

**Polymorphism Identification and Improved Genome Annotation of *Brassica rapa*  
Through Deep RNA Sequencing**

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**DOI: [10.1534/g3.114.012526](https://doi.org/10.1534/g3.114.012526)**

**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	CCCCTATGTAAGTACCAGACATA	GGGTAATCAAACATTAGTTACTCTGG
A03:3325120-3325420_23	GACTTGGACCTGGTTGATTGAG	GCAGACAAGACAAGTATCAGCA
A03:1011952-1012252_31	TTGGTTTGCTTATGTATTATAGCAAGT	GAACTTTCACGGAATGTGTTTAAAG
A02:24429642-24429942_38	GAATGGCAAACCTGAGTGTAGTTT	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	TGAAATTTACATGTCACATAACCC	TTTTGAGAGAGAGAGAGAGACGTTG

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	CTAAAACCCAAAATCTCAAAACGTA
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	GCTCTACCGTATTACAGCAG	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	CCTTGTCTTGTCTTTTAGCTCTTG	TAAACGTCAAACTGTTTAGGGAAG
A02:21573870-21574170_31	CCGATGTCTCCGTTGAAGAT	GATTTCACTCAGATCTTCGATTCAT
A02:19686549-19686849_37	TAAGAAGTGTCTCTCAGATCCT	TCAGCAACCACTTTATAGTGTCAA
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	TAGTGAGCGTGTGTTTTTGTGATT	GATGAGTTGATAAGGCTAGCTGAAG
A01:16389091-16389391_28	ATAGCATGCATATTGGGGTCTCT	TCTGTTCCAGACAAGATACGTCTAA
A01:7930221-7930521_37	CTCACC AATATCAGGACCAAGTAGT	TGAAAGTCTCAGTTTTTGTGTTGGT
A01:7064816-7065116_36	AAGTCGTACAATCTTGTCTGGTCAT	GGCGTATTCTCTCTACCCCTACTAGA
A09:11632252-11632552_26	ATGTTTTCCATGTTCTGCTTTCT	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	GAAATCAGATTTCGAAGTTTCAGAG
A05:23123778-23124078_32	CGCTGCGGTTAAGGTAATATAGTTT	CATCCAAACTGAGAAAGACTGAATAA
A05:737763-738063_27	ATCTAAGCTTTTGCAAGACATCCA	AGAATCCGATAACTTCATTTGTGAC
A05:1001717-1002017_28	TTCTTTTTCTTCTTCTTTTAGGTTT	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	TCACCTTCCTTATTTCAGTAATTG	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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**Table S2 List of primers used for semi-quantitative RT-PCR validations.**

