

An Effective Model of the Retinoic Acid Induced HL-60 Differentiation Program

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Abstract

In this study, we present an effective model All-Trans Retinoic Acid (ATRA)-induced differentiation of HL-60 cells. The model describes a key architectural feature of ATRA-induced differentiation, positive feedback between an ATRA-inducible signalsome complex involving many proteins including Vav1, a guanine nucleotide exchange factor, and the activation of the mitogen activated protein kinase (MAPK) cascade. The model, which was developed by integrating logical rules with kinetic modeling, was significantly smaller than previous models. However, despite its simplicity, it captured key features of ATRA induced differentiation of HL-60 cells. We identified an ensemble of effective model parameters using measurements taken from ATRA-induced HL-60 cells. Using these parameters, model analysis predicted that MAPK activation was bistable as a function of ATRA exposure. Conformational experiments supported ATRA-induced bistability. These findings, combined with other literature evidence, suggest that positive feedback is central to a diversity of cell fate programs.

1 Introduction

2 Understanding the architecture of differentiation programs is an important therapeutic
3 challenge. Differentiation induction chemotherapy (DIC), using agents such as the vita-
4 min A derivative all-trans retinoic acid (ATRA), is a promising approach for the treatment
5 of many cancers (1–3). For example, ATRA treatment induces remission in 80–90% of
6 promyelocytic leukemia (APL) PML-RAR α -positive patients (4), thereby transforming a
7 fatal diagnosis into a manageable disease. However, remission is sometimes not durable
8 and relapsed cases exhibit emergent ATRA resistance (5, 6). To understand the basis of
9 this resistance, we must first understand the ATRA-induced differentiation program. To-
10 ward this challenge, lessons learned in model systems, such as the lineage-uncommitted
11 human myeloblastic cell line HL-60, could inform our analysis of the more complex dif-
12 ferentiation programs occurring in patients. Patient derived HL-60 leukemia cells have
13 been a durable experimental model since the 1970's to study differentiation (7). HL-60
14 undergoes cell cycle arrest and either myeloid or monocytic differentiation following stim-
15 ulation; ATRA induces G1/G0-arrest and myeloid differentiation in HL-60 cells, while 1,25-
16 dihydroxy vitamin D3 (D3) induces arrest and monocytic differentiation. Commitment to
17 cell cycle arrest and differentiation requires approximately 48 hr of treatment, during which
18 HL-60 cells undergo two division cycles.

19 Sustained mitogen-activated protein kinase (MAPK) activation is a defining feature of
20 ATRA-induced HL-60 differentiation. ATRA drives sustained MEK-dependent activation
21 of the Raf/MEK/ERK pathway, leading to arrest and differentiation (8). MEK inhibition re-
22 sults in the loss of ERK and Raf phosphorylation, and the failure to arrest and differentiate
23 (9). ATRA (and its metabolites) are ligands for the hormone activated nuclear transcrip-
24 tion factors retinoic acid receptor (RAR) and retinoid X receptor (RXR) (10). RAR/RXR
25 activation is necessary for ATRA-induced Raf phosphorylation (9), and the formation of
26 an ATRA-inducible signalsome complex at the membrane which drives MAPK activation

27 through a yet to be identified kinase activity. While the makeup of the signalsome com-
28 plex is not yet known, we do know that it is composed of Src family kinases Fgr and Lyn,
29 PI3K, c-Cbl, Slp76, and KSR, as well as IRF-1 transcription factors (11–15). Signalsome
30 formation and activity is driven by ATRA-induced expression of CD38 and the putative
31 heterotrimeric Gq protein-coupled receptor BLR1 (16, 17). BLR1, identified as an early
32 ATRA (or D3)-inducible gene using differential display (18), is necessary for MAPK ac-
33 tivation and differentiation (17), and is also involved with signalsome activity. Studies
34 of the BLR1 promoter identified a 5' 17bp GT box approximately 1 kb upstream of the
35 transcriptional start that conferred ATRA responsiveness (17). Members of the BLR1
36 transcriptional activator complex, e.g. NFATc3 and CREB, are phosphorylated by ERK,
37 JNK or p38 MAPK family members suggesting positive feedback between the signal-
38 some and MAPK activation (19). BLR1 overexpression enhanced Raf phosphorylation
39 and accelerated terminal differentiation, while Raf inhibition reduced BLR1 expression
40 and differentiation (20). BLR1 knock-out cells failed to activate Raf or differentiate in
41 the presence of ATRA (20). Interestingly, both the knockdown or inhibition of Raf, also
42 reduced BLR1 expression and functional differentiation (20). Thus, the expression of
43 signalsome components e.g., BLR1 was Raf dependent, while Raf activation depended
44 upon the siganlsome. A recent computational study of ATRA-induced differentiation in
45 HL-60 cells suggested that the BLR1-MAPK positive feedback circuit was sufficient to ex-
46 plain ATRA-induced sustained MAPK activation, and the expression of a limited number
47 of functional differentiation markers (21). Model analysis also suggested that Raf was the
48 most distinct of the MAPK proteins. However, this previous study developed and analyzed
49 a complex model, thus leaving open the critical question of what is the minimal positive
50 feedback circuit required to drive ATRA-induced differentiation.

51 In this study, we explored this question using a minimal mathematical model of the
52 key architectural feature of ATRA induced differentiation of HL-60 cells, namely positive

53 feedback between an ATRA-inducible signalsome complex and MAPK activation. The
54 ATRA responsive signalsome-MAPK circuit was then used to drive a downstream gene
55 expression program which encoded for the expression of functional differentiation mark-
56 ers. The effective model used a novel framework which integrated logical rules with ki-
57 netic modeling to describe gene expression and protein regulation, while largely relying
58 upon biophysical parameters from the literature. This formulation significantly reduced
59 the size and complexity of the model compared to the previous study of Tasseff et al.,
60 while increasing the breadth of the biology described (21). The effective model, despite
61 its simplicity, captured key features of ATRA induced differentiation of HL-60 cells. Model
62 analysis predicted the bistability of MAPK activation as a function of ATRA exposure; con-
63 formational experiments supported ATRA-induced bistability. Model simulations were also
64 consistent with measurements of the influence of MAPK inhibitors, and the failure of BLR1
65 knockout cells to differentiate when exposed to ATRA. Lastly, we showed by through im-
66 munoprecipitation studies, that the guanine nucleotide exchange factor Vav1 is potentially
67 a new ATRA-inducible member of the siganlsome complex. Taken together, these findings
68 when combined with other literature evidence, suggested that positive feedback architec-
69 tures are central to differentiation programs generally, and necessary for ATRA-induced
70 differentiation.

71 **Results**

72 We constructed an effective model of ATRA-induced HL-60 differentiation which described
73 signaling and gene expression events following the addition of ATRA (Fig. 1). The model
74 connectivity was developed from literature and the studies presented here (Table 1). We
75 decomposed the ATRA program into three modules; a signal initiation module that sensed
76 and transformed the ATRA signal into activated cRaf-pS621 and the ATRA-RXR/RAR
77 (Trigger) signals (Fig. 1A); a signal integration module that controlled the expression of
78 upstream transcription factors given cRaf-pS621 and activated Trigger signals (Fig. 1B);
79 and a phenotype module which encoded the expression of functional differentiation mark-
80 ers from the ATRA-inducible transcription factors (Fig. 1C). Each component of these
81 modules was described by a mRNA and protein balance equation. Additionally, the sig-
82 nal initiation module also described the abundance of activated species e.g., Trigger and
83 cRaf-pS621 whose values were derived from unactivated Trigger and cRaf protein levels.
84 Lastly, because the population of HL-60 cells was dividing (at least before ATRA-induced
85 cell cycle arrest), we also considered a dilution term in all balance equations. The sig-
86 nal initiation module contained nine differential equations, while the signal integration and
87 phenotype modules were collectively encoded by 54 differential equations. Model pa-
88 rameters were taken literature, or estimated from experimental data taken from literature
89 using heuristic optimization (see materials and methods).

90 The signal initiation module recapitulated sustained signalsome and MAPK activation
91 following exposure to $1\mu\text{M}$ ATRA (Fig. 2A-B). An ensemble of effective model param-
92 eters was estimated by minimizing the difference between simulations and time-series
93 measurements of BLR1 mRNA and cRaf-pS621 following the addition of $1\mu\text{M}$ ATRA. We
94 focused on the S621 phosphorylation site of cRaf since enhanced phosphorylation at
95 this site is a defining characteristic of sustained MAPK activation in HL-60. The effective
96 model captured both ATRA-induced BLR1 expression (Fig. 2A) and sustained phospho-

97 phosphorylation of cRaf-pS621 (Fig. 2B) in a growing population of HL-60 cells. Together, the
98 reinforcing positive feedback between the signalsome and MAPK led to sustained activation
99 over multiple cellular generations. However, the effective model failed to capture the
100 decline of BLR1 message after 48 hr of ATRA exposure. This suggested that we captured
101 the logic leading to the onset of differentiation, but failed to describe program shutdown.
102 Next, we tested the response of the signal initiation module to different ATRA dosages.

103 The signal initiation model was bistable with respect to ATRA induction (Fig. 2C-D).
104 Phaseplane analysis predicted two stable steady-states when ATRA was present below
105 a critical threshold (Fig. 2C). In the lower stable state, neither the signalsome nor cRaf-
106 pS621 were present (thus, the differentiation program was deactivated). However, at
107 the high stable state, both the signalsome and cRaf-pS621 were present, allowing for
108 sustained activation and differentiation. Interestingly, when ATRA was above a critical
109 threshold, only the activated state was accessible (Fig. 2D). To test these findings, we
110 first identified the ATRA threshold. We exposed HL-60 cells to different ATRA concen-
111 trations for 72 hr (Fig. 2E). Morphological changes associated with differentiation were
112 visible for ATRA $\geq 0.25 \mu\text{M}$, suggesting the critical ATRA threshold was near this concen-
113 tration. Next, we conducted ATRA washout experiments to determine if activated cells
114 remained activated in the absence of ATRA. HL-60 cells locked into an activated state
115 remained activated following ATRA withdraw (Fig. 3). This sustained activation resulted
116 from reinforcing feedback between the signalsome and the MAPK pathway. Thus, follow-
117 ing activation, if we inhibited or removed elements from the signal initiation module we
118 expected the siganlsome and MAPK signals to decay. We simulated ATRA induced acti-
119 vation in the presence of kinase inhibitors, and without key circuit elements. Consistent
120 with experimental results using multiple MAPK inhibitors, ATRA activation in the presence
121 of MAPK inhibitors lowered the steady-state value of signalsome (Fig. 3A). In the pres-
122 ence of BLR1, the signalsome and cRaf-pS621 signals were maintained following ATRA

123 withdraw (Fig. 3B, gray). On the other hand, BLR1 deletion removed the ability of the
124 circuit to maintain a sustained MAPK response following the withdraw of ATRA (Fig. 3B,
125 blue). Lastly, washout experiments in which cells were exposed to $1\mu\text{M}$ ATRA for 24 hr,
126 and then transferred to fresh media without ATRA, confirmed the persistence of the self
127 sustaining activated state for up to 144 hr (Fig. 3C). Thus, these experiments confirmed
128 that reinforcing positive feedback likely drives the ATRA-induced differentiation program.
129 Next, we analyzed the ATRA-induced downstream gene expression program following
130 signalsome and cRaf activation.

