

Supplementary Table S10. T98G GBM Panther Gene Ontology Reactome Analysis of DEGS Upregulated in Normoxia Sorted by P-value.

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|---|--------------------------------------|---|-----------------|---|---------------------|----------|-----------------------|--|----------------------------|--|--------------------|
| Analysis Type: | | PANTHER Overrepresentation Test (Released 20221013) | | | | | | | | | |
| Annotation Version and Release Date: | | Reactome version 77 Released 2021-10-01 | | | | | | | | | |
| Analyzed List: | upload_1 (Homo sapiens) | | | | | | | | | | |
| Reference List: | Homo sapiens (all genes in database) | | | | | | | | | | |
| Test Type: FISHER | | | | | | | | | | | |
| Correction: | BONFERRONI | | | | | | | | | | |
| Bonferroni count: | 2229 | | | | | | | | | | |
| Reactome pathways | Homo sapiens - | REFLIST (20589) | upload_1 (1340) | | upload_1 (expected) | | upload_1 (over/under) | | upload_1 (fold Enrichment) | | upload_1 (P-value) |
| Unclassified (UNCLASSIFIED) | | 10082 | 454 | | 656.17 | | - | | .69 | | 0.00E00 |
| Cell Cycle (R-HSA-1640170) | | 648 | 171 | | 42.17 | | + | | 4.05 | | 1.69E-44 |
| Cell Cycle, Mitotic (R-HSA-69278) | | 517 | 136 | | 33.65 | | + | | 4.04 | | 1.72E-34 |
| Metabolism of RNA (R-HSA-8953854) | | 661 | 143 | | 43.02 | | + | | 3.32 | | 1.70E-28 |
| Cell Cycle Checkpoints (R-HSA-69620) | | 271 | 90 | | 17.64 | | + | | 5.10 | | 4.82E-28 |
| Gene expression (Transcription) (R-HSA-74160) | | 1454 | 197 | | 94.63 | | + | | 2.08 | | 5.46E-17 |
| Mitotic G1 phase and G1/S transition (R-HSA-453279) | 147 | 53 | 9.57 | + | 5.54 | 6.47E-17 | | | | | |
| G1/S Transition (R-HSA-69206) | 130 | 50 | 8.46 | + | 5.91 | 8.28E-17 | | | | | |
| Mitotic Metaphase and Anaphase (R-HSA-2555396) | 228 | 65 | 14.84 | + | 4.38 | 1.04E-16 | | | | | |
| M Phase (R-HSA-68886) | 375 | 84 | 24.41 | + | 3.44 | 1.80E-16 | | | | | |
| DNA Replication (R-HSA-69306) | 159 | 54 | 10.35 | + | 5.22 | 2.59E-16 | | | | | |
| Mitotic Anaphase (R-HSA-68882) | 227 | 64 | 14.77 | + | 4.33 | 3.24E-16 | | | | | |
| S Phase (R-HSA-69242) | 161 | 54 | 10.48 | + | 5.15 | 4.11E-16 | | | | | |
| Synthesis of DNA (R-HSA-69239) | 119 | 46 | 7.74 | + | 5.94 | 2.26E-15 | | | | | |
| Process Capped Intron-Cont Pre-mRNA (R-HSA-72203) | 238 | 64 | 15.49 | + | 4.13 | 2.43E-15 | | | | | |
| G2/M Checkpoints (R-HSA-69481) | 150 | 49 | 9.76 | + | 5.02 | 4.72E-14 | | | | | |
| DNA Repair (R-HSA-73894) | 310 | 70 | 20.18 | + | 3.47 | 1.61E-13 | | | | | |
