| **Gene name and annotation** | **Average Coverage** | **Average Length** | **Reason For Exclusion** | **Final Aligned Length** | **Final Aligned PI sites** |
| --- | --- | --- | --- | --- | --- |
| GSMUA\_Achr1T00810\_001\_40S\_ribosomal\_protein\_S17:0-438 | 51.2369 | 355 | BLAST | NA | NA |
| GSMUA\_Achr1T05180\_001\_Cell\_division\_protease\_ftsH\_homolog\_5\_mitochondrial:738-1215 | 20.9064 | 272 | BLAST | NA | NA |
| GSMUA\_Achr1T12760\_001\_NADH\_dehydrogenase\_ubiquinone\_flavoprotein\_1\_mitochondrial:375-1476 | 58.757 | 324 | BLAST | NA | NA |
| GSMUA\_Achr1T16990\_001\_40S\_ribosomal\_protein\_S10:331-614 | 29.5233 | 256 | BLAST | NA | NA |
| GSMUA\_Achr1T18800\_001\_Threonyl-tRNA\_synthetase\_mitochondrial:1095-1317 | 23.7382 | 245 | BLAST | NA | NA |
| GSMUA\_Achr1T21900\_001\_60S\_ribosomal\_protein\_L27a-3:0-243 | 38.0711 | 292 | BLAST | NA | NA |
| GSMUA\_Achr2T01220\_001\_30S\_ribosomal\_protein\_3\_chloroplastic:378-657 | 42.6104 | 335 | BLAST | NA | NA |
| GSMUA\_Achr2T01640\_001\_40S\_ribosomal\_protein\_S4:498-936 | 39.1549 | 330 | BLAST | NA | NA |
| GSMUA\_Achr2T08960\_001\_Hypothetical\_protein:0-525 | 36.6441 | 258 | BLAST | NA | NA |
| GSMUA\_Achr2T16990\_001\_ADPATP\_carrier\_protein\_1\_chloroplastic:639-906 | 35.7079 | 307 | BLAST | NA | NA |
| GSMUA\_Achr2T21060\_001\_Isocitrate\_dehydrogenase\_NAD\_regulatory\_subunit\_1\_mitochondrial:516-756 | 24.6677 | 265 | BLAST | NA | NA |
| GSMUA\_Achr2T22080\_001\_40S\_ribosomal\_protein\_S16:0-210 | 25.2083 | 227 | BLAST | NA | NA |
| GSMUA\_Achr3T01440\_001\_60S\_ribosomal\_protein\_L26-2:0-462 | 45.886 | 288 | BLAST | NA | NA |
| GSMUA\_Achr3T20140\_001\_transposon\_protein\_putative\_CACTA\_En\_Spm\_sub-class\_expressed:0-290 | 33.1032 | 260 | BLAST | NA | NA |
| GSMUA\_Achr3T26310\_001\_Glycine\_dehydrogenase\_decarboxylating\_mitochondrial:0-677 | 42.7956 | 295 | BLAST | NA | NA |
| GSMUA\_Achr4T00030\_001\_Glycyl-tRNA\_synthetase\_1\_mitochondrial:960-1366 | 37.2716 | 308 | BLAST | NA | NA |
| GSMUA\_Achr4T04240\_001\_60S\_ribosomal\_protein\_L23:13-298 | 39.2681 | 274 | BLAST | NA | NA |
| GSMUA\_Achr4T08480\_001\_Cell\_division\_protease\_ftsH\_homolog\_11\_chloroplastic\_mitochondrial:1830-2112 | 22.7986 | 216 | BLAST | NA | NA |
| GSMUA\_Achr4T11890\_001\_calcium-binding\_mitochondrial\_protein\_anon-60Da\_putative\_expressed:1436-1608 | 32.1168 | 318 | BLAST | NA | NA |
| GSMUA\_Achr4T19830\_001\_Heat\_shock\_70\_kDa\_protein\_mitochondrial:798-1419 | 23.7254 | 217 | BLAST | NA | NA |
| GSMUA\_Achr4T26620\_001\_60S\_ribosomal\_protein\_L21-1:0-237 | 30.3798 | 345 | BLAST | NA | NA |
| GSMUA\_Achr5T00710\_001\_Putative\_aconitate\_hydratase\_cytoplasmic:2085-2565 | 62.8748 | 461 | BLAST | NA | NA |
| GSMUA\_Achr5T01070\_001\_60S\_ribosomal\_protein\_L3:501-911 | 48.9493 | 301 | BLAST | NA | NA |
| GSMUA\_Achr5T17120\_001\_Cysteine\_synthase\_chloroplastic\_chromoplastic:387-651 | 43.3195 | 341 | BLAST | NA | NA |
| GSMUA\_Achr5T18740\_001\_60S\_ribosomal\_protein\_L8:440-786 | 70.1945 | 403 | BLAST | NA | NA |
| GSMUA\_Achr6T06280\_001\_60S\_ribosomal\_protein\_L27a-3:123-531 | 40.7298 | 315 | BLAST | NA | NA |
| GSMUA\_Achr6T31150\_001\_60S\_ribosomal\_protein\_L15:247-414 | 29.4814 | 262 | BLAST | NA | NA |
| GSMUA\_Achr7T00810\_001\_Succinate\_dehydrogenase\_ubiquinone\_flavoprotein\_subunit\_mitochondrial:934-1122 | 23.0254 | 315 | BLAST | NA | NA |
| GSMUA\_Achr7T05470\_001\_Cytochrome\_c1-1\_heme\_protein\_mitochondrial:278-558 | 34.273 | 258 | BLAST | NA | NA |
| GSMUA\_Achr7T24720\_001\_Pyruvate\_kinase\_isozyme\_G\_chloroplastic:1167-1343 | 41.5436 | 268 | BLAST | NA | NA |
| GSMUA\_Achr7T25110\_001\_60S\_ribosomal\_protein\_L27-3:0-408 | 36.2971 | 270 | BLAST | NA | NA |
| GSMUA\_Achr8T01550\_001\_60S\_ribosomal\_protein\_L10:10-512 | 47.95 | 368 | BLAST | NA | NA |
| GSMUA\_Achr8T06120\_001\_50S\_ribosomal\_protein\_L3-1\_chloroplastic:0-379 | 26.2331 | 226 | BLAST | NA | NA |
| GSMUA\_Achr8T09450\_001\_Putative\_Solute\_carrier\_family\_35\_member\_E1:369-828 | 40.8934 | 327 | BLAST | NA | NA |
| GSMUA\_Achr8T18300\_001\_60S\_ribosomal\_protein\_L26-2:0-462 | 45.8681 | 285 | BLAST | NA | NA |
| GSMUA\_Achr8T23840\_001\_60S\_ribosomal\_protein\_L12:0-501 | 57.881 | 412 | BLAST | NA | NA |
| GSMUA\_Achr8T30200\_001\_40S\_ribosomal\_protein\_S9-2:28-410 | 29.1247 | 274 | BLAST | NA | NA |
| GSMUA\_Achr9T07000\_001\_Hypothetical\_protein:625-878 | 36.4 | 250 | BLAST | NA | NA |
| GSMUA\_Achr9T20320\_001\_60S\_ribosomal\_protein\_L19-2:235-549 | 49.511 | 364 | BLAST | NA | NA |
| GSMUA\_Achr9T21710\_001\_ATP\_synthase\_subunit\_beta\_mitochondrial:1017-1242 | 49.0334 | 580 | BLAST | NA | NA |
| GSMUA\_Achr9T21710\_001\_ATP\_synthase\_subunit\_beta\_mitochondrial:1242-1554 | 46.236 | 437 | BLAST | NA | NA |
| GSMUA\_Achr9T21710\_001\_ATP\_synthase\_subunit\_beta\_mitochondrial:858-1017 | 28.3174 | 276 | BLAST | NA | NA |
| GSMUA\_Achr9T22420\_001\_Chaperone\_protein\_ClpB\_2:1410-2340 | 31.2425 | 275 | BLAST | NA | NA |
| GSMUA\_Achr9T30160\_001\_Ubiquitin-60S\_ribosomal\_protein\_L40:0-234 | 49.0379 | 296 | BLAST | NA | NA |
| GSMUA\_Achr10T10700\_001\_Protease\_Do-like\_10\_mitochondrial:610-806 | 43.2479 | 298 | BLAST | NA | NA |
| GSMUA\_Achr10T12900\_001\_60S\_ribosomal\_protein\_L10:10-512 | 56.3963 | 410 | BLAST | NA | NA |
| GSMUA\_Achr10T14230\_001\_Putative\_mitochondrial\_2-oxoglutarate\_malate\_carrier\_protein:269-631 | 44.1061 | 279 | BLAST | NA | NA |
| GSMUA\_Achr10T19100\_001\_ribosomal\_protein\_L23\_family\_protein\_putative\_expressed:0-484 | 40.8498 | 304 | BLAST | NA | NA |
| GSMUA\_Achr11T00740\_001\_60S\_ribosomal\_protein\_L8:152-498 | 61.5246 | 408 | BLAST | NA | NA |
| GSMUA\_Achr11T02700\_001\_40S\_ribosomal\_protein\_S17:0-426 | 56.1486 | 377 | BLAST | NA | NA |
| GSMUA\_Achr11T08740\_001\_Succinate\_dehydrogenase\_ubiquinone\_iron-sulfur\_subunit\_2\_mitochondrial:0-683 | 32.2105 | 282 | BLAST | NA | NA |
| GSMUA\_Achr11T09050\_001\_60S\_ribosomal\_protein\_L3:501-911 | 56.0026 | 318 | BLAST | NA | NA |
| GSMUA\_Achr11T10220\_001\_Putative\_mitochondrial\_2-oxoglutarate-malate\_carrier\_protein:266-628 | 37.0433 | 316 | BLAST | NA | NA |
| GSMUA\_Achr11T16110\_001\_Probable\_NADH\_dehydrogenase\_ubiquinone\_1\_alpha\_subcomplex\_subunit\_5\_mitochondrial:0-340 | 47.3632 | 356 | BLAST | NA | NA |
| GSMUA\_Achr11T22610\_001\_60S\_ribosomal\_protein\_L8:0-440 | 35.0194 | 305 | BLAST | NA | NA |
| GSMUA\_AchrUn\_randomT00030\_001\_Ubiquitin-40S\_ribosomal\_protein\_S27a-1:0-474 | 66.8384 | 367 | BLAST | NA | NA |
| GSMUA\_AchrUn\_randomT03040\_001\_Cell\_division\_protease\_ftsH\_homolog\_2\_chloroplastic:522-836 | 39.6379 | 321 | BLAST | NA | NA |
| GSMUA\_AchrUn\_randomT08730\_001\_RuBisCO\_large\_subunit-binding\_protein\_subunit\_alpha\_chloroplastic:994-1446 | 39.6211 | 403 | BLAST | NA | NA |
| GSMUA\_AchrUn\_randomT10300\_001\_protein\_kinase\_APK1B\_chloroplast\_precursor\_putative\_expressed:706-1098 | 36.3959 | 269 | BLAST | NA | NA |
| GSMUA\_AchrUn\_randomT18700\_001\_Cell\_division\_protease\_ftsH\_homolog\_8\_mitochondrial:1032-1800 | 48.9364 | 344 | BLAST | NA | NA |
| GSMUA\_AchrUn\_randomT22440\_001\_ATP-dependent\_Clp\_protease\_ATP-binding\_subunit\_clpC\_homolog\_chloroplastic:2937-3177 | 33.2733 | 228 | BLAST | NA | NA |
| GSMUA\_AchrUn\_randomT26360\_001\_ATP\_synthase\_subunit\_beta\_mitochondrial:1305-1656 | 51.2105 | 454 | BLAST | NA | NA |
| GSMUA\_AchrUn\_randomT28100\_001\_Chlorophyll\_a-b\_binding\_protein\_CP29.2\_chloroplastic:69-441 | 24.1654 | 242 | BLAST | NA | NA |
