Figure S3 A

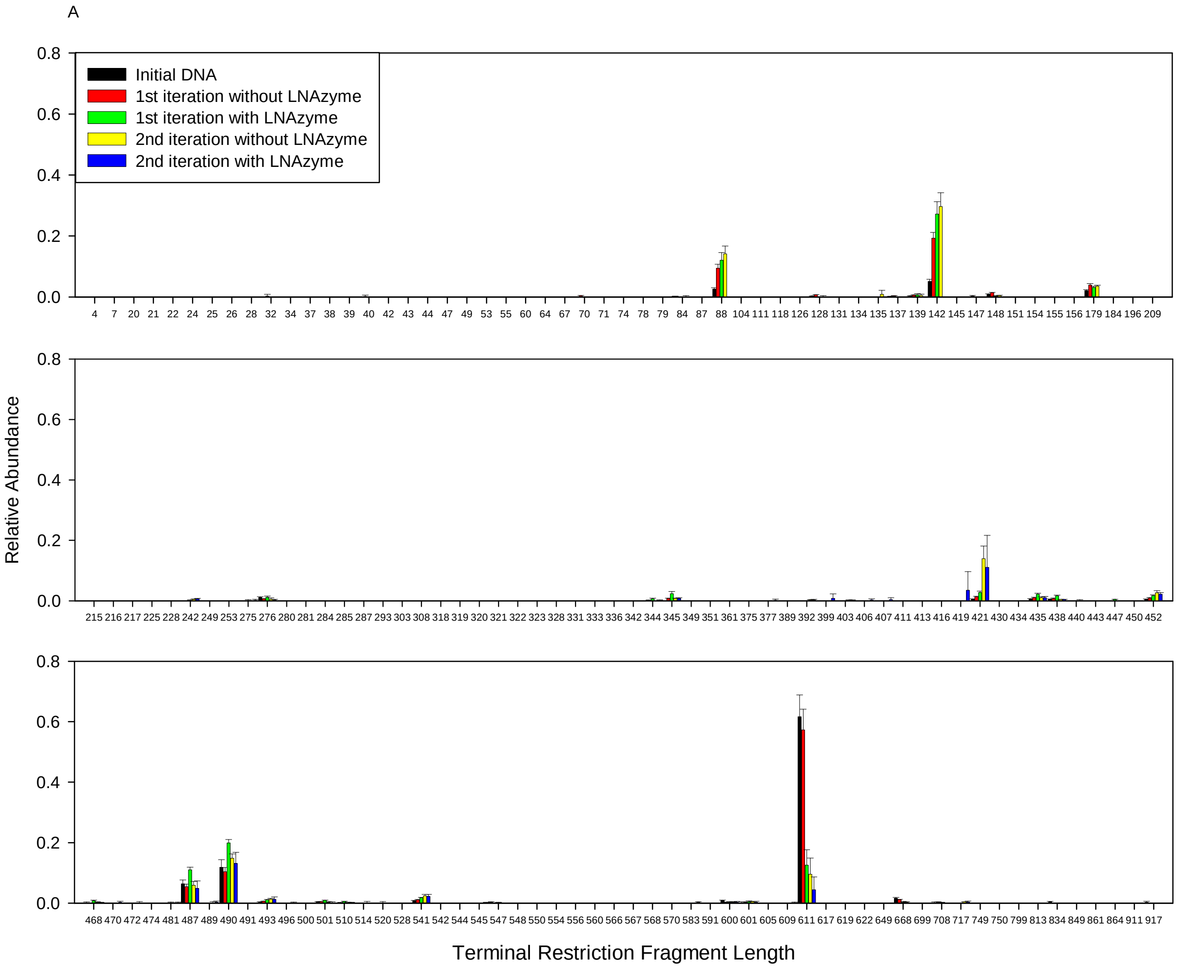
A
Initial DNA
1st iteration without LNAzyme
1st iteration with LNAzyme
2nd iteration without LNAzyme
2nd iteration with LNAzyme
Relative Abundance
0.0
0.2
0.4
0.6
0.8
4 7 20 21 22 24 25 26 28 32 34 37 38 39 40 42 43 44 47 49 53 55 60 64 67 70 71 74 78 79 84 87 88 104 111 118 126 128 131 134 135 137 139 142 145 147 148 151 154 155 156 179 184 196 209
215 216 217 225 228 242 249 253 275 276 280 281 284 285 287 293 303 308 318 319 320 321 322 323 328 331 333 336 342 344 345 349 351 361 375 377 389 392 399 403 406 407 411 413 416 419 421 430 434 435 438 440 443 447 450 452
468 470 472 474 481 487 489 490 491 493 496 500 501 510 514 520 528 541 542 544 545 547 548 550 554 556 560 566 567 568 570 583 591 600 601 605 609 611 617 619 622 649 668 699 708 717 749 750 799 813 834 849 861 864 911 917
Terminal Restriction Fragment Length

