

# MIMOSA 23 SETTINGS

---

Elena Rocco

Nikhef-Utrecht University

24<sup>th</sup> October 2013

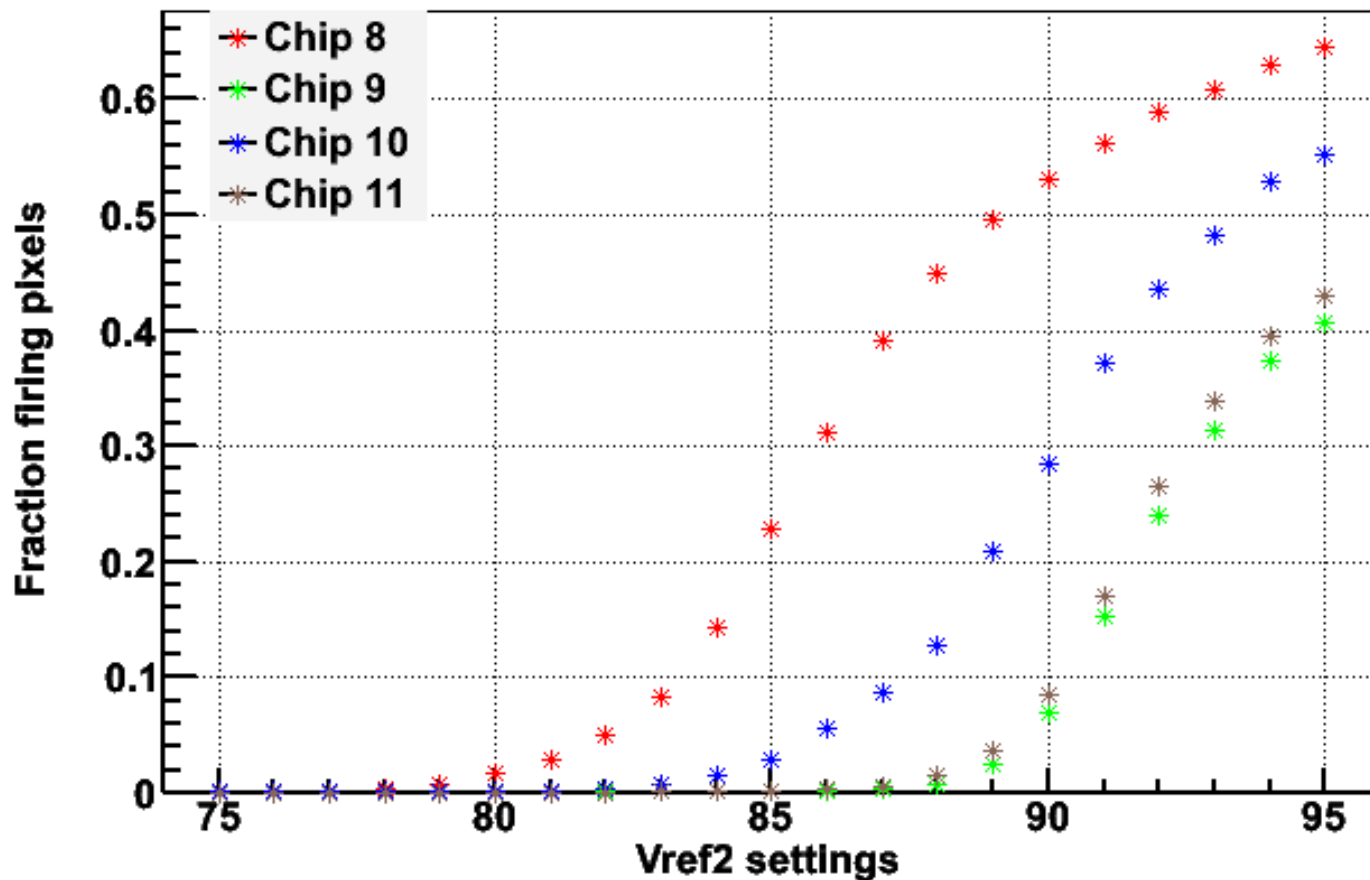
# Current status

- **Detector in use:** FoCal prototype; 24 layers , 96 chips (MIMOSA 23)
- **Non uniform response:** from the testbeam data analysis we noticed that we have large variation in sensitivity from chip to chip
- **Settings in use:** settings used during the test beam:  $V_{ref2}=80$   $V_{ref1}$  optimised per single chip
- **Tests in lab:**
  - “pedestal” measurements -> systematic studies in  $V_{ref1}$  and  $V_{ref2}$
  - Cosmic data taking (for given threshold settings to study the MIP response)
- **Only digital R/O available** (no voltage reading)

