

Support information

Table

Table S1 The top 10 differentially expressed lncRNAs and mRNAs detected among newly diagnosed ITP patients (P1) and chronic recurrent ITP patients (P2) versus healthy controls (N). Chr: chromosomal derivation of the lncRNAs.

Up regulated lncRNAs (Top 10)								
P1 vs N			P2 vs N			P2 vs P1		
Seqname	Fold change	Chr	Seqname	Fold change	Chr	Seqname	Fold change	Chr
NR_037166	18.2377081	chr6	TCONS_00000918	13.8725523	chr1	TCONS_00000918	47.2823881	chr1
ENST00000548900	18.1087074	chr12	uc021qqx.1	10.1056578	chr11	ENST00000433329	21.8240659	chr11
ENST00000584923	8.9689743	chr17	TCONS_00015370	9.1304376	chr8	TCONS_00015370	9.2468052	chr8
ENST00000416930	7.1770311	chr5	ENST00000584923	8.2404169	chr17	ENST00000495536	7.7226179	chr17
uc002tjp.2	7.1516394	chr2	ENST00000506807	7.6350715	chr5	ENST00000456949	5.8869017	chr2
uc021qqx.1	6.9547501	chr11	ENST00000565617	6.7524638	chr8	ENST00000522640	3.5316593	chr8
ENST00000549744	6.9239533	chr1	uc001ius.1	6.4281176	chr10	ENST00000510134	3.2442283	chr12
ENST00000420058	6.5006426	chr7	NR_037166	6.4092114	chr6	TCONS_00006917	3.235654	chr3
TCONS_00020260	6.2875894	chr12	uc010rog.2	6.2485806	chr11	ENST00000533082	3.0889278	chr11
ENST00000565617	5.9105553	chr8	ENST00000561476	6.167089	chr9	ENST00000571085	2.9884129	chr17

Down regulated lncRNAs (Top 10)								
P1 vs N			P2 vs N			P2 vs P1		
Seqname	Fold change	Chr	Seqname	Fold change	Chr	Seqname	Fold change	Chr
TCONS_00003870	93.5865198	chr2	TCONS_00003870	186.430574	chr2	ENST00000548900	12.9519822	chr12
ENST00000418209	16.9953205	chr2	ENST00000418209	20.8072582	chr2	ENST00000549744	7.2689115	chr1
NR_033950	10.8826475	chr12	NR_033950	19.8316343	chr12	uc021zvt.1	5.8821884	chr6_ssto_hap7
ENST00000555024	9.2826559	chr14	ENST00000566457	14.585414	chr8	ENST00000583122	4.9552471	chr18
uc003iwy.1	9.2268419	chr4	NR_037867	14.4200774	chr4	TCONS_00019322	4.7813245	chr11
NR_037867	8.9431568	chr4	uc021zvt.1	11.9010847	chr6_ssto_hap7	uc002vwe.1	4.4615402	chr2
uc004bit.1	8.8717241	chr9	ENST00000526431	10.1349362	chr11	uc003tgm.1	4.4227775	chr7
ENST00000462083	8.2446257	chr7	ENST00000433576	9.2168025	chr1	TCONS_00020579	4.4151517	chr12
ENST00000566457	8.0775457	chr8	ENST00000511918	8.6740855	chr5	ENST00000414404	4.0962365	chr2
ENST00000554458	7.3623602	chr14	ENST00000513492	8.5693523	chr5	ENST00000430247	4.0316941	chr21

c		Up regulated mRNAs (Top 10)			
P1 vs N		P2 vs N		P2 vs P1	
Seqname	Fold change	Seqname	Fold change	Seqname	Fold change
NM_001008	68.1959583	NM_001008	83.996744	ENST00000361255	5.4032584
NM_005252	12.0921622	NM_000518	17.6057669	NM_000342	4.9596057
NM_001105576	11.5632457	NM_001925	12.839404	ENST00000371929	4.1031664
NM_001925	11.0687712	ENST00000538966	10.0503453	ENST00000326783	3.9826266
NM_005139	8.600461	NM_000519	9.623382	ENST00000358184	3.306514
NM_000518	7.670751	ENST00000407724	9.0112745	ENST00000330807	3.0748338
NM_181869	6.1910645	NM_001105576	7.3669298	NM_001134848	3.042129
NM_022468	6.1327111	NM_001134875	6.6100721	ENST00000538966	2.9653773
NM_022835	6.0124056	NM_005252	6.4802344	NM_022917	2.8134851
NM_004907	5.8018339	NM_005217	6.4127641	NM_144594	2.7963582

d		Down regulated mRNAs (Top 10)			
P1 vs N		P2 vs N		P2 vs P1	
Seqname	Fold change	Seqname	Fold change	Seqname	Fold change
NM_002090	48.4059001	NM_002090	84.3707683	NM_003246	8.3846913
ENST00000380232	47.617952	NM_032413	42.7441674	NM_032822	8.1778243
NM_001547	18.5086402	ENST00000380232	24.0068021	NM_001073	6.4513854
NM_001657	17.2589246	NM_007115	19.9544139	NM_001432	6.2296013
NM_007115	13.8223659	NM_005502	17.1951365	NM_182488	5.5925413
NM_000891	11.7036774	NM_001547	15.5488359	NM_006498	5.4806234
NM_002852	11.0527822	NM_018370	15.021882	NM_004073	4.7665805
NM_016584	10.3014963	NM_000891	14.3852794	NM_012072	4.757599
NM_018370	9.666134	NM_002089	14.2551897	NM_005502	4.6576665
NM_032413	9.6592645	NM_012118	12.4579173	NM_004566	4.6008391

e

Different expressed Antisense lncRNAs and related gene(Top 10)

