Target Genes and their Regulators

# WT

SMP1

* Regulators: CIN5, FHL1, PHD1, & SMP1
  + Significant p-values: PHD1 (0.001676)
  + Insignificant: CIN5 (0.064), FHL1 (0.4454), & SMP1 (0.6046)
* Dynamics
  + Slightly negative; its degradation/dilution rate must be less than its production value
  + PHD1 represses SMP1 🡪 this result makes sense due to its significant p-value compared to its co-regulators which had insignificant p-value results
  + Would not expect to see great dynamical change if solely CIN5 and FHL1 regulated this gene, so the fact that the dynamics are small agrees with assumptions

MSS11

* Regulators: CIN5, SKN7, & SKO1
  + Significant: SKN7 (0.0228)
  + Insignificant: CIN5 (0.064) & SKO1 (0.133)
* Dynamics
  + Negative dynamics that change see initial decrease after T0
  + It’s degradation rate must be greater than its production rate
  + All regulators appear to be activators (SKN7 and CIN5 appear to be significant in the GRNSight’s visualized network)

YAP6

* Regulators: CIN5, FHL1, FKH2, PHD1, SKN7, SKO1, YAP6
  + Significant: PHD1 (0.00168), SKN7 (0.0228), YAP6 (0.00026)
  + Insignificant: CIN5 (0.064), FHL1 (0.4454), FKH2 (0.127), SKO1 (0.133)
* Dynamics
  + Negative and the dynamics are great/near 1
  + Degradation must be greater than its production rate
  + It possesses two of everything – two grey, two cyan, and two magenta – in the visualized network
  + It represses itself and receives repression cues from FKH2, while CIN5 and SKN7 activate it
    - YAP6 and SKN7 both have significant p-values while the other two colored lines do not

PHD1

* Regulators: CIN5, FHL1, PHD1, SKN7, SKO1, SWI4, SWI6
  + Significant: PHD1 (0.00168), SKN7 (0.0228)
  + Insignificant: CIN5 (0.064), FHL1 (0.4454), SKO1 (0.133), SWI4 (0.637), & SWI6 (0.467)
* Dynamics
  + Up-regulation that sees a decrease toward T60
    - Slight concave down
  + Probably receives dynamics from self-regulation and SKN7 while the other insignificant regulators contribute minimal dynamics…?
  + Highly regulated with 7 TFs looking over it 🡪 suggests that due to that regulation, dynamics may be smaller over a course of time

CIN5

* Regulators: CIN5, PHD1, SKO1, YAP6
  + Significant: PHD1 (0.00168), SKN7 (0.0228)
  + Insignificant: CIN5 (0.064), SKO1 (0.133)
* Dynamics
  + Greatly positive and increasing at a steady rate
  + Odd because it receives repression cues from all these genes except itself (activates)
    - Production rate must be far greater than its degradation rate
  + Significance could influence the data greatly, but it appears that its self-regulation has an influence on the dynamics, not just p-value

HOT1

* Regulators: CIN5 & SKN7
  + Significant: SKN7 (0.0228)
  + Insignificant: CIN5 (0.064)
* Dynamics
  + Slight negative degrease, appears linear
  + Both are repressor
  + Appears that CIN5 may have more influence insofar as the little variance/change in dynamics until reaching T60…

HMO1

* Regulators: FHL1 (0.4454), insignificant
* Dynamics
  + Greatly positive/increasing 🡪 odd because its regulator doesn’t have significance, but the gene’s expression does (0.0409)
  + Makes sense when looking at visualized network 🡪 calls for activation/up-regulation

FKH2

* Regulators: FHL1 & FKH2
  + Significant: None
  + Insignificant: FHL1 (0.4454) & FKH2 (0.127)
* Dynamics
  + Great initial negative dynamics and end at ~1
  + Degradation rate must be greater than its production rate
    - Represses itself while FHL1 activates it
  + Shouldn’t see any major dynamics for wt

ACE2

* Regulators: ZAP1 & FKH2
  + Significant: ZAP1 (0.0086)
  + Insignificant: FKH2 (0.127)
* Dynamics
  + No dynamics whatsoever 🡪 yay!
    - Doesn’t account for ZAP1’s influence on the gene however
  + See activation from both, but with ZAP1 being significant, you’d expect more positive dynamics