| Separation of Sister Chromatids (R-HSA-2467813) | 187 | 51 | 12.17 | + | 4.19 | 5.09E-12 | | | | | |
| Mitotic Spindle Checkpoint (R-HSA-69618) | 109 | 38 | 7.09 | + | 5.36 | 3.44E-11 | | | | | |
| DNA Double-Strand Break Repair (R-HSA-5693532) | 149 | 44 | 9.70 | + | 4.54 | 4.10E-11 | | | | | |
| Amp sig kinetochore MAD2 inhib sig (R-HSA-141444) | 92 | 35 | 5.99 | + | 5.85 | 4.61E-11 | | | | | |

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| Amplif of signal from the kinetochores (R-HSA-141424) | 92 | 35 | 5.99 | + | 5.85 | 4.61E-11 |
| RNA Polymerase II Transcription (R-HSA-73857) | 1319 | 164 | 85.84 | + | 1.91 | 1.38E-10 |
| Resolu of Sister Chromatid Cohesion (R-HSA-2500257) | 123 | 39 | 8.01 | + | 4.87 | 1.93E-10 |
| Mitotic Prometaphase (R-HSA-68877) | 199 | 49 | 12.95 | + | 3.78 | 4.82E-10 |
| mRNA Splicing - Major Pathway (R-HSA-72163) | 180 | 46 | 11.71 | + | 3.93 | 8.60E-10 |
| tRNA processing (R-HSA-72306) | 104 | 35 | 6.77 | + | 5.17 | 8.70E-10 |
| Chromosome Maintenance (R-HSA-73886) | 120 | 37 | 7.81 | + | 4.74 | 1.67E-09 |
| Homology Directed Repair (R-HSA-5693538) | 120 | 37 | 7.81 | + | 4.74 | 1.67E-09 |
| DNA Replication Pre-Initiation (R-HSA-69002) | 116 | 36 | 7.55 | + | 4.77 | 2.91E-09 |
| DNA strand elongation (R-HSA-69190) | 32 | 21 | 2.08 | + | 10.08 | 2.97E-09 |
| mRNA Splicing (R-HSA-72172) | 188 | 46 | 12.24 | + | 3.76 | 3.17E-09 |
| Activation of pre-replicative complex (R-HSA-68962) | 33 | 21 | 2.15 | + | 9.78 | 4.58E-09 |
| EML4 and NUDC mitotic spindle form (R-HSA-9648025) | 115 | 35 | 7.48 | + | 4.68 | 9.44E-09 |
| Activation of ATR in res to rep stress (R-HSA-176187) | 37 | 21 | 2.41 | + | 8.72 | 2.32E-08 |
| Transcriptional Regulation by TP53 (R-HSA-3700989) | 360 | 64 | 23.43 | + | 2.73 | 4.47E-08 |
| HDR Homologous Recomb/(SSA) (R-HSA-5693567) | 114 | 33 | 7.42 | + | 4.45 | 1.17E-07 |
| HDR Homologous Recomb (HRR) (R-HSA-5685942) | 66 | 25 | 4.30 | + | 5.82 | 2.58E-07 |
| snRNP Assembly (R-HSA-191859) | 50 | 22 | 3.25 | + | 6.76 | 3.47E-07 |
| Metabolism of non-coding RNA (R-HSA-194441) | 50 | 22 | 3.25 | + | 6.76 | 3.47E-07 |
| RHO GTPases Activate Formins (R-HSA-5663220) | 136 | 35 | 8.85 | + | 3.95 | 4.69E-07 |
| TCA cycle and respira electron trans (R-HSA-1428517) | 176 | 40 | 11.45 | + | 3.49 | 6.05E-07 |
| Homologous DNA Pair/Strand Excha (R-HSA-5693579) | 42 | 20 | 2.73 | + | 7.32 | 7.95E-07 |
| Switching origins to post-replicat state (R-HSA-69052) | 90 | 28 | 5.86 | + | 4.78 | 8.56E-07 |
| Generic Transcription Pathway (R-HSA-212436) | 1197 | 139 | 77.90 | + | 1.78 | 9.58E-07 |
