Supplementary Table S4: Identification, subcellular localization and characterization of the *MATE* genes in *G. arboreum* and *G. raimondii*

|  |  |  |  |  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- |
| Gene ID | Gene name | Exon | Length (aa) | Chromosome location | pI | MW Da | TM | Subcellular Localization | | |
| wolfpsort | TargetP | Pprowler |
| Cotton\_A\_10319 | GaMATE1 | 1 | 448 | Chr01:1214119-1215465:+ | 6.23 | 48617.2 | 9 | Plas | \_ | other |
| Cotton\_A\_23601 | GaMATE2 | 1 | 520 | Chr01:56204050-56205612:- | 8.21 | 56550 | 10 | Plas | \_ | SP |
| Cotton\_A\_12209 | GaMATE3 | 6 | 478 | Chr01:84346317-84349104:+ | 7.08 | 52237.8 | 11 | Plas | \_ | other |
| Cotton\_A\_12208 | GaMATE4 | 6 | 477 | Chr01:84391840-84395218:+ | 5.6 | 52193.4 | 11 | Plas | \_ | other |
| Cotton\_A\_36630 | GaMATE5 | 8 | 518 | Chr01:113075149-113079824:- | 8.01 | 56677 | 12 | Plas | \_ | SP |
| Cotton\_A\_36631 | GaMATE6 | 8 | 514 | Chr01:113081945-113087024:- | 5.31 | 55755.7 | 12 | Plas | \_ | SP |
| Cotton\_A\_20416 | GaMATE7 | 7 | 470 | Chr02:53016569-53020719:- | 6.33 | 51393.7 | 12 | Plas | S | SP |
| Cotton\_A\_08859 | GaMATE8 | 9 | 450 | Chr02:90640922-90644666:+ | 9.53 | 48077.1 | 3 | Chlo | \_ | SP |
| Cotton\_A\_40180 | GaMATE9 | 7 | 471 | Chr03:2201588-2204829:- | 8.64 | 52822.8 | 12 | Plas | M | other |
| Cotton\_A\_30984 | GaMATE10 | 7 | 480 | Chr03:17596347-17605251:+ | 5 | 53619.5 | 10 | Plas | \_ | other |
| Cotton\_A\_36352 | GaMATE11 | 8 | 480 | Chr03:36588393-36591230:+ | 6.54 | 53128.9 | 10 | Plas | \_ | other |
| Cotton\_A\_38142 | GaMATE12 | 8 | 499 | Chr03:45921421-45919587:- | 6.61 | 55324.3 | 11 | Plas | \_ | other |
| Cotton\_A\_39721 | GaMATE13 | 8 | 490 | Chr03:58538281-58541064:- | 6.98 | 54017.2 | 8 | Plas | \_ | other |
| Cotton\_A\_00148 | GaMATE14 | 6 | 470 | Chr04:38580252-38585855:+ | 9.08 | 51616.8 | 11 | vacu | \_ | other |
| Cotton\_A\_04850 | GaMATE15 | 2 | 510 | Chr04:42742962-42744571:- | 6.93 | 55162.1 | 11 | Plas | \_ | other |
| Cotton\_A\_06267 | GaMATE16 | 7 | 484 | Chr04:91644390-91648624:- | 5.68 | 53096.6 | 12 | Plas | C | other |
| Cotton\_A\_33036 | GaMATE17 | 8 | 472 | Chr04:95474017-95477248:- | 6.81 | 51217 | 12 | Plas | S | SP |
| Cotton\_A\_17154 | GaMATE18 | 1 | 499 | Chr04:111216612-111218111:+ | 8.7 | 53978.4 | 10 | Plas | \_ | SP |
| Cotton\_A\_17155 | GaMATE19 | 1 | 493 | Chr04:111223144-111224625:+ | 9.28 | 53693.3 | 10 | Plas | \_ | SP |
| Cotton\_A\_24370 | GaMATE20 | 4 | 722 | Chr05:19885593-19889406:- | 5.74 | 78899.6 | 12 | Plas | C | other |
| Cotton\_A\_16784 | GaMATE21 | 7 | 444 | Chr05:111712723-111715847:+ | 9 | 48515.5 | 11 | Plas | \_ | other |
