

Species	Genome (Mb)	Coverage (X fold)	C	CG	CHG	CHH	CA	CC	CT
<i>Oryza sativa</i>	372.6	9.6	18.6%	50.0%	27.4%	5.2%	ND	ND	ND
<i>Selaginella moellendorffii</i>	101.1	9.2	5.1%	12.5%	9.0%	.92%	ND	ND	ND
<i>Physcomitrella patens</i>	454.2	6.0	24.6%	29.5%	29.7%	23.2%	ND	ND	ND
<i>Chlorella</i> sp. NC64A	42.4	3.1	20.7%	80.5%	2.2%	.25%	ND	ND	ND
<i>Volvox carteri</i>	125.9	7.9	.77%	2.6%	.08%	.08%	ND	ND	ND
<i>Tetraodon nigroviridis</i>	302.3	7.3	10.7%	65.5%	.25%	.34%	ND	ND	ND
<i>Ciona intestinalis</i>	141.2	15.3	4.7%	21.6%	.28%	.28%	ND	ND	ND
<i>Apis mellifera</i>	231.0	11.3	.28%	.51%	.11%	.16%	ND	ND	ND
<i>Tribolium castaneum</i>	151.3	2.3	.12%	.11%	.12%	.12%	ND	ND	ND
<i>Bombyx mori</i>	431.8	4.7	.24%	.71%	.08%	.09%	ND	ND	ND
<i>Drosophila melanogaster</i>	162.4	5.6	.11%	.12%	.11%	.11%	ND	ND	ND
<i>Nematostella vectensis</i>	297.4	10.8	1.8%	9.4%	.16%	.15%	ND	ND	ND
<i>Phycomyces blakesleeanus</i>	51.1	11.8	1.3%	4.9%	ND	ND	.78%	.82%	.35%
<i>Coprinopsis cinerea</i>	35.9	14.3	4.2%	12.2%	ND	ND	1.4%	1.0%	.69%
<i>Laccaria bicolor</i>	58.7	11.3	5.4%	20.3%	ND	ND	1.3%	1.0%	.52%
<i>Postia placenta</i>	69.0	15.1	5.1%	12.1%	ND	ND	2.4%	2.2%	2.1%
<i>Uncinocarpus reesii</i>	22.1	23.0	1.9%	.67%	ND	ND	2.1%	1.8%	3.0%

Table S1. Bulk methylation statistics for the nuclear genome of indicated organisms. ND = not determined; for the last three fungal species, the mitochondrial genome sequence was not available. NA = not applicable.