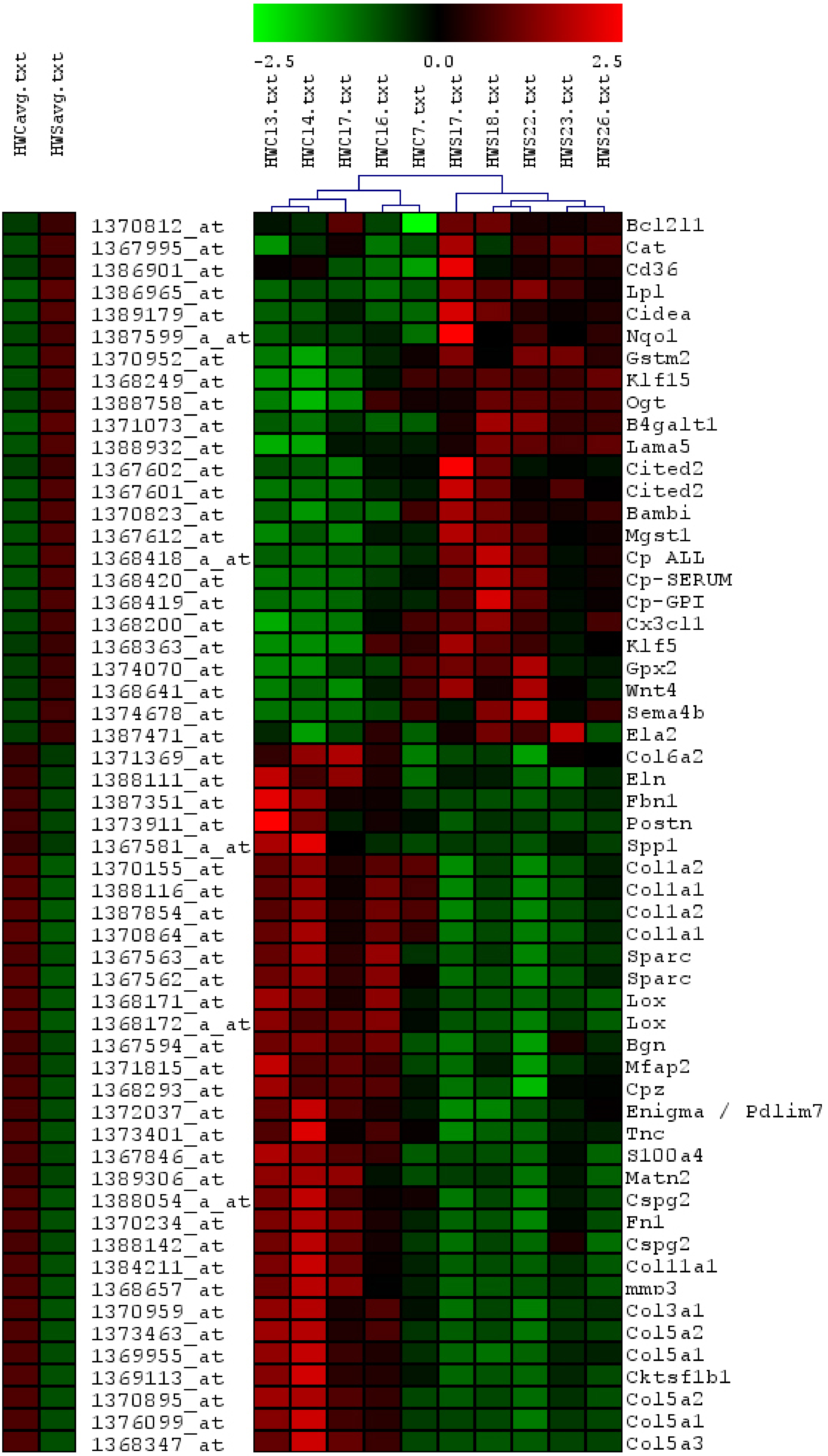
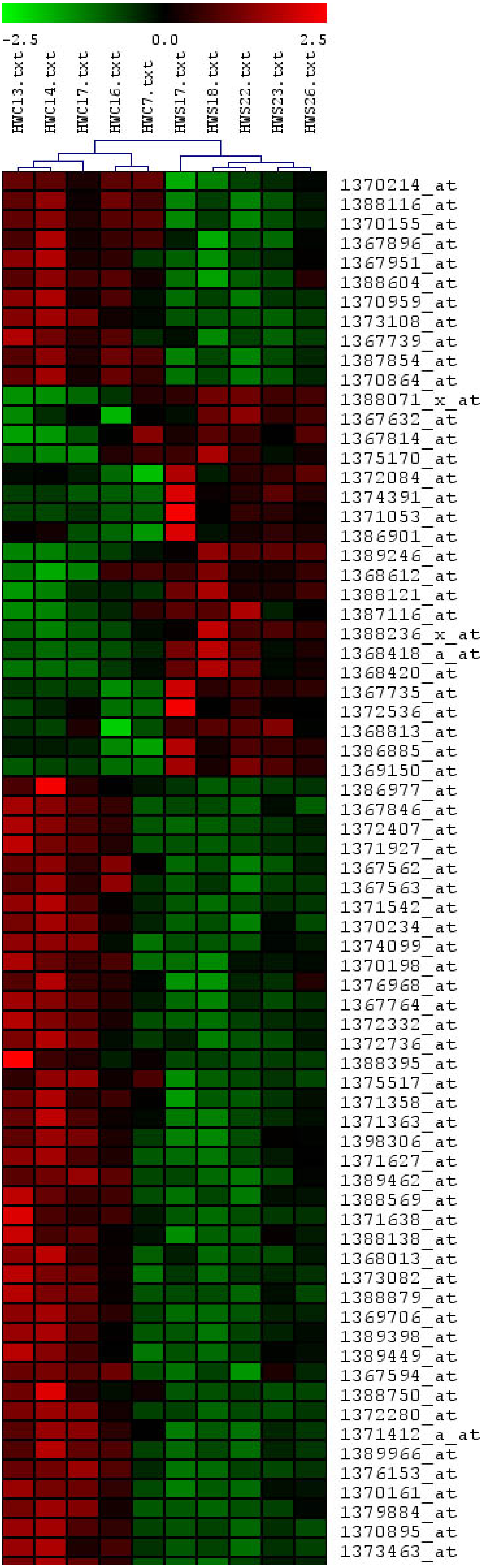


Supplemental Display of Array Data: TIGR MeV 3.1 software based hierarchical clustering of all control (HWC) and diabetic (HWS) samples using expression values (from the Affymetrix CHP files) for those genes