| Cotton\_A\_16785 | GaMATE22 | 7 | 468 | Chr05:111739554-111742081:+ | 8.57 | 51061.5 | 11 | Plas | \_ | other |
| Cotton\_A\_16786 | GaMATE23 | 7 | 484 | Chr05:111860606-111864929:+ | 5.2 | 52958 | 12 | Plas | S | SP |
| Cotton\_A\_34394 | GaMATE24 | 7 | 494 | Chr06:2559823-2562299:- | 5.83 | 53563.6 | 9 | Plas | \_ | other |
| Cotton\_A\_04689 | GaMATE25 | 7 | 518 | Chr06:20256164-20259322:+ | 5.52 | 55996.9 | 11 | Plas | S | SP |
| Cotton\_A\_19523 | GaMATE26 | 2 | 554 | Chr06:22090072-22091858:+ | 7.47 | 60379.2 | 12 | Plas | S | SP |
| Cotton\_A\_02516 | GaMATE27 | 7 | 471 | Chr06:51422467-51425639:- | 8.56 | 51216.7 | 10 | Plas | \_ | SP |
| Cotton\_A\_04051 | GaMATE28 | 1 | 461 | Chr06:81024422-81025807:+ | 6.31 | 50352.9 | 11 | Plas | \_ | other |
| Cotton\_A\_13693 | GaMATE29 | 6 | 405 | Chr06:111243182-111245731:- | 9 | 43601.6 | 9 | Plas | \_ | other |
| Cotton\_A\_09978 | GaMATE30 | 1 | 535 | Chr07:14248070-14249677:- | 8.08 | 58377.9 | 11 | nucl | \_ | SP |
| Cotton\_A\_14530 | GaMATE31 | 1 | 509 | Chr07:23324252-23325781:+ | 8.36 | 55590.5 | 10 | E.R | C | SP |
| Cotton\_A\_06827 | GaMATE32 | 12 | 503 | Chr07:53087857-53092108:+ | 9.43 | 53677 | 9 | vacu | C | other |
| Cotton\_A\_29724 | GaMATE33 | 8 | 489 | Chr07:76586217-76589109:+ | 7.93 | 53641.4 | 11 | Plas | \_ | SP |
| Cotton\_A\_29722 | GaMATE34 | 8 | 489 | Chr07:76613642-76616182:+ | 8.75 | 53935.3 | 11 | Plas | \_ | other |
| Cotton\_A\_12986 | GaMATE35 | 12 | 529 | Chr07:84377620-84380346:- | 9.12 | 56336.3 | 8 | vacu | \_ | other |
| Cotton\_A\_38174 | GaMATE36 | 1 | 435 | Chr08:8142836-8144143:+ | 8.19 | 47488.4 | 9 | Plas | \_ | other |
| Cotton\_A\_18824 | GaMATE37 | 1 | 474 | Chr08:21325243-21326667:+ | 7.92 | 51155.5 | 8 | Plas | \_ | other |
| Cotton\_A\_25640 | GaMATE38 | 8 | 341 | Chr08:74860718-74866292:- | 6.14 | 36672.7 | 7 | Plas | S | SP |
| Cotton\_A\_24645 | GaMATE39 | 7 | 514 | Chr08:92301132-92305621:+ | 8.1 | 56642.3 | 10 | Plas | \_ | other |
| Cotton\_A\_20939 | GaMATE40 | 4 | 455 | Chr09:19400142-19403212:- | 5.86 | 49738.5 | 7 | Plas | C | SP |
| Cotton\_A\_35736 | GaMATE41 | 7 | 506 | Chr09:36821292-36824647:- | 5.34 | 54762.4 | 12 | Plas | S | SP |
| Cotton\_A\_35442 | GaMATE42 | 7 | 485 | Chr09:38177546-38180011:- | 6.98 | 52393.9 | 10 | vacu | \_ | other |
| Cotton\_A\_11428 | GaMATE43 | 6 | 469 | Chr09:78515400-78519385:+ | 8.64 | 52395.9 | 10 | Plas | \_ | other |
| Cotton\_A\_01420 | GaMATE44 | 7 | 445 | Chr09:120155937-120160133:- | 6.93 | 48300.4 | 11 | Plas | C | other |
| Cotton\_A\_01338 | GaMATE45 | 1 | 547 | Chr09:120816975-120818618:+ | 6.69 | 59754.5 | 11 | Plas | \_ | SP |
