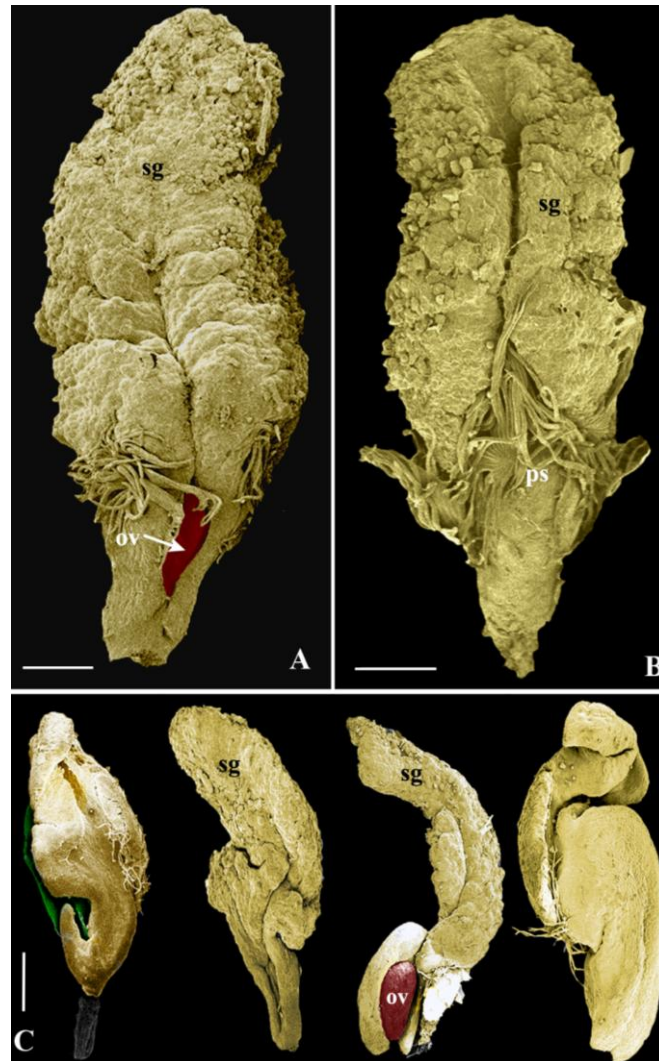
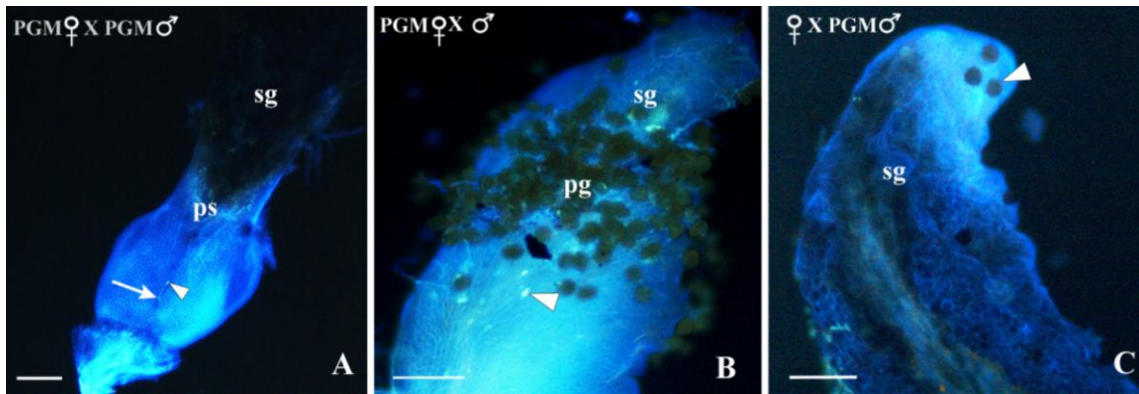


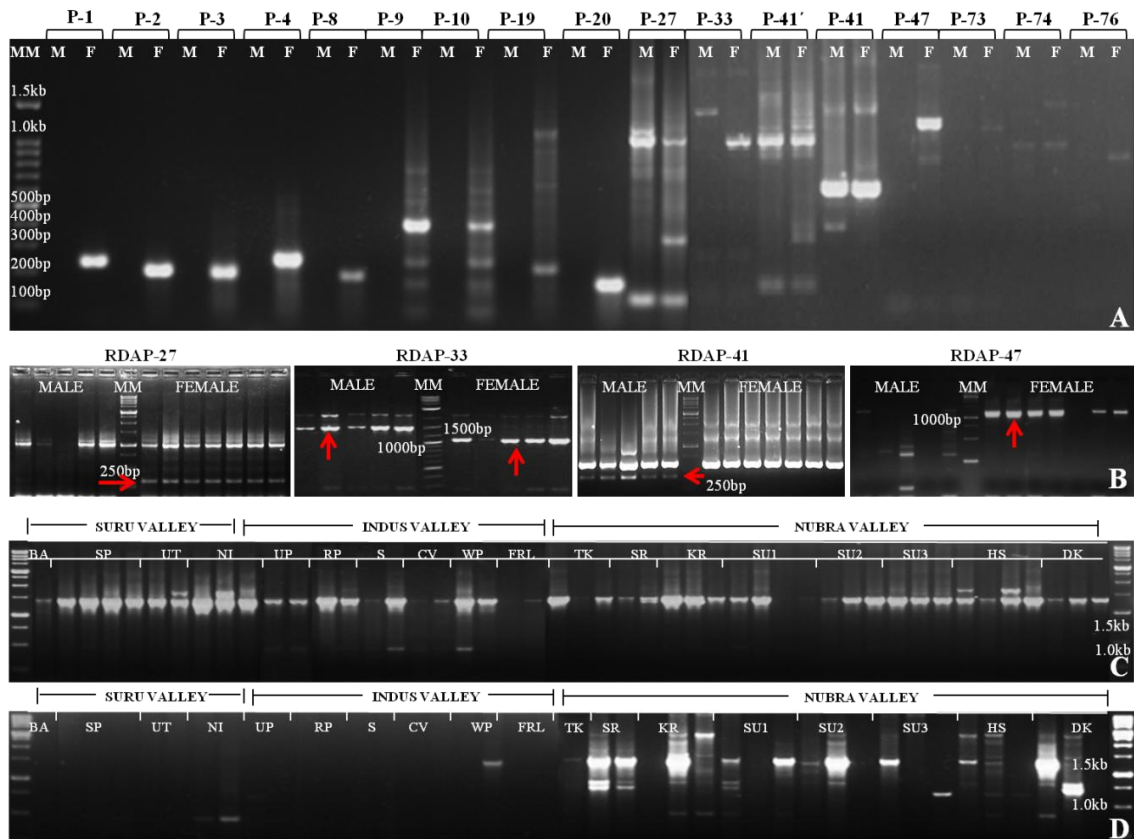
**Figure. S1:** Scanning electron micrographs of the gynoecia of female flower from the PGM plants. **A.** Ventral, **B.** Dorsal view of gynoecium. Note the presence of expanded stigma (sg), very restricted pseudostyle (ps) and ovary (ov). Opposite margins of carpel are wide apart at the pseudostyle region and appressed at the ovarian region making ovule slightly naked (arrow) at the otherwise conduplicate region (a). Numerous dendroid trichomes are present at stigma-pseudostyle junction (b). **C.** a panel showing sterile gynoecia (i) carpelloid type, (ii) sterile and without an ovule (arrow) (iii) with naked ovule and (iv) without definite morphology. *Scale bars:* A-C= 200  $\mu$ m



**Figure. S2:** Epi-fluorescence micrographs showing pollen grains and pollen tubes on manually pollinated gynoecia from PGM plants (A and B) and female plant (C). The respective crosses are marked on the pictures. pg; pollen grain, sg; stigma, ps; pseudostyle. Scale bars: A=500  $\mu$ m; B=100  $\mu$ m; C=200  $\mu$ m



**Figure. S3:** Gel profiles showing A. 17 primers (P-1 etc. designed from RDA derived sequences) showing gender specific amplicons (either in male or in female/size different) selected from RP population. B. Amplification of RDAP-27, RDAP-33, RDAP-41 & RDAP-47 only in case of RP population. C and D. Testing with primer pair SCAR-33 in the populations sampled across three valleys. A male specific amplicon of size ~1.5 kb in samples collected from Indus valley (RP, UP, RP, S, CV & FRL) and Suru valley (BA, SP, UT and NI) (C); while marker did not hold gender specificity for the samples tested from nine populations from Nubra valley (D). Refer Supplementary Data Table S1 for population codes.



