|  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- |
| **Supplementary Table S1 sequencing information of samples** | | | |  |  |  |
| **sample** | **ReadsNum** | **BaseNum（bp）** | **TotalBase（bp）** | **Q20** | **Q30** | **GC** |
| DDA | 20,723,900 | 3,108,585,000 | 6,217,170,000 | 96.92% | 91.90% | 37.94% |
| 20,723,900 | 3,108,585,000 | 95.54% | 88.88% | 38.05% |
| DDB | 35,459,106 | 5,318,865,900 | 10,637,731,800 | 97% | 92.33% | 37.46% |
| 35,459,106 | 5,318,865,900 | 95.95% | 90.01% | 37.57% |
| DDC | 20,993,258 | 3,148,988,700 | 6,297,977,400 | 97.44% | 93.39% | 37.36% |
| 20,993,258 | 3,148,988,700 | 96.33% | 90.68% | 37.48% |
| DDD | 23,941,886 | 3,591,282,900 | 7,182,565,800 | 96.93% | 92.41% | 35.97% |
| 23,941,886 | 3,591,282,900 | 94.80% | 87.98% | 36.20% |
| DDE | 22,285,493 | 3,342,823,950 | 6,685,647,900 | 96.86% | 92.29% | 35.66% |
| 22,285,493 | 3,342,823,950 | 95.24% | 88.90% | 35.93% |
| DDF | 24,254,504 | 3,638,175,600 | 7,276,351,200 | 97.03% | 92.64% | 35.69% |
| 24,254,504 | 3,638,175,600 | 94.89% | 88.17% | 35.94% |
| DDG | 28,130,768 | 4,219,615,200 | 8,439,230,400 | 97.13% | 92.81% | 35.68% |
| 28,130,768 | 4,219,615,200 | 95.03% | 88.44% | 35.93% |
| DDH | 24,503,503 | 3,675,525,450 | 7,351,050,900 | 96.91% | 92.41% | 35.93% |
| 24,503,503 | 3,675,525,450 | 94.50% | 87.41% | 36.21% |
| DZA | 33,717,984 | 5,057,697,600 | 10,115,395,200 | 97.44% | 93.34% | 37.91% |
| 33,717,984 | 5,057,697,600 | 94.91% | 87.64% | 37.91% |
| DZB | 21,480,041 | 3,222,006,150 | 6,444,012,300 | 97.45% | 93.42% | 37.79% |
| 21,480,041 | 3,222,006,150 | 96.74% | 91.69% | 37.84% |
| DZC | 22,028,312 | 3,304,246,800 | 6,608,493,600 | 97.51% | 93.56% | 38.05% |
| 22,028,312 | 3,304,246,800 | 96.42% | 90.92% | 38.16 |
| DZD | 34,689,427 | 5,203,414,050 | 10,406,828,100 | 97.14% | 92.89% | 35.91% |
| 34,689,427 | 5,203,414,050 | 95.29% | 89.02% | 36.17% |
| DZE | 21,525,755 | 3,228,863,250 | 6,457,726,500 | 96.82% | 92.23% | 35.58% |
| 21,525,755 | 3,228,863,250 | 95.82% | 90.12% | 35.85% |
| DZF | 21,428,741 | 3,214,311,150 | 6,428,622,300 | 96.89% | 92.34% | 35.34% |
| 21,428,741 | 3,214,311,150 | 95.65% | 89.68% | 35.60% |
| DZG | 22,876,559 | 3,431,483,850 | 6,862,967,700 | 96.91% | 92.35% | 35.50% |
| 22,876,559 | 3,431,483,850 | 95.49% | 89.34% | 35.77% |
| XZA | 22,686,317 | 3,402,947,550 | 6,805,895,100 | 97.11% | 92.68% | 37.84% |
| 22,686,317 | 3,402,947,550 | 95.71% | 89.44% | 37.91% |
| XZB | 21,364,819 | 3,204,722,850 | 6,409,445,700 | 97.56% | 93.67% | 37.85% |
| 21,364,819 | 3,204,722,850 | 95.98% | 89.89% | 37.93% |
| XZC | 30,018,417 | 4,502,762,550 | 9,005,525,100 | 97.09% | 92.66% | 38.31% |
| 30,018,417 | 4,502,762,550 | 96.25% | 90.75% | 38.38% |
| XZD | 25,581,507 | 3,837,226,050 | 7,674,452,100 | 97.44% | 93.26% | 35.40% |
| 25,581,507 | 3,837,226,050 | 95.49% | 89.17% | 35.43% |
| XZE | 31,852,241 | 4,777,836,150 | 9,555,672,300 | 97.30% | 93.02% | 35.90% |
| 31,852,241 | 4,777,836,150 | 95.42% | 89.09% | 36.02% |
| XZF | 22,348,085 | 3,352,212,750 | 6,704,425,500 | 96.95% | 92.46% | 36.25% |
| 22,348,085 | 3,352,212,750 | 94.53% | 87.42% | 36.53% |
| XZG | 27,263,957 | 4,089,593,550 | 8,179,187,100 | 96.85% | 92.33% | 36.36% |
| 27,263,957 | 4,089,593,550 | 95.19% | 88.88% | 36.64% |
| XZH | 23,043,485 | 3,456,522,750 | 6,913,045,500 | 97.12% | 92.82% | 36.35% |
| 23,043,485 | 3,456,522,750 | 95.06% | 88.54% | 36.65% |
| Sample-1-1 | 6,065,015 | 909,752,250 | 1,819,504,500 | 97.35% | 93.09% | 35.69% |
| 6,065,015 | 909,752,250 | 95.67% | 89.53% | 35.81% |
| Sample-1-2 | 4,077,952 | 611,692,800 | 1,223,385,600 | 96.80% | 92.09% | 35.56% |
| 4,077,952 | 611,692,800 | 96.19% | 90.68% | 35.63% |
| Sample-1-3 | 6,129,640 | 919,446,000 | 1,838,892,000 | 96.88% | 92.28% | 36.34% |
| 6,129,640 | 919,446,000 | 94.89% | 88.16% | 36.59% |
| Sample-1-4 | 9,309,179 | 1,396,376,850 | 2,792,753,700 | 97.13% | 93.03% | 37.58% |
| 9,309,179 | 1,396,376,850 | 95.99% | 90.59% | 37.83% |
| Sample-1-5 | 7,410,670 | 1,111,600,500 | 2,223,201,000 | 96.84% | 92.32% | 37.63% |
| 7,410,670 | 1,111,600,500 | 95.81% | 90.08% | 37.84% |
| Sample-1-6 | 8,295,529 | 1,244,329,350 | 2,488,658,700 | 96.94% | 92.58% | 37.90% |
| 8,295,529 | 1,244,329,350 | 93.92% | 86.41% | 38.42% |
| Sample-1-7 | 10,049,986 | 1,507,497,900 | 3,014,995,800 | 97.17% | 93.09% | 38.01% |
| 10,049,986 | 1,507,497,900 | 95.73% | 89.97% | 38.27% |
| Sample-1-8 | 6,723,531 | 1,008,529,650 | 2,017,059,300 | 97.32% | 93.55% | 38.54% |
| 6,723,531 | 1,008,529,650 | 96.16% | 90.87% | 38.82% |
| Sample-1-9 | 7,692,236 | 1,153,835,400 | 2,307,670,800 | 97.24% | 93.32% | 38.41% |
| 7,692,236 | 1,153,835,400 | 95.60% | 89.70% | 38.74% |
| Sample-1-10 | 22,543,636 | 3,381,545,400 | 6,763,090,800 | 37.34% | 96.93% | 92.13% |
| 22,543,636 | 3,381,545,400 | 37.20% | 95.48% | 89.08% |
| Sample-1-11 | 24,140,114 | 3,621,017,100 | 7,242,034,200 | 37.74% | 96.98% | 92.27% |
| 24,140,114 | 3,621,017,100 | 37.62% | 95.60% | 89.28% |
| Sample-1-12 | 22,284,356 | 3,342,653,400 | 6,685,306,800 | 37.59% | 96.61% | 91.44% |
| 22,284,356 | 3,342,653,400 | 37.52% | 95.82% | 89.80% |
| Sample-1-13 | 23,237,902 | 3,485,685,300 | 6,971,370,600 | 37.64% | 96.58% | 91.59% |
| 23,237,902 | 3,485,685,300 | 37.56% | 95.56% | 89.37% |
| Sample-1-14 | 28,430,752 | 4,264,612,800 | 8,529,225,600 | 38.52% | 96.47% | 91.42% |
| 28,430,752 | 4,264,612,800 | 38.42% | 95.64% | 89.61% |
| Sample-1-15 | 23,062,994 | 3,459,449,100 | 6,918,898,200 | 37.82% | 97.01% | 92.35% |
| 23,062,994 | 3,459,449,100 | 37.67% | 95.89% | 89.91% |
| Sample-1-16 | 20,250,271 | 3,037,540,650 | 6,075,081,300 | 37.24% | 97.31% | 92.71% |
| 20,250,271 | 3,037,540,650 | 37.21% | 97.46% | 93.12% |
| Sample-1-17 | 22,264,585 | 3,339,687,750 | 6,679,375,500 | 37.93% | 96.72% | 91.89% |
| 22,264,585 | 3,339,687,750 | 37.78% | 95.36% | 88.96% |
| Sample-1-18 | 21,047,402 | 3,157,110,300 | 6,314,220,600 | 37.17% | 96.81% | 92.17% |
| 21,047,402 | 3,157,110,300 | 37.20% | 95.76% | 89.67% |
| Sample-1-19 | 22,208,362 | 3,331,254,300 | 6,662,508,600 | 37.53% | 97.51% | 93.64% |
| 22,208,362 | 3,331,254,300 | 37.54% | 96.51% | 91.69% |
| Sample-1-20 | 25,111,428 | 3,766,714,200 | 7,533,428,400 | 36.66% | 97.78% | 93.82% |
| 25,111,428 | 3,766,714,200 | 36.70% | 96.73% | 91.86% |
| Sample-1-21 | 30,810,970 | 4,621,645,500 | 9,243,291,000 | 36.84% | 97.49% | 93.26% |
| 30,810,970 | 4,621,645,500 | 36.85% | 95.80% | 89.67% |
| Sample-1-22 | 23,715,371 | 3,557,305,650 | 7,114,611,300 | 37.65% | 97.71% | 94.00% |
| 23,715,371 | 3,557,305,650 | 37.58% | 96.57% | 91.50% |
| Sample-1-23 | 23,779,136 | 3,566,870,400 | 7,133,740,800 | 37.11% | 97.81% | 93.88% |
| 23,779,136 | 3,566,870,400 | 37.14% | 96.64% | 91.62% |
| Sample-1-24 | 23,314,785 | 3,497,217,750 | 6,994,435,500 | 37.42% | 97.39% | 93.27% |
| 23,314,785 | 3,497,217,750 | 37.28% | 95.78% | 89.53% |
| Sample-1-25 | 22,572,341 | 3,385,851,150 | 6,771,702,300 | 37.07% | 97.78% | 93.81% |
| 22,572,341 | 3,385,851,150 | 37.18% | 96.61% | 91.65% |
| Sample-1-26 | 22,940,719 | 3,441,107,850 | 6,882,215,700 | 37.40% | 97.36% | 93.04% |
| 22,940,719 | 3,441,107,850 | 37.30% | 95.63% | 89.28% |
| Sample-1-27 | 29,835,223 | 4,475,283,450 | 8,950,566,900 | 37.34% | 97.44% | 93.25% |
| 29,835,223 | 4,475,283,450 | 37.32% | 96.71% | 91.93% |
| Sample-1-28 | 25,822,365 | 3,873,354,750 | 7,746,709,500 | 37.08% | 97.71% | 93.70% |
| 25,822,365 | 3,873,354,750 | 37.11% | 96.22% | 90.71% |
| Sample-1-29 | 24,691,376 | 3,703,706,400 | 7,407,412,800 | 37.85% | 97.69% | 93.92% |
| 24,691,376 | 3,703,706,400 |  | 37.76% | 96.06% | 90.31% |
| Sample-1-30 | 27,789,043 | 4,168,356,450 | 8,336,712,900 | 37.47% | 97.54% | 93.62% |
| 27,789,043 | 4,168,356,450 | 37.42% | 96.10% | 90.57% |
| Sample-1-31 | 21,817,525 | 3,272,628,750 | 6,545,257,500 | 37.80% | 97.66% | 93.95% |
| 21,817,525 | 3,272,628,750 | 37.71% | 96.08% | 90.57% |
| Sample-1-32 | 23,980,423 | 3,597,063,450 | 7,194,126,900 | 37.25% | 97.77% | 94.12% |
| 23,980,423 | 3,597,063,450 | 37.15% | 96.73% | 91.94% |
| Sample-2-1 | 26,900,333 | 4,035,049,950 | 8,070,099,900 | 96.70% | 92.04% | 38.06% |
| 26,900,333 | 4,035,049,950 | 95.49% | 89.12% | 38.00% |
| Sample-2-2 | 26,111,098 | 3,916,664,700 | 7,833,329,400 | 96.72% | 92.01% | 37.56% |
| 26,111,098 | 3,916,664,700 | 95.18% | 88.43% | 37.50% |
| Sample-2-3 | 27,799,947 | 4,169,992,050 | 8,339,984,100 | 96.68% | 92.02% | 37.28% |
| 27,799,947 | 4,169,992,050 | 95.24% | 88.68% | 37.26% |
| Sample-2-4 | 20,359,683 | 3,053,952,450 | 6,107,904,900 | 96.51% | 91.50% | 37.92% |
| 20,359,683 | 3,053,952,450 | 95.79% | 89.81% | 37.99% |
| Sample-2-5 | 17,825,796 | 2,673,869,400 | 5,347,738,800 | 96.36% | 91.63% | 38.79% |
| 17,825,796 | 2,673,869,400 | 95.36% | 89.25% | 38.78% |
| Sample-2-6 | 23,252,192 | 3,487,828,800 | 6,975,657,600 | 96.67% | 91.94% | 36.17% |
| 23,252,192 | 3,487,828,800 | 96.64% | 91.51% | 35.98% |
| Sample-2-7 | 22,709,177 | 3,406,376,550 | 6,812,753,100 | 96.60% | 91.89% | 37.58% |
| 22,709,177 | 3,406,376,550 | 95.41% | 89.08% | 37.56% |
| Sample-2-8 | 21,301,693 | 3,195,253,950 | 6,390,507,900 | 96.60% | 91.84% | 37.63% |
| 21,301,693 | 3,195,253,950 | 95.08% | 88.36% | 37.58% |
| Sample-2-9 | 31,880,234 | 4,782,035,100 | 9,564,070,200 | 96.54% | 91.82% | 38.17% |
| 31,880,234 | 4,782,035,100 | 95.23% | 88.76% | 38.10% |
| Sample-2-10 | 36,248,379 | 5,437,256,850 | 10,874,513,700 | 96.44% | 91.68% | 38.29% |
| 36,248,379 | 5,437,256,850 | 95.22% | 88.79% | 38.26% |
| Sample-2-11 | 25,641,863 | 3,846,279,450 | 7,692,558,900 | 96.29% | 91.22% | 38.51% |
| 25,641,863 | 3,846,279,450 | 95.48% | 89.28% | 38.54% |
| Sample-2-12 | 39,395,740 | 5,909,361,000 | 11,818,722,000 | 96.53% | 91.60% | 38.91% |
| 39,395,740 | 5,909,361,000 | 94.14% | 86.59% | 39.05% |
| Sample-2-13 | 21,747,670 | 3,262,150,500 | 6,524,301,000 | 96.18% | 90.73% | 38.84% |
| 21,747,670 | 3,262,150,500 | 94.49% | 87.21% | 38.90% |
| Sample-2-14 | 29,091,831 | 4,363,774,650 | 8,727,549,300 | 96.64% | 91.86% | 38.52% |
| 29,091,831 | 4,363,774,650 | 94.30% | 86.84% | 38.47% |
| Sample-2-15 | 27,677,872 | 4,151,680,800 | 8,303,361,600 | 96.50% | 91.34% | 38.63% |
| 27,677,872 | 4,151,680,800 | 94.27% | 86.64% | 38.70% |
| Sample-2-16 | 19,345,598 | 2,901,839,700 | 5,803,679,400 | 37.49% | 97.66% | 93.67% |
| 19,345,598 | 2,901,839,700 | 37.61% | 96.05% | 90.71% |
| Sample-2-17 | 17,282,689 | 2,592,403,350 | 5,184,806,700 | 37.52% | 97.57% | 93.75% |
| 17,282,689 | 2,592,403,350 | 37.49% | 96.61% | 91.94% |
| Sample-2-18 | 30,985,675 | 4,647,851,250 | 9,295,702,500 | 36.43% | 97.49% | 93.31% |
| 30,985,675 | 4,647,851,250 | 36.43% | 96.76% | 91.87% |
| Sample-2-19 | 25,175,545 | 3,776,331,750 | 7,552,663,500 | 37.48% | 97.70% | 93.96% |
| 25,175,545 | 3,776,331,750 | 37.48% | 97.02% | 92.63% |
| Sample-2-20 | 30,146,272 | 4,521,940,800 | 9,043,881,600 | 36.96% | 97.67% | 93.92% |
