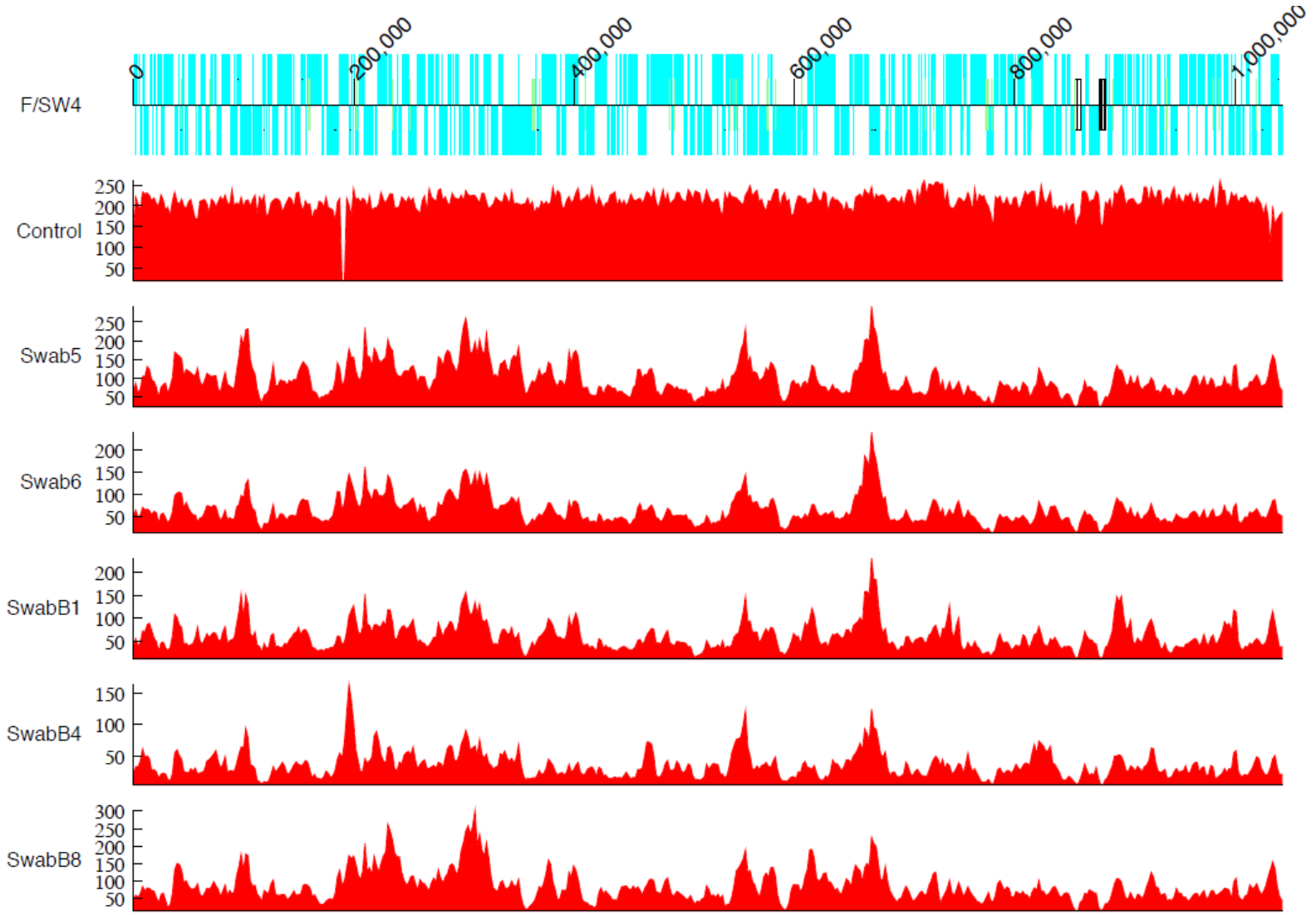
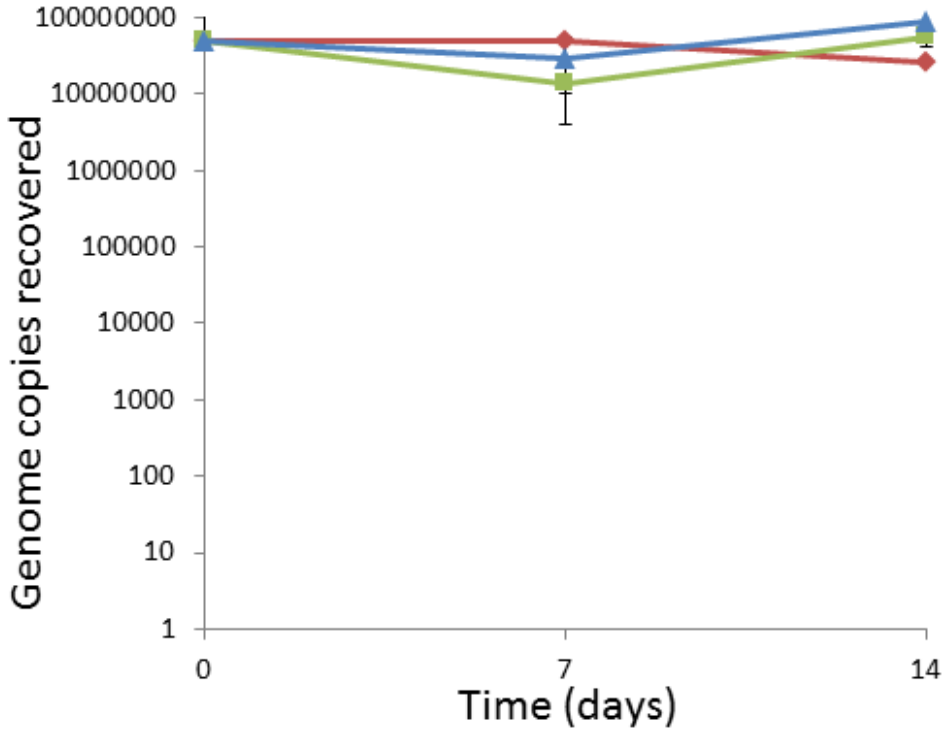
Supplemental files

