteriaceae</i> ECO1457F/ECO1652R	CATTGACGTTACCCGCAGAAGAAGC	CTCTACGAGACTCAAGCTTGC	(Bartosch et al, 2004)	60	193
<i>P.goldsteinii</i> /ASF519	TTGCCGTTGAAACTGGTTGA	GGAGTTCTGCGTGATATCTATGCA	(Cahenzli et al, 2013)	60	90

Tan: Annealing temperature, in Celsius.

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