

Supplementary Table 2. Genes induced specifically in RCB_r.

| Br_SEQ_ID | At_Locus | Gene Annotation | Probe Intensity | | Fold Change |
|------------------|---------------|---|-----------------|--------|-------------|
| | | | RCBr | Chiifu | RCBr/Chiifu |
| Brapa_ESTC019795 | AT1G09500.3 | Symbols: cinnamyl-alcohol dehydrogenase chr1:3066813-3068246 FORWARD | 19558 | 30 | 654.1 |
| Brapa_ESTC045273 | AT2G15700 | copla-like retrotransposon family | 9550 | 15 | 653.2 |
| Brapa_ESTC032343 | AT1G57750.1 | Symbols: cytochrome P450, putative chr1:21387851-21389344 REVERSE | 11872 | 32 | 370.2 |
| Brapa_ESTC046555 | AT3G43575 | non-LTR retrotransposon family (LINE) | 7080 | 20 | 357.0 |
| Brapa_ESTC008670 | AT1G57750.1 | Symbols: cytochrome P450, putative chr1:21387851-21389344 REVERSE | 4395 | 14 | 318.5 |
| Brapa_ESTC033111 | no_hits_found | ----- | 27622 | 92 | 301.2 |
| Brapa_ESTC032362 | AT1G57750.1 | Symbols: cytochrome P450, putative chr1:21387851-21389344 REVERSE | 19450 | 67 | 290.9 |
| Brapa_ESTC039728 | AT2G15700 | copla-like retrotransposon family | 2706 | 15 | 185.8 |
| Brapa_ESTC034449 | AT1G76520.2 | Symbols: auxin efflux carrier family protein chr1:28720278-28722183 FORWARD | 6683 | 38 | 174.1 |
| Brapa_ESTC037638 | AT5G11910.1 | Symbols: esterase/lipase/thioesterase family protein chr5:3836561-3838183 REVERSE | 12922 | 75 | 172.9 |
| Brapa_ESTC032934 | no_hits_found | ----- | 5856 | 34 | 172.2 |
| Brapa_ESTC039253 | AT5G28823 | Zinc knuckle (CCHC-type) family protein | 16148 | 111 | 145.3 |
| Brapa_ESTC001844 | AT2G38540.1 | Symbols: LTP1, ATLTP1, LP1 LP1 (nonspecific lipid transfer protein 1) chr2:16137496-16137971 FORWARD | 14923 | 104 | 143.5 |
| Brapa_ESTC034325 | AT2G07210 | Mutator-like transposase family | 5971 | 46 | 130.9 |
| Brapa_ESTC038115 | AT5G34860.1 | Symbols: similar to unknown protein [Arabidopsis thaliana] (TAIR:AT2G06908.1); similar to putative transposon protein [Oryza sativa (japonica cultivar-group)] (GB:AAR88574.1); contains InterPro domain HMG-I and HMG-Y, DNA-binding; (InterPro:IPR000637) | 7822 | 66 | 119.0 |
| Brapa_ESTC050413 | no_hits_found | ----- | 4057 | 36 | 112.5 |
| Brapa_ESTC046022 | no_hits_found | ----- | 16151 | 146 | 110.4 |
| Brapa_ESTC008729 | AT1G20130.1 | Symbols: family II extracellular lipase, putative chr1:6978101-6985306 FORWARD | 2772 | 29 | 96.8 |
| Brapa_ESTC028268 | AT5G20240.1 | Symbols: PI PI (PISTILLATA); DNA binding / transcription factor chr5:6829205-6831210 FORWARD | 4123 | 43 | 95.0 |
| Brapa_ESTC028837 | no_hits_found | ----- | 4728 | 50 | 94.1 |
| Brapa_ESTC010397 | AT1G57750.1 | Symbols: cytochrome P450, putative chr1:21387851-21389344 REVERSE | 18785 | 201 | 93.4 |

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|------------------|---------------|--|-----------------|--------|-------------|
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| Brapa_ESTC023275 | AT1G43780.1 | Symbols: SCPL44 SCPL44 (serine carboxypeptidase-like 44); serine carboxypeptidase chr1:16566251-16569839 FORWARD | 2780 | 34 | 80.8 |
| Brapa_ESTC039308 | AT3G32914 | non-LTR retrotransposon family (LINE) | 2710 | 34 | 80.6 |
| Brapa_ESTC046752 | AT5G02880.1 | Symbols: UPL4 UPL4 (ubiquitin-protein ligase 4) chr5:662641-668845 FORWARD | 11723 | 147 | 79.8 |
| Brapa_ESTC044414 | no_hits_found | ----- | 2381 | 30 | 79.4 |
| Brapa_ESTC049628 | AT2G40660.1 | Symbols: tRNA-binding region domain-containing protein chr2:16973089-16975944 FORWARD | 2751 | 36 | 75.8 |
| Brapa_ESTC030965 | no_hits_found | ----- | 2190 | 30 | 72.7 |
| Brapa_ESTC033604 | AT2G45080.1 | Symbols: CYCP3;1 CYCP3;1 (cyclin p3;1); cyclin-dependent protein kinase chr2:18598763-18599518 FORWARD | 1471 | 21 | 69.8 |
| Brapa_ESTC042407 | AT1G79680.1 | Symbols: wall-associated kinase, putative chr1:29985081-29987642 REVERSE | 1161 | 17 | 68.6 |
| Brapa_ESTC039567 | AT1G14500.1 | Symbols: ankyrin repeat family protein chr1:4960370-4961775 FORWARD | 4639 | 68 | 68.2 |
| Brapa_ESTC006493 | AT5G48210.1 | Symbols: similar to unknown protein [Arabidopsis thaliana] | 2761 | 41 | 67.8 |
| Brapa_ESTC033110 | AT3G49640.1 | Symbols: FAD binding / oxidoreductase chr3:18411465-18415412 REVERSE | 10933 | 162 | 67.4 |
| Brapa_ESTC005377 | AT1G75900.1 | Symbols: family II extracellular lipase 3 (EXL3) chr1:28502840-28504604 FORWARD | 5316 | 80 | 66.3 |
| Brapa_ESTC032615 | no_hits_found | ----- | 5839 | 94 | 62.3 |
| Brapa_ESTC040246 | no_hits_found | ----- | 8536 | 140 | 61.1 |
| Brapa_ESTC032235 | no_hits_found | ----- | 2887 | 47 | 61.0 |
| Brapa_ESTC034499 | no_hits_found | ----- | 6452 | 108 | 59.6 |
| Brapa_ESTC017479 | AT1G12860.1 | Symbols: basic helix-loop-helix (bHLH) family protein / F-box family protein chr1:4382221-4386390 FORWARD | 1301 | 22 | 59.1 |
| Brapa_ESTC033247 | no_hits_found | ----- | 21591 | 404 | 53.4 |
| Brapa_ESTC032382 | AT5G08139.1 | Symbols: zinc finger (C3HC4-type RING finger) family protein chr5:2616488-2617618 FORWARD | 6259 | 118 | 53.1 |
| Brapa_ESTC032285 | AT1G56110.1 | Symbols: NOP56 NOP56 (ARABIDOPSIS HOMOLOG OF NUCLEOLAR PROTEIN NOP56) chr1:20988209-20990558 REVERSE | 6701 | 131 | 51.1 |
| Brapa_ESTC010741 | AT1G23600.2 | Symbols: similar to unknown protein [Arabidopsis thaliana] (TAIR:AT1G23570.2); similar to OBP32pep (GB:AAA79703.1); contains InterPro domain Protein of unknown function DUF220; (InterPro:IPR003863) chr1:8361187-8362347 REVERSE | 3200 | 63 | 50.7 |

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| Brapa_ESTC025908 | AT5G15800.1 | Symbols: AGL2, SEP1 SEP1 (SEPALLATA1); DNA binding / transcription factor chr5:5151597-5153770 REVERSE | 1629 | 32 | 50.6 |
| Brapa_ESTC019697 | AT4G23340.1 | Symbols: oxidoreductase, 2OG-Fe(II) oxygenase family protein chr4:12195729-12196662 REVERSE | 17151 | 341 | 50.3 |
| Brapa_ESTC032348 | no_hits_found | ----- | 2615 | 53 | 49.3 |
| Brapa_ESTC039444 | AT1G09880.1 | Symbols: lyase chr1:3208830-3211655 REVERSE | 3978 | 81 | 49.2 |
| Brapa_ESTC034812 | AT5G33075 | copla-like retrotransposon family | 3028 | 62 | 48.5 |
| Brapa_ESTC048287 | AT4G34450.1 | Symbols: coatomer gamma-2 subunit, putative / gamma-2 coat protein, putative / gamma-2 COP, putative chr4:16471960-16476799 FORWARD | 1989 | 42 | 47.7 |
| Brapa_ESTC036983 | AT3G29265.1 | Symbols: similar to zinc knuckle (CCHC-type) family protein [Arabidopsis thaliana] (TAIR:AT5G32482.1); similar to Zinc knuckle containing protein [Brassica oleracea] (GB:ABD64973.1) chr3:11232949-11233659 FORWARD | 7567 | 163 | 46.6 |
| Brapa_ESTC040022 | AT1G26390.1 | Symbols: FAD-binding domain-containing protein chr1:9130151-9131743 REVERSE | 4053 | 87 | 46.4 |
| Brapa_ESTC038593 | no_hits_found | ----- | 8153 | 184 | 44.3 |
| Brapa_ESTC040086 | AT1G26140.1 | Symbols: similar to unknown protein [Arabidopsis thaliana] (TAIR:AT3G25597.1); similar to hypothetical protein [Oryza sativa (japonica cultivar-group)] (GB:AAL87149.1); similar to Os02g0709300 [Oryza sativa (japonica cultivar-group)] (GB:NP_001047889.1) | 2390 | 54 | 44.1 |
| Brapa_ESTC046226 | AT4G16020 | copla-like retrotransposon family | 5094 | 117 | 43.4 |
| Brapa_ESTC042007 | AT2G39310.1 | Symbols: jacalin lectin family protein chr2:16421340-16423401 REVERSE | 4689 | 109 | 43.1 |
| Brapa_ESTC038230 | no_hits_found | ----- | 7610 | 181 | 41.9 |
| Brapa_ESTC035780 | no_hits_found | ----- | 13722 | 330 | 41.6 |
| Brapa_ESTC046377 | no_hits_found | ----- | 18748 | 466 | 40.2 |
| Brapa_ESTC029772 | AT3G20110.1 | Symbols: CYP705A20 CYP705A20 (cytochrome P450, family 705, subfamily A, polypeptide 20); oxygen binding chr3:7021501-7023119 FORWARD | 4420 | 111 | 39.9 |
| Brapa_ESTC034302 | no_hits_found | ----- | 15277 | 391 | 39.0 |
| Brapa_ESTC044893 | AT4G33150.2 | Symbols: LKR/SDH, LKR, SDH LKR (SACCHAROPINE DEHYDROGENASE) chr4:15985482-15991072 REVERSE | 7371 | 189 | 39.0 |
| Brapa_ESTC044326 | no_hits_found | ----- | 4147 | 110 | 37.8 |
| Brapa_ESTC046430 | no_hits_found | ----- | 11322 | 306 | 36.9 |
| Brapa_ESTC038507 | AT4G17486.1 | Symbols: Identical to UPF0326 protein At4g17486 [Arabidopsis Thaliana] (GB:Q93VG8;GB:O23591;GB:Q9FPJ0); similar to unknown protein [Arabidopsis thaliana] (TAIR:AT5G47310.1); similar to hypothetical protein 40.t00020 [Brassica oleracea] (GB:ABD65143.1); | 11072 | 307 | 36.1 |

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| | | | RCBr | Chiifu | RCBr/Chiifu |
| Brapa_ESTC046429 | no_hits_found | ----- | 10558 | 297 | 35.5 |
| Brapa_ESTC020438 | no_hits_found | ----- | 4886 | 139 | 35.2 |
| Brapa_ESTC032467 | no_hits_found | ----- | 15100 | 432 | 34.9 |
| Brapa_ESTC009361 | AT3G22510.1 | Symbols: similar to unknown protein [Arabidopsis thaliana] (TAIR:AT5G27990.1); similar to hypothetical protein MtrDRAFT_AC135320g16v1 [Medicago truncatula] (GB:ABE82968.1); contains domain gb def: At3g22510 (PTHR21250:SF8); contains | 5607 | 161 | 34.9 |
| Brapa_ESTC043621 | no_hits_found | ----- | 5107 | 147 | 34.8 |
| Brapa_ESTC039058 | no_hits_found | ----- | 2197 | 65 | 33.9 |
| Brapa_ESTC044045 | AT2G40116.1 | Symbols: phosphoinositide-specific phospholipase C family protein chr2:16758860-16761389 FORWARD | 4466 | 133 | 33.7 |
| Brapa_ESTC040697 | AT5G39095 | copla-like retrotransposon family | 4898 | 149 | 33.0 |
| Brapa_ESTC042413 | AT3G01510.1 | Symbols: 5'-AMP-activated protein kinase beta-1 subunit-related chr3:198862-201689 REVERSE | 2257 | 69 | 32.9 |
| Brapa_ESTC031417 | AT5G38383 | gypsy-like retrotransposon family (Athila) | 3709 | 113 | 32.8 |
| Brapa_ESTC008655 | AT5G40260.2 | Symbols: nodulin MtN3 family protein chr5:16107070-16108666 FORWARD | 1003 | 31 | 32.5 |
| Brapa_ESTC036982 | AT4G04313 | copla-like retrotransposon family | 3607 | 111 | 32.5 |
| Brapa_ESTC043407 | AT2G42120.1 | Symbols: POLD2 DNA polymerase delta small subunit-related chr2:17570360-17573043 REVERSE | 12996 | 405 | 32.1 |
| Brapa_ESTC040402 | AT1G69120.1 | Symbols: AP1 AP1 (APETALA1); DNA binding / transcription factor chr1:25986239-25989765 REVERSE | 8412 | 267 | 31.5 |
| Brapa_ESTC033734 | no_hits_found | ----- | 5638 | 180 | 31.3 |
| Brapa_ESTC033735 | no_hits_found | ----- | 7654 | 246 | 31.2 |
| Brapa_ESTC034737 | no_hits_found | ----- | 6916 | 226 | 30.6 |
| Brapa_ESTC051810 | no_hits_found | ----- | 3412 | 112 | 30.5 |
| Brapa_ESTC042120 | AT2G46490.1 | Symbols: similar to unknown protein [Arabidopsis thaliana] | 9695 | 328 | 29.6 |
| Brapa_ESTC038732 | AT3G55960.1 | Symbols: NLI interacting factor (NIF) family protein chr3:20771776-20773871 REVERSE | 1916 | 65 | 29.5 |
| Brapa_ESTC043945 | no_hits_found | ----- | 2196 | 75 | 29.3 |

