

SUPPLEMENTARY FILES IMAGES

Perturbed gene	Cluster of variants	Genes in modules
TP53	2	- Module 1: MT-ND1, MT-ND5, MT-ND6, NDUFA10, NDUFA9, NDUFAF4, NDUFS2 - Module 2: C12orf65, MRPL10, MRPL13, MRPL45, MRPL49, MRPS18A, MTIF2 - Module 3: BOP1, BRIX1, C1D, EIF1, EIF2S1, EIF5, EXOSC1, EXOSC3, EXOSC8, GRWD1, NOP58, RPS27A, RPS27L, UTP18, WDR74 - Module 4: ACTB, ALDOA, CDKN1A, DERA, E2F1, EPHX1, FN1, GAPDH, GPX2, GSTO1, ITGAV, JUN, MGST1, MGST2, MYH9, MYL12A, MYL12B, PDHB, PKM, SFN, SPP1, TP53, TXNDC12
	3	- Module 1: DHX9, EIF4A3, EIF4E, ELAVL1, HNRNPDL, HNRNPR, ILF2, MAGO, RAN, SRSF3, SSB, XRCC6 - Module 2: ACTB, ACTG1, ALDOA, AREG, CD24, CD44, DERA, EEF1A1, EGFR, EIF2AK2, FN1, GAPDH, HMOX1, HNRNPDL, HPRT1, IRS1, MRPL13, MYC, NCL, NPM1, PHGDH, PKM, SMARCB1, SOX2, SPP1, STAT3, TP53
KRAS	1	- Module 1: ACTB, ALDOA, CD44, CTNNB1, ENO1, G6PC3, GAPDH, HIF1A, NFE2L2, PDHB, PFKP, PGK1, PKM, SRC, TKT, TP53 - Module 2: AHNAK, AHNAK2, ANXA1, ANXA2, CDC42, EZR, MYOF, S100A4, S100A6, TP53
	3	- Module 1: ACAT2, FDPS, HMGCS1, IDI1, SQLE, DHCR7, FDFT1 - Module 2: GSTO1, HACD1, HACD3, MGST1, SCD, ACTB, CD44, CYP1B1, EGFR, EPHX1, HSD17B12, JUN, KRAS, SREBF1, STAT3, TP53
	4	Module 1: BLVRB, GLRX, GPX2, GSTO1, HMOX1, NQO1, SEPHS1, TALDO1, TKT, TXNRD1, TXNRD2, VKORC1L1, NFE2L2, POR, STAT3, TP53
	5	- Module 1: DHCR7, EGFR, FDFT1, GAPDH, HMGCS1, HSP90AA1, KRAS, SQLE, STAT3 - Module 2: GLRX, GPX2, GSR, GSTO1, TXNRD1

Anx. 1: Genes in each detected MCODE module with significantly expressed genes in red, added intermediators in yellow, and significantly expressed added intermediators in green.

