

SUPPLEMENTARY MATERIAL

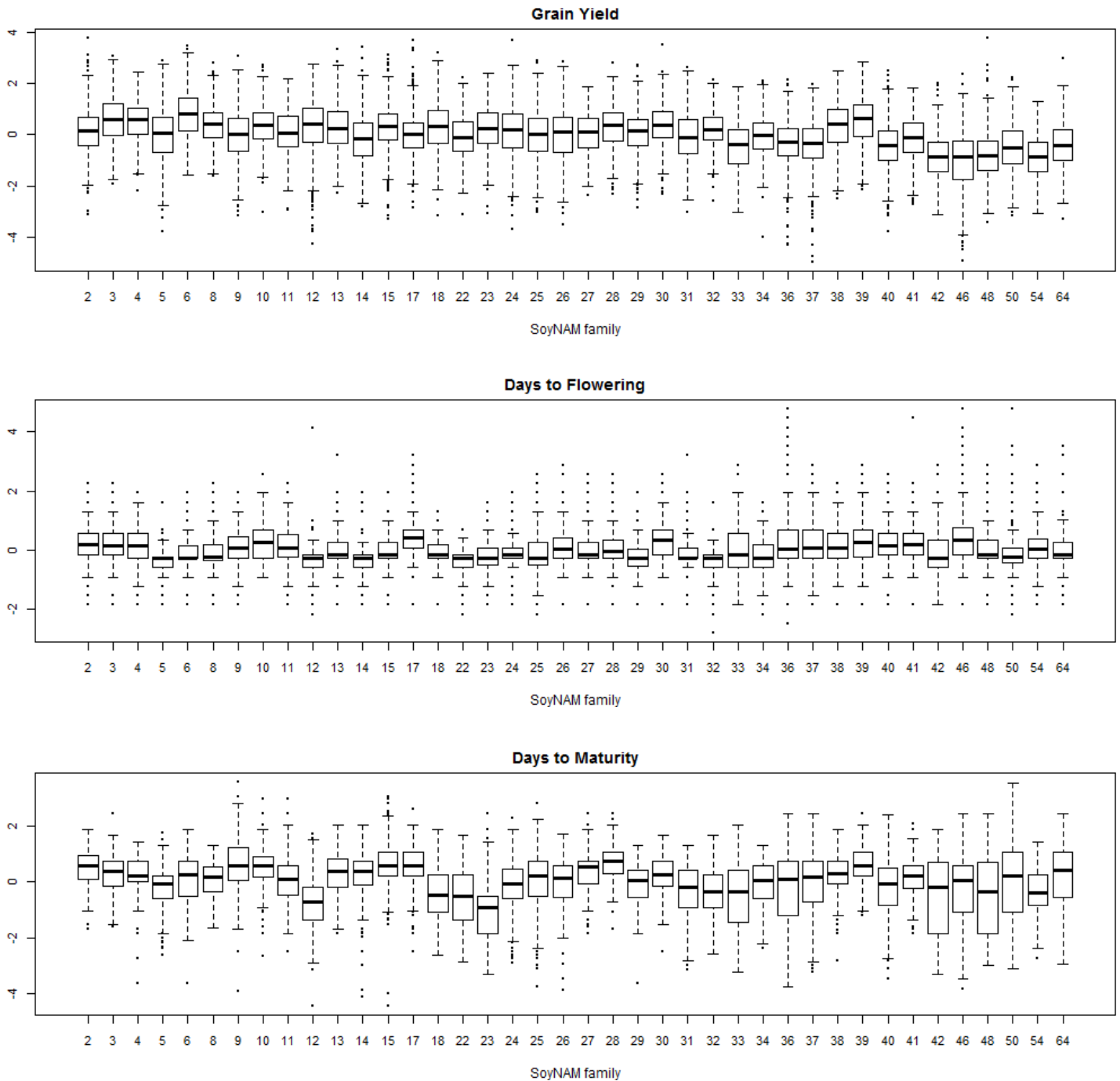
File S1: Descriptive Population Parameters Estimated by Family

1. Table of genomic narrow-sense heritability of soybean quantitative traits collected from 40 biparental families that compose the SoyNAM population in Indiana from 2012 to 2015. Data was normalized by year. Estimates were computed using Gibbs sampling implemented in the R package NAM.

