Supplementary Material:

TABLE 1S: Primers used in this study

Primer	Sequence (5' – 3')
M13_for	CGCCAGGGTTTTCCCAGTCACGAC
T7 promoter	TAATACGACTCACTATAGGG
T3 promoter	ATTAACCCTCACTAAAGGGA
T7 terminator	GCTAGTTATTGCTCAGCGG
M13_20	GTAAAACGACGGCCAGT
M13_rev	GGAAACAGCTATGACCATG
aldR_for	CTATCCGGTTCGGACAAGGACTGG
aldR_rev	ATGAGAAAGTGCGAGCGGTTTGAC
dlhR_for	CATATGATTCCTTCGCATGTTCC
dlhR_rev	AAGCTTGACCTTACGAAGGCTC
hitR_for	GGTTTCTCGACGGTTGAAACTG
hitR_rev	CGTGCTGCAAATGCCTGATG
hydR_for	GCTTCATGTGCACGTCATCG
hydR_rev	AGCACCTGGAGGAGATCGATG
qsdR1_for	CGCCATATGCCGCATGCAGAAACAA
qsdR1_rev	ACTGCTCGAGTGAGTCCCAGACGA
qsdR2_for	CTTTCCGCGGCAAGCGTAAC
qsdR2_rev	CGCATCTCTAACTGGCTCATATGTC

*inserted restriction sites are underlined

TABLE 2S: Putative hydrolases found in NGR234

ORF ID	Annotated/predicted Function	Size of protein (no.of AA)
NGR_c10830	putative hydrolase	208
NGR_c28340	putative esterase/hydrolase	349
NGR_c16700	putative hydrolase	251
NGR_c17080	probable hydrolase	306
NGR_b05590	putative hydrolase or acyltransferase (alpha/beta hydrolase superfamily)	314
NGR_b05410	putative esterase of the alpha/beta hydrolase superfamily	261
NGR_b21240	beta-ketoadipate enol-lactone hydrolase	273
NGR_c08550	putative hydrolase	203
NGR_c04450	putative hydrolase	392
NGR_b15930	probable hydrolase	219
NGR_b14140	putative esterase of the alpha/beta hydrolase fold	205
NGR_c21350	hydrolase of the alpha/beta fold family	318
NGR_c05550	putative hydrolase	221
NGR_c08180	putative hydrolase	300

TABLE 3S: Putative QQ cosmid clones (this study) with their properties and positions

Cosmid clone	Location	ORF ID	Coordinates [bp]*	Insert size [bp]	No. of ORFs
pWEB-TNC-A5	cNGR234	NGR_c35340-NGR_c35730	3 752 569 – 3 793 031	40462	39
pWEB-TNC-B2	pNGR234*b*	NGR_b21920-NGR_b22210	2 252 689 – 2 286 730	34041	30
pWEB-TNC-B9	cNGR234	NGR_c15790-NGR_c16240	1 630 075 – 1 671 235	41160	45
pWEB-TNC-C6	pNGR234*b*	NGR_b16700-NGR_b17020	1 696 835 – 1 734 543	37708	33
pWEB-TNC-G2	cNGR234	NGR_c23130-NGR_c23380	2 397 554 – 2 430 912	33358	26

*orientated to *recA*