

Table S1. Characteristics of four resistant lines (S&P 7129, S&P 7168, S&P 7521, and S&P 7522) and three susceptible lines (S&P 7130, S&P 7175, and S&P 7483) provided by ‘Seeds & People’ Co., Ltd. (Yeonggwang, Korea).

Onion line	Resistant or Susceptible to gray mold	Bulb color	Maturity date
S&P 7129	Resistant	Brown	Moderate
S&P 7168	Resistant	Brown	Late
S&P 7521	Resistant	Brown	Late
S&P 7522	Resistant	Brown	Late
S&P 7130	Susceptible	Brown	Moderate
S&P 7175	Susceptible	Brown	Late
S&P 7483	Susceptible	Brown	Late

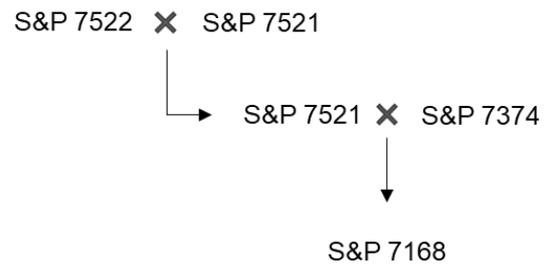
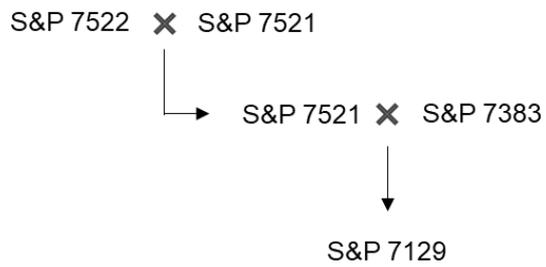
Table S2. Sequence information of 40 OPERON random primers used for RAPD analysis.

No	Random primer	Sequence	No	Random primer	Sequence
1	OPAN-1	5'-ACT CCA CGT C-3'	21	OPL-1	5'-GGC ATG ACC T-3'
2	OPAN-2	5'-CAC CGC AGT T-3'	22	OPL-2	5'-TGG GCG TCA A-3'
3	OPAN-3	5'-AGC CAG GCT G-3'	23	OPL-3	5'-CCA GCA GCT T-3'
4	OPAN-4	5'-GGC GTA AGT C-3'	24	OPL-4	5'-GAC TGC ACA C-3'
5	OPAN-5	5'-GGG TGC AGT T-3'	25	OPL-5	5'-ACG CAG GCA C-3'
6	OPAN-6	5'-GGG AAC CCG T-3'	26	OPL-6	5'-GAG GGA AGA G-3'
7	OPAN-7	5'-TCG CTG CGG A-3'	27	OPL-7	5'-AGG CGG GAA C-3'
8	OPAN-8	5'-AAG GCT GCT G-3'	28	OPL-8	5'-AGC AGG TGG A-3'
9	OPAN-9	5'-GGG GGA GAT G-3'	29	OPL-9	5'-TGC GAG AGT C-3'
10	OPAN-10	5'-CTG TGT GCT C-3'	30	OPL-10	5'-ACG ATG AGC C-3'
11	OPAN-11	5'-GTC CAT GCA G-3'	31	OPL-11	5'-ACG ATG AGC C-3'
12	OPAN-12	5'-AAC GGC GGT C-3'	32	OPL-12	5'-GGG CGG TAC T-3'
13	OPAN-13	5'-CTT CCA GGA C-3'	33	OPL-13	5'-ACC GCC TGC T-3'
14	OPAN-14	5'-AGC CGG GTA A-3'	34	OPL-14	5'-GTG ACA GGC T-3'
15	OPAN-15	5'-TGA TGC CGC T-3'	35	OPL-15	5'-AAG AGAGGG G-3'
16	OPAN-16	5'-GTG TCG AGT C-3'	36	OPL-16	5'-AGG TTG CAG G-3'
17	OPAN-17	5'-TCA GCA CAG G-3'	37	OPL-17	5'-AGC CTG AGC C-3'
18	OPAN-18	5'-TGT CCT GCG T-3'	38	OPL-18	5'-ACC ACC CAC C-3'
19	OPAN-19	5'-ACC ACG CCT T-3'	39	OPL-19	5'-GAG TGG TGA C-3'
20	OPAN-20	5'-GAG TCC TCA C-3'	40	OPL-20	5'-TGG TGG ACC A-3'

