Dorsoventral (DV) embryonic patterning relies on precisely controlled interpretation of morphogen signaling. In all vertebrates, DV axis specification is informed by gradients of Bone Morphogenetic Proteins (BMPs). Interestingly, the intrinsically stochastic production distribution of the BMP morphogen source is buffered and is integrated into precise and reproducible DV gradients of PSmad, a readout of BMP signaling. To quantify the inputs and outputs in this pathway, we developed a novel wavelet-based nuclei and object segmentation algorithm, that contains five main steps including 2D continuous wavelet transform, multi-scale object identification, 3D alignment, object division, and outlier removal. Using single-molecule mRNA quantification in zebrafish embryos, we determine the quantified bmp2b gene expression with single mRNA resolution throughout the embryo composed of between 8,000-10,000 cells. We applied similar wavelet-based segmentation algorithms for mature mRNA and nascent mRNA spot size. Next, we applied least-square algorithm to fit the intensity distribution of total fluorescence intensity for all mature mRNA spots and calculated individual mRNA molecule intensity. We evaluated the cell-to-cell and embryo-to-embryo levels of bmp2b mRNA and PSmad signaling in zebrafish. The results are consistent with a noisy morphogen source is averaged by extracellular diffusion to lead to greater precision in signaling output.