

Cytogenetic Band	Locus (Mb)	Minimal Common Region				MCR Recurrence		Information about MCR/gene				Comparison with other datasets
		position (Mb)	size (Mb)	peak value	# genes	Gain/Loss %	Amp/Del %	viral integration site	miRNA	Cancer Gene	Murine Glioma	KLL/DNL Human Expression Dataset
<b>Gain/Amplification</b>												
1p35.2-1p35.1	31.5-32.31	31.5-32.18	0.67	0.78	12	21.6	8.1					KPNA6, DKFZp451J011
1p32.3-1p32.3	51.13-52.21	51.13-52.21	1.08	1.03	12	8.1	2.7		EPS15			
1p31.1-1p22.3	76.09-86.93	76.09-86.93	10.82	0.46	47	13.5	5.4	Bcl10	BCL10			C1orf29, IFI44, and CTBS
1p13.3-1p12	109.09-120.05	109.09-120.05	10.96	0.80	131	10.8	2.7	Rap1a, Nras	hsa-mir-197 TRIM33, NRAS			
1q21.3-1q21.3	150-150.12	150-150.12	0.11	0.57	3	16.2	5.4					IVL
1q21.3-1q22	151.37-152.53	151.37-152.53	1.15	0.60	39	16.2	5.4					
1q31.3-1q31.3	195.02-195.46	195.02-195.46	0.44	1.49	2	13.5	5.4					
1q32.1-1q32.1	198.16-198.58	198.16-198.58	0.41	1.00	4	16.2	5.4					ORC1L
1q32.1-1q32.1	199.03-199.6	199.03-199.6	0.56	1.60	7	13.5	2.7					
1q32.1-1q32.2	200.47-203.99	200.47-203.99	3.51	1.86	59	13.5	2.7		hsa-mir-135b			SOX13
1q42.3-1q43	231.04-234.33	231.04-234.33	3.27	1.62	22	13.5	2.7	D6Erd233e				
1q44-1q44	240.54-241.86	240.54-241.86	1.31	1.90	11	13.5	2.7					PNAS-4
2p25.1-2p25.1	10.14-10.54	10.14-10.54	0.39	0.77	5	8.1	2.7					TIEG2, RRM2
2q33.1-2q33.2	201.36-203.68	201.6-201.92	0.32	0.95	5	13.5	8.1					CFLAR, CASP10, CASP8
3p26.3-3p24.3	0.42-21.46	10.95-11.58	0.62	1.18	5	10.8	5.4					SLC6A11
3p26.3-3p24.3	0.42-21.46	12.91-13.84	0.92	1.18	5	10.8	5.4					
3p24.1-3p21.32	29.91-44.43	29.91-44.43	14.51	0.94	96	5.4	2.7	Ckfst7	hsa-mir-128 MLH1, CTNNB1			RBMA3, PLCD1, MYD88, OSR1
3p21.31-3p21.31	49.18-49.85	49.18-49.85	0.65	0.40	21	5.4	2.7					
3p21.1-3p13	52.91-73.2	52.91-73.2	20.28	0.67	82	5.4	2.7	Il17rb				PRKCD, WNT5A, CAST, FHIT, PITPRG, LRIG1
3q26.1-3q27.1	166.17-184.22	166.17-184.22	18.04	0.55	66	10.8	5.4	Evi1	EVH1, MDS1	ST6GAL1		BCHC, TLOC1, NLGN1, BAF53A, USP13, SOX2
4p12-4p12	47.43-47.91	47.43-47.91	0.47	0.96	4	5.4	2.7					
4q11-4q13.1	52.8-62.6	53.45-56.08	2.63	2.43	11	8.1	5.4	Kit	FIP1L1, CHIC2, PDGFRA, PDGFRA and KDR			NRG2, PURA, and DTR
5q31.2-5q31.2	138.98-139.9	138.98-139.9	0.91	0.49	11	10.8	2.7					
