TABLE S1 Primers used in this study

Primer name	Oligonucleotide sequence (5’→3’)
Over-expression experiments	
pf279-XbaI-F	TATGCTCTAGAATGCGACGTCGCAC
pf279-HindIII-R	TATGCAAGCTTTCACCGGGATTCCC
pf774- XbaI- F	GATCATTCTAGAGTGAGTCGGTCGGGACGG
pf774- HindIII-R	GATCATAAGCTTTCACGCCTCCGCAGAGCC
Inactivation experiments	
KO-*pf279*- XbaI-F	GATCTTTCTAGAAGCCCTCGCTGCTGTCTTGA
KO-*pf279*- BamHI-R	GATCTTGGATCCAGGAGTCGGACAGGCATTCG
KO-*pf774*- XbaI-F	GATCTTTCTAGAGGTTGCGTTCCTGTTGCTGA
KO-*pf774*- BamHI-R	GATCTTGGATCCAGCAGGTTCGCGTCAAGGTT

Underlined sequences indicate the position of restriction sites

FIG S1 ClustalW multiple sequence alignment of 61 to 240 bp of pf279 gene encoding a secreted esterase in 21 wild strains of *Propionibacterium freudenreichii*

```
                        61                                                         120
PFCIRM118_05600         GCCCAGGCCGCACCCGCCAGTGCCGACGGGGGCACCAGTTCCACCCCACGCAGCGTGGCG
PFCIRM123_09055         GCCCAGGCCGCACCCGCCAGTGCCGACGGGGGCACCAGTTCCACCCCACGCAGCGTGGCG
PFCIRM134_10180-        GCCCAGGCCGCACCCGCCAGTGCCGACGGGGGCACCAGTTCCACCCCACGCAGCGTGGCG
PFCIRM456_09555         GCCCAGGCCGCACCCGCCAGTGCCGACGGGGGCACCAGTTCCACCCCACGCAGCGTGGCG
PFCIRM508_01655         GCCCAGGCCGCACCCGCCAGTGCCGACGGGGGCACCAGTTCCACCCCACGCAGCGTGGCG
ITGP9_09195             GCCCAGGCCGCACCCGCCAGTGCCGACGGGGGCACCAGTTCCACCCCACGCAGCGTGGCG
PFCIRM9_06320           GCCCAGGCCGCACCCGCCAGTGCCGACGGGGGCACCAGTTCCACCCCACGCAGCGTGGCG
ITGP23_03080            GCCCAGGCCGCACCCGCCAGTGCCGACGGGGGCACCAGTTCCACCCCACGCAGCGTGGCG
PFCIRM527_10700         GCCCAGGCCGCACCCGCCAGTGCCGACGGGGGCACCAGTTCCACCCCACGCAGCGTGGCG
ITGP18_00520            GCCCAGGCCGCACCCGCCAGTGCCGACGGGGGCACCAGTTCCACCCCACGCAGCGTGGCG
CIRM1-PFREUD_04340      GCCCAGGCCGCACCCGCCAGTGCCGACGGGGGCACCAGTTCCACCCCACGCAGCGTGGCG
PFCIRM513_04955-        GCCCAGGCCGCACCCGCCAGTGCCGACGGGGGCACCAGTTCCACCCCACGCAGCGTGGCG
ITGP20_08925            GCCCAGGCCGCACCCGCCAGTGCCGACGGGGGCACCAGTTCCACCCCACGCAGCGTGGCG
PFCIRM512_02550         GCCCAGGCCGCACCCGCCAGTGCCGACGGGGGCACCAGTTCCACCCCACGCAGCGTGGCG
PFCIRM135_09305         GCCCAGGCCGCACCCGCCAGTGCCGACGGGGGCACCAGTTCCACCCCACGCAGCGTGGCG
PFCIRM122_07375         GCCCAGGCCGCACCCGCCAGTGCCGACGGGGGCACCAGTTCCACCCCACGCAGCGTGGCG
