Supplementary Material

Table S1 Summary of 26 cases of MDS/AML with del(5q) and/or -7/del(7q)

Group	Case #	Age (y) /Sex	WBC ($\times 10^9$/L)	Diagnosis	G-banding	FISH	Array CGH
I: Cases with del(5q) (n=6)	1B	69/M	43.2	AML	45,XY,del(5)(q31),del(9)(p13),-17[14]/46,XY[7]	N/A	arr cgh 5q23.2qter(122,435,964-180,814,162)×1,9p23p22.3(13,626,392-14,149,100)×1,9q13qter(70,222,356-140,246538)×1,17pterq11.1(5,157-22,889,443)×1,17q11.2(25,090,767-27,404,425)×1,18q12.1(26,072,951-28,026,852)×1,18q21.31(18q21.31)×1,18q21.31q21.32(54,090,980-54,499,468)×3,18q23qter(75,996,798-76,114624)×3,21q22.13qter (36,771,128-46,923,366)×3
	2B	59/F	2	AML	46,XX,t(1;2)(q21;q31),der(3),del(5)(q13q33),dup(6)(q21q25)[4]/44,idem,-17,-18[13]/44,idem,der(11)[2]/46,XX[1]	N/A	arr cgh 5q14.1(79,391,019-80,776,929)×1,5q14.3q33.2(82,909,072-154,319,730)×1,17pterqter(5,157-78,649,123)×1,18pterqter(15,636-76,114,624)×1,21q22.12(35,138,293-35,197,013)×1
	3B	53/M	6.5	MDS	44,XY,del(1)(p22p33),+der(1)add(1)(q21),+der(3)add(3)(q29),-4,del(5)(q31q35),+6,-8,+der(9)add(9)(p13),der(10)t(10;14)(p10;q10),?del(10)(q22),der(12)add(12)(q24.3),?t(12;17)(p11.2;q11.2),-13,-14,-15,der(19)t(15;19)(p10;	N/A	arr cgh 1q21.1q23.1(143,890,003-157,211,867)×3,1q23.1q23.2(157,222,018-157,390,091)×1,1q23.2(157,397,735-157,833,758)×3,1q23.2(157,859,148-158,282,384)×1,1q23.2(158,287,749-158,780,299)×3,1q23.2q23.3(158,781,342-159,119,771)×1,1q23.3(159,148,599-159,918,934)×3,1q23.3(159,922,293-160,123,338)×1,1q23.3(160,134,353-160,692,736)×3,1q23.3q25.2(160,696,819-175,055,137)×1,3p26.3p11.1(40,700-90,354,250)×1,3p11.1qter(90,361,769-199,381,714)×3,4q11q12(52,392,021-55,514,601)×3,4q12qter(55,516,661-191,220,565)×1,5pterp12(91,422-44,801,689)×3,5q35.1(170,271,170-170,321,516)×1,6pterqter(5,745-170,884,586)×3,8p23.3p23.1(1,398,855-6,811,479)×1,8p23.1(8

					q13.4),-21[19]/46,XY[2]		,673,707-10,602,515)×1,8p23.1p12(10,774,453-36,424,907)×1,8p12p11.21(37,368,568-41,184,709)×3,8p11.21(41,309,692-42,220,588)×3,8p11.21(42,444,912-42,668,435)×1,8p11.2q13.1(42,786,704-66,983,620)×1,9pter(33,972-833,923)×3,10p15.3p15.1(61,561-5,261,849)×1,10p15.1p12.1(6,286,817-27,500,094)×1,10p11.22p11.21(31,909,019-38,718,217)×1,10q22.3q26.13(80,187,784-123,790,725)×1,0q26.13qter(123,964,128-135,327635)×1,12pterp13.33(33,393-698,376)×3,12q24.33qter(131,952,751-132,283,285)×1,13q11q21.31(18,016,985-62,813,466)×1,17pterq11.1(5,157-22,359,411)×1,17q12q21.31(34,505,486-39,466,810)×3,17q21.33q22(47,020,289-50,456,516)×1,17q22q23.1(50,759,923-55,163,608)×1,9q12q13.2(34,723,709-46,443,628)×3,19q13.2qter(46,446,528-63,786,148)×1,Xq11.1qter(61,847,932-154,895,334)×3
	4L*	44/M	5.7	MDS	44,X,-Y,-5,der(6)(5;6)(p12;q12),del(11)(q23),der(12)?t(12;18)(p11.2;q11.2),der(17)t(6;17)(q21;p13),-18,+r(?)[18]/45,idem,+mar[6]/46,XY[4]	nuc ish (D5S23,D5S721x2,EGR1x1)[85/200]	arr cgh 1p36.21(15,222,238-15,461,176)×3,5q11.2qter(54,446,262-180,814,162)×1,11q22.1q25(97,040,020-130,675,009)×3
	5B*	66/M	1.6	AML	45,XY,der(2),der(3),-5,der(14),der(17)[13]/45,XY,der(2),der(3),-5,der(17)[2]/ 46,XY[6]	N/A	arr cgh 1q25.1q25.2(174,039,010-174,566,349)×1,2p14(68,183,556-68,663,172)×1, 2p14p11.2(69,512,801-85,362,374)×1,3p21.31p11.1(45,674,598-89,897,373)×1,5q14.1qter(80,793,477-180,814,162)×1,6q23.2(131,487,338-131,751,303)×1,11q21qter(92,914,678-134,444,816)×3,14q12(24,568,914-24,629,456)×3,14q23.2(62,867,794-63,222,028)×3,17p13.3p13.1(5,157-7,054,250)×1,17p13.1(7,201,733-7,974,536)×1
	6B	33/M	27.9	AML	N/A	N/A	arr cgh 5pterq11.2(67,513-52,232,859)×3,5q11.2q12.1(52,237,381-60,826,805)×1,5q12.1(60,833,558-61,509,286)×3,5q12.1q13.3(61,514,797-74,234,934)×1,5q13.3(74,243,978-75,054,956)×3,5q13.3q14.3(75,059,178-89,603,782)×1,5q14.3(89,609,383-90,924,602)×3,5q14.3q33.3(90,927,144-157,171,850)×1,5q33.4q34(157,177,738-161,652,692)×3,5q34

