

Supplementary Table 16 Gene ontology enrichment analysis of MRs differentially activated in ATRX mutant compared with ATRX wild type LGM6 glioma.
 Supplementary Table 16b Gene ontology terms significantly enriched for the inferred targets of the 10 most active MRs in ATRX wild type.

GO Term	originalGeneSetSize	actualGeneSetSize	Genes	Fold Enrichment	p-value	q-value
STRUCTURAL CONSTITUENT OF RIBOSOME	706	105	RPL18, MRPS	11.49	1.21E-89	1.84E-86
RIBOSOME	757	119	MRPL40, RPL	9.35	9.12E-89	1.30E-85
MITOCHONDRION	757	236	MRPL40, MR	3.67	1.79E-77	2.55E-74
RIBOSOMAL SUBUNIT	757	86	MRPS36, RPL	11.34	8.76E-74	1.25E-70
TRANSLATION	762	127	EIF6, RPL18,	6.81	6.52E-73	1.14E-69
RIBONUCLEOPROTEIN COMPLEX	757	151	MRPS36, RPL	4.95	7.70E-66	1.10E-62
MITOCHONDRIAL PART	757	162	MRPS36, MR	4.60	7.95E-66	1.13E-62
TRANSLATIONAL ELONGATION	762	64	RPL18, RPL3	11.25	1.80E-53	3.13E-50
CYTOSOLIC RIBOSOME	757	57	RPL18, RPL13	11.88	3.01E-50	4.29E-47
MITOCHONDRIAL INNER MEMBRANE	757	101	NDUJFAB1, S	5.57	1.79E-48	2.55E-45
MITOCHONDRIAL ENVELOPE	757	115	TSPO, NDUJF	4.63	3.11E-46	4.43E-43
ORGANELLE INNER MEMBRANE	757	102	EIF6, NDUJFA	5.23	3.86E-46	5.50E-43
MITOCHONDRIAL MEMBRANE	757	111	TSPO, NDUJF	4.76	8.80E-46	1.25E-42
CYTOSOLIC PART	757	66	RPL18, RPL13	7.33	5.95E-40	8.48E-37
LARGE RIBOSOMAL SUBUNIT	757	45	RPL18, MRPL	11.34	3.91E-38	5.57E-35
MITOCHONDRIAL MEMBRANE PART	757	57	UQCRC2, TIM	7.70	7.29E-36	1.04E-32
SMALL RIBOSOMAL SUBUNIT	757	42	MRPS36, MR	11.26	2.33E-35	3.32E-32
ORGANELLE ENVELOPE	757	125	EIF6, TSPO, N	3.40	2.62E-35	3.74E-32
ENVELOPE	757	125	EIF6, TSPO, N	3.39	3.68E-35	5.24E-32
ORGANELLAR RIBOSOME	757	36	MRPS36, MR	12.66	4.44E-33	6.32E-30
MITOCHONDRIAL RIBOSOME	757	36	MRPS36, MR	12.66	4.44E-33	6.32E-30
STRUCTURAL MOLECULE ACTIVITY	706	114	RPL18, MRPS	3.31	8.16E-31	1.25E-27
GENERATION OF PRECURSOR METABOLITES AND ENERGY	762	78	UQCRC2, LDH	4.42	1.93E-29	3.36E-26
RESPIRATORY CHAIN	757	40	UQCRC2, ND	9.01	2.02E-28	2.88E-25
OXIDATIVE PHOSPHORYLATION	762	44	UQCRC2, ND	7.97	3.47E-28	6.04E-25
ELECTRON TRANSPORT CHAIN	762	45	UQCRC2, ND	7.01	5.29E-26	9.21E-23
CYTOSOLIC SMALL RIBOSOMAL SUBUNIT	757	29	MRPS36, RPS	12.24	7.04E-26	1.50E-22
MITOCHONDRIAL RESPIRATORY CHAIN	757	35	UQCRC2, ND	9.23	2.43E-23	3.47E-22
ORGANELLE MEMBRANE	757	152	EIF6, TSPO, V	2.34	2.34E-24	3.34E-21
CYTOSOL	757	172	ITGB3BP, RP	2.18	2.81E-24	4.00E-21
