Suppl. Table 1a. Copy number alterations in C57/B1

region	gain	homologue region in human	
		cytoband	position (GRCh37/hg19)
3F3-H4	x1	1p22.1-p12 4q26 4q22.3-q26 1p31.3-p22.2 7q11.23	1:93905157-120696915 4:119596924-120703320 4:95284699-119338945 1:68589539-89738135 7:76282730-76575579
6A1-qter	x2	7q21.2-q21.3 7p22.1-p21.3 7q31.1-q36.1 7q36.1 7p15.3-p14.3 4q22.1-q22.3 4q27 1p31.3 2p11.2 2p13.3-p11.2 3q21.2-q21.3 3p25.2-p25.1 3p14.1-p12.3 3p26.3-p25.2 3q21.3-q22.1 10q11.21-q11.22 12p13.33 22q11.1-q11.21 12p13.31 12p13.33-p13.31 12p11.21 12p13.31-p11.21 12p11.21	7:92745197-97502117 7:7132996-12536829 7:112138919-149583263 7:150032467-150558657 7:23254035-33103246 4:89178698-95273100 4:121018693-122194687 1:67631910-68317098 2:88302422-89174373 2:68715037-87095119 3:125725101-129038484 3:12939278-15163105 3:64017713-75322601 3:61304-12897767 3:129094932-129632650 10:43277986-46218167 12:66113-2823666 22:17565811-18659740 12:8071763-9214464 12:2903120-7695890 12:30985917-31165338 12:9901365-30943693 12:31424829-32537434
8B3-C5	x1	4q32.2-q35.2 8p22-p21.3 19p13.12-p13.11 22q12.3 4q31.1-q31.23 19p13.2-p13.12 16q11.2-q22.1	4:163504024-190884657 8:18227877-20177976 19:16163040-19774937 22:33658332-35953121 4:141251922-150892329 19:12745060-14683008 16:46693273-69976105
10A1-qter	x1	6q22.31-q25.2 6q16.3-q22.1 6q22.1-q22.31 2q12.3-q13 10q21.1-q22.1 22q11.22-q11.23 21q22.3 19p13.12 19p13.3 12q23.3 22q12.3 12q13.2-q23.3	6:123289910-154997844 6:100545979-116923157 6:117047677-123151435 2:109065537-110402734 10:55366623-74862972 22:23396488-25031504 21:45278940-48084912 19:15052169-15262910 19:281181-4173052 12:104359309-108176937 22:32783299-33472414 12:55351591-104351507
18A1-qter	x1	10p11.21 10p12.1-p11.22 10p12.1 10p11.21 18p11.32 18q11.1-q12.3 2q14.3 5q22.1-q22.2 5q31.2-q32 5q22.2-q23.3 5q32-q33.1 18p11.22-p11.21 18q21.31-q21.32 18p11.21 18q12.3-q21.31 18q22.1-q23	10:35284099-35521818 10:28950711-32678701 10:27747786-28722506 10:35676708-37094546 18:112543-599224 18:18528605-41073893 2:127805408-128786667 5:110280120-112296881 5:137225085-147624774 5:112310736-130339352 5:147647374-150177176 18:10202644-11518916 18:54267924-58201586 18:11649353-13871680 18:41355914-54244819 18:66339761-78010601

region	loss	homologue region in human	
		cytoband	position (GRCh37/hg19)
No Loss			
region	**breakpoint**	**homologue region in human**	
		cytoband	potential tumor associated genes
3F3	t	1p21.1	1:103342023-103574052 (*COL11A1*)
5A	dic	7q21.2	7:91875548-92030698 (*ANKIB1*)
9A1	dic	11q22.3	11:107373452-107436472 (*ALKBH8*)
10A1	dic	6q25.1	6:149068464-149398126 (*UST*)
12A	idic	2p25.1	2:11674242-11782914 (*GREB1*)
13A3	t	6p22.3~p22.2	6:27107076-27108418 (*HIST1H4I*)
15A1	idic	5p13.1~p12	5:42423879-42721979 (*GHR*)
16A1	idic	16p13.3	16:6069095-7763340 (*RBFOX1*)
18A	idic	18p11.2	18:19230858-19284766 (*ABHD3*)

Legend: The regions of gain and loss of copy numbers, as well of breakpoints of balanced rearrangements, observed in C57/B1 and the corresponding homologue regions in humans, are listed as cytoband and position (GRCh37/hg19).

