

Figure 1. Schema used to model the information from different biological databases about enhancers and their relations with other entities. The colored boxes specify the different subgraphs or subdomains: enhancer sequences (crm graph - orange on the top), and their relations with other biological entities of interest, such as target genes (crm2gene graph - yellow on the bottom), transcription factors (crm2tfac graph - brown on the right), and phenotypes (crm2phen graph - red on the left). The blue classes constitute the central entities of each graph, while the green classes are biological classes of interest that were not modeled in detail because they are already present in the BioGateway KG, schema that is interoperable with this one.

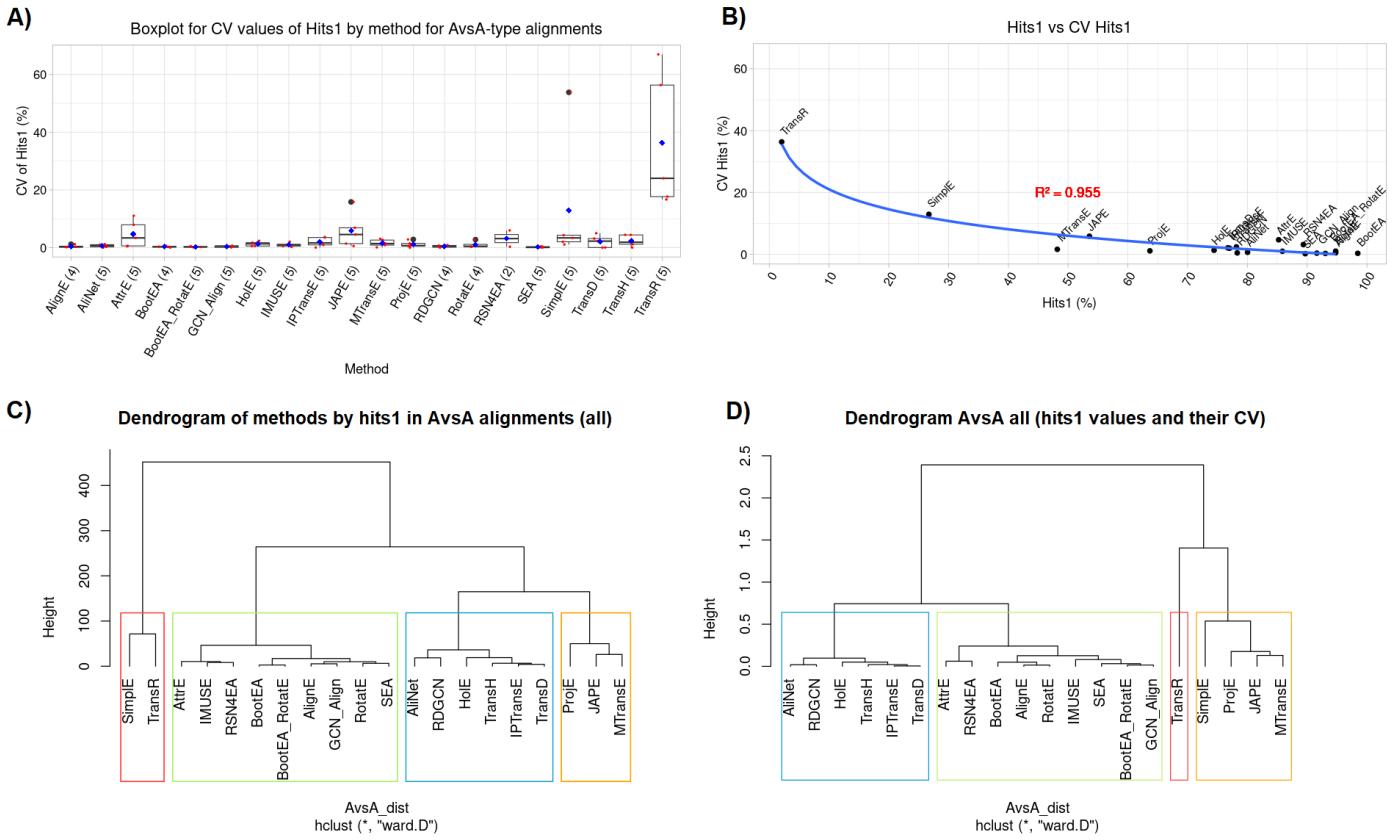


Figure 2. Results associated to hits@1 values in AvsA-all alignments and considering 5 datasets (ENdb, EnDisease, DiseaseEnhancer, VISTA and RefSeq). A) Boxplot for the coefficients of variation (CV) of hits@1 values between replicates for each method. B) Observed log trend between the hits@1 values and their CV, derived by running replicates. C and D) Comparison of methods classified from dendograms using hits@1 values (C) and using hits@1 values and the CV of hits@1 values between replicates (D). The clusters remain mainly without changes, with two clusters (red and orange) associated with methods with low hits@1 values, one cluster (green) with good results, that could be subdivided in two subclusters, and one cluster with intermediate results (blue).

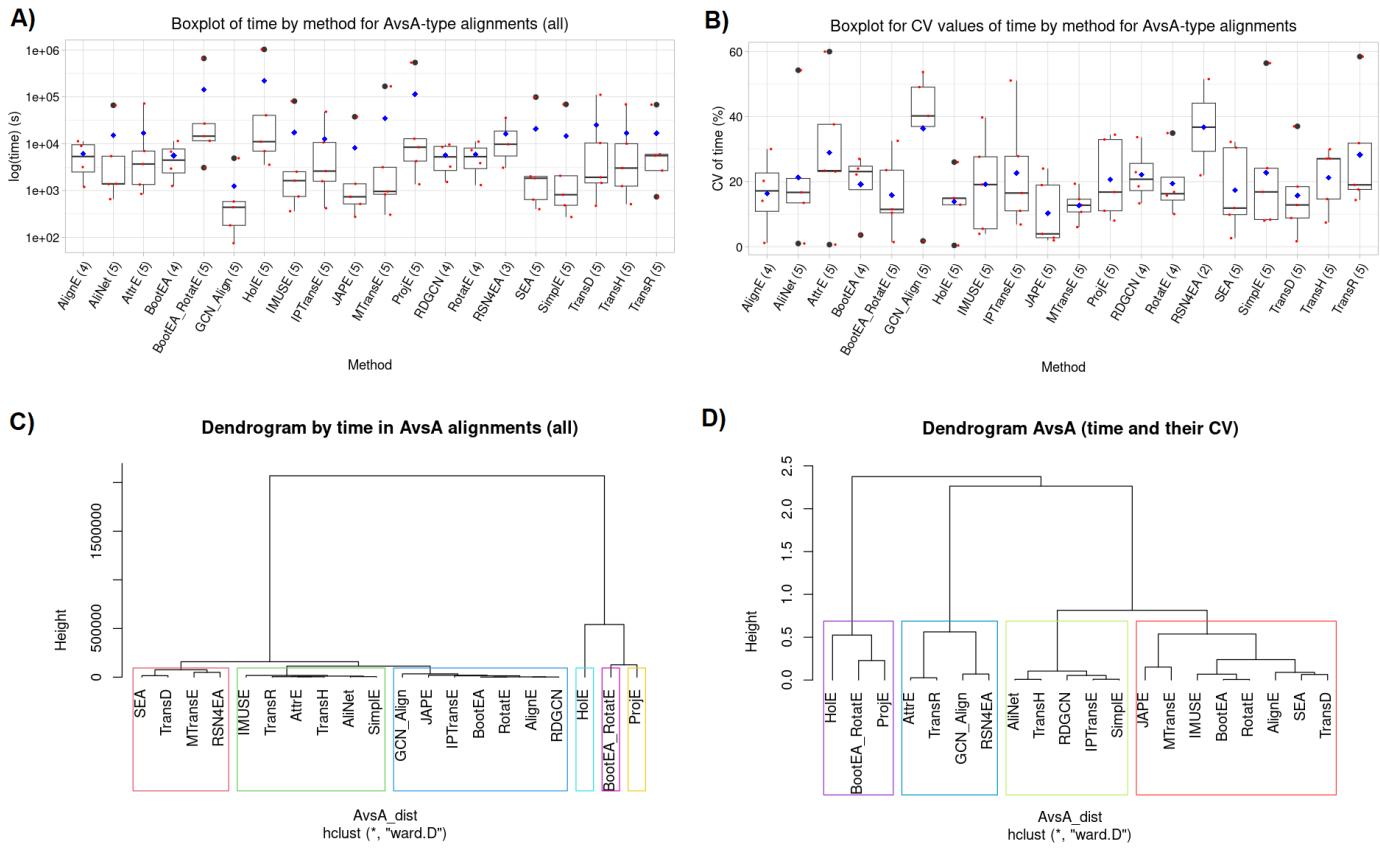


Figure 3. Results associated to time values in AvsA all alignments and considering 5 datasets (ENdb, EnDisease, DiseaseEnhancer, VISTA and RefSeq). A) Boxplot by method of time values. B) Boxplot of CV values of time. C) Dendrogram of methods using time values. Two main branches stand out. The left branch is associated with low run times and the right branch with high run times. These branches can in turn be subdivided into sub-clusters with more specific time profiles. D) Dendrogram of methods using time values and their CV. The inclusion of CV values of time does not improve the generation of clusters with homogeneous methods.

Relation between number of triples and mean time of execution by method

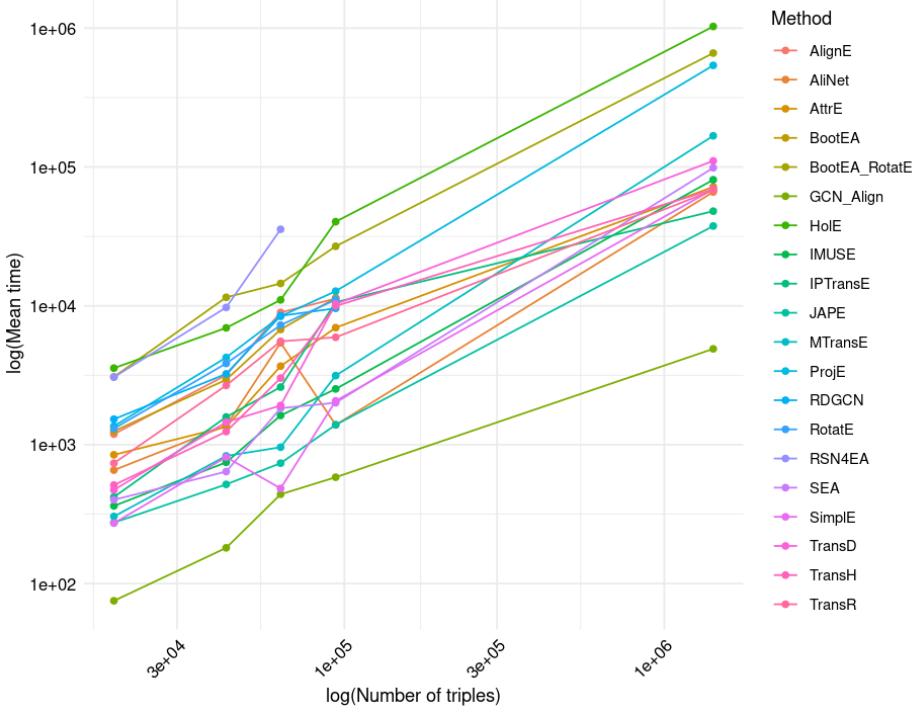


Figure 4. Representation of the number of triples against execution time for each alignment method used and each database.

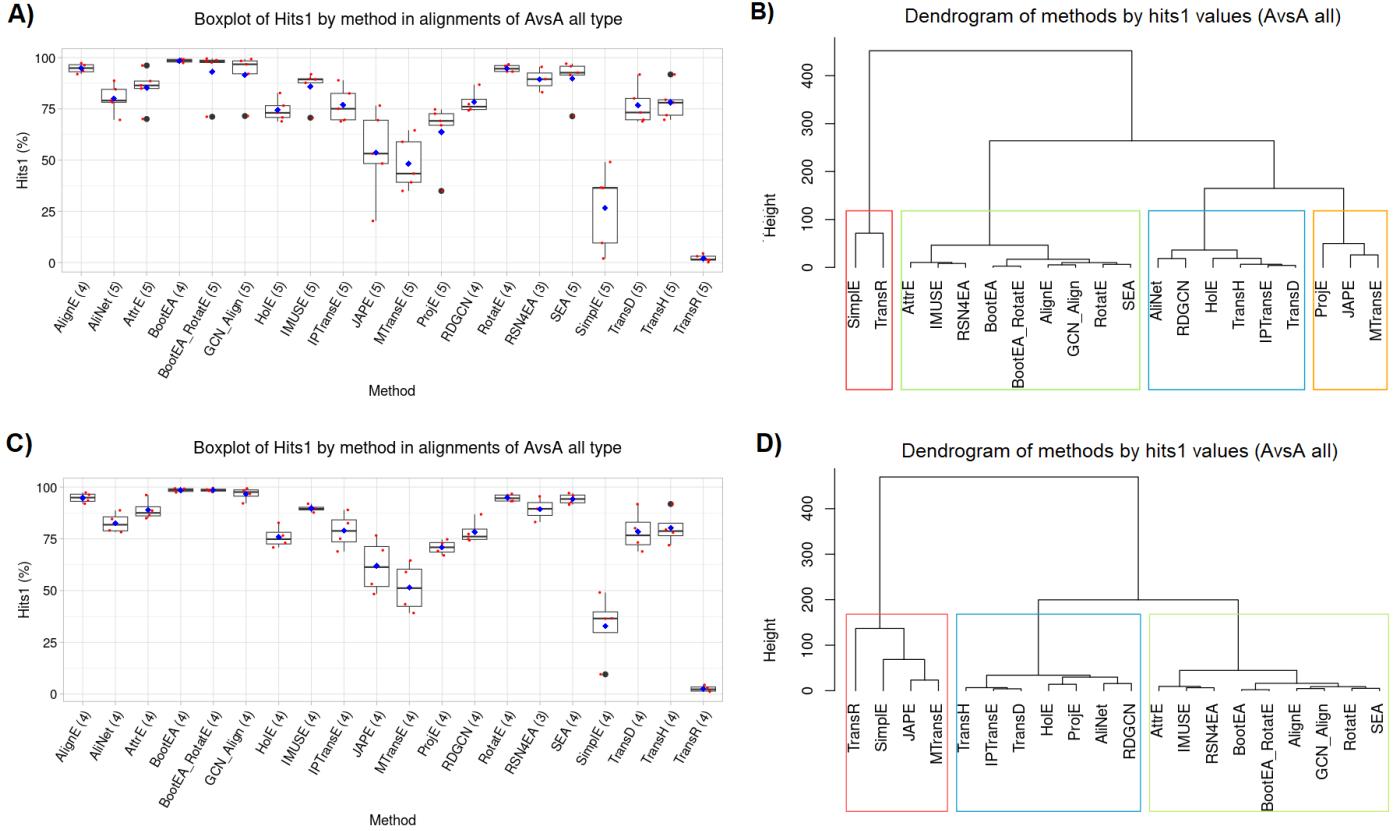
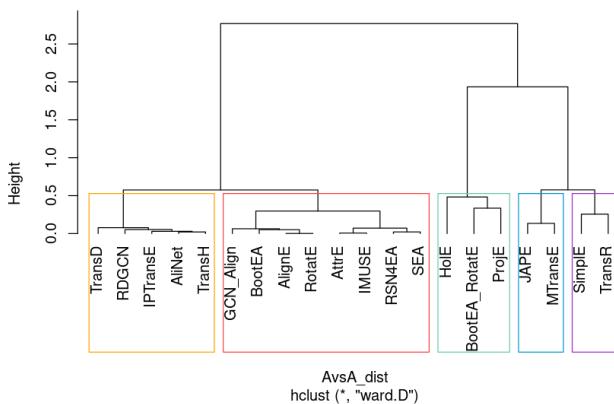


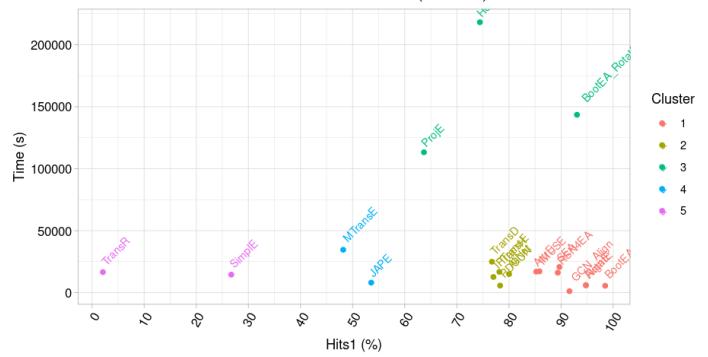
Figure 5. The hits@1 of the AvsA all alignments using five datasets (ENdb, EnDisease, DiseaseEnhancer, VISTA and RefSeq) (A and B) are compared to those obtained when RefSeq is removed due to non-alignments in some methods (C and D).