# Open points (1)

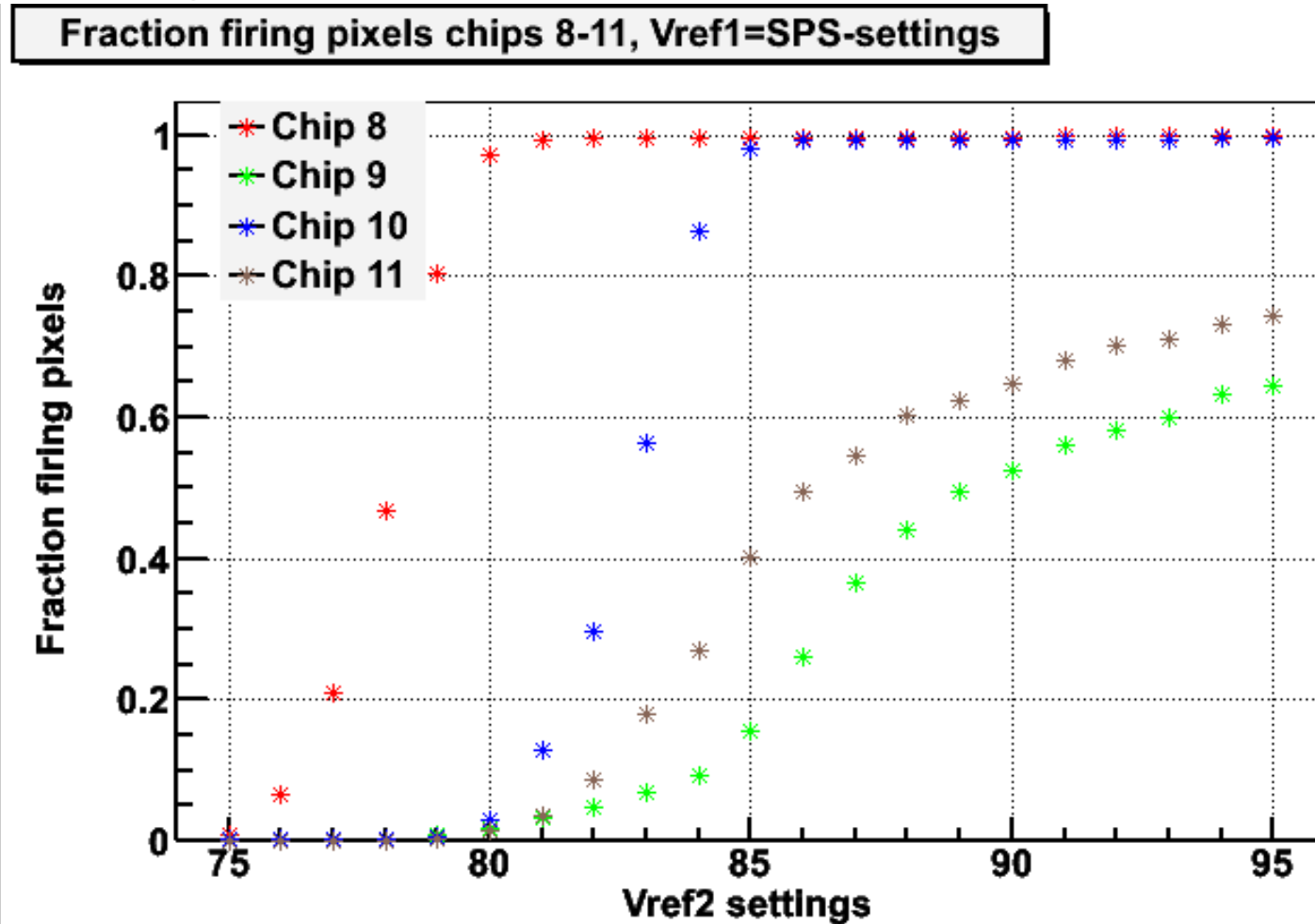
1. Impossibility to get the discriminator transfer function normalised from 0 to 1

