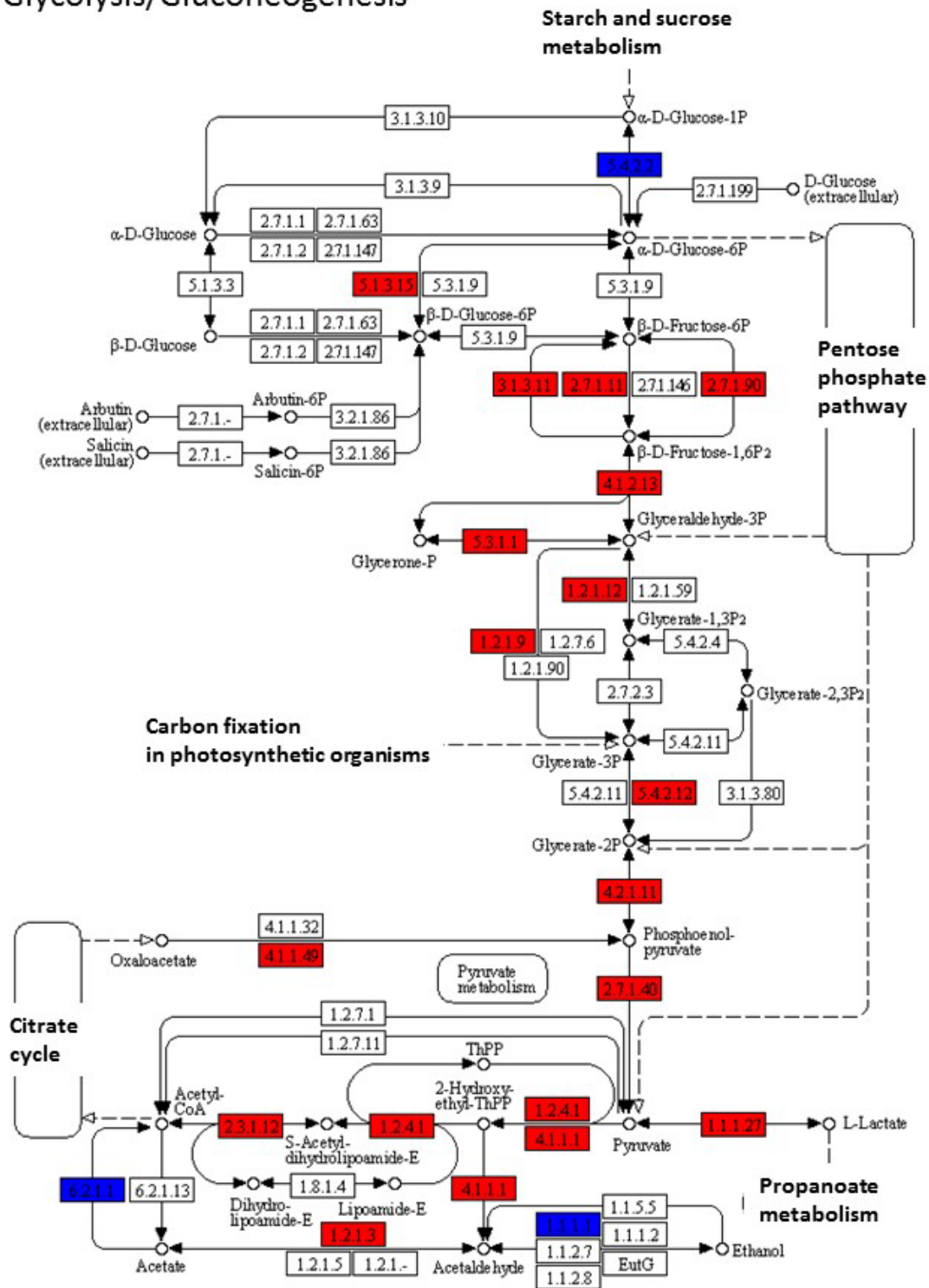


**Figure S1.** Daylength and average air temperatures (based on 8 measures/day) in Bet Dagan, Israel during growth season 2015-2016

