

Supplementary Information for

A Mechanism for Temporary Bioadhesion

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Fig. S1. Organization of Lysine-Arginine repeats in Mlig-ap1

(A) schematic illustration of Mlig-ap1 protein sequence. The three Lysine-Arginine rich repeat regions are highlighted in purple-green (KR region A), yellow (KR region B) and red (KR region C). (**B-D**) alignments of the different KR-rich repeats. Diagrams indicate the percentage of amino acids in the repeats. Amino acids are color-coded according to polarity colors: green neutral polar, black neutral nonpolar, red acidic polar, blue basic polar.



Fig. S2. Organization of Repeat A and Repeat B in Mlig-ap2

(A) schematic illustration of Mlig-ap2 protein sequence. Repeat region A is colored in green, repeat region B in purple. (B) alignment of repeat A, (C) alignment of repeat B. Amino acids are color-coded according to Polarity colors: green neutral polar, black neutral nonpolar, red acidic polar, blue basic polar.



Fig. S3. Mlig-ap1 at a glance

Schematic illustration of Mlig-ap1 protein with the isoelectric point of protein regions and domains, location of according transcripts found in the transcriptome MLRNA110815, cloned regions, location of *in situ* hybridization probes and RNAi target sites as well as Antibody binding sites. *aa* amino acids, *C8* domain of 8 conserved Cysteines, *c-Lect* C-type lectin binding domain, *EGF* epidermal growth factor-like domain, *KR region* Lysine-Arginine rich repeat region, *TIL* Trypsin inhibitor-like domain, *vWD* von Willebrand domain.



Fig. S4. Mlig-ap2 at a glance

Schematic illustration of Mlig-ap2 protein with the location of according transcripts found in the transcriptome MLRNA110815, cloned regions, location of *in situ* hybridization probes and RNAi target sites as well as antibody binding sites. *aa* amino acids, *C8* domain of 8 conserved Cysteines, *LDL* low-density lipoprotein receptor-like domain, *TSP-1* Thrombospondin-1-like domain, *TIL* Trypsin inhibitor-like domain, *vWD* von Willebrand domain.



Fig. S5. Multiple *in situ* hybridization probes confirm the expression of both adhesive genes in adhesive organs

Independent transcripts of the MLRNA110815 transcriptome (1) are partial sequences of Mlig-ap1 (red frame) or Mlig-ap2 (green frame) and are expressed in the adhesive gland cells. This panel corroborates the expression of these transcripts in earlier *in situ* hybridization screens (2, 3). *In situ* hybridization with different probes belonging to Mlig-ap1 and Mlig-ap2. (A-F) *in situ* probes generated according to transcriptomic data that target Mlig-ap1 expression (red frame). (G-J) *in situ* probes made using transcripts all belonging to Mlig-ap2 (green frame). Scale bar: 100 µm.





Confocal projection (A-C) control PNA labelling with strong signal in frontal glands in the head region (B) and adhesive glands in the tail plate (C). (D-E) Labelling with PNA pre-incubated with 0.4 M D-galactose. Note that no fluorescent signal can be detected in the frontal glands (E) or the adhesive glands. Dotted white lines indicate the outline of the animals, white stars indicate the region of the eyes. *tp* tail plate. Scale bars: $100 \ \mu m$ (A), $50 \ \mu m$ (B, C).



Fig. S7. Coexpression of Mlig-ap1 and Mlig-ap2

Confocal projection: (A-C) PNA labelling of Mlig-ap2 (green) combined with fluorescence in situ hybridization for *Mlig-ap1* (red). Note that the expression of *Mlig-ap1* RNA is restricted to adhesive gland cell bodies while PNA labels adhesive gland vesicles in the cell bodies and the adhesive gland necks. (D-F) double fluorescence *in situ* hybridization for *Mlig-ap1* (green, in adhesive gland cell bodies) and *macif1* (red, in anchor cells) (4). *agb* adhesive gland body, *agn* adhesive gland neck. Scale bar: 20 µm



Fig. S8. Staining of Mlig-ap1 and Mlig-ap2 with Antibodies

Confocal projections of double labelling with antibodies against Mlig-ap1 or Mlig-ap2 combined with PNA staining. (A-C) antibody binding to Mlig-ap1 KR region B (green) and PNA (red). (D-F) Antibody raised against Mlig-ap1 KR region C and PNA. (G-I) antibody against Mlig-ap2 repeat 1 and PNA. (J-L) Antibody binding to Mlig-ap2 repeat 2 and PNA. For location of antibody binding sites of Mlig-ap1 and Mlig-ap2 see Figs. S3 and S4, respectively. Scale bar: 40 µm.



Fig. S9. Footprint labelled with Mlig-ap1 and Mlig-ap1

Confocal projection of double-labelled footprint with antibody against Mlig-ap1 KR region A (A) and PNA (B). White rectangle in the overlay (C) indicates the area of enlargement (inset). Note the dot-like labelling of Mlig-ap1 surrounding the PNA-positive Mlig-ap2 (white arrowheads). Scale bar: 10 μ m.



Fig. S10. Labelling of footprints after detachment

Confocal projection (A-C), footprints double-labelled with Antibody against Mlig-ap1 and PHA-E (4). (D-F) footprints double-labelled with Antibody against Mlig-ap2 and PHA-E. The lack of PHA-E staining indicated that no glycocalyx of the microvilli remained on the footprint. Scale bars: 20 µm.