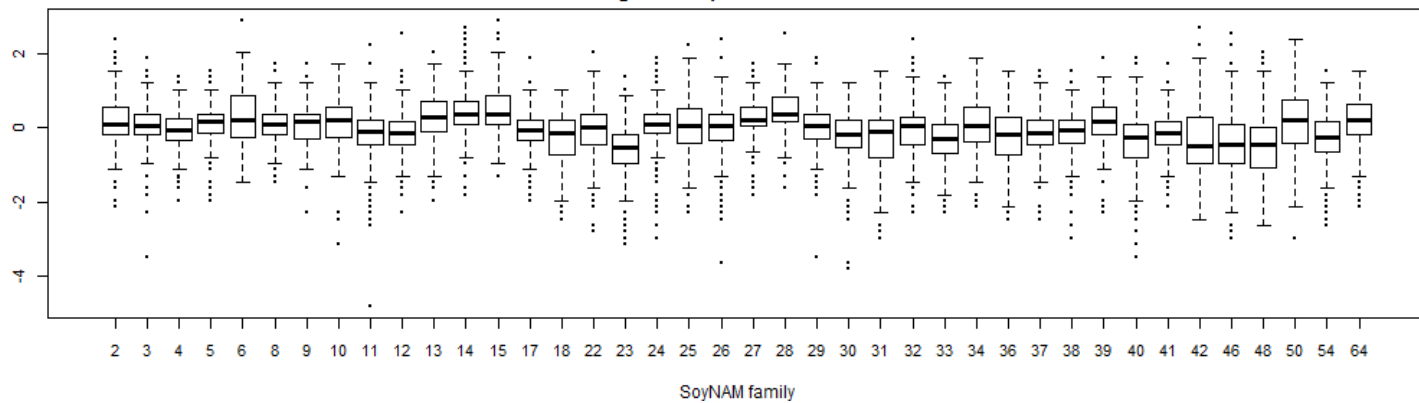
Family	Yld [†]	Flo	Mat	Rep	Hgt	Ldg	Acc	Rcc	LSh	Nde	Pod	PN	SW	Int
2	0.497	0.684	0.530	0.454	0.809	0.365	0.395	0.461	0.519	0.598	0.571	0.521	0.530	0.565
3	0.579	0.399	0.545	0.517	0.792	0.455	0.587	0.538	0.541	0.502	0.379	0.358	0.746	0.750
4	0.434	0.560	0.354	0.417	0.697	0.384	0.409	0.464	0.515	0.438	0.411	0.555	0.606	0.631
5	0.428	0.381	0.749	0.494	0.664	0.444	0.413	0.487	0.417	0.472	0.552	0.551	0.834	0.817
6	0.382	0.391	0.403	0.320	0.518	0.335	0.363	0.462	0.390	0.343	0.288	0.329	0.666	0.639
8	0.366	0.418	0.388	0.366	0.549	0.465	0.590	0.346	0.482	0.446	0.536	0.426	0.513	0.556
9	0.452	0.454	0.709	0.530	0.722	0.739	0.420	0.409	0.415	0.665	0.618	0.566	0.683	0.676
10	0.500	0.491	0.617	0.405	0.597	0.528	0.519	0.293	0.348	0.467	0.533	0.434	0.668	0.686
11	0.617	0.792	0.409	0.430	0.665	0.549	0.348	0.359	0.521	0.348	0.402	0.418	0.365	0.365
12	0.519	0.373	0.446	0.374	0.752	0.587	0.363	0.447	0.270	0.449	0.512	0.477	0.403	0.397
13	0.502	0.576	0.519	0.526	0.857	0.542	0.562	0.341	0.316	0.348	0.380	0.403	0.555	0.640
14	0.490	0.539	0.405	0.460	0.697	0.510	0.494	0.582	0.484	0.440	0.547	0.532	0.663	0.651
15	0.445	0.514	0.684	0.472	0.819	0.687	0.520	0.485	0.399	0.672	0.573	0.451	0.619	0.598
17	0.513	0.442	0.412	0.412	0.603	0.399	0.529	0.500	0.533	0.468	0.378	0.465	0.529	0.442
18	0.446	0.296	0.317	0.362	0.286	0.353	0.315	0.271	0.379	0.322	0.282	0.270	0.285	0.279
22	0.433	0.464	0.482	0.380	0.601	0.611	0.378	0.398	0.540	0.607	0.566	0.537	0.473	0.439
23	0.431	0.490	0.375	0.429	0.503	0.419	0.580	0.383	0.363	0.526	0.475	0.458	0.404	0.398
24	0.681	0.407	0.636	0.506	0.675	0.545	0.655	0.507	0.440	0.759	0.676	0.418	0.284	0.279
25	0.499	0.553	0.686	0.380	0.822	0.529	0.640	0.537	0.372	0.518	0.579	0.580	0.438	0.431
26	0.451	0.402	0.628	0.370	0.664	0.418	0.478	0.501	0.506	0.401	0.564	0.563	0.403	0.344
27	0.447	0.595	0.570	0.531	0.709	0.435	0.427	0.545	0.522	0.352	0.480	0.402	0.296	0.312
28	0.413	0.455	0.682	0.583	0.713	0.575	0.496	0.622	0.359	0.445	0.381	0.338	0.408	0.427
29	0.378	0.348	0.360	0.323	0.623	0.351	0.462	0.512	0.302	0.310	0.362	0.363	0.305	0.347
30	0.438	0.543	0.618	0.534	0.795	0.582	0.492	0.392	0.310	0.606	0.457	0.423	0.630	0.594
31	0.391	0.449	0.367	0.396	0.488	0.357	0.411	0.451	0.383	0.362	0.405	0.524	0.344	0.334
32	0.349	0.341	0.330	0.354	0.609	0.357	0.326	0.350	0.378	0.324	0.370	0.403	0.343	0.358
33	0.428	0.554	0.443	0.337	0.361	0.595	0.363	0.324	0.384	0.354	0.390	0.371	0.411	0.476
34	0.509	0.382	0.413	0.329	0.433	0.396	0.310	0.407	0.340	0.491	0.373	0.363	0.371	0.344
36	0.425	0.507	0.490	0.382	0.506	0.433	0.418	0.374	0.408	0.378	0.307	0.363	0.323	0.293
37	0.399	0.306	0.434	0.356	0.493	0.286	0.352	0.380	0.341	0.352	0.347	0.338	0.365	0.351
38	0.439	0.658	0.426	0.353	0.839	0.659	0.643	0.425	0.441	0.570	0.603	0.451	0.272	0.346
39	0.440	0.561	0.716	0.440	0.707	0.591	0.419	0.572	0.362	0.509	0.416	0.375	0.343	0.281
40	0.298	0.366	0.467	0.403	0.454	0.341	0.466	0.359	0.317	0.403	0.447	0.452	0.292	0.303
41	0.554	0.647	0.438	0.445	0.672	0.632	0.438	0.481	0.415	0.447	0.435	0.440	0.283	0.304
42	0.370	0.473	0.629	0.499	0.470	0.355	0.351	0.381	0.298	0.455	0.548	0.449	0.350	0.287
46	0.283	0.484	0.547	0.402	0.576	0.401	0.350	0.327	0.356	0.371	0.436	0.410	0.386	0.435
48	0.468	0.271	0.355	0.390	0.390	0.354	0.458	0.401	0.335	0.339	0.350	0.346	0.314	0.291
50	0.368	0.452	0.579	0.406	0.453	0.533	0.306	0.295	0.384	0.329	0.351	0.360	0.330	0.309
54	0.293	0.336	0.265	0.310	0.413	0.358	0.417	0.335	0.350	0.491	0.336	0.277	0.312	0.320
64	0.345	0.315	0.371	0.347	0.351	0.354	0.379	0.352	0.320	0.299	0.342	0.365	0.301	0.294