| GSMUA\_Achr6T22780\_001\_Maturase\_K:0-459 | 906.101 | 339 | high coverage | NA | NA |
| GSMUA\_Achr6T36680\_001\_NADPH-quinone\_oxidoreductase\_subunit\_H\_chloroplastic:144-762:0 | 976.63 | 265 | high coverage | NA | NA |
| GSMUA\_Achr6T36680\_001\_NADPH-quinone\_oxidoreductase\_subunit\_H\_chloroplastic:144-762:3 | 1696.92 | 326 | high coverage | NA | NA |
| GSMUA\_Achr10T02890\_001\_Hypothetical\_protein:0-252 | 479.839 | 237 | high coverage | NA | NA |
| GSMUA\_Achr11T15530\_001\_50S\_ribosomal\_protein\_L22\_chloroplastic:0-390 | 1410.99 | 381 | high coverage | NA | NA |
| GSMUA\_AchrUn\_randomT03080\_001\_Ribosomal\_protein\_S12\_mitochondrial:0-378 | 249.096 | 276 | high coverage | NA | NA |
| GSMUA\_AchrUn\_randomT05630\_001\_NADH-ubiquinone\_oxidoreductase\_27\_kDa\_subunit:0-573 | 556.039 | 573 | high coverage | NA | NA |
| GSMUA\_AchrUn\_randomT10060\_001\_60S\_ribosomal\_protein\_L2\_mitochondrial:863-1317 | 306.494 | 460 | high coverage | NA | NA |
| GSMUA\_AchrUn\_randomT10070\_001\_Ribosomal\_protein\_S19\_mitochondrial:0-279 | 242.879 | 366 | high coverage | NA | NA |
| GSMUA\_AchrUn\_randomT10550\_001\_Apocytochrome\_f:517-786 | 675.16 | 242 | high coverage | NA | NA |
| GSMUA\_AchrUn\_randomT15230\_001\_ATP\_synthase\_subunit\_alpha\_mitochondrial:841-1426 | 232.038 | 273 | high coverage | NA | NA |
| GSMUA\_AchrUn\_randomT15230\_001\_ATP\_synthase\_subunit\_alpha\_mitochondrial:86-841 | 574.525 | 564 | high coverage | NA | NA |
| GSMUA\_AchrUn\_randomT21760\_001\_ATP\_synthase\_subunit\_b\_chloroplastic:0-267 | 912.333 | 280 | high coverage | NA | NA |
| GSMUA\_AchrUn\_randomT21780\_001\_Hypothetical\_protein:0-322 | 199.754 | 181 | high coverage | NA | NA |
| GSMUA\_AchrUn\_randomT21780\_001\_Hypothetical\_protein:14271-15628 | 306.993 | 203 | high coverage | NA | NA |
| GSMUA\_AchrUn\_randomT21780\_001\_Hypothetical\_protein:322-550 | 1390.89 | 263 | high coverage | NA | NA |
| GSMUA\_AchrUn\_randomT21780\_001\_Hypothetical\_protein:550-14271 | 2951.5 | 445 | high coverage | NA | NA |
| GSMUA\_AchrUn\_randomT21790\_001\_Photosystem\_I\_P700\_chlorophyll\_a\_apoprotein\_A1:0-196 | 876.13 | 221 | high coverage | NA | NA |
| GSMUA\_AchrUn\_randomT21790\_001\_Photosystem\_I\_P700\_chlorophyll\_a\_apoprotein\_A1:196-558 | 2860.15 | 372 | high coverage | NA | NA |
| GSMUA\_AchrUn\_randomT29040\_001\_NADPH-quinone\_oxidoreductase\_subunit\_I\_chloroplastic:0-369 | 1767.9 | 372 | high coverage | NA | NA |
| GSMUA\_Achr5T17250\_001\_Protein\_transport\_protein\_Sec61\_subunit\_alpha:0-344:[0-9][0-9]- | 36.5085 | 364 | introduced frame shift | NA | NA |
| GSMUA\_Achr5T17250\_001\_Protein\_transport\_protein\_Sec61\_subunit\_alpha:0-344:[0-9][0-9][0-9]-344 | 45.9691 | 323 | introduced frame shift | NA | NA |
| GSMUA\_Achr5T17250\_001\_Protein\_transport\_protein\_Sec61\_subunit\_alpha:1188-1428 | 27.8343 | 254 | introduced frame shift | NA | NA |
| GSMUA\_Achr5T17250\_001\_Protein\_transport\_protein\_Sec61\_subunit\_alpha:572-927 | 51.1876 | 427 | introduced frame shift | NA | NA |
| GSMUA\_Achr1T20200\_001\_Actin-1:364-978 | 29.6714 | 341 | skewed tree length | NA | NA |
| GSMUA\_Achr1T22900\_001\_Sulfite\_reductase\_ferredoxin:174-951 | 19.8652 | 264 | skewed tree length | NA | NA |
| GSMUA\_Achr1T28070\_001\_Putative\_Importin\_subunit\_beta-1:0-856 | 28.608 | 244 | skewed tree length | NA | NA |
| GSMUA\_Achr1T28070\_001\_Putative\_Importin\_subunit\_beta-1:856-2324 | 46.5931 | 338 | skewed tree length | NA | NA |
| GSMUA\_Achr2T02040\_001\_Dihydrolipoyl\_dehydrogenase\_mitochondrial:246-785 | 48.0778 | 329 | skewed tree length | NA | NA |
| GSMUA\_Achr2T02040\_001\_Dihydrolipoyl\_dehydrogenase\_mitochondrial:785-1407 | 39.0781 | 282 | skewed tree length | NA | NA |
| GSMUA\_Achr2T03830\_001\_Hypothetical\_protein:209-411 | 44.4746 | 305 | skewed tree length | NA | NA |
| GSMUA\_Achr2T12390\_001\_Tubulin\_alpha-3\_chain:1037-1353 | 48.4475 | 334 | skewed tree length | NA | NA |
| GSMUA\_Achr2T14040\_001\_Thiazole\_biosynthetic\_enzyme\_chloroplastic:0-375 | 22.3311 | 250 | skewed tree length | NA | NA |
| GSMUA\_Achr2T14200\_001\_Ribose-phosphate\_pyrophosphokinase\_3:68-384 | 26.6951 | 316 | skewed tree length | NA | NA |
| GSMUA\_Achr3T00530\_001\_Putative\_Ubiquilin-1:241-1015 | 26.8965 | 277 | skewed tree length | NA | NA |
| GSMUA\_Achr3T01410\_001\_DEAD-box\_ATP-dependent\_RNA\_helicase\_21:501-999 | 33.1532 | 289 | skewed tree length | NA | NA |
| GSMUA\_Achr3T04890\_001\_LRR\_receptor-like\_Serine-threonine-protein\_kinase\_FEI\_1:850-1183 | 23.8483 | 264 | skewed tree length | NA | NA |
| GSMUA\_Achr3T08780\_001\_Putative\_4-alpha-glucanotransferase:1473-1716 | 30.3487 | 328 | skewed tree length | NA | NA |
| GSMUA\_Achr3T18630\_001\_ATP-dependent\_Clp\_protease\_ATP-binding\_subunit\_clpA\_homolog\_CD4B\_chloroplastic:1011-1227 | 25.9992 | 385 | skewed tree length | NA | NA |
| GSMUA\_Achr4T27850\_001\_Nuclear\_transcription\_factor\_Y\_subunit\_B-3:0-386 | 72.3659 | 407 | skewed tree length | NA | NA |
| GSMUA\_Achr5T03620\_001\_6-phosphogluconate\_dehydrogenase\_decarboxylating:221-1170 | 36.1793 | 323 | skewed tree length | NA | NA |
| GSMUA\_Achr5T08520\_001\_Clathrin\_heavy\_chain\_1:2891-3894 | 57.7728 | 760 | skewed tree length | NA | NA |
| GSMUA\_Achr5T08970\_001\_Putative\_Speckle-type\_POZ\_protein:0-401 | 45.8869 | 360 | skewed tree length | NA | NA |
| GSMUA\_Achr5T14620\_001\_Hypothetical\_protein:0-172 | 36.0912 | 288 | skewed tree length | NA | NA |
| GSMUA\_Achr5T28260\_001\_Putative\_Zinc\_finger\_CCCH\_domain-containing\_protein\_66:70-1086 | 53.6057 | 378 | skewed tree length | NA | NA |
| GSMUA\_Achr6T12250\_001\_26S\_protease\_regulatory\_subunit\_6B\_homolog:150-381 | 47.9889 | 313 | skewed tree length | NA | NA |
| GSMUA\_Achr6T36390\_001\_Chitinase-like\_protein\_1:0-679 | 35.1145 | 292 | skewed tree length | NA | NA |
| GSMUA\_Achr7T08250\_001\_Putative\_Probable\_disease\_resistance\_protein\_At4g33300:1083-1439 | 28.0946 | 319 | skewed tree length | NA | NA |
| GSMUA\_Achr7T24390\_001\_Eukaryotic\_translation\_initiation\_factor\_1A:0-435 | 57.0108 | 330 | skewed tree length | NA | NA |
| GSMUA\_Achr8T00950\_001\_UDP-glucuronate\_4-epimerase\_6:606-1332 | 38.0426 | 309 | skewed tree length | NA | NA |
| GSMUA\_Achr9T01620\_001\_Serine\_hydroxymethyltransferase\_2:0-678 | 56.3328 | 387 | skewed tree length | NA | NA |
| GSMUA\_Achr9T03520\_001\_26S\_proteasome\_non-ATPase\_regulatory\_subunit\_14:130-308 | 32.4236 | 272 | skewed tree length | NA | NA |
| GSMUA\_Achr9T29870\_001\_ABC\_transporter\_F\_family\_member\_4:963-1448 | 32.5227 | 282 | skewed tree length | NA | NA |
| GSMUA\_Achr10T23290\_001\_serine-threonine-protein\_kinase\_HT1\_putative\_expressed:0-899 | 28.3207 | 248 | skewed tree length | NA | NA |
| GSMUA\_Achr10T29540\_001\_Formate-tetrahydrofolate\_ligase:312-524 | 38.0574 | 283 | skewed tree length | NA | NA |
| GSMUA\_Achr10T29540\_001\_Formate-tetrahydrofolate\_ligase:524-1359 | 43.6662 | 366 | skewed tree length | NA | NA |
| GSMUA\_Achr11T10020\_001\_Heat\_shock\_protein\_81-3:918-1398 | 43.5256 | 361 | skewed tree length | NA | NA |
| GSMUA\_Achr11T17170\_001\_HEAT\_repeat\_family\_protein\_putative\_expressed:1777-3543 | 20.1884 | 271 | skewed tree length | NA | NA |
| GSMUA\_Achr11T19070\_001\_Putative\_Basic\_leucine\_zipper\_and\_W2\_domain-containing\_protein\_2:501-995 | 26.6537 | 277 | skewed tree length | NA | NA |