Fig. S11. Peptides found in mass spectrometry for Mlig-ap1

Mlig-ap1 protein sequence. Peptides found in mass spectrometry are indicated in grey. To highlight the K-R content, all lysines (K) (except the ones included in the mass spec peptides) are marked in green; all arginines (R) (except the ones included in the mass spec peptides) are labelled yellow.

Mlig-ap2:

GEDGAAEDACRKEIVIHFRGVPRCPTDTRVSIRGRSVRVVOLDTDGRNSSRTVAELRLGGDSEGDDDDDRLPASVPLLLRSFDS LARSCLRDSFVEVAGSAAAYATARRFLLSSRGRDCNSGGRSGAACRDGRAVLSLCHRRCPDRCAALRRLPPLMCALAPLCACAP PRLLDSRGRCVEEAECPCRHGNRIYHRGERFTKDCQTCSCLGNNNWRCASSDCGRVCLATPGQVVTFDGQKISFVDNRNDYYLI EPDDSKIPLAVKFSRSSPARLEVSWQGQQVLVYHRPATDSESGDFFIQLGDRSQKLAIGEHLRVGLGFFLHRVTSHYIRLRVAD LLRVDFNGGTVELAASRRLRGARRLRGLCGRYDGSSENDLWPRRGRAAADSLSVARSYLVKAISPAGGPKRTTISREAVRTCYD LFOHSGOFORCARTENLOPFLRNCEAAGDRDSVCYIAFNAMRLCARSGYKIHWRLLPOLRNCALLACPRGGSSFRLCANTCOAT CASLARPDRCPSGCYFGCQCPRGRYLMADGRCVTKSQCTCFDSATGRQRQPGEKFSRRNENCKCQDGRAVCQAAQSASANGRVA CPKNQVWRRAQPGECWPRRCEDPVKDGSRCQSPDSAAEERCRCPAGLFATDSGLCVNRSDCPCRYGGRELLTGSVLTAQCPGRV GDEIRVLOGRIIAGLRHVDGEAVVLTATAALGGLHFLRIGVSIVWDRGTRLTINAARPRSGOPIGGLCGSFNGDATDDYRTPGG LLALSPDEFGRSWTLESDYAQPIPESEYDQGCLKSRENFDWSFARCGLLRDQRGPFGRCLSVLNEDRLEFLHDACLREACRCRR ${\tt TVKDAANCDGLCNLMAAAADECAGLNVTVDWRSAAFCPYNCPEGTAYTSCGQLQSPFVFANGPDVQCLEDCRCRMGGQWTQAAG}$ SCTEASHVCRYRAAVYQTGDSAKLGCRQCTCREGKWIRCDNKDCYRNTTIELNNLSTVAPCTGHSFACRNSDACLHRSKVCDGV PDCSDGSDEMSCEGCPAFKLKCRRSNLCIAKSEVCDGKHQCRLGNSTDDSDEENCATGATTSAPQKKPIEGTDSCYRPLLQSGL IKESQVRITENFAPTHGYRRAELLDSRKRPYLLSKGRTVFELRLSPAGSAVRVSSVLLQIQSNHRRGLKAIRLYANSNKTWQLL EAKESNIACTRCLIKLNKLPFAAEKLKFKIQSRSSMKIQLEINGCPGQNLESGRCRRLPATACIVKVYKSITYNREYSGEEKSR LVLPRTEYSLLNQGSSEIVIGVPEMVRICAVIIKSKLPSDGKPTANVVSFVYDKKLSELTLVSKLPISTNTTTITISKPTNEYK AVLYSKDPIRISIEIQVKKQPVTKNEPKQQKIACKGSLPDSEVSGKVRVLRMTALDSRQEYTQSDRRQLLRKGAALSSGRTDVL VQFSLKQTDVIEALQVLTTTPGADAKVTARELQLCTRDRCSKVKMSTPSVQQTNMVIRARARFLKIILDSPTSRYAKNAKLKFD FCSRNKPHVCKERYLERCNVPLMKSITFGKRYDAYTVKALLQGRPVRLLRGYTKITLINLNLAESVILKKTGGRRPLKLIISLT TTNERKRKTTITKFDTVYSAKLPTGYTKMIITIKSKEPSKLALFKKECQKPNKIPNREPKTAAHTTTIAPATTTLEPTKRPTTA STAAAKTTKAPVLTTTTKRRRVCKKKMAFDSNVLRPEDVVEVK<mark>RVPQNEPYDEPEKK</mark>SLLPGRRGLPLRK<mark>GDTLVRIDLSRLPE</mark> <mark>GSRVAEIK</mark>VSADKPKRITK<mark>VSVTEVTNNERTPVGK</mark>AEQPGDEPLSRDDLESIPLTPTRRTPDLIEVR</mark>IRRGSKRPVRVTLEVKV TTASTAAAKTTKAPVLTTTTKRRRVCKKKMAFDSNVLRPEDVVEVK<mark>RVPQNEPYDEPEKK</mark>SLLPGRRGLPLRK<mark>GDTLVRIDLSR</mark> <mark>LPEGSRVAEIK</mark>VSADKPKRITK<mark>VSVTEVTNNER<mark>TPVGK</mark>AEQPGDEPLSRDDLESIPLTPTRRTPDLIEVR</mark>IRRGSKRPVRVTLE VKVCLKKKPATTTTQSTTTSATTTRRPSTAGLTTETTRTTRGTPAGEKVTFPMPSITSRKSTGRTTRQKKSTTTAGRSTTSTST KRPTTASTAAAKTTKAPVLTTTTKRRRVCKKKMAFDSNVLRPEDVVEVK<mark>RVPQNEPYDEPEKK</mark>SLLPGRRGLPLRK<mark>GDTLVRID</mark> <mark>LSRLPEGSRVAEIK</mark>VSADKPKRITK<mark>VSVTEVTNNER<mark>TPVGK</mark>AEQPGDEPLSRDDLESIPLTPTRRTPDLIEVR</mark>IRRGSKRPVRV TLEVKVCLKKKPATTTTQSTTTSATTTRRPSTAGLTTETTRTTRGTPAGEKVTFPMPSITSRKSTGRTTRQKKSTTTAGRSTTS