| Diseases of DNA repair (R-HSA-9675135) | 33 | 18 | 2.15 | + | 8.38 | 1.13E-06 |
| tRNA processing in the nucleus (R-HSA-6784531) | 55 | 22 | 3.58 | + | 6.15 | 1.47E-06 |
| Presynaptic homolo DNA strd exch (R-HSA-5693616) | 39 | 19 | 2.54 | + | 7.49 | 1.63E-06 |
| Trans of Mat Transcript to Cytoplasm (R-HSA-72202) | 80 | 26 | 5.21 | + | 4.99 | 1.67E-06 |
| Orc1 removal from chromatin (R-HSA-68949) | 70 | 23 | 4.56 | + | 5.05 | 1.33E-05 |

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| Cellular responses to stress (R-HSA-2262752) | 718 | 91 | 46.73 | + | 1.95 | 3.21E-05 |
| Def HDR PALB2 BRCA2/RAD51/RAD51C-(HSA-9704646) 24 | | 14 | 1.56 | + | 8.96 | 5.09E-05 |
| Diseases of DNA Dble-Strd Break Rep (R-HSA-9675136) 24 | | 14 | 1.56 | + | 8.96 | 5.09E-05 |
| Def HDR (HRR) due to PALB2 loss fxn (R-HSA-9701193) 24 | | 14 | 1.56 | + | 8.96 | 5.09E-05 |
| Def HDR (HRR) due to BRCA1 loss fxn (R-HSA-9701192) 24 | | 14 | 1.56 | + | 8.96 | 5.09E-05 |
| Def HDR (HRR) PALB2 loss BRCA1 bin (R-HSA-9704331) 24 | | 14 | 1.56 | + | 8.96 | 5.09E-05 |
| Interact of Rev with host cellular prot (R-HSA-177243) 34 | | 16 | 2.21 | + | 7.23 | 5.24E-05 |
| Extension of Telomeres (R-HSA-180786) 51 | | 19 | 3.32 | + | 5.72 | 5.39E-05 |
| Trans mRNAs Intronless Transcripts (R-HSA-159234) 40 | | 17 | 2.60 | + | 6.53 | 6.29E-05 |
| Trans mRNA Intron-ContTranscript (R-HSA-159236) 71 | | 22 | 4.62 | + | 4.76 | 6.80E-05 |
| Assembly of the pre-replicative cmplx (R-HSA-68867) 99 | | 26 | 6.44 | + | 4.04 | 6.83E-05 |
| Cellular responses to stimuli (R-HSA-8953897) 732 | | 91 | 47.64 | + | 1.91 | 9.44E-05 |
| Resolun of D-loop Strd Anneal (SDSA) (R-HSA-5693554) 26 | | 14 | 1.69 | + | 8.27 | 1.09E-04 |
| Respiratory electron transport (R-HSA-611105) 102 | | 26 | 6.64 | + | 3.92 | 1.14E-04 |
| Reg of HSF1-med heat shock resp (R-HSA-3371453) 68 | | 21 | 4.43 | + | 4.75 | 1.46E-04 |
| Res Holliday Junction Intermediates (R-HSA-5693568) 32 | | 15 | 2.08 | + | 7.20 | 1.50E-04 |
| Rev-mediated nucexport HIV RNA (R-HSA-165054) 32 | | 15 | 2.08 | + | 7.20 | 1.50E-04 |
| Tran SLBP Dependant Mature mRNA (R-HSA-159230) 33 | | 15 | 2.15 | + | 6.98 | 2.05E-04 |
| Resolution of D-Loop Structures (R-HSA-5693537) 33 | | 15 | 2.15 | + | 6.98 | 2.05E-04 |
| G1/S-Specific Transcription (R-HSA-69205) 28 | | 14 | 1.82 | + | 7.68 | 2.21E-04 |
| Trans mRNA intronless Transcript (R-HSA-159231) 39 | | 16 | 2.54 | + | 6.30 | 2.37E-04 |
| SUMOylation (R-HSA-2990846) 163 | | 33 | 10.61 | + | 3.11 | 2.37E-04 |
| G2/M DNA damage checkpoint (R-HSA-69473) 78 | | 22 | 5.08 | + | 4.33 | 2.73E-04 |
