

Metabolic control of germ layer proportions through regulation of Nodal and Wnt signalling

Kristina S. Stapornwongkul,^{1,*} Elisa Hahn,^{1,6} Laura Salamo Palau,^{1,6} Krisztina Arato,¹ Nicola Gritti,¹ Kerim Anlas,¹ Patryk Poliński,¹ Mireia Osuna Lopez,² Miki Eibisuya,^{1,4,5,*} Vikas Trivedi^{1,3,*,#}

During embryonic development, cells exit pluripotency to give rise to the three germ layers. Metabolic pathways influence cell fate decisions by modulating the epigenetic, transcriptional, and signalling states of cells. However, the interplay between metabolism and the major signalling pathways that drive the emergence of ectoderm, mesoderm, and endoderm remains poorly understood. Here, we demonstrate an instructive role of glycolytic activity in activating signalling pathways involved in mesoderm and endoderm induction. Using an *in vitro* model system for mouse gastrulation, we observed that inhibiting glycolysis prevents the upregulation of primitive streak markers, resulting in a significant increase in ectodermal cell fates at the expense of mesodermal and endodermal lineages. We demonstrate that this relationship is dose-dependent, enabling metabolic control of germ layer proportions through exogenous glucose levels. Mechanistically, we found that glycolysis inhibition leads to the downregulation of Wnt, Nodal, and Fgf signalling. Notably, this metabolic phenotype was rescued by Nodal or Wnt signalling agonists in the absence of glycolytic activity, suggesting that glycolytic activity acts upstream of both signalling pathways. Our work underscores the dependence of specific signalling pathways on metabolic conditions and provides mechanistic insight into the nutritional regulation of cell fate decision making.

1 Introduction

2 Research in the field of stem cell biology has been critical
3 in uncovering the mechanisms that underlie the intricate
4 interplay between metabolism and cell fate determination
5 [1, 2]. It is now widely acknowledged that metabolic
6 pathways not only fulfil the bioenergetic needs of cells but
7 also act as regulators of differentiation. The underlying mechanisms range from metabolite-driven post-translational modifications and metabolite-protein interactions to moonlighting metabolic enzymes, and can affect the epigenetic as well as the signalling state of cells [3–6]. This perspective has gained support from *in vivo* studies that underscore the mechanistic role of metabolism during embryonic development [7–14]. Regulation of cellular metabolic state has been exploited to enhance the efficiency of differentiation and reprogramming protocols [15]. Therefore, a comprehensive understanding of the complex interactions between metabolism, signalling and differentiation will open new avenues for engineering reproducible tissue patterns *in vitro*. In a broader context such an approach will guide our efforts to study the effects of genetic metabolic disorders, malnutrition and maternal diabetes on embryonic development.

23 One of the earliest cell fate decisions is the exit from pluripotency resulting in the emergence of the three germ layers: the ectoderm, mesoderm and endoderm. In the embryo, prospective mesodermal and endodermal cells migrate through a transient structure known as the primitive streak (PS) while remaining epiblast cells will adapt an ectodermal cell fate [16]. Much attention has focused on how a cell's preference for either aerobic glycolysis or oxidative phosphorylation changes during

differentiation [15]. Pluripotent stem cells (PSCs) are thought to rely on high glycolytic activity to maintain their characteristic histone acetylation patterns [17]. While some studies have suggested that metabolic switching is a prerequisite for epigenetic remodelling and differentiation [17,18], others have found that a shift towards oxidative metabolism is germ-layer specific and only occurs in mesodermal and endodermal cells [19]. In contrast to these findings from directed differentiation of cells using extrinsic signals, a study in the developing tailbud (neuromesodermal progenitors, NMPs) found that inhibition of glycolysis increased the proportion of neuroectoderm at the expense of the presomitic mesoderm via regulation of Wnt signalling [14]. Unlike the bipotent NMPs, cells of the early embryo can still give rise to all future cell types. Therefore, the relationship between metabolism and signalling during the earliest stages of differentiation of pluripotent embryonic cells into the three germ layers remains unresolved. Recent studies, both *in vitro* and *in vivo*, have reported spatiotemporal restriction of different glucose transporters that accompany germ layer patterning and how metabolism affects signalling particularly during mesoderm specification [20, 21]. However, the simultaneous control of the three germ layers and their cell type-specific interplay between glycolysis and signalling remains obscure.

25 In this study, we further elucidate the interplay between glycolysis and the signalling pathways that coordinate germ layer differentiation. Using 3D mouse gastruloids, a stem-cell based model system that allows the co-differentiation of the three germ layers [22], we found that glycolysis plays a crucial role in both endoderm and mesoderm induction by activating Nodal, Wnt and Fgf signalling. Importantly, exogenous glucose (Glc) concentration has a dose-dependent effect on PS marker expression and the development of endodermal and mesodermal cell type derivatives. Thus, we show for the first time that glycolytic activity is not merely permissive but rather acts as an instructive signal which can be used to control germ layer proportions. Moreover, we were able to decouple the metabolic phenotype of glycolysis

¹Tissue Biology and Disease Modelling European Molecular Biology Laboratory (EMBL) Barcelona, Spain. ²Genomics Core Facility, European Molecular Biology Laboratory (EMBL) Heidelberg, Germany. ³Developmental Biology, European Molecular Biology Laboratory (EMBL) Heidelberg, Germany. ⁴Cluster of Excellence Physics of Life, TU Dresden, Dresden, Germany. ⁵Max Planck Institute of Molecular Cell Biology and Genetics, Dresden, Germany. ⁶These authors contributed equally. *Corresponding authors: kristina.stapornwongkul@embl.es, eibisuya@embl.es, trivedi@embl.es, #Lead Contact: trivedi@embl.es

