

Table S1. Regions of copy number alteration and the corresponding genes among four tumors from Atad5+/m mice.

ChrNumber	ProbeName	Start	Stop	Deletion	Amplification
chr1	A_67_P04010830	9884081	9884140	0	25
chr1	A_53_P127556	17723913	17723972	0	25
chr1	A_53_P127556	17723913	17723972	0	25
chr1	A_53_P127556	17723913	17723972	0	25
chr1	A_53_P127501	17741507	17741566	0	25
chr1	A_67_P04055333	32621242	32621301	25	0
chr1	A_53_P163710	36210559	36210618	0	25
chr1	A_53_P111377	39494205	39494264	0	25
chr1	A_67_P04111240	58801090	58801149	0	25
chr1	A_67_P00100290	72235377	72235436	25	0
chr1	A_67_P04212616	106703566	106703625	25	0
chr1	A_67_P04316715	157349593	157349652	50	0
chr1	A_67_P00238028	165814781	165814840	0	25
chr1	A_67_P00247956	171555916	171555975	0	25
chr1	A_67_P04379846	184316327	184316386	0	25
chr2	A_53_P122881	4900498	4900557	0	25
chr2	A_53_P140447	29688284	29688338	25	0
chr2	A_53_P140339	29690643	29690702	25	0
chr2	A_53_P126333	29694550	29694604	25	0
chr2	A_53_P149149	30007128	30007187	0	25
chr2	A_53_P142959	38182019	38182069	25	0
chr2	A_53_P142959	38182019	38182069	25	0
chr2	A_53_P142959	38182019	38182069	25	0
chr2	A_67_P04497742	42163870	42163929	50	0
chr2	A_53_P124470	65156156	65156214	0	25
chr2	A_67_P04546499	65179814	65179873	0	25
chr2	A_67_P04546499	65179814	65179873	0	25
chr2	A_67_P04546499	65179814	65179873	0	25
chr2	A_67_P04610311	93668807	93668866	25	0
chr2	A_53_P143963	102910708	102910767	25	0
chr2	A_53_P130345	127057207	127057258	0	50
chr2	A_53_P165807	127057461	127057519	0	50
chr2	A_53_P146037	127058196	127058246	0	50
chr2	A_53_P142604	127078793	127078852	0	50
chr2	A_53_P142604	127078793	127078852	0	50
chr2	A_53_P142604	127078793	127078852	0	50
chr2	A_53_P175034	132537535	132537594	0	25
chr2	A_53_P122355	132546377	132546436	0	25
chr2	A_53_P108325	132555577	132555636	0	25
chr2	A_67_P04754545	157053447	157053506	25	0
chr2	A_53_P133949	167875056	167875115	25	0
chr2	A_53_P138401	167892101	167892160	25	0
chr2	A_53_P137188	167895601	167895660	25	0
chr2	A_53_P137188	167895601	167895660	25	0
chr2	A_53_P137188	167895601	167895660	25	0
chr2	A_53_P173360	167901807	167901866	25	0
chr2	A_53_P130759	172627871	172627930	50	0
chr2	A_53_P150980	172634873	172634932	50	0
chr2	A_53_P119738	172645445	172645504	50	0
chr2	A_53_P124390	181599311	181599370	25	0
chr3	A_53_P165905	67061180	67061239	25	0
chr3	A_53_P165905	67061180	67061239	25	0
chr3	A_53_P165905	67061180	67061239	25	0
chr3	A_53_P111210	67063507	67063566	25	0
chr3	A_53_P144597	67068194	67068253	25	0
chr3	A_53_P168889	105097650	105097709	25	0
chr3	A_67_P05025592	108722263	108722322	0	25
chr3	A_53_P104868	127553166	127553225	0	25
chr3	A_53_P153389	127554177	127554236	0	25
chr3	A_53_P119858	127578083	127578142	0	25
chr3	A_53_P119858	127578083	127578142	0	25
chr3	A_53_P119858	127578083	127578142	0	25