| NEP/NS2 Inter Cellular Export Machin (R-HSA-168333) 29 | | 14 | 1.89 | + | 7.42 | 3.09E-04 |
| Mitochondrial protein import (R-HSA-1268020) 65 | | 20 | 4.23 | + | 4.73 | 3.14E-04 |
| Host Interactions of HIV factors (R-HSA-162909) 124 | | 28 | 8.07 | + | 3.47 | 3.15E-04 |
| Translation (R-HSA-72766) 293 | | 47 | 19.07 | + | 2.46 | 3.27E-04 |
| Regulation of mitotic cell cycle (R-HSA-453276) 87 | | 23 | 5.66 | + | 4.06 | 3.81E-04 |
| APC/C-mediated degr of cell cycle prot (R-HSA-174143) 87 | | 23 | 5.66 | + | 4.06 | 3.81E-04 |

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| Regulation of TP53 Activity (R-HSA-5633007) | 159 | 32 | 10.35 | + | 3.09 | 4.13E-04 |
| Resp ATP syn uncoupling prot (R-HSA-163200) | 126 | 28 | 8.20 | + | 3.41 | 4.19E-04 |
| Export Viral Ribonucleoprot Nucleus (R-HSA-168274) | 30 | 14 | 1.95 | + | 7.17 | 4.28E-04 |
| Processing of DNA dble-strd break (R-HSA-5693607) | 81 | 22 | 5.27 | + | 4.17 | 4.74E-04 |
| Unwinding of DNA (R-HSA-176974) | 12 | 10 | .78 | + | 12.80 | 5.14E-04 |
| Nuclear import of Rev protein (R-HSA-180746) | 31 | 14 | 2.02 | + | 6.94 | 5.86E-04 |
| GPCR ligand binding (R-HSA-500792) | 463 | 6 | 30.13 | - | .20 | 5.95E-04 |
| HDR (SSA) (R-HSA-5685938) | 37 | 15 | 2.41 | + | 6.23 | 6.68E-04 |
| Transport SLBP indep Mature mRNA (R-HSA-159227) | 32 | 14 | 2.08 | + | 6.72 | 7.96E-04 |
| SUMOylation of SUMOylation proteins (R-HSA-4085377) | 32 | 14 | 2.08 | + | 6.72 | 7.96E-04 |
| HIV Infection (R-HSA-162906) | 227 | 39 | 14.77 | + | 2.64 | 8.71E-04 |
| Reg TP53 Activity through Phosphory(R-HSA-6804756) | 92 | 23 | 5.99 | + | 3.84 | 8.86E-04 |
| E2F mediated reg of DNA replication (R-HSA-113510) | 22 | 12 | 1.43 | + | 8.38 | 8.96E-04 |
| rRNA processing nucleus cytosol (R-HSA-8868773) | 192 | 35 | 12.50 | + | 2.80 | 9.00E-04 |
| Metabolism (R-HSA-1430728) | 2087 | 197 | 135.83 | + | 1.45 | 9.92E-04 |
| SUMOylation DNA damage response(R-HSA-3108214) | 71 | 20 | 4.62 | + | 4.33 | 1.03E-03 |
| Nuclear Pore Complex Disassembly (R-HSA-3301854) | 33 | 14 | 2.15 | + | 6.52 | 1.07E-03 |
| CDT1 assoc with the CDC6:ORC:origin (R-HSA-68827) | 58 | 18 | 3.77 | + | 4.77 | 1.18E-03 |
| Mitochondrial translation (R-HSA-5368287) | 94 | 23 | 6.12 | + | 3.76 | 1.22E-03 |
| Metabolism of proteins (R-HSA-392499) | 1914 | 183 | 124.57 | + | 1.47 | 1.25E-03 |
| Telomere C-strand (Lagging Strd) Syn (R-HSA-174417) | 34 | 14 | 2.21 | + | 6.33 | 1.43E-03 |
| Mitochondrial translation elongation (R-HSA-5389840) | 88 | 22 | 5.73 | + | 3.84 | 1.57E-03 |
