**Supplemental Table 1.** RepeatMasker results.

| Type                        | N elements | Length (bp) | Percent of sequence |
|-----------------------------|------------|-------------|---------------------|
| **Retroelements**           |            |             |                     |
| Retroelements               | 5,004      | 360,562     | 0.16%               |
| SINEs                       | 20         | 1,919       | 0.00%               |
| Penelope                    | 658        | 46,476      | 0.02%               |
| LINEs                       | 2,115      | 154,766     | 0.07%               |
| L2/CR1/Rex                  | 73         | 3,824       | 0.00%               |
| R1/LOA/Jockey               | 28         | 2,514       | 0.00%               |
| R2/R4/NeSL                  | 13         | 1,250       | 0.00%               |
| RTE/Bov-B                   | 208        | 19,795      | 0.01%               |
| L1/CIN4                     | 737        | 50,727      | 0.02%               |
| **LTR elements**            |            |             |                     |
| BEL/Pao                     | 265        | 24,018      | 0.01%               |
| Ty1/Copia                   | 31         | 7,678       | 0.00%               |
| Gypsy/DIRS1                 | 838        | 62,256      | 0.03%               |
| Retroviral                  | 1,218      | 70,865      | 0.03%               |
| **DNA transposons**         |            |             |                     |
| hobo-Activator              | 3,206      | 204,429     | 0.09%               |
| Tc1-IS630-Pogo              | 632        | 102,005     | 0.05%               |
| PiggyBac                    | 90         | 4,603       | 0.00%               |
| Tourist/Harbinger           | 794        | 43,897      | 0.02%               |
| Other (Mirage, P-element, Transib) | 139    | 6,220       | 0.00%               |
| **Rolling-circles**         | 425        | 27,897      | 0.01%               |
| **Unclassified**            | 1,387      | 156,892     | 0.07%               |
| **Total interspersed repeats** | 1,266,419 | 1,266,419   | 0.57%               |
| **Small RNA**               | 277        | 32,089      | 0.01%               |
| **Satellites**              | 660        | 68,592      | 0.03%               |
| **Simple repeats**          | 247,811    | 11,358,037  | 5.08%               |
| **Low complexity**          | 50,265     | 2,718,971   | 1.22%               |
| **Total bases masked**      | .          | 15,396,268  | 6.89%               |
### Supplemental Table 2. Enriched InterPro signatures.

| Test set            | Reference set | Enriched InterPro signature | InterPro name                                                                 | Functional importance | FDR     | p-value     | N test set | N ref set |
|---------------------|---------------|-----------------------------|-------------------------------------------------------------------------------|-----------------------|---------|-------------|------------|-----------|
| A. dorsale-only genes | IPK001992     |                             | Integration host factor (IHF) like DNA-binding domain                         | microsome             | 0.00425  | 9.62E-06    | 5          | 0         |
| A. dorsale-only genes | IPK001127     |                             | Bacterial phosphoionlypyruvate: sugar phosphotransferase system (PTS)         | microsome             | 0.00784  | 3.95E-06    | 6          | 1         |
| A. dorsale-only genes | IPK003984     |                             | Integrase, catalytic core                                                    | transposable element  | 0.004091 | 3.12E-07    | 8          | 2         |
| A. dorsale-only genes | IPK025526     |                             | Pigg-like transposable element-derived protein                               | transposable element  | 0.00784  | 6.86E-06    | 8          | 5         |
| A. dorsale-only genes | IPK035537     |                             | Retrotransposon 1/rop-like                                                   | transposable element  | 0.004091 | 8.71E-07    | 6          | 0         |
| Single copy universal genes | IPK006618 |                             | Insert outside protein                                                        | growth and development | 3.77E-04 | 6.06E-07    | 39         | 38        |
| Single copy universal genes | IPK001111 |                             | Transforming growth factor beta 1                                            | growth and development | 8.23E-05 | 1.06E-06    | 12         | 2         |
| Single copy universal genes | IPK008759 |                             | Transforming growth factor beta, C-terminal                                   | growth and development | 8.23E-05 | 1.06E-06    | 13         | 3         |
| Single copy universal genes | IPK0105622 |                             | Hsomoynph juvenile hormone binding                                           | growth and development | 8.48E-05 | 1.37E-07    | 20         | 13        |
| Single copy universal genes | IPK005743 |                             | Dual domain                                                                  | molecular chaperone    | 2.22E-05 | 1.92E-08    | 35         | 39        |
| Single copy universal genes | IPK002423 |                             | Chaperonin TCP-4                                                             | molecular chaperone    | 9.24E-05 | 1.34E-07    | 16         | 7         |
| Single copy universal genes | IPK001035 |                             | GroES-like superfamily                                                        | molecular chaperone    | 1.95E-05 | 1.36E-08    | 20         | 10        |
| Single copy universal genes | IPK006669 |                             | Small GTPase superfamily, ARF/SAR type                                       | signal transduction    | 0.009370 | 4.73E-05    | 19         | 22        |
| A. multifeo-only genes | IPK000159     |                             | Ras-associated (RA) domain                                                    | signal transduction    | 8.44E-08 | 3.62E-10    | 21         | 81        |
| A. multifeo-only genes | IPK000479     |                             | PDE                                                                         | signal transduction    | 2.10E-07 | 7.37E-09    | 40         | 38        |
| A. multifeo-only genes | IPK000653     |                             | Ras-like guanine nucleotide exchange factor, N-terminal                      | signal transduction    | 6.12E-05 | 3.32E-07    | 11         | 30        |
| A. multifeo-only genes | IPK000004     |                             | PAS                                                                         | signal transduction    | 3.34E-04 | 2.22E-06    | 8          | 16        |
| A. multifeo-only genes | IPK009895     |                             | Ras guanine-nucleotide exchange factors catalytic domain                     | signal transduction    | 3.34E-04 | 2.22E-06    | 11         | 38        |
| A. multifeo-only genes | IPK000131     |                             | Rap GTPase activating protein domain                                          | signal transduction    | 9.92E-04 | 7.30E-06    | 10         | 35        |
| A. multifeo-only genes | IPK000073     |                             | 5'-5' cyclic nucleotides phosphodiesterase, catalytic domain                 | signal transduction    | 0.004984 | 1.63E-05    | 10         | 39        |