Supplement Table 1. The regions of gain and loss of copy numbers, as well of breakpoints of balanced rearrangements, observed in MTLC1 and the corresponding homologue regions in humans, are listed as cytoband and position (GRCh37/hg19). The chromosomal rearrangements are reported according to ISCN (2020)[29]

region	gain of copies basic copy number 6	homologue region in human	
		cytoband	position (GRCh37/hg19)
2A1-C1	+2	10p15.1-p12.1	10:5915452-27157072
		10p12.1	10:27398972-27531240
		2q22.1	2:138721435-139545160
		2q13	2:113723845-114137444
		9q34.11-q34.3	9:131071714-141019156
		9q33.2-q34.11	9:123526077-131061546
		2q22.1-q23.3	2:140065297-151873807
3F1-G3	+2	1q21.2-q23.1	1:150226467-158154741
		1p22.1-p12	1:93905157-120696915
		4q26	4:119596924-120703320
		4q22.3-q24	4:95284699-101730246
15A-qter	+3	5p15.31-p12	5:8927745-42888975
		8q22.1-q24.3	8:97446632-146158346
		22q12.3-q13.33	22:35962951-51222438
		12p11.1	12:33476533-34210697
		12q12-q13.2	12:38607141-55072925
17A-qter	+1	6q25.2-q25.3	6:155053083-160101646
		6q27	6:167120855-167552070
		6q25.3-q27	6:160103032-166797236
		6q27	6:167859539-170893754
		5q15-q21.1	5:96202316-98405239
		16p13.3	16:222880-3208490
		5q35.1	5:171946752-172722349
		6p21.32-p21.2	6:33359177-39058058
		21q22.3	21:43490502-45122943
		19p13.12	19:15270296-15808207
		19p13.2	19:8366687-8811037
		6p22.1-p21.32	6:29322703-33098080
		6p21.32	6:33098080- 33297218
		6p21.2-p12.3	6:39266498-49681826
		3p25.1-p24.3	3:16307846-20231899
		2q12.2-q12.3	2:107383985-108798215
		19p13.3	19:4229082-6862967
		5q21.1-q22.1	5:102759315-110063021
		18p11.32-p11.22	18:2534401-9972541
		2p23.2-p16.3	2:29033520-51699597
		2p16.3-p16.2	2:51709987-53282184
		18p11.32	18:861722-2534400

region	loss	homologue region in human	
		cytoband	position (GRCh37/hg19)
3A-F1	-2	8q21.11-q21.3	8:76197937-87035414
		8q12.3-q13.1	8:64075897-67315825
		3q24-q25.1	3:148467535-148965303
		3q26.2-q26.32	3:167857105-178105807
		3q26.32-q27.1	3:178137517-182818465
		4q27-q31.1	4:122242382-141190230
		9p11.2	9:45446787-46098069
		21p11.2	21:10369840-10592667
		9p12	9:42028291-42246766
		9q13	9:68139917-68294733
		13q13.2-q14.11	13:34463185-41254213
		3q25.1-q26.2	3:149055816-167822106
		4q31.23-q32.2	4:150966383-163096512
		1q21.1-q21.2	1:144676687-150226467