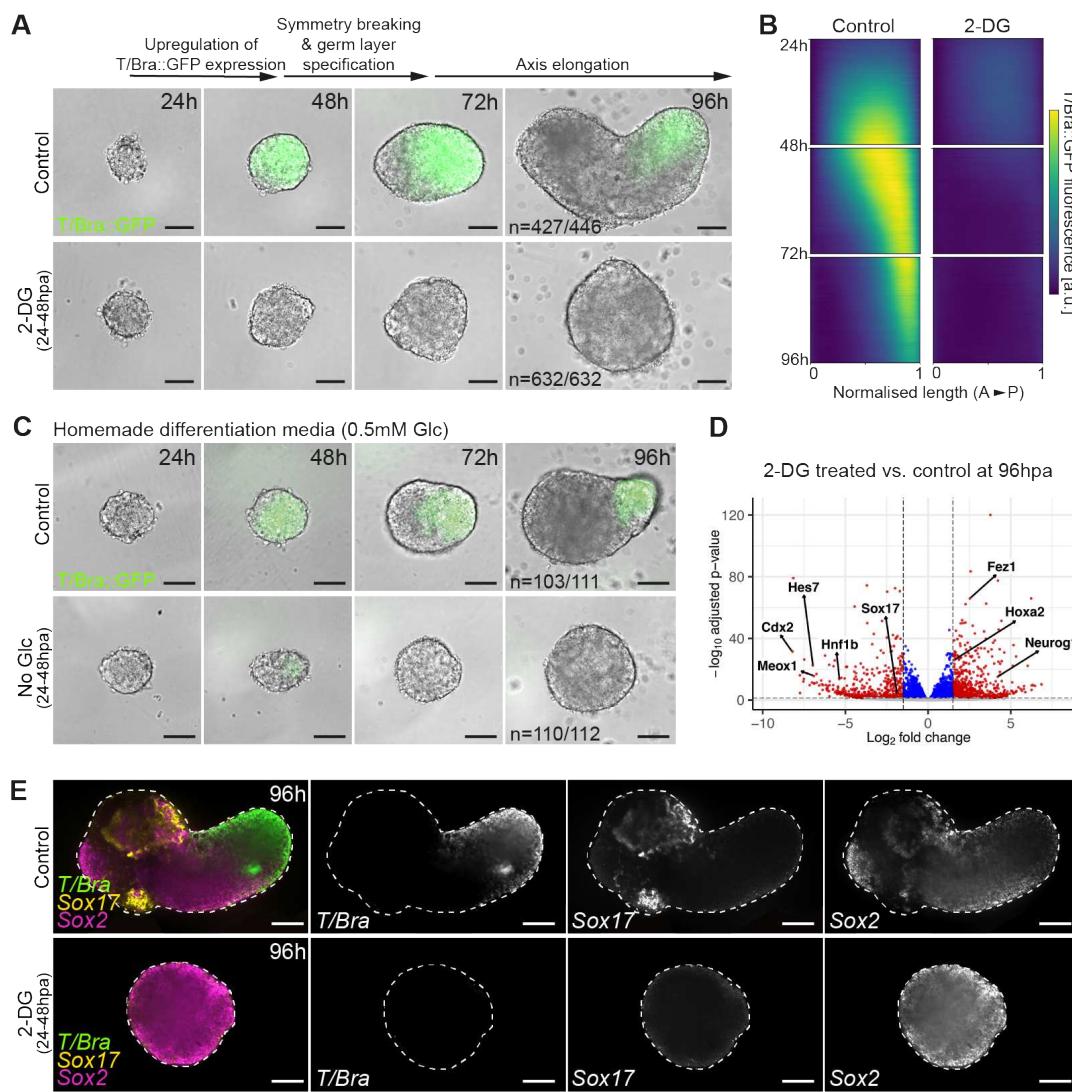


Fig. 1. Glycolysis is required for T/Bra expression, mesoderm and endoderm induction. (A) In control gastruloids, T/Bra::GFP reporter expression is first present throughout gastruloid and then gets polarised before gastruloid elongation. Glycolysis inhibition between 24-48hpa (6mM 2-DG) results in loss of T/Bra::GFP expression and impaired gastruloid development. N numbers from $N_{exp} = 12$. Scale bars: 100μm. (B) Kymographs of control and 2-DG treated gastruloids. Polarisation of T/Bra::GFP fluorescence in controls while 2-DG treated gastruloids fail to upregulate T/Bra::GFP expression. Normalised length from anterior (A) to posterior (P). Kymographs were generated by averaging T/Bra::GFP fluorescence of $n = 30$ gastruloids for each condition. (C) Gastruloids in homemade differentiation media containing 0.5mM Glc express T/Bra::GFP and break symmetry. Removing Glc between 24-48hpa results in loss of T/Bra::GFP expression. N numbers from $N_{exp} = 3$. Scale bars: 100μm. (D) Volcano plot describing differentially expressed genes between 2-DG treated and control gastruloids at 96hpa based on RNA-seq. Red dots describe significantly differentially expressed genes that pass thresholds for $\log_2FC = 1.5$ (vertical lines) and adjusted p value = 0.05 (horizontal line). $n = 6$ for both conditions. (E) HCR stainings of control and 2-DG treated gastruloids at 96hpa. Single confocal slices are shown. $N_{exp} = 3$, $n = 107$ (control), $n = 104$ (2-DG). Scale bars: 100μm.

inhibition from its effects on gastruloid development by rescuing mesoderm and endoderm induction with agonists of the Nodal and Wnt signalling pathways. This demonstrates that glycolytic activity is not a bioenergetic prerequisite for endoderm and mesoderm induction, but instead functions as an important activator of Nodal and Wnt signalling. These findings demonstrate how metabolic activity acts as a regulator of morphogen signalling and cell fate determination and opens new possibilities for metabolic control of cell type proportions in *in vitro* systems.

Results

Glycolysis is needed for T/Bra expression and symmetry breaking in gastruloids

To address the role of metabolism during germ layer specification, we used gastruloids, aggregates of mouse embryonic stem cells (mESCs) which specify cell types of all three germ layers while establishing an anterior-posterior (AP) axis [22]. Between 24 and 48 hours post aggregation (hpa), gastruloids upregulate the PS and early mesoderm marker Brachyury (T/Bra) throughout the tissue (Figure 1A) [23,24]. In a symmetry-breaking event, the posterior pole is then

81
82
83
84
85
86
87
88
89
90
91
92

93 specified by the polarisation of T/Bra expression. At 72hpa,
94 markers of all three germ layers can be detected and further
95 culture results in gastruloid elongation along the AP axis [25].
96 In contrast to previous culture protocols, we did not add
97 the glycogen synthase kinase-3 (GSK3) inhibitor and Wnt
98 signalling activator CHIR99021 (CHIR) to provide a clean
99 delineation between signalling and metabolic activity. Even
100 in the absence of CHIR treatment, we find that 95% of
101 gastruloids generated from E14 T/Bra::GFP mESCs break
102 spontaneously symmetry and elongate when they were
103 previously maintained in serum/LIF conditions (Figure 1A).

104 To investigate the role of Glc metabolism during germ layer
105 specification, we used 2-Deoxy-D-glucose (2-DG) to inhibit
106 glycolysis in gastruloids (Figure S1A). Using a T/Bra::GFP
107 reporter line, we found that 2-DG treatment between 24 and
108 48hpa resulted in the loss of T/Bra::GFP expression and
109 subsequent failure of symmetry breaking and axis elongation
110 (Figure 1A). Time lapse imaging showed upregulation of
111 T/Bra::GFP expression in control gastruloids between 24
112 and 48hpa, while 2-DG treated gastruloids did not start
113 expressing the PS marker even after 2-DG withdrawal (Figure
114 1B and Movie S1,2). It has been reported that the effects of
115 2-DG are not limited to the inhibition of glycolysis but could
116 also affect other cellular functions due to breakdown products
117 of 2-DG [26]. To test whether the phenotype is specific to
118 Glc metabolism, we prepared N2B27 differentiation medium
119 with 0.5mM Glc, reflecting physiological Glc levels in the
120 uterine fluid [27]. While this is around 40 times less than
121 the Glc concentration used in commercially available N2B27
122 medium, it not only supported T/Bra::GFP expression and
123 symmetry breaking sufficiently, but also allowed to remove
124 Glc between 24 and 48hpa of gastruloid development by
125 repeated washes with Glc-free medium. Similar to the
126 2-DG treatment, lack of Glc in this time window resulted
127 in reduced T/Bra::GFP upregulation and failure to polarise,
128 suggesting that the observed 2-DG phenotype was indeed
129 mediated by reduced glycolytic activity (Figure 1C). These
130 experiments suggest that active glycolysis is needed during
131 early gastruloid development to ensure T/Bra expression and
132 subsequent symmetry breaking. To test if loss of T/Bra::GFP
133 is specific to glycolysis inhibition, we next treated gastruloids
134 with sodium azide (NaN₃), a Complex IV inhibitor that
135 blocks oxidative phosphorylation (OxPhos) (Figure S1A).
136 While the treatment resulted in an effective block of OxPhos,
137 as measured by loss of oxygen consumption as well as reduced
138 gastruloid growth, we did not observe loss of T/Bra::GFP
139 expression and symmetry breaking (Figure S1B,C). These
140 results suggest that metabolic inhibition and reduced cell
141 proliferation does not affect T/Bra::GFP expression per se
142 and indicates that glycolysis might play a specific role in
143 gastruloid development.

144 2-DG suppresses mesoderm and endoderm formation

145 Gastruloids display post-occipital cell types of all three germ
146 layers which are spatially organised along an AP axis [28].
147 We next asked how the early inhibition of glycolysis affects
148 cell fate decision making during gastruloid development.
149 To assess the presence of different cell types, we performed
150 single-gastruloid RNA-seq on control and 2-DG treated
151 gastruloids at 96hpa. We found that markers of mesodermal
152 derivatives, such as *Hes7* and *Meox1* were strongly downregulated
153 (Figure 1D, Figure S2A) [29,30]. Similarly, endodermal
154 markers, such as *Sox17* and *Hnf1b* were reduced in 2-DG
155 treated gastruloids (Figure 1D, Figure S2B) [31]. In contrast,
156 transcripts associated with neural cell fates, such as *Neurog1*
157 and *Fez1*, were upregulated (Figure 1D, Figure S2C) [32,33].
158 Furthermore, we found an upregulation of the most anterior
159

160 Hox gene and hindbrain marker *Hoxa2* while posterior Hox
161 genes and *Cdx2*, which marks the posterior embryo, were
162 strongly reduced (Figure 1D, Figure S2E) [34, 35]. This
163 suggests an anteriorisation of 2-DG treated gastruloids.

164 The shift in germ layer proportions was further confirmed
165 by *in situ* hybridisation chain reaction (HCR) showing that
166 in contrast to control gastruloids, cells expressing *T/Bra*
167 (PS/early mesoderm) and *Sox17* (definitive endoderm)
168 transcripts were strongly reduced in 2-DG treated gastruloids
169 (Figure 1E). Instead, *Sox2* (ectoderm/pluripotent) was
170 expressed throughout the glycolysis inhibited gastruloids.
171 Further stainings showed that the *Sox2*⁺ domain was sub-
172 divided in clusters of cells expressing the neuroectodermal
173 marker *Sox1* or the pluripotency marker *Nanog* (Figure
174 S2F) [36, 37]. Both of these markers were overrepresented
175 compared to control gastruloids, confirming the transcript-
176 omics results (Figure S2C,D). These results show that the
177 inhibition of glycolysis between 24 and 48hpa has long-term
178 effects on gastruloid development and results in a shift of
179 germ layer proportions away from posterior mesodermal and
180 endodermal derivatives towards more anterior neuroecto-
181 dermal cell fates.

