

## **Resistance to Arsenite and Arsenate in *Saccharomyces cerevisiae* Arises through the Subtelomeric Expansion of a Cluster of Yeast Genes**

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### **Supplementary results:**

Details of the assembly unitigs found to match with the *ARR* genes cluster in SG60 and SGU90.

## Supplementary Tables

### Table S1

**Strains used in this study.** For each strain, the isolation source and the assays in which the corresponding strain was used are reported.

Stefanini et al. 2012: Stefanini I., Dapporto L., Legras J.L., Calabretta A., Di Paola M., De Filippo C., Viola R., Capretti P., Polsinelli M., Turillazzi S., Cavalieri D. Role of social wasps in *Saccharomyces cerevisiae* ecology and evolution. *Proc Natl Acad Sci U S A*. 2012 Aug 14;109(33):13398-403. doi: 10.1073/pnas.1208362109;

Mortimer R.K. and Johnston J.R. (1986) Genealogy of principal strains of the yeast genetic stock center. *Genetics* 113: 35–43;

Cavalieri et al. 1998: Cavalieri D., Barberio C., Casalone E., Pinzauti F., Sebastiani F., Mortimer R., Polsinelli M. Genetic and Molecular Diversity in *Saccharomyces cerevisiae* natural populations. *Food Technology and Biotechnology*, 1998, 36(1):45-50;

Kane and Roth 1974: Kane S.M. and Roth R. Carbohydrate metabolism during ascospore development in yeast. *J Bacteriol*, 1974, 118(1):8-14;

Stern M., Jensen R., Herskowitz I. Five SWI genes are required for expression of the HO gene in yeast. *J. Mol. Biol.* 1984, 178, 853–868, doi:10.1016/0022-2836(84)90315-2;

Winston F., Dollard C., Ricupero-Hovasse S.L. Construction of a set of convenient *Saccharomyces cerevisiae* strains that are isogenic to S288C. *Yeast*, 1995, 11(1):53-5

Strain name	Isolation source	Used in assay	reference
1014	Frape for vinsanto fermentation	Phenotypic tests, CGH, whole genome sequencing, SNPs comparison, transcriptomics	Stefanini et al. 2012
EM93	laboratory	Phenotypic tests, CGH, whole genome sequencing, SNPs comparison, transcriptomics	Mortimer and Johnston 1986
M12	Montalcino grape	Phenotypic tests, transcriptomics	Cavalieri et al. 1998
M28	Montalcino grape	Phenotypic tests, SNPs comparison (3 meiotic segregants from the same ascus), transcriptomics	Cavalieri et al. 1998
M57	Montalcino grape	Phenotypic tests, transcriptomics	Cavalieri et al. 1998
SG60	San Giovese must	Phenotypic tests, CGH, whole genome sequencing, SNPs comparison, transcriptomics	Stefanini et al. 2012
SGU89	San Giovese grape	Phenotypic tests, transcriptomics	Stefanini et al. 2012
SGU90	San Giovese grape	Phenotypic tests, CGH, whole genome sequencing, SNPs comparison, transcriptomics	Stefanini et al. 2012
SGU114	San Giovese grape	Phenotypic tests, transcriptomics	Stefanini et al. 2012
SGU406	San Giovese grape	Phenotypic tests, transcriptomics	Stefanini et al. 2012

SGU407	San Giovese grape	Phenotypic tests, transcriptomics	Stefanini et al. 2012
SK1	laboratory	Phenotypic tests, SNPs comparison, transcriptomics	Kane and Roth 1974
W303	laboratory	Phenotypic tests, transcriptomics	Stern et al. 1984
BY4742	laboratory	Phenotypic tests	Winston et al. 1995
BY4743	laboratory	CGH	Winston et al. 1995

**Growth of *Saccharomyces cerevisiae* cells in the presence of sodium arsenite and sodium arsenate.** 100, 1000, and 10000 cells for each tested strain were spotted onto YPD medium supplemented with sodium arsenate or sodium arsenite at the reported concentrations. Growth was scored after 4 days incubation at 30 °C: 0= no growth, += growth, ++= as in control (YPD).

[illegible]

**Table S3**

List of CGH samples

<b>Accession number</b>	<b>Strain 1 (Cy5)</b>	<b>Strain 2 (Cy3)</b>	<b>replicate</b>
GSM4050898	1014	BY4743	1
GSM4050899	1014	BY4743	2
GSM4050900	EM93	BY4743	1
GSM4050901	EM93	BY4743	2
GSM4050902	M28	BY4743	1
GSM4050903	M28	BY4743	2
GSM4050904	M57	BY4743	1
GSM4050905	M57	BY4743	2
GSM4050906	SG60	BY4743	1
GSM4050907	SG60	BY4743	2
GSM4050908	SGU114	BY4743	1
GSM4050909	SGU114	BY4743	2
GSM4050910	SGU406	BY4743	1
GSM4050911	SGU406	BY4743	2
GSM4050912	SGU407	BY4743	1
GSM4050913	SGU407	BY4743	2
GSM4050914	SGU90	BY4743	1
GSM4050915	SGU90	BY4743	2
GSM4050916	SK1	BY4743	1
GSM4050917	SK1	BY4743	2
GSM4050918	W303	BY4743	1
GSM4050919	W303	BY4743	2

**Table S4**

**Sequencing details and stats.** ENA\_sample= ID of the data submitted to ArrayExpress; Filtered reads= number of reads remaining after the initial filtering carried out as described in materials and methods; Coverage (average)= average depth of coverage over the entire genome; Mapped reads= number of reads mapped against the genome of the reference strain S288C; % mapped reads= % of reads mapped against the S288C genome over the total number of reads. (S)= Sensitive to arsenic; (R)= Resistant to arsenic.

strain	Reads_SRA_ID	Filtered reads	Coverage (average)	Mapped reads	Assembly_SRA_ID	% mapped reads
1014 (S)	ERX240908	18,235,568	150	17,545,681	SAMN12640820	96.2
EM93 (S)	ERX240933	18,699,970	153.8	18,005,019	SAMN12640821	96.3
SG60 (R)	ERX240914	7,540,524	90.6	7,318,387	SAMN12640822	97.1
SGU90 (R)	ERX240918	6,889,632	82.7	6,735,090	SAMN12640823	97.8

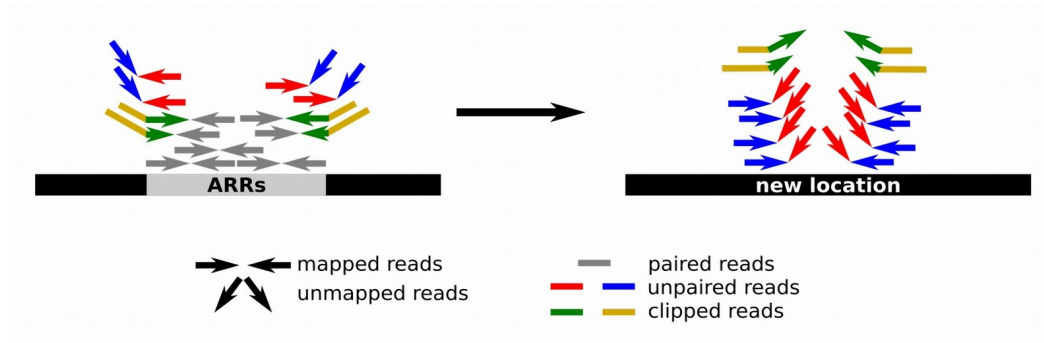
Note: SRA project ID for sequencing data (also including other strains' sequences)= PRJEB1871; SRA project ID for assembly=PRJNA562447.

