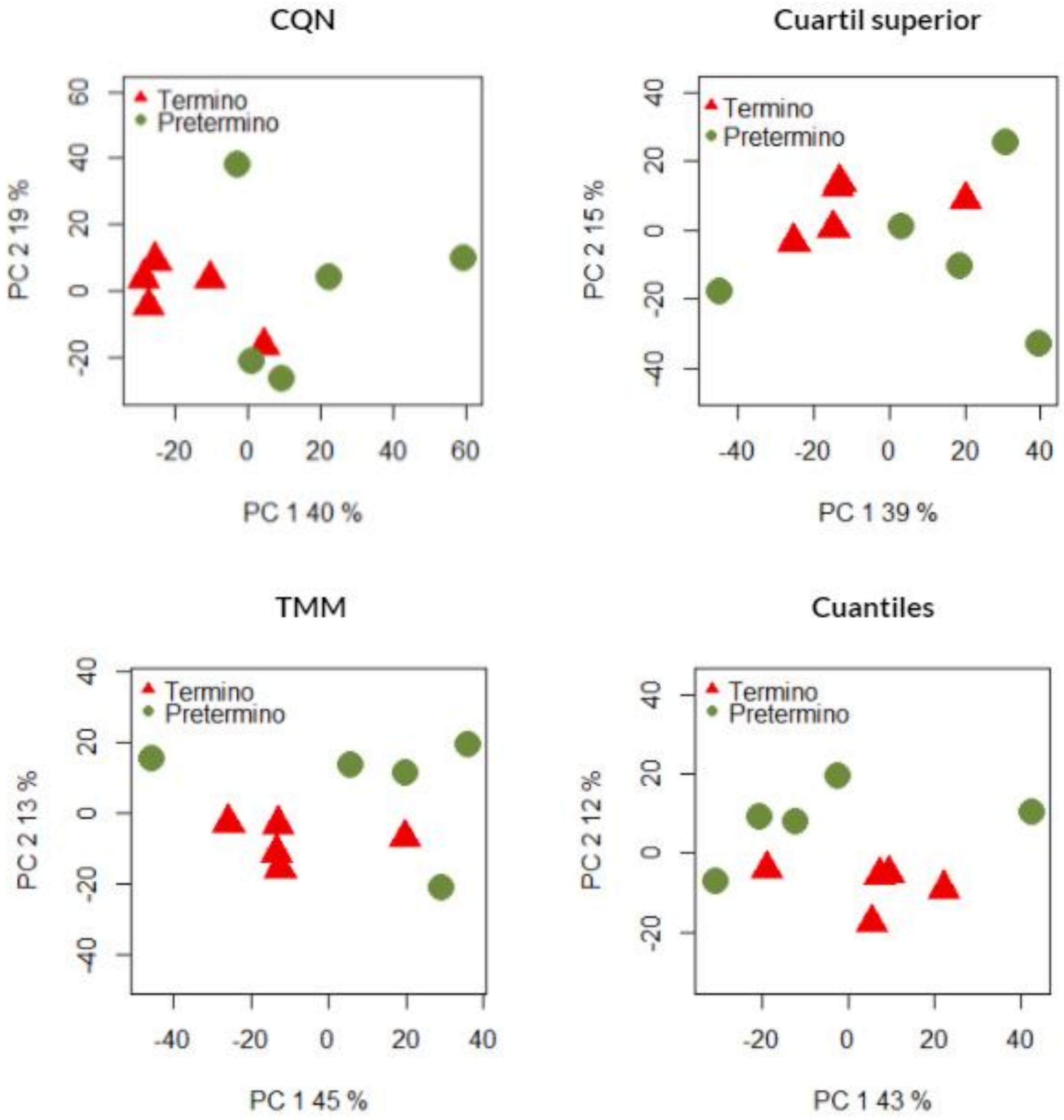
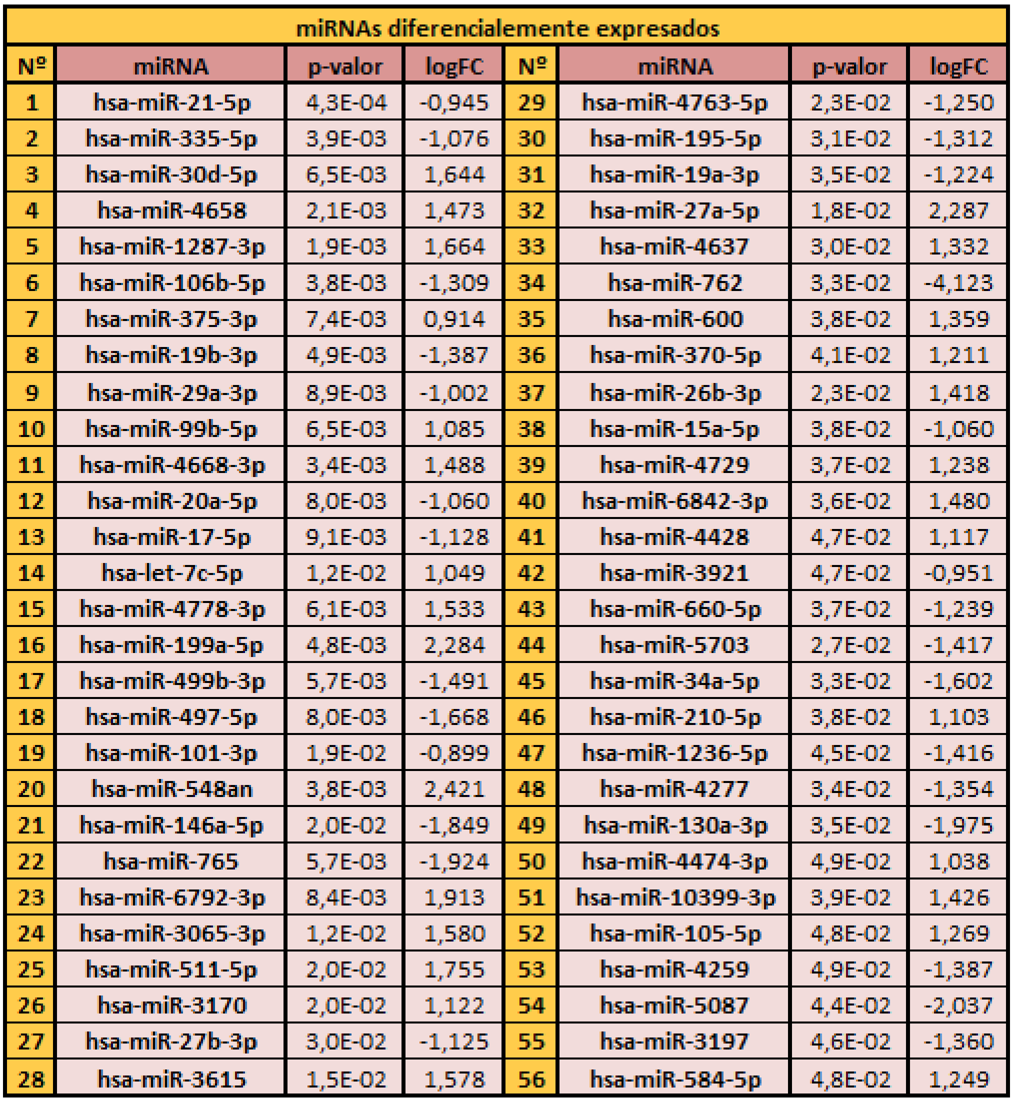
Anexos

1. **Anexo 1:** gráficos de *scores* de PCA de los cuatro métodos de normalización aplicados a los datos de transcriptómica de MAPQ1 tras el filtro CPM > 2

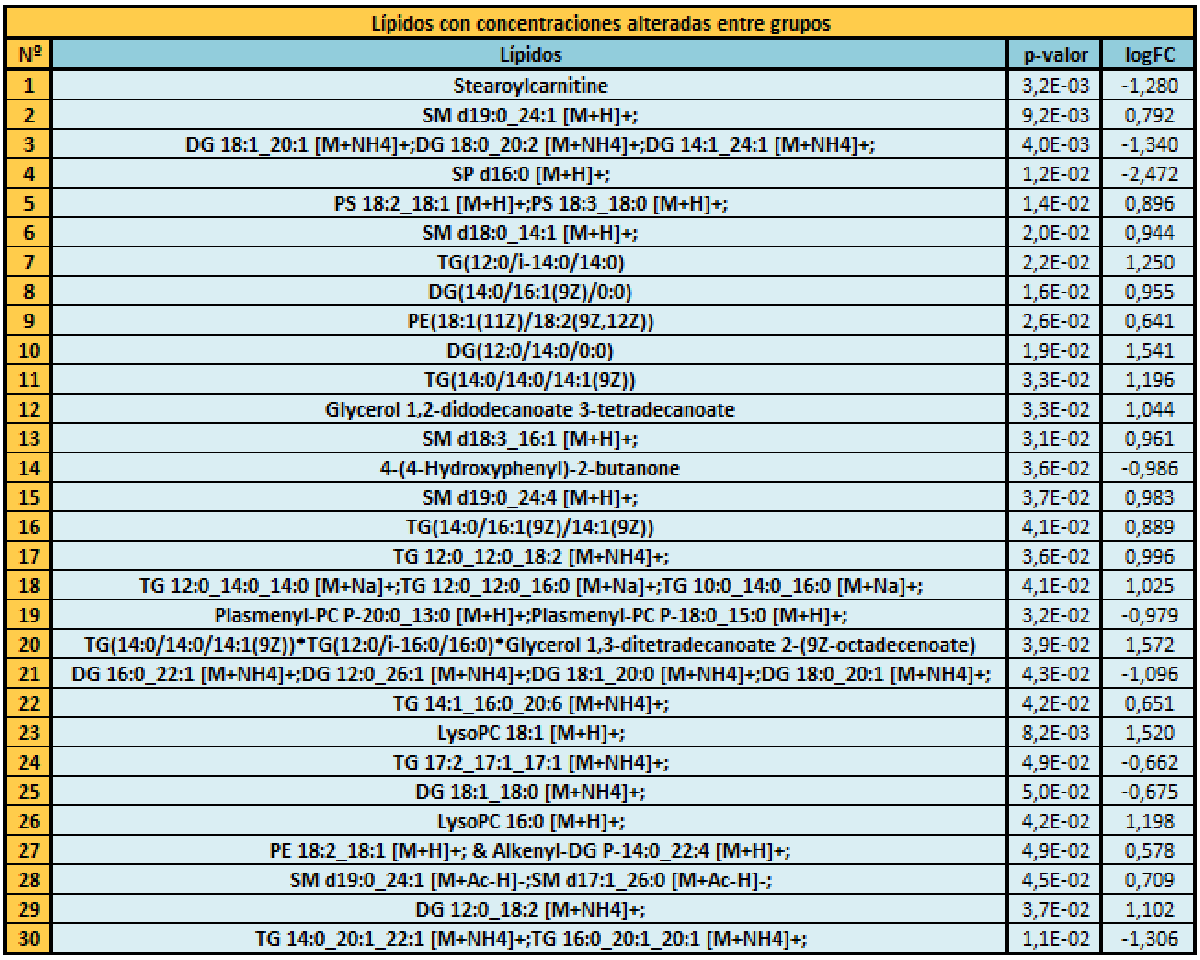


2. **Anexo 2:** listado de los miRNAs diferencialmente expresados con p-valor y logFC



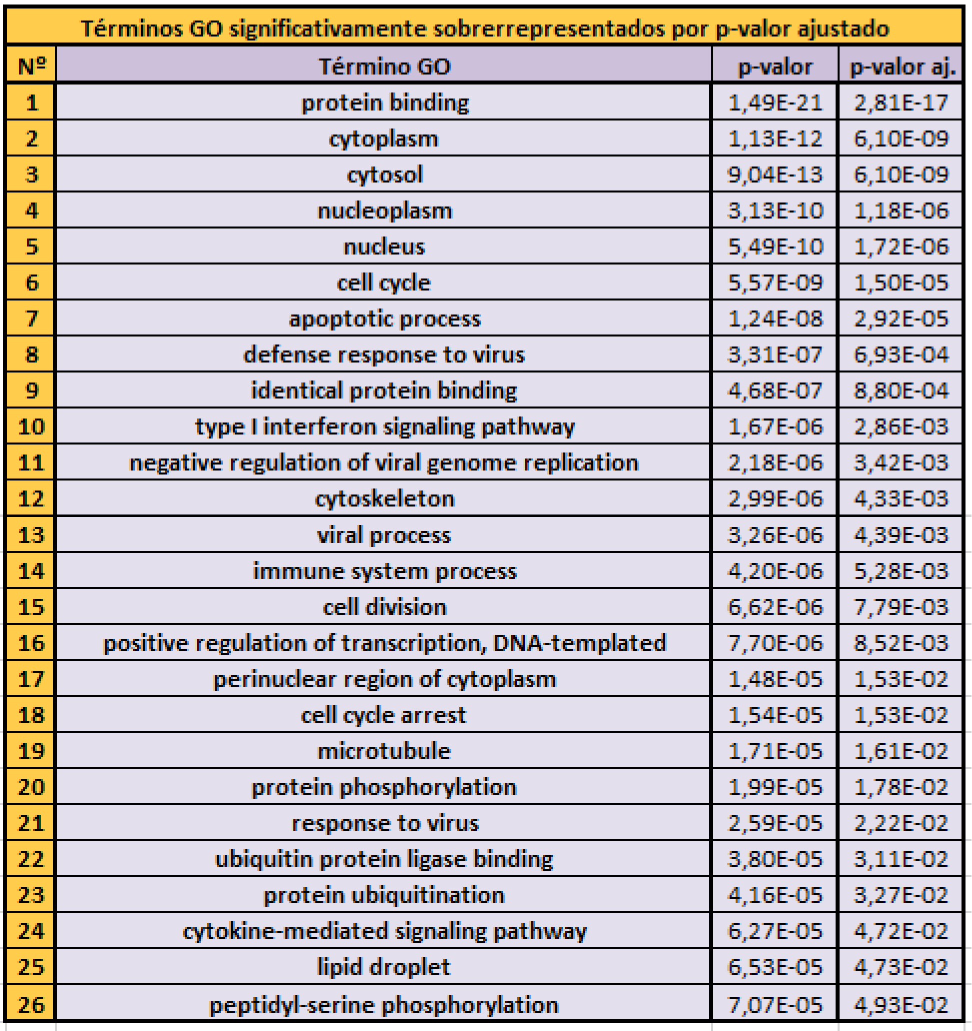
miRNAs diferencialmente expresados							
Nº	**miRNA**	**p-valor**	**logFC**	**Nº**	**miRNA**	**p-valor**	**logFC**
1	**hsa-miR-21-5p**	4,3E-04	-0,945	**29**	**hsa-miR-4763-5p**	2,3E-02	-1,250
2	**hsa-miR-335-5p**	3,9E-03	-1,076	**30**	**hsa-miR-195-5p**	3,1E-02	-1,312
3	**hsa-miR-30d-5p**	6,5E-03	1,644	**31**	**hsa-miR-19a-3p**	3,5E-02	-1,224
4	**hsa-miR-4658**	2,1E-03	1,473	**32**	**hsa-miR-27a-5p**	1,8E-02	2,287
5	**hsa-miR-1287-3p**	1,9E-03	1,664	**33**	**hsa-miR-4637**	3,0E-02	1,332
6	**hsa-miR-106b-5p**	3,8E-03	-1,309	**34**	**hsa-miR-762**	3,3E-02	-4,123
