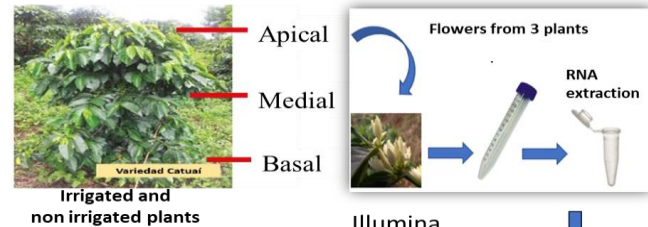
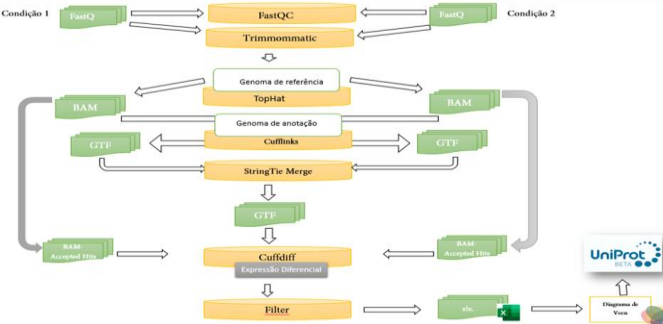


Introduction. Floral development significantly impacts coffee productivity and quality, and environmental conditions and soil water capacity playing vital roles on it. To study the effects on plant flowering, we conducted a transcriptome analysis on flowers buds from various plant sections, from plants under irrigated and non-irrigated conditions.

Material/Methods



Galaxy Pipeline



Results

Table 1. Coffee flowers transcriptome data analysis

	Basal	Medial	Apical	Ap Irrigated	Ap Non Irrigated	Md Irrigated	Md Non Irrigated
Reads	23.139.288	23.572.530	25.757.440	75.875.364	25.757.440	71.191.793	23.572.530
Aligned reads %	79.60	86.20	85.40	84.1	89.2	76.1	85.4
# Contigs	10.968	10.938	10.925	10.317	10.393	10.334	10.358
Unique genes	54	30	51	0	4	0	1
Upregulated	145	46	110	123	40	125	5
Down Regulated	1	98	17	293	126	450	60

- ✓ 92 genes differentially expressed between the apical and medial regions, 58 genes between the apical and basal regions, and 151 genes between the medial and basal regions.
- ✓ higher number of upregulated genes in flowers from irrigated plants, both in the medial region (450 genes) and the apical region (293 genes).

Conclusion/Perspectives

- ✓ a comprehensive panel of differentially expressed genes, both under irrigated/non-irrigated conditions and across different plant regions is provided.
- ✓ under irrigated conditions, upregulated genes included stress-responsive ones like stress-induced protein K1N2-like, nsLTPs, and LEA 1-like, commonly associated with water stress.