

Peak Data										Normalized Peak Area							
No.	Label	Size	Ref. size	Size diff.	MRC size	Height	Width	Area	Area	Ref. Mean	Ref. SD	Ref. Weigh	Position p-tel band	Dist. Ratio	1.0 in SD	low high	
3	64 -	60.78	60.65	0.13	64	104	7.3	761	0.378	1.438	0.213	0.89	64 nt	0.26	-5.0*		
4	70 -	66.69	66.46	0.23	70	153	18.6	2852	1.416	0.773	0.104	0.98	70 nt	1.83	6.2*		
5	76 -	72.74	72.37	0.37	76	145	18.8	2730	1.356	1.055	0.125	1.12	76 nt	1.29	2.4		
6	82 -	78.68	78.56	0.12	82	114	15.0	1713	0.851	0.734	0.097	1.00	82 nt	1.16	1.2		
Ctrl: Q-fragments					Mean	129	15.0	2014	1.000	1.000	0.134	1.00	(CV: 0.54)	1.16			
7	6 a	85.20	84.95	0.25	88	1087	12.1*	13151	0.600	0.834	0.103	0.95	6p21.3 CpG isl.	0.72	-2.3		
9	2 a	90.39	90.17	0.22	92	1495	10.5	15675	0.715	0.824	0.081	1.20	2q14 synt.	0.87	-1.4		
10	1 a	96.76	96.50	0.26	96	2573	11.8*	30483	1.390	1.685	0.232	0.85	MV 36 1p36 CpG isl.	0.83	-1.3		
Ctrl: D-fragments					Mean	1718	11.5	19770	0.902	1.115	0.138	1.00	(CV: 0.10)	0.81			
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	126.26	126.04	0.22	130	1985	11.2	22161	1.011	1.133	0.040	1.25	1.14 1p36.33	0.89	-3.0		
19	1 A	176.61	176.49	0.12	178	1707	11.9	20243	0.923	0.839	0.046	0.81	1.75 1p36.33	1.10	1.8		
17	1 A	164.68	164.53	0.15	166	1955	11.5	22527	1.027	1.090	0.052	0.94	1.95 1p36.33	0.94	-1.2		
1p36 (1p-deletion)					Mean	1882	11.5	21644	0.987	1.021	0.046	1.00	(CV: 0.11)	0.96			
33	2 B	264.85	264.89	-0.04	267	1574	13.5	21250	1.049	0.910	0.038	1.17	58.30 2p16.1	1.15	3.7		
59	2 D	481.58	481.31	0.27	486	1079	20.0	21610	1.014	1.072	0.063	0.83	61.00 2p16.1	0.95	-0.9		
"2p16.1 deletion syndrome"					Mean	1327	16.8	21430	1.032	0.991	0.050	1.00	(CV: 0.13)	1.07			
52	3 D	416.70	416.46	0.24	418	1496	18.2	27183	1.276	1.230	0.057	1.15	198.51 3q29	1.04	0.8	.	
45	3 C	354.52	354.58	-0.06	359	1515	15.9	24050	1.068	0.959	0.061	0.85	198.28 3q29	1.11	1.8		
"3q29 deletion syndrome"					Mean	1506	17.0	25617	1.172	1.094	0.059	1.00	(CV: 0.05)	1.07			
28	4 B	230.60	230.47	0.13	232	1391	12.5	17444	0.861	0.896	0.058	0.88	1.81 4p16.3	0.96	-0.6	.	
55	4 D	443.43	443.03	0.40	445	997	19.2	19147	0.899	0.880	0.045	1.12	1.90 4p16.3	1.02	0.4	.	
4p16.3 Wolf-Hirschhorn region					Mean	1194	15.9	18296	0.880	0.888	0.052	1.00	(CV: 0.04)	0.99			
54	5 D	435.83	435.58	0.25	436	638	18.4	11719	0.550	0.655	0.037	1.02	1.34 5p15.33	0.84	-2.9		
35	5 C	281.43	281.39	0.04	283	1503	14.6	21920	0.973	1.053	0.061	0.98	1.40 5p15.33	0.92	-1.3		
Cri du Chat syndrome					Mean	1071	16.5	16820	0.762	0.854	0.049	1.00	(CV: 0.07)	0.88			
15	5 A	151.63	151.42	0.21	154	3816	10.9	41531	1.894	0.972	0.047	0.98	176.62 5q35.3	1.95	19.7*		
56	5 D	453.25	453.02	0.23	454	2331	19.2	44866	2.106	1.134	0.052	1.02	176.65 5q35.3	1.86	18.7*		
Sotos syndrome					Mean	3074	15.1	43199	2.000	1.053	0.049	1.00	(CV: 0.03)	1.90			
39	7 C	310.40	310.40	0.00	310	1623	15.0	24374	1.082	1.047	0.040	1.13	73.08 7q11.23	1.03	0.9	.	
46	7 C	363.41	363.46	-0.05	364	1334	16.4	21822	0.969	0.995	0.048	0.88	73.11 7q11.23	0.97	-0.5	.	
49	7 D	390.01	389.95	0.06	391	898	17.0	15269	0.717	0.774	0.034	0.99	73.15 7q11.23	0.93	-1.7		
Williams syndrome					Mean	1285	16.1	20488	0.923	0.938	0.041	1.00	(CV: 0.06)	0.98			
50	8 D	399.90	399.69	0.21	401	923	17.5	16136	0.757	0.753	0.051	0.88	116.75 8q24.12	1.01	0.1	.	