[†] Yld, grain yield; Flo, flowering; Mat, maturity; Rep, length of reproductive period; Hgt, plant height; Ldg, lodging score; Acc, average canopy coverage; Rcc, rate of canopy closure; LSh, leaflet shape; Node, number of reproductive nodes; Pod, pods in the main stem; P/N, pods per node; SW, 100-seed weight; Int, internode length.

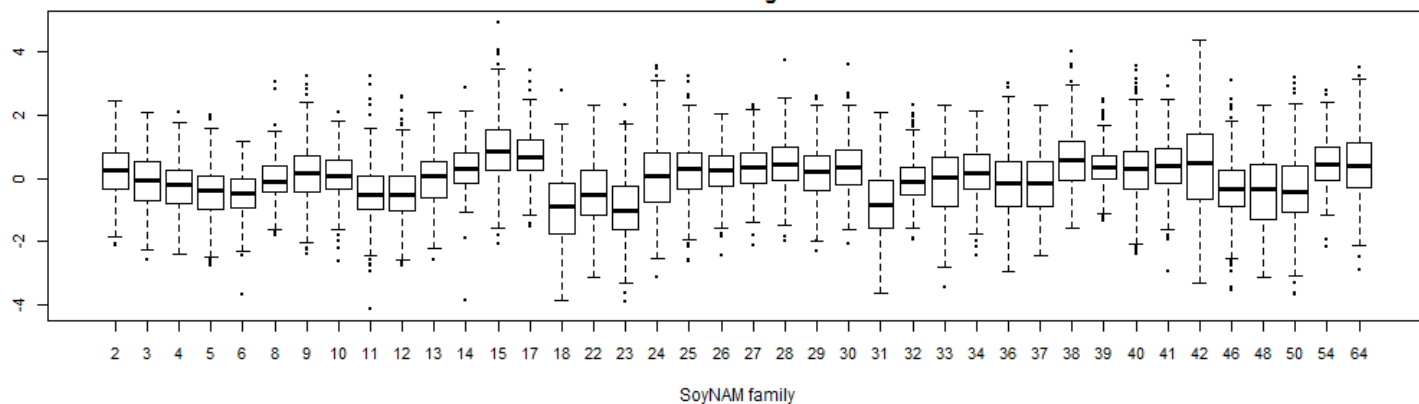
2. Box-and-whiskers plot of soybean quantitative traits collected from 40 biparental families that compose the SoyNAM population in Indiana from 2012 to 2015. Data was normalized by year. The box represents the three quartiles (25%, median, 75%), whiskers represent the range, and dots are the outliers.