Suppl. Table 1b. Copy number alterations in B16-F0

region	gain	homologue region in human	
		cytoband	position (GRCh37/hg19)
1A3-B	x1	6p12.2-p12.3	6:49813958-52703905
		6p12.1-q13	6:56359076-73210217
		8q13.1-q21.13	8:66403591-75214401
4A1-C6	x2	1p31.3-p32.1	1:58654679-67096416
		9p21.2-p24.1	9:6847129-27300708
		9p13.1-p21.2	9:27325075-38472102
		9q21.31-q21.32	9:80378606-83600221
		9q22.33-q33.2	9:97275612-120726664
		6q15-q16.3	6:87084169-99797137
		8q21.3-q22.1	8:86044134-96234554
		8q12.3	8:62182367-63105957
		8q12.1-q12.3	8:55737745-61783006
6A1-qter	x2	7q21.2-q21.3	7:92745197-97502117
		7p22.1-p21.3	7:7132996-12536829
		7q31.1-q36.1	7:112138919-149583263
		7q36.1	7:150032467-150558657
		7p15.3-p14.3	7:23254035-33103246
		4q22.1-q22.3	4:89178698-95273100
		4q27	4:121018693-122194687
		1p31.3	1:67631910-68317098
		2p11.2	2:88302422-89174373
		2p13.3-p11.2	2:68715037-87095119
		3q21.2-q21.3	3:125725101-129038484
		3p25.2-p25.1	3:12939278-15163105
		3p14.1-p12.3	3:64017713-75322601
		3p26.3-p25.2	3:61304-12897767
		3q21.3-q22.1	3:129094932-129632650
		10q11.21-q11.22	10:43277986-46218167
		12p13.33	12:66113-2823666
		22q11.1-q11.21	22:17565811-18659740
		12p13.31	12:8071763-9214464
		12p13.33-p13.31	12:2903120-7695890
		12p11.21	12:30985917-31165338
		12p13.31-p11.21	12:9901365-30943693
		12p11.21	12:31424829-32537434
8C4-D2	x1	16q11.2-q22.1	16:46659361-69942202
9F3-F4	x1	3p22.2-p24.1	3:27712199-37219649
		3p21.31-p22.2	3:37227752-46381878
11B1-E2	x1	5q35.3	5:177531363-180585244
		5q23.3-q31.1	5:130484032-134063627
		5q33.1-q33.2	5:150381711-154330989
		1q42.13	1:227919753-228703212
		17p11.2	17:16917258-21343117
		17p12-p11.2	17:15731601-16472951
		17p13.3-p12	17:0-15625804
		17q11.1-q11.2	17:25525650-28853901
		17q11.2-q12	17:29058377-36200511
		17q21.32-q23.2	17:45560334-60326198
		17q12-q21.31	17:36351926-43638822
		17q21.31-q21.32	17:43706746-45150591
		17q21.32	17:45188646-45518436
		17q23.2-q24.1	17:60483588-62760387
		17q24.1-q24.2	17:62990972-66110690
		17q24.2-q25.3	17:66224207-81175056
17B3-D	x1	6p12.3-p21.2	6:39298722-49714113
		19p13.2-p13.3	19:4229085-6940562
		2q12.3	2:106767529-108195055
		3p24.3-p25.1	3:16266324-20190407

