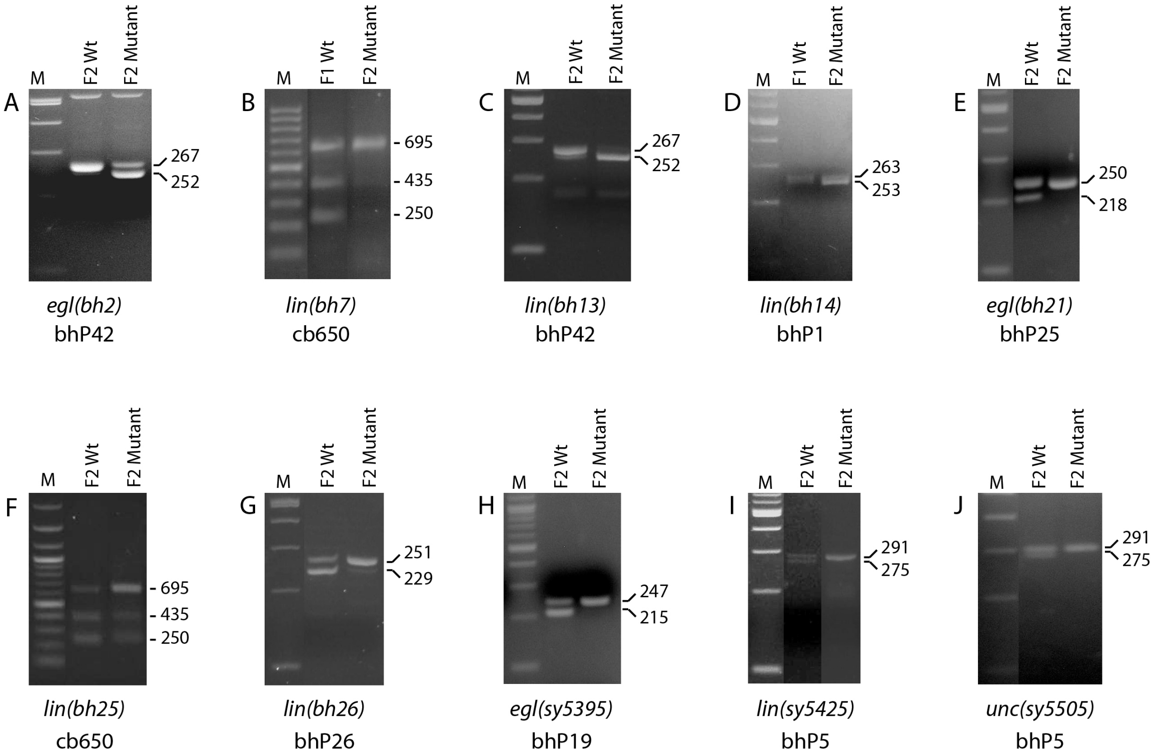

**Figure S1** Mutation mapping using indel and snip-SNP polymorphisms. The images show DNA bands on 4% (for indels) and 1% (for snip-SNPs) agarose gels. The polymorphisms have been previously described (KOBOLDT *et al.* 2010). See Materials and Methods and Table 3 for details. M: DNA molecular weight marker, F1 Wt: DNA from F1 heterozygous animals, F2 Wt: DNA from phenotypically wild type pool of F2 animals, F2 Mutant: DNA from phenotypically mutant pool of F2 animals.

