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Read Depth Analyses

For all 15 strains of the *Armillaria gallica* fungus the global average read depths and the total number of sites, based on the reference genome, are shown in table 1.

Table 1. Goba Average Read Depths and Number of Reads for Each Strain

Strain	Global Average Read Depth	Total Global Number of Reads
Ar73	111.0507	69955093
Ar109	117.6863	70143802
Ar119	112.4868	70015910
Ar142	109.3741	70068064
Ar159	104.3773	69875550
Ar170	112.3987	70033946
Ar174	113.4283	70022954
Ar175	73.79959	69545937
Ar176	73.21531	69583274
Ar179	117.2196	70061598
Ar188	63.61699	68627951
Ar194	67.88522	69488072
Ar196	113.9182	70027951
Ar201	68.39596	69488227
Ar213	110.9612	69988055

Table 1 shows that all fifteen strains which we can work with have a similar number of

sites which reads were aligned to. This number of aligned reads was between 68.6 million and 70.1 million for all strains. The global average read depths (average read depth of all sites where reads were aligned) varied much more. The low end for global average read depths was for the strain Ar188 which had average of 63.6 reads, when reads were aligned, and the high end for average read depth was 117.7 for the strain Ar109. Hao had mentioned that Ar 188 was not used in his analyses because it was different in some way to the other strains. Ar188 is the strain with the lowest number of reads and lowest total number of reads aligned.

The average number of reads within strains was also calculated, these results can be found in figures , , , and .

