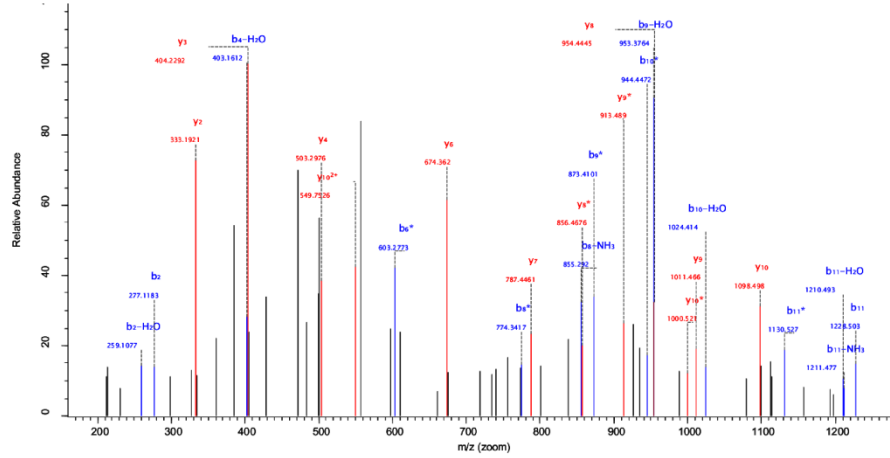
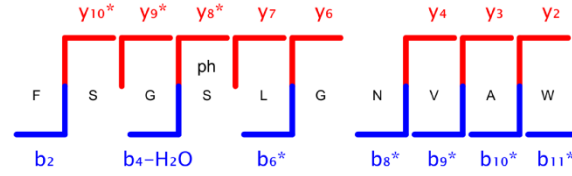
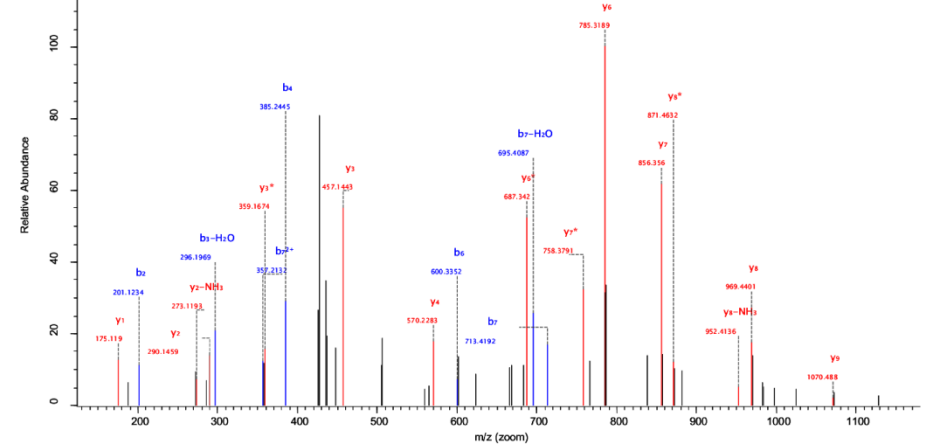
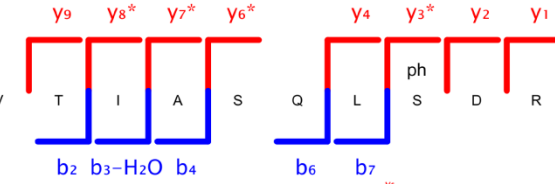


Figure S6

A



B



C

Sequence alignment of the RING-finger Domain and Hypervariable region I across various Bradi species. The alignment shows conserved residues in bold and modified residues in red. Specific regions are highlighted as Transmembrane region I and II. The alignment is as follows:

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BrcESa1 Bradi2g34240.1 - M A A G N G V M A G S H R N R E F V M I R H D G D A P A G K Q A K G V N G O V C O I C C G D V G V S A H G D V F Y A G E C A F P V C R P C Y E Y E R K E G Q C P O C K T R Y K R L K G S P F W Q D E E E D V D D C D N E F N Y K Q G N G K G P E W Q L H G - - - - - Q G E D I D L S S - - - - - S S R 143
BrcESa2 Bradi1g04597.1 - M G C G C G E A S K S R - - - - - K L A G C A C C O I C C G D V G V A D G E L F T A C D V C G F P V C R P C Y E Y E R K E G Q C P O C K T R Y K R K R S P F I R D E S D V D A D A S D L S M P V S G N D R K R H K I P E R I L T W R M N S G T D D V G R - - - - - A K Y S G E I G L P K Y D S G 143
BrcESa9 Bradi4g30540.1 - M E A G A G L V A G S H R N R E L V L I R G H - - - - - E D H K P V R A L S G Q V C E I C C G D E V R T A D G D L F V A G E C A F P V C R P C Y E Y E R R E G C D C P O C K T R Y K R L K G S P F W Q D E E E D I D D E H E F N I D D D Q K R A I Q L H N N S H I T E A M L H G - - - - - R M S Y C R - - - - - A S E D G G E G - - - - - N N T 155
BrcESa4 Bradi2g49912.1 - M M E S G T - - - - - H H P C A C C G D D A R - - - - - A A C R A C S Y A I C R A C L D E D A A E G R T V C A R G G G Y A A F D - T A H G K A S A V E E K E E E E V E D H H A A E G L R G - - - - - R V T I A S - - - - - Q L D 92
BrcESa7 Bradi3g28350.1 - M D T G G E - - - - - P K A I A K A C R A C C G D V L R D G D - O P F V A G E C A F P V C R P C Y E Y E R K E G Q C P O C N T R Y K R L K G S P F W Q D E E D A D D D E E E F Q A K S P K K A A H E P - - - - - A P F D V L S - - - - - E N G E 111
BrcESa8 Bradi1g64260.1 - M D V D A G - A V K S G - - - - - R H G G C G V C T C C G G V G T T A D G - E V F A P G V G G F P V C R P C Y E Y E R K E G Q C P O C K T R Y K R K H K G S P F A T R G E E G D D T A D G - S D F N P A S G T E D E K O K I I A D R M R S W R N H A G S C G D V G S I G L A K Y D - G E I G L S K Y D G G 146
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Transmembrane region I  
BrcESa1 Bradi2g34240.1 H E P H R R P R L T S G Q O L S G D I P D A S P D R S I R S P T S S V V D P S V P V P R I V D P S K - D L N S Y G I N S V D W K E R V E S W R V R K D N M M Q V I N K Y P D A R G G D M E G - - - - - T G S N G E D M Q M D D A R L P L S R I V P I P A N Q L I R R V L R L L L C F L O Y R V T I H P P D A V C L W L V G 307

Hypervariable region I  
BrcESa1 Bradi2g34240.1 E G W I M A D G T A W P G N N R D H P G M I Q V F L G S G G L D T D G E L P R L Y V Y S R E K R P G F Q H H K K A G A M N A L I R V S A V L T N A P E I L N L D C D H Y N N S K A R E A M C F L M D P L G R K I C Y V Q F P O R F D G I A D R D R Y A N R N I V F F D I N M K L G D I G G P V V G T G C F N R Q A L Y G V D P V L 647

Transmembrane region II  
BrcESa1 Bradi2g34240.1 T E A D - - - - - L E F N I V V K S C G G R K K K N K S - - - - - Y M D N K N R M K R T S S A P I F N - - - - - M E D I E E G - I E G V D - E R S L M S Q R L E K R F G S P I F A S T F M T G G G L P P - - - - - S I N P A S L L K E A I H V I S C G Y E D K T E W G K E I G W I Y G S V T E D I 778