							qter(161,655,228-180,814,286)×1,8pterqter(170-46,262,982)×3,15q11.1q15.1(18,308,582-40,594,528)×1,15q15.1qter(40,597,795-100,320,705)×3,16pterqter(11,631-88,813,426)×1,21q11.2q21.3(13,302,567-26,763,083)×1,21q21.3(26,766,298-27,475,785)×3,21q21.3q22.11(27,565,349-32,176,361)×1,21q22.11(32,178,049-34,430,032)×3,21q22.11q22.12(34,435,306-35,124,705)×1,21q22.12qter(35,199,183-46,933,606)×3
II: Cases with -7/ del(7q) (n=11)	7B	49/F	4.8	AML	46,XX,del(7)(q22)[17]/46,XX[3]	N/A	arr cgh 3q26.2qter(170,169,281-199,381,713)×3,7q21.2qter(92,264,231-158,816,034)×1
	8L	61/M	NA	AML	45,XY,-7[12]/ 46,XY[8]	N/A	arr cgh 7pterqter(127,598-158,816,034)×1,12q13.3(55,840,247-55,922,168)×3,20q11.23(36,222,297-36,308,982)×3
	9B	60/M	4.7	MDS	46,XY,t(3;21)(q26;q22)[8]/45,idem,-7[10],46,XY[2]	N/A	arr cgh 7pterqter(127,598-158,816,034)×1
	10L	72/M	NA	AML	46,XY,del(7)(q22q34)[19]/46,XY[1]	N/A	arr cgh 7q21.11qter(79,566,594-158,816,034)×1,9q34.11q34.12(132,494,565-132,783,811)×3,11p14.3p14.2(25,616,706-26,621,268)×1,14q23.3qter(65,662,126-106,342,076)×3,20p12(8,026,284-8,584,915)×1,21q22.12(35,126,513-35,405,617)×1
	11B	59/M	34.4	AML	46,XY,del(7)[1]/46,XY[15]	nuc ish (D7S486x1,ELNx2)[195/200]	arr cgh 7pterp22.2(127,598-2,413,029)×1,7q22.1qter(102,913,354-158,816,034)×1
	12B	37/M	6	Relapse AML	45,der(X)t(X;?8)(q26;?q21),Y,add(1)(p36.1),del(7)(q21),-8,?t(9;16)(q22;p13.1),-9,add(19)(p13),+mar[18]/46,XY[2]	N/A	arr cgh 1pterp36.32(32,108-2,686,732)×3,1p36.32p36.23(3,208,081-7,216,894)×1,7q21.11qter(85,054,707-158,816,034)×1,9p23p21.1(10,459,186-30,576,907)×1,9q13q21.13(70,151,353-76,337,036)×1,9q22.32q22.33(97,708,787-100,251,136)×1,16q23.3(81,664,303-81,717,816)×1,17q21.31qter(38,784,938-78,649,123)×3,18q11.2(16,880,553-16,909,471

							)×1
	13B	40/F	2.1	Relapse AML	45,XX,inv(3)(p12q26),t(5;6)(q13;p25),-7[9]/46,XX[15]	N/A	arr cgh 7pterqter(127,598-158,816,034)×1
	14B	27/F	11.1	AML	45,XX,-7[20]	N/A	arr cgh 7pterqter(127,598-158,816,034)×1
	15L+	2/F	32.8	AML	47,XX,+21c[20];	nuc ish (D5S23,D5S721/EGR1x2)[200],(D7S486/ELN)x1 [160/200]	arr cgh 1q32.1qter(198,420,115-247,175,936)×3,7pterqter(127,598-158,816,034)×1,13q22.1qter(73,509,574-114,117,364)×3, 21pterqter (9,892,286-46,923,366)×3
	16B	61/M	63.8	AML	46,XY,-7,?+mar[10]/45,XY,-7[5]/ 46,XY[5]	N/A	arr cgh 7pterqter(127,598-158,816,034)×1
	17B	66/F	38.6	AML	N/A	N/A	arr cgh 3q26.2qter(170,262,958-199,381,714)×3,7q21.2qter(92,258,287-158,816,034)×1
III: Cases with concurrent del(5q) and del(7q) (n=9)	18B	17/M	4.5	Relapse AML	46,XY,?del(2)(p21),?inv(3)(q21q27),-5,del(7)(q11.2),del(12)(p11.2),+mar[15]/46,XY[7].	nuc ish 7q31(D7S486-)[158]/(D7S486x2)[42]	arr cgh 5q14.2qter(81,635,615-180,718,374)×1,7q21.2qter(92,193,469-158,816,034)×1,12p13.2p11.22(11,203,139-29,748,969)×1,13q12.2q21.32(27,371,962-67,034,363)×1,20q13.13(48,483,706-48,562,494)×1,Xp11.3(44,712,172-44,947,274)×1
	19B*	56/M	14.9	AML	44,XY,?del(3)(q12q26),del(5)(q31q35),-7,add(12)(p11.2),add(14)(p11.2),add(14)(q32),-15,add(16)(q12.1),-17,add(20)(q11.	N/A	arr cgh 1pterp36.32(580,411-4,330,405)×3,3q12.3q24(104,164,436-148,061,383)×1,5q23.1q23.2(119,563,771-125,702,460)×1,5q31.1qter(131,192,129-180,814,162)×1,6q23.1q23.2(130,697,296-133,902,829)×1,7q11.21qter(61,834,419-158,816,034)×1,12q13.12(47,609,890-48,221,668)×1,14q11.2(22,233,733-22,728,120)×1,14q24.1(67,417,008-69,091,990

