

| | cov | pid | 2881 | 9 | 0 | 3000 |
|---------------------|--------|--------|------|------------------------------------|--|---|
| 1 ARG2_SC328C | 100.0% | 100.0% | CC | TGCGGCTAC | CAAGAGGACCGAAGCTACCTTGGCC | TGGGAGACATTGAAGGATC--CCATGCGGAGGTGGAAGCAACAGAAACCTTCCGACC--ACGCCGGAGAGATCTCACAAGT |
| 2 ARG2_Keller | 100.0% | 100.0% | CC | TGCGGCTAC | CAAGAGGACCGAAGCTACCTTGGCC | TGGGAGACATTGAAGGATC--CCATGCGGAGGTGGAAGCAACAGAAACCTTCCGACC--ACGCCGGAGAGATCTCACAAGT |
| 3 ARG2_SC237 | 100.0% | 100.0% | CC | TGCGGCTAC | CAAGAGGACCGAAGCTACCTTGGCC | TGGGAGACATTGAAGGATC--CCATGCGGAGGTGGAAGCAACAGAAACCTTCCGACC--ACGCCGGAGAGATCTCACAAGT |
| 4 ARG2_Rio | 100.0% | 100.0% | CC | TGCGGCTAC | CAAGAGGACCGAAGCTACCTTGGCC | TGGGAGACATTGAAGGATC--CCATGCGGAGGTGGAAGCAACAGAAACCTTCCGACC--ACGCCGGAGAGATCTCACAAGT |
| 5 arg2_CS265 | 97.0% | 92.3% | ---- | GCTATCAGAGGACCGAAGCTACCTTGAACC | TGGGAGACGTTGAAGGATC--CAGAGTGGAGGTGGAAGCAACAGAAACCTTCCGACC--G--TGGCTGGAGAGATCTCACAAGT | |
| 6 arg2_TAM428 | 97.5% | 87.5% | CC | TGCGGCTATCAGATGACCGAAGCTACCTTGAACC | TGGGAGACGTTGAAGGATCTCCCAATACG | CAGGTGGAAGCAACAGAAACCTTCTTGAT----ATGGCAGAGAGATCTCACAAGT |
| 7 arg2_BTx642 | 97.5% | 87.5% | CC | TGCGGCTATCAGATGACCGAAGCTACCTTGAACC | TGGGAGACGTTGAAGGATCTCCCAATACG | CAGGTGGAAGCAACAGAAACCTTCTTGAT----ATGGCAGAGAGATCTCACAAGT |
| 8 arg2_SC23 | 97.5% | 87.5% | CC | TGCGGCTATCAGATGACCGAAGCTACCTTGAACC | TGGGAGACGTTGAAGGATCTCCCAATACG | CAGGTGGAAGCAACAGAAACCTTCTTGAT----ATGGCAGAGAGATCTCACAAGT |
| 9 arg2_IS9830 | 97.5% | 87.5% | CC | TGCGGCTATCAGATGACCGAAGCTACCTTGAACC | TGGGAGACGTTGAAGGATCTCCCAATACG | CAGGTGGAAGCAACAGAAACCTTCTTGAT----ATGGCAGAGAGATCTCACAAGT |
| 10 arg2_PQ434 | 97.5% | 87.5% | CC | TGCGGCTATCAGATGACCGAAGCTACCTTGAACC | TGGGAGACGTTGAAGGATCTCCCAATACG | CAGGTGGAAGCAACAGAAACCTTCTTGAT----ATGGCAGAGAGATCTCACAAGT |
| 11 arg2_IS18760 | 97.5% | 87.5% | CC | TGCGGCTATCAGATGACCGAAGCTACCTTGAACC | TGGGAGACGTTGAAGGATCTCCCAATACG | CAGGTGGAAGCAACAGAAACCTTCTTGAT----ATGGCAGAGAGATCTCACAAGT |
| 12 arg2_ICSV745 | 99.6% | 89.1% | CC | TGCGGCTATCAGATGACCGAAGCTACCTTGAACC | TGGGAGACGTTGAAGGATCTCCCAATACG | CAGGTGGAAGCAACAGAAACCTTCTTGATGACCATGCCTGCCAGAGAGATCTCACAAGT |
| 13 arg2_IS8525 | 99.6% | 89.2% | CC | TGCGGCTATCAGATGACCGAAGCTACCTTGAACC | TGGGAGACGTTGAAGGATCTCCCAATACG | CAGGTGGAAGCAACAGAAACCTTCTTGATGACCATGCCTGCCAGAGAGATCTCACAAGT |
| 14 arg2_Malisor84-7 | 99.6% | 89.1% | CC | TGCGGCTATCAGATGACCGAAGCTACCTTGAACC | TGGGAGACGTTGAAGGATCTCCCAATACG | CAGGTGGAAGCAACAGAAACCTTCTTGATGACCATGCCTGCCAGAGAGATCTCACAAGT |
| 15 arg2_BTx623 | 99.6% | 89.1% | CC | TGCGGCTATCAGATGACCGAAGCTACCTTGAACC | TGGGAGACGTTGAAGGATCTCCCAATACG | CAGGTGGAAGCAACAGAAACCTTCTTGATGACCATGCCTGCCAGAGAGATCTCACAAGT |

