

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	low high
2	64 -	60.77	60.65	0.12	64	64	6.0	382	0.192	1.438	0.213	0.89	64 nt	0.13	-5.9*	.
3	70 -	66.81	66.46	0.35	70	131	18.2	2381	1.198	0.773	0.104	0.98	70 nt	1.55	4.1*	.
4	76 -	72.51	72.37	0.14	76	167	17.6	2933	1.476	1.055	0.125	1.12	76 nt	1.40	3.4	.
5	82 -	78.65	78.56	0.09	82	141	16.0	2254	1.134	0.734	0.097	1.00	82 nt	1.55	4.1*	.
Ctrl: Q-fragments					Mean	126	14.4	1988	1.000	1.000	0.134	1.00	(CV: 0.55)	1.19		
7	6 a	85.15	84.95	0.20	88	1697	11.7*	19903	0.817	0.834	0.103	0.95	6p21.3 CpG isl.	0.98	-0.2	.
9	2 a	90.39	90.17	0.22	92	2199	10.3*	22624	0.929	0.824	0.081	1.20	2q14 synt.	1.13	1.3	.
10	1 a	96.74	96.50	0.24	96	3379	11.4*	38400	1.576	1.685	0.232	0.85	MV 36 1p36 CpG isl.	0.94	-0.5	.
Ctrl: D-fragments					Mean	2425	11.1	26976	1.107	1.115	0.138	1.00	(CV: 0.10)	1.03		
	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:)			
11	1 A	126.21	126.04	0.17	130	2557	10.8	27680	1.136	1.133	0.040	1.25	1.14 1p36.33	1.00	0.1	.
19	1 A	176.54	176.49	0.05	178	1852	11.2	20790	0.853	0.839	0.046	0.81	1.75 1p36.33	1.02	0.3	.
17	1 A	164.62	164.53	0.09	166	2168	11.0	23830	0.978	1.090	0.052	0.94	1.95 1p36.33	0.90	-2.2	.
1p36 (1p-deletion)					Mean	2192	11.0	24100	0.989	1.021	0.046	1.00	(CV: 0.07)	0.97		
33	2 B	264.91	264.89	0.02	267	1446	13.1	18879	0.851	0.910	0.038	1.17	58.30 2p16.1	0.93	-1.6	.
59	2 D	481.61	481.31	0.30	486	1232	18.9	23243	1.068	1.072	0.063	0.83	61.00 2p16.1	1.00	-0.1	.
"2p16.1 deletion syndrome"					Mean	1339	16.0	21061	0.959	0.991	0.050	1.00	(CV: 0.04)	0.96		
52	3 D	416.56	416.46	0.10	418	1594	17.3	27568	1.267	1.230	0.057	1.15	198.51 3q29	1.03	0.6	.
45	3 C	354.59	354.58	0.01	359	1640	14.8	24335	1.030	0.959	0.061	0.85	198.28 3q29	1.07	1.2	.
"3q29 deletion syndrome"					Mean	1617	16.1	25952	1.149	1.094	0.059	1.00	(CV: 0.03)	1.05		
28	4 B	230.63	230.47	0.16	232	1701	12.1	20500	0.924	0.896	0.058	0.88	1.81 4p16.3	1.03	0.5	.
55	4 D	443.29	443.03	0.26	445	1050	17.8	18729	0.860	0.880	0.045	1.12	1.90 4p16.3	0.98	-0.4	.
4p16.3 Wolf-Hirschhorn region					Mean	1376	14.9	19615	0.892	0.888	0.052	1.00	(CV: 0.04)	1.00		
54	5 D	435.74	435.58	0.16	436	824	17.0	13978	0.642	0.655	0.037	1.02	1.34 5p15.33	0.98	-0.4	.
35	5 C	281.44	281.39	0.05	283	1991	13.5	26917	1.140	1.053	0.061	0.98	1.40 5p15.33	1.08	1.4	.
Cri du Chat syndrome					Mean	1408	15.2	20448	0.891	0.854	0.049	1.00	(CV: 0.07)	1.03		
15	5 A	151.55	151.42	0.13	154	2296	10.0	22977	0.943	0.972	0.047	0.98	176.62 5q35.3	0.97	-0.6	.
56	5 D	453.17	453.02	0.15	454	1314	18.5	24349	1.119	1.134	0.052	1.02	176.65 5q35.3	0.99	-0.3	.
Sotos syndrome					Mean	1805	14.3	23663	1.031	1.053	0.049	1.00	(CV: 0.01)	0.98		
39	7 C	310.31	310.40	-0.09	310	1845	14.2	26213	1.110	1.047	0.040	1.13	73.08 7q11.23	1.06	1.6	.
