

Supplementary Table 3: Data collected from 26-plex pre-amplification of reference RNA dilution series (see also Fig. 4). Slopes and median standard deviations of triplicate pre-amplifications (SD) were shown. (A) Uncorrected C_T values. (B) C_T values were corrected by the arithmetic average of the three SIR transcripts. The slopes were close to 0.0. The median SD of triplicates of the same concentration for all assays except OAZ1 is reduced. Also the SD's of the ΔC_T values determined between 100 and 0.1 ng show that there is no variability due to total RNA concentration.

| | | ANXA2 | DUSP1 | H3F3A | IL1B | IL8 | OAZ1 | RPL37 | S100A8 | S100P | SAT | 3SIRs | |
|----------|--|-----------|-------|-------|-------|-------|-------|-------|--------|-------|-------|-------|-------|
| A | C_T values | slope | -3.68 | -3.63 | -3.43 | -3.76 | -3.62 | -3.50 | -3.90 | -3.63 | -3.63 | -3.64 | -3.77 |
| | | median SD | 0.30 | 0.52 | 0.52 | 0.77 | 0.30 | 0.21 | 0.45 | 0.47 | 0.42 | 0.25 | 0.35 |
| B | ΔC_T values (normalized by 3 SIRs) | slope | 0.05 | 0.11 | 0.06 | 0.04 | 0.09 | 0.24 | -0.16 | 0.11 | 0.10 | 0.10 | |
| | | median SD | 0.20 | 0.17 | 0.35 | 0.37 | 0.28 | 0.28 | 0.12 | 0.11 | 0.20 | 0.15 | |
| | SD of measurments from 100 to 0.1 ng | | 0.21 | 0.21 | 0.27 | 0.35 | 0.25 | 0.45 | 0.26 | 0.19 | 0.27 | 0.16 | |