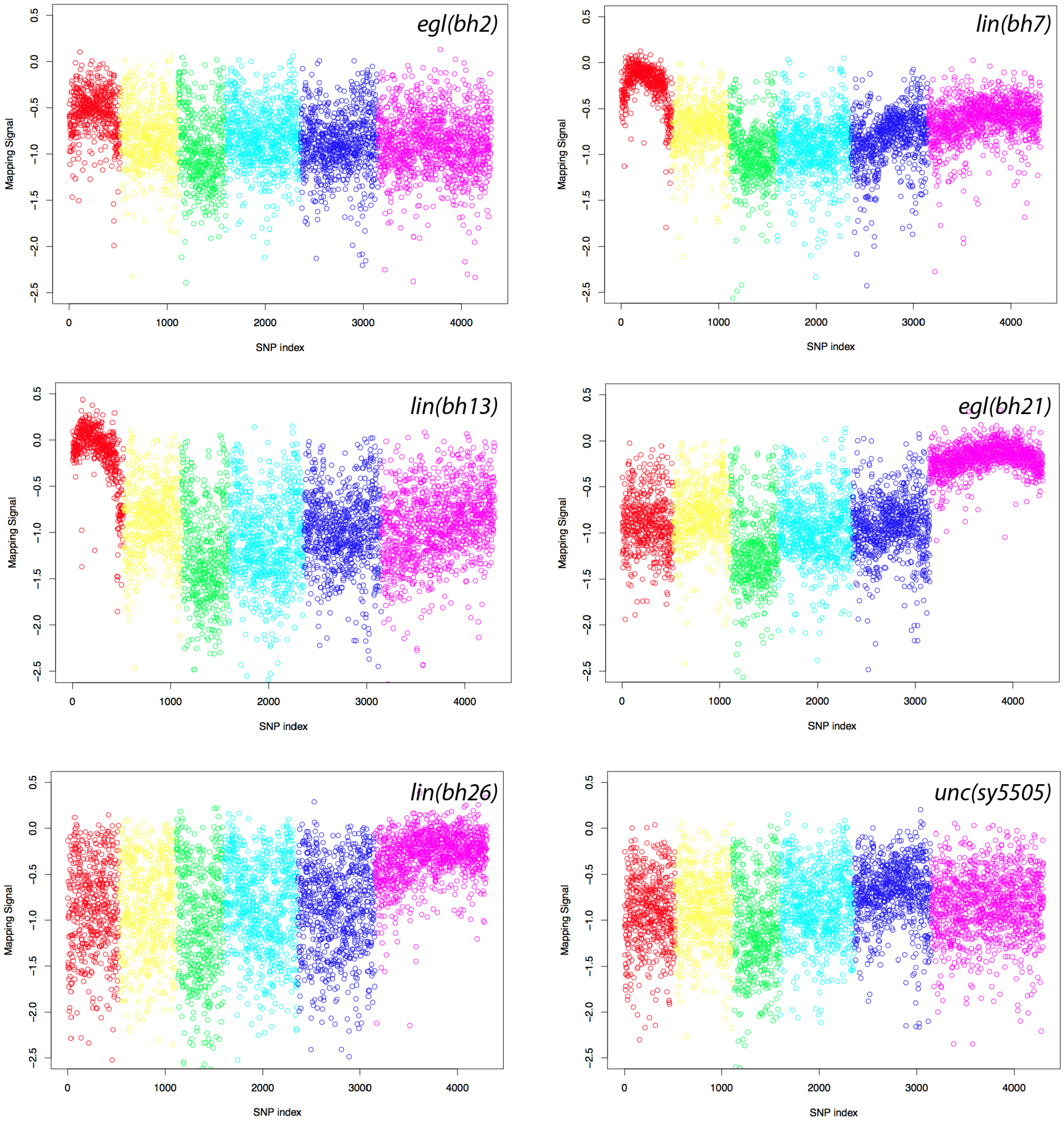

**Figure S2** Mutation mapping using SNP-chip. Each tiny colored circle represents the mapping signal for a single SNP. Chromosomes are color coded (starting from 1 to 5 and X, in that order). See Materials and Methods and Zhao et al. study (ZHAO *et al.* 2010) for details.

## *Cbr-lin-11* cDNA sequence (1239 bp)

```
   1  ATGCATTCTT  CTTCGTCCAT  CATCACCACC  CTGGAAGAAG  AAGAGAAGAA  GCCTCCTGCT
  61  CATCTTCATC  AATATCATCA  TCATCTTCAT  CAACAGTCAG  TAGAAGACGT  CGGAAGTGCC
 121  ACCTCATCAG  CCACGCTGCT  TCTTCTGGAT  ACTTCCGCTG  CCACGTGGAT  GATGCCGTCC
 181  TCGACGACGC  ACCCTCAAAT  CTCCGAGATA  AGCGGAAATG  AATGCGCTGC  ATGTGCACAG
 241  CCTATTCTTG  ACAG|ATATGT  ATTCACCGTT  CTTGGCAAAT  GTTGGCATCA  ATCATGTCTC
 301  CGATGTTGCG  ATTGTCGAGC  TCCAATGTCG  ATGACTTGTT  TCAGTAAAGA  TGGCCTGATA
 361  TTGTGTAAAA  CAGACTATTC  AAG|AAGGTAC  GGTCATCGAT  GCGCTGGATG  TGATGGAAAA
 421  CTGGAAAAAG  AGGATTTAGT  AAGGAGAGCA  AGAGACAAAG  TATTTCATAT  TCGATGTTTT
 481  CAATGTTCAG  TATGTCAAAG  GCTCTTGGAT  ACGGGTGATC  AG|CTTTATAT  CATGGAGGGA
 541  AATCGATTCA  TGTGTCAAAA  TGATTTTCAA  ACGGCTACCA  AAACATCGAC  TCCAACATCA
 601  ATGCACCGTC  CAA|TATCCAA  TGGATCCGAA  TGTAATTCCG  ATATCGAGGA  AGATAACGTG
 661  GATGCTTGTG  ACGAG|GGTGG  TCTTGACGAC  GTTGATGGTG  ACTGTGGAAA  GGATAACTCT
 721  GATGACTCAA  ACTCTGCAAA  ACGGCGGGGT  CCTCGAACAA  CAATCAAAGC  TAAACAG|CTT
 781  GAAACATTGA  AAAATGCATT  CGCTGCGACC  CCGAAACCAA  CTCGACACAT  CCGTGAACAA
 841  CTTGCTGCCG  AGACAGGGCT  GAACATGAGA  GTCATTCAG|G  TGTGGTTCCA  AAATCGACGA
 901  AGCAAGGAAC  GTCGAATGAA  ACAGCTTCGA  TACGGTGGAT  ATCGTCAATC  CAGAAGACAA
 961  CGTCGAGAGG  ATATCGTTGA  TATGTTTCCG  AATG|ACCAAC  AGTTCTACCC  TCCACCACCT
1021  CCATCAAACG  TTCAATTCTT  CTGTGACCCA  TATGGAAGTC  CTCCAAATAA  CGGAGAGTCG
1081  ATGCAAATTC  CATCACAATT  CACAGTACCT  CCGGAGACTA  TGAATATGGT  GCCAG|AACCA
1141  TATGCCGAAT  CATCGTCAAC  ACCACCAGAG  TTCAATGAAG  ATGCATTCAC  ATGCATTTAT
1201  TCCACTGATG  TCGGAAAACC  AACTCCAGTT  TCATGGTAG
```