## Glycolysis/Gluconeogenesis



00010 4/12/18  
(c) Kanehisa Laboratories

**Figure S2.** Pathways of glycolysis and gluconeogenesis in imbibed and stratified garlic seeds as revealed by KEGG algorithm osa00010. Over-representation in stratified seeds is marked in red, over-representation in imbibed seeds is marked in blue

**Table S1.** List of 61 homologous genes associated with seed dormancy and germination, proliferation, glycolysis and glucose transport and meristem identity in seeds of *Allium sativum*. Short description according to UniProt database and literature survey.

NN	Short name	Full name	Trinity ID	Putative function
<b>SEED DORMANCY AND GERMINATION</b>				
<b>1</b>	<b>DOG1</b>	<i>DELAY OF GERMINATION1</i>	TR221356 c0_g1	The level of DOG1 protein in freshly harvested seeds determines the level of seed dormancy through temperature control of the gibberellins metabolism. Regulates seed dormancy and flowering time through an influence on levels of miR156 and miR172
<b>2</b>	<b>RGL1</b>	<i>RGA-like1</i>	TR228129 c0_g2	Transcriptional regulator that acts as a repressor of the gibberellin (GA) signaling pathway. Regulates seed germination and floral development
<b>3</b>	<b>HSP90.2</b>	<i>HEAT SHOCK PROTEIN 90.2</i>	TR140681 c0_g2	Plants with reduced HSP90.2 activity are hypersensitive to ABA in seed germination
<b>4</b>	<b>TAR2</b>	<i>TRYPTOPHAN AMINOTRANSFERASE-RELATED PROTEIN 2</i>	TR207941 c0_g1	Important for embryo development and seedling growth in the auxin signaling pathway.
<b>5</b>	<b>PM41</b>	<i>SEED MATURATION PROTEIN PM41</i>	TR148223 c0_g1	Involved in seed development and dormancy. Show differential expression in maize kernel in response to drought.
<b>6</b>	<b>LEA D34</b>	<i>LATE EMBRYOGENESIS ABUNDANT D34</i>	TR208624 c0_g1	Late embryonic proteins abundant in higher plant seed embryos. Promotes seed heat-resistant
<b>7</b>	<b>LEA B19.4</b>	<i>LATE EMBRYOGENESIS ABUNDANT B19.4</i>	TR207222 c0_g1	Late embryonic proteins abundant in higher plant seed embryos. Differentially expressed by abscisic acid and osmotic stress.
<b>8</b>	<b>GLUP4</b>	<i>GLUTELIN PRECURSOR 4</i>	TR230284 c0_g2	It is thought to provide protection for the cytoplasm during the desiccation stage of embryo development.

