

Supplementary Materials

Prioritisation of candidate genes in QTL regions for seed germination and early seedling growth in bread wheat (*Triticum aestivum*) under salt-stress conditions

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Table S1. Physiological traits used in QTL analysis and Phenotypic variation of traits for RILs and their parents in salinity treatment
^a, N, S₁ and S₂ normal, first and second Salt Stress conditions, respectively; ^b, Recombinant Inbred Line (RIL); ^c, Standard Deviation (σ)

Trait description	Abbreviation	Index ^a	Parental means		RIL ^b			
			Roshan	SuperHead#2	Minimum	Maximum	Mean	Std. Deviation ^c
I. Germination								
<i>Germination Speed</i> (day)	GS	N	73.73	62.92	75	80	76.17	1.64
		S ₁	78.55	58.56	65	75	66.97	2.25
		S ₂	87.66	74.69	0	75	66.56	7.54
<i>Germination Percentage</i> (%)	GP	N	84.71	57.33	40	100	87.25	15.36
		S ₁	96.13	82.16	20	100	88.65	15.76
		S ₂	97.78	77.63	0	100	68.60	22.87
II. Early Seedling								
<i>Total Fresh Weight</i> (g)	TFW	N	0.25	0.1	0.07	0.56	0.19	0.06
		S ₁	0.32	0.13	0.07	0.28	0.18	0.03
		S ₂	0.34	0.15	0	1.59	0.12	0.15
<i>Total Dry Weight</i> (g)	TDW	N	0.025	0.01	0.008	0.255	0.02	0.028
		S ₁	0.074	0.05	0.002	0.082	0.018	0.005
		S ₂	0.036	0.016	0	0.153	0.015	0.013
<i>Primary leaf-Fresh Weight</i> (g)	PFW	N	0.19	0.1	0.01	0.6	0.078	0.05
		S ₁	0.28	0.09	0	0.29	0.035	0.025
		S ₂	0.23	0.079	0	1.2	0.053	0.112
<i>Primary leaf-Dry Weight</i> (g)	PDW	N	0.02	0.01	0	0.018	0.007	0.002
		S ₁	0.12	0.08	0	0.011	0.003	0.001
		S ₂	0.02	0.01	0	0.103	0.004	0.009
<i>Primary leaf Number</i>	PN	N	2.23	1.2	0.71	3.4	1.72	0.37
		S ₁	2.58	1.44	0	2.2	1.13	0.36
		S ₂	3.18	1.29	0	20	1.21	1.55
<i>Primary leaf Length</i> (cm)	PL	N	15.02	9.63	4.44	37.2	17.67	6.11
		S ₁	11.81	9.83	0	24	5.83	3.5
		S ₂	30.94	16.95	0	20	6.57	3.19
<i>Coleoptile Fresh Weight</i> (g)	CFW	N	0.119	0.08	0.002	0.61	0.04	0.04
		S ₁	0.21	0.11	0.01	9.28	0.11	0.71
		S ₂	0.15	0.072	0	0.28	0.05	0.03
<i>Coleoptile Dry Weight</i> (g)	CDW	N	0.013	0.008	0	0.015	0.004	0.001
		S ₁	0.016	0.01	0	0.085	0.007	0.01
		S ₂	0.013	0.007	0	0.04	0.005	0.003
<i>Coleoptile Length</i> (cm)	CL	N	5.25	3.25	2	10	4.40	1.198
		S ₁	5.05	3.05	0.007	10.44	3.08	1.42
		S ₂	6.37	4.38	0	30	3.62	2.91
<i>Radicle Fresh Weight</i> (g)	RFW	N	0.13	0.09	0.02	1.92	0.08	0.16
		S ₁	0.28	0.11	0.01	3.42	0.11	0.25
		S ₂	0.2	0.093	0	1.0	0.062	0.075
<i>Radicle Dry Weight</i> (g)	RDW	N	0.014	0.008	0.001	0.02	0.006	0.002
		S ₁	0.068	0.048	0.001	0.11	0.01	0.016
		S ₂	0.018	0.009	0	0.05	0.005	0.004
<i>Radicle Number</i>	RN	N	9.23	7.22	1.1	79.5	25.01	16.00
		S ₁	12.52	10.6	0.008	46.25	9.558	8.23
		S ₂	30.81	22.87	0	67.5	5.49	5.78
<i>Radicle Length</i> (cm)	RL	N	6.52	4.54	1.6	9	4.55	0.99
		S ₁	6.46	4.51	1.4	10.62	4.47	1.57

S ₂	6.51	4.61	0	61	4.90	5.53
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Table S2a. Correlations analysis between traits in RIL population derived from Roshan and SuperHead#2 in normal [N] condition by SAS
 Germination Speed (GS, day), Germination Percentage (GP, %), Total Fresh Weight (TFW, g), Total Dry Weight (TDW, g), Primary leaf Fresh Weight (PFW, g),
 Primary leaf Dry Weight (PDW, g), Primary leaf Number (PN), Primary leaf Length (PL, cm), Coleoptile Fresh Weight (CFW, g), Coleoptile Dry Weight (CDW, g),
 Coleoptile Length (CL, cm), Radicle Fresh Weight (RFW, g), Radicle Dry Weight (RDW, g), Radicle Length (RL, cm), and Radicle Number (RN).

*, **, significant at ($P < 0.05$), ($P < 0.01$), respectively.

	GS	GP	TFW	TDW	PFW	PDW	PN	PL	CFW	CDW	CL	RFW	RDW	RL	RN
GS	1														
GP	-0.480**	1													
TFW	0.028	-0.027	1												
TDW	0.054	-0.017	0.205**	1											
PFW	-0.010	0.031	0.275**	0.131	1										
PDW	-0.074	0.002	0.553**	0.152*	0.409**	1									
PN	-0.067	0.033	0.325**	0.084	0.302**	0.584**	1								
PL	-0.101	0.012	0.346**	0.028	0.347**	0.727**	0.443**	1							
CFW	-0.046	-0.105	0.286**	-0.006	0.131	0.302**	0.021	0.275**	1						
CDW	0.012	-0.166*	0.300**	-0.067	0.217**	0.485**	0.079	0.589**	0.500**	1					
CL	-0.041	-0.073	0.235**	-0.060	0.222**	0.492**	0.073	0.767**	0.381**	0.751**	1				
RFW	-0.036	0.081	0.285**	0.059	0.110	0.162*	0.050	0.117	0.088	0.157*	0.075	1			
RDW	-0.123	0.110	0.598**	0.179*	0.128	0.300**	0.104	0.215**	0.240**	0.306**	0.146*	0.442**	1		
RL	-0.109	0.241**	0.568**	0.278**	0.408**	0.443**	0.258**	0.288**	0.138	0.036	0.061	0.265**	0.512**	1	
RN	-0.109	0.023	0.308**	-0.031	0.232**	0.441**	0.113	0.735**	0.292**	0.644**	0.694**	0.113	0.300**	0.185*	1

Table S2b. Correlations analysis between traits in RIL population derived from Roshan and SuperHead#2 in first salinity [S₁] condition by SAS

Germination Speed (GS, day), Germination Percentage (GP, %), Total Fresh Weight (TFW, g), Total Dry Weight (TDW, g), Primary leaf Fresh Weight (PFW, g), Primary leaf Dry Weight (PLDW, g), Primaryleaf Number (PN), Primaryleaf Length (PL, cm), Coleoptile Fresh Weight (CFW, g), Coleoptile Dry Weight (CDW, g), Coleoptile Length (CL, cm), Radicle Fresh Weight (RFW, g), Radicle Dry Weight (RDW, g), Radicle Length (RL, cm), and Radicle Number (RN).

*, **, significant at $P < 0.05$, $P < 0.01$, respectively.

	<i>GS</i>	<i>GP</i>	<i>TFW</i>	<i>TDW</i>	<i>PFW</i>	<i>PDW</i>	<i>PN</i>	<i>PL</i>	<i>CFW</i>	<i>CDW</i>	<i>CL</i>	<i>RFW</i>	<i>RDW</i>	<i>RL</i>	<i>RN</i>
<i>GS</i>	1														
<i>GP</i>	-0.719**	1													
<i>TFW</i>	0.056	-0.084	1												
<i>TDW</i>	-0.024	0.002	0.404**	1											
<i>PFW</i>	-0.077	0.018	0.349**	0.183*	1										
<i>PDW</i>	-0.126	0.111	0.379**	0.202**	0.474**	1									
<i>PN</i>	-0.024	-0.044	0.138	0.058	0.173*	0.712**	1								
<i>PL</i>	-0.034	0.017	0.285**	0.145*	0.350**	0.750**	0.792**	1							
<i>CFW</i>	-0.017	-0.087	0.073	0.023	0.040	0.070	0.107	-0.034	1						
<i>CDW</i>	-0.073	0.016	0.179*	0.086	0.023	0.164*	0.232**	0.117	0.518**	1					
<i>CL</i>	0.004	0.024	0.106	-0.041	0.007	0.415**	0.494**	0.407**	-0.107	0.098	1				
<i>RFW</i>	-0.018	-0.106	0.120	0.033	0.042	0.012	0.029	-0.090	0.957**	0.483**	-0.151*	1			
<i>RDW</i>	0.034	-0.172*	0.147*	0.045	-0.053	0.104	0.132	0.013	0.361**	0.237**	0.142	0.346**	1		
<i>RL</i>	-0.140	0.160*	0.175*	0.065	0.236**	0.561**	0.449**	0.546**	-0.064	0.121	0.423**	-0.100	0.059	1	
<i>RN</i>	-0.101	0.074	0.084	0.033	0.068	0.571**	0.720**	0.574**	0.046	0.289**	0.535**	-0.022	0.206**	0.579**	1

Table S2c. Correlations analysis between traits in RIL population derived from Roshan and SuperHead#2 in second salinity [S₂] condition by SAS.

Germination Speed (GS, day), Germination Percentage (GP, %), Total Fresh Weight (TFW, g), Total Dry Weight (TDW, g), Primary leaf Fresh Weight (PFW, g), Primary leaf Dry Weight (PLDW, g), Primary leaf Number (PN), Primary leaf Length (PL, cm), Coleoptile Fresh Weight (CFW, g), Coleoptile Dry Weight (CDW, g), Coleoptile Length (CL, cm), Radicle Fresh Weight (RFW, g), Radicle Dry Weight (RDW, g), Radicle Length (RL, cm), and Radicle Number (RN).

*, **, significant at $P < 0.05$, $P < 0.01$, respectively.

