FNBtools: A Software to Identify Homozygous Deletions in FNB Mutant Populations

Supplemental Material

Files in this Data Supplement:

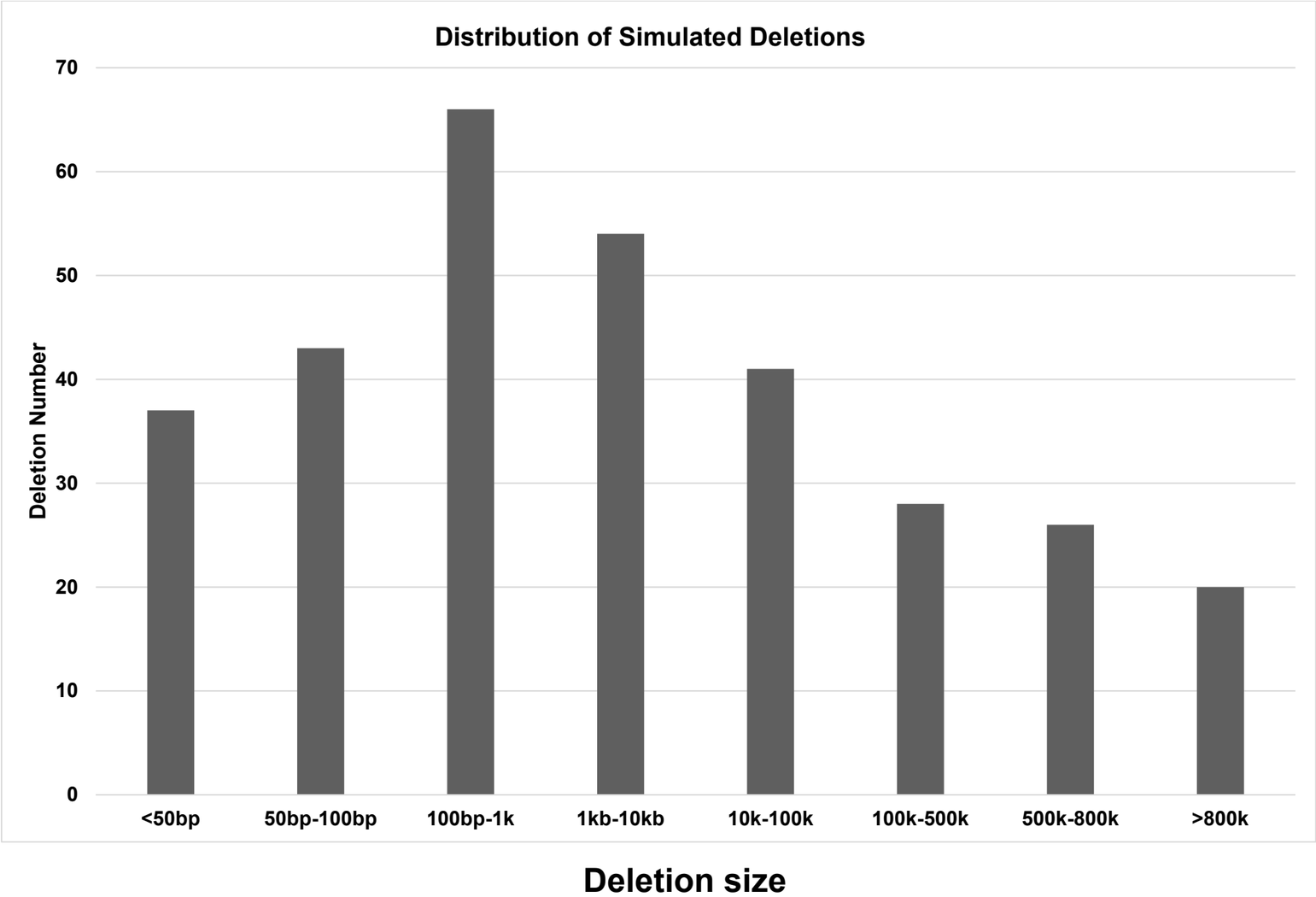
- **Supplementary_Table S1.pdf**
- **Supplementary_Table S2.pdf**
- **Supplementary_Fig_S1.pdf**
- **Supplementary_Fig_S2.pdf**
- **Supplementary_Fig_S3.pdf**
- **Supplementary_file1.excel**

