```
###################### DIST-1 (J,M:DEIB) ######################

#  1
AccRnaseq = SELECT(manually_curated__tumor_tag == "acc" AND
                   manually_curated__tissue_status == "tumoral"; at:CINECA)
                                               CINECA.HG19_TCGA_rnaseqv2_gene;

#  2
AccExp = COVER(1, ANY; aggregate: mean_exp as AVG(normalized_count); at:CINECA)
AccRnaseq;

#  3
AccExpFilt = SELECT(region: mean_exp > 1000; at:CINECA) AccExp;

#  4
Myc = SELECT(gcm_curated__cell_line == "H1-hESC" AND
             target__name == "MYC-human" AND
             file__output_type == "conservative idr thresholded peaks"; at:DEIB)
                                         DEIB.HG19_ENCODE_NARROW_2019_01;

#  5
GeneMyc = JOIN(dist < 0; output: left_distinct; at:DEIB) AccExpFilt Myc;

#  6
myMutation = SELECT(at:LOCAL) myMutation;

#  7
myMutationMerge = MERGE(at:LOCAL) myMutation;

#  8
GeneMycMut= MAP(count_name: mut_count; at:DEIB) GeneMyc myMutationMerge;

#  9
ResGenes = SELECT(region:mut_count > 0; at:DEIB) GeneMycMut;

# 10
MATERIALIZE ResGenes INTO ResGenes;

###################### DIST-1 (J,M:DEIB) ######################
```

```
######################## DIST-2 (J,M:CINECA) ########################

#  1
AccRnaseq = SELECT(manually_curated__tumor_tag == "acc" AND
                   manually_curated__tissue_status == "tumoral"; at:CINECA)
                                              CINECA.HG19_TCGA_rnaseqv2_gene;

#  2
AccExp = COVER(1, ANY; aggregate: mean_exp as AVG(normalized_count); at:CINECA)
AccRnaseq;

#  3
AccExpFilt = SELECT(region: mean_exp > 1000; at:CINECA) AccExp;

#  4
Myc = SELECT(gcm_curated__cell_line == "H1-hESC" AND
             target__name == "MYC-human" AND
             file__output_type == "conservative idr thresholded peaks"; at:DEIB)
                                          DEIB.HG19_ENCODE_NARROW_2019_01;

#  5
GeneMyc = JOIN(dist < 0; output: left_distinct; at:CINECA) AccExpFilt Myc;

#  6
myMutation = SELECT(at:LOCAL) myMutation;

#  7
myMutationMerge = MERGE(at:LOCAL) myMutation;

#  8
GeneMycMut= MAP(count_name: mut_count; at:CINECA) GeneMyc myMutationMerge;

#  9
ResGenes = SELECT(region:mut_count > 0; at:CINECA) GeneMycMut;

# 10
MATERIALIZE ResGenes INTO ResGenes;

######################## DIST-2 (J,M:CINECA) ########################
```

```
###################### DIST-3 (J:DEIB,M:GECO) ######################

#  1
AccRnaseq = SELECT(manually_curated__tumor_tag == "acc" AND
                   manually_curated__tissue_status == "tumoral"; at:CINECA)
                                               CINECA.HG19_TCGA_rnaseqv2_gene;

#  2
AccExp = COVER(1, ANY; aggregate: mean_exp as AVG(normalized_count); at:CINECA)
AccRnaseq;

#  3
AccExpFilt = SELECT(region: mean_exp > 1000; at:CINECA) AccExp;

#  4
Myc = SELECT(gcm_curated__cell_line == "H1-hESC" AND
             target__name == "MYC-human" AND
             file__output_type == "conservative idr thresholded peaks"; at:DEIB)
                                               DEIB.HG19_ENCODE_NARROW_2019_01;

#  5
GeneMyc = JOIN(dist < 0; output: left_distinct; at:DEIB) AccExpFilt Myc;

#  6
myMutation = SELECT(at:GeCo ) myMutation;

#  7
myMutationMerge = MERGE(at:LOCAL) myMutation;

#  8
GeneMycMut= MAP(count_name: mut_count; at:LOCAL) GeneMyc myMutationMerge;

#  9
ResGenes = SELECT(region:mut_count > 0; at:LOCAL) GeneMycMut;

# 10
MATERIALIZE ResGenes INTO ResGenes;

###################### DIST-3 (J:DEIB,M:GECO) ######################
```

```
####################### DIST-4 (J:CINECA,M:GECO) #######################

