

SUPPLEMENTARY

MH-22A			
region	gain	homologue region in human	
		cytoband	position (GRCh37/hg19)
2A3-B	+1	10p12.31-p12.1 2q22.1 2q13 9q33.2-q34.3	10:20105168-27531068 2:138721590-139537918 2:113730780-114036527 9:123514256-141019076
2H1	+1	20q11.21-q11.23	20:30028322-37207504
3C-C	+1	4q28.3-q31.1	4:138440072-141075338
5pter-B3	+2	7q11.23-q21.13 7q22.1-q22.3 7p15.3 7q36.1-q36.3 7p15.3 2p23.3-p23.2 18p11.32 22q12.2-q12.3 4p16.3 4p16.3-p16.1	7:76751751-92219708 7:102389418-105208124 7:22852251-23240630 7:150642049-157210133 7:22765503-22771621 2:26395960-29025806 18:721592-812327 22:32014477-32509016 4:1160720-3770251 4:6783102-8873543
5B3-C1	+1	4p16.3-p16.1 4p15.33-p15.2	4:4190530-10686489 4:11394774-27027003
5F-qter	+1	12q24.31-q24.33 7p22.3-p22.1 7p11.2 7q11.21-q11.23 7q21.3-q22.1 13q12.13-q12.3	12:122277433-132336328 7:192969-6866401 7:55861237-56184093 7:65338254-76648340 7:97613996-102283316 13:26706253-31549639
6pter-qter	+1	1p31.3 2p13.3-p11.2 2p11.2 3p26.3-p25.1 3p14.1-p12.3 3q21.2-q22.1 4q22.1-q22.3 4q27 7p22.1-p21.3 7p15.3-p14.3 7q21.2-q21.3 7q31.1-q36.1 10q11.21-q11.22 12p13.33-p11.21 22q11.1-q11.21	1:59041099-68299150 2:68694693-87089047 2:88326724-90044439 3:238279-15140670 3:64079543-74570291 3:125725198-129612419 4:89011416-95264027 4:120980577-122302214 7:7196565-12443567 7:23275586-33102409 7:92759368-97501854 7:112405787-150558592 10:43278249-47949417 12:175931-32536567 22:17565844-20745048
7D3-E3	+2	15q25.3-q26.1 15q25.1-q25.3 11p11.12 11q13.4-q14.3 11p15.4-p15.1	15:88402982-91565833 15:80351910-85682376 11:49168187-49230222 11:71639747-89322779 11:3659733-6704632
7F5-qter	+1	11p15.5-p15.4 11q13.3-q13.4	11:167784-3253616 11:68747490-71239227
10D2-D2	+1	12q14.3-q15	12:66217911-69995350
12pter-B1	+2	2p25.3-p25.1 7q22.3-q31.1 7p21.3-p21.1 7q31.1	2:38814-10271545 7:105205567-107643700 7:12610203-19748710 7:110303110-112130942

12F1-qter	+1	14q32.2-q32.33 7q36.3 7p21.1-p15.3	14:100204030-106237742 7:157331750-158937649 7:19758933-22396763
14C1-D1	+1	14q11.2 14q22.1-q23.1 14q11.2-q12 14q12 13q12.12 13q12.11 13q14.2 13q12.13 13q12.12	14:21359558-21424595 14:52734431-58764857 14:20215587-24977471 14:25042728-25103473 13:24995064-25497018 13:20207788-22278637 13:49822047-50159719 13:25735822-26625198 13:24734861-24896096
15D1-D1	+1	8q24.21	8:130760442-131455906
Xpter-qter	+1	Xp11.23-p11.22 Xp21.1-p11.23 Xq23-q24 gap Xq24-q27.1 Xq27.2-q28 Xq23 Xp22.31-p22.2 Xp22.33 Xp22.11-p21.1 Xq11.1-q23 Yp11.2 Xp11.22 Xp11.22 Xp11.22-p11.21 Xp22.2 Xp22.2 Xp22.2-p22.11	X:47967365-52790617 X:31089360-47991995 X:115301975-117590949 X:117629861-139866723 X:140269934-154688276 X:114795501-114885181 X:9935392-9936134 X:3522411-3631649 X:23851470-37316548 X:62854847-114468635 Y:4868267-5610265 X:51149767-51151687 X:52920336-53024651 X:53078273-56593443 X:9693386-9936134 X:9935392-9936134 X:10413350-23804343
region	loss	homologue region in human	
		cytoband	position (GRCh37/hg19)
2B-C3	-1	9q33.2-q33.3 2q22.1-q31.3	9:125288637-127952218 2:140988992-180871840
4E2-E2	-1	1p36.33-p36.31	1:1981909-6526255
5C1-F	-1	4p15.1-p11 4q12-q22.1 1p22.2-p22.1 4p16.3 12q24.33 22q11.23-q12.1 12q23.3-q24.11 12q24.11-q24.31 12q24.31	4:30722037-49064098 4:52709166-89152474 1:89829605-93828149 4:492989-1107350 12:132379196-133532892 22:25202188-29153503 12:108523248-122270562 12:110562140-121623876 12:121647660-122270562
10B1-B2	-1	6q21	6:107473761-111804918
12B1-F1	-1	7q31.1 14q12-q22.1 14q23.1-q32.2	7:107788082-108215294 14:25278862-52197445 14:58666798-100408397
13D1-qter	-1	5q11.1-q12.3 5p12	5:49692026-65479443 5:43486803-45696253
14pter-B	-1	3p14.3-p14.1 3p24.3-p24.1 14q22.1 6p21.2 10q22.1-q22.3 3p21.1-p14.3 3p25.1 10q11.2-q11.23 10q23.1-q23.2	3:57994127-64009658 3:23244511-27525911 14:52292913-52536545 6:39071840-39290744 10:74870217-81965433 3:52350335-57914895 3:15247659-16378822 10:46549955-51732941 10:82031576-88951225