Table S3. Results of raw data obtained by RNA-seq, trimming, and mapping.

Sample ID	Raw data			Trimmed data		Mapped read	Mapped bp	Unmapped read
	Raw_read	Total_bp	Q30 (%)	Total_read	Total_bp			
S&P 7522	37,514,342	5,664,665,642	96.32	23,922,326	3,562,440,647	18,752,581	2,785,954,539	5,169,745
S&P 7521	41,664,542	5,664,665,642	96.19	26,580,416	3,954,227,261	20,870,020	3,100,221,092	5,710,396
S&P 7129	36,936,016	6,291,345,842	95.84	27,932,656	4,156,538,263	21,958,205	3,262,554,110	5,974,451
S&P 7168	34,603,666	5,577,338,416	96.3	22,483,100	3,347,031,254	19,118,370	2,543,407,213	5,364,730
S&P 7130	38,048,776	5,225,153,566	96.35	25,465,920	3,791,674,247	19,439,752	2,887,423,932	6,026,168
S&P 7175	28,899,894	4,363,883,994	96.15	20,744,300	2,780,687,046	16,852,911	2,058,017,975	4,891,389
S&P 7483	35,628,426	5,379,892,326	96.01	23,254,768	3,464,681,101	18,176,165	2,700,897,987	5,078,603

(A)



(B)

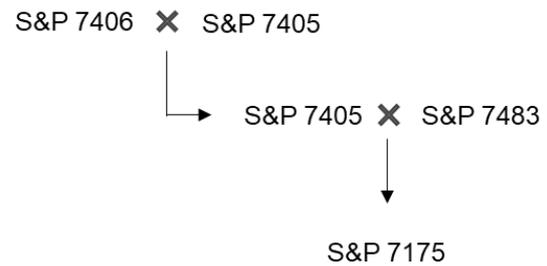
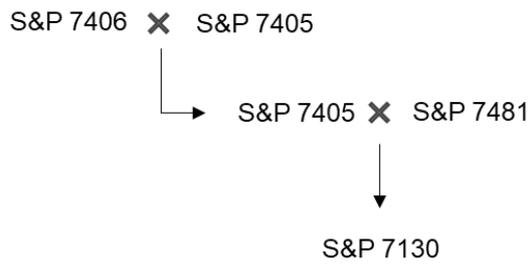


Figure S1. The pedigree of onion lines provided by 'Seeds & People' Co. (A) The pedigree of four resistant lines (S&P 7129, S&P 7168, S&P 7521, and S&P 7522). (B) The pedigree of three susceptible lines (S&P 7130, S&P 7175, and S&P 7483).