Supplemental Table S1: Accuracy test for sample S1

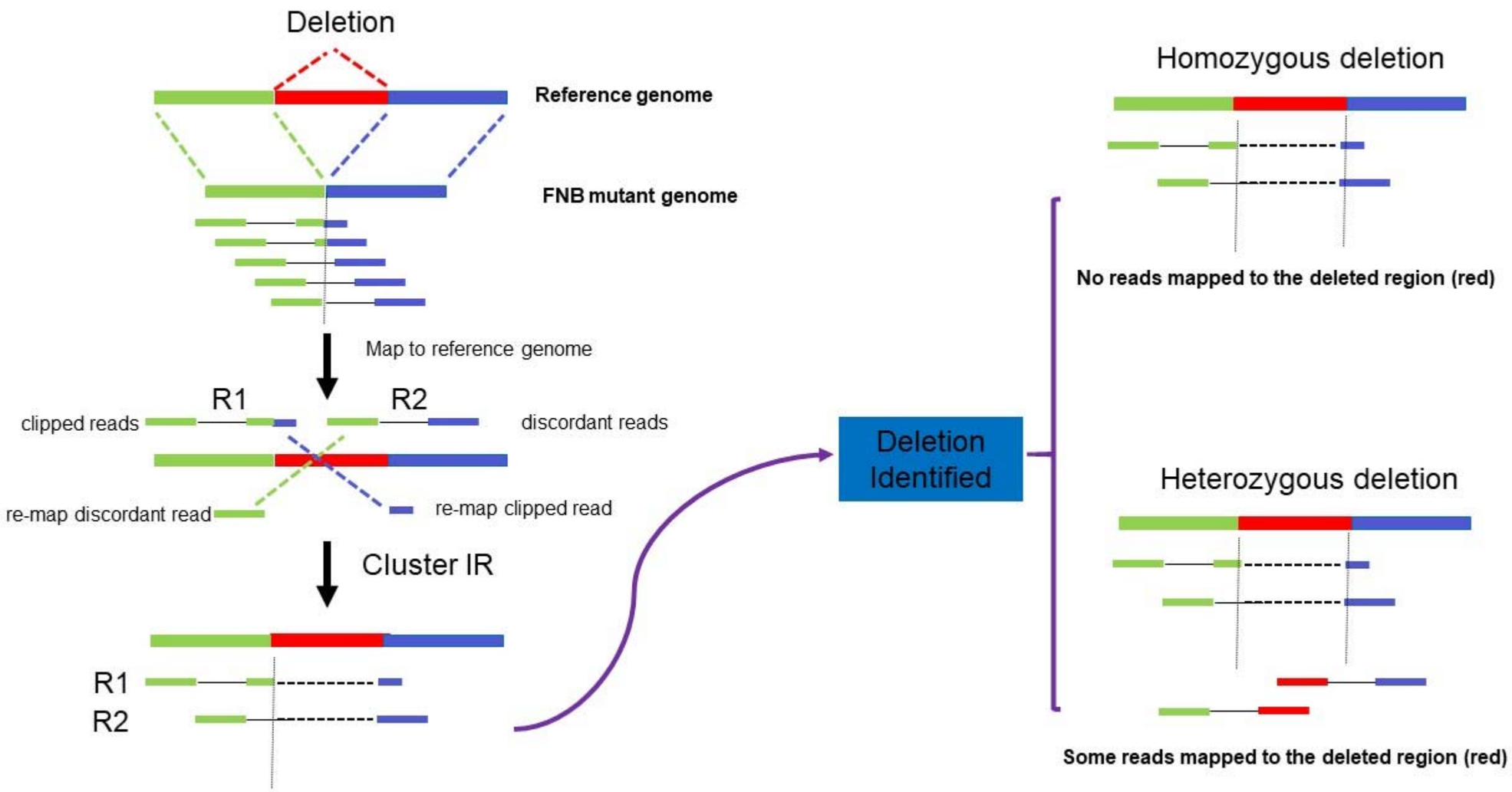
Deletion ID	Chr	Breakpoint Start	Breakpoint End	Deletion Size (bp)	Supportive Read Number	Gap Starts	Gap Ends	Del_mutant	Del_control	Homo_Unique	Confirmation
25	chr1	1284048	1284049	1	CLR=0;CRR=0;SMD=3;FLR=2;FRR=26	1284048	1284049	Yes	Yes	No	No
109	chr1	7702199	7702205	6	CLR=0;CRR=0;SMD=3;FLR=7;FRR=3	7702199	7702205	Yes	Yes	No	Yes
267	chr1	29717335	29717336	1	CLR=0;CRR=0;SMD=3;FLR=3;FRR=3	29717335	29717336	Yes	Yes	No	Yes
540	chr2	15321685	15321687	2	CLR=0;CRR=0;SMD=3;FLR=6;FRR=2	15321685	15321687	Yes	Yes	No	Yes
543	chr2	15331444	15331445	1	CLR=0;CRR=0;SMD=3;FLR=3;FRR=3	15331444	15331445	Yes	No	Yes	Yes
755	chr3	21965675	21965676	1	CLR=0;CRR=0;SMD=3;FLR=3;FRR=8	21965675	21965676	Yes	Yes	No	Yes
768	chr3	23588052	23588053	1	CLR=0;CRR=0;SMD=3;FLR=3;FRR=2	23588052	23588053	Yes	No	Yes	Yes
985	chr4	13164475	13164479	4	CLR=0;CRR=0;SMD=3;FLR=12;FRR=3	13164475	13164479	Yes	Yes	No	No
275	chr1	31035828	31035847	19	CLR=3;CRR=0;SMD=0;FLR=3;FRR=4	31035828	31035847	Yes	Yes	No	No
709	chr3	12721653	12721704	51	CLR=3;CRR=0;SMD=0;FLR=7;FRR=5	12721654	12721704	Yes	Yes	No	Yes
