Figure S 1: Power comparisons between DECMDR (D), SNPHarvester (H), MACOED (M), AntEpiSeeker (S), HS-MMGKG (G), SEE (E) and SHEIB-AGM (A) with the DME and DNME 1000 dataset. The bars represent powers of the algorithms.
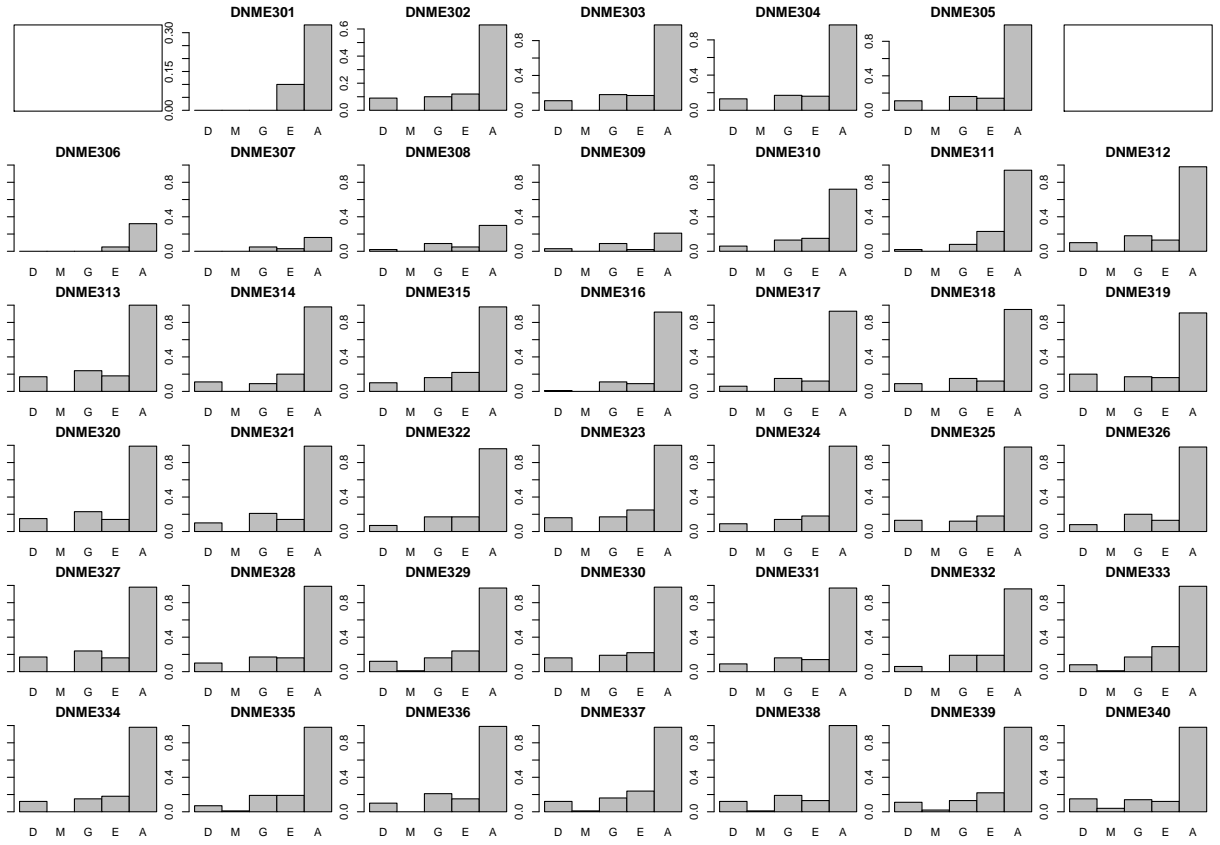
Figure S 2: Power comparisons between DECMDR (D), MACOED (M), HS-MMGKG (G), SEE (E) and SHEIB-AGM (A) with the DNME3 100 dataset. The bars represent powers of the algorithms.
