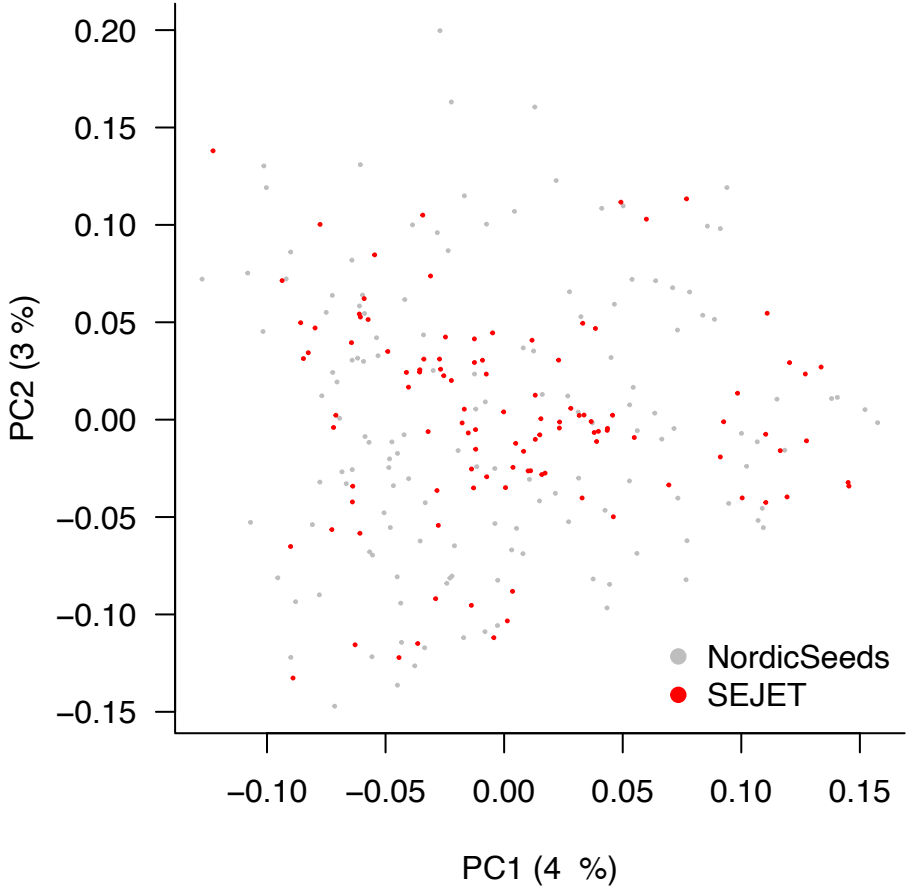


Genome-wide Association Study for Grain Protein in Wheat

Genotypic Data

Array_Name	#SNPs	#Samples	Company
7K	6731	41	Sejet
15K	13006	25	Sejet
20K	17267	23	Sejet
25K	24145	20	Sejet
25K	24145	146	NordicSeeds
Total		255	

chromum	chr	SNPs
1	chr1A	954
2	chr2A	944
3	chr3A	965
4	chr4A	638
5	chr5A	1169
6	chr6A	897
7	chr7A	1193
8	chr1B	1214
9	chr2B	1256
10	chr3B	1302
11	chr4B	612
12	chr5B	1328
13	chr6B	1027
14	chr7B	901
15	chr1D	462
16	chr2D	456
17	chr3D	266
18	chr4D	130
19	chr5D	350
20	chr6D	305
21	chr7D	315
22	chrUn	161
23	unmapped	7300
		24145

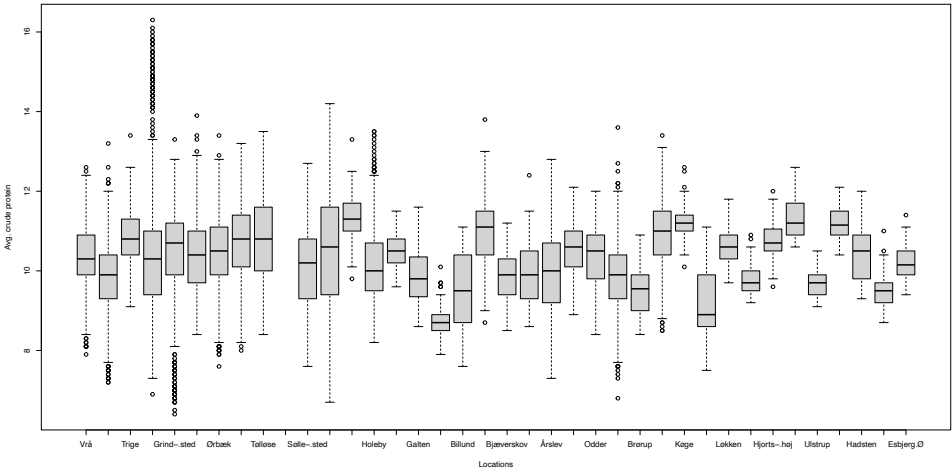
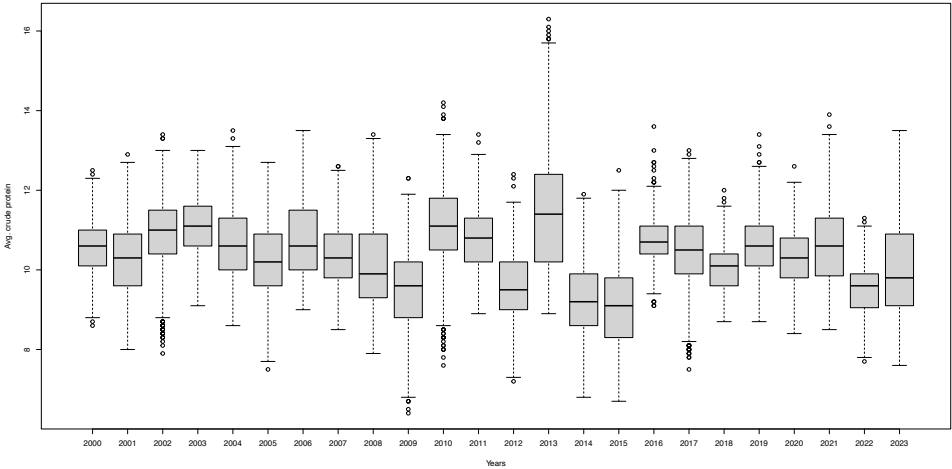


