

A recurrent de novo MAX p.Arg60Gln variant causes a syndromic overgrowth disorder through differential expression of c-Myc target genes.

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Supplementary Data

Supplementary Data 1: Colour and oral fluorescein angiogram photos of right eye of P1.

Supplementary Data 2: Table of significantly (adjusted p-valued <0.05) up-regulated genes in MAX-R60Q transfected HEK293 cells relative to MAX-WT transfected cells.

Supplementary Data 3: Table of significantly (adjusted p-valued <0.05) down-regulated genes in MAX-R60Q transfected HEK293 cells relative to MAX-WT transfected cells.

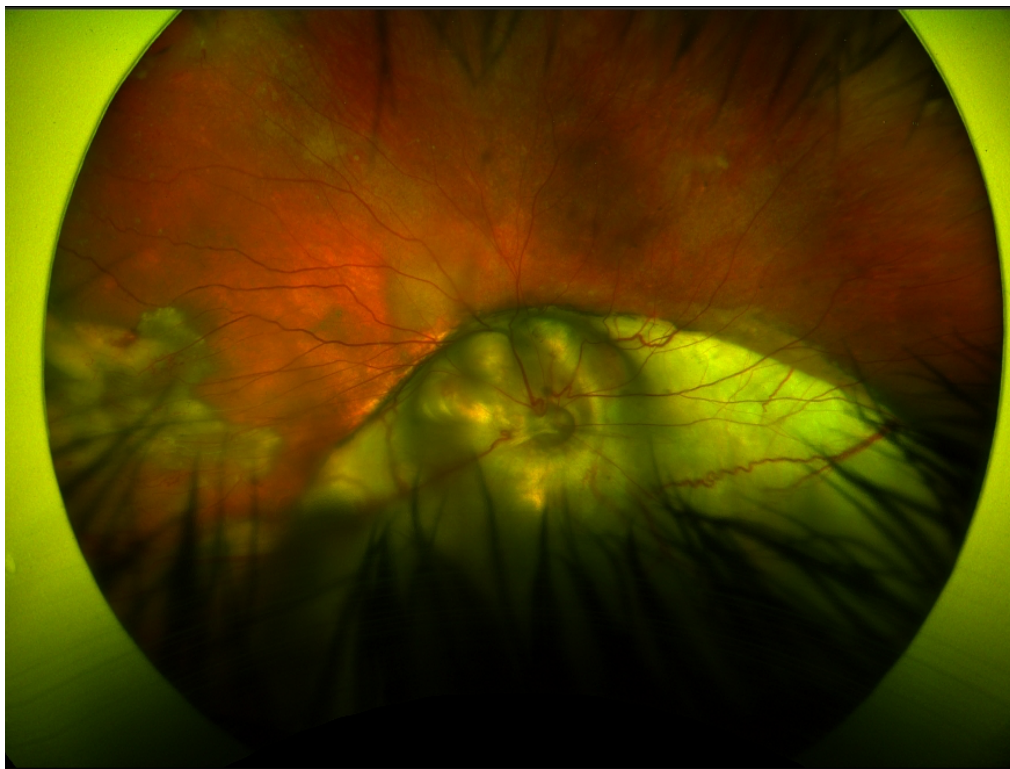
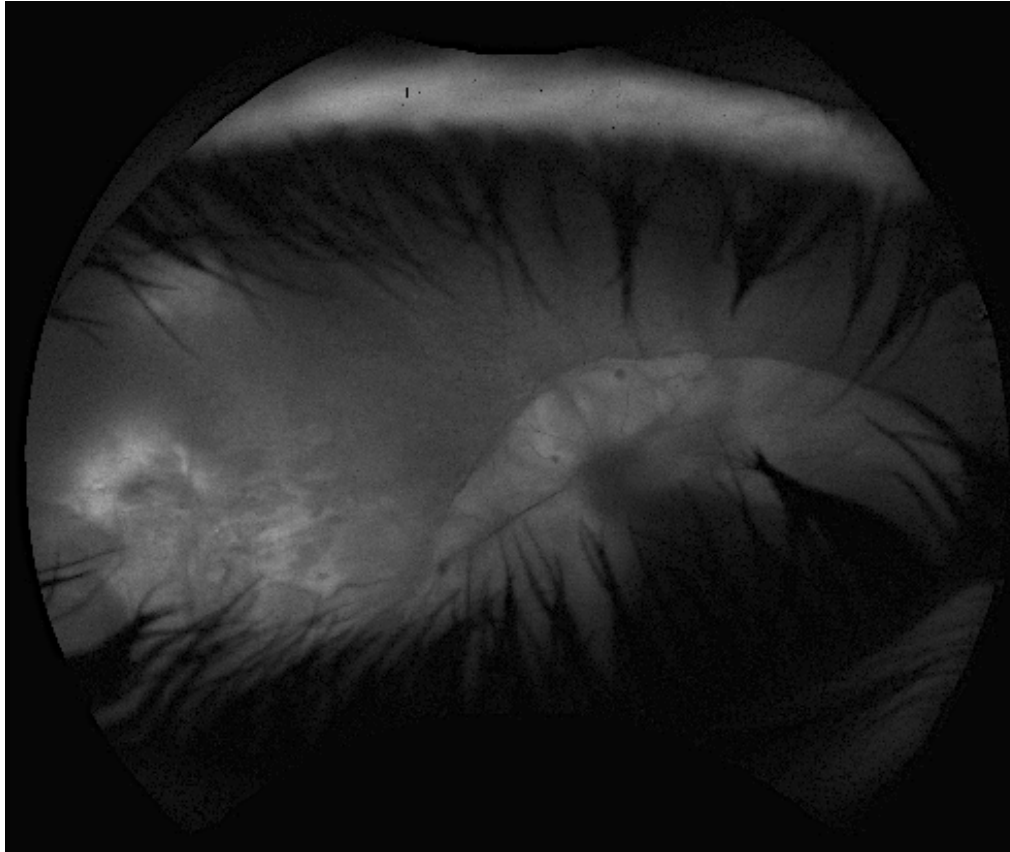
Supplementary Data 4: Table of significantly enriched reactome pathways using all MAX-R60Q differentially expressed genes.

Supplementary Data 5: Table of significantly enriched reactome pathways using genes up-regulated by MAX-R60Q.

Supplementary Data 6: Table of significantly enriched reactome pathways using genes down-regulated by MAX-R60Q.

Supplementary Data 1: Colour and oral fluorescein angiogram photos of right eye of P1.

P1 has bilateral microphthalmia, which is more severe in his left eye which has never had any vision. Images show large chorio-retinal coloboma and retinal exudation of the temporal retina. The patient subsequently developed retinal exudation in both eyes requiring cryotherapy. He has since developed a right cataract associated with intraocular inflammation.



Supplementary Data 2: Table of significantly (adjusted p-valued <0.05) up-regulated genes in MAX-R60Q transfected HEK293 cells relative to MAX-WT transfected cells. Genes are sorted by log2fold change.

Gene Name	baseMean	log2FoldChange	p.value	p.adj
CD164L2	9.289463546	2.04146228	0.00566094	0.01966121
RPL23AP65	9.019419	1.96099671	0.00768035	0.02528652
GGTLC2	17.06058332	1.9204666	0.00043141	0.00228315
NKX6-2	13.42459724	1.89861122	0.00156549	0.0067532
BGLAP	7.497282248	1.88647393	0.01635661	0.04696081
PTH2	14.087248	1.83124951	0.00435956	0.01588143
FAM90A25P	10.78175175	1.82909266	0.0058676	0.02022709
RPS28P4	21.02737954	1.81493198	0.00025057	0.00143468
RPL17P36	8.650323194	1.79311231	0.01516389	0.04411226
KCNK7	13.45109008	1.77015175	0.00384708	0.0143182
ATP4A	14.91652958	1.76072311	0.00177135	0.00748723
PRPH	40.75357664	1.75501369	3.02E-06	3.32E-05
TECRP1	217.6670336	1.64776032	4.00E-12	4.15E-10
S100A2	11.44870978	1.64013885	0.00974478	0.03066642
RPL36AP7	10.22468155	1.63385665	0.01358937	0.04036526
LRRC26	18.83359326	1.63306604	0.00186437	0.00781815
CFAP65	15.54299217	1.63237138	0.00816188	0.02661982
DDX11L16	22.61036963	1.60460239	0.00105541	0.0048387
MATN4	19.35374449	1.59360814	0.00397752	0.01473072
RPL10P6	13.88104217	1.5734863	0.00631389	0.02151878
RPS26P3	15.18671381	1.56227268	0.00441262	0.01604352
JAKMIP1	23.26439769	1.55035003	0.00091337	0.00429896
NEURL2	13.20663288	1.54236833	0.01300911	0.03898194
FAM110D	18.84182881	1.53396616	0.00231828	0.00940665
LKAAEAR1	12.87659886	1.52865392	0.01739882	0.04935596
RPS28P7	1186.842767	1.52809627	9.33E-17	5.43E-14
LINC02356	24.3152445	1.51714577	0.00241552	0.00972679
PRTN3	17.31658451	1.48406798	0.01559452	0.04515375
PFN1P1	15.06664116	1.4705261	0.00699105	0.0234106
SNHG25	35.65325341	1.46899844	9.55E-05	0.00063006
TMOD4	17.77693387	1.46220505	0.00379263	0.01415892
CCDC85B	3163.626476	1.45942392	2.47E-19	2.79E-16
RPL3L	53.86395256	1.45044308	2.28E-06	2.63E-05
CRACR2B	230.3443978	1.4440464	0.00255675	0.01020436
HBA1	131.6746567	1.41377951	8.78E-08	1.61E-06
MTND1P23	74.82643993	1.40548195	1.24E-07	2.16E-06
LINC00852	29.3379363	1.39650712	0.00038084	0.00205406
SLC9B1	16.10935381	1.377788	0.00861364	0.02777678
PSLNR	48.2670017	1.33608104	0.0001736	0.00105247
C4orf48	2077.908267	1.33280693	1.70E-16	8.74E-14

Gene Name	baseMean	log2FoldChange	p.value	p.adj
PPIAP31	40.93069746	1.33040473	0.00013606	0.00085269
RPL35P5	26.60324948	1.32910033	0.00202043	0.00838032
NME2P1	17.99191797	1.3277845	0.01197961	0.03642094
ARL6IP4	21.43040662	1.32650939	0.00643275	0.02187426
MRPL12	2627.714975	1.32252149	1.97E-16	9.86E-14
HES7	360.9569618	1.32009568	0.00337585	0.0128102
PLPPR3	772.8814158	1.31707968	0.0015339	0.00664078
LERFS	23.25347814	1.31431543	0.00317569	0.01217878
CLDND2	50.33091194	1.3097028	4.37E-05	0.0003272
UTF1	244.4803538	1.30450807	6.85E-07	9.34E-06
HBA2	114.0318839	1.29523249	1.08E-06	1.36E-05
RPL13P12	959.0493952	1.29488564	3.82E-12	4.01E-10
LGALS9	20.71409322	1.28410931	0.01591303	0.04592912
CHD4	1469.81304	1.27894102	1.41E-15	5.91E-13
SNHG19	895.1718072	1.27758211	2.77E-10	1.29E-08
SNORD104	48.23448072	1.26751106	0.00016154	0.00098631
RPL7AP62	27.23828482	1.26658156	0.00324669	0.01241146
CNFN	200.3584553	1.26563612	8.89E-11	4.86E-09
RPL5P34	70.98113368	1.26439793	5.25E-05	0.0003787
PLCB2	52.43458791	1.26155507	6.42E-05	0.00044978
IER2	866.7688909	1.26111192	0.00343525	0.01298915
NPW	28.05334063	1.25550428	0.0023271	0.00943393
APOA1	22.8477865	1.25259853	0.00538389	0.01888811
RPSAP19	319.1062263	1.25178828	1.22E-13	2.60E-11
NRTN	346.9441965	1.25168505	1.41E-08	3.44E-07
GARIN5A	108.2871	1.25027365	3.13E-06	3.43E-05
CTXN1	1699.124561	1.25001011	2.12E-12	2.50E-10
C19orf81	449.7558175	1.24487199	7.91E-14	1.76E-11
GALNT9	18.03074841	1.24425116	0.0169796	0.04838744
TNNI3	199.7226044	1.24072298	4.76E-06	4.90E-05
ATP5F1D	4923.070042	1.23864501	1.14E-14	4.11E-12
INAFM1	261.0645343	1.2297405	3.70E-09	1.09E-07
PPIAP29	298.89289	1.22788406	1.05E-14	3.93E-12
RPS26P58	48.94214919	1.22700164	0.00014274	0.00088743
RPL21P28	1080.337651	1.22449176	1.86E-10	9.26E-09
NDUFS6	2738.238565	1.22387112	9.32E-16	4.31E-13
ABHD17AP6	68.94438555	1.22386677	6.39E-06	6.34E-05
CERS1	323.4341137	1.22256752	9.81E-11	5.30E-09
CSNK2B	802.9390675	1.22199866	4.91E-13	8.25E-11
RPLP2	31981.88111	1.21489705	5.66E-12	5.43E-10
RPL32P18	96.6482181	1.21464957	5.66E-07	7.96E-06
NAA10	2368.483733	1.2139811	1.09E-15	4.94E-13
PPP1R14BP3	154.8606774	1.21023739	1.16E-08	2.90E-07
RPS28	21946.46397	1.20903322	3.60E-12	3.85E-10

Gene Name	baseMean	log2FoldChange	p.value	p.adj
ETFB	911.10206	1.20878747	5.05E-14	1.32E-11
RPL3P4	760.287313	1.20219404	6.94E-10	2.72E-08
GAPDHP1	132.1499826	1.20061886	3.01E-07	4.62E-06
SPATC1L	770.613258	1.20007237	6.57E-12	6.02E-10
PHLDA2	292.4146077	1.19961259	5.79E-08	1.15E-06
ATP5ME	2347.899767	1.19755526	2.91E-14	8.75E-12
F12	575.9514798	1.19704555	4.01E-11	2.52E-09
JTB	1151.919674	1.1961867	6.81E-14	1.58E-11
CITED4	246.0208304	1.19159919	2.49E-11	1.78E-09
SH2B2	260.4860189	1.18778939	1.01E-09	3.71E-08
HSPB1	3518.983626	1.18616919	1.39E-12	1.84E-10
GJC2	24.40059805	1.18500157	0.0114123	0.03504124
RPL7P32	62.03875554	1.18163904	3.36E-05	0.00026066
FAM174C	1221.253687	1.18045408	2.66E-12	2.98E-10
EGFL7	1083.098763	1.17909589	5.06E-09	1.43E-07
RPL24P8	55.78995727	1.17843347	0.00014627	0.00090717
METTL26	2751.15582	1.1753293	1.01E-19	1.21E-16
MZT2B	4272.483442	1.17521706	2.02E-10	9.89E-09
HSD17B1	46.51645207	1.17500604	0.00022955	0.00133594
HBQ1	562.2397947	1.17453449	5.68E-11	3.35E-09
ARHGDIG	416.0289365	1.16906486	5.01E-10	2.13E-08
POLR2L	3122.848122	1.16711431	8.52E-13	1.23E-10
MRPL23	4145.764032	1.16544303	8.78E-16	4.17E-13
TMEM86B	35.23525851	1.16504891	0.00213409	0.00877656
HNRNPA1P4	24.24322951	1.1638118	0.00669827	0.0225982
CYBA	4006.699622	1.16365304	7.92E-13	1.15E-10
RPL13AP25	115.0181249	1.16088386	2.72E-06	3.04E-05
RPLP0P9	448.7729367	1.16069852	6.14E-11	3.56E-09
RABAC1	808.3627414	1.15965625	5.89E-13	9.16E-11
NDUFA3	2809.323696	1.15852716	3.82E-13	6.97E-11
NDUFAF8	2570.477009	1.15762079	7.80E-13	1.14E-10
LINC01896	51.82870751	1.15630653	0.00037903	0.00204622
STAP2	87.60099526	1.15499241	1.63E-05	0.00014024
TMEM205	673.8530625	1.15495975	2.05E-09	6.83E-08
ATOX1	1218.453393	1.15278828	3.33E-13	6.39E-11
RPL28	20921.49566	1.14929272	6.64E-10	2.63E-08
DHRS12	53.05786267	1.14904058	0.00111897	0.00508357
TUBB8B	19.14473072	1.14844302	0.01398357	0.04131134
H2AC20	63.65146747	1.14842344	0.00037353	0.00202249
CLEC11A	356.99895	1.14580775	1.01E-09	3.71E-08
CALY	121.8080021	1.14451657	7.34E-05	0.00050463
POMC	46.90583403	1.14049547	0.00178772	0.00754406
HES4	6032.036328	1.13489938	4.73E-10	2.03E-08
RPL24P4	70.51197268	1.1338154	4.01E-05	0.00030345