7	**hsa-miR-375-3p**	7,4E-03	0,914	**35**	**hsa-miR-600**	3,8E-02	1,359
8	**hsa-miR-19b-3p**	4,9E-03	-1,387	**36**	**hsa-miR-370-5p**	4,1E-02	1,211
9	**hsa-miR-29a-3p**	8,9E-03	-1,002	**37**	**hsa-miR-26b-3p**	2,3E-02	1,418
10	**hsa-miR-99b-5p**	6,5E-03	1,085	**38**	**hsa-miR-15a-5p**	3,8E-02	-1,060
11	**hsa-miR-4668-3p**	3,4E-03	1,488	**39**	**hsa-miR-4729**	3,7E-02	1,238
12	**hsa-miR-20a-5p**	8,0E-03	-1,060	**40**	**hsa-miR-6842-3p**	3,6E-02	1,480
13	**hsa-miR-17-5p**	9,1E-03	-1,128	**41**	**hsa-miR-4428**	4,7E-02	1,117
14	**hsa-let-7c-5p**	1,2E-02	1,049	**42**	**hsa-miR-3921**	4,7E-02	-0,951
15	**hsa-miR-4778-3p**	6,1E-03	1,533	**43**	**hsa-miR-660-5p**	3,7E-02	-1,239
16	**hsa-miR-199a-5p**	4,8E-03	2,284	**44**	**hsa-miR-5703**	2,7E-02	-1,417
17	**hsa-miR-499b-3p**	5,7E-03	-1,491	**45**	**hsa-miR-34a-5p**	3,3E-02	-1,602
18	**hsa-miR-497-5p**	8,0E-03	-1,668	**46**	**hsa-miR-210-5p**	3,8E-02	1,103
19	**hsa-miR-101-3p**	1,9E-02	-0,899	**47**	**hsa-miR-1236-5p**	4,5E-02	-1,416
