

Table S4 DEGs KEGG pathway enrichment result. (Pathways related to terpenoid biosynthesis, plant hormone signal transduction, plant-pathogen interaction were written in bold)

Term	ID	Input number	FDR(NSs vs WT)	KEGG_ID/KO	Entrez_ID	Hyperlink
DNA replication	ath03030	15	2.31E-05	ath:AT2G07690 ath:AT1G07370 ath:AT2G16440 ath:AT1G44900 ath:AT1G23750 ath:AT5G67100 ath:AT3G52630 ath:AT5G44635 ath:AT5G61000 ath:AT4G02060 ath:AT1G67630 ath:AT2G25100 ath:AT1G67320 ath:AT5G41880 ath:AT5G08020	815415 83724 9 816142 84109 838985 836845 824429 834492 836221 828153 843086 817048 843052 834193 830696	http://www.genome.jp/kegg-bin/show_pathway?ath03030/ath:AT5G41880%09red/ath:AT3G52630%09red/ath:AT2G16440%09red/ath:AT2G07690%09red/ath:AT5G08020%09red/ath:AT5G61000%09red/ath:AT1G67630%09red/ath:AT5G67100%09red/ath:AT1G07370%09red/ath:AT5G44635%09red/ath:AT1G44900%09red/ath:AT1G67320%09red/ath:AT1G23750%09red/ath:AT5G08020%09red/
Steroid biosynthesis	ath00100	7	0.1272	ath:AT4G37760 ath:AT3G19820 ath:AT5G13710 ath:AT1G58440 ath:AT4G34650 ath:AT1G47290 ath:AT3G45130	829932 821519 831216 842213 829617 841132 823649	http://www.genome.jp/kegg-bin/show_pathway?ath00100/ath:AT3G19820%09red/ath:AT1G58440%09red/ath:AT3G45130%09red/ath:AT5G13710%09red/ath:AT4G34650%09red/ath:AT4G37760%09red/
Pentose and glucuronate interconversions	ath00040	9	0.34086	ath:AT1G67750 ath:AT3G54920 ath:AT3G07010 ath:AT1G04680 ath:AT5G63180 ath:AT3G53190 ath:AT4G02330 ath:AT3G10720 ath:AT5G48900	843100 824657 819886 839452 836439 82485 828064 820241 834948	http://www.genome.jp/kegg-bin/show_pathway?ath00040/ath:AT1G67750%09red/ath:AT3G07010%09red/ath:AT5G48900%09red/ath:AT4G02330%09red/ath:AT5G63180%09red/ath:AT3G10720%09red/ath:AT3G54920%09red/ath:AT3G53190%09red/

Photosynthesis - antenna proteins	ath00196	4	822391 81505 5 839870 815058	0.34086	ath:AT3G27690 ath:AT2G05070 ath:AT1G29920 ath:AT2G05100	822391 81505 5 839870 815058	http://www.genome.jp/kegg-bin/show_pathway?ath00196/ath:AT1G29920%09red/ath:AT2G05100%09red/ath:AT3G27690%09red/ath:AT2G05070%09red/
Phagosome	ath04145	9	825225 84391 1 817504 837365 839405 832451 834459 836391 841425	0.34086	ath:AT3G60540 ath:AT1G75780 ath:AT2G29550 ath:AT1G08450 ath:AT1G50010 ath:AT5G23860 ath:AT5G44340 ath:AT5G62700 ath:AT1G50010	825225 84391 1 817504 837365 841425 832451 834459 836391 841425	http://www.genome.jp/kegg-bin/show_pathway?ath04145/ath:AT3G60540%09red/ath:AT5G23860%09red/ath:AT1G08450%09red/ath:AT1G75780%09red/ath:AT1G50010%09red/ath:AT5G62700%09red/ath:AT5G44340%09red/
Cutin, suberine and wax biosynthesis	ath00073	4	842857 82952 1 828019 843628	0.34086	ath:AT5G41040 ath:AT4G33790 ath:AT4G00360 ath:AT1G72970	834106 82952 1 828019 843628	http://www.genome.jp/kegg-bin/show_pathway?ath00073/ath:AT4G33790%09red/ath:AT1G72970%09red/ath:AT4G00360%09red/ath:AT5G41040%09red/
Vitamin B6 metabolism	ath00750	3	836175 838347 820850	0.34086	ath:AT5G60540 ath:AT1G17710 ath:AT3G16050	836175 838347 820850	http://www.genome.jp/kegg-bin/show_pathway?ath00750/ath:AT3G16050%09red/ath:AT5G60540%09red/ath:AT1G17710%09red/
ABC transporters	ath02010	4	822519 83935 3 828702 822463	0.34086	ath:AT3G28860 ath:AT1G02520 ath:AT4G25960 ath:AT3G28345	822519 83935 3 828702 822463	http://www.genome.jp/kegg-bin/show_pathway?ath02010/ath:AT3G28345%09red/ath:AT4G25960%09red/ath:AT1G02520%09red/ath:AT3G28860%09red/
Tropane, piperidine and pyridine alkaloid biosynthesis	ath00960	5	842580 817479 817483 833613 826838	0.34086	ath:AT1G62810 ath:AT2G29300 ath:AT2G29320 ath:AT5G36160 ath:AT4G12290	842580 817479 817481 833613 826838	http://www.genome.jp/kegg-bin/show_pathway?ath00960/ath:AT4G12290%09red/ath:AT1G62810%09red/ath:AT2G29300%09red/ath:AT2G29320%09red/ath:AT5G36160%09red/