**Figure. S3-E.** Alignment of the two fragments (1kb and ~1.5kb) obtained from RDAP-33 primers, Shows scattered insertions only in the male sequence in a size range of 1-31bp. (RP: Ranbirpura, M:male; F:female)

```

RPM3      ACGGCGCTAAAAACTTGATGCGTAATTTTCGCAAGTGTACGAATCGTTCAAGTAATAAAGT
RPM1      ACGGCGCTAAAAACTTGATGCGTAATTTTCGCAAGTGTACGAATCGTTCAAGTAATAAAGT
RPM2      ACGGCGCTAAAAACTTGATGCGTAATTTTCGCAAGTGTACGAATCGTTCAAGTAATAAAGT
RPF1      ACGGCGCTAAAAA-CTTGATGCTTATTTTTCAACAAGTGTACAAATCATTCAAGTAATAAAGT
RPF2      ACG-CGCTAAAA-CT-GATGCT-ATTTTTACA-GTGTACAAATCATC--AGTA-TAAAGT
RPF3      ACGGCGCTAAAAACTTGATGCTTATTT-CACAAGTGTACAAATCATTCAAGTAATAAAGT
          ***  *****  **  *****  *  **  *  **  *****  *****  *  *****  *****

RPM3      ATACAAAAGTACGAATATCGAACCCACAAGGAATGGCGTTACTAAGTACCGAAAATTGACT
RPM1      ATACAAAAGTACGAATATCGAACCCACAAGGAATGGCGTTACTAAGTACCGAAAATTGACT
RPM2      ATACAAAAGTACGAATATCGAACCCACAAGGAATGGCGTTACTAAGTACCGAAAATTGACT
RPF1      GTACAAAAGTACGGATATCGAACCCACAAGGAATGGCGTTACTAAGTACCGAAAATTGACT
RPF2      GTACAAA-GTACGGATATCGAACCCACAAGGAATGGCGTTACTAAGTACCGAAAATTGACT
RPF3      GTACAAAAGTACGGATATCGAACCCACAAGGAATGGCGTTACTAAGTACCGAAAATTGACT
          *****  *****  *****

RPM3      AATCCGAATTTTTATTTGAAAACCGAATTTTTGAATTTGTTTAAAGAGTAAATTAAC TTAA
RPM1      AATCCGAATTTTTATTTGAAAACCGAATTTTTGAATTTGTTTAAAGAGTAAATTAAC TTAA
RPM2      AATCCGAATTTTTATTTGAAAACCGAATTTTTGAATTTGTTTAAAGAGTAAATTAAC TTAA
RPF1      AATCCTAATTTTTATTTGAAAACCGAATTTGTTGAAATTTGTTTAAAGAGTAAATTAAC TTAA
RPF2      AATCCTAATTTTTATTTGAAAACCGAATTTGTTGAAATTTGTT-AAAGAGTAAATTAAC TTAA
RPF3      AATCCTAGTTTTATTTGAAAACCGAATTTGTTGAAATTTGTTTAAAGAGTAAATTAAC TTAA
          *****  *  *****  *****  *****  *****  *****  *****

RPM3      AACTAA-CGCAAATAACAAAATTTAATGTTGTTTACAAATGATTAAAAATGCTAAGGCAT
RPM1      AACTAA-CGCAAATAACAAAATTTGATGTTGTTTACAAATGATTAAAAATGCTAAGGCAT
RPM2      AACTAA-CGCAAATAACAAAATTTAATGTTGTTTACAAATGATTAAAAATGCTAAGGCAT
RPF1      AACTAAATGCAAATAACACAATTTGAATGTTGTTTACAAATAATTAATAATGCTGAGGTAT
RPF2      AACTAAATGCAAATAACACAATTTGAATGTTGTTTACAAATAATTAATAATGCTGAGGTAT
RPF3      AACTAAATGCAAATAACACAATTTGAATGTTGTTTACAAATAATTAATAATGCTGAGGTAT
          *****  *****  *****  *****  *****  *****  *****  **  **

RPM3      TTGATTTTCGCTAAATCAATTCAATCCGATTTCAAGTTATGTTATATGAGAATCAAAGTTA
RPM1      TTGATTTTCGCTAAATCAATTCAATCCGATTTCAAGTTATGTTATATGAGAATCAAAGTTA
RPM2      TTGATTTTCGCTAAATCAATTCAATCCGATTTCAAGTTATGTTATATGAGAATCAAAGTTA
RPF1      TTGATTTTTCGCTAAATCAATTCAATTTCAAGTCATCTTATATGAGAATCAAAGCTA
RPF2      TTGATTTTTCGCTAAATCAATTCAATTTCAAGTCATCTTATATGAGAATCAAAGCTA
RPF3      TTGATTTTTCGCTAAATCAATTCAATTTCAAGTCATCTTATATGAGAATCAAAGCTA
          *****  *****  *****  *  *****  **  *****  *****  **

RPM3      AAAGTGATGGTTGAAAACCCAAATTTACGTAATACTCTCTCT-CGAGTTATATTAGAAT
RPM1      AAAGTGATGGTTGAAAACCCAAATTTACGTAATACTCTCTCTTCGAGTTATATTAGAAT
RPM2      AAAGTGATGGTTGAAAACCCAAATTTACGTAATACTCTCTCT-CGAGTTATATTAGAAT
RPF1      AAAGTAATGGTTGAAAACCCAAATTTACCTAATACTCTCTCT-CGAGTTATATTAGAAT
RPF2      AAAGTAATGGTTGAAAACCCAAATTTACCTAATACTCTCTCT-CGAGTTATATTAGAAT
RPF3      AAAGTAATGGTTGAAAACCCAAATTTACCTAATA-TCTCTCT-CGAGTTATATTAGAAT
          *****  *****  *****  *****  *****  *****  *****

RPM3      TACTTATCTATGAAA-TCGACTATATTTCTATTAAGAAATTAATCGCAAACAAGCACAA-
RPM1      TACTTTTTTATGAAA-TCGACTATATTTCTATTAAGA-TTTAATCACAACAAGCACAA-
RPM2      TACTTATCTATGAAA-TCGACTATATTTCTATTAAGA-TTTAATCACAACAAGCACAA-
RPF1      TACTTATCTATGAAAACCAACTATATTTCTATGAAGA-TTTAATCACAACAAGCACAT-
RPF2      TACTTATCTATGAAAACCAACTATATTTCTATGAAGA-TTTAATCACAACAAGCACAT-
RPF3      TACTTATCTATGAAAACCAACTATATTTCTATGAAGA-TTTAATCACAACAAGCACAT-
          *****  *  *****  *  *****  *****  *****  *****

RPM3      TACGATTTATGGAATTTCTAGAATAACCACA-TACATCATGCATTAGTTCTCACACTCGC
RPM1      TACGATTTATGGAATTTCTAGAATAACCACAATACATCATGCATTAGTTCTCACACTCGC
RPM2      TACGATTTATGGAATTTCTAGAATAACCACA-TACATCATGCATTAGTTCTCACACTCGC
RPF1      TACGATTTATGGAATTTCTAGAATAACCACA-TACATCATGCATTAGTTCTCACACTCGC
RPF2      TACGATTTATGGAATTTCTAGAATAACCACA-TACATCATGCATTAGTTCTCACACTCGC

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RPF3 TACGATTTATGGAATTTCTAGAATAACCACA-TACATCATGCATTAGGTCTCACACTCGC  
\*\*\*\*\*

RPM3 ATTCAACATACGGTATTT-ATCACAAGGAAGCGTTCATTACACATCTAAAATGAATTGATT  
RPM1 ATTCAACATACGGTATTTTATCACAAGGAAGCGTTCATTACACATCTAAAATGAATTGATT  
RPM2 ATTCAACATACGGTATTT-ATCACAAGGAAGCGTTCATTACACATCTAAAATGAATTGATT  
RPF1 ATTCAACATACGGTATTT-ATCACAAGGAAGCATTTCATTACACATCT----CCTCTCGGTC  
RPF2 ATTCAACATACGGTATTT-ATCACAAGGAAGCATTTCATTACACATCT----CCTCTCGGTC  
RPF3 ATTCAACATACGGTATTT-ATCACAAGGAAGCATTTCATTACACATCT----CCTCTCGGTC  
\*\*\*\*\* \* \* \*

RPM3 TTATTTTTATTCAAGATTTTTATATTAAGAATGTTAGAGAGAAATATATTATTTTTTCATTA  
RPM1 TTATTTTTATTCAAGATTTTTATATTAAGAATGTTAGAGAGAAATATATTATTTTTTCATTA  
RPM2 TTATTTTTATTCAAGATTTTTATATTAAGAATGTTAGAGAGAAATATATTATTTTTTCATTA  
RPF1 TCA-----ATAT----AATGC----AGAAA---ATCATCT-----  
RPF2 TCA-----ATAT----AATGC----AGAAA---ATCATCT-----  
RPF3 TCA-----ATAT----AATGC----AGAAA---ATCATCT-----  
\* \* \* \* \* \* \* \* \* \* \* \* \* \* \*

RPM3 CAAACTTAAATCTGAAAATTAGATTTTAAGGTTTATCCGGTCTGATTTAGAGTAGT  
RPM1 CAAACTTAAATCTGAAAATTAGATTTTAAGGTTTATCCGGTCTGATTTAGAGTAGT  
RPM2 CAAACTTAAATCTGAAAATTAGATTTTAAGGTTTATCCGGTCTGATTTAGAGTAGT  
RPF1 -AAATCTTGGCCAGAAATTTAAA-----AGCA--  
RPF2 -AAATCT-TGCCAGAAATTTAAA-----AGCA--  
RPF3 -AAATCTTGGCCAGAAATTTAAA-----AGCA--  
\*\*\* \* \* \* \* \* \* \* \* \* \* \* \* \* \*

RPM3 GCTCTTTTATTTGTTGGTACAATCGCCCGATAGTTAAAGTGAAGCTCTATTTCAAAAAGTT  
RPM1 GCTCTTTTATTTGTTGGTACAATCGCCCGATAGTTAAAGTGAAGCTCTATTTCAAAAAGTT  
RPM2 GCTCTTTTATTTGTTGGTACAATCGCCCGATAGTTAAAGTGAAGCTCTATTTCAAAAAGTT  
RPF1 -----TTAAGCGTGGAAATAA-----ATACTCAAATTGAA-----AACAA-  
RPF2 -----TTAAGCATGGAATAA-----ATACTCAAATTGAA-----AACAA-  
