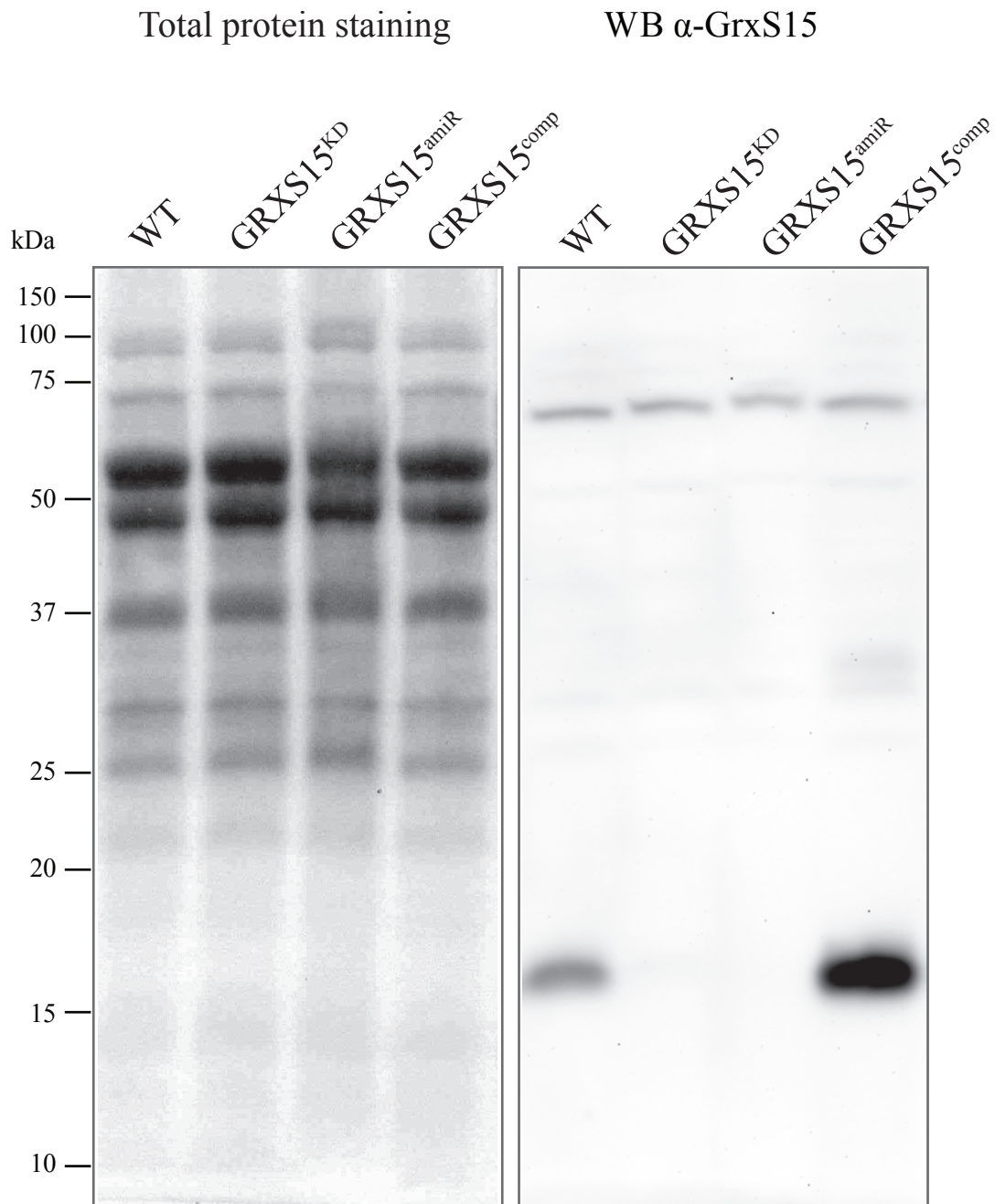


Supplementary Figure 1

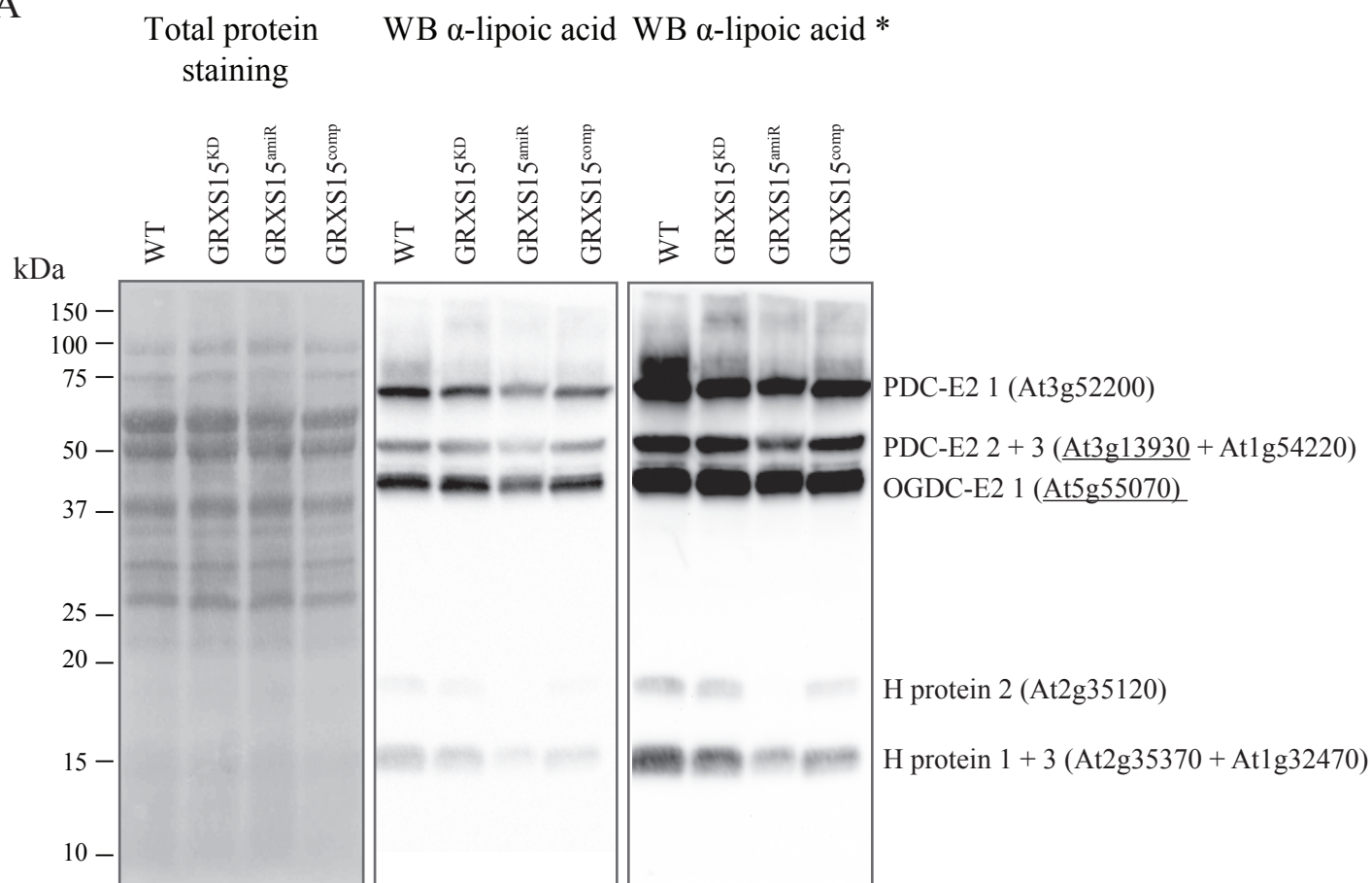
Phenotypic analysis of WT, GrxS15^{KD}, GrxS15^{amiR} and GrxS15^{comp}. Plants were grown under (A) long and short day conditions on soil and (B) long day conditions on MS agar plates. Exemplary images are shown.