CYTOSOLIC LARGE RIBOSOMAL SUBUNIT	757	27	RPL18, RPL13	12.00	1.04E-23	1.48E-20
NADH DEHYDROGENASE (UBIQUINONE) ACTIVITY	706	27	NDUJF3, ND	11.55	1.38E-22	2.11E-19
NADH DEHYDROGENASE ACTIVITY	706	27	NDUJF3, ND	11.55	1.38E-22	2.11E-19
NADH DEHYDROGENASE (QUINONE) ACTIVITY	706	27	NDUJF3, ND	11.55	1.38E-22	2.11E-19
MITOCHONDRIAL RESPIRATORY CHAIN COMPLEX I	757	27	NDUJF3, ND	10.85	5.06E-22	7.21E-19
RESPIRATORY CHAIN COMPLEX I	757	27	NDUJF3, ND	10.85	5.06E-22	7.21E-19
NADH DEHYDROGENASE COMPLEX	757	27	NDUJF3, ND	10.85	5.06E-22	7.21E-19
MITOCHONDRIAL ELECTRON TRANSPORT, NADH TO UBIQUINONE	762	26	NDUJF3, ND	10.99	3.82E-21	6.65E-18
RNA BINDING	706	105	RPL18, RPL3	2.69	4.77E-21	7.28E-18
CELLULAR RESPIRATION	762	37	UQCRC2, ND	6.77	7.96E-21	1.39E-17
OXIDOREDUCTASE ACTIVITY, ACTING ON NADH OR NADPH, QUINONE OR SIMILAR COMPOUND AS ACCEPTOR	706	27	NDUJF3, ND	10.13	1.38E-20	2.11E-17
MITOCHONDRIAL LUMEN	757	56	MRPS36, MR	4.17	5.59E-20	7.97E-17
MITOCHONDRIAL MATRIX	757	56	MRPS36, MR	4.17	5.59E-20	7.97E-17
ATP SYNTHESIS COUPLED ELECTRON TRANSPORT	762	28	NDUJF3, ND	8.88	1.68E-19	2.93E-16
MITOCHONDRIAL ATP SYNTHESIS COUPLED ELECTRON TRANSPORT	762	28	NDUJF3, ND	8.88	1.68E-19	2.93E-16
RESPIRATORY ELECTRON TRANSPORT CHAIN	762	29	NDUJF3, ND	8.04	9.39E-19	1.64E-15
MEMBRANE-ENCLOSED LUMEN	757	19	ITGB3BP, RP	1.80	3.89E-18	5.58E-15
ENERGY DERIVATION BY OXIDATION OF ORGANIC COMPOUNDS	762	40	UQCRC2, ND	9.23	2.43E-17	3.47E-14
INTRACELLULAR ORGANELLE LUMEN	706	186	EIF6, MRPS3	1.77	9.13E-16	1.27E-12
OXIDOREDUCTASE ACTIVITY, ACTING ON NADH OR NADPH	706	29	NDUJF3, ND	6.43	1.30E-15	2.03E-12
HYDROGEN ION TRANSMEMBRANE TRANSPORTER ACTIVITY	706	30	ATP6V0E1, C	6.13	1.69E-15	2.54E-12
ORGANELLE LUMEN	757	187	EIF6, MRPS3	1.73	4.16E-15	6.01E-12
MONOVALENT INORGANIC CATION TRANSMEMBRANE TRANSPORTER ACTIVITY	706	30	ATP6V0E1, C	5.30	1.13E-13	1.73E-10
ORGANELLAR LARGE RIBOSOMAL SUBUNIT	757	14	MRPL1, MRP	13.13	6.38E-13	9.09E-10
MITOCHONDRIAL LARGE RIBOSOMAL SUBUNIT	757	14	MRPL1, MRP	13.13	6.38E-13	9.09E-10
NCRNA PROCESSING	762	40	HSD17B10, P	3.80	6.84E-13	1.19E-09
RNA PROCESSING	762	74	RPL36A, RPL	2.40	3.30E-12	5.74E-09
RIBOSOME BIOGENESIS	762	31	EIF6, RPL14,	4.51	3.90E-12	6.80E-09
RIBONUCLEOPROTEIN COMPLEX BIOGENESIS	762	38	EIF6, RPL14,	3.75	4.26E-12	7.41E-09
OXIDATION REDUCTION	762	80	UQCRC2, SEF	2.22	2.08E-11	3.62E-08