3G3-qter	-2	4q24-q26	4:101730246-119338945
		1p31.3-p22.2	1:68589539-89738135
		7q11.23	7:76282730-76575579
4A1-A4	-3	8q12.1-q12.3	8:56650304-62695565
		8q21.3-q22.1	8:87057363-97246782
		8q12.3	8:63094926-64018516
		6q14.3-q16.1	6:87793887-94723614
5A1-E5	-2	7q11.23-q21.2	7:76702246-92676514
		7q22.1-q22.3	7:102331617-105210094
		7p15.3	7:22903126-23240676
		7q36.1-q36.3	7:150588373-157179154
		7q36.1	7:149628652-149959756
		7p15.3	7:22595306-22772664
		2p23.3	2:26394466-27256616
		2p23.3	2:27256674-27749458
		2p23.3-p23.2	2:27759882-29024462
		18p11.32	18:683166-844532
		22q12.2-q12.3	22:32022117-32511666
		4p16.3	4:1109142-3830658
		4p16.3-p11	4:4184743-49083612
		4q12-q21.22	4:52689038-83815615
5E5-qter	-3	4q21.22-q22.1	4: 83815615-89000187
		1p22.2-p22.1	1:89950168-93744300
		4p16.3	4:493106-1023731
		12q24.33	12:132378991-133522542
		22q11.23-q12.1	22:25201765-29156283
		12q23.3-q24.11	12:108325357-110486420
		12q24.11-q24.31	12:110488793-121497537
		12q24.31-q24.33	12:121577100-132336561
		7p11.2	7:56019352-56184138
		7q11.21-q11.22	7:66808098-72045725
		7q11.23	7:72536306-76149827
		7q22.1	7:99552841-102191754
		7p22.3-p22.1	7:169204-6771649
		7q21.3-q22.1	7:97598308-99229367
		13q12.13-q13.2	13:26784894-34260463
6A1-D	-2	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
		2p11.2	2:88302422-89174373
		2p13.3-p11.2	2:68715037-87095119
		3q21.2-q21.3	3:125725101-128215999
7A1-qter	-2	19q13.42-q13.43	19:54368915-57485284
		19q13.43	19:58523795-59089552
		19q13.31-q13.33	19:45010010-48707700
		19q12-q13.31	19:30093064-44860951
		19q12	19:28589680-30085362
		19q13.33-q13.41	19:48800017-51921957
		16p13.11	16:16252815-16388674
		11p15.1-p14.3	11:17403485-25251145
		15q11.2	15:22833222-23086601
		15q11.2-q13.1	15:23914751-28586067
		15q13.1-q13.3	15:29107424-32578594
		15q26.3	15:99080385-102265870
		15q26.1-q26.3	15:91593058-99078056
		15q25.3-q26.1	15:85829657-91565912
		15q25.1-q25.3	15:80253398-85682414
		11p11.12	11:49250334-49827246
		11q13.4-q14.3	11:71627032-89350901
		10p11.21	10:37191655-37402201

		11p15.4-p15.1	11:3631069-17360027
		16p13.11	16:15260325-15369270
		16p13.11-p12.3	16:16681590-18325190
		16p12.3-p12.2	16:18608156-21351663
		16p12.2-p11.2	16:21572755-28339524
		16p11.2	16:28390845-29030948
		16p11.2	16:29661006-31520748
		10q26.11-q26.3	10:121224592-135295738
		11p15.5-p15.4	11:192898-3098752
		11q13.3-q13.4	11:68728143-71212974
9A1-C	-2	11q14.3-q22.3	11:89860533-107436639
		19p13.2	19:8919008-11689880
		7p14.3-p14.2	7:33134362-36494039
		11q22.3-q25	11:107452617-134843539
		15q21.2	15:51349622-51942502
		15q21.2-q22.2	15:51961808-61689774
9C-qter	-1	15q22.2-q25.1	15:61689774-78956872
		6p12.2-p12.1	6:52656530-55784577
		6q13-q14.3	6:74104388-86360515
		15q25.1	15:79042978-80196839
		3q22.3-q24	3:138372654-148087492
		3q22.1-q22.3	3:129931635-138353358
		3p21.31-p21.1	3:46446256-52346387
		3p24.1-p22.2	3:27753690-37261140
		3p22.2-p21.31	3:37269243-46423369
11A1-E2	-3	22q12.1-q12.2	22:29251511-32022116
		7p13-p11.2	7:43906144-55317931
		2p16.2-p14	2:53882943-68694726
		5q35.1-q35.2	5:172736725-173663599
		5q33.2-q35.1	5:154331837-171932313
		5q35.3	5:177531363-180585244
		5q23.3-q31.1	5:130484032-134063627
		5q33.1-q33.2	5:150381711-154330989
		17p11.2	17:16917258-21343117
		17p12-p11.2	17:15731601-16472951
		17p13.3-p12	17:2-15625804
		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-q24.3	17:66224207-67158507
11E1-qter	-1	17q24.3-q25.3	17:67158507-81175056
12A1-A3	-2	2p25.1-p23.3	2:10303009-26361943
		2p25.1	2:9354723-9994801
		2p25.1	2:9996101-10284917
		2p25.3-p25.1	2:140908-9278318
		7q22.3-q31.1	7:105210238-107772185
		7p21.3-p21.2	7:12561752-15205762
12A3-B3	-4	7p21.2-p21.1	7: 15205762-19748810
		7q31.1	7:107772206-112136146
		14q12	14:25157192-26697245
12B3-E	-2	14q12-q22.1	14: 26697245-52251174
		14q23.1-q32.31	14:58666612-101479263
13A-qter	-2	10p15.3-p15.1	10:138698-5865622
		1q42.3-q43	1:235330060-240084659
		7p14.2-p13	7:36524506-43605930
		6p22.3-p22.1	6:20065223-28502803
		6p25.3-p23	6:181261-15099150
		6p23-p22.3	6:15104709-20060798
		9q22.1-q22.32	9:91031851-97067712