| | cov | pid | 3001 | 1 | 3049 |
|---------------------|--------|--------|------|--------------------------------------|---------|
| 1 ARG2_SC328C | 100.0% | 100.0% | GATC | CAACCAACACGACCAACAGTGAATCCAGCCCCTTC | TACTTGA |
| 2 ARG2_Keller | 100.0% | 100.0% | GATC | CAACCAACACGACCAACAGTGAATCCAGCCCCTTC | TACTTGA |
| 3 ARG2_SC237 | 100.0% | 100.0% | GATC | CAACCAACACGACCAACAGTGAATCCAGCCCCTTC | TACTTGA |
| 4 ARG2_Rio | 100.0% | 100.0% | GATC | CAACCAACACGACCAACAGTGAATCCAGCCCCTTC | TACTTGA |
| 5 arg2_CS265 | 97.0% | 92.3% | GATC | CAACTAGCCACGACCAACAGTGAATCCAGCCCTTC | TACTTGA |
| 6 arg2_TAM428 | 97.5% | 87.5% | GATC | CAACCAACACGACCAACAGTGAATCCAGCCCCTTC | TACTTGA |
| 7 arg2_BTx642 | 97.5% | 87.5% | GATC | CAACCAACACGACCAACAGTGAATCCAGCCCCTTC | TACTTGA |
| 8 arg2_SC23 | 97.5% | 87.5% | GATC | CAACCAACACGACCAACAGTGAATCCAGCCCCTTC | TACTTGA |
| 9 arg2_IS9830 | 97.5% | 87.5% | GATC | CAACCAACACGACCAACAGTGAATCCAGCCCCTTC | TACTTGA |
| 10 arg2_PQ434 | 97.5% | 87.5% | GATC | CAACCAACACGACCAACAGTGAATCCAGCCCCTTC | TACTTGA |
| 11 arg2_IS18760 | 97.5% | 87.5% | GATC | CAACCAACACGACCAACAGTGAATCCAGCCCCTTC | TACTTGA |
| 12 arg2_ICSV745 | 99.6% | 89.1% | GATC | CAACCAACACGACCAACAGTGAATCCAGACTGCTTC | TACTTGA |
| 13 arg2_IS8525 | 99.6% | 89.2% | GATC | CAACCAACACGACCAACAGTGAATCCAGACTGCTTC | TACTTGA |
| 14 arg2_Malisor84-7 | 99.6% | 89.1% | GATC | CAACCAACACGACCAACAGTGAATCCAGACTGCTTC | TACTTGA |
| 15 arg2_BTx623 | 99.6% | 89.1% | GATC | CAACCAACACGACCAACAGTGAATCCAGACTGCTTC | TACTTGA |

Data S1. Alignment of the ARG2 nucleotide sequences from 15 sorghum lines.

