

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	Dist. Ratio	1.0 in SD	1.0 low high
19	64 -	60.45	60.91	-0.46	64	1143	11.0	12553	1.358	1.185	0.134	1.13	64 nt	1.15	1.3	↓
20	70 -	66.68	66.95	-0.27	70	683	11.8	8038	0.869	0.816	0.139	0.75	70 nt	1.07	0.4	↓
23	76 -	72.94	73.13	-0.19	76	781	10.9	8522	0.922	1.034	0.115	1.15	76 nt	0.89	-1.0	↓
24	82 -	79.31	79.41	-0.10	82	625	12.6	7870	0.851	0.962	0.126	0.97	82 nt	0.89	-0.9	↓
<b>Ctrl: Q-fragments</b>					Mean	808	11.6	9246	1.000	0.999	0.129	1.00	(CV: 0.13)	<b>0.99</b>		
25	6 a	85.69	85.90	-0.21	88	4413	9.2*	40645	2.113	2.027	1.250	0.43	6p21.3 CpG isl.	1.04	0.1	.
26	2 a	91.08	91.30	-0.22	92	2785	6.2	17391	0.904	0.956	0.138	1.85	2q14 synt.	0.95	-0.4	↓
27	1 a	97.19	97.34	-0.15	96	1909	6.1	11609	0.603	0.961	0.360	0.72	1p36.3 CpG isl.	0.63	-1.0	
<b>Ctrl: D-fragments</b>					Mean	3036	7.2	23215	1.207	1.314	0.583	1.00	(CV: 0.20)	<b>0.88</b>		
28	X a	100.91	101.15	-0.24	100	1855	5.8	10713	0.557	0.629	0.067	0.97	Xq23	0.88	-1.1	↓
29	Y a	105.45	105.67	-0.22	105	2902	6.1	17805	0.925	0.987	0.099	1.03	Yq11.21	0.94	-0.6	↓
<b>Ctrl: X- &amp; Y-fragments</b>					Mean	2379	6.0	14259	0.741	0.808	0.083	1.00	(CV: 0.04)	<b>0.91</b>		
60	13 C	356.69	356.65	0.04	355	1984	8.2	16315	1.256	1.214	0.060	1.13	13q13.1	1.04	0.7	.
39	13 A	178.23	178.41	-0.18	178	2913	6.3	18339	0.953	1.059	0.045	1.31	13q13.3	0.90	-2.3	↓
46	13 B	219.76	219.76	0.00	220	3519	6.4	22442	1.231	1.283	0.065	1.10	13q14.2	0.96	-0.8	.
64	13 D	398.61	398.45	0.16	400	2514	7.8	19680	1.296	1.287	0.098	0.74	13q14.2	1.01	0.1	.
51	13 B	263.69	263.72	-0.03	265	1902	6.8	13013	0.714	0.899	0.063	0.80	13q21.33	0.79	-3.0	
34	13 A	147.06	147.13	-0.07	148	3678	6.2	22765	1.183	1.273	0.063	1.13	13q32.1	0.93	-1.4	↓
68	13 D	443.86	443.79	0.07	445	2189	8.3	18075	1.191	1.243	0.083	0.84	13q34	0.96	-0.6	.
56	13 C	310.22	310.35	-0.13	310	1924	7.0	13437	1.035	1.130	0.067	0.95	13q34	0.92	-1.4	↓
<b>Chromosome 13</b>					Mean	2578	7.1	18008	1.107	1.173	0.068	1.00	(CV: 0.07)	<b>0.94</b>		
55	18 C	299.35	299.41	-0.06	301	2170	7.1	15350	1.182	1.261	0.073	0.94	18p11.32	0.94	-1.1	↓
67	18 D	435.29	435.32	-0.03	436	2109	8.2	17247	1.136	1.117	0.069	0.89	18p11.21	1.02	0.3	.
45	18 B	211.18	211.24	-0.06	211	3393	6.4	21749	1.193	1.163	0.068	0.93	18q11.2	1.03	0.4	.
63	18 D	390.60	390.52	0.08	391	2551	7.9	20142	1.327	1.376	0.058	1.29	18q11.2	0.96	-0.8	.
33	18 A	141.10	141.15	-0.05	142	4082	6.2	25166	1.308	1.408	0.067	1.14	18q21.1	0.93	-1.5	↓
38	18 A	171.36	171.52	-0.16	172	3901	6.4	24920	1.295	1.302	0.053	1.35	18q21.32	0.99	-0.1	.
59	18 C	346.42	346.50	-0.08	346	1490	7.3	10833	0.834	0.845	0.064	0.73	18q21.33	0.99	-0.2	.
50	18 B	254.15	254.03	0.12	256	2766	6.8	18794	1.031	1.207	0.090	0.73	18q23	0.85	-2.0	↓
<b>Chromosome 18</b>					Mean	2808	7.0	19275	1.163	1.210	0.068	1.00	(CV: 0.05)	<b>0.97</b>		
49	21 B	246.23	246.23	0.00	247	5591	6.6	37056	2.032	1.485	0.080	1.06	21q11.2	1.37	6.9*	
44	21 B	202.28	202.31	-0.03	202	5238	6.3	33188	1.820	1.290	0.082	0.90	21q21.1	1.41	6.5*	