#  1
AccRnaseq = SELECT(manually_curated__tumor_tag == "acc" AND
                   manually_curated__tissue_status == "tumoral"; at:CINECA)
                                               CINECA.HG19_TCGA_rnaseqv2_gene;

#  2
AccExp = COVER(1, ANY; aggregate: mean_exp as AVG(normalized_count); at:CINECA)
AccRnaseq;

#  3
AccExpFilt = SELECT(region: mean_exp > 1000; at:CINECA) AccExp;

#  4
Myc = SELECT(gcm_curated__cell_line == "H1-hESC" AND
             target__name == "MYC-human" AND
             file__output_type == "conservative idr thresholded peaks"; at:DEIB)
                                         DEIB.HG19_ENCODE_NARROW_2019_01;

#  5
GeneMyc = JOIN(dist < 0; output: left_distinct; at:CINECA) AccExpFilt Myc;

#  6
myMutation = SELECT(at:GeCo ) myMutation;

#  7
myMutationMerge = MERGE(at:LOCAL) myMutation;

#  8
GeneMycMut= MAP(count_name: mut_count; at:LOCAL) GeneMyc myMutationMerge;

#  9
ResGenes = SELECT(region:mut_count > 0; at:LOCAL) GeneMycMut;

# 10
MATERIALIZE ResGenes INTO ResGenes;

####################### DIST-4 (J:CINECA,M:GECO) #######################
```

```
####################### CENT-1 (DEIB) #######################

#  1
AccRnaseq = SELECT(manually_curated__tumor_tag == "acc" AND
                   manually_curated__tissue_status == "tumoral"; at:CINECA)
                                               CINECA.HG19_TCGA_rnaseqv2_gene;


#  2
AccExp = COVER(1, ANY; aggregate: mean_exp as AVG(normalized_count); at:DEIB) AccRnaseq;


#  3
AccExpFilt = SELECT(region: mean_exp > 1000; at:DEIB) AccExp;


#  4
Myc = SELECT(gcm_curated__cell_line == "H1-hESC" AND
             target__name == "MYC-human" AND
             file__output_type == "conservative idr thresholded peaks"; at:DEIB)
                                               DEIB.HG19_ENCODE_NARROW_2019_01;


#  5
GeneMyc = JOIN(dist < 0; output: left_distinct; at:DEIB) AccExpFilt Myc;


#  6
myMutation = SELECT(at:LOCAL) myMutation;


#  7
myMutationMerge = MERGE(at:DEIB) myMutation;


#  8
GeneMycMut= MAP(count_name: mut_count; at:DEIB) GeneMyc myMutationMerge;


#  9
ResGenes = SELECT(region:mut_count > 0; at:DEIB) GeneMycMut;


# 10
MATERIALIZE ResGenes INTO ResGenes;

####################### CENT-1 (DEIB) #######################
```

```
###################### CENT-2 (CINECA) ######################

#  1
AccRnaseq = SELECT(manually_curated__tumor_tag == "acc" AND
                   manually_curated__tissue_status == "tumoral"; at:CINECA)
                                        CINECA.HG19_TCGA_rnaseqv2_gene;

#  2
AccExp = COVER(1, ANY; aggregate: mean_exp as AVG(normalized_count); at:CINECA)
AccRnaseq;

#  3
AccExpFilt = SELECT(region: mean_exp > 1000; at:CINECA) AccExp;

#  4
Myc = SELECT(gcm_curated__cell_line == "H1-hESC" AND
             target__name == "MYC-human" AND
             file__output_type == "conservative idr thresholded peaks"; at:DEIB)
                                        DEIB.HG19_ENCODE_NARROW_2019_01;

#  5
GeneMyc = JOIN(dist < 0; output: left_distinct; at:CINECA) AccExpFilt Myc;

#  6
myMutation = SELECT(at:LOCAL) myMutation;

#  7
myMutationMerge = MERGE(at:CINECA) myMutation;

#  8
GeneMycMut= MAP(count_name: mut_count; at:CINECA) GeneMyc myMutationMerge;

#  9
ResGenes = SELECT(region:mut_count > 0; at:CINECA) GeneMycMut;

# 10
MATERIALIZE ResGenes INTO ResGenes;

###################### CENT-2 (CINECA) ######################
```

```
####################### CENT-3 (GECO) #######################

#  1
AccRnaseq = SELECT(manually_curated__tumor_tag == "acc" AND
                   manually_curated__tissue_status == "tumoral"; at:CINECA)