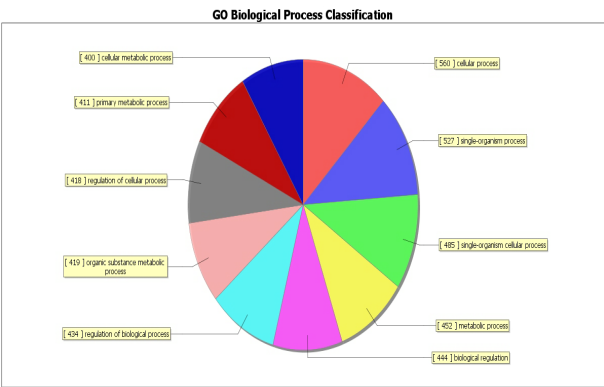
Group	Seqname	lncRNA-fold change	lncRNA-regulation	related gene symbol	mRNA-regulation
P1 vs N	uc010kun.2	24.223358	down	IL6	down
	ENST00000509463	16.7895012	up	FAM198B	up
	ENST00000514381	15.6585429	up	FAM198B	up
	ENST00000503611	9.1841852	up	FAM198B	up
	ENST00000530510	8.3998758	up	KCNE3	up
	ENST00000462083	8.2446257	down	PRKAG2	up
	ENST00000559553	8.1839918	down	C15orf48	down
	uc021qqx.1	6.9547501	up	BACE1	up
	ENST00000420058	6.5006426	up	FBXL13	up
	ENST00000523005	6.1090789	up	DUSP1	up
P2 vs N	ENST00000559553	46.3305702	down	C15orf48	down
	uc010kun.2	10.3194383	down	IL6	down
	uc021qqx.1	10.1056578	up	BACE1	up
	ENST00000557226	7.9182214	down	WARS	down
	uc003can.3	6.1619276	down	ANKRD28	down
	ENST00000420058	5.8899947	up	FBXL13	up
	NR_038951	5.7122412	down	FAM212B	up
	ENST00000560280	5.3144901	up	RORA	down
	NR_027954	4.49397	down	TIPARP	down
	NR_037595	4.3609119	down	HHIP	down
P2 vs P1	ENST00000559553	5.6611213	down	C15orf48	down
	ENST00000505646	4.6993706	down	UGT2B11	down
	ENST00000426775	4.6352828	down	PTGER3	down
	ENST00000560769	4.1859237	down	THBS1	down
	NR_038926	3.4808224	down	PRKAG2	down
	ENST00000435915	3.4574055	down	ABCA1	down
	NR_045406	3.3534203	down	HIF1A	down
	ENST00000502725	3.27797	down	NRG3	down
	ENST00000523005	3.2480271	down	DUSP1	down
	NR_037166	2.8455463	down	ACAT2	down

Table S2 Primers for quantitative real-time polymerase chain reaction (qRT-PCR)

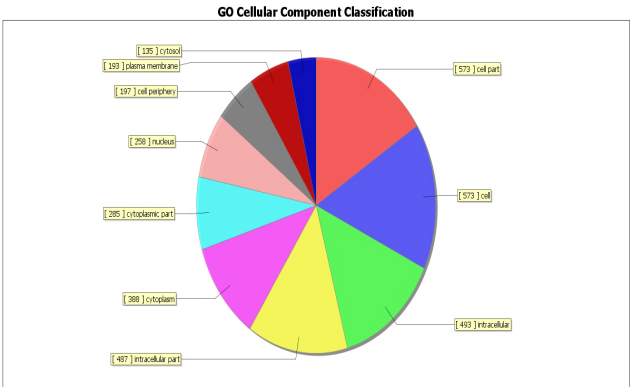
Seq-name	primer sequences
β -actin	F:5' GTGCCGAGGACTTTGATTG3' R:5' CCTGTAACAACGCATCTCATATT3'
ENST00000521756	F:5'TGAAGATCATGGAAGGCAAGTC3' R:5'TCTGGCTGCACGAAAGAAGG3'
ENST00000552576	F:5'CCACGCTACCCAGTCAATCA3' R:5'TGGAAGCACAGACCTTGTCAA3'
ENST00000528366	F:5'CCCCGTAGTAGACACCTAAAGC3' R:5'CCATGCTCTAATCCCAAATGTC3'
ENST00000436506	F:5'AGGAGAAAGCCAGGTAACTACG3' R:5' GAAGGAGATGATGACACCCAGA3'
uc002ubt.1	F:5'GAGAAAGCCAGAAAATGGAGAA3' R:5' GAAGGAGATGATGACACCCAGA3'
ENST00000440492	F:5'CTTGTTGCTTCAGGAGTCGG3' R:5' TGCTCATGCCATCGTTTTC3'
ENST00000412084	F:5'ACCAACACGCCAGAAAGGA3' R:5' AGGCATGTCTTGTCTTAAGGTG3'
ENST00000417932	F:5'TGATCCCAAAGCCCACATG3' R:5' TCTTGCTTCAGGACTTGACAGG3'
ENST00000440436	F:5'AAAGCCAGGCATTTGTAGTCC3' R:5' CTGGGTGAGGTCATTCTGGTC3'
NR_038920	F:5'CAGGGAGCCATCAACGACTA3' R:5' TTCAAGTTGGTTTGTGGTCCT3'
ENST00000509463	F:5'GAGACACGGCACAGAAGA3' R:5' GGAAGCAGGACATTGTTGGAT3'
uc010kun.2	F:5'GGCAGAAAGGGGGAGAATACT3' R:5'TACAGGGAGAGGGAGCGATAA3'
TCONS_00000918	F:5'CCAAGGACCAAGCAATAAGATC3' R:5' CAGGAAGATGAAAAGGGTAGCC3'
TCONS_00003870	F:5'GAAACCAAGAACGGGCATCAC3' R:5' AGGCTCCCCACCAGTAGATTAG3'
CCR7	F:5'GTGCCCCGCTCCTTCTCATCAG3' R:5'GGCCAGGACCACCCCATTTAG3'
CXCR1	F:5'TCCTGCTGGCAGACACCC3' R:5'AAATCCCAGAATCTCAGTGG3'
CD274	F:5'CAAAGAAGCAAAGTGATACACATT3' R:5'AAATGTGTATCACTTTGCTTCTTTG3'
CCRL2	F:5'GCCATGATCTACACCCGTTTCTTAAAAGGCAGTCTG3' R:5'CACTTCGGTGGAATGGTCAGGTTCTTCCTC3'

