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| **Supplemental Table S2:** The expressed level of differential proteins in *Ricinus communis* L. inflorescences by mass spectrometry (MS) analysis. | | | | | |
| **Spot no.** | **Protein ID** | **Description** | **single female inflorescence** | **female with marker Inflorescence** | **bisexual inflorescence** |
| **4 euphylla stage** | | | | | |
| 1 | XP\_002526446.1 | Heat shock protein | 0.576±0.0076 | 0.094±0.0163 | \* |
| 2 | XP\_002534347.2 | ruBisCO large subunit binding protein | 0.388±0.0029 | 0.893±0.0209 | 0.148±0.0850 |
| 3 | XP\_002523404.1 | Rubiscosu bunit binding protein beta subunit | 0.234±0.0037 | 0.237±0.0090 | 0.151±0.0816 |
| 4 | XP\_002524206.1 | Ribulose bisphosphat carboxylase/oxygenase activase 1 | 0.117±0.0028 | 0.040±0.0379 | 0.070±0.0145 |
| 5 | XP\_002530503.1 | Ran binding protein | 0.220±0.0125 | 0.190±0.0458 | 0.360±0.0419 |
| 6 | XP\_002510253.1 | 26S proteasome non ATPase regulatory subunit ribulose bisphosphat | 0.113±0.0124 | \* | 0.010±0.0163 |
| 10 | XP\_015577917.1 | carboxylase/oxygenase activase 2 | 0.099±0.0047 | \* | 0.092±0.0377 |
| 11 | XP\_015572366.1 | S-adenosylmethionine synthase | 0.582±0.0249 | 0.609±0.0402 | 0.313±0.0419 |
| 12 | XP\_002522586.1 | O-methyltransferase | 0.511±0.0045 | 0.360±0.0386 | 0.265±0.0141 |
| 13 | XP\_002513928.1 | 14-3-3 protein | 0.307±0.0082 | 0.145±0.0249 | 0.966±0.0141 |
| 14 | XP\_002522386.1 | Oxygen-evolving enhancer protein 1 | 0.060±0.0094 | 0.100±0.0283 | 0.200±0.0136 |
| 15 | XP\_002530987.1 | Uncharacterized protein | 0.105±0.0357 | 0.110±0.0294 | 0.219±0.0245 |
| 16 | XP\_002512288.1 | Tubulin alpha chain | 0.788±0.0250 | 0.813±0.0054 | 0.048±0.0029 |
| 37 | XP\_002523376.1 | 14-3-3 protein | 0.4110±0.002 | \* | 0.342±0.0419 |
| 38 | XP\_002514900.1 | nuclear transport factor 2B | 0.257±0.0141 | 0.332±0.0283 | 0.717±0.0236 |
| 39 | XP\_002522386.1 | Oxygen-evolving enhancer protein 1 | 0.151±0.0004 | 0.007±0.0294 | 0.486±0.0170 |
| **5 euphylla stage** | | | | | |
| 18 | XP\_002528199.1 | Heat shock 70 kDa protein | 0.141±0.0403 | \* | 0.138±0.0130 |
| 20 | XP\_002518324.1 | Heat shock protein | 0.124±0.0125 | 0.204±0.0099 | \* |
| 21 | XP\_002509580.1 | Heat shock protein 70 (HSP70)interacting protein | 0.121±0.0287 | \* | \* |
| 22 | XP\_002524159.1 | Protein binding protein | 0.408±0.017 | 0.079±0.0109 | 0.197±0.0089 |
| 24 | XP\_002525204.1 | Glutathione-s-transferase omega | 0.079±0.0108 | \* | \* |
| 25 | XP\_015574043.1 | Inosine triphosphate pyrophosphatase | 0.25±0.0162 | 0.129±0.0156 | 0.044±0.0039 |
| 26 | XP\_002533008.1 | Uncharacterized protein | 0.255±0.0037 | 0.763±0.0061 | 0.841±0.0041 |
| 27 | XP\_002528522.1 | Thioredoxin reductase NTRB | 0.198±0.0147 | 0.32±0.0366 | \* |
| 28 | XP\_002515980.1 | Protein transport protein sec13 | 0.074±0.0244 | \* | \* |
| 30 | XP\_015571753.1 | uncharacterized protein | 0.048±0.0062 | \* | \* |
| 31 | XP\_002532190.2 | ribosome-inactivating | 0.062±0.0059 | \* | \* |
| 32 | XP\_002527995.1 | Proteasome subunit beta type | 0.096±0.0054 | \* | \* |
| 33 | XP\_002512222.1 | Uncharacterized protein | 0.027±0.0156 | 0.015±0.0164 | \* |
| 34 | XP\_002520127.1 | Ubiquitin-conjugating enzyme rad6 | 0.045±0.025 | 0.041±0.0076 | \* |
| **Main stem heading stage** | | | | | |
| 23 | XP\_002510911.1 | Enolase | 0.117±0.0125 | 0.084±0.001 | 0.11±0.0063 |
| 29 | XP\_002531606.1 | Inositol-1-monophosphatase | 0.055±0.0134 | 0.113±0.0108 | 0.012±0.0252 |
| 40 | XP\_002519500.1 | Transitional endoplasmic reticulum ATPase | 0.099±0.0104 | \* | \* |
