

**Table S1** List of primers used to validate SNPs between R500/IMB211 genotypes of *B. rapa*

| Primer name              | Forward primer              | Reverse primer              |
|--------------------------|-----------------------------|-----------------------------|
| A01:2641459-2641759_37   | ATGATGTTGATGATATCGAGAATGA   | TTGAAAACAGACACAACCTAACAACA  |
| A01:2504268-2504568_23   | CAAGCTGTCTTTGTGCTCCTAC      | TAAGAGGGAACGTGCAGAAATCTAT   |
| A01:2409444-2409744_35   | GAATAATCATTGTGTGGAACCAGAT   | CAAGATACCGAAGGATGTCACTACT   |
| A01:2430717-2431017_29   | ACTGTCATTATTTGGCTAAACTCG    | TTTCTTGGTAACAATTTTCCCTGTA   |
| A10:4784864-4785164_29   | GACTTTCAAATTAACAATAGGGTAG   | CTTTTGCTAGCCCCGAAATAACTC    |
| A10:126179-126479_26     | CCATTCTTATAAATTACGGGAAGAT   | TGGGTTTACGATTTTAAATCAATGTT  |
| A09:25567566-25567866_81 | AATATCCCGGTCCAGAATCTAGT     | GAAACTATAGGAGGCCATGACTACA   |
| A08:16903736-16904036_81 | AGCCTACGCCGTACCTTCT         | GTGTGGTAAGGGAGCATCGT        |
| A07:21482713-21483013_66 | GAATCCAAAATTGTAATTGCATGAT   | TAGAGATATGCTTTTCTTTGCCATC   |
| A07:11721587-11721887_41 | AGTCCATACAAGCTCACCTCTCTAA   | TAAAATCCAAGGAAATGTGTTTTGT   |
| A07:8435288-8435588_28   | TTCTTTTTGGATAAATTCTTGAGTTC  | CAAGTACGAGCATACAACCTTGAGAA  |
| A07:4582105-4582405_29   | TGCTATCATAGTTGTGAATCTTTGTT  | GTTTAAACATGAGCTAGCACAAACA   |
| A06:9950425-9950725_67   | TAACCAAAAATTAATGTGGACATGG   | AATGGTTTTATCTTTCGATCTGATG   |
| A06:6389021-6389321_27   | CTACCAGGAGAGGAAGTGATTGATA   | GTGACTAAAGCAATGCAACATGAAT   |
| A05:21349588-21349888_26 | TACTCTCGAAATGAGTTCATGAAT    | AACCGAAAGAGTTCGGTATAGGAC    |
| A05:1290236-1290536_38   | CATCTAGAAGAACTCTCGAGCAAG    | AGAGGTTGAGGAAGAAGAGGTAATC   |
| A04:13577963-13578263_24 | ACGTGAATTGGAGAAGGGACTA      | TCCTTCTTTTATCCTCTCCTCTCT    |
| A04:5923147-5923447_34   | AGCATATAGTTATTGTGACATAGGTTG | TTTGGAACATTTTATACACATGATGA  |
| A04:1864440-1864740_32   | CCCACTATGTAAGTACCAGACATA    | GGGTAATCAAACATTAGTTACTCTGG  |
| A03:3325120-3325420_23   | GACTTGGACCTGGTTGATTGAG      | GCAGACAAGACAACCTAGTATCAGCA  |
| A03:1011952-1012252_31   | TTGGTTTGCTTATGTATTATAGCAAGT | GAACTTTCACGGAATGTGTTTAAAG   |
| A02:24429642-24429942_38 | GAATGGCAAACCTGAGTGTTAGTTT   | TACACGAAGACAGCTATGTCACAC    |
| A02:23763206-23763506_59 | GATAAGACAAAATGACTGCAACAA    | CACATTAAAGTCAGGCAAAGGTT     |