The ARG2 coding sequences in four resistant (SC328C, Keller, SC237 and Rio) and 11 susceptible lines were aligned. The alignment shows four different ARG2 alleles. ARG2 allele in SC328C is similar to that in Keller, SC237 and Rio. The susceptibility ARG2 allele from SC265 is a unique allele. TAM428, BTx642, SC23, IS9830, PQ434 and IS18760 show the same allele. ICSV745, IS8525, Malisor84-7 carry the susceptibility allele like BTx623. The premature stop codons are shaded in red. The premature stop codons are shaded in red. These amino acid sequences were aligned using “multiple sequence alignment” tools: kalign [www.ebi.ac.uk/Tools/msa/kalign/] and mview [www.ebi.ac.uk/Tools/msa/mview/].

| | cov | pid | 961 | 0 | 1018 |
|-----------------|--------|--------|-------|---|-------|
| 1 ARG2_SC328C | 100.0% | 100.0% | R | QEDRSYHCLCDTEGSHFEEVETESIPDFACEISQVITFTTTNSEQPA | SSStP |
| 2 ARG2_Rio | 100.0% | 100.0% | R | QEDRSYHCLCDTEGSHFEEVETESIPDFACEISQVITFTTTNSEQPA | SSStP |
| 3 ARG2_DS13 | 100.0% | 100.0% | R | QEDRSYHCLCDTEGSHFEEVETESIPDFACEISQVITFTTTNSEQPA | SSStP |
| 4 ARG2_DS49 | 100.0% | 100.0% | R | QEDRSYHCLCDTEGSHFEEVETESIPDFACEISQVITFTTTNSEQPA | SSStP |
| 5 arg2_DS26 | 83.1% | 93.2% | ----- | ----- | ----- |
| 6 arg2_DS06 | 60.9% | 84.9% | ----- | ----- | ----- |
| 7 arg2_DS25 | 60.9% | 84.9% | ----- | ----- | ----- |
| 8 arg2_DS50 | 60.9% | 84.9% | ----- | ----- | ----- |
| 9 arg2_DS57 | 60.9% | 84.9% | ----- | ----- | ----- |
| 10 arg2_IS18760 | 60.9% | 84.9% | ----- | ----- | ----- |
| 11 arg2_TAM428 | 60.9% | 84.9% | ----- | ----- | ----- |
| 12 arg2_DS10 | 99.8% | 82.9% | R | SDDRSYHDEEDVEGSPMRRWKQONPFLTMFAREISQVITFTTTNSEQTA | SSStP |
| 13 arg2_DS12 | 99.8% | 83.0% | R | SDDRSYHDEEDVEGSPMRRWKQONPFLTMFAREISQVITFTTTNSEQTA | SSStP |
| 14 arg2_DS17 | 99.8% | 82.9% | R | SDDRSYHDEEDVEGSPMRRWKQONPFLTMFAREISQVITFTTTNSEQTA | SSStP |
| 15 arg2_BTx623 | 99.8% | 82.9% | R | SDDRSYHDEEDVEGSPMRRWKQONPFLTMFAREISQVITFTTTNSEQTA | SSStP |

Data S2. Alignment of the ARG2 amino acid sequences in 15 sorghum lines.

