

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	Dist. Ratio	1.0 in SD	low high
15	64 -	60.54	60.65	-0.11	64	329	9.7	3198	1.284	1.190	0.371	0.75	64 nt	1.08	0.3	↓
16	70 -	66.63	66.46	0.17	70	175	12.3	2156	0.865	0.913	0.264	0.80	70 nt	0.95	-0.2	↓
17	76 -	73.11	72.37	0.74 *	76	220	11.8	2602	1.044	1.138	0.170	1.55	76 nt	0.92	-0.5	↓
19	82 -	79.34	78.56	0.78 *	82	168	12.0	2009	0.806	0.787	0.204	0.90	82 nt	1.02	0.1	↓
Ctrl: Q-fragments					Mean	223	11.5	2491	1.000	1.007	0.252	1.00	(CV: 0.07)	0.98		
21	6 a	85.72	84.95	0.77 *	88	1938	5.3 *	10202	1.161	0.981	0.152	1.02	6p21.3 CpG isl.	1.18	1.2	↓
23	2 a	91.01	90.17	0.84 *	92	1677	5.4 *	9065	1.032	0.967	0.135	1.13	2q14 synt.	1.07	0.5	↓
24	1 a	97.12	96.50	0.62 *	96	3912	5.7 *	22258	2.533	1.641	0.304	0.85	MV 36 1p36 CpG isl.	1.54	2.9	↓
Ctrl: D-fragments					Mean	2509	5.5	13842	1.575	1.197	0.197	1.00	(CV: 0.19)	1.24		
28	Y a	115.19	114.50	0.69 *	118	1268	5.9 *	7434	0.846	0.811	0.088	1.03	13.54 Yq11	1.04	0.4	↓
26	Y a	105.33	104.34	0.99 *	108	789	5.7 *	4503	0.512	0.566	0.065	0.97	14.10 Yq11	0.91	-0.8	↓
Ctrl: Y-fragments (male ref.)					Mean	1029	5.8	5969	0.679	0.688	0.076	1.00	(CV: 0.10)	0.98		
29	1 A	126.70	126.04	0.66 *	130	2040	5.2	10664	1.214	1.200	0.054	1.30	1.14 1p36.33	1.01	0.3	↓
37	1 A	177.40	176.49	0.91 *	178	1721	5.4	9319	1.061	0.942	0.074	0.75	1.75 1p36.33	1.13	1.6	↓
35	1 A	165.16	164.53	0.63 *	166	2053	5.4	11013	1.253	1.181	0.073	0.95	1.95 1p36.33	1.06	1.0	↓
1p36 (1p-deletion)					Mean	1938	5.3	10332	1.176	1.108	0.067	1.00	(CV: 0.05)	1.06		
51	2 B	266.06	264.89	1.17 *	267	1166	6.6	7640	0.842	0.948	0.040	1.36	58.30 2p16.1	0.89	-2.6	↓
77	2 D	481.89	481.31	0.58 *	486	1001	10.0	10034	1.100	1.121	0.101	0.64	61.00 2p16.1	0.98	-0.2	↓
"2p16.1 deletion syndrome"					Mean	1084	8.3	8837	0.971	1.034	0.071	1.00	(CV: 0.07)	0.92		
70	3 D	417.03	416.46	0.57 *	418	1200	9.0	10786	1.183	1.268	0.073	0.96	198.51 3q29	0.93	-1.2	↓
63	3 C	355.14	354.58	0.56 *	359	1210	7.8	9434	1.035	1.039	0.056	1.04	198.28 3q29	1.00	-0.1	↓
"3q29 deletion syndrome"					Mean	1205	8.4	10110	1.109	1.154	0.064	1.00	(CV: 0.05)	0.97		
46	4 B	231.80	230.47	1.33 *	232	1142	5.9	6684	0.737	0.944	0.063	0.88	1.81 4p16.3	0.78	-3.3	↓
73	4 D	443.99	443.03	0.96 *	445	886	9.2	8195	0.899	0.879	0.046	1.12	1.90 4p16.3	1.02	0.4	↓
4p16.3 Wolf-Hirschhorn region					Mean	1014	7.6	7440	0.818	0.912	0.054	1.00	(CV: 0.19)	0.92		
72	5 D	436.64	435.58	1.06 *	436	657	9.1	5978	0.656	0.659	0.053	0.88	1.34 5p15.33	1.00	-0.1	↓
53	5 C	282.01	281.39	0.62 *	283	1452	6.7	9685	1.063	1.115	0.071	1.12	1.40 5p15.33	0.95	-0.7	↓
Cri du Chat syndrome					Mean	1055	7.9	7832	0.859	0.887	0.062	1.00	(CV: 0.03)	0.97		
33	5 A	152.47	151.42	1.05 *	154	1918	5.4	10334	1.176	1.127	0.052	1.03	176.62 5q35.3	1.04	0.9	↓
74	5 D	453.30	453.02	0.28	454	999	9.5	9483	1.040	1.123	0.055	0.97	176.65 5q35.3	0.93	-1.5	↓
