

**Table S3. important TD genes information.**

<b>GeneID</b>	<b>Chr</b>	<b>Start</b>	<b>End</b>	<b>Str:Family</b>	<b>TypeInfo</b>	<b>isTDorNot</b>
<b>TPS genes</b>						
VIT_12s0059g02710	chr12	7438986	7441486 +	G98	TPS	TD
VIT_12s0059g02720	chr12	7461794	7463233 +	G98	TPS	TD
VIT_12s0134g00020	chr12	7533163	7535905 -	G98	TPS-b	TD
VIT_12s0134g00030	chr12	7549484	7552781 -	G98	TPS-b	TD
VIT_13s0067g00380	chr13	19765857	19769243 +	G98	TPS-b	TD
VIT_13s0067g00370	chr13	19771350	19773899 +	G98	TPS-b	TD
VIT_13s0067g00130	chr13	19898393	19900842 -	G98	TPS-b	TD
VIT_13s0067g00050	chr13	19964640	19967848 +	G98	TPS-b	TD
VIT_13s0067g03700	chr13	22538253	22540752 -	G98	TPS-b	TD
VIT_13s0067g03740	chr13	22560789	22563116 +	G98	TPS-b	TD
VIT_13s0067g03790	chr13	22589414	22591902 +	G98	TPS-b	TD
VIT_13s0067g03830	chr13	22630720	22632966 +	G98	TPS-b	TD
VIT_13s0019g00060	chr13	22740519	22743003 +	G98	TPS-b	TD
VIT_18s0001g05520	chr18	31889810	31898087 +	G61	TPS-a	TD
VIT_18s0001g05470	chr18	31899384	31909042 +	G61	TPS-a	TD
VIT_18s0001g05460	chr18	31914899	31916090 +	G61	TPS-a	TD
VIT_18s0001g05430	chr18	31923932	31926139 +	G61	TPS-a	TD
VIT_18s0001g05360	chr18	31950323	31955047 +	G61	TPS-a	TD
VIT_18s0001g05290	chr18	31973944	31986715 +	G61	TPS-a	TD
VIT_18s0001g05240	chr18	32014137	32016389 +	G61	TPS-a	TD
VIT_18s0001g05230	chr18	32024044	32026321 -	G61	TPS-a	TD
VIT_18s0001g04870	chr18	32192342	32194578 -	G61	TPS-a	TD
VIT_18s0001g04780	chr18	32248823	32251297 +	G61	TPS-a	TD
VIT_18s0001g04510	chr18	32353880	32355134 -	G61	TPS-a	TD
VIT_18s0001g04280	chr18	32435669	32438130 -	G61	TPS-a	TD
VIT_18s0001g04220	chr18	32468242	32470450 -	G61	TPS-a	TD

VIT_18s0001g04170	chr18	32482794	32485087 -	G61	TPS-a	TD
VIT_18s0001g04120	chr18	32513865	32516312 +	G61	TPS-a	TD
VIT_18s0001g04080	chr18	32538566	32548051 -	G61	TPS-a	TD
VIT_18s0001g04050	chr18	32562442	32564785 -	G61	TPS-a	TD
VIT_19s0014g01060	chr19	1119857	1123798 +	G61	TPS-a	TD
VIT_19s0014g01070	chr19	1126915	1130051 -	G61	TPS-a	TD
VIT_19s0014g02550	chr19	2630096	2638773 -	G61	TPS-a	TD
VIT_19s0014g02580	chr19	2649604	2653203 -	G61	TPS-a	TD
VIT_19s0014g02590	chr19	2667926	2670239 -	G61	TPS-a	TD
VIT_19s0014g04800	chr19	5138070	5153191 -	G61	TPS-a	TD
VIT_19s0014g04810	chr19	5156208	5159153 -	G61	TPS-a	TD
VIT_19s0014g04900	chr19	5226851	5232162 -	G61	TPS-a	TD
VIT_19s0014g04930	chr19	5254957	5257671 +	G61	TPS-a	TD
VIT_07s0151g01040	chr7	1605733	1612151 -	G1716	TPS-c	TD
VIT_07s0151g01070	chr7	1633647	1639678 -	G1716	TPS-c	TD
VIT_10s0116g00750	chr10	4370158	4374523 -	G1802	TPS-f	notTD
VIT_00s0450g00010	chr10	4416112	4418955 +	G159	TPS-a	notTD
VIT_13s0084g00010	chr13	21923387	21926049 -	G98	TPS-b	notTD
VIT_19s0015g02070	chr19	11275953	11278623 -	G61	TPS-a	notTD
VIT_19s0085g00830	chr19	23957285	23964901 -	G1716	TPS-e	notTD

### STS genes

VIT_10s0042g00930	chr10	19721140	19722874 -	G34	STS	TD
VIT_10s0042g00920	chr10	19727108	19728704 -	G34	STS	TD
VIT_10s0042g00910	chr10	19741924	19743475 -	G34	STS	TD
VIT_10s0042g00890	chr10	19761954	19763059 -	G34	STS	TD
VIT_14s0068g00920	chr14	24673459	24675059 +	G34	STS	TD
VIT_14s0068g00930	chr14	24686995	24688542 +	G34	STS	TD
VIT_16s0022g01140	chr16	14459402	14460328 +	G34	STS	TD
VIT_16s0022g01190	chr16	14557320	14558246 +	G34	STS	TD

VIT_16s0100g00750	chr16	17749915	17751633 +	G34	STS	TD
VIT_16s0100g00760	chr16	17763444	17764515 +	G34	STS	TD
VIT_16s0100g00770	chr16	17779694	17781560 +	G34	STS	TD
VIT_16s0100g00780	chr16	17787520	17789266 +	G34	STS	TD
VIT_16s0100g00800	chr16	17797744	17799029 -	G34	STS	TD
VIT_16s0100g00810	chr16	17800279	17801828 -	G34	STS	TD
VIT_16s0100g00830	chr16	17846607	17848432 +	G34	STS	TD
VIT_16s0100g00840	chr16	17854026	17855468 -	G34	STS	TD
VIT_16s0100g00850	chr16	17857368	17858900 -	G34	STS	TD
VIT_16s0100g00860	chr16	17860847	17862396 -	G34	STS	TD
VIT_16s0100g00880	chr16	17877762	17879367 -	G34	STS	TD
VIT_16s0100g00900	chr16	17896834	17907999 -	G34	STS	TD
VIT_16s0100g00910	chr16	17909184	17910942 +	G34	STS	TD
VIT_16s0100g00920	chr16	17916025	17917483 -	G34	STS	TD
VIT_16s0100g00930	chr16	17919268	17920789 -	G34	STS	TD
VIT_16s0100g00940	chr16	17922707	17924268 -	G34	STS	TD
VIT_16s0100g00960	chr16	17951602	17952568 -	G34	STS	TD
VIT_16s0100g00990	chr16	17977689	17979588 -	G34	STS	TD
VIT_16s0100g01000	chr16	17987894	17989631 -	G34	STS	TD
VIT_16s0100g01010	chr16	18002363	18004082 -	G34	STS	TD
VIT_16s0100g01020	chr16	18014561	18016118 -	G34	STS	TD
VIT_16s0100g01030	chr16	18018676	18020429 -	G34	STS	TD
VIT_16s0100g01040	chr16	18020430	18023685 +	G34	STS	TD
VIT_16s0100g01070	chr16	18037091	18038893 -	G34	STS	TD
VIT_16s0100g01100	chr16	18066665	18068451 -	G34	STS	TD
VIT_16s0100g01120	chr16	18126465	18128209 -	G34	STS	TD
VIT_16s0100g01130	chr16	18129941	18135657 -	G34	STS	TD
VIT_16s0100g01140	chr16	18138317	18140121 -	G34	STS	TD
VIT_16s0100g01150	chr16	18154999	18156754 -	G34	STS	TD
VIT_16s0100g01160	chr16	18184851	18186495 -	G34	STS	TD



VIT_11s0052g00200	chr11	17665848	17669845 +	G56	NBS-LRR	TD
VIT_11s0052g00210	chr11	17677140	17680684 +	G56	CC-NBS-LRR	TD
VIT_12s0121g00050	chr12	13090874	13094737 +	G10	CC-NBS-LRR	TD
VIT_12s0121g00060	chr12	13227199	13231374 -	G10	NBS-LRR	TD
VIT_12s0034g00850	chr12	18238522	18244329 +	G39	TIR-NBS-LRR	TD
VIT_12s0034g00910	chr12	18312773	18320014 +	G39	TIR-NBS-LRR	TD
VIT_12s0034g01460	chr12	19072154	19075404 +	G10	NBS-LRR	TD
VIT_12s0034g01470	chr12	19077214	19088046 +	G10	NBS-LRR	TD
VIT_12s0034g01480	chr12	19097739	19101743 +	G10	NBS-LRR	TD
VIT_12s0034g01490	chr12	19115744	19119373 +	G10	NBS-LRR	TD
VIT_12s0034g02310	chr12	20287229	20291308 +	G10	NBS-LRR	TD
VIT_12s0034g02440	chr12	20504618	20510846 -	G10	NBS-LRR	TD
VIT_12s0034g02500	chr12	20545270	20549661 -	G10	NBS-LRR	TD
VIT_12s0035g00410	chr12	21316657	21318448 +	G10	NBS	TD
VIT_12s0035g01260	chr12	22613421	22621094 +	G368	CC-NBS-LRR	TD
VIT_12s0035g01280	chr12	22669016	22672221 +	G368	NBS-LRR	TD
VIT_13s0067g00740	chr13	408641	410725 -	G20	NBS-LRR	TD
VIT_13s0067g00750	chr13	414991	417136 -	G20	NBS	TD
VIT_13s0067g00760	chr13	421193	426855 -	G20	NBS-LRR	TD
VIT_13s0067g00780	chr13	448334	455249 -	G20	CC-NBS	TD
VIT_13s0067g00790	chr13	456630	461257 -	G20	NBS-LRR	TD
VIT_13s0067g00810	chr13	463533	468515 -	G20	CC-NBS-LRR	TD
VIT_13s0067g00830	chr13	473988	480826 +	G20	NBS-LRR	TD
VIT_13s0047g00730	chr13	17369804	17373604 -	G44	NBS-LRR	TD
VIT_13s0067g03570	chr13	22462678	22466355 +	G44	NBS-LRR	TD
VIT_13s0067g03590	chr13	22472865	22476834 +	G44	NBS-LRR	TD
VIT_13s0067g03640	chr13	22489605	22493684 +	G44	NBS-LRR	TD
VIT_13s0019g00380	chr13	22917892	22932646 +	G44	CC-NBS-LRR	TD
VIT_13s0139g00010	chr13	23061203	23069455 +	G44	NBS-LRR	TD
VIT_13s0139g00030	chr13	23079886	23099495 +	G44	CC-NBS-LRR	TD