MGA2

* Regulators: GLN3 & SMP1
  + Significant: None
  + Insignificant: GLN3 (0.412) & SMP1 (0.605)
* Dynamics
  + Increases at a steady initial rate, why when the p-values are insignificant?
  + Even this gene’s B&H p-value is insignificant so what gives?
    - Receives activation cues from GLN3 in the visualized network (magenta) but grey repression cues

GLN3

* Regulators: GLN3 & MAL33
  + Significant: MAL33 (0.0101)
  + Insignificant: GLN3 (0.412)
* Dynamics
  + Odd because of the initial dip, but then its dynamics appear to increase only slightly
  + Only moves maybe a quarter of one (1/4… don’t know why I said it that way?)
  + Represses itself (initial dip…?) and then MAL33 wins over with its activating cues

MAL33

* Regulators: MBP1 & SKO1
  + Significant: None
  + Insignificant: MBP1 (0.524) & SKO1 (0.127)
* Dynamics
  + Greatly increasing within the first 15 minutes…
  + The gene’s p-value is 0.0101
  + Receives activation cues from SKo1 and repression cues from MBP1 although both are insignificant as defined by their p-values

SWI4

* Regulators: MBP1, MAL33, SWI6, SWI4, PHD1, YAP6
  + Significant: MAL33 (0.0101), PHD1 (0.00168), & YAP6 (0.00026)
  + Insignificant: MBP1 (0.524), SWI4 (0.637), & SWI6 (0.118)
* Dynamics
  + Slight negative, ends around the 0.5 point for gene expression
  + Degradation rate must be greater than the production rate
    - It also receives repression cues from pretty much every single regulator regardless of significance
  + Its dynamics appear linear

MBP1

* Regulators: MBP1 (0.524), insignificant
* Dynamics
  + Dynamics are increasing and reach 0.5 expression levels
  + It’s also odd because it represses itself, but it has positive dynamics
    - Degradation rate is lower than production rate

Overall Conclusions

p-value of controllers, from what I’ve seen, do not specifically allow one to have a better understanding of what the results could be

* Most genes do not have one, lone regulator such that even knowing the p-value’s significance would not identify which regulator had the most influence on the gene

# dCIN5

SMP1

* Regulators: CIN5, FHL1, SMP1, PHD1
  + Significant: None
  + Insignificant: CIN5 (0.921), FHL1 (0.963), SMP1 (0.053), PHD1 (0.464)
* Dynamics
  + Slightly negative, but the pattern resembles that of positive auto-regulation
  + The fit is poor, especially at T15 and T60
  + End point appears around 0.25/0.30
  + Degradation rate higher than its production rate

MSS11

* Regulators: CIN5, SKO1, SKN7
  + Significant: SKN7 (0.018)
  + Insignificant: CIN5 (0.921) & SKO1 (0.201)
* Dynamics
  + Very small dynamics; almost negligible/expression level at 0
  + Fits the data well

YAP6

* Regulators: CIN5, FHL1, FKH2, PHD1, SKN7, SKO1, YAP6
  + Significant: SKN7 (0.018)
  + Insignificant: CIN5 (0.921), FHL1 (0.962), FKH2 (0.0570), PHD1 (0.464), SKO1 (0.201), & YAP6 (0.072)
* Dynamics
  + Slight and negative, reaching around -0.2
  + Fit is decent and reaches the average points
  + Degradation must be slightly greater than its production rate

PHD1

* Regulators: CIN5, FHL1, PHD1, SKN7, SKO1, SWI4, SWI6
  + Significant: SKN7 (0.018)
  + Insignificant: CIN5 (0.921), FHL1 (0.962), PHD1 (0.464), SKO1 (0.201), SWI4 (0.437), & SWI6 (0.634)
* Dynamics
  + Slightly negative and the data points wide
  + Fit: decent, but not great 🡪 could be due to wide range of data points collected

CIN5

* Regulators: CIN5, PHD1, SKO1, YAP6
  + Significant: None
  + Insignificant: CIN5 (0.921), PHD1 (0.464), SKO1 (0.201), YAP6 (0.072)
* Dynamics
  + Deletion strain; therefore, no dynamics
  + Regulators do not seem to matter

HOT1

* Regulators: CIN5 & SKN7
  + Significant: SKN7 (0.018)
  + Insignificant: CIN5 (0.921)
* Dynamics
  + Slightly negative dynamics; doesn’t change much
  + Fit is poor for T15, but the other two seem to be fine
  + Deletion of CIN5 may have an impact on the dynamics 🡪 not as repressed as before