Pathway name	Entities found	Entities Total	Entities ratio	Entities pValue	Entities FDR	Reactions found	Reactions total
NFE2L2 regulates pentose phosphate pathway genes	2	15	0.001	5.52E-6	8.28E-5	2	8
Nuclear events mediated by NFE2L2	2	144	0.009	5.03E-4	3.52E-3	2	85
KEAP1-NFE2L2 pathway	2	181	0.012	7.92E-4	3.96E-3	2	117
Cellular response to chemical stress	2	301	0.019	2.17E-3	6.51E-3	2	173
Insulin effects increased synthesis of Xylulose-5-Phosphate	1	10	0.001	2.56E-3	7.67E-3	2	3
Metabolism of carbohydrates	2	453	0.029	4.85E-3	9.69E-3	5	232
Pentose phosphate pathway	1	46	0.003	1.17E-2	1.55E-2	4	20
Non-integrin membrane-ECM interactions	1	61	0.004	1.55E-2	1.55E-2	1	22
Cellular responses to stress	2	1,034	0.066	2.4E-2	2.4E-2	2	500
Cellular responses to stimuli	2	1,052	0.067	2.48E-2	2.48E-2	2	531
Glycolysis	1	112	0.007	2.84E-2	2.84E-2	1	24
Glucose metabolism	1	132	0.008	3.34E-2	3.34E-2	1	41
Integration of energy metabolism	1	153	0.01	3.86E-2	3.86E-2	2	73
Extracellular matrix organization	1	328	0.021	8.13E-2	8.13E-2	1	319
Metabolism	2	3,766	0.241	2.47E-1	2.47E-1	5	2,341
Pathway name	Entities found	Entities Total	Entities ratio	Entities pValue	Entities FDR	Reactions found	Reactions total
Interleukin-4 and Interleukin-13 signaling	2	211	0.013	2.64E-3	2.95E-2	1	47
Formyl peptide receptors bind formyl peptides and many other ligands	1	11	0.001	4.22E-3	2.95E-2	2	3
Smooth Muscle Contraction	1	61	0.004	2.32E-2	7.12E-2	1	16
Signaling by Interleukins	2	658	0.042	2.37E-2	7.12E-2	1	505
Cytokine Signaling in Immune system	2	1,099	0.07	6.13E-2	1.05E-1	1	785
Peptide ligand-binding receptors	1	203	0.013	7.54E-2	1.05E-1	2	83
Muscle contraction	1	232	0.015	8.58E-2	1.05E-1	1	53
G alpha (q) signalling events	1	285	0.018	1.05E-1	1.05E-1	3	35
Class A/1 (Rhodopsin-like receptors)	1	414	0.026	1.49E-1	1.49E-1	2	185
G alpha (i) signalling events	1	426	0.027	1.53E-1	1.53E-1	3	74
GPCR ligand binding	1	609	0.039	2.12E-1	2.12E-1	2	217
GPCR downstream signalling	1	795	0.051	2.69E-1	2.69E-1	6	175
Immune System	2	2,664	0.17	2.72E-1	2.72E-1	1	1,723
Signaling by GPCR	1	876	0.056	2.93E-1	2.93E-1	8	392
Signal Transduction	1	3,054	0.195	7.29E-1	7.29E-1	8	2,572

Anx. 2: Reactome annotations of modules 1 (top) and 2 (bottom) of cluster 1 of variants for KRAS experiment (Vastrik et al., 2007).

Pathway name	Entities found	Entities Total	Entities ratio	Entities pValue	Entities FDR	Reactions found	Reactions total
Activation of gene expression by SREBF (SREBP)	8	71	0.005	1.11E-16	6.66E-16	8	42
Regulation of cholesterol biosynthesis by SREBF (SREBF)	8	87	0.006	1.11E-16	6.66E-16	8	52
Metabolism of steroids	9	335	0.021	9.33E-15	3.73E-14	15	251
Cholesterol biosynthesis	5	77	0.005	7.16E-10	2.15E-9	7	37
Metabolism of lipids	9	1,503	0.096	6.42E-9	1.28E-8	15	981
Metabolism	9	3,766	0.241	2.14E-5	4.29E-5	15	2,341
PPARA activates gene expression	2	173	0.011	5.2E-3	5.2E-3	1	41
Regulation of lipid metabolism by PPARalpha	2	175	0.011	5.31E-3	5.31E-3	1	45
LDL clearance	1	28	0.002	1.78E-2	1.78E-2	1	20
Plasma lipoprotein clearance	1	46	0.003	2.9E-2	2.9E-2	1	36
Plasma lipoprotein assembly, remodeling, and clearance	1	102	0.007	6.34E-2	6.34E-2	1	86
Transport of small molecules	1	1,016	0.065	4.89E-1	4.89E-1	1	464
Pathway name	Entities found	Entities Total	Entities ratio	Entities pValue	Entities FDR	Reactions found	Reactions total
Fatty acyl-CoA biosynthesis	4	78	0.005	4.27E-8	1.2E-6	2	25
Synthesis of very long-chain fatty acyl-CoAs	3	51	0.003	1.92E-6	2.69E-5	1	12
NR1H2 & NR1H3 regulate gene expression linked to lipogenesis	2	17	0.001	3.3E-5	2.54E-4	2	8
Fatty acid metabolism	4	429	0.027	3.64E-5	2.54E-4	2	220
Metabolism	7	3,766	0.241	2.98E-4	1.43E-3	9	2,341
Metabolism of lipids	5	1,503	0.096	3.59E-4	1.43E-3	4	981
Glutathione conjugation	2	68	0.004	5.21E-4	1.58E-3	2	14
Activation of gene expression by SREBF (SREBP)	2	71	0.005	5.67E-4	1.58E-3	2	42
Gene and protein expression by JAK-STAT signaling after Interleukin-12 stimulation	2	73	0.005	6E-4	1.58E-3	1	36
Interleukin-12 signaling	2	84	0.005	7.92E-4	1.58E-3	1	56
NR1H2 and NR1H3-mediated signaling	2	85	0.005	8.1E-4	1.62E-3	2	60
Regulation of cholesterol biosynthesis by SREBF (SREBF)	2	87	0.006	8.48E-4	1.7E-3	2	52
Interleukin-12 family signaling	2	96	0.006	1.03E-3	2.06E-3	1	114
Phase II - Conjugation of compounds	2	262	0.017	7.36E-3	1.18E-2	3	72
Metabolism of steroids	2	335	0.021	1.18E-2	1.18E-2	2	251
Vitamin C (ascorbate) metabolism	1	26	0.002	1.32E-2	1.32E-2	1	9
Signaling by Nuclear Receptors	2	388	0.025	1.56E-2	1.56E-2	2	196
Aflatoxin activation and detoxification	1	49	0.003	2.48E-2	2.48E-2	1	18
Methylation	1	52	0.003	2.63E-2	2.63E-2	1	13
Biological oxidations	2	547	0.035	2.98E-2	2.98E-2	4	192