6p25.2-6p25.1	3.09-4.95	3.09-4.95	1.84	0.55	11	13.5	2.7					
6p21.2-6p21.2	37.71-39.11	37.71-39.11	1.39	0.85	5	8.1	2.7					[PIM1 oncogene at 37.19]
7p22.3-7p22.1	0.66-6.22	0.66-6.22	5.55	0.70	56	61.1	5.4	Gna12, Actb, Matk, hsa-mir-339 PMS2				NUDT1, JTV1, HRI
7p14.1-7p14.1	38.04-38.2	38.04-38.2	0.15	1.16	23	68.5	10.8					
7p14.1-7p12.3	39.27-48.47	39.27-48.47	9.18	0.68	62	66.7	10.8					CDC2L5, STK17A, BLVRA, YKT6, OGDH, IGFBP3
7p12.3-7p12.1	49.72-50.86	50.28-50.86	0.57	4.27	4	66.7	16.2					ZNFN1A1
7p11.2-7p11.2	54.41-56.44	54.41-56.27	0.85	4.39	4	75.9	37.8					EGFR
7q11.21-7q22.1	63.42-99.68	66.67-97.49	10.82	0.65	64	83.3	10.8					ODAG, ASB4
7q22.1-7q22.1	100.03-100.14	100.03-100.14	0.10	0.87	6	72.2	5.4					ARS2, ACHE
7q22.1-7q32.1	101.7-126.61	115.79-121.3	5.50	2.70	18	77.8	18.9					MGC33190, HBP1 and CAV1
7q36.1-7q36.3	149.61-158.24	149.61-158.24	8.62	0.65	67	79.6	13.5		hsa-mir-153-2			KCNH2, SHH
8q22.1-8q23.1	96.07-107.79	96.07-107.79	11.72	0.69	65	16.2	2.7		COX6C			ODF1, TIEG, FZD6, RIMS2, ST7
8q23.1-8q24.3	109.86-146.26	144.87-145.13	0.25	0.99	9	18.9	8.1					MYC, LRRC14, ZNF7
9p23-9p22.3	12.69-16.41	12.69-16.41	3.71	0.55	16	8.1	2.7					NFIB, SNAPC3
9p21.2-9p13.2	26.83-37.63	32.44-32.54	0.09	0.93	3	10.8	5.4					
9q33.2-9q33.3	122.66-122.97	122.66-122.97	0.31	1.06	8	5.4	2.7					OLFML2A
9q34.11-9q34.11	128.34-128.67	128.34-128.67	0.32	0.47	11	8.1	2.7					
9q34.3-9q34.3	135.62-136.58	135.62-136.58	0.95	0.42	18	13.5	2.7		SET			CACNA1B and CARD9
9q34.3-9q34.3	137.33-138.3	137.33-138.3	0.95	0.54	27	10.8	2.7					
10p15.3-10p11.2	0.28-35.97	30.64-35.97	5.33	0.84	18	13.5	8.1	Map3k8				
11q13.1-11q13.1	64.65-65.45	64.65-65.45	0.79	0.52	33	5.4	2.7					
11q13.5-11q14.1	77.26-78.05	77.26-78.05	0.78	3.40	9	5.4	2.7					
11q21-11q21	92.52-95.21	92.52-95.21	2.69	0.71	23	5.4	2.7					ZF, SRP46

12p13.33-12p13.0:17-1.78	0.17-1.78	1.60	0.46	15	16.2	2.7		ELKS	JARID1A, PRKWNK1, ELKS, FBXL14, CACNA1C
12p13.32-12p13.3:26-6.81	3.81-5.48	1.66	2.45	16	18.9	10.8		Ccnd2	CCND2, KCNA5
12p13.31-12p13.3:6.81-12.17	6.86-7.78	0.91	0.78	21	18.9	8.1	HcpH	hsa-mir-200c, hsa-mir-141	
12p12.3-12q12	15.02-37.98	21.59-29.56	7.96	2.56		16.2	13.5		PPFIBP1