VIT_13s0139g00070	chr13	23137902	23141390 +	G44	CC-NBS-LRR	TD
VIT_13s0139g00210	chr13	23297898	23305683 -	G44	CC-NBS-LRR	TD
VIT_13s0139g00220	chr13	23308392	23312770 -	G44	NBS-LRR	TD
VIT_13s0139g00270	chr13	23377909	23381253 +	G10	NBS-LRR	TD
VIT_13s0139g00290	chr13	23393438	23400015 +	G10	NBS-LRR	TD
VIT_13s0139g00320	chr13	23410012	23413176 +	G10	NBS-LRR	TD
VIT_13s0139g00340	chr13	23418221	23421764 +	G10	NBS-LRR	TD
VIT_13s0019g01050	chr13	24846069	24856338 -	G535	CC-NBS-LRR	TD
VIT_13s0019g01120	chr13	24888821	24890550 -	G535	NBS	TD
VIT_13s0019g01880	chr13	25308524	25314466 +	G10	CC-NBS-LRR	TD
VIT_13s0019g01950	chr13	25345245	25349091 +	G10	NBS-LRR	TD
VIT_13s0158g00430	chr13	25637214	25646219 +	G10	NBS-LRR	TD
VIT_13s0158g00400	chr13	25684061	25688390 +	G10	NBS-LRR	TD
VIT_13s0158g00290	chr13	25844579	25850422 -	G10	NBS-LRR	TD
VIT_13s0158g00260	chr13	25870805	25874584 -	G10	NBS-LRR	TD
VIT_13s0064g00140	chr13	26280378	26289742 +	G44	NBS-LRR	TD
VIT_13s0064g01790	chr13	28344556	28346379 -	G10	NBS	TD
VIT_13s0064g01800	chr13	28354608	28358892 -	G10	NBS-LRR	TD
VIT_13s0064g01850	chr13	28379122	28383006 -	G10	CC-NBS-LRR	TD
VIT_13s0064g01870	chr13	28393778	28399716 -	G10	NBS-LRR	TD
VIT_13s0156g00500	chr13	28555759	28560015 +	G10	NBS-LRR	TD
VIT_13s0156g00480	chr13	28571739	28576083 +	G501	CC-NBS	TD
VIT_13s0156g00450	chr13	28610822	28612143 +	G501	CC-NBS	TD
VIT_14s0030g00130	chr14	3797710	3799911 -	G56	NBS-LRR	TD
VIT_14s0030g00840	chr14	5084147	5087361 -	G56	NBS-LRR	TD
VIT_14s0030g00870	chr14	5094731	5100392 -	G56	CC-NBS-LRR	TD
VIT_14s0030g00960	chr14	5254285	5275694 -	G56	NBS-LRR	TD
VIT_14s0030g00990	chr14	5293868	5311280 -	G56	CC-NBS-LRR	TD
VIT_14s0030g01160	chr14	5552260	5557543 -	G56	NBS-LRR	TD
VIT_14s0030g01170	chr14	5563100	5565424 -	G56	NBS-LRR	TD

VIT_14s0030g01200	chr14	5671014	5674017 -	G56	NBS-LRR	TD
VIT_14s0081g00780	chr14	9273608	9280327 -	G56	NBS-LRR	TD
VIT_14s0081g00800	chr14	9306048	9317036 -	G56	CC-NBS-LRR	TD
VIT_14s0036g00010	chr14	9382342	9384014 -	G578	CC-NBS	TD
VIT_14s0036g00030	chr14	9397163	9398059 -	G578	NBS	TD
VIT_14s0036g00070	chr14	9463706	9470147 -	G56	NBS-LRR	TD
VIT_14s0036g00120	chr14	9575313	9587255 -	G56	CC-NBS-LRR	TD
VIT_14s0036g00240	chr14	9701598	9707217 -	G578	NBS-LRR	TD
VIT_14s0036g00260	chr14	9715660	9716787 -	G578	CC-NBS	TD
VIT_14s0036g00290	chr14	9735291	9742878 +	G578	CC-NBS	TD
VIT_14s0036g00310	chr14	9771968	9779302 -	G56	CC-NBS-LRR	TD
VIT_14s0036g00330	chr14	9827334	9840401 -	G56	CC-NBS-LRR	TD
VIT_14s0036g01350	chr14	12453010	12454836 +	G56	NBS-LRR	TD
VIT_14s0036g01360	chr14	12463695	12466138 +	G56	NBS-LRR	TD
VIT_15s0024g00400	chr15	582271	585735 -	G10	NBS-LRR	TD
VIT_15s0024g00440	chr15	619199	623235 -	G10	NBS-LRR	TD
VIT_15s0024g00470	chr15	724149	747196 +	G10	NBS	TD
VIT_15s0045g00920	chr15	7482066	7488247 +	G664	NBS-LRR	TD
VIT_15s0045g00980	chr15	7560406	7562199 +	G20	NBS	TD
VIT_15s0045g01020	chr15	7660173	7662104 +	G20	NBS-LRR	TD
VIT_15s0046g02730	chr15	19454696	19457671 +	G20	NBS-LRR	TD
VIT_15s0046g02750	chr15	19500365	19503350 +	G20	NBS-LRR	TD
VIT_15s0046g02800	chr15	19528135	19530195 +	G20	NBS-LRR	TD
VIT_15s0046g02810	chr15	19535684	19538497 +	G20	NBS-LRR	TD
VIT_15s0046g02820	chr15	19542369	19545367 +	G20	NBS-LRR	TD
VIT_00s0144g00220	chr16	11672512	11674048 -	G148	NBS	TD
VIT_00s0144g00190	chr16	11722792	11725233 -	G148	NBS-LRR	TD
VIT_00s0144g00120	chr16	11940951	11944527 -	G148	NBS-LRR	TD
VIT_17s0000g03070	chr17	3025189	3029641 +	G148	NBS-LRR	TD
VIT_17s0000g03080	chr17	3031910	3038630 +	G148	CC-NBS-LRR	TD

VIT_17s0000g03090	chr17	3039120	3041513 +	G148	CC-NBS-LRR	TD
VIT_18s0075g00480	chr18	24902487	24906911 -	G216	NBS-LRR	TD
VIT_18s0041g00190	chr18	27991695	27997119 -	G39	TIR-NBS	TD
VIT_18s0041g00200	chr18	28008376	28011207 -	G39	NBS-LRR	TD
VIT_18s0041g01330	chr18	29396028	29417319 -	G39	TIR-NBS-LRR	TD
VIT_18s0041g01340	chr18	29433834	29438272 -	G39	TIR-NBS-LRR	TD
VIT_18s0041g02180	chr18	30736006	30741164 -	G639	NBS	TD
VIT_18s0041g02190	chr18	30741182	30742836 -	G639	NBS	TD
VIT_18s0001g06380	chr18	31459460	31463235 -	G39	TIR-NBS-LRR	TD
VIT_18s0001g06340	chr18	31483133	31489122 -	G39	TIR-NBS-LRR	TD
VIT_18s0001g06240	chr18	31538506	31542848 +	G39	TIR-NBS-LRR	TD
VIT_18s0089g00100	chr18	33037039	33057421 -	G216	TIR-NBS-LRR	TD
VIT_19s0014g00570	chr19	581396	582941 +	G11	NBS-LRR	TD
VIT_19s0014g00580	chr19	600125	606739 +	G11	CC-NBS	TD
VIT_19s0014g00870	chr19	897695	916258 -	G11	CC-NBS-LRR	TD
VIT_19s0014g00900	chr19	929691	938363 -	G11	NBS-LRR	TD
VIT_19s0014g00920	chr19	957484	960645 -	G11	CC-NBS-LRR	TD
VIT_19s0014g05150	chr19	5432059	5434734 -	G11	NBS-LRR	TD
VIT_19s0014g05160	chr19	5439530	5442340 +	G11	NBS-LRR	TD
VIT_19s0014g05180	chr19	5477937	5480948 +	G11	CC-NBS-LRR	TD
VIT_19s0090g00240	chr19	6358719	6365615 -	G56	CC-NBS-LRR	TD
VIT_19s0090g00260	chr19	6368383	6371752 -	G56	NBS-LRR	TD
VIT_19s0027g01330	chr19	21995759	22008917 +	G148	NBS-LRR	TD
VIT_19s0027g01350	chr19	22049719	22053240 +	G148	NBS-LRR	TD
VIT_19s0027g01590	chr19	22513152	22515293 -	G11	NBS-LRR	TD
VIT_19s0027g01700	chr19	22640066	22641703 -	G11	CC-NBS	TD
VIT_19s0027g01740	chr19	22695811	22698202 -	G11	CC-NBS-LRR	TD
VIT_19s0027g01750	chr19	22727575	22730253 -	G11	CC-NBS-LRR	TD
VIT_19s0027g01780	chr19	22739784	22748143 -	G11	CC-NBS-LRR	TD
VIT_03s0038g01520	chr3	1044307	1047456 -	G20	NBS-LRR	TD