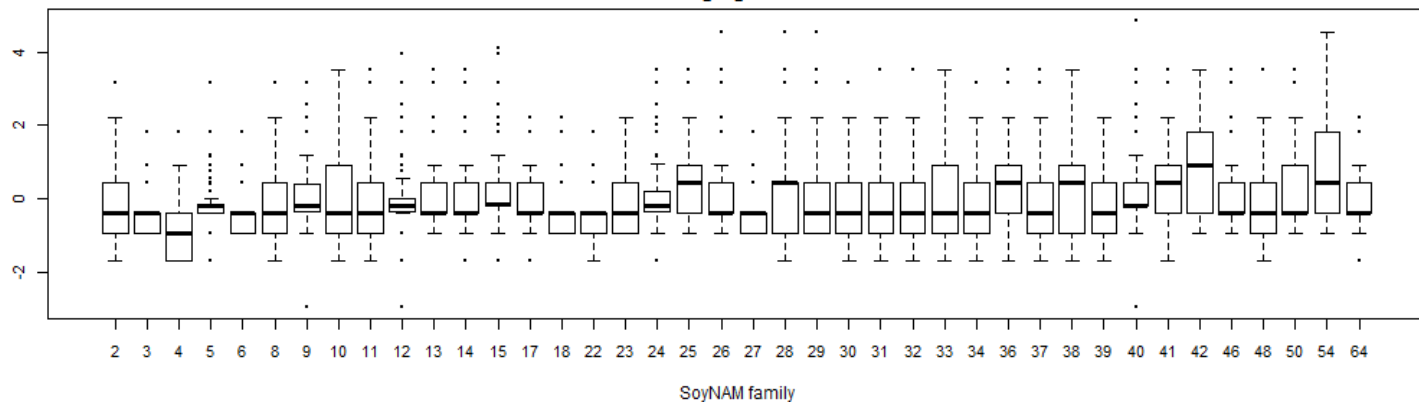
Length of Reproductive Period



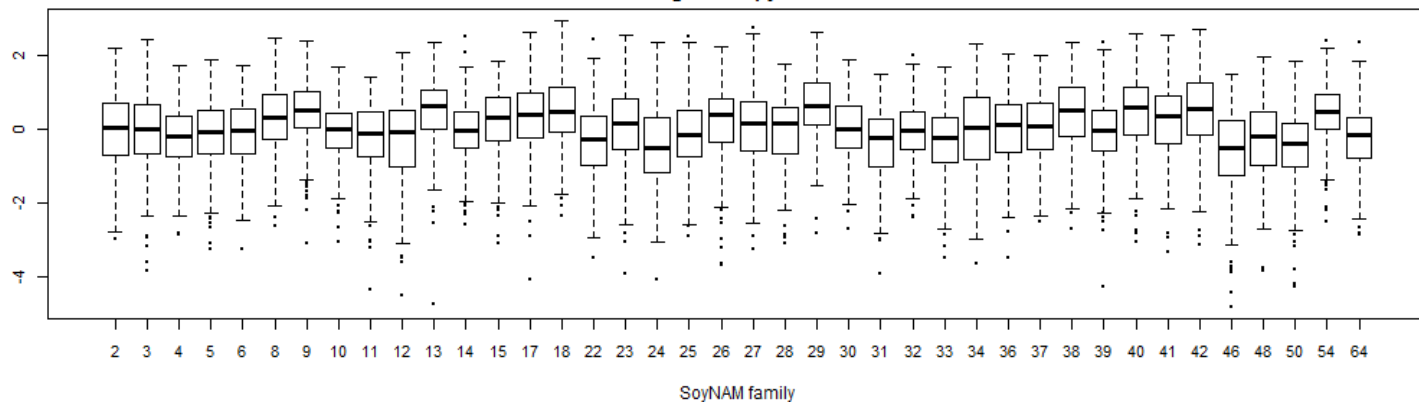
Plant Height



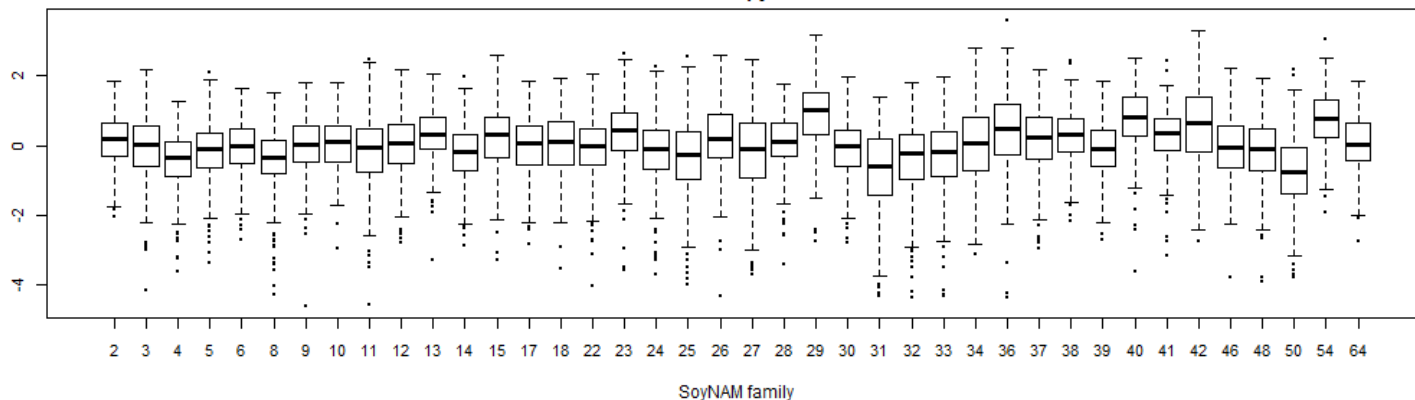