| 30,146,272 | 4,521,940,800 | 36.91% | 96.83% | 92.20% |
| Sample-3-1 | 7,939,563 | 1,190,934,450 | 2,381,868,900 | 96.33% | 90.78% | 35.39% |
| 7,939,563 | 1,190,934,450 | 95.24% | 88.53% | 35.49% |
| Sample-3-2 | 12,523,266 | 1,878,489,900 | 3,756,979,800 | 96.23% | 90.68% | 36.13% |
| 12,523,266 | 1,878,489,900 | 94.68% | 87.59% | 36.29% |
| Sample-3-3 | 8,907,182 | 1,336,077,300 | 2,672,154,600 | 96.25% | 90.70% | 36.28% |
| 8,907,182 | 1,336,077,300 | 93.72% | 85.66% | 36.46% |
| Sample-3-4 | 7,826,634 | 1,173,995,100 | 2,347,990,200 | 96.51% | 91.11% | 35.76% |
| 7,826,634 | 1,173,995,100 | 94.74% | 87.67% | 35.92% |
| Sample-3-5 | 7,287,528 | 1,093,129,200 | 2,186,258,400 | 96.38% | 90.93% | 35.95% |
| 7,287,528 | 1,093,129,200 | 94.89% | 87.89% | 36.09% |
| Sample-3-6 | 9,052,662 | 1,357,899,300 | 2,715,798,600 | 96.32% | 90.89% | 36.17% |
| 9,052,662 | 1,357,899,300 | 94.96% | 88.11% | 36.33% |
| Sample-3-7 | 8,585,238 | 1,287,785,700 | 2,575,571,400 | 96.32% | 90.85% | 36.25% |
| 8,585,238 | 1,287,785,700 | 95.13% | 88.41% | 36.41% |
| Sample-3-8 | 8,233,291 | 1,234,993,650 | 2,469,987,300 | 96.28% | 90.76% | 35.97% |
| 8,233,291 | 1,234,993,650 | 94.53% | 87.26% | 36.15% |
| Sample-3-9 | 8,130,254 | 1,219,538,100 | 2,439,076,200 | 96.39% | 90.90% | 35.28% |
| 8,130,254 | 1,219,538,100 | 95.70% | 89.55% | 35.42% |
| Sample-3-10 | 10,325,141 | 1,548,771,150 | 3,097,542,300 | 96.28% | 90.75% | 36.03% |
| 10,325,141 | 1,548,771,150 | 94.19% | 86.58% | 36.22% |
| Sample-3-11 | 8,596,962 | 1,289,544,300 | 2,579,088,600 | 96.30% | 90.78% | 35.93% |
| 8,596,962 | 1,289,544,300 | 94.31% | 86.76% | 36.10% |
| Sample-3-12 | 8,780,480 | 1,317,072,000 | 2,634,144,000 | 96.39% | 90.96% | 35.95% |
| 8,780,480 | 1,317,072,000 | 94.43% | 87.00% | 36.17% |
| Sample-3-13 | 8,129,666 | 1,219,449,900 | 2,438,899,800 | 96.34% | 90.86% | 35.37% |
| 8,129,666 | 1,219,449,900 | 94.61% | 87.39% | 35.54% |
| Sample-3-14 | 9,138,360 | 1,370,754,000 | 2,741,508,000 | 96.13% | 90.44% | 36.32% |
| 9,138,360 | 1,370,754,000 | 94.49% | 87.20% | 36.43% |
| Sample-3-15 | 9,182,160 | 1,377,324,000 | 2,754,648,000 | 96.22% | 90.65% | 35.85% |
| 9,182,160 | 1,377,324,000 | 93.67% | 85.63% | 36.04% |
| Sample-3-16 | 8,981,467 | 1,347,220,050 | 2,694,440,100 | 96.17% | 90.53% | 36.41% |
| 8,981,467 | 1,347,220,050 | 94.31% | 86.86% | 36.62% |
| Sample-3-17 | 8,426,261 | 1,263,939,150 | 2,527,878,300 | 96.24% | 90.68% | 35.94% |
| 8,426,261 | 1,263,939,150 | 95.01% | 88.15% | 36.09% |
| Sample-3-18 | 7,962,244 | 1,194,336,600 | 2,388,673,200 | 96.24% | 90.65% | 36.01% |
| 7,962,244 | 1,194,336,600 | 94.81% | 87.80% | 36.20% |
| Sample-3-19 | 10,596,717 | 1,589,507,550 | 3,179,015,100 | 96.25% | 90.70% | 36.04% |
| 10,596,717 | 1,589,507,550 | 94.59% | 87.37% | 36.23% |
| Sample-3-20 | 8,453,286 | 1,267,992,900 | 2,535,985,800 | 96.20% | 90.59% | 36.38% |
| 8,453,286 | 1,267,992,900 | 93.50% | 85.33% | 36.60% |
| Sample-3-21 | 9,089,063 | 1,363,359,450 | 2,726,718,900 | 96.15% | 90.58% | 36.91% |
| 9,089,063 | 1,363,359,450 | 94.05% | 86.57% | 37.21% |
| Sample-3-22 | 10,540,786 | 1,581,117,900 | 3,162,235,800 | 96.09% | 90.39% | 36.64% |
| 10,540,786 | 1,581,117,900 | 93.69% | 85.78% | 36.89% |
| Sample-3-23 | 9,909,794 | 1,486,469,100 | 2,972,938,200 | 96.34% | 90.92% | 36.10% |
| 9,909,794 | 1,486,469,100 | 94.56% | 87.32% | 36.31% |
| Sample-3-24 | 10,295,828 | 1,544,374,200 | 3,088,748,400 | 96.27% | 90.78% | 36.49% |
| 10,295,828 | 1,544,374,200 | 93.98% | 86.16% | 36.73% |
| Sample-4-1 | 4,960,102 | 744,015,300 | 1,488,030,600 | 96.98% | 92.41% | 36.28% |
| 4,960,102 | 744,015,300 | 93.76% | 85.78% | 36.57% |
| Sample-4-2 | 3,527,826 | 529,173,900 | 1,058,347,800 | 96.68% | 91.89% | 36.49% |
| 3,527,826 | 529,173,900 | 95.26% | 88.72% | 36.67% |
| Sample-4-3 | 4,948,556 | 742,283,400 | 1,484,566,800 | 96.70% | 91.97% | 36.35% |
| 4,948,556 | 742,283,400 | 95.64% | 89.56% | 36.55% |
| Sample-4-4 | 5,836,172 | 875,425,800 | 1,750,851,600 | 96.80% | 92.14% | 36.07% |
| 5,836,172 | 875,425,800 | 95.99% | 90.24% | 36.23% |
| Sample-4-5 | 4,694,289 | 704,143,350 | 1,408,286,700 | 94.78% | 88.03% | 36.12% |
| 4,694,289 | 704,143,350 | 93.25% | 85.58% | 36.30% |
| Sample-4-6 | 5,767,238 | 865,085,700 | 1,730,171,400 | 96.99% | 92.44% | 36.17% |
| 5,767,238 | 865,085,700 | 94.72% | 87.65% | 36.41% |
| Sample-4-7 | 5,288,652 | 793,297,800 | 1,586,595,600 | 96.93% | 92.37% | 36.68% |
| 5,288,652 | 793,297,800 | 95.39% | 89.17% | 36.93% |
| Sample-4-8 | 7,230,381 | 1,084,557,150 | 2,169,114,300 | 96.99% | 92.47% | 36.25% |
| 7,230,381 | 1,084,557,150 | 94.87% | 87.97% | 36.52% |
| Sample-4-9 | 6,039,386 | 905,907,900 | 1,811,815,800 | 96.93% | 92.32% | 36.56% |
| 6,039,386 | 905,907,900 | 94.03% | 86.38% | 36.89% |
| Sample-4-10 | 5,391,021 | 808,653,150 | 1,617,306,300 | 97.19% | 92.77% | 36.04% |
| 5,391,021 | 808,653,150 | 94.19% | 86.61% | 36.24% |
| Sample-4-11 | 4,518,530 | 677,779,500 | 1,355,559,000 | 96.44% | 91.55% | 36.18% |
| 4,518,530 | 677,779,500 | 95.09% | 88.55% | 36.39% |
| Sample-4-12 | 4,723,945 | 708,591,750 | 1,417,183,500 | 96.76% | 92.06% | 36.07% |
| 4,723,945 | 708,591,750 | 95.98% | 90.22% | 36.24% |
| Sample-4-13 | 4,949,062 | 742,359,300 | 1,484,718,600 | 96.22% | 91.00% | 35.99% |
| 4,949,062 | 742,359,300 | 92.17% | 83.22% | 36.26% |
| Sample-4-14 | 4,339,694 | 650,954,100 | 1,301,908,200 | 96.61% | 91.76% | 36.21% |
| 4,339,694 | 650,954,100 | 95.80% | 89.91% | 36.38% |
| Sample-4-15 | 5,040,645 | 756,096,750 | 1,512,193,500 | 96.93% | 92.37% | 36.37% |
| 5,040,645 | 756,096,750 | 95.01% | 88.31% | 36.63% |
| Sample-4-16 | 4,999,660 | 749,949,000 | 1,499,898,000 | 94.88% | 88.18% | 36.01% |
| 4,999,660 | 749,949,000 | 93.91% | 86.73% | 36.15% |
| Sample-4-17 | 5,263,243 | 789,486,450 | 1,578,972,900 | 96.96% | 92.42% | 36.80% |
| 5,263,243 | 789,486,450 | 92.98% | 84.49% | 37.09% |
| Sample-4-18 | 4,918,388 | 737,758,200 | 1,475,516,400 | 96.96% | 92.42% | 36.03% |
| 4,918,388 | 737,758,200 | 94.95% | 88.12% | 36.23% |
| Sample-4-19 | 4,694,040 | 704,106,000 | 1,408,212,000 | 96.87% | 92.14% | 35.87% |
| 4,694,040 | 704,106,000 | 95.22% | 88.64% | 36.03% |
| Sample-4-20 | 7,034,631 | 1,055,194,650 | 2,110,389,300 | 97.04% | 92.60% | 35.80% |
| 7,034,631 | 1,055,194,650 | 95.35% | 88.91% | 36.00% |
| Sample-4-21 | 5,895,453 | 884,317,950 | 1,768,635,900 | 96.97% | 92.35% | 35.90% |
| 5,895,453 | 884,317,950 | 96.11% | 90.42% | 36.10% |
| Sample-4-22 | 3,786,489 | 567,973,350 | 1,135,946,700 | 96.39% | 91.14% | 36.07% |
| 3,786,489 | 567,973,350 | 95.09% | 88.37% | 36.28% |
| Sample-4-23 | 3,571,665 | 535,749,750 | 1,071,499,500 | 96.52% | 91.28% | 35.90% |
| 3,571,665 | 535,749,750 | 95.89% | 89.95% | 36.07% |
| Sample-4-24 | 4,366,218 | 654,932,700 | 1,309,865,400 | 96.58% | 91.42% | 35.99% |
| 4,366,218 | 654,932,700 | 95.65% | 89.38% | 36.14% |
| Sample-4-25 | 5,517,951 | 827,692,650 | 1,655,385,300 | 97.09% | 92.66% | 36.63% |
| 5,517,951 | 827,692,650 | 94.67% | 87.55% | 36.77% |
| Sample-4-26 | 4,067,794 | 610,169,100 | 1,220,338,200 | 96.61% | 91.45% | 35.74% |
| 4,067,794 | 610,169,100 | 95.11% | 88.20% | 35.95% |
| Sample-4-27 | 5,409,878 | 811,481,700 | 1,622,963,400 | 97.03% | 92.59% | 35.98% |
| 5,409,878 | 811,481,700 | 95.16% | 88.51% | 36.17% |
| Sample-4-28 | 6,120,709 | 918,106,350 | 1,836,212,700 | 97.11% | 92.73% | 36.50% |
| 6,120,709 | 918,106,350 | 95.84% | 89.95% | 36.67% |
| Sample-4-29 | 3,712,976 | 556,946,400 | 1,113,892,800 | 96.48% | 91.26% | 35.78% |
| 3,712,976 | 556,946,400 | 94.68% | 87.48% | 35.98% |
| Sample-4-30 | 4,831,933 | 724,789,950 | 1,449,579,900 | 97.10% | 92.63% | 35.90% |
| 4,831,933 | 724,789,950 | 95.87% | 89.96% | 36.02% |

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| --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- |
| **Supplementary Table S2 PCA analysis of hypothetical standard samples** | | | | | | | | |  |  |  |
| Sample | PC1 | PC2 | PC3 | PC4 | PC5 | PC6 | PC7 | PC8 | PC9 | PC10 | Variety |
| DDA | -0.3436 | -0.2255 | -0.6058 | -0.0109 | 0.12579 | -0.4157 | 0.4692 | -0.0041 | 0.00974 | 0.00847 | XZ |
| DDB | -0.1564 | 0.033 | -0.013 | 0.09478 | 0.05595 | -0.0106 | -0.1619 | 0.09471 | 0.18957 | 0.05215 | XZ |
| DDC | 0.12511 | -0.386 | -0.1924 | -0.7116 | 0.07451 | 0.04496 | -0.4419 | 0.17198 | -0.0875 | 0.00975 | DZ |
| DDD | -0.0679 | 0.21389 | -0.0241 | 0.00049 | -0.0113 | 0.0283 | -0.0119 | 0.11619 | -0.1528 | 0.00184 | XZ |
| DDE | -0.1171 | 0.19787 | -0.0412 | -0.0673 | -0.0832 | 0.12755 | 0.03656 | 0.15014 | -0.267 | -0.1655 | XZ |
| DDF | -0.0973 | 0.18852 | -0.0367 | -0.0386 | -0.0325 | 0.06793 | -0.0056 | 0.1171 | -0.0586 | 0.03204 | XZ |
| DDG | 0.25577 | 0.09338 | 0.02545 | -0.0543 | -0.0017 | -0.0901 | 0.08443 | -0.052 | 0.09705 | 0.14688 | DZ |
| DDH | 0.23448 | 0.07761 | 0.01342 | -0.065 | -0.0138 | -0.0599 | 0.09668 | -0.0852 | 0.06574 | 0.05221 | DZ |
| DZA | 0.33155 | -0.0391 | 0.16326 | 0.29068 | 0.35792 | -0.5631 | -0.2114 | 0.06025 | -0.3324 | -0.0524 | DZ |
| DZB | 0.1329 | -0.4489 | -0.0615 | 0.37731 | -0.7373 | 0.00219 | -0.0864 | 0.1607 | -0.094 | 0.00478 | DZ |
| DZC | 0.18471 | -0.3665 | -0.0175 | 0.28449 | 0.48476 | 0.60899 | 0.25109 | 0.17382 | -0.0509 | 0.01 | DZ |
| DZD | 0.2688 | 0.08007 | 0.05973 | 0.01188 | 0.02404 | -0.115 | 0.00137 | -0.0208 | 0.14911 | 0.13554 | DZ |
| DZE | 0.21154 | 0.04969 | 0.00721 | -0.1242 | -0.0982 | 0.04732 | 0.21018 | -0.2569 | 0.0913 | 0.34083 | DZ |
| DZF | 0.21848 | 0.04367 | 0.01418 | -0.153 | -0.1113 | 0.06798 | 0.20252 | -0.2808 | 0.26754 | -0.6554 | DZ |
| DZG | 0.21956 | 0.05451 | 0.02523 | -0.0692 | -0.0619 | -0.0188 | 0.12403 | -0.1306 | 0.07964 | 0.0357 | DZ |
| XZA | -0.2696 | -0.1246 | -0.0634 | 0.15966 | 0.07262 | 0.14154 | -0.3453 | -0.7895 | -0.1978 | 0.06299 | XZ |
| XZB | -0.3933 | -0.3161 | 0.74201 | -0.2074 | -0.0075 | -0.1466 | 0.27612 | 0.01319 | -0.0237 | 0.02802 | XZ |
| XZC | -0.2096 | -0.0507 | 0.01181 | 0.2114 | 0.13572 | -0.065 | -0.339 | 0.14103 | 0.62572 | -0.2196 | XZ |
| XZD | -0.1349 | 0.16672 | -0.026 | -0.022 | -0.0762 | 0.1355 | -0.02 | 0.09159 | 0.14598 | 0.43263 | XZ |
| XZE | -0.0672 | 0.21579 | 0.01333 | 0.0712 | 0.00794 | 0.00376 | -0.0996 | 0.10513 | 0.09593 | 0.10092 | XZ |
| XZF | -0.0909 | 0.2041 | -0.015 | -0.0039 | -0.0374 | 0.10649 | 0.01858 | 0.05385 | -0.2341 | -0.0126 | XZ |
| XZG | -0.0899 | 0.18911 | 0.01666 | 0.03051 | -0.0211 | 0.03036 | -0.06 | 0.07539 | 0.02648 | 0.01472 | XZ |
| XZH | -0.093 | 0.20724 | 0.00055 | -0.0029 | -0.0505 | 0.08251 | -0.0008 | 0.09117 | -0.3112 | -0.3542 | XZ |

|  |  |  |  |  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- |
| **Supplementary Table S3 376 SNPs for varieties identification and resistan fuction**  **(Note: Highlight marks indicate SNPs related to stress resistance. Yellow highlight indicates that the mutation occurs upstream of the gene.Green highlights indicate non-synonymous mutations.)** | | | | | | | | | | |