VIT_03s0038g01530	chr3	1050448	1058022 -	G20	NBS	TD
VIT_03s0038g01540	chr3	1062491	1063732 -	G20	CC-NBS	TD
VIT_03s0038g01550	chr3	1066258	1068897 -	G20	CC-NBS-LRR	TD
VIT_03s0038g01580	chr3	1077896	1078534 -	G20	NBS	TD
VIT_03s0038g01610	chr3	1084197	1085815 -	G20	CC-NBS	TD
VIT_03s0038g01620	chr3	1088445	1096163 -	G20	CC-NBS-LRR	TD
VIT_03s0038g01630	chr3	1111137	1113800 -	G20	CC-NBS	TD
VIT_03s0038g01670	chr3	1168819	1177208 -	G20	CC-NBS	TD
VIT_03s0017g00900	chr3	17482618	17484357 +	G289	NBS-LRR	TD
VIT_03s0017g00920	chr3	17513185	17515837 +	G289	NBS-LRR	TD
VIT_05s0020g04940	chr5	6796470	6797069 -	G20	NBS	TD
VIT_05s0051g00140	chr5	10994256	10998864 -	G216	NBS-LRR	TD
VIT_05s0029g00750	chr5	16368592	16373862 -	G39	NBS-LRR	TD
VIT_05s0029g00780	chr5	16383433	16393132 -	G39	NBS	TD
VIT_05s0029g00870	chr5	16688368	16692897 -	G39	NBS-LRR	TD
VIT_05s0029g00880	chr5	16708097	16712020 -	G39	NBS-LRR	TD
VIT_05s0102g01010	chr5	23455268	23458492 +	G289	NBS-LRR	TD
VIT_05s0102g01030	chr5	23468582	23471320 +	G289	NBS-LRR	TD
VIT_05s0102g01040	chr5	23523144	23526203 +	G289	NBS-LRR	TD
VIT_00s0226g00050	chr5	23854321	23858000 -	G289	NBS-LRR	TD
VIT_00s0226g00080	chr5	23899455	23903534 +	G289	NBS-LRR	TD
VIT_06s0009g01350	chr6	14109804	14112581 -	G20	NBS-LRR	TD
VIT_06s0009g01360	chr6	14134742	14141440 -	G20	NBS-LRR	TD
VIT_07s0005g06180	chr7	11420122	11422881 -	G20	NBS-LRR	TD
VIT_07s0005g06200	chr7	11475778	11479494 -	G20	NBS-LRR	TD
VIT_07s0005g06210	chr7	11510892	11513696 +	G20	NBS-LRR	TD
VIT_07s0005g06220	chr7	11518294	11521590 -	G20	NBS-LRR	TD
VIT_07s0005g06240	chr7	11646327	11648375 -	G20	NBS-LRR	TD
VIT_07s0197g00250	chr7	18472555	18476051 +	G164	NBS-LRR	TD
VIT_07s0197g00240	chr7	18484919	18488688 +	G164	CC-NBS-LRR	TD

VIT_07s0197g00230	chr7	18492872	18496539 +	G164	NBS	TD
VIT_07s0197g00210	chr7	18511045	18514798 +	G164	CC-NBS-LRR	TD
VIT_07s0197g00170	chr7	18527707	18531296 +	G164	CC-NBS-LRR	TD
VIT_07s0197g00140	chr7	18549335	18552572 +	G164	CC-NBS-LRR	TD
VIT_07s0197g00130	chr7	18558908	18564035 +	G164	NBS	TD
VIT_07s0197g00090	chr7	18615627	18619463 +	G164	NBS-LRR	TD
VIT_08s0007g08420	chr8	21772646	21775973 +	G148	CC-NBS-LRR	TD
VIT_09s0002g03270	chr9	2985146	2987797 +	G11	CC-NBS-LRR	TD
VIT_09s0002g03300	chr9	3004166	3012627 +	G11	CC-NBS-LRR	TD
VIT_09s0002g03790	chr9	3471674	3472774 -	G11	CC-NBS	TD
VIT_09s0002g03800	chr9	3474831	3478940 -	G11	CC-NBS-LRR	TD
VIT_09s0002g03820	chr9	3483757	3496747 -	G11	NBS-LRR	TD
VIT_09s0002g03840	chr9	3523496	3527617 -	G11	CC-NBS-LRR	TD
VIT_09s0002g03860	chr9	3565039	3567852 -	G11	CC-NBS-LRR	TD
VIT_09s0002g03870	chr9	3570947	3574796 -	G11	CC-NBS-LRR	TD
VIT_09s0002g04890	chr9	4487070	4489307 +	G11	NBS-LRR	TD
VIT_09s0002g04910	chr9	4497767	4508868 +	G11	CC-NBS	TD
VIT_09s0002g04940	chr9	4543340	4545577 +	G11	NBS-LRR	TD
VIT_09s0002g04950	chr9	4551701	4554535 +	G11	CC-NBS-LRR	TD
VIT_09s0002g05000	chr9	4632649	4635980 +	G11	NBS-LRR	TD
VIT_09s0002g05040	chr9	4670594	4673853 +	G11	CC-NBS-LRR	TD
VIT_09s0002g05050	chr9	4681771	4683987 +	G11	NBS-LRR	TD
VIT_09s0002g05070	chr9	4722218	4726125 +	G11	CC-NBS-LRR	TD
VIT_09s0002g05840	chr9	5642255	5645259 +	G11	CC-NBS-LRR	TD
VIT_09s0002g05870	chr9	5688927	5697812 -	G11	NBS-LRR	TD
VIT_09s0002g05920	chr9	5737378	5739597 -	G11	NBS-LRR	TD
VIT_09s0002g06210	chr9	6143188	6146349 +	G11	NBS-LRR	TD
VIT_09s0002g06260	chr9	6189802	6192901 +	G11	CC-NBS-LRR	TD
VIT_09s0096g00420	chr9	11826647	11829340 -	G11	CC-NBS-LRR	TD
VIT_09s0002g03980	chr9	3688933	3691944 +	G11	CC-NBS-LRR	notTD

VIT_09s0002g04420	chr9	4024160	4026364 +	G11	NBS-LRR	notTD
VIT_09s0002g05220	chr9	4889366	4892529 -	G11	CC-NBS-LRR	notTD
VIT_09s0002g06140	chr9	5979258	5981877 +	G11	NBS-LRR	notTD
VIT_09s0002g06320	chr9	6240665	6244472 +		NBS	notTD
VIT_09s0002g07890	chr9	8351350	8355376 -	G44	CC-NBS-LRR	notTD
VIT_09s0002g08020	chr9	8543746	8546548 -	G44	CC-NBS-LRR	notTD
VIT_09s0002g08160	chr9	8760287	8786178 +	G44	NBS-LRR	notTD
VIT_09s0002g08240	chr9	8865567	8868600 +	G44	CC-NBS-LRR	notTD
VIT_09s0002g08290	chr9	8971667	8975510 -	G44	CC-NBS-LRR	notTD
VIT_09s0002g08300	chr9	9099745	9103465 -	G10	CC-NBS-LRR	notTD
VIT_09s0018g00480	chr9	16666088	16668229 -	G11	NBS-LRR	notTD
VIT_09s0054g01870	chr9	22940972	22945636 +	G2876	TIR-NBS	notTD
VIT_09s0070g00350	chr9	13493838	13495988 +	G11	CC-NBS	notTD
VIT_09s0096g00140	chr9	11553906	11556825 +	G11	NBS	notTD
VIT_09s0096g00200	chr9	11641012	11643369 -	G11	NBS-LRR	notTD
VIT_09s0096g00760	chr9	12342021	12344832 +	G11	CC-NBS-LRR	notTD
VIT_09s0096g00830	chr9	12490597	12491130 +	G1400	NBS	notTD
VIT_00s0184g00120	chr7	14640801	14644523 +	G39	TIR-NBS	notTD
VIT_07s0095g00040	chr7	12781763	12785780 +	G535	NBS-LRR	notTD
VIT_07s0141g00700	chr7	16159295	16162469 -	G44	CC-NBS-LRR	notTD
VIT_07s0141g01030	chr7	15117200	15121252 -	G44	NBS-LRR	notTD
VIT_06s0009g01660	chr6	14763829	14766777 +	G11	CC-NBS-LRR	notTD
VIT_06s0061g00170	chr6	18542961	18553017 -	G10	NBS-LRR	notTD
VIT_05s0051g00170	chr5	11049913	11052491 -	G39	NBS-LRR	notTD
VIT_05s0051g00230	chr5	11142107	11146091 -	G216	NBS-LRR	notTD
VIT_05s0102g00870	chr5	23240908	23244632 -	G289	NBS-LRR	notTD
VIT_05s0102g00940	chr5	23339948	23341681 +	G289	NBS-LRR	notTD
VIT_05s0102g01100	chr5	23614930	23618046 -	G289	NBS-LRR	notTD
VIT_04s0023g02380	chr4	19307517	19310251 +	G20	CC-NBS-LRR	notTD
VIT_03s0017g01620	chr3	19065496	19066596 +	G417	NBS	notTD

