Supporting Information:

High throughput, comprehensive single cell proteomics analysis of *Xenopus laevis* embryos at 50-cell stage using a microplate-based MICRO-FASP system

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Associated content

Clustergrams and cell identifications for blastomeres isolated from single embryos.

Figure S1. Clustergram for blastomeres isolated from embryo 2 using CMFM buffer.

Figure S2. Clustergram for blastomeres isolated from embryo 3 using CMFM buffer.

Figure S3. Clustergram for blastomeres isolated from embryo 4 using CMFM buffer.

Figure S4. Clustergram for blastomeres isolated from embryo 5 using CMFM buffer.

Figure S5. Clustergram for blastomeres isolated from embryo 8 using Newport buffer.

Figure S6. Clustergram for blastomeres isolated from embryo 9 using Newport buffer.

Figure S7. Clustergram for blastomeres isolated from embryo 10 using Newport buffer.

Excel spreadsheets with protein and peptide identifications.

Samples collected in the CMFM buffer

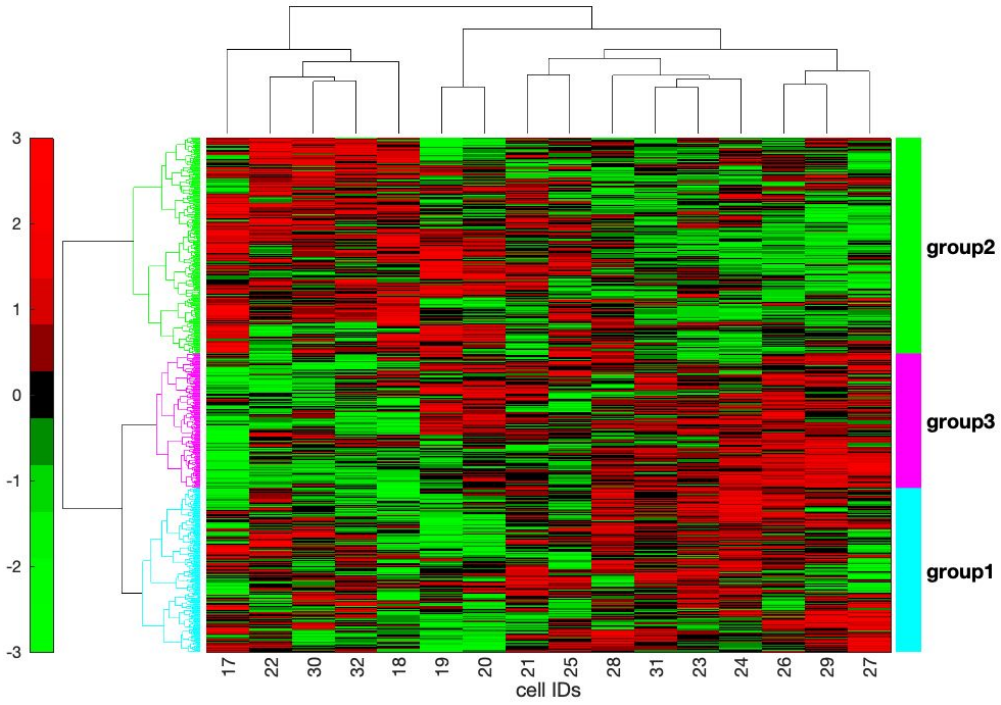


Figure S1. Clustergram for 16 blastomers isolated from Embryo 2 using the CMFM buffer. Top-micrograph of embryo during microdisection, with blastomeres numbered. Those proteins with the highest 15% variance after normalization were used to construct the clustergram using the Ward linkage option.

