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Supporting Information

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QIP, a Protein That Converts Duplex siRNA Into Single Strands, Is Required for Meiotic Silencing by Unpaired DNA

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-900 CAACCTTATCCAACCGTTTGCATGACATGCCTTTATCTGATCAGCAGCAGTCATTTTACTTGTGATTAGTCTGTAAGGCCGGCCAGGGAATCGTCTTTT
 -800 CCCTTCACAGGAATTGCCATTTCTCCTCTTTGCCAAGTGGGGTCTTTAATCAACACTTACTTATTGTTCCGTCCTTTGTGAACCTACAGTGGGGCA
 -700 CCTGTAGGCCTCATACCTGACCTCAAATCGTACCACCTCAACGGGTAGTTGCGATTCTGTTCACTTATCTGTGATCGCTCCTCCATTTTCGTCCTTT
 -600 CTAGTGTCTGTTGGGAGCCTCCACTGACGCGCCGCTCACTCGACCTCCGCGTTGGTTGAAGTACTGCTCAAGACCATTATCACTTGAAGAATT
 -500 AAGGAGCCTAAATCCGTTTCACTAAGTACCTGACCAATCTGAACAAAATAGGTTTTCCGGATGAGAAGTTTGGCCACTATCCAGGGCTCCCATTCACCTCCATTG
 -400 TGCTGCCTAAGGACTATTTATATTTCCCTCGCTCACCTCTTCCGAAATATCTATCCCTCCCGGACAATCGCTTCCGCGAAGCCTCCGCCAGCA
 -300 ACGACAACCGCCTACGACTCGCGGAGCCCACTTCGTTCAAGCGACGCTTTTCTTCCCTTCAATTCGCATCCTACCTACGACAGTAAAGTGAAT
 -200 ATCGTAGCAGAGACCTAGGCTGAGATCTCCATTTGCCGAAAACGTCCTTCCAGATCAGCCGCCCTCATATTGCTGGCCATACCCACACCCGA
 -100 GAGACATACCAGATCAAGATTAGAATCGCCGGCTGCACTTCTGTCGAAGGCTAAGTATCTTACTGCTCCTAACCAGAACTATCGCTCGCCACC
 1 ATGGAGGACGAGCAGTTCATGCAACAGCTGCGGAACCTTACCTGCCAGACTGTGACTGGAGCGGATTTCGATCCTTCAAGTGGCGGACGAAAGACATCA
 M E D E Y Q L F M Q Q L R N L T C A Q T V D W S G F D P S K W R D E D I 33
 101 ATGATGGGACATTAGTGTAGCGCCAGGGTGTAGGAGCAGCAATTAATGATCCGACGCTTCTATCCTGAGCGCCGCTTGGATCCCTTTAAGCT
 N D W D I S D D A Q G D E D D N Y A S D A S I L S A R H L D P F N V 67
 201 CAAACCTGCTACTGCCCTCACCATACTGCCCTACCTCCTTGGCATTGAGGACGTGACCGACGACGAGGAAGAGTACCGCGATGCTTCGGACTTGGAG
 K P A T R P H H T G P T S L R I E D V T D E Q E E Y R D A S D L E 100
 301 AACATCAGTGGCCAGAAGTCAAGTGGAGCAGGGGAGATCGATCCATTACAGAACTCTTACTCCCTGGAGAATGGTTCTGGAGTATCCCAACCTGT
 N I S W P E V S V E Q G E I D P I T E L F T P W R M V L E Y P N L 133
 401 TTGTTGGCAAGCGAACGGCGGAGG *GTGAGACCCATCATCGCAGTATGGATGAGTGTGACGCTAACAGTTCTGCCAAGGCTCGGCTCTTTTACGC*
 F V G K R N G A R A R P L F T 148
 501 TCGAGCGCTACACGAAAACCGCATATGGGATCT *GTAAGAGTTGAGGTCTTATCGGGTGTGAGTCCACGACACTGTGTTAACACGCTCCAGATTCTACC*
 L E S L H E N R I W D L F Y 162
 601 TCTACCGCGCTCCAACGAGGGGAACAATACTTGTATCTTCTGCCAACCTACCAGATGCAGCACCTACTCGAGCTATAAACAGAAAACCTTGACGT
 L Y R P S N E G N N N P L I F V P T Y Q M Q H L L D V I N R K L D V 196
 701 AGAGTTCAGTTCCTCCTCGCGGACATCAAGACATGTTCCGATGCCATTTGGGAGAGTAATACAGCGAAAACCGGATTCTTGGCCGTTCCAGATCGCC
 E F T F P R G H Q D M F A M P F G Q S N T A K P R F L G R S R S A 229
 801 GAGGAATGGAAGCAGCTTACGAACAACGTCGCCGCGTAAGCCGGAGACAGTCCGAAAATGCTCCTTCCCTTCCCAAGCAGGAGCTCACACGCCGT
 E E W K Q L T N N V P A R K P G D T S E N A P F L A K Q E L T R R 262