VIT_03s0017g01840	chr3	19525099	19526758 -	G417	NBS	notTD
VIT_03s0038g01400	chr3	978958	982622 +	G20	NBS-LRR	notTD
VIT_02s0012g02720	chr2	10620819	10623614 -	G20	NBS-LRR	notTD
VIT_02s0033g00520	chr2	14670377	14678952 +	G368	NBS-LRR	notTD
VIT_19s0014g03950	chr19	4190151	4190744 +		NBS	notTD
VIT_19s0015g01800	chr19	10527535	10530538 +	G2876	TIR-NBS	notTD
VIT_19s0027g00660	chr19	20487774	20490614 +	G148	NBS-LRR	notTD
VIT_19s0027g01070	chr19	21270458	21282840 -	G10	NBS-LRR	notTD
VIT_19s0027g01170	chr19	21732322	21742383 +	G148	NBS-LRR	notTD
VIT_19s0027g01400	chr19	22168322	22176636 +	G148	NBS-LRR	notTD
VIT_19s0027g01490	chr19	22308564	22312139 +	G148	NBS-LRR	notTD
VIT_19s0085g00440	chr19	23479442	23483784 +	G44	NBS-LRR	notTD
VIT_19s0093g00050	chr19	15176573	15181990 +	G148	NBS-LRR	notTD
VIT_19s0093g00380	chr19	15891532	15894603 -	G11	CC-NBS-LRR	notTD
VIT_18s0001g03260	chr18	27353125	27358518 +	G39	TIR-NBS-LRR	notTD
VIT_18s0001g03710	chr18	32781118	32788529 +	G39	TIR-NBS-LRR	notTD
VIT_18s0001g03900	chr18	32654657	32662032 +	G39	TIR-NBS-LRR	notTD
VIT_18s0001g05050	chr18	32090817	32095023 -	G39	TIR-NBS-LRR	notTD
VIT_18s0001g07270	chr18	5499153	5501603 -	G501	NBS	notTD
VIT_18s0001g11250	chr18	9566593	9570177 +	G164	NBS-LRR	notTD
VIT_18s0041g00250	chr18	28050204	28053963 -	G39	TIR-NBS-LRR	notTD
VIT_18s0041g00270	chr18	28070513	28074155 +	G44	NBS-LRR	notTD
VIT_18s0041g01620	chr18	29898448	29904360 +	G39	TIR-NBS-LRR	notTD
VIT_18s0041g01750	chr18	29993681	30002750 -	G216	NBS-LRR	notTD
VIT_18s0041g02120	chr18	30661818	30666793 +	G39	TIR-NBS-LRR	notTD
VIT_18s0041g02450	chr18	31022362	31025778 +	G11	NBS-TIR	notTD
VIT_18s0072g01230	chr18	23908904	23915819 -	G39	NBS	notTD
VIT_18s0089g00090	chr18	32987889	32993788 -	G39	TIR-NBS-LRR	notTD
VIT_18s0089g00600	chr18	33638394	33643653 -	G39	TIR-NBS-LRR	notTD
VIT_18s0117g00020	chr18	26044017	26045809 -	G39	NBS	notTD

VIT_18s0117g00080	chr18	26120416	26123324 +	G39	NBS-LRR	notTD
VIT_18s0117g00360	chr18	26653665	26658508 +	G39	TIR-NBS-LRR	notTD
VIT_17s0000g02830	chr17	2722902	2725337 -	G148	NBS-LRR	notTD
VIT_00s0144g00270	chr16	11463597	11466323 -	G148	NBS-LRR	notTD
VIT_16s0022g01330	chr16	14814938	14816839 +	G20	NBS-LRR	notTD
VIT_15s0021g00130	chr15	9397833	9398768 -	G664	NBS	notTD
VIT_15s0024g01760	chr15	3728979	3732547 -	G39	NBS	notTD
VIT_15s0045g00680	chr15	7123874	7126567 +	G20	CC-NBS-LRR	notTD
VIT_15s0045g00710	chr15	7193005	7207457 -	G56	NBS-LRR	notTD
VIT_15s0045g00880	chr15	7433123	7435822 +	G20	CC-NBS-LRR	notTD
VIT_15s0046g03660	chr15	20161262	20163943 +	G20	CC-NBS-LRR	notTD
VIT_15s0107g00290	chr15	5259743	5262574 +	G39	NBS-LRR	notTD
VIT_14s0030g01050	chr14	5382575	5390214 -	G56	LRR-CC-NBS	notTD
VIT_14s0036g01110	chr14	11819414	11822260 +	G56	CC-NBS-LRR	notTD
VIT_14s0036g01230	chr14	12105751	12118092 +	G56	CC-NBS-LRR-NBS-LRR	notTD
VIT_13s0019g01140	chr13	24905916	24909956 -	G10	CC-NBS-LRR	notTD
VIT_13s0047g00950	chr13	17796458	17800768 -	G44	CC-NBS-LRR	notTD
VIT_13s0047g01010	chr13	17958583	17968155 -	G44	NBS-LRR	notTD
VIT_13s0064g00060	chr13	26185289	26213059 +	G44	CC-NBS-LRR-NBS-LRR	notTD
VIT_13s0064g00320	chr13	26519740	26531797 +	G44	NBS-LRR	notTD
VIT_13s0064g00530	chr13	26919072	26921420 -		NBS-LRR	notTD
VIT_13s0064g00550	chr13	26949303	26950175 -	G417	NBS	notTD
VIT_13s0064g01830	chr13	28373202	28377073 -	G501	CC-NBS	notTD
VIT_13s0067g00650	chr13	19645945	19646874 +	G535	NBS	notTD
VIT_13s0067g00910	chr13	19484033	19491645 +	G10	NBS-LRR	notTD
VIT_13s0067g01100	chr13	19392475	19395831 +	G10	NBS-LRR	notTD
VIT_13s0067g01310	chr13	19262378	19264144 +	G501	NBS	notTD
VIT_13s0067g01490	chr13	19165286	19175181 +	G10	NBS-LRR	notTD
VIT_13s0067g02430	chr13	20033514	20039292 +	G10	NBS-LRR	notTD
VIT_13s0067g02580	chr13	20106367	20112985 +	G10	NBS-LRR	notTD

VIT_13s0074g00130	chr13	7605731	7609912 +	G44	NBS-LRR	notTD
VIT_13s0084g00060	chr13	21840689	21843727 +	G10	NBS-LRR	notTD
VIT_13s0084g00360	chr13	21242658	21246641 -	G44	NBS-LRR	notTD
VIT_13s0084g00420	chr13	21150192	21154305 -	G44	NBS-LRR	notTD
VIT_13s0084g00510	chr13	21020551	21029113 -	G44	NBS-LRR	notTD
VIT_13s0084g00750	chr13	20458428	20463308 +	G44	NBS-LRR	notTD
VIT_13s0101g00300	chr13	12085661	12089974 -	G44	CC-NBS-LRR	notTD
VIT_13s0106g00020	chr13	9383806	9391697 +	G10	NBS-LRR	notTD
VIT_13s0139g00100	chr13	23161429	23168234 +		NBS	notTD
VIT_13s0139g00130	chr13	23198933	23210292 +	G44	NBS-LRR-NBS-LRR	notTD
VIT_13s0158g00010	chr13	26086547	26090124 -	G44	NBS-LRR	notTD
VIT_13s0158g00170	chr13	25935411	25938877 +	G10	CC-NBS-LRR	notTD
VIT_13s0158g00190	chr13	25922980	25924428 -	G535	CC-NBS	notTD
VIT_13s0158g00210	chr13	25895031	25899077 -	G10	NBS-LRR	notTD
VIT_12s0034g01030	chr12	18432532	18448098 -	G10	CC-NBS-LRR	notTD
VIT_12s0034g01070	chr12	18479038	18481971 -	G10	NBS-LRR	notTD
VIT_12s0034g01270	chr12	18850408	18856151 +	G39	TIR-NBS-LRR	notTD
VIT_12s0034g01350	chr12	18904766	18911280 +	G39	TIR-NBS-LRR	notTD
VIT_12s0034g01580	chr12	19204709	19206799 -	G10	NBS	notTD
VIT_12s0034g01660	chr12	19344438	19347511 +	G10	NBS-LRR	notTD
VIT_12s0034g01750	chr12	19445921	19454590 +	G10	NBS-LRR	notTD
VIT_12s0034g02340	chr12	20338054	20339761 +	G501	NBS	notTD
VIT_12s0034g02400	chr12	20470240	20476893 -	G10	NBS-LRR	notTD
VIT_12s0035g00440	chr12	21333410	21337746 +		NBS	notTD
VIT_12s0035g01330	chr12	22755949	22761565 +	G368	CC-NBS-LRR	notTD
VIT_12s0035g01470	chr12	22894644	22898234 -	G368	NBS-LRR	notTD
VIT_12s0035g01630	chr12	23214144	23221820 -	G368	NBS-LRR-NBS-LRR	notTD
VIT_12s0035g01680	chr12	23336363	23341442 +	G368	NBS	notTD
VIT_12s0055g00560	chr12	15928582	15931791 -	G368	NBS-LRR	notTD
VIT_12s0121g00240	chr12	13719845	13743177 -	G417	NBS	notTD

