**Table S1, List of *de novo* mutations identified in two species of duckweed**

|  |  |  |  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- | --- | --- | --- |
| **Genotype** | **Scaffold** | **Position** | **Line** | **Validation** | **Reference coverage** | **Non-reference coverage** | **Site type** | **Base change** | **Effect** |
| **CC** | CP019093.1 | 4723004 | H | - | 15 | 5 | non CpG | C->G | intergenic variant |
|  | CP019097.1 | 4764451 | D | - | 14 | 5 | CpG | C->T | intergenic variant |
|  | CP019098.1 | 2797447 | P | - | 28 | 5 | CpG | C->A | missense variant |
|  | CP019100.1 | 2235140 | P | - | 19 | 5 | non CpG | C->T | intergenic variant |
|  | CP019108.1 | 782390 | N | - | 24 | 5 | non CpG | C->A | intergenic variant |
|  | CP019112.1 | 653683 | B | - | 17 | 5 | non CpG | A->T | intergenic variant |
|  | CP019095.1 | 8394653 | K | - | 26 | 6 | non CpG | C->T | intron variant |
|  | CP019105.1 | 1846849 | D | - | 15 | 6 | non CpG | A->T | intergenic variant |
|  | CP019094.1 | 7988664 | K | - | 9 | 7 | CpG | C->G | missense variant |
|  | CP019096.1 | 7777428 | K | - | 10 | 7 | non CpG | C->T | intergenic variant |
|  | CP019101.1 | 6813954 | F | - | 13 | 8 | CpG | C->T | intron variant |
|  | CP019109.1 | 2721723 | A | - | 20 | 9 | non CpG | C->T | intergenic variant |
|  | CP019093.1 | 9622614 | A | - | 18 | 11 | non CpG | C->T | intergenic variant |
|  | CP019098.1 | 7624791 | I | Pass | 9 | 13 | CpG | C->T | intergenic variant |
|  | CP019099.1 | 6962338 | C | Pass | 20 | 5 | CpG | C->T | intergenic variant |
|  | CP019101.1 | 3587320 | B | - | 25 | 5 | CpG | C->T | intergenic variant |
|  | CP019098.1 | 876453 | B | - | 15 | 6 | CpG | C->T | intergenic variant |
|  | CP019096.1 | 5852363 | D | - | 10 | 7 | CpG | C->T | intergenic variant |
|  | CP019112.1 | 199698 | P | Pass | 28 | 15 | non CpG | A->T | intergenic variant |
|  | CP019096.1 | 7993588 | C | Fail | 19 | 9 | CpG | C->T | NA |
|  |  |  |  |  |  |  |  |  |  |
| **GP23** | CP019094.1 | 9744127 | D | Pass | 22 | 5 | non CpG | C->T | intron variant |
|  | CP019094.1 | 10922385 | I | - | 16 | 5 | non CpG | C->T | intergenic variant |
|  | CP019095.1 | 5049789 | N | - | 35 | 5 | CpG | C->A | 5 prime UTR variant |
|  | CP019096.1 | 2739883 | P | - | 32 | 5 | CpG | C->A | intron variant |
|  | CP019103.1 | 3501136 | J | - | 13 | 5 | CpG | C->T | intergenic variant |
|  | CP019095.1 | 1536194 | N | - | 28 | 7 | non CpG | C->A | intron variant |
|  | CP019099.1 | 2234049 | D | - | 20 | 7 | CpG | C->T | intergenic variant |
|  | CP019099.1 | 5403453 | A | - | 38 | 7 | non CpG | A->G | intergenic variant |
|  | CP019103.1 | 3690446 | J | Pass | 12 | 7 | CpG | C->T | intergenic variant |
|  | CP019107.1 | 4253782 | H | - | 17 | 7 | non CpG | A->G | intergenic variant |
|  | CP019108.1 | 2476 | P | - | 30 | 7 | non CpG | C->T | intergenic variant |
|  | CP019111.1 | 3525994 | I | - | 25 | 8 | non CpG | A->G | intergenic variant |
|  | CP019108.1 | 3744394 | F | - | 10 | 9 | CpG | C->T | intergenic variant |
|  | CP019097.1 | 4835779 | P | - | 32 | 10 | CpG | C->T | intergenic variant |
|  | CP019099.1 | 6581448 | I | - | 22 | 10 | non CpG | C->T | intergenic variant |
|  | CP019104.1 | 3445982 | E | - | 19 | 10 | CpG | C->A | intergenic variant |
|  | CP019106.1 | 3255737 | O | - | 21 | 10 | CpG | C->T | missense variant |