RPF3 -----TTAAGCATGGAATAA-----ATACTCAAATTGAA-----AACAA-  
\*\*\* \* \* \* \* \* \* \* \* \* \* \* \* \* \*

RPM3 TTTATAAGAATTATCATCTGAAAATGTATTGACAACACGTTTTTCAGTAGTGGTTTTAAAA  
RPM1 TTTATAAGAATTATCATCTGAAAATGTATTGACAACACGTTTTTCAGTAGTGGTTTTAAAA  
RPM2 TTTATAAGAATTATCATCTGAAAATGTATTGACAACACGTTTTTCAGTAGTGGTTTTAAAA  
RPF1 -----GAAT--TCATATAACAAT-----AACAA-----AAA-  
RPF2 -----GAAT--TCATATAACAAT-----AACAA-----AAA-  
RPF3 -----GAAT--TCATATAACAAT-----AACAA-----AAA-  
\*\*\*\*\* \* \* \* \* \* \* \* \* \* \* \* \* \* \*

RPM3 CTTGAAAGTTAGTACTCGGATAACTAAATTCCTTAGGTTTAAATTTGGACACCTTGAATAAA  
RPM1 CTTGAAAGTTAGTACTCGGATAACTAAATTCCTTAGGTTTAAATTTGGACACCTTGAATAAA  
RPM2 CTTGAAAGTTAGTACTCGGATAACTAAATTCCTTAGGTTTAAATTTGGACACCTTGAATAAA  
RPF1 ---GAAA-----TCAGAT-----TTTCTTGATTCAACT---ACATCAT-----  
RPF2 ---GAAA-----TCAGAT-----TTTCTTGATTCAACT---ACATCAT-----  
RPF3 ---GAAA-----TCAGAT-----TTTCTTGATTCAACT---ACATCAT-----  
\*\*\*\*\* \*\* \* \* \* \* \* \* \* \* \* \* \* \* \* \*

RPM3 GTTTAAACTGTCTAACCTCACCAAAGGTGGCATTAAATGGTTTCATTTTCAATCTCTTAG  
RPM1 GTTTAAACTGTCTAACCTCACCAAAGGTGGCATTAAATGGTTTCATTTTCAATCTCTTAG  
RPM2 GTTTAAACTGTCTAACCTCACCAAAGGTGGCATTAAATGGTTTCATTTTCAATCTCTTAG  
RPF1 -----AGCCTTAGCAAAAATG--ATTTA----GTTTCAT----AATAT-----  
RPF2 -----AGCCTTAGCAAAAATG--ATTTA----GTTTCAT----AATAT-----  
RPF3 -----AGCCTTAGCAAAAATG--ATTTA----GTTTCAT----AATAT-----  
\* \* \* \* \* \* \* \* \* \* \* \* \* \* \*

RPM3 AAAAAAGGAATTAATTTAATTAACCAAATAGTTATCAACCCACCCATAGGTGTTAATT  
RPM1 AAAAAAGGAATTAATTTAATTAACCAAATAGTTATCAACCCACCCATAGGTGTTAATT  
RPM2 AAAAAAGGAATTAATTTAATTAACCAAATAGTTATCAACCCACCCATAGGTGTTAATT  
RPF1 -AAATAAGAA-----CAAACATATTCTCAATTGAATCCATGAAT-----  
RPF2 -AAATAAGAA-----CAAACATATTCTCAATTGAATCCATGAAT-----

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RPF3  -AAATAAGAA-----CAAACATAT-CTCAATTGAATCCATGAAT-----
      *** * ***          ***** * ***** * ***** *
RPM3  GATTTGTTTAGTTAACAAAGAATATCTAACCCACCAAAGGTGGTATTTCATACAAGAAAG
RPM1  GATTTGTTTAGTTAACAAAGGATATCTAACCCACCAAAGGTGGTATTTCATACAAGAAAG
RPM2  GATTTGTTTAGTTAACAAAGAATATCTAACCCACCAAAGGTGGTATTTCATACAAGAAAG
RPF1  -----AACAAA-----TCTGA-----ATAAAATGTAGAAA--ATAAA-GCTAA
RPF2  -----AACAAA-----TCTGA-----ATAAAATGTAGAAA--ATAAAAGCTAA
RPF3  -----AACAAA-----TCTGA-----ATAAAATGTAGAAA--ATAAAAGCTAA
      *****          *** *          * ***** * * * ***** * * *
RPM3  GGAGAATCAATAAATATCAATTATATCTTTAATAACCTAAATAATATGAGCAAGCATAA
RPM1  GGAGAATCAATAAATATCAATTATATCTTTAATAACCTAAATAATATGAGCAAGCATAA
RPM2  GGAGAATCAATAAATATCAATTATATCTTTAATAACCTAAATAATATGAGCAAGCATAA
RPF1  GGAGAAGAGATGAAAAAC-----TCTTGAAGA---TGAA-----GACTTGGTAGAA
RPF2  GGAGAAGAGATGAAAAAC-----TCTTGAAGA---TGAA-----GACTTGGTAGAA
RPF3  GGAGAAGAGATGAAAAAC-----TCTTGAAGA---TGAA-----GACTTGGTAGAA
      ***** ** * * * *          ***** * *          * **          ** * * **
RPM3  TTAACCTTAGTTATTATATCCTTAAATACTCCACTATTTATAAAAAGATAAAATTTGCATGA
RPM1  TTAACCTTAGTTATTATATCCTTAAATACTCCACTATTTATAAAAAGATAAAATTTGCATGA
RPM2  TTAACCTTAGTTATTATATCCTTAAATACTCCACTATTTATAAAAAGATAAAATTTGCATGA
RPF1  ACAA--TGGTGACGAT--CCTTCAA-GCTTCTCCA-----AACTT-----
RPF2  ACAA--TGGTGACGAT--CCTTCAA-GCTTCTCCA-----AACTT-----
RPF3  ACAA--TGGTGACGAT--CCTTCAA-GCTTCTCCA-----AACTT-----
      ** * * * * ** ***** ** * * * *          ** **
RPM3  ATGTTTATTGAATCTATGTTTAAATTTTCTGTAAGTAGATTAAAAACACAAAAACCCCAA
RPM1  ATGTTTATTGAATCTATGTTTAAATTTTCTGTAAGTAGATTAAAAACACAAAAACCCCAA
RPM2  ATGTTTATTGAATCTATGTTTAAATTTTCTGTAAGTAGATTAAAAACACAAAAACCCCAA
RPF1  -TCTCTCCAAAAT--TGCCT--TTTCTC-----CTCCAA
RPF2  -TCTCTCCAAAAT--TGCCT--TTTCTC-----CTCCAA
RPF3  -TCTCTCCAAAAT--TGCCT--TTTCTC-----CTCCAA
      * * *          ***          ** *          *****          * *****
RPM3  AATTTTCGTGACAGGATGTTTAGGATTTAATTTTGTTTTTAAAAGTTTGAATAATAAATTA
RPM1  AATTTTCGTGACAGGATGTTTAGGATTTAATTTTGTTTTTAAAAGTTTGAATAATAAATTA
RPM2  AATTTTCGTGACAGGATGTTTAGGATTTAATTTTGTTTTTAAAAGTTTGAATAATAAATTA
RPF1  AA-----ATGTCTTAGACCT--CCTCTCTCTAC-----
RPF2  AA-----ATGTCTTAGACCT--CCTCTCTCTAC-----
RPF3  AA-----ATGTCTTAGACCT--CCTCTCTCTAC-----
      **          ***** * ** *          * * * **
RPM3  AAAACCACATACATTCCTTCCTTAGATCGACCTTGAGAGTATACTTATCATTTTCTACGA
RPM1  AAAACCACATACATTCCTTCCTTAGATCGACCTTGAGAGTATACTTATCATTTTCTACGA
RPM2  AAAACCACATACATTCCTTCCTTAGATCGACCTTGAGAGTATACTTATCATTTTCTACGA
RPF1  -----CGTGGCCTCTTTC-----TCCATCTT-ATAGTATATACA-----
RPF2  -----CGTGGCCTCTTTC-----TCCATCTT-ATAGTATATATA-----
RPF3  -----CGTGGCCTCTTTC-----TCCATCTT-ATAGTATATATA-----
      * *          ** ***          ** * ***** * ***** *
RPM3  AATGATTCGTGCACTTGCGAGAATTTTATAAATATAAAAACCAAAGTATTGGCAGGAATCG
RPM1  AATGATTCGTGCACTTGCGAGAATTTTATAAATATAAAAACCAAAGTATTGGCAGGAATCG
RPM2  AATGATTCGTGCACTTGCGAGAATTTTATAAATATAAAAACCAAAGTATTGGCAGGAATCG
RPF1  ---GATATAGGGTTTTGCGGAAATTTTG-GAACAAA-CAACAAAAAA-TTGT-GTTT-CG
RPF2  ---GATATAGGGTTTTGCGGAAATTTTG-GAACAAAACAACAAAAAAATTGT-GTTTTCG
RPF3  ---GATATAGG-TTTTTGCGGAAATTTTG-GAACAAAACA-CAAAAAA-TTGT-GTTTTCG
      ***          * ***** *****          ** * *          * ***** * * * **
RPM3  GCGATGCAAGTTTTTCGTTCAATAAAGTATTTGGCGATCACGATTCTGCTCATCAAGTTTT
RPM1  GCGATGCAAGTTTTTCGTTCAATAAAGTATTTGGCGATCACGATTCTGCTCATCAAGTTTT
RPM2  GCGATGCAAGTTTTTCGTTCAATAAAGTATTTGGCGATCACGATTCTGCTCATCAAGTTTT
RPF1  --GACGAAA--CTCGCCCGC-----AGCGA--A-TTATTCTCATCAG--TTT

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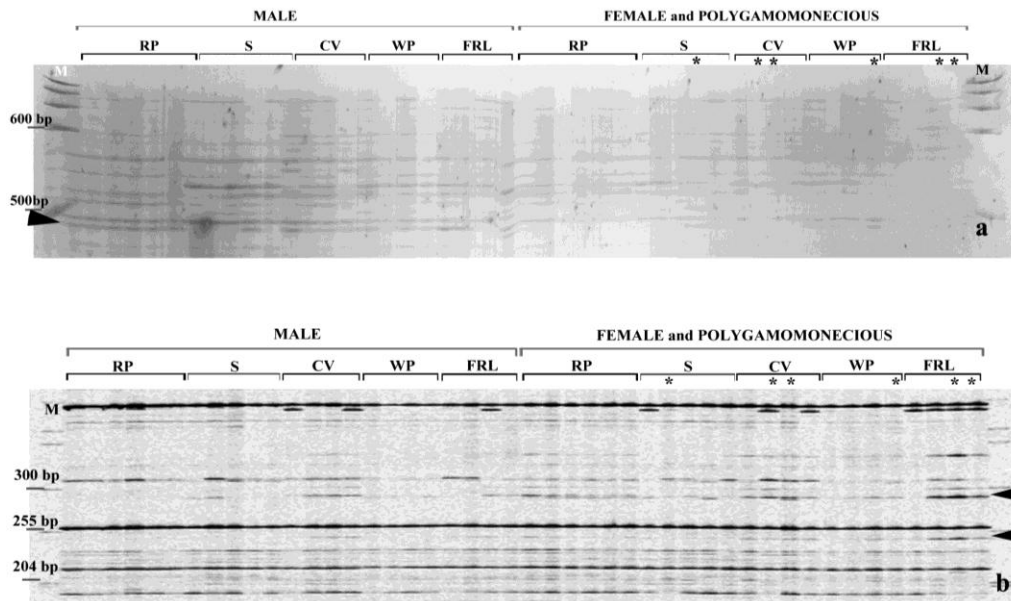
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RPF3      --GACGAAA--CTCGCCCGC-----AGCGA--AATTATTCTCATCAAG--TT
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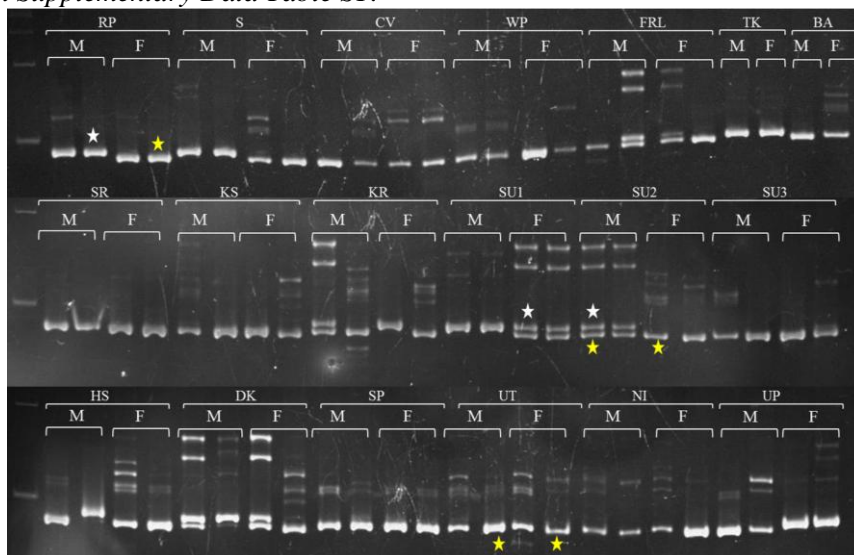
RPM3      TAGCGCCGT
RPM1      TAGCGCCGT
RPM2      TAGCGCCGT
RPF1      TAGCGC-GT
RPF2      TAGCGCCGT
RPF3      TAGCGC-GT
          ***** **

