

Peak Data										Normalized Peak Area								
No.	Label	Size	Ref. size	Size diff.	MRC	Height	Width	Area	Peak Area	Ref. Mean	Ref. SD	Ref. Weigh	Position p-tel band	Dist. Ratio	1.0 in SD	1.0 low high		
3	64 -	60.80	60.65	0.15	64	208	10.3	2134	0.699	1.438	0.213	0.89	64 nt	0.49	-3.5	.		
4	70 -	66.66	66.46	0.20	70	202	18.9	3809	1.247	0.773	0.104	0.98	70 nt	1.61	4.6*			
5	76 -	72.33	72.37	-0.04	76	192	17.6	3387	1.109	1.055	0.125	1.12	76 nt	1.05	0.4	.		
6	82 -	78.68	78.56	0.12	82	185	15.6	2888	0.945	0.734	0.097	1.00	82 nt	1.29	2.2			
Ctrl: Q-fragments					Mean	197	15.6	3055	1.000	1.000	0.134	1.00	(CV: 0.41)	1.12				
7	6 a	85.04	84.95	0.09	88	1349	12.4*	16684	0.979	0.834	0.103	0.95	6p21.3 CpG isl.	1.17	1.4			
9	2 a	90.30	90.17	0.13	92	1689	10.5	17659	1.036	0.824	0.081	1.20	2q14 synt.	1.26	2.6			
11	1 a	96.60	96.50	0.10	96	3076	11.3*	34722	2.038	1.685	0.232	0.85	MV 36 1p36 CpG isl.	1.21	1.5			
Ctrl: D-fragments					Mean	2038	11.4	23022	1.351	1.115	0.138	1.00	(CV: 0.04)	1.22				
	Y a	114.50			118					0.811			13.54 Yq11					
	Y a	104.34			108					0.566			14.10 Yq11					
ctrl: Y-fragments (male ref.)					Mean							1.00	(CV:)					
12	1 A	126.10	126.04	0.06	130	1676	11.4	19134	1.123	1.133	0.040	1.25	1.14 1p36.33	0.99	-0.2	.		
20	1 A	176.53	176.49	0.04	178	1427	11.6	16540	0.971	0.839	0.046	0.81	1.75 1p36.33	1.16	2.8			
18	1 A	164.53	164.53	0.00	166	1655	11.4	18907	1.110	1.090	0.052	0.94	1.95 1p36.33	1.02	0.4	.		
1p36 (1p-deletion)					Mean	1586	11.5	18194	1.068	1.021	0.046	1.00	(CV: 0.08)	1.04				
34	2 B	264.86	264.89	-0.03	267	1093	12.6	13813	0.823	0.910	0.038	1.17	58.30 2p16.1	0.90	-2.3	.		
60	2 D	481.35	481.31	0.04	486	955	18.4	17609	1.135	1.072	0.063	0.83	61.00 2p16.1	1.06	1.0	.		
"2p16.1 deletion syndrome"					Mean	1024	15.5	15711	0.979	0.991	0.050	1.00	(CV: 0.11)	0.97				
53	3 D	416.44	416.46	-0.02	418	1090	16.6	18120	1.168	1.230	0.057	1.15	198.51 3q29	0.95	-1.1	.		
46	3 C	354.62	354.58	0.04	359	1189	14.6	17350	1.015	0.959	0.061	0.85	198.28 3q29	1.06	0.9	.		
"3q29 deletion syndrome"					Mean	1140	15.6	17735	1.091	1.094	0.059	1.00	(CV: 0.08)	1.00				
29	4 B	230.50	230.47	0.03	232	1160	11.9	13826	0.823	0.896	0.058	0.88	1.81 4p16.3	0.92	-1.2	.		
56	4 D	443.00	443.03	-0.03	445	774	17.4	13505	0.870	0.880	0.045	1.12	1.90 4p16.3	0.99	-0.2	.		
4p16.3 Wolf-Hirschhorn region					Mean	967	14.7	13666	0.847	0.888	0.052	1.00	(CV: 0.05)	0.96				
55	5 D	435.55	435.58	-0.03	436	616	17.3	10644	0.686	0.655	0.037	1.02	1.34 5p15.33	1.05	0.8	.		
36	5 C	281.43	281.39	0.04	283	1321	13.7	18163	1.063	1.053	0.061	0.98	1.40 5p15.33	1.01	0.2	.		
Cri du Chat syndrome					Mean	969	15.5	14404	0.874	0.854	0.049	1.00	(CV: 0.03)	1.03				
16	5 A	151.46	151.42	0.04	154	1629	10.1	16413	0.963	0.972	0.047	0.98	176.62 5q35.3	0.99	-0.2	.		
57	5 D	453.01	453.02	-0.01	454	953	17.5	16720	1.077	1.134	0.052	1.02	176.65 5q35.3	0.95	-1.1	.		
Sotos syndrome					Mean	1291	13.8	16567	1.020	1.053	0.049	1.00	(CV: 0.03)	0.97				
40	7 C	310.45	310.40	0.05	310	1263	14.0	17657	1.033	1.047	0.040	1.13	73.08 7q11.23	0.99	-0.3	.		
47	7 C	363.45	363.46	-0.01	364	976	15.3	14981	0.876	0.995	0.048	0.88	73.11 7q11.23	0.88	-2.4	.		
50	7 D	390.05	389.95	0.10	391	693	16.1	11182	0.721	0.774	0.034	0.99	73.15 7q11.23	0.93	-1.6	.		
Williams syndrome					Mean	977	15.2	14607	0.877	0.938	0.041	1.00	(CV: 0.06)	0.94				