Fraction firing pixels (new definition) chips 8-11, Vref1=SPS-settings



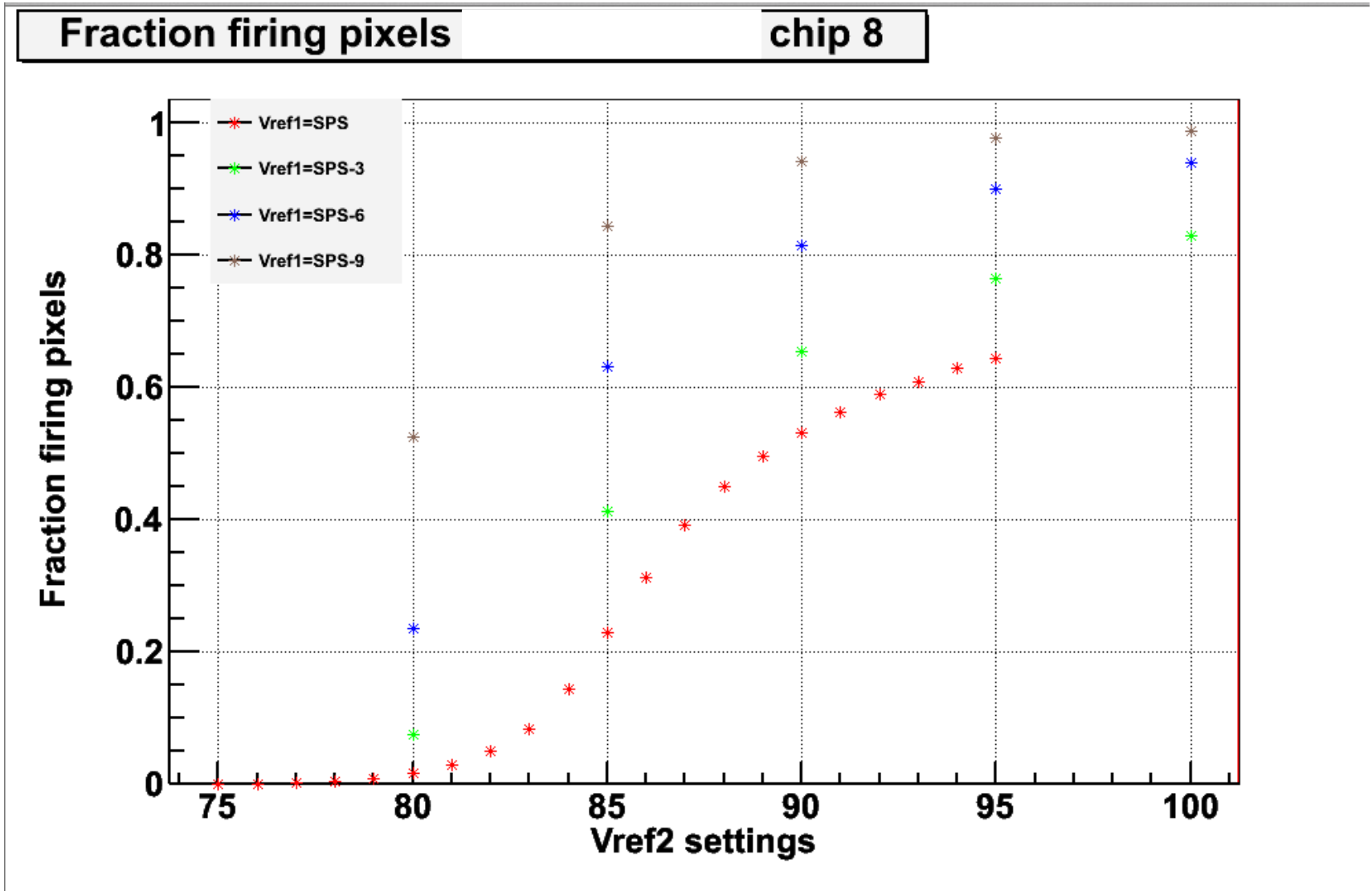
# Open point (2)

- The normalisation of the firing pixels to 1 hides possible pathological behaviour