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| Brapa_ESTC038618 | AT4G09710 | non-LTR retrotransposon family (LINE) | 1140 | 39 | 29.3 |
| Brapa_ESTC046817 | no_hits_found | ----- | 12192 | 418 | 29.2 |
| Brapa_ESTC032026 | AT1G70460.1 | Symbols: protein kinase, putative chr1:26559818-26562657 FORWARD | 2046 | 75 | 27.5 |
| Brapa_ESTC037319 | AT5G67500.1 | Symbols: porin, putative chr5:26952449-26954349 FORWARD | 1170 | 43 | 27.2 |
| Brapa_ESTC024069 | AT5G37300.1 | Symbols: similar to unknown protein [Arabidopsis thaliana] (TAIR:AT2G38995.1); similar to Protein of unknown function DUF1298 [Medicago truncatula] (GB:ABE82755.1); contains InterPro domain Protein of unknown function UPF0089; (InterPro:IPR004255); | 6897 | 255 | 27.1 |
| Brapa_ESTC033112 | no_hits_found | ----- | 3305 | 123 | 26.8 |
| Brapa_ESTC038915 | AT3G59270.1 | Symbols: syntaxin-related family protein chr3:21917570-21918849 REVERSE | 2647 | 100 | 26.4 |
| Brapa_ESTC012936 | AT1G52560.1 | Symbols: 26.5 kDa class I small heat shock protein-like (HSP26.5-P) chr1:19578452-19579435 REVERSE | 8118 | 311 | 26.1 |
| Brapa_ESTC029845 | AT5G07200.1 | Symbols: GA20OX3, ATGA20OX3 YAP169 (Gibberellin 20 oxidase 3); gibberellin 20-oxidase chr5:2243836-2245158 REVERSE | 4761 | 183 | 26.1 |
| Brapa_ESTC044293 | no_hits_found | ----- | 1942 | 75 | 26.0 |
| Brapa_ESTC041801 | AT2G37940.1 | Symbols: similar to phosphatidic acid phosphatase-related / PAP2-related [Arabidopsis thaliana] (TAIR:AT3G54020.1); similar to Os01g0850100 [Oryza sativa (japonica cultivar-group)] (GB:NP_001044812.1); similar to hypothetical protein PY02331 [Plasmodium | 9834 | 388 | 25.3 |
| Brapa_ESTC008039 | AT3G02310.1 | Symbols: AGL4, SEP2 SEP2 (SEPALLATA2); DNA binding / transcription factor chr3:464561-466694 REVERSE | 5018 | 200 | 25.0 |
| Brapa_ESTC030240 | no_hits_found | ----- | 3068 | 123 | 24.9 |
| Brapa_ESTC031450 | no_hits_found | ----- | 4568 | 188 | 24.3 |
| Brapa_ESTC011597 | AT5G15800.1 | Symbols: AGL2, SEP1 SEP1 (SEPALLATA1); DNA binding / transcription factor chr5:5151597-5153770 REVERSE | 2267 | 94 | 24.2 |
| Brapa_ESTC005886 | AT3G02310.1 | Symbols: AGL4, SEP2 SEP2 (SEPALLATA2); DNA binding / transcription factor chr3:464561-466694 REVERSE | 1654 | 69 | 24.0 |
| Brapa_ESTC051814 | no_hits_found | ----- | 2099 | 88 | 23.8 |
| Brapa_ESTC010258 | AT4G14730.1 | Symbols: transmembrane protein-related chr4:8448602-8449996 FORWARD | 3244 | 137 | 23.7 |
| Brapa_ESTC036545 | no_hits_found | ----- | 6771 | 286 | 23.7 |
| Brapa_ESTC039929 | AT1G22220.1 | Symbols: F-box family protein chr1:7846683-7847627 FORWARD | 3973 | 169 | 23.6 |
| Brapa_ESTC008514 | AT5G22430.1 | Symbols: similar to unknown protein [Arabidopsis thaliana] (TAIR:AT2G27385.1); similar to hypothetical protein [Oryza sativa (japonica cultivar-group)] (GB:BAD27801.1) chr5:7433916-7434649 FORWARD | 8159 | 347 | 23.5 |

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| Brapa_ESTC035286 | AT2G14710.1 | Symbols: F-box family protein chr2:6306018-6307106 FORWARD | 2409 | 104 | 23.2 |
| Brapa_ESTC036761 | AT4G17530.1 | Symbols: AtRab1C, AtRABD2c, RAB1C RAB1C; GTP binding chr4:9773734-9775437 REVERSE | 3205 | 139 | 23.1 |
| Brapa_ESTC044307 | no_hits_found | ----- | 1479 | 66 | 22.5 |
| Brapa_ESTC050414 | no_hits_found | ----- | 2519 | 112 | 22.5 |
| Brapa_ESTC038924 | no_hits_found | ----- | 1872 | 85 | 22.0 |
| Brapa_ESTC031186 | no_hits_found | ----- | 2739 | 126 | 21.7 |
| Brapa_ESTC039980 | no_hits_found | ----- | 2071 | 96 | 21.7 |
| Brapa_ESTC034163 | no_hits_found | ----- | 1761 | 82 | 21.5 |
| Brapa_ESTC036572 | AT4G18830.1 | Symbols: ATOFP5, OFP5 ATOFP5/OFP5 (ARABIDOPSIS THALIANA OVATE FAMILY PROTEIN 5) chr4:10337460-10338509 FORWARD | 5806 | 274 | 21.2 |
| Brapa_ESTC010485 | AT3G54340.1 | Symbols: AP3 AP3 (APETALA 3); DNA binding / transcription factor chr3:20130406-20132065 REVERSE | 2902 | 138 | 21.0 |
| Brapa_ESTC044108 | no_hits_found | ----- | 2787 | 134 | 20.8 |
| Brapa_ESTC038763 | no_hits_found | ----- | 2860 | 138 | 20.7 |
| Brapa_ESTC008198 | AT4G18960.1 | Symbols: AG AG (AGAMOUS); transcription factor chr4:10383928-10388283 FORWARD | 1927 | 93 | 20.6 |
| Brapa_ESTC017264 | AT1G69120.1 | Symbols: AP1 AP1 (APETALA1); DNA binding / transcription factor chr1:25986239-25989765 REVERSE | 4988 | 242 | 20.6 |
| Brapa_ESTC039255 | no_hits_found | ----- | 2019 | 99 | 20.5 |
| Brapa_ESTC020245 | AT5G63810 | member of Glycoside Hydrolase Family 35 | 3015 | 148 | 20.4 |
| Brapa_ESTC051633 | no_hits_found | ----- | 5662 | 280 | 20.2 |
| Brapa_ESTC031913 | AT2G36325.1 | Symbols: hydrolase, acting on ester bonds chr2:15238488-15240303 FORWARD | 1876 | 93 | 20.2 |
| Brapa_ESTC036168 | AT3G51000.1 | Symbols: epoxide hydrolase, putative chr3:18956239-18957480 REVERSE | 3973 | 198 | 20.1 |
| Brapa_ESTC045715 | AT5G15800.1 | Symbols: AGL2, SEP1 SEP1 (SEPALATA1); DNA binding / transcription factor chr5:5151597-5153770 REVERSE | 7932 | 402 | 19.7 |
| Brapa_ESTC038782 | AT2G07682 | gypsy-like retrotransposon family | 2450 | 126 | 19.4 |

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| | | | RCBr | Chiifu | RCBr/Chiifu |
| Brapa_ESTC047207 | no_hits_found | ----- | 2531 | 132 | 19.2 |
| Brapa_ESTC031079 | AT3G02310.1 | Symbols: AGL4, SEP2 SEP2 (SEPALLATA2); DNA binding / transcription factor chr3:464561-466694 REVERSE | 4813 | 254 | 19.0 |
| Brapa_ESTC040252 | no_hits_found | ----- | 4251 | 226 | 18.8 |
| Brapa_ESTC008651 | AT1G69120.1 | Symbols: AP1 AP1 (APETALA1); DNA binding / transcription factor chr1:25986239-25989765 REVERSE | 5851 | 313 | 18.7 |
| Brapa_ESTC034243 | no_hits_found | ----- | 5387 | 289 | 18.7 |
| Brapa_ESTC033362 | AT4G31520.1 | Symbols: SDA1 family protein chr4:15278287-15281745 REVERSE | 7916 | 429 | 18.4 |
| Brapa_ESTC038227 | no_hits_found | ----- | 1430 | 78 | 18.3 |
| Brapa_ESTC032483 | AT5G19660.1 | Symbols: subtilase family protein chr5:6642120-6646420 REVERSE | 4749 | 266 | 17.8 |
| Brapa_ESTC032429 | AT5G58784.1 | Symbols: dehydrololichyl diphosphate synthase, putative / DEDOL-PP synthase, putative chr5:23757176-23758220 REVERSE | 1572 | 89 | 17.7 |
| Brapa_ESTC008132 | AT5G20240.1 | Symbols: PI PI (PISTILLATA); DNA binding / transcription factor chr5:6829205-6831210 FORWARD | 6436 | 365 | 17.7 |
| Brapa_ESTC045693 | no_hits_found | ----- | 1472 | 83 | 17.7 |
| Brapa_ESTC021994 | no_hits_found | ----- | 4915 | 283 | 17.3 |
| Brapa_ESTC043740 | AT3G16320.1 | Symbols: binding chr3:5529540-5534471 FORWARD | 1148 | 66 | 17.3 |
| Brapa_ESTC006467 | AT5G22430.1 | Symbols: similar to unknown protein [Arabidopsis thaliana] (TAIR:AT2G27385.1); similar to hypothetical protein [Oryza sativa (japonica cultivar-group)] (GB:BAD27801.1) chr5:7433916-7434649 FORWARD | 4712 | 274 | 17.2 |
| Brapa_ESTC051809 | no_hits_found | ----- | 6339 | 373 | 17.0 |
| Brapa_ESTC028783 | no_hits_found | ----- | 4200 | 249 | 16.9 |
| Brapa_ESTC020499 | no_hits_found | ----- | 7386 | 448 | 16.5 |
| Brapa_ESTC017153 | AT5G24940.1 | Symbols: protein phosphatase 2C, putative / PP2C, putative chr5:8591410-8593604 REVERSE | 4244 | 261 | 16.3 |
| Brapa_ESTC042059 | no_hits_found | ----- | 4965 | 306 | 16.2 |
| Brapa_ESTC011306 | AT3G05600.1 | Symbols: epoxide hydrolase, putative chr3:1623491-1624710 REVERSE | 1528 | 96 | 15.9 |
| Brapa_ESTC032885 | AT2G34200.1 | Symbols: zinc finger (C3HC4-type RING finger) family protein chr2:14448184-14448961 FORWARD | 5343 | 336 | 15.9 |

