

## Per patient final QC assessment plots after quality control and removal of low quality colonies

Page 1) Top panel: An SNV and table detailing the pairwise overlap of loci that failed filtering. The diagonal elements give the proportion of failed loci that have failed each filter. The off-diagonal elements give the proportion of failed loci that fail both the corresponding filters. Lower panel: Plot of number of per sample SNV (Caveman) calls vs Depth.

Page 2) Upper panel- Per colony VAF distribution at Caveman sites that pass all filters. Lower panel- Per colony VAF distribution at Caveman sites that are identified as germline. Boxes are filled red if the VAF is less than 0.35 with significance level 0.01. Boxes are filled grey if less than 100 mutations are recorded. Borders are red if median depth  $\leq 7$ . Colonies corresponding to filled red or grey boxes were subsequently excluded.

Page 3) Upper panel- Number of loci failing each filter on a log scale. Lower panel- Number of loci that uniquely fail each filter on a log scale. This measures the effect of removing a single filter.

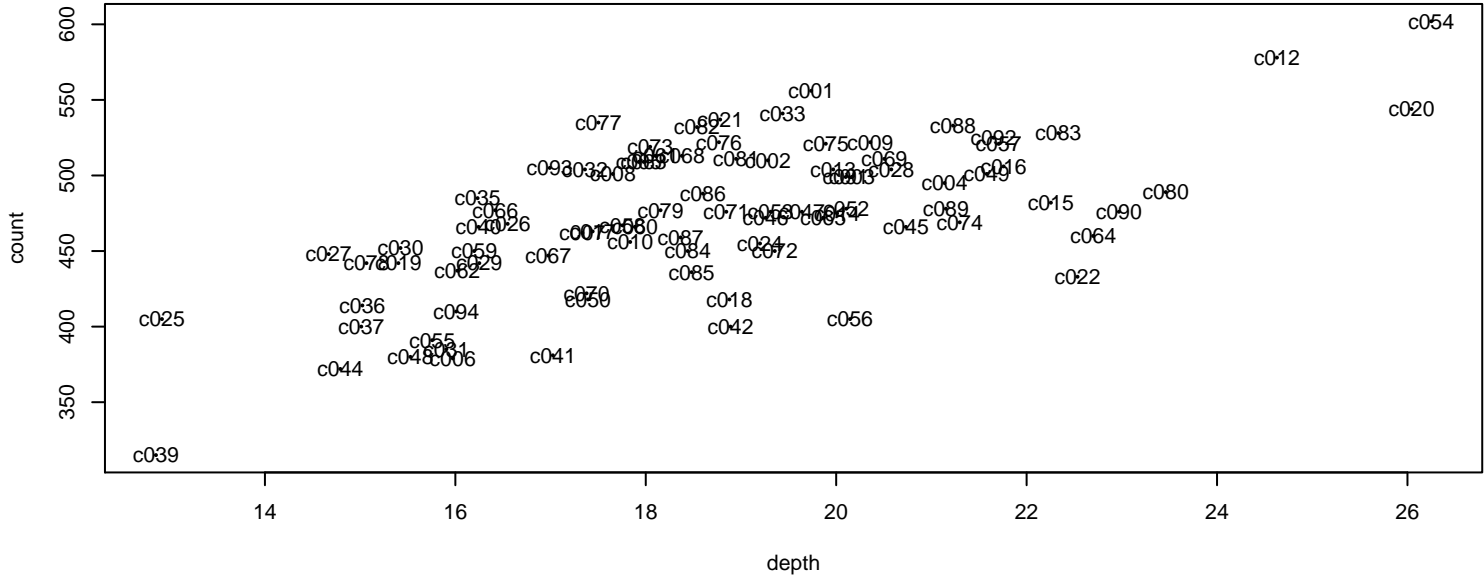
Page 4-6) As Page 1-3 but for mutations that are indels.

PD7271 : SNVs

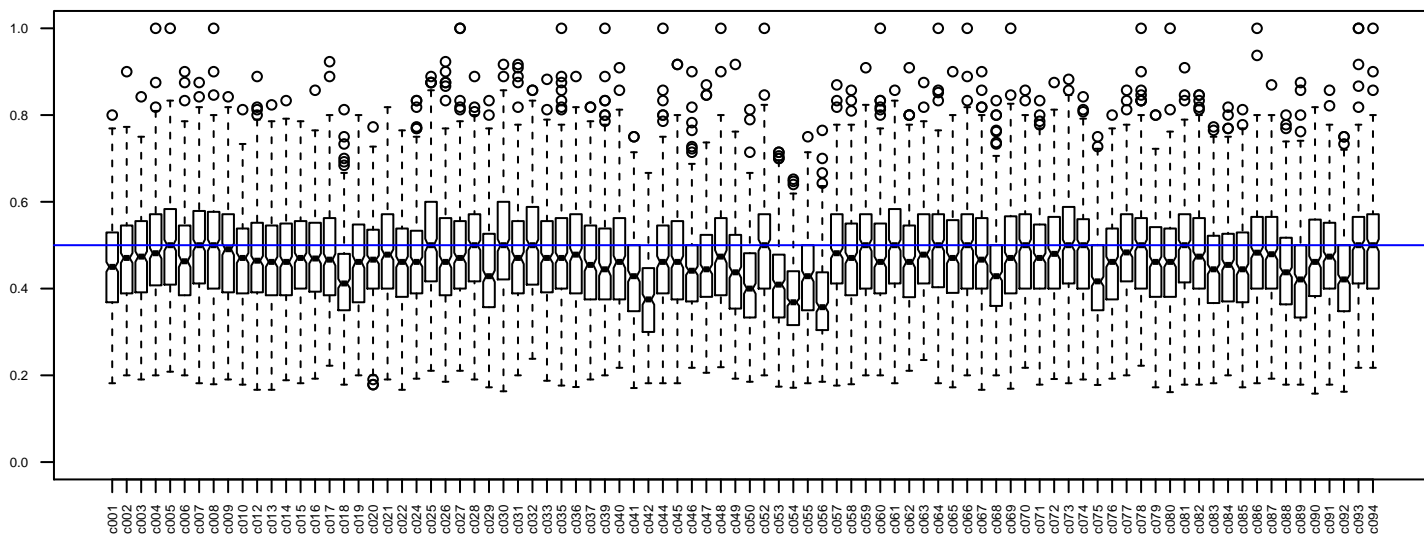
SNV:Pairwise Filter Overlap (% Filtered Variants):Total Fail=37491/Pass=38860

	near_indel	too_close	max_miss	max_gmiss	count	bgld	vaf_too_low_s	vaf_too_low_m2	vaf_zg_too_noisy	manual_exclude	
near_indel	0.1	0.0	0.0	0.0	0.0	0.0	0.0	0.1	0.1	0.0	
too_close	0.0	1.5	0.0	0.0	1.0	1.0	0.0	0.1	0.0	0.0	
max_miss	0.0	0.0	0.1	0.0	0.1	0.1	0.0	0.0	0.0	0.0	
max_gmiss	0.0	0.0	0.0	0.5	0.1	0.2	0.3	0.4	0.4	0.0	
count	0.0	1.0	0.1	0.1	95.9	94.7	0.7	1.0	0.9	0.0	
bgld	0.0	1.0	0.1	0.2	94.7	97.7	0.2	0.4	0.4	0.0	
vaf_too_low_s	0.0	0.0	0.0	0.3	0.7	0.2	1.1	1.1	1.0	0.0	
vaf_too_low_m2	0.1	0.1	0.0	0.4	1.0	0.4	1.1	1.8	1.2	0.0	
vaf_zg_too_noisy	0.1	0.0	0.0	0.4	0.9	0.4	1.0	1.2	1.4	0.0	
manual_exclude	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	

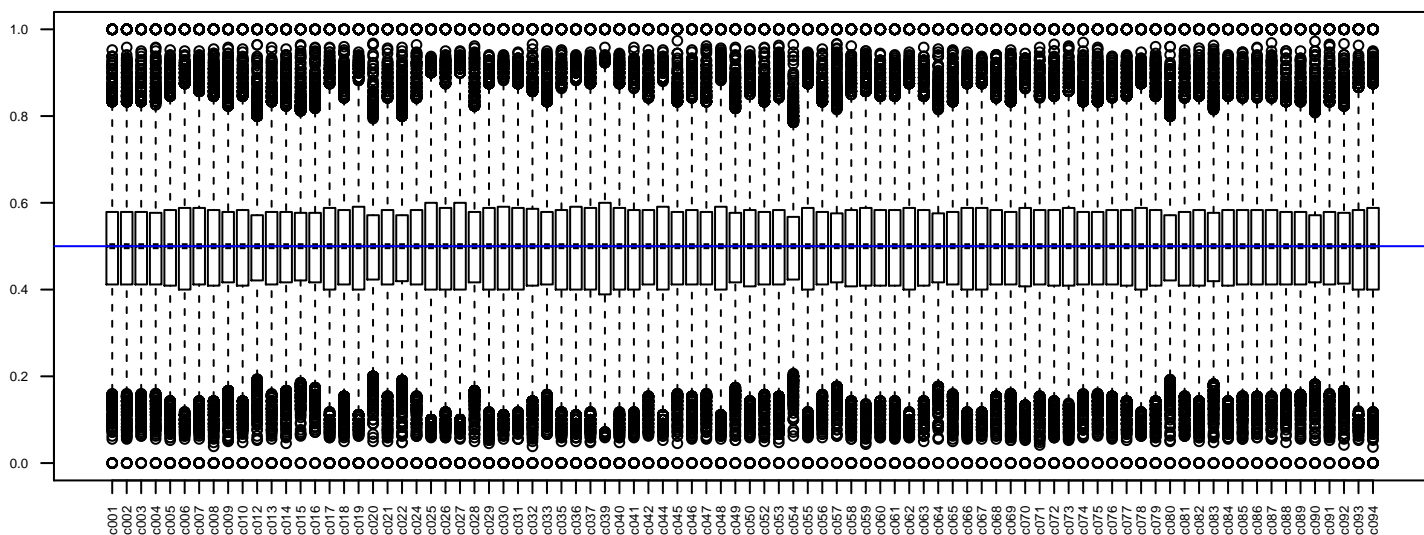
Called SNV Count vs Average Depth



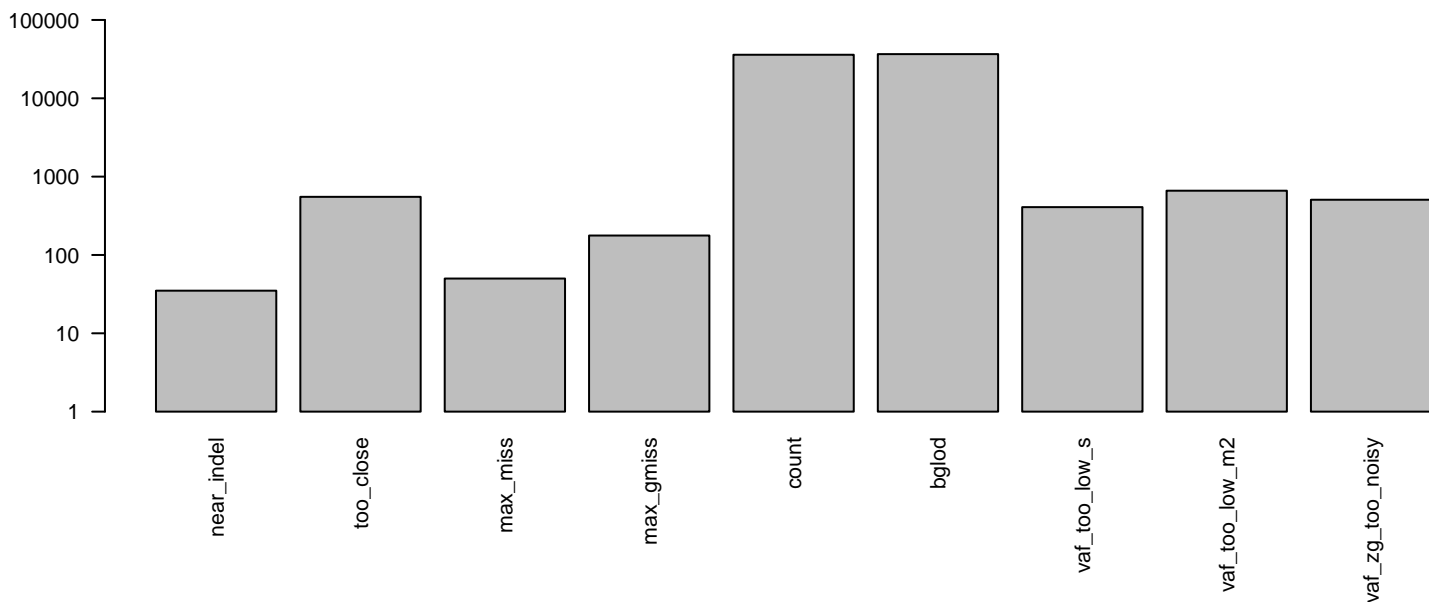
PD7271: SNV : VAF Distribution at Somatic (pass all filters) sites called in Caveman



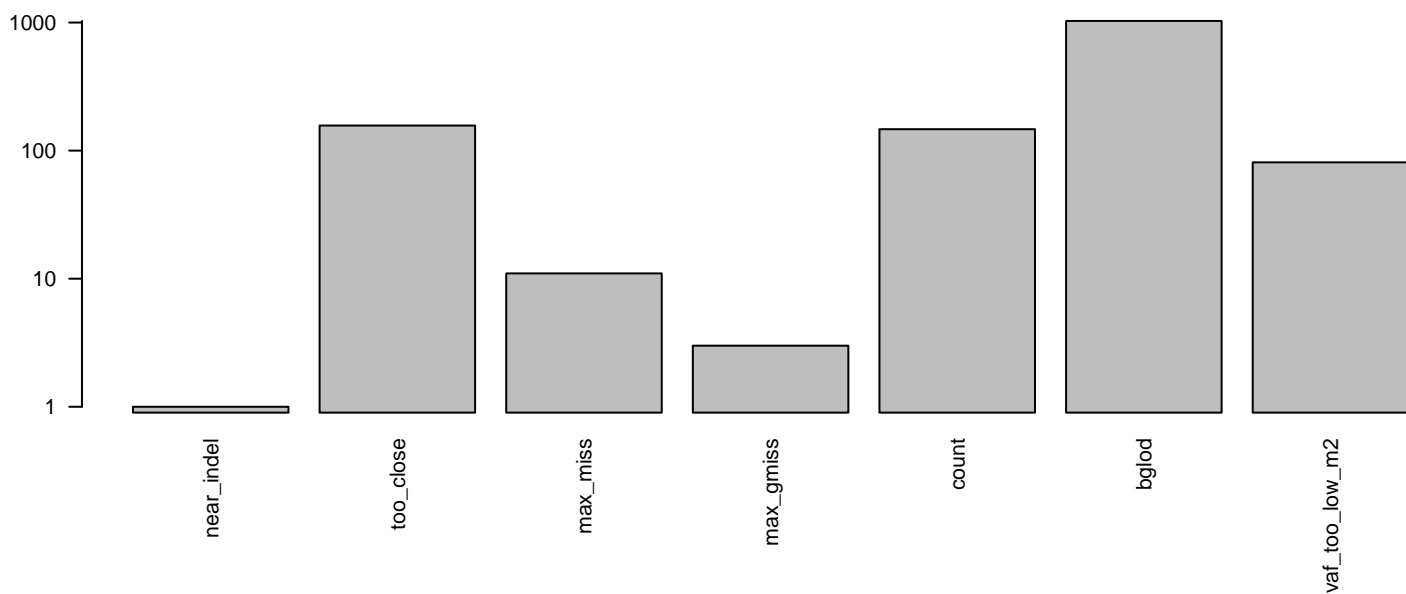
PD7271: SNV : VAF Distribution at Germline [Based on the Matched Normal] sites called in Caveman



PD7271: SNV: No. Sites removed by each filter



PD7271: SNV: No. Sites UNIQUELY removed by each filter

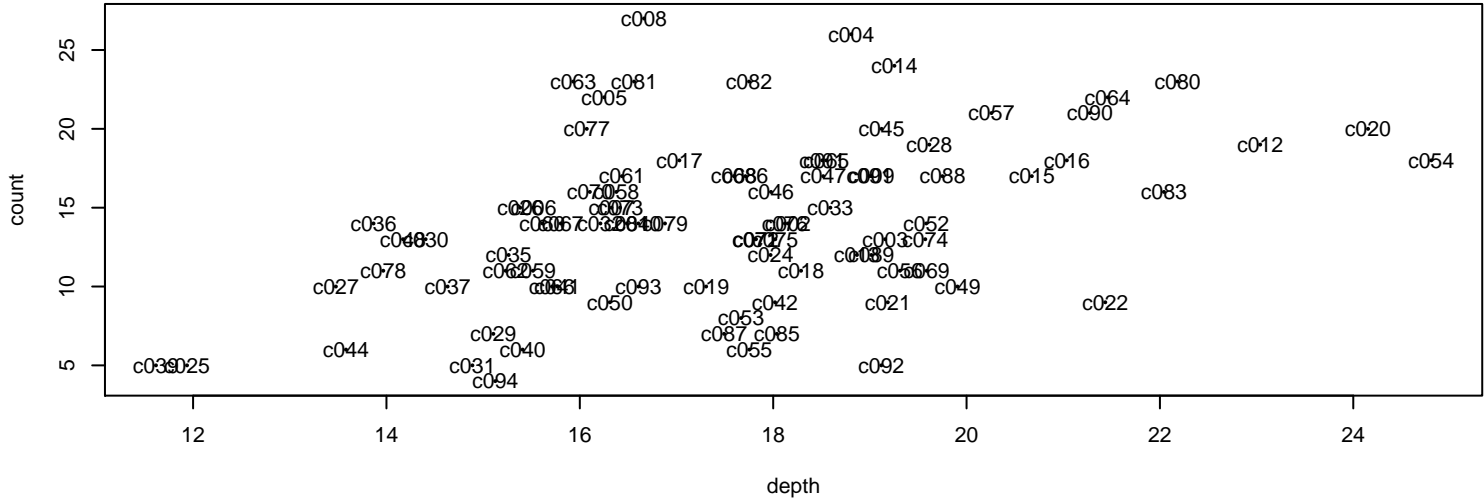


PD7271 : Indels

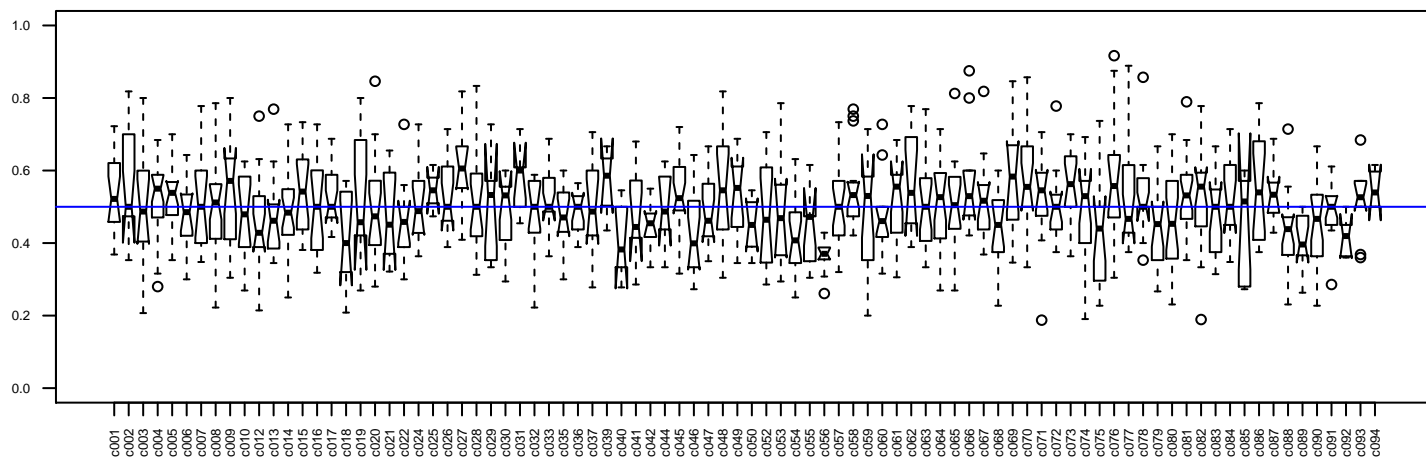
Indels:Pairwise Filter Overlap (% Filtered Variants):Total Fail=5427/Pass=1099

	too_close	max_miss	max_gmiss	count	bgld	vaf_too_low_s	vaf_too_low_m2	vaf_zg_too_noisy	manual_exclude	
too_close	3.7	2.5	1.4	2.2	2.8	0.1	0.4	0.4	0.0	
max_miss	2.5	24.2	8.8	15.6	21.4	0.0	0.0	0.0	0.0	
max_gmiss	1.4	8.8	13.4	3.0	8.2	1.5	3.6	2.9	0.0	
count	2.2	15.6	3.0	74.1	71.4	0.4	1.7	1.3	0.0	
bgld	2.8	21.4	8.2	71.4	86.6	0.6	1.6	1.3	0.0	
vaf_too_low_s	0.1	0.0	1.5	0.4	0.6	2.2	2.2	2.2	0.0	
vaf_too_low_m2	0.4	0.0	3.6	1.7	1.6	2.2	11.5	8.6	0.0	
vaf_zg_too_noisy	0.4	0.0	2.9	1.3	1.3	2.2	8.6	8.8	0.0	
manual_exclude	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	

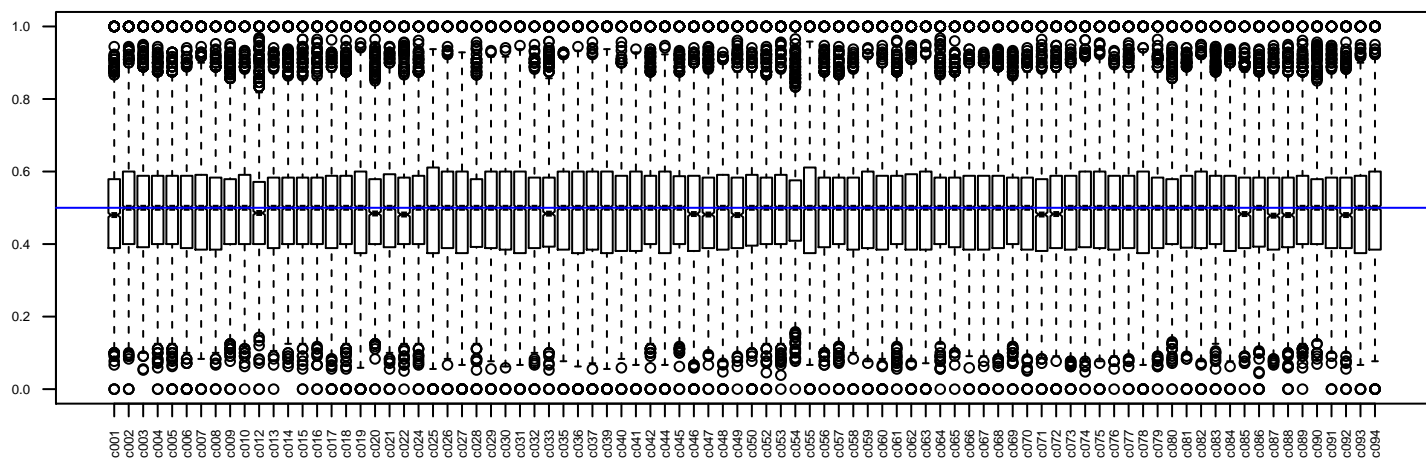
Called INDEL Count vs Average Depth



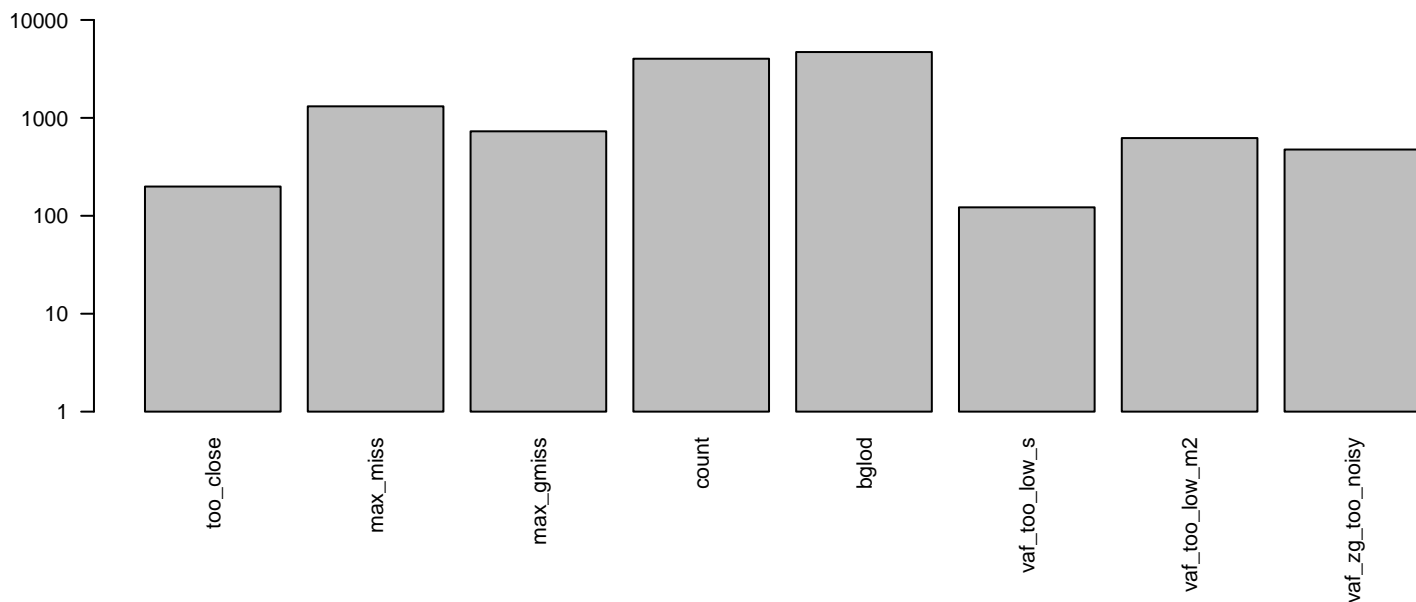
**PD7271: INDEL : VAF Distribution at Somatic (pass all filters) sites called in Pindel**



