

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	Dist. Ratio	1.0 in SD	1.0 low high	
2	64 -	60.91	60.65	0.26	64	191	10.0	1904	0.798	1.438	0.213	0.89	64 nt	0.56	-3.0	.	
3	70 -	66.59	66.46	0.13	70	106	18.5	1965	0.824	0.773	0.104	0.98	70 nt	1.07	0.5	.	
4	76 -	72.77	72.37	0.40	76	143	21.8	3113	1.306	1.055	0.125	1.12	76 nt	1.24	2.0		
5	82 -	78.80	78.56	0.24	82	155	16.5	2556	1.072	0.734	0.097	1.00	82 nt	1.46	3.5		
<b>Ctrl: Q-fragments</b>					Mean	149	16.7	2385	1.000	1.000	0.134	1.00	(CV: 0.34)	<b>1.10</b>			
6	6 a	85.10	84.95	0.15	88	1520	12.9*	19670	0.937	0.834	0.103	0.95	6p21.3 CpG isl.	1.12	1.0	.	
8	2 a	90.32	90.17	0.15	92	1865	11.2	20831	0.992	0.824	0.081	1.20	2q14 synt.	1.20	2.1		
9	1 a	96.63	96.50	0.13	96	3252	11.9*	38761	1.847	1.685	0.232	0.85	MV 36 1p36 CpG isl.	1.10	0.7	.	
<b>Ctrl: D-fragments</b>					Mean	2212	12.0	26421	1.259	1.115	0.138	1.00	(CV: 0.05)	<b>1.15</b>			
	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	126.11	126.04	0.07	130	2106	11.9	25015	1.192	1.133	0.040	1.25	1.14 1p36.33	1.05	1.5	.	
19	1 A	176.55	176.49	0.06	178	1422	12.2	17392	0.829	0.839	0.046	0.81	1.75 1p36.33	0.99	-0.2	.	
17	1 A	164.58	164.53	0.05	166	2026	12.3	24867	1.185	1.090	0.052	0.94	1.95 1p36.33	1.09	1.8	.	
<b>1p36 (1p-deletion)</b>					Mean	1851	12.1	22425	1.068	1.021	0.046	1.00	(CV: 0.04)	<b>1.05</b>			
33	2 B	264.92	264.89	0.03	267	1285	14.4	18524	0.859	0.910	0.038	1.17	58.30 2p16.1	0.94	-1.4	.	
62	2 D	481.25	481.31	-0.06	486	945	20.3	19188	0.999	1.072	0.063	0.83	61.00 2p16.1	0.93	-1.2	.	
<b>"2p16.1 deletion syndrome"</b>					Mean	1115	17.4	18856	0.929	0.991	0.050	1.00	(CV: 0.01)	<b>0.94</b>			
55	3 D	416.56	416.46	0.10	418	1113	19.3	21473	1.118	1.230	0.057	1.15	198.51 3q29	0.91	-2.0	.	
46	3 C	354.63	354.58	0.05	359	1229	16.4	20147	0.994	0.959	0.061	0.85	198.28 3q29	1.04	0.6	.	
<b>"3q29 deletion syndrome"</b>					Mean	1171	17.8	20810	1.056	1.094	0.059	1.00	(CV: 0.09)	<b>0.96</b>			
28	4 B	230.70	230.47	0.23	232	1456	13.5	19724	0.915	0.896	0.058	0.88	1.81 4p16.3	1.02	0.3	.	
58	4 D	443.23	443.03	0.20	445	933	19.3	18007	0.938	0.880	0.045	1.12	1.90 4p16.3	1.07	1.3	.	
<b>4p16.3 Wolf-Hirschhorn region</b>					Mean	1195	16.4	18866	0.926	0.888	0.052	1.00	(CV: 0.03)	<b>1.05</b>			
57	5 D	435.62	435.58	0.04	436	640	19.6	12558	0.654	0.655	0.037	1.02	1.34 5p15.33	1.00	0.0	.	
35	5 C	281.44	281.39	0.05	283	1580	14.8	23438	1.156	1.053	0.061	0.98	1.40 5p15.33	1.10	1.7	.	
<b>Cri du Chat syndrome</b>					Mean	1110	17.2	17998	0.905	0.854	0.049	1.00	(CV: 0.07)	<b>1.05</b>			
15	5 A	151.46	151.42	0.04	154	1980	10.7	21169	1.009	0.972	0.047	0.98	176.62 5q35.3	1.04	0.8	.	
59	5 D	453.11	453.02	0.09	454	1052	19.6	20601	1.073	1.134	0.052	1.02	176.65 5q35.3	0.95	-1.2	.	
<b>Sotos syndrome</b>					Mean	1516	15.1	20885	1.041	1.053	0.049	1.00	(CV: 0.06)	<b>0.99</b>			
39	7 C	310.39	310.40	-0.01	310	1571	15.5	24341	1.201	1.047	0.040	1.13	73.08 7q11.23	1.15	3.9	.	
47	7 C	363.48	363.46	0.02	364	1214	16.4	19944	0.984	0.995	0.048	0.88	73.11 7q11.23	0.99	-0.2	.	
52	7 D	390.09	389.95	0.14	391	821	17.5	14337	0.747	0.774	0.034	0.99	73.15 7q11.23	0.97	-0.8	.	
<b>Williams syndrome</b>					Mean	1202	16.5	19541	0.977	0.938	0.041	1.00	(CV: 0.10)	<b>1.04</b>			
53	8 D	399.81	399.69	0.12	401	796	17.9	14239	0.742	0.753	0.051	0.88	116.75 8q24.12	0.99	-0.2	.	