	<i>GS</i>	<i>GP</i>	<i>TFW</i>	<i>TDW</i>	<i>PFW</i>	<i>PDW</i>	<i>PN</i>	<i>PL</i>	<i>CFW</i>	<i>CDW</i>	<i>CL</i>	<i>RFW</i>	<i>RDW</i>	<i>RL</i>	<i>RN</i>
<i>GS</i>	1														
<i>GP</i>	0.537**	1													
<i>TFW</i>	-0.161*	-0.283**	1												
<i>TDW</i>	-0.172*	-0.310**	0.865**	1											
<i>PFW</i>	-0.673**	-0.361**	0.383**	0.326**	1										
<i>PDW</i>	-0.639**	-0.330**	0.421**	0.353**	0.994**	1									
<i>PN</i>	-0.182*	-0.289**	0.865**	0.756**	0.384**	0.427**	1								
<i>PL</i>	-0.109	-0.279**	0.402**	0.332**	0.157*	0.174*	0.535**	1							
<i>CFW</i>	-0.131	-0.268**	0.643**	0.524**	0.239**	0.255**	0.716**	0.771**	1						
<i>CDW</i>	-0.096	-0.194**	0.644**	0.510**	0.223**	0.242**	0.727**	0.748**	0.980**	1					
<i>CL</i>	-0.211**	-0.339**	0.769**	0.656**	0.311**	0.326**	0.839**	0.650**	0.862**	0.859**	1				
<i>RFW</i>	-0.131	-0.243**	0.900**	0.801**	0.318**	0.355**	0.888**	0.257**	0.533**	0.554**	0.716**	1			
<i>RDW</i>	0.012	-0.068	0.194**	0.180*	-0.031	-0.037	0.204**	0.232**	0.358**	0.348**	0.304**	0.300**	1		
<i>RL</i>	-0.085	-0.134	0.249**	0.196**	0.066	0.042	0.219**	0.520**	0.555**	0.555**	0.569**	0.132	0.257**	1	
<i>RN</i>	-0.198**	-0.287**	0.826**	0.720**	0.348**	0.368**	0.888**	0.515**	0.766**	0.782**	0.920**	0.825**	0.299**	0.556**	1

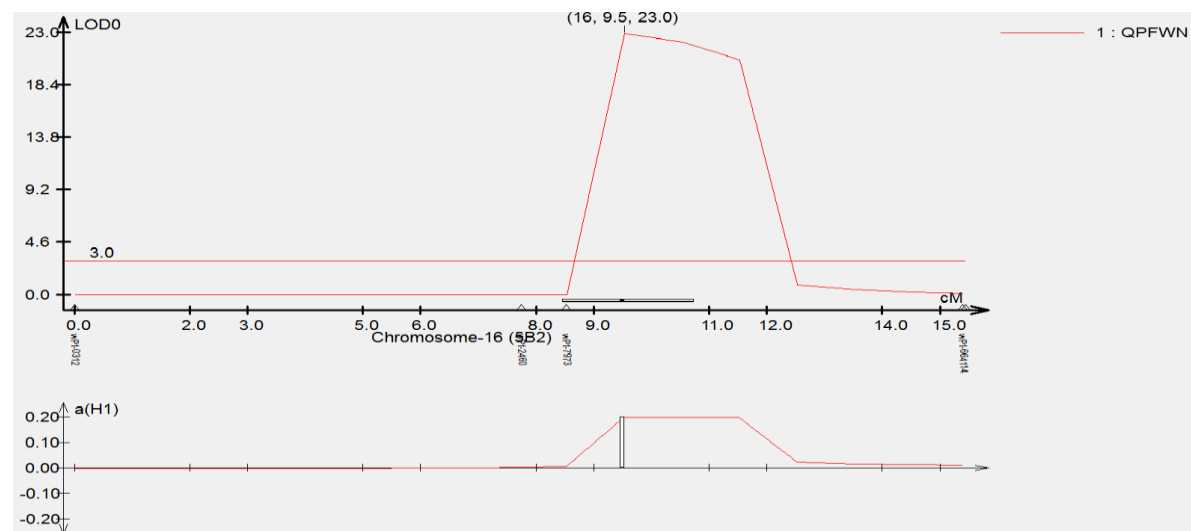


Fig. S1a. Chart obtained by QTL analysis of various attributes by QTL Cartographer. *QPfw-5B₂* (a); *Plumule Leaf Fresh Weight* trait, and in the linkage group 5B₂ (*wpt-7973 - wpt-664114* interval); the LOD score threshold is 3.

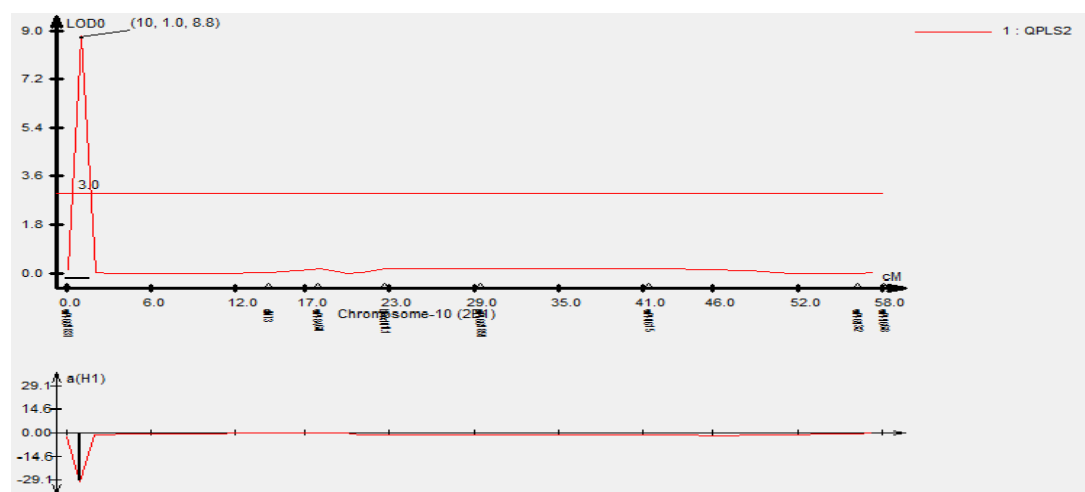


Fig. S1b. Chart obtained by QTL analysis of various attributes by QTL Cartographer. *QPI-2B₁* (b); *Plumule Leaf Length* trait, and in the linkage group 2B₁ (*wpt-669837 - cfd73* interval); the LOD score threshold is 3.

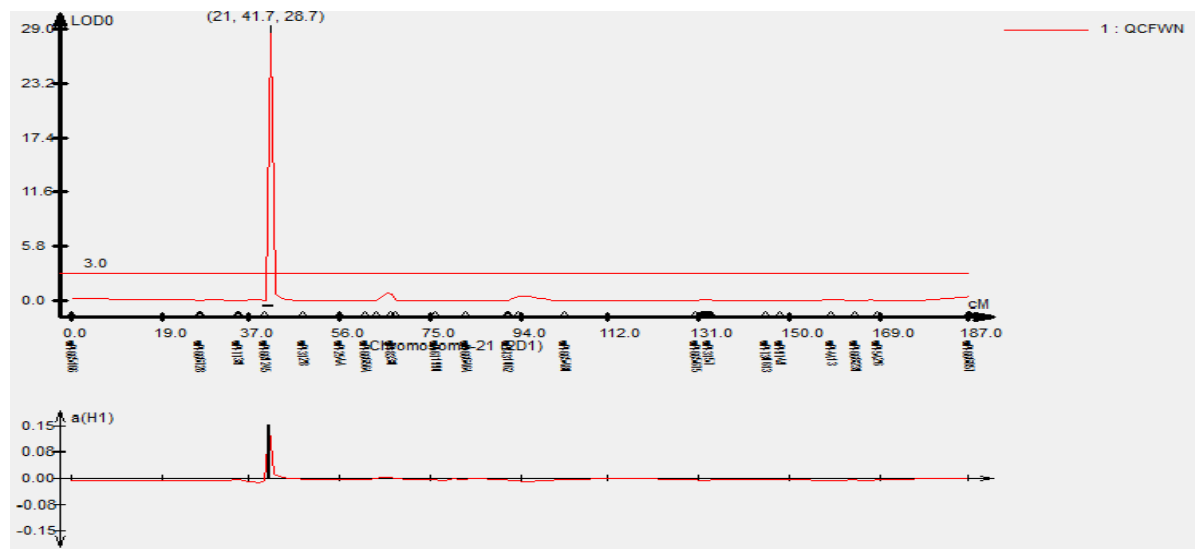


Fig. S1c. Chart obtained by QTL analysis of various attributes by QTL Cartographer. *QCfw-2D_{1.2}* (c); *Coleoptile Fresh Weight* trait, and in the linkage group 2D₁ (*wpt-669245* - *wpt-3728* interval); the LOD score threshold is 3.

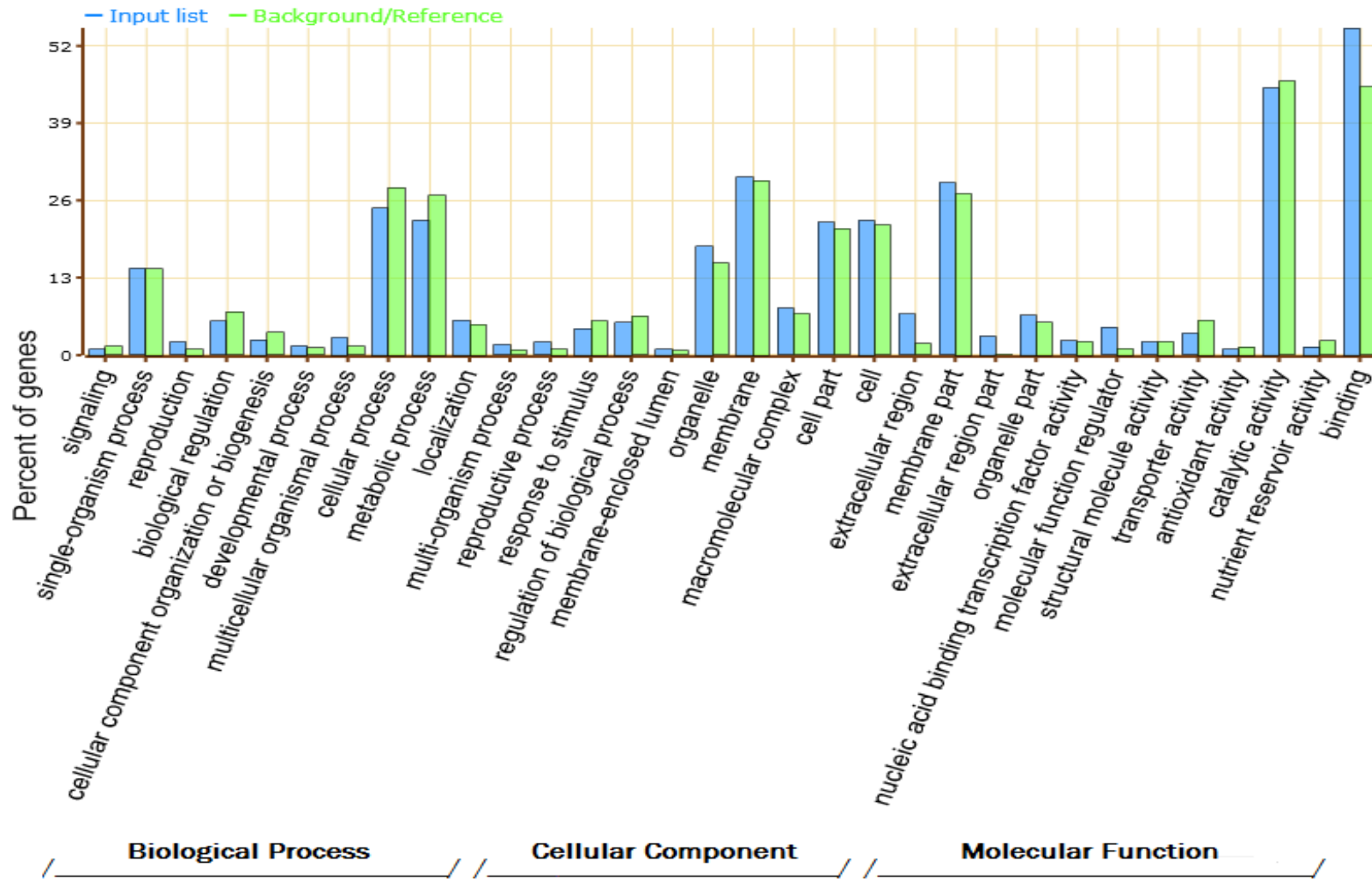


Fig. S2a. Agri GO annotation information in group A (a): Germination Speed (GS) trait QTLs (QGS-3B, QGS-2D₁, QGS-7D, QGS-6A, and QGS-7D).