Phenotypic Data

Downloaded from SortInfo from 2000- 2023

- Crude Protien
- Grain Yiled

	Showing 74 of 74 rows	Vrå	Horsens	Trige	Holste- bro	Grind- sted	Sønder- borg	Ørbæk	Nykøbing F	Tølløse	Avg.
1	02/09	-	10.7	11.3	9.8	10.6	9.3	10.9	10	10.7	10.4
2	01/06	-	11	10.2	9.6	10.3	9.5	10.7	10.7	11	10.4
3	Asketis	10.9	-	11.1	11.4	10.8	-	11.5	11.4	12.1	11.3
4	Askro	-	10.3	10.3	10.3	9.5	9.4	10.1	10.3	11.6	10.2
5	Aspect	11.2	-	11.5	11	10.6	-	11.3	11.9	12	11.4
6	Baltimor	10.7	-	11.1	9.7	10.8	-	11.2	10.9	11.5	10.8
7	Bauxit	-	10.4	10.6	9.9	10.5	9.5	10.3	10.3	11	10.3
8	Bill	10.6	-	10.5	9.3	10.6	-	10.8	11	11	10.5
9	Biscay	10.7	-	10.4	9.9	10.4	-	11.1	10.6	11.1	10.6
10	Blanding,vi-hved	10.8	10.6	10.5	9.8	10	9.4	10.5	10.6	11.2	10.4
11	Boston	10.9	-	10.5	11.1	10.5	-	10.5	11.2	11.4	10.9
12	Brandt	11	-	11	10	10.5	-	10.8	11.6	11.7	10.9
13	Buccaneer	11	-	10.8	8.9	10.5	-	10.1	10	10.7	10.3
14	CPB-T W63	10.4	-	11	9.4	10.5	-	10.8	10.7	11.1	10.6
15	Cardos	11.1	-	11.8	11.3	11.1	-	11.3	11.1	10.9	11.2
16	Claire	10.6	-	10.5	9.1	10.5	-	10.5	11.1	10.8	10.4
17	Classic	11.6	-	11.5	9.9	10.9	-	11.6	11.6	11.8	11.3
18	Cockpit	10.4	-	10.9	9.9	10.1	-	10.8	11.3	10.7	10.6
19	Comet	-	10.8	10.1	9.1	9.9	9.1	10.4	10.2	11.4	10.1
20	Compleat	11.4	-	11.4	10.7	10.6	-	11.3	12.3	11.6	11.3
21	Cortez	10.1	-	10.1	9.1	9.9	-	10.2	10.7	11.8	10.3
22	Deben	10.9	-	10.3	9.4	10.1	-	10	10.8	11.3	10.4
23	Diabas	10.6	-	10.2	10.3	9.7	-	11.1	11.5	12.5	10.8
24	Dirigent	10.4	-	10.5	9.4	9.9	-	9.5	10	10.9	10.1
25	Efal	10.3	-	11.2	9.4	9.9	-	9.9	10.7	10.9	10.3
26	Excellenz	-	10.7	10.5	9.9	10.6	9.6	10.6	10.4	11.1	10.4
27	Flair	10.8	-	11.3	10.4	10.1	-	10.2	10.9	12.3	10.9
28	Flio	-	10.5	10.1	9.9	10.6	9.5	9.9	10.2	11.3	10.3



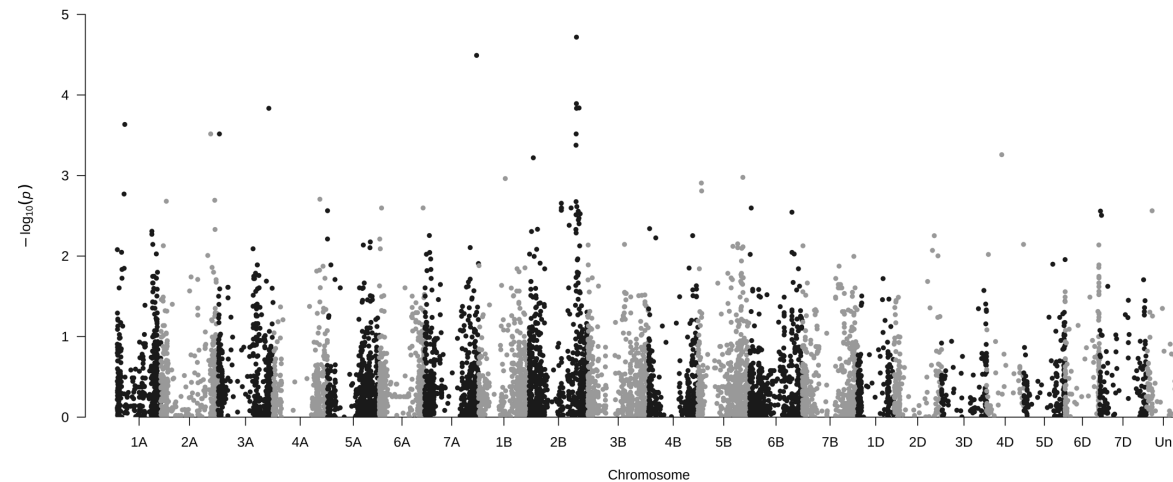
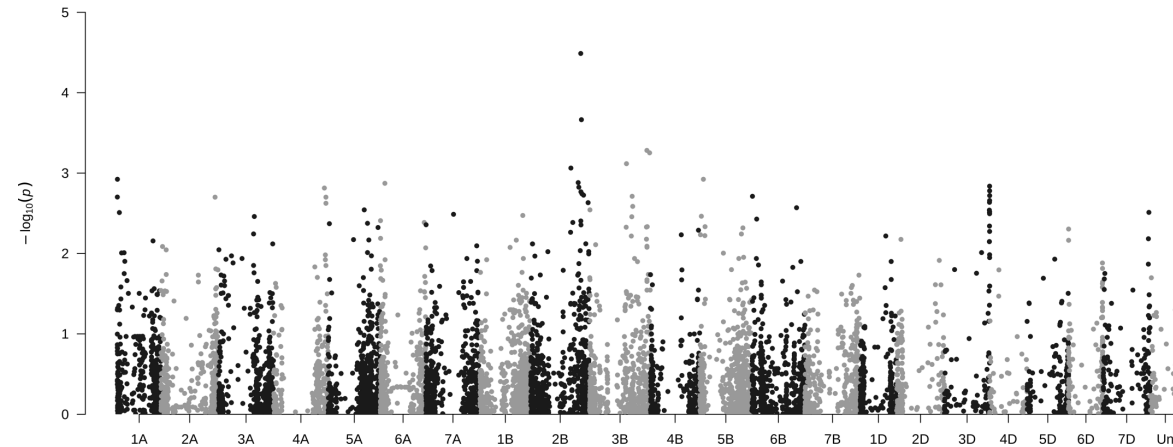
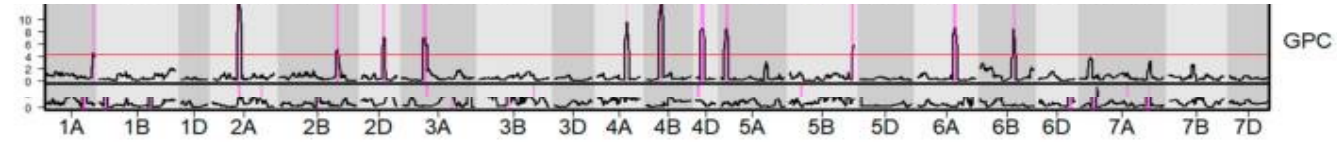
Download data for NT and OVT from 2000 to 2023