| A02:20219025-20219325_34 | TTACGTTCAAATGTGAAGGCTATT    | AAAGAGAGCTATTGGTCCATGTCTA   |
| A02:18093943-18094243_63 | TTAAAGCTTCATTTCAATTCGAGTG   | ACATAAGCTAAAATGCAAATGTCAA   |
| A02:16080177-16080477_30 | AAACAGTAAAGAAATCAACCATTG    | TTATATATCGTGTGGCTTGGAGAAT   |
| A02:15281374-15281674_32 | CGTTGGAGATGAAGAAGCTGAT      | AGCCTTGCTGTTTTGAGAGAAC      |
| A01:24666619-24666919_38 | CTCCACGAGAGAGATCAGCTTT      | ATGTAGGCAACACCAAGTCTTCT     |
| A01:22687697-22687997_32 | AGTGTCAGAGAAGATGAAGCTTGTG   | CCAACAACATTTCTAGCAAACCTTA   |
| A01:12763247-12763547_81 | GGAGACTGTAGTCGAAAGTTCA      | AACAGCAAAGAAAGACAAGAACAC    |
| A01:10484884-10485184_26 | AAGAAGAGATGTGTGCGTTTGTAT    | TTTTTCTATATGGTTCTTCTCACTT   |
| A01:7221153-7221453_27   | AGAAAATCATTCCATCCTGAACAC    | TGTGGTTCAACTTAAGAAAATGTTAGA |
| A01:3818667-3818967_40   | AAAGTAGCGCACATGATATTCAAA    | CTTAACACCGACAGTGGAACCTTAT   |
| A01:3469236-3469536_35   | TGAAATTTACATGTCACATAACCAC   | TTTTGAGAGAGAGAGAGAGACGTTG   |

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| A01:2913765-2914065_32   | AGAGGACGGGGAAATGATCT        | GTGACACCGAGAATACAAGAGTTTT   |
| A09:23861226-23861526_39 | CTTTATGCGAGATTTTGAATCTGTT   | GTAGAAACTGGGCTATAACAATCCA   |
| A09:16171653-16171953_37 | CATTGAGTTTCCATAAATCCCATTA   | TCCGTGTATAGATCATAGTGGGAAG   |
| A09:6242303-6242603_28   | CAAATAGGAGCATGAGCTGAGAAG    | ATATATCAGAGACGGCGGTTGAAG    |
| A08:9873219-9873519_39   | GTTTTTGGTGGTTAGTCTGAGTGAG   | GTGATTCTCTTGAGGATCGGTCT     |
| A07:14481590-14481890_30 | AAAACCACACAGGACTAAAAATATAAA | CTAAAACCCAAAATCTCAAACGTA    |
| A07:10890009-10890309_41 | CACTTGTGATTCTCTCAGTCCTCA    | GAAACTAAAATCAGAAAGCCAACCT   |
| A07:7433306-7433606_52   | AAGTACAGCAGCATAAGAAGACCTG   | TGCGCTATCTAGTTGTGTGATTCTA   |
| A07:1449431-1449731_61   | TTAAACCTAAAAACACCACCAAAAA   | CTAGAATCCACGGTTTCTGATGTT    |
| A06:8961822-8962122_39   | GAATACGACCGTCAAATGAATAAG    | CATGAAATGTCTTTAGCTAGTTTTTGA |
| A06:4775258-4775558_40   | TAATTGATTATGTGTATTGCCATTG   | TATGTTCTTGTCTTGAATGACTGT    |
| A05:18736009-18736309_36 | GCCCATCTAACCAGGTAGTGATTAT   | GTAGTACACGTGGCTTCTGTGAGT    |
| A05:2137672-2137972_80   | GCTCTACCGTATTCAGCAG         | TGATTTGTTCTACTAAGACAGCAG    |
| A04:12349509-12349809_35 | TCACCAAAAAGAGTAACCACCTTACA  | GTTCCGAATATGTGTGAATGAGAT    |
| A04:7348232-7348532_36   | ATTAACGAGAGTGCTAAGATGTGGA   | GTACTTGCGTAATTTTGTACTTCT    |
