**Table S1** Summary of the sequencing data production (Clean\_Data).

|  |  |  |  |
| --- | --- | --- | --- |
| **Genotype** | **Quality value >=20** | **Production** | |
| **Rate (%)** | **Reads (M)** | **Bases (Gb)** |
| *sur2-1gl1* | 96.88 | 47.72 | 4.29 |
| *494* | 96.20 | 50.49 | 4.54 |
| *2035* | 96.80 | 47.65 | 4.29 |

Note: “Clean data”: the data which have deleted adapter and removed the reads that the rate of low quality (quality value <=5) is more than or equal to 50% of these reads. M, million reads; Gb, giga base pairs.

**Table S2** Summary of the alignment results.

|  |  |  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- | --- | --- |
| **Genotype** | **Insert size**  **(bp)** | **Coverage rate**  **(%)** | **Mapped**  **data** | | **UniqMapped data** | | **Average depth** | |
| **Reads rate**  **(%)** | **Base rate (%)** | **Reads rate**  **(%)** | **Base rate (%)** | **Sequencing (X)** | **Effective**  **(X)** |
| *sur2-1gl1* | 460 | 93.50 | 91.39 | 91.30 | 63.84 | 63.76 | 35.89 | 32.81 |
| *494* | 475 | 94.34 | 89.19 | 89.09 | 70.00 | 69.91 | 37.97 | 33.88 |
| *2035* | 471 | 94.05 | 90.29 | 90.18 | 71.40 | 71.30 | 35.83 | 32.36 |

Note: The genome size of TAIR10 is 119.67 Mb while the effective size is 119.48 Mb (not including the N base in the reference). Average sequencing depth = Clean data bases / the reference genome size. Average effective depth = Mapped data bases / the effective genome size.

**Table S3** Annotation of homozygous mutations identified by sequencing the genome of *494* after four backcrosses. In bold, the causal suppressor mutation.

|  |  |  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- | --- | --- |
| **Ch** | **Position** | **Mutation** | **Sequencing depth** | **Feature annotation** | **Mutated**  **codon** | **Mutated**  **amino acid** | **Type** | **Gene id** |
| 1 | 100887 | G-to-A | 25 | CDS | GGA-to-AGA | G-to-R | Nonsyn | AT1G01240 |
| 114810 | G-to-A | 19 | CDS | GTG-to-GTA | V-to-V | Syn | AT1G01290 |
| 13627084 | C-to-G | 9 | Transposon | - | - | - | AT1G36260 |
| 2 | 9498172 | T-to-C | 18 | CDS | ATA-to-ACA | I-to-T | Nonsyn | AT2G22360 |
| 15555113 | T-to-C | 25 | 3`UTR | - | - | - | AT2G37035 |
| 3 | 222161 | C-to-T | 32 | CDS | AAG-to-AAA | K-to-K | Syn | AT3G01570 |
| 682611 | C-to-T | 22 | CDS | GAC-to-GAT | D-to-D | Syn | AT3G03030 |
| 2307400 | G-to-A | 29 | CDS | ATC-to-ATT | I-to-I | Syn | AT3G07250 |
| 2528826 | A-to-G | 30 | Intergenic | - | - | - | - |
| 3007848 | G-to-A | 34 | Intronic | - | - | - | AT3G09800 |
| 3375369 | G-to-A | 28 | CDS | CGG-to-CAG | R-to-Q | Nonsyn | AT3G10780 |
| 4300078 | G-to-A | 28 | CDS | GCG-to-ACG | A-to-T | Nonsyn | AT3G13290 |
| 5992709 | G-to-A | 14 | 5`UTR | - | - | - | AT3G17510 |
| 9337434 | C-to-A | 18 | Intergenic | - | - | - | - |
| 9840905 | G-to-A | 24 | CDS | GCT-to-GTT | A-to-V | Nonsyn | AT3G26750 |
| 9979474 | G-to-A | 12 | Intronic | - | - | - | AT3G27050 |
| 4 | 628659 | G-to-A | 26 | Intergenic | - | - | - | - |
| 833997 | C-to-T | 18 | CDS | CTC-to-CTT | L-to-L | Syn | AT4G01925 |
| **1130414** | **G-to-A** | **23** | **CDS** | **AAG-to-AAA** | **K-to-K** | **Syn** | **AT4G02570** |
| 1635305 | G-to-A | 18 | Transposon | - | - | - | AT4G03690 |
| 3427119 | C-to-T | 22 | Intergenic | - | - | - | - |
| 4854122 | T-to-G | 22 | Intergenic | - | - | - | - |
| 5520544 | T-to-A | 15 | Intergenic | - | - | - | - |
| 5599216 | C-to-T | 29 | CDS | GGT-to-GAT | G-to-D | Nonsyn | AT4G08770 |
| 5712042 | C-to-T | 26 | Intergenic | - | - | - | - |
| 5718505 | C-to-A | 12 | Intergenic | - | - | - | - |
| 6055177 | C-to-T | 14 | Intergenic | - | - | - | - |
| 9186808 | C-to-A | 12 | Intergenic | - | - | - | - |
| 5 | 22935555 | C-to-T | 36 | Intronic | - | - | - | AT5G56660 |
| 24835327 | C-to-T | 22 | Intronic | - | - | - | AT5G61820 |
| 24906145 | C-to-T | 24 | Intergenic | - | - | - | - |
| 25357936 | C-to-T | 17 | Intergenic | - | - | - | - |
| 26295563 | C-to-T | 27 | Intergenic | - | - | - | - |