| GSMUA\_Achr11T22900\_001\_Ubiquitin-fold\_modifier-conjugating\_enzyme\_1:0-395 | 33.1192 | 301 | skewed tree length | NA | NA |
| GSMUA\_AchrUn\_randomT06180\_001\_Tubulin\_beta-7\_chain:696-978 | 83.4275 | 318 | skewed tree length | NA | NA |
| GSMUA\_Achr1T00220\_001\_DEAD-box\_ATP-dependent\_RNA\_helicase\_6:804-1056 | 19.553 | 234 |  | 170 | 50 |
| GSMUA\_Achr1T02360\_001\_Probable\_aquaporin\_PIP2-6:0-292 | 38.8117 | 352 |  | 230 | 77 |
| GSMUA\_Achr1T04330\_001\_Coatomer\_subunit\_alpha-2:1590-2131 | 25.7 | 289 |  | 158 | 53 |
| GSMUA\_Achr1T07110\_001\_ZOS9-17-C2H2\_zinc\_finger\_protein\_expressed:225-674 | 57.4104 | 354 |  | 263 | 42 |
| GSMUA\_Achr1T07620\_001\_Endoplasmin\_homolog:1779-2184:0123 | 31.1818 | 278 |  | 380 | 109 |
| GSMUA\_Achr1T07620\_001\_Endoplasmin\_homolog:1779-2184:1516 | 42.769 | 289 | merged | NA | NA |
| GSMUA\_Achr1T07700\_001\_Lon\_protease\_homolog\_2\_peroxisomal:1523-1737 | 19.619 | 282 |  | 170 | 58 |
| GSMUA\_Achr1T08940\_001\_4-hydroxy-3-methylbut-2-en-1-yl\_diphosphate\_synthase:783-1014 | 52.1309 | 366 |  | 230 | 66 |
| GSMUA\_Achr1T09070\_001\_Phenylalanine\_ammonia-lyase:389-1773 | 28.6982 | 300 |  | 167 | 44 |
| GSMUA\_Achr1T10100\_001\_Putative\_Transmembrane\_9\_superfamily\_member\_4:771-1077 | 41.9114 | 376 |  | 245 | 71 |
| GSMUA\_Achr1T10550\_001\_26S\_proteasome\_non-ATPase\_regulatory\_subunit\_1:1470-1691 | 40.2234 | 342 |  | 464 | 142 |
| GSMUA\_Achr1T10550\_001\_26S\_proteasome\_non-ATPase\_regulatory\_subunit\_1:2183-2700 | 42.6733 | 393 | merged | NA | NA |
| GSMUA\_Achr1T12930\_001\_S-adenosylmethionine\_synthase\_1:216-1407 | 32.1281 | 329 |  | 194 | 62 |
| GSMUA\_Achr1T13970\_001\_Protease\_Do-like\_1\_chloroplastic:773-972 | 30.2061 | 278 |  | 170 | 43 |
| GSMUA\_Achr1T14710\_001\_T-complex\_protein\_1\_subunit\_zeta:936-1141 | 24.5045 | 278 |  | 161 | 43 |
| GSMUA\_Achr1T14740\_001\_Cullin-1:240-426 | 32.6784 | 317 |  | 170 | 44 |
| GSMUA\_Achr1T19130\_001\_Putative\_uncharacterized\_protein\_Sb07g010440:6562-7845:4 | 28.1556 | 380 |  | 497 | 133 |
| GSMUA\_Achr1T19130\_001\_Putative\_uncharacterized\_protein\_Sb07g010440:6562-7845:89 | 24.6845 | 406 | merged | NA | NA |
| GSMUA\_Achr1T19130\_001\_Putative\_uncharacterized\_protein\_Sb07g010440:9120-9525 | 23.8067 | 369 | merged | NA | NA |
| GSMUA\_Achr1T22920\_001\_Probable\_cellulose\_synthase\_A\_catalytic\_subunit\_8\_UDP-forming:974-1320 | 45.401 | 336 |  | 218 | 54 |
| GSMUA\_Achr1T24870\_001\_DEAD-box\_ATP-dependent\_RNA\_helicase\_24:1215-1518 | 51.4165 | 328 |  | 356 | 107 |
| GSMUA\_Achr1T24870\_001\_DEAD-box\_ATP-dependent\_RNA\_helicase\_24:442-1134 | 28.8221 | 250 | merged | NA | NA |
| GSMUA\_Achr1T25100\_001\_heat\_shock\_protein\_binding\_protein\_putative\_expressed:510-728 | 25.8312 | 373 |  | 383 | 105 |
| GSMUA\_Achr1T25100\_001\_heat\_shock\_protein\_binding\_protein\_putative\_expressed:728-906 | 33.9745 | 380 | merged | NA | NA |
| GSMUA\_Achr1T25530\_001\_Probable\_pyridoxal\_biosynthesis\_protein\_PDX1.1:0-675 | 30.9489 | 360 |  | 308 | 91 |
| GSMUA\_Achr1T27340\_001\_Uncharacterized\_urease\_accessory\_protein\_ureG-like:321-523 | 37.2262 | 330 |  | 203 | 62 |
| GSMUA\_Achr2T01410\_001\_Tubulin\_beta-1\_chain:559-1035 | 67.8319 | 547 |  | 362 | 114 |
| GSMUA\_Achr2T01660\_001\_ATKINESIN-13A\_KINESIN-13A\_putative\_expressed:1001-1331 | 29.7017 | 253 |  | 188 | 61 |
| GSMUA\_Achr2T01800\_001\_T-complex\_protein\_1\_subunit\_beta:635-1121 | 49.857 | 320 |  | 230 | 75 |
| GSMUA\_Achr2T01990\_001\_Protein\_translocase\_subunit\_secA\_chloroplastic:657-876 | 33.9486 | 288 |  | 191 | 43 |
| GSMUA\_Achr2T03840\_001\_Pyruvate\_kinase\_cytosolic\_isozyme:489-1035 | 42.3664 | 251 |  | 173 | 50 |
| GSMUA\_Achr2T04510\_001\_Mannosyl-oligosaccharide\_12-alpha-mannosidase\_MNS1:1320-1491 | 29.0354 | 252 |  | 161 | 49 |
| GSMUA\_Achr2T05230\_001\_Pre-mRNA-processing-splicing\_factor\_8:2301-2606 | 30.9451 | 322 |  | 1592 | 414 |
| GSMUA\_Achr2T05230\_001\_Pre-mRNA-processing-splicing\_factor\_8:3852-4106 | 32.9062 | 310 | merged | NA | NA |
| GSMUA\_Achr2T05230\_001\_Pre-mRNA-processing-splicing\_factor\_8:4106-4723 | 72.3354 | 780 | merged | NA | NA |
| GSMUA\_Achr2T05230\_001\_Pre-mRNA-processing-splicing\_factor\_8:4830-5085 | 34.739 | 349 | merged | NA | NA |
| GSMUA\_Achr2T05230\_001\_Pre-mRNA-processing-splicing\_factor\_8:5085-5559 | 41.708 | 339 | merged | NA | NA |
| GSMUA\_Achr2T05230\_001\_Pre-mRNA-processing-splicing\_factor\_8:5919-6198 | 25.5519 | 271 | merged | NA | NA |
| GSMUA\_Achr2T06520\_001\_Histone\_deacetylase\_6:312-753 | 40.6362 | 286 |  | 161 | 34 |
| GSMUA\_Achr2T06800\_001\_Ferredoxin-dependent\_glutamate\_synthase\_chloroplastic:2736-2976 | 33.6289 | 385 |  | 212 | 59 |
| GSMUA\_Achr2T06890\_001\_Putative\_Magnesium-chelatase\_subunit\_H:1668-2523 | 61.0222 | 749 |  | 647 | 189 |
| GSMUA\_Achr2T08110\_001\_Calcium-dependent\_protein\_kinase\_SK5:0-556 | 44.6051 | 275 |  | 191 | 51 |
| GSMUA\_Achr2T09260\_001\_E3\_ubiquitin-protein\_ligase\_SINAT5:579-942 | 26.0703 | 306 |  | 173 | 59 |
| GSMUA\_Achr2T09300\_001\_Chlorophyll\_a-b\_binding\_protein\_3C\_chloroplastic:0-804 | 59.8279 | 746 |  | 671 | 205 |
| GSMUA\_Achr2T11540\_001\_Protein\_ETHYLENE\_INSENSITIVE\_3:0-1815 | 47.1731 | 291 |  | 197 | 58 |
| GSMUA\_Achr2T12670\_001\_37\_kDa\_inner\_envelope\_membrane\_protein\_chloroplastic:263-570 | 46.7461 | 382 |  | 275 | 82 |
| GSMUA\_Achr2T13670\_001\_histone-like\_transcription\_factor\_and\_archaeal\_histone\_putative\_expressed:0-417 | 62.9506 | 340 |  | 221 | 54 |
| GSMUA\_Achr2T14120\_001\_Sugar\_carrier\_protein\_C:456-1086 | 38.1269 | 263 |  | 167 | 56 |
| GSMUA\_Achr2T14960\_001\_Chlorophyll\_a-b\_binding\_protein\_4\_chloroplastic:206-622 | 45.2237 | 316 |  | 224 | 66 |
| GSMUA\_Achr2T16160\_001\_Actin-101:454-1068:0 | 71.5982 | 516 |  | 938 | 262 |
| GSMUA\_Achr2T16160\_001\_Actin-101:454-1068:3 | 57.7281 | 285 | merged | NA | NA |
| GSMUA\_Achr2T16160\_001\_Actin-101:60-454 | 72.767 | 591 | merged | NA | NA |
| GSMUA\_Achr2T16710\_001\_V-type\_proton\_ATPase\_subunit\_B2:385-594 | 41.6037 | 348 |  | 191 | 47 |
| GSMUA\_Achr2T19080\_001\_Histone\_H2B.6:0-432 | 58.8201 | 386 |  | 272 | 83 |
| GSMUA\_Achr2T19320\_001\_Mitogen-activated\_protein\_kinase\_1:453-786 | 36.1492 | 301 |  | 155 | 39 |
| GSMUA\_Achr2T19700\_001\_Probable\_cellulose\_synthase\_A\_catalytic\_subunit\_1\_UDP-forming:2059-2256 | 40.8684 | 341 |  | 404 | 122 |
| GSMUA\_Achr2T19700\_001\_Probable\_cellulose\_synthase\_A\_catalytic\_subunit\_1\_UDP-forming:992-1314 | 43.1999 | 352 | merged | NA | NA |
| GSMUA\_Achr2T20610\_001\_Transmembrane\_9\_superfamily\_member\_3:1156-1530 | 31.4402 | 297 |  | 416 | 122 |
| GSMUA\_Achr2T20610\_001\_Transmembrane\_9\_superfamily\_member\_3:1530-1804 | 35.3814 | 334 | merged | NA | NA |
| GSMUA\_Achr3T00140\_001\_Dolichyl-diphosphooligosaccharide--protein\_glycosyltransferase\_subunit\_STT3:1023-1478 | 33.0443 | 273 |  | 170 | 48 |
| GSMUA\_Achr3T01430\_001\_Vacuolar\_protein\_sorting-associated\_protein\_4:512-711 | 33.3775 | 316 |  | 203 | 47 |
| GSMUA\_Achr3T01900\_001\_Sucrose\_synthase\_2:1008-1182 | 26.9943 | 263 |  | 155 | 47 |
| GSMUA\_Achr3T04010\_001\_Putative\_heat\_shock\_protein\_HSP\_90-beta-3:1228-1692 | 36.8 | 279 |  | 413 | 129 |
| GSMUA\_Achr3T04010\_001\_Putative\_heat\_shock\_protein\_HSP\_90-beta-3:549-765 | 32.5051 | 302 | merged | NA | NA |
| GSMUA\_Achr3T04370\_001\_Putative\_U5\_small\_nuclear\_ribonucleoprotein\_40\_kDa\_protein:0-514 | 46.6932 | 342 |  | 224 | 64 |