The ARG2 amino acid sequences in four resistant (SC328C, Keller, SC237 and Rio) and 11 susceptible lines were aligned. The alignment shows four different ARG2 alleles. ARG2 allele in SC328C is similar to that in Keller, SC237 and Rio. The susceptible ARG2 allele from SC265 is a unique allele. TAM428, BTx642, SC23, IS9830, PQ434 and IS18760 show the same allele. ICSV745, IS8525, Malisor84-7 carry the susceptible allele like BTx623. The premature stop codons are shaded in red. These deduced amino acid sequences were aligned using “multiple sequence alignment” tools: kalign [www.ebi.ac.uk/Tools/msa/kalign/] and mview [www.ebi.ac.uk/Tools/msa/mview/].

```

cov    pid    1 [
1 arg2_SC265 100.0% 100.0% MAETALSLKSLGSAISKVA SAAGTEISILMGVQKEWFKDEKTKMQLFQAPQTEKKDKLVKWEQ RDLSYD EDCDEFVHVGSHLSKQLMK KDRHRIAVQRN KSR E
2 arg2_TAM428 99.5% 84.5% MAETALIMKSLGSAISKVA SAAGTEISILMGVQKEWFKDEKTKMQLFQAPQTEKKDKLVKWEQ RDLSYD EDCDEFVHVGSHLSKQLMK KDRHRIAVQRN KSR E
cov    pid    121
1 arg2_SC265 100.0% 100.0% ELSRNRYNLIKTESSNNTDDSDN EYIRNNAAWNDE ELVGFDAFKRELIALIDVITDGPDKVVCVVGSGGLGKTTLRKTYESREDT KSEFYRAWITVQSFSRRGILQDMIS
2 arg2_TAM428 99.5% 84.5% ELSNRNRYNLIKTESSNNTDDSDN EDIRNNSASNDE ELVGFDAFKRELIAMIDVITDGPDKVVCVVGSGGLGKTTLRKTYESREDT KSEFYRAWITVQSFSRRAMIQDMIN
cov    pid    241
1 arg2_SC265 100.0% 100.0% KIEGVSALNDLLKQPAKQVLEODLATSIRQK EDKRYFIVFDD WE DHWNCIRGVALPMSNNRGSRRIMITTRDVGLAHCTSSENN--LYHKHIQIDAIKLLQKKTNI THEE DKDE
2 arg2_TAM428 99.5% 84.5% QIEGPDALKKLLIQVCKVLEODGLASYIRQK EDKRYFIVFDD WE NHWNNTSGIALESNNRGSRRIVTTRDAGLARHCTS--ELLIVDKPIETDAIKLLQKKTNI THEE DKDE
cov    pid    361
1 arg2_SC265 100.0% 100.0% NISTIVKIVKRCYLPPLAIL IGGVLAKKKKEWENFYQK CSEVESNPSFAIRRVNLSYNHLESRLKCELYLSFPEEDYEKRSHLYRWIAEFVRKVCITDEVCKEYFDEI
2 arg2_TAM428 99.5% 84.5% NISTIVKIVKRCYLPPLAIL IGGVLAKKKKEWENFYQK PSEVESNPSFAIRRVNLSYNHLESRLKCELYLSFPEEDYEKRSHLYRWIAEFVRKVCITDEVCKEYFDEI
cov    pid    481
1 arg2_SC265 100.0% 100.0% ISRSMIQSSELGMECSVKICRVDHIDRDITIVSTRREENEVHIVQSNQNNVAEENFRHVAYHDSKQKQKGMWRHRSITDFTECSSGLGLDITPSSIKRMLRVLDLVGQNFRIQDQ
2 arg2_TAM428 99.5% 84.5% ISRSMIQSSELGMECSVKICRVDHIDRDITIVSTRREENEVHIVQSNQNNVPEENFRHVAYHDSKQKQKGMWRHRSITDFTECSSGLGLDITPSSIKRMLRVLDLVGQNFRIQDQ
cov    pid    601
1 arg2_SC265 100.0% 100.0% NIKIVLLCHLYKYNVSDW
2 arg2_TAM428 99.5% 84.5% NIKIVLLCHLYKLVNRTY

```

Data S3. Comparison of the ARG2 allele in SC265 and TAM428 (15.5% non-synonymous codon).

| | | cov | pid | 1 | | | | | | 1 | | 120 | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
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| 1 | ARG2_SC328C | 100.0% | 100.0% | L | N | R | S | L | Q | S | S | R | L | G | E | S | K | T | C | R | V | H | D | L | M | R | D | L | I | V | S | S | R | E | N | F | H | L | V | Q | S | N | N | V | A | E | E | N | F | R | V | A | Y | H | D | S | K | Q | K | E | G | N | D | W | R | H | R | S | L | T | F | F | T | E | G | S | S | L | G | L | D | T | S | S | K | R | L | R | V | I | D | L | V | G | N | F | R | T | Q | G |
| 2 | arg2_BTx623 | 97.7% | 79.3% | L | N | R | S | L | Q | S | S | R | L | G | E | S | K | T | C | R | V | H | D | L | M | R | D | L | I | V | S | S | R | E | N | F | H | L | V | Q | S | N | N | V | A | E | E | N | F | R | V | A | Y | H | D | S | K | Q | K | E | G | N | D | W | R | H | R | S | L | T | F | F | T | E | G | S | S | L | G | L | D | T | S | S | K | R | L | R | V | I | D | L | V | G | N | F | R | T | Q | G |