 901 TGAACAGCATCTTTCAATCCAAGACAAGAGCAAGAAGACCAAGAACAACAGTACAAGCAAGCAATCTTACCAGCCTGGGGAAAAATATCAAGAG
 L N S I F S I Q D K S K K T K N N Q Y K R S N L H R A W G K N I K R 296
 1001 GGTTCAGCGGTATCTCGGCTTCCGCGCAGAGTTTATCTGACCCGGAAGTGTATCATATACCCCGCTGGATCTACCCAGCCTACTGGCATCCAGCGC
 V Q R Y L G L R R R V L S D P E V S Y T P L D L T Q P T G I Q P 329
 1101 GAGAAGTGTGCTGTTGTGGCGATTGACCTTGAAGGCTTATGACTGGACCAAAGCATATACCAGGTCGCGCTGGCAATCTTGTATACCCGCGGAGA
 E K S V V F V A I D L E A Y E L D Q S I I T E V G L A I L D T A E 362
 1201 TCACAAATGTTGCTCCTGGTGAAGGCAGCAAGAACTGGTTCGACTTCATCAAGCAGCAGATATTCGCGTCAAGGAGTTTTCTGGGGCCAAAACCTCCAG
 I T N V A P G E G S K N W F D F I K A R H I R V K E F S W A Q N S R 396
 1301 GCATGTCCAAGGCGCCGAATACTTTGACTTTGGGTATGTGTATCTATCCCTATCCTTGGCCCTGTCCTTGGCCAAAACCGAAAACCGAATTACTA
 H V Q G R A E Y F D F G 408
 1401 *ACAATGTCCAGCGAGAGCAGTTCATCGAGTTCGCGAAGATCGCCAGCGTTCTGAAGGAGACCATCGAGGAGAGTCTCCATCGGTGGTGGGGAGCAA*
 E S E F I E V A K I A S V L K E T I E G E S S I G G E G A 437
 1501 AGCGCCCGTGGTCTTGTATCCACGACCAATCTCAAGATCTCAAATACATTCGCATGCTTGGCTATGATGTGGCCAGCGCGACAACATTTTGGAGGT
 K R P V V L V F H D Q S Q D L K Y I R M L G Y D V A S A D N I L E V 471
 1601 GGTAGACACTCGAGAGATGTACCAGTATCTCAGCCGTTCAAGCAACGCCTCAAACCTTTCGAATGTTTGTGGTACCTCGACATTCCTGGAAAGCAATG
 V D T R E M Y Q Y L S R S N N A S K L S N V C G Y L D I P W K N M 504
 1701 CACAACGCTGAAAATGACGCGGTCTACTCTTCAAGCCATGATGGCTTGGCCATTGACATCGCGCAGAGAGCTTGGAGAGGGCTGCTCGAAGGCTT
 H N A G N D A V Y T L Q A M M G L A I D M R Q K S L E R A A A K A 537
 1801 CAAAGCGAATACGAGTAAAGTCTTCAAGAAAGGCGCACAGCGCGGACGAAGTGTGATATAATCATGTTTCTTTTAGTAACGATGGTTACGTTACTT
 S K A N T S N D G Y V T 549
 1901 ACTCTGAATTCACCGCAGCAAGGAGGACGTGATGAGGGTGGATCAGCACCGGGAGCTGTCTGATGGTGGCAACCAAGCTTGGTATGGCGCGAG
 Y S E F T A T K E D V D E G W I S T G E L S D G G E P S L V M A A S 583
 2001 CACCGTCCCTAATCCGTCGTTGAGACTACTGTGTGAAAACCTGGGAGTTGTAATGGCTATGAGACTACCATATTTCCACCACCACTGCCAGGGCGTA
 T V P N S V V E T T V C E N W E L * 600
 2101 GGTGTACTGGGAAAAGTTAGCTGATAAACTGGAGTCAAGCAAGGCAAGGGGCACAGGCGGCAAGAAAAGGTGAAAAGGCTGCACTCCAGCCAAAG
 CGAGCATCAAACAGCATCTGGCAATGTTGTAACGCGCATCATAGTCTACGGCGTGTATACAGTAAAAGGAGAACCGCTAAACTATTCAGTCCATGT
 2201 GGCACAGAACACAATAATCGTATTGGTCTAATATTTTACATGGGTATGTTATTCAAGTTGTGCAAAAGCTACAAAAGCCTCCTACTTTTTTCCATCC
 2301 AAGCCACCCGCAAGCAAAAACCGTCAACGCCAGTGTATGAAGAACCATATGTGTGTTTTTGTGTAAGAATAGGGTAAGGAGCTTGTCTGAGGC
 2401 CAATGTGTAGTAGCAGCGGTATCATCATGGCGTAGGTCTTTCTGATCGAACTCTGCTCTGCTCGCGGCTCAGGCTTACGAGATGCTGCTGTAATC
 2501 GAGTACCGCAGTGTCCGCTAGCAGTGTGACGACTACCGTAGCCGAGCTGCATACCCCAACCACTCAGCCCACTGAGGCGACACTGGTATCGTCGTA
 2601 ACAGACAACTCGAGCTGGAGTTGGAGAGTGGTGAAGGATGCAATCTGATTGTTGCTGTGTAAGACTCCAGAGACTCTAGACTCGCTCTCAC
 2701 AGTTCATCTGTCGAGATCGATCAAATTAATCGCTCGCATGGCGTTGACTGCATCGAGCAGGATTGGACCGAACAGATTGATCGGTCAACGAGATCAAT

