

ANEXO 1: MATERIAL SUPLEMENTARIO

Tabla S1. Valores de VP, VN, FP, FN, VP_v y FN_v usados para calcular las métricas de cada uno de los programas para cada una de las especies.

Especie	Programa	VP	VN	FP	FN	VP _v	FN _v
<i>A.thaliana</i>	FEELnc	6163	13488	1	219	118	7
<i>O.sativa</i>	FEELnc	4462	11527	0	284	25	0
<i>Z.mays</i>	FEELnc	8285	32161	2	2414	13	3
<i>S.lycopersicum</i>	FEELnc	7889	8709	0	100	17	2
<i>C.sativus</i>	FEELnc	5984	8697	0	610	5	1
<i>A.thaliana</i>	CPAT	12041	13188	411	1558	127	17
<i>O.sativa</i>	CPAT	9234	11407	158	2331	21	19
<i>Z.mays</i>	CPAT	20800	31424	820	11597	19	7
<i>S.lycopersicum</i>	CPAT	6215	8548	191	2526	17	2
<i>C.sativus</i>	CPAT	6438	8583	169	2315	7	1
<i>A.thaliana</i>	CPC2	13419	12572	1027	180	141	3
<i>O.sativa</i>	CPC2	11554	10959	606	11	37	3
<i>Z.mays</i>	CPC2	31328	30043	2354	1069	25	1
<i>S.lycopersicum</i>	CPC2	8573	8354	387	168	18	1
<i>C.sativus</i>	CPC2	8513	8319	434	240	8	0
<i>A.thaliana</i>	LncADeep	12292	13112	487	1307	129	15
<i>O.sativa</i>	LncADeep	10834	11027	538	731	39	1
<i>Z.mays</i>	LncADeep	26619	30409	1988	5778	24	2
<i>S.lycopersicum</i>	LncADeep	8239	8505	236	502	18	1
<i>C.sativus</i>	LncADeep	7119	8543	210	1634	8	0
<i>A.thaliana</i>	lncRNA_Mdeep	12532	13038	561	1067	134	10
<i>O.sativa</i>	lncRNA_Mdeep	10469	11271	294	1096	34	6
<i>Z.mays</i>	lncRNA_Mdeep	25060	31330	1067	7337	20	6
<i>S.lycopersicum</i>	lncRNA_Mdeep	7746	8488	253	995	17	2
<i>C.sativus</i>	lncRNA_Mdeep	7506	8457	296	1247	7	1

Tabla S2. Métricas de evaluación de cada uno de los programas para cada especie.

Especie	Programa	Exactitud	Ratio error	Sensibilidad	Sensibilidad validados	Especificidad	Precisión	VPN	PuntuaciónF1
<i>A.thaliana</i>	FEELnc	98,89	1,11	96,57	94,40	99,99	99,98	98,40	98,25
<i>O.sativa</i>	FEELnc	98,25	1,75	94,02	100,00	100,00	100,00	97,60	96,92
<i>Z.mays</i>	FEELnc	94,36	5,64	77,44	81,25	99,99	99,98	93,02	87,27
<i>S.lycopersicum</i>	FEELnc	99,40	0,60	98,75	89,47	100,00	100,00	98,86	99,37
<i>C.sativus</i>	FEELnc	96,01	3,99	90,75	83,33	100,00	100,00	93,45	95,15
<i>A.thaliana</i>	CPAT	92,76	7,24	88,54	88,19	96,98	96,70	89,43	92,44
<i>O.sativa</i>	CPAT	89,24	10,76	79,84	52,50	98,63	98,32	83,03	88,12
<i>Z.mays</i>	CPAT	80,79	19,21	64,20	73,08	97,46	96,21	73,04	77,01
<i>S.lycopersicum</i>	CPAT	84,46	15,54	71,10	89,47	97,81	97,02	77,19	82,06
<i>C.sativus</i>	CPAT	85,81	14,19	73,55	87,50	98,07	97,44	78,76	83,83
<i>A.thaliana</i>	CPC2	95,56	4,44	98,68	97,92	92,45	92,89	98,59	95,70
<i>O.sativa</i>	CPC2	97,33	2,67	99,90	92,50	94,76	95,02	99,90	97,40
<i>Z.mays</i>	CPC2	94,72	5,28	96,70	96,15	92,73	93,01	96,56	94,82
<i>S.lycopersicum</i>	CPC2	96,83	3,17	98,08	94,74	95,57	95,68	98,03	96,86
<i>C.sativus</i>	CPC2	96,15	3,85	97,26	100,00	95,04	95,15	97,20	96,19
<i>A.thaliana</i>	LncADeep	93,40	6,60	90,39	89,58	96,42	96,19	90,94	93,20
<i>O.sativa</i>	LncADeep	94,51	5,49	93,68	97,50	95,35	95,27	93,78	94,47
<i>Z.mays</i>	LncADeep	88,01	11,99	82,17	92,31	93,86	93,05	84,03	87,27
<i>S.lycopersicum</i>	LncADeep	95,78	4,22	94,26	94,74	97,30	97,22	94,43	95,71
<i>C.sativus</i>	LncADeep	89,47	10,53	81,33	100,00	97,60	97,13	83,94	88,53
<i>A.thaliana</i>	lncRNA_Mdeep	94,01	5,99	92,15	93,06	95,87	95,72	92,44	93,90
<i>O.sativa</i>	lncRNA_Mdeep	93,99	6,01	90,52	85,00	97,46	97,27	91,14	93,77
<i>Z.mays</i>	lncRNA_Mdeep	87,03	12,97	77,35	76,92	96,71	95,92	81,03	85,64
<i>S.lycopersicum</i>	lncRNA_Mdeep	92,86	7,14	88,62	89,47	97,11	96,84	89,51	92,54
<i>C.sativus</i>	lncRNA_Mdeep	91,19	8,81	85,75	87,50	96,62	96,21	87,15	90,68

