Table S3. Strains of the Bean Beetles *Callosobruchus* spp. Used in This Study.

Strain	Insect species Original locality	Collection year and collector	PCR of *wsp* and *ftsZ* genes[1]	Infection status based on *wsp*[2, 3]	Description[4]	Transferred genes detected[5]
Callosobruchus chinensis						
jC	Kyoto, Kyoto Japan	1936 T. Uchida	positive	C, O, (A)	A inbred laboratory line established in 1930's; infected with Con and Ori; chromosomal Aus detected.	-
jC^{Aus}			positive	Φ (A)	A tetracycline-treated line derived from jC; no infection; chromosomal Aus detected.	57/205
k10	Kasukabe, Saitama Japan	1998 N. Kondo	positive	C, O	An isofemale line originating from kkC98 population; infected with Con and Ori; chromosomal Aus not detected.	-
k10U2			negative	Φ	A tetracycline-treated line derived from k10; no infection; chromosomal Aus undetected.	40/205
r13	Maruoka, Fukui Japan	1998 N. Kondo	positive	C, O	An isofemale line originating from mrC98 population; infected with Con and Ori; chromosomal Aus undetected.	-
r13U1			negative	Φ	A tetracycline-treated line derived from r13; no infection; chromosomal Aus undetected.	40/205
Rm	Kenting, Taiwan	2004 N. Kondo	positive	O	A mass-rearing line originating from Kenting, Taiwan; infected with Ori; chromosomal Aus undetected.	-
Rm^{tet}			negative	Φ	A tetracycline-treated line derived from Rm; no infection; chromosomal Aus undetected.	31/205
Callosobruchus maculatus						
hQ	Bunkyo-ku, Tokyo Japan	1988 M. Shimada	negative	Φ	A laboratory line of a congenic species; no infection.	0/57
Callosobruchus rhodesianus						
ZH	Zimbabwe	1993 D. Giga	negative	Φ	A laboratory line of a congenic species; no infection.	0/57

[1]Diagnostic PCR detection of *wsp* and *ftsZ* genes by using universal primers as described [Kondo et al. 2002b].

[2]Diagnostic PCR detection of *wsp* gene from Con, Ori and Aus by using specific primers as described [Kondo et al. 2002b].

[3]C, infected with Con; O, infected with Ori; Φ, no infection; (A), chromosomal Aus detected by specific PCR detection of *wsp* gene.

[4]Geographic information of the populations described previously [Kondo et al. 2002b].
[5][Number of genes detected by PCR]/[number of genes subjected to PCR assay].