Exon 1: 254 bp (1 - 254)
2: 129 bp (255 - 383)
3: 139 bp (384 - 522)
4: 91 bp (523 - 613)
5: 62 bp (614 - 675)
6: 102 bp (676 - 777)
7: 102 bp (778 - 879)
8: 115 bp (880 - 994)
9: 141 bp (995 - 1135)
10: 104 bp (1136 - 1239)

**Figure S3** *Cbr-lin-11* cDNA sequence. The positions of exon-intron boundaries are marked.

**Table S1 List of PCR and sequencing primers used in this study.**

| Oligo | Sequence (5’ to 3’) |
|---|---|
| GL380 | GCTTCCCAATTCTCTGAGACGTCACA |
| GL381 | GCCAAATTGCACAATTCCAGTTCAG |
| GL382 | GTCCCGTTGAGACACACTTACATTG |
| GL383 | CTCTGCTAGCTCCGACCACATTTC |
| GL384 | AGGCTACTGTAGTTCTCATTTTAGGACCTA |
| GL385 | GGTCAAAGCTAGAAGCCTATTAGAGCG |
| GL389 | TTACGGTATTGGACGCCTAGGTAACC |
| GL390 | GAGAAGTTCACACCTGCTGAGCTAC |
| GL391 | GCAACAATGGAGCATCTACAGTAAGATCCC |
| GL392 | AACAGGATACTGTGGTCCTGCTCCAATC |
| GL793 | AGCTTCACATCTTGGTTCG |
| GL795 | AAGAAACTCTGGATGGGCTC |
| GL800 | CGGGAAGTTTGTGGAACG |
| GL801 | GACAGAGTGCAGGAACAGC |
| GL802 | GGCTCTCCTAATACATTCACG |
| GL806 | TCCGAATAAGCGTAGGAGAC |
| GL807 | AGCAGTCACTGTCCTTCC |
| GL808 | AGATCCGTGTTGTCCAAGG |
| GL809 | AGCTTCCTTGTCTACGGTC |
| GL810 | GAGGTAGCGCCCAATTTATG |
| GL812 | CCTCTATTCCAGCCAGAAACC |
| cb-lin-11-up-1 | CCATGCATTCTTCTTCGTCCATCATCAC |
| cb-lin-11-up-2 | TCTTCTGCAGTTCCGTTCTCGTTCATTTTCC |
| cb-lin-11-up-4 | GGAAGTCCTCCAAATAACGGAGAG |
| cb-lin-11-up-5 | GTCTTGACGACGTTGATGGTGACTGTG |
| cb-lin-11-up-6 | GGAAATGAATGCGCTGCATGTGCAC |
| cb-lin-11-up-7 | GATTCTACCATCTTTCCCACGCTGTAG |
| cb-lin-11-up-8 | CTGGCTCTCCTCATCTAACTG |
| cb-lin-11-up-9 | CTGGTCAATCGTACAGGGTTC |
| cb-lin-11-down-1 | CCCTGCAGTGAAACTGGAGTTGGTTTTCC |
| cb-lin-11-down-2 | GTGATGATGGACGAAGAAGAATGCATG |
| cb-lin-11-down-5 | CTGAAAATGAAATGACTGGTCGGAGGG |
| cb-lin-11-down-7 | GAACCCTGTGTGTCTCCTCTACTTC |
| cb-lin-11-down-8 | GATAACTGACTCCAAATAGACGTAGGC |