

601 **Supplementary Figure Legends**

602 **Supplementary Figure 1. Strategies, strains and constructs related to Figure 1. A.**

603 Schematic of thermotaxis assays and behavior. (Left) Schematic of the behavioral choice
604 assays used in most studies, in which animals are placed at the middle of the gradient,
605 and allowed to migrate towards their preferred temperature region (shaded grey), where
606 they perform isothermal tracking. (Right) Schematic of the assay using in this study, in
607 which animal start sites (circles) were placed in an “H” configuration and trained to prefer
608 20C (shaded area in middle of assay), as to better capture behaviors of animals
609 performing gradient migration up or down the gradient as they transition into isothermal
610 tracking. **B.** Schematic and sequence information for the *inx-1(ola375)* allele isolated in
611 this study from forward genetic screens. **C.** Schematic of the subtractive labeling
612 strategy to identify the INX-1 site of action. A promoter fragment of 2.5kb can drive
613 expression of *inx-1* cDNA and rescue the observed thermotaxis defects for the *inx-1*
614 mutants, while a promoter fragment of 1.5 kb is insufficient to do so. By creating
615 transcriptional fusions of both promoter fragments, we identified candidate neurons which
616 are uniquely labeled by the rescuing promoter fragment. **D.** Schematic of part of the
617 thermotaxis circuit, highlighting the AIY interneuron position as the primary interneurons
618 downstream of the thermosensory neuron AFD. **E.** Schematic of *inx-1(ola278)* a floxed
619 allele engineered for conditional knockdowns of the *inx-1* gene.

620 **Supplementary Figure 2. Examination of AIY coupling by INX-1, related to Figure 3.**

621 GCaMP6 signal strength over time in clamped AIY (AIY_c) and unclamped AIY (AIY_{uc}) of
622 wild type (A and C) and the *inx-1* mutants (B and D). Shown here are results of individual

623 animals normalized by the peak fluorescent signal of AIY_c. C and D are the same as
624 Figure 3 C and D, and represent the cumulative results of the individual animals.

625 **Supplementary Figure 3. Thermotaxis modeling parameterization and Pearson**
626 **coefficient firing between AIY pairs. A.** Data from a freely moving animal during a
627 straight run, displaying the position of the nose tip (dots) and fit with a sinusoidal curve.
628 **B.** Histogram of the speeds of runs of animals trained at 25C and placed at 20C, and
629 moving up the gradient towards their preferred temperature, with a lognormal fit (in red).
630 **C.** Pearson's coefficient in AIY pairs between wild-type animals (n = 8) and *inx-1(tm3524)*
631 (n = 7). Values are shown as mean ± SE. the asterisks *** denote p < 0.0005 from two-
632 tailed Mann-Whitney test.

633 **Supplemental Movies.**

634 **Movie 1.** Calcium responses of AIYs (ventral view) in wild type animals stimulated by
635 simulated isotherm (+/- 0.01°C oscillations surrounding T_c, 20°C, related for Figure 4D)
636 **Movie 2.** As Movie 1, but in *inx-1(tm3524)* mutants.

637 **Supplemental Strain Table.**

Strain	Genotype	Source
N2	Bristol wild-type strain	CGC
CB4856	Hawaiian wild-type strain	CGC
DCR3056	<i>olals17 [Pmod-1::GCaMP6s (25ng/ul), Ptx-3::mCherry (25ng/ul), Punc-122::dsRed (40ng/ul)]</i> I	(57)
DCR3542	<i>pkc-1(nj1) V; inx-1(ola375) X</i>	This study
DCR3682	<i>inx-1(tm3524) X; olaEx2136[Pinx-1(2.5kb)::INX-1gene::SL2::GFP (10 ng/ul), Punc-122::RFP (35 ng/ul)]</i>	This study