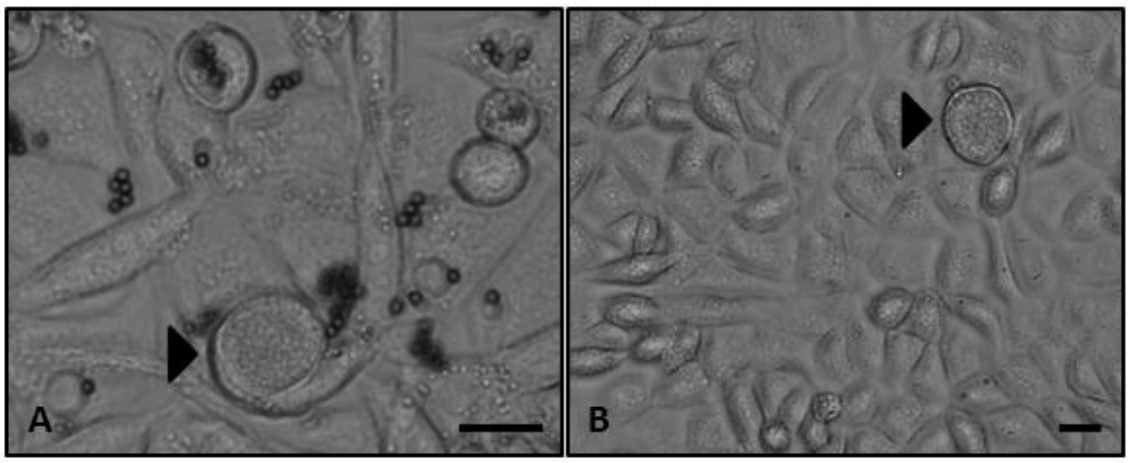
Supplemental Figure S1. Moving window plots of chromosome coverage of the sequence data from a cultured control strain and five IMS-MDA clinical samples mapped against a reference genome (F/SW4). The samples that have been subject to MDA show far greater variation in coverage than the control sample. Above the plots is a representation of the reference genome with annotated coding sequences coloured in blue, tRNAs in green, rRNA operons indicated by boxes and a scale indicating base position.