Anx. 3: Reactome annotations of modules 1 (top) and 2 (bottom) of cluster 3 of variants for KRAS experiment (Vastrik et al., 2007).

Pathway name	Entities found	Entities Total	Entities ratio	Entities pValue	Entities FDR	Reactions found	Reactions total
Activation of gene expression by SREBF (SREBP)	8	71	0.005	1.11E-16	6.66E-16	8	42
Regulation of cholesterol biosynthesis by SREBP (SREBF)	8	87	0.006	1.11E-16	6.66E-16	8	52
Metabolism of steroids	9	335	0.021	9.33E-15	3.73E-14	15	251
Cholesterol biosynthesis	5	77	0.005	7.16E-10	2.15E-9	7	37
Metabolism of lipids	9	1,503	0.096	6.42E-9	1.28E-8	15	981
Metabolism	9	3,766	0.241	2.14E-5	4.29E-5	15	2,341
PPARA activates gene expression	2	173	0.011	5.2E-3	5.2E-3	1	41
Regulation of lipid metabolism by PPARalpha	2	175	0.011	5.31E-3	5.31E-3	1	45
LDL clearance	1	28	0.002	1.78E-2	1.78E-2	1	20
Plasma lipoprotein clearance	1	46	0.003	2.9E-2	2.9E-2	1	36
Plasma lipoprotein assembly, remodeling, and clearance	1	102	0.007	6.34E-2	6.34E-2	1	86
Transport of small molecules	1	1,016	0.065	4.89E-1	4.89E-1	1	464

Anx. 4: Reactome annotations of modules 1 (top) of cluster 4 of variants for KRAS experiment (Vastrik et al., 2007).

Pathway name	Entities found	Entities Total	Entities ratio	Entities pValue	Entities FDR	Reactions found	Reactions total
Activation of gene expression by SREBF (SREBP)	6	71	0.005	8.77E-15	7.02E-14	6	42
Regulation of cholesterol biosynthesis by SREBP (SREBF)	6	87	0.006	2.98E-14	1.19E-13	6	52
Metabolism of steroids	6	335	0.021	9.69E-11	1.94E-10	10	251
PPARA activates gene expression	4	173	0.011	2.21E-7	2.32E-7	2	41
Regulation of lipid metabolism by PPARalpha	4	175	0.011	2.32E-7	2.32E-7	2	45
Metabolism of lipids	6	1,503	0.096	7.91E-7	7.91E-7	10	981
Cholesterol biosynthesis	3	77	0.005	2.36E-6	2.36E-6	4	37
Metabolism	6	3,766	0.241	1.96E-4	1.96E-4	10	2,341