chr4	A_53_P171194	6871304	6871363	25	0
chr4	A_53_P117023	25292463	25292522	0	25
chr4	A_53_P158856	108075973	108076032	25	0
chr4	A_53_P153893	116145076	116145135	0	25
chr4	A_53_P175041	116148266	116148325	0	25
chr4	A_53_P119710	116189464	116189523	0	25
chr4	A_53_P119710	116189464	116189523	0	25
chr4	A_53_P119710	116189464	116189523	0	25
chr4	A_53_P141513	116201120	116201179	0	25
chr4	A_67_P00991319	131533937	131533996	25	0
chr4	A_53_P153557	131547829	131547888	25	0
chr4	A_53_P179626	135292419	135292478	0	25
chr4	A_53_P127264	143718531	143718590	25	0
chr4	A_53_P127264	143718531	143718590	25	0
chr4	A_53_P127264	143718531	143718590	25	0
chr4	A_53_P176506	143718719	143718778	25	0
chr4	A_53_P159738	143719730	143719789	25	0
chr4	A_53_P135204	143727277	143727336	25	0
chr4	A_53_P149697	154036955	154037014	25	0
chr5	A_67_P01045598	17326606	17326665	25	0
chr5	A_53_P126590	23170604	23170663	0	25
chr5	A_53_P126590	23170604	23170663	0	25
chr5	A_53_P126590	23170604	23170663	0	25
chr5	A_53_P138609	23193207	23193266	0	25
chr5	A_53_P135438	33414961	33415020	0	25
chr5	A_67_P01077607	38089212	38089271	25	0
chr5	A_53_P108165	38108535	38108594	25	0
chr5	A_53_P175486	38109073	38109119	25	0

chr5	A_53_P123082	38109346	38109390	25	0
chr5	A_53_P162874	38111207	38111260	25	0
chr5	A_53_P173329	38113363	38113417	25	0
chr5	A_53_P128190	66556144	66556203	0	25
chr5	A_53_P171803	96198914	96198970	0	25
chr5	A_53_P174588	96211239	96211298	0	25
chr5	A_53_P167185	111078276	111078335	0	25
chr5	A_53_P122821	114719268	114719327	0	25
chr5	A_53_P168074	119026225	119026284	0	25
chr5	A_53_P124387	124864339	124864398	0	25
chr5	A_53_P172781	125678195	125678254	25	0
chr5	A_67_P05743100	130129644	130129703	25	0
chr5	A_53_P137728	136404662	136404715	25	0
chr6	A_53_P176344	18046851	18046910	25	0
chr6	A_53_P161420	40379374	40379430	25	0
chr6	A_53_P133411	51379645	51379704	0	25
chr6	A_53_P107943	51386191	51386250	0	25
chr6	A_53_P116958	53749223	53749268	0	25
chr6	A_53_P163759	53751299	53751358	0	25
chr6	A_67_P05912680	58269139	58269198	25	0
chr6	A_53_P142840	64648433	64648492	0	25
chr6	A_67_P01346282	64649017	64649076	0	25
chr6	A_67_P05924178	64668172	64668231	0	25
chr6	A_53_P166406	64669896	64669953	0	25
chr6	A_53_P177216	64671111	64671170	0	25
chr6	A_67_P05928394	66896082	66896141	0	25
chr6	A_53_P159421	81891515	81891574	0	25
chr6	A_53_P121320	83736104	83736163	25	0
chr6	A_53_P140954	90314274	90314333	0	25
chr6	A_53_P166377	90439821	90439880	0	25
chr6	A_53_P132201	92026420	92026476	0	25
chr6	A_53_P163911	92041255	92041314	0	25
chr6	A_53_P145850	92042425	92042484	0	25
chr6	A_53_P125111	113504292	113504351	0	25
chr6	A_53_P102294	113504962	113505021	0	25
chr6	A_53_P121700	114398210	114398269	0	25
chr6	A_53_P121700	114398210	114398269	0	25
chr6	A_53_P121700	114398210	114398269	0	25
chr6	A_53_P163903	115742122	115742178	0	25
