

Table S2 Read mapping statistics.

Sample	Number of sequenced reads	Aligned reads (%)
Reference strain, untreated, 1	11 568 834	79.98
Reference strain, untreated, 2	14 894 686	88.54
Reference strain, untreated, 3	15 360 372	81.30
Reference strain, CdCl ₂ treated, 1	14 327 487	80.41
Reference strain, CdCl ₂ treated, 2	15 640 405	82.04
Reference strain, CdCl ₂ treated, 3	14 210 634	82.39
<i>ΔatfA</i> mutant, untreated, 1	15 698 460	88.04
<i>ΔatfA</i> mutant, untreated, 2	14 517 442	88.41
<i>ΔatfA</i> mutant, untreated, 3	16 011 236	90.19
<i>ΔatfA</i> mutant, CdCl ₂ treated, 1	14 219 473	91.1
<i>ΔatfA</i> mutant, CdCl ₂ treated, 2	14 747 338	89.53
<i>ΔatfA</i> mutant, CdCl ₂ treated, 3	15 069 078	90.16