958	chr4	11234103	11234221	118	CLR=3;CRR=0;SMD=0;FLR=4;FRR=4	11234103	11234221	Yes	Yes	No	No
1279	chr4	43194196	43194314	118	CLR=3;CRR=0;SMD=0;FLR=16;FRR=18	43194197	43194313	Yes	Yes	No	No
1620	chr6	4956772	4956804	32	CLR=3;CRR=0;SMD=0;FLR=3;FRR=11	4956772	4956804	Yes	Yes	No	Yes
12	chr3	23588052	23588053	1	CLR=0;CRR=0;SMD=3;FLR=3;FRR=2	23588052	23588053	Yes	No	Yes	Yes
24	chr5	30952197	30952198	1	CLR=0;CRR=0;SMD=3;FLR=3;FRR=4	30952197	30952198	Yes	No	Yes	No
38	chr8	42384569	42384573	4	CLR=0;CRR=0;SMD=3;FLR=2;FRR=3	42384569	42384573	Yes	No	Yes	Yes
666	chr3	3928202	3928277	75	CLR=4;CRR=0;SMD=0;FLR=4;FRR=4	3928202	3928277	Yes	Yes	No	Yes
700	chr3	10421730	10421774	44	CLR=4;CRR=0;SMD=0;FLR=4;FRR=13	10421730	10421774	Yes	Yes	No	Yes
1	chr1	3325600	3325601	1	CLR=0;CRR=0;SMD=4;FLR=5;FRR=5	3325600	3325601	Yes	No	Yes	Yes
25	chr5	33844610	33844611	1	CLR=0;CRR=0;SMD=4;FLR=3;FRR=6	33844610	33844611	Yes	No	Yes	Yes
42	scaffold0124	26758	26759	1	CLR=0;CRR=0;SMD=4;FLR=4;FRR=2	26758	26759	Yes	No	Yes	Yes
27	chr6	30824164	30824165	1	CLR=0;CRR=0;SMD=6;FLR=6;FRR=6	30824164	30824165	Yes	No	Yes	Yes
10	chr2	26959662	26959663	1	CLR=0;CRR=0;SMD=7;FLR=6;FRR=6	26959662	26959663	Yes	No	Yes	Yes