					2),+mar[19]/46,XY[1]		)×1,14q24.2(69,419,342-70,469,644)×1,14q24.2(72,550,744-72,878,714)×1,14q32.33(103,377,866-104,943,386)×1,15q21.1q22.2(45,991,638-61,395,696)×1,16p11.2q12.1(33,716,834-49,263,169)×1,16q12.2qter(51,848,759-88,715,037)×1,17p11.2(18,754,135-19,253,042)×1,17q25.3(75,622,107-77,074,800)×1,20q11.22q13.2(32,176,283-50,148,479)×1
	20B	66/F	1	MDS	44,XX,?t(2;6),del(5)(q15q31),der(7)t(7;17)(q11.2;q21),-14,-15,der(17),?der(20) t(20;?)(q11.2;?),-21,+2mar[cp24]	N/A	arr cgh 2q37.1q37.3(233,655,397-242,706,291)×1,5q13.1q13.2(67,553,568-68,862,326)×1,5q13.2qter(73,268,152-180,814,162)×1,6p24.1(12,633,684-12,995,778)×3,6p22.3(16,879,115-20,175,927)×1,6p22.3(20,181,941-20,666,700)×3,6p22.2(24,938,466-25,204,156)×1,7p14.3q11.2(34,031,823-67,164,074)×1,7q11.22(68,321,159-69,174,607)×3,7q11.23q21.11(76,648,107-77,686,631)×3,7q21.11qter(78,245,210-158,816,034)×1,15q13.1q15.3(26,289,079-42,645,934)×1,15q15.3q21.1(42,647,815-43,502,237)×3,15q21.1q22.2(44,528,701-60,065,631)×1,15q22.2q22.31(60,075,217-64,030,397)×3,16pterqter(18,227-88,715,032)×1,17pterp11.2(5,157-17,392,536)×1,20p12.3(5,010,254-8,551,180)×3,20p12.3p12.1(8,556,989-11,951,978)×1,20p12.1(12,414,108-12,876,437)×1,20p12.1q11.1(16,809,249-28,087,291)×1,20q11.21q11.22(29,297,619-33,889,652)×3,20q12q13.12(38,842,710-41,923,291)×1,20q13.13(47,167,391-48,842,788)×1,21q11.2q21.1(13,485,159-15,739,693)×1,21q21.1(15,760,312-17,865,359)×3,21q21.1(17,868,739-20,628,907)×1, 21q22.11q22.13 (34,226,820-37,377,277)×1
	21B*	73/M	2	MDS	44,XY,der(1)add(1)(q21),-3,-5,der(9)t(3;9)(q21;q34),der(11)add(11)(p12), ?der(15)add(15)(q15),der(16)add(16)(q24),-17,-19,-20,+3mar[3],42,idem,-7,-14[13]/46,XY[6]	N/A	arr cgh 1q21.1q23.3(152,223,514-159,394,673)×1,1q44qter(245,368,717-247,175,936)×1,3p21.21p21.1(50,693,649-51,814,822)×1,3p21.1p14.3(52,550,778-54,463,119)×1,3p13q13.31(74,088,860-115,995,146)×1,3q13.31q21.2(118,556,523-127157575)×1,3q22.1(133,565,943-134,196,842)×1,5pterp14.2(91,422-24,175,610)×1,5q13.2q14.1(71,867,294-79,106,944)×1,5q21.3q22.1(107,810,143-110,186,114)×1,5q22.2qter(111,548,569-180,814,162)×1,6q16.1(97,497,032-98,576,634)×1,6q16.2(99,148,362-99,752,062)×1,6q22.31

							q22.33(122,367,145-128,880,044)×1,6q22.33q23.2(130,184,062-32,050,742)×1,6q23.3(135,348,698-138,338,744)×1,7p22.2(3,286,887-3,873,152)×1,7p22.1p12.1(7,009,946-52,824,182)×1,7p12.1q21.3(52,828,766-94,971,635)×3,7q21.3(94,975,376-97,509,219)×1,7q22.1q36.2(102,214,571-153,339,984)×1,7q36.2qter(153,346,388-158,816,034)×3,14q31.3(86,190,809-86,837,463)×1,15q14q15.3(36,572,299-41,786,195)×1,16q22.2q23.3(69,765,645-82,484,118)×1,17p13.3(2,890,389-3,368,301)×1,17p13.1q11.2(8,203,433-28,674,099)×1,18q23(76,086,211-76,114,624)×3,22q11.1q13.33(14,434,579-49,568,253)×3
	22B	66/F	16.3	MDS	45,X,-X,-3,del(5)(q31q32),del(7)(q22q34),add(8)(q24),add(11)(p15),-11,-20,+3mar[5]/44,idem,-6[3]/45,X,del(X)(q22-24),der(2)t(2;3)(p21;q12),-3,del(5)(q31;q32),add(6)(p23),del(7)(q22q34),-7,add(8)(q24),der(11)t(7;11)(q11;p15),-11,add(20)(p11.2),+2mar[11]	N/A	arr cgh 3p22.3p12.1(36,461,221-83,339,999)×1,3p12.1q13.2(85,952,522-114,785,323)×1,3q13.31(117,539,305-118,698,638)×3,3q21.1(124,407,359-125,023,219)×1,3q21.1(127,422,012-127,603,036)×1,3q21.3(128,747,248-129,056,694)×1,5q31.1qter(130,562,020-180,814,162)×1,6pterp24.1(5,745-13,431,147)×1,7pterp12.1(127,598-53,567,518)×1,7q22.1q36.1(99,774,428-149,033,790)×1,8pterp23.2(7,702-4,716,408)×3,8p22qter(17,712,776-146,264,232)×3,11pter(66,612-2,936,409)×1,11p15.1p12(19,386,476-40,404,974)×1,11q12.2q12.3(60,842,513-61,609,561)×1,20pterp13(15,928-1,483,130)×1,20p13(1,941,394-3,348,964)×3,20p12.3p11.1(8,183,733-26,177,033)×1,Xq13.1q21.32(68,519,908-92,257,677)×1,Xq21.33q25(95,875,232-128,456,387)×1,Xq25q26.2(129,379,323-131,847,556)×1,Xq26.2q26.3(132,406,559-133,700,035)×1,Xq26.3qter(134,671,855-154,895,334)×1
	23B*	67/M	0.3	AML	43,X,-Y,-5,der(7),der(12),-16,der(21)[2]/43,idem,der(5)[5]/43,idem,der(11)[13]	N/A	arr cgh 5q11.1qter(49,611,041-180,814,162)×1,7q21.3qter(92,613,505-158,816,034)×1,11q13.3(69,667,422-70,005,435)×3,11q14.1(77,095,878-77,453,011)×3,11q14.1(78,845,684-81,376,072)×3,11q21(95,357,177-95,707,050)×3,11q21(95,707,455-96,521,482)×1,11q21q23.3(96,523,941-117,900,930)×3,11q24.2qter(125,947,002-134,444,816)×3,12p13.2p12.3(10,158,247-17,908,124)×1,15q14(32,405,050-35,333,353)×3,15q15.2q21.1(40,9

