

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	
2	64 -	60.59	60.65	-0.06	64	97	9.8	948	0.489	1.190	0.371	0.75	64 nt	0.41	-1.9	.	
3	70 -	66.49	66.46	0.03	70	76	22.1	1678	0.865	0.913	0.264	0.80	70 nt	0.95	-0.2	.	
4	76 -	72.41	72.37	0.04	76	170	22.2	3770	1.944	1.138	0.170	1.55	76 nt	1.71	4.7*		
5	82 -	78.75	78.56	0.19	82	122	11.2	1361	0.702	0.787	0.204	0.90	82 nt	0.89	-0.4	.	
Ctrl: Q-fragments					Mean	116	16.3	1939	1.000	1.007	0.252	1.00	(CV: 0.51)	1.13			
7	6 a	85.04	84.95	0.09	88	1153	12.4*	14269	0.792	0.981	0.152	1.02	6p21.3 CpG isl.	0.81	-1.2	.	
9	2 a	90.30	90.17	0.13	92	1801	10.8	19410	1.077	0.967	0.135	1.13	2q14 synt.	1.11	0.8	.	
10	1 a	96.68	96.50	0.18	96	2814	11.8*	33148	1.840	1.641	0.304	0.85	MV 36 1p36 CpG isl.	1.12	0.7	.	
Ctrl: D-fragments					Mean	1923	11.6	22276	1.237	1.197	0.197	1.00	(CV: 0.18)	1.01			
14	Y a	114.58	114.50	0.08	118	1474	10.6	15632	0.868	0.811	0.088	1.03	13.54 Yq11	1.07	0.7	.	
12	Y a	104.42	104.34	0.08	108	992	10.8	10760	0.597	0.566	0.065	0.97	14.10 Yq11	1.06	0.5	.	
ctrl: Y-fragments (male ref.)					Mean	1233	10.7	13196	0.733	0.688	0.076	1.00	(CV: 0.01)	1.06			
15	1 A	126.14	126.04	0.10	130	1877	11.6	21699	1.205	1.200	0.054	1.30	1.14 1p36.33	1.00	0.1	.	
23	1 A	176.51	176.49	0.02	178	1394	11.9	16651	0.924	0.942	0.074	0.75	1.75 1p36.33	0.98	-0.2	.	
21	1 A	164.59	164.53	0.06	166	1838	11.8	21694	1.204	1.181	0.073	0.95	1.95 1p36.33	1.02	0.3	.	
1p36 (1p-deletion)					Mean	1703	11.8	20015	1.111	1.108	0.067	1.00	(CV: 0.02)	1.00			
37	2 B	264.97	264.89	0.08	267	1316	13.7	18019	0.964	0.948	0.040	1.36	58.30 2p16.1	1.02	0.4	.	
64	2 D	481.45	481.31	0.14	486	1004	19.6	19680	1.165	1.121	0.101	0.64	61.00 2p16.1	1.04	0.4	.	
"2p16.1 deletion syndrome"					Mean	1160	16.6	18850	1.064	1.034	0.071	1.00	(CV: 0.01)	1.02			
56	3 D	416.48	416.46	0.02	418	1220	17.7	21644	1.281	1.268	0.073	0.96	198.51 3q29	1.01	0.2	.	
49	3 C	354.66	354.58	0.08	359	1264	15.7	19784	1.050	1.039	0.056	1.04	198.28 3q29	1.01	0.2	.	
"3q29 deletion syndrome"					Mean	1242	16.7	20714	1.165	1.154	0.064	1.00	(CV: 0.00)	1.01			
32	4 B	230.55	230.47	0.08	232	1317	12.4	16391	0.877	0.944	0.063	0.88	1.81 4p16.3	0.93	-1.1	.	
59	4 D	443.17	443.03	0.14	445	816	18.8	15307	0.906	0.879	0.046	1.12	1.90 4p16.3	1.03	0.6	.	
4p16.3 Wolf-Hirschhorn region					Mean	1067	15.6	15849	0.891	0.912	0.054	1.00	(CV: 0.07)	0.99			
58	5 D	435.69	435.58	0.11	436	607	18.5	11215	0.664	0.659	0.053	0.88	1.34 5p15.33	1.01	0.1	.	
39	5 C	281.45	281.39	0.06	283	1390	14.4	20069	1.065	1.115	0.071	1.12	1.40 5p15.33	0.96	-0.7	.	
Cri du Chat syndrome					Mean	999	16.5	15642	0.864	0.887	0.062	1.00	(CV: 0.04)	0.98			
19	5 A	151.46	151.42	0.04	154	1740	10.9	18934	1.051	1.127	0.052	1.03	176.62 5q35.3	0.93	-1.5	.	