**LTP   BioSample accession**

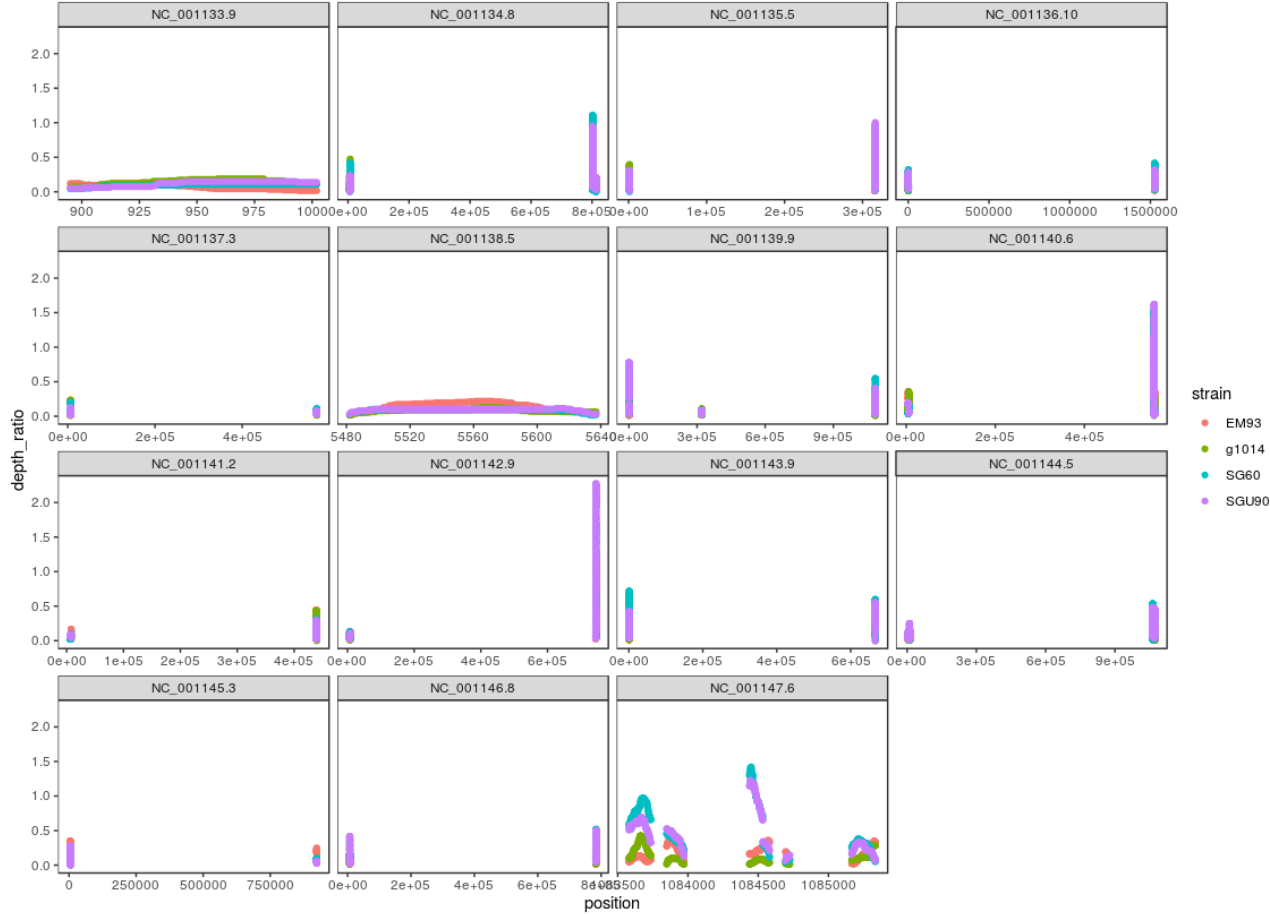
**FZC25   SAMN12640820   1014**  
**FZC26   SAMN12640821   EM93**  
**FZC27   SAMN12640822   SG60**  
**FZC28   SAMN12640823   SGU90**

## Supplementary Figures

**Figure S1:** Schematic representation of the approach used to identify the potential location of the duplicated region. Unpaired reads mapping against the region of interests (red arrows) were identified and their read mates (blue arrows) were extracted. Such read mates were then aligned against the whole genome of the reference strain to identify the potential location of the additional copies of the region of interest.