                                           CINECA.HG19_TCGA_rnaseqv2_gene;

#  2
AccExp = COVER(1, ANY; aggregate: mean_exp as AVG(normalized_count); at:LOCAL) AccRnaseq;

#  3
AccExpFilt = SELECT(region: mean_exp > 1000; at:LOCAL) AccExp;

#  4
Myc = SELECT(gcm_curated__cell_line == "H1-hESC" AND
             target__name == "MYC-human" AND
             file__output_type == "conservative idr thresholded peaks"; at:DEIB)
                                       DEIB.HG19_ENCODE_NARROW_2019_01;

#  5
GeneMyc = JOIN(dist < 0; output: left_distinct; at:LOCAL) AccExpFilt Myc;

#  6
myMutation = SELECT(at:LOCAL) myMutation;

#  7
myMutationMerge = MERGE(at:LOCAL) myMutation;

#  8
GeneMycMut= MAP(count_name: mut_count; at:LOCAL) GeneMyc myMutationMerge;

#  9
ResGenes = SELECT(region:mut_count > 0; at:LOCAL) GeneMycMut;

# 10
MATERIALIZE ResGenes INTO ResGenes;

####################### CENT-3 (GECO) #######################
```

```
###################### BEST ######################

#  1
AccRnaseq = SELECT(manually_curated__tumor_tag == "acc" AND
                   manually_curated__tissue_status == "tumoral"; at:CINECA)
                                               CINECA.HG19_TCGA_rnaseqv2_gene;


#  2
AccExp = COVER(1, ANY; aggregate: mean_exp as AVG(normalized_count); at:CINECA)
AccRnaseq;

#  3
AccExpFilt = SELECT(region: mean_exp > 1000; at:LOCAL) AccExp;

#  4
Myc = SELECT(gcm_curated__cell_line == "H1-hESC" AND
             target__name == "MYC-human" AND
             file__output_type == "conservative idr thresholded peaks"; at:DEIB)
                                        DEIB.HG19_ENCODE_NARROW_2019_01;

#  5
GeneMyc = JOIN(dist < 0; output: left_distinct; at:LOCAL) AccExpFilt Myc;

#  6
myMutation = SELECT(at:LOCAL) myMutation;

#  7
myMutationMerge = MERGE(at:LOCAL) myMutation;

#  8
GeneMycMut= MAP(count_name: mut_count; at:LOCAL) GeneMyc myMutationMerge;

#  9
ResGenes = SELECT(region:mut_count > 0; at:LOCAL) GeneMycMut;

# 10
MATERIALIZE ResGenes INTO ResGenes;

###################### BEST ######################
```

The log file of run of the Best execution

```
2019-07-29 15:49:38,350 Starting Federated query job_canakoglu_best_20190729_154937
2019-07-29 15:49:38,350 Splitting the computation DAG
2019-07-29 15:49:38,359 Getting DAGs to execute remotely
2019-07-29 15:49:38,363 Starting the federated query
2019-07-29 15:49:38,387 Sending sub-query to CINECA
2019-07-29 15:50:34,404 Execution time at remote (CINECA): 56 s.
2019-07-29 15:50:34,404 Moving temp_0 (metadata) from CINECA to LOCAL
2019-07-29 15:50:35,427 Execution time of moving from CINECA to LOCAL: 1 s.
2019-07-29 15:50:35,450 Sending sub-query to CINECA
2019-07-29 15:55:16,591 Execution time at remote (CINECA): 281s.
2019-07-29 15:55:16,591 Moving temp_1 (region) from CINECA to LOCAL
2019-07-29 15:55:19,616 Execution time of moving from CINECA to LOCAL: 3 s.
2019-07-29 15:55:19,638 Sending sub-query to DEIB
2019-07-29 15:55:58,969 Execution time at remote (DEIB): 39s.
2019-07-29 15:55:58,969 Moving temp_2 (metadata) from DEIB to LOCAL
2019-07-29 15:55:59,990 Execution time of moving from DEIB to LOCAL: 1 s.
2019-07-29 15:56:00,011 Sending sub-query to DEIB
2019-07-29 15:56:46,803 Execution time at remote (DEIB): 46s.
2019-07-29 15:56:46,803 Moving temp_3 (region) from DEIB to LOCAL
2019-07-29 15:56:47,827 Execution time of moving from DEIB to LOCAL: 1 s.
2019-07-29 15:56:47,828 Executing local query
2019-07-29 15:57:32,025 Execution time at local: 44 s.
2019-07-29 15:57:32,025 Total response time: 473 s.
```