

(A)

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> Megabalanus_rosa_Mr-lcp1-122k
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59% coverage
 72% identity

34% coverage
 65% identity

29% coverage
 66% identity

20% coverage
 69% identity

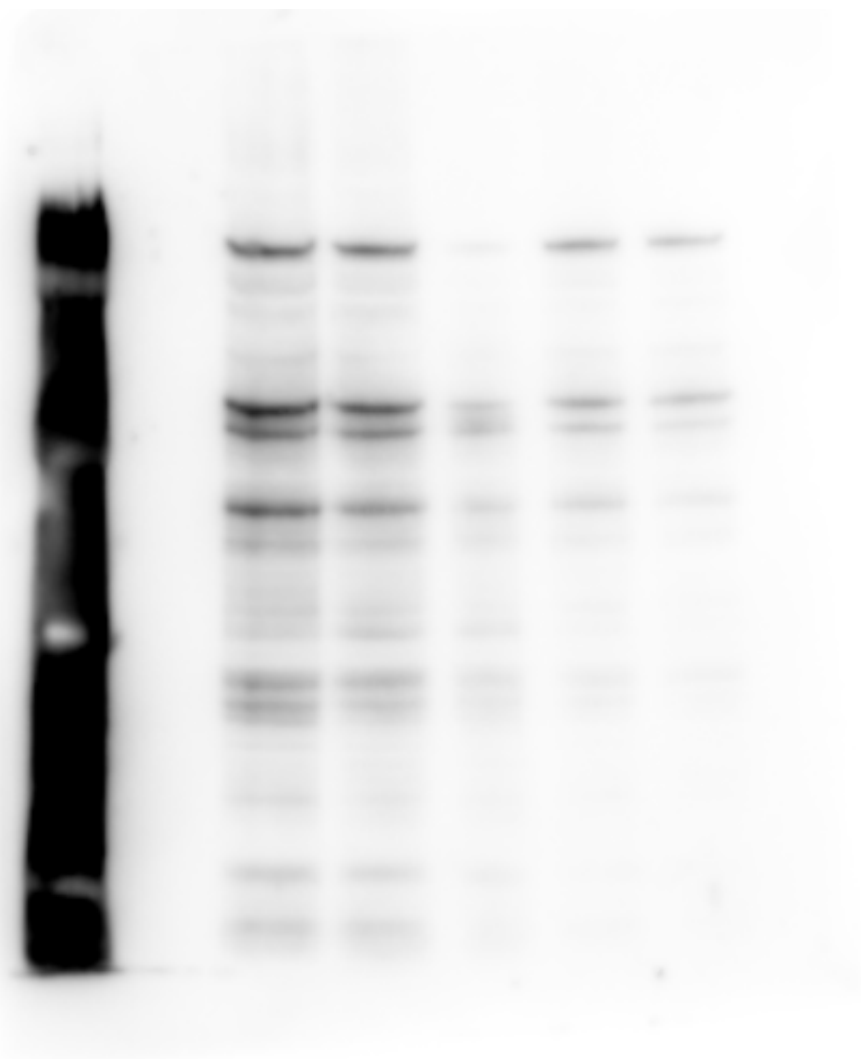
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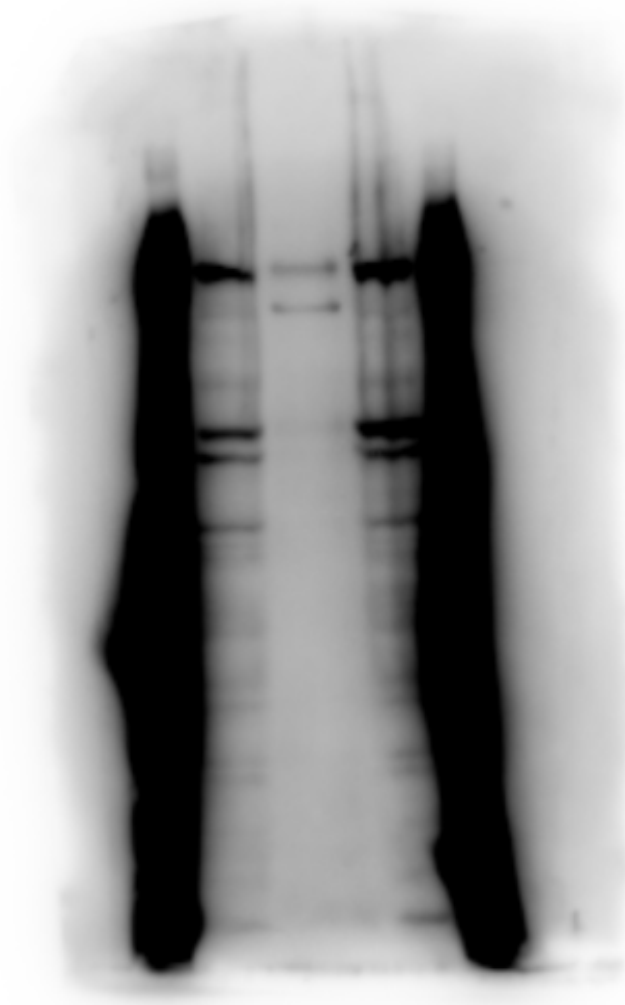
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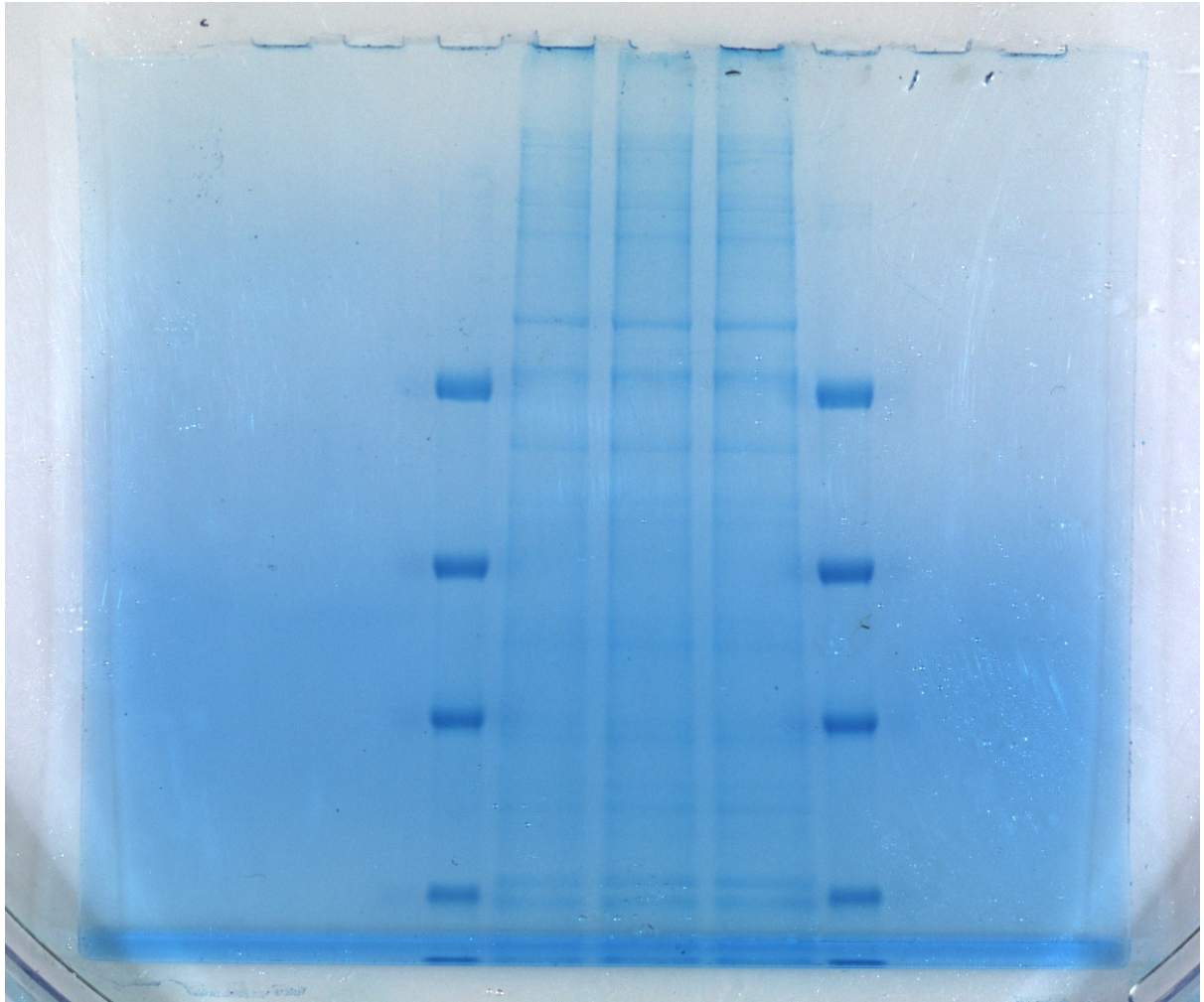
Supplementary Figure 1: Identification of a cement gland-specific Mr-lcp1-122k by MS/MS, and alignment to equivalent sequences in the *B. amphitrite* transcriptome. **A)** MS/MS-generated peptides mapped onto (left) the *M. rosa* full-length sequence and (right) four contigs from the *B. amphitrite* transcriptome. **B)** Mapping of the *B. amphitrite* sequences onto the *M. rosa* sequence. Sequences sharing significant identity are indicated by their colour. The coverage of the respective *B. amphitrite* sequence and its identity match to the equivalent stretch of *M. rosa* sequence are indicated for each *B. amphitrite* contig.