```

**Figure. S4.** Part of representative AFLP profiles with selective primer combinations **a.** E-AGC+M-CAT; showing a fragment in male plants across five populations. **b.** E-AGG+M-CAGT; showing female-specific fragments (arrow heads). M: DNA size marker. Population codes are as per *Supplementary Table S1*.



**Figure. S5-A:** PAGE (6%) profiles showing amplification products of SCAR-32 marker in different populations collected from 3 different geographically located valleys. Observe the product size variation between male & female and among populations. White and yellow asterisk marked bands were eluted, Cloned and sequenced. The sequence alignment (*in Figure. S5-B*) showed a 12bp insertion (225 bp). *Population codes are same as given in Supplementary Data Table S1.*



**Figure. S5-B:** Alignment of cloned sequences of male (M) and female (F), obtained from SCAR-32 marker. The population codes are same as given in supplementary file 1. LB (Yellow asterisk): 213 bp fragment, UB (white asterisk): 225 bp fragment as marked in *Figure. S5-A*.

```

RP-F-LB      GTCATGTCACACAATCAAATGAGTTGACTA-GTCAAACCACACAAGCA----CAAAGAGA
SU2-F-LB    GTCATGTCACACAATCAAATGAGTTGACTATGGCAAACCACACAAGCAAGCACAAGAGA
UT-F-LB     GTCATGTCACACAATCAAATGAGTTGATTA-GGCAAACCACACAAGCA----CAAAGAGA
SU2-M-LB    -----GTCACACAATCAAATGAGTTGACTA-GCCCAACCACACAAGCA----CAAAGAGA
UT-M-LB     GTCATGTCACACAATCAAATGAGTTGACTA-GGCAAACCACACAAGCA----CAAAGAGA
RP-M-UB     GTCATGTCACACAATCAAATGAGTTGACTA-GGCAAACCACACAAGCA----CAAAGAGA
SU2-M-UB    GTCATGTCACACAATCAAATGAGTTGACTA-GGCAAACCACACAAGCA----CAAAGAGA
SU1-F-UB    GTCATGTCACACAATCAAATGAGTTGACTA-GGCAAACCACACAAGCA----CAAAGAGA
              ***** ** * * *****

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```

RP-F-LB      GAATCATATCACCCCGCGT-----GTGAGGAGGATGAAACGTGTGTACAGTAT
SU2-F-LB    GAATCATATCACCCCGCGT-----GTGAGGAGGACGAAACGTGTGTACAGTGT
UT-F-LB     GAATCATATCACCCCGCGT-----GTGAGGAGGATGAAACGTGTGTACAGTGT
SU2-M-LB    GAATCATATCACCCCGCGT-----GTGAGGAGGATGAAACGTGTGTACAGTAT
UT-M-LB     GAATCATATCACCCCGCGT-----GCGAGGAGGATGAAACATGTGTACAGTGT
RP-M-UB     GAATCATATCACCCCGCGTATCACCCCGCATGTGAGGAGGATGAAACGTGTGTACAGTGT
SU2-M-UB    GAATCATATCACCCCGCGTATCACCCCGCATGTGAGGAGGATGAAACGTGTGTACAGTGT
SU1-F-UB    GAATCATATCACCCCGCGTATCACCCCGCATGTGAGGAGGATGAAACGTGTGTACAGTGT
              ***** * *****

```

```

RP-F-LB      TAGCATAACGTTCAATCCAAGTGCAAAAAATTGGTCAACATGCCACATGTCACTAACTCAG
SU2-F-LB    TAGCATAATGTTCAATCCAAGTGCGAACATTGGTCAACATGCCACATGTCACTAACTCAC
UT-F-LB     TAGCATAACATACAATCCAAGTGCGAAAAATTGGTCAACATGCCAGATGTCACTAACTCAA
SU2-M-LB    TAGCATAACGTTCAATCCAAGTGCAAAAAATTGGTCAACATGCCACATGTCACTAACTCAG
UT-M-LB     TAGCATAACGTTCAATCCAAGTGCAAAAAATTGGTCAACATGCCACATGTTACTAACTCAG
RP-M-UB     TAGCATAACGTTCAATCCAAGTGCAAAAAATTGGTCAACATGCCACATGTCACTAACTCAG
SU2-M-UB    TAGCATAACGTTCAATCCAAGTGCAAAAAATTGGTCAACATGCCACATGTCACTAACTCAG
SU1-F-UB    TAGCATAACGTTCAATCCAAGTGCAAAAAATTGGTCAACATGCCACATGTCACTAACTCAG
              ***** * *****

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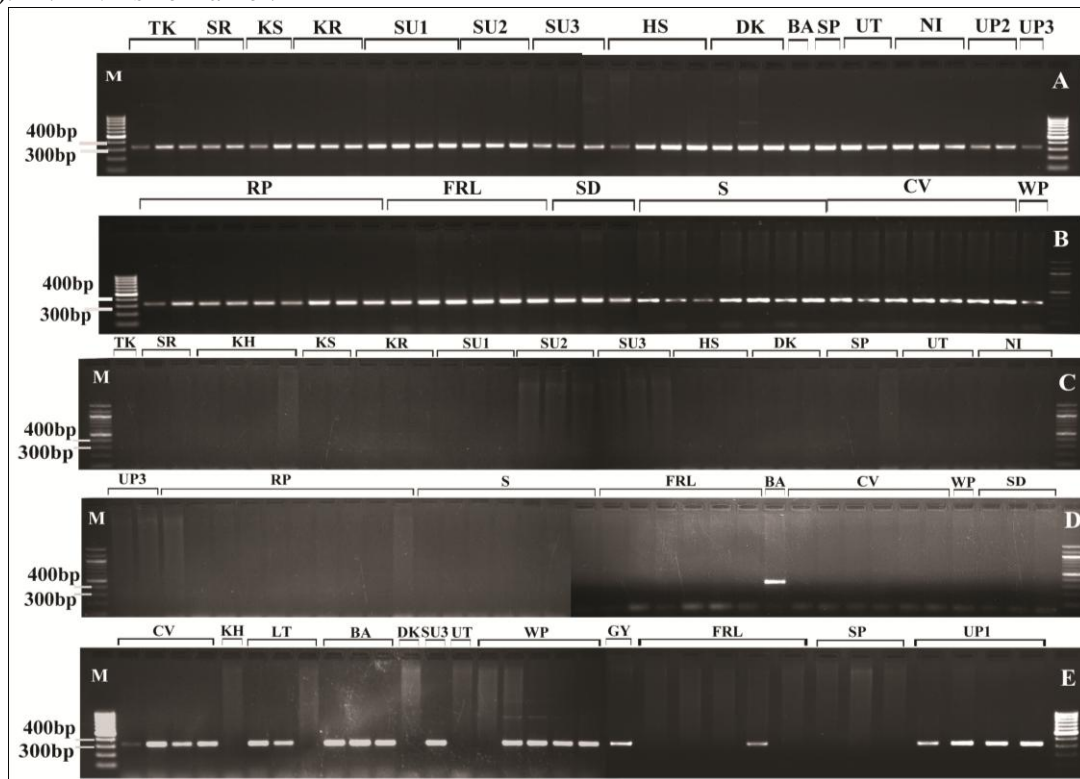
  

```

RP-F-LB      CGAGCATTGCCTCTAATCGGTCTCCCCTATCATGTGTGCGTCCCTAAATT
SU2-F-LB    CGAGCATTGCCTCTAATCGGTCTCCCCTATCATGTGTGCGTCCCTAAATT
UT-F-LB     CGAGCATTGCCTCTAATCGGTCTCCCCTATCATGTGTGCGTCCCTAAATT
SU2-M-LB    CGAGCATTGCCTCTAATCGGTCTCCCCTATCATGTGTGCGTCCCTAAATT
UT-M-LB     CGAGCATTGCCTCTAATCGGTCTCCCCTATCATGTGTGCGTCCCTAAATT
RP-M-UB     CGAGCATTGCCTTTAATCGGTTTCCCCTATCATGTGTGCGTCCCTAAATT
SU2-M-UB    CGAGCATTGCCTTTAATCGGTTTCCCCTATCATGTGTGCGTCCCTAAATT
SU1-F-UB    CGAGCATTGCCTTTAATCGGTTTCCCCTATCATGTGTGCGTCCCTAAATT
              *****

```

**Figure. S6-A.** Amplification product with SCAR primer pair HRML1 and HRML2. **a-b.** male plants. **c-d.** female plants. **e.** polygamomonoecious plants. Lanes are marked with population codes (*Supplementary Data Table S1*). M: DNA size marker.



**Figure. S6-B.** Alignment of male-specific region (consensus sequence obtained from 3 clones, HRML region) amplified with primer pair HRML1 and HRML2 across populations collected from geographically isolated valleys of Leh-Ladakh. *Refer Supplementary Data Table S1 for population codes.*

```

CV          GGTTCAATTTCTGTTACTCTGATGCCTAACTATTTACTCAATGGTCCCCCTCCTACGCCCG 60
WP          GGTTCAATTTCTGTTACTCTGATGCCTAACTATTTACTCAATGGTCCCCCTCCTACGCCCG 60
SD          GGTTCAATTTCTGTTACTCTGATGCCTAACTATTTACTCAATGGTCCCCCTCCTACGCCCG 60
HS          GGTTCAATTTCTGTTACTCTGATGCCTAACTATTTACTCAATGGTCCCCCTCCTACGCCCG 60
SU2        GGTTCAATTTCTGTTACTCTGATGCCTAACTATTTACTCAATGGTCCCCCTCCTACGCCCG 60
UP3        GGTTCAATTTCTGTTACTCTGATGCCTAACTATTTACTCAATGGTCCCCCTCCTACGCCCG 60
RP          GGTTCAATTTCTGTTACTCTGATGCCTAACTATTTACTCAATGGTCCCCCTCCTACGCCCG 60
KS          GGTTCAATTTCTGTTACTCTGATGCCTAACTATTTACTCAATGGTCCCCCTCCTACGCCCG 60
NI          GGTTCAATTTCTGTTACTCTGATGCCTAACTATTTACTCAATGGTCCCCCTCCTACGCCCG 60
FRL        GGTTCAATTTCTGTTACTCTGATGCCTAACTATTTACTCAATGGTCCCCCTCCTACGCCCG 60
SR          GGTTCAATTTCTGTTACTCTGATGCCTAACTATTTACTCAATGGTCCCCCTCCTACGCCCG 60
*****

CV          TTCTGTGTTATCATGTGCTCAGTTGCACCCACTGCGTGCCGCATGTGTGTTGGTTGTTGC 120
WP          TTCTGTGTTATCATGTGCTCAGTTGCACCCACTGCGTGCCGCATGTGTGTTGGTTGTTGC 120
SD          TTCTGTGTTATCATGTGCTCAGTTGCACCCACTGCGTGCCGCATGTGTGTTGGTTGTTGC 120
HS          TTCTGTGTTATCATGTGCTCAGTTGCACCCACTGCGTGCCGCATGTGTGTTGGTTGTTGC 120
SU2        TTCTGTGTTATCATGTGCTCAGTTGCACCCACTGCGTGCCGCATGTGTGTTGGTTGTTGC 120
UP3        TTCTGTGTTATCATGTGCTCAGTTGCACCCACTGCGTGCCGCATGTGTGTTGGTTGTTGC 120
RP          TTCTGTGTTATCATGTGCTCAGTTGCACCCACTGCGTGCCGCATGTGTGTTGGTTGTTGC 120
KS          TTCTGTGTTATCATGTGCTCAGTTGCACCCACTGCGTGCCGCATGTGTGTTGGTTGTTGC 120
NI          TTCTGTGTTATCATGTGCTCAGTTGCACCCACTGCGTGCCGCATGTGTGTTGGTTGTTGC 120
FRL        TTCTGTGTTATCATGTGCTCAGTTGCACCCACTGCGTGCCGCATGTGTGTTGGTTGTTGC 120
SR          TTCTGTGTTATCATGTGCTCAGTTGCACCCACTGCGTGCCGCATGTGTGTTGGTTGTTGC 120
*****

