

Table 1: RNA sequence results showing black raspberry genes that are upregulated when comparing untreated (wild-type) vs. *Verticillium*-infected ‘Jewel’ roots.

Gene-type category	Bras_Gene ID	Rubus Linkage Group	Black Raspberry Scaffold Locus	Wild-type FPKM1	Verticillium-infected FPKM2	log2 fold change	p-value	Uniprot Annotation
R-like	G23625	SNM	S0475:78736-79332	45.62	996.62	4.45	5.00E ⁻⁰⁵	PDF1.4: Defensin-like protein 19 (<i>Arabidopsis thaliana</i>)
	G10513	SNM	S0072:81640-92172	0.57	12.31	4.42	5.00E ⁻⁰⁵	(3S,6E)-nerolidol synthase 1, chloroplastic (<i>Fragaria vesca</i>)
	G04810	2	S0019:29109-30316	20.63	358.95	4.12	5.00E ⁻⁰⁵	AOC4: Allene oxide cyclase 4, chloroplastic (<i>Arabidopsis thaliana</i>)
	G20341	SNM	S0304:204059-204607	2.97	50.72	4.10	2.60E ⁻⁰³	(-)-alpha-pinene synthase (<i>Fragaria vesca</i>)
	G02684	SNM	S0008:1004709-1006221	2.67	44.20	4.05	2.00E ⁻⁰⁴	RBCS: Ribulose bisphosphate carboxylase small chain, chloroplastic (<i>Pyrus pyrifolia</i>)
	G05636	6	S0024:305572-306601	5.33	88.05	4.05	5.00E ⁻⁰⁵	TRPA1: Tryptophan synthase alpha chain (<i>Arabidopsis thaliana</i>)
	G01273	1	S0003:2152532-2153635	5.93	82.87	3.80	5.00E ⁻⁰⁵	Endochitinase (<i>Pisum sativum</i>)
	G12710	7	S0104:279729-280510	2.75	29.82	3.44	5.50E ⁻⁰⁴	23 kDa jasmonate-induced protein (<i>Hordeum vulgare</i>)
	G23083	SNM	S0438:104827-108328	3.10	32.89	3.41	1.00E ⁻⁰⁴	Thaumatococin-like protein 1 (<i>Prunus persica</i>)
	G24696	SNM	S0559:48833-49469	6.74	67.16	3.32	1.50E ⁻⁰⁴	UBP8: Ubiquitin carboxyl-terminal hydrolase 8 (<i>Arabidopsis thaliana</i>)
TF	G11629	1	S0088:30091-32344	1.04	9.19	3.14	8.95E ⁻⁰³	ABR1: Ethylene-responsive transcription factor ABR1 (<i>Arabidopsis thaliana</i>)
	G01734	5	S0005:356081-356846	4.50	37.56	3.06	9.00E ⁻⁰⁴	At1g01500: Uncharacterized protein At1g01500 (<i>Arabidopsis thaliana</i>)
	G11097	6	S0079:441741-442965	12.49	103.45	3.05	5.00E ⁻⁰⁵	At5g58410: E3 ubiquitin-protein ligase listerin (<i>Arabidopsis thaliana</i>)
	G01102	1	S0003:1143991-1158167	20.26	167.21	3.05	5.00E ⁻⁰⁵	DHN1: Dehydrin DHN1 (<i>Hordeum vulgare</i>)
	G12712	7	S0104:284377-285142	3.10	24.59	2.99	7.25E ⁻⁰³	23 kDa jasmonate-induced protein (<i>Hordeum vulgare</i>)
	G07238	5	S0038:153298-154550	2.96	21.07	2.83	1.05E ⁻⁰³	SRG1: Protein SRG1 (<i>Arabidopsis thaliana</i>)
TF	G03027	SNM	S0009:1160229-1160877	14.07	99.28	2.82	5.00E ⁻⁰⁵	ERF017: Ethylene-responsive transcription factor ERF017 (<i>Arabidopsis thaliana</i>)
	G12918	SNM	S0108:355317-356918	1.36	9.09	2.74	1.50E ⁻⁰²	BG: Basic 7S globulin (<i>Glycine max</i>)