chr6	A_53_P163903	115742122	115742178	0	25
chr6	A_53_P163903	115742122	115742178	0	25
chr6	A_53_P165299	122301705	122301764	0	25
chr6	A_53_P130502	129363053	129363112	0	25
chr6	A_53_P170910	132533042	132533101	0	25
chr6	A_53_P110677	132536497	132536556	0	25
chr6	A_67_P06090397	140487543	140487602	0	50
chr6	A_67_P06090397	140487543	140487602	0	50
chr6	A_67_P06090397	140487543	140487602	0	50
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chr7	A_53_P161898	19188507	19188566	0	50
chr7	A_53_P136562	30274044	30274092	25	0
chr7	A_53_P136316	30276685	30276741	25	0
chr7	A_53_P167236	30287447	30287496	25	0
chr7	A_53_P163206	44394346	44394391	25	0
chr7	A_53_P113508	44419097	44419156	25	0
chr7	A_53_P107873	45558921	45558977	25	0
chr7	A_53_P119967	47474727	47474786	0	50
chr7	A_53_P147158	102452475	102452519	25	0
chr7	A_53_P149239	102461767	102461815	25	0
chr7	A_67_P06334011	115801929	115801988	25	0
chr7	A_67_P06385766	136789565	136789624	0	25
chr7	A_53_P114561	141202973	141203032	0	25
chr7	A_53_P114840	141312737	141312796	25	0
chr7	A_53_P124983	141321624	141321668	25	0
chr7	A_53_P158538	141324859	141324909	25	0
chr7	A_53_P101441	141325525	141325576	25	0
chr7	A_53_P147986	141325836	141325882	25	0
chr7	A_53_P120897	141331624	141331683	25	0
chr7	A_53_P129660	141336674	141336733	25	0
chr8	A_53_P140537	10006559	10006617	0	25
chr8	A_53_P119390	23895107	23895166	25	0
chr8	A_53_P104738	55600809	55600868	25	0
chr8	A_53_P104738	55600809	55600868	25	0
chr8	A_53_P104738	55600809	55600868	25	0
chr8	A_67_P06529067	63773877	63773936	25	0
chr8	A_67_P06540414	69431029	69431088	0	25
chr8	A_67_P06540813	69645876	69645935	0	25
chr8	A_67_P01761875	72688021	72688080	25	25
chr8	A_53_P153143	72697767	72697826	25	25
chr8	A_53_P153143	72697767	72697826	25	25
chr8	A_53_P153143	72697767	72697826	25	25
chr8	A_53_P126910	72698917	72698976	25	25
chr8	A_53_P156271	72700060	72700119	25	25
chr8	A_53_P156271	72700060	72700119	25	25
chr8	A_53_P156271	72700060	72700119	25	25
chr8	A_67_P06546672	72721301	72721360	50	25
chr8	A_67_P06558081	78030417	78030476	25	0
chr8	A_53_P123989	86323615	86323674	0	25
chr8	A_53_P157640	86328704	86328763	0	25
chr8	A_53_P103525	86870864	86870912	25	0
chr8	A_67_P01785026	88298941	88299000	25	0
chr8	A_53_P169689	88308075	88308134	25	0

chr8	A_53_P133367	88310330	88310389	25	0
chr8	A_53_P130056	97113053	97113112	25	25
chr8	A_53_P130056	97113053	97113112	25	25
chr8	A_53_P130056	97113053	97113112	25	25
chr8	A_53_P134681	97122574	97122633	25	0
chr8	A_53_P134681	97122574	97122633	25	0
chr8	A_53_P134681	97122574	97122633	25	0
chr8	A_53_P151421	97977104	97977163	25	0
chr8	A_53_P117960	97994145	97994204	25	0
chr8	A_53_P128807	108158406	108158465	0	25
chr8	A_53_P139728	108163589	108163647	0	25
chr8	A_67_P06642295	114380612	114380671	25	0
chr8	A_67_P06673097	126685325	126685384	25	0
chr8	A_53_P170387	126703183	126703242	25	0
