Table S4. Prediction of tyrosine-phosphorylation sites for Beps of Bep clade 9 using NetPhos2.0 [52], ScanSite [53], and KinasePhos [54]. Except for BARCL_1035, tandem-repeated motifs were detected in all genes of Bep clade 9.

| Locus_tag | Species | Pos. | NetPhos2.0 prediction[a] | | ScanSite prediction[b] | | | KinasePhos prediction[c] | |
			Motif	Score	High	Medium	predicted kinase	100% specificity	predicted kinase
B11C_150019	*B. sp.* 1-1C	255	SSGIYTNYN	0.966	no	yes	Grb2 SH2, Lck kinase	yes	INSR kinase
B11C_150019	*B. sp.* 1-1C	278	SSGIYTNYN	0.966	no	yes	Grb2 SH2, Lck kinase	yes	INSR kinase
B11C_150019	*B. sp.* 1-1C	297	SEEEYSAIY	0.989	yes	yes	Shc SH2, **INSR kinase**	yes	Src kinase
B11C_150019	*B. sp.* 1-1C	317	NEEEYSGIY	0.979	yes	yes	**Fgr**, Lck, INSR kinases, **Shc SH2**	yes	Src, INSR kinases
B11C_150019	*B. sp.* 1-1C	321	YSGIYESYD	0.899	yes	yes	**Src**, Lck kinases, Lck SH2	yes	Syk, INSR kinases
B11C_150019	*B. sp.* 1-1C	340	NEEEYSGIY	0.979	yes	yes	**Fgr**, Lck, INSR kinases, **Shc SH2**	yes	Syk, INSR kinases
B11C_150019	*B. sp.* 1-1C	344	YSGIYANYD	0.923	yes	yes	Fgr, Lck, Src, **Grb2 SH**	yes	INSR kinase
B11C_150019	*B. sp.* 1-1C	363	NEEEYSGIY	0.979	yes	yes	**Fgr**, Lck, INSR kinases, **Shc SH2**	yes	Src, INSR kinases
B11C_150019	*B. sp.* 1-1C	367	YSGIYANCD	0.898	no	yes	Itk SH2	yes	INSR kinase
B11C_150019	*B. sp.* 1-1C	396	NDDIYDNKD	0.987	no	yes	Src kinase	yes	Syk, INSR kinases
B11C_150019	*B. sp.* 1-1C	402	NKDIYDSAN	0.983	no	no	-	yes	EGFR, INSR kinases
B11C_150019	*B. sp.* 1-1C	414	NDDIYDNKD	0.987	no	yes	Src kinase	yes	Syk, INSR kinases
B11C_150019	*B. sp.* 1-1C	420	NKDIYDSAN	0.983	no	no	-	yes	EGFR, INSR kinases
B11C_150019	*B. sp.* 1-1C	432	NDDIYDNKD	0.987	no	yes	Src kinase	yes	Syk, INSR kinases
B11C_150019	*B. sp.* 1-1C	438	NKDIYDNPN	0.99	yes	yes	**Abl**, **Nck**, Crk, Itk SH2	yes	Syk, EGFR, INSR kinases
B11C_150019	*B. sp.* 1-1C	660	KEDDYQTLA	0.991	no	no	-	yes	Syk, EGFR, INSR kinases
BARRO_80017	*B. rochalimae*	4	-MPNYVLVP	0.969	no	yes	PDFGR kinase, PLCg SH2	no	-
BARRO_80017	*B. rochalimae*	253	QEGIYANYN	0.979	yes	yes	Fgr, **Lck**, Abl, Src kinases	yes	INSR kinase
BARRO_80017	*B. rochalimae*	277	NEDIYDTTD	0.986	yes	yes	Lck, **Src**, Abl kinases	yes	Syk, Jak, EGFR, INSR kinases
BARRO_80017	*B. rochalimae*	283	TTDIYDNPD	0.964	yes	yes	**Abl**, Crk, **Nck**, Itk SH2	yes	Syk, INSR kinases
BARRO_80017	*B. rochalimae*	301	EEDIYANYN	0.993	yes	yes	**Fgr**, **Lck**, **Src**, Abl kinases, **Grb2, Itk SH2**	yes	Src, Syk, INSR kinasess
BARRO_80017	*B. rochalimae*	320	NEGEYSDTY	0.986	no	no	-	yes	Srk, EGFR, INSR kinases
BARRO_80017	*B. rochalimae*	324	YSDTYNTTG	0.938	no	no	-	yes	Syk kinases
BARRO_80017	*B. rochalimae*	330	TTGIYENPD	0.927	yes	yes	**Abl**, Lck, Itk SH2	yes	INSR kinase

