

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	low high
18	64 -	60.78	60.78	0.00	64	59	15.7	925	1.423	1.423	0.100	1.42	64 nt	1.00	0.0	.
19	70 -	67.21	67.21	0.00	70	53	11.3	598	0.920	0.920	0.100	0.92	70 nt	1.00	0.0	.
	76 -		72.75		76					1.143	0.100		76 nt			.
20	82 -	78.14	78.14	0.00	82	59	7.2	427	0.657	0.657	0.100	0.66	82 nt	1.00	0.0	.
Ctrl: Q-fragments					Mean	57	11.4	650	1.000	1.000	0.100	1.00	(CV: 0.00)	1.00		
22	2 a	91.55	91.56	-0.01	94	2648	7.0	18601	0.715	0.770	0.093	1.00	2q14 synt.	0.93	-0.6	.
Ctrl: Synthetic control probe					Mean	2648	7.0	18601	0.715	0.770	0.093	1.00	(CV:)	0.93		
27	5 A	127.97	127.94	0.03	130	3206	6.8	21696	0.834	0.842	0.025	0.96	c 5q31.1	0.99	-0.3	.
28	4 A	133.87	133.89	-0.02	136	3339	7.2	24199	0.930	0.895	0.028	0.90	c 4q11	1.04	1.2	.
32	6 A	152.90	152.82	0.08	154	4358	7.0	30650	1.178	1.187	0.019	1.73	c 6p21.3	0.99	-0.5	.
35	3 A	172.18	172.00	0.18	172	3957	7.0	27564	1.059	1.076	0.031	0.97	c 3p22	0.98	-0.6	.
42	10 B	221.02	220.70	0.32	220	2400	7.3	17426	1.079	1.072	0.038	0.81	c 10q22	1.01	0.2	.
46	16 B	258.94	258.40	0.54 *	256	2524	7.6	19238	1.191	1.153	0.031	1.06	c 16q24.3	1.03	1.2	.
49	16 B	275.04	274.60	0.44	274	1586	7.4	11787	0.730	0.775	0.035	0.63	c 16q22.1	0.94	-1.3	.
53	3 C	310.82	310.47	0.35	310	2053	7.9	16159	1.022	1.008	0.043	0.67	c 3p25.3	1.01	0.3	.
56	3 C	329.52	329.10	0.42	328	1747	8.8	15308	0.968	0.974	0.039	0.70	c 3q12	0.99	-0.2	.
63	5 C	382.62	382.93	-0.31	382	1805	8.8	15959	1.010	1.018	0.040	0.72	c 5q33.1	0.99	-0.2	.
66	2 D	407.15	407.60	-0.45	409	1503	9.4	14117	1.213	1.192	0.023	1.47	c 2p14	1.02	0.9	.
69	1 D	434.56	434.96	-0.40	436	963	9.9	9521	0.818	0.805	0.018	1.30	c 1p36	1.02	0.8	.
72	13 D	460.36	460.65	-0.29	463	1116	10.1	11275	0.969	1.003	0.026	1.08	c 13q14.2	0.97	-1.3	.
Reference fragments					Mean	2351	8.1	18069	1.000	1.000	0.030	1.00	(CV: 0.02)	1.00		
26	Y a	115.71	115.65	0.06	118	1850	7.0	12954	0.498	0.588	0.105	1.00	c Y	0.85	-0.9	.
Male Y					Mean	1850	7.0	12954	0.498	0.588	0.105	1.00	(CV:)	0.85		
61	5 c	374.80	375.07	-0.27	373	1069	8.8	9406	0.595	0.601	0.042	0.78	176.5 5q35.1-qter ex1	0.99	-0.1	.
59	5 c	354.39	354.47	-0.08	355	1393	9.0	12568	0.795	0.813	0.036	1.22	176.5 5q35.1-qter ex	0.98	-0.5	.
Before NSD1					Mean	1231	8.9	10987	0.695	0.707	0.039	1.00	(CV: 0.01)	0.98		
57	5 c	337.99	337.62	0.37	337	693	9.0	6206	0.393	0.378	0.022	0.66	176.6 NSD1 exon 1a	1.04	0.7	.
34	5 a	166.21	166.16	0.05	166	3504	7.0	24537	0.943	0.969	0.047	0.78	176.6 NSD1 exon 1	0.97	-0.5	.
55	5 c	319.79	319.49	0.30	319	1386	8.2	11298	0.715	0.701	0.024	1.08	176.6 NSD1 exon 2	1.02	0.6	.
52	5 c	299.91	299.81	0.10	301	1010	8.0	8043	0.509	0.510	0.027	0.71	176.6 NSD1 exon 3	1.00	0.0	.
29	5 a	141.39	141.37	0.02	142	3537	6.7	23779	0.914	0.944	0.021	1.68	176.6 NSD1 exon 4	0.97	-1.4	.
50	5 b	283.61	283.29	0.32	283	1381	7.6	10561	0.654	0.639	0.033	0.73	176.6 NSD1 exon 5	1.02	0.4	.
47	5 b	267.14	266.67	0.47	265	963	7.7	7390	0.458	0.443	0.023	0.74	176.6 NSD1 exon 6	1.03	0.6	.
37	5 a	185.26	185.20	0.06	184	3554	7.1	25378	0.975	1.010	0.023	1.64	176.6 NSD1 exon 7	0.97	-1.5	.
