

Supplementary Material

Integrated transcriptomics and metabolomics reveal induction of hierarchies of resistance genes in potato against late blight

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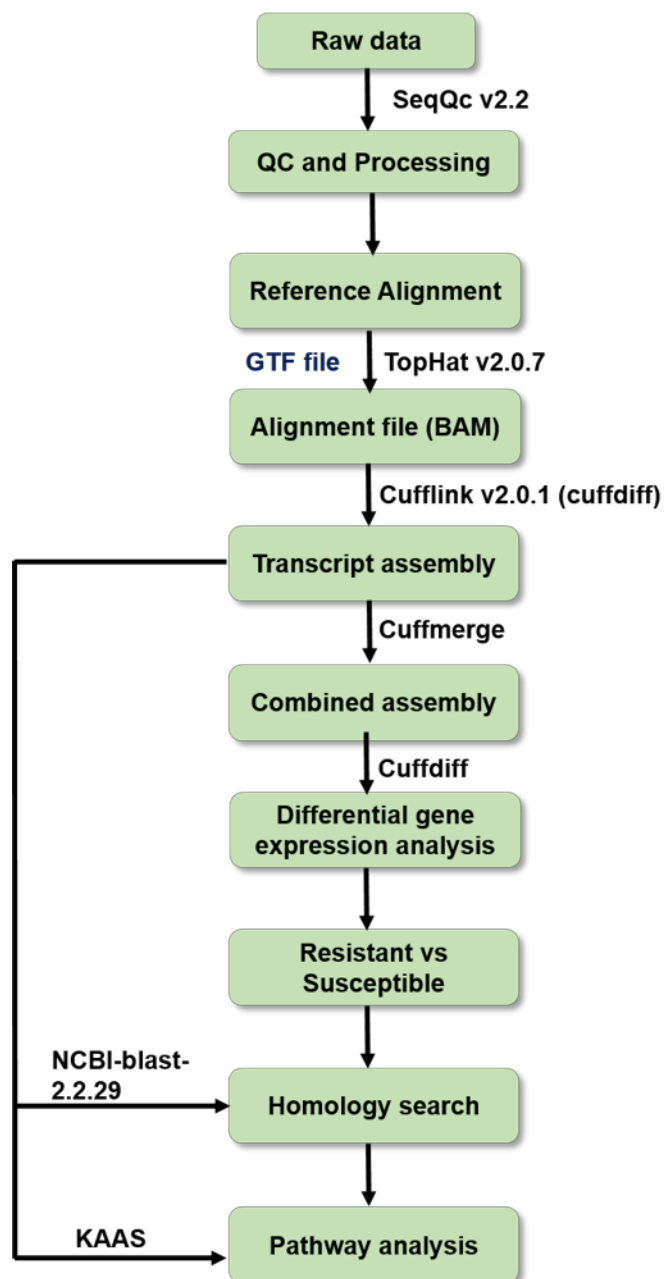
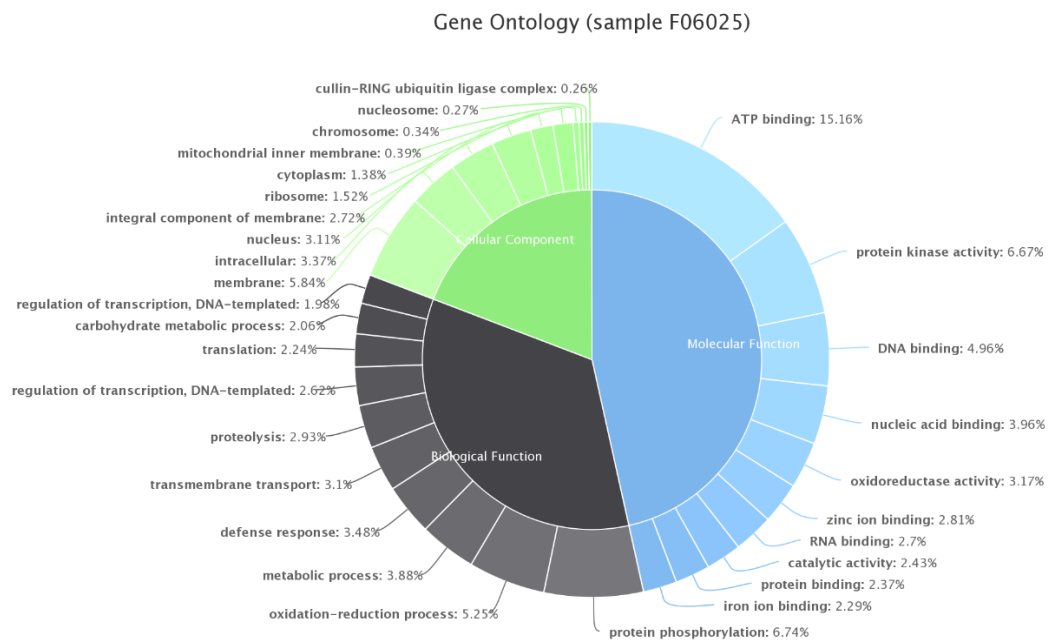