Supplemental Table S2: Genetic linkage analysis of 12 unique homozygous deletions in sample S2

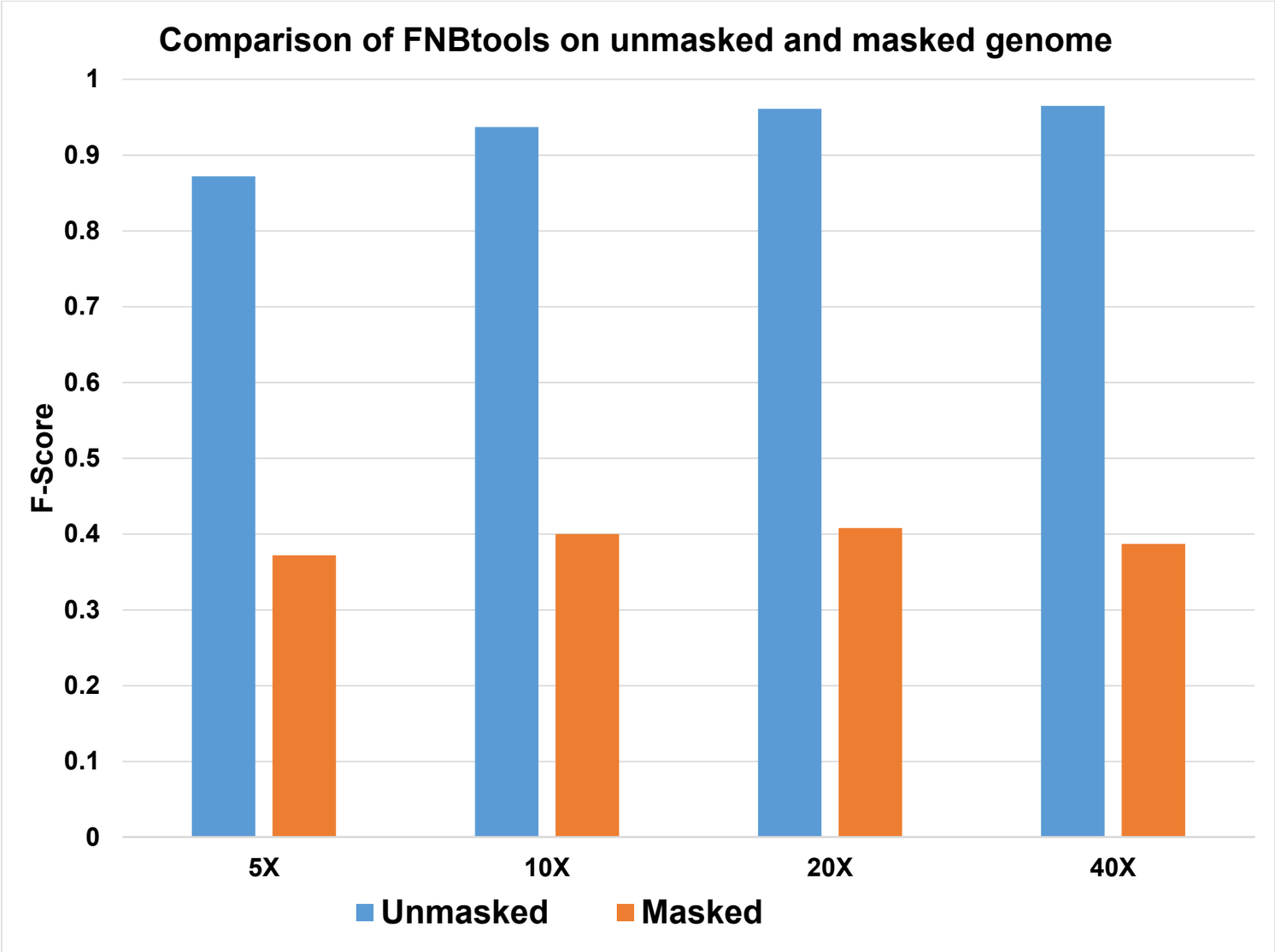
Deletion ID	Chr	Start_position	End_position	Deletion size (bp)	Supportive reads	Gap Starts	Gap Ends	Del_mutant	Del_control	Homo_Unique	Annotation	Linkage
1	chr1	42780901	42780902	1	CLR=0;CRR=0;SMD=20;FLR=20;FRR=18	42780901	42780902	Yes	No	Yes	['Medtr1g095050']	25%
2	chr2	4912716	4912717	1	CLR=0;CRR=0;SMD=8;FLR=9;FRR=8	4912716	4912717	Yes	No	Yes	['Medtr2g016200']	31%
3	chr2	29170197	29170198	1	CLR=0;CRR=0;SMD=9;FLR=8;FRR=9	29170197	29170198	Yes	No	Yes	[]	43%
4	chr3	34323306	34323314	8	CLR=0;CRR=0;SMD=19;FLR=20;FRR=19	34323306	34323314	Yes	No	Yes	['Medtr3g075410']	35%
5	chr4	28247742	28247749	7	CLR=0;CRR=0;SMD=13;FLR=14;FRR=14	28247745	28247749	Yes	No	Yes	['Medtr4g074220']	23%
6	chr4	52426842	52426846	4	CLR=0;CRR=0;SMD=23;FLR=25;FRR=24	52426842	52426846	Yes	No	Yes	['Medtr4g126140']	41%
7	chr5	2830713	2830715	2	CLR=0;CRR=0;SMD=24;FLR=25;FRR=24	2830713	2830714	Yes	No	Yes	['Medtr5g010520']	42%
8	chr5	17668358	17668360	2	CLR=0;CRR=0;SMD=16;FLR=15;FRR=15	17668358	17668360	Yes	No	Yes	[]	37%
