

Peak Data										Normalized Peak Area								
No.	Label	Size	Ref. size	Size diff.	MRC	Height	Width	Area	Area	Ref. Mean	Ref. SD	Ref. Weigh	Position p-tel band	Ratio	Dist. in SD	1.0 low high		
3	64 -	60.87	60.65	0.22	64	281	9.5	2669	0.444	1.190	0.371	0.75	64 nt	0.37	-2.0	.		
4	70 -	66.87	66.46	0.41	70	408	19.1	7807	1.297	0.913	0.264	0.80	70 nt	1.42	1.5	.		
5	76 -	72.36	72.37	-0.01	76	340	22.4	7622	1.267	1.138	0.170	1.55	76 nt	1.11	0.8	.		
6	82 -	78.65	78.56	0.09	82	269	22.2	5974	0.993	0.787	0.204	0.90	82 nt	1.26	1.0	.		
<b>Ctrl: Q-fragments</b>					Mean	325	18.3	6018	1.000	1.007	0.252	1.00	(CV: <b>0.38</b> )	<b>1.07</b>				
7	6 a	85.17	84.95	0.22	88	1338	11.6*	15586	0.840	0.981	0.152	1.02	6p21.3 CpG isl.	0.86	-0.9	.		
9	2 a	90.39	90.17	0.22	92	1516	10.4	15760	0.849	0.967	0.135	1.13	2q14 synt.	0.88	-0.9	.		
10	1 a	96.71	96.50	0.21	96	2952	11.7*	34478	1.857	1.641	0.304	0.85	MV 36 1p36 CpG isl.	1.13	0.7	.		
<b>Ctrl: D-fragments</b>					Mean	1935	11.2	21941	1.182	1.197	0.197	1.00	(CV: <b>0.16</b> )	<b>0.94</b>				
14	Y a	114.70	114.50	0.20	118	1513	10.6	15981	0.861	0.811	0.088	1.03	13.54 Yq11	1.06	0.6	.		
12	Y a	104.49	104.34	0.15	108	920	10.5	9623	0.518	0.566	0.065	0.97	14.10 Yq11	0.92	-0.7	.		
<b>ctrl: Y-fragments (male ref.)</b>					Mean	1217	10.5	12802	0.690	0.688	0.076	1.00	(CV: <b>0.10</b> )	<b>0.99</b>				
15	1 A	126.38	126.04	0.34	130	2224	11.1	24604	1.325	1.200	0.054	1.30	1.14 1p36.33	1.10	2.3	.		
23	1 A	176.67	176.49	0.18	178	1460	11.2	16408	0.884	0.942	0.074	0.75	1.75 1p36.33	0.94	-0.8	.		
21	1 A	164.65	164.53	0.12	166	2029	11.6	23541	1.268	1.181	0.073	0.95	1.95 1p36.33	1.07	1.2	.		
<b>1p36 (1p-deletion)</b>					Mean	1904	11.3	21518	1.159	1.108	0.067	1.00	(CV: <b>0.08</b> )	<b>1.05</b>				
38	2 B	265.15	264.89	0.26	267	1290	13.4	17232	1.077	0.948	0.040	1.36	58.30 2p16.1	1.14	3.2	.		
64	2 D	481.66	481.31	0.35	486	431	19.9	8578	0.734	1.121	0.101	0.64	61.00 2p16.1	0.66	-3.8	.		
<b>"2p16.1 deletion syndrome"</b>					Mean	861	16.6	12905	0.905	1.034	0.071	1.00	(CV: <b>0.32</b> )	<b>0.98</b>				
57	3 D	416.70	416.46	0.24	418	906	17.3	15717	1.345	1.268	0.073	0.96	198.51 3q29	1.06	1.1	.		
50	3 C	354.73	354.58	0.15	359	773	15.1	11664	0.747	1.039	0.056	1.04	198.28 3q29	0.72	-5.3*	.		
<b>"3q29 deletion syndrome"</b>					Mean	840	16.2	13691	1.046	1.154	0.064	1.00	(CV: <b>0.27</b> )	<b>0.88</b>				