Gene Name	baseMean	log2FoldChange	p.value	p.adj
TMEM160	2179.109626	1.13125387	1.72E-15	7.06E-13
POLR2I	993.4293252	1.12933101	9.17E-13	1.29E-10
RPL23AP42	68.4872118	1.12833744	7.34E-05	0.00050463
RPS24P19	45.6652562	1.12748335	0.00052963	0.00270915
MT2A	690.3448498	1.12510285	6.33E-12	5.88E-10
ATP1A3	207.3246394	1.121419	4.55E-07	6.61E-06
PRR22	222.2279262	1.11935942	5.04E-10	2.14E-08
TMEM52	219.7881644	1.11926989	1.03E-08	2.65E-07
RBP7	54.55131298	1.11739695	0.0008018	0.00384508
H2AJ	290.522549	1.11234375	3.69E-07	5.49E-06
ARL2	1510.903069	1.10975057	6.01E-12	5.65E-10
JUND	4530.240106	1.10843087	2.97E-08	6.50E-07
CORO7	267.6345316	1.10705684	4.43E-09	1.28E-07
NT5C	1180.18162	1.10600055	1.84E-13	3.73E-11
MICOS13	1880.03066	1.10363578	6.64E-13	1.00E-10
VKORC1	659.2990303	1.10283119	5.73E-10	2.38E-08
BBLN	1281.810195	1.10269299	2.00E-10	9.84E-09
ZNF414	599.8975832	1.10141361	2.95E-12	3.20E-10
SLC9A3R2	1417.195054	1.10131733	5.20E-14	1.34E-11
STXBP2	160.470034	1.09856113	4.54E-06	4.72E-05
CTSD	1567.333402	1.0980819	3.83E-11	2.44E-09
PPAN	458.8425707	1.09612971	2.07E-09	6.85E-08
CCDC124	4813.634266	1.09599497	2.60E-11	1.83E-09
REEP6	533.7873848	1.09498597	1.26E-09	4.52E-08
ROMO1	3892.772445	1.09489925	1.23E-15	5.41E-13
RPL13AP7	30.48762039	1.09439576	0.00464833	0.01675741
AP2S1	4582.237704	1.09294751	1.55E-11	1.19E-09
NPIP10P	33.04899642	1.09042498	0.01115722	0.03438681
NTNG2	108.7712312	1.09019569	8.14E-05	0.00055063
MCRIP2	1314.617515	1.08945138	3.60E-13	6.76E-11
TEPP	57.35245933	1.08638638	0.00105135	0.00482375
NDUFA11	1497.247463	1.08391077	1.94E-13	3.89E-11
PRAC2	54.37356147	1.08334355	0.00149651	0.00649606
RPS15	47987.19577	1.08294528	5.28E-13	8.57E-11
LINC01297	81.45300777	1.08236501	0.00012886	0.00081571
GADD45GIP1	4856.476643	1.0820258	4.48E-16	2.18E-13
FXYD5	1056.047025	1.08090347	1.83E-07	3.03E-06
SDF2L1	2265.390833	1.08047838	1.25E-12	1.66E-10
TMSB10	11569.75057	1.07805287	1.76E-11	1.32E-09
MRPS34	5241.21669	1.07774978	1.96E-12	2.38E-10
MZT2A	5004.862975	1.07758991	6.56E-10	2.62E-08
C20orf27	3555.238468	1.07692711	2.18E-11	1.59E-09
PCSK1N	2113.539583	1.07682118	6.04E-11	3.53E-09
EDF1	4894.415185	1.07627368	5.71E-14	1.41E-11

Gene Name	baseMean	log2FoldChange	p.value	p.adj
CNIH2	92.81783671	1.07585384	1.31E-05	0.00011628
CPT1C	378.1348403	1.07559481	2.58E-09	8.12E-08
SNHG9	163.2729031	1.07547234	9.62E-07	1.24E-05
CRYBG2	66.92928103	1.07256348	0.00010364	0.00067732
ISG15	172.5660194	1.07103846	6.21E-06	6.18E-05
DYNLT2B	68.18792864	1.07032567	0.00032682	0.00180206
CHCHD10	4914.845024	1.06993334	1.76E-18	1.51E-15
ZNNT1	41.8212952	1.06955153	0.00340217	0.01289651
FAM89B	137.6798517	1.06910874	2.30E-07	3.66E-06
PPDPF	3762.276848	1.06842926	2.43E-09	7.79E-08
LAGE3	2667.862396	1.06787781	2.67E-13	5.24E-11
RPL26	3334.576488	1.06731034	1.78E-10	9.01E-09
UQCR10	2666.530537	1.06684863	1.62E-14	5.43E-12
RCN3	116.3746817	1.06623166	1.16E-05	0.00010463
TOP3BP1	164.1726491	1.06593547	9.77E-07	1.25E-05
PPP1R14B	7080.89534	1.0642172	1.15E-17	8.14E-15
COPS9	2229.392181	1.06181176	3.59E-14	1.01E-11
EBP	1261.814859	1.06177077	6.40E-13	9.79E-11
GAL	2581.17754	1.05894343	3.30E-13	6.39E-11
NDUFS8	4345.205374	1.05886413	1.18E-11	9.68E-10
METRNL	1326.02631	1.05790461	1.41E-12	1.84E-10
MRPL41	3500.136069	1.05736377	3.89E-14	1.06E-11
ATP5F1E	6206.234579	1.05706942	5.14E-13	8.49E-11
RPL18	35030.77036	1.05542815	1.06E-10	5.67E-09
NUDT1	965.9335121	1.05520341	3.42E-11	2.27E-09
RPL13	83346.98683	1.05488851	1.71E-10	8.68E-09
TIMM13	4460.535859	1.0537551	1.08E-12	1.47E-10
ZNHIT2	600.0909284	1.05346128	2.31E-11	1.67E-09
NKX2-5	1739.131099	1.05052933	8.60E-13	1.23E-10
FBXL15	1030.50167	1.04982945	5.43E-12	5.32E-10
SRM	5516.319785	1.04861606	2.98E-12	3.22E-10
CARMIL2	362.5926845	1.0484424	7.63E-08	1.43E-06
RPS19	48922.88061	1.04771668	9.29E-12	7.90E-10
RPS15P4	189.0934094	1.04512693	2.73E-08	6.09E-07
NDUFB11	4200.070794	1.04486447	3.67E-13	6.82E-11
C2CD4A	31.42940916	1.04371894	0.00663562	0.02243572
DHRS4L2	431.4085793	1.04020254	3.13E-11	2.13E-09
RPL36	35764.60648	1.03890916	2.41E-10	1.14E-08
BATF3	323.7432313	1.03696472	5.87E-10	2.41E-08
SERGEF	613.005934	1.03611669	3.55E-07	5.31E-06
BCYRN1	309.4598995	1.03536572	4.58E-08	9.34E-07
TMEM158	399.7249669	1.03449607	1.02E-08	2.63E-07
ZNF296	245.9156411	1.03390414	2.08E-08	4.81E-07
SMIM4	558.7532069	1.03305176	4.59E-10	1.98E-08

Gene Name	baseMean	log2FoldChange	p.value	p.adj
LDHB	5351.811452	1.03145452	1.63E-14	5.43E-12
EEF1A1P11	1301.470559	1.03075009	9.49E-10	3.53E-08
SLC25A10	834.4812136	1.02814304	6.69E-10	2.64E-08
C12orf57	575.3950118	1.02723856	1.31E-08	3.21E-07
TBC1D3F	60.08889195	1.02698766	0.00033001	0.00181745
FAM181B	60.65386352	1.02601867	0.0007315	0.00356507
SULT2B1	89.37418765	1.02526126	0.00027105	0.00153634
SLC39A4	844.0724244	1.02349153	8.41E-11	4.67E-09
C19orf73	88.2067749	1.01960557	3.20E-05	0.00025023
MESP1	513.6984767	1.01848094	2.30E-09	7.45E-08
U2AF1L4	65.83565105	1.01829067	0.00021906	0.00128363
ZNF580	1493.398317	1.01800191	2.49E-11	1.78E-09
METRNL	625.6904438	1.01768308	6.63E-07	9.10E-06
CAHM	36.17247568	1.01692796	0.00477003	0.0171245
TMEM31	29.34522484	1.01688559	0.01582816	0.04572748
KRT10	857.9641456	1.01497383	5.81E-11	3.41E-09
SQOR	35.03611735	1.01315811	0.016944	0.04830887
ASPHD1	79.36717416	1.01287069	0.00010715	0.00069742
POLA2	765.418681	1.01160631	1.38E-12	1.82E-10
STARD10	678.9799672	1.0113744	1.50E-10	7.65E-09
RNF208	334.592051	1.01091978	5.19E-07	7.38E-06
RPL18A	43451.15399	1.01080166	2.13E-11	1.57E-09
CTU1	673.2961514	1.01037321	5.54E-13	8.92E-11
LSM7	3788.109087	1.01016919	4.02E-14	1.08E-11
DUSP15	109.4958854	1.00991532	9.72E-05	0.00064039
RPL35	46907.68012	1.00865243	3.67E-12	3.90E-10
CAMK2N2	79.58142133	1.0072726	0.00024411	0.00140516
ATP5PO	2497.805923	1.00608178	7.58E-13	1.12E-10
ZFPM1	333.3191763	1.00550598	1.21E-06	1.49E-05
MICOS10	271.0882502	1.00545997	7.04E-08	1.35E-06
ZFAS1	1064.35518	1.00432687	0.0086723	0.02794097
ECH1	1466.916147	1.0023118	1.95E-10	9.63E-09
RPL21P119	1032.834452	1.001513	1.78E-09	6.03E-08
HAGHL	930.7783142	1.00031398	3.63E-07	5.41E-06

Supplementary Data 3: Table of significantly (adjusted p-valued <0.05) down-regulated genes in MAX-R60Q transfected HEK293 cells relative to MAX-WT transfected cells.

Gene Name	baseMean	log2FoldChange	p.value	p.adj
CEP170P1	96.46939551	-3.127763389	8.50E-27	2.56E-23
PLXNB3	8.205721404	-3.005240077	0.002481941	0.009954257
FPGT-TNNI3K	7.988997018	-2.655781543	0.002742822	0.01081065
GABPAP	19.81495391	-2.633593846	3.23E-06	3.52E-05
LINC02211	37.47884116	-2.57626135	1.11E-09	4.03E-08
SLC18A2	7.601939656	-2.572028636	0.002765966	0.010892351
TBX20	31.80578247	-2.554830494	4.61E-08	9.39E-07
MFSD14A	34.19784887	-2.531113992	1.92E-09	6.47E-08
ZSCAN23	39.37945052	-2.486873896	3.43E-10	1.53E-08
BCLAF1P2	239.3367127	-2.41687399	3.71E-05	0.000283764
RNA5SP18	10.13772032	-2.395429091	0.001778265	0.007511194
PFN1P2	14.52754213	-2.393279501	0.000249511	0.001429993
BEND3P3	17.42101423	-2.356605665	4.99E-05	0.000362576
XIST	13192.81056	-2.352057035	5.66E-05	0.000403256
CRYBG3	196.2049688	-2.337447674	1.39E-20	2.08E-17
CMTM1	16.10352155	-2.301514458	5.55E-05	0.000397245
TCAF1P1	465.419724	-2.293816546	4.14E-08	8.62E-07
TCAF2C	10.31896778	-2.235180095	0.002875798	0.011256054
ACKR4	13.07611304	-2.216556979	0.00074805	0.003629763
HLTF	1168.308127	-2.216427561	8.73E-30	3.93E-26
ARHGAP5	397.9876289	-2.213927023	2.80E-42	5.05E-38
ZNF658B	8.088927346	-2.196592218	0.006452412	0.021916671
KLHL11	251.9740384	-2.194770418	4.28E-32	2.57E-28
GOLGA2P7	9.098652984	-2.190072011	0.007221014	0.024033623
SHPRH	328.5093298	-2.181259683	3.00E-24	6.76E-21
PKD1P4	497.4665071	-2.17182922	4.18E-24	8.39E-21
DLEU2L	7.879052387	-2.159158112	0.007093854	0.023684702
LTB4R2	31.53409452	-2.152781367	5.35E-07	7.57E-06
ACAD11	41.80033383	-2.148780503	2.99E-08	6.53E-07
MRPS31P5	11.38476556	-2.140094831	0.003660091	0.013735621
ZNF770	436.3283851	-2.115409869	7.90E-22	1.30E-18
USP32P4	20.33813888	-2.107636826	6.07E-05	0.000429159
GRM2	9.679353895	-2.107066764	0.004302269	0.015701281
HERC2P3	159.8638116	-2.069250339	1.82E-17	1.22E-14
FREM1	7.457046214	-2.057607652	0.010531739	0.032703002
HOXA6	130.0800419	-2.039024887	4.37E-13	7.72E-11
NFAT5	532.1360258	-2.031386112	7.57E-28	2.73E-24
NCKAP5	11.05590118	-2.026916948	0.005578118	0.019433443
INHBE	21.45544339	-1.985709526	0.000239375	0.001382001
USP37	190.6219658	-1.981486304	5.33E-20	6.87E-17
PKD1P3	334.1420916	-1.981072381	2.23E-06	2.58E-05

Gene Name	baseMean	log2FoldChange	p.value	p.adj
KRT38	14.47324303	-1.974311487	0.004385213	0.015958778
LRIG1	224.3976478	-1.955158104	5.56E-14	1.39E-11
TOP3B	9.614449779	-1.952806149	0.007396403	0.024495321
CEP295	351.4850893	-1.952459283	2.13E-23	3.84E-20
TLR1	8.653337393	-1.928225145	0.008892531	0.028528228
RNF169	356.5063448	-1.906628976	2.09E-25	5.39E-22
TRAPPC6B	96.6329666	-1.900978239	2.01E-12	2.38E-10
PGM5P2	13.70993255	-1.886682507	0.003930907	0.014588032
ADAMTS20	65.28632689	-1.875774958	1.26E-08	3.13E-07
EML5	93.90108304	-1.868199624	5.62E-12	5.43E-10
ACER2	34.27189935	-1.867466974	2.83E-06	3.13E-05
ZNF322P1	117.8425199	-1.858795225	2.09E-11	1.55E-09
PKD1P6	59.87003812	-1.855653873	1.64E-08	3.90E-07
UBE4A	457.5479863	-1.828291788	4.25E-15	1.67E-12
IGF2BP3	524.8038213	-1.822715332	6.33E-18	5.19E-15
HAUS6P1	8.214886945	-1.822140168	0.016098228	0.046386729
USP34	808.5070084	-1.803701334	3.88E-35	3.49E-31
TSTD2	221.7864672	-1.783275375	1.08E-18	1.06E-15
HAUS6P3	20.32277081	-1.77727266	0.001309751	0.00579982
FMN1	9.63917513	-1.770363384	0.017324252	0.049175355
SEN3-EIF4A1	8.846662232	-1.762764196	0.01590023	0.045906282
PCDHGC3	44.96487555	-1.73185272	4.70E-05	0.000345449
CERKL	17.29662045	-1.729363851	0.00130974	0.00579982
FAM169A	225.5639302	-1.688817464	1.57E-14	5.43E-12
TSSK5P	41.92159169	-1.685532344	4.11E-06	4.34E-05
PKD1P2	410.3503357	-1.685410854	7.22E-18	5.66E-15
TMEFF1	72.74835722	-1.680153735	1.95E-07	3.19E-06
RECQL	439.3393718	-1.66236434	3.34E-05	0.000259683
OCLNP1	24.28255297	-1.641705981	0.000281381	0.001580501
CSNK2A3	11.07681017	-1.623877705	0.017546106	0.049695599
KIAA1614	25.5116257	-1.617629076	0.000262231	0.001492927
NCR3LG1	497.896916	-1.615019851	7.50E-05	0.000513671
RNA5SP312	15.91343591	-1.614216152	0.005810103	0.020065012
CYP51A1	94.24692279	-1.604067571	4.94E-07	7.06E-06
RNA5SP315	14.41131752	-1.600537527	0.007701176	0.025334505
NSFP1	327.9465027	-1.599750347	4.33E-11	2.67E-09
LINC00624	19.22073642	-1.59202373	0.004324068	0.015761701
SMC4	2859.319161	-1.58563477	4.50E-19	4.78E-16
ASAP2	163.0135809	-1.578132228	3.36E-11	2.25E-09
ZNF460	57.95486636	-1.576463922	6.74E-06	6.62E-05
TCP11L2	59.48357708	-1.561787263	1.63E-07	2.73E-06
SEC24C	522.6973156	-1.561251115	6.01E-13	9.27E-11
CCDC144CP	17.0015359	-1.557349759	0.006786657	0.022836593
NRIP1	276.9917598	-1.554697099	8.78E-18	6.60E-15

