

----- Peak Data -----													----- Normalized Peak Area -----					
No.	Label	Size	Ref. size	Size diff.	MRC	Height	Width	Area	Area	Ref. Mean	Ref. SD	Ref. Weigh	Position	Dist.	1.0			
													p-tel	band	Ratio	in SD	low	high
4	64 -	60.59	60.65	-0.06	64	72	5.2	375	0.171	1.190	0.371	0.75	64 nt	0.14	-2.7	.		
5	70 -	66.40	66.46	-0.06	70	133	20.6	2738	1.251	0.913	0.264	0.80	70 nt	1.37	1.3			
6	76 -	72.49	72.37	0.12	76	147	22.3	3271	1.495	1.138	0.170	1.55	76 nt	1.31	2.1			
7	82 -	78.68	78.56	0.12	82	128	18.5	2369	1.083	0.787	0.204	0.90	82 nt	1.38	1.5			
Ctrl: Q-fragments					Mean	120	16.6	2188	1.000	1.007	0.252	1.00	(CV: 0.48)	1.12				
8	6 a	85.16	84.95	0.21	88	1329	11.4*	15179	0.994	0.981	0.152	1.02	6p21.3 CpG isl.	1.01	0.1	.		
10	2 a	90.37	90.17	0.20	92	1307	10.4*	13631	0.893	0.967	0.135	1.13	2q14 synt.	0.92	-0.6	.		
11	1 a	96.78	96.50	0.28	96	2536	11.4*	28832	1.888	1.641	0.304	0.85	MV 36 1p36 CpG isl.	1.15	0.8			
Ctrl: D-fragments					Mean	1724	11.1	19214	1.258	1.197	0.197	1.00	(CV: 0.11)	1.02				
16	Y a	114.68	114.50	0.18	118	1255	10.4	13038	0.854	0.811	0.088	1.03	13.54 Yq11	1.05	0.5	.		
13	Y a	104.40	104.34	0.06	108	813	10.2	8300	0.544	0.566	0.065	0.97	14.10 Yq11	0.96	-0.3	.		
ctrl: Y-fragments (male ref.)					Mean	1034	10.3	10669	0.699	0.688	0.076	1.00	(CV: 0.07)	1.01				
17	1 A	126.31	126.04	0.27	130	1808	10.9	19651	1.287	1.200	0.054	1.30	1.14 1p36.33	1.07	1.6	.		
25	1 A	176.58	176.49	0.09	178	1444	11.5	16596	1.087	0.942	0.074	0.75	1.75 1p36.33	1.15	2.0			
23	1 A	164.53	164.53	0.00	166	1629	11.0	17855	1.169	1.181	0.073	0.95	1.95 1p36.33	0.99	-0.2	.		
1p36 (1p-deletion)					Mean	1627	11.1	18034	1.181	1.108	0.067	1.00	(CV: 0.07)	1.07				
39	2 B	264.91	264.89	0.02	267	1274	13.2	16807	1.045	0.948	0.040	1.36	58.30 2p16.1	1.10	2.4	.		
65	2 D	481.73	481.31	0.42	486	936	19.7	18449	1.076	1.121	0.101	0.64	61.00 2p16.1	0.96	-0.4	.		
"2p16.1 deletion syndrome"					Mean	1105	16.5	17628	1.061	1.034	0.071	1.00	(CV: 0.09)	1.06				
58	3 D	416.73	416.46	0.27	418	1350	17.3	23413	1.366	1.268	0.073	0.96	198.51 3q29	1.08	1.3	.		
51	3 C	354.59	354.58	0.01	359	1298	15.0	19479	1.057	1.039	0.056	1.04	198.28 3q29	1.02	0.3	.		
"3q29 deletion syndrome"					Mean	1324	16.2	21446	1.211	1.154	0.064	1.00	(CV: 0.04)	1.05				
34	4 B	230.69	230.47	0.22	232	1206	11.8	14224	0.885	0.944	0.063	0.88	1.81 4p16.3	0.94	-1.0	.		
61	4 D	443.36	443.03	0.33	445	811	18.0	14584	0.851	0.879	0.046	1.12	1.90 4p16.3	0.97	-0.6	.		
4p16.3 Wolf-Hirschhorn region					Mean	1009	14.9	14404	0.868	0.912	0.054	1.00	(CV: 0.02)	0.95				
60	5 D	435.86	435.58	0.28	436	596	17.6	10471	0.611	0.659	0.053	0.88	1.34 5p15.33	0.93	-0.9	.		
41	5 C	281.40	281.39	0.01	283	1419	13.6	19297	1.047	1.115	0.071	1.12	1.40 5p15.33	0.94	-1.0	.		
Cri du Chat syndrome					Mean	1008	15.6	14884	0.829	0.887	0.062	1.00	(CV: 0.01)	0.93				
21	5 A	151.48	151.42	0.06	154	1774	10.5	18601	1.218	1.127	0.052	1.03	176.62 5q35.3	1.08	1.7	.		
62	5 D	453.34	453.02	0.32	454	1034	18.7	19333	1.128	1.123	0.055	0.97	176.65 5q35.3	1.00	0.1	.		
Sotos syndrome					Mean	1404	14.6	18967	1.173	1.125	0.054	1.00	(CV: 0.05)	1.04				
45	7 C	310.29	310.40	-0.11	310	1306	14.5	18912	1.026	1.116	0.056	0.99	73.08 7q11.23	0.92	-1.6	.		
52	7 C	363.52	363.46	0.06	364	1184	15.9	18869	1.023	1.029	0.040	1.27	73.11 7q11.23	0.99	-0.2	.		
55	7 D	390.24	389.95	0.29	391	789	16.5	12993	0.758	0.748	0.050	0.74	73.15 7q11.23	1.01	0.2	.		