Tabla S3. Ejemplo de las 20 primeras líneas del fichero de salida de Deseq2

ID_transcript	baseMean	log2FoldChange	lfcSE	stat	pvalue	padj	COLD-S1_S1	OLD-S2_S2	COLD-S3_S3	NT-S11_S8	NT-S1_S5	NT-S2_S7	ID_Gene	log10baseMean	Type	ID
maker-chr01-exonerate_est2genome-gene-0,0-mRNA-1	2,44E+13	4,85E-01	8,06E-02	6,03E+14	1,69E+05	5,48E+05	2,81E+14	2,89E+14	2,83E+14	2,08E+13	2,04E+14	1,98E+14	maker-chr01	3,39E+14	up-regulated	mRNA
maker-chr01-exonerate_est2genome-gene-0,1-mRNA-1	1,33E+13	2,44E-01	1,07E-01	2,28E+14	0,02288176	0,03409788	1,47E+14	1,34E+14	1,53E+13	1,14E+14	1,27E+13	1,25E+14	maker-chr01	3,13E+13	up-regulated	mRNA
maker-chr01-exonerate_est2genome-gene-0,2-mRNA-1	3,34E+14	-1,03E+14	1,35E-01	-7,64E+14	2,21E+00	1,01E+00	2,22E+14	2,13E+14	2,25E+14	4,34E+14	4,64E+14	4,46E+14	maker-chr01	2,53E+14	down-regulated (<=-1)	mRNA
maker-chr01-exonerate_est2genome-gene-0,3-mRNA-1	1,02E+14	-1,43E+13	1,22E-01	-1,18E+14	4,66E-18	5,37E-17	6,19E+14	4,72E+14	5,69E+14	1,56E+14	1,47E+14	1,45E+14	maker-chr01	4,01E+13	down-regulated (<=-1)	mRNA
maker-chr01-exonerate_est2genome-gene-0,4-mRNA-1	6,48E+14	1,77E+13	1,40E-01	1,27E+14	9,64E-23	1,33E-21	9,81E+14	1,12E+14	9,04E+13	2,77E+14	3,15E+14	2,90E+14	maker-chr01	2,81E+14	up-regulated (>=1)	mRNA
maker-chr01-exonerate_est2genome-gene-0,5-mRNA-1	1,50E+14	-1,91E+12	1,42E-01	-1,35E+13	1,55E-27	2,62E-26	6,92E+14	4,98E+14	6,93E+14	2,36E+14	2,40E+14	2,33E+14	maker-chr01	4,18E+14	down-regulated (<=-1)	mRNA
maker-chr01-exonerate_est2genome-gene-0,6-mRNA-1	2,97E+14	-5,36E-01	1,71E-01	-3,14E+14	0,00167204	0,00294235	2,64E+14	2,02E+14	2,64E+14	3,56E+14	3,30E+13	3,64E+14	maker-chr01	2,47E+13	down-regulated	mRNA
maker-chr01-exonerate_est2genome-gene-0,7-mRNA-1	4,95E+14	4,82E+14	5,86E-01	8,23E+14	1,92E-02	9,96E-03	7,32E+14	1,19E+14	9,45E+14	2,45E+13	3,63E+14	3,98E+14	maker-chr01	1,70E+14	up-regulated (>=1)	mRNA
maker-chr01-exonerate_est2genome-gene-0,8-mRNA-1	1,49E+14	-9,18E-01	2,06E-01	-4,46E+14	8,23E+08	1,90E+09	1,07E+14	1,05E+14	9,62E+14	2,26E+14	1,91E+14	1,68E+14	maker-chr01	2,18E+14	down-regulated	mRNA
maker-chr01-exonerate_est2genome-gene-0,9-mRNA-1	1,78E+14	6,15E-01	1,75E-01	3,51E+14	0,00044197	0,00084041	2,29E+14	2,26E+14	1,92E+14	1,07E+14	1,46E+14	1,70E+14	maker-chr01	3,25E+14	up-regulated	mRNA