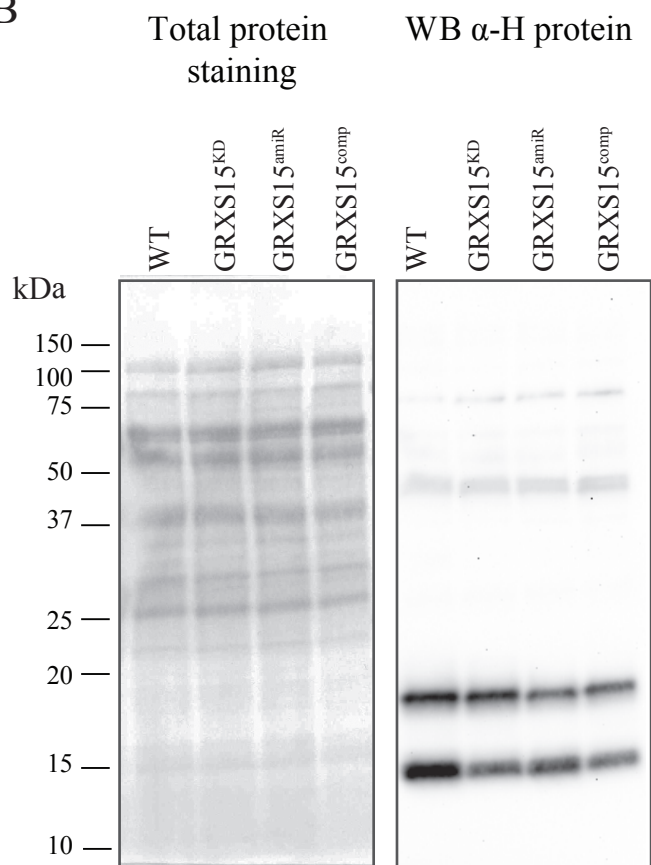
Supplementary Figure 2

Western blot of mitochondria isolated from whole tissue of WT, GrxS15^{KD}, GrxS15^{amiR} and GrxS15^{comp} using specific antibodies raised against GrxS15 (right). On the left, total protein staining of the membrane was performed with Ponceau and used for normalisation. N=4, exemplary image shown.