Lodging Score



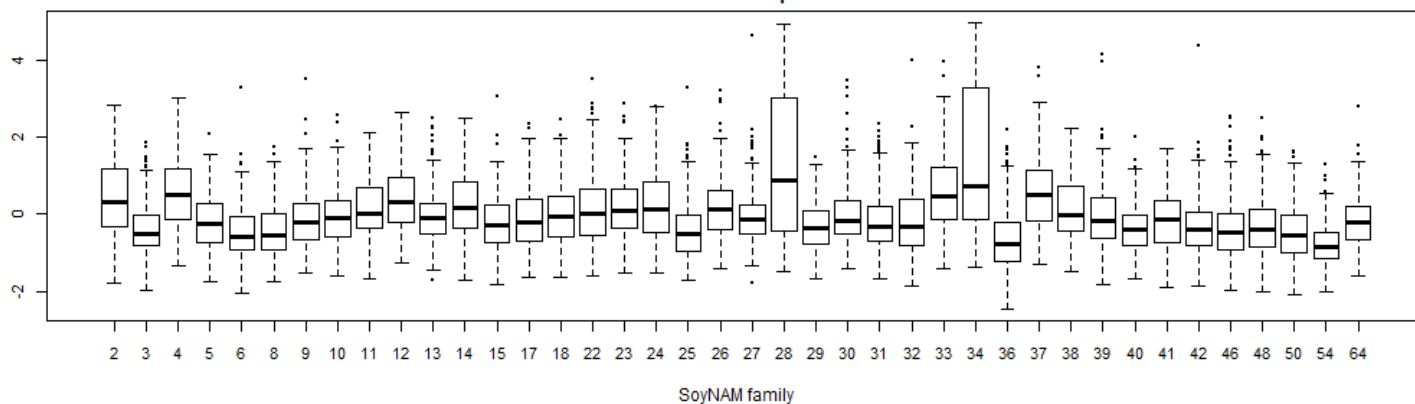
Average Canopy Closure



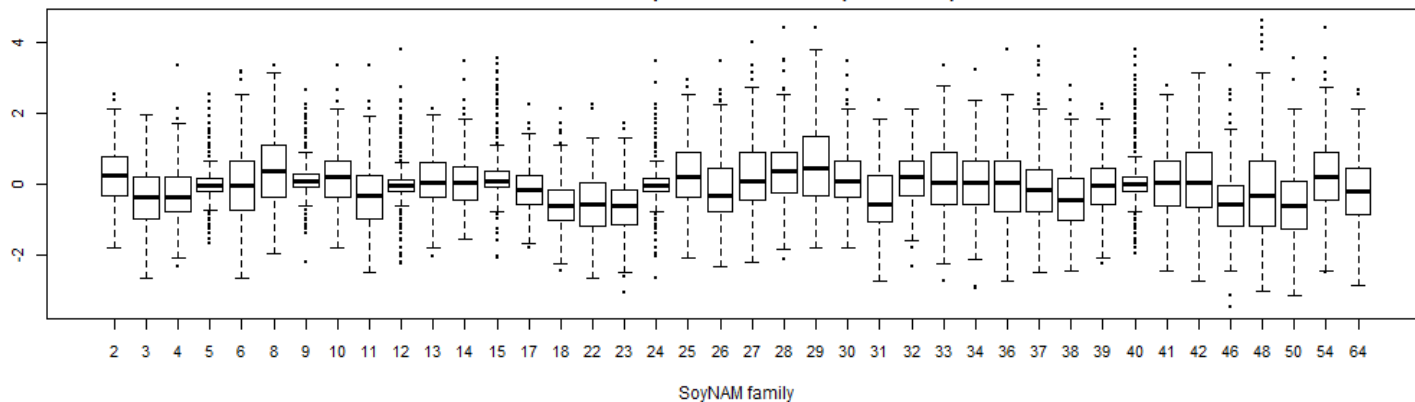
Rate of Canopy Closure



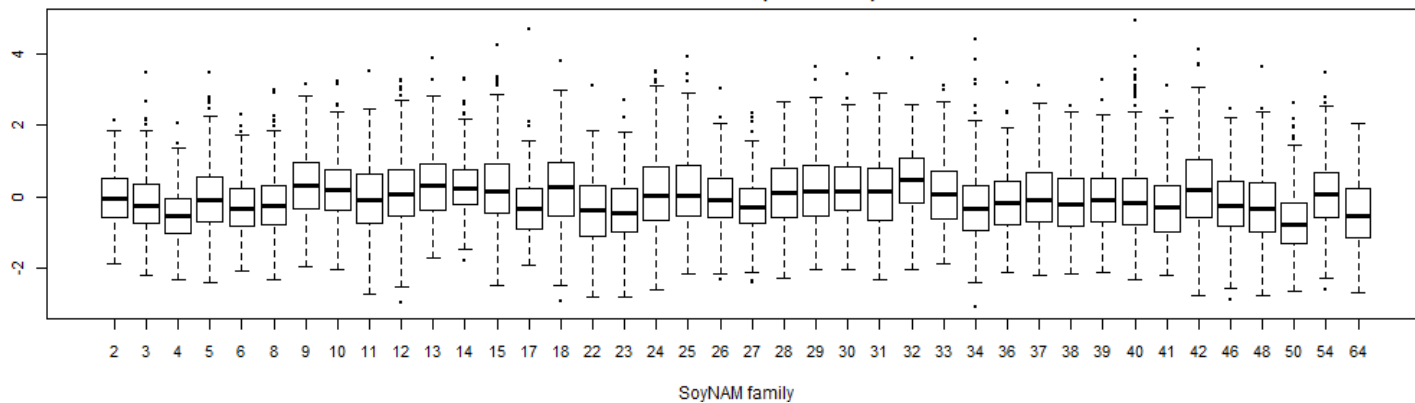