Circadian rhythm - plant	ath04712	5	0.34086	832518 83073 0 8309 96 838 883 83 6132	ath:AT5G244 70 ath:AT5G 08330 ath:AT 5G11260 ath :AT1G22770 ath:AT5G601 00	832518 83073 0 830996 8388 83 836132	http://www.genom e.jp/kegg- bin/show_pathway? ath04712/ath:AT5G 11260%09red/ath:A T5G08330%09red/at h:AT5G60100%09re d/ath:AT5G24470%0 9red/ath:AT1G2277
				82396 3 8270 89 818 710 81 5949 8 27114 81870 9 8357 01 824 355 81 7165 8 28457 83569 9 8393 95 829 179 82 8713	ath:AT3G48 080 ath:AT4 G14440 ath: AT3G56800 ath:AT2G14 610 ath:AT4 G14640 ath: AT2G41100 ath:AT5G56 010 ath:AT3 G51920 ath: AT2G26250 ath:AT4G23 570 ath:AT5 G56010 ath: AT1G01120 ath:AT4G30 ath:AT4G393 30 ath:AT2G 34060 ath:AT 5G54160 ath :AT5G51890 ath:AT5G583 90 ath:AT2G 37040 ath:AT 2G30490 ath :AT5G48930 ath:AT2G371 30 ath:AT1G 26560 ath:AT 3G47010 ath :AT4G36220 ath:AT3G601 30	823963 8270 89 824847 81 5949 827114 818709 8356 99 824355 81 7165 828457 835699 8393 95 829179 82 8713	http://www.geno me.jp/kegg- bin/show_pathway ?ath04626/ath:AT 2G26250%09red/at h:AT2G41100%09r ed/ath:AT3G48080 %09red/ath:AT3G5 1920%09red/ath:A T4G23570%09red/ ath:AT4G30560%0 9red/ath:AT4G144 40%09red/ath:AT2 G14610%09red/ath :AT5G56010%09re d/ath:AT4G26070% 09red/ath:AT3G56 http://www.genom e.jp/kegg- bin/show_pathway? ath00940/ath:AT2G 30490%09red/ath:A T5G54160%09red/at h:AT5G48930%09re d/ath:AT2G37130%0 9red/ath:AT5G5839 0%09red/ath:AT3G4 7010%09red/ath:AT 5G51890%09red/ath :AT4G39330%09red/ ath:AT2G37040%09r ed/ath:AT4G36220% 09red/ath:AT3G601 30%09red/ath:AT1G
Plant-pathogen interaction	ath04626	14	0.34086	830088 81796 7 8355 04 835 264 83 5952 8 18280 817599 83495 1 8182 89 839 196 82 3854 8 29779 825183	ath:AT3G48 080 ath:AT4 G14440 ath: AT3G56800 ath:AT2G14 610 ath:AT4 G14640 ath: AT2G41100 ath:AT5G56 010 ath:AT3 G51920 ath: AT2G26250 ath:AT4G23 570 ath:AT5 G56010 ath: AT1G01120 ath:AT4G30 ath:AT4G393 30 ath:AT2G 34060 ath:AT 5G54160 ath :AT5G51890 ath:AT5G583 90 ath:AT2G 37040 ath:AT 2G30490 ath :AT5G48930 ath:AT2G371 30 ath:AT1G 26560 ath:AT 3G47010 ath :AT4G36220 ath:AT3G601 30	830088 81796 7 835504 8352 64 835952 818 280 817599 83 4951 818289 8 39196 823854 829779 82518 3	http://www.genom e.jp/kegg- bin/show_pathway? ath00940/ath:AT2G 30490%09red/ath:A T5G54160%09red/at h:AT5G48930%09re d/ath:AT2G37130%0 9red/ath:AT5G5839 0%09red/ath:AT3G4 7010%09red/ath:AT 5G51890%09red/ath :AT4G39330%09red/ ath:AT2G37040%09r ed/ath:AT4G36220% 09red/ath:AT3G601 30%09red/ath:AT1G
Phenylpropanoid biosynthesis	ath00940	13	0.34086	838985 83622 1 8244 29 830 696 83 7249	ath:AT1G237 50 ath:AT5G 61000 ath:AT 3G52630 ath :AT5G08020 ath:AT1G073 70	838985 83622 1 824429 8306 96 837249	http://www.genom e.jp/kegg- bin/show_pathway? ath03430/ath:AT1G 23750%09red/ath:A T3G52630%09red/at h:AT1G07370%09re d/ath:AT5G08020%0 9red/ath:AT5G6100
				838985 83622 1 8244 29 830 696 83 7249	ath:AT1G237 50 ath:AT5G 61000 ath:AT 3G52630 ath :AT5G08020 ath:AT1G073 70	838985 83622 1 824429 8306 96 837249	http://www.genom e.jp/kegg- bin/show_pathway? ath03430/ath:AT1G 23750%09red/ath:A T3G52630%09red/at h:AT1G07370%09re d/ath:AT5G08020%0 9red/ath:AT5G6100
Mismatch repair	ath03430	5	0.34086	838985 83622 1 8244 29 830 696 83 7249	ath:AT1G237 50 ath:AT5G 61000 ath:AT 3G52630 ath :AT5G08020 ath:AT1G073 70	838985 83622 1 824429 8306 96 837249	http://www.genom e.jp/kegg- bin/show_pathway? ath03430/ath:AT1G 23750%09red/ath:A T3G52630%09red/at h:AT1G07370%09re d/ath:AT5G08020%0 9red/ath:AT5G6100
				838985 83622 1 8244 29 830 696 83 7249	ath:AT1G237 50 ath:AT5G 61000 ath:AT 3G52630 ath :AT5G08020 ath:AT1G073 70	838985 83622 1 824429 8306 96 837249	http://www.genom e.jp/kegg- bin/show_pathway? ath03430/ath:AT1G 23750%09red/ath:A T3G52630%09red/at h:AT1G07370%09re d/ath:AT5G08020%0 9red/ath:AT5G6100