A)

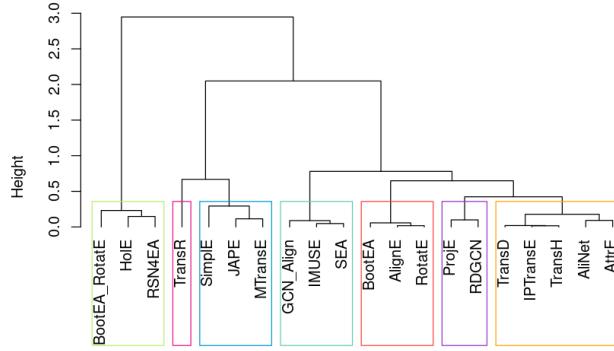
Dendrogram by hits1 and time (AvsA all and 5 datasets)



Mean Hits1 vs Mean Time (AvsA all)

**B)**

Dendrogram by hits1 and time (AvsA all and without RefSeq)



Mean Hits1 vs Mean Time (AvsA all)

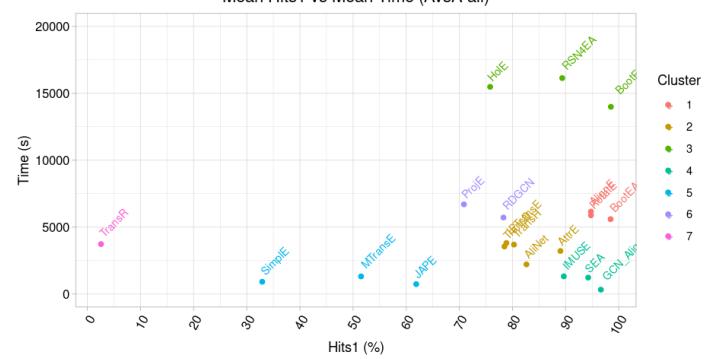
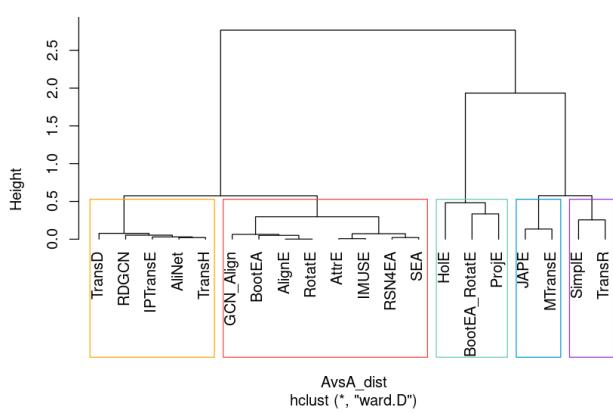


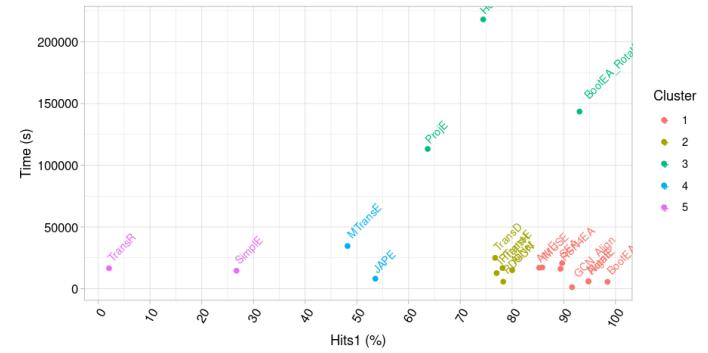
Figure 6. Dendograms and representation of the clusters generated by grouping the methods by hits@1 and time values obtained in the AvsA-all type alignments. A) Results obtained by using the alignments of the 5 databases. B) Results when we omit the alignment corresponding to RefSeq, because different methods were not able to complete the alignment corresponding to this dataset.

A)

Dendrogram by hits1 and time (AvsA all)

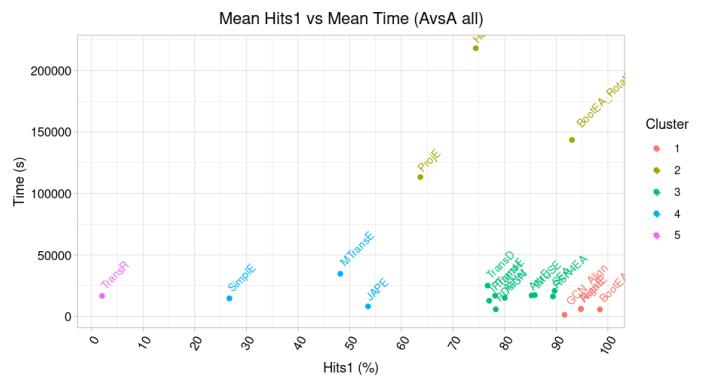
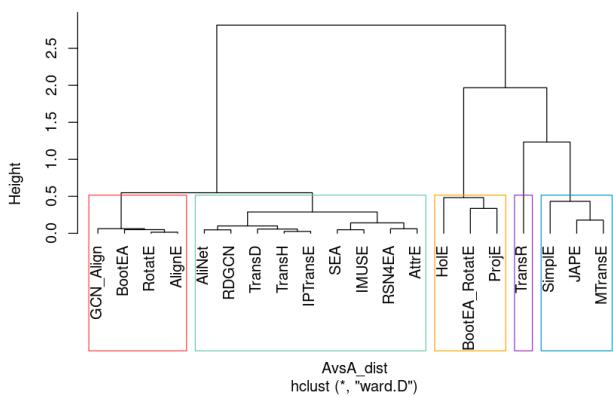


Mean Hits1 vs Mean Time (AvsA all)

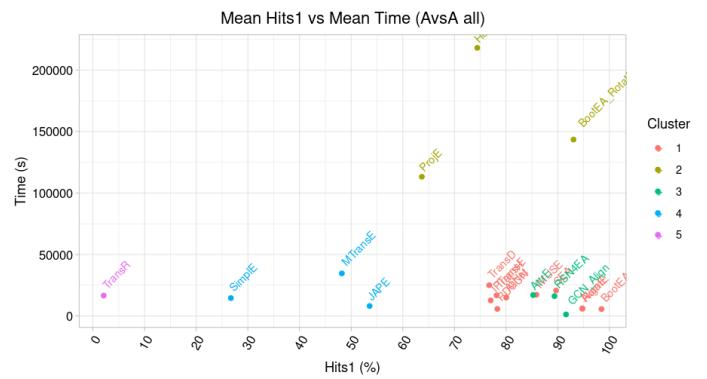
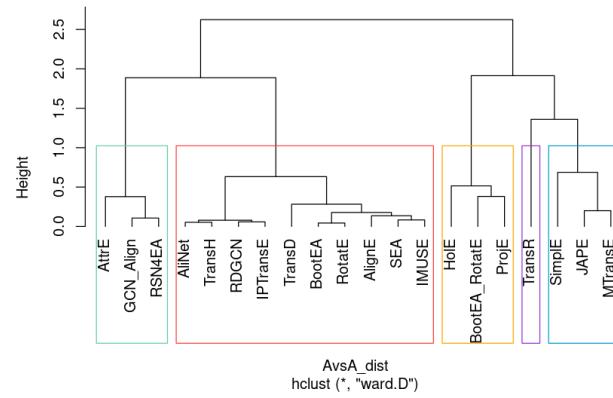


B)

Dendrogram AvsA (hits1, time and CV hits1)

**C)**

Dendrogram AvsA (hits1, time and CVs)

**D)**

Dendrogram AvsA (all metrics)

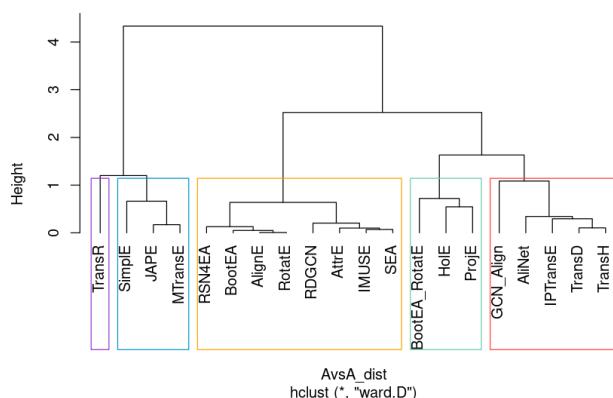
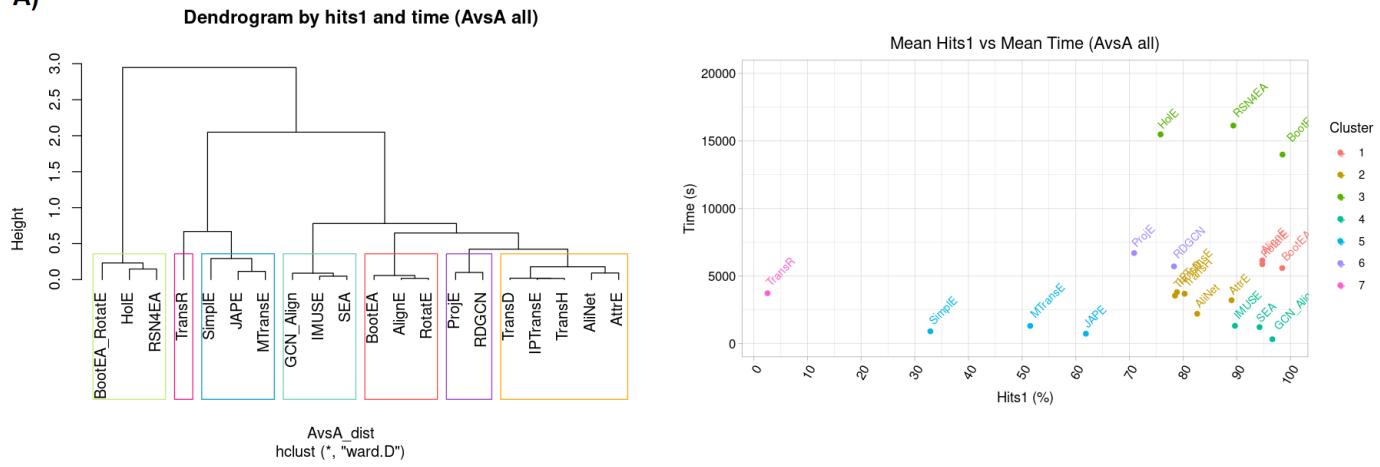
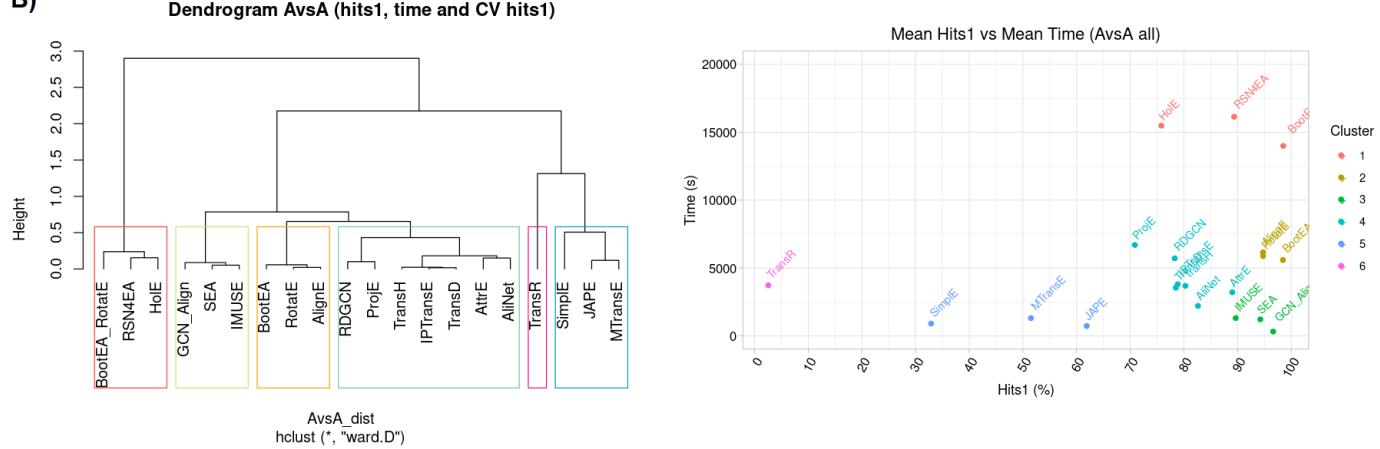
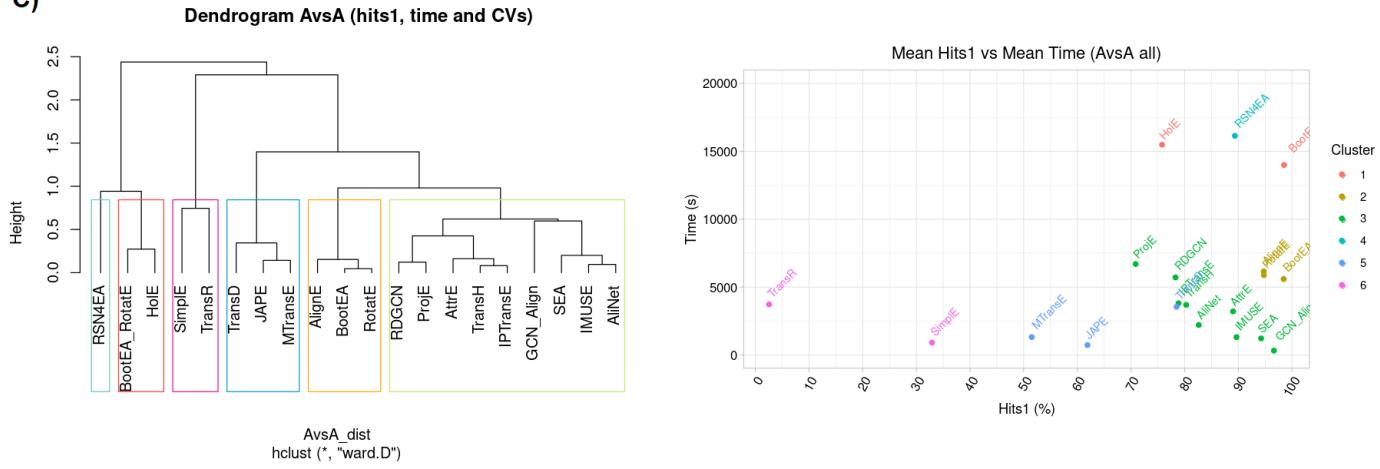


Figure 7. Effects of including coefficient of variance values of hits@1 and time, and other combination of scaled alignment metrics (hits@1, hits@5, hits@10, mr, mrr, time) in the clustering of methods (AvsA-all type alignments: alignment of equal graphs with all the data domains which contain the databases that constitute the graphs). A) Dendrogram and plot using hits@1 and time values. B) Dendrogram and plot after adding CV values of hits@1. C) Dendrogram and plot after adding CV values of hits@1 and time. D) Dendrogram and plot considering all metrics returned in the alignment (hits@1, hits5, hits@10, mr, mrr and time).