46	7 C	363.62	363.46	0.16	364	1579	15.7	24861	1.053	0.995	0.048	0.88	73.11 7q11.23	1.06	1.2	.
49	7 D	390.06	389.95	0.11	391	1034	16.2	16762	0.770	0.774	0.034	0.99	73.15 7q11.23	1.00	-0.1	.
Williams syndrome					Mean	1486	15.4	22612	0.978	0.938	0.041	1.00	(CV: 0.04)	1.04		
50	8 D	399.81	399.69	0.12	401	1063	16.5	17575	0.807	0.753	0.051	0.88	116.75 8q24.12	1.07	1.1	.
53	8 D	424.68	424.33	0.35	427	1080	17.8	19194	0.882	0.897	0.048	1.12	117.73 8q24.11	0.98	-0.3	.
Langer-Giedion syndrome					Mean	1072	17.2	18385	0.845	0.825	0.049	1.00	(CV: 0.06)	1.02		
40	9 C	319.28	319.40	-0.12	319	2219	14.2	31494	1.334	1.194	0.050	0.92	100.95 9q22.33	1.12	2.8	.
51	9 D	408.21	408.03	0.18	409	1514	17.1	25895	1.190	1.115	0.040	1.08	100.95 9q22.33	1.07	1.8	.
"9q22.3 deletion syndrome"					Mean	1867	15.6	28695	1.262	1.155	0.045	1.00	(CV: 0.03)	1.09		
12	10 A	132.75	132.56	0.19	136	2038	11.0	22397	0.919	0.895	0.048	0.90	8.14 10p	1.03	0.5	.
44	10 C	349.32	349.23	0.09	349	1477	15.1	22238	0.942	0.938	0.041	1.10	10.59 10p15.1	1.00	0.1	.
DiGeorge region 2 (10p)					Mean	1758	13.0	22318	0.930	0.917	0.044	1.00	(CV: 0.02)	1.01		
26	11 B	218.76	218.68	0.08	220	2153	11.9	25607	1.154	1.184	0.062	1.00	31.78 11p13	0.97	-0.5	.
WAGR syndrome					Mean	2153	11.9	25607	1.154	1.184	0.062	1.00	(CV:)	0.97		
25	15 B	213.58	213.54	0.04	214	2281	11.7	26721	1.204	1.162	0.060	0.90	21.48 15q11.2	1.04	0.7	.
30	15 B	245.19	245.06	0.13	247	1673	12.6	21131	0.952	0.909	0.047	0.90	22.65 15q12	1.05	0.9	.
36	15 C	289.88	289.75	0.13	292	1717	13.6	23311	0.987	0.932	0.035	1.25	22.76 15q12	1.06	1.6	.
16	15 A	158.08	158.00	0.08	160	1834	11.1	20416	0.838	0.838	0.041	0.95	23.17 15q12	1.00	0.0	.
Prader-Willi / Angelman					Mean	1876	12.3	22895	0.995	0.960	0.046	1.00	(CV: 0.02)	1.04		
21	15 A	189.80	189.75	0.05	190	2559	11.2	28548	1.172	1.228	0.057	1.07	72.50 15q24.1	0.95	-1.0	.
41	15 C	326.31	326.43	-0.12	325	1114	14.5	16138	0.683	0.753	0.040	0.93	72.80 15q24.1	0.91	-1.7	.
"15q24 deletion syndrome"					Mean	1837	12.8	22343	0.928	0.990	0.049	1.00	(CV: 0.03)	0.93		
18	16 A	170.95	170.91	0.04	172	2196	11.0	24077	0.988	0.921	0.053	1.00	3.87 16p13.3	1.07	1.3	.
Rubinstein-Taybi syndrome					Mean	2196	11.0	24077	0.988	0.921	0.053	1.00	(CV:)	1.07		
13	17 A	139.09	138.97	0.12	142	2585	11.2	28934	1.188	1.138	0.031	1.42	2.51 17p13.3	1.04	1.6	.
29	17 B	236.31	236.22	0.09	238	1692	12.2	20644	0.930	0.859	0.058	0.58	2.52 17p13.3	1.08	1.2	.
Miller-Dieker region					Mean	2139	11.7	24789	1.059	0.999	0.044	1.00	(CV: 0.02)	1.05		
57	17 D	463.45	463.07	0.38	465	1700	18.4	31358	1.441	1.385	0.097	0.75	17.53 17p11.2-##	1.04	0.6	.