131 The signal integration and phenotype modules described ATRA-induced gene expres-
132 sion events in wild-type HL-60 cells (Fig. 4). The signal initiation module produced two
133 outputs, activated Trigger and cRaf-pS621 which drove the expression of ATRA-induced
134 transcription factors, which then in turn activated the phenotypic program. In particular,
135 Trigger, which is a surrogate for the RAR α /RXR transcriptional complex, regulated the ex-
136 pression of the transcription factors CCATT/enhancer binding protein α (C/EBP α), PU.1,
137 and EGR1. In turn, these transcription factors, in combination with cRaf-pS621, regulated
138 the expression of downstream phenotypic markers such as CD38, CD11b or P47Phox.
139 We assembled the connectivity of the signal integration and phenotypic programs driven
140 by Trigger and cRaf-pS621 from literature (Table 1). We estimated the parameters which
141 appeared in the control laws regulating these programs from steady-state and dynamic
142 measurements of transcription factor and phenotypic marker expression following the ad-
143 dition of ATRA [REFHERE]. However, the bulk of the remaining model parameters were
144 taken from directly from literature (22) and were not estimated in this study (see mate-
145 rials and methods). The model simulations captured the time dependent expression of
146 CD38 and CD11b following the addition ATRA (Fig. 4A), and the steady-state for sig-
147 nal integration and phenotypic markers (Fig. 4B). Taken together, the signal integration
148 and phenotypic simulations were consistent with measurements, thereby validating the

149 assumed molecular connectivity.

150 The composition of the siganlsome, and the kinase ultimately responsible for medi-
151 ating ATRA-induced Raf activation is currently unknown. To explore this question, we
152 conducted immunoprecipitation and subsequent Western blotting to identify physical in-
153 teractions between Raf and 19 putative interaction partners. A panel of 19 possible Raf
154 interaction partners (kinases, GTPases, scaffolding proteins etc) was constructed based
155 upon known signaling pathways. We did not consider the most likely binding partner, the
156 small GTPase RAS, as previous studies have ruled it out in MAPK activation in HL-60 cells
157 (20, 23). Total Raf was used as a bait protein for the immunoprecipitation studies. Interro-
158 gation of the Raf interactome suggested Vav1 was involved with ATRA-induced initiation
159 of MAPK activity (Fig. 5). Western blot analysis using total Raf and pS621 Raf specific
160 antibodies confirmed the presence of the bait protein, total and phosphorylated forms, in
161 the immunoprecipitate (Fig. 5A). Of the 19 proteins sampled, Vav1, Src, CK2, Akt, and
162 14-3-3 precipitated with Raf, suggesting a direct physical interaction was possible. How-
163 ever, only the associations between Raf and Vav1 and Raf and Src were ATRA-inducible
164 (Fig. 5). Furthermore, the Vav1 and Src associations were correlated with pS621 Raf
165 abundance in the precipitate. Others proteins e.g., CK2, Akt and 14-3-3, generally bound
166 Raf regardless of phosphorylation status or ATRA treatment. The remaining 14 proteins
167 were expressed in whole cell lysate (Fig. 5B), but were not detectable in the precipitate
168 of Raf IP. Treatment with the Raf kinase inhibitor GW5074 following ATRA exposure re-
169 duced the association of both Vav1 with Raf and Src with Raf (Fig. 5), although the signal
170 intensity for Src was notably weak. However, GW5074 did not influence the association
171 of CK2 or 14-3-3 with Raf, further demonstrating their independence from Raf phospho-
172 rylation. Interestingly, the Raf-Akt interaction qualitatively increased following treatment
173 with GW5074; however, it remained unaffected by treatment with ATRA. Src family ki-
174 nases are known to be important in myeloid differentiation (24) and their role in HL-60

175 differentiation has been investigated elsewhere (11). Given the existing work and variable
176 reproducibility in the context of the Raf immunoprecipitate, we did not investigate the role
177 of Src further in this study. Taken together, the immunoprecipitation and GW5074 results
178 implicated Vav1 association to be correlated with Raf activation following ATRA-treatment.
179 Previous studies demonstrated that a Vav1-Slp76-Cbl-CD38 complex plays an important
180 role in ATRA-induced MAPK activation and differentiation of HL-60 cells (13). Here we
181 did not observe direct interaction of Raf with Cbl or Slp76; however, this complex could
182 be involved upstream.

183 Next, we considered the effect of the Raf kinase inhibitor GW5074 on functional mark-
184 ers of ATRA-induced growth arrest and differentiation. Inhibition of Raf kinase activity
185 modulated MAPK activation and differentiation markers following ATRA exposure (Fig.
186 5D-F). ATRA treatment alone statistically significantly increased the G1/G0 percentage
187 over the untreated control, while GW5074 alone had a negligible effect on the cell cycle
188 distribution (Fig. 5D). Surprisingly, the combination of GW5074 and ATRA statistically
189 significantly increased the G1/G0 population ($82 \pm 1\%$) compared with ATRA alone (61
190 $\pm 0.5\%$). Increased G1/G0 arrest following the combined treatment with GW5074 and
191 ATRA was unexpected, as the combination of ATRA and the MEK inhibitor (PD98059) has
192 been shown previously to decrease ATRA-induced growth arrest (8). However, growth ar-
193 rest is not the sole indication of functional differentiation. Expression of the cell surface
194 marker CD11b has also been shown to coincide with HL-60 cells myeloid differentiation
195 (25). We measured CD11b expression, for the various treatment groups, using immuno-
196 fluorescence flow cytometry 48 hr post-treatment. As with G1/G0 arrest, ATRA alone
197 increased CD11b expression over the untreated control, while GW5074 further enhanced
198 ATRA-induced CD11b expression (Fig. 5E). GW5074 alone had no statistically significant
199 effect on CD11b expression, compared with the untreated control. Lastly, the inducible re-
200 active oxygen species (ROS) response was used as a functional marker of differentiated

201 neutrophils (16). We measured the ROS response induced by the phorbol ester 12-O-
202 tetradecanoylphorbol-13-acetate (TPA) using flow cytometry. Untreated cells showed no
203 discernible TPA response, with only $7.0 \pm 3.0\%$ ROS induction (Fig. 5F). Cells treated
204 with ATRA had a significantly increased TPA response, $53 \pm 7\%$ ROS induction 48 hr
205 post-treatment. Treatment with both ATRA and GW5074 statistically significantly reduced
206 ROS induction ($22 \pm 0.6\%$) compared to ATRA alone. Interestingly, Western blot analy-
207 sis did not detect a GW5074 effect on ATRA-induced expression of p47phox, a required
208 upstream component of the ROS response (Fig. 5F, bottom). Thus, the inhibitory effect
209 of GW5074 on inducible ROS might occur downstream of p47phox expression. How-
210 ever, the ROS producing complex is MAPK dependent, therefore it is also possible that
211 GW5074 inhibited ROS production by interfering with MAPK activation (in which case the
212 p47Phox marker might not accurately reflect phenotypic conversion and differentiation).

213 **Discussion**

214 In this study, we presented an effective model of ATRA-inducible differentiation of HL-60
215 cells which encoded positive feedback between the ATRA-inducible signalsome complex
216 and the MAPK pathway. Despite its simplicity, the model captured key features of the
217 ATRA induced differentiation such as sustained MAPK activation, and bistability with re-
218 spect to ATRA exposure. We also reported a new ATRA-inducible component of the
219 signalsome, Vav1. Vav1 is a guanine nucleotide exchange factor for Rho family GTPases
220 that activate pathways leading to actin cytoskeletal rearrangements and transcriptional al-
221 terations (26). The Vav1/Raf association correlated with Raf activity, was ATRA-inducible
222 and decreased after treatment with GW5074. The presence of Vav1 in Raf/Grb2 com-
223 plexes has been shown to correlate with increased Raf activity in mast cells (27). Fur-
224 thermore, studies on Vav1 knockout mice demonstrated that the loss of Vav1 resulted
225 in deficiencies of ERK signaling for both T-cells as well as neutrophils (28, 29). While its
226 function in the signalsome is unclear, Vav1 has been shown to associate with a Cbl-Slp76-
227 CD38 complex in an ATRA-dependent manner; furthermore, transfection of HL-60 cells
228 with Cbl mutants that fail to bind CD38, yet still bind Slp76 and Vav1, prevented ATRA-
229 induced MAPK activation (13). Thus, interaction of Cbl-Slp76-Vav1 and CD38 appears to
230 be required for transmission of the ATRA signal by the signalsome.

231 We conducted immunoprecipitation studies and identified a limited number of ATRA-
232 dependent and -independent Raf interaction partners. While we were unable to detect
233 the association of Raf with common kinases and GTPases such as PKC, PKA, p38, Rac
234 and Rho, we did establish potential interactions between Raf and key partners such as
235 Vav1, Src, Akt, CK2 and 14-3-3. All of these partners are known to be associated with Raf
236 activation or function. Src is known to bind Raf through an SH2 domain, and this associ-
237 ation has been shown to be dependent of the serine phosphorylation of Raf (30). Thus,
238 an ATRA inducible Src/Raf association may be a result of ATRA-induced Raf phospho-

239 phosphorylation at S259 or S621. We also identified an interaction between Raf and the Ser/Thr
240 kinases Akt and CK2. Akt can phosphorylate Raf at S259, as demonstrated by studies
241 in a human breast cancer line (31). CK2 can also phosphorylate Raf, although the lit-
242 erature has traditionally focused on S338 and not S621 or S259(32). However, neither
243 of these kinase interactions were ATRA-inducible, suggesting their association with Raf
244 alone was not associated with ATRA-induced Raf phosphorylation. The adapter protein
245 14-3-3 was also constitutively associated with Raf. The interaction between Raf and 14-
246 3-3 has been associated with both S621 and S259 phosphorylation and activity (33).
247 Additionally, the association of Raf with 14-3-3 not only stabilized S621 phosphorylation,
248 but also reversed the S621 phosphorylation from inhibitory to activating (34). Finally, we
249 found that Vav1/Raf association correlated with Raf activity, was ATRA-inducible and de-
250 creased after treatment with GW5074. The presence of Vav1 in Raf/Grb2 complexes has
251 been shown to correlate with increased Raf activity in mast cells (27). Furthermore, stud-
252 ies on Vav1 knockout mice demonstrated that the loss of Vav1 resulted in deficiencies of
253 ERK signaling for both T-cells as well as neutrophils (28, 29). Interestingly, while an in-
254 tegrin ligand-induced ROS response was blocked in Vav1 knockout neutrophils, TPA was
255 able to bypass the Vav1 requirement and stimulate both ERK phosphorylation and ROS
256 induction (29). In this study, the TPA-induced ROS response was dependent upon Raf
257 kinase activity, and was mitigated by the addition of GW5074. It is possible that Vav1 is
258 downstream of various integrin receptors but upstream of Raf in terms of inducible ROS
259 responses. Vav1 has also been shown to associate with a Cbl-Slp76-CD38 complex in an
260 ATRA-dependent manner; furthermore, transfection of HL-60 cells with Cbl mutants that
261 fail to bind CD38, yet still bind Slp76 and Vav1, prevents ATRA-induced MAPK activation
262 (13). The literature suggest a variety of possible receptor-signaling pathways, which in-
263 volve Vav1, for MAPK activation; moreover, given the ATRA-inducible association Vav1
264 may play a direct role in Raf activation.