Gene Name	baseMean	log2FoldChange	p.value	p.adj
RBL2	735.0618735	-1.545959531	1.58E-16	8.36E-14
RAB11FIP1	340.0075311	-1.539435554	1.86E-14	6.00E-12
LRRC37A4P	162.9226295	-1.537460565	9.81E-13	1.36E-10
CCNE2	155.5327599	-1.525867433	1.28E-09	4.59E-08
EMBP1	14.56502577	-1.522761084	0.014222763	0.041880733
CERS6	420.705183	-1.519241744	3.71E-20	5.14E-17
NUS1P1	86.44995578	-1.516794083	3.75E-08	7.93E-07
DLG5	595.7181099	-1.51469235	4.71E-13	8.17E-11
IGSF10	25.76419796	-1.513227514	0.000397882	0.002131966
TJP2	14.52326746	-1.497294447	0.008444476	0.027338822
TBC1D14	367.2903177	-1.492964773	3.14E-12	3.38E-10
UBE2Q2P1	33.40957837	-1.48589917	0.00013838	0.0008645
FNBP1P1	30.74721407	-1.481108433	0.000461512	0.002407121
TATDN2P2	49.69957059	-1.478900775	3.76E-06	4.01E-05
ZFYVE16	489.6009072	-1.478222982	1.79E-13	3.66E-11
HMCN1	44.97445177	-1.473182491	4.58E-05	0.000339318
CLUL1	15.70209342	-1.472743432	0.007688244	0.025299245
SOGA3	22.50284832	-1.472221252	0.001431845	0.006262067
REL	132.0324727	-1.468977846	3.53E-11	2.31E-09
B3GNT5	137.7646091	-1.467306768	2.37E-09	7.66E-08
ZNF731P	85.63301425	-1.461344449	8.07E-07	1.07E-05
TCEA1P2	65.71390317	-1.453584738	1.89E-06	2.21E-05
GOLGA8H	120.6746047	-1.448935563	6.98E-09	1.90E-07
PARGP1	16.65267548	-1.428993845	0.00746126	0.024681665
PTGFR	32.90165485	-1.42866223	0.000630445	0.003141949
DNAH10	25.20046919	-1.425434131	0.001507506	0.006537482
SRGAP2D	99.4250749	-1.416180927	8.25E-07	1.08E-05
FAM13C	29.07402989	-1.401007591	0.000545882	0.002779652
SYTL4	89.41129368	-1.400746765	4.19E-08	8.66E-07
PKD1P1	284.290262	-1.399019729	6.74E-11	3.84E-09
TIMM23B-AGAP6	16.3938373	-1.398127932	0.011778135	0.035926903
TLK2P1	13.8493871	-1.397786628	0.013034694	0.039045631
NID2	305.8929601	-1.387671345	3.62E-14	1.01E-11
TMPPE	19.09674164	-1.387213103	0.013760565	0.040793155
FSIP2	22.46465081	-1.378912154	0.003289684	0.012538619
DYNC1LI2	841.7631865	-1.375446441	1.74E-13	3.60E-11
TMEM140	114.6301831	-1.371569987	3.18E-07	4.85E-06
HSPG2	218.2047534	-1.370727594	1.86E-10	9.26E-09
IKZF2	41.06530011	-1.369424604	0.000111746	0.00072368
RALGAPA1P1	27.09179385	-1.369279551	0.001328361	0.005862793
HMG20A	871.2161287	-1.360259412	1.12E-18	1.06E-15
TSSK4	33.27541937	-1.356744615	0.002383973	0.009627706
PCDHGA11	38.09248043	-1.356366577	0.000168865	0.001025818
SYT16	62.0454448	-1.345335588	8.17E-05	0.000552198

Gene Name	baseMean	log2FoldChange	p.value	p.adj
ERBB4	24.92897989	-1.342885241	0.001464689	0.006380948
ZDBF2	717.440899	-1.340141382	3.94E-17	2.37E-14
ETS1	29.18803517	-1.333037152	0.000730876	0.00356507
INPP5D	31.33378548	-1.33300639	0.000807003	0.003865032
SS18L1	311.2830302	-1.331601928	4.88E-13	8.25E-11
DCHS1	81.56296968	-1.331291836	4.56E-07	6.62E-06
ADAM17	503.601171	-1.327210992	2.71E-11	1.89E-09
ANKRD10-IT1	42.65245151	-1.322654091	0.000422299	0.002241492
DHFRP1	316.882971	-1.31767841	1.26E-09	4.52E-08
NOD2	16.96507847	-1.305004046	0.013110694	0.039208172
JMJD7-PLA2G4B	36.09267979	-1.302378201	0.000471701	0.002449914
ZNF700	53.58887295	-1.294418376	0.000115371	0.000743683
ANKRD12	208.8501967	-1.294243539	3.96E-13	7.14E-11
USP54	373.5111945	-1.29041618	5.18E-13	8.49E-11
STAG1	489.0693273	-1.289271067	0.00193476	0.008077623
LRRC37A9P	16.06637893	-1.289041166	0.015385041	0.044654748
CCNK	232.2213639	-1.288423924	7.79E-12	6.86E-10
ZNF23	22.29693407	-1.285111705	0.005539708	0.019329499
CDON	295.2502104	-1.281048668	4.09E-12	4.19E-10
CARD14	17.66476996	-1.279580499	0.016673786	0.047666571
JAM3	463.69099	-1.279155583	4.48E-10	1.94E-08
HSP90AA2P	23.04344447	-1.27755135	0.004270026	0.015618371
EDA	125.7902641	-1.277066006	3.83E-08	8.09E-07
RAF1	770.0264746	-1.277056405	2.71E-10	1.26E-08
SNORD17	75.38426261	-1.276910994	1.27E-05	0.000113215
RAB23	179.7702602	-1.268988635	3.77E-07	5.58E-06
WDR48	604.8200312	-1.265907543	1.19E-11	9.68E-10
SAMD9	37.71652707	-1.26545785	0.001085401	0.004954771
FBXO11	605.6952124	-1.261573807	1.57E-18	1.42E-15
JMJD1C	535.8183746	-1.261437006	2.30E-14	7.02E-12
ERCC5	36.16421263	-1.256604176	0.000715772	0.003501398
PIGCP1	65.85088477	-1.25435041	1.62E-05	0.000139599
PROX1	104.131078	-1.254187751	7.17E-08	1.36E-06
WWC2	705.3040375	-1.252039402	3.61E-14	1.01E-11
AHCTF1P1	45.93360299	-1.240967591	0.000139699	0.000871534
IRS1	99.0088305	-1.238818859	1.73E-07	2.89E-06
NFATC3	277.5650296	-1.236769127	2.27E-07	3.62E-06
PI15	36.48881405	-1.226711538	0.001680389	0.007159815
ZSWIM4	60.31645902	-1.225327169	3.05E-05	0.00023971
CNOT1	3380.521925	-1.222675189	1.76E-14	5.78E-12
ATG9A	447.9766272	-1.221151969	7.22E-08	1.37E-06
WNT8B	27.64458786	-1.220300191	0.00498547	0.017766205
ONECUT1	18.53115254	-1.219456041	0.015579625	0.045117874
POLK	324.1169142	-1.212566075	1.29E-09	4.60E-08

Gene Name	baseMean	log2FoldChange	p.value	p.adj
TTN	143.9229768	-1.212078858	1.22E-06	1.51E-05
FAT3	113.1160145	-1.209243056	1.04E-07	1.85E-06
MYLK	115.3382551	-1.208350731	7.76E-07	1.03E-05
POM121B	299.1871049	-1.207078746	9.04E-09	2.38E-07
LINC02256	22.16948217	-1.201755257	0.011374484	0.034942972
SPIRE1	331.4283694	-1.1976956	1.82E-11	1.36E-09
EPHA3	266.4533691	-1.196694499	2.47E-12	2.84E-10
LRRIQ1	36.56234931	-1.186537885	0.002670502	0.010590409
PKD1P5	724.2912518	-1.186360924	6.84E-12	6.23E-10
EPN2	394.6902497	-1.1856327	5.21E-09	1.47E-07
ZNF852	76.24679316	-1.18361531	5.63E-05	0.000401692
FREM2	361.7936637	-1.182781695	7.02E-14	1.60E-11
PLCL1	37.34675252	-1.181474737	0.000708211	0.003472041
NBEAP2	18.9614263	-1.180455756	0.014061319	0.041486985
MYO9A	497.5581889	-1.178006037	3.67E-17	2.28E-14
EPHA5	43.10136237	-1.177549956	0.001041062	0.004783845
TOMM40P4	36.8735546	-1.17337967	0.002288234	0.009303558
PLPPR4	37.96860081	-1.165969499	0.001479486	0.006435071
TEX14	24.0496925	-1.165878953	0.006722771	0.022663904
ZNF805	153.8927358	-1.164178605	1.97E-08	4.61E-07
CYP1B1	79.17942059	-1.163785463	4.95E-05	0.000360744
DOP1A	208.1533106	-1.163648788	6.67E-11	3.81E-09
CD302	76.76419879	-1.159568566	2.35E-05	0.00019273
GCNT4	27.50105147	-1.156022666	0.004978019	0.017747293
PIK3R1	240.1376212	-1.154129445	5.11E-09	1.44E-07
MKRN2	475.2356174	-1.151785021	8.16E-11	4.56E-09
DPY19L2P3	57.09272743	-1.149559123	0.000278715	0.001568454
PLCXD2	101.4649966	-1.146419465	1.62E-06	1.93E-05
KAT6B	482.4959336	-1.146305289	5.41E-14	1.37E-11
ZNF608	249.3069849	-1.145611892	5.15E-07	7.33E-06
GPR50	85.87698053	-1.145599973	8.11E-06	7.73E-05
EXOC7	743.3392411	-1.14292466	1.12E-07	1.97E-06
TNC	38.89284996	-1.142481626	0.001818198	0.007656554
ADGRA2	305.1734358	-1.141936477	6.98E-12	6.27E-10
RAB43	24.18870716	-1.139393143	0.009432881	0.029910592
WDR17	176.6882497	-1.138850894	1.05E-09	3.84E-08
CNTNAP3C	44.46846743	-1.134303927	0.000395137	0.002119779
BAZ2B	272.3026794	-1.134026607	4.59E-10	1.98E-08
MPDZ	345.0743413	-1.131386269	3.58E-13	6.76E-11
HS6ST1P1	33.57195958	-1.129698095	0.006818965	0.022932472
KIAA1109	511.370412	-1.129582858	3.61E-11	2.34E-09
HBP1	247.2358477	-1.129534512	3.38E-10	1.51E-08
ELF1	419.8971846	-1.129189181	1.48E-11	1.17E-09
NEMF	532.6146825	-1.126220885	5.23E-10	2.20E-08

Gene Name	baseMean	log2FoldChange	p.value	p.adj
CCDC186	384.6155529	-1.125768097	4.33E-11	2.67E-09
NCOA3	399.0585042	-1.124233483	9.48E-13	1.32E-10
NHS	65.57664543	-1.122856762	0.000149834	0.000923899
ASH1L	770.1252601	-1.121023709	5.76E-13	9.16E-11
BDP1	932.1436152	-1.118366686	2.77E-12	3.05E-10
UTRN	806.7658553	-1.116247092	2.54E-15	1.02E-12
SNX14	110.0919041	-1.113380537	1.19E-05	0.000106949
GOLGA6L5P	51.20475668	-1.110685904	0.000610047	0.003058885
ATRX	1357.693366	-1.110626196	1.05E-16	5.75E-14
GOLGA7	361.2386955	-1.109800492	9.27E-11	5.05E-09
ZNF518A	552.58159	-1.107864395	2.72E-12	3.01E-10
GHR	53.4687272	-1.106053858	0.001780336	0.007518177
ABCA1	48.05962207	-1.104627484	0.002836887	0.011125483
TENM1	879.4559107	-1.104534376	6.06E-10	2.45E-08
PTPRG	523.9033788	-1.104493682	3.05E-11	2.08E-09
SRCAP	177.932939	-1.102188569	1.31E-07	2.26E-06
AFF4	1449.593615	-1.101025578	1.17E-17	8.14E-15
MICAL3	639.8380793	-1.098755229	7.76E-15	2.98E-12
MPHOSPH9	722.6770289	-1.092070279	4.79E-12	4.85E-10
ADAMTS6	37.50613866	-1.091929042	0.002587224	0.010312304
LINC01876	34.75963212	-1.091663891	0.003545393	0.013360782
CASP8AP2	985.7215499	-1.090642892	6.68E-13	1.00E-10
CFAP126	115.0700063	-1.090310136	1.08E-05	9.79E-05
RALGAPA1	563.1161714	-1.089875257	7.03E-13	1.05E-10
PHC1P1	255.0419136	-1.088833782	8.56E-11	4.72E-09
ATP11B	733.943988	-1.088028434	3.27E-14	9.68E-12
MEF2A	672.6614048	-1.087839069	1.92E-14	6.08E-12
SRXN1	57.56545204	-1.083467318	0.003729057	0.013954026
PAG1	365.145285	-1.083264612	1.00E-11	8.43E-10
NAB1	439.7770448	-1.083009714	1.15E-12	1.55E-10
FOXN2	319.9673711	-1.082505568	2.30E-08	5.25E-07
RASAL2	433.062549	-1.076898958	1.56E-12	2.01E-10
TBC1D8B	175.6715288	-1.07630395	1.41E-07	2.41E-06
LINC00630	141.6303809	-1.07415389	1.49E-07	2.52E-06
ATP1A1	4791.061415	-1.072737281	4.66E-09	1.34E-07
RAPGEF2	404.3269159	-1.071138044	4.83E-09	1.38E-07
AHNAK2	142.0815197	-1.070807682	3.69E-05	0.00028265
LHFPL5	38.51921672	-1.069730286	0.006025105	0.02069882
SYT2	59.75077465	-1.069453598	0.000446947	0.00234756
ITPR1	200.9233601	-1.064802164	3.71E-08	7.87E-07
ZKSCAN8	903.2776901	-1.063012627	1.63E-14	5.43E-12
CD109	192.0227379	-1.061918927	7.67E-09	2.06E-07
ZNF337	50.693072	-1.060839847	0.001441344	0.006295977
STAT5A	32.30909835	-1.060322971	0.007082336	0.023659385

Gene Name	baseMean	log2FoldChange	p.value	p.adj
ALDH1L2	900.0831445	-1.058611924	9.33E-14	2.03E-11
SOX5	59.99334778	-1.05789629	0.000283444	0.001589335
BOD1L1	941.3469619	-1.056947114	1.33E-15	5.72E-13
ITGA4	141.7763451	-1.055918286	9.49E-07	1.22E-05
PAN2	510.6737783	-1.055114828	5.15E-09	1.45E-07
ZBTB45P2	50.8903174	-1.054229695	0.005720358	0.019824661
HIVEP1	194.9505244	-1.054229158	3.71E-07	5.51E-06
SEMA3D	145.8467255	-1.053204705	3.04E-07	4.66E-06
PIK3C2A	1115.001082	-1.045394689	9.62E-12	8.10E-10
ITPR3	728.7054297	-1.044299	2.62E-12	2.97E-10
ANKRD18CP	29.33032697	-1.042606027	0.010044342	0.031495089
ZNF140	34.22037916	-1.041753673	0.004081242	0.015022301
ROR1	226.5862594	-1.03877099	1.24E-07	2.16E-06
LRP1B	130.2363941	-1.033127125	1.37E-06	1.67E-05
SHANK1	82.83010791	-1.03259295	0.000771733	0.003720668
NDNF	126.7308271	-1.032345008	3.52E-06	3.79E-05
FAT4	132.3722627	-1.032226343	3.14E-06	3.43E-05
PKD2	324.580123	-1.029726839	3.23E-09	9.69E-08
PABPC4L	335.266113	-1.029513832	1.14E-08	2.86E-07
LCA5	131.8000613	-1.027444711	1.54E-05	0.000133599
CARF	61.65524445	-1.026787028	0.002681473	0.010614293
PTPN13	1559.210443	-1.026012932	4.85E-13	8.25E-11
HEATR1	1941.982272	-1.025958258	4.37E-09	1.26E-07
ATXN1L	599.8605399	-1.025692416	3.76E-11	2.41E-09
N4BP2	357.4733399	-1.025604146	3.24E-08	7.02E-07
RTEL1-TNFRSF6B	55.32741725	-1.024429873	0.00328788	0.012537043
TP53BP1	623.9332114	-1.024000152	2.28E-07	3.64E-06
FOXO3B	397.268701	-1.023281683	3.56E-07	5.31E-06
FGD5	30.36902438	-1.022165794	0.016636476	0.04761274
FGD6	127.1405203	-1.020235174	2.58E-06	2.90E-05
PLIN4	34.72715375	-1.018235224	0.010738977	0.03326261
XRN1	631.6286953	-1.017972891	6.53E-12	6.01E-10
PKD1	1050.020152	-1.017112613	9.30E-10	3.48E-08
SMAP1	183.0395159	-1.0169176	2.35E-06	2.70E-05
BTAF1	1220.199636	-1.016870251	3.79E-10	1.67E-08
ZNF384	376.8574074	-1.015580178	8.05E-08	1.49E-06
ZRANB1	293.6494398	-1.015030194	4.85E-07	6.96E-06
HIPK3	425.3527148	-1.014941487	6.48E-10	2.60E-08
NT5C2	266.3523483	-1.014837912	1.38E-05	0.000121342
ZNF536	140.6499435	-1.009370811	1.23E-06	1.52E-05
SCN8A	85.01961804	-1.007167319	4.67E-05	0.000344055
MYO5B	105.5306962	-1.005829963	6.85E-05	0.00047598
ZNF780A	157.8856033	-1.004105693	2.68E-05	0.000214136
KCNN3	30.33549346	-1.003526856	0.014348137	0.042181417

Gene Name	baseMean	log2FoldChange	p.value	p.adj
EP300	1256.224	-1.003149541	8.07E-14	1.78E-11
LONRF3	252.4757782	-1.002835152	1.65E-08	3.91E-07
RP2	435.4533723	-1.002699216	3.08E-09	9.31E-08
KMT2D	1922.71433	-1.002697323	5.33E-12	5.26E-10
RUBCN	126.6524247	-1.001015098	5.77E-05	0.000410345
DNAH6	59.69996057	-1.000574782	0.001170516	0.005281816

Supplementary Data 4: Table of significantly enriched reactome pathways using all MAX-R60Q differentially expressed genes.