20	**hsa-miR-548an**	3,8E-03	2,421	**48**	**hsa-miR-4277**	3,4E-02	-1,354
21	**hsa-miR-146a-5p**	2,0E-02	-1,849	**49**	**hsa-miR-130a-3p**	3,5E-02	-1,975
22	**hsa-miR-765**	5,7E-03	-1,924	**50**	**hsa-miR-4474-3p**	4,9E-02	1,038
23	**hsa-miR-6792-3p**	8,4E-03	1,913	**51**	**hsa-miR-10399-3p**	3,9E-02	1,426
24	**hsa-miR-3065-3p**	1,2E-02	1,580	**52**	**hsa-miR-105-5p**	4,8E-02	1,269
25	**hsa-miR-511-5p**	2,0E-02	1,755	**53**	**hsa-miR-4259**	4,9E-02	-1,387
26	**hsa-miR-3170**	2,0E-02	1,122	**54**	**hsa-miR-5087**	4,4E-02	-2,037
27	**hsa-miR-27b-3p**	3,0E-02	-1,125	**55**	**hsa-miR-3197**	4,6E-02	-1,360
28	**hsa-miR-3615**	1,5E-02	1,578	**56**	**hsa-miR-584-5p**	4,8E-02	1,249

3. **Anexo 3:** listado de los lípidos con concentraciones alteradas entre ambos grupos con p-valor y logFC



Lípidos con concentraciones alteradas entre grupos			
Nº	**Lípidos**	**p-valor**	**logFC**
1	Stearoylcarnitine	3,2E-03	-1,280
2	SM d19:0_24:1 [M+H]+;	9,2E-03	0,792