TSTKRPTTASTAAAKTTKAPVLTTTTKRRRVCKKKMAFDSNVLRPEDVVEVK<mark>RVPQNEPYDEPEKK</mark>SLLPGRRGLPLRK<mark>GDTLV</mark> <mark>RIDLSRLPEGSRVAEIK</mark>VSADKPKRITK<mark>VSVTEVTNNER<mark>TPVGK</mark>AEQPGDEPLSRDDLESIPLTPTRRTPDLIEVR</mark>IRRGSKRP VRVTLEVKVCLKKKPATTTTQSTTTSATTTRRPSTAGLTTETTRTTRGTPAGEKVTFPMPSITSRKSTGRTTRQKKSTTTAGRS TTSTSTKRPTTASTAAAKTTKAPVLTTTKRRRVCKKKMAFDSNVLRPEDVVEVK<mark>RVPONEPYDEPEKK</mark>SLLPGRRGLPLRK<mark>GD</mark> TLVRIDLSRLPEGSRVAEIK</mark>VSADKPKRITK<mark>VSVTEVTNNERTPVGKAEQPGDEPLSRDDLESIPLTPTRRTPDLIEVR</mark>IRRGS KRPVRVTLEVKVCLKKKPATTTTQSTTTSATTTRRPSTAGLTTETTRTTRGTPAGEKVTFPMPSITSRKSTGRTTRQKKSTTTA ${\tt GRSTTSTSTKRPTTASTAAAKTTKAPVLTTTTKRRRVCKKKMAFDSNVLRPEDVVEVK } {\tt RVPQNEPYDEPEKK} {\tt SLLPGRRGLPLR}$ K<mark>GDTLVRIDLSRLPEGSRVAEIK</mark>VSADKPKRITK<mark>VSVTEVTNNERTPVGKAEOPGDEPLSRDDLESIPLTPTRRTPDLIEVR</mark>IR RGSKRPVRVTLEVKVCLKKKPATTTTQSTTTSATTTRRPSTAGLTTETTRTTRGTPAGEKVTFPMPSITSRKSTGRTTRQKKST ${\tt TTAGRSTTSTSTKRPTTASTAAAKTTKAPVLTTTKRRRVCKKKMAFDSNVLRPEDVVEVK {\tt RVPONEPYDEPEKK} {\tt SLLPGRRGL}$ PLRK<mark>GDTLVRIDLSRLPEGSRVAEIK</mark>VSADKPKRITK<mark>VSVTEVTNNERTPVGKAEOPGDEPLSRDDLESIPLTPTRRTPDLIEV</mark> RIRRGSKRPVRVTLEVKVCLKKKPATTTTQSTTTSATTTRRPSTAGLTTETTRTTRGTPAGEKVTFPMPSITSRKSTGRTTRQK KSTTTAGRSTTSTSTKRPTTASTAAAKTTKAPVLTTTTKRRRVCKKKMAFDSNVLRPEDVVEVK<mark>RVFQNEPYDEPEKK</mark>SLLPGR RGLPLRK<mark>SDTLVRIDLSRLPEGSRVAEIK</mark>VSADKPKRITK<mark>VSVTEVTNNERTPVGKAEOPGDEPLSRDDLESIPLTPTRRTPDL</mark> IEVRINGSKRPVRVTLEVKVCLKKKPATTTTQSTTTSATTTRRPSTAGLTTETTRTTRGTPAGEKVTFPMPSITSRKSTGRTT RQKKSTTTAGRSTTSTSTKRPTTASTAAAKTTKAPVLTTTTKRRRVCKKKMAFDSNVLRPEDVVEVK<mark>RVPQNEPYDEPEKK</mark>SLL PGRRGLPLRK<mark>GDTLVRIDLSRLPEGSRVAEIK</mark>VSADKPKRITK<mark>VSVTEVTNNERTPVGK</mark>AEQPGDEPLSRDDLESIPLTPTRRT PDLIEVR IRRGSKRPVRVTLEVKVCLKKKPATTTTQSTTTSATTTRRPSTAGLTTETTRTTRGTPAGEKVTFPMPSITSRKSTG RTTRQKKSTTTAGRSTTSTSTKRPTTASTAAAKTTKAPVLTTTTKRRRVCKKKMAFDSNVLRPEDVVEVK<mark>RVPQNEPYDEPEKI</mark> SLLPGRRGLPLRK<mark>GDTLVRIDLSRLPEGSRVAEIK</mark>VSADKPKRITK<mark>VSVTEVTNNERTPVGKAEQPGDEPLSRDDLESIPLTP</mark> RRTPDLIEVR RKSTGRTTRQKKSTTTAGRSTTSTSTKRPTTASTAAAKTTKAPVLTTTTKRRRVCKKKMAFDSNVLRPEDVVEVK<mark>RVPQNEPYL</mark> EPEKK<mark>SLLPGRRGLPLRK<mark>GDTLVRIDLSRLPEGSRVAEIK</mark>VSADKPKRITK<mark>VSVTEVTNNER</mark>TPVGKAEQPGDEPLSRDDLE</mark> PLTPTRRTPDLIEVE I TSRKSTGRTTRQKKSTTTAGRSTTSTSTKRPTTASTAAAKTTKAPVLTTTTKRRRVCKKKMAFDSNVLRPEDVVEVK<mark>RVPQN</mark> <mark>PYDEPEKK</mark>SLLPGRRGLPLRK<mark>GDTLVRIDLSRLPEGSRVAEIK</mark>VSADKPKRITK<mark>VSVTEVTNNER<mark>TPVGK</mark>AEQPGDEPLSRDDI</mark> <mark>SIPLTPTRRTPDLIEVR</mark>IRRGSKRPVRVTLEVKVCLKKKPATTTTQSTTTSATTTRRPSTAGLTTETTRTTRGTPAGEKVTFP MPSITSRKSTGRTTRQKKSTTTAGRSTTSTSTKRPTTASTAAAKTTKAPVLTTTTKRRRVCKKKMAFDSNVLRPEDVVEVK<mark>RVF</mark> NEPYDEPEKK</mark>SLLPGRRGLPLRK<mark>GDTLVR IDLSRLPEGSRVAE IK</mark>VSADKPKRITK<mark>VSVTEVTNNER TPVGKAEOPGDE</mark>I DDLESIPLTPTRRTPDLIEVR</mark>IRRGSKRPVRVTLEVKVCLKKKPATTTTQSTTTSATTTRRPSTAGLTTETTRTTRGTPAGEKV ${\tt TFPMPS} {\tt ITSRKSTGRTTRQKKSTTTAGRSTTSTSTKRPTTASTAAAKTTKAPVLTTTKRRRVCKKKMAFDSNVLRPEDVVEVK$ <mark>RVPQNEPYDEPEKK</mark>SLLPGRRGLPLRK<mark>GDTLVRIDLSRLPEGSRVAEIK</mark>VSADKPKRITK<mark>VSVTEVTNNER</mark>TPVGK