| Cotton\_A\_36951 | GaMATE46 | 1 | 536 | Chr10:820154-822078:+ | 8.15 | 58806.8 | 11 | Plas | \_ | SP |
| Cotton\_A\_12471 | GaMATE47 | 1 | 436 | Chr10:8382835-8384145:+ | 7.05 | 47494.4 | 9 | Plas | \_ | other |
| Cotton\_A\_25608 | GaMATE48 | 5 | 153 | Chr10:23136120-23137506:- | 6.26 | 16719.6 | 3 | vacu | C | SP |
| Cotton\_A\_25605 | GaMATE49 | 7 | 480 | Chr10:23153932-23156942:- | 6.15 | 52438 | 11 | Plas | \_ | other |
| Cotton\_A\_25604 | GaMATE50 | 7 | 488 | Chr10:23162462-23166161:- | 6.15 | 53288.9 | 12 | Plas | \_ | other |
| Cotton\_A\_27875 | GaMATE51 | 2 | 520 | Chr10:37106806-37108463:- | 6 | 56441.6 | 12 | Plas | \_ | other |
| Cotton\_A\_07599 | GaMATE52 | 8 | 508 | Chr10:53567501-53571514:- | 8.34 | 55601.8 | 11 | Plas | C | SP |
| Cotton\_A\_07598 | GaMATE53 | 8 | 497 | Chr10:53573112-53576147:- | 8.35 | 54115.2 | 12 | Plas | \_ | SP |
| Cotton\_A\_07545 | GaMATE54 | 1 | 503 | Chr10:54101338-54102849:+ | 8.53 | 54969.5 | 11 | Plas | S | SP |
| Cotton\_A\_37422 | GaMATE55 | 7 | 491 | Chr10:67392878-67397073:+ | 5.17 | 54096.7 | 11 | Plas | S | SP |
| Cotton\_A\_01824 | GaMATE56 | 12 | 521 | Chr10:80140952-80143803:- | 5.42 | 55886.2 | 7 | Plas | \_ | other |
| Cotton\_A\_01858 | GaMATE57 | 3 | 502 | Chr10:80700916-80702929:- | 5.49 | 54245.3 | 11 | cyto | C | SP |
| Cotton\_A\_14741 | GaMATE58 | 8 | 498 | Chr10:103394324-103399525:+ | 5.79 | 53778.2 | 10 | Plas | \_ | other |
| Cotton\_A\_18103 | GaMATE59 | 1 | 524 | Chr11:57852209-57854089:+ | 8.62 | 56906.7 | 10 | Chlo | S | SP |
| Cotton\_A\_09404 | GaMATE60 | 1 | 447 | Chr11:59764310-59765653:- | 7.06 | 48510.2 | 9 | Plas | \_ | other |
| Cotton\_A\_02806 | GaMATE61 | 8 | 492 | Chr11:98467497-98474098:+ | 5.52 | 53992.2 | 10 | Plas | \_ | SP |
| Cotton\_A\_15329 | GaMATE62 | 13 | 508 | Chr12:20710664-20713866:+ | 8.49 | 54599.1 | 10 | vacu | \_ | other |
| Cotton\_A\_00294 | GaMATE63 | 13 | 557 | Chr12:70391575-70394399:+ | 8.7 | 59133.7 | 9 | Chlo | \_ | SP |
| Cotton\_A\_00704 | GaMATE64 | 15 | 570 | Chr13:8027202-8031183:- | 8.02 | 62423.3 | 9 | Plas | C | SP |
| Cotton\_A\_00703 | GaMATE65 | 12 | 489 | Chr13:8032855-8036525:- | 8.76 | 53546.6 | 7 | Plas | C | SP |
| Cotton\_A\_00702 | GaMATE66 | 14 | 560 | Chr13:8037393-8043443:- | 7.59 | 60889.3 | 8 | Chlo | \_ | SP |
| Cotton\_A\_38110 | GaMATE67 | 8 | 487 | scaffold1237:86439-90792:+ | 8.32 | 53694.8 | 11 | cyto | \_ | SP |
| Cotton\_A\_37169 | GaMATE68 | 8 | 491 | scaffold2861:84269-86852:- | 6.54 | 53957.7 | 12 | Plas | S | SP |
| Gorai.001G009200 | GrMATE1 | 1 | 503 | Chr01:867204-868912:+ | 6.59 | 55181.8 | 10 | cyto | S | SP |