A)**B)****C)**

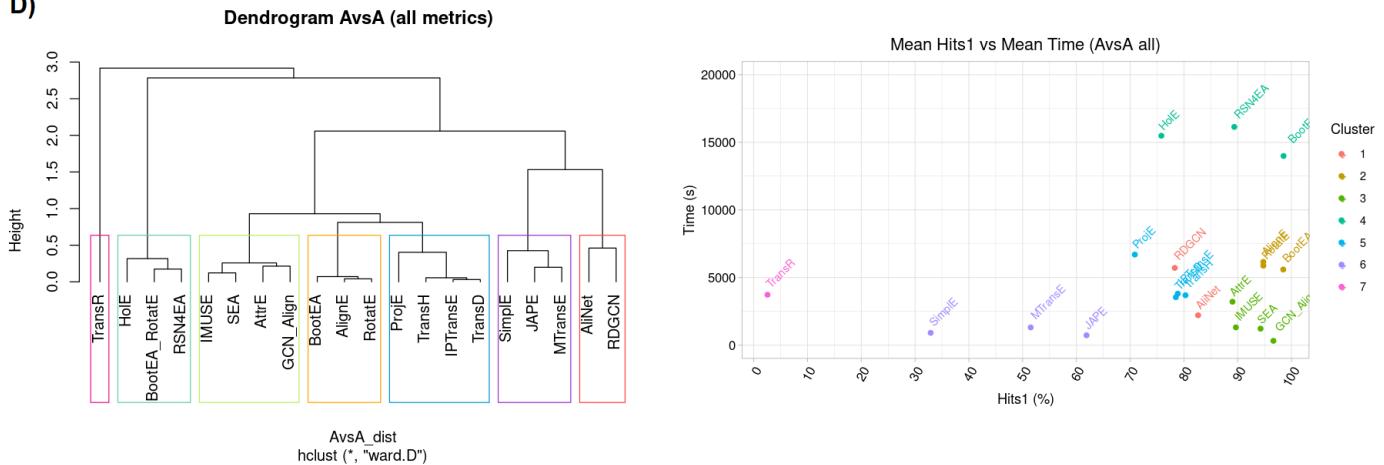
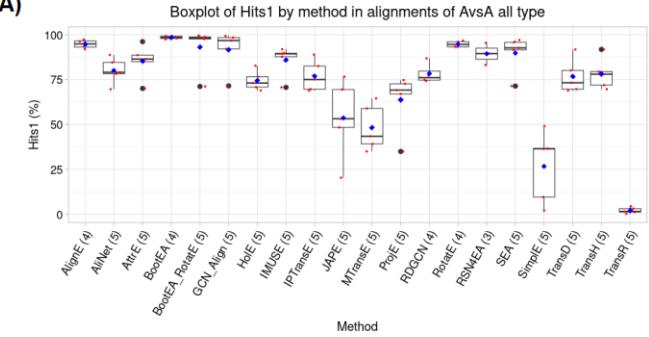
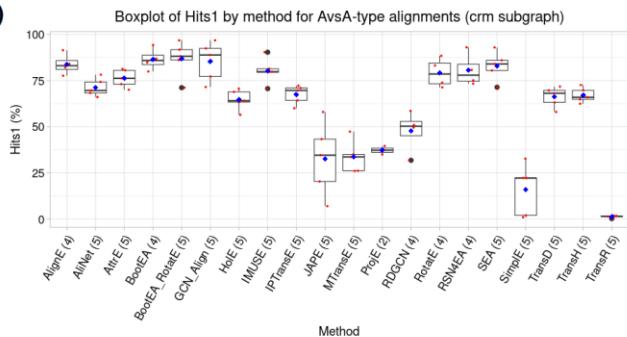
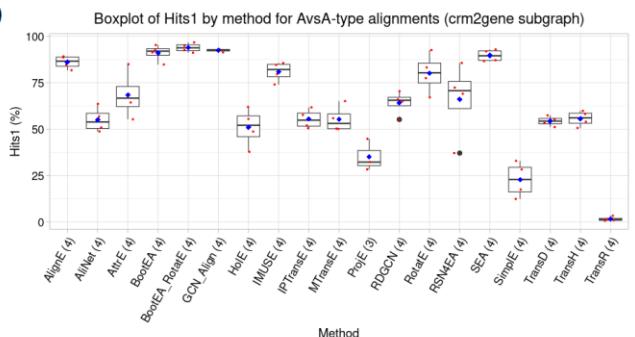
D)

Figure 8. Effects of including coefficient of variance values of hits@1 and time, and other combination of scaled alignment metrics (hits@1, hits@5, hits@10, mr, mrr, time) in the clustering of methods (AvsA-all type alignments). The results of RefSeq were omitted from this report because different methods were not able to align this dataset. A) Dendrogram and plot using hits@1 and time values. B) Dendrogram and plot after adding CV values of hits@1. C) Dendrogram and plot after adding CV values of hits@1 and time. D) Dendrogram and plot considering all metrics returned in the alignment (hits@1, hits5, hits@10, mr, mrr and time).

A)**B)****C)**

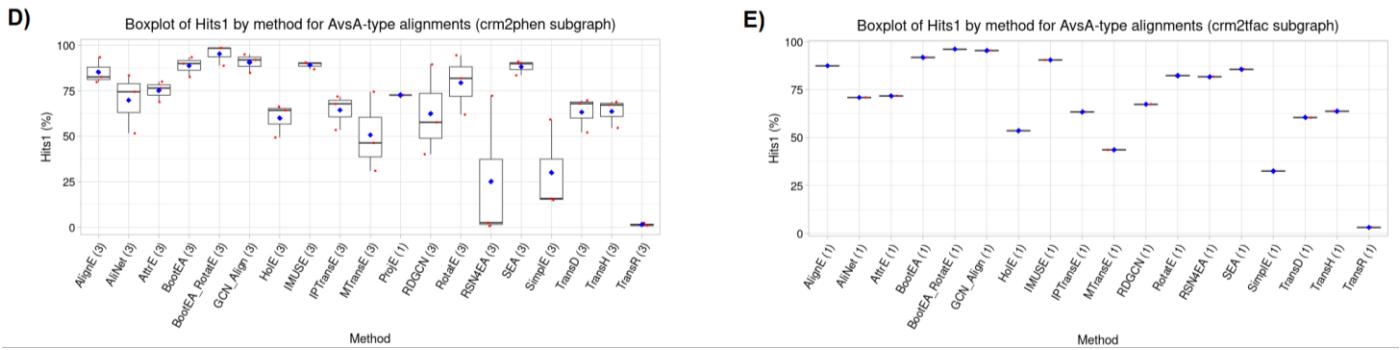


Figure 9. Boxplot of hits@1 values obtained in AvsA-type alignment using all the information from the source database (A), and subdomains of data: crm sequences (B), relations between crm and genes (C), relations between crm and phenotypes (D), and relations between crm and transcription factors (E).

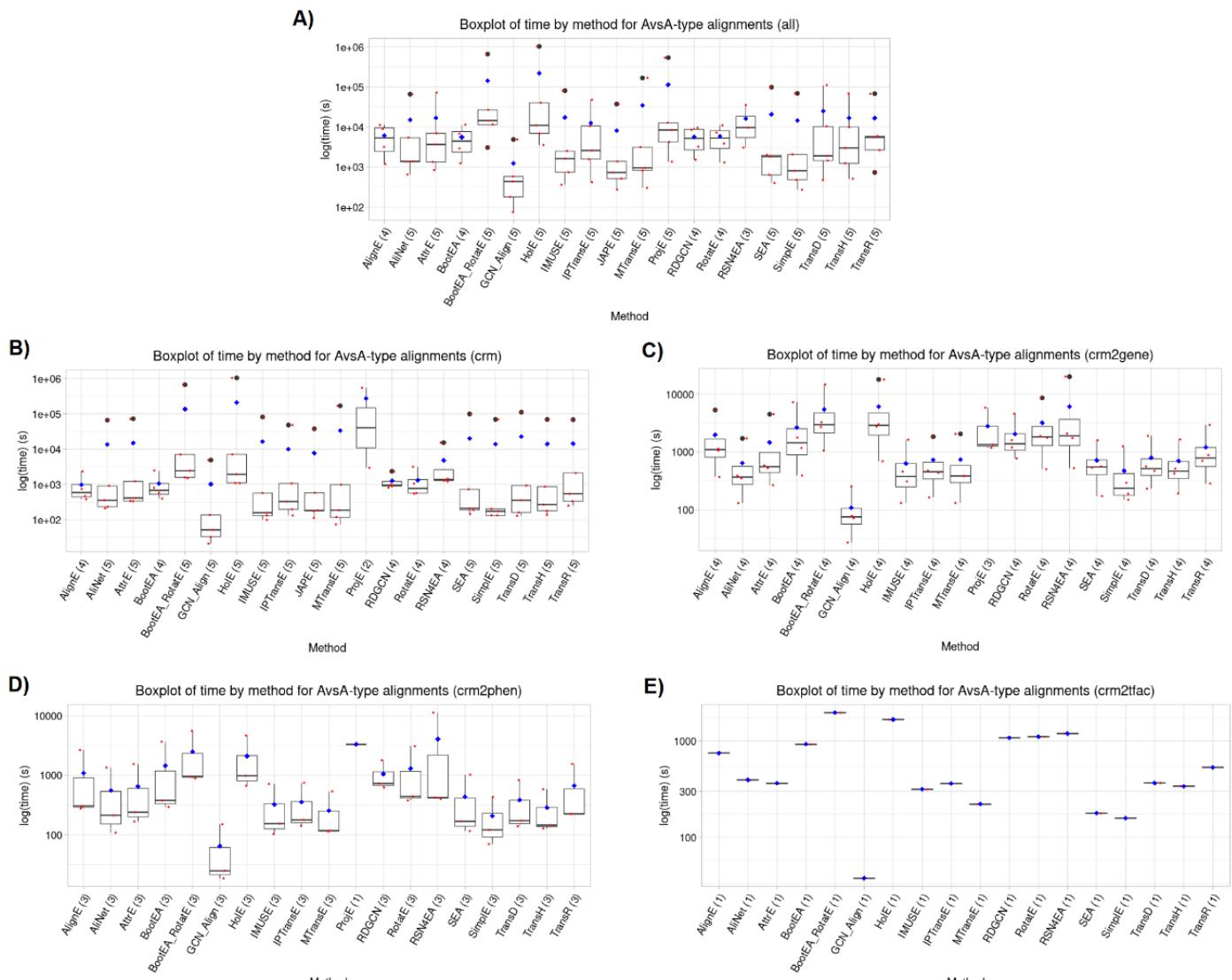


Figure 10. Boxplot of time values obtained in AvsA-type alignment using all the data domains from the source database (A), and different data subdomains: crm sequences (B), relations between crm and genes (C), relations between crm and phenotypes (D), and relations between crm and transcription factors (E).

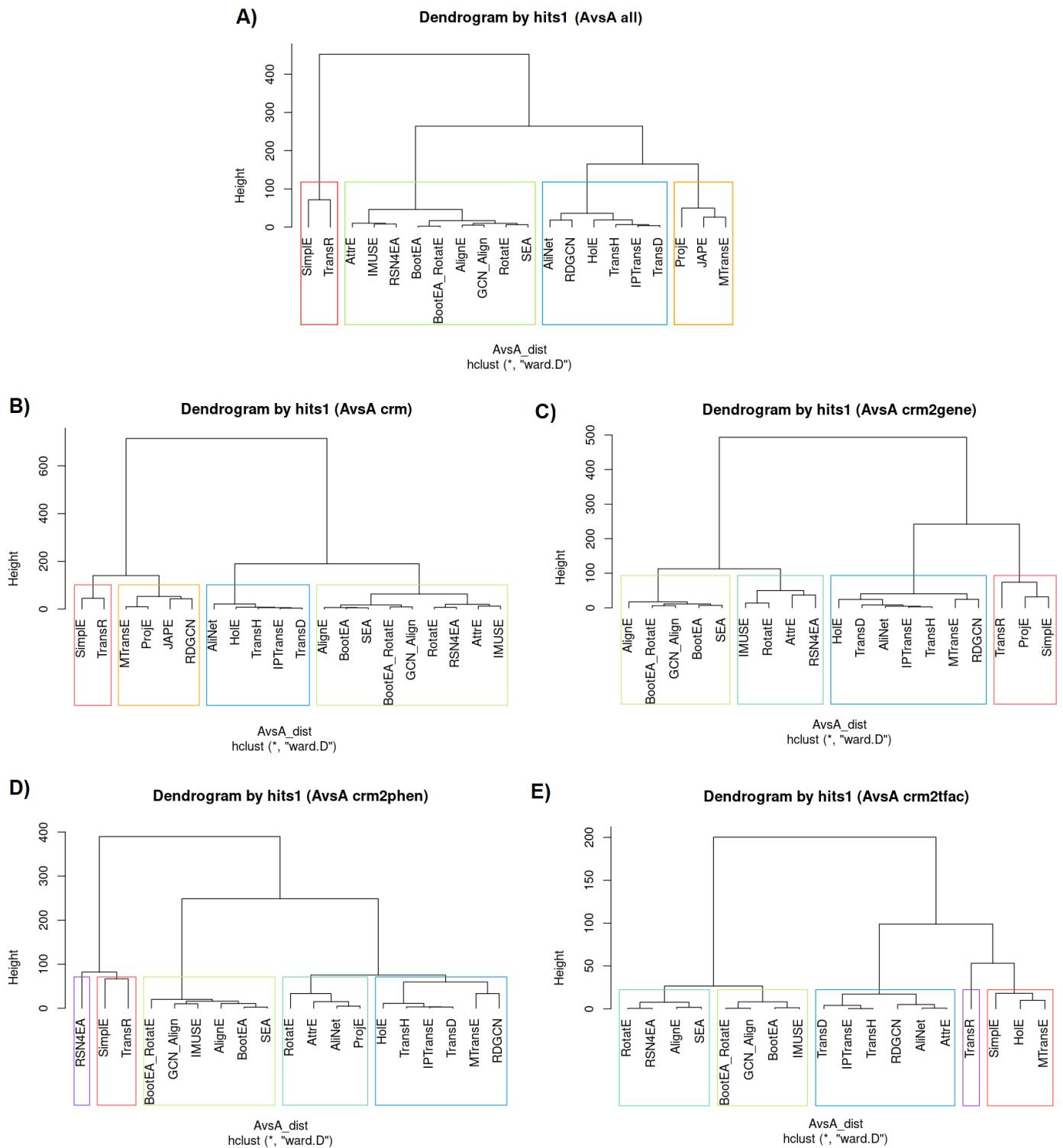


Figure 11. Dendrograms of methods using hits@1 values in AvsA type graph alignments using all the information from the source database (A), and subdomains of data: CRM sequences (B), relations between CRM and genes (C), relations between CRM and phenotypes (D), and relations between CRM and transcription factors (E).