HMO1

* Regulators: FHL1 (0.921), insignificant
* Dynamics
  + Significant changes/dynamics in HMO1
  + Greatly up-regulated
  + Data points are wide, and the fit is not the best for T15 or T60

FKH2

* Regulators: FHL1 & FKH2
  + Significant: None
  + Insignificant: FHL1 (0.963) & FKH2 (0.0570)
* Dynamics
  + Negative and closer to 1
  + Dynamics are the same as those for wt 🡪 makes sense, not connected to dCIN5
  + Fit: poor for these values and data points are not too wide/varied

ACE2

* Regulators: ZAP1 & FKH2
  + Significant: None
  + Insignificant: ZAP1 (0.281) & FKH2 (0.0570)
* Dynamics
  + Initial decrease before heading back up to original expression level (relatively 0)
  + Tight data points for 15 and 60 🡪 makes fit better
  + Seems to be affected by deletion of CIN5 🡪 altered from wt graph

MGA2

* Regulators: GLN3 & SMP1
  + Significant: None
  + Insignificant: GLN3 (0.547) & SMP1 (0.057)
* Dynamics
  + Dynamics are slightly up-regulated with tight data points at 15 & 30
  + Affected by the deletion of CIN5 🡪 dynamics are not as high as wt
  + Fit is pretty good overall; goes along with the data points

GLN3

* Regulators: GLN3 & MAL33
  + Significant: None
  + Insignificant: GLN3 (0.546) & MAL33 (0.770)
* Dynamics
  + Dynamics are slightly increasing, but reach a steady state pretty quickly
  + Data points are tight for T30, but wider for 15 and 60
  + Different from wt in that there isn’t an initial deep 🡪 affected dCIN5

SWI4

* Regulators: MBP1, MAL33, SWI6, SWI4, PHD1, YAP6
  + Significant: None
  + Insignificant: MBP1 (0.938), MAL33 (0.770), SWI6 (0.635), SWI4 (0.437), PHD1 (0.464), & YAP6 (0.072)
* Dynamics
  + Clearly affected by deletion of CIN5
    - Instead of down-regulation, we see steady up regulation
  + Up-regulation slight and ends up around 0.5
  + None of the regulators are significant 🡪 shouldn’t see much dynamics, but we do…

MBP1

* Regulators: MBP1 (0.524), insignificant
* Dynamics
  + Slightly positive/up-regulation
  + Data points are not as widespread as wt, which had more of a curve than the dCIN5

SWI6

* No regulators
* Dynamics
  + Slightly increasing
  + Data points range; there are a few tight spots , but overall gaps within each time point
  + The fit is decent, but not the best
    - T30 and T15 could better 🡪 not close enough to the average

ZAP1

* Regulators: ZAP1 (0.281), insignificant
* Dynamics
  + Large up-regulation & seems to be insignificantly different than the wt dynamics
  + Data points are widespread with a poor fit for T15 & T60
    - T30 time point does not look great

# dGLN3

SMP1

* Regulators: CIN5, FHL1, PHD1, & SMP1
  + Significant: CIN5 (0.016)
  + Insignificant: FHL1 (0.677), PHD1 (0.156), & SMP1 (0.938)
* Dynamics
  + Slightly negative with poor fit at T60; data points are tight in general
  + Degradation must be greater than production rate 🡪 CIN5 also represses it

HMO1

* Regulators: FHL1 (0.677), insignificant
* Dynamics
  + Great dynamics 🡪 similar to the wt?
  + Fits the data well, especially at T30 & 60

PHD1

* Regulators: CIN5, FHL1, PHD1, SKN7, SKO1, SWI4, SWI6
  + Significant: CIN5 (0.016)
  + Insignificant: FHL1 (0.677), PHD1 (0.156), SKN7 (0.160), SKO1 (0.655), SWI4 (0.388), & SWI6 (0.456)
* Dynamics
  + Concave down/sees initial production before reaching its peak and decreasing its level of expression
  + Data points are evenly spaced for T30 and an outlier for T60
  + Fits the data decently; misses the average for T15 & T30

YAP6

* Regulators: CIN5, FHL1, FKH2, PHD1, SKN7, SKO1, YAP6
  + Significant: CIN5 (0.016) & YAP6 (0.029)
  + Insignificant: FHL1 (0.677), FKH2 (0.896), PHD1 (0.156), SKN7 (0.160), SKO1 (0.655), & SWI6 (0.456)
* Dynamics
  + Slight initial increase before it has negative dynamics
  + Data points are tight at T15 and T 60, but wide for T30 🡪 fit of the model is good for data points

