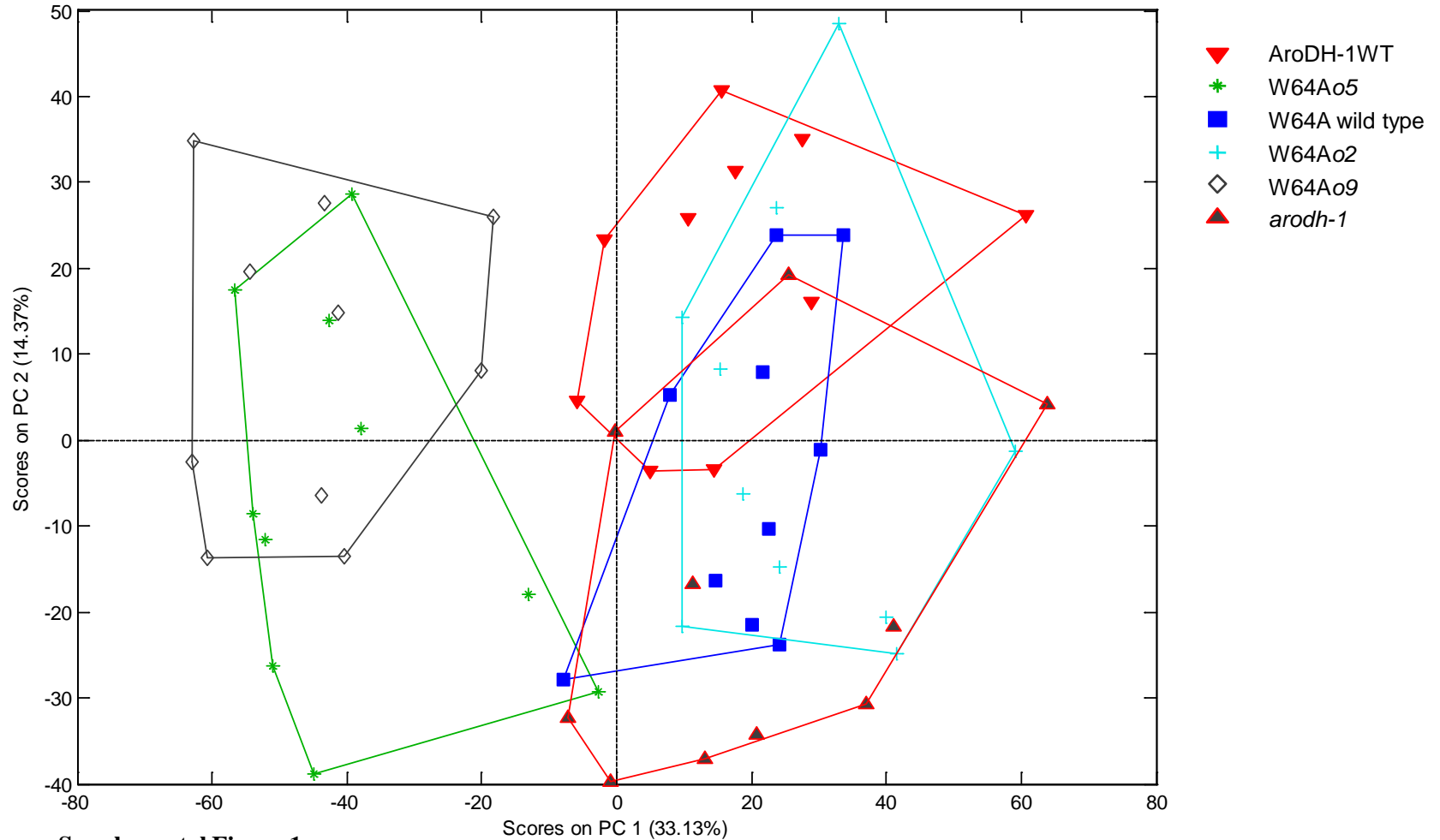


Identification and characterization of the maize arogenate dehydrogenase gene family

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Supplemental Figure 1. PCA metabolites in *arodh-1* and other W64A lines