37	21 A	165.58	165.62	-0.04	166	4696	6.4	29860	1.552	1.139	0.089	0.73	21q21.1	1.36	4.7*	
58	21 C	336.89	336.97	-0.08	337	2594	7.3	18986	1.462	1.026	0.060	0.97	21q21.3	1.42	7.2*	
66	21 D	425.37	425.28	0.09	427	2360	8.6	20216	1.332	0.973	0.055	1.00	21q22.11	1.37	6.5*	
54	21 C	289.49	289.48	0.01	292	2847	6.8	19265	1.484	1.127	0.071	0.90	21q22.11	1.32	5.0*	
32	21 A	134.12	134.22	-0.10	136	5835	6.2	36071	1.875	1.443	0.060	1.36	21q22.13	1.30	7.2*	
62	21 D	381.88	381.85	0.03	382	2396	7.7	18564	1.223	0.954	0.050	1.09	21q22.3	1.28	5.4*	
<b>Chromosome 21</b>					Mean	3945	7.0	26651	1.597	1.180	0.068	1.00	(CV: 0.04)	<b>1.35</b>	<b>P= 0.000%</b>	
61	X C	363.20	363.20	0.00	364	1360	7.4	10089	0.777	0.775	0.057	1.05	Xp22.12	1.00	0.0	.
47	X B	229.74	229.70	0.04	229	1569	6.8	10649	0.584	0.681	0.052	1.02	Xp21.3	0.86	-1.9	↓
69	X D	452.85	452.74	0.11	454	851	8.4	7182	0.473	0.477	0.039	0.95	Xp21.1	0.99	-0.1	.
52	X B	272.04	272.05	-0.01	274	1664	6.8	11372	0.624	0.657	0.055	0.93	Xp11.4**	0.95	-0.6	↓
35	X A	154.03	154.05	-0.02	154	2072	6.2	12868	0.669	0.630	0.037	1.31	Xq12	1.06	1.0	↓
41	X A	184.61	184.77	-0.16	184	1343	6.4	8616	0.448	0.426	0.045	0.73	Xq23**	1.05	0.5	↓
65	X D	407.68	407.65	0.03	409	1022	7.8	7989	0.526	0.573	0.043	1.04	Xq25	0.92	-1.1	↓
57	X C	318.06	318.19	-0.13	319	824	7.5	6151	0.474	0.622	0.050	0.96	Xq28	0.76	-3.0	
<b>Chromosome X</b>					Mean	1338	7.2	9365	0.572	0.605	0.047	1.00	(CV: 0.11)	<b>0.95</b>		
36	Y A	159.43	159.59	-0.16	160	2679	6.4	17142	0.891	0.893	0.085	0.92	Yp11.31	1.00	0.0	.
43	Y A	192.72	192.83	-0.11	193	1394	6.3	8759	0.455	0.427	0.058	0.65	Yp11.31	1.07	0.5	↓
53	Y B	281.03	281.03	0.00	283	2386	6.8	16238	0.890	0.827	0.052	1.39	Yp11.3	1.08	1.2	↓
48	Y B	239.07	239.11	-0.04	238	1395	6.7	9339	0.512	0.508	0.042	1.05	Yq11.21	1.01	0.1	.
<b>Chromosome Y</b>					Mean	1964	6.5	12870	0.687	0.664	0.059	1.00	(CV: 0.04)	<b>1.04</b>		
<b>Mean values</b>				-0.03		2589	7.0	17719	<b>1.063</b>	1.000	0.062	4		1.05	Total of all except	
<b>Standard deviations</b>				0.08		(Coef. of variance: 0.441)			0.419	0.314				0.18	Ctrl and '?' peaks	

Quality assessment	Quality limits	Quality
Mean A-group area / mean Q-frag. area	>0.65 (1.50)	2.08
Mean CpG-area / mean A-group area	>0.30 (0.65)	1.36
Mean height of first probes AB	> 450 ( 800)	3101
Mean height of last probes CD	> 280 ( 500)	1949
Ratio of mean heights AB/CD ('slope')	<3.00 (2.50)	1.59
Mean group CV of weighted ratio	<0.20 (0.15)	0.07
4 unidentified peak areas / 41 peak areas	< (0.02)	0.00

The weighted mean ratios are tested for being outside ratio 1 ± 0.10 for chromosome 13, 18, 21 and female X  
 1 ± 0.13 for male X and 1 ± 0.24 for Y.  
 (One-tailed significance is high for p<=1%, and low for p<=5%)

**High significance P= 0.000%** **Male Reference**  
**Trisomy 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 335 (14 peaks). CV of ROX heights for peaks above 100 nt is: 0.08

Ratio 1.35 is found. Theoretically 'Trisomy 21' has ratio 1.5