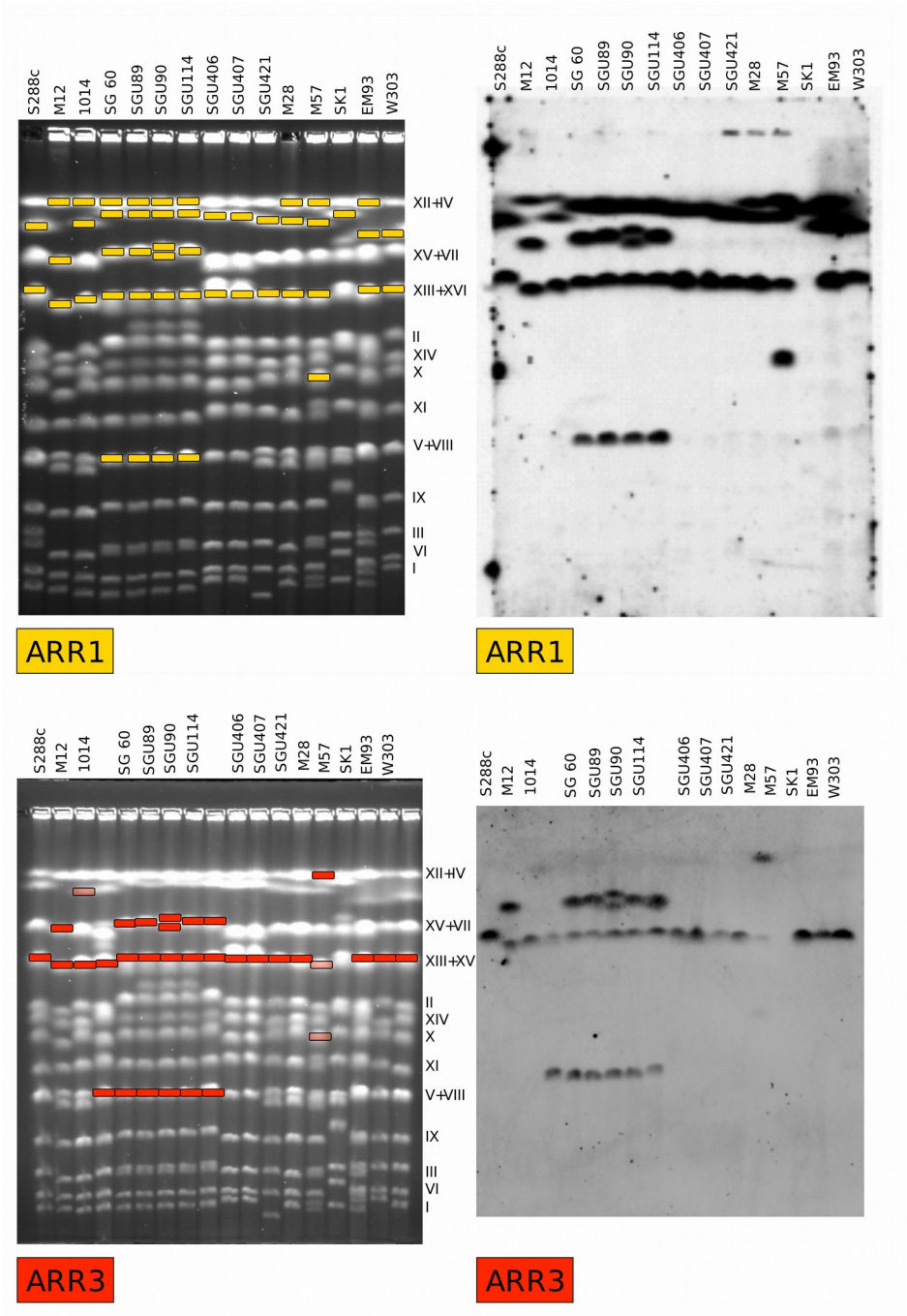


**Figure S2:**  
Genomic regions potential recipients of the additional copies of the *ARR* genes cluster.



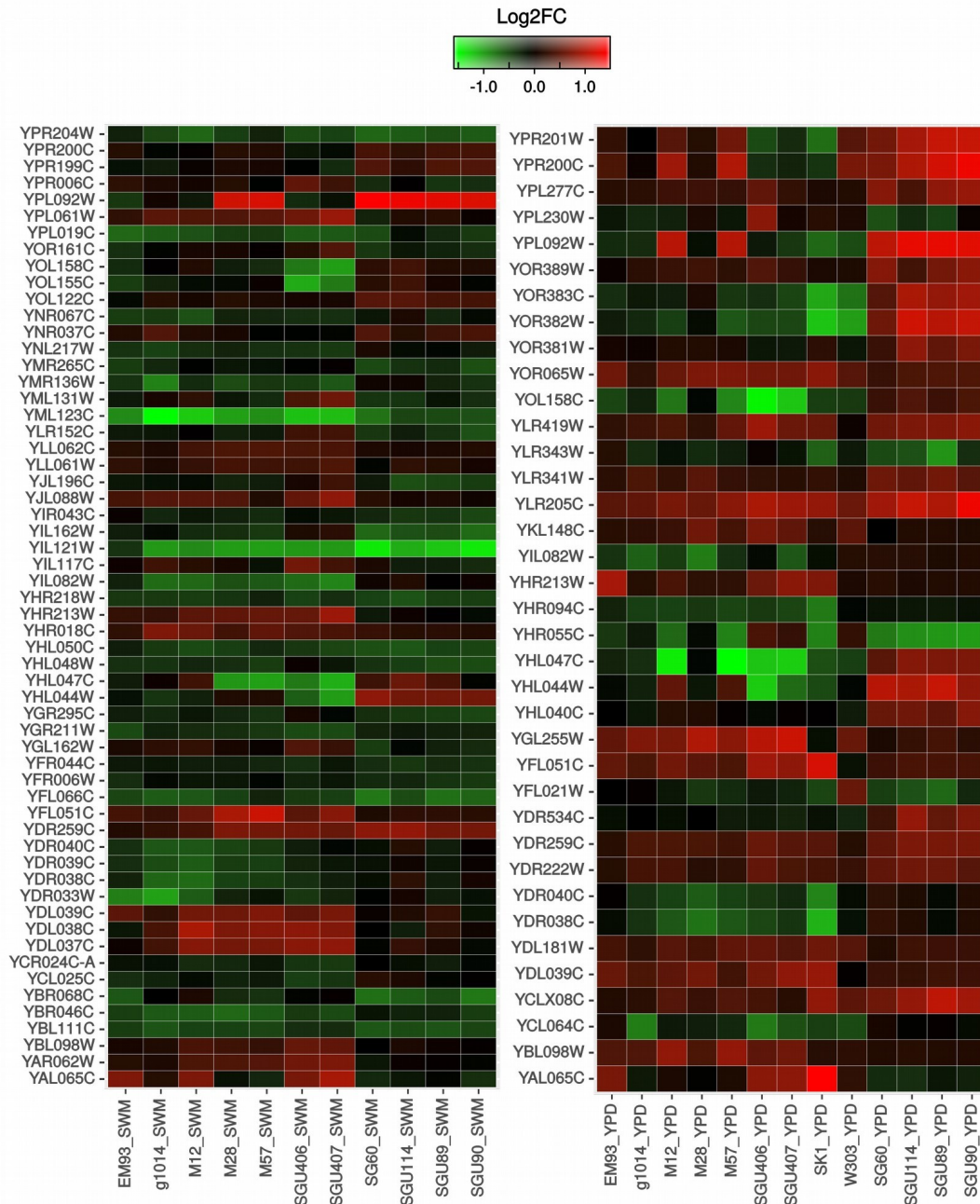


**Figure S3:**  
**Pulsed-Field Gel Electrophoresis (PFGE) and ARR1 or ARR3 hybridization confirm the new location of ARR genes cluster in strains resistant to arsenic.** After the PFGE run, DNA was transferred through southern blot and hybridised with *ARR1* or *ARR2* labelled probes. Colored rectangles represent the bands identified through *ARR1*, *ARR3*, or both genes hybridization, as indicated in the legend at the bottom of the figure. The tested strain names are listed on top of the figure. Strains resistant to arsenic are SG60, SGU89, SGU90, and SGU114. Missing labels refer to strains not investigated in other assays.



**Figure S4:**

**Heatmap of genes differentially expressed in YPD or SWM.** heatmap reporting the expression levels of genes expressed at levels significantly differing among resistant and sensitive strains in either SWM (left) or YPD (right). Log2FC was calculated as the log2 transformation of the ratio: expression level (fluorescence of microarray hybridized gene) in the sample/ expression level in the control (BY4743 strains, grown in the same conditions of the sample). Only genes with Log2FC >0.5 or < -0.5 in at least three strains are shown.