12p11.21-12p11.3:32.38-33.46	32.38-33.46	1.07	0.61	6	10.8	2.7			
12q13.13-12q13.5:52-52.16	52-52.16	0.15	4.55	5	5.4	2.7			
12q13.2-12q13.3:54.51-55.28	54.88-55.28	0.39	0.89	17	10.8	8.1			STAT2
12q13.3-12q14.1:55.31-57.56	56.21-56.49	0.28	3.64	3	32.4	24.3			
12q14.2-12q14.2:62.87-63.4	62.87-63.4	0.52	1.92	6	10.8	2.7			GNS
12q14.3-12q15	65.02-66.89	65.02-66.89	1.85	2.61	6	8.1	5.4		DYRK2
12q15-12q15	66.92-69.81	67-67.96	0.95	4.28	10	24.3	21.6	Rap1b	
12q21.1-12q21.1:70.26-71.35	70.26-71.35	1.08	2.61	9	8.1	5.4			
12q21.1-12q21.2:73.73-74.71	73.73-74.71	0.98	1.13	6	5.4	2.7			HRB2, PHLD1A
12q21.31-12q21.1:81.24-84.88	81.24-84.88	3.63	1.88	10	5.4	2.7			
12q21.33-12q21.1:89.84-91.05	89.84-91.05	1.20	1.39	8	5.4	2.7		BTG1	DCN
12q24.33-12q24.1:130.94-131.08	130.94-131.08	0.12	1.26	3	5.4	2.7			
13q32.1-13q32.2:95.21-97.48	95.21-97.48	2.26	0.47	7	8.1	2.7			RAP2A
13q33.1-13q34	101.17-114.12	107.68-114.12	6.43	0.57	46	10.8	5.4	irs2, Rasa3	IRS2, ING1, F7
14q11.2-14q11.2:19.4-19.6	19.4-19.6	0.19	0.49	7	5.4	2.7			
15q13.1-15q13.1:27.34-27.88	27.34-27.88	0.52	0.55	2	5.4	2.7			
15q23-15q24.1	68.12-72.26	71.38-71.8	0.41	0.67	6	16.2	8.1		HEXA, BBS4, NEO1, and PML
15q25.1-15q25.1:76.42-77.01	76.42-77.01	0.57	0.78	11	10.8	2.7			
15q25.3-15q26.2:85.92-92.83	85.92-92.83	6.90	0.83	60	16.2	2.7	Sema4b	hsa-mir-7-2 NTRK3, BLM	
15q26.3-15q26.3:99.66-100.21	99.66-100.21	0.54	0.60	5	10.8	2.7			
16p13.3-16p13.3:2.16-2.23	2.16-2.23	0.06	0.91	6	5.4	2.7			
16p13.3-16p13.3:4.34-4.49	4.34-4.49	0.14	0.69	4	5.4	2.7			
16q24.1-16q24.1:82.81-83.69	82.81-83.69	0.87	0.58	10	8.1	5.4	Cot11, Zdhhc7		
17q21.33-17q21.1:45.71-46.42	45.71-46.42	0.47	0.53	18	5.4	5.4			
18p11.31-18p11.1:5.22-10.67	5.22-10.67	5.43	0.64	23	13.5	2.7			DLGAP1
18q11.2-18q11.2:17.33-18.87	17.33-18.87	1.52	0.81	8	5.4	2.7		hsa-mir-133a-1, hsa-mir-1-2	ZFP161
18q12.1-18q12.3:26.82-39.11	26.82-39.11	12.27	0.82	44	5.4	2.7	Mapre2	hsa-mir-187	RBBP8
18q21.31-18q21.1:53.47-56.2	53.47-56.2	2.72	0.78	15	5.4	2.7		hsa-mir-122MALT1	DTNA, ZNF271, GALNT1, PIK3C3
18q22.3-18q23	68.35-76.02	70.07-76.02	5.95	0.59	31	8.1	5.4	Nfatc1	NEDD4L
19p13.2-19p13.2:11.54-12.5	11.54-12.5	0.95	0.57	25	48.6	5.4			CYB5, ATP9B