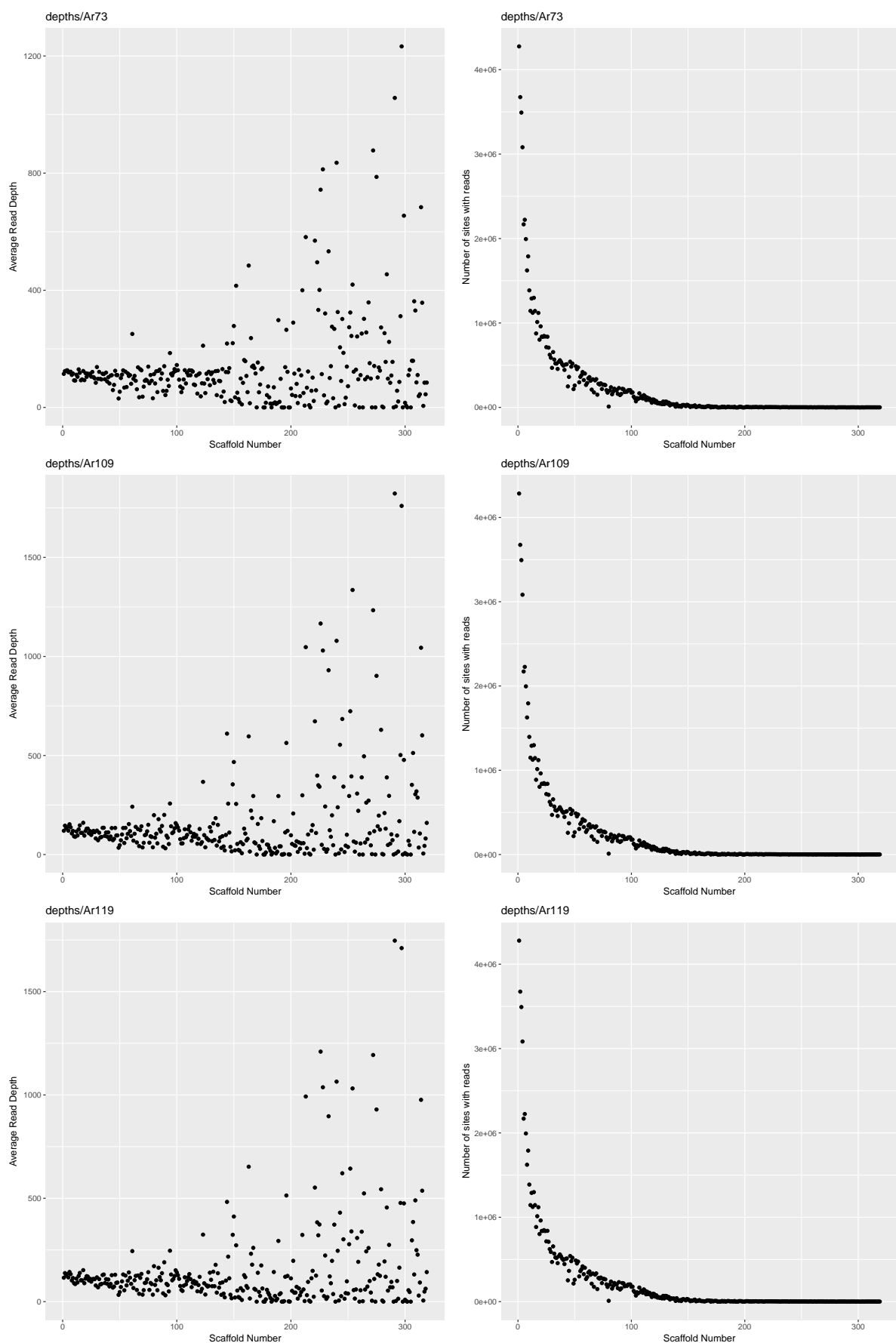


Figure 1. Average Read Depth Per scaffold, Ar:73, 109, 119. Left are the average read depth vs scaffold number graphs and Right are the total number of sites with reads aligned to them per scaffold