**Table S4** Annotation of homozygous mutations identified by sequencing the genome of *2035* after two backcrosses.

|  |  |  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- | --- | --- |
| **Ch** | **Position** | **Mutation** | **Sequencing depth** | **Feature annotation** | **Mutated**  **codon** | **Mutated**  **amino acid** | **Type** | **Gene id** |
| 1 | 13627084 | C-to-G | 9 | CDS | GGA-to-AGA | G-to-R | Nonsyn | AT1G01240 |
| 15216659 | T-to-C | 13 | Transposon | - | - | - | AT1G40127 |
| 16056590 | C-to-A | 20 | Transposon | - | - | - | AT1G42697 |
| 24475466 | A-to-T | 28 | CDS | GAT-to-GTT | D-to-V | Nonsyn | AT1G65800 |
| 5 | 65186 | A-to-C | 28 | Intergenic | - | - | - | - |
| 5631842 | T-to-C | 29 | Transposon | - | - | - | AT5G17125 |
| 12431671 | T-to-A | 23 | Transposon | - | - | - | AT5G33125 |
| 15481247 | G-to-A | 24 | Intronic | - | - | - | AT5G38690 |
| 15874695 | G-to-A | 9 | Intergenic | - | - | - | - |
| 16035276 | G-to-A | 19 | CDS | GAA-to-AAA | E-to-K | Nonsyn | AT5G40060 |
| 16317006 | G-to-A | 25 | Intergenic | - | - | - | - |
| 17108752 | G-to-A | 28 | CDS | GGT-to-AGT | G-to-S | Nonsyn | AT5G42670 |
| 17238058 | G-to-A | 31 | CDS | GCT-to-GTT | A-to-V | Nonsyn | AT5G42970 |
| 17651948 | G-to-A | 26 | Intergenic | - | - | - | - |
| 18149319 | G-to-A | 31 | Intergenic | - | - | - | - |
| 19218560 | G-to-A | 32 | Intergenic | - | - | - | - |
| 19952813 | G-to-A | 20 | Intergenic | - | - | - | - |
| 20196832 | G-to-A | 32 | mRNA | AAC-to-AAT | N-to-N | Syn | AT5G49710 |
| 20896589 | G-to-A | 16 | CDS | GAT-to-AAT | D-to-N | Nonsyn | AT5G51450 |
| 21766071 | G-to-A | 33 | mRNA | CAC-to-CAT | H-to-H | Syn | AT5G53580 |
| 22282208 | G-to-A | 19 | Intronic | - | - | - | AT5G54850 |
| 22430399 | G-to-A | 15 | CDS | ACC-to-ATC | T-to-I | Nonsyn | AT5G55310 |
| 22641127 | G-to-A | 25 | CDS | CCG-to-TCG | P-to-S | Nonsyn | AT5G55910 |
| 23609681 | G-to-A | 37 | CDS | GAT-to-AAT | D-to-N | Nonsyn | AT5G58410 |
| 24186916 | G-to-A | 8 | Intergenic | - | - | - | - |
| 24478071 | G-to-A | 30 | Intergenic | - | - | - | - |