Figures

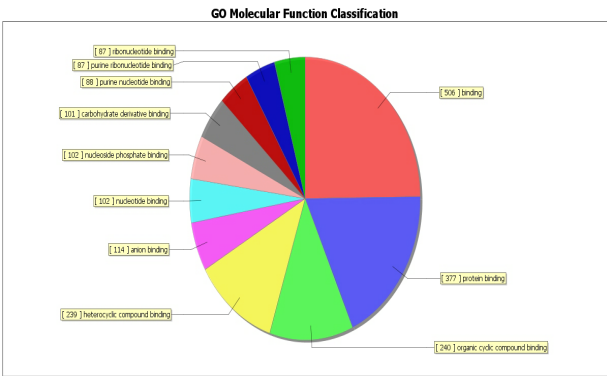
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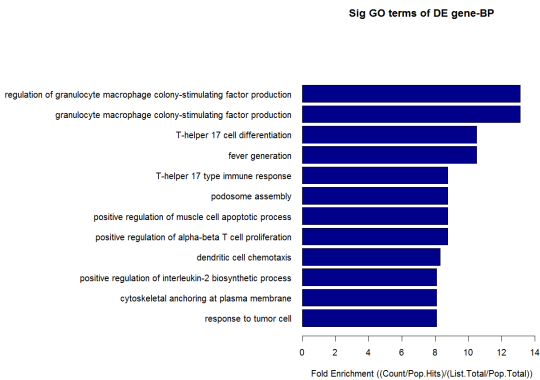
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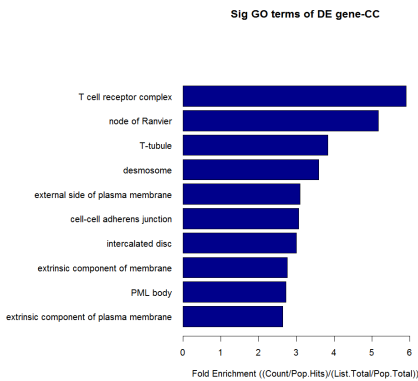
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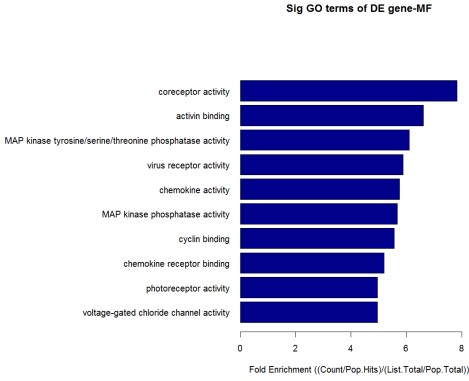
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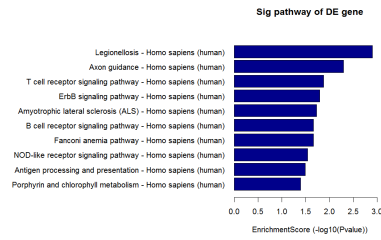
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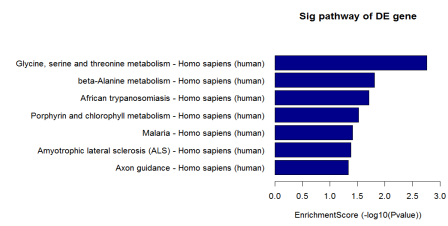
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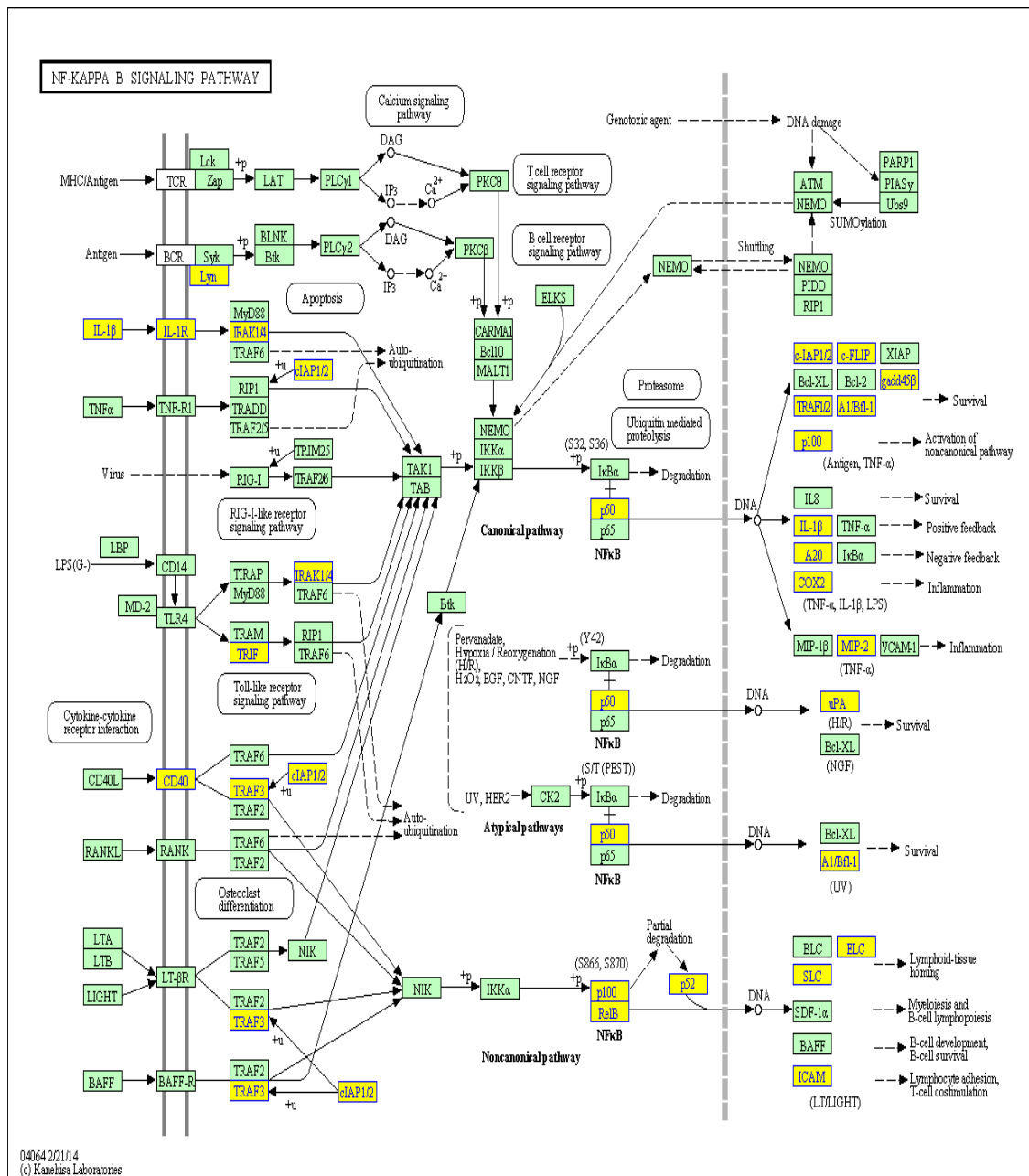
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f