| Chrom | Position | MinGT  (DZ) | MaxGT  (DZ) | Hp  (DZ) | MinGT  (XZ) | MaxGT(XZ) | Hp  (XZ) | Fst | Annotation | Resistant Fuction |
| Chr1 | 584053 | 0(N) | 2(G) | 0 | 0(N) | 12(A) | 0 | 1 | Non-Gene | - |
| Chr1 | 6831772 | 0(N) | 12(G) | 0 | 0(N) | 8(A) | 0 | 1 | Non-Gene | - |
| Chr1 | 12362823 | 0(N) | 8(T) | 0 | 0(N) | 10(C) | 0 | 1 | LOC102610930.1:(-),ATA->ATG,I->M,no-syn,exon-2,Note=uncharacterized LOC102610930 | - |
| Chr1 | 12410091 | 0(N) | 6(G) | 0 | 0(N) | 12(A) | 0 | 1 | Non-Gene | - |
| Chr1 | 12410124 | 0(N) | 8(C) | 0 | 0(N) | 12(T) | 0 | 1 | Non-Gene | - |
| Chr1 | 13067574 | 0(N) | 2(C) | 0 | 0(N) | 16(A) | 0 | 1 | Non-Gene | - |
| Chr1 | 13152824 | 0(N) | 4(A) | 0 | 0(N) | 16(C) | 0 | 1 | Non-Gene | - |
| Chr1 | 13475517 | 0(N) | 4(A) | 0 | 0(N) | 12(G) | 0 | 1 | Non-Gene | - |
| Chr1 | 13832874 | 0(N) | 2(T) | 0 | 0(N) | 10(G) | 0 | 1 | Non-Gene | - |
| Chr1 | 14173160 | 0(N) | 4(A) | 0 | 0(N) | 12(G) | 0 | 1 | LOC112498796.1:(-),up-1344bp,Note=putative UPF0481 protein At3g02645 | diseases resistance(Basim et al., 2021) |
| Chr1 | 14792781 | 0(N) | 2(G) | 0 | 0(N) | 14(A) | 0 | 1 | Non-Gene | - |
| Chr1 | 14862393 | 0(N) | 2(T) | 0 | 0(N) | 16(C) | 0 | 1 | Non-Gene | - |
| Chr1 | 15073708 | 0(N) | 4(C) | 0 | 0(N) | 16(T) | 0 | 1 | LOC102619144.1:(-),intron-2,Note=probable disease resistance protein At5g63020, transcript variant X2 | - |
| Chr1 | 15163178 | 0(N) | 6(A) | 0 | 0(N) | 8(G) | 0 | 1 | LOC102619144.1:(-),intron-2,Note=probable disease resistance protein At5g63020, transcript variant X2 | - |
| Chr1 | 15631908 | 0(N) | 2(C) | 0 | 0(N) | 14(T) | 0 | 1 | LOC107176971.1:(-),down-820bp,Note=uncharacterized LOC107176971 | - |
| Chr1 | 16007544 | 0(N) | 2(T) | 0 | 0(N) | 12(C) | 0 | 1 | LOC102624063.1:(-),down-896bp,Note=putative disease resistance protein At5g05400 | - |
| Chr1 | 16022899 | 0(N) | 2(T) | 0 | 0(N) | 16(C) | 0 | 1 | Non-Gene | - |
| Chr1 | 16022925 | 0(N) | 6(G) | 0 | 0(N) | 12(C) | 0 | 1 | Non-Gene | - |
| Chr1 | 16451243 | 0(N) | 2(A) | 0 | 0(N) | 16(G) | 0 | 1 | LOC102629499.1:(+),GAC->GGC,D->G,no-syn,exon-1,Note=probable disease resistance protein At5g63020 | disease resistance(Lin et al., 2010; Giraldo-Gonzalez et al., 2021) |
| Chr1 | 16716791 | 0(N) | 4(A) | 0 | 0(N) | 16(G) | 0 | 1 | LOC102607577.1:(+),intron-1,Note=pleiotropic drug resistance protein 1-like | |
| Chr1 | 17608279 | 0(N) | 14(A) | 0 | 0(N) | 8(G) | 0 | 1 | LOC102611408.1:(-),TTT->CTT,F->L,no-syn,exon-4,Note=probable LRR receptor-like serine/threonine-protein kinase At3g47570 | disease and possible drought resistance(Wang et al., 2018) |
| Chr1 | 17817997 | 0(N) | 2(G) | 0 | 0(N) | 14(T) | 0 | 1 | LOC102621812.2:(-),up-1345bp,Note=probable sulfate transporter 3.4, transcript variant X2 | drought and salt resistance( Medina-Puche et. al, 2020) |
| Chr1 | 18508212 | 0(N) | 2(T) | 0 | 0(N) | 14(A) | 0 | 1 | LOC102619243.1:(+),intron-8,Note=malonate--CoA ligase | - |
| Chr1 | 18515606 | 0(N) | 12(A) | 0 | 0(N) | 2(G) | 0 | 1 | Non-Gene | - |
| Chr1 | 18969299 | 0(N) | 14(A) | 0 | 0(N) | 14(T) | 0 | 1 | Non-Gene | - |
| Chr1 | 19110060 | 0(N) | 4(A) | 0 | 0(N) | 16(T) | 0 | 1 | Non-Gene | - |
| Chr1 | 19110061 | 0(N) | 6(A) | 0 | 0(N) | 16(T) | 0 | 1 | Non-Gene | - |
| Chr1 | 19132725 | 0(N) | 4(C) | 0 | 0(N) | 10(T) | 0 | 1 | Non-Gene | - |
| Chr1 | 21144684 | 0(N) | 4(A) | 0 | 0(N) | 16(T) | 0 | 1 | LOC102625846.1:(+),intron-0,Note=protein ROOT HAIR DEFECTIVE 3-like | - |
| Chr1 | 22085829 | 0(N) | 8(G) | 0 | 0(N) | 12(A) | 0 | 1 | Non-Gene | - |
| Chr1 | 22085847 | 0(N) | 2(G) | 0 | 0(N) | 16(A) | 0 | 1 | Non-Gene | - |
| Chr1 | 22430915 | 0(N) | 2(T) | 0 | 0(N) | 14(G) | 0 | 1 | Non-Gene | - |
| Chr1 | 23279740 | 0(N) | 14(A) | 0 | 0(N) | 16(T) | 0 | 1 | LOC102629046.1:(-),intron-1,Note=classical arabinogalactan protein 2 | - |
| Chr1 | 23279741 | 0(N) | 6(A) | 0 | 0(N) | 16(T) | 0 | 1 | LOC102629046.1:(-),intron-1,Note=classical arabinogalactan protein 2 | - |
| Chr1 | 23960111 | 0(N) | 14(A) | 0 | 0(N) | 12(C) | 0 | 1 | Non-Gene | - |
| Chr1 | 23960112 | 0(N) | 12(A) | 0 | 0(N) | 12(C) | 0 | 1 | Non-Gene | - |
| Chr1 | 24337929 | 0(N) | 2(C) | 0 | 0(N) | 16(T) | 0 | 1 | LOC102621427.1:(+),up-990bp,Note=BTB/POZ domain-containing protein At3g49900 | - |
| Chr1 | 24990295 | 0(N) | 2(G) | 0 | 0(N) | 14(C) | 0 | 1 | LOC102626934.1:(+),up-456bp,Note=putative oxidoreductase C1F5.03c | - |
| Chr1 | 25569921 | 0(N) | 2(G) | 0 | 0(N) | 16(T) | 0 | 1 | LOC102630693.1:(+),intron-2,Note=uncharacterized LOC102630693, transcript variant X3;LOC102630693.2:(+),intron-2,Note=uncharacterized LOC102630693, transcript variant X3;LOC102630693.3:(+),intron-2,Note=uncharacterized LOC102630693, transcript variant X3 | - |
| Chr2 | 309096 | 0(N) | 4(C) | 0 | 0(N) | 16(T) | 0 | 1 | LOC102620598.1:(+),up-35bp,Note=phosphoglycolate phosphatase 2 | - |
| Chr2 | 320100 | 0(N) | 10(A) | 0 | 0(N) | 16(T) | 0 | 1 | LOC102621149.1:(+),intron-1,Note=hypothetical protein, transcript variant X1;LOC102621149.2:(+),intron-0,Note=hypothetical protein, transcript variant X1 | - |
| Chr2 | 482992 | 0(N) | 10(C) | 0 | 0(N) | 12(A) | 0 | 1 | LOC102631413.1:(+),intron-5,Note=protein ENDOSPERM DEFECTIVE 1 | - |
| Chr2 | 482993 | 0(N) | 12(T) | 0 | 0(N) | 14(A) | 0 | 1 | LOC102631413.1:(+),intron-5,Note=protein ENDOSPERM DEFECTIVE 1 | - |
| Chr2 | 482995 | 0(N) | 6(C) | 0 | 0(N) | 12(G) | 0 | 1 | LOC102631413.1:(+),intron-5,Note=protein ENDOSPERM DEFECTIVE 1 | - |
| Chr2 | 482997 | 0(N) | 10(T) | 0 | 0(N) | 6(G) | 0 | 1 | LOC102631413.1:(+),intron-5,Note=protein ENDOSPERM DEFECTIVE 1 | - |
| Chr2 | 1161987 | 0(N) | 6(A) | 0 | 0(N) | 10(T) | 0 | 1 | Non-Gene | - |
| Chr2 | 1753827 | 0(N) | 10(G) | 0 | 0(N) | 4(A) | 0 | 1 | LOC102625299.1:(-),up-1328bp,Note=chlorophyll a-b binding protein of LHCII type 1 | - |
| Chr2 | 1779170 | 0(N) | 14(T) | 0 | 0(N) | 2(A) | 0 | 1 | Non-Gene | - |
| Chr2 | 1974642 | 0(N) | 10(C) | 0 | 0(N) | 16(A) | 0 | 1 | LOC102614001.1:(+),intron-1,Note=eukaryotic translation initiation factor 4E-1-like | - |
| Chr2 | 1974654 | 0(N) | 14(G) | 0 | 0(N) | 16(C) | 0 | 1 | LOC102614001.1:(+),intron-1,Note=eukaryotic translation initiation factor 4E-1-like | - |
| Chr2 | 2006643 | 0(N) | 6(A) | 0 | 0(N) | 16(T) | 0 | 1 | LOC102615756.1:(+),up-1907bp,Note=pentatricopeptide repeat-containing protein At4g18975, chloroplastic | - |
| Chr2 | 2346740 | 0(N) | 6(A) | 0 | 0(N) | 10(G) | 0 | 1 | LOC102630700.3:(-),down-992bp,Note=uncharacterized LOC102630700, transcript variant X3 | - |
| Chr2 | 2346750 | 0(N) | 6(A) | 0 | 0(N) | 12(G) | 0 | 1 | LOC102630700.3:(-),down-982bp,Note=uncharacterized LOC102630700, transcript variant X3 | - |
| Chr2 | 2666402 | 0(N) | 14(T) | 0 | 0(N) | 4(A) | 0 | 1 | LOC102619643.2:(-),down-991bp,Note=pentatricopeptide repeat-containing protein At1g28690, mitochondrial, transcript variant X2 | - |
| Chr2 | 2714931 | 0(N) | 6(C) | 0 | 0(N) | 2(T) | 0 | 1 | LOC102621435.1:(-),down-306bp,Note=nudix hydrolase 15, mitochondrial | - |
| Chr2 | 2959499 | 0(N) | 10(G) | 0 | 0(N) | 8(A) | 0 | 1 | LOC102606911.1:(+),up-1269bp,Note=glutaredoxin-C9 | Arsenic resistance(Singh et. al, 2020) |
| Chr2 | 3165828 | 0(N) | 14(A) | 0 | 0(N) | 16(T) | 0 | 1 | Non-Gene | - |
| Chr2 | 3165829 | 0(N) | 6(A) | 0 | 0(N) | 16(T) | 0 | 1 | Non-Gene | - |
| Chr2 | 4389356 | 0(N) | 4(C) | 0 | 0(N) | 16(T) | 0 | 1 | Non-Gene | - |
| Chr2 | 4389392 | 0(N) | 4(G) | 0 | 0(N) | 16(T) | 0 | 1 | Non-Gene | - |
| Chr2 | 4424596 | 0(N) | 4(A) | 0 | 0(N) | 14(T) | 0 | 1 | LOC102622014.1:(-),up-316bp,Note=cysteine-rich repeat secretory protein 38-like | - |
| Chr2 | 5273751 | 0(N) | 6(A) | 0 | 0(N) | 10(T) | 0 | 1 | Non-Gene | - |
| Chr2 | 5280271 | 0(N) | 4(G) | 0 | 0(N) | 12(A) | 0 | 1 | Non-Gene | - |
| Chr2 | 5995917 | 0(N) | 6(T) | 0 | 0(N) | 10(A) | 0 | 1 | LOC102612415.1:(-),up-1161bp,Note=SH3 domain-containing protein 1-like | cold resistance(Sasaki ei al, 2008) |
| Chr2 | 5996061 | 0(N) | 2(C) | 0 | 0(N) | 14(A) | 0 | 1 | LOC102612415.1:(-),up-1305bp,Note=SH3 domain-containing protein 1-like |
| Chr2 | 7550435 | 0(N) | 8(A) | 0 | 0(N) | 12(G) | 0 | 1 | LOC102628955.1:(-),up-1326bp,Note=berberine bridge enzyme-like 8 | - |
| Chr2 | 7550450 | 0(N) | 12(C) | 0 | 0(N) | 12(T) | 0 | 1 | LOC102628955.1:(-),up-1341bp,Note=berberine bridge enzyme-like 8 | - |
| Chr2 | 7956812 | 0(N) | 6(A) | 0 | 0(N) | 14(T) | 0 | 1 | LOC102616538.1:(-),down-567bp,Note=LOB domain-containing protein 4 | - |
| Chr2 | 7956813 | 0(N) | 6(A) | 0 | 0(N) | 14(T) | 0 | 1 | LOC102616538.1:(-),down-566bp,Note=LOB domain-containing protein 4 | - |
| Chr2 | 8466001 | 0(N) | 2(C) | 0 | 0(N) | 16(T) | 0 | 1 | LOC102614396.1:(+),down-911bp,Note=patatin-like protein 1, transcript variant X1 | - |
| Chr2 | 9045554 | 0(N) | 4(C) | 0 | 0(N) | 12(T) | 0 | 1 | Non-Gene | - |
| Chr2 | 9463631 | 0(N) | 4(G) | 0 | 0(N) | 14(A) | 0 | 1 | Non-Gene | - |
| Chr2 | 9997364 | 0(N) | 2(A) | 0 | 0(N) | 14(T) | 0 | 1 | Non-Gene | - |
| Chr2 | 10001117 | 0(N) | 2(C) | 0 | 0(N) | 14(T) | 0 | 1 | LOC102615463.1:(-),down-1707bp,Note=rust resistance kinase Lr10-like | - |
| Chr2 | 10044709 | 0(N) | 2(G) | 0 | 0(N) | 14(A) | 0 | 1 | Non-Gene | - |
| Chr2 | 10667331 | 0(N) | 6(A) | 0 | 0(N) | 10(G) | 0 | 1 | Non-Gene | - |
| Chr2 | 11281916 | 0(N) | 2(A) | 0 | 0(N) | 16(T) | 0 | 1 | LOC102621335.1:(-),up-666bp,Note=putative pentatricopeptide repeat-containing protein At2g01510 | Aluminum resistance(Zhou et al., 2015) |
| Chr2 | 12011597 | 0(N) | 2(T) | 0 | 0(N) | 10(C) | 0 | 1 | LOC102623792.1:(+),up-305bp,Note=ras-related protein Rab11D | diseases resistance(Xie et. al, 2017) |
| Chr2 | 12208579 | 0(N) | 2(G) | 0 | 0(N) | 12(T) | 0 | 1 | Non-Gene | - |
| Chr2 | 12211177 | 0(N) | 4(A) | 0 | 0(N) | 12(T) | 0 | 1 | Non-Gene | - |
| Chr2 | 12335828 | 0(N) | 4(C) | 0 | 0(N) | 16(T) | 0 | 1 | LOC102607689.3:(-),up-827bp,Note=protein CONSERVED ONLY IN THE GREEN LINEAGE 160, chloroplastic, transcript variant X3 | salt resistance(Cho et. al, 2021) |
| Chr2 | 12487873 | 0(N) | 2(T) | 0 | 0(N) | 16(G) | 0 | 1 | Non-Gene | - |
| Chr2 | 14136058 | 0(N) | 6(C) | 0 | 0(N) | 12(T) | 0 | 1 | Non-Gene | - |
| Chr2 | 20773977 | 0(N) | 2(A) | 0 | 0(N) | 14(C) | 0 | 1 | Non-Gene | - |
| Chr2 | 21381290 | 0(N) | 12(A) | 0 | 0(N) | 12(C) | 0 | 1 | LOC107175812.1:(+),intron-2,Note=putative pre-16S rRNA nuclease | - |
| Chr2 | 26213743 | 0(N) | 2(A) | 0 | 0(N) | 14(G) | 0 | 1 | Non-Gene | - |
| Chr2 | 26293183 | 0(N) | 2(C) | 0 | 0(N) | 12(T) | 0 | 1 | LOC102623306.1:(+),intron-1,Note=methionine S-methyltransferase-like, transcript variant X1 | - |
| Chr2 | 26394367 | 0(N) | 2(A) | 0 | 0(N) | 14(T) | 0 | 1 | Non-Gene | - |
| Chr2 | 27011296 | 0(N) | 10(T) | 0 | 0(N) | 4(A) | 0 | 1 | Non-Gene | - |
| Chr2 | 27288651 | 0(N) | 2(A) | 0 | 0(N) | 16(T) | 0 | 1 | LOC102623125.1:(+),up-1356bp,Note=oleosin 18.2 kDa | - |
| Chr2 | 27288707 | 0(N) | 2(T) | 0 | 0(N) | 14(C) | 0 | 1 | LOC102623125.1:(+),up-1300bp,Note=oleosin 18.2 kDa | - |