A

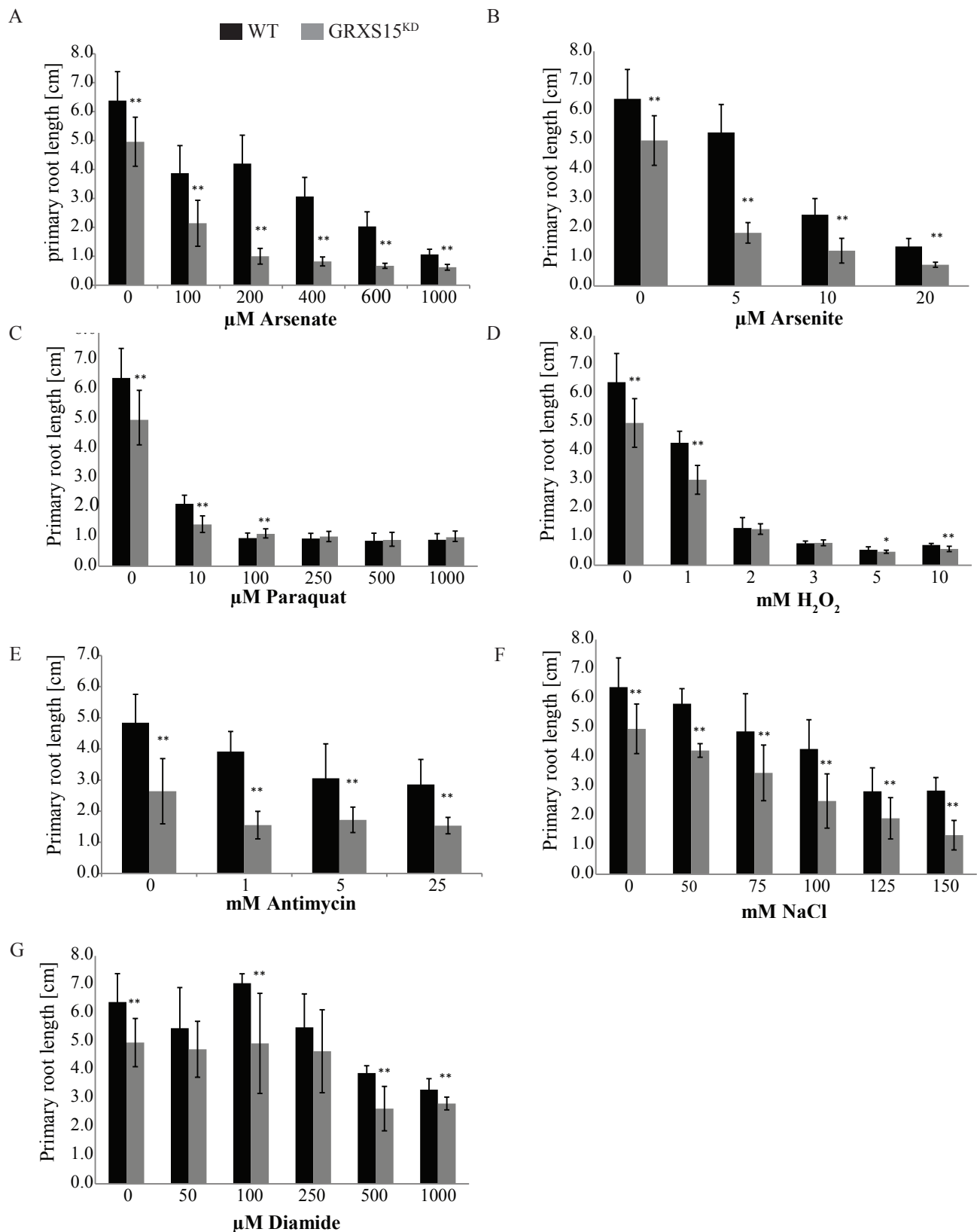


B



Supplementary Figure 3

Western blot of isolated mitochondria from whole tissue of WT, GrxS15^{KD}, GrxS15^{amiR} and GrxS15^{comp} using specific antibodies raised against lipoic acid (A) and H protein (B). On the left, total protein staining of the membrane was performed with Ponceau and used for normalisation. On the right, the fluorescent signal can be seen. In A, images are taken with different exposure times, * indicates the longer exposure time. Bands are labelled with protein name and AGI number. N=4 (anti-H protein), N=6 (anti-lipoic acid), exemplary images are shown.



Supplementary Figure 4

Analysis of primary root length of WT and GRXS15^{KD} grown on vertical MS agar plates for 10 d under medium day growth conditions. Different concentrations of the following effectors have been used: Arsenate (A), Arsenite (B), Paraquat (C), H₂O₂ (D), Antimycin (E), NaCl (F) and Diamide (G). Average and standard deviation are displayed. Student's *t*-test were performed, * indicates $p < 0.05$ ** indicates $p < 0.01$, $n = 6-32$.

Supplementary Figure 5. A two –way ANOVA with Tukey post hoc test for the rosette area data set using IBM SPSS version 21.