Primer name	Forward primer	Reverse primer
BRME_31321	GGATGAAGATACAGTGTGAAGTGTG	ATCTGGTAAGTTTCGGAGCTAAGAT
BRME_27825	TTGAATATGAAGTGTGGTTGAAGAA	AATTATGAAGTGTCTAGGCCTTTGG
BRME_26899	ATTTTAAGCATGAGACAAATGGAGA	CACTTCAAATACGATCTCGACTCTT
BRME_26899	TATTTGGTTTTGGTTCTTTGACAAT	CTCATTTTGCATTAACCTTTCCACT
BRME_26751	GAGATAAACAAATGGACGGAGTTAGA	CAAGAACAAAGCTTTACCTCTCAAG
BRME_25902	AACCATTCAAACATTTTGTCTCTC	AAGACTACGAGCTGATAGCAAAGAC
BRME_24665	GCCAAAATACTCAAACATCAAACCT	TGTTTCTTCAAAGTCTCCTTGTCT
BRME_23842	AGTCAAATAATGGGTGAGTTAGCAG	GATGAGTCTTTTCAGTCAAGTGGAT
BRME_22309	TAAACATCAGAAAAAGATCGACACA	TGAAATTGCAGATTGAACAAGAATA
BRME_21821	CTTGAAGAAAGCTTGGTTCGAAT	CATATATCTCTGGCCATGTAAAC
BRME_21506	GATGCAGGTAGACGGGTTAGC	GACACAAAACCTATTGAAATCCTTAGC
BRME_20969	TTGGATTGTTGATGATCATGTTTAC	AATCAAACGAAATAGGGATTAGACC
BRME_20091	AGAATATCACATCCTGGAATTGTGT	GTTAAGAGATCACCCGAGATCAATA
BRME_19801	TTGGATACCAATTGTTGGAGATAGT	CTTCTGCCTGTAATGAGTTATGGTT
BRME_1524	CACCTGGTTAGTGAGATTTTCAGTT	TTGATTCTATGGAAAACCGTATCAT
BRME_13109	GAGAAACAATGAAAACCTAAAACCA	TAGCTCCATGACCAGATAAGATTTTC
BRME_12328	ATGAGTTGATTGTCCATTGTACCTT	TCGATAATGTGTTTTTCAGTTTTTGA
BRME_11851	ACAGGATTCTTTTCCTTTTACATC	GTATCGTTCAGATTTCGATCTGTTTT
BRME_10091	AACACACTCCAAGATTCATTTTGAT	AGTCCGTGTACCAACAGCTTAATAG
BRME_10018	AAACTAACTCCTCAGAAAATGAGCA	ATCAAAAACCTCCATTATATTCCACA
comp220607_c0_seq1	AAACTCTCGTTTTTCACTAACATGC	GGATCTATCAAGCAGTGACGACTAT
comp252005_c0_seq2	CATGTCGTTTGTATAGCTCTGATG	ATGTTCAATCAAAGAGAGCAAGACT
comp268777_c0_seq1	TTTGATACTCCAAATCTGCTTTACC	ACCTGGAAAGTAGAATCTGACACAG
comp227753_c0_seq1	ACGAAATAGCAATTTAGATGTGGAG	TGGGTATATGAGAAACATCAAGGAT
comp265888_c0_seq2	ACCTGACAGTTATCAATCACCGTAT	GAATTTACTCATCGTTTACAACCTT
comp249517_c0_seq1	ACAGACAAACACAAATCAAACAAGA	GTAGATTAGCGACGATTAGGTCAAA
comp247229_c0_seq1	ATCTGCCACAGGAAGTCACC	GTCAAGAAGGGGTCATGGAA

comp91267_c0_seq2	CTCTTGCAACCATCAAAGCA	GGAACAAACTGGTGGAGGAA
comp264288_c0_seq1	AGCGTTGTTTATTAGACACCTTACG	TCAAGAAAAGTAGAGATGGAATCGT
comp260850_c0_seq1	ATCTCTACCGCAATAATTCAAACCTG	AGAAGAAAGCATCTTTGCTGTAA
comp257801_c0_seq2	TGATGCTTGATTGTTTGTGAAGTT	ATGAGAACTCTGTCAAATTGATCC
comp255347_c0_seq2	AGGAGTTGAAGTATCACCCCTTCT	TTGGTTGAGAGATCAGAGGAATATC
comp250423_c0_seq1	ACAAAACAAGATCAATATCATCACC	TTTACAAACCTTATTCAAGGCAAAG
comp249273_c0_seq1	TGGGGAGATCAATGAACTATCTTA	CATCCCTCAACTTTGTAATTTTGT
comp247416_c0_seq1	GATGATCATGGAGAAAGAGTTCAGT	TAAACAGAGAAGGAAGGTTGAAATG
comp246096_c1_seq1	GAGACTACGATCACTGGAGTTTGAT	GTATCCACATACCTTCTACCAATC
comp238537_c0_seq1	TGTC AACACAATGGTCTTGAAATC	AATGTAGAGCATCTGGAGATCAAAC
comp230719_c0_seq1	GTCATCATCTTCTTCTGCTATCAT	CTCTTACCGTAGAGAAACAAGGCTA
comp223271_c0_seq2	TTCGTAACCAATAAGAGCTTTCTGT	CGACGAAAAATAAGAAAGAAATGAA
comp206339_c0_seq1	ACATTTTAGCATACTTTTTCGGAAC	AACAACCTCTTTTAGCCAAGGTTTT
TCONS_00000072	AAAACCTCTCTGTATCCGTTTCT	GTAGAACTTATCCCCAACTCTTC
TCONS_00003667	ACGTTATCCACTATATTGCCAGAAG	GCTCTTTCTAAATTTCTTTGGGTT
TCONS_00000059	TCTCACATACGACACATCTCAAAAA	GTAAAGCTTCTTCAGTCTCTCAAC
TCONS_00000058	TATTTGTTTTGTTTGTAGGGTCGAT	TACGCCTTCTTAAACTAAGAGCAGA
TCONS_00003635	CACACAGATATATCCCATCATGAAA	CCTTGGATGTCTGAAACCTTTATATT
TCONS_00003634	CACACAGATATATCCCATCATGAAA	CCTTGGATGTCTGAAACCTTTATATT
TCONS_00003593	GGGAAGATAGGACCATTGAGTTTAT	AACTTGATAGAACCAGTGACTGAGC
TCONS_00015281	AACACAAAACGGCACATCAA	CGTCTTGGCATTGGGACTAT
TCONS_00008509	CCTCCGTCTGAGAACCAGAG	TTGAGCATTGGTTGCATGTT
TCONS_00015207	TCATCATCTGCTCCGATTCA	AGCTGCCGTACCATTGAGAC
TCONS_00008391	TGTCTCACAGTCACGGGAAC	GAAGCGAGCAAGGATCACAT
TCONS_00011686	TCTCGACTCATCCATCCACA	GGTCACGACTGAATCTGCAA
TCONS_00007791	TAAGCTGGCTGGTCCATTCT	TGGGATGTTGGGTTCACTTT
TCONS_00006570	TCCGCTTGAGAGTTTCAGGT	ACCATCACCAGAGGCGTAAC
TCONS_00006529	GGTCGTGGTCGAAAAGTTGT	CTCTGAATGAGGAGGCCTTG
TCONS_00006527	CGATTTGAGGAGCCTCTTTG	CAGAAACGTTGTGCAGGAGA