## Supplementary results

### ARR1

SGU90_contig6667	AGATAATGGCAAAACCGCGTGGAAGAAAAGGCGGCAGGAAGCCTTCACTTACTCCACCTA	3273
SG60_contig8180	AGATAATGGCAAAACCGCGTGGAAGAAAAGGCGGCAGGAAGCCTTCACTTACTCCACCTA	3397
EM93_cotig25909	AGATAATGGCAAAACCGCGTGGAAGAAAAGGCGGCAGGAAGCCTTCACTTACTCCACCTA	3750
1014_contig8644	AGATAATGGCAAAACCGCGTGGAAGAAAAGGCGGCAGGAAGCCTTCACTTACTCCACCTA	4080
ARR1	-----ATGGCAAAACCGCGTGGAAGAAAAGGCGGCAGGAAGCCTTCACTTACTCCACCTA	55
*****		
SGU90_contig6667	AAAATAAGAGAGCTGCGCAACTTAGAGCATCCCAAAACGCATTTAGAAAACGAAAGTTGG	3333
SG60_contig8180	AAAATAAGAGAGCTGCGCAACTTAGAGCATCCCAAAACGCATTTAGAAAACGAAAGTTGG	3457
EM93_cotig25909	AAAATAAGAGAGCTGCGCAACTTAGAGCATCCCAAAACGCATTTAGAAAACGAAAGTTGG	3810
1014_contig8644	AAAATAAGAGAGCTGCGCAACTTAGAGCATCCCAAAACGCATTTAGAAAACGAAAGTTGG	4140
ARR1	AAAATAAGAGAGCTGCGCAACTTAGAGCATCCCAAAACGCATTTAGAAAACGAAAGTTGG	115
*****		
SGU90_contig6667	AAAGATTAGAAGAACTAGAGAAGAAAGAAGCTCAGCTAACGGTAACAAATGATCAAATTC	3393
SG60_contig8180	AAAGATTAGAAGAACTAGAGAAGAAAGAAGCTCAGCTAACGGTAACAAATGATCAAATTC	3517
EM93_cotig25909	AAAGATTAGAAGAACTAGAGAAGAAAGAAGCTCAGCTAACGGTAACAAATGATCAAATTC	3870
1014_contig8644	AAAGATTAGAAGAACTAGAGAAGAAAGAAGCTCAGCTAACGGTAACAAATGATCAAATTC	4200
ARR1	AAAGATTAGAAGAACTAGAGAAGAAAGAAGCTCAGCTAACGGTAACAAATGATCAAATTC	175
*****		
SGU90_contig6667	ACATATTAAAGAAGGAAAAATGAACCTCTCCATTTTATGTTGAGGAGTCTTTTGACTGAGA	3453
SG60_contig8180	ACATATTAAAGAAGGAAAAATGAACCTCTCCATTTTATGTTGAGGAGTCTTTTGACTGAGA	3577
EM93_cotig25909	ACATATTAAAGAAGGAAAAATGAACCTCTCCATTTTATGTTGAGGAGTCTTTTGACTGAGA	3930
1014_contig8644	ACATATTAAAGAAGGAAAAATGAACCTCTCCATTTTATGTTGAGGAGTCTTTTGACTGAGA	4260
ARR1	ACATATTAAAGAAGGAAAAATGAACCTCTCCATTTTATGTTGAGGAGTCTTTTGACTGAGA	235
*****		
SGU90_contig6667	GGAACATGCCTTCTGATGAACGGAACATTAGTAAGGCCTGTTGTGAAGAAAAACCGCCCA	3513
SG60_contig8180	GGAACATGCCTTCTGATGAACGGAACATTAGTAAGGCCTGTTGTGAAGAAAAACCGCCCA	3637
EM93_cotig25909	GGAACATGCCTTCTGATGAACGGAACATTAGTAAGGCCTGTTGTGAAGAAAAACCGCCCA	3990
1014_contig8644	GGAACATGCCTTCTGATGAACGGAACATTAGTAAGGCCTGTTGTGAAGAAAAACCGCCCA	4320
ARR1	GGAACATGCCTTCTGATGAACGGAACATTAGTAAGGCCTGTTGTGAAGAAAAACCGCCCA	295
*****		
SGU90_contig6667	CATGTAACACTCTCGATGGTAGTGTGGTTCTTTCCCTCCACATATAATTCCCTTGAAATAC	3573
SG60_contig8180	CATGTAACACTCTCGATGGTAGTGTGGTTCTTTCCCTCCACATATAATTCCCTTGAAATAC	3697
EM93_cotig25909	CATGTAACACTCTCGATGGTAGTGTGGTTCTTTCCCTCCACATATAATTCCCTTGAAATAC	4050
1014_contig8644	CATGTAACACTCTCGATGGTAGTGTGGTTCTTTCCCTCCACATATAATTCCCTTGAAATAC	4380
ARR1	CATGTAACACTCTCGATGGTAGTGTGGTTCTTTCCCTCCACATATAATTCCCTTGAAATAC	355
*****		
SGU90_contig6667	AACAATGCTACGTATTTTTCAAGCAACTGCTCTCAGTGTGTGTTGGAAAGAATTGTACAG	3633
SG60_contig8180	AACAATGCTACGTATTTTTCAAGCAACTGCTCTCAGTGTGTGTTGGAAAGAATTGTACAG	3757
EM93_cotig25909	AACAATGCTACGTATTTTTCAAGCAACTGCTCTCAGTGTGTGTTGGAAAGAATTGTACAG	4110
1014_contig8644	AACAATGCTACGTATTTTTCAAGCAACTGCTCTCAGTGTGTGTTGGAAAGAATTGTACAG	4440
ARR1	AACAATGCTACGTATTTTTCAAGCAACTGCTCTCAGTGTGTGTTGGAAAGAATTGTACAG	415
*****		
SGU90_contig6667	TGCCGTCACCGTTGAATTCCTTTGATCGGTCCTTCTATCCCATAGGCTGTACGAATCTCT	3693
SG60_contig8180	TGCCGTCACCGTTGAATTCCTTTGATCGGTCCTTCTATCCCATAGGCTGTACGAATCTCT	3817
EM93_cotig25909	TGCCGTCACCGTTGAATTCCTTTGATCGGTCCTTCTATCCCATAGGCTGTACGAATCTCT	4170
1014_contig8644	TGCCGTCACCGTTGAATTCCTTTGATCGGTCCTTCTATCCCATAGGCTGTACGAATCTCT	4500
ARR1	TGCCGTCACCGTTGAATTCCTTTGATCGGTCCTTCTATCCCATAGGCTGTACGAATCTCT	475
*****		
SGU90_contig6667	CAAATGACATACCAGGCTATTCTTTTCTAAATGATGCAATGAGTGAGATTCATACGTTTG	3753
SG60_contig8180	CAAATGACATACCAGGCTATTCTTTTCTAAATGATGCAATGAGTGAGATTCATACGTTTG	3877
EM93_cotig25909	CAAATGACATACCAGGCTATTCTTTTCTAAATGATGCAATGAGTGAGATTCATACGTTTG	4230
1014_contig8644	CAAATGACATACCAGGCTATTCTTTTCTAAATGATGCAATGAGTGAGATTCATACGTTTG	4560
ARR1	CAAATGACATACCAGGCTATTCTTTTCTAAATGATGCAATGAGTGAGATTCATACGTTTG	535
*****		
SGU90_contig6667	GTGACTTTAATGGGGAACCTTGATAGTACCTTTTTGGAGTTTAGTGGGACTGAAATAAAGG	3813
SG60_contig8180	GTGACTTTAATGGGGAACCTTGATAGTACCTTTTTGGAGTTTAGTGGGACTGAAATAAAGG	3937
EM93_cotig25909	GTGACTTTAATGGGGAACCTTGATAGTACCTTTTTGGAGTTTAGTGGGACTGAAATAAAGG	4290
1014_contig8644	GTGACTTTAATGGGGAACCTTGATAGTACCTTTTTGGAGTTTAGTGGGACTGAAATAAAGG	4620
ARR1	GTGACTTTAATGGGGAACCTTGATAGTACCTTTTTGGAGTTTAGTGGGACTGAAATAAAGG	595
*****		

SGU90_contig6667	AGCCAAATAATTTCTATTACTGAAAACACTAATGCAATAGAAAACAGCGGCAGCGAGCATGG	3873
SG60_contig8180	AGCCAAATAATTTCTATTACTGAAAACACTAATGCAATAGAAAACAGCGGCAGCGAGCATGG	3997
EM93_cotig25909	AGCCAAATAATTTCTATTACTGAAAACACTAATGCAATAGAAAACAGCGGCAGCGAGCATGG	4350
1014_contig8644	AGCCAAATAATTTCTATTACTGAAAACACTAATGCAATAGAAAACAGCGGCAGCGAGCATGG	4680
ARR1	AGCCAAATAATTTCTATTACTGAAAACACTAATGCAATAGAAAACAGCGGCAGCGAGCATGG *****	655
SGU90_contig6667	TGATTAGGCAGGGTTTCCATCCAAGACAGTATTATACAGTGGATGCTTTTGGAGGGGACG	3933
SG60_contig8180	TGATTAGGCAGGGTTTCCATCCAAGACAGTATTATACAGTGGATGCTTTTGGAGGGGACG	4057
EM93_cotig25909	TGATTAGGCAGGGTTTCCATCCAAGACAGTATTATACAGTGGATGCTTTTGGAGGGGACG	4410
1014_contig8644	TGATTAGGCAGGGTTTCCATCCAAGACAGTATTATACAGTGGATGCTTTTGGAGGGGACG	4740
ARR1	TGATTAGGCAGGGTTTCCATCCAAGACAGTATTATACAGTGGATGCTTTTGGAGGGGACG *****	715
SGU90_contig6667	TCCTATTAAGTGCGATGGATATTTGGAGTTTTATGAAAGTGCATCCAAAGGTTAACACAT	3993
SG60_contig8180	TCCTATTAAGTGCGATGGATATTTGGAGTTTTATGAAAGTGCATCCAAAGGTTAACACAT	4117
EM93_cotig25909	TCCTATTAAGTGCGATGGATATTTGGAGTTTTATGAAAGTGCATCCAAAGGTTAACACAT	4470
1014_contig8644	TCCTATTAAGTGCGATGGATATTTGGAGTTTTATGAAAGTGCATCCAAAGGTTAACACAT	4800
ARR1	TCCTATTAAGTGCGATGGATATTTGGAGTTTTATGAAAGTGCATCCAAAGGTTAACACAT *****	775
SGU90_contig6667	TTGACCTTGAAATTTTGGGAACAGAACTTAAGAAAAGTGCTACGTGTTCTAATTTTGATA	4053
SG60_contig8180	TTGACCTTGAAATTTTGGGAACAGAACTTAAGAAAAGTGCTACGTGTTCTAATTTTGATA	4177
EM93_cotig25909	TTGACCTTGAAATTTTGGGAACAGAACTTAAGAAAAGTGCTACGTGTTCTAATTTTGATA	4530
1014_contig8644	TTGACCTTGAAATTTTGGGAACAGAACTTAAGAAAAGTGCTACGTGTTCTAATTTTGATA	4860
ARR1	TTGACCTTGAAATTTTGGGAACAGAACTTAAGAAAAGTGCTACGTGTTCTAATTTTGATA *****	835
SGU90_contig6667	TTTTAATTAGCCTCAAGCATTTTCATTAAGGTCTTTTCGTCAAAATTATAATATTCTTCCT	4113
SG60_contig8180	TTTTAATTAGCCTCAAGCATTTTCATTAAGGTCTTTTCGTCAAAATTATAATATTCTTCCT	4237
EM93_cotig25909	TTTTAATTAGCCTCAAGCATTTTCATTAAGGTCTTTTCGTCAAAATTATAATATTCTTCCT	4590
1014_contig8644	TTTTAATTAGCCTCAAGCATTTTCATTAAGGTCTTTTCGTCAAAATTATAATATTCTTCCT	4920
ARR1	TTTTAATTAGCCTCAAGCATTTTCATTAAGGTCTTTTCGTCAAAATTATAA----- *****	885

