

**Data selection & animations**

Clicking on the buttons below will cause animated transitions between different two-way QFA comparisons. Click on any point in the graph to select it - selected points will remain highlighted between datasets.

These animations work best in Chrome or Firefox. Use the controls on the right to customise the speed of the animation, or turn it off.

**Speed:**

Medium (default) ▾

**Disable:** 

cdc13-1 **pol2-12 (Pol epsilon)** cdc2-2 (Pol delta) pol1-4 (Pol alpha) HU\_100mM

**Colour key**

The points on the scatterplot are coloured according to a number of criteria:

- Gene (hover for gene names)
- Significant Gene (improved fitness)
- Significant Gene (reduced fitness)
- Selected Gene
- Selected and Significant Gene

**Keyboard shortcuts**

A number of keyboard shortcuts help with navigation of the datasets and gene lists:

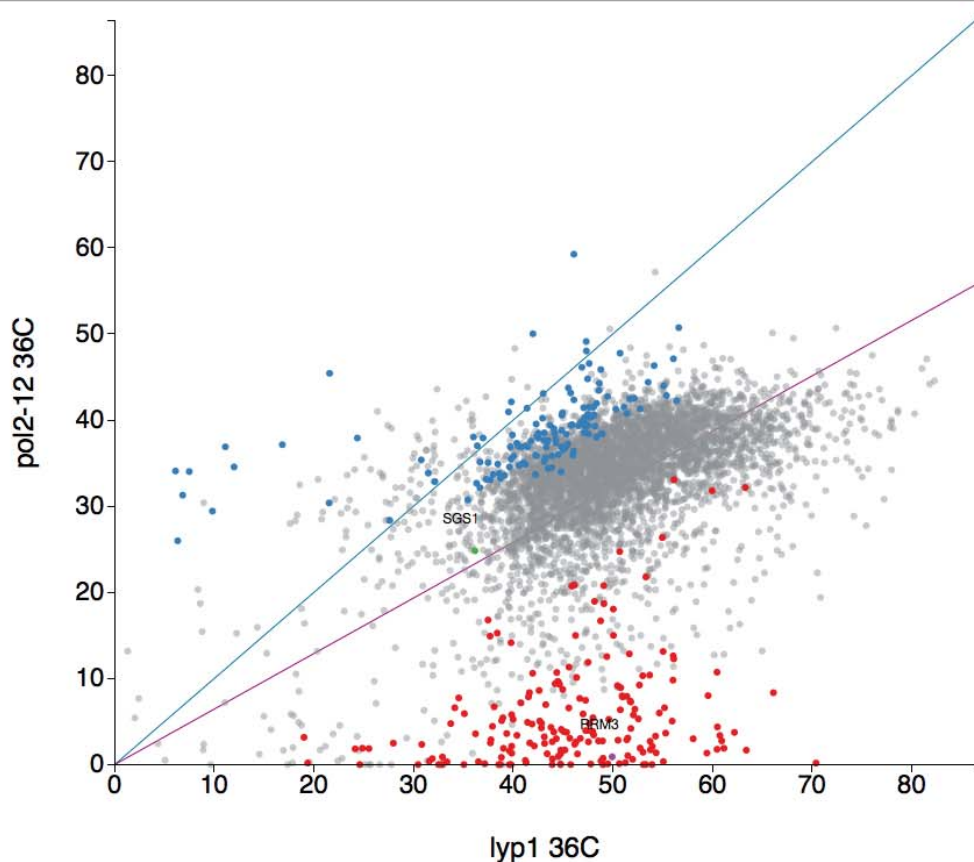
Key	Function
c	Clear currently selected points
.	Select 'previous' dataset (button to left of current dataset).
,	Select 'next' dataset (button to right of current dataset).
Up arrow	Move up through current list of Genesets
Down arrow	Move down through current list of Genesets
Shift+Click	Open gene in SGD

**Vector graphics**

Click button to generate a saveable (.SVG) version of the current graph which will appear at the foot of this page.

**Further customisations**

Reverse significant points colouring:

**Search for genes**

RRM3, SGS1,

Use the text box above to search for genes of interest. Searches will auto-complete based on gene name or systematic ORF name.

Paste in comma-separated lists to select groups of genes.

If searching by standard gene name does not return any result, please try searching by systematic ORF name instead.

If searching by systematic ORF name does not return any result, this means that the gene disruption was not present in the library screened.

**Selected Genes Info**

Gene: RRM3

DNA helicase involved in rDNA replication and Ty1 transposition; relieves replication fork pauses at telomeric regions; structurally and functionally related to Pif1p

Gene: SGS1

Nucleolar DNA helicase of the RecQ family; involved in genome integrity maintenance; regulates chromosome synapsis and meiotic joint molecule/crossover formation; potential role as repressor of a subset of rapamycin responsive genes; rapidly lost in response to rapamycin in Rrd1p-dependent manner; similar to human BLM and WRN proteins implicated in Bloom and Werner syndromes

**Genesets**

Select gene sets from the lists below to highlight groups of interest. Use the up and down arrows on your keyboard to cycle through the currently selected list of lists.

Functional Complexes

GO Annotation

Telomere related genes  
MTC/RTCs  
Spermidine synthase complex  
nuclear telomere cap complex  
Accelerated senescence: liq, culture  
Accelerated entry into & escape from senescence: liq, culture  
Normal senescence: liq, culture  
Most dissimilar to wild-type senescence curve  
Most similar to rad52D senescence curve  
Most dissimilar to rad52D senescence curve

**Figure S4: DIXY illustrates *rrm3Δ* and *sgs1Δ* genetic interactions with Pol  $\epsilon$**   
**A-C)** Snapshot of DIXY web page. Static scatter plots exported from DIXY shows the mean fitness of *rrm3Δ* and *sgs1Δ* mutants in *pol2-12* screen versus *lyp1Δ* control screen.