3	DG 18:1_20:1 [M+NH4]+;DG 18:0_20:2 [M+NH4]+;DG 14:1_24:1 [M+NH4]+;	4,0E-03	-1,340
4	SP d16:0 [M+H]+;	1,2E-02	-2,472
5	PS 18:2_18:1 [M+H]+;PS 18:3_18:0 [M+H]+;	1,4E-02	0,896
6	SM d18:0_14:1 [M+H]+;	2,0E-02	0,944
7	TG(12:0/i-14:0/14:0)	2,2E-02	1,250
8	DG(14:0/16:1(9Z)/0:0)	1,6E-02	0,955
9	PE(18:1(11Z)/18:2(9Z,12Z))	2,6E-02	0,641
10	DG(12:0/14:0/0:0)	1,9E-02	1,541
11	TG(14:0/14:0/14:1(9Z))	3,3E-02	1,196
12	Glycerol 1,2-didodecanoate 3-tetradecanoate	3,3E-02	1,044
13	SM d18:3_16:1 [M+H]+;	3,1E-02	0,961
14	4-(4-Hydroxyphenyl)-2-butanone	3,6E-02	-0,986
15	SM d19:0_24:4 [M+H]+;	3,7E-02	0,983
16	TG(14:0/16:1(9Z)/14:1(9Z))	4,1E-02	0,889
17	TG 12:0_12:0_18:2 [M+NH4]+;	3,6E-02	0,996
18	TG 12:0_14:0_14:0 [M+Na]+;TG 12:0_12:0_16:0 [M+Na]+;TG 10:0_14:0_16:0 [M+Na]+;	4,1E-02	1,025
19	Plasmenyl-PC P-20:0_13:0 [M+H]+;Plasmenyl-PC P-18:0_15:0 [M+H]+;	3,2E-02	-0,979
20	TG(14:0/14:0/14:1(9Z))*TG(12:0/i-16:0/16:0)*Glycerol 1,3-ditetradecanoate 2-(9Z-octadecenoate)	3,9E-02	1,572