## ARR2

SG60_contig8180	GAAAACTTGACAATCCAGCAAGCGTAATGGTAAGCTTCATAACGCTCTAGGCAACTCAAGG	2739
SGU90_contig6667	GAAAACTTGACAATCCAGCAAGCGTAATGGTAAGCTTCATAACGCTCTAGGCAACTCAAGG	2615
EM93_cotig25909	GAAAACTTGACAATCCAGCAAGCGTAATGGTAAGCTTCATAACGCTCTAGGCAACTCAAGG	3091
1014_contig8644	GAAAACTTGACAATCCAGCAAGCGTAATGGTAAGCTTCATAACGCTCTAGGCAACTCAAGG	3420
ARR2	-----ATGGTAAGCTTCATAACGCTCTAGGCAACTCAAGG *****	34
SG60_contig8180	GCCTAATTGAAAATCAGAGGAAGGATTTTCAAGTTGTTGATCTTCGAAGAGAAGATTTTG	2799
SGU90_contig6667	GCCTAATTGAAAATCAGAGGAAGGATTTTCAAGTTGTTGATCTTCGAAGAGAAGATTTTG	2675
EM93_cotig25909	GCCTAATTGAAAATCAGAGGAAGGATTTTCAAGTTGTTGATCTTCGAAGAGAAGATTTTG	3151
1014_contig8644	GCCTAATTGAAAATCAGAGGAAGGATTTTCAAGTTGTTGATCTTCGAAGAGAAGATTTTG	3480
ARR2	GCCTAATTGAAAATCAGAGGAAGGATTTTCAAGTTGTTGATCTTCGAAGAGAAGATTTTG *****	94
SG60_contig8180	CACGTGATCATATTACAAACGCTTGGCATGTTCCAGTAACAGCACAGATTACAGAGAAGC	2859
SGU90_contig6667	CACGTGATCATATTACAAACGCTTGGCATGTTCCAGTAACAGCACAGATTACAGAGAAGC	2735
EM93_cotig25909	CACGTGATCATATTACAAACGCTTGGCATGTTCCAGTAACAGCACAGATTACAGAGAAGC	3211
1014_contig8644	CACGTGATCATATTACAAACGCTTGGCATGTTCCAGTAACAGCACAGATTACAGAGAAGC	3540
ARR2	CACGTGATCATATTACAAACGCTTGGCATGTTCCAGTAACAGCACAGATTACAGAGAAGC *****	154
SG60_contig8180	AACTGAATCAATTAATTAAGGTTTATCGGATACTTTCTCAAGTTCTCAATTTCGTCAAAG	2919
SGU90_contig6667	AACTGAATCAATTAATTAAGGTTTATCGGATACTTTCTCAAGTTCTCAATTTCGTCAAAG	2795
EM93_cotig25909	AACTGAATCAATTAATTAAGGTTTATCGGATACTTTCTCAAGTTCTCAATTTCGTCAAAG	3271
1014_contig8644	AACTGAATCAATTAATTAAGGTTTATCGGATACTTTCTCAAGTTCTCAATTTCGTCAAAG	3600
ARR2	AACTGAATCAATTAATTAAGGTTTATCGGATACTTTCTCAAGTTCTCAATTTCGTCAAAG *****	214
SG60_contig8180	TGATATTTTCATTGTACTGGGTCCAAGAATAGGGGACCAAAAGTAGCTGCTAAATTCGAAA	2979
SGU90_contig6667	TGATATTTTCATTGTACTGGGTCCAAGAATAGGGGACCAAAAGTAGCTGCTAAATTCGAAA	2855
EM93_cotig25909	TGATATTTTCATTGTACTGGGTCCAAGAATAGGGGACCAAAAGTAGCTGCTAAATTCGAAA	3331
1014_contig8644	TGATATTTTCATTGTACTGGGTCCAAGAATAGGGGACCAAAAGTAGCTGCTAAATTCGAAA	3660
ARR2	TGATATTTTCATTGTACTGGGTCCAAGAATAGGGGACCAAAAGTAGCTGCTAAATTCGAAA *****	274
SG60_contig8180	CCTACTTACAAGAAGAAGATATTACAAGTAAGTTTGAGAGTTGCATCCTCGTTGGAGGTT	3039
SGU90_contig6667	CCTACTTACAAGAAGAAGATATTACAAGTAAGTTTGAGAGTTGCATCCTCGTTGGAGGTT	2915

EM93_cotig25909	CCTACTTACAAGAAGAAGATATTACAAGTAAGTTTGAGAGTTGCATCCTCGTTGGAGGTT	3391
1014_contig8644	CCTACTTACAAGAAGAAGATATTACAAGTAAGTTTGAGAGTTGCATCCTCGTTGGAGGTT	3720
ARR2	CCTACTTACAAGAAGAAGATATTACAAGTAAGTTTGAGAGTTGCATCCTCGTTGGAGGTT	334
	*****	

SG60_contig8180	TTTACGCTTGGGAGACCCATTGTAGAGAGAGTAACCTTAAATTGATTGTTAGTGGTTGAG	3099
SGU90_contig6667	TTTACGCTTGGGAGACCCATTGTAGAGAGAGTAACCTTAAATTGATTGTTAGTGGTTGAG	2975
EM93_cotig25909	TTTACGCTTGGGAGACCCATTGTAGAGAGAGTAACCTTAAATTGATTGTTAGTGGTTGAG	3451
1014_contig8644	TTTACGCTTGGGAGACCCATTGTAGAGAGAGTAACCTTAAATTGATTGTTAGTGGTTGAG	3780
ARR2	TTTACGCTTGGGAGACCCATTGTAGAGAGAGTAACCTTAAATTGATTGTTAGTGGTTGA-	393
	*****	

### ARR3

SGU90_contig6667	ATTAATTTCTATTGTTCCATATATAATATGGTTTAAAGGATCCTCGCGACTATTGCCAAAA	1175
SG60_contig8180	ATTAATTTCTATTGTTCCATATATAATATGGTTTAAAGGATCCTCGCGACTATTGCCAAAA	1299
EM93_cotig25909	ATTAATTTCTATTGTTCCATATATAATATGGTTTAAAGGATCCTCGCGACTATTGCCAAAA	1651
1014_contig8644	ATTAATTTCTATTGTTCCATATATAATATGGTTTAAAGGATCCTCGCGACTATTGCCAAAA	1980
ARR3_YPR201W	-TTAATTTCTATTGTTCCATATATAATATGGTTTAAAGGATCCTCGCGACTATTGCCAAAA	59
	*****	

SGU90_contig6667	TCAATAAAATTGGAACCTTCTAGCAACGGCCCAAATGTTGCAGCTATTGCTTGCTTGCTAT	1235
SG60_contig8180	TCAATAAAATTGGAACCTTCTAGCAACGGCCCAAATGTTGCAGCTATTGCTTGCTTGCTAT	1359
EM93_cotig25909	TCAATAAAATTGGAACCTTCTAGCAACGGCCCAAATGTTGCAGCTATTGCTTGCTTGCTAT	1711
1014_contig8644	TCAATAAAATTGGAACCTTCTAGCAACGGCCCAAATGTTGCAGCTATTGCTTGCTTGCTAT	2040
ARR3_YPR201W	TCAATAAAATTGGAACCTTCTAGCAACGGCCCAAATGTTGCAGCTATTGCTTGCTTGCTAT	119
	*****	

