Supplementary Table 7: CNV region from Egan, et al overlapping with ours

chromosome	start	end	overlap (bp)	Percent of overlap with CNVs in this study	Percent of overlap with SD	Number of pairwise alignments	Average identity	CNV	Class
chr12	55997156	56223667	197365	87%	76%	5	99.46%	CNV37	Class III
chr12	82921102	82982766	47612	77%	100%	1	99.99%	CNV36	Class III
chr13	65323845	67308411	1810193	91%	89%	2069	94.72%	CNV31b	Class III
chr14	24708036	25126745	386425	92%	89%	6	99.98%	CNV29	Class III
chr14	51709828	52636158	559191	60%	91%	28	97.23%	CNV21	Class II
chr14	68207457	68425918	113813	52%	0%	52	95.74%	CNV20	Class I
chr17	6175796	6573190	317834	80%	63%	1	99.86%	CNV30	Class III
chr17	14697982	14758748	60641	100%	100%	21	92.02%	CNV27	Class II
chr17	27015633	27176394	139501	87%	0%	303	94.87%	CNV22	Class II
chr4	121183994	122047766	495490	57%	74%	141	93.56%	CNV23	Class II
chr5	14905798	15228152	231105	72%	84%	35	92.92%	CNV28	Class II
chr6	47047173	47100393	41987	79%	100%	9	92.22%	CNV35	Class III
chr7	3319721	3517429	156868	79%	96%	15	95.56%	CNV33	Class III
chr7	19219816	23047261	3092216	81%	95%	2031	96.41%	CNV38	Class III
chrX	143047623	145439992	2056539	86%	98%	1007	95.73%	CNV32	Class III
Total of all CNVs			9706780	74%	81%				

15 of 38 CNVs and 74% of total base pairs (9.7 Mb) reported by Egan et al overlap with CNVs detected in our study; we identify an additional 57 Mb corresponding to 2189 regions as CNV; Class I CNVs are those that arose once within B6, Class II arose once within B6 but more than once in all strains, Class III arose more than once among B6 substrains. Class II and III are recurrent