FIGURE S1.—The nucleotide and amino-acid sequence of *qip* (NCU00076). The intron sequences are italicized. The DNA sequence listed here corresponds to the reverse complement of nucleotides 2528149-2531948 of *N. crassa* supercontig 3 (<http://www.broadinstitute.org/annotation/genome/neurospora/MultiHome.html>).

TABLE S1**Primers used in this study**

Primer	Sequence (5' to 3')	Amplification of
Act-507F	507 CGTTGGTTCGTCCTCCCGTTATCATG 529	cDNA spanning <i>actin</i> intron 4
Act-811R	811 TGGGAGCCTCGGTAAGAAGGACG 789	cDNA spanning <i>actin</i> intron 4
Gfp-t-hph-F1	GGGGCA-3060 GGAGCTGGTGCAGGCGCTGGAGCCAT 3035	<i>gfp-hph</i>
Gfp-t-hph-R1	331 GCCCTTGTTAACTGATATTGAAGGAGCAT 359	<i>gfp-hph</i>
Qjp-298792R	313 CCAGAAGTCAGCGTGGAGCAG 333	cDNA spanning <i>qip</i> introns 1-4
Qjp-297127F	1978 GTTCGCCACCATCAGACAGCTC 1957	cDNA spanning <i>qip</i> introns 1-4
Qjp-299824R	-720 GTGAACTC- <u>TCTAGA</u> -GGGGCACCTGTAGG -693	<i>qip</i> for frameshift construction
Qjp-296819F	2286 GTTTA- <u>GCGGCCGC</u> -CCTTTTCACTGTATACAC 2256	<i>qip</i> for frameshift construction
Qjp-299128R	-24 CTA- <u>ACTAGT</u> -CTATCGCTCGCCACCAT 2	<i>qip</i> for <i>gfp</i> fusion ¹
Qjp-297035F	2070 GTAGTCTCAT- <u>TTAATTAA</u> -CAACTCCCAGTTTTTC 2038	<i>qip</i> for <i>gfp</i> fusion ¹
Qjp-A	793 GATCTGCCGAGGAATGGAAGCAG 815	<i>qip</i> left flank for <i>gfp</i> fusion ²
Qjp-gfp1	CAGCGCCTGCACCAGCTCCTGCCCC- 2052 CAACTCCCAGTTTTTCACACACAGTAGTC 2025	<i>qip</i> left flank for <i>gfp</i> fusion ²
Qjp-gfp2	CTCCTTCAATATCAGTTAACAAGGGC - 2219 CTGGCAATGTTGTAACGCGCATC 2241	<i>qip</i> right flank for <i>gfp</i> fusion ²
Qjp-B	3322 TGTTTCAGTCCGCCTTGTCTGTTGT 3300	<i>qip</i> right flank for <i>gfp</i> fusion ²
Sad1-A	5420 ATACACGCACAAGCGATGGCAAG 5441	<i>sad-1</i> left flank for <i>gfp</i> fusion ²
Sad1-gfp-1	CAGCGCCTGCACCAGCTCCTGCCCC- 6372 AAGCGCCGCCATCTGTGCATAAC 6350	<i>sad-1</i> left flank for <i>gfp</i> fusion ²
Sad1-gfp-2	CTCCTTCAATATCAGTTAACAAGGGC- 6630 CCCCATCCTCATCTTCCATCACC 6652	<i>sad-1</i> right flank for <i>gfp</i> fusion ²
Sad1-B	7923 CACTACCTCGAATCCCCACCAA 7901	<i>sad-1</i> right flank for <i>gfp</i> fusion ²
Sms2-107713F	107713 CTCTTGCCCTCAACCAGTACC- <u>ACTAGT</u> -ATGTCTGCTCCTGG 107752	<i>sms-2</i> for <i>rfp</i> fusion ¹
Sms2-110724R	110724 GCCAAAGCGACCAAG- <u>TCTAGA</u> -CCCACCACATGGTGTGTTGTG 110685	<i>sms-2</i> for <i>rfp</i> fusion ¹

Restriction sites, including *NotI* (GCGGCCGC), *SpeI* (ACTAGT), *PacI* (TTAATTAA), and *XbaI* (TCTAGA) are underlined. Nucleotide positions for *qip* are numbered according to Figure S1. ¹*his-3* integration. ²Native integration.