# Open point (3)

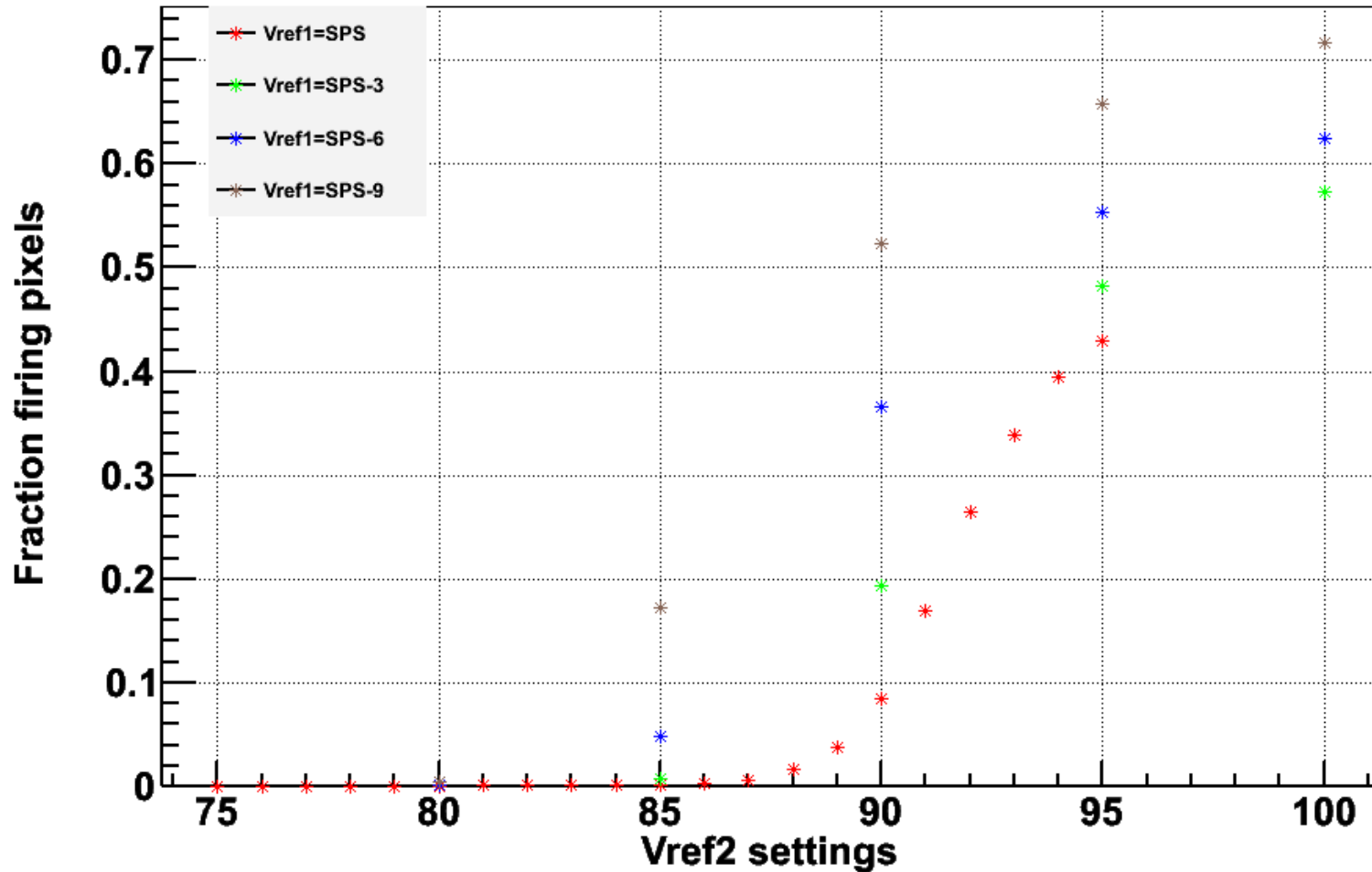
Different Vref1 settings -> different discriminator transfer functions