182 Glucose has a dose-dependent effect on the proportion of T/Bra::GFP expressing cells

183 The observed effects of 2-DG treatment on gastruloid develop-
184 opment raise the question whether glycolytic activity has a
185 permissive or instructive role in T/Bra expression and germ
186 layer induction. A permissive role would suggest the existence
187 of a certain threshold of cellular glycolytic activity needed
188 to allow T/Bra upregulation in gastruloids. If instead the
189 glycolytic activity acted as an instructive signal, one would
190 expect a dose-dependent effect on T/Bra gene expression. To
191 address this question, we aimed to modulate the glycolytic
192 activity in gastruloids to assess the effect on T/Bra::GFP
193 expression and germ layer proportions. Taking advantage of
194 our *in vitro* system, we varied exogenous Glc levels in the
195 differentiation medium and found that this changes glycolytic
196 activity effectively in 2D cultured cells (Figure 2A). In the
197 absence of Glc, cells relied entirely on OxPhos for ATP pro-
198 duction (Figure S3A). Raising Glc levels resulted in increased
199 glycolytic activity which plateaued around 12.5mM Glc.
200 At this concentration, glycolysis and OxPhos contributed
201 approximately evenly to the total ATP production rate
202 (Figure S3A). To test whether Glc and glycolytic activity
203 have a dose-dependent effect on T/Bra::GFP expression, we
204 generated gastruloids in medium containing different amounts
205 of Glc. At 48hpa, when T/Bra::GFP expression is present
206 throughout the gastruloid, a positive correlation between Glc
207 concentration and GFP signal was observed (Figure 2B).
208 However, it was also apparent that gastruloids grown in lower
209 Glc concentrations were strongly reduced in size suggesting
210 that Glc was growth limiting.

211 To exclude the possibility that size and not glycolytic
212 activity is affecting T/Bra::GFP expression, we generated
213 gastruloids from different initial cell numbers resulting in
214 similar sized gastruloids at different Glc concentrations
215 (Figure 2C, see insets). By assessing the percentage of
216 GFP⁺ cells using flow cytometry at 0.02mM Glc, 0.1mM
217 Glc, 0.5mM Glc and 2.5mM Glc over four different initial
218 cell numbers (350, 700, 1050 and 1400 cells), we found that
219 the percentage of GFP⁺ cells was indeed dependent on Glc
220 concentration and not gastruloid size (Figure 2C, Figure
221 S3B). We further wondered if Glc concentration not only
222 determines the percentage of T/Bra::GFP expressing cells
223 but also cellular T/Bra::GFP expression levels. Based on
224 flow cytometry histograms, we detected no noticeable shift
225 in typical GFP peak intensity levels suggesting that cellular
226

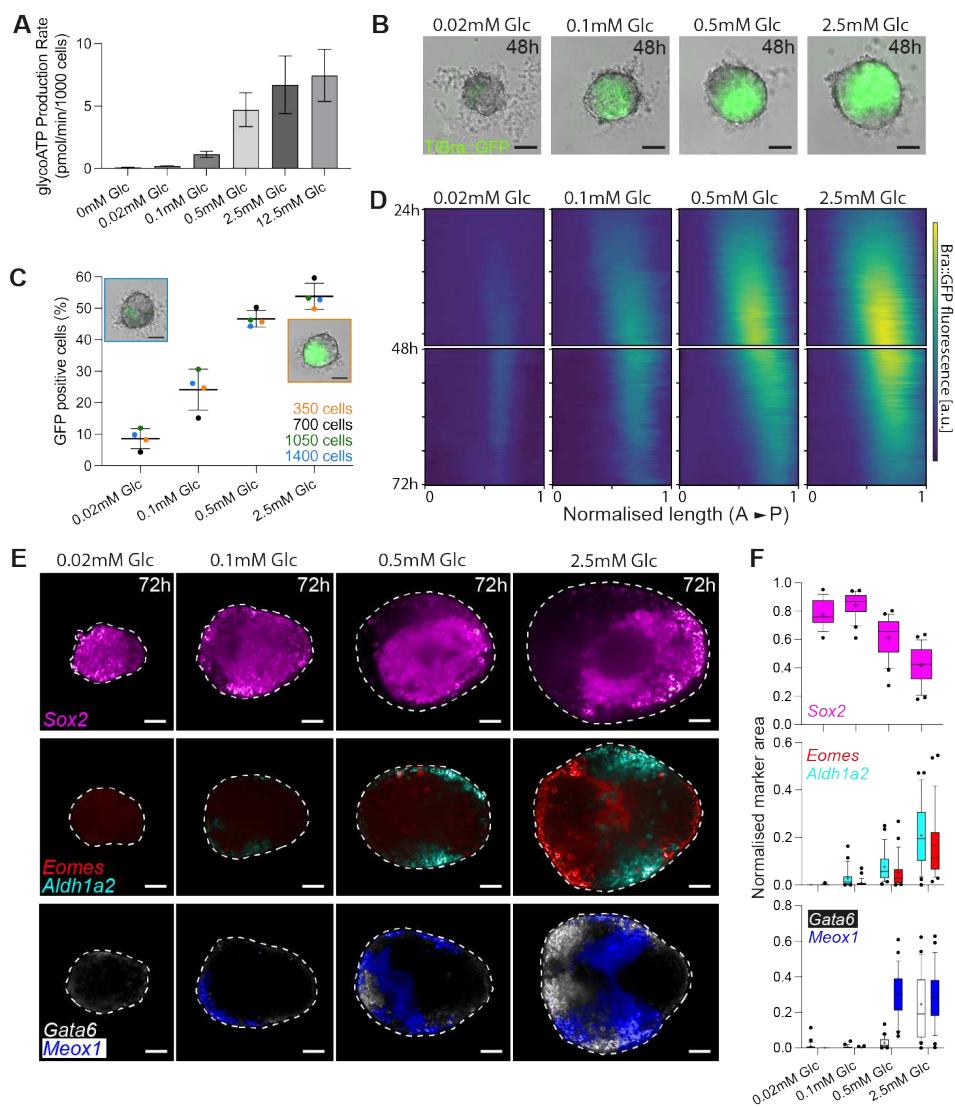


Fig. 2. Glucose has a dose-dependent effect on T/Bra::GFP expressing cells and germ layer proportions. (A) Changes in mean glycoATP production rate depending on exogenous Glc levels. Error bars indicate SD. $N_{exp} = 3$ for all conditions. (B) Raising exogenous Glc concentration results in increasing levels of T/Bra expression in gastruloids. $N_{exp} = 7$, $n \geq 315$ for each condition. Scale bars: 100 μ m. (C) Mean percentage of GFP⁺ cells in T/Bra::GFP gastruloids at 48hpa which were generated by aggregating 350, 700, 1050 and 1400 cells and cultured in different Glc concentrations. Error bars indicate SD. Insets show images of gastruloids generated by aggregation of 1400 (blue frame) and 350 (orange frame) initial cells and grown in 0.02mM and 2.5mM Glc respectively. At 48hpa, gastruloids are similar sized but express different levels of T/Bra::GFP. Scale bars: 100 μ m. (D) Kymographs of T/Bra::GFP intensity in gastruloids developing in different Glc concentrations from 24 to 72hpa. Kymographs were generated by averaging $n = 10$ gastruloids for each condition. (E) Germ layer marker expression in gastruloids at 72hpa which developed at different Glc concentrations. Single confocal slices are shown. $n = 3$, $N_{exp} \geq 31$ for each condition. Scale bars: 50 μ m. (F) Marker area quantifications on average Z-projections of the batch of gastruloids shown in (E). Marker area was normalised to gastruloid area. Sox2: $n = 18$ (0.02mM Glc), $n = 22$ (0.1mM Glc), $n = 23$ (0.5mM Glc), $n = 22$ (2.5mM Glc). Eomes/Aldh1a2: $n = 18$ (0.02mM Glc), $n = 26$ (0.1mM Glc), $n = 25$ (0.5mM Glc), $n = 25$ (2.5mM Glc). Gata6/Meox1: $n = 10$ (0.02mM Glc), $n = 18$ (0.1mM Glc), $n = 22$ (0.5mM Glc), $n = 20$ (2.5mM Glc).