Average the data by year and location

Pheno ~ (1 | sample) + (1 | variable) + (1 | year) + (1 | sample:variable)

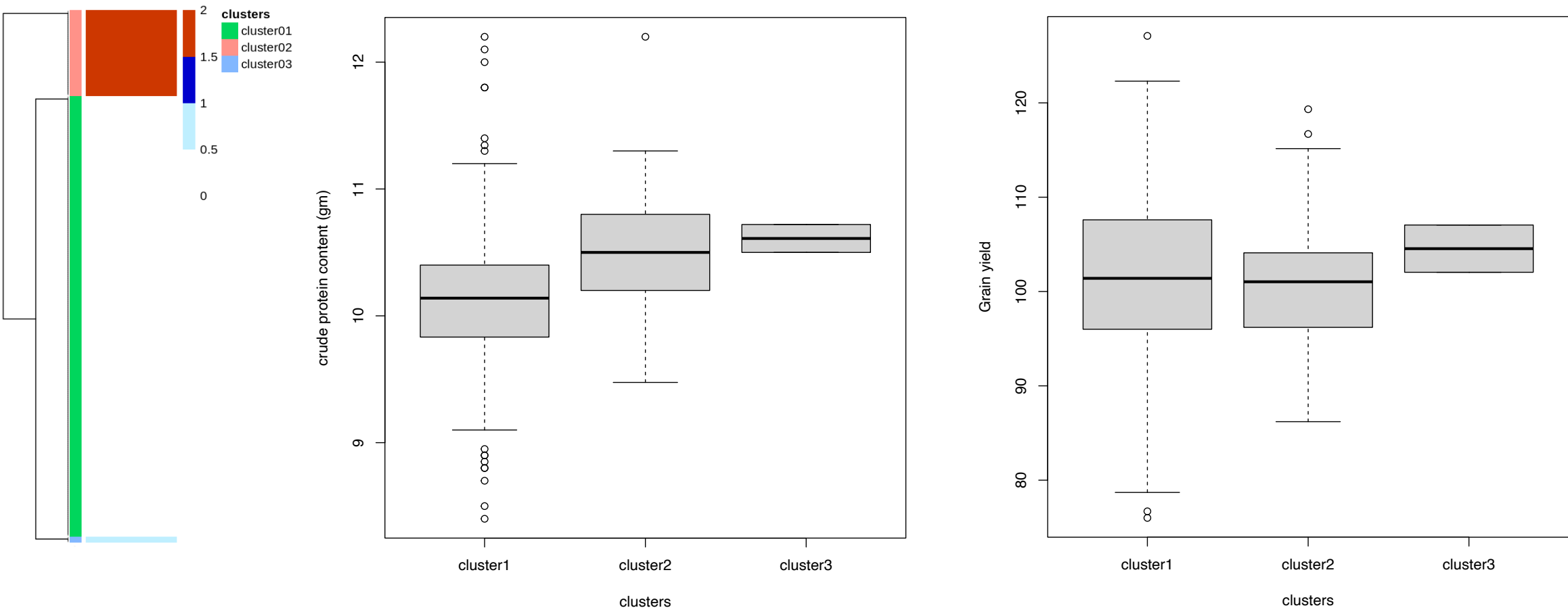
GWAS-Crude Protein

#Samples: 255
SNPs: 11,219 (<30% missing)

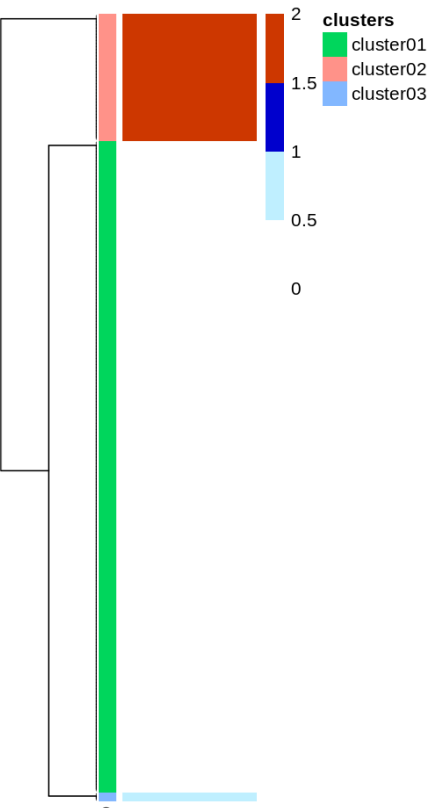


GWAS-Crude Protein

BS00022717_51 chr 2B 680573507 A/G 0.167



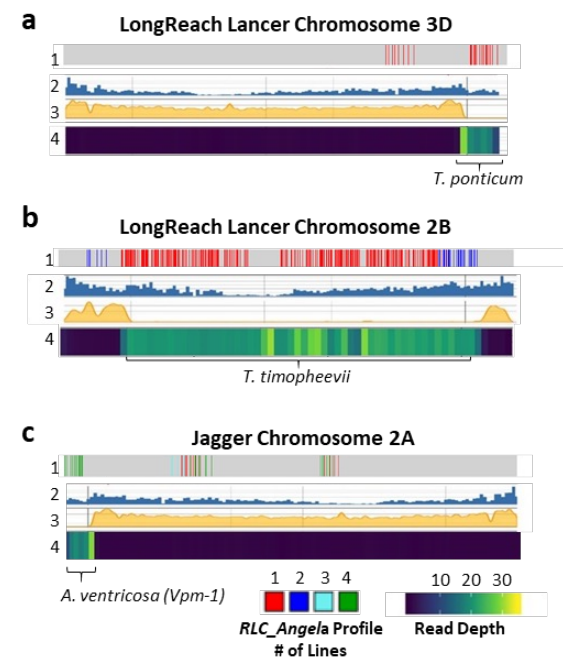
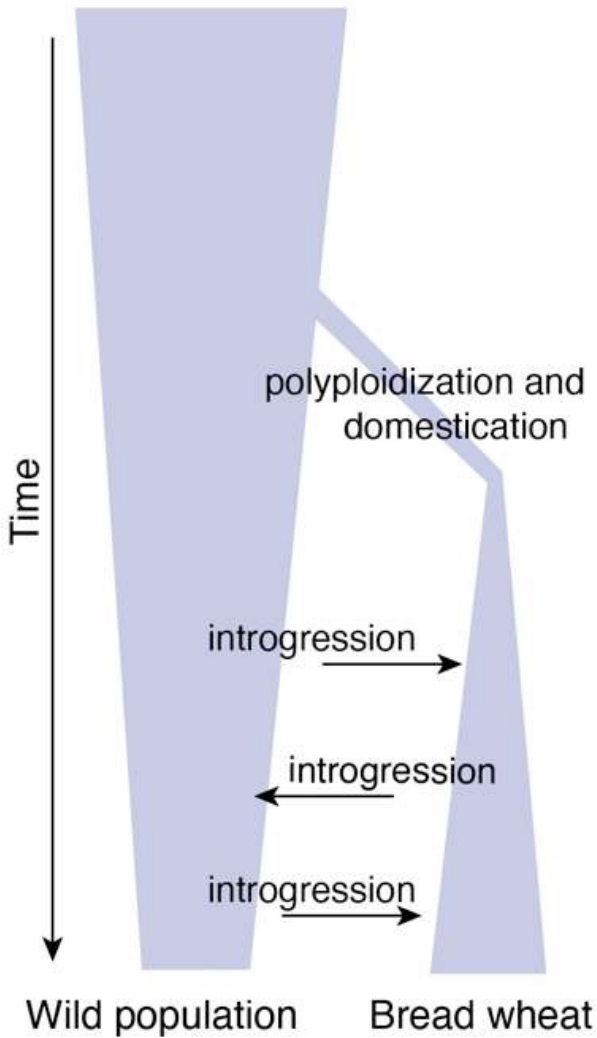
GWAS-Crude Protein