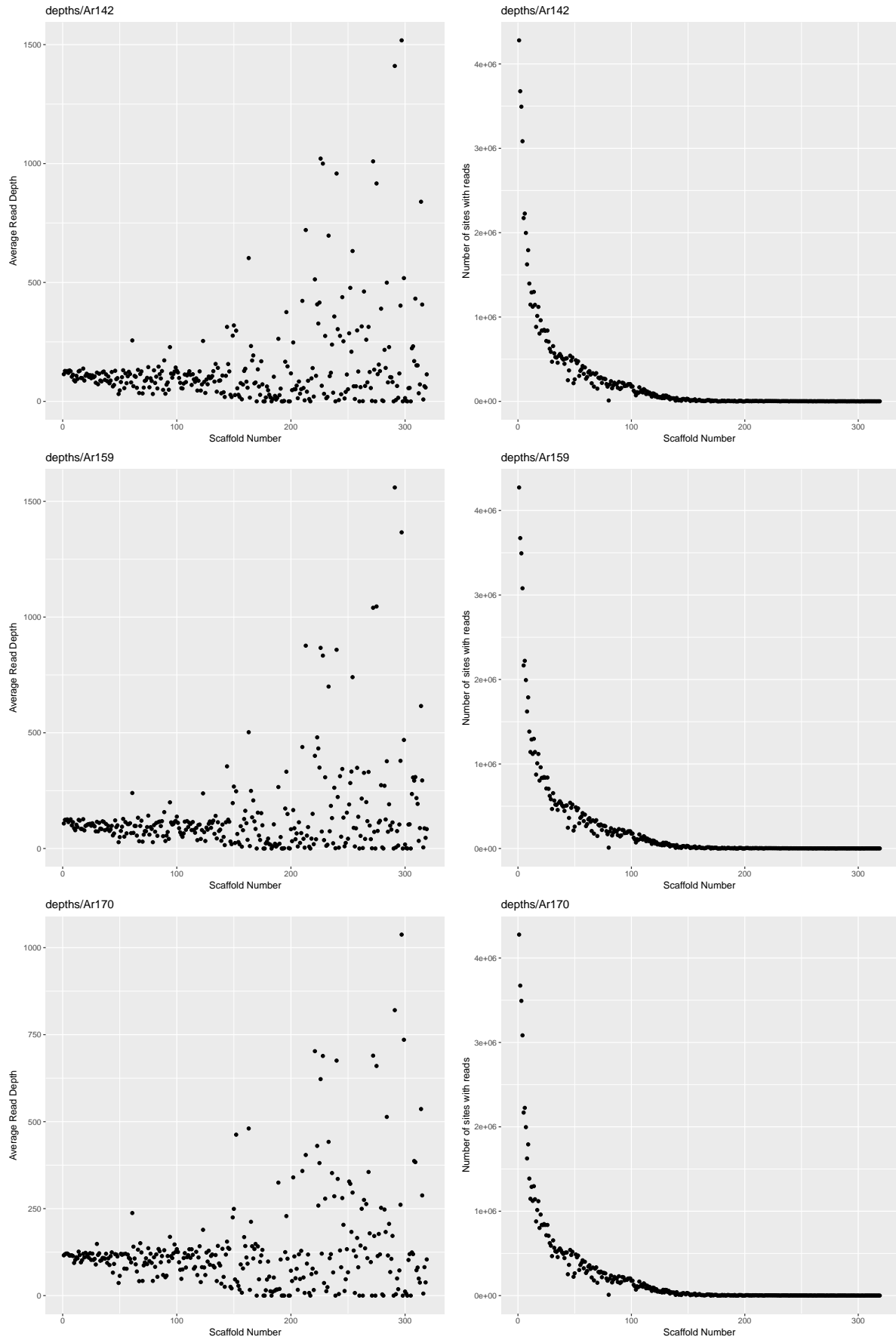


Figure 2. Average Read Depth Per scaffold, Ar: 142, 159, 170. Left are the average read depth vs scaffold number graphs and Right are the total number of sites with reads aligned to them per scaffold