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| | | | RCBr | Chiifu | RCBr/Chiifu |
| Brapa_ESTC034838 | AT3G54650.1 | Symbols: F-box family protein (FBL17) chr3:20236982-20239860 REVERSE | 3958 | 250 | 15.9 |
| Brapa_ESTC039781 | AT3G19540.1 | Symbols: similar to unknown protein [Arabidopsis thaliana] (TAIR:AT1G49840.1); similar to Protein of unknown function DUF620 [Medicago truncatula] (GB:ABD33276.1); contains InterPro domain Protein of unknown function DUF620; (InterPro:IPR006873) | 2369 | 150 | 15.8 |
| Brapa_ESTC012973 | AT1G15330.1 | Symbols: CBS domain-containing protein chr1:5274363-5275494 FORWARD | 4622 | 301 | 15.4 |
| Brapa_ESTC005296 | no_hits_found | ----- | 1062 | 70 | 15.1 |
| Brapa_ESTC033909 | AT3G15310.1 | Symbols: similar to unknown protein [Arabidopsis thaliana] (TAIR:AT5G32621.1); similar to hypothetical protein 24.t00017 [Brassica oleracea] (GB:ABD64939.1); contains InterPro domain Protein of unknown function DUF635; (InterPro:IPR006912); contains InterPro | 1034 | 69 | 15.1 |
| Brapa_ESTC005549 | AT1G40129.1 | Symbols: similar to unknown protein [Arabidopsis thaliana] (TAIR:AT4G07350.1) chr1:15242994-15246477 FORWARD | 3264 | 219 | 14.9 |
| Brapa_ESTC020226 | AT3G14410.1 | Symbols: transporter-related chr3:4815989-4817859 REVERSE | 2977 | 200 | 14.9 |
| Brapa_ESTC047634 | no_hits_found | ----- | 3752 | 254 | 14.8 |
| Brapa_ESTC032361 | AT1G57750.1 | Symbols: cytochrome P450, putative chr1:21387851-21389344 REVERSE | 2053 | 139 | 14.8 |
| Brapa_ESTC048017 | no_hits_found | ----- | 5211 | 353 | 14.7 |
| Brapa_ESTC033146 | no_hits_found | ----- | 1991 | 136 | 14.6 |
| Brapa_ESTC033763 | AT3G07670.1 | Symbols: SET domain-containing protein chr3:2451657-2454623 FORWARD | 4527 | 311 | 14.5 |
| Brapa_ESTC039773 | AT5G24775 | CACTA-like transposase family (En/Spm) | 1618 | 112 | 14.4 |
| Brapa_ESTC036055 | AT1G40129.1 | Symbols: similar to unknown protein [Arabidopsis thaliana] (TAIR:AT4G07350.1) chr1:15242994-15246477 FORWARD | 1862 | 132 | 14.2 |
| Brapa_ESTC046111 | AT5G47600.1 | Symbols: heat shock protein-related chr5:19317171-19317682 REVERSE | 2574 | 185 | 13.9 |
| Brapa_ESTC027440 | AT5G07200.1 | Symbols: GA20OX3, ATGA20OX3 YAP169 (Gibberellin 20 oxidase 3); gibberellin 20-oxidase chr5:2243836-2245158 REVERSE | 1114 | 81 | 13.7 |
| Brapa_ESTC045950 | AT5G40720.1 | Symbols: similar to zinc finger (C3HC4-type RING finger) family protein [Arabidopsis thaliana] (TAIR:AT3G27330.1); similar to Os08g0121900 [Oryza sativa (japonica cultivar-group)] (GB:NP_001060883.1); similar to zinc finger (C3HC4-type RING finger) protein | 1971 | 148 | 13.4 |
| Brapa_ESTC031825 | no_hits_found | ----- | 1343 | 101 | 13.3 |
| Brapa_ESTC030765 | AT5G17970.1 | Symbols: disease resistance protein (TIR-NBS-LRR class), putative chr5:5949001-5951621 REVERSE | 1975 | 149 | 13.3 |
| Brapa_ESTC006608 | AT2G15020.1 | Symbols: similar to unknown protein [Arabidopsis thaliana] (TAIR:AT5G64190.1); similar to hypothetical protein [Oryza sativa (japonica cultivar-group)] (GB:AAP46203.1) chr2:6498788-6500368 REVERSE | 2315 | 181 | 12.8 |
| Brapa_ESTC050496 | no_hits_found | ----- | 5845 | 460 | 12.7 |

Supplementary Table 2. Genes induced specifically in RCB_r.

| Br_SEQ_ID | At_Locus | Gene Annotation | Probe Intensity | | Fold Change |
|------------------|---------------|--|-----------------|--------|-------------|
| | | | RCBr | Chiifu | RCBr/Chiifu |
| Brapa_ESTC037616 | AT5G21120.1 | Symbols: EIL2 EIL2 (ETHYLENE-INSENSITIVE3-LIKE 2); transcription factor chr5:7182632-7184188 FORWARD | 1460 | 116 | 12.6 |
| Brapa_ESTC040278 | AT5G22530.1 | Symbols: similar to unknown protein [Arabidopsis thaliana] (TAIR:AT5G22520.1) chr5:7480627-7481046 FORWARD | 3968 | 320 | 12.4 |
| Brapa_ESTC034888 | AT4G14815.1 | Symbols: protease inhibitor/seed storage/lipid transfer protein (LTP) family protein chr4:8505117-8505755 FORWARD | 1711 | 138 | 12.4 |
| Brapa_ESTC035505 | no_hits_found | ----- | 3614 | 294 | 12.3 |
| Brapa_ESTC032247 | AT3G59720 | copa-like retrotransposon family | 1172 | 97 | 12.0 |
| Brapa_ESTC034409 | AT2G28930.3 | Symbols: APK1B APK1B (Arabidopsis protein kinase 1B); kinase chr2:12431628-12433642 FORWARD | 3827 | 321 | 11.9 |
| Brapa_ESTC042955 | no_hits_found | ----- | 2741 | 235 | 11.7 |
| Brapa_ESTC048288 | AT4G34450.1 | Symbols: coatomer gamma-2 subunit, putative / gamma-2 coat protein, putative / gamma-2 COP, putative chr4:16471960-16476799 FORWARD | 1885 | 162 | 11.7 |
| Brapa_ESTC036711 | AT1G22240.1 | Symbols: APUM8 APUM8 (ARABIDOPSIS PUMILIO 8); RNA binding chr1:7853073-7854952 FORWARD | 1570 | 135 | 11.6 |
| Brapa_ESTC044923 | AT5G32484 | copa-like retrotransposon family | 1813 | 161 | 11.3 |
| Brapa_ESTC035347 | no_hits_found | ----- | 2364 | 211 | 11.2 |
| Brapa_ESTC020325 | no_hits_found | ----- | 1926 | 173 | 11.2 |
| Brapa_ESTC046798 | no_hits_found | ----- | 1630 | 147 | 11.1 |
| Brapa_ESTC040646 | no_hits_found | ----- | 1186 | 108 | 11.0 |
| Brapa_ESTC042772 | AT3G07900.1 | Symbols: similar to unknown protein [Arabidopsis thaliana] (TAIR:AT2G44500.1); similar to Plant protein family, putative [Medicago truncatula] (GB:ABE79402.1); similar to H+-transporting two-sector ATPase, delta (OSCP) subunit; Hypothetical plant protein | 4024 | 374 | 10.8 |
| Brapa_ESTC033230 | AT1G04700.1 | Symbols: protein kinase family protein chr1:1316918-1320652 FORWARD | 2082 | 194 | 10.8 |
| Brapa_ESTC029810 | AT3G15310.1 | Symbols: similar to unknown protein [Arabidopsis thaliana] (TAIR:AT5G32621.1); similar to hypothetical protein 24.t00017 [Brassica oleracea] (GB:ABD64939.1); contains InterPro domain Protein of unknown function DUF635; (InterPro:IPR006912); contains InterPro | 2653 | 247 | 10.8 |
| Brapa_ESTC017454 | AT3G56150.1 | Symbols: ATEIF3C-1, EIF3C-1, ATTIF3C1, TIF3C1, EIF3C EIF3C (EUKARYOTIC TRANSLATION INITIATION FACTOR 3) chr3:20844769-20847799 REVERSE | 4553 | 425 | 10.7 |
| Brapa_ESTC048090 | no_hits_found | ----- | 3228 | 303 | 10.7 |
| Brapa_ESTC049557 | AT2G36620.1 | Symbols: RPL24A RPL24A (RIBOSOMAL PROTEIN L24); structural constituent of ribosome chr2:15357627-15358898 REVERSE | 2221 | 211 | 10.5 |
| Brapa_ESTC045834 | AT3G15310.1 | Symbols: similar to unknown protein [Arabidopsis thaliana] (TAIR:AT5G32621.1); similar to hypothetical protein 24.t00017 [Brassica oleracea] (GB:ABD64939.1); contains InterPro domain Protein of unknown function DUF635; (InterPro:IPR006912); contains InterPro | 1026 | 97 | 10.5 |

Supplementary Table 2. Genes induced specifically in RCB_r.

| Br_SEQ_ID | At_Locus | Gene Annotation | Probe Intensity | | Fold Change |
|------------------|---------------|--|-----------------|--------|-------------|
| | | | RCBr | Chiifu | RCBr/Chiifu |
| Brapa_ESTC030234 | no_hits_found | ----- | 2376 | 226 | 10.5 |
| Brapa_ESTC030530 | no_hits_found | ----- | 2601 | 249 | 10.5 |
| Brapa_ESTC032657 | AT2G21410.1 | Symbols: (VACUOLAR PROTON ATPASE A2); ATPase chr2:9169783-9175221 FORWARD | 1884 | 181 | 10.4 |
| Brapa_ESTC039157 | no_hits_found | ----- | 1910 | 185 | 10.3 |
| Brapa_ESTC031662 | AT5G38383 | gypsy-like retrotransposon family (Athila) | 1674 | 162 | 10.3 |
| Brapa_ESTC038013 | AT1G74820.1 | Symbols: cupin family protein chr1:28115543-28116226 REVERSE | 2189 | 213 | 10.3 |
| Brapa_ESTC044007 | AT2G11630 | pseudogene, similar to P0005C02.7 | 1009 | 98 | 10.3 |
| Brapa_ESTC042103 | AT2G45680.1 | Symbols: TCP family transcription factor, putative chr2:18827791-18828861 REVERSE | 3852 | 377 | 10.2 |
| Brapa_ESTC044186 | no_hits_found | ----- | 2862 | 283 | 10.1 |
| Brapa_ESTC036541 | no_hits_found | ----- | 2038 | 204 | 10.0 |
| Brapa_ESTC044341 | no_hits_found | ----- | 2939 | 302 | 9.7 |
| Brapa_ESTC010942 | AT2G45650.1 | Symbols: AGL6 AGL6 (AGAMOUS LIKE-6); DNA binding / transcription factor chr2:18811527-18813365 FORWARD | 1086 | 112 | 9.7 |
| Brapa_ESTC031561 | no_hits_found | ----- | 1311 | 136 | 9.7 |
| Brapa_ESTC040203 | AT1G30050.1 | Symbols: similar to unknown protein [Arabidopsis thaliana] (TAIR:AT5G01970.1); similar to Os05g0315200 [Oryza sativa (japonica cultivar-group)] (GB:NP_001055171.1); similar to hypothetical protein MtrDRAFT_AC136139g6v1 [Medicago truncatula] | 2343 | 243 | 9.7 |
| Brapa_ESTC019275 | AT5G20240.1 | Symbols: PI PI (PISTILLATA); DNA binding / transcription factor chr5:6829205-6831210 FORWARD | 3390 | 359 | 9.4 |
| Brapa_ESTC033098 | AT4G05470.1 | Symbols: F-box family protein (FBL21) chr4:2763253-2767954 REVERSE | 3037 | 323 | 9.4 |
| Brapa_ESTC045274 | no_hits_found | ----- | 1834 | 196 | 9.4 |
| Brapa_ESTC018123 | AT4G18960.1 | Symbols: AG AG (AGAMOUS); transcription factor chr4:10383928-10388283 FORWARD | 2371 | 253 | 9.4 |
| Brapa_ESTC030919 | no_hits_found | ----- | 1959 | 210 | 9.3 |
| Brapa_ESTC041087 | AT2G22140.1 | Symbols: similar to unknown protein [Arabidopsis thaliana] (TAIR:AT2G21800.1); similar to hypothetical protein MtrDRAFT_AC141113g18v1 [Medicago truncatula] (GB:ABE94626.1); similar to OSJNBa0010D21.8 [Oryza sativa (japonica cultivar- | 1950 | 210 | 9.3 |
| Brapa_ESTC000137 | AT3G16490.1 | Symbols: IQD26 IQD26 (IQ-domain 26); calmodulin binding chr3:5603968-5605495 REVERSE | 1915 | 210 | 9.1 |

Supplementary Table 2. Genes induced specifically in RCB_r.