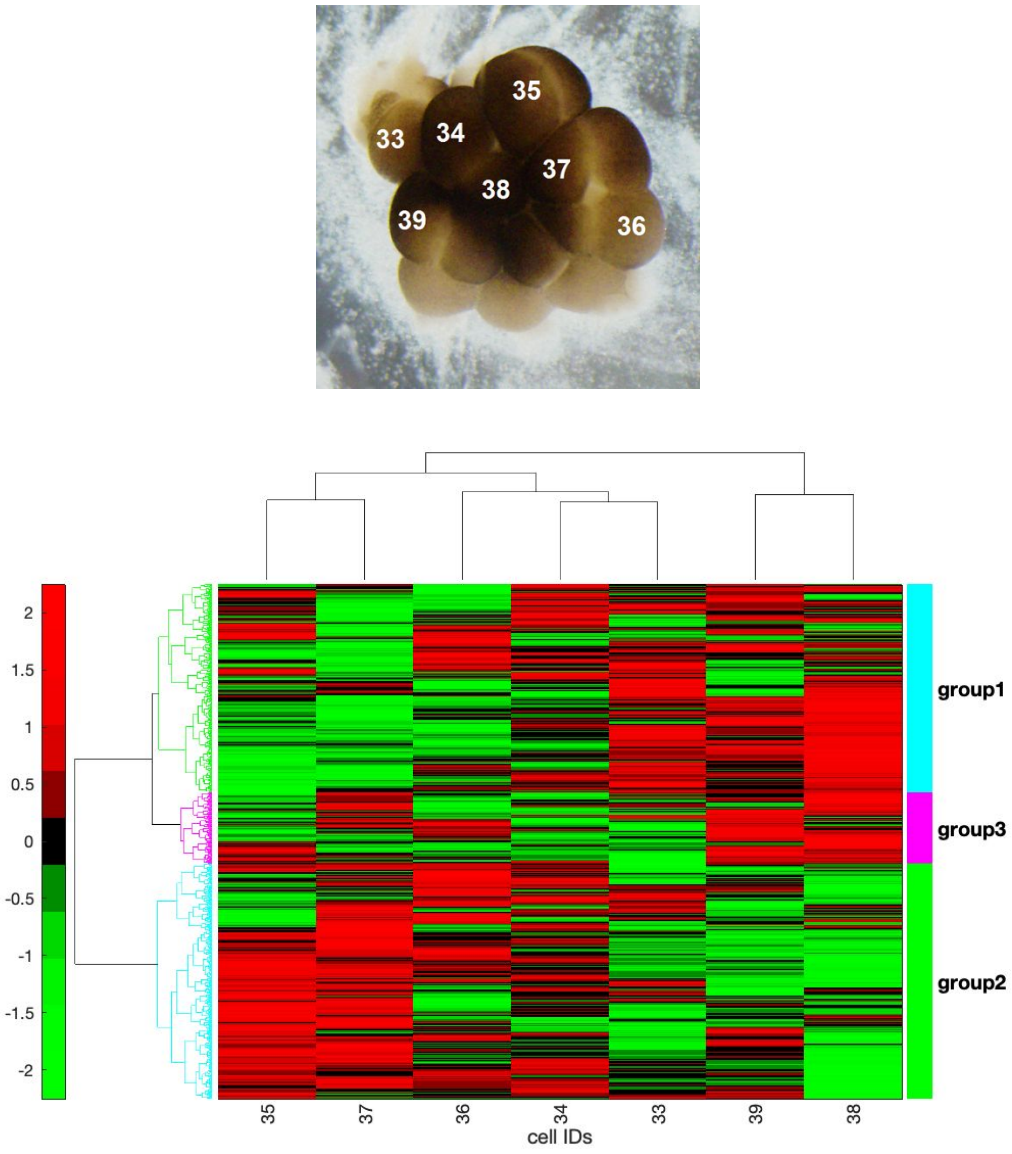


Figure S2. Clustergram for blastomers isolated from seven blastomers isolated from Embryo 3 using the CMFM buffer. Top-micrograph of embryo during microdisection, with blastomeres numbered. Those proteins with the highest 15% variance after normalization were used to construct the clustergram using the Ward linkage option.