							78,158-44,120,335)×3,15q21.1q21.2(45,611,894-47,896,186)×3,15q21.3(52,175,548-53,948,510)×3,15q21.3q22.31(55,788,381-64,815,870)×3,16pterp12.3(18,227-18,310,634)×1,16p12.2p12.1(21,446,560-23,428,313)×3,16p11.2(28,072,168-30,238,886)×3,16p11.2qter(30,482,761-88,715,037)×1,18q21.2(48,557,322-50,804,845)×3,21p11.2qter(9,892,286-46,923,366)×3
	24B*	68/M	2.1	AML	49-53,XY,?der(5),-7,+11,der(16)t(5q;16q),?der(17),?der(18),+21,+21,+21,+22,mar1-3[7]/48-52,XY,?der(5),-7,+11,der(16)t(5q;16q),?der(17),-18,+21,+21,+21,+22,mar1-3[8]/46,XY[5]	N/A	arr cgh 1pterp31.1(32,108-72,498,773)×3,5p15.2p14.1(13,902,471-27,433,539)x1,5p14.1p11(27,441,968-46,148,641)×3,5q11.1q12.1(49,600,885-59,580,424)×1,5q14.2q33.1(82,357,337-150,625,216)×1,7q11.21qter(62,620,413-158,816,034)×1,11pterqter(66,612-13,4444,816)×3,17pterp12(5,157-15,360,833)×1,17q11.1q11.2(23,121,145-26,336,746)×1,17q11.2(26,340,489-26,906,705)×3,17q11.2(26,915,037-27,747,652)×1,17q11.2q21.31(27,765,651-40,426,890)×3,17q21.31(40,433,668-40,479,835)×1,17q21.31(40,487,029-40,537,503)×3,17q21.31q21.32(40,546,941-42,329,690)×1,17q22q23.2(54,762,968-55,818,301)×1,17q23.2(55,824,843-56,321,573)×3,17q23.2q23.3(56,335,052-58,853,934)×1,17q23.3q24.1(58,857,723-60,214,125)×3,17q24.1q24.2(60,222,313-63,079,901)×1,17q24.2(63,087,813-63,263,493)×3,17q24.2q25.3(64,494,110-73,720,084)×3,17q25.3(73,731,949-75,524,297)×1,17q25.3(75,538,482-76,736,539)×3,17q25.3(76,743,450-78,649,123)×1,18pterqter(15,636-76,114,624)×1,21p11.2qter(9,892,266-46,923,366)×3,22q11.1q13.33(14,434,579-49,568,253)×3
	25B	66/M	215	AML	N/A	N/A	arr cgh 2pterq11.2(19,799-99,110,607)×3,2q11.2(99,121,784-100,519,403)×1,5q15(95,036,103-95,171,967)×1,5q15qter(95,277,745-180,814,162)×1,7p14.1p13(37,828,776-3,951,674)×1,7p13(44,051,445-44,787,539)×3,7p13p12.1(44,804,878-52,411,616)×1,7p12.1p11.2(53,746,152-55,528,062)×3,7q11.22qter(67,855,593-158,816,034)×1,9pterp24.3(33,972-1,270,648)×3,9p24.2(2,478,133-3,526,152)×1,9p24.2p24.1(4,182,024-5,802,114)×3,9p24.1p22.3(7,568,405-15,238,267)×1,9p22.3p21.1(16,158,968-31,906,806)×1,9p21.1

							p13.1(32,239,402-38,363,312)×3,9q13q34.3(70,222,356-140,246,538)×1,11q14.1q14.2(85,015,265-85,405,269)×3,11q21qter(94,728,103-134,444,816)×3,12pterqter(33,393-132,283,285)×1,16pterq24.3(18,227-88,715,037)×1,19q13.11qter(39,601,770-63,786,148)×3
	26B	72/F	159.1	AML	N/A	N/A	arr cgh 2q14.3(123,636,784-126,418,676)×1,2q21.2qter(134,230,501-242,706,291)×1,5q21.3q34(104,803,921-63,613,351)×1,6pterp22.3(5,745-20,863,427)×1,6p22.3(21,633,472-23,033,705)×1,6p12.3(46,636,975-48,985,866)×1,6p12.1(53,188,225-54,602,203)×3,6q14.1(77,663,323-78,596,890)×1,6q14.1q14.2(79,537,205-83,998,638)×1,6q14.3q15(84,978,276-87,778,166)×1,6q15q16.1(89,983,896-95,245,621)×1,6q24.2(143,923,599-144,506,122)×1,7q31.31qter(119,547,309-158,816,034)×1,8p21.1p12(28,309,706-31,525,769)×1,8p12p11.22(37,863,150-39,608,080)×1,8p11.22p11(39,635,074-43,694,868)×3,8q11.21q24.3(50,233,257-146,176,344)×3,12pterp13.32(33,393-4,242,649)×1,12p13.31p13.2(8,647,392-12,138,458)×1,12p13.1p12.3(14,387,078-15,198,833)×1,13q21.2qter(58,275,596-114,117,364)×3,17p11.2(19,082,873-20,155,203)×1,18p11.32(15,636-1,085,785)×1

B: Bone marrow sample

L: Leukemic blood sample

N/A: not available due to cultural failure or study was not been performed.