19p13.12-19p13.1:15.77-40.21	19.75-24.14	4.38	0.77	33	56.8	8.1			ZNF85, ZNF43, ZNF91 and LOC91120
19q13.2-19q13.3:47.62-48.62	47.62-48.62	0.99	0.49	24	35.1	2.7			PSG11
19q13.33-19q13.3:53.8-53.96	53.8-53.96	0.15	0.84	13	32.4	2.7			FUT1
19q13.43-19q13.3:61.82-63.47	62.33-63.19	0.85	0.51	36	43.2	5.4		GRLF1	ZNF134
20p11.23-20p11.1:18.41-25.55	18.41-25.55	7.12	0.52	67	43.2	5.4			INSM1, NKX2-2, SSTR4

#### Loss/Deletion

1p36.33-1p36.33:0.95-1.29	0.95-1.29	0.34	-0.41	16	10.8	2.7		hsa-mir-200b, hsa-mir-200a		
1p36.33-1p36.22:1.55-9.36	7.83-9.13	1.28	-0.68	14	24.3	13.5		gene		
1p36.22-1p36.21:9.72-15.41	9.72-15.41	5.68	-0.58	65	10.8	2.7			CLCN6	
1p36.12-1p36.11:23.63-25.88	23.63-25.88	2.24	-0.45	37	8.1	2.7	Idk3   E2f2, Cnr2, Runx3			
1p36.11-1p36.3:27.62-28.65	27.62-28.65	1.02	-0.62	16	10.8	2.7				
1p31.1-1p22.2:77.73-89.04	78.12-87.53	9.40	-0.48	41	13.5	5.4	Bcl10	BCL10		
1p22.1-1p21.1:92.51-103.81	92.51-103.81	11.29	-0.47	53	13.5	2.7	Gri1	hsa-mir-137	BTG2	
1p13.3-1p13.3:107.82-108.96	107.82-108.96	1.13	-0.99	8	16.2	2.7			AGL, EXTL2	
1q24.3-1q24.3:168.33-168.5	168.33-168.5	0.16	-1.06	3	5.4	2.7				
1q32.2-1q42.12	203.98-223.13	214.89-220.66	5.76	-0.63	31	18.9	10.8			
1q42.2-1q42.3	230.11-231.05	230.11-231.05	0.94	-1.02	5	16.2	5.4		hsa-mir-215, hsa-mir-194-1	MCP and CAMK1G

1q43-1q44	236.39-245.43	244.52-244.86	0.32	-1.19	14	10.8	10.8				
2p23.3-2p23.3	24.9-25.3	24.9-25.3	0.39	-0.50	6	5.4	2.7				
2q11.1-2q11.2	95.37-100.47	95.37-100.47	5.09	-0.49	60	5.4	2.7	LincR   D430024K22Rik	LAF4	INPP4A, RWI1, U5-200KD	
2q36.1-2q36.1	223.26-224.57	223.26-224.57	1.30	-0.76	7	8.1	5.4				
2q37.1-2q37.1	233.25-234.04	233.25-234.04	0.78	-0.60	10	13.5	5.4				
2q37.3-2q37.3	241.26-242.24	241.26-242.24	0.97	-0.45	17	16.2	5.4				
3p24.3-3p24.3	19.55-20	19.55-20	0.44	-1.64	4	13.5	8.1				
3p24.1-3p21.31	29.91-47.44	29.91-47.44	17.52	-0.60	147	24.3	8.1	hsa-mir-128MLH1, CTNNE1		UGCRC1, BSN, DHX30, DOCK3, SACM1L	
3p21.31-3p21.31	48.57-49.03	48.57-49.03	0.45	-0.60	12	24.3	8.1				
3p13-3p12.3	71.09-74.4	71.09-74.4	3.30	-0.60	11	13.5	8.1				
3q12.3-3q13.13	102.96-112.8	102.96-112.8	9.83	-0.60	30	5.4	2.7				
3q29-3q29	194.47-199.26	194.47-199.26	4.78	-0.45	54	10.8	2.7		TFRC	ACK1, BDH	
4p13-4p12	44.01-48.73	47.77-48.73	0.95	-0.55	10	8.1	5.4		TEC		