265 We hypothesized that Vav1 is a member of an ATRA-inducible complex which propels
266 sustained MAPK activation, arrest and differentiation. Initially, ATRA-induced Vav1 ex-
267 pression drives increased association between Vav1 and Raf. This increased interaction
268 facilitates phosphorylation and activation of Raf by pre-bound Akt and/or CK2 at S621
269 or perhaps S259. Constitutively bound 14-3-3 may also stabilize the S621 phosphory-
270 lation, modulate the activity and/or up-regulate autophosphorylation. Activated Raf can
271 then drive ERK activation, which in turn closes the positive feedback loop by activating
272 Raf transcription factors, e.g. Sp1 and/or STAT1 (35–38). We tested this working hy-
273 pothesis using mathematical modeling. The model recapitulated both ATRA time-course
274 data as well as the GW5074 inhibitor effects. This suggested the proposed Raf-Vav1
275 architecture was at least consistent with the experimental studies. Further, analysis of
276 the Raf-Vav1 model identified bistability in ppERK levels. Thus, two possible MAPK ac-
277 tivation branches were possible for experimentally testable ATRA values. The analysis
278 also suggested the ATRA-induced Raf-Vav1 architecture could be locked into a sustained
279 signaling mode (high ppERK) even in the absence of a ATRA signal. This locked-in prop-
280 erty could give rise to an ATRA-induction memory. We validated the treatment memory
281 property predicted by the Raf-Vav1 circuit experimentally using ATRA-washout experi-
282 ments. ERK phosphorylation levels remained high for more then 96 hr after ATRA was
283 removed. Previous studies demonstrated that HL-60 cells possessed an inheritable mem-
284 ory of ATRA stimulus (39). Although the active state was self-sustaining, the inactive state
285 demonstrated considerable robustness to perturbation. For example, we found that 50x
286 overexpression of Raf was required to reliably lock MAPK into the activated state, while
287 small perturbations had almost no effect on ppERK levels over the entire ensemble. CD38
288 expression correlated with the ppERK, suggesting its involvement in the signaling com-
289 plex. Our computational and experimental results showed that positive feedback, through
290 ERK-dependent Raf expression, could sustain MAPK signaling through many division cy-

291 cles. Such molecular mechanisms could underly aspects of cellular memory associated
292 to consecutive ATRA treatments.

293 Several engineered, or naturally occurring systems involved in cell fate decisions incor-
294 porate positive feedback and bistability (40). One of the most well studied cell fate circuits
295 is the Mos mitogen-activated protein kinase cascade in *Xenopus* oocytes. This cascade
296 is activated when oocytes are induced by the steroid hormone progesterone (41). The
297 MEK-dependent activation of p42 MAPK stimulates the accumulation of the Mos onco-
298 protein, which in turn activates MEK, thereby closing the feedback loop. This is similar to
299 the differentiation circuit presented here; ATRA drives signalsome which activates MAPK,
300 cell-cycle arrest, differentiation and signalsome. Thus, while HL-60 and *Xenopus* oocytes
301 are vastly different biological models, they share similar cell fate decision architectures.
302 Other unrelated cell fate decisions such as programmed cell death have also been sug-
303 gested to be bistable (42). Still more biochemical networks important to human health,
304 for example the human coagulation or complement cascades, also feature strong positive
305 feedback elements (43). Thus, while positive feedback is sometimes not desirable in man-
306 made systems, it may be at the core of a diverse variety of cell fate programs and other
307 networks important to human health.

308 Model performance was impressive given its limited size. However, there were several
309 issues to explore further. First, there was likely missing connectivity in the effective differ-
310 entiation circuit. Decreasing BLR1 expression with simultaneously sustained cRaf-pS261
311 activation was not captured by the current network architecture. This suggested that
312 signalsome, once activated, had a long lifetime as decreased BLR1 expression did not
313 impact cRaf-pS261 abundance. We could model this by separating signalsome formation
314 into an inactive precursor pool that is transformed to a long-lived activated signalsome by
315 MAPK activation. We should also explore adding additional downstream biological mod-
316 ules to this skeleton model, for example the upregulation of reactive oxygen markers such

317 as p47Phox or cell cycle arrest components to capture the switch from an actively prolif-
318 erating population to a population in G0-arrest. Next, the choice of max/min integration
319 rules or the particular form of the transfer functions could also be explored. Integration
320 rules other than max/min could be used, such as the mean or the product, assuming the
321 range of the transfer functions is always $f \in [0, 1]$. Alternative integration rules might
322 have different properties which could influence model identification or performance. For
323 example, a mean integration rule would be differentiable, allowing derivative-based opti-
324 mization approaches to be used. The form of the transfer function could also be explored.
325 We choose hill-like functions because of their prominence in the systems and synthetic
326 biology community. However, many other transfer functions are possible.

327 **Materials and Methods**

328 *Gene expression model equations.* We decomposed the ATRA-induced differentiation
329 program into three modules; a signal initiation module that sensed and transformed the
330 ATRA signal into activated cRaf-pS621 and the ATRA-RXR/RAR (activated Trigger) sig-
331 nals; a signal integration module that controlled the expression of upstream transcription
332 factors given cRaf-pS621 and activated Trigger signals; and a phenotype module which
333 encoded the expression of functional differentiation markers from the ATRA-inducible tran-
334 scription factors. The output of the signal initiation module was the input to the gene ex-
335 pression model. For each gene $j = 1, 2, \dots, \mathcal{G}$, we modeled both the mRNA (m_j) and
336 protein (p_j) abundance:

$$\frac{dm_j}{dt} = r_{T,j} - (\mu + \theta_{m,j}) m_j + \lambda_j \quad (1)$$

$$\frac{dp_j}{dt} = r_{X,j} - (\mu + \theta_{p,j}) p_j \quad (2)$$

337 The terms $r_{T,j}$ and $r_{X,j}$ denote the specific rates of transcription, and translation while
338 the terms $\theta_{m,j}$ and $\theta_{p,j}$ denote first-order degradation constants for mRNA and protein,
339 respectively. The specific transcription rate $r_{T,j}$ was modeled as the product of a kinetic
340 term $\bar{r}_{T,j}$ and a control term u_j which described how the abundance of transcription fac-
341 tors, or other regulators influenced the expression of gene j . The kinetic transcription
342 term $\bar{r}_{T,j}$ was modeled as:

$$\bar{r}_{T,j} = V_T^{max} \left(\frac{L_{T,o}}{L_{T,j}} \right) \left(\frac{G_j}{K_T + G_j} \right) \quad (3)$$

343 where the maximum gene expression rate V_T^{max} was defined as the product of a char-
344 acteristic transcription rate constant (k_T) and the abundance of RNA polymerase (R_1),
345 $V_T^{max} = k_T (R_1)$. The $(L_{T,o}/L_{T,j})$ term denotes the ratio of transcription read lengths; $L_{T,o}$

346 represents a characteristic gene length, while $L_{T,j}$ denotes the length of gene j . Thus,
 347 the ratio $(L_{T,o}/L_{T,j})$ is a gene specific correction to the characteristic transcription rate
 348 V_T^{max} . The degradation rate constants were defined as $\theta_{m,j}$ and $\theta_{p,j}$ denote characteristic
 349 degradation constants for mRNA and protein, respectively. Lastly, the λ_j term denotes the
 350 constitutive rate of expression of gene j .

351 The gene expression control term $0 \leq u_j \leq 1$ depended upon the combination of fac-
 352 tors which influenced the expression of gene j . If the expression of gene j was influenced
 353 by $1, \dots, m$ factors, we modeled this relationship as $u_j = \mathcal{I}_j(f_{1j}(\cdot), \dots, f_{mj}(\cdot))$ where
 354 $0 \leq f_{ij}(\cdot) \leq 1$ denotes a regulatory transfer function quantifying the influence of factor i
 355 on the expression of gene j , and $\mathcal{I}_j(\cdot)$ denotes an integration rule which combines the
 356 individual regulatory inputs for gene j into a single control term. In this study, the integra-
 357 tion rule governing gene expression was the weighted fraction of promoter configurations
 358 that resulted in gene expression [REFHERE]:

$$u_j = \frac{W_{R_{1,j}} + \sum_n W_{nj} f_{nj}}{1 + W_{R_{1,j}} + \sum_d W_{dj} f_{dj}} \quad (4)$$

359 The numerator, the weighted sum (with weights W_{nj}) of promoter configurations leading to
 360 gene expression, was normalized by all possible promoter configurations. The likelihood
 361 of each configuration was quantified by the transfer function f_{nj} (which we modeled using
 362 hill like functions), while the lead term in the numerator $W_{R_{1,j}}$ denotes the weight of con-
 363 stitutive expression for gene j . Given this formulation, the rate of constitutive expression
 364 was then given by:

$$\lambda_j = \bar{r}_{T,j} \left(\frac{W_{R_{1,j}}}{1 + W_{R_{1,j}}} \right) \quad (5)$$

365 If a gene expression process had no modifying factors, $u_j = 1$. Lastly, the specific trans-

366 lation rate was modeled as:

$$r_{X,j} = V_X^{max} \left(\frac{L_{X,o}}{L_{X,j}} \right) \left(\frac{m_j}{K_X + m_j} \right) \quad (6)$$

367 where V_X^{max} denotes a characteristic maximum translation rate estimated from literature,
368 and K_X denotes a translation saturation constant. The characteristic maximum translation
369 rate was defined as the product of a characteristic translation rate constant (k_X) and
370 the Ribosome abundance (R_2), $V_X^{max} = k_X (R_2)$. As was the case for transcription, we
371 corrected the characteristic translation rate by the ratio of the length of a characteristic
372 transcription normalized by the length of transcript j .

373 *Signaling model equations.* The signal initiation, and integration modules required the
374 level of cRaf-pS621 and ATRA-RXR/RAR (activated Trigger) as inputs. However, our
375 base model described only the abundance of inactive proteins e.g., cRaf or RXR/RAR
376 but not the activated forms. To address this issue, we estimated pseudo steady state
377 approximations for the abundance of cRaf-pS621 and activated Trigger. The abundance
378 of activated trigger ($x_{a,1}$) was estimated directly from the RXR/RAR abundance ($x_{u,1}$):

$$x_{a,1} \sim x_{u,1} \left(\frac{\alpha \cdot \text{ATRA}}{1 + \alpha \cdot \text{ATRA}} \right) \quad (7)$$

379 where α denotes a gain parameter; $\alpha = 0.0$ if ATRA is less than a threshold, and $\alpha = 0.1$
380 if ATRA is greater than the differentiation threshold. The abundance of cRaf-pS621 was
381 estimated by making the pseudo steady state approximation on the cRaf-pS621 balance.
382 The abundance of an activated signaling species i was given by:

$$\frac{dx_i}{dt} = r_{+,i}(\mathbf{x}, \mathbf{k}) - (\mu + k_{d,i}) x_i \quad i = 1, \dots, \mathcal{M} \quad (8)$$

383 The quantity x_i denotes concentration of signaling species i , while \mathcal{R} and \mathcal{M} denote
 384 the number of signaling reactions and signaling species in the model, respectively. The
 385 term $r_{+,i}(\mathbf{x}, \mathbf{k})$ denotes the rate of generation of activated species i , while μ denotes
 386 the specific growth rate, and $k_{d,i}$ denotes the rate constant controlling the non-specific
 387 degradation of x_i . We neglected deactivation reactions e.g., phosphatase activities. We
 388 assumed that signaling processes were fast compared to gene expression; this allowed
 389 us to approximate the signaling balance as:

$$x_i^* \simeq \frac{r_{+,i}(\mathbf{x}, \mathbf{k})}{(\mu + k_{d,i})} \quad i = 1, \dots, \mathcal{M} \quad (9)$$