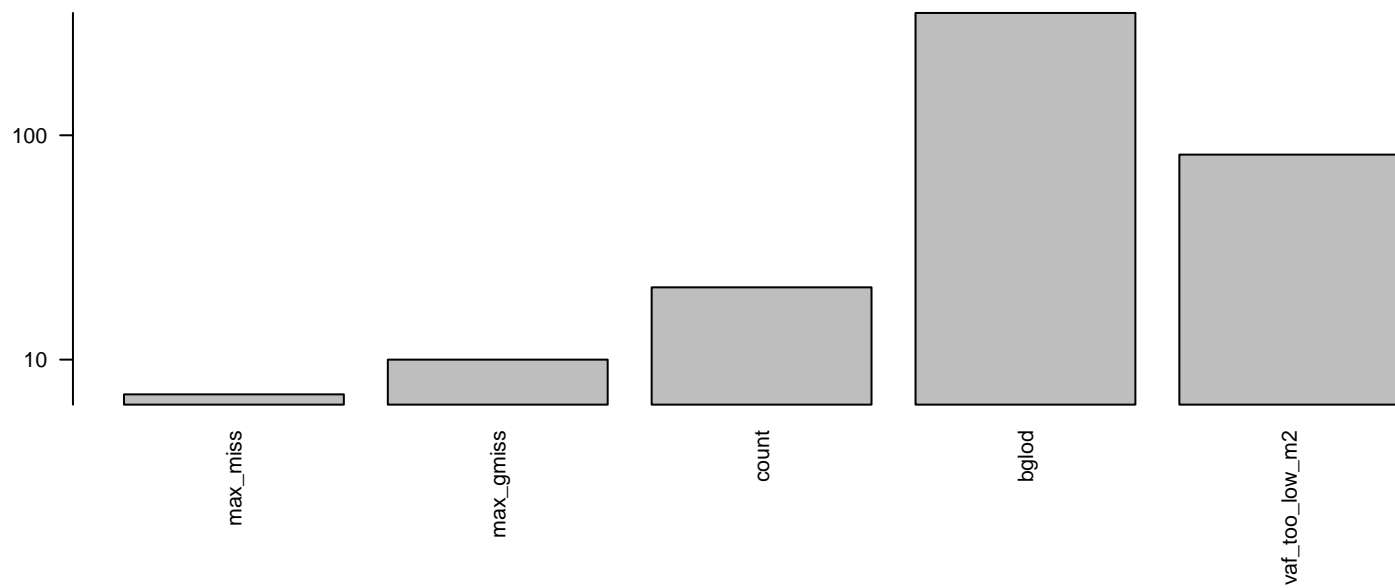
**PD7271: INDEL : VAF Distribution at Germline [Based on the Matched Normal] sites called in Pindel**



**PD7271: INDEL: No. Sites removed by each filter**



**PD7271: INDEL: No. Sites UNIQUELY removed by each filter**

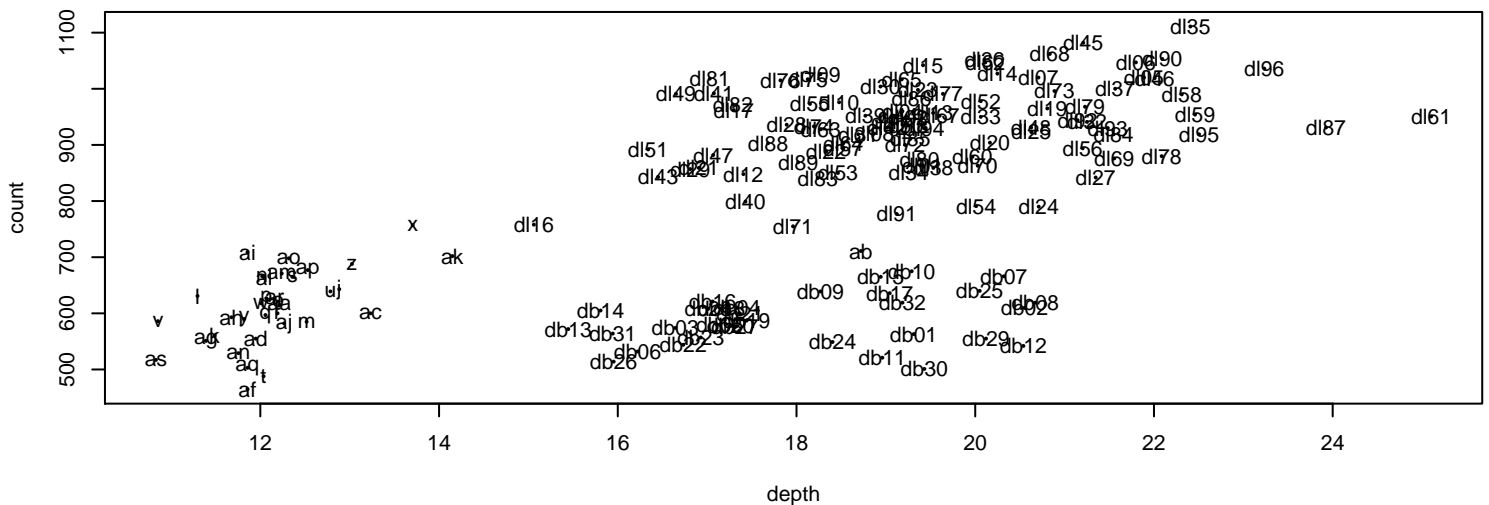


## PD5182 : SNVs

**SNV:Pairwise Filter Overlap (% Filtered Variants):Total Fail=39364/Pass=101598**

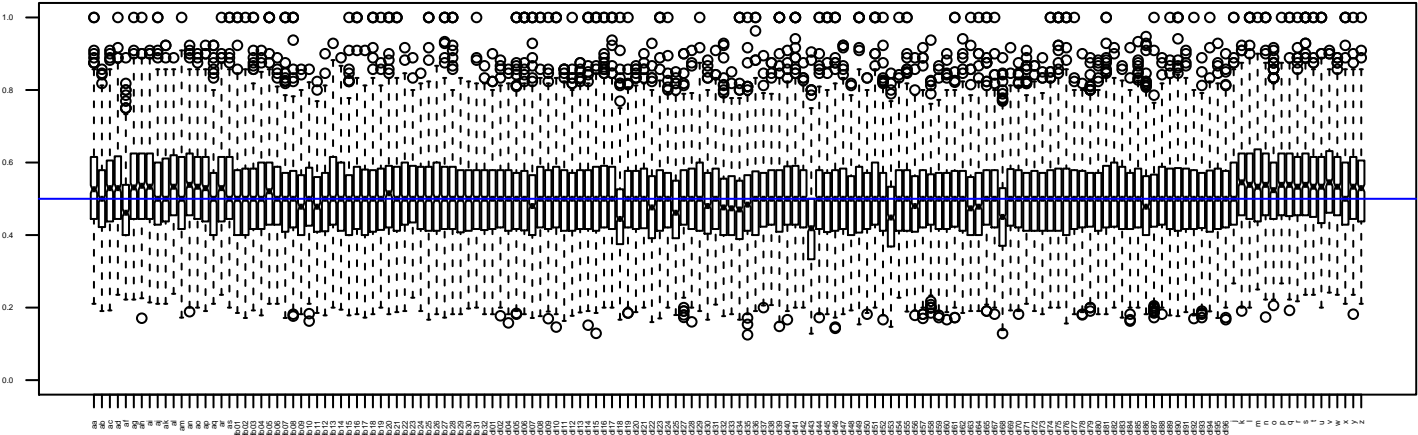
[illegible]

## Called SNV Count vs Average Depth

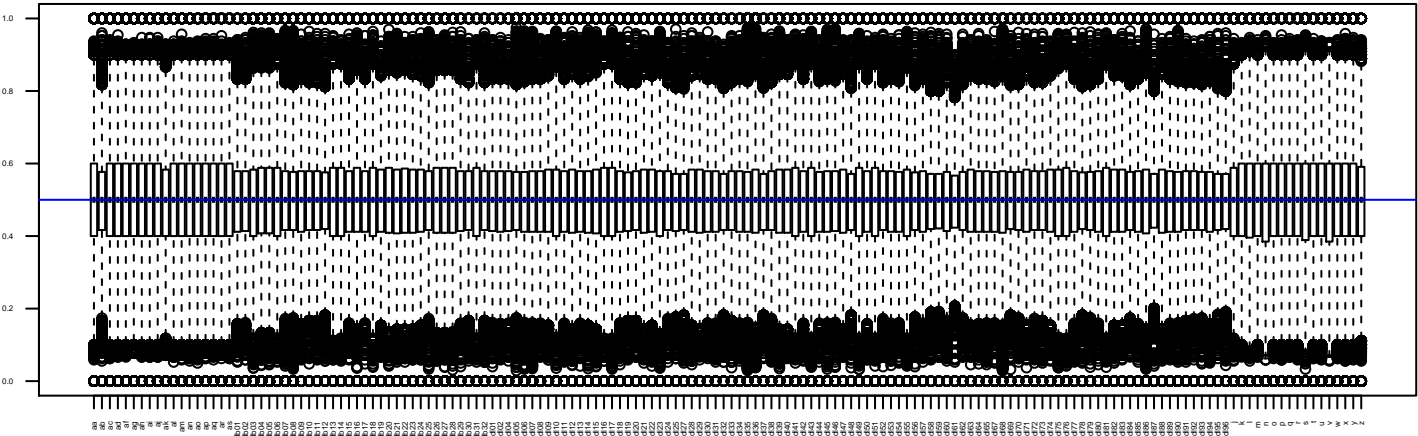




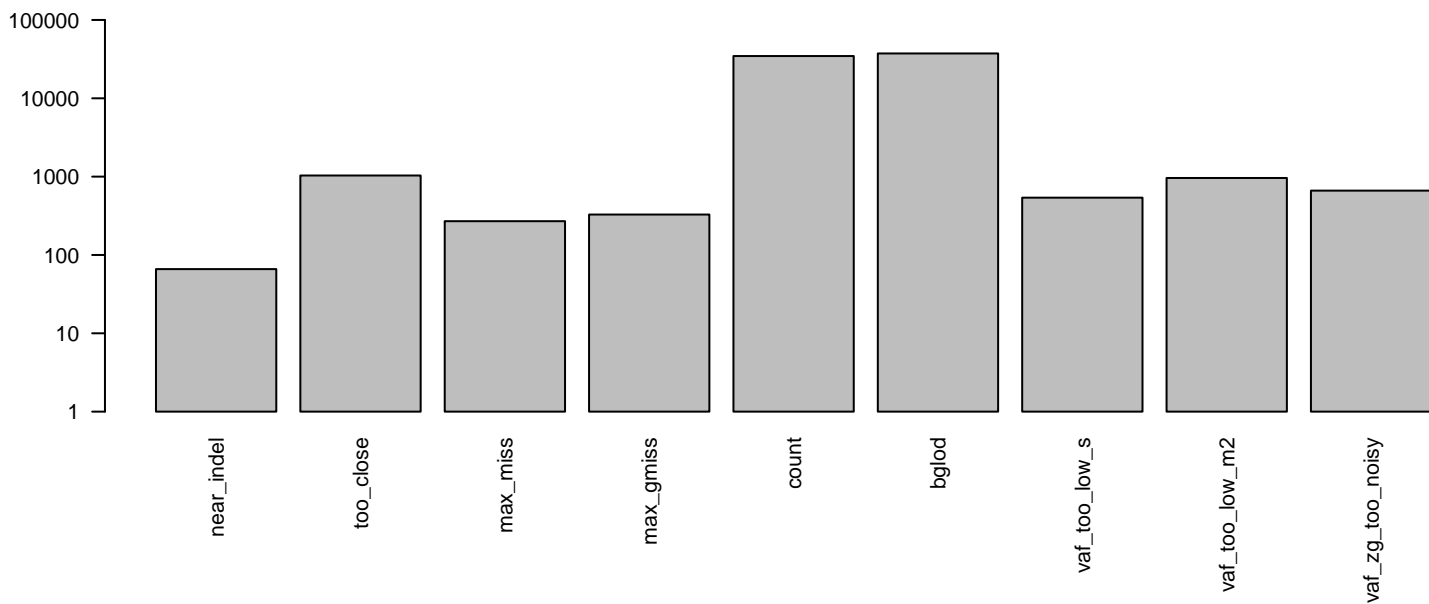
PD5182: SNV : VAF Distribution at Somatic (pass all filters) sites called in Caveman



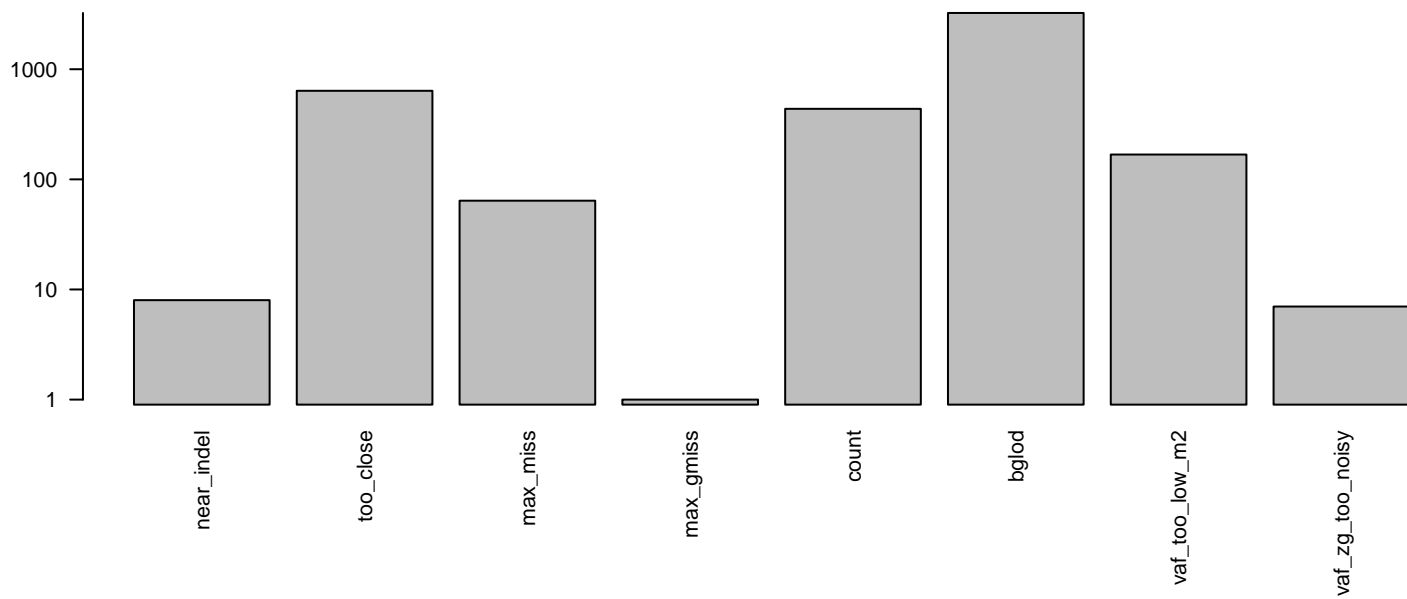
PD5182: SNV : VAF Distribution at Germline [Based on the Matched Normal] sites called in Caveman



PD5182: SNV: No. Sites removed by each filter



PD5182: SNV: No. Sites UNIQUELY removed by each filter

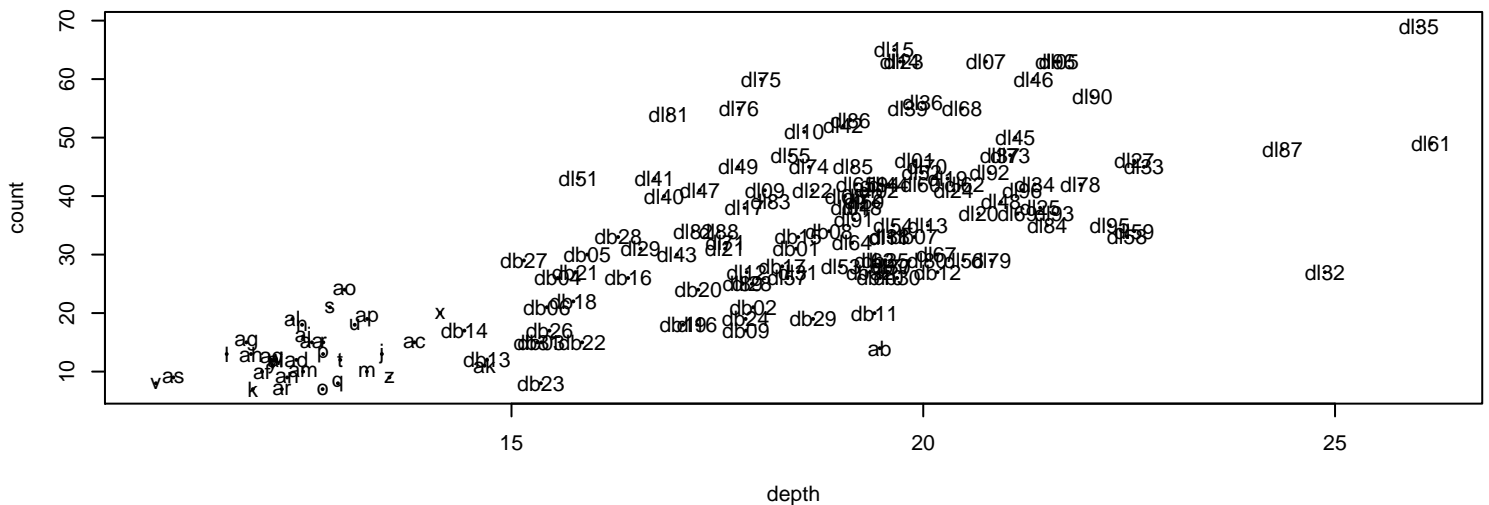


## PD5182 : Indels

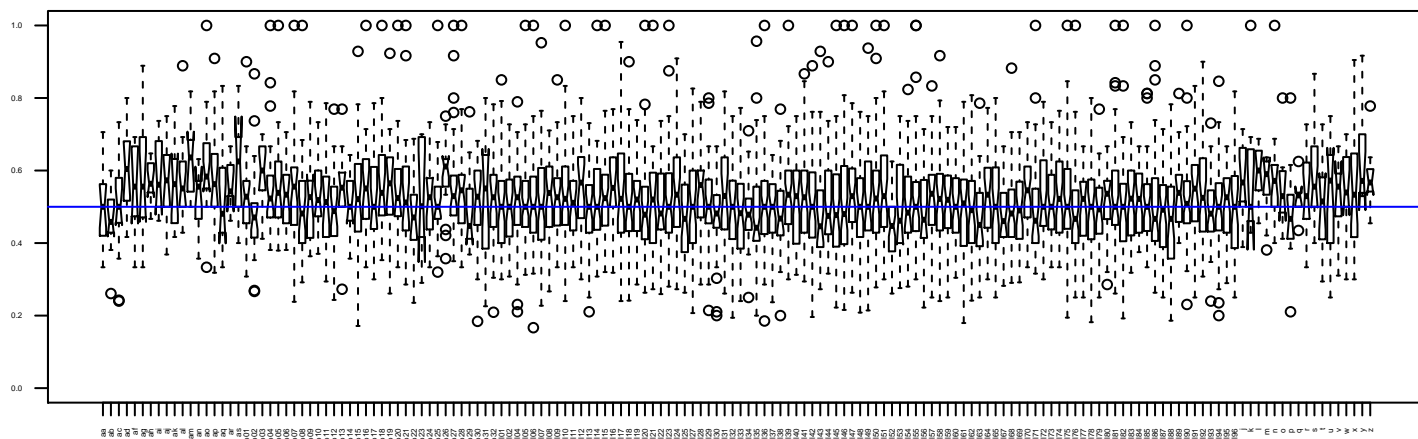
**Indels:Pairwise Filter Overlap (% Filtered Variants):Total Fail=7721/Pass=3624**

[illegible]

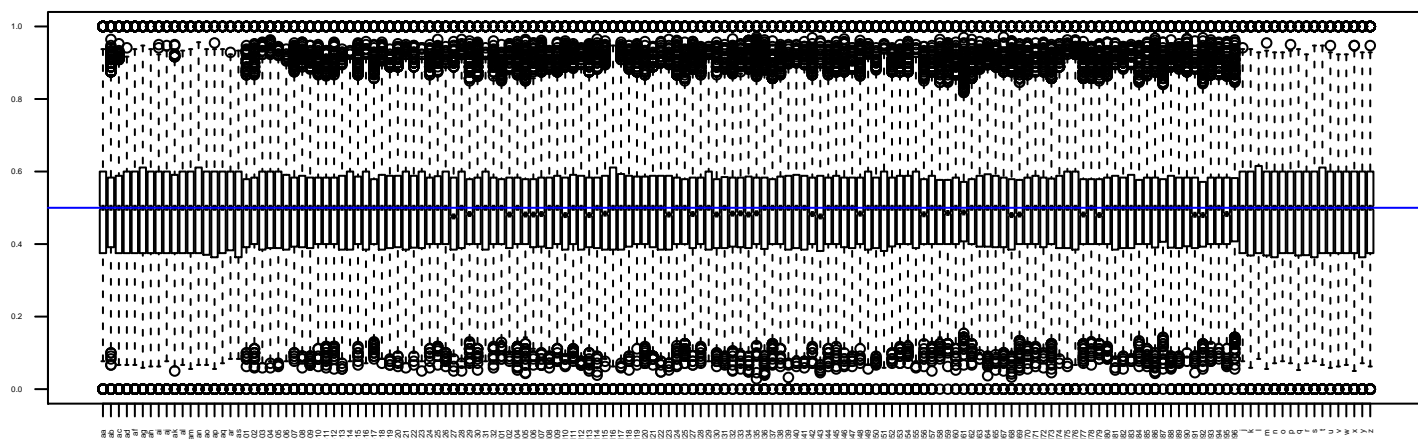
### Called INDEL Count vs Average Depth



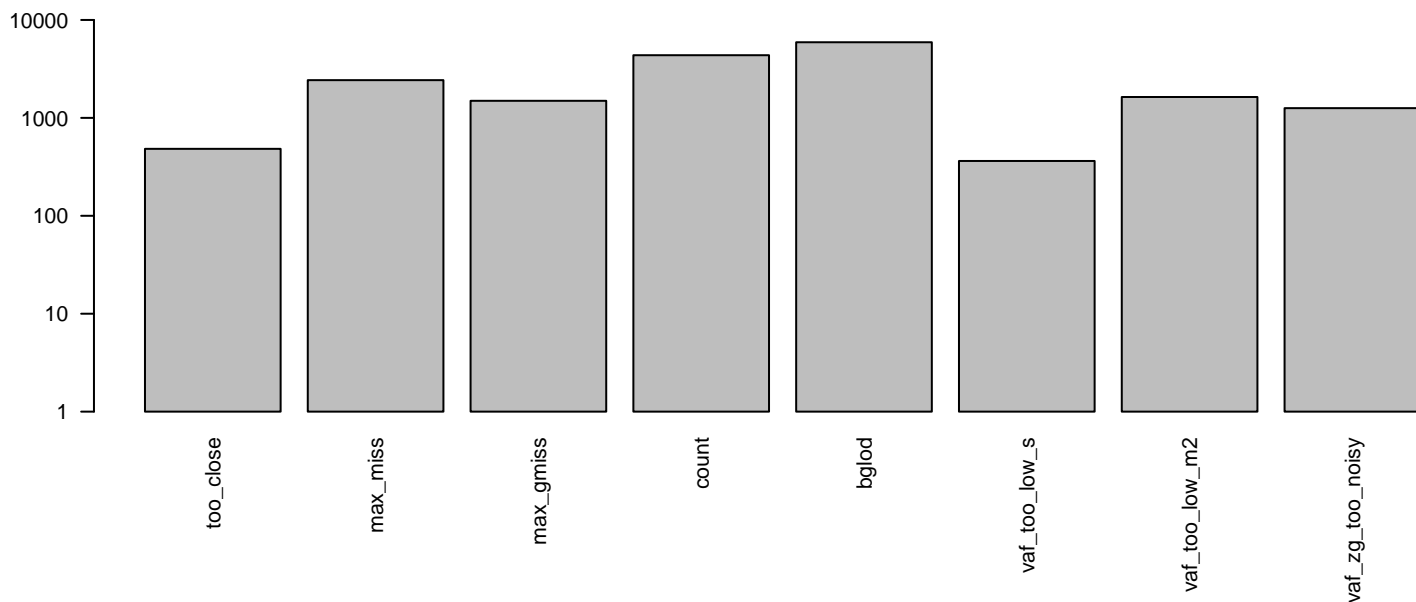
PD5182: INDEL : VAF Distribution at Somatic (pass all filters) sites called in Pindel