Analysis Type: PANTHER Overrepresentation Test
Annotation Version and Release Date: Reactome version 77
Reference List: Homo sapiens (all genes)
Test Type: FISHER
Correction: FDR

Reactome pathways	Homo sapiens - REFLIST (20589)	MAX-R60Q (5736)	MAX-R60Q (expected)	MAX-R60Q (fold Enrichment)	MAX-R60Q (raw P-value)	MAX-R60Q (FDR)
Metabolism of proteins (R-HSA-392499)	1914	784	533.23	1.47	8.04E-21	1.00E-17
Translation (R-HSA-72766)	293	192	81.63	2.35	4.19E-19	3.48E-16
Metabolism of RNA (R-HSA-8953854)	661	335	184.15	1.82	1.96E-18	1.22E-15
Cellular responses to stress (R-HSA-2262752)	718	344	200.03	1.72	3.10E-16	1.54E-13
Cellular responses to stimuli (R-HSA-8953897)	732	349	203.93	1.71	3.88E-16	1.61E-13
Formation of a pool of free 40S subunits (R-HSA-72689)	101	91	28.14	3.23	4.03E-15	1.44E-12
Signaling by ROBO receptors (R-HSA-376176)	215	143	59.9	2.39	5.82E-15	1.61E-12
Signaling by Rho GTPases, Miro GTPases and RHOBTB3 (R-HSA-9716542)	685	325	190.84	1.7	7.00E-15	1.75E-12
Signaling by Rho GTPases (R-HSA-194315)	670	317	186.66	1.7	1.75E-14	3.96E-12
SRP-dependent cotranslational protein targeting to membrane (R-HSA-1799339)	112	94	31.2	3.01	2.49E-14	5.18E-12
L13a-mediated translational silencing of Ceruloplasmin expression (R-HSA-156827)	111	93	30.92	3.01	3.71E-14	7.11E-12
RHO GTPase cycle (R-HSA-9012999)	448	233	124.81	1.87	4.54E-14	8.08E-12
GTP hydrolysis and joining of the 60S ribosomal subunit (R-HSA-72706)	112	93	31.2	2.98	4.90E-14	8.14E-12
Influenza Viral RNA Transcription and Replication (R-HSA-168273)	133	103	37.05	2.78	6.47E-14	1.01E-11
Regulation of expression of SLITs and ROBOs (R-HSA-9010553)	169	119	47.08	2.53	7.31E-14	1.07E-11
Eukaryotic Translation Initiation (R-HSA-72613)	119	96	33.15	2.9	9.67E-14	1.15E-11
Cap-dependent Translation Initiation (R-HSA-72737)	119	96	33.15	2.9	9.67E-14	1.21E-11
Response of EIF2AK4 (GCN2) to amino acid deficiency (R-HSA-9633012)	101	87	28.14	3.09	9.51E-14	1.25E-11

Reactome pathways	Homo sapiens - REFLIST (20589)	MAX-R60Q (5736)	MAX-R60Q (expected)	MAX-R60Q (fold Enrichment)	MAX-R60Q (raw P-value)	MAX-R60Q (FDR)
rRNA processing (R-HSA-72312)	202	133	56.28	2.36	9.06E-14	1.25E-11
Eukaryotic Translation Elongation (R-HSA-156842)	94	83	26.19	3.17	1.33E-13	1.51E-11
Viral mRNA Translation (R-HSA-192823)	89	80	24.79	3.23	1.68E-13	1.74E-11
rRNA processing in the nucleus and cytosol (R-HSA-8868773)	192	128	53.49	2.39	1.77E-13	1.77E-11
Peptide chain elongation (R-HSA-156902)	89	80	24.79	3.23	1.68E-13	1.82E-11
Selenocysteine synthesis (R-HSA-2408557)	93	82	25.91	3.16	2.00E-13	1.91E-11
Nervous system development (R-HSA-9675108)	574	276	159.91	1.73	2.61E-13	2.41E-11
Major pathway of rRNA processing in the nucleolus and cytosol (R-HSA-6791226)	182	122	50.7	2.41	3.94E-13	3.28E-11
Eukaryotic Translation Termination (R-HSA-72764)	93	81	25.91	3.13	3.93E-13	3.38E-11
Axon guidance (R-HSA-422475)	549	266	152.95	1.74	4.20E-13	3.38E-11
Nonsense-Mediated Decay (NMD) (R-HSA-927802)	115	91	32.04	2.84	8.08E-13	6.10E-11
Nonsense Mediated Decay (NMD) enhanced by the Exon Junction Complex (EJC) (R-HSA-975957)	115	91	32.04	2.84	8.08E-13	6.29E-11
Gene expression (Transcription) (R-HSA-74160)	1454	571	405.08	1.41	1.49E-12	1.09E-10
Nonsense Mediated Decay (NMD) independent of the Exon Junction Complex (EJC) (R-HSA-975956)	95	80	26.47	3.02	1.98E-12	1.41E-10
Cellular response to starvation (R-HSA-9711097)	156	107	43.46	2.46	5.17E-12	3.58E-10
Selenoamino acid metabolism (R-HSA-2408522)	116	88	32.32	2.72	8.93E-12	6.02E-10
Cell Cycle (R-HSA-1640170)	648	292	180.53	1.62	1.90E-11	1.25E-09
RNA Polymerase II Transcription (R-HSA-73857)	1319	513	367.47	1.4	8.15E-11	5.08E-09
Membrane Trafficking (R-HSA-199991)	626	280	174.4	1.61	8.03E-11	5.13E-09
Signal Transduction (R-HSA-162582)	2500	882	696.49	1.27	2.25E-10	1.30E-08
Respiratory electron transport, ATP synthesis by chemiosmotic coupling, and heat production by uncoupling proteins. (R-HSA-163200)	126	87	35.1	2.48	3.23E-10	1.83E-08
The citric acid (TCA) cycle and respiratory electron transport (R-HSA-1428517)	176	108	49.03	2.2	4.50E-10	2.49E-08
Disease (R-HSA-1643685)	1679	620	467.76	1.33	8.01E-10	4.25E-08
Post-translational protein modification (R-HSA-597592)	1396	529	388.92	1.36	9.38E-10	4.87E-08
DNA Repair (R-HSA-73894)	310	158	86.36	1.83	2.19E-09	1.11E-07

Reactome pathways	Homo sapiens - REFLIST (20589)	MAX-R60Q (5736)	MAX-R60Q (expected)	MAX-R60Q (fold Enrichment)	MAX-R60Q (raw P-value)	MAX-R60Q (FDR)
Metabolism (R-HSA-1430728)	2087	742	581.43	1.28	2.91E-09	1.45E-07
Cell Cycle, Mitotic (R-HSA-69278)	517	229	144.03	1.59	9.46E-09	4.63E-07
Generic Transcription Pathway (R-HSA-212436)	1197	455	333.48	1.36	1.17E-08	5.59E-07
Infectious disease (R-HSA-5663205)	895	356	249.34	1.43	1.47E-08	6.80E-07
Mitochondrial translation initiation (R-HSA-5368286)	88	64	24.52	2.61	1.71E-08	7.50E-07
Mitochondrial translation elongation (R-HSA-5389840)	88	64	24.52	2.61	1.71E-08	7.63E-07
Mitochondrial translation termination (R-HSA-5419276)	88	64	24.52	2.61	1.71E-08	7.77E-07
Diseases of signal transduction by growth factor receptors and second messengers (R-HSA-5663202)	418	192	116.45	1.65	2.28E-08	9.82E-07
Respiratory electron transport (R-HSA-611105)	102	70	28.42	2.46	2.37E-08	9.84E-07
Mitochondrial translation (R-HSA-5368287)	94	66	26.19	2.52	3.76E-08	1.54E-06
Transcriptional Regulation by TP53 (R-HSA-3700989)	360	168	100.29	1.68	6.47E-08	2.56E-06
M Phase (R-HSA-68886)	375	171	104.47	1.64	1.85E-07	7.10E-06
Formation of the ternary complex, and subsequently, the 43S complex (R-HSA-72695)	51	43	14.21	3.03	2.35E-07	8.76E-06
Metabolism of amino acids and derivatives (R-HSA-71291)	369	167	102.8	1.62	3.44E-07	1.24E-05
Organelle biogenesis and maintenance (R-HSA-1852241)	293	138	81.63	1.69	6.78E-07	2.41E-05
Vesicle-mediated transport (R-HSA-5653656)	725	286	201.98	1.42	7.57E-07	2.66E-05
Activation of the mRNA upon binding of the cap-binding complex and eIFs, and subsequent binding to 43S (R-HSA-72662)	59	45	16.44	2.74	1.00E-06	3.47E-05
Complex I biogenesis (R-HSA-6799198)	57	44	15.88	2.77	1.26E-06	4.29E-05
Translation initiation complex formation (R-HSA-72649)	58	44	16.16	2.72	1.48E-06	4.92E-05
Ribosomal scanning and start codon recognition (R-HSA-72702)	58	44	16.16	2.72	1.48E-06	4.99E-05
RAC1 GTPase cycle (R-HSA-9013149)	183	95	50.98	1.86	1.73E-06	5.69E-05
Chromatin organization (R-HSA-4839726)	240	116	66.86	1.73	2.07E-06	6.53E-05
Chromatin modifying enzymes (R-HSA-3247509)	240	116	66.86	1.73	2.07E-06	6.62E-05
Processing of Capped Intron-Containing Pre-mRNA (R-HSA-72203)	238	114	66.31	1.72	3.49E-06	1.09E-04
mRNA Splicing (R-HSA-72172)	188	94	52.38	1.79	8.22E-06	2.44E-04
SUMO E3 ligases SUMOylate target proteins (R-HSA-3108232)	157	81	43.74	1.85	1.24E-05	3.63E-04

Reactome pathways	Homo sapiens - REFLIST (20589)	MAX-R60Q (5736)	MAX-R60Q (expected)	MAX-R60Q (fold Enrichment)	MAX-R60Q (raw P-value)	MAX-R60Q (FDR)
Mitotic Anaphase (R-HSA-68882)	227	107	63.24	1.69	1.29E-05	3.75E-04
Mitotic Metaphase and Anaphase (R-HSA-2555396)	228	107	63.52	1.68	1.37E-05	3.89E-04
Class I MHC mediated antigen processing & presentation (R-HSA-983169)	378	160	105.31	1.52	1.41E-05	3.94E-04
Antigen processing: Ubiquitination & Proteasome degradation (R-HSA-983168)	308	135	85.81	1.57	1.64E-05	4.54E-04
mRNA Splicing - Major Pathway (R-HSA-72163)	180	89	50.15	1.77	2.01E-05	5.50E-04
Beta-catenin independent WNT signaling (R-HSA-3858494)	142	74	39.56	1.87	2.16E-05	5.79E-04
SUMOylation (R-HSA-2990846)	163	82	45.41	1.81	2.34E-05	6.21E-04
Cell Cycle Checkpoints (R-HSA-69620)	271	121	75.5	1.6	2.55E-05	6.69E-04
Deubiquitination (R-HSA-5688426)	282	124	78.56	1.58	3.52E-05	9.13E-04
Separation of Sister Chromatids (R-HSA-2467813)	187	90	52.1	1.73	3.71E-05	9.53E-04
Signaling by Receptor Tyrosine Kinases (R-HSA-9006934)	505	199	140.69	1.41	4.46E-05	1.13E-03
Nucleotide Excision Repair (R-HSA-5696398)	110	60	30.65	1.96	5.21E-05	1.31E-03
Cellular response to chemical stress (R-HSA-9711123)	154	77	42.9	1.79	5.47E-05	1.36E-03
CDC42 GTPase cycle (R-HSA-9013148)	154	76	42.9	1.77	7.59E-05	1.84E-03
Developmental Biology (R-HSA-1266738)	1090	383	303.67	1.26	8.33E-05	1.96E-03
Mitotic Prometaphase (R-HSA-68877)	199	92	55.44	1.66	1.05E-04	2.45E-03
RAC3 GTPase cycle (R-HSA-9013423)	93	52	25.91	2.01	1.06E-04	2.46E-03
RHO GTPase Effectors (R-HSA-195258)	288	123	80.24	1.53	1.09E-04	2.47E-03
Neddylation (R-HSA-8951664)	233	104	64.91	1.6	1.08E-04	2.48E-03
mRNA Splicing - Minor Pathway (R-HSA-72165)	52	35	14.49	2.42	1.18E-04	2.65E-03
Cristae formation (R-HSA-8949613)	31	25	8.64	2.89	1.31E-04	2.88E-03
Mitochondrial protein import (R-HSA-1268020)	65	40	18.11	2.21	1.30E-04	2.90E-03
Cytoprotection by HMOX1 (R-HSA-9707564)	120	62	33.43	1.85	1.36E-04	2.94E-03
PCP/CE pathway (R-HSA-4086400)	91	51	25.35	2.01	1.35E-04	2.95E-03
trans-Golgi Network Vesicle Budding (R-HSA-199992)	72	43	20.06	2.14	1.51E-04	3.21E-03
RAC2 GTPase cycle (R-HSA-9013404)	87	49	24.24	2.02	1.49E-04	3.21E-03

Reactome pathways	Homo sapiens - REFLIST (20589)	MAX-R60Q (5736)	MAX-R60Q (expected)	MAX-R60Q (fold Enrichment)	MAX-R60Q (raw P-value)	MAX-R60Q (FDR)
Signaling by WNT (R-HSA-195721)	297	125	82.74	1.51	1.71E-04	3.61E-03
ESR-mediated signaling (R-HSA-8939211)	187	86	52.1	1.65	2.11E-04	4.38E-03
Mitochondrial biogenesis (R-HSA-1592230)	92	50	25.63	1.95	2.20E-04	4.53E-03
Clathrin-mediated endocytosis (R-HSA-8856828)	144	70	40.12	1.74	2.29E-04	4.69E-03
Regulation of cholesterol biosynthesis by SREBP (SREBF) (R-HSA-1655829)	53	34	14.77	2.3	2.32E-04	4.70E-03
Intra-Golgi and retrograde Golgi-to-ER traffic (R-HSA-6811442)	203	91	56.55	1.61	2.71E-04	5.44E-03
Dual incision in TC-NER (R-HSA-6782135)	65	39	18.11	2.15	2.91E-04	5.80E-03
Intracellular signaling by second messengers (R-HSA-9006925)	291	121	81.07	1.49	2.94E-04	5.81E-03
Signaling by VEGF (R-HSA-194138)	104	54	28.97	1.86	3.17E-04	6.17E-03
Transcriptional regulation by RUNX1 (R-HSA-8878171)	204	90	56.83	1.58	3.68E-04	7.06E-03
Mitotic G2-G2/M phases (R-HSA-453274)	197	87	54.88	1.59	4.94E-04	9.33E-03
DNA Double-Strand Break Repair (R-HSA-5693532)	149	70	41.51	1.69	5.13E-04	9.54E-03
TP53 Regulates Metabolic Genes (R-HSA-5628897)	83	45	23.12	1.95	5.25E-04	9.69E-03
UCH proteinases (R-HSA-5689603)	95	50	26.47	1.89	5.34E-04	9.80E-03
Transcription-Coupled Nucleotide Excision Repair (TC-NER) (R-HSA-6781827)	78	43	21.73	1.98	5.44E-04	9.91E-03
RHO GTPase cycle (R-HSA-9013408)	73	41	20.34	2.02	5.60E-04	9.97E-03
Cilium Assembly (R-HSA-5617833)	201	88	56	1.57	5.56E-04	9.98E-03
PTEN Regulation (R-HSA-6807070)	137	65	38.17	1.7	5.83E-04	1.02E-02
Golgi Associated Vesicle Biogenesis (R-HSA-432722)	54	33	15.04	2.19	6.10E-04	1.04E-02
S Phase (R-HSA-69242)	161	74	44.85	1.65	5.98E-04	1.04E-02
G2/M Transition (R-HSA-69275)	195	86	54.33	1.58	6.02E-04	1.04E-02
RHO GTPase cycle (R-HSA-9013409)	54	33	15.04	2.19	6.10E-04	1.05E-02
Estrogen-dependent gene expression (R-HSA-9018519)	118	58	32.87	1.76	6.39E-04	1.08E-02
HDR through Homologous Recombination (HRR) or Single Strand Annealing (SSA) (R-HSA-5693567)	114	56	31.76	1.76	7.38E-04	1.23E-02
Signaling by Nuclear Receptors (R-HSA-9006931)	261	108	72.71	1.49	7.34E-04	1.23E-02
Signaling by TGFB family members (R-HSA-9006936)	103	52	28.7	1.81	8.20E-04	1.35E-02