| GSMUA\_Achr3T04520\_001\_Putative\_Transmembrane\_9\_superfamily\_member\_4:471-1341 | 37.6522 | 282 |  | 179 | 52 |
| GSMUA\_Achr3T04920\_001\_Eukaryotic\_translation\_initiation\_factor\_3\_subunit\_C:1722-2679 | 27.1699 | 276 |  | 167 | 52 |
| GSMUA\_Achr3T05060\_001\_Histone\_H4:0-312 | 25.1159 | 306 |  | 218 | 54 |
| GSMUA\_Achr3T05800\_001\_Putative\_Ethylene-responsive\_transcription\_factor\_1:280-537 | 22.0681 | 275 |  | 164 | 54 |
| GSMUA\_Achr3T05890\_001\_3-oxoacyl-acyl-carrier-protein\_synthase\_I\_chloroplastic:450-882 | 45.1695 | 410 |  | 266 | 73 |
| GSMUA\_Achr3T06150\_001\_Putative\_U4-U6\_small\_nuclear\_ribonucleoprotein\_Prp31:228-1121 | 46.5842 | 436 |  | 245 | 77 |
| GSMUA\_Achr3T07850\_001\_Phospholipid\_diacylglycerol\_acyltransferase\_1:693-977 | 43.3477 | 389 |  | 266 | 84 |
| GSMUA\_Achr3T10970\_001\_Heat\_shock\_protein\_81-3:930-1540 | 31.8971 | 315 |  | 155 | 47 |
| GSMUA\_Achr3T11550\_001\_Transketolase\_chloroplastic:1299-2256 | 54.7612 | 419 |  | 317 | 111 |
| GSMUA\_Achr3T12250\_001\_lung\_seven\_transmembrane\_domain\_containing\_protein\_putative\_expressed:276-1179 | 71.1379 | 614 |  | 515 | 162 |
| GSMUA\_Achr3T12630\_001\_Peptidyl-prolyl\_cis-trans\_isomerase:0-456 | 23.4992 | 209 |  | 167 | 51 |
| GSMUA\_Achr3T12710\_001\_Probable\_pre-mRNA-splicing\_factor\_ATP-dependent\_RNA\_helicase:476-1561 | 24.1228 | 305 |  | 185 | 58 |
| GSMUA\_Achr3T12780\_001\_S-adenosylmethionine\_synthase:0-1185:2 | 33.8866 | 281 |  | 344 | 111 |
| GSMUA\_Achr3T12780\_001\_S-adenosylmethionine\_synthase:0-1185:67 | 29.6497 | 278 | merged | NA | NA |
| GSMUA\_Achr3T14360\_001\_Catalase\_isozyme\_A:390-1167:1689 | 68.857 | 612 |  | 701 | 235 |
| GSMUA\_Achr3T14360\_001\_Catalase\_isozyme\_A:390-1167:4 | 49.9715 | 391 | merged | NA | NA |
| GSMUA\_Achr3T17720\_001\_ABC\_transporter\_B\_family\_member\_20:1393-1622 | 26.8276 | 317 |  | 467 | 148 |
| GSMUA\_Achr3T17720\_001\_ABC\_transporter\_B\_family\_member\_20:3258-3759 | 64.0986 | 446 | merged | NA | NA |
| GSMUA\_Achr3T17740\_001\_Calcium-transporting\_ATPase\_1\_endoplasmic\_reticulum-type:2312-2541 | 26.4015 | 300 |  | 179 | 57 |
| GSMUA\_Achr3T19120\_001\_Probable\_Serine-threonine-protein\_kinase\_At1g01540:1023-1233 | 22.6075 | 307 |  | 173 | 50 |
| GSMUA\_Achr3T19370\_001\_MYB\_family\_transcription\_factor\_putative\_expressed:0-496 | 55.3253 | 346 |  | 275 | 84 |
| GSMUA\_Achr3T19770\_001\_tyrosine\_protein\_kinase\_domain\_containing\_protein\_putative\_expressed:130-450 | 41.7842 | 308 |  | 173 | 47 |
| GSMUA\_Achr3T19880\_001\_Pyrophosphate-energized\_vacuolar\_membrane\_proton\_pump:1121-1443 | 41.0938 | 264 |  | 188 | 57 |
| GSMUA\_Achr3T23490\_001\_Tubulin\_beta-1\_chain:559-1025 | 61.5882 | 529 |  | 347 | 109 |
| GSMUA\_Achr3T25040\_001\_Calmodulin:76-450 | 54.9512 | 347 |  | 230 | 70 |
| GSMUA\_Achr3T25050\_001\_Magnesium-protoporphyrin\_IX\_monomethyl\_ester\_oxidative\_cyclase\_chloroplastic:518-846 | 55.0201 | 387 |  | 287 | 70 |
| GSMUA\_Achr3T26080\_001\_Coatomer\_subunit\_gamma-2:954-1205 | 32.4126 | 306 |  | 227 | 64 |
| GSMUA\_Achr3T27400\_001\_Probable\_voltage-gated\_potassium\_channel\_subunit\_beta:132-489 | 27.5082 | 264 |  | 203 | 60 |
| GSMUA\_Achr3T27470\_001\_Caffeic\_acid\_3-O-methyltransferase:416-727 | 32.2399 | 276 |  | 161 | 47 |
| GSMUA\_Achr4T01550\_001\_Thylakoid\_lumenal\_19\_kDa\_protein\_chloroplastic:0-729 | 21.3485 | 271 |  | 167 | 48 |
| GSMUA\_Achr4T01890\_001\_Proteasome\_subunit\_beta\_type-3:6-188 | 37.9655 | 342 |  | 173 | 52 |
| GSMUA\_Achr4T02120\_001\_Pentatricopeptide\_repeat-containing\_protein\_At5g10690:731-1225 | 35.2027 | 334 |  | 173 | 52 |
| GSMUA\_Achr4T05570\_001\_Mitogen-activated\_protein\_kinase\_2:432-765 | 37.6519 | 269 |  | 185 | 61 |
| GSMUA\_Achr4T05850\_001\_26S\_protease\_regulatory\_subunit\_4\_homolog:833-1050 | 41.8395 | 288 |  | 197 | 65 |
| GSMUA\_Achr4T06270\_001\_E3\_ubiquitin-protein\_ligase\_UPL1:8558-9654 | 25.8078 | 259 |  | 161 | 47 |
| GSMUA\_Achr4T07140\_001\_Tryptophan\_synthase\_beta\_chain\_2\_chloroplastic:225-582 | 37.5462 | 312 |  | 173 | 59 |
| GSMUA\_Achr4T08600\_001\_Eukaryotic\_translation\_initiation\_factor\_1A:0-435 | 72.8861 | 422 |  | 332 | 88 |
| GSMUA\_Achr4T09920\_001\_Protein\_TOPLESS:2481-2661 | 52.0592 | 307 |  | 176 | 52 |
| GSMUA\_Achr4T11560\_001\_ECT5\_putative\_expressed:1317-1530 | 29.0674 | 285 |  | 200 | 57 |
| GSMUA\_Achr4T11590\_001\_amino\_acid\_permease\_family\_protein\_putative\_expressed:0-489 | 39.88 | 326 |  | 230 | 63 |
| GSMUA\_Achr4T11940\_001\_Luminal-binding\_protein\_4:494-709 | 30.2324 | 282 |  | 212 | 64 |
| GSMUA\_Achr4T17120\_001\_Photosystem\_I\_reaction\_center\_subunit\_II\_chloroplastic:0-624 | 17.266 | 210 |  | 164 | 36 |
| GSMUA\_Achr4T17710\_001\_Oryzain\_alpha\_chain:415-651 | 35.3382 | 328 |  | 191 | 66 |
| GSMUA\_Achr4T17930\_001\_Pre-mRNA\_branch\_site\_p14-like\_protein:0-378 | 59.8088 | 369 |  | 278 | 77 |
| GSMUA\_Achr4T21470\_001\_5-methyltetrahydropteroyltriglutamate-homocysteine\_methyltransferase:137-491 | 53.1711 | 391 |  | 470 | 147 |
| GSMUA\_Achr4T21470\_001\_5-methyltetrahydropteroyltriglutamate-homocysteine\_methyltransferase:1620-1871 | 40.1842 | 283 | merged | NA | NA |
| GSMUA\_Achr4T23500\_001\_RNA\_recognition\_motif\_containing\_protein\_putative\_expressed:37-301 | 36.1481 | 311 |  | 218 | 66 |
| GSMUA\_Achr4T24420\_001\_Putative\_Serine-threonine-protein\_kinase\_HT1:659-834 | 29.8918 | 266 |  | 173 | 52 |
| GSMUA\_Achr4T25210\_001\_Serine-threonine-protein\_phosphatase\_PP1:178-738 | 33.0362 | 295 |  | 173 | 49 |
| GSMUA\_Achr4T25930\_001\_SNF2\_family\_N-terminal\_domain\_containing\_protein\_expressed:2045-2264 | 27.622 | 317 |  | 161 | 44 |
| GSMUA\_Achr4T26250\_001\_Tubulin\_beta-7\_chain:664-1341 | 62.62 | 411 |  | 278 | 71 |
| GSMUA\_Achr4T28510\_001\_Pyruvate\_kinase\_isozyme\_A\_chloroplastic:476-955 | 38.4354 | 294 |  | 170 | 48 |
| GSMUA\_Achr4T29300\_001\_Serine-threonine-protein\_phosphatase\_PP1:738-957 | 26.9126 | 321 |  | 176 | 42 |
| GSMUA\_Achr4T30080\_001\_Putative\_casein\_kinase\_II\_subunit\_beta-4:546-712 | 23.4096 | 288 |  | 164 | 53 |
| GSMUA\_Achr4T30650\_001\_14-3-3-like\_protein\_GF14-C:0-317 | 46.5053 | 347 |  | 272 | 86 |
| GSMUA\_Achr4T31270\_001\_Glutamate\_decarboxylase\_1:86-291 | 44.4489 | 279 |  | 197 | 60 |
| GSMUA\_Achr4T31670\_001\_Ferredoxin-NADP\_reductase\_root\_isozyme\_chloroplastic:887-1146 | 20.4373 | 237 |  | 155 | 49 |
| GSMUA\_Achr4T33040\_001\_Chlorophyll\_a-b\_binding\_protein\_151\_chloroplastic:143-795:[0-9]- | 48.5533 | 456 |  | 605 | 194 |
| GSMUA\_Achr4T33040\_001\_Chlorophyll\_a-b\_binding\_protein\_151\_chloroplastic:143-795:[0-9][0-9][0-9]- | 35.215 | 337 | merged | NA | NA |
| GSMUA\_Achr5T00040\_001\_Hypothetical\_protein:164-390 | 28.534 | 343 |  | 182 | 45 |
| GSMUA\_Achr5T00120\_001\_Ethylene\_receptor:81-450 | 36.8437 | 291 |  | 161 | 52 |
| GSMUA\_Achr5T00290\_001\_Tubulin\_beta-1\_chain:559-1035 | 58.8509 | 325 |  | 212 | 60 |
| GSMUA\_Achr5T01170\_001\_Protein\_SENSITIVE\_TO\_PROTON\_RHIZOTOXICITY\_1:226-1036:1367 | 51.7796 | 335 |  | 419 | 138 |
| GSMUA\_Achr5T01170\_001\_Protein\_SENSITIVE\_TO\_PROTON\_RHIZOTOXICITY\_1:226-1036:2 | 36.319 | 336 | merged | NA | NA |
| GSMUA\_Achr5T02310\_001\_Putative\_Tuftelin-interacting\_protein\_11:0-1587 | 39.2566 | 330 |  | 164 | 47 |
| GSMUA\_Achr5T03040\_001\_emp24\_gp25L\_p24\_family\_protein\_putative\_expressed:222-409 | 25.9653 | 252 |  | 179 | 52 |
| GSMUA\_Achr5T03690\_001\_Putative\_Peptide\_transporter\_PTR2:1179-1638 | 29.3014 | 320 |  | 353 | 96 |