21	DG 16:0_22:1 [M+NH4]+;DG 12:0_26:1 [M+NH4]+;DG 18:1_20:0 [M+NH4]+;DG 18:0_20:1 [M+NH4]+;	4,3E-02	-1,096
22	TG 14:1_16:0_20:6 [M+NH4]+;	4,2E-02	0,651
23	LysoPC 18:1 [M+H]+;	8,2E-03	1,520
24	TG 17:2_17:1_17:1 [M+NH4]+;	4,9E-02	-0,662
25	DG 18:1_18:0 [M+NH4]+;	5,0E-02	-0,675
26	LysoPC 16:0 [M+H]+;	4,2E-02	1,198
27	PE 18:2_18:1 [M+H]+; & Alkenyl-DG P-14:0_22:4 [M+H]+;	4,9E-02	0,578
28	SM d19:0_24:1 [M+Ac-H]-;SM d17:1_26:0 [M+Ac-H]-;	4,5E-02	0,709
29	DG 12:0_18:2 [M+NH4]+;	3,7E-02	1,102
30	TG 14:0_20:1_22:1 [M+NH4]+;TG 16:0_20:1_20:1 [M+NH4]+;	1,1E-02	-1,306

4. **Anexo 4:** listado de términos GO significativamente sobrerrepresentados por p-valor ajustado



Términos GO significativamente sobrerrepresentados por p-valor ajustado			
Nº	**Término GO**	**p-valor**	**p-valor aj.**
1	protein binding	1,49E-21	2,81E-17
2	cytoplasm	1,13E-12	6,10E-09
3	cytosol	9,04E-13	6,10E-09
4	nucleoplasm	3,13E-10	1,18E-06
5	nucleus	5,49E-10	1,72E-06
6	cell cycle	5,57E-09	1,50E-05
7	apoptotic process	1,24E-08	2,92E-05