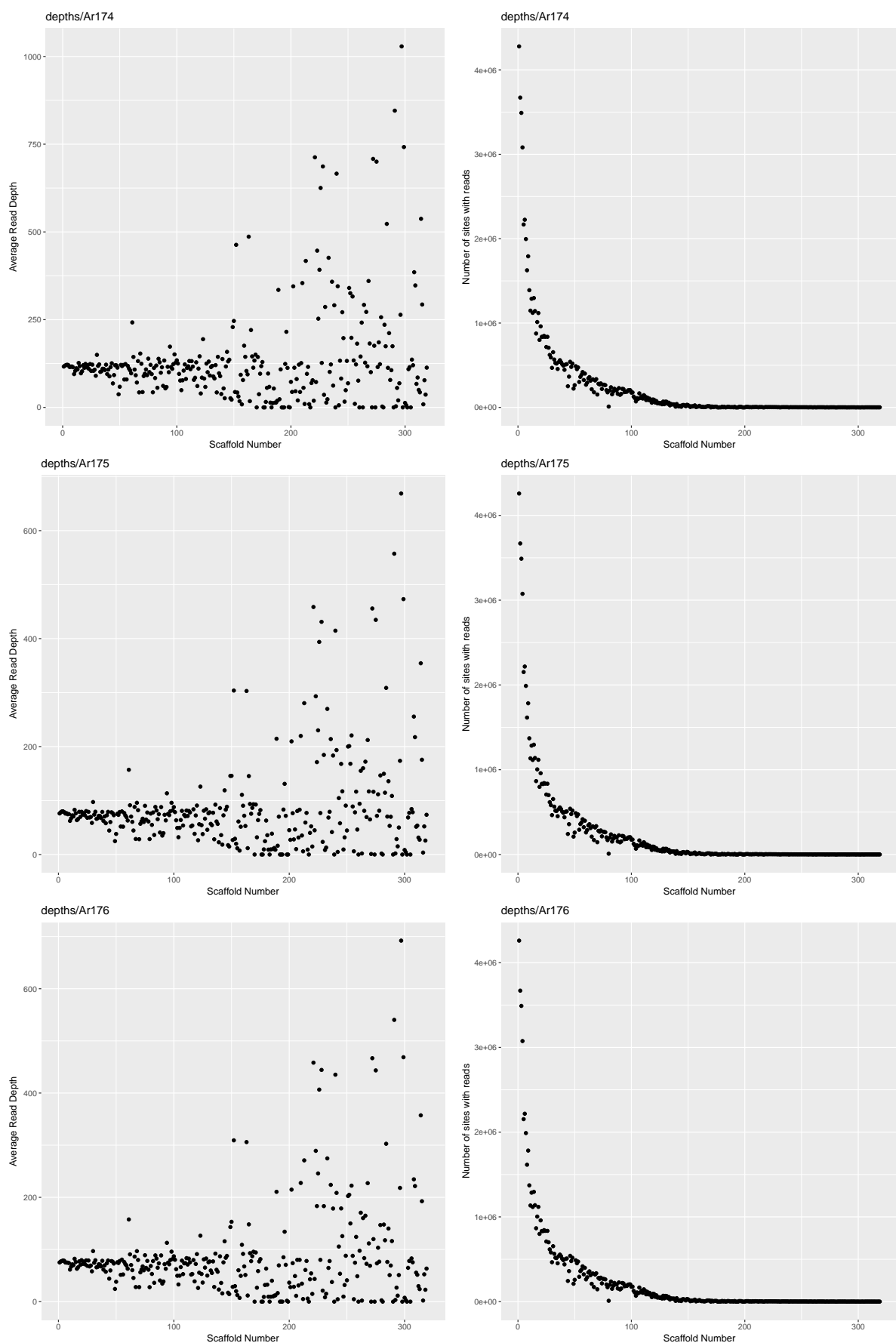


Figure 3. Average Read Depth Per scaffold, Ar:174, 175, 176. Left are the average read depth vs scaffold number graphs and Right are the total number of sites with reads aligned to them per scaffold