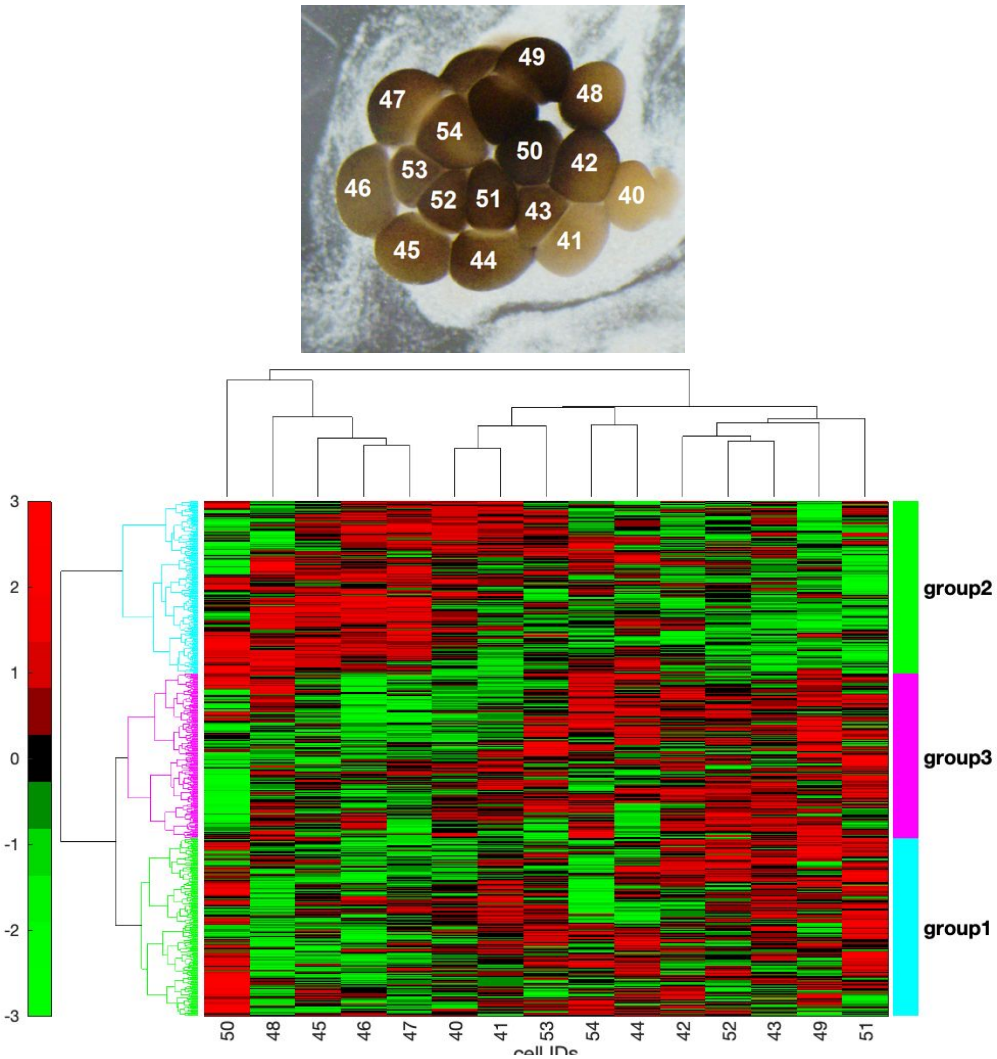
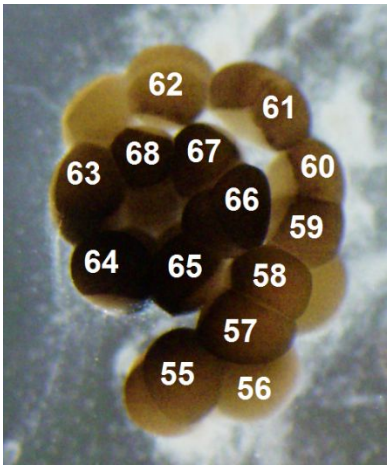


Figure S3. Clustergram for blastomers isolated from 15 blastomers isolated from Embryo 4 using the CMFM buffer. Top-micrograph of embryo during microdisection, with blastomeres numbered. Those proteins with the highest 15% variance after normalization were used to construct the clustergram using the Ward linkage option.