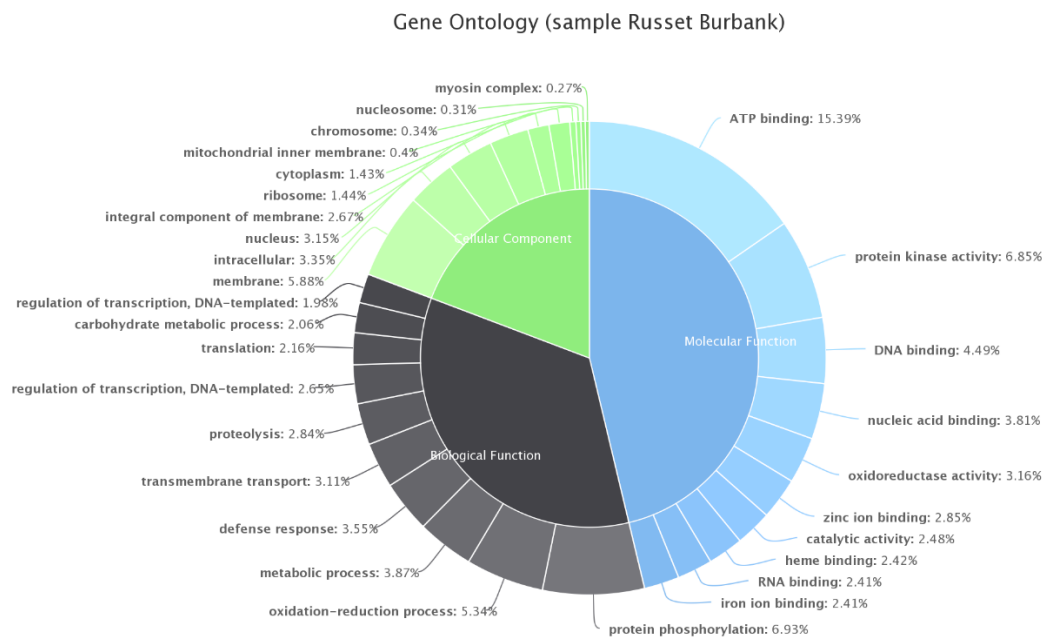
Fig. S1. Flowchart, illustrating an overview of different steps followed for sequencing, assembly of the HiSeq2000 Illumina reads, and subsequent annotation and validation of the resulting transcriptome.