| Chr2 | 27657117 | 0(N) | 8(T) | 0 | 0(N) | 14(C) | 0 | 1 | Non-Gene | - |
| Chr2 | 27657120 | 0(N) | 2(T) | 0 | 0(N) | 14(A) | 0 | 1 | Non-Gene | - |
| Chr2 | 29261479 | 0(N) | 10(A) | 0 | 0(N) | 10(C) | 0 | 1 | Non-Gene | - |
| Chr2 | 29261484 | 0(N) | 8(A) | 0 | 0(N) | 10(C) | 0 | 1 | Non-Gene | - |
| Chr2 | 29261485 | 0(N) | 8(G) | 0 | 0(N) | 12(C) | 0 | 1 | Non-Gene | - |
| Chr2 | 29261552 | 0(N) | 4(T) | 0 | 0(N) | 6(A) | 0 | 1 | Non-Gene | - |
| Chr2 | 30569246 | 0(N) | 2(A) | 0 | 0(N) | 16(G) | 0 | 1 | Non-Gene | - |
| Chr3 | 58780 | 0(N) | 4(A) | 0 | 0(N) | 16(G) | 0 | 1 | Non-Gene | - |
| Chr3 | 495722 | 0(N) | 2(C) | 0 | 0(N) | 14(T) | 0 | 1 | Non-Gene | - |
| Chr3 | 1790354 | 0(N) | 6(A) | 0 | 0(N) | 10(G) | 0 | 1 | LOC112497559.1:(-),down-1121bp,Note=uncharacterized LOC112497559 | - |
| Chr3 | 2564547 | 0(N) | 4(G) | 0 | 0(N) | 14(A) | 0 | 1 | LOC102622820.1:(+),up-1305bp,Note=protein PHR1-LIKE 1, transcript variant X4 | repressing microbially driven plant immune system outputs(Castrillo et. al, 2017) |
| Chr3 | 2564564 | 0(N) | 6(A) | 0 | 0(N) | 12(C) | 0 | 1 | LOC102622820.1:(+),up-1288bp,Note=protein PHR1-LIKE 1, transcript variant X4 |
| Chr3 | 2582886 | 0(N) | 2(C) | 0 | 0(N) | 12(T) | 0 | 1 | Non-Gene | - |
| Chr3 | 2595143 | 0(N) | 10(G) | 0 | 0(N) | 14(A) | 0 | 1 | Non-Gene | - |
| Chr3 | 3114227 | 0(N) | 6(T) | 0 | 0(N) | 14(A) | 0 | 1 | LOC102613624.1:(+),down-1104bp,Note=putative disease resistance protein At3g14460 | - |
| Chr3 | 3413436 | 0(N) | 6(G) | 0 | 0(N) | 14(A) | 0 | 1 | Non-Gene | - |
| Chr3 | 3725688 | 0(N) | 4(C) | 0 | 0(N) | 14(T) | 0 | 1 | Non-Gene | - |
| Chr3 | 3839616 | 0(N) | 6(A) | 0 | 0(N) | 14(C) | 0 | 1 | Non-Gene | - |
| Chr3 | 3952469 | 0(N) | 2(A) | 0 | 0(N) | 14(T) | 0 | 1 | Non-Gene | - |
| Chr3 | 4079656 | 0(N) | 4(A) | 0 | 0(N) | 14(G) | 0 | 1 | LOC102609931.1:(+),up-1571bp,Note=serine/threonine-protein kinase SRK2A | drought and salt resistance(Soma et. al, 2017; 2020) |
| Chr3 | 4079657 | 0(N) | 2(G) | 0 | 0(N) | 14(T) | 0 | 1 | LOC102609931.1:(+),up-1570bp,Note=serine/threonine-protein kinase SRK2A |
| Chr3 | 4603544 | 0(N) | 8(A) | 0 | 0(N) | 6(G) | 0 | 1 | LOC112497608.1:(-),down-1373bp,Note=putative disease resistance protein RGA4 | - |
| Chr3 | 4713359 | 0(N) | 4(G) | 0 | 0(N) | 12(A) | 0 | 1 | LOC102621536.1:(-),down-1695bp,Note=putative disease resistance protein RGA1, transcript variant X11 | - |
| Chr3 | 5192865 | 0(N) | 2(A) | 0 | 0(N) | 16(T) | 0 | 1 | Non-Gene | - |
| Chr3 | 5192873 | 0(N) | 6(C) | 0 | 0(N) | 16(G) | 0 | 1 | Non-Gene | - |
| Chr3 | 5507048 | 0(N) | 2(C) | 0 | 0(N) | 10(T) | 0 | 1 | Non-Gene | - |
| Chr3 | 6327528 | 0(N) | 8(G) | 0 | 0(N) | 10(A) | 0 | 1 | Non-Gene | - |
| Chr3 | 6604056 | 0(N) | 4(C) | 0 | 0(N) | 14(T) | 0 | 1 | Non-Gene | - |
| Chr3 | 6819795 | 0(N) | 14(T) | 0 | 0(N) | 6(G) | 0 | 1 | Non-Gene | - |
| Chr3 | 6956568 | 0(N) | 8(T) | 0 | 0(N) | 16(C) | 0 | 1 | LOC102624277.1:(-),intron-1,Note=cytochrome P450 82A3-like | - |
| Chr3 | 7179540 | 0(N) | 2(A) | 0 | 0(N) | 12(G) | 0 | 1 | LOC112497615.1:(-),intron-1,Note=uncharacterized mitochondrial protein AtMg00810-like | - |
| Chr3 | 7374077 | 0(N) | 2(A) | 0 | 0(N) | 16(T) | 0 | 1 | LOC102625129.1:(-),up-217bp,Note=salicylate/benzoate carboxyl methyltransferase-like | diseases resistance(Huang et. al, 2020) |
| Chr3 | 7396168 | 0(N) | 14(C) | 0 | 0(N) | 2(T) | 0 | 1 | Non-Gene | - |
| Chr3 | 7894013 | 0(N) | 4(A) | 0 | 0(N) | 12(T) | 0 | 1 | LOC102611269.1:(+),intron-1,Note=putative disease resistance RPP13-like protein 3 | - |
| Chr3 | 8204323 | 0(N) | 2(A) | 0 | 0(N) | 16(T) | 0 | 1 | LOC102615383.1:(-),intron-1,Note=COBRA-like protein 6 | - |
| Chr3 | 8658108 | 0(N) | 12(A) | 0 | 0(N) | 8(G) | 0 | 1 | LOC102617644.1:(+),up-1937bp,Note=nascent polypeptide-associated complex subunit alpha-like protein 1, transcript variant X1 | diseases resistance(Wang et. al, 2020) |
| Chr3 | 8751885 | 0(N) | 2(A) | 0 | 0(N) | 14(G) | 0 | 1 | LOC102620416.1:(-),up-412bp,Note=uncharacterized LOC102620416 | - |
| Chr3 | 8994293 | 0(N) | 6(G) | 0 | 0(N) | 12(T) | 0 | 1 | LOC102623904.1:(-),intron-2,Note=disease resistance protein At4g27190-like;LOC107176104.1:(-),intron-4,Note=probable disease resistance protein At4g27220, transcript variant X2 | - |
| Chr3 | 9041233 | 0(N) | 8(A) | 0 | 0(N) | 6(G) | 0 | 1 | LOC102623904.1:(-),intron-2,Note=disease resistance protein At4g27190-like;LOC107176104.1:(-),intron-4,Note=probable disease resistance protein At4g27220, transcript variant X2 | - |
| Chr3 | 9041235 | 0(N) | 6(C) | 0 | 0(N) | 8(T) | 0 | 1 | LOC102623904.1:(-),intron-2,Note=disease resistance protein At4g27190-like;LOC107176104.1:(-),intron-4,Note=probable disease resistance protein At4g27220, transcript variant X2 | - |
| Chr3 | 9086358 | 0(N) | 4(T) | 0 | 0(N) | 12(C) | 0 | 1 | LOC102623904.1:(-),intron-2,Note=disease resistance protein At4g27190-like;LOC107176104.1:(-),intron-4,Note=probable disease resistance protein At4g27220, transcript variant X2 | - |
| Chr3 | 9239579 | 0(N) | 10(G) | 0 | 0(N) | 4(C) | 0 | 1 | LOC102613243.1:(-),CAG->GAG,Q->E,no-syn,exon-5,Note=probable disease resistance protein At4g27220, transcript variant X2;LOC102613243.2:(-),CAG->GAG,Q->E,no-syn,exon-5,Note=probable disease resistance protein At4g27220, transcript variant X2 | disease resistance(Li et al., 2018) |
| Chr3 | 9395761 | 0(N) | 14(T) | 0 | 0(N) | 12(C) | 0 | 1 | Non-Gene | - |
| Chr3 | 10065205 | 0(N) | 2(T) | 0 | 0(N) | 14(C) | 0 | 1 | Non-Gene | - |
| Chr3 | 10069597 | 0(N) | 6(C) | 0 | 0(N) | 12(T) | 0 | 1 | Non-Gene | - |
| Chr3 | 10993058 | 0(N) | 4(A) | 0 | 0(N) | 6(G) | 0 | 1 | Non-Gene | - |
| Chr3 | 11704424 | 0(N) | 4(A) | 0 | 0(N) | 12(G) | 0 | 1 | Non-Gene | - |
| Chr3 | 11704738 | 0(N) | 10(T) | 0 | 0(N) | 10(C) | 0 | 1 | Non-Gene | - |
| Chr3 | 11746162 | 0(N) | 8(C) | 0 | 0(N) | 6(T) | 0 | 1 | LOC102607123.1:(-),intron-5,Note=uncharacterized LOC102607123 | - |
| Chr3 | 11833964 | 0(N) | 14(A) | 0 | 0(N) | 10(T) | 0 | 1 | LOC102609368.1:(-),intron-7,Note=DNA (cytosine-5)-methyltransferase CMT2-like, transcript variant X1;LOC102609368.2:(-),intron-7,Note=DNA (cytosine-5)-methyltransferase CMT2-like, transcript variant X1 | - |
| Chr3 | 11895133 | 0(N) | 6(C) | 0 | 0(N) | 16(T) | 0 | 1 | LOC102612432.1:(+),down-501bp,Note=secretory carrier-associated membrane protein 4 | - |
| Chr3 | 12031712 | 0(N) | 2(T) | 0 | 0(N) | 10(C) | 0 | 1 | LOC102614699.1:(+),up-565bp,Note=DEAD-box ATP-dependent RNA helicase 5 | - |
| Chr3 | 12633086 | 0(N) | 4(G) | 0 | 0(N) | 10(A) | 0 | 1 | Non-Gene | - |
| Chr3 | 12832413 | 0(N) | 2(A) | 0 | 0(N) | 14(C) | 0 | 1 | LOC107176170.1:(-),up-744bp,Note=uncharacterized LOC107176170 | - |
| Chr3 | 13335187 | 0(N) | 6(C) | 0 | 0(N) | 14(T) | 0 | 1 | LOC102625984.1:(-),up-1506bp,Note=ubiquitin carboxyl-terminal hydrolase 12-like | - |
| Chr3 | 15325388 | 0(N) | 8(G) | 0 | 0(N) | 10(A) | 0 | 1 | LOC102628023.1:(-),intron-12,Note=importin subunit alpha-2-like, transcript variant X3;LOC102628023.2:(-),intron-12,Note=importin subunit alpha-2-like, transcript variant X3;LOC102628023.3:(-),intron-11,Note=importin subunit alpha-2-like, transcript variant X3;LOC102628023.6:(-),intron-10,Note=importin subunit alpha-2-like, transcript variant X3 | - |
| Chr3 | 15399323 | 0(N) | 4(A) | 0 | 0(N) | 12(G) | 0 | 1 | LOC102628023.1:(-),intron-7,Note=importin subunit alpha-2-like, transcript variant X3;LOC102628023.2:(-),intron-7,Note=importin subunit alpha-2-like, transcript variant X3;LOC102628023.3:(-),intron-7,Note=importin subunit alpha-2-like, transcript variant X3;LOC102628023.6:(-),intron-7,Note=importin subunit alpha-2-like, transcript variant X3;LOC102628023.7:(-),intron-7,Note=importin subunit alpha-2-like, transcript variant X3 | - |
| Chr3 | 15455648 | 0(N) | 8(A) | 0 | 0(N) | 6(G) | 0 | 1 | Non-Gene | - |
| Chr3 | 15455664 | 0(N) | 12(C) | 0 | 0(N) | 6(T) | 0 | 1 | Non-Gene | - |
| Chr3 | 16144097 | 0(N) | 6(T) | 0 | 0(N) | 16(G) | 0 | 1 | Non-Gene | - |
| Chr3 | 16349526 | 0(N) | 6(A) | 0 | 0(N) | 10(T) | 0 | 1 | LOC112497652.1:(+),intron-1,Note=uncharacterized LOC112497652 | - |
| Chr3 | 16786533 | 0(N) | 4(A) | 0 | 0(N) | 12(T) | 0 | 1 | Non-Gene | - |
| Chr3 | 16862073 | 0(N) | 2(G) | 0 | 0(N) | 16(A) | 0 | 1 | LOC102620695.1:(-),intron-1,Note=cysteine-rich receptor-like protein kinase 10 | - |
| Chr3 | 17135768 | 0(N) | 2(G) | 0 | 0(N) | 12(A) | 0 | 1 | Non-Gene | - |
| Chr3 | 17234844 | 0(N) | 4(C) | 0 | 0(N) | 16(A) | 0 | 1 | LOC102610252.1:(+),CAC->AAC,H->N,no-syn,exon-4,Note=probable disease resistance protein At4g27220 | disease resistance(Li et al., 2018) |
| Chr3 | 17768651 | 0(N) | 6(G) | 0 | 0(N) | 10(A) | 0 | 1 | LOC107176292.1:(-),up-1701bp,Note=putative disease resistance protein RGA4 | diseases resistance(Okuyama et. al, 2011) |
| Chr3 | 18036219 | 0(N) | 10(G) | 0 | 0(N) | 12(T) | 0 | 1 | LOC107176273.1:(-),intron-2,Note=disease resistance protein RGA2-like | - |
| Chr3 | 19478622 | 0(N) | 4(G) | 0 | 0(N) | 16(A) | 0 | 1 | Non-Gene | - |
| Chr3 | 19587699 | 0(N) | 2(C) | 0 | 0(N) | 16(T) | 0 | 1 | LOC102609839.1:(+),up-462bp,Note=uncharacterized protein At4g06744-like, transcript variant X1 | diseases and drought resisitance(Tang et. al, 2013; Bengyella et. al, 2015) |
| Chr3 | 20632163 | 0(N) | 2(T) | 0 | 0(N) | 16(C) | 0 | 1 | LOC102614616.1:(+),intron-1,Note=oligopeptide transporter 2-like | - |
| Chr3 | 20706560 | 0(N) | 2(C) | 0 | 0(N) | 14(T) | 0 | 1 | LOC102607519.2:(+),up-1263bp,Note=probable rhamnogalacturonate lyase B, transcript variant X2 | - |
| Chr3 | 21121042 | 0(N) | 14(A) | 0 | 0(N) | 16(T) | 0 | 1 | LOC107176314.1:(-),down-226bp,Note=60 kDa heat shock protein, mitochondrial-like | - |
| Chr3 | 21121043 | 0(N) | 14(A) | 0 | 0(N) | 8(T) | 0 | 1 | LOC107176314.1:(-),down-225bp,Note=60 kDa heat shock protein, mitochondrial-like | - |
| Chr3 | 21235158 | 0(N) | 6(T) | 0 | 0(N) | 12(G) | 0 | 1 | Non-Gene | - |
| Chr3 | 21572765 | 0(N) | 2(A) | 0 | 0(N) | 16(T) | 0 | 1 | LOC102622831.4:(+),down-1449bp,Note=serine/threonine-protein kinase SAPK2, transcript variant X2 | - |
| Chr3 | 22415879 | 0(N) | 2(T) | 0 | 0(N) | 16(C) | 0 | 1 | LOC102609644.1:(-),up-713bp,Note=uncharacterized LOC102609644 | - |
| Chr3 | 22614307 | 0(N) | 4(T) | 0 | 0(N) | 16(C) | 0 | 1 | LOC102619579.1:(+),down-327bp,Note=DIS3-like exonuclease 2, transcript variant X1;LOC102619579.2:(+),down-327bp,Note=DIS3-like exonuclease 2, transcript variant X1 | - |
| Chr3 | 22931149 | 0(N) | 14(T) | 0 | 0(N) | 6(A) | 0 | 1 | LOC102608592.1:(+),intron-2,Note=IAA-amino acid hydrolase ILR1-like 6 | - |
| Chr3 | 23146391 | 0(N) | 2(A) | 0 | 0(N) | 14(T) | 0 | 1 | LOC102617840.1:(+),down-1935bp,Note=thylakoidal processing peptidase 1, chloroplastic-like | - |
| Chr3 | 23156387 | 0(N) | 2(T) | 0 | 0(N) | 16(G) | 0 | 1 | LOC102625596.1:(+),down-838bp,Note=amino acid permease 3 | - |