56	8 D	424.53	424.33	0.20	427	782	21.0*	16432	0.856	0.897	0.048	1.12	117.73 8q24.11	0.95	-0.9	.	
<b>Langer-Giedion syndrome</b>					Mean	789	19.5	15336	0.799	0.825	0.049	1.00	(CV: 0.02)	<b>0.97</b>			
40	9 C	319.42	319.40	0.02	319	1450	14.4	20941	1.033	1.194	0.050	0.92	100.95 9q22.33	0.87	-3.2	.	
54	9 D	408.16	408.03	0.13	409	1231	18.0	22192	1.156	1.115	0.040	1.08	100.95 9q22.33	1.04	1.0	.	
<b>"9q22.3 deletion syndrome"</b>					Mean	1341	16.2	21567	1.094	1.155	0.045	1.00	(CV: 0.13)	<b>0.96</b>			
12	10 A	132.70	132.56	0.14	136	1649	12.0	19733	0.940	0.895	0.048	0.90	8.14 10p	1.05	0.9	.	
45	10 C	349.25	349.23	0.02	349	1219	16.0	19463	0.960	0.938	0.041	1.10	10.59 10p15.1	1.02	0.5	.	
<b>DiGeorge region 2 (10p)</b>					Mean	1434	14.0	19598	0.950	0.917	0.044	1.00	(CV: 0.02)	<b>1.04</b>			
26	11 B	218.74	218.68	0.06	220	1899	12.8	24262	1.125	1.184	0.062	1.00	31.78 11p13	0.95	-1.0	.	
<b>WAGR syndrome</b>					Mean	1899	12.8	24262	1.125	1.184	0.062	1.00	(CV: )	<b>0.95</b>			
25	15 B	213.63	213.54	0.09	214	1901	12.8	24270	1.126	1.162	0.060	0.90	21.48 15q11.2	0.97	-0.6	.	
30	15 B	245.17	245.06	0.11	247	1282	14.0	17989	0.834	0.909	0.047	0.90	22.65 15q12	0.92	-1.6	.	
36	15 C	289.71	289.75	-0.04	292	1336	14.9	19863	0.980	0.932	0.035	1.25	22.76 15q12	1.05	1.4	.	
16	15 A	158.07	158.00	0.07	160	1502	12.1	18165	0.865	0.838	0.041	0.95	23.17 15q12	1.03	0.7	.	
<b>Prader-Willi / Angelman</b>					Mean	1505	13.4	20072	0.951	0.960	0.046	1.00	(CV: 0.06)	<b>1.00</b>			
21	15 A	189.88	189.75	0.13	190	2041	12.3	25123	1.197	1.228	0.057	1.07	72.50 15q24.1	0.97	-0.5	.	
42	15 C	326.49	326.43	0.06	325	1030	14.4	14868	0.733	0.753	0.040	0.93	72.80 15q24.1	0.97	-0.5	.	
<b>"15q24 deletion syndrome"</b>					Mean	1536	13.4	19996	0.965	0.990	0.049	1.00	(CV: 0.00)	<b>0.97</b>			
18	16 A	170.94	170.91	0.03	172	1661	12.2	20207	0.963	0.921	0.053	1.00	3.87 16p13.3	1.05	0.8	.	
<b>Rubinstein-Taybi syndrome</b>					Mean	1661	12.2	20207	0.963	0.921	0.053	1.00	(CV: )	<b>1.05</b>			
13	17 A	139.09	138.97	0.12	142	1982	12.0	23868	1.137	1.138	0.031	1.42	2.51 17p13.3	1.00	0.0	.	
29	17 B	236.23	236.22	0.01	238	1301	13.2	17138	0.795	0.859	0.058	0.58	2.52 17p13.3	0.93	-1.1	.	
<b>Miller-Dieker region</b>					Mean	1642	12.6	20503	0.966	0.999	0.044	1.00	(CV: 0.05)	<b>0.98</b>			
60	17 D	463.16	463.07	0.09	465	1469	19.8	29159	1.519	1.385	0.097	0.75	17.53 17p11.2-##	1.10	1.4	.	
34	17 B	271.93	271.90	0.03	274	1373	14.7	20154	0.935	0.934	0.038	1.30	17.83 17p11.2	1.00	0.0	.	
38	17 C	302.95	302.90	0.05	303	1091	15.2	16540	0.816	0.796	0.044	0.95	18.08 17p11.2	1.03	0.5	.	
<b>Smith-Magenis syndrome</b>					Mean	1311	16.6	21951	1.090	1.038	0.060	1.00	(CV: 0.05)	<b>1.03</b>			
32	17 B	258.38	258.33	0.05	260	775	13.9	10810	0.501	0.578	0.041	0.94	26.56 17q11.2	0.87	-1.9	.	
43	17 C	334.50	334.45	0.05	335	1488	16.2	24071	1.187	1.044	0.065	1.06	26.58 17q11.2	1.14	2.2	.	
<b>NF1 microdeletion syndrome</b>					Mean	1132	15.1	17441	0.844	0.811	0.053	1.00	(CV: 0.19)	<b>1.01</b>			
61	17 D	470.50	470.58	-0.08	472	668	19.9	13313	0.693	0.728	0.046	0.78	41.26 17q21.31	0.95	-0.8	.	
27	17 B	224.87	224.79	0.08	226	1967	13.4	26301	1.220	1.273	0.049	1.26	41.44 17q21.31	0.96	-1.1	.	
44	17 C	341.84	341.78	0.06	342	1242	16.4	20418	1.007	0.896	0.046	0.95	41.45 17q21.31	1.12	2.4	.	
<b>"17q21.31 microdeletion"</b>					Mean	1292	16.6	20011	0.974	0.966	0.047	1.00	(CV: 0.09)	<b>1.01</b>			