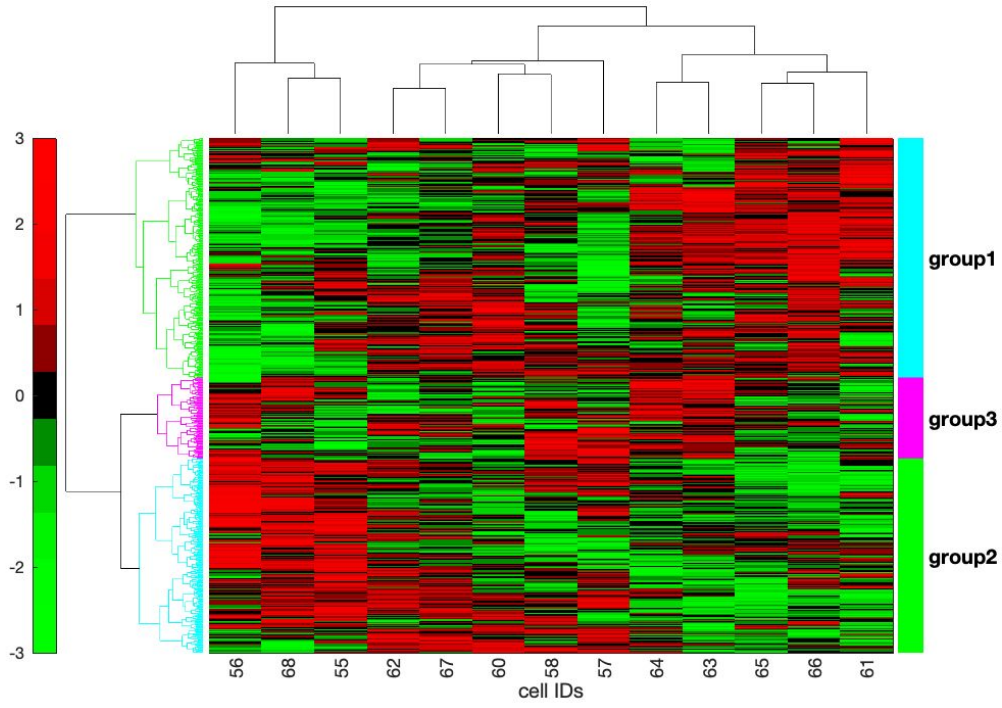


Figure S4. Clustergram for blastomers isolated from 13 blastomers isolated from Embryo 5 using the CMFM buffer. Top-micrograph of embryo during microdisection, with blastomeres numbered. Those proteins with the highest 15% variance after normalization were used to construct the clustergram using the Ward linkage option.

Samples collected in the Newport buffer.

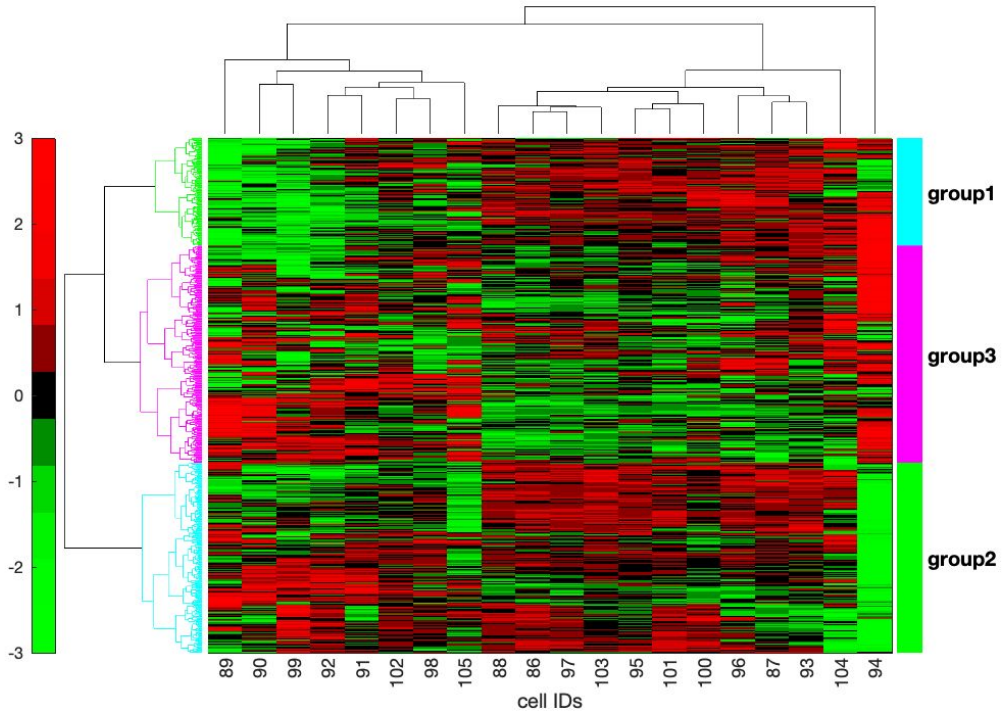


Figure S5. Clustergram for blastomers isolated from 20 blastomers isolated from Embryo 8 using the Newport buffer. Top-micrograph of embryo during microdisection, with blastomeres numbered. Those proteins with the highest 15% variance after normalization were used to construct the clustergram using the Ward linkage option.