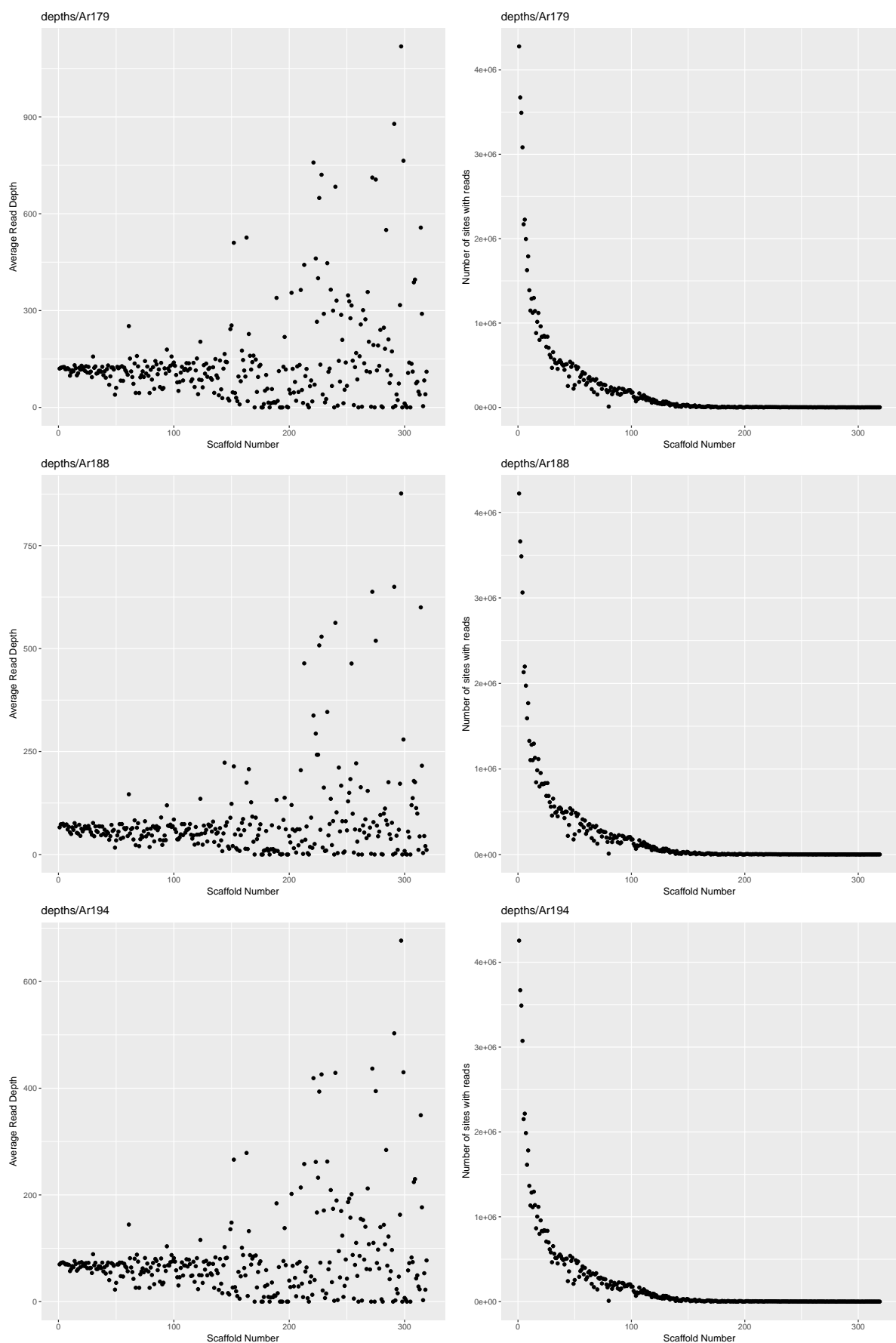


Figure 4. Average Read Depth Per scaffold, Ar:179, 188, 194. Left are the average read depth vs scaffold number graphs and Right are the total number of sites with reads aligned to them per scaffold