390 The generation rate was written as the product of a kinetic term ($\bar{r}_{+,i}$) and a control term
 391 (v_i). The control terms $0 \leq v_j \leq 1$ depended upon the combination of factors which in-
 392 fluenced rate process j . If rate j was influenced by $1, \dots, m$ factors, we modeled this
 393 relationship as $v_j = \mathcal{I}_j(f_{1j}(\cdot), \dots, f_{mj}(\cdot))$ where $0 \leq f_{ij}(\cdot) \leq 1$ denotes a regulatory
 394 transfer function quantifying the influence of factor i on rate j . The function $\mathcal{I}_j(\cdot)$ is an
 395 integration rule which maps the output of regulatory transfer functions into a control vari-
 396 able. In this study, we used $\mathcal{I}_j \in \{\min, \max\}$ and hill transfer functions (44). If a process
 397 had no modifying factors, $v_j = 1$. The kinetic rate of cRaf-pS621 generation $\bar{r}_{+,cRaf}$ was
 398 modeled as:

$$\bar{r}_{+,cRaf} = k_{+,cRaf} x_s \left(\frac{x_{cRaf}}{K_{+,cRaf} + x_{cRaf}} \right) \quad (10)$$

399 where x_s denotes the signalsome abundance, and $K_{+,cRaf}$ denotes a saturation constant
 400 governing cRaf-pS621 formation. The formation of cRaf-pS621 was regulated by only a
 401 single factor, the abundance of MAPK inhibitor, thus $v_{+,cRaf}$ took the form:

$$v_{+,cRaf} = \left(1 - \frac{I}{K_D + I} \right) \quad (11)$$

402 where I denotes the abundance of the MAPK inhibitor, and K_D denotes the inhibitor
403 affinity.

404 *Estimation of model parameters.* We estimated parameters appearing in the mRNA and
405 protein balances, and the abundance of polymerases and ribosomes, from estimates of
406 transcription and translation rates, the half-life of a typical mRNA and protein, and typi-
407 cal values for the copies per cell of RNA polymerase and ribosomes from literature (Table
408 ZZ). For the remaining parameters, e.g., the W_{ij} appearing in the control laws, or parame-
409 ters appearing in the transfer functions f_{d_j} , were estimated from the gene expression and
410 signaling data sets discussed here. The saturation constants K_X and K_T were adjusted
411 so that gene expression and translation resulted in gene products on a biologically realis-
412 tic concentration scale. Lastly, we calculated the concentration for gene G_j by assuming,
413 on average, that a cell had two copies of each gene at any given time. Thus, the bulk
414 of our gene expression parameters were based directly upon literature values, and were
415 not adjusted during model identification. The values used for the characteristic transcrip-
416 tion/translation parameters, degradation constants and macromolecular copy number are
417 given in the supplemental materials along with the specific formulas required to calculate
418 all derived constants.

419 Signal and gene expression model parameters were estimated by minimizing the
420 squared difference between simulations and experimental data set j :

$$E_j(\mathbf{k}) = \sum_{i=1}^{\mathcal{T}_j} \left(\hat{M}_{ij} - \hat{y}_{ij}(\mathbf{k}) \right)^2 + \left(\frac{\mathcal{M}'_{ij} - \max y_{ij}}{\mathcal{M}'_{ij}} \right)^2 \quad (12)$$

421 The terms \hat{M}_{ij} and \hat{y}_{ij} denote scaled experimental observations and simulation outputs
422 at time i from training set j , where \mathcal{T}_j denoted the number of time points for data set j .
423 The first term in Eqn. (12) quantified the relative simulation error. We used immunoblot
424 intensity measurements for model training. Thus, we trained the model on the *relative*

425 change between bands within each data set. Suppose we have the intensity of species x
426 at time $\{t_1, t_2, \dots, t_n\}$ in condition j . The scaled value $0 \leq \hat{\mathcal{M}}_{ij} \leq 1$ is given by:

$$\hat{\mathcal{M}}_{ij} = (\mathcal{M}_{ij} - \min_i \mathcal{M}_{ij}) / (\max_i \mathcal{M}_{ij} - \min_i \mathcal{M}_{ij}) \quad (13)$$

427 where $\hat{\mathcal{M}}_{ij} = 0$ and $\hat{\mathcal{M}}_{ij} = 1$ describe the lowest (highest) intensity bands. A similar
428 scaling was used for the simulation output. The second term in the objective function
429 ensured a realistic concentration scale was estimated by the model. We set the highest
430 intensity band to $\mathcal{M}'_{ij} = 10$ [AU] for all simulations. We minimized the total model residual
431 $\sum_j E_j$ using heuristic optimization starting from a random initial parameter guess.

432 The signaling and gene expression model equations were implemented in the Julia
433 programming language, and solved using the CVODE routine of the Sundials package (45,
434 46). The model code and parameter ensemble is freely available under an MIT software
435 license and can be downloaded from <http://www.varnerlab.org>.

436 *Cell culture and treatment* Human myeloblastic leukemia cells (HL-60 cells) were grown
437 in a humidified atmosphere of 5% CO₂ at 37°C and maintained in RPMI 1640 from Gibco
438 (Carlsbad, CA) supplemented with 5% heat inactivated fetal bovine serum from Hyclone
439 (Logan, UT) and 1× antibiotic/antimicotic (Gibco, Carlsbad, CA). Cells were cultured in
440 constant exponential growth (47). Experimental cultures were initiated at 0.1×10^6 cells/mL
441 24 hr prior to ATRA treatment; if indicated, cells were also treated with GW5074 (2 μ M) 18
442 hr before ATRA treatment. For the cell culture washout experiments, cells were treated
443 with ATRA for 24 hr, washed 3x with prewarmed serum supplemented culture medium
444 to remove ATRA, and reseeded in ATRA-free media as described. Western blot analysis
445 was performed at incremental time points after removal of ATRA.

446 *Chemicals* All-Trans Retinoic Acid (ATRA) from Sigma-Aldrich (St. Louis, MO) was dis-
447 solved in 100% ethanol with a stock concentration of 5mM, and used at a final concen-

448 tration of $1\mu\text{M}$ (unless otherwise noted). The cRaf inhibitor GW5074 from Sigma-Aldrich
449 (St. Louis, MO) was dissolved in DMSO with a stock concentration of 10mM , and used
450 at a final concentration of $2\mu\text{M}$. HL-60 cells were treated with $2\mu\text{M}$ GW5074 with or with-
451 out ATRA ($1\mu\text{M}$) at 0 hr. This GW5074 dosage had a negligible effect on the cell cycle
452 distribution, compared to ATRA treatment alone.

453 *Immunoprecipitation and western blotting* Approximately 1.2×10^7 cells were lysed using
454 $400\mu\text{L}$ of M-Per lysis buffer from Thermo Scientific (Waltham, MA). Lysates were cleared
455 by centrifugation at $16,950 \times g$ in a micro-centrifuge for 20 min at 4°C . Lysates were
456 pre-cleared using $100\mu\text{L}$ protein A/G Plus agarose beads from Santa Cruz Biotechnology
457 (Santa Cruz, CA) by inverting overnight at 4°C . Beads were cleared by centrifugation and
458 total protein concentration was determined by a BCA assay (Thermo Scientific, Waltham,
459 MA). Immunoprecipitations were setup by bringing lysate to a concentration of 1g/L in a
460 total volume of $300\mu\text{L}$ (M-Per buffer was used for dilution). The anti-Raf antibody was
461 added at $3\mu\text{L}$. A negative control with no bait protein was also used to exclude the di-
462 rect interaction of proteins with the A/G beads. After 1 hr of inversion at 4°C , $20\mu\text{L}$ of
463 agarose beads was added and samples were left to invert overnight at 4°C . Samples
464 were then washed three times with M-Per buffer by centrifugation. Finally proteins were
465 eluted from agarose beads using a laemmli loading buffer. Eluted proteins were resolved
466 by SDS-PAGE and Western blotting. Total lysate samples were normalized by total protein
467 concentration ($20\mu\text{g}$ per sample) and resolved by SDS-PAGE and Western blotting. Sec-
468 ondary HRP bound antibody was used for visualization. All antibodies were purchased
469 from Cell Signaling (Boston, MA) with the exception of α -p621 Raf which was purchased
470 from Biosource/Invitrogen (Carlsbad, CA), and α -CK2 from BD Biosciences (San Jose,
471 CA).

472 *Morphology assessment* Untreated and ATRA-treated HL-60 cells were collected after
473 72 hr and cytocentrifuged for 3 min at 700 rpm onto glass slides. Slides were air-dried

⁴⁷⁴ and stained with Wright's stain. Slide images were captured at 40X (Leica DM LB 100T
⁴⁷⁵ microscope, Leica Microsystems).

⁴⁷⁶ **Competing interests**

⁴⁷⁷ The authors declare that they have no competing interests.

⁴⁷⁸ **Author's contributions**

⁴⁷⁹ J.V and A.Y directed the study. R.T, H.J and J.C conducted the cell culture measurements. J.V and W.D developed the reduced order HL-60 models and the parameter ensemble. W.D analyzed the model ensemble, and generated figures for the manuscript.

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494 **References**

- 495 1. Bushue N, Wan YJY (2010) Retinoid pathway and cancer therapeutics. *Adv Drug*
496 *Deliv Rev* 62: 1285-98.
- 497 2. Tang XH, Gudas LJ (2011) Retinoids, retinoic acid receptors, and cancer. *Annu Rev*
498 *Pathol* 6: 345-64.
- 499 3. Cheung FSG, Lovicu FJ, Reichardt JKV (2012) Current progress in using vitamin d
500 and its analogs for cancer prevention and treatment. *Expert Rev Anticancer Ther* 12:
501 811-37.
- 502 4. Nilsson B (1984) Probable in vivo induction of differentiation by retinoic acid of
503 promyelocytes in acute promyelocytic leukaemia. *Br J Haematol* 57: 365-71.
- 504 5. Warrell RP Jr (1993) Retinoid resistance in acute promyelocytic leukemia: new mech-
505 anisms, strategies, and implications. *Blood* 82: 1949-53.
- 506 6. Freemantle SJ, Spinella MJ, Dmitrovsky E (2003) Retinoids in cancer therapy and
507 chemoprevention: promise meets resistance. *Oncogene* 22: 7305-15.
- 508 7. Breitman TR, Selonick SE, Collins SJ (1980) Induction of differentiation of the human
509 promyelocytic leukemia cell line (HL-60) by retinoic acid. *Proc Natl Acad Sci U S A*
510 77: 2936–2940.
- 511 8. Yen A, Roberson MS, Varvayanis S, Lee AT (1998) Retinoic acid induced
512 mitogen-activated protein (MAP)/extracellular signal-regulated kinase (ERK) kinase-
513 dependent MAP kinase activation needed to elicit HL-60 cell differentiation and
514 growth arrest. *Cancer Res* 58: 3163–3172.
- 515 9. Hong HY, Varvayanis S, Yen A (2001) Retinoic acid causes MEK-dependent RAF
516 phosphorylation through RARalpha plus RXR activation in HL-60 cells. *Differentiation*
517 68: 55–66.
- 518 10. Mangelsdorf DJ, Ong ES, Dyck JA, Evans RM (1990) Nuclear receptor that identifies
519 a novel retinoic acid response pathway. *Nature* 345: 224–229.

