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PCA plot

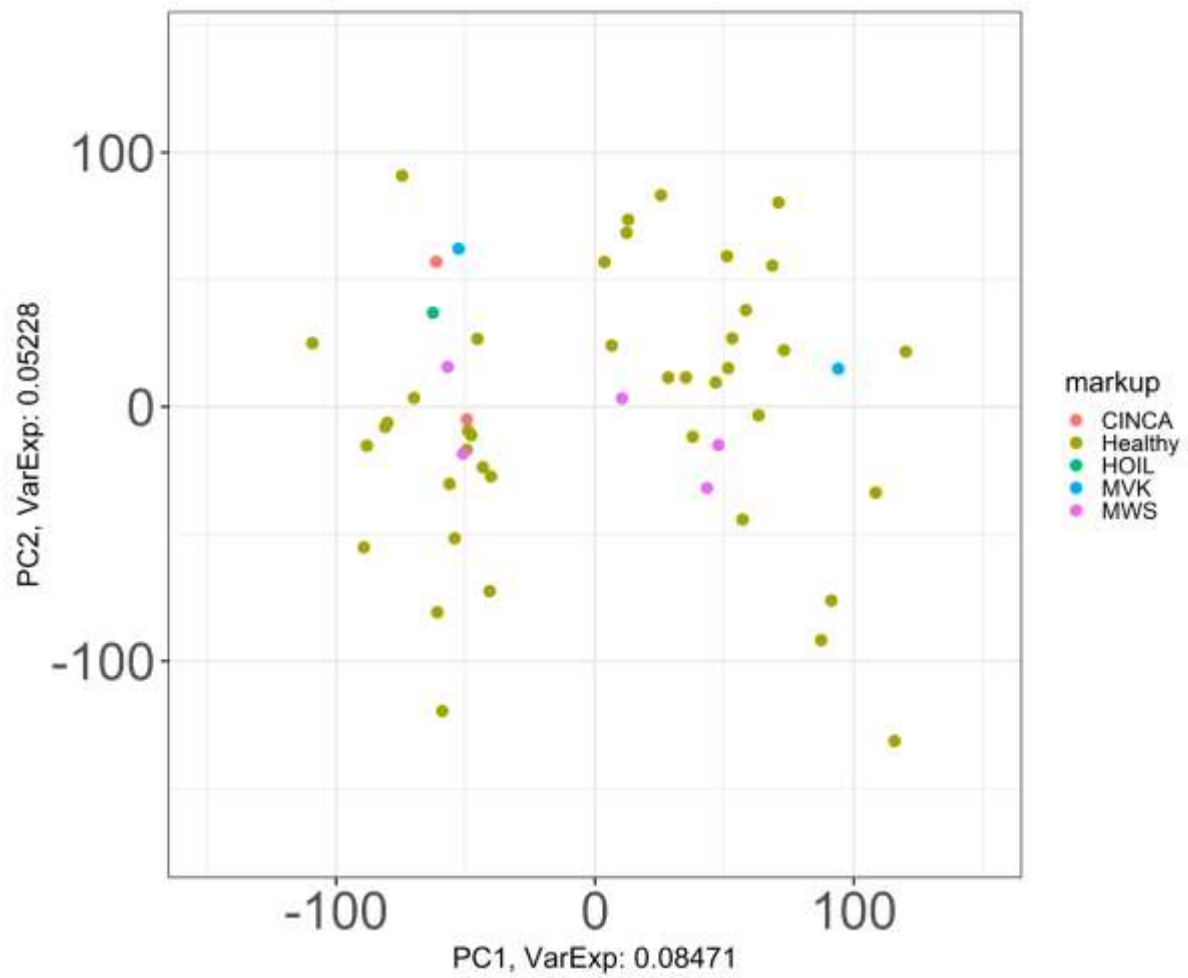


Fig. 1. Principal Component Analysis. The PCA of raw expression data. The colored dots represent groups of examined samples' deficiencies.

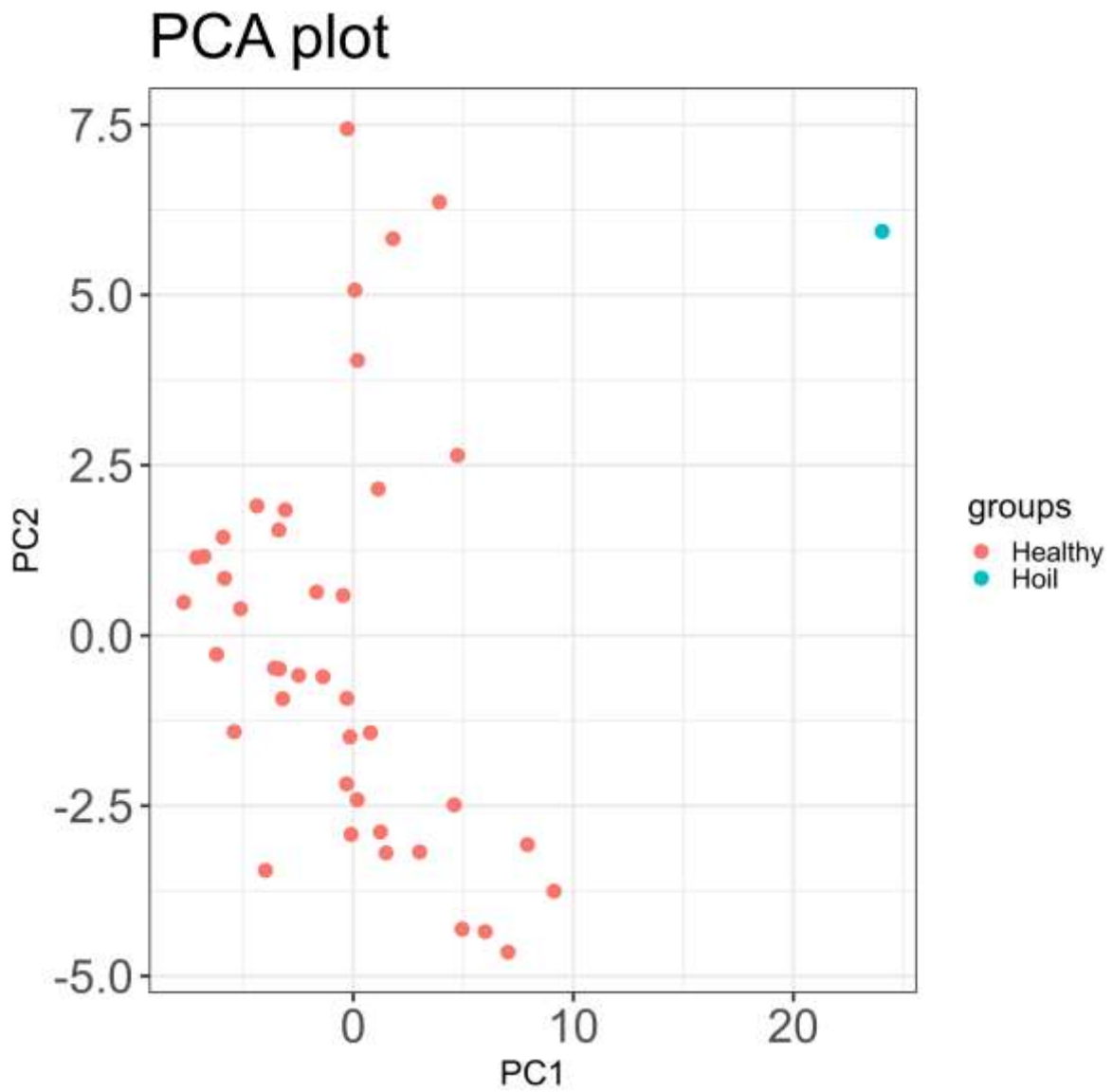


Fig. 2. Principal Component Analysis. The PCA of gene expression data in comparison between healthy and RBCK1 disease samples. Only down-regulated genes were presented in this data. Colors show groups of examined samples' deficiencies.

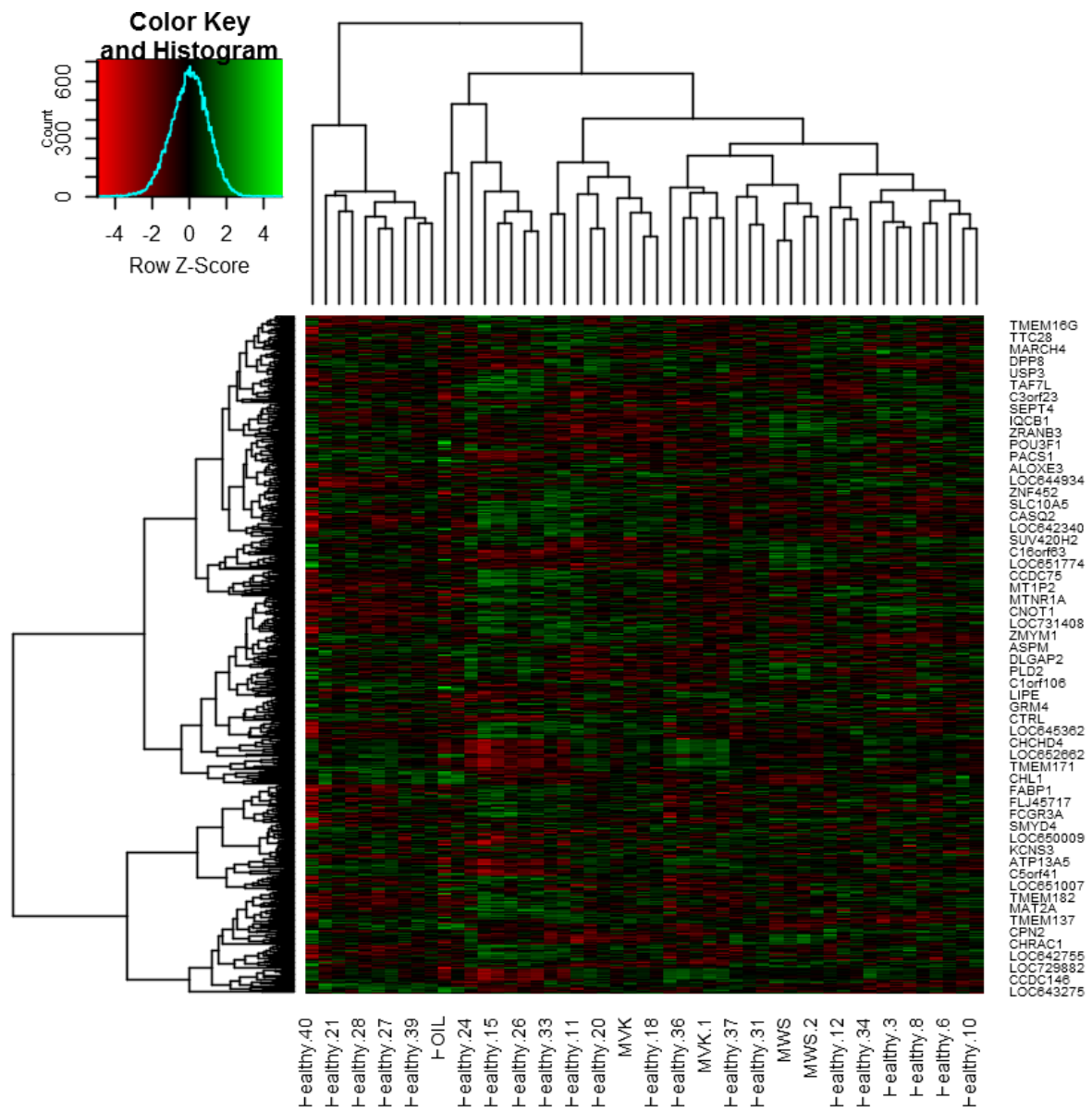


Fig. 3. Heatmap of expression data after normalization. Each column represents the expression levels of all genes from one of the examined samples (healthy, RBCK1, CINCA, MWS, MVK). Each row represents the expression levels of a gene across all samples.

RBCK1 deficiency versus healthy samples

EnhancedVolcano

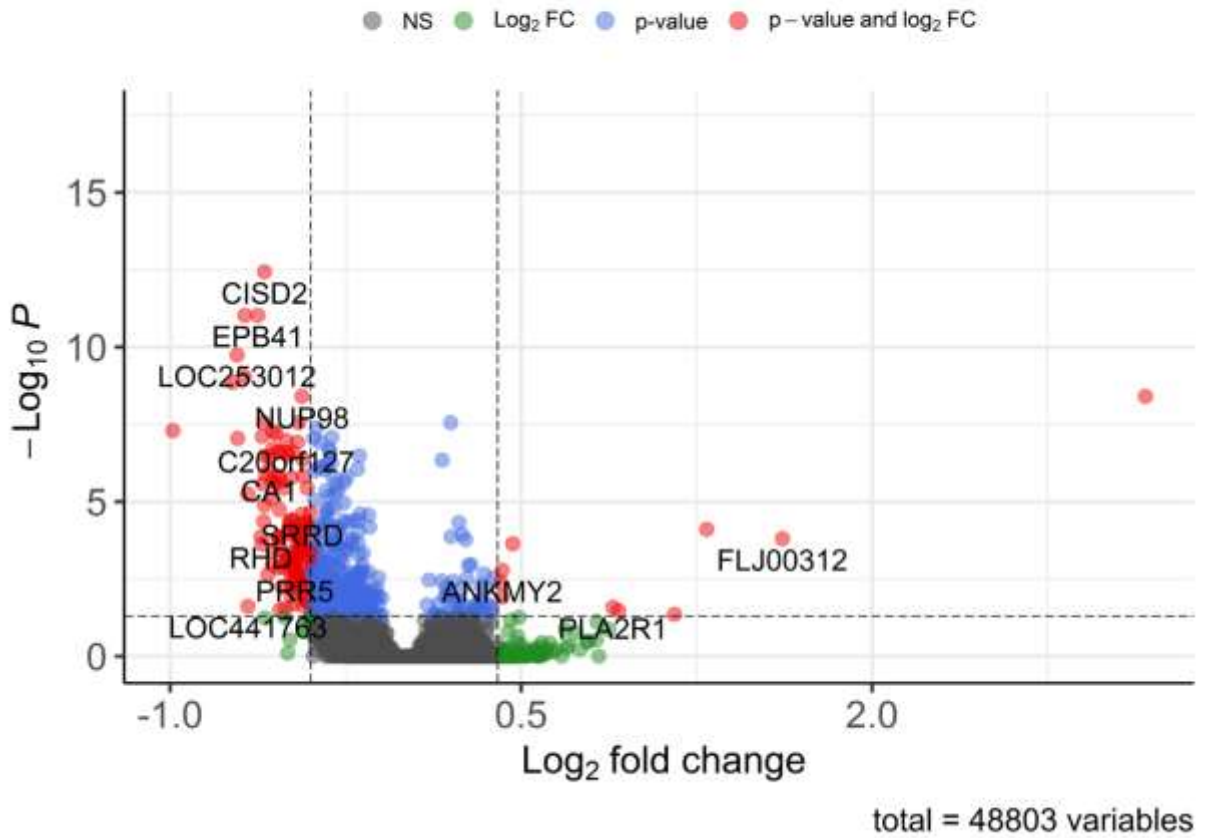


Fig. 4. Volcano Plot. Volcano plots showing differential expression between healthy and diseased samples. X axis represents Fold Change value, while Y axis represents P value. Red dots represent differentially expressed genes.

