*Referee comments are in italic.*

Our responses to the referees are in blue.

Changes made to the manuscript are in red.

We would first like to summarize our answers to two general points that were addressed from various aspects by all three reviewers. For consistency and easier reference, we are providing the combined changes here.

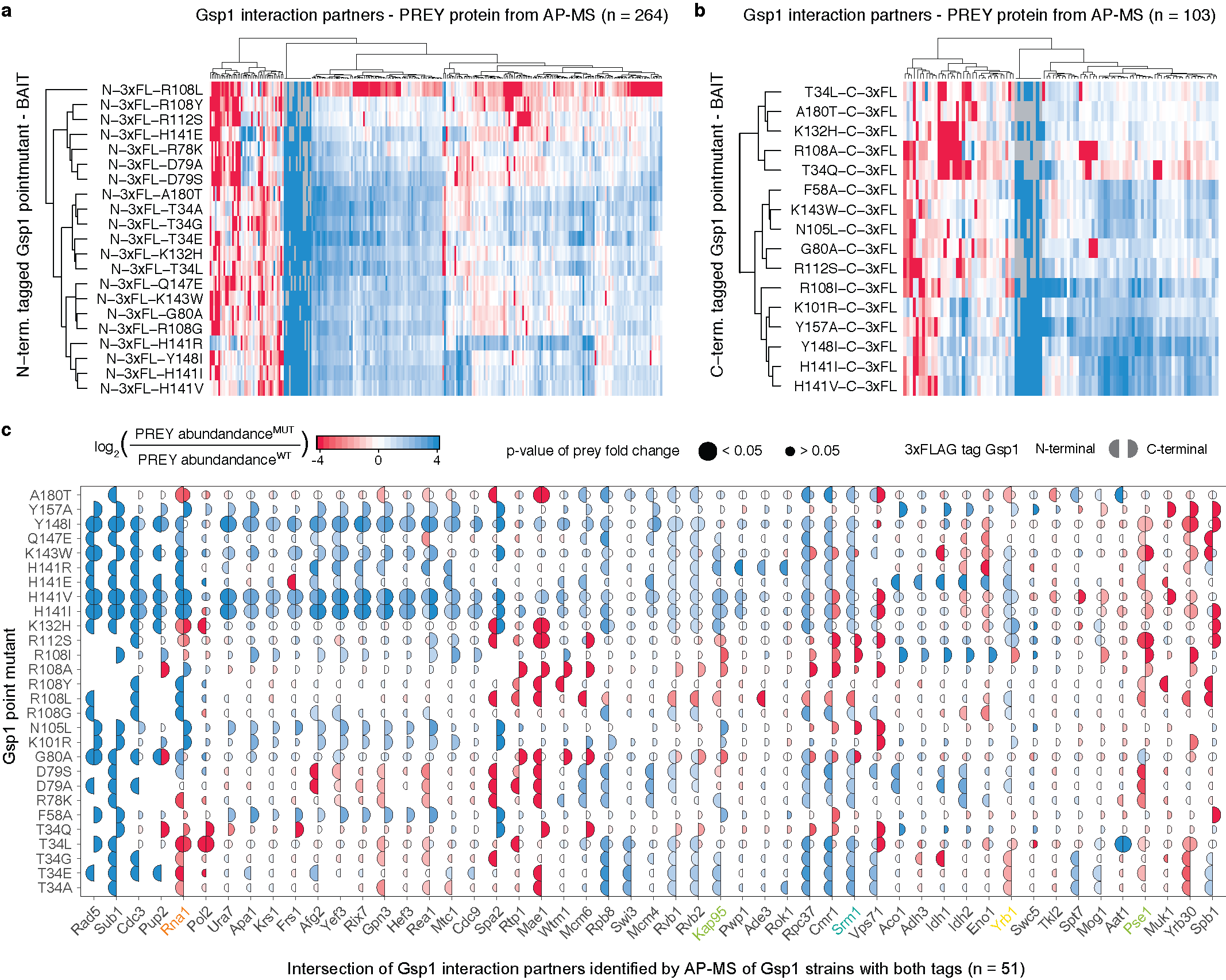
**POINT 1: Representation of the AP-MS data.** We reworked the figures and text referring to the rewiring of physical protein-protein interactions.:

The main text Figure 2, Extended Data Figures 4 and 5:

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**Figure 2 Gsp1 point mutations in the interfaces with protein partners globally rewire the interactions with the switch regulators GEF (Srm1) and GAP (Rna1).** **a**, Schematic representation of the AP-MS experimental design. The change in abundance partner pulled down with Gsp1 mutants is represented as log2-transformed fold change between abundance pulled-down with mutant versus with the wild-type Gsp1. **b**, Change in abundance of pulled-down physical interaction partners for which there are co-complex X-ray crystal structures (Rna1, Srm1, Yrb1, Kap95, Pse1, Srp1). On average, when the point mutation is in the core of the interface with the partner mean log2-transformed fold change of abundance is lower ( mean(log2FC) = -1), than when the mutation is not in the interface core with the pulled down partner (mean(log2FC) = 0.73), t-test p-value = 1.6x10-5. **c**, Change in abundance of pulled-down Rna1 (GAP) and Srm1 (GEF). There is significant change in abundance of pulled-down central regulators for most tested mutants, even when the mutations are not in the cores of GAP or GEF interfaces, for example for mutations at the Thr34 position. **d,** Threonine 34 is neither in the interface with the Rna1 (GAP, PDB id: 1k5d), nor the Srm1 (GEF, PDB id: 2i1m).



**Extended Data Figure 4 Interface point mutations in Gsp1 rewire its physical interaction network**. **a,** Amino- and **b,** -carboxy terminally 3xFLAG-tagged Gsp1 point mutants (rows) and prey proteins identified by AP-MS (columns) hierarchically clustered by the log2-transformed fold change in prey abundance pulled-down with either the mutant or wild-type Gsp1 with the corresponding 3xFLAG-tag (log2(abundance(PREY)MUT/abundance(PREY)WT)). **c**, Prey proteins pulled down by both amino- and carboxy-terminal tagged constructs. Left semi-circle represents an amino-terminal 3xFLAG-tagged Gsp1 point mutant, and right semi-circle represents carboxy-terminal 3xFLAG-tagged Gsp1 point mutant. Semi-circle size is proportional to the significance of the log2-transformedfold change (false discovery rate adjusted p-value) of the prey abundance in pulled-down complexes with a Gsp1 mutant compared to complexes with the wild-type Gsp1. Overall we identified 316 high-confidence prey partner proteins, with the amino- and carboxy-terminally tagged Gsp1 mutants pulling down 264 and 103 preys, respectively, including 51 overlapping preys. The difference in preys identified by experiments with N- or C-terminal tags illustrates the sensitivity of the interaction network to perturbation of Gsp1. To account for possible tag effects, we always computed the fold change in prey abundance only relative to the wild-type protein with the corresponding tag. In **a, b,** and **c,** decreased abundance compared to pull-down with wild-type Gsp1 is annotated in red and increased abundance in blue. The log2-transformed fold change values are capped at +/- 4.

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**Extended Data Figure 5 Gsp1 interface mutations rewire the protein-protein interactions with the partners of Gsp1 for which there are co-complex X-ray crystal structures (core regulators Srm1 and Rna1, and effectors Yrb1, Kap95, Pse1, and Srp1). a,** Changes in pulled-down prey partner abundance when the point mutation is in the core of the Gsp1 interface with the prey partner. **b,** Changes in pulled-down prey partner abundance for core regulators Srm1 and Rna1, and effectors Yrb1, Kap95, Pse1, and Srp1. Change in pulled-down prey partner abundance is expressed as log2(PREY abundanceMUT/PREY abundanceWT)). N-3xFL and C-3xFL labelled mutants are tagged with an amino- or carboxy-terminal triple FLAG tag, respectively. **c,** Distribution showing the variation in log2-transformed fold change in abundance of all prey proteins pulled down with the Gsp1 mutants, as defined by interquartile range (IQR) across mutants. Values for core partners shown as arrows (Rna1 orange, Srm1 teal, Yrb1 yellow, Kap95 green, Pse1 light green, Srp1 pink). Mean and +1 standard deviation of IQR values are highlighted with a dark gray and a light gray arrow, respectively. The extent to which the abundance of the two cycle regulators Rna1 and Srm1 changed across the Gsp1 point mutants was significantly larger than the change of an average prey protein. All IQR values are provided in **Supplementary File 1 Table 5.**