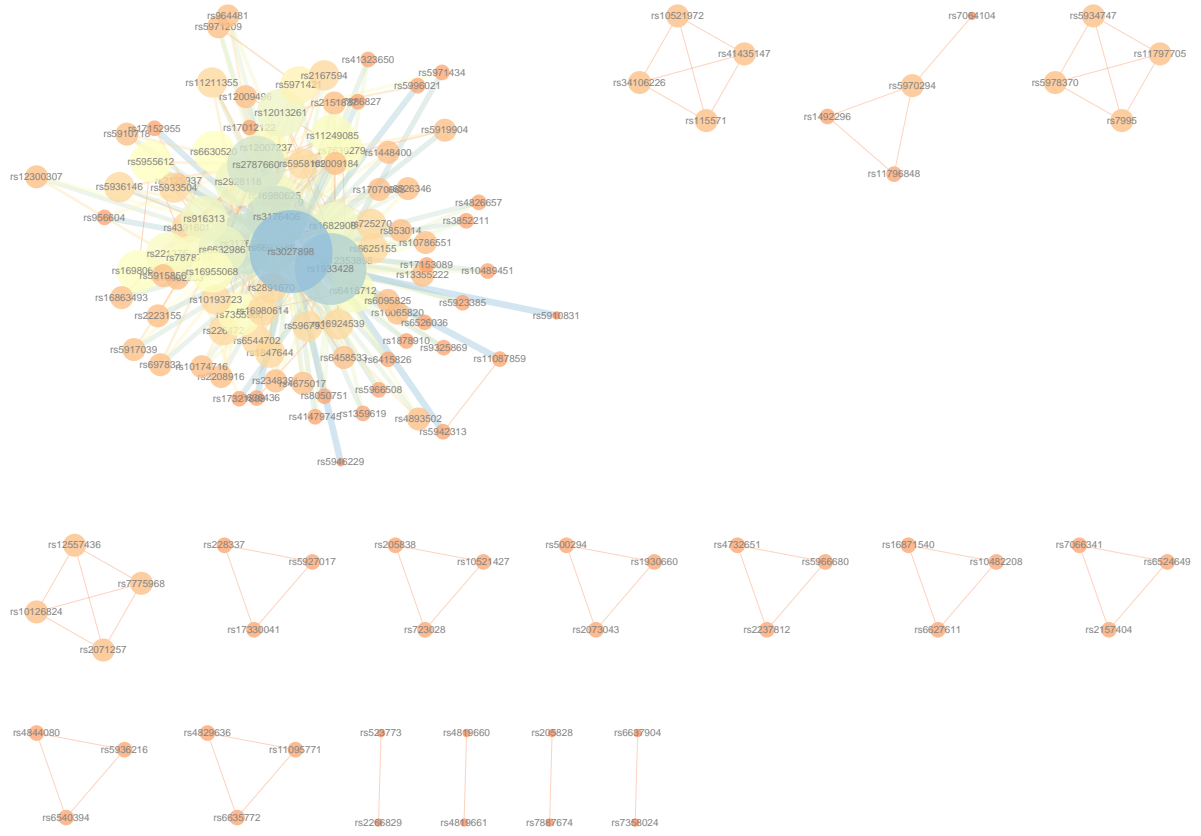
Figure S 3: The SNP network of the epistatic interactions detected for Coronary Artery Disease (only 400 SNP pairs with minimum p-values of G-test).