*: -5 or -7 by GTL banding were re-designated as a deletion or rearrangement involving chromosomes 5 or 7 by array CGH.

+: del(5q) was detected by array CGH and confirmed by FISH.

Table S2. Summary of genomic CNAs detected by array CGH

Group	Size of Imbalances		Number of Imbalances			
			Chromosome 5	Chromosome 7	Other Chromosomes	**Total**
I	≥5Mb	Gains	2	0	11	13
		Losses	9	0	24	33
	<5Mb	Gains	4	0	17	21
		Losses	2	0	20	22
II	≥5Mb	Gains	0	0	7	7
		Losses	0	11	2	13
	<5Mb	Gains	0	0	4	4
		Losses	0	1	7	8
III	≥5Mb	Gains	1	2	18	21
		Losses	14	14	41	69
	<5Mb	Gains	0	4	34	38
		Losses	3	2	64	69
Total			**35**	**34**	**249**	**318**

Table S3 Characterizations of the deletion of chromosomes 5 and 7 in the three groups

Group	Chromosome	Simple deletion		Complex deletion	
		Interstitial	Terminal	Interstitial + Interstitial	Interstitial + Terminal
I	5	1	3	1	1
II	7	0	5	0	0
III	5	1	3	1	4
	7	1	6	1	1

Table S4 Recurrent ‘other CNAs’ in three groups

	Group	**Chromosome (n)**	**Genomic Annotation (bp) hg18**	**Size (Mb)**	**Interesting Genes***
Gain	I only	21p11.2-qter (3)	9,892,266-46,923,366	37.031	*RUNX1, NRIP1, ETS2, ERG*
	II only	None			
	III only	9p24.3 (2)	33,972-833,923	0.8	*FOXD4, KANK1*
		15q22.2-q22.31 (3)	60,075,217-64,030,397	3.955	*DAPK2*
		22q11.1-q13.33 (2)	14,434,579-49,568,253	35.134	*MN1, PDGFB, BCR, BCL2L13*
	I & II	3q26.2-qter (3)	170,262,958-199,381,714	29.119	*MECOM, ZMAT3, SKIL*
	I & III	1p36.21 (2)	15,222,238-15,461,176	0.239	*KAZN, TMEM51, C1orf126*
		3q13.31 (2)	117,539,305-118,698,638	1.159	*LSAMP*
		8p11.22-8p11.21 (3)	39,635,074-42,220,588	2.586	*ADAM18, ADAM2, KAT6A, GOLGA7, ZMAT4, SFRP, GINS4, ANK1, AP3M2, PLAT*
		8q11.21-q24.3 (2)	50,233,257-146,176,344	95.943	*RIPK2, MYC, TRPS1, RUNX1T1*

		11q21 (3)	95,357,177-95,707,050	0.35	*MAML2*
		11q22.1-q23.3 (4)	97,040,020-117,860,864	20.821	*PDGFD, MLL, ATM, CASP1, CASP4, CASP5, PPP2R1B*
		11q24.2-q25 (4)	125,947,002-130,675,009	4.728	*ETS1, ADAMTS8, TP53AIP1*
		15q15.3-q21.1 (3)	42,647,815-43,502,237	0.854	*SPG11, B2M, PATL2, SHF*
		15q21.1-q21.2 (2)	45,611,894-47,896,186	2.284	*FGF7*
		18q23 (2)	76,086,211-76,114,624	0.028	*PARD6G*
		19q13.11-q13.2 (2)	39,601,770-46,443,628	6.842	*MLL4, AKT2, AXL, FXYD3, SPRED3*
	II & III	1pter-p36.32 (3)	580,411-2,686,732	2.106	*CDK11A, CDK11B, SKI*
		13q22.1-qter (2)	73,509,574-114,117,364	40.608	*KLF12, GPC6. GPC5*
		17q21.31-q21.31 (3)	38,784,938-39,466,810	0.682	*MPP2*
		17q23.2 (2)	55,824,843-56,321,573	0.497	*PPM1D, APPBP2*
		17q23.3-q24.1 (2)	58,857,723-60,214,125	1.356	*ERN1, PECAM1, DDX5, PSMC5, STRADA, MAP3K3, ICAM2*
		17q24.2 (2)	63,087,813-63,263,493	0.176	*BPTF*
		17q24.2-q25.3 (2)	64,494,110-73,720,084	9.226	*MAP2K6, GRB2, SEPT9, LLGL2, TTYH2, FOXJ1, JMJD6*
		17q25.3 (2)	75,538,482-76,736,539	1.198	*CARD14, RPTOR, AATK*
		21q22.13-qter (2)	36,771,128-46,923,366	10.152	*ETS2, ERG*
	I, II & III	17q21.31 (2)	40,487,029-40,537,503	0.05	*MAML2*
Loss	I only	None			
	II only	None			
	III only	2q37.1-q37.3 (2)	233,655,397-242,706,291	9.051	*GPC1*
		3q21.1 (3)	124,407,359-125,023,219	0.616	*SEC22A, ADCY5, MYLK, PTPLB*
		3q21.1 (2)	127,422,012-127,603,036	0.181	*KLF15, CCDC37*
		3q21.3 (2)	128,747,248-129,056,694	0.309	*TPRA1, ABTB1, MGLL*
		3q22.1 (2)	133,565,943-134,196,842	0.631	*ACPP, ACAD11, CCRL1, UBA5, NPHP3, DNAJC13*