Reactome pathways	Homo sapiens - REFLIST (20589)	MAX-R60Q (5736)	MAX-R60Q (expected)	MAX-R60Q (fold Enrichment)	MAX-R60Q (raw P-value)	MAX-R60Q (FDR)
RHOC GTPase cycle (R-HSA-9013106)	73	40	20.34	1.97	8.48E-04	1.39E-02
Transcriptional regulation by RUNX3 (R-HSA-8878159)	93	48	25.91	1.85	9.56E-04	1.54E-02
Homology Directed Repair (R-HSA-5693538)	120	58	33.43	1.73	9.56E-04	1.55E-02
HDR through Homologous Recombination (HRR) (R-HSA-5685942)	66	37	18.39	2.01	1.09E-03	1.73E-02
ER to Golgi Anterograde Transport (R-HSA-199977)	155	70	43.18	1.62	1.12E-03	1.76E-02
PIP3 activates AKT signaling (R-HSA-1257604)	251	103	69.93	1.47	1.16E-03	1.82E-02
Regulation of TP53 Activity through Phosphorylation (R-HSA-6804756)	92	47	25.63	1.83	1.27E-03	1.96E-02
Regulation of TP53 Activity (R-HSA-5633007)	159	71	44.3	1.6	1.27E-03	1.97E-02
Hedgehog 'off' state (R-HSA-5610787)	112	54	31.2	1.73	1.27E-03	1.98E-02
Signaling by EGFR (R-HSA-177929)	48	29	13.37	2.17	1.36E-03	2.09E-02
Gap-filling DNA repair synthesis and ligation in TC-NER (R-HSA-6782210)	64	36	17.83	2.02	1.40E-03	2.09E-02
Signaling by ALK in cancer (R-HSA-9700206)	53	31	14.77	2.1	1.40E-03	2.10E-02
Signaling by ALK fusions and activated point mutants (R-HSA-9725370)	53	31	14.77	2.1	1.40E-03	2.11E-02
VEGFA-VEGFR2 Pathway (R-HSA-4420097)	94	47	26.19	1.79	1.44E-03	2.12E-02
Signaling by Hedgehog (R-HSA-5358351)	148	67	41.23	1.62	1.53E-03	2.24E-02
Regulation of RAS by GAPs (R-HSA-5658442)	66	36	18.39	1.96	1.65E-03	2.39E-02
Hedgehog 'on' state (R-HSA-5632684)	84	43	23.4	1.84	1.66E-03	2.39E-02
Transport to the Golgi and subsequent modification (R-HSA-948021)	186	80	51.82	1.54	1.64E-03	2.39E-02
Resolution of D-loop Structures through Synthesis-Dependent Strand Annealing (SDSA) (R-HSA-5693554)	26	19	7.24	2.62	1.87E-03	2.65E-02
Homologous DNA Pairing and Strand Exchange (R-HSA-5693579)	42	26	11.7	2.22	1.85E-03	2.66E-02
Asymmetric localization of PCP proteins (R-HSA-4608870)	63	35	17.55	1.99	1.93E-03	2.72E-02
RHOA GTPase cycle (R-HSA-8980692)	148	66	41.23	1.6	2.00E-03	2.81E-02
Degradation of beta-catenin by the destruction complex (R-HSA-195253)	82	42	22.84	1.84	2.07E-03	2.87E-02
MAPK6/MAPK4 signaling (R-HSA-5687128)	88	44	24.52	1.79	2.06E-03	2.87E-02
Transcriptional regulation by RUNX2 (R-HSA-8878166)	117	55	32.6	1.69	2.09E-03	2.88E-02
MAPK family signaling cascades (R-HSA-5683057)	308	120	85.81	1.4	2.11E-03	2.89E-02

Reactome pathways	Homo sapiens - REFLIST (20589)	MAX-R60Q (5736)	MAX-R60Q (expected)	MAX-R60Q (fold Enrichment)	MAX-R60Q (raw P-value)	MAX-R60Q (FDR)
RHOQ GTPase cycle (R-HSA-9013406)	59	33	16.44	2.01	2.13E-03	2.90E-02
Activation of gene expression by SREBF (SREBP) (R-HSA-2426168)	40	25	11.14	2.24	2.28E-03	3.08E-02
Formation of ATP by chemiosmotic coupling (R-HSA-163210)	18	15	5.01	2.99	2.39E-03	3.20E-02
CDK-mediated phosphorylation and removal of Cdc6 (R-HSA-69017)	72	38	20.06	1.89	2.37E-03	3.20E-02
APC/C:Cdc20 mediated degradation of Securin (R-HSA-174154)	67	36	18.67	1.93	2.51E-03	3.35E-02
APC/C:Cdh1 mediated degradation of Cdc20 and other APC/C:Cdh1 targeted proteins in late mitosis/early G1 (R-HSA-174178)	73	38	20.34	1.87	2.53E-03	3.36E-02
Diseases of DNA repair (R-HSA-9675135)	33	22	9.19	2.39	2.67E-03	3.52E-02
RNA polymerase II transcribes snRNA genes (R-HSA-6807505)	74	38	20.62	1.84	2.76E-03	3.57E-02
Signaling by TGF-beta Receptor Complex (R-HSA-170834)	74	38	20.62	1.84	2.76E-03	3.59E-02
G2/M Checkpoints (R-HSA-69481)	150	66	41.79	1.58	2.76E-03	3.60E-02
Autodegradation of Cdh1 by Cdh1:APC/C (R-HSA-174084)	63	34	17.55	1.94	2.82E-03	3.63E-02
Formation of TC-NER Pre-Incision Complex (R-HSA-6781823)	53	30	14.77	2.03	3.02E-03	3.82E-02
Regulation of RUNX3 expression and activity (R-HSA-8941858)	53	30	14.77	2.03	3.02E-03	3.84E-02
p53-Dependent G1 DNA Damage Response (R-HSA-69563)	64	34	17.83	1.91	3.09E-03	3.85E-02
p53-Dependent G1/S DNA damage checkpoint (R-HSA-69580)	64	34	17.83	1.91	3.09E-03	3.86E-02
Establishment of Sister Chromatid Cohesion (R-HSA-2468052)	11	11	3.06	3.59	3.27E-03	4.01E-02
Global Genome Nucleotide Excision Repair (GG-NER) (R-HSA-5696399)	84	42	23.4	1.79	3.23E-03	4.01E-02
Cdc20:Phospho-APC/C mediated degradation of Cyclin A (R-HSA-174184)	72	37	20.06	1.84	3.41E-03	4.17E-02
Asparagine N-linked glycosylation (R-HSA-446203)	305	117	84.97	1.38	3.56E-03	4.32E-02
Recruitment of mitotic centrosome proteins and complexes (R-HSA-380270)	80	40	22.29	1.79	3.68E-03	4.44E-02
APC:Cdc20 mediated degradation of cell cycle proteins prior to satisfaction of the cell cycle checkpoint (R-HSA-179419)	73	37	20.34	1.82	3.71E-03	4.45E-02
Centrosome maturation (R-HSA-380287)	80	40	22.29	1.79	3.68E-03	4.46E-02
Regulation of PTEN stability and activity (R-HSA-8948751)	68	35	18.94	1.85	3.96E-03	4.70E-02
APC/C:Cdc20 mediated degradation of mitotic proteins (R-HSA-176409)	75	38	20.89	1.82	3.99E-03	4.71E-02
Apoptosis (R-HSA-109581)	173	73	48.2	1.51	3.95E-03	4.72E-02

Reactome pathways	Homo sapiens - REFLIST (20589)	MAX-R60Q (5736)	MAX-R60Q (expected)	MAX-R60Q (fold Enrichment)	MAX-R60Q (raw P-value)	MAX-R60Q (FDR)
Defective HDR through Homologous Recombination Repair (HRR) due to PALB2 loss of BRCA1 binding function (R-HSA-9704331)	24	17	6.69	2.54	4.12E-03	4.73E-02
Defective HDR through Homologous Recombination (HRR) due to BRCA1 loss-of-function (R-HSA-9701192)	24	17	6.69	2.54	4.12E-03	4.75E-02
HDR through Single Strand Annealing (SSA) (R-HSA-5685938)	37	23	10.31	2.23	4.16E-03	4.76E-02
Vif-mediated degradation of APOBEC3G (R-HSA-180585)	52	29	14.49	2	4.19E-03	4.77E-02
RHOB GTPase cycle (R-HSA-9013026)	70	36	19.5	1.85	4.30E-03	4.77E-02
Defective HDR through Homologous Recombination (HRR) due to PALB2 loss of function (R-HSA-9701193)	24	17	6.69	2.54	4.12E-03	4.78E-02
RND3 GTPase cycle (R-HSA-9696264)	42	25	11.7	2.14	4.28E-03	4.78E-02
Regulation of RUNX2 expression and activity (R-HSA-8939902)	70	36	19.5	1.85	4.30E-03	4.79E-02
MicroRNA (miRNA) biogenesis (R-HSA-203927)	24	17	6.69	2.54	4.12E-03	4.80E-02
SUMOylation of transcription cofactors (R-HSA-3899300)	42	25	11.7	2.14	4.28E-03	4.80E-02
Signaling by MET (R-HSA-6806834)	76	38	21.17	1.79	4.25E-03	4.80E-02
Diseases of DNA Double-Strand Break Repair (R-HSA-9675136)	24	17	6.69	2.54	4.12E-03	4.82E-02
Activation of APC/C and APC/C:Cdc20 mediated degradation of mitotic proteins (R-HSA-176814)	76	38	21.17	1.79	4.25E-03	4.82E-02
Defective HDR through Homologous Recombination Repair (HRR) due to PALB2 loss of BRCA2/RAD51/RAD51C binding function (R-HSA-9704646)	24	17	6.69	2.54	4.12E-03	4.84E-02
Resolution of D-Loop Structures (R-HSA-5693537)	33	21	9.19	2.28	4.41E-03	4.86E-02

Supplementary Data 5: Table of significantly enriched reactome pathways using genes up-regulated by MAX-R60Q.

Analysis Type: PANTHER Overrepresentation Test
Annotation Version and Release Date: Reactome version 77
Reference List: Homo sapiens (all genes)
Test Type: FISHER
Correction: FDR

Reactome pathways	Homo sapiens - REFLIST (20589)	MAX-R60Q (2665)	MAX-R60Q (expected)	MAX-R60Q (fold Enrichment)	MAX-R60Q (raw P-value)	MAX-R60Q (FDR)
Translation (R-HSA-72766)	293	180	37.93	4.75	6.52E-52	1.62E-48
Metabolism of RNA (R-HSA-8953854)	661	254	85.56	2.97	2.11E-43	2.63E-40
rRNA processing (R-HSA-72312)	202	124	26.15	4.74	5.80E-36	4.82E-33
rRNA processing in the nucleus and cytosol (R-HSA-8868773)	192	119	24.85	4.79	7.56E-35	4.71E-32
Formation of a pool of free 40S subunits (R-HSA-72689)	101	89	13.07	6.81	2.36E-34	1.18E-31
SRP-dependent cotranslational protein targeting to membrane (R-HSA-1799339)	112	92	14.5	6.35	7.86E-34	3.27E-31
Major pathway of rRNA processing in the nucleolus and cytosol (R-HSA-6791226)	182	114	23.56	4.84	9.74E-34	3.47E-31
Eukaryotic Translation Initiation (R-HSA-72613)	119	93	15.4	6.04	5.26E-33	1.46E-30
Cap-dependent Translation Initiation (R-HSA-72737)	119	93	15.4	6.04	5.26E-33	1.64E-30
L13a-mediated translational silencing of Ceruloplasmin expression (R-HSA-156827)	111	90	14.37	6.26	7.97E-33	1.99E-30
GTP hydrolysis and joining of the 60S ribosomal subunit (R-HSA-72706)	112	90	14.5	6.21	1.28E-32	2.90E-30
Regulation of expression of SLITs and ROBOs (R-HSA-9010553)	169	108	21.88	4.94	1.41E-32	2.94E-30
Eukaryotic Translation Elongation (R-HSA-156842)	94	83	12.17	6.82	3.64E-32	6.98E-30
Peptide chain elongation (R-HSA-156902)	89	80	11.52	6.94	2.07E-31	3.69E-29
Selenocysteine synthesis (R-HSA-2408557)	93	81	12.04	6.73	3.85E-31	5.64E-29
Eukaryotic Translation Termination (R-HSA-72764)	93	81	12.04	6.73	3.85E-31	5.99E-29
Response of EIF2AK4 (GCN2) to amino acid deficiency (R-HSA-9633012)	101	83	13.07	6.35	1.18E-30	1.63E-28

Reactome pathways	Homo sapiens - REFLIST (20589)	MAX-R60Q (2665)	MAX-R60Q (expected)	MAX-R60Q (fold Enrichment)	MAX-R60Q (raw P-value)	MAX-R60Q (FDR)
Nonsense Mediated Decay (NMD) independent of the Exon Junction Complex (EJC) (R-HSA-975956)	95	80	12.3	6.51	4.32E-30	5.67E-28
Cellular response to starvation (R-HSA-9711097)	156	98	20.19	4.85	3.05E-29	3.45E-27
Nonsense-Mediated Decay (NMD) (R-HSA-927802)	115	85	14.89	5.71	4.57E-29	4.74E-27
Nonsense Mediated Decay (NMD) enhanced by the Exon Junction Complex (EJC) (R-HSA-975957)	115	85	14.89	5.71	4.57E-29	4.95E-27
Cellular responses to stimuli (R-HSA-8953897)	732	231	94.75	2.44	5.93E-29	5.91E-27
Cellular responses to stress (R-HSA-2262752)	718	227	92.94	2.44	1.96E-28	1.88E-26
Signaling by ROBO receptors (R-HSA-376176)	215	113	27.83	4.06	2.06E-28	1.90E-26
Selenoamino acid metabolism (R-HSA-2408522)	116	84	15.01	5.59	2.67E-28	2.37E-26
Metabolism (R-HSA-1430728)	2087	471	270.14	1.74	4.61E-28	3.97E-26
Respiratory electron transport, ATP synthesis by chemiosmotic coupling, and heat production by uncoupling proteins. (R-HSA-163200)	126	86	16.31	5.27	1.21E-27	1.01E-25
Metabolism of proteins (R-HSA-392499)	1914	440	247.74	1.78	1.42E-27	1.14E-25
The citric acid (TCA) cycle and respiratory electron transport (R-HSA-1428517)	176	99	22.78	4.35	9.62E-27	7.49E-25
Metabolism of amino acids and derivatives (R-HSA-71291)	369	145	47.76	3.04	1.10E-25	8.31E-24
Respiratory electron transport (R-HSA-611105)	102	69	13.2	5.23	2.73E-22	2.00E-20
Mitochondrial translation initiation (R-HSA-5368286)	88	63	11.39	5.53	2.19E-21	1.52E-19
Mitochondrial translation elongation (R-HSA-5389840)	88	63	11.39	5.53	2.19E-21	1.56E-19
Mitochondrial translation (R-HSA-5368287)	94	64	12.17	5.26	6.98E-21	4.70E-19
Mitochondrial translation termination (R-HSA-5419276)	88	62	11.39	5.44	8.15E-21	5.35E-19
Infectious disease (R-HSA-5663205)	895	223	115.85	1.92	3.78E-17	2.36E-15
Complex I biogenesis (R-HSA-6799198)	57	43	7.38	5.83	1.27E-15	7.51E-14
Formation of the ternary complex, and subsequently, the 43S complex (R-HSA-72695)	51	41	6.6	6.21	1.26E-15	7.66E-14
Axon guidance (R-HSA-422475)	549	152	71.06	2.14	4.82E-15	2.80E-13
Activation of the mRNA upon binding of the cap-binding complex and eIFs, and subsequent binding to 43S (R-HSA-72662)	59	42	7.64	5.5	1.13E-14	6.39E-13
Translation initiation complex formation (R-HSA-72649)	58	41	7.51	5.46	2.76E-14	1.49E-12
Ribosomal scanning and start codon recognition (R-HSA-72702)	58	41	7.51	5.46	2.76E-14	1.53E-12

