Fig 1. <Figure Title – Bcd raw data> (A-D) Representative embryos from Lines 2.49.3 and 9.31.2 which have been stained for Bicoid (A,C) and counterstained by DAPI (B,D). Images are from the midsagittal section. (E-H) Fluorescence intensity data extracted to show the Bcd protein gradient profile plotted over absolute length (E, G) and relative egg length (F, H). Also shown are mean profiles from the *bcdE1* null mutant to be used for background subtraction. (n = x and y, respectively)

Fig 2. Mean Bicoid protein gradient profiles of Lines 2.49.3 and 9.31.2 demonstrate convergence. (A, B) The mean profiles were plotted over absolute length (A) and relative egg length (B).

Fig 3. Within-line scaling is lost for embryos from Line 2.49.3. (A, B) Profile data from these embryos were bifurcated according to egg length plotted over absolute length (A) and relative egg length (B).

Fig 4. Aggregate Bcd fluorescence from mean profiles. (A) Shown here are the sum of Bcd fluorescence intensities from the mean profiles from Line 2.49.3 (Blue) and Line 9.31.2 (Red). (A, inset) Recorded values of the aggregate intensities.

Fig 5. <Figure Title 2 – Hb raw data> (A-D) Shown here are raw Hunchback profiles from fluorescent in situ hybridization in embryos from Line 2.49.3 and 9.31.2 plotted over absolute length (A, C) and relative egg length (B, D).

Fig 6. Convergence of mean Hunchback profiles are indicative of scaling. (A, B) Shown here are mean profiles from Hunchback in situ data plotted over absolute length (A) and relative egg length (B).

Fig 7. Bicoid mRNA fluorescent in situ hybridization in Lines 2.49.3 and 9.31.2 reveal disparities in distribution of maternally deposited products. (A) Shown here are raw immunofluorescent images of Bicoid mRNA in early embryos; contours outlining the embryo (Green), specific signal (Blue) and posterior reciprocal (Red) are overlaid. (see text)

Fig 8. Bicoid mRNA intensity is correlated with embryo size. (A) Shown here are aggregated fluorescence intensity values of Bcd mRNA in early embryos plotted over egg length (A) and estimated egg volume (B). [Also shown here are previously published intensity values from similar lines (tbd, will have to convert to relative dose or convert from intensity to relative dose to intensity via 2 std curves)].

Fig 9. Bicoid mRNA contour area is significantly larger in Line 2.49.3. (A-C) Shown here are the total areas from the Bicoid in situ hybridization specific signal bounded by calculated contour lines plotted over egg length (A), estimated egg volume (B), and Egg Area[dimensions can be directly compared; functionally meaningless] (C).

Fig S1. <Figure Title 3 – Genomic Sequencing Data> TBD

Fig S2. <Figure Title 4 - Cuticle> TBD

Fig S3 <Figure Title 5 – Even-skipped> Eve data – C. Miles. [Can be moved to main section or cut entirely, tbd].