Starch and sucrose metabolism	ath00500	15	0.34086	818212	ath:AT2G363	http://www.genom
				82795	90 ath:AT4G	e.jp/kegg-
				9 8429	00490 ath:AT	bin/show_pathway?
				61 839	1G66430 ath	ath00500/ath:AT2G
				467 82	:AT1G02730	36390%09red/ath:A
				9167 8	ath:AT4G304	818212 82795
				35220	40 ath:AT5G	9 842961 8394
				821965	51460 ath:AT	67 829167 835
				82806	3G23820 ath	220 821965 82
				4 8202	:AT4G02330	8064 820241 8
				41 839	ath:AT3G107	39196 821499
				196 82	20 ath:AT1G	823854 83369
				1499 8	26560 ath:AT	2 825183 8280
				23854	3G19620 ath	81
				833692	:AT3G47010	ath:AT4G02280%09r
Fatty acid biosynthesis	ath00061	5	0.34086	82518	ath:AT5G371	ed/ath:AT5G37180%
				3 2872	80 ath:AT3G	09red/ath:AT4G304
				1286	60130 ath:AT	40%09red/ath:AT3G
					4G02280	60130%09red/ath:A
						T1G26560%09red/at
						http://www.genom
						e.jp/kegg-
						bin/show_pathway?
						ath00061/ath:AT5G
						16390%09red/ath:A
						T1G64400%09red/at
						h:AT3G23790%09re
						d/ath:AT1G77590%0
						9red/ath:AT1G4943
				Plant hormone signal transduction	ath04075	20
83150	90 ath:AT5G	me.jp/kegg-				
0 8413	16390 ath:AT	bin/show_pathway				
67 844	1G49430 ath	?ath04075/ath:AT				
094 84	:AT1G77590	1G77920%09red/at				
2748	ath:AT1G644	h:AT5G18010%09r				
	00	ed/ath:AT2G27050				
		%09red/ath:AT1G7				
		7690%09red/ath:A				
		T3G15540%09red/				
		ath:AT2G46690%0				
		9red/ath:AT2G146				
		10%09red/ath:AT1				
		G04240%09red/ath				
		:AT2G21050%09re				

Cysteine and methionine metabolism	ath00270	9	829933 81970 8 8210 03 826 317 81 8260 8 22186 833613 83287 3 8433 13	0.3504	ath:AT4G3770 ath:AT3G05430 ath:AT3G17390 ath:AT4G08040 ath:AT2G36880 ath:AT3G25900 ath:AT5G36160 ath:AT5G28030 ath:AT1G69770	829933 81970 8 821003 826317 818260 822186 833613 832873 843313	http://www.genome.jp/kegg-bin/show_pathway?ath00270/ath:AT2G36880%09red/ath:AT5G36160%09red/ath:AT4G08040%09red/ath:AT5G28030%09red/ath:AT3G25900%09red/ath:AT3G17390%09red/ath:AT3G05430%09red/ath:AT1G69770%09red/
Homologous recombination	ath03440	6	836221 83651 3 8389 85 824 429 83 0696 8 19743	0.3504	ath:AT5G6100 ath:AT5G63920 ath:AT1G23750 ath:AT3G52630 ath:AT5G08020 ath:AT3G05740	836221 83651 3 838985 824429 830696 819743	http://www.genome.jp/kegg-bin/show_pathway?ath03440/ath:AT3G52630%09red/ath:AT5G61000%09red/ath:AT3G05740%09red/ath:AT1G23750%09red/ath:AT5G63920%09red/
Other glycan degradation	ath00511	3	817355 84310 9 8295 75	0.3504	ath:AT2G28100 ath:AT1G67830 ath:AT4G34260	817355 84310 9 829575	http://www.genome.jp/kegg-bin/show_pathway?ath00511/ath:AT2G28100%09red/ath:AT4G34260%09red/ath:AT1G67830%09red/
Fatty acid metabolism	ath01212	7	817548 84409 4 8219 61 842 748 84 1367 8 37117 831500	0.3762	ath:AT2G29980 ath:AT1G77590 ath:AT3G23790 ath:AT1G64400 ath:AT1G49430 ath:AT1G06080 ath:AT5G16390	817548 84409 4 821961 842748 841367 837117 831500	http://www.genome.jp/kegg-bin/show_pathway?ath01212/ath:AT2G29980%09red/ath:AT1G49430%09red/ath:AT5G16390%09red/ath:AT1G64400%09red/ath:AT3G23790%09red/ath:AT1G06080%09red/ath:AT5G16390%09red/
Cyanoamino acid metabolism	ath00460	6	840543 83229 0 8391 96 829 910 82 3854 8 25183	0.38965	ath:AT1G36370 ath:AT5G22300 ath:AT1G26560 ath:AT4G37550 ath:AT3G47010 ath:AT3G60130	840543 83229 0 839196 829910 823854 825183	http://www.genome.jp/kegg-bin/show_pathway?ath00460/ath:AT1G26560%09red/ath:AT5G22300%09red/ath:AT3G47010%09red/ath:AT3G60130%09red/ath:AT4G37550%09red/
Sesquiterpenoid and triterpenoid biosynthesis	ath00909	3	829932 842213 829 617	0.47709	ath:AT4G37760 ath:AT1G58440 ath:AT4G34650	829932 842213 829617	http://www.genome.jp/kegg-bin/show_pathway?ath00909/ath:AT4G34650%09red/ath:AT4G37760%09red/ath:AT1G58440%09red/