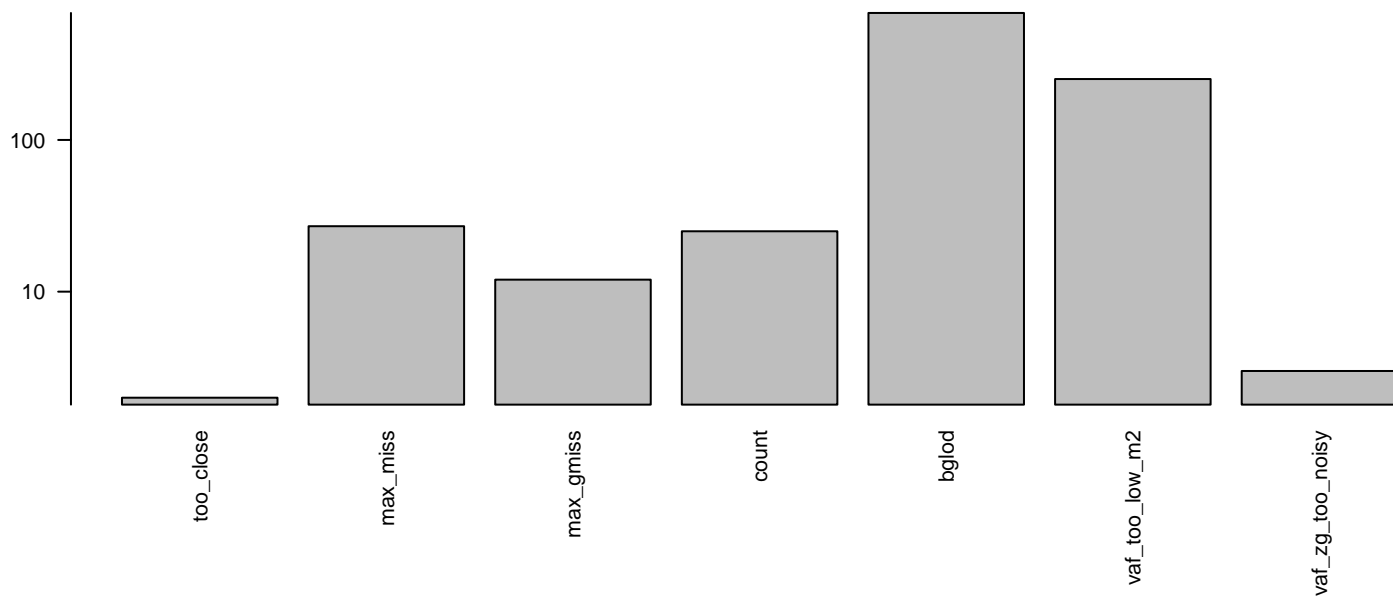
PD5182: INDEL : VAF Distribution at Germline [Based on the Matched Normal] sites called in Pindel



PD5182: INDEL: No. Sites removed by each filter



PD5182: INDEL: No. Sites UNIQUELY removed by each filter

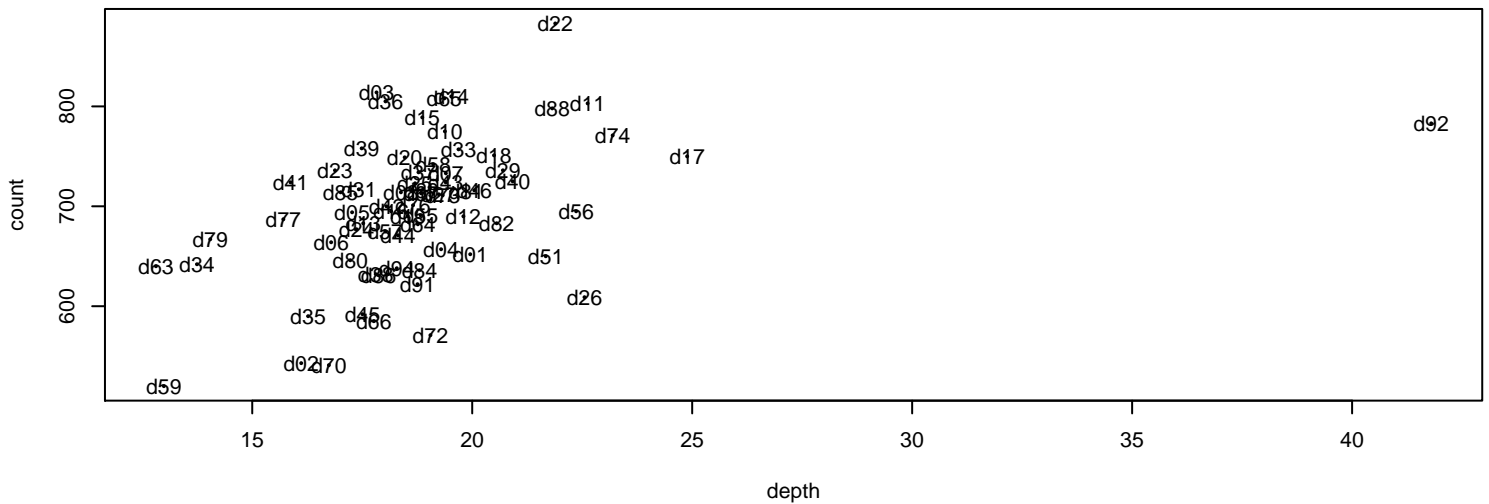


## PD5163 : SNVs

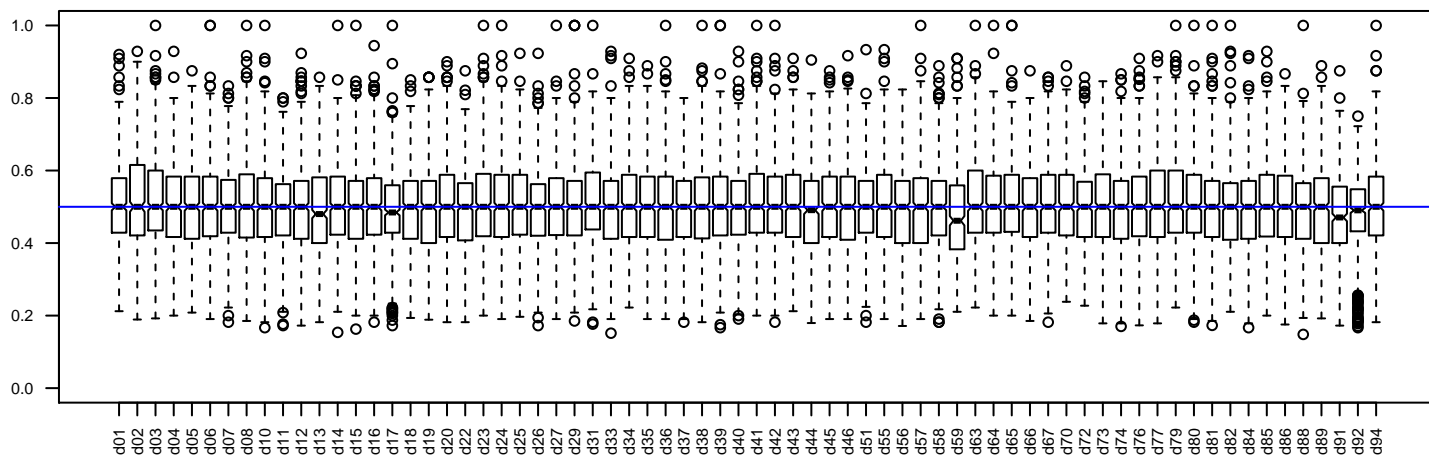
**SNV:Pairwise Filter Overlap (% Filtered Variants):Total Fail=86594/Pass=45282**

[illegible]

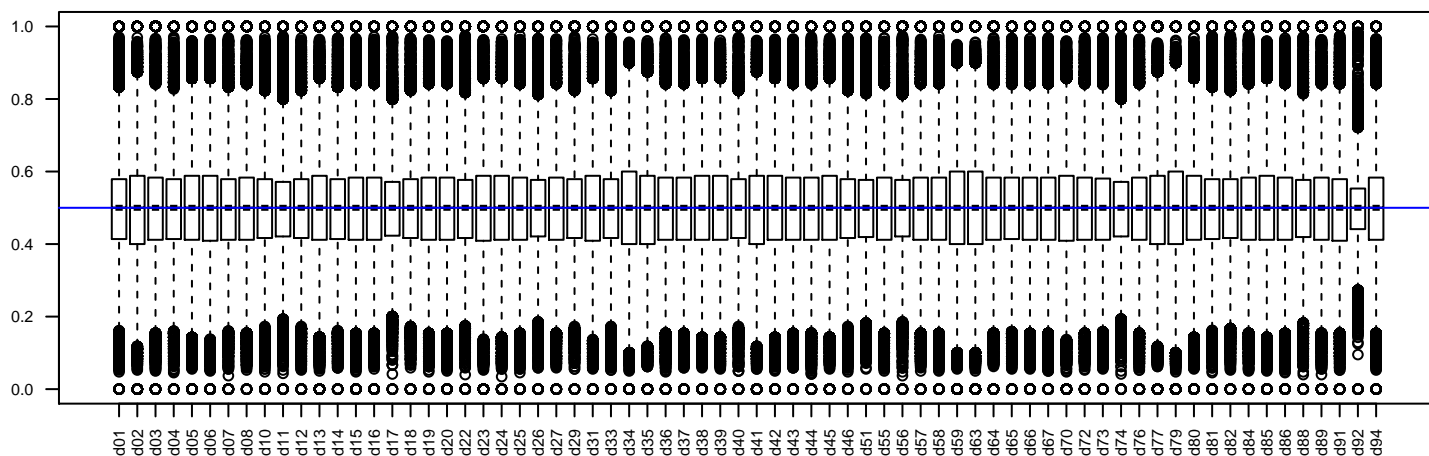
## Called SNV Count vs Average Depth



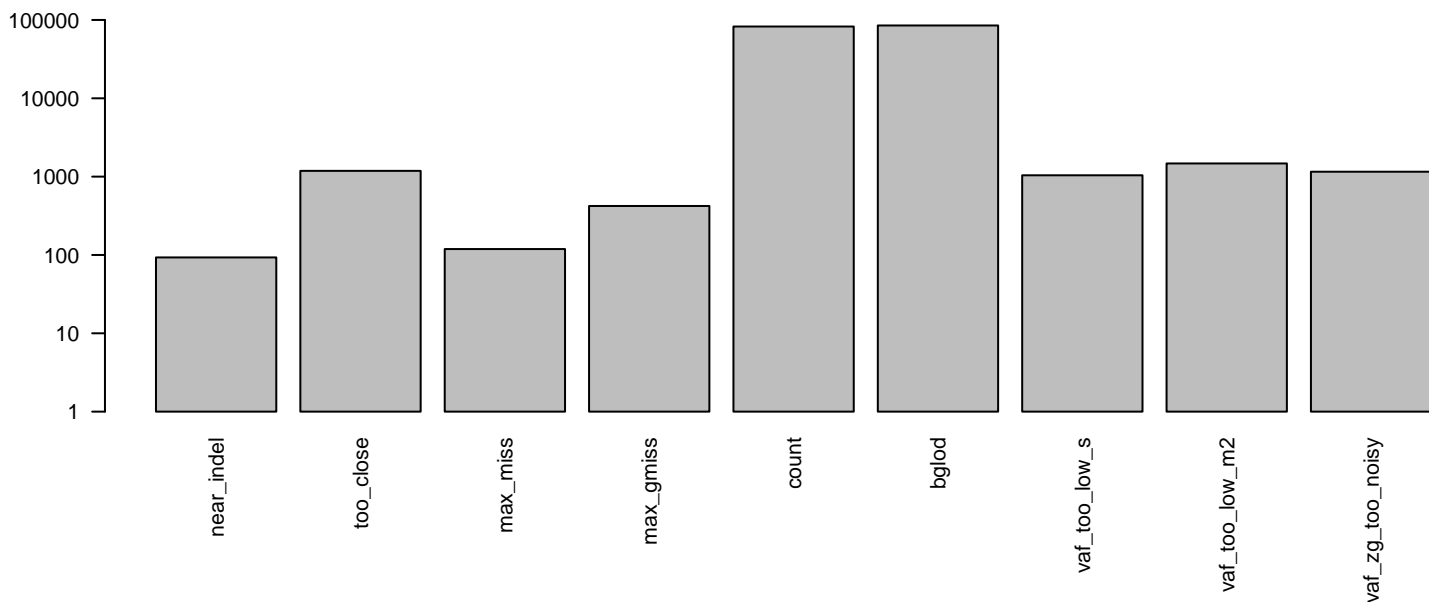
PD5163: SNV : VAF Distribution at Somatic (pass all filters) sites called in Caveman



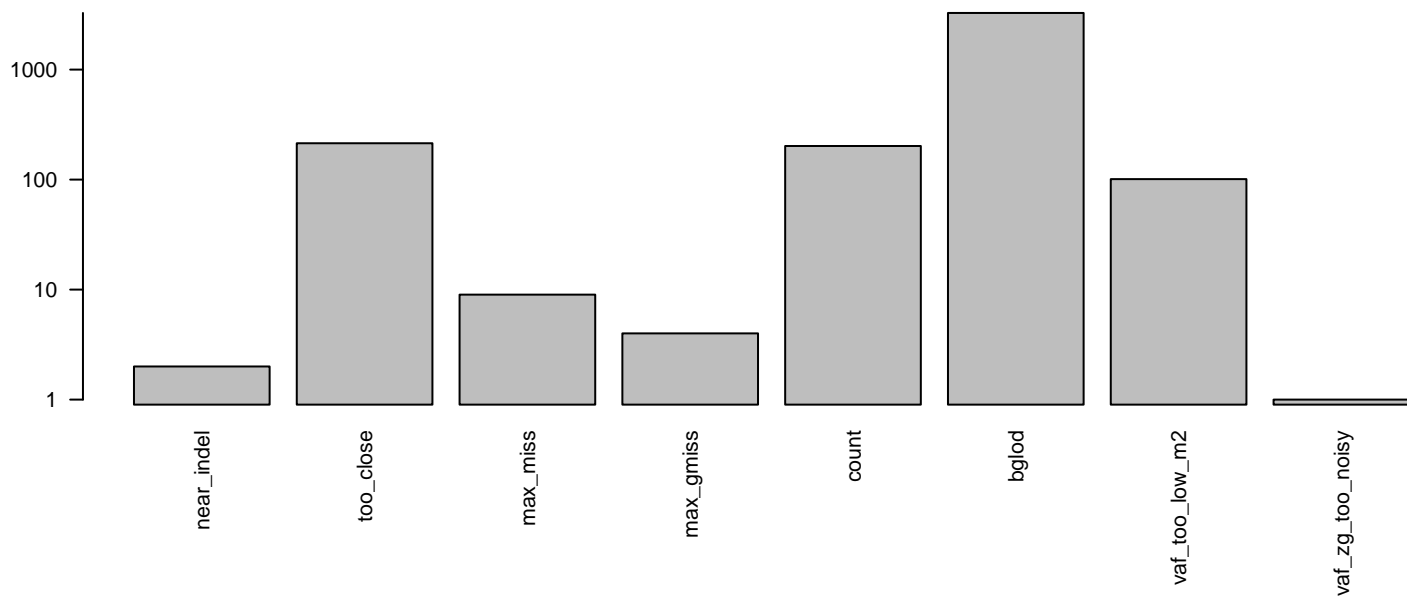
PD5163: SNV : VAF Distribution at Germline [Based on the Matched Normal] sites called in Caveman



**PD5163: SNV: No. Sites removed by each filter**



**PD5163: SNV: No. Sites UNIQUELY removed by each filter**



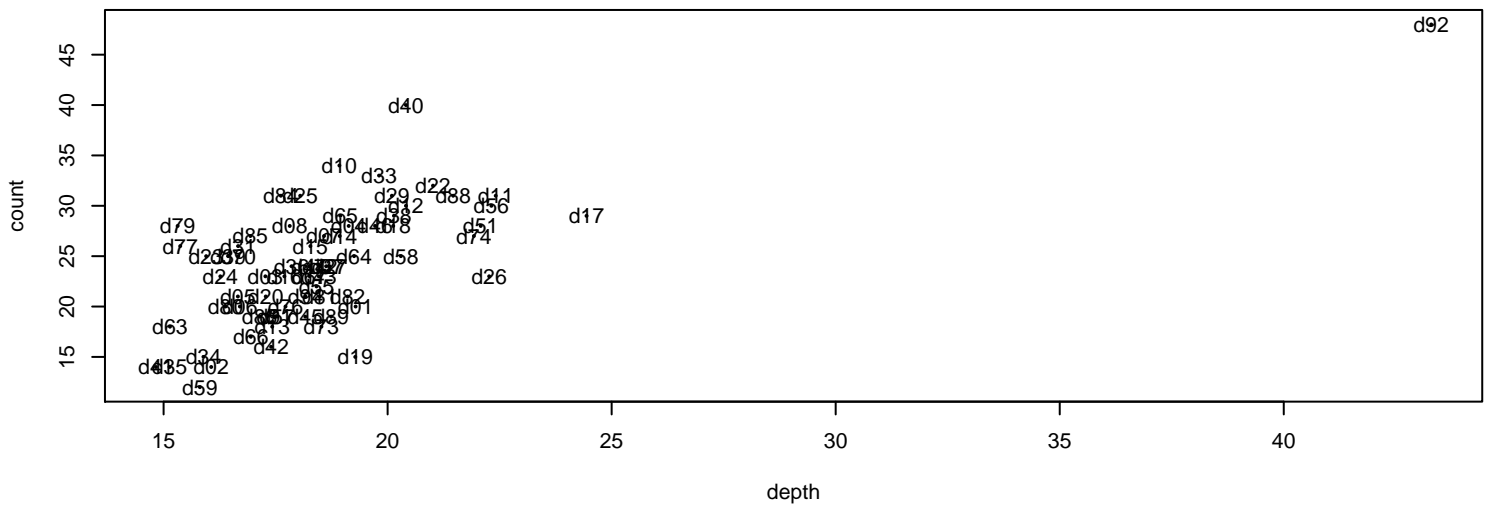


## PD5163 : Indels

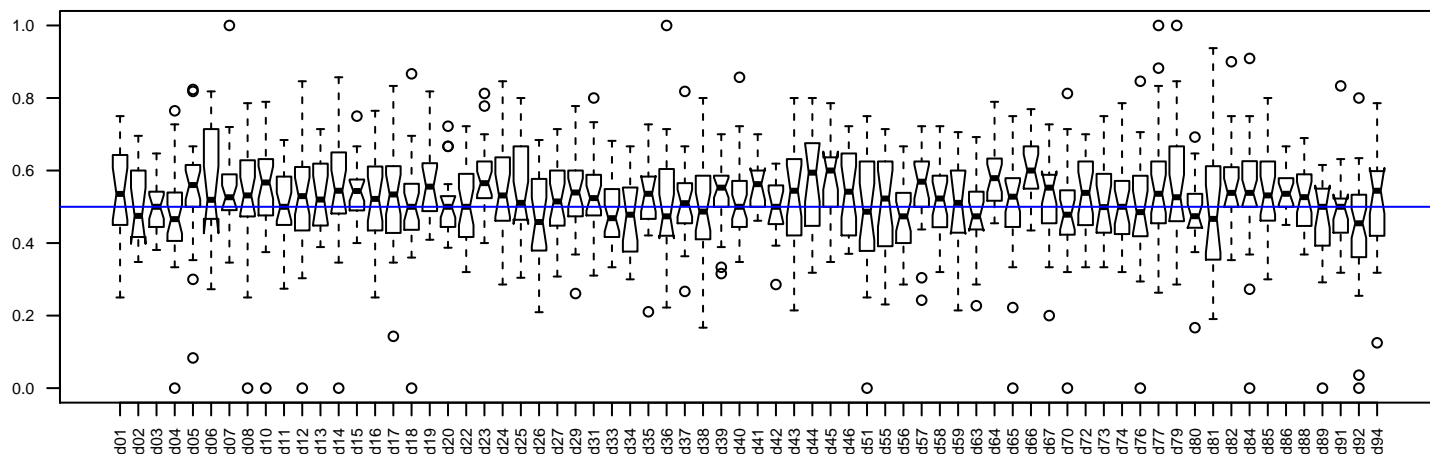
**Indels:Pairwise Filter Overlap (% Filtered Variants):Total Fail=10508/Pass=1493**

[illegible]

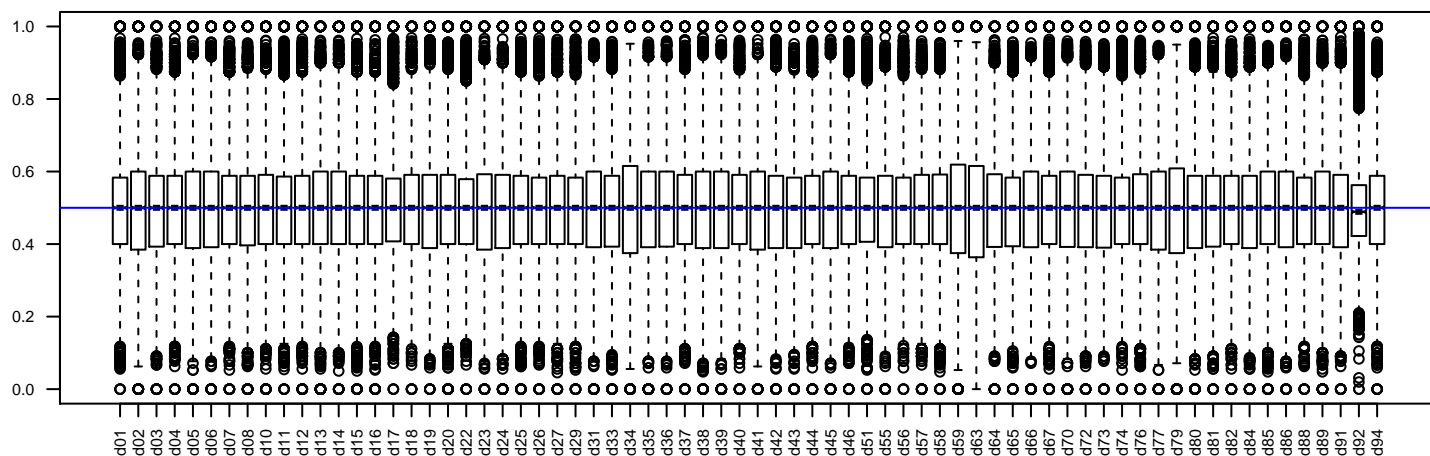
## Called INDEL Count vs Average Depth



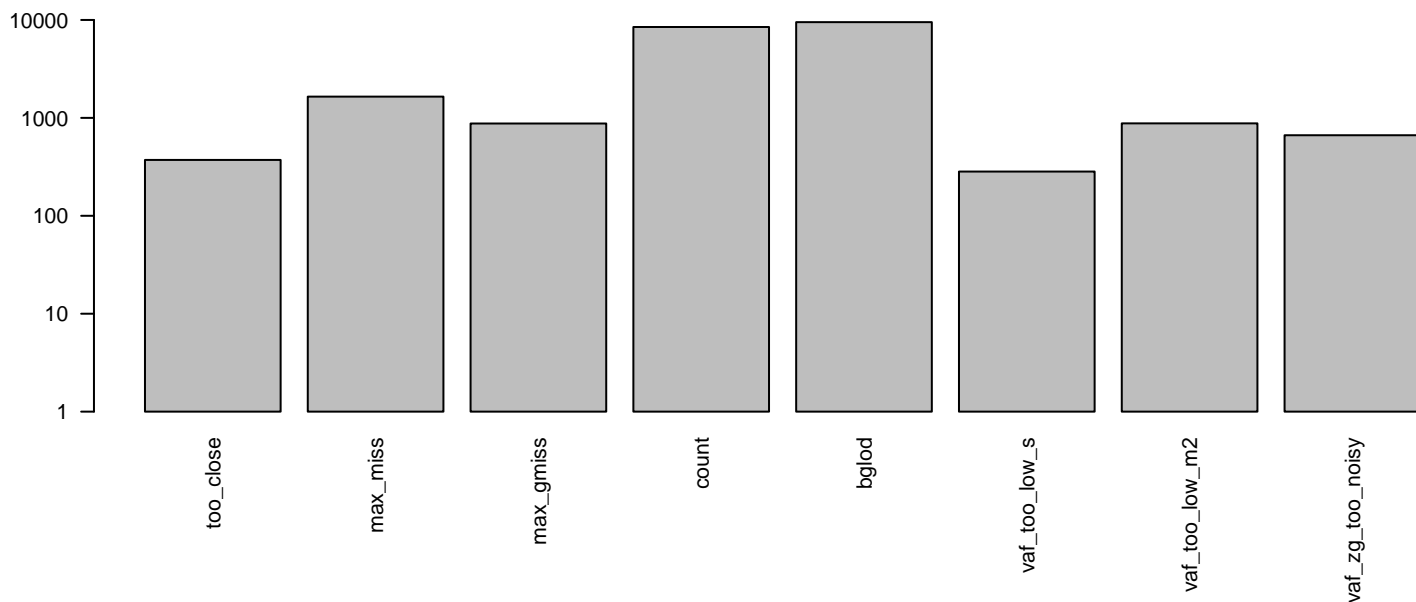
**PD5163: INDEL : VAF Distribution at Somatic (pass all filters) sites called in Pindel**