SGU90_contig6667	TGTTACCATATAAGGAAATAGCAATTGCCAGGGATAGTTCAAAATTATTTGAAGCCATAG	1295
SG60_contig8180	TGTTACCATATAAGGAAATAGCAATTGCCAGGGATAGTTCAAAATTATTTGAAGCCATAG	1419
EM93_cotig25909	TGTTACCATATAAGGAAATAGCAATTGCCAGGGATAGTTCAAAATTATTTGAAGCCATAG	1771
1014_contig8644	TGTTACCATATAAGGAAATAGCAATTGCCAGGGATAGTTCAAAATTATTTGAAGCCATAG	2100
ARR3_YPR201W	TGTTACCATATAAGGAAATAGCAATTGCCAGGGATAGTTCAAAATTATTTGAAGCCATAG	179
	*****	

SGU90_contig6667	TGAAACATTGCGTCATCGTAATAGAAAAGCTAGCTTCACAAGACTTTCTTCCCCAGACCC	1355
SG60_contig8180	TGAAACATTGCGTCATCGTAATAGAAAAGCTAGCTTCACAAGACTTTCTTCCCCAGACCC	1479
EM93_cotig25909	TGAAACATTGCGTCATCGTAATAGAAAAGCTAGCTTCACAAGACTTTCTTCCCCAGACCC	1831
1014_contig8644	TGAAACATTGCGTCATCGTAATAGAAAAGCTAGCTTCACAAGACTTTCTTCCCCAGACCC	2160
ARR3_YPR201W	TGAAACATTGCGTCATCGTAATAGAAAAGCTAGCTTCACAAGACTTTCTTCCCCAGACCC	239
	*****	

SGU90_contig6667	TCTTTAAAAGTAGTTCTTGGTCACAGCTACATTCTCTTTGTGTATCACTCCTAGATATTG	1415
SG60_contig8180	TCTTTAAAAGTAGTTCTTGGTCACAGCTACATTCTCTTTGTGTATCACTCCTAGATATTG	1539
EM93_cotig25909	TCTTTAAAAGTAGTTCTTGGTCACAGCTACATTCTCTTTGTGTATCACTCCTAGATATTG	1891
1014_contig8644	TCTTTAAAAGTAGTTCTTGGTCACAGCTACATTCTCTTTGTGTATCACTCCTAGATATTG	2220
ARR3_YPR201W	TCTTTAAAAGTAGTTCTTGGTCACAGCTACATTCTCTTTGTGTATCACTCCTAGATATTG	299
	*****	

SGU90_contig6667	ATAAGTACCTCATTAATGCGAAGGTCAAAAACCATGCAATAAAGAAGTAAAGCACCAATG	1475
SG60_contig8180	ATAAGTACCTCATTAATGCGAAGGTCAAAAACCATGCAATAAAGAAGTAAAGCACCAATG	1599
EM93_cotig25909	ATAAGTACCTCATTAATGCGAAGGTCAAAAACCATGCAATAAAGAAGTAAAGCACCAATG	1951
1014_contig8644	ATAAGTACCTCATTAATGCGAAGGTCAAAAACCATGCAATAAAGAAGTAAAGCACCAATG	2280
ARR3_YPR201W	ATAAGTACCTCATTAATGCGAAGGTCAAAAACCATGCAATAAAGAAGTAAAGCACCAATG	359
	*****	

SGU90_contig6667	GGACAAAGCACAAATATTGCAGAACCAATTTCTGGGATAAATTGATAACCTCTACTAATAA	1535
SG60_contig8180	GGACAAAGCACAAATATTGCAGAACCAATTTCTGGGATAAATTGATAACCTCTACTAATAA	1659
EM93_cotig25909	GGACAAAGCACAAATATTGCAGAACCAATTTCTGGGATAAATTGATAACCTCTACTAATAA	2011
1014_contig8644	GGACAAAGCACAAATATTGCAGAACCAATTTCTGGGATAAATTGATAACCTCTACTAATAA	2340
ARR3_YPR201W	GGACAAAGCACAAATATTGCAGAACCAATTTCTGGGATAAATTGATAACCTCTACTAATAA	419
	*****	

SGU90_contig6667	AAATAACAAATAAAGTGTAATGAAATCCGATCATTGCCCATGGAGAAATAAATCTCAAAA	1595
SG60_contig8180	AAATAACAAATAAAGTGTAATGAAATCCGATCATTGCCCATGGAGAAATAAATCTCAAAA	1719
EM93_cotig25909	AAATAACAAATAAAGTGTAATGAAATCCGATCATTGCCCATGGAGAAATAAATCTCAAAA	2071
1014_contig8644	AAATAACAAATAAAGTGTAATGAAATCCGATCATTGCCCATGGAGAAATAAATCTCAAAA	2400
ARR3_YPR201W	AAATAACAAATAAAGTGTAATGAAATCCGATCATTGCCCATGGAGAAATAAATCTCAAAA	479
	*****	

SGU90_contig6667	TGTATTTTTCATAATTACTTTTACCAGCTATGGTAAGACTTCCCAAACGTATGATAATGC	1655
SG60_contig8180	TGTATTTTTCATAATTACTTTTACCAGCTATGGTAAGACTTCCCAAACGTATGATAATGC	1779
EM93_cotig25909	TGTATTTTTCATAATTACTTTTACCAGCTATGGTAAGACTTCCCAAACGTATGATAATGC	2131
1014_contig8644	TGTATTTTTCATAATTACTTTTACCAGCTATGGTAAGACTTCCCAAACGTATGATAATGC	2460