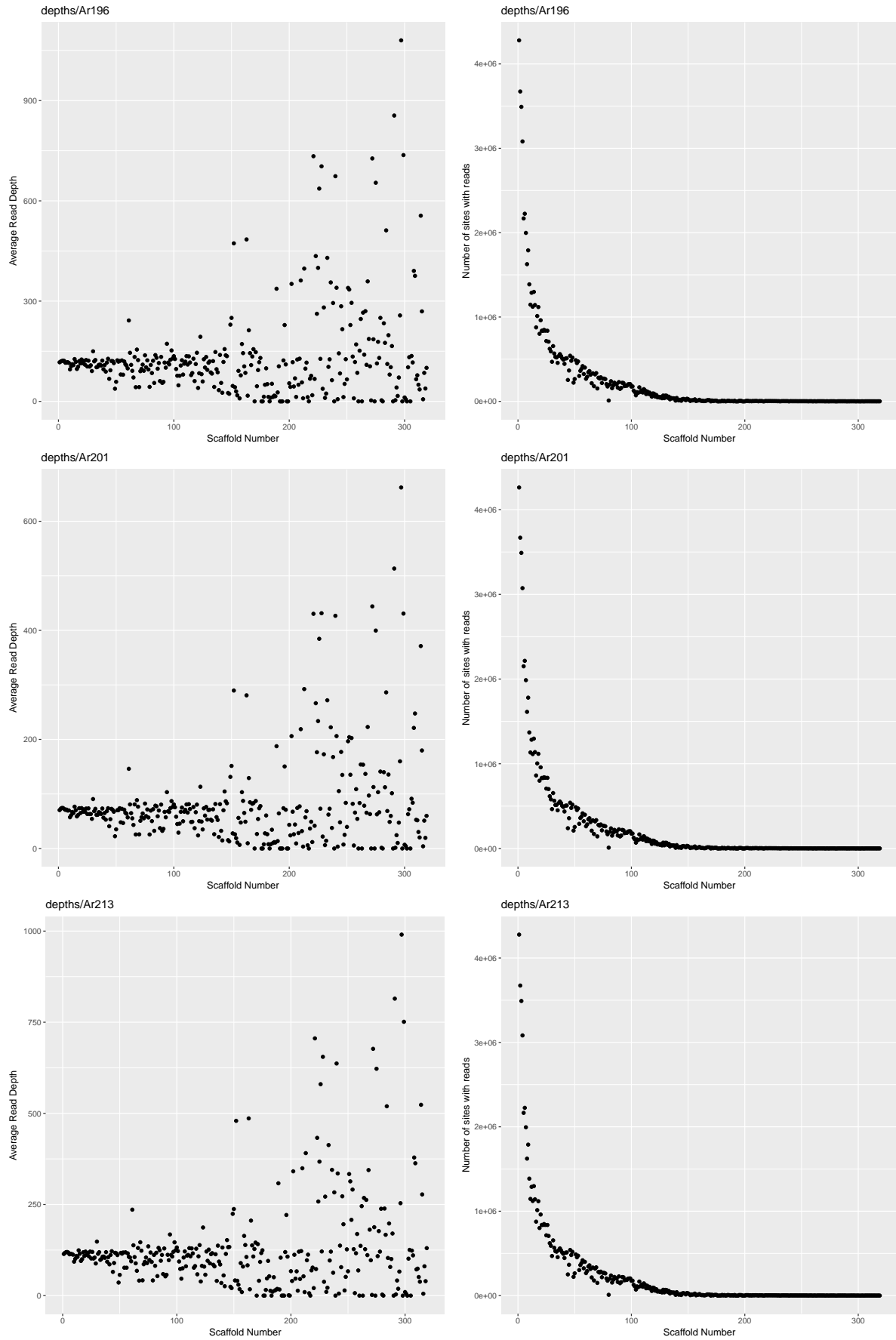


Figure 5. Average Read Depth Per scaffold, Ar:196, 201, 213. Left are the average read depth vs scaffold number graphs and Right are the total number of sites with reads aligned to them per scaffold

Indel Analysis

Indels in *Armillaria gallica*

Through previous studies on the *Armillaria gallica* fungus, several strains were sequenced in Illumina. These strains were analyzed using samtools and an additional package called bcftools.

Through the use of bcftools, labels were added to the output which indicated various other information about the indel found such as: maximum number of reads supporting an indel, raw read depth, the number of reads that support the indel and other information.

Strain No.	Scaffold No.	Location	No. of Reads Supporting	Raw Read Depth
Ar159	1	7762	41	116
	1	10784	28	100
	1	16154	3	85
Ar170	1	7762	73	222
	1	10784	61	194
	1	12340	72	193
Ar174	1	7762	63	201
	1	9593	72	218
	1	10784	45	184
Ar175	1	7762	47	141
	1	10784	28	108
	1	12340	35	102
Ar176	1	7762	39	141
	1	9593	43	129
	1	10784	33	115
Ar179	1	7762	63	193
	1	9593	64	205
	1	10784	50	195
Ar188	1	7762	17	62
	1	10784	11	47
	1	12340	24	54
Ar194	1	7762	35	133
	1	10784	32	105
	1	12340	35	110
Ar196	1	7762	72	224
	1	10784	53	169
	1	12340	72	192
Ar201	1	7762	38	110
	1	10784	44	116
	1	12340	50	102
Ar213	1	7762	76	220
	1	9593	63	196
	1	10784	48	188

Figure 6. A summary table of the first three indels found in each of the strains which includes the scaffold number, the location at which the indel is found, the number of reads that support that indel and the raw read depth