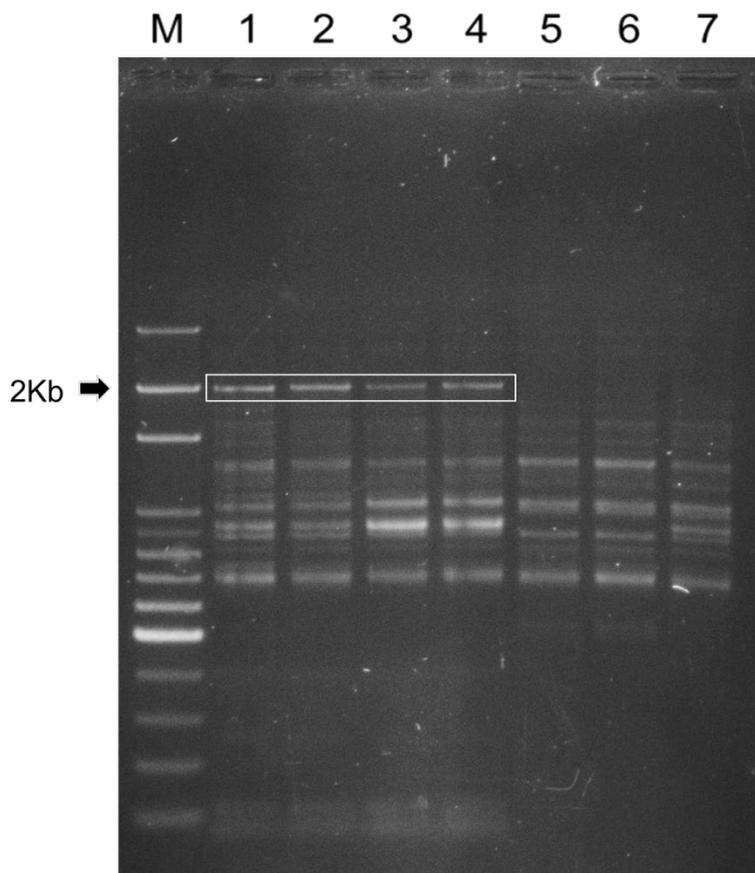


Figure S2. RAPD analysis of resistant and susceptible lines provided by 'Seeds & People' Co. by using the OPAN-1 random primer. The 2Kb bands were amplified in the resistant lines S&P 7522, S&P 7521, S&P 7129, and S&P 7168. M; 100bp DNA ladder marker, Lane 1; S&P 7522, Lane 2; S&P 7521, Lane 3; S&P 7129, Lane 4; S&P 7168, Lane 5; S&P 7483, Lane 6; S&P 7130, Lane 7; S&P 7175.