(a)



Highcharts.com

(b)



Highcharts.com

(c)

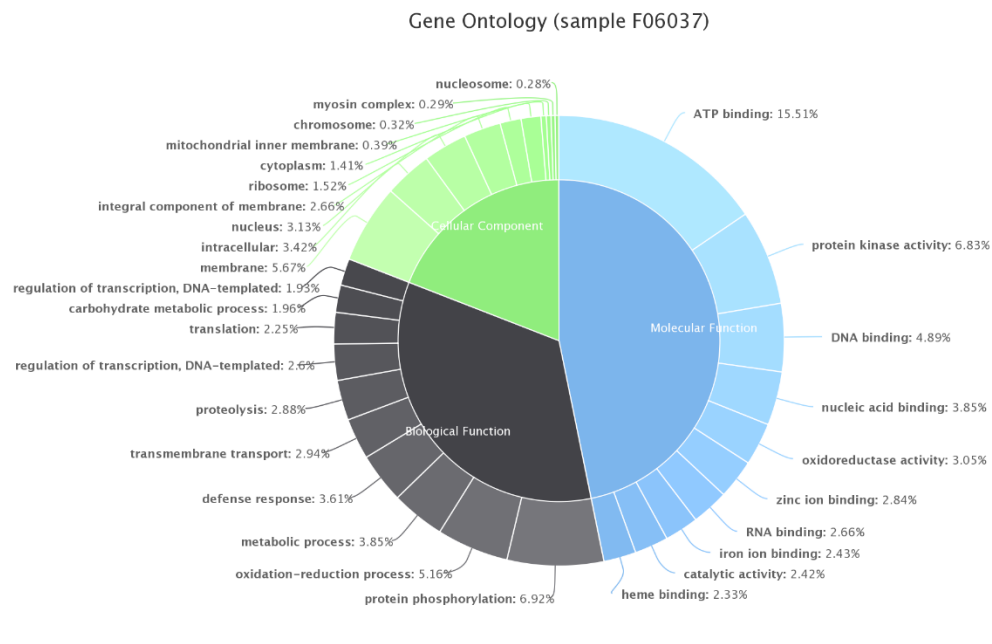


Fig. S2. Gene Ontology (GO) analysis and functional classification of potato genotypes: (a) F06025; (b) F06037; (c) Russet Burbank. This chart is representing top 10 GO including molecular function, biological process and cellular components.