| Cellular response to heat stress (R-HSA-3371556) | 88 | 22 | 5.73 | + | 3.84 | 1.57E-03 |
| Mitochondrial translation initiation (R-HSA-5368286) | 88 | 22 | 5.73 | + | 3.84 | 1.57E-03 |
| rRNA processing (R-HSA-72312) | 202 | 36 | 13.15 | + | 2.74 | 1.62E-03 |
| Trans Ribonucleoproteins Nucleus (R-HSA-168271) | 29 | 13 | 1.89 | + | 6.89 | 1.68E-03 |
| rRNA modification nucleus/cytosol (R-HSA-6790901) | 60 | 18 | 3.90 | + | 4.61 | 1.78E-03 |
| Nuclear Envelope Breakdown (R-HSA-2980766) | 47 | 16 | 3.06 | + | 5.23 | 1.83E-03 |
| rRNA processing nucleolus/cytosol (R-HSA-6791226) | 182 | 33 | 11.85 | + | 2.79 | 2.12E-03 |

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| SUMO E3 ligases SUMOylate (R-HSA-3108232) | 157 | 30 | 10.22 | + | 2.94 | 2.55E-03 |
| Lagging Strand Synthesis (R-HSA-69186) | 20 | 11 | 1.30 | + | 8.45 | 2.58E-03 |
| Vpr-mediated nuc import of PICs (R-HSA-180910) | 31 | 13 | 2.02 | + | 6.44 | 3.04E-03 |
| SUMOylation of DNA replication prot (R-HSA-4615885) | 43 | 15 | 2.80 | + | 5.36 | 3.13E-03 |
| Telomere Maintenance (R-HSA-157579) | 93 | 22 | 6.05 | + | 3.63 | 3.47E-03 |
| NS1 Mediated Effect Host Pathways (R-HSA-168276) | 38 | 14 | 2.47 | + | 5.66 | 4.15E-03 |
| Antiviral mech by IFN-stim genes (R-HSA-1169410) | 79 | 20 | 5.14 | + | 3.89 | 4.23E-03 |
| Regof APC/C actvs G1/S anaphase (R-HSA-176408) | 80 | 20 | 5.21 | + | 3.84 | 4.98E-03 |
| Sig Rho GTPases RHOBTB3 (R-HSA-9716542) | 685 | 80 | 44.58 | + | 1.79 | 5.19E-03 |
| Mitochondrial translation term(R-HSA-5419276) | 88 | 21 | 5.73 | + | 3.67 | 5.29E-03 |
| Mitotic Prophase (R-HSA-68875) | 104 | 23 | 6.77 | + | 3.40 | 5.44E-03 |
| RNA Polymerase II Transcription Term (R-HSA-73856) | 66 | 18 | 4.30 | + | 4.19 | 5.63E-03 |
| SCF(Skp2) degradation of p27/p21 (R-HSA-187577) | 59 | 17 | 3.84 | + | 4.43 | 5.69E-03 |
| Cyclin E associated G1/S transition (R-HSA-69202) | 82 | 20 | 5.34 | + | 3.75 | 6.88E-03 |
| Interactions of Vpr with host cell prot (R-HSA-176033) | 34 | 13 | 2.21 | + | 5.87 | 6.94E-03 |
| APC/C:Cdc20 med deg mitotic prot (R-HSA-176409) | 75 | 19 | 4.88 | + | 3.89 | 7.53E-03 |
| Nucleosome assembly (R-HSA-774815) | 54 | 16 | 3.51 | + | 4.55 | 8.27E-03 |
| Dep CENPA nucleosomes centromere (R-HSA-606279) | 54 | 16 | 3.51 | + | 4.55 | 8.27E-03 |
| Viral Messenger RNA Synthesis (R-HSA-168325) | 41 | 14 | 2.67 | + | 5.25 | 8.60E-03 |
| Reg by Glucokinase Regulatory Protein (R-HSA-170822) | 29 | 12 | 1.89 | + | 6.36 | 8.65E-03 |
| Def TPR suscep thyroid pap carci (R-HSA-5619107) | 29 | 12 | 1.89 | + | 6.36 | 8.65E-03 |