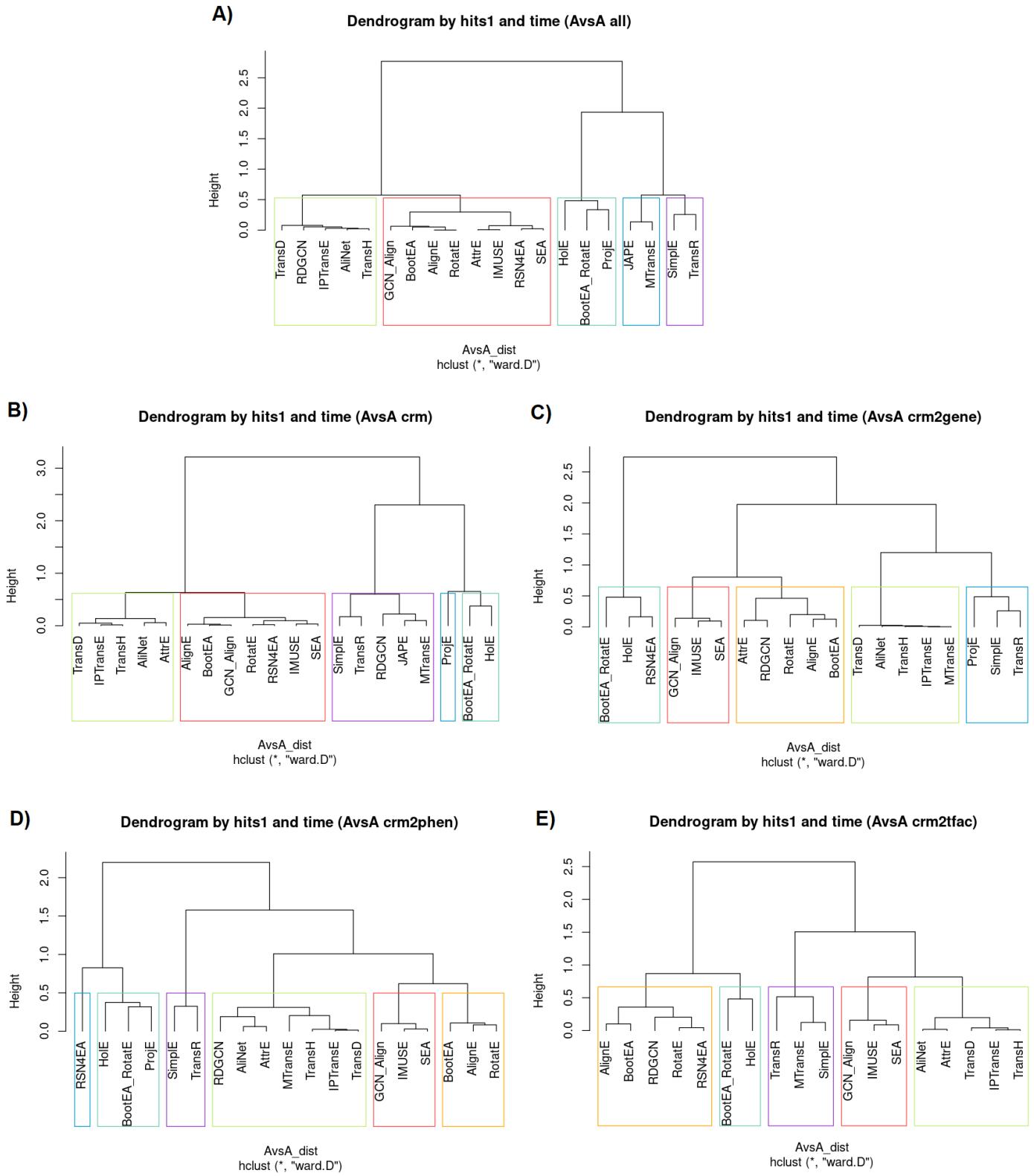
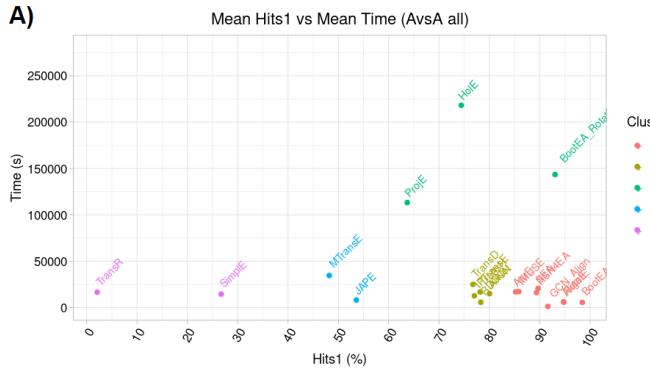
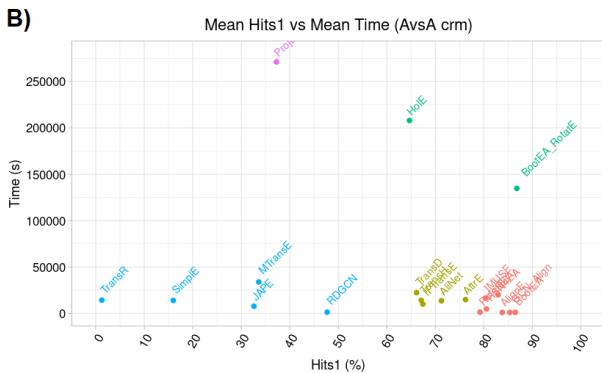
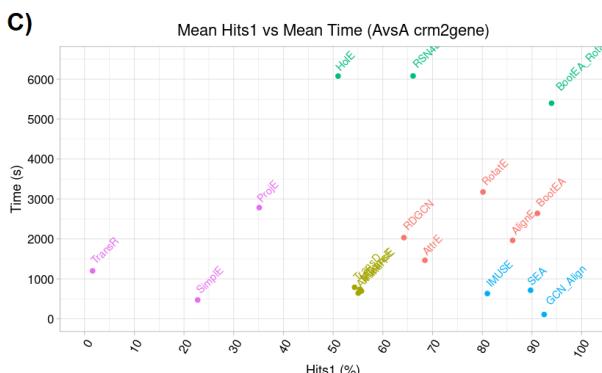
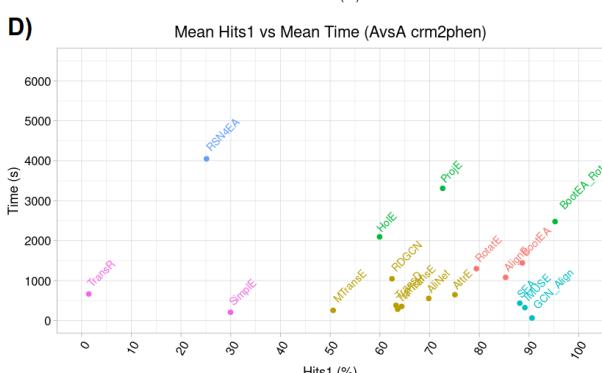
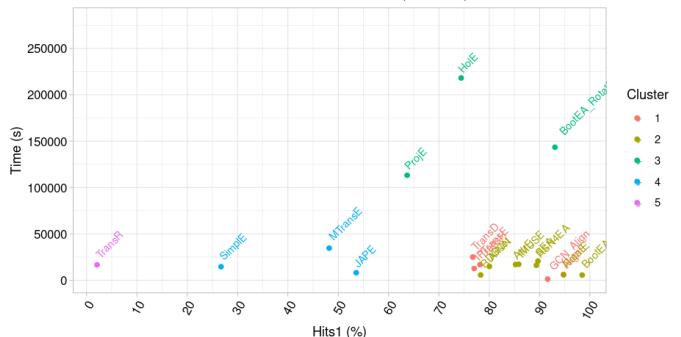


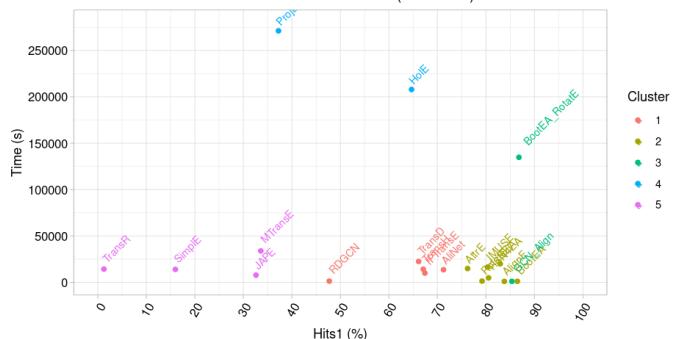
Figure 12. Dendrograms of methods using hits@1 and time values in AvsA type graph alignments with all data domain from the source databases (A), and subdomains of data: crm sequences (B), relations between crm and genes (C), relations between crm and phenotypes (D), and relations between crm and transcription factors (E).

A)**B)****C)****D)**

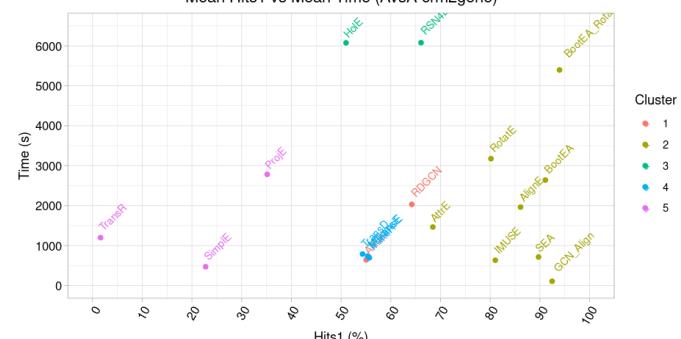
Mean Hits1 vs Mean Time (AvsA all)



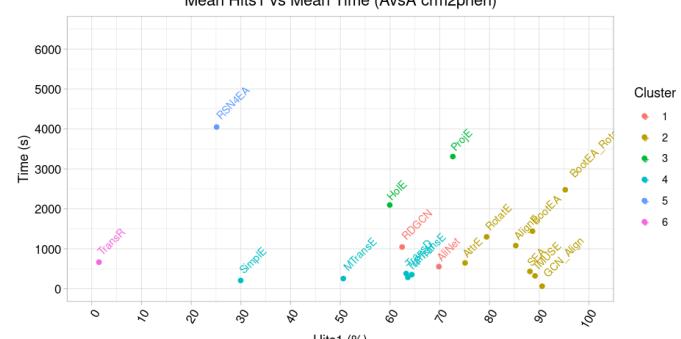
Mean Hits1 vs Mean Time (AvsA crm)



Mean Hits1 vs Mean Time (AvsA crm2gene)



Mean Hits1 vs Mean Time (AvsA crm2phen)



E)

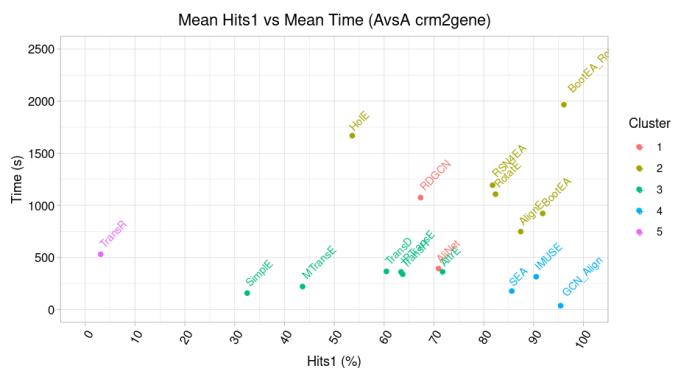
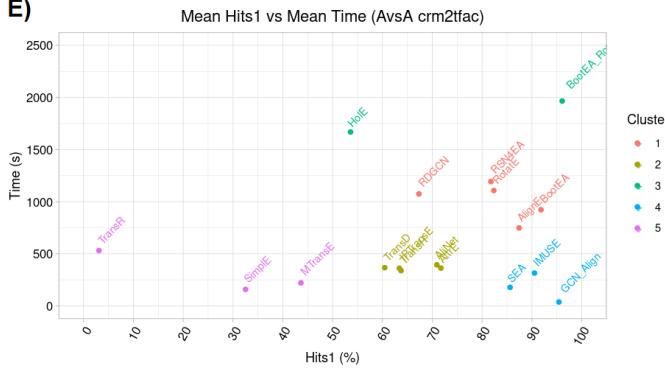
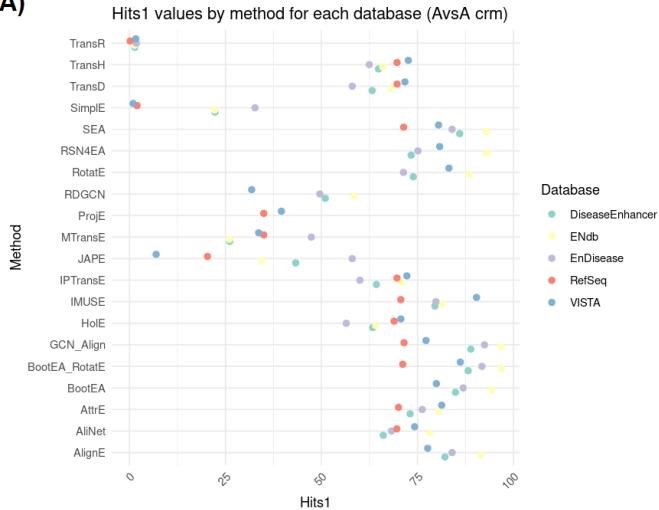


Figure 13. Left: Plot of methods grouped according to the clusters obtained in the dendograms by hits@1 and time values (Supplementary Figure 17), AvsA type graph alignments. Right: Plot of methods grouped according to the clusters obtained in the dendograms including all the alignment metrics (hits@1, hits@5, hits@10, mr, mrr, time). Each row corresponds to a different subdomain of data: all data (A), crm (B), crm2phen (C), crm2tfac (E).

A)

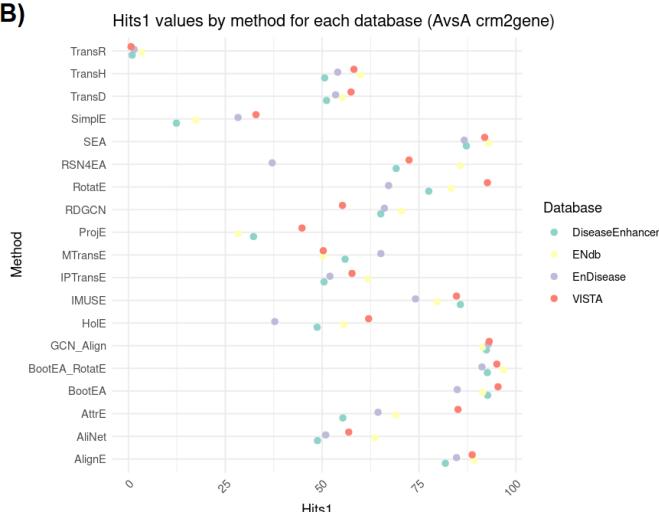


	database	first	second	third	fourth	fifth	weight
1	DiseaseEnhancer	0	4	7	8	1	10.8
2	ENdb	9	3	5	2	1	15.4
3	EnDisease	4	4	5	2	5	12
4	RefSeq	0	5	2	2	11	8.2
5	VISTA	7	4	1	6	2	13.6

	database	first	second	third	fourth	fifth	weight
1	DiseaseEnhancer	0	1	5	2	0	4.6
2	ENdb	6	2	0	0	0	7.6
3	EnDisease	0	4	3	1	0	5.4
4	RefSeq	0	0	0	0	8	1.6
5	VISTA	2	1	0	5	0	4.8

	database	first	second	third	fourth	fifth	weight
1	DiseaseEnhancer	0	1	2	2	0	2.8
2	ENdb	3	2	0	0	0	4.6
3	EnDisease	0	2	3	0	0	3.4
4	RefSeq	0	0	0	0	5	1
5	VISTA	2	0	0	3	0	3.2

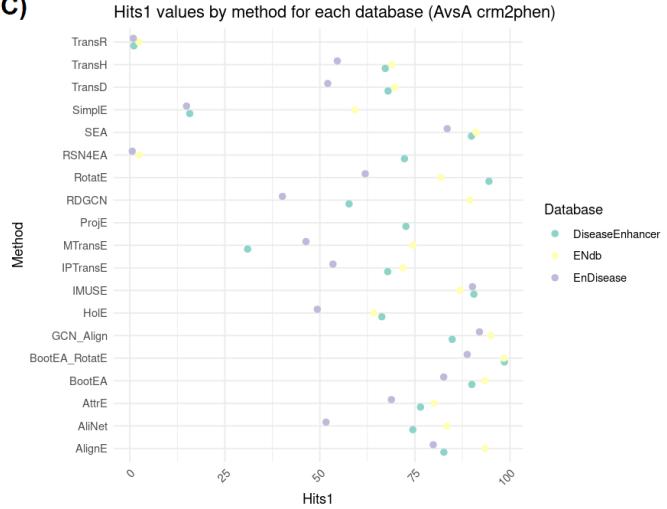
B)



	database	first	second	third	fourth	weight
1	DiseaseEnhancer	1	3	8	7	9
2	ENdb	9	4	4	2	14.5
3	EnDisease	1	4	6	8	9
4	VISTA	8	8	1	2	15

	database	first	second	third	fourth	weight
1	DiseaseEnhancer	1	1	4	2	4.25
2	ENdb	3	2	2	1	5.75
3	EnDisease	0	1	2	5	3
4	VISTA	4	4	0	0	7

	database	first	second	third	fourth	weight
1	DiseaseEnhancer	1	0	3	1	2.75
2	ENdb	2	1	1	1	3.5
3	EnDisease	0	1	1	3	2
4	VISTA	2	3	0	0	4.25

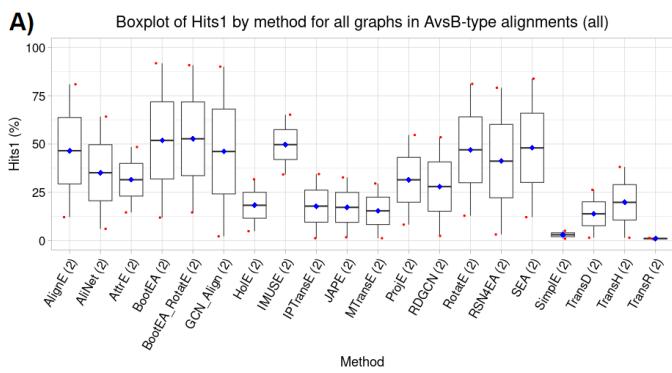
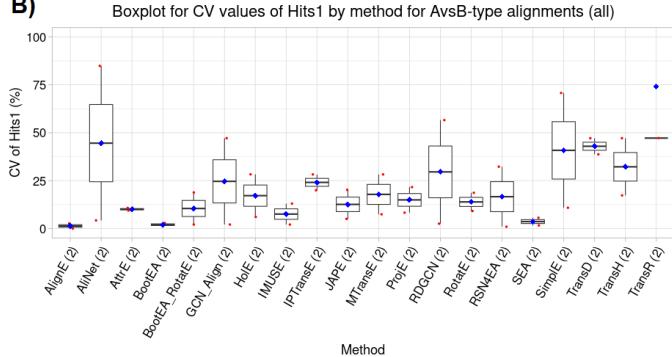
C

database	first	second	third	weight
1 DiseaseEnhancer	6	11	2	14
2 ENdb	13	5	1	16.67
3 EnDisease	0	3	16	7.33