ARR3_YPR201W	TGTATTTTTTCATAATTACTTTTACCAGCTATGGTAAGACTTCCCAAACGTATGATAATGC *****	539
SGU90_contig6667	CAATTCCCAGTGGTATGCCGAGAAAACTCCGACAGACTTTGCAACCTCTTCGAATAATA	1715
SG60_contig8180	CAATTCCCAGTGGTATGCCGAGAAAACTCCGACAGACTTTGCAACCTCTTCGAATAATA	1839
EM93_cotig25909	CAATTCCCAGTGGTATGCCGAGAAAACTCCGACAGACTTTGCAACCTCTTCGAATAATA	2191
1014_contig8644	CAATTCCCAGTGGTATGCCGAGAAAACTCCGACAGACTTTGCAACCTCTTCGAATAATA	2520
ARR3_YPR201W	CAATTCCCAGTGGTATGCCGAGAAAACTCCGACAGACTTTGCAACCTCTTCGAATAATA *****	599
SGU90_contig6667	CCCTATTTGAAGTATTTCAGGTGGTCATGAGAAATAACATAACAGTAAAATATCTGCAATG	1775
SG60_contig8180	CCCTATTTGAAGTATTTCAGGTGGTCATGAGAAATAACATAACAGTAAAATATCTGCAATG	1899
EM93_cotig25909	CCCTATTTGAAGTATTTCAGGTGGTCATGAGAAATAACATAACAGTAAAATATCTGCAATG	2251
1014_contig8644	CCCTATTTGAAGTATTTCAGGTGGTCATGAGAAATAACATAACAGTAAAATATCTGCAATG	2580
ARR3_YPR201W	CCCTATTTGAAGTATTTCAGGTGGTCATGAGAAATAACATAACAGTAAAATATCTGCAATG *****	659
SGU90_contig6667	GTGCATATAATACCATCTGTAAAAGCGAGTTTGTAAATAACAAGCAGCAGCAGAGATCAT	1835
SG60_contig8180	GTGCATATAATACCATCTGTAAAAGCGAGTTTGTAAATAACAAGCAGCAGCAGAGATCAT	1959
EM93_cotig25909	GTGCATATAATACCATCTGTAAAAGCGAGTTTGTAAATAACAAGCAGCAGCAGAGATCAT	2311
1014_contig8644	GTGCATATAATACCATCTGTAAAAGCGAGTTTGTAAATAACAAGCAGCAGCAGAGATCAT	2640
ARR3_YPR201W	GTGCATATAATACCATCTGTAAAAGCGAGTTTGTAAATAACAAGCAGCAGCAGAGATCAT *****	719
SGU90_contig6667	TGTCTCCTCCAGCAATCTGATTCCAAATTAGCACCATTGGCAATGCATCTAGCTACTCCGA	1895
SG60_contig8180	TGTCTCCTCCAGCAATCTGATTCCAAATTAGCACCATTGGCAATGCATCTAGCTACTCCGA	2019
EM93_cotig25909	TGTCTCCTCCAGCAATCTGATTCCAAATTAGCACCATTGGCAATGCATCTAGCTACTCCGA	2371
1014_contig8644	TGTCTCCTCCAGCAATCTGATTCCAAATTAGCACCATTGGCAATGCATCTAGCTACTCCGA	2700
ARR3_YPR201W	TGTCTCCTCCAGCAATCTGATTCCAAATTAGCACCATTGGCAATGCATCTAGCTACTCCGA *****	779
SGU90_contig6667	TCATAATAATGCCTTGACGGTATTCTTATAATCGAATAGCGCCATCCACGCCAATGCTG	1955
SG60_contig8180	TCATAATAATGCCTTGACGGTATTCTTATAATCGAATAGCGCCATCCACGCCAATGCTG	2079
EM93_cotig25909	TCATAATAATGCCTTGACGGTATTCTTATAATCGAATAGCGCCATCCACGCCAATGCTG	2431
1014_contig8644	TCATAATAATGCCTTGACGGTATTCTTATAATCGAATAGCGCCATCCACGCCAATGCTG	2760
ARR3_YPR201W	TCATAATAATGCCTTGACGGTATTCTTATAATCGAATAGCGCCATCCACGCCAATGCTG *****	839
SGU90_contig6667	TCATCAACAAGGACCGATGACCCAAATTCAAAAATAACGAGAGGGCTAGTTGCTTCCTTA	2015
SG60_contig8180	TCATCAACAAGGACCGATGACCCAAATTCAAAAATAACGAGAGGGCTAGTTGCTTCCTTA	2139
EM93_cotig25909	TCATCAACAAGGACCGATGACCCAAATTCAAAAATAACGAGAGGGCTAGTTGCTTCCTTA	2491
1014_contig8644	TCATCAACAAGGACCGATGACCCAAATTCAAAAATAACGAGAGGGCTAGTTGCTTCCTTA	2820
ARR3_YPR201W	TCATCAACAAGGACCGATGACCCAAATTCAAAAATAACGAGAGGGCTAGTTGCTTCCTTA *****	899
SGU90_contig6667	TATAGCTCCTGTAGAAGTACTTGTGAATAGACTCCCAGGAAACTTTGCAGATCGGGGGAA	2075
SG60_contig8180	TATAGCTCCTGTAGAAGTACTTGTGAATAGACTCCCAGGAAACTTTGCAGATCGGGGGAA	2199
EM93_cotig25909	TATAGCTCCTGTAGAAGTACTTGTGAATAGACTCCCAGGAAACTTTGCAGATCGGGGGAA	2551
1014_contig8644	TATAGCTCCTGTAGAAGTACTTGTGAATAGACTCCCAGGAAACTTTGCAGATCGGGGGAA	2880
ARR3_YPR201W	TATAGCTCCTGTAGAAGTACTTGTGAATAGACTCCCAGGAAACTTTGCAGATCGGGGGAA *****	959
SGU90_contig6667	TCATCATTACAATCATACCAACAGTCAAAGGAATGGACACTCCCATTAGATTGGGATGAC	2135
SG60_contig8180	TCATCATTACAATCATACCAACAGTCAAAGGAATGGACACTCCCATTAGATTGGGATGAC	2259
EM93_cotig25909	TCATCATTACAATCATACCAACAGTCAAAGGAATGGACACTCCCATTAGATTGGGATGAC	2611
1014_contig8644	TCATCATTACAATCATACCAACAGTCAAAGGAATGGACACTCCCATTAGATTGGGATGAC	2940
ARR3_YPR201W	TCATCATTACAATCATACCAACAGTCAAAGGAATGGACACTCCCATTAGATTGGGATGAC *****	1019
SGU90_contig6667	CTTCAGCGTCAAAAGTGTGACGGGAAGAAGGCACATAGACAGAAATTATTACTGCAATGA	2195
SG60_contig8180	CTTCAGCGTCAAAAGTGTGACGGGAAGAAGGCACATAGACAGAAATTATTACTGCAATGA	2319
EM93_cotig25909	CTTCAGCGTCAAAAGTGTGACGGGAAGAAGGCACATAGACAGAAATTATTACTGCAATGA	2671
1014_contig8644	CTTCAGCGTCAAAAGTGTGACGGGAAGAAGGCACATAGACAGAAATTATTACTGCAATGA	3000
ARR3_YPR201W	CTTCAGCGTCAAAAGTGTGACGGGAAGAAGGCACATAGACAGAAATTATTACTGCAATGA *****	1079
SGU90_contig6667	TTATGGAGAGAATTATAGTAAATGGCAACATCAAGTCAAGCCATGACAATGACTTGATCG	2255
SG60_contig8180	TTATGGAGAGAATTATAGTAAATGGCAACATCAAGTCAAGCCATGACAATGACTTGATCG	2379
EM93_cotig25909	TTATGGAGAGAATTATAGTAAATGGCAACATCAAGTCAAGCCATGACAATGACTTGATCG	2731
1014_contig8644	TTATGGAGAGAATTATAGTAAATGGCAACATCAAGTCAAGCCATGACAATGACTTGATCG	3060
ARR3_YPR201W	TTATGGAGAGAATTATAGTAAATGGCAACATCAAGTCAAGCCATGACAATGACTTGATCG *****	1139
SGU90_contig6667	TAGTCAGTATATCGGTGCGATTACCATATTAACCTTAGAAGGTACCGAATTTTCACTTT	2315
SG60_contig8180	TAGTCAGTATATCGGTGCGATTACCATATTAACCTTAGAAGGTACCGAATTTTCACTTT	2439

EM93_cotig25909	TAGTCAGTATATCGGTGCGATTACCATATTAACCTTAGAAGGTACCGAATTTTCACTTT	2791
1014_contig8644	TAGTCAGTATATCGGTGCGATTACCATATTAACCTTAGAAGGTACCGAATTTTCACTTT	3120
ARR3_YPR201W	TAGTCAGTATATCGGTGCGATTACCATATTAACCTTAGAAGGTACCGAATTTTCACTTT	1199
	*****	
SGU90_contig6667	TTTGATCTTCTGACATTATTCTACTAACCTGATGATTTGTTGGTTGGGTTCTCTTGAATT	2375
SG60_contig8180	TTTGATCTTCTGACATTATTCTACTAACCTGATGATTTGTTGGTTGGGTTCTCTTGAATT	2499
EM93_cotig25909	TTTGATCTTCTGACATTATTCTACTAACCTGATGATTTGTTGGTTGGGTTCTCTTGAATT	2851
1014_contig8644	TTTGATCTTCTGACATTATTCTACTAACCTGATGATTTGTTGGTTGGGTTCTCTTGAATT	3180
ARR3_YPR201W	TTTGATCTTCTGACAT-----	1215
	*****	

Details of the assembly unitigs found to match with the *ARR* genes cluster in SG60 and SGU90. 1014 and EM93 (sensitive strains) unitigs are not reported because if partially matching with chr XVI the portion of the unitig not matching with chr XVI matched with multiple chromosomes. After the sequence of each relevant unitig (formatted as described in the color legend), the coordinates of the mapping are reported, with the position of the *ARR* genes cluster sequence being referred to the *ARR* genes cluster (considered to start from nucleotide 925,709 of chromosome XVI).