| GSMUA\_Achr5T03690\_001\_Putative\_Peptide\_transporter\_PTR2:354-896 | 27.5978 | 264 | merged | NA | NA |
| GSMUA\_Achr5T04520\_001\_26S\_protease\_regulatory\_subunit\_6A\_homolog:288-480 | 30.2824 | 328 |  | 170 | 53 |
| GSMUA\_Achr5T06320\_001\_Probable\_histone\_deacetylase\_19:810-1041 | 24.1175 | 229 |  | 173 | 44 |
| GSMUA\_Achr5T09230\_001\_Chlorophyll\_a-b\_binding\_protein\_40\_chloroplastic:234-402 | 39.7429 | 222 |  | 164 | 47 |
| GSMUA\_Achr5T09710\_001\_eukaryotic\_translation\_initiation\_factor\_5B\_putative\_expressed:885-1293 | 41.4027 | 305 |  | 194 | 61 |
| GSMUA\_Achr5T10720\_001\_Tubulin\_beta-1\_chain:725-1088 | 90.8613 | 462 |  | 302 | 64 |
| GSMUA\_Achr5T12220\_001\_DEAD-box\_ATP-dependent\_RNA\_helicase\_6:330-565 | 28.784 | 252 |  | 170 | 45 |
| GSMUA\_Achr5T13160\_001\_Pyrophosphate-energized\_membrane\_proton\_pump\_3:730-903 | 31.0524 | 321 |  | 164 | 38 |
| GSMUA\_Achr5T13570\_001\_Elongation\_factor\_G\_chloroplastic:247-823:2 | 48.6924 | 432 |  | 563 | 155 |
| GSMUA\_Achr5T13570\_001\_Elongation\_factor\_G\_chloroplastic:247-823:89 | 31.2108 | 281 | merged | NA | NA |
| GSMUA\_Achr5T13570\_001\_Elongation\_factor\_G\_chloroplastic:972-1494 | 26.4606 | 247 | merged | NA | NA |
| GSMUA\_Achr5T14780\_001\_Photosystem\_I\_reaction\_center\_subunit\_II\_chloroplastic:0-624 | 41.2611 | 355 |  | 284 | 72 |
| GSMUA\_Achr5T14830\_001\_Tubulin\_alpha-3\_chain:528-1037 | 54.4837 | 521 |  | 236 | 65 |
| GSMUA\_Achr5T15500\_001\_Cell\_division\_cycle\_protein\_48\_homolog:1770-2130 | 36.236 | 340 |  | 719 | 229 |
| GSMUA\_Achr5T15500\_001\_Cell\_division\_cycle\_protein\_48\_homolog:427-1194:12 | 38.6968 | 479 | merged | NA | NA |
| GSMUA\_Achr5T15500\_001\_Cell\_division\_cycle\_protein\_48\_homolog:427-1194:4 | 48.1035 | 488 | merged | NA | NA |
| GSMUA\_Achr5T16500\_001\_Putative\_Outer\_membrane\_lipoprotein\_blc:0-378 | 15.0463 | 235 |  | 185 | 69 |
| GSMUA\_Achr5T18560\_001\_Phenylalanine\_ammonia-lyase\_1:380-1770 | 59.651 | 375 |  | 215 | 70 |
| GSMUA\_Achr5T18760\_001\_UDP-glucuronate\_4-epimerase\_3:0-1380 | 38.0137 | 288 |  | 227 | 77 |
| GSMUA\_Achr5T20780\_001\_Putative\_Pre-mRNA-processing\_factor\_6:922-2191:2 | 31.3016 | 389 |  | 362 | 98 |
| GSMUA\_Achr5T20780\_001\_Putative\_Pre-mRNA-processing\_factor\_6:922-2191:5 | 37.9973 | 375 | merged | NA | NA |
| GSMUA\_Achr5T21370\_001\_Putative\_Structural\_maintenance\_of\_chromosomes\_protein\_1A:1415-1686 | 40.7027 | 335 |  | 209 | 58 |
| GSMUA\_Achr5T23480\_001\_Pyrophosphate-energized\_vacuolar\_membrane\_proton\_pump:238-813 | 27.8043 | 310 |  | 155 | 46 |
| GSMUA\_Achr5T23640\_001\_Diaminopimelate\_decarboxylase\_1\_chloroplastic:1020-1206 | 20.7315 | 285 |  | 158 | 50 |
| GSMUA\_Achr5T25020\_001\_Serine-threonine-protein\_kinase\_PBS1:517-909 | 49.0722 | 362 |  | 227 | 74 |
| GSMUA\_Achr5T25450\_001\_Serine-threonine\_protein\_phosphatase\_2A\_59\_kDa\_regulatory\_subunit\_B\_gamma\_isoform:264-1026:1 | 28.0892 | 360 |  | 473 | 148 |
| GSMUA\_Achr5T25450\_001\_Serine-threonine\_protein\_phosphatase\_2A\_59\_kDa\_regulatory\_subunit\_B\_gamma\_isoform:264-1026:45 | 38.4291 | 420 | merged | NA | NA |
| GSMUA\_Achr5T26680\_001\_Tubulin\_beta-1\_chain:0-177 | 32.2094 | 320 |  | 461 | 138 |
| GSMUA\_Achr5T26680\_001\_Tubulin\_beta-1\_chain:559-1035 | 66.1313 | 420 | merged | NA | NA |
| GSMUA\_Achr5T26800\_001\_Copper-transporting\_ATPase\_RAN1:1610-1953 | 40.1488 | 316 |  | 194 | 57 |
| GSMUA\_Achr5T26990\_001\_Elongation\_factor\_TS:2399-2733 | 24.1412 | 255 |  | 167 | 61 |
| GSMUA\_Achr5T28610\_001\_ADP-ribosylation\_factor\_GTPase-activating\_protein\_AGD7:54-527 | 31.7676 | 228 |  | 161 | 43 |
| GSMUA\_Achr6T01660\_001\_Transcriptional\_corepressor\_LEUNIG:1440-1683 | 39.8729 | 289 |  | 170 | 51 |
| GSMUA\_Achr6T01750\_001\_Eukaryotic\_initiation\_factor\_4A-1:606-1242 | 33.898 | 309 |  | 206 | 66 |
| GSMUA\_Achr6T02020\_001\_Elongation\_factor\_1-alpha\_putative\_expressed:199-675 | 66.3373 | 531 |  | 320 | 94 |
| GSMUA\_Achr6T03030\_001\_expressed\_protein:780-1713 | 35.6029 | 326 |  | 188 | 50 |
| GSMUA\_Achr6T04090\_001\_Elongation\_factor\_1-alpha:21-552 | 32.068 | 347 |  | 161 | 52 |
| GSMUA\_Achr6T06520\_001\_Serine\_hydroxymethyltransferase\_1:0-389 | 41.869 | 336 |  | 353 | 117 |
| GSMUA\_Achr6T06520\_001\_Serine\_hydroxymethyltransferase\_1:389-600 | 45.2208 | 312 | merged | NA | NA |
| GSMUA\_Achr6T06690\_001\_Elongation\_factor\_Tu\_chloroplastic:312-627 | 36.7238 | 262 |  | 173 | 46 |
| GSMUA\_Achr6T06830\_001\_Protein\_transport\_protein\_Sec61\_subunit\_alpha:146-374 | 32.9447 | 349 |  | 167 | 49 |
| GSMUA\_Achr6T07940\_001\_Glutamate-1-semialdehyde\_21-aminomutase\_chloroplastic:357-1425 | 30.6084 | 297 |  | 182 | 58 |
| GSMUA\_Achr6T08040\_001\_ATP-dependent\_Clp\_protease\_ATP-binding\_subunit\_clpA\_homolog\_CD4A\_chloroplastic:453-671 | 31.8738 | 411 |  | 416 | 139 |
| GSMUA\_Achr6T08040\_001\_ATP-dependent\_Clp\_protease\_ATP-binding\_subunit\_clpA\_homolog\_CD4A\_chloroplastic:837-1530 | 51.2816 | 311 | merged | NA | NA |
| GSMUA\_Achr6T09310\_001\_calpain\_putative\_expressed:6186-6492 | 42.6014 | 344 |  | 257 | 84 |
| GSMUA\_Achr6T10120\_001\_paramyosin\_putative\_expressed:855-2473 | 24.8411 | 282 |  | 164 | 54 |
| GSMUA\_Achr6T10570\_001\_Putative\_MYST-like\_histone\_acetyltransferase\_1:258-471 | 33.8669 | 335 |  | 191 | 49 |
| GSMUA\_Achr6T10590\_001\_ABC\_transporter\_F\_family\_member\_5:786-1128 | 30.2174 | 311 |  | 173 | 55 |
| GSMUA\_Achr6T11210\_001\_Deoxyhypusine\_synthase:805-1041 | 25.0874 | 274 |  | 152 | 49 |
| GSMUA\_Achr6T11910\_001\_Putative\_Protein\_ALWAYS\_EARLY\_3:1908-2087 | 33.3474 | 277 |  | 158 | 52 |
| GSMUA\_Achr6T15480\_001\_Serine-threonine-protein\_kinase\_PBS1:478-870 | 41.3928 | 306 |  | 179 | 50 |
| GSMUA\_Achr6T16370\_001\_Chalcone\_synthase\_2:178-669 | 29.1014 | 238 |  | 167 | 50 |
| GSMUA\_Achr6T16670\_001\_Chaperone\_protein\_ClpB\_2:1626-2553 | 55.7384 | 385 |  | 278 | 84 |
| GSMUA\_Achr6T17750\_001\_Serine\_hydroxymethyltransferase\_1:987-1393 | 17.5804 | 262 |  | 179 | 53 |
| GSMUA\_Achr6T18780\_001\_Patellin-3:531-1215 | 45.5412 | 322 |  | 215 | 70 |
| GSMUA\_Achr6T18890\_001\_V-type\_proton\_ATPase\_16\_kDa\_proteolipid\_subunit\_c1\_c3\_c5:76-362 | 52.7428 | 340 |  | 227 | 65 |
| GSMUA\_Achr6T19490\_001\_Carbamoyl-phosphate\_synthase\_small\_chain:750-1098 | 54.9136 | 393 |  | 233 | 69 |
| GSMUA\_Achr6T19990\_001\_Tubulin\_beta-1\_chain:394-664 | 37.5556 | 271 |  | 374 | 105 |
| GSMUA\_Achr6T19990\_001\_Tubulin\_beta-1\_chain:855-1071 | 44.2328 | 315 | merged | NA | NA |
| GSMUA\_Achr6T20210\_001\_expressed\_protein:3151-3751 | 43.5445 | 346 |  | 230 | 62 |
| GSMUA\_Achr6T23120\_001\_Probable\_E3\_ubiquitin-protein\_ligase\_ARI2:1046-1595 | 34.8159 | 276 |  | 497 | 145 |
| GSMUA\_Achr6T23120\_001\_Probable\_E3\_ubiquitin-protein\_ligase\_ARI2:565-1046 | 51.6603 | 414 | merged | NA | NA |
| GSMUA\_Achr6T23290\_001\_T-complex\_protein\_1\_subunit\_gamma:513-791 | 29.1422 | 291 |  | 197 | 55 |
| GSMUA\_Achr6T28370\_001\_Stromal\_70\_kDa\_heat\_shock-related\_protein\_chloroplastic:1058-1248 | 22.1047 | 238 |  | 407 | 128 |
| GSMUA\_Achr6T28370\_001\_Stromal\_70\_kDa\_heat\_shock-related\_protein\_chloroplastic:1248-1647 | 46.7396 | 322 | merged | NA | NA |
| GSMUA\_Achr6T31540\_001\_Hypothetical\_protein:442-790 | 37.946 | 324 |  | 245 | 78 |
| GSMUA\_Achr6T31810\_001\_Cellulose\_synthase\_A\_catalytic\_subunit\_4\_UDP-forming:806-1152 | 21.8163 | 234 |  | 170 | 35 |
