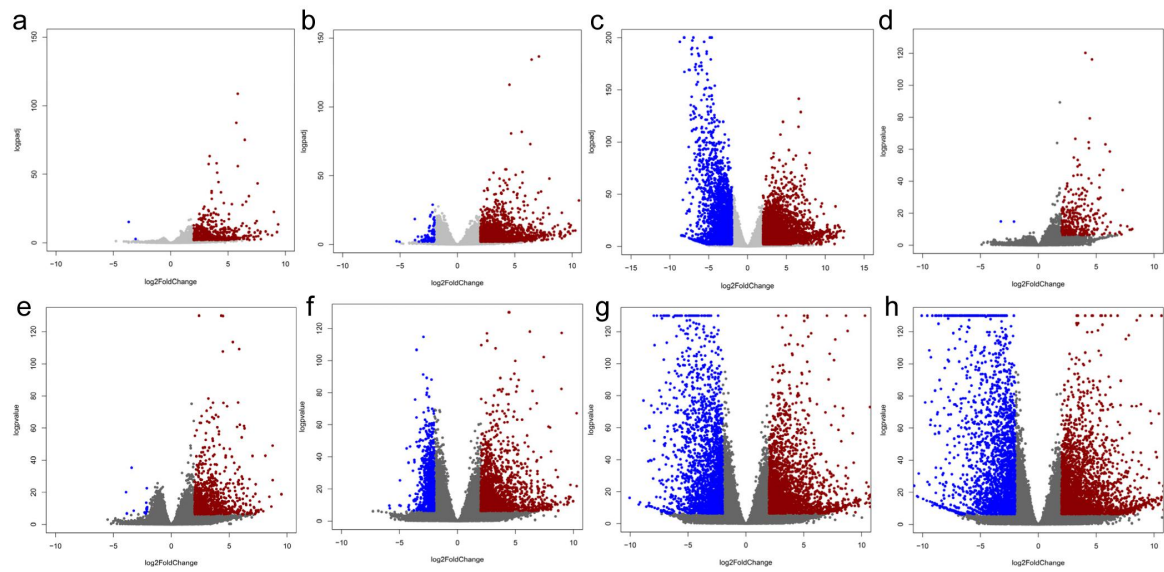
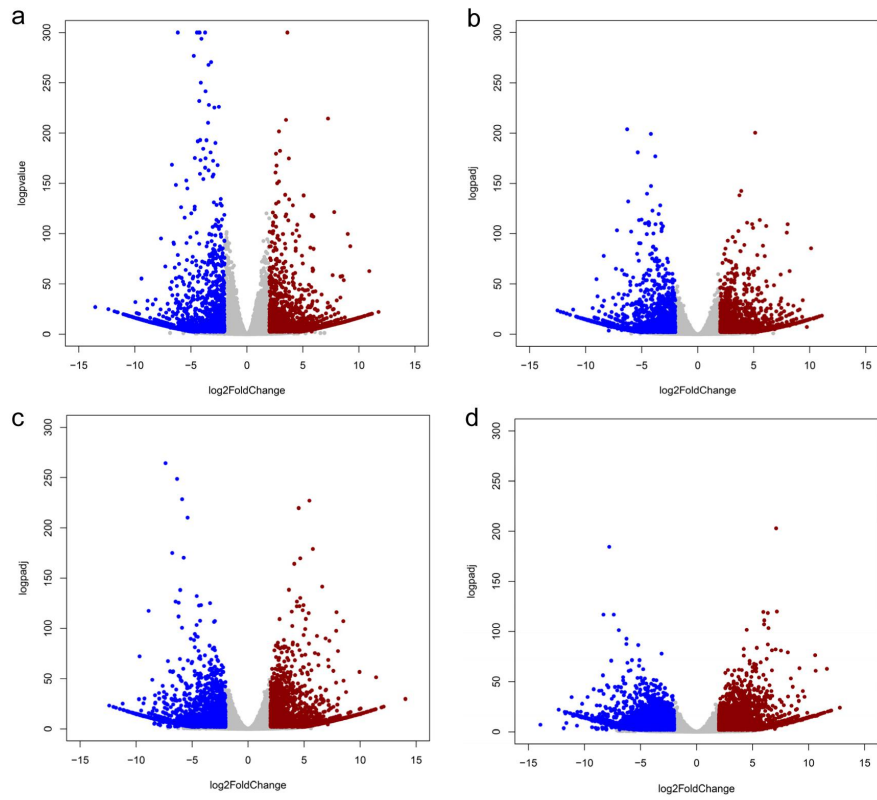