		6pter-p24.1 (2)	5,745-13,431,147	13.425	*FOXQ1, FOXF2, IRF4, FOXC1, PRPF4B, NEDD9, RREB1, HUS1B*
		8p21.1-p12 (2)	28,309,706-31,525,769	3.216	*FBXO16, PPP2CB*
		12p13.2 (3)	11,203,139-12,138,458	0.935	*ETV6, BCL2L14*
		12p13.1-p12.3 (3)	14,387,078-15,198,833	0.812	*RERG*
		15q21.1-q22.2 (2)	45,991,638-60,065,631	14.074	*GABPB1, FGF7, CCNB2, POLR2M*
		16p11.2-q12.1 (2)	33,716,834-49,263,169	15.546	*ZNF423, BRD7*
		20p12.1-p11.1 (2)	16,809,249-26,177,033	9.367	*FOXA2, RBBP9, NXT1, PAX1*
		20q12-q13.12 (2)	38,842,710-41,923,291	3.081	*TOP1, PTPRT, MYBL2*
		20q13.13 (3)	48,483,706-48,562,494	0.079	*PTPN1*
	I & II	None			
	I & III	1q23.1-q23.2 (2)	157,222,018-157,390,091	0.168	*IFI16, AIM2*
		1q23.2 (2)	157,859,148-158,282,384	0.423	*CRP, CD2*
		1q23.2-1q23.3 (2)	158,781,342-159,119,771	0.338	*CD84, CD48, CD244, CY9,*
		1q25.1-25.2 (2)	174,039,010-174,566,349	0.527	*RFWD2*
		3p21.21-p21.1 (4)	50,693,649-51,814,822	1.121	*MANF*
		3p21.1-p14.3 (4)	52,550,778-54,463,119	1.912	*PBRM1, GNL3, PRKCD, DCP1A*
		3p13-p12.1 (4)	74,088,860-83,339,999	9.251	*ROBO1*
		3p12.1-p11.2 (4)	85,952,522-89,897,373	1.726	*EPHA3, CGGBP1*
		6q23.2 (3)	131,487,338-131,751,303	0.264	*AKAP7*
		13q12.2-q21.31 (2)	27,371,962-62,813,466	35.442	*NEBA, FOXO1, FLT3, FLT1, SMAD9, CCNA1*
		15q14-q15.1 (3)	36,572,299-40,594,528	4.022	*THBS1, BMF, PAK6*
		16pter-qter (3)	18,227-88,715,032	88.697	*N/A*
		17pter-p12 (5)	5,157-15,360,833	15.356	*TP53, WRAP53, NLRP1*
		17p11.2 (5)	19,082,873-19,253,042	0.17	*MAPK7*
		17q11.2 (2)	25,090,767-26,336,746	1.246	*CRLF3, RNF135*

		17q11.2 (2)	26,915,037-27,404,425	0.489	*SUZ12*
		17q22-q23.1 (2)	54,762,968-55,163,608	0.401	*CLTC*
		18pter-qter (2)	15,636-76,114,624	76.099	*N/A*
		21q11.2-q21.1 (2)	13,485,159-15,739,693	2.255	*NRIP1*
		21q21.1(2)	17,868,739-20,628,907	2.706	*BTG3*
	II & III	9p22.3-p21.1 (2)	16,158,968-30,576,907	14.418	*CDKN2A, CDKN2B, TUSC1, ADAMTSL1, TEK*
		11p14.3-p14.2 (2)	25,616,706-26,621,268	1.005	*MUC15, ANO3*
		16q23.3 (4)	81,664,303-81,717,816	0.054	*CDH13*
		20p12.3 (3)	8,556,989-8,584,915	0.028	*PLCB1*
	I, II & III	9p23-p22.3 (3)	13,626,392-14,149,100	0.523	*NFIB*
		9q13-q21.13 (3)	70,151,353-76,337,036	6.186	*RORB*
		9q22.32-q22.33 (3)	97,708,787-100,251,136	2.542	*CDC14B*
		21q22.12 (3)	35,138,293-35,197,013	0.059	*RUNX1*

n: number of cases

*: selected from UCSC Genome browser (http://genome.ucsc.edu/) and NCBI (http://www.ncbi.nlm.nih.gov/gene/) based on function described.

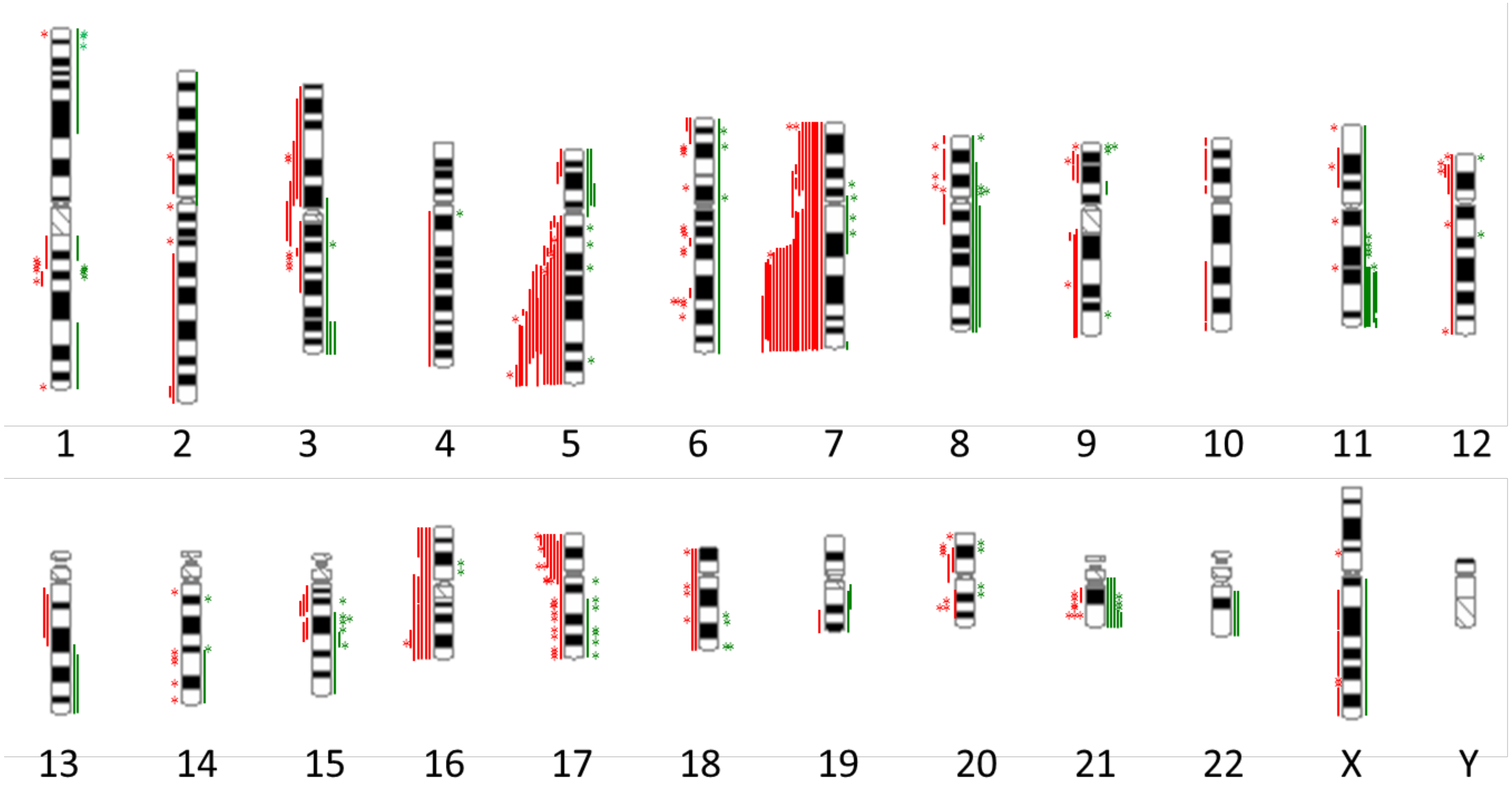
Table S5 Selected interesting tumor-associated genes* from the recurrent ‘other CNAs’

