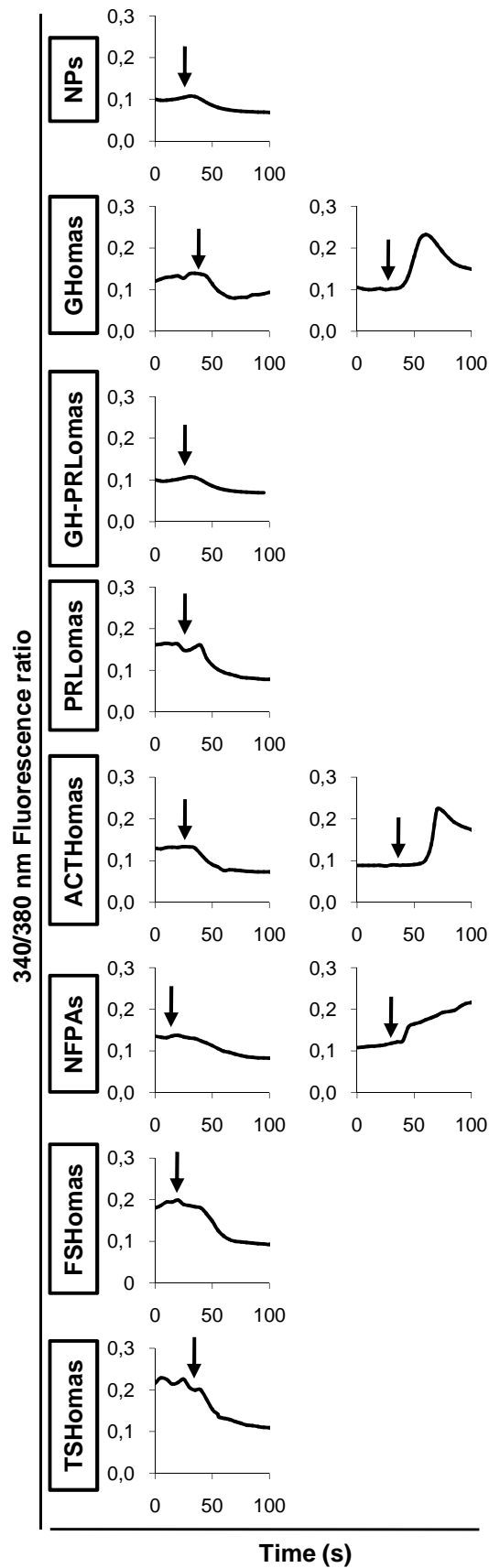


**BIM-23A760 influences key functional endpoints in pituitary adenomas and normal pituitaries: molecular mechanisms underlying the differential response in adenomas**

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**Supplemental table-1.** Absolute cDNA copy number/50ng total RNA of gene transcripts in the whole pituitary versus primary pituitary cell cultures (control groups) of female baboons, as determined by quantitative real-time PCR. Values represent means  $\pm$  SEM (from 3 separate whole pituitary extracts and primary pituitary cell cultures of the same baboons).

| <b>Gene</b>           | <b>Whole pituitary</b> | <b>Primary pituitary cell cultures</b> |
|-----------------------|------------------------|--|
| <b>sst2</b>           | 2,182 $\pm$ 229        | 2,018 $\pm$ 309                        |
| <b>sst5</b>           | 4,465 $\pm$ 357        | 3,809 $\pm$ 479                        |
| <b>D<sub>2</sub>T</b> | 28,269 $\pm$ 4,239     | 20,347 $\pm$ 2,785                     |
| <b>D<sub>2</sub>L</b> | 16,116 $\pm$ 3,077     | 11,420 $\pm$ 1,620                     |
| <b>Cyclophilin A</b>  | 79,469 $\pm$ 5,578     | 88,280 $\pm$ 1,626                     |



**Supplemental Figure 1.** Representative profiles of changes in  $[Ca^{2+}]_i$  in primary cell culture from normal pituitaries (NPs,  $n=4$ ) as well as from GHomas ( $n=20$ ), mixed GH/PRLomas ( $n=5$ ), PRLomas ( $n=6$ ), ACTHomas ( $n=10$ ), NFPAs ( $n=16$ ), FSHomas ( $n=1$ ) and TSHomas ( $n=2$ ) in response to BIM-23A760 administration (100 nM; arrow).