Supplementary information

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Molecular Analysis of Desmoid Tumors with a High-Density Single-Nucleotide Polymorphism Array Identifies New Molecular Candidate Lesions

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Table 2. Summary of duplications amplifications and deletions found in desmoid tumor patients (n = 9) by SNP array analysis.

pt ID	Chromosome		Chromosomal position	CN	Gains/ losses	Mean log2 ratio	Length in base pairs	Genes	Candidate genes
1	*5*	*q21-23*	*109,159,524-126,849,318*	*1*	*l*	*-0,36*	*17,689,795 bp*	*>50*	*APC, FER, TNFAIP8*
1	*10*	*q11*	*46,467,015-46,483,124*	*1*	*l*	*-0,62*	*16,110 bp*	*1*	*ANXA8*
1	6		monosomy 6	1	l	-0,31	-	-	-
1	10	p	monosomy 10p	1	l	-0,36	-	-	-
1	*8*	*p23*	*3,822,506-3,949,083*	*1*	*l*	*-0,82*	*126,578 bp*	*1*	*CSMD1*
1	13	q	monosomy 13q	1	l	-0,32	-	-	-
2	*8*	*p23*	*3,504,412-4,005,702*	*1*	*l*	*-0,27*	*501,291 bp*	*1*	*CSMD1*
5	*10*	*q11*	*46,475,717-46,479,771*	*1*	*l*	*-0,77*	*4,055 bp*	*1*	*ANXA8*
8	*8*	*p23*	*3,404,597-3,967,184*	*1*	*l*	*-0,63*	*562,588 bp*	*1*	*CSMD1*
8	*5*	*q21-23*	*108,082,004-114,238,177*	*1*	*l*	*-0,86*	*6,156,174 bp*	*>30*	*APC,FER*
8	5	q21-23	118,704,428-120,153,552	1	l	-0,78	1,449,125 bp	4	TNFAIP8, PRR16
8	5	q21-23	122,092,320-122,993,400	1	l	-0,85	901,081 bp	8	SNX2, PRDM6
8	6	q	monosomy 6q	1	l	-0,99	-	-	-
9	*5*	*q13.3-q31.1*	*89,283,665-132,923,792*	*1*	*l*	*-0,77*	*43,640,128 bp*	*>50*	*APC, FER, TNFAIP8*
6	*8*	*p23*	*3,626,762-3,958,912*	*1*	*l*	*-0,4*	*332,151 bp*	*1*	*CSMD1*

pt ID	Chromosome		Chromosomal position	CN	Gains/ losses	Mean log2 ratio	Length in base pairs	Genes	Candidate genes
2	7	p21	13,867,256-14,094,188	3	g	0,3	226,933 bp	1	ETV1
2	7	p11	55,074,690-55,192,821	3	g	0,29	118,132 bp	1	EGFR
2	*8*	*q21.3*	*93,043,558-93,367,880*	*3*	g	*0,35*	*324,323 bp*	*2*	*RUNX1T1, MTG8*
2	10	p14-13	12,121,392-12,417,027	3	g	0,42	295,636 bp	8	NUDT5, DHTKD1
1	*17*	*q12*	*35,019,965-35,163,526*	*3*	*g*	*0,45*	*143,562 bp*	*12*	*Erbb2, HER2*
4	*17*	*q12*	*35,043,688-35,163,526*	*3*	*g*	*0,32*	*119,839 bp*	*12*	*Erbb2, HER2*
4	*8*	*q21.3*	*93,021,306-93,135,521*	*3*	*g*	*0,3*	*114,216 bp*	*3*	*RUNX1T1, MTG8*
4	11	p12	40,006,070-40,182,957	3	g	0,29	176,888 bp	1	LRRC4C
4	3	p24	25,392,531-25,610,771	3	g	0,29	218,241 bp	3	RARB
4	9	q33.1	120,982,463-121,087,494	3	g	0,31	105,032 bp	1	DBC1
4	16	q21	63,542,288-63,655,828	3	g	0,29	113,541 bp	2	CDH11, AK021537
4	2	p13	71,614,084-71,688,184	4	g	0,43	74,101 bp	1	DYSF
2	8	q24.12	120,563,653-120,683,338	3	g	0,31	119,686 bp	1	ENPP2
9	9	p23	10,435,439-10,536,257	3	g	0,48	100,819 bp	1	PTPRD
5	14	q23	64,939,273-65,205,532	3	g	0,38	266,260 bp	3	FUT8
3	20		trisomy	3	g	0,44	-	-	-
3	3	p24	26,586,501-26,651,318	3	g	0,41	64,818 bp	1	LRRC3B
3	12	q23	99,066,414-99,112,329	4	g	0,59	45,916 bp	5	GOLGA2L1
3	14	q23	60,616,779-60,662,863	4	g	0,58	46,085 bp	1	SLC38A6
6	*8*	*q21.3*	*93,050,167-93,150,570*	*3*	*g*	*0,31*	*100,404 bp*	*2*	*RUNX1T1, MTG1*
7	*8*	*q21.3*	*93,056,436-93,135,521*	*3*	*g*	0,31	*79,086 bp*	*2*	*RUNX1T1*
8	20	q11.23	35,129,973-35,156,244	3	g	0,43	26,272 bp	1	RBL1
6	7	q32.1	127,419,244-127,473,427	3	g	0,33	54,184 bp	4	SND1 ;LRC4

chr = chromosome; CN = copy number, gain = g; loss = l.
CNAs that occurred more than once are indicated in italics.