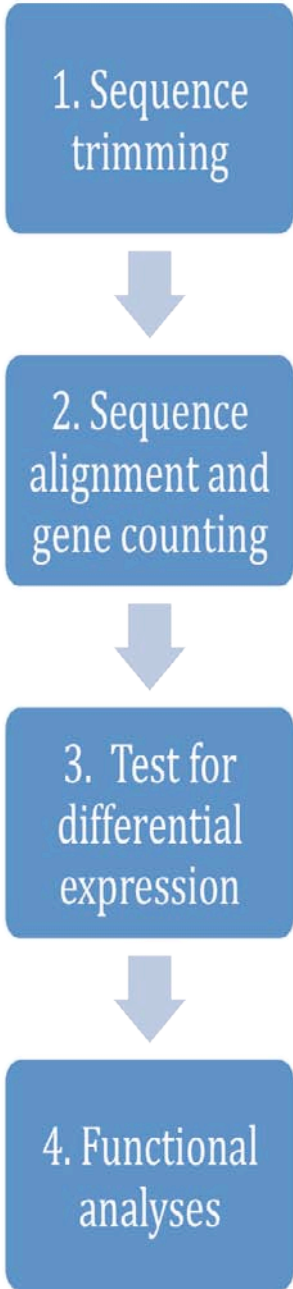


Analysis pipeline

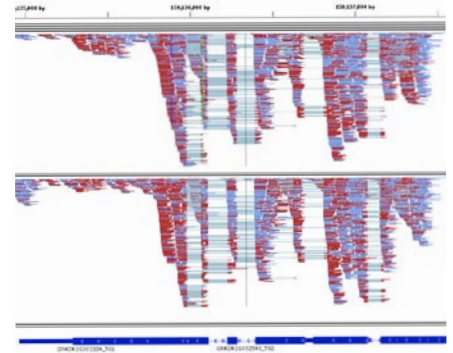


1. Quality check of sequence data

Data	Raw Reads	Trimmed Reads	Raw Read Len.	Trimmed Read Len.	Trimmed %
Sample 1	24,737,600	23,347,979	75	72	94.4%
Sample 2	23,116,137	21,674,741	75	71	93.8%

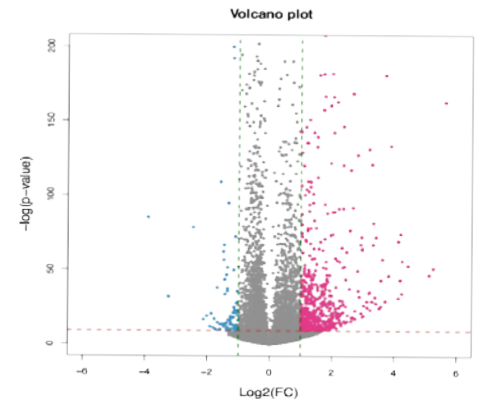
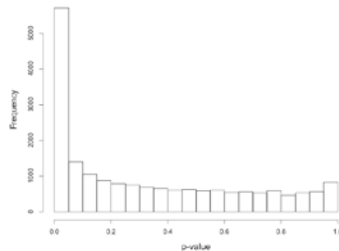
2. Sequence alignment to reference genome and alignment visualisation

Data	No. mapped reads	No. uniquely mapped reads	No. uniquely mapped reads to genes
Sample 1	11,821,711	11,024,188	9,218,760
Sample 2	11,030,851	10,435,290	8,858,178



3. Pair-wise comparison of gene expression

No. Up	No. Down	Up (<=-1)	Down (>=-1)	Up (>1)	Down (<-1)	No. genes tested ²
674	701	330	520	344	181	11,555
5.8%	6.1%	2.9%	4.5%	3.0%	1.6%	100%



5. Visualization of differential expressed gene pathway and Gene ontology analysis