| Br_SEQ_ID | At_Locus | Gene Annotation | Probe Intensity | | Fold Change |
|------------------|---------------|--|-----------------|--------|-------------|
| | | | RCBr | Chiifu | RCBr/Chiifu |
| Brapa_ESTC031881 | AT1G03020.1 | Symbols: glutaredoxin family protein chr1:698207-698515 REVERSE | 1506 | 168 | 9.0 |
| Brapa_ESTC017036 | AT1G26310.1 | Symbols: CAL1, AGL10, CAL CAL (CAULIFLOWER); DNA binding / transcription factor chr1:9100317-9103497 REVERSE | 2570 | 287 | 9.0 |
| Brapa_ESTC026107 | AT5G59080.1 | Symbols: similar to unknown protein [Arabidopsis thaliana] (TAIR:AT5G02020.1) chr5:23864917-23865629 REVERSE | 3362 | 377 | 8.9 |
| Brapa_ESTC029566 | no_hits_found | ----- | 3847 | 432 | 8.9 |
| Brapa_ESTC019477 | AT5G01250.1 | Symbols: alpha 1,4-glycosyltransferase family protein / glycosyltransferase sugar-binding DXD motif-containing protein chr5:102369-103592 REVERSE | 2732 | 312 | 8.8 |
| Brapa_ESTC009267 | AT1G01310.1 | Symbols: allergen V5/Tpx-1-related family protein chr1:120221-120946 FORWARD | 1535 | 178 | 8.6 |
| Brapa_ESTC039631 | AT1G16640.1 | Symbols: transcriptional factor B3 family protein chr1:5686756-5687526 FORWARD | 3901 | 455 | 8.6 |
| Brapa_ESTC010075 | AT5G57685.1 | Symbols: similar to unknown protein [Arabidopsis thaliana] (TAIR:AT4G25760.1); similar to At5g57685 [Medicago truncatula] (GB:ABE81292.1) chr5:23383582-23384028 REVERSE | 1665 | 198 | 8.4 |
| Brapa_ESTC031327 | no_hits_found | ----- | 1690 | 201 | 8.4 |
| Brapa_ESTC037802 | no_hits_found | ----- | 1200 | 143 | 8.4 |
| Brapa_ESTC045377 | AT5G07200.1 | Symbols: GA20OX3, ATGA20OX3 YAP169 (Gibberellin 20 oxidase 3); gibberellin 20-oxidase chr5:2243836-2245158 REVERSE | 1296 | 155 | 8.4 |
| Brapa_ESTC027297 | AT3G13400.1 | Symbols: SKS13 SKS13 (SKU5 Similar 13); copper ion binding / oxidoreductase chr3:4355264-4357312 FORWARD | 1750 | 210 | 8.3 |
| Brapa_ESTC041729 | no_hits_found | ----- | 1395 | 168 | 8.3 |
| Brapa_ESTC031029 | AT1G21525 | pseudogene of unknown protein | 3803 | 460 | 8.3 |
| Brapa_ESTC035232 | AT5G18040 | unknown protein | 2621 | 320 | 8.2 |
| Brapa_ESTC034231 | no_hits_found | ----- | 2670 | 327 | 8.2 |
| Brapa_ESTC041214 | AT1G30300.1 | Symbols: similar to phosphonate metabolism protein-related [Arabidopsis thaliana] (TAIR:AT4G03610.1); similar to Os03g0643200 [Oryza sativa (japonica cultivar-group)] (GB:NP_001050752.1); similar to Os12g0615500 [Oryza sativa (japonica cultivar-group)] | 3719 | 456 | 8.2 |
| Brapa_ESTC034883 | AT5G25980.3 | Symbols: TGG2 TGG2 (GLUCOSIDE GLUCOHYDROLASE 2); hydrolase, hydrolyzing O-glycosyl compounds chr5:9072733-9075146 FORWARD | 3654 | 449 | 8.1 |
| Brapa_ESTC035379 | AT1G32890 | non-LTR retrotransposon family (LINE) | 2039 | 250 | 8.1 |
| Brapa_ESTC041785 | no_hits_found | ----- | 2028 | 249 | 8.1 |
| Brapa_ESTC033550 | AT1G15050.1 | Symbols: IAA34 IAA34 (indoleacetic acid-induced protein 34); transcription factor chr1:5182251-5183238 REVERSE | 2023 | 250 | 8.1 |

Supplementary Table 2. Genes induced specifically in RCB_r.

| Br_SEQ_ID | At_Locus | Gene Annotation | Probe Intensity | | Fold Change |
|------------------|---------------|--|-----------------|--------|-------------|
| | | | RCBr | Chiifu | RCBr/Chiifu |
| Brapa_ESTC040728 | AT2G21820.1 | Symbols: similar to seed maturation protein PM41, putative [Medicago truncatula] (GB:ABE86900.1) chr2:9310063-9310299 REVERSE | 3044 | 376 | 8.1 |
| Brapa_ESTC043894 | AT3G59480.1 | Symbols: pfkB-type carbohydrate kinase family protein chr3:21994080-21995417 FORWARD | 2922 | 362 | 8.1 |
| Brapa_ESTC033999 | AT4G25200.1 | Symbols: ATHSP23.6-MITO ATHSP23.6-MITO (MITOCHONDRION-LOCALIZED SMALL HEAT SHOCK PROTEIN 23.6) chr4:12917099-12917868 FORWARD | 3878 | 484 | 8.0 |
| Brapa_ESTC046280 | AT2G07760 | Zinc knuckle (CCHC-type) family protein | 1554 | 197 | 7.9 |
| Brapa_ESTC036199 | AT4G15396.1 | Symbols: CYP702A6 CYP702A6 (cytochrome P450, family 702, subfamily A, polypeptide 6); heme binding / iron ion binding / monooxygenase chr4:8807574-8810419 FORWARD | 1873 | 238 | 7.9 |
| Brapa_ESTC051217 | AT3G48020.1 | Symbols: similar to F-box family protein-related [Arabidopsis thaliana] (TAIR:AT5G62860.1); similar to IS10 transposase, putative [Lycopersicon esculentum] (GB:ABI34274.1) chr3:17735578-17735985 FORWARD | 1223 | 159 | 7.7 |
| Brapa_ESTC017338 | AT1G69760.1 | Symbols: similar to unknown protein [Arabidopsis thaliana] (TAIR:AT1G26920.1); similar to hypothetical protein [Ricinus communis] (GB:CAH56540.1) chr1:26243757-26244290 REVERSE | 2806 | 371 | 7.6 |
| Brapa_ESTC044174 | AT4G18960.1 | Symbols: AG AG (AGAMOUS); transcription factor chr4:10383928-10388283 FORWARD | 2787 | 369 | 7.5 |
| Brapa_ESTC045669 | AT5G13990.1 | Symbols: ATEXO70C2 ATEXO70C2 (exocyst subunit EXO70 family protein C2); protein binding chr5:4514682-4516769 REVERSE | 2379 | 316 | 7.5 |
| Brapa_ESTC003732 | no_hits_found | ----- | 2101 | 281 | 7.5 |
| Brapa_ESTC043749 | AT4G10400.2 | Symbols: F-box family protein chr4:6446331-6447711 REVERSE | 2489 | 338 | 7.4 |
| Brapa_ESTC018063 | AT4G37580.1 | Symbols: COP3, HLS1 HLS1 (HOOKLESS 1); N-acetyltransferase chr4:17658926-17660558 FORWARD | 1133 | 155 | 7.3 |
| Brapa_ESTC012595 | AT4G36880.1 | Symbols: cysteine proteinase, putative chr4:17374689-17376177 REVERSE | 1244 | 171 | 7.3 |
| Brapa_ESTC041853 | AT2G39310.2 | Symbols: jacalin lectin family protein chr2:16421340-16423401 REVERSE | 1362 | 187 | 7.3 |
| Brapa_ESTC043513 | AT3G51300.1 | Symbols: ARAC11, ROP1, ROP1AT, AtROP1 ARAC11/AtROP1/ROP1/ROP1AT (rho-related protein from plants 1); GTP binding / GTPase/ protein binding chr3:19054176-19055194 FORWARD | 2382 | 331 | 7.2 |
| Brapa_ESTC021792 | AT5G39150.1 | Symbols: germin-like protein, putative chr5:15687236-15688017 REVERSE | 2505 | 348 | 7.2 |
| Brapa_ESTC034579 | AT1G65480.1 | Symbols: FT FT (FLOWERING LOCUS T) chr1:24335173-24337352 FORWARD | 1985 | 278 | 7.1 |
| Brapa_ESTC029997 | AT3G15310.1 | Symbols: similar to unknown protein [Arabidopsis thaliana] (TAIR:AT5G32621.1); similar to hypothetical protein 24.t00017 [Brassica oleracea] (GB:ABD64939.1); contains InterPro domain Protein of unknown function DUF635; (InterPro:IPR006912); contains InterPro | 1489 | 210 | 7.1 |
| Brapa_ESTC050589 | AT5G05810.1 | Symbols: ATL43 ATL43; protein binding / zinc ion binding chr5:1746939-1748000 FORWARD | 2262 | 319 | 7.1 |
| Brapa_ESTC048481 | no_hits_found | ----- | 1584 | 226 | 7.0 |
| Brapa_ESTC035619 | AT1G70720.1 | Symbols: invertase/pectin methylesterase inhibitor family protein chr1:26670089-26670691 FORWARD | 1629 | 232 | 7.0 |

Supplementary Table 2. Genes induced specifically in RCB_r.

| Br_SEQ_ID | At_Locus | Gene Annotation | Probe Intensity | | Fold Change |
|------------------|---------------|---|-----------------|--------|-------------|
| | | | RCBr | Chiifu | RCBr/Chiifu |
| Brapa_ESTC048639 | AT5G57785.1 | Symbols: contains InterPro domain Helix-loop-helix DNA-binding; (InterPro:IPR011598) chr5:23426331-23426552 REVERSE | 3215 | 462 | 7.0 |
| Brapa_ESTC020774 | AT3G29680.1 | Symbols: transferase family protein chr3:11533928-11535283 REVERSE | 1107 | 160 | 6.9 |
| Brapa_ESTC019217 | AT1G80160.1 | Symbols: lactoylglutathione lyase family protein / glyoxalase I family protein chr1:30155993-30156822 FORWARD | 3055 | 441 | 6.9 |
| Brapa_ESTC038685 | AT1G17250.1 | Symbols: leucine-rich repeat family protein chr1:5901162-5903432 REVERSE | 1626 | 235 | 6.9 |
| Brapa_ESTC020937 | AT1G07060.1 | Symbols: similar to hypothetical protein LOC_Os12g01540 [Oryza sativa (japonica cultivar-group)] (GB:ABA95616.1); similar to Os12g0106100 [Oryza sativa (japonica cultivar-group)] (GB:NP_001065937.1) chr1:2167137-2168396 REVERSE | 3030 | 440 | 6.9 |
| Brapa_ESTC035485 | AT2G32530.1 | Symbols: CSLB03, ATCSLB3, ATCSLB03 ATCSLB03 (Cellulose synthase-like B3); transferase/ transferase, transferring glycosyl groups chr2:13816360-13820564 FORWARD | 2400 | 350 | 6.9 |
| Brapa_ESTC001519 | no_hits_found | ----- | 1482 | 217 | 6.8 |
| Brapa_ESTC041594 | no_hits_found | ----- | 2433 | 357 | 6.8 |
| Brapa_ESTC030802 | no_hits_found | ----- | 2788 | 409 | 6.8 |
| Brapa_ESTC033232 | AT1G04700.1 | Symbols: protein kinase family protein chr1:1316918-1320652 FORWARD | 3137 | 461 | 6.8 |
| Brapa_ESTC017652 | AT5G09780.1 | Symbols: transcriptional factor B3 family protein chr5:3036957-3038485 REVERSE | 1251 | 184 | 6.8 |
| Brapa_ESTC048568 | no_hits_found | ----- | 1840 | 273 | 6.7 |
| Brapa_ESTC035504 | no_hits_found | ----- | 1231 | 183 | 6.7 |
| Brapa_ESTC044612 | AT5G38383 | gypsy-like retrotransposon family (Athila) | 1621 | 242 | 6.7 |
| Brapa_ESTC043892 | AT3G59480.1 | Symbols: pfkB-type carbohydrate kinase family protein chr3:21994080-21995417 FORWARD | 2518 | 377 | 6.7 |
| Brapa_ESTC041068 | AT5G35130 | pseudogene, similar to putative helicase | 1856 | 278 | 6.7 |
| Brapa_ESTC049168 | AT5G19150.2 | Symbols: carbohydrate kinase family chr5:6426282-6428404 REVERSE | 1625 | 244 | 6.7 |
| Brapa_ESTC032448 | AT2G24850.1 | Symbols: TAT, TAT3 TAT3 (TYROSINE AMINOTRANSFERASE 3); transaminase chr2:10590149-10592231 REVERSE | 2815 | 423 | 6.7 |
| Brapa_ESTC019558 | AT2G39855.2 | Symbols: similar to unknown protein [Arabidopsis thaliana] (TAIR:AT3G55646.1) chr2:16644923-16645930 FORWARD | 3316 | 499 | 6.6 |
| Brapa_ESTC030866 | AT4G02780.1 | Symbols: ABC33, GA1 GA1 (GA REQUIRING 1); ent-copalyl diphosphate synthase chr4:1237881-1244766 REVERSE | 1464 | 221 | 6.6 |
| Brapa_ESTC027337 | AT3G06420.1 | Symbols: ATG8H ATG8H (AUTOPHAGY 8H); microtubule binding chr3:1955225-1956280 REVERSE | 2757 | 418 | 6.6 |

Supplementary Table 2. Genes induced specifically in RCB.