	G26677	SNM	S0832:19992-23592	28.55	187.94	2.72	5.00E ⁻⁰⁵	ADH1: Alcohol dehydrogenase 1 (<i>Trifolium repens</i>)

	G25479	SNM	S0637:82772-84084	37.41	235.66	2.66	5.00E ⁻⁰⁵	ROMT: Trans-resveratrol di-O-methyltransferase (<i>Vitis vinifera</i>)
	G03808	6	S0013:478100-484695	3.37	17.96	2.41	3.00E ⁻⁰⁴	CYP94B3: Cytochrome P450 94B3 (<i>Arabidopsis thaliana</i>)
	G12919	SNM	S0108:357560-358871	2.89	15.38	2.41	5.00E ⁻⁰⁵	BG: Basic 7S globulin (<i>Glycine max</i>)
	G16111	4	S0174:196896-197673	6.41	32.80	2.36	4.00E ⁻⁰⁴	At5g65560: Pentatricopeptide repeat-containing protein At5g65560 (<i>Arabidopsis thaliana</i>)
R-like	G06290	3	S0029:582802-584511	2.74	13.92	2.34	1.90E ⁻⁰³	NPK1: Mitogen-activated protein kinase kinase kinase NPK1 (<i>Nicotiana tabacum</i>)
	G09676	2	S0062:480088-480961	5.06	25.32	2.32	5.00E ⁻⁰⁴	EDL3: EID1-like F-box protein 3 (<i>Arabidopsis thaliana</i>)
	G19956	3	S0289:60290-61637	44.99	224.37	2.32	5.00E ⁻⁰⁵	PUB21: U-box domain-containing protein 21 (<i>Arabidopsis thaliana</i>)
	G14616	SNM	S0141:93130-97411	3.51	17.40	2.31	4.50E ⁻⁰⁴	WRKY12: Probable WRKY transcription factor 12 (<i>Arabidopsis thaliana</i>)
	G12916	SNM	S0108:336691-338775	4.77	23.35	2.29	5.00E ⁻⁰⁵	BG: Basic 7S globulin (<i>Glycine max</i>)
	G16846	1	S0192:77322-78940	1.72	8.44	2.29	2.10E ⁻⁰³	LE: Gibberellin 3-beta-dioxygenase 1 (<i>Pisum sativum</i>)
	G14387	5	S0137:32097-34333	8.25	40.15	2.28	5.00E ⁻⁰⁵	ANS: Leucoanthocyanidin dioxygenase (<i>Malus domestica</i>)
	G07799	7	S0043:445793-446264	125.48	601.10	2.26	5.00E ⁻⁰⁵	HSP17.6C: 17.6 kDa class I heat shock protein 3 (<i>Arabidopsis thaliana</i>)
	G22050	SNM	S0381:173658-175485	3.41	16.01	2.23	2.10E ⁻⁰³	TI572: Seed trypsin/chymotrypsin inhibitor TI5-72 (<i>Pisum sativum</i>)
	G11171	1	S0081:121691-123688	9.17	42.26	2.20	5.00E ⁻⁰⁵	XTH6: Probable xyloglucan endotransglucosylase/hydrolase protein 6 (<i>Arabidopsis thaliana</i>)
TF	G06013	3	S0027:115749-116316	12.46	56.06	2.17	5.00E ⁻⁰⁵	NFYB3: Nuclear transcription factor Y subunit B-3 (<i>Arabidopsis thaliana</i>)
	G07584	6	S0041:597347-598550	10.41	45.63	2.13	5.00E ⁻⁰⁵	PUB23: E3 ubiquitin-protein ligase PUB23 (<i>Arabidopsis thaliana</i>)
	G07239	5	S0038:173896-175168	13.03	54.53	2.06	5.00E ⁻⁰⁵	SRG1: Protein SRG1 (<i>Arabidopsis thaliana</i>)
	G00307	4	S0001:1772722-1780326	136.61	561.16	2.04	5.00E ⁻⁰⁵	GOLS1: Galactinol synthase 1 (<i>Ajuga reptans</i>)
	G02234	2	S0007:217892-218372	154.47	631.61	2.03	5.00E ⁻⁰⁵	ATJ11: Chaperone protein dnaJ 11, chloroplastic (<i>Arabidopsis thaliana</i>)