4q11-4q12	52.8-54.7	52.8-54.7	1.89	-0.57	7	5.4	2.7		FIP1L1		
4q12-4q13.1	57.63-66.02	57.63-66.02	8.38	-0.57	9	5.4	2.7				
4q26-4q27	114.66-122.42	114.66-122.42	7.75	-0.41	28	10.8	2.7				
4q31.23-4q32.1	148.81-157.11	148.81-157.11	8.29	-0.72	41	16.2	8.1				
4q33-4q34.1	171.01-175.63	171.01-175.63	4.61	-0.67	15	16.2	10.8				
5p15.33-5p15.31	0.23-0.69	0.91-3.66	2.74	-0.51	19	24.3	8.1				
5q13.1-5q13.2	67.62-71.06	67.62-71.06	3.42	-0.43	30	10.8	2.7				
5q23.1-5q31.3	118.2-140.59	118.2-140.59	22.38	-0.67	181	13.5	10.8	I5   Irf1, Klf3		C5orf19, CTNNA1, HNRPA0, NDUFA2, NMES, SPOCK	
5q34-5q35.1	167.87-172.6	167.87-172.6	4.71	-0.59	31	16.2	10.8	hsa-mir-103 TLX3, NPM1			
5q35.3-5q35.3	177.59-180.62	177.59-180.62	3.02	-0.58	44	18.9	10.8	hsa-mir-340 FLT4		CLTB, MAPK9, SNCB	
6p25.3-6p22.3	0.29-17.72	0.29-0.36	0.06	-1.33	2	21.6	8.1	IRF4			
6p22.1-6p22.1	26.5-27.9	26.5-27.9	1.39	-0.47	28	16.2	5.4	HIST1H4I			
6p21.32-6p21.32	32.47-32.72	32.47-32.72	0.25	-0.81	7	13.5	5.4				
6p12.3-6p12.2	49.5-52.48	49.5-52.48	2.97	-0.49	19	16.2	5.4	hsa-mir-206, hsa-mir-133b			
6p12.1-6p12.1	53.89-55.73	53.89-55.73	1.83	-0.64	9	18.9	5.4				
6q14.1-6q15	79.7-88.06	79.7-88.06	8.34	-0.76	30	33.3	27.0	A930014C21Rik			
6q16.2-6q21	99.42-107.23	105.28-105.84	0.55	-0.65	5	40.7	24.1				
6q21-6q21	109.41-109.88	109.41-109.88	0.46	-0.63	8	37.0	20.4				
6q23.3-6q23.3	136.59-138.25	136.59-138.25	1.65	-0.76	11	44.4	25.9				
6q25.3-6q25.3	158.06-160.18	158.06-160.06	2.01	-0.70	17	44.4	24.1	Zdhhc14			
6q26-6q26	161.55-162.45	161.55-162.45	0.89	-0.70	3	40.7	22.2				
7p15.2-7p15.2	26.9-27	26.9-27	0.09	-0.59	10	8.1	2.7	Hoxa7   Hoxa9	hsa-mir-196 HOXA9, HOXA11		
7q11.23-7q11.23	72.45-75.57	72.45-75.57	3.11	-0.42	43	10.8	2.7		HIP1	GTF2I, STX1A, WBSR1	
8p23.3-8p23.2	0.18-3.13	0.18-3.13	2.94	-0.44	16	8.1	2.7				
8p22-8p12	13.3-30.05	16.01-17.14	1.12	-0.78	6	13.5	8.1				
8p12-8q12.1	35.77-57.19	35.77-57.19	21.42	-0.53	99	13.5	2.7	Plekha2	VHSC1L1, FGFR1	NEF3, NEFL, XPO7, KIF13B, PNMA2, PPP2R2A, EPB49	
8q24.21-8q24.21	127.63-130.93	127.63-130.93	3.28	-0.52	7	5.4	2.7	Myc   Pvt1	MYC	AP3M2, POLB, VDAC3	
9p24.3-9p21.1	0.2-30.55	21.06-22	0.93	-2.30	22	55.6	46.30		hsa-mir-31	CDKN2A	