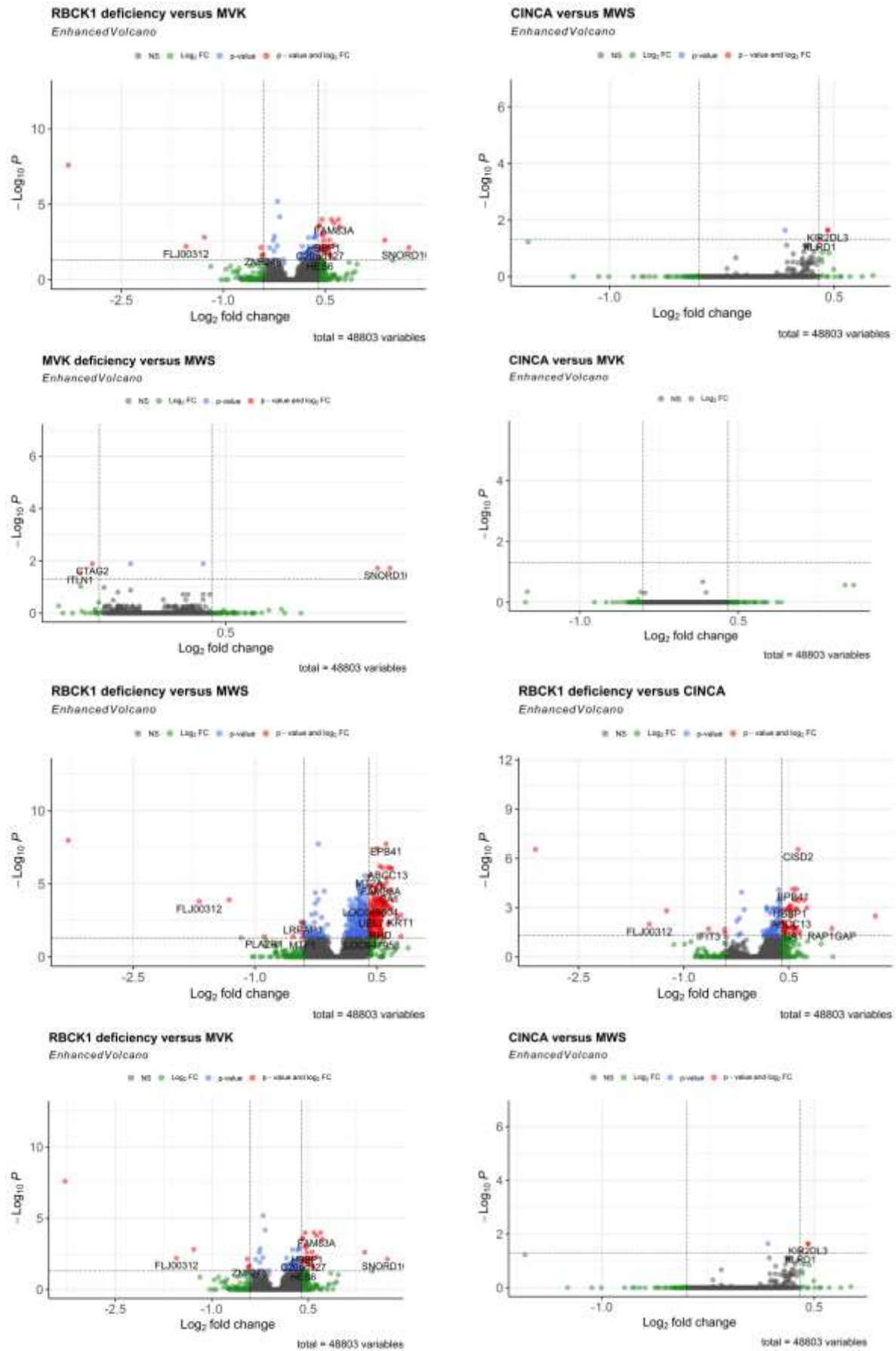


Fig. 5. Volcano Plot. Volcano plots showing differential expression between all diseased samples. X-axis represents Fold Change value, while Y-axis represents P value. Red dots represent differentially expressed genes.

Table 1. Top 10 most differentially expressed downregulated genes from comparison between healthy and RBCK1 samples

	Gene name	P-value	logFC
1	HBBP1	1.141737e-06	0.4786540
2	C20orf127	6.579816e-06	0.4264092
3	MAOA	2.440151e-06	0.6300522
4	RFFL	3.421255e-06	0.5362195
5	EPB41	2.627018e-07	0.4556318
6	FAM83A	2.497823e-08	0.6278024
7	NSUN3	5.924530e-08	0.4098833
8	PPM1A	4.976705e-06	0.5563138
9	HES6	6.051238e-05	0.4230913
10	STOM	5.554047e-05	0.4090811

Table 2. Top 10 most differentially expressed upregulated genes in comparison between RBCK1 deficiency and MWS

	Gene name	P-value	logFC
1	RHD	4.681915e-05	0.5447136
2	CA1	2.060478e-08	0.6516630
3	UBL7	4.361623e-06	0.4322227
4	HBBP1	1.284623e-08	0.4898661
5	LOC647958	3.833628e-04	0.4407032
6	PRR5	2.400870e-05	0.5007257
7	LOC649604	3.972521e-07	0.4215989
8	C20orf127	6.046749e-09	0.4938760
9	RNF123	1.022530e-06	0.4021701
10	MAOA	1.650408e-08	0.6626294

Table 3. Differentially expressed genes, involved into several significant pathways, obtained from KEGG

	Signaling pathway	Leishmaniasis	Hematopoietic cell lineage	Dilated cardiomyopathy	Pantothenate and CoA biosynthesis	<i>Vibrio cholerae</i> infection	Primary immune-deficiency
1	TIAM1	FCGR2A	MME	TPM3	VNN1	TCIRG1	CD79A
2	FOXO3	PTGS2	HLA-DRB5	ACTG1	UPB1	ACTG1	CD8B
3	STAT1	HLA-DRB5	CD8B	ITGB1	VNN2	PRKACB	CD8A
4	GNB4	FCGR3B	IL1R2	ITGA4	ZNF586		
5	GRB2	NCF4	CSF3R	PRKACB	VNN3		
6	CXCL5	TLR2	CD8A				
7	PIK3CG	IL1B	IL1B				
8	ROCK1	NCF2					
9	PIK3R1						
10	VAV3						

Table 4. Groups of genes involved in several significant pathways obtained from KEGG

	Natural killer cell mediated cytotoxicity	Antigen processing and presentation	<i>Staphylococcus aureus</i> infection	RIG-I-like receptor signalling pathway
1	KIR2DL3	KIR2DL3	FCGR2A	CXCL8
2	KIR2DL1	KIR2DL1	KRT23	MAPK13
3	KIR2DS5	KIR2DS5	FCGR1A	CXCL10
4	KIR3DL1	KIR2DL4	FCAR	ISG15
5	KLRC1	KIR3DL1	FPR2	
6	SH2D1B	KLRC1		
7	PRF1	KLRD1		
8	FASLG	KLRC2		
9	KLRD1	KIR3DL3		
10	KLRC2	KIR2DS3		
11	KIR3DL3	KIR3DL2		
12	GZMB	IFNG		
13	KIR2DS3			
14	KIR3DL2			

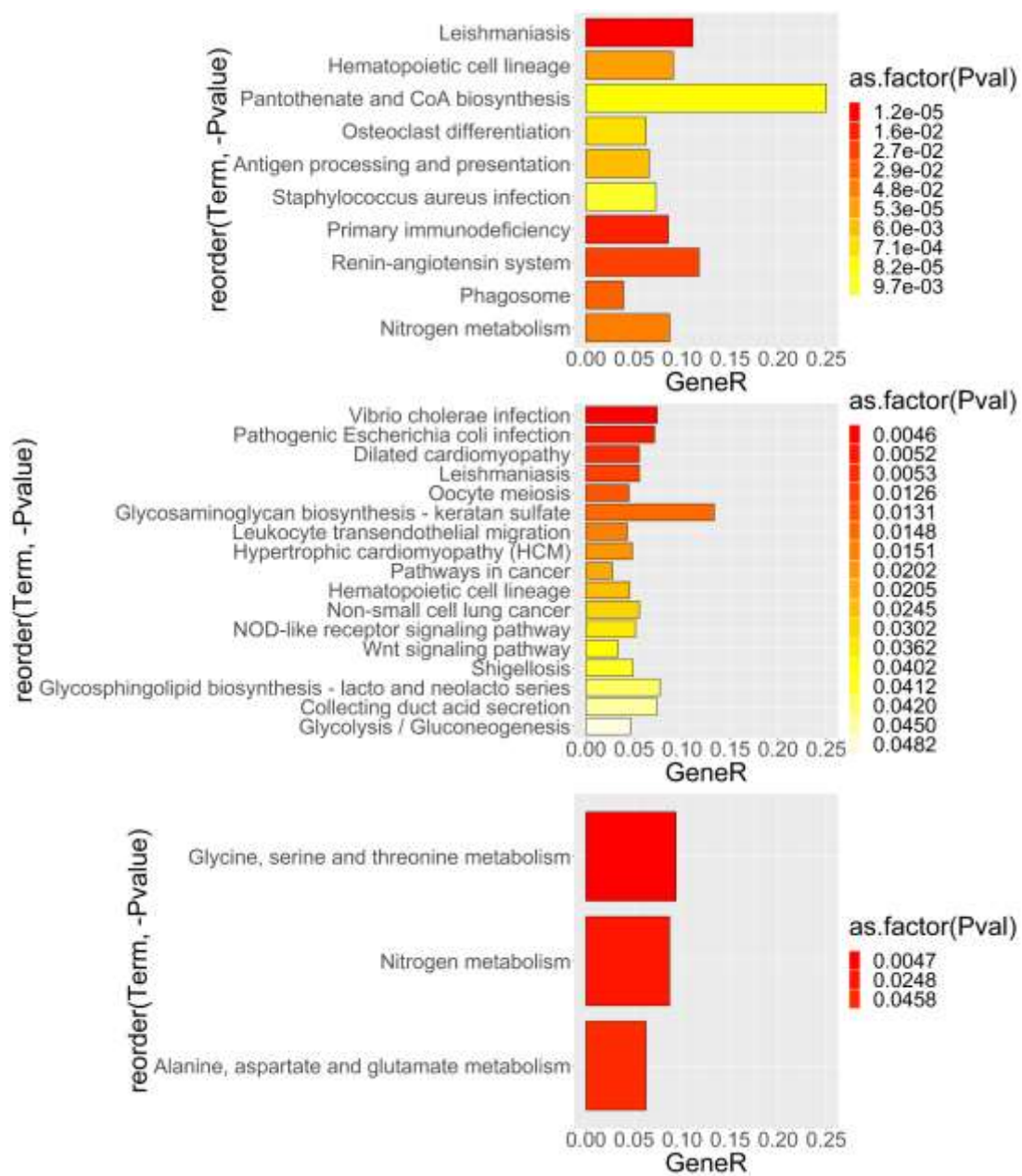


Fig. 6. Over representation analysis (ORA). Barplots showing groups of pathways found in the three clusters of highly expressed genes. X-axis represents the ratio of the group of genes from the input cluster found in the pathway to the total number of genes presented in it.

