

Supplementary Table 1: Mouse Duplicated Loci: FISH vs. Computational Detection of Segmental Duplications

BAC	Mouse build36 location		end	size (kb)	FISH		WGAC Analysis			WSSD Analysis		# of computational analyses supporting duplication
	chrom	start			copies	Duplicated fraction	Number of pairwise duplications	Total alignment length (bp)	WSSD_DRR	WSSD_DOC		
AC122877.3	chr14	50,578,851	50,765,399	187	4	70%	193	1,509,448	92851	92851	3	
AC124452.4	chr7	22,527,129	22,704,734	178	2	100%	232	2,274,441	177606	177606	3	
AC124511.4	chr12	24,589,359	24,660,862	72	4	100%	245	1,259,903	71504	71504	3	
AL451076.14	chrX	33,504,896	33,708,476	204	2	0%			50476	48476	2	
AL713974.9	chrX	52,415,106	52,606,708	192	2	72%	186	909,127	57341	75581	3	
AL731663.12	chr4	145,950,966	146,131,998	181	5	100%	98	625,892	179033	181033	3	
AL929496.10	chrX	25,519,678	25,773,749	254	5	100%	318	7,268,347	254072	254072	3	
RP23-110E20	chr9	20,600,331	20,802,196	202	6	99%	38	315846	0	0	1	
RP23-113M24	chr17	13,127,073	13,318,149	191	2	70%	193	1509448	65149	154259	3	
RP23-117M12	chr17	30,157,845	30,353,697	196	2	100%	232	2274441	0	0	1	
RP23-120M19	chr12	55,946,291	56,014,587	68	4	100%	245	1259903	14153	17587	3	
RP23-148B16	chr16	11,958,968	12,067,729	109	2	67%	17	110238	0	0	1	
RP23-163B8	chr7	14,323,243	14,533,887	211	2	72%	186	909127	159909	160645	3	
RP23-17N2	chr2	177,054,464	177,245,046	191	2	100%	98	625892	182582	190582	3	
RP23-193H8	chr5_random	716,299	929,912	214	2	43%	3	46120	201613	213613	3	
RP23-206D2	chr8	104,730,266	104,840,208	110	5	100%	318	7268347	0	0	1	
RP23-222O20	chr12	24,409,571	24,558,572	149	4	91%	44	282757	149001	149001	3	
RP23-263M19	chr16	37,454,777	37,564,876	110	19	18%	2	6278	0	0	1	
RP23-305K11	chr2	160,342,571	160,525,802	183	2	73%	150	1010418	0	0	1	
RP23-39A3	chr1	175,332,537	175,562,389	230	2	100%	361	2802863	16000	111625	3	
RP23-41G19	chr18	12,601,359	12,899,093	298	2	100%	534	3829128	11596	0	2	
RP23-5C1	chr9	19,428,868	19,596,387	168	2	86%	16	136374	28549	27000	3	
RP23-67O16	chr1	173,112,758	173,274,955	162	3	56%	11	76686	0	0	1	
RP23-6I17	chr7	143,310,381	143,506,735	196	2	1%	1	1219	0	0	0	

BAC clones that previously showed evidence of multisite signals by FISH are mapped to mouse build36 coordinates. The number of copies identified by metaphase FISH are shown. Segmental duplication content of region was assessed by WGAC (whole genome assembly comparison, WSSD_DRR (whole genome shotgun sequence detection using divergent read ratio) and WSSD_DOC (whole genome shotgun sequence detection using depth of coverage) (see supplementary note for details of computational methodology but note that the WSSD method detects only duplications >94% sequence identical). The number of computational approaches supporting a duplicated BAC are summarized. 21/24 of the clones show evidence of duplication (>50% of the BAC duplicated) by the assembly-based comparison while 23/24 show evidence of duplication by one of the three different measures. *We did not include three clones that showed as single signals by metaphase FISH but are mapped within regions of tandem duplication.