continued

<mark>AEQPGDEPLSRDDLESIPLTPTRRTPDLIEVR</mark>IRRGSKRPVRVTLEVKVCLKKKPATTTTQSTTTSATTTRPSTAGLTTETTR ${\tt TTRGTPAGEKVTFPMPSITSRKSTGRTTRQKKSTTTAGRSTTSTSTKRPTTASTAAAKTTKAPVLTTTTKRRRVCKKKMAFDSN$ VLRPEDVVEVK<mark>RVPQNEPYDEPEKK</mark>SLLPGRRGLPLRK<mark>GDTLVRIDLSRLPEGSRVAEIK</mark>VSADKPKRITK<mark>VSVTEVTNNERT</mark>P <mark>VGKAEQPGDEPLSRDDLESIPLTPTRRTPDLIEVR</mark>IRRGSKRPVRVTLEVKVCLKKKPATTTTQSTTTSATTTRRPSTAGLTTE ${\tt TRTTRGTPAGEKVTFPMPSITSRKSTGRTTRQKKSTTTAGRSTTSTSTKRPTTASTAAAKTTKAPVLTTTKRRRVCKKKMAF$ DSNVLRPEDVVEVK<mark>RVPQNEPYDEPEKK</mark>SLLPGRRGLPLRK<mark>GDTLVRIDLSRLPEGSRVAEIK</mark>VSADKPKRITK<mark>VSVTEVT</mark> <mark>R TPVGKAEOPGDEPLSRDDLES I PLT PTRRTPDLIEVR</mark>IRRGSKRPVRVTLEVKVCLKKKPATTTTOSTTTSATTTRPSTAGL TTETTRTTRGTPAGEKVTFPMPSITSRKSTGRTTRQKKSTTTAGRSTTSTSTKRPTTASTAAAKTTKAPVLTTTTKRRRVCKKKMAFDSNVLRPEDVVEVK<mark>RVPQNEPYDEPEKK</mark>SLLPGRRGLPLRK<mark>GDTLVRIDLSRLPEGSRVAEIK</mark>VSADKPKRITK<mark>VSVTEV</mark> NNER<mark>TPVGK</mark>AE<mark>QPGDEPLSRDDLESIPLTPTRRTPDLIEVR</mark>IRRGSKRPVRVTLEVKVCLKKKPATTTTQSTTTSATTTRRPST AGLTTETTRTTRGTPAGEKVTFPMPSITSRKSTGRTTRQKKSTTTAGRSTTSTSTKRPTTASTAAAKTTKAPVLTTTTKRRRVC KKKMAFDSNVLRPEDVVEVK<mark>RVPQNEPYDEPEKK</mark>SLLPGRRGLPLRK<mark>GDTLVRIDLSRLPEGSRVAEIK</mark>VSADKPKRITK<mark>VSV</mark> VTNNER<mark>TPVGK</mark>AEQPGDEPLSRDDLESIPLTPTRRTPDLIEVR</mark>IRRGSKRPVRVTLEVKVCLKKKPATTTTQSTTTSATTTRR PSTAGLTTETTRTTRGTPAGEKVTSPMPSITSRKSTGRTTRQKKSTTTAGRSTTSTSTKRPTTASTAAAKTTKAPVLTTTTKRR RVCKKKMAFDSNVLRPEDVVEVK<mark>RVPQNEPYDEPEKK</mark>SLLPGRRGLPLRK<mark>GDTLVRIDLSRLPEGSRVAEIK</mark>VSADKPKRITK<mark>V</mark> <mark>SVTEVTNNER<mark>TPVGK</mark>AEQPGDEPLSRDDLESIPLTPTRRTPDLIEVR</mark>IRRGSKRPVRVTLEVKVCLKKKPATTTTQSTTTSATT TRRPSTAGLTTETTRTTRGTPAGEKVTFPMPSITSRKSTGRTTRQKKSTTTAGRSTTSTSTKRPTTASTAAARTTNASLLTMKT TKILPSIRVSSRRKTTTTPAPTTTTRRPAVCLRKSVK<mark>LFESGELPSDALTK</mark>AEKLPEKKEFTPKER<mark>KEALLPSGSGLPVKR(</mark> IQLTFQVDRLPK</mark>TASLMKVVLK<mark>SSTPDSVR</mark>EVTVFVADEDKPEK<mark>YVQVNRE</mark>TPKEPK<mark>KALSPSQLENVEFPELPK</mark>LPKFVRVVL KTLPGKATSVRAELKACHKPKTTVRTTQQTTTTTGRTTPSTTSRKPGSPAAEKLTFPMPSMPGATGKTTTTPAPTTTTRRPAVC LRKSVK<mark>LFESGELPSDALTK</mark>AEKLPEKKEFTPKER<mark>KEALLPSGSGLPVKRGGSTQLTFQVDR</mark>LPK</mark>TASLMKVVLK<mark>SSTPDSVRE</mark> <mark>VTVFVADEDKPEKYVQVNRETPKEPK<mark>KALSPSQLENVEFPELPKLPKFVRVVLK</mark>TLPGKATSVRAELKACHKPKTTVRTTQQTT</mark> TTTGRTTPSTTSRKPGSPAAEKLTFPMPSMPGATGKTTTTPAPTTTTRRPAVCLRKSVK<mark>LFESGELPSDALTK</mark>AEKLPEKKEFT