9p21.1-9p13.3	31.24-34.99	31.24-32.97	1.72	-0.56	7	37.0	21.6				
9p13.3-9p13.2	35.04-38.54	35.72-35.9	0.17	-0.72	8	29.6	13.5				
9p13.3-9p13.2	35.04-38.54	37.55-38.39	0.84	-0.56	9	29.6	13.5				
9q21.11-9q21.2	69.23-77.27	69.23-77.27	8.02	-0.67	29	14.8	10.8	Anxa1   1500015L2	hsa-mir-204		
9q22.33-9q31.1	98.57-99.71	98.57-99.71	1.13	-0.64	7	10.8	8.1		NR4A3		
9q31.3-9q32	108.69-112.73	110.71-112.32	1.60	-0.58	12	13.5	8.1				
10p15.3-10p13	0.28-12.91	0.28-3.82	3.53	-0.64	15	72.2	40.7		COPEB		
10p12.1-10p12.1	27.44-29.02	27.44-29.02	1.57	-0.64	12	72.2	38.9				
10q11.22-10q11.1	47.99-51.26	47.99-51.26	3.27	-0.64	29	72.2	35.2		NCOA4		
10q11.23-10q22	51.26-71.86	69.66-70.64	0.98	-0.80	15	79.6	46.3				
10q22.1-10q24.3	74.43-102.76	84.73-89.6	4.86	-1.38	28	85.2	46.3	hsa-mir-346	EMPR1A	TNFRSF6	

10q22.1-10q24.3	74.43-102.76	90.68-91.06	0.37	-2.13	5	81.5	44.4			TNFRSF6	BTAF1 and FER1L3		
10q22.1-10q24.3	74.43-102.76	92.49-102.74	10.24	-0.64	104	81.5	44.4	Hhex, Frat1, KIAA0608			C10orf6, CHUK, MMS19L and SEC31L2		
10q24.32-10q25.1	104.38-112.04	104.38-112.04	7.65	-0.64	36	79.6	40.7			SUFU	NEURL	GFRA1, MXI1, GSTO1, NEURL, SLK	
10q25.2-10q26.3	112.04-135.25	120.43-121.39	0.95	-1.27	9	83.3	48.1					TRUB1, ATRNL1, EF3S10	
10q25.2-10q26.3	112.04-135.25	123.71-129.79	6.08	-1.27	48	85.2	48.1			Ptprc		FGFR2, DOCK1, GALNAC2S-6ST, OAT, BUB3	
10q25.2-10q26.3	112.04-135.25	133.87-135.00	1.16	-1.27	17	85.2	48.1						
11p15.4-11p15.4	4.56-5.71	4.56-5.71	1.14	-0.57	75	29.6	16.7						
11p15.4-11p15.4	5.71-5.82	5.73-5.8	0.07	-3.11	6	22.2	5.6						
11p15.4-11p15.4	5.83-5.87	5.83-5.87	0.03	-0.57	3	33.3	14.3						
11p11.2-11p11.2	46.83-48.15	46.83-48.15	1.31	-0.55		18.9	8.1			DDB2		MADD	
11q11-11q11	54.86-55.04	54.86-55.04	0.17	-0.55	8	27.0	2.7						
11q11-11q11	55.07-55.3	55.09-55.2	0.09	-2.43	3	43.2	18.9						
11q11-11q12.3	55.32-63.1	57.34-61.92	4.57	-0.47	114	18.9	5.4			Cd6		COX8A, NXF1, FLJ36198	
11q13.4-11q13.4	71.39-71.97	71.39-71.97	0.57	-0.45	14	13.5	2.7						
11q13.5-11q14.1	77.26-78.05	77.26-78.05	0.78	-0.80	9	18.9	5.4			NUMA1			
11q14.1-11q23.1	82.21-112.63	85.82-89.57	3.73	-0.58	20	24.3	8.1						
11q14.1-11q23.1	82.21-112.63	93.55-94.45	0.89	-0.93	10	21.6	10.8						