Isoquinoline alkaloid biosynthesis	ath00950	3	842580 833613 826838	0.47709	ath:AT1G62810 ath:AT5G36160 ath:AT4G12290	842580 833613 826838	http://www.genome.jp/kegg-bin/show_pathway?ath00950/ath:AT4G12290%09red/ath:AT1G62810%09red/ath:AT5G36160%09red/
Phenylalanine metabolism	ath00360	9	817967 835264 842580 835952 817599 818289 833613 826838 818280	0.48065	ath:AT2G34060 ath:AT5G51890 ath:AT1G62810 ath:AT5G58390 ath:AT2G30490 ath:AT2G37130 ath:AT5G36160 ath:AT4G12290 ath:AT2G37040	817967 835264 842580 835952 817599 818289 833613 826838 818280	http://www.genome.jp/kegg-bin/show_pathway?ath00360/ath:AT2G34060%09red/ath:AT5G51890%09red/ath:AT1G62810%09red/ath:AT5G58390%09red/ath:AT2G37040%09red/ath:AT2G34060%09red/
Nucleotide excision repair	ath03420	6	836221 837249 838564 838985 824429 830696	0.51427	ath:AT5G61000 ath:AT1G07370 ath:AT1G19750 ath:AT1G23750 ath:AT3G52630 ath:AT5G08020	836221 837249 838564 838985 824429 830696	http://www.genome.jp/kegg-bin/show_pathway?ath03420/ath:AT3G52630%09red/ath:AT5G61000%09red/ath:AT1G07370%09red/ath:AT1G23750%09red/ath:AT1G19750%09red/
Fatty acid degradation	ath00071	4	821961 844094 841367 842748	0.51621	ath:AT3G23790 ath:AT1G77590 ath:AT1G49430 ath:AT1G64400	821961 844094 841367 842748	http://www.genome.jp/kegg-bin/show_pathway?ath00071/ath:AT1G64400%09red/ath:AT3G23790%09red/ath:AT1G77590%09red/ath:AT1G49430%09red/
Ether lipid metabolism	ath00565	3	815261 819730 824021	0.51621	ath:AT2G06925 ath:AT3G05630 ath:AT3G48610	815261 819730 824021	http://www.genome.jp/kegg-bin/show_pathway?ath00565/ath:AT3G05630%09red/ath:AT3G48610%09red/ath:AT2G06925%09red/
Nicotinate and nicotinamide metabolism	ath00760	2	832129 825377	0.55367	ath:AT5G20070 ath:AT3G62040	832129 825377	http://www.genome.jp/kegg-bin/show_pathway?ath00760/ath:AT5G20070%09red/ath:AT3G62040%09red/

Base excision repair	ath03410	4	820453 83449 7 835908 837249	0.55912	ath:AT3G12710 ath:AT5G44680 ath:AT5G57970 ath:AT1G07370	820453 83449 7 835908 837249	http://www.genome.jp/kegg-bin/show_pathway?ath03410/ath:AT1G07370%09red/ath:AT5G44680%09red/ath:AT3G12710%09red/ath:AT5G57970%09red/
Carotenoid biosynthesis	ath00906	3	841665 834570 827663	0.57051	ath:AT1G52340 ath:AT5G45340 ath:AT4G19230	841665 834570 827663	http://www.genome.jp/kegg-bin/show_pathway?ath00906/ath:AT5G45340%09red/ath:AT4G19230%09red/ath:AT1G52340%09red/
Fatty acid elongation	ath00062	3	817165 839395 827089	0.58702	ath:AT2G26250 ath:AT1G01120 ath:AT4G14440	817165 839395 827089	http://www.genome.jp/kegg-bin/show_pathway?ath00062/ath:AT2G26250%09red/ath:AT4G14440%09red/ath:AT1G01120%09red/
Arachidonic acid metabolism	ath00590	2	815261 831196	0.58702	ath:AT2G06925 ath:AT5G13520	815261 831196	http://www.genome.jp/kegg-bin/show_pathway?ath00590/ath:AT5G13520%09red/ath:AT2G06925%09red/
Ubiquinone and other terpenoid-quinone biosynthesis	ath00130	3	817599 829413 833613	0.58702	ath:AT2G30490 ath:AT4G32770 ath:AT5G36160	817599 829413 833613	http://www.genome.jp/kegg-bin/show_pathway?ath00130/ath:AT2G30490%09red/ath:AT4G32770%09red/ath:AT5G36160%09red/
Peroxisome	ath04146	6	832129 844094 842748 829521 841367 821961	0.58702	ath:AT5G20070 ath:AT1G77590 ath:AT1G64400 ath:AT4G33790 ath:AT1G49430 ath:AT3G23790	832129 844094 842748 829521 841367 821961	http://www.genome.jp/kegg-bin/show_pathway?ath04146/ath:AT4G33790%09red/ath:AT1G49430%09red/ath:AT3G23790%09red/ath:AT5G20070%09red/ath:AT1G77590%09red/
Pyrimidine metabolism	ath00240	8	831309 836845 843086 832710 819971 823847 834193 843052	0.58702	ath:AT5G14580 ath:AT5G67100 ath:AT1G67630 ath:AT5G26667 ath:AT3G07800 ath:AT3G46940 ath:AT5G41880 ath:AT1G67320	831309 836845 843086 832710 819971 823847 834193 843052	http://www.genome.jp/kegg-bin/show_pathway?ath00240/ath:AT5G41880%09red/ath:AT3G07800%09red/ath:AT1G67630%09red/ath:AT5G67100%09red/ath:AT5G26667%09red/ath:AT1G67320%09red/