60	5 D	453.08	453.02	0.06	454	1008	19.1	19230	1.138	1.123	0.055	0.97	176.65 5q35.3	1.01	0.3	.	
Sotos syndrome					Mean	1374	15.0	19082	1.095	1.125	0.054	1.00	(CV: 0.06)	0.97			
43	7 C	310.43	310.40	0.03	310	1383	15.2	21013	1.115	1.116	0.056	0.99	73.08 7q11.23	1.00	0.0	.	
50	7 C	363.47	363.46	0.01	364	1104	16.7	18420	0.977	1.029	0.040	1.27	73.11 7q11.23	0.95	-1.3	.	
53	7 D	389.95	389.95	0.00	391	737	17.1	12605	0.746	0.748	0.050	0.74	73.15 7q11.23	1.00	0.0	.	
Williams syndrome					Mean	1075	16.3	17346	0.946	0.964	0.049	1.00	(CV: 0.03)	0.98			
54	8 D	399.62	399.69	-0.07	401	794	17.5	13885	0.822	0.776	0.036	1.06	116.75 8q24.12	1.06	1.3	.	
57	8 D	424.42	424.33	0.09	427	879	18.8	16564	0.980	0.895	0.047	0.94	117.73 8q24.11	1.10	1.8	.	
Langer-Giedion syndrome					Mean	837	18.2	15225	0.901	0.835	0.042	1.00	(CV: 0.02)	1.08			
44	9 C	319.40	319.40	0.00	319	1633	15.1	24615	1.306	1.292	0.072	1.05	100.95 9q22.33	1.01	0.2	.	
55	9 D	408.02	408.03	-0.01	409	1145	17.7	20286	1.201	1.119	0.069	0.95	100.95 9q22.33	1.07	1.2	.	
"9q22.3 deletion syndrome"					Mean	1389	16.4	22451	1.253	1.206	0.070	1.00	(CV: 0.04)	1.04			
16	10 A	132.67	132.56	0.11	136	1511	11.4	17249	0.958	0.948	0.043	1.16	8.14 10p	1.01	0.2	.	
48	10 C	349.33	349.23	0.10	349	1132	15.5	17590	0.933	0.979	0.060	0.84	10.59 10p15.1	0.95	-0.8	.	
DiGeorge region 2 (10p)					Mean	1322	13.5	17420	0.945	0.963	0.052	1.00	(CV: 0.04)	0.99			
30	11 B	218.74	218.68	0.06	220	1907	12.4	23653	1.265	1.246	0.061	1.00	31.78 11p13	1.02	0.3	.	
WAGR syndrome					Mean	1907	12.4	23653	1.265	1.246	0.061	1.00	(CV:)	1.02			
29	15 B	213.58	213.54	0.04	214	1764	12.4	21917	1.172	1.226	0.047	1.34	21.48 15q11.2	0.96	-1.1	.	
34	15 B	245.13	245.06	0.07	247	1202	13.5	16170	0.865	0.962	0.058	0.86	22.65 15q12	0.90	-1.7	.	
40	15 C	289.80	289.75	0.05	292	1339	14.3	19209	1.019	1.018	0.061	0.86	22.76 15q12	1.00	0.0	.	
20	15 A	158.07	158.00	0.07	160	1503	11.7	17595	0.977	0.930	0.051	0.94	23.17 15q12	1.05	0.9	.	
Prader-Willi / Angelman					Mean	1452	13.0	18723	1.008	1.034	0.054	1.00	(CV: 0.06)	0.98			
25	15 A	189.74	189.75	-0.01	190	2087	11.8	24546	1.363	1.299	0.130	0.78	72.50 15q24.1	1.05	0.5	.	
45	15 C	326.42	326.43	-0.01	325	1011	15.1	15306	0.812	0.771	0.049	1.22	72.80 15q24.1	1.05	0.8	.	
"15q24 deletion syndrome"					Mean	1549	13.5	19926	1.087	1.035	0.090	1.00	(CV: 0.00)	1.05			
22	16 A	170.97	170.91	0.06	172	1446	11.6	16730	0.929	1.018	0.063	1.00	3.87 16p13.3	0.91	-1.4	.	
Rubinstein-Taybi syndrome					Mean	1446	11.6	16730	0.929	1.018	0.063	1.00	(CV:)	0.91			
17	17 A	139.00	138.97	0.03	142	1814	11.9	21505	1.194	1.248	0.053	1.27	2.51 17p13.3	0.96	-1.0	.	
33	17 B	236.20	236.22	-0.02	238	1117	12.9	14418	0.771	0.900	0.067	0.73	2.52 17p13.3	0.86	-1.9	.	
