

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	Ratio	Dist. in SD	1.0 low high	
3	64 -	60.66	60.65	0.01	64	232	19.5	4523	1.360	1.190	0.371	0.75	64 nt	1.14	0.5	↓	
4	70 -	66.21	66.46	-0.25	70	179	18.7	3341	1.004	0.913	0.264	0.80	70 nt	1.10	0.3	↓	
5	76 -	72.39	72.37	0.02	76	148	25.1	3712	1.116	1.138	0.170	1.55	76 nt	0.98	-0.1	↓	
6	82 -	78.55	78.56	-0.01	82	111	15.6	1730	0.520	0.787	0.204	0.90	82 nt	0.66	-1.3	III	
Ctrl: Q-fragments					Mean	168	19.7	3327	1.000	1.007	0.252	1.00	(CV: 0.21)	0.96			
7	6 a	84.87	84.95	-0.08	88	1246	11.9*	14857	0.936	0.981	0.152	1.02	6p21.3 CpG isl.	0.95	-0.3	↓	
9	2 a	90.09	90.17	-0.08	92	1348	10.3	13837	0.871	0.967	0.135	1.13	2q14 synt.	0.90	-0.7	↓	
10	1 a	96.50	96.50	0.00	96	2398	11.6*	27871	1.755	1.641	0.304	0.85	MV 36 1p36 CpG isl.	1.07	0.4	↓	
Ctrl: D-fragments					Mean	1664	11.3	18855	1.187	1.197	0.197	1.00	(CV: 0.09)	0.97			
14	Y a	114.34	114.50	-0.16	118	1194	10.2	12179	0.767	0.811	0.088	1.03	13.54 Yq11	0.95	-0.5	↓	
12	Y a	104.24	104.34	-0.10	108	897	10.4	9355	0.589	0.566	0.065	0.97	14.10 Yq11	1.04	0.4	↓	
Ctrl: Y-fragments (male ref.)					Mean	1046	10.3	10767	0.678	0.688	0.076	1.00	(CV: 0.07)	0.99			
15	1 A	125.96	126.04	-0.08	130	1786	11.2	19987	1.259	1.200	0.054	1.30	1.14 1p36.33	1.05	1.1	↓	
23	1 A	176.42	176.49	-0.07	178	1244	11.2	13876	0.874	0.942	0.074	0.75	1.75 1p36.33	0.93	-0.9	↓	
21	1 A	164.40	164.53	-0.13	166	1613	11.0	17795	1.121	1.181	0.073	0.95	1.95 1p36.33	0.95	-0.8	↓	
1p36 (1p-deletion)					Mean	1548	11.1	17219	1.084	1.108	0.067	1.00	(CV: 0.07)	0.99			
37	2 B	264.90	264.89	0.01	267	1095	12.8	14021	0.889	0.948	0.040	1.36	58.30 2p16.1	0.94	-1.5	↓	
63	2 D	481.36	481.31	0.05	486	980	18.8	18394	1.135	1.121	0.101	0.64	61.00 2p16.1	1.01	0.1	↓	
"2p16.1 deletion syndrome"					Mean	1038	15.8	16208	1.012	1.034	0.071	1.00	(CV: 0.05)	0.96			
56	3 D	416.40	416.46	-0.06	418	1189	16.9	20146	1.243	1.268	0.073	0.96	198.51 3q29	0.98	-0.4	↓	
49	3 C	354.61	354.58	0.03	359	1132	15.1	17095	1.032	1.039	0.056	1.04	198.28 3q29	0.99	-0.1	↓	
"3q29 deletion syndrome"					Mean	1161	16.0	18621	1.137	1.154	0.064	1.00	(CV: 0.01)	0.99			
32	4 B	230.44	230.47	-0.03	232	1286	12.0	15394	0.976	0.944	0.063	0.88	1.81 4p16.3	1.03	0.5	↓	
59	4 D	443.11	443.03	0.08	445	770	17.9	13802	0.851	0.879	0.046	1.12	1.90 4p16.3	0.97	-0.6	↓	
4p16.3 Wolf-Hirschhorn region					Mean	1028	14.9	14598	0.914	0.912	0.054	1.00	(CV: 0.05)	1.00			
58	5 D	435.57	435.58	-0.01	436	639	17.6	11276	0.696	0.659	0.053	0.88	1.34 5p15.33	1.06	0.7	↓	
39	5 C	281.36	281.39	-0.03	283	1317	13.3	17513	1.057	1.115	0.071	1.12	1.40 5p15.33	0.95	-0.8	↓	
Cri du Chat syndrome					Mean	978	15.5	14395	0.876	0.887	0.062	1.00	(CV: 0.08)	1.00			
19	5 A	151.30	151.42	-0.12	154	1634	10.2	16699	1.052	1.127	0.052	1.03	176.62 5q35.3	0.93	-1.4	↓	
60	5 D	452.94	453.02	-0.08	454	1063	17.7	18822	1.161	1.123	0.055	0.97	176.65 5q35.3	1.03	0.7	↓	
Sotos syndrome					Mean	1349	14.0	17761	1.106	1.125	0.054	1.00	(CV: 0.07)	0.98			
43	7 C	310.20	310.40	-0.20	310	1426	14.2	20227	1.221	1.116	0.056	0.99	73.08 7q11.23	1.09	1.9	↓	
50	7 C	363.48	363.46	0.02	364	1130	15.4	17409	1.051	1.029	0.040	1.27	73.11 7q11.23	1.02	0.5	↓	
53	7 D	389.94	389.95	-0.01	391	828	16.0	13244	0.817	0.748	0.050	0.74	73.15 7q11.23	1.09	1.4	↓	
Williams syndrome					Mean	1128	15.2	16960	1.030	0.964	0.049	1.00	(CV: 0.04)	1.06			