8	defense response to virus	3,31E-07	6,93E-04
9	identical protein binding	4,68E-07	8,80E-04
10	type I interferon signaling pathway	1,67E-06	2,86E-03
11	negative regulation of viral genome replication	2,18E-06	3,42E-03
12	cytoskeleton	2,99E-06	4,33E-03
13	viral process	3,26E-06	4,39E-03
14	immune system process	4,20E-06	5,28E-03
15	cell division	6,62E-06	7,79E-03
16	positive regulation of transcription, DNA-templated	7,70E-06	8,52E-03
17	perinuclear region of cytoplasm	1,48E-05	1,53E-02
18	cell cycle arrest	1,54E-05	1,53E-02
19	microtubule	1,71E-05	1,61E-02
20	protein phosphorylation	1,99E-05	1,78E-02
21	response to virus	2,59E-05	2,22E-02
22	ubiquitin protein ligase binding	3,80E-05	3,11E-02
23	protein ubiquitination	4,16E-05	3,27E-02
24	cytokine-mediated signaling pathway	6,27E-05	4,72E-02
25	lipid droplet	6,53E-05	4,73E-02
26	peptidyl-serine phosphorylation	7,07E-05	4,93E-02

5. **Anexo 5:** componentes alterados de la uta de señalización PI3K obtenida con la herramienta “KEGG mapper”