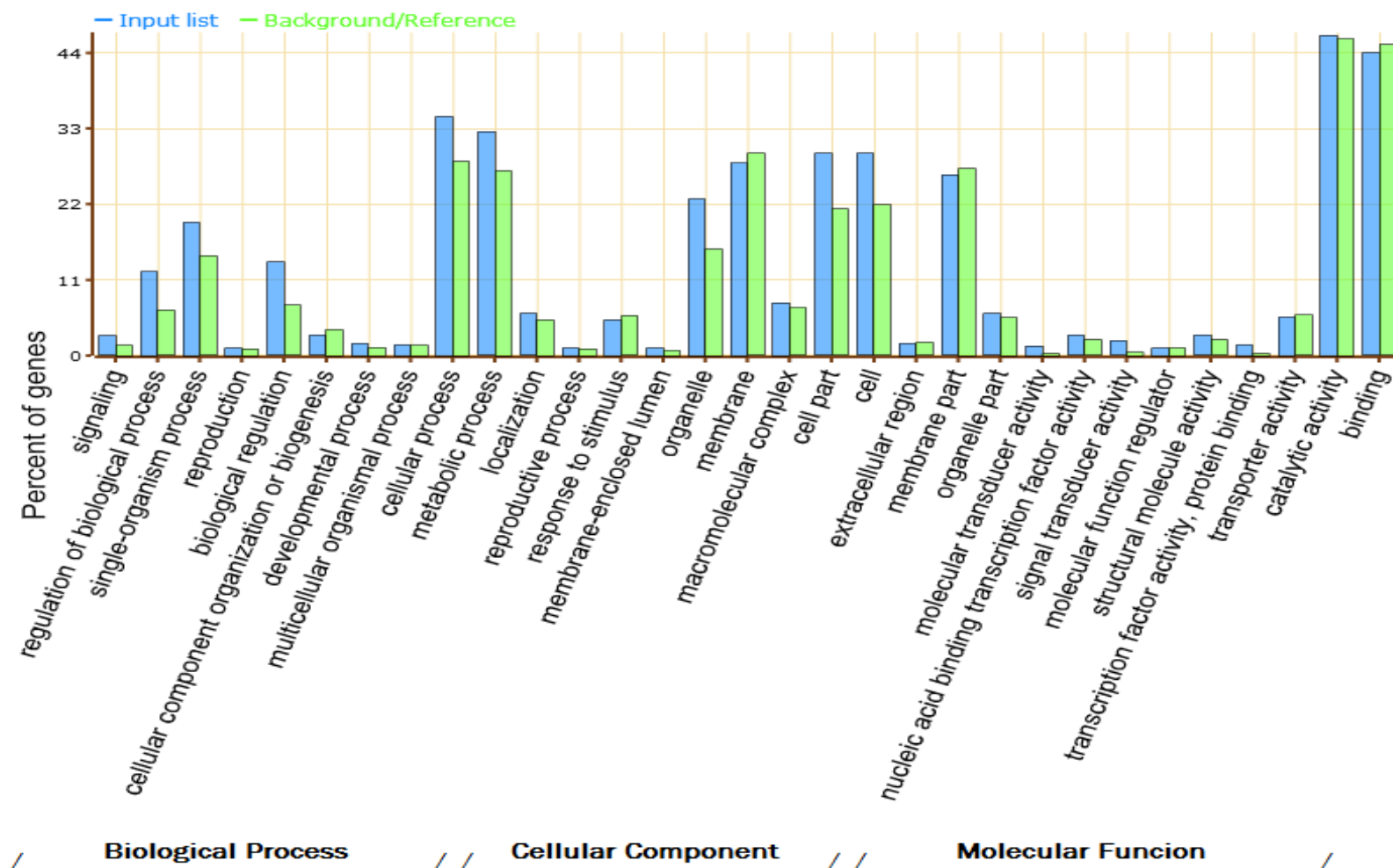


Fig. S2b. Agri GO annotation information in group B (b): Germination Percentage trait (GP) QTLs (*QGP-4A* and *QGP-3B*).

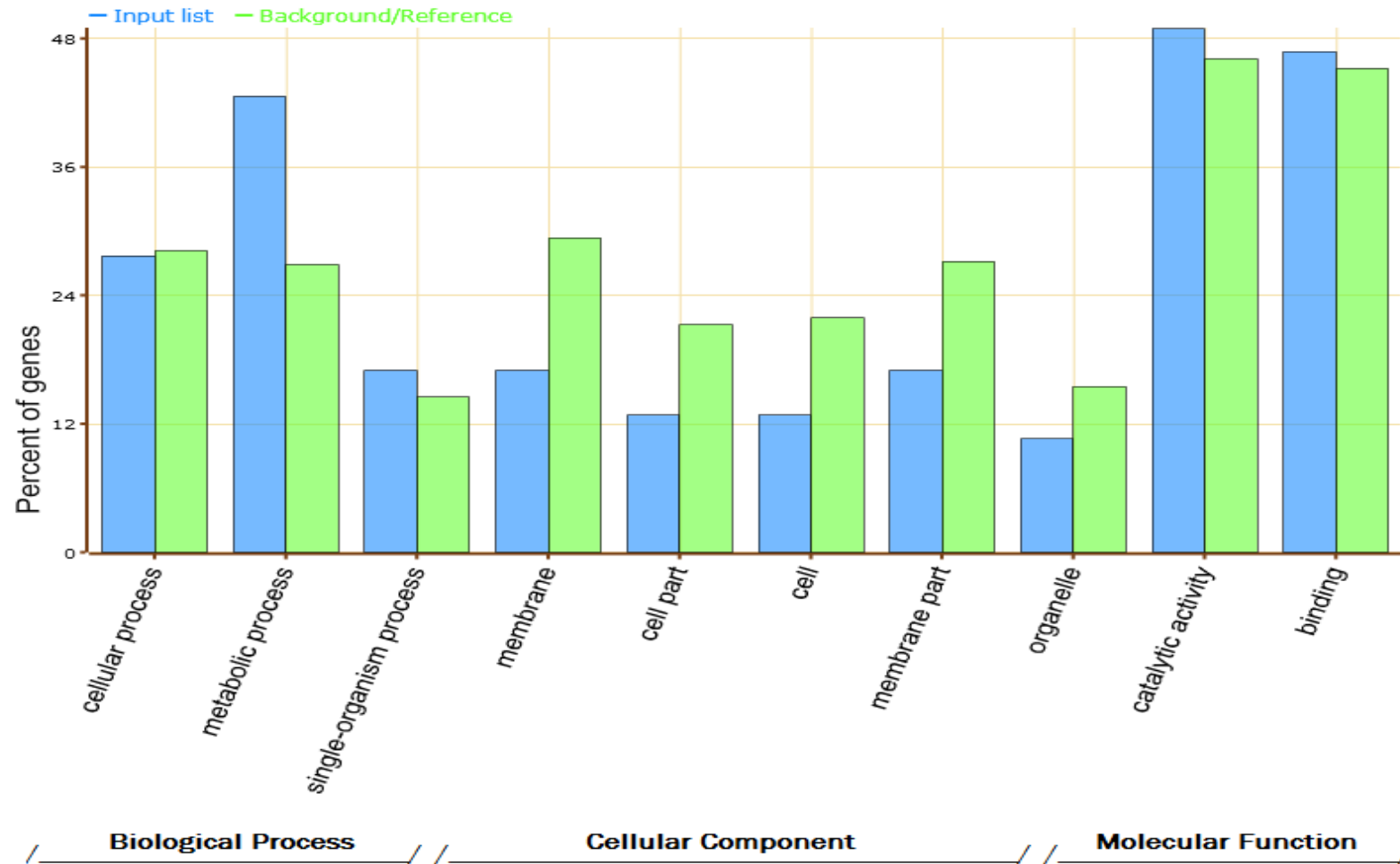


Fig. S2c. Agri GO annotation information in group C (c): Total Fresh Weight (TFW) trait QTL (*QTfw-3A*).

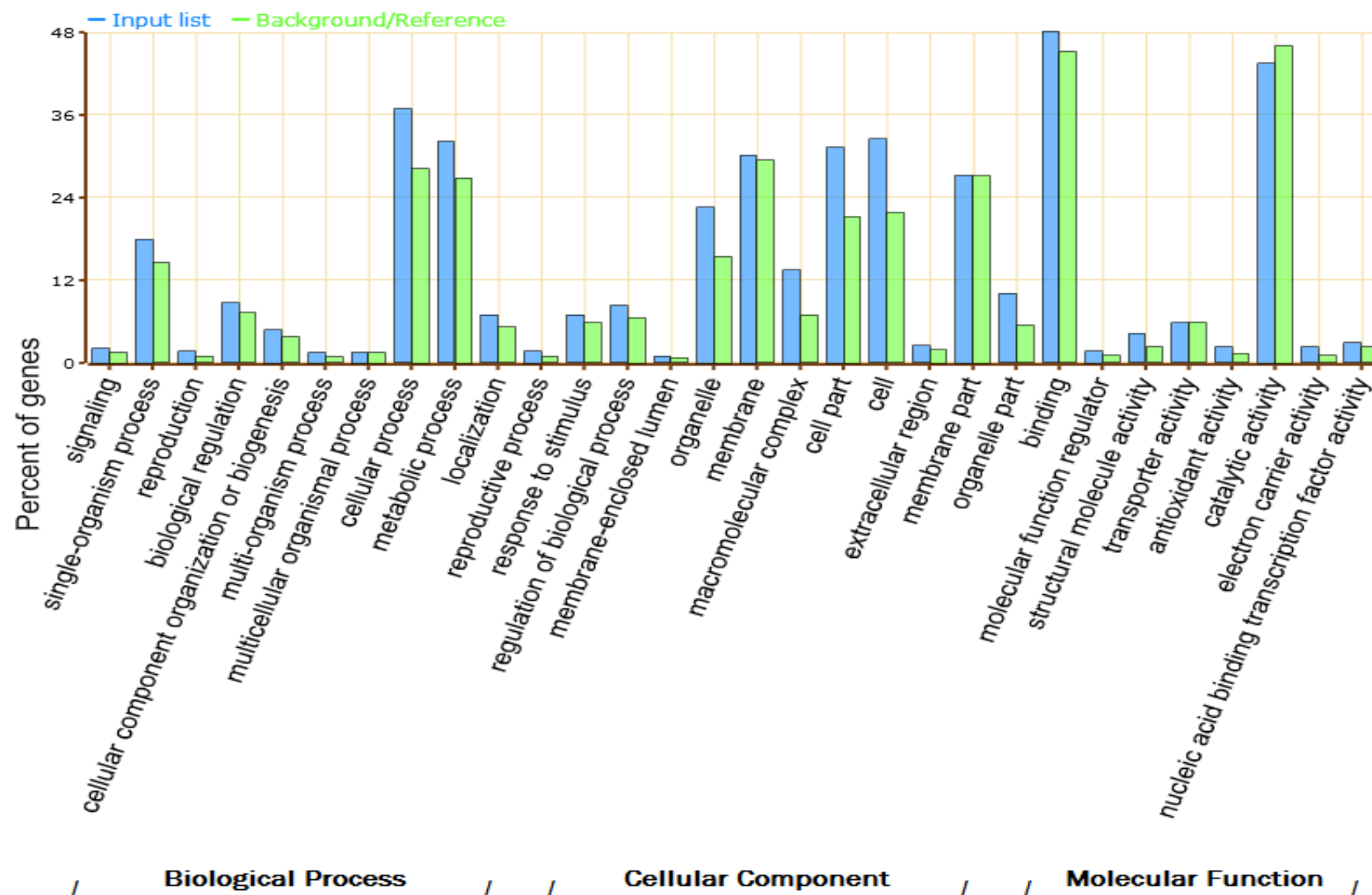


Fig. S2d. Agri GO annotation information in group D (d): Total Dry Weight (TDW) trait QTL (QT_{dw-2D_1}).