| GSMUA\_Achr6T31900\_001\_Calcium-dependent\_protein\_kinase\_3:36-412 | 51.6666 | 322 |  | 245 | 63 |
| GSMUA\_Achr6T32910\_001\_Putative\_Zinc\_finger\_CCCH\_domain-containing\_protein\_66:0-1076 | 55.9515 | 347 |  | 266 | 91 |
| GSMUA\_Achr6T33650\_001\_Cell\_division\_protease\_ftsH\_homolog\_7\_chloroplastic:1083-1407 | 31.9559 | 293 |  | 176 | 62 |
| GSMUA\_Achr6T33660\_001\_Phosphomethylpyrimidine\_synthase:1404-2081 | 84.3637 | 705 |  | 803 | 247 |
| GSMUA\_Achr6T33660\_001\_Phosphomethylpyrimidine\_synthase:577-1404 | 51.8141 | 355 | merged | NA | NA |
| GSMUA\_Achr6T33760\_001\_Pleckstrin\_homology\_domain-containing\_protein\_1:0-471 | 38.1825 | 285 |  | 188 | 49 |
| GSMUA\_Achr6T33840\_001\_Alpha-glucan\_phosphorylase\_H\_isozyme:372-549 | 27.7129 | 291 |  | 176 | 49 |
| GSMUA\_Achr6T33940\_001\_26S\_proteasome\_non-ATPase\_regulatory\_subunit\_14:399-576 | 39.2312 | 377 |  | 173 | 49 |
| GSMUA\_Achr6T33980\_001\_Mannose-1-phosphate\_guanyltransferase\_beta:414-762 | 16.3061 | 296 |  | 167 | 57 |
| GSMUA\_Achr6T36560\_001\_Probable\_methyltransferase\_PMT8:612-1207 | 62.8666 | 476 |  | 368 | 111 |
| GSMUA\_Achr7T02100\_001\_Probable\_cellulose\_synthase\_A\_catalytic\_subunit\_5\_UDP-forming:2691-3276 | 53.2966 | 398 |  | 221 | 66 |
| GSMUA\_Achr7T05110\_001\_Probable\_GDP-L-fucose\_synthase\_1:0-993 | 29.9595 | 270 |  | 197 | 58 |
| GSMUA\_Achr7T05550\_001\_Probable\_receptor-like\_protein\_kinase\_At2g42960:351-707 | 39.2916 | 356 |  | 224 | 69 |
| GSMUA\_Achr7T10170\_001\_Phospholipase\_D\_alpha\_1:801-1189 | 22.6062 | 216 |  | 161 | 52 |
| GSMUA\_Achr7T10410\_001\_Actin-101:454-1068 | 56.3976 | 341 |  | 641 | 188 |
| GSMUA\_Achr7T10410\_001\_Actin-101:60-454 | 72.3478 | 606 | merged | NA | NA |
| GSMUA\_Achr7T14490\_001\_ABC\_transporter\_E\_family\_member\_2:996-1182 | 23.8036 | 289 |  | 173 | 54 |
| GSMUA\_Achr7T15160\_001\_Heat\_shock\_cognate\_70\_kDa\_protein:396-671 | 31.2545 | 239 |  | 383 | 122 |
| GSMUA\_Achr7T15160\_001\_Heat\_shock\_cognate\_70\_kDa\_protein:747-1074 | 46.8853 | 358 | merged | NA | NA |
| GSMUA\_Achr7T15260\_001\_Histone\_H2B.6:0-459 | 39.0125 | 252 |  | 179 | 58 |
| GSMUA\_Achr7T15350\_001\_Ankyrin\_repeat-containing\_protein\_At3g12360:0-439 | 21.7158 | 245 |  | 338 | 114 |
| GSMUA\_Achr7T15350\_001\_Ankyrin\_repeat-containing\_protein\_At3g12360:439-849 | 41.7877 | 283 | merged | NA | NA |
| GSMUA\_Achr7T15530\_001\_PHD\_finger\_protein\_At5g26210:477-729 | 41.1275 | 340 |  | 224 | 75 |
| GSMUA\_Achr7T17620\_001\_26S\_protease\_regulatory\_subunit\_S10B\_homolog\_B:834-1059 | 22.3998 | 271 |  | 164 | 46 |
| GSMUA\_Achr7T17740\_001\_Putative\_U-box\_domain-containing\_protein\_13:3352-5566 | 36.4717 | 438 |  | 161 | 50 |
| GSMUA\_Achr7T18320\_001\_Trans-cinnamate\_4-monooxygenase:850-1446 | 30.5434 | 256 |  | 188 | 58 |
| GSMUA\_Achr7T20920\_001\_Probable\_WRKY\_transcription\_factor\_19:162-586 | 34.8385 | 325 |  | 164 | 55 |
| GSMUA\_Achr7T21280\_001\_Proteasome\_subunit\_alpha\_type-4:0-564 | 28.4967 | 274 |  | 158 | 47 |
| GSMUA\_Achr7T21790\_001\_Probable\_methylenetetrahydrofolate\_reductase:0-222 | 28.8378 | 252 |  | 158 | 43 |
| GSMUA\_Achr7T21890\_001\_23-bisphosphoglycerate-independent\_phosphoglycerate\_mutase:645-1070 | 48.3826 | 344 |  | 227 | 76 |
| GSMUA\_Achr7T21960\_001\_26S\_protease\_regulatory\_subunit\_6B\_homolog:22-693 | 59.5629 | 371 |  | 500 | 145 |
| GSMUA\_Achr7T21960\_001\_26S\_protease\_regulatory\_subunit\_6B\_homolog:693-924 | 46.2754 | 349 | merged | NA | NA |
| GSMUA\_Achr7T22040\_001\_Vacuolar-sorting\_receptor\_1:301-994 | 54.9125 | 439 |  | 320 | 106 |
| GSMUA\_Achr7T22310\_001\_PRA1\_family\_protein\_B4:132-567 | 37.8631 | 300 |  | 215 | 88 |
| GSMUA\_Achr7T23140\_001\_Probable\_ion\_channel\_POLLUX:2289-2553 | 32.8482 | 268 |  | 161 | 41 |
| GSMUA\_Achr8T00820\_001\_Acyl-acyl-carrier-protein\_desaturase\_chloroplastic:48-334 | 39.5932 | 293 |  | 194 | 60 |
| GSMUA\_Achr8T02520\_001\_Mannose-1-phosphate\_guanyltransferase\_beta:723-1392 | 37.1902 | 290 |  | 194 | 61 |
| GSMUA\_Achr8T04480\_001\_Probable\_histone\_H2A\_variant\_3:108-405 | 54.2054 | 343 |  | 242 | 84 |
| GSMUA\_Achr8T06200\_001\_S-adenosylmethionine\_synthase:0-1182 | 48.6756 | 397 |  | 212 | 67 |
| GSMUA\_Achr8T07200\_001\_DNA\_damage-binding\_protein\_1:1776-2051 | 32.3106 | 296 |  | 197 | 60 |
| GSMUA\_Achr8T07340\_001\_Polyubiquitin:0-303 | 40.4666 | 268 |  | 182 | 64 |
| GSMUA\_Achr8T08130\_001\_Uncharacterized\_protein\_At5g49945:0-1179 | 39.902 | 327 |  | 209 | 74 |
| GSMUA\_Achr8T08750\_001\_Acyl-acyl-carrier-protein\_desaturase\_chloroplastic:125-624 | 52.8212 | 381 |  | 275 | 87 |
| GSMUA\_Achr8T08980\_001\_Serine-threonine\_protein\_phosphatase\_2A\_57\_kDa\_regulatory\_subunit\_B\_theta\_isoform:90-459 | 25.9443 | 352 |  | 170 | 41 |
| GSMUA\_Achr8T09960\_001\_Probable\_chromatin-remodeling\_complex\_ATPase\_chain:1584-1805 | 33.7529 | 336 |  | 191 | 60 |
| GSMUA\_Achr8T10620\_001\_Probable\_ATP-citrate\_synthase:1640-1925 | 34.7081 | 264 |  | 167 | 50 |
| GSMUA\_Achr8T11090\_001\_glycosyl\_transferase\_8\_domain\_containing\_protein\_putative\_expressed:143-402 | 31.5189 | 308 |  | 173 | 57 |
| GSMUA\_Achr8T12670\_001\_Putative\_Pre-mRNA-processing\_factor\_39:863-1224 | 58.0385 | 390 |  | 245 | 47 |
| GSMUA\_Achr8T13360\_001\_Catalase\_isozyme\_2:390-1167 | 35.1569 | 357 |  | 239 | 82 |
| GSMUA\_Achr8T15940\_001\_kinesin\_motor\_domain\_containing\_protein\_putative\_expressed:1268-1487 | 28.9424 | 363 |  | 194 | 56 |
| GSMUA\_Achr8T16150\_001\_Actin-7:60-454 | 43.7456 | 406 |  | 176 | 53 |
| GSMUA\_Achr8T16590\_001\_T-complex\_protein\_1\_subunit\_eta:147-408 | 38.4413 | 304 |  | 203 | 57 |
| GSMUA\_Achr8T17490\_001\_Adenosylhomocysteinase:426-963 | 43.5342 | 297 |  | 206 | 68 |
| GSMUA\_Achr8T19830\_001\_hAT\_dimerisation\_domain-containing\_protein\_putative\_expressed:67-1684 | 25.956 | 273 |  | 161 | 40 |
| GSMUA\_Achr8T20830\_001\_Heat\_shock\_cognate\_70\_kDa\_protein:214-1947:1 | 57.7661 | 348 |  | 1412 | 480 |
| GSMUA\_Achr8T20830\_001\_Heat\_shock\_cognate\_70\_kDa\_protein:214-1947:5 | 65.0006 | 864 | merged | NA | NA |
| GSMUA\_Achr8T20830\_001\_Heat\_shock\_cognate\_70\_kDa\_protein:214-1947:78 | 59.4001 | 621 | merged | NA | NA |
| GSMUA\_Achr8T21320\_001\_CBL-interacting\_protein\_kinase\_18:224-676 | 32.8981 | 267 |  | 191 | 67 |
| GSMUA\_Achr8T23480\_001\_Probable\_LRR\_receptor-like\_Serine-threonine-protein\_kinase\_At5g10290:1108-1503 | 70.015 | 461 |  | 563 | 172 |
| GSMUA\_Achr8T23480\_001\_Probable\_LRR\_receptor-like\_Serine-threonine-protein\_kinase\_At5g10290:766-1108 | 43.3362 | 349 | merged | NA | NA |
| GSMUA\_Achr8T24130\_001\_Geranylgeranyl\_diphosphate\_reductase\_chloroplastic:0-648 | 22.3699 | 225 |  | 551 | 156 |
| GSMUA\_Achr8T24130\_001\_Geranylgeranyl\_diphosphate\_reductase\_chloroplastic:648-932 | 32.5243 | 302 | merged | NA | NA |
| GSMUA\_Achr8T24130\_001\_Geranylgeranyl\_diphosphate\_reductase\_chloroplastic:932-1368 | 51.8694 | 338 | merged | NA | NA |
| GSMUA\_Achr8T24670\_001\_Eukaryotic\_initiation\_factor\_4A-15:175-606 | 68.2076 | 467 |  | 512 | 155 |
| GSMUA\_Achr8T24670\_001\_Eukaryotic\_initiation\_factor\_4A-15:714-1131 | 35.3035 | 282 | merged | NA | NA |
| GSMUA\_Achr8T24860\_001\_expressed\_protein:3277-5491:1 | 57.2892 | 503 |  | 707 | 235 |
| GSMUA\_Achr8T24860\_001\_expressed\_protein:3277-5491:2 | 31.8607 | 345 | merged | NA | NA |
| GSMUA\_Achr8T24860\_001\_expressed\_protein:5491-5946 | 36.7567 | 304 | merged | NA | NA |
