

Supplementary Table 16 Gene ontology enrichment analysis of MRs differentially activated in ATRX mutant compared with ATRX wild type LGM6 glioma.

Supplementary Table 16a Gene ontology terms significantly enriched for the inferred targets of the 10 most active MRs in ATRX mutant.

GO Term	originalGeneSetSize	actualGeneSetSize	Genes	Fold Enrichment	p-value	q-value
NON-MEMBRANE-BOUNDED ORGANELLE	552	205	ALS2, TGOLN2, CTTNBP2N	1.83	7.91E-21	1.12E-17
INTRACELLULAR NON-MEMBRANE-BOUNDED ORGANELLE	552	205	ALS2, TGOLN2, CTTNBP2N	1.83	7.91E-21	1.12E-17
TRANSCRIPTION	665	184	EIF2C2, EIF2C1, ARNT2, HIRA	1.78	2.84E-16	5.88E-13
REGULATION OF TRANSCRIPTION	665	212	EIF2C2, EIF2C1, HIRA, ZNF638	1.66	1.79E-15	3.13E-12
CYTOSKELETON	552	123	CTTNBP2NL, ALS2, DYNC1L1	2.06	2.74E-15	3.92E-12
MICROTUBULE CYTOSKELETON	552	67	ALS2, DYNC1L12, KIAA0368	2.83	2.15E-14	3.03E-11
ZINC ION BINDING	652	187	PLEKHM1, ZXDB, ZNF638, ZNF639	1.61	2.55E-12	3.84E-09
DNA BINDING	652	186	PRR12, ARNT2, HIRA, ZNF638	1.59	1.10E-11	1.65E-08
CHROMATIN MODIFICATION	665	43	RSF1, SETD1B, HIRA, TRRAP	3.19	4.00E-11	7.07E-08
CYTOSKELETAL PART	552	84	ALS2, DYNC1L12, KIAA0368	2.04	3.45E-10	4.87E-07
NUCLEAR LUMEN	552	112	TGOLN2, ARNT2, ZNF638	1.79	6.42E-10	9.07E-07
CHROMOSOME ORGANIZATION	665	57	RSF1, ARID4B, HIRA, BRPF1	2.39	1.86E-09	3.28E-06
TRANSCRIPTION FACTOR BINDING	652	59	ARNT2, HIRA, ZEB1, FOXO3	2.29	4.45E-09	6.69E-06
TRANSITION METAL ION BINDING	652	201	PDP2, PLEKHM1, ZNF638, ZNF639	1.44	9.04E-09	1.36E-05
CHROMATIN ORGANIZATION	665	47	RSF1, SETD1B, ARID4B, HIRA	2.53	1.10E-08	1.95E-05
NUCLEOPLASM PART	552	55	ARNT2, YLPM1, ZNF638, ZNF639	2.29	1.54E-08	2.18E-05
HEART DEVELOPMENT	665	32	RBP4, BBS5, PRKDC, SOX6	3.03	6.42E-08	1.13E-04
CELL PROJECTION	552	62	GNA13, ALS2, ADCY4, SH3BP1	2.06	8.63E-08	1.22E-04
CELLULAR COMPONENT MORPHOGENESIS	665	46	ALS2, BBS5, SSH1, SHROCK4	2.36	1.33E-07	2.35E-04
NUCLEOPLASM	552	72	ARNT2, YLPM1, ZEB1, ZNF638	1.89	1.94E-07	2.73E-04
REGULATION OF TRANSCRIPTION FROM RNA POLYMERASE	665	69	PPARA, ARNT2, HIRA, ZEB1	1.93	1.84E-07	3.25E-04
TRANSCRIPTION REGULATOR ACTIVITY	652	120	ARNT2, HIRA, FOXO3, FOXO4	1.58	2.43E-07	3.66E-04
CELL MORPHOGENESIS	665	42	ALS2, BBS5, SSH1, SHROCK4	2.40	3.16E-07	5.58E-04
GTPASE REGULATOR ACTIVITY	652	46	ALS2, USP6, RABGAP1, RABGAP2	2.27	3.95E-07	5.94E-04