We have also rewritten the text in the main manuscript to match the simplified, more streamlined version of Fig. 2 and Extended Data Figures 4 and 5. The paragraph about the affinity purification mass spectrometry and protein-protein interaction rewiring now reads:

**Physical interactions of Gsp1 mutants.**

To investigate further why the GI profiles of Gsp1 mutations did not group based on targeted specific physical interactions of Gsp1, we sought to determine how the physical interaction network of Gsp1 changes in response to the interface point mutations. We tagged wild-type Gsp1 and 28 mutants covering all interface residues shown in **Fig. 1e** with an amino- or carboxy-terminal 3xFLAG tag and quantified the abundance of each of the ‘prey’ partner proteins in complex with Gsp1 by AP-MS (**Fig. 2a**, **Extended Data Fig. 4**, **Supplementary File 4**). We refer to the prey partner protein abundance in the pulled-down Gsp1 complexes simply as “abundance” below. In our AP-MS experiment, we could quantify the abundance changes of the core regulators Rna1 (GAP) and Srm1 (GEF), and effectors Yrb1, Kap95, Pse1 and Srp1. On average, when the Gsp1 mutation was in the interface core with the prey partner the abundance of the prey partner was decreased (**Fig. 2b, Extended Data Fig. 5a**). However, we can also see notable changes in abundance with the two core GTPase cycle regulators, GAP (Rna1) and GEF (Srm1) (**Fig. 2c**, **Extended Data Fig. 5**, **Supplementary File 1 Table 5**), even for the mutations that are outside either of the interfaces. For example mutations at the position 34, which is in the core of the interface with Yrb1, increase the levels of pulled-down GEF, and decrease the levels of pulled-down GAP, even though the residue is outside either of the interfaces (**Fig. 2c-d**). In summary, the AP-MS experiments confirm that the point mutations, in addition to targeted interactions also introduce extensive changes to the physical interaction network of Gsp1 that cannot simply be explained by the interface location of the mutations.

**POINT 2: Our general framework for building models of systems level function by combining functional genomics with mechanistic biochemical measurements.**

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NOTE FOR TANJA and CHRIS: Here, mainly for the editor, I want to have a general summary of our approach, from phenotype, and then choosing representative mutants, and doing follow up investigation that is following a path of discovery towards mechanistic details. Tanja said the editor liked that we present our work as a framework/platform to be followed. Maybe we can double down on this (I made a placeholder cartoon for this above – cartoon needs work!). That should address all the complaints from Reviewer 2 and 3 in one concise way. Even if those two schmucks don’t get it, the editor(s) might. Points to hit:

1. why it’s enough to do representative mutants, why we don’t have to measure all possible parameters of the GTPase cycle – because yes, they are broad strokes, but they explain a lot of the observed phenotype

2. our model is of how one switch can perform multiple cellular functions, not about predicting how individual point mutations in Gsp1 will affect the cell.

3. our null-hypothesis that we need to explicitly show can be discarded is that simply position in the interface can explain the phenotype:

a) analysis of functional genomics data shows that residue position in the interface does not explain the data

b) even though the “signal” is stronger when instead of functional interactions we only look at physical interactions, and the mutations on average perturb (positively of negatively) the interface directly, we can also see the global rewiring in physical interactions, and among all the physical interactions rewired – rewiring with the two core GTPase cycle regulators stands out (IQR plot quantifies that they stand out, all other data also shows it qualitatively)

CLEAN TEXT FOR THE EDITOR: Several of the comments by reviewers 2 and 3 can be summarized as questioning whether the completeness of our data limits our interpretations. We were surprised by these comments, but we hope that more explicit discussion of our research platform will help clarify our results and remove doubt.

We believe one of the main strengths of our work is the discovery approach we have taken, where we first quantified the effects of endogenously expressed mutations on the complex cellular phenotype, and then experimentally followed up groups of mutations with increasing resolution of mechanistic detail, to finally arrive to a simple set of biophysical parameters that explain the complex phenotype to a surprising extent.

From functional genomics experiments we saw that half of our mutants have rich phenotypes and half have very weak effects, comparable to wild type. Among the mutants with strong phenotype effects, we could see that they further group by their profile similarities with genes representing a handful of distinct cellular processes (gene sets from Supplementary File 5). But most importantly we saw that the simplest hypothesis, that position of the mutation in the interface could sufficiently explain the observed phenotype profiles, did not hold true.

We next sought to find the biophysical basis for the observed phenotype. As both AP-MS and kinetics experiments are extremely laborious and expensive, we selected mutants from each of the phenotype categories for further characterization: weak and strong, as well as from each of the phenotypic groups of strong mutants.

**Referee #1:**

*In their manuscript, Perica and colleagues describe a detailed system-wide genetic, cellular and biophysical analysis of a molecular switch protein in order to analyse the molecular mechanism by which these central regulators of signal transduction differentially affect multiple biological functions. To carry out this work the authors focused on the small GTPase Ran/Gsp1, which is a very good choice as its activity is modulated by one main GEF and one main GAP, but forms protein-protein interactions with many different binding partners. High resolution crystal structures for 16 of such complexes are available, which allowed the authors to carry out a detailed analysis of the protein interfaces involved and design 56 point mutations that would likely interfere with a given interaction, and allow analysis of their functional significance on the biological processes regulated by Gsp1.*

*Making use of the genetic power of yeast the authors carry out a careful genetic interaction screen of the mutations selected, followed by mapping the physical interactions of the mutants by AP-MS. The AP-MS experiments indicated that many mutations had significant effects on the interaction with GAP and GEF proteins, which prompted the authors to quantify the effect of the mutations on GAP-mediated GTP hydrolysis and GEF-mediated nucleotide exchange, followed by NMR analysis of the effect of mutations on the conformational behaviour of active site residues with respect to GTP status.*

*This is a well-executed, exciting and insightful study that makes a fundamental contribution to our understanding of protein interaction networks and how a single switch protein can independently regulate multiple cellular processes. A key, and unexpected finding, of this study is the observation that the GI profiles did not group according to their location on the Gsp1 surface and binding partner interfaces, and hence that functional specificity is not determined solely by interaction with a given binding partner. Instead, the data show that the kinetic parameters of the GTPase cycle of Gsp1 are allosterically regulated by distal interface mutations. This leads the authors to suggest that the effect of a mutation on a biological process depends on its sensitivity to different properties of the GTPase cycle. This is an appealing and novel concept that will attract a lot of attention. The discovery of novel allosteric sites in a GTPase is particularly interesting given the link of mutations to disease and efforts to target their activity therapeutically.*

We would like to thank Reviewer 1 on this summary of our work and on the shared enthusiasm for our results. We especially appreciate this approval knowing that Reviewer 1 is an expert in small GTPases.

*Specific points:*

*- Ext. Data Fig. 2*

*Some mutants show quite a lot of variation between replicates and differ up to 6-fold from WT. Is this really close to WT expression? How may this effect the genetic interaction profiles?*

There are indeed 2 outlier data points in our Western blot data that deviate 6-fold from the mean WT expression, but also from the other replicates for those mutants. One of the mutants with an outlier point is K154M, which shows a weak phenotype in E-MAP screens, meaning it does not show significant genetic interactions and we do not follow up on this mutant in other parts of this study. The second mutant with the outlier value is one of the strong mutants, R108G, however, for the other two replicates of R108G expression levels, expression is in the same range as the WT Gsp1.

We are convinced that these are deviations due to technical variations, but in the light of our efforts towards reproducibility and transparency of scientific research, we chose not to exclude any datapoints.

However, the reviewer does raise a valid point we should address in more detail in our manuscript. We added a third panel to the Extended Data Figure 2, where we now show more explicitly that the variation in expression levels is not predictive of the differences between the mutants with strong and weak phenotype profiles.

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**Extended Data Figure 2. Expression levels of endogenously expressed Gsp1 protein in *S. cerevisiae* strains with genomically integrated Gsp1 point mutations profiled by Western Blot.** Expression levels are relative to the expression levels of wild-type Gsp1 protein. **a,** Expression data for strong mutants, defined as mutants with more than nine significant GIs. **b,** Expression data for weak mutants, defined as mutants with fewer than nine significant GIs. Bar heights indicate averages over 2 or more biological replicates (n) with error bars indicating one standard deviation for n >= 3. Overlaid points indicate individual biological replicates (each an average over at least 12 technical replicates per biological replicate for wild-type and MAT-α strains, and between one and six technical replicates per biological replicate for mutant strains). Dashed red line indicates expression at the level of wild-type Gsp1 (fold change of 1). **c,** Distributions of relative expression changes for strong mutants and weak mutants, colored by biological replicate. All strains in a replicate were grown in parallel. Larger circles indicate mean relative change of all strong or all weak mutants from a given replicate.