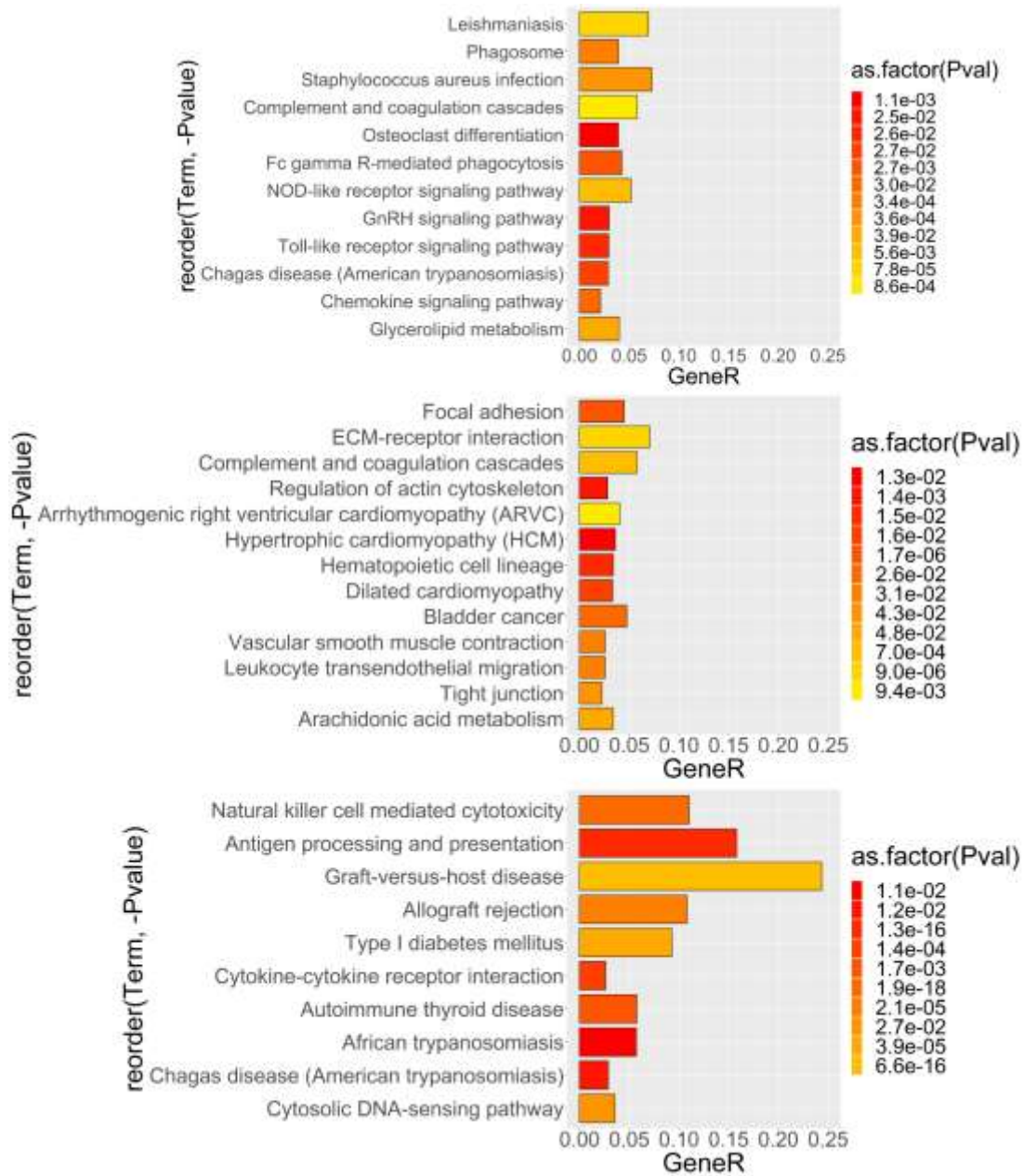


Fig. 7. Over representation analysis (ORA). Barplots showing groups of pathways found in the three clusters of highly expressed genes. X-axis represents the ratio of the group of genes from the input cluster found in the pathway to the total number of genes presented in it.

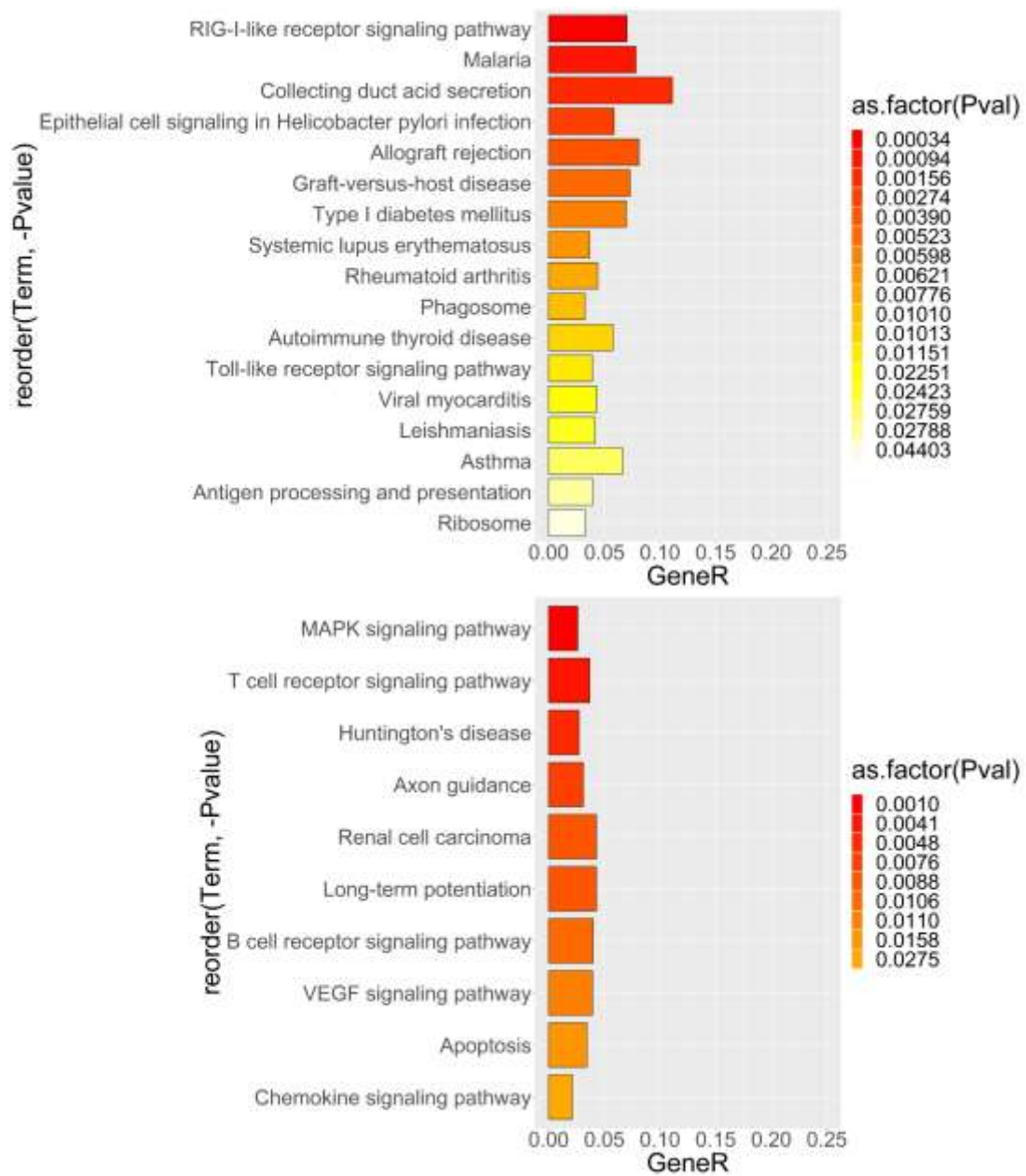


Fig. 8. Over representation analysis (ORA). Barplots showing groups of pathways found in the two clusters of highly expressed genes. X-axis represents the ratio of the group of genes from the input cluster found in the pathway to the total number of genes presented in it.

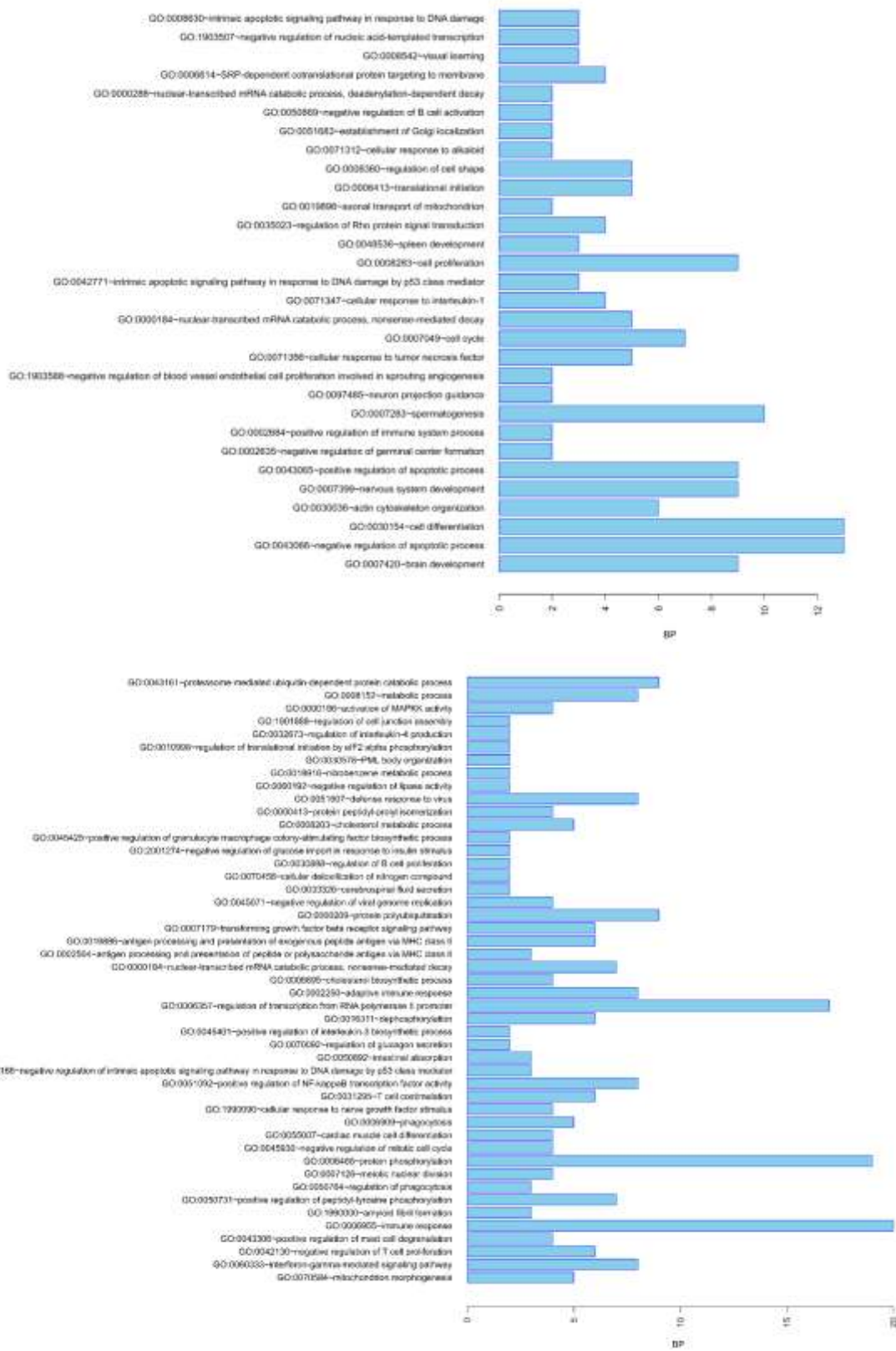


Fig. 9. Gene Ontology (GO). Barplots showing groups of GO pathways found in the co-expression genes clusters (1, 2). X-axis represents the number of genes presented in a pathway. The presented category is a Biological Process (BP).

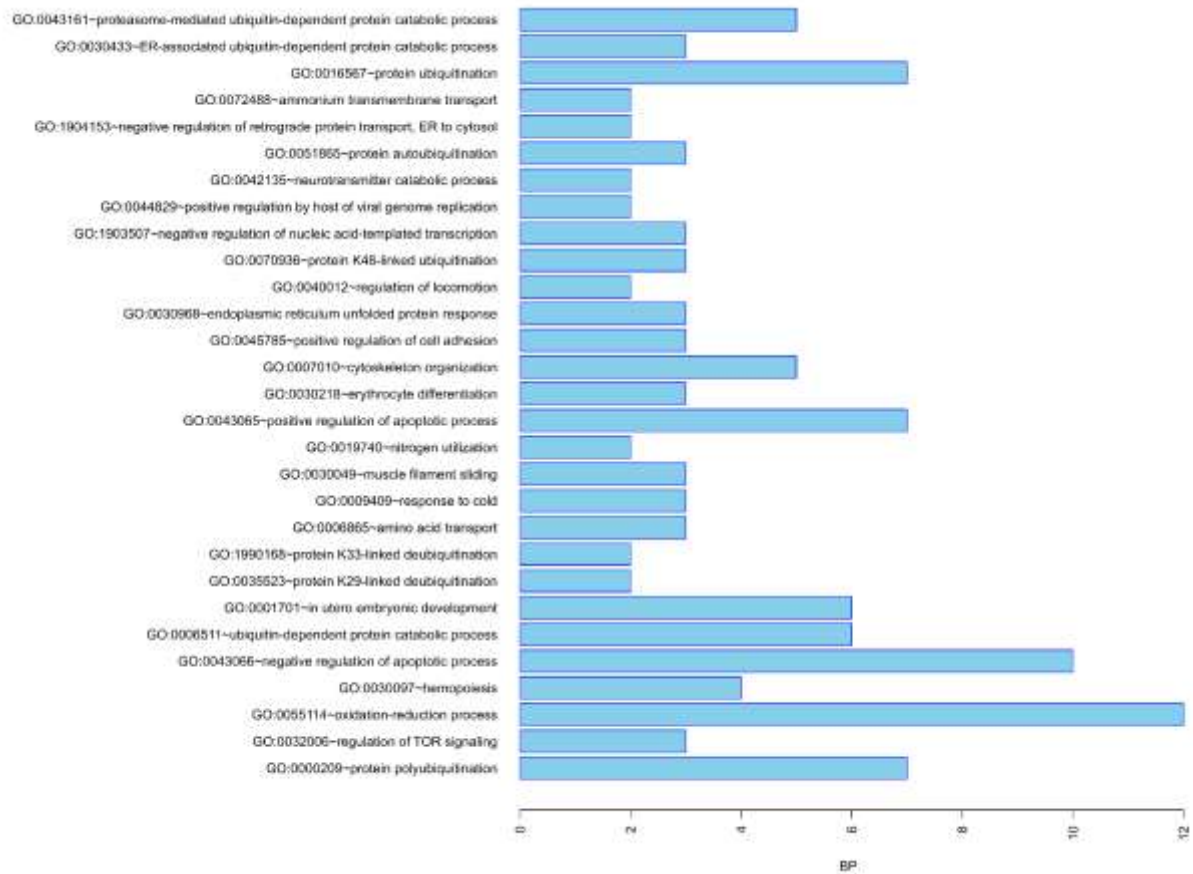
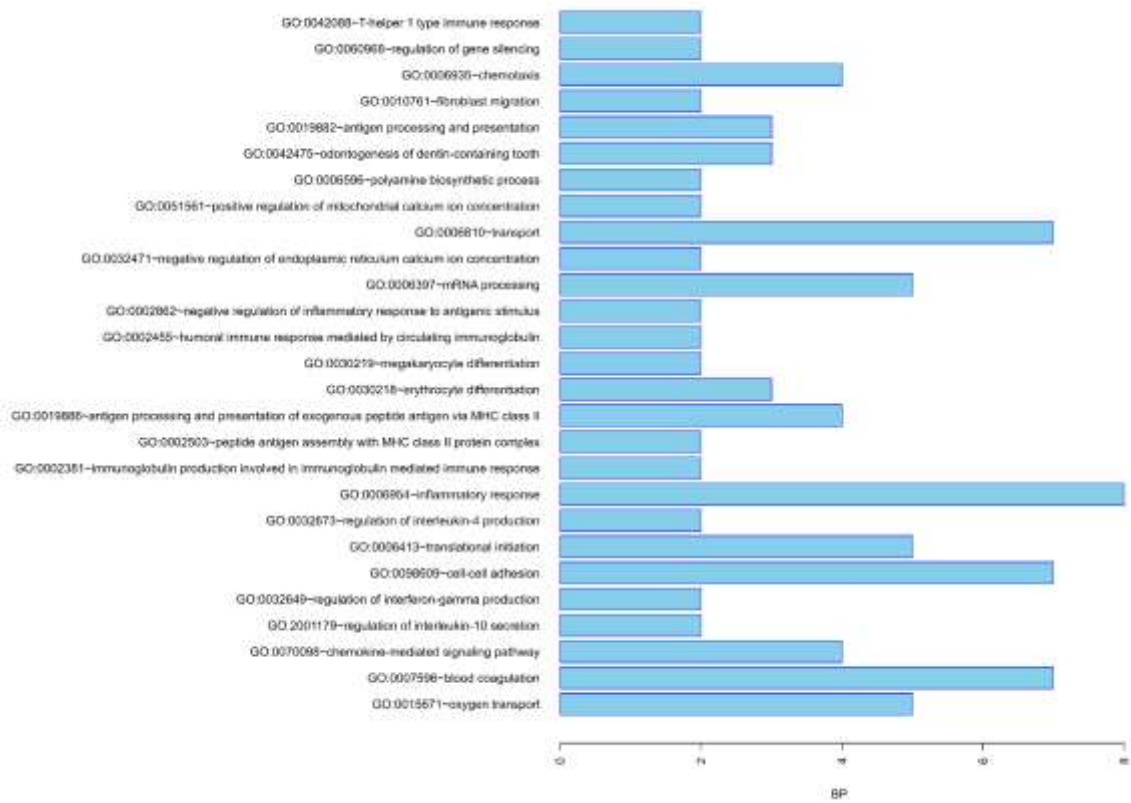