POSITIVE REGULATION OF TRANSCRIPTION	665	57	PPARA, RSF1, ARNT2, FOXO3	2.06	3.57E-07	6.30E-04
MICROTUBULE ORGANIZING CENTER	552	31	ALS2, PPP4R2, BBS5, RAB11	2.84	4.77E-07	6.73E-04
METAL ION BINDING	652	267	ADCY4, EIF2C2, PDP2, PLEKHM1	1.28	4.65E-07	6.99E-04
MICROTUBULE-BASED MOVEMENT	665	21	KIF3B, KIF3A, OPA1, KIF5B	3.78	5.33E-07	9.40E-04
NUCLEOSIDE-TRIPHOSPHATASE REGULATOR ACTIVITY	652	46	ALS2, USP6, RABGAP1, RABGAP2	2.22	7.32E-07	1.10E-03
NEGATIVE REGULATION OF GENE EXPRESSION	665	52	PPARA, EIF2C2, RSF1, EIF2C1	2.10	7.01E-07	1.24E-03
MICROTUBULE-BASED PROCESS	665	33	KIF13A, PTK2, MACF1, KIF13B	2.65	8.26E-07	1.46E-03
POSITIVE REGULATION OF GENE EXPRESSION	665	57	PPARA, RSF1, ARNT2, FOXO3	2.00	9.35E-07	1.65E-03
CHORDATE EMBRYONIC DEVELOPMENT	665	39	ALS2, GNA13, ZFAND5, RAB11	2.40	9.40E-07	1.66E-03
CATION BINDING	652	267	ADCY4, EIF2C2, PDP2, PLEKHM1	1.27	1.12E-06	1.68E-03
CELL PART MORPHOGENESIS	665	33	ALS2, BBS5, COX10, MYO5A	2.62	1.08E-06	1.90E-03
EMBRYONIC DEVELOPMENT ENDING IN BIRTH OR EGG HATCHING	665	39	ALS2, GNA13, ZFAND5, RAB11	2.38	1.17E-06	2.06E-03
NEURON PROJECTION	552	36	MYO5A, ALS2, ADCY4, GRB2	2.44	1.83E-06	2.59E-03
ION BINDING	652	269	ADCY4, EIF2C2, PDP2, PLEKHM1	1.26	1.88E-06	2.82E-03
REGULATION OF TRANSCRIPTION, DNA-DEPENDENT	665	130	ARNT2, HIRA, FOXO3, FOXO4	1.49	1.73E-06	3.06E-03
CYTOSKELETON ORGANIZATION	665	46	ABLIM1, SSH1, SHROOM4	2.15	1.86E-06	3.29E-03
POSITIVE REGULATION OF NUCLEOBASE, NUCLEOSIDE, NUCLEOTIDE METABOLISM	665	59	PPARA, RSF1, ARNT2, FOXO3	1.92	1.91E-06	3.37E-03
MICROTUBULE	552	31	DYNC1L12, KIF13A, INCENP	2.62	2.57E-06	3.63E-03
CYTOSKELETAL PROTEIN BINDING	652	51	HIP1R, TLN2, FER, PACSIN1	2.01	2.88E-06	4.33E-03
INTRACELLULAR ORGANELLE LUMEN	552	116	TGOLN2, PDP2, ARNT2, ZNF638	1.51	3.25E-06	4.60E-03
ATP BINDING	652	113	ADCY4, DYNC1L12, PRPF4B	1.52	3.70E-06	5.56E-03
MICROTUBULE MOTOR ACTIVITY	652	16	KIF3B, KIF3A, KIF5B, KIF5A	4.14	5.27E-06	7.92E-03
CHROMATIN BINDING	652	23	SATB2, SVEP1, UPF1, MLL2	3.05	5.50E-06	8.27E-03
TRANSCRIPTION COFACTOR ACTIVITY	652	40	HIRA, HCF1, ZEB1, TRRAP	2.19	5.73E-06	8.61E-03
POSITIVE REGULATION OF NITROGEN COMPOUND METABOLISM	665	59	PPARA, RSF1, ARNT2, FOXO3	1.86	5.14E-06	9.07E-03
IN UTERO EMBRYONIC DEVELOPMENT	665	25	ALS2, GNA13, ZFAND5, RAB11	2.89	5.32E-06	9.39E-03
REGULATION OF RNA METABOLIC PROCESS	665	130	ARNT2, HIRA, FOXO3, FOXO4	1.46	5.45E-06	9.62E-03