	G00616	2	S0002:817491-817788	24.38	99.04	2.02	8.90E ⁻⁰³	CML27: Probable calcium-binding protein CML27 (<i>Arabidopsis thaliana</i>)
TF	G25293	7	S0618:45497-46217	19.50	79.18	2.02	5.00E ⁻⁰⁵	ERF2: Ethylene-responsive transcription factor 2 (<i>Nicotiana tabacum</i>)
	G19628	3	S0279:15421-20001	16.60	66.55	2.00	5.00E ⁻⁰⁵	BAG6: BAG family molecular chaperone regulator 6 (<i>Arabidopsis thaliana</i>)

TF	G26901	SNM	S0878:22918-23293	7.51	29.58	1.98	1.22E ⁻⁰²	At5g66910: Probable disease resistance protein At5g66910 (<i>Arabidopsis thaliana</i>)
	G17001	6	S0196:280932-281790	157.41	619.07	1.98	5.00E ⁻⁰⁵	CAF1-9: Probable CCR4-associated factor 1 homolog 9 (<i>Arabidopsis thaliana</i>)
	G13718	6	S0123:340360-342831	41.52	162.99	1.97	5.00E ⁻⁰⁵	NRT2.1: High-affinity nitrate transporter 2.1 (<i>Arabidopsis thaliana</i>)
	G20671	SNM	S0318:122140-122941	4.67	18.27	1.97	4.85E ⁻⁰³	LECRK71: L-type lectin-domain containing receptor kinase VII.1 (<i>Arabidopsis thaliana</i>)
	G04271	1	S0015:1076712-1077456	19.92	77.81	1.97	5.00E ⁻⁰⁵	OBF1: Ocs element-binding factor 1 (<i>Zea mays</i>)
	G20062	SNM	S0293:242462-245978	1.90	7.39	1.96	8.50E ⁻⁰⁴	At5g02620: Ankyrin repeat-containing protein At5g02620 (<i>Arabidopsis thaliana</i>)
	G01886	5	S0005:1295762-1305712	2.86	10.98	1.94	5.00E ⁻⁰⁵	SWEET14: Bidirectional sugar transporter SWEET14 (<i>Oryza sativa</i> subsp. <i>japonica</i>)
TF	G07836	7	S0043:665277-666717	66.12	251.40	1.93	5.00E ⁻⁰⁵	HSPRO2: Nematode resistance protein-like HSPRO2 (<i>Arabidopsis thaliana</i>)
	G26210	SNM	S0743:39348-40529	3370.65	12772.50	1.92	5.00E ⁻⁰⁵	Glycine-rich protein DC9.1 (<i>Daucus carota</i>)
	G04522	2	S0017:592510-594159	16.06	60.21	1.91	5.00E ⁻⁰⁵	HSP17.9-D: 17.9 kDa class II heat shock protein (<i>Glycine max</i>)
	G10526	SNM	S0072:151866-153185	5.96	22.20	1.90	3.00E ⁻⁰⁴	PSBQ2: Oxygen-evolving enhancer protein 3-2, chloroplastic (<i>Arabidopsis thaliana</i>)
	G17756	SNM	S0219:159868-173269	140.28	515.05	1.88	5.00E ⁻⁰⁵	ARGAH1: Arginase 1, mitochondrial (<i>Arabidopsis thaliana</i>)
	G25480	SNM	S0637:89699-91284	320.22	1167.99	1.87	5.00E ⁻⁰⁵	ROMT: Trans-resveratrol di-O-methyltransferase (<i>Vitis vinifera</i>)
	G27328	SNM	S0998:22639-26316	9.76	35.30	1.85	5.00E ⁻⁰⁵	LAC14: Laccase-14 (<i>Arabidopsis thaliana</i>)
	G13623	6	S0122:18514-25893	8.87	31.84	1.84	5.00E ⁻⁰⁵	At1g80440: F-box/kelch-repeat protein At1g80440 (<i>Arabidopsis thaliana</i>)
	G10471	2	S0071:393748-396686	2.86	10.24	1.84	9.50E ⁻⁰⁴	FMO1: Probable flavin-containing monooxygenase 1 (<i>Arabidopsis thaliana</i>)