<i>DCR4116</i>	<i>olaEx2390[Pinx-1(2.5kb)::GFP, Pinx-1(1.5kb)::mCherry, Punc-122::GFP]</i>	This study
<i>DCR4466</i>	<i>olals17 [Pmod-1::GCaMP6s (25ng/ul), Ptx-3::mCherry (25ng/ul), Punc-122::dsRed (40ng/ul)] I; inx-1(tm3524) X</i>	This study
<i>DCR4708</i>	<i>inx-1(ola278) X</i>	This study
<i>DCR4984</i>	<i>inx-1(ola278) X; olaEx2943[Pinx-1(2.5kb)::nCRE (25 ng/ul), Punc-122::RFP]</i>	This study
<i>DCR4990</i>	<i>inx-1(ola278) X; olaEx2949[Pinx-1(1kb)::nCRE (25 ng/ul), Punc-122::RFP]</i>	This study
<i>DCR4995</i>	<i>tmls777[Prgef-1::cre, Punc-119::venus]; inx-1(ola278) X</i>	This study
<i>DCR5027</i>	<i>inx-1(ola278) X; olaEx2976[Pce-1::nCRE (25 ng/ul), Punc-122::RFP]</i>	This study
<i>DCR5030</i>	<i>inx-1(ola278) X; olaEx2979[Podr-2b3a::nCRE (25 ng/ul), Punc-122::RFP]</i>	This study
<i>DCR5035</i>	<i>inx-1(ola278) X; olaEx2984[Ptx-3::SL2::nCRE (25ng/ml), Punc122::RFP] #1</i>	This study
<i>DCR5036</i>	<i>inx-1(ola278) X; olaEx2985[Ptx-3::SL2::nCRE (25ng/ml), Punc122::RFP] #2</i>	This study
<i>DCR5043</i>	<i>tmls1091[Ptx-3::nCRE, Plin-44::GFP]; inx-1(ola278) X</i>	This study
<i>DCR5080</i>	<i>olals17 [Pmod-1::GCaMP6s (25ng/ul), Ptx-3::mCherry (25ng/ul), Punc-122::dsRed (40ng/ul)] I; inx-1(ola278) X</i>	This study
<i>DCR5087</i>	<i>olals17 [Pmod-1::GCaMP6s (25ng/ul), Ptx-3::mCherry (25ng/ul), Punc-122::dsRed (40ng/ul)] I; inx-1(ola278) X; olaEx3023[Pinx-1(2.5kb)::nCRE (25 ng/ul), Pmyo-3::RFP]</i>	This study
<i>DCR5108</i>	<i>inx-1(ola278) X; olaEx3041[Pceh-16::nCRE, Punc-122::RFP]</i>	This study
<i>DCR5121</i>	<i>olals17 [Pmod-1::GCaMP6s (25ng/ul), Ptx-3::mCherry (25ng/ul), Punc-122::dsRed (40ng/ul)] I; tmls1091[Ptx-3::nCRE, Plin-44::GFP]; inx-1(ola278) X</i>	This study
<i>DCR5122</i>	<i>olals17 [Pmod-1::GCaMP6s (25ng/ul), Ptx-3::mCherry (25ng/ul), Punc-122::dsRed (40ng/ul)] I; inx-1(ola278) X; olaEx3053[Pinx-1(2.5kb)::nCRE (25 ng/ul), Pmyo-3::RFP]</i>	This study
<i>DCR5281</i>	<i>inx-1(tm3524) X outcrossed 6 times</i>	This study
<i>DCR5282</i>	<i>inx-1(ola278) X outcrossed 5 times</i>	This study
<i>DCR5283</i>	<i>inx-1(gk580946) X outcrossed 4 times</i>	This study
<i>DCR5438</i>	<i>olals17 [Pmod-1::GCaMP6s (25ng/ul), Ptx-3::mCherry (25ng/ul), Punc-122::dsRed (40ng/ul)] I; inx-1(gk580946) X</i>	This study

<i>DCR5790</i>	<i>olals17 [Pmod-1::GCaMP6s (25ng/ul), Ptx-3::mCherry (25ng/ul), Punc-122::dsRed (40ng/ul)] I; olals72 [Pelt-7::mCherry (25ng/ul), Ptx-3::Cx36::mCherry (25ng/ul)]</i>	(57)
<i>DCR7342</i>	<i>inx-1(ola375) X outcrossed 1 time</i>	This study
<i>DCR8285</i>	<i>olals72 [Pelt-7::mCherry (25ng/ul), Ptx-3::Cx36::mCherry (25ng/ul)]; inx-1(tm3524) X</i>	This study
<i>DCR8945</i>	<i>olals17 [Pmod-1::GCaMP6s (25ng/ul), Ptx-3::mCherry (25ng/ul), Punc-122::dsRed (40ng/ul)] I; inx-1(tm3524) X; olaEx5354[Ptx-3::SL2::Cx36::mCherry (25ng/ul), Pelt-7::mCherry (25ng/ul)]</i>	This study
<i>DCR8946</i>	<i>olals17 [Pmod-1::GCaMP6s (25ng/ul), Ptx-3::mCherry (25ng/ul), Punc-122::dsRed (40ng/ul)] I; inx-1(tm3524) X; olaEx5355[Ptx-3::SL2::Cx36::mCherry (25ng/ul), Pelt-7::mCherry (25ng/ul)]</i>	This study
<i>DCR8947</i>	<i>inx-1(tm3524) X; olaEx5356[Ptx-3::SL2::Cx36::mCherry (25ng/ul), Pelt-7::mCherry (25ng/ul)]</i>	This study
<i>FX03524</i>	<i>inx-1(tm3524) X</i>	Shohei Mitani/ NBRP
<i>FX14215</i>	<i>tmls777[Prgef-1::cre, Punc-119::venus]</i>	Shohei Mitani/ NBRP
<i>FX16643</i>	<i>tmls1091[Ptx-3::nCRE, Plin-44::GFP]</i>	Shohei Mitani/ NBRP
<i>IK105</i>	<i>pkc-1(nj1) V</i>	CGC
<i>VC40335</i>	<i>inx-1(gk580946) X</i>	CGC