Williams syndrome					Mean	1093	15.6	16925	0.936	0.964	0.049	1.00	(CV: 0.05)	0.97				
56	8 D	400.10	399.69	0.41	401	751	17.0	12773	0.745	0.776	0.036	1.06	116.75 8q24.12	0.96	-0.8	.		
59	8 D	424.93	424.33	0.60*	427	910	17.9	16322	0.952	0.895	0.047	0.94	117.73 8q24.11	1.06	1.2	.		
Langer-Giedion syndrome					Mean	831	17.5	14548	0.849	0.835	0.042	1.00	(CV: 0.07)	1.01				
46	9 C	319.13	319.40	-0.27	319	1823	14.3	26096	1.415	1.292	0.072	1.05	100.95 9q22.33	1.10	1.7	.		
57	9 D	408.39	408.03	0.36	409	1212	17.1	20688	1.207	1.119	0.069	0.95	100.95 9q22.33	1.08	1.3	.		
"9q22.3 deletion syndrome"					Mean	1518	15.7	23392	1.311	1.206	0.070	1.00	(CV: 0.01)	1.09				
18	10 A	132.93	132.56	0.37	136	1363	10.8	14692	0.962	0.948	0.043	1.16	8.14 10p	1.01	0.3	.		
50	10 C	349.21	349.23	-0.02	349	1226	14.9	18207	0.988	0.979	0.060	0.84	10.59 10p15.1	1.01	0.1	.		
DiGeorge region 2 (10p)					Mean	1295	12.8	16450	0.975	0.963	0.052	1.00	(CV: 0.00)	1.01				
32	11 B	218.82	218.68	0.14	220	1872	11.9	22354	1.390	1.246	0.061	1.00	31.78 11p13	1.12	2.3	.		
WAGR syndrome					Mean	1872	11.9	22354	1.390	1.246	0.061	1.00	(CV:)	1.12				
31	15 B	213.61	213.54	0.07	214	1816	11.9	21661	1.347	1.226	0.047	1.34	21.48 15q11.2	1.10	2.6	.		
36	15 B	245.24	245.06	0.18	247	1378	12.9	17775	1.105	0.962	0.058	0.86	22.65 15q12	1.15	2.5	.		
42	15 C	289.79	289.75	0.04	292	1282	13.5	17315	0.939	1.018	0.061	0.86	22.76 15q12	0.92	-1.3	.		
22	15 A	158.04	158.00	0.04	160	1590	11.0	17487	1.145	0.930	0.051	0.94	23.17 15q12	1.23	4.2*			
Prader-Willi / Angelman					Mean	1517	12.3	18560	1.134	1.034	0.054	1.00	(CV: 0.11)	1.10				
27	15 A	189.77	189.75	0.02	190	1968	11.3	22165	1.451	1.299	0.130	0.78	72.50 15q24.1	1.12	1.2	.		
47	15 C	326.17	326.43	-0.26	325	970	14.5	14046	0.762	0.771	0.049	1.22	72.80 15q24.1	0.99	-0.2	.		
"15q24 deletion syndrome"					Mean	1469	12.9	18106	1.107	1.035	0.090	1.00	(CV: 0.09)	1.04				
24	16 A	170.90	170.91	-0.01	172	1422	11.0	15601	1.022	1.018	0.063	1.00	3.87 16p13.3	1.00	0.1	.		
Rubinstein-Taybi syndrome					Mean	1422	11.0	15601	1.022	1.018	0.063	1.00	(CV:)	1.00				
19	17 A	139.18	138.97	0.21	142	913	11.7*	10641	0.697	1.248	0.053	1.27	2.51 17p13.3	0.56	-10.5*	.		
35	17 B	236.24	236.22	0.02	238	623	11.8	7329	0.456	0.900	0.067	0.73	2.52 17p13.3	0.51	-6.7*	.		
Miller-Dieker region					Mean	768	11.7	8985	0.576	1.074	0.060	1.00	(CV: 0.07)	0.54				
63	17 D	463.46	463.07	0.39	465	1247	18.9	23577	1.375	1.331	0.092	0.83	17.53 17p11.2-##	1.03	0.5	.		
40	17 B	271.90	271.90	0.00	274	1112	13.2	14701	0.914	0.940	0.043	1.25	17.83 17p11.2	0.97	-0.6	.		
44	17 C	302.83	302.90	-0.07	303	1030	14.0	14443	0.783	0.839	0.053	0.91	18.08 17p11.2	0.93	-1.0	.		
Smith-Magenis syndrome					Mean	1130	15.4	17574	1.024	1.037	0.063	1.00	(CV: 0.05)	0.98				
38	17 B	258.40	258.33	0.07	260	824	13.2	10850	0.675	0.621	0.038	0.88	26.56 17q11.2	1.09	1.4	.		
48	17 C	334.38	334.45	-0.07	335	1402	14.9	20918	1.135	1.118	0.053	1.12	26.58 17q11.2	1.01	0.3	.		
NF1 microdeletion syndrome					Mean	1113	14.0	15884	0.905	0.870	0.046	1.00	(CV: 0.05)	1.05				
64	17 D	470.92	470.58	0.34	472	646	18.8	12137	0.708	0.719	0.047	0.70	41.26 17q21.31	0.99	-0.2	.		
33	17 B	224.99	224.79	0.20	226	1846	12.3	22645	1.408	1.325	0.050	1.21	41.44 17q21.31	1.06	1.7	.		
49	17 C	341.67	341.78	-0.11	342	1196	15.5	18501	1.003	0.932	0.039	1.09	41.45 17q21.31	1.08	1.8	.		
"17q21.31 microdeletion"					Mean	1229	15.5	17761	1.									