Pathway name	Entities found	Entities Total	Entities ratio	Entities pValue	Entities FDR	Reactions found	Reactions total
NFE2L2 regulating anti-oxidant/detoxification enzymes	2	39	0.002	9.28E-5	2.99E-3	2	28
Cellular response to chemical stress	3	301	0.019	1.37E-4	2.99E-3	4	173
Detoxification of Reactive Oxygen Species	2	65	0.004	2.57E-4	2.99E-3	2	34
Gene and protein expression by JAK-STAT signaling after Interleukin-12 stimulation	2	73	0.005	3.23E-4	2.99E-3	1	36
Interconversion of nucleotide di- and triphosphates	2	80	0.005	3.88E-4	2.99E-3	4	33
Interleukin-12 signaling	2	84	0.005	4.27E-4	2.99E-3	1	56
Interleukin-12 family signaling	2	96	0.006	5.57E-4	3.34E-3	1	114
TP53 Regulates Metabolic Genes	2	128	0.008	9.84E-4	4.92E-3	2	34
Nuclear events mediated by NFE2L2	2	144	0.009	1.24E-3	5.85E-3	2	85
PPARA activates gene expression	2	173	0.011	1.78E-3	5.85E-3	1	41
Regulation of lipid metabolism by PPARalpha	2	175	0.011	1.82E-3	5.85E-3	1	45
KEAP1-NFE2L2 pathway	2	181	0.012	1.95E-3	5.85E-3	2	117
Metabolism of ingested MeSeO2H into MeSeH	1	9	0.001	3.45E-3	7.79E-3	2	2
Uptake and function of diphtheria toxin	1	10	0.001	3.83E-3	7.79E-3	1	5
Metabolism of nucleotides	2	256	0.016	3.85E-3	7.79E-3	4	142
Metabolism	5	3,766	0.241	3.89E-3	7.79E-3	15	2,341
Cellular responses to stress	3	1,034	0.066	4.97E-3	9.94E-3	4	500
Cellular responses to stimuli	3	1,052	0.067	5.22E-3	9.94E-3	4	531
Synthesis of 12-eicosatetraenoic acid derivatives	1	19	0.001	7.27E-3	9.94E-3	2	6
Synthesis of 15-eicosatetraenoic acid derivatives	1	22	0.001	8.42E-3	9.94E-3	1	4

Anx. 5: Reactome annotations of modules 1 (top) and 2 (bottom) of cluster 5 of variants for KRAS experiment (Vastrik et al., 2007).