T/Bra::GFP expression levels are similar in GFP⁺ cells across different Glc concentrations (Figure S3C). Exogenous Glc concentration thus determines the likelihood of a cell to switch into a T/Bra expressing state in a dose-dependent manner. As a result, gastruloids developing in higher Glc concentration display a higher percentage of T/Bra::GFP at 48hpf, resulting in a higher overall T/Bra::GFP intensity level. These results indicate that glycolytic activity plays an instructive role in T/Bra induction during gastruloid

development, especially between 0mM Glc and 0.5mM Glc where dose-dependency is most prominent (Figure S3B). Interestingly, Glc concentration in the uterine fluid has been measured to be around 0.6mM [27]. Thus, it is conceivable that the *in vivo* embryo develops in a regime where Glc can act as an instructive regulator of PS induction.

249 **Glucose has a dose-dependent effect on germ layer
250 proportions**

251 Next, we were wondering whether the dose-dependent effect
252 of Glc on the relative number of T/Bra::GFP expressing
253 cells further translates into a change of the proportion of
254 cell types deriving from the different germ layers. We first
255 determined the dynamics of T/Bra::GFP reporter activity
256 at different Glc concentrations by performing time lapse
257 imaging. Kymographs of T/Bra::GFP reporter intensity
258 showed that gastruloids developing at 0.02mM Glc failed to
259 polarise (Figure 2D). Instead a weak stripe of T/Bra::GFP
260 expression formed, a phenotype previously described in gas-
261 truloids treated with Nodal or Fgf signalling inhibitors [25].
262 Despite differences in reporter intensities, the dynamics of
263 symmetry breaking at 0.1mM, 0.5mM and 2.5mM Glc were
264 comparable (Figure 2D). Next, we performed HCR stainings
265 for *Sox2* and markers of PS derived cell fates. We found that
266 the proportion of *Sox2* expressing cells decreased with rising
267 Glc concentration (Figure 2E,F). In contrast, mesodermal
268 and endodermal markers, such as *Eomes* (endoderm/anterior
269 mesoderm), *Gata6* (cardiac mesoderm/endoderm), *Aldh1a2*
270 (trunk mesoderm) and *Meox1* (paraxial mesoderm) were
271 absent in gastruloids cultured at 0.02mM Glc but showed an
272 increase in proportion with rising Glc concentration (Figure
273 2E,F). Our results show for the first time that exogenous Glc
274 levels can bias the emergence of specific cell types deriving
275 from the three germ layers in a dose-dependent manner.
276 Thus, increasing Glc levels lead to a greater proportion of
277 mesodermal and endodermal cell derivatives, accompanied by
278 lower proportions of ectodermal cell fates. This demonstrates
279 how glucose concentration can be used as tool to modulate
280 the proportions of cell lineages in gastruloids.

281
282 **Nodal, Wnt and Fgf signalling pathway activity
283 is dependent on glycolysis**

284 We next wanted to understand the mechanism by which
285 glycolytic activity regulates changes in cell fate decision
286 making. PS markers are induced and maintained by major
287 developmental signalling pathways, such as Nodal, Wnt and
288 Fgf signalling [38–41]. To test whether the effect of glycolysis
289 inhibition on mesoderm and endoderm development is me-
290 diated by reduced signalling, we performed single-gastruloid
291 RNA-seq on control and 2-DG treated gastruloids immedi-
292 ately at the end of the treatment period at 48hpa of gastruloid
293 development. We found that transcription of Nodal, Wnt3a
294 and Fgf8 ligands, as well as many of their target genes, such
295 as *T/Bra*, *Eomes* and *Dusp6* were downregulated upon 24
296 hours of glycolysis inhibition (Figure 3A). Among the most
297 upregulated transcripts were *Meis2*, *Irx3* and *Chrdl1*, all genes
298 associated with neural development (Figure S4A) [42–44].
299 These results suggest that the effect of reduced glycolytic
300 activity on germ layer proportions can indeed be explained
301 by the reduced activity of Nodal, Wnt and Fgf signalling.

302
303
304 **Development of glycolysis inhibited gastruloids
305 can be rescued by Nodal or Wnt signalling pathway
306 activation**

307 The observation that Nodal, Wnt and Fgf signalling pathways
308 are downregulated upon glycolysis inhibition raises the
309 question whether glycolytic activity acts as an activator
310 of signalling pathways or whether signalling is just not
311 functional under the bioenergetic constraints related to the
312 lack of glycolytic activity. If glycolysis is solely required to
313 activate these pathways or to promote cells required to induce
314 these signalling pathways, it should be possible to rescue the
315 2-DG phenotype by activating signalling pathways during
316 the treatment period. Indeed, simultaneous activation of the

317 Nodal signalling pathway with Activin A (Act-A) during
318 2-DG treatment between 24 and 48hpa, was able to partially
319 rescue T/Bra::GFP expression at 48hpa (Figure 3B,C). Even
320 though T/Bra::GFP expression was not reaching control
321 levels at 48hpa, symmetry breaking was robust in these
322 rescued gastruloids and elongation was observed in 70% of
323 the cases. We further performed HCR stainings at 96hpa to
324 validate whether cells of all three germ layers can be found in
325 the rescued gastruloids. Quantifications of the relative area
326 of T/Bra and Sox17 expression confirmed that mesoderm and
327 endoderm development was rescued (Figure 3D,E). Further
328 stainings also confirmed the presence of paraxial mesoderm
329 (*Meox1*) and cardiac precursors (*Gata6*) in these gastruloids
330 (Figure S4B). These results confirm that Nodal signalling
331 activation during glycolysis inhibition was sufficient to rescue
332 the development of mesodermal and endodermal cell types.
333 Activation of Wnt signalling using CHIR was also able to
334 rescue gastruloid development, albeit in a less reproducible
335 manner (Figure S4C,D). Even though elongation occurred in
336 34% of gastruloids, endodermal and cardiac cell derivatives
337 were mostly absent, most likely because Wnt signalling
338 strongly promotes differentiation towards posterior mesoderm
339 (Figure S4B,E). We also added Fgf8 simultaneously with 2-
340 DG but did not observe a rescue of T/Bra::GFP induction and
341 polarisation (Figure S4F). Our rescue experiments suggest
342 that Nodal and Wnt signalling activation are downstream
343 of glycolytic activity and can rescue the 2-DG mediated
344 phenotype on gastruloid development.

345
346
347 **Glycolytic activity is not rescued by Nodal and
348 Wnt signalling**

349 The signalling, epigenetic and metabolic state of cells are
350 highly integrated through several feedback mechanisms that
351 ensure coordination of cellular behaviour [1, 4, 6, 45]. In
352 cancer cells, Wnt signalling is a crucial regulator of metabolic
353 reprogramming resulting in increased Glc uptake and its
354 preferential fermentation to lactate even in the presence of
355 oxygen, known as the Warburg effect [46]. Similarly, Wnt,
356 Fgf and Nodal signalling have been suggested to promote
357 glycolysis in the context of normal embryonic development
358 and homeostasis as well as in cancerous tissue [13, 47–50].

359 To rule out the possibility that Nodal or Wnt signalling
360 activation rescue the 2-DG mediated glycolysis inhibition, we
361 first analysed gastruloid size that is expected to be affected
362 by 2-DG treatment [51]. Indeed, we detected a significant
363 reduction in gastruloid size upon the 24h 2-DG treatment
364 period. In contrast to T/Bra::GFP intensity levels, neither
365 Nodal nor Wnt signalling activation rescued the gastruloid
366 size phenotype suggesting that anabolic metabolism driving
367 proliferation and tissue growth was not restored in these
368 gastruloids (Figure 3F; Figure S4G). To look at a more
369 direct readout of metabolic state, we next measured the ATP
370 production rate from glycolysis (glycoATP production rate).
371 Control cells cultured for two days in differentiation medium
372 displayed a significantly higher glycoATP production rate
373 than cells that had been treated with 2-DG for 24h prior
374 measurement (Figure 3G). We found that the addition of
375 Nodal signalling agonist Act-A did not rescue the glycoATP
376 production rate of 2-DG treated cells. This was also the
377 case when Act-A and CHIR were added simultaneously to
378 cells (Figure S4H). These results were further supported
379 by the finding that T/Bra::GFP expression and symmetry
380 breaking of gastruloids in Glc-free medium (24–48hpa) was
381 also rescued by the addition of Act-A and CHIR (Figure
382 S3I). Here, the absence of Glc abolishes any possibility of
383 reactivating glycolytic activity. Together, these experiments
384 suggest that even though signalling activation can rescue
385 gastruloid development, it does not rescue the metabolic