Figure S3 B

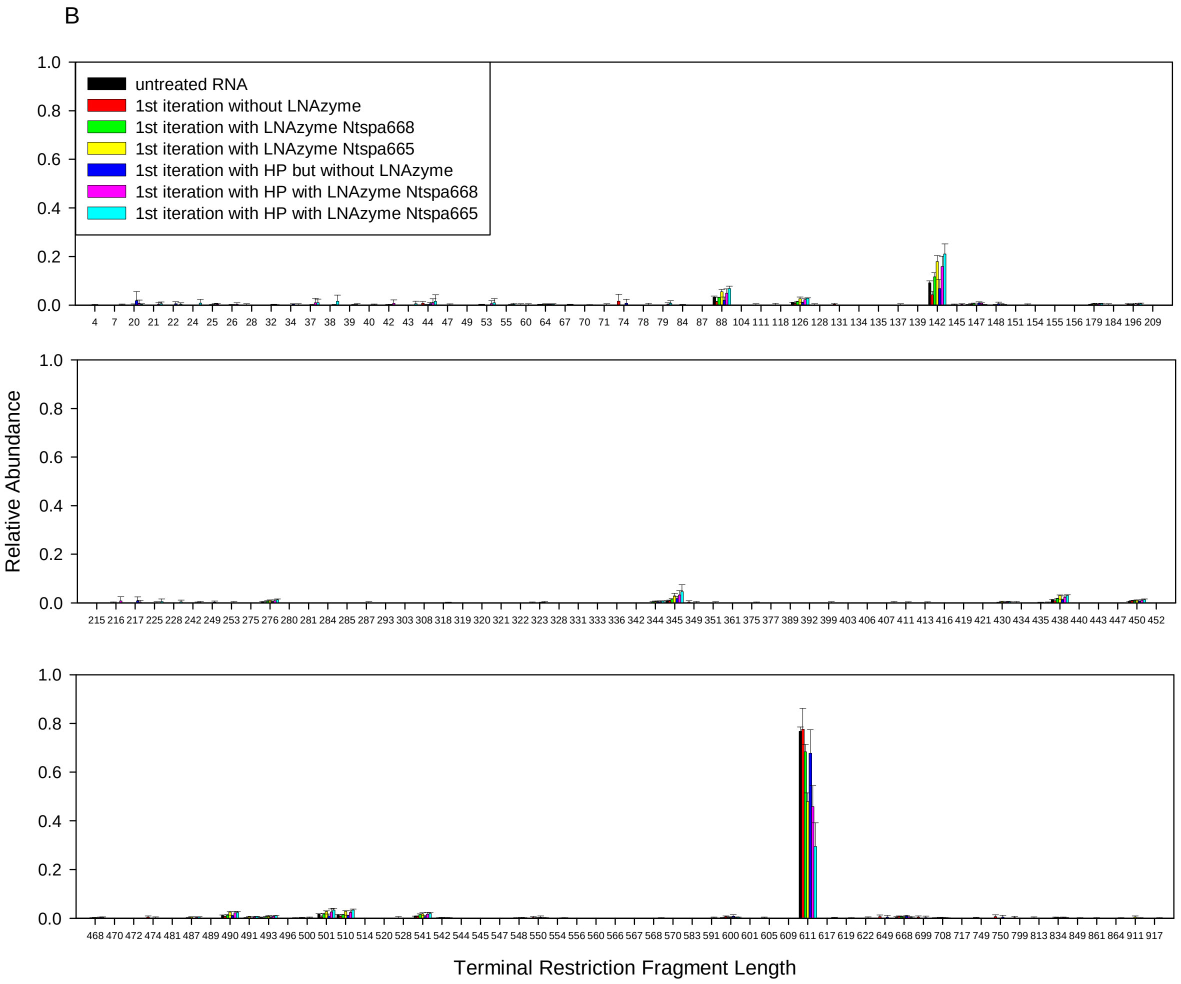

Fig. S3. Depletion of the 16S rRNA of *Ca*. N. defluvii from (A) DNA or (B) native RNA that was extracted from the *Ca*. N. defluvii enrichment culture. The bars show the relative abundances of the 16S rRNA genes of *Ca*. N. defluvii and of other bacteria before and after one or two iterations of the LNAzyme-mediated depletion. Control experiments without added LNAzymes are also shown (the second iteration without LNAzyme was performed after a first iteration with LNAzyme). The relative abundances were determined by T-RFLP analysis. This figure shows the complete T-RFLP profiles, whereas Fig. 4 (main text) contains selected peaks only. Applied LNAzymes were Ntspa668 (panel A) and Ntspa668 or Ntspa665 (panel B, which also shows the effects of additional helper probes on the efficiency of target depletion). HP = helper probes. Error bars depict standard deviations of three replicate experiments.