Treatment	Stationary phase (µg ml ⁻¹ OD600 ⁻¹)												_	Treatmont	Bacteroids										
Ireatment													_	reatment		(µg g ⁻¹ fresh weight)									
phaZ (NGR_b03370)	0.773 ± 0.020	a												WT		47.6 ± 4.4	a								
riangle phbC1	0.762 ± 0.011	a	b											riangle phaPl		47.3 ± 4.5	a								
WT	0.758 ± 0.020	a	b											phaZ (NGR_b03370)		47.0 ± 6.7	a								
riangle phaP3	0.746 ± 0.063	a	b											$\triangle phbCl$		47.4 ± 10.9	а	b							
$\triangle phbC1C2+C2$	0.721 ± 0.050	a	b	c										$\triangle phbC1C2+C2$		45.0 ± 7.5	а	b							
riangle phaP4	0.709 ± 0.060	a	b	c										riangle phaP2		43.4 ± 9.5	a	b	c						
$\triangle phaP3P4$	0.695 ± 0.063	a	b	c	d									$\triangle phaP2P3+P3$		39.9 ± 2.0	а	b	c	d	l				
riangle phaP1	0.615 ± 0.094		b	c	d	e								$\triangle phaP1P4$		33.1 ± 5.9		b	c	d		e			
$\triangle phaP1P4$	0.538 ± 0.034			c	d	e	f							riangle phaP4		31.3 ± 5.0			c	d		e	f		
$\triangle phaP1P3$	0.529 ± 0.022			c	d	e	f							$\triangle phaP1P2$		30.0 ± 2.4			c	d		e	f		
riangle phaP2	0.516 ± 0.093				d	e	f	g						$\triangle phaP1P3$		27.6 ± 5.0				d		e	f		
$\triangle phaP2P3$	0.464 ± 0.036					e	f	g	h					$\triangle phaP3$		23.8 ± 5.3					G	e	f	g	
$\triangle phaP2P3+P3$	0.375 ± 0.030					e	f	g	h	i	i			riangle phaP2P4		22.1 ± 3.8					(e	f	g	
riangle phaP2P4	0.310 ± 0.024						f	g	h	i	i	j		$\triangle phaP3P4$		14.1 ± 1.1							f	g	h
riangle phaP1P2	0.060 ± 0.004							g	h	i	i	j		$\triangle phaP2P3$		9.8 ± 1.3								g	h
$\triangle phaP1P2P3P4$	0.056 ± 0.002								h	i	i	j		$\triangle phaP1P2P3$		9.4 ± 1.0								g	h
$\triangle phaP1P2P3$	0.045 ± 0.006									i	i	j		$\triangle phbC1C2$		8.0 ± 0.3									h
$\triangle phbC1C2$	0.028 ± 0.002											j		$\triangle phaP1P2P3P4$		7.5 ± 1.4									h
riangle phbC2	0.026 ± 0.002											j	_	$\triangle phbC2$		7.5 ± 0.5									h

Table S1. PHB content of NGR234 and test mutants.

Brown-Forsythe Test (P value < 0.05) rejects the assumption of equal variances. Different letters indicate significant difference between means (average \pm SD is shown; n=9 from three independent experiments) based on multiple comparisons (q value < 0.05, Two-stage linear step-up procedure of Benjamini, Krieger and Yekutieli) after Kruskal-Wallis test.

Treatment	Chlorophyll c (SPAD val	content lue)	Shoot dry we (g/plant)	ight	Number of plants	Number of independent experiments			
Control	22.2 ± 1.2	(*)	0.21 ± 0.01	(*)	45	5			
WT	43.3 ± 1.0		0.34 ± 0.01		47	5			
riangle phaP1	39.7 ± 0.9	(ns)	0.32 ± 0.02	(ns)	19	2			
riangle phaP2	43.1 ± 1.6	(ns)	0.33 ± 0.03	(ns)	19	2			
riangle phaP3	40.3 ± 0.9	(ns)	0.30 ± 0.02	(ns)	20	2			
riangle phaP4	39.7 ± 1.6	(ns)	0.38 ± 0.02	(ns)	20	2			
riangle phaP1P2	40.5 ± 1.4	(ns)	0.26 ± 0.02	(ns)	20	2			
$\triangle phaP1P3$	44.7 ± 1.7	(ns)	0.31 ± 0.02	(ns)	20	2			
riangle phaP2P3	42.9 ± 1.6	(ns)	0.26 ± 0.02	(ns)	20	2			
$\triangle phaP2P3+P3$	41.3 ± 1.2	(ns)	0.28 ± 0.02	(ns)	30	3			
$\triangle phaP1P2P3$	40.0 ± 1.6	(ns)	0.30 ± 0.02	(ns)	20	2			
$\triangle phaP1P2P3P4$	44.8 ± 1.4	(ns)	0.33 ± 0.01	(ns)	29	3			
riangle phbC1	40.7 ± 1.1	(ns)	0.37 ± 0.03	(ns)	19	2			
riangle phbC2	40.0 ± 1.0	(ns)	0.36 ± 0.02	(ns)	28	3			
$\triangle phbC1C2$	40.7 ± 1.1	(ns)	0.24 ± 0.01	(*)	29	3			
$\triangle phbC1C2+C2$	40.6 ± 1.4	(ns)	0.29 ± 0.005	(ns)	30	3			
phaZ (NGR_b03370)	41.3 ± 1.0	(ns)	0.32 ± 0.01	(ns)	20	2			

Table S2. Symbiotic phenotypes of NGR234 and test mutants on Vigna unguiculata.

* and ns, significant and non-significant difference between means of each treatment and wild-type strain (average ± SEM). Duncan's test for chlorophyll content and Kruskal-Wallis test followed by Mann-Whitney test (Bonferroni correction) for shoot dry weight.



Figure S1 Pictures of ultrathin sections of nodules obtained under transmission electronic microscopy. Red arrows indicate PHB granules.

Figure S2 Nodule occupancy by NGR234 and mutants on *Vigna unguiculata*. Values represent means \pm standard error of the mean based on 286~367 nodules per treatment from three independent experiments. *, significant difference between means of wild-type (WT) and indicated mutant (t-test, P < 0.05).

Figure S3. Isolation of PHB associated proteins from NGR234 and strains lacking *phaP1* and/or *phaP2*. (A) The PHB granule layer (located between 1.66 M and 1.33 M sucrose solution). (B) SDS-PAGE of proteins from soluble and insoluble fractions, and those associated with PHB granules from wild-type NGR234. (C) SDS-PAGE of PHB associated proteins from NGR234, $\triangle phaP1$, $\triangle phaP2$ and $\triangle phaP1P2$. Granule-associated protein samples from these strains were used in subsequent nanospray ESI-MS analysis. Three identified phasins are indicated in red.