

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	in SD	1.0 low high			
5	64 -	60.86	61.20	-0.34	64	1437	18.3	26288	1.065	0.897	0.243	0.68	64 nt	1.19	0.7				
6	70 -	66.61	66.91	-0.30	70	1093	17.7	19346	0.783	0.751	0.145	0.96	70 nt	1.04	0.2	.			
7	76 -	72.57	72.54	0.03	76	1448	18.5	26773	1.084	1.111	0.183	1.12	76 nt	0.98	-0.1	.			
8	82 -	78.78	78.43	0.35	82	1472	17.9	26369	1.068	1.241	0.185	1.24	82 nt	0.86	-0.9	.			
Ctrl: Q-fragments									Mean	1363	18.1	24694	1.000	1.000	0.189	1.00	(CV: 0.13)	0.99	
10	2 A	90.38	90.17	0.21	94	764	9.3	7124	0.821	0.993	0.108	1.00	2q14 synt.	0.83	-1.6	.			
Synthetic control probe									Mean	764	9.3	7124	0.821	0.993	0.108	1.00	(CV:)	0.83	
15	13 A	146.10	145.92	0.18	148	1118	8.9	9934	1.145	1.437	0.075	1.29	13q32.1	0.80	-3.9	.			
21	13 A	177.37	177.35	0.02	178	1026	10.8	11089	1.278	0.990	0.072	0.92	13q13.3	1.29	4.0				
27	13 B	218.93	218.82	0.11	220	909	11.2	10158	1.336	1.332	0.076	1.18	13q14.2	1.00	0.0	.			
32	13 B	262.60	262.45	0.15	265	630	10.0	6329	0.832	0.951	0.069	0.92	13q21.33	0.88	-1.7	.			
39	13 C	309.97	309.93	0.04	310	602	11.1	6691	0.953	1.315	0.084	1.05	13q34	0.72	-4.3*	.			
44	13 C	355.41	355.19	0.22	355	822	11.5	9486	1.351	1.209	0.069	1.18	13q13.1	1.12	2.1	.			
50	13 D	398.52	398.39	0.13	400	758	12.2	9223	1.351	1.278	0.110	0.78	13q14.2	1.06	0.7	.			
54	13 D	442.76	442.59	0.17	445	383	14.3	5471	0.801	0.990	0.097	0.68	13q34	0.81	-1.9	.			
Chromosome 13									Mean	781	11.3	8548	1.131	1.188	0.081	1.00	(CV: 0.20)	0.96	
13	18 A	140.30	140.07	0.23	142	1161	8.9	10314	1.189	1.531	0.090	1.13	18q21.1	0.78	-3.8	.			
19	18 A	170.84	170.78	0.06	172	1163	9.4	10931	1.260	1.112	0.083	0.90	18q21.32	1.13	1.8	.			
26	18 B	209.99	209.88	0.11	211	1037	10.8	11219	1.475	1.191	0.072	1.10	18q11.2	1.24	3.9				
31	18 B	252.96	252.77	0.19	256	946	10.0	9485	1.247	1.489	0.074	1.35	18q23	0.84	-3.3	.			
37	18 C	299.02	298.88	0.14	301	617	10.5	6465	0.921	1.238	0.088	0.93	18p11.32	0.74	-3.6	.			
43	18 C	346.14	346.18	-0.04	346	412	13.8*	5704	0.812	0.680	0.058	0.79	18q21.33	1.19	2.3				
49	18 D	390.08	389.97	0.11	391	545	13.3	7248	1.061	1.473	0.094	1.04	18q11.2	0.72	-4.4*	.			
53	18 D	433.94	433.86	0.08	436	773	13.1	10163	1.488	1.140	0.099	0.76	18p11.21	1.31	3.5				
Chromosome 18									Mean	832	11.2	8941	1.182	1.232	0.082	1.00	(CV: 0.25)	0.97	
12	21 A	133.13	132.90	0.23	136	1464	10.5	15432	1.779	1.526	0.080	1.23	21q22.13	1.17	3.1				
18	21 A	164.70	164.56	0.14	166	801	9.3	7480	0.862	1.248	0.081	1.00	21q21.1	0.69	-4.8*	.			
25	21 B	200.97	200.81	0.16	202	987	10.0	9848	1.295	1.272	0.082	1.00	21q21.1	1.02	0.3	.			