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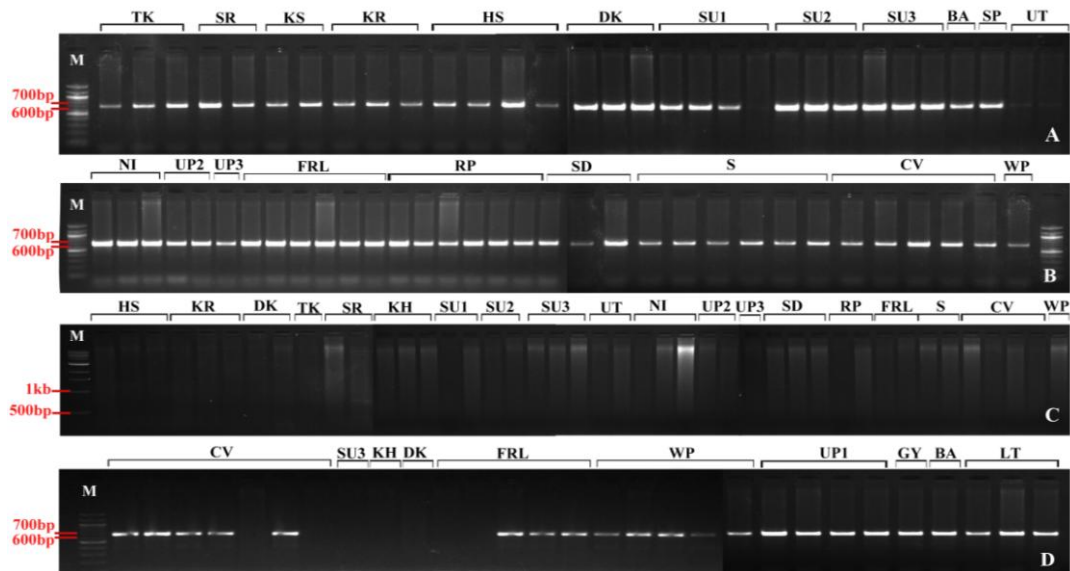
CV GTGCGCGGTTGTGCGAGTAGAATCTTCATGTAACATTTCTCCCTCTCTTTCAAAATCCTT 180  
WP GTGCGCGGTTGTGCGAGTAGAATCTTCATGTAACATTTCTCCCTCTCTTTCAAAATCCTT 180  
SD GTGCGCGGTTGTGCGAGTAGAATCTTCATGTAACATTTCTCCCTCTCTTTCAAAATCCTT 180  
HS GTGCGCGGTTGTGCGAGTAGAATCTTCATGTAACATTTCTCCCTCTCTTTCAAAATCCTT 180  
SU2 GTGCGCGGTTGTGCGAGTAGAATCTTCATGTAACATTTCTCCCTCTCTTTCAAAATCCTT 180  
UP3 GTGCGCGGTTGTGCGAGTAGAATCTTCATGTAACATTTCTCCCTCTCTTTCAAAATCCTT 180  
RP GTGCGCGGTTGTGCGAGTAGAATCTTCATGTAACATTTCTCCCTCTCTTTCAAAATCCTT 180  
KS GTGCGCGGTTGTGCGAGTAGAATCTTCATGTAACATTTCTCCCTCTCTTTCAAAATCCTT 180  
NI GTGCGCGGTTGTGCGAGTAGAATCTTCATGTAACATTTCTCCCTCTCTTTCAAAATCCTT 180  
FRL GTGCGCGGTTGTGCGAGTAGAATCTTCATGTAACATTTCTCCCTCTCTTTCAAAATCCTT 180  
SR GTGCGCGGTTGTGCGAGTAGAATCTTCATGTAACATTTCTCCCTCTCTTTCAAAATCCTT 180  
\*\*\*\*\*

CV GTCCACAAGGATGAAGTCAGGATAGGACTTGGAGAAGCGCCATTCATTCTCCCAACTAGC 240  
WP GTCCACAAGGATGAAGTCAGGATAGGACTTGGAGAAGCGCCATTCATTCTCCCAACTAGC 240  
SD GTCCACAAGGATGAAGTCAGGATAGGACTTGGAGAAGCGCCATTCATTCTCCCAACTAGC 240  
HS GTCCACAAGGATGAAGTCAGGATAGGACTTGGAGAAGCGCCATTCATTCTCCCAACTAGC 240  
SU2 GTCCACAAGGATGAAGTCAGGATAGGACTTGGAGAAGCGCCATTCATTCTCCCAACTAGC 240  
UP3 GTCCACAAGGATGAAGTCAGGATAGGACTTGGAGAAGCGCCATTCATTCTCCCAACTAGC 240  
RP GTCCACAAGGATGAAGTCAGGATAGGACTTGGAGAAGCGCCATTCATTCTCCCAACTAGC 240  
KS GTCCACAAGGATGAAGTCAGGATAGGACTTGGAGAAGCGCCATTCATTCTCCCAACTAGC 240  
NI GTCCACAAGGATGAAGTCAGGATAGGACTTGGAGAAGCGCCATTCATTCTCCCAACTAGC 240  
FRL GTCCACAAGGATGAAGTCAGGATAGGACTTGGAGAAGCGCCATTCATTCTCCCAACTAGC 240  
SR GTCCACAAGGATGAAGTCAGGATAGGACTTGGAGAAGCGCCATTCATTCTCCCAACTAGC 240  
\*\*\*\*\*

CV TACCTCGGTTGGAGCCCCCTACCCATTTGACCAGAATTTCAAATTTTGGTTGATATCTATC 300  
WP TGCCTCGGTTGGAGCCCCCTACCCATTTGACCAGAATTTCAAATTTTGGTTGATATCTATC 300  
SD TGCCTCGGTTGGAGCCCCCTACCCATTTGACCAGAATTTCAAATTTTGGTTGATATCTATC 300  
HS TGCCTCGGTTGGAGCCCCCTACCCATTTGACCAGAATTTCAAATTTTGGTTGATATCTATC 300  
SU2 TGCCTCGGTTGGAGCCCCCTACCCATTTGACCAGAATTTCAAATTTTGGTTGATATCTATC 300  
UP3 TGCCTCGGTTGGAGCCCCCTACCCATTTGACCAGAATTTCAAATTTTGGTTGATATCTATC 300  
RP TGCCTCGGTTGGAGCCCCCTACCCATTTGACCAGAATTTCAAATTTTGGTTGATATCTATC 300  
KS TGCCTCGGTTGGAGCCCCCTACCCATTTGACCAGAATTTCAAATTTTGGTTGATATCTATC 300  
NI TGCCTCGGTTGGAGCCCCCTACCCATTTGACCAGAATTTCAAATTTTGGTTGATATCTATC 300  
FRL TGCCTCGGTTGGAGCCCCCTACCCATTTGACCAGAATTTCAAATTTTGGTTGATATCTATC 300  
SR TGCCTCGGTTGGAGCCCCCTACCCATTTGACCAGAATTTCAAATTTTGGTTGATATCAAAC 300  
\* .\*\*\*\*\* \* \*

CV CTTCTGAATCACTCGGCGCTCTAGGATAG 329  
WP CTTCTGAATCACTCGGCGCTCTAGGATAG 329  
SD CTTCTGAATCACTCGGCGCTCTAGGATAG 329  
HS CTTCTGAATCACTCGGCGCTCTAGGATAG 329  
SU2 CTTCTGAATCACTCGGCGCTCTAGGATAG 329  
UP3 CTTCTGAATCACTCGGCGCTCTAGGATAG 329  
RP CTTCTGAATCACTCGGCGCTCTAGGATAG 329  
KS CTTCTGAATCACTCGGCGCTCTAGGATAG 329  
NI CTTCTGAATCACTCGGCGCTCTAGGATAG 329  
FRL CTTCTGAATCACTCGGCGCTCTAGGATAG 329  
SR GTTCTGAATCACTCGGCGCTCTAGGATAG 329  
\*\*\*\*\*

**Figure. S7-A.** Representative agarose gels (1.5%) showing amplification with primers HRML1 and HRML3, in male plants (A-B). No amplification was observed in female plants (C). Some polygamomonoecious plants samples also showed amplification (D). *Lanes of gels are marked with the population code (See Supplementary Data Table S1).* M: DNA size marker.



**Figure. S7-B.** Alignment of sequence (consensus sequence of three clones) of region amplified (~676 bp) with primer pair HRML1 and HRML3 in male plants. This region showed male-specificity across the populations distributed in three geographically isolated valleys. *Population codes are as given in Supplementary Data Table S1.*

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SU1    GGTTCAATTTCTGTTACTCTGATGCCTAACTATTTACTCAATGGTCCCCCTCCTACGCCCG
SU2    GGTTCAATTTCTGTTACTCTGATGCCTAACTATTTACTCAATGGTCCCCCTCCTACGCCCG
SD     GGTTCAATTTCTGTTACTCTGATGCCTAACTATTTACTCAATGGTCCCCCTCCTACGCCCG
WP     GGTTCAATTTCTGTTACTCTGATACCTAACTATTTACTCAATGGTCCCCCTCCTACGCCCG
CV     GGTTCAATTTCTGTTACTCTGATGCCTAACTATTTACTCAATGGTCCCCCTCCTACGCCCG
*****
SU1    TTCTGTGTTATCATGTGCTCAGTTGCACCCACTGCGTGCCGCATGTGTGTTGGTTGTTGC
SU2    TTCTGTGTTATCATGTGCTCAGTTGCACCCACTGCGTGCCGCATGTGTGTTGGTTGTTGC
SD     TTCTGTGTTATCATGTGCTCAGTTGCACCCACTGCGTGCCGCATGTGTGTTGGTTGTTGC
WP     TTCTGTGTTATCATGTGCTCAGTTGCACCCACTGCGTGCCGCATGTGTGTTGGTTGTTGC
CV     TTCTGTGTTATCATGTGCTCAGTTGCACCCACTGCGTGCCGCATGTGTGTTGGTTGTTGC
*****
SU1    GTGCGCGGTTGTGCGAGTAGAATCTTCATGTAACATTTCTCCCTCTCTTTCAAAATCCTT
SU2    GTGCGCGGTTGTGCGAGTAGAATCTTCATGTAACATTTCTCCCTCTCTTTCAAAATCCTT
SD     GTGCGCGGTTGTGCGAGTAGAATCTTCATGTAACATTTCTCCCTCTCTTTCAAAATCCTT
WP     GTGCGCGGTTGTGCGAGTAGAATCTTCATGTAACATTTCTCCCTCTCTTTCAAAATCCTT
CV     GTGCGCGGTTGTGCGAGTAGAATCTTCATGTAACATTTCTCCCTCTCTTTCAAAATCCTT
*****
SU1    GTCCACAAGGATGAAGTCAGGATAGGACTTGGAGAAAGCGCCATTCAATCTCCCAACTAGC
SU2    GTCCACAAGGATGAAGTCAGGATAGGACTTGGAGAAAGCGCCATTCAATCTCCCAACTAGC
SD     GTCCACAAGGATGAAGTCAGGATAGGACTTGGAGAAAGCGCCATTCAATCTCCCAACTAGC
WP     GTCCACAAGGATGAAGTCAGGATAGGACTTGGAGAAAGCGCCATTCAATCTCCCAACTAGC
CV     GTCCACAAGGATGAAGTCAGGATAGGACTTGGAGAAAGCGCCATTCAATCTCCCAACTAGC
*****