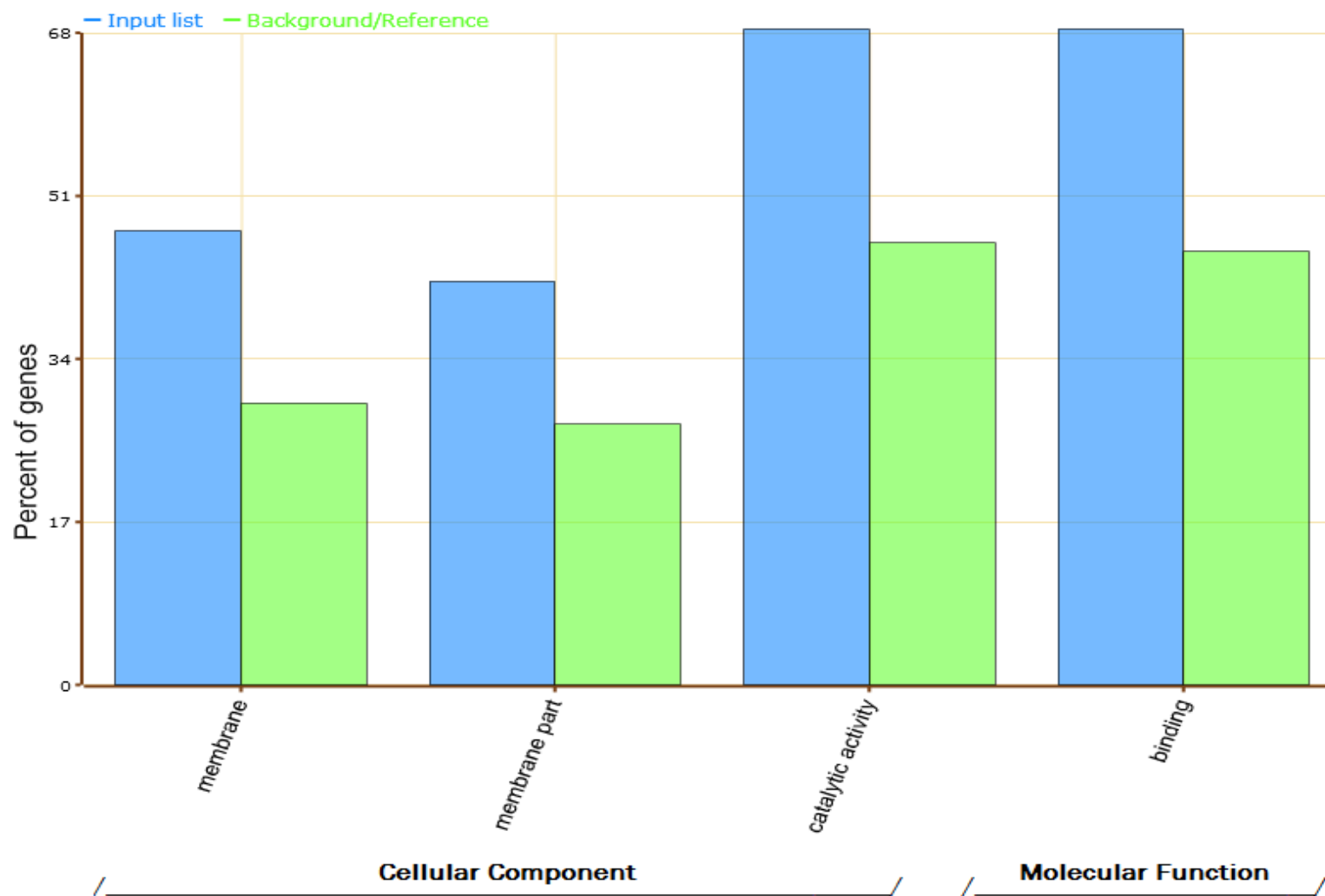


Fig. S2e. Agri GO annotation information in group E (e): Primary leaf Fresh Weight (*PFW*) trait QTL (*QPfw-3B*).

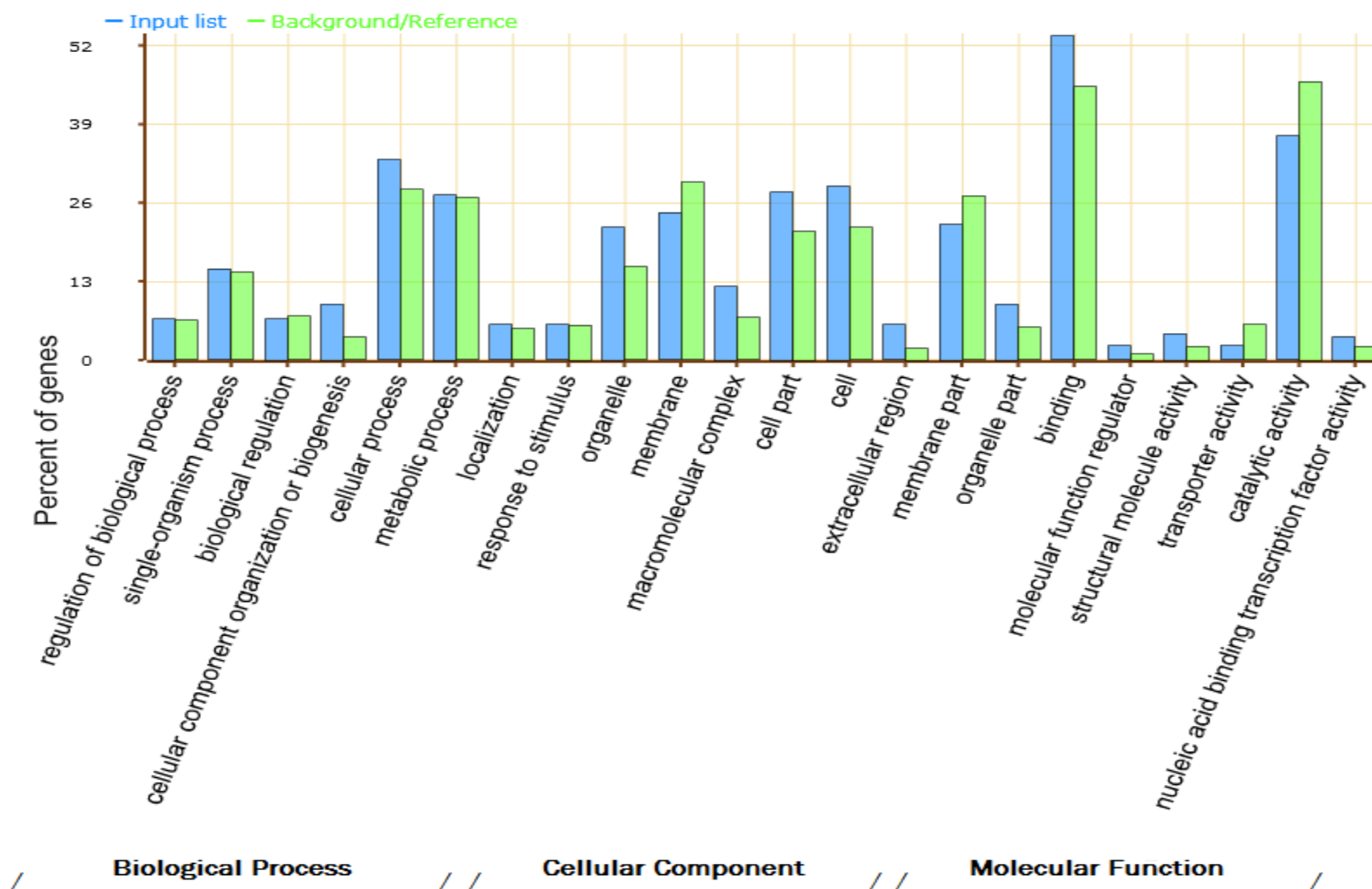


Fig. S2f. Agri GO annotation information in group F (f): Primary leaf Dry Weight (PDW) trait QTL (QPdw-5B₂).

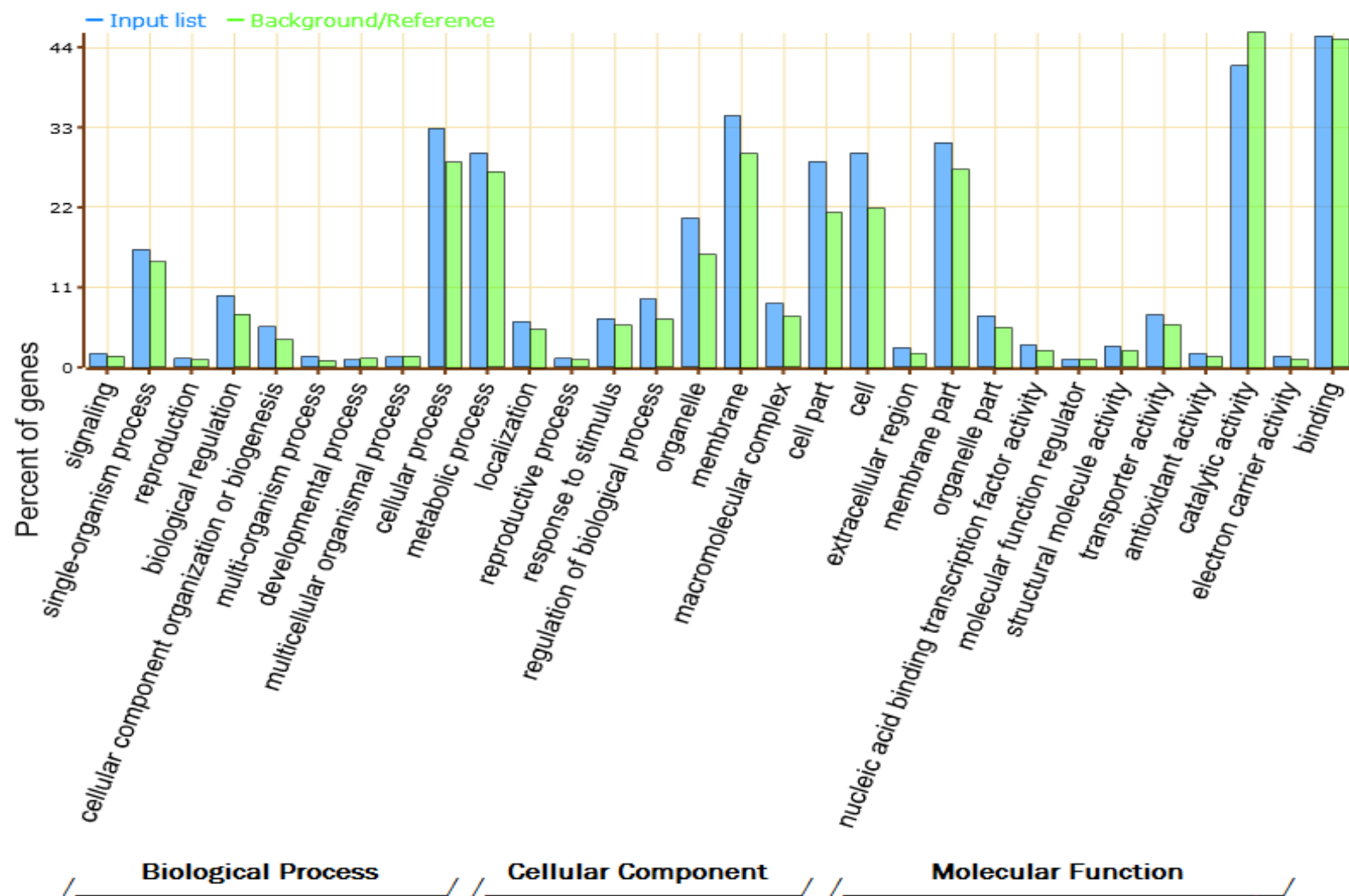


Fig. S2g. Agri GO annotation information in group G (g): Primary leafLength (PL) trait QTLs (QPI-4A and QPI-2B₁).