PFCIRM121_09415         GCCCAGGCCGCACCCGCCAGTGCCGACGGGGGCACCAGTTCCACCCCACGCAGCGTGGCG
PFCIRM119_12075         GCCCAGGCCGCACCCGCCAGTGCCGACGGGGGCACCAGTTCCACCCCACGCAGCGTGGCG
LSP108                  GCCCAGGCCGCACCCGCCAGTGCCGACGGGGGCACCAGTTCCACCC-ACGCAGCGTGGCG
CIRM514                 GCCCAGGCCGCACCCGCCAGTGCCGACGGGGGCACCAGTTCCACCC-ACGCAGCGTGGCG
PFCIRM516_06470         GCCCAGGCCGCACCCGCCAGTGCCGACGGGGGCACCAGTTCCACCCCACGCAGCGTGGCG
Clustal consensus       ********************************************** *************

                        121                                                        180
PFCIRM118_05600         ACATCGACGTCGTCCGCTGGCGTGGACCCGGCGTCGGCATGTGGCGACCTGGTGCAGCTG
PFCIRM123_09055         ACATCGACGTCGTCCGCTGGCGTGGACCCGGCGTCGGCATGTGGCGACCTGGTGCAGCTG
PFCIRM134_10180-        ACATCGACGTCGTCCGCTGGCGTGGACCCGGCGTCGGCATGTGGCGACCTGGTGCAGCTG
PFCIRM456_09555         ACATCGACGTCGTCCGCTGGCGTGGACCCGGCGTCGGCATGTGGCGACCTGGTGCAGCTG
PFCIRM508_01655         ACATCGACGTCGTCCGCTGGCGTGGACCCGGCGTCGGCATGTGGCGACCTGGTGCAGCTG
ITGP9_09195             ACATCGACGTCGTCCGCTGGCGTGGACCCGGCGTCGGCATGTGGCGACCTGGTGCAGCTG
PFCIRM9_06320           ACATCGACGTCGTCCGCTGGCGTGGACCCGGCGTCGGCATGTGGCGACCTGGTGCAGCTG
ITGP23_03080            ACATCGACGTCGTCCGCTGGCGTGGACCCGGCGTCGGCATGTGGCGACCTGGTGCAGCTG
PFCIRM527_10700         ACATCGACGTCGTCCGCTGGCGTGGACCCGGCGTCGGCATGTGGCGACCTGGTGCAGCTG
ITGP18_00520            ACATCGACGTCGTCCGCTGGCGTGGACCCGGCGTCGGCATGTGGCGACCTGGTGCAGCTG
CIRM1-PFREUD_04340      ACATCGACGTCGTCCGCTGGCGTGGACCCGGCGTCGGCATGTGGCGACCTGGTGCAGCTG
PFCIRM513_04955-        ACATCGACGTCGTCCGCTGGCGTGGACCCGGCGTCGGCATGTGGCGACCTGGTGCAGCTG
ITGP20_08925            ACATCGACGTCGTCCGCTGGCGTGGACCCGGCGTCGGCATGTGGCGACCTGGTGCAGCTG
PFCIRM512_02550         ACATCGACGTCGTCCGCTGGCGTGGACCCGGCGTCGGCATGTGGCGACCTGGTGCAGCTG
PFCIRM135_09305         ACATCGACGTCGTCCGCTGGCGTGGACCCGGCGTCGGCATGTGGCGACCTGGTGCAGCTG
PFCIRM122_07375         ACATCGACGTCGTCCGCTGGCGTGGACCCGGCGTCGGCATGTGGCGACCTGGTGCAGCTG
PFCIRM121_09415         ACATCGACGTCGTCCGCTGGCGTGGACCCGGCGTCGGCATGTGGCGACCTGGTGCAGCTG
PFCIRM119_12075         ACATCGACGTCGTCCGCTGGCGTGGACCCGGCGTCGGCATGTGGCGACCTGGTGCAGCTG
LSP108                  ACATCGACGTCGTCCGCTGGCGTGGACCCGGCGTCGGCATGTGGCGACCTGGTGCAGCTG