34	17 B	272.00	271.90	0.10	274	1527	13.4	20395	0.919	0.934	0.038	1.30	17.83 17p11.2	0.98	-0.4	.
38	17 C	302.85	302.90	-0.05	303	1342	14.0	18795	0.796	0.796	0.044	0.95	18.08 17p11.2	1.00	0.0	.
Smith-Magenis syndrome					Mean	1523	15.3	23516	1.052	1.038	0.060	1.00	(CV: 0.03)	1.00		
32	17 B	258.39	258.33	0.06	260	481	12.9	6191	0.279	0.578	0.041	0.94	26.56 17q11.2	0.48	-7.4*	.
42	17 C	334.46	334.45	0.01	335	980	14.6	14301	0.606	1.044	0.065	1.06	26.58 17q11.2	0.58	-6.7*	.
NF1 microdeletion syndrome					Mean	731	13.7	10246	0.442	0.811	0.053	1.00	(CV: 0.13)	0.53		
58	17 D	470.75	470.58	0.17	472	841	18.6	15637	0.718	0.728	0.046	0.78	41.26 17q21.31	0.99	-0.2	.
27	17 B	224.97	224.79	0.18	226	2485	12.3	30516	1.375	1.273	0.049	1.26	41.44 17q21.31	1.08	2.1	.
43	17 C	341.79	341.78	0.01	342	1451	15.0	21695	0.919	0.896	0.046	0.95	41.45 17q21.31	1.02	0.5	.
"17q21.31 microdeletion"					Mean	1592	15.3	22616	1.004	0.966	0.047	1.00	(CV: 0.05)	1.04		

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	
22	22 A	195.35	195.29	0.06	196	1687	10.9	18405	0.755	0.767	0.034	1.08	17.89 22q11.21	0.99	-0.3	.	
24	22 B	208.10	207.99	0.11	208	2163	11.8	25504	1.149	1.070	0.053	0.96	18.09 22q11.21	1.07	1.5	↓	
47	22 D	371.62	371.47	0.15	373	1124	17.1	19222	0.883	0.942	0.047	0.96	19.57 22q11.21	0.94	-1.3	↓	
22q11.21 (DiGeorge)					Mean	1658	13.3	21044	0.929	0.926	0.044	1.00	(CV: 0.07)	1.00			
31	22 B	252.07	251.96	0.11	253	2272	13.1	29673	1.337	1.330	0.090	0.75	49.49 22q13.33-##	1.01	0.1	.	
48	22 D	382.18	382.09	0.09	382	1713	16.7	28666	1.317	1.436	0.059	1.25	49.50 22q13.33-#	0.92	-2.0	↓	
22q13 (Phelan-McDermid)					Mean	1993	14.9	29170	1.327	1.383	0.075	1.00	(CV: 0.06)	0.95			
37	X C	295.42	295.46	-0.04	297	2395	13.5	32314	1.368	1.392	0.054	1.00	32.29 Xp21.2	0.98	-0.4	.	
Chromosome X control probe					Mean	2395	13.5	32314	1.368	1.392	0.054	1.00	(CV:)	0.98			
23	X B	199.76	199.64	0.12	202	1811	11.0	19855	0.895	0.895	0.045	1.00	153.02 Xq28	1.00	0.0	.	
14	X A	147.05	146.82	0.23	148	2285	10.1	22974	0.943	0.964	0.056	0.86	152.95 Xq28	0.98	-0.4	.	
20	X A	183.18	183.16	0.02	184	2710	11.3	30535	1.253	1.214	0.053	1.14	152.94 Xq28-#	1.03	0.7	.	
Xq28 (RETT / MECP2)					Mean	2269	10.8	24455	1.030	1.025	0.051	1.00	(CV: 0.03)	1.01			
Mean values			0.10			1720	13.9	22897	0.997	1.000	0.050	4		0.99	Total of all except		
Standard deviations			0.10			(Coef. of variance: 0.232)			0.230	0.196				0.11	Ctrl and '?' peaks		

Quality assessment	Quality limits	Quality
Mean A-group area / mean Q-frag. area	>1.00 (1.75)	12.26
Mean CpG-area / mean A-group area	>0.55 (0.85)	1.20
Mean height of first probes AB	> 450 (800)	2019
Mean height of last probes CD	> 280 (500)	1433
Ratio of mean heights AB/CD ('slope')	<2.00 (1.55)	1.41
Mean group CV of weighted ratio	<0.20 (0.15)	0.05
1 unidentified peak area / 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: 17q11.2 17q11.2

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 279 (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)