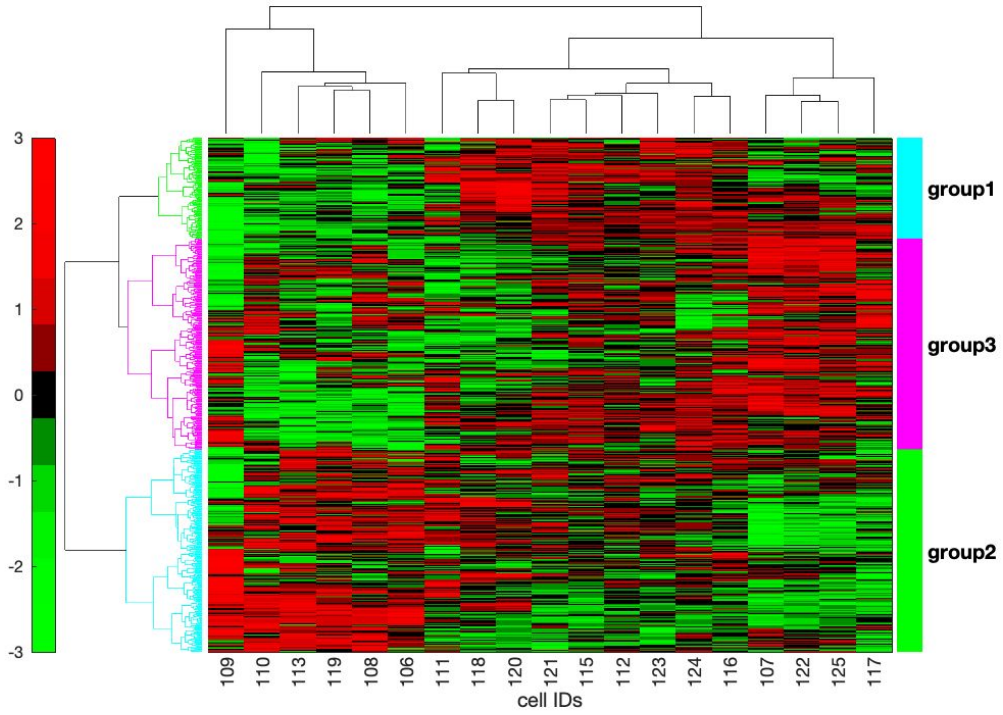


Figure S6. Clustergram for blastomers isolated from 20 blastomers isolated from Embryo 9 using the Newport buffer. Top-micrograph of embryo during microdisection, with blastomeres numbered. Those proteins with the highest 15% variance after normalization were used to construct the clustergram using the Ward linkage option.

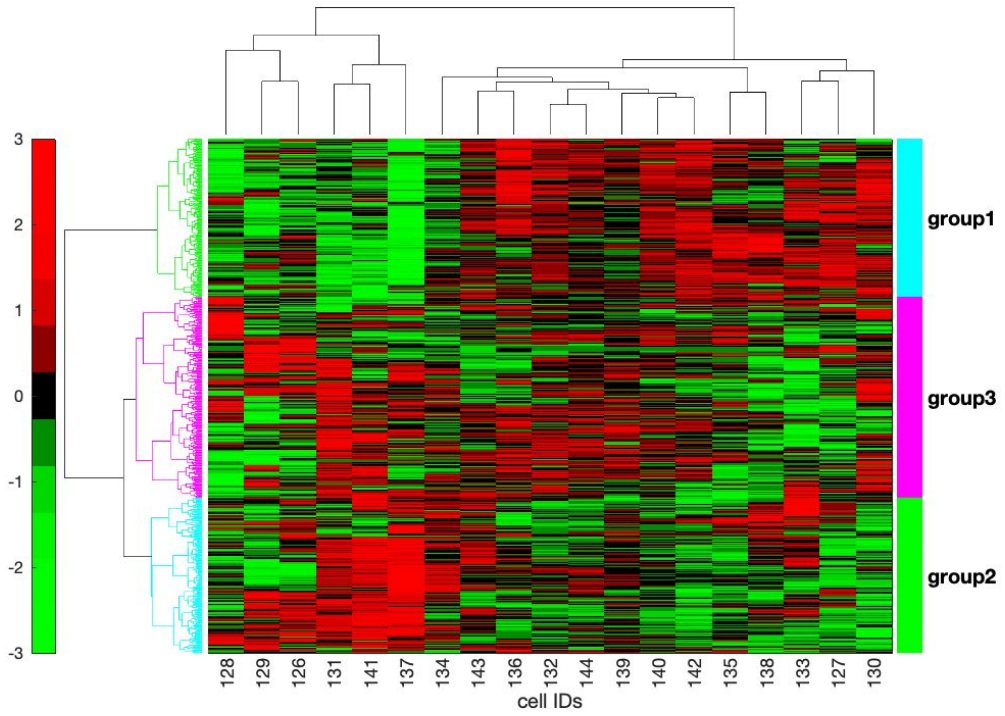


Figure S7. Clustergram for blastomers isolated from 20 blastomers isolated from Embryo 10 using the Newport buffer. Top-micrograph of embryo during microdisection, with blastomeres numbered. Those proteins with the highest 15% variance after normalization were used to construct the clustergram using the Ward linkage option.