51	8 D	399.71	399.69	0.02	401	679	16.4	11117	0.716	0.753	0.051	0.88	116.75 8q24.12	0.95	-0.7	.		
54	8 D	424.36	424.33	0.03	427	778	17.3	13436	0.866	0.897	0.048	1.12	117.73 8q24.11	0.97	-0.6	.		
Langer-Giedion syndrome					Mean	729	16.8	12277	0.791	0.825	0.049	1.00	(CV: 0.01)	0.96				
41	9 C	319.49	319.40	0.09	319	1471	14.2	20935	1.225	1.194	0.050	0.92	100.95 9q22.33	1.03	0.6	.		
52	9 D	408.10	408.03	0.07	409	1109	16.7	18484	1.191	1.115	0.040	1.08	100.95 9q22.33	1.07	1.9	.		
"9q22.3 deletion syndrome"					Mean	1290	15.4	19710	1.208	1.155	0.045	1.00	(CV: 0.03)	1.05				
13	10 A	132.60	132.56	0.04	136	1288	11.0	14226	0.835	0.895	0.048	0.90	8.14 10p	0.93	-1.3	.		
45	10 C	349.33	349.23	0.10	349	1100	14.2	15624	0.914	0.938	0.041	1.10	10.59 10p15.1	0.97	-0.6	.		
DiGeorge region 2 (10p)					Mean	1194	12.6	14925	0.874	0.917	0.044	1.00	(CV: 0.03)	0.96				
27	11 B	218.69	218.68	0.01	220	1570	11.6	18269	1.088	1.184	0.062	1.00	31.78 11p13	0.92	-1.6	.		
WAGR syndrome					Mean	1570	11.6	18269	1.088	1.184	0.062	1.00	(CV:)	0.92				
26	15 B	213.58	213.54	0.04	214	1733	12.1	20883	1.244	1.162	0.060	0.90	21.48 15q11.2	1.07	1.3	.		
31	15 B	245.12	245.06	0.06	247	1197	12.7	15225	0.907	0.909	0.047	0.90	22.65 15q12	1.00	0.0	.		
37	15 C	289.77	289.75	0.02	292	1206	13.2	15973	0.934	0.932	0.035	1.25	22.76 15q12	1.00	0.1	.		
17	15 A	158.08	158.00	0.08	160	1393	11.4	15830	0.929	0.838	0.041	0.95	23.17 15q12	1.11	2.2	.		
Prader-Willi / Angelman					Mean	1382	12.3	16978	1.003	0.960	0.046	1.00	(CV: 0.05)	1.04				
22	15 A	189.80	189.75	0.05	190	1706	11.3	19322	1.134	1.228	0.057	1.07	72.50 15q24.1	0.92	-1.6	.		
42	15 C	326.52	326.43	0.09	325	813	14.2	11521	0.674	0.753	0.040	0.93	72.80 15q24.1	0.90	-2.0	.		
"15q24 deletion syndrome"					Mean	1260	12.7	15422	0.904	0.990	0.049	1.00	(CV: 0.02)	0.91				
19	16 A	170.95	170.91	0.04	172	1425	11.2	16027	0.941	0.921	0.053	1.00	3.87 16p13.3	1.02	0.4	.		
Rubinstein-Taybi syndrome					Mean	1425	11.2	16027	0.941	0.921	0.053	1.00	(CV:)	1.02				
14	17 A	139.00	138.97	0.03	142	1811	11.5	20784	1.220	1.138	0.031	1.42	2.51 17p13.3	1.07	2.6	.		
30	17 B	236.20	236.22	-0.02	238	1264	12.1	15318	0.912	0.859	0.058	0.58	2.52 17p13.3	1.06	0.9	.		
Miller-Dieker region					Mean	1538	11.8	18051	1.066	0.999	0.044	1.00	(CV: 0.01)	1.07				
58	17 D	463.07	463.07	0.00	465	1162	18.0	20948	1.350	1.385	0.097	0.75	17.53 17p11.2-##	0.97	-0.4	.		
35	17 B	271.83	271.90	-0.07	274	1083	13.1	14192	0.845	0.934	0.038	1.30	17.83 17p11.2	0.91	-2.3	.		
39	17 C	302.92	302.90	0.02	303	972	13.6	13260	0.776	0.796	0.044	0.95	18.08 17p11.2	0.97	-0.5	.		
Smith-Magenis syndrome					Mean	1072	14.9	16133	0.990	1.038	0.060	1.00	(CV: 0.04)	0.94				
33	17 B	258.38	258.33	0.05	260	779	12.9	10026	0.597	0.578	0.041	0.94	26.56 17q11.2	1.03	0.5	.		
43	17 C	334.59	334.45	0.14	335	1270	14.8	18751	1.097	1.044	0.065	1.06	26.58 17q11.2	1.05	0.8	.		
NF1 microdeletion syndrome					Mean	1025	13.8	14389	0.847	0.811	0.053	1.00	(CV: 0.01)	1.04				
59	17 D	470.52	470.58	-0.06	472	971	18.2	17637	1.137	0.728	0.046	0.78	41.26 17q21.31	1.56	8.9*			
28	17 B	224.83	224.79	0.04	226	2498	12.4	31026	1.848	1.273	0.049	1.26	41.44 17q21.31	1.45	11.7*			
44	17 C	341.86	341.78	0.08	342	1528	14.9	22730	1.330	0.896	0.046	0.95	41.45 17q21.31	1.48	9.4*			
"17q21.31 microdeletion"					Mean	1666	15.2	23798	1.438	0.966	0.047	1.00	(CV: 0.04)	1.49				