Finally, we do observe up to 2-fold increase in expression levels of some of the strong mutants, and although we do not know how biologically significant this difference is, it might play a role in defining the complex cellular phenotype. We have modified a sentence (in red) in our Discussion section which now reads:

“Other effects such as direct perturbations of interactions, binding partner competition, and small changes in expression of Gsp1 or its partners undoubtedly also play a role in modulating the phenotype of our Gsp1 mutations. Nevertheless, our model explains to a remarkable degree how a single molecular switch motif can differentially control subsets of biological processes by using one of the three functional modes.”

*- The authors present an enormous amount of data in this manuscript, which has resulted in some of the figures being overloaded and difficult to follow. I understand that there are restrictions to the number of figures in the main text, and hence the authors have tried to include a lot of subpanels. However, this has resulted in some of the figures not being as easy to interpret as they should be. This is particularly relevant to the figures depicting protein structures. They are crucial to the manuscript as they visualise some of the key messages of this story. Hence the authors should rethink how to illustrate these points and at least add additional structure figures to Supplementary.*

*Examples:*

*- The structures shown in Fig. 1c are not sufficient to allow the reader to fully understand the special relationship of the different protein surfaces mutated and their importance in the interaction with binding partners. The authors should consider showing a surface representation in addition in which the different protein interfaces are highlighted, maybe coloured according to the number of times they have been detected in protein-protein interactions.*

We agree with the reviewer, readers, especially those that are not used to looking at structures of small GTPases might need much more visual guidance to grasp the features of Gsp1 interfaces and conformations. We have therefore replaced the Extended Data Fig. 1 panel a, and instead of simply showing all the RAN/Gsp1 complexes in the same orientation, we show the same representation of the GTPase in the GTP and GDP conformations as in the main text Fig. 1c, with the Cα atoms of mutated residues in sphere representation, coloured by the different interfaces. We have moved the panel with the complexes to the Supplementary File 1.

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Extended Data Figure 1 **Extended Data Figure 1 Design of interface point mutations in *S. cerevisiae* Gsp1.** **a-f,** Structures of Ran/Gsp1 in the GTP-bound (marine, PDB ID: 1ibr) and GDP-bound (gray, PDB ID: 3gj0) states. Mutated Gsp1 residues are shown as spheres. Interface residues are coloured by the type of partner protein: **a,** Srm1 (GEF) interface core (dark teal) and interface rim and support (light teal); **b,** Rna1 (GAP) interface core (dark orange) and interface rim and support (light orange); **c,** Ntf2 interface core (dark purple) and interface rim and support (light purple); **d,** Residues that are in both the core of the Yrb1 and Yrb2 interfaces (dark yellow), and in only one of the two interfaces (light yellow); **e,** Srp1 interface core (dark pink) and interface rim and support (light pink); f, Residues that are in the core of more than four (dark green), two to three (green) and one (light green) karyopherin interface. Karyopherins are: Kap95, Crm1, Los1, Kap104, Msn5, Cse1, Mtr10. **g,** Location of Gsp1 residues in partner interfaces. Interface positions (core, rim/support) were defined by the difference in relative surface accessible surface area (ΔrASA) between monomer and complex, as previously described{Levy, 2010, p00824} (**Supplementary File 1 Table 2**). Residues within 5 Å of the nucleotide, in the canonical P-loop, or in the switch I or II regions are indicated and were not mutated. Chosen Gsp1 point mutation substitutions are provided in **Supplementary File 1 Table 3**.

*- Similarly, the structures shown in Fig. 2d-f are not intuitive and don’t sufficiently convey the message. It may help to add figures with Gsp1 in a surface representation with the position of the different residues described indicated.*

We appreciate the comments from Reviewer 1 and 2, as they made it clear to us that the previous version of Fig. 2 did not convey the message we wanted to present to the reader. We have now completely reworked the Fig. 2 and adjusted the text. We think that the new, simplified version of Figure 2 presented in the beginning of this letter better presents the main points we aim to make with the AP-MS data.

*Minor points*

*- Suppl. Table 2 and Ext. Data Fig. 1:*

*Please provide the definition for rim and support.*

We have added the definition of the support, rim and core interface residues (described in Levy, JMB, 2012) to the Methods section: In brief, the three types of interface residues were defined as: SUPPORT residues have a ΔrASA > 0 & rASAmonomer < 25%, RIM residues have a ΔrASA > 0 & rASAcomplex > 25%, and CORE residues have ΔrASA > 0 & rASAm > 25% & rASAcomplex < 25%.

*- Page 46*

*The authors use the S. pombe homologue of the Gsp1 GAP Rna1 for their kinetic experiments as the S. cerevisiae homologue forms soluble aggregates. They should provide a brief comment on how they think this may (or may not) affect the kinetic parameters determined.*

We put in a significant effort in optimizing a purification protocol for the *S. cerevisiae* RNA1, but we were reluctant to perform kinetics measurements with an enzyme for which the effective concentration was so unclear. We ultimately chose to use the ortholog from *S. pombe* as that was the only RanGAP for which there is a structure in complex with (mammalian) Ran (PDB ids: 1k5d and 1k5g).

We have now added a sequence alignment between yeast, *S. pombe* and human GAP (Supplementary File 1 Fig. 14).

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**Supplementary Figure 2 Multiple sequence alignment between Rna1 from *S. cerevisiae* (Rna1\_yeast) and *S. pombe* (Rna1\_Schpo), as well as human RanGAP (RAGP1\_human).** Interface core residues (based on the X-ray crystal structure between Rna1\_Schpo and mammalian RAN, PDB ID: 1k5d) are highlighted in orange. All residues except Pro108 in Rna1\_Schpo, which corresponds to Leu122 in Rna\_yeast are conserved in sequence between *S. cerevisiae* and *S. pombe* Rna1.

We also added as supplementary discussion about using an orthogonal GAP to the Supplementary File 1 Supplementary Discussion section:

**Caveats about using the GAP (Rna1) from *S. pombe.***

All of our GAP-mediated GTP hydrolysis kinetics experiments were done using the wild type and mutant Gsp1 from *S. cerevisiae*, but Rna1 GAP from *S. pombe*. We chose to use the ortholog from *S. pombe* as the *S. cerevisiae* ortholog formed soluble aggregates and *S. pombe* Rna1 was the only RanGAP for which there was a structure in complex with Ran (PDB IDs: 1k5d and 1k5g).

As our GEF-mediated nucleotide exchange data are for a S. cerevisiae system, and our GAP-mediated GTP hydrolysis data are for a mixed orthogonal system there are three things to keep in mind when interpreting our results.

1.) **Sequence conservation between *S. cerevisiae* and *S. pombe* GAP.** Although we cannot know for sure which residues from *S. cerevisiae* Rna1 form the interface with *S. cerevisiae* Gsp1, based on a sequence alignment between S*. pombe* and *S. cerevisiae* Rna1 the residues that form the interface in the PDB ID file 1k5d structure are highly conserved. Overall sequence identity values can be seen in **Supplementary File 1 Table 1**.

A sequence alignment between *S. cerevisiae*, *S. pombe* and human GAP shows that all but one interface core residue is absolutely conserved in sequence (**Supplementary File 1 Supplementary Fig. 14**). Overall, out of the 1290 Å2 buried by *S. pombe* RNA1 upon interface formation with Gsp1 (PDB ID: 1k5d), 997 Å2 (77%)is buried by residues that are perfectly conserved in sequence between *S. pombe* and *S. cerevisiae*.

2.) **Comparable kinetic values to the human RAN/RANGAP1 pair.** The kinetic values for our *S. cerevisiae* Gsp1 and *S. pombe* Rna1 GAP are comparable to the kinetic values for the human RAN and human RAGP1 reported by Klebe *et al.*[1](#_ENREF_1). They estimate the Km of 0.45 μM and kcat of 2.1 s-1 at 25˚C, while our values for the wild type *S. cerevisiae* Gsp1 and *S. pombe* GAP at 30˚C are Km of 0.4 μM and kcat of 8.9 s-1.