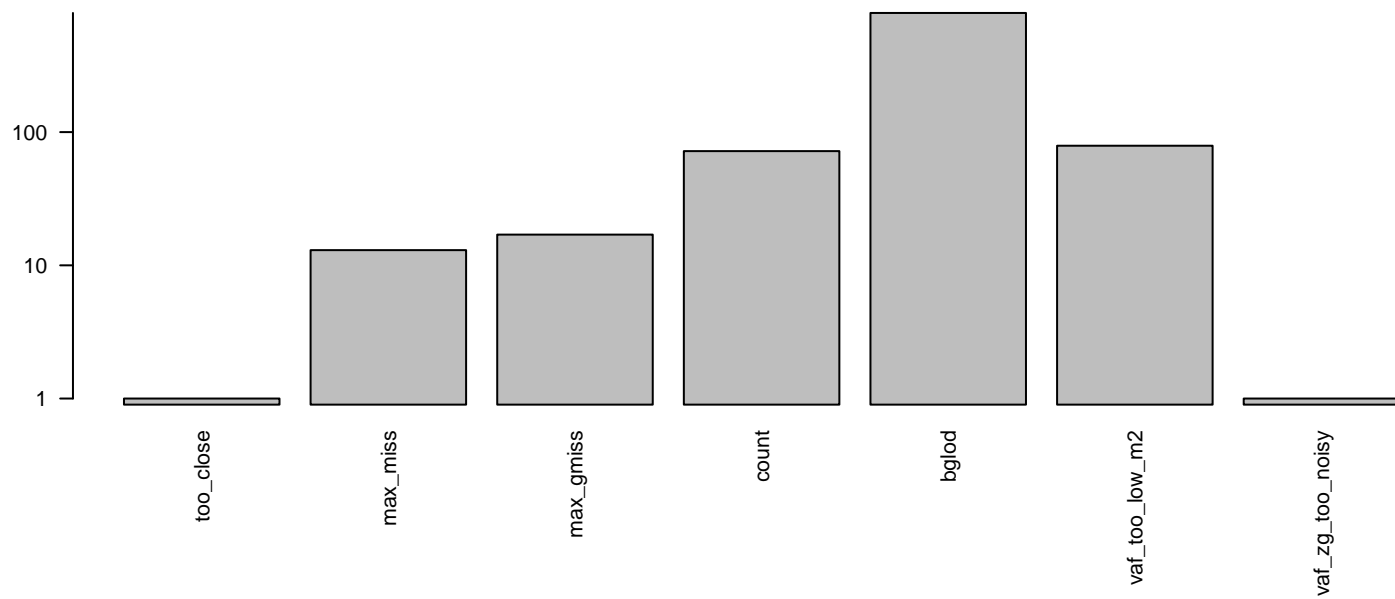
**PD5163: INDEL : VAF Distribution at Germline [Based on the Matched Normal] sites called in Pindel**



PD5163: INDEL: No. Sites removed by each filter

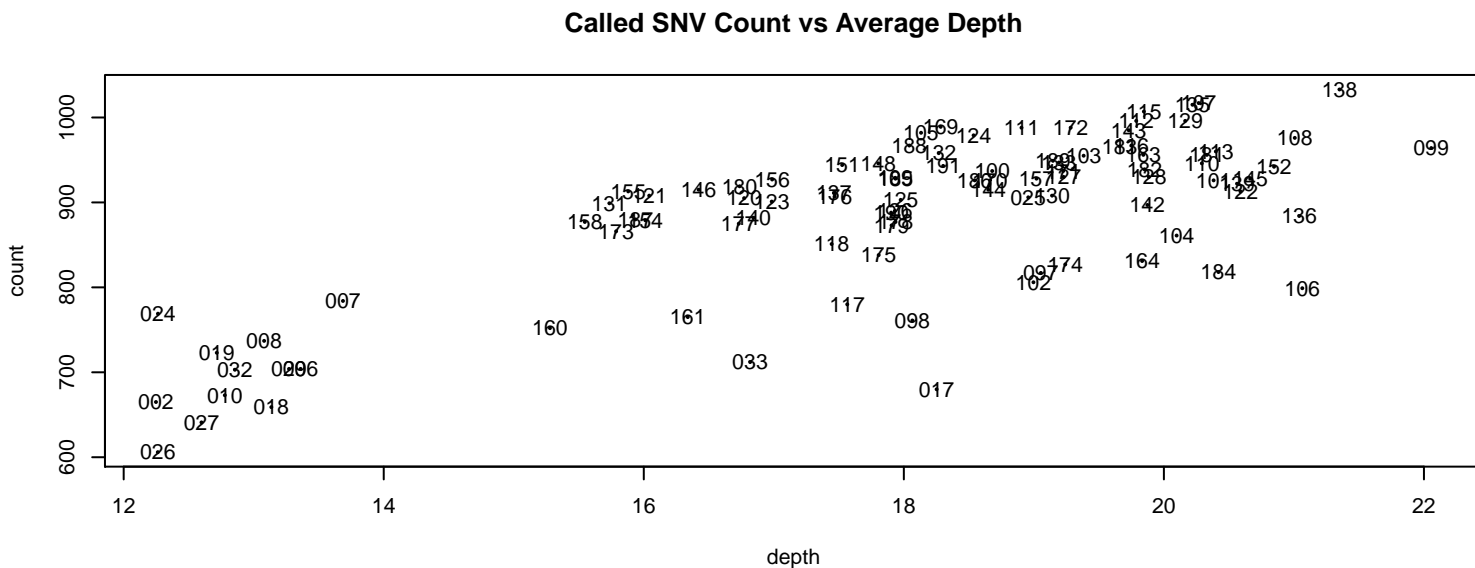


PD5163: INDEL: No. Sites UNIQUELY removed by each filter

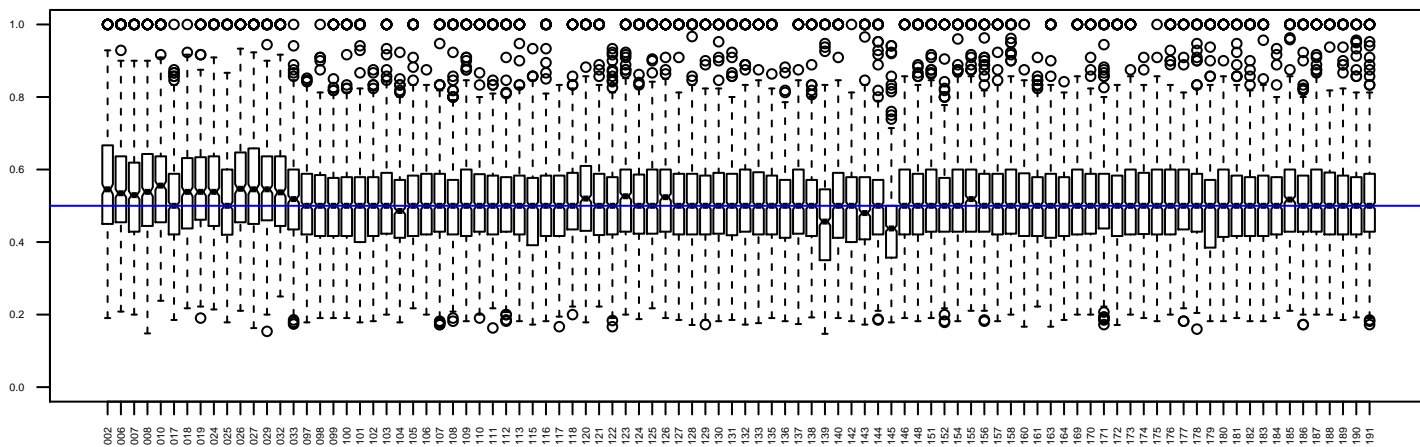


## PD5847 : SNVs

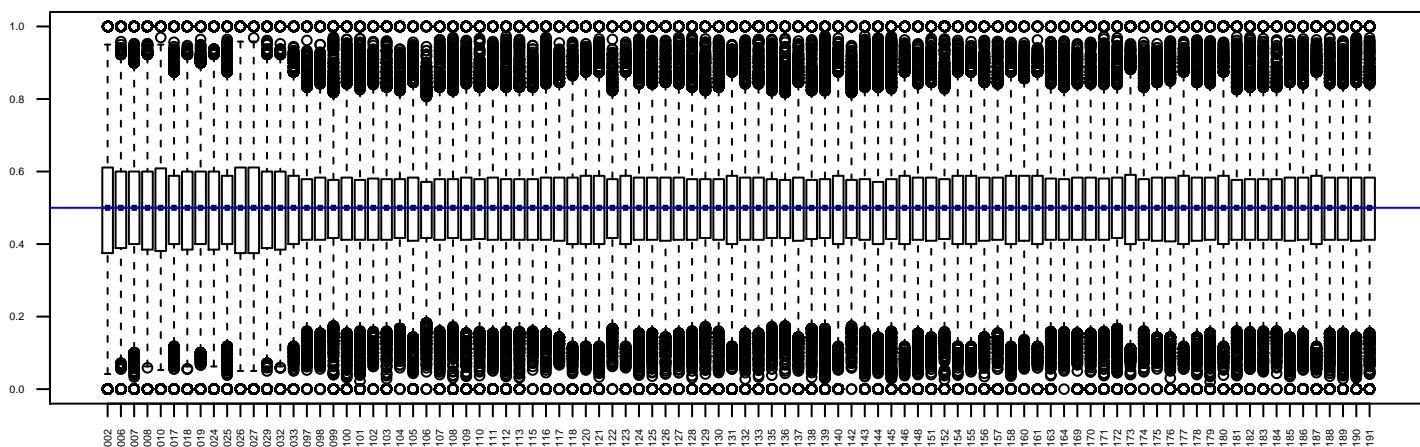
**SNV:Pairwise Filter Overlap (% Filtered Variants):Total Fail=38076/Pass=32508**

[illegible]

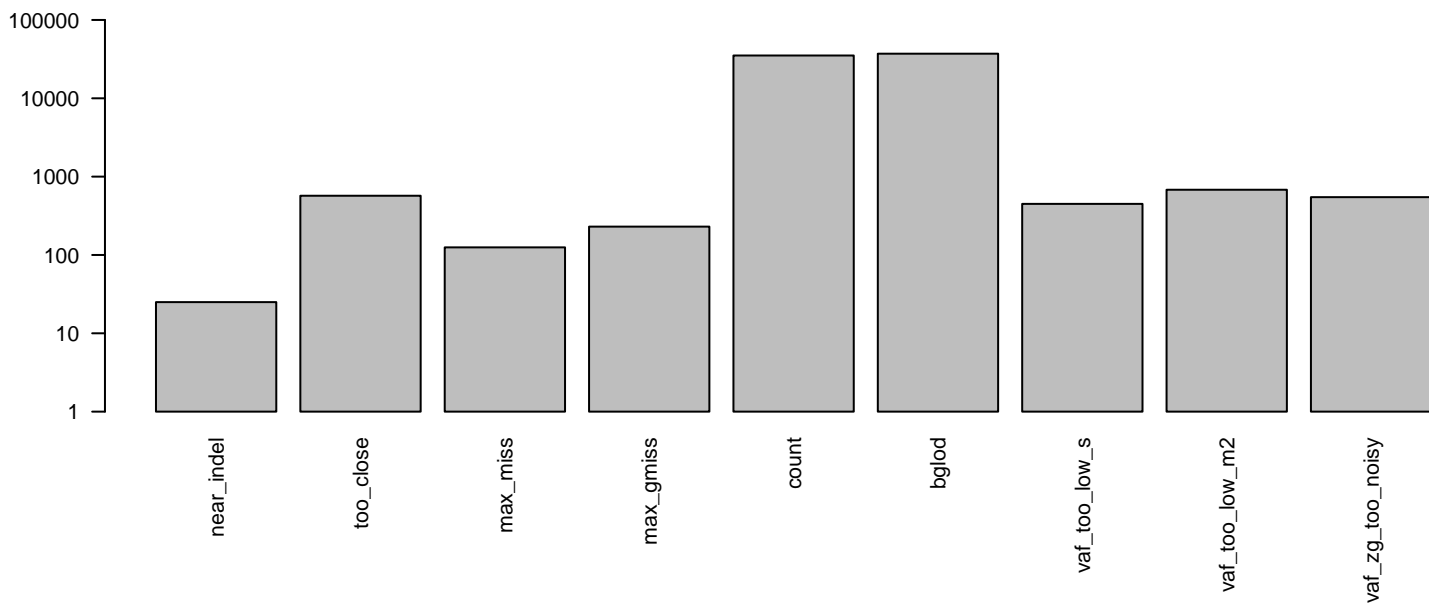
PD5847: SNV : VAF Distribution at Somatic (pass all filters) sites called in Caveman



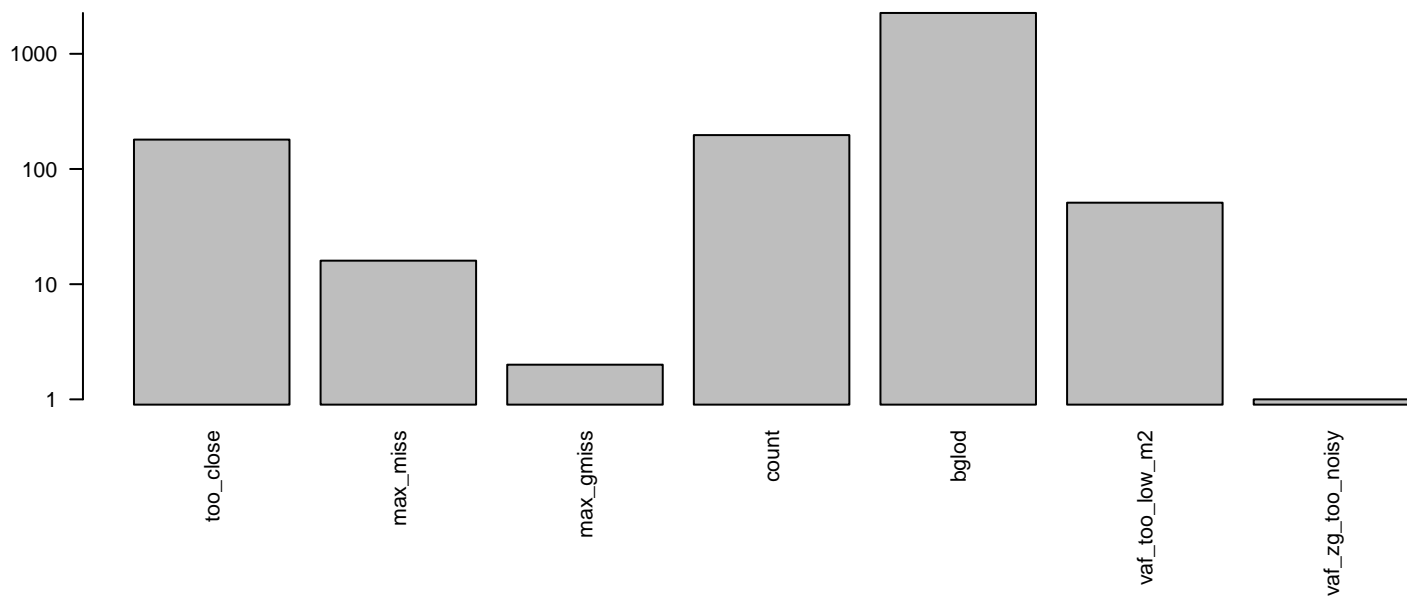
PD5847: SNV : VAF Distribution at Germline [Based on the Matched Normal] sites called in Caveman



PD5847: SNV: No. Sites removed by each filter



PD5847: SNV: No. Sites UNIQUELY removed by each filter

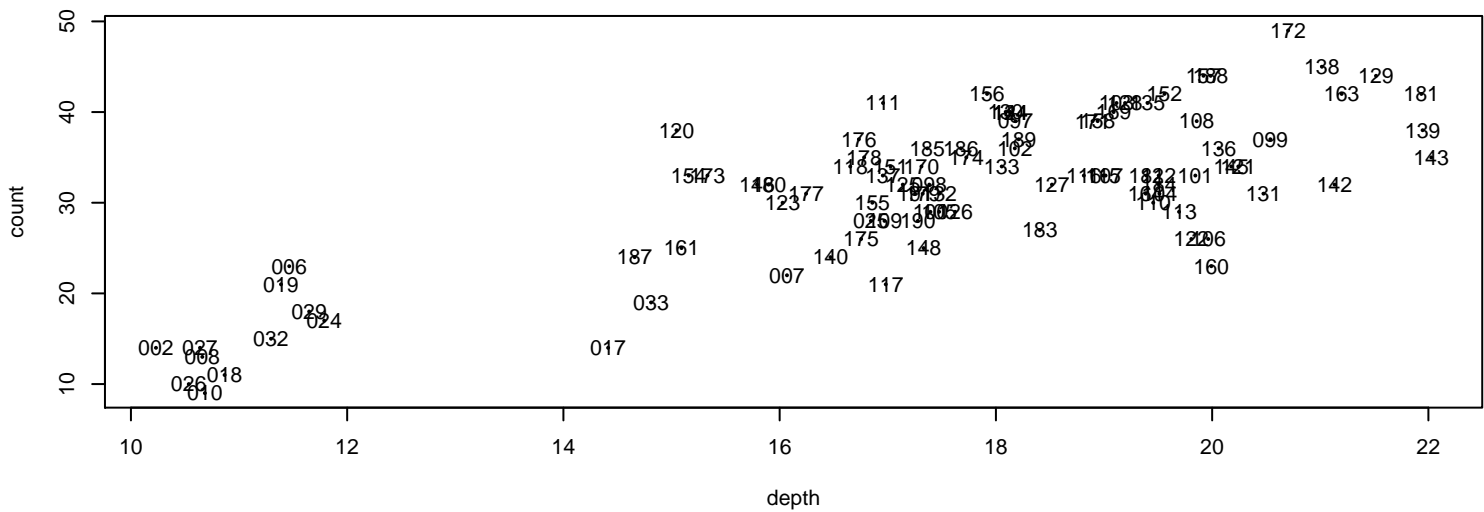


PD5847 : Indels

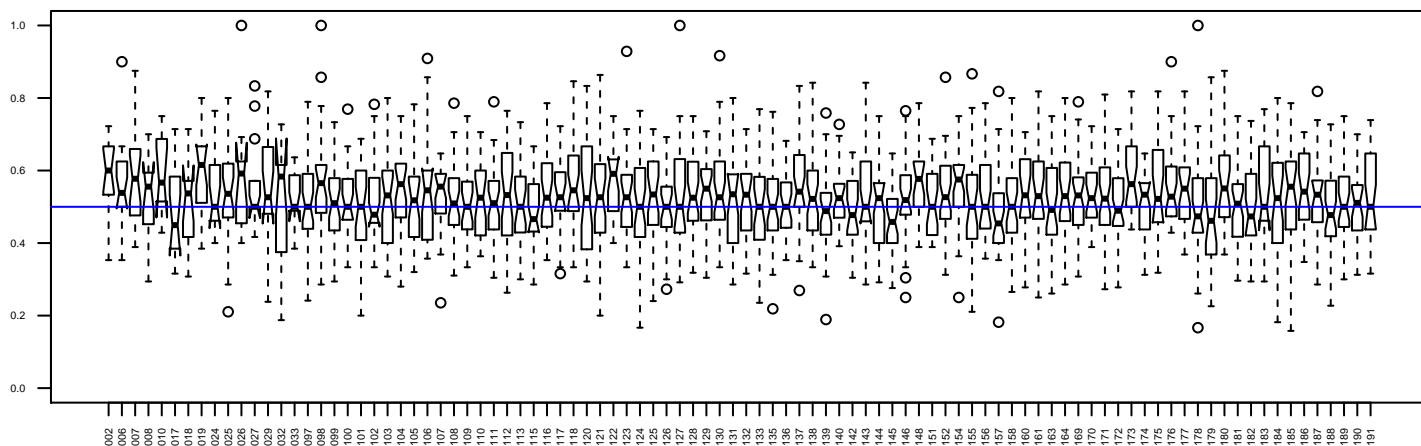
Indels:Pairwise Filter Overlap (% Filtered Variants):Total Fail=5775/Pass=1183

	too_close	max_miss	max_gmiss	count	bgld	vaf_too_low_s	vaf_too_low_m2	vaf_zg_too_noisy	manual_exclude	
too_close	4.4	2.9	1.3	2.8	3.4	0.1	0.3	0.2	0.0	
max_miss	2.9	25.5	9.0	16.0	21.6	0.0	0.0	0.0	0.0	
max_gmiss	1.3	9.0	13.5	2.8	7.5	1.8	3.5	2.9	0.0	
count	2.8	16.0	2.8	71.0	67.5	0.6	2.2	1.5	0.0	
bgld	3.4	21.6	7.5	67.5	84.2	1.0	1.7	1.5	0.0	
vaf_too_low_s	0.1	0.0	1.8	0.6	1.0	3.0	3.0	2.8	0.0	
vaf_too_low_m2	0.3	0.0	3.5	2.2	1.7	3.0	12.7	9.2	0.0	
vaf_zg_too_noisy	0.2	0.0	2.9	1.5	1.5	2.8	9.2	9.4	0.0	
manual_exclude	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	