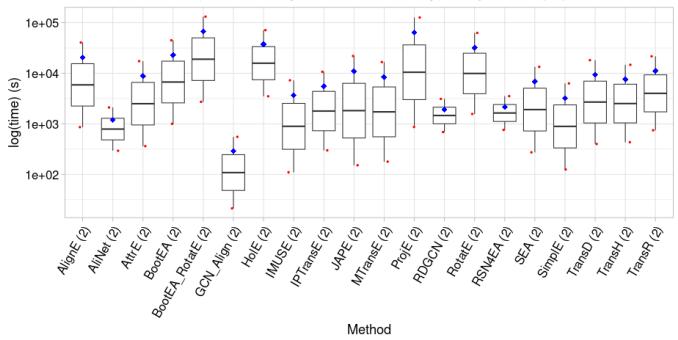
database	first	second	third	weight
1 DiseaseEnhancer	3	4	1	6
2 ENdb	5	2	1	6.67
3 EnDisease	0	2	6	3.33

database	first	second	third	weight
1 DiseaseEnhancer	2	2	1	3.67
2 ENdb	3	1	1	4
3 EnDisease	0	2	3	2.33

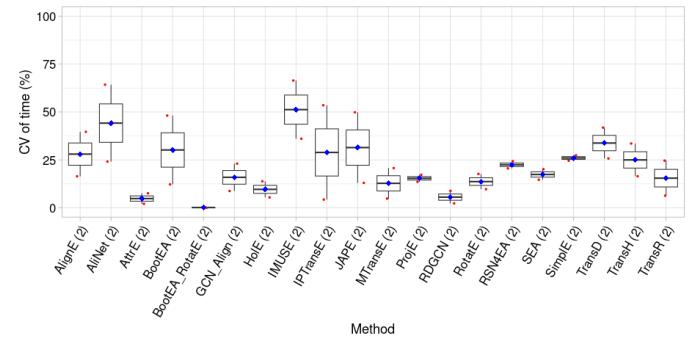
Figure 14. Left: Plot of hits@1 values by method and dataset in AvsA-type alignments, and considering different data subdomains of the datasets: crm sequences (A), relations crm2gene (B) and crm2phen (C). Right: Count the position of each method in a ranking by hits@1 values and different method combinations: all the methods (first table), eight methods (second table: GCN Align, SEA, IMUSE, BootEA, AlignE, RotatE, AttrE and BootEA-RotatE) and five methods (third table: GCN Align, SEA, IMUSE, AttrE and BootEA-RotatE).

A**B**

Boxplot of time by method for AvsB-type alignments (all)



Boxplot for CV values of time by method for AvsB-type alignments (all)



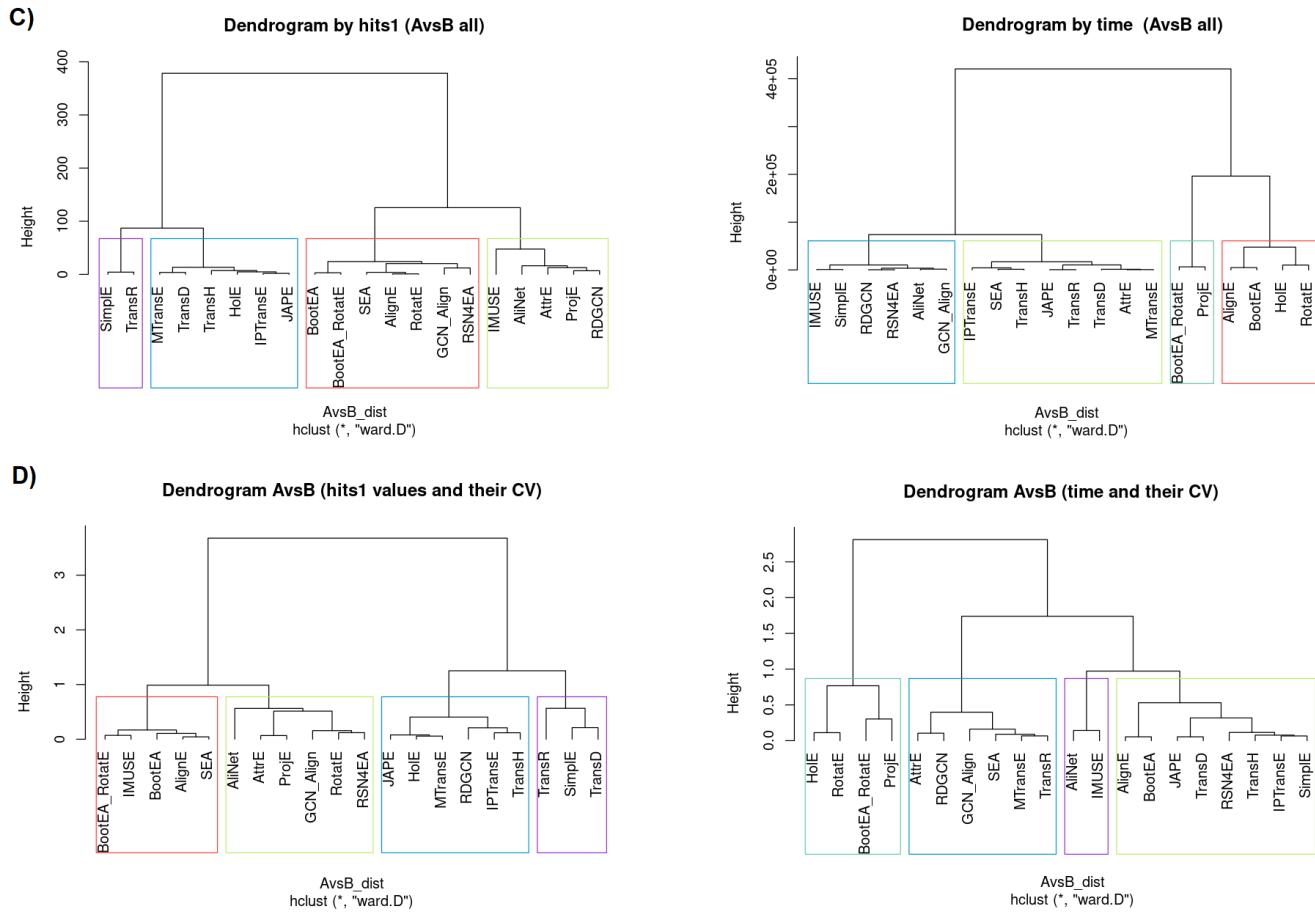


Figure 15. Results corresponding to AvsB-all alignments, and using two pairs: EnDisease-DiseaseEnhancer and RefSeq-VISTA. Left: hits@1 values. Right: Time values. A) Boxplot of hits@1 and time values. B) Coefficients of variation of hits@1 and time values. C) Dendrogram of methods with 4 clusters using hits@1 values and time values. D) Alternative dendrograms obtained by adding the coefficients of variation to the hits@1 and time values.

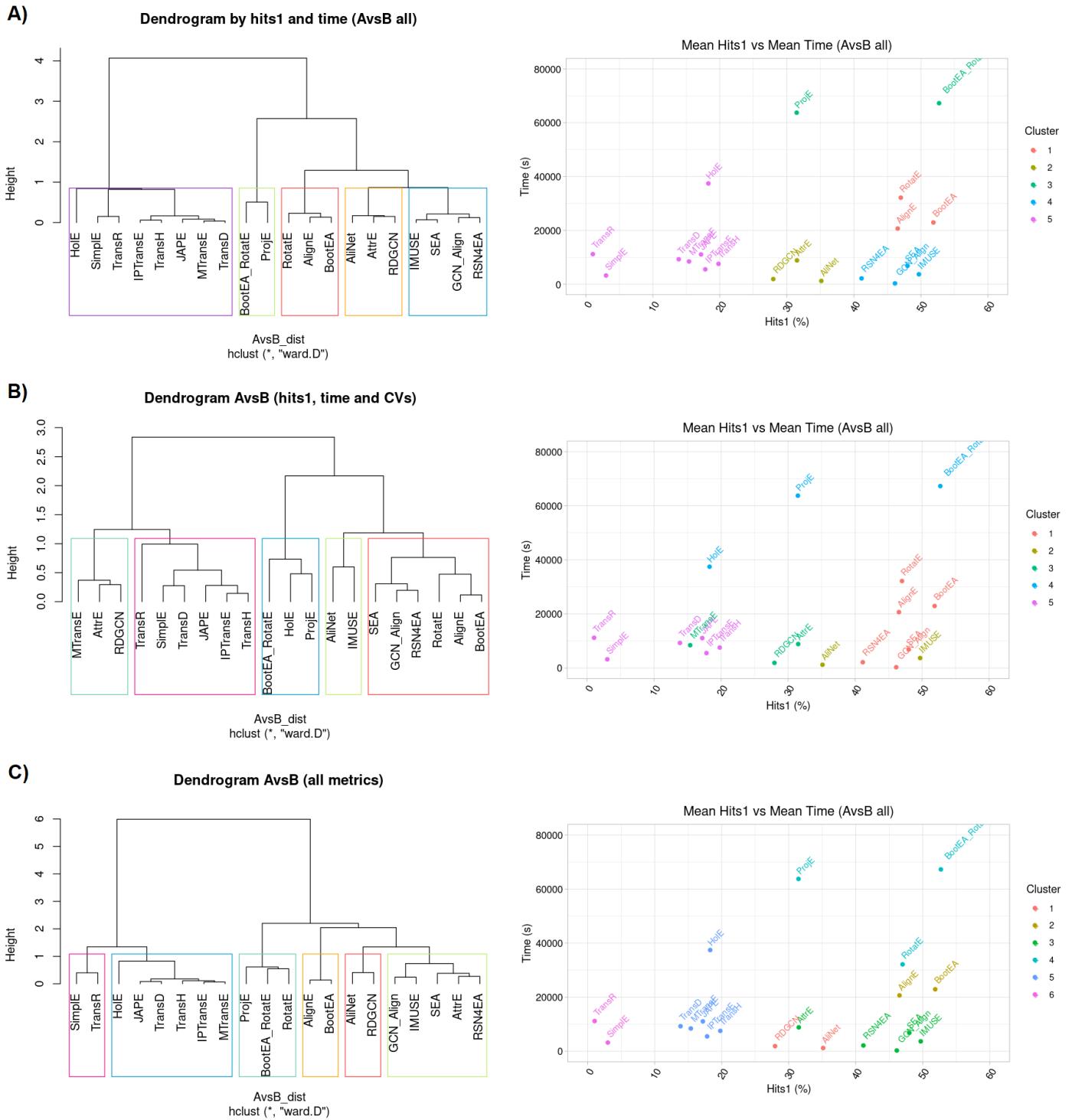


Figure 16. Clustering of methods using: hits@1 and time values (A); hits@1, time and their coefficients of variation (B); and using all metrics (hits@1, hits@5, hits@10, mr, mrr, time) (C). Values associated with AvsB-all alignments, using the pairs EnDisease-DiseaseEnhancer, and RefSeq-VISTA.

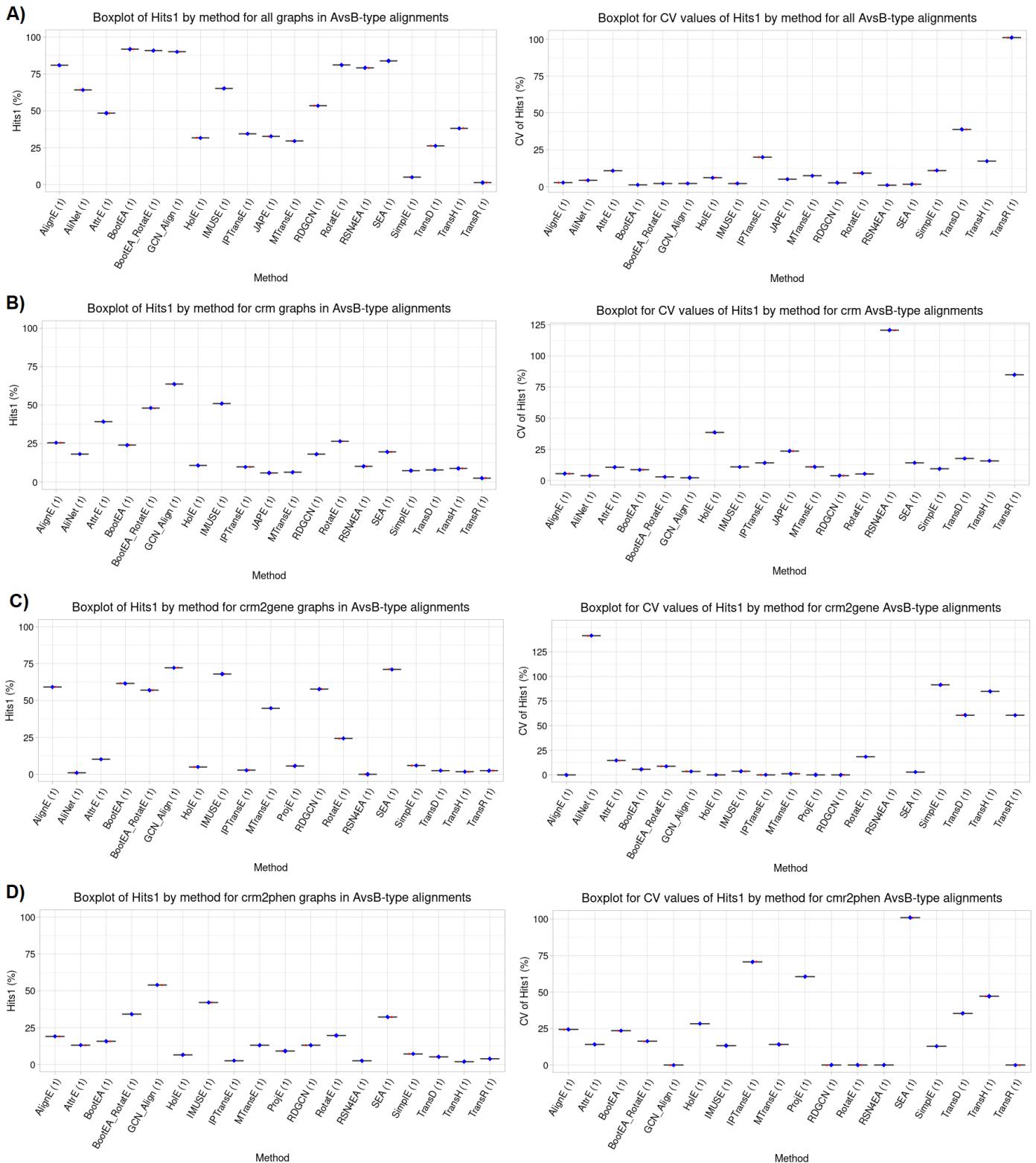


Figure 17. Boxplot for hits@1 values (left) and their coefficients of variation (right) in AvsB type alignments for EnDisease-DiseaseEnhancer, which is the pair that has different subgraphs and enough common entities to train a model. Values using all data (A) and the different subgraphs (B: crm, C: crm2gene, D: crm2phen).