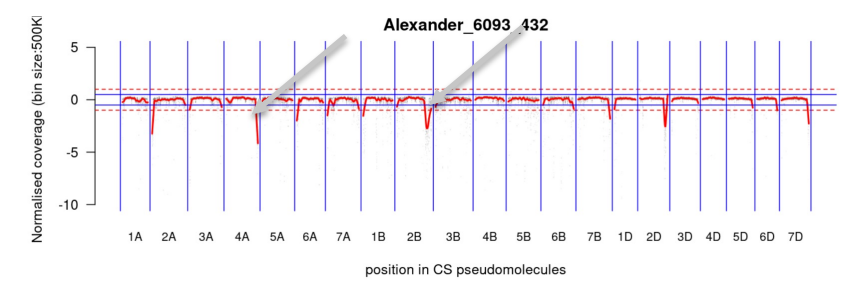
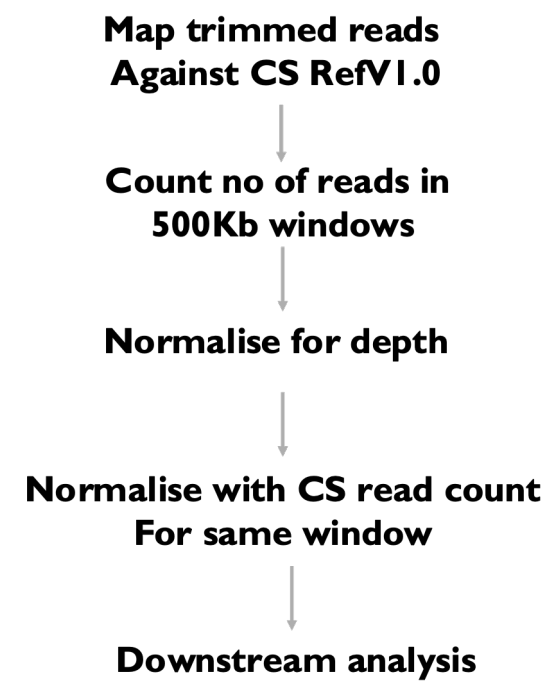
Sample	#years	First year	GPD_LS MEANS	Cluster
Torp	9	2010	-0.28	1
KWS_Lili	6	2013	-0.23	1
Sheriff	6	2013	-0.09	1
Kvarn	4	2015	-0.05	1
Pistoria	8	2011	-0.04	1
Substance	6	2012	0.00	1
Benchmark	7	2012	0.04	2
KWS_Magic	3	2011	0.42	1
KWS_Zyatt	3	2016	0.43	2
Ohio	7	2012	0.65	2

(source: Lars Erik Bonde, www.SortInfo.dk)

