

**Table S4** Illumina sequenced *P. tritici-repentis* isolate read alignment under different stringencies

	All repeats/Best hit*		No repeats/Best hit*		No repeats/Unique hit**	
	(Low Stringency)		(Medium Stringency)		(High Stringency)	
	DW7	SD20	DW7	SD20	DW7	SD20
PE alignment (M)	75.59	56.87	22.18	44.10	21.65	36.40
SE alignment (M)	5.80	9.11	0.52	3.43	0.41	2.20
Unmapped (M)	2.92	17.26	6.72	19.56	7.36	28.49
Paired read count (M)	14.71	33.54				
<b>Total read count (M)</b>	<b>29.42</b>	<b>67.09</b>				

\*Best hit = up to 4 mismatches; \*\*Unique = no mismatches; Mapping performed with SOAP2