g



h

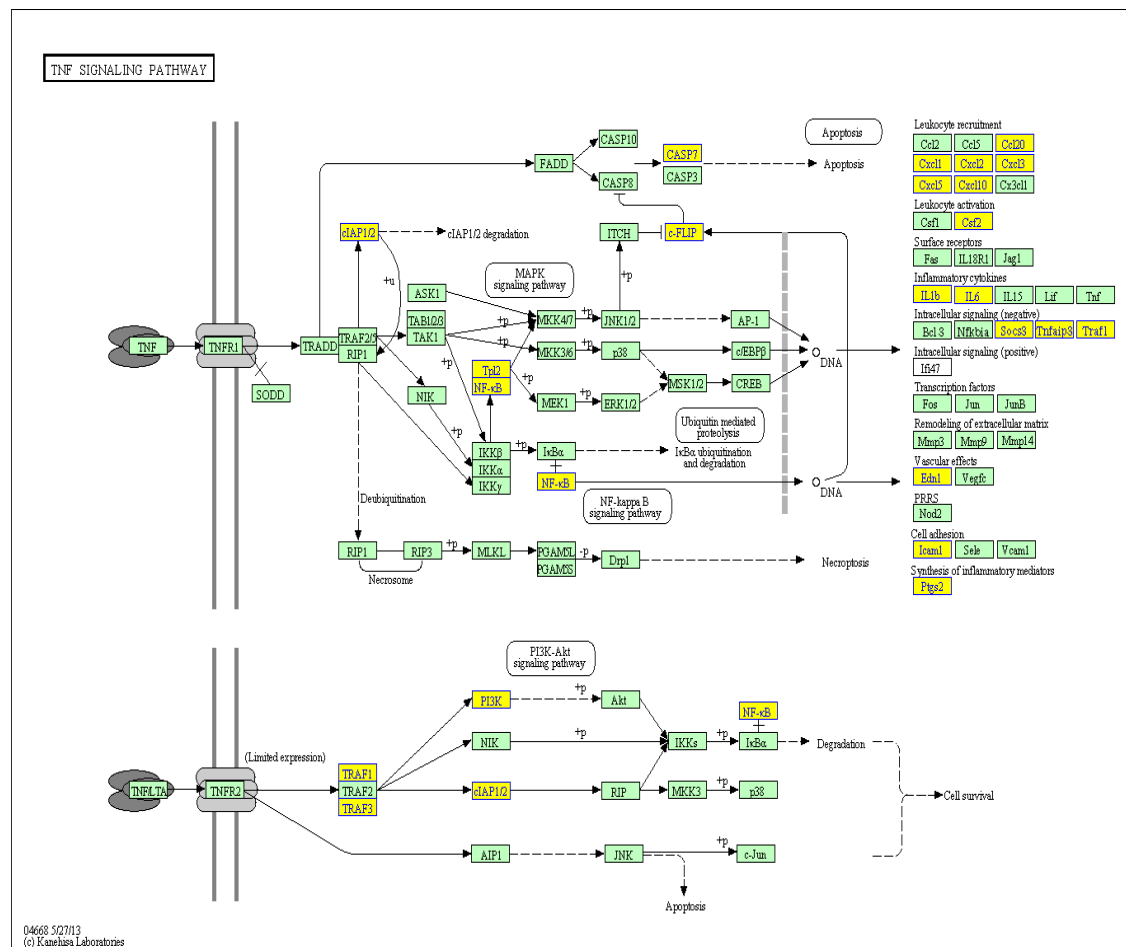


Figure S2. (a-c) pathway analysis for down-regulated transcripts in p1 vs control, p2 vs control, p2 vs p1, separately. (d-f) pathway analysis for up-regulated transcripts in p1 vs control, p2 vs control, p2 vs p1, separately. (g) NF-KPPA B signaling pathway. (h) TNF signaling pathway.