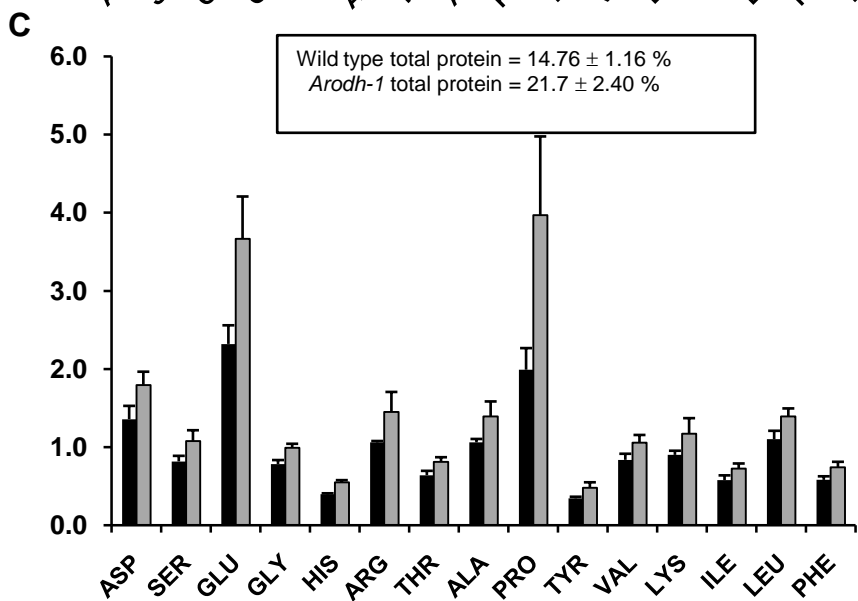
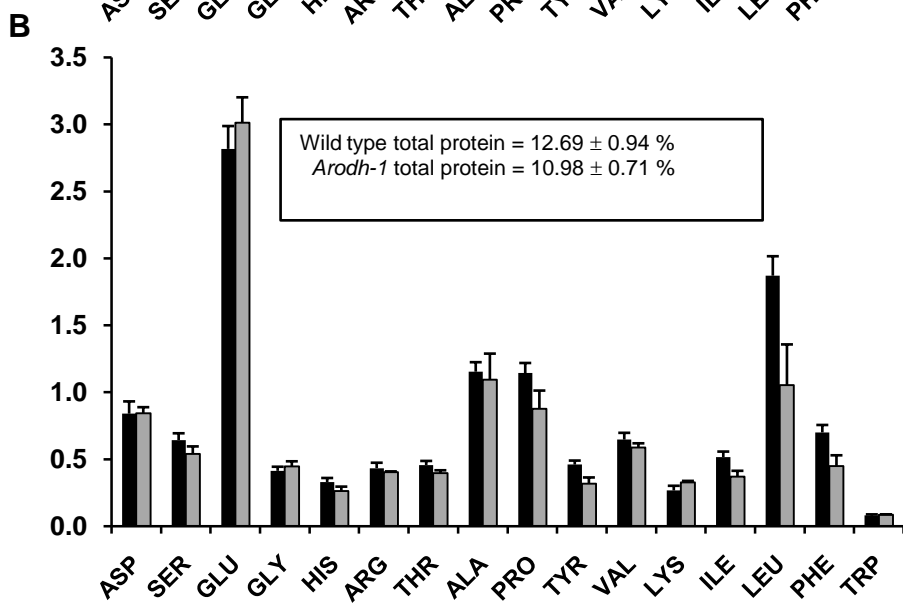
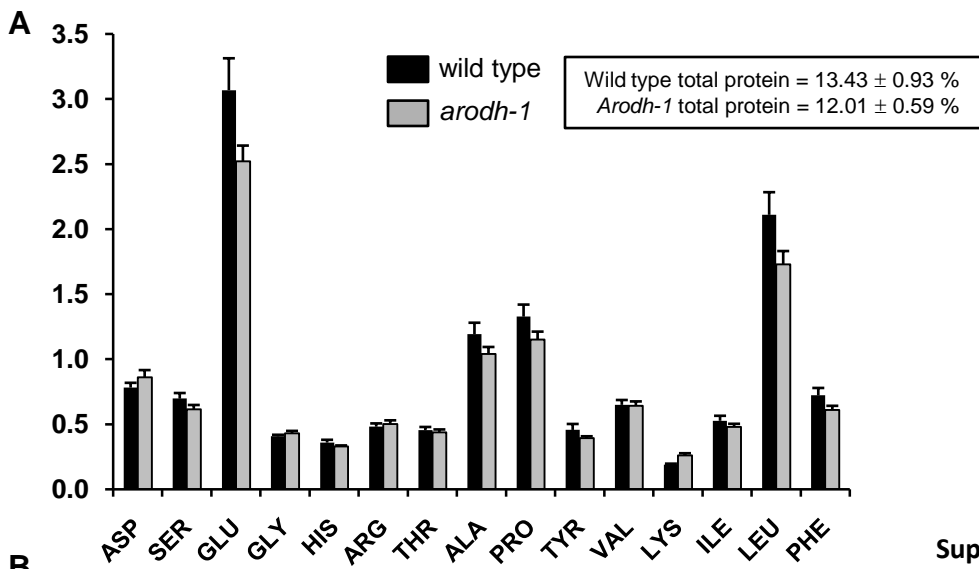


Supplemental Figure 1

Principle Component Analysis (PCA) scores plot of leaf tissue metabolite profiles obtained from W64A *arodh-1*, W64A *AroDH-1* wild-type isolate, W64Ao2, W64Ao5, W64o9 and W64A wild type.

PCA was performed on the m/z value \times retention time matrix of metabolite fingerprinting data following Z-scoring using the Eigenvector PLS Toolbox software. Group boundaries for samples of each genotype are shown with solid lines. The W64Ao5 and W64Ao9 sample groups form a cluster that is distinct from W64A *arodh-1*, which overlaps with sample groups of W64A wild type and W64Ao2.

Supplemental Figure 2. Protein bound amino acid content of *arodh-1* mutant and wild type tissues



Supplemental Figure 2
Protein bound amino acid profiles
of *arodh-1* mutant and wild type
tissues

A; mature endosperm, B; 20 DAP developing endosperm, C; 20 DAP developing embryo.

Key in A also refers to B and C. Values shown are % of endosperm dry weight \pm standard deviation (three biological replicates). Insert boxes showing total protein are also expressed as the percent of dry weight; tryptophan data were only available for developing endosperm samples.

Supplemental table 1. Data from MPSS analysis of Zm AroDH genes in wild type B73 maize tissues

	Chrm	Seed	Endosperm	Aleurone	Starchy endosperm	Chalazal endosperm	Embryo	Pericarp	Ear meristem	Silk	Tassel	Pollen	Anther	SAM	Leaf	Root	Stem
AroDH-1	5	233	129	74	28	240	23	178	133	89	0	0	128	175	274	534	286
AroDH-2	5	-	-	-	-	-	-	-	30	30	-	-	-	-	33	-	22
AroDH-3	6	49	27	82	-	96	-	72	-	24	112	-	187	11	448	459	336
AroDH-4	9	20	78	-	-	75	-	-	13	-	-	-	-	-	79	113	-