Reactome pathways	Homo sapiens - REFLIST (20589)	MAX-R60Q (2665)	MAX-R60Q (expected)	MAX-R60Q (fold Enrichment)	MAX-R60Q (raw P-value)	MAX-R60Q (FDR)
Nervous system development (R-HSA-9675108)	574	152	74.3	2.05	9.93E-14	5.27E-12
Mitochondrial protein import (R-HSA-1268020)	65	39	8.41	4.64	4.95E-12	2.57E-10
mRNA Splicing (R-HSA-72172)	188	69	24.33	2.84	8.07E-12	4.10E-10
mRNA Splicing - Major Pathway (R-HSA-72163)	180	66	23.3	2.83	2.43E-11	1.21E-09
Processing of Capped Intron-Containing Pre-mRNA (R-HSA-72203)	238	78	30.81	2.53	4.80E-11	2.35E-09
Cellular response to chemical stress (R-HSA-9711123)	154	59	19.93	2.96	6.60E-11	3.16E-09
Disease (R-HSA-1643685)	1679	317	217.33	1.46	5.83E-10	2.74E-08
Protein localization (R-HSA-9609507)	158	57	20.45	2.79	9.09E-10	4.20E-08
Cristae formation (R-HSA-8949613)	31	23	4.01	5.73	6.48E-09	2.94E-07
Cytoprotection by HMOX1 (R-HSA-9707564)	120	46	15.53	2.96	9.02E-09	4.01E-07
mRNA Splicing - Minor Pathway (R-HSA-72165)	52	28	6.73	4.16	2.84E-08	1.22E-06
PCP/CE pathway (R-HSA-4086400)	91	37	11.78	3.14	6.45E-08	2.72E-06
Autodegradation of Cdh1 by Cdh1:APC/C (R-HSA-174084)	63	30	8.15	3.68	7.66E-08	3.18E-06
APC/C:Cdc20 mediated degradation of Securin (R-HSA-174154)	67	31	8.67	3.57	7.77E-08	3.18E-06
Vif-mediated degradation of APOBEC3G (R-HSA-180585)	52	27	6.73	4.01	8.83E-08	3.55E-06
APC/C:Cdh1 mediated degradation of Cdc20 and other APC/C:Cdh1 targeted proteins in late mitosis/early G1 (R-HSA-174178)	73	32	9.45	3.39	1.28E-07	4.90E-06
Cell Cycle (R-HSA-1640170)	648	139	83.88	1.66	1.86E-07	7.03E-06
UCH proteinases (R-HSA-5689603)	95	37	12.3	3.01	2.54E-07	9.46E-06
Negative regulation of NOTCH4 signaling (R-HSA-9604323)	52	26	6.73	3.86	2.68E-07	9.83E-06
CDK-mediated phosphorylation and removal of Cdc6 (R-HSA-69017)	72	31	9.32	3.33	2.73E-07	9.86E-06
ROS sensing by NFE2L2 (R-HSA-8932339)	56	27	7.25	3.72	2.79E-07	9.93E-06
Oxygen-dependent proline hydroxylation of Hypoxia-inducible Factor Alpha (R-HSA-1234176)	65	29	8.41	3.45	3.67E-07	1.29E-05
The role of GTSE1 in G2/M progression after G2 checkpoint (R-HSA-8852276)	78	32	10.1	3.17	4.16E-07	1.44E-05
APC/C:Cdc20 mediated degradation of mitotic proteins (R-HSA-176409)	75	31	9.71	3.19	5.52E-07	1.88E-05
Synthesis of DNA (R-HSA-69239)	119	41	15.4	2.66	5.57E-07	1.88E-05
Ubiquitin Mediated Degradation of Phosphorylated Cdc25A (R-HSA-69601)	51	25	6.6	3.79	6.01E-07	1.95E-05

Reactome pathways	Homo sapiens - REFLIST (20589)	MAX-R60Q (2665)	MAX-R60Q (expected)	MAX-R60Q (fold Enrichment)	MAX-R60Q (raw P-value)	MAX-R60Q (FDR)
p53-Independent DNA Damage Response (R-HSA-69610)	51	25	6.6	3.79	6.01E-07	1.97E-05
p53-Independent G1/S DNA damage checkpoint (R-HSA-69613)	51	25	6.6	3.79	6.01E-07	2.00E-05
Activation of APC/C and APC/C:Cdc20 mediated degradation of mitotic proteins (R-HSA-176814)	76	31	9.84	3.15	6.92E-07	2.21E-05
Cdc20:Phospho-APC/C mediated degradation of Cyclin A (R-HSA-174184)	72	30	9.32	3.22	7.31E-07	2.31E-05
Regulation of HMOX1 expression and activity (R-HSA-9707587)	64	28	8.28	3.38	7.89E-07	2.46E-05
Degradation of DVL (R-HSA-4641258)	56	26	7.25	3.59	8.07E-07	2.48E-05
APC:Cdc20 mediated degradation of cell cycle proteins prior to satisfaction of the cell cycle checkpoint (R-HSA-179419)	73	30	9.45	3.17	9.19E-07	2.79E-05
Formation of ATP by chemiosmotic coupling (R-HSA-163210)	18	15	2.33	6.44	1.02E-06	2.99E-05
Regulation of RUNX3 expression and activity (R-HSA-8941858)	53	25	6.86	3.64	1.04E-06	2.99E-05
Regulation of activated PAK-2p34 by proteasome mediated degradation (R-HSA-211733)	49	24	6.34	3.78	1.02E-06	3.01E-05
Degradation of beta-catenin by the destruction complex (R-HSA-195253)	82	32	10.61	3.01	1.00E-06	3.01E-05
AUF1 (hnRNP D0) binds and destabilizes mRNA (R-HSA-450408)	53	25	6.86	3.64	1.04E-06	3.02E-05
Degradation of AXIN (R-HSA-4641257)	54	25	6.99	3.58	1.36E-06	3.77E-05
FBXL7 down-regulates AURKA during mitotic entry and in early mitosis (R-HSA-8854050)	54	25	6.99	3.58	1.36E-06	3.81E-05
NIK-->noncanonical NF-kB signaling (R-HSA-5676590)	58	26	7.51	3.46	1.35E-06	3.83E-05
Stabilization of p53 (R-HSA-69541)	55	25	7.12	3.51	1.76E-06	4.53E-05
Ubiquitin-dependent degradation of Cyclin D (R-HSA-75815)	51	24	6.6	3.64	1.76E-06	4.57E-05
Vpu mediated degradation of CD4 (R-HSA-180534)	51	24	6.6	3.64	1.76E-06	4.61E-05
Asymmetric localization of PCP proteins (R-HSA-4608870)	63	27	8.15	3.31	1.69E-06	4.62E-05
Autodegradation of the E3 ubiquitin ligase COP1 (R-HSA-349425)	51	24	6.6	3.64	1.76E-06	4.66E-05
Dectin-1 mediated noncanonical NF-kB signaling (R-HSA-5607761)	59	26	7.64	3.4	1.74E-06	4.66E-05
SCF(Skp2)-mediated degradation of p27/p21 (R-HSA-187577)	59	26	7.64	3.4	1.74E-06	4.71E-05
p53-Dependent G1 DNA Damage Response (R-HSA-69563)	64	27	8.28	3.26	2.14E-06	5.38E-05
p53-Dependent G1/S DNA damage checkpoint (R-HSA-69580)	64	27	8.28	3.26	2.14E-06	5.44E-05
Switching of origins to a post-replicative state (R-HSA-69052)	90	33	11.65	2.83	2.37E-06	5.68E-05

Reactome pathways	Homo sapiens - REFLIST (20589)	MAX-R60Q (2665)	MAX-R60Q (expected)	MAX-R60Q (fold Enrichment)	MAX-R60Q (raw P-value)	MAX-R60Q (FDR)
DNA Repair (R-HSA-73894)	310	76	40.13	1.89	2.32E-06	5.68E-05
Mitotic Anaphase (R-HSA-68882)	227	61	29.38	2.08	2.30E-06	5.69E-05
Regulation of Apoptosis (R-HSA-169911)	52	24	6.73	3.57	2.29E-06	5.72E-05
Mitotic Metaphase and Anaphase (R-HSA-2555396)	228	61	29.51	2.07	2.41E-06	5.72E-05
ER-Phagosome pathway (R-HSA-1236974)	90	33	11.65	2.83	2.37E-06	5.73E-05
M Phase (R-HSA-68886)	375	87	48.54	1.79	2.81E-06	6.62E-05
Metabolism of polyamines (R-HSA-351202)	57	25	7.38	3.39	2.92E-06	6.80E-05
Cellular response to hypoxia (R-HSA-1234174)	74	29	9.58	3.03	2.96E-06	6.83E-05
Nucleotide Excision Repair (R-HSA-5696398)	110	37	14.24	2.6	3.05E-06	6.97E-05
Regulation of RUNX2 expression and activity (R-HSA-8939902)	70	28	9.06	3.09	3.18E-06	7.14E-05
G2/M Transition (R-HSA-69275)	195	54	25.24	2.14	3.17E-06	7.19E-05
APC/C-mediated degradation of cell cycle proteins (R-HSA-174143)	87	32	11.26	2.84	3.27E-06	7.22E-05
Regulation of mitotic cell cycle (R-HSA-453276)	87	32	11.26	2.84	3.27E-06	7.28E-05
G1/S DNA Damage Checkpoints (R-HSA-69615)	66	27	8.54	3.16	3.39E-06	7.41E-05
CDT1 association with the CDC6:ORC:origin complex (R-HSA-68827)	58	25	7.51	3.33	3.73E-06	8.08E-05
SCF-beta-TrCP mediated degradation of Emi1 (R-HSA-174113)	54	24	6.99	3.43	3.83E-06	8.23E-05
Regulation of ornithine decarboxylase (ODC) (R-HSA-350562)	50	23	6.47	3.55	3.87E-06	8.24E-05
DNA Replication (R-HSA-69306)	159	47	20.58	2.28	4.26E-06	9.00E-05
Degradation of GLI1 by the proteasome (R-HSA-5610780)	59	25	7.64	3.27	4.73E-06	9.75E-05
Degradation of GLI2 by the proteasome (R-HSA-5610783)	59	25	7.64	3.27	4.73E-06	9.83E-05
GLI3 is processed to GLI3R by the proteasome (R-HSA-5610785)	59	25	7.64	3.27	4.73E-06	9.91E-05
Hh mutants are degraded by ERAD (R-HSA-5362768)	55	24	7.12	3.37	4.91E-06	1.00E-04
Mitotic G2-G2/M phases (R-HSA-453274)	197	54	25.5	2.12	5.20E-06	1.05E-04
Regulation of mRNA stability by proteins that bind AU-rich elements (R-HSA-450531)	85	31	11	2.82	5.26E-06	1.06E-04
Cell Cycle, Mitotic (R-HSA-69278)	517	110	66.92	1.64	5.62E-06	1.11E-04
Regulation of APC/C activators between G1/S and early anaphase (R-HSA-176408)	80	30	10.36	2.9	5.60E-06	1.12E-04

Reactome pathways	Homo sapiens - REFLIST (20589)	MAX-R60Q (2665)	MAX-R60Q (expected)	MAX-R60Q (fold Enrichment)	MAX-R60Q (raw P-value)	MAX-R60Q (FDR)
Antigen processing-Cross presentation (R-HSA-1236975)	106	35	13.72	2.55	7.63E-06	1.50E-04
Separation of Sister Chromatids (R-HSA-2467813)	187	51	24.2	2.11	8.56E-06	1.67E-04
Activation of NF-kappaB in B cells (R-HSA-1169091)	66	26	8.54	3.04	8.77E-06	1.68E-04
Regulation of RAS by GAPs (R-HSA-5658442)	66	26	8.54	3.04	8.77E-06	1.70E-04
Hh mutants abrogate ligand secretion (R-HSA-5387390)	58	24	7.51	3.2	1.00E-05	1.89E-04
Downstream signaling events of B Cell Receptor (BCR) (R-HSA-1168372)	79	29	10.23	2.84	1.01E-05	1.90E-04
Regulation of PTEN stability and activity (R-HSA-8948751)	68	26	8.8	2.95	1.34E-05	2.49E-04
rRNA modification in the nucleus and cytosol (R-HSA-6790901)	60	24	7.77	3.09	1.57E-05	2.87E-04
Defective CFTR causes cystic fibrosis (R-HSA-5678895)	60	24	7.77	3.09	1.57E-05	2.90E-04
Beta-catenin independent WNT signaling (R-HSA-3858494)	142	41	18.38	2.23	2.10E-05	3.82E-04
Cross-presentation of soluble exogenous antigens (endosomes) (R-HSA-1236978)	49	21	6.34	3.31	2.33E-05	4.21E-04
Signaling by NOTCH4 (R-HSA-9013694)	80	28	10.36	2.7	2.57E-05	4.60E-04
Orc1 removal from chromatin (R-HSA-68949)	70	26	9.06	2.87	2.83E-05	5.04E-04
Transcription-Coupled Nucleotide Excision Repair (TC-NER) (R-HSA-6781827)	78	27	10.1	2.67	4.13E-05	7.25E-04
PTEN Regulation (R-HSA-6807070)	137	39	17.73	2.2	4.31E-05	7.51E-04
Transcriptional Regulation by TP53 (R-HSA-3700989)	360	79	46.6	1.7	5.40E-05	9.35E-04
Hedgehog ligand biogenesis (R-HSA-5358346)	64	24	8.28	2.9	5.83E-05	1.00E-03
Dual incision in TC-NER (R-HSA-6782135)	65	24	8.41	2.85	6.39E-05	1.09E-03
RUNX1 regulates transcription of genes involved in differentiation of HSCs (R-HSA-8939236)	98	31	12.68	2.44	6.76E-05	1.15E-03
Assembly of the pre-replicative complex (R-HSA-68867)	99	31	12.81	2.42	7.29E-05	1.23E-03
DNA Replication Pre-Initiation (R-HSA-69002)	116	34	15.01	2.26	8.60E-05	1.44E-03
S Phase (R-HSA-69242)	161	43	20.84	2.06	8.73E-05	1.45E-03
Transcriptional regulation by RUNX2 (R-HSA-8878166)	117	34	15.14	2.25	9.51E-05	1.57E-03
MAPK6/MAPK4 signaling (R-HSA-5687128)	88	28	11.39	2.46	1.06E-04	1.73E-03
Gap-filling DNA repair synthesis and ligation in TC-NER (R-HSA-6782210)	64	23	8.28	2.78	1.14E-04	1.85E-03
ABC transporter disorders (R-HSA-5619084)	77	26	9.97	2.61	1.25E-04	2.02E-03