		10q22.3-q23.1	10:81315608-81742370
14D1-qter	-2	8p23.1 8p21.3-p12 13q14.11-q14.2 13q14.3-q33.1	8:9911778-11422113 8:21547915-29120641 13:41506056-49783888 13:53226844-103054124
16pter-B1	-1	16p13.3-p13.11 16p13.11 8q11.21 12p11.21 22q11.21(-q11.23) 3q27.1-q27.3	16:3254247-15609205 16:15528152-16236931 8:48173167-49834299 12:32552463-33049774 22:18893541-23265085 3:182840001-187463515
16C3-qter	-1	21q21.1-q22.3	21:18884700-46351904
18pter-B3	-1	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	10:35297479-35501886 10:28966271-32667726 10:27793197-28909928 10:35535953-35930362 18:158483-581524 18:18529701-40857615 2:127413509-128785694 5:110405760-112258236 5:137223657-147719412
region	breakpoint	homologue region in human	
		cytoband	potential tumor associated genes
2A3	inv/del	10p12.31	PLXDC2
2B	inv/del	9q33.2	OR1J4, OR1N1
2C3	inv/del	2q31.3	CWC22
2H1	inv/del	20q11.21	DEFB123
5B1	inv dic	2p23.2	BRE
5B3	inv dic	4p16.1	KIAA0232
5C1	inv dic	4p15.1	PCDH7
5F	t	12q24.31	SETD1B
7D3	ins	15q25.3	NTRK3
7E3	ins	11p15.4	MRPL17
10B1	del	6q21	REV3L
10B2	del	6q21	PDSS2
12A1	dup	2p25.1	ASAP2
12B1	dup	7q31.1	LRRN3
12F1	t	14q32.2	EML1
13D1	del	5q12.3	SREK1
13D2	del	5p12	C5orf34
14C1	t	14q11.2	RNASE2
14C2	t	14q11.2	RNASE2
14C3	t	14q11.2	ZFX2
14D1	t	13q12.12	SPATA13
16B1	dup	3q27.3	BCL6
16C3	dup	21q21.1	CXADR
16C4	dup	21q22.3	ZNF295
18B3	t	5q32	SPINK9
Hepa 1-6			
region	gain	homologue region in human	
		cytoband	position (GRCh37/hg19)
1pter-qter	+1	8q11.21-q12.1 8q13.1-q21.11 6p12.3-p12.2 6q11-q13 6p12.1-p11.2 2q14.3-q21.1 2q11.2-q12.2 13q33.1	8:50767106-56535248 8:67336477-76107163 6:49796129-52568703 6:61967179-73920868 6:56223874-58686221 2:128848553-131914911 2:97151065-106819719 13:103237605-103533914