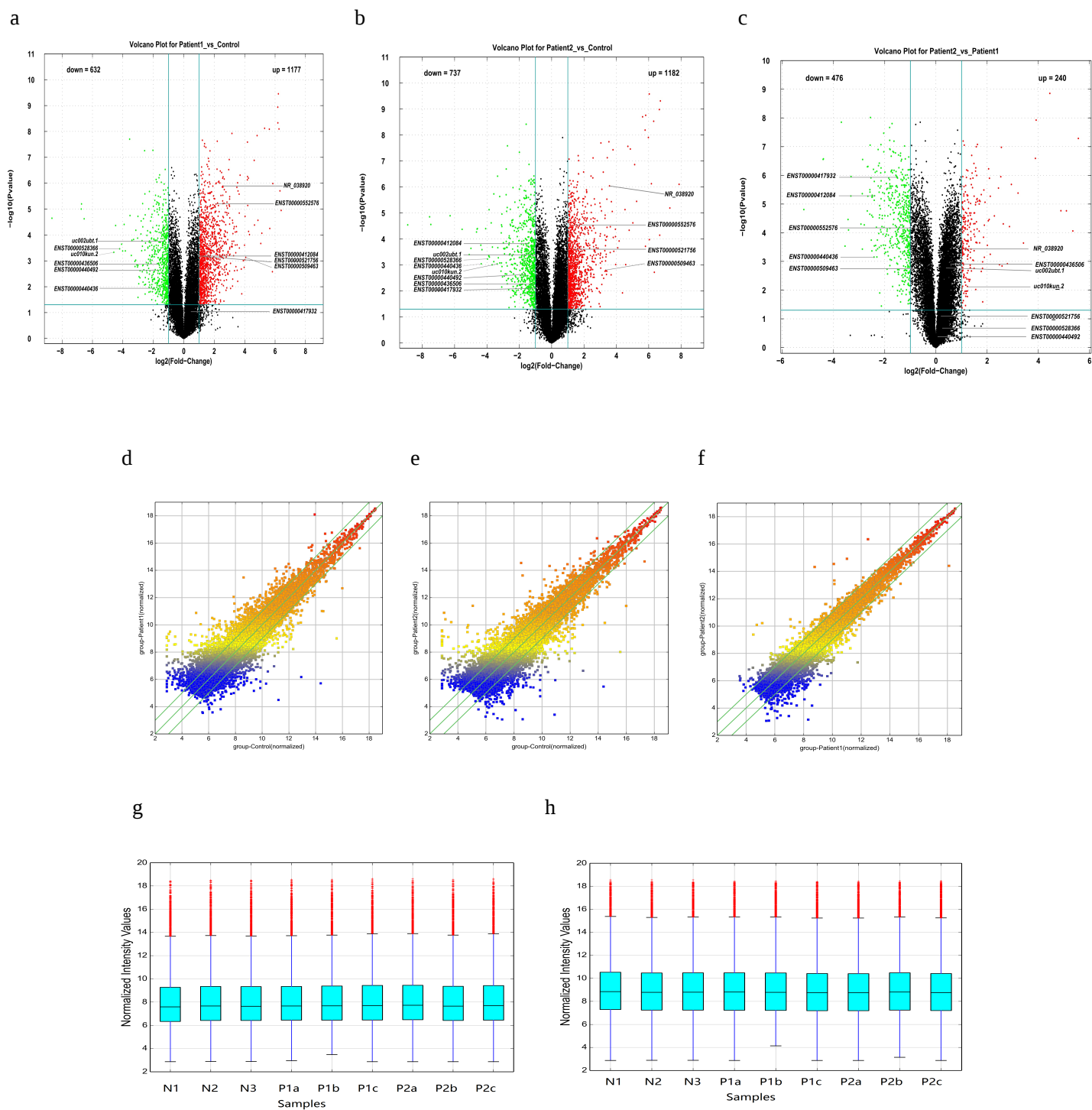
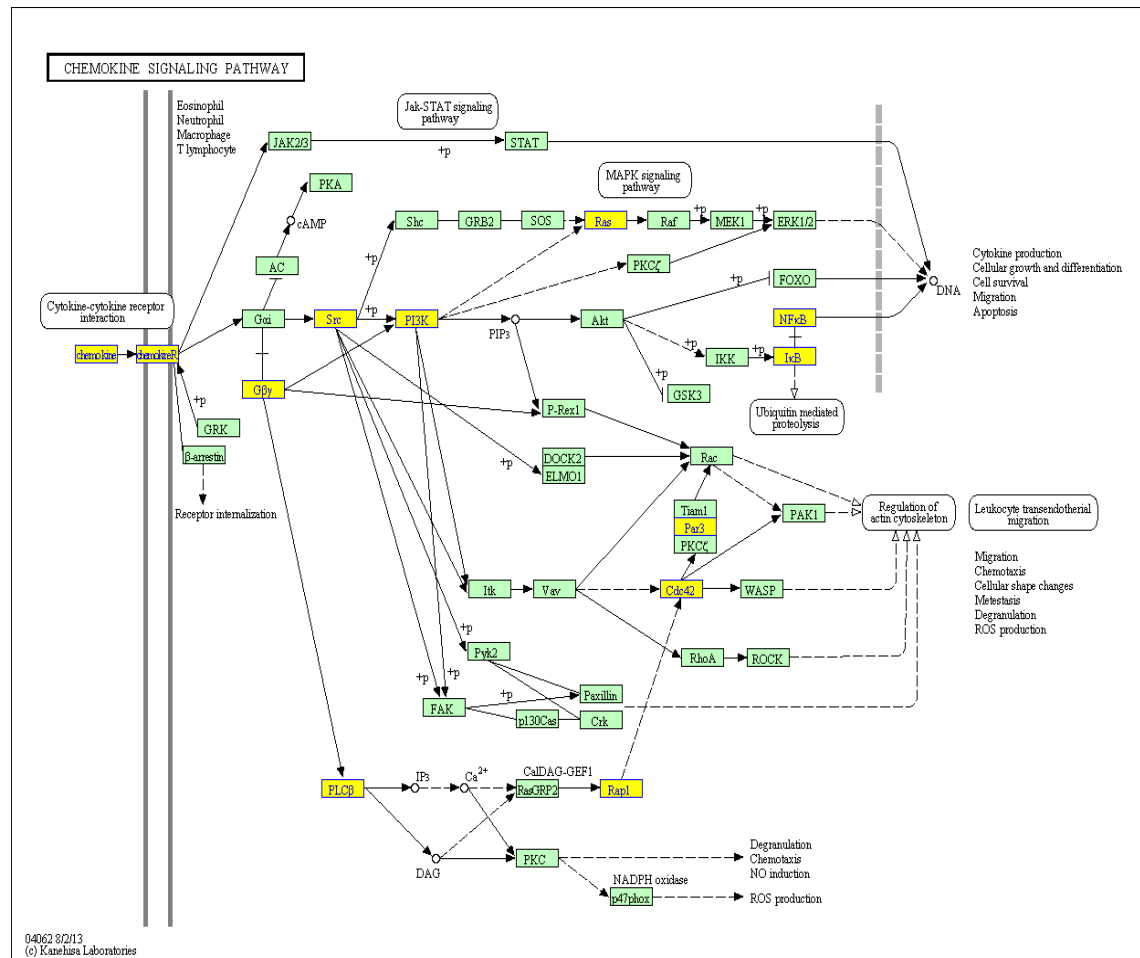