maker-chr01-exonerate_est2genome-gene-1,0-mRNA-1	5,32E+14	-3,16E-01	1,64E-01	-1,92E+14	0,05434383	0,07597723	5,31E+14	4,34E+14	4,58E+14	6,87E+14	5,84E+13	5,00E+14	maker-chr01	2,73E+14	non-significant	mRNA
maker-chr01-exonerate_est2genome-gene-1,1-mRNA-1	6,78E+14	-3,51E-01	1,46E-01	-2,41E+14	0,01593242	0,02437683	6,00E+14	5,05E+14	6,88E+14	7,48E+14	7,55E+14	7,76E+14	maker-chr01	2,83E+14	down-regulated	mRNA
maker-chr01-exonerate_est2genome-gene-1,11-mRNA-1	1,37E+14	-1,58E+14	1,80E-01	-8,77E+14	1,86E-04	1,09E-03	7,83E+14	4,88E+14	7,88E+14	2,14E+14	1,95E+14	2,05E+14	maker-chr01	4,14E+14	down-regulated (<=-1)	mRNA
maker-chr01-exonerate_est2genome-gene-1,12-mRNA-1	9,14E+14	-4,82E-01	9,68E-02	-4,98E+14	6,44E+07	1,67E+08	7,60E+14	7,83E+14	7,44E+14	1,05E+14	1,08E+13	1,07E+14	maker-chr01	2,96E+13	down-regulated	mRNA
maker-chr01-exonerate_est2genome-gene-1,13-mRNA-1	4,73E+14	-4,40E+14	1,18E-01	-3,74E+14	2,15E-292	3,42E-288	4,33E+14	4,00E+14	4,48E+14	9,68E+14	8,00E+14	9,39E+14	maker-chr01	3,67E+14	down-regulated (<=-1)	mRNA
maker-chr01-exonerate_est2genome-gene-1,2-mRNA-1	1,59E+14	7,10E-01	1,99E-01	3,56E+14	0,00036955	0,00070971	1,87E+14	2,07E+14	1,98E+14	8,18E+14	1,40E+14	1,41E+14	maker-chr01	3,20E+14	up-regulated	mRNA
maker-chr01-exonerate_est2genome-gene-1,3-mRNA-1	4,74E+14	9,41E-01	1,85E-01	5,09E+14	3,57E+07	9,50E+07	6,56E+14	6,63E+14	5,49E+14	2,81E+14	4,07E+14	2,86E+14	maker-chr01	2,68E+14	up-regulated	mRNA
maker-chr01-exonerate_est2genome-gene-1,4-mRNA-1	5,68E+13	-1,91E+14	1,40E-01	-1,36E+14	2,52E-28	4,37E-27	2,29E+14	2,67E+14	2,17E+14	9,50E+13	8,34E+14	9,12E+14	maker-chr01	2,76E+14	down-regulated (<=-1)	mRNA
maker-chr01-exonerate_est2genome-gene-1,5-mRNA-1	1,35E+14	-6,48E-01	2,38E-01	-2,73E+13	0,00640316	0,01038633	8,49E+14	1,05E+13	1,27E+13	1,37E+14	1,71E+14	1,86E+14	maker-chr01	2,13E+14	down-regulated	mRNA
maker-chr01-exonerate_est2genome-gene-1,7-mRNA-1	4,25E+14	4,64E+14	6,43E-01	7,22E+14	5,07E+01	2,11E+01	6,17E+13	1,21E+14	6,26E+13	1,18E+14	3,53E+14	4,95E+14	maker-chr01	1,64E+14	up-regulated (>=1)	mRNA

Tabla S4: Ejemplo de las 20 primeras filas de las parejas de ARNm y ARNnci localizados a menos de 10 kb aguas arriba/abajo y sus respectivos log2FC.