Reactome pathways	Homo sapiens - REFLIST (20589)	MAX-R60Q (2665)	MAX-R60Q (expected)	MAX-R60Q (fold Enrichment)	MAX-R60Q (raw P-value)	MAX-R60Q (FDR)
Hedgehog 'on' state (R-HSA-5632684)	84	27	10.87	2.48	1.29E-04	2.07E-03
G2/M Checkpoints (R-HSA-69481)	150	40	19.42	2.06	1.31E-04	2.09E-03
Neddylation (R-HSA-8951664)	233	55	30.16	1.82	1.70E-04	2.70E-03
Developmental Biology (R-HSA-1266738)	1090	190	141.09	1.35	1.74E-04	2.75E-03
Cell Cycle Checkpoints (R-HSA-69620)	271	61	35.08	1.74	1.76E-04	2.76E-03
tRNA processing (R-HSA-72306)	104	31	13.46	2.3	1.85E-04	2.84E-03
Hedgehog 'off' state (R-HSA-5610787)	112	32	14.5	2.21	1.96E-04	2.99E-03
Cyclin E associated events during G1/S transition (R-HSA-69202)	82	26	10.61	2.45	2.01E-04	3.03E-03
TNFR2 non-canonical NF-kB pathway (R-HSA-5668541)	98	29	12.68	2.29	2.30E-04	3.44E-03
Mitochondrial biogenesis (R-HSA-1592230)	92	28	11.91	2.35	2.35E-04	3.47E-03
Metabolism of nucleotides (R-HSA-15869)	92	28	11.91	2.35	2.35E-04	3.49E-03
Cyclin A:Cdk2-associated events at S phase entry (R-HSA-69656)	84	26	10.87	2.39	2.59E-04	3.73E-03
Global Genome Nucleotide Excision Repair (GG-NER) (R-HSA-5696399)	84	26	10.87	2.39	2.59E-04	3.75E-03
Transcriptional regulation by RUNX3 (R-HSA-8878159)	93	28	12.04	2.33	2.57E-04	3.75E-03
Telomere Maintenance (R-HSA-157579)	93	28	12.04	2.33	2.57E-04	3.77E-03
Chromosome Maintenance (R-HSA-73886)	120	33	15.53	2.12	3.01E-04	4.29E-03
Interleukin-1 signaling (R-HSA-9020702)	100	29	12.94	2.24	4.03E-04	5.61E-03
Resolution of Abasic Sites (AP sites) (R-HSA-73933)	36	15	4.66	3.22	4.22E-04	5.84E-03
Mitotic G1 phase and G1/S transition (R-HSA-453279)	147	38	19.03	2	4.24E-04	5.84E-03
Prefoldin mediated transfer of substrate to CCT/TriC (R-HSA-389957)	28	13	3.62	3.59	4.52E-04	6.16E-03
Formation of TC-NER Pre-Incision Complex (R-HSA-6781823)	53	19	6.86	2.77	5.17E-04	6.96E-03
G1/S Transition (R-HSA-69206)	130	34	16.83	2.02	5.15E-04	6.98E-03
Post-translational protein modification (R-HSA-597592)	1396	230	180.7	1.27	5.93E-04	7.83E-03
Deubiquitination (R-HSA-5688426)	282	60	36.5	1.64	7.95E-04	1.00E-02
ABC-family proteins mediated transport (R-HSA-382556)	102	28	13.2	2.12	8.24E-04	1.03E-02
CLEC7A (Dectin-1) signaling (R-HSA-5607764)	96	27	12.43	2.17	8.81E-04	1.09E-02

Reactome pathways	Homo sapiens - REFLIST (20589)	MAX-R60Q (2665)	MAX-R60Q (expected)	MAX-R60Q (fold Enrichment)	MAX-R60Q (raw P-value)	MAX-R60Q (FDR)
RNA Polymerase III Transcription Initiation (R-HSA-76046)	35	14	4.53	3.09	8.95E-04	1.10E-02
TP53 Regulates Metabolic Genes (R-HSA-5628897)	83	24	10.74	2.23	1.14E-03	1.37E-02
Interconversion of nucleotide di- and triphosphates (R-HSA-499943)	28	12	3.62	3.31	1.28E-03	1.54E-02
Base Excision Repair (R-HSA-73884)	70	21	9.06	2.32	1.44E-03	1.71E-02
Cooperation of Prefoldin and TricCCT in actin and tubulin folding (R-HSA-389958)	33	13	4.27	3.04	1.51E-03	1.78E-02
Apoptosis (R-HSA-109581)	173	40	22.39	1.79	1.59E-03	1.86E-02
TCF dependent signaling in response to WNT (R-HSA-201681)	201	45	26.02	1.73	1.66E-03	1.93E-02
DNA Damage Recognition in GG-NER (R-HSA-5696394)	38	14	4.92	2.85	1.69E-03	1.96E-02
Programmed Cell Death (R-HSA-5357801)	202	45	26.15	1.72	1.71E-03	1.97E-02
Organelle biogenesis and maintenance (R-HSA-1852241)	293	60	37.93	1.58	1.76E-03	2.02E-02
RNA Polymerase II Transcription Termination (R-HSA-73856)	66	20	8.54	2.34	1.80E-03	2.06E-02
Class I MHC mediated antigen processing & presentation (R-HSA-983169)	378	73	48.93	1.49	2.17E-03	2.46E-02
Detoxification of Reactive Oxygen Species (R-HSA-3299685)	35	13	4.53	2.87	2.30E-03	2.60E-02
Signaling by WNT (R-HSA-195721)	297	60	38.44	1.56	2.45E-03	2.74E-02
Protein folding (R-HSA-391251)	97	26	12.56	2.07	2.45E-03	2.76E-02
Neutrophil degranulation (R-HSA-6798695)	477	88	61.74	1.43	2.60E-03	2.89E-02
RNA Polymerase III Transcription Initiation From Type 1 Promoter (R-HSA-76061)	27	11	3.49	3.15	2.77E-03	3.05E-02
RNA Polymerase III Transcription Initiation From Type 3 Promoter (R-HSA-76071)	27	11	3.49	3.15	2.77E-03	3.06E-02
Transcriptional regulation by RUNX1 (R-HSA-8878171)	204	44	26.41	1.67	3.42E-03	3.74E-02
RNA Polymerase III Transcription (R-HSA-74158)	40	14	5.18	2.7	3.87E-03	4.11E-02
Formation of the Early Elongation Complex (R-HSA-113418)	33	12	4.27	2.81	3.85E-03	4.13E-02
RNA Polymerase III Abortive And Retractive Initiation (R-HSA-749476)	40	14	5.18	2.7	3.87E-03	4.13E-02
Translesion synthesis by REV1 (R-HSA-110312)	16	8	2.07	3.86	3.99E-03	4.21E-02
Signaling by NOTCH (R-HSA-157118)	201	43	26.02	1.65	4.39E-03	4.62E-02
Signaling by Hedgehog (R-HSA-5358351)	148	34	19.16	1.77	4.64E-03	4.86E-02
Gene expression (Transcription) (R-HSA-74160)	1454	229	188.2	1.22	4.78E-03	4.92E-02

Reactome pathways	Homo sapiens - REFLIST (20589)	MAX-R60Q (2665)	MAX-R60Q (expected)	MAX-R60Q (fold Enrichment)	MAX-R60Q (raw P-value)	MAX-R60Q (FDR)
Gap-filling DNA repair synthesis and ligation in GG-NER (R-HSA-5696397)	25	10	3.24	3.09	4.73E-03	4.93E-02
Inhibition of DNA recombination at telomere (R-HSA-9670095)	48	15	6.21	2.41	4.77E-03	4.93E-02

Supplementary Data 6: Table of significantly enriched reactome pathways using genes down-regulated by MAX-R60Q.

Analysis Type:	PANTHER Overrepresentation Test
Annotation Version and Release Date:	Reactome version 77
Reference List:	Homo sapiens (all genes in database)
Test Type:	FISHER
Correction:	FDR

Reactome pathways	Homo sapiens - REFLIST (20589)	MAX-R60Q (3090)	MAX-R60Q (expected)	MAX-R60Q (fold Enrichment)	MAX-R60Q (raw P-value)	MAX-R60Q (FDR)
RHO GTPase cycle (R-HSA-9012999)	448	178	67.24	2.65	5.07E-25	1.27E-21
Signaling by Rho GTPases, Miro GTPases and RHOBTB3 (R-HSA-9716542)	685	229	102.8	2.23	1.62E-23	2.02E-20
Signaling by Rho GTPases (R-HSA-194315)	670	224	100.55	2.23	4.55E-23	3.78E-20
Signal Transduction (R-HSA-162582)	2500	568	375.2	1.51	2.70E-20	1.68E-17
Unclassified (UNCLASSIFIED)	10082	1260	1513.11	0.83	1.76E-17	8.78E-15
Gene expression (Transcription) (R-HSA-74160)	1454	344	218.22	1.58	3.62E-14	1.29E-11
Membrane Trafficking (R-HSA-199991)	626	183	93.95	1.95	3.60E-14	1.50E-11
RAC1 GTPase cycle (R-HSA-9013149)	183	81	27.46	2.95	4.90E-14	1.53E-11
RNA Polymerase II Transcription (R-HSA-73857)	1319	312	197.96	1.58	8.14E-13	2.25E-10
Generic Transcription Pathway (R-HSA-212436)	1197	283	179.65	1.58	1.00E-11	2.50E-09
CDC42 GTPase cycle (R-HSA-9013148)	154	65	23.11	2.81	9.57E-11	2.17E-08
Class A/1 (Rhodopsin-like receptors) (R-HSA-373076)	331	11	49.68	0.22	4.09E-10	7.84E-08
Vesicle-mediated transport (R-HSA-5653656)	725	185	108.81	1.7	3.84E-10	7.97E-08
GPCR ligand binding (R-HSA-500792)	463	23	69.49	0.33	9.19E-10	1.64E-07
Immunoregulatory interactions between a Lymphoid and a non-Lymphoid cell (R-HSA-198933)	197	3	29.57	0.1	5.11E-09	8.50E-07
Diseases of signal transduction by growth factor receptors and second messengers (R-HSA-5663202)	418	118	62.73	1.88	8.11E-09	1.26E-06
Post-translational protein modification (R-HSA-597592)	1396	301	209.51	1.44	1.18E-08	1.74E-06
Chromatin organization (R-HSA-4839726)	240	78	36.02	2.17	2.09E-08	2.48E-06

Reactome pathways	Homo sapiens - REFLIST (20589)	MAX-R60Q (3090)	MAX-R60Q (expected)	MAX-R60Q (fold Enrichment)	MAX-R60Q (raw P-value)	MAX-R60Q (FDR)
Chromatin modifying enzymes (R-HSA-3247509)	240	78	36.02	2.17	2.09E-08	2.60E-06
RAC2 GTPase cycle (R-HSA-9013404)	87	41	13.06	3.14	2.02E-08	2.65E-06
RAC3 GTPase cycle (R-HSA-9013423)	93	43	13.96	3.08	1.94E-08	2.69E-06
Signaling by Receptor Tyrosine Kinases (R-HSA-9006934)	505	132	75.79	1.74	4.65E-08	5.27E-06
Keratinization (R-HSA-6805567)	217	6	32.57	0.18	1.14E-07	1.24E-05
RHOA GTPase cycle (R-HSA-8980692)	148	54	22.21	2.43	1.60E-07	1.66E-05
SUMO E3 ligases SUMOylate target proteins (R-HSA-3108232)	157	56	23.56	2.38	1.86E-07	1.85E-05
Peptide ligand-binding receptors (R-HSA-375276)	196	5	29.42	0.17	2.53E-07	2.42E-05
SUMOylation (R-HSA-2990846)	163	57	24.46	2.33	2.84E-07	2.62E-05
Translation (R-HSA-72766)	293	13	43.97	0.3	3.23E-07	2.88E-05
RHOC GTPase cycle (R-HSA-9013106)	73	34	10.96	3.1	3.92E-07	3.37E-05
RHOB GTPase cycle (R-HSA-9013026)	70	33	10.51	3.14	4.67E-07	3.88E-05
Regulation of cholesterol biosynthesis by SREBP (SREBF) (R-HSA-1655829)	53	28	7.95	3.52	6.01E-07	4.83E-05
Cell Cycle (R-HSA-1640170)	648	154	97.25	1.58	6.24E-07	4.86E-05
RHOJ GTPase cycle (R-HSA-9013409)	54	28	8.1	3.45	7.99E-07	6.04E-05
Respiratory electron transport, ATP synthesis by chemiosmotic coupling, and heat production by uncoupling proteins. (R-HSA-163200)	126	1	18.91	0.05	8.42E-07	6.17E-05
Intra-Golgi and retrograde Golgi-to-ER traffic (R-HSA-6811442)	203	63	30.47	2.07	2.18E-06	1.51E-04
Metabolism of amino acids and derivatives (R-HSA-71291)	369	22	55.38	0.4	2.15E-06	1.53E-04
Signaling by MET (R-HSA-6806834)	76	32	11.41	2.81	4.88E-06	3.04E-04
DNA Repair (R-HSA-73894)	310	83	46.52	1.78	7.21E-06	4.38E-04
RHOQ GTPase cycle (R-HSA-9013406)	59	27	8.85	3.05	7.67E-06	4.55E-04
Signaling by ALK in cancer (R-HSA-9700206)	53	25	7.95	3.14	1.10E-05	5.95E-04
Signaling by ALK fusions and activated point mutants (R-HSA-9725370)	53	25	7.95	3.14	1.10E-05	6.09E-04
Organelle biogenesis and maintenance (R-HSA-1852241)	293	79	43.97	1.8	1.17E-05	6.21E-04
ESR-mediated signaling (R-HSA-8939211)	187	56	28.06	2	1.98E-05	9.87E-04
Transcriptional Regulation by TP53 (R-HSA-3700989)	360	91	54.03	1.68	2.02E-05	9.89E-04

Reactome pathways	Homo sapiens - REFLIST (20589)	MAX-R60Q (3090)	MAX-R60Q (expected)	MAX-R60Q (fold Enrichment)	MAX-R60Q (raw P-value)	MAX-R60Q (FDR)
RHOG GTPase cycle (R-HSA-9013408)	73	30	10.96	2.74	2.20E-05	1.06E-03
RND3 GTPase cycle (R-HSA-9696264)	42	21	6.3	3.33	2.80E-05	1.27E-03
RND1 GTPase cycle (R-HSA-9696273)	42	21	6.3	3.33	2.80E-05	1.29E-03
Cell Cycle, Mitotic (R-HSA-69278)	517	120	77.59	1.55	2.79E-05	1.31E-03
rRNA processing (R-HSA-72312)	202	9	30.32	0.3	3.14E-05	1.40E-03
RHOA GTPase cycle (R-HSA-9013420)	39	20	5.85	3.42	3.28E-05	1.43E-03
PI Metabolism (R-HSA-1483255)	84	32	12.61	2.54	3.81E-05	1.61E-03
Heme signaling (R-HSA-9707616)	47	22	7.05	3.12	3.98E-05	1.63E-03
Resolution of D-loop Structures through Synthesis-Dependent Strand Annealing (SDSA) (R-HSA-5693554)	26	16	3.9	4.1	3.92E-05	1.63E-03
Resolution of D-Loop Structures (R-HSA-5693537)	33	18	4.95	3.63	4.36E-05	1.67E-03
RHOD GTPase cycle (R-HSA-9013405)	51	23	7.65	3	4.22E-05	1.70E-03
Diseases of DNA repair (R-HSA-9675135)	33	18	4.95	3.63	4.36E-05	1.70E-03
Activation of gene expression by SREBF (SREBP) (R-HSA-2426168)	40	20	6	3.33	4.32E-05	1.71E-03
Mitotic Prometaphase (R-HSA-68877)	199	57	29.87	1.91	4.98E-05	1.82E-03
RHOV GTPase cycle (R-HSA-9013424)	37	19	5.55	3.42	5.06E-05	1.83E-03
Cilium Assembly (R-HSA-5617833)	201	57	30.17	1.89	5.48E-05	1.95E-03
Defective HDR through Homologous Recombination Repair (HRR) due to PALB2 loss of BRCA1 binding function (R-HSA-9704331)	24	15	3.6	4.16	5.98E-05	1.99E-03
Defective HDR through Homologous Recombination (HRR) due to BRCA1 loss-of-function (R-HSA-9701192)	24	15	3.6	4.16	5.98E-05	2.02E-03
Defective HDR through Homologous Recombination (HRR) due to PALB2 loss of function (R-HSA-9701193)	24	15	3.6	4.16	5.98E-05	2.04E-03
Diseases of DNA Double-Strand Break Repair (R-HSA-9675136)	24	15	3.6	4.16	5.98E-05	2.07E-03
Defective HDR through Homologous Recombination Repair (HRR) due to PALB2 loss of BRCA2/RAD51/RAD51C binding function (R-HSA-9704646)	24	15	3.6	4.16	5.98E-05	2.10E-03
trans-Golgi Network Vesicle Budding (R-HSA-199992)	72	28	10.81	2.59	6.83E-05	2.24E-03
Complement cascade (R-HSA-166658)	120	3	18.01	0.17	7.24E-05	2.28E-03
Cohesin Loading onto Chromatin (R-HSA-2470946)	10	10	1.5	6.66	7.47E-05	2.30E-03