	G08287	6	S0048:5747-7391	146.34	506.70	1.79	5.00E ⁻⁰⁵	At3g01520: Universal stress protein A-like protein (<i>Arabidopsis thaliana</i>)
	G10047	5	S0066:299132-299696	20.86	72.22	1.79	5.00E ⁻⁰⁵	GLR2.7: Glutamate receptor 2.7 (<i>Arabidopsis thaliana</i>)
	G19145	1	S0263:78391-78775	75.24	255.18	1.76	5.00E ⁻⁰⁵	CP12-2: Calvin cycle protein CP12-2, chloroplastic (<i>Arabidopsis thaliana</i>)
	G22766	6	S0420:35791-37671	36.87	123.35	1.74	5.00E ⁻⁰⁵	MYB4: Myb-related protein Myb4 (<i>Oryza sativa</i> subsp. <i>japonica</i>)
	G19292	SNM	S0267:184511-190742	2.39	7.91	1.72	6.00E ⁻⁰⁴	HT1: Serine/threonine-protein kinase HT1 (<i>Arabidopsis thaliana</i>)
	G15264	6	S0155:139554-140352	105.04	342.30	1.70	5.00E ⁻⁰⁵	At1g63220: C2 domain-containing protein At1g63220 (<i>Arabidopsis thaliana</i>)

TF	G13301	4	S0116:169053-171538	5.32	17.29	1.70	5.00E ⁻⁰⁵	MYB86: Transcription factor MYB86 (<i>Arabidopsis thaliana</i>)
	G05565	2	S0023:869840-870368	8.91	28.93	1.70	1.12E ⁻⁰²	PSB27-1: Photosystem II repair protein PSB27-H1, chloroplastic (<i>Arabidopsis thaliana</i>)
	G10966	2	S0077:451486-451798	133.44	427.52	1.68	5.00E ⁻⁰⁵	DIR1: Putative lipid-transfer protein DIR1 (<i>Arabidopsis thaliana</i>)
	G19752	SNM	S0283:44038-46284	2.27	7.23	1.67	1.75E ⁻⁰³	AAE11: Butyrate--CoA ligase AAE11, peroxisomal (<i>Arabidopsis thaliana</i>)
	G00512	2	S0002:269367-270150	221.59	703.09	1.67	5.00E ⁻⁰⁵	ZAT10: Zinc finger protein ZAT10 (<i>Arabidopsis thaliana</i>)
	G18164	7	S0232:149260-155305	771.59	2443.64	1.66	5.00E ⁻⁰⁵	SAP8: Zinc finger A20 and AN1 domain-containing stress-associated protein 8 (<i>Oryza sativa</i> subsp. <i>japonica</i>)
	G16585	7	S0184:251031-252042	10.37	32.85	1.66	5.00E ⁻⁰⁵	BG: Basic 7S globulin (<i>Glycine max</i>)
	G08827	3	S0054:9644-11541	39.87	125.60	1.66	5.00E ⁻⁰⁵	TIFY9: Protein TIFY 9 (<i>Arabidopsis thaliana</i>)
	G08258	6	S0047:575336-580694	2.51	7.87	1.65	1.04E ⁻⁰²	PCMP-E93: Pentatricopeptide repeat-containing protein At3g18970 (<i>Arabidopsis thaliana</i>)
	G13716	6	S0123:306544-309563	9.99	31.32	1.65	5.00E ⁻⁰⁵	NRT2.1: High-affinity nitrate transporter 2.1 (<i>Arabidopsis thaliana</i>)
	G02048	3	S0006:400759-411644	11.66	36.10	1.63	5.00E ⁻⁰⁵	ZAT12: Zinc finger protein ZAT12 (<i>Arabidopsis thaliana</i>)
	G14179	6	S0133:23183-28197	22.64	69.85	1.63	1.11E ⁻⁰²	Auxin-induced protein 6B (<i>Glycine max</i>)
	G19637	3	S0279:76323-80750	32.43	99.68	1.62	5.00E ⁻⁰⁵	At4g01130: GDSL esterase/lipase At4g01130 (<i>Arabidopsis thaliana</i>)