Supplemental Figure S2: Recovery of amplified *C. trachomatis* DNA after storage of IMS beads at a series of temperatures for up to 14 days. The blue line indicates storage at -20°C, the green line indicates storage at +4°C and the red line indicates storage at +20°C. Error bars indicate standard deviation from duplicate experiments.



Supplemental Figure S3. McCoy cells infected with *C. trachomatis* samples post-IMS, shown by phase contrast microscopy. A. Inclusion (indicated with an arrowhead) in a confluent McCoy cell monolayer, produced after infection using Dynabead substrate. Dynabeads (2.8 μm diameter) can also be seen. **B.** Inclusion (indicated with an arrowhead) in a confluent McCoy cell monolayer, produced after infection with *C. trachomatis* eluted from Dynabeads post-IMS. Scale bar indicates 20 μm in both images.



Supplemental Table S1. Effect of MDA on dilutions of Chlamydial DNA.
*: estimated value from serial dilution.

Sample	Sample DNA concen-tration (pg/μl)	Sample *Ct* genome copies (/μl)	Approx sample % *Ct* DNA	Post-MDA DNA concen-tration (pg/μl)	Post-MDA *Ct* genome copies (/μl)	Post-MDA % *Ct* DNA	Increase in amount *Ct* DNA	Reduction in % *Ct* DNA (fold)
A	3,480	740,000	21	792,000	21,400,000	2.7	578	8
B	7,140	530,000	7	720,000	19,300,000	2.7	728	2.5
C	5,300	300,000	5.7	746,000	9,630,000	1.3	642	4.3
D	4,980	12,000	0.2	782,000	521,000	0.07	868	2.9
E	5,680	3,700	0.07	816,000	184,000	0.02	994	3.5
F	5,800	925*	0.02*	752,000	31,300	0.004	677*	5*

Supplemental Table S2. Comparison of sequence data derived by extraction or IMS-MDA.

*Extracted DNA samples run with read length of 100 and 36 samples per lane; IMS samples run with read length of 75 cycles and 48 samples per lane. All samples were run on Illumina Hiseq machines and all produced 100% chromosome coverage.

Sample	Extracted DNA*					IMS-MDA*					SNPs between extracted and IMS samples	*ompA* genotype
	Input copies (per μl)	Total yield for tag (kb)	Depth of coverage (mean)	Chromosome CV (std/mean)	Hetero-geneous sites	Post-MDA copies (per μl)	Total yield for tag (kb)	Depth of coverage (mean)	Chromosome CV (std/mean)	Hetero-geneous sites		
R26833	26,500,000	362,066	294.3	0.10	5	146,000,000	594,171	93.7	0.35	16	0	E
R33512	19,000,000	385,786	82.3	0.15	4513	6,450,000	571,539	15.6	0.47	5258	0	K & E
R32100	17,900,000	59,360	127.4	0.13	9	546,000,000	661,294	237.1	0.33	7	0	E
R28017	13,800,000	49,623	37.9	0.20	36	218,000,000	504,548	180.7	0.38	10	0	E
R4175	10,500,000	451,126	146.5	0.10	11	25,700,000	556,219	127.5	0.48	11	0	G
R36176	6,090,000	459,234	156.9	0.09	11	525,000	121,648	37.4	0.26	44	0	G
R27091	4,790,000	63,087	49.4	0.17	25	193,000,000	548,186	86.2	0.70	22	0	E
R3059	1,040,000	539,129	156.6	0.11	13	150,000	65,361	14.4	0.33	875	0	G

Supplemental Table S3. Analysis of data from archived samples successfully sequenced after IMS-MDA.

Chromosome coverage was determined through mapping against the genome of strain L2/434 (EMBL accession AM884176). N/A: samples from previous culture in McCoy cells. M: samples from males. All samples were run on Illumina Hiseq machines and all produced 100% chromosome coverage.