- 520 11. Congleton J, MacDonald R, Yen A (2012) Src inhibitors, PP2 and dasatinib, increase
521 retinoic acid-induced association of Lyn and c-Raf (S259) and enhance MAPK-
522 dependent differentiation of myeloid leukemia cells. Leukemia 26: 1180-8.
- 523 12. Shen M, Bunaci R, Congleton J, Jensen H, Sayam L, et al. (2011) Interferon regula-
524 tory factor-1 binds c-Cbl, enhances mitogen activated protein kinase signaling and
525 promotes retinoic acid-induced differentiation of HL-60 human myelo-monoblastic
526 leukemia cells. Leuk Lymphoma 52: 2372-9.
- 527 13. Shen M, Yen A (2009) c-Cbl tyrosine kinase-binding domain mutant G306E abolishes
528 the interaction of c-Cbl with CD38 and fails to promote retinoic acid-induced cell dif-
529 ferentiation and G0 arrest. J Biol Chem 284: 25664–25677.
- 530 14. Yen A, Varvayanis S, Smith J, Lamkin T (2006) Retinoic acid induces expression of
531 SLP-76: expression with c-FMS enhances ERK activation and retinoic acid-induced
532 differentiation/G0 arrest of HL-60 cells. Eur J Cell Biol 85: 117–132.
- 533 15. Marchisio M, Bertagnolo V, Colamussi ML, Capitani S, Neri LM (1998) Phosphatidyli-
534 nositol 3-kinase in HL-60 nuclei is bound to the nuclear matrix and increases during
535 granulocytic differentiation. Biochem Biophys Res Commun 253: 346-51.
- 536 16. Congleton J, Jiang H, Malavasi F, Lin H, Yen A (2011) ATRA-induced HL-60 myeloid
537 leukemia cell differentiation depends on the CD38 cytosolic tail needed for membrane
538 localization, but CD38 enzymatic activity is unnecessary. Exp Cell Res 317: 910–
539 919.
- 540 17. Wang J, Yen A (2004) A novel retinoic acid-responsive element regulates retinoic acid
541 induced BLR1 expression. Mol Cell Biol 24: 2423 - 2443.
- 542 18. Yen A (1990) HL-60 cells as a model of growth and differentiation: the significance of
543 variant cells. Hematology Review 4: 5-46.
- 544 19. Yang T, Xiong Q, Enslen H, Davis R, Chow CW (2002) Phosphorylation of NFATc4 by
545 p38 mitogen-activated protein kinases. Mol Cell Biol 22: 3892–3904.

- 546 20. Wang J, Yen A (2008) A MAPK-positive Feedback Mechanism for BLR1 Signaling
547 Propels Retinoic Acid-triggered Differentiation and Cell Cycle Arrest. *J Biol Chem*
548 283: 4375–4386.
- 549 21. Tasseff R, Nayak S, Song S, Yen A, Varner J (2011) Modeling and analysis of retinoic
550 acid induced differentiation of uncommitted precursor cells. *Integr Biol* 3: 578 - 591.
- 551 22. Milo R, Jorgensen P, Moran U, Weber G, Springer M (2010) Bionumbers—the
552 database of key numbers in molecular and cell biology. *Nucleic Acids Res* 38: D750-
553 3.
- 554 23. Katagiri K, Hattori S, Nakamura S, Yamamoto T, Yoshida T, et al. (1994) Activation
555 of ras and formation of gap complex during tpa-induced monocytic differentiation of
556 hl-60 cells. *Blood* 84: 1780–1789.
- 557 24. Miranda MB, Johnson DE (2007) Signal transduction pathways that contribute to
558 myeloid differentiation. *Leukemia* 21: 1363–1377.
- 559 25. Hickstein DD, Back AL, Collins SJ (1989) Regulation of expression of the cd11b and
560 cd18 subunits of the neutrophil adherence receptor during human myeloid differenti-
561 ation. *J Biol Chem* 264: 21812–21817.
- 562 26. Hornstein I, Alcover A, Katzav S (2004) Vav proteins, masters of the world of cy-
563 toskeleton organization. *Cell Signal* 16: 1-11.
- 564 27. Song JS, Gomez J, Stancato LF, Rivera J (1996) Association of a p95 vav-containing
565 signaling complex with the fcepsilonlonri gamma chain in the rbl-2h3 mast cell line. ev-
566 idence for a constitutive in vivo association of vav with grb2, raf-1, and erk2 in an
567 active complex. *J Biol Chem* 271: 26962–26970.
- 568 28. Costello PS, Walters AE, Mee PJ, Turner M, Reynolds LF, et al. (1999) The rho-family
569 gtp exchange factor vav is a critical transducer of t cell receptor signals to the calcium,
570 erk, and nf-kappab pathways. *Proc Natl Acad Sci U S A* 96: 3035–3040.
- 571 29. Graham D, Robertson C, Bautista J, Mascarenhas F, Diacovo M, et al. (2007)

- 572 Neutrophil-mediated oxidative burst and host defense are controlled by a Vav-
573 PLCgamma2 signaling axis in mice. *J Clin Invest* 117: 3445–3452.
- 574 30. Cleghon V, Morrison DK (1994) Raf-1 interacts with fyn and src in a non-
575 phosphotyrosine-dependent manner. *J Biol Chem* 269: 17749–17755.
- 576 31. Zimmermann S, Moelling K (1999) Phosphorylation and regulation of raf by akt (pro-
577 tein kinase b). *Science* 286: 1741–1744.
- 578 32. Ritt DA, Zhou M, Conrads TP, Veenstra TD, Copeland TD, et al. (2007) Ck2 is a
579 component of the ksr1 scaffold complex that contributes to raf kinase activation. *Curr*
580 *Biol* 17: 179–184.
- 581 33. Hekman M, Wiese S, Metz R, Albert S, Troppmair J, et al. (2004) Dynamic changes in
582 c-raf phosphorylation and 14-3-3 protein binding in response to growth factor stimula-
583 tion: differential roles of 14-3-3 protein binding sites. *J Biol Chem* 279: 14074–14086.
- 584 34. Dhillon AS, Yip YY, Grindlay GJ, Pakay JL, Dangers M, et al. (2009) The c-terminus
585 of raf-1 acts as a 14-3-3-dependent activation switch. *Cell Signal* 21: 1645–1651.
- 586 35. Kim HS, Lim IK (2009) Phosphorylated extracellular signal-regulated protein kinases
587 1 and 2 phosphorylate sp1 on serine 59 and regulate cellular senescence via tran-
588 scription of p21sdi1/cip1/waf1. *J Biol Chem* 284: 15475–15486.
- 589 36. Milanini-Mongiat J, Pouyss?gur J, Pag?as G (2002) Identification of two sp1 phospho-
590 rylation sites for p42/p44 mitogen-activated protein kinases: their implication in vas-
591 cular endothelial growth factor gene transcription. *J Biol Chem* 277: 20631–20639.
- 592 37. Zhang Y, Cho YY, Petersen BL, Zhu F, Dong Z (2004) Evidence of stat1 phospho-
593 lation modulated by mapks, mek1 and msk1. *Carcinogenesis* 25: 1165–1175.
- 594 38. Li Z, Theus MH, Wei L (2006) Role of erk 1/2 signaling in neuronal differentiation of
595 cultured embryonic stem cells. *Dev Growth Differ* 48: 513–523.
- 596 39. Yen A, Reece SL, Albright KL (1984) Dependence of hl-60 myeloid cell differentiation
597 on continuous and split retinoic acid exposures: precommitment memory associated

- 598 with altered nuclear structure. *J Cell Physiol* 118: 277–286.
- 599 40. Ferrell J (2002) Self-perpetuating states in signal transduction: positive feedback,
600 double-negative feedback and bistability. *Curr Opin Cell Biol* 14: 140-8.
- 601 41. Xiong W, Ferrell J (2003) A positive-feedback-based bistable 'memory module' that
602 governs a cell fate decision. *Nature* 426: 460-5.
- 603 42. Bagci EZ, Vodovotz Y, Billiar TR, Ermentrout GB, Bahar I (2006) Bistability in apop-
604 tosis: roles of bax, bcl-2, and mitochondrial permeability transition pores. *Biophys J*
605 90: 1546-59.
- 606 43. Luan D, Zai M, Varner JD (2007) Computationally derived points of fragility of a human
607 cascade are consistent with current therapeutic strategies. *PLoS Comput Biol* 3:
608 e142.
- 609 44. Wayman JA, Sagar A, Varner JD (2015) Dynamic modeling of cell-free biochemical
610 networks using effective kinetic models. *Processes* 3: 138.
- 611 45. Bezanson J, Edelman A, Karpinski S, Shah VB (2014) Julia: A fresh approach to
612 numerical computing. *CoRR* abs/1411.1607.
- 613 46. Hindmarsh A, Brown P, Grant K, Lee S, Serban R, et al. (2005) Sundials: Suite of non-
614 linear and differential/algebraic equation solvers. *ACM Transactions on Mathematical
615 Software* 31: 363-396.
- 616 47. Brooks SC, Kazmer S, Levin AA, Yen A (1996) Myeloid differentiation and retinoblas-
617 toma phosphorylation changes in HL-60 cells induced by retinoic acid receptor- and
618 retinoid X receptor-selective retinoic acid analogs. *Blood* 87: 227–237.
- 619 48. Rishi AK, Gerald TM, Shao ZM, Li XS, Baumann RG, et al. (1996) Regulation of the
620 human retinoic acid receptor alpha gene in the estrogen receptor negative human
621 breast carcinoma cell lines skbr-3 and mda-mb-435. *Cancer Res* 56: 5246-52.
- 622 49. Mueller BU, Pabst T, Fos J, Petkovic V, Fey MF, et al. (2006) Atra resolves the differ-
623 entiation block in t(15;17) acute myeloid leukemia by restoring pu.1 expression. *Blood*

- 624 107: 3330-8.
- 625 50. Friedman AD (2007) Transcriptional control of granulocyte and monocyte develop-
626 ment. *Oncogene* 26: 6816-28.
- 627 51. Luo XM, Ross AC (2006) Retinoic acid exerts dual regulatory actions on the expres-
628 sion and nuclear localization of interferon regulatory factor-1. *Exp Biol Med (May-
629 wood)* 231: 619-31.
- 630 52. Sylvester I, Schöler HR (1994) Regulation of the oct-4 gene by nuclear receptors.
631 *Nucleic Acids Res* 22: 901-11.
- 632 53. Drach J, McQueen T, Engel H, Andreeff M, Robertson KA, et al. (1994) Retinoic acid-
633 induced expression of cd38 antigen in myeloid cells is mediated through retinoic acid
634 receptor-alpha. *Cancer Res* 54: 1746-52.
- 635 54. Liu M, Iavarone A, Freedman LP (1996) Transcriptional activation of the human
636 p21(waf1/cip1) gene by retinoic acid receptor. correlation with retinoid induction of
637 u937 cell differentiation. *J Biol Chem* 271: 31723-8.
- 638 55. Bunaciu RP, Yen A (2013) 6-formylindolo (3,2-b)carbazole (ficz) enhances retinoic
639 acid (ra)-induced differentiation of hl-60 myeloblastic leukemia cells. *Mol Cancer* 12:
640 39.
- 641 56. Balmer JE, Blomhoff R (2002) Gene expression regulation by retinoic acid. *J Lipid
642 Res* 43: 1773-808.
- 643 57. Rosen ED, Hsu CH, Wang X, Sakai S, Freeman MW, et al. (2002) C/ebpalpha induces
644 adipogenesis through ppargamma: a unified pathway. *Genes Dev* 16: 22-6.
- 645 58. Varley CL, Bacon EJ, Holder JC, Southgate J (2009) Foxa1 and irf-1 intermediary
646 transcriptional regulators of ppargamma-induced urothelial cytodifferentiation. *Cell
647 Death Differ* 16: 103-14.
- 648 59. Bruemmer D, Yin F, Liu J, Berger JP, Sakai T, et al. (2003) Regulation of the growth
649 arrest and dna damage-inducible gene 45 (gadd45) by peroxisome proliferator-

