Table S2 ***Chaos3*** **-specific and Mammary Tumor-specific Recurrent Deletions Overlapping Human Breast Cancer CNAs.**

					Tumors								
Mouse CNA	**Gene**	**Hum Chr**	**Human CNA**	***Chaos3* CNA**	**A**	**B**	**C**	**D**	**E**	**F**	**G**	**H**	**I**
Mmu Chr 4 148.4-149.5 Mb	SLC2A7	1	FALSE	33%		x			x				
	SLC2A5	1	FALSE	50%		x			x	x			
	GPR157	1	FALSE	50%		x			x	x			
	MIR34A	1	FALSE	50%		x			x	x			
	H6PD	1	FALSE	57%		x			x	x	x		
	SPSB1	1	FALSE	86%		x	x		x	x	x	x	
	SLC25A33	1	FALSE	86%		x	x		x	x	x	x	
	TMEM201	1	FALSE	86%		x	x		x	x	x	x	
	PIK3CD	1	FALSE	86%		x		x	x	x	x	x	
	CLSTN1	1	FALSE	71%		x		x	x		x	x	
	CTNNBIP1	1	FALSE	71%		x		x	x		x	x	
	LZIC	1	FALSE	71%		x		x	x		x	x	
	NMNAT1	1	FALSE	71%		x		x	x		x	x	
	RBP7	1	FALSE	71%		x		x	x		x	x	
	UBE4B	1	TRUE	71%		x		x	x		x	x	
	KIF1B	1	TRUE	71%		x		x	x		x	x	
	PGD	1	TRUE	33%		x		x				x	
	APITD1	1	TRUE	33%		x		x				x	
	CORT	1	TRUE	33%		x		x				x	
	DFFA	1	TRUE	33%		x		x				x	
	PEX14	1	TRUE	33%		x		x				x	
	CASZ1	1	TRUE	33%		x		x					
	TARDBP	1	FALSE	17%		x							
	MASP2	1	FALSE	17%		x							
	SRM	1	FALSE	17%		x							
Mmu Chr 5 122-125 Mb	CLIP1	12	FALSE	43%	x	x					x		
	ZCCHC8	12	FALSE	43%	x	x					x		
	RSRC2	12	FALSE	43%	x	x					x		
	KNTC1	12	FALSE	71%	x	x		x			x		x
	GPR81	12	FALSE	71%	x	x		x			x		x
	DENR	12	FALSE	71%	x	x		x			x		x
	CCDC62	12	FALSE	71%	x	x		x			x		x
	HIP1R	12	FALSE	71%	x	x		x			x		x
	VPS37B	12	FALSE	86%	x	x	x	x			x		x
	ABCB9	12	FALSE	86%	x	x	x	x			x		x
	OGFOD2	12	FALSE	86%	x	x	x	x			x		x
	ARL6IP4	12	FALSE	86%	x	x	x	x			x		x
	PITPNM2	12	FALSE	86%	x	x	x	x			x		x
	MPHOSPH9	12	FALSE	86%	x	x	x	x			x		x
	CDK2AP1	12	FALSE	86%	x	x	x	x			x		x
	SBNO1	12	FALSE	86%	x	x	x	x			x		x

	SETD8	12	FALSE	86%	x	x	x	x			x		x
	RILPL2	12	FALSE	86%	x	x	x	x			x		x
	SNRNP35	12	FALSE	100%	x	x	x	x			x	x	x
	RILPL1	12	FALSE	100%	x	x	x	x			x	x	x
	TMED2	12	FALSE	100%	x	x	x	x			x	x	x
	DDX55	12	FALSE	100%	x	x	x	x			x	x	x
	EIF2B1	12	FALSE	100%	x	x	x	x			x	x	x
	GTF2H3	12	FALSE	100%	x	x	x	x			x	x	x
	TCTN2	12	FALSE	100%	x	x	x	x			x	x	x
	ATP6V0A2	12	FALSE	43%						x		x	x
	CCDC92	12	FALSE	29%								x	x
	Zfp664	12	FALSE	14%								x	
	Fam101a	12	TRUE	14%								x	
	Ncor2	12	TRUE	14%								x	
	Scarb1	12	FALSE	14%								x	
Mmu Chr 11	WSB1	17	FALSE	100%	x	x	x	*	x	*	x	x	x*
78-79.6 Mb	KSR1	17	TRUE	100%	x	x	x	*	x	*	x	x	x*
	LGALS9	17	TRUE	57%		x		x*		x*		x	x*
	NOS2	17	TRUE	57%		x		x*		*		x	
	NLK	17	FALSE	43%		x				x*		x	
	TMEM97	17	FALSE	29%		x				*		x	
	IFT20	17	FALSE	29%		x				*		x	
	TNFAIP1	17	FALSE	29%		x				x*		x	
	POLDIP2	17	FALSE	29%		x						x	
	TMEM199	17	FALSE	29%		x						x	
	SEBOX	17	FALSE	29%		x						x	
	VTN	17	FALSE	29%		x						x	
	SARM1	17	FALSE	29%		x						x	
	SLC46A1	17	FALSE	29%		x						x	
	SLC13A2	17	FALSE	29%		x						x	
	FOXN1	17	FALSE	29%		x						x	
	UNC119	17	FALSE	17%		x							
	PIGS	17	FALSE	17%		x							
	ALDOC	17	FALSE	17%		x							
	NF1	17	TRUE	100%	x	x	x	x*	x	x*	x	x	x
	OMG	17	TRUE	86%	x	x	x	x*	x		x		x
	EVI2B	17	TRUE	86%	x	x	x	*	x		x		x
	EVI2A	17	TRUE	71%	x	x	x	*	x		x		
	RAB11FIP4	17	TRUE	57%	x	x	x	x*	x				

Legend. x= deleted as determined by aCGH analysis. Some qPCR genotyping from the Chr 11 interval was added, and deleted probes are indicated as x*. Presumed deleted probes are indicated by "*". Tumor Codes: A: 2044B; B: 12353A; C: 12351L; D: 12352; E: 15259; F: 16168; G: 12115B; H: 16898; I: 11929A. Mmu = *Mus musculus*. Some of the deletions extend further than indicated. The True (deleted) and False (not deleted) calls for human gene deletions are from TCGA level 4 data (see Methods) and refer to whether that locus is deleted at levels statistically above background. Human genes in red are potentially cancer-relevant if deleted. Red shaded regions are the "critical regions" of a deletion set. Note that the Mmu Chr 11 deletion cluster is organized in the human genome order, which is inverted and has an insertion. Thus, the critical region is actually contiguous. The "Chaos3 CNA" column refers to the % of Chaos3 mammary tumors analyzed by aCGH that contained deletions of that particular locus. ND=no data.