3.) **Our conclusions are based on relative values between the wild-type Gsp1 and its point mutants.** Although we report the absolute values of the kinetics parameters, when we compare the kinetics parameters with the phenotype (from functional genomics or proteomics) we always use the relative parameters as compared to the wild type. And even though there could be epistasis between the sequence variation in Rna1 and the point mutations in Gsp1, we do not expect it to have a significant effect, as the GAP-mediated GTP hydrolysis rates corelate with the intrinsic GTP hydrolysis rates.

*Suppl. Tables 6-8*

*Please rearrange these tables such that the order of mutants listed is the same across all tables to make a comparison between them easier, ideally in ascending aa sequence.*

We agree with the reviewer about this suggestion. We originally ordered the mutants in these tables by the measured values, but relative ordering of the mutants by effects on the nucleotide exchange and hydrolysis is already clear from Fig. 3a-b, as well as Extended Data Figure 5. A reader would most likely used the Supplementary Data Tables for specific value lookup, for which an easy ordering of the mutants by residue number makes most sense. We have now changed the three tables accordingly.

*- Suppl. Figs 2 and 3*

*The authors should show plots for GAP-mediated GTP hydrolysis and GEF-mediated nucleotide exchange for all their mutants.*

STILL TO DO

*- Page 11, line 213:*

*Is anything known about PTMs modifying K101 in yeast? Are any proteomic data sets available that may allow the authors to comment on this?*

We would like to thank the reviewer, for, together with Reviewer 3 raising this point. We indeed did not do an appropriate job backing up our explanation of the K101R, an outlier that groups with GAP hydrolysis mutants, even though it clearly affects the GEF nucleotide exchange in our *in vitro* experiments*,* with appropriate citations. Although we cited the work showing the corresponding residue, K99, is acetylated in human RAN (Choudhary, C. *et al.*, 2009), as well as that the acetylation of human Ran at the K99 position (corresponding to position K101 in Gsp1) perturbs GEF-mediated nucleotide exchange of human RAN *in vitro* (de Boor, S. *et al,* 2015). We should have also cited more recent work by C. Choudhary and colleagues that shows K101 is also acetylated in *S. cerevisiae* (Henriksen et al, Mol Cell Proteomics, 2012).

The modified section in the main text now read (changed sentence in red):

A clear outlier of this ordering is the K101R mutant, which primarily affects GEF-mediated nucleotide exchange *in vitro* but, by GI profiles, groups with mutations affecting the efficiency of GTP hydrolysis. The lysine at this position was found to be acetylated in both *S. cerevisiae*(Henriksen, 2012) and human cells(Choudhary, 2009). The acetylation at this position in human RAN was shown to reduce the efficiency of nucleotide release from the RAN:GDP:GEF complex(de Boor, 2015). We hypothesize that while our K101R mutation affected the interaction with the GEF, it also likely broke a critical mechanism by which the cell reduces GEF activity, phenocopying the mutants with reduced GTP hydrolysis activity. This observation suggests the possibility that the allosteric sites discovered here might be used to control cellular functions *via* posttranslational modifications.

REFERENCES

Choudhary, C. *et al.* Lysine acetylation targets protein complexes and co-regulates major cellular functions. *Science* **325,** 834–840 (2009).

de Boor, S. *et al.* Small GTP-binding protein Ran is regulated by posttranslational lysine acetylation. *Proceedings of the National Academy of Sciences* **112,** E3679–88 (2015).

Henriksen, P. *et al.* Proteome-wide Analysis of Lysine Acetylation Suggests its Broad Regulatory Scope in Saccharomyces cerevisiae. *Mol. Cell Proteomics* **11,** 1510–1522 (2012).

*Referee #2:*

*This manuscript by Kortemme, Krogan and coworkers addresses a very interesting question of how molecular switches regulate multiple processes. The authors use mutations as molecular perturbations to the input and output pathways of the switch and integrate systems level approaches with molecular and biophysical methods to tackle this problem. The conclusions are also exciting in that the switch cycle properties seem to tune the sensitivity of biological processes to this particular switch. Overall, the manuscript is written clearly and the authors have made a commendable effort to catalogue the methodology underlying the numerous methods they have used.*

*However, I have a number of major and minor reservations listed below that need to be addressed before the manuscript can be considered for publication.*

*Major questions:*

*1) The main conclusion from this work is a model for Gsp1 function, where different biological processes are sensitive to different aspects of the switching cycle, either cycling, GTP hydrolysis or nucleotide exchange (GDP to GTP). The authors ended up with this model starting with mutations to perturb various Gsp1-protein interaction interfaces. The power of this model is that it can now predict which processes will be affected if various parts of the cycle are tickled. However, this model has not been validated. The authors must now go the reverse direction, rationally design mutations to perturb the three aspects of the switch (cycling, activation and nucleotide exchange) and demonstrate that the model can successfully predict the effects of these mutations on downstream biological processes. Without this validation step, the predictive power of the model remains unclear and the manuscript remains one-sided.*

While we think that the reviewer raises an interesting point, we would like to use this opportunity to discuss more precisely what exactly we mean when we use the word “model” in our manuscript.

We would like to clarify that based on our results we propose a model by which a single switch can regulate multiple cellular processes.

Furthermore, one of the additional important points of our work is that due to the widespread allostery in small GTPases, we cannot rationally design mutations that will differentially perturb the two sides of the GTPase cycle, leading to a specific ratio of the two parameters and, in turn specific functional consequences, with notable success. We thus, as is important to emphasize, **do not** propose that we can model the effects of point mutations in Gsp1 on cellular phenotype.

Any attempt to do what the reviewer suggests, would necessarily lead to designing a range of new mutants, some of which will indeed behave as predicted, but many would either have weak effects on the phenotype, and many more would have (additional) unpredicted allosteric effects. To reach that distinction, we would need to test both the kinetics parameters of those mutants *in vitro*, as well as measure their effects on the phenotype by performing E-MAP screens. This would ultimately lead to the same manuscript we have now, just with more mutants tested.

While it is of course hard to argue against more data that would support our findings, as indeed, more data always lead to increased confidence in a conclusion, we want to emphasize here that our study is already unprecedented in the number of mutants that were tested both biochemically as well as endogenously *in vivo*. In addition, we would like to also emphasize that the financial cost and the time required to increase the scope of this study in this manner would be significant.

One might assume we could use mutations that will directly affect the GTPase cycle, for example, by using mutations to the catalytic residues that break GTP hydrolysis, or mutations analogous to the constitutively active GTPase KRAS G12C mutants. However, although we have not tested each of those mutants ourselves, based on our unsuccessful attempts in making endogenous mutations to the switch I and switch II regions, we are confident that those mutants would not be viable in *S. cerevisiae*, and we would therefore not be able to perform the unbiased functional screens.

The experiment we believe would really address the Reviewer’s point would be to specifically perturb the two sides of the GTPase cycle by perturbing the GAP or the GEF directly. However, the genetics tools for doing that in a systematic way are not established, and their development would require a full study that would include substantial methods development and be similar to this one in its scope.

In any case we would like to thank the reviewer, and we acknowledge their point and have therefore, to avoid this misconception with the readers, crafted some of our wording in the discussion more carefully.

TO DO Wording to change in the manuscript/added discussion points to address this?

*2) I have concerns listed below with the Michaelis-Menten data acquisition and analysis that need to be addressed because the enzyme data form a linchpin for the correlations and the eventual model generated in this paper.*

Although we share the reviewer’s enthusiasm for understanding the enzyme kinetics of small GTPases, we want to refine the claim that the kinetics data form the linchpin of our paper. Although we agree that the kinetics data are essential for the claims we make, our conclusions are not based on the fine-grained resolution of the complex kinetics of the GTPase cycling, but rather on combining the (approximate, yet informative) GTPase cycle kinetics parameters with the functional genomics data for a phenotypically diverse set of point mutants. This point may sound like an overly precise distinction, but we believe it is an important one to keep in mind when assessing our responses to many of the points made by Reviewer 2.

*a) As far as I could gather from the Methods section, the GAP-mediated GTP hydrolysis kcat and Km values have been obtained from data acquired at a single substrate concentration [S] >> Km (in contrast to GEF-mediated nucleotide exchange where 0.25 um - [S] >> Km have been used) and not by varying [S]. A single substrate concentration >> Km is insufficient to determine both kcat and Km reliably. At high [S], only kcat can be obtained since the velocity of the reaction becomes independent of Km. If the velocity is forcibly fit to kcat and Km, Km and kcat/Km values will be error-prone and this may explain why errors are larger in the GTP hydrolysis data than in GEF data (Extended data figure 5 panels a,b vs c,d). Since kcat/Km values are central to their conclusions, the authors must determine Km reliably using multiple [S] data.*

The reviewer’s reading of our Methods section is correct, and indeed the error bars for the GAP kinetics data are higher. We would like to discuss three, somewhat intertwined points about our GAP-mediated GTP hydrolysis assay and the reviewer’s comments about its quality.