- activated receptor gamma in vascular smooth muscle cells. Circ Res 93: e38-47.
- 650
651 60. Delerive P, De Bosscher K, Besnard S, Vanden Berghe W, Peters JM, et al. (1999)
652 Peroxisome proliferator-activated receptor alpha negatively regulates the vascular in-
653 flammatory gene response by negative cross-talk with transcription factors nf-kappab
654 and ap-1. J Biol Chem 274: 32048-54.
- 655 61. Altioik S, Xu M, Spiegelman BM (1997) Ppargamma induces cell cycle withdrawal:
656 inhibition of e2f/dp dna-binding activity via down-regulation of pp2a. Genes Dev 11:
657 1987-98.
- 658 62. Fei J, Cook C, Gillespie M, Yu B, Fullen K, et al. (2011) Atherogenic ω -6 lipids modu-
659 late ppar- egr-1 crosstalk in vascular cells. PPAR Res 2011: 753917.
- 660 63. Song EK, Lee YR, Kim YR, Yeom JH, Yoo CH, et al. (2012) Naadp mediates insulin-
661 stimulated glucose uptake and insulin sensitization by ppar γ in adipocytes. Cell Rep
662 2: 1607-19.
- 663 64. Szanto A, Nagy L (2005) Retinoids potentiate peroxisome proliferator-activated re-
664 ceptor gamma action in differentiation, gene expression, and lipid metabolic pro-
665 cesses in developing myeloid cells. Mol Pharmacol 67: 1935-43.
- 666 65. Han S, Sidell N, Fisher PB, Roman J (2004) Up-regulation of p21 gene expression
667 by peroxisome proliferator-activated receptor gamma in human lung carcinoma cells.
668 Clin Cancer Res 10: 1911-9.
- 669 66. Von Knethen A, Brüne B (2002) Activation of peroxisome proliferator-activated recep-
670 tor gamma by nitric oxide in monocytes/macrophages down-regulates p47phox and
671 attenuates the respiratory burst. J Immunol 169: 2619-26.
- 672 67. Dispirito JR, Fang B, Wang F, Lazar MA (2013) Pruning of the adipocyte peroxisome
673 proliferator-activated receptor γ cistrome by hematopoietic master regulator pu.1. Mol
674 Cell Biol 33: 3354-64.
- 675 68. Chen H, Ray-Gallet D, Zhang P, Hetherington CJ, Gonzalez DA, et al. (1995) Pu.1

- 676 (spi-1) autoregulates its expression in myeloid cells. *Oncogene* 11: 1549-60.
- 677 69. Steidl U, Rosenbauer F, Verhaak RGW, Gu X, Ebralidze A, et al. (2006) Essential role
678 of jun family transcription factors in pu.1 knockdown-induced leukemic stem cells. *Nat*
679 *Genet* 38: 1269-77.
- 680 70. Laslo P, Spooner CJ, Warmflash A, Lancki DW, Lee HJ, et al. (2006) Multilineage
681 transcriptional priming and determination of alternate hematopoietic cell fates. *Cell*
682 126: 755-66.
- 683 71. Pahl HL, Scheibe RJ, Zhang DE, Chen HM, Galson DL, et al. (1993) The proto-
684 oncogene pu.1 regulates expression of the myeloid-specific cd11b promoter. *J Biol*
685 *Chem* 268: 5014-20.
- 686 72. Yuki H, Ueno S, Tatetsu H, Niiro H, Iino T, et al. (2013) Pu.1 is a potent tumor sup-
687 pressor in classical hodgkin lymphoma cells. *Blood* 121: 962-70.
- 688 73. Li SL, Schlegel W, Valente AJ, Clark RA (1999) Critical flanking sequences of pu.1
689 binding sites in myeloid-specific promoters. *J Biol Chem* 274: 32453-60.
- 690 74. Dahl R, Walsh JC, Lancki D, Laslo P, Iyer SR, et al. (2003) Regulation of macrophage
691 and neutrophil cell fates by the pu.1:c/ebpalpha ratio and granulocyte colony-
692 stimulating factor. *Nat Immunol* 4: 1029-36.
- 693 75. Timchenko N, Wilson DR, Taylor LR, Abdelsayed S, Wilde M, et al. (1995) Autoreg-
694 ulation of the human c/ebp alpha gene by stimulation of upstream stimulatory factor
695 binding. *Mol Cell Biol* 15: 1192-202.
- 696 76. Lidonnici MR, Audia A, Soliera AR, Prisco M, Ferrari-Amorotti G, et al. (2010) Expres-
697 sion of the transcriptional repressor gfi-1 is regulated by c/ebpalpha and is involved
698 in its proliferation and colony formation-inhibitory effects in p210bcr/abl-expressing
699 cells. *Cancer Res* 70: 7949-59.
- 700 77. D'Alo' F, Johansen LM, Nelson EA, Radomska HS, Evans EK, et al. (2003) The amino
701 terminal and e2f interaction domains are critical for c/ebp alpha-mediated induction

- 702 of granulopoietic development of hematopoietic cells. Blood 102: 3163-71.
- 703 78. Pan Z, Hetherington CJ, Zhang DE (1999) Ccaat/enhancer-binding protein activates
704 the cd14 promoter and mediates transforming growth factor beta signaling in mono-
705 cyte development. J Biol Chem 274: 23242-8.
- 706 79. Harris TE, Albrecht JH, Nakanishi M, Darlington GJ (2001) Ccaat/enhancer-binding
707 protein-alpha cooperates with p21 to inhibit cyclin-dependent kinase-2 activity and
708 induces growth arrest independent of dna binding. J Biol Chem 276: 29200-9.
- 709 80. Bauvois B, Durant L, Laboureau J, Barthélémy E, Rouillard D, et al. (1999) Upreg-
710 ulation of cd38 gene expression in leukemic b cells by interferon types i and ii. J
711 Interferon Cytokine Res 19: 1059-66.
- 712 81. Passioura T, Dolnikov A, Shen S, Symonds G (2005) N-ras-induced growth suppres-
713 sion of myeloid cells is mediated by irf-1. Cancer Res 65: 797-804.
- 714 82. Dahl R, Iyer SR, Owens KS, Cuylear DD, Simon MC (2007) The transcriptional re-
715 pressor gfi-1 antagonizes pu.1 activity through protein-protein interaction. J Biol
716 Chem 282: 6473-83.
- 717 83. Duan Z, Horwitz M (2003) Targets of the transcriptional repressor oncoprotein gfi-1.
718 Proc Natl Acad Sci U S A 100: 5932-7.
- 719 84. Chen H, Zhang P, Radomska HS, Hetherington CJ, Zhang DE, et al. (1996) Octamer
720 binding factors and their coactivator can activate the murine pu.1 (spi-1) promoter. J
721 Biol Chem 271: 15743-52.
- 722 85. Behre G, Whitmarsh AJ, Coghlan MP, Hoang T, Carpenter CL, et al. (1999) c-jun
723 is a jnk-independent coactivator of the pu.1 transcription factor. J Biol Chem 274:
724 4939-46.
- 725 86. Kardassis D, Papakosta P, Pardali K, Moustakas A (1999) c-jun transactivates the
726 promoter of the human p21(waf1/cip1) gene by acting as a superactivator of the ubiq-
727 uitous transcription factor sp1. J Biol Chem 274: 29572-81.

- 728 87. Johnson DG, Ohtani K, Nevins JR (1994) Autoregulatory control of e2f1 expression
729 in response to positive and negative regulators of cell cycle progression. *Genes Dev*
730 8: 1514-25.
- 731 88. Fu M, Zhang J, Lin Y, Zhu X, Ehrengruber MU, et al. (2002) Early growth response
732 factor-1 is a critical transcriptional mediator of peroxisome proliferator-activated
733 receptor-gamma 1 gene expression in human aortic smooth muscle cells. *J Biol
734 Chem* 277: 26808-14.
- 735 89. Mak KS, Funnell APW, Pearson RCM, Crossley M (2011) Pu.1 and haematopoietic
736 cell fate: Dosage matters. *Int J Cell Biol* 2011: 808524.
- 737 90. Chen F, Wang Q, Wang X, Studzinski GP (2004) Up-regulation of egr1 by 1,25-
738 dihydroxyvitamin d3 contributes to increased expression of p35 activator of cyclin-
739 dependent kinase 5 and consequent onset of the terminal phase of hl60 cell differen-
740 tiation. *Cancer Res* 64: 5425-33.
- 741 91. Suh J, Jeon YJ, Kim HM, Kang JS, Kaminski NE, et al. (2002) Aryl hydrocarbon
742 receptor-dependent inhibition of ap-1 activity by 2,3,7,8-tetrachlorodibenzo-p-dioxin
743 in activated b cells. *Toxicol Appl Pharmacol* 181: 116-23.
- 744 92. Shen M, Bunaciu RP, Congleton J, Jensen HA, Sayam LG, et al. (2011) Interferon
745 regulatory factor-1 binds c-cbl, enhances mitogen activated protein kinase signaling
746 and promotes retinoic acid-induced differentiation of hl-60 human myelo-monoblastic
747 leukemia cells. *Leuk Lymphoma* 52: 2372-9.
- 748 93. Bunaciu RP, Yen A (2011) Activation of the aryl hydrocarbon receptor ahr promotes
749 retinoic acid-induced differentiation of myeloblastic leukemia cells by restricting ex-
750 pression of the stem cell transcription factor oct4. *Cancer Res* 71: 2371-80.
- 751 94. Jensen HA, Yourish HB, Bunaciu RP, Varner JD, Yen A (2015) Induced myelomono-
752 cytic differentiation in leukemia cells is accompanied by noncanonical transcription
753 factor expression. *FEBS Open Bio* 5: 789-800.

754

Table 1: Myelomonocytic transcription factor connectivity used in the signal integration and phenotype modules.