| Chr3 | 25386483 | 0(N) | 8(G) | 0 | 0(N) | 6(A) | 0 | 1 | LOC102618133.1:(-),up-268bp,Note=uncharacterized LOC102618133 | - |
| Chr3 | 25593748 | 0(N) | 2(G) | 0 | 0(N) | 16(A) | 0 | 1 | Non-Gene | - |
| Chr3 | 25593756 | 0(N) | 4(G) | 0 | 0(N) | 14(A) | 0 | 1 | Non-Gene | - |
| Chr3 | 25990958 | 0(N) | 14(T) | 0 | 0(N) | 10(A) | 0 | 1 | LOC102620625.1:(+),intron-5,Note=uncharacterized LOC102620625, transcript variant X1;LOC102620625.2:(+),intron-5,Note=uncharacterized LOC102620625, transcript variant X1;LOC102620625.3:(+),intron-5,Note=uncharacterized LOC102620625, transcript variant X1;LOC102620625.4:(+),intron-5,Note=uncharacterized LOC102620625, transcript variant X1 | - |
| Chr3 | 26256134 | 0(N) | 4(A) | 0 | 0(N) | 14(G) | 0 | 1 | Non-Gene | - |
| Chr3 | 27817177 | 0(N) | 2(C) | 0 | 0(N) | 16(T) | 0 | 1 | Non-Gene | - |
| Chr4 | 225881 | 0(N) | 2(G) | 0 | 0(N) | 14(C) | 0 | 1 | LOC102620545.1:(+),up-333bp,Note=uncharacterized LOC102620545 | - |
| Chr4 | 332912 | 0(N) | 6(A) | 0 | 0(N) | 16(T) | 0 | 1 | LOC107176483.1:(+),up-28bp,Note=uncharacterized LOC107176483, transcript variant X1 | - |
| Chr4 | 7754760 | 0(N) | 2(C) | 0 | 0(N) | 14(T) | 0 | 1 | Non-Gene | - |
| Chr4 | 8596262 | 0(N) | 8(C) | 0 | 0(N) | 8(T) | 0 | 1 | Non-Gene | - |
| Chr4 | 8876310 | 0(N) | 10(C) | 0 | 0(N) | 14(T) | 0 | 1 | Non-Gene | - |
| Chr5 | 1233864 | 0(N) | 4(C) | 0 | 0(N) | 14(T) | 0 | 1 | LOC112498341.1:(+),TCC->TCT,S->S,syn,exon-1,Note=protein FAR1-RELATED SEQUENCE 5-like | - |
| Chr5 | 2649964 | 0(N) | 12(G) | 0 | 0(N) | 4(T) | 0 | 1 | LOC112498301.1:(+),up-880bp,Note=germin-like protein subfamily T member 2 | - |
| Chr5 | 3228227 | 0(N) | 12(A) | 0 | 0(N) | 14(G) | 0 | 1 | Non-Gene | - |
| Chr5 | 3228236 | 0(N) | 8(T) | 0 | 0(N) | 10(A) | 0 | 1 | Non-Gene | - |
| Chr5 | 5384842 | 0(N) | 2(T) | 0 | 0(N) | 12(C) | 0 | 1 | Non-Gene | - |
| Chr5 | 6631212 | 0(N) | 2(A) | 0 | 0(N) | 16(T) | 0 | 1 | LOC102613666.1:(-),down-1420bp,Note=ACT domain-containing protein ACR8, transcript variant X1 | - |
| Chr5 | 7660355 | 0(N) | 4(A) | 0 | 0(N) | 10(T) | 0 | 1 | Non-Gene | - |
| Chr5 | 7690921 | 0(N) | 2(C) | 0 | 0(N) | 16(T) | 0 | 1 | Non-Gene | - |
| Chr5 | 7913395 | 0(N) | 6(G) | 0 | 0(N) | 8(T) | 0 | 1 | Non-Gene | - |
| Chr5 | 7969644 | 0(N) | 4(A) | 0 | 0(N) | 14(C) | 0 | 1 | Non-Gene | - |
| Chr5 | 9706966 | 0(N) | 6(C) | 0 | 0(N) | 16(T) | 0 | 1 | Non-Gene | - |
| Chr5 | 9830937 | 0(N) | 2(G) | 0 | 0(N) | 16(A) | 0 | 1 | LOC102608042.1:(-),down-787bp,Note=kinesin-like protein NACK1, transcript variant X1 | - |
| Chr5 | 9849633 | 0(N) | 2(G) | 0 | 0(N) | 12(A) | 0 | 1 | LOC102608621.1:(-),intron-11,Note=(E)-beta-farnesene synthase-like | - |
| Chr5 | 10138662 | 0(N) | 2(T) | 0 | 0(N) | 14(G) | 0 | 1 | Non-Gene | - |
| Chr5 | 10676938 | 0(N) | 2(T) | 0 | 0(N) | 16(C) | 0 | 1 | Non-Gene | - |
| Chr5 | 10676957 | 0(N) | 4(C) | 0 | 0(N) | 12(A) | 0 | 1 | Non-Gene | - |
| Chr5 | 11040618 | 0(N) | 2(T) | 0 | 0(N) | 12(C) | 0 | 1 | Non-Gene | - |
| Chr5 | 11040674 | 0(N) | 10(C) | 0 | 0(N) | 6(A) | 0 | 1 | Non-Gene | - |
| Chr5 | 11840211 | 0(N) | 14(A) | 0 | 0(N) | 10(T) | 0 | 1 | Non-Gene | - |
| Chr5 | 12131108 | 0(N) | 4(G) | 0 | 0(N) | 16(A) | 0 | 1 | LOC102612871.1:(-),intron-2,Note=exopolygalacturonase | - |
| Chr5 | 12131116 | 0(N) | 4(T) | 0 | 0(N) | 16(C) | 0 | 1 | LOC102612871.1:(-),intron-2,Note=exopolygalacturonase | - |
| Chr5 | 12221935 | 0(N) | 2(T) | 0 | 0(N) | 12(C) | 0 | 1 | Non-Gene | - |
| Chr5 | 12576612 | 0(N) | 2(C) | 0 | 0(N) | 16(T) | 0 | 1 | Non-Gene | - |
| Chr5 | 12619495 | 0(N) | 4(A) | 0 | 0(N) | 10(T) | 0 | 1 | LOC107176928.1:(+),up-550bp,Note=uncharacterized LOC107176928 | - |
| Chr5 | 12655050 | 0(N) | 6(T) | 0 | 0(N) | 6(A) | 0 | 1 | LOC107176931.1:(+),up-175bp,Note=drebrin-like | - |
| Chr5 | 12845606 | 0(N) | 2(G) | 0 | 0(N) | 12(T) | 0 | 1 | Non-Gene | - |
| Chr5 | 14087888 | 0(N) | 12(A) | 0 | 0(N) | 2(G) | 0 | 1 | Non-Gene | - |
| Chr5 | 14511960 | 0(N) | 2(T) | 0 | 0(N) | 12(G) | 0 | 1 | LOC102617573.1:(-),up-168bp,Note=protein BOBBER 1 | - |
| Chr5 | 14590619 | 0(N) | 4(T) | 0 | 0(N) | 12(G) | 0 | 1 | Non-Gene | - |
| Chr5 | 14779944 | 0(N) | 4(C) | 0 | 0(N) | 16(T) | 0 | 1 | Non-Gene | - |
| Chr5 | 14857198 | 0(N) | 12(T) | 0 | 0(N) | 4(G) | 0 | 1 | Non-Gene | - |
| Chr5 | 14876650 | 0(N) | 2(A) | 0 | 0(N) | 16(G) | 0 | 1 | Non-Gene | - |
| Chr5 | 15068914 | 0(N) | 6(C) | 0 | 0(N) | 8(T) | 0 | 1 | Non-Gene | - |
| Chr5 | 15227300 | 0(N) | 8(A) | 0 | 0(N) | 16(T) | 0 | 1 | Non-Gene | - |
| Chr5 | 15664429 | 0(N) | 2(G) | 0 | 0(N) | 16(A) | 0 | 1 | Non-Gene | - |
| Chr5 | 15913870 | 0(N) | 12(G) | 0 | 0(N) | 8(A) | 0 | 1 | Non-Gene | - |
| Chr5 | 15936259 | 0(N) | 4(T) | 0 | 0(N) | 12(C) | 0 | 1 | Non-Gene | - |
| Chr5 | 16194497 | 0(N) | 2(C) | 0 | 0(N) | 14(T) | 0 | 1 | Non-Gene | - |
| Chr5 | 16741267 | 0(N) | 2(C) | 0 | 0(N) | 14(T) | 0 | 1 | Non-Gene | - |
| Chr5 | 16753758 | 0(N) | 8(G) | 0 | 0(N) | 16(A) | 0 | 1 | Non-Gene | - |
| Chr5 | 17676891 | 0(N) | 6(G) | 0 | 0(N) | 8(A) | 0 | 1 | Non-Gene | - |
| Chr5 | 17711146 | 0(N) | 6(C) | 0 | 0(N) | 10(G) | 0 | 1 | LOC102619108.1:(+),intron-5,Note=immune-associated nucleotide-binding protein 9-like | - |
| Chr5 | 18845149 | 0(N) | 8(A) | 0 | 0(N) | 12(G) | 0 | 1 | LOC102606770.1:(-),down-1734bp,Note=B-box zinc finger protein 23-like | - |
| Chr5 | 18979349 | 0(N) | 6(C) | 0 | 0(N) | 12(T) | 0 | 1 | Non-Gene | - |
| Chr5 | 19253875 | 0(N) | 12(A) | 0 | 0(N) | 16(T) | 0 | 1 | LOC102614164.1:(-),intron-1,Note=RNA-binding protein 24, transcript variant X4;LOC102614164.2:(-),intron-1,Note=RNA-binding protein 24, transcript variant X4;LOC102614164.3:(-),intron-1,Note=RNA-binding protein 24, transcript variant X4;LOC102614164.4:(-),intron-1,Note=RNA-binding protein 24, transcript variant X4;LOC102614164.5:(-),intron-1,Note=RNA-binding protein 24, transcript variant X4;LOC102614164.6:(-),intron-1,Note=RNA-binding protein 24, transcript variant X4;LOC102614164.7:(-),intron-1,Note=RNA-binding protein 24, transcript variant X4 | - |
| Chr5 | 19372409 | 0(N) | 4(A) | 0 | 0(N) | 14(T) | 0 | 1 | Non-Gene | - |
| Chr5 | 19871922 | 0(N) | 12(C) | 0 | 0(N) | 2(A) | 0 | 1 | LOC102611773.1:(+),down-1870bp,Note=protein SUPPRESSOR OF npr1-1, CONSTITUTIVE 1-like | - |
| Chr5 | 19871923 | 0(N) | 14(T) | 0 | 0(N) | 4(G) | 0 | 1 | LOC102611773.1:(+),down-1871bp,Note=protein SUPPRESSOR OF npr1-1, CONSTITUTIVE 1-like | - |
| Chr5 | 20931985 | 0(N) | 4(G) | 0 | 0(N) | 12(T) | 0 | 1 | Non-Gene | - |
| Chr5 | 21465784 | 0(N) | 2(A) | 0 | 0(N) | 12(G) | 0 | 1 | Non-Gene | - |
| Chr5 | 22034519 | 0(N) | 4(G) | 0 | 0(N) | 12(A) | 0 | 1 | LOC102614450.1:(-),intron-10,Note=MLO-like protein 1 | - |
| Chr5 | 22037741 | 0(N) | 6(G) | 0 | 0(N) | 10(T) | 0 | 1 | LOC102614450.1:(-),intron-3,Note=MLO-like protein 1 | - |
| Chr5 | 22484220 | 0(N) | 2(T) | 0 | 0(N) | 12(G) | 0 | 1 | LOC102616685.1:(+),up-255bp,Note=2-alkenal reductase (NADP(+)-dependent)-like | - |
| Chr5 | 22484225 | 0(N) | 8(A) | 0 | 0(N) | 12(C) | 0 | 1 | LOC102616685.1:(+),up-250bp,Note=2-alkenal reductase (NADP(+)-dependent)-like | - |
| Chr5 | 23187194 | 0(N) | 6(A) | 0 | 0(N) | 6(C) | 0 | 1 | Non-Gene | - |
| Chr5 | 23212396 | 0(N) | 10(T) | 0 | 0(N) | 10(G) | 0 | 1 | Non-Gene | - |
| Chr5 | 23853867 | 0(N) | 2(C) | 0 | 0(N) | 14(T) | 0 | 1 | Non-Gene | - |
| Chr5 | 23912716 | 0(N) | 12(C) | 0 | 0(N) | 6(T) | 0 | 1 | Non-Gene | - |
| Chr5 | 23912722 | 0(N) | 6(G) | 0 | 0(N) | 12(A) | 0 | 1 | Non-Gene | - |
| Chr5 | 24125495 | 0(N) | 4(T) | 0 | 0(N) | 6(C) | 0 | 1 | Non-Gene | - |
| Chr5 | 24360123 | 0(N) | 12(A) | 0 | 0(N) | 12(T) | 0 | 1 | Non-Gene | - |
| Chr5 | 24490099 | 0(N) | 4(T) | 0 | 0(N) | 14(C) | 0 | 1 | Non-Gene | - |
| Chr5 | 24490120 | 0(N) | 2(C) | 0 | 0(N) | 16(T) | 0 | 1 | Non-Gene | - |
| Chr5 | 24615151 | 0(N) | 4(A) | 0 | 0(N) | 14(G) | 0 | 1 | Non-Gene | - |
| Chr5 | 24640995 | 0(N) | 2(A) | 0 | 0(N) | 12(G) | 0 | 1 | Non-Gene | - |
| Chr5 | 25497322 | 0(N) | 6(A) | 0 | 0(N) | 14(T) | 0 | 1 | Non-Gene | - |
| Chr5 | 25854191 | 0(N) | 4(C) | 0 | 0(N) | 12(T) | 0 | 1 | Non-Gene | - |
| Chr5 | 26254705 | 0(N) | 2(A) | 0 | 0(N) | 14(G) | 0 | 1 | Non-Gene | - |
| Chr5 | 26631651 | 0(N) | 4(A) | 0 | 0(N) | 16(G) | 0 | 1 | Non-Gene | - |
| Chr5 | 26631662 | 0(N) | 4(T) | 0 | 0(N) | 14(C) | 0 | 1 | Non-Gene | - |
| Chr5 | 26631664 | 0(N) | 2(G) | 0 | 0(N) | 14(A) | 0 | 1 | Non-Gene | - |
| Chr5 | 26631676 | 0(N) | 6(T) | 0 | 0(N) | 12(C) | 0 | 1 | Non-Gene | - |
| Chr5 | 26631678 | 0(N) | 2(G) | 0 | 0(N) | 12(T) | 0 | 1 | Non-Gene | - |
| Chr5 | 27068389 | 0(N) | 4(T) | 0 | 0(N) | 12(A) | 0 | 1 | LOC107177164.1:(+),intron-3,Note=NAC domain-containing protein 13-like | - |
| Chr5 | 28436222 | 0(N) | 4(C) | 0 | 0(N) | 10(G) | 0 | 1 | LOC102614057.1:(+),down-697bp,Note=pentatricopeptide repeat-containing protein At5g18390, mitochondrial, transcript variant X2 | - |
| Chr5 | 29048098 | 0(N) | 12(T) | 0 | 0(N) | 14(G) | 0 | 1 | Non-Gene | - |
| Chr5 | 29048129 | 0(N) | 10(G) | 0 | 0(N) | 10(A) | 0 | 1 | Non-Gene | - |
| Chr5 | 29840503 | 0(N) | 10(T) | 0 | 0(N) | 16(G) | 0 | 1 | LOC102611982.1:(-),intron-5,Note=probable zinc metalloprotease EGY1, chloroplastic | - |
| Chr5 | 31654245 | 0(N) | 2(A) | 0 | 0(N) | 16(T) | 0 | 1 | LOC102607454.1:(+),intron-3,Note=uncharacterized LOC102607454 | - |
| Chr5 | 35384075 | 0(N) | 2(T) | 0 | 0(N) | 16(C) | 0 | 1 | LOC102623258.1:(-),intron-1,Note=PE-PGRS family protein PE\_PGRS33-like | - |
| Chr5 | 36021288 | 0(N) | 2(A) | 0 | 0(N) | 16(G) | 0 | 1 | Non-Gene | - |
| Chr5 | 36058041 | 0(N) | 2(A) | 0 | 0(N) | 14(G) | 0 | 1 | Non-Gene | - |
| Chr6 | 15553 | 0(N) | 6(A) | 0 | 0(N) | 10(C) | 0 | 1 | Non-Gene | - |
| Chr6 | 29567 | 0(N) | 8(T) | 0 | 0(N) | 14(A) | 0 | 1 | Non-Gene | - |
| Chr6 | 92093 | 0(N) | 8(T) | 0 | 0(N) | 10(C) | 0 | 1 | Non-Gene | - |
| Chr6 | 100198 | 0(N) | 10(C) | 0 | 0(N) | 2(T) | 0 | 1 | Non-Gene | - |
| Chr6 | 609010 | 0(N) | 2(A) | 0 | 0(N) | 12(G) | 0 | 1 | LOC107177287.1:(-),down-1886bp,Note=uncharacterized LOC107177287 | - |
| Chr6 | 13685249 | 0(N) | 4(G) | 0 | 0(N) | 12(C) | 0 | 1 | LOC107177486.1:(-),intron-2,Note=receptor-like protein 13 | - |
| Chr6 | 14294125 | 0(N) | 2(A) | 0 | 0(N) | 12(G) | 0 | 1 | Non-Gene | - |
| Chr7 | 15373 | 0(N) | 14(C) | 0 | 0(N) | 10(T) | 0 | 1 | Non-Gene | - |
| Chr7 | 3242526 | 0(N) | 14(A) | 0 | 0(N) | 14(T) | 0 | 1 | Non-Gene | - |
| Chr7 | 13124883 | 0(N) | 4(T) | 0 | 0(N) | 10(A) | 0 | 1 | Non-Gene | - |
| Chr7 | 13590242 | 0(N) | 6(G) | 0 | 0(N) | 12(C) | 0 | 1 | Non-Gene | - |
| Chr7 | 14886910 | 0(N) | 6(A) | 0 | 0(N) | 4(G) | 0 | 1 | Non-Gene | - |
| Chr7 | 15031743 | 0(N) | 4(C) | 0 | 0(N) | 12(T) | 0 | 1 | LOC107177821.2:(+),ACC->ACT,T->T,syn,exon-1,Note=zinc finger MYM-type protein 1-like, transcript variant X3;LOC107177821.3:(+),ACC->ACT,T->T,syn,exon-1,Note=zinc finger MYM-type protein 1-like, transcript variant X3 | - |