Inositol phosphate metabolism	ath00562	5	835981 83078 83380 14819 98782 4021	0.58702	ath:AT5G58670 ath:AT5G09290 ath:AT1G14520 ath:AT3G07960 ath:AT3G48610	835981 83078 83380 14819 87824021	http://www.genome.jp/kegg-bin/show_pathway?
Glycerophospholipid metabolism	ath00564	6	819730 83955 88240 21828 14082 7165 815261	0.5929	ath:AT3G05630 ath:AT1G02390 ath:AT3G48610 ath:AT4G00400 ath:AT4G01950 ath:AT2G06925	819730 83955 8824021 828140 827165 815261	http://www.genome.jp/kegg-bin/show_pathway?
Amino sugar and nucleotide sugar metabolism	ath00520	8	839467 844193 829167 823908 842961 818066 821499 821965	0.64008	ath:AT1G02730 ath:AT1G78570 ath:AT4G30440 ath:AT3G47540 ath:AT1G66430 ath:AT2G35020 ath:AT3G19620 ath:AT3G23820	839467 844193 829167 823908 842961 818066 821499 821965	http://www.genome.jp/kegg-bin/show_pathway?
One carbon pool by folate	ath00670	2	840543 819022	0.64008	ath:AT1G36370 ath:AT2G44160	840543 819022	http://www.genome.jp/kegg-bin/show_pathway?

Metabolic pathways	ath01100	98	0.64761	837610	ath:AT1G106	837610 83884	http://www.genom
				83884	70 ath:AT1G	7 837931 8395	e.jp/kegg-
				7 8379	22410 ath:AT	58 836845 839	bin/show_pathway?
				31 839	1G13700 ath	870 818066 83	ath01100/ath:AT5G
				558 83	:AT1G02390	0867 829167 8	67100%09red/ath:A
				6845 8	ath:AT5G671	17481 828019	T5G09290%09red/at
				39870	00 ath:AT1G	830788 83078	h:AT3G47010%09re
				818066	29920 ath:AT	9 826838 8238	d/ath:AT4G39330%0
				83086	2G35020 ath	54 815261 835	9red/ath:AT2G2930
				7 8291	:AT5G01320	220 830985 83	0%09red/ath:AT1G1
				67 817	ath:AT4G304	2234 822186 8	0670%09red/ath:AT
				483 82	40 ath:AT2G	41367 827165	4G37770%09red/ath
				8019 8	29320 ath:AT	835981 84296	:AT1G66430%09red/
				30788	4G00360 ath	1 820241 8190	ath:AT1G13700%09r
				830789	:AT5G09290	22 832873 823	ed/ath:AT5G58670%
				82683	ath:AT5G093	847 819730 82	09red/ath:AT4G004
				8 8238	00 ath:AT4G	6317 834951 8	00%09red/ath:AT1G
				54 815	12290 ath:AT	21499 825183	67630%09red/ath:A
				261 83	3G47010 ath	828064 83369	T3G05430%09red/at
				5220 8	:AT2G06925	2 829413 8336	h:AT3G25900%09re
				30985	ath:AT5G514	13 830088 829	d/ath:AT4G34650%0
				832234	60 ath:AT5G	933 829932 81	9red/ath:AT1G6732
				82218	11160 ath:AT	6244 821072 8	0%09red/ath:AT3G1
				6 8413	5G21100 ath	19971 842213	7390%09red/ath:AT
				67 827	:AT3G25900	844094 84219	2G37040%09red/ath
				165 83	ath:AT1G494	8 821003 8150	:AT2G35020%09red/
				5981 8	30 ath:AT4G	55 829779 815	ath:AT2G30490%09r
				42961	01950 ath:AT	058 836625 84	ed/ath:AT1G02390%
				820241	5G58670 ath	1665 824592 8	09red/ath:AT1G094
Flavonoid biosynthesis	ath00941	2	0.64761	817599	ath:AT2G304	817599 83495	e.jp/kegg-
				83495	90 ath:AT5G	1	bin/show_pathway?
		1		48930			ath00941/ath:AT2G
							30490%09red/ath:A
							T5G48930%09red