Fig. 10. Gene Ontology (GO). Barplots showing groups of GO pathways found in the co-expression genes clusters (3, 4) (Biological Process category).

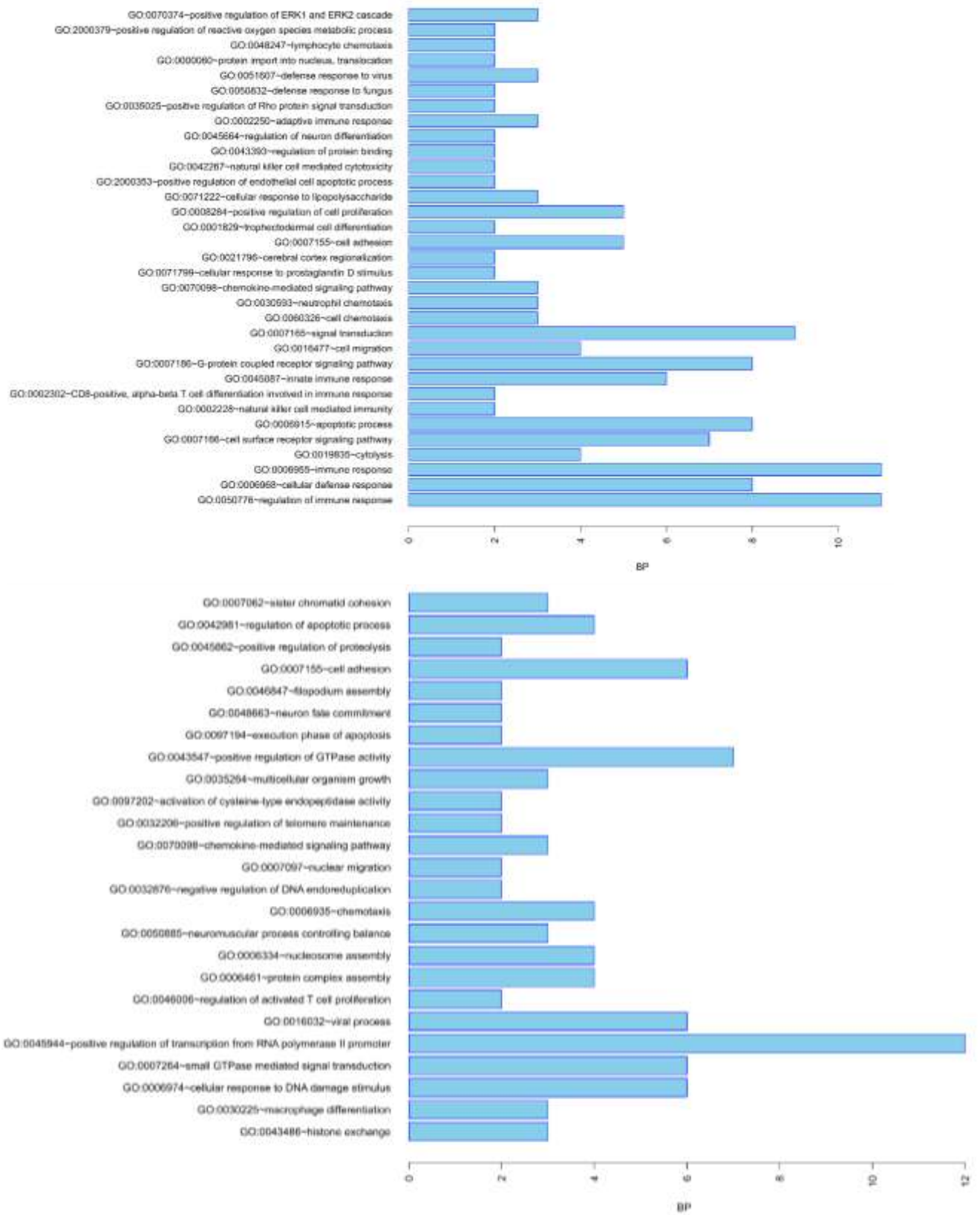


Fig. 11. Gene Ontology (GO). Barplots showing groups of GO pathways found in the co-expression genes clusters (5, 6) (Biological Process category).

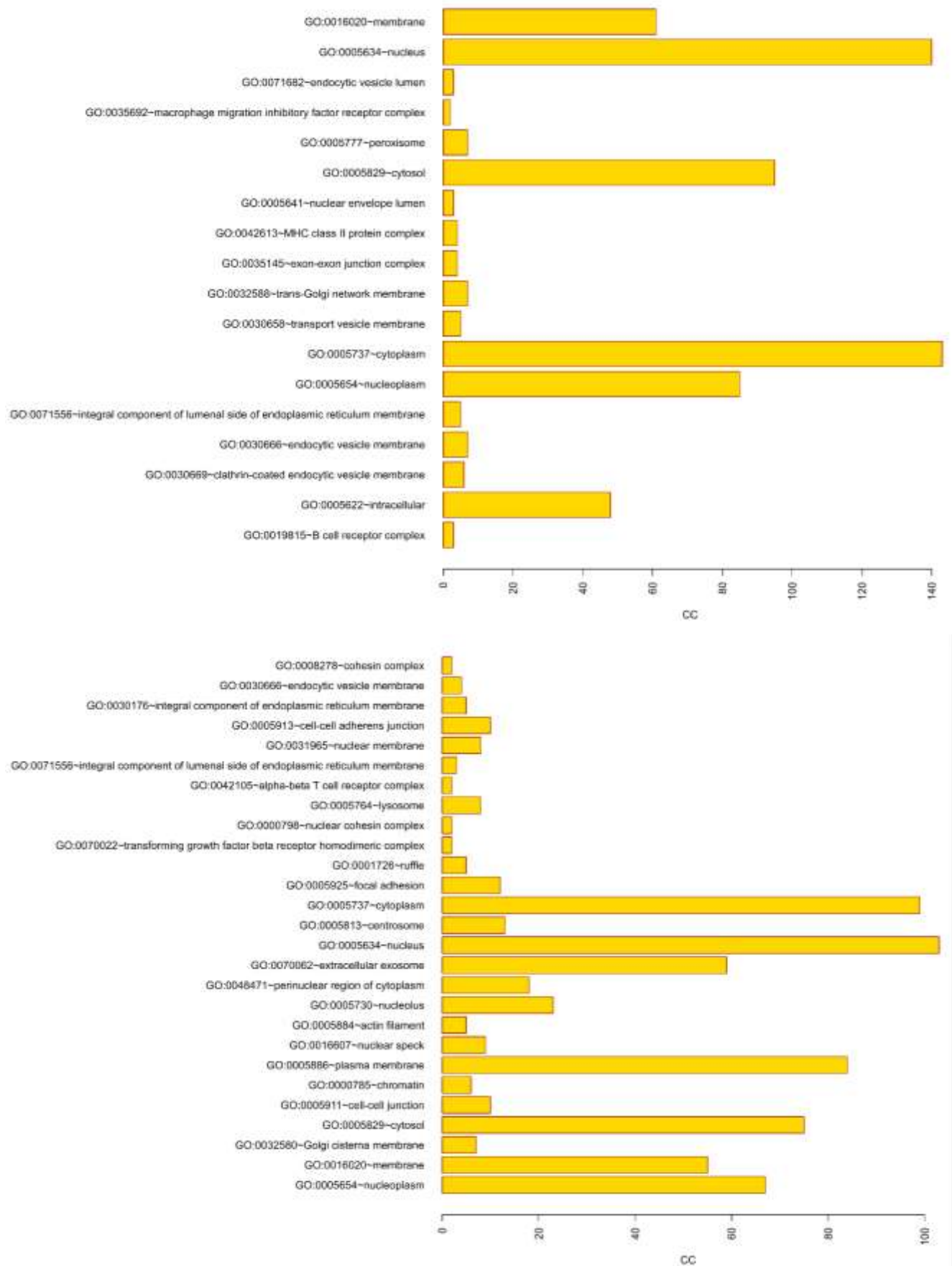


Fig. 12. Gene Ontology (GO). Barplots showing groups of GO pathways found in the co-expression genes clusters (1, 2) (Cellular Component category).

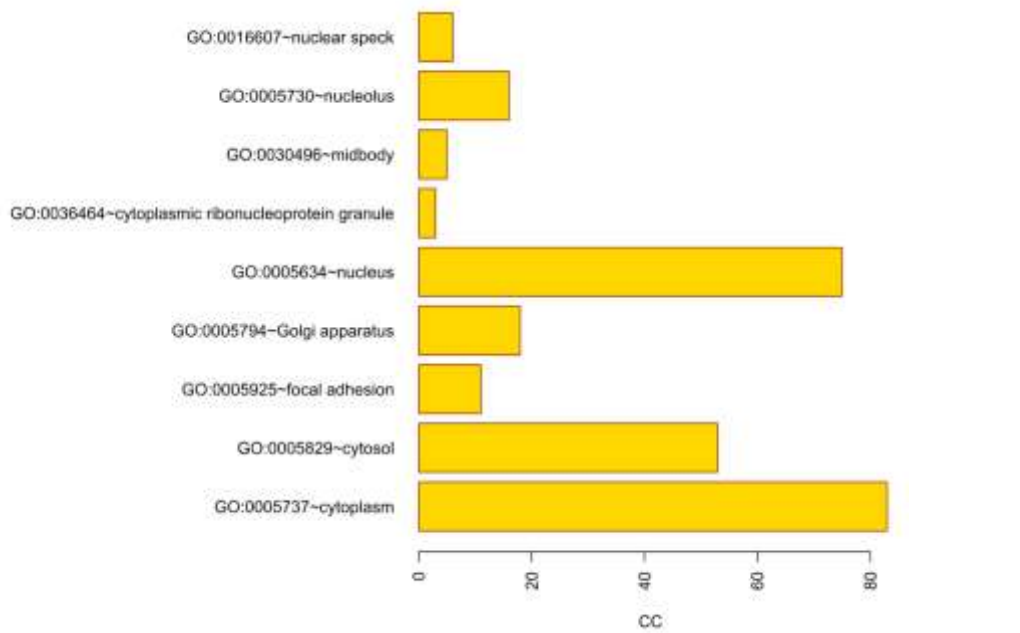
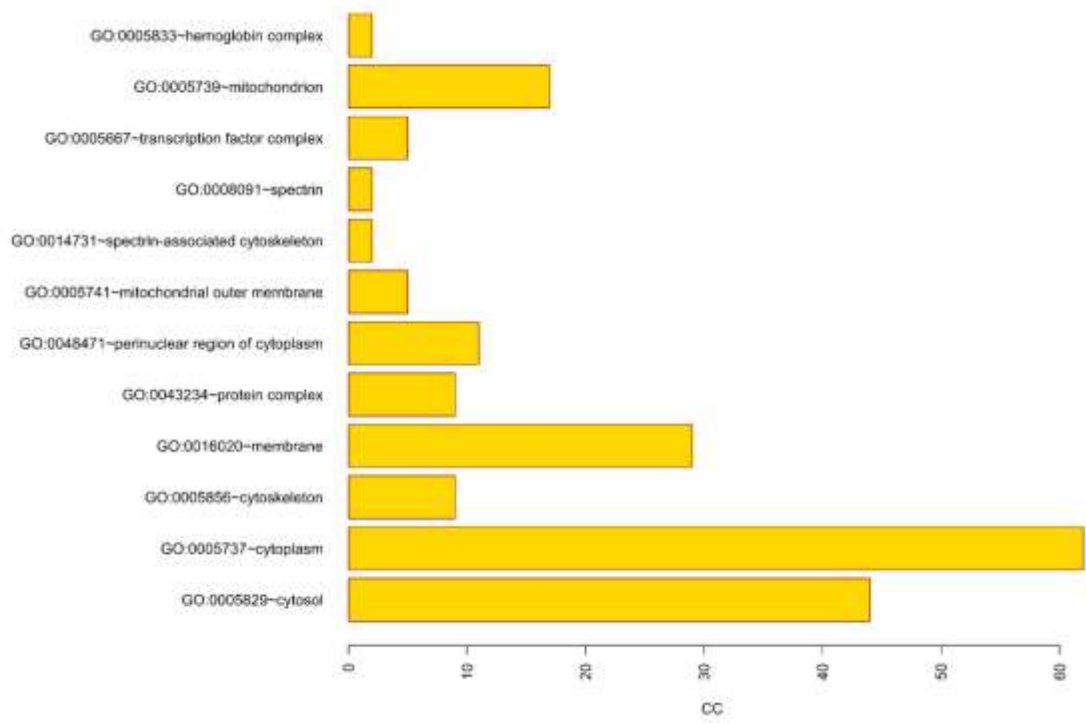


Fig. 13. Gene Ontology (GO). Barplots showing groups of GO pathways found in the co-expression genes clusters (3, 4) (Cellular Component category).

