Supplementary Material

Supplementary Figure 1: **LRA2 is HSP90.2. (A)** Map based cloning of lra2 mutants began with genetic definition of a 52 kB interval on the lower arm of Chromosome V using the markers shown on the left and right. This region was contained on the P1 clone MDA7 (Kaneko et al., 1998). Candidate clones, including all three of the constitutively expressed cytosolic HSP90s in Arabidopsis, are given in green with the arrow pointing in the direction of transcription.

Supplementary Figure 2: **Phenotypic pleiotropy in hsp90.2 mutants suggests functions in additional Arabidopsis processes.** While overall morphology is unaffected (row 1), hsp90.2 mutants show slight flattening of the leaves (adaxial view row 2 and abaxial view row 3), and young flower buds are not completely closed (row 4). Leaves often appeared somewhat flattened in hsp90.2. We often found that all the buds in a flower cluster were slightly opened prematurely. We did not observe a difference in gross morphological architecture of the roots. These phenotypes were weak and the bud phenotype was variably penetrant in all hsp90.2 alleles, in contrast to the disease resistance phenotype. We recapitulated heat shock conditions known to cause loss of $R$ function in other systems, notably the tobacco $N$ gene, but failed to see an effect on $RPM1$ function in wild type plants at 30°C. These same conditions also revealed no pronounced phenotypic effects in hsp90.2 plants.

Supplementary Figure 3: **SGT1a and Sgt1b contain strong structural similarity to two different HSP90 co-chaperones, HOP and p23. (A)** The TPR motifs of AtSGT1s are predicted to fold like the TPR motif of the HSP90 co-chaperone, HOP (seen here).
(B) The CS domain found in AtSGT1s is predicted to fold in a similar conformation as p23 (seen here).
Sup. Fig. 1

A

Chromosome V
MDA7 551 T/A
1 Recombinant/
1878 Meioses

MDA7 52632 C/A
3 Recombinants/
1878 Meioses

P1 Clone MDA7
Unknown
Unknown
CBL2

HSP90.4
HSP90.2
Receptor kinase-like
Unknown

Unknown
Nicotianamine synthase
Unknown

Unknown
Similar to cytochrome oxidase assembly factor

SALK_058553 at 23453 bp
M558A
Sup. Fig. 2
Sup. Fig. 3