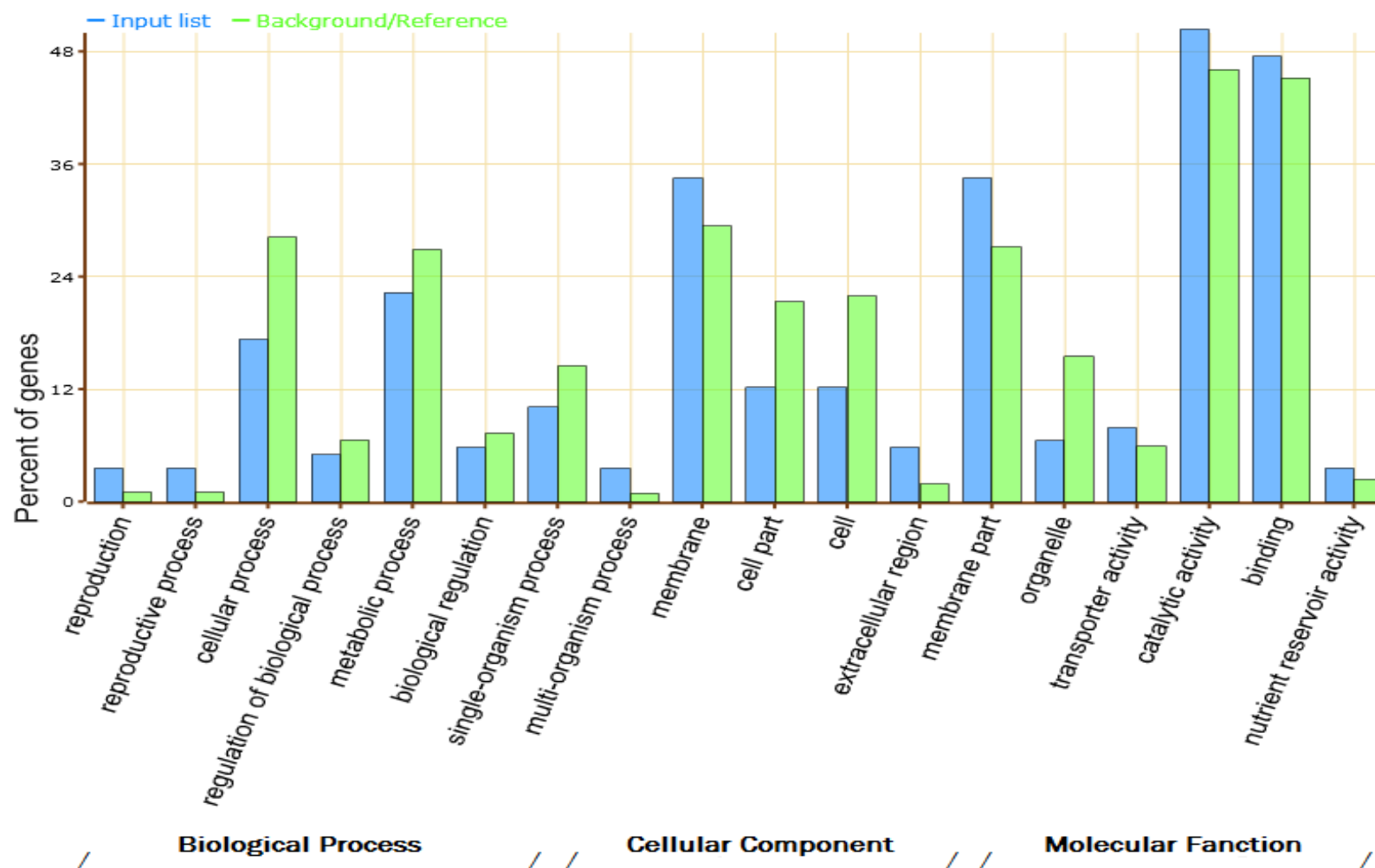


Fig. S2h. Agri GO annotation information in group H (h): Coleoptile Fresh Weight (CFW) trait QTLs (*QCfw-2D_{1.1}* and *QCfw-3B*).

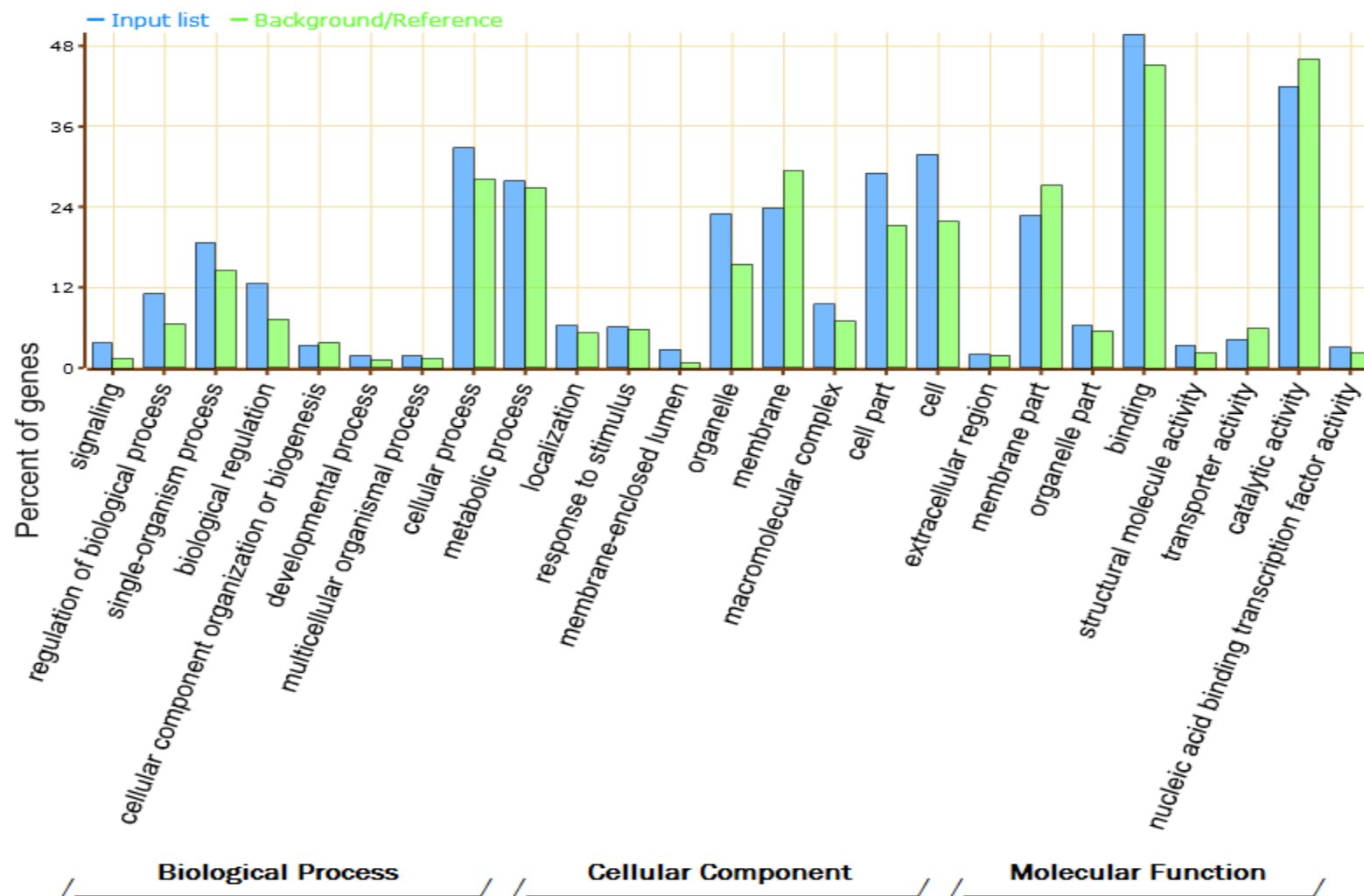


Fig. S2i. Agri GO annotation information in group I (i): Coleoptile Dry Weight (CDW) trait QTLs.

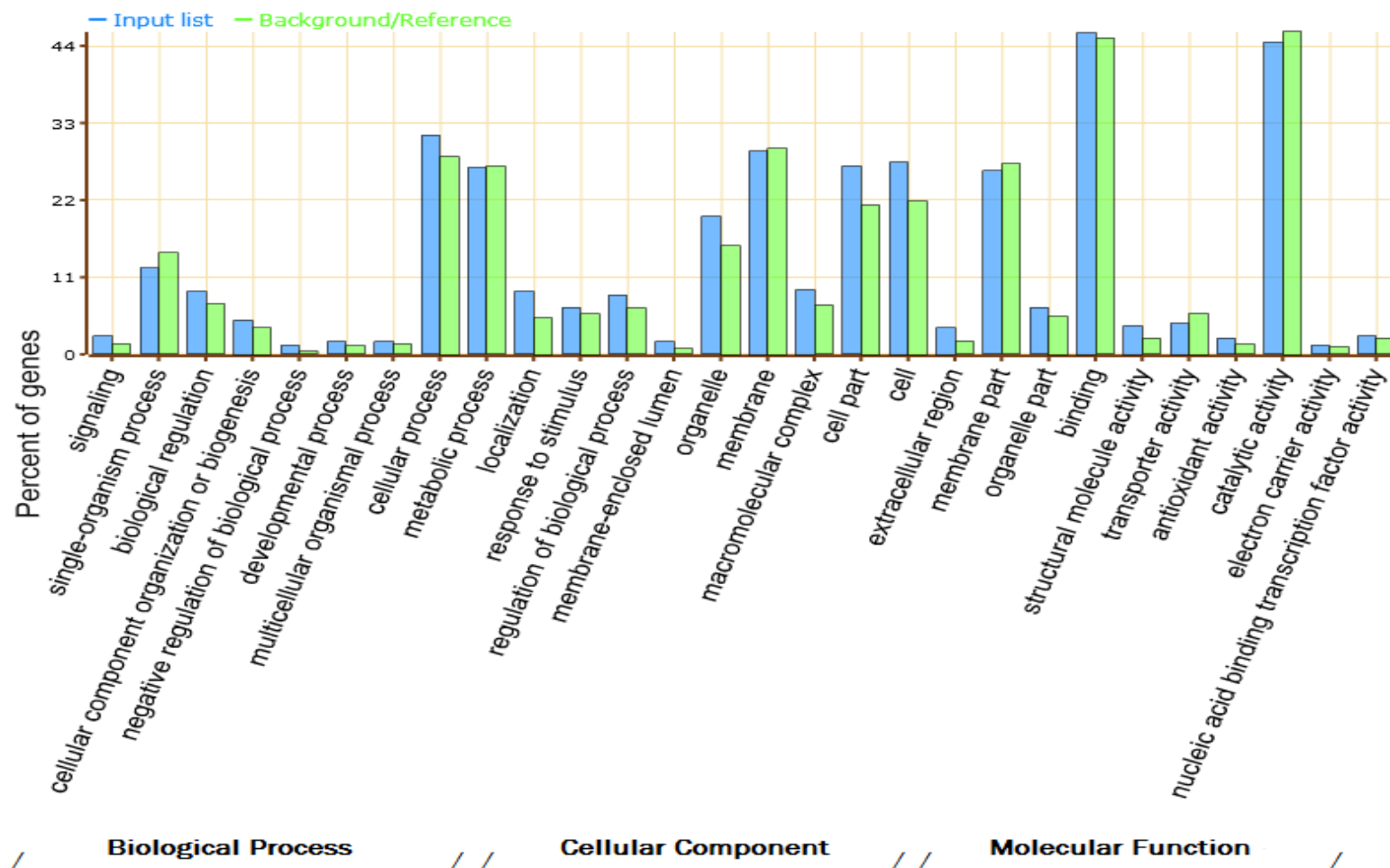


Fig. S2j. Agri GO annotation information in group J(j): Coleoptile Length (CL) trait QTL (QCl-3B).