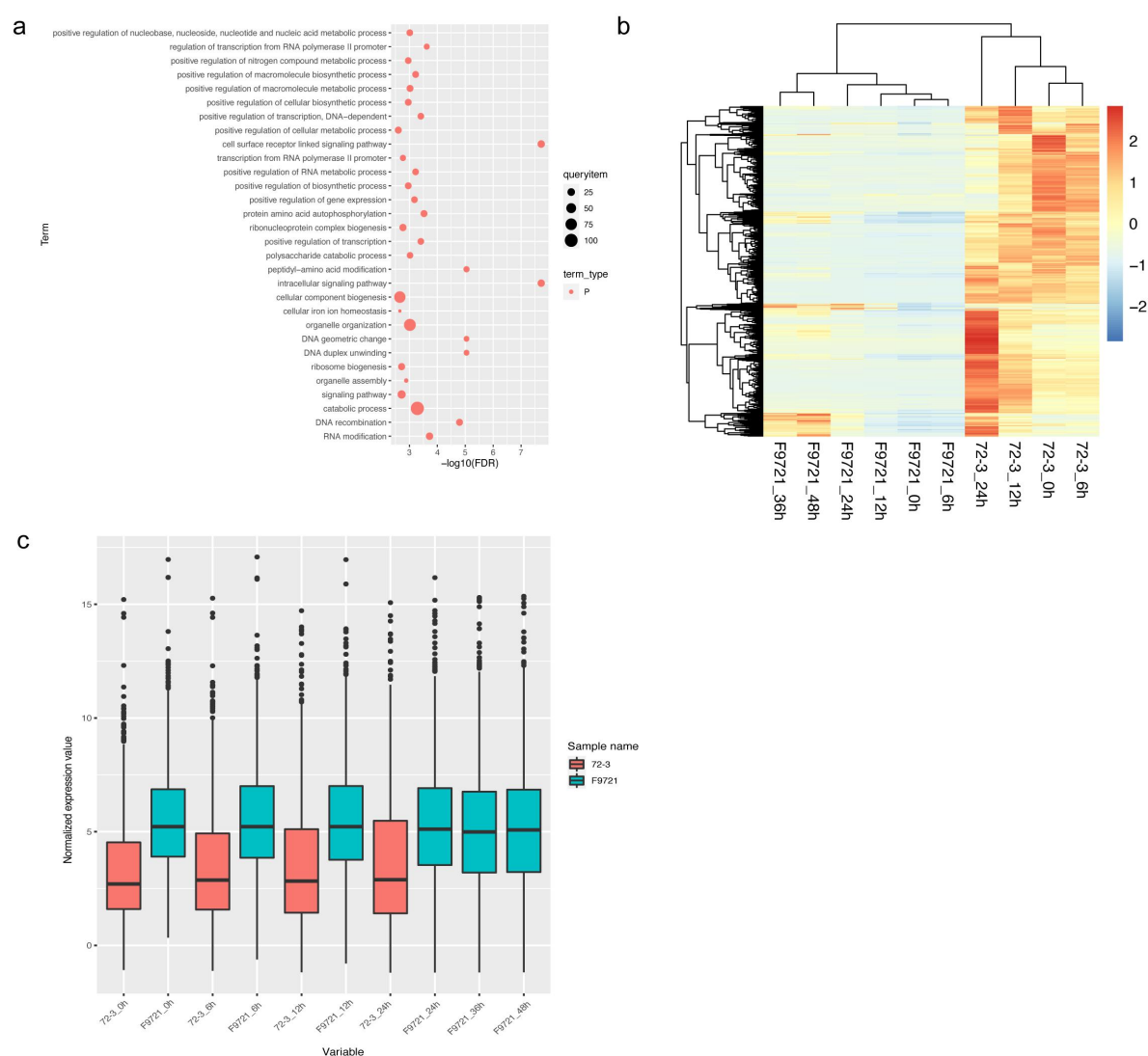
Supplementary Figure S1: Overall analysis of the transcriptome data. (a) PCA plot of the two inbred lines transcriptome change during seed germination. (b) Pearson correlation coefficients heat map between samples from 72-3 and F9721 at six germination stages.



Supplementary Figure S2: Volcano plots of DEGs between different imbibition stages. (a) Volcano plot of DEGs for 72-3 6 HAI versus 0 HAI. (b) Volcano plot of DEGs for 72-3 12HAI versus 0 HAI. (c) Volcano plot of DEGs for 72-3 24 HAI versus 0 HAI. (d) Volcano plot of DEGs for F9721 6 HAI versus 0 HAI. (e) Volcano plot of DEGs for F9721 12 HAI versus 0 HAI. (f) Volcano plot of DEGs for F9721 24 HAI versus 0 HAI. (g) Volcano plot of DEGs for F9721 36 HAI versus 0 HAI. (h) Volcano plot of DEGs for F9721 48 HAI versus 0 HAI.



