Table S4 qPCR analysis of *Nf1* locus in tumors

Geno & Type	Tumor #	*Nf1* 5'	*Nf1* 3' (*Omg*)
Chaos3 MT	15259	17.4	52.9
Chaos3 MT	12351 L	35.5	12.0
Chaos3 MT	12353A	25.5	16.7
Chaos3 MT	12352	12.7	0.7
Chaos3 MT	2044B CL	63.7	48.0
Chaos3 MT	11929A	16.7	16.3
Chaos3 MT	16168	9.2	ND
Chaos3 MT	16898	9.6	75.1
Chaos3 MT	12115B	31.2	38.7
Chaos3 MT	2042 CL	78.9	92.3
Chaos3 MT	919 CL	51.8	0.1
Chaos3 MT	21040	0.1	0.1
Chaos3 MT	21253	0.3	0.2
Chaos3 MT	20317	29.5	48.7
Chaos3 MT	19957	32.7	5.4
Chaos3 MT	19958	11.2	12.4
Chaos3 MT	19959	14.4	72.4
Chaos3 MT	20783	7.0	10.4
Chaos3 MT	20164	20.6	22.8
Chaos3 MT	20888	27.3	26.0
Chaos3 MT	20892	6.4	34.9
Chaos3 MT	20893	7.4	24.5
Chaos3 MT	20138	41.1	10.8
Chaos3 MT	21039	68.4	66.7
Chaos3 MT	21809	62.0	60.0
Chaos3 MT	20894	85.1	67.1
Chaos3 MT	20889	12.0	18.4
Chaos3 MT	21333	40.8	71.4
Chaos3 MT	20626	36.7	22.6
Chaos3 MT	20318	14.5	24.9
Chaos3 MT	20890	13.6	38.9
Chaos3 MT	20891	2.5	1.4
Chaos3 MT	21123	34.7	39.0
Chaos3 MT	19660	44.8	48.3
Chaos3 MT	20459	53.7	69.8
Chaos3 MT	21597	28.6	5.3
Chaos3 MT	22182	62.6	78.2
Chaos3 MT	21416	63.8	56.8
Chaos3 MT	22236	31.6	8.0
Chaos3 MT	22418	24.9	24.2
Chaos3 MT	22180	23.9	49.0
Chaos3 MT	22235	8.1	8.2
Chaos3 MT	22166	21.7	21.0
Chaos3 MT	22168	8.0	7.6
Chaos3 MT	22238	3.4	3.4

Chaos3 MT	21417	3.3	14.8
Chaos3 MT	21419	19.2	50.6
Chaos3 MT	21255	7.0	6.1
Chaos3 MT	21124	8.5	29.1
Chaos3 MT	21810	26.3	27.0
Chaos3 MT	21811	47.3	51.7
Chaos3 MT	21254	9.5	7.9
Chaos3 MT	21041	24.4	21.2
Chaos3 MT	22420	40.5	17.1
Chaos3 MT	22476	75.5	70.7
Chaos3 MT	22414	3.3	17.1
Chaos3 MT	22416	3.5	14.6
Chaos3 MT	22417	7.1	19.4
Chaos3 MT	23116	11.2	10.8
Chaos3 MT	22418	115.0	110.3
Chaos3 non-MT	19160	198.2	207.5
Chaos3 non-MT	10658	87.1	ND
Chaos3 non-MT	16862	98.5	101.2
Chaos3 non-MT	17883	97.0	88.0
PyVT		96.3	105.1
MMTV-neu1		108.6	93.2
MMTV-neu2		103.8	104.4
Chaos3 +/+ MT		107.3	109.4

Legend. qPCR values are presented as the percentage vs C3H DNA. *Nf1* probes were at the 5' and 3' ends of the gene. The 3’ probe actually corresponds to the *Omg* gene that lies within an *Nf1* intron near the 3' end. Note that copy number differences between the *Nf1* 5' and 3' are observed in some tumors, indicating a breakpoint within *Nf1*. Deletion calls were made as follows: Heterozygous = 15-80%; Homozygous = <15%. If either *Nf1* or *Omg* were <15%, the tumor sample was called as homozygous deleted because full *Nf1* transcripts cannot be made. MT = mammary tumor.

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