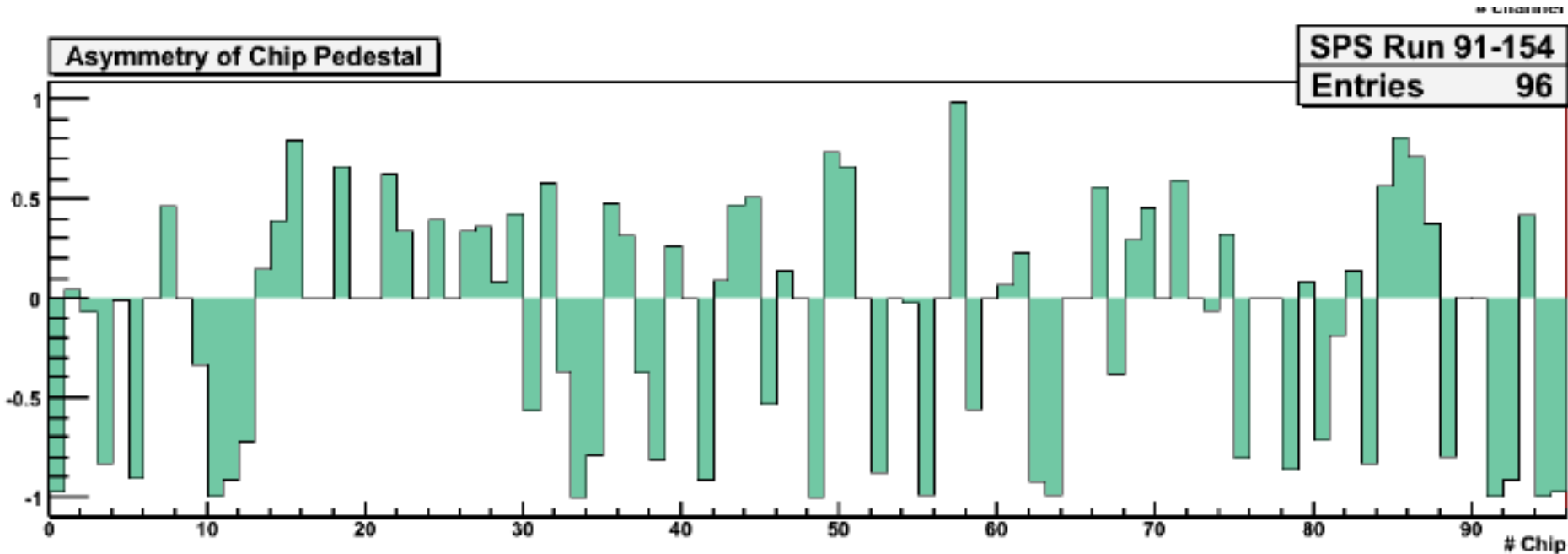
# Open point (3) another example

Fraction firing pixels

chip 11



# Open point (4): unbalance left-right

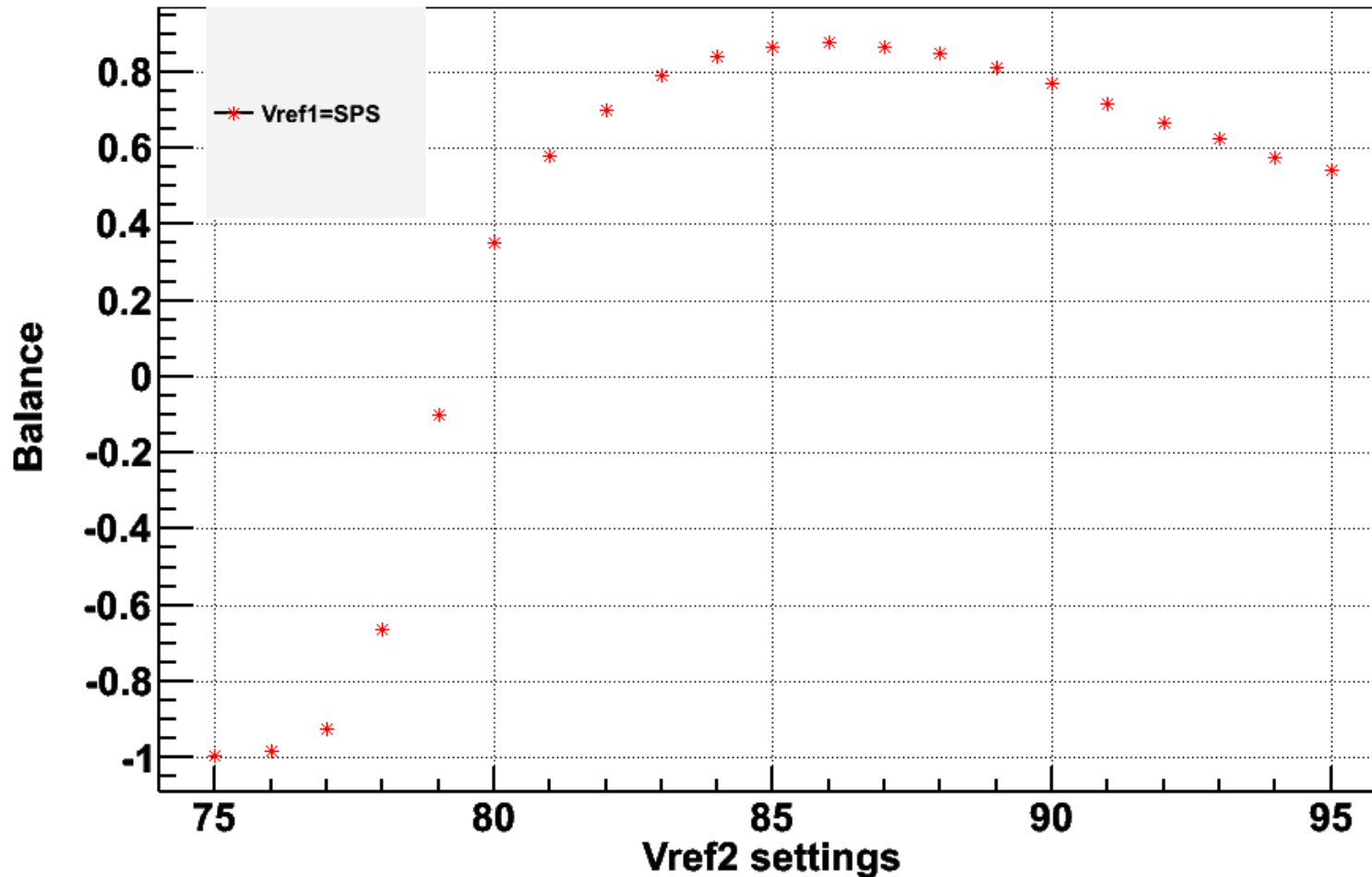


All the chips have  $V_{ref2}=80$ : unexpected unbalance!!!  
Some unbalanced chips present hot columns/rows/pixels