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TCONS_00009672	CTGTTTACCCACTTCTTAACCAAA	TACAAAAACACCCCTATAAAACAA
TCONS_00014998	TCTTTTCTCGAAGCTATTAAGGTGA	GAGTAAGTTGAAACAAGGACTCAGC
TCONS_00007585	GAACTTCTTCTCGTCTGTAACCTCG	AAGACAAGGTATGTAGGTGCAGAAC
TCONS_00002126	ACCATCTAACAGAACAAGCACTCTT	AGCCTTTGTGCTCTTATCCTTAGTT
TCONS0_00002441	GCCGTCGTTCAATCTCTCTAA	AGATGCAGCTCCGCTTTCAT
TCONS0_00003629	CAATTGAGATGGATGGCTGA	CAATGTTGCCCAAGTTGTTG
TCONS0_00006299	TGGGGAAAACACCAAGAGAC	GGCTAGGGTTTGTGATTCCA
TCONS0_00021925	TCTGACGCACAGGACAGTTC	CTGAATGCACGTGTCAGCTT
TCONS0_00021930	CCATGATCTCTTCCCATGCT	TGGCATTATCCTCCAGCTCT
TCONS0_00033329	CTCCTTTGCTTATGCATGGATAC	TAACGAAACCGGTTCAAAGG
TCONS0_00033336	TTGGCAGAGAGTCAATGGAA	AAGCTTGCTCATAGCCCAAA
TCONS0_00036293	TCATCTCCAGCTTTGTTCC	TACGTCAGGCACATCAGCTC
TCONS0_00058472	CCATTTCTCTATCCCCCAAA	CACCCTCCGTAAGTGTGCGAT
TCONS0_00072042	CGTTATCGGAGGCAACATTT	GAACAGCTTCTGCTCGCTTT
Actin	ATGTTGGGATGGGTCAAAAA	ACGGAGCTCGTTGTAGAAAGT

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BRME: These primers are for Velvet-Oases assembly validation, comp: These primers are for Trinity assembly validation, TCONS: These primers are for TopHat-Cufflink assembly “u” transcripts validation and TCONS0: These primers are for TopHat-Cufflink assembly “o” transcripts validation.