| A04:815297-815597_36     | GTAAGGGTGTGTCTTACCGTATG     | GATAGCATCCTACAAAGACACAACA   |
| A03:2501877-2502177_41   | TAACACATATGAATTGAACCCCAA    | TTGTTTCTAGTGCTAACATTTCCAA   |
| A03:637010-637310_26     | CCATATCAAAGTTTTTGGGTAGATT   | GAAAGTTTATACAAAGATGAGGGAAA  |
| A02:22284015-22284315_40 | CCTTGCTTTTGTCTTTTAGCTCTTG   | TAAACGTCAAACCTGTTTAGGGAAG   |
| A02:21573870-21574170_31 | CCGATGTCTCCGTTGAAGAT        | GATTTCACTCAGATCTTCGATTCAT   |
| A02:19686549-19686849_37 | TAAGAAGTGTCTCTCAGATCCT      | TCAGCAACCACTTTATAGTGCAA     |
| A02:16920930-16921230_32 | AAGAGGGAGAGAAAAAGAAACAAAA   | AAAAGGGATCTAAGAAACAAAGCAT   |
| A02:15918417-15918717_33 | TGATGCATGTTAAACTGCTATAAAGA  | GCCTTTCTCTATTCTGTTTTTATG    |
| A02:15544401-15544701_40 | TGAGAATCTGAAGGCATAAACTAGG   | CTCTTATGAGTCGGACGGAAAC      |
| A02:1775927-1776227_38   | GACTTCCAAGTGACAGTGCATAAAC   | AGATCCGGCTAAGTTTAACTCATT    |
| A02:867202-867502_41     | ATCATCAACCACAGGCACATAA      | AAGATTTAATTACTGTTTTGGTGCAG  |
| A02:100144-100444_38     | GGGGGAAGTCCACTAGTTGTT       | GTACTTCCACTGAATTTTCGATCTC   |
| A01:27324412-27324712_28 | GAATCTGCAGAGACATACTGGTTG    | AAATAGAATCTCCGATTCAAACAG    |
| A01:18850930-18851230_40 | TAGTGAGCGTGTGTTTTGTGTATT    | GATGAGTTGATAAGGCTAGCTGAAG   |
| A01:16389091-16389391_28 | ATAGCATGCATATTGGGGTCTCT     | TCTGTTCCAGACAAGATACGTCTAA   |
| A01:7930221-7930521_37   | CTCACC AATATCAGGACCAAGTAGT  | TGAAAGTCTCAGTTTTTGTGTTGGT   |
| A01:7064816-7065116_36   | AAGTCGTACAATCTTGCTGGTCAT    | GGCGTATTCTCTCTACCCCTACTAGA  |
| A09:11632252-11632552_26 | ATGTTTTCCATGTTCCGTTTCT      | ATATCAAGAAGATGCAGATGGAAGT   |
| A09:9394381-9394681_26   | ATTACCGCCGTGATAATATGC       | TCTCTCTCTCTCTCTGACTTACACA   |
| A09:3795646-3795946_37   | AGTTGGCGATGAAGGAGATG        | ACTGGTACAAGCACTTCCACTAGAC   |
| A08:9418706-9419006_37   | ATCAGACAAAATGTCACAATCAATG   | AGTCAAATTGAAGAGGAGAGTCTGA   |
| A07:13264897-13265197_60 | TGTATGATATATGTGCAGTTTCTTGG  | AATAACACTCACAAAGACCAAGAGG   |
| A07:10399471-10399771_26 | TTGCGTCTCTGACTATGGACTTAAT   | GTCCATTCTCTCTAACCACAGAAA    |
| A07:5290237-5290537_25   | TAGCGATCAGTGATGAGAAGAAAC    | TTGCAGAGATAAGCAGAGTTAACAA   |

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| A07:62937-63237_67       | TCTAATAAGTAATCACCAAGGAAGAGG | TTAAATCAGGTCTCTTCGTCTGTCT  |