Biosynthesis of secondary metabolites	ath01110	53	837610 81796 7 8355 34060 ath:AT5G54160 ath:AT1G52340 665 83 8847 8 37931 824592 83662 5 8263 17 834 951 81 8066 8 17165 830867 82364 9 8251 83 837 465 82 1003 8 18212 831216 81838 3 8359 52 817 483 84 2580 8 30789 833613	0.69157	ath:AT1G10670 ath:AT2G34060 ath:AT5G54160 ath:AT1G52340 6625 826317 834951 818066 10 ath:AT1G13700 ath:AT3G54250 ath:AT5G65010 ath:AT4G08040 ath:AT5G48930 ath:AT2G35020 ath:AT2G26250 ath:AT5G01320 ath:AT3G45130 ath:AT3G60130 ath:AT1G09420 ath:AT3G17390 ath:AT2G36390 ath:AT5G13710 ath:AT2G38050 ath:AT5G58390 ath:AT2G29320 ath:AT1G62810 ath	837610 81796 7 835504 84165 838847 837931 824592 836625 826317 834951 818066 817165 830867 823649 82513 837465 821003 818212 831216 818383 835952 817481 842580 830789 833613 826838 821519 82309red/ath:AT1G10620 ath:AT3G45130 ath:AT3G60130 ath:AT1G09420 9 818260 818289 822186 839196 817479 831500 835006 818280 842213 829617 844193 842198 823908 829413 832584 832585 831G62810 ath	http://www.genome.jp/kegg-bin/show_pathway?ath01110/ath:AT5G54160%09red/ath:A548930%09red/ath:AT5G36160%09red/ath:AT1G52340%09red/ath:AT5G16390%09red/ath:AT3G47540%09red/ath:AT3G17390%09red/ath:AT3G47010%09red/ath:AT1G78570%09red/ath:AT2G29300%09red/ath:AT1G10670%09red/ath:AT2G45130%09red/ath:A37130%09red/ath:AT4G37770%09red/ath:AT1G62810%09red/ath:AT3G19820%09red/ath:AT1G13700%09red/ath:AT3G45130%09red/ath:AT5G13710%09red/ath:AT5G58390%09red/ath:AT4G12290%09red/ath:AT5G49460%09red/ath:AT1G01120%09red/ath:AT2G38050%09red/ath:AT4G12290
		3	842580 833613 826838	0.69157	ath:AT1G62810 ath:AT5G36160 ath:AT4G12290	842580 833613 826838	http://www.genome.jp/kegg-bin/show_pathway?ath00350/ath:AT4G12290%09red/ath:AT1G62810%09red/ath:AT5G36160%09red/ath:AT4G12290
		1	818383	0.71285	ath:AT2G38050	818383	http://www.genome.jp/kegg-bin/show_pathway?ath00905/ath:AT2G38050%09red/ath:AT2G38050
		3	829910 821072 833738	0.71285	ath:AT4G37550 ath:AT3G03910 ath:AT5G37600	829910 821072 833738	http://www.genome.jp/kegg-bin/show_pathway?ath00910/ath:AT3G03910%09red/ath:AT4G37550%09red/ath:AT5G37600%09red/ath:AT4G37550
		1	817599	0.71375	ath:AT2G30490	817599	http://www.genome.jp/kegg-bin/show_pathway?ath01220/ath:AT2G30490%09red/ath:AT2G30490
		1	815261	0.71375	ath:AT2G06925	815261	http://www.genome.jp/kegg-bin/show_pathway?ath00591/ath:AT2G06925%09red/ath:AT2G06925

Riboflavin metabolism	ath00740	1	838035	0.71375	ath:AT1G14700	838035	http://www.genome.jp/kegg-bin/show_pathway?ath00740/ath:AT1G14700%09red
Stilbenoid, diarylheptanoid and gingerol biosynthesis	ath00945	4	817599 83495 832584 832585	0.73433	ath:AT2G30490 ath:AT5G48930 ath:AT5G25130 ath:AT5G25140	817599 83495 832584 832585	http://www.genome.jp/kegg-bin/show_pathway?ath00945/ath:AT2G30490%09red/ath:AT5G25130%09red/ath:AT5G25140%09red/ath:AT5G48930%09red
Phosphatidylinositol signaling system	ath04070	4	830788 83598 819987 818710	0.75641	ath:AT5G09290 ath:AT5G58670 ath:AT3G07960 ath:AT3G56800	830788 83598 819987 824847	http://www.genome.jp/kegg-bin/show_pathway?ath04070/ath:AT3G56800%09red/ath:AT5G09290%09red/ath:AT5G58670%09red/ath:AT3G07960%09red
Alanine, aspartate and glutamate metabolism	ath00250	3	836625 821072 833738	0.75641	ath:AT5G65010 ath:AT3G03910 ath:AT5G37600	836625 821072 833738	http://www.genome.jp/kegg-bin/show_pathway?ath00250/ath:AT5G65010%09red/ath:AT3G03910%09red/ath:AT5G37600%09red
Thiamine metabolism	ath00730	1	817513	0.75641	ath:AT2G29630	817513	http://www.genome.jp/kegg-bin/show_pathway?ath00730/ath:AT2G29630%09red
Glycerolipid metabolism	ath00561	3	839558 828140 827165	0.8038	ath:AT1G02390 ath:AT4G00400 ath:AT4G01950	839558 828140 827165	http://www.genome.jp/kegg-bin/show_pathway?ath00561/ath:AT1G02390%09red/ath:AT4G01950%09red/ath:AT4G00400%09red
Fructose and mannose metabolism	ath00051	3	838689 837752 842961	0.8038	ath:AT1G20950 ath:AT1G12000 ath:AT1G66430	838689 837752 842961	http://www.genome.jp/kegg-bin/show_pathway?ath00051/ath:AT1G66430%09red/ath:AT1G12000%09red/ath:AT1G20950%09red
Biosynthesis of unsaturated fatty acids	ath01040	2	837117 817548	0.88024	ath:AT1G06080 ath:AT2G29980	837117 817548	http://www.genome.jp/kegg-bin/show_pathway?ath01040/ath:AT2G29980%09red/ath:AT1G06080%09red