33	4 B	230.73	230.47	0.26	232	737	11.8	8684	0.543	0.944	0.063	0.88	1.81 4p16.3	0.57	-6.4*	.		
60	4 D	443.29	443.03	0.26	445	236	18.6	4398	0.376	0.879	0.046	1.12	1.90 4p16.3	0.43	-11.0*	.		
<b>4p16.3 Wolf-Hirschhorn region</b>					Mean	487	15.2	6541	0.460	0.912	0.054	1.00	(CV: <b>0.21</b> )	<b>0.49</b>				
59	5 D	435.75	435.58	0.17	436	368	18.5	6814	0.583	0.659	0.053	0.88	1.34 5p15.33	0.89	-1.4	.		
40	5 C	281.60	281.39	0.21	283	1418	14.0	19842	1.271	1.115	0.071	1.12	1.40 5p15.33	1.14	2.2	.		
<b>Cri du Chat syndrome</b>					Mean	893	16.3	13328	0.927	0.887	0.062	1.00	(CV: <b>0.17</b> )	<b>1.03</b>				
19	5 A	151.53	151.42	0.11	154	1926	11.1	21317	1.148	1.127	0.052	1.03	176.62 5q35.3	1.02	0.4	.		
61	5 D	453.25	453.02	0.23	454	740	18.5	13663	1.169	1.123	0.055	0.97	176.65 5q35.3	1.04	0.8	.		
<b>Sotos syndrome</b>					Mean	1333	14.8	17490	1.159	1.125	0.054	1.00	(CV: <b>0.02</b> )	<b>1.03</b>				
44	7 C	310.58	310.40	0.18	310	1331	14.6	19417	1.244	1.116	0.056	0.99	73.08 7q11.23	1.11	2.3	.		
51	7 C	363.60	363.46	0.14	364	903	16.3	14674	0.940	1.029	0.040	1.27	73.11 7q11.23	0.91	-2.2	.		
54	7 D	390.14	389.95	0.19	391	592	16.7	9896	0.847	0.748	0.050	0.74	73.15 7q11.23	1.13	2.0	.		
<b>Williams syndrome</b>					Mean	942	15.9	14662	1.010	0.964	0.049	1.00	(CV: <b>0.12</b> )	<b>1.03</b>				
55	8 D	399.91	399.69	0.22	401	659	17.2	11328	0.969	0.776	0.036	1.06	116.75 8q24.12	1.25	5.3*	.		
58	8 D	424.71	424.33	0.38	427	573	18.2	10403	0.890	0.895	0.047	0.94	117.73 8q24.11	0.99	-0.1	.		
<b>Langer-Giedion syndrome</b>					Mean	616	17.7	10866	0.930	0.835	0.042	1.00	(CV: <b>0.16</b> )	<b>1.13</b>				
45	9 C	319.51	319.40	0.11	319	1303	14.6	19061	1.221	1.292	0.072	1.05	100.95 9q22.33	0.95	-1.0	.		
56	9 D	408.28	408.03	0.25	409	973	17.4	16941	1.450	1.119	0.069	0.95	100.95 9q22.33	1.30	4.8*	.		
<b>"9q22.3 deletion syndrome"</b>					Mean	1138	16.0	18001	1.336	1.206	0.070	1.00	(CV: <b>0.22</b> )	<b>1.11</b>				
16	10 A	132.87	132.56	0.31	136	1472	11.1	16274	0.877	0.948	0.043	1.16	8.14 10p	0.92	-1.7	.		
49	10 C	349.42	349.23	0.19	349	1080	15.6	16859	1.080	0.979	0.060	0.84	10.59 10p15.1	1.10	1.7	.		
<b>DiGeorge region 2 (10p)</b>					Mean	1276	13.3	16567	0.978	0.963	0.052	1.00	(CV: <b>0.12</b> )	<b>1.00</b>				
31	11 B	218.92	218.68	0.24	220	1769	12.0	21192	1.324	1.246	0.061	1.00	31.78 11p13	1.06	1.3	.		
<b>WAGR syndrome</b>					Mean	1769	12.0	21192	1.324	1.246	0.061	1.00	(CV: )	<b>1.06</b>				