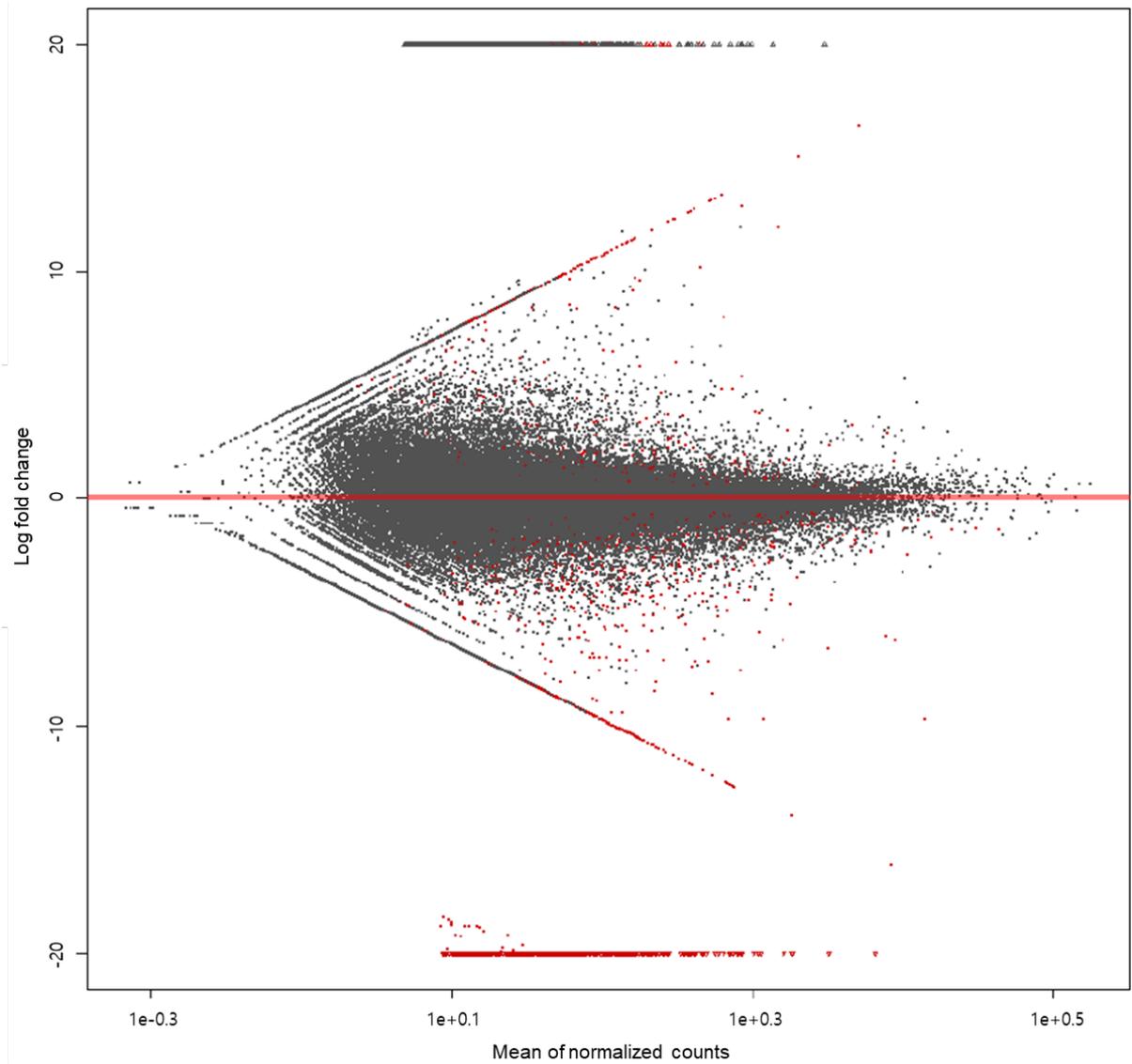


Figure S3. MA plot to verify significantly expressed genes in groups of resistant and susceptible lines. False discovery rate (FDR) of less than 0.05 is indicated in red. It was verified that the significantly expressed genes (red color) were identified to be sufficient for subsequent resistance-related gene analysis.