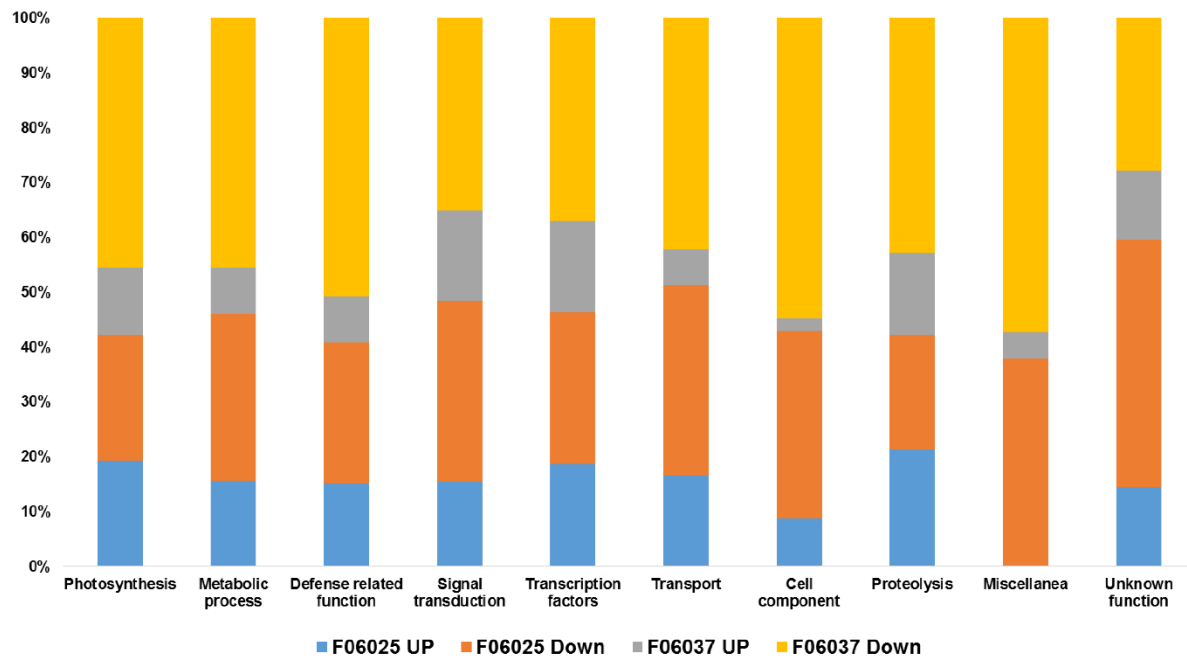
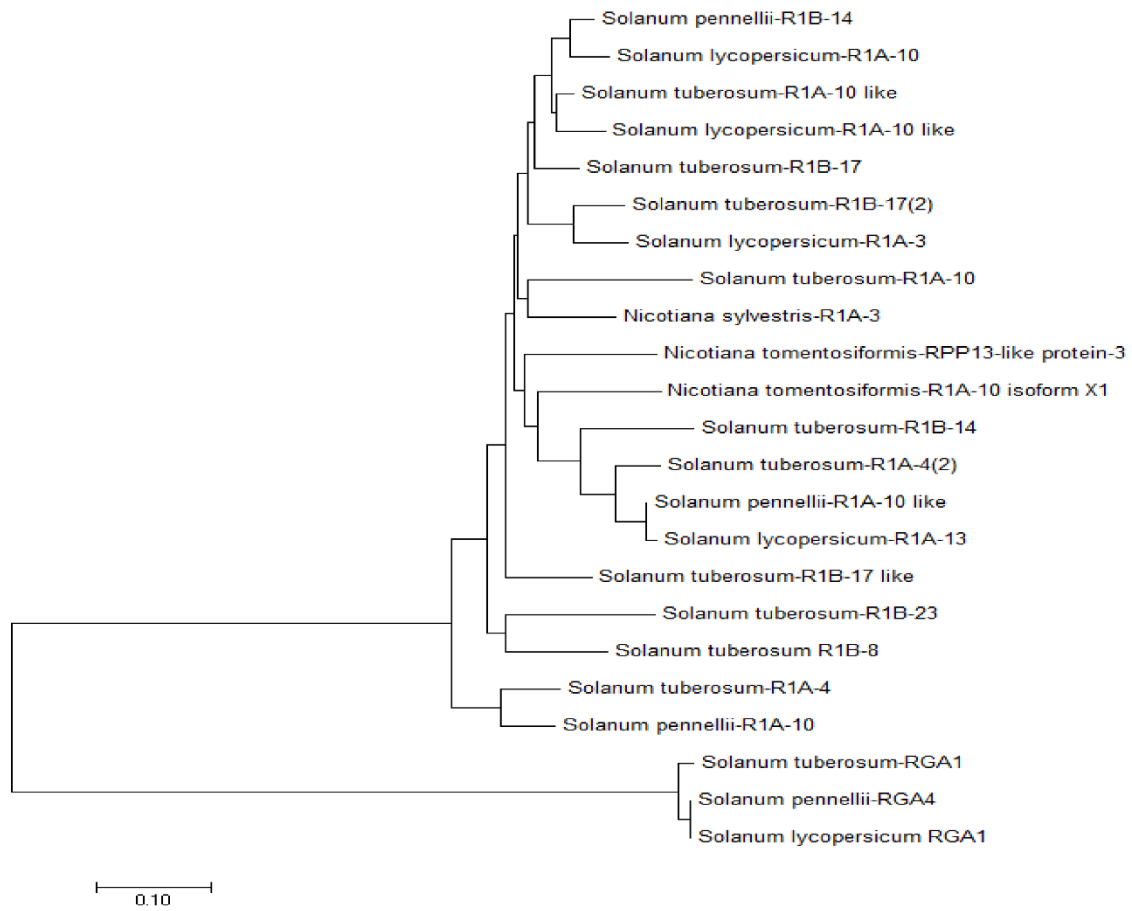