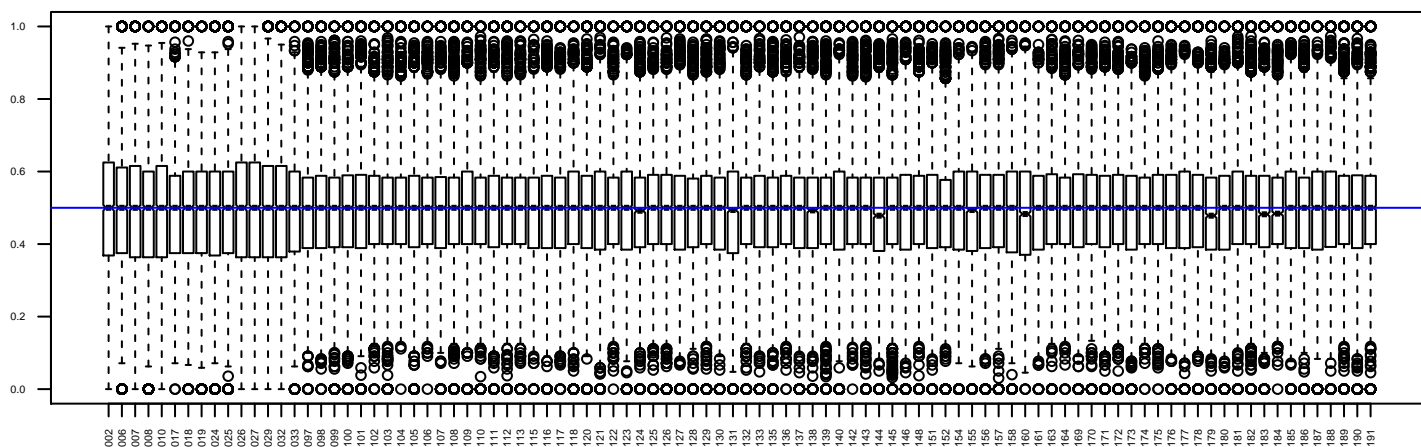
Called INDEL Count vs Average Depth



**PD5847: INDEL : VAF Distribution at Somatic (pass all filters) sites called in Pindel**

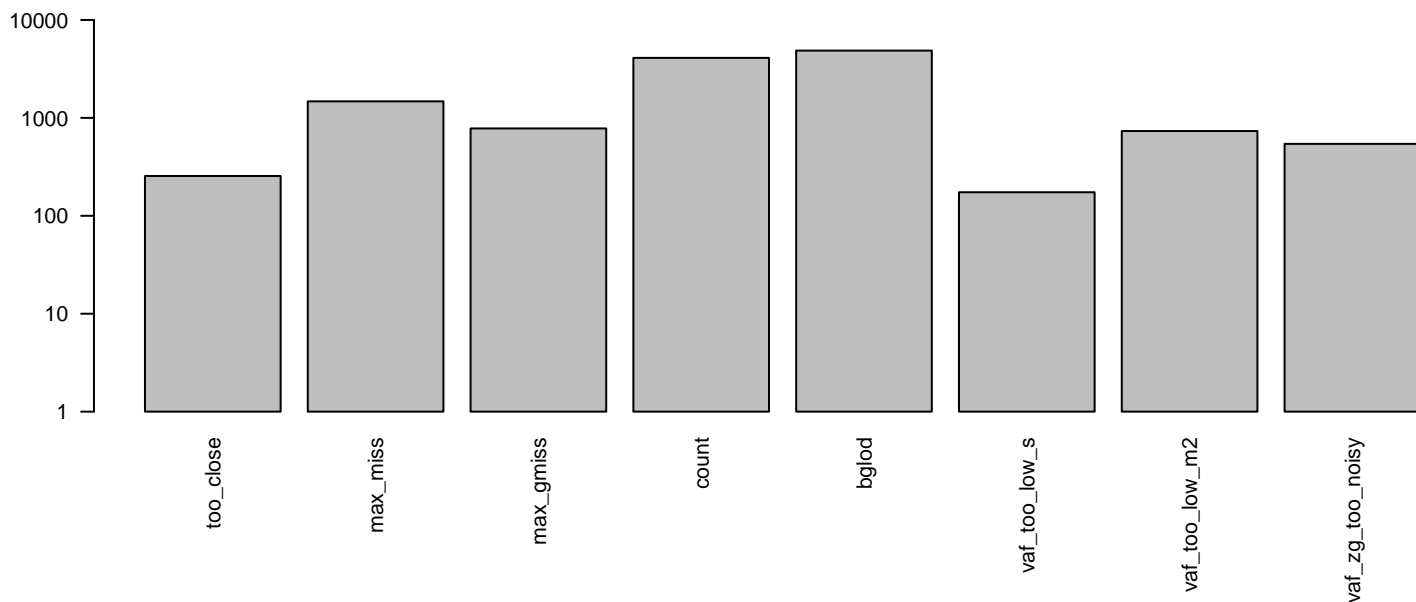


**PD5847: INDEL : VAF Distribution at Germline [Based on the Matched Normal] sites called in Pindel**

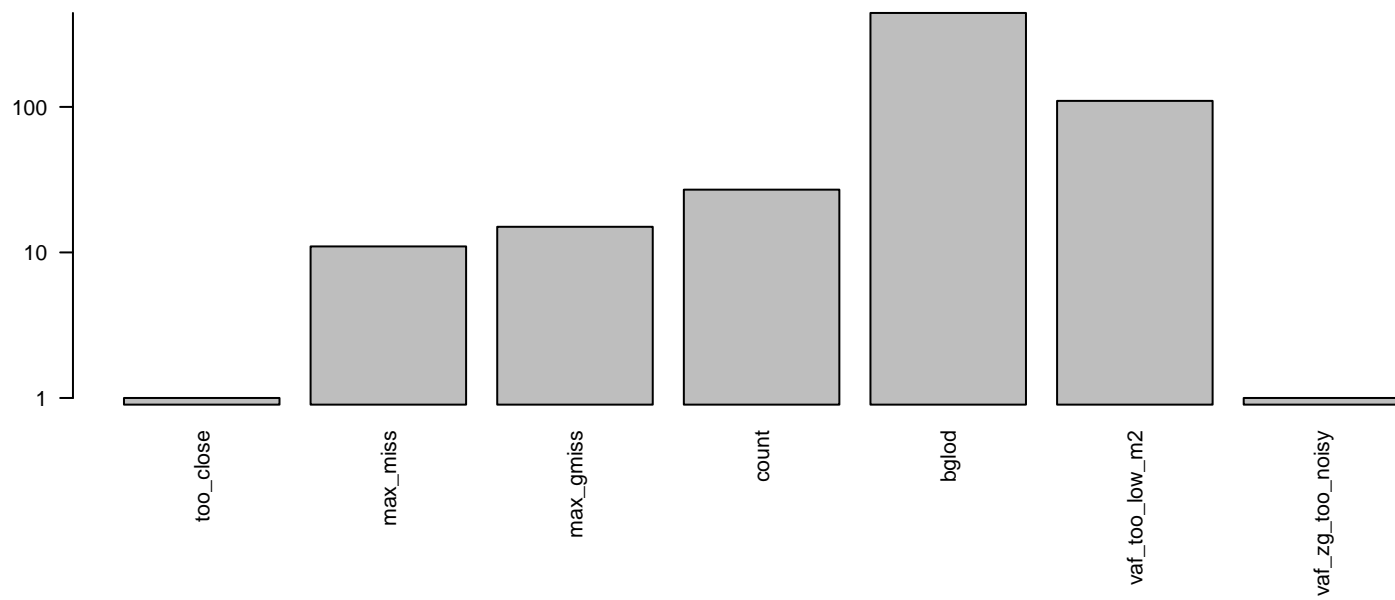




PD5847: INDEL: No. Sites removed by each filter



PD5847: INDEL: No. Sites UNIQUELY removed by each filter

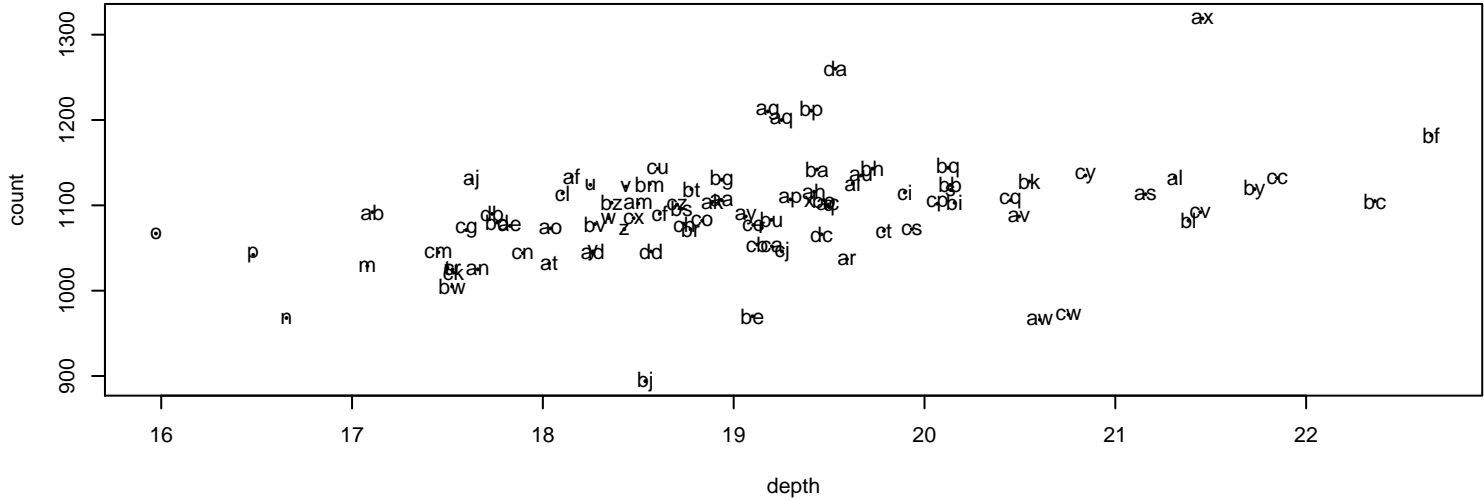


PD5179 : SNVs

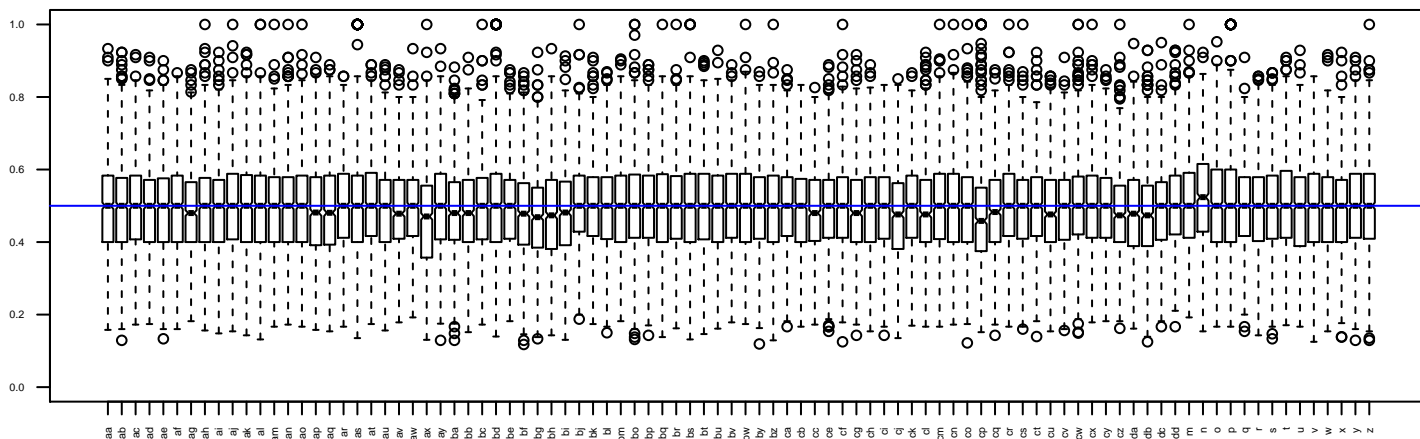
SNV:Pairwise Filter Overlap (% Filtered Variants):Total Fail=38741/Pass=37215

	near_indel	too_close	max_miss	max_gmiss	count	bgld	vaf_too_low_s	vaf_too_low_m2	vaf_zg_too_noisy	manual_exclude	
near_indel	<b>0.2</b>	0.0	0.0	0.1	0.0	0.1	0.1	0.1	0.1	0.0	
too_close	0.0	<b>1.9</b>	0.0	0.0	1.0	1.0	0.0	0.0	0.0	0.0	
max_miss	0.0	0.0	<b>0.2</b>	0.1	0.1	0.1	0.0	0.0	0.0	0.0	
max_gmiss	0.1	0.0	0.1	<b>0.6</b>	0.2	0.2	0.4	0.5	0.4	0.0	
count	0.0	1.0	0.1	0.2	<b>93.9</b>	91.6	0.7	0.9	0.8	0.0	
bgld	0.1	1.0	0.1	0.2	91.6	<b>96.3</b>	0.2	0.3	0.3	0.0	
vaf_too_low_s	0.1	0.0	0.0	0.4	0.7	0.2	<b>1.0</b>	1.0	1.0	0.0	
vaf_too_low_m2	0.1	0.0	0.0	0.5	0.9	0.3	1.0	<b>1.6</b>	1.2	0.0	
vaf_zg_too_noisy	0.1	0.0	0.0	0.4	0.8	0.3	1.0	1.2	<b>1.3</b>	0.0	
manual_exclude	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	<b>0.0</b>	

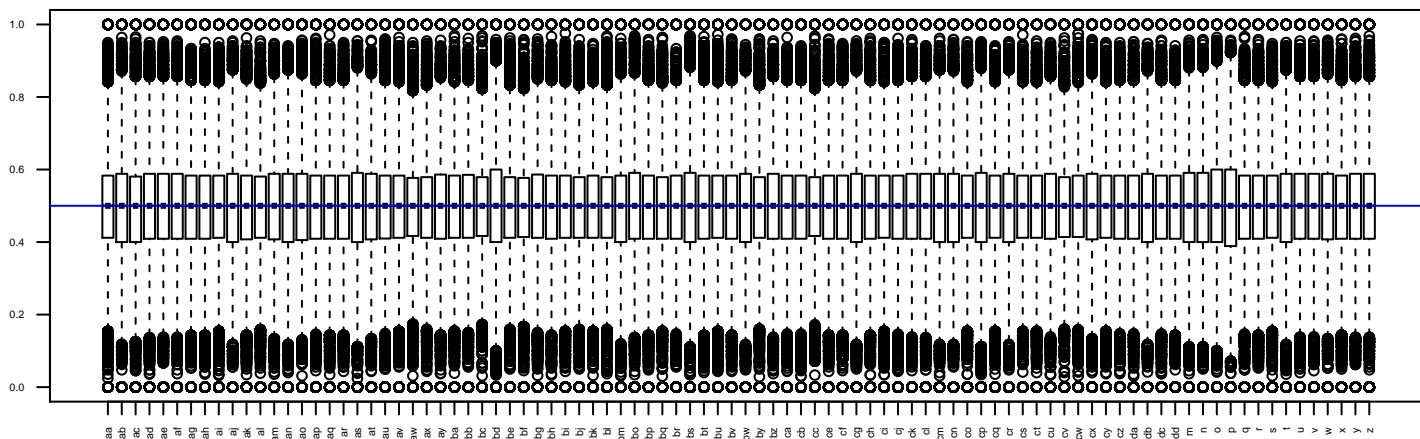
Called SNV Count vs Average Depth



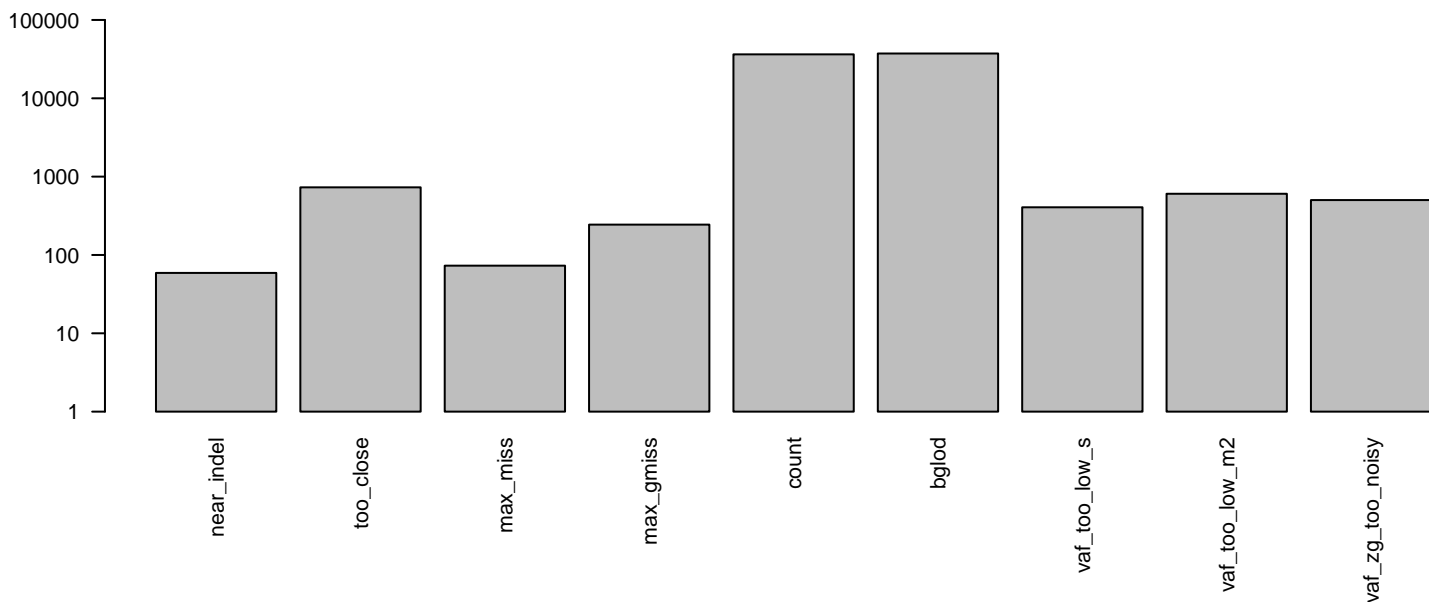
PD5179: SNV : VAF Distribution at Somatic (pass all filters) sites called in Caveman



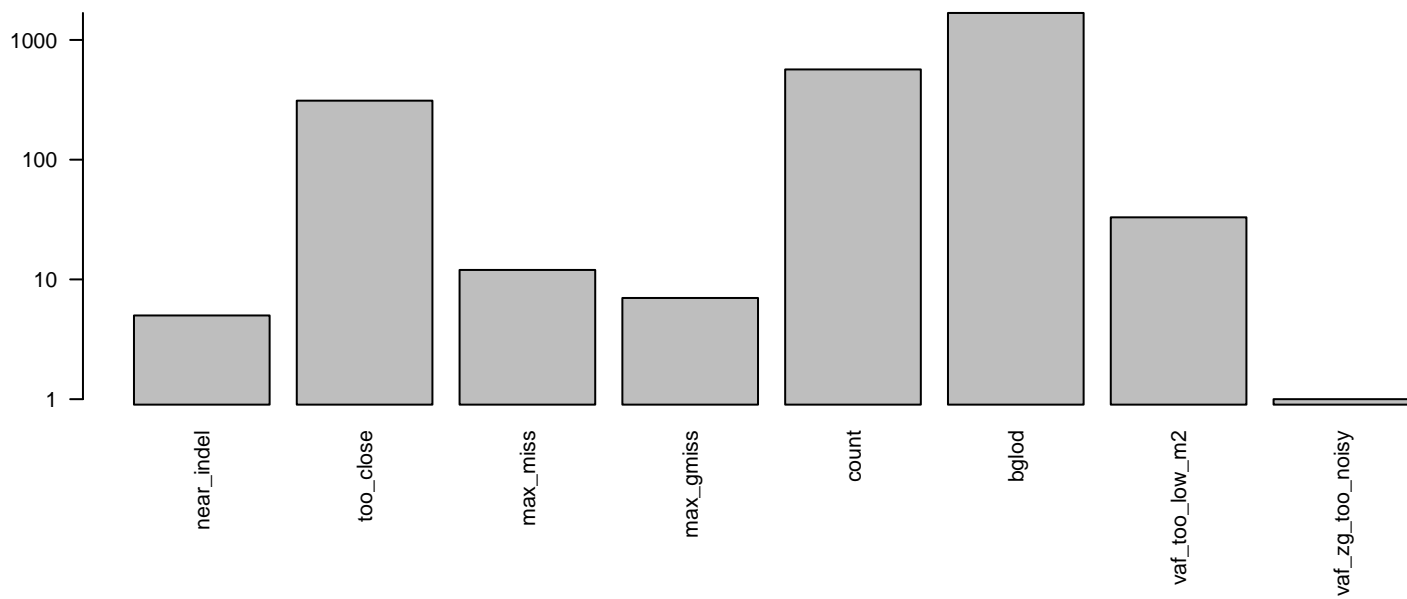
PD5179: SNV : VAF Distribution at Germline [Based on the Matched Normal] sites called in Caveman



PD5179: SNV: No. Sites removed by each filter



PD5179: SNV: No. Sites UNIQUELY removed by each filter

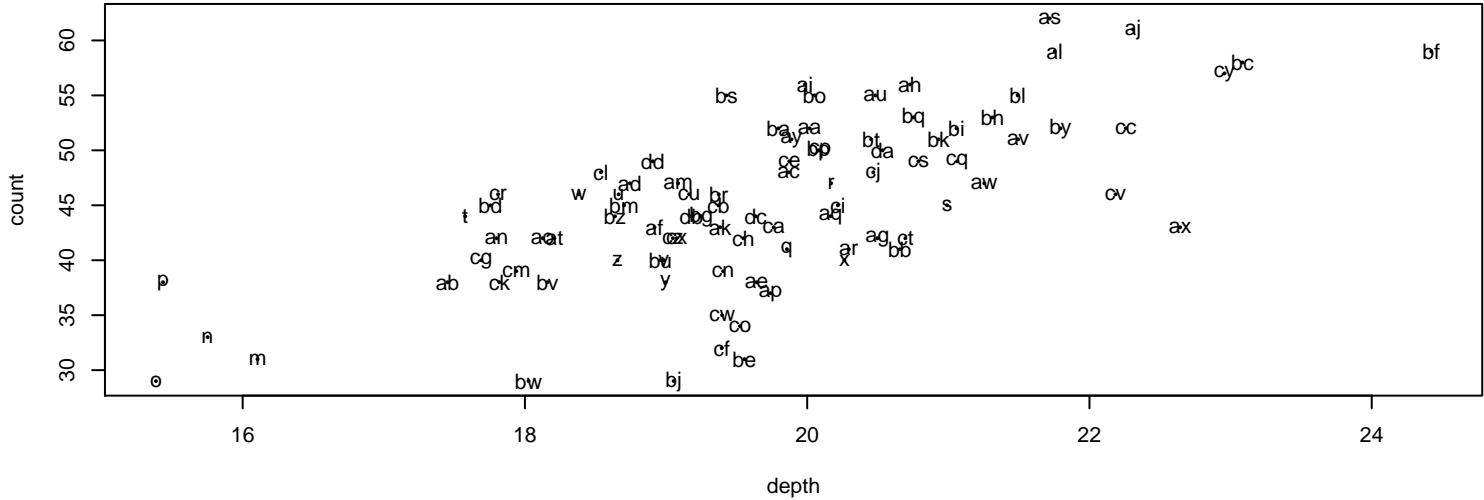


PD5179 : Indels

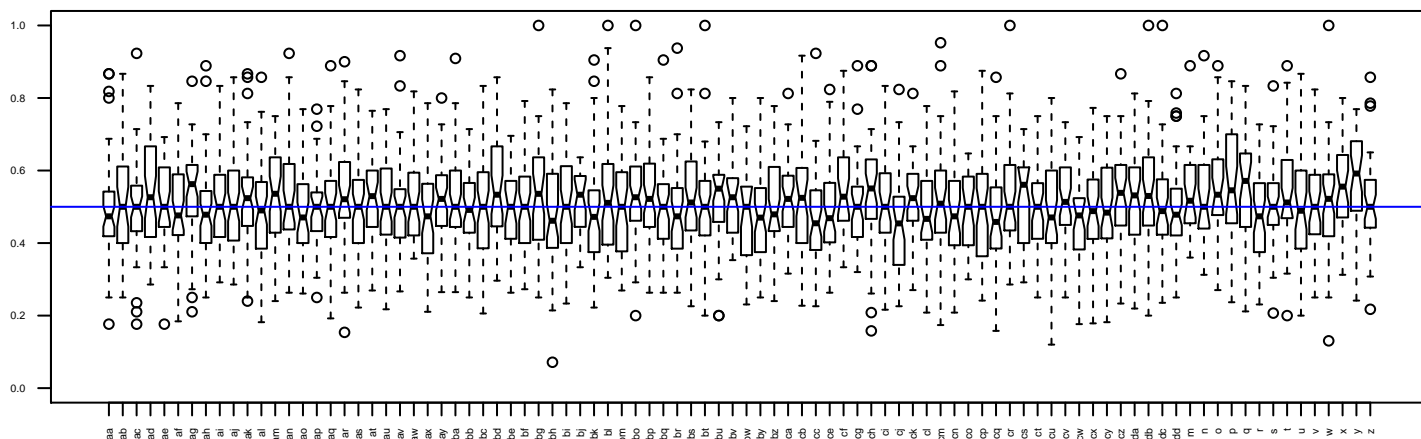
Indels:Pairwise Filter Overlap (% Filtered Variants):Total Fail=6949/Pass=1307

	too_close	max_miss	max_gmiss	count	bglod	vaf_too_low_s	vaf_too_low_m2	vaf_zg_too_noisy	manual_exclude	
too_close	4.9	2.9	1.4	2.9	3.0	0.1	0.3	0.2	0.0	
max_miss	2.9	20.8	7.3	12.5	14.0	0.0	0.0	0.1	0.0	
max_gmiss	1.4	7.3	13.8	1.4	4.3	2.2	4.4	3.8	0.0	
count	2.9	12.5	1.4	67.6	61.7	0.7	3.4	2.4	0.0	
bglod	3.0	14.0	4.3	61.7	74.2	0.9	1.9	2.1	0.0	
vaf_too_low_s	0.1	0.0	2.2	0.7	0.9	3.7	3.7	3.6	0.0	
vaf_too_low_m2	0.3	0.0	4.4	3.4	1.9	3.7	18.1	13.0	0.0	
vaf_zg_too_noisy	0.2	0.1	3.8	2.4	2.1	3.6	13.0	13.9	0.0	
manual_exclude	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	

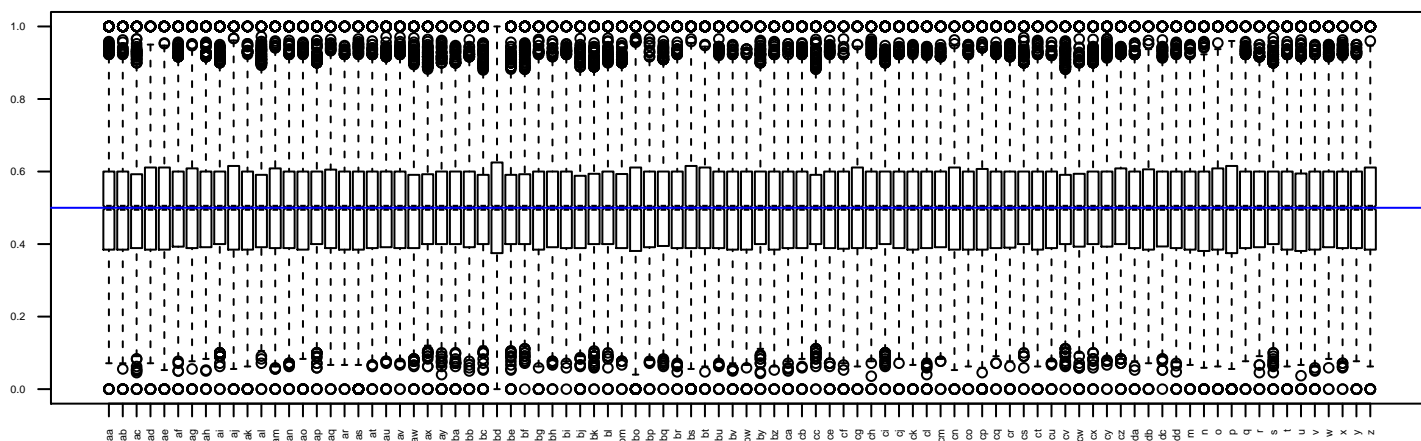
Called INDEL Count vs Average Depth



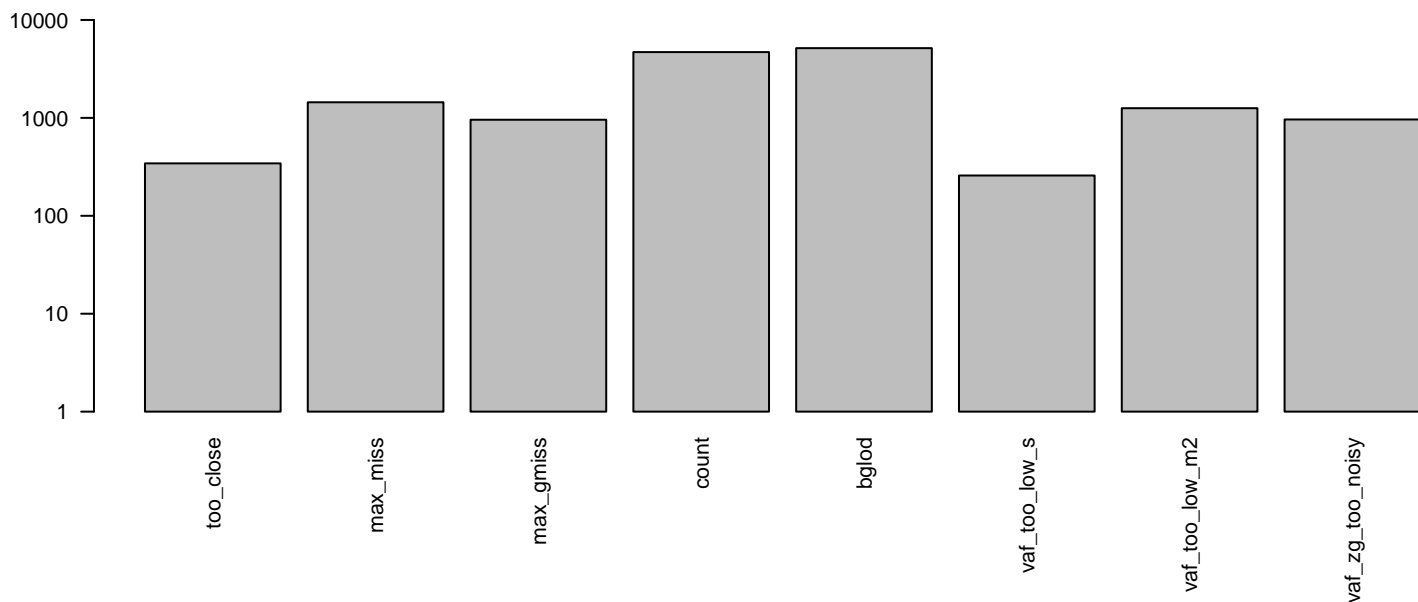
PD5179: INDEL : VAF Distribution at Somatic (pass all filters) sites called in Pindel