|  | CP019093.1 | 3254558 | P | - | 44 | 12 | non CpG | C->T | splice region variant |
|  | CP019107.1 | 122485 | P | Fail | 23 | 12 | CpG | C->G | NA |
|  | CP019107.1 | 2770689 | I | - | 24 | 12 | non CpG | C->T | intergenic variant |
|  | CP019094.1 | 4157362 | A | Pass | 46 | 15 | non CpG | C->G | intergenic variant |
|  | CP019093.1 | 7920465 | H | - | 17 | 5 | non CpG | C->A | intergenic variant |
|  | CP019094.1 | 2158224 | E | - | 10 | 5 | non CpG | C->T | intergenic variant |
|  | CP019099.1 | 5294879 | J | - | 20 | 6 | CpG | C->T | intergenic variant |
|  | CP019103.1 | 2366057 | P | Fail | 46 | 5 | CpG | C->T | NA |
|   | CP019106.1  | 1753773 | A | Fail | 40 | 15 | CpG | C->G | NA |
|  | CP019106.1 | 3921984 | F | Fail | 17 | 10 | non CpG | A->G | NA |
|  |  |  |  |  |  |  |  |  |  |
| **GPL7** | lcl|lminor\_contig83 | 53005 | G | - | 19 | 5 | non CpG | A->C | intergenic variant |
|  | lcl|lminor\_contig645 | 31133 | A | - | 14 | 5 | CpG | C->T | intergenic variant |
|  | lcl|lminor\_contig1647 | 41425 | L | - | 14 | 5 | CpG | C->T | intergenic variant |
|  | lcl|lminor\_contig4622 | 11588 | F | - | 21 | 5 | CpG | C->T | intergenic variant |
|  | lcl|lminor\_contig7461 | 3344 | B | - | 19 | 5 | non CpG | C->T | intergenic variant |
|  | lcl|lminor\_contig7937 | 1139 | K | - | 12 | 5 | non CpG | C->T | intergenic variant |
|  | lcl|lminor\_contig12792 | 398 | O | - | 9 | 5 | non CpG | C->T | intergenic variant |
|  | lcl|lminor\_contig281 | 88447 | L | - | 17 | 6 | CpG | C->G | intergenic variant |
|  | lcl|lminor\_contig496 | 14769 | D | - | 21 | 6 | non CpG | C->T | intergenic variant |
|  | lcl|lminor\_contig560 | 25886 | A | - | 7 | 6 | non CpG | A->G | intergenic variant |
|  | lcl|lminor\_contig4164 | 4665 | A | - | 14 | 6 | CpG | C->G | intergenic variant |
|  | lcl|lminor\_contig4176 | 20576 | E | - | 10 | 6 | non CpG | C->T | intergenic variant |
|  | lcl|lminor\_contig4301 | 20542 | M | - | 16 | 6 | CpG | C->T | intergenic variant |
|  | lcl|lminor\_contig18559 | 3799 | M | - | 11 | 6 | non CpG | C->T | intergenic variant |
|  | lcl|lminor\_contig30843 | 905 | B | - | 21 | 6 | non CpG | C->T | intergenic variant |
|  | lcl|lminor\_contig1541 | 36664 | D | - | 19 | 7 | non CpG | C->T | intergenic variant |
|  | lcl|lminor\_contig4321 | 1841 | D | - | 9 | 7 | non CpG | C->T | intergenic variant |
|  | lcl|lminor\_contig4637 | 12478 | O | - | 8 | 7 | CpG | C->G | intergenic variant |
|  | lcl|lminor\_contig5967 | 746 | D | - | 15 | 7 | non CpG | C->T | intergenic variant |
|  | lcl|lminor\_contig15751 | 5324 | F | - | 9 | 7 | non CpG | C->T | intergenic variant |
|  | lcl|lminor\_contig181 | 2513 | B | - | 8 | 8 | CpG | C->T | intergenic variant |
|  | lcl|lminor\_contig5326 | 7604 | D | - | 12 | 8 | CpG | C->T | intergenic variant |
|  | lcl|lminor\_contig8410 | 1781 | K | - | 10 | 8 | CpG | C->T | intergenic variant |
|  | lcl|lminor\_contig13862 | 4502 | M | - | 15 | 8 | CpG | C->T | intergenic variant |
|  | lcl|lminor\_contig32793 | 1391 | D | - | 11 | 8 | non CpG | C->T | intergenic variant |
|  | lcl|lminor\_contig7725 | 11398 | M | - | 11 | 10 | CpG | C->T | intergenic variant |
|  | lcl|lminor\_contig2059 | 2826 | L | - | 9 | 5 | CpG | C->T | intergenic variant |
|  | lcl|lminor\_contig5191 | 11534 | D | - | 13 | 6 | CpG | C->T | intergenic variant |
|  | lcl|lminor\_contig10179 | 10642 | D | - | 18 | 10 | CpG | C->T | intergenic variant |