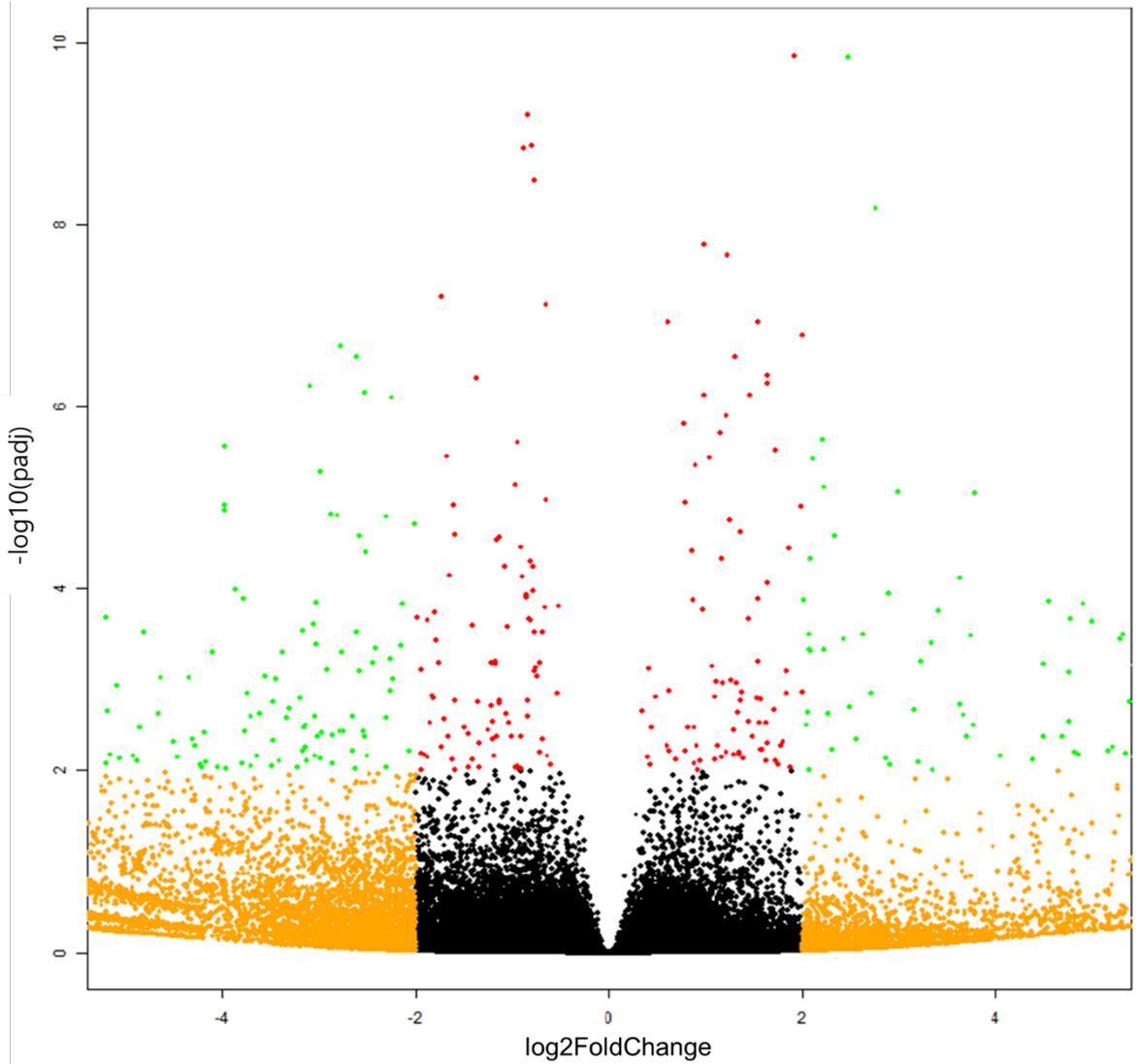
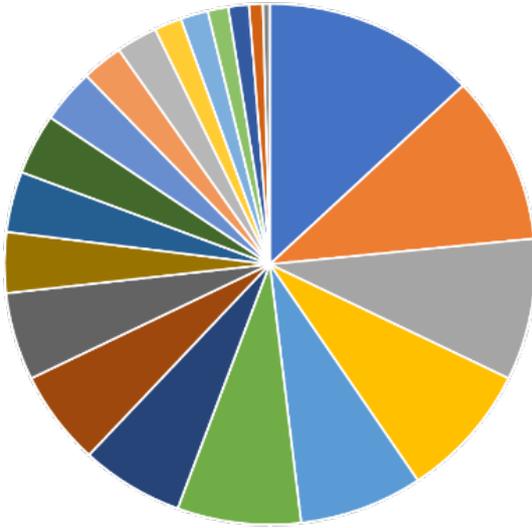