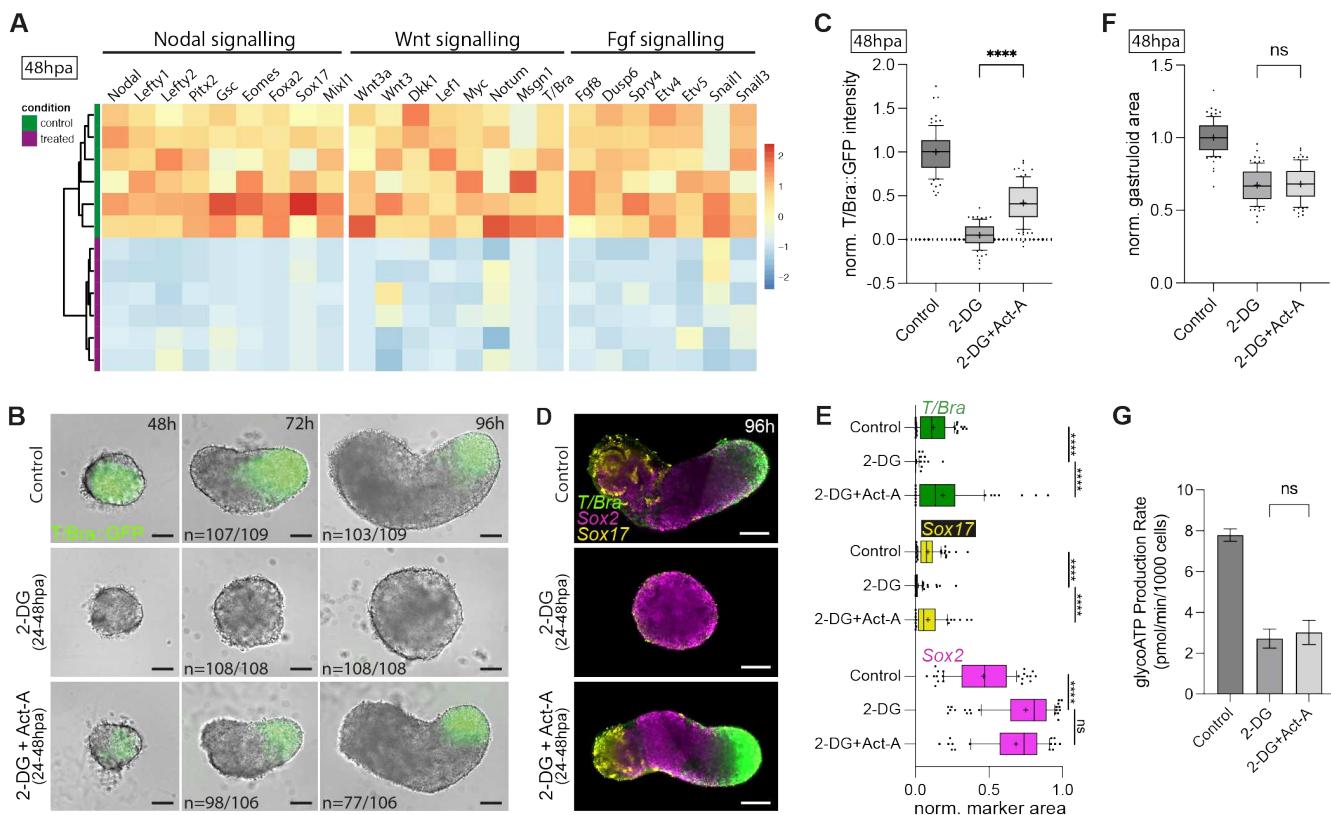


Fig. 3. Nodal signalling activation can rescue the 2-DG phenotype in the absence of glycolytic activity. (A) Heatmap depicting relative transcript levels of selected genes in 2-DG treated vs. control gastruloids at 48hpa, based on RNA-seq. List was manually curated based on typical genes for selected signalling pathways. Heatmap columns are normalised per gene. Lower and higher expression in blue and red, respectively. Each row represents a single gastruloid with applied hierarchical clustering. (B) Gastruloids developing under control conditions, glycolysis inhibition or Nodal signalling rescue condition. N numbers for symmetry breaking at 48hpa and axis elongation at 96hpa from $N_{exp} = 4$. Scale bars: 100µm. (C) T/Bra::GFP intensity of gastruloids at 48hpa for different treatment conditions. Background was subtracted and intensities were normalised to mean control intensity. $N_{exp} = 3$, $n = 87$ (control), $n = 85$ (2-DG), $n = 87$ (2-DG+Act-A). ***p < 0.0001 for t-test. (D) Images of HCR stainings for control, 2-DG and Nodal signalling rescue. T/Bra: PS/early mesoderm (green), Sox2: ectoderm/pluripotent (magenta), Sox17: definitive endoderm (yellow). Single confocal slices are shown. Scale bars: 100µm. (E) Area quantifications of germ layer markers using average Z-projections of HCR stainings as shown in (D). Area was normalised to total gastruloid area. Line in box plot indicates median, + indicates mean, whiskers indicate 10 to 90 percentiles. $N_{exp} = 3$, $n = 107$ (control), $n = 104$ (2-DG), $n = 70$ (2-DG+Act-A). ****p < 0.0001 for t-test. (F) Gastruloid area at 48hpa for different treatment conditions. Area was normalised to mean control area. $N_{exp} = 3$, $n = 87$ (control), $n = 85$ (2-DG), $n = 87$ (2-DG+Act-A). t-test was not significant (ns). (G) Mean glycoATP production rate of cells cultured for 48h in differentiation medium. Inhibitor and growth factor treatment was started 24h prior to measurements. $N_{exp} = 3$, error bars indicate SD. t-test was not significant (ns).

phenotype on the level of glycolytic activity in 2-DG treated cells. This implies that glycolytic activity is not needed for the activation of T/Bra::GFP expression as long as signalling pathways are active. Therefore, glycolysis activity is a crucial inducer of mesodermal and endodermal cell fates but does solely act through the activation of signalling rather than posing bioenergetic constraints on the specification of certain cell types.

395

396

397

398

Discussion

An instructive role of glycolytic activity for mesoderm and endoderm induction

Spatial metabolic patterns observed during amphibian gastrulation in the 1930s sparked early hypotheses about the metabolic regulation of embryonic development [52–54].

In recent years, both *in vitro* and *in vivo* studies have contributed to our understanding of the mechanistic link between metabolic pathways and cell fate specification [4, 55]. Here, we found an important role of glycolytic activity in the induction of endoderm and mesoderm using both a glycolysis inhibitor and Glc-free medium. Most importantly, we demonstrate that this relationship is dose-dependent. As glycolytic activity increases, so does the probability of cells committing to mesodermal and endodermal cell fates. This suggests that glycolysis acts as an instructive cue, rather than merely a permissive factor.

Differences in our findings compared to a prior study [19], which indicated that cells differentiating into endoderm and mesoderm required a shift from high glycolysis to high Ox-Phos, might be attributed to the use of directed differentiation protocols involving growth factor-containing germ layer-specific media. In our gastruloid system, cells of all three germ layers co-emerge without the need for exogenous signalling agonists. This allowed us to demonstrate the importance of gly-

406
407
408
409
410
411
412
413
414
415
416

417
418
419
420
421
422
423
424

425 colytic activity in the induction of mesoderm and endoderm
426 via Wnt signalling and Nodal signalling activation. Since ag-
427 onists of these signalling pathways are part of the directed
428 differentiation protocol, it is conceivable that the importance
429 of glycolytic activity for the activation of these pathways could
430 not be detected previously.

431 Our findings align with another recent study that showed
432 adverse effects of 2-DG treatment on mesoderm specification
433 in gastruloids, highlighting the reproducibility of this pheno-
434 type [21]. Contrary to our results, the authors did, however,
435 not observe a phenotype in Glc-free medium and concluded
436 that glycolytic activity is dispensable for mesoderm develop-
437 ment in gastruloids. A possible explanation might be that the
438 experiments were conducted in the presence of CHIR, a con-
439 dition that is analogous to our rescue experiments. Since even
440 low amounts of Glc are sufficient for Bra induction, residual
441 Glc after washing out high-Glc differentiation media might be
442 another potential explanation for the observed differences.

443 In accordance with our findings, an important role of gly-
444 colysis has been suggested for mesoderm development at later
445 stages of embryonic development when bipotent NMPs com-
446 mit to either a neural tube or presomitic mesoderm fate [13].
447 In NMPs it is however still disputed whether glycolytic activi-
448 ty has a promoting or inhibitory function on Wnt and Fgf
449 signalling [12, 14]. Concurrently with our research, another
450 preprint has identified metabolic activity as a key driver of
451 phenotypic variation through integrated molecular-phenotypic
452 profiling of trunk-like structures, an *in vitro* model system
453 for neural tube and somite formation [56]. Specifically, they
454 demonstrate that an early imbalance in OxPhos and glycolysis
455 leads to aberrant morphology and biases cells towards the
456 neural lineage, consistent with our findings during germ layer
457 formation.