VIT_12s0121g00290	chr12	13851761	13873056 -	G417	NBS	notTD
VIT_12s0142g00570	chr12	217073	219367 +	G417	NBS	notTD
VIT_12s0178g00120	chr12	11294907	11300974 -	G417	NBS	notTD
VIT_12s0178g00190	chr12	11415478	11416668 -	G417	NBS	notTD
VIT_11s0016g01860	chr11	1506369	1508546 -	G11	NBS-LRR	notTD
VIT_11s0016g03990	chr11	3251962	3254889 -	G20	NBS-LRR	notTD
VIT_11s0037g01270	chr11	10877902	10879097 -	G1400	NBS	notTD
VIT_11s0052g00270	chr11	17751482	17754683 -	G56	CC-NBS-LRR	notTD
VIT_00s0515g00020	chr10	1749919	1753861 -	G20	NBS-LRR	notTD
VIT_10s0042g00250	chr10	20954070	20959990 +	G56	CC-NBS-LRR	notTD
VIT_10s0042g00370	chr10	20792042	20797588 +	G56	NBS-LRR	notTD
VIT_01s0011g01120	chr1	972356	975005 -	G148	NBS-LRR	notTD
VIT_01s0026g01120	chr1	10521391	10529397 +	G39	TIR-NBS-LRR	notTD

#### CYP75 genes

VIT_06s0009g02860	chr6	16923856	16925874 +	G66	K13083; CYP75A; flavonoid 3',5'-hydroxylase [EC:1.14.14.81]	TD
VIT_06s0009g02920	chr6	17081481	17083296 +	G66	K13083; CYP75A; flavonoid 3',5'-hydroxylase [EC:1.14.14.81]	TD
VIT_06s0009g03110	chr6	17353534	17354457 +	G66	K13083; CYP75A; flavonoid 3',5'-hydroxylase [EC:1.14.14.81]	TD
VIT_06s0009g03140	chr6	17444153	17446396 -	G66	K13083; CYP75A; flavonoid 3',5'-hydroxylase [EC:1.14.14.81]	TD
VIT_06s0009g03010	chr6	17173732	17175410 +	G66	K13083; CYP75A; flavonoid 3',5'-hydroxylase [EC:1.14.14.81]	TD
VIT_06s0009g02880	chr6	17039830	17041297 +	G66	K13083; CYP75A; flavonoid 3',5'-hydroxylase [EC:1.14.14.81]	TD
VIT_06s0009g02810	chr6	16795211	16796950 +	G66	K13083; CYP75A; flavonoid 3',5'-hydroxylase [EC:1.14.14.81]	TD
VIT_06s0009g03040	chr6	17231742	17232665 +	G66	K13083; CYP75A; flavonoid 3',5'-hydroxylase [EC:1.14.14.81]	TD
VIT_06s0009g02840	chr6	16843274	16845502 +	G66	K13083; CYP75A; flavonoid 3',5'-hydroxylase [EC:1.14.14.81]	TD
VIT_06s0009g02970	chr6	17133919	17136112 +	G66	K13083; CYP75A; flavonoid 3',5'-hydroxylase [EC:1.14.14.81]	TD
VIT_06s0009g02830	chr6	16839623	16840989 +	G66	K13083; CYP75A; flavonoid 3',5'-hydroxylase [EC:1.14.14.81]	TD
VIT_06s0009g03050	chr6	17233378	17234253 +	G66	K13083; CYP75A; flavonoid 3',5'-hydroxylase [EC:1.14.14.81]	TD

#### chalcone synthase genes

VIT_10s0042g00920	chr10	19727108	19728704 -	G34	K00660; CHS; chalcone synthase [EC:2.3.1.74]	TD
-------------------	-------	----------	------------	-----	--	----

VIT_16s0100g00750	chr16	17749915	17751633	+	G34	K00660; CHS; chalcone synthase [EC:2.3.1.74]	TD
VIT_16s0100g01020	chr16	18014561	18016118	-	G34	K00660; CHS; chalcone synthase [EC:2.3.1.74]	TD
VIT_14s0068g00930	chr14	24686995	24688542	+	G34	K00660; CHS; chalcone synthase [EC:2.3.1.74]	TD
VIT_16s0100g00770	chr16	17779694	17781560	+	G34	K00660; CHS; chalcone synthase [EC:2.3.1.74]	TD
VIT_16s0100g01150	chr16	18154999	18156754	-	G34	K00660; CHS; chalcone synthase [EC:2.3.1.74]	TD
VIT_16s0100g00880	chr16	17877762	17879367	-	G34	K00660; CHS; chalcone synthase [EC:2.3.1.74]	TD
VIT_10s0042g00930	chr10	19721140	19722874	-	G34	K00660; CHS; chalcone synthase [EC:2.3.1.74]	TD
VIT_16s0100g00960	chr16	17951602	17952568	-	G34	K00660; CHS; chalcone synthase [EC:2.3.1.74]	TD
VIT_16s0022g01140	chr16	14459402	14460328	+	G34	K00660; CHS; chalcone synthase [EC:2.3.1.74]	TD
VIT_16s0100g00930	chr16	17919268	17920789	-	G34	K00660; CHS; chalcone synthase [EC:2.3.1.74]	TD
VIT_16s0100g00920	chr16	17916025	17917483	-	G34	K00660; CHS; chalcone synthase [EC:2.3.1.74]	TD
VIT_10s0042g00910	chr10	19741924	19743475	-	G34	K00660; CHS; chalcone synthase [EC:2.3.1.74]	TD
VIT_16s0100g01100	chr16	18066665	18068451	-	G34	K00660; CHS; chalcone synthase [EC:2.3.1.74]	TD
VIT_16s0100g00910	chr16	17909184	17910942	+	G34	K00660; CHS; chalcone synthase [EC:2.3.1.74]	TD
VIT_16s0100g00760	chr16	17763444	17764515	+	G34	K00660; CHS; chalcone synthase [EC:2.3.1.74]	TD
VIT_16s0100g00850	chr16	17857368	17858900	-	G34	K00660; CHS; chalcone synthase [EC:2.3.1.74]	TD
VIT_16s0100g01140	chr16	18138317	18140121	-	G34	K00660; CHS; chalcone synthase [EC:2.3.1.74]	TD
VIT_16s0022g01190	chr16	14557320	14558246	+	G34	K00660; CHS; chalcone synthase [EC:2.3.1.74]	TD
VIT_16s0100g00830	chr16	17846607	17848432	+	G34	K00660; CHS; chalcone synthase [EC:2.3.1.74]	TD
VIT_16s0100g01120	chr16	18126465	18128209	-	G34	K00660; CHS; chalcone synthase [EC:2.3.1.74]	TD
VIT_16s0100g01170	chr16	18193499	18195215	-	G34	K00660; CHS; chalcone synthase [EC:2.3.1.74]	TD
VIT_16s0100g01160	chr16	18184851	18186495	-	G34	K00660; CHS; chalcone synthase [EC:2.3.1.74]	TD
VIT_16s0100g01070	chr16	18037091	18038893	-	G34	K00660; CHS; chalcone synthase [EC:2.3.1.74]	TD
VIT_16s0100g00940	chr16	17922707	17924268	-	G34	K00660; CHS; chalcone synthase [EC:2.3.1.74]	TD
VIT_10s0042g00890	chr10	19761954	19763059	-	G34	K00660; CHS; chalcone synthase [EC:2.3.1.74]	TD
VIT_14s0068g00920	chr14	24673459	24675059	+	G34	K00660; CHS; chalcone synthase [EC:2.3.1.74]	TD
VIT_16s0100g01040	chr16	18020430	18023685	+	G34	K00660; CHS; chalcone synthase [EC:2.3.1.74]	TD
VIT_16s0100g00860	chr16	17860847	17862396	-	G34	K00660; CHS; chalcone synthase [EC:2.3.1.74]	TD
VIT_16s0100g01000	chr16	17987894	17989631	-	G34	K00660; CHS; chalcone synthase [EC:2.3.1.74]	TD
VIT_16s0100g00840	chr16	17854026	17855468	-	G34	K00660; CHS; chalcone synthase [EC:2.3.1.74]	TD