	Group	**Gene Symbol***	**Chromosome Location**	**Gene Description (NCBI)**	**Associated Cancers**	**Role in Carcinogenesis/Leukemogenesis**
Gain	I only	None				
	II only	None				
	III only	None				
	I & II	*SKIL*	3q26.2	SKI-like oncogene	Breast, esophageal, colorectal, and ovarian cancers	A component of the SMAD pathway, which regulates cell growth and differentiation through transforming growth factor-beta (TGFB)
	I & III	*PDGFD*	11q22.3	Platelet-derived growth factor D	Prostate, pancreatic, and renal cancers, glioblastoma, melanoma	Mitogenic factor for cells of mesenchymal origin; a newly recognized growth factor that can regulate many cellular processes, including cell proliferation, transformation, invasion, and angiogenesis by specifically binding to and activating its cognate receptor PDGFR-beta
		MLL	11q23.3	Mixed-lineage leukemia	AML, acute lymphoblastic leukemia (ALL)	Regulation of hematopoiesis
		ETS1	11q24.3	V-ets erythroblastosis virus E26 oncogene homolog 1	Myelodysplastic syndrome (MDS), gastric, colon, lung, cervical, and breast cancer, lymphoma	Either as transcriptional activators or repressors of numerous genes involved in stem cell development, cell senescence and death, and tumorigenesis
		ADAMTS8	11q24.3	ADAM metallopeptidase with thrombospondin type 1	Lung, brain, thyroid and breast cancers	With anti-angiogenic properties

	II & III	*SKI*	1p36.33	V-ski sarcoma viral oncogene homolog	Leukemia, breast, esophageal, cervical, prostate, and ovarian cancers	It functions as a repressor of TGF-beta signaling
		RUNX1	21q22.12	Runt-related transcription factor 1	Several types of leukemia	Involvement in development of normal hematopoiesis
	I, II & III	*ETS2*	21q22.2	V-ets erythroblastosis virus E26 oncogene homolog 2	Acute myeloid leukemia (AML), breast, gastric, lung, pancreatic, and prostate cancers	A proto-oncogene; regulating genes involved in development and apoptosis; involved in regulation of telomerase
		ERG	21q22.2	Ets-related isoform 1	AML, prostate cancer	Regulators of embryonic development, cell proliferation, differentiation, angiogenesis, inflammation, and apoptosis; regulation of hematopoiesis, and the differentiation and maturation of megakaryocytic cells
Loss	I only	None				
	II only	None				
	III only	*ADCY5*	3q21.1	Adenylate cyclase 5	Chronic lymphocytic leukemia (CLL), ALL	Mediate G protein-coupled receptor signaling through the synthesis of the second messenger cAMP
		ETV6	12p13.2	Ets variant 6	Leukemia, breast cancer, mucoepidermoid carcinoma	Involvement in hematopoiesis and maintenance of the developing vascular network
		BCL2L14	12p13.2	BCL2-like 14	Lung, breast, hepatic, and laryngeal cancers, ALL	Anti- or pro-apoptotic regulator involved in a wide variety of cellular activities
		RERG	12p12.3	RAS-like estrogen-regulated	MDS, breast and colorectal cancers	TSG, a member of the RAS superfamily of GTPases, inhibits cell proliferation and tumor formation

				growth inhibitor		
		PTPN1	20q13.13	Protein tyrosine phosphatase non-receptor type1	AML, CML, lymphoma, colorectal, breast, and prostate cancers	A signaling molecule that regulates cell growth, differentiation, mitotic cycle, and oncogenic transformation
	I & II	None				
	I & III	*MANF*	3p21.31 - 3p21.2	Mesencephalic astrocyte-derived neurotrophic factor	Pancreatic, lung, breast, prostate, and renal cancers	Inhibits cell proliferation and endoplasmic reticulum (ER) stress-induced cell death
		TP53	17p13.1	Tumor protein p53	Leukemia, many types of cancers	Cell cycle arrest, apoptosis, senescence, DNA repair, or changes in metabolism
		WRAP53	17p13.1	WD repeat domain 79	Rectal and ovarian cancers	Required for telomere synthesis; regulation of p53 expression at the post- transcriptional level
	II & III	*CDH13*	16q23.3	Cadherin 13 preproprotein	Many types of cancer	A negative regulator of axon growth during neural differentiation; protecting vascular endothelial cells from apoptosis
	I, II & III	*RUNX1*	21q22.12	Runt-related transcription factor 1	Several types of leukemia	Involvement in development of normal hematopoiesis

* Genes are selected based on the function described from UCSC Genome browser (http://genome.ucsc.edu/) and NCBI (http://www.ncbi.nlm.nih.gov/gene/).