	G10797	3	S0075:340795-342632	3.77	11.59	1.62	4.70E ⁻⁰³	RCCR: Red chlorophyll catabolite reductase, chloroplastic (<i>Arabidopsis thaliana</i>)
	G07128	4	S0037:205899-206730	11.90	36.41	1.61	1.00E ⁻⁰⁴	GXM1: Glucuronoxylan 4-O-methyltransferase 1 (<i>Arabidopsis thaliana</i>)
R-like	G18386	SNM	S0239:116137-139577	4.23	12.89	1.61	5.00E ⁻⁰⁵	CHIA1: Endochitinase 1 (<i>Theobroma cacao</i>)
	G15332	3	S0156:224169-225732	9.45	28.69	1.60	5.00E ⁻⁰⁵	At1g06800: Phospholipase A1-Igama1, chloroplastic (<i>Arabidopsis thaliana</i>)
	G21291	SNM	S0346:155480-155912	33.62	100.95	1.59	5.00E ⁻⁰⁵	ALMT9: Aluminum-activated malate transporter 9 (<i>Arabidopsis thaliana</i>)
TF	G05470	2	S0023:161860-162703	18.94	56.62	1.58	5.00E ⁻⁰⁵	MYB44: Transcription factor MYB44 (<i>Arabidopsis thaliana</i>)
R-like	G10778	3	S0075:218677-219730	24.72	72.43	1.55	5.00E ⁻⁰⁵	MEKK1: Mitogen-activated protein kinase kinase kinase 1 (<i>Arabidopsis thaliana</i>)
	G24310	SNM	S0525:32081-33692	12.81	37.45	1.55	5.00E ⁻⁰⁵	At1g51880: Probable LRR receptor-like serine/threonine-protein kinase At1g51880 (<i>Arabidopsis thaliana</i>)
R-like	G03203	1	S0010:1224137-1224701	16.35	47.70	1.54	1.00E ⁻⁰⁴	PR-1: Pathogenesis-related protein PR-1 (<i>Medicago truncatula</i>)

	G10965	2	S0077:449009-450603	52.37	152.41	1.54	5.00E ⁻⁰⁵	At5g48480: Uncharacterized protein At5g48480 (<i>Arabidopsis thaliana</i>)
	G18552	SNM	S0243:201868-203398	2140.15	6228.22	1.54	5.00E ⁻⁰⁵	Auxin-repressed 12.5 kDa protein (<i>Fragaria ananassa</i>)
	G00372	4	S0001:2153115-2156350	15.04	43.67	1.54	5.00E ⁻⁰⁵	ILL1: IAA-amino acid hydrolase ILR1-like 1 (<i>Oryza sativa</i> subsp. <i>indica</i>)
TF	G11781	5	S0090:229024-230047	106.53	307.02	1.53	5.00E ⁻⁰⁵	ERF5: Ethylene-responsive transcription factor 5 (<i>Arabidopsis thaliana</i>)
	G05793	3	S0025:433007-434105	10.16	29.23	1.53	5.00E ⁻⁰⁵	PUP4: Probable purine permease 4 (<i>Arabidopsis thaliana</i>)
	G24322	SNM	S0525:112583-113801	0.00	94.38	inf	5.00E ⁻⁰⁵	VAT1: Acetolactate synthase small subunit 1, chloroplastic (<i>Arabidopsis thaliana</i>)
	G13997	7	S0129:141194-143320	0.00	11.79	inf	1.45E ⁻⁰³	TPP8: Probable trehalose-phosphate phosphatase 8 (<i>Oryza sativa</i> subsp. <i>japonica</i>)
	G05888	5	S0026:123054-123661	0.00	9.21	inf	1.45E ⁻⁰³	Phytochrome (<i>Picea abies</i>)

FPKM: Fragments Per Kilobase of target sequence per Million reads mapped. SNM: Scaffold not mapped (Bushakra et al. submitted). Inf: Indicates missing data. TF: Transcription factor. R-like: Resistance-like gene.