Reactome pathways	Homo sapiens - REFLIST (20589)	MAX-R60Q (3090)	MAX-R60Q (expected)	MAX-R60Q (fold Enrichment)	MAX-R60Q (raw P-value)	MAX-R60Q (FDR)
Circadian Clock (R-HSA-400253)	67	27	10.06	2.69	7.46E-05	2.32E-03
Major pathway of rRNA processing in the nucleolus and cytosol (R-HSA-6791226)	182	8	27.31	0.29	7.86E-05	2.39E-03
rRNA processing in the nucleus and cytosol (R-HSA-8868773)	192	9	28.82	0.31	8.14E-05	2.44E-03
Synthesis of PIPs at the plasma membrane (R-HSA-1660499)	53	23	7.95	2.89	9.11E-05	2.67E-03
Resolution of D-loop Structures through Holliday Junction Intermediates (R-HSA-5693568)	32	17	4.8	3.54	9.05E-05	2.69E-03
Synthesis of PIPs at the early endosome membrane (R-HSA-1660516)	16	12	2.4	5	9.54E-05	2.77E-03
Signaling by Nuclear Receptors (R-HSA-9006931)	261	68	39.17	1.74	9.80E-05	2.81E-03
Signaling by TGFB family members (R-HSA-9006936)	103	35	15.46	2.26	1.04E-04	2.96E-03
Signaling by VEGF (R-HSA-194138)	104	35	15.61	2.24	1.12E-04	3.07E-03
Ca2+ pathway (R-HSA-4086398)	59	24	8.85	2.71	1.14E-04	3.10E-03
Downstream signal transduction (R-HSA-186763)	26	15	3.9	3.84	1.17E-04	3.13E-03
Establishment of Sister Chromatid Cohesion (R-HSA-2468052)	11	10	1.65	6.06	1.26E-04	3.34E-03
Signaling by KIT in disease (R-HSA-9669938)	17	12	2.55	4.7	1.43E-04	3.73E-03
Signaling by phosphorylated juxtamembrane, extracellular and kinase domain KIT mutants (R-HSA-9670439)	17	12	2.55	4.7	1.43E-04	3.77E-03
VEGFA-VEGFR2 Pathway (R-HSA-4420097)	94	32	14.11	2.27	1.61E-04	4.14E-03
Formation of a pool of free 40S subunits (R-HSA-72689)	101	2	15.16	0.13	1.70E-04	4.29E-03
Clathrin-mediated endocytosis (R-HSA-8856828)	144	43	21.61	1.99	1.77E-04	4.42E-03
Signaling by EGFR (R-HSA-177929)	48	21	7.2	2.92	1.89E-04	4.67E-03
RHO GTPase Effectors (R-HSA-195258)	288	72	43.22	1.67	1.94E-04	4.75E-03
RORA activates gene expression (R-HSA-1368082)	18	12	2.7	4.44	2.11E-04	5.10E-03
Golgi Associated Vesicle Biogenesis (R-HSA-432722)	54	22	8.1	2.71	2.21E-04	5.21E-03
Regulation of Complement cascade (R-HSA-977606)	110	3	16.51	0.18	2.17E-04	5.21E-03
Signaling by SCF-KIT (R-HSA-1433557)	39	18	5.85	3.08	2.24E-04	5.21E-03
L13a-mediated translational silencing of Ceruloplasmin expression (R-HSA-156827)	111	3	16.66	0.18	2.20E-04	5.23E-03
GTP hydrolysis and joining of the 60S ribosomal subunit (R-HSA-72706)	112	3	16.81	0.18	2.28E-04	5.26E-03
Biological oxidations (R-HSA-211859)	220	13	33.02	0.39	2.67E-04	6.11E-03

Reactome pathways	Homo sapiens - REFLIST (20589)	MAX-R60Q (3090)	MAX-R60Q (expected)	MAX-R60Q (fold Enrichment)	MAX-R60Q (raw P-value)	MAX-R60Q (FDR)
MET promotes cell motility (R-HSA-8875878)	40	18	6	3	2.85E-04	6.47E-03
Signaling by Hippo (R-HSA-2028269)	19	12	2.85	4.21	3.03E-04	6.75E-03
Antigen processing: Ubiquitination & Proteasome degradation (R-HSA-983168)	308	75	46.22	1.62	3.01E-04	6.76E-03
Nervous system development (R-HSA-9675108)	574	124	86.15	1.44	3.14E-04	6.94E-03
Mitotic Telophase/Cytokinesis (R-HSA-68884)	13	10	1.95	5.13	3.19E-04	6.97E-03
The role of GTSE1 in G2/M progression after G2 checkpoint (R-HSA-8852276)	78	1	11.71	0.09	3.31E-04	7.19E-03
Signaling by Erythropoietin (R-HSA-9006335)	23	13	3.45	3.77	3.83E-04	8.09E-03
Regulation of MECP2 expression and activity (R-HSA-9022692)	30	15	4.5	3.33	3.82E-04	8.13E-03
The citric acid (TCA) cycle and respiratory electron transport (R-HSA-1428517)	176	9	26.41	0.34	3.89E-04	8.15E-03
Intracellular signaling by second messengers (R-HSA-9006925)	291	71	43.67	1.63	3.81E-04	8.19E-03
PLC beta mediated events (R-HSA-112043)	49	20	7.35	2.72	4.35E-04	8.96E-03
Retrograde transport at the Trans-Golgi-Network (R-HSA-6811440)	49	20	7.35	2.72	4.35E-04	9.04E-03
G-protein mediated events (R-HSA-112040)	54	21	8.1	2.59	4.77E-04	9.75E-03
Class I MHC mediated antigen processing & presentation (R-HSA-983169)	378	87	56.73	1.53	4.84E-04	9.80E-03
Antimicrobial peptides (R-HSA-6803157)	91	2	13.66	0.15	5.17E-04	1.04E-02
Selenoamino acid metabolism (R-HSA-2408522)	116	4	17.41	0.23	5.51E-04	1.10E-02
Regulation of TP53 Activity through Phosphorylation (R-HSA-6804756)	92	30	13.81	2.17	6.01E-04	1.19E-02
SUMOylation of DNA damage response and repair proteins (R-HSA-3108214)	71	25	10.66	2.35	6.30E-04	1.24E-02
Homologous DNA Pairing and Strand Exchange (R-HSA-5693579)	42	18	6.3	2.86	6.78E-04	1.31E-02
NRAGE signals death through JNK (R-HSA-193648)	59	22	8.85	2.48	6.84E-04	1.31E-02
Regulation of PTEN mRNA translation (R-HSA-8943723)	9	8	1.35	5.92	6.76E-04	1.32E-02
Protein localization (R-HSA-9609507)	158	8	23.71	0.34	7.03E-04	1.34E-02
Regulation of TP53 Activity (R-HSA-5633007)	159	44	23.86	1.84	7.16E-04	1.35E-02
DNA Double-Strand Break Repair (R-HSA-5693532)	149	42	22.36	1.88	7.24E-04	1.36E-02
RND2 GTPase cycle (R-HSA-9696270)	43	18	6.45	2.79	7.61E-04	1.39E-02
Mitochondrial translation initiation (R-HSA-5368286)	88	2	13.21	0.15	7.58E-04	1.40E-02

Reactome pathways	Homo sapiens - REFLIST (20589)	MAX-R60Q (3090)	MAX-R60Q (expected)	MAX-R60Q (fold Enrichment)	MAX-R60Q (raw P-value)	MAX-R60Q (FDR)
Mitochondrial translation elongation (R-HSA-5389840)	88	2	13.21	0.15	7.58E-04	1.41E-02
Scavenging of heme from plasma (R-HSA-2168880)	74	1	11.11	0.09	7.87E-04	1.43E-02
Metabolism of proteins (R-HSA-392499)	1914	347	287.25	1.21	8.09E-04	1.46E-02
RAB GEFs exchange GTP for GDP on RABs (R-HSA-8876198)	89	29	13.36	2.17	8.15E-04	1.46E-02
HDR through Single Strand Annealing (SSA) (R-HSA-5685938)	37	16	5.55	2.88	8.56E-04	1.52E-02
HDMs demethylate histones (R-HSA-3214842)	26	13	3.9	3.33	9.22E-04	1.63E-02
Post-transcriptional silencing by small RNAs (R-HSA-426496)	7	7	1.05	6.66	9.48E-04	1.66E-02
M Phase (R-HSA-68886)	375	85	56.28	1.51	9.71E-04	1.69E-02
Estrogen-dependent gene expression (R-HSA-9018519)	118	35	17.71	1.98	9.87E-04	1.71E-02
Laminin interactions (R-HSA-3000157)	30	14	4.5	3.11	1.00E-03	1.72E-02
RHOF GTPase cycle (R-HSA-9035034)	41	17	6.15	2.76	1.16E-03	1.97E-02
DAG and IP3 signaling (R-HSA-1489509)	41	17	6.15	2.76	1.16E-03	1.99E-02
BMAL1:CLOCK,NPAS2 activates circadian gene expression (R-HSA-1368108)	27	13	4.05	3.21	1.20E-03	2.03E-02
Transport to the Golgi and subsequent modification (R-HSA-948021)	186	48	27.91	1.72	1.23E-03	2.06E-02
Formation of the cornified envelope (R-HSA-6809371)	129	6	19.36	0.31	1.25E-03	2.06E-02
HDR through Homologous Recombination (HRR) (R-HSA-5685942)	66	23	9.91	2.32	1.25E-03	2.08E-02
Phospholipid metabolism (R-HSA-1483257)	212	53	31.82	1.67	1.28E-03	2.10E-02
Mitochondrial translation (R-HSA-5368287)	94	3	14.11	0.21	1.32E-03	2.16E-02
Signaling by PDGF (R-HSA-186797)	54	20	8.1	2.47	1.38E-03	2.21E-02
PKMTs methylate histone lysines (R-HSA-3214841)	47	18	7.05	2.55	1.40E-03	2.23E-02
Regulation of RUNX1 Expression and Activity (R-HSA-8934593)	17	10	2.55	3.92	1.43E-03	2.26E-02
Signaling by FLT3 fusion proteins (R-HSA-9703465)	17	10	2.55	3.92	1.43E-03	2.28E-02
Role of ABL in ROBO-SLIT signaling (R-HSA-428890)	8	7	1.2	5.83	1.58E-03	2.46E-02
Competing endogenous RNAs (ceRNAs) regulate PTEN translation (R-HSA-8948700)	8	7	1.2	5.83	1.58E-03	2.47E-02
Olfactory Signaling Pathway (R-HSA-381753)	66	1	9.91	0.1	1.63E-03	2.49E-02
Mitochondrial protein import (R-HSA-1268020)	65	1	9.76	0.1	1.63E-03	2.50E-02

Reactome pathways	Homo sapiens - REFLIST (20589)	MAX-R60Q (3090)	MAX-R60Q (expected)	MAX-R60Q (fold Enrichment)	MAX-R60Q (raw P-value)	MAX-R60Q (FDR)
Synthesis of PIPs at the late endosome membrane (R-HSA-1660517)	11	8	1.65	4.85	1.65E-03	2.51E-02
Signaling by FGFR1 in disease (R-HSA-5655302)	32	14	4.8	2.92	1.62E-03	2.51E-02
Disease (R-HSA-1643685)	1679	305	251.98	1.21	1.71E-03	2.59E-02
Presynaptic phase of homologous DNA pairing and strand exchange (R-HSA-5693616)	39	16	5.85	2.73	1.78E-03	2.68E-02
Axon guidance (R-HSA-422475)	549	114	82.39	1.38	1.90E-03	2.84E-02
Golgi-to-ER retrograde transport (R-HSA-8856688)	135	37	20.26	1.83	1.97E-03	2.89E-02
Regulation of lipid metabolism by PPARalpha (R-HSA-400206)	115	33	17.26	1.91	1.96E-03	2.90E-02
Signaling by PDGFR in disease (R-HSA-9671555)	18	10	2.7	3.7	1.97E-03	2.91E-02
Response of EIF2AK4 (GCN2) to amino acid deficiency (R-HSA-9633012)	101	4	15.16	0.26	2.14E-03	3.12E-02
Signaling by TGF-beta Receptor Complex (R-HSA-170834)	74	24	11.11	2.16	2.20E-03	3.19E-02
Cellular response to starvation (R-HSA-9711097)	156	9	23.41	0.38	2.33E-03	3.36E-02
FLT3 Signaling (R-HSA-9607240)	36	15	5.4	2.78	2.44E-03	3.46E-02
RUNX1 interacts with co-factors whose precise effect on RUNX1 targets is not known (R-HSA-8939243)	36	15	5.4	2.78	2.44E-03	3.48E-02
Signaling by Leptin (R-HSA-2586552)	9	7	1.35	5.18	2.49E-03	3.49E-02
ALK mutants bind TKIs (R-HSA-9700645)	12	8	1.8	4.44	2.44E-03	3.49E-02
Rab regulation of trafficking (R-HSA-9007101)	121	34	18.16	1.87	2.49E-03	3.50E-02
Mitochondrial translation termination (R-HSA-5419276)	88	3	13.21	0.23	2.70E-03	3.74E-02
Resolution of Sister Chromatid Cohesion (R-HSA-2500257)	123	34	18.46	1.84	2.70E-03	3.76E-02
PPARA activates gene expression (R-HSA-1989781)	114	32	17.11	1.87	2.83E-03	3.86E-02
Netrin-1 signaling (R-HSA-373752)	49	18	7.35	2.45	2.81E-03	3.86E-02
HDR through Homologous Recombination (HRR) or Single Strand Annealing (SSA) (R-HSA-5693567)	114	32	17.11	1.87	2.83E-03	3.88E-02
Factors involved in megakaryocyte development and platelet production (R-HSA-983231)	158	41	23.71	1.73	2.87E-03	3.88E-02
RUNX2 regulates osteoblast differentiation (R-HSA-8940973)	23	11	3.45	3.19	2.94E-03	3.94E-02
Nephrin family interactions (R-HSA-373753)	23	11	3.45	3.19	2.94E-03	3.96E-02
Anchoring of the basal body to the plasma membrane (R-HSA-5620912)	96	28	14.41	1.94	3.04E-03	4.06E-02
Insulin processing (R-HSA-264876)	27	12	4.05	2.96	3.09E-03	4.08E-02

Reactome pathways	Homo sapiens - REFLIST (20589)	MAX-R60Q (3090)	MAX-R60Q (expected)	MAX-R60Q (fold Enrichment)	MAX-R60Q (raw P-value)	MAX-R60Q (FDR)
FLT3 signaling in disease (R-HSA-9682385)	27	12	4.05	2.96	3.09E-03	4.10E-02
IGF1R signaling cascade (R-HSA-2428924)	43	16	6.45	2.48	3.21E-03	4.15E-02
G alpha (12/13) signalling events (R-HSA-416482)	80	25	12.01	2.08	3.17E-03	4.15E-02
IRS-related events triggered by IGF1R (R-HSA-2428928)	43	16	6.45	2.48	3.21E-03	4.17E-02
Intra-Golgi traffic (R-HSA-6811438)	43	16	6.45	2.48	3.21E-03	4.19E-02
Oncogene Induced Senescence (R-HSA-2559585)	33	14	4.95	2.83	3.43E-03	4.38E-02
Homology Directed Repair (R-HSA-5693538)	120	33	18.01	1.83	3.51E-03	4.40E-02
Regulation of KIT signaling (R-HSA-1433559)	13	8	1.95	4.1	3.49E-03	4.40E-02
Constitutive Signaling by EGFRvIII (R-HSA-5637810)	13	8	1.95	4.1	3.49E-03	4.42E-02
Signaling by EGFRvIII in Cancer (R-HSA-5637812)	13	8	1.95	4.1	3.49E-03	4.44E-02
Signaling by NTRKs (R-HSA-166520)	131	35	19.66	1.78	3.61E-03	4.48E-02
Deubiquitination (R-HSA-5688426)	282	64	42.32	1.51	3.69E-03	4.48E-02
Regulation of expression of SLITs and ROBOs (R-HSA-9010553)	169	11	25.36	0.43	3.67E-03	4.48E-02
Non-integrin membrane-ECM interactions (R-HSA-3000171)	59	20	8.85	2.26	3.64E-03	4.50E-02
ER to Golgi Anterograde Transport (R-HSA-199977)	155	40	23.26	1.72	3.67E-03	4.51E-02
PI3K/AKT Signaling in Cancer (R-HSA-2219528)	92	27	13.81	1.96	3.72E-03	4.51E-02
Signaling by PDGFRA transmembrane, juxtamembrane and kinase domain mutants (R-HSA-9673767)	10	7	1.5	4.66	3.76E-03	4.51E-02
Estrogen-dependent nuclear events downstream of ESR-membrane signaling (R-HSA-9634638)	24	11	3.6	3.05	3.79E-03	4.52E-02
Signaling by PDGFRA extracellular domain mutants (R-HSA-9673770)	10	7	1.5	4.66	3.76E-03	4.53E-02
Myogenesis (R-HSA-525793)	28	12	4.2	2.86	3.90E-03	4.57E-02
EGR2 and SOX10-mediated initiation of Schwann cell myelination (R-HSA-9619665)	28	12	4.2	2.86	3.90E-03	4.59E-02
Signaling by ERBB2 (R-HSA-1227986)	46	17	6.9	2.46	3.90E-03	4.60E-02
Transcriptional activity of SMAD2/SMAD3:SMAD4 heterotrimer (R-HSA-2173793)	46	17	6.9	2.46	3.90E-03	4.62E-02
RHOBTB GTPase Cycle (R-HSA-9706574)	35	14	5.25	2.67	4.18E-03	4.85E-02
Interleukin-3, Interleukin-5 and GM-CSF signaling (R-HSA-512988)	47	17	7.05	2.41	4.18E-03	4.87E-02