

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	in SD	1.0 low high		
3	64 -	60.86	60.65	0.21	64	209	12.6	2624	0.732	1.438	0.213	0.89	64 nt	0.51	-3.3	.		
4	70 -	66.76	66.46	0.30	70	169	22.1	3732	1.041	0.773	0.104	0.98	70 nt	1.35	2.6			
5	76 -	72.34	72.37	-0.03	76	216	20.0	4329	1.208	1.055	0.125	1.12	76 nt	1.15	1.2			
6	82 -	78.52	78.56	-0.04	82	218	16.8	3653	1.019	0.734	0.097	1.00	82 nt	1.39	2.9			
<b>Ctrl: Q-fragments</b>					Mean	203	17.9	3585	1.000	1.000	0.134	1.00	(CV: 0.35)	1.11				
7	6 a	85.01	84.95	0.06	88	1605	12.3*	19815	0.790	0.834	0.103	0.95	6p21.3 CpG isl.	0.95	-0.4	.		
9	2 a	90.25	90.17	0.08	92	2062	11.0*	22699	0.905	0.824	0.081	1.20	2q14 synt.	1.10	1.0			
10	1 a	96.61	96.50	0.11	96	3655	12.2*	44700	1.782	1.685	0.232	0.85	MV 36 1p36 CpG isl.	1.06	0.4			
<b>Ctrl: D-fragments</b>					Mean	2441	11.9	29071	1.159	1.115	0.138	1.00	(CV: 0.08)	1.04				
	Y a	114.50			118					0.811			13.54 Yq11					
	Y a	104.34			108					0.566			14.10 Yq11					
<b>ctrl: Y-fragments (male ref.)</b>					Mean							1.00	(CV: )					
11	1 A	126.08	126.04	0.04	130	2234	11.5	25796	1.028	1.133	0.040	1.25	1.14 1p36.33	0.91	-2.6	.		
19	1 A	176.48	176.49	-0.01	178	2047	12.0	24622	0.981	0.839	0.046	0.81	1.75 1p36.33	1.17	3.1			
17	1 A	164.58	164.53	0.05	166	2208	11.8	25951	1.034	1.090	0.052	0.94	1.95 1p36.33	0.95	-1.1	.		
<b>1p36 (1p-deletion)</b>					Mean	2163	11.8	25456	1.015	1.021	0.046	1.00	(CV: 0.14)	0.99				
33	2 B	264.91	264.89	0.02	267	1569	13.9	21885	0.926	0.910	0.038	1.17	58.30 2p16.1	1.02	0.4	.		
59	2 D	481.22	481.31	-0.09	486	1089	19.9	21722	1.031	1.072	0.063	0.83	61.00 2p16.1	0.96	-0.7	.		
<b>"2p16.1 deletion syndrome"</b>					Mean	1329	16.9	21804	0.979	0.991	0.050	1.00	(CV: 0.04)	0.99				
52	3 D	416.53	416.46	0.07	418	1642	18.2	29921	1.421	1.230	0.057	1.15	198.51 3q29	1.16	3.4			
45	3 C	354.58	354.58	0.00	359	1545	16.1	24905	0.959	0.959	0.061	0.85	198.28 3q29	1.00	0.0	.		
<b>"3q29 deletion syndrome"</b>					Mean	1594	17.2	27413	1.190	1.094	0.059	1.00	(CV: 0.10)	1.09				
28	4 B	230.52	230.47	0.05	232	1626	12.7	20639	0.873	0.896	0.058	0.88	1.81 4p16.3	0.97	-0.4	.		
55	4 D	443.11	443.03	0.08	445	871	19.1	16604	0.788	0.880	0.045	1.12	1.90 4p16.3	0.90	-2.0	.		
<b>4p16.3 Wolf-Hirschhorn region</b>					Mean	1249	15.9	18622	0.831	0.888	0.052	1.00	(CV: 0.06)	0.93				
54	5 D	435.57	435.58	-0.01	436	644	18.7	12036	0.571	0.655	0.037	1.02	1.34 5p15.33	0.87	-2.3	.		
35	5 C	281.29	281.39	-0.10	283	1710	14.6	24993	0.962	1.053	0.061	0.98	1.40 5p15.33	0.91	-1.5	.		
<b>Cri du Chat syndrome</b>					Mean	1177	16.7	18515	0.767	0.854	0.049	1.00	(CV: 0.03)	0.89				
15	5 A	151.53	151.42	0.11	154	2396	10.7	25711	1.025	0.972	0.047	0.98	176.62 5q35.3	1.05	1.1			
56	5 D	453.13	453.02	0.11	454	1300	19.2	24901	1.182	1.134	0.052	1.02	176.65 5q35.3	1.04	0.9	.		
<b>Sotos syndrome</b>					Mean	1848	14.9	25306	1.104	1.053	0.049	1.00	(CV: 0.01)	1.05				
39	7 C	310.34	310.40	-0.06	310	1776	15.4	27382	1.054	1.047	0.040	1.13	73.08 7q11.23	1.01	0.2	.		
46	7 C	363.51	363.46	0.05	364	1441	16.7	24044	0.926	0.995	0.048	0.88	73.11 7q11.23	0.93	-1.4	.		
49	7 D	390.03	389.95	0.08	391	970	17.8	17223	0.818	0.774	0.034	0.99	73.15 7q11.23	1.06	1.3			
<b>Williams syndrome</b>					Mean	1396	16.6	22883	0.933	0.938	0.041	1.00	(CV: 0.06)	1.00				
50	8 D	399.72	399.69	0.03	401	903	17.6	15853	0.753	0.753	0.051	0.88	116.75 8q24.12	1.00	0.0	.		