53	8 D	424.68	424.33	0.35	427	1051	18.6	19524	0.916	0.897	0.048	1.12	117.73 8q24.11	1.02	0.4	.	
Langer-Giedion syndrome					Mean	987	18.0	17830	0.837	0.825	0.049	1.00	(CV: 0.01)	1.02			
40	9 C	319.42	319.40	0.02	319	1913	14.9	28525	1.267	1.194	0.050	0.92	100.95 9q22.33	1.06	1.4		
51	9 D	408.28	408.03	0.25	409	1339	17.7	23643	1.110	1.115	0.040	1.08	100.95 9q22.33	1.00	-0.1	.	
"9q22.3 deletion syndrome"					Mean	1626	16.3	26084	1.188	1.155	0.045	1.00	(CV: 0.05)	1.03			
12	10 A	132.85	132.56	0.29	136	1607	11.5	18432	0.841	0.895	0.048	0.90	8.14 10p	0.94	-1.1		
44	10 C	349.25	349.23	0.02	349	1376	15.4	21256	0.944	0.938	0.041	1.10	10.59 10p15.1	1.01	0.1	.	
DiGeorge region 2 (10p)					Mean	1492	13.5	19844	0.892	0.917	0.044	1.00	(CV: 0.05)	0.98			
26	11 B	218.65	218.68	-0.03	220	2196	12.4	27160	1.341	1.184	0.062	1.00	31.78 11p13	1.13	2.5		
WAGR syndrome					Mean	2196	12.4	27160	1.341	1.184	0.062	1.00	(CV:)	1.13			
25	15 B	213.48	213.54	-0.06	214	1996	12.2	24254	1.197	1.162	0.060	0.90	21.48 15q11.2	1.03	0.6	.	
30	15 B	245.18	245.06	0.12	247	1494	13.4	20019	0.988	0.909	0.047	0.90	22.65 15q12	1.09	1.7		
36	15 C	289.82	289.75	0.07	292	1544	13.8	21360	0.948	0.932	0.035	1.25	22.76 15q12	1.02	0.5	.	
16	15 A	158.16	158.00	0.16	160	1674	11.6	19369	0.883	0.838	0.041	0.95	23.17 15q12	1.05	1.1		
Prader-Willi / Angelman					Mean	1677	12.7	21251	1.004	0.960	0.046	1.00	(CV: 0.03)	1.04			
21	15 A	189.79	189.75	0.04	190	2323	11.5	26773	1.221	1.228	0.057	1.07	72.50 15q24.1	0.99	-0.1	.	
41	15 C	326.38	326.43	-0.05	325	1069	15.2	16198	0.719	0.753	0.040	0.93	72.80 15q24.1	0.96	-0.8	.	
"15q24 deletion syndrome"					Mean	1696	13.3	21486	0.970	0.990	0.049	1.00	(CV: 0.03)	0.98			
18	16 A	170.98	170.91	0.07	172	1680	11.5	19289	0.880	0.921	0.053	1.00	3.87 16p13.3	0.96	-0.8	.	
Rubinstein-Taybi syndrome					Mean	1680	11.5	19289	0.880	0.921	0.053	1.00	(CV:)	0.96			
13	17 A	139.18	138.97	0.21	142	2280	11.9*	27056	1.234	1.138	0.031	1.42	2.51 17p13.3	1.08	3.1		
29	17 B	236.20	236.22	-0.02	238	1539	13.0	19953	0.985	0.859	0.058	0.58	2.52 17p13.3	1.15	2.2		
Miller-Dieker region					Mean	1910	12.4	23505	1.109	0.999	0.044	1.00	(CV: 0.04)	1.10			
57	17 D	463.37	463.07	0.30	465	1281	19.2	24651	1.157	1.385	0.097	0.75	17.53 17p11.2-##	0.84	-2.3		
34	17 B	271.88	271.90	-0.02	274	1370	13.8	18839	0.930	0.934	0.038	1.30	17.83 17p11.2	1.00	-0.1	.	
38	17 C	302.88	302.90	-0.02	303	1164	14.5	16824	0.747	0.796	0.044	0.95	18.08 17p11.2	0.94	-1.1		
Smith-Magenis syndrome					Mean	1272	15.8	20105	0.945	1.038	0.060	1.00	(CV: 0.08)	0.94			
32	17 B	258.31	258.33	-0.02	260	957	13.7	13108	0.647	0.578	0.041	0.94	26.56 17q11.2	1.12	1.7		
42	17 C	334.45	334.45	0.00	335	1746	15.5	27108	1.204	1.044	0.065	1.06	26.58 17q11.2	1.15	2.4		
NF1 microdeletion syndrome					Mean	1352	14.6	20108	0.925	0.811	0.053	1.00	(CV: 0.02)	1.14			
58	17 D	470.81	470.58	0.23	472	736	19.4	14259	0.669	0.728	0.046	0.78	41.26 17q21.31	0.92	-1.3		
27	17 B	224.86	224.79	0.07	226	2080	12.7	26411	1.304	1.273	0.049	1.26	41.44 17q21.31	1.02	0.6	.	
43	17 C	341.77	341.78	-0.01	342	1298	15.6	20270	0.900	0.896	0.046	0.95	41.45 17q21.31	1.00	0.1	.	
"17q21.31 microdeletion"					Mean	1371	15.9	20313	0.958	0.966	0.047	1.00	(CV: 0.05)	0.99			