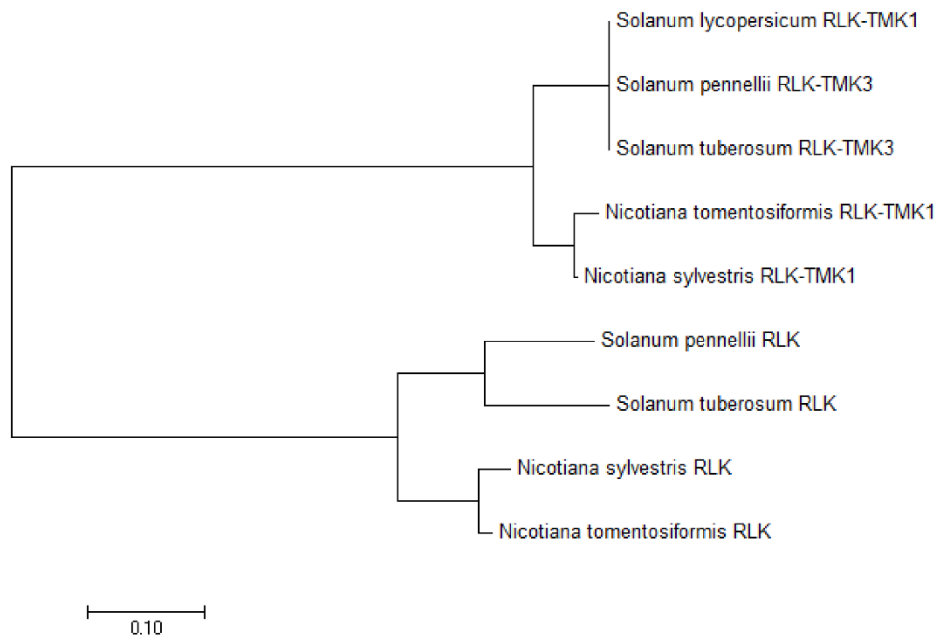