**phenylalanine ammonia-lyase (PAL) genes**

VIT_16s0039g01110	chr16	603763	610090 -	G163	K10775; PAL; phenylalanine ammonia-lyase [EC:4.3.1.24]	TD
VIT_11s0016g01660	chr11	1327977	1330009 +	G163	K10775; PAL; phenylalanine ammonia-lyase [EC:4.3.1.24]	TD
VIT_16s0039g01300	chr16	706775	712536 +	G163	K10775; PAL; phenylalanine ammonia-lyase [EC:4.3.1.24]	TD
VIT_16s0039g01240	chr16	688542	691191 +	G163	K10775; PAL; phenylalanine ammonia-lyase [EC:4.3.1.24]	TD
VIT_16s0039g01130	chr16	619822	622337 +	G163	K10775; PAL; phenylalanine ammonia-lyase [EC:4.3.1.24]	TD
VIT_16s0039g01120	chr16	613506	616051 -	G163	K10775; PAL; phenylalanine ammonia-lyase [EC:4.3.1.24]	TD
VIT_16s0039g01360	chr16	777110	779568 +	G163	K10775; PAL; phenylalanine ammonia-lyase [EC:4.3.1.24]	TD
VIT_16s0039g01100	chr16	598409	601085 -	G163	K10775; PAL; phenylalanine ammonia-lyase [EC:4.3.1.24]	TD
VIT_11s0016g01640	chr11	1318994	1321292 +	G163	K10775; PAL; phenylalanine ammonia-lyase [EC:4.3.1.24]	TD
VIT_16s0039g01280	chr16	700063	702582 +	G163	K10775; PAL; phenylalanine ammonia-lyase [EC:4.3.1.24]	TD
VIT_16s0039g01170	chr16	649907	652554 +	G163	K10775; PAL; phenylalanine ammonia-lyase [EC:4.3.1.24]	TD

**beta-glucosidase genes**

VIT_13s0073g00530	chr13	14485790	14488917 -	G334	K05349; bglX; beta-glucosidase [EC:3.2.1.21]	TD
VIT_06s0009g00800	chr6	12851902	12854640 +	G334	K05349; bglX; beta-glucosidase [EC:3.2.1.21]	TD
VIT_06s0009g00790	chr6	12798181	12799747 +	G334	K05349; bglX; beta-glucosidase [EC:3.2.1.21]	TD
VIT_13s0073g00550	chr13	14509890	14518271 -	G334	K05349; bglX; beta-glucosidase [EC:3.2.1.21]	TD
VIT_19s0014g03250	chr19	3377492	3381785 -	G78	K05350; bglB; beta-glucosidase [EC:3.2.1.21]	TD
VIT_19s0014g03240	chr19	3368204	3377120 -	G78	K05350; bglB; beta-glucosidase [EC:3.2.1.21]	TD
VIT_06s0009g00810	chr6	12868021	12872596 -	G334	K01188; E3.2.1.21; beta-glucosidase [EC:3.2.1.21]	TD
VIT_13s0064g01640	chr13	28210888	28215502 -	G78	K01188; E3.2.1.21; beta-glucosidase [EC:3.2.1.21]	TD
VIT_13s0064g01690	chr13	28260597	28274233 -	G2956	K01188; E3.2.1.21; beta-glucosidase [EC:3.2.1.21]	TD
VIT_13s0064g01530	chr13	28124722	28128040 -	G2380	K01188; E3.2.1.21; beta-glucosidase [EC:3.2.1.21]	TD
VIT_14s0036g01050	chr14	11629989	11632704 -	G334	K01188; E3.2.1.21; beta-glucosidase [EC:3.2.1.21]	TD
VIT_13s0064g01560	chr13	28145910	28149615 -	G2380	K01188; E3.2.1.21; beta-glucosidase [EC:3.2.1.21]	TD
VIT_07s0005g00370	chr7	3499557	3501863 +	G78	K01188; E3.2.1.21; beta-glucosidase [EC:3.2.1.21]	TD
VIT_13s0064g01540	chr13	28132344	28144899 -	G78	K01188; E3.2.1.21; beta-glucosidase [EC:3.2.1.21]	TD
VIT_07s0005g00410	chr7	3518499	3527906 +	G78	K01188; E3.2.1.21; beta-glucosidase [EC:3.2.1.21]	TD

VIT_13s0064g01720	chr13	28282996	28289988 -	G78	K01188; E3.2.1.21; beta-glucosidase [EC:3.2.1.21]	TD
VIT_07s0005g00390	chr7	3502718	3511571 +	G78	K01188; E3.2.1.21; beta-glucosidase [EC:3.2.1.21]	TD
VIT_01s0011g00750	chr1	668056	673607 -	G78	K01188; E3.2.1.21; beta-glucosidase [EC:3.2.1.21]	TD
VIT_01s0011g00760	chr1	679670	685040 -	G78	K01188; E3.2.1.21; beta-glucosidase [EC:3.2.1.21]	TD
VIT_07s0005g00360	chr7	3494896	3499084 +	G78	K01188; E3.2.1.21; beta-glucosidase [EC:3.2.1.21]	TD
VIT_13s0064g01700	chr13	28274278	28275020 -	G2956	K01188; E3.2.1.21; beta-glucosidase [EC:3.2.1.21]	TD
VIT_13s0064g01740	chr13	28310959	28316219 -	G78	K01188; E3.2.1.21; beta-glucosidase [EC:3.2.1.21]	TD
VIT_06s0004g01430	chr6	1721538	1743560 +	G78	K01188; E3.2.1.21; beta-glucosidase [EC:3.2.1.21]	TD
VIT_13s0064g01570	chr13	28153654	28161816 -	G78	K01188; E3.2.1.21; beta-glucosidase [EC:3.2.1.21]	TD
VIT_14s0036g01040	chr14	11599164	11601834 -	G334	K01188; E3.2.1.21; beta-glucosidase [EC:3.2.1.21]	TD
VIT_13s0064g01580	chr13	28163048	28183444 -	G78	K01188; E3.2.1.21; beta-glucosidase [EC:3.2.1.21]	TD
VIT_06s0004g01420	chr6	1699485	1713361 +	G78	K01188; E3.2.1.21; beta-glucosidase [EC:3.2.1.21]	TD
VIT_13s0064g01600	chr13	28188984	28190704 -	G78	K01188; E3.2.1.21; beta-glucosidase [EC:3.2.1.21]	TD
VIT_13s0064g01760	chr13	28328405	28332965 -	G78	K01188; E3.2.1.21; beta-glucosidase [EC:3.2.1.21]	TD
VIT_13s0064g01660	chr13	28232965	28239332 -	G78	K01188; E3.2.1.21; beta-glucosidase [EC:3.2.1.21]	TD
VIT_06s0004g01440	chr6	1749828	1768489 +	G78	K01188; E3.2.1.21; beta-glucosidase [EC:3.2.1.21]	TD
VIT_13s0064g01710	chr13	28275397	28276676 -	G78	K01188; E3.2.1.21; beta-glucosidase [EC:3.2.1.21]	TD
VIT_13s0064g01750	chr13	28316947	28328282 -	G78	K01188; E3.2.1.21; beta-glucosidase [EC:3.2.1.21]	TD

#### **cinnamyl-alcohol dehydrogenase genes**

VIT_00s0174g00280	chr7	17153887	17156457 +	G71	K00083; CAD; cinnamyl-alcohol dehydrogenase [EC:1.1.1.195]	TD
VIT_04s0044g00190	chr4	21735345	21738107 -	G71	K00083; CAD; cinnamyl-alcohol dehydrogenase [EC:1.1.1.195]	TD
VIT_04s0044g00210	chr4	21741715	21744162 -	G71	K00083; CAD; cinnamyl-alcohol dehydrogenase [EC:1.1.1.195]	TD
VIT_00s0346g00110	chr7	19434629	19438455 +	G71	K00083; CAD; cinnamyl-alcohol dehydrogenase [EC:1.1.1.195]	TD
VIT_03s0180g00250	chr3	6179858	6181360 -	G71	K00083; CAD; cinnamyl-alcohol dehydrogenase [EC:1.1.1.195]	TD
VIT_00s0346g00100	chr7	19418590	19421270 +	G71	K00083; CAD; cinnamyl-alcohol dehydrogenase [EC:1.1.1.195]	TD
VIT_02s0025g03100	chr2	2446725	2449138 +	G71	K00083; CAD; cinnamyl-alcohol dehydrogenase [EC:1.1.1.195]	TD
VIT_00s0346g00080	chr7	19404853	19407222 +	G71	K00083; CAD; cinnamyl-alcohol dehydrogenase [EC:1.1.1.195]	TD
VIT_00s0346g00090	chr7	19407223	19418024 +	G71	K00083; CAD; cinnamyl-alcohol dehydrogenase [EC:1.1.1.195]	TD
VIT_02s0025g03110	chr2	2455964	2456863 +	G71	K00083; CAD; cinnamyl-alcohol dehydrogenase [EC:1.1.1.195]	TD

VIT_03s0180g00260	chr3	6212329	6214039 -	G71	K00083; CAD; cinnamyl-alcohol dehydrogenase [EC:1.1.1.195]	TD
-------------------	------	---------	-----------	-----	--	----