| Gorai.001G084200 | GrMATE2 | 7 | 474 | Chr01:8943300-8947514:- | 5.76 | 51621.7 | 10 | cyto | \_ | other |
| Gorai.001G084300 | GrMATE3 | 7 | 229 | Chr01:8964559-8966634:- | 8.23 | 24778.3 | 5 | cyto | S | SP |
| Gorai.002G011300 | GrMATE4 | 7 | 481 | Chr02:748807-755439:- | 8.9 | 52295.4 | 11 | Plas | \_ | other |
| Gorai.002G068800 | GrMATE5 | 7 | 484 | Chr02:7971895-7976018:+ | 5.68 | 53065.4 | 12 | Plas | C | other |
| Gorai.002G130000 | GrMATE6 | 9 | 483 | Chr02:20259150-20263595:+ | 7.51 | 52469.2 | 12 | Plas | \_ | SP |
| Gorai.002G230300 | GrMATE7 | 13 | 502 | Chr02:58952759-58956155:+ | 8.49 | 53722.1 | 10 | vacu | \_ | other |
| Gorai.002G266300 | GrMATE8 | 11 | 489 | Chr02:62577175-62580522:+ | 8.62 | 51751 | 10 | chlo | S | SP |
| Gorai.003G162500 | GrMATE9 | 1 | 520 | Chr03:43166486-43168048:- | 8.35 | 56568.1 | 10 | Plas | \_ | SP |
| Gorai.003G167400 | GrMATE10 | 1 | 499 | Chr03:43725189-43727633:- | 8.86 | 54190.6 | 10 | Plas | \_ | SP |
| Gorai.004G037400 | GrMATE11 | 11 | 487 | Chr04:3087006-3091901:+ | 9.43 | 52033.1 | 9 | vacu | S | SP |
| Gorai.004G172500 | GrMATE12 | 12 | 550 | Chr04:47314770-47318736:- | 9.25 | 58510.1 | 9 | vacu | \_ | other |
| Gorai.004G208200 | GrMATE13 | 2 | 601 | Chr04:54046928-54050094:+ | 8.8 | 66275.4 | 11 | chlo | \_ | SP |
| Gorai.004G253200 | GrMATE14 | 6 | 495 | Chr04:59057969-59062569:+ | 8.87 | 54619.4 | 11 | Plas | \_ | other |
| Gorai.004G253300 | GrMATE15 | 5 | 308 | Chr04:59067519-59069924:+ | 8.74 | 33941.7 | 7 | Plas | \_ | other |
| Gorai.004G281900 | GrMATE16 | 1 | 509 | Chr04:61363979-61365926:+ | 7.12 | 55617.3 | 11 | chlo | C | SP |
| Gorai.005G061400 | GrMATE17 | 2 | 510 | Chr05:6449192-6451116:- | 6.53 | 55056.8 | 11 | Plas | \_ | other |
| Gorai.005G149900 | GrMATE18 | 7 | 505 | Chr05:41168257-41172297:+ | 5.47 | 54787.4 | 12 | Plas | S | SP |
| Gorai.005G178900 | GrMATE19 | 8 | 505 | Chr05:52404202-52409063:- | 8.3 | 55107.3 | 12 | Plas | \_ | SP |
| Gorai.005G179100 | GrMATE20 | 8 | 554 | Chr05:52437991-52442663:- | 5.33 | 60707.5 | 12 | Plas | S | SP |
| Gorai.005G194400 | GrMATE21 | 7 | 489 | Chr05:56448829-56452509:- | 7.89 | 53370.1 | 12 | Plas | \_ | other |
| Gorai.005G194500 | GrMATE22 | 7 | 490 | Chr05:56469101-56473235:- | 7.43 | 53463.2 | 12 | Plas | \_ | other |
| Gorai.005G247400 | GrMATE23 | 12 | 471 | Chr05:62732765-62737327:- | 8.17 | 51251.1 | 8 | chlo | C | SP |
| Gorai.005G247500 | GrMATE24 | 14 | 541 | Chr05:62738552-62742565:- | 8.55 | 58671.7 | 7 | chlo | C | SP |
| Gorai.005G247600 | GrMATE25 | 13 | 546 | Chr05:62743005-62749566:- | 7.12 | 59414.6 | 8 | chlo | C | SP |
