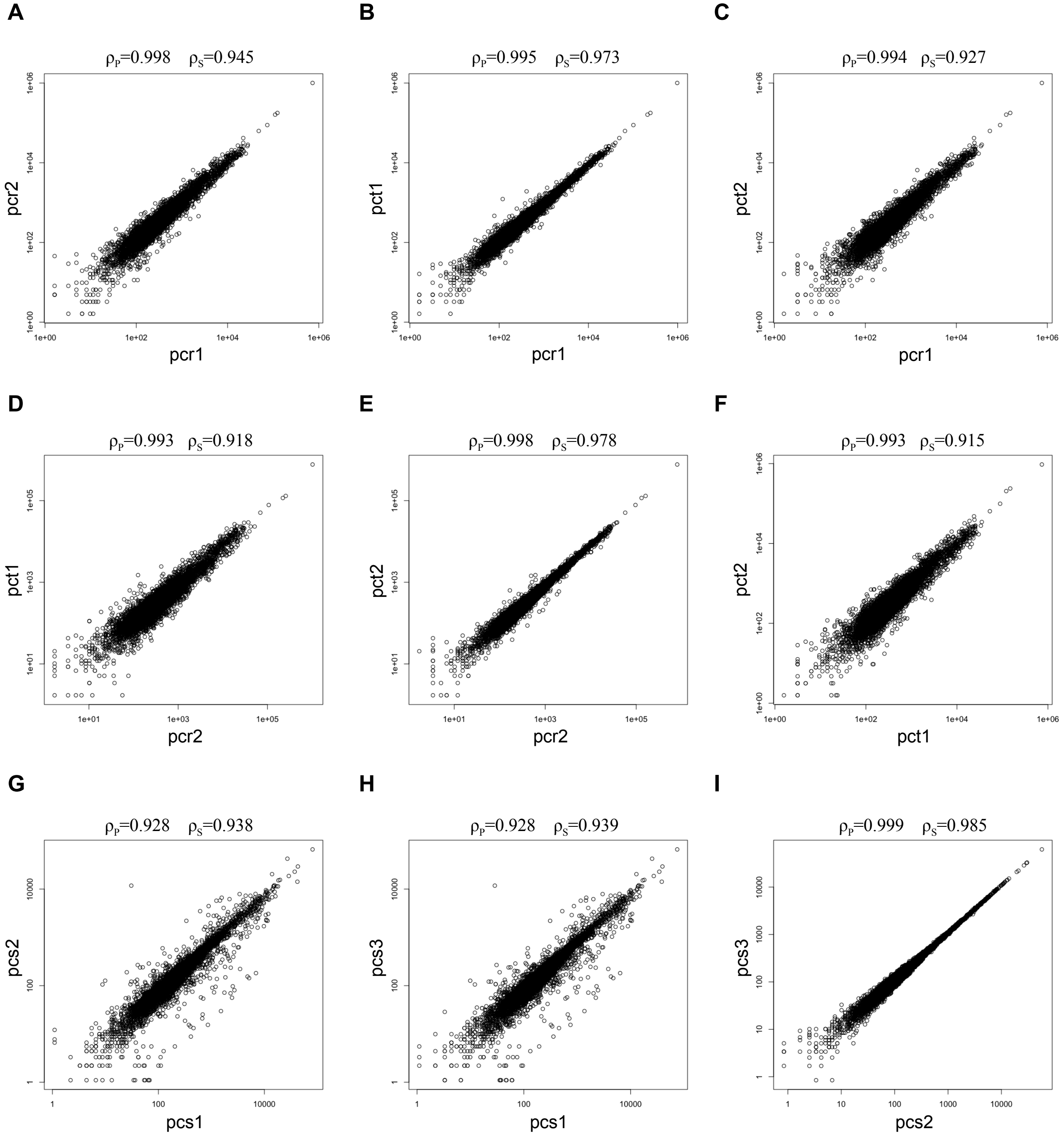

Figure S1. Comparison of technical and biological replica data sets. (*A-I*) Transcript abundance measures were derived from the number of reads (not including end-reads) that align within a 500-nucleotide window at the 5' end of the transcript (for the SL-libraries) or at the 3' end (for the poly-A enriched libraries; random primed or oligo(dT) primed). Shown above each graph are the Pearson's correlation coefficient (ρ_P) and the Spearman's rank correlation coefficient (ρ_S). *Pcr*, *pct* and *pcs* indicate libraries from procyclic cells prepared with random primers, oligo(dT) primer and SL primer (for the second cDNA strand), respectively.