Locus_tag	Species	Pos.	NetPhos2.0 prediction[a]		ScanSite prediction[b]			KinasePhos prediction[c]	
			Motif	Score	High	Medium	predicted kinase	100% specificity	predicted kinase
BARRO_80017	*B. rochalimae*	350	FSDIYDTTD	0.954	no	yes	Nck SH2	no	-
BARRO_80017	*B. rochalimae*	356	TTDIYDNPD	0.964	yes	yes	**Abl**, Crk, **Nck**, Itk SH2	yes	Syk, INSR kinases
BARRO_80017	*B. rochalimae*	374	EEDIYANYN	0.993	yes	yes	**Fgr, Lck, Src**, Abl kinases, **Itk, Grb2 SH2**	yes	Src, Syk, INSR kinasess
BARRO_80017	*B. rochalimae*	393	NKGEYSDTY	0.973	no	no	-	yes	INSR kinase
BARRO_80017	*B. rochalimae*	397	YSDTYNTTG	0.938	no	no	-	yes	Syk kinase
BARRO_80017	*B. rochalimae*	403	TTGIYENPD	0.927	yes	yes	**Abl**, Lck, Itk SH2	yes	INSR kinase
BARRO_80017	*B. rochalimae*	421	EEDIYANYN	0.993	yes	yes	**Fgr, Lck, Src**, Abl kinases, **Grb2, Itk SH2**	yes	Src, Syk, INSR kinasess
BARRO_80017	*B. rochalimae*	440	NKGEYSDTY	0.973	no	no	-	yes	INSR kinase
BARRO_80017	*B. rochalimae*	444	YSDTYNTTG	0.938	no	no	-	yes	Syk kinase
BARRO_80017	*B. rochalimae*	450	TTGIYENPD	0.927	yes	yes	**Abl**, Lck, Itk SH2	yes	INSR kinase
BARRO_80017	*B. rochalimae*	468	EENIYENYN	0.99	yes	yes	**Src, Lck**, Fgr kinases, **Fgr**, Lck, **Grb2, Itk**, Shc SH2	yes	Src, Syk, INSR kinasess
BARRO_80017	*B. rochalimae*	675	KENDYQTLA	0.98	no	no	-	yes	Syk
BAR15_160030	*B. sp.* AR 15-3	255	DQNIYESYD	0.866	yes	yes	**Src kinase**	yes	Syk, INSR kinases
BAR15_160030	*B. sp.* AR 15-3	285	IDSIYDNPS	0.84	yes	yes	**Abl**, Crk, **Nck SH2**	yes	Syk, INSR kinases
BAR15_160030	*B. sp.* AR 15-3	296	VDPVYANYT	0.929	yes	yes	Abl, Lck kinases, **Grb2**, Itk SH2	no	-
BAR15_160030	*B. sp.* AR 15-3	323	VDPVYDDPS	0.928	yes	yes	Abl kinase, **Nck**, Abl, Crk SH2	yes	Syk kinases
BAR15_160030	*B. sp.* AR 15-3	340	IDSIYDNPS	0.84	yes	yes	**Abl**, Crk, **Nck SH2**	yes	Syk, INSR kinases
BAR15_160030	*B. sp.* AR 15-3	351	VDPVYANYT	0.929	yes	yes	Abl, Lck kinases, **Grb2**, Itk SH2	no	-
BAR15_160030	*B. sp.* AR 15-3	378	IDPVYDDPS	0.908	yes	yes	Abl kinase, **Nck**, Abl, Crk SH2	yes	Syk kinases
BAR15_160030	*B. sp.* AR 15-3	395	IDSIYDNPS	0.84	yes	yes	**Abl**, Crk, **Nck SH2**	yes	Syk, INSR kinases
BAR15_160030	*B. sp.* AR 15-3	406	VDPVYANYT	0.929	yes	yes	Abl, Lck kinases, **Grb2**, Itk SH2	no	-
BAR15_160030	*B. sp.* AR 15-3	433	VDPVYDDPS	0.928	yes	yes	Abl kinase, **Nck**, Abl, Crk SH2	yes	Syk kinase
BAR15_160030	*B. sp.* AR 15-3	450	IDSIYDNPS	0.84	yes	yes	**Abl**, Crk, **Nck SH2**	yes	Syk, INSR kinases
BAR15_160030	*B. sp.* AR 15-3	461	VDPVYANYT	0.929	yes	yes	Abl, Lck kinases, **Grb2**, Itk SH2	no	-
BAR15_160030	*B. sp.* AR 15-3	488	IDPVYDDPS	0.908	yes	yes	Abl kinase, **Nck**, Abl, Crk SH2	yes	Syk kinases
BAR15_160030	*B. sp.* AR 15-3	608	KNPRYKQAK	0.948	no	no	-	no	-
BARCL_1034	*B. clarridgeiae*	14	NSEIYENSE	0.981	no	yes	Src kinase, Fgr SH2	yes	Syk, EGFR, INSR kinases
BARCL_1034	*B. clarridgeiae*	20	NSEIYDNPA	0.983	yes	yes	**Abl, Nck SH2**	yes	Syk, INSR kinasess

