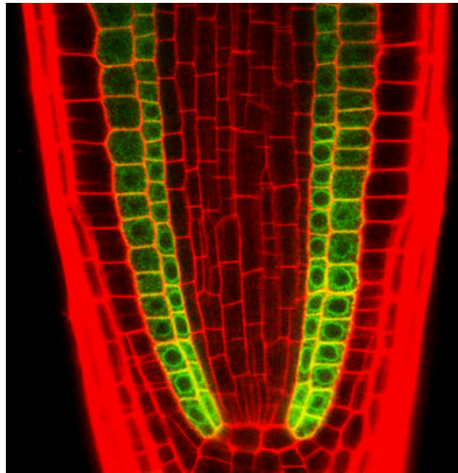


# PRACTICE 1: UNDERSTANDING THE ROLE OF CELL-TYPE SPECIFIC FACTORS



*wt J0571*



*shr2 J0571*



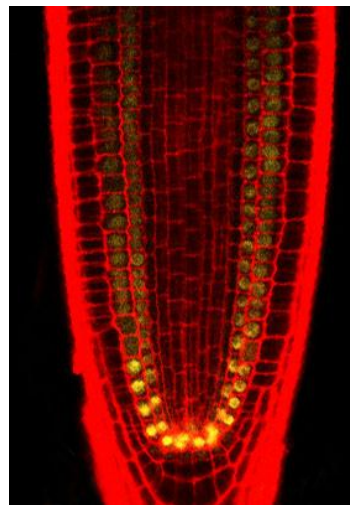
*SHORT-ROOT*



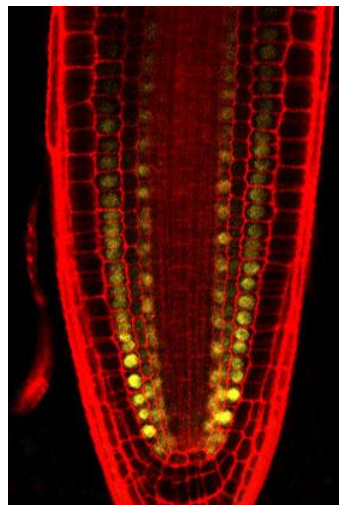
*pSCR:GFP:SCR*



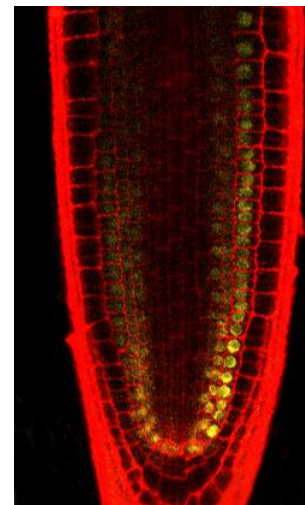
*Rec-JKD-YFP*



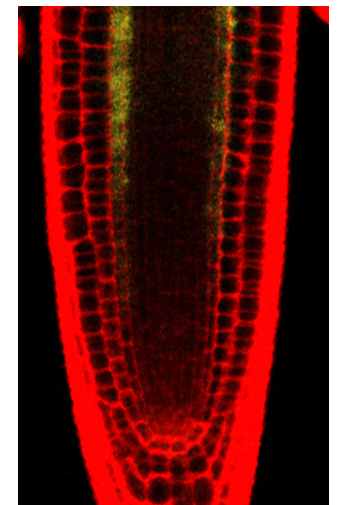
*Rec-MGP-YFP*



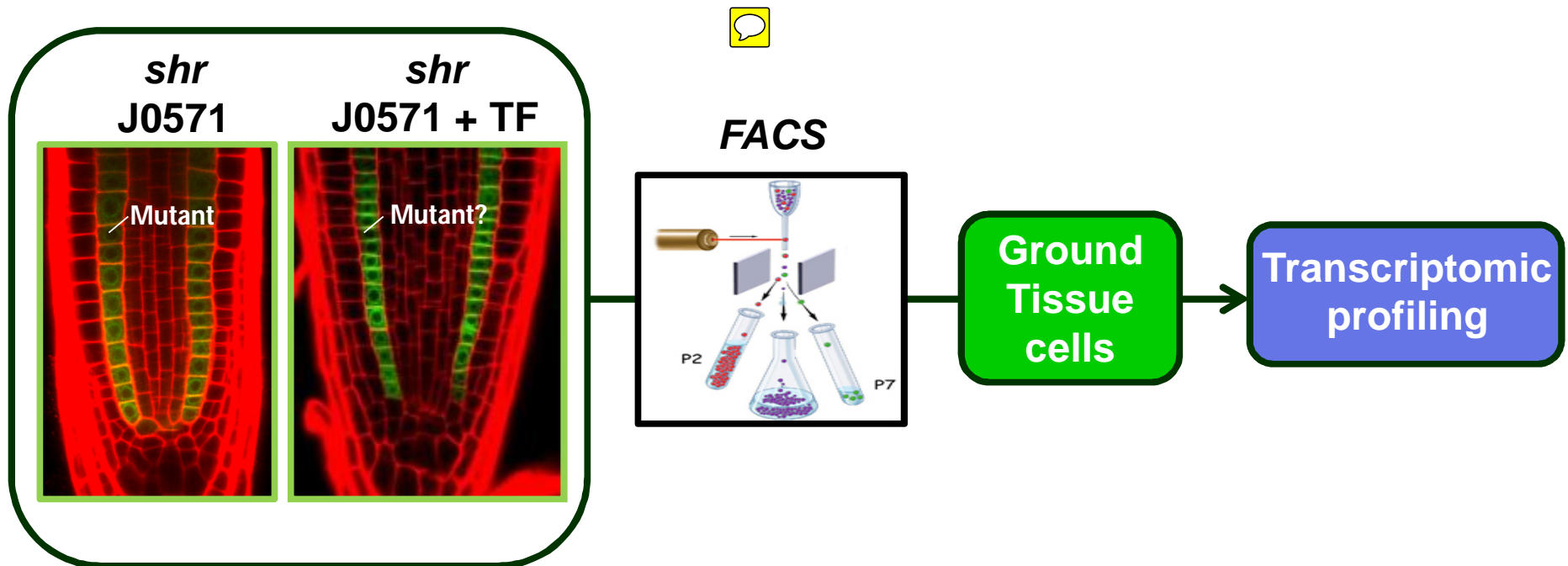
*pNUC-NUCs-YFP*



*Rec-BLJ-YFP*



# PRACTICE 1: EXPERIMENTAL DESIGN





# PRACTICE 1 EXERCICES

1. -Calculate relationships among ground tissue cells in *shr* mutant, the wild type and the complemented lines with the transcription factors BLUEJAY (BLJ), JACKDAW (JKD), MAGPIE (MGP), NUTCRACKER(NUC), IMPERIAL EAGEL (IME) and SCARECROW (SCR). File = table.csv
- 2.- Create intermediate transcriptomes between *shr* mutant and the wild which represent 25%, 50% and 75% of complementation. Recalculate relationships. What role may you establish for of these transcription factors?
- 3.- Add the transcriptome of cells corresponding to SCR domain. What might you conclude for several of these transcription factors?
- 4.- Find the most important genes which contribute to these transcriptomic changes. Investigate their expression patterns across samples. What do you observe?