| A06:7722860-7723160_32   | CAAATCATCAGAGATGAGTGACTGT   | GAAGTCAGATTTCGAAGTTTCAGAG  |
| A05:23123778-23124078_32 | CGCTGCGGTTAAGGTAATATAGTTT   | CATCCAAACTGAGAAAGACTGAATAA |
| A05:737763-738063_27     | ATCTAAGCTTTTGCAAGACATCCA    | AGAATCCGATAACTTCATTTGTGAC  |
| A05:1001717-1002017_28   | TTCTTTTTCTTCTCTTTTAGGTTT    | GAGTTCTTGAACAAGCTCTCTGAAC  |
| A04:8387375-8387675_32   | CGAGAGCAATGAAATAGTACTAAAAAG | TGCAGAGAGAATCATCGCTAGTAGT  |
| A04:4062660-4062960_35   | AGTGGTCCGGCGATTATTCT        | TGAAAATTATGTAAAAGTAGCAATGG |
| A04:21937-22237_37       | CCACCACCAGATCTTTTCTGTT      | CCTTCAGTGTTTACCCATCATCTTA  |
| A03:1789842-1790142_41   | GAGGAGATTAGTCCAAAGTCGTGT    | CAAAGAAGTAGTCCGAGAGTTGGTA  |
| A03:61334-61634_36       | GACACAAGAGCGCTCAAACC        | ACCTAAATCAAGCTAGGGCTTTAAC  |
| A02:24174743-24175043_41 | AGATTAGCTTACCATTGAAACAGCA   | GATATTGGATTGAGGATAGCTACG   |
| A02:20541059-20541359_41 | GACGATAGATGTTCTGATTGGCTA    | TTCTACATCCACAAGACTGCATAAC  |
| A02:19059447-19059747_34 | CTCTTTTCTTGAGGGATAACATTGA   | TAACTGAGGAGATACAAGGAGCACT  |
| A02:16536391-16536691_41 | CGAGTCCGGAGAAGATTCACT       | AGCTTCAAGTCAAAGTTACTCTGT   |
| A02:15823477-15823777_29 | CCAAAGATTTCTTCTGGTTTCC      | CAGCTATTTGTGTTGTTGTCTATGC  |
| A02:12835309-12835609_21 | CACGGAGGAGTCTTGAAGC         | ATCCCTGCGTACATCAATCC       |
| A01:10977047-10977347_25 | CTCTCTTATCCTCCTCCCTCTC      | GTACCTCTTCCGGTAACCACTT     |
| A01:4743386-4743686_30   | AAGTGTACCTGCAAACAGAAGAGAG   | ATTTTCACAATATCAGCCATTGTTT  |
| A01:2636910-2637210_41   | TCACCTTCCTCATTTCAGTAATTG    | CGACATATGTAGAAGTGACCAACAG  |
| A01:2623564-2623864_60   | TCACGTGAAAAATGACGTTACAAT    | AATTTTCATTGGCAAATCAGAAATTA |
| A01:2500749-2501049_21   | TTTATCGACGTTTGGCGTTT        | GAGATGAGATTGGGAAAGTGAAGT   |
| A01:2491118-2491418_26   | TTTTACCTGCATTATCCTTATTAC    | GGATAATCACAGAGAAAAGCCAAT   |
| A01:2488957-2489257_26   | ATCTGAGCTGCATTCAAGCTGT      | CGGCAGATTATTCACAGATAGAGTT  |
| A01:4327607-4327907      | TCAGGTATTACACTCGTTGAAGAAA   | TCATATTGGTTTGACTCTCCATTTT  |
| A09:7510144-7510444      | ATGATCATCTCCGACACATATTTT    | AATCAGTAGTTTAAAGTGCTCCACA  |
| A01:2647195-2647495_62   | GGGTTACCGATCTTTATCTTCAACT   | GTTAACCACCACCACCATACAAT    |
| A01:7654999-7655299_27   | GTAGGAGCAGGAATGATATGTTCAC   | TACTGATGATGGTGACACATAGGAT  |

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