Leaflet Shape



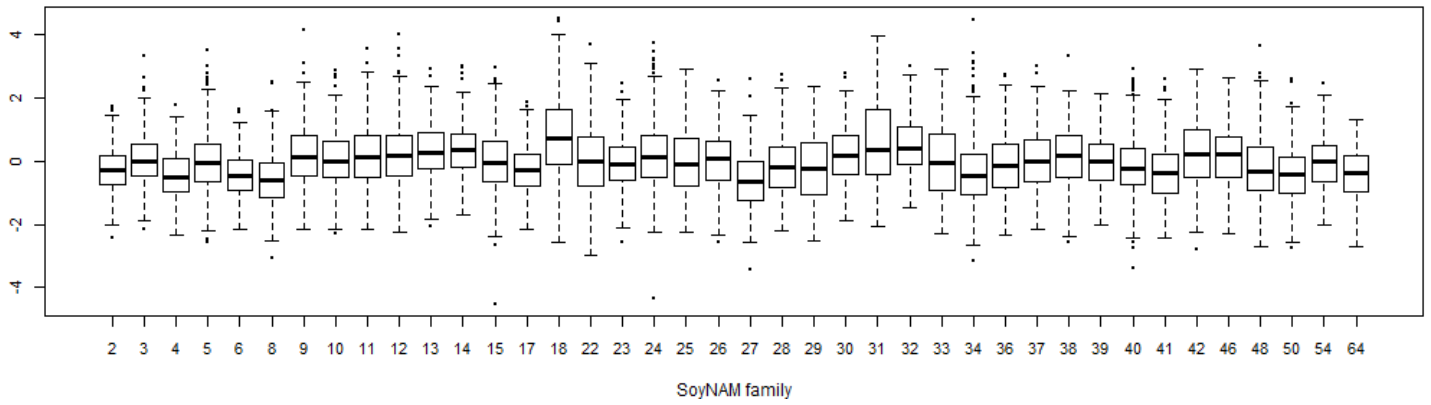
Number of Reproductive Nodes (main stem)



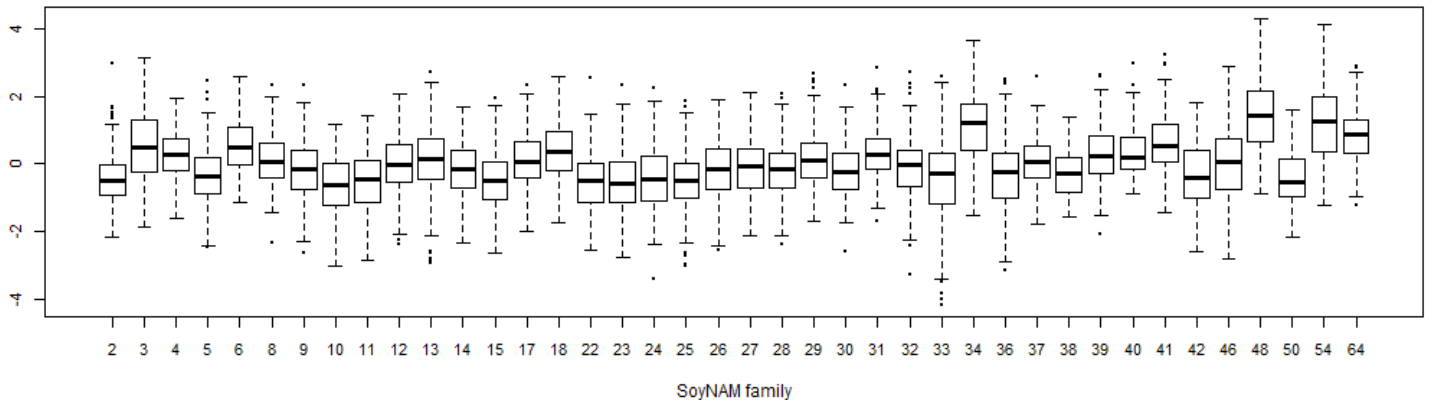
Number of Pods (main stem)