chr8	A_53_P125806	127759543	127759602	25	0
chr8	A_53_P132183	127779173	127779232	25	0
chr8	A_53_P132183	127779173	127779232	25	0
chr8	A_53_P132183	127779173	127779232	25	0
chr8	A_53_P120427	127779694	127779753	25	0
chr8	A_53_P101229	127781274	127781333	25	0
chr8	A_53_P120650	127796302	127796361	25	0
chr9	A_53_P139458	20867691	20867747	25	0
chr9	A_53_P150466	21023842	21023901	25	0
chr9	A_53_P162938	21023844	21023902	25	0
chr9	A_67_P01881858	21034772	21034831	25	0
chr9	A_67_P01882231	21243514	21243573	25	0
chr9	A_53_P126751	21830204	21830263	25	0
chr9	A_53_P173333	39159483	39159542	25	0
chr9	A_53_P125743	46020556	46020615	25	0
chr9	A_67_P06818387	63908740	63908799	25	0
chr9	A_67_P01969536	72476042	72476101	0	25
chr9	A_53_P158355	100757025	100757084	25	25
chr9	A_53_P158355	100757025	100757084	25	25
chr9	A_53_P158355	100757025	100757084	25	25
chr9	A_53_P162858	100766218	100766277	0	25
chr9	A_53_P162858	100766218	100766277	0	25
chr9	A_53_P162858	100766218	100766277	0	25
chr9	A_53_P112402	100781741	100781800	25	25
chr9	A_53_P117142	108240429	108240488	0	25
chr10	A_67_P06966003	6571112	65711171	25	0
chr10	A_67_P06966068	6595657	6595716	25	0
chr10	A_67_P06966068	6595657	6595716	25	0
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chr10	A_67_P06974685	10521792	10521851	50	0
chr10	A_67_P06974704	10537281	10537340	50	0
chr10	A_67_P06974704	10537281	10537340	50	0
chr10	A_67_P06974704	10537281	10537340	50	0
chr10	A_53_P180466	51444579	51444638	0	25
chr10	A_53_P120731	51447163	51447222	0	25
chr10	A_53_P120731	51447163	51447222	0	25
chr10	A_53_P120731	51447163	51447222	0	25
chr10	A_53_P179423	74979039	74979095	0	25
chr10	A_53_P104449	78690108	78690167	25	0
chr10	A_53_P171067	78712875	78712934	25	0
chr10	A_53_P101125	79386680	79386732	25	0
chr10	A_67_P07121650	79551705	79551759	25	0
chr10	A_67_P02168468	79560111	79560170	25	0
chr10	A_53_P110235	80029727	80029786	25	0
chr10	A_53_P103331	80737944	80737990	25	0
chr10	A_53_P140786	80741755	80741812	25	0
chr10	A_53_P139712	80751620	80751677	25	0
chr10	A_67_P02170711	80758816	80758875	25	0
chr10	A_53_P160230	80896536	80896580	25	0
chr10	A_53_P158295	80905798	80905848	25	0
chr10	A_67_P02171033	80914889	80914948	25	0
chr10	A_53_P172610	80926954	80927005	25	0
chr10	A_67_P07180313	105155301	105155360	0	25
chr10	A_53_P102134	127134674	127134733	25	0
chr11	A_53_P154523	49929144	49929195	0	25
chr11	A_67_P02330042	54925251	54925308	0	25
chr11	A_53_P102218	54944222	54944281	0	25
chr11	A_53_P113782	54950125	54950184	0	25
chr11	A_53_P152998	60053092	60053137	0	25
chr11	A_53_P179821	60054094	60054147	0	25
chr11	A_53_P151013	60054326	60054371	0	25
chr11	A_53_P155742	60719571	60719630	0	25
chr11	A_53_P106635	60722980	60723036	0	25
chr11	A_53_P137263	60741985	60742044	0	25
chr11	A_53_P127978	60745553	60745612	0	25
chr11	A_53_P179944	77729608	77729666	25	0