44	5 b	240.39	239.87	0.52 *	238	2652	7.3	19343	1.198	1.235	0.041	1.15	176.6 NSD1 exon 8	0.97	-0.9	.
51	5 c	291.55	291.35	0.20	292	2087	7.8	16375	1.036	1.004	0.045	0.84	176.6 NSD1 exon 9	1.03	0.7	.
39	5 b	201.27	201.34	-0.07	202	3523	7.4	25940	1.606	1.654	0.097	0.64	176.6 NSD1 exon 10	0.97	-0.5	.
45	5 b	249.29	248.61	0.68 *	247	1611	7.4	11995	0.743	0.718	0.034	0.79	176.6 NSD1 exon 11	1.03	0.7	.
70	5 d	443.97	444.30	-0.33	445	661	10.0	6632	0.570	0.527	0.032	0.63	176.6 NSD1 exon 12	1.08	1.3	.
31	5 a	146.50	146.37	0.13	148	4165	6.8	28476	1.094	1.092	0.027	1.53	176.6 NSD1 exon 13	1.00	0.1	.
43	5 b	229.87	229.39	0.48	229	2142	7.0	15003	0.929	0.963	0.046	0.79	176.6 NSD1 exon 14	0.97	-0.7	.
58	5 c	346.26	346.03	0.23	346	635	8.7	5495	0.348	0.343	0.017	0.78	176.6 NSD1 exon 15	1.01	0.3	.
33	5 a	159.18	159.01	0.17	160	2565	7.0	17925	0.689	0.674	0.024	1.04	176.6 NSD1 exon 16	1.02	0.6	.
41	5 b	211.77	211.49	0.28	211	1602	7.3	11631	0.720	0.714	0.025	1.06	176.6 NSD1 exon 17	1.01	0.3	.
65	5 d	399.12	399.61	-0.49	400	1575	9.4	14748	1.267	1.296	0.036	1.34	176.6 NSD1 exon 18	0.98	-0.8	.
68	5 d	426.01	426.42	-0.41	427	1349	9.8	13169	1.132	1.109	0.040	1.04	176.6 NSD1 exon 19	1.02	0.6	.
67	5 d	416.77	417.23	-0.46	418	701	9.5	6679	0.574	0.550	0.031	0.67	176.6 NSD1 exon 20	1.04	0.8	.
71	5 d	453.10	453.20	-0.10	454	1765	9.9	17511	1.505	1.495	0.038	1.47	176.6 NSD1 exon 21	1.01	0.2	.
60	5 c	363.95	364.06	-0.11	364	1961	9.0	17674	1.118	1.180	0.039	1.14	176.6 NSD1 exon 22	0.95	-1.6	.
36	5 a	177.43	177.28	0.15	178	3534	7.0	24871	0.956	1.009	0.036	1.07	176.6 NSD1 exon 23	0.95	-1.5	.
NSD1					Mean	2023	8.0	15444	0.877	0.882	0.035	1.00	(CV: 0.03)	1.00		
64	5 d	390.88	391.19	-0.31	391	1194	9.3	11161	0.959	0.998	0.048	1.01	180.0 5q34-q35	0.96	-0.8	.
38	5 b	193.23	193.09	0.14	193	3489	7.2	25128	1.556	1.564	0.077	0.99	180.6 5q35.3	0.99	-0.1	.
After NSD1					Mean	2342	8.3	18145	1.257	1.281	0.063	1.00	(CV: 0.02)	0.98		
Mean values				0.07	2098	8.1	16114	0.915	0.922	0.036	3		0.99	Total of all except		
Standard deviations				0.31	(Coef. of variance: 0.423)			0.299	0.305				0.04	Ctrl and '?' peaks		
Quality assessment					Quality limits	Quality										
Mean A-group area / mean Q-frag. area					>0.65 (1.50)	40.04										
Mean height of first probes AB					> 450 (800)	3053										
Mean height of last probes CD					> 280 (500)	1531										
Ratio of mean heights AB/CD ('slope')					<3.00 (2.50)	1.99										
CV of Control Probes					<0.20 (0.15)	0.02										
8 unidentified peak areas / 43 peak areas					< (0.02)	0.02	high									

Weighted mean ratios are tested for being outside ratio 1±0.13
 One-tailed significance is high for p<=1%, and low for p<=5%.
 Individual peaks having normalized area > 4.0 SD from the ref.
 mean and ratio <0.65 or >1.3 indicate 'abnormal' probe area.

Female & male ref.
 Normal probes

1 quality warning!

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 516 (14 peaks), 100*CV of ROX heights for peaks above 100 nt is: 10.67

(Ctrl probes are used for quality evaluation only)