| Br_SEQ_ID | At_Locus | Gene Annotation | Probe Intensity | | Fold Change |
|------------------|---------------|---|-----------------|--------|-------------|
| | | | RCBr | Chiifu | RCBr/Chiifu |
| Brapa_ESTC042014 | no_hits_found | ----- | 1033 | 157 | 6.6 |
| Brapa_ESTC040477 | AT1G71910.1 | Symbols: unknown protein chr1:27068885-27069406 FORWARD | 1586 | 247 | 6.4 |
| Brapa_ESTC040630 | no_hits_found | ----- | 1235 | 194 | 6.4 |
| Brapa_ESTC049045 | AT3G02310.1 | Symbols: AGL4, SEP2 SEP2 (SEPALATA2); DNA binding / transcription factor chr3:464561-466694 REVERSE | 1242 | 197 | 6.3 |
| Brapa_ESTC049821 | no_hits_found | ----- | 1618 | 257 | 6.3 |
| Brapa_ESTC049830 | no_hits_found | ----- | 1104 | 176 | 6.3 |
| Brapa_ESTC031676 | no_hits_found | ----- | 2639 | 425 | 6.2 |
| Brapa_ESTC049381 | no_hits_found | ----- | 1692 | 273 | 6.2 |
| Brapa_ESTC004632 | no_hits_found | ----- | 1891 | 305 | 6.2 |
| Brapa_ESTC042374 | no_hits_found | ----- | 1662 | 268 | 6.2 |
| Brapa_ESTC019569 | AT4G15396.1 | Symbols: CYP702A6 CYP702A6 (cytochrome P450, family 702, subfamily A, polypeptide 6); heme binding / iron ion binding / monooxygenase chr4:8807574-8810419 FORWARD | 1227 | 198 | 6.2 |
| Brapa_ESTC042178 | AT2G47750.1 | Symbols: GH3.9 auxin-responsive GH3 family protein chr2:19567377-19570044 REVERSE | 2766 | 447 | 6.2 |
| Brapa_ESTC008559 | AT5G02540.1 | Symbols: short-chain dehydrogenase/reductase (SDR) family protein chr5:568607-570718 FORWARD | 2121 | 343 | 6.2 |
| Brapa_ESTC047347 | no_hits_found | ----- | 2418 | 395 | 6.1 |
| Brapa_ESTC040391 | AT1G25380.1 | Symbols: mitochondrial substrate carrier family protein chr1:8903713-8905805 FORWARD | 1234 | 203 | 6.1 |
| Brapa_ESTC044773 | AT4G31100.1 | Symbols: wall-associated kinase, putative chr4:15123868-15126432 FORWARD | 1690 | 281 | 6.0 |
| Brapa_ESTC034232 | no_hits_found | ----- | 2122 | 353 | 6.0 |
| Brapa_ESTC023518 | AT2G36080.1 | Symbols: DNA-binding protein, putative chr2:15155691-15158490 REVERSE | 1036 | 173 | 6.0 |
| Brapa_ESTC034400 | AT5G53240.1 | Symbols: similar to unknown protein [Arabidopsis thaliana] (TAIR:AT5G55270.1); contains InterPro domain Protein of unknown function DUF295; (InterPro:IPR005174) chr5:21618773-21619858 FORWARD | 2975 | 500 | 5.9 |
| Brapa_ESTC003989 | AT1G76890.2 | Symbols: AT-GT2, GT2 GT2 (GT2); transcription factor chr1:28878105-28880097 REVERSE | 1178 | 199 | 5.9 |
| Brapa_ESTC042121 | AT2G46500.2 | Symbols: phosphatidylinositol 3- and 4-kinase family protein / ubiquitin family protein chr2:19093813-19095606 REVERSE | 2120 | 359 | 5.9 |

Supplementary Table 2. Genes induced specifically in RCB_r.

| Br_SEQ_ID | At_Locus | Gene Annotation | Probe Intensity | | Fold Change |
|------------------|---------------|--|-----------------|--------|-------------|
| | | | RCBr | Chiifu | RCBr/Chiifu |
| Brapa_ESTC041510 | AT2G30130.1 | Symbols: PCK1, LBD12, ASL5 ASL5 (phosphoenolpyruvate carboxykinase1) chr2:12875817-12876761 FORWARD | 1689 | 288 | 5.9 |
| Brapa_ESTC032349 | no_hits_found | ----- | 2538 | 433 | 5.9 |
| Brapa_ESTC032308 | AT4G01030.1 | Symbols: pentatricopeptide (PPR) repeat-containing protein chr4:448336-449838 REVERSE | 2192 | 374 | 5.9 |
| Brapa_ESTC030501 | no_hits_found | ----- | 1741 | 303 | 5.7 |
| Brapa_ESTC032163 | AT5G25390.2 | Symbols: SHN2 SHN2 (SHINE2); DNA binding / transcription factor chr5:8820640-8821744 FORWARD | 1763 | 307 | 5.7 |
| Brapa_ESTC042528 | no_hits_found | ----- | 1143 | 201 | 5.7 |
| Brapa_ESTC019151 | AT1G73830.1 | Symbols: BEE3 BEE3 (BR ENHANCED EXPRESSION 3); DNA binding / transcription factor chr1:27763688-27765007 FORWARD | 2796 | 496 | 5.6 |
| Brapa_ESTC021310 | AT5G22290.1 | Symbols: ANAC089 ANAC089 (Arabidopsis NAC domain containing protein 89); transcription factor chr5:7376047-7377501 REVERSE | 1579 | 281 | 5.6 |
| Brapa_ESTC003972 | no_hits_found | ----- | 2022 | 362 | 5.6 |
| Brapa_ESTC039436 | no_hits_found | ----- | 1766 | 317 | 5.6 |
| Brapa_ESTC020500 | AT2G36030.1 | Symbols: unknown protein chr2:15134638-15134850 REVERSE | 2012 | 363 | 5.5 |
| Brapa_ESTC004590 | AT5G65660.1 | Symbols: hydroxyproline-rich glycoprotein family protein chr5:26262670-26263471 REVERSE | 2669 | 483 | 5.5 |
| Brapa_ESTC033875 | AT1G06770.1 | Symbols: zinc finger (C3HC4-type RING finger) family protein chr1:2079221-2081706 REVERSE | 1171 | 213 | 5.5 |
| Brapa_ESTC036677 | AT1G12050.1 | Symbols: fumarylacetoacetase, putative chr1:4072902-4075854 FORWARD | 1281 | 233 | 5.5 |
| Brapa_ESTC021534 | AT3G29190.1 | Symbols: terpene synthase/cyclase family protein chr3:11160610-11163800 REVERSE | 1506 | 274 | 5.5 |
| Brapa_ESTC005850 | AT3G14010.3 | Symbols: CID4 CID4 (CTC-Interacting Domain 4) chr3:4637171-4640698 FORWARD | 2335 | 427 | 5.5 |
| Brapa_ESTC050456 | no_hits_found | ----- | 1117 | 207 | 5.4 |
| Brapa_ESTC032590 | no_hits_found | ----- | 2098 | 391 | 5.4 |
| Brapa_ESTC051916 | no_hits_found | ----- | 1481 | 276 | 5.4 |
| Brapa_ESTC031357 | no_hits_found | ----- | 1036 | 195 | 5.3 |
| Brapa_ESTC042529 | no_hits_found | ----- | 1115 | 210 | 5.3 |

Supplementary Table 2. Genes induced specifically in RCB.

| Br_SEQ_ID | At_Locus | Gene Annotation | Probe Intensity | | Fold Change |
|------------------|---------------|---|-----------------|--------|-------------|
| | | | RCBr | Chiifu | RCBr/Chiifu |
| Brapa_ESTC037254 | AT2G36950.1 | Symbols: heavy-metal-associated domain-containing protein chr2:15522295-15523833 FORWARD | 1834 | 346 | 5.3 |
| Brapa_ESTC040227 | AT1G30960.1 | Symbols: GTP-binding protein (ERG) chr1:11037736-11039958 REVERSE | 1224 | 232 | 5.3 |
| Brapa_ESTC019941 | AT1G65480.1 | Symbols: FT FT (FLOWERING LOCUS T) chr1:24335173-24337352 FORWARD | 2432 | 462 | 5.3 |
| Brapa_ESTC031762 | AT3G28880.1 | Symbols: ankyrin repeat family protein chr3:10893672-10897009 FORWARD | 1082 | 206 | 5.3 |
| Brapa_ESTC029753 | AT3G62455 | copia-like retrotransposon family | 1341 | 255 | 5.3 |
| Brapa_ESTC009958 | AT5G58040.1 | Symbols: ATFIP1[V] ATFIP1[V] (ARABIDOPSIS HOMOLOG OF YEAST FIP1 [V]); RNA binding chr5:23506091-23511226 FORWARD | 2265 | 434 | 5.2 |
| Brapa_ESTC044067 | AT2G03020.2 | Symbols: heat shock protein-related chr2:882926-884080 REVERSE | 2185 | 419 | 5.2 |
| Brapa_ESTC049829 | no_hits_found | ----- | 1458 | 280 | 5.2 |
| Brapa_ESTC030731 | no_hits_found | ----- | 1400 | 270 | 5.2 |
| Brapa_ESTC043599 | AT3G53310.1 | Symbols: transcriptional factor B3 family protein chr3:19777905-19779346 REVERSE | 1018 | 196 | 5.2 |
| Brapa_ESTC029945 | AT3G20395.1 | Symbols: protein binding / zinc ion binding chr3:7112026-7113798 REVERSE | 1869 | 360 | 5.2 |
| Brapa_ESTC044874 | no_hits_found | ----- | 1635 | 316 | 5.2 |
| Brapa_ESTC040931 | AT1G52810.1 | Symbols: 2-oxoglutarate-dependent dioxygenase-related chr1:19670795-19671905 FORWARD | 1174 | 228 | 5.2 |
| Brapa_ESTC017640 | AT1G22380.1 | Symbols: transcription factor/ transferase, transferring glycosyl groups chr1:7900511-7902321 REVERSE | 2350 | 457 | 5.1 |
| Brapa_ESTC018195 | AT5G49360.1 | Symbols: ATBXL1, BXL1 BXL1 (BETA-XYLOSIDASE 1); hydrolase, hydrolyzing O-glycosyl compounds chr5:20029405-20033885 REVERSE | 2401 | 467 | 5.1 |
| Brapa_ESTC040454 | AT1G69560.1 | Symbols: AtMYB105, MYB105 MYB105 (myb domain protein 105); DNA binding / transcription factor chr1:26161418-26162569 FORWARD | 1409 | 277 | 5.1 |
| Brapa_ESTC048537 | AT5G03230.1 | Symbols: similar to unknown protein [Arabidopsis thaliana] (TAIR:AT5G60680.1); similar to Protein of unknown function DUF584 [Medicago truncatula] (GB:ABD32800.1); contains InterPro domain Protein of unknown function DUF584; (InterPro:IPR007608) | 2408 | 474 | 5.1 |
| Brapa_ESTC032650 | AT3G17010.1 | Symbols: transcriptional factor B3 family protein chr3:5800466-5802309 FORWARD | 1224 | 241 | 5.1 |
| Brapa_ESTC025273 | AT3G57530.1 | Symbols: ATCPK32, CDPK32, CPK32 CPK32 (CALCIUM-DEPENDENT PROTEIN KINASE 32); calcium- and calmodulin-dependent protein kinase/ kinase chr3:21307875-21310328 REVERSE | 1504 | 297 | 5.1 |
| Brapa_ESTC027110 | no_hits_found | ----- | 1234 | 246 | 5.0 |
| Brapa_ESTC038723 | AT1G10530.1 | Symbols: similar to unknown protein [Arabidopsis thaliana] (TAIR:AT1G60010.1); similar to T10024.15, related [Lycopersicon esculentum] (GB:AAX95759.1) chr1:3471806-3472527 REVERSE | 1198 | 239 | 5.0 |

Supplementary Table 2. Genes induced specifically in RCB.

| Br_SEQ_ID | At_Locus | Gene Annotation | Probe Intensity | | Fold Change |
|------------------|---------------|--|-----------------|--------|-------------|
| | | | RCBr | Chiifu | RCBr/Chiifu |
| Brapa_ESTC026388 | AT2G39510.1 | Symbols: nodulin MtN21 family protein chr2:16498436-16500163 REVERSE | 2026 | 405 | 5.0 |
| Brapa_ESTC024156 | AT3G10870.1 | Symbols: hydrolase, alpha/beta fold family protein chr3:3401233-3402617 REVERSE | 2426 | 487 | 5.0 |
| Brapa_ESTC045189 | no_hits_found | ----- | 1846 | 372 | 5.0 |
| Brapa_ESTC038248 | no_hits_found | ----- | 1739 | 351 | 5.0 |
| Brapa_ESTC019205 | AT5G50790.1 | Symbols: nodulin MtN3 family protein chr5:20673687-20675053 REVERSE | 1250 | 256 | 4.9 |
| Brapa_ESTC013587 | AT2G31980.1 | Symbols: cysteine proteinase inhibitor-related chr2:13616323-13616847 REVERSE | 1599 | 328 | 4.9 |
| Brapa_ESTC020132 | AT4G29050.1 | Symbols: lectin protein kinase family protein chr4:14314876-14316885 REVERSE | 1686 | 349 | 4.8 |
| Brapa_ESTC048691 | no_hits_found | ----- | 1440 | 298 | 4.8 |
| Brapa_ESTC031054 | no_hits_found | ----- | 1042 | 216 | 4.8 |
| Brapa_ESTC036909 | AT3G11680.1 | Symbols: similar to unknown protein [Arabidopsis thaliana] (TAIR:AT1G08440.1); similar to Protein of unknown function UPF0005; Rho GTPase activation protein [Medicago truncatula] (GB:ABD32183.1); contains InterPro domain Protein of unknown function | 1585 | 329 | 4.8 |
| Brapa_ESTC017372 | AT1G20630.1 | Symbols: CAT1 CAT1 (CATALASE 1); catalase chr1:7146802-7149599 FORWARD | 2244 | 468 | 4.8 |
| Brapa_ESTC035080 | no_hits_found | ----- | 1480 | 309 | 4.8 |
| Brapa_ESTC022490 | AT2G03750 | P-loop containing nucleoside triphosphate hydrolases superfamily protein | 1125 | 236 | 4.8 |
| Brapa_ESTC031900 | AT1G02850.2 | Symbols: glycosyl hydrolase family 1 protein chr1:630569-633085 FORWARD | 1244 | 262 | 4.8 |
| Brapa_ESTC036628 | AT2G20290.1 | Symbols: ATXIG, XIG XIG (Myosin-like protein XIG); motor/ protein binding chr2:8750356-8758959 REVERSE | 2286 | 484 | 4.7 |
| Brapa_ESTC000474 | no_hits_found | ----- | 2069 | 441 | 4.7 |
| Brapa_ESTC045415 | AT5G06470.1 | Symbols: glutaredoxin family protein chr5:1974660-1975379 REVERSE | 1272 | 272 | 4.7 |
| Brapa_ESTC019960 | AT3G53530.1 | Symbols: heavy-metal-associated domain-containing protein chr3:19856177-19857561 FORWARD | 1128 | 242 | 4.7 |
| Brapa_ESTC048538 | AT5G03230.1 | Symbols: similar to unknown protein [Arabidopsis thaliana] (TAIR:AT5G60680.1); similar to Protein of unknown function DUF584 [Medicago truncatula] (GB:ABD32800.1); contains InterPro domain Protein of unknown function DUF584; (InterPro:IPR007608) | 1566 | 336 | 4.7 |
| Brapa_ESTC030783 | AT5G18000.1 | Symbols: transcriptional factor B3 family protein chr5:5960073-5961475 REVERSE | 1211 | 260 | 4.7 |
| Brapa_ESTC050075 | no_hits_found | ----- | 1197 | 257 | 4.7 |