ID_transcript	ID_IncRNA	log2FC_IncRNA	log2FC_mRNA
maker-chr01-exonerate_est2genome-gene-118.3-m...	MSTRG.768.1	-2.2501079	-0.5127701
maker-chr01-exonerate_est2genome-gene-118.3-m...	MSTRG.774.2	4.7564580	-0.5127701
maker-chr01-exonerate_est2genome-gene-118.3-m...	MSTRG.774.1	1.7492346	-0.5127701
maker-chr01-exonerate_est2genome-gene-118.4-m...	MSTRG.768.1	-2.2501079	2.3555790
maker-chr01-exonerate_est2genome-gene-118.4-m...	MSTRG.774.1	1.7492346	2.3555790
maker-chr01-exonerate_est2genome-gene-118.4-m...	MSTRG.774.2	4.7564580	2.3555790
maker-chr01-exonerate_est2genome-gene-118.5-m...	MSTRG.774.1	1.7492346	2.6160581
maker-chr01-exonerate_est2genome-gene-118.5-m...	MSTRG.774.2	4.7564580	2.6160581
maker-chr01-exonerate_est2genome-gene-149.41-...	MSTRG.898.1	1.9040826	0.5526302
maker-chr01-exonerate_est2genome-gene-197.22-...	MSTRG.1157.4	1.7203557	0.8879218
maker-chr01-exonerate_est2genome-gene-278.34-...	MSTRG.1477.42	1.2530796	-0.3809477
maker-chr01-exonerate_est2genome-gene-302.3-m...	MSTRG.1608.2	-8.8823056	-0.3924978
maker-chr01-exonerate_est2genome-gene-302.3-m...	MSTRG.1608.5	-2.6696582	-0.3924978
maker-chr01-exonerate_est2genome-gene-302.4-m...	MSTRG.1608.2	-8.8823056	0.4356979
maker-chr01-exonerate_est2genome-gene-302.4-m...	MSTRG.1608.5	-2.6696582	0.4356979
maker-chr01-exonerate_est2genome-gene-324.6-m...	MSTRG.1826.1	-1.4116113	-1.3380051
maker-chr01-exonerate_est2genome-gene-324.7-m...	MSTRG.1826.1	-1.4116113	-3.4961570
maker-chr01-exonerate_est2genome-gene-335.1-m...	MSTRG.1952.3	1.0921980	0.9200227
maker-chr01-exonerate_est2genome-gene-335.10-...	MSTRG.1950.4	2.0871976	0.4714210
maker-chr01-exonerate_est2genome-gene-335.11-...	MSTRG.1950.4	2.0871976	1.5167210

Tabla S5. Ejemplo de las 20 primeras filas del fichero que contiene las parejas de ARNm y ARNnci localizados a menos de 10 kb aguas arriba/abajo y los correspondientes términos GO de los ARNm.