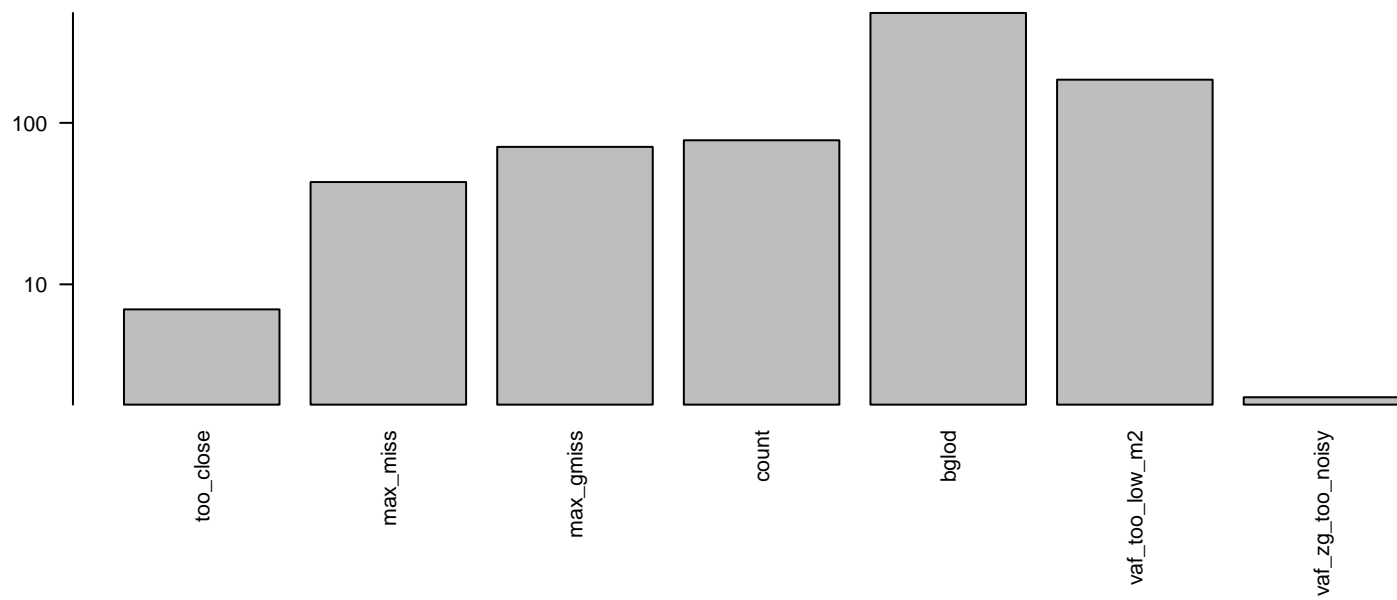
PD5179: INDEL : VAF Distribution at Germline [Based on the Matched Normal] sites called in Pindel



PD5179: INDEL: No. Sites removed by each filter



PD5179: INDEL: No. Sites UNIQUELY removed by each filter

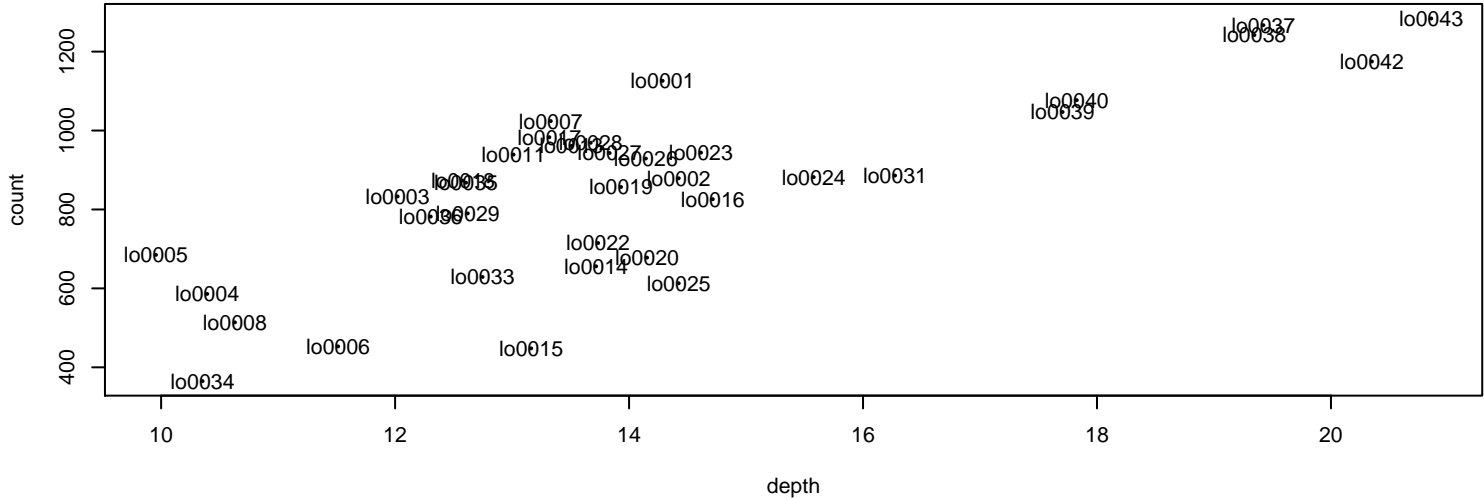


PD6634 : SNVs

SNV:Pairwise Filter Overlap (% Filtered Variants):Total Fail=36193/Pass=16531

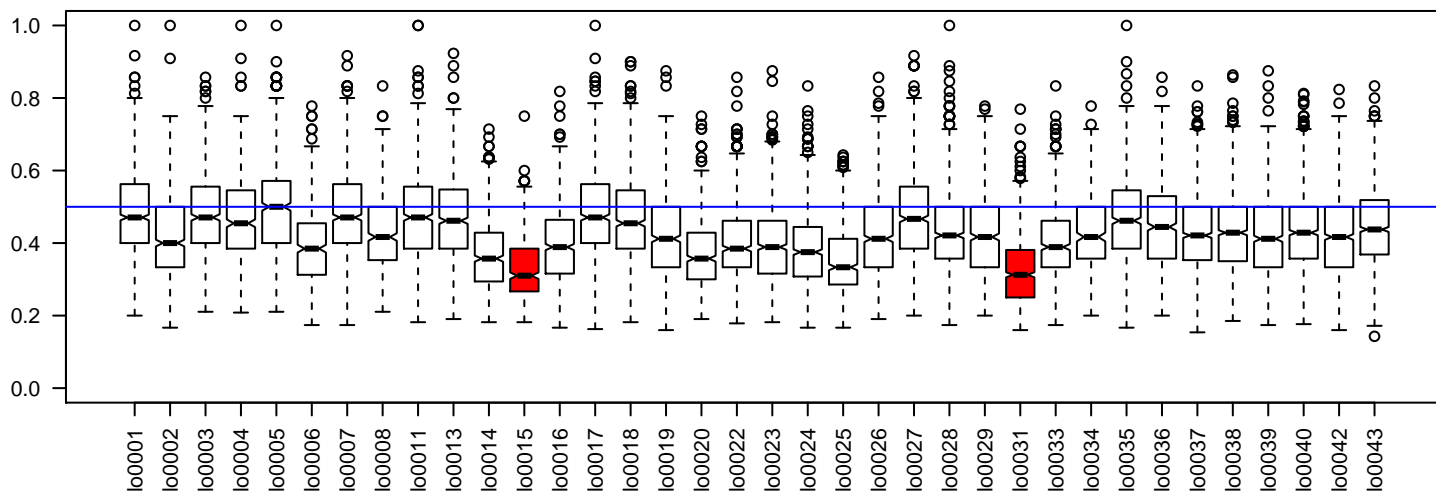
	near_indel	too_close	max_miss	max_gmiss	count	bgld	vaf_too_low_s	vaf_too_low_m2	vaf_zg_too_noisy	manual_exclude	
near_indel	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	
too_close	0.0	1.3	0.0	0.0	0.9	0.9	0.0	0.0	0.0	0.0	
max_miss	0.0	0.0	1.2	0.3	0.9	1.0	0.0	0.0	0.0	0.0	
max_gmiss	0.0	0.0	0.3	0.7	0.4	0.3	0.2	0.4	0.3	0.0	
count	0.0	0.9	0.9	0.4	95.4	93.8	0.5	0.7	0.5	0.0	
bgld	0.0	0.9	1.0	0.3	93.8	97.6	0.0	0.1	0.0	0.0	
vaf_too_low_s	0.0	0.0	0.0	0.2	0.5	0.0	0.7	0.7	0.5	0.0	
vaf_too_low_m2	0.0	0.0	0.0	0.4	0.7	0.1	0.7	1.0	0.7	0.0	
vaf_zg_too_noisy	0.0	0.0	0.0	0.3	0.5	0.0	0.5	0.7	0.7	0.0	
manual_exclude	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	

Called SNV Count vs Average Depth

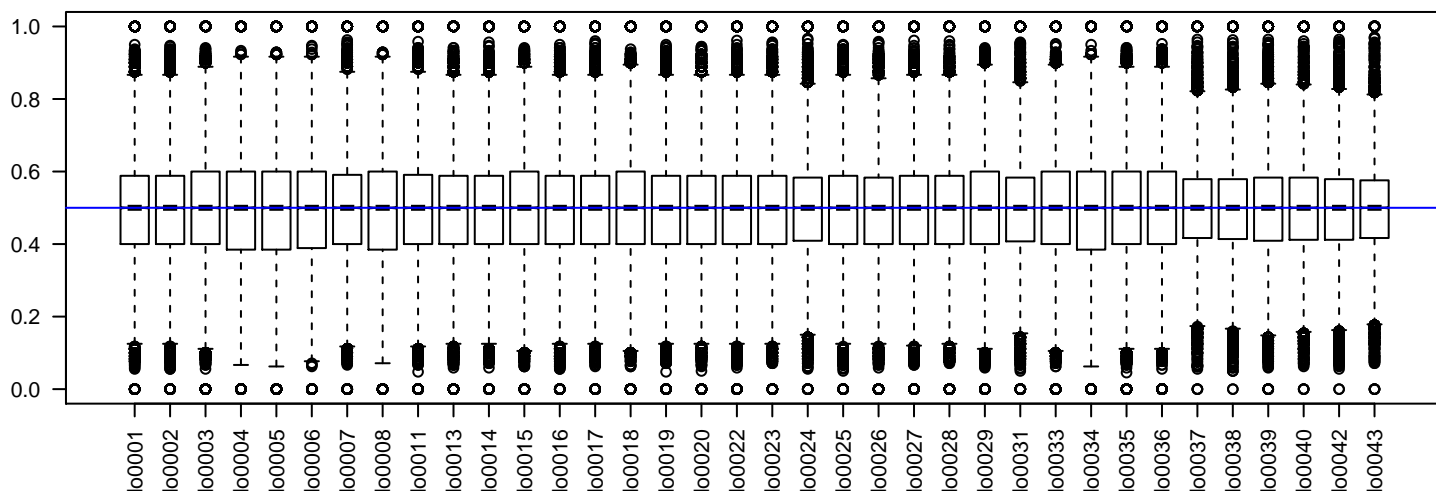




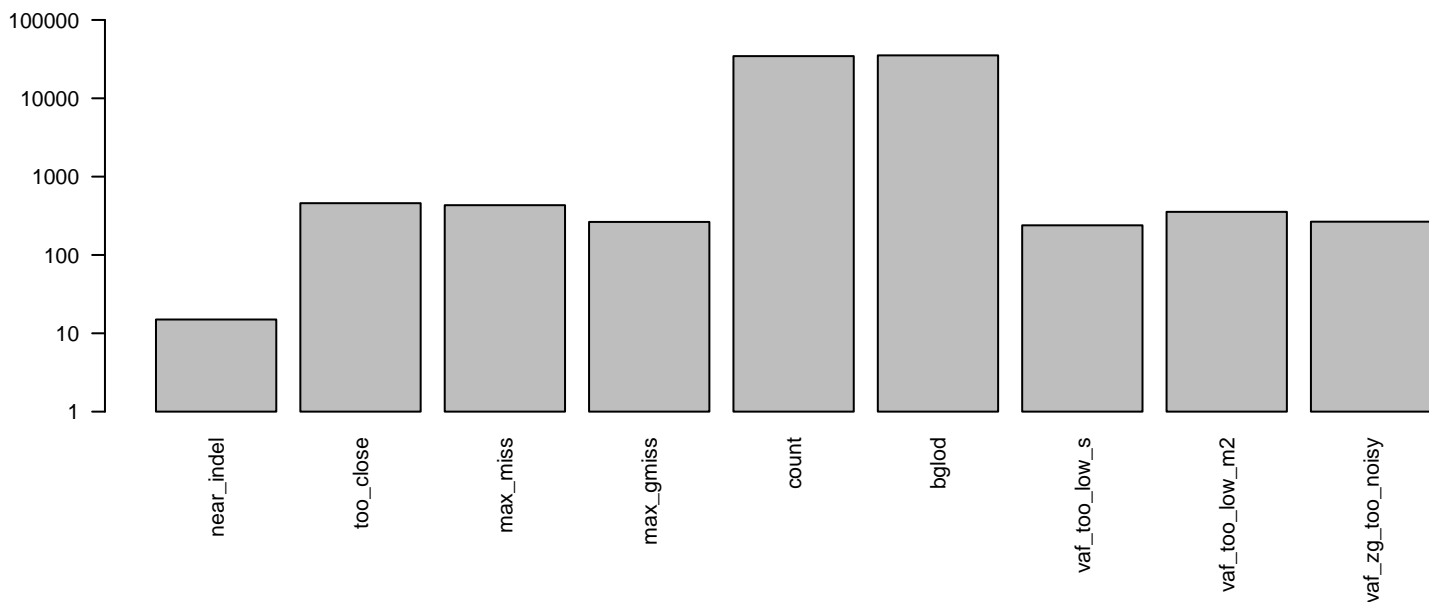
PD6634: SNV : VAF Distribution at Somatic (pass all filters) sites called in Caveman



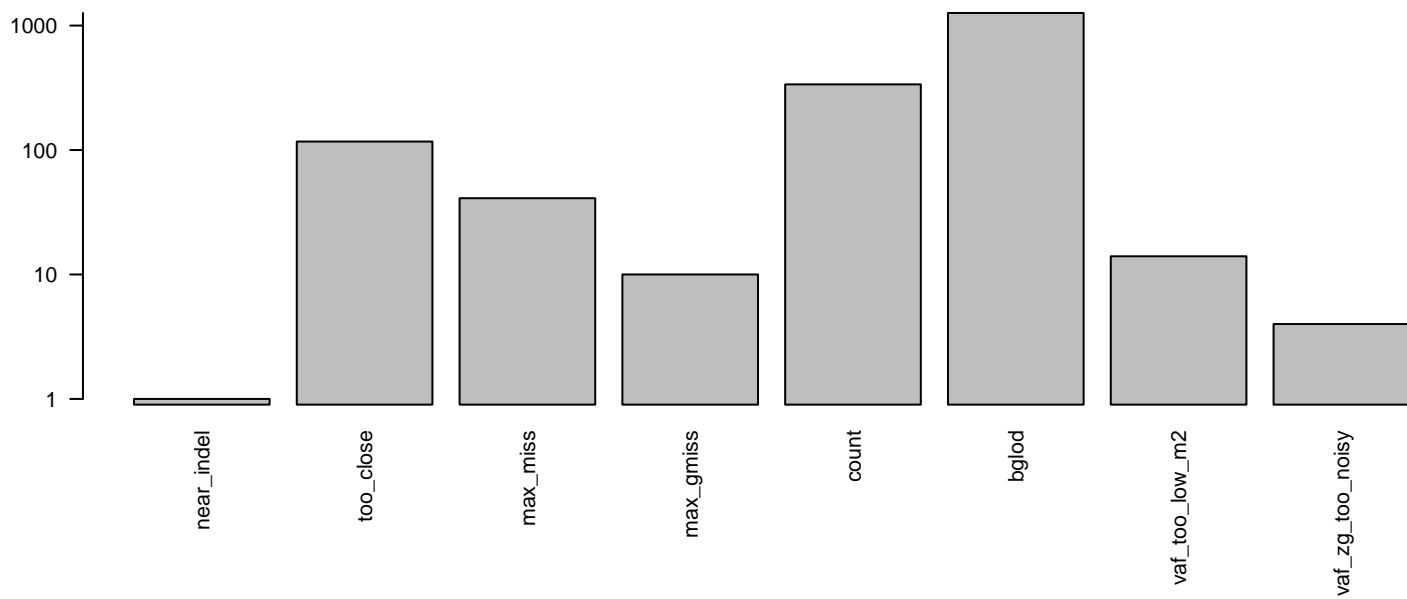
PD6634: SNV : VAF Distribution at Germline [Based on the Matched Normal] sites called in Caveman



PD6634: SNV: No. Sites removed by each filter



PD6634: SNV: No. Sites UNIQUELY removed by each filter

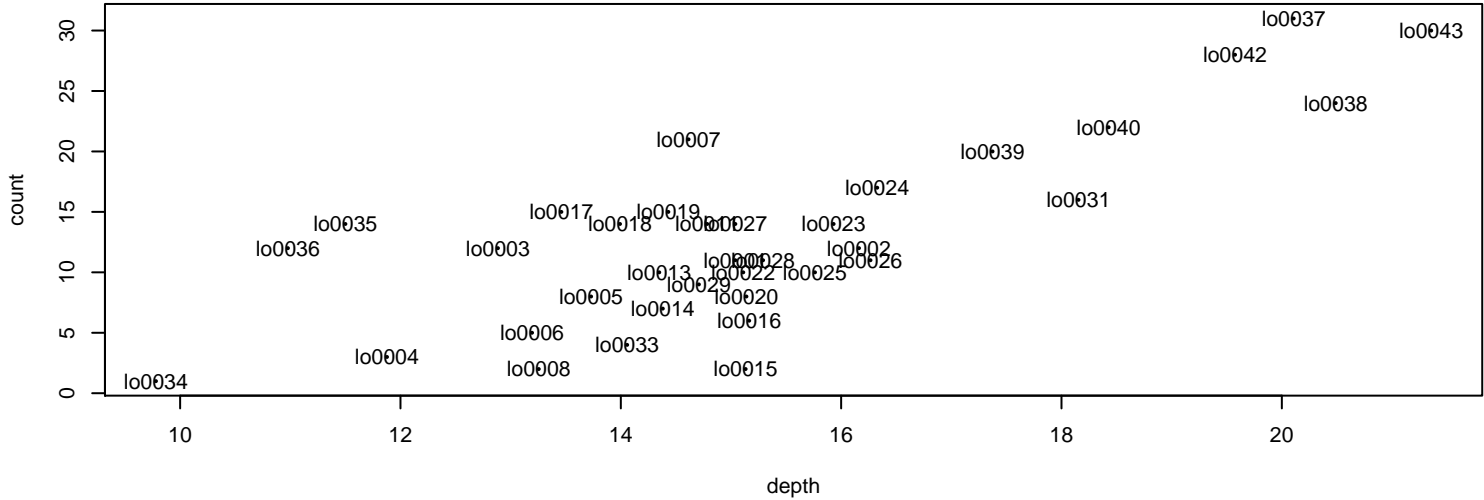


PD6634 : Indels

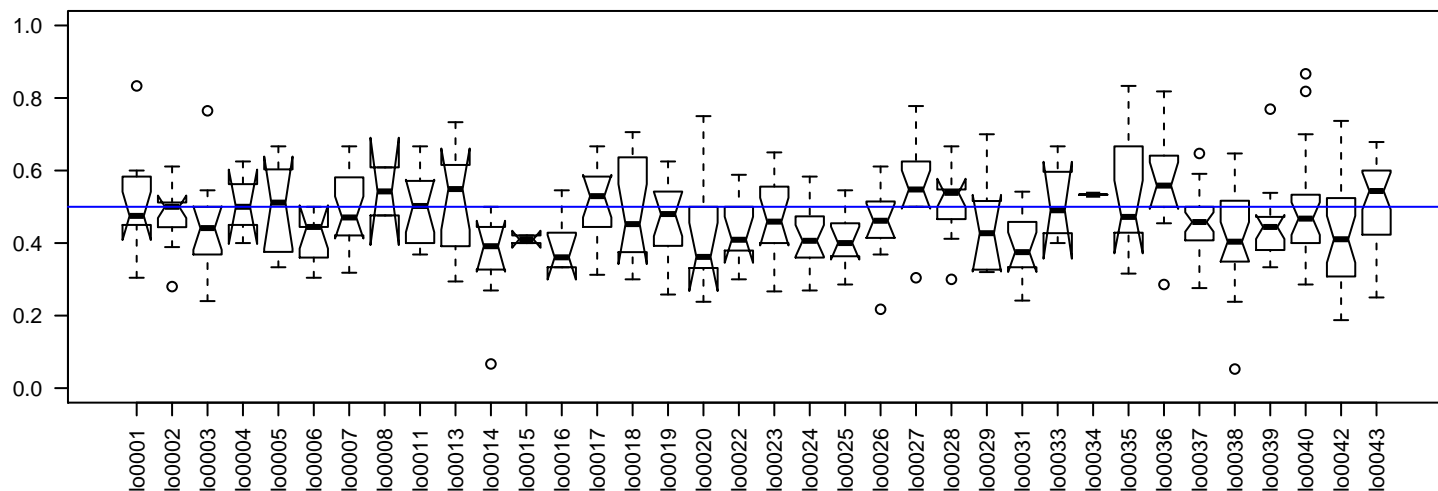
Indels:Pairwise Filter Overlap (% Filtered Variants):Total Fail=3421/Pass=278

	too_close	max_miss	max_gmiss	count	bgld	vaf_too_low_s	vaf_too_low_m2	vaf_zg_too_noisy	manual_exclude	
too_close	0.5	0.1	0.1	0.3	0.4	0.0	0.0	0.0	0.0	
max_miss	0.1	13.8	5.5	9.6	12.6	0.0	0.0	0.0	0.0	
max_gmiss	0.1	5.5	7.2	3.2	5.1	0.1	0.9	0.6	0.0	
count	0.3	9.6	3.2	87.0	85.5	0.6	1.1	0.7	0.0	
bgld	0.4	12.6	5.1	85.5	95.8	0.3	0.6	0.3	0.0	
vaf_too_low_s	0.0	0.0	0.1	0.6	0.3	0.8	0.8	0.5	0.0	
vaf_too_low_m2	0.0	0.0	0.9	1.1	0.6	0.8	2.9	1.7	0.0	
vaf_zg_too_noisy	0.0	0.0	0.6	0.7	0.3	0.5	1.7	1.7	0.0	
manual_exclude	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	

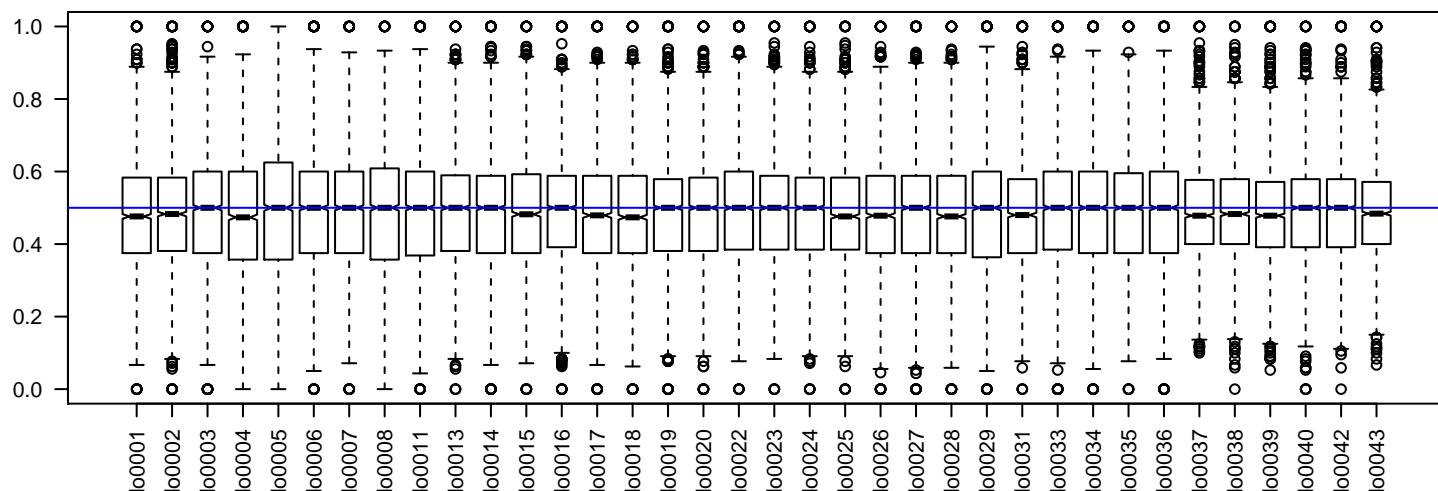
Called INDEL Count vs Average Depth



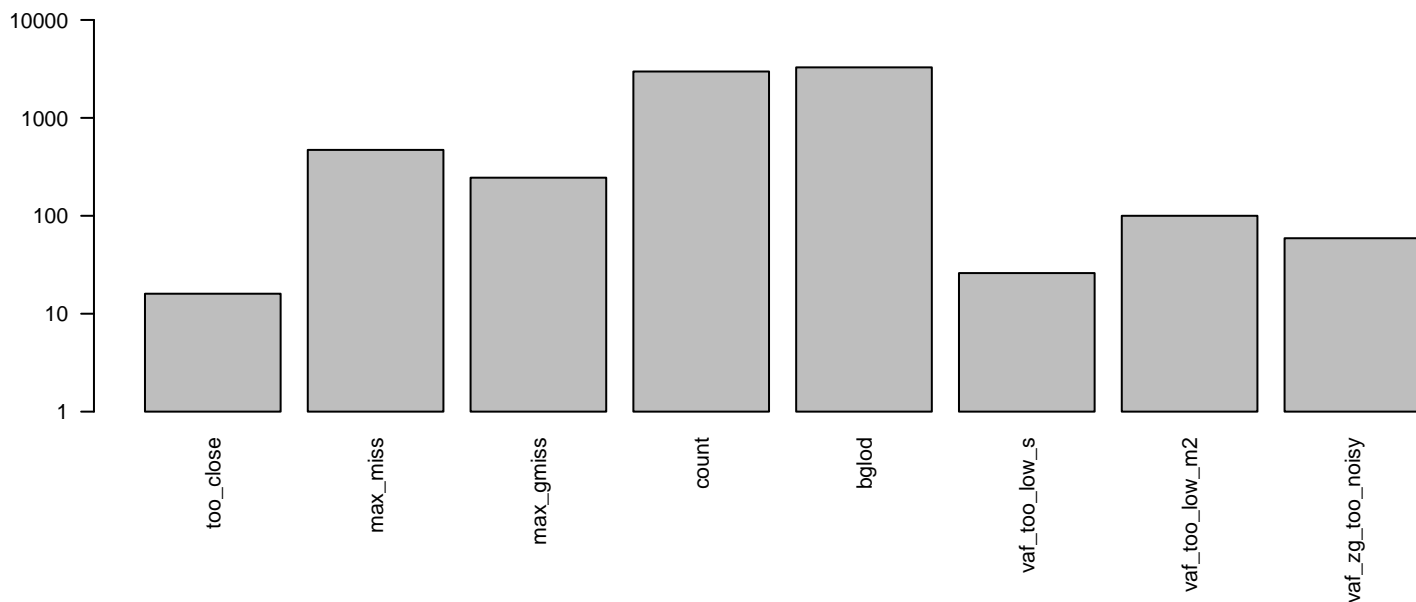
**PD6634: INDEL : VAF Distribution at Somatic (pass all filters) sites called in Pindel**