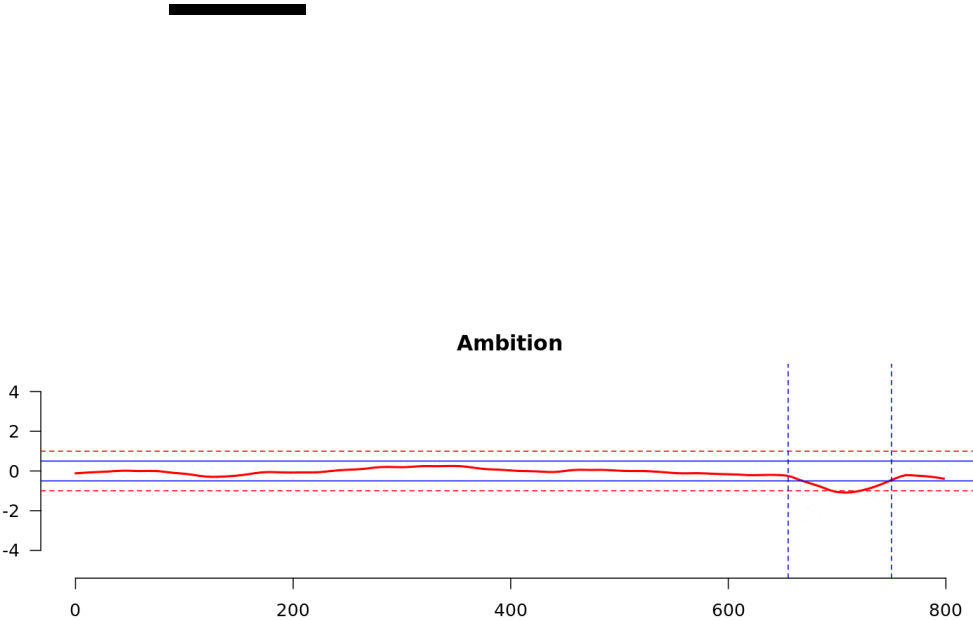
Alien Introgressions in Hexaploid Wheat



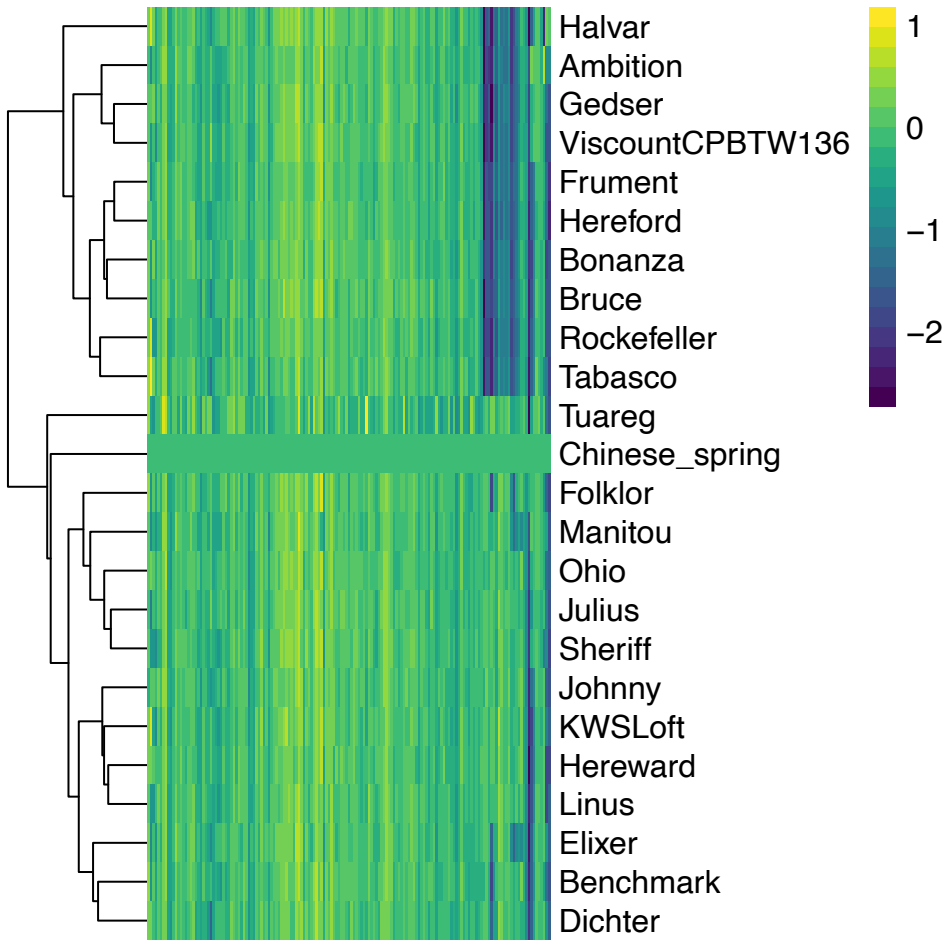
Walkowiak et al., (10+ wheat genome)
IB/IR rye introgression



Correlation of GPC with chr2B introgression?

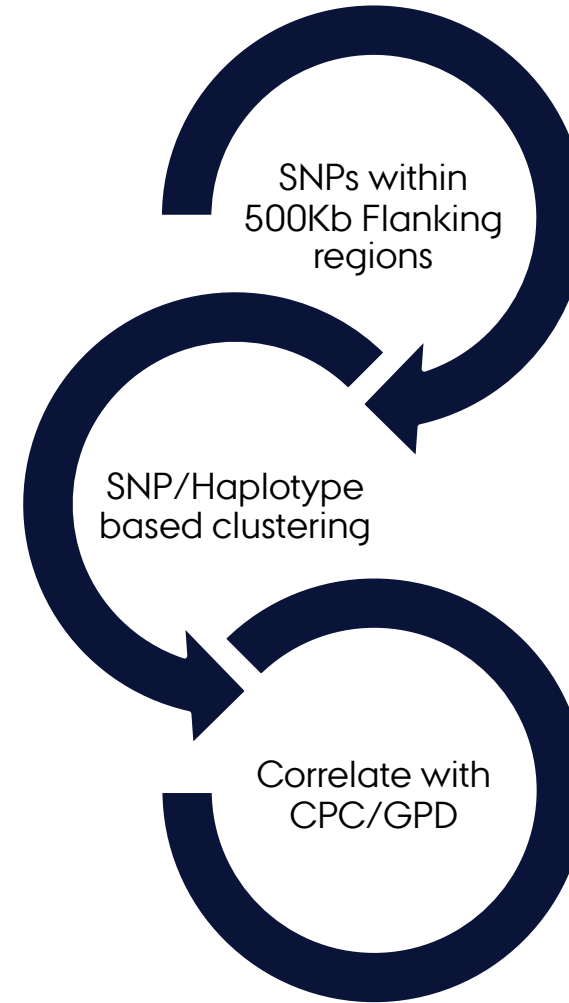


Sample	Cluster
Ambition	1
Bonanza	1
Bruce	1
Frument	1
Gedser	1
Halvar	1
Hereford	1
Hereward	1
KWSLoft	1
Linus	1
Manitou	1
Rockefeller	1
Sheriff	1
Tabasco	1
Tuareg	1
Benchmark	2
Dichter	2
Elixer	2
Folklor	2
Johnny	2
Julius	2
Ohio	2