considered significant. The above heat map displays those genes included in Tables 1 and 2. The included CHP values for each gene/row were normalized using MeV for display purposes. Thus, each CHP expression value was adjusted using the mean and the standard deviation of the row of the matrix to which the value belongs, using the following formula:

value = [(value) – mean(gene)]/[standard deviation(gene)]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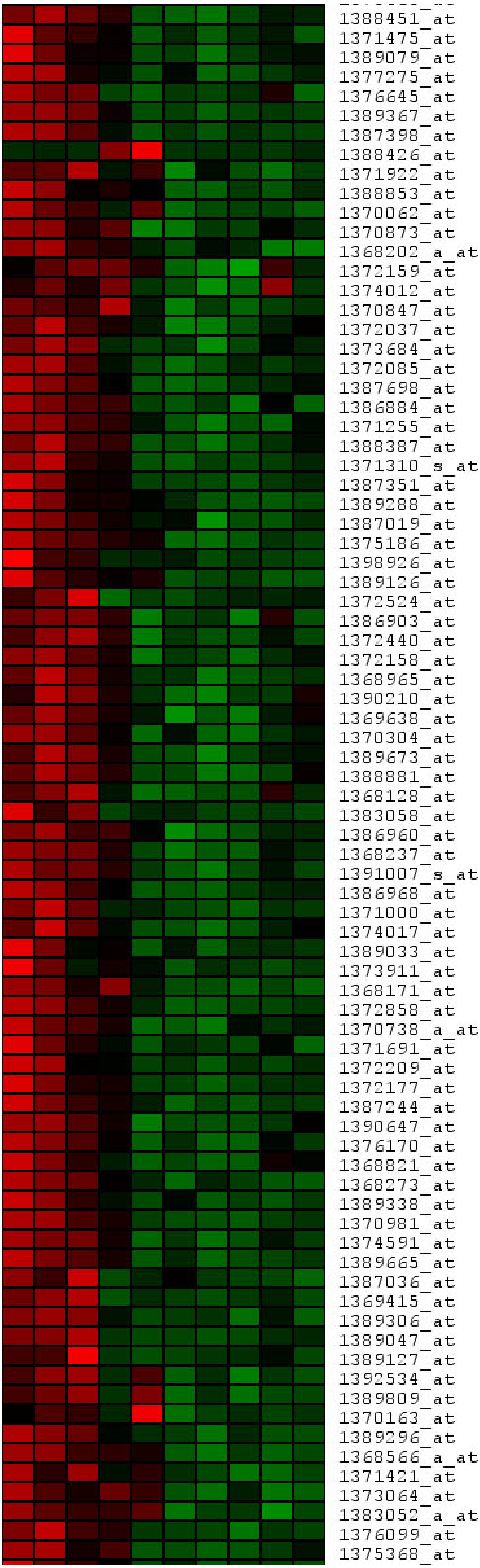
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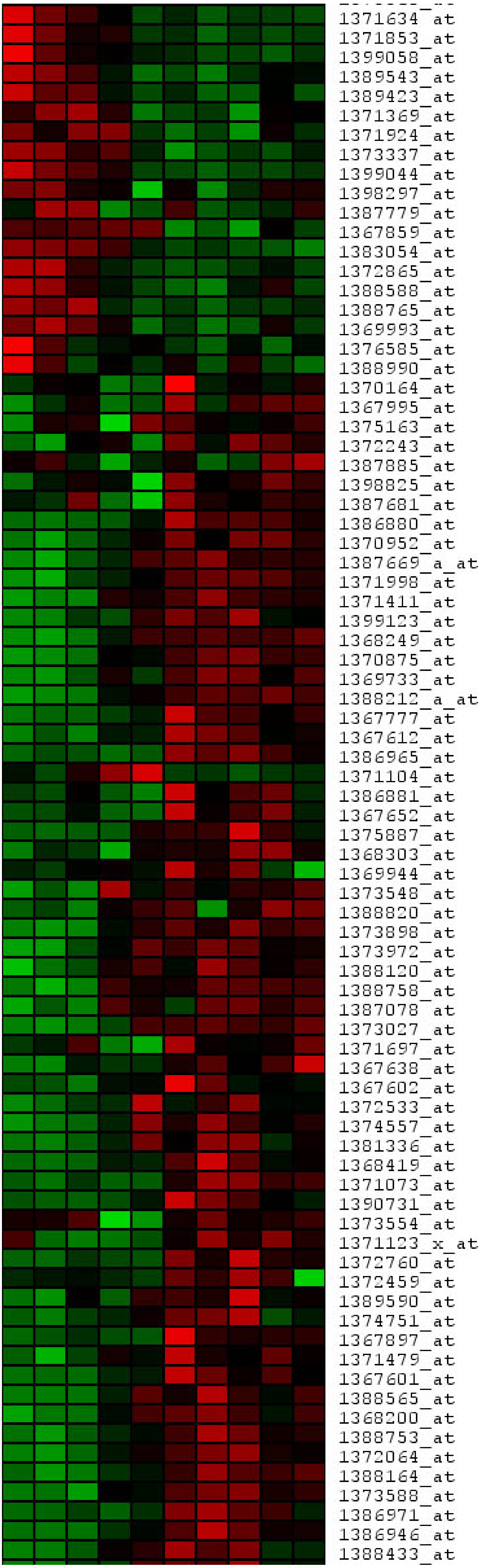