| Locus_tag | Species | Pos. | NetPhos2.0 prediction[a] | | ScanSite prediction[b] | | | KinasePhos prediction[c] | |
			Motif	Score	High	Medium	predicted kinase	100% specificity	predicted kinase
BARCL_1034	*B. clarridgeiae*	30	DSGIYDTPA	0.891	yes	yes	**Abl kinase, Nck, Crk**, Abl SH2	yes	Syk, INSR kinases
BARCL_1034	*B. clarridgeiae*	40	NSEIYDNPA	0.983	yes	yes	Abl kinase, **Abl, Nck**, Crk, Itk SH2	yes	Syk, INSR kinases
BARCL_1034	*B. clarridgeiae*	50	DSGIYDTPA	0.891	yes	yes	**Abl kinase, Nck, Crk**, Abl SH2	yes	Syk, INSR kinases
BARCL_1034	*B. clarridgeiae*	60	NSEIYGNPA	0.978	no	yes	Abl, Srk kinases, Abl, Itk SH2	yes	INSR kinase
BARCL_1034	*B. clarridgeiae*	70	DSGIYDTPA	0.891	yes	yes	**Abl kinase, Nck, Crk,** Abl SH2	yes	Syk, INSR kinase
BARCL_1034	*B. clarridgeiae*	80	NSEIYENSE	0.981	no	yes	Src kinase	yes	Syk, EGFR, INSR kinases
BARCL_1034	*B. clarridgeiae*	86	NSEIYGNPA	0.978	no	yes	Abl kinase, Abl, Nck, Crk, Itk SH2	yes	INSR kinase
BARCL_1034	*B. clarridgeiae*	96	DSGIYDTPA	0.891	yes	yes	**Abl kinase, Nck, Crk,** Abl SH2	yes	Syk, INSR kinases
BARCL_1034	*B. clarridgeiae*	106	NSEIYENSE	0.981	no	yes	Src kinase	yes	Syk, EGFR, INSR kinases
BARCL_1034	*B. clarridgeiae*	112	NSEIYGNSA	0.973	no	yes	Src kinase	yes	INSR kinase
BARCL_1034	*B. clarridgeiae*	122	DSEIYENYD	0.983	yes	yes	**Src, Lck, Fgr kinases, Grb2**, Fgr SH2	yes	Syk, INSR kinases
BARCL_1034	*B. clarridgeiae*	128	NYDTYKKNK	0.844	no	no	-	no	-
BARCL_1034	*B. clarridgeiae*	318	RNNEYKLLA	0.84	no	no	-	no	-
BARCL_1032	*B. clarridgeiae*	17	QEVEYTEVH	0.949	no	yes	Fyn, Lck, Src SH2	no	-
BARCL_1032	*B. clarridgeiae*	42	QEVEYAEIR	0.962	no	yes	Lck kinase	no	-
BARCL_1035	*B. clarridgeiae*	16	EEVEYAEVF	0.971	no	yes	Src, Lck, INSR, PDFGR kinase, PLCg SH2	yes	Syk, INSR kinases
BARCL_1035	*B. clarridgeiae*	197	SKPVYMLSR	0.89	no	yes	PCLg SH2	no	-

[a]For NetPhos2.0 predictions a threshold of 0.8 was used.

[b]Scansite was used with the high stringency and the medium stringency filter. Kinases depicted in bold type were predicted with high stringency filter.

[c]For KinasePhos predictions the 100% specificity filter was used.