**1. Comparison of GEF and GAP assays.**

A general difficulty with precise measurements of both GAP and GEF GTPase kinetics of RAN/Gsp1 is the low Km and high kcat values compared to the *in vitro* values for other small GTPases and their GAPs and GEFs. This is due to the fact that *in vitro* conditions represent more biologically relevant values for the RAN cycle (RAN/Gsp1 is highly abundant and freely distributed in the cell), unlike for other GTPases whose interactions with their GAPs and GEFs are facilitated by membrane interactions.

For the GEF assay we could obtain very reproducible measurements between biological replicates because we avoided the nucleotide loading step by measuring the decrease in Trp fluorescence upon the tryptophan to mant-group FRET (described in Klebe *et al*. Biochemistry, 1995a).

Using intrinsic Trp fluorescence can in theory be used to measure GTP hydrolysis, as was used initially by Klebe et al, Biochemistry, 1995a, but the small change of fluorescence (10%, compared to 40% upon to Trp to mant FRET) is not compatible with a plate reader measurement, which was necessary for our large number of samples (for the GEF assay, we have measured more than 1000 nucleotide exchange curves). That being said, we note that using the intrinsic Trp fluorescence Klebe et al estimate the Km of 0.45 μM and kcat of 2.1 s-1 at 25˚C for mammalian RAN and *S. pombe* GAP, while our values for the wild type *S. cerevisiae* Gsp1 and *S. pombe* GAP at 30˚C are Km of 0.4 μM and kcat of 8.9 s-1.

The Km values of GEF-mediated exchange were high enough for us to obtain the Km and kcat by fitting the data for a range of Gsp1 concentrations to the exponential form of the Michaelis-Menten equation. However, as the Km for the GAP-mediated hydrolysis for many of the Gsp1 variants is 0.1-0.4 μM, to obtain the kcat and the Km from the fitting the data for a range of [Gsp1:GTP] we would need to measure GTP hydrolysis at concentration of Gsp1:GTP of <50 nM, which is too low for reliable measurement of fluorescence signal increase by the phosphate sensor.

**2. Estimating the kcat and Km parameters using an accurate solution to the integrated Michaelis-Menten equation.**

Estimation of the kinetics parameters by the accurate solution of the integrated Michaelis-Menten equation by the Lambert ω function was shown to be precise by others (e.g. by Goudar et al, 1999), and the reason it was rarely used in the past were computational limitations.

If the experiment is set up correctly: (i) with the [Gsp1:GTP] >> Km, (ii) [GAP] <<< [Gsp1:GTP], and (iii) the reaction time course F(t) was measured to completion (i.e. until it approached equilibrium), as our experiments were, the F(t) samples a concentration range from [Gsp1:GTP] (at t = 0) >> Km to [Gsp1:GTP] (at t = final time) << Km.

The entire F(t) can then be directly analyzed by a non-linear fit with the analytical solution for the integrated Michaelis-Menten equation. As the initial linear phase of the time course is well measured, kcat can be well determined. As the exponential phase and transition region of the time course are also well measured the maximum likelihood Km can be determined.

**3. Comparing the accuracy of the approaches to estimating the Michaelis-Menten parameters.**

While we do agree with the reviewer that there are limitations in the accuracy of the method, and in the ideal case we would want to determine the kcat and the Km parameters by measuring initial velocity for a wide range of [Gsp1:GTP], we would argue that given the low Km values and accuracy limitations of other methods rather than using the phosphate sensor, significant limitations exist even if we use the approach the reviewer suggests. For example, if we did a range of Gsp1 concentrations, in the cases where [Gsp1] is above Km the curve cannot be fitted to an exponential (as can be seen in our Supplementary File 1 Figure 3). Traditionally the initial velocity would be estimated from those data by a linear fit of the first 10% of the reaction, but the accuracy of the linear fit to the initial data is also imperfect for a number of reasons. The very beginning of the reaction is, for technical reasons, always missed and the very high rate in the beginning necessarily means that the ratio of time points to concentration change is low. In many ways, using all of the collected data is more meaningful.

The confidence of the calculated kcat and Km depend primarily on the accuracy of the enzyme [GAP] and substrate [Gsp1] concentrations. As the kcat/Km values for the GAP-mediated GTP hydrolysis are relatively high, in order not to miss much of the initial hydrolysis we used picomolar concentrations of the enzyme which were below the limit for accurate protein concentration measurements (by Bradford or UV spectroscopy), meaning that there was necessarily some error in enzyme concentration estimate. Furthermore, unlike for our nucleotide exchange experiments, each biological replicate measurement required loading the Gsp1 (mutant) with GTP. Despite having standardized the loading protocol we could not avoid some variations in the loading efficiency, which we have estimated from the final phosphate amounts based on phosphate sensor fluorescence upon reaction completion. This means that for each replicate there was also an associated error in effective concentration of GTP-bound Gsp1, which would propagate and contribute to the error of the measured hydrolysis kinetics parameters.

Also, as we calculated the kcat and the Km from each individual curve, we reported the error bars by propagating the standard deviation of the individual kcat and Km measurements, which means that our error bars for kcat/Km are often higher than the reproducibility of the kcat/Km ratio (which we use for our downstream analyses).

Finally, both our biophysical and our phenotype measurements (functional genomics as well as proteomics) measure small differences, but the conclusions we make are based on grouping the mutants by the measured effects. Even though each measurement has different types of noise associated with it, the signal is strong enough for us to see clear groupings, both in Fig. 4a (now Extended Data Fig. 7a) and Fig. 4b (now Fig. 4a)

As we want to be as forward about the limitations of our data, and as clear about the significance of our results, we have now added additional discussion about the limitations of our kinetics to the Supplementary File 1 Supplementary Discussion.

*b) Interpretation: Enzyme kinetics data in Gsp1 must be interpreted with care because there are multiple steps involved in each reaction. The authors are referred to work on the Hsp70 chaperone system which is very similar to this switch in having ATP hydrolysis-enhancing factors (J-proteins) and nucleotide exchange factors (NEFs) facilitating the cycle. Careful enzyme kinetics work by the groups of Philip Christen, Roger McMacken, Bernd Bukau and others show that multiple steps must be considered in building a model (Hu, Mayer and Tomita, BiophysJ 2006). Some of the questions that authors need to consider are:*

The reviewer is correct, the GTPase cycle is only approximated by the two reactions forming the two sides of the cycle (exchange and hydrolysis) represented as simple enzyme-substrate Michaelis-Menten reactions. Especially the GEF-mediated nucleotide exchange is a multi-step reaction, and the individual steps for the RAN GTPase were worked out by Klebe *et al*. (Klebe et al., Biochemistry, 1995a).

The same authors (Klebe et al, Biochemistry, 1995b) have also proposed that both reactions can be described enzymatically, and this approach has been regularly used for other small GTPases. (We will discuss this point further in our reply to comment (iv)).

In general, we do agree with the reviewer that GTPase kinetics data needs to be interpreted with care, and we believe we have done so. The point we want to acknowledge, and we thank the reviewer for making us revisit this, is that we might not have done a thorough enough job explicitly discussing all the details in our manuscript.

We hope that our responses to the reviewer’s questions, as well as the additional discussion we added to the paper, will rectify this.

*(i) How is the basal GTPase activity of Gsp1 taken into account? The authors have mentioned controls in the Methods. Equations used for correcting for the basal rate and equations used for fitting the data should be stated.*

RAN/Gsp1 has very low intrinsic nucleotide exchange and hydrolysis rates, which are low even compared to other small GTPases, and both the GAP and the GEF increase the reactions 105-fold (Klebe et al, Biochemistry, 1995b). Although we do report the intrinsic hydrolysis rate for our mutants, all the intrinsic rates remain orders of magnitude below the enzyme facilitated reactions and we do not add the intrinsic exchange/hydrolysis term when we fit the data.