54	8 D	399.62	399.69	-0.07	401	780	16.3	12752	0.787	0.776	0.036	1.06	116.75 8q24.12	1.01	0.3	↓	
57	8 D	424.33	424.33	0.00	427	751	17.1	12837	0.792	0.895	0.047	0.94	117.73 8q24.11	0.88	-2.2	↓	
Langer-Giedion syndrome					Mean	766	16.7	12795	0.789	0.835	0.042	1.00	(CV: 0.10)	0.95			
44	9 C	319.23	319.40	-0.17	319	1582	14.1	22305	1.347	1.292	0.072	1.05	100.95 9q22.33	1.04	0.8	↓	
55	9 D	408.03	408.03	0.00	409	1092	16.6	18137	1.119	1.119	0.069	0.95	100.95 9q22.33	1.00	0.0	↓	
"9q22.3 deletion syndrome"					Mean	1337	15.4	20221	1.233	1.206	0.070	1.00	(CV: 0.03)	1.02			
16	10 A	132.58	132.56	0.02	136	1386	11.1	15397	0.970	0.948	0.043	1.16	8.14 10p	1.02	0.5	↓	
48	10 C	349.22	349.23	-0.01	349	1096	14.6	15960	0.964	0.979	0.060	0.84	10.59 10p15.1	0.98	-0.3	↓	
DiGeorge region 2 (10p)					Mean	1241	12.8	15679	0.967	0.963	0.052	1.00	(CV: 0.03)	1.01			
30	11 B	218.66	218.68	-0.02	220	1608	11.8	18979	1.203	1.246	0.061	1.00	31.78 11p13	0.97	-0.7	↓	
WAGR syndrome					Mean	1608	11.8	18979	1.203	1.246	0.061	1.00	(CV:)	0.97			
29	15 B	213.50	213.54	-0.04	214	1635	11.9	19450	1.233	1.226	0.047	1.34	21.48 15q11.2	1.01	0.2	↓	
34	15 B	245.04	245.06	-0.02	247	1172	13.0	15188	0.963	0.962	0.058	0.86	22.65 15q12	1.00	0.0	↓	
40	15 C	289.68	289.75	-0.07	292	1206	13.5	16335	0.986	1.018	0.061	0.86	22.76 15q12	0.97	-0.5	↓	
20	15 A	157.89	158.00	-0.11	160	1285	11.2	14427	0.908	0.930	0.051	0.94	23.17 15q12	0.98	-0.4	↓	
Prader-Willi / Angelman					Mean	1325	12.4	16350	1.023	1.034	0.054	1.00	(CV: 0.02)	0.99			
25	15 A	189.63	189.75	-0.12	190	2003	11.4	22783	1.435	1.299	0.130	0.78	72.50 15q24.1	1.10	1.0	↓	
45	15 C	326.20	326.43	-0.23	325	905	14.3	12909	0.779	0.771	0.049	1.22	72.80 15q24.1	1.01	0.2	↓	
"15q24 deletion syndrome"					Mean	1454	12.8	17846	1.107	1.035	0.090	1.00	(CV: 0.06)	1.05			
22	16 A	170.79	170.91	-0.12	172	1648	10.9	17991	1.133	1.018	0.063	1.00	3.87 16p13.3	1.11	1.8	↓	
Rubinstein-Taybi syndrome					Mean	1648	10.9	17991	1.133	1.018	0.063	1.00	(CV:)	1.11			
17	17 A	138.92	138.97	-0.05	142	1748	11.3	19751	1.244	1.248	0.053	1.27	2.51 17p13.3	1.00	-0.1	↓	
33	17 B	236.20	236.22	-0.02	238	1139	12.1	13800	0.875	0.900	0.067	0.73	2.52 17p13.3	0.97	-0.4	↓	
Miller-Dieker region					Mean	1444	11.7	16776	1.059	1.074	0.060	1.00	(CV: 0.02)	0.99			
61	17 D	463.14	463.07	0.07	465	1252	18.3	22850	1.409	1.331	0.092	0.83	17.53 17p11.2-##	1.06	0.9	↓	
38	17 B	271.85	271.90	-0.05	274	1224	13.1	16039	1.017	0.940	0.043	1.25	17.83 17p11.2	1.08	1.8	↓	
42	17 C	302.80	302.90	-0.10	303	1070	14.0	15020	0.907	0.839	0.053	0.91	18.08 17p11.2	1.08	1.3	↓	
Smith-Magenis syndrome					Mean	1182	15.1	17970	1.111	1.037	0.063	1.00	(CV: 0.01)	1.08			
36	17 B	258.27	258.33	-0.06	260	722	13.2	9520	0.604	0.621	0.038	0.88	26.56 17q11.2	0.97	-0.5	↓	
46	17 C	334.24	334.45	-0.21	335	1223	14.6	17839	1.077	1.118	0.053	1.12	26.58 17q11.2	0.96	-0.8	↓	
NF1 microdeletion syndrome					Mean	973	13.9	13680	0.840	0.870	0.046	1.00	(CV: 0.01)	0.97			
62	17 D	470.61	470.58	0.03	472	665	18.0	11941	0.737	0.719	0.047	0.70	41.26 17q21.31	1.03	0.4	↓	
31	17 B	224.79	224.79	0.00	226	1784	12.0	21474	1.362	1.325	0.050	1.21	41.44 17q21.31	1.03	0.7	↓	
47	17 C	341.66	341.78	-0.12	342	1085	14.9	16139	0.974	0.932	0.039	1.09	41.45 17q21.31	1.05	1.1	↓	
"17q21.31 microdeletion"					Mean	1178	15.0	16518	1.024	0.992	0.046	1.00	(CV: 0.01)	1.03			