11q14.1-11q23.1	82.21-112.63	95.2-102.07	6.87	-0.62	19	27.0	8.1						
11q23.2-11q23.3	113.77-117.5	113.77-117.5	3.72	-0.64	28	24.3	5.4						
11q23.3-11q25.1	120.68-133.78	127.83-133.78	5.93	-0.69	34	24.3	8.1			Flil   Ets1		FLI1	SC5DL, UBE4A
12p13.2-12p13.1	11.31-14.55	12.37-12.84	0.46	-0.62	7	10.8	5.4						
12p13.1-12p12.3	14.54-15.65	14.54-15.65	1.09	-0.62	15	10.8	5.4						
12q12-12q13.11	37.97-45.76	37.97-45.76	7.78	-0.56	33	10.8	8.1					Slc38a2	
12q14.1-12q14.1	57.55-58.47	57.55-58.47	0.91	-0.76	2	10.8	5.4						
12q14.2-12q15.1	63.17-67.45	63.39-67.45	4.05	-0.65	27	21.6	8.1			Rep1b		HMG2A	
12q15-12q21.1	69.11-71.35	69.11-71.35	2.23	-0.65	13	16.2	5.4						
12q21.1-12q21.3	73.73-80.16	73.73-75.66	1.92	-0.65	10	24.3	8.1						
12q22-12q24.23	94.19-119	97.43-97.5	0.07	-0.65	2	13.5	8.1						
12q22-12q24.23	94.19-119	105.88-112.3	6.40	-0.51	81	16.2	8.1						
12q24.32-12q24.1	127.71-127.83	127.71-127.83	0.11	-0.51	3	10.8	5.4			PTPN11		IKIP ARPC3, ALDH2, PTPN11	
12q24.32-12q24.1	127.99-131.1	130.94-131.06	0.12	-1.19	3	18.9	16.2						
12q24.33-12q24.1	131.09-132.35	131.09-132.35	1.25	-0.64	19	10.8	5.4					ULK1	
13q12.11-13q13.1	19.14-35.65	19.66-20.65	0.99	-0.60	11	32.4	18.9						
13q12.11-13q13.1	19.14-35.65	22.32-25.69	3.36	-0.71	24	29.7	18.9						
13q14.2-13q21.1	47.41-57.2	47.41-57.2	9.78	-1.40	54	37.0	27.8						
14q11.2-14q11.2	19.4-19.56	19.4-19.52	0.11	-0.68	3	33.3	25.9						
14q11.2-14q11.2	19.57-19.66	19.57-19.66	0.08	-0.55	5	18.9	8.1						
14q13.1-14q13.2	33.97-34.95	33.97-34.95	0.97	-0.62	13	27.0	10.8			Nrkbia			
14q23.1-14q23.1	59.60-59	59.60-59	1.59	-0.57	19	32.4	16.2						
14q32.32-14q32.1	102.03-106.34	102.03-106.34	4.29	-0.67	233	18.5	13.5			lgh-4, Akt1, Crip2	hsa-mir-203		
14q32.12-14q32.1	90.79-101.47	90.79-101.47	10.67	-0.67		18.9	13.5				342, hsa-	GOLGA5,	CHGA, MEG3, MOAP1, C14orf132, DICER1
15q11.2-15q11.2	19.36-20.56	19.36-20.56	1.19	-0.57	18	24.3	8.1						
15q13.3-15q15.3	30.71-41.88	40.43-41.03	0.59	-0.68	8	22.2	16.2						
15q15.3-15q21.2	41.88-50.67	42.64-50.39	7.75	-0.68	58	18.5	10.8						
15q21.3-15q22.2	53.9-57.18	53.9-57.18	3.27	-0.61	19	21.6	5.4			Tcf12		TCF12	
15q23-15q25.1	67.13-79.06	67.13-79.06	11.92	-0.57	122	24.3	5.4						