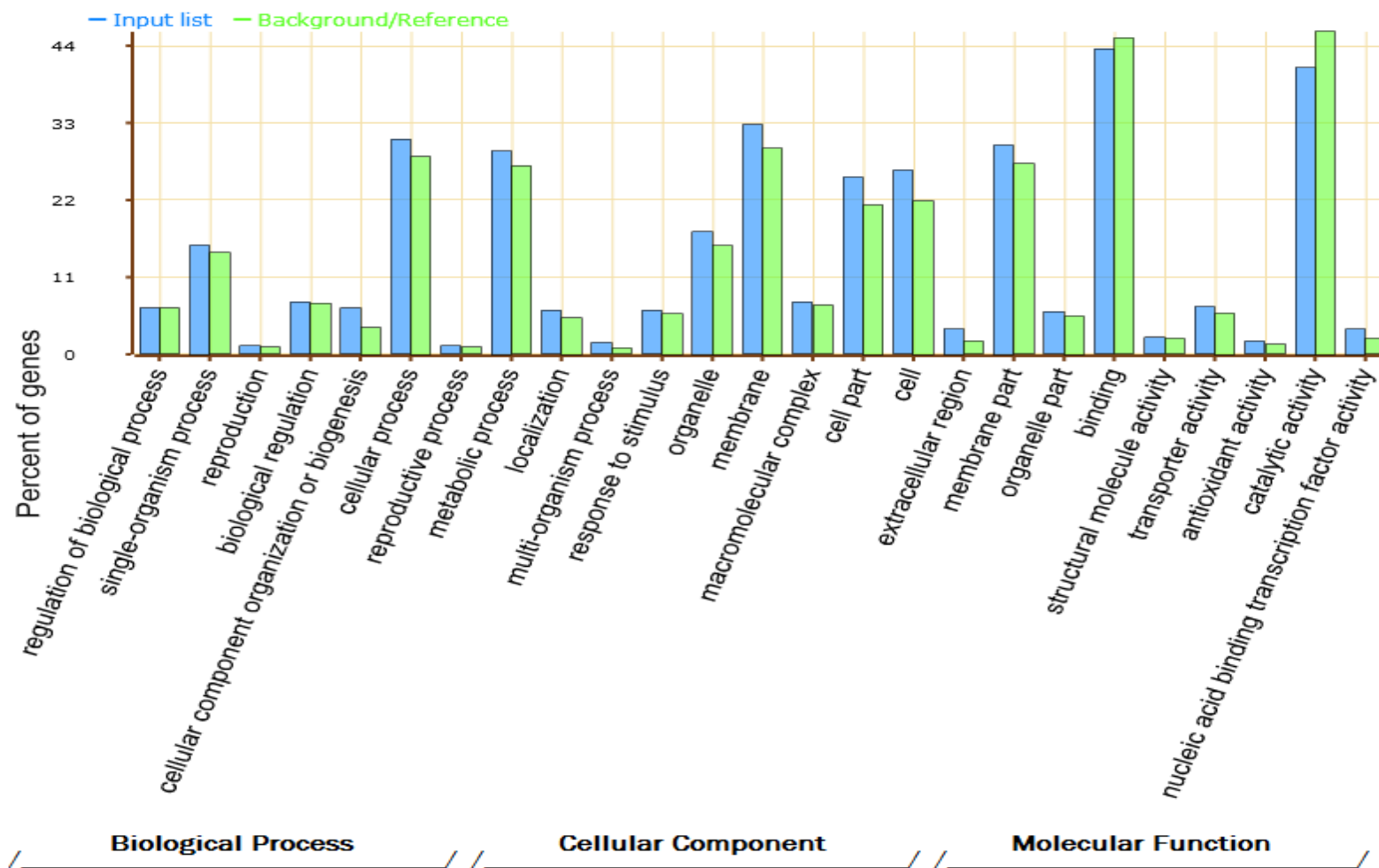


Fig. S2k. Agri GO annotation information in group K (k): Radicle Dry Weight (RDW) trait QTLs (*QRdw-2B_{1.1}* and *QRdw-3B*).

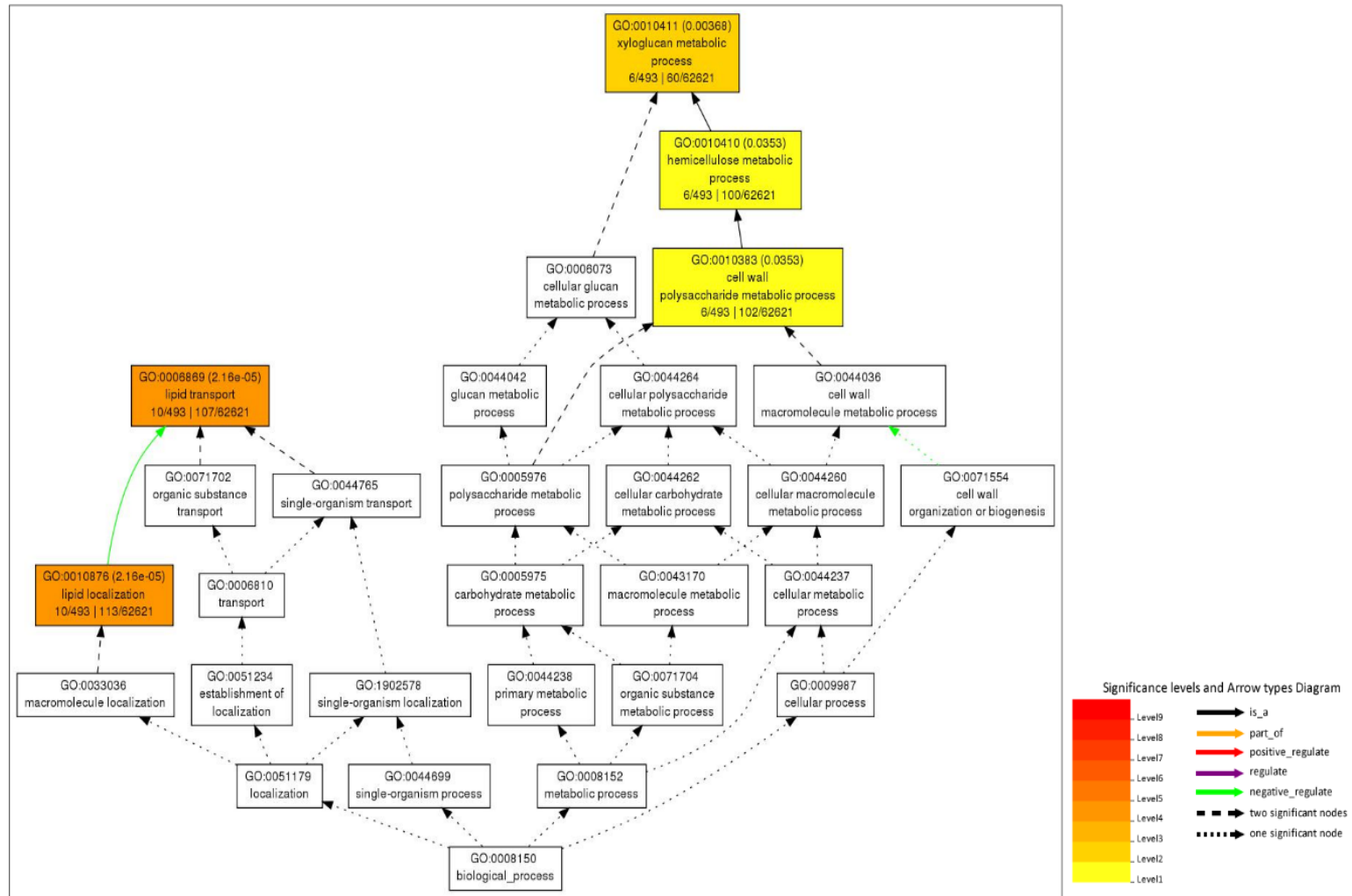


Fig. S3a. Agri GO analysis of Biological Process in group A (a): Germination Speed (GS) trait QTLs (QGS-3B, QGS-2D₁, QGS-7D, QGS-6A, and QGS-7D).

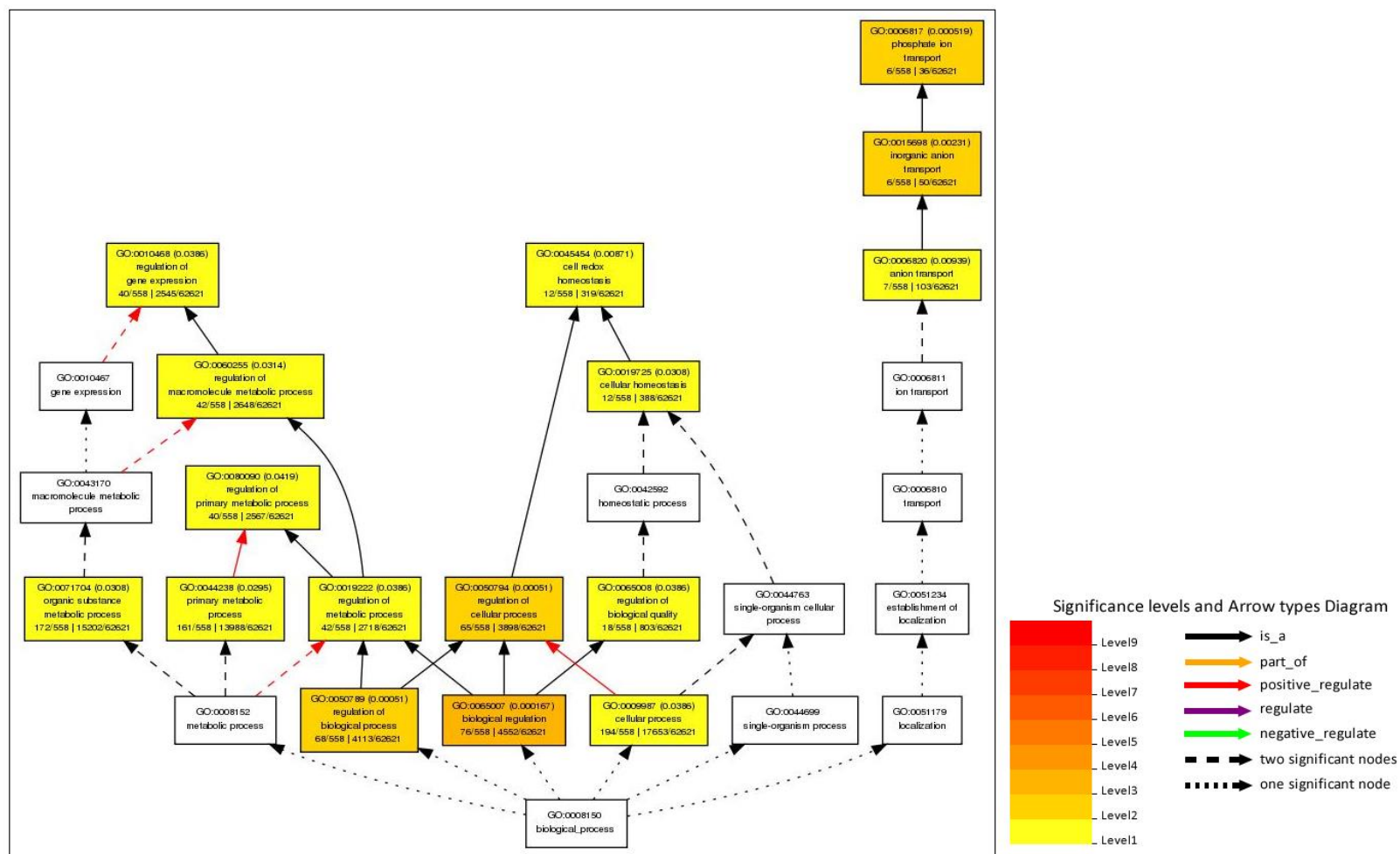


Fig. S3b. Agri GO analysis of Biological Process in group B (b): Germination Percentage trait (GP) QTLs (*QGP-4A* and *QGP-3B*).