755

Actor	Effect	Target	Cite
RAR α	+	RAR α	(48)
	+	PU.1	(49)
	+	C/EBP α	(50)
	+	IRF-1	(51)
	-	Oct4	(52)
	+	CD38	(53)
	+	p21	(54)
	+	AhR	(55)
	+	EGR1	(56)
PPAR γ	+	C/EBP α	(57)
	+	IRF-1	(58)
	+	Oct1	(59)
	-	AP-1	(60)
	-	E2F	(61)
	-	EGR1	(62)
	+	CD38	(63)
	+	CD14	(64)
	+	p21	(65)
	-	p47phox	(66)
PU.1	-	PPAR γ	(67)
	+	PU.1	(68)
	+	AP-1	(69)
	+	EGR1	(70)
	+	CD11b	(71)
	+	p21	(72)
	+	p47phox	(73)
C/EBP α	+	PPAR γ	(57)
	+	PU.1	(74)
	+	C/EBP α	(75)
	+	Gfi-1	(76)
	-	E2F	(77)
	+	CD14	(78)
	+	p21	(79)
IRF-1	+	CD38	(80)
	+	p21	(81)
	-	PU.1	(82)
	-	C/EBP α	(83)
	-	E2F	(83)
	-	EGR1	(70)
	-	p21	(83)
Oct1	+	PU.1	(84)

AP-1	-	PPAR γ	(60)
	+	PU.1	(85)
	+	p21	(86)
E2F	+	E2F	(87)
EGR1	+	PPAR γ	(88)
	-	Gfi-1	(89)
	+	CD14	(90)
AhR	+	AP-1	(91)
	+	IRF-1	(92)
	-	Oct4	(93)
	-	PU.1	

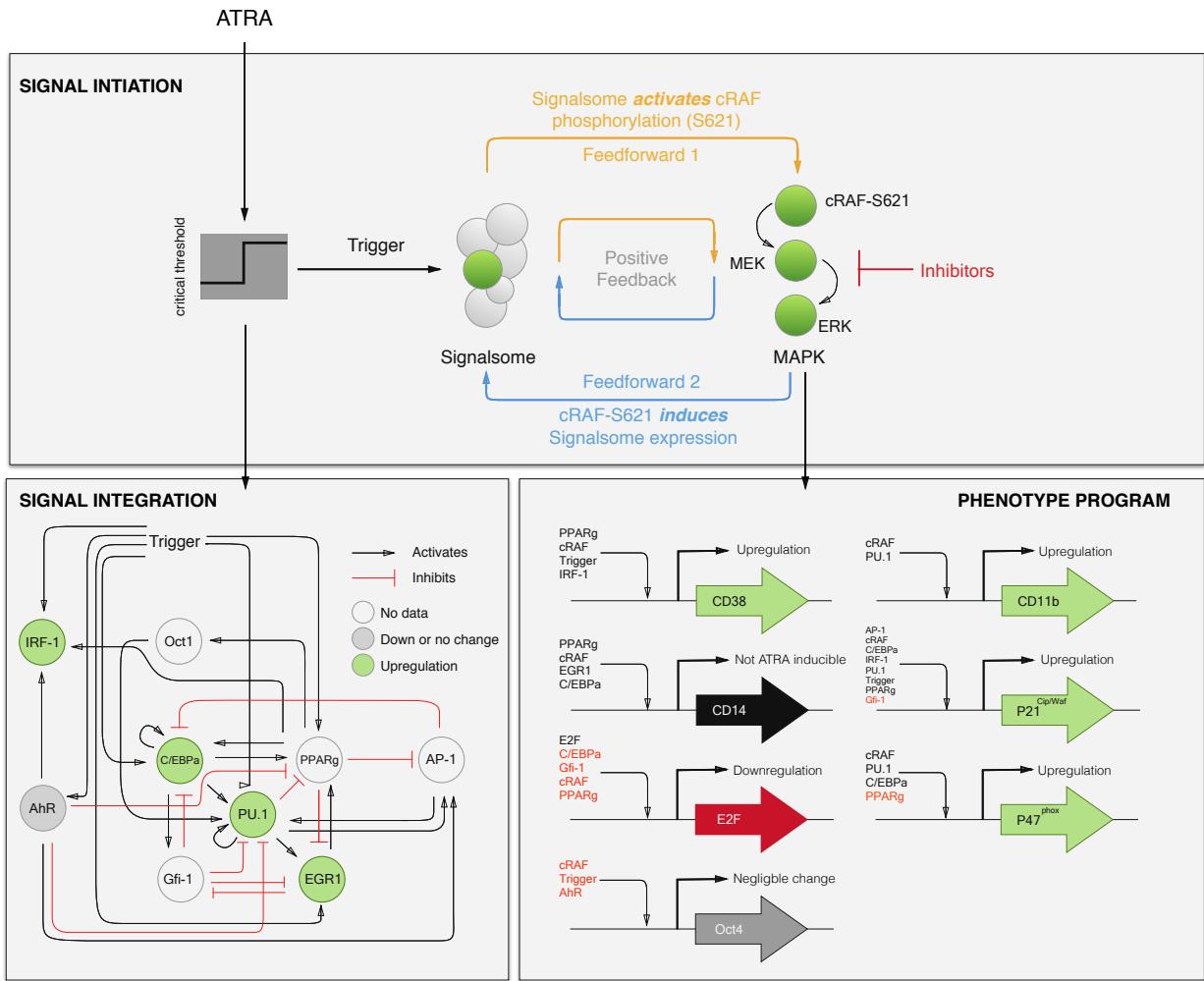


Fig. 1: Schematic of the effective ATRA differentiation circuit. Above a critical threshold, ATRA activates an upstream Trigger, which induces signalsome complex formation. Signalsome activates the mitogen-activated protein kinase (MAPK) cascade which in turn drives the differentiation program and signalsome formation. Both Trigger and activated cRaf-pS621 drive a phenotype gene expression program responsible for differentiation. Trigger activates the expression of a series of transcription factors which in combination with cRaf-pS621 result in phenotypic change.

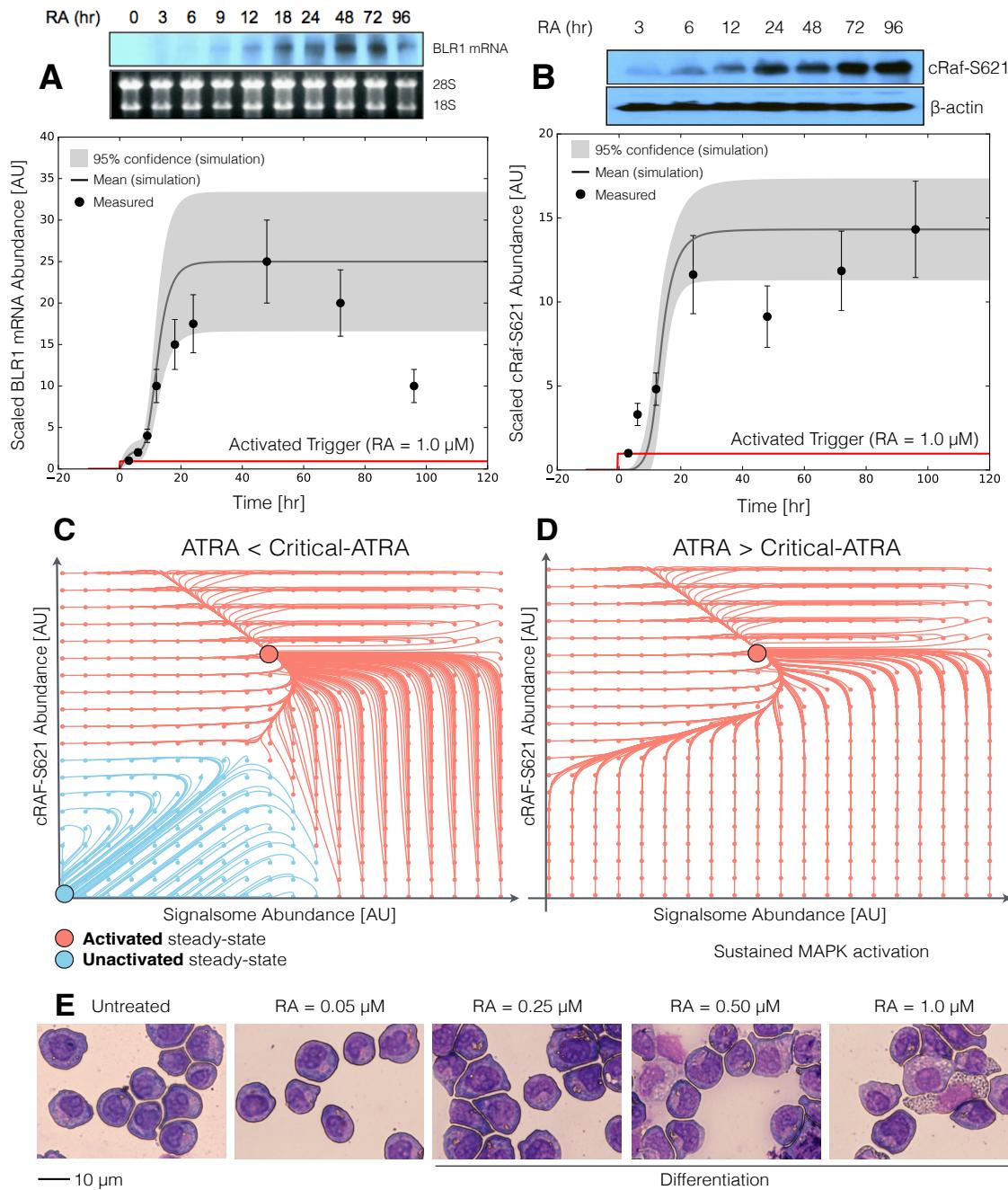


Fig. 2: Model analysis for ATRA-induced HL-60 differentiation. A: BLR1 mRNA versus time following exposure to 1 μ M ATRA at t = 0 hr. B: cRaf-pS621 versus time following exposure to 1 μ M ATRA at t = 0 hr. Points denote experimental measurements, solid lines denote the mean model performance. Shaded regions denote the 99% confidence interval calculated over the parameter ensemble. C: Signalsome and cRaf-pS621 nullclines for ATRA below the critical threshold. The model had two stable steady states and a single unstable state in this regime. D: Signalsome and cRaf-pS621 nullclines for ATRA above the critical threshold. In this regime the model had only a single stable steady state. E: Morphology of HL-60 as a function of ATRA concentration (t = 72 hr).