# Open point (4)

- Scan in Vref2 looking at the unbalance left-right

## Balance of chip 8

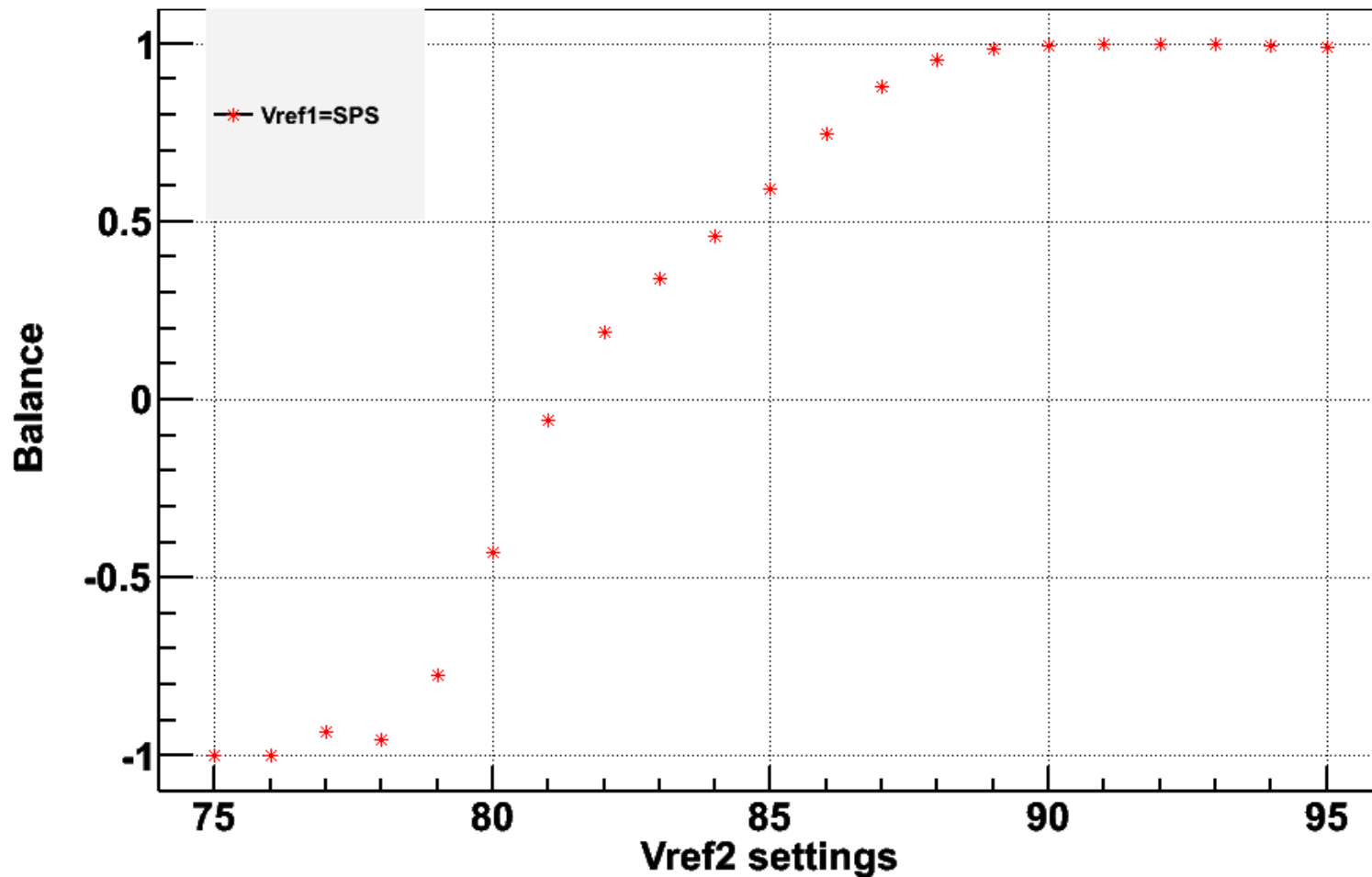




# Open point (4) another example

- Scan in Vref2 looking at the unbalance left-right

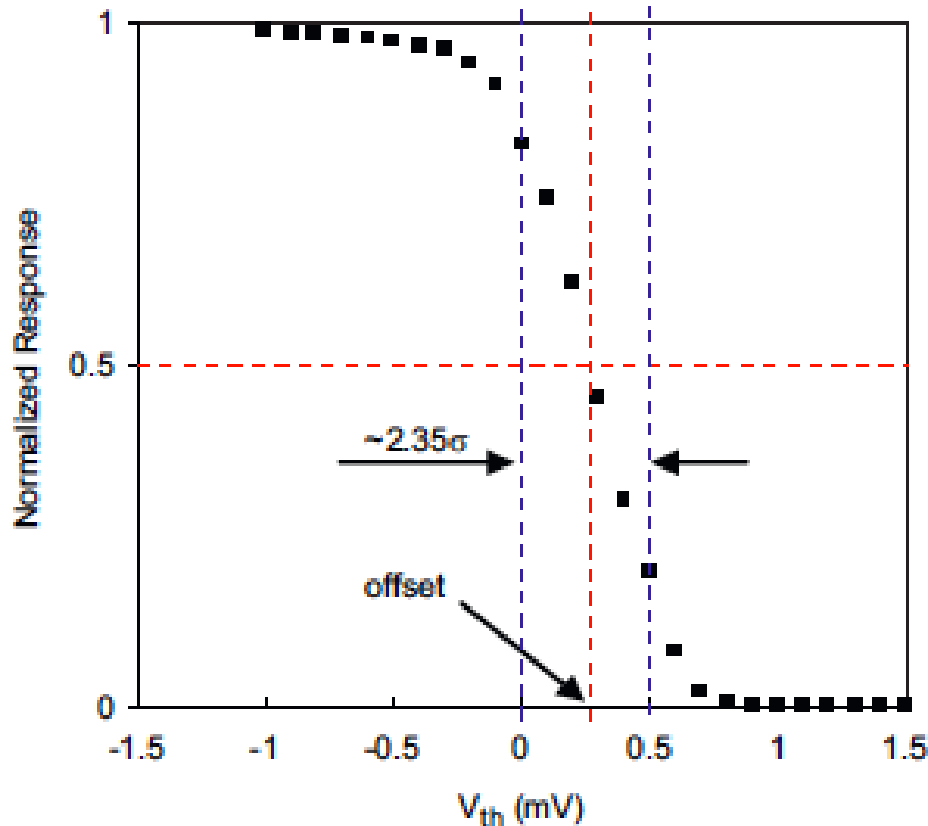
## Balance of chip 9



Which is the procedure to get the best Vref2 value then?