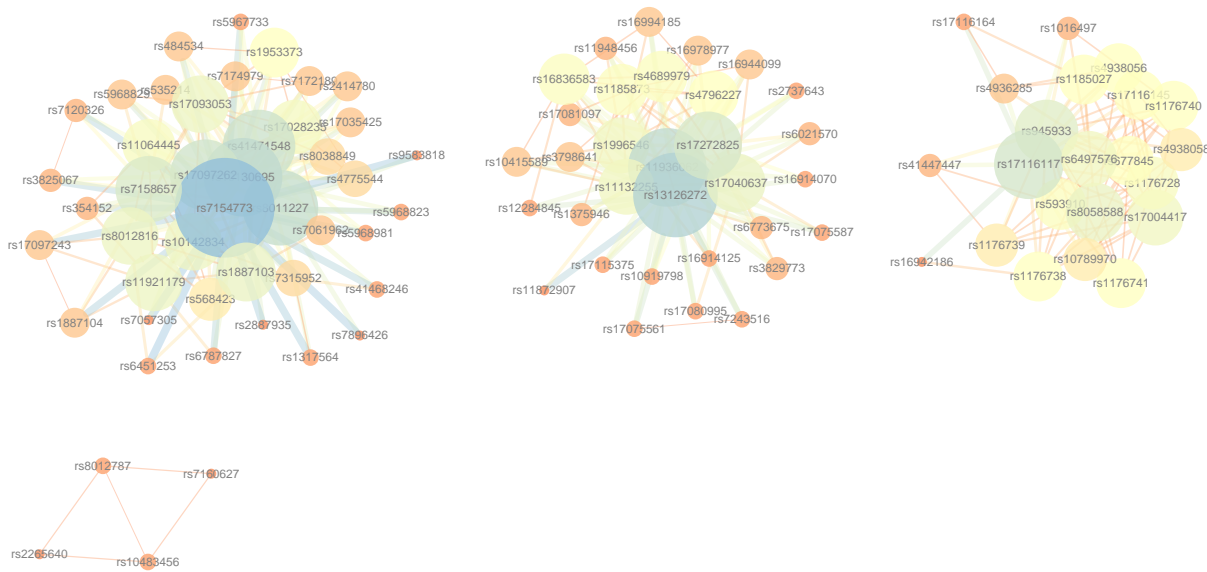

Figure S 4: The SNP network of the epistatic interactions detected for Crohn's Disease (only 400 SNP pairs with minimum p-values of G-test).
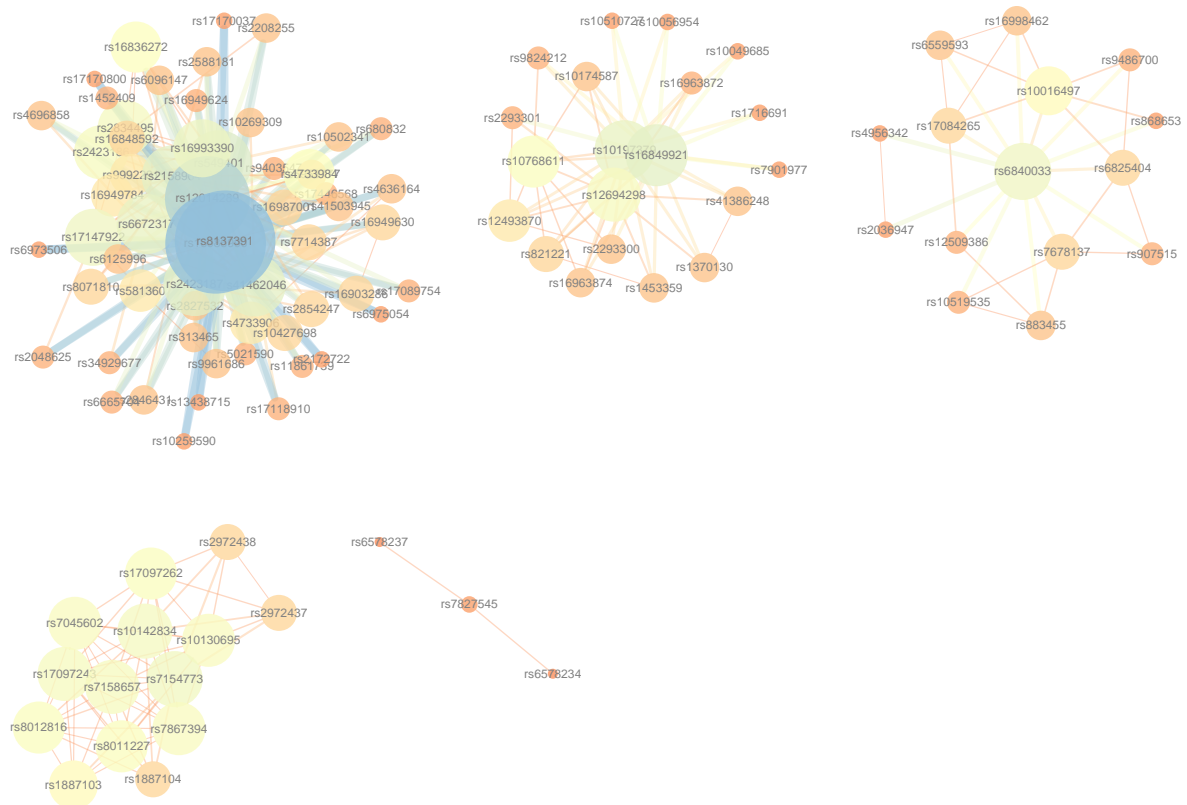
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Figure S 5: The SNP network of the epistatic interactions detected for Hypertension (only 400 SNP pairs with minimum p-values of G-test).