Sotos syndrome					Mean	1459	7.4	9909	1.108	1.125	0.054	1.00	(CV: 0.08)	0.99		
57	7 C	310.44	310.40	0.04	310	1602	7.3	11710	1.285	1.116	0.056	0.99	73.08 7q11.23	1.15	3.0	↓
64	7 C	363.48	363.46	0.02	364	1262	8.0	10083	1.107	1.029	0.040	1.27	73.11 7q11.23	1.07	1.9	↓
67	7 D	389.91	389.95	-0.04	391	735	8.6	6336	0.695	0.748	0.050	0.74	73.15 7q11.23	0.93	-1.1	↓
Williams syndrome					Mean	1200	8.0	9376	1.029	0.964	0.049	1.00	(CV: 0.10)	1.06		
68	8 D	400.34	399.69	0.65 *	401	760	8.6	6504	0.713	0.776	0.036	1.06	116.75 8q24.12	0.92	-1.7	↓
71	8 D	425.77	424.33	1.44 *	427	898	9.1	8192	0.898	0.895	0.047	0.94	117.73 8q24.11	1.00	0.1	↓
Langer-Giedion syndrome					Mean	829	8.8	7348	0.806	0.835	0.042	1.00	(CV: 0.06)	0.96		
58	9 C	319.49	319.40	0.09	319	1483	7.3	10855	1.191	1.292	0.072	1.05	100.95 9q22.33	0.92	-1.4	↓
69	9 D	408.32	408.03	0.29	409	1142	8.7	9914	1.087	1.119	0.069	0.95	100.95 9q22.33	0.97	-0.5	↓
"9q22.3 deletion syndrome"					Mean	1313	8.0	10385	1.139	1.206	0.070	1.00	(CV: 0.04)	0.95		
30	10 A	133.28	132.56	0.72 *	136	1572	5.4 *	8545	0.972	0.948	0.043	1.16	8.14 10p	1.03	0.6	↓
62	10 C	349.68	349.23	0.45	349	1276	7.7	9863	1.082	0.979	0.060	0.84	10.59 10p15.1	1.11	1.7	↓
DiGeorge region 2 (10p)					Mean	1424	6.6	9204	1.027	0.963	0.052	1.00	(CV: 0.05)	1.06		
44	11 B	219.49	218.68	0.81 *	220	2013	5.9	11961	1.319	1.246	0.061	1.00	31.78 11p13	1.06	1.2	↓
WAGR syndrome					Mean	2013	5.9	11961	1.319	1.246	0.061	1.00	(CV:)	1.06		
43	15 B	214.46	213.54	0.92 *	214	2299	5.9	13486	1.487	1.226	0.047	1.34	21.48 15q11.2	1.21	5.5 *	↓
48	15 B	246.36	245.06	1.30 *	247	1447	6.5	9367	1.033	0.962	0.058	0.86	22.65 15q12	1.07	1.2	↓
54	15 C	290.15	289.75	0.40	292	1275	6.9	8823	0.968	1.018	0.061	0.86	22.76 15q12	0.95	-0.8	↓
34	15 A	158.88	158.00	0.88 *	160	1610	5.3	8595	0.978	0.930	0.051	0.94	23.17 15q12	1.05	0.9	↓
Prader-Willi / Angelman					Mean	1658	6.1	10068	1.116	1.034	0.054	1.00	(CV: 0.10)	1.09		
39	15 A	190.57	189.75	0.82 *	190	1997	5.5	11028	1.255	1.299	0.130	0.78	72.50 15q24.1	0.97	-0.3	↓
59	15 C	325.66	326.43	-0.77 *	325	947	7.3	6911	0.758	0.771	0.049	1.22	72.80 15q24.1	0.98	-0.3	↓
"15q24 deletion syndrome"					Mean	1472	6.4	8970	1.007	1.035	0.090	1.00	(CV: 0.01)	0.98		
36	16 A	171.52	170.91	0.61 *	172	1717	5.3	9153	1.042	1.018	0.063	1.00	3.87 16p13.3	1.02	0.4	↓
Rubinstein-Taybi syndrome					Mean	1717	5.3	9153	1.042	1.018	0.063	1.00	(CV:)	1.02		
31	17 A	140.04	138.97	1.07 *	142	1829	5.3	9730	1.107	1.248	0.053	1.27	2.51 17p13.3	0.89	-2.7	↓
47	17 B	236.94	236.22	0.72 *	238	1482	5.8	8570	0.945	0.900	0.067	0.73	2.52 17p13.3	1.05	0.7	↓
Miller-Dieker region					Mean	1656	5.6	9150	1.026	1.074	0.060	1.00	(CV: 0.12)	0.95		
75	17 D	463.57	463.07	0.50	465	1710	9.9	16863	1.849	1.331	0.092	0.83	17.53 17p11.2-##	1.39	5.6 *	↓
52	17 B	272.48	271.90	0.58 *	274	1219	6.3	7667	0.845	0.940	0.043	1.25	17.83 17p11.2	0.90	-2.2	↓