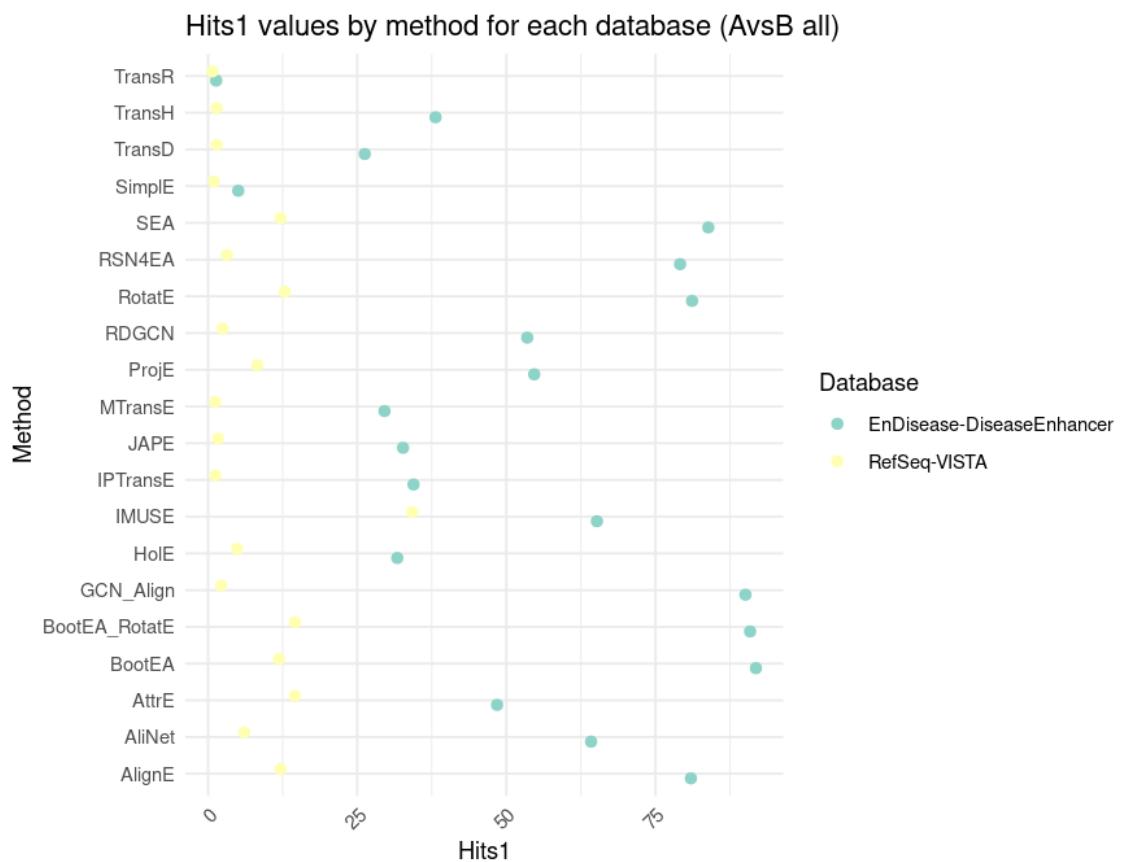


Figure 18. Plot of hits@1 values by method and dataset in AvsB-all alignments.

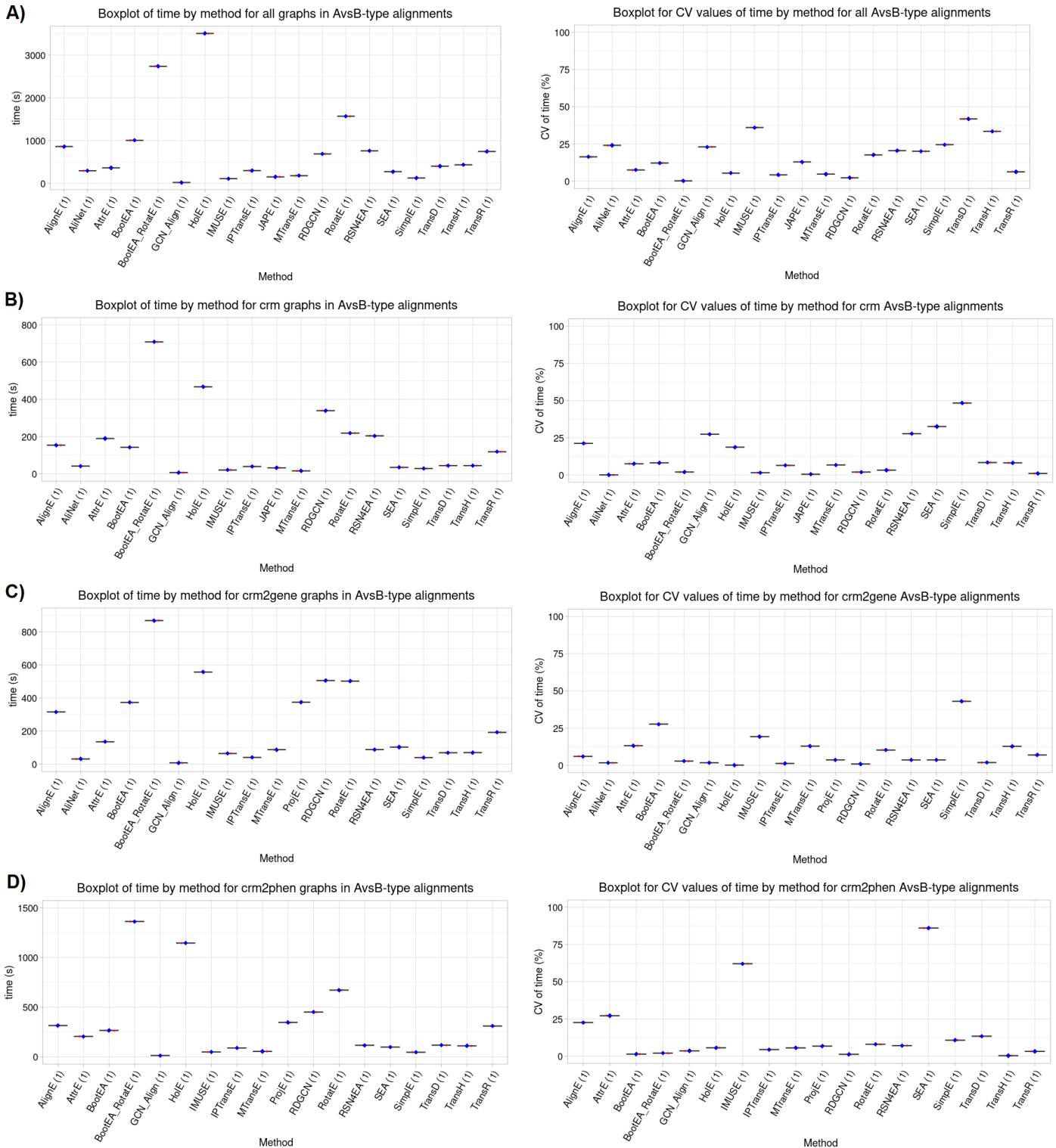


Figure 19. Plot for time values (left) and their coefficients of variation (right) in AvsB type alignments for EnDisease-DiseaseEnhancer, which is the pair that has different subgraphs and enough common entities to train a model. Values using all data (A) and the different subgraphs (B: crm, C: crm2gene, D: crm2phen).

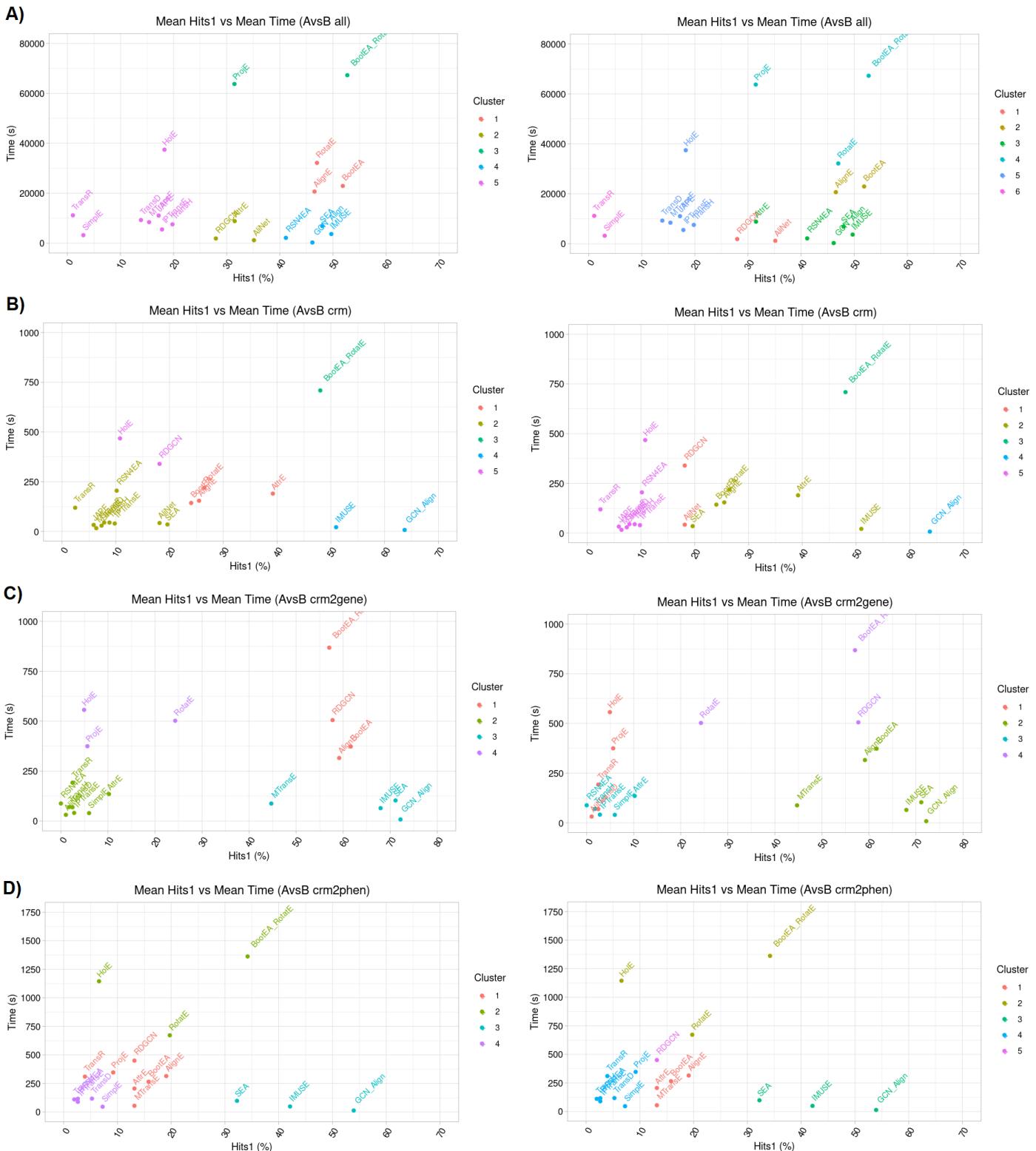


Figure 20. Left: Plot of methods grouped according to the clusters obtained in the dendograms by hits@1 and time values, AvsB type graph alignments. Right: Plot of methods grouped according to the clusters obtained in the dendograms including all the alignment metrics. Each row corresponds to a different subdomain of data: all data (A), crm (B), crm2gene (C), crm2phen (D). Note that the results of A correspond to the average obtained from two different alignments: EnDisease-DiseaseEnhancer and RefSeq-VISTA. On the contrary, B-D correspond to the results of EnDisease-DiseaseEnhancer.

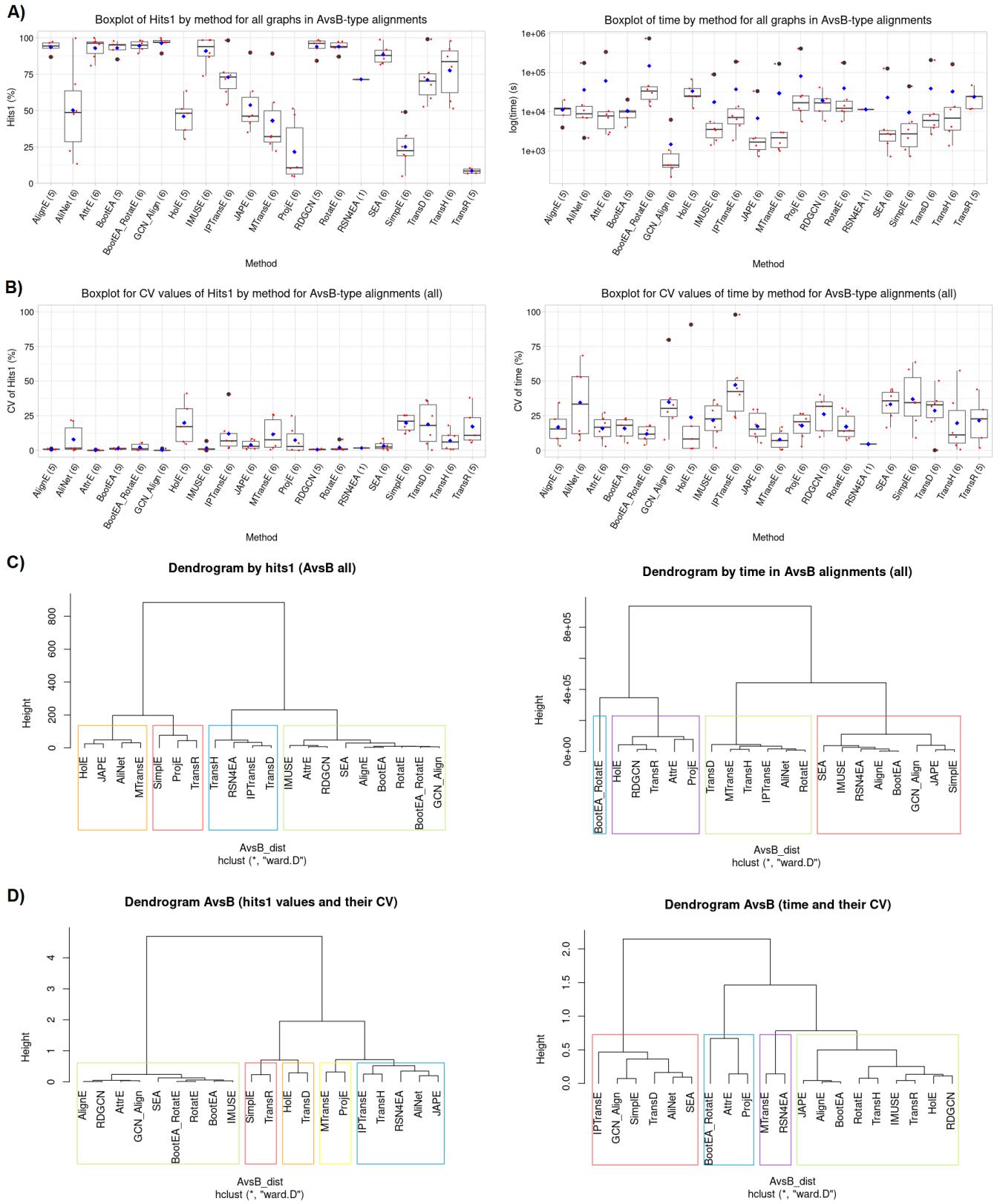
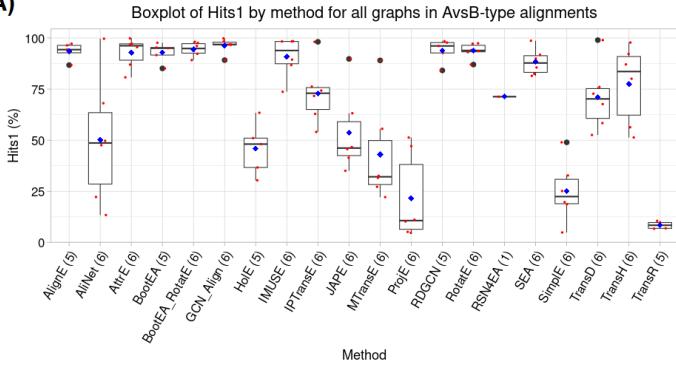
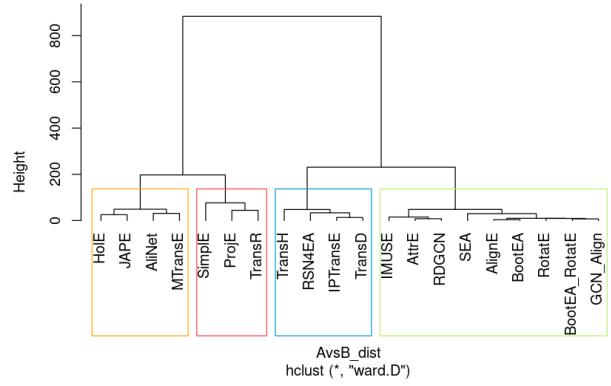
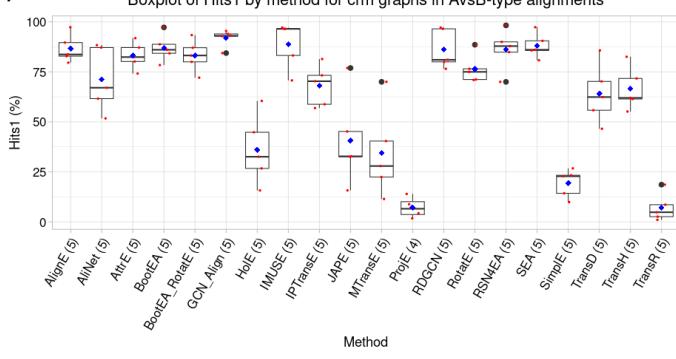


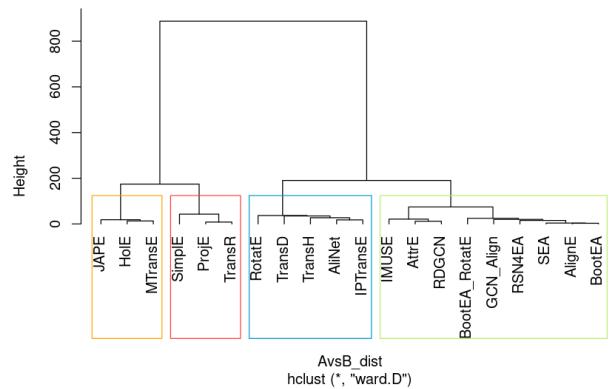
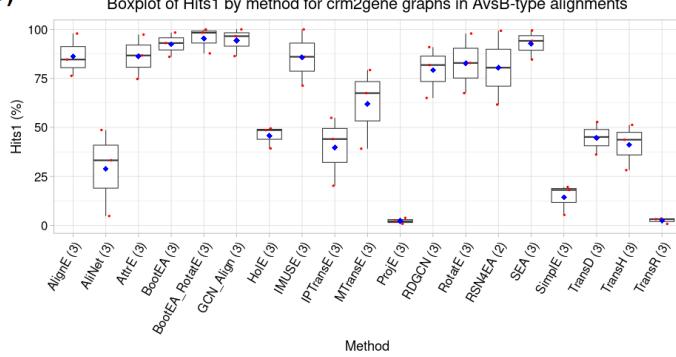
Figure 21. Results corresponding to modified AvsB-all alignments (A+B vs B+A). Left: hits@1 values. Right: Time values. A) Boxplot of hits@1, and time values. B) Boxplot of coefficients of variation of hits@1, and time values. C) Dendrogram of methods with 4 clusters using hits@1 values, and time values. D) Alternative dendograms obtained by adding the coefficients of variation to the hits@1, and time values.