Name_transcript	GO_term	Function	Ubication	ID_transcript	ID_IncRNA
MELO3C001983.2	GO:0016020	cellular_component	membrane	maker-chr12-exonerate_est2genome-gene-256.13-...	MSTRG.21985.4
MELO3C002014.2	GO:0005484	molecular_function	SNAP receptor activity	maker-chr12-exonerate_est2genome-gene-254.7-m...	MSTRG.21955.1
MELO3C002014.2	GO:0015031	biological_process	protein transport	maker-chr12-exonerate_est2genome-gene-254.7-m...	MSTRG.21955.1
MELO3C002014.2	GO:0006810	biological_process	transport	maker-chr12-exonerate_est2genome-gene-254.7-m...	MSTRG.21955.1
MELO3C002014.2	GO:0007049	biological_process	cell cycle	maker-chr12-exonerate_est2genome-gene-254.7-m...	MSTRG.21955.1
MELO3C002014.2	GO:0051301	biological_process	cell division	maker-chr12-exonerate_est2genome-gene-254.7-m...	MSTRG.21955.1
MELO3C002014.2	GO:0005886	cellular_component	plasma membrane	maker-chr12-exonerate_est2genome-gene-254.7-m...	MSTRG.21955.1
MELO3C002014.2	GO:0051707	biological_process	response to other organism	maker-chr12-exonerate_est2genome-gene-254.7-m...	MSTRG.21955.1
MELO3C002014.2	GO:0016021	cellular_component	integral component of membrane	maker-chr12-exonerate_est2genome-gene-254.7-m...	MSTRG.21955.1
MELO3C002014.2	GO:0009737	biological_process	response to abscisic acid	maker-chr12-exonerate_est2genome-gene-254.7-m...	MSTRG.21955.1
MELO3C002014.2	GO:0016192	biological_process	vesicle-mediated transport	maker-chr12-exonerate_est2genome-gene-254.7-m...	MSTRG.21955.1
MELO3C002014.2	GO:0016020	cellular_component	membrane	maker-chr12-exonerate_est2genome-gene-254.7-m...	MSTRG.21955.1
MELO3C002014.2	GO:0061025	biological_process	membrane fusion	maker-chr12-exonerate_est2genome-gene-254.7-m...	MSTRG.21955.1
MELO3C002014.2	GO:0005515	molecular_function	protein binding	maker-chr12-exonerate_est2genome-gene-254.7-m...	MSTRG.21955.1
MELO3C002014.2	GO:0009507	cellular_component	chloroplast	maker-chr12-exonerate_est2genome-gene-254.7-m...	MSTRG.21955.1
MELO3C002014.2	GO:0009612	biological_process	response to mechanical stimulus	maker-chr12-exonerate_est2genome-gene-254.7-m...	MSTRG.21955.1
MELO3C002014.2	GO:0009504	cellular_component	cell plate	maker-chr12-exonerate_est2genome-gene-254.7-m...	MSTRG.21955.1
MELO3C002014.2	GO:0000911	biological_process	cytokinesis by cell plate formation	maker-chr12-exonerate_est2genome-gene-254.7-m...	MSTRG.21955.1
MELO3C002015.2	GO:0005515	molecular_function	protein binding	maker-chr12-exonerate_est2genome-gene-254.6-m...	MSTRG.21955.1
MELO3C002044.2	GO:0003677	molecular_function	DNA binding	maker-chr12-exonerate_est2genome-gene-252.15-...	MSTRG.21923.5

ANEXO 2: CÓDIGOS SUPLEMENTARIOS

Código 1. Programa de Python usado para eliminar los transcritos con código de clases correspondientes a los errores (p, r, s).

```
#!/usr/bin/env python3
# -*- coding: utf-8 -*-

"""
This script is aim to remove transcripts with class codes not interesting or incorrectly assembled
(p,r,s).
"""

## MODULES

import sys

## PIPELINE

path_GTF_initial = sys.argv[1]
path_GTF_filtered = sys.argv[2]

GTF_initial = open(path_GTF_initial, "r+")
GTF_filtered = open(path_GTF_filtered, "w")

for line in GTF_initial:
    line=line.rstrip().split("\t")

    if line[2] == "transcript":
        if ('class_code "p"' not in line[-1]) and \
            ('class_code "r"' not in line[-1]) and \
            ('class_code "s"' not in line[-1]):
            var="+"
            GTF_filtered.write("%s\n"%("\t".join(line)))
        else:
            var="-"

    elif line[2]=="exon":
        if var=="+":
            GTF_filtered.write("%s\n"%("\t".join(line)))
```

Código 2. Programa de Python usado para seleccionar los transcritos con código de clases correspondientes a los ARNncl (u, x, i, o, e).

```
#!/usr/bin/env python3
# -*- coding: utf-8 -*-

"""
This script is aim to select the class codes: "x" (antisense), "i" (intronic), "u" (intergenic) and "o"/"e"
(exon sense) as novel transcripts.
"""

## MODULES

import sys

## PIPELINE

path_GTF_initial = sys.argv[1]
path_GTF_filtered = sys.argv[2]

GTF_initial = open(path_GTF_initial, "r+")
GTF_filtered = open(path_GTF_filtered, "w")

for line in GTF_initial:
    line=line.rstrip().split("\t")

    if line[2] == "transcript":
        if ('class_code "x"' in line[-1]) or \
            ('class_code "u"' in line[-1]) or \
            ('class_code "i"' in line[-1]) or \
            ('class_code "o"' in line[-1]) or \
            ('class_code "e"' in line[-1]):
            var="+"
            GTF_filtered.write("%s\n"%("\t".join(line)))
        else:
            var="-"

    elif line[2]=="exon":
        if var=="+":
            GTF_filtered.write("%s\n"%("\t".join(line)))
```