PKER<mark>KEALLPSGSGLPVKRGGSTQLTFQVDRLPK</mark>TASLMKVVLK<mark>SSTPDSVREVTVFVADEDKPEK</mark>YVQVNRETPKEPK<mark>KALSP</mark> <mark>SQLENVEFPELPKLPKFVRVVLK</mark>TLPGKATSVRAELKACHKPKTTVRTTQQTTTTTGRTTPSTTSRKPGSPAAEKLTFPMPSMP GATGKTTTTPAPTTTTRRPAVCLRKSVK<mark>LFESGELPSDALTK</mark>AEKLPEKKEFTPKER<mark>KEALLPSGSGLP</mark> <mark>LPK</mark>TASLMKVVLK<mark>SSTPDSVREVTVFVADEDKPEK</mark>YVQVNRETPKEPKKALSPSQLENVEFPELPK<mark>LPKE</mark>VRVIVQILAEMSTN VSLDLFSCQDDFYPCMNCTHNGTSYIEGSIVSLNGVKCDHHVCRKRSWEPLYDCSSWSSWSNCSSECDAGFKTRMKICRSSFRD LIARQNLTSLEKCFNQVEREPCFNRRCSKTECNPAEWGPWSPCSGECSTLLSERKRQPGSAVLSEFCKKVQLPESRLCPKTEKC LCKDPNAAWNNCSNOCPFTCGHLSEOSACVMTSACVPGCACKPGYYLODGRCVPOSOCRCPGLTPTTLAISTTALTTPSTGAAA ${\tt RASMLIPMLPGKPAATPVKPATTATAPTPTTPVRIRGTAAPDGVNLLIPTLSLGSAANTTTMAPSTTVPTTTAAASVSTVASVN}$ GIPAAPSNAATPGAFAPGVTSGSSGSFTVKGFVSPAQGLGKANTMGAFRVTSLLNMKRPPPPPPPPRPGGNHGRFQHSAFRLPPK FHLPAPSGGRPAFRLPGQFKPPPAFRPPGGGSFGKFNPGKPVFRLPGAGSFNPPGKPGTKNSSPSVPHTPAAASPAQPVTPKSS ASTPAPPPGLKPVPSGQQASVAPTKPTTKAPVPMSSQGTRIRGTAADDRVDLRIPTLPNLLPLPTSPRTKLFTKRSTPSTRSMP KTTCVGGHEDSLAAWSTWTAWSNCSAHCGQGKQYRFRQCSGPACVGNGHANESRACTGVDCYCVFSRAKLQWLLTDDYYHAEMW VERDGKPGLSSPLETVNDGDRLESGSVLQVGCLRCTCKDGGFACKLQRCASDCQWSAWQPWATCSATCGGGLQTRLRTIHKPAV ADGAPCQASGFTDTQACNLDPCPGCSWSSWSQWSNCTGSATSDIGVRERRRQPIGSCKEADRDLQPCQLRPAQSKCKPGQLHSA CHNVTGCEVACSAGANARTLCSQTDACLSGCLCPKGQVMGPNGQCVATDKCRCLPKSINCSNCFKPVCLNGQPTCLPDMNCQRL ${\tt YTEWSAWSACSAACGEGLSHRTRQLLQEGRRPAGCGKSDLIETRHCNARPCGYACKDRNGDLYTEGQAMPALDQCSMCFCRANR}$ TECVSKAKVGEPVPTPVWSAWSTWSSCVSAAANNRRQERRRRCVRICPDDPRKCGEFFDKEESVEWKACLPKTPLLKRDCIVSP DWIEGTCYANCMVRSAVARGFRTLYRRILOLPANGGAPCPELRREDVPCTKTCPVDCSOTAWSAWGACVRASNSGCSGLOVRSR GVLVPPANGGRACEDAKQLRSCLAPGCQTSACRAPMTKQPLQQSRCIVRCSDLASEDKCAPVQAANAAAVNATVCACPAGQYEQ DGRCVAKQACRCRWNEELMGQRSPGTREEFAAGERLVMGCKNCTCQDGVFKCNRLSSCSDECHWSNWRPEGKCTAGCRLKPGLQ KFVRSPRNSDYLPTKACQGPSVKYELCSSTRSCDSLCPSGQRYNEFGECDEQCYSAGSLGQPQRQRCPEQACVCARGLVKRGDS CVPKSECYKCSSGNTTLPDGGYSVDLAACQIVTCDKGRTSAVPLSVDQMPACSLEDERIAQSAPKAKDPNRCCYRASASACSRE EVSISKLDDSCLLTSPIRVPHCRGQCPQASPLIAPRRSDVVAAEVAAADSSQVYLLKLPGAHCTGCLPDRVQYSPTTLTVKCKS GESRQLRMPIVGACHCKQVPCPSTA