| RHO GTPase Effectors (R-HSA-195258) | 288 | 43 | 18.74 | + | 2.29 | 8.76E-03 |
| APC/C APC/C:Cdc20 med deg mit prot (R-HSA-176814) | 76 | 19 | 4.95 | + | 3.84 | 8.87E-03 |
| SUMO ubiquitinylation proteins (R-HSA-3232142) | 35 | 13 | 2.28 | + | 5.71 | 8.99E-03 |
| Cyclin A:Cdk2-assoc S phase entry (R-HSA-69656) | 84 | 20 | 5.47 | + | 3.66 | 9.40E-03 |
| Leading Strand Synthesis (R-HSA-69109) | 14 | 9 | .91 | + | 9.88 | 9.63E-03 |
| Polymerase switching (R-HSA-69091) | 14 | 9 | .91 | + | 9.88 | 9.63E-03 |
| Postmitotic nucpore complex (R-HSA-9615933) | 24 | 11 | 1.56 | + | 7.04 | 1.01E-02 |
| Folding of actin by CCT/TrIC (R-HSA-390450) | 10 | 8 | .65 | + | 12.29 | 1.07E-02 |

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| tRNA Aminoacylation (R-HSA-379724) | 42 | 14 | 2.73 | + | 5.12 | 1.08E-02 |
| Nuclear Envelope (NE) Reassembly (R-HSA-2995410) | 70 | 18 | 4.56 | + | 3.95 | 1.13E-02 |
| Glucose metabolism (R-HSA-70326) | 86 | 20 | 5.60 | + | 3.57 | 1.27E-02 |
| ISG15 antiviral mechanism (R-HSA-1169408)71 | 18 | 4.62 | + | 3.90 | 1.34E-02 | |
| SUMOylationRNA binding proteins (R-HSA-4570464) | 43 | 14 | 2.80 | + | 5.00 | 1.36E-02 |
| Res AP sites multiple-nucleotide (R-HSA-110373) | 25 | 11 | 1.63 | + | 6.76 | 1.38E-02 |
| CDK-med Phosphor removal of Cdc6 (R-HSA-69017) | 72 | 18 | 4.69 | + | 3.84 | 1.58E-02 |
| Cdc20:Phospho-APC/C deg Cyclin A (R-HSA-174184) | 72 | 18 | 4.69 | + | 3.84 | 1.58E-02 |
| Signaling by GPCR (R-HSA-372790) | 697 | 18 | 45.36 | - | .40 | 1.69E-02 |
| Signaling by Rho GTPases (R-HSA-194315) | 670 | 77 | 43.61 | + | 1.77 | 1.74E-02 |
| CDC6 assoc w/ORC:origin complex (R-HSA-68689) | 11 | 8 | .72 | + | 11.17 | 1.75E-02 |
| Polymerase switch C-strand telomere (R-HSA-174411) | 26 | 11 | 1.69 | + | 6.50 | 1.85E-02 |
| APC:Cdc20 deg cell cycle checkpoint (R-HSA-179419) | 73 | 18 | 4.75 | + | 3.79 | 1.86E-02 |
| G1/S DNA Damage Checkpoints (R-HSA-69615) | 66 | 17 | 4.30 | + | 3.96 | 2.02E-02 |
| HIV Life Cycle (R-HSA-162587) | 149 | 27 | 9.70 | + | 2.78 | 2.02E-02 |
| GPCR downstream signalling (R-HSA-388396) | 624 | 15 | 40.61 | - | .37 | 2.39E-02 |
| SUMOylation of chromatin org (R-HSA-4551638) | 53 | 15 | 3.45 | + | 4.35 | 2.63E-02 |
| Transcriptional Regulation by E2F6 (R-HSA-8953750) | 34 | 12 | 2.21 | + | 5.42 | 3.21E-02 |
| Class A/1 (Rhodopsin-like receptors) (R-HSA-373076) | 331 | 4 | 21.54 | - | .19 | 3.27E-02 |
| Diseases of programmed cell death (R-HSA-9645723) | 70 | 17 | 4.56 | + | 3.73 | 3.89E-02 |
| E2F inhibition of pre-replication comp (R-HSA-113507) 9 | | 7 | .59 | + | 11.95 | 4.90E-02 |