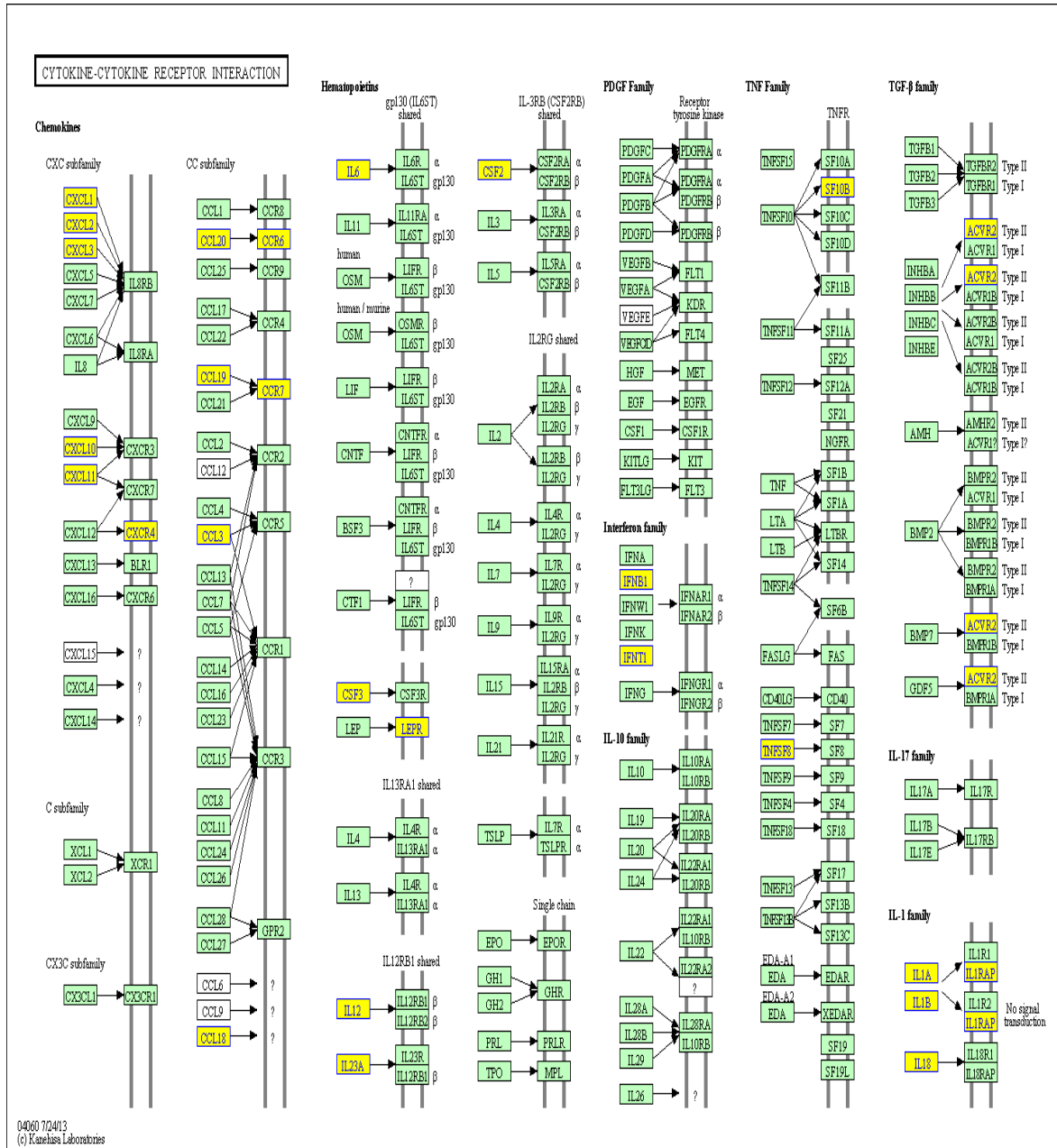