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	
26	22 A	195.15	195.29	-0.14	196	1319	11.0	14554	0.916	0.890	0.065	0.83	17.89 22q11.21	1.03	0.4	.	
28	22 B	207.94	207.99	-0.05	208	1494	11.6	17303	1.097	1.109	0.061	1.11	18.09 22q11.21	0.99	-0.2	.	
51	22 D	371.57	371.47	0.10	373	898	16.6	14922	0.920	0.920	0.053	1.06	19.57 22q11.21	1.00	0.0	.	
22q11.21 (DiGeorge)					Mean	1237	13.1	15593	0.978	0.973	0.060	1.00	(CV: 0.02)	1.00			
35	22 B	252.03	251.96	0.07	253	1769	12.9	22856	1.449	1.321	0.100	1.05	49.49 22q13.33-##	1.10	1.3	↓	
52	22 D	382.08	382.09	-0.01	382	1443	16.5	23747	1.465	1.442	0.120	0.95	49.50 22q13.33-#	1.02	0.2	.	
22q13 (Phelan-McDermid)					Mean	1606	14.7	23302	1.457	1.382	0.110	1.00	(CV: 0.05)	1.06			
41	X C	295.33	295.46	-0.13	297	917	13.1	12007	0.725	0.751	0.048	1.00	32.29 Xp21.2	0.97	-0.5	.	
Chromosome X control probe					Mean	917	13.1	12007	0.725	0.751	0.048	1.00	(CV:)	0.97			
27	X B	199.59	199.64	-0.05	202	693	10.3	7132	0.452	0.457	0.047	0.99	153.02 Xq28	0.99	-0.1	.	
18	X A	146.78	146.82	-0.04	148	905	9.3	8427	0.531	0.538	0.065	0.84	152.95 Xq28	0.99	-0.1	.	
24	X A	183.03	183.16	-0.13	184	963	11.2	10790	0.679	0.678	0.060	1.16	152.94 Xq28-#	1.00	0.0	.	
Xq28 (RETT / MECP2)					Mean	854	10.3	8783	0.554	0.558	0.057	1.00	(CV: 0.01)	0.99			
Mean values			-0.05			1216	13.7	16271	1.010	1.000	0.060	4		1.01	Total of all except		
Standard deviations			0.08			(Coef. of variance: 0.237)			0.240	0.224				0.05	Ctrl and '?' peaks		

Quality assessment	Quality limits	Quality
Mean A-group area / mean Q-frag. area	>1.00 (1.75)	4.77
Mean CpG-area / mean A-group area	>0.55 (0.85)	1.35
Mean height of first probes AB	> 450 (800)	1381
Mean height of last probes CD	> 280 (500)	1058
Ratio of mean heights AB/CD ('slope')	<2.00 (1.55)	1.31
Mean group CV of weighted ratio	<0.20 (0.15)	0.04
3 unidentified peak areas / 54 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.

Male Reference

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 352 (14 peaks). CV of ROX heights for peaks above 100 nt is: 0.06

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