9	PHYA	<i>PHYTOCHROME A</i>	TR231741 c0_g1	Regulates phototropic responses both in the nucleus (e.g. hypocotyl elongation and cotyledon opening under high-irradiance conditions and seed germination under very-low-fluency conditions) and in the cytoplasm (e.g. negative gravitropism in blue light and red-enhanced phototropism). Also involved in flowering time regulation.
10	SBP65	<i>SEED BIOTIN-CONTAINING PROTEIN65</i>	TR202704 c0_g1	May serve as a biotin provider for several growth-limiting enzymes that are necessary during seed development and the subsequent germination stages, and thus may play some roles in determining seed germination capacity
11	LHW	<i>LONESOME HIGHWAY</i>	TR220058 c0_g1	Regulates root development; promotes the production of stele cells in roots.
12	PHOT2	<i>PHOTOTROPIN2</i>	TR231376 c2_g33	Regulates a wide range of physiological activities in plants that maximize the efficiency of photosynthesis, Involved in hypocotyl phototropism.
13	LEA D29	<i>LATE EMBRYOGENESIS ABUNDANT D29</i>	TR212691 c1_g1	Late embryonic proteins abundant in higher plant seed embryos. Storage proteins involved in post-embryonic development.
14	LEA D8	<i>LATE EMBRYOGENESIS ABUNDANT D8</i>	TR204749 c0_g3	Late embryonic proteins abundant in higher plant seed embryos. Involved in seed maturation independent of embryo morphogenesis.
15	LEA Dc3	<i>LATE EMBRYOGENESIS ABUNDANT Dc3</i>	TR169709 c2_g2	Late embryonic proteins abundant in higher plant seed embryos. Involved in the response to abscisic acid.
16	PNH1	<i>PINHEAD HOMOLOG1</i>	TR227482 c2_g5	Main component of the RNA-induced silencing complex (RISC) that binds to a short guide RNA such as a miRNA or siRNA. Essential for multiple processes in development. Plays a role in the maintenance of the indeterminate state of the stem cells in the shoot apical meristem (SAM).
17	PHOT1A	<i>PHOTOTROPIN1A</i>	TR212212 c0_g5	Protein kinase that acts as a blue light photoreceptor in a signal-transduction pathway. Necessary for root phototropism. Involved in hypocotyl phototropism under a low rate.
18	LEA14	<i>LATE EMBRYOGENESIS ABUNDANT 14</i>	TR189555 c0_g1	Late embryonic proteins abundant in higher plant seed embryos. Upregulated by high light, drought, cold, and salt stresses.
19	NRT1	<i>NITRATE TRANSPORTER 1.1</i>	TR233132 c2_g1	Acts as a nitrate sensor that trigger a specific signaling pathway stimulating lateral root growth and seed germination

20	HDAC1	HISTONE DEACETYLASE1	TR215568 c1_g1	Histone deacetylation gives a tag for epigenetic repression and plays an important role in transcriptional regulation. Regulates negatively the expression of the NAC48/NAC6 gene that controls root growth in seedlings.
21	LUG	LEUNIG	TR221609 c2_g6	Involved in post-synthesis cell wall modifications necessary for mucilage extrusion from seeds upon imbibition. Implicated in embryo and floral development.
22	LEA	LATE EMBRYOGENESIS ABUNDANT D	TR193346 c0_g6 TR162936 c0_g1 TR336079 c0_g1 TR215760 c0_g1	Late embryonic proteins abundant in higher plant seed embryos.
PROLIFERATION				
23	MBR2	MED25-BINDING RING-H2 PROTEIN 2	TR77112 c0_g2	Plays a role in cell proliferation by HAL3, HAL3 may lead to the degradation of cell cycle suppressors, resulting in enhancement of cell division and plant growth. Also involve in flowering through degradation of MED25 seems to activate its function as positive regulator of FT
24	MCM2	MINICHROMOSOM E MAINTENANCE PROTEIN 2	TR236252 c0_g1	Plays a crucial role in the control of de-differentiation and cell proliferation processes required for lateral root formation. Is essential for embryo development.
25	RABA2a	RAS-RELATED PROTEIN RABA2A	TR121383 c0_g1	Rab-A2 and Rab-A3 GTPases define a trans-Golgi endosomal membrane domain in Arabidopsis that contributes substantially to the cell plate
26	PPC2	PHOSPHOENOLPY RUVATE CARBOXYLASE 2	TR231660 c0_g1	Involve in bud formation by stabling abscisic acid receptors.
27	ACT7	ACTIN 7	TR227686 c7_g3	Essential component of cell cytoskeleton; plays an important role in cell division. Considered as one of the vegetative actins involved in the regulation of hormone-induced plant cell proliferation and callus formation.
28	CDC48	CELL DIVISION CONTROL 48	TR216875 c0_g1	Probably functions in cell division and growth processes.
29	CDC2	CELL DIVISION CONTROL 2	TR225341 c3_g3	Involved in the control of the cell cycle. Essential for both G1/S and G2/M (mitosis) phase transitions.
30	NCAPD2	NON-SMC CONDENSIN I COMPLEX SUBUNIT D2	TR201684 c0_g1	Part of complex of proteins governing cell-cycle.