Fig. S12. Peptides found in mass spectrometry for Mlig-ap2 Peptides identified by Mass Spectrometry. Color code: Footprints Trypsin; Footprints LysC; Footprints V8



Fig. S13. RNAi knock-down of Mlig-ap1 and Mlig-ap2

(A) schematic illustration of Mlig-ap1 protein with location of RNAi probes and different *in situ* hybridization probes. (**B-G**) RNAi experiment for Mlig-ap1. *Mlig-ap1* expression in the tail region shown by three different *in situ* hybridization probes (R1, R2, R4) in control animals (**B-D**) and dsRNA treated animals (**E-G**). (**H**) schematic illustration of Mlig-ap2 protein with location of dsRNA probe and *in situ* hybridization probes (R1, R2, R3). (**I-N**) RNAi experiment for Mlig-ap2. *In situ* hybridization in the tail region against three different regions of Mlig-ap2 in control animals (**I-K**) and dsRNA treated animals (**L-N**). Scale bar: 50 µm.



Fig. S14. Empty adhesive glands after mechanical disturbance of animals

(A, B) ultrastructural analysis (TEM) of adhesive organs immediately after mechanically disturbing animals for 5 minutes in longitudinal (A) and cross section (B). Note that no adhesive vesicles can be found in the tips of adhesive glands. However, vesicles are still present in the cell bodies of the adhesive gland cells (A, black arrows). Notably, other adhesive organs of the same animals exhibited vesicles in the adhesive gland cell tip. *acmv* anchor cell microvilli, *agn* adhesive gland neck, *ep* epidermis, *rgn* releasing gland neck, *rh* rhabdite. Scale bar: $2 \mu m$.





Average number of attachments per minute under different culture conditions (salinity, temperature, and pH). Scale bars indicate SD (n=10).





Fluorescence images of footprints stained with PNA on SAMs with decreasing hydration from EG6 (A) to EG1 (D). White dotted indicate the border from coated to uncoated area. Note that on EG6, EG4 and EG2 footprints can only be found on the uncoated areas (A-C). White stars in C indicate adhering mucus on the EG2 coated area. White arrowheads in D indicate footprints in EG1-coated area. Scale bar: 50 μ m.



Fig. S17. Interference of attachment with sulfated sugars

(A) average number of attachments per minute with 2% of 2-O-desulfated- (2OS-H), 6-O-desulfated- (6OS-H), N-desulfated-re-N-acetylated- (NDR-H) Heparin, and Chondroitin Sulfate (Ch-S), respectively. (B) average number of attachments per minute with 10mM Glucose, 10mM Galactose, 100mM Glycine, and 10μ g/ml PNA added to the ASW respectively. Scale bars indicate SD (n=10).



Fig. S18. Heparin treatment on deposited footprints

Confocal projection of double labelling with Mlig-ap1 antibody (green) and for Mlig-ap2 by Lectin PNA (red) on footprints. (A-C) control footprints. (D-F) footprints were treated with 2% Heparin in ASW. Note that Mlig-ap1 is present - in contrast to footprints where Heparin was added to the medium before footprint collection. Scale bar: $2 \mu m$.



Fig. S19. Labelling of carbohydrates and nitrogen distribution in adhesive gland cells.