**peroxidase genes**

VIT_18s0001g06890	chr18	5121954	5123595 +	G49	K00430; E1.11.1.7; peroxidase [EC:1.11.1.7]	TD
VIT_05s0020g02110	chr5	3842855	3844012 +	G31	K00430; E1.11.1.7; peroxidase [EC:1.11.1.7]	TD
VIT_12s0059g02410	chr12	7187086	7188356 +	G31	K00430; E1.11.1.7; peroxidase [EC:1.11.1.7]	TD
VIT_14s0060g00510	chr14	462201	463332 -	G31	K00430; E1.11.1.7; peroxidase [EC:1.11.1.7]	TD
VIT_01s0010g02000	chr1	19848445	19849874 -	G49	K00430; E1.11.1.7; peroxidase [EC:1.11.1.7]	TD
VIT_01s0010g02010	chr1	19853262	19854412 -	G49	K00430; E1.11.1.7; peroxidase [EC:1.11.1.7]	TD
VIT_12s0028g01830	chr12	2459848	2461510 -	G49	K00430; E1.11.1.7; peroxidase [EC:1.11.1.7]	TD
VIT_11s0016g05280	chr11	4611416	4626713 -	G31	K00430; E1.11.1.7; peroxidase [EC:1.11.1.7]	TD
VIT_11s0016g05320	chr11	4652400	4653819 -	G31	K00430; E1.11.1.7; peroxidase [EC:1.11.1.7]	TD
VIT_14s0060g00520	chr14	465057	466070 -	G31	K00430; E1.11.1.7; peroxidase [EC:1.11.1.7]	TD
VIT_06s0004g07750	chr6	8545354	8546653 -	G49	K00430; E1.11.1.7; peroxidase [EC:1.11.1.7]	TD
VIT_08s0058g00970	chr8	10330209	10332083 +	G49	K00430; E1.11.1.7; peroxidase [EC:1.11.1.7]	TD
VIT_08s0058g00990	chr8	10343071	10344275 +	G49	K00430; E1.11.1.7; peroxidase [EC:1.11.1.7]	TD
VIT_01s0010g01980	chr1	19834869	19836149 +	G49	K00430; E1.11.1.7; peroxidase [EC:1.11.1.7]	TD
VIT_01s0010g01960	chr1	19817071	19818341 +	G49	K00430; E1.11.1.7; peroxidase [EC:1.11.1.7]	TD
VIT_01s0010g01970	chr1	19828600	19829880 +	G49	K00430; E1.11.1.7; peroxidase [EC:1.11.1.7]	TD
VIT_05s0020g02120	chr5	3846138	3847499 +	G31	K00430; E1.11.1.7; peroxidase [EC:1.11.1.7]	TD
VIT_06s0004g07770	chr6	8561978	8564357 +	G49	K00430; E1.11.1.7; peroxidase [EC:1.11.1.7]	TD
VIT_08s0058g00980	chr8	10337019	10338975 +	G49	K00430; E1.11.1.7; peroxidase [EC:1.11.1.7]	TD
VIT_14s0060g00540	chr14	475653	476746 -	G31	K00430; E1.11.1.7; peroxidase [EC:1.11.1.7]	TD
VIT_12s0055g01000	chr12	15015547	15016691 -	G31	K00430; E1.11.1.7; peroxidase [EC:1.11.1.7]	TD
VIT_01s0010g02020	chr1	19864341	19865553 +	G49	K00430; E1.11.1.7; peroxidase [EC:1.11.1.7]	TD
VIT_06s0004g01190	chr6	1267641	1274454 -	G49	K00430; E1.11.1.7; peroxidase [EC:1.11.1.7]	TD
VIT_12s0055g01030	chr12	14971055	14972322 -	G31	K00430; E1.11.1.7; peroxidase [EC:1.11.1.7]	TD
VIT_12s0055g00980	chr12	15035642	15037245 +	G31	K00430; E1.11.1.7; peroxidase [EC:1.11.1.7]	TD
VIT_18s0001g06840	chr18	5092164	5094226 +	G49	K00430; E1.11.1.7; peroxidase [EC:1.11.1.7]	TD
VIT_12s0028g01840	chr12	2468084	2469873 -	G49	K00430; E1.11.1.7; peroxidase [EC:1.11.1.7]	TD

VIT_18s0001g06850	chr18	5102796	5105019 +	G49	K00430; E1.11.1.7; peroxidase [EC:1.11.1.7]	TD
VIT_06s0004g01180	chr6	1261685	1263352 -	G49	K00430; E1.11.1.7; peroxidase [EC:1.11.1.7]	TD
VIT_01s0010g01920	chr1	19753771	19754575 +	G49	K00430; E1.11.1.7; peroxidase [EC:1.11.1.7]	TD
VIT_12s0055g01080	chr12	14848903	14857336 -	G31	K00430; E1.11.1.7; peroxidase [EC:1.11.1.7]	TD
VIT_01s0010g01950	chr1	19801427	19802551 -	G49	K00430; E1.11.1.7; peroxidase [EC:1.11.1.7]	TD
VIT_12s0059g02420	chr12	7190475	7199637 +	G31	K00430; E1.11.1.7; peroxidase [EC:1.11.1.7]	TD
VIT_12s0055g01010	chr12	14999381	15000790 -	G31	K00430; E1.11.1.7; peroxidase [EC:1.11.1.7]	TD
VIT_12s0055g01020	chr12	14975322	14976482 -	G31	K00430; E1.11.1.7; peroxidase [EC:1.11.1.7]	TD
VIT_11s0016g05310	chr11	4636943	4651752 -	G31	K00430; E1.11.1.7; peroxidase [EC:1.11.1.7]	TD

#### small auxin-up RNA (SAUR) genes

VIT_03s0038g00930	chr3	736435	737319 +	G1372	K14488; SAUR; SAUR family protein	TD
VIT_03s0038g01120	chr3	867890	868156 +	G53	K14488; SAUR; SAUR family protein	TD
VIT_09s0054g00730	chr9	21569331	21569744 +	G146	K14488; SAUR; SAUR family protein	TD
VIT_06s0061g00400	chr6	18965662	18966093 +	G146	K14488; SAUR; SAUR family protein	TD
VIT_03s0038g01210	chr3	894854	895141 -	G53	K14488; SAUR; SAUR family protein	TD
VIT_03s0038g01310	chr3	921733	927965 +	G53	K14488; SAUR; SAUR family protein	TD
VIT_04s0023g00490	chr4	17100613	17100903 -	G53	K14488; SAUR; SAUR family protein	TD
VIT_04s0023g00570	chr4	17148746	17149040 -	G53	K14488; SAUR; SAUR family protein	TD
VIT_04s0023g00560	chr4	17146276	17146771 -	G53	K14488; SAUR; SAUR family protein	TD
VIT_09s0054g00680	chr9	21487058	21487600 +	G146	K14488; SAUR; SAUR family protein	TD
VIT_09s0054g00670	chr9	21482997	21483422 -	G146	K14488; SAUR; SAUR family protein	TD
VIT_03s0038g01270	chr3	908817	909399 +	G53	K14488; SAUR; SAUR family protein	TD
VIT_04s0023g00550	chr4	17136441	17137012 -	G53	K14488; SAUR; SAUR family protein	TD
VIT_03s0038g01260	chr3	905892	906181 +	G53	K14488; SAUR; SAUR family protein	TD
VIT_04s0023g00540	chr4	17134287	17134600 -	G53	K14488; SAUR; SAUR family protein	TD
VIT_04s0023g00580	chr4	17151931	17152421 -	G53	K14488; SAUR; SAUR family protein	TD
VIT_03s0038g01170	chr3	885397	885684 -	G53	K14488; SAUR; SAUR family protein	TD
VIT_03s0038g01190	chr3	892009	892382 +	G53	K14488; SAUR; SAUR family protein	TD
VIT_03s0038g01150	chr3	880653	881315 -	G53	K14488; SAUR; SAUR family protein	TD

VIT_03s0038g01180	chr3	888635	888955 +	G53	K14488; SAUR; SAUR family protein	TD
VIT_01s0146g00210	chr1	23042231	23042737 +	G2636	K14488; SAUR; SAUR family protein	TD
VIT_03s0038g01220	chr3	897891	898180 +	G53	K14488; SAUR; SAUR family protein	TD
VIT_03s0038g00940	chr3	738127	738887 +	G1372	K14488; SAUR; SAUR family protein	TD
VIT_06s0061g00390	chr6	18946425	18946861 +	G146	K14488; SAUR; SAUR family protein	TD
VIT_09s0054g00740	chr9	21572109	21572643 -	G146	K14488; SAUR; SAUR family protein	TD
VIT_03s0038g01080	chr3	858886	859170 -	G53	K14488; SAUR; SAUR family protein	TD
VIT_03s0038g01160	chr3	883689	883976 -	G53	K14488; SAUR; SAUR family protein	TD
VIT_18s0001g13980	chr18	11987475	11987922 -	G53	K14488; SAUR; SAUR family protein	TD
VIT_03s0038g01110	chr3	866357	866897 +	G53	K14488; SAUR; SAUR family protein	TD
VIT_04s0023g00520	chr4	17122551	17122853 -	G53	K14488; SAUR; SAUR family protein	TD
VIT_03s0038g01090	chr3	862995	863398 +	G53	K14488; SAUR; SAUR family protein	TD
VIT_04s0023g00530	chr4	17132411	17132780 -	G53	K14488; SAUR; SAUR family protein	TD
VIT_03s0038g01280	chr3	910867	911175 -	G53	K14488; SAUR; SAUR family protein	TD
VIT_09s0054g00660	chr9	21457322	21457844 +	G146	K14488; SAUR; SAUR family protein	TD
VIT_18s0001g14000	chr18	12002927	12003389 +	G53	K14488; SAUR; SAUR family protein	TD
VIT_04s0023g00500	chr4	17102184	17102480 -	G53	K14488; SAUR; SAUR family protein	TD
VIT_03s0038g01230	chr3	900918	901205 +	G53	K14488; SAUR; SAUR family protein	TD
VIT_03s0038g01130	chr3	869586	872380 +	G53	K14488; SAUR; SAUR family protein	TD
VIT_01s0146g00180	chr1	22986065	22987155 -	G2636	K14488; SAUR; SAUR family protein	TD
VIT_03s0038g01100	chr3	864608	864876 +	G53	K14488; SAUR; SAUR family protein	TD

