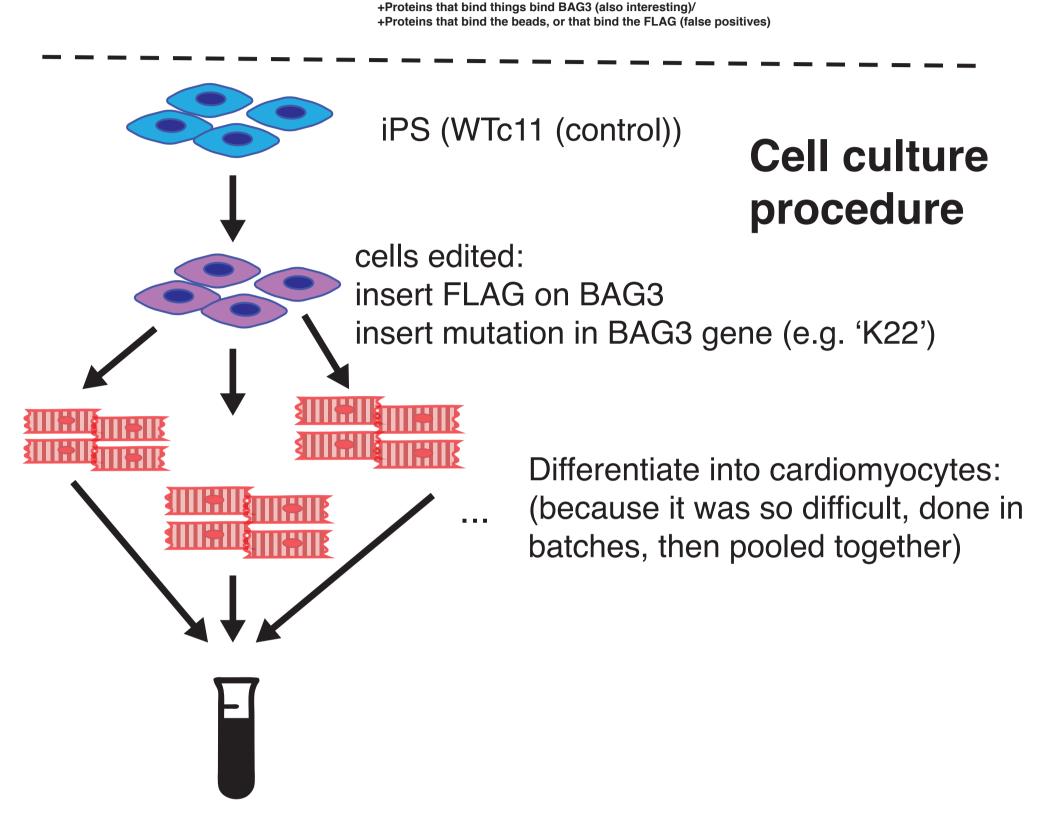
## **AP-MS** basics Starting material: cell lysate. BAG3 is fused with a 3xFLAG tag Magnetic Beads (bind the 3xFLAG) 3xFLAG **Affinity Purification** To Mass Spectrometry (MS) **Basic Steps:** 1.-Cut protein into peptides 2.-MS1: quantify peptide intensity 3.-MS2: identify the peptides (sequence) A small fraction is retained. 'protein intensity' is just summed peptide intensity Most of the proteome is discarded This contains:

+Proteins that bind BAG3 (true positives)



## Frozen cell pellet for later processing