| | | cov | pid | 121 | | | | | | 2 | | 240 | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
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| 1 | ARG2_SC328C | 100.0% | 100.0% | I | N | K | I | V | L | L | C | H | K | Y | L | N | S | A | W | S | E | Y | T | L | P | S | G | I | G | N | O | G | I | R | I | L | D | N | G | Y | T | C | L | T | T | P | T | N | T | K | R | D | H | V | I | L | C | N | R | I | P | Y | R | Y | D | E | N | E | P | V | D | C | L | E | G | T | R | D | P | F | L | L | D | S | H | S | R | A | R | A | I | N | E | L | H | M | C | S | S | G | W | S | R | L | G | Y | G |
| 2 | arg2_BTx623 | 97.7% | 79.3% | I | N | K | I | V | L | L | C | H | K | Y | L | N | S | A | W | S | E | Y | T | L | P | S | G | I | G | N | O | G | I | R | I | L | D | N | G | Y | T | C | L | T | T | P | T | N | T | K | R | D | H | V | I | L | C | N | R | I | P | Y | R | Y | D | E | N | E | P | V | D | C | L | E | G | T | R | D | P | F | L | L | D | S | H | S | R | A | R | A | I | N | E | L | H | M | C | S | S | G | W | S | R | L | G | Y | G |

| | | cov | pid | 241 | | | | | | 3 | | 360 | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
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| 1 | ARG2_SC328C | 100.0% | 100.0% | R | V | P | R | G | I | C | N | K | E | Q | L | I | E | S | D | R | R | T | S | S | K | A | V | K | E | L | E | L | T | R | R | K | L | A | I | G | T | D | W | S | K | K | K | K | L | I | C | S | L | E | K | S | S | R | S | L | T | V | A | G | E | H | O | R | G | L | G | L | I | S | S | S | S | P | P | P | H | R | S | L | S | L | Y | C | Y | I | G | E | T | D | W | F | R | N | T | H | L | V | K | L | S |
| 2 | arg2_BTx623 | 97.7% | 79.3% | R | V | P | R | G | I | C | N | K | E | Q | L | I | E | S | D | R | R | T | S | S | K | A | V | K | E | L | E | L | T | R | R | K | L | A | I | G | T | D | W | S | K | K | K | K | L | I | C | S | L | E | K | S | S | R | S | L | T | V | A | G | E | H | O | R | G | L | G | L | I | S | S | S | S | P | P | P | H | R | S | L | S | L | Y | C | Y | I | G | E | T | D | W | F | R | N | T | H | L | V | K | L | S |

| | | cov | pid | 361 | | | | | | 4 | | 480 | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
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| 1 | ARG2_SC328C | 100.0% | 100.0% | Y | K | S | Q | K | E | D | K | T | M | E | L | C | E | L | P | K | L | M | L | L | R | D | Y | H | A | Y | --- | L | D | K | I | A | P | G | A | F | N | R | R | D | E | W | D | S | D | N | K | E | T | R | F | E | E | C | A | S | R | Q | M | E | R | E | N | F | C | L | K | S | G | I | I | G | K | H | L | C | L | K | V | I | S | L | I | C | - | S | K | V | A | R | L | G | M | L | E | E | N | A | H |
| 2 | arg2_BTx623 | 97.7% | 79.3% | W | D | S | Q | K | E | D | K | T | M | E | L | C | E | L | P | K | L | M | L | L | R | D | Y | H | A | Y | --- | L | D | K | I | A | P | G | A | F | N | R | R | D | E | W | D | S | D | N | K | E | T | R | F | E | E | C | A | S | R | Q | M | E | R | E | N | F | C | L | K | S | G | I | I | G | K | H | L | C | L | K | V | I | S | L | I | C | - | S | K | V | A | R | L | G | M | L | E | E | N | A | H |

| | | cov | pid | 481 | | | | | | 5 | | 546 | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
|---|-------------|--------|--------|-----|---|---|---|---|---|---|---|-----|---|---|---|---|---|---|---|---|---|---|---|-----|---|---|-----|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| 1 | ARG2_SC328C | 100.0% | 100.0% | E | N | R | F | V | L | R | Q | E | D | R | S | Y | H | C | L | G | D | E | S | --- | H | E | --- | V | E | T | E | S | L | D | H | A | G | E | S | O | V | T | P | T | T | N | S | E | Q | S |
| 2 | arg2_BTx623 | 97.7% | 79.3% | E | N | R | F | V | L | R | Q | E | D | R | S | Y | H | C | L | G | D | E | S | --- | H | E | --- | V | E | T | E | S | L | D | H | A | G | E | S | O | V | T | P | T | T | N | S | E | Q | S |

Data S4. Comparison of the amino acid sequences of the LRR domain of ARG2 in SC328C and BTx623.