#### **pathogenesis-related genes**

VIT_03s0088g00690	chr3	8895244	8909155 -	G141	K13449; PR1; pathogenesis-related protein 1	TD
VIT_03s0088g00750	chr3	8949588	8950233 -	G141	K13449; PR1; pathogenesis-related protein 1	TD
VIT_03s0088g00910	chr3	9119915	9130668 -	G141	K13449; PR1; pathogenesis-related protein 1	TD
VIT_03s0088g00940	chr3	9150089	9150575 -	G141	K13449; PR1; pathogenesis-related protein 1	TD
VIT_03s0088g00720	chr3	8923838	8924209 -	G141	K13449; PR1; pathogenesis-related protein 1	TD
VIT_03s0088g00680	chr3	8883856	8884465 -	G141	K13449; PR1; pathogenesis-related protein 1	TD
VIT_03s0088g00700	chr3	8911524	8912111 -	G141	K13449; PR1; pathogenesis-related protein 1	TD

VIT_03s0088g00810	chr3	9044529	9045211 -	G141	K13449; PR1; pathogenesis-related protein 1	TD
VIT_03s0088g00780	chr3	8986184	8986955 -	G141	K13449; PR1; pathogenesis-related protein 1	TD
VIT_03s0088g00710	chr3	8916223	8916893 -	G141	K13449; PR1; pathogenesis-related protein 1	TD
VIT_03s0088g00890	chr3	9101007	9101495 -	G141	K13449; PR1; pathogenesis-related protein 1	TD
VIT_03s0088g00900	chr3	9106967	9110222 -	G141	K13449; PR1; pathogenesis-related protein 1	TD

### disease resistance genes

VIT_03s0038g01670	chr3	1168819	1177208 -	G20	K13457; RPM1, RPS3; disease resistance protein RPM1	TD
VIT_03s0038g01620	chr3	1088445	1096163 -	G20	K13457; RPM1, RPS3; disease resistance protein RPM1	TD
VIT_01s0011g00960	chr1	812008	816090 +	G20	K13457; RPM1, RPS3; disease resistance protein RPM1	TD
VIT_01s0011g00950	chr1	806983	809670 +	G20	K13457; RPM1, RPS3; disease resistance protein RPM1	TD
VIT_01s0011g00990	chr1	865318	867702 +	G20	K13457; RPM1, RPS3; disease resistance protein RPM1	TD
VIT_01s0011g00970	chr1	850780	857788 +	G20	K13457; RPM1, RPS3; disease resistance protein RPM1	TD
VIT_05s0020g04940	chr5	6796470	6797069 -	G20	K13457; RPM1, RPS3; disease resistance protein RPM1	TD
VIT_05s0020g04930	chr5	6784989	6786602 -	G20	K13457; RPM1, RPS3; disease resistance protein RPM1	TD
VIT_06s0009g01360	chr6	14134742	14141440 -	G20	K13457; RPM1, RPS3; disease resistance protein RPM1	TD
VIT_01s0011g01020	chr1	901077	903884 +	G20	K13457; RPM1, RPS3; disease resistance protein RPM1	TD
VIT_01s0011g01000	chr1	872585	888273 +	G20	K13457; RPM1, RPS3; disease resistance protein RPM1	TD
VIT_07s0005g06180	chr7	11420122	11422881 -	G20	K13457; RPM1, RPS3; disease resistance protein RPM1	TD
VIT_07s0005g06220	chr7	11518294	11521590 -	G20	K13457; RPM1, RPS3; disease resistance protein RPM1	TD
VIT_12s0057g01140	chr12	9420074	9426959 +	G193	K13457; RPM1, RPS3; disease resistance protein RPM1	TD
VIT_07s0005g06210	chr7	11510892	11513696 +	G20	K13457; RPM1, RPS3; disease resistance protein RPM1	TD
VIT_07s0005g06200	chr7	11475778	11479494 -	G20	K13457; RPM1, RPS3; disease resistance protein RPM1	TD
VIT_06s0009g01350	chr6	14109804	14112581 -	G20	K13457; RPM1, RPS3; disease resistance protein RPM1	TD
VIT_15s0045g00980	chr15	7560406	7562199 +	G20	K13457; RPM1, RPS3; disease resistance protein RPM1	TD
VIT_03s0038g01610	chr3	1084197	1085815 -	G20	K13457; RPM1, RPS3; disease resistance protein RPM1	TD
VIT_03s0038g01630	chr3	1111137	1113800 -	G20	K13457; RPM1, RPS3; disease resistance protein RPM1	TD
VIT_09s0002g03820	chr9	3483757	3496747 -	G11	K13459; RPS2; disease resistance protein RPS2	TD
VIT_09s0002g03870	chr9	3570947	3574796 -	G11	K13459; RPS2; disease resistance protein RPS2	TD

VIT_19s0014g00870	chr19	897695	916258 -	G11	K13459; RPS2; disease resistance protein RPS2	TD
VIT_19s0014g05140	chr19	5423967	5430360 +	G11	K13459; RPS2; disease resistance protein RPS2	TD
VIT_19s0027g01580	chr19	22485251	22486783 -	G11	K13459; RPS2; disease resistance protein RPS2	TD
VIT_09s0096g00390	chr9	11808577	11809362 +	G11	K13459; RPS2; disease resistance protein RPS2	TD
VIT_19s0027g01750	chr19	22727575	22730253 -	G11	K13459; RPS2; disease resistance protein RPS2	TD
VIT_09s0002g04910	chr9	4497767	4508868 +	G11	K13459; RPS2; disease resistance protein RPS2	TD
VIT_19s0027g01630	chr19	22547885	22550086 +	G11	K13459; RPS2; disease resistance protein RPS2	TD
VIT_09s0002g05070	chr9	4722218	4726125 +	G11	K13459; RPS2; disease resistance protein RPS2	TD
VIT_09s0002g03270	chr9	2985146	2987797 +	G11	K13459; RPS2; disease resistance protein RPS2	TD
VIT_11s0052g00210	chr11	17677140	17680684 +	G56	K13459; RPS2; disease resistance protein RPS2	TD
VIT_19s0014g00920	chr19	957484	960645 -	G11	K13459; RPS2; disease resistance protein RPS2	TD
VIT_19s0014g05180	chr19	5477937	5480948 +	G11	K13459; RPS2; disease resistance protein RPS2	TD
VIT_14s0081g00780	chr14	9273608	9280327 -	G56	K13459; RPS2; disease resistance protein RPS2	TD
VIT_19s0027g01600	chr19	22525847	22527133 +	G11	K13459; RPS2; disease resistance protein RPS2	TD
VIT_09s0002g04940	chr9	4543340	4545577 +	G11	K13459; RPS2; disease resistance protein RPS2	TD
VIT_19s0027g01740	chr19	22695811	22698202 -	G11	K13459; RPS2; disease resistance protein RPS2	TD
VIT_12s0035g01280	chr12	22669016	22672221 +	G368	K13459; RPS2; disease resistance protein RPS2	TD
VIT_12s0035g01260	chr12	22613421	22621094 +	G368	K13459; RPS2; disease resistance protein RPS2	TD
VIT_19s0027g01700	chr19	22640066	22641703 -	G11	K13459; RPS2; disease resistance protein RPS2	TD
VIT_09s0002g03790	chr9	3471674	3472774 -	G11	K13459; RPS2; disease resistance protein RPS2	TD
VIT_19s0014g05160	chr19	5439530	5442340 +	G11	K13459; RPS2; disease resistance protein RPS2	TD
VIT_09s0002g03300	chr9	3004166	3012627 +	G11	K13459; RPS2; disease resistance protein RPS2	TD
VIT_19s0027g01590	chr19	22513152	22515293 -	G11	K13459; RPS2; disease resistance protein RPS2	TD
VIT_19s0027g01780	chr19	22739784	22748143 -	G11	K13459; RPS2; disease resistance protein RPS2	TD
VIT_19s0027g01570	chr19	22475590	22477146 -	G11	K13459; RPS2; disease resistance protein RPS2	TD
VIT_09s0002g05920	chr9	5737378	5739597 -	G11	K13459; RPS2; disease resistance protein RPS2	TD
VIT_09s0002g04950	chr9	4551701	4554535 +	G11	K13459; RPS2; disease resistance protein RPS2	TD
VIT_19s0014g00580	chr19	600125	606739 +	G11	K13459; RPS2; disease resistance protein RPS2	TD
VIT_11s0052g00200	chr11	17665848	17669845 +	G56	K13459; RPS2; disease resistance protein RPS2	TD
VIT_19s0027g01540	chr19	22395374	22395547 -	G491	K13459; RPS2; disease resistance protein RPS2	TD

VIT_19s0014g05150	chr19	5432059	5434734 -	G11	K13459; RPS2; disease resistance protein RPS2	TD
VIT_09s0002g05840	chr9	5642255	5645259 +	G11	K13459; RPS2; disease resistance protein RPS2	TD
VIT_19s0014g00900	chr19	929691	938363 -	G11	K13459; RPS2; disease resistance protein RPS2	TD
VIT_09s0096g00420	chr9	11826647	11829340 -	G11	K13459; RPS2; disease resistance protein RPS2	TD
VIT_09s0002g03800	chr9	3474831	3478940 -	G11	K13459; RPS2; disease resistance protein RPS2	TD