A)

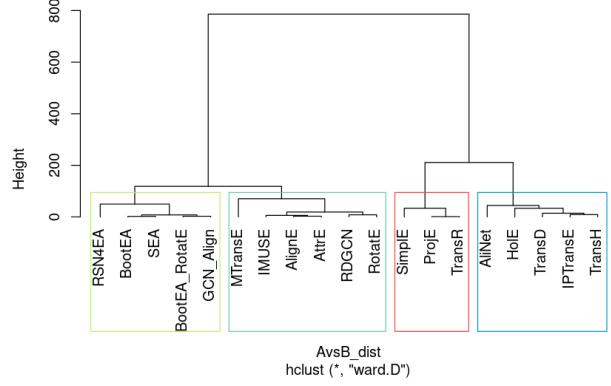
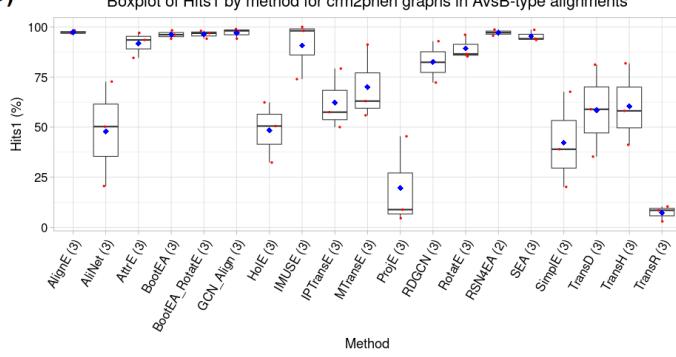
Dendrogram by hits1 (AvsB all)

**B)**

Dendrogram by hits1 (AvsB crm)

**C)**

Dendrogram by hits1 (AvsB crm2gene)

**D)**

Dendrogram by hits1 (AvsB crm2phen)

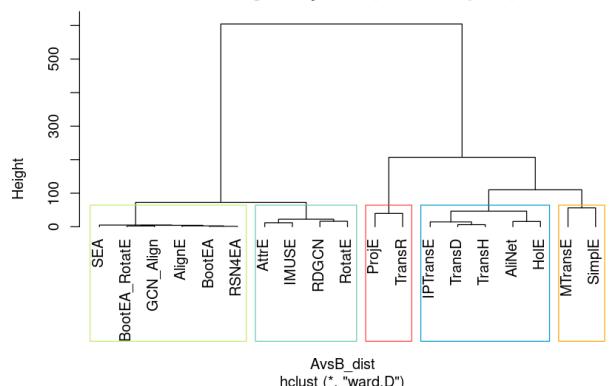
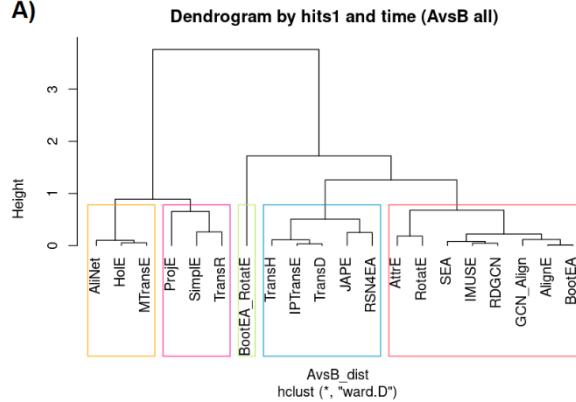
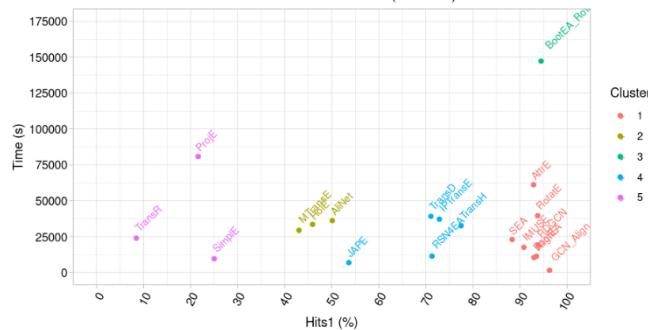
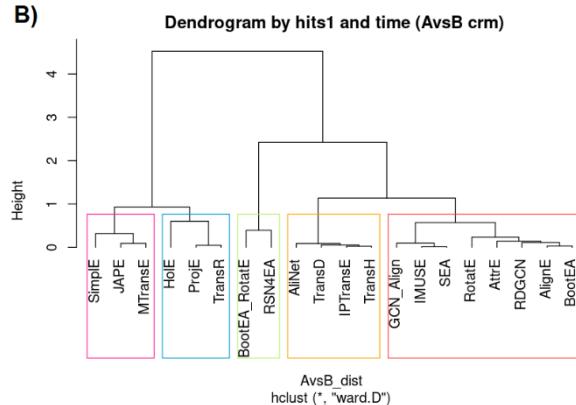


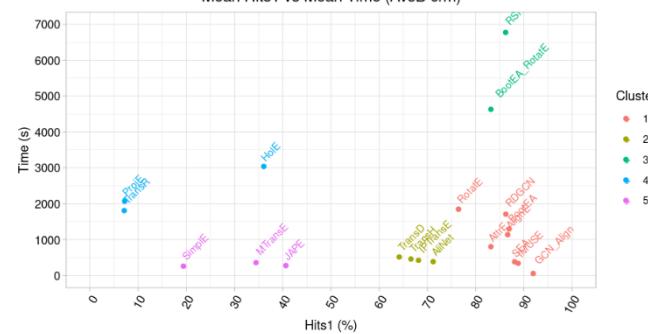
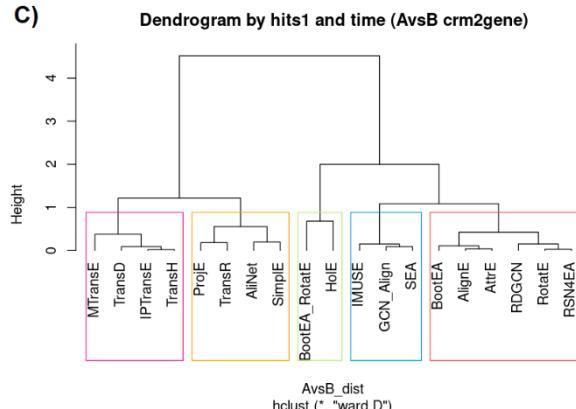
Figure 22. Boxplot and dendograms in modified AvsB alignments (A+B vs B+A) using hits@1 values and different data subdomains: all (A), crm (B), crm2gene (C) and crm2phen (D).

A)

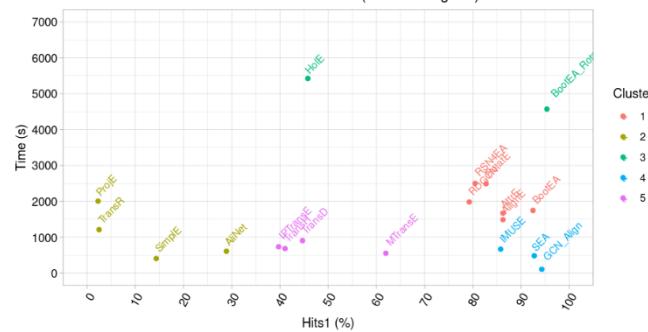
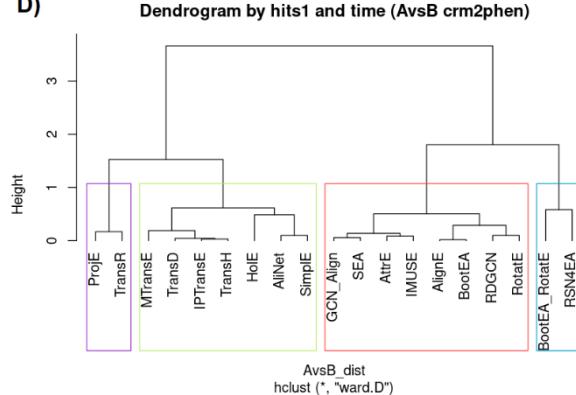
Mean Hits1 vs Mean Time (AvsB all)

**B)**

Mean Hits1 vs Mean Time (AvsB.crm)

**C)**

Mean Hits1 vs Mean Time (AvsB.crm2gene)

**D)**

Mean Hits1 vs Mean Time (AvsB.crm2phen)

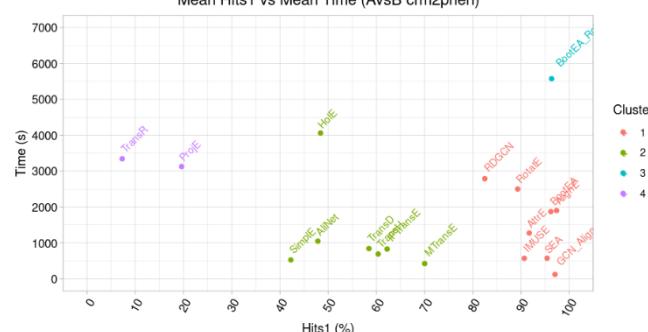


Figure 23. Clustering methods by hits@1 and time, using different data domains: all data (A), crm (B), crm2gene (C), and crm2phen (D). Modified AvsB alignments (A+B vs B+A).

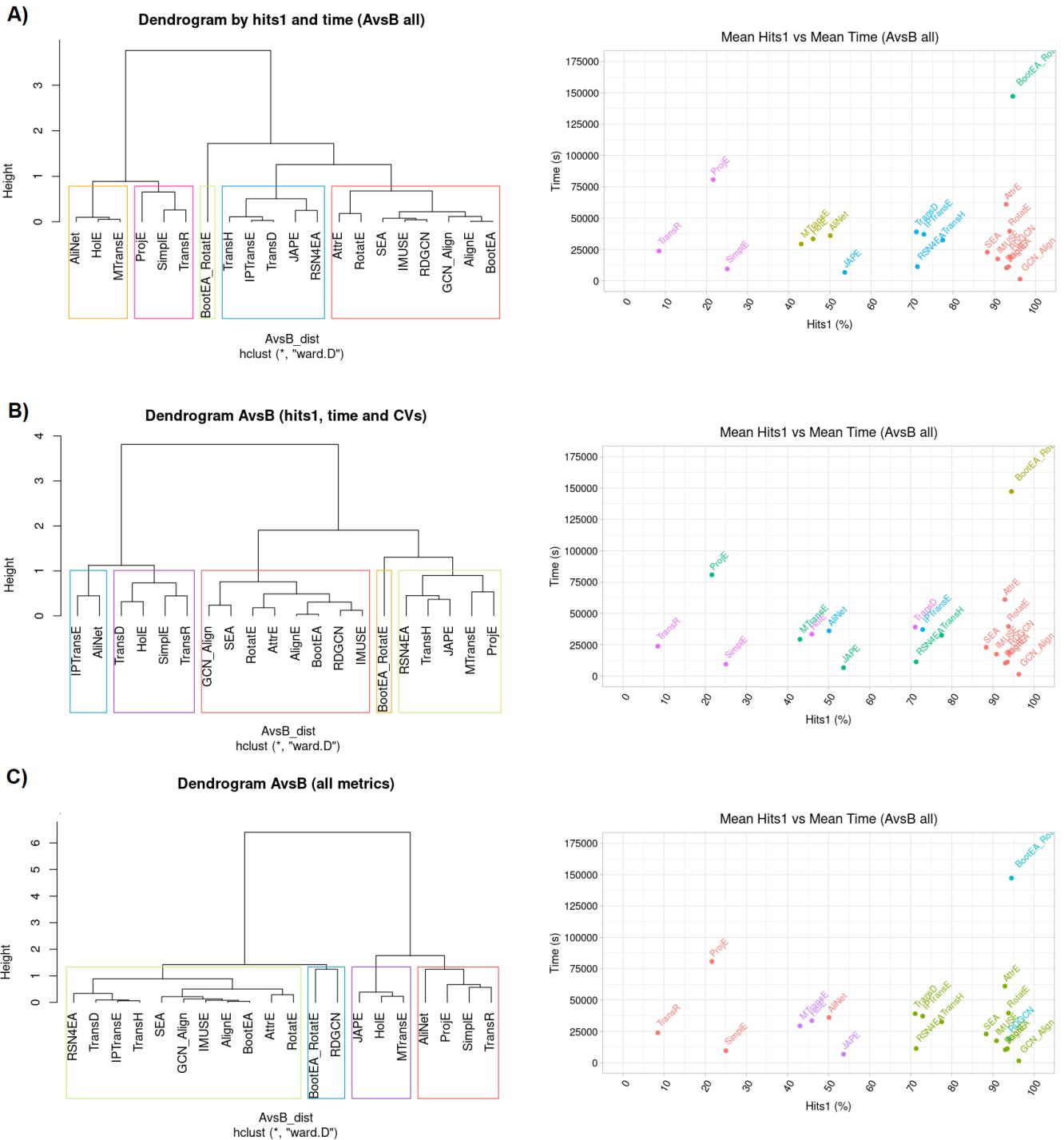


Figure 24. Clustering of methods, in modified AvsB alignments, by hits@1 and time values (A), and including CV values (B), and considering all alignment metrics (C).