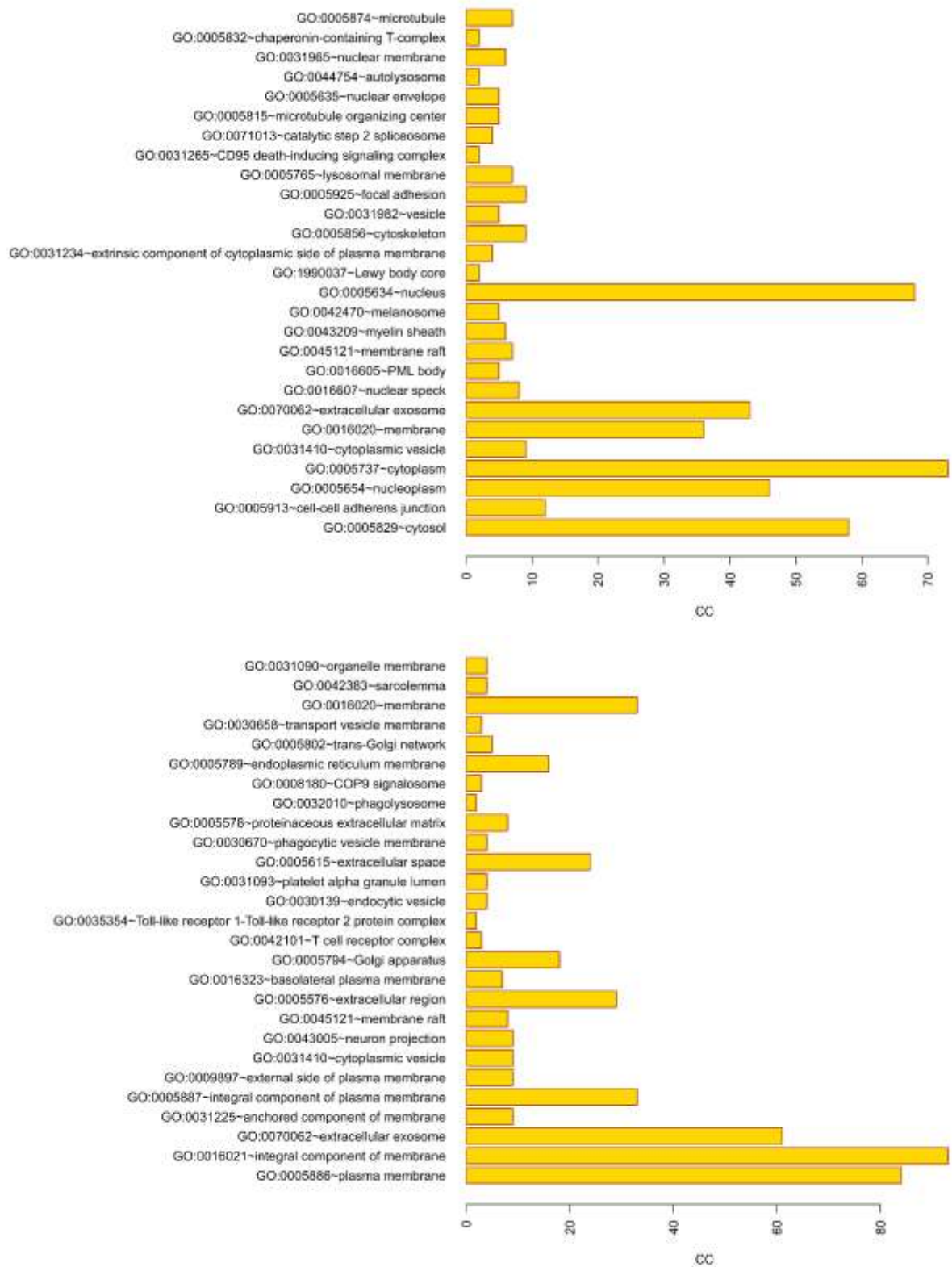


Fig. 14. Gene Ontology (GO). Barplots showing groups of GO pathways found in the co-expression genes clusters (5, 6) (Cellular Component category).

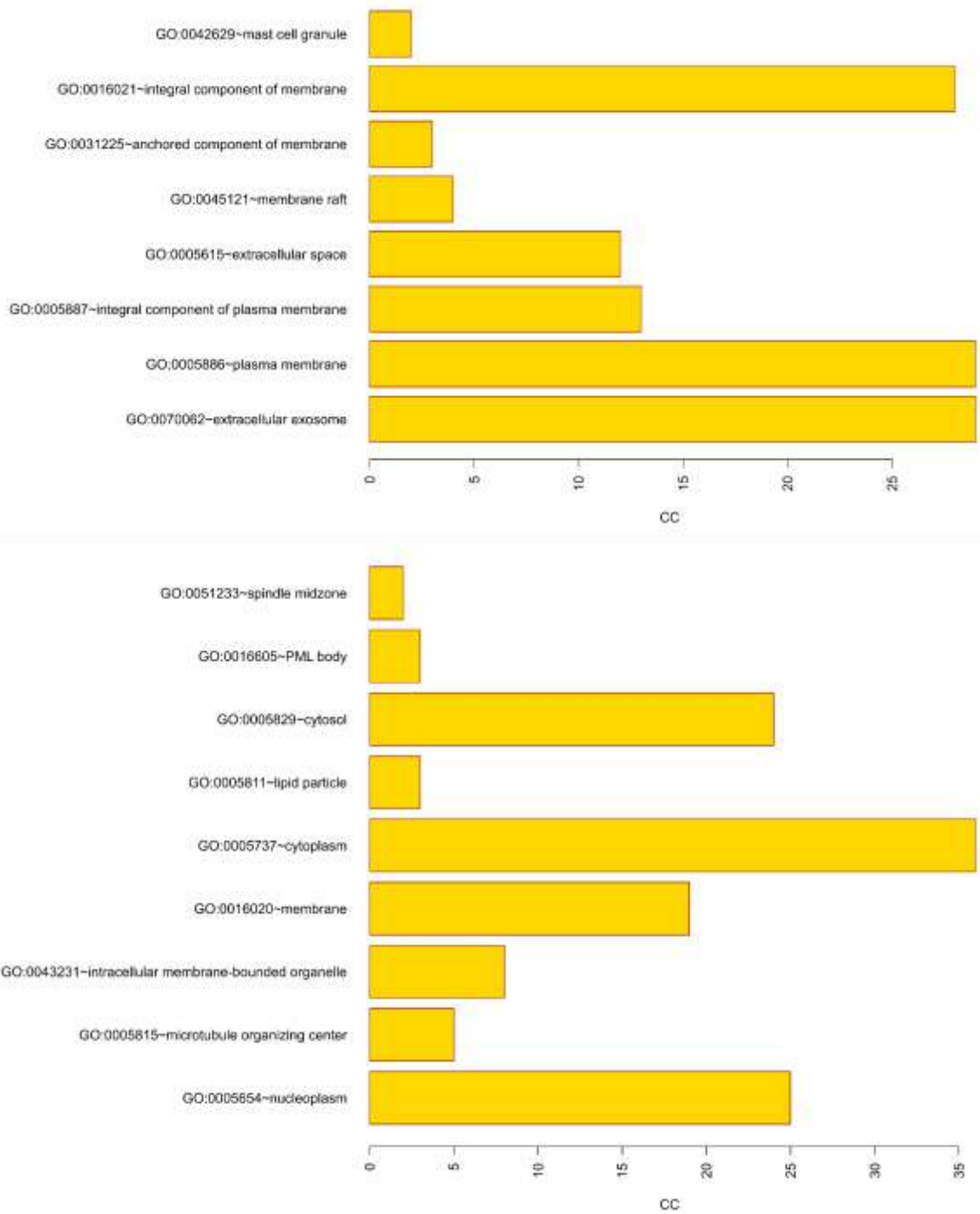


Fig. 15. Gene Ontology (GO). Barplots showing groups of GO pathways found in the co-expression genes clusters (7, 8) (Cellular Component category).

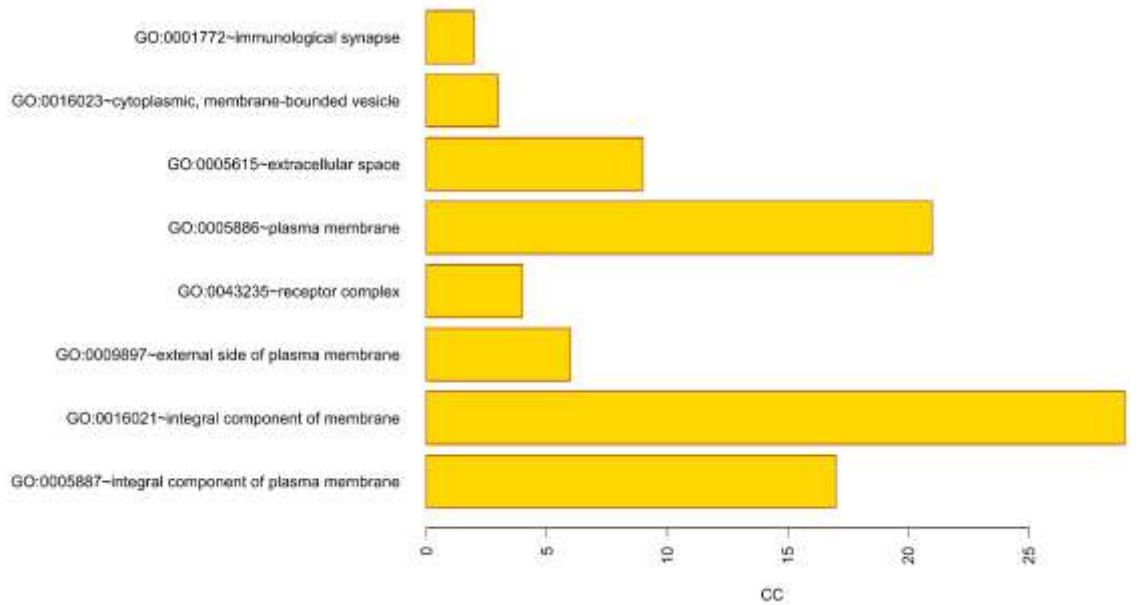
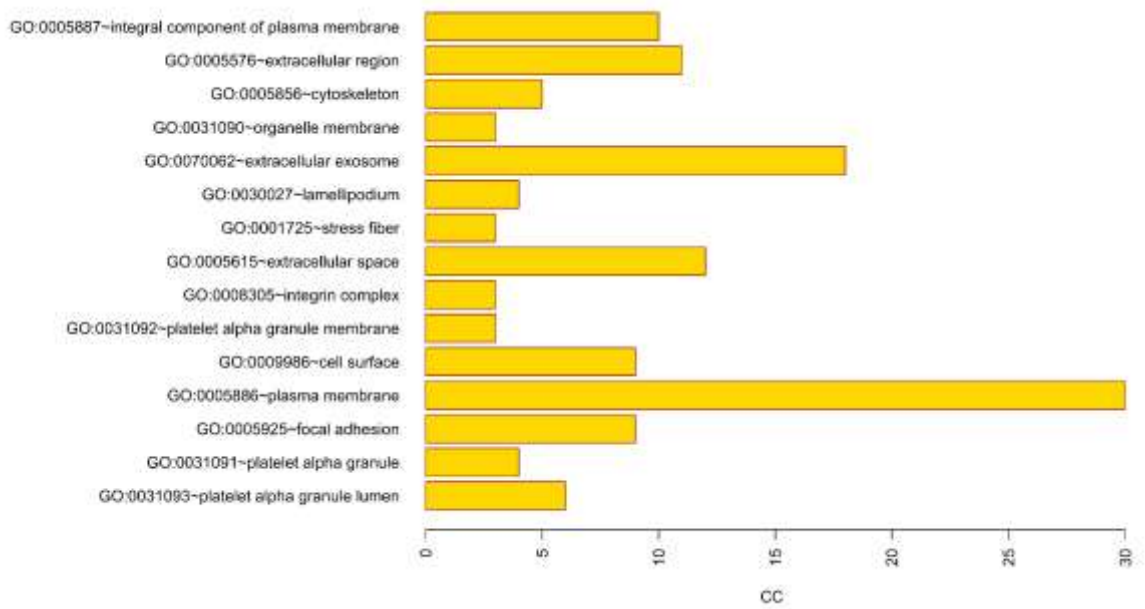


Fig. 16. Gene Ontology (GO). Barplots showing groups of GO pathways found in the co-expression genes clusters (9, 10) (Cellular Component category).