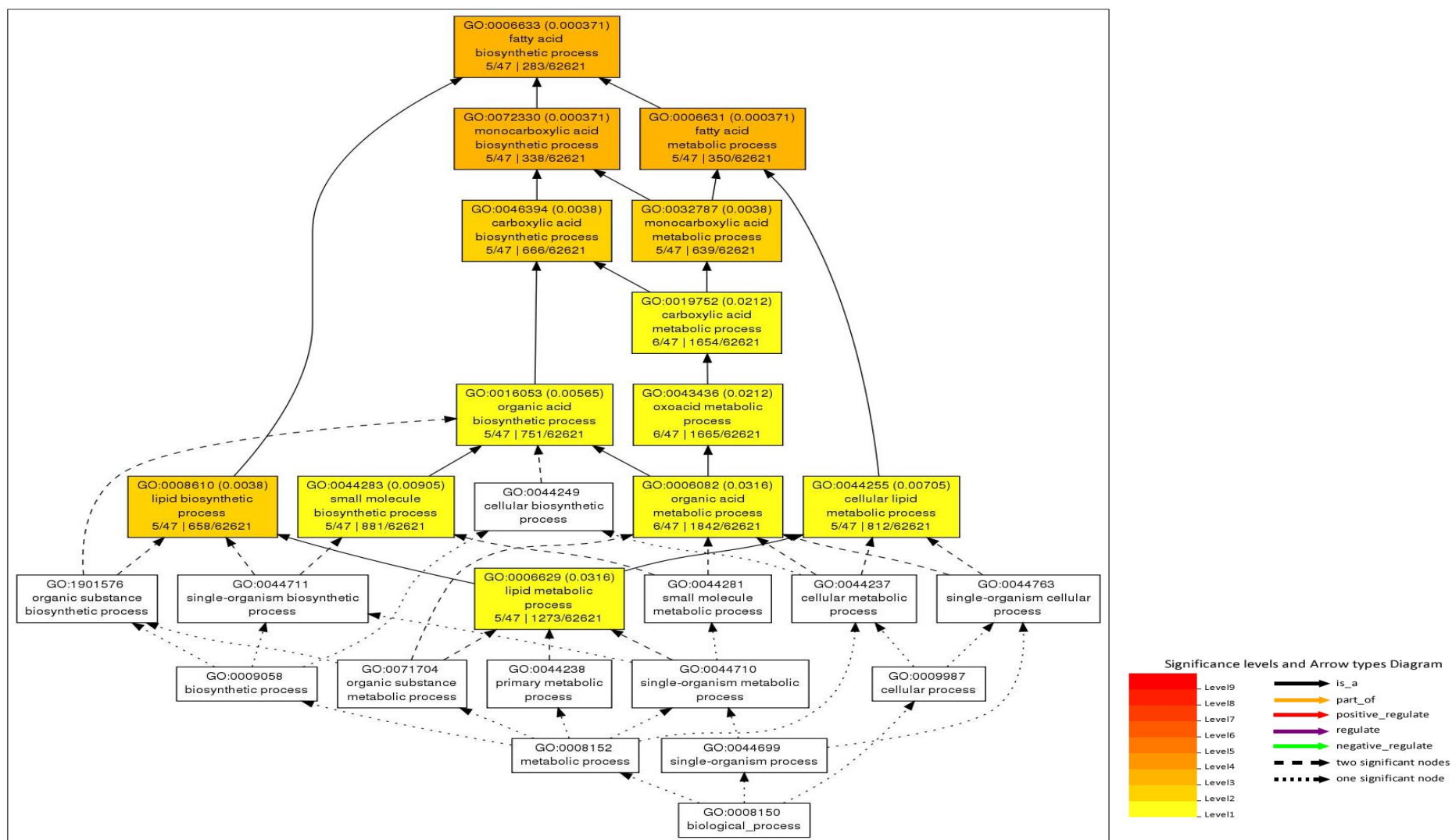


Fig. S3c. Agri GO analysis of Biological Process in group C (c): Total Fresh Weight (TFW) trait QTL (*QTfw-3A*).

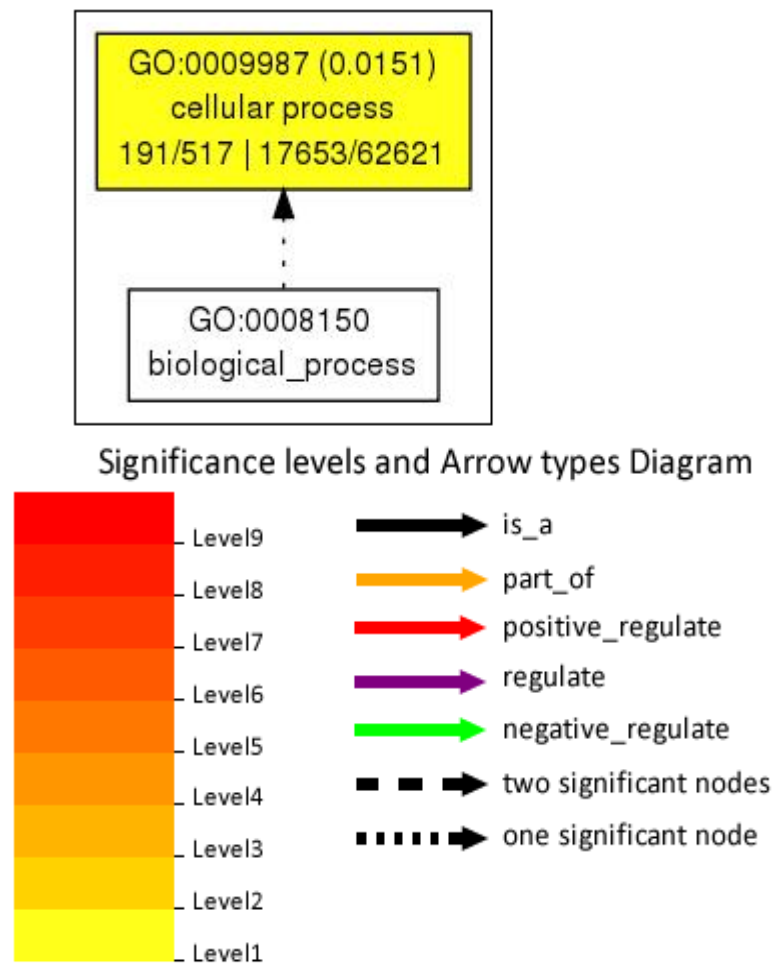


Fig. S3d. Agri GO analysis of Biological Process in group D (d): Total Dry Weight (TDW) trait QTL (QT_{dw-2D_1}).

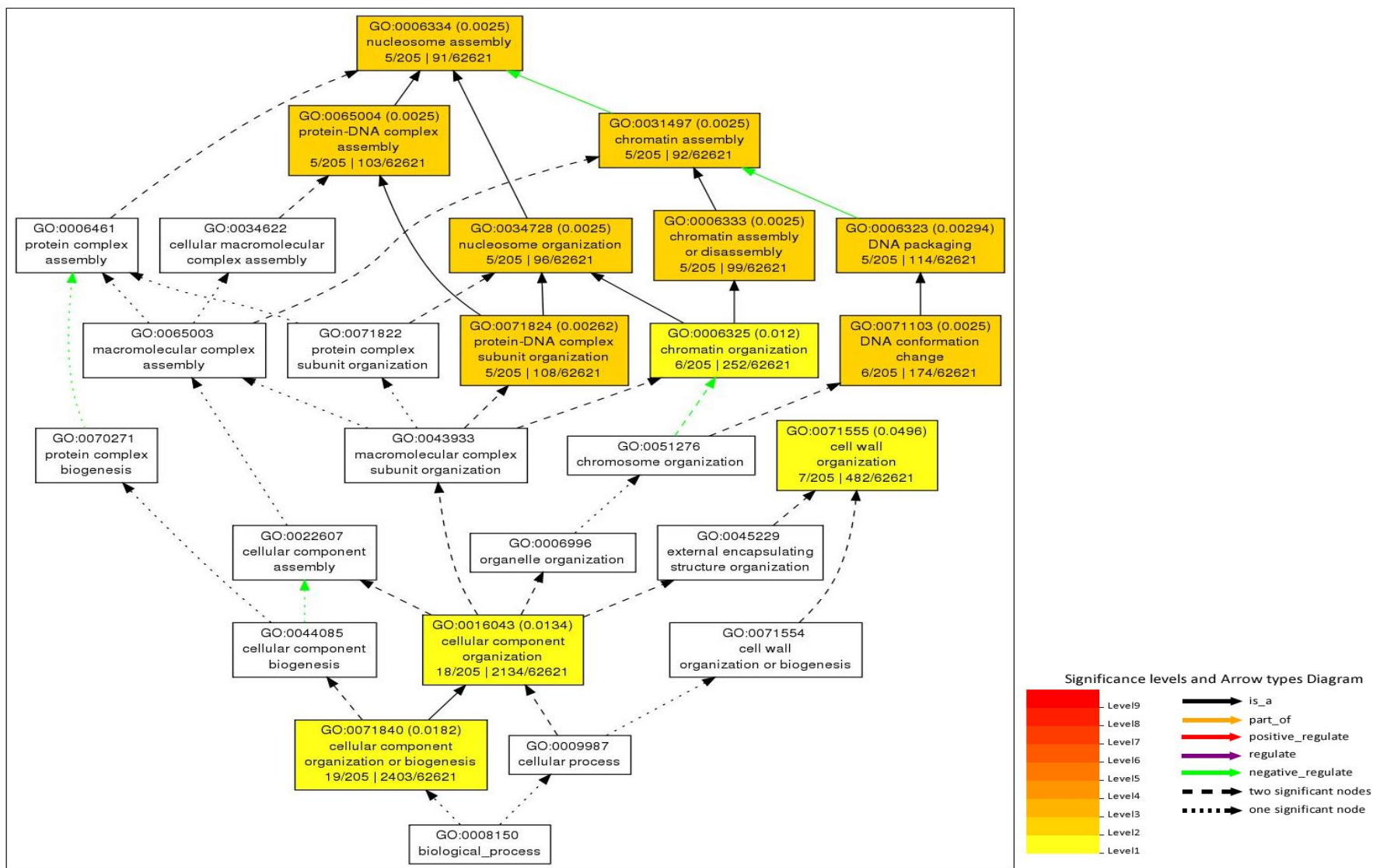


Fig. S3e. Agri GO analysis of Biological Process in group F (f): Primary leaf Dry Weight (*PDW*) trait QTL (*QPdw-5B₂*).

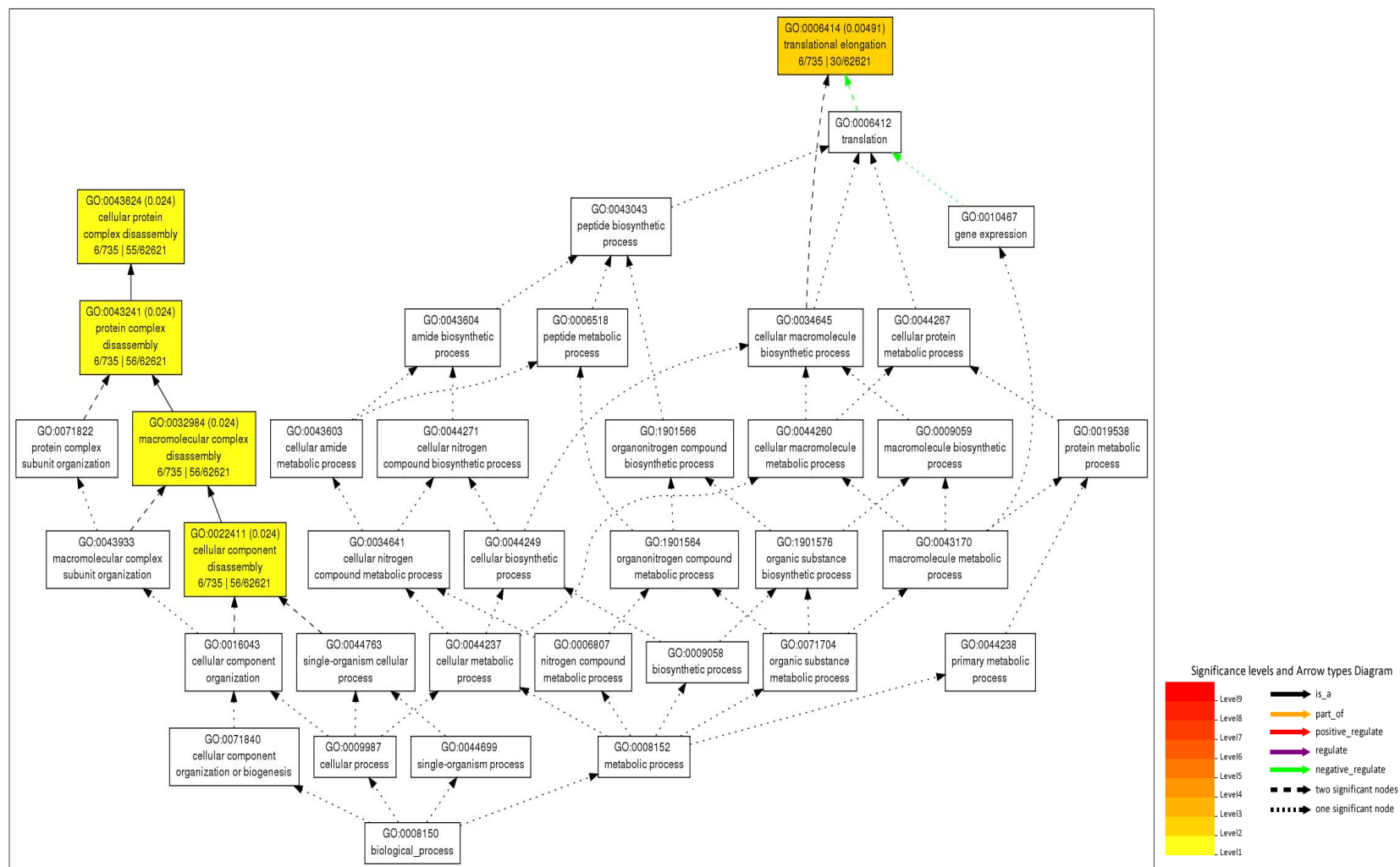


Fig. S3f. Agri GO analysis of Biological Process in group G (g): Primaryleaf Length (PL) trait QTLs (*QPL-4A* and *QPL-2B₁*).

