

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	
7	64 -	59.69	61.20	-1.51 *	64	979	18.4	18024	0.951	0.897	0.243	0.68	64 nt	1.06	0.2	-.	
8	70 -	66.10	66.91	-0.81 *	70	603	20.6	12404	0.654	0.751	0.145	0.96	70 nt	0.87	-0.7	.	
9	76 -	72.20	72.54	-0.34	76	1211	20.6	24983	1.318	1.111	0.183	1.12	76 nt	1.19	1.1	-.	
10	82 -	78.60	78.43	0.17	82	936	21.8	20427	1.077	1.241	0.185	1.24	82 nt	0.87	-0.9	.	
Ctrl: Q-fragments					Mean	932	20.4	18960	1.000	1.000	0.189	1.00	(CV: 0.16)	0.99			
12	2 A	90.28	90.17	0.11	94	3832	10.1	38745	1.125	0.993	0.108	1.00	2q14 synt.	1.13	1.2	-.	
Synthetic control probe					Mean	3832	10.1	38745	1.125	0.993	0.108	1.00	(CV:)	1.13			
16	13 A	145.97	145.92	0.05	148	4303	10.1	43324	1.258	1.437	0.075	1.29	13q32.1	0.88	-2.4	.	
21	13 A	177.36	177.35	0.01	178	3361	10.1	34088	0.990	0.990	0.072	0.92	13q13.3	1.00	0.0	.	
27	13 B	218.82	218.82	0.00	220	3727	11.0	40931	1.163	1.332	0.076	1.18	13q14.2	0.87	-2.2	.	
32	13 B	262.44	262.45	-0.01	265	2413	11.6	27974	0.795	0.951	0.069	0.92	13q21.33	0.84	-2.3	.	
37	13 C	309.89	309.93	-0.04	310	2146	12.9	27660	1.037	1.315	0.084	1.05	13q34	0.79	-3.3	.	
41	13 C	355.20	355.19	0.01	355	1738	14.9	25859	0.970	1.209	0.069	1.18	13q13.1	0.80	-3.5	.	
46	13 D	398.49	398.39	0.10	400	2397	14.9	35721	1.304	1.278	0.110	0.78	13q14.2	1.02	0.2	.	
50	13 D	442.55	442.59	-0.04	445	2010	15.7	31566	1.152	0.990	0.097	0.68	13q34	1.16	1.7	-.	
Chromosome 13					Mean	2762	12.6	33390	1.083	1.188	0.081	1.00	(CV: 0.13)	0.90			
15	18 A	140.13	140.07	0.06	142	5136	10.4	53229	1.546	1.531	0.090	1.13	18q21.1	1.01	0.2	.	
20	18 A	170.81	170.78	0.03	172	3473	10.3	35877	1.042	1.112	0.083	0.90	18q21.32	0.94	-0.8	.	
26	18 B	209.90	209.88	0.02	211	3976	11.0	43900	1.247	1.191	0.072	1.10	18q11.2	1.05	0.8	.	
31	18 B	252.77	252.77	0.00	256	4574	11.7	53396	1.517	1.489	0.074	1.35	18q23	1.02	0.4	.	
36	18 C	298.92	298.88	0.04	301	2626	12.7	33464	1.255	1.238	0.088	0.93	18p11.32	1.01	0.2	.	
40	18 C	346.23	346.18	0.05	346	1347	13.9	18751	0.703	0.680	0.058	0.79	18q21.33	1.03	0.4	.	
45	18 D	389.98	389.97	0.01	391	2673	14.4	38479	1.404	1.473	0.094	1.04	18q11.2	0.95	-0.7	.	
49	18 D	433.88	433.86	0.02	436	1785	15.4	27435	1.001	1.140	0.099	0.76	18p11.21	0.88	-1.4	.	
Chromosome 18					Mean	3199	12.5	38066	1.214	1.232	0.082	1.00	(CV: 0.05)	0.99			
14	21 A	132.95	132.90	0.05	136	4654	10.7	49731	1.444	1.526	0.080	1.23	21q22.13	0.95	-1.0	.	
19	21 A	164.56	164.56	0.00	166	3744	10.4	38991	1.132	1.248	0.081	1.00	21q21.1	0.91	-1.4	.	
25	21 B	200.73	200.81	-0.08	202	4267	10.9	46432	1.319	1.272	0.082	1.00	21q21.1	1.04	0.6	.	
30	21 B	245.32	245.33	-0.01	247	3061	12.2	37321	1.060	1.048	0.048	1.40	21q11.2	1.01	0.3	.	