53	8 D	424.44	424.33	0.11	427	1056	18.5	19552	0.928	0.897	0.048	1.12	117.73 8q24.11	1.04	0.7	.		
<b>Langer-Giedion syndrome</b>					Mean	980	18.0	17703	0.841	0.825	0.049	1.00	(CV: 0.02)	1.02				
40	9 C	319.31	319.40	-0.09	319	2073	15.2	31537	1.214	1.194	0.050	0.92	100.95 9q22.33	1.02	0.4	.		
51	9 D	408.10	408.03	0.07	409	1485	17.9	26593	1.263	1.115	0.040	1.08	100.95 9q22.33	1.13	3.7			
<b>"9q22.3 deletion syndrome"</b>					Mean	1779	16.6	29065	1.238	1.155	0.045	1.00	(CV: 0.08)	1.08				
12	10 A	132.64	132.56	0.08	136	1718	11.6	19957	0.795	0.895	0.048	0.90	8.14 10p	0.89	-2.1	.		
44	10 C	349.25	349.23	0.02	349	1375	15.7	21622	0.832	0.938	0.041	1.10	10.59 10p15.1	0.89	-2.6	.		
<b>DiGeorge region 2 (10p)</b>					Mean	1547	13.7	20790	0.814	0.917	0.044	1.00	(CV: 0.00)	0.89				
26	11 B	218.64	218.68	-0.04	220	2364	12.6	29774	1.260	1.184	0.062	1.00	31.78 11p13	1.06	1.2			
<b>WAGR syndrome</b>					Mean	2364	12.6	29774	1.260	1.184	0.062	1.00	(CV: )	1.06				
25	15 B	213.57	213.54	0.03	214	2148	12.7	27345	1.157	1.162	0.060	0.90	21.48 15q11.2	1.00	-0.1	.		
30	15 B	245.10	245.06	0.04	247	1750	13.5	23549	0.996	0.909	0.047	0.90	22.65 15q12	1.10	1.9			
36	15 C	289.72	289.75	-0.03	292	1782	14.0	24990	0.962	0.932	0.035	1.25	22.76 15q12	1.03	0.9	.		
16	15 A	158.01	158.00	0.01	160	2045	11.9	24285	0.968	0.838	0.041	0.95	23.17 15q12	1.16	3.1			
<b>Prader-Willi / Angelman</b>					Mean	1931	13.0	25042	1.021	0.960	0.046	1.00	(CV: 0.06)	1.07				
21	15 A	189.72	189.75	-0.03	190	2433	11.5	28054	1.118	1.228	0.057	1.07	72.50 15q24.1	0.91	-1.9	.		
41	15 C	326.33	326.43	-0.10	325	1160	15.4	17829	0.686	0.753	0.040	0.93	72.80 15q24.1	0.91	-1.6	.		
<b>"15q24 deletion syndrome"</b>					Mean	1797	13.5	22942	0.902	0.990	0.049	1.00	(CV: 0.00)	0.91				
18	16 A	170.86	170.91	-0.05	172	2082	11.7	24435	0.974	0.921	0.053	1.00	3.87 16p13.3	1.06	1.0			
<b>Rubinstein-Taybi syndrome</b>					Mean	2082	11.7	24435	0.974	0.921	0.053	1.00	(CV: )	1.06				
13	17 A	139.00	138.97	0.03	142	2476	11.8	29287	1.167	1.138	0.031	1.42	2.51 17p13.3	1.03	0.9	.		
29	17 B	236.26	236.22	0.04	238	1635	13.2	21517	0.910	0.859	0.058	0.58	2.52 17p13.3	1.06	0.9			
<b>Miller-Dieker region</b>					Mean	2056	12.5	25402	1.039	0.999	0.044	1.00	(CV: 0.02)	1.04				
57	17 D	463.05	463.07	-0.02	465	1421	19.5	27682	1.314	1.385	0.097	0.75	17.53 17p11.2-##	0.95	-0.7	.		
34	17 B	271.89	271.90	-0.01	274	1487	13.9	20625	0.873	0.934	0.038	1.30	17.83 17p11.2	0.93	-1.6	.		
38	17 C	302.86	302.90	-0.04	303	1276	14.7	18795	0.724	0.796	0.044	0.95	18.08 17p11.2	0.91	-1.6	.		
<b>Smith-Magenis syndrome</b>					Mean	1395	16.0	22367	0.970	1.038	0.060	1.00	(CV: 0.02)	0.93				
32	17 B	258.32	258.33	-0.01	260	1070	13.9	14845	0.628	0.578	0.041	0.94	26.56 17q11.2	1.09	1.2			
42	17 C	334.38	334.45	-0.07	335	1666	15.9	26477	1.019	1.044	0.065	1.06	26.58 17q11.2	0.98	-0.4	.		
<b>NF1 microdeletion syndrome</b>					Mean	1368	14.9	20661	0.824	0.811	0.053	1.00	(CV: 0.08)	1.03				
58	17 D	470.52	470.58	-0.06	472	728	19.6	14241	0.676	0.728	0.046	0.78	41.26 17q21.31	0.93	-1.1	.		
27	17 B	224.81	224.79	0.02	226	2452	13.0	31893	1.349	1.273	0.049	1.26	41.44 17q21.31	1.06	1.6			
43	17 C	341.77	341.78	-0.01	342	1476	16.2	23977	0.923	0.896	0.046	0.95	41.45 17q21.31	1.03	0.6	.		
<b>"17q21.31 microdeletion"</b>					Mean	1552	16.3	23370	0.983	0.966	0.047	1.00	(CV: 0.06)	1.02				