*ii) What are the relative affinities of GDP and GTP for Gsp1? This is important, for example, in deciding how much excess GTP is needed in a nucleotide exchange experiment.*

Ran binds GTP specifically and with high affinity (> 19 M-1) (Klebe et al., 1995b). A low dissociation rate leads to almost irreversible binding of the guanine nucleotide. Ran:GDP and Ran:GTP complexes have half-lives of several hours (Bischoff and Ponstingl, 1991; Klebe et al., 1995a; Klebe et al., 1995b). The low intrinsic dissociation rates of GDP and GTP are paralleled by a low intrinsic rate of Ran·GTP hydrolysis.

As we state in our Methods, for most of our exchange experiments, we used 200 μM mant-GTP, going up to 1 mM mant-GTP for higher concentrations of Gsp1. The starting value of 200 μM was taken from the first published nucleotide exchange experiment using mant-labeled nucleotides in Klebe et al, Biochemistry, 1995b.

*(iii) Factors such as GAP and GEF may have residual affinities for the products of the enzyme reaction (GDP-Gsp1 and GTP-Gsp1 respectively). Are these numbers known to be negligible? If not, they have to be taken into account in determining 'kcat' and 'Km'.*

TO DO Find difference in affinity for GDP and GTP bound RAN for Rna1?

However, due to GEFs comparable affinity for mant-labelled and unlabeled bound Gsp1, for higher concentrations of Gsp1, where the relative excess of mant-nucleotide is smaller, we estimated the initial rates from the linear fits to the very beginning of the reaction, when levels of mant-nucleotide-bound Gsp1 are low.

*(iv) Is there justification for using the Michaelis-Menten equations for these two reactions, instead of approximation-free A=B=C reaction kinetics? Is [ES] at a steady-state and very close to zero throughout the reaction?*

*Overall, I would like to see a more careful analysis of the enzyme kinetics data in the context of the entire cycle.*

We think that there is a justification for using Michaelis-Menten equations for describing the GTPase cycle, as has indeed been done in the past by different labs, and for different small GTPases: Ran (Klebe et al, 1995a), Ras (Gideon et al, 1992), or Rap (Brinkmann et al, 2002).

For RAN/Gsp1 specifically, both the hydrolysis and the exchange are measured using enzymatic levels of the GAP or the GEF (orders of magnitude less than the substrate). In the case of the GEF-mediated nucleotide exchange, the free nucleotide is also in excess.

Go through precedent in the literature. Perhaps could address with qualifying discussion on assumptions in the kinetics. Consult an expert… (Geeta?)

References for replies to point 2:

Brinkmann, T. *et al.* Rap-specific GTPase Activating Protein follows an Alternative Mechanism. *Journal of Biological Chemistry* **277,** 12525–12531 (2002).

Gideon, P. *et al.* Mutational and kinetic analyses of the GTPase-activating protein (GAP)-p21 interaction: the C-terminal domain of GAP is not sufficient for full activity. *Molecular and Cellular Biology* **12,** 2050–2056 (1992).

Klebe, C., Prinz, H., Wittinghofer, A. & Goody, R. S. The Kinetic Mechanism of Ran-Nucleotide Exchange Catalyzed by RCC1. *Biochemistry* **34,** 12543–12552 (1995).)

Klebe, C., Bischoff, F. R., Ponstingl, H. & Wittinghofer, A. Interaction of the nuclear GTP-binding protein Ran with its regulatory proteins RCC1 and RanGAP1. *Biochemistry* **34,** 639–647 (1995).

Bischoff, F. R. & Ponstingl, H. Mitotic regulator protein RCC1 is complexed with a nuclear ras-related polypeptide. *Proceedings of the National Academy of Sciences* **88,** 10830–10834 (1991).

Goudar, C. T., Sonnad, J. R. & Duggleby, R. G. Parameter estimation using a direct solution of the integrated Michaelis-Menten equation. *Biochimica et biophysica acta* **1429,** 377–383 (1999).

Mishra, A. K. & Lambright, D. G. High-throughput assay for profiling the substrate specificity of Rab GTPase-activating proteins. *Methods Mol. Biol.* **1298,** 47–60 (2015).

*3) Lines 183-186: "Taken together, the 31P NMR and kinetic data support a molecular mechanism whereby Gsp1 interface mutations allosterically shift the conformational distribution at the active site which in turn alters the GTPase switch cycle". This conclusion is too strong for the amount of data available to support it, though the data does indeed suggest such a possibility. Given that the allostery in Gsp1 is only an interesting side-story in this manuscript, the authors can tone down this conclusion.*

*a) The correlation in Fig. 3f looks much weaker when I plot the data without the log scale on the y-axis. It is equally likely to state from the plot that the y-ratio (without log) remains between 0.05 and 0.5 regardless of what the % of the second conformation is.*

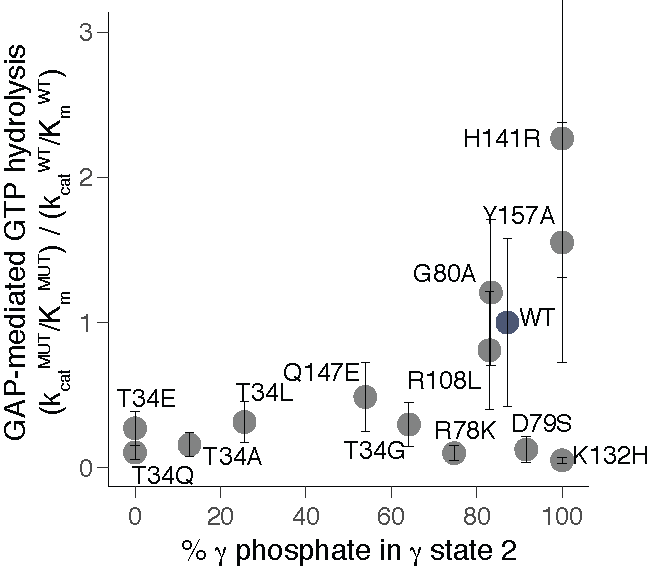
*b) While the 31P NMR data show that there are two conformations in slow exchange, they definitely don't indicate what the structural changes are between the two states and whether the conformational differences are local or global. For all we know, there may be two peaks because some sidechain is flipping in the vicinity, resulting in two peaks for 31P. Without data on other nuclei and strong correlations to structure across the entire protein, it is unwise to draw strong conclusions regarding the conformational exchange.*

OK, tone down (but refer to other work on the conformations). Say reviewer is right that we do not know the structural details. But we do know effects are not just in the vicinity of the gamma phosphate as mutations are distal.

Combined answer to point 3:

We appreciate the reviewer’s call to attention with regards to relating the 31P NMR data to the differences in GAP-mediated GTP hydrolysis. We had reservations on how to present this data, and these criticisms allowed us to more carefully consider the relationship between the conformational distributions of GTP-bound Gsp1 mutants and the GAP-mediated hydrolysis values.

With regards to the correlation in Fig. 3f, we initially chose this data representation to emphasize the monotonically increasing relationship between the fraction of GTP-bound Gsp1 in state 2 and the *kcat/Km* of GAP-mediated hydrolysis. We agree that a true log-linear relationship for these variables is not expected *a priori* (and, in fact, unlikely)*,* and acknowledge that the exact functional form of the relationship is impossible to fit using reaction kinetics formalisms without some means of directly measuring the *kcat and Km* values for state 1 and state 2 separately (which is not to our knowledge feasible). To more accurately make our point, we have modified our figure to no longer include an overlaid regression line, and to instead state the Spearman rank correlation statistic, which concisely summarizes the monotonically increasing relationship.