#### Color legend:

Mapping vs *ARR* genes cluster

Mapping vs chr VIII

Mapping vs chr XV

#### >SG60\_unitig 1787

TACAGTATTACTGATGATATGTTATTTAGTGCTGTCCGTATGTCCTCTGTTCTTTTTTGGGCTACAATTTAATTGATGGGGTGTATG  
CTTACGATATTTCAATTATGTTAATATTTAGTATGTTTATATCTTCTCATTAAATGAATGGTTAATTTTAA  
[matches with chr VIII from 555,989 to 556,053]  
[matches with *ARR* genes cluster from 16,636 to 16,730]

#### >SG60\_unitig5436

TTAGATTGGAATTCGAACCGCTTCTGCTCAACTAGAAAGGTGGCGTTTCAATAATTACATTCTTACGAAAAGCGTTTACATAACTGAATG  
ATAAATGGCATCATCAATACATATTACTGATGATATGTTATTTAGTGCTGTACGTATGCCCTCTGTTCTTTTTTGGGCTACAATTT  
AATTGATGGAGTGTATGTTTACGATATTTCAATTATGTTAATATTTAGTATGTTTATATCTTCTCATTAAATGAATAGTTAATTTTAC  
GTTTAGGTGA  
[mapping vs chr VIII (ref) from 555882 to 556053]  
[matches with *ARR* genes cluster from 16,636 to 16,741]

#### >SG60\_unitig6295

TCACCTAAACGTAAAAATTAATCTATTCATTAATGAGAAGATATAAACATACTAAATATTAACATAATTGAAATATCGTAAACATAACAC  
CCCATCAATTAAATTTGTAGCCCAAAAAAGAACAGGAGACATACGGACAGCACTAAATAACATATCATCAGTAATACTGTA  
[mapping vs chr VIII (ref) from 556052 to 555989]  
[matches with *ARR* genes cluster from 16,636 to 16,741]

#### >SG60\_unitig4277

TTTTTGAGCTTTCTAATAGTGCTCCTGAGCAAAAGATCCGGCATCTACGCTCAATCTCTATGTATCACTTTATCAAGAAATATGTATCT  
GATATCAAGAAATAGAAATGTAAGAAAATGAAATTAGATTATACAAGTTGTATTGAGAAAAGTGAAGAGAAACCTGTGAAATATGTTAAA  
ATCACAACACAACATTCTTGGCAAGTTTGTCTTGTATTGTAAAAATACTACCATCCCATCTTGTAGCAGTTTTGTGTTCAACAACAAAA  
ATATCCTTTGCAATTTTATCCAGCAATCTGAAATCGTGAGATACGACAACAACACCACCGTTAAATTCAGGATAGCTTCAGCCAAAGA  
ATCAATAGTTGGAATGTCCAGACCGTTAGTAGGTTTATCCAGTAGTAGAACATTGGGCTGCTCAAGGGCTAGCAATGCAAAAACAACAC  
GCGAAGCTTTGCTTCAGATAATGTACCCATTGGACCGTTTGACCTTCACCTGTTAAACCGTAAACGTCCTAATTGACCCCTCCAGTAT  
TGGAAATCTTTGTGAGATGTTTGGATATTTGTACGAACAATTCAGGGCAGATTTTGTAAATCTAATTGATCTTGAGAATGTTGTGA  
GTAAACTCCCAATTTAACATGTGTACGCCCTAAGAAACAGTGATATTCTATAGCCTGATTTTGCCTCGTTGGTTTTCTTAGGGCATAT  
TGCCTTCATGTATATTGAAGATTTTCTCTATGCTTTGTGTCTTAAAGCATAATTAACTCAACCAACCAACGATGTTTCAACAGCCAGA  
GGTTTCTTTTCACTTTTGAAGGTTAAAGCAATACTCCATTGAGGACCAGTTTCTCTCAAAAGGCTTTGTAGACATATGTCTTGAAT  
ACGTAGTGAGCACTTGTGGAATGCTTTCTTCTACCCGTTTATGGGTAAATCCATTTAATCGCTTCTCTTTAATTTACCACGTACGGAT  
GTAGCCTCTAGAAGATCTCAGTCTGATTCAATGCTCTAGTACCTCTAGTAATTATGAATTGAAAATCATGACTTAGGAAGGATTGACTG  
CGGACGTCGAAATCTGTGTGTTCCAATACCTCGGAGTTGCCTATAAAGGACCAGTAAAGGTTGTTTTTAAAGAATCCAGTTAGAGTTC  
AGCCCTTTCAGATCTTTGGGTAAGTACGGAATTTTGAATCCGCACTTGAAGTGTGCAATAGATACGTTGTTTCAATTTAGAAGTGGG  
CATACAACAATCTTTCTTTTCGGATGATACTGCTTGGACATGGTACGCTTTAGAGTTTTTATTCAGCTTCATGAAAAAATGCCATA  
CTGTGCTAAATATTGAAGACGTCGGTAAAGGGCTGCCATGTGCTCACATTTAATCCTACTCCTTATAATTATGGCAGTGATTGATCG  
GGTGGCACTAAATACCATATTAGGAACAATACATTCCCTTACGTAACGGAACCCCTAAAACGTCCTTTTTTGCAGGCTTAAATAATCA  
CAGTAGTTGCAGACGGCCTTATAGGCATATTGCGGGCTTTGCTATTCTGAAGGATGAGAAGTGAAGGAAATGCACTTTTATGAATCAA  
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GGTGGCGTTAGATTGTAAAGATTTTCATCGAAGATTTCTCCCTGTTCTGTCTCTCTCTTTCTGCCTCGAACAGAACTATCGAGTTCT  
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CCGAGTCTAGTAGCCCATAGGATGTCCATAAAAAATGCAGTCCACCATACTTTCTTCTTGCATCTGTTCTGCCTTCGGTCTGTCACAC  
ATTGCTTACTTCTCTATGCATCCCTAACATTATAGCAGTCGATAAGGCGAGCCAGTGTAGGTGAAACCAGAAATTTACTCTATTCCATC



CTTGAGAGTATATAGCAAAACAAAAGCAATGTTCTGACTGTATCTAAGGTGGGCTCTTCAATCGGTTTCATGGAATAATGTGAGGGCTGTC  
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ATTCATTTTTCTTCCATTTTTTTGATATCAGTGTCCAGCACTGAAATTTTTCCCTGGATTTTAAAGGGTAGGTGCAACTATTGCCATTGC  
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[matches with chr XV from 1,054,629 to 1,067,195]  
[matches with ARR genes cluster from 1483 to 1575]

>SGU90\_unitig1536

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[matches with chr VIII from 555989 to 556053]  
[matches with ARR genes cluster from 16,636 to 16,730]

>SGU90\_unitig1784

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[matches with chr VIII from 556161 to 555989]  
[matches with ARR genes cluster from 16,636 to 16,741]

>SGU90\_unitig4710

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[matches with ARR genes cluster from 16,636 to 16,741]

>SGU90\_unitig1284

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GTCTTCAATATTTAGCAGACGATATGGCAATTTTTTTCATGAAGCTGAATAAAAACTCTAAAGCGTACCATGTCCAGCAGTATCATCCG  
AAAGGAAAGATTGTTTGTATGCCCACTTCTAAATGAACAACGTATCTATTGCACACTTTCAAGTTGCGGATTTCAAAAATTTCCGTACTT  
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GTGAGATCTTCTAGAGGCTACATCCGTACGTGGTAAATTAAGAGAAGCGATTAAATGGATTTACCCATAACCGGTGAGAAGAAAGCAT

TCCACAAGTTGCTCACTACGTATTCAAGACATATGTCTACAAAGCCTTTGTGAGAATGAACTGGTCCTCAATGGAGTATTGCTTTAACC  
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TATCTGAAGGACAACGTTTCGCGTGTGTTTTTGCATTGCTAGCCCTTGAGCAGCCCAATGTTCTACTACTGGATGAACCTACTAACGGT  
CTGGACATTCCAACCTATTGATTCTTTGGCTGAAGCTATCCTTGAATTTAACGGTGGTGTGTTGTTGTCGTATCTCACGATTTTCAATTGCT  
GGATAAAATTGCAAAGGATATTTTTGTTGTTGAACACAAAACCTGCTACAAGATGGGATGGTAGTATTTTACAATACAAGAACAACCTTG  
CCAAGAATGTTGTGTTGTGATTTTAACATATTTACAGGTTTCTCTTCACTTTTCTCAATACAACCTGTATAATCTAATTTTCAATTTCT  
TACATTTCTATTCTTGATATCAGATACATATTTCTTGATAAAGTGATACATAGAGATTGAGCGTAGATGCCGGATCTTTTGCTCAGGAG  
CACTATTAGAAAGCTCAAAAAAA

[matches with DBVPG6765 chr XV from 1,067,200 to 1,069,547]

[matches with *ARR* genes cluster from 1,483 to 1,575]