FKH2

* Regulators: FHL1 & FKH2
  + Significant: None
  + Insignificant: FHL1 (0.677) & FKH2 (0.896)
* Dynamics
  + Negative dynamics with wide range of data points
  + Hits the average data point at 15; fits the data good enough to follow the trend
  + Degradation rate must be greater than production because it receives activation cues from both itself and FHL1

ACE2

* Regulators: ZAP1 & FKH2
  + Significant: None
  + Insignificant: ZAP1 (0.232) & FKH2 (0.896)
* Dynamics
  + See initial dip before slight up-regulation
  + Misses the mark completely at T15 and the data points are widespread for T30 such that it would be slightly more difficult to model
  + The fact that there are no significant regulators could indicate that the model has more freedoms in plotting what occurred at the various time points…?

MGA2 (regulated by GLN3)

* Regulators: GLN3 & SMP1
  + Significant: None
  + Insignificant: GLN3 (0.616) & SMP1 (0.938)
* Dynamics
  + Data points are closely knit
  + Fit: well in that it reaches somewhere in the midst of all the data points, but falls either slightly above or slightly below the average
  + There is slight up-regulation of the gene

GLN3 (self-regulated)

* Regulators: GLN3 & MAL33
  + Significant: MAL33 (0.015)
  + Insignificant: GLN3 (0.616)
* Dynamics
  + Nothing because it is the deletion strain

MAL33

* Regulators: MBP1 & SKO1
  + Significant: None
  + Insignificant: MBP1 (0.978) & SKO1 (0.655)
* Dynamics
  + Highly up-regulated before dipping slightly back down after its peak
  + Data points are spread out, specifically at T30 and 60
  + Model does not fit data for T15 and reaches too high for T30

SWI4

* Regulators: MBP1, MAL33, SWI6, SWI4, PHD1, YAP6
  + Significant: MAL33 (0.015) & YAP6 (0.029)
  + Insignificant: MBP1 (0.978), SWI6 (0.456), SWI4 (0.388), & PHD1 (0.156)
* Dynamics
  + Linearly negative
  + Data points are generally evenly spaced out amongst each other, but the model does not fit the average of them 🡪 probably modeling closer to the wt b/c GLN3 & SWI4 aren’t connected whatsoever

MBP1

* Regulators: MBP1 (0.978), insignificant
* Dynamics
  + Slightly increasing, but the data points are wide for T15 and evenly spaced for T60
    - Tight for 30
  + Misses the mark for T30 & 60 (slightly above average)

CIN5

* Regulators: CIN5, PHD1, SKO1, YAP6
  + Significant: CIN5 (0.016) & YAP6 (0.029)
  + Insignificant: PHD1 (0.156) & SKO1 (0.655)
* Dynamics
  + Dynamics are great, but it makes sense because it activates itself with activation cues from YAP6 too
  + Doesn’t fit the average for T60, but other time points are ok; a little above average for 15

AFT2

* Regulators: AFT2 & SKN7
  + Significant:
  + Insignificant: SKN7 (0.160)
* Dynamics
  + Initial up-regulation before down-regulation
  + Fit of the model is decent; not really the average for 15 or 30 but follows the trends seen

HOT1

* Regulators: CIN5 & SKN7
  + Significant: CIN5 (0.016)
  + Insignificant: SKN7 (0.160)
* Dynamics
  + Initial up-regulation before down-regulated greatly
  + Does not fit the data well whatsoever; above data points for T15, T30 and doesn’t fit T60

MSS11

* Regulators: CIN5, SKN7, SKO1
  + Significant: CIN5 (0.016)
  + Insignificant: SKN7 (0.160) & SKO1 (0.655)
* Dynamics
  + Appears stationary before slight up-regulation
  + Fits the average for all the points

SKN7

* Regulators: SKN7 (0.160), insignificant
* Dynamics
  + Crazy up regulation, but it doesn’t reach the T15 and doesn’t fall to the T60 time point (degradation rate isn’t great enough to bring it back down)
  + Fit is very poor though

ZAP1

* Regulators: ZAP1 (0.232), insignificant
* Dynamics
  + Linear negative dynamics, but the data points are widespread
  + Doesn’t fit the data well 🡪 T15 & T60 model line is above the average