31	ALIS1	ALA-INTERACTING SUBUNIT 1	TR210966 c0_g1	Important part of the Golgi machinery required for secretory processes during plant development. Expressed in root peripheral cells.
<b>KEY GENES IN GLYCOLYSIS AND GLUCOSE TRANSPORT</b>				
32	KINB1	SNF1-related kinase regulatory subunit beta-1-like isoform X1	TR196482 c1_g1	Play a role in a signal transduction cascade regulating gene expression and carbohydrate metabolism.
33	FBA	FRUCTOSE- BIPHOSPHATE ADOLASE	TR217854 c5_g9	Plays a key role in glycolysis and gluconeogenesis.
34	ATHB13	HOMEODOMAIN- LEUCINE ZIPPER ATHB13	TR146602 c0_g1	Transcription factor that may act in the sucrose-signaling pathway.
35	PV42A	SNF1-RELATED KINASE REGULATORY SUBUNIT GAMMA- LIKE PV42a	TR212684 c1_g1	Member of family of central metabolic sensors, activated when environmental stress conditions deplete carbon and energy supply and which are known to link the sugar status with organ growth.
<b>MERISTEM IDENTITY GENES</b>				
36	AP2	APETALA2	TR195452 c0_g1	Required subsequently for the transition of an inflorescence meristem into a floral meristem. Acts through the maternal sporophyte and endosperm genomes to control seed weight and seed yield.
37	LHY	LATE ELONGATED HYPOCOTYL	TR206379 c1_g1	LHY and CCA1 accelerate flowering in part by reducing the abundance of SVP and thereby antagonizing its capacity to repress FT expression under LL
38	VEL2	VIN3-LIKE PROTEIN 2	TR223059 c7_g1	May be involved in both the vernalization and photoperiod pathways by regulating gene expression. Binds preferentially to dimethylated histone H3 'Lys-9' (H3K9me2). Promotes flowering in non-inductive photoperiods (e.g. short days) through the maintenance of the epigenetically repressed state of MAF5 via H3K9me2 and plant homeodomain/polycomb repressive complex 2 (PHD-PRC2)-dependent H3K27me3.
39	LD	LUMINIDEPEN- DENT	TR191950 c0_g1	Play a role in the regulation of flowering time in the autonomous flowering pathway by repressing FLOWERING LOCUS C expression.
40	JMJ14	JUMONJI 14	TR231068 c4_g3	Represses FT and TSF expression to inhibit the floral transition. Regulates gene expression and flowering time, probably by the promotion of RNA-mediated gene silencing.