35	21 C	289.16	289.12	0.04	292	2640	12.2	32329	1.212	1.167	0.072	1.04	21q22.11	1.04	0.6	.	
39	21 C	337.46	337.42	0.04	337	1862	13.5	25133	0.943	1.008	0.094	0.69	21q21.3	0.93	-0.7	.	
44	21 D	381.50	381.44	0.06	382	1924	13.8	26573	0.970	1.051	0.078	0.87	21q22.3	0.92	-1.0	.	
48	21 D	424.70	424.65	0.05	427	1393	15.8	21965	0.802	1.005	0.083	0.78	21q22.11	0.80	-2.5	.	
Chromosome 21					Mean	2943	12.4	34809	1.110	1.166	0.077	1.00	(CV: 0.08)	0.96			
17	X A	152.80	152.75	0.05	154	2839	10.4	29630	0.861	0.624	0.047	1.17	Xq12	1.38	5.0 *	-	
23	X A	183.59	183.64	-0.05	184	2685	9.9	26506	0.770	0.504	0.048	0.94	Xq23	1.53	5.6 *	-	
28	X B	228.50	228.55	-0.05	229	2916	10.9	31882	0.906	0.649	0.052	1.11	Xp21.3	1.40	5.0 *	-	
33	X B	271.59	271.57	0.02	274	2571	11.8	30420	0.864	0.666	0.054	1.10	Xp11.4	1.30	3.7	-	
38	X C	317.77	317.74	0.03	319	1474	13.3	19544	0.733	0.606	0.057	0.94	Xq28	1.21	2.2	-	
42	X C	362.47	362.44	0.03	364	2027	13.8	27897	1.046	0.776	0.076	0.91	Xp22.12	1.35	3.6	-	
47	X D	407.77	407.76	0.01	409	1477	14.9	22020	0.804	0.596	0.051	1.04	Xq25	1.35	4.1 *	-	
51	X D	451.31	451.33	-0.02	454	791	16.1	12717	0.464	0.467	0.053	0.79	Xp21.1	0.99	-0.1	.	
Chromosome X					Mean	2098	12.6	25077	0.806	0.611	0.055	1.00	(CV: 0.11)	1.32	P= 0.37%		
18	Y A	158.42	158.46	-0.04	160	1251	10.2	12757	0.370	0.588	0.064	0.88	Yp11.31	0.63	-3.4	.	
24	Y A	191.64	191.66	-0.02	193	1022	10.9	11126	0.323	0.446	0.070	0.61	Yp11.31	0.72	-1.8	.	
29	Y B	238.02	238.00	0.02	238	1414	10.9	15407	0.438	0.629	0.074	0.82	Yq11.21	0.70	-2.6	.	
34	Y B	280.56	280.49	0.07	283	1687	11.8	19969	0.567	0.772	0.044	1.68	Yp11.3	0.73	-4.6 *	.	
Chromosome Y					Mean	1344	11.0	14815	0.425	0.609	0.063	1.00	(CV: 0.07)	0.70	P= 4.61%		
Mean values			0.02		2627	12.3	31047	0.987	1.000	0.074	2		1.01	Total of all except			
Standard deviations			0.04		(Coef. of variance:	0.352)	0.311	0.328					0.21	Ctrl and '?' peaks			

Quality assessment	Quality limits	Quality
Mean A-group area / mean Q-frag. area	>0.65 (1.50)	1.82
Mean height of first probes AB	> 450 (800)	3186
Mean height of last probes CD	> 280 (500)	1894
Ratio of mean heights AB/CD ('slope')	<3.00 (2.50)	1.68
Mean group CV of weighted ratio	<0.20 (0.15)	0.09
3 unidentified peak areas / 37 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 $p \leq 1\%$, and low for $p \leq 5\%$)

High significance P= 0.37%

Male Reference

Contamination by mat. DNA or 69,XXY?

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 189 (14 peaks). 100%CV of ROX heights for peaks above 100 nt is: 4.72

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