		5q35.2-q35.3	5:173750964-177039611
		5q31.1-q31.2	5:134073478-137090938
		9q21.32-q21.33	9:86231955-90340399
		9q22.32-q22.33	9:97320957-99417669
		9p13.1	9:38810965-40707569
		9q12-q13	9:65585614-65901647
		9p11.2	9:43623473-43941731
		8q22.1	8:97247028-97373828
		5p15.33-p15.31	5:191425-7935441
		5q14.3-q15	5:84566270-96144383
		5q13.2-q14.3	5:70265557-84371909
		5q11.1-q13.2	5:49569996-68922426
		1p11.2	1:121149401-121350677
		5p12	5:43446298-46118514
14A1-E2	-1	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-q21.33	13:53226033-69786475
18A-E1	-2	10p11.21	10:35284099-35521818
		10p12.1-p11.22	10:28950711-32678701
		10p12.1	10:27747786-28722506
		10p11.21	10:35676708-37094546
		18p11.32	18:112543-599224
		18q11.1-q12.3	18:18528605-41073893
		2q14.3	2:127805408-128786667
		5q22.1-q22.2	5:110280120-112296881
		5q31.2-q32	5:137225085-147624774
		5q22.2-q23.3	5:112310736-130339352
		5q32-q33.1	5:147647374-150177176
		18p11.22-p11.21	18:10202644-11518916
		18q21.31-q21.32	18:54267924-57096691
18E1-qter	-1	18q21.32	18:57096691- 58201586
		18p11.21	18:11649353-13871680
		18q12.3-q21.31	18:41355914-54244819
		18q22.1-q23	18:66339761-78010601
19A1-D1	-3	11q12.1-q13.3	11:57844834-68709722
		9q21.11-q21.31	9:69086307-82777364
		2q13	2:114171139-114321953
		9p24.3-p24.1	9:51374-6659223
		10q11.23-q21.1	10:51917603-54540082
		10q23.2-q24.33	10:89234113-105317067
19D1-qter	-4	10q24.33-q26.11	10: 105317067-121219507
XA1-A6	-2	Xp11.23-p11.22	X:48262014-51358982
		Xp21.1-p11.23	X:37364439-47520178
		Xq23-q24	X:115210308-117585111
		Xq24-q26.3	X:117586665-136267340

XA6-A7	-3	Xq26.3-q27.1 Xq27.2-q28	X:136267340-140073167 X:140429142-152161695
XA7-qter	-2	Xq28 Xq23 Xp22.31-p22.2 Xp22.11-p21.1 Xq11.1-q23 Yp11.2 Xp11.22-p11.21 Xp22.2 Xp22.2-p22.11	X:152161695-154494231 X:114569624-114885545 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	idic	8q12.1	8:56014949-56454613 (*XKR4*)
2C1	del/inv.	2q23.3	2:151324709-151395525 (*RND3*)
3F1	del	1q21.3	1:152881021-152884362 (*IVL*)
3G3	del	4q25	4:110661852-110723335 (*CFI*)
4A4	del	6q16.1	6:93949738-94129265 (*EPHA7*)
5E5	del	No homologues	No homologues
6D1	del	No homologues	No homologues
9C	del	13q22.2	13:76123619-76180085 (*UCHL3*)
11E1	dic/del	17q24.3	17:67410839-67539472 (*MAP2K6*)
12A3	del	7q37.3	2:238875469-238951236 (*UBE2F*)
12B3	del/dup	14q12	14:25278862-25519503 (*STXBP6*)
12E	del	14q32.33	14:106610313-106610852 (*IGHV3-15*)
14E2	t	13q21.33	13:70274726-70682591 (*KLHL1*)
15A1	idic	5p12	5:42799982-42887494 (*SEPP1*)
17B1	t/del	6p22.1	6:29523292-29527702 (*UBD*)
18E1	t	18q21.32	18:57098172-57364612 (*CCBE1*)
19D1	t	10q25.1	10:106400859-107024993 (*SORCS3*)

Legend: del - deletion; dic - dicentric; dup - duplication; idic - isodicentric chromosome, inv - inversion; t - translocation.