| 41 | XP\_002517625.1 | phospholipase D alpha | 0.214±0.0219 | 0.131±0.0156 | 0.109±0.0201 |
| 42 | XP\_002513353.1 | Phosphoglycerate kinase | 0.213±0.0349 | \* | 0.085±0.0104 |
| 46 | XP\_015575717.1 | ferritin-3 | 0.154±0.0317 | 0.182±0.026 | 0.056±0.0122 |
| 47 | XP\_002527995.1 | Proteasome subunit beta type | 0.017±0.0257 | \* | \* |
| 48 | XP\_002513523.1 | Polyadenylate-binding protein | 0.06±0.0131 | 0.10±0.032 | 0.048±0.0136 |
| 49 | XP\_002521740.1 | Uncharacterized protein | 0.017±0.0227 | 0.022±0.04 | \* |
| 50 | XP\_002526500.1 | ATP binding protein | 0.033±0.0297 | 0.042±0.025 | 0.072±0.0142 |
| 52 | XP\_002530503.1 | Ran binding protein | 0.148±0.032 | 0.145±0.025 | \* |
| 53 | XP\_002523376.1 | 14-3-3 protein | 0.068±0.0314 | 0.115±0.031 | 0.048±0.0156 |
| 55 | XP\_002511200.1 | Elongation factor 1-beta | 0.108±0.0118 | 0.07±0.016 | \* |
| 57 | XP\_002518856.1 | 26S proteasome non-atpase regulatory subunit | 0.334±0.0341 | 0.185±0.033 | 0.445±0.0283 |
| 58 | XP\_002529248.1 | Triosephosphate isomerase | 0.032±0.022 | \* | 0.043±0.0221 |
| 59 | XP\_002516232.1 | Groes chaperonin | 0.05±0.038 | \* | 0.04±0.0137 |
| 60 | XP\_002526510.1 | UMP-CMP kinase | 0.054±0.0254 | \* | \* |
| 61 | XP\_002528798.1 | synthase delta chain, mitochondrial | 0.042±0.0116 | 0.041±0.024 | \* |
| 62 | XP\_002523979.1 | Tubulin-specific chaperone A | 0.021±0.0172 | 0.026±0.003 | \* |
| 63 | XP\_015584449.1 | eukaryotic translation initiation factor 5A | 0.06±0.0185 | \* | \* |
| 64 | XP\_002521598.1 | 40S ribosomal protein S12 | 0.09±0.0104 | 0.151±0.026 | \* |
| 67 | XP\_002533607.1 | Uncharacterized protein | 0.356±0.0219 | 0.324±0.0201 | \* |
| 71 | XP\_002528517.1 | Isocitrate dehydrogenase | 0.114±0.1192 | 0.120±0.1783 | \* |
| 74 | XP\_002531508.1 | Fructose-bisphosphate aldolase | 0.217±0.0277 | 0.276±0.013 | 0.135±0.017 |
| 91 | XP\_002512253.1 | cysteine synthase | 0.046±0.0119 | 0.148±0.0178 | 0.111±0.012 |
| **Second-level branching stage** | | | | | |
| 68 | XP\_002527736.1 | Heat shock protein | 0.21±0.0092 | \* | \* |
| 69 | XP\_002522194.1 | Actin | 0.396±0.0123 | 0.027±0.0141 | \* |
| 70 | XP\_002521293.1 | Nascent polypeptide associated complex alpha subunit | 0.261±0.0362 | \* | \* |
| 78 | XP\_002525552.1 | cysteine proteinase inhibitor | 0.042±0.0276 | 0.023±0.018 | \* |
| 79 | XP\_002516930.1 | Translationally-controlled tumor protein | 0.156±0.0131 | 0.187±0.0238 | 0.339±0.0219 |
| 80 | XP\_002517071.1 | 1,2-dihydroxy-3-keto-5-methylthiopentene dioxyge | 0.034±0.0306 | 0.043±0.0069 | 0.085±0.0233 |
| 83 | XP\_002524472.1 | Uncharacterized protein | 0.069±0.0196 | 0.067±0.0246 | 0.147±0.0159 |
| 85 | XP\_002526922.1 | Glycine-rich RNA-binding protein | 0.087±0.0134 | 0.058±0.0127 | 0.041±0.012 |
| 86 | XP\_002528580.1 | enolase | 0.051±0.0125 | \* | 0.023±0.0168 |
| 87 | XP\_002524262.1 | Malate dehydrogenase | 0.05±0.0109 | \* | \* |
| 88 | XP\_015582143.1 | annexin | 0.188±0.0131 | 0.178±0.0207 | \* |
| 89 | XP\_002532823.1 | Glutathione s-transferase | 0.037±0.0217 | \* | \* |
| 90 | XP\_015583123.1 | proteasome subunit alpha type-3 | 0.049±0.0124 | \* | 0.053±0.0165 |
| 93 | XP\_002528580.1 | enolase | 0.097±0.0219 | 0.077±0.0134 | 0.208±0.0237 |
| 94 | XP\_002515309.1 | Protein disulfide isomerase | 0.046±0.0226 | 0.014±0.0174 | 0.079±0.0126 |
| 95 | XP\_002512288.1 | Superoxide dismutase [Cu-Zn] | 0.129±0.0118 | 0.048±0.0103 | 0.043±0.0184 |
| 96 | XP\_002522546.1 | Malate dehydrogenase | 0.118±0.0112 | 0.158±0.0245 | \* |

\*: Protein is not expressed; Data are reported as mean ± SD from three biological repetition.