| Gorai.006G008600 | GrMATE26 | 7 | 498 | Chr06:1800720-1805532:- | 6.09 | 53853.4 | 10 | Plas | \_ | other |
| Gorai.006G046500 | GrMATE27 | 1 | 536 | Chr06:14761763-14763792:+ | 8.15 | 58840.8 | 11 | Plas | \_ | SP |
| Gorai.006G050100 | GrMATE28 | 7 | 491 | Chr06:17112065-17117253:- | 5.37 | 54083.8 | 11 | Plas | S | other |
| Gorai.006G063900 | GrMATE29 | 13 | 441 | Chr06:23570178-23573203:- | 4.88 | 46780.6 | 9 | Plas | C | other |
| Gorai.006G128800 | GrMATE30 | 13 | 545 | Chr06:38213510-38217000:- | 5.28 | 58869.7 | 8 | Plas | C | SP |
| Gorai.006G131300 | GrMATE31 | 3 | 502 | Chr06:38579915-38582825:- | 5.8 | 54192.2 | 11 | cyto | S | SP |
| Gorai.006G234700 | GrMATE32 | 1 | 467 | Chr06:48295470-48296873:+ | 6.5 | 50697.20 | 10 | Plas | \_ | SP |
| Gorai.007G004900 | GrMATE33 | 8 | 545 | Chr07:384248-387284:- | 8.17 | 59622.5 | 10 | Plas | \_ | SP |
| Gorai.007G010300 | GrMATE34 | 1 | 533 | Chr07:807159-808842:+ | 8.2 | 58233.2 | 11 | Plas | \_ | SP |
| Gorai.007G212500 | GrMATE35 | 2 | 522 | Chr07:23268178-23271777:- | 5.13 | 56170.4 | 12 | extra | C | other |
| Gorai.007G235800 | GrMATE36 | 8 | 490 | Chr07:31360881-31364028:- | 6.98 | 54006.1 | 10 | Plas | \_ | other |
| Gorai.007G249400 | GrMATE37 | 8 | 483 | Chr07:39181754-39185030:+ | 6.25 | 53567.3 | 10 | Plas | \_ | other |
| Gorai.007G251500 | GrMATE38 | 7 | 491 | Chr07:39830030-39833600:+ | 5.3 | 54891.9 | 10 | Plas | \_ | other |
| Gorai.007G251700 | GrMATE39 | 7 | 496 | Chr07:39956490-39964802:+ | 4.59 | 55342 | 10 | Plas | \_ | other |
| Gorai.007G251800 | GrMATE40 | 8 | 487 | Chr07:40072853-40075770:+ | 7.51 | 53953.7 | 11 | Plas | \_ | other |
| Gorai.008G058000 | GrMATE41 | 7 | 459 | Chr08:9023324-9026554:- | 8.41 | 50529.8 | 10 | Plas | \_ | other |
| Gorai.008G097100 | GrMATE42 | 8 | 506 | Chr08:26692254-26695826:- | 6.99 | 54571.3 | 10 | vacu | \_ | other |
| Gorai.008G120800 | GrMATE43 | 7 | 509 | Chr08:35743417-35748173:+ | 5.14 | 55626.3 | 10 | Plas | S | SP |
| Gorai.008G280200 | GrMATE44 | 1 | 543 | Chr08:55723888-55725519:- | 8.03 | 59214.1 | 11 | Plas | \_ | SP |
| Gorai.008G288100 | GrMATE45 | 8 | 475 | Chr08:56335708-56341003:+ | 6.24 | 51506.1 | 12 | Plas | C | other |
| Gorai.009G027800 | GrMATE46 | 1 | 537 | Chr09:2108215-2110297:+ | 7.51 | 58429.4 | 10 | chlo | S | SP |
| Gorai.009G178100 | GrMATE47 | 7 | 518 | Chr09:13750831-13754011:- | 5.78 | 56131.1 | 11 | Plas | S | SP |
| Gorai.009G225600 | GrMATE48 | 2 | 553 | Chr09:17632735-17634837:+ | 7.47 | 60366.3 | 12 | Plas | S | SP |
| Gorai.009G232700 | GrMATE49 | 8 | 491 | Chr09:18336486-18339526:+ | 6.78 | 53982.7 | 10 | Plas | S | SP |