| Chr7 | 15031787 | 0(N) | 2(A) | 0 | 0(N) | 14(G) | 0 | 1 | LOC107177821.2:(+),aat->aGt,X->X,syn,exon-1,Note=zinc finger MYM-type protein 1-like, transcript variant X3;LOC107177821.3:(+),aat->aGt,X->X,syn,exon-1,Note=zinc finger MYM-type protein 1-like, transcript variant X3 | - |
| Chr7 | 16053731 | 0(N) | 4(G) | 0 | 0(N) | 12(A) | 0 | 1 | Non-Gene | - |
| Chr7 | 17615541 | 0(N) | 10(A) | 0 | 0(N) | 4(G) | 0 | 1 | LOC107177829.1:(+),up-459bp,Note=uncharacterized LOC107177829 | - |
| Chr7 | 18281984 | 0(N) | 4(A) | 0 | 0(N) | 14(C) | 0 | 1 | Non-Gene | - |
| Chr7 | 20630814 | 0(N) | 10(T) | 0 | 0(N) | 8(A) | 0 | 1 | Non-Gene | - |
| Chr7 | 20630816 | 0(N) | 4(C) | 0 | 0(N) | 10(A) | 0 | 1 | Non-Gene | - |
| Chr7 | 22285736 | 0(N) | 4(A) | 0 | 0(N) | 14(G) | 0 | 1 | Non-Gene | - |
| Chr7 | 25433370 | 0(N) | 2(A) | 0 | 0(N) | 10(G) | 0 | 1 | Non-Gene | - |
| Chr7 | 25662215 | 0(N) | 6(T) | 0 | 0(N) | 16(A) | 0 | 1 | Non-Gene | - |
| Chr7 | 27150886 | 0(N) | 4(C) | 0 | 0(N) | 12(A) | 0 | 1 | Non-Gene | - |
| Chr7 | 27413907 | 0(N) | 2(A) | 0 | 0(N) | 12(G) | 0 | 1 | LOC102623191.1:(+),up-800bp,Note=ribulose bisphosphate carboxylase small chain, chloroplastic-like | - |
| Chr8 | 4637442 | 0(N) | 4(T) | 0 | 0(N) | 12(A) | 0 | 1 | Non-Gene | - |
| Chr8 | 4875438 | 0(N) | 2(A) | 0 | 0(N) | 14(G) | 0 | 1 | Non-Gene | - |
| Chr8 | 5386076 | 0(N) | 2(C) | 0 | 0(N) | 12(T) | 0 | 1 | LOC102615542.1:(+),up-922bp,Note=protein CASPARIAN STRIP INTEGRITY FACTOR 1-like | - |
| Chr8 | 5907210 | 0(N) | 2(C) | 0 | 0(N) | 14(A) | 0 | 1 | Non-Gene | - |
| Chr8 | 6369630 | 0(N) | 2(G) | 0 | 0(N) | 12(A) | 0 | 1 | Non-Gene | - |
| Chr8 | 6726501 | 0(N) | 2(G) | 0 | 0(N) | 14(T) | 0 | 1 | Non-Gene | - |
| Chr8 | 6726693 | 0(N) | 2(G) | 0 | 0(N) | 16(T) | 0 | 1 | Non-Gene | - |
| Chr8 | 7541279 | 0(N) | 2(T) | 0 | 0(N) | 14(C) | 0 | 1 | LOC102625290.2:(+),down-1662bp,Note=probable amidase At4g34880, transcript variant X1 | - |
| Chr8 | 8035643 | 0(N) | 2(G) | 0 | 0(N) | 16(A) | 0 | 1 | Non-Gene | - |
| Chr8 | 8123236 | 0(N) | 6(C) | 0 | 0(N) | 8(T) | 0 | 1 | Non-Gene | - |
| Chr8 | 8535172 | 0(N) | 2(G) | 0 | 0(N) | 12(C) | 0 | 1 | Non-Gene | - |
| Chr8 | 8937466 | 0(N) | 8(C) | 0 | 0(N) | 14(T) | 0 | 1 | Non-Gene | - |
| Chr8 | 9582294 | 0(N) | 2(A) | 0 | 0(N) | 16(T) | 0 | 1 | LOC102613308.1:(-),intron-10,Note=CCR4-NOT transcription complex subunit 11, transcript variant X1;LOC102613308.2:(-),intron-10,Note=CCR4-NOT transcription complex subunit 11, transcript variant X1 | - |
| Chr8 | 10233109 | 0(N) | 6(C) | 0 | 0(N) | 6(T) | 0 | 1 | Non-Gene | - |
| Chr8 | 10471258 | 0(N) | 6(C) | 0 | 0(N) | 8(T) | 0 | 1 | Non-Gene | - |
| Chr8 | 10650252 | 0(N) | 2(A) | 0 | 0(N) | 10(T) | 0 | 1 | Non-Gene | - |
| Chr8 | 10668038 | 0(N) | 2(T) | 0 | 0(N) | 12(C) | 0 | 1 | LOC107178223.2:(-),up-1644bp,Note=zinc finger BED domain-containing protein RICESLEEPER 2-like, transcript variant X2 | - |
| Chr8 | 10993248 | 0(N) | 2(G) | 0 | 0(N) | 14(T) | 0 | 1 | Non-Gene | - |
| Chr8 | 11204315 | 0(N) | 2(T) | 0 | 0(N) | 14(C) | 0 | 1 | Non-Gene | - |
| Chr8 | 11204584 | 0(N) | 2(C) | 0 | 0(N) | 16(T) | 0 | 1 | Non-Gene | - |
| Chr8 | 11347545 | 0(N) | 8(A) | 0 | 0(N) | 6(G) | 0 | 1 | LOC107178207.1:(+),intron-2,Note=uncharacterized LOC107178207 | - |
| Chr8 | 11563653 | 0(N) | 8(G) | 0 | 0(N) | 2(A) | 0 | 1 | Non-Gene | - |
| Chr8 | 12440996 | 0(N) | 4(A) | 0 | 0(N) | 16(T) | 0 | 1 | Non-Gene | - |
| Chr8 | 12495167 | 0(N) | 2(A) | 0 | 0(N) | 14(T) | 0 | 1 | Non-Gene | - |
| Chr8 | 12630099 | 0(N) | 4(C) | 0 | 0(N) | 14(T) | 0 | 1 | Non-Gene | - |
| Chr8 | 12647984 | 0(N) | 2(C) | 0 | 0(N) | 16(T) | 0 | 1 | Non-Gene | - |
| Chr8 | 12792677 | 0(N) | 8(A) | 0 | 0(N) | 12(T) | 0 | 1 | Non-Gene | - |
| Chr8 | 13164844 | 0(N) | 8(G) | 0 | 0(N) | 10(A) | 0 | 1 | Non-Gene | - |
| Chr8 | 13889498 | 0(N) | 2(T) | 0 | 0(N) | 14(A) | 0 | 1 | Non-Gene | - |
| Chr8 | 14591907 | 0(N) | 8(G) | 0 | 0(N) | 2(A) | 0 | 1 | LOC107178261.1:(-),TTG->CTG,L->L,syn,exon-1,Note=protein NYNRIN-like | - |
| Chr8 | 14793413 | 0(N) | 6(T) | 0 | 0(N) | 10(A) | 0 | 1 | Non-Gene | - |
| Chr8 | 14795155 | 0(N) | 8(T) | 0 | 0(N) | 8(A) | 0 | 1 | Non-Gene | - |
| Chr8 | 14974523 | 0(N) | 10(A) | 0 | 0(N) | 14(T) | 0 | 1 | Non-Gene | - |
| Chr8 | 14974524 | 0(N) | 8(A) | 0 | 0(N) | 14(T) | 0 | 1 | Non-Gene | - |
| Chr8 | 15052535 | 0(N) | 4(C) | 0 | 0(N) | 14(T) | 0 | 1 | Non-Gene | - |
| Chr8 | 15052536 | 0(N) | 8(A) | 0 | 0(N) | 14(G) | 0 | 1 | Non-Gene | - |
| Chr8 | 16039414 | 0(N) | 2(G) | 0 | 0(N) | 12(C) | 0 | 1 | Non-Gene | - |
| Chr8 | 16121343 | 0(N) | 2(A) | 0 | 0(N) | 12(C) | 0 | 1 | Non-Gene | - |
| Chr8 | 16408119 | 0(N) | 2(T) | 0 | 0(N) | 16(C) | 0 | 1 | LOC102610209.1:(+),intron-0,Note=photosystem II reaction center W protein, chloroplastic-like | - |
| Chr8 | 17964111 | 0(N) | 4(A) | 0 | 0(N) | 12(G) | 0 | 1 | Non-Gene | - |
| Chr8 | 22156105 | 0(N) | 2(T) | 0 | 0(N) | 16(G) | 0 | 1 | LOC102626643.1:(-),down-165bp,Note=U-box domain-containing protein 44-like | - |
| Chr8 | 22388326 | 0(N) | 6(A) | 0 | 0(N) | 12(T) | 0 | 1 | LOC102610331.1:(-),down-1874bp,Note=protein LIGHT-DEPENDENT SHORT HYPOCOTYLS 6-like | - |
| Chr9 | 5901307 | 0(N) | 2(T) | 0 | 0(N) | 14(C) | 0 | 1 | LOC107178426.1:(+),down-1458bp,Note=FHA domain-containing protein At4g14490-like | - |
| Chr9 | 6336211 | 0(N) | 2(T) | 0 | 0(N) | 14(G) | 0 | 1 | Non-Gene | - |
| Chr9 | 7160702 | 0(N) | 4(T) | 0 | 0(N) | 12(A) | 0 | 1 | Non-Gene | - |
| Chr9 | 7211845 | 0(N) | 10(G) | 0 | 0(N) | 12(A) | 0 | 1 | Non-Gene | - |
| Chr9 | 7700186 | 0(N) | 2(G) | 0 | 0(N) | 14(T) | 0 | 1 | LOC102630000.1:(-),up-1809bp,Note=protein tas | - |
| Chr9 | 7839120 | 0(N) | 10(G) | 0 | 0(N) | 8(T) | 0 | 1 | LOC112495633.1:(+),up-1986bp,Note=early nodulin-75-like | - |
| Chr9 | 8486810 | 0(N) | 2(A) | 0 | 0(N) | 12(T) | 0 | 1 | Non-Gene | - |
| Chr9 | 8560085 | 0(N) | 2(A) | 0 | 0(N) | 12(G) | 0 | 1 | LOC102610218.1:(+),up-1698bp,Note=cellulose synthase-like protein D1, transcript variant X1 | droughtresistance(Li et. al, 2018) |
| Chr9 | 8674578 | 0(N) | 2(A) | 0 | 0(N) | 12(T) | 0 | 1 | Non-Gene | - |
| Chr9 | 8972396 | 0(N) | 4(C) | 0 | 0(N) | 14(T) | 0 | 1 | LOC102608384.1:(+),intron-1,Note=UPF0481 protein At3g47200-like, transcript variant X1;LOC102608384.2:(+),intron-1,Note=UPF0481 protein At3g47200-like, transcript variant X1 | - |
| Chr9 | 9129948 | 0(N) | 8(A) | 0 | 0(N) | 12(G) | 0 | 1 | LOC102608384.1:(+),intron-1,Note=UPF0481 protein At3g47200-like, transcript variant X1;LOC102608384.2:(+),intron-1,Note=UPF0481 protein At3g47200-like, transcript variant X1 | - |
| Chr9 | 9757824 | 0(N) | 4(T) | 0 | 0(N) | 8(C) | 0 | 1 | Non-Gene | - |
| Chr9 | 9890321 | 0(N) | 2(T) | 0 | 0(N) | 16(G) | 0 | 1 | Non-Gene | - |
| Chr9 | 10989715 | 0(N) | 8(A) | 0 | 0(N) | 16(T) | 0 | 1 | LOC107178518.1:(-),down-1095bp,Note=NAC transcription factor 32-like | - |
| Chr9 | 10989716 | 0(N) | 6(A) | 0 | 0(N) | 16(T) | 0 | 1 | LOC107178518.1:(-),down-1094bp,Note=NAC transcription factor 32-like | - |
| Chr9 | 10989717 | 0(N) | 6(A) | 0 | 0(N) | 16(T) | 0 | 1 | LOC107178518.1:(-),down-1093bp,Note=NAC transcription factor 32-like | - |
| Chr9 | 11249420 | 0(N) | 6(A) | 0 | 0(N) | 14(G) | 0 | 1 | Non-Gene | - |
| Chr9 | 11249471 | 0(N) | 10(A) | 0 | 0(N) | 8(C) | 0 | 1 | Non-Gene | - |
| Chr9 | 11584657 | 0(N) | 2(A) | 0 | 0(N) | 16(T) | 0 | 1 | LOC107178529.1:(-),up-1754bp,Note=probable LRR receptor-like serine/threonine-protein kinase At3g47570 | - |
| Chr9 | 11811467 | 0(N) | 14(A) | 0 | 0(N) | 6(T) | 0 | 1 | LOC107178542.1:(-),up-1959bp,Note=uncharacterized LOC107178542 | - |
| Chr9 | 12222505 | 0(N) | 4(C) | 0 | 0(N) | 14(T) | 0 | 1 | Non-Gene | - |
| Chr9 | 12338763 | 0(N) | 6(T) | 0 | 0(N) | 12(C) | 0 | 1 | LOC107178555.1:(+),down-483bp,Note=putative disease resistance protein RGA1 | - |
| Chr9 | 12351418 | 0(N) | 2(C) | 0 | 0(N) | 14(T) | 0 | 1 | Non-Gene | - |
| Chr9 | 12392000 | 0(N) | 2(A) | 0 | 0(N) | 16(G) | 0 | 1 | LOC102622913.1:(+),intron-1,Note=disease resistance protein RGA2-like | - |
| Chr9 | 12430161 | 0(N) | 8(G) | 0 | 0(N) | 10(A) | 0 | 1 | LOC107178568.3:(+),GCC->ACC,A->T,no-syn,exon-2,Note=disease resistance protein RGA2-like, transcript variant X3 | disease resistance(Marimon et al., 2020) |
| Chr9 | 12536448 | 0(N) | 2(A) | 0 | 0(N) | 14(G) | 0 | 1 | Non-Gene | - |
| Chr9 | 12650244 | 0(N) | 6(G) | 0 | 0(N) | 10(C) | 0 | 1 | LOC102623211.1:(+),down-379bp,Note=putative disease resistance protein RGA1 | - |
| Chr9 | 12650254 | 0(N) | 6(C) | 0 | 0(N) | 14(T) | 0 | 1 | LOC102623211.1:(+),down-389bp,Note=putative disease resistance protein RGA1 | - |
| Chr9 | 12704887 | 0(N) | 2(T) | 0 | 0(N) | 16(C) | 0 | 1 | LOC112495652.1:(-),down-1754bp,Note=F-box protein At5g49610-like | - |
| Chr9 | 12704892 | 0(N) | 4(T) | 0 | 0(N) | 12(C) | 0 | 1 | LOC112495652.1:(-),down-1749bp,Note=F-box protein At5g49610-like | - |
| Chr9 | 12704913 | 0(N) | 2(T) | 0 | 0(N) | 16(C) | 0 | 1 | LOC112495652.1:(-),down-1728bp,Note=F-box protein At5g49610-like | - |
| Chr9 | 12754353 | 0(N) | 10(C) | 0 | 0(N) | 6(G) | 0 | 1 | LOC107178564.1:(-),up-1112bp,Note=uncharacterized LOC107178564 | - |
| Chr9 | 13389506 | 0(N) | 4(A) | 0 | 0(N) | 14(G) | 0 | 1 | Non-Gene | - |
| Chr9 | 13946494 | 0(N) | 2(C) | 0 | 0(N) | 12(T) | 0 | 1 | Non-Gene | - |
| Chr9 | 13946498 | 0(N) | 2(T) | 0 | 0(N) | 12(C) | 0 | 1 | Non-Gene | - |
| Chr9 | 14302585 | 0(N) | 2(C) | 0 | 0(N) | 16(T) | 0 | 1 | Non-Gene | - |
| Chr9 | 14302599 | 0(N) | 2(T) | 0 | 0(N) | 16(C) | 0 | 1 | Non-Gene | - |
| Chr9 | 14313601 | 0(N) | 4(C) | 0 | 0(N) | 12(T) | 0 | 1 | Non-Gene | - |
| Chr9 | 14381929 | 0(N) | 4(A) | 0 | 0(N) | 16(G) | 0 | 1 | LOC102612019.1:(+),up-1884bp,Note=non-functional NADPH-dependent codeinone reductase 2 | - |
| Chr9 | 14781887 | 0(N) | 4(C) | 0 | 0(N) | 14(A) | 0 | 1 | Non-Gene | - |
| Chr9 | 14783720 | 0(N) | 2(T) | 0 | 0(N) | 16(A) | 0 | 1 | Non-Gene | - |
| Chr9 | 14959939 | 0(N) | 8(G) | 0 | 0(N) | 8(A) | 0 | 1 | Non-Gene | - |
| Chr9 | 15182347 | 0(N) | 4(G) | 0 | 0(N) | 8(A) | 0 | 1 | LOC102631206.1:(+),CGG->CAG,R->Q,no-syn,exon-4,Note=putative lipase YOR059C, transcript variant X1;LOC102631206.2:(+),CGG->CAG,R->Q,no-syn,exon-4,Note=putative lipase YOR059C, transcript variant X1 | - |
| Chr9 | 15230522 | 0(N) | 10(A) | 0 | 0(N) | 10(T) | 0 | 1 | LOC102606612.1:(+),GCA->GCT,A->A,syn,exon-6,Note=ankyrin repeat-containing protein ITN1-like, transcript variant X1;LOC102606612.2:(+),GCA->GCT,A->A,syn,exon-6,Note=ankyrin repeat-containing protein ITN1-like, transcript variant X1;LOC102606612.3:(+),GCA->GCT,A->A,syn,exon-6,Note=ankyrin repeat-containing protein ITN1-like, transcript variant X1;LOC102606612.4:(+),GCA->GCT,A->A,syn,exon-6,Note=ankyrin repeat-containing protein ITN1-like, transcript variant X1 | - |
| Chr9 | 15764163 | 0(N) | 10(G) | 0 | 0(N) | 4(A) | 0 | 1 | LOC102630100.1:(+),down-497bp,Note=subtilisin-like protease SBT1.3 | - |
| Chr9 | 16409731 | 0(N) | 14(C) | 0 | 0(N) | 6(G) | 0 | 1 | Non-Gene | - |