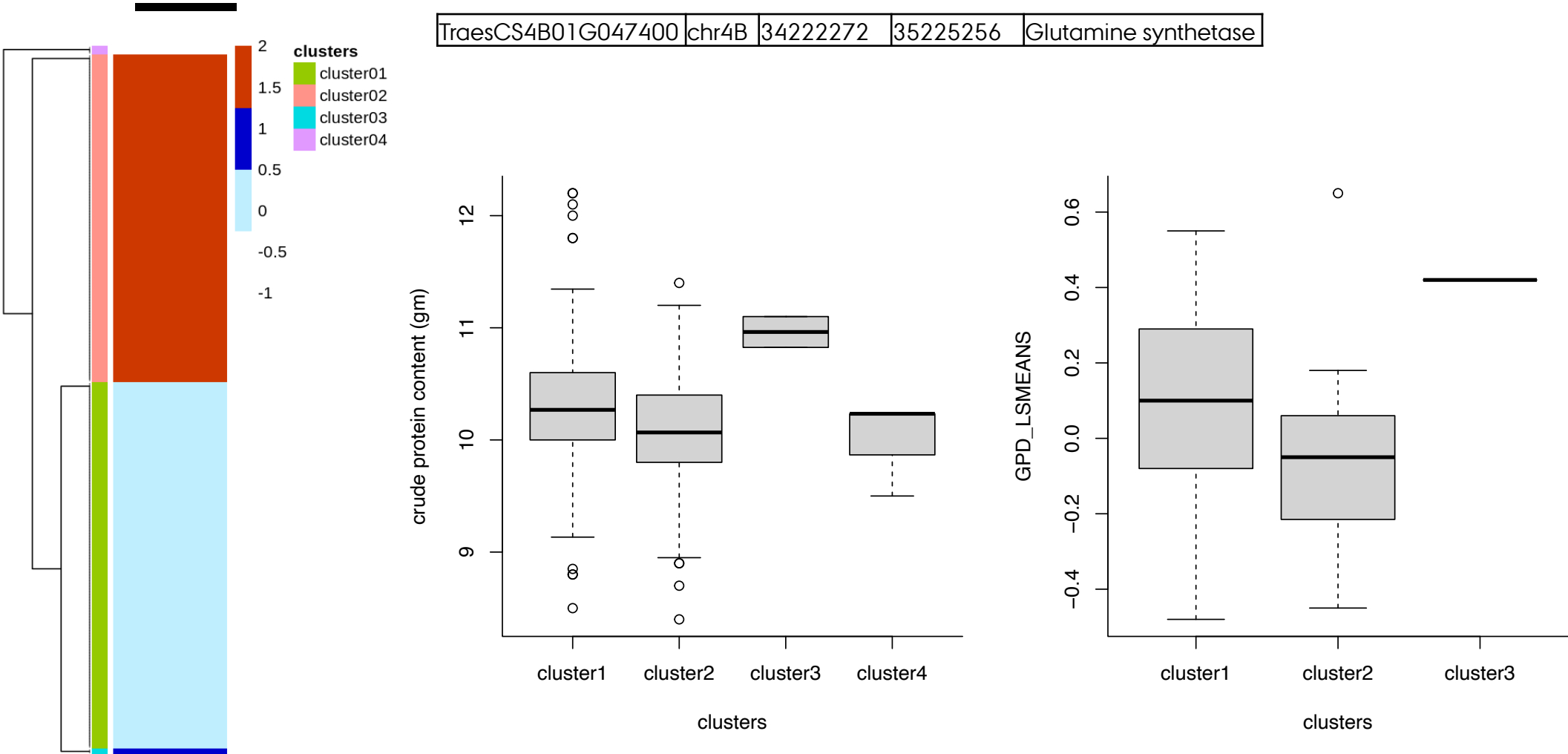


Candidate gene-based analysis

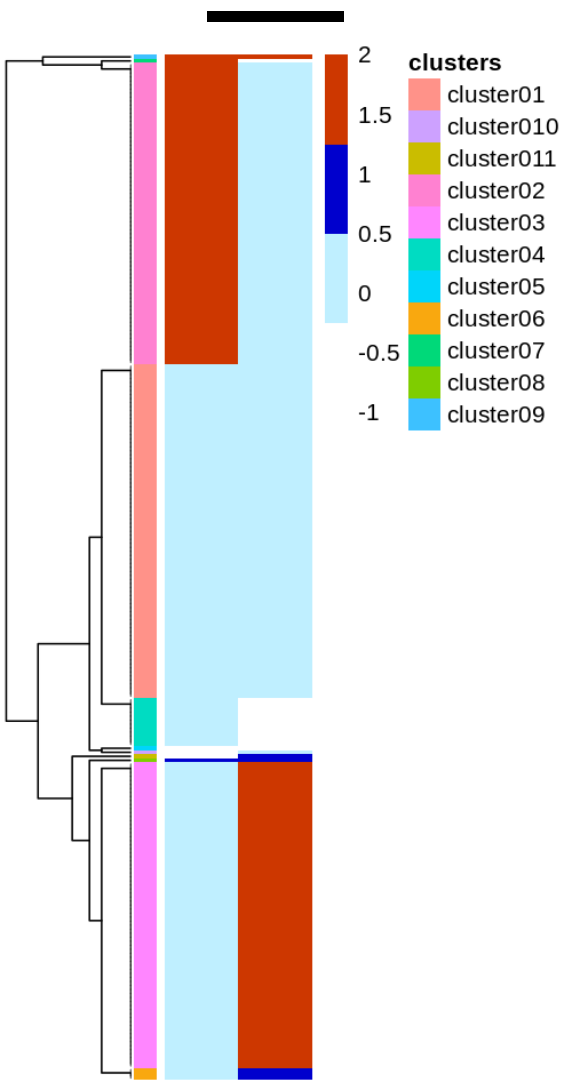
N uptake	Position on RefSeq V1.0	Gene Name
NRT2 cluster	6A:15727844-16410137	13 NRT2s
TraesCS2A02G130600	2A:78328734-78346097	FD-GOGAT-2A
TraesCS2D02G132900	2D:78375985-78392563	FD-GOGAT-2D
TraesCS6A02G298100	6A:531394366-531398363	GS1.1-6A
TraesCS4B02G04740	4B:34722272-34725256	GS1.3-4B
TraesCS4D02G047400	4D:22946578-22949866	GS1.3-4D
TraesCS2A02G500400	2A:729293649-729297303	GS2-2A
TraesCS2B02G528300	2B:722629776-722634436	GS2-2B
TraesCS3A02G266300	3A:490922100-490932750	NADH-GOGAT-3A
TraesCS6A02G333900	6A:564882616-564886300	NiR-6A
TraesCS4B02G029600	4B:21928977-21936945	NPF2.4-4B
TraesCS4D02G026800	4D:11862455-11867655	NPF2.4-4D
TraesCS3B02G095900	3B:64314648-64316600	NPF6.1-3B
TraesCS1A02G031300	1A:14519757-14525659	NPF6.2-1A
TraesCS1D02G032700	1D:13040668-13043201	NPF6.2-1D
TraesCS2D02G182900	2D:127113821-127117419	NPF7.1-2D
TraesCS6A02G017500	6A:8694483-8700180	NR1.1-6A
TraesCS6B02G024900	6B:15128191-15134280	NR1.1-6B
TraesCS6D02G020700	6D:8149929-8155961	NR1.1-6D
TraesCS4A02G376700	4A:651365942-651370213	NR1.2-4A
TraesCS7A02G078500	7A:43180494-43185382	NR1.2-7A
TraesCS7D02G073700	7D:43212472-43217253	NR1.2-7D
TraesCS7D02G297000	7D:374564870-374572229	NRT1.1A-7D
TraesCS1D02G214200	1D:299575952-299578670	NRT1.1B-1D2
TraesCS5A02G537100	5A:693632703-693642408	NRT1.1C-5A
TraesCS2A02G074800	2A:33054150-33056031	NRT2.3-2A
TraesCS2D02G073500	2D:30787486-30789242	NRT2.3-2D
TraesCS1D02G035700	1D:16504613-16506169	NRT2.4-1D
TraesCS3A02G254000	3A:475304797-475306341	NRT2.5-3A
TraesCS7A02G428500	7A:621910950-621913739	NRT2.6-7A
TraesCS7B02G328700	7B:583923053-583926829	NRT2.6-7B
TraesCS7D02G420900	7D:540617018-540627808	NRT2.6-7D