Supplementary Figure S3: Volcano plots of DEGs between 72-3 and F9721 (a) Volcano plot of DEGs for 72-3 versus F9721 at 0 HAI. (b) Volcano plot of DEGs for 72-3 versus F9721 at 6 HAI. (c) Volcano plot of DEGs for 72-3 versus F9721 at 12 HAI. (d) Volcano plot of DEGs for 72-3 versus F9721 at 24 HAI.



Supplementary Figure S4: Expression pattern of differential expressed stored mRNAs and GO enrichment. (a) GO enrichment of differential expressed stored mRNAs in dry seeds between 72-3 and F9721. (b) Expression pattern of up-regulated stored mRNAs in 72-3 versus F9721 during seed germination. (c) Expression pattern of down-regulated stored mRNAs in 72-3 versus F9721 during seed germination.

Supplementary Table S1: Summary of reads alignment with B73 reference genome
APGv4

| Samples | Pair-end reads number | GC content (%) | Mapping rate |
|-------------|-----------------------|----------------|--------------|
| 72-3_0h_1 | 11655657;11655657 | 54;54 | 92.78% |
| 72-3_0h_2 | 11791262;11791262 | 54;54 | 92.66% |
| 72-3_0h_3 | 12061984;12061984 | 53;53 | 92.78% |
| 72-3_12h_1 | 17835078;17835078 | 53;53 | 93.25% |
| 72-3_12h_2 | 14910260;14910260 | 55;55 | 93.92% |
| 72-3_12h_3 | 11815028;11815028 | 54;54 | 92.97% |
| 72-3_24h_1 | 16773188;16773188 | 54;54 | 95.12% |
| 72-3_24h_2 | 12216469;12216469 | 53;52 | 94.22% |
| 72-3_24h_3 | 14059372;14059372 | 53;53 | 95.62% |
| 72-3_6h_1 | 13305083;13305083 | 55;54 | 93.00% |
| 72-3_6h_2 | 14112810;14112810 | 56;56 | 93.54% |
| 72-3_6h_3 | 13893967;13893967 | 55;55 | 93.23% |
| F9721_0h_1 | 15375316;15375316 | 55;55 | 90.06% |
| F9721_0h_2 | 12888583;12888583 | 55;55 | 88.53% |
| F9721_0h_3 | 14573350;14573350 | 54;54 | 88.31% |
| F9721_12h_1 | 17303918;17303918 | 57;57 | 88.99% |
| F9721_12h_2 | 17143408;17143408 | 56;56 | 89.57% |
| F9721_12h_3 | 14655576;14655576 | 55;55 | 88.58% |
| F9721_24h_1 | 13682849;13682849 | 55;55 | 90.04% |
| F9721_24h_2 | 14605629;14605629 | 55;55 | 88.17% |
| F9721_24h_3 | 15558163;15558163 | 55;55 | 89.49% |
| F9721_36h_1 | 13495568;13495568 | 53;53 | 90.44% |
| F9721_36h_2 | 14579617;14579617 | 54;54 | 89.99% |
| F9721_36h_3 | 13066391;13066391 | 51;51 | 91.06% |
| F9721_48h_1 | 12172336;12172336 | 54;53 | 91.20% |
| F9721_48h_2 | 13249328;13249328 | 54;54 | 90.70% |
| F9721_48h_3 | 13868005;13868005 | 51;51 | 90.92% |
| F9721_6h_1 | 12888169;12888169 | 54;54 | 88.95% |
| F9721_6h_2 | 15938142;15938142 | 56;56 | 88.63% |
| F9721_6h_3 | 15904529;15904529 | 56;56 | 88.96% |