**Table S3** Accession numbers of the read sequences submitted to NCBI SRA.

<b>Run</b>	<b>NCBI SRA Accession number</b>	<b>Run</b>	<b>NCBI SRA Accession number</b>
R500_Lane1	SRR1227842	IMB211_Lane1	SRR1238059
R500_Lane2	SRR1228204	IMB211_Lane2	SRR1238060
R500_Lane3	SRR1228205	IMB211_Lane3	SRR1238061
R500_Lane4	SRR1228206	IMB211_Lane4	SRR1238062
R500_Lane5	SRR1228207	IMB211_Lane5	SRR1238063
R500_Lane6	SRR1228208	IMB211_Lane6	SRR1238064
R500_Lane7	SRR1228209	IMB211_Lane7	SRR1238065
R500_Lane8	SRR1228210	IMB211_Lane8	SRR1238066
R500_Lane9	SRR1228211	IMB211_Lane9	SRR1238067
R500_Lane10	SRR1228212	IMB211_Lane10	SRR1238068
R500_Lane11	SRR1238051	IMB211_Lane11	SRR1238069
R500_Lane12	SRR1238052	IMB211_Lane12	SRR1238070
R500_Lane13	SRR1238054	IMB211_Lane13	SRR1238071
R500_Lane14	SRR1238055	IMB211_Lane14	SRR1238072
R500_Lane15	SRR1238056	IMB211_Lane15	SRR1238073
R500_Lane16	SRR1238057	IMB211_Lane16	SRR1238074
R500_Lane17	SRR1238058		



**Table S4** *In-silico* validation of novel transcripts generated using *de novo* and reference based assemblies and annotation

Gene id	RNA-Seq coverage	Our annotation	Special note
Bra1000030	Same	Correct	-
Bra1000066	Same	Correct	-
Bra1000106	Same	Correct	-
Bra1000128	Same	Wrong	-
Bra1000159	Same	Correct	-
Bra1000243	Same	Correct	-
Bra1000273	Same	Correct	-
Bra1000310	Same	Wrong	-
Bra1000360	Same	Correct	-
Bra1000369	Same	Correct	-
Bra1000489	Same	Wrong	-
Bra1000598	Not same	Correct	-
Bra1000632	Same	Correct	-
Bra1000652	Not same	Correct	-
Bra1000682	Same	Correct	-
Bra1000711	Same	Correct	-
Bra1000719	Same	Correct	-
Bra1000737	Same	Correct	-
Bra1000912	Same	Correct	-
Bra1001005	Not same	Probably Correct	No coverage in Chiifu
Bra1001027	Same	Correct	-
Bra1001094	Same	Correct	-
Bra1001111	Same	Correct	-
Bra1001150	Same	Correct	-
Bra1001380	Same	Wrong	-
Bra1001421	Same	Correct	-
Bra1001488	Same	Correct	-
Bra1001549	Same	Correct	-
Bra1001620	Same	Correct	-
Bra1001652	Same	Correct	-
Bra1001656	Not same	Annotation matches Chiifu	-
Bra1001755	Same	not sure	No coverage in R500 & Chiifu

Bra1001808	Same	Correct	-
Bra1001848	Same	Wrong	-
Bra1001880	Same	Correct	-
Bra1001890	Same	Correct	-
Bra1001918	Same	Correct	-
Bra1001941	Same	Wrong	-
Bra1002075	Not same	Probably Correct	No coverage in Chiifu
Bra1002133	Same	Correct	-
Bra1002196	Same	Correct	-
Bra1002282	Same	Correct	-
Bra1002286	Same	Wrong	-
Bra1002485	Same	Correct	-
Bra1002547	Same	Correct	-
Bra1002627	Same	Correct	-
Bra1002685	Probably same	Probably Correct	No coverage in Chiifu
Bra1002774	Probably same	Probably Correct	No coverage in Chiifu
Bra1003501	Same	Wrong	-
Bra1003474	Probably same	Probably Correct	No coverage in Chiifu
Bra1003432	Same	Correct	-
Bra1003361	Same	Correct	-
Bra1003495	Not same	Correct	-
Bra1003501	Same	Wrong	-
Bra1003474	Not sure	not sure	Both coverage and annotation is unsure
Bra1003432	Same	Correct	-
Bra1003436	Same	Correct	-
Bra1003361	Same	Correct	-
Bra1003282	Same	Wrong	-
Bra1003179	Same	Wrong	-

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**Table S5** *In-silico* validation of PASA updated transcript annotations