🟩: gain, 🟥: loss, *: gain ≤ 5.0Mb, *: loss ≤ 5.0Mb

Figure S1 An overview of the genomic imbalances found in 26 MDS/AML cases with del(5q) and/or -7/del(7q)

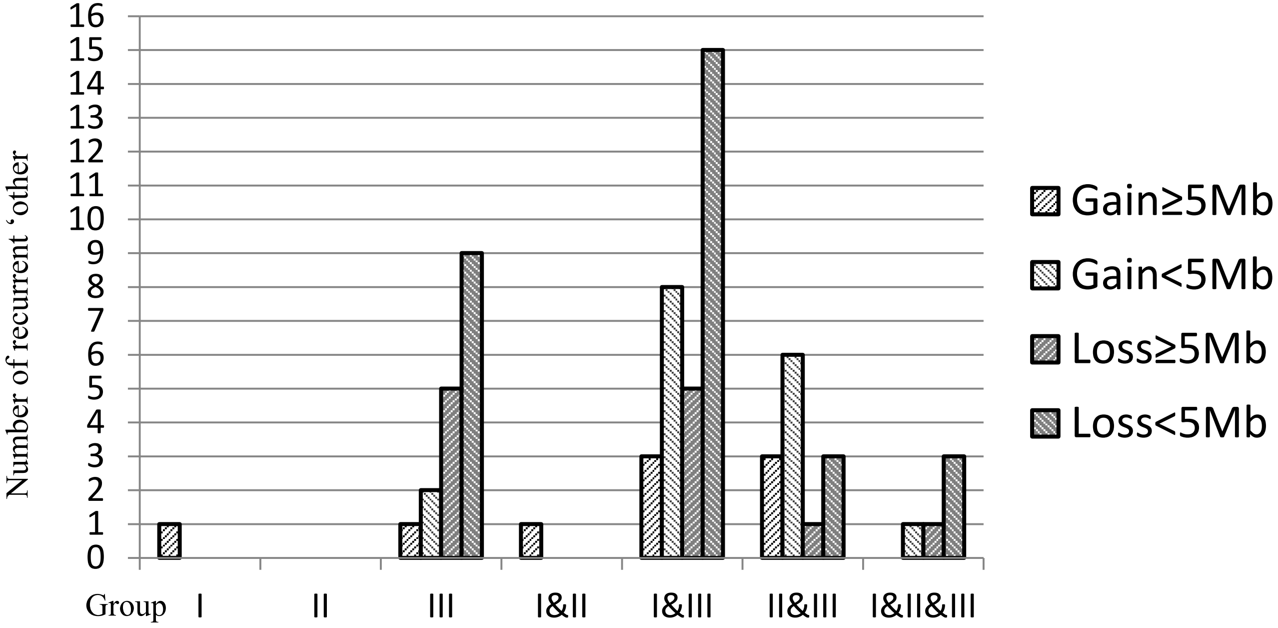


Figure S2 The group and size distribution of 68 recurrent ‘other CNAs’

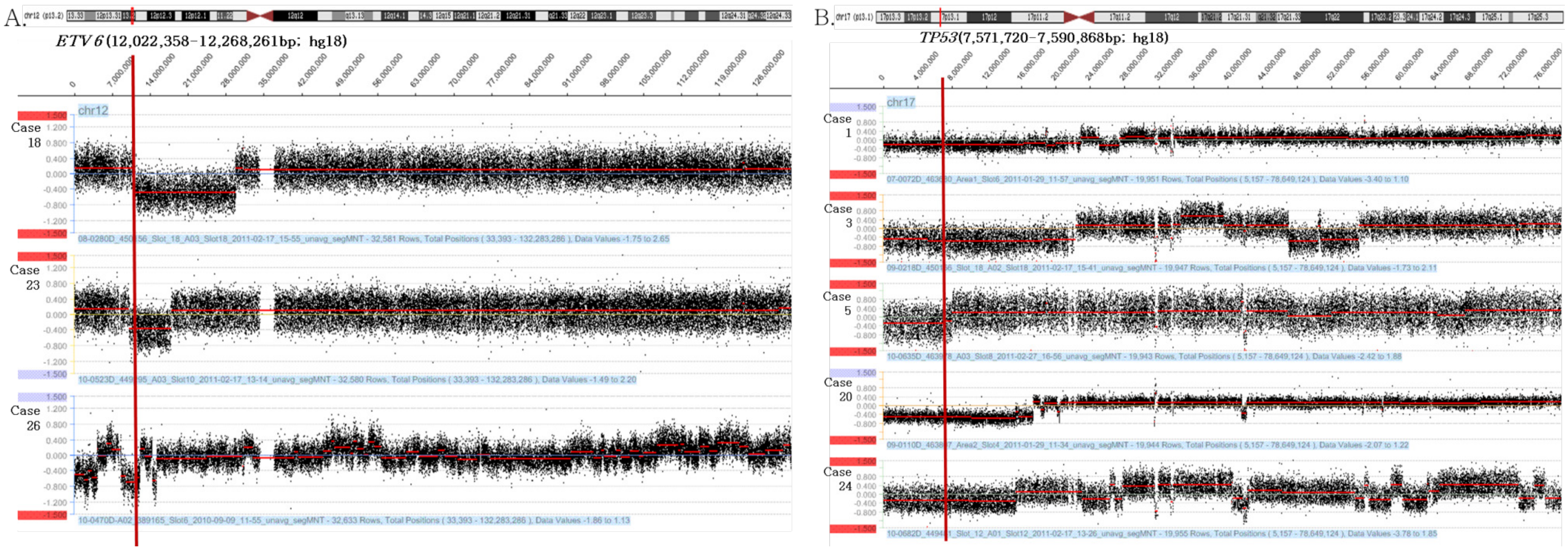


Figure S3 Losses of 12p13.2 including *ETV6* gene in three cases (A) and 17p harboring *TP53* gene in four cases (B) were detected by array CGH. Red vertical line indicates the location gene is located.