458 While the relationship between glycolysis and mesoderm
459 development has been explored in several studies, little is
460 known about the metabolic control of endoderm specification.
461 Previous studies have also found that glycolysis can promote
462 endoderm differentiation [57, 58]. One suggested mechanism
463 involves the Lin41 protein kinase as a non-canonical phos-
464 phorylation target of glycolytic enzyme Pfkp, resulting in
465 the suppression of Sox2 and leading to increased endodermal
466 differentiation of ESCs [57]. Here, we show that glycolytic
467 activity is needed for the activation of endoderm-promoting
468 Nodal signalling and therefore introduce an additional layer
469 of metabolic control to our understanding of endoderm
470 specification.

471 **Bioenergetic versus signalling function of glycolysis**

472 Metabolism plays a vital role in generating the necessary
473 building blocks and energy required for growth and prolifera-
474 tion. Differentiating cells might display unique bioenergetic
475 demands which must be met to ensure the proper develop-
476 ment of certain cell types [59, 60]. For instance, the energetic
477 requirements of prospective mesodermal and endodermal
478 cells migrating through the PS might differ significantly from
479 epithelial cells fated to become neuroectoderm. However, our
480 finding that the metabolic phenotype of glycolysis inhibition
481 can be rescued through the activation of Nodal and Wnt
482 signalling pathways in the absence of glycolytic activity
483 strongly indicates that the phenotype is not related to ener-
484 getic constraints. Since glycolysis is not reactivated in these
485 rescued gastruloids, it seems to primarily act as an activator
486 of developmental signalling pathways. This implies that
487 glycolytic activity is not an absolute necessity for mesoderm
488 and endoderm differentiation as long as these signalling
489 pathways are activated to coordinate gastruloid develop-
490 ment by inducing T/Bra upregulation between 24-48hpa. Since

491 morphogenetic movements in the gastruloid model system
492 are not comparable with *in vivo* gastrulation, it is however
493 conceivable that a bioenergetic function of glycolysis plays
494 a role in the migration of mesodermal and endodermal
495 cells [7, 20].

496 An open question is how changes in glycolytic activity can
497 regulate Nodal, Wnt and Fgf signalling during germ layer in-
498 duction. Metabolite-driven posttranslational modifications,
499 moonlighting glycolytic enzymes and metabolite-protein in-
500 teractions are possible links between metabolism and sig-
501 nalling [4, 6, 61]. For instance, high glycolytic activity pro-
502 motes acetyl-CoA levels which can be rate-limiting for protein
503 acetylation [62]. Interestingly, the activity of Nodal and Wnt
504 signalling transducers is known to be modulated by acetylation
505 [63–65]. It has been also suggested that glycolysis-driven
506 changes in the intracellular pH may further favour β -catenin
507 acetylation and nuclear translocation during NMP differenti-
508 ation [14]. Glycolytic activity also feeds into the production
509 of the building blocks necessary for glycosylation [66, 67]. Re-
510 cently, it was proposed that 2-DG treatment affects mesoderm
511 specification due to reduced glycosylation, based on the knowl-
512 edge that several proteins involved in Wnt and Fgf signalling
513 transduction are known to be glycosylated [20, 21, 68].

514 Besides post-translational modifications, glycolytic activity
515 has also been shown to affect cellular localisation of glycolytic
516 enzymes, thereby allowing them to perform non-canonical
517 functions. For instance, translocation of Pfkl and Aldoa into
518 the nucleus has been hypothesised to modulate Wnt signalling
519 during somitogenesis [12]. Moreover, metabolites might also
520 modulate protein activity by direct binding. Sentinel metabo-
521 lites such as fructose-1,6-bisphosphate (FBP) whose concen-
522 tration changes with glycolytic activity might be interesting
523 targets for metabolite-protein allosteromes as suggested by
524 Miyazawa and colleagues [12].

525 Most of the previous work has been focused on Wnt
526 signalling and mesoderm specification. Currently, we know
527 only little about how glycolytic activity modulates the Nodal
528 signalling pathway and endoderm differentiation. Future
529 work will be also important to identify actual changes in
530 acetylation and glycosylation patterns of signalling compo-
531 nents and functionally link them to their activity, as well as
532 probe non-canonical glycolytic enzyme function and possible
533 metabolite-protein interactions.

534 **Relevance for *in vivo* mouse gastrulation**

535 The observation that exogenous Glc concentrations ranging
536 from 0.02mM to 2.5mM have a dose-dependent effect on
537 germ layer proportions, raises the question whether Glc
538 levels within the embryonic environment fall within this
539 regulatory range and whether glycolytic activity may indeed
540 function as an instructive cue during *in vivo* gastrulation.
541 Notably, measurements of Glc levels in uterine fluid suggest
542 a concentration of approximately 0.6mM [27]. Interestingly,
543 dose dependency is almost linear until 0.5mM and starts
544 plateauing afterwards (Figure S3B). Hence, it is conceivable
545 that differential expression of Glc transporters and glycolytic
546 enzymes could account for spatial variations in glycolytic
547 activity, thereby impacting cell fate decision making. This
548 notion gains added significance when considered alongside
549 recent findings that demonstrate the spatiotemporal coordi-
550 nation of Glc transporter expression during mouse gastrula-
551 tion [20].

552 Our study provides new insights into the interplay between
553 metabolism and signalling pathways that coordinate the dif-
554 ferentiation of pluripotent cells into the three germ layers.
555 The demonstrated instructive role of exogenous Glc concen-
556 tration on cell fate decision-making represents an initial stride
557 toward establishing nutritional control of cell type composi-
558

tion in complex *in vitro* model systems. Future work in this emerging research field will further improve our understanding of how metabolism is integrated into cellular behaviour and how metabolic conditions affect embryonic development.