chr11	A_53_P115779	94055296	94055355	25	0
chr11	A_53_P163046	94055785	94055840	25	0
chr11	A_53_P158758	94056647	94056699	25	0
chr11	A_67_P07447225	94073941	94074000	25	0
chr11	A_53_P158918	94489888	94489947	0	25
chr11	A_53_P125833	94829857	94829916	25	0
chr11	A_53_P145038	94838417	94838476	25	0
chr11	A_53_P139517	94842731	94842781	25	0
chr11	A_53_P120174	112503933	112503988	0	25
chr11	A_53_P140072	118149288	118149347	25	0
chr11	A_53_P105331	121532307	121532366	0	25
chr11	A_53_P105331	121532307	121532366	0	25

chr11	A_53_P105331	121532307	121532366	0	25
chr12	A_67_P07540943	12362435	12362494	25	0
chr12	A_67_P07583382	34526953	34527012	25	0
chr12	A_67_P07583401	34537196	34537255	25	0
chr12	A_53_P140161	45076245	45076304	25	0
chr12	A_67_P07604830	45086611	45086670	25	0
chr12	A_67_P07629427	57246480	57246539	0	25
chr12	A_67_P07663410	74001467	74001526	0	25
chr12	A_53_P153412	81886135	81886192	0	25
chr12	A_53_P122053	99200727	99200786	0	25
chr12	A_53_P101282	103801250	103801309	0	25
chr12	A_53_P178876	103807346	103807405	0	25
chr12	A_53_P166953	103807850	103807909	0	25
chr13	A_67_P07800274	18792185	18792244	0	50
chr13	A_67_P07810826	23885875	23885934	0	25
chr13	A_53_P154257	23895497	23895556	0	25
chr13	A_53_P154257	23895497	23895556	0	25
chr13	A_53_P154257	23895497	23895556	0	25
chr13	A_53_P173873	23902797	23902856	0	25
chr13	A_67_P07818090	27155183	27155242	25	0
chr13	A_67_P07818169	27210860	27210919	25	0
chr13	A_53_P170219	101714168	101714227	0	25
chr13	A_53_P178026	101842739	101842798	25	0
chr13	A_53_P120963	105288825	105288884	0	25
chr13	A_53_P146207	105295215	105295274	0	25
chr13	A_53_P168106	105299626	105299685	0	25
chr13	A_53_P163495	106134302	106134361	0	25
chr13	A_53_P163495	106134302	106134361	0	25
chr13	A_53_P163495	106134302	106134361	0	25
chr14	A_67_P08046141	19320156	19320215	25	0
chr14	A_67_P02806702	19808158	19808216	0	25
chr14	A_53_P164346	46302419	46302478	0	25
chr14	A_53_P150330	46316577	46316636	0	25
chr14	A_67_P09541093	51406262	51406321	25	0
chr14	A_67_P09541099	51409109	51409168	25	0
chr14	A_53_P139209	51411970	51412025	25	0
chr14	A_67_P09541122	51417164	51417223	25	0
chr14	A_67_P08122673	56086711	56086770	25	0
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chrY	A_67_P09496951	784675	784734	0	75
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chrY	A_67_P09496955	786004	786063	0	75
chrY	A_67_P09496956	786266	786325	0	75
chrY	A_67_P09496957	786751	786810	0	75
chrY	A_67_P09496958	787301	787360	0	75
chrY	A_67_P09496959	787604	787663	0	75

chrY	A_67_P09496960	788271	788330	0	75
chrY	A_67_P09496961	788604	788663	0	75
chrY	A_67_P09496962	788991	789050	0	75
chrY	A_67_P09496964	790418	790477	0	50
chrY	A_67_P09496965	790754	790813	0	75
chrY	A_67_P09496967	791059	791118	0	50
chrY	A_67_P09496969	791570	791629	0	50
chrY	A_67_P09496970	792056	792115	0	50