Tests of Between-Subjects Effects

Dependent Variable: area

Source	Type III Sum of Squares	df	Mean Square	F	Sig.
Corrected Model	22789.121 ^a	11	2071.738	74.672	.000
Intercept	53768.543	1	53768.543	1937.991	.000
genotype	14845.390	3	4948.463	178.359	.000
treatment	6393.443	2	3196.722	115.220	.000
genotype * treatment	1600.479	6	266.747	9.614	.000
Error	5992.806	216	27.744		
Total	80714.948	228			
Corrected Total	28781.927	227			

a. R Squared = .792 (Adjusted R Squared = .781)

Post Hoc Tests

genotype

Multiple Comparisons

Dependent Variable: area

Tukey HSD

(I) genotype	(J) genotype	Mean Difference (I-J)	Std. Error	Sig.	95% Confidence Interval	
					Lower Bound	Upper Bound
WT	GrxS15KD	11.6594*	.99105	.000	9.0934	14.2253
	GrxS15amiR	21.0883*	.98666	.000	18.5337	23.6429
	GrxS15comp	4.0822*	.98239	.000	1.5386	6.6257
GrxS15KD	WT	-11.6594*	.99105	.000	-14.2253	-9.0934
	GrxS15amiR	9.4289*	.99105	.000	6.8630	11.9949
	GrxS15comp	-7.5772*	.98681	.000	-10.1322	-5.0222
GrxS15amiR	WT	-21.0883*	.98666	.000	-23.6429	-18.5337
	GrxS15KD	-9.4289*	.99105	.000	-11.9949	-6.8630
	GrxS15comp	-17.0061*	.98239	.000	-19.5497	-14.4626
GrxS15comp	WT	-4.0822*	.98239	.000	-6.6257	-1.5386
	GrxS15KD	7.5772*	.98681	.000	5.0222	10.1322
	GrxS15amiR	17.0061*	.98239	.000	14.4626	19.5497

Based on observed means.

The error term is Mean Square(Error) = 27.744.

*. The mean difference is significant at the 0.05 level.

treatment

Multiple Comparisons

Dependent Variable: area

Tukey HSD

(I) treatment	(J) treatment	Mean Difference (I-J)	Std. Error	Sig.	95% ...
					Lower Bound
control	5 uM arsenite	11.7518*	.86539	.000	9.7095
	200 uM arsenate	11.5166*	.86792	.000	9.4683
5 uM arsenite	control	-11.7518*	.86539	.000	-13.7941
	200 uM arsenate	-.2351	.83546	.957	-2.2068
200 uM arsenate	control	-11.5166*	.86792	.000	-13.5649
	5 uM arsenite	.2351	.83546	.957	-1.7366

Supplementary Figure 6. A two –way ANOVA with Tukey post hoc test for the root length data set using IBM SPSS version 21.

Tests of Between-Subjects Effects

Dependent Variable: rootlength

Source	Type III Sum of Squares	df	Mean Square	F	Sig.
Corrected Model	291.777 ^a	11	26.525	258.134	.000
Intercept	625.019	1	625.019	6082.474	.000
genotype	153.394	3	51.131	497.595	.000
treatment	113.270	2	56.635	551.154	.000
genotype * treatment	27.207	6	4.534	44.128	.000
Error	34.115	332	.103		
Total	948.197	344			
Corrected Total	325.893	343			

a. R Squared = .895 (Adjusted R Squared = .892)

Post Hoc Tests

genotype

Multiple Comparisons

Dependent Variable: rootlength
Tukey HSD

(I) genotype	(J) genotype	Mean Difference (I-J)	Std. Error	Sig.	95% Confidence Interval	
					Lower Bound	Upper Bound
WT	GrxS15KD	1.0286 [*]	.04891	.000	.9023	1.1549
	GrxS15amir	1.7767 [*]	.04947	.000	1.6489	1.9044
	GrxS15comp	.4321 [*]	.04918	.000	.3051	.5591
GrxS15KD	WT	-1.0286 [*]	.04891	.000	-1.1549	-.9023
	GrxS15amir	.7480 [*]	.04862	.000	.6225	.8736
	GrxS15comp	-.5965 [*]	.04833	.000	-.7213	-.4717
GrxS15amir	WT	-1.7767 [*]	.04947	.000	-1.9044	-1.6489
	GrxS15KD	-.7480 [*]	.04862	.000	-.8736	-.6225
	GrxS15comp	-1.3445 [*]	.04889	.000	-1.4708	-1.2183
GrxS15comp	WT	-.4321 [*]	.04918	.000	-.5591	-.3051
	GrxS15KD	.5965 [*]	.04833	.000	.4717	.7213
	GrxS15amir	1.3445 [*]	.04889	.000	1.2183	1.4708

Based on observed means.