Figure S 6: The SNP network of the epistatic interactions detected for Rheumatoid Arthritis (only 400 SNP pairs with minimum p-values of G-test).
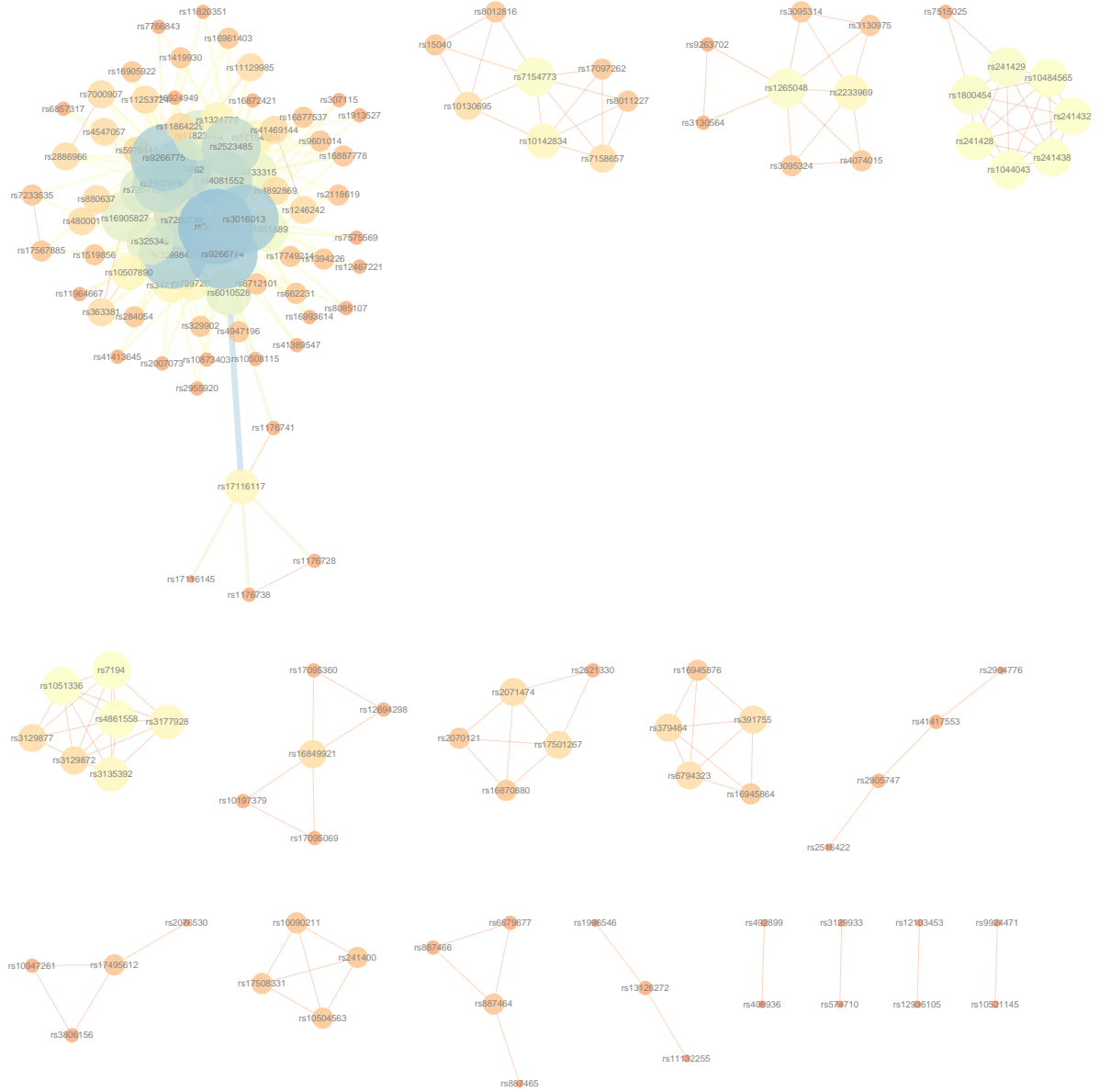
Figure S 7: The SNP network of the epistatic interactions detected for Type 1 Diabetes (only 400 SNP pairs with minimum p-values of G-test).