41	U2AF35B	<i>SPLICING FACTOR U2AF SMALL SUBUNIT B</i>	TR200517 c0_g3	Necessary for the splicing of pre-mRNA (by similarity). Probably active at the 3' splice sites. Mutants showed altered flowering time.
42	ZHD4	<i>ZINC-FINGER HOMEODOMAIN 4</i>	TR210252 c0_g1	Putative transcription factor. Probably involved in the regulation of floral induction
43	STO	<i>SALT TOLERANCE</i>	TR190403 c0_g1	Acts as negative regulator of seedling photomorphogenesis and light-regulated inhibition of hypocotyl elongation. Negative regulator of photomorphogenic UV-B responses by interacting with both COP1 and HY5.
44	FBH4	<i>TRANSCRIPTION FACTOR BHLH130</i>	TR213978 c0_g1	Positively regulate CO transcription for photoperiodic flowering.
45	RAV2	<i>RELATED TO ABI3/VP1 2</i>	TR209075 c0_g2	Transcriptional repressor of flowering time on long day plants. Acts directly on FT expression by binding 5'-CAACA-3' and 5'-CACCTG-3 sequences.
46	COL9	<i>CONSTANS-LIKE 9</i>	TR212015 c0_g1	Involved in regulation of flowering time by repressing the expression of CO, concomitantly reducing the expression of FT and delaying floral transition.
47	CDKG2	<i>CYCLIN- DEPENDENT KINASE G 2</i>	TR234706 c1_g2	The flowering of salinity-stressed cdkg2 mutant plants was earlier and that of the CDKG2 over-expressors later than of control plants.
48	ESD7	<i>EARLY IN SHORT DAYS7</i>	TR232574 c4_g6	Required for flowering repression through a mechanism involving epigenetic gene silencing.
49	GATA22	<i>PUTATIVE GATA TRANSCRIPTION FACTOR 22</i>	TR223189 c0_g1	Prevents the accumulation of SOC1 during flowering.
50	APL1	<i>ADP GLUCOSE PYROPHOSPHORYL ASE 1</i>	TR205688 c1_g1	Mutants showed delayed flowering under long days.
51	CRY2	<i>CRYPTOCHROME2</i>	TR223854 c0_g2	Photoreceptor that mediates primarily blue light inhibition of hypocotyl elongation and photoperiodic control of floral initiation, and regulates other light responses, including circadian rhythms, tropic growth, root development, cell cycles, apical dominance, seed dormancy. Regulates the timing of flowering by promoting the expression of FT in vascular bundles. Negatively regulated by FLC. Inhibits COP1-mediated degradation of transcription factors (e.g. CO and HY5).
52	CDC73	<i>CELL DIVISION CONTROL PROTEIN 73</i>	TR223980 c9_g2	Required for the expression of the flowering repressors FLC and MADS-box genes of the MAF family by histone H3 trimethylation on 'Lys-4' (H3K4me3).

53	<b>CDF1</b>	<i>CYCLIC DOF FACTOR 1</i>	TR231460 c0_g1	Regulates photoperiodic flowering response. Transcriptional repressor of CONSTANS expression. The DNA-binding ability is not modulated by GIGANTEA but the stability of CDF1 is controlled by the proteasome-dependent pathway.
54	<b>ATHB16</b>	<i>HOMEODOMAIN-LEUCINE ZIPPER ATHB16</i>	TR184651 c0_g1	Transcription factor that may function as a negative regulator of the flowering time response to photoperiod.
55	<b>CCA1</b>	<i>CIRCADIAN CLOCK ASSOCIATED 1</i>	TR224608 c0_g2	Transcription factor involved in the circadian clock and in the phytochrome regulation.
56	<b>RVE2</b>	<i>REVEILLE 2</i>	TR215430 c0_g3	Positive regulator for cold-responsive gene expression and cold tolerance. Part of a regulatory feedback loop that controls a subset of the circadian outputs and modulates the central oscillator, including germination.
57	<b>FLL1</b>	<i>FLX-LIKE 1</i>	TR179555 c0_g1	Part of the FLC expressor gene family, function is unknown but it bind to FCA (that regulate RNA silencing in FLC locus).
58	<b>PRR9</b>	<i>PSEUDO-RESPONSE REGULATOR 9</i>	TR191441 c1_g1	Repressor of CCA1 and LHY, and positive regulator of LWD1 and LWD2 expression. Controls photoperiodic flowering response and temperature compensation.
59	<b>FIP1</b>	<i>FRIGIDA INTERACTING PROTEIN 1</i>	TR200375 c1_g1	Interacts directly with FRI in the vernalization pathway, function unknown.
60	<b>AGL14</b>	<i>AGAMOUS-LIKE14</i>	TR135509 c0_g1	Involved in the regulation of shoot apical meristem (SAM) cell identities and transitions. Promotes flowering transition and participates in flower meristem maintenance and determinacy. Positively regulates TFL1 and WUS expression.
61	<b>HDA19</b>	<i>HISTONE DEACETYLASE19</i>	TR215568 c1_g1	HDA19 Acts with APETALA2 to negatively regulates multiple floral organ identity genes.