Figure S3. A comparison of P1, P2, and control (N) lncRNA data in volcano plots (a-c) and in scatter plots to evaluate repeatability (d-f). Box plots of lncRNA (g) and mRNA (h) data are presented to evaluate probe distribution in microarray.

a



b



C

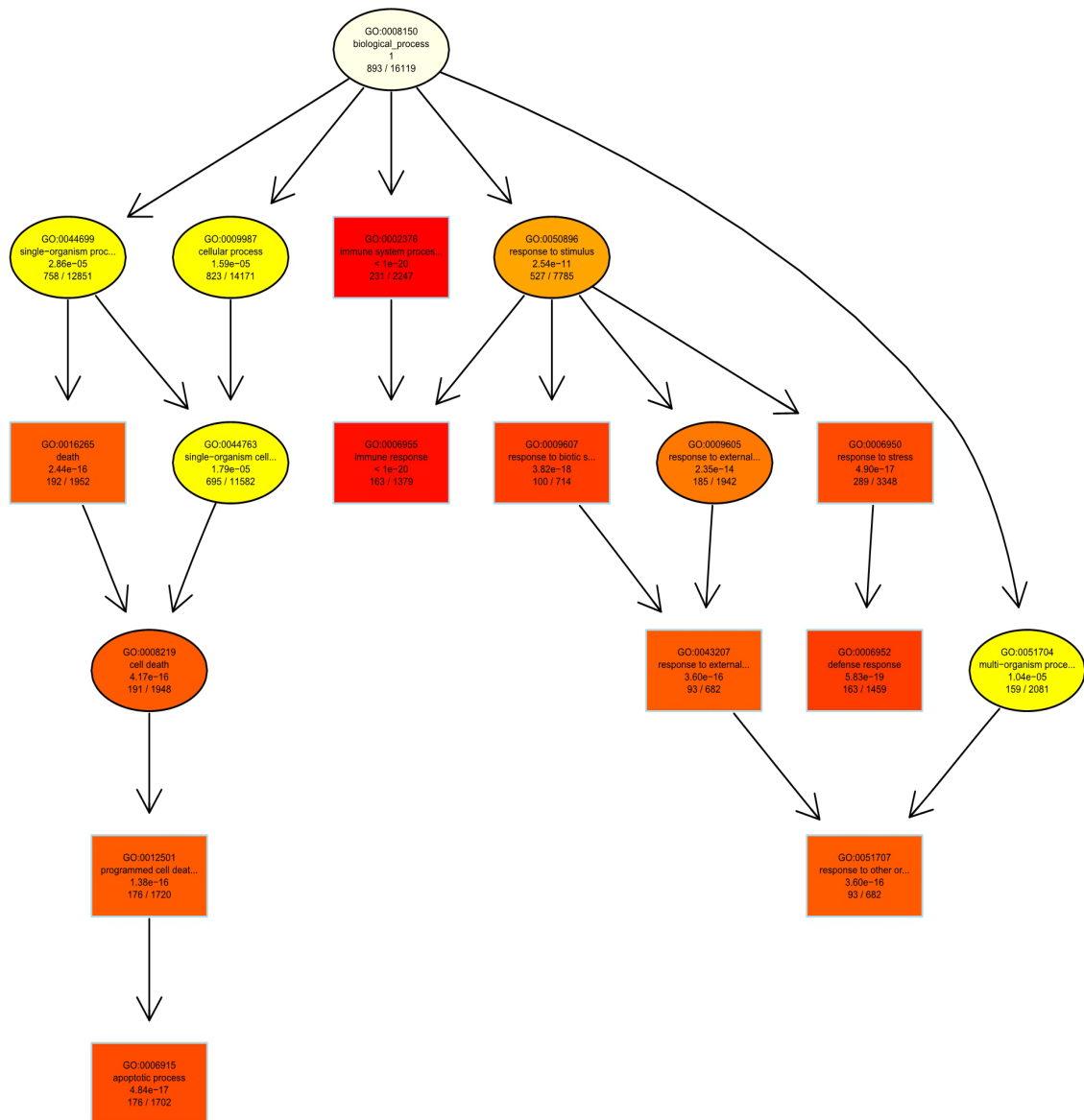


Figure S4. overview of the “chemokine signaling pathway-Homosapiens(human)” (a) and