Supplementary Table 15 List of MRs differentially activated in *ATRX* mutant compared with *ATRX* wild type high-grade LGm6 glioma.

MRs	originalGeneSetCount	actualGeneSetCount	NES	odd_NES	logit2_NES	p-value	q-value	fold activity	p-value_wTest	q-value_wTest
KTN1	122	122	0.8338	5.0177	2.3270	3.43E-37	8.57E-37	0.7088	3.20E-05	3.24E-02
DST	244	244	0.8642	6.3638	2.6699	1.17E-85	2.92E-84	0.8028	3.20E-05	3.24E-02
CBL	162	162	0.7905	3.7737	1.9160	2.44E-37	6.49E-37	0.5946	6.77E-05	4.57E-02
CHD2	162	162	0.8563	5.9566	2.5745	2.92E-55	1.64E-54	0.8084	4.46E-04	6.17E-02
TRIP11	144	144	0.7975	3.9382	1.9775	6.08E-35	1.31E-34	0.5732	5.12E-04	6.17E-02
NSD1	201	201	0.8512	5.7193	2.5158	3.76E-66	3.36E-65	0.6989	5.86E-04	6.17E-02
GOLGA4	110	110	0.7543	3.0699	1.6182	2.99E-20	4.20E-20	0.4770	6.69E-04	6.17E-02
FOXN3	151	151	0.7554	3.0888	1.6270	2.20E-27	3.76E-27	0.5413	6.69E-04	6.17E-02
MAML2	206	206	0.8162	4.4394	2.1503	3.01E-55	1.64E-54	0.6731	6.69E-04	6.17E-02
KLF13	229	229	0.8470	5.5344	2.4684	2.77E-73	3.85E-72	0.6901	7.63E-04	6.72E-02
PHF3	110	110	0.8054	4.1374	2.0487	1.75E-28	3.08E-28	0.6434	9.85E-04	7.10E-02
PROX1	157	157	0.7914	3.7933	1.9234	1.89E-36	4.38E-36	0.6306	1.12E-03	7.10E-02
HELZ	143	143	0.8203	4.5653	2.1907	5.72E-40	1.79E-39	0.6294	1.26E-03	7.10E-02
NCOR1	251	251	0.8309	4.9126	2.2965	5.45E-73	6.81E-72	0.6790	1.26E-03	7.10E-02
WDFY3	202	202	0.8612	6.2023	2.6328	3.41E-70	3.28E-69	0.8037	1.42E-03	7.59E-02
SKIL	101	101	0.7891	3.7412	1.9035	9.72E-24	1.54E-23	0.5295	1.60E-03	7.73E-02
MGA	104	104	0.8228	4.6424	2.2149	5.29E-30	9.87E-30	0.6566	1.60E-03	7.73E-02
CLIP1	191	191	0.7662	3.2768	1.7123	6.20E-37	1.52E-36	0.5252	1.80E-03	8.29E-02
SLTM	207	207	0.8063	4.1629	2.0576	3.26E-52	1.57E-51	0.6257	2.26E-03	9.75E-02
MYST3	191	191	0.8434	5.3861	2.4292	2.66E-60	1.96E-59	0.7271	2.26E-03	9.75E-02
ROCK1	128	128	0.8020	4.0516	2.0185	3.54E-32	7.37E-32	0.5877	2.82E-03	1.10E-01
ZFHX3	230	230	0.7971	3.9278	1.9737	1.94E-54	1.01E-53	0.5965	3.14E-03	1.20E-01
SON	317	317	0.7985	3.9630	1.9866	8.57E-75	1.34E-73	0.6148	3.89E-03	1.29E-01
CLOCK	78	78	0.7697	3.3417	1.7406	1.75E-16	2.21E-16	0.5196	4.31E-03	1.30E-01
ZMIZ1	320	320	0.7888	3.7347	1.9010	9.24E-71	9.63E-70	0.5748	4.31E-03	1.30E-01
GOLGB1	247	247	0.7485	2.9765	1.5736	2.49E-41	8.00E-41	0.4877	4.77E-03	1.33E-01
ARHGEF12	188	188	0.7465	2.9446	1.5581	1.92E-31	3.88E-31	0.5261	4.77E-03	1.33E-01
NCOA3	124	124	0.7989	3.9721	1.9899	1.30E-30	2.50E-30	0.6131	5.28E-03	1.36E-01