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SU1 TGCCTCGGTTGGAGCCCCACCCATTTGACCAGAAATTTCAAATTTTGGTTGATATCTATC  
SU2 TGCCTCGGTTGGAGCCCCACCCATTTGACCAGAAATTTCAAATTTTGGTTGATATCTATC  
SD TGCCTCGGTTGGAGCCCCACCCATTTGACCAGAAATTTCAAATTTTGGTTGATATCTATC  
WP TGCCTCGGTTGGAGCCCCACCCATTTGACCAGAAATTTCAAATTTTGGTTGATATCTATC  
CV TGCCTCGGTTGGAGCCCCACCCATTTGACCAGAAATTTCAAATTTTGGTTGATATCTATC  
\*\*\*\*\*

SU1 CTTCTGAATCACTCGGCGCTCTAGGATAGCTTCAGGCTGTTGCATGATCGTTGAGTGTTTC  
SU2 CTTCTGAATCACTCGGCGCTCTAGGATAGCTTCAGGCTGTTGCATGATCGTTGAGTGTTTC  
SD CTTCTGAATCACTCGGCGCTCTAGGATAGCTTCAGGCTGTTGCATGATCGTTGAGTGTTTC  
WP CTTCTGAATCACTCGGCGCTCTAGGATAGCTTCAGGCTGTTGCATGATCGTTGAGTGTTTC  
CV CTTCTGAATCACTCGGCGCTCTAGGATAGCTTCAGGCTGTTGCATGATCGTTGAGTGTTTC  
\*\*\*\*\*

SU1 TGAGATTGAAGTTAGTTGGGAGATGGTAGGGGTAATGGTCCTTATGTGCTTCTTCAACAT  
SU2 TGAGATTGAAGTTAGTTGGGAGATGGTAGGGGTAATGGTCCTTATGTGCTTCTTCAACAT  
SD TGAGATCGAAGTTAGTTGGGAGATGGTAGGGGTAATGGTCCTCATGTGCTTCTTCAACAT  
WP TGAGATTGAAGTTAGTTGGGAGATGGTAGGGGTAATGGTCCTTATGTGCTTCTTCAACAT  
CV TGAGATTGAAGTTAGTTGGGAGATGGTAGGGGTAATGGTCCTTATGTGCTTCTTCAACAT  
\*\*\*\*\*

SU1 GTTAACATGGAACACATCGTGTATCTATGAGTTTAGAGGTAGAAGTGCCTGTAGGCTAC  
SU2 GTTAACATGGAACACATCGTGTATCTATGAGTTTAGAGGTAGAAGTGCCTGTAGGCTAC  
SD GTTAACATGGAACACATCGTGTATCTATGAGTTTAGAGGTAGAAGTGCCTGTAGGCTAC  
WP GTTAACATGGAACACATCGTGTATCTATGAGTTTAGAGGTAGAAGTGCCTGTAGGCTAC  
CV GTTAACATGGAACACATCGTGTATCTATGAGTTTAGAGGTAGAAGTGCCTGTAGGCTAC  
\*\*\*\*\*

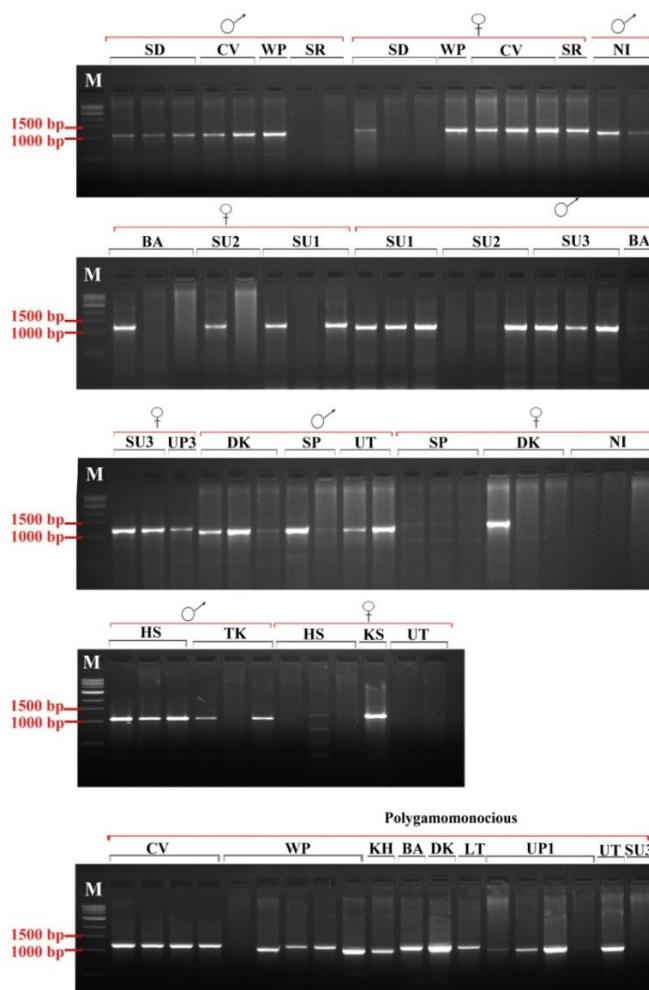
SU1 TAGACCAATTTTCTCAATAACCATTTAAGGTCCAAAGAAGCATTGAGCAAGCTTCATAAA  
SU2 TAGACCAATTTTCTCAATAACCATTTAAGGTCCAAAGAAGCATTGAGCAAGCTTCATAAA  
SD TAGACCAATTTTCTCAATAACCATATAAGGTCCAAAGAAGCGTTGAGCAAGCTTCATAAA  
WP TAGACCAATTTTCTCAATAACCATATAAGGTCCAAAGAAGCGTTGAGCGAGCTTCATAAA  
CV TAGACCAATTTTCTCAATAACCATATAAGGTCCAAAGAAGCGTTGAGCGAGCTTCATAAA  
\*\*\*\*\*

SU1 TTAACGAAAAGCTACAAAAGTCTACTGATAGGGTTGTAGCTTCAAATAGACATATTCTCC  
SU2 TTAACGAAAAGCTACAAAAGTCTACTGATAGGGTTGTAGCTTCAAATAGACATATTCTCC  
SD TTAACGAAAAGCTACAAAAGTCTACTGATAGGGTTGTAGCTTCAAATAGACATATTCTCC  
WP TTAACGAAAAGCTACAAAAGTCTACTGATAGGGTTGTAGCTTCAAATAGACATATTCTCC  
CV TTAACGAAAAGCTACAAAAGTCTACTGATAGGGTTGTAGCTTCAAATAGACATATTCTCC  
\*\*\*\*\*

SU1 TAGTAGGAAGGAGAGCTCTCTTCTATGTTGATCGGTTTTACACTTCATACAGTTTTGAGC  
SU2 TAGTAGGAAGGAGAGCTCTCTTCTATGTTGATCGGTTTTACACTTCATACAGTTTTGAGC  
SD TAGTAGGAAGGAGAGCTCTCTTCTATGTTGATCGGTTTTACACTTCATACAGTTTTGAGC  
WP TAGTAGGAAGGAGAGCTCTCTTCTATGTTGATCGGTTTTACACTTCATACAGTTTTGAGC  
CV TAGTAGGAAGGAGAGCTCTCTTCTATGTTGATCGGTTTTACACTTCATACAGTTTTGAGC  
\*\*\*\*\*

SU1 TTGTAGAATACTGGGG  
SU2 TTGTAGAATACTGTGG  
SD TTGTAGAATACTGTGG  
WP TTGTAGAATACTGTGG  
CV TTGTAGAATACTGGGG  
\*\*\*\*\* \*\*

**Figure. S8-A.** Representative agarose gel (1.5%) showing product size variation with primer pair: HRSS1 and HRML2, in male (~1100 base pair), female plants (~1200 base pair) and PGM plants. *Samples lanes in gels are marked with the population code (given in Supplementary Data Table S1). M: DNA size marker.*



**Figure. S8-B.** Alignment of (consensus sequences of three clones) sequences from male and female plants generated through sequencing of a region amplified using primer pair HRSS1 and HRML2. In female plants ~100bp additional fragment is present at the SCAR locus which splits the HRMS1 primer (Boxed).

SDM1	TGACAACGAGCCAATTCT-TCAGCAGCAAATTTGAAAACAT-GTAGTTAATWTGCTAGAG	58
CVM1	TGACAACGAGCCAATTCT-TCAGCAGCAAATTTGAAAACAT-GTAGTTAATWTGCTAGAG	58
DKMI	TGACAASGAGCCAATTYT-TCAGCAGCAAATTTGAAAACAT-GTAGTTAATWTGCTAGAG	58
KSMI	TGACAACGASCCAATTCT-TCAGCAGCAAATTTGAAAACAT-GTAGTTAATWTGCTAGAG	58
HSM1	TGACAACGASCCAATTCT-TCAGCAGCAAATTTGAAAACAT-GTAGTTAATWTGCTAGAG	58
SU1M1	TGACAACGRGCCAATYY-TCMGCAGCAAATTTGAAAACMTTGTAGTTAATWTGCTAGR	59
HSF1	TGACAACGASCCAATYYTCTCAGCAGCAAATTTGAAMACWGTGTAGTTAATWTGSKRGR	60
KSF1	TGACAACGAGCCMATTYTCTCRGCAGCAAATTTGAAAMCWT-GTRGTTAATATGCTRGR	59
SU1F1	TGACAACGAGCCMATTCT-TCRGCAGCAAATTTGAAAMCWT-GTRGTTAATWTGCTRGR	58
DKF1	TGACAACGMGCYTAWTTYTTTCRGCAGCAAATTTGAAACACWGTGAKTTAATWTGSTRGR	60
SDF1	TGAMACGAGCCW ATTCT-TCASCAGCAAATTTGAAAACAT-GTWGTTAATATGCTRAG	57
CVF1	TGACAACGRGCCAATTCT-TCAGCAGCAAATTTGAAAACMT-GTAGTTAATWTGCTAGAG	58
	*** * * * * ** ***** ** *** * * *	
SDM1	G-TACATGAATAAGAAAAMMAGAGTAAAATTACCAT-CACGCAAAT-CACTTTAATCGCA	115
CVM1	G-TACATGAATAAGAAAAACAGAGTAAAATTACCAT-CACGCAAAT-CACTTTAATCGCA	115
DKMI	G-TACATGAATAAGAAAAMCAGAGTAAAATTACCAT-CACGCAAAT-CACTTTAATCGCA	115
KSMI	G-TACATGAATAAGAAAAMCRGRGTAAAATTMCCAT-CACGCAAAT-CACTTTAATCGCA	115
HSM1	G-TACATGAATAAGAAAAMCAGAGTAAAATTMCCAT-CACGCAAAT-CACTTTAATCGCA	115