30	15 B	213.73	213.54	0.19	214	1853	12.0	22156	1.384	1.226	0.047	1.34	21.48 15q11.2	1.13	3.4	.		
35	15 B	245.29	245.06	0.23	247	1144	13.5	15476	0.967	0.962	0.058	0.86	22.65 15q12	1.01	0.1	.		
41	15 C	289.88	289.75	0.13	292	1060	14.1	14983	0.960	1.018	0.061	0.86	22.76 15q12	0.94	-1.0	.		
20	15 A	158.17	158.00	0.17	160	1630	11.3	18425	0.992	0.930	0.051	0.94	23.17 15q12	1.07	1.2	.		
<b>Prader-Willi / Angelman</b>					Mean	1422	12.7	17760	1.076	1.034	0.054	1.00	(CV: <b>0.08</b> )	<b>1.05</b>				
26	15 A	189.94	189.75	0.19	190	2169	11.2	24237	1.305	1.299	0.130	0.78	72.50 15q24.1	1.01	0.1	.		
46	15 C	326.59	326.43	0.16	325	747	14.9	11108	0.712	0.771	0.049	1.22	72.80 15q24.1	0.92	-1.2	.		
<b>"15q24 deletion syndrome"</b>					Mean	1458	13.0	17673	1.009	1.035	0.090	1.00	(CV: <b>0.06</b> )	<b>0.96</b>				
22	16 A	170.99	170.91	0.08	172	1724	11.2	19248	1.037	1.018	0.063	1.00	3.87 16p13.3	1.02	0.3	.		
<b>Rubinstein-Taybi syndrome</b>					Mean	1724	11.2	19248	1.037	1.018	0.063	1.00	(CV: )	<b>1.02</b>				
17	17 A	139.26	138.97	0.29	142	2108	11.3	23920	1.288	1.248	0.053	1.27	2.51 17p13.3	1.03	0.8	.		
34	17 B	236.35	236.22	0.13	238	1018	12.9	13143	0.821	0.900	0.067	0.73	2.52 17p13.3	0.91	-1.2	.		
<b>Miller-Dieker region</b>					Mean	1563	12.1	18532	1.055	1.074	0.060	1.00	(CV: <b>0.08</b> )	<b>0.99</b>				
62	17 D	463.26	463.07	0.19	465	701	19.0	13330	1.141	1.331	0.092	0.83	17.53 17p11.2-##	0.86	-2.1	.		
39	17 B	272.08	271.90	0.18	274	1063	13.0	13845	0.865	0.940	0.043	1.25	17.83 17p11.2	0.92	-1.7	.		
43	17 C	303.04	302.90	0.14	303	924	14.3	13173	0.844	0.839	0.053	0.91	18.08 17p11.2	1.01	0.1	.		
<b>Smith-Magenis syndrome</b>					Mean	896	15.4	13449	0.950	1.037	0.063	1.00	(CV: <b>0.08</b> )	<b>0.93</b>				
37	17 B	258.52	258.33	0.19	260	744	13.5	10049	0.628	0.621	0.038	0.88	26.56 17q11.2	1.01	0.2	.		
47	17 C	334.59	334.45	0.14	335	1049	15.6	16335	1.047	1.118	0.053	1.12	26.58 17q11.2	0.94	-1.3	.		
<b>NF1 microdeletion syndrome</b>					Mean	897	14.5	13192	0.837	0.870	0.046	1.00	(CV: <b>0.05</b> )	<b>0.97</b>				
63	17 D	470.95	470.58	0.37	472	412	19.5	8042	0.688	0.719	0.047	0.70	41.26 17q21.31	0.96	-0.6	.		
32	17 B	225.06	224.79	0.27	226	1766	12.6	22274	1.392	1.325	0.050	1.21	41.44 17q21.31	1.05	1.3	.		
48	17 C	341.92	341.78	0.14	342	1014	15.6	15828	1.014	0.932	0.039	1.09	41.45 17q21.31	1.09	2.1	.		