		2q32.1-q32.2 2q32.2-q37.3 5q21.1 18q21.32-q22.1 2q14.3 2q14.1-q14.3 2q21.2-q22.1 1q32.1-q32.2 1q21.1 1p11.2 1q23.1-q32.1 Yq11.23 1q43-q44 4q26 1q32.2-q42.13	2:189007277-190504466 2:190506076-242812118 5:98439740-102728411 18:58351903-65328593 2:122585948-126347698 2:114436107-122578025 2:133138389-138607743 1:206075775-207534964 1:143881371-144095755 1:120754434-120887322 1:158516903-205922697 Y:28358518-28544030 1:240253393-247125743 4:119339188-119512723 1:207575939-227644727
2G-qter	+1	20p13-p11.21 20p13 20q11.21-q13.32 20q13.32-q13.33	20:1736101-25606620 20:102147-1447942 20:29933153-58056214 20:58148222-62907435
3pter-qter	+1	8q21.11-q21.3 8q12.3-q13.1 3q24-q25.1 3q26.2-q26.32 3q26.32-q27.1 4q27-q31.1 9p11.2 21p11.2 9p12 9q13 13q13.2-q14.11 3q25.1-q26.2 4q31.23-q32.2 1q21.1-q23.1 1p22.1-p12 4q26 4q22.3-q26 1p31.3-p22.2 7q11.23	8:76197937-87035414 8:64075897-67315825 3:148467535-148965303 3:167857105-178105807 3:178137517-182818465 4:122242382-141190230 9:45446787-46098069 21:10369840-10592667 9:42028291-42246766 9:68139917-68294733 13:34463185-41254213 3:149055816-167822106 4:150966383-163096512 1:144676687-158154741 1:93905157-120696915 4:119596924-120703320 4:95284699-119338945 1:68589539-89738135 7:76282730-76575579
6E3-qter	+1	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	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
7F2-qter	+2	16p13.11-p12.3 16p12.3-p12.2 16p12.2-p11.2 16p11.2 16p11.2 10q26.11-q26.3 11p15.5-p15.4 11q13.3-q13.4	16:16681590-18325190 16:18608156-21351663 16:21572755-28339524 16:28390845-29030948 16:29661006-31520748 10:121224592-135295738 11:192898-3098752 11:68728143-71212974
8pter-qter	+1	19p13.2 13q33.1-q34 8p23.3-p23.2 8p23.2-p23.1	19:7112183-8071013 13:103533915-115092930 8:591286-5358752 8:5368147-6693649

		13q14.3 8p11.23-p11.21 8p11.21 8p12 8p23.1 8p23.1-p22 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 16q22.1-q24.3 1q42.13-q42.3 10p11.22-p11.21	13:52435459-53211718 8:36716542-42505949 8:42691750-43058925 8:29190466-36677574 8:8108776-9640417 8:12579073-17958954 4:163504024-190884657 8:18227877-20177976 19:16163040-19774937 22:33658332-35953121 4:141251922-150892329 19:12745060-14683008 16:46693273-69976105 16:70109527-90110030 1:229404294-235324774 10:33112469-35152269
10pter-qter	+1	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
11pter-qter	+1	22q12.1-q12.2 7p13-p11.2 2p16.2-p14 5q35.1-q35.2 5q33.2-q35.1 5q35.3 5q23.3-q31.1 5q33.1-q33.2 1q42.13 17p11.2 17p12-p11.2 17p13.3-p12 17q11.1-q11.2 17q11.2-q12 17q21.32-q23.2 17q12-q21.31 17q21.31-q21.32 17q21.32 17q23.2-q24.1 17q24.1-q24.2 17q24.2-q25.3	22:29251511-32022116 7:43906144-55317931 2:53882943-68694726 5:172736725-173663599 5:154331837-171932313 5:177531363-180585244 5:130484032-134063627 5:150381711-154330989 1:227919753-228703212 17:16917258-21343117 17:15731601-16472951 17:2-15625804 17:25525650-28853901 17:29058377-36200511 17:45560334-60326198 17:36351926-43638822 17:43706746-45150591 17:45188646-45518436 17:60483588-62760387 17:62990972-66110690 17:66224207-81175056
15pter-F1	+4	5p15.31-p12 8q22.1-q24.3 22q12.3-q13.33 12p11.1	5:8927745-42888975 8:97446632-146158346 22:35962951-51222438 12:33476533-34210697
15F1-qter	+2	12q12-q13.2	12:38607141-55072925
16B5-qter	+1	3q11.1-q21.2 3p12.3-p11.1 21q11.2-q22.3 21q11.2 18p11.21 2q21.1	3:93527487-125343459 3:75865702-90309600 21:15515528-43438088 21:14535253-14714360 18:15016525-15155234 2:132604281-132757591