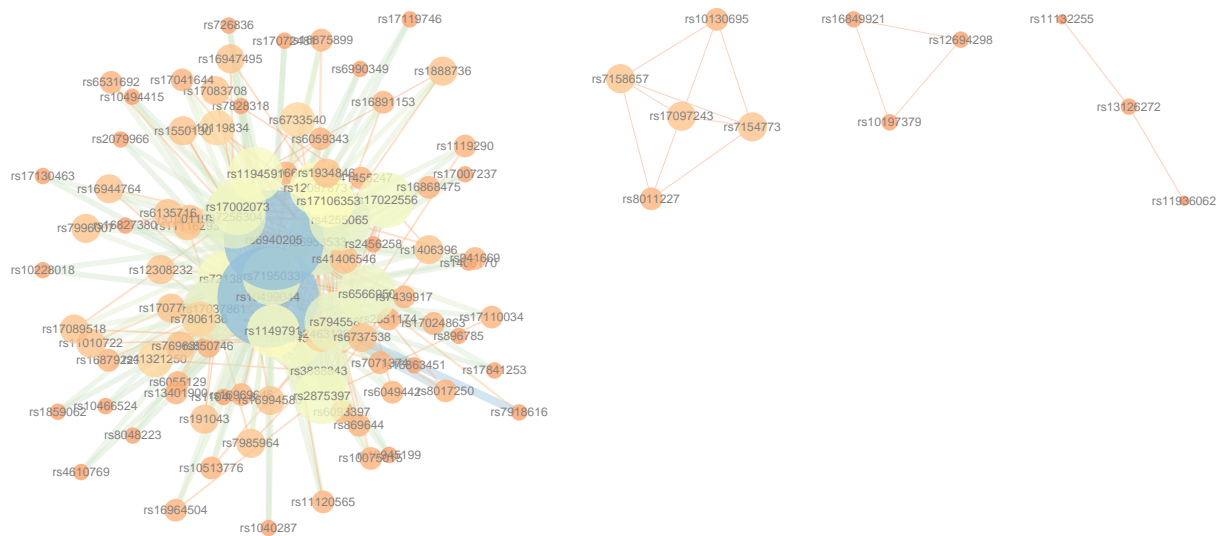
Figure S 8: The SNP network of the epistatic interactions detected for Type 2 Diabetes (only 400 SNP pairs with minimum p-values of G-test).

Figure S 9: The gene network of the epistatic interactions detected for Coronary Disease (only 400 gene pairs with the highest frequency of occurrence).

Figure S 10: The gene network of the epistatic interactions detected for Crohn's Disease (only 400 gene pairs with the highest frequency of occurrence).

Figure S 11: The gene network of the epistatic interactions detected for Hypertension (only 400 gene pairs with the highest frequency of occurrence).