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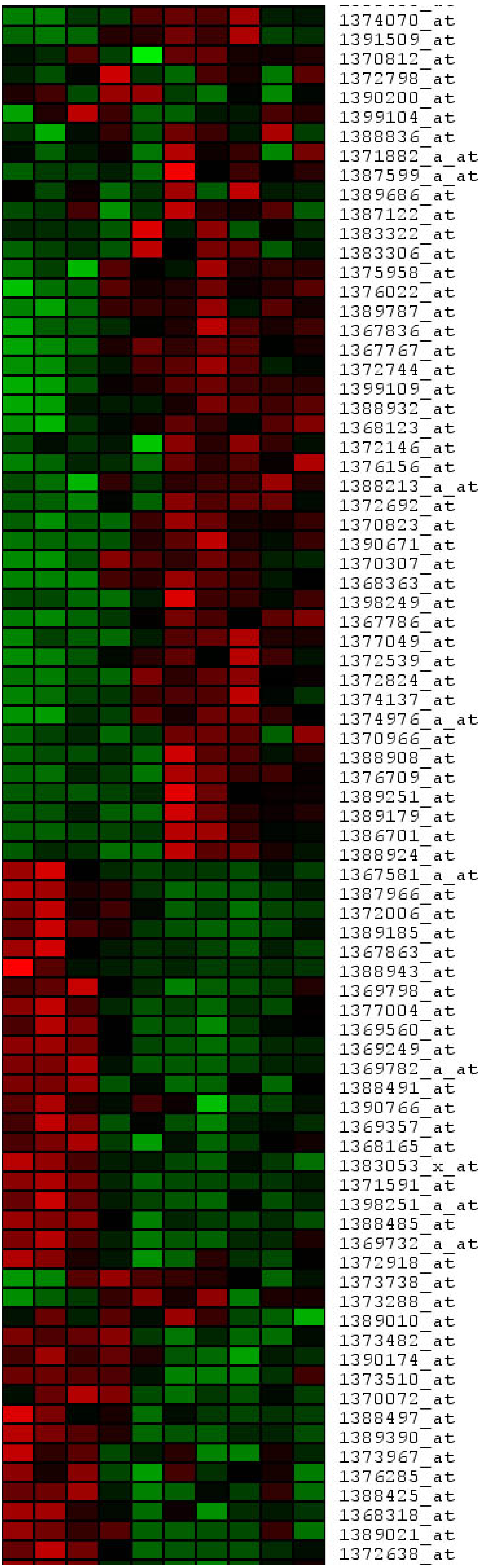
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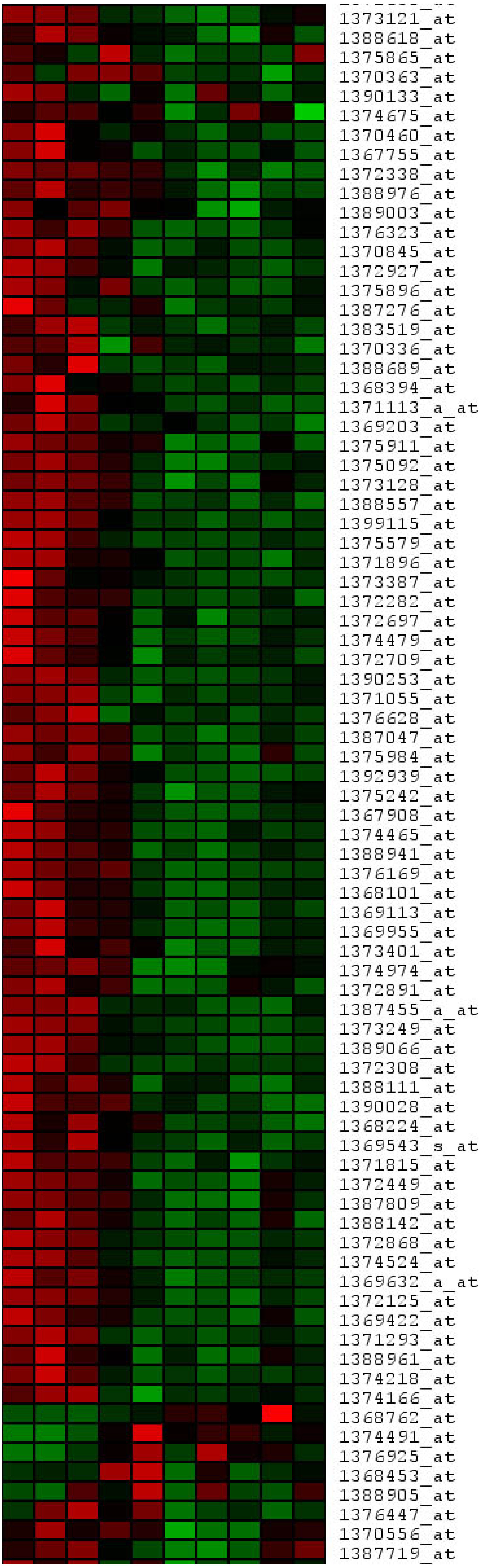
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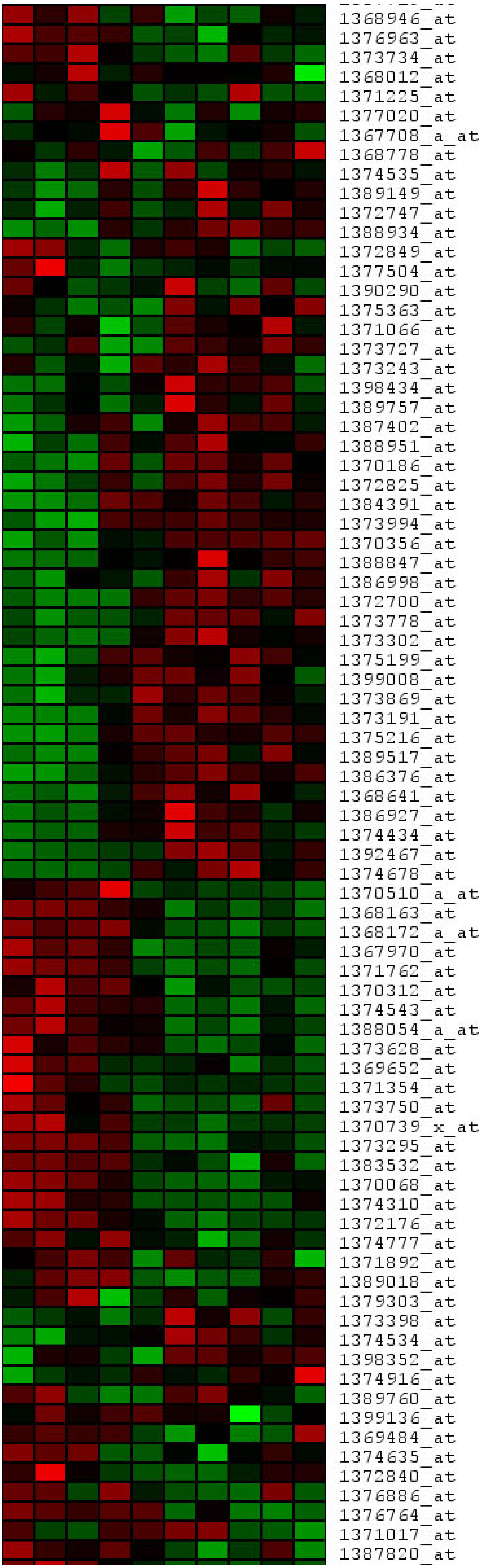