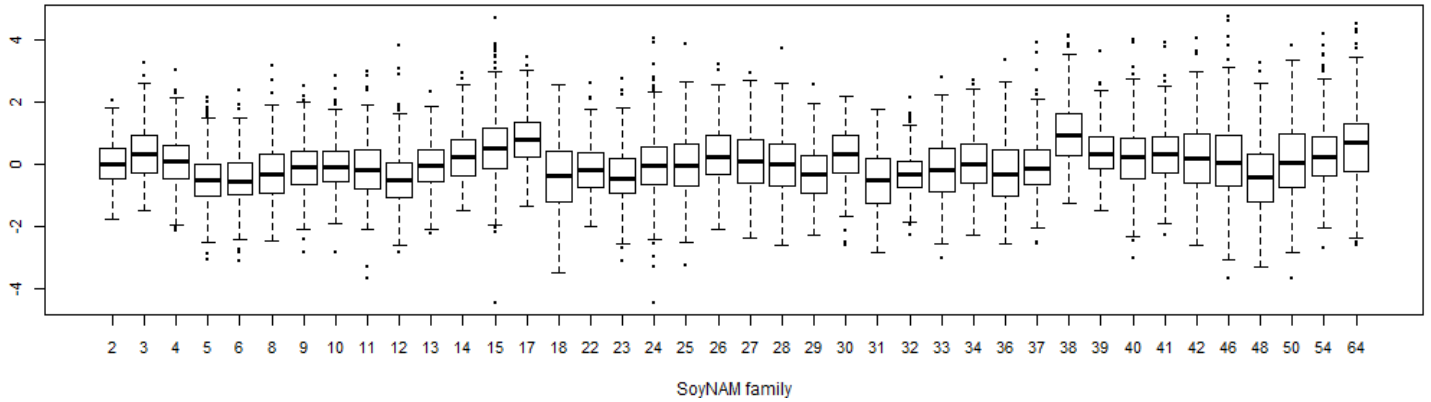
Number of Pods per Node



Seed Weight



Internode Length



3. Heatmap of genetic correlation (upper-right diagonal, blue), environmental correlation (lower-left diagonal, green) and heritabilities (main diagonal, bold letters, yellow) of soybean quantitative traits collected from the SoyNAM population in Indiana from 2012 to 2015. Genetic and environmental correlation were obtained using a multivariate mixed models fitted via Gibbs sampler implemented in GIBBS3F90, using genomic data to specify relatedness among genotypes.

Trait†	Yld	Flo	Mat	Rep	Hgt	Ldg	Acc	Rcc	LSh	Node	Pod	P/N	SW	Int
Yld	0.63	-0.29	0.69	0.8	0.55	0.5	0.73	0.53	0.08	0.58	0.44	0.15	0.09	0.08
Flo	-0.05	0.70	0.21	-0.54	0.39	0.32	0.04	-0.07	-0.33	-0.07	-0.12	-0.21	0.13	0.42
Mat	0.34	0.13	0.82	0.71	0.86	0.71	0.61	0.29	-0.14	0.47	0.19	-0.17	0.21	0.49
Rep	0.25	-0.64	0.54	0.72	0.45	0.38	0.5	0.3	0.1	0.48	0.26	-0.01	0.11	0.08
Hgt	0.27	0.13	0.47	0.16	0.88	0.89	0.77	0.52	-0.29	0.39	0.22	-0.07	0.21	0.67
Ldg	0.09	0.03	0.23	0.11	0.35	0.66	0.83	0.65	-0.42	0.57	0.45	0.15	0.07	0.41
Acc	0.36	-0.06	0.18	0.13	0.46	0.29	0.73	0.9	-0.36	0.54	0.43	0.17	0.21	0.31
Rcc	0.2	-0.01	0.06	0.05	0.21	0.14	0.5	0.60	-0.32	0.38	0.3	0.12	0.16	0.2
LSh	0.1	-0.05	-0.02	0.01	-0.06	-0.15	-0.15	-0.03	0.59	-0.03	-0.04	-0.04	-0.08	-0.27
Node	0.22	-0.003	0.22	0.15	0.36	0.22	0.31	0.19	-0.05	0.82	0.83	0.38	-0.07	-0.42
Pod	0.2	-0.04	0.1	0.1	0.2	0.19	0.23	0.09	-0.03	0.63	0.84	0.83	-0.23	-0.48
P/N	0.08	-0.06	-0.06	0.002	-0.05	0.06	0.05	-0.02	0.003	0	0.78	0.75	-0.32	-0.41
SW	0.02	-0.1	-0.07	-0.07	-0.01	-0.03	0.04	-0.01	0.001	-0.05	-0.04	-0.02	0.40	0.27
Int	0.05	0.12	0.23	0.03	0.57	0.12	0.14	0.04	-0.01	-0.54	-0.38	-0.06	0.03	0.85

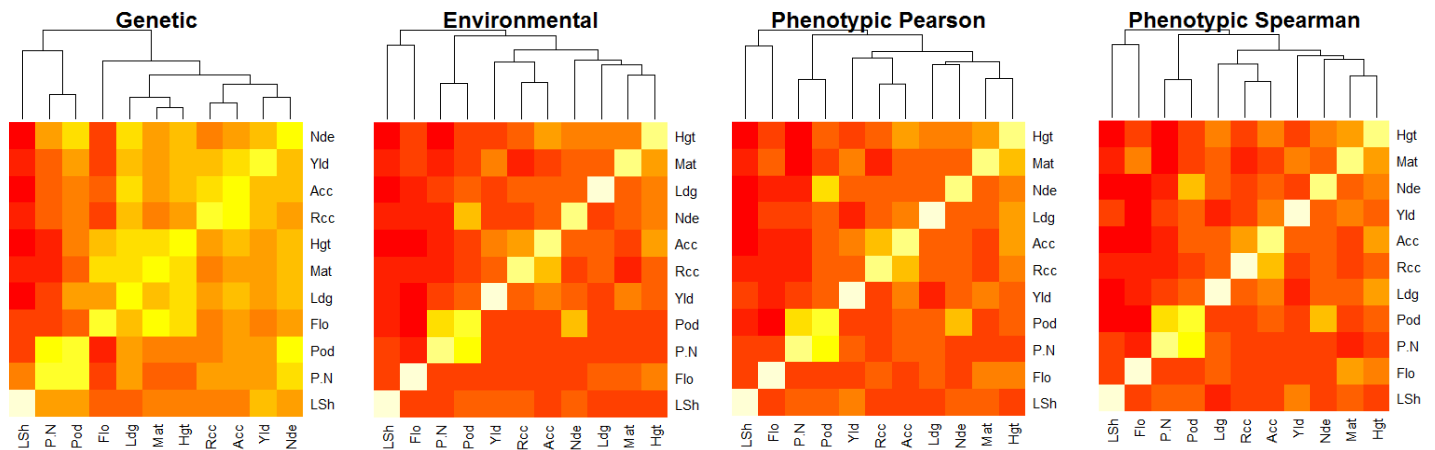
† Yld, grain yield; Flo, flowering; Mat, maturity; Rep, length of reproductive period; Hgt, plant height; Ldg, lodging score; Acc, average canopy closure; Rcc, rate of canopy closure; LSh, leaflet shape; Node, number of reproductive nodes; Pod, pods in the main stem; P/N, pods per node; SW, 100-seed weight; Int, internode length.