the “cytokine-cytokine receptor interaction” (b) pathways and their components. (c) A tree map of the Go analysis that included GO:0050896(response to stimulus) and GO: 0009987(cellular process).

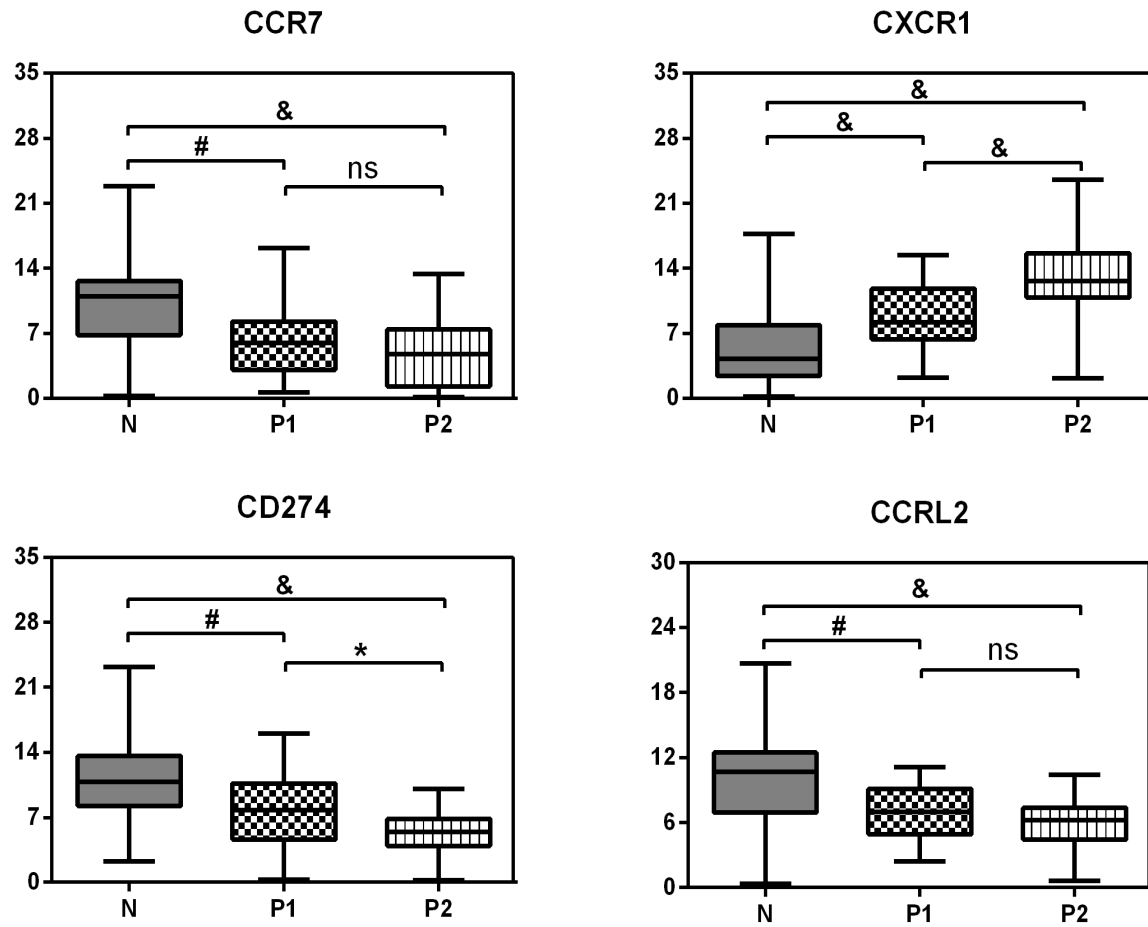


Figure S5. qRT-PCR results of CCR7, CXCR1, CD274, CCRL2 in N, P1, P2 groups. * $P < 0.05$, # $P < 0.01$, & $P < 0.001$.