Supplementary Table 2. Genes induced specifically in RCB_r.

| Br_SEQ_ID | At_Locus | Gene Annotation | Probe Intensity | | Fold Change |
|------------------|---------------|---|-----------------|--------|-------------|
| | | | RCBr | Chiifu | RCBr/Chiifu |
| Brapa_ESTC012753 | AT3G20395.1 | Symbols: protein binding / zinc ion binding chr3:7112026-7113798 REVERSE | 1265 | 275 | 4.6 |
| Brapa_ESTC041180 | AT2G21220.1 | Symbols: auxin-responsive protein, putative chr2:9096461-9096775 FORWARD | 1028 | 224 | 4.6 |
| Brapa_ESTC042180 | AT1G45191.2 | Symbols: glycosyl hydrolase family 1 protein chr1:17118484-17121516 FORWARD | 1879 | 411 | 4.6 |
| Brapa_ESTC040243 | no_hits_found | ----- | 1133 | 248 | 4.6 |
| Brapa_ESTC004129 | AT4G35070.2 | Symbols: similar to SBP1 (S-RIBONUCLEASE BINDING PROTEIN 1), protein binding / zinc ion binding [Arabidopsis thaliana] (TAIR:AT1G45976.1); similar to S-RNase binding protein 1 [Solanum chacoense] (GB:AAS76633.1); contains domain RING/U-box | 2001 | 438 | 4.6 |
| Brapa_ESTC031464 | AT3G16380.1 | Symbols: PAB6 PAB6 (POLY(A) BINDING PROTEIN 6); RNA binding / translation initiation factor chr3:5558682-5560999 REVERSE | 1034 | 227 | 4.6 |
| Brapa_ESTC040994 | no_hits_found | ----- | 2069 | 455 | 4.5 |
| Brapa_ESTC037159 | AT1G21620.1 | Symbols: APUM20 APUM20 (ARABIDOPSIS PUMILIO 20); RNA binding chr1:7579118-7580160 FORWARD | 1314 | 289 | 4.5 |
| Brapa_ESTC027150 | AT2G31980.1 | Symbols: cysteine proteinase inhibitor-related chr2:13616323-13616847 REVERSE | 1773 | 391 | 4.5 |
| Brapa_ESTC031485 | AT1G27180.1 | Symbols: disease resistance protein (TIR-NBS-LRR class), putative chr1:9439846-9445805 FORWARD | 1307 | 289 | 4.5 |
| Brapa_ESTC030533 | AT1G66170.1 | Symbols: MMD1 MMD1 (MALE MEIOCYTE DEATH 1); DNA binding chr1:24642456-24644885 REVERSE | 1777 | 395 | 4.5 |
| Brapa_ESTC051664 | no_hits_found | ----- | 1623 | 362 | 4.5 |
| Brapa_ESTC022367 | AT5G01300.1 | Symbols: phosphatidylethanolamine-binding family protein chr5:121642-122447 REVERSE | 1938 | 432 | 4.5 |
| Brapa_ESTC012481 | AT4G23496.1 | Symbols: SPI15 SPI15 (SPIRAL1-LIKE5) chr4:12257924-12258307 REVERSE | 1177 | 263 | 4.5 |
| Brapa_ESTC031418 | no_hits_found | ----- | 2173 | 487 | 4.5 |
| Brapa_ESTC003383 | AT2G22570.1 | Symbols: ATNIC1 isochorismatase hydrolase family protein chr2:9596684-9597926 REVERSE | 1853 | 420 | 4.4 |
| Brapa_ESTC018021 | AT1G20880.1 | Symbols: RNA recognition motif (RRM)-containing protein chr1:7262868-7264823 REVERSE | 1199 | 273 | 4.4 |
| Brapa_ESTC029991 | no_hits_found | ----- | 1031 | 235 | 4.4 |
| Brapa_ESTC030315 | no_hits_found | ----- | 1073 | 245 | 4.4 |
| Brapa_ESTC026170 | AT1G24160.1 | Symbols: similar to unknown protein [Arabidopsis thaliana] (TAIR:AT1G70100.3); similar to Targeting for Xklp2 [Medicago truncatula] (GB:ABE84619.1) chr1:8553658-8555819 REVERSE | 1850 | 425 | 4.4 |
| Brapa_ESTC044891 | AT4G33150.2 | Symbols: LKR/SDH, LKR, SDH LKR (SACCHAROPINE DEHYDROGENASE) chr4:15985482-15991072 REVERSE | 2070 | 475 | 4.4 |

Supplementary Table 2. Genes induced specifically in RCB_r.

| Br_SEQ_ID | At_Locus | Gene Annotation | Probe Intensity | | Fold Change |
|------------------|---------------|--|-----------------|--------|-------------|
| | | | RCBr | Chiifu | RCBr/Chiifu |
| Brapa_ESTC025442 | AT5G15310.1 | Symbols: AtMYB16, AtMIXTA AtMIXTA/AtMYB16 (myb domain protein 16); DNA binding / transcription factor chr5:4974897-4976109 FORWARD | 1817 | 419 | 4.3 |
| Brapa_ESTC040884 | AT5G18510.1 | Symbols: similar to unknown protein [Arabidopsis thaliana] (TAIR:AT1G51538.1); similar to unknown protein [Arabidopsis thaliana] (TAIR:AT1G50830.1); similar to hypothetical protein [Oryza sativa (japonica cultivar-group)] (GB:AAO60015.1); contains InterPro | 1692 | 392 | 4.3 |
| Brapa_ESTC019325 | AT2G03980.1 | Symbols: GDSL-motif lipase/hydrolase family protein chr2:1260904-1262405 FORWARD | 1284 | 299 | 4.3 |
| Brapa_ESTC036878 | no_hits_found | ----- | 1656 | 388 | 4.3 |
| Brapa_ESTC040339 | no_hits_found | ----- | 1703 | 401 | 4.3 |
| Brapa_ESTC040673 | AT1G77390.1 | Symbols: CYCA1, CYCA1;2 CYCA1;2 (CYCLIN A1;2); cyclin-dependent protein kinase regulator chr1:29086798-29089031 REVERSE | 1292 | 304 | 4.2 |
| Brapa_ESTC022565 | AT5G28750.1 | Symbols: thylakoid assembly protein, putative chr5:10784146-10785681 REVERSE | 1261 | 298 | 4.2 |
| Brapa_ESTC033379 | AT5G10990.1 | Symbols: auxin-responsive family protein chr5:3476885-3477331 FORWARD | 1786 | 422 | 4.2 |
| Brapa_ESTC037861 | AT1G73880.1 | Symbols: UDP-glucuronosyl/UDP-glucosyl transferase family protein chr1:2778804-27790225 FORWARD | 1343 | 318 | 4.2 |
| Brapa_ESTC044093 | AT4G16400.1 | Symbols: similar to unknown protein [Arabidopsis thaliana] (TAIR:AT3G13175.1); similar to hypothetical protein MA4_112110.14 [Musa acuminata] (GB:ABF70146.1) chr4:9260587-9262125 FORWARD | 1538 | 368 | 4.2 |
| Brapa_ESTC043886 | no_hits_found | ----- | 1372 | 329 | 4.2 |
| Brapa_ESTC001266 | AT1G63300.1 | Symbols: similar to unknown protein [Arabidopsis thaliana] (TAIR:AT5G41140.1); similar to putative myosin [Oryza sativa (japonica cultivar-group)] (GB:AAO72668.1); contains domain MYOSIN HEAVY CHAIN-RELATED (PTHR23160) chr1:23485858-23489732 | 1854 | 446 | 4.2 |
| Brapa_ESTC049958 | no_hits_found | ----- | 1137 | 275 | 4.1 |
| Brapa_ESTC033102 | AT4G10250.1 | Symbols: ATHSP22.0 ATHSP22.0 (Arabidopsis thaliana heat shock protein 22.0) chr4:6370533-6371120 FORWARD | 1119 | 272 | 4.1 |
| Brapa_ESTC014892 | AT2G28110.1 | Symbols: FRA8 FRA8 (FRAGILE FIBER8); transferase chr2:11985101-11986718 REVERSE | 2028 | 496 | 4.1 |
| Brapa_ESTC009306 | AT3G13400.1 | Symbols: SKS13 SKS13 (SKU5 Similar 13); copper ion binding / oxidoreductase chr3:4355264-4357312 FORWARD | 1433 | 350 | 4.1 |
| Brapa_ESTC005937 | AT4G18630.1 | Symbols: similar to unknown protein [Arabidopsis thaliana] (TAIR:AT5G45850.1); similar to Protein of unknown function DUF688 [Medicago truncatula] (GB:ABE80249.1); contains InterPro domain Protein of unknown function DUF688; (InterPro:IPR007789) | 1165 | 285 | 4.1 |
| Brapa_ESTC049670 | no_hits_found | ----- | 1593 | 391 | 4.1 |
| Brapa_ESTC031731 | no_hits_found | ----- | 1107 | 274 | 4.0 |
| Brapa_ESTC006053 | AT4G11640.1 | Symbols: ATSR ATSR (ARABIDOPSIS THALIANA SIGNAL-RESPONSIVE); serine racemase chr4:7021764-7023246 FORWARD | 1509 | 376 | 4.0 |
| Brapa_ESTC033092 | AT4G24140.1 | Symbols: hydrolase, alpha/beta fold family protein chr4:12530042-12533674 REVERSE | 1749 | 436 | 4.0 |

Supplementary Table 2. Genes induced specifically in RCB_r.

| Br_SEQ_ID | At_Locus | Gene Annotation | Probe Intensity | | Fold Change |
|------------------|---------------|--|-----------------|--------|-------------|
| | | | RCBr | Chiifu | RCBr/Chiifu |
| Brapa_ESTC049533 | AT2G04350.2 | Symbols: long-chain-fatty-acid--CoA ligase family protein / long-chain acyl-CoA synthetase family protein (LACS8) chr2:1516083-1519175 FORWARD | 1742 | 437 | 4.0 |
| Brapa_ESTC032819 | AT5G01580.1 | Symbols: OSH1 OSH1 (OAS HIGH ACCUMULATION 1); catalytic chr5:222759-223851 REVERSE | 1362 | 342 | 4.0 |
| Brapa_ESTC047641 | no_hits_found | ----- | 1586 | 399 | 4.0 |
| Brapa_ESTC050885 | no_hits_found | ----- | 1018 | 257 | 4.0 |
| Brapa_ESTC031268 | no_hits_found | ----- | 1634 | 420 | 3.9 |
| Brapa_ESTC031882 | AT1G03010.1 | Symbols: phototropic-responsive NPH3 family protein chr1:693480-696188 FORWARD | 1214 | 313 | 3.9 |
| Brapa_ESTC032977 | no_hits_found | ----- | 1299 | 335 | 3.9 |
| Brapa_ESTC000221 | AT1G20530.1 | Symbols: similar to unknown protein [Arabidopsis thaliana] (TAIR:AT2G17110.1); similar to Os09g0547300 [Oryza sativa (japonica cultivar-group)] (GB:NP_001063849.1); similar to bzjp-related transcription factor -like [Oryza sativa (japonica cultivar-group)] | 1921 | 497 | 3.9 |
| Brapa_ESTC004448 | AT1G20823.1 | Symbols: zinc finger (C3HC4-type RING finger) family protein chr1:7238869-7239462 FORWARD | 1063 | 277 | 3.8 |
| Brapa_ESTC049255 | no_hits_found | ----- | 1600 | 417 | 3.8 |
| Brapa_ESTC000703 | AT2G32710.1 | Symbols: ACK2, ICK7, KRP4 KRP4 (KIP-RELATED PROTEIN 4) chr2:13880573-13882427 FORWARD | 1258 | 328 | 3.8 |
| Brapa_ESTC018312 | AT4G27450.1 | Symbols: similar to unknown protein [Arabidopsis thaliana] (TAIR:AT3G15450.1); similar to unknown [Glycine max] (GB:AAG00940.1); contains domain no description (G3D.3.60.20.10); contains domain N-terminal nucleophile aminohydrolases (Ntn | 1793 | 470 | 3.8 |
| Brapa_ESTC026222 | AT1G05440.1 | Symbols: similar to Os03g0747100 [Oryza sativa (japonica cultivar-group)] (GB:NP_001051255.1) chr1:1596373-1597842 REVERSE | 1017 | 269 | 3.8 |
| Brapa_ESTC020635 | AT1G29195.1 | Symbols: similar to unknown protein [Arabidopsis thaliana] (TAIR:AT2G30230.1); similar to unknown protein [Oryza sativa (japonica cultivar-group)] (GB:BAB90229.1) chr1:10202659-10203240 REVERSE | 1520 | 402 | 3.8 |
| Brapa_ESTC021214 | no_hits_found | ----- | 1061 | 281 | 3.8 |
| Brapa_ESTC051781 | no_hits_found | ----- | 1510 | 401 | 3.8 |
| Brapa_ESTC026773 | AT5G60890.1 | Symbols: AtMYB34, ATR1, ATR ATR1 (ALTERED TRYPTOPHAN REGULATION); DNA binding / kinase/ transcription factor chr5:24512255-24513446 FORWARD | 1226 | 326 | 3.8 |
| Brapa_ESTC003624 | no_hits_found | ----- | 1790 | 480 | 3.7 |
| Brapa_ESTC050076 | no_hits_found | ----- | 1141 | 306 | 3.7 |
| Brapa_ESTC019836 | AT4G26420.1 | Symbols: GAMT1 GAMT1; S-adenosylmethionine-dependent methyltransferase/ gibberellin carboxyl-O-methyltransferase chr4:13350904-13352495 REVERSE | 1067 | 287 | 3.7 |
| Brapa_ESTC039683 | no_hits_found | ----- | 1512 | 408 | 3.7 |