We also agree that the conclusion as stated could be toned down, as the 31P data do not provide structural detail on the differences between the two states across the entire protein. However, we assert that the data do reveal that differences between states cannot be local to the active site, as the point mutations are in distal interfaces (>18 Å away). This is consistent with previous work using 31P NMR to study conformational equilibria in human Ran bound to GTP analogs (Geyer et al 1999). That study found that while WT RAN was only ~70% in state 1 at 30˚C, active site mutants RAN(F35L) and RAN(T42A) are only observable in state 1 at 25˚C and the strength of their interaction with RanBP1 (the human homolog of Yrb1) at 25˚C is decreased >100-fold from 3.7 nM (WT) to 492.0 nM and 651.0 nM, respectively. Critically, RanBP1 does not bind F35, T42, or any other active site residues on RAN, as seen in the published complex (Seewald et al, 2001, PDB ID: 1k5d). This energetic coupling between the active site and the distal RanBP1 binding interaction is supporting evidence that the states are correlated with structural changes not confined to the active site. Nonetheless, we agree with the reviewer that the limitations of the 31P NMR data in establishing a relationship to GAP kinetics should be clearly stated in the text, and have modified the text as follows: CHRIS WILL (RELUCTANTLY) MODIFY TEXT but he realized he needs to think about the intrinsic hydrolysis plot in the supplement as well. If we remove the correlation from the main figure do we need to remove it from the hydrolysis plot? That relationship **should** be linear (but not log-linear)

Prior work on human Ran (22) and the related GTPase Ras (23) had implicated the γ2 state conformation in effector binding. Here we observe a striking linear relationship when plotting the γ2 state population in the different Gsp1 mutants against their effects on relative catalytic efficiency of GAP-mediated GTP hydrolysis (Fig. 3f) and intrinsic GTP hydrolysis (Supplementary File 1 Table 8, Fig. S6b, c). These experiments directly quantify the allosteric effects of the mutations and indicate that the γ2 state represents the hydrolysis- competent conformation of Gsp1:GTP. Exceptions to the linear relationship are the K132H mutation, which is in the core of the GAP interface and is hence expected to directly affect the interaction with the GAP, and the D79S and R78K mutations, which are on the edge of the GTPase switch II region (from residues 69 to 77) and could lead to additional perturbations of the nucleotide binding site geometry. Taken together, the 31P NMR and kinetic data support a molecular mechanism whereby Gsp1 interface mutations allosterically shift the conformational distribution at the active site which in turn alters the GTPase switch cycle. Interestingly, the allosteric mutations we show here to tune the distribution of the catalytically competent state of Gsp1 (T34, H141, Q147, and Y157, Fig. 3d, e) do not overlap with either allosteric inhibitor pocket successfully targeted by small molecule inhibitors in Ras (24–26) (Fig. S6d).

References:

Geyer, M., Assheuer, R., Klebe, C., Kuhlmann, J., Becker, J., Wittinghofer, A., & Kalbitzer, H. R. (1999). Conformational states of the nuclear GTP-binding protein Ran and its complexes with the exchange factor RCC1 and the effector protein RanBP1. *Biochemistry*, *38*(35), 11250–11260.

Seewald, M. J., Körner, C., Wittinghofer, A., & Vetter, I. R. (2002). RanGAP mediates GTP hydrolysis without an arginine finger. *Nature*, *415*(6872), 662-666.

*4) I find it difficult from the data to disentangle the effects of the mutations on the binding and on the cycle. A part of this problem is because the some of the mutations are directly at the interface of Srm1 and Rna1, which facilitate the cycle turnover. Secondly, I find the representation of AP-MS data in Fig. 2b/c very confusing. Particularly in Fig. 2b,*

*a) Why have only 6 prey proteins been quantified out of 16 whose interfaces were to be perturbed? How do we estimate how the interactions with the other 10 proteins have been affected?*

Can try to address in discussion. For MS, the 6 are the ones we see. For the others, the reviewer is right, we don’t know. But most importantly, the interface locations of the mutations do not explain the GI data. Could replot that just for the 6 interfaces where we have MS data?

*b) Kap95 has 7 core residues at the interface with Gsp1 from Ext. Data Fig. 1b (79, 80, 112, 143, 147, 154 and 157). In Fig. 2b for Kap95, I don't see 7 circles/half-circles of the same size. Has the classification of core residues changed?*

We have reworked the presentation of AP-MS data (Fig. 2 and Extended Data Figure 4 and 5 above), but for clarity, core residues are defined as ΔrASA > 0 & rASAm > 0.25 & rASAcomplex < 0.25 (we have now, in addition to the original reference, added explicit definitions of interface residues in the Methods section). While we do not have AP-MS data for residue 154. but points representing residues 79, 80, 112, 143, 147, and 157 are in visible in the previous version of Fig. 2b.

c) Again, for example, Kap95 seems to have approximately the same number of reds and blues. Pse1 has two reds and one blue. Srm1 has four bluish tinges and four reddish tinges. Excepting Yrb1, I don't find this evidence convincing for the statement that the introduced mutations perturb the interactions they were meant to perturb (lines 130 and 142 in the manuscript.

Check this and explain. We can apologize that we were confusing – the reviewer is right, the mutations sometimes perturb, sometimes not, and most of the time rewire. Can show the sina plots – abundance fold changes for mutations in and not in interfaces. For mutations in interfaces distribution expected (shifted to lower abundance). But when mutant not in interface then wide distribution.

Overall, I am not convinced of the extent to which the mutations introduced in this work perturb the interfaces of the 16 interactors of Supplementary File 1 Table 1. The authors should purify the mutant Gsp1 proteins and measure their interactions with the partners whose interactions the mutations were meant to perturb, using robust biophysical methods such as ITC to settle this point.

Could try to argue but probably need to do at least some of these binding exp (as reviewer #3 also argues for them). Perhaps we can pick some strategic ones that would satisfy the 2 reviewers.

The point we want to make is that although we do see a trend on average (Fig. 2b), it is important to look at the data in more detail. However, the reviewers helped us realize that the way we chose to represent the data did not convey that massage successfully. We hope that the simplified presentation of the AP-MS data makes these points clearer and have rewritten the section about the AP-MS data analysis and interpretation.

*Minor changes:*

*1) It will help to put the function of the 16 proteins in Supplementary File 1 Table 1 as a separate column.*

We have now added the protein names and functions of the binding partner proteins to Supplementary File 1 Table 1



2) Line 320, "highlighted in yellow": I was unable to locate the yellow colouring in Fig. 3c.

We apologize for this, it seems that the transparent yellow box got converted to a gray box during the file conversion process. We have now changed the Figure to contain a yellow box without fill, to make it more robust for file conversions and printing.

3) Line 844 should read "run in parallel".

We have now fixed that grammatical error in our Methods text.

4) Numbers seem to be slightly off in line 155: R78K and T34Q are ~10-fold, but T34A is 6.3 and T34E is 3.7, hardly 10-fold.

fix

5) I find it very interesting that a cycling between two forms of a switch is necessary rather than one or the other conformation. A similar effect has been observed in a cis-trans molecular switch in the circadian clock (Partch and coworkers, Mol. Cell, 2017, 66:447). Perhaps the authors can comment on a possible mechanism of how cycle dynamics, rather end populations can impact downstream biological processes?

Cite that paper and add discussion. This is actually a deeper point that was also brought up by David after my talk in Seattle. Perhaps discuss the ultrasensitivity work more in this context.

We should go overboard about how this is a brilliant addition to our paper!

6) While reading the manuscript, I felt that the work was not sufficiently placed in perspective of what is known about the mode of operation of other molecular switches. A short paragraph on this may help the manuscript.

Ok add that.

Data presentation:

1) Fig. 2b/c is extremely confusing and took me a long time to interpret. They depict quantitative AP-MS data as semi-qualitative colours which do not help in making quantitative assessments.

a) Why are some half-circles missing their counterparts?

The half circles represent either the N or C terminally FLAG tagged mutants. Although we attempted to make each of the mutants with both tags, for most of the mutants we only managed to obtain viable yeast strains for only one of the tags. This is explained in the Methods section, and we assume this is due to the negative epistasis of the tags (both of which unfortunately affect the function of Gsp1) and the interface point mutations.

b) The meaning of circle size has changed between panels b and c. While this is indeed mentioned both on the plot and in the legend, it makes it very difficult to grasp the import of the figures.

c) In panel b, I found it very difficult to get a reliable estimate of circle size, which reports on the key DASA parameter, without actually using a ruler. Why has the core/rim classification of Ext. Data Fig. 1b changed though it portrays the same parameter? Consistency between these two figures will help.

Fig. 2b/c has to be reworked so that it is easier to understand the data. A simple histogram may work.

We have now completely reworked Fig. 2 in the main text to streamline and simplify our interpretation of the AP-MS data as per combined suggestions by Reviewers 1 and 2. The new version of Fig. 2 is above, and the accompanying Extended Data Fig. 5 now contains the stacked bar plots representing log2(fold change) for a) the mutations which are in the core of the prey interface and b) all preys with structural information.