CIRM514                 ACATCGACGTCGTCCGCTGGCGTGGACCCGGCGTCGGCATGTGGCGACCTGGTGCAGCTG
PFCIRM516_06470         ACATCGACGTCGTCCGCTGGCGTGGACCCGGCGTCGGCATGTGGCGACCTGGTGCAGCTG
Clustal consensus       ************************************************************

                        181                                                        240
PFCIRM118_05600         GCGCCGGTGCTGAGTTCCGACCACACGCCCGACGGCAAGCAGATCACGCCGAAGCCCACC
PFCIRM123_09055         GCGCCGGTGCTGAGTTCCGACCACACGCCCGACGGCAAGCAGATCACGCCGAAGCCCACC
PFCIRM134_10180-        GCGCCGGTGCTGAGTTCCGACCACACGCCCGACGGCAAGCAGATCACGCCGAAGCCCACC
PFCIRM456_09555         GCGCCGGTGCTGAGTTCCGACCACACGCCCGACGGCAAGCAGATCACGCCGAAGCCCACC
PFCIRM508_01655         GCGCCGGTGCTGAGTTCCGACCACACGCCCGACGGCAAGCAGATCACGCCGAAGCCCACC
ITGP9_09195             GCGCCGGTGCTGAGTTCCGACCACACGCCCGACGGCAAGCAGATCACGCCGAAGCCCACC
PFCIRM9_06320           GCGCCGGTGCTGAGTTCCGACCACACGCCCGACGGCAAGCAGATCACGCCGAAGCCCACT
ITGP23_03080            GCGCCGGTGCTGAGTTCCGACCACACGCCCGACGGCAAGCAGATCACGCCGAAGCCCACT
PFCIRM527_10700         GCGCCGGTGCTGAGTTCCGACCACACGCCCGACGGCAAGCAGATCACGCCGAAGCCCACT
ITGP18_00520            GCGCCGGTGCTGAGTTCCGACCACACGCCCGACGGCAAGCAGATCACGCCGAAGCCCACT
CIRM1-PFREUD_04340      GCGCCGGTGCTGGGTTCCGACCACACGCCCGACGGCAAGCAGATCACGCCGAAGCCCACT
PFCIRM513_04955         GCGCCGGTGCTGGGTTCCGACCACACGCCCGACGGCAAGCAGATCACGCCGAAGCCCACT
ITGP20_08925            GCGCCGGTGCTGAGTTCCGACCACACGCCCGACGGCAAGCAGATCACGCCGAAGCCCACT
PFCIRM512_02550         GCGCCGGTGCTGAGTTCCGACCACACGCCCGACGGCAAGCAGATCACGCCGAAGCCCACT
PFCIRM135_09305         GCGCCGGTGCTGAGTTCCGACCACACGCCCGACGGCAAGCAGATCACGCCGAAGCCCACT
PFCIRM122_07375         GCGCCGGTGCTGAGTTCCGACCACACGCCCGACGGCAAGCAGATCACGCCGAAGCCCACT
PFCIRM121_09415         GCGCCGGTGCTGAGTTCCGACCACACGCCCGACGGCAAGCAGATCACGCCGAAGCCCACT
PFCIRM119_12075         GCGCCGGTGCTGAGTTCCGACCACACGCCCGACGGCAAGCAGATCACGCCGAAGCCCACT
LSP108                  GCGCCGGTGCTGAGTTCCGACCACACGCCCGACGGCAAGCAGATCACGCCGAAGCCCACC
CIRM514                 GCGCCGGTGCTGAGTTCCGACCACACGCCCGACGGCAAGCAGATCACGCCGAAGCCCACT
PFCIRM516_06470         GCGCCGGTGCTGAGCTCCGACCACACGCCCGATGGCAAGCAGATCACGCCGAAGCCCACC
Clustal consensus       ************ * ***************** **************************
```