# Open point (5)

- The discriminator transfer function fit

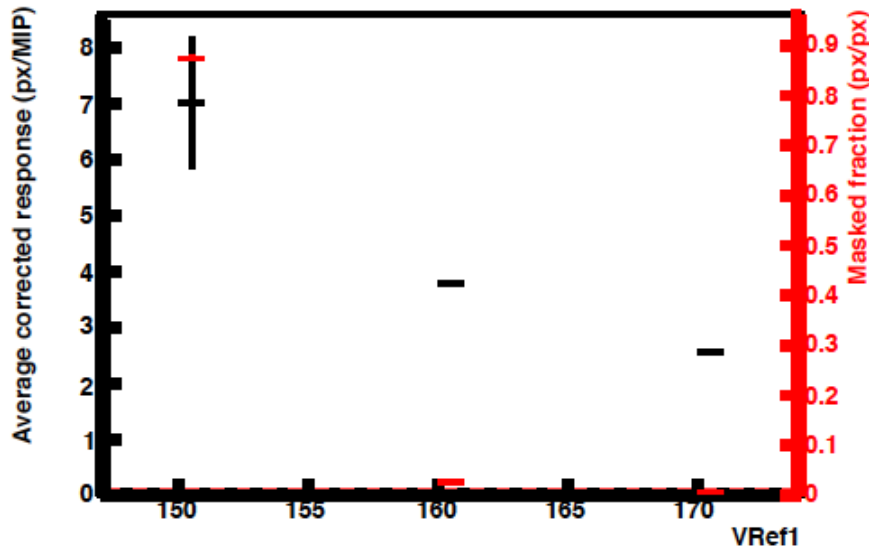


From the paper (NIM A 602 (2009) 461-466). “..One can fit with an erf (error function) to this curve. Its derivative gives a gaussian (normal) distribution.the FWHM is  $\sim 2.35 \sigma$ , and its mean give the offset of the comparator, where  $\sigma$  is the rms temporal noise.”