Referee #3:

*Perica et al. interrogate the small GTPase Gsp1 to identify the effects of directed point mutations, largely in interface regions. Through multiple assays, including genetic interaction, protein-protein interactions, NMR, and enzyme kinetics, they determine that mutations fall into three categories, affecting overall function, GTPase function, or GTP loading.*

*Unfortunately, despite starting the manuscript with 56 mutants, at the end, through multiple rounds of experimentation, the authors manage to describe the functional impact of mutating 11 sites in Gsp1. The core findings, that mutating 11 disparate sites in a GTPase affects its overall function and that many mutations affect function through allosteric regulation, are somewhat dissatisfying. Perhaps because of the systems-level scale of the analysis, there appears to be a lack of depth of understanding for any given mutation. For instance, how does T34Q (or any other amino acid substitution at the T34 position) lead to a strong change in GAP function?*

*Points to address:*

*1. 2-9 replicates for Michaelis-Menten measurements? Why were there different numbers of replicates for some mutants compared to others?*

We knew we needed to do some more.

*2. Correlation plots for AP-MS experiments are disconcerting, as they show that, in many cases, the replicate pull-downs for a given mutant do not cluster together. For instance, the WT pulldown replicates do not cluster. Even more disconcerting is that the replicates for each mutant appear to have correlation values that are much less than 1.*

From Danielle: My hypothesis here is that this is due to these all being mutants of the same protein. When we have different baits, yes we expect them to all be more different, but in APMS experiments, >95% of proteins identified are background proteins (i.e. not PPIs deterministic of a given mutant). With this, in mind when we analyze highly similar baits, such as a large set of mutants of the same bait, it would be expected imperfect clustering due to high similarity in the total peptide signature identified in each sample.

To the comment about correlations between replicates: Looks like generally we are in the .6-.8 range for correlations. It's not amazing, but also it's not terrible. Also, this correlation is done before any normalization procedure. We could also argue that APMS is an involved protocol (many washes etc.) that reduce reproducibility, but this might hurt the argument made above. Other ideas might be just to say, this is why we do rigorous statistical analysis, or point towards your other analysis with the functional separations and say, despite these less than ideal correlations, we still are able to extract data that separates the mutants accurately by function.

Maybe the point to emphasize: correlation is raw data. Confess the batch effects – because we so focused on biological replicates

Is there a way to illustrate that extracted high-confidence data is much more reliable.

Or some other way to assess the quality of raw data that is not correlations. Abundances?

*3. Orthogonal validation experiments would strengthen the AP-Ms data. For instance, it should be fairly straightforward to perform co-IP western blots to demonstrate the loss of binding of SRM1 to T34A, as an example.*

IPs. But the specific mutant asked about is tricky because effect may be too small for resolution of IP… Strategic mutants / partners and biophysics, as for reviewer #2?

*4. p 11: The discussion of K101R and acetylation is speculative. The authors do not show that this lysine is acetylated in yeast.*

We have now added a reference showing that this lysine is also acetylated in yeast. (Please see our reply to reviewer 1 regarding the same point).

Reference: Henriksen, P. *et al.* Proteome-wide Analysis of Lysine Acetylation Suggests its Broad Regulatory Scope in Saccharomyces cerevisiae. *Mol. Cell Proteomics* **11,** 1510–1522 (2012).

*5. The authors start with 56 mutants, but then drop to 22 mutants that ‘express and purify well’. What does this say about the other 34 mutants? Did they not express well? If so, then the GI and AP-MS data for these mutants should be removed.*

Do you even have a biochemistry degree?! Let us explain to you a little thing called overexpression, as well as stability of small GTPases at 1-2 mM concentration when you add 10 mM EDTA for 3 hours at room temperature! In any case, you should be banned from doing science, because you just suggested us to cherry pick our data. Your parents should be ashamed of you.

We would like to thank the reviewer for this comment. We should have been far more precise in our language, and now that the reviewer has brought it up, it has become clear that we wrote this in a misleading way. All of the mutants we tried to express did express in *E. coli* at similar levels to the wild type, and we could purify all of them. However, GAP assay and NMR experiments required a highly concentrated pure protein sample (> 1 mM), and, more importantly, both experiments required loading the protein with GTP, by using enough EDTA to chelate the Mg2+. Removal of Mg2+ increases the off-rate for nucleotide binding of small GTPases, and chelation of divalent cathions is therefore a common method for nucleotide loading of small GTPases. As was the case in our hands, and was also noted by others early on (Klebe et al) RAN/Gsp1 is more unstable than other small GTPases when in nucleotide-free form. Those 34 mutants not included were not stable enough as pure, highly concentrated samples to enable the sample preparation necessary for the precise biochemical and biophysical assays.

In addition, we have shown by Western blots (Extended Data Figure 2) that all the mutants express from endogenous locus at levels similar to wild type, and that there is no significant difference in protein expression levels between mutants with weak and strong phenotype profiles.

Again, we would like to thank the reviewer for catching that. It might be a minor point, but we can see how our language could have been misleading. We now rewrote that sentence to say:

To address the question whether the mutations act directly or indirectly (i.e. by altering the competition between physical interaction partners in the cell), we recombinantly expressed and purified wild-type and 22 Gsp1 mutants and measured their effects on GAP-mediated GTP hydrolysis and GEF-mediated nucleotide exchange *in vitro.*

*6. Similar note regarding the AP-MS experiments. 56 mutants were used for GI, but only 28 for AP-MS? The other 28, even if they were not in interface regions, should have been assessed for altered protein interactions, even as controls. Are the 22 mutants for enzyme kinetics a subset of the 28 mutants for AP-MS?*

In general, we are surprised by reviewers points 6, 7 and 8 (well, not really, all sorts of idiots walk among us every day). We could have removed E-MAP and AP-MS data and presented the whole paper with just 22 mutants for which we have all three experiments, but we think it is conceptually an important point, that we started from global phenotype measurements, and then delved deeper into elucidating the mechanism behind it. We did not know before we did the experiments which mutants will have strong effects on the phenotype, and we have screened relatively many. As both AP-MS and especially biophysics are extremely laborious, expensive and time-consuming experiments, we chose representative sets of mutants to follow up.

All the mutants were in interfaces, did you even read the paper, dude? We chose representative mutants, always making sure to cover strong and weak, and representatives from all the clusters of mutants. Even by taking a representative set the scope of our AP-MS dataset is unprecedented.

From Danielle: I am unaware of any PPI study doing this many mutants. Do you know of any?  We could do a bit more literature digging just to make sure, but I think that we could just state, that this is the largest PPI study of point mutations on a single protein, it is unrealistic for the review to request more, when we have already done more than anyone else. (We will write this in a more scholarly manner and back up with flashy papers that have much much fewer mutants)

Second note from Danielle: Myself and 2 other people in the Krogan lab have done literature searches looking for APMS work on mutants, and we are unable to find any paper doing more than a couple mutants.  I think that responding to the reviewers with a statement like to the effect of:  to the best of our knowledge, this work represents by far the largest analysis of point mutants on a single protein by APMS, and for this reason thus it is unreasonable for the reviewers to suggest that we should double our efforts to attempt to perform APMS on additional mutants

Discuss scope with editor. AP-MS does not matter for main conclusion. We may not get away with it but perhaps Nevan can make the point.

*7. Were only 13 of the mutants used for NMR?*

How many NMR datasets have you collected for the paper that got you this job?

I think we can argue here, as the NMR mutants span the entire range so we could not learn more if doing more.

Yes, only 13 of the mutants were used for NMR. As described above, adequate signal for the 31P NMR studies required relatively large volumes (400 µL) of very highly concentrated samples of purified protein (> 800 µM) after GTP-loading (which in our hands dilutes samples to ~40% initial concentration). Thus, our workflow began with concentration of purified Gsp1-GDP mutants to well over 1 mM. Attempts to concentrate several mutants to these high concentrations were unfortunately in vain as the protein crashed out, despite these mutants being readily purified at lower concentrations, active in the GEF and GAP assays, and stably folded as confirmed by CD spectroscopy (Supplementary Figure 11 and Supplementary Table 9). Despite these obstacles, we believe the dataset we have collected spans the entire range of observable behaviours in the assay, as it includes two mutants only observed in state 1, two mutants only observed in state 2, the WT variant, two mutants with WT-like distributions, and several intermediate mutants. While we would have been eager to collect a larger set of spectra if the samples were attainable, we do not believe those additional mutants would significantly change our claims.

*8. In Supp. Tables 6-8 the authors include std. dev. and std. error values. Often these values are of similar magnitude to the measured value, indicating that the confidence in the measured value is low. Yet it seems that these measured values were still used in the main figures, with no indication of the error. Some indication of significance should be assigned to these figures.*

Explain more (editor wants to consult additional “stats” reviewer). Probably there are only a few high-error values and some / most of those may go down with additional GAP assays (?)