REFERENCES AND NOTES

- Shohini Ghosh-Choudhary, Jie Liu, Toren Finkel, *Trends in Cell Biology* **30**, 201–212 (2020).
- James G. Ryall, Tim Cliff, Stephen Dalton, Vittorio Sartorelli, *Cell Stem Cell* **17**, 651–662 (2015).
- Xinjian Li, Gabor Egervari, Yugang Wang, Shelley L. Berger, Zhimin Lu, *Nature Reviews Molecular Cell Biology* **19**, 563–578 (2018).
- Hidenobu Miyazawa, Alexander Aulehla, *Development* **145** (2018).
- Chaoyun Pan, Bo Li, M. Celeste Simon, *Molecular Cell* **81**, 3760–3774 (2021).
- Oscar A. Tarazona, Olivier Pourquié, *Developmental Cell* **54**, 282–292 (2020).
- Debadrita Bhattacharya, Ana Paula Azambuja, Marcos Simoes-Costa, *Developmental Cell* **53**, 199–211.e6 (2020).
- Vinay Bulusu, Nicole Prior, Marteinn T. Snaebjörnsson, Andreas Kuehne, Katharina F. Sonnen, Jana Kress, Frank Stein, Carsten Schultz, Uwe Sauer, Alexander Aulehla, *Developmental Cell* **40**, 331–341.e4 (2017).
- Fangtao Chi, Mark S. Sharpley, Raghavendra Nagaraj, Shubhendu Sen Roy, Utpal Banerjee, *Developmental Cell* **53**, 9–26.e4 (2020).
- Jaroslav Ferenc, Aissam Ikmi, *Development* **150** (2023).
- Alexandra MacColl Garfinkel, Nelli Mnatsakanyan, Jeet H. Patel, Andrea E. Wills, Amy Shteyman, Peter J.S. Smith, Kambiz N. Alavian, Elizabeth Ann Jonas, Mustafa K. Khokha, *Developmental Cell* **58**, 2597–2613.e4 (2023).
- Hidenobu Miyazawa, Marteinn T Snaebjörnsson, Nicole Prior, Eleni Kafkia, Henrik M Hammarén, Nobuko Tsuchida-Straeten, Kiran R Patil, Martin Beck, Alexander Aulehla, *eLife* **11** (2022).
- Masayuki Oginuma, Philippe Moncquet, Fengzhu Xiong, Edward Karoly, Jérôme Chal, Karine Guevorkian, Olivier Pourquié, *Developmental Cell* **40**, 342–353.e10 (2017).
- Masayuki Oginuma, Yukiko Harima, Oscar A. Tarazona, Margarete Diaz-Cuadros, Arthur Michaut, Tohru Ishitani, Fengzhu Xiong, Olivier Pourquié, *Nature* **584**, 98–101 (2020).
- Enkhtuul Tsogtbaatar, Chelsea Landin, Katherine Minter-Dykhouse, Clifford D. L. Folmes, *Frontiers in Cell and Developmental Biology* **8** (2020).
- Lila Solnica-Krezel, Diane S. Sepich, *Annual Review of Cell and Developmental Biology* **28**, 687–717 (2012).
- Arieh Moussaieff, Matthieu Rouleau, Daniel Kitsberg, Merav Cohen, Gahl Levy, Dinorah Barasch, Alina Nemirovski, Shai Shen-Orr, Ilana Laevsky, Michal Amit, David Bomze, Bénédicte Elena-Herrmann, Tali Scherf, Malka Nissim-Rafinia, Stefan Kempa, Joseph Itskovitz-Eldor, Eran Meshorer, Daniel Aberdam, Yaakov Nahmias, *Cell Metabolism* **21**, 392–402 (2015).
- Wen Gu, Xavier Gaeta, Anna Sahakyan, Alanna B. Chan, Candice S. Hong, Rachel Kim, Daniel Braas, Kathrin Plath, William E. Lowry, Heather R. Christofk, *Cell Stem Cell* **19**, 476–490 (2016).
- Timothy S. Cliff, Tiamming Wu, Benjamin R. Boward, Amelia Yin, Hang Yin, John N. Glushka, James H. Prestegaard, Stephen Dalton, *Cell Stem Cell* **21**, 502–516.e9 (2017).
- Dominica Cao, Liangwen Zhong, Anupama Hemalatha, Jenna Bergmann, Andy L. Cox, Valentina Greco, Berna Sozen, *bioRxiv* (2023).
- Chaitanya Dingare, Jenny Yang, Ben Steventon, *bioRxiv* (2023).
- van den Susanne C. Brink, Peter Baillie-Johnson, Tina Balayo, Anna-Katerina Hadjantonakis, Sonja Nowotschin, David A. Turner, Alfonso Martinez Arias, *Development* **141**, 4231–4242 (2014).
- R. S. P. Beddington, P. Rashbass, V. Wilson, *Development* **116**, 157–165 (1992).
- David G. Wilkinson, Sangita Bhatt, Bernhard G. Herrmann, *Nature* **343**, 657–659 (1990).
- Kerim Anlaş, Nicola Gritti, David Oriola, Krisztina Arató, Fumio Nakaki, Jia Le Lim, James Sharpe, Vikas Trivedi, *bioRxiv* (2021).
- Clotilde Laussel, Sébastien Léon, *Biochemical Pharmacology* **182**, 114213 (2020).
- Sarah E. Harris, Nadia Gopichandran, Helen M. Picton, Henry J. Leese, Nicolas M. Orsi, *Theriogenology* **64**, 992–1006 (2005).
- Leonardo Beccari, Naomi Moris, Mehmet Girgin, David A. Turner, Peter Baillie-Johnson, Anne-Catherine Cossy, Matthias P. Lutolf, Denis Duboule, Alfonso Martinez Arias, *Nature* **562**, 272–276 (2018).
- Yasumasa Bessho, Goichi Miyoshi, Ryoichi Sakata, Ryoichiro Kageyama, *Genes to Cells* **6**, 175–185 (2001).
- Baljinder S. Mankoo, Susan Skuntz, Ian Harrigan, Elena Grigorieva, Al Candia, Christopher V. E. Wright, Heinz Arnheiter, Vassilis Pachnis, *Development* **130**, 4655–4664 (2003).
- Nicholas R.F. Hannan, Robert P. Fordham, Yasir A. Syed, Victoria Moignard, Andrew Berry, Ruben Bautista, Neil A. Hanley, Kim B. Jensen, Ludovic Vallier, *Stem Cell Reports* **1**, 293–306 (2013).
- Qiu Ma, Lukas Sommer, Peter Cserjesi, David J. Anderson, *The Journal of Neuroscience* **17**, 3644–3652 (1997).
- Caroline Whitehouse, Julie Chambers, Kathy Howe, Martyn Cobourne, Paul Sharpe, Ellen Solomon, *European Journal of Biochemistry* **269**, 538–545 (2002).
- F. Beck, T. Erler, A. Russell, R. James, *Developmental Dynamics* **204**, 219–227 (1995).
- Anthony Gavalas, Marc Davenne, Andrew Lumsden, Pierre Chambon, Filippo M. Rijli, *Development* **124**, 3693–3702 (1997).
- Kaoru Mitsui, Yoshimi Tokuzawa, Hiroaki Itoh, Kohichi Segawa, Mirei Murakami, Kazutoshi Takahashi, Masayoshi Maruyama, Mitsuyo Maeda, Shinya Yamanaka, *Cell* **113**, 631–642 (2003).
- Larysa H. Pevny, Shantini Sockanathan, Marysia Placzek, Robin Lovell-Badge, *Development* **125**, 1967–1978 (1998).
- Sebastian J. Arnold, Elizabeth J. Robertson, *Nature Reviews Molecular Cell Biology* **10**, 91–103 (2009).
- Frank L. Conlon, Karen M. Lyons, Norma Takaesu, Katrin S. Barth, Andreas Kispert, Bernhard Herrmann, Elizabeth J. Robertson, *Development* **120**, 1919–1928 (1994).
- Paul Gadue, Tara L. Huber, Patrick J. Paddison, Gordon M. Keller, *Proceedings of the National Academy of Sciences* **103**, 16806–16811 (2006).
- X. Sun, E. N. Meyers, M. Lewandoski, G. R. Martin, *Genes and Development* **13**, 1834–1846 (1999).
- Francesco Cecconi, Gabriele Proetzel, Gonzalo Alvarez-Bolado, Desmond Jay, Peter Gruss, *Developmental Dynamics* **210**, 184–190 (1997).
- Catherine Coffinier, Uyen Tran, Juan Larraín, E.M. De Robertis, *Mechanisms of Development* **100**, 119–122 (2001).
- Dana R. Cohen, Chi Wa Cheng, Shuk Han Cheng, Chi-chung Hui, *Mechanisms of Development* **91**, 317–321 (2000).
- Matthew H. Sieber, Allan C. Spradling, *Current Opinion in Genetics and Development* **45**, 58–68 (2017).
- Matthew G. Vander Heiden, Lewis C. Cantley, Craig B. Thompson, *Science* **324**, 1029–1033 (2009).
- Haipeng Fu, Tingyu Wang, Xiaohui Kong, Kun Yan, Yang Yang, Jingyi Cao, Yafei Yuan, Nan Wang, Kehkooi Kee, Zhi John Lu, Qiaoran Xi, *Nature Communications* **13** (2022).
- Junchen Liu, Guo Chen, Zezhen Liu, Shaoyou Liu, Zhiqian Cai, Pan You, Yuepeng Ke, Li Lai, Yun Huang, Hongchang Gao, Liangcai Zhao, Helene Pelicano, Peng Huang, Wallace L. McKeehan, Chin-Lee Wu, Cong Wang, Weide Zhong, Fen Wang, *Cancer Research* **78**, 4459–4470 (2018).
- Kira T. Pate, Chiara Stringari, Stephanie Sprowl-Tanio, Kehui Wang, Tara TeStaa, Nate P. Hoverter, Miriam M. McQuade, Chad Garner, Michelle A. Digman, Michael A. Teitelbaum, Robert A. Edwards, Enrico Gratton, Marian L. Waterman, *The EMBO Journal* **33**, 1454–1473 (2014).
- Jaswinder K. Sethi, Antonio Vidal-Puig, *Biochemical Journal* **427**, 1–17 (2010).
- B. Pajak, E. Siwiak, M. Sołtyka, A. Priebe, R. Zieliński, I. Fokt, M. Ziemiąk, A. Jaśkiewicz, R. Borowski, T. Domoradzki, W. Priebe, *International Journal of Molecular Sciences* **21**, 234 (2019).
- E. J. Boell, J. Needham, *Proceedings of the Royal Society of London. Series B - Biological Sciences* **127**, 356–362 (1939).
- N. G. Heatley, C. H. Waddington, J. Needham, *Proceedings of the Royal Society of London. Series B - Biological Sciences* **122**, 403–412 (1937).
- J. NEEDHAM, E. J. BOELL, VERONICA ROGERS, *Nature* **141**, 973–973 (1938).
- Clifford D. L. Folmes, Andre Terzic, *Reproduction, Fertility and Development* **27**, 82 (2015).
- A. Villaronga Luque, R. Savill, N. López-Anguita, A. Bolondi, S. Garai, S. Ipek Gassaloglu, A. Poddar, A. Bulut-Karslioglu, J. V. Veenvliet, *bioRxiv* (2023).
- Leixi Cao, Ruijin Wang, Guangzhi Liu, Yuwei Zhang, Rick Francis Thorne, Xu Dong Zhang, Jimming Li, Yang Xia, Lili Guo, Fengmin Shao, Hao Gu, Mian Wu, *EMBO reports* **24** (2023).
- Ina Huppertz, Joel I. Perez-Perry, Panagiotis Mantas, Thileepan Sekaran, Thomas Schwarzel, Francesco Russo, Dunja Ferring-Appel, Zuzana Koskova, Lyudmila Dimitrova-Paternoga, Eleni Kafkia, Janosch Hennig, Pierre A. Neveu, Kiran Patil, Matthias W. Hentze, *Molecular Cell* **82**, 2666–2680.e11 (2022).
- Nioosha Nekooie Marnay, Redouane Fodil, Sophie Férél, Alwyn Dady, Marine Depp, Frédéric Relaix, Roberto Motterlini, Roberta Foresti, Jean-Loup Duband, Sylvie Dufour, *Journal of Cell Science* **136** (2023).
- Zheng Wang, Dongdong Wei, Ennan Bin, Jiao Li, Kewu Jiang, Tingting Lv, Xiaoxu Mao, Fengchao Wang, Huaping Dai, Nan Tang, *Cell Stem Cell* **30**, 1028–1042.e7 (2023).
- Ng Shyh-Chang, Huck-Hui Ng, *Genes and Development* **31**, 336–346 (2017).
- Lei Shi, Benjamin P. Tu, *Current Opinion in Cell Biology* **33**, 125–131 (2015).
- Ana Chocarro-Calvo, Jose Manuel García-Martínez, Soraya Artila-González, Antonio De la Vieja, Custodia García-Jiménez, *Molecular Cell* **49**, 474–486 (2013).
- Y. Inoue, Y. Itoh, K. Abe, T. Okamoto, H. Daitoku, A. Fukamizu, K. Onozaki, H. Hayashi, *Oncogene* **26**, 500–508 (2006).
- Andrea W. Tu, Kunxin Luo, *Journal of Biological Chemistry* **282**, 21187–21196 (2007).
- Alysta Panque, Harvey Fortus, Julia Zheng, Guy Werlen, Estela Jacinto, *Genes* **14**, 933 (2023).
- Colin Reily, Tyler J. Stewart, Matthew B. Renfrow, Jan Novak, *Nature Reviews Nephrology* **15**, 346–366 (2019).
- Yohé Hayashi, Yukiko Tando, Yumi Ito-Matsuoka, Kaho Ikuta, Asuka Takehara, Katsutaro Morino, Hiroshi Maegawa, Yasuhisa Matsui, *EMBO reports* **24** (2023).
- Frank L. Conlon, Karen M. Lyons, Norma Takaesu, Katrin S. Barth, Andreas Kispert, Bernhard Herrmann, Elizabeth J. Robertson, *Development* **120**, 1919–1928 (1994).
- Paul Gadue, Tara L. Huber, Patrick J. Paddison, Gordon M. Keller, *Proceedings of the National Academy of Sciences* **103**, 16806–16811 (2006).
- X. Sun, E. N. Meyers, M. Lewandoski, G. R. Martin, *Genes and Development* **13**, 1834–1846 (1999).
- Francesco Cecconi, Gabriele Proetzel, Gonzalo Alvarez-Bolado, Desmond Jay, Peter Gruss, *Developmental Dynamics* **210**, 184–190 (1997).
- Catherine Coffinier, Uyen Tran, Juan Larraín, E.M. De Robertis, *Mechanisms of Development* **100**, 119–122 (2001).
- Dana R. Cohen, Chi Wa Cheng, Shuk Han Cheng, Chi-chung Hui, *Mechanisms of Development* **91**, 317–321 (2000).
- Matthew H. Sieber, Allan C. Spradling, *Current Opinion in Genetics and Development* **45**, 58–68 (2017).
- Matthew G. Vander Heiden, Lewis C. Cantley, Craig B. Thompson, *Science* **324**, 1029–1033 (2009).
- Haipeng Fu, Tingyu Wang, Xiaohui Kong, Kun Yan, Yang Yang, Jingyi Cao, Yafei Yuan, Nan Wang, Kehkooi Kee, Zhi John Lu, Qiaoran Xi, *Nature Communications* **13** (2022).
- Junchen Liu, Guo Chen, Zezhen Liu, Shaoyou Liu, Zhiqian Cai, Pan You, Yuepeng Ke, Li Lai, Yun Huang, Hongchang Gao, Liangcai Zhao, Helene Pelicano, Peng Huang, Wallace L. McKeehan, Chin-Lee Wu, Cong Wang, Weide Zhong, Fen Wang, *Cancer Research* **78**, 4459–4470 (2018).
- Ina Huppertz, Joel I. Perez-Perry, Panagiotis Mantas, Thileepan Sekaran, Thomas Schwarzel, Francesco Russo, Dunja Ferring-Appel, Zuzana Koskova, Lyudmila Dimitrova-Paternoga, Eleni Kafkia, Janosch Hennig, Pierre A. Neveu, Kiran Patil, Matthias W. Hentze, *Molecular Cell* **82**, 2666–2680.e11 (2022).
- Nioosha Nekooie Marnay, Redouane Fodil, Sophie Férél, Alwyn Dady, Marine Depp, Frédéric Relaix, Roberto Motterlini, Roberta Foresti, Jean-Loup Duband, Sylvie Dufour, *Journal of Cell Science* **136** (2023).
- Zheng Wang, Dongdong Wei, Ennan Bin, Jiao Li, Kewu Jiang, Tingting Lv, Xiaoxu Mao, Fengchao Wang, Huaping Dai, Nan Tang, *Cell Stem Cell* **30**, 1028–1042.e7 (2023).
- Ng Shyh-Chang, Huck-Hui Ng, *Genes and Development* **31**, 336–346 (2017).
- Lei Shi, Benjamin P. Tu, *Current Opinion in Cell Biology* **33**, 125–131 (2015).
- Ana Chocarro-Calvo, Jose Manuel García-Martínez, Soraya Artila-González, Antonio De la Vieja, Custodia García-Jiménez, *Molecular Cell* **49**, 474–486 (2013).
- Y. Inoue, Y. Itoh, K. Abe, T. Okamoto, H. Daitoku, A. Fukamizu, K. Onozaki, H. Hayashi, *Oncogene* **26**, 500–508 (2006).
- Andrea W. Tu, Kunxin Luo, *Journal of Biological Chemistry* **282**, 21187–21196 (2007).
- Alysta Panque, Harvey Fortus, Julia Zheng, Guy Werlen, Estela Jacinto, *Genes* **14**, 933 (2023).
- Colin Reily, Tyler J. Stewart, Matthew B. Renfrow, Jan Novak, *Nature Reviews Nephrology* **15**, 346–366 (2019).
- Yohé Hayashi, Yukiko Tando, Yumi Ito-Matsuoka, Kaho Ikuta, Asuka Takehara, Katsutaro Morino, Hiroshi Maegawa, Yasuhisa Matsui, *EMBO reports* **24** (2023).