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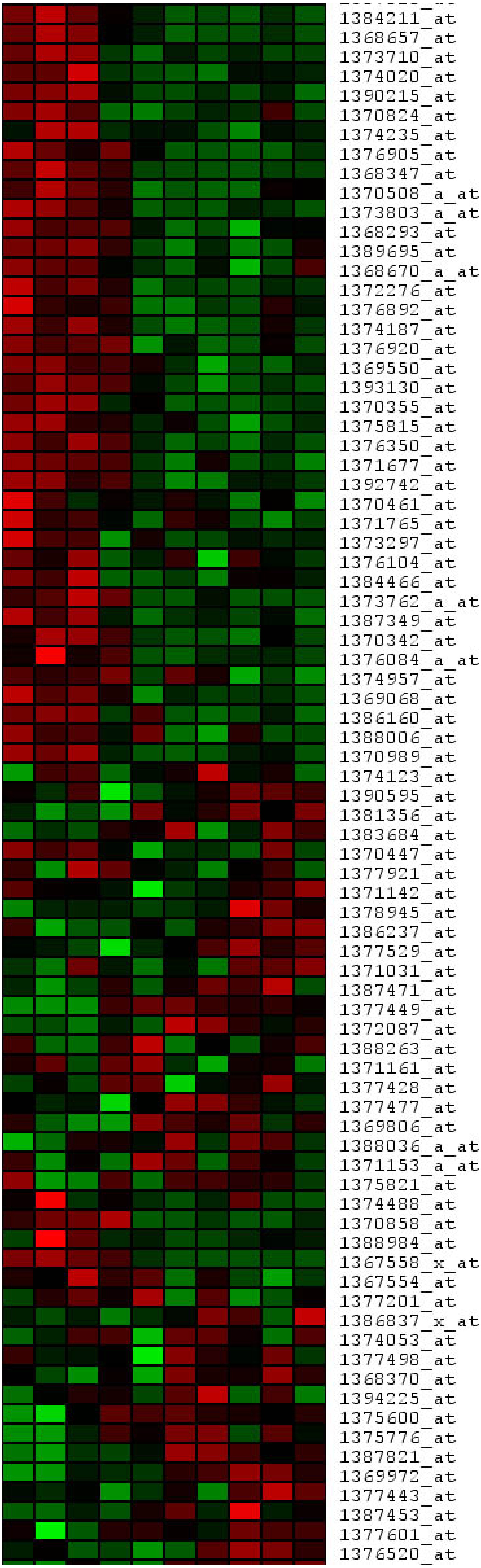
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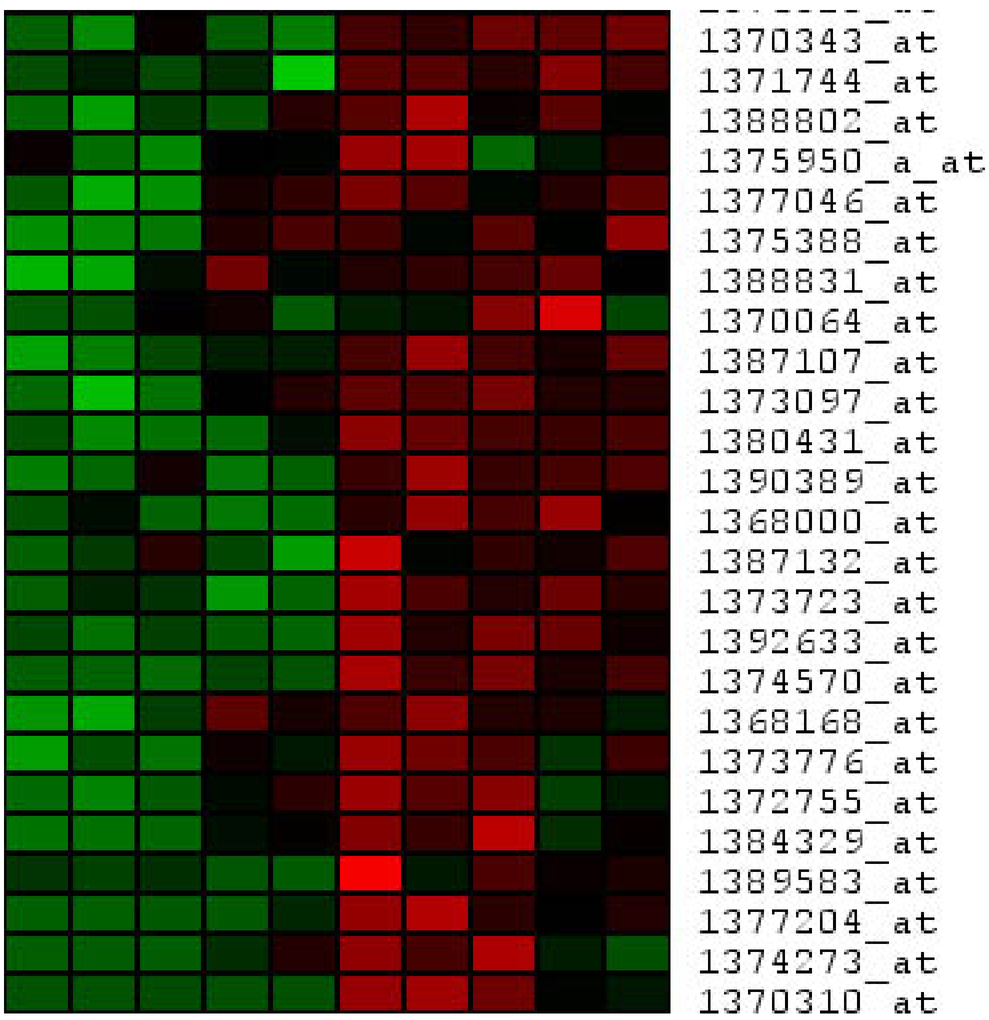

Supplemental Display of Array Data: TIGR MeV 3.1 software based hierarchical clustering of all control (HWC) and diabetic (HWS) samples using expression values (from the Affymetrix CHP files) for those genes considered significant. The above heat map displays those genes considered significant. The included CHP values for each gene/row were normalized using MeV for display purposes.