Table 2: RNA sequence results showing black raspberry genes that are downregulated when comparing untreated (wild-type) vs. *Verticillium*-infected ‘Jewel’ roots.

Gene-type category	Bras_Gene ID	Rubus Linkage Group	Black Raspberry Scaffold Locus	Wild-type FPKM1	Verticillium-infected FPKM2	log2 fold change	p-value	Uniprot Annotation
	G04354	7	S0016:744502-746959	30.10	2.94	-3.36	5.00E ⁻⁰⁵	FRO2: Ferric reduction oxidase 2 (<i>Arabidopsis thaliana</i>)
	G08068	3	S0046:39573-41277	314.15	31.90	-3.30	5.00E ⁻⁰⁵	F6'H1: Feruloyl CoA ortho-hydroxylase 1 (<i>Arabidopsis thaliana</i>)
	G06936	3	S0035:149753-151591	687.25	73.99	-3.22	5.00E ⁻⁰⁵	F6'H2: Feruloyl CoA ortho-hydroxylase 2 (<i>Arabidopsis thaliana</i>)
	G11399	7	S0084:406267-407122	808.35	106.40	-2.93	5.00E ⁻⁰⁵	CHLN: Nicotianamine synthase (<i>Solanum lycopersicum</i>)
	G22736	2	S0418:83378-84197	8.04	1.20	-2.74	1.10E ⁻⁰²	At4g34330: UPF0496 protein At4g34330 (<i>Arabidopsis thaliana</i>)
	G02839	SNM	S0009:136092-136779	373.62	57.41	-2.70	5.00E ⁻⁰⁵	At3g43660: Vacuolar iron transporter homolog 4 (<i>Arabidopsis thaliana</i>)
	G21523	4	S0357:56896-64178	75.58	11.74	-2.69	5.00E ⁻⁰⁵	PDR3: Pleiotropic drug resistance protein 3 (<i>Nicotiana tabacum</i>)
	G19106	SNM	S0262:41049-41736	84.60	13.66	-2.63	5.00E ⁻⁰⁵	At3g43660: Vacuolar iron transporter homolog 4 (<i>Arabidopsis thaliana</i>)
	G06587	2	S0032:141875-145958	22.33	3.73	-2.58	5.00E ⁻⁰⁵	NPF7.3: Protein NRT1/ PTR FAMILY 7.3 (<i>Arabidopsis thaliana</i>)

	G02650	SNM	S0008:816549-817899	51.50	9.41	-2.45	2.40E ⁻⁰³	PCR12: Protein PLANT CADMIUM RESISTANCE 12 (<i>Arabidopsis thaliana</i>)
	G22735	2	S0418:80574-81582	41.53	7.59	-2.45	5.00E ⁻⁰⁵	At4g34330: UPF0496 protein At4g34330 (<i>Arabidopsis thaliana</i>)
	G25863	SNM	S0690:5739-12553	234.65	42.93	-2.45	5.00E ⁻⁰⁵	G6PD: Glucose-6-phosphate 1-dehydrogenase chloroplastic (<i>Spinacia oleracea</i>)
TF	G21225	SNM	S0342:89852-101290	122.72	22.48	-2.45	5.00E ⁻⁰⁵	FIT: Transcription factor FER-LIKE IRON DEFICIENCY-INDUCED TRANSCRIPTION FACTOR (<i>Arabidopsis thaliana</i>)
R-like	G16397	SNM	S0180:157516-163419	11.25	2.09	-2.43	5.00E ⁻⁰⁵	MLO3: MLO-like protein 3 (<i>Arabidopsis thaliana</i>)
	G14016	7	S0129:231550-235394	6.53	1.23	-2.41	1.10E ⁻⁰³	CBSDUF5: DUF21 domain-containing protein At5g52790 (<i>Arabidopsis thaliana</i>)
TF	G05429	2	S0022:763428-767225	7.72	1.51	-2.36	3.00E ⁻⁰³	Myb-related protein Zm1 (<i>Zea mays</i>)
TF	G26784	7	S0856:17532-19870	66.24	13.30	-2.32	5.00E ⁻⁰⁵	ORG2: Transcription factor ORG2 (<i>Arabidopsis thaliana</i>)