MECP2	181	181	0.7483	2.9737	1.5723	8.93E-31	1.77E-30	0.4805	5.83E-03	1.36E-01
THRAP3	55	55	0.7801	3.5473	1.8267	6.58E-13	7.61E-13	0.5530	5.83E-03	1.36E-01
SP2	131	131	0.7815	3.5777	1.8390	8.51E-29	1.52E-28	0.6088	5.83E-03	1.36E-01
HUWE1	245	245	0.7566	3.1087	1.6363	1.31E-43	4.30E-43	0.4819	6.43E-03	1.37E-01
NCOA2	182	182	0.7699	3.3466	1.7427	3.07E-36	6.98E-36	0.5307	6.43E-03	1.37E-01
MED13L	178	178	0.7769	3.4823	1.8000	2.99E-37	7.63E-37	0.5536	6.43E-03	1.37E-01
AFF4	190	190	0.7414	2.8670	1.5195	1.58E-30	2.99E-30	0.4749	7.08E-03	1.37E-01
FYCO1	181	181	0.7685	3.3198	1.7311	1.09E-35	2.43E-35	0.5317	7.08E-03	1.37E-01
TRIM44	219	219	0.7947	3.8720	1.9531	3.68E-51	1.64E-50	0.5668	7.08E-03	1.37E-01
SPEN	178	178	0.8172	4.4710	2.1606	2.42E-48	1.01E-47	0.6775	7.08E-03	1.37E-01
RSF1	205	205	0.8390	5.2129	2.3821	5.73E-63	4.77E-62	0.7405	7.78E-03	1.40E-01
EP300	149	149	0.7669	3.2897	1.7179	2.25E-29	4.08E-29	0.4892	9.37E-03	1.52E-01
KLF3	75	75	0.7809	3.5635	1.8333	3.97E-17	5.11E-17	0.5176	9.37E-03	1.52E-01
HOXC13	73	73	0.2109	0.2672	-1.9039	1.28E-17	1.69E-17	-0.6232	9.37E-03	1.52E-01
MED7	178	178	0.2167	0.2767	-1.8537	6.61E-39	1.97E-38	-0.5450	9.37E-03	1.52E-01
SNRPB2	112	112	0.2284	0.2960	-1.7562	2.94E-23	4.53E-23	-0.5265	9.37E-03	1.52E-01
ING4	246	246	0.2324	0.3027	-1.7239	1.84E-47	7.17E-47	-0.4891	9.37E-03	1.52E-01
HOXD11	35	35	0.2178	0.2784	-1.8449	7.46E-09	7.83E-09	-0.6402	8.54E-03	1.48E-01
AIP	179	179	0.2510	0.3351	-1.5774	1.30E-30	2.50E-30	-0.4528	8.54E-03	1.48E-01
SCAND1	162	162	0.1997	0.2495	-2.0027	8.88E-40	2.71E-39	-0.5412	7.78E-03	1.40E-01
RPL27	343	343	0.1953	0.2427	-2.0427	5.45E-84	1.14E-82	-0.6053	7.08E-03	1.37E-01
NR5A2	215	215	0.2546	0.3415	-1.5500	2.19E-35	4.81E-35	-0.4817	7.08E-03	1.37E-01
RPL35A	210	210	0.1924	0.2382	-2.0698	2.22E-53	1.11E-52	-0.6220	6.43E-03	1.37E-01
SNRPC	112	112	0.1976	0.2462	-2.0221	1.88E-28	3.27E-28	-0.5748	5.83E-03	1.36E-01
SMARCD3	179	179	0.2217	0.2849	-1.8117	8.24E-38	2.34E-37	-0.5116	5.83E-03	1.36E-01
RNF7	154	154	0.1998	0.2496	-2.0022	6.78E-38	1.97E-37	-0.6505	5.28E-03	1.36E-01
NDUFA13	168	168	0.1897	0.2341	-2.0947	7.59E-44	2.56E-43	-0.5547	5.28E-03	1.36E-01
PFDN5	350	350	0.1805	0.2203	-2.1823	5.91E-94	2.46E-92	-0.6159	4.77E-03	1.33E-01
OGG1	107	107	0.2426	0.3203	-1.6425	3.43E-20	4.76E-20	-0.4900	4.77E-03	1.33E-01
HSBP1	195	195	0.1972	0.2456	-2.0256	3.11E-48	1.25E-47	-0.6017	4.31E-03	1.30E-01
EIF3I	179	179	0.1570	0.1863	-2.4245	1.63E-56	1.07E-55	-0.6623	3.89E-03	1.29E-01