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	195.31	195.29	0.02	196	1411	11.0	15575	0.710	0.767	0.034	1.08	17.89 22q11.21	0.93	-1.7	I.			
24	22 B	208.00	207.99	0.01	208	1624	12.1	19678	0.971	1.070	0.053	0.96	18.09 22q11.21	0.91	-1.9	I.			
47	22 D	371.47	371.47	0.00	373	1193	18.0*	21502	1.009	0.942	0.047	0.96	19.57 22q11.21	1.07	1.4	I.			
22q11.21 (DiGeorge)					Mean	1409	13.7	18918	0.897	0.926	0.044	1.00	(CV: 0.09)	0.97					
31	22 B	251.98	251.96	0.02	253	1780	13.6	24255	1.197	1.330	0.090	0.75	49.49 22q13.33-##	0.90	-1.5	I.			
48	22 D	382.13	382.09	0.04	382	1485	17.7	26278	1.233	1.436	0.059	1.25	49.50 22q13.33-#	0.86	-3.4	I.			
22q13 (Phelan-McDermid)					Mean	1633	15.7	25267	1.215	1.383	0.075	1.00	(CV: 0.03)	0.87					
37	X C	295.40	295.46	-0.06	297	2460	14.3	35153	1.561	1.392	0.054	1.00	32.29 Xp21.2	1.12	3.1	I.			
Chromosome X control probe					Mean	2460	14.3	35153	1.561	1.392	0.054	1.00	(CV:)	1.12					
23	X B	199.68	199.64	0.04	202	1644	11.2	18470	0.912	0.895	0.045	1.00	153.02 Xq28	1.02	0.4	.			
14	X A	147.07	146.82	0.25	148	1787	9.5	17039	0.777	0.964	0.056	0.86	152.95 Xq28	0.81	-3.3	II.			
20	X A	183.21	183.16	0.05	184	1815	11.9	21509	0.981	1.214	0.053	1.14	152.94 Xq28-#	0.81	-4.4*	II.			
Xq28 (RETT / MECP2)					Mean	1749	10.9	19006	0.890	1.025	0.051	1.00	(CV: 0.14)	0.88					
Mean values			0.10			1585	14.5	22184	1.032	1.000	0.050	4		1.03	Total of all except				
Standard deviations			0.12			(Coef. of variance: 0.281)			0.287	0.196				0.20	Ctrl and '?' peaks				

Quality assessment	Quality limits	Quality
Mean A-group area / mean Q-frag. area	>1.00 (1.75)	10.89
Mean CpG-area / mean A-group area	>0.55 (0.85)	0.99
Mean height of first probes AB	> 450 (800)	1820
Mean height of last probes CD	> 280 (500)	1360
Ratio of mean heights AB/CD ('slope')	<2.00 (1.55)	1.34
Mean group CV of weighted ratio	<0.20 (0.15)	0.06
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: 5q35.3 5q35.3

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 113 (14 peaks). CV of ROX heights for peaks above 100 nt is: 0.10

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