Supplementary Table S2: Gene list of 2 Mb candidate locus

| Gene id | Description |
|----------------|---|
| Zm00001d004505 | drug resistance transporter-like ABC domain protein |
| Zm00001d007916 | uncharacterized |
| Zm00001d011289 | Malic enzyme1 |
| Zm00001d012623 | Malic enzyme 2 |
| Zm00001d018978 | uncharacterized |
| Zm00001d025415 | phosphoprotein phosphatase inhibitors |
| Zm00001d027292 | scarecrow-like protein 6 |
| Zm00001d027293 | signal recognition particle receptor homolog 1 |
| Zm00001d027295 | beta tubulin1 |
| Zm00001d027296 | DUF3527 domain protein |
| Zm00001d027298 | uncharacterized LOC100275685 |
| Zm00001d027299 | mediator of RNA polymerase II transcription subunit 12-like |
| Zm00001d027300 | protein PAIR1 |
| Zm00001d027302 | uncharacterized |
| Zm00001d027303 | Pleiotropic drug resistance protein 2 |
| Zm00001d027304 | ATPase 9, plasma membrane-type |
| Zm00001d027305 | uncharacterized |
| Zm00001d027306 | F-box protein |
| Zm00001d027307 | cingulin |
| Zm00001d027308 | RING/U-box superfamily protein |
| Zm00001d027309 | uncharacterized |
| Zm00001d027310 | vegetative cell wall protein gp1 |
| Zm00001d027311 | uncharacterized |
| Zm00001d027312 | putative RING zinc finger domain superfamily protein |
| Zm00001d027313 | hydrolase protein 32 |
| Zm00001d027314 | uncharacterized |
| Zm00001d027315 | uncharacterized |
| Zm00001d027317 | rolled leaf 2 |
| Zm00001d027318 | uncharacterized |
| Zm00001d027319 | 4-phosphopantetheinyl transferase sfp |
| Zm00001d027320 | CemA-like proton extrusion protein-related |
| Zm00001d027321 | putative peptidyl-prolyl cis-trans isomerase family protein |
| Zm00001d027322 | Protein weak chloroplast movement under blue light 1 |
| Zm00001d027323 | uncharacterized |
| Zm00001d027324 | THO complex subunit 1 |
| Zm00001d027325 | peptidoglycan-binding LysM domain-containing protein |
| Zm00001d027326 | uncharacterized |
| Zm00001d027329 | DNA cytosine methyltransferase Zmet 3 |
| Zm00001d027330 | uncharacterized |
| Zm00001d027332 | Nonspecific lipid-transfer protein |

| | |
|----------------|---|
| Zm00001d027333 | uncharacterized |
| Zm00001d027334 | uncharacterized |
| Zm00001d027335 | trihelix transcription factor GTL1 |
| Zm00001d027337 | kinesin-like protein KIN-14E |
| Zm00001d027338 | uncharacterized |
| Zm00001d027339 | RNA binding protein |
| Zm00001d027340 | ATP binding protein |
| Zm00001d027341 | ATP binding protein |
| Zm00001d027342 | uncharacterized |
| Zm00001d027343 | fertility restorer |
| Zm00001d027344 | molybdate-anion transporter |
| Zm00001d027345 | mitochondrial import inner membrane translocase subunit TIM23-2 |
| Zm00001d027346 | early nodulin-like protein 1 |
| Zm00001d027347 | uncharacterized |
| Zm00001d027348 | uncharacterized |
| Zm00001d027349 | pentatricopeptide repeat-containing protein At3g53170 |
| Zm00001d027350 | uncharacterized |
| Zm00001d027351 | uncharacterized |
| Zm00001d027352 | Pyridoxine/pyridoxamine 5'-phosphate oxidase 2 |
| Zm00001d027353 | retinol dehydrogenase 12 |
| Zm00001d027354 | mitochondrial inner membrane protein OXA1-like |
| Zm00001d027355 | membrane protein |
| Zm00001d027359 | uncharacterized |
| Zm00001d027360 | Probable protein phosphatase 2C 33 |
| Zm00001d027361 | ATPP2-A13 |
| Zm00001d027362 | uncharacterized |
| Zm00001d027363 | uncharacterized |
| Zm00001d027365 | vacuolar protein 8 |
| Zm00001d027366 | Peroxisomal membrane protein PEX11-1 |
| Zm00001d027367 | riboflavin biosynthesis protein ribD |
| Zm00001d027368 | xyloglucan endotransglucosylase/hydrolase protein 5 |
| Zm00001d027369 | Protein-ribulosamine 3-kinase chloroplastic |
| Zm00001d027370 | uncharacterized LOC100192905 |
| Zm00001d027371 | putative TCP-1/cpn60 chaperonin family protein |
| Zm00001d039633 | uncharacterized |
| Zm00001d040069 | Probable glucuronoxylan glucuronosyltransferase IRX7 |
| Zm00001d047177 | TATA-binding protein-associated factor BTAF1 |
| Zm00001d048502 | COP9 signalosome complex subunit 1 |
| Zm00001d048507 | uncharacterized |
| Zm00001d048510 | uncharacterized |
| Zm00001d048511 | AP-2 complex subunit alpha-2 |
| Zm00001d048527 | rolled leaf 1 |
| Zm00001d048536 | SKP1-like protein 21 |

| | |
|----------------|------------------------------|
| Zm00001d048541 | uncharacterized |
| Zm00001d049814 | uncharacterized |
| Zm00001d051566 | LOC100191766-like pseudogene |
| Zm00001d051742 | uncharacterized |