ANAPHASE-PROMOTING COMPLEX-DEPENDENT PROTEASOMAL UBIQUITIN-DEPENDENT PROTEIN CATABOLIC PROCESS	762	22	ANAPC10, CE	6.01	2.50E-11	4.34E-08
NEGATIVE REGULATION OF UBIQUITIN-PROTEIN LIGASE ACTIVITY DURING MITOTIC CELL CYCLE	762	22	ANAPC10, CE	6.01	2.50E-11	4.34E-08
THREONINE-TYPE ENDOPEPTIDASE ACTIVITY	706	13	PSMA7, PSM	11.95	5.06E-11	7.72E-08
THREONINE-TYPE PEPTIDASE ACTIVITY	706	13	PSMA7, PSM	11.95	5.06E-11	7.72E-08
NEGATIVE REGULATION OF UBIQUITIN-PROTEIN LIGASE ACTIVITY	762	22	ANAPC10, CE	5.83	4.79E-11	8.34E-08
NEGATIVE REGULATION OF LIGASE ACTIVITY	762	22	ANAPC10, CE	5.83	4.79E-11	8.34E-08
NEGATIVE REGULATION OF PROTEIN UBIQUITINATION	762	22	ANAPC10, CE	5.83	4.79E-11	8.34E-08
POSITIVE REGULATION OF UBIQUITIN-PROTEIN LIGASE ACTIVITY DURING MITOTIC CELL CYCLE	762	22	ANAPC10, CE	5.74	6.57E-11	1.04E-07
PROTEASOME CORE COMPLEX	757	13	PSMA7, PSM	10.98	1.37E-10	1.95E-07
POSITIVE REGULATION OF UBIQUITIN-PROTEIN LIGASE ACTIVITY	762	22	ANAPC10, CE	5.58	1.21E-10	2.11E-07
NCRNA METABOLIC PROCESS	762	41	HSD17B10, E	3.16	1.37E-10	2.38E-07
REGULATION OF UBIQUITIN-PROTEIN LIGASE ACTIVITY DURING MITOTIC CELL CYCLE	762	22	ANAPC10, CE	5.50	1.63E-10	2.84E-07
POSITIVE REGULATION OF LIGASE ACTIVITY	762	22	ANAPC10, CE	5.35	2.90E-10	5.06E-07
INTRACELLULAR NON-MEMBRANE-BOUNDED ORGANELLE	757	224	ITGB3BP, RP	1.46	3.71E-10	5.29E-07
NON-MEMBRANE-BOUNDED ORGANELLE	757	224	ITGB3BP, RP	1.46	3.71E-10	5.29E-07
INORGANIC CATION TRANSMEMBRANE TRANSPORTER ACTIVITY	706	31	ATP6V0E1, C	7.78	4.68E-10	7.14E-07
MITOCHONDRIAL SMALL RIBOSOMAL SUBUNIT	757	12	MRPS36, MR	11.26	6.27E-10	8.93E-07
ORGANELLAR SMALL RIBOSOMAL SUBUNIT	757	12	MRPS36, MR	11.26	6.27E-10	8.93E-07
POSITIVE REGULATION OF PROTEIN UBIQUITINATION	762	23	NDJF1, ANA	4.86	8.02E-10	1.40E-06
RRNA PROCESSING	762	24	RPL35A, RPL	4.63	9.01E-10	1.57E-06
PROTON-TRANSPORTING ATP SYNTHASE COMPLEX, COUPLING FACTOR F(0)	757	11	ATP5J2, ATP	12.38	1.13E-09	1.61E-06
REGULATION OF PROTEIN UBIQUITINATION	762	25	NDJF1, ANA	4.44	9.57E-10	1.67E-06
REGULATION OF UBIQUITIN-PROTEIN LIGASE ACTIVITY	762	22	ANAPC10, CE	5.01	1.12E-09	1.95E-06
PROTEASOMAL UBIQUITIN-DEPENDENT PROTEIN CATABOLIC PROCESS	762	25	DERL2, ANAF	4.35	1.47E-09	2.57E-06
PROTEASOMAL PROTEIN CATABOLIC PROCESS	762	25	DERL2, ANAF	4.35	1.47E-09	2.57E-06