Peak Data										Normalized Peak Area							
No.	Label	Size	Ref. size	Size diff.	MRC size	Height	Width	Area	Peak Area	Ref. Mean	Ref. SD	Ref. Weigh	Position p-tel band	Ratio	Dist. in SD	1.0 low high	
23	22 A	195.27	195.29	-0.02	196	1214	10.9	13249	0.778	0.767	0.034	1.08	17.89 22q11.21	1.01	0.3	.	
25	22 B	208.09	207.99	0.10	208	1458	12.0	17458	1.040	1.070	0.053	0.96	18.09 22q11.21	0.97	-0.6	.	
48	22 D	371.44	371.47	-0.03	373	906	16.6	15024	0.968	0.942	0.047	0.96	19.57 22q11.21	1.03	0.6	.	
22q11.21 (DiGeorge)					Mean	1193	13.2	15244	0.928	0.926	0.044	1.00	(CV: 0.03)	1.00			
32	22 B	251.94	251.96	-0.02	253	1693	13.0	21926	1.306	1.330	0.090	0.75	49.49 22q13.33-##	0.98	-0.3	.	
49	22 D	382.14	382.09	0.05	382	1381	16.6	22938	1.478	1.436	0.059	1.25	49.50 22q13.33-#	1.03	0.7	.	
22q13 (Phelan-McDermid)					Mean	1537	14.8	22432	1.392	1.383	0.075	1.00	(CV: 0.03)	1.01			
38	X C	295.37	295.46	-0.09	297	1787	13.4	23901	1.398	1.392	0.054	1.00	32.29 Xp21.2	1.00	0.1	.	
Chromosome X control probe					Mean	1787	13.4	23901	1.398	1.392	0.054	1.00	(CV:)	1.00			
24	X B	199.67	199.64	0.03	202	1384	11.0	15179	0.904	0.895	0.045	1.00	153.02 Xq28	1.01	0.2	.	
15	X A	146.96	146.82	0.14	148	1747	10.1	17719	1.040	0.964	0.056	0.86	152.95 Xq28	1.08	1.4	↓	
21	X A	183.17	183.16	0.01	184	1904	11.6	22012	1.292	1.214	0.053	1.14	152.94 Xq28-#	1.06	1.5	↓	
Xq28 (RETT / MECP2)					Mean	1678	10.9	18303	1.079	1.025	0.051	1.00	(CV: 0.03)	1.05			
Mean values			0.03			1281	13.8	17051	1.028	1.000	0.050	4		1.03	Total of all except		
Standard deviations			0.05			(Coef. of variance: 0.231)			0.235	0.196				0.13	Ctrl and '?' peaks		

Quality assessment	Quality limits	Quality
Mean A-group area / mean Q-frag. area	>1.00 (1.75)	5.58
Mean CpG-area / mean A-group area	>0.55 (0.85)	1.51
Mean height of first probes AB	> 450 (800)	1491
Mean height of last probes CD	> 280 (500)	1079
Ratio of mean heights AB/CD ('slope')	<2.00 (1.55)	1.38
Mean group CV of weighted ratio	<0.20 (0.15)	0.04
2 unidentified peak areas / 52 peak areas	< (0.02)	0.00

Individual peaks having normalized area > 4.0 SD from the ref. mean and ratio <0.65 or >1.3 indicate 'abnormal' probe area.

Female Reference

Abn. peaks: 17q21.31 17q21.31 17q21.31

An "*" marks: Size Diff.>0.5, Peak Height>7000, unexpected peak width, and "Dist. in SD">4.0.
 Ratio group mean and coefficient of variance (CV) are weighted by the ref. weights
 Labels A,B,... define normalization groups; a,b,... labeled probes do not contribute to normalization.
 Mean Rox height is 260 (14 peaks). CV of ROX heights for peaks above 100 nt is: 0.05

("#" marked probes are often low when CpG-D-fragments are low)