CCRN4L	205	205	0.2418	0.3189	-1.6488	2.89E-37	7.52E-37	-0.5092	3.89E-03	1.29E-01
GTF3A	81	81	0.2488	0.3312	-1.5940	5.34E-15	6.42E-15	-0.4665	3.89E-03	1.29E-01
GTF2B	221	221	0.2204	0.2827	-1.8226	1.28E-46	4.58E-46	-0.5469	3.50E-03	1.27E-01
TCEB2	181	181	0.1997	0.2496	-2.0023	3.40E-44	1.18E-43	-0.5691	2.82E-03	1.10E-01
CCNH	119	119	0.2247	0.2898	-1.7868	3.07E-25	5.12E-25	-0.5364	2.82E-03	1.10E-01
HOXA1	27	27	0.2233	0.2874	-1.7987	6.40E-07	6.46E-07	-0.5324	2.53E-03	1.07E-01
STRAP	123	123	0.2253	0.2908	-1.7821	6.28E-26	1.06E-25	-0.5637	2.26E-03	9.75E-02
PFDN1	146	146	0.1498	0.1762	-2.5050	2.17E-48	9.35E-48	-0.7235	1.60E-03	7.73E-02
SSBP1	144	144	0.1535	0.1814	-2.4629	8.94E-47	3.29E-46	-0.7077	1.60E-03	7.73E-02
RCHY1	215	215	0.2017	0.2526	-1.9849	1.89E-51	8.73E-51	-0.5465	1.42E-03	7.59E-02
COX7B	285	285	0.1301	0.1495	-2.7414	1.16E-102	1.45E-100	-0.7622	1.26E-03	7.10E-02
POLR2K	209	209	0.1315	0.1514	-2.7237	1.88E-75	3.35E-74	-0.7404	1.26E-03	7.10E-02
HOXC6	49	49	0.1728	0.2089	-2.2589	2.26E-15	2.75E-15	-0.6904	1.26E-03	7.10E-02
ZNHIT1	281	281	0.1569	0.1861	-2.4261	2.15E-87	6.71E-86	-0.6861	1.26E-03	7.10E-02
COPS5	166	166	0.2147	0.2734	-1.8711	6.45E-37	1.55E-36	-0.5243	1.26E-03	7.10E-02
MESP1	167	167	0.2169	0.2770	-1.8519	1.43E-36	3.37E-36	-0.5164	1.26E-03	7.10E-02
POLR3K	181	181	0.1601	0.1906	-2.3910	3.98E-56	2.37E-55	-0.6727	9.85E-04	7.10E-02
ZNF593	201	201	0.1744	0.2112	-2.2432	3.96E-57	2.75E-56	-0.6304	9.85E-04	7.10E-02
ELK1	127	127	0.2453	0.3251	-1.6210	3.51E-23	5.35E-23	-0.5029	9.85E-04	7.10E-02
CNBP	143	143	0.2048	0.2576	-1.9570	3.35E-34	7.09E-34	-0.6007	6.69E-04	6.17E-02
PRPF19	98	98	0.2269	0.2934	-1.7689	8.86E-21	1.28E-20	-0.5151	6.69E-04	6.17E-02
C1QBP	184	184	0.1449	0.1694	-2.5614	4.37E-62	3.41E-61	-0.6908	5.86E-04	6.17E-02
SEC13	146	146	0.1936	0.2401	-2.0584	1.90E-37	5.17E-37	-0.6835	5.12E-04	6.17E-02
MED31	317	317	0.1510	0.1778	-2.4913	1.53E-101	9.55E-100	-0.6612	5.12E-04	6.17E-02
BRF2	105	105	0.2117	0.2686	-1.8964	1.76E-24	2.90E-24	-0.5867	5.12E-04	6.17E-02
MRPL24	142	142	0.2133	0.2712	-1.8826	3.87E-32	7.94E-32	-0.5265	3.87E-04	6.17E-02
ZNHIT3	227	227	0.1533	0.1810	-2.4657	1.45E-72	1.65E-71	-0.6791	2.15E-04	6.17E-02
TCEB1	162	162	0.1402	0.1631	-2.6161	2.54E-56	1.59E-55	-0.7758	1.84E-04	6.17E-02
SUPT4H1	161	161	0.1699	0.2046	-2.2888	2.01E-47	7.62E-47	-0.6592	1.13E-04	4.60E-02
POLR2I	129	129	0.1733	0.2097	-2.2538	1.26E-37	3.49E-37	-0.6340	1.13E-04	4.60E-02