Table 3 SNP locations in YP-1, *S. galapagense,* and *S. pimpinellifolium.* Annotations are based on ITAG2.3 predictions for H1706. Numbers in parenthesis indicate percentage of the region containing SNPs. *S. gal = S. galapagense*; *S. pim = S. pimpinellifolium*; nonsyn=nonsynonymous.

SNP Location	# of SNPs (% of region)*		
	YP-1	*S. gal*	*S. pim*
Total SNPs	539,406 (0.07%)	4,665,765 (0.6%)	6,016,177 (0.8%)
Intergenic	339,858 (0.05%)	4,318,821 (0.5%)	5,589,364 (0.8%)
Genic	42,117 (0.04%)	346,944 (0.3%)	426,813 (0.4%)
Genic - noncoding	26,025 (0.04%)	241,551 (0.3%)	304,830 (0.4%)
Genic - coding	16,092 (0.04%)	105,393 (0.3%)	121,983 (0.3%)
coding nonsyn.	10,118	62,432	70,474
coding synonymous	15,457	40,622	40,703
stop gained	288	1,427	1,781
stop lost	144	497	541
splice site donor	49	271	320
start lost	64	258	326
splice site acceptor	55	251	255
synonymous stop	21	120	152
nonsyn. start	14	53	54

* some SNPs are counted more than once since they are in more than one gene model