PROTON-TRANSPORTING TWO-SECTOR ATPASE COMPLEX, PROTON-TRANSPORTING DOMAIN	757	13	ATP5J2, ATP	9.15	2.35E-09	3.35E-06
PROTON-TRANSPORTING TWO-SECTOR ATPASE COMPLEX	757	17	ATP5J2, ATP	6.38	2.46E-09	3.51E-06
RNA METABOLIC PROCESS	762	24	RPL35A, RPL	4.44	2.23E-09	3.86E-06
REGULATION OF LIGASE ACTIVITY	762	22	ANAPC10, CE	4.82	2.38E-09	4.14E-06
PROTON-TRANSPORTING ATP SYNTHASE COMPLEX	757	12	ATP5J2, ATP	9.65	5.89E-09	8.40E-06
PROTEASOME COMPLEX	757	19	PSMA7, PSM	5.26	7.58E-09	1.08E-05
MITOCHONDRION ORGANIZATION	762	28	BID, TSPO, S	3.60	1.06E-08	1.84E-05
MITOCHONDRIAL PROTON-TRANSPORTING ATP SYNTHASE COMPLEX	757	11	ATP5J2, ATP	9.78	2.80E-08	3.99E-05
NEGATIVE REGULATION OF PROTEIN MODIFICATION PROCESS	762	25	TAF7, ANAP	3.73	3.76E-08	6.55E-05
OXIDOREDUCTASE ACTIVITY, ACTING ON HEME GROUP OF DONORS, OXYGEN AS ACCEPTOR	706	12	COX7A2, COX	7.88	1.03E-07	1.57E-04
OXIDOREDUCTASE ACTIVITY, ACTING ON HEME GROUP OF DONORS	706	12	COX7A2, COX	7.88	1.03E-07	1.57E-04
CYTOCHROME-C OXIDASE ACTIVITY	706	12	COX7A2, COX	7.88	1.03E-07	1.57E-04
HEME-COPPER TERMINAL OXIDASE ACTIVITY	706	12	COX7A2, COX	7.88	1.03E-07	1.57E-04
RRNA BINDING	706	12	MRPL11, MR	7.61	1.58E-07	2.41E-04
ATP SYNTHESIS COUPLED PROTON TRANSPORT	762	14	ATP6V1C2, A	6.21	1.49E-07	2.59E-04
ENERGY COUPLED PROTON TRANSPORT, DOWN ELECTROCHEMICAL GRADIENT	762	14	ATP6V1C2, A	6.21	1.49E-07	2.59E-04
PROTON TRANSPORT	762	16	ATP6V0E1, A	4.66	9.69E-07	1.69E-03
TRANSLATION REGULATOR ACTIVITY	706	11	MRPL11, DA2	6.98	1.63E-06	2.49E-03
PROTEIN LOCALIZATION IN MITOCHONDRION	762	12	BID, TSPO, T	6.27	1.44E-06	2.51E-03
PROTEIN TARGETING TO MITOCHONDRION	762	12	BID, TSPO, T	6.27	1.44E-06	2.51E-03
HYDROGEN TRANSPORT	762	16	ATP6V0E1, A	4.51	1.51E-06	2.63E-03
IRON-SULFUR CLUSTER BINDING	706	14	FOX1, UQCRC	5.13	1.75E-06	2.67E-03
METAL CLUSTER BINDING	706	14	FOX1, UQCRC	5.13	1.75E-06	2.67E-03
RNA ELONGATION FROM RNA POLYMERASE II PROMOTER	762	14	POLR2H, POL	5.18	1.57E-06	2.74E-03
NUCLEAR LUMEN	757	128	EIF6, ITGB3B	1.49	2.43E-06	3.46E-03
ION TRANSMEMBRANE TRANSPORT	762	14	ATP6V1C2, A	5.07	2.03E-06	3.53E-03
RNA ELONGATION	762	14	POLR2H, POL	4.87	3.32E-06	5.77E-03
PEROXIDASE ACTIVITY	706	11	MGST3, GPX	6.32	4.53E-06	6.92E-03
OXIDOREDUCTASE ACTIVITY, ACTING ON PEROXIDE AS ACCEPTOR	706	11	MGST3, GPX	6.32	4.53E-06	6.92E-03
COFACTOR METABOLIC PROCESS	762	29	LDHB, TSPO,	2.64	4.45E-06	7.75E-03