

		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
3	64 - 70 -	61.17	61.20 66.91	-0.03	64 70	403	16.2	6537	0.614	0.911 0.782	0.156 0.147	0.83	64 nt 70 nt	0.67	-1.9	
6	76 - 82 -	72.72	72.54 78.43	0.18	76 82	592 687	19.2 20.5	11339 14083	1.064 1.322	1.126 1.178	0.128 0.184	1.26 0.91	76 nt 82 nt	0.95 1.12	-0.5 0.8	
Ctrl: Q-fragments					Mean	561	18.6	10653	1.000	1.072	0.156	1.00	(CV: 0.23)	0.92		
9	2 A	90.18	90.17	0.01	94	2134	11.0	23381	0.758	0.786	0.064	1.00	2q14 synt.	0.96	-0.4	.
Synthetic control probe					Mean	2134	11.0	23381	0.758	0.786	0.064	1.00	(CV:)	0.96		
12	13 A	146.00	145.92	0.08	148	3065	12.1	37091	1.203	1.167	0.051	1.48	13q32.1	1.03	0.7	.
16	13 A	177.26	177.35	-0.09	178	1994	13.1	26159	0.848	0.852	0.062	0.89	13q13.3	1.00	-0.1	.
20	13 B	218.83	218.82	0.01	220	2282	15.0	34198	0.999	1.077	0.050	1.40	13q14.2	0.93	-1.6	
24	13 B	262.41	262.45	-0.04	265	1435	16.6	23841	0.696	0.777	0.057	0.88	13q21.33	0.90	-1.4	
28	13 C	309.87	309.93	-0.06	310	1378	18.9	26085	1.146	1.125	0.067	1.09	13q34	1.02	0.3	.
32	13 C	355.44	355.19	0.25	355	978	21.9	21424	0.942	1.017	0.073	0.90	13q13.1	0.93	-1.0	
36	13 D	398.65	398.39	0.26	400	900	23.1	20750	0.945	1.094	0.120	0.59	13q14.2	0.86	-1.2	
40	13 D	442.93	442.59	0.34	445	864	24.4	21117	0.962	0.855	0.074	0.75	13q34	1.13	1.4	
Chromosome 13					Mean	1612	18.1	26333	0.968	0.995	0.069	1.00	(CV: 0.08)	0.98		
11	18 A	140.15	140.07	0.08	142	3111	12.1	37692	1.222	1.236	0.061	1.25	18q21.1	0.99	-0.2	.
15	18 A	170.66	170.78	-0.12	172	2081	13.1	27313	0.886	0.868	0.073	0.73	18q21.32	1.02	0.2	.
19	18 B	209.91	209.88	0.03	211	2021	14.6	29418	0.859	0.965	0.041	1.44	18q11.2	0.89	-2.6	
23	18 B	252.82	252.77	0.05	256	2501	16.5	41143	1.202	1.191	0.057	1.29	18q23	1.01	0.2	.
27	18 C	298.81	298.88	-0.07	301	1242	18.7	23261	1.022	1.037	0.066	0.97	18p11.32	0.99	-0.2	.
31	18 C	346.24	346.18	0.06	346	663	20.4	13541	0.595	0.607	0.060	0.63	18q21.33	0.98	-0.2	.
35	18 D	390.07	389.97	0.10	391	1370	22.2	30399	1.385	1.276	0.079	0.99	18q11.2	1.09	1.4	
39	18 D	434.19	433.86	0.33	436	907	24.5	22219	1.012	1.055	0.094	0.69	18p11.21	0.96	-0.5	.
Chromosome 18					Mean	1737	17.8	28123	1.023	1.030	0.066	1.00	(CV: 0.06)	0.99		
10	21 A	132.99	132.90	0.09	136	2957	12.1	35805	1.161	1.169	0.115	0.71	21q22.13	0.99	-0.1	.
14	21 A	164.55	164.56	-0.01	166	2616	12.9	33631	1.090	1.046	0.070	1.04	21q21.1	1.04	0.6	.
18	21 B	200.83	200.81	0.02	202	2532	14.0	35370	1.033	1.026	0.067	1.07	21q21.1	1.01	0.1	.
22	21 B	245.32	245.33	-0.01	247	1923	16.3	31302	0.914	0.851	0.046	1.28	21q11.2	1.07	1.4	
26	21 C	289.13	289.12	0.01	292	1276	18.1	23111	1.016	1.000	0.099	0.70	21q22.11	1.02	0.2	.
30	21 C	337.29	337.42	-0.13	337	1152	20.1	23163	1.018	0.884	0.070	0.88	21q21.3	1.15	1.9	
34	21 D	381.51	381.44	0.07	382	939	22.4	21055	0.959	0.931	0.056	1.16	21q22.3	1.03	0.5	.
38	21 D	424.81	424.65	0.16	427	716	24.0	17190	0.783	0.911	0.055	1.15	21q22.11	0.86	-2.3	
Chromosome 21					Mean	1764	17.5	27578	0.997	0.977	0.072	1.00	(CV: 0.08)	1.02		
13	X A	152.82	152.75	0.07	154	2506	12.3	30874	1.001	1.049	0.065	1.11	Xq12	0.95	-0.7	.
17	X A	183.61	183.64	-0.03	184	1766	13.7	24223	0.785	0.828	0.056	1.01	Xq23	0.95	-0.7	
21	X B	228.60	228.55	0.05	229	2490	15.3	38051	1.111	1.079	0.067	1.10	Xp21.3	1.03	0.5	.
25	X B	271.56	271.57	-0.01	274	2265	17.3	39179	1.144	1.034	0.050	1.41	Xp11.4	1.11	2.2	
29	X C	317.54	317.74	-0.20	319	1191	20.2	24070	1.058	1.039	0.113	0.63	Xq28	1.02	0.2	.
33	X C	362.65	362.44	0.21	364	1250	21.2	26448	1.162	1.291	0.083	1.07	Xp22.12	0.90	-1.6	
37	X D	407.83	407.76	0.07	409	1039	23.1	24037	1.095	1.061	0.097	0.75	Xq25	1.03	0.3	.
41	X D	451.62	451.33	0.29	454	720	24.9	17920	0.816	0.816	0.061	0.92	Xp21.1	1.00	0.0	.
Chromosome X					Mean	1653	18.5	28100	1.022	1.024	0.074	1.00	(CV: 0.07)	1.00		
	Y a	158.46			160					0.588			Yp11.31			
	Y a	191.66			193					0.446			Yp11.31			
	Y b	238.00			238					0.629			Yq11.21			
	Y b	280.49			283					0.772			Yp11.3			
Chromosome Y					Mean							1.00	(CV:)			

Mean values 0.06 1705 17.8 27408 **0.995** 1.000 0.070 2 1.00 Total of all except
Standard deviations 0.13 (Coef. of variance: 0.257) 0.170 0.157 0.07 Ctrl and '?' peaks

Quality assessment	Quality limits	Quality
Mean A-group area / mean Q-frag. area	>0.65 (1.50)	2.90
Mean height of first probes AB	> 450 (800)	2334
Mean height of last probes CD	> 280 (500)	1037
Ratio of mean heights AB/CD ('slope')	<3.00 (2.50)	2.25
Mean group CV of weighted ratio	<0.20 (0.15)	0.07
0 unidentified peak areas / 33 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%)

Female Reference
Normal 13, 18, 21, XX

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 128 (15 peaks). 100*CV of ROX heights for peaks above 100 nt is: 21.02

(Ctrl probes are used for quality evaluation only)