Supplementary Table 2. Genes induced specifically in RCB_r.

| Br_SEQ_ID | At_Locus | Gene Annotation | Probe Intensity | | Fold Change |
|------------------|---------------|---|-----------------|--------|-------------|
| | | | RCBr | Chiifu | RCBr/Chiifu |
| Brapa_ESTC004044 | no_hits_found | ----- | 1126 | 305 | 3.7 |
| Brapa_ESTC034674 | AT5G57840.1 | Symbols: transferase family protein chr5:23450171-23452387 REVERSE | 1142 | 311 | 3.7 |
| Brapa_ESTC034036 | AT5G22290.1 | Symbols: ANAC089 ANAC089 (Arabidopsis NAC domain containing protein 89); transcription factor chr5:7376047-7377501 REVERSE | 1104 | 301 | 3.7 |
| Brapa_ESTC048624 | no_hits_found | ----- | 1813 | 497 | 3.6 |
| Brapa_ESTC003250 | AT1G17590.3 | Symbols: CCAAT-binding transcription factor (CBF-B/NF-YA) family protein chr1:6050474-6051977 REVERSE | 1089 | 302 | 3.6 |
| Brapa_ESTC018157 | AT2G46535.1 | Symbols: similar to unknown protein [Arabidopsis thaliana] (TAIR:AT3G61840.1) chr2:19116770-19117392 FORWARD | 1214 | 338 | 3.6 |
| Brapa_ESTC024200 | AT3G60670.1 | Symbols: zinc-binding protein, putative chr3:22435670-22437049 REVERSE | 1622 | 451 | 3.6 |
| Brapa_ESTC031576 | no_hits_found | ----- | 1475 | 411 | 3.6 |
| Brapa_ESTC022443 | AT3G28100.1 | Symbols: nodulin MtN21 family protein chr3:10457388-10462050 FORWARD | 1527 | 431 | 3.5 |
| Brapa_ESTC030511 | no_hits_found | ----- | 1308 | 370 | 3.5 |
| Brapa_ESTC046594 | AT1G24706 | Encodes a component of the putative Arabidopsis THO/TREX complex | 1128 | 320 | 3.5 |
| Brapa_ESTC003546 | no_hits_found | ----- | 1638 | 472 | 3.5 |
| Brapa_ESTC020005 | AT3G44716.1 | Symbols: similar to hypothetical protein MtrDRAFT_AC150566g28v1 [Medicago truncatula] (GB:ABE89140.1) chr3:16274217-16274738 FORWARD | 1465 | 424 | 3.5 |
| Brapa_ESTC033000 | no_hits_found | ----- | 1427 | 414 | 3.4 |
| Brapa_ESTC003610 | no_hits_found | ----- | 1098 | 321 | 3.4 |
| Brapa_ESTC040299 | no_hits_found | ----- | 1075 | 315 | 3.4 |
| Brapa_ESTC035373 | no_hits_found | ----- | 1326 | 389 | 3.4 |
| Brapa_ESTC008846 | AT4G24780.1 | Symbols: pectate lyase family protein chr4:12770641-12772237 REVERSE | 1341 | 398 | 3.4 |
| Brapa_ESTC002709 | AT5G06270.1 | Symbols: similar to unknown protein [Arabidopsis thaliana] (TAIR:AT3G11600.1); similar to H0913C04.5 [Oryza sativa (indica cultivar-group)] (GB:CAJ86164.1); similar to Os04g0415000 [Oryza sativa (japonica cultivar-group)] (GB:NP_001052757.1); similar to | 1680 | 499 | 3.4 |
| Brapa_ESTC050334 | no_hits_found | ----- | 1575 | 468 | 3.4 |
| Brapa_ESTC042612 | no_hits_found | ----- | 1072 | 319 | 3.4 |

Supplementary Table 2. Genes induced specifically in RCB_r.

| Br_SEQ_ID | At_Locus | Gene Annotation | Probe Intensity | | Fold Change |
|------------------|---------------|--|-----------------|--------|-------------|
| | | | RCBr | Chiifu | RCBr/Chiifu |
| Brapa_ESTC019746 | AT5G60540.1 | Symbols: EMB2407, ATPDX2, PDX2 ATPDX2/EMB2407/PDX2 (PYRIDOXINE BIOSYNTHESIS 2); glutaminase/ glutamyl-tRNA(Gln) amidotransferase/ protein heterodimerization chr5:24354100-24355873 REVERSE | 1263 | 376 | 3.4 |
| Brapa_ESTC036144 | AT1G72720.1 | Symbols: similar to unknown protein [Arabidopsis thaliana] (TAIR:AT2G19460.1); similar to putative protein [Brassica oleracea] (GB:AAF19806.1) chr1:27380565-27380948 REVERSE | 1576 | 470 | 3.3 |
| Brapa_ESTC044866 | AT4G33280.1 | Symbols: DNA binding / transcription factor chr4:16047361-16049314 REVERSE | 1607 | 480 | 3.3 |
| Brapa_ESTC029822 | AT5G07280.1 | Symbols: EXS, EMS1 EMS1 (EXCESS MICROSPOROCYTES1); kinase chr5:2285089-2288667 FORWARD | 1568 | 470 | 3.3 |
| Brapa_ESTC019197 | AT2G03060.2 | Symbols: similar to AGL102, DNA binding / transcription factor [Arabidopsis thaliana] (TAIR:AT1G18750.1); similar to SRF-type transcription factor family protein [Oryza sativa (japonica cultivar-group)] (GB:ABA95182.1); contains InterPro domain Transcription | 1325 | 401 | 3.3 |
| Brapa_ESTC027745 | AT2G17033.2 | Symbols: pentatricopeptide (PPR) repeat-containing protein chr2:7408287-7410289 FORWARD | 1477 | 449 | 3.3 |
| Brapa_ESTC011555 | AT5G01010.1 | Symbols: similar to emp24/gp25L/p24 [Medicago truncatula] (GB:ABE93045.1); contains InterPro domain emp24/gp25L/p24; (InterPro:IPR000348); contains InterPro domain GOLD; (InterPro:IPR009038) chr5:1527-4923 REVERSE | 1388 | 423 | 3.3 |
| Brapa_ESTC049687 | AT1G76080.1 | Symbols: ATCDSP32, CDSP32 ATCDSP32/CDSP32 (CHLOROPLASTIC DROUGHT-INDUCED STRESS PROTEIN OF 32 KD); thiol-disulfide exchange intermediate chr1:28552957-28554242 REVERSE | 1475 | 451 | 3.3 |
| Brapa_ESTC039787 | AT5G33385 | gypsy-like retrotransposon family (Athila) | 1353 | 414 | 3.3 |
| Brapa_ESTC051281 | AT5G02600 | Heavy metal transport/detoxification superfamily protein | 1406 | 431 | 3.3 |
| Brapa_ESTC016099 | AT5G24750.1 | Symbols: similar to UDP-glucose:sterol glucosyltransferase, putative [Arabidopsis thaliana] (TAIR:AT1G43620.3); similar to OsO2g0210800 [Oryza sativa (japonica cultivar-group)] (GB:NP_001046269.1); similar to glucosyltransferase [Xanthomonas campestris | 1502 | 463 | 3.2 |
| Brapa_ESTC041311 | no_hits_found | ----- | 1472 | 455 | 3.2 |
| Brapa_ESTC035076 | AT3G57700.1 | Symbols: protein kinase, putative chr3:21395894-21396916 FORWARD | 1510 | 470 | 3.2 |
| Brapa_ESTC001067 | AT5G47635.1 | Symbols: similar to unknown protein [Arabidopsis thaliana] (TAIR:AT2G40113.1); similar to hypothetical protein 31.t00008 [Brassica oleracea] (GB:ABD65108.1) chr5:19324507-19325075 REVERSE | 1380 | 436 | 3.2 |
| Brapa_ESTC036362 | AT3G26490.1 | Symbols: phototropic-responsive NPH3 family protein chr3:9705379-9707398 FORWARD | 1252 | 396 | 3.2 |
| Brapa_ESTC037347 | no_hits_found | ----- | 1343 | 425 | 3.2 |
| Brapa_ESTC033238 | AT2G33060.1 | Symbols: leucine-rich repeat family protein chr2:14032738-14035164 FORWARD | 1176 | 372 | 3.2 |
| Brapa_ESTC038934 | AT5G59380.1 | Symbols: MBD6 MBD6 (methyl-CpG-binding domain 6); DNA binding chr5:23969547-23970711 FORWARD | 1385 | 439 | 3.2 |
| Brapa_ESTC041273 | AT3G51240.1 | Symbols: TT6, F3H, F3'H F3H (TRANSPARENT TESTA 6); naringenin 3-dioxygenase chr3:19036388-19037637 FORWARD | 1089 | 347 | 3.1 |
| Brapa_ESTC038306 | AT3G62300.1 | Symbols: agenet domain-containing protein chr3:23065222-23068056 FORWARD | 1089 | 348 | 3.1 |
| Brapa_ESTC050377 | AT2G21480.1 | Symbols: protein kinase family protein chr2:9209833-9212448 REVERSE | 1168 | 374 | 3.1 |

Supplementary Table 2. Genes induced specifically in RCB_r.

| Br_SEQ_ID | At_Locus | Gene Annotation | Probe Intensity | | Fold Change |
|------------------|---------------|--|-----------------|--------|-------------|
| | | | RCBr | Chiifu | RCBr/Chiifu |
| Brapa_ESTC028636 | no_hits_found | ----- | 1253 | 403 | 3.1 |
| Brapa_ESTC050077 | no_hits_found | ----- | 1463 | 471 | 3.1 |
| Brapa_ESTC002241 | AT1G20640.2 | Symbols: RWP-RK domain-containing protein chr1:7155191-7157976 FORWARD | 1408 | 455 | 3.1 |
| Brapa_ESTC024230 | AT5G05810.1 | Symbols: ATL43 ATL43; protein binding / zinc ion binding chr5:1746939-1748000 FORWARD | 1505 | 488 | 3.1 |
| Brapa_ESTC035665 | AT4G21600.1 | Symbols: bifunctional nuclease, putative chr4:11485331-11487247 FORWARD | 1140 | 375 | 3.0 |
| Brapa_ESTC030637 | AT1G05690.1 | Symbols: BT3 BT3 (BTB and TAZ domain protein 3); protein binding / transcription regulator chr1:1707808-1709131 FORWARD | 1143 | 378 | 3.0 |
| Brapa_ESTC018153 | AT2G24420.2 | Symbols: DNA repair ATPase-related chr2:10387227-10389704 FORWARD | 1194 | 397 | 3.0 |
| Brapa_ESTC005962 | AT3G5680.1 | Symbols: dehydration-responsive protein-related chr3:20821505-20823033 REVERSE | 1060 | 354 | 3.0 |
| Brapa_ESTC001255 | AT5G37790.1 | Symbols: protein kinase family protein chr5:15025663-15028255 REVERSE | 1246 | 417 | 3.0 |
| Brapa_ESTC014094 | AT4G26180.1 | Symbols: mitochondrial substrate carrier family protein chr4:13260272-13261896 REVERSE | 1365 | 457 | 3.0 |
| Brapa_ESTC047080 | no_hits_found | ----- | 1158 | 388 | 3.0 |
| Brapa_ESTC043089 | no_hits_found | ----- | 1040 | 351 | 3.0 |
| Brapa_ESTC006096 | AT3G26740.1 | Symbols: CCL CCL (CCR-LIKE) chr3:9829105-9829698 FORWARD | 1460 | 493 | 3.0 |
| Brapa_ESTC027933 | AT5G42120.1 | Symbols: lectin protein kinase family protein chr5:16850301-16852376 REVERSE | 1327 | 451 | 2.9 |
| Brapa_ESTC000634 | no_hits_found | ----- | 1141 | 390 | 2.9 |
| Brapa_ESTC042873 | AT3G12720.1 | Symbols: AtY53, AtMYB67 AtMYB67/AtY53 (myb domain protein 67); DNA binding / transcription factor chr3:4043414-4044529 REVERSE | 1358 | 467 | 2.9 |
| Brapa_ESTC048964 | no_hits_found | ----- | 1404 | 485 | 2.9 |
| Brapa_ESTC024889 | AT2G35550.4 | Symbols: BPC7, BBR/BPC7, ATBPC7 ATBPC7/BBR/BPC7/BPC7 (BASIC PENTACYSSTEINE 7) chr2:14937017-14937697 FORWARD | 1373 | 475 | 2.9 |
| Brapa_ESTC027885 | no_hits_found | ----- | 1182 | 413 | 2.9 |
| Brapa_ESTC042104 | no_hits_found | ----- | 1154 | 404 | 2.9 |
| Brapa_ESTC035820 | AT5G23340.1 | Symbols: protein binding chr5:7856317-7857986 FORWARD | 1015 | 356 | 2.8 |