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**Supplementary Table S4 PCA analysis of 106 samples to be identified**

|  |  |  |  |  |  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- |
| Sample | Variety | PC1 | PC2 | PC3 | PC4 | PC5 | PC6 | PC7 | PC8 | PC9 | PC10 |
| Sample-1-1 | XZ | -0.138519 | 0.029743 | -0.04386 | -0.012857 | -0.04483 | 0.0404425 | 0.0187477 | 0.833001 | -0.10096 | 0.265352 |
| Sample-1-2 | XZ | -0.126738 | -0.067407 | -0.020868 | 0.0750846 | 0.0165607 | 0.0111998 | 0.188014 | -0.802806 | 0.0307889 | -0.29357 |
| Sample-1-3 | XZ | -0.126096 | -0.039068 | -0.20822 | -0.035359 | -0.060902 | -0.088588 | 0.0267141 | -0.751044 | 0.0204711 | -0.301998 |
| Sample-1-4 | XZ | -0.131911 | 0.0342959 | -0.035323 | -0.147126 | -0.049335 | -0.084821 | -0.0701 | -0.850094 | 0.0585639 | -0.091757 |
| Sample-1-5 | XZ | -0.117129 | 0.006223 | -0.034511 | -0.103331 | -0.07559 | -0.026544 | -0.048957 | 0.898442 | -0.109667 | 0.270134 |
| Sample-1-6 | XZ | -0.135158 | -0.070222 | 0.0336094 | -0.005144 | -0.087595 | 0.0065222 | 0.0817396 | -0.827146 | 0.132818 | -0.293774 |
| Sample-1-7 | XZ | -0.148314 | 0.0678176 | 0.0159054 | 0.0729717 | 0.0603641 | 0.0336811 | 0.0575022 | -0.819804 | -0.126915 | 0.165999 |
| Sample-1-8 | XZ | -0.094403 | -0.104433 | 0.167547 | -0.117383 | 0.0080624 | -0.069819 | -0.247581 | -0.855569 | 0.125146 | 0.122036 |
| Sample-1-9 | XZ | -0.120957 | 0.110471 | 0.0689491 | 0.009725 | 0.131322 | -0.000392 | 0.0421826 | -0.864957 | 0.118356 | -0.162611 |
| Sample-1-10 | DZ | 0.213133 | -0.228493 | -0.261711 | 0.0484968 | 0.11501 | -0.076787 | -0.065555 | 0.876343 | -0.004878 | 0.140955 |
| Sample-1-11 | DZ | 0.160268 | 0.269568 | -0.041214 | 0.241274 | 0.194814 | 0.0198623 | 0.243092 | -0.840382 | 0.0203151 | -0.048292 |
| Sample-1-12 | DZ | 0.204068 | 0.273924 | -0.010492 | -0.191196 | 0.204254 | -0.15454 | -0.441989 | -0.727967 | 0.0135497 | -0.125236 |
| Sample-1-13 | DZ | 0.196818 | 0.302115 | 0.119825 | 0.0951092 | -0.313739 | 0.185177 | -0.20269 | 0.799023 | -0.018456 | 0.073266 |
| Sample-1-14 | DZ | 0.185106 | 0.244034 | -0.067616 | 0.086796 | -0.035516 | -0.200525 | 0.386672 | -0.761277 | 0.0286526 | -0.158946 |
| Sample-1-15 | DZ | 0.1952 | 0.328278 | -0.15537 | 0.0566515 | 0.108071 | 0.239741 | -0.208573 | -0.819689 | -0.0394 | -0.114887 |
| Sample-1-16 | DZ | 0.1697 | -0.332054 | -0.290656 | -0.027619 | -0.208198 | 0.136311 | -0.467903 | 0.679735 | -0.035283 | 0.0212967 |
| Sample-1-17 | DZ | 0.229518 | 0.319391 | -0.178302 | 5.87E-05 | -0.182987 | 0.0667745 | -0.074952 | 0.851062 | -0.001541 | 0.164504 |
| Sample-1-18 | XZ | -0.14902 | 0.0314889 | -0.021154 | 0.0666346 | 0.0874897 | -0.037343 | 0.0829169 | -0.849505 | 0.189909 | -0.241965 |
| Sample-1-19 | DZ | 0.1881 | 0.447319 | -0.290722 | 0.068065 | -0.017203 | 0.154292 | -0.34481 | 0.705099 | 0.0374437 | -0.10169 |
| Sample-1-20 | DZ | 0.18228 | 0.299379 | 0.0549985 | 0.0587041 | -0.072542 | -0.12093 | 0.623934 | -0.648776 | 0.0752051 | -0.067194 |
| Sample-1-21 | XZ | -0.144815 | -0.046893 | -0.009133 | -0.092752 | 0.0572433 | 0.0705142 | -0.038183 | -0.906861 | 0.0333061 | -0.07663 |
| Sample-1-22 | XZ | -0.142368 | -0.033185 | -0.016689 | 0.0684632 | -0.00818 | 0.0601071 | 0.235962 | 0.874224 | 0.169849 | -0.045605 |
| Sample-1-23 | XZ | -0.141847 | -0.047524 | 0.0116407 | 0.0079968 | -0.071789 | 0.0391936 | 0.0881667 | -0.859251 | 0.0310203 | -0.388118 |
| Sample-1-24 | XZ | -0.154887 | 0.0284485 | -0.047477 | 0.0206008 | 0.0179093 | 0.0305486 | -0.155119 | -0.866693 | -0.096565 | 0.297878 |
| Sample-1-25 | XZ | -0.153249 | -0.025646 | -0.046921 | -0.023264 | -0.000405 | -0.077123 | 0.0745164 | 0.890222 | -0.062034 | 0.0302771 |
| Sample-1-26 | XZ | -0.161223 | 0.0033759 | -0.004164 | -0.009252 | 0.0259156 | -0.016033 | 0.020667 | 0.804073 | -0.29314 | -0.247415 |
| Sample-1-27 | XZ | -0.142742 | -0.015246 | 0.0547759 | -0.082874 | 0.0283728 | -0.022881 | -0.076677 | -0.936825 | 0.039258 | 0.0326626 |
| Sample-1-28 | XZ | -0.158917 | -0.021802 | -0.052664 | -0.081561 | 0.0115309 | 0.0440273 | -0.063024 | -0.793702 | 0.308389 | 0.195215 |
| Sample-1-29 | XZ | -0.152066 | 0.0003143 | 0.0144181 | -0.005456 | 0.0221421 | -0.053335 | 0.0386382 | 0.76838 | -0.001277 | -0.4508 |
| Sample-1-30 | XZ | -0.155629 | -0.06057 | 0.0019456 | -0.016944 | -0.026113 | -0.005377 | -0.011589 | -0.881093 | 0.153447 | -0.009178 |
| Sample-1-31 | XZ | -0.157428 | 0.0212861 | 0.0375079 | 0.0169765 | -0.002095 | -0.034343 | 0.0013246 | 0.941543 | -0.014843 | 0.0193542 |
| Sample-1-32 | XZ | -0.150636 | 0.0054098 | -0.021978 | -0.013743 | 0.0052474 | 0.0244962 | -0.11374 | 0.829856 | -0.181683 | 0.300556 |
| Sample-2-1 | XZ | -0.146956 | -0.003311 | 0.0213804 | -0.071483 | 0.0124579 | 0.0090657 | 0.0428049 | -0.868743 | -0.049124 | -0.281947 |
| Sample-2-2 | XZ | -0.143551 | -0.003925 | -0.015606 | 0.0185608 | 0.0121391 | -0.011649 | -0.039049 | -0.943667 | 0.0863034 | -0.113203 |
| Sample-2-3 | XZ | -0.148059 | 0.0320399 | -0.017828 | -0.017448 | -0.022602 | 0.0196884 | -0.059854 | -0.626914 | 0.641049 | -0.003848 |
| Sample-2-4 | XZ | -0.139181 | 0.0628137 | 0.0176154 | 0.0123757 | 0.0270045 | -0.079048 | -0.224072 | 0.910941 | -0.113176 | 0.093643 |
| Sample-2-5 | XZ | -0.147973 | 0.0160937 | 0.0278381 | -0.051677 | -0.035686 | -0.022138 | -0.006306 | 0.866129 | -0.215052 | -0.288708 |
| Sample-2-6 | XZ | -0.155429 | 0.0238595 | -0.011758 | 0.0270182 | 0.0081017 | 0.0440216 | -0.018605 | -0.874152 | -0.061111 | 0.250858 |
| Sample-2-7 | XZ | -0.153097 | 0.0779041 | 0.009646 | 0.0729079 | -0.038319 | -0.000264 | -0.060047 | 0.92768 | -0.036986 | 0.156564 |
| Sample-2-8 | XZ | -0.156708 | 0.0177265 | 0.0193553 | -0.007145 | -0.060416 | 0.0207525 | -0.14048 | -0.703964 | 0.0468357 | -0.369662 |
| Sample-2-9 | XZ | -0.142897 | -0.05101 | 0.0106758 | -0.061432 | -0.035328 | -0.043863 | -0.049208 | -0.924029 | -0.023512 | -0.10899 |
| Sample-2-10 | XZ | -0.164939 | -0.017106 | -0.053743 | -0.019413 | -0.00765 | 0.0278708 | -0.064375 | -0.670126 | 0.0460644 | -0.566278 |
| Sample-2-11 | XZ | -0.147621 | 0.0215524 | 0.0222655 | 0.0291257 | 0.0097144 | 0.0364944 | 0.0771972 | -0.813996 | -0.423951 | 0.153078 |
| Sample-2-12 | XZ | -0.143566 | 0.0012103 | 0.0495924 | 0.0067013 | 0.067488 | -0.006166 | -0.042954 | -0.901785 | 0.0550841 | -0.178009 |
| Sample-2-13 | DZ | 0.170821 | 0.332497 | -0.156579 | 0.0971328 | 0.0375436 | 0.0061752 | -0.501994 | 0.734534 | -0.022106 | 0.103747 |
| Sample-2-14 | DZ | 0.197585 | 0.394002 | -0.138957 | 0.121093 | 0.132184 | -0.016121 | 0.265073 | 0.807236 | -0.024591 | 0.0902446 |
| Sample-2-15 | DZ | 0.195885 | 0.107813 | -0.044387 | 0.113011 | 0.23408 | -0.18193 | 0.119271 | -0.899391 | 0.0102508 | -0.012796 |
| Sample-2-16 | DZ | 0.145166 | 0.0936046 | 0.622471 | 0.0444972 | 0.0166268 | 0.169229 | 0.105173 | -0.687055 | 0.0481864 | -0.094104 |
| Sample-2-17 | DZ | 0.169181 | 0.46125 | -0.2803 | 0.0651588 | 0.176548 | 0.0634199 | 0.341089 | -0.70952 | 0.0626166 | 0.0154011 |
| Sample-2-18 | DZ | 0.146855 | 0.164107 | -0.222567 | -0.054686 | -0.177559 | -0.247672 | -0.126846 | -0.8614 | -0.132251 | -0.020716 |
| Sample-2-19 | DZ | 0.156433 | -0.125235 | -0.375977 | 0.0950656 | 0.016585 | -0.320188 | 0.504718 | 0.652728 | -0.029903 | 0.0574846 |
| Sample-2-20 | DZ | 0.185608 | -0.356038 | -0.194965 | 0.0165182 | 0.0614602 | 0.0974852 | -0.330928 | 0.803907 | -0.012929 | -0.068727 |
| Sample-3-1 | DZ | 0.120313 | -0.376346 | -0.198463 | 0.170228 | 0.0774681 | -0.267563 | -0.362392 | 0.736634 | 0.0128985 | 0.0154962 |
| Sample-3-2 | DZ | 0.149925 | -0.542501 | -0.256075 | -0.027978 | 0.152615 | -0.019002 | 0.564209 | -0.496354 | 0.0351204 | 0.0132123 |
| Sample-3-3 | DZ | 0.0618417 | -0.013306 | -0.568675 | 0.0454368 | -0.349073 | -0.475956 | -0.535944 | -0.061772 | -0.005061 | 0.012429 |
| Sample-3-4 | DZ | 0.0760902 | -0.645488 | -0.109307 | 0.0194766 | 0.143442 | -0.109911 | -0.287061 | -0.634537 | 0.08708 | -0.112008 |
| Sample-3-5 | DZ | 0.117715 | -0.622223 | -0.044212 | -0.157309 | 0.206949 | -0.077081 | -0.513687 | -0.470042 | 0.018246 | 0.108007 |
| Sample-3-6 | DZ | 0.0986027 | 0.474258 | -0.383488 | 0.0330082 | -0.210267 | 0.190952 | 0.437868 | 0.54669 | -0.00375 | -0.103765 |
| Sample-3-7 | DZ | 0.0447292 | 0.35983 | -0.558655 | 0.191905 | 0.127729 | -0.04854 | 0.453486 | -0.504987 | 0.0340716 | 0.0673203 |
| Sample-3-8 | DZ | 0.102269 | 0.652538 | -0.183661 | -0.062958 | -0.093209 | 0.0202546 | 0.239542 | -0.639789 | 0.103409 | -0.101678 |
| Sample-3-9 | DZ | 0.118454 | 0.427795 | -0.382053 | 0.128751 | 0.19509 | -0.064926 | 0.282917 | -0.706807 | 0.0151055 | -0.092599 |
| Sample-3-10 | DZ | 0.114886 | -0.351145 | -0.247544 | 0.105198 | -0.175211 | 0.331727 | -0.708564 | -0.334417 | -0.005762 | 0.0540705 |
| Sample-3-11 | DZ | 0.0779559 | -0.270443 | -0.443179 | 0.0538109 | -0.016583 | 0.573295 | -0.393878 | -0.447956 | 0.0302028 | -0.101973 |
| Sample-3-12 | DZ | 0.0922525 | -0.697078 | 0.206044 | -0.084321 | -0.112253 | 0.0838643 | -0.294046 | 0.568081 | -0.040528 | -0.061042 |
| Sample-3-13 | DZ | 0.111451 | -0.225294 | -0.387301 | 0.274338 | 0.329797 | -0.520827 | -0.251508 | -0.492203 | 0.0655812 | 0.0497025 |
| Sample-3-14 | DZ | 0.0554208 | 0.414186 | -0.30887 | 0.344516 | 0.145718 | 0.0304511 | -0.466491 | 0.544913 | -0.058752 | 0.087744 |
| Sample-3-15 | DZ | 0.119831 | -0.541113 | -0.195828 | 0.154042 | 0.356534 | -0.343253 | 0.539163 | -0.239886 | -0.092008 | -0.055767 |
| Sample-3-16 | DZ | 0.131377 | -0.568684 | 0.149481 | -0.000313 | 0.279182 | -0.379381 | -0.471848 | -0.387653 | 0.0543784 | 0.0624258 |
| Sample-3-17 | DZ | 0.0997302 | 0.394403 | -0.431168 | 0.085913 | 0.1513 | -0.161293 | -0.634032 | 0.40709 | 0.0530208 | 0.0416254 |
| Sample-3-18 | DZ | 0.133929 | 0.511418 | -0.26741 | -0.154623 | 0.165728 | -0.100688 | -0.11055 | -0.724137 | 0.0216639 | 0.0425227 |
| Sample-3-19 | DZ | 0.130678 | -0.610967 | 0.187826 | -0.059591 | 0.158659 | -0.159239 | -0.289256 | -0.636733 | -0.003261 | 0.0466776 |
| Sample-3-20 | DZ | 0.116654 | -0.635522 | 0.272296 | 0.0879092 | 0.0973396 | 0.0214458 | 0.67841 | 0.0221605 | 0.0865901 | 0.0684471 |
| Sample-3-21 | DZ | 0.111011 | 0.652699 | -0.185095 | 0.0146614 | -0.058433 | 0.0623331 | 0.228438 | 0.646296 | -0.087882 | 0.0317011 |
| Sample-3-22 | DZ | 0.150395 | 0.322176 | -0.167063 | -0.22312 | 0.264808 | 0.228907 | 0.715061 | -0.37241 | -0.005976 | 0.0268222 |
| Sample-3-23 | DZ | 0.0906478 | -0.426925 | -0.396294 | 0.0303999 | 0.433081 | 0.299352 | -0.489123 | 0.31907 | 0.005452 | -0.05267 |
| Sample-3-24 | DZ | 0.0913699 | -0.450213 | -0.205274 | -0.043158 | -0.364789 | 0.185612 | -0.433548 | -0.611913 | 0.0183675 | -0.027161 |
| Sample-4-1 | XZ | -0.106698 | 0.0155988 | -0.089702 | -0.052302 | -0.040936 | 0.0569257 | -0.228178 | 0.871978 | -0.167876 | -0.20006 |
| Sample-4-2 | XZ | -0.131396 | -0.037108 | 0.006991 | 0.0278656 | -0.150118 | -0.13147 | -0.055683 | -0.848916 | -0.05546 | 0.180952 |