| GSMUA\_Achr8T29000\_001\_frigida\_putative\_expressed:0-1039 | 42.2521 | 356 |  | 197 | 69 |
| GSMUA\_Achr8T29950\_001\_Probable\_glutamyl\_endopeptidase\_chloroplastic:1553-2012 | 23.9353 | 318 |  | 170 | 54 |
| GSMUA\_Achr8T31320\_001\_RNA\_recognition\_motif\_containing\_protein\_putative\_expressed:198-682 | 55.6361 | 394 |  | 239 | 71 |
| GSMUA\_Achr8T31890\_001\_ATP-dependent\_RNA\_helicase-like\_protein\_DB10:717-1068 | 53.9632 | 412 |  | 308 | 102 |
| GSMUA\_Achr8T32300\_001\_PHD\_finger\_protein\_At5g26210:133-362 | 50.5188 | 267 |  | 182 | 47 |
| GSMUA\_Achr8T33760\_001\_AAA-type\_ATPase\_family\_protein\_putative\_expressed:2712-2897 | 42.0151 | 338 |  | 182 | 49 |
| GSMUA\_Achr9T00100\_001\_Mitogen-activated\_protein\_kinase\_kinase\_1:180-393 | 28.3954 | 362 |  | 206 | 54 |
| GSMUA\_Achr9T01630\_001\_Adenosylhomocysteinase:531-1068 | 43.1218 | 277 |  | 182 | 55 |
| GSMUA\_Achr9T03250\_001\_Vacuolar\_protein\_sorting-associated\_protein\_2\_homolog\_1:273-534 | 50.139 | 326 |  | 230 | 71 |
| GSMUA\_Achr9T03960\_001\_Heat\_shock\_cognate\_70\_kDa\_protein:0-214 | 36.7115 | 298 |  | 200 | 64 |
| GSMUA\_Achr9T04060\_001\_Probable\_histone\_H2B.1:66-354 | 53.2875 | 361 |  | 284 | 80 |
| GSMUA\_Achr9T05610\_001\_Ras-related\_protein\_Rab11D:0-221 | 44.886 | 283 |  | 407 | 121 |
| GSMUA\_Achr9T05610\_001\_Ras-related\_protein\_Rab11D:221-648 | 40.5831 | 304 | merged | NA | NA |
| GSMUA\_Achr9T05910\_001\_protein\_kinase\_putative\_expressed:449-1453 | 43.983 | 333 |  | 200 | 53 |
| GSMUA\_Achr9T06900\_001\_Hypothetical\_protein:16-414 | 39.4483 | 321 |  | 257 | 76 |
| GSMUA\_Achr9T07750\_001\_Stromal\_70\_kDa\_heat\_shock-related\_protein\_chloroplastic:0-369 | 19.1783 | 223 |  | 149 | 47 |
| GSMUA\_Achr9T11540\_001\_Probable\_potassium\_transporter\_14:1174-1429 | 37.0186 | 316 |  | 200 | 59 |
| GSMUA\_Achr9T12260\_001\_Probable\_cellulose\_synthase\_A\_catalytic\_subunit\_3\_UDP-forming:2835-3255 | 40.2706 | 318 |  | 182 | 56 |
| GSMUA\_Achr9T12680\_001\_Putative\_heat\_shock\_protein\_HSP\_90-beta-3:1228-1677 | 36.365 | 324 |  | 230 | 74 |
| GSMUA\_Achr9T15340\_001\_Hypothetical\_protein:0-1425 | 68.3005 | 432 |  | 326 | 94 |
| GSMUA\_Achr9T17280\_001\_Calmodulin-3:76-450 | 46.4847 | 215 |  | 176 | 56 |
| GSMUA\_Achr9T17850\_001\_Putative\_zinc\_finger\_C3HC4\_type\_domain\_containing\_protein\_expressed:5151-5379 | 26.3873 | 284 |  | 167 | 53 |
| GSMUA\_Achr9T19880\_001\_expressed\_protein:6-818 | 30.6853 | 263 |  | 182 | 62 |
| GSMUA\_Achr9T20870\_001\_Histone\_H3.3:138-342 | 29.048 | 269 |  | 182 | 58 |
| GSMUA\_Achr9T23240\_001\_RuBisCO\_large\_subunit-binding\_protein\_subunit\_beta\_chloroplastic:612-855 | 39.5344 | 372 |  | 197 | 60 |
| GSMUA\_Achr9T23340\_001\_Cell\_division\_cycle\_5-like\_protein:177-1899 | 74.9838 | 431 |  | 308 | 95 |
| GSMUA\_Achr9T23710\_001\_Luminal-binding\_protein\_5:712-1192 | 47.3559 | 373 |  | 290 | 96 |
| GSMUA\_Achr9T23810\_001\_DEAD-box\_ATP-dependent\_RNA\_helicase\_34:0-257 | 52.0465 | 367 |  | 230 | 70 |
| GSMUA\_Achr9T26220\_001\_Hypothetical\_protein:222-558 | 41.4336 | 334 |  | 203 | 54 |
| GSMUA\_Achr9T27600\_001\_Ribose-phosphate\_pyrophosphokinase\_4:116-432 | 26.8408 | 297 |  | 167 | 47 |
| GSMUA\_Achr9T29080\_001\_Putative\_phagocytic\_receptor\_1b:1077-1562 | 19.3788 | 205 |  | 155 | 51 |
| GSMUA\_Achr9T29100\_001\_Peptide\_transporter\_PTR2:381-938 | 29.2295 | 338 |  | 197 | 56 |
| GSMUA\_Achr10T00180\_001\_phosphoesterase\_family\_protein\_putative\_expressed:0-496 | 18.5316 | 217 |  | 164 | 58 |
| GSMUA\_Achr10T01510\_001\_Calmodulin:76-450 | 56.0572 | 418 |  | 356 | 117 |
| GSMUA\_Achr10T01790\_001\_Developmentally-regulated\_GTP-binding\_protein\_2:215-396 | 23.6724 | 316 |  | 179 | 45 |
| GSMUA\_Achr10T03250\_001\_Elongation\_factor\_1-alpha:417-654 | 36.0618 | 276 |  | 209 | 70 |
| GSMUA\_Achr10T03520\_001\_Heat\_shock\_protein\_81-2:705-1542 | 54.5462 | 526 |  | 344 | 119 |
| GSMUA\_Achr10T03730\_001\_Actin-2:60-454 | 56.8018 | 587 |  | 266 | 76 |
| GSMUA\_Achr10T05860\_001\_TBC\_domain\_containing\_protein\_expressed:1267-1692 | 43.8025 | 359 |  | 248 | 85 |
| GSMUA\_Achr10T06510\_001\_WD\_domain\_G-beta\_repeat\_domain\_containing\_protein\_expressed:2678-4068 | 48.9056 | 324 |  | 236 | 71 |
| GSMUA\_Achr10T07400\_001\_SKP1-like\_protein\_1A:0-306 | 38.9388 | 290 |  | 203 | 60 |
| GSMUA\_Achr10T07890\_001\_ankyrin\_repeat\_domain\_containing\_protein\_expressed:0-1012 | 35.3323 | 290 |  | 194 | 68 |
| GSMUA\_Achr10T09380\_001\_Digalactosyldiacylglycerol\_synthase\_1\_chloroplastic:1254-1497 | 27.3203 | 290 |  | 215 | 61 |
| GSMUA\_Achr10T12360\_001\_Glyceraldehyde-3-phosphate\_dehydrogenase\_A\_chloroplastic:156-461 | 33.2634 | 304 |  | 167 | 46 |
| GSMUA\_Achr10T12740\_001\_UDP-sulfoquinovose\_synthase\_chloroplastic:0-771 | 23.2092 | 266 |  | 158 | 50 |
| GSMUA\_Achr10T13400\_001\_Calcium-transporting\_ATPase\_1\_endoplasmic\_reticulum-type:684-951 | 39.3811 | 265 |  | 179 | 55 |
| GSMUA\_Achr10T16310\_001\_expressed\_protein:1844-2453 | 48.2358 | 413 |  | 473 | 128 |
| GSMUA\_Achr10T16310\_001\_expressed\_protein:843-1113 | 41.2652 | 309 | merged | NA | NA |
| GSMUA\_Achr10T17010\_001\_Putative\_E3\_ubiquitin-protein\_ligase\_UPL1:8294-9390:7 | 29.1751 | 343 |  | 665 | 206 |
| GSMUA\_Achr10T17010\_001\_Putative\_E3\_ubiquitin-protein\_ligase\_UPL1:8294-9390:9 | 21.9448 | 261 | merged | NA | NA |
| GSMUA\_Achr10T17330\_001\_Calnexin\_homolog\_1:151-1278:1 | 42.3311 | 297 |  | 1145 | 404 |
| GSMUA\_Achr10T17330\_001\_Calnexin\_homolog\_1:151-1278:4 | 78.5617 | 468 | merged | NA | NA |
| GSMUA\_Achr10T17710\_001\_EF\_hand\_family\_protein\_expressed:0-474 | 24.8652 | 332 |  | 275 | 92 |
| GSMUA\_Achr10T18810\_001\_Probable\_methyltransferase\_PMT2:0-645 | 31.5571 | 265 |  | 164 | 44 |
| GSMUA\_Achr10T19930\_001\_Ribulose\_bisphosphate\_carboxylase\_small\_chain\_chloroplastic:246-477 | 36.2272 | 289 |  | 224 | 66 |
| GSMUA\_Achr10T20580\_001\_Proteasome\_subunit\_alpha\_type-1-A:351-798 | 20.3119 | 219 |  | 173 | 51 |
| GSMUA\_Achr10T21400\_001\_Elongation\_factor\_2:1950-2316 | 34.8554 | 338 |  | 563 | 158 |
| GSMUA\_Achr10T21400\_001\_Elongation\_factor\_2:702-1950 | 36.8178 | 510 | merged | NA | NA |
| GSMUA\_Achr10T21400\_001\_Elongation\_factor\_2:91-702 | 46.7248 | 330 | merged | NA | NA |
| GSMUA\_Achr10T22980\_001\_Elongation\_factor\_1-alpha:103-570 | 67.5662 | 509 |  | 377 | 108 |
| GSMUA\_Achr10T23400\_001\_Coatomer\_subunit\_beta-1:1884-2394 | 31.4225 | 281 |  | 197 | 64 |
| GSMUA\_Achr10T24850\_001\_Riboflavin\_biosynthesis\_protein\_ribBA\_chloroplastic:1110-1407 | 47.2325 | 367 |  | 293 | 105 |
| GSMUA\_Achr10T26630\_001\_IWS1\_C-terminus\_family\_protein\_putative\_expressed:624-845 | 29.9572 | 301 |  | 197 | 55 |
| GSMUA\_Achr10T27140\_001\_26S\_protease\_regulatory\_subunit\_8\_homolog\_A:755-912 | 31.7297 | 273 |  | 155 | 45 |
| GSMUA\_Achr10T27330\_001\_Protein\_GIGANTEA:1293-2829 | 42.4491 | 337 |  | 206 | 70 |
| GSMUA\_Achr10T28040\_001\_Putative\_Transmembrane\_9\_superfamily\_member\_2:1333-2046:1 | 44.4299 | 373 |  | 392 | 122 |
| GSMUA\_Achr10T28040\_001\_Putative\_Transmembrane\_9\_superfamily\_member\_2:1333-2046:3 | 28.8174 | 235 | merged | NA | NA |
| GSMUA\_Achr10T28260\_001\_Lysyl-tRNA\_synthetase:897-1180 | 28.3403 | 301 |  | 158 | 50 |
| GSMUA\_Achr10T29400\_001\_Ubiquitin-activating\_enzyme\_E1\_2:1308-2177 | 49.3064 | 415 |  | 341 | 119 |
| GSMUA\_Achr10T30470\_001\_Chlorophyll\_a-b\_binding\_protein\_CP24\_10A\_chloroplastic:0-450 | 11.866 | 296 |  | 176 | 47 |