Fig. S3. Specificity of transcriptional changes in inoculated resistant (F06025 and F06037) genotypes within functional categories. Percentage of genes modulated in F06025 (up-blue and down-orange) and F06037 (up-grey and down-yellow) at 2 dpi.



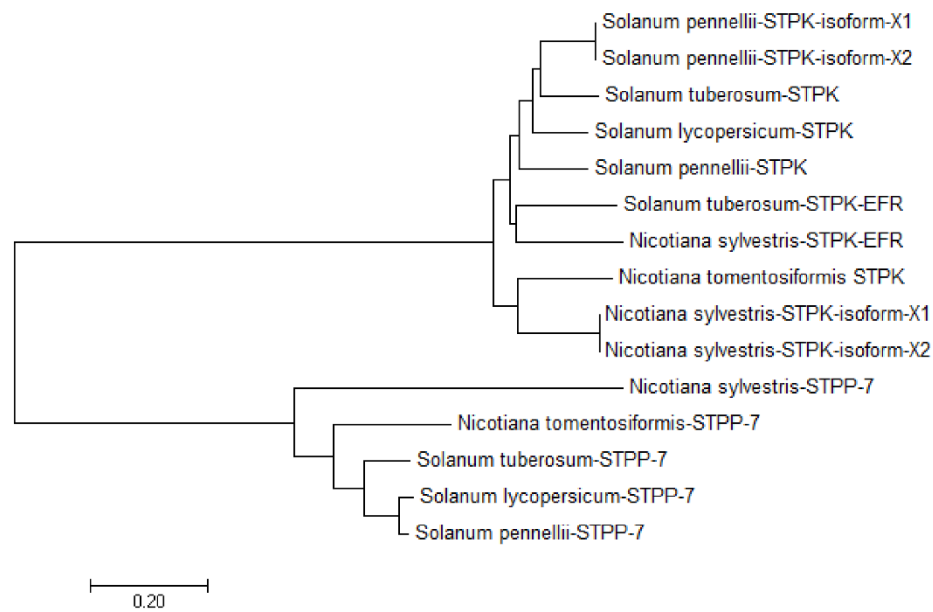


Fig. S4. Phylogenetic relationships of RLK-LRRs (a), *R* gene homologs (b), and MAPKs (c) with other sequences retrieved from NCBI database. The evolutionary history was inferred using the Neighbor-Joining method. The tree is drawn to scale, with branch lengths in the same units as those of the evolutionary distances used to infer the phylogenetic tree. Evolutionary analyses were conducted in MEGA7.

Table S1. Primer sequences used for biomass quantification and validation of RNA seq data in potato genotypes

Genbank name	Gene name	Forward primer (5'-3')	Reverse primer (5'-3')
A. Biomass quantification			
GQ371195.1	O-8	GAAAGGCATAGAAGGTAGA	TAACCGACCAAGTAGTAAA
AB061263.1	StEf1- α	ATTGGAAACGGATATGCTCCA	TCCTTACCTGAACGCCTGTCA
Z33382.1	β -tubulin	ATGTTCAAGGCGCAAGGCTT	TCTGCAACCGGGTCATT CAT
B. qRT-PCR primers			
PGSC0003DMT400026625	Chitinase	TGTTGCTAAGTGCAGCAAATG	GCAGGAGTAGTGCCACAATAA
PGSC0003DMT400027377	Allene oxide synthase	GGGTAACCTCTTTCGGCTATTGA	GAACGATGCTTCGTGGTTAGA
PGSC0003DMT400069030	Endochitinase 2	CTTGTGCTCCTGGAAGGAAATA	GATCCACTCCAATGACTCTTCC
PGSC0003DMT400087614	F-box	GCATGGAGGACGACGAATATAA	GCAGGTATTGCATACCGAACTA
PGSC0003DMT400033720	Receptor protein kinase	CACCCAAATGCTGTTCTTTAC	CGCCAAACTATCTCCTGGTATG
PGSC0003DMT400036586	Patatin-2-Kuras 4	GCTCCAGAATTGGATGCTAAGA	GCAACACCACCATCAACAAG
PGSC0003DMT400029181	UDP-glucuronate 5-epimerase	GTATCGGGTCACTTGACACTTC	CCGGAGACGTATTACCCAAATTA
PGSC0003DMT400052746	Isoflavone reductase	TGACGTGGCAACATACACTATAA	TCCCCTTGGCTATCAATTCC

Table S2. Raw data processing of RNA seq data in potato genotypes

Samples	Platform	Type of the reads	Total number of processed reads
F06025	Illumina Hiseq	2 x Paired end (100bp max)	113.34 million
F06037	Illumina Hiseq	2 x Paired end (100bp max)	111.38 million
Russet Burbank	Illumina Hiseq	2 x Paired end (100bp max)	129.7 million

Table S3. Transcripts Annotation of RNA seq data in potato genotypes

Transcripts annotation summary	Transcripts		
	F06025	F06037	Russet Burbank
Total transcripts	53302	52958	52402
Total annotated transcripts	42725	42104	42681
Total unannotated transcripts	10577	10854	9721
percent annotated	80.15	79.5	81.44

* Mapped on the *Solanum tuberosum* Group Phureja DM genome

Table S4. Differentially expressed genes detected in resistant potato genotypes compared to susceptible genotype following *P. infestans* inoculation.

[See separate Excel file]

Table S5. Resistance related metabolites upregulated in resistant potato genotypes compared to susceptible genotype following *P. infestans* inoculation.

[See separate Excel file]