Miller-Dieker region					Mean	1466	12.4	17962	0.982	1.074	0.060	1.00	(CV: 0.07)	0.92			
61	17 D	463.30	463.07	0.23	465	1192	18.4	21936	1.298	1.331	0.092	0.83	17.53 17p11.2-##	0.98	-0.4	.	
38	17 B	271.95	271.90	0.05	274	1197	13.7	16347	0.874	0.940	0.043	1.25	17.83 17p11.2	0.93	-1.5	.	
42	17 C	302.96	302.90	0.06	303	1069	14.6	15564	0.826	0.839	0.053	0.91	18.08 17p11.2	0.98	-0.2	.	
Smith-Magenis syndrome					Mean	1153	15.5	17949	0.999	1.037	0.063	1.00	(CV: 0.03)	0.96			
36	17 B	258.37	258.33	0.04	260	843	14.2	11930	0.638	0.621	0.038	0.88	26.56 17q11.2	1.03	0.4	.	
46	17 C	334.47	334.45	0.02	335	1507	15.7	23693	1.257	1.118	0.053	1.12	26.58 17q11.2	1.12	2.6	.	
NF1 microdeletion syndrome					Mean	1175	14.9	17812	0.948	0.870	0.046	1.00	(CV: 0.06)	1.08			
63	17 D	470.73	470.58	0.15	472	639	17.4	11107	0.657	0.719	0.047	0.70	41.26 17q21.31	0.91	-1.3	.	
31	17 B	224.83	224.79	0.04	226	1892	12.8	24215	1.295	1.325	0.050	1.21	41.44 17q21.31	0.98	-0.6	.	
47	17 C	341.77	341.78	-0.01	342	1119	16.1	18063	0.958	0.932	0.039	1.09	41.45 17q21.31	1.03	0.7	.	
"17q21.31 microdeletion"					Mean	1217	15.4	17795	0.970	0.992	0.046	1.00	(CV: 0.05)	0.98			

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	
26	22 A	195.32	195.29	0.03	196	1808	11.9	21495	1.193	0.890	0.065	0.83	17.89 22q11.21	1.34	4.6*	.		
28	22 B	208.05	207.99	0.06	208	2410	12.4	29931	1.601	1.109	0.061	1.11	18.09 22q11.21	1.44	8.1*	.		
51	22 D	371.45	371.47	-0.02	373	857	17.7	15157	0.897	0.920	0.053	1.06	19.57 22q11.21	0.98	-0.4	.		
22q11.21 (DiGeorge)					Mean	1692	14.0	22194	1.230	0.973	0.060	1.00	(CV: 0.20)	1.25				
35	22 B	251.99	251.96	0.03	253	2043	13.8	28101	1.503	1.321	0.100	1.05	49.49 22q13.33-##	1.14	1.8	.		
52	22 D	382.17	382.09	0.08	382	1430	17.2	24559	1.453	1.442	0.120	0.95	49.50 22q13.33-#	1.01	0.1	.		
22q13 (Phelan-McDermid)					Mean	1737	15.5	26330	1.478	1.382	0.110	1.00	(CV: 0.09)	1.08				
41	X C	295.51	295.46	0.05	297	1185	13.9	16457	0.873	0.751	0.048	1.00	32.29 Xp21.2	1.16	2.5	.		
Chromosome X control probe					Mean	1185	13.9	16457	0.873	0.751	0.048	1.00	(CV:)	1.16				
27	X B	199.68	199.64	0.04	202	673	10.3*	6899	0.369	0.457	0.047	0.99	153.02 Xq28	0.81	-1.9	. .		
18	X A	146.91	146.82	0.09	148	947	10.0	9431	0.524	0.538	0.065	0.84	152.95 Xq28	0.97	-0.2	.		
24	X A	183.18	183.16	0.02	184	1006	12.0	12109	0.672	0.678	0.060	1.16	152.94 Xq28-#	0.99	-0.1	.		
Xq28 (RETT / MECP2)					Mean	875	10.7	9480	0.522	0.558	0.057	1.00	(CV: 0.11)	0.92				
Mean values			0.05			1308	14.5	18379	1.016	1.000	0.060	4		1.01	Total of all except			
Standard deviations			0.05			(Coef. of variance: 0.256)			0.256	0.224				0.10	Ctrl and '?' peaks			

Quality assessment	Quality limits	Quality
Mean A-group area / mean Q-frag. area	>1.00 (1.75)	9.29
Mean CpG-area / mean A-group area	>0.55 (0.85)	1.32
Mean height of first probes AB	> 450 (800)	1527
Mean height of last probes CD	> 280 (500)	1099
Ratio of mean heights AB/CD ('slope')	<2.00 (1.55)	1.39
Mean group CV of weighted ratio	<0.20 (0.15)	0.06
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: 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 140 (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)