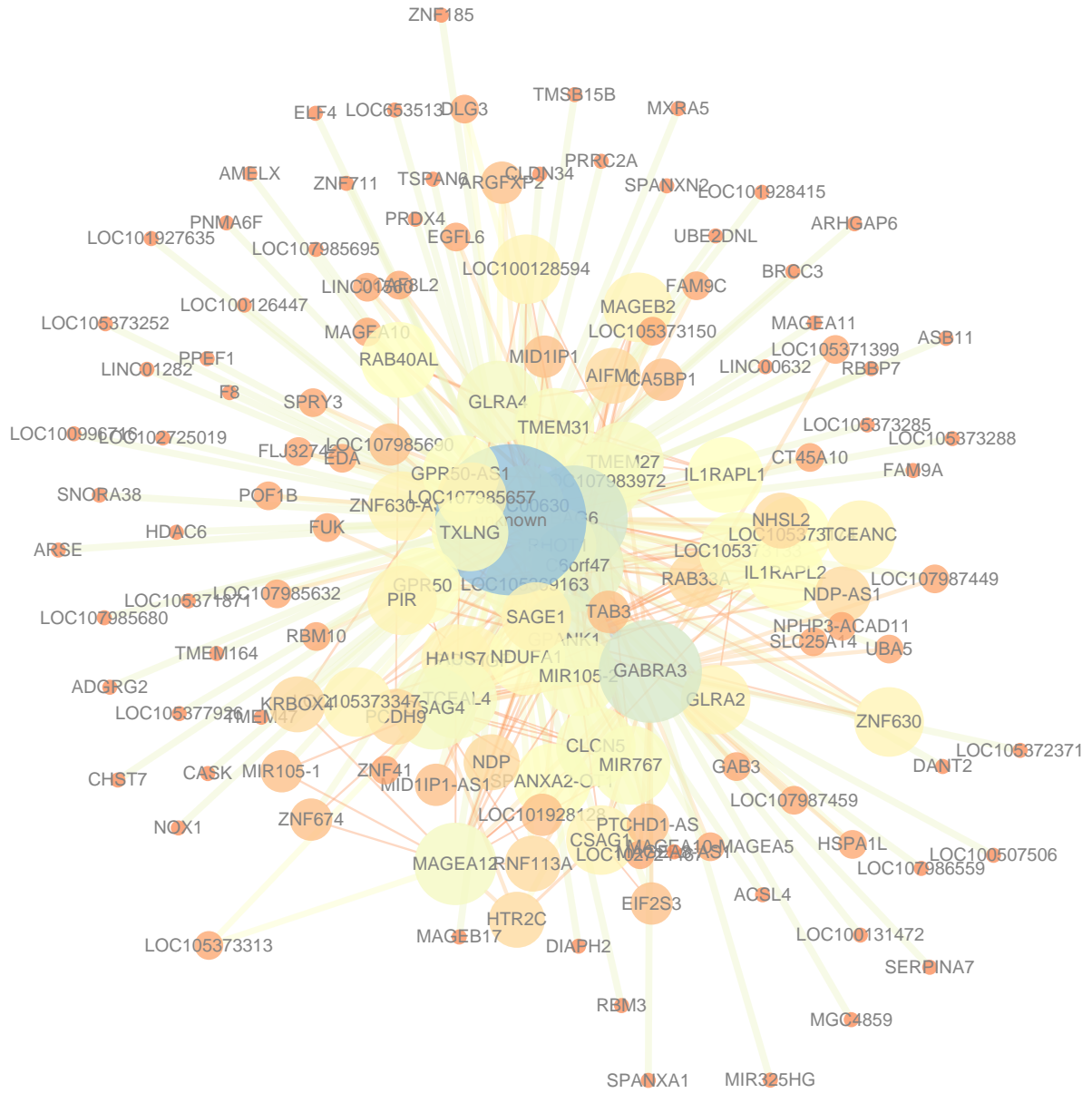
Figure S 12: The gene network of the epistatic interactions detected for Rheumatoid Arthritis (only 400 gene pairs with the highest frequency of occurrence).

Figure S 13: The gene network of the epistatic interactions detected for Type 1 Diabetes (only 400 gene pairs with the highest frequency of occurrence).

Figure S 14: The gene network of the epistatic interactions detected for Type 2 Diabetes (only 400 gene pairs with the highest frequency of occurrence).