region	loss	homologue region in human	
		cytoband	position (GRCh37/hg19)
1D-E1	x1	5q21.1-q21.2	5:99084032-103392710
1F-H6	x1	1q32.2-q42.13	1:207402594-227457026
		1q43-q44	1:240057965-246962441
		1q23.1-q32.2	1:158547113-207361619
3F3-H4	x1	1p22.2-p31.3	1:68121446-89272452
		4q22.3-q27	4:94363548-119782165
		1p11.2-p22.1	1:93439600-120801119
4D-qter	x1	1p32.1-ptr	1:933238-58547094
5D-F	x1	1q22.1-q22.2	1:89498675-93369782
		4p16.3	4:559243-1058871
		4p16.3-q22.1	4:4183016-88079035
		12q24.33	12:131894446-132945956
		22q11.23-q12.1	22:24805798-28760295
		12q23.3-q24.11	12:107931580-110048615
8A4-C2	x1	21p11.2	21:9594592-9809818
		4q32.2-qtr	4:162582872-189963502
		4q31.21-q31.3	4:140330768-149971177
		22q12.3	22:33262346-35459147
		19p13.11-q13.12	19:16052230-19664128
		8p21.3-p22	8:18135309-20320465
12A3-C1	x1	14q12-q22.1	14:24687986-51784456
		7q31.1	7:108131761-112496091
		2q11.1	2:94607466-94720140
		9p11.2	9:40364174-40478572
		cent.	9:42990554-43106968
		9q13-q21.11	9:64504248-66012148
		7p21.1-p21.3	7:12522126-19709187
13A1-A3	x1	6p22.1-p22.3	6:20064992-28544283
		7p13-p14.2	7:36484897-43566331
		1q42.3-q43	1:235166745-239921359
		10p15.1-p15.3	10:92758-5823659
15A1-B3	x1	5p12-p15.31	5:8927633-42888873
14A1-qter	x1	3p14.3-p14.1	3:57993765-64009700
		3p24.3-p24.1	3:23146386-27721393
		14q22.1	14:52272055-52598781
		6p21.2	6:39069766-39266486
		10q22.1-q22.3	10:74870164-81255099
		3p21.1-p14.3	3:52350060-57931230
		3p25.1	3:15245114-16307845
		10q11.2-q11.23	10:46488677-51727392
		10q23.1-q23.2	10:82019368-88976316
		14q22.1-q23.1	14:52688635-58629894
		14q11.2-q12	14:20211286-24987352
		14q12	14:25040539-25149959
		13q12.12	13:25188452-25511922
		13q12.11	13:20207279-23370461
		13q14.2	13:49821990-50161404
		13q12.13	13:25685086-26668986
		13q12.12	13:23853398-24896355
		13q14.2-q14.3	13:50192169-52356487
		8p23.1	8:9744629-11737304
		8p21.3-p12	8:20206584-29151199
		13q14.11-q14.2	13:41469941-49799059
		13q14.3-q33.1	13:53226033-103089581
19A-B	x1	11q12.1-q13.3	11:58108647-68942254
		9q21.11-q21.31	9:68221841-80162449
XD-F5	x1	Xp22.11-p22.2	X:10447551-23831475
		Xp11.11-p11.22	X:52958297-56292129
		Xp22.2	X:9720195-9949488
		Xq21.33-q23	X:94193017-115283323
		Xq11.1-q21.33	X:63633840-94173088
		Yp11.2	Y:3057265-6133938

region	Break point	homologue region in human	
		cytoband	potential tumor associated genes
1A3	t	8q21.11	8:74692332-74791145 (*UBE2W*)
1E2	del	18q22.1	18:64168320-642714098 (*CDH19*)
3F3	t	1p21.1	1:103342023-103574052 (*COL11A1*)
4C6	t	1p31.3	1:64239693-64647181 (*ROR1*)
6B2	inv	7q35	7:143657027-143658108 (*OR2F1*)
6G1	inv	12p11.21	12:32259769-32536567 (*BICD1*)
7A	dic	19q13.42	19:54818353-54824409 (*LILRA5*)
9A5	t	11q24.1	11:123396344-123498482 (*GRAMD1B*)
13A3	t	6p22.3	6:20534688-21232635 (*CDKAL1*)
16A	t	16p13.3	16:6069095-7763340 (*RBFOXI*)
19A	dic	11q13.3	11:68671310-68708070 (*IGHMBP2*)

Legend: The regions of gain and loss of copy numbers, as well of breakpoints of balanced rearrangements, observed in B16-F0 and the corresponding homologue regions in humans, are listed as cytoband and position (GRCh37/hg19).