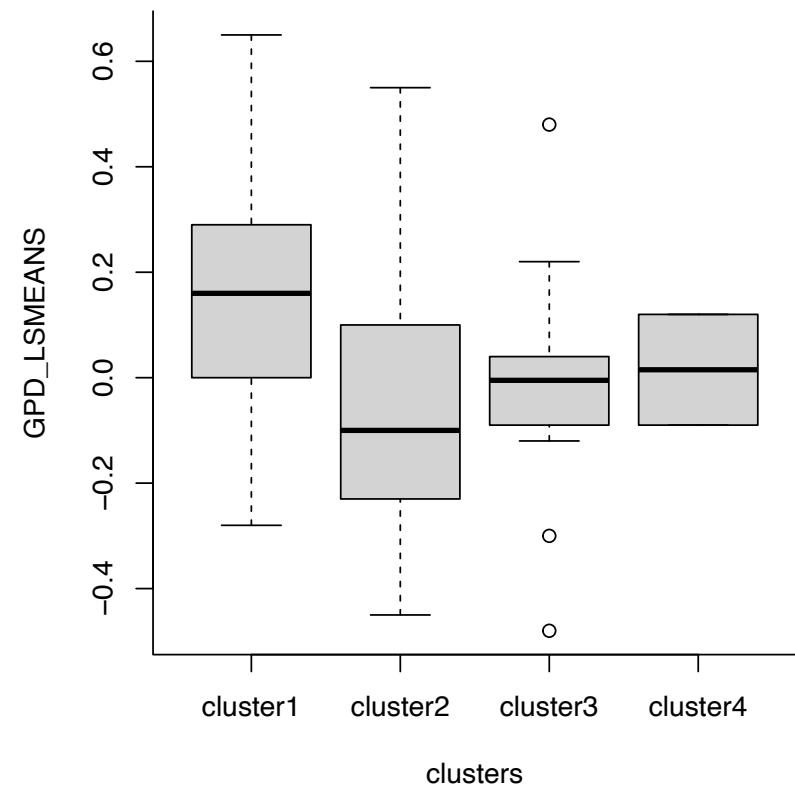
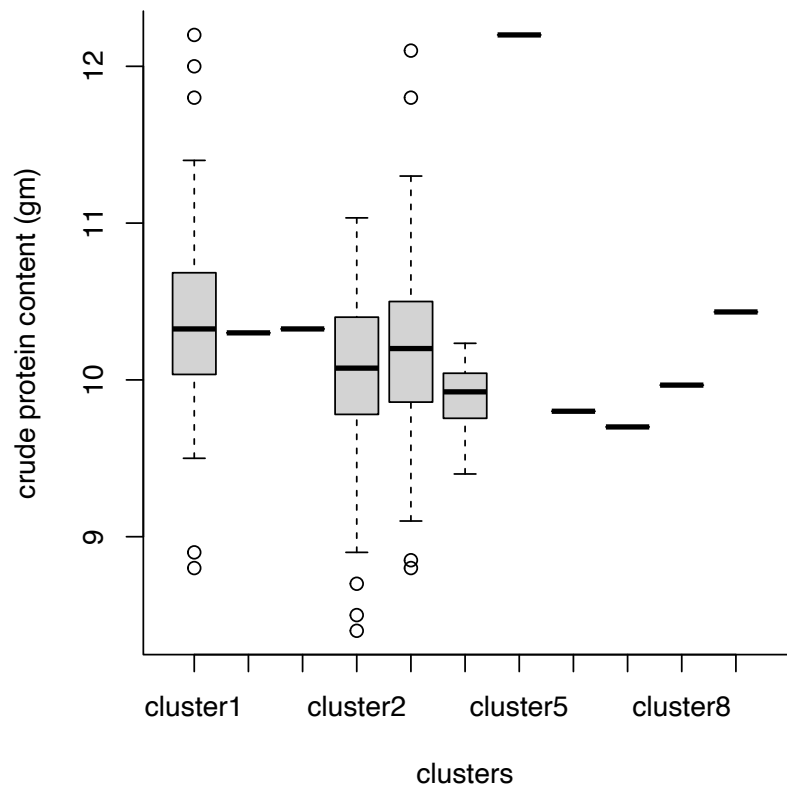
Candidate gene-based analysis



Candidate gene-based analysis



TraesCS6A02G032500	TraesCS6A01G032500	chr6A	15598637	16600163	High affinity nitrate transporter
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SNP list