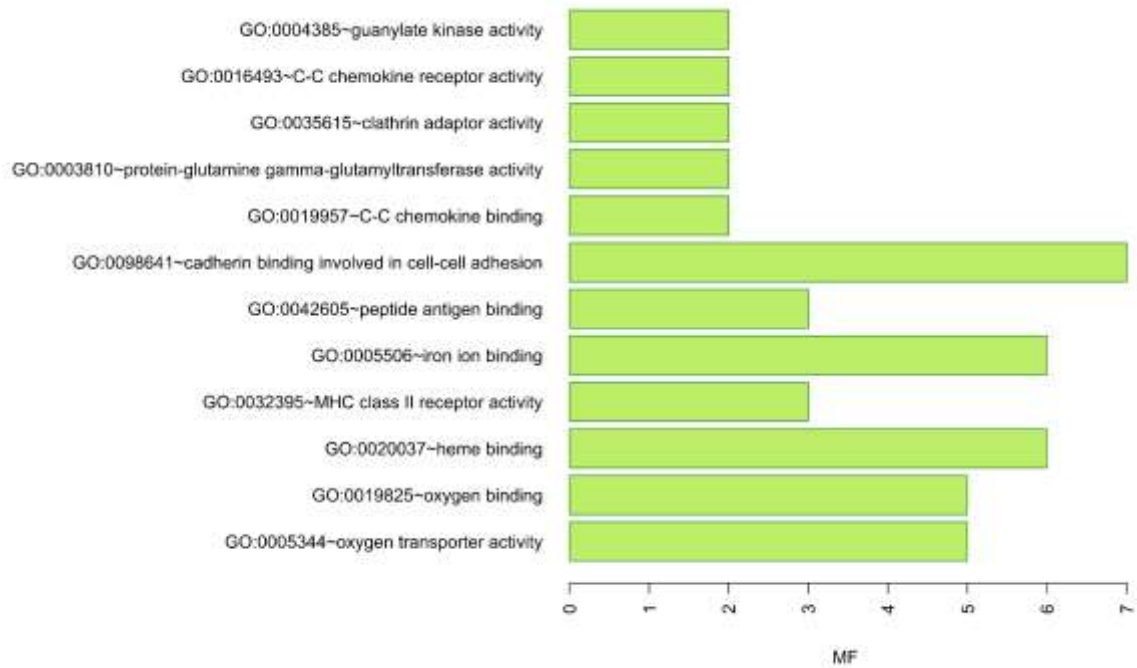
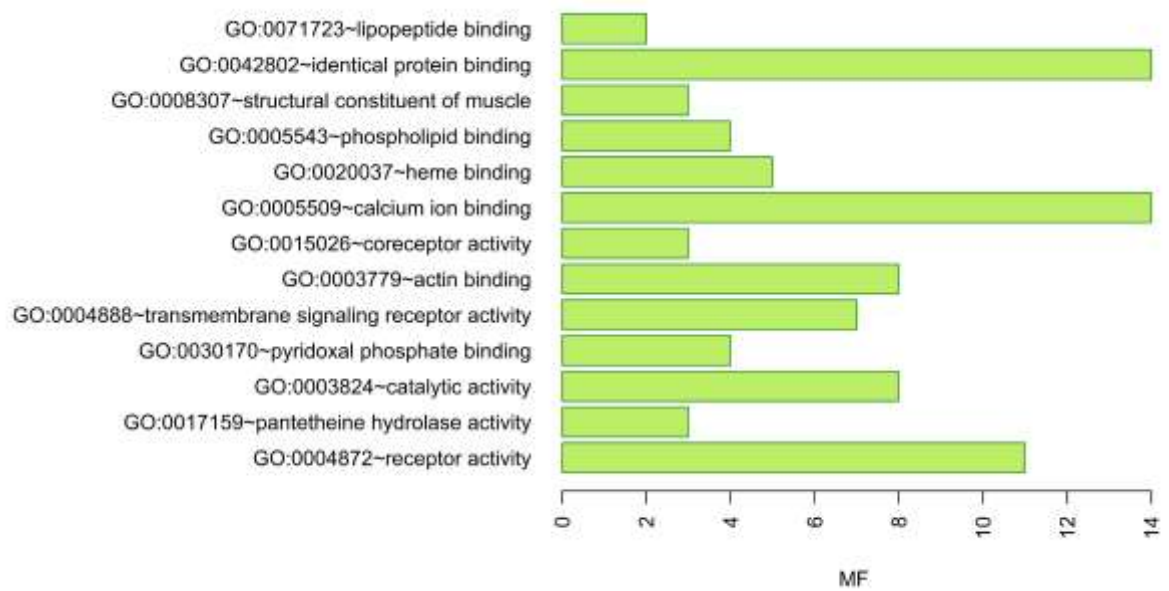


Fig. 17. Gene Ontology (GO). Barplots showing groups of GO pathways found in the co-expression genes clusters (1, 2) (Molecular Function category).

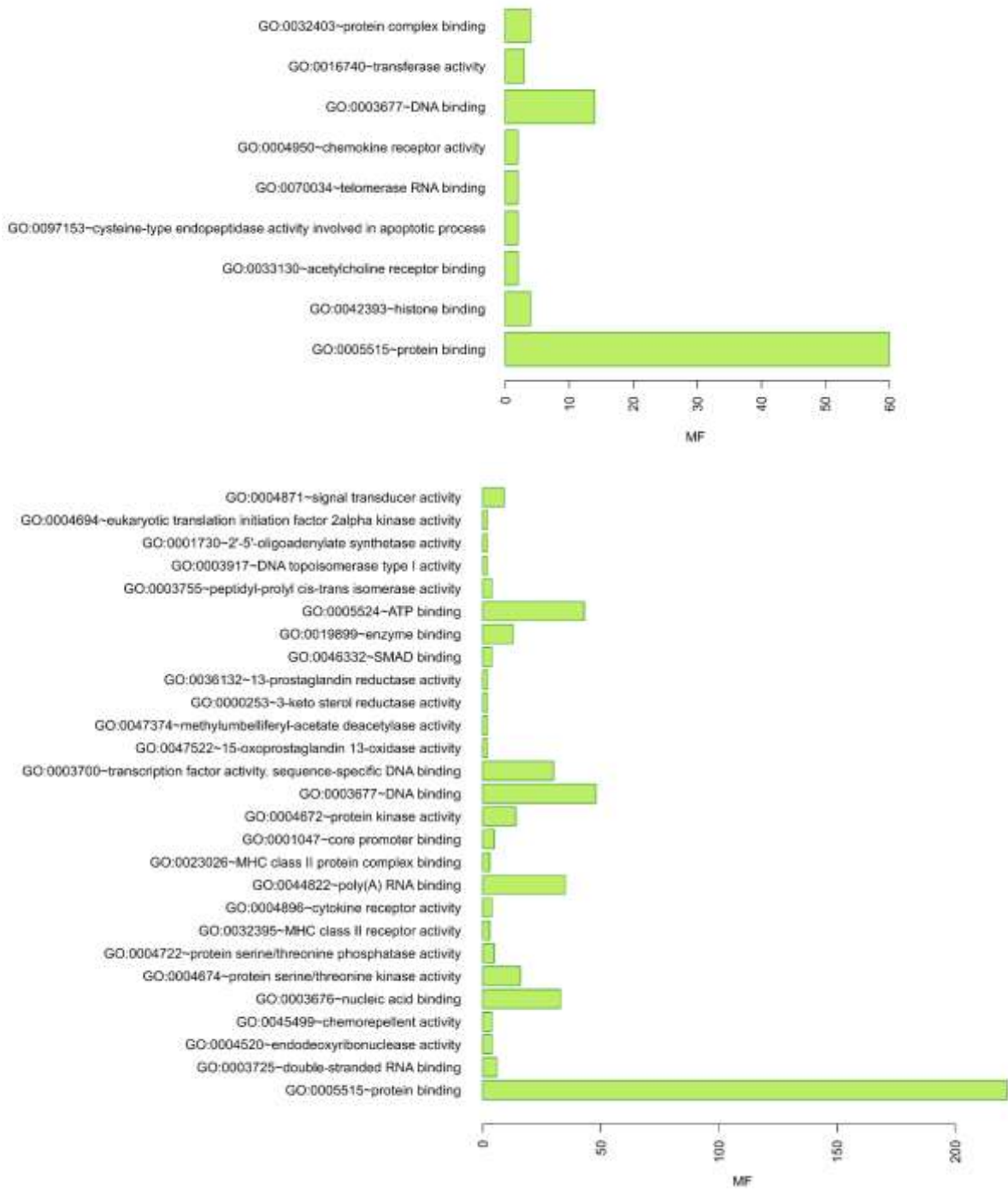


Fig. 18. Gene Ontology (GO). Barplots showing groups of GO pathways found in the co-expression genes clusters (3, 4) (Molecular Function category).

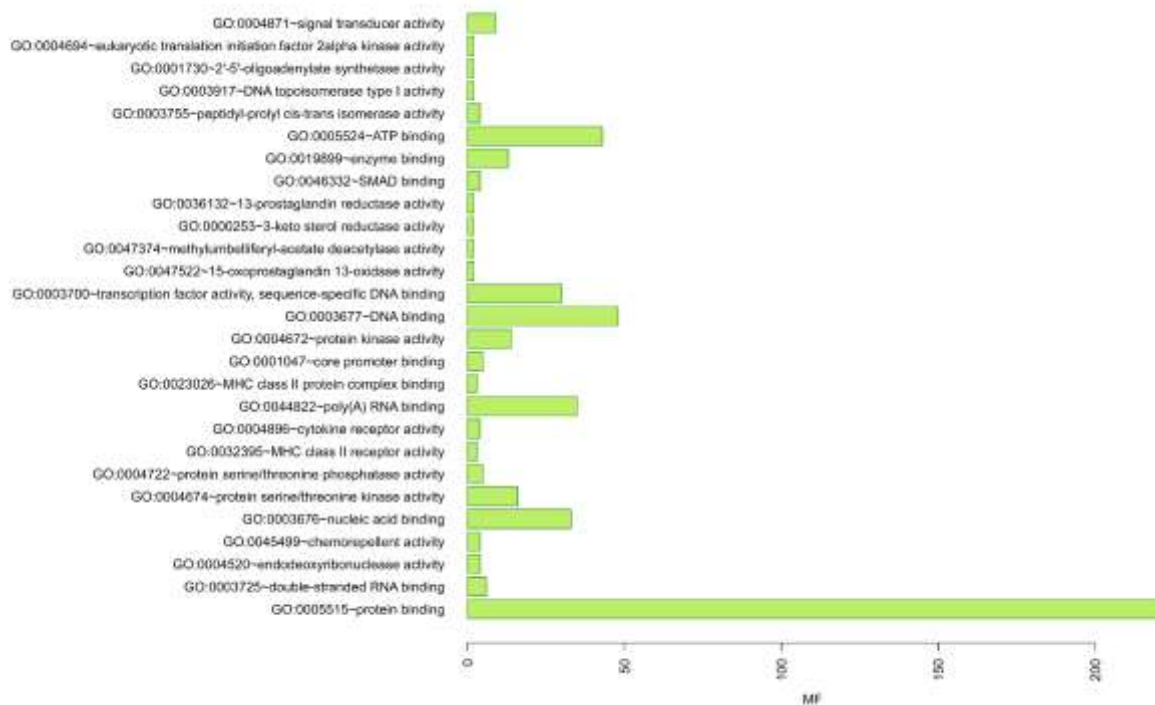
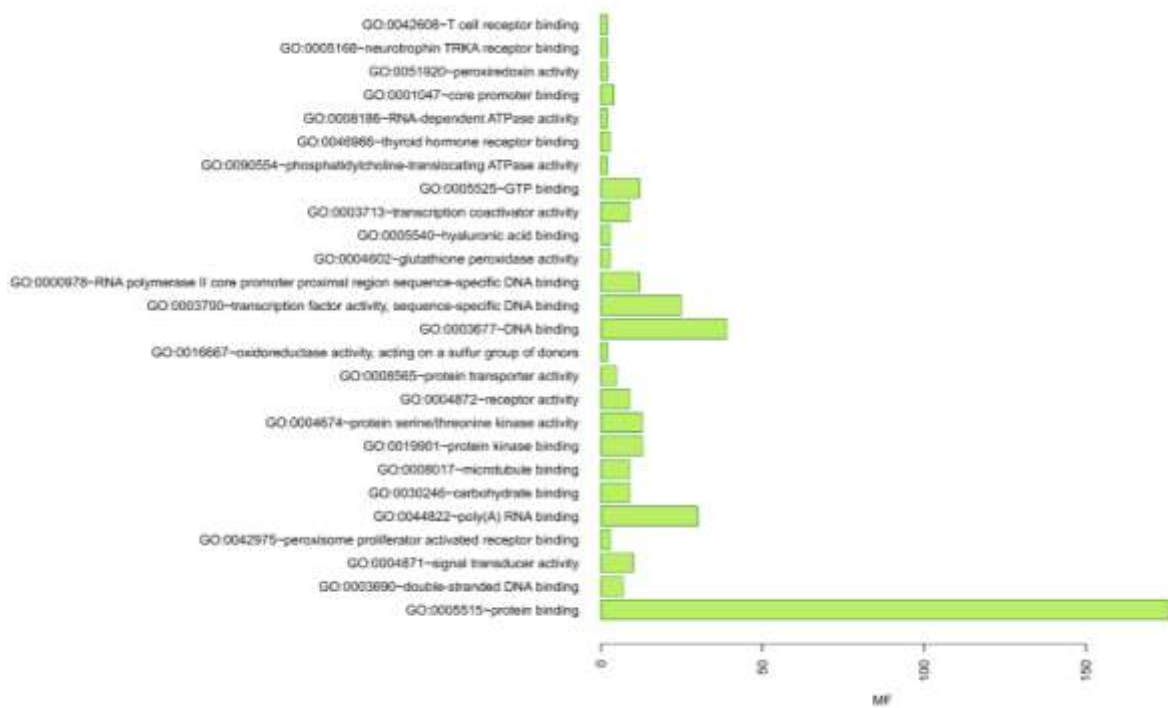


Fig. 19. Gene Ontology (GO). Barplots showing groups of GO pathways found in the co-expression genes clusters (5, 6) (Molecular Function category).