SU1M1 G-TMCATGAATAAGAAAAACRGRGTAAAAATTMCCMT-CMCGCAAAT-CACTTTAATCGCA 116  
HSF1 G-YACATGAATAAGAAAAACRAGTAAAAATTMCCMTCCACGCAAATCCAYTTWAATCGCA 119  
KSF1 G-TMCATGAATAAGAAAAACRGRGTAAAAATTMCCMT-CMCGCAAAY-CACTTTAATCGCA 116  
SU1F1 G-TACATGAATAAGAAAAACRGRGTAAAAATTACCMT-CMMGCAAAT-CACTTTWATCGCA 115  
DKF1 GGTMCWTGAATAAGAAAAACRGRGTAAAAATTWCCMTCMCCGCAAATCMYTTTTAATCGCA 120  
SDF1 G-TMCATGAATAAGAAAAACRAGTAAAAATTMCCMT-CACGCAAAT-CACTTTAATCGCA 114  
CVF1 G-TACMTGAATAAGAAAAACRGRGTAAAAATTMCCMT-CMCGCAAAT-CACTTTAATCGCA 115  
\* \* \*\*\*\*\* \* \*\*\*\*\* \*\* \* \*\*\*\*\* \*\* \*\*\*\*\*

SDM1 TGATG-ACATACATTGGCCTTT-CAAGCGGGGGCATG-CCACTTTG-TTATCTCACAT-A 170  
CVM1 TGATG-ACATACATTGGCCTTT-CAAGCGGGGGCATG-CCACTTTG-TTATCTCACAT-A 170  
DKMI TGATG-ACATACATTGGCCTTT-CAAGCGGGGGCATG-CCACTTTG-TTATCTCACAT-A 170  
KSMI TGATG-ACATACATTGGCCTTT-CAAGCGGGGGCATG-CCACTTTG-TTATCTCACAT-A 170  
HSM1 TGATG-ACATACATTGGCCTTT-CAAGCGGGGGCATG-CCACTTTG-TTATCTCACAT-A 170  
SU1M1 TGATG-ACATACATTGGCCTTT-CAAGCGGGGGCATG-CCACTTTG-TTATCTCACAT-A 171  
HSF1 TGATGACCATACATTGGCCTTTTTCAASGGGGGCAWCCCAATTTG-TTWTCTCACAT-A 177  
KSF1 TGATG-ACATMCATTGGCCTTT-CAAACGGGGGCATG-CCACTTTG-TTATCTCACAT-A 171  
SU1F1 TGATG-ACATMCATTGGCCTTT-CAAACGGGGGCATG-CCACTTTG-TTATCTCACAT-A 170  
DKF1 TGATG-ACATACATTGGCCTTTTTCAASGGGGGCAW-CCACTTTGGTTATCTCACATAA 178  
SDF1 TGATG-ACATMCATTGGCCTTT-CAAACGGGGGCATG-CCACTTTG-TTATCTCACAT-A 169  
CVF1 TGATG-ACATMCATTGGCCTTT-CAAACGGGGGCATG-CCACTTTG-TTATCTCACAT-A 170  
\*\*\*\*\* \*\* \*\*\*\*\* \*\* \*\*\*\*\* \* \*\* \*\*\*\*\* \*\* \*\*\*\*\* \*\*

SDM1 AAAATAATTATTTAATCCTTTGGGGAAGCACATACTGTAAAAATCCTCTAT-CTCAT-AAT 228  
CVM1 AAAATAATTATTTAATCCTTTGGGGAAGCACATACTGTAAAAATCCTCTAT-CTCAT-AAT 228  
DKMI AAAATAATTATTTAATCCTTTGGGGAAGCACATACTGTAAAAATCCTCTAT-CTCAT-AAT 228  
KSMI AAAATAATTATTTAATCCTTTGGGGAAGCACATACTGTAAAAATCCTCTAT-CTCAATAAT 229  
HSM1 AAGATAATTATTTAATCCTTTGGGGAAGCACATACTGTAAAAATCCTCTAT-CTCAT-AAT 228  
SU1M1 AAAATAATTATTTAATCCTTTGGGGAAGCACATACTGTAAAAATCCTCTATTCTCAT-AAT 230  
HSF1 AAAATAATTATTTAATCCTTTGGGGAAGCACATACTGTAAAAATCCTCTWTTCTCAT-AAT 236  
KSF1 AAAATAATTATTTWATCCTTTGGGGAAGCACATACTGTAAAAATCCTCTATTCTCAT-AAT 230  
SU1F1 AAAATAATTATTTAATCCTTTGGGGAAGCACATACTGTAAAAATCCTCTATTCTCAT-AAT 229  
DKF1 AAAATAATTATTTAATCCTTTGGGGAAGCACATACTGTAAAAATCCTYTTATCTCAT-AAT 237  
SDF1 AAAATAATTATTTAATCCTTTGGGGAAGCACATACTGTAAAAATCCTCTTATCTCAT-AAT 228  
CVF1 AAAATAATTATTTAATCCTTTGGGGAAGCACATACTGTAAAAATCCTCTAATCTCAT-AAT 229  
\*\* \*\*\*\*\* \*\*\*\*\* \*\*\*\*\* \* \*\*\*\*\* \*\* \*\*\*\*\* \*\*

SDM1 TGCATAAAAGAGAAATTAGAATTCTCTACTTAGTCTAACCCAAATAGAATAAGATTATCA 288  
CVM1 TGCATAAAAGAGAAATTAGAATTCTCTACTTAGTCTAACCCAAATAGAATAAGATTATCA 288  
DKMI TGCATAAAAGAGAAATTAGAATTCTCTACTTAGTCTAACCCAAATAGAATAAGATTATCA 288  
KSMI TGCATAAAAGAGAAATTAGAATTCTCTACTTAGTCTAACCCAAATAGAATAAGATTATCA 289  
HSM1 TGCATAAAAGAGAAATTAGAATTCTCTACTTAGTCTAACCCAAATAGAATAAGATTATCA 288  
SU1M1 TGCATAAAAGAGAAATTAGAATTCTCTACTTAGTCTAACCCAAATAGAATAAGATTATCA 290  
HSF1 TGCATAAAAGAGAAATTAGAATTCTCTACTTAGTCTAACCCAAATAGAATAAGATTATCA 296  
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DKF1 TGCATAAAAGAGAAATTAGAATTCTCTACTTAGTCTAACCCAAATAGAATAAGATTATCA 297  
SDF1 TGCATAAAAGAGAAATTAGAATTCTCTACTTAGTCTAACCCAAATAGAATAAGATTATCA 288  
CVF1 TGCATAAAAGAGAAATTAGAATTCTCTACTTAGTCTAACCCAAATAGAATAAGATTATCA 289  
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CVM1 TATAAACTAGAAAAGCATACTTTGACTCTTAGCCAATAGCTCAATCACCG-TATATGCAA 347  
DKMI TATAAACTAGAAAAGCATACTTTGACTCTTAGCCAATAGCTCAATCACCG-TATATGCAA 347  
KSMI TATAAACTAGAAAAGCATACTTTGACTCTTAGCCAATAGCTCAATCACCG-TATATGCAA 348  
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SU1M1 TATAAACTAGAAAAGCATACTTTGACTCTTAGCCAATAGCTCAATCACCG-TATATGCAA 349  
HSF1 TATAAACTAGAAAAGCATACTTTGACTCTTAGCCAATAGCTCAATCACCG-TATATGCAA 355  
KSF1 TATAAACTAGAAAAGCATACTTTGACTCTTAGCCAATAGCTCAATCACCGGTATATGCAA 350  
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DKF1 TATAAACTAGAAAAGCATACTTTGACTCTTAGCCAATAGCTCAATCACCG-TATATGCAA 356  
SDF1 TATAAACTAGAAAAGCATACTTTGACTCTTAGCCAATAGCTCAATCACCG-TATATGCAA 347

CVF1 TATAAACTAGAAAAGCATACTTTGACTCTTAGCCAATAGCTCAATCACCG-TATATGCAA 348  
\*\*\*\*\*

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CVM1 GTAAAAAAAAATTGAATAGAATCATTAAATTGGTCGGAAACACAGTAATAACCCCTTTGAAG 407  
DKMI GTAAAAAAAAATTGAATAGAATCATTAAATTGGTCGGAAACACAGTAATAACCCCTTTGAAG 407  
KSM1 GTAAAAAAAAATTGAATAGAATCATTAAATTGGTCGGAAACACAGTAATAACCCCTTTGAAG 408  
HSM1 GTAAAAAAAAATTGAATAGAATCATTAAATTGGTCGGAAACACAGTAATAACCCCTTTGAAG 407  
SU1M1 GTAAAAAAAAATTGAATAGAATCATTAAATTGGTCGGAAACACAGTAATAACCCCTTTGAAG 409  
HSF1 GTAAAAAAAAATTGAATAGAATCATTAAATTGGTCGGAAACACAGTAATAACCCCTTTGAAG 415  
KSF1 GTAAAAAAAAATTGAATAGAATCATTAAATTGGTCGGAAACACAGTAATAACCCCTTTGAAG 410  
SU1F1 GTAAAAAAAAATTGAATAGAATCATTAAATTGGTCGGAAACACAGTAATAACCCCTTTGAAG 408  
DKF1 GTAAAAAAAAATTGAATAGAATCATTAAATTGGTCGGAAACACAGTAATAACCCCTTTGAAG 416  
SDF1 GTAAAAAAAAATTGAATAGAATCATTAAATTGGTCGGAAACACAGTAATAACCCCTTTGAAG 407  
CVF1 GTAAAAAAAAATTGAATAGAATCATTAAATTGGTCGGAAACACAGTAATAACCCCTTTGAAG 408  
\*\*\*\*\*

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CVM1 AAAAGGAAAAGAACTGAAGAAACCTTATTTAGAAGATGAATCAAAGGCATAAAACAAATA 467  
DKMI AAAAGGAAAAGAACTGAAGAAACCTTATTTAGAAGATGAATCAAAGGCATAAAACAAATA 467  
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SU1M1 TAAAAAGACAGAAGTAACACCAAGAACACTAGGTTATATACATCTTTATACTCAACCCCT 529  
HSF1 TAAAAAGACAGAAGTAACACCAAGAACACTAGGTTATATACATCTTTATACTCAACCCCT 535  
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DKF1 TAAAAAGACAGAAGTAACACCAAGAACACTAGGTTATATACATCTTTATACTCAACCCCT 536  
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CVF1 TAAAAAGACAGAAGTAACACCAAGAACACTAGGTTATATACATCTTTATACTCAACCCCT 528  
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HSM1 CCTTCTCAAACCATATAAGTAACTTCTACTTGATAATATTCCTCACGAGCTTCCGTAGAA 587  
SU1M1 CCTTCTCAAACCATATAAGTAACTTCTACTTGATAATATTCCTCACGAGCTTCCGTAGAA 589  
HSF1 CCTTCTCAAACCATATAAGTAACTTCTACTTGATAATATTCCTCACGAGCTTCCGCAGAA 595  
KSF1 CCTTCTCAAACCATATAAGTAACTTCTACTTGATAATATTCCTCACGAGCTTCCGTAGAA 590  
SU1F1 CCTTCTCAAACCATATAAGTAACTTCTACTTGATAATATTCCTCACGAGCTTCCGTAGAA 588  
DKF1 CCTTCTCAAACCATATAAGTAACTTCTACTTGATAATATTCCTCACGAGCTTCCGTAGAA 596  
SDF1 CCTTCTCAAACCATATAAGTAACTTCTACTTGATAATATTCCTCACGAGCTTCCGTAGAA 587  
CVF1 CCTTCTCAAACCATATAAGTAACTTCTACTTGATAATATTCCTCACGAGCTTCCGTAGAA 588  
\*\*\*\*\*