Pathway name	Entities found	Entities Total	Entities ratio	Entities pValue	Entities FDR	Reactions found	Reactions total
Complex I biogenesis	6	71	0.005	7.29E-13	9.48E-12	9	14
Respiratory electron transport	6	196	0.013	3.16E-10	1.9E-9	10	47
Aerobic respiration and respiratory electron transport	6	360	0.023	1.18E-8	4.73E-8	10	117
FASTK family proteins regulate processing and stability of mitochondrial RNAs	3	19	0.001	1.5E-7	4.5E-7	4	4
Mitochondrial RNA degradation	3	30	0.002	5.89E-7	1.18E-6	8	10
tRNA processing in the mitochondrion	3	45	0.003	1.98E-6	3.96E-6	2	3
Mitochondrial protein degradation	3	104	0.007	2.4E-5	2.4E-5	2	20
tRNA processing	3	182	0.012	1.26E-4	1.26E-4	2	54
rRNA processing in the mitochondrion	2	40	0.003	2.33E-4	2.33E-4	1	6
rRNA processing	2	245	0.016	8.22E-3	8.22E-3	1	21
Metabolism	6	3,766	0.241	8.25E-3	8.25E-3	10	2,341
Metabolism of RNA	3	839	0.054	1.02E-2	1.02E-2	10	199
Metabolism of proteins	3	2,347	0.15	1.41E-1	1.41E-1	2	847
Pathway name	Entities found	Entities Total	Entities ratio	Entities pValue	Entities FDR	Reactions found	Reactions total
Mitochondrial translation initiation	6	88	0.007	1.18E-12	5.25E-12	3	4
Mitochondrial translation	6	94	0.008	1.75E-12	5.25E-12	13	17
Mitochondrial translation termination	5	88	0.007	4.72E-10	4.72E-10	5	5
Mitochondrial translation elongation	5	88	0.007	4.72E-10	4.72E-10	5	8
Translation	6	294	0.025	1.61E-9	1.61E-9	13	99
Metabolism of proteins	6	2,067	0.175	1.7E-4	1.7E-4	13	830
Pathway name	Entities found	Entities Total	Entities ratio	Entities pValue	Entities FDR	Reactions found	Reactions total
Major pathway of rRNA processing in the nucleolus and cytosol	7	183	0.015	1.57E-10	6.11E-9	7	7
rRNA processing in the nucleus and cytosol	7	193	0.016	2.27E-10	6.11E-9	8	15
rRNA processing	7	203	0.017	3.22E-10	6.11E-9	8	21
mRNA decay by 3' to 5' exonuclease	3	16	0.001	5.39E-7	5.17E-6	1	3
Tristetraprolin (TTP, ZFP36) binds and destabilizes mRNA	3	17	0.001	6.47E-7	5.17E-6	1	4
KSRP (KHSRP) binds and destabilizes mRNA	3	17	0.001	6.47E-7	5.17E-6	1	5
Butyrate Response Factor 1 (BRF1) binds and destabilizes mRNA	3	17	0.001	6.47E-7	5.17E-6	1	6
Metabolism of RNA	7	729	0.062	2.03E-6	1.42E-5	17	199
ATF4 activates genes in response to endoplasmic reticulum stress	3	27	0.002	2.58E-6	1.55E-5	1	7
PERK regulates gene expression	3	32	0.003	4.28E-6	2.14E-5	1	11
Deadenylation-dependent mRNA decay	3	56	0.005	2.26E-5	1.13E-4	1	10
Regulation of mRNA stability by proteins that bind AU-rich elements	3	88	0.007	8.61E-5	3.44E-4	3	26
Unfolded Protein Response (UPR)	3	93	0.008	1.01E-4	4.05E-4	1	99
Ribosomal scanning and start codon recognition	2	59	0.005	1.59E-3	6.35E-3	2	2
GTP hydrolysis and joining of the 60S ribosomal subunit	2	113	0.01	5.65E-3	1.7E-2	3	3
Cellular responses to stress	4	780	0.066	6.09E-3	1.83E-2	5	492
Cap-dependent Translation Initiation	2	120	0.01	6.35E-3	1.9E-2	10	18
Eukaryotic Translation Initiation	2	120	0.01	6.35E-3	1.9E-2	11	21
Cellular responses to stimuli	4	794	0.067	6.48E-3	1.95E-2	5	523
Translation	2	294	0.025	3.45E-2	6.91E-2	23	99
Pathway name	Entities found	Entities Total	Entities ratio	Entities pValue	Entities FDR	Reactions found	Reactions total
TP53 Regulates Transcription of Cell Cycle Genes	7	65	0.004	1.32E-11	2.75E-9	13	42
TP53 Regulates Transcription of Genes Involved in G1 Cell Cycle Arrest	5	20	0.001	2.21E-10	2.29E-8	8	17
Transcriptional activation of cell cycle inhibitor p21	3	6	0	1.46E-7	7.6E-6	4	5
Transcriptional activation of p53 responsive genes	3	6	0	1.46E-7	7.6E-6	4	5
Transcriptional Regulation by TP53	8	486	0.031	8.26E-7	3.38E-5	16	258
Defective binding of RB1 mutants to E2F1,(E2F2, E2F3)	3	17	0.001	3.28E-6	9.52E-5	1	1
Aberrant regulation of mitotic G1/S transition in cancer due to RB1 defects	3	17	0.001	3.28E-6	9.52E-5	1	2
FOXO-mediated transcription of cell cycle genes	3	27	0.002	1.3E-5	3.38E-4	5	22
Aberrant regulation of mitotic cell cycle due to RB1 defects	3	36	0.002	3.05E-5	6.45E-4	1	3
FOXO-mediated transcription	4	110	0.007	3.24E-5	6.45E-4	6	85
Diseases of mitotic cell cycle	3	38	0.002	3.58E-5	6.45E-4	1	5
Transcriptional regulation by RUNX3	4	118	0.008	4.25E-5	7.23E-4	4	47
TFAP2 (AP-2) family regulates transcription of cell cycle factors	2	6	0	4.76E-5	7.62E-4	3	4
G2 Phase	2	7	0	6.47E-5	9.06E-4	2	2
RUNX3 regulates CDKN1A transcription	2	8	0.001	8.44E-5	1.08E-3	3	6
Cyclin D associated events in G1	3	52	0.003	9.04E-5	1.08E-3	8	17
G1 Phase	3	52	0.003	9.04E-5	1.08E-3	8	17
RUNX3 Regulates Immune Response and Cell Migration	2	10	0.001	1.32E-4	1.32E-3	1	5
Generic Transcription Pathway	10	1,586	0.101	1.32E-4	1.32E-3	37	880
Gene expression (Transcription)	11	1,941	0.124	1.38E-4	1.36E-3	42	1,103

Anx. 6: Reactome annotations of modules 1 (top), 2 (second), 3 (third) and 4 (bottom) of cluster 2 of variants for TP53 experiment (Vastrik et al., 2007).