	G05213	3	S0021:241654-243068	118.66	25.47	-2.22	5.00E ⁻⁰⁵	TAX10: 3'-N-debenzoyl-2'-deoxytaxol N-benzoyltransferase (<i>Taxus canadensis</i>)
	G08272	6	S0047:639811-642171	22.00	5.01	-2.13	5.00E ⁻⁰⁵	AKR1: Probable aldo-keto reductase 1 (<i>Glycine max</i>)
	G12333	7	S0098:334261-345942	16.66	3.85	-2.11	5.00E ⁻⁰⁵	PECS-2.1: Pectinesterase 2 (<i>Citrus sinensis</i>)
	G19196	SNM	S0264:126094-126565	625.04	145.39	-2.10	5.00E ⁻⁰⁵	COPT1: Copper transporter 1 (<i>Arabidopsis thaliana</i>)
	G20447	SNM	S0308:199172-204373	13.54	3.18	-2.09	5.00E ⁻⁰⁵	RABC2A: Ras-related protein RABC2a (<i>Arabidopsis thaliana</i>)
	G11061	5	S0078:528534-536505	195.19	46.09	-2.08	5.00E ⁻⁰⁵	SALR: Salutaridine reductase (<i>Papaver bracteatum</i>)
	G14201	6	S0133:235501-245313	6.43	1.55	-2.05	7.50E ⁻⁰⁴	NEC3: Bifunctional monodehydroascorbate reductase and carbonic anhydrase nectarin-3 (<i>Nicotiana langsdorffii</i> x <i>Nicotiana sanderae</i>)
	G17154	3	S0201:101936-106091	21.07	5.34	-1.98	5.00E ⁻⁰⁵	CNGC1: Cyclic nucleotide-gated ion channel 1 (<i>Arabidopsis thaliana</i>)
	G20665	SNM	S0318:74632-75398	2569.14	679.36	-1.92	5.00E ⁻⁰⁵	MT2: Metallothionein-like protein type 3 (<i>Malus domestica</i>)
	G10038	5	S0066:189810-190047	544.05	147.59	-1.88	5.00E ⁻⁰⁵	CLE1: CLAVATA3/ESR (CLE)-related protein 1 (<i>Arabidopsis thaliana</i>)
	G03261	5	S0011:185563-186169	51.41	14.31	-1.85	5.00E ⁻⁰⁵	CML45: Probable calcium-binding protein CML45 (<i>Arabidopsis thaliana</i>)
	G05665	6	S0024:505386-509732	35.15	9.96	-1.82	5.00E ⁻⁰⁵	IREG2: Solute carrier family 40 member 2 (<i>Arabidopsis thaliana</i>)
	G04179	1	S0015:487534-489685	9.97	2.83	-1.82	3.50E ⁻⁰⁴	GH3.1: Probable indole-3-acetic acid-amido synthetase GH3.1 (<i>Arabidopsis thaliana</i>)
	G24554	SNM	S0546:22372-27856	31.90	9.24	-1.79	5.00E ⁻⁰⁵	ALATS: Alanine--tRNA ligase (<i>Arabidopsis thaliana</i>)
	G03231	5	S0011:74073-75428	818.99	244.16	-1.75	5.00E ⁻⁰⁵	GSTU9: Glutathione S-transferase U9 (<i>Arabidopsis thaliana</i>)

	G25563	7	S0647:8608-9859	12.92	3.85	-1.74	1.35E ⁻⁰³	At4g34330: UPF0496 protein At4g34330 (<i>Arabidopsis thaliana</i>)
	G00701	2	S0002:1356630-1367969	28.09	8.40	-1.74	5.00E ⁻⁰⁵	CCD1: Carotenoid 9,10(9',10')-cleavage dioxygenase 1 (<i>Pisum sativum</i>)
TF	G01967	5	S0005:1783558-1788323	8.56	2.64	-1.69	5.00E ⁻⁰⁵	GTE10: Transcription factor GTE10 (<i>Arabidopsis thaliana</i>)
	G21969	SNM	S0377:75547-76580	95.94	29.77	-1.69	5.00E ⁻⁰⁵	CYP75B1: Flavonoid 3'-monooxygenase (<i>Arabidopsis thaliana</i>)