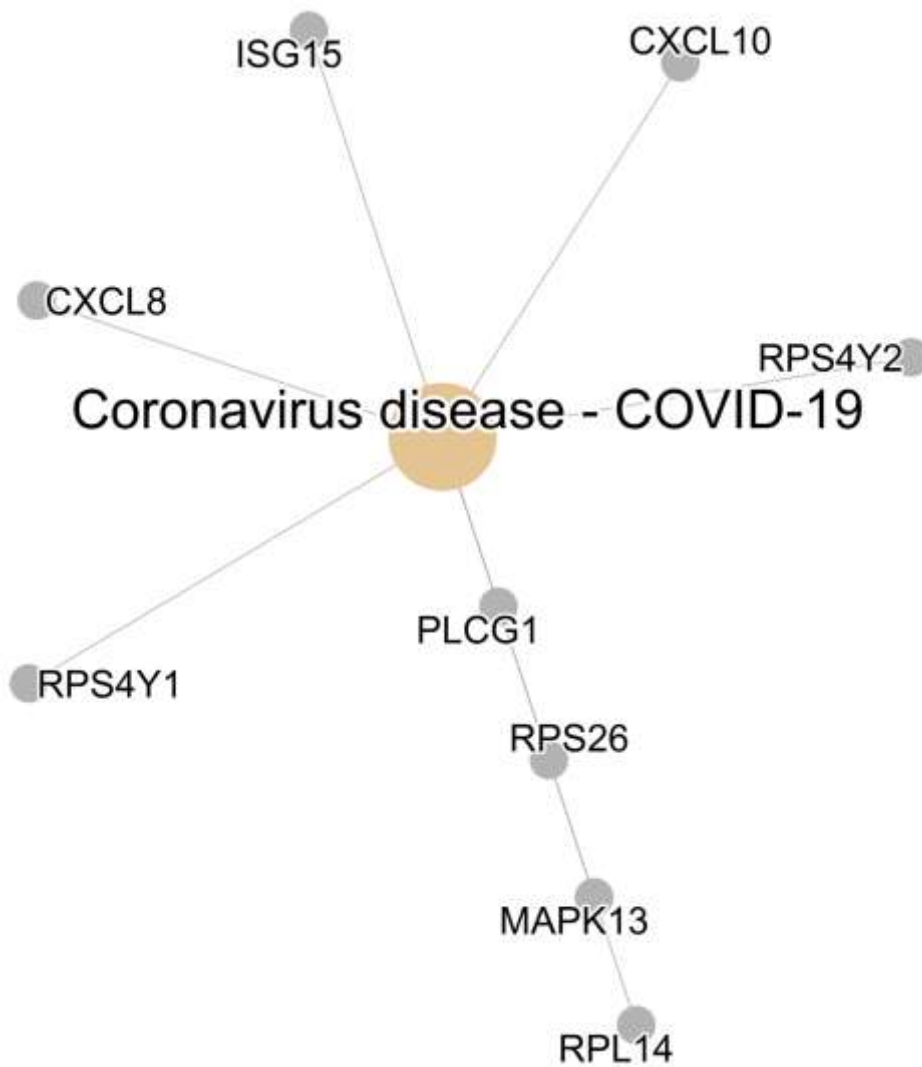


Fig. 20. KEGG graph. Barplots showing groups of pathways found in the two clusters of highly expressed genes. X-axis represents the ratio of the group of genes from the input cluster found in the pathway to the total number of genes presented in it.

Table 5. Pathways found in WikiPathways database

	ID	Pathway name	Genes
1	WP5115	Network map of SARS-CoV-2 signaling pathway	FAM83A HP IFI27
2	WP5039	SARS-CoV-2 innate immunity evasion and cell-specific immune response	NUP98
3	WP5098	T-cell activation SARS-CoV-2	TSC1

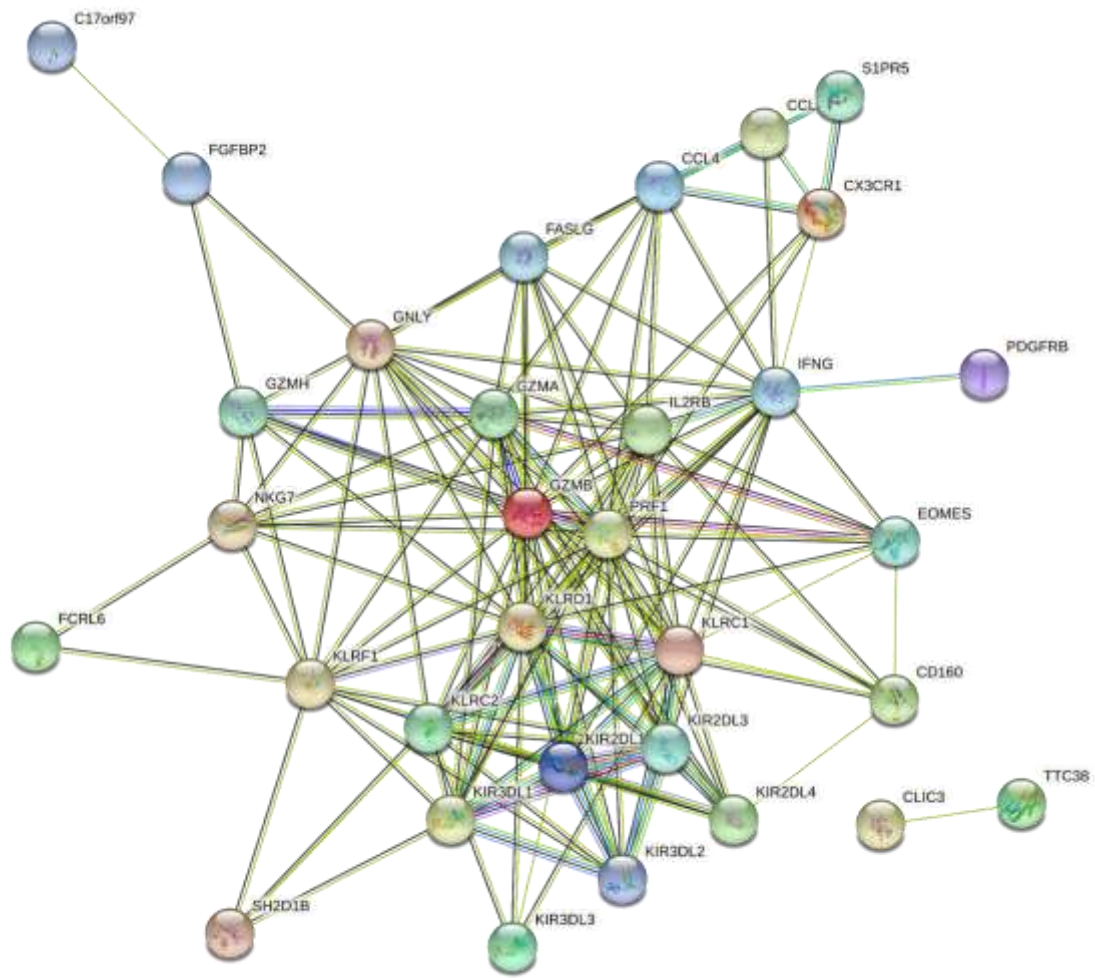


Fig. 21. STRING graph. Protein-protein interactions graph from STRING. Contains genes from one of the co-expression modules, created with CemiTool.

Table 6. DEGs from STRING graph

Gene ID	P-value	Log FC
KIR2DL4	0.00209788651071389	-0.205005232102024
KIR3DL3	0.00814053762563458	-0.216763412869406
KLRD1	0.000135183376061967	-0.249270886125981
KLRC1	0.000207571425358897	-0.259263386490044
KIR2DL1	0.0354069148029456	-0.168799854782198
KIR2DL3	0.000139918664310681	-0.260887263850761
KIR3DL2	0.365968629026214	-0.0719313216278259

Table 7. 380 DEGs found in our study

Gene ID	P-value	Log FC
Down-regulated genes (Healthy vs CINCA)		
IFIT3	1.74609331700504e-05	-0.448294716210724
LOC441763	1.47233982896637e-05	-0.609014232620713
SOD2	2.78149438373382e-07	-0.58012265425286
IKZF3	1.31806278781658e-05	-0.423217419210266
Down-regulated genes (Healthy vs RBCK1 deficiency)		
RHD	3.06377501094136e-07	-0.611200490393251
CA1	7.79560593336739e-10	-0.576206913434433
GLUL	8.6252507011449e-08	-0.433818845743858
HBBP1	2.21004809448002e-10	-0.493952695553687
LOC730996	5.4158206826892e-07	-0.429182308276256
PRR5	6.15756364362851e-06	-0.466970969137613
C20ORF127	4.29196932508036e-11	-0.503823086693028
MAOA	3.45635687661528e-11	-0.71149687967469
EPB41	1.05073344811606e-06	-0.524086955692296
RFFL	1.7787876243623e-07	-0.463262474363137
SRRD	3.69305686343315e-08	-0.435308561743468
EPB41	4.10834311666971e-16	-0.625604788043923
BZRPL1	2.57994400142045e-06	-0.471173744671184
FAM83A	5.44854038181488e-12	-0.599507727918373
C18ORF10	1.09048508902326e-07	-0.428416420839521
ISCA1L	1.52691122702879e-10	-0.501956290642989
UBE2H	5.90301268371945e-08	-0.474685055389697
LOC389293	9.7265992847629e-07	-0.444237498423597
MARCH8	1.56620224759829e-05	-0.415145328541088
ABCC13	2.51980754979099e-11	-0.606438102500972
YOD1	2.61445184502943e-07	-0.429200889815241
MAP2K3	3.2094776830514e-07	-0.535762246169115
ICAM4	8.13314317075278e-06	-0.440589759357464
GYPB	5.35537151818344e-06	-0.535621231895341
GPR146	1.01136419337272e-08	-0.567645214457263
USP12	2.99253437362475e-09	-0.605356436449592
PPM1A	2.03539778781035e-09	-0.528857796785936
LOC643008	1.73442878109425e-05	-0.485040439363551
NFIX	5.22268953523978e-06	-0.4724728396363
HMBS	1.4693732690123e-05	-0.424183404232344
STOM	1.24284526630849e-10	-0.531310670851352
TSTA3	1.34938350092169e-10	-0.477282328432734
KLC3	2.05774537169341e-05	-0.405164523068791
LOC441763	0.000181082483566001	-0.667692304622325
ARL4A	7.26925152801753e-08	-0.489367144774149
KLF1	0.000135750708139281	-0.404669273020196
ALAS2	2.35459034179256e-06	-0.502284988409139
ABCC13	1.90891282700382e-11	-0.547661149453971
CMBL	0.000251673924439325	-0.531786088886633
ENDOGL1	1.42332012702017e-09	-0.431639051878824
TTC25	9.73324861047136e-07	-0.443481768944991
SLC6A9	1.26902867532115e-07	-0.491538129593716
MT1G	1.361860014615e-09	-0.537206194645534
KANK2	1.97993569285184e-05	-0.468624785292866
C5ORF4	2.35196973740107e-09	-0.561928828951184
FBXO9	4.97135009981045e-06	-0.419062143443751
APOBEC2	4.17733010579391e-09	-0.511778758016943
CTNNA1	2.0166448384343e-10	-0.596649699430933
SFRP2	2.91591303469987e-07	-0.5367816022116
DARC	2.23228930373954e-06	-0.506758228600563

CDKL1	5.18558137141098e-11	-0.456240499526942
NR2C2	2.74471210362574e-07	-0.467063780892068
UBE2V1	4.22395050446097e-09	-0.414052200088762
NUP98	5.96598638237005e-13	-0.436454846129473
KRT1	0.000149381819429962	-0.472058867502659
PIP5K1B	1.61607968161147e-06	-0.40278495445915
TMOD1	8.08685868503521e-07	-0.457177922927007
ACSL6	1.6920257303265e-09	-0.482186233547585
BCL2L1	4.07848891215034e-06	-0.56278357895157
ARL4A	2.44775976433304e-07	-0.498357318723835
TRIM10	0.000136589544130928	-0.406188853239464
DDB1	2.19904311913089e-06	-0.411424516867145
HK1	1.06124279949703e-05	-0.44169750081173
TSC1	1.77847714750638e-05	-0.468256438090652
NEK7	0.000170349220630892	-0.433066819325831
XK	2.00592319972554e-06	-0.489141940758087
NRIP3	8.15990365932026e-08	-0.421844535724224
LOC441019	9.06644866645905e-11	-0.561183032184118
MBNL3	2.95767777019393e-06	-0.500129854672688
GLUL	2.74896382034478e-09	-0.546312230012825
TCP11L2	1.26769591795187e-06	-0.471494396335578
FECH	5.41086882496622e-06	-0.511414227978014
TBCEL	3.94419209473046e-06	-0.478551678063247
RAP1GAP	1.33890086146641e-11	-0.988635102618676
OSBP2	7.3910625318555e-08	-0.600874698724962
TMEM56	6.12390440720877e-05	-0.483039958948652
RHOT1	1.10308558627238e-05	-0.446354148644388
GSTA5	0.000209202795444071	-0.506344731509343
BPGM	3.35779076418107e-07	-0.539997871952786
TMEM158	2.72463341738246e-06	-0.407924550530202
CISD2	7.53793555390848e-18	-0.596995403396861
MAP2K3	6.33459801757628e-07	-0.607553874348244
SIAH2	1.38346158335195e-07	-0.410553400629246
LOC253012	1.4820449345248e-14	-0.714106701309741
DPM2	1.31973076649606e-06	-0.444373234792454
SLC14A1	3.61407330577942e-06	-0.472533746138953
C14ORF45	1.06861423592279e-05	-0.406521505707906
TSPAN7	9.74035130571459e-06	-0.582083373265941
RHAG	8.55144551318859e-07	-0.438406584483529
OR2W3	3.35702401663645e-05	-0.478425163113573
GYPE	0.000108299870959704	-0.419783780145331
MAP2K3	2.62556504967366e-08	-0.533593365911246
HS.568705	1.19878618554507e-06	-0.401117514638576
HS.563750	1.53991608195374e-11	-0.562247486891869
BNIP3L	8.67977553186154e-07	-0.437108330372131
IFI27	3.07621715357289e-05	-0.522310561539633
FAM10A7	3.06701055612153e-10	-0.431638059297229
TSPAN7	1.79002824480927e-08	-0.597581551791717
CTNNA1	1.20238873602371e-09	-0.591752492581158
ITLN1	3.35065885877735e-06	-0.470439194740778
C18ORF10	1.43867425110084e-06	-0.444342452561307
TCP11L2	2.2293531169601e-05	-0.444685661263156
FAM83A	1.70381102055525e-13	-0.733775779774681
HPS1	5.38685063353283e-07	-0.441403240291118
ALAS2	6.87503728242588e-09	-0.668295016947645
MGC13057	1.55986789814511e-07	-0.456397469333022
LOC253012	7.08472253869593e-06	-0.4814632803348
EPB41	9.43861898867066e-14	-0.681606254770784
NUP98	3.24830943058539e-08	-0.40065020402267
TRIM23	4.83350492483459e-07	-0.445110561057617
CHD2	6.2799392701495e-12	-0.450443690611727