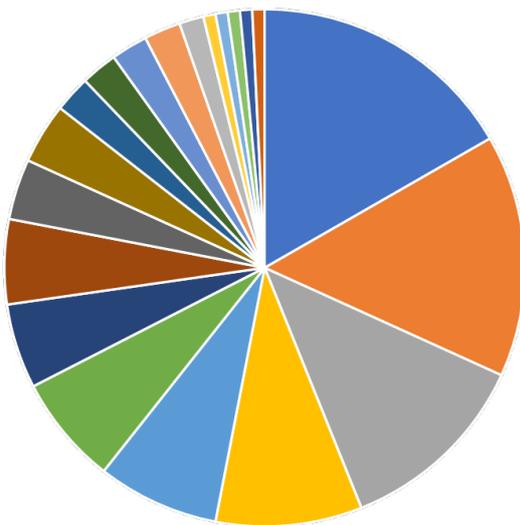
Figure S4. Volcano plot of transcripts satisfied following condition: $FDR < 0.05$, $|\log_2 \text{fold change}| \geq 2$. Red; $FDR < 0.01$ & $|\log_2 \text{fold change}| \leq 2$, green; $FDR < 0.01$ & $|\log_2 \text{fold change}| > 2$, orange; $FDR \geq 0.01$ & $|\log_2 \text{fold change}| > 2$.

(A) Cellular Component



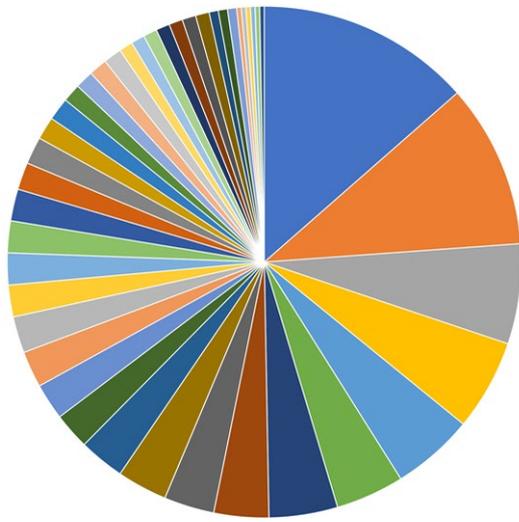
GO Cellular Component	Gene count
nucleus	31
chloroplast	25
cytoplasm	21
other intracellular components	20
plastid	18
mitochondrion	18
cytosol	15
plasma membrane	14
other membranes	13
thylakoid	9
other cellular components	9
Golgi apparatus	9
extracellular region	8
vacuole	6
nucleolus	6
endoplasmic reticulum	4
endosome	4
cell wall	3
ribosome	3
peroxisome	2
nucleoplasm	1

(B) Molecular Function



GO Molecular Function	Gene count
protein binding	22
catalytic activity	20
other binding	16
transferase activity	12
DNA binding	10
RNA binding	9
hydrolase activity	7
nucleic acid binding	7
transporter activity	5
DNA-binding transcription factor activity	5
kinase activity	3
lipid binding	3
unknown molecular functions	3
signaling receptor activity	3
enzyme regulator activity	2
nucleotide binding	1
carbohydrate binding	1
translation factor activity, RNA binding	1
structural molecule activity	1
nuclease activity	1

(C) Biological Process



GO Biological Process	Gene count
other cellular processes	47
other metabolic processes	36
response to stress	22
biosynthetic process	20
response to chemical	18
multicellular organism development	15
anatomical structure development	15
nucleobase-containing compound metabolic process	12
cellular component organization	11
response to external stimulus	11
response to abiotic stimulus	10
reproduction	8
cellular protein modification process	8
response to light stimulus	8
post-embryonic development	8
transport	7
response to endogenous stimulus	7
response to biotic stimulus	7
protein metabolic process	7
lipid metabolic process	6
signal transduction	6
growth	5
catabolic process	5
cell growth	4
cell communication	4
photosynthesis	4
carbohydrate metabolic process	4
cell differentiation	3
regulation of molecular function	3
cellular homeostasis	3
unknown biological processes	3
embryo development	3
pollination	3
translation	3
flower development	2
DNA metabolic process	2
generation of precursor metabolites and energy	2
tropism	1
secondary metabolic process	1
cell cycle	1
circadian rhythm	1
cell death	1
other biological processes	1

Figure S5. GO annotation of 182 transcripts with increased expression levels. (A); Cellular component, (B); Molecular function, (C); Biological process.