	G09723	6	S0063:92602-98952	46.34	15.12	-1.62	5.00E ⁻⁰⁵	SAG101: Senescence-associated carboxylesterase 101 (<i>Arabidopsis thaliana</i>)
	G06418	4	S0030:708310-710160	88.38	28.98	-1.61	5.00E ⁻⁰⁵	SRG1: Protein SRG1 (<i>Arabidopsis thaliana</i>)
	G19195	SNM	S0264:122100-122496	67.12	22.17	-1.60	2.60E ⁻⁰³	COPT6: Copper transporter 6 (<i>Arabidopsis thaliana</i>)
	G02943	SNM	S0009:700347-702229	25.41	8.44	-1.59	5.00E ⁻⁰⁵	UBA1C: UBP1-associated proteins 1C (<i>Arabidopsis thaliana</i>)
	G04081	1	S0014:807919-813112	12.34	4.11	-1.59	5.00E ⁻⁰⁵	Ent-copalyl diphosphate synthase, chloroplastic (<i>Pisum sativum</i>)
	G03560	5	S0012:406649-409775	28.58	9.52	-1.59	5.00E ⁻⁰⁵	DTXL2: MATE efflux family protein 6 (<i>Arabidopsis thaliana</i>)
	G20257	SNM	S0301:35633-46087	7.17	2.39	-1.58	7.50E ⁻⁰⁴	MATE: MATE efflux family protein 1 (<i>Arabidopsis thaliana</i>)
	G13393	3	S0118:126733-136952	19.44	6.54	-1.57	5.00E ⁻⁰⁵	At5g40240: WAT1-related protein At5g40240 (<i>Arabidopsis thaliana</i>)
TF	G16081	7	S0173:327773-331036	7.91	2.67	-1.57	7.95E ⁻⁰³	BHLH123: Transcription factor bHLH123 (<i>Arabidopsis thaliana</i>)
	G17820	6	S0221:290510-293346	93.97	31.78	-1.56	5.00E ⁻⁰⁵	Endo-1,3,1,4-beta-D-glucanase (<i>Zea mays</i>)
	G05802	3	S0025:490704-492629	9.64	3.26	-1.56	5.85E ⁻⁰³	PER7: Peroxidase 7 (<i>Arabidopsis thaliana</i>)
	G12576	5	S0102:127863-135517	166.22	56.62	-1.55	5.00E ⁻⁰⁵	CEVI57: Proteinase inhibitor type-2 CEVI57 (<i>Solanum lycopersicum</i>)
	G25471	SNM	S0637:6054-9982	61.73	21.14	-1.55	5.00E ⁻⁰⁵	CYP716B1: Cytochrome P450 716B1 (<i>Picea sitchensis</i>)
	G20378	5	S0306:76017-77194	14.19	4.94	-1.52	8.05E ⁻⁰³	RCOM_1259250: Casparian strip membrane protein RCOM_1259250 (<i>Ricinus communis</i>)
	G00970	1	S0003:455423-457473	82.26	28.63	-1.52	5.00E ⁻⁰⁵	CML41: Probable calcium-binding protein CML41 (<i>Arabidopsis thaliana</i>)
	G16450	SNM	S0181:180805-184264	273.24	95.83	-1.51	5.00E ⁻⁰⁵	KA01: Ent-kaurenoic acid oxidase 1 (<i>Arabidopsis thaliana</i>)
	G24511	SNM	S0541:100633-105123	22.62	7.97	-1.51	5.00E ⁻⁰⁵	PHB6: Prohibitin-6, mitochondrial (<i>Arabidopsis thaliana</i>)
	G09454	7	S0060:275814-276072	21.60	0.00	-inf	1.35E ⁻⁰³	CLE14: CLAVATA3/ESR (CLE)-related protein 2 (<i>Arabidopsis thaliana</i>)

FPKM: Fragments Per Kilobase of target sequence per Million reads mapped. SNM: Scaffold not mapped (Bushakra et al. submitted). Inf: Indicates missing data. TF: Transcription factor. R-like: Resistance-like gene.