



CEPLAS

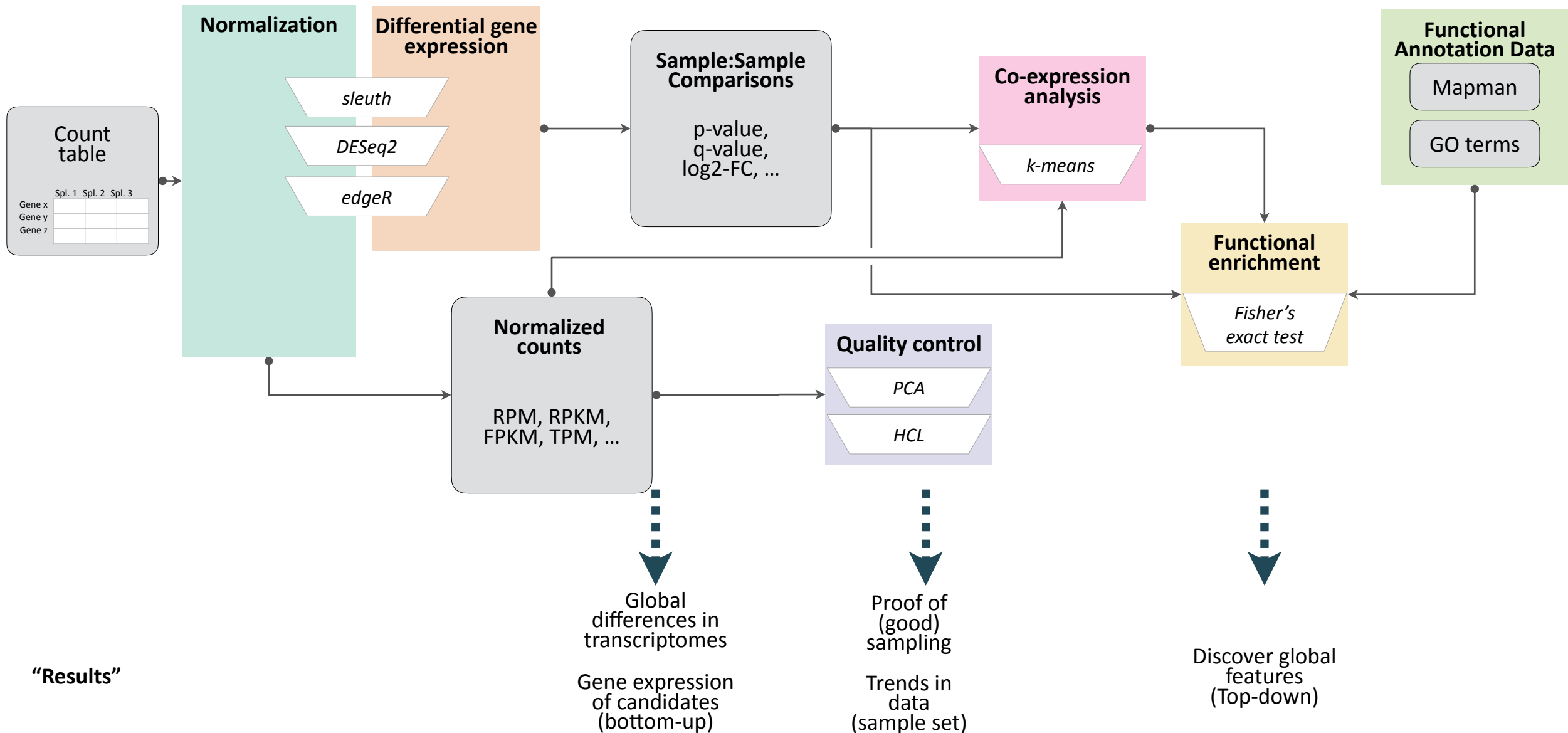
Cluster of Excellence on Plant Sciences

Reads to finding





# Biological knowledge extraction





# RPM, RPKM, FPKM, TPM,...

- RPM (*reads per million*)
  - $\text{RPM}_{\text{GeneX}} = \text{ReadCount}_{\text{GeneX}} / \text{ReadCount}_{\text{Total}} / 10^6$
- RPKM (*reads per kilobase million*)
  - $\text{RPKM}_{\text{GeneX}} = \text{RPM}_{\text{GeneX}} / \text{GeneLength}_{\text{GeneX}}$
- FPKM (*fragments per kilobase million*)
  - Same as RPKM except for paired-end reads
  - Takes into account that two reads can map to one fragment
- TPM (*transcripts per kilobase million*)
  - $\text{RPK}_{\text{GeneX}} = \text{ReadCount}_{\text{GeneX}} / \text{GeneLength}_{\text{GeneX}}$
  - $\text{TPM}_{\text{GeneX}} = \text{RPK}_{\text{GeneX}} / \text{RPK}_{\text{Total}} / 10^6$