9	chr5	41319722	41319732	10	CLR=0;CRR=0;SMD=14;FLR=19;FRR=15	41319722	41319732	Yes	No	Yes	[]	32%
10	chr7	28316601	28316609	8	CLR=0;CRR=0;SMD=20;FLR=23;FRR=26	28316603	28316609	Yes	No	Yes	['Medtr7g075260']	35%
11	chr7	48837558	48837644	86	CLR=19;CRR=0;SMD=0;FLR=22;FRR=25	48837558	48837643	Yes	No	Yes	[]	100%
12	scaffold0352	2591	2597	6	CLR=0;CRR=0;SMD=18;FLR=20;FRR=18	2591	2597	Yes	No	Yes	[]	68%



Supplemental Figure S1. Distribution of simulated deletions in *Medicago truncatula* genome A17



Supplemental Figure S2. A methodology flowchart for deletion detection. Step 1: map all reads (R1, R2, and so on) to the reference genome and extract all informative reads (IR) from SAM files. Step 2: cluster all informative reads based on mapping positions. Step 3: identify homozygous deletions according to the gap information



Supplemental Figure S3. Comparison of FNBtools performance in unmasked and masked *Medicago truncatula* genome. Significantly reduced F-scores were observed from the masked reference genome due to undetectable deletions in the masked repetitive regions.