<b>"17q21.31 microdeletion"</b>					Mean	1064	15.9	15381	1.031	0.992	0.046	1.00	(CV: <b>0.06</b> )	<b>1.04</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 high	
27	22 A	195.50	195.29	0.21	196	1364	11.5	15697	0.845	0.890	0.065	0.83	17.89 22q11.21	0.95	-0.7	.	
29	22 B	208.23	207.99	0.24	208	1487	11.8	17581	1.099	1.109	0.061	1.11	18.09 22q11.21	0.99	-0.2	.	
52	22 D	371.65	371.47	0.18	373	795	17.5	13884	1.188	0.920	0.053	1.06	19.57 22q11.21	1.29	5.1*	.	
<b>22q11.21 (DiGeorge)</b>					Mean	1215	13.6	15721	1.044	0.973	0.060	1.00	(CV: <b>0.17</b> )	<b>1.09</b>			
36	22 B	252.18	251.96	0.22	253	1647	13.1	21554	1.347	1.321	0.100	1.05	49.49 22q13.33-##	1.02	0.3	.	
53	22 D	382.27	382.09	0.18	382	1025	17.0	17385	1.488	1.442	0.120	0.95	49.50 22q13.33-#	1.03	0.4	.	
<b>22q13 (Phelan-McDermid)</b>					Mean	1336	15.0	19470	1.417	1.382	0.110	1.00	(CV: <b>0.01</b> )	<b>1.03</b>			
42	X C	295.55	295.46	0.09	297	912	13.6	12445	0.797	0.751	0.048	1.00	32.29 Xp21.2	1.06	1.0	.	
<b>Chromosome X control probe</b>					Mean	912	13.6	12445	0.797	0.751	0.048	1.00	(CV: )	<b>1.06</b>			
28	X B	199.92	199.64	0.28	202	696	10.0*	6938	0.434	0.457	0.047	0.99	153.02 Xq28	0.95	-0.5	. .	
18	X A	147.05	146.82	0.23	148	796	9.6	7681	0.414	0.538	0.065	0.84	152.95 Xq28	0.77	-1.9	.  .	
24	X A	183.31	183.16	0.15	184	873	10.5	9205	0.496	0.678	0.060	1.16	152.94 Xq28-#	0.73	-3.1	.   .	
<b>Xq28 (RETT / MECP2)</b>					Mean	788	10.1	7941	0.448	0.558	0.057	1.00	(CV: <b>0.14</b> )	<b>0.81</b>			
<b>Mean values</b>			0.21			1141	14.2	15234	<b>0.990</b>	1.000	0.060	4		0.99	Total of all except		
<b>Standard deviations</b>			0.07			(Coef. of variance: 0.337)			0.292	0.224				0.16	Ctrl and '?' peaks		

Quality assessment	Quality limits	Quality
Mean A-group area / mean Q-frag. area	>1.00 (1.75)	3.09
Mean CpG-area / mean A-group area	>0.55 (0.85)	1.35
Mean height of first probes AB	> 450 ( 800)	1458
Mean height of last probes CD	> 280 ( 500)	837
Ratio of mean heights AB/CD ('slope')	<2.00 (1.55)	1.74 <b>high</b>
Mean group CV of weighted ratio	<0.20 (0.15)	0.12
4 unidentified peak areas / 54 peak areas	< (0.02)	0.01

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

**Male Reference**  
**Abn. peaks: 4p16.3 4p16.3**

**1 quality warning!**

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 144 (14 peaks). CV of ROX heights for peaks above 100 nt is: 0.09

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