| GSMUA\_Achr10T31340\_001\_Probable\_phosphatidylinositol\_4-kinase\_type\_2-beta\_At1g26270:439-996 | 63.0907 | 420 |  | 311 | 93 |
| GSMUA\_Achr10T31490\_001\_Chloride\_channel\_protein\_CLC-f:369-772 | 46.8063 | 417 |  | 443 | 125 |
| GSMUA\_Achr10T31490\_001\_Chloride\_channel\_protein\_CLC-f:772-967 | 24.3662 | 318 | merged | NA | NA |
| GSMUA\_Achr11T00490\_001\_Ubiquitin-fold\_modifier-conjugating\_enzyme\_1:0-395 | 39.2091 | 385 |  | 176 | 50 |
| GSMUA\_Achr11T01900\_001\_Protochlorophyllide\_reductase\_B\_chloroplastic:676-1035 | 32.6306 | 274 |  | 185 | 48 |
| GSMUA\_Achr11T03500\_001\_Putative\_Methionine\_gamma-lyase:673-1267 | 32.0773 | 288 |  | 194 | 55 |
| GSMUA\_Achr11T04800\_001\_Pto-interacting\_protein\_1:463-737 | 47.0674 | 364 |  | 257 | 83 |
| GSMUA\_Achr11T05030\_001\_Probable\_ATP-citrate\_synthase:1466-1751 | 31.4744 | 298 |  | 185 | 57 |
| GSMUA\_Achr11T08060\_001\_V-type\_proton\_ATPase\_catalytic\_subunit\_A:1098-1293 | 48.0692 | 333 |  | 191 | 52 |
| GSMUA\_Achr11T10550\_001\_Probable\_methylenetetrahydrofolate\_reductase:426-600 | 26.0917 | 301 |  | 161 | 46 |
| GSMUA\_Achr11T15050\_001\_Proteasome\_subunit\_beta\_type-4:459-645 | 36.6606 | 357 |  | 185 | 61 |
| GSMUA\_Achr11T17980\_001\_Putative\_Protein\_transport\_protein\_SEC23:438-2259 | 23.426 | 259 |  | 149 | 46 |
| GSMUA\_Achr11T19060\_001\_Putative\_CUB\_and\_sushi\_domain-containing\_protein\_2:0-435 | 33.1012 | 232 |  | 170 | 58 |
| GSMUA\_Achr11T19850\_001\_Vacuolar-sorting\_receptor\_1:298-991 | 71.1959 | 509 |  | 344 | 110 |
| GSMUA\_Achr11T24320\_001\_Ribulose\_bisphosphate\_carboxylase\_oxygenase\_activase\_2\_chloroplastic:557-1030 | 32.4018 | 299 |  | 167 | 39 |
| GSMUA\_Achr11T25560\_001\_Serine-threonine-protein\_phosphatase\_BSL1\_homolog:234-434 | 23.9934 | 293 |  | 173 | 46 |
| GSMUA\_AchrUn\_randomT01480\_001\_Clathrin\_heavy\_chain\_1:2876-3879:1 | 44.1161 | 349 |  | 650 | 186 |
| GSMUA\_AchrUn\_randomT01480\_001\_Clathrin\_heavy\_chain\_1:2876-3879:3 | 63.0585 | 347 | merged | NA | NA |
| GSMUA\_AchrUn\_randomT01480\_001\_Clathrin\_heavy\_chain\_1:3879-4365 | 37.9983 | 300 | merged | NA | NA |
| GSMUA\_AchrUn\_randomT02630\_001\_Phosphatidylinositol-4-phosphate\_5-kinase\_9:1485-1673 | 23.3856 | 329 |  | 167 | 44 |
| GSMUA\_AchrUn\_randomT04950\_001\_Probable\_cellulose\_synthase\_A\_catalytic\_subunit\_3\_UDP-forming:1034-1380 | 33.1127 | 263 |  | 593 | 166 |
| GSMUA\_AchrUn\_randomT04950\_001\_Probable\_cellulose\_synthase\_A\_catalytic\_subunit\_3\_UDP-forming:2340-2691 | 52.4951 | 407 | merged | NA | NA |
| GSMUA\_AchrUn\_randomT04950\_001\_Probable\_cellulose\_synthase\_A\_catalytic\_subunit\_3\_UDP-forming:2691-3276 | 35.3233 | 293 | merged | NA | NA |
| GSMUA\_AchrUn\_randomT07140\_001\_expressed\_protein:1350-1524 | 32.2208 | 309 |  | 167 | 37 |
| GSMUA\_AchrUn\_randomT09460\_001\_Probable\_cellulose\_synthase\_A\_catalytic\_subunit\_2\_UDP-forming:1938-2289 | 68.3175 | 423 |  | 299 | 87 |
| GSMUA\_AchrUn\_randomT09650\_001\_Glucosamine--fructose-6-phosphate\_aminotransferase\_isomerizing\_2:1282-1533 | 31.947 | 421 |  | 509 | 138 |
| GSMUA\_AchrUn\_randomT09650\_001\_Glucosamine--fructose-6-phosphate\_aminotransferase\_isomerizing\_2:1648-1904 | 33.5262 | 364 | merged | NA | NA |
| GSMUA\_AchrUn\_randomT09650\_001\_Glucosamine--fructose-6-phosphate\_aminotransferase\_isomerizing\_2:960-1282 | 26.2971 | 325 | merged | NA | NA |
| GSMUA\_AchrUn\_randomT09700\_001\_Clathrin\_heavy\_chain\_1:2841-3327 | 65.6665 | 684 |  | 344 | 100 |
| GSMUA\_AchrUn\_randomT21380\_001\_auxin\_efflux\_carrier\_component\_putative\_expressed:574-1179 | 27.9549 | 267 |  | 164 | 62 |
| GSMUA\_AchrUn\_randomT25710\_001\_Elongation\_factor\_1-alpha:159-574 | 28.8289 | 455 |  | 212 | 64 |
| GSMUA\_AchrUn\_randomT27420\_001\_Polyubiquitin\_10:0-279 | 67.1779 | 316 |  | 245 | 78 |
| GSMUA\_AchrUn\_randomT27920\_001\_Charged\_multivesicular\_body\_protein\_1:0-387 | 59.6364 | 373 |  | 266 | 74 |
| whole plastid | 400 | 112193 | introns and intergenic spacers removed | 56202 | 8336 |
| accD | 180.955 | 1508 |  | 2333 | 426 |
| atpA | 327.729 | 1523 |  | 1535 | 226 |
| atpB | 287.432 | 1495 |  | 1517 | 192 |
| atpE | 207.245 | 408 |  | 407 | 58 |
| atpF | 715.442 | 1352 |  | 551 | 94 |
| atpH | 139.034 | 246 |  | 245 | 26 |
| atpI | 233.304 | 744 |  | 746 | 83 |
| ccsA | 172.912 | 985 |  | 1115 | 222 |
| cemA | 178.681 | 688 |  | 704 | 121 |
| clpP | 187.296 | 2107 |  | 650 | 185 |
| infA | 109.673 | 235 |  | 263 | 72 |
| matK | 685.711 | 1536 |  | 1613 | 337 |
| ndhA | 265.892 | 2147 |  | 1091 | 148 |
| ndhB | 452.896 | 2233 | skewed tree length | NA | NA |
| ndhC | 188.864 | 363 |  | 359 | 34 |
| ndhD | 866.049 | 1506 |  | 1526 | 290 |
| ndhE | 145.404 | 306 |  | 308 | 42 |
| ndhF | 186.075 | 2213 |  | 2618 | 505 |
| ndhG | 188.565 | 530 |  | 533 | 94 |
| ndhH | 2860.15 | 1182 |  | 1184 | 163 |
| ndhI | 2079.06 | 542 |  | 551 | 81 |
| ndhJ | 190.557 | 479 |  | 476 | 52 |
| ndhK | 248.12 | 773 |  | 887 | 107 |
| petA | 1411.07 | 963 |  | 959 | 116 |
| petB | 210.765 | 1463 |  | 650 | 65 |
| petD | 207.859 | 1234 |  | 479 | 60 |
| petG | 37.8546 | 110 |  | 110 | 9 |
| petL | 19.0491 | 90 | skewed tree length | NA | NA |
| petN | 16.9701 | 83 | skewed tree length | NA | NA |
| psaA | 2328.49 | 2253 |  | 2405 | 208 |
| psaB | 2411.99 | 2205 |  | 2207 | 201 |
| psaC | 137.404 | 246 |  | 242 | 40 |
| psaI | 31.4816 | 107 |  | 107 | 12 |
| psaJ | 48.4175 | 127 |  | 131 | 14 |
| psbA | 249.214 | 1062 |  | 1058 | 131 |
| psbB | 265.342 | 1527 | skewed tree length | NA | NA |
| psbC | 222.367 | 1422 |  | 1418 | 147 |
| psbD | 268.887 | 1062 |  | 1058 | 86 |
| psbE | 152.877 | 252 |  | 248 | 22 |
| psbF | 69.308 | 119 | skewed tree length | NA | NA |
| psbH | 104.955 | 221 |  | 218 | 24 |
| psbI | 27.1717 | 106 | skewed tree length | NA | NA |
| psbJ | 60.2015 | 122 |  | 125 | 14 |
| psbK | 78.0455 | 184 |  | 182 | 33 |
| psbL | 55.4941 | 116 | skewed tree length | NA | NA |
| psbM | 32.6341 | 101 |  | 101 | 9 |
| psbN | 62.5067 | 131 |  | 128 | 15 |
| psbT | 28.2031 | 101 |  | 110 | 8 |
| psbZ | 96.0475 | 188 |  | 185 | 15 |
| rbcL | 226.655 | 1458 |  | 1490 | 180 |
| rpl14 | 176.613 | 369 |  | 389 | 74 |
| rpl16 | 160.171 | 1317 |  | 407 | 87 |
| rpl2 | 155.415 | 390 |  | 827 | 35 |
| rpl20 | 1806.14 | 392 |  | 668 | 89 |
| rpl22 | 209.933 | 283 |  | 530 | 102 |
| rpl23 | 416.872 | 1487 | skewed tree length | NA | NA |
| rpl32 | 67.9864 | 171 |  | 242 | 39 |
| rpl33 | 99.5671 | 201 |  | 233 | 42 |
| rpl36 | 37.2246 | 112 | skewed tree length | NA | NA |
| rpoA | 204.112 | 1021 |  | 1052 | 196 |
| rpoB | 345.951 | 3229 |  | 3563 | 477 |
| rpoC1 | 239.031 | 2800 |  | 2168 | 308 |
| rpoC2 | 246.265 | 4140 |  | 4586 | 782 |
| rps11 | 181.792 | 416 |  | 452 | 121 |
| rps12 | 340.496 | 914 |  | 380 | 26 |
| rps14 | 158.51 | 303 |  | 302 | 58 |
| rps15 | 177.986 | 272 |  | 284 | 66 |
| rps16 | 173.363 | 1088 |  | 254 | 39 |
| rps18 | 145.327 | 319 |  | 431 | 50 |
| rps19 | 174.1 | 279 |  | 368 | 79 |
| rps2 | 210.657 | 711 |  | 737 | 153 |
| rps3 | 215.101 | 647 |  | 680 | 169 |
| rps4 | 201.868 | 609 |  | 659 | 95 |
| rps7 | 305.829 | 475 |  | 599 | 65 |
| rps8 | 143.959 | 397 |  | 407 | 73 |
| ycf1 | 260.843 | 5554 | alignment uncertainty | NA | NA |
| ycf15 | 265.772 | 495 |  | 509 | 28 |
| ycf2 | 419.459 | 6841 | skewed tree length | NA | NA |
| ycf3 | 229.438 | 2015 | skewed tree length | NA | NA |
| ycf4 | 177.162 | 535 |  | 584 | 116 |
| ycf68 | 597.076 | 385 | skewed tree length | NA | NA |