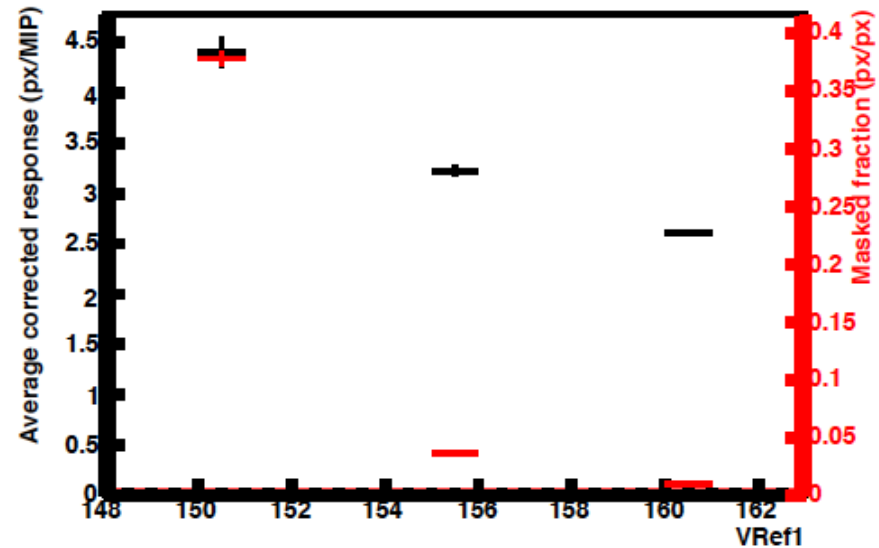
Question: can we do the same operation but with the digital readout?

# Open point (6): clustersize (chip 8&9)

Corrected response profile for chip 8

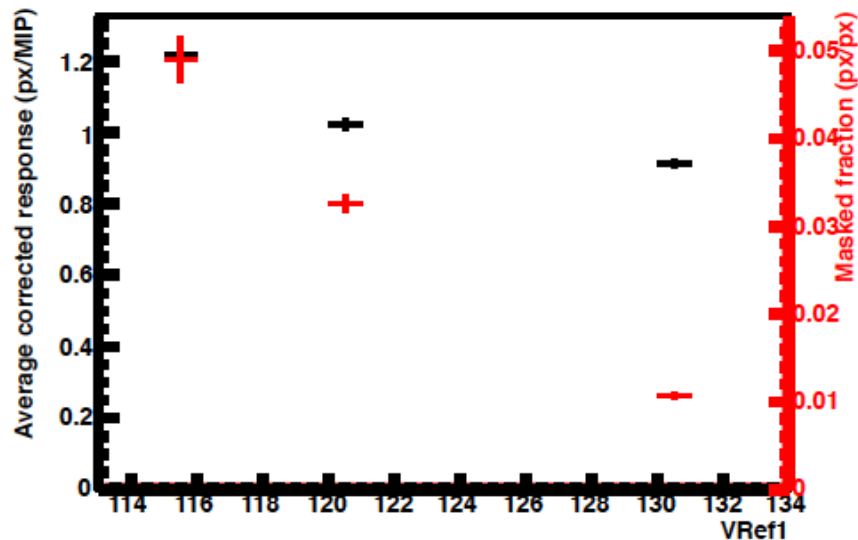


Corrected response profile for chip 9

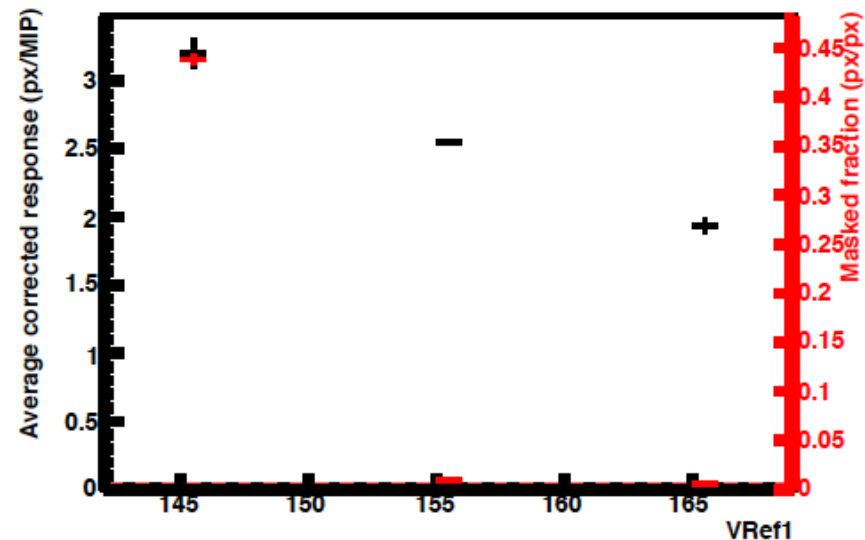


# Open point (6): clustersize (chip 10&11)

Corrected response profile for chip 10



Corrected response profile for chip 11



More questions might come....

**THANK YOU!**