15q25.2-15q26.3	80.2-97.5	80.2-97.5	7.97	-0.57	73	24.3	8.1			hsa-mir-184 PML	CSPG4	SDFR1, ARNT2, RASGRF1	
16q11.2-16q12.1	45.25-48.83	45.25-48.83	3.57	-0.71	25	10.8	5.4			hsa-mir-7-2 NTRK3	ABHD2	SLCO3A1	
16q23.1-16q23.2	73.98-79.15	73.98-79.15	5.16	-0.71	18	13.5	5.4			MAF			
17p13.1-17p11.2	7.5-20.85	7.5-20.85	13.35	-0.48	187	13.5	2.7			Trp53		TP53, GAS7, MAP2K4, BF-ALDH3A2, LOC220594, MAP2K4, ULK2, GAS7	
17q21.1-17q21.2	35.4-35.77	35.4-35.77	0.36	-0.52	11	8.1	2.7			Cdc6		RARA	
17q21.2-17q21.2	35.77-36.98	35.77-36.98	0.07	-2.45	4	18.9	13.5						

17q21.2-17q21.2	36.99-37.24	36.99-37.24	0.25	-0.52	10	8.1	2.7				
17q21.31-17q21.3	40.54-46.3	44.04-44.3	0.25	-0.92	7	16.2	8.1	hsa-mir-196a-1		LUC7A, NPEPPS, NSF, TOB1	
17q24.3-17q24.3	65.04-67.64	65.04-67.64	2.58	-0.64	7	10.8	5.4				
18p11.32-18p11.3	0.2-10.67	6.95-10.67	3.71	-0.70	16	27.0	18.9		DLGAP1	ANKRD12, KIAA0802, VAPA	
18p11.21-18q11.1	12.02-17.47	12.02-17.47	5.44	-0.58	30	16.2	5.4				
18q21.1-18q21.2	46.58-50.12	46.58-50.12	3.53	-0.73	10	16.2	8.1				
18q21.33-18q22.2	57.37-70.21	57.37-70.21	12.84	-0.58	40	16.2	8.1	Tnfrsf11a	BCL2		
19p13.3-19p13.2	2.2-7.6	2.2-7.6	5.39	-0.35		8.1	2.7	3	MLLT1	TLE2, TUBB5	
19q13.12-19q13.1	40.71-41.63	40.71-41.63	0.92	-0.48		10.8	5.4				
19q13.2-19q13.2	43.81-43.82	43.81-43.82	0.00	-0.48		10.8	5.4				
19q13.2-19q13.4	47.16-63.77	47.78-48.56	0.77	-0.97	19	24.3	10.8				
19q13.2-19q13.4	47.16-63.77	53.06-54.84	1.76	-0.59	84	24.3	10.8	hsa-mir-150	GRLF1	KLK6, SLC8A2, SEPW1, PLA2G4C, SNRP70, CA11	
20p13-20p11.21	0.02-25.61	7.9-18.72	10.81	-0.85	61	8.1	5.4	Snx5			
20p13-20p11.21	0.02-25.61	19.96-24.6	4.63	-0.73	44	8.1	5.4				
20q11.23-20q11.1	34.28-35.38	34.28-35.38	1.10	-0.41	18	5.4	2.7				
21p11.2-21q22.1	9.93-31.11	14.4-15.26	0.85	-0.69	7	21.6	8.1				
21q22.3-21q22.3	45.75-46.44	45.75-46.44	0.67	-0.69	7	13.5	5.4				
22q11.21-22q11.1	19.74-22.06	19.74-22.06	2.32	-0.55	129	27.0	2.7	hsa-mir-130BCR		UBE2L3	
22q12.1-22q13.1	27.85-37.86	27.85-37.86	9.99	-0.39		10.8	5.4		ZNF278,	KIAA0063, NPTXR, PRKCABP, PVALB, UNC84B	
22q13.1-22q13.2	37.94-40.25	37.94-40.25	2.30	-0.42	35	29.7	2.7	St13	PDGFB, EP300		
22q13.2-22q13.3	40.24-49.5	42.22-49.34	7.11	-0.60	75	37.8	10.8	Parvb	hsa-let-7a-3, hsa-let-7b		