4. Heatmap of Phenotypic correlation: Pearson's correlation (upper-right diagonal) and Spearman's correlation (lower-left diagonal) of soybean quantitative traits collected from the SoyNAM population in Indiana from 2012 to 2015. Correlation were obtained using a phenotypes normalized by environment.

Trait†	Yld	Flo	Mat	Rep	Hgt	Ldg	Acc	Rcc	LSh	Node	Pod	P/N	SW	Int
Yld	-	-0.06	0.31	0.31	0.13	0.01	0.31	0.13	0.12	0.2	0.18	0.06	0.07	-0.06
Flo	-0.05	-	0.21	-0.53	0.19	0.07	-0.01	0.02	-0.06	-0.001	-0.04	-0.06	0.05	0.13
Mat	0.3	0.3	-	0.59	0.42	0.17	0.18	0.05	-0.003	0.21	0.1	-0.07	0.03	0.15
Rep	0.41	-0.24	0.75	-	0.21	0.1	0.13	0.03	0.02	0.22	0.13	-0.01	-0.02	0.01
Hgt	0.12	0.23	0.4	0.3	-	0.35	0.44	0.25	-0.05	0.34	0.28	-0.01	-0.02	0.42
Ldg	0.03	0.05	0.18	0.13	0.38	-	0.3	0.21	-0.13	0.19	0.19	0.07	0.002	0.11
Acc	0.3	-0.01	0.18	0.17	0.43	0.31	-	0.53	-0.13	0.3	0.24	0.06	0.09	0.09
Rcc	0.12	0.05	0.06	0.03	0.24	0.23	0.5	-	-0.05	0.21	0.14	0.02	0.03	0.05
LSh	0.15	-0.03	-0.001	-0.003	-0.05	-0.14	-0.11	-0.04	-	-0.03	-0.03	-0.01	-0.03	-0.03
Node	0.2	-0.01	0.23	0.3	0.39	0.24	0.29	0.2	-0.05	-	0.51	-0.03	-0.01	-0.27
Pod	0.18	-0.05	0.1	0.18	0.28	0.21	0.23	0.15	-0.01	0.6	-	0.78	-0.06	-0.2
P/N	0.07	-0.06	-0.06	-0.02	0.02	0.08	0.06	0.03	0.02	0.03	0.77	-	-0.06	-0.04
SW	0.08	0.08	0.05	0.01	-0.02	0.01	0.1	0.02	-0.05	-0.02	-0.06	-0.06	-	0.06
Int	-0.05	0.16	0.15	0.01	0.43	0.12	0.1	0.05	-0.03	-0.32	-0.21	-0.04	0.06	-

† Yld, grain yield; Flo, flowering; Mat, maturity; Rep, length of reproductive period; Hgt, plant height; Ldg, lodging score; Acc, average canopy closure; Rcc, rate of canopy closure; LSh, leaflet shape; Node, number of reproductive nodes; Pod, pods in the main stem; P/N, pods per node; SW, 100-seed weight; Int, internode length.

- Classification heatmap of correlation matrices of soybean quantitative traits collected from the SoyNAM population in Indiana from 2012 to 2015. Plots were generated using the built-in R function *heatmap* with default settings.



Yld, grain yield; Flo, flowering; Mat, maturity; Hgt, plant height; Ldg, lodging score; Acc, average canopy closure; Rcc, rate of canopy closure; LSh, leaflet shape; Nde, number of reproductive nodes; Pod, pods in the main stem; P.N, pods per node.

- Scatterplot among various types of correlations of soybean quantitative traits collected from 40 biparental families that compose the SoyNAM population in Indiana from 2012 to 2015, including phenotypic Pearson (linear), phenotypic Spearman (non-linear), genetic, and environmental correlations. Phenotypic correlations were obtained using R built-in function, genetic and environmental correlation were obtained using a multivariate mixed models fit via Gibbs sampler implemented in GIBBS3F90, using genomic data to specify relatedness among genotypes.