SDM1 AGAGATGAAAGAGAAGAAAAC TAATAAGTTATTAATTTTTTCAAAGAAAACCGAGTTTCAG 647  
CVM1 AGAGATGAAAGAGAAGAAAAC TAATAAGTTATTAATTTTTTCAAAGAAAACCGAGTTTCAG 647  
DKMI AGAGATGAAAGAGAAGAAAAC TAATAAGTTATTAATTTTTTCAAAGAAAACCGAGTTTCAG 647  
KSM1 AGAGATGAAAGAGAAGAAAAC TAATAAGTTATTAATTTTTTCAAAGAAAACCGAGTTTCAG 648

HSM1 AGAGATGAAAGAGAAGAAAAC TAATAAGTTATTAATTTTTCAAAGAAAACCGAGTTTCAG 647  
SU1M1 AGAGATGAAAGAGAAGAAAAC TAATAAGTTGTTAATTTTTCAAAGAAAACCGAGTTTCAG 649  
HSF1 AGAGATGAAAGAGAAGAAAAC TAATAAGTTATTAATTTTTCAAAGAAAACCGAGTTTCAG 655  
KSF1 AGAGATGAAAGAGAAGAAAAC TAATAAGTTATTAATTTTTCAAAGAAAACCGAGTTTCAG 650  
SU1F1 AGAGATGAAAGAGAAGAAAAC TAATAAGTTATTAATTTTTCAAAGAAAACCGAGTTTCAG 648  
DKF1 AGAGATGAAAGAGAAGAAAAC TAATAAGTTATTAATTTTTCAAAGAAAACCGAGTTTCAG 656  
SDF1 AGAGATGAAAGAGAAGAAAAC TAATAAGTTATTAATTTTTCAAAGAAAACCGAGTTTCAG 647  
CVF1 AGAGATGAAAGAGAAGAAAAC TAATAAGTTATTAATTTTTCAAAGAAAACCGAGTTTCAG 648  
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SDM1 AAAGAAAAATATTTAAATCTTTGCCAGCTTATTAATAATCAATCTGTTAGGGTTATTTTG 707  
CVM1 AAAGAAAAATATTTAAATCTTTGCCAGCTTATTAATAATCAATCTGTTAGGGTTATTTTG 707  
DKMI AAAGAAAAATATTTAAATCTTTGCCAGCTTATTAATAATCAATCTGTTAGGGTTATTTTG 707  
KSMI AAAGAAAAATATTTAAATCTTTGCCAGCTTATTAATAATCAATCTGTTAGGGTTATTTTG 708  
HSM1 AAAGAAAAATATTTAAATCTTTGCCAGCTTATTAATAATCAATCTGTTAGGGTTATTTTG 707  
SU1M1 AAAGAAAAATATTTAAATCTTTGCCAGCTTATTAATAATCAATCTGTTAGGGTTATTTTG 709  
HSF1 AAAGAAAAATATTTAAATCTTTGCCAGCTTATTAATAATCAATCTGTTAGGGTTATTTTG 715  
KSF1 AAAGAAAAATATTTAAATCTTTGCCAGCTTATTAATAATCAATCTGTTAGGGTTATTTTG 710  
SU1F1 AAAGAAAAATATTTAAATCTTTGCCAGCTTATTAATAATCAATCTGTTAGGGTTATTTTG 708  
DKF1 AAAGAAAAATATTTAAATCTTTGCCAGCTTATTAATAATCAATCTGTTAGGGTTATTTTG 716  
SDF1 AAAGAAAAATATTTAAATCTTTGCCAGCTTATTAATAATCAATCTGTTAGGGTTATTTTG 707  
CVF1 AAAGAAAAATATTTAAATCTTTGCCAGCTTATTAATAATCAATCTGTTAGGGTTATTTTG 708  
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SDM1 TAGAATTCAGCAGAATAGAATGAGAGAGAAAGAGAAAAGAGAGTTAGGGAGGCAGAGGG 767  
CVM1 TAGAATTCAGCAGAATAGAATGAGAGAGAAAGAGAAAAGAGAGTTAGGGAGGCAGAGGG 767  
DKMI TAGAATTCAGCAGAATAGAATGAGAGAGAAAGAGAAAAGAGAGTTAGGGAGGCAGAGGG 767  
KSMI TAGAATTCAGCAGAATAGAATGAGAGAGAAAGAGAAAAGAGAGTTAGGGAGGCAGAGGG 768  
HSM1 TAGAATTCAGCAGAATAGAATGAGAGAGAAAGAGAAAAGAGAGTTAGGGAGGCAGAGGG 767  
SU1M1 TAGAATTCAGCAGAATAGAATGAGAGAGAAAGAGAAAAGAGAGTTAGGGAGGCAGAGGG 769  
HSF1 TAGAATTCAGCAGAATAGAATGAGAGAGAAAGAGAAAAGAGAGTTAGGGAGGCAGAGGG 775  
KSF1 TAGAATTCAGCAGAATAGAATGAGAGAGAAAGAGAAAAGAGAGTTAGGGAGGCAGAGGG 770  
SU1F1 TAGAATTCAGCAGAATAGAATGAGAGAGAAAGAGAAAAGAGAGTTAGGGAGGCAGAGGG 768  
DKF1 TAGAATTCAGCAGAATAGAATGAGAGAGAAAGAGAAAAGAGAGTTAGGGAGGCAGAGGG 776  
SDF1 TAGAATTCAGCAGAATAGAATGAGAGAGAAAGAGAAAAGAGAGTTAGGGAGGCAGAGGG 767  
CVF1 TAGAATTCAGCAGAATAGAATGAGAGAGAAAGAGAAAAGAGAGTTAGGGAGGCAGAGGG 768  
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SDM1 ATAATTGGGTTCAATTTCTGTTACTCT----- 793  
CVM1 ATAATTGGGTTCAATTTCTGTTACTCT----- 793  
DKMI ATAATTGGGTTCAATTTCTGTTACTCT----- 793  
KSMI ATAATTGGGTTCAATTTCTGTTACTCT----- 794  
HSM1 ATAATTGGGTTCAATTTCTGTTACTCT----- 793  
SU1M1 ATAATTGGGTTCAATTTCTGTTACTCT----- 795  
HSF1 ATAATTGGGTTCAATTTCTGTTACTCTTTATTCCAATCATTGGACTATATATAGCTTTACA 835  
KSF1 ATAATTGGGTTCAATTTCTGTTACTCTTTATTCCAATCATTGGACTATATATAGCTTTACA 830  
SU1F1 ATAATTGGGTTCAATTTCTGTTACTCTTTATTCCAATCATTGGACTATATATAGCTTTACA 828  
DKF1 ATAATTGGGTTCAATTTCTGTTACTCTTTATTCCAATCATTGGACTATATATAGCTTTACA 836  
SDF1 ATAATTGGGTTCAATTTCTGTTACTCTTTATTCCAATCATTGGACTATATATAGCTTTACA 827  
CVF1 ATAATTGGGTTCAATTTCTGTTACTCTTTATTCCAATCATTGGACTATATATAGCTTTACA 828  
\*\*\*\*\*

SDM1 -----  
CVM1 -----  
DKMI -----  
KSMI -----  
HSM1 -----  
SU1M1 -----  
HSF1 TATGCGTGATTAAAAGGACAGAGAATGCTAAGGAATTGGCTCCAATATGATAACCAACTC 895  
KSF1 TATGCGTGATTAAAAGGACAGAGAATGCTAAGGAATTGGCTCCAATATGATAACCAACTC 890  
SU1F1 TATGCGTGATTAAAAGGACAGAGAATGCTAAGGAATTGGCTCCAATATGATAACCAACTC 888  
DKF1 TATGCGTGATTAAAAGGACAGAGAATGCTAAGGAATTGGCTCCAATATGATAACCAACTC 896





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KSM1      CCGGTTGG-AGCCCCTACCCATTT-GACCAGAAWTT-CAAAATTTTGGGTKGAWAWCTAT 1078
HSM1      TCGGTTGG-AGCCCCTACCCATTT-GACCAGAATTT-CAAATTTT--GGTTGAWATCTAT 1075
SU1M1    CCGGTTGG-AGCCCCTACCCATTT-GACCAGAATTT-CAAATTTT--GGTTGAWATCTAT 1078
HSF1     CCGGTTGG-AGCCCCTACCCATTT-GACCARAATTT-CAAATTTT--GGTTGRWAWCTAW 1181
KSF1     CCGGTTGG-RGCCCCWACCCATTT-GACCAGAATTT-CAAATTTT--GGTKGRWAWCTAW 1175
SU1F1    CCGGTTGG-AGCCCCTACCCATTT-GACCARAATTT-CAAATTTT--GGTTGRWAWCYAW 1173
DKF1     CCGGTGTGGAGCCCCYMCCCWTTT-GMCCARAATTW-MAAATTTK--GGKTGAWAWMWCA 1183
SDF1     YCGGTTGG-AGCCCCTACCCWTTT-GACCARAATTT---CAAATTTTGGTTGAWAWCWAW 1173
CVF1     CCGGTTGGAGCCCCWACCCMTTTT-GACCAGAATATYCAAAATTTTGGGTKGAWAWCYAA 1187
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SDM1      -CCTTCTG---AATCACT-CGGCGCTCT-AGGATAG 1104
CVM1      -CCTTCTG---AATCACT-CGGCGCTCT-AGGAWAG 1104
DKMI      -CCTTCTG---AATCACT-CGGCGCTCT-AGGAWAG 1104
KSM1      CCCTTCTG---AAWCACTCCGGCGCTCTTAGGATAG 1111
HSM1      -CCTTCTG---AATCACT-CGGCGCTCT-AGGAWAG 1105
SU1M1    -CCTTCTG---AATCACT-CGGCGCTCT-AGGAWAG 1108
HSF1     -CCTTCTG---AATCACTCCGGCGCTCT-AGGATAG 1212
KSF1     -CCTTCTG---AATMACT-CSGCG-KCT-AGGATAG 1204
SU1F1    -CCYTCYG---AATCACT-CSGCGCTCT-AGGAWAG 1203
DKF1     YCCYTCTG---ARWMACY-CSGCGCYCY-AGGATAG 1209
SDF1     -CCYTCTS---AAWCACT-CSGCGCYCTCARGAWAG 1204
CVF1     -TCCTCTCTCGAAWCAMTTCCGGCGCSCTYTAG---- 1218
          * ** * * * ** *

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**Figure S9.** DOT Blot assay: Each dot (encircle) represent the loaded cloned sequence of HRMSSR obtained from genome walking. The numbers show the address of the sequence as depicted in main Figure 3c. Hybridization was carried out with female (a) and male (b) genomic DNA.