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	1.0 high
22	22 A	195.31	195.29	0.02	196	805	10.2*	8181	0.326	0.767	0.034	1.08	17.89 22q11.21	0.43	-13.1*	.	
24	22 B	208.04	207.99	0.05	208	1054	12.2	12862	0.544	1.070	0.053	0.96	18.09 22q11.21	0.51	-9.9*	.	
47	22 D	371.59	371.47	0.12	373	574	18.0	10334	0.491	0.942	0.047	0.96	19.57 22q11.21	0.52	-9.7*	.	
<b>22q11.21 (DiGeorge)</b>					Mean	811	13.5	10459	0.454	0.926	0.044	1.00	(CV: <b>0.11</b> )	<b>0.48</b>			
31	22 B	251.94	251.96	-0.02	253	2209	13.9	30810	1.303	1.330	0.090	0.75	49.49 22q13.33-##	0.98	-0.3		.
48	22 D	382.24	382.09	0.15	382	1736	17.7	30708	1.458	1.436	0.059	1.25	49.50 22q13.33-#	1.02	0.4		.
<b>22q13 (Phelan-McDermid)</b>					Mean	1973	15.8	30759	1.381	1.383	0.075	1.00	(CV: <b>0.02</b> )	<b>1.00</b>			
37	X C	295.43	295.46	-0.03	297	2632	14.4	37844	1.457	1.392	0.054	1.00	32.29 Xp21.2	1.05	1.2		.
<b>Chromosome X control probe</b>					Mean	2632	14.4	37844	1.457	1.392	0.054	1.00	(CV: )	<b>1.05</b>			
23	X B	199.68	199.64	0.04	202	1809	11.7	21250	0.899	0.895	0.045	1.00	153.02 Xq28	1.00	0.1		.
14	X A	146.98	146.82	0.16	148	2493	10.4	25858	1.031	0.964	0.056	0.86	152.95 Xq28	1.07	1.2		↓
20	X A	183.14	183.16	-0.02	184	2597	12.3	31854	1.270	1.214	0.053	1.14	152.94 Xq28-#	1.05	1.0		.
<b>Xq28 (RETT / MECP2)</b>					Mean	2300	11.5	26321	1.066	1.025	0.051	1.00	(CV: <b>0.03</b> )	<b>1.04</b>			
<b>Mean values</b>			0.02			1654	14.7	23321	<b>0.977</b>	1.000	0.050	4		0.97	Total of all except		
<b>Standard deviations</b>			0.06			(Coef. of variance: 0.264 )			0.252	0.196				0.15	Ctrl and '?' peaks		

Quality assessment	Quality limits	Quality
Mean A-group area / mean Q-frag. area	>1.00 (1.75)	7.00
Mean CpG-area / mean A-group area	>0.55 (0.85)	1.29
Mean height of first probes AB	> 450 ( 800)	1946
Mean height of last probes CD	> 280 ( 500)	1373
Ratio of mean heights AB/CD ('slope')	<2.00 (1.55)	1.42
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: 22q11.21 22q11.21 22q11.21**

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 229 (14 peaks). CV of ROX heights for peaks above 100 nt is: 0.08

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