56	17 C	303.45	302.90	0.55 *	303	1105	7.1	7825	0.859	0.839	0.053	0.91	18.08 17p11.2	1.02	0.4	↓
Smith-Magenis syndrome					Mean	1345	7.7	10785	1.184	1.037	0.063	1.00	(CV: 0.23)	1.07		
50	17 B	258.99	258.33	0.66 *	260	769	6.4	4934	0.544	0.621	0.038	0.88	26.56 17q11.2	0.88	-2.0	↓
60	17 C	334.76	334.45	0.31	335	1312	7.6	9935	1.090	1.118	0.053	1.12	26.58 17q11.2	0.98	-0.5	↓
NF1 microdeletion syndrome					Mean	1041	7.0	7435	0.817	0.870	0.046	1.00	(CV: 0.08)	0.93		
76	17 D	471.59	470.58	1.01 *	472	664	9.6	6349	0.696	0.719	0.047	0.70	41.26 17q21.31	0.97	-0.5	↓
45	17 B	226.45	224.79	1.66 *	226	2062	5.9	12255	1.351	1.325	0.050	1.21	41.44 17q21.31	1.02	0.5	↓
61	17 C	341.60	341.78	-0.18	342	1094	7.9	8609	0.945	0.932	0.039	1.09	41.45 17q21.31	1.01	0.3	↓
"17q21.31 microdeletion"					Mean	1273	7.8	9071	0.997	0.992	0.046	1.00	(CV: 0.02)	1.01		

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		
40	22 A	196.43	195.29	1.14 *	196	1484	5.5	8182	0.931	0.890	0.065	0.83	17.89 22q11.21	1.05	0.6	.		
42	22 B	209.21	207.99	1.22 *	208	1672	5.8	9704	1.070	1.109	0.061	1.11	18.09 22q11.21	0.96	-0.7	.		
65	22 D	371.66	371.47	0.19	373	1075	8.8 *	9495	1.041	0.920	0.053	1.06	19.57 22q11.21	1.13	2.3	↓		
22q11.21 (DiGeorge)					Mean	1410	6.7	9127	1.014	0.973	0.060	1.00	(CV: 0.08)	1.05				
49	22 B	253.21	251.96	1.25 *	253	2297	6.2	14171	1.562	1.321	0.100	1.05	49.49 22q13.33-##	1.18	2.4	↓		
66	22 D	382.59	382.09	0.50	382	1588	8.5	13423	1.472	1.442	0.120	0.95	49.50 22q13.33-#	1.02	0.2	.		
22q13 (Phelan-McDermid)					Mean	1943	7.3	13797	1.517	1.382	0.110	1.00	(CV: 0.10)	1.11				
55	X C	295.61	295.46	0.15	297	1233	6.8	8385	0.920	0.751	0.048	1.00	32.29 Xp21.2	1.23	3.5	↓		
Chromosome X control probe					Mean	1233	6.8	8385	0.920	0.751	0.048	1.00	(CV:)	1.23				
41	X B	201.07	199.64	1.43 *	202	931	5.6	5181	0.571	0.457	0.047	0.99	153.02 Xq28	1.25	2.4	↓		
32	X A	147.72	146.82	0.90 *	148	1079	5.2	5616	0.639	0.538	0.065	0.84	152.95 Xq28	1.19	1.5	↓		
38	X A	184.33	183.16	1.17 *	184	1068	5.6	5937	0.676	0.678	0.060	1.16	152.94 Xq28-#	1.00	0.0	.		
Xq28 (RETT / MECP2)					Mean	1026	5.4	5578	0.629	0.558	0.057	1.00	(CV: 0.12)	1.13				
Mean values			0.69			1370	7.0	9253	1.025	1.000	0.060	4		1.02	Total of all except			
Standard deviations			0.48			(Coef. of variance: 0.260)			0.265	0.224				0.11	Ctrl and '?' peaks			

Quality assessment	Quality limits	Quality
Mean A-group area / mean Q-frag. area	>1.00 (1.75)	3.53
Mean CpG-area / mean A-group area	>0.55 (0.85)	1.85
Mean height of first probes AB	> 450 (800)	1608
Mean height of last probes CD	> 280 (500)	1143
Ratio of mean heights AB/CD ('slope')	<2.00 (1.55)	1.41
Mean group CV of weighted ratio	<0.20 (0.15)	0.09
3 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: 17p11.2-##

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 224 (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)