

**Supplemental Table 3.-** Hybridization intensities and expression ratios of flavanone 3-hydroxylase cDNAs detected in microarray experiment comparing seed coat RNAs of isogenic lines of the *Wp* locus in soybean.

Clone ID <sup>a</sup>	GenBank Acc. No.	Intensities <sup>b</sup>				Expression Ratios			Functional Annotation
		Replicate 1		Replicate 2		Line 1/Line 2			
		Line 1 ( <i>Wp/Wp</i> )	Line 2 ( <i>wp/wp</i> )	Line 1 ( <i>Wp/Wp</i> )	Line 2 ( <i>wp/wp</i> )	( <i>Wp/Wp</i> ) / ( <i>wp/wp</i> )			
		Cy 5	Cy3	Cy3	Cy5	Rep 1	Rep 2	Ave <sup>c</sup>	
Gm-c1012-683	AI900038	1075	280	1021	311	3.839	3.283	3.547	Flavanone 3-hydroxylase
Gm-c1012-683	AI900038	918	213	1011	330	4.310	3.097	3.573	Flavanone 3-hydroxylase
Gm-c1019-2646	AW277481	909	121	1133	151	7.512	7.503	7.507	Flavanone 3-hydroxylase
Gm-c1019-2646	AW277481	925	141	1132	213	6.560	5.315	5.811	Flavanone 3-hydroxylase
Gm-c1012-683	AI900038	716	217	440	177	3.300	2.486	2.934	Flavanone 3-hydroxylase
Gm-c1012-683	AI900038	752	215	592	199	3.498	2.975	3.246	Flavanone 3-hydroxylase
Gm-c1019-2646	AW277481	860	145	749	206	5.931	3.636	4.584	Flavanone 3-hydroxylase
Gm-c1019-2646	AW277481	795	122	823	158	6.516	5.209	5.779	Flavanone 3-hydroxylase
Gm-c1012-683	AI900038	504	146	474	213	3.452	2.225	2.724	Flavanone 3-hydroxylase
Gm-c1012-683	AI900038	508	129	667	219	3.938	3.091	3.405	Flavanone 3-hydroxylase
Gm-c1019-2646	AW277481	649	88	724	149	7.375	4.859	5.793	Flavanone 3-hydroxylase
Gm-c1019-2646	AW277481	548	106	680	76	5.170	8.947	6.747	Flavanone 3-hydroxylase
Gm-c1012-683	AI900038	548	182	677	209	3.011	3.239	3.133	Flavanone 3-hydroxylase
Gm-c1012-683	AI900038	574	142	771	230	4.042	3.352	3.616	Flavanone 3-hydroxylase
Gm-c1019-2646	AW277481	946	170	989	138	5.565	7.167	6.282	Flavanone 3-hydroxylase
Gm-c1019-2646	AW277481	763	131	973	167	5.824	5.826	5.826	Flavanone 3-hydroxylase
<b>Mean Ratio</b>						<b>4.990</b>	<b>4.513</b>	<b>4.656</b>	

(a) Both clone IDs represent the same F3H sequence except Gm-c1012-683 is 60 bases longer at the 5' end than the Gm-c-1019-2646.

(b) Intensities after background subtraction and global normalization between replicates and within each slide are shown.

(c) The average ratio of both microarray slides is calculated as follows:  
 $(\text{Line 1 Rep 1 intensity} + \text{Line 1 Rep2 intensity}) / (\text{Line 2 Rep 1 intensity} + \text{Line2 Rep 2 intensity})$