Sample	Source	Location	Genome copies post IMS-MDA (per μl)	Read length (bp)	Tags per lane	Total yield for tag (kb)	Depth of coverage (mean)	Chromosome CV (std/mean)	Reads mapping to human genome (%)	*ompA* genotype
HPA1IMS	rectal (M)	UK	10,000,000	100	48	524,824	23.2	0.60	6.6	L2b
HPA17IMS	rectal (M)	UK	6,000,000	100	24	2,260,806	333.7	0.40	9.2	L2b
HPA21IMS	rectal (M)	UK	100,000,000	100	24	2,848,198	1137.2	0.44	26.1	L2b
HPA27IMS	rectal (M)	UK	28,000,000	100	48	527,731	52.1	0.42	0.2	L2b
HPA29IMS	rectal (M)	UK	10,000,000	100	48	445,825	28.1	0.60	1.0	L2b
HPA31IMS	rectal (M)	UK	2,000,000	100	48	488,732	98.1	0.65	57.5	L2b
HPA34IMS	rectal (M)	UK	1,600,000	100	48	553,242	18.6	0.65	84.5	L2b
LGV98	M	South Africa	6,000,000	75	13	908,726	170.9	0.56	N/A	L1
LGV913	M	South Africa	20,000,000	75	13	808,490	671.3	0.57	N/A	L1
LGV1339	urethral (M)	South Africa	5,000,000	75	13	749,073	396.8	0.88	N/A	L1

Supplemental Table S4. ENA Accession numbers.

Sample	Data from	ENA accession number		Sample	Data from	ENA accession number
Control L2	Table 1	ERR033884		R26833extract	Table S2	ERR111601
Dilution1		ERR173903		R33512extract		ERR111613
Dilution2		ERR173907		R32100extract		ERR111602
Dilution3		ERR173904		R28017extract		ERR111603
Dilution4		ERR173908		R4175extract		ERR111614
Dilution5		ERR173905		R36176extract		ERR111611
Dilution6		ERR173909		R27091extract		ERR111604
Dilution7		ERR173906		R3059extract		ERR111612
Dilution8		ERR173910		R26833IMS		ERR111562
GA3	Table 3	ERR140770		R33512IMS		ERR111572
GA3MDA		ERR140788		R32100IMS		ERR111563
GA4		ERR140785		R28017IMS		ERR111565
GA4MDA		ERR140789		R4175IMS		ERR111573
GA5		ERR140772		R36176IMS		ERR111570
GA5MDA		ERR140790		R27091IMS		ERR111566
GA9		ERR140786		R3059IMS		ERR111571
GA9MDA		ERR140791		H1IMS	Table S3	ERR164659
GA10MDA		ERR140792		H17IMS		ERR140766
GA11		ERR140787		H21IMS		ERR140767
GA11MDA		ERR140793		H27IMS		ERR164661
GA12		ERR140776		H29IMS		ERR164662
GA12MDA		ERR140794		H31IMS		ERR164663
Swab1	Table 4	ERR024694		H34IMS		ERR164665
Swab2		ERR024698		LGV98		ERR071990
Swab3		ERR024699		LGV913		ERR071991
Swab5		ERR024700		LGV1339		ERR071992
Swab6		ERR024701				
Swab7		ERR024702				
Swab8		ERR024703				
Swab B1		ERR173901				
Swab B4		ERR034345				
Swab B8		ERR034346				
Swab B11		ERR173902				

Supplemental Table S5. Variations to the standard protocol.

rpm: revolutions per minute; ops: oscillations per second

Source	Vol beads used	Vol Antibody	# washes	Incubation temperature	Incubation movement
Swab5	3	25	3	4 ^{o}C	Platform, 50 ops
Swab6	3	25	3	4 ^{o}C	Platform, 50 ops
SwabB1	3	2.75	2	20 ^{o}C	Shaker, 200 rpm
SwabB4	3	25	3	4 ^{o}C	Platform, 50 ops
SwabB8	3	25	3	4 ^{o}C	Platform, 50 ops
Cultured, 2 wells of 24WT	5	0.6	2	20 ^{o}C	Shaker, 200 rpm
Archived, passaged	2	0.3	2	20 ^{o}C	Platform, 50 ops