beta-Alanine metabolism	ath00410	2	842580 82683 8	0.92246	ath:AT1G62810 ath:AT4G12290	842580 826838	http://www.genome.jp/kegg-bin/show_pathway?ath00410/ath:AT4G12290%09red/ath:AT1G62810%09red
Sulfur metabolism	ath00920	2	832873 83078 8	0.92246	ath:AT5G28030 ath:AT5G09290	832873 830788	http://www.genome.jp/kegg-bin/show_pathway?ath00920/ath:AT5G28030%09red/ath:AT5G09290%09red
Ascorbate and aldarate metabolism	ath00053	2	838014 83223 4	0.92246	ath:AT1G14520 ath:AT5G21100	838014 832234	http://www.genome.jp/kegg-bin/show_pathway?ath00053/ath:AT1G14520%09red/ath:AT5G21100%09red
Glyoxylate and dicarboxylate metabolism	ath00630	3	840543 82991 0 8337 38	0.92246	ath:AT1G36370 ath:AT4G37550 ath:AT5G37600	840543 829910 833738	http://www.genome.jp/kegg-bin/show_pathway?ath00630/ath:AT5G37600%09red/ath:AT1G36370%09red/ath:AT4G37550%09red
Glucosinolate biosynthesis	ath00966	1	838210	0.92246	ath:AT1G16400	838210	http://www.genome.jp/kegg-bin/show_pathway?ath00966/ath:AT1G16400%09red
Tryptophan metabolism	ath00380	2	832667 83266 9	0.94811	ath:AT5G25980 ath:AT5G26000	832667 832669	http://www.genome.jp/kegg-bin/show_pathway?ath00380/ath:AT5G26000%09red/ath:AT5G25980%09red
Glycine, serine and threonine metabolism	ath00260	3	840543 84258 0 8268 38	0.94811	ath:AT1G36370 ath:AT1G62810 ath:AT4G12290	840543 842580 826838	http://www.genome.jp/kegg-bin/show_pathway?ath00260/ath:AT4G12290%09red/ath:AT1G62810%09red/ath:AT1G36370%09red
Propanoate metabolism	ath00640	1	831500	0.94811	ath:AT5G16390	831500	http://www.genome.jp/kegg-bin/show_pathway?ath00640/ath:AT5G16390%09red
Glutathione metabolism	ath00480	4	819386 84225 7 8375 76 837 465	0.94811	ath:AT2G47730 ath:AT1G59670 ath:AT1G10370 ath:AT1G09420	819386 842257 837576 837465	http://www.genome.jp/kegg-bin/show_pathway?ath00480/ath:AT1G10370%09red/ath:AT2G47730%09red/ath:AT1G59670%09red/ath:AT1G09420%09red

Endocytosis	ath04144	5	838263 820102 819987 819730 829691	0.9487	ath:AT1G16920 ath:AT3G09440 ath:AT3G07960 ath:AT3G05630 ath:AT4G35380	838263 820102 819987 819730 829691	http://www.genome.jp/kegg-bin/show_pathway?ath04144/ath:AT3G05630%09red/ath:AT3G09440%09red/ath:AT1G16920%09red/ath:AT4G35380%09red/ath:AT3G07960%09red/
Protein export	ath03060	2	825225 838100	0.99817	ath:AT3G60540 ath:AT1G15310	825225 838100	http://www.genome.jp/kegg-bin/show_pathway?ath03060/ath:AT1G15310%09red/ath:AT3G60540%09red/
Pentose phosphate pathway	ath00030	2	837931 837465	0.99817	ath:AT1G13700 ath:AT1G09420	837931 837465	http://www.genome.jp/kegg-bin/show_pathway?ath00030/ath:AT1G13700%09red/ath:AT1G09420%09red/
Phenylalanine, tyrosine and tryptophan biosynthesis	ath00400	2	838847 833613	0.99966	ath:AT1G22410 ath:AT5G36160	838847 833613	http://www.genome.jp/kegg-bin/show_pathway?ath00400/ath:AT1G22410%09red/ath:AT5G36160%09red/
Terpenoid backbone biosynthesis	ath00900	2	816244 824592	0.99966	ath:AT2G17370 ath:AT3G54250	816244 824592	http://www.genome.jp/kegg-bin/show_pathway?ath00900/ath:AT3G54250%09red/ath:AT2G17370%09red/
Purine metabolism	ath00230	6	831309 836845 830985 843086 843052 834193	0.99966	ath:AT5G14580 ath:AT5G67100 ath:AT5G11160 ath:AT1G67630 ath:AT1G67320 ath:AT5G41880	831309 836845 830985 843086 843052 834193	http://www.genome.jp/kegg-bin/show_pathway?ath00230/ath:AT5G41880%09red/ath:AT5G14580%09red/ath:AT1G67630%09red/ath:AT5G67100%09red/ath:AT5G11160%09red/ath:AT1G67320%09red/
alpha-Linolenic acid metabolism	ath00592	1	815261	0.99966	ath:AT2G06925	815261	http://www.genome.jp/kegg-bin/show_pathway?ath00592/ath:AT2G06925%09red/
Citrate cycle (TCA cycle)	ath00020	2	837610 835006	0.99966	ath:AT1G10670 ath:AT5G49460	837610 835006	http://www.genome.jp/kegg-bin/show_pathway?ath00020/ath:AT5G49460%09red/ath:AT1G10670%09red/