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
28	22 A	195.26	195.29	-0.03	196	1265	11.0	13863	0.908	0.890	0.065	0.83	17.89 22q11.21	1.02	0.3	.	.
30	22 B	208.18	207.99	0.19	208	1508	11.7	17683	1.100	1.109	0.061	1.11	18.09 22q11.21	0.99	-0.2	.	.
53	22 D	371.65	371.47	0.18	373	935	17.0	15937	0.930	0.920	0.053	1.06	19.57 22q11.21	1.01	0.2	.	.
22q11.21 (DiGeorge)					Mean	1236	13.2	15828	0.979	0.973	0.060	1.00	(CV: 0.01)	1.01			
37	22 B	252.20	251.96	0.24	253	1552	12.9	20026	1.245	1.321	0.100	1.05	49.49 22q13.33-##	0.94	-0.8	.	.
54	22 D	382.34	382.09	0.25	382	1354	16.7	22636	1.321	1.442	0.120	0.95	49.50 22q13.33-#	0.92	-1.0	.	.
22q13 (Phelan-McDermid)					Mean	1453	14.8	21331	1.283	1.382	0.110	1.00	(CV: 0.02)	0.93			
43	X C	295.39	295.46	-0.07	297	1165	13.4	15625	0.847	0.751	0.048	1.00	32.29 Xp21.2	1.13	2.0	.	.
Chromosome X control probe					Mean	1165	13.4	15625	0.847	0.751	0.048	1.00	(CV:)	1.13			
29	X B	199.75	199.64	0.11	202	713	10.3	7325	0.455	0.457	0.047	0.99	153.02 Xq28	1.00	0.0	.	.
20	X A	147.04	146.82	0.22	148	790	9.3	7317	0.479	0.538	0.065	0.84	152.95 Xq28	0.89	-0.9	.	.
26	X A	183.18	183.16	0.02	184	828	11.1	9167	0.600	0.678	0.060	1.16	152.94 Xq28-#	0.88	-1.3	.	.
Xq28 (RETT / MECP2)					Mean	777	10.2	7936	0.512	0.558	0.057	1.00	(CV: 0.07)	0.92			
Mean values			0.13			1232	13.9	16776	1.002	1.000	0.060	4		1.00	Total of all except		
Standard deviations			0.18			(Coef. of variance: 0.267)			0.263	0.224				0.12	Ctrl and '?' peaks		

Quality assessment	Quality limits	Quality
Mean A-group area / mean Q-frag. area	>1.00 (1.75)	6.98
Mean CpG-area / mean A-group area	>0.55 (0.85)	1.44
Mean height of first probes AB	> 450 (800)	1355
Mean height of last probes CD	> 280 (500)	1115
Ratio of mean heights AB/CD ('slope')	<2.00 (1.55)	1.22
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: 17p13.3 17p13.3

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 120 (14 peaks). CV of ROX heights for peaks above 100 nt is: 0.10

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