<b>Gene id</b>	<b>RNA-Seq coverage</b>	<b>Original annotation</b>	<b>PASA updated annotation</b>	<b>Special note</b>
Bra022192	Same	Wrong	Correct	-
Bra033775	Same	Wrong	Correct	-
Bra033776	Same	Wrong	Correct	-
Bra033769	Same	Wrong	Correct	-
Bra020977	Same	Wrong	Correct	-
Bra020971	Not same	Correct	Probably correct	Alternative splicing
Bra021634	Same	Wrong	Correct	-
Bra021651	Same	Wrong	Correct	-
Bra021661	Same	Wrong	Correct	-
Bra004312	Same	Wrong	Correct	-
Bra004127	Same	Wrong	Correct	-
Bra007104	Same	Wrong	Correct	-
Bra004312	Same	Wrong	Correct	-
Bra003912	Same	Wrong	Correct	-
Bra002554	Same	Correct	Probably correct	Alternative splicing
		Correct according		
Bra002518	Not same	to Chiifu	Correct according to R500	-
Bra002519	Same	Wrong	Correct	-
Bra029936	Same	Wrong	Correct	-
Bra030270	Same	Wrong	Correct	-
Bra001264	Same	Wrong	Correct	-
Bra001267	Same	Wrong	Correct	-
Bra001271	Same	Wrong	Correct	-
Bra001274	Same	Wrong	Correct	-
Bra001283	Same	Wrong	Correct	-
Bra030267	Same	Wrong	Correct	-
Bra030262	Same	Wrong	Correct	-
Bra030256	Same	Wrong	Correct	-
Bra030244	Not same	Wrong	Wrong	-
Bra030229	Same	Wrong	Correct	-
Bra032283	Same	Wrong	Correct	-
		Correct accroding		
Bra032273	Not same	to Chiifu	Correct according to R500	-

Bra019452	Same	Wrong	Correct	-
Bra019445	Same	Wrong	Correct	-
Bra019433	Same	Wrong	Correct	-
Bra038606	Same	Wrong	Correct	-
Bra011921	Same	Wrong	Correct	-
Bra011920	Same	Wrong	Correct	-
Bra011913	Same	Wrong	Correct	-
Bra011912	Same	Wrong	Correct	-
Bra011910	Same	Wrong	Correct	-
Bra003134	Same	Wrong	Wrong	-
Bra003143	Same	Wrong	Correct	-
Bra003146	Same	Wrong	Correct	-
Bra020982	Same	Wrong	Correct	-
Bra020977	Same	Wrong	Correct	-
Bra020975	Same	Correct	Probably correct	Small exon problem
Bra020971	Same	Correct	Probably correct	Alternative splicing
Bra020963	Same	Wrong	Correct	-
Bra028046	Same	Wrong	Correct	-
Bra025750	Same	Wrong	Correct	-
Bra002568	Same	Wrong	Correct	-
Bra002536	Same	Wrong	Correct	-
Bra002527	Same	Wrong	Correct	-
Bra002517	Same	Wrong	Correct	-
Bra002515	Same	Wrong	Correct	-
Bra002512	Same	Wrong	Correct	-
Bra002508	Same	Wrong	Correct	-
Bra002501_Bra				
002502	Same	Correct	Not sure	Alternative splicing
Bra002498	Same	Wrong	Correct	-
Bra002485	Same	Wrong	Wrong	-

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## Files S1-S11

Available for download at [www.g3journal.org/lookup/suppl/doi:10.1534/g3.114.012526/-/DC1](http://www.g3journal.org/lookup/suppl/doi:10.1534/g3.114.012526/-/DC1)

**File S1** - R500 vs. IMB211 vcf file

**File S2** - R500 vs. Chiifu vcf file

**File S3** - IMB211 vs. Chiifu vcf file

**File S4** - *B. rapa* Chiifu final CDS in fasta format

**File S5** - *B. rapa* Chiifu unanchored transcript sequences in fasta format

**File S6** - *B. rapa* Chiifu unanchored transcript sequences gene descriptions

**File S7** - *In-silico* RNA-Seq coverage and genome annotation validation of PASA updated *B. rapa* transcripts (IGV screen shots)

**File S8** - *B. rapa* Chiifu annotation file in bed format

**File S9** - *B. rapa* Chiifu transcript sequences gene descriptions

**File S10** - *In-silico* RNA-Seq coverage and genome annotation validation of novel *B. rapa* transcripts (IGV screen shots)

**File S11** - *B. rapa* GO annotations