Limonene and pinene degradation	ath00903	2	832584 832585	0.99966	ath:AT5G25130 ath:AT5G25140	832584 832585	http://www.genome.jp/kegg-bin/show_pathway?ath00903/ath:AT5G25130%09red/ath:AT5G25140%09red
Protein processing in endoplasmic reticulum	ath04141	8	825225 832267 820102 837252 837365 820091 835701 835699	0.99966	ath:AT3G60540 ath:AT5G22060 ath:AT3G09440 ath:AT1G07400 ath:AT1G08450 ath:AT3G09350 ath:AT5G56010 ath:AT5G56010	825225 832267 820102 837252 837365 820091 835699	http://www.genome.jp/kegg-bin/show_pathway?ath04141/ath:AT3G60540%09red/ath:AT1G08450%09red/ath:AT3G09440%09red/ath:AT5G56010%09red/ath:AT5G22060%09red/ath:AT3G09350%09red/ath:AT5G56010%09red
Arginine and proline metabolism	ath00330	2	821072 833738	0.99966	ath:AT3G03910 ath:AT5G37600	821072 833738	http://www.genome.jp/kegg-bin/show_pathway?ath00330/ath:AT3G03910%09red/ath:AT5G37600%09red
Porphyrin and chlorophyll metabolism	ath00860	1	842198	0.99966	ath:AT1G58290	842198	http://www.genome.jp/kegg-bin/show_pathway?ath00860/ath:AT1G58290%09red
Valine, leucine and isoleucine degradation	ath00280	1	830789	0.99966	ath:AT5G09300	830789	http://www.genome.jp/kegg-bin/show_pathway?ath00280/ath:AT5G09300%09red
Proteasome	ath03050	1	841815	0.99966	ath:AT1G53780	841815	http://www.genome.jp/kegg-bin/show_pathway?ath03050/ath:AT1G53780%09red
Carbon metabolism	ath01200	7	837931 840543 819022 829910 832873 831500 837465	0.99966	ath:AT1G13700 ath:AT1G36370 ath:AT2G44160 ath:AT4G37550 ath:AT5G28030 ath:AT5G16390 ath:AT1G09420	837931 840543 819022 829910 832873 831500 837465	http://www.genome.jp/kegg-bin/show_pathway?ath01200/ath:AT1G13700%09red/ath:AT5G28030%09red/ath:AT1G09420%09red/ath:AT5G16390%09red/ath:AT2G44160%09red/ath:AT1G36370%09red/ath:AT1G13700%09red
Spliceosome	ath03040	5	830597 820698 830033 831313 820102	0.99966	ath:AT5G07060 ath:AT3G14700 ath:AT4G38780 ath:AT5G14610 ath:AT3G09440	830597 820698 830033 831313 820102	http://www.genome.jp/kegg-bin/show_pathway?ath03040/ath:AT3G09440%09red/ath:AT3G14700%09red/ath:AT5G07060%09red/ath:AT4G38780%09red/ath:AT5G14610%09red

Biosynthesis of amino acids	ath01230	7	838847 840543 821003 818260 833613 832873 833738	0.99966	ath:AT1G22410 ath:AT1G36370 ath:AT3G17390 ath:AT2G36880 ath:AT5G36160 ath:AT5G28030 ath:AT5G37600	838847 840543 821003 818260 833613 832873 833738	http://www.genome.jp/kegg-bin/show_pathway?ath01230/ath:AT2G36880%09red/ath:AT5G36160%09red/ath:AT3G17390%09red/ath:AT1G22410%09red/ath:AT5G37600%09red/ath:AT5G37600%09red/ath:AT5G37600%09red/
RNA degradation	ath03018	2	830371 831309	0.99966	ath:AT5G04895 ath:AT5G14580	830371 831309	http://www.genome.jp/kegg-bin/show_pathway?ath03018/ath:AT5G14580%09red/ath:AT5G04895%09red/
2-Oxocarboxylic acid metabolism	ath01210	1	838210	0.99966	ath:AT1G16400	838210	http://www.genome.jp/kegg-bin/show_pathway?ath01210/ath:AT1G16400%09red/
Pyruvate metabolism	ath00620	1	831500	0.99966	ath:AT5G16390	831500	http://www.genome.jp/kegg-bin/show_pathway?ath00620/ath:AT5G16390%09red/
Ribosome biogenesis in eukaryotes	ath03008	1	824963	0.99966	ath:AT3G57940	824963	http://www.genome.jp/kegg-bin/show_pathway?ath03008/ath:AT3G57940%09red/
Ubiquitin mediated proteolysis	ath04120	2	817943 838564	0.99966	ath:AT2G33770 ath:AT1G19750	817943 838564	http://www.genome.jp/kegg-bin/show_pathway?ath04120/ath:AT2G33770%09red/ath:AT1G19750%09red/
Glycolysis / Gluconeogenesis	ath00010	1	830867	0.99966	ath:AT5G01320	830867	http://www.genome.jp/kegg-bin/show_pathway?ath00010/ath:AT5G01320%09red/
mRNA surveillance pathway	ath03015	1	841887	0.99966	ath:AT1G54450	841887	http://www.genome.jp/kegg-bin/show_pathway?ath03015/ath:AT1G54450%09red/
Oxidative phosphorylation	ath00190	1	836388	0.99966	ath:AT5G62670	836388	http://www.genome.jp/kegg-bin/show_pathway?ath00190/ath:AT5G62670%09red/