The error term is Mean Square(Error) = .103.

*. The mean difference is significant at the 0.05 level.

treatment

Multiple Comparisons

Dependent Variable: rootlength
Tukey HSD

(I) treatment	(J) treatment	Mean Difference (I-J)	Std. Error	Sig.	95% ...
					Lower Bound
control	5 uM arsenite	1.3890 [*]	.04228	.000	1.2895
	200 uM arsenate	.6444 [*]	.04228	.000	.5448
5 uM arsenite	control	-1.3890 [*]	.04228	.000	-1.4886
	200 uM arsenate	-.7447 [*]	.04246	.000	-.8446
200 uM arsenate	control	-.6444 [*]	.04228	.000	-.7439
	5 uM arsenite	.7447 [*]	.04246	.000	.6447

Supplementary Figure 7. A two –way ANOVA with Tukey post hoc test for the root tip respiration data set using IBM SPSS version 21.

Tests of Between-Subjects Effects

Dependent Variable: normOCR

Source	Type III Sum of Squares	df	Mean Square	F	Sig.
Corrected Model	2020072.53 ^a	11	183642.958	23.866	.000
Intercept	4193625.822	1	4193625.822	544.995	.000
genotype	1562016.074	3	520672.025	67.665	.000
treatment	225323.739	2	112661.870	14.641	.000
genotype * treatment	147410.496	6	24568.416	3.193	.005
Error	2008341.569	261	7694.795		
Total	9063262.953	273			
Corrected Total	4028414.103	272			

a. R Squared = .501 (Adjusted R Squared = .480)

Post Hoc Tests

genotype

Multiple Comparisons

Dependent Variable: normOCR

Tukey HSD

(I) genotype	(J) genotype	Mean Difference (I-J)	Std. Error	Sig.	95% Confidence Interval	
					Lower Bound	Upper Bound
WT	GrxS15KD	8.1693	15.10320	.949	-30.8824	47.2210
	GrxS15amiR	120.1868 [*]	15.10320	.000	81.1351	159.2385
	GrxS15comp	-97.9660 [*]	15.10320	.000	-137.0177	-58.9143
GrxS15KD	WT	-8.1693	15.10320	.949	-47.2210	30.8824
	GrxS15amiR	112.0175 [*]	14.93444	.000	73.4021	150.6329
	GrxS15comp	-106.1353 [*]	14.93444	.000	-144.7506	-67.5199
GrxS15amiR	WT	-120.1868 [*]	15.10320	.000	-159.2385	-81.1351
	GrxS15KD	-112.0175 [*]	14.93444	.000	-150.6329	-73.4021
	GrxS15comp	-218.1528 [*]	14.93444	.000	-256.7681	-179.5374
GrxS15comp	WT	97.9660 [*]	15.10320	.000	58.9143	137.0177
	GrxS15KD	106.1353 [*]	14.93444	.000	67.5199	144.7506
	GrxS15amiR	218.1528 [*]	14.93444	.000	179.5374	256.7681

Based on observed means.

The error term is Mean Square(Error) = 7694.795.

*. The mean difference is significant at the 0.05 level.

treatment

Multiple Comparisons

Dependent Variable: normOCR

Tukey HSD

(I) treatment	(J) treatment	Mean Difference (I-J)	Std. Error	Sig.	95% ...
					Lower Bound
control	5 uM arsenite	40.9355 [*]	13.36186	.007	9.4394
	200 uM arsenate	-45.6524 [*]	13.36186	.002	-77.1485
5 uM arsenite	control	-40.9355 [*]	13.36186	.007	-72.4316
	200 uM arsenate	-86.5879 [*]	16.01540	.000	-124.3388
200 uM arsenate	control	45.6524 [*]	13.36186	.002	14.1563
	5 uM arsenite	86.5879 [*]	16.01540	.000	48.8369