Distribution of polysaccharides (A) shown by Periodic Acid-Thiocarbohadrazide- Silverproteinate staining (PAS) (TEM). The staining indicates the presence of carbohydrates in the releasing vesicles (arrows). Glycogen (arrowheads) is stained in the epidermal cell and in the adhesive gland cell. (B) Recording of nitrogen distribution in false color (green) in ultrathin sections by Electron Spectroscopic Imaging (ESI). Comparatively little nitrogen (i.e. reflecting protein) is present in the releasing vesicles (arrows) in relation to the high nitrogen (i.e. protein) content (green) of the adhesive vesicles (asterisk). *acmv* anchor cell microvilli; *agc* adhesive gland cell; *ci* cilium; *ep* epidermal cell; *mv* microvilli; *rgc* releasing gland cell. Scale bars: (A) 1 μ m, (B) 200 nm.

Table S1. Attachment assays

Attachments per minute upon addition of different chemicals to the culture medium. Conditions and concentrations where animals showed an unnatural overall behavior were not counted (labelled with red).

		Ad	he sion w	rithin 1 m	inute						F	F	-	
Category	Individuals	1	2	e	4	2	9	7	8	6	10	Average	STDEV	Comment
ľ	control ASW	2	2	10	∞	5	80	11	5	9	11	7,4	2,5	
ortro	control ASW	10	5	4	4	e	12	5	4	11	7	6,5	3,3	
cor	control ASW	13	6	9	9	11	0	6	12	00	4	8,3	3,1	
	D-Glucose 10-8M in ASW	7	7	10	15	12	8	10	5	3	5	8,2	3,6	
	D-Glucose 10-6M in ASW	4	13	20	6	9	7	9	9	5	œ	7,9	5,1	
	D-Glucose 10-4M in ASW	4	13	4	8	6	3	17	18	14	с	9,3	5,9	
	D-Glucose 10-2M in ASW	2	4	12	14	12	11	5	11	2	∞	8,4	4,1	
	D-Galactose 10-8M in ASW	7	13	∞	6	16	∞	10	11	2	m	8,7	4,2	
	D-Galactose 10-6M in ASW	4	8	2	9	2	11	ŝ	6	13	5	6,6	3,6	
	D-Galactose 10-4M in ASW	12	4	4	12	9	ŝ	2	4	m	-	5,1	3,9	
	D-Galactose 10-2M in ASW	17	7	7	8	11	7	5	0	5	5	7,2	4,4	
sreț	D-Galactose 0.1Min ASW	2	9	6	7	7	5	5	5	9	4	5,6	1,9	
€ns	Glycogen 0,05M in ASW													unnatural behaviour
	PNA lectin 50µg/ml in ASW	2	2	2	4	2	7	4	2	m	80	3,9	2,2	
	PNA lectin 10µg/ml in ASW	7	4	e	e	5	e	1	5	1	2	3,4	1,9	
uit	PNA lectin 5µg/ml in ASW	11	10	4	9	7	2	6	2	m	c	5,7	3,4	
сэл	PNA lectin 500µg/ml in ASW	2	4	4	2	T	T		1	1	T	1,9	1,2 0	unnatural behaviour
	Glycine 1M in ASW													unnatural behaviour
	Glycine 1M in ddH2O													unnatural behaviour
spi	Glycine 0.1M in ASW	15	12	9	4	16	80	11	5	6	6	9,5	4,0	
рĄ	Glutamate 5% in ASW													unnatural behaviour
oui	Glutamate 2% in ASW													unnatural behaviour
mΑ	Glutamate 1% in ASW	16	18	16	7	11	4	6	14	15	7	11,7	4,8	
,	GABA 5% in ASW													unnatural behaviour
itte	GABA 2% in ASW													unnatural behaviour
ws	GABA 1% in ASW													unnatural behaviour
ner:	GABA 0.5% in ASW													unnatural behaviour
noi	GABA 0.25% in ASW													unnatural behaviour
юN	GABA 0.1% in ASW	12	10	4	6	6	12	m	7	14	2	8,2	4,1	
	Antibody Mlig-ap1 R1 1:10 in ASW													unnatural behaviour
s	Antibody Mlig-ap1 R2 1:10 in ASW	12	14	9	∞	6	7	12	15	5	11	6'6	3,4	
dA	Antibody Mlig-ap2 R2 1:10 in ASW	18	7	10	16	5	13	10	9	4	10	6'6	4,7	
	NaCl 33 Promill in ddH2O													unnatural behaviour
вЭ	NaCl 33 Promill + CaCl 1.2% in dd H2O													unnatural behaviour
sa	He parin 0.5% in ASW	m	1	0	0	0	1	1	0	2	0	0,8	1,0	
iter	He parin 1.0% in ASW	2	1	0	1	0	1	0	0	0	0	0,5	0,7	
рĥι	He parin 2.0% in ASW	0	0	0	0	1	0	1	0	0	0	0,2	0,4	
lod.	2-O-desulfates Heparin 2% in ASW	0	0	7	2	1	0	2	0	0	0	0,6	0,8	
iedi	6-O-desulfated Heparin 2% in ASW	e	2	2	2	4	1	0	0	m	2	2,2	1,6	
) bé	N-desulfated Heparin 2% in ASW													unnatural behaviour
ətet	N-desulfated-Reacetylated Heparin 2% in ASW	4	3	4	2	0	3	1	5	1	2	2,5	1,6	
Ins	Chondroitin Sulfate 2% in ASW	0	0	1	0	2	0	0	0	0	-	0,4	0,7	

Table S2. Primer list

Primers used for PCR for *in situ* hybridisation Probe synthesis and dsRNA probe synthesis for Mlig-ap1 and Mlig-ap2.