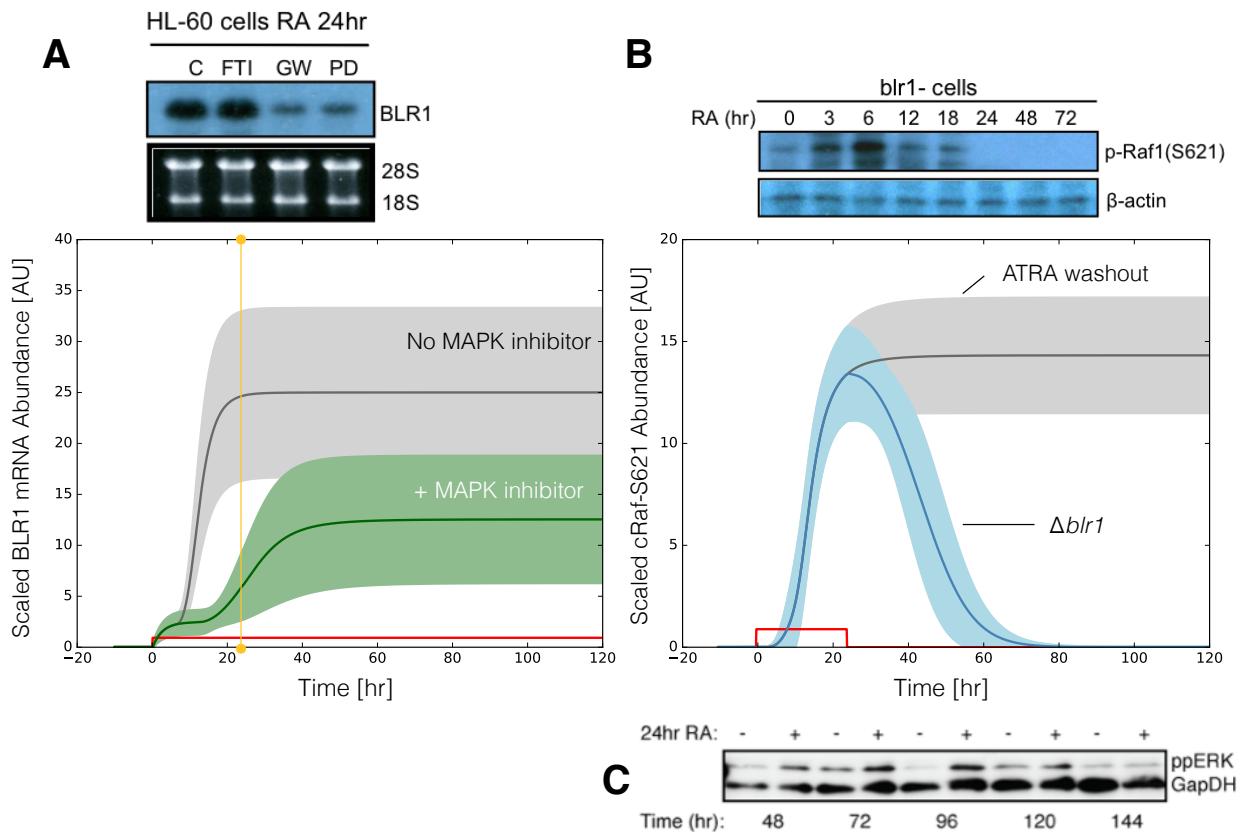


Fig. 3: Model simulation following exposure to $1\mu\text{M}$ ATRA. A: BLR1 mRNA versus time with and without MAPK inhibitor. B: cRaf-pS621 versus time following pulsed exposure to $1\mu\text{M}$ ATRA with and without BLR1. Solid lines denote the mean model performance, while shaded regions denote the 99% confidence interval calculated over the parameter ensemble. C: Western blot analysis of phosphorylated ERK1/2 in ATRA washout experiments. Experimental data in panels A and B were reproduced from Wang and Yen (20), data in panel C is reported in this study.

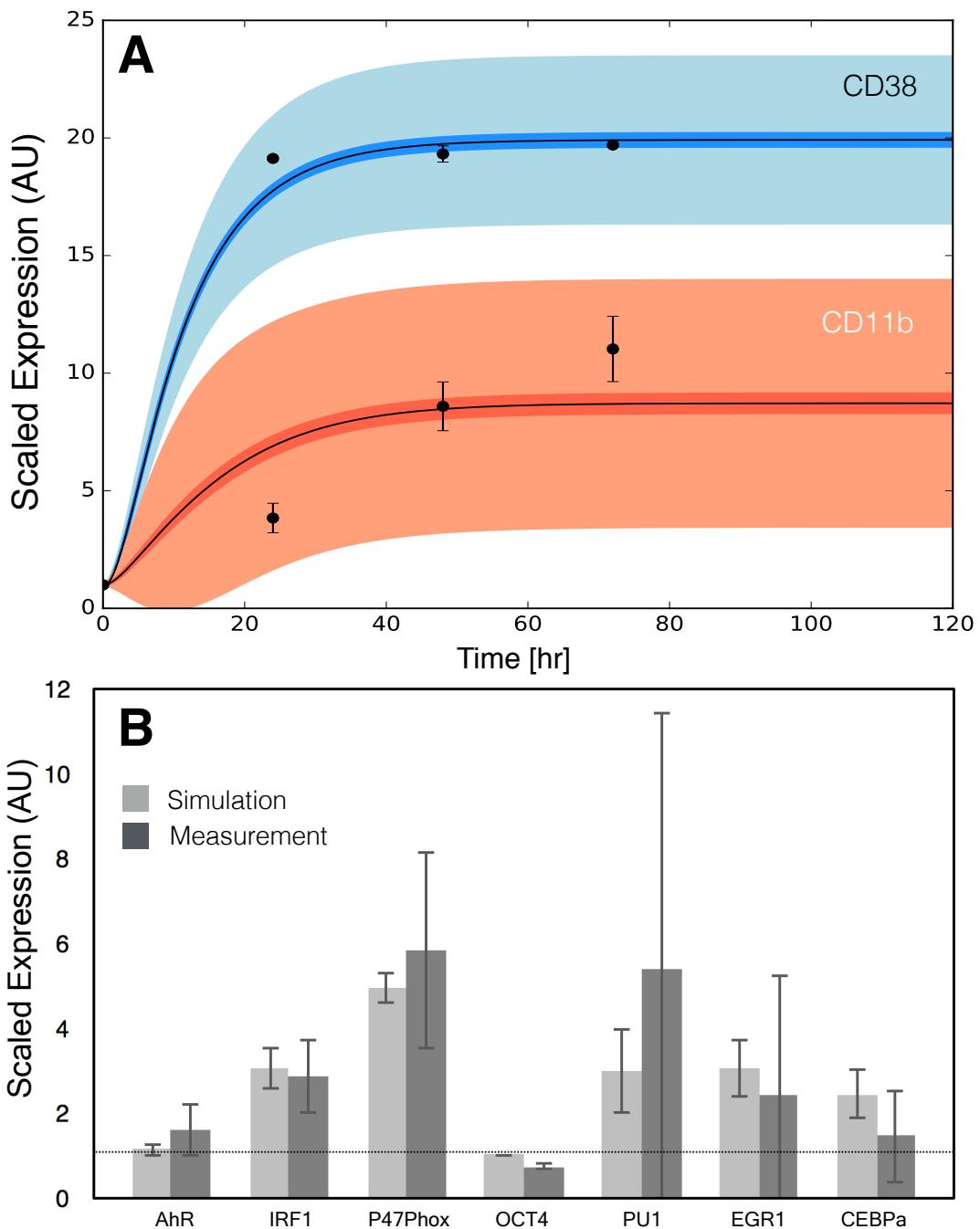


Fig. 4: Model simulation of the HL-60 gene expression program following exposure to $1\mu\text{M}$ ATRA at $t = 0$ hr. A: CD38 and CD11b expression versus time following ATRA exposure at time $t = 0$ hr. B: Gene expression at $t = 48$ hr following ATRA exposure. Experimental data in panels A and B were reproduced from Jensen et al. (94).

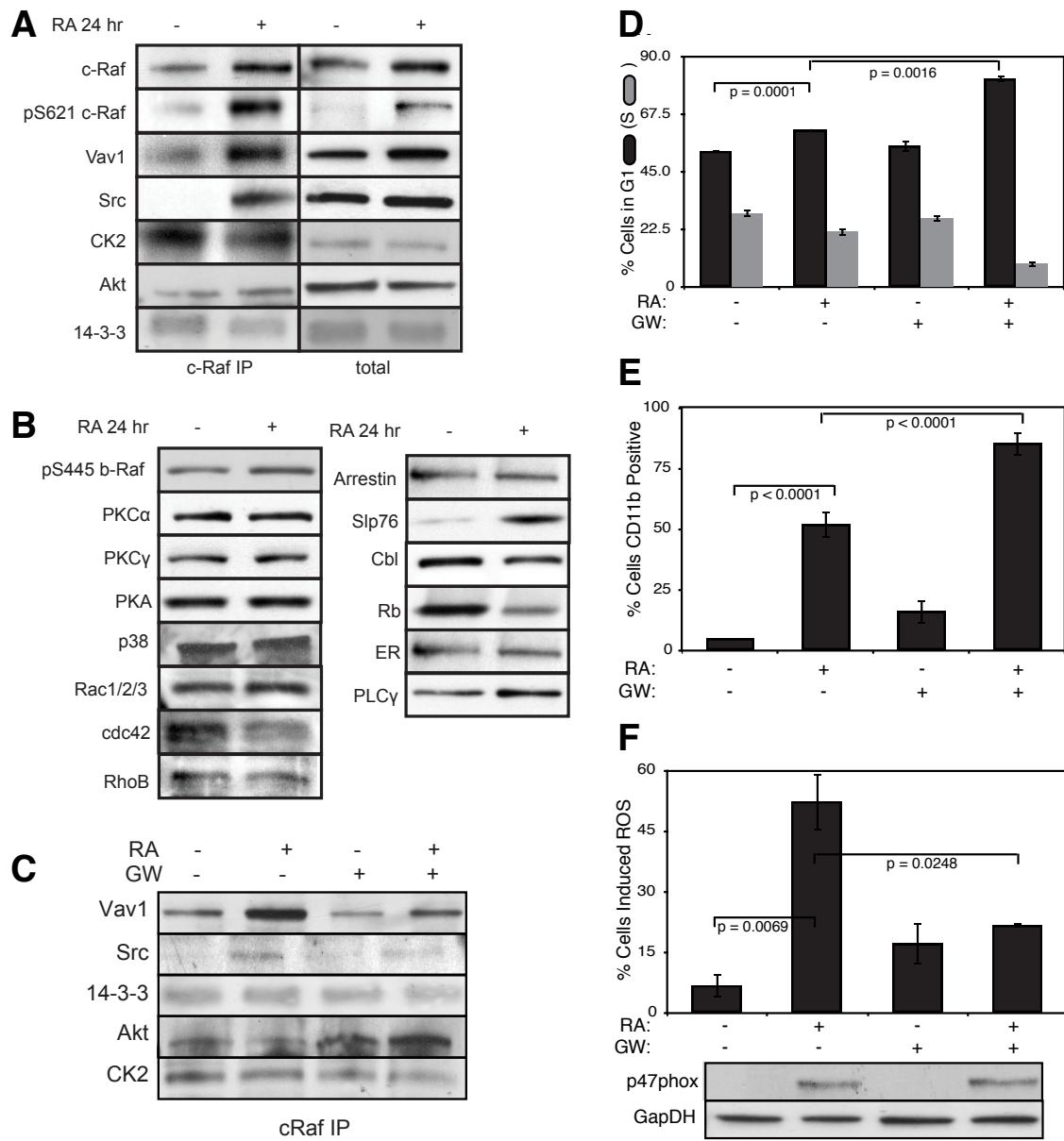


Fig. 5: Investigation of a panel of possible Raf interaction partners in the presence and absence of ATRA. A: Species identified to precipitate out with Raf: first column shows Western blot analysis on total Raf immunoprecipitation with and without 24 hr ATRA treatment and the second on total lysate. B: The expression of species considered that did not precipitate out with Raf at levels detectable by Western blot analysis on total lysate. C: Effect of the Raf inhibitor GW5074 on Raf interactions as determined by Western blot analysis of total Raf immunoprecipitation. The Authors note the signal associated with Src was found to be weak. D: Cell Cycle distribution as determined by flow cytometry indicated arrest induced by ATRA, which was increased by the addition of GW5074. E: Expression of the cell surface marker CD11b as determined by flow cytometry indicated increased expression induced by ATRA, which was enhanced by the addition of GW5074. F: Inducible reactive oxygen species (ROS) as determined by DCF flow cytometry. The functional differentiation response of ATRA treated cells was mitigated by GW5074.