Supplementary Table 2. Genes induced specifically in RCB_r.

| Br_SEQ_ID | At_Locus | Gene Annotation | Probe Intensity | | Fold Change |
|------------------|---------------|--|-----------------|--------|-------------|
| | | | RCBr | Chiifu | RCBr/Chiifu |
| Brapa_ESTC007773 | AT2G40850.1 | Symbols: phosphatidylinositol 3- and 4-kinase family protein chr2:17058653-17060338 FORWARD | 1346 | 474 | 2.8 |
| Brapa_ESTC043129 | AT3G17650.1 | Symbols: PDE321, YSL5 YSL5 (YELLOW STRIPE LIKE 5); oligopeptide transporter chr3:6034313-6037093 FORWARD | 1016 | 358 | 2.8 |
| Brapa_ESTC032947 | no_hits_found | ----- | 1268 | 446 | 2.8 |
| Brapa_ESTC050120 | AT2G38110.1 | Symbols: ATGPAT6, GPAT6 ATGPAT6/GPAT6 (GLYCEROL-3-PHOSPHATE ACYLTRANSFERASE 6); 1-acylglycerol-3-phosphate O-acyltransferase/ acyltransferase chr2:15959894-15962442 REVERSE | 1101 | 391 | 2.8 |
| Brapa_ESTC036448 | AT1G08180.1 | Symbols: similar to unknown protein [Arabidopsis thaliana] (TAIR:AT5G02420.1) chr1:2564738-2565073 REVERSE | 1075 | 386 | 2.8 |
| Brapa_ESTC032225 | AT1G49990.1 | Symbols: similar to F-box family protein [Arabidopsis thaliana] (TAIR:AT3G26010.1); contains InterPro domain Cyclin-like F-box; (InterPro:IPR001810); contains InterPro domain Galactose oxidase, central; (InterPro:IPR011043) chr1:18517364-18518656 FORWARD | 1352 | 488 | 2.8 |
| Brapa_ESTC036536 | AT3G14950.1 | Symbols: TTL2 TTL2 (TETRATRICOPETIDE-REPEAT THIOREDOXIN-LIKE 2); binding chr3:5030223-5032899 REVERSE | 1067 | 386 | 2.8 |
| Brapa_ESTC044459 | no_hits_found | ----- | 1106 | 405 | 2.7 |
| Brapa_ESTC044429 | no_hits_found | ----- | 1187 | 436 | 2.7 |
| Brapa_ESTC046660 | no_hits_found | ----- | 1294 | 475 | 2.7 |
| Brapa_ESTC027705 | AT3G10320.1 | Symbols: similar to unknown protein [Arabidopsis thaliana] (TAIR:AT2G41640.1); similar to glycosyltransferase [Medicago truncatula] (GB:CAI30145.1); contains InterPro domain Protein of unknown function DUF563; (InterPro:IPR007657) chr3:3195446- | 1224 | 451 | 2.7 |
| Brapa_ESTC044393 | AT3G25510.1 | Symbols: disease resistance protein (TIR-NBS-LRR class), putative chr3:9262075-9270034 REVERSE | 1213 | 448 | 2.7 |
| Brapa_ESTC016536 | AT3G15720.2 | Symbols: glycoside hydrolase family 28 protein / polygalacturonase (pectinase) family protein chr3:5325336-5327624 REVERSE | 1317 | 493 | 2.7 |
| Brapa_ESTC031832 | AT3G59830.1 | Symbols: ankyrin protein kinase, putative chr3:22113983-22116300 REVERSE | 1081 | 408 | 2.6 |
| Brapa_ESTC033416 | no_hits_found | ----- | 1314 | 497 | 2.6 |
| Brapa_ESTC036212 | AT4G15475.1 | Symbols: F-box family protein (FBL4) chr4:8845925-8848699 FORWARD | 1309 | 496 | 2.6 |
| Brapa_ESTC043424 | AT4G20900.1 | Symbols: TDM1, MS5 MS5 (MALE-STERILE 5); binding chr4:11184114-11185855 REVERSE | 1002 | 381 | 2.6 |
| Brapa_ESTC051627 | no_hits_found | ----- | 1203 | 464 | 2.6 |
| Brapa_ESTC021796 | AT2G48080.1 | Symbols: oxidoreductase, 2OG-Fe(II) oxygenase family protein chr2:19672262-19674162 REVERSE | 1013 | 391 | 2.6 |
| Brapa_ESTC042768 | AT3G07970.1 | Symbols: polygalacturonase, putative / pectinase, putative chr3:2541012-2543376 FORWARD | 1018 | 397 | 2.6 |
| Brapa_ESTC024939 | AT5G43530.1 | Symbols: SNF2 domain-containing protein / helicase domain-containing protein / RING finger domain-containing protein chr5:17506555-17512058 FORWARD | 1008 | 393 | 2.6 |

Supplementary Table 2. Genes induced specifically in RCB_r.

| Br_SEQ_ID | At_Locus | Gene Annotation | Probe Intensity | | Fold Change |
|------------------|---------------|---|-----------------|--------|-------------|
| | | | RCBr | Chiifu | RCBr/Chiifu |
| Brapa_ESTC037270 | AT4G28040.4 | Symbols: nodulin MtN21 family protein chr4:13940887-13942207 FORWARD | 1032 | 404 | 2.6 |
| Brapa_ESTC045391 | AT5G06839.1 | Symbols: bZIP family transcription factor chr5:2120912-2126218 FORWARD | 1162 | 455 | 2.6 |
| Brapa_ESTC010446 | AT1G28610.2 | Symbols: GDSL-motif lipase, putative chr1:10053863-10055651 REVERSE | 1161 | 455 | 2.6 |
| Brapa_ESTC045531 | AT5G12920.1 | Symbols: similar to unnamed protein product [Ostreococcus tauri] (GB:CAL53992.1); similar to Os02g0591600 [Oryza sativa (japonica cultivar-group)] (GB:NP_001047287.1); contains InterPro domain WD40-like; (InterPro:IPR011046) chr5:4077920-4082064 REVERSE | 1082 | 425 | 2.5 |
| Brapa_ESTC017122 | AT3G26932.2 | Symbols: DRB3 DRB3 (DSRNA-BINDING PROTEIN 3); double-stranded RNA binding chr3:9931697-9932951 REVERSE | 1027 | 405 | 2.5 |
| Brapa_ESTC010720 | AT1G67350.2 | Symbols: unknown protein chr1:25239580-25240446 FORWARD | 1145 | 453 | 2.5 |
| Brapa_ESTC022393 | no_hits_found | ----- | 1226 | 488 | 2.5 |
| Brapa_ESTC015752 | AT5G66740.1 | Symbols: similar to unknown protein [Arabidopsis thaliana] (TAIR:AT1G75160.1); similar to BAC19.5 [Lycopersicon esculentum] (GB:AAG01120.1); contains InterPro domain Protein of unknown function DUF620; (InterPro:IPR006873) chr5:26664956-26665784 | 1121 | 448 | 2.5 |
| Brapa_ESTC037031 | no_hits_found | ----- | 1089 | 436 | 2.5 |
| Brapa_ESTC020463 | AT5G61865.1 | Symbols: unknown protein chr5:24864621-24866932 FORWARD | 1001 | 403 | 2.5 |
| Brapa_ESTC031091 | AT3G02100.1 | Symbols: UDP-glucuronosyl/UDP-glucosyl transferase family protein chr3:368847-370491 REVERSE | 1069 | 432 | 2.5 |
| Brapa_ESTC039268 | AT4G38370.1 | Symbols: phosphoglycerate/bisphosphoglycerate mutase family protein chr4:17970106-17971216 REVERSE | 1174 | 476 | 2.5 |
| Brapa_ESTC010412 | AT1G68200.1 | Symbols: zinc finger (CCCH-type) family protein chr1:25565781-25567611 FORWARD | 1073 | 435 | 2.5 |
| Brapa_ESTC002332 | AT1G35310.1 | Symbols: MLP168 Bet v I allergen family protein chr1:12956406-12957002 REVERSE | 1117 | 453 | 2.5 |
| Brapa_ESTC004186 | AT1G60060.1 | Symbols: similar to unknown protein [Arabidopsis thaliana] (TAIR:AT5G53900.2); similar to Os02g0742700 [Oryza sativa (japonica cultivar-group)] (GB:NP_001048090.1); similar to unknown protein [Oryza sativa (japonica cultivar-group)] (GB:BAD37771.1); similar | 1019 | 419 | 2.4 |
| Brapa_ESTC017107 | AT2G32530.1 | Symbols: CSLB03, ATCSLB3, ATCSLB03 ATCSLB03 (Cellulose synthase-like B3); transferase/ transferase, transferring glycosyl groups chr2:13816360-13820564 FORWARD | 1064 | 439 | 2.4 |
| Brapa_ESTC028695 | AT4G01470.1 | Symbols: GAMMA-TIP3, TIP1;3 GAMMA-TIP3/TIP1;3 (tonoplast intrinsic protein 1;3); water channel chr4:625092-625850 REVERSE | 1070 | 443 | 2.4 |
| Brapa_ESTC019662 | AT2G41510.1 | Symbols: ATCKX1, CKX1 ATCKX1/CKX1 (CYTOKININ OXIDASE/DEHYDROGENASE 1); cytokinin dehydrogenase chr2:17321704-17323939 FORWARD | 1195 | 499 | 2.4 |
| Brapa_ESTC022453 | AT3G22490.1 | Symbols: late embryogenesis abundant protein, putative / LEA protein, putative chr3:7969792-7970745 REVERSE | 1089 | 456 | 2.4 |
| Brapa_ESTC019328 | AT5G58170.1 | Symbols: glycerophosphoryl diester phosphodiesterase family protein chr5:23557487-23560318 REVERSE | 1122 | 470 | 2.4 |
| Brapa_ESTC039306 | no_hits_found | ----- | 1037 | 434 | 2.4 |

Supplementary Table 2. Genes induced specifically in RCB_r.

| Br_SEQ_ID | At_Locus | Gene Annotation | Probe Intensity | | Fold Change |
|------------------|---------------|---|-----------------|--------|-------------|
| | | | RCBr | Chiifu | RCBr/Chiifu |
| Brapa_ESTC035154 | AT4G32280.1 | Symbols: IAA29 IAA29 (indoleacetic acid-induced protein 29); transcription factor chr4:15583485-15584634 FORWARD | 1126 | 472 | 2.4 |
| Brapa_ESTC004428 | AT5G10930.1 | Symbols: SnRK3.24, CIPK5 CIPK5 (CBL-INTERACTING PROTEIN KINASE 5); kinase chr5:3445570-3446907 REVERSE | 1112 | 467 | 2.4 |
| Brapa_ESTC036282 | AT3G15760.1 | Symbols: similar to unknown protein [Arabidopsis thaliana] (TAIR:AT1G52565.1); similar to conserved hypothetical protein [Medicago truncatula] (GB:ABD28733.1) chr3:5337741-5338226 FORWARD | 1069 | 451 | 2.4 |
| Brapa_ESTC035134 | AT5G53660.1 | Symbols: AtGRF7 AtGRF7 (GROWTH-REGULATING FACTOR 7) chr5:21811862-21813155 FORWARD | 1094 | 464 | 2.4 |
| Brapa_ESTC043677 | AT3G54350.3 | Symbols: EMB1967 EMB1967 (EMBRYO DEFECTIVE 1967) chr3:20133276-20137009 REVERSE | 1039 | 441 | 2.4 |
| Brapa_ESTC026017 | AT1G47510.1 | Symbols: endonuclease/exonuclease/phosphatase family protein chr1:17438431-17440736 REVERSE | 1161 | 495 | 2.3 |
| Brapa_ESTC005357 | AT5G48740.1 | Symbols: leucine-rich repeat family protein / protein kinase family protein chr5:19782550-19786540 REVERSE | 1116 | 485 | 2.3 |
| Brapa_ESTC017040 | AT1G15360.1 | Symbols: SHN1, WIN1 SHN1/WIN1 (SHINE1); DNA binding / transcription factor chr1:5283604-5284501 FORWARD | 1064 | 464 | 2.3 |
| Brapa_ESTC027067 | AT5G10140.1 | Symbols: FLF, AGL25, FLC FLC (FLOWERING LOCUS C); transcription factor chr5:3173725-3179340 REVERSE | 1108 | 485 | 2.3 |
| Brapa_ESTC037470 | no_hits_found | ----- | 1025 | 457 | 2.2 |
| Brapa_ESTC021084 | AT2G18090.1 | Symbols: PHD finger family protein / SWIB complex BAF60b domain-containing protein / GYF domain-containing protein chr2:7871583-7874399 FORWARD | 1070 | 497 | 2.2 |
| Brapa_ESTC048164 | no_hits_found | ----- | 1024 | 476 | 2.1 |
| Brapa_ESTC050850 | AT4G22545 | pseudogene of unknown protein | 1020 | 486 | 2.1 |
| Brapa_ESTC044956 | AT2G16420 | non-LTR retrotransposon family (LINE), | 1006 | 480 | 2.1 |
| Brapa_ESTC003844 | AT1G77590.1 | Symbols: LACS9 LACS9 (LONG CHAIN ACYL-COA SYNTHETASE 9); long-chain-fatty-acid-CoA ligase chr1:29153395-29156670 REVERSE | 1026 | 495 | 2.1 |
| Brapa_ESTC032215 | no_hits_found | ----- | 1016 | 493 | 2.1 |