| Sample-4-3 | XZ | -0.112447 | -0.035975 | -0.016165 | 0.132489 | 0.057085 | 0.0027983 | 0.151755 | -0.884378 | -0.095017 | 0.18852 |
| Sample-4-4 | XZ | -0.12643 | -0.047028 | -0.079896 | 0.0197154 | -0.032003 | 0.105665 | -0.082196 | 0.881711 | -0.188858 | 0.146261 |
| Sample-4-5 | XZ | -0.106113 | 0.0742809 | 0.0884396 | -0.010313 | 0.0915473 | -0.006219 | 0.25527 | 0.87306 | -0.097387 | 0.198338 |
| Sample-4-6 | XZ | -0.131462 | -0.061767 | 0.123223 | -0.080903 | -0.012102 | -0.07364 | 0.20592 | 0.844513 | -0.093302 | 0.165818 |
| Sample-4-7 | XZ | -0.138437 | 0.0282444 | 0.0391954 | 0.0413159 | -0.029455 | 0.0412555 | -0.049378 | -0.816269 | 0.118042 | -0.251814 |
| Sample-4-8 | XZ | -0.131622 | 0.0982212 | 0.097783 | -0.036342 | 0.0558485 | -0.083738 | 0.0415111 | 0.846355 | -0.073048 | 0.24755 |
| Sample-4-9 | XZ | -0.127653 | 0.0961611 | -0.000328 | -0.041093 | 0.0900891 | -0.184818 | 0.152353 | 0.869892 | -0.135161 | 0.177591 |
| Sample-4-10 | XZ | -0.142601 | -0.023421 | 0.0256334 | 0.0375477 | 0.0005415 | 0.188649 | 0.109708 | -0.821355 | -0.037207 | -0.17663 |
| Sample-4-11 | XZ | -0.134927 | 0.0032723 | -0.027849 | 0.0855616 | -0.081283 | 0.0179275 | 0.190914 | -0.780413 | -0.091044 | -0.332963 |
| Sample-4-12 | XZ | -0.129141 | -0.048894 | -0.020604 | -0.06155 | 0.0926977 | 5.29E-05 | 0.0057814 | -0.921427 | 0.0651105 | 0.132212 |
| Sample-4-13 | XZ | -0.117067 | -0.008813 | 0.0183068 | 0.0445964 | -0.158574 | -0.045487 | 0.380663 | 0.775255 | -0.076508 | 0.173178 |
| Sample-4-14 | XZ | -0.120201 | 0.160575 | 0.0605885 | 0.137693 | -0.033162 | -0.121426 | -0.217719 | 0.819287 | 0.121727 | -0.274152 |
| Sample-4-15 | XZ | -0.146216 | -0.0417 | 0.113777 | 0.0020373 | 0.0209591 | 0.0751211 | -0.04216 | 0.830952 | 0.0921749 | 0.228176 |
| Sample-4-16 | XZ | -0.137684 | -0.058235 | 0.0069048 | -0.048964 | 0.0546839 | 0.10258 | 0.114805 | 0.85593 | 0.0986703 | -0.224959 |
| Sample-4-17 | XZ | -0.122448 | 0.0291096 | 0.0471156 | 0.034956 | 0.0469505 | -0.113405 | 0.069319 | 0.849921 | -0.049367 | 0.239876 |
| Sample-4-18 | XZ | -0.108317 | 0.0861466 | 0.0643105 | -0.013824 | -0.044256 | 0.0556662 | 0.0087468 | -0.919131 | 0.103495 | -0.140228 |
| Sample-4-19 | XZ | -0.128686 | 0.0134705 | -0.047617 | -0.021405 | -0.10806 | -0.004442 | 0.149481 | -0.912574 | 0.157152 | -0.091563 |
| Sample-4-20 | XZ | -0.133208 | 0.00155 | 0.0282156 | 0.0569932 | 0.120877 | -0.010568 | 0.127989 | 0.862684 | -0.215213 | 0.118607 |
| Sample-4-21 | XZ | -0.12023 | -0.023577 | 0.0419434 | 0.0626138 | 0.0016591 | -0.078273 | 0.1186 | 0.86943 | -0.145887 | 0.209176 |
| Sample-4-22 | XZ | -0.125806 | -0.079495 | -0.018221 | -0.070283 | 0.028681 | 0.0859315 | -0.276723 | -0.878522 | 0.116558 | -0.137132 |
| Sample-4-23 | XZ | -0.124194 | -0.137401 | 0.0559615 | -0.178622 | -0.028178 | 0.102502 | 0.0430262 | 0.849102 | -0.07714 | -0.094077 |
| Sample-4-24 | XZ | -0.144288 | -0.172377 | 0.0175295 | 0.0114941 | -0.015661 | -0.048419 | -0.014806 | -0.808012 | -0.013682 | 0.232078 |
| Sample-4-25 | XZ | -0.143402 | 0.0146192 | 0.0307742 | 0.182757 | -0.042184 | -0.05808 | 0.162777 | 0.849601 | -0.110196 | -0.187777 |
| Sample-4-26 | XZ | -0.139053 | 0.0493422 | -0.020226 | 0.0153169 | 0.075981 | 0.0462318 | 0.0006225 | -0.819677 | -0.148075 | 0.28228 |
| Sample-4-27 | XZ | -0.112038 | -0.019207 | 0.0403113 | -0.065447 | -0.0219 | -0.052015 | -0.179313 | -0.92163 | 0.0238112 | 0.0329466 |
| Sample-4-28 | XZ | -0.141533 | -0.002389 | 0.0241859 | -0.020856 | 0.0312741 | -0.023684 | 0.0092247 | 0.86771 | -0.075793 | 0.246453 |
| Sample-4-29 | XZ | -0.124626 | 0.0221255 | 0.0504477 | -0.064337 | -0.027281 | 0.0081382 | -0.138739 | -0.837446 | 0.0965431 | 0.260782 |
| Sample-4-30 | DZ | 0.0692633 | 0.410028 | -0.441471 | -0.0899042 | -0.154795 | 0.287345 | 0.562852 | -0.393381 | 0.0455105 | -0.0592727 |

**Supplementary Table S5 Differences between DZ and XZ in morphological phenotype, volatile oil content and flavonoids content**

|  |  |  |
| --- | --- | --- |
|  | DZ | XZ |
| weight of fruit/g | 95.46±3.79 | 95.83±11.03 |
| fruit shape index | 1.19±0.01 | 1.18±0.01 |
| moisture content of peel/% | 0.78±0.02 | 0.78±0.01 |
| ratio of abortive seeds/% | 19.52±11.12 | 15.83±9.19 |
| weight of flesh peel/g | 19.28±0.88 | 18.23±1.05 |
| weight of dry peel/g | 4.42±0.34 | 4.74±0.21 |
| dry peel yield peer fruit/% | 4.66±0.36 | 5.08±0.56 |
| thickness of flesh peel/mm | 2.13±0.16 | 2.15±0.17 |
| thickness of dry peel/mm | 0.91±0.08 | 1.01±0.03 |
| secretion cavity diameter/mm | 1.53±0.02 | 1.59±0.03 |
| number of secretion cavity peer field | 11.70±1.74 | 14.70±1.48 |
| volatile oil content of fresh peel/mL/g(DW) | 0.13±0.02 | 0.14±0.02 |
| total flavonoids content/mg/g(DW) | 7.25±0.56 | 6.24±0.90 |
| nobiletin content/mg/g(DW) | 2.91±1.12 | 1.11±0.07 |
| tangeretin content/mg/g(DW) | 5.41±0.67 | 4.30±0.42 |
| hesperidins content/mg/g(DW) | 23.72±2.01 | 15.14±2.38 |

**Supplementary Table S6 Normal temperature aromatic component of *Citrus reticulata* cv. Chachiensis(Note: '-' indicates that the component was not detected in all three repetitions.)**

|  |  |  |  |  |
| --- | --- | --- | --- | --- |
| CAS Number | Chemical Compound | Molecular Formula | Peak Area/% | |
| DZ | XZ |
| 71773-95-0 | (2S)-2-amino-N-ethylpropanamide | C5H12N2O | - | 0.02±0.00 |
| 80-56-8 | alpha-Pinene | C10H16 | 2.39±0.60 | 2.55±0.41 |
| 18172-67-3 | β-Pinene | C10H16 | 1.67±0.26 | 1.69±0.006 |
| 555-10-2 | β-phellandrene | C10H16 | 0.30±0.02 | 0.27±0.03 |
| 123-35-3 | Myrcene | C10H16 | 3.60±0.12 | 3.50±0.15 |
| 99-83-2 | α-phellandrene | C10H16 | 0.13±0.01 | - |
| 99-86-5 | a-Terpin | C10H16 | 0.70±0.13 | 0.70±0.04 |
| 5989-27-5 | d-limonene | C10H16 | 59.80±3.94 | 56.96±2.29 |
| 555-10-2 | β-phellandrene | C10H16 | 0.43±0.03 | 0.40±0.02 |
| 99-85-4 | γ-terpinene | C10H16 | 24.87±2.60 | 25.89±0.87 |
| 527-84-4 | o-Cymene | C10H14 | 1.18±0.10 | 1.48±0.34 |
| 29050-33-7 | δ-4-carene | C10H16 | 2.06±0.34 | 2.10±0.17 |
| 3681-71-8 | Leaf acetate | C8H14O2 | - | 0.05±0.03 |
| 15537-55-0 | sabinene hydrate | C10H18O | 0.06±0.02 | 0.06±0.01 |
| 3856-25-5 | α-copaene | C15H24 | - | 0.11±0.04 |
| 112-31-2 | decanal | C10H20O | 0.13±0.06 | 0.08±0.02 |
| 78-70-6 | linalool | C10H18O | 0.12±0.02 | 0.08±0.01 |
| 29803-81-4 | 2-Cyclohexen-1-ol, 1-methyl-4-(1-methylethyl)-, trans- | C10H18O | 0.08±0.03 | 0.08±0.01 |
| 87-44-5 | (-)-β-caryophyllene | C15H24 | 0.30±0.14 | 0.53±0.11 |
| 562-74-3 | 4-terpineol | C10H18O | 0.10±0.03 | 0.12±0.02 |
| 98-55-5 | α-terpineol | C10H18O | 0.24±0.09 | 0.34±0.04 |
| 502-61-4 | (E,E)-α-farnesene | C15H24 | 0.27±0.29 | 0.35±0.10 |
| 523-47-7 | b-Cadinene | C15H24 | - | 0.04±0.02 |
| 85-91-6 | Methyl 2-(methylamino)benzoate | C9H11NO2 | 0.80±0.01 | 2.12±0.67 |

**Supplementary Table S7 Volatile oil components of *Citrus reticulata* cv. Chachiensis(Note: '-' indicates that the component was not detected in all three repetitions.)**

|  |  |  |  |  |
| --- | --- | --- | --- | --- |
| CAS Number | Molecular Formula | Chemical  Compound | Peak Area/% | |
| DZ | XZ |
| 123-35-3 | .beta.-Myrcene | C10H16 | 3.77±0.14 | 3.83±0.09 |
| 29050-33-7 | (+)-4-Carene | C10H16 | 0.76±0.08 | 0.97±0.07 |
| 5989-27-5 | D-Limonene | C10H16 | 61.82±1.62 | 57.41±1.67 |
| 555-10-2 | .beta.-Phellandrene | C10H16 | 0.50±0.01 | 0.50±0.01 |
| 99-85-4 | .gamma.-Terpinene | C10H16 | 22.65±0.58 | 23.70±0.62 |
| 527-84-4 | o-Cymene | C10H14 | - | 2.42±0.25 |
| 586-62-9 | Terpinolene | C10H16 | 1.74±0.12 | 2.02±0.09 |
| 768-49-0 | Benzene, (2-methyl-1-propenyl)- | C10H12 | - | 0.01±0.01 |
| 18368-95-1 | 1,3,8-p-Menthatriene | C10H14 | - | 0.01±0.01 |
| 1195-92-2 | 7-Oxabicyclo[4.1.0]heptane, 1-methyl-4-(1-methylethenyl)- | C10H16O | 0.02±0.01 | 0.01±0.00 |
| 6909-30-4 | (+)-(E)-Limonene oxide | C10H16O | 0.02±0.01 | - |
| 2385-77-5 | 6-Octenal, 3,7-dimethyl-, (R)- | C10H18O | 0.03±0.01 | - |
| 3856-25-5 | Copaene | C15H24 | 0.04±0.01 | 0.03±0.01 |
| 112-31-2 | Decanal | C10H20O | 0.19±0.07 | 0.15±0.03 |
| 13744-15-5 | 1H-Cyclopenta[1,3]cyclopropa[1,2]benzene, octahydro-7-methyl-3-methylene-4-(1-methylethyl)-, [3aS-(3a.alpha.,3b.beta.,4.beta.,7 | C15H24 | 0.02±0.01 | 0.02±0.01 |
| 78-70-6 | 1,6-Octadien-3-ol, 3,7-dimethyl- | C10H18O | 0.13±0.03 | 0.14±0.02 |
| 29803-81-4 | 2-Cyclohexen-1-ol, 1-methyl-4-(1-methylethyl)-, trans- | C10H18O | 0.01±0.00 | 0.01±0.00 |
| 515-13-9 | Cyclohexane, 1-ethenyl-1-methyl-2,4-bis(1-methylethenyl)-, [1S-(1. alpha., 2. beta.,4. beta.)]- | C15H24 | - | 0.01±0.00 |
| 31574-44-4 | Benzene, 1-methoxy-4-methyl-2-(1-methylethyl)- | C11H16O | - | 0.01±0.00 |
| 87-44-5 | Caryophyllene | C15H24 | 0.23±0.01 | 0.18±0.02 |
| 20126-76-5 | 3-Cyclohexen-1-ol, 4-methyl-1-(1-methylethyl)-, (R)- | C10H18O | 0.33±0.04 | 0.49±0.18 |
|  | trans-p-Mentha-2,8-dienol | C10H16O | 0.02±0.00 | - |
| 6753-98-6 | Humulene | C15H24 | 0.03±0.00 | 0.02±0.00 |
| 3886-78-0 | cis-p-Mentha-2,8-dien-1-ol | C10H16O | 0.01±0.00 | - |
| 98-55-5 | .alpha.-Terpineol | C10H18O | 0.39±0.05 | 0.66±0.25 |
| 112-54-9 | Dodecanal | C12H24O | - | 0.06±0.01 |
| 17699-05-7 | Bicyclo[3.1.1]hept-2-ene, 2,6-dimethyl-6-(4-methyl-3-pentenyl)- | C15H24 | 0.08±0.01 | 0.06±0.01 |
| 6485-40-1 | (-)-Carvone | C10H14O | 0.03±0.01 | 0.02±0.01 |
| 502-61-4 | .alpha.-Farnesene | C15H24 | 0.41±0.06 | 0.35±0.07 |
| 483-76-1 | Naphthalene, 1,2,3,5,6,8a-hexahydro-4,7-dimethyl-1-(1-methylethyl)-, (1S-cis)- | C15H24 | 0.07±0.01 | 0.06±0.01 |
| 106-22-9 | Citronellol | C10H20O | 0.06±0.01 | 0.06±0.01 |
| 2111-75-3 | 1-Cyclohexene-1-carboxaldehyde, 4-(1-methylethenyl)- | C10H14O | 0.10±0.01 | - |
| 106-25-2 | 2,6-Octadien-1-ol, 3,7-dimethyl-, (Z)- | C10H18O | - | 0.02±0.01 |
| 50764-55-1 | Bicyclo[3.1.1]hept-2-en-6-ol, 2,7,7-trimethyl-, acetate, [1S-(1.alpha.,5.alpha.,6.beta.)]- | C12H18O2 | 0.02±0.00 | 0.02±0.01 |
| 1197-06-4 | 2-Cyclohexen-1-ol, 2-methyl-5-(1-methylethenyl)-, cis- | C10H16O | 0.02±0.00 | 0.02±0.01 |
| 1197-01-9 | Benzenemethanol, .alpha.,.alpha.,4-trimethyl- | C10H14O | 0.01±0.01 | - |
| 4826-62-4 | 2-Dodecenal | C12H22O | 0.04±0.01 | 0.03±0.01 |
| 99-48-9 | Carveol | C10H16O | 0.01±0.00 | 0.01±0.00 |
| 124-25-4 | Tetradecanal | C14H28O | 0.01±0.00 | - |
| 29548-13-8 | p-Mentha-1(7),8(10)-dien-9-ol | C10H16O | 0.01±0.00 | 0.01±0.01 |
| 536-59-4 | 1-Cyclohexene-1-methanol, 4-(1-methylethenyl)- | C10H16O | - | 0.01±0.01 |
| 85-91-6 | Methyl 2-(methylamino)benzoate | C9H11NO2 | 2.34±0.52 | 2.44±0.39 |
| 639-99-6 | Cyclohexanemethanol, 4-ethenyl-.alpha.,.alpha.,4-trimethyl-3-(1-methylethenyl)-, [1R-(1.alpha.,3.alpha.,4.beta.)]- | C15H26O | - | 0.01±0.00 |
| 147254-33-9 | 2(3H)-Furanone, 5-hexyldihydro-4-methyl-, trans- | C11H20O2 | 0.01±0.00 | - |
| 89-83-8 | Thymol | C10H14O | 0.10±0.04 | 0.07±0.01 |
| 88034-74-6 | Bergamotol, Z-.alpha.-trans- | C15H24O | 0.02±0.00 | - |
| 17909-77-2 | 2,6,9,11-Dodecatetraenal, 2,6,10-trimethyl-, (E,E,E)- | C15H22O | 0.41±0.08 | 0.27±0.01 |