Supplementary Figure 2: A chemiluminescence western blot using wheat germ agglutinin to label whole-cyprid extract, resolved using SDS-PAGE.



Supplementary Figure 3: A chemiluminescence western blot using wheat germ agglutinin to label cyprid cement glands, resolved using SDS-PAGE.



Supplementary Figure 4: An SDS-PAGE gel of whole-cyprid extract immunoprecipitated using wheat germ agglutinin.



Supplementary Figure 5: A chemiluminescence western blot using the chitin-binding domain to label whole-cyprid extract, resolved using SDS-PAGE.



Supplementary Figure 6: A chemiluminescence western blot using an antibody to Mr-lcp1-122k to label whole-cyprid extract, resolved using SDS-PAGE.

Supplementary Table 1: A summary of MS/MS data (Supplementary Data 1 & Supplementary Table 2), produced from WGA-immunoprecipitated cyprid proteins, used to identify 4 contigs from the *B. amphitrite* transcriptome that matched the Mr-lcp1-122k cement gland-specific protein in *M. rosa*.

Representative <i>B. amphitrite</i> contig	Identity with equivalent <i>M. rosa</i> 122 kDa sequence	No. related contigs matched by MS/MS	No. peptides per related contig	Representative contig (column 1) coverage by MS/MS peptides (column 4)
k55_2957215	72 %	4	4;2;2;1	59 %
k75_2477949	65 %	3	3;3;3	34 %
k75_2510032	66 %	3	3;3;2	29 %
K55_979678	69 %	3	3;3;2	20 %

Supplementary Table 2: Amino acid sequence fragments identified by Edman degradation of gel bands, relating to Mr-lcp1-122k.

Band1-PS1	K or R / xLPsNTVstiqqa
Band1-PS2	K or R / LTPGILQAAr
Band1-PS3	K or R / xxglv
Band1-PS4	K or R / AFQPVPYLQY-
Band1-PS5	K or R / FsLTDnef-