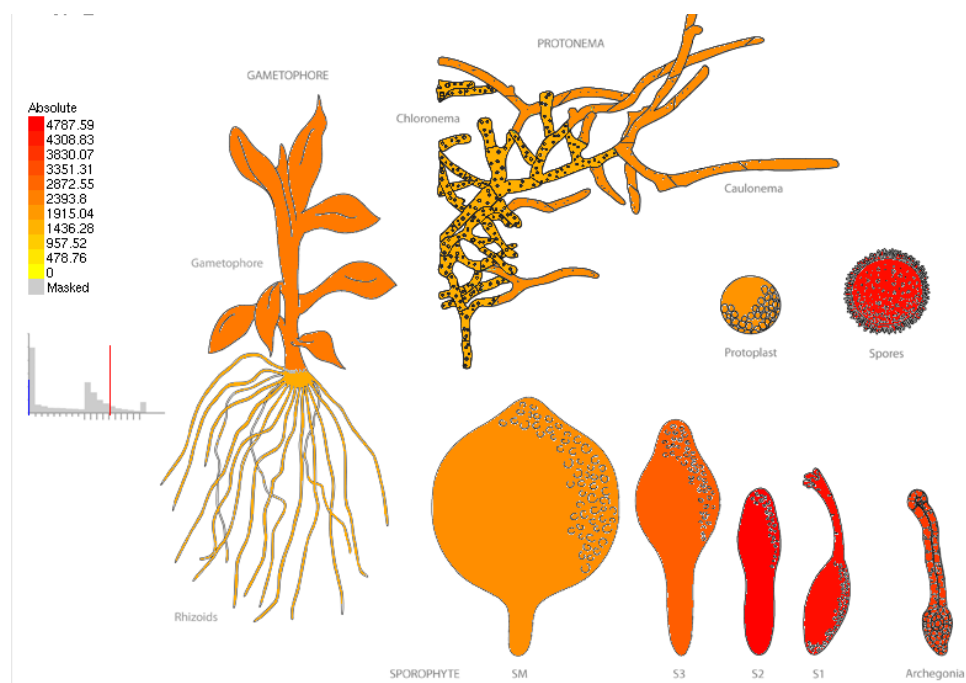
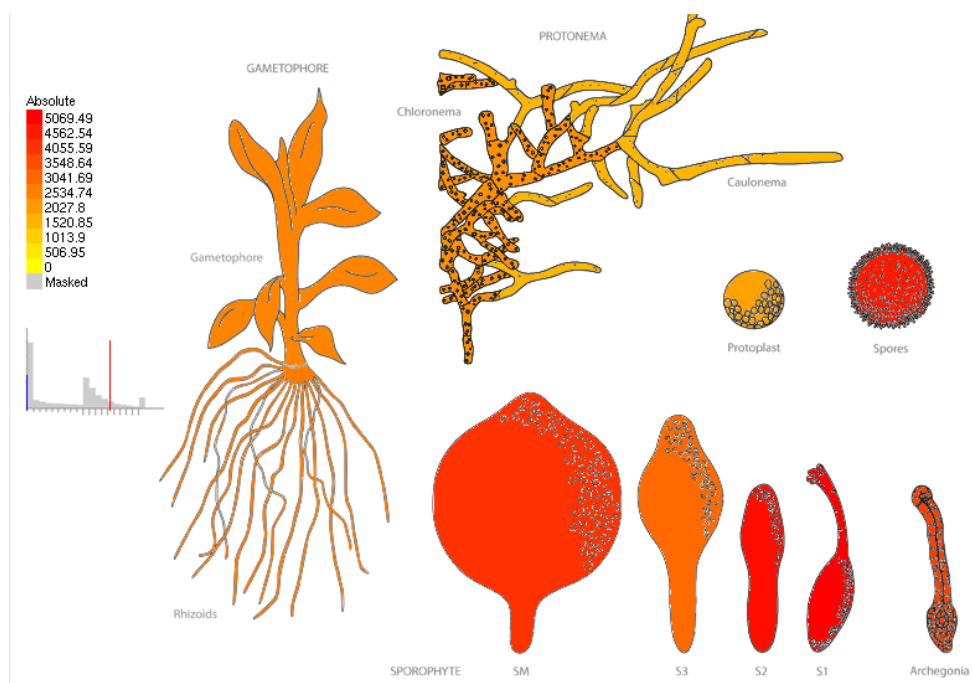
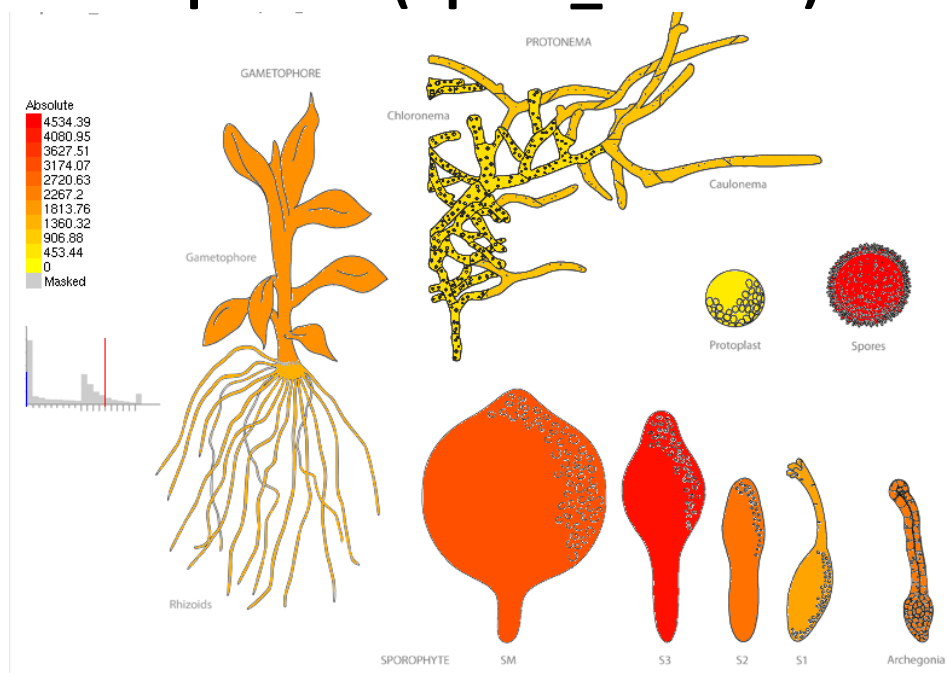
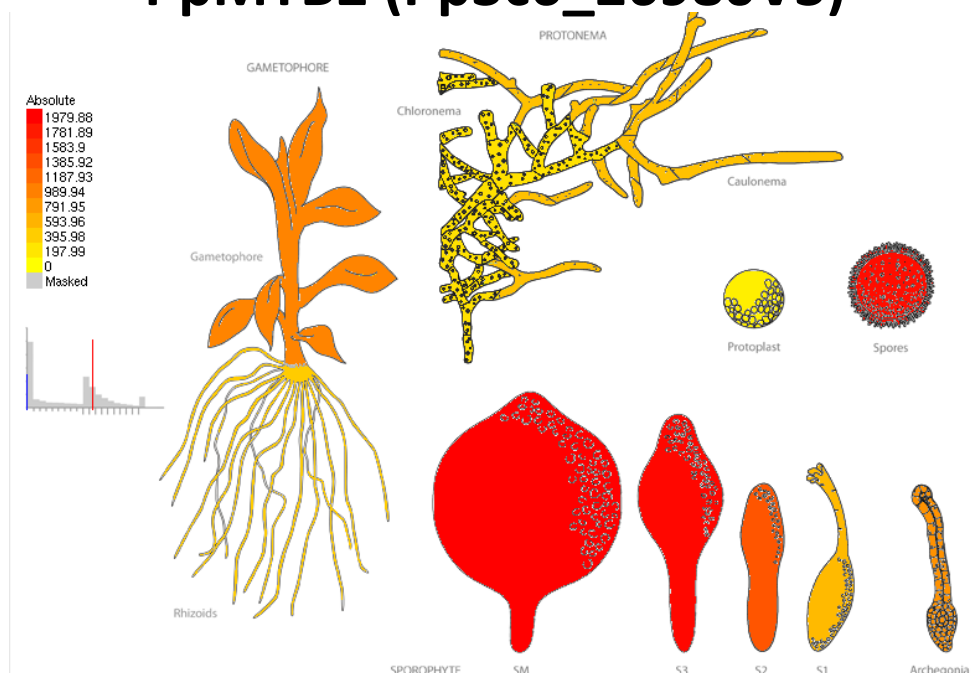


**(a)****PpMTA (Pp3c1\_32590V3)****(b)****PpFIP37 (Pp3c8\_10480V3)****(c)****PpMTB1 (Pp3c5\_5900V3)****(d)****PpMTB2 (Pp3c6\_26980V3)**

**Figure S4. The accumulation of methyltransferase complex transcripts is larger during sporophyte development.**

Gene expression maps for **(a)** *PpMTA*, **(b)** *PpFIP37*, **(c)** *PpMTB1* and **(d)** *PpMTB2* were obtained from the eFP browser ([http://bar.utoronto.ca/efp\\_physcomitrella/cgi-bin/efpWeb.cgi](http://bar.utoronto.ca/efp_physcomitrella/cgi-bin/efpWeb.cgi)). In these schemes we observe the absolute accumulation of the transcripts that encode for the MTC components in *P. patens*. For all of them, the highest expression observed is in the developing sporophyte and in the mature spore.