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639 **inx-1(ola278) sequence (insertions in bold)**

640 gaggcacagttgaaaataaaatttaattcattgtatgtttttcttggggctaaaaatgataaacggtacaaa
 641 actacaaaaaactccataagtcttatttcataattttgaaattttattcaaatgcacaagatccatttatcatatttagttct
 642 tcattcttttttaatatccctttgttttattcggtccatacgtgctctcaactttttcattttgacttaataagaaaaat
 643 ggcataaaaaattggccgaagaggcgatggacggatggaaatctactaaaaggattataactcaatttgatatgctct
 644 tcgggaggatcctcctgacgagatggaaaagaagaagaagaagaagctgtcatcggtcatcgcaaaaga
 645 gacgggtggacattagaccacgccccacagggaaaccttcgagttcatccacccctgtctgttaacatattgtttttcta
 646 gotctattttctccgcctactgcgtactttgcataattctattctaagtctgatcattataagtatcatcctgaacatcgac
 647 ctaaacatcctggc**ATAACTTCGTATAGCATACATTATACGAAGTTAT**cggcacggatgaagta
 648 gtttcattcattgcattgttgcgggaATGCTTCTATATTATCTGGCGGCCATTCAAGGGCTTA
 649 CATCCGCGAGTCGACGACGATTGTGGACAAGCTCAATTACTACTATACTTCTGC
 650 TATTATATTTCGCGTTGCGATTATTGTGTCTGCCAAGCAGTAGCTAGGtaagtctgatttcat
 651 taattcagctctgcgcctacccttcacgttaaaatcaattacttcagGTTATCCGATACAATGTTGGGTG
 652 CCTGCGCAGTTCACCGATGCTGGAACAGTACACCGAAAATATTGTTGGGTGG

696 caagggtggcaaaacgcaatgaatgcctgtgacaggcggctccataaattcattagataaccta
697 attacagAGTCCAATCGAGATGTTGAAGGCAGGTCACTCAGTCACCTAGCAAATT
698 AGACGCCAATTCAAAACGTGGCTCTCGGCCAGACGAGgtgagtcaagatggacacatgt
699 ctgacacgctgacatgtgaaaattgcaaaaatttagacttcagctgtcaacgtttttttcaagt
700 gacgtgatagtaatttgtaaatgtcaaagtatgtatggatgtcgctgttacggcaaaact
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782 ccataaccacgttaattcttcataattcaaaccgtgatttgtctgtactgattccaaccgtgtacacaacaacgcctggctttaa
783 gtgcttctcgccctgaaattttcagattctagaaaattttaggtaacgctgaaagagcctaatttgaacaagtgattgct
784 ggcacgcacattcaggtgaaaacccgatgacgggtgtccataactatgcccttattaataatacattacggctaaac
785 atcctagtcagtgtacgtactagaaggcatgaa

786 **Genotyping protocols**

787

788 Genotyping the *inx-1(tm3524)* X allele:

789 *inx1_tm_F*: GCCTGTCAGTTGCCAAATCT

790 *inx1_tm_R1*: GCAGTGTCCATGTTCCATTG

791 *inx1_tm_R2*: ATGTGTGTCCAGAAGCGATG

792 Anneal at 55°C, elongate for 1 min at 72°C. Run amplified products on a 2% agarose
793 gel. Homozygous wild-type will produce 542bp & 159bp bands, homozygous *inx-*
794 *1(tm3524)* X will produce a single 304bp band, and a heterozygous *inx-1(+/tm3524)* X
795 will produce three bands at 542bp, 304bp & 159bp.

796

797 Primer set for *inx-1* exome sequencing:

798 *ex1_inx1_F*: CGGCACGGATGAAGTAGTTT

799 *ex1_inx1_R*: TTGGTTTCATCTCCCGTTTC

800 *ex1_inx1* product: 576bp

801 *ex2_inx1_F*: AGACGGGAGACCTACGTTGT

802 *ex2_inx1_R*: CCGCAACTTAGCCGATCTTA

803 *ex2_inx1* product: 982bp

804 *ex3_inx1_F*: AAACACGCAATTTCTGCAA

805 *ex3_inx1_R*: CACACACGCACATCCATACA

806 *ex3_inx1* product: 994bp

807 *ex4_inx1_F*: CTGCTGTCTGCTCGCTAATG

808 *ex4_inx1_R*: ACGTGGTCGGGTTAGATGAG

809 *ex4_inx1* product: 250bp

810 Anneal at 55°C, elongate for 1 min 15 seconds at 72°C. Send resulting products for
811 Sanger Sequencing performed by GENEWIZ (Azenta Life Sciences).

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