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	195.35	195.29	0.06	196	1557	11.5	17897	0.853	0.767	0.034	1.08	17.89 22q11.21	1.11	2.6	.	↓
24	22 B	208.14	207.99	0.15	208	1863	13.1	24426	1.133	1.070	0.053	0.96	18.09 22q11.21	1.06	1.2	.	↓
49	22 D	371.59	371.47	0.12	373	886	16.6	14725	0.767	0.942	0.047	0.96	19.57 22q11.21	0.81	-3.8	.	
<b>22q11.21 (DiGeorge)</b>					Mean	1435	13.7	19016	0.917	0.926	0.044	1.00	(CV: <b>0.16</b> )	<b>1.00</b>			
31	22 B	251.97	251.96	0.01	253	3129	14.4	44943	2.085	1.330	0.090	0.75	49.49 22q13.33-##	1.57	8.3*	.	
51	22 D	382.17	382.09	0.08	382	2415	17.8	42926	2.236	1.436	0.059	1.25	49.50 22q13.33-#	1.56	13.6*	.	
<b>22q13 (Phelan-McDermid)</b>					Mean	2772	16.1	43935	2.160	1.383	0.075	1.00	(CV: <b>0.00</b> )	<b>1.56</b>			
37	X C	295.46	295.46	0.00	297	1941	14.7	28530	1.407	1.392	0.054	1.00	32.29 Xp21.2	1.01	0.3	.	
<b>Chromosome X control probe</b>					Mean	1941	14.7	28530	1.407	1.392	0.054	1.00	(CV: )	<b>1.01</b>			
23	X B	199.76	199.64	0.12	202	1703	11.8	20087	0.932	0.895	0.045	1.00	153.02 Xq28	1.04	0.8	.	
14	X A	146.84	146.82	0.02	148	1981	9.8	19470	0.928	0.964	0.056	0.86	152.95 Xq28	0.96	-0.6	.	
20	X A	183.27	183.16	0.11	184	2276	12.6	28625	1.364	1.214	0.053	1.14	152.94 Xq28-#	1.12	2.8	↓	
<b>Xq28 (RETT / MECP2)</b>					Mean	1987	11.4	22727	1.074	1.025	0.051	1.00	(CV: <b>0.08</b> )	<b>1.05</b>			
<b>Mean values</b>			0.07			1475	15.0	21263	<b>1.038</b>	1.000	0.050		<b>Note: High CV of ROX peaks</b>	1.03	Total of all except		
<b>Standard deviations</b>			0.06			(Coef. of variance: 0.296 )			0.307	0.196				0.13	Ctrl and '?' peaks		

Quality assessment	Quality limits	Quality
Mean A-group area / mean Q-frag. area	>1.00 (1.75)	8.80
Mean CpG-area / mean A-group area	>0.55 (0.85)	1.39
Mean height of first probes AB	> 450 ( 800)	1755
Mean height of last probes CD	> 280 ( 500)	1206
Ratio of mean heights AB/CD ('slope')	<2.00 (1.55)	1.46
Mean group CV of weighted ratio	<0.20 (0.15)	0.07
5 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: 22q13.33-## 22q13.33-#**

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 202 (14 peaks). CV of ROX heights for peaks above 100 nt is: 0.22 (High!)

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