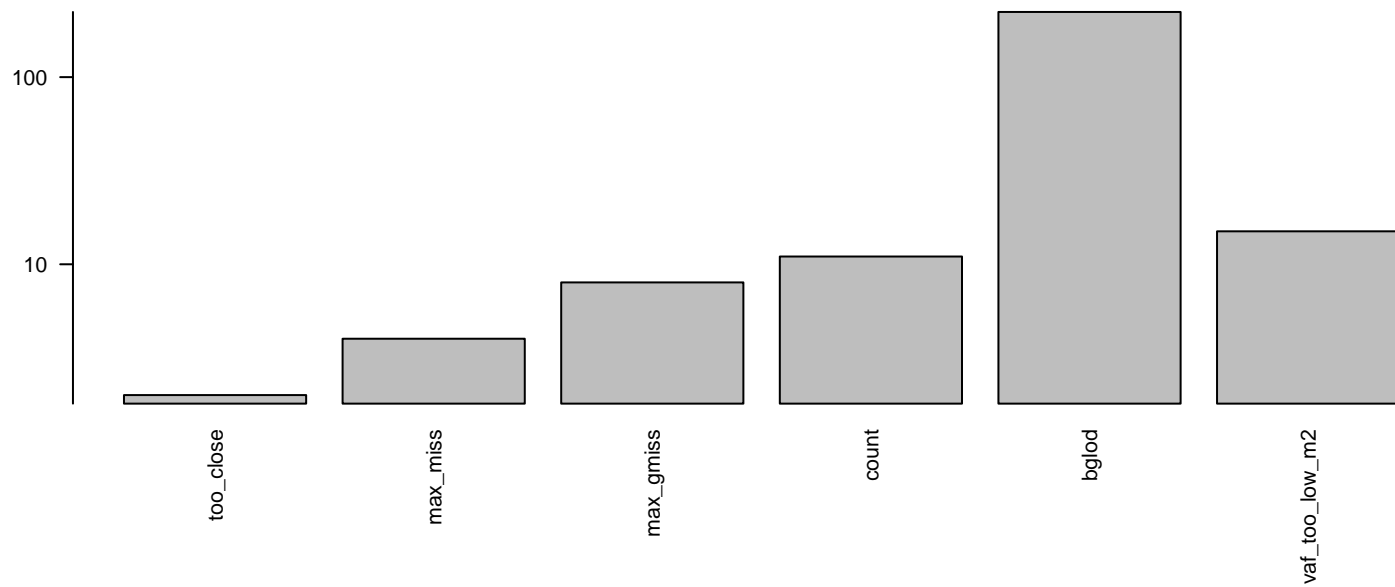
**PD6634: INDEL : VAF Distribution at Germline [Based on the Matched Normal] sites called in Pindel**



PD6634: INDEL: No. Sites removed by each filter

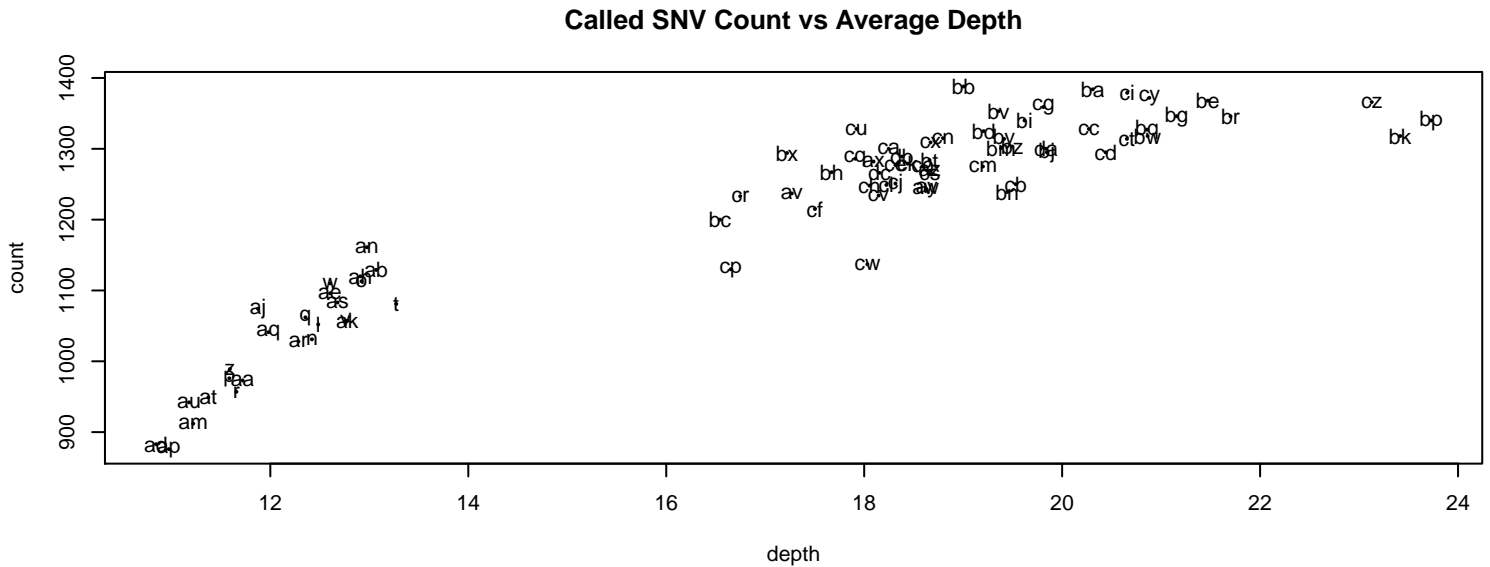


PD6634: INDEL: No. Sites UNIQUELY removed by each filter

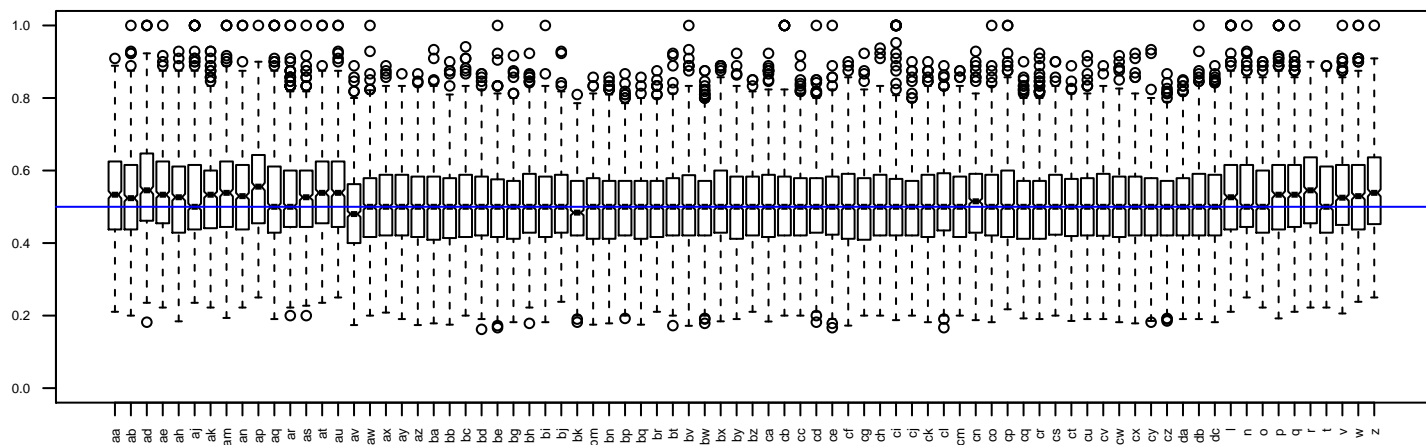


PD9478 : SNVs

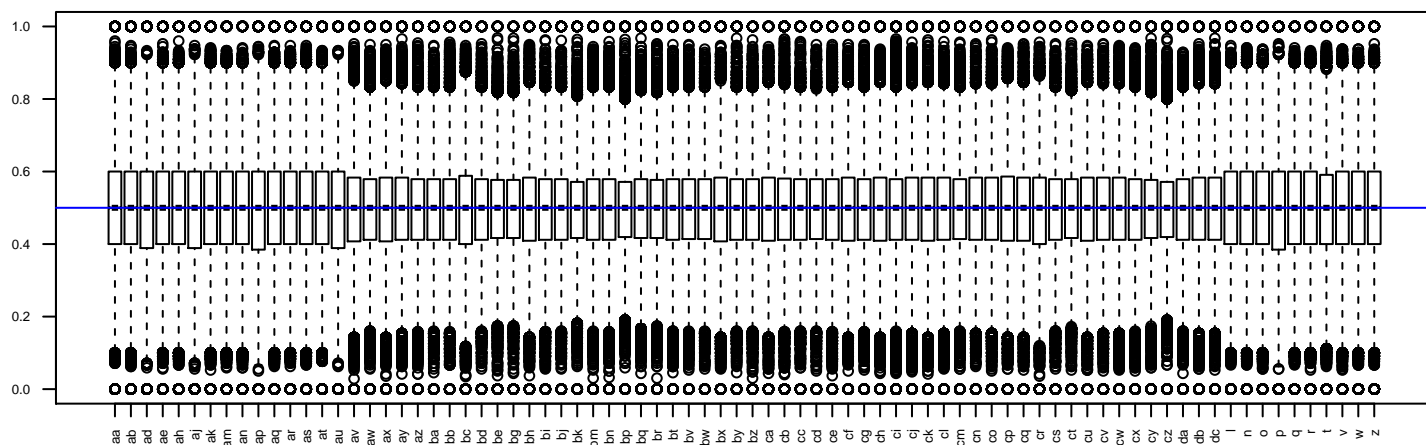
**SNV:Pairwise Filter Overlap (% Filtered Variants):Total Fail=36931/Pass=33660**

[illegible]

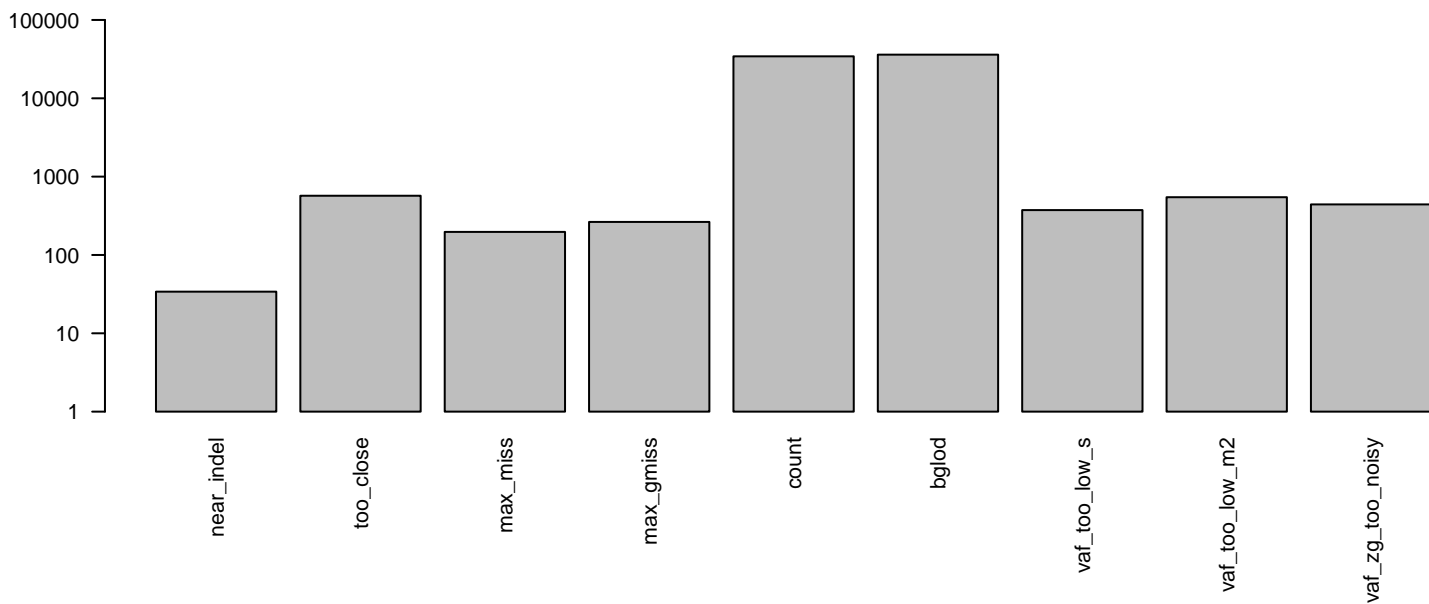
PD9478: SNV : VAF Distribution at Somatic (pass all filters) sites called in Caveman



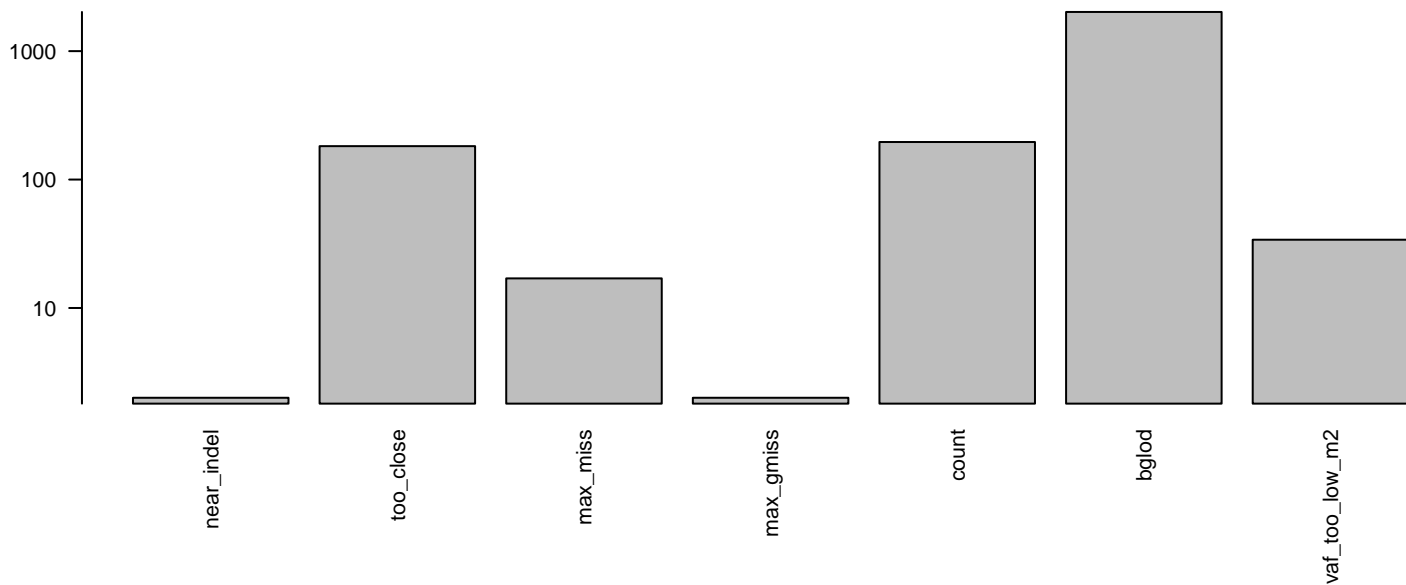
PD9478: SNV : VAF Distribution at Germline [Based on the Matched Normal] sites called in Caveman



**PD9478: SNV: No. Sites removed by each filter**



**PD9478: SNV: No. Sites UNIQUELY removed by each filter**



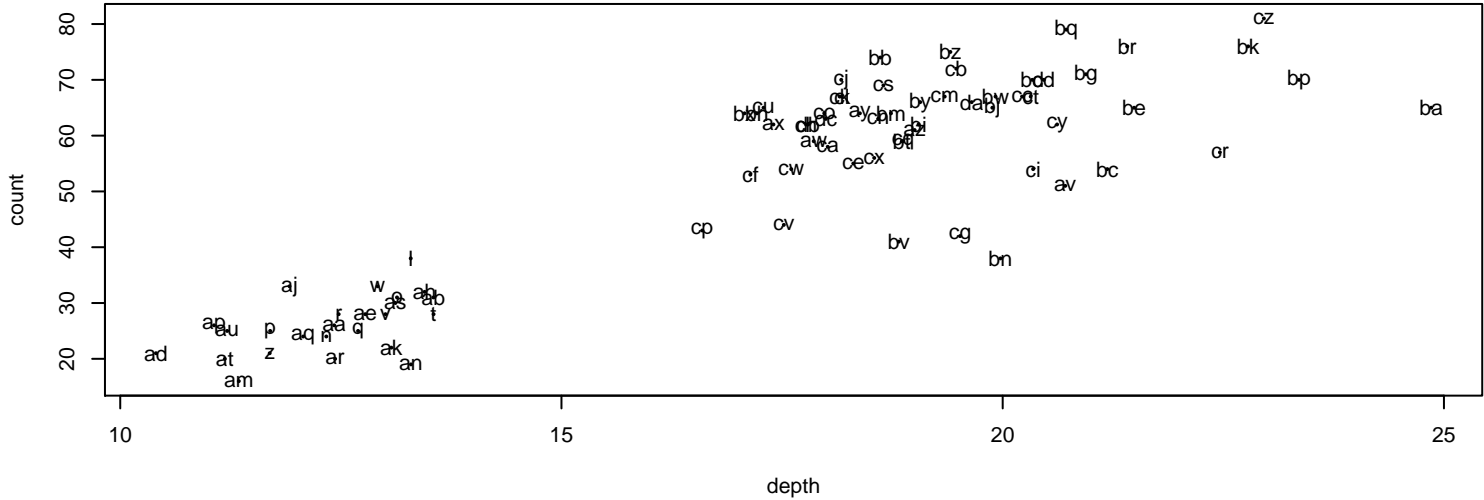


PD9478 : Indels

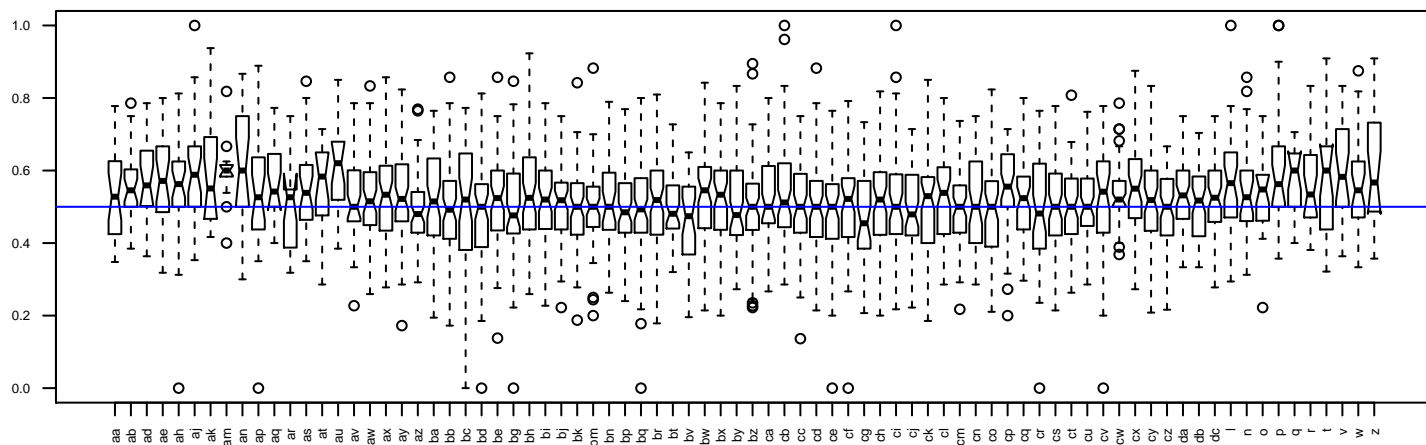
Indels:Pairwise Filter Overlap (% Filtered Variants):Total Fail=5810/Pass=1292

	too_close	max_miss	max_gmiss	count	bgld	vaf_too_low_s	vaf_too_low_m2	vaf_zg_too_noisy	manual_exclude	
too_close	3.1	2.4	1.3	1.8	1.9	0.0	0.2	0.1	0.0	
max_miss	2.4	27.4	11.5	16.7	19.4	0.1	0.2	0.1	0.0	
max_gmiss	1.3	11.5	16.6	3.8	6.8	1.5	4.1	3.1	0.0	
count	1.8	16.7	3.8	68.9	63.2	0.5	2.9	1.7	0.0	
bgld	1.9	19.4	6.8	63.2	77.0	0.8	1.7	1.3	0.0	
vaf_too_low_s	0.0	0.1	1.5	0.5	0.8	2.5	2.5	2.4	0.0	
vaf_too_low_m2	0.2	0.2	4.1	2.9	1.7	2.5	15.5	9.8	0.0	
vaf_zg_too_noisy	0.1	0.1	3.1	1.7	1.3	2.4	9.8	10.1	0.0	
manual_exclude	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	

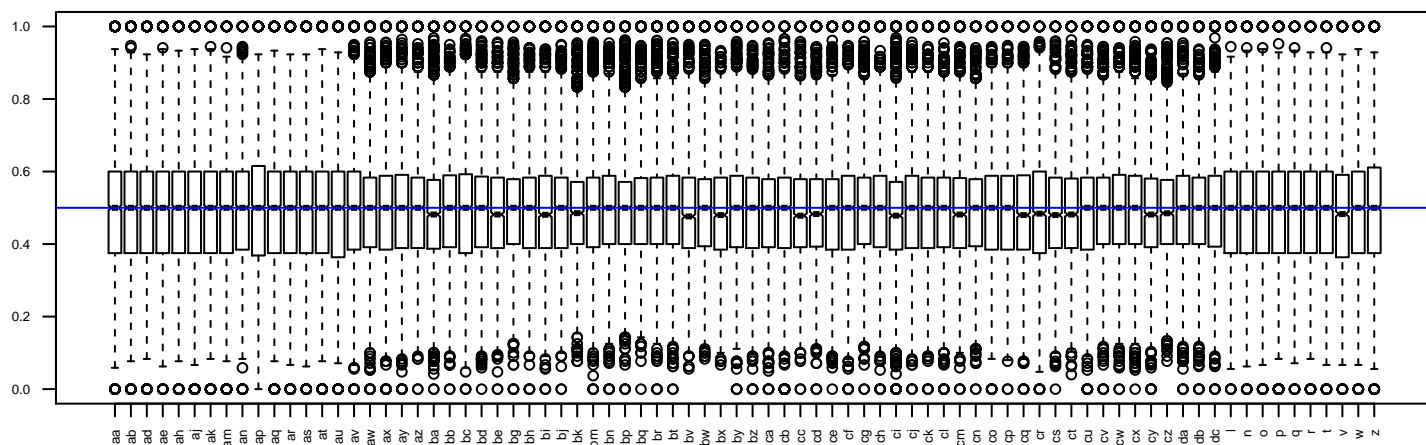
Called INDEL Count vs Average Depth



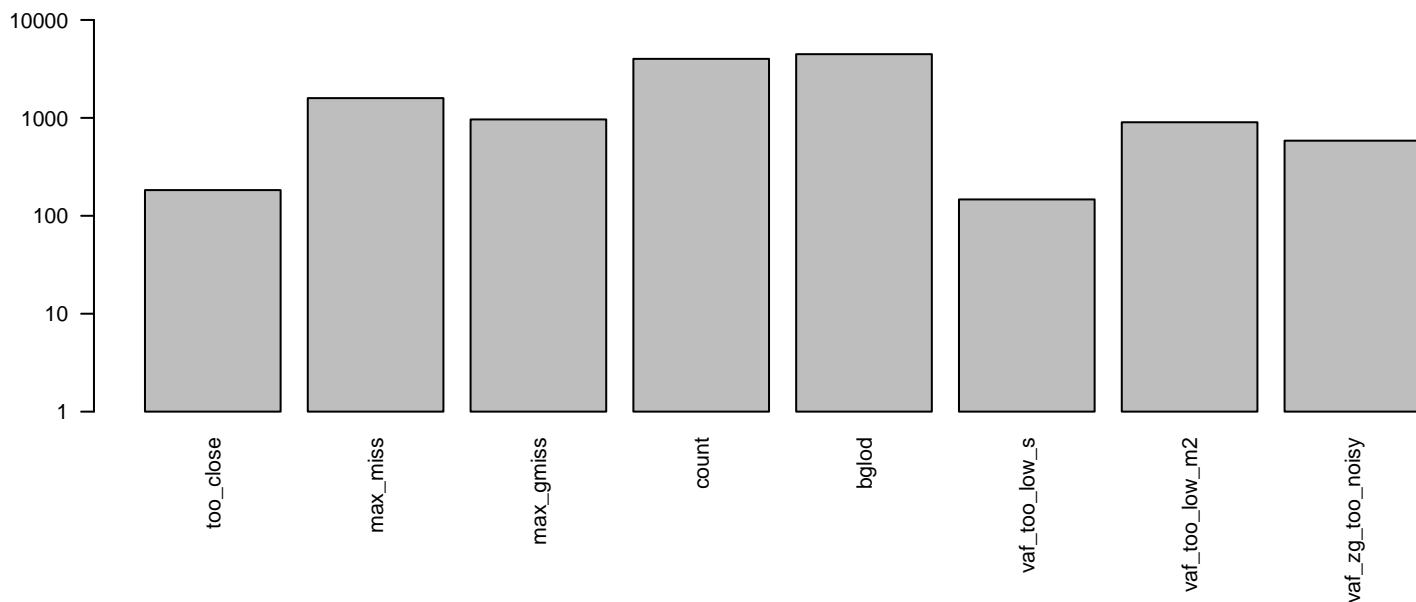
PD9478: INDEL : VAF Distribution at Somatic (pass all filters) sites called in Pindel