Mlig-ap1					
Primer Name	FW Primer	RV Primer			
RNA815_13121.1	ACAAGTGGCTCCACCAACA	CTCGAGCGGTTCGTTTCTCT			
RNA815_13121.2	GAGTCACAGTGGCCTCAAGC	ACATGCGACTGTCCTTTTGC			
RNA815_13121.3	TTTCCTAGGCTTGTCAATGTGC	TCAGCTAGGCCTTGACATCG			
RNA815_317.1	AAGGCCAATTGTATCAACAAACG	AAATTTCTTATTGGCGCACTCG			
RNA815_27695.1	AGCGAGGAAGAGTGGACTGAAG	CTATCATGCGCATTTTGGGTAT			
RNA815_27695.2	AGTGGATTGACGAAGGAGAAGC	AAGTTGAGACGGGGCAGTAGC			
RNA815_13121.1b	TCAGGTAGAAAGTTGACGAAGC	GTCAATGATGGTTGTCTCATCG			
RNA815_317.1a	CAGAGGAACGACGGCTACG	AGTCTTTTGGTTTGGTCACAGC			
RNA815_317.1c	CTCTGCGAGGACATCAACG	TGTAGCCGTCTCCATAGTAACC			
Mlig-ap2					
Primer Name	FW Primer	RV Primer			
RNA815_21583	GCGCGTAATAGTTCAAGTTTTGG	ATTCTGGCAGTTGAACTTCTTGC			
RNA815_23142	ACCCAGCTGAAACATCAGATTGAG	CTTGTTGTTTAATCGTCGCACTTG			
RNA815_300	AAGACTACGGACGATTCACAAGC	CGAAGAACTCTCCGCACTTCC			
RNA815_16605a	CTGTGCTGACTACAACCACCAAG	CGATGTCGTAGTACTCTGCGTTG			
Mlig013356.g2-A	CAATACCCGAGTCCGAGTACG	TCAATGGGCTTCTTCTGAGG			
Mlig013356g2-B	CTAACTTCTTTGCCCTGTGAAGC	CCACCTCCACGAAAGAATCG			

Table S3. Advancing and receding contact angles, and ellipsometric thicknesses for the used SAMs.

	Advancing contact	Receding contact	Ellipsometric
SAM	angle (deg)	angle (deg)	thickness (Å)
C16	110 ± 1	106 ± 1	20.8 ± 0.5
MHA	32 ± 2	< 10	22.7 ± 0.4
NH2	35 ± 2	< 10	21.2 ± 0.5
EG1	26 ± 1	15 ± 1	24.4 ± 0.4
EG2	31 ± 1	19 ± 1	26.5 ± 0.3
EG4	33 ± 1	25 ± 1	31.4 ± 0.4
EG6	36 ± 1	23 ± 1	37.7 ± 0.5

Movie S1. adhesive papillae are in contact with surface

Attachment behaviour of control *M. lignano*, squeezing preparation of a life animal with detailed view on the tail plate.

Movie S2. RNAi experiment: control animals adhere strongly to substrate

Live observation of RNAi control *M. lignano* after 9 days of tail regeneration

Movie S3. RNAi experiment: Mlig-ap1 RNAi leads to non-adhesive phenotype

Live observation of Mlig-ap1 dsRNA treated M. lignano after 9 days of tail regeneration

Movie S4. RNAi experiment: Mlig-ap2 RNAi leads to non-adhesive phenotype

Live observation of Mlig-ap2 dsRNA treated M. lignano after 9 days of tail regeneration

Movie S5. RNAi experiment: double RNAi leads to non-adhesive phenotype

Live observation of Mlig-ap1 and Mlig-ap2 dsRNA treated M. lignano after 9 days of tail regeneration

Movie S6. Adhesive organs are used sequentially

Live observation of the attachment in a squeezed animal with detailed view on the tail plate

Movie S7. MgCl2 hinders the release

Live observation of M. lignano in 80% MgCl₂ in ASW

Movie S8. 1-Phenoxy-2-Propanol does not impair the release

Live observation of M. lignano in 0,1% 1-Phenoxy-2-Propanol in ASW

Movie S9. Arginine and Lysine hinder the release

Live observation of M. lignano in 8% Arginine and 3% Lysine in ASW

Datasets D1, D2, D3 (separate files)

Mass spectrometry analyses

Datasets D1 - D3 are Excel files (Mass Spectrometry analyses output) showing peptides found in different mass spectrometry analyses. Single experiments are displayed on different sheets. Mlig-ap1 and Mlig-ap2 are colored in yellow in all files.

References

- 1. Arbore R, et al. (2015) Positional RNA-Seq identifies candidate genes for phenotypic engineering of sexual traits. *Front Zool* **12**:14.
- 2. Lengerer B, et al. (2018) Organ specific gene expression in the regenerating tail of Macrostomum lignano. *Dev Biol* **433**:448–460.
- 3. Weber M, et al. (2018) A targeted in situ hybridization screen identifies putative seminal fluid proteins in a simultaneously hermaphroditic flatworm. *Bmc Evol Biol* **18**:81.
- 4. Lengerer B, Hennebert E, Flammang P, Salvenmoser W, Ladurner P (2016) Adhesive organ regeneration in Macrostomum lignano. *Bmc Dev Biol* **16**:20.