MARCH8	2.56157544228178e-06	-0.474205738912535
BPGM	1.45034368022173e-10	-0.542350150009864
BPGM	6.20859756105282e-05	-0.423679510669356
FECH	1.15231264764613e-06	-0.561792657767508
LOC253012	5.73998378461065e-16	-0.681069526086712
SOX6	4.1110047227485e-05	-0.444872082134934
RHCE	2.39065579240491e-10	-0.576783549807026
PPM1A	6.58118313415536e-08	-0.486525770111466
Down-regulated genes (Healthy vs MVK)		
OR7D2	7.04254590259349e-07	-0.445190246204898
CTAG2	1.37293178849356e-08	-0.425508982145102
Down-regulated genes (Healthy vs MWS)		
MAPK8IP1	3.23183843676115e-08	-0.426087995959029
GPR128	3.21031089903406e-09	-0.404337799088839
HP	4.72312538568793e-08	-0.410948832911504
Up-regulated gene (Healthy vs CINCA)		
HS.332360	1.35896745487404e-06	1.61321965741775
Up-regulated genes (Healthy vs RBCK1 deficiency)		
PLA2R1	0.000199207127737016	0.892439400436565
FLJ00312	3.6401154176701e-07	1.61761590151659
HIST1H2BI	0.000278443535449758	0.916727064236308
ANKMY2	6.5171254938158e-06	0.418964835449505
HS.551123	6.45879094685694e-13	3.16870105950953
HS.19339	6.03473284790242e-07	0.464301646441145
HS.542923	0.000384929864622159	1.15592770980196
HS.531457	7.58513792049983e-05	0.419426602559435
HS.552143	1.58377723350902e-07	1.29376182615501
RPS29	1.97801903881016e-05	0.412319477580699
Up-regulated genes (Healthy vs MWS)		
SNORD101	2.98981619650048e-06	1.59871466324165
GPM6B	2.67626160499603e-06	1.50880585329478
Up-regulated genes (Healthy vs MVK)		
HBBP1	1.14173704941383e-06	0.478653983440068
C20ORF127	6.5798157203638e-06	0.426409184547074
MAOA	2.44015082103226e-06	0.630052228582019
RFFL	3.4212549477718e-06	0.536219474675563
EPB41	2.62701820835691e-07	0.455631839848625
FAM83A	2.49782329060035e-08	0.627802381539782
NSUN3	5.92453035266978e-08	0.409883315641316
PPM1A	4.9767051917542e-06	0.556313765226818
HES6	6.05123772618859e-05	0.423091284342303
STOM	5.5540472638423e-05	0.409081086031493
TSTA3	3.08936535341488e-06	0.446142229778541
SNORD101	4.65225998118568e-06	1.73120617955731
ABCC13	4.26519783082112e-05	0.401252510049555
CDKL1	2.74858844333723e-07	0.466255440087856
NUP98	4.30772014356358e-08	0.414001599570805
ARL4A	2.77034252417117e-05	0.571251272351404
NRIP3	6.49414101845174e-06	0.459589541823844
LOC441019	1.03497404016182e-05	0.490979582676609
RAP1GAP	1.04200655288737e-06	1.37706133345479
TMEM158	1.78835519450909e-05	0.559385168815898
CISD2	1.23869398791649e-08	0.451745023155612
LOC253012	4.14821610170912e-06	0.509662208073758
HS.563750	9.33931440883221e-09	0.694052147312873
DLEU1	1.02150679853994e-05	0.407460618680324
TSPAN7	4.46178512125141e-05	0.583825631997659
FAM83A	5.82403503434797e-08	0.716128748862842
MGC13057	1.0208393292274e-06	0.562824585588067
EPB41	1.33267826006951e-05	0.474380549237925

LOC253012	1.26166462171332e-08	0.591032442962684
RHD	4.68191484876829e-05	0.544713595508595
CA1	2.06047810631241e-08	0.651662978151937
UBL7	4.36162281188699e-06	0.43222274890705
HBBP1	1.28462310982546e-08	0.489866086735082
LOC647958	0.000383362786234934	0.440703192818126
PRR5	2.40086999810563e-05	0.500725742709894
LOC649604	3.97252123322445e-07	0.421598944894415
C20ORF127	6.04674921396216e-09	0.493875977182491
RNF123	1.02252963207917e-06	0.402170050385184
MAOA	1.65040803323732e-08	0.662629399111838
EPB41	4.04818708736332e-06	0.571534194122536
RFFL	4.36928552031925e-07	0.50126076803325
SRRD	6.32067667126842e-08	0.50809310388097
IL8	0.000272491635030956	0.519572710602466
EPB41	1.11037747907479e-12	0.61376653038594
BZRPL1	2.59792648055488e-05	0.4674987344675
FAM83A	3.15290102299894e-09	0.549987798669722
C18ORF10	8.84190869638946e-08	0.520311590223252
ISCA1L	9.25098466804627e-08	0.46685158442946
UBE2H	4.77034298342347e-06	0.44939447214597
LOC389293	4.17040770960571e-05	0.418600401897941
MARCH8	2.09227487366482e-05	0.466603449391998
ABCC13	9.22291033587986e-10	0.623913001131426
HEMGN	0.000215227363138166	0.50033548218047
SELENBP1	0.000260401675898387	0.438454752769696
MAP2K3	7.46960733594107e-07	0.627315147141768
ICAM4	4.25403295045977e-07	0.599718856369376
GYPB	8.39764478181565e-05	0.543099112457328
GPR146	3.78960136847208e-07	0.59138099461057
MT2A	6.35641211903385e-10	0.40388776467241
LOC648494	9.42154149048378e-05	0.410876933648217
USP12	5.19880411907117e-07	0.57168872780835
PPM1A	2.98834086031698e-07	0.512038220299723
LOC643008	7.8122957880705e-05	0.523612511975364
NFIX	0.000103552658660884	0.46031550073921
HMBS	9.40772810791819e-06	0.519528868249405
GYPE	5.00144461172661e-06	0.469349239965135
STOM	1.92970428396748e-07	0.470839892557033
TSTA3	1.95839887121962e-07	0.418946026914881
KLC3	2.87953451192714e-06	0.53631519092312
LOC731777	6.68848823094516e-09	0.420562734994813
ARL4A	7.33536142402827e-07	0.516517393054458
KLF1	3.33451938955765e-05	0.530399521284292
SLC1A5	8.0633068761184e-06	0.407613444980876
ALAS2	0.000348240844414221	0.428177897524068
ABCC13	1.29727963495995e-10	0.633767571117769
ENDOGL1	3.03023226440504e-08	0.448878491800459
TTC25	1.63648860335468e-07	0.587559079322214
LOC653907	6.15650827577892e-07	0.462612801441705
CDC34	5.55536752274364e-07	0.446120248844223
HBZ	0.000277612301403654	0.79537438340555
SLC6A9	6.88671458523452e-06	0.469482963389481
MT1G	8.9791739665621e-07	0.470419748096149
FBXO7	1.73488026848113e-05	0.481788633054943
KANK2	0.000366028395393602	0.424609722586072
C5ORF4	1.24485021519584e-07	0.565798121664606
FBXO9	2.96510615876494e-07	0.58757516476698
APOBEC2	2.21806225235802e-07	0.489803241343539
CTNNAL1	1.24040350325174e-06	0.493379551531111
SFRP2	3.34359368888017e-05	0.463411053916889

DARC	2.25783961407591e-05	0.528664494774814
CDKL1	6.50921484748966e-11	0.537051601953825
UBE2V1	3.7812540373462e-08	0.442588997903417
GMPR	5.99658044108212e-05	0.441335619895896
DPM2	3.48768685960766e-06	0.508894129919738
LOC730996	3.55269424723149e-06	0.422913672641048
MARCH3	1.19530713929392e-05	0.430021567487154
LOC648434	2.64934138634416e-05	0.405649016842396
KRT1	3.68833039983947e-06	0.793756801295169
TMOD1	9.31921474299839e-06	0.479441098399924
ACSL6	1.15099810839809e-07	0.475726296902466
KEL	0.00015979425315366	0.495765144346225
RNF175	8.14193233315393e-05	0.404272097979131
HPS1	1.51749795631051e-06	0.536099902719691
RAB3IL1	0.000229363980086953	0.453281380795621
BCL2L1	1.6218970547731e-05	0.647949310506331
ARL4A	2.23271085433759e-06	0.532406349497287
TRIM10	0.000262942628753118	0.453164798941961
SYT15	2.33838538676627e-06	0.444391684122992
LOC440313	0.000172076514979739	0.541371888950144
HK1	2.03357213049933e-05	0.492493436887975
RUNDC3A	0.000223036401103234	0.588696458313033
TSC1	0.000153981890851736	0.452460418004396
XK	2.46749073305039e-05	0.505571664720605
IFIT1L	1.34550305910812e-05	0.486306770858157
LOC441019	1.67750250102536e-10	0.684281074856468
MBNL3	7.12632969691523e-06	0.55238029339834
GLUL	6.9836212740305e-08	0.58209151568982
SNCA	2.33871691224687e-06	0.46564760974609
SLC6A10P	0.000242715735417517	0.418746743447086
TCP11L2	1.05921338508118e-06	0.569823508504849
BRD4	3.83583436131254e-06	0.430824788913916
LOC650898	9.99309026221346e-05	0.415270015889231
ARL4A	0.000217586238613028	0.545382456664364
TBCEL	2.69587457292362e-05	0.50296901613574
RAP1GAP	5.42618312187792e-06	0.742882073475464
OSBP2	1.1386739571916e-06	0.669506292993562
PBX1	1.33425273483343e-05	0.419138025518595
RHOT1	0.000156127600192038	0.429560256462088
MGC13057	2.19152045812114e-06	0.407075110368549
GSTA5	0.000378270612556844	0.559254146538072
BPGM	4.39159953683287e-07	0.629161726961319
C20ORF175	5.32190218659349e-05	0.433336000705182
CISD2	3.32951900002514e-12	0.499800982635026
MAP2K3	8.82066030756384e-05	0.550400306445956
LOC253012	1.0341116410218e-10	0.662639156919313
DPM2	4.94692074399743e-07	0.56194631281929
SLC14A1	1.37380349953298e-05	0.524725486864942
TSPAN7	2.45142072261846e-05	0.638428257956705
RHAG	2.82675206007722e-06	0.470113359050469
OR2W3	5.96909940043465e-05	0.555800488682924
GYPE	0.000272742639864919	0.451120886055731
MAP2K3	6.23382249041453e-06	0.485190073258051
HBD	4.51159282687686e-06	0.558520973967356
HS.568705	1.64607246917726e-06	0.440454739957978
HS.563750	1.60829923569124e-08	0.499334740032373
RP11-529I10.4	3.79531846417734e-06	0.487165736219161
TSPAN7	4.24316380774168e-07	0.617612090122576
CTNNAL1	5.66791939967482e-06	0.478277555850092
PIP5K2A	0.000286334197788232	0.407700080870365
ITLN1	1.20852658613045e-07	0.699120999650875

C18ORF10	2.19639314991728e-06	0.522244970813161
TCP11L2	1.84754512609556e-05	0.537697590514322
LOC388931	9.11037571975723e-06	0.420583047275303
FAM83A	2.35133825673221e-09	0.615388106324918
HPS1	1.3717818409742e-07	0.576192314176819
ALAS2	8.04326362135468e-07	0.67401247539983
MGC13057	1.63797088915475e-07	0.517491538633812
LOC253012	5.26296607264634e-05	0.501360285430449
MBNL3	4.11697885109786e-05	0.405879635475871
EPB41	6.8721583696329e-09	0.571674725863154
TRIM23	8.00947566589959e-06	0.447847245538033
MARCH8	3.10350308650188e-05	0.501903280577696
CHD2	4.03524533351963e-09	0.420455571667781
MARCH8	1.61263195902561e-06	0.591780232707442
BPGM	7.31919750054256e-09	0.57663903012379
FECH	0.000388278498753792	0.453261769492885
HAGH	8.25879624009117e-05	0.410057922274795
LOC253012	1.29770172634334e-10	0.567851589068332
RHCE	1.73573544650488e-07	0.527718143432599
PPM1A	1.79429219936815e-06	0.496416883349792
HPS1	3.58586332548645e-07	0.550024732917581