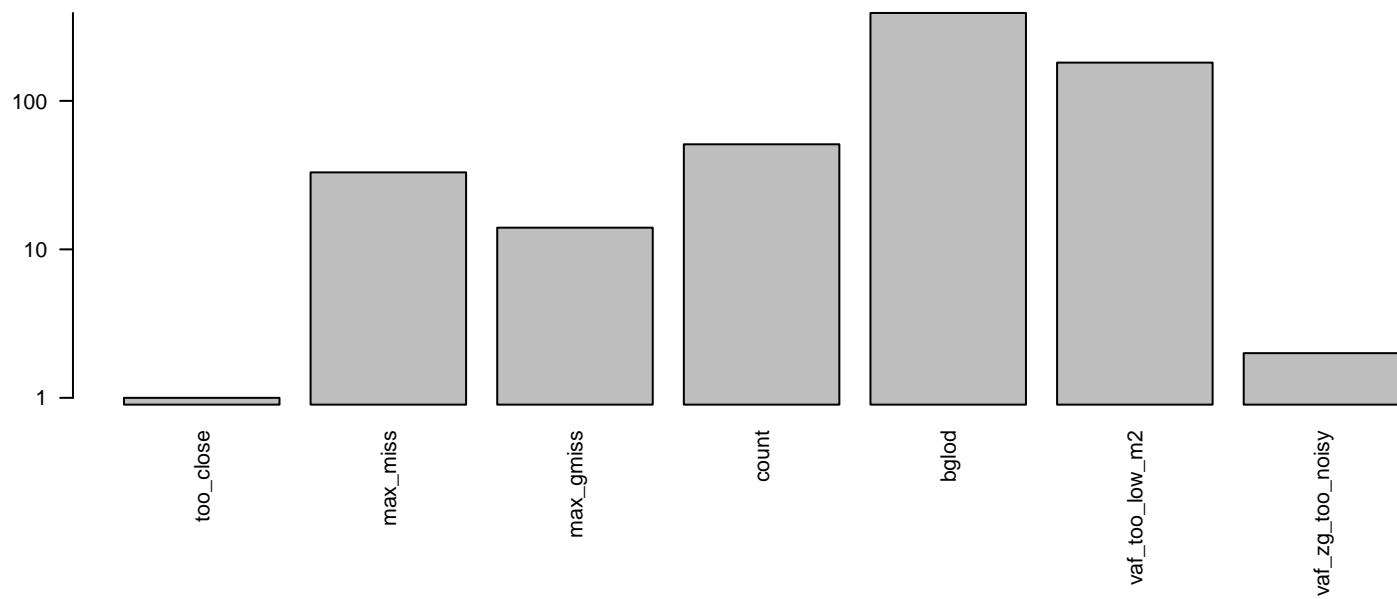
PD9478: INDEL : VAF Distribution at Germline [Based on the Matched Normal] sites called in Pindel



**PD9478: INDEL: No. Sites removed by each filter**



**PD9478: INDEL: No. Sites UNIQUELY removed by each filter**

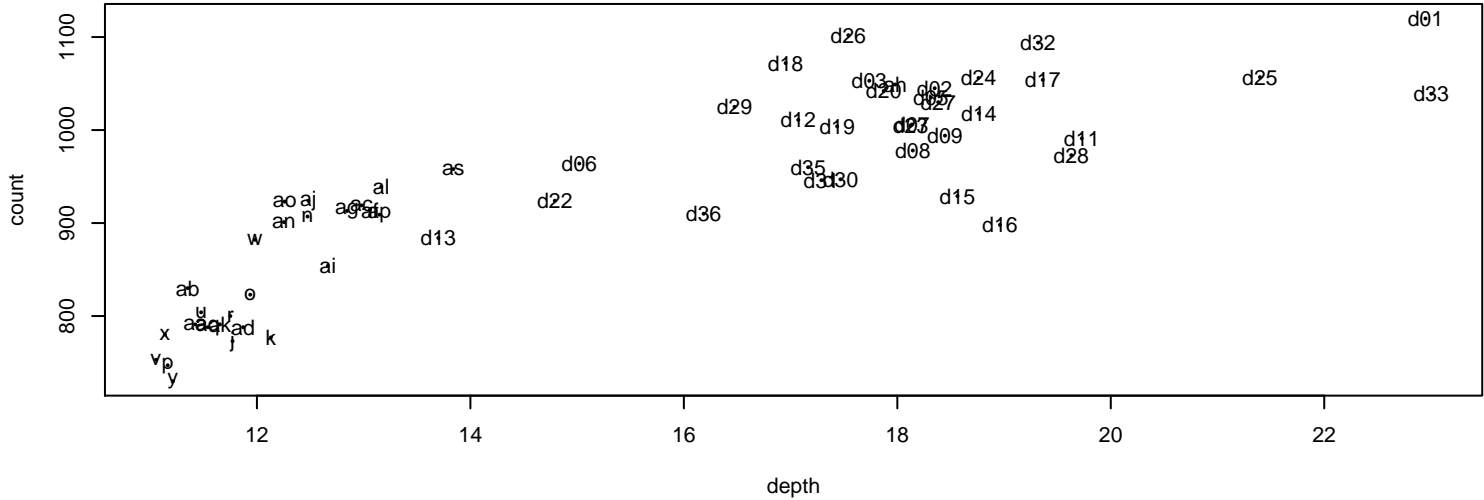


PD6629 : SNVs

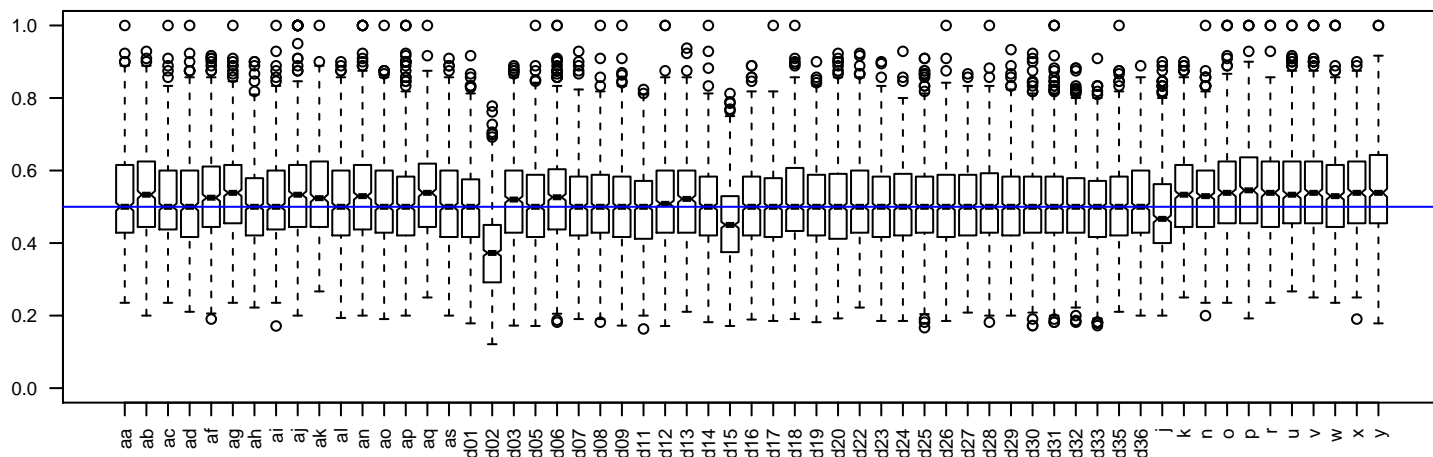
SNV:Pairwise Filter Overlap (% Filtered Variants):Total Fail=34522/Pass=31318

	near_indel	too_close	max_miss	max_gmiss	count	bgld	vaf_too_low_s	vaf_too_low_m2	vaf_zg_too_noisy	manual_exclude	
near_indel	0.1	0.0	0.0	0.1	0.0	0.0	0.0	0.1	0.1	0.0	
too_close	0.0	1.5	0.0	0.0	0.9	1.0	0.0	0.0	0.0	0.0	
max_miss	0.0	0.0	1.3	0.3	0.8	0.9	0.0	0.0	0.0	0.0	
max_gmiss	0.1	0.0	0.3	0.9	0.3	0.3	0.3	0.5	0.4	0.0	
count	0.0	0.9	0.8	0.3	92.8	91.3	0.6	0.8	0.6	0.0	
bgld	0.0	1.0	0.9	0.3	91.3	97.1	0.1	0.2	0.1	0.0	
vaf_too_low_s	0.0	0.0	0.0	0.3	0.6	0.1	0.9	0.9	0.8	0.0	
vaf_too_low_m2	0.1	0.0	0.0	0.5	0.8	0.2	0.9	1.4	1.0	0.0	
vaf_zg_too_noisy	0.1	0.0	0.0	0.4	0.6	0.1	0.8	1.0	1.1	0.0	
manual_exclude	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	

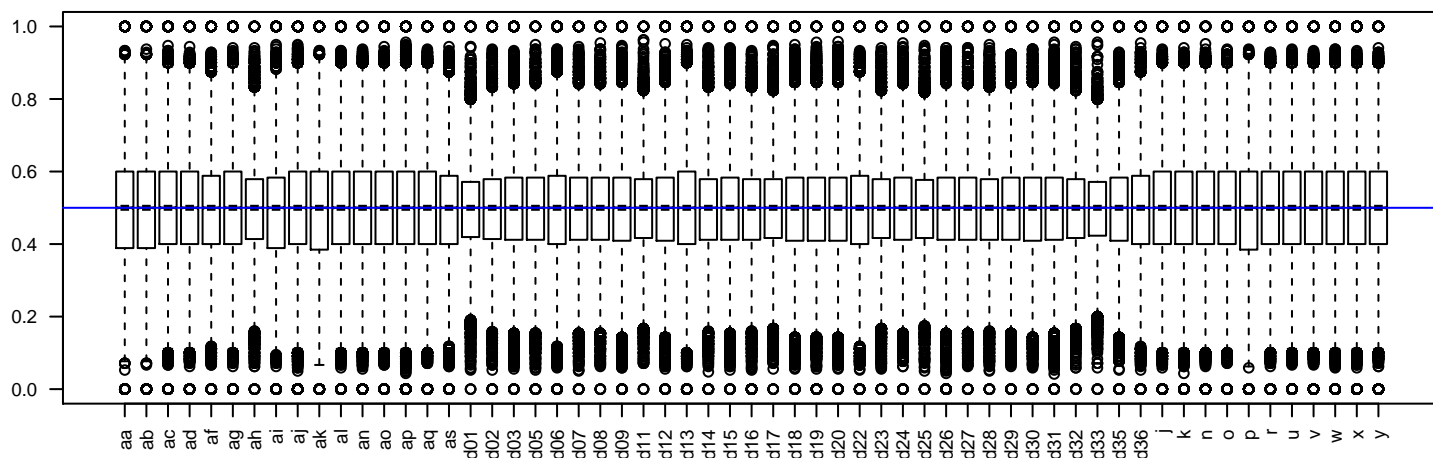
Called SNV Count vs Average Depth



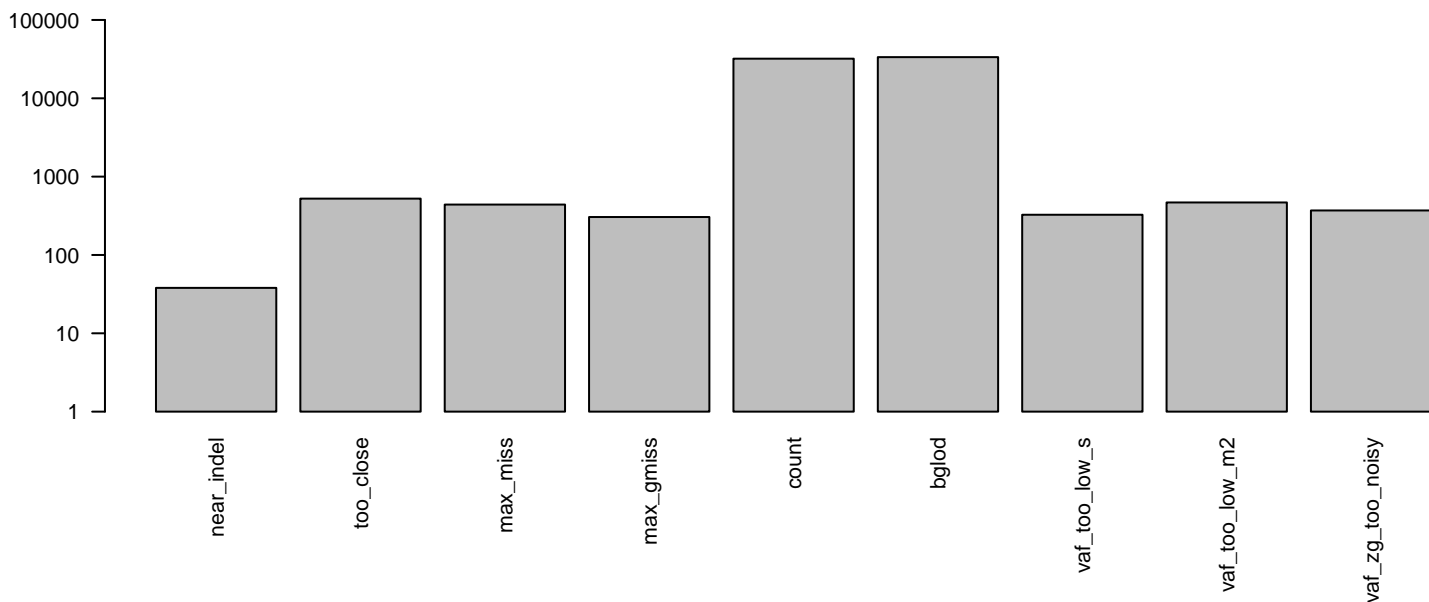
PD6629: SNV : VAF Distribution at Somatic (pass all filters) sites called in Caveman



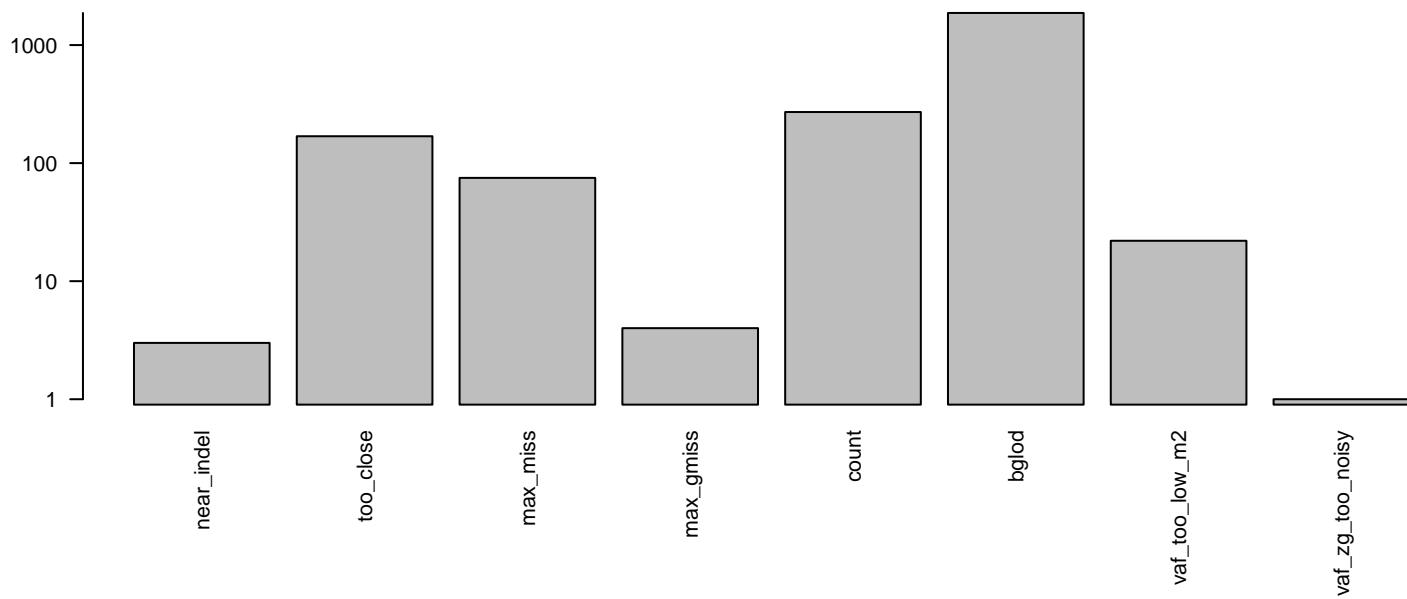
PD6629: SNV : VAF Distribution at Germline [Based on the Matched Normal] sites called in Caveman



PD6629: SNV: No. Sites removed by each filter



PD6629: SNV: No. Sites UNIQUELY removed by each filter

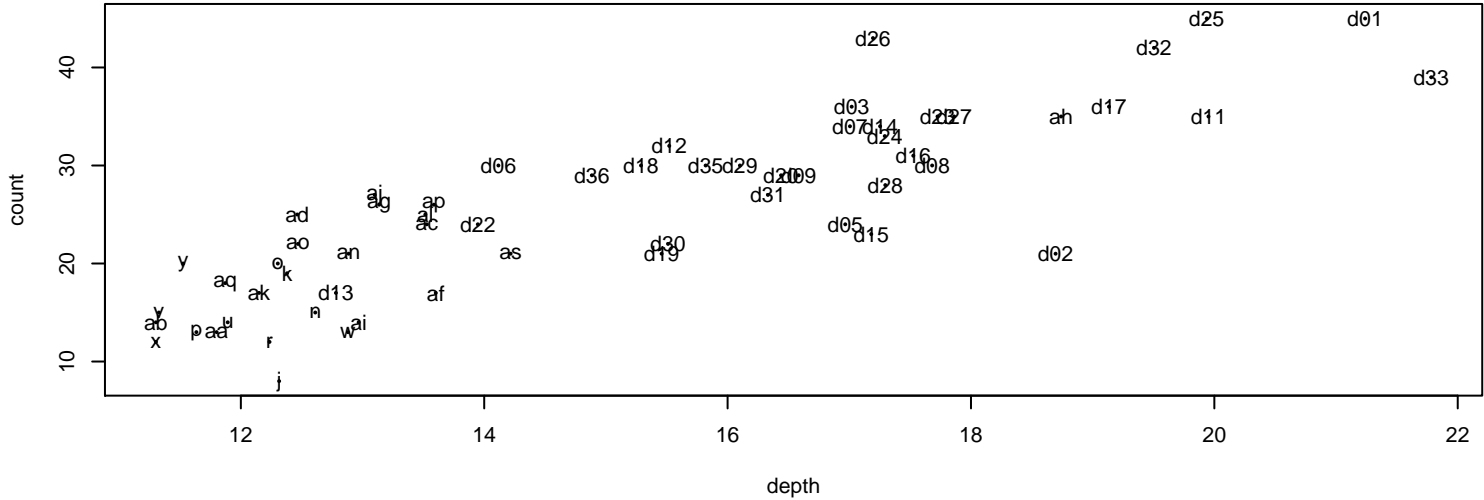


PD6629 : Indels

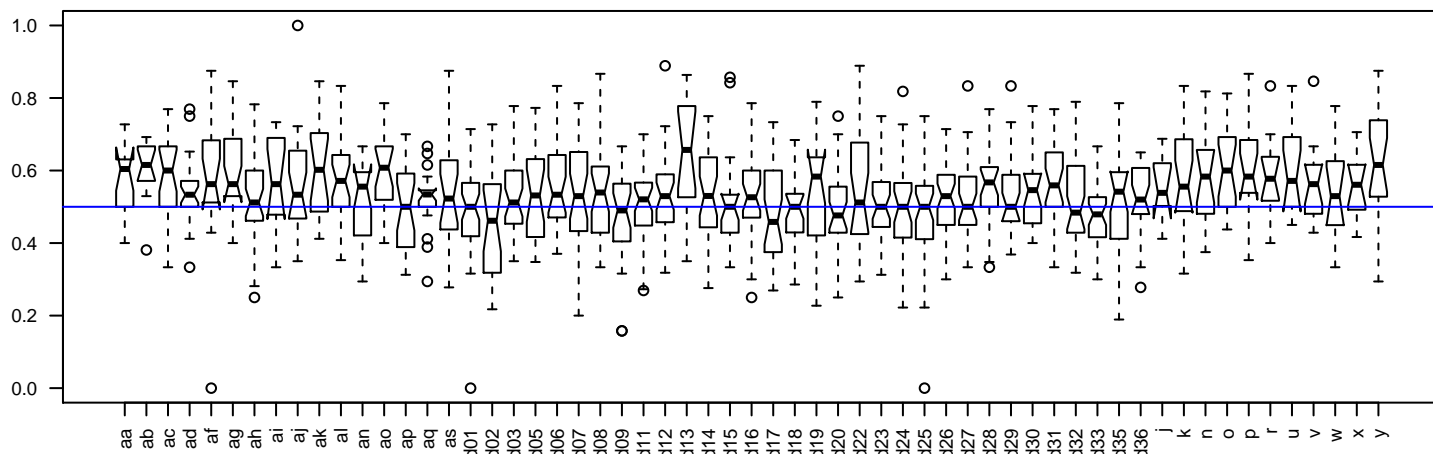
Indels:Pairwise Filter Overlap (% Filtered Variants):Total Fail=3909/Pass=909

	too_close	max_miss	max_gmiss	count	bgld	vaf_too_low_s	vaf_too_low_m2	vaf_zg_too_noisy	manual_exclude	
too_close	1.4	1.1	0.6	0.9	1.0	0.0	0.0	0.0	0.0	
max_miss	1.1	24.9	11.2	16.7	22.5	0.0	0.1	0.2	0.0	
max_gmiss	0.6	11.2	13.8	5.3	10.2	0.5	1.8	1.5	0.0	
count	0.9	16.7	5.3	80.7	78.7	0.3	1.1	0.9	0.0	
bgld	1.0	22.5	10.2	78.7	93.3	0.3	0.8	0.7	0.0	
vaf_too_low_s	0.0	0.0	0.5	0.3	0.3	0.9	0.9	0.9	0.0	
vaf_too_low_m2	0.0	0.1	1.8	1.1	0.8	0.9	4.4	2.6	0.0	
vaf_zg_too_noisy	0.0	0.2	1.5	0.9	0.7	0.9	2.6	2.9	0.0	
manual_exclude	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	

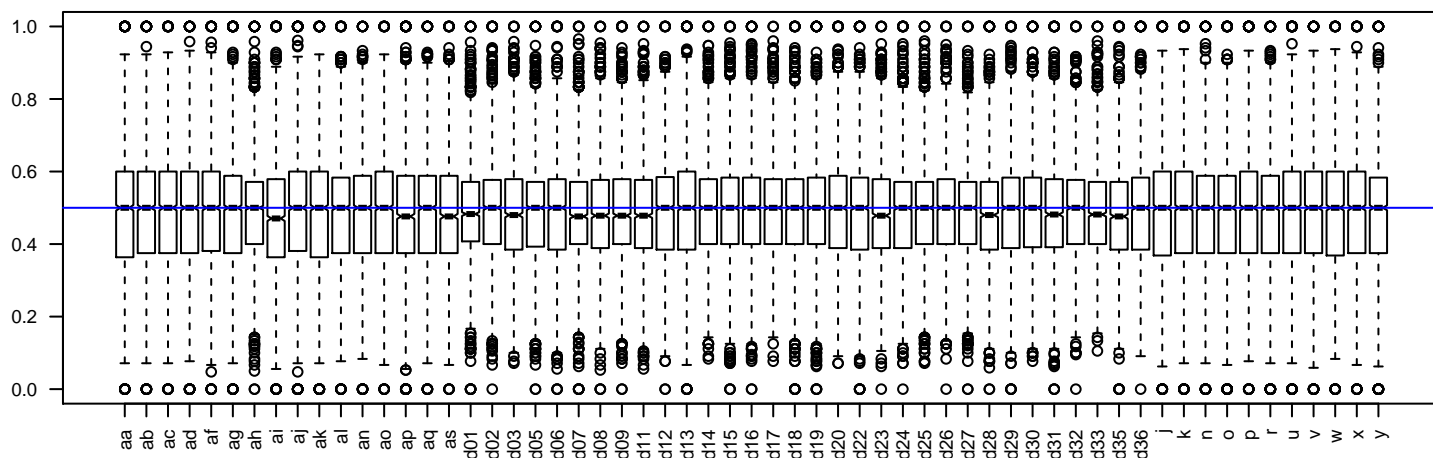
Called INDEL Count vs Average Depth



**PD6629: INDEL : VAF Distribution at Somatic (pass all filters) sites called in Pindel**