| Gorai.009G293400 | GrMATE50 | 1 | 461 | Chr09:25436155-25437893:+ | 6.58 | 50247.9 | 11 | Plas | \_ | other |
| Gorai.009G342600 | GrMATE51 | 7 | 473 | Chr09:40051467-40054133:+ | 5.67 | 51626.6 | 9 | Plas | \_ | other |
| Gorai.009G344000 | GrMATE52 | 12 | 467 | Chr09:40675759-40678326:- | 6.65 | 49561 | 12 | Plas | \_ | SP |
| Gorai.009G381600 | GrMATE53 | 7 | 471 | Chr09:51805024-51809269:+ | 7.52 | 51406.8 | 12 | Plas | C | other |
| Gorai.009G381900 | GrMATE54 | 7 | 472 | Chr09:51833050-51839370:+ | 8.75 | 51844 | 11 | Plas | S | SP |
| Gorai.009G382800 | GrMATE55 | 7 | 471 | Chr09:51953274-51958986:+ | 6.33 | 51716 | 12 | Plas | S | other |
| Gorai.009G387100 | GrMATE56 | 5 | 259 | Chr09:52486525-52489456:+ | 9.1 | 28826.5 | 4 | Plas | \_ | SP |
| Gorai.009G390400 | GrMATE57 | 7 | 468 | Chr09:52959768-52962707:+ | 9.12 | 50889.5 | 12 | Plas | \_ | other |
| Gorai.010G030900 | GrMATE58 | 2 | 536 | Chr10:2641941-2643776:+ | 6.7 | 58182.6 | 12 | Plas | S | SP |
| Gorai.010G037100 | GrMATE59 | 8 | 492 | Chr10:3455469-3461205:+ | 5.27 | 53867.2 | 10 | Plas | \_ | SP |
| Gorai.010G077700 | GrMATE60 | 1 | 524 | Chr10:11216014-11217919:+ | 8.61 | 57096 | 10 | chlo | S | SP |
| Gorai.011G014800 | GrMATE61 | 7 | 522 | Chr11:1050455-1056445:+ | 6.32 | 57040 | 12 | Plas | S | SP |
| Gorai.011G110400 | GrMATE62 | 8 | 492 | Chr11:13205067-13209662:+ | 8.22 | 53980 | 12 | cyto | \_ | other |
| Gorai.011G128600 | GrMATE63 | 1 | 466 | Chr11:18506547-18507947:- | 8.19 | 50764.3 | 10 | Plas | \_ | SP |
| Gorai.011G192200 | GrMATE64 | 2 | 509 | Chr11:46234238-46236329:- | 7.48 | 55037.9 | 8 | cyto | \_ | SP |
| Gorai.012G158400 | GrMATE65 | 13 | 588 | Chr12:33156447-33161611:+ | 9.5 | 62981.9 | 9 | mito | C | SP |
| Gorai.013G114200 | GrMATE66 | 8 | 486 | Chr13:28049589-28054141:+ | 8.32 | 53629.8 | 11 | Plas | \_ | other |
| Gorai.013G169900 | GrMATE67 | 7 | 478 | Chr13:45626372-45629380:+ | 8.76 | 52030.6 | 12 | Plas | \_ | other |
| Gorai.013G170000 | GrMATE68 | 6 | 449 | Chr13:45663844-45666364:+ | 8.83 | 48883.8 | 10 | Plas | \_ | other |
| Gorai.013G170200 | GrMATE69 | 7 | 486 | Chr13:45720801-45725054:+ | 4.92 | 53239.3 | 12 | Plas | S | SP |
| Gorai.013G246100 | GrMATE70 | 7 | 486 | Chr13:56489344-56492648:+ | 8.78 | 52992.9 | 11 | Plas | \_ | SP |

PI: isoelectric value; Length (aa); protein lengths in amino acid bases; MW: molecular weight in Dalton; TM: transmembrane domain; Plas: plasma membrane; mito: mitochondrion; extra: extracellular organelles; E.R: endoplasmic reticulum; cyto: cytoplasm; vacu: vacuole; C: cytoplasm; S/SP: secretory pathway -: other regions; M: mitochondrion.