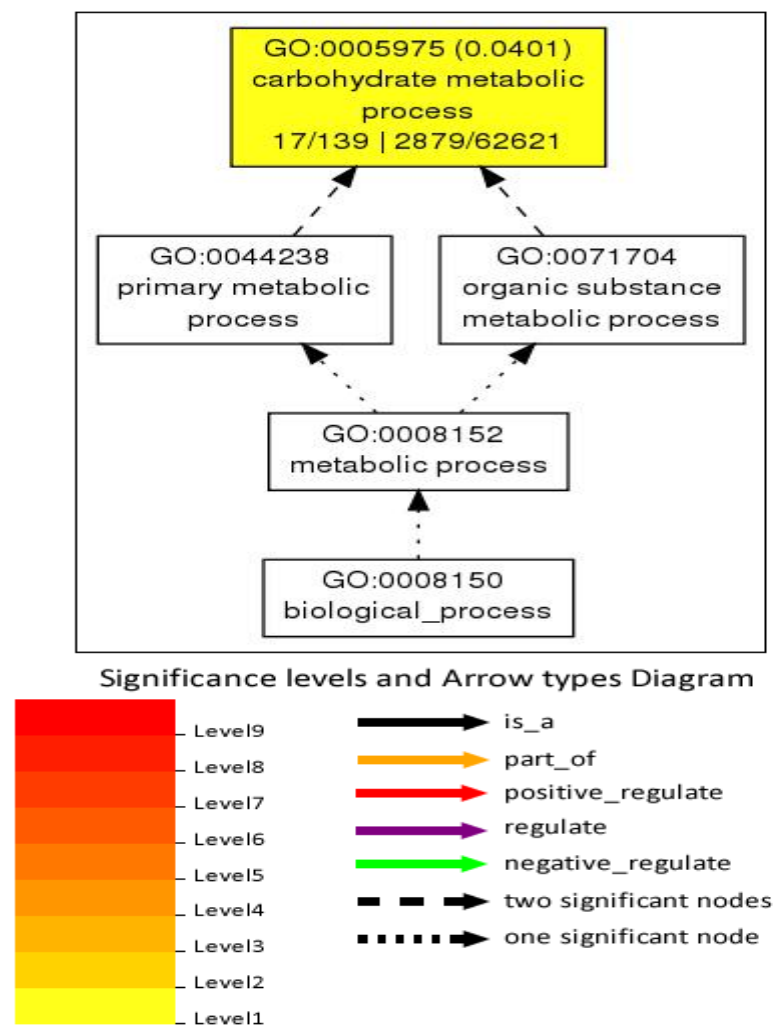


Fig. S3g. Agri GO analysis of Biological Process in group H (h): Coleoptile Fresh Weight (CFW) trait QTLs (*QCfw-2D_{1.1}* and *QCfw-3B*).

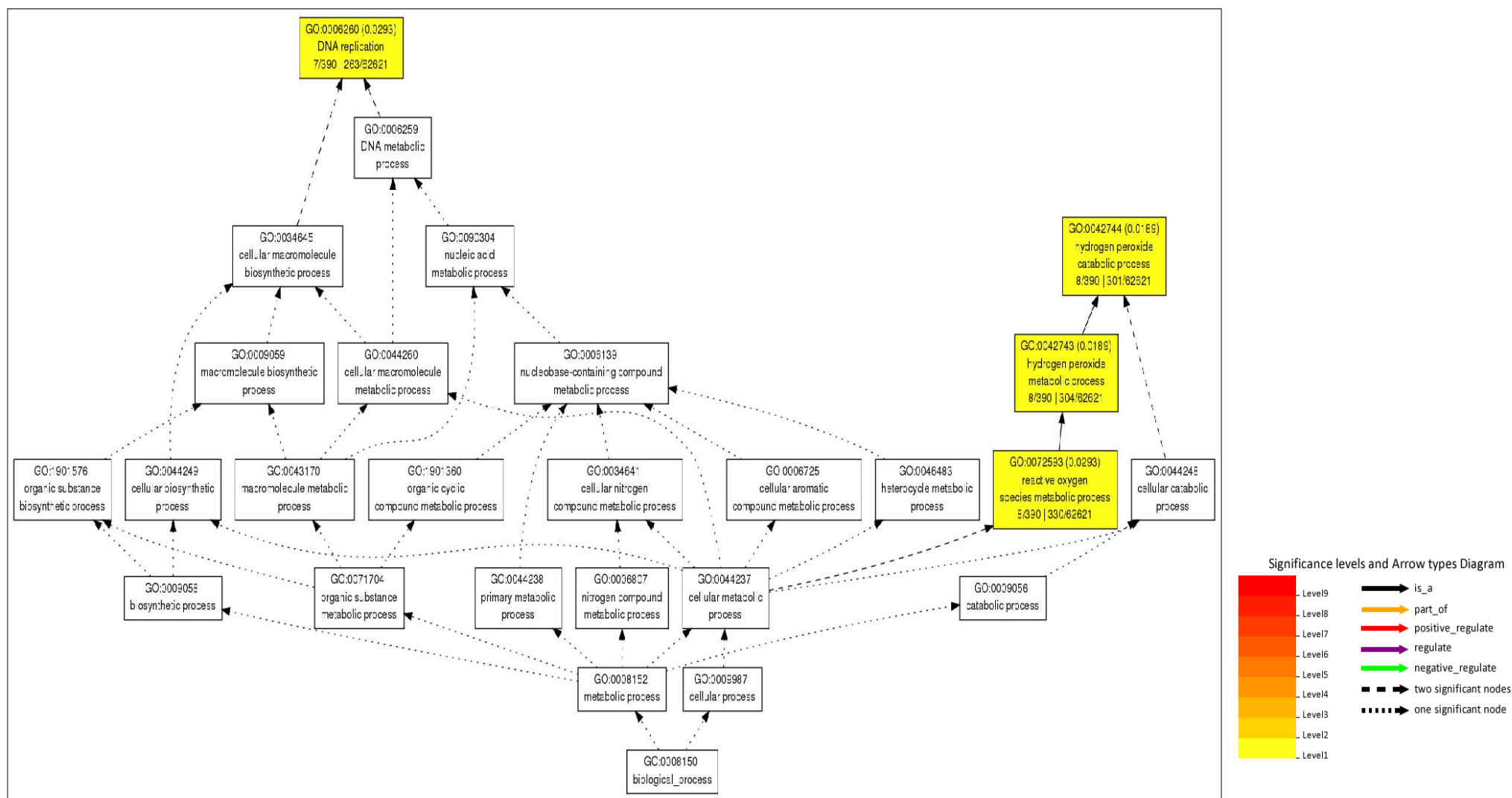


Fig. S3i. Agri GO analysis of Biological Process in group J (j): Coleoptile Length (CL) trait QTL (QCI-3B).

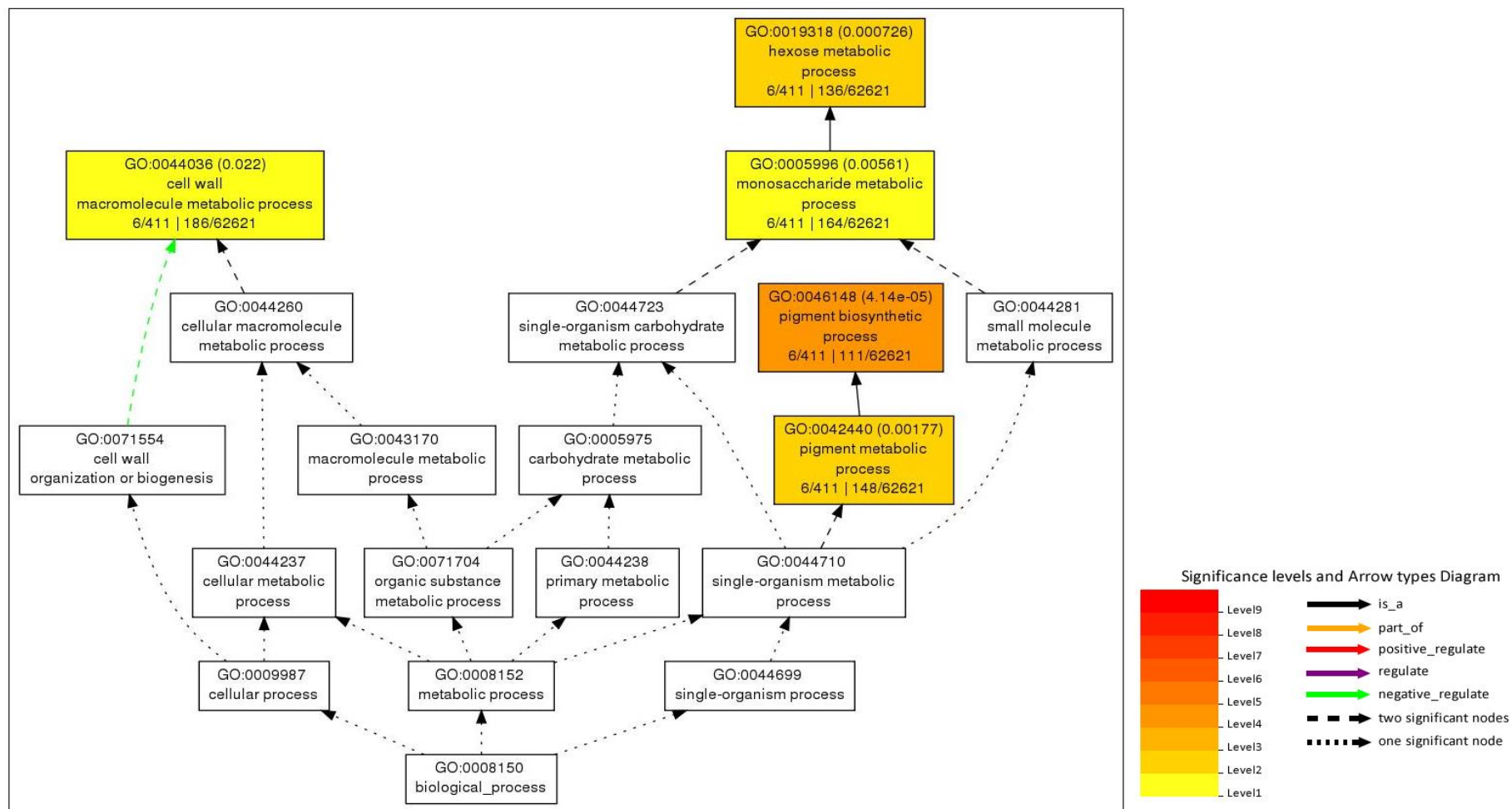


Fig. S3j. Agri GO analysis of Biological Process in group K (k): Radicle Dry Weight (RDW) trait QTLs (*QRdw-2B_{1.1}* and *QRdw-3B*).