Pathway name	Entities found	Entities Total	Entities ratio	Entities pValue	Entities FDR	Reactions found	Reactions total
Processing of Capped Intron-Containing Pre-mRNA	3	299	0.019	3.65E-4	1.24E-2	18	34
Metabolism of RNA	4	839	0.054	4.88E-4	1.24E-2	24	199
Gene and protein expression by JAK-STAT signaling after Interleukin-12 stimulation	2	73	0.005	6E-4	1.24E-2	1	36
Interleukin-12 signaling	2	84	0.005	7.92E-4	1.24E-2	1	56
Transport of Mature Transcript to Cytoplasm	2	90	0.006	9.07E-4	1.24E-2	5	13
Interleukin-12 family signaling	2	96	0.006	1.03E-3	1.24E-2	1	114
Cytokine Signaling in Immune system	4	1,099	0.07	1.36E-3	1.49E-2	3	785
Antiviral mechanism by IFN-stimulated genes	2	172	0.011	3.24E-3	2.92E-2	2	71
mRNA Splicing - Major Pathway	2	213	0.014	4.92E-3	3.53E-2	9	10
mRNA Splicing	2	224	0.014	5.43E-3	3.53E-2	9	15
Z-decay: degradation of maternal mRNAs by zygotically expressed factors	1	16	0.001	8.16E-3	3.53E-2	4	4
RNA Polymerase III Transcription Termination	1	23	0.001	1.17E-2	3.53E-2	1	2
mTORC1-mediated signalling	1	28	0.002	1.42E-2	3.53E-2	2	8
Deadenylation of mRNA	1	30	0.002	1.53E-2	3.53E-2	4	4
MicroRNA (miRNA) biogenesis	1	31	0.002	1.58E-2	3.53E-2	2	8
Postmitotic nuclear pore complex (NPC) reformation	1	32	0.002	1.63E-2	3.53E-2	4	10
Interferon Signaling	2	397	0.025	1.63E-2	3.53E-2	2	119
Transport of the SLBP independent Mature mRNA	1	39	0.002	1.98E-2	3.53E-2	1	3
Transport of the SLBP Dependant Mature mRNA	1	40	0.003	2.03E-2	3.53E-2	1	3
Nuclear import of Rev protein	1	41	0.003	2.08E-2	3.53E-2	3	7
Pathway name	Entities found	Entities Total	Entities ratio	Entities pValue	Entities FDR	Reactions found	Reactions total
Insulin-like Growth Factor-2 mRNA Binding Proteins (IGF2BPs/IMPs/VICKZs) bind RNA	5	13	0.001	4.58E-12	4.58E-10	2	3
RUNX3 Regulates Immune Response and Cell Migration	2	10	0.001	7E-5	3.47E-3	1	5
NFE2L2 regulating tumorigenic genes	2	17	0.001	2E-4	6.59E-3	2	12
Metabolism of RNA	5	839	0.054	2.75E-3	6.81E-2	2	199
Gene and protein expression by JAK-STAT signaling after Interleukin-12 stimulation	2	73	0.005	3.54E-3	6.81E-2	1	36
Interleukin-12 signaling	2	84	0.005	4.65E-3	6.81E-2	1	56
Integrin cell surface interactions	2	86	0.006	4.86E-3	6.81E-2	5	55
Interleukin-12 family signaling	2	96	0.006	6.02E-3	7.22E-2	1	114
Transcriptional regulation by RUNX3	2	118	0.008	8.95E-3	8.71E-2	1	47
Inhibition of Signaling by Overexpressed EGFR	1	8	0.001	9.68E-3	8.71E-2	1	2
Signaling by Overexpressed Wild-Type EGFR in Cancer	1	8	0.001	9.68E-3	8.71E-2	1	2
Nuclear events mediated by NFE2L2	2	144	0.009	1.31E-2	9.14E-2	2	85
EGFR interacts with phospholipase C-gamma	1	11	0.001	1.33E-2	9.14E-2	3	3
Degradation of the extracellular matrix	2	148	0.009	1.38E-2	9.14E-2	2	105
Metabolism of carbohydrates	3	453	0.029	1.67E-2	9.14E-2	6	232
Neutrophil degranulation	3	478	0.031	1.92E-2	9.14E-2	4	10
GRB2 events in EGFR signaling	1	16	0.001	1.93E-2	9.14E-2	2	3
Interferon gamma signaling	2	177	0.011	1.93E-2	9.14E-2	2	23
KEAP1-NFE2L2 pathway	2	181	0.012	2.01E-2	9.14E-2	2	117
Hyaluronan uptake and degradation	1	18	0.001	2.17E-2	9.14E-2	3	10

Anx. 7: Reactome annotations of modules 1 (top) and 2 (bottom) of cluster 3 of variants for TP53 experiment (Vastrik et al., 2007).