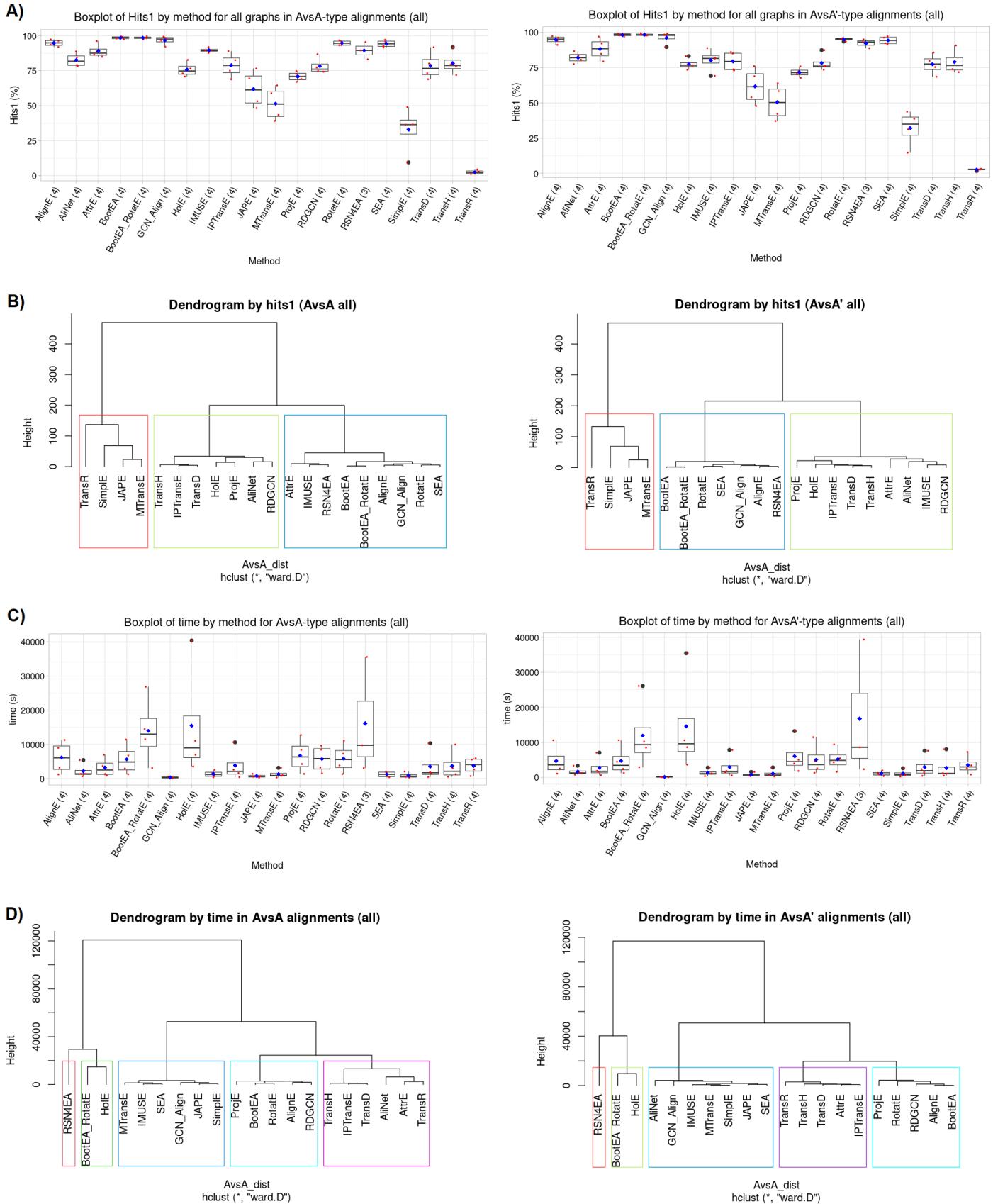


Figure 25. Boxplot and comparative dendrograms of hits@1 and time values between alignment results of AvsA (left) and AvsA' (right) type. All data domains were used.

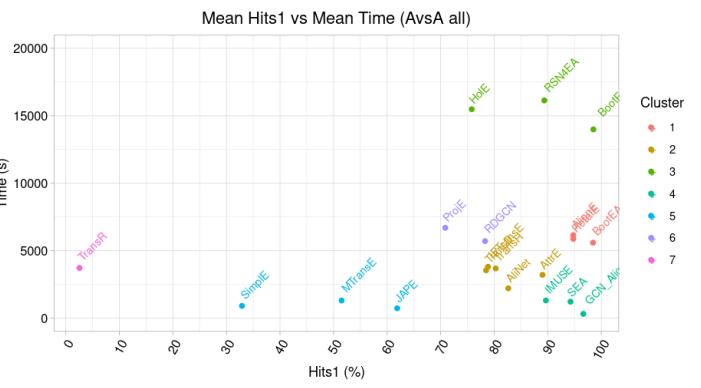
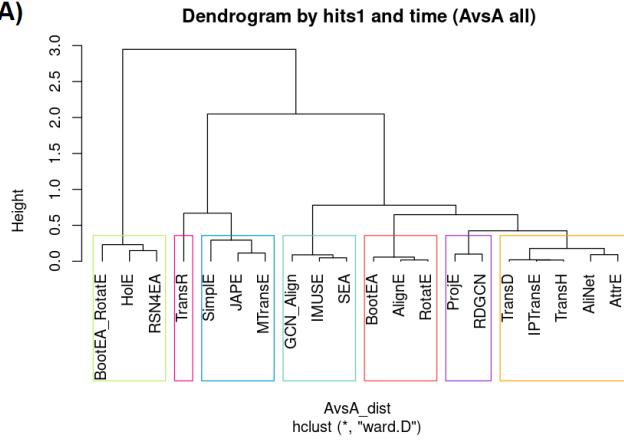
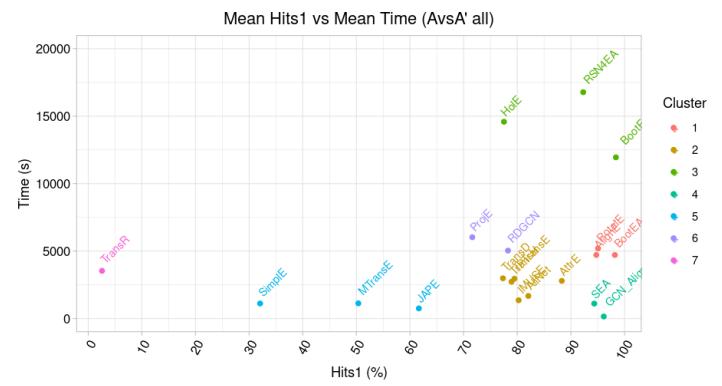
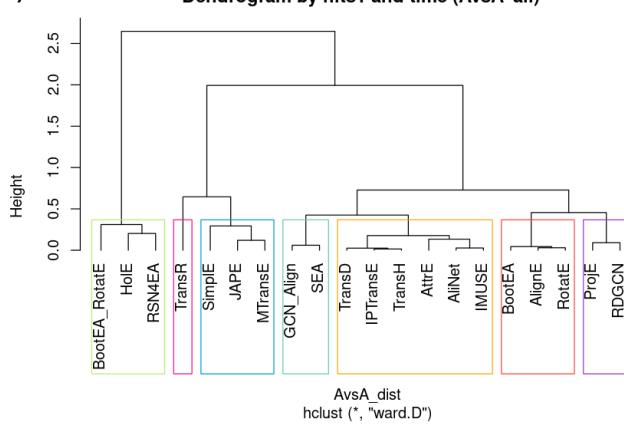
A)**B)**

Figure 26. Comparison of dendograms and plots of methods using hits@1 and time values. A) AvsA type alignments. B) AvsA' type alignments. All data domains were used.

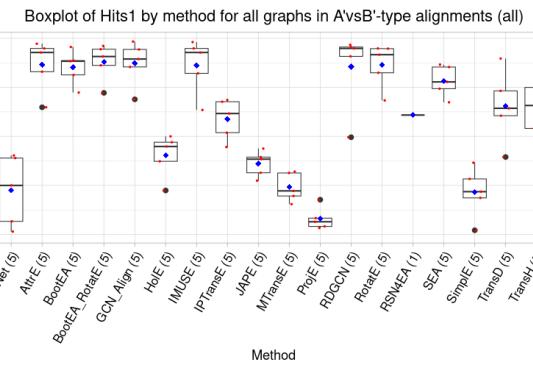
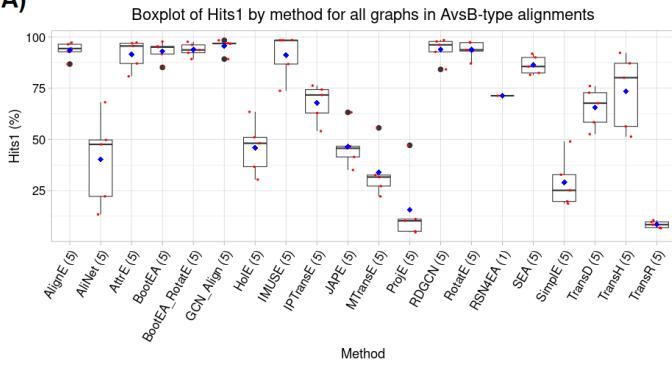
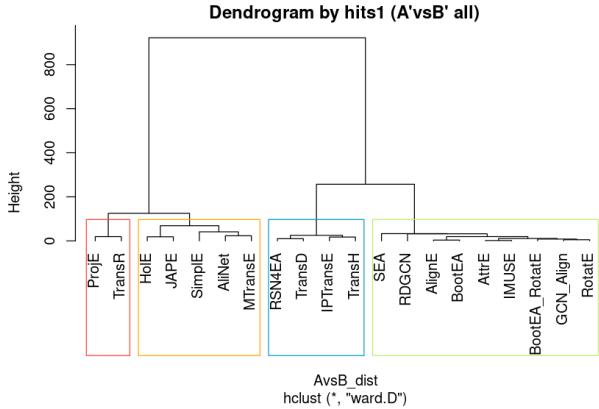
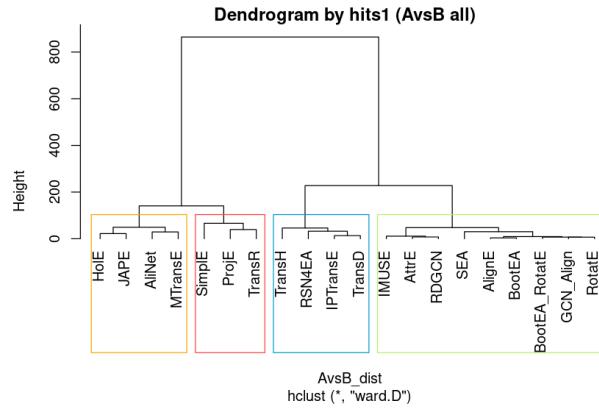
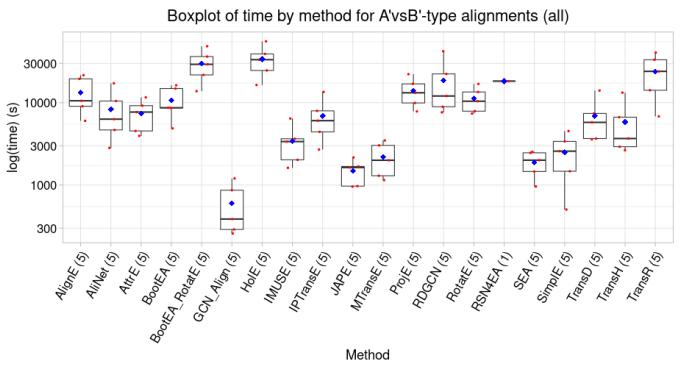
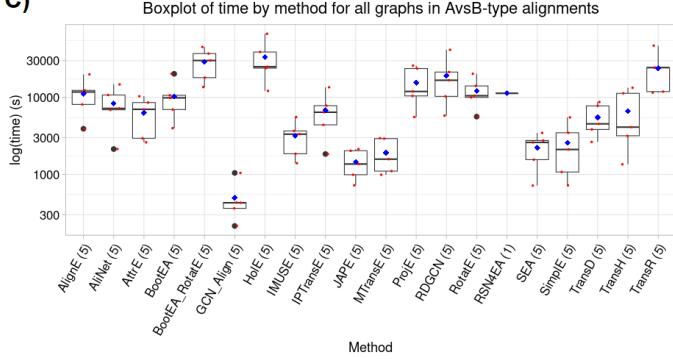
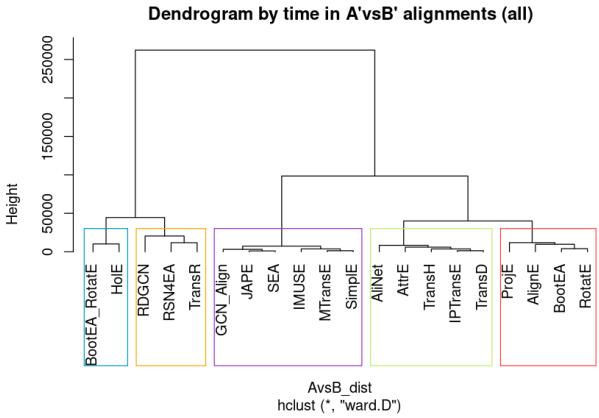
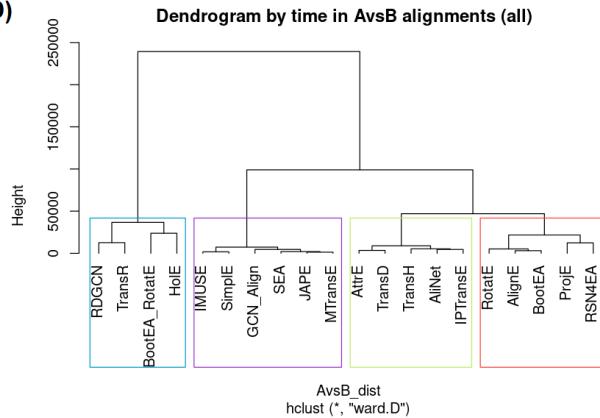
A)**B)****C)****D)**

Figure 27. Boxplot and comparative dendrograms of hits@1 and time values between alignment results of modified AvsB (left) and A'vsB' (right) type. All data domains were used.

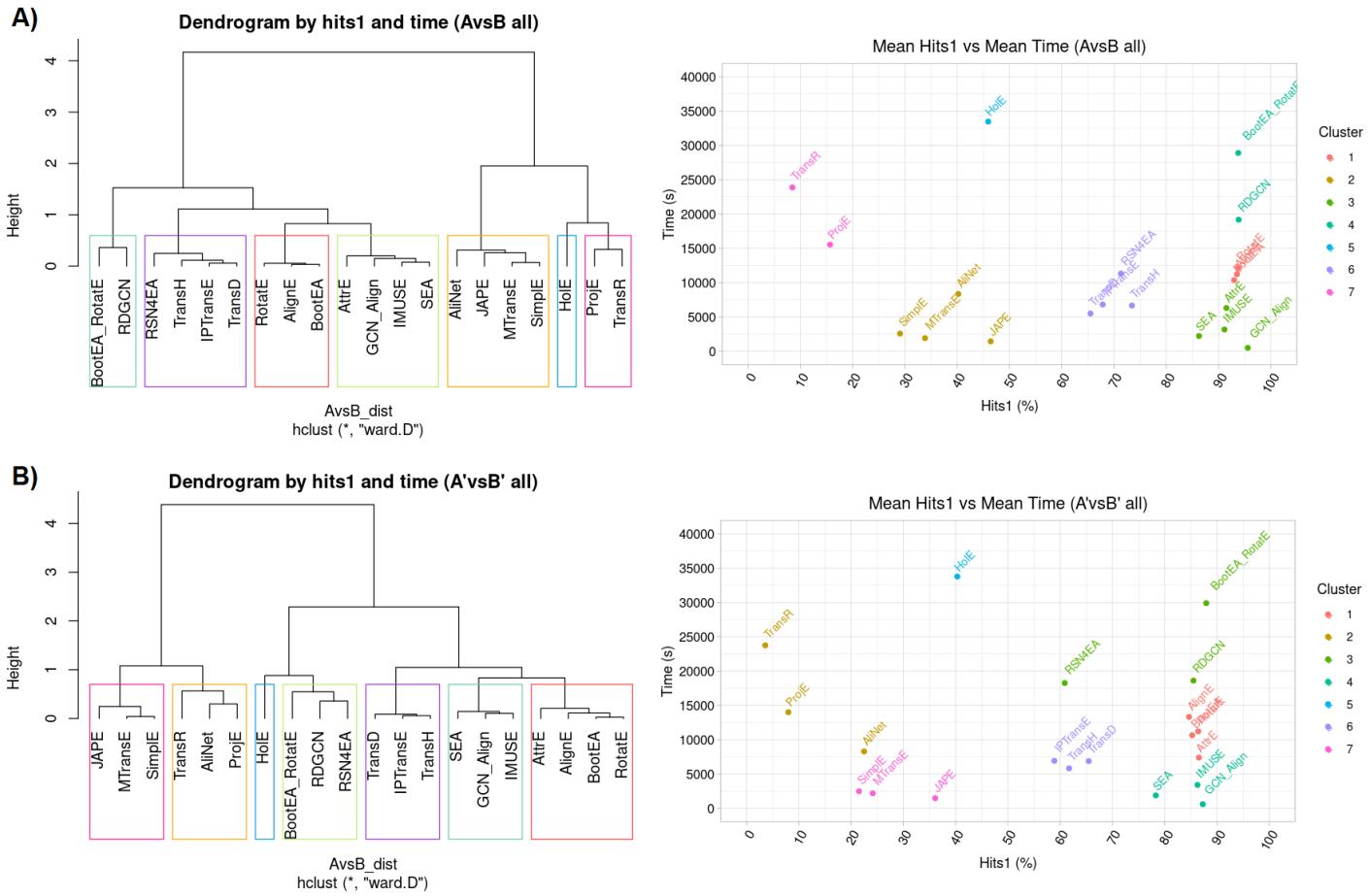


Figure 28. Comparison of dendograms and plots of methods using hits@1 and time values. A) Modified AvsB type alignments. B) A'vsB' type alignments. All data domains were used.