

Supplemental Table S13. Mycoplasma contamination

Species ^a	Genome (bp)	HEK293			A23		
		Reads ^b	Read rate ($\times 10^{-6}$) ^c	Copy number ($\times 10^{-2}$) ^d	Reads ^b	Read rate ($\times 10^{-6}$) ^e	Copy number ($\times 10^{-2}$) ^f
<i>M. hominis</i> ATCC 23114	665 445	0	0.0	0.0	262	7.9	5.6
<i>M. hyorhinae</i> MCLD	829 709	47	1.2	0.9	195	5.9	3.4
<i>M. fermentans</i> M64	1 118 751	0	0.0	0.0	2060	62.0	26.3
<i>A. laidlawii</i> PG-8A ^g	1 496 992	0	0.0	0.0	0	0.0	0.0
<i>M. pneumoniae</i> M129	816 394	0	0.0	0.0	0	0.0	0.0

^a RefSeq numbers NC_013511.1, NC_017519.1, NC_014921.1, NC_010163.1, NC_000912.1, respectively.

^b Based on 1 bp mismatch. Identical read numbers obtained using 4 bp mismatch.

^c (Mycoplasma reads/{aligned HEK293 reads = 40 128 368}) $\times 10^6$ (c.f. Supplemental Tables S3, S4).

^d $2 \cdot (\text{Mycoplasma reads}/\{(\text{aligned HEK293 reads} = 40\,128\,368) - (\text{HEK293 mitochondrial reads} = 153\,367)\}) \cdot (\{\text{human genome} = 3\,088\,269\,832\text{ bp}\}/\text{mycoplasma genome}) \times 100$ (c.f. Supplemental Tables S3, S4).

^e (Mycoplasma reads/{aligned A23 reads = 33 234 329}) $\times 10^6$ (c.f. Supplemental Tables S3, S4).

^f $2 \cdot (\text{Mycoplasma reads}/\{(\text{aligned A23 reads} = 33\,234\,329) - (\text{A23 mitochondrial reads} = 95\,975)\}) \cdot (\{\text{hamster genome} = 2\,368\,906\,908\text{ bp}\}/\text{mycoplasma genome}) \times 100$ (c.f. Supplemental Tables S3, S4).

^g *Acholeplasma laidlawii* PG-8A.