Acknowledgments

We thank the Mesoscopic Imaging Facility (MIF) at the European Molecular Biology Laboratory (EMBL) for support. We further thank the EMBL Genomics Core Facility for sequencing or data processing and the EMBL Genome Biology Computational Support for data management and submission. We thank Joshua Frenster for advice on gastruloid dissociation and flow cytometry. We thank all members of the Trivedi and Ebisuya labs for insightful discussions and feedback throughout the project. We thank Idse Heemskerk, Katharina Sonnen, Charisios Tsiairis for feedback on the manuscript.

Author contributions

Conceptualization: K.S.S., M.E., V.T.; Methodology: K.S.S., M.E., V.T.; Software: N.G.; Validation: K.S.S., E.H., L.S.P., Kr.A.; Formal analysis: K.S.S., L.S.P., Ke.A., P.P., M.O.L.; Investigation: K.S.S., E.H., L.S.P.; Writing - original draft: K.S., V.T.; Visualization: K.S.S., V.T.; Supervision: K.S.S., M.E., V.T.; Project administration: V.T.; Funding acquisition: K.S.S., M.E., V.T.

Competing interests

The authors have no competing interests.

728 **Funding**

729 This work was supported by funds from the European Molecular Biology Lab-
730 oratory to V.T. K.S.S. was supported by an EMBL Interdisciplinary Postdoc
731 (EIPOD4) fellowship under H2020 Marie Skłodowska- Curie Actions COFUND
732 4 (847543) and a Human Frontier Science Program long-term postdoctoral fellow-
733 ship (LT000685/2021). M.E. was supported by the European Research Council
734 (ERC) under the European Union's Horizon 2020 research and innovation program
735 (grant agreement No. 101002564).

736 **Supplementary information**

737 Materials and methods, Supplementary figures and Supplementary movies.