chrY	A_67_P09496971	792392	792451	0	50
chrY	A_67_P09496972	793534	793593	0	75
chrY	A_67_P09496974	794678	794737	0	75
chrY	A_67_P09496976	795254	795313	0	50
chrY	A_67_P09496977	795793	795845	0	50
chrY	A_67_P09496979	796130	796189	0	50
chrY	A_67_P09496981	796753	796812	0	50
chrY	A_67_P09496982	798108	798167	0	50
chrY	A_67_P09496983	798920	798974	0	50
chrY	A_67_P09496984	799215	799274	0	50
chrY	A_67_P09496985	799656	799715	0	50
chrY	A_67_P09496987	800431	800490	0	50
chrY	A_67_P09496988	800792	800851	0	50
chrY	A_67_P09496989	801169	801228	0	50
chrY	A_67_P09496990	801874	801933	0	50
chrY	A_67_P09497449	1602758	1602817	0	25
chrY	A_67_P09497453	1604555	1604614	0	25
chrY	A_67_P09497459	1607051	1607110	0	25
chrY	A_67_P09497467	1609749	1609800	0	25
chrY	A_67_P09497471	1611237	1611288	0	25
chrY	A_67_P09497483	1620306	1620365	0	25
chrY	A_67_P09497492	1623398	1623449	0	25
chrY	A_67_P09497497	1625424	1625483	0	25
chrY	A_67_P09497502	1627320	1627379	0	25
chrY	A_67_P09497528	1641299	1641358	0	25
chrY	A_67_P09497556	1667176	1667235	0	25
chrY	A_67_P09497564	1669747	1669806	0	25
chrY	A_67_P09497565	1670249	1670308	0	25
chrY	A_67_P09497570	1671998	1672057	0	25
chrY	A_67_P09497573	1672749	1672808	0	25
chrY	A_67_P09497582	1677061	1677120	0	25
chrY	A_67_P09497601	1684098	1684157	0	25
chrY	A_67_P09497603	1684861	1684920	0	25
chrY	A_67_P09497606	1685953	1686012	0	25
chrY	A_67_P09497612	1699586	1699645	0	50
chrY	A_67_P09497615	1700636	1700695	0	50
chrY	A_67_P09497618	1702869	1702923	0	25
chrY	A_67_P09497620	1703624	1703673	0	50
chrY	A_67_P09497630	1708607	1708666	0	25
chrY	A_67_P09497631	1709117	1709167	0	25
chrY	A_67_P09497633	1709788	1709847	0	25
chrY	A_67_P09497635	1710446	1710498	0	25
chrY	A_67_P09497637	1711122	1711181	0	25
chrY	A_67_P09497643	1712381	1712435	0	25
chrY	A_67_P09497645	1712871	1712930	0	25
chrY	A_67_P09497647	1713604	1713661	0	25
chrY	A_67_P09497649	1714487	1714546	0	25
chrY	A_67_P09497671	1731943	1732001	0	25
chrY	A_67_P09497710	1756587	1756646	0	25
chrY	A_67_P09497721	1772303	1772362	0	25
chrY	A_67_P09497749	1788059	1788107	0	25
chrY	A_67_P09497751	1788886	1788945	0	25
chrY	A_67_P09497753	1789482	1789541	0	25
chrY	A_67_P09497762	1798851	1798910	0	50
chrY	A_67_P09497766	1800150	1800206	0	50
chrY	A_67_P09497768	1806959	1807018	0	25
chrY	A_67_P09497777	1813416	1813475	0	25
chrY	A_67_P09497778	1813881	1813940	0	25
chrY	A_67_P09497805	1823971	1824026	0	50
chrY	A_67_P09497818	1830151	1830210	0	50
chrY	A_67_P09497819	1830633	1830692	0	50
chrY	A_67_P09497821	1832953	1833012	0	50
chrY	A_67_P09497822	1834587	1834646	0	50
chrY	A_67_P09497824	1835307	1835366	0	50

The locations of copy number gain or loss observed from tumors in the mouse genome and the genes present in those regions
Deletion and amplification columns are percentage of tumors with a deletion or amplification.