30	21 B	245.43	245.33	0.10	247	982	9.8	9641	1.268	1.048	0.048	1.40	21q11.2	1.21	4.6*				
36	21 C	289.32	289.12	0.20	292	660	10.7	7073	1.007	1.167	0.072	1.04	21q22.11	0.86	-2.2	.			
42	21 C	337.31	337.42	-0.11	337	638	12.1	7748	1.103	1.008	0.094	0.69	21q21.3	1.09	1.0	.			
48	21 D	381.57	381.44	0.13	382	372	10.8	4024	0.589	1.051	0.078	0.87	21q22.3	0.56	-5.9*	.			
52	21 D	424.80	424.65	0.15	427	459	13.2	6074	0.889	1.005	0.083	0.78	21q22.11	0.88	-1.4	.			
Chromosome 21									Mean	795	10.8	8415	1.099	1.166	0.077	1.00	(CV: 0.24)	0.96	
16	X A	152.94	152.75	0.19	154	798	10.4	8329	0.960	0.624	0.047	1.17	Xq12	1.54	7.1*				
23	X A	183.64	183.64	0.00	184	529	11.6*	6157	0.710	0.504	0.048	0.94	Xq23	1.41	4.3*				
28	X B	228.60	228.55	0.05	229	606	10.1	6110	0.803	0.649	0.052	1.11	Xp21.3	1.24	3.0	.			
34	X B	271.72	271.57	0.15	274	705	11.2	7862	1.034	0.666	0.054	1.10	Xp11.4	1.55	6.8*				
40	X C	317.71	317.74	-0.03	319	453	10.5	4753	0.677	0.606	0.057	0.94	Xq28	1.12	1.2	.			
45	X C	362.61	362.44	0.17	364	483	11.3	5453	0.776	0.776	0.076	0.91	Xp22.12	1.00	0.0	.			
51	X D	407.84	407.76	0.08	409	546	12.1	6597	0.966	0.596	0.051	1.04	Xq25	1.62	7.3*				
55	X D	451.47	451.33	0.14	454	247	12.5	3099	0.454	0.467	0.053	0.79	Xp21.1	0.97	-0.3	.			
Chromosome X									Mean	546	11.2	6045	0.797	0.611	0.055	1.00	(CV: 0.19)	1.33	P= 3.22%
17	Y A	158.93	158.46	0.47	160	167	9.1	1527	0.176	0.588	0.064	0.88	Yp11.31	0.30	-6.4*				
24	Y A	192.39	191.66	0.73*	193	197	11.9*	2345	0.270	0.446	0.070	0.61	Yp11.31	0.61	-2.5				
29	Y B	236.52	238.00	-1.48*	238	91	7.1*	647	0.085	0.629	0.074	0.82	Yq11.21	0.14	-7.4*				
35	Y B	281.45	280.49	0.96*	283	87	11.0	954	0.125	0.772	0.044	1.68	Yp11.3	0.16	-14.6*				
Chromosome Y									Mean	136	9.8	1368	0.164	0.609	0.063	1.00	(CV: 0.73)	0.26	P= 0.61%
Mean values			0.12	674	10.9	7248	0.950	1.000	0.074	2	0.96	Total of all except							
Standard deviations			0.33	(Coef. of variance:	0.437)	0.391	0.328	0.36	Ctrl and '?' peaks										

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

Mean A-group area / mean Q-frag. area >0.65 (1.50) 0.35 **Too low!**

Mean height of first probes AB > 450 (800) 770 **low**

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

Ratio of mean heights AB/CD ('slope') <3.00 (2.50) 1.40

Mean group CV of weighted ratio <0.20 (0.15) 0.28 **Too high!**

9 unidentified peak areas / 37 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%)

High significance P= 0.61% **Male 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!

Theoretically X and Y ratios of 69,XXY are 1.33 and 0.66