18D-qter	+1	5q22.2-q23.3 5q32-q33.1 18p11.22-p11.21 18q21.31-q21.32 18p11.21 18q12.3-q21.31 18q22.1-q23	5:112310736-130339352 5:147647374-150177176 18:10202644-11518916 18:54267924-58201586 18:11649353-13871680 18:41355914-54244819 18:66339761-78010601
19pter-qter	+2	11q12.1-q13.3 9q21.11-q21.31 2q13 9p24.3-p24.1 10q11.23-q21.1	11:57844834-68709722 9:69086307-82777364 2:114171139-114321953 9:51374-6659223 10:51917603-54540082
Xpter-A3	+4	Xp11.23-p11.22 Xp21.1-p11.23 Xq23-q24	X:48262014-51358982 X:37364439-47520178 X:115210308-117585111
region	loss	homologue region in human	
		cytoband	position (GRCh37/hg19)
4C4-C6	-1	9p24.1-p21.2 1p32.1-p31.3	9:6847129-27220407 1:59120351-67562260
4D2-qter	-1	1p36.33-p32.2~1	1:894315-59012766
5pter-A1	-1	7q11.23-q21.2	7:76702246-92676514
5A2-F	-2	7q22.1-q22.3 7p15.3 7q36.1-q36.3 7q36.1 7p15.3 2p23.3 2p23.3 2p23.3-p23.2 18p11.32 22q12.2-q12.3 4p16.3 4p16.3-p11 4q12-q22.1 1p22.2-p22.1 4p16.3 12q24.33 22q11.23-q12.1 12q23.3-q24.11	7:102331617-105210094 7:22903126-23240676 7:150588373-157179154 7:149628652-149959756 7:22595306-22772664 2:26394466-27256616 2:27256674-27749458 2:27759882-29024462 18:683166-844532 22:32022117-32511666 4:1109142-3830658 4:4184743-49083612 4:52689038-89000187 1:89950168-93744300 4:493106-1023731 12:132378991-133522542 22:25201765-29156283 12:108325357-110486420
14A3-qter	-1	3p21.1-p14.3 3p25.1 10q11.2-q11.23 10q23.1-q23.2 14q22.1-q23.1 14q11.2-q12 14q12 13q12.12 13q12.11 13q14.2 13q12.13 13q12.12 13q14.2-q14.3 8p23.1 8p21.3-p12 13q14.11-q14.2 13q14.3-q33.1	3:52350060-57931230 3:15245114-16307845 10:46488677-51727392 10:82019368-88976316 14:52688635-58629894 14:20211286-24987352 14:25040539-25149959 13:25188452-25511922 13:20207279-23370461 13:49821990-50161404 13:25685086-26668986 13:23853398-24896355 13:50192169-52356487 8:9744629-11737304 8:20206584-29151199 13:41469941-49799059 13:53226033-103089581
19D2-qter	-1	10q23.2-q26.11	10:89234113-121219507
XA3-qter	-1	Xq24-q27.1 Xq27.2-q28 Xq23	X:117586665-140073167 X:140429142-154494231 X:114569624-114885545

		Xp22.31-p22.2 Xp22.11-p21.1 Xq11.1-q23 Yp11.2 Xp11.22-p11.21 Xp22.2 Xp22.2-p22.11	X:8784578-9687806 X:23850309-37316857 X:62853720-114517895 Y:4132374-5642381 X:52987493-56318562 X:9688235-9917528 X:10415591-23849592
region	breakpoint	homologue region in human	
		cytoband	potential tumor associated genes
1A1	dic	8q12.1	XKR4
2G	t	20p11.23	SLC24A3
4E2	t	1p36.32	AJAP1
4D2	del	1p34.3	ZMYM6
4C4	del	9p21.3	CDKN2A
4C6	del	1p32.2	DAB1
5A1	t	7q21.12	KIAA1324L
5F	t	12q24.11	C12orf34
6E3	del	3p26.1	GRM7
7F2	t	No homologues	
8A1	dic	8p23.1	MCPH1
14A3	del	3p14.3	ERC2
18D	del	5q23.1	TNFAIP8
19D2	t	10q25.2	RBM20
XA3	del	Xq24	DOCK11

Table The regions of gain and loss of copy numbers, as well of breakpoints of balanced rearrangements observed in MH-22A and Hepa 1-6 the corresponding homologous regions in humans are listed as cytoband and position (GRCh37/hg19).