

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	
5	64 -	60.86	61.20	-0.34	64	1437	18.3	26288	1.065	0.911	0.156	0.89	64 nt	1.17	1.0	..	
6	70 -	66.61	66.91	-0.30	70	1093	17.7	19346	0.783	0.782	0.147	0.81	70 nt	1.00	0.0	.	
7	76 -	72.57	72.54	0.03	76	1448	18.5	26773	1.084	1.126	0.128	1.34	76 nt	0.96	-0.3	.	
8	82 -	78.78	78.43	0.35	82	1472	17.9	26369	1.068	1.178	0.184	0.97	82 nt	0.91	-0.6	..	
Ctrl: Q-fragments					Mean	1363	18.1	24694	1.000	0.999	0.154	1.00	(CV: 0.11)	1.00			
10	2 A	90.38	90.17	0.21	94	764	9.3	7124	0.801	0.786	0.064	1.00	2q14 synt.	1.02	0.2	.	
Synthetic control probe					Mean	764	9.3	7124	0.801	0.786	0.064	1.00	(CV:)	1.02			
15	13 A	146.10	145.92	0.18	148	1118	8.9	9934	1.117	1.167	0.051	1.48	13q32.1	0.96	-1.0	.	
21	13 A	177.37	177.35	0.02	178	1026	10.8	11089	1.246	0.852	0.062	0.89	13q13.3	1.46	6.4*	..	
27	13 B	218.93	218.82	0.11	220	909	11.2	10158	1.247	1.077	0.050	1.40	13q14.2	1.16	3.4	..	
32	13 B	262.60	262.45	0.15	265	630	10.0	6329	0.777	0.777	0.057	0.88	13q21.33	1.00	0.0	.	
39	13 C	309.97	309.93	0.04	310	602	11.1	6691	1.087	1.125	0.067	1.09	13q34	0.97	-0.6	.	
44	13 C	355.41	355.19	0.22	355	822	11.5	9486	1.541	1.017	0.073	0.90	13q13.1	1.51	7.2*	..	
50	13 D	398.52	398.39	0.13	400	758	12.2	9223	1.541	1.094	0.120	0.59	13q14.2	1.41	3.7	..	
54	13 D	442.76	442.59	0.17	445	383	14.3	5471	0.914	0.855	0.074	0.75	13q34	1.07	0.8	..	
Chromosome 13					Mean	781	11.3	8548	1.184	0.995	0.069	1.00	(CV: 0.20)	1.16	P= 23.39%		
13	18 A	140.30	140.07	0.23	142	1161	8.9	10314	1.159	1.236	0.061	1.25	18q21.1	0.94	-1.3	..	
19	18 A	170.84	170.78	0.06	172	1163	9.4	10931	1.229	0.868	0.073	0.73	18q21.32	1.42	4.9*	..	
26	18 B	209.99	209.88	0.11	211	1037	10.8	11219	1.377	0.965	0.041	1.44	18q11.2	1.43	9.9*	..	
31	18 B	252.96	252.77	0.19	256	946	10.0	9485	1.164	1.191	0.057	1.29	18q23	0.98	-0.5	.	
37	18 C	299.02	298.88	0.14	301	617	10.5	6465	1.050	1.037	0.066	0.97	18p11.32	1.01	0.2	.	
43	18 C	346.14	346.18	-0.04	346	412	13.8*	5704	0.927	0.607	0.060	0.63	18q21.33	1.53	5.3*	..	
49	18 D	390.08	389.97	0.11	391	545	13.3	7248	1.211	1.276	0.079	0.99	18q11.2	0.95	-0.8	..	
53	18 D	433.94	433.86	0.08	436	773	13.1	10163	1.698	1.055	0.094	0.69	18p11.21	1.61	6.8*	..	
Chromosome 18					Mean	832	11.2	8941	1.227	1.030	0.066	1.00	(CV: 0.23)	1.19	P= 19.27%		
12	21 A	133.13	132.90	0.23	136	1464	10.5	15432	1.735	1.169	0.115	0.71	21q22.13	1.48	4.9*	..	
18	21 A	164.70	164.56	0.14	166	801	9.3	7480	0.841	1.046	0.070	1.04	21q21.1	0.80	-2.9	..	
25	21 B	200.97	200.81	0.16	202	987	10.0	9848	1.209	1.026	0.067	1.07	21q21.1	1.18	2.7	..	
30	21 B	245.43	245.33	0.10	247	982	9.8	9641	1.183	0.851	0.046	1.28	21q11.2	1.39	7.2*	..	
36	21 C	289.32	289.12	0.20	292	660	10.7	7073	1.149	1.000	0.099	0.70	21q22.11	1.15	1.5	..	
42	21 C	337.31	337.42	-0.11	337	638	12.1	7748	1.259	0.884	0.070	0.88	21q21.3	1.42	5.4*	..	
48	21 D	381.57	381.44	0.13	382	372	10.8	4024	0.672	0.931	0.056	1.16	21q22.3	0.72	-4.6*	..	
52	21 D	424.80	424.65	0.15	427	459	13.2	6074	1.015	0.911	0.055	1.15	21q22.11	1.11	1.9	..	
Chromosome 21					Mean	795	10.8	8415	1.133	0.977	0.072	1.00	(CV: 0.25)	1.14			
16	X A	152.94	152.75	0.19	154	798	10.4	8329	0.936	1.049	0.065	1.11	Xq12	0.89	-1.7	..	
23	X A	183.64	183.64	0.00	184	529	11.6*	6157	0.692	0.828	0.056	1.01	Xq23	0.84	-2.4	..	
28	X B	228.60	228.55	0.05	229	606	10.1	6110	0.750	1.079	0.067	1.10	Xp21.3	0.70	-4.9*	..	
34	X B	271.72	271.57	0.15	274	705	11.2	7862	0.965	1.034	0.050	1.41	Xp11.4	0.93	-1.4	..	
40	X C	317.71	317.74	-0.03	319	453	10.5	4753	0.772	1.039	0.113	0.63	Xq28	0.74	-2.4	..	
45	X C	362.61	362.44	0.17	364	483	11.3	5453	0.886	1.291	0.083	1.07	Xp22.12	0.69	-4.9*	..	
51	X D	407.84	407.76	0.08	409	546	12.1	6597	1.102	1.061	0.097	0.75	Xq25	1.04	0.4	..	
55	X D	451.47	451.33	0.14	454	247	12.5	3099	0.518	0.816	0.061	0.92	Xp21.1	0.63	-4.9*	..	
Chromosome X					Mean	546	11.2	6045	0.828	1.024	0.074	1.00	(CV: 0.17)	0.81	P= 5.29%		
17	Y a	158.93	158.46	0.47	160	167	9.1	1527	0.172	0.588			Yp11.31	0.29	?		
24	Y a	192.39	191.66	0.73*	193	197	11.9*	2345	0.264	0.446			Yp11.31	0.59	?		
29	Y b	236.52	238.00	-1.48*	238	91	7.1*	647	0.079	0.629			Yq11.21	0.13	?		
35	Y b	281.45	280.49	0.96*	283	87	11.0	954	0.117	0.772			Yp11.3	0.15	?		
Chromosome Y					Mean					1.00			(CV:)				
Mean values			0.12		739	11.1	7961	1.084	1.000	0.070	2			1.07	Total of all except		
Standard deviations			0.08		(Coef. of variance:	0.318)	0.290	0.157						0.27	Ctrl and '?' peaks		

Quality assessment **Quality limits** **Quality**

Mean A-group area / mean Q-frag. area >0.65 (1.50) 0.36 **Too low!**

Mean height of first probes AB > 450 (800) 919

Mean height of last probes CD > 280 (500) 548

Ratio of mean heights AB/CD ('slope') <3.00 (2.50) 1.68

Mean group CV of weighted ratio <0.20 (0.15) 0.21 **Too high!**

9 unidentified peak areas / 33 peak areas < (0.02) 0.03 **high**

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%)

P= 5.29% is NOT significant! **Female Reference**
BAD: Too low DNA!

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 212 (14 peaks). 100*CV of ROX heights for peaks above 100 nt is: 7.37

Poor Quality!
Note the Y peaks!
 Ratio=0.81 (but a normal ratio 1.0 was expected)