Site_Name	chr_num	Physical_Position	Number_of_Taxa	Ref	Alt	Major_Allele	Major_Allele_Gametes	Major_Allele_Proportion	Major_Allele_Frequency	cp_R2	gpd_R2	favourable cluster	RefSeqV1.1_gene_id	RefSeqV1.0_gene_id	chr	start	end	Function
AX-94482613	2	729175030	255	C	T	T	349	0.68431	0.93817	1.97	4.03	cluster3	TraesCS2A02G500400	TraesCS2A01G500400	chr2A	728793649	729797303	Glutamine synthetase
BS00057059_51	2	729287912	255	G	A	A	476	0.93333	0.93333	1.97	4.03	cluster3	TraesCS2A02G500400	TraesCS2A01G500400	chr2A	728793649	729797303	Glutamine synthetase
BS00057060_51	2	729288310	255	C	T	T	476	0.93333	0.93333	1.97	4.03	cluster3	TraesCS2A02G500400	TraesCS2A01G500400	chr2A	728793649	729797303	Glutamine synthetase
AX-94504542	2	729298626	255	G	C	C	349	0.68431	0.93316	1.97	4.03	cluster3	TraesCS2A02G500400	TraesCS2A01G500400	chr2A	728793649	729797303	Glutamine synthetase
Excalibur_rep_c105463_330	6	15766571	255	G	A	A	349	0.68431	0.69246	3.03	4.14	cluster1	TraesCS6A02G030700	TraesCS6A01G030700	chr6A	15227844	16229367	High affinity nitrate transporter
Excalibur_rep_c105463_330	6	15766571	255	G	A	A	349	0.68431	0.69246	3.03	4.14	cluster1	TraesCS6A02G030800	TraesCS6A01G030800	chr6A	15234520	16236043	High affinity nitrate transporter
Excalibur_rep_c105463_330	6	15766571	255	G	A	A	349	0.68431	0.69246	3.03	4.14	cluster1	TraesCS6A02G030900	TraesCS6A01G030900	chr6A	15247526	16249383	High-affinity nitrate transporter
Excalibur_rep_c105463_330	6	15766571	255	G	A	A	349	0.68431	0.69246	3.03	4.14	cluster1	TraesCS6A02G031000	TraesCS6A01G031000	chr6A	15256560	16258437	High affinity nitrate transporter
Excalibur_rep_c105463_330	6	15766571	255	G	A	A	349	0.68431	0.69246	3.03	4.14	cluster1	TraesCS6A02G031100	TraesCS6A01G031100	chr6A	15265759	16267783	High affinity nitrate transporter
Excalibur_rep_c105463_330	6	15766571	255	G	A	A	349	0.68431	0.69246	3.03	4.14	cluster1	TraesCS6A02G031200	TraesCS6A01G031200	chr6A	15281020	16282725	High affinity nitrate transporter
Excalibur_rep_c105463_330	6	15766571	255	G	A	A	349	0.68431	0.69246	3.03	4.14	cluster1	TraesCS6A02G032400	TraesCS6A01G032400	chr6A	15451566	16453536	High affinity nitrate transporter
Excalibur_rep_c105463_330	6	15766571	255	G	A	A	349	0.68431	0.69246	10.69	8.3	cluster1	TraesCS6A02G032500	TraesCS6A01G032500	chr6A	15598637	16600163	High affinity nitrate transporter
BS00077789_51	6	16569122	255	G	T	T	323	0.63333	0.67012	10.69	8.3	cluster1	TraesCS6A02G032500	TraesCS6A01G032500	chr6A	15598637	16600163	High affinity nitrate transporter
BS00074752_51	6	531101136	255	T	G	G	406	0.79608	0.95305	1.11	5.06	cluster2	TraesCS6A02G298100	TraesCS6A01G298100	chr6A	530894366	531898363	Glutamine synthetase
BS00073872_51	6	531522344	255	C	T	T	408	0.8	0.95327	1.11	5.06	cluster2	TraesCS6A02G298100	TraesCS6A01G298100	chr6A	530894366	531898363	Glutamine synthetase
Tdurum_contig69065_319	6	564515617	255	A	G	G	421	0.82549	0.98826	1.24	4.03	cluster2	TraesCS6A02G333900	TraesCS6A01G333900	chr6A	564382616	565386300	Nitrite reductase
GENE-4204_738	6	564974986	255	T	C	C	394	0.77255	0.92056	1.24	4.03	cluster2	TraesCS6A02G333900	TraesCS6A01G333900	chr6A	564382616	565386300	Nitrite reductase
wsnp_Ra_c26491_36054023	7	621582998	255	C	T	T	486	0.95294	0.95294	0.91	-0.56		TraesCS7A02G428500	TraesCS7A01G428500	chr7A	621410950	622413739	High-affinity nitrate transporter 2
BS00022717_51	9	680573507	255	A	G	A	425	0.83333	0.83333	15.95	13.1	cluster2/3	MTA for crude protein		chr2B	675573507	680573507	
AX-94547426	9	722637559	255	C	T	T	221	0.43333	0.59091	1.37	2.4		TraesCS2B02G528300	TraesCS2B01G528300	chr2B	722129776	723134436	Glutamine synthetase
Tdurum_contig63537_2050	11	34721738	255	G	A	A	266	0.52157	0.52778	6.97	10.13	cluster1	TraesCS4B02G047400	TraesCS4B01G047400	chr4B	34222272	35225256	Glutamine synthetase
wsnp_Ex_c56091_58346859	13	26633165	255	C	T	T	353	0.69216	0.82477	2.41	0.89		TraesCS6B02G044000	TraesCS6B01G044000	chr6B	26091111	27092640	High affinity nitrate transporter
wsnp_Ex_c56091_58346859	13	26633165	255	C	T	T	353	0.69216	0.82477	2.32	6.09	cluster6	TraesCS6B02G044100	TraesCS6B01G044100	chr6B	26096252	27097775	High affinity nitrate transporter
wsnp_Ex_c56091_58346859	13	26633165	255	C	T	T	353	0.69216	0.82477	2.32	6.09	cluster6	TraesCS6B02G044200	TraesCS6B01G044200	chr6B	26116491	27118567	High affinity nitrate transporter
wsnp_Ex_c56091_58346859	13	26633165	255	C	T	T	353	0.69216	0.82477	2.32	6.09	cluster6	TraesCS6B02G044300	TraesCS6B01G044300	chr6B	26125403	27126926	High affinity nitrate transporter
wsnp_Ex_c56091_58346859	13	26633165	255	C	T	T	353	0.69216	0.82477	2.32	6.09	cluster6	TraesCS6B02G044400	TraesCS6B01G044400	chr6B	26133039	27134966	High-affinity nitrate transporter 2.2
wsnp_Ex_c56091_58346859	13	26633165	255	C	T	T	353	0.69216	0.82477	2.32	6.09	cluster6	TraesCS6B02G044500	TraesCS6B01G044500	chr6B	26144113	27145632	High-affinity nitrate transporter 2.2
wsnp_Ex_c56091_58346859	13	26633165	255	C	T	T	353	0.69216	0.82477	2.32	6.09	cluster6	TraesCS6B02G045600	TraesCS6B01G045600	chr6B	26622861	27624387	High affinity nitrate transporter
RAC875_c68849_153	13	26633918	255	T	C	C	306	0.6	0.75	2.41	0.89	cluster6	TraesCS6B02G044000	TraesCS6B01G044000	chr6B	26091111	27092640	High affinity nitrate transporter
RAC875_c68849_153	13	26633918	255	T	C	C	306	0.6	0.75	2.32	6.09	cluster6	TraesCS6B02G044100	TraesCS6B01G044100	chr6B	26096252	27097775	High affinity nitrate transporter
RAC875_c68849_153	13	26633918	255	T	C	C	306	0.6	0.75	2.32	6.09	cluster6	TraesCS6B02G044200	TraesCS6B01G044200	chr6B	26116491	27118567	High affinity nitrate transporter
RAC875_c68849_153	13	26633918	255	T	C	C	306	0.6	0.75	2.32	6.09	cluster6	TraesCS6B02G044300	TraesCS6B01G044300	chr6B	26125403	27126926	High affinity nitrate transporter
RAC875_c68849_153	13	26633918	255	T	C	C	306	0.6	0.75	2.32	6.09	cluster6	TraesCS6B02G044400	TraesCS6B01G044400	chr6B	26133039	27134966	High-affinity nitrate transporter 2.2
RAC875_c68849_153	13	26633918	255	T	C	C	306	0.6	0.75	2.32	6.09	cluster6	TraesCS6B02G044500	TraesCS6B01G044500	chr6B	26144113	27145632	High-affinity nitrate transporter 2.2
RAC875_c68849_153	13	26633918	255	T	C	C	306	0.6	0.75	2.32	6.09	cluster6	TraesCS6B02G045600	TraesCS6B01G045600	chr6B	26622861	27624387	High affinity nitrate transporter
D_F5X2DLF02G9H4M_286	21	43037081	255	G	A	A	299	0.58627	0.70188	3.84	2	cluster1	TraesCS7D02G073700	TraesCS7D01G073700	chr7D	42712472	43717253	Nitrate reductase
BS00064892_51	21	43366397	255	G	A	A	292	0.57255	0.68868	3.84	2	cluster1	TraesCS7D02G073700	TraesCS7D01G073700	chr7D	42712472	43717253	Nitrate reductase





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Activities in 2024

Activities in 2024:

- Literature review with a view to updating the catalogue (delivery in 2023) with the latest marker candidates.
- Analysis of genomic profiles of Danish winter wheat varieties in relation to variation in genomic regions, involved in protein content in the nucleus and N-mobilization. Particular attention will be paid to regions which, according to previous studies, do not have a negative impact on yield.
- Participation in national or international conference where results from AP2 are presented.

Deliverables in 2024:

- Note with an updated catalogue of markers and candidate genes that have a function in relation to protein content in the nucleus, Grain Protein Deviation (GPD) (the deviation of the negative regression between protein content and core yield) and N metabolism relative to N remobilization. The memo is delivered to breeders and published on the project site.

Activities in 2024-25:

In 2024-25, validation will be carried out in breeding material from the wheat breeders, which consists of crossing populations based on the varieties characterised in 2023. The question will be whether the good protein properties can be found in offspring populations together with the markers that will be selected in 2023. For the winter wheat varieties characterized in AP1 in terms of mobilization of N from straw to core, the correlation to the selected markers will also be investigated. During 2023, it will be determined which crossing populations are relevant to investigate in 2024-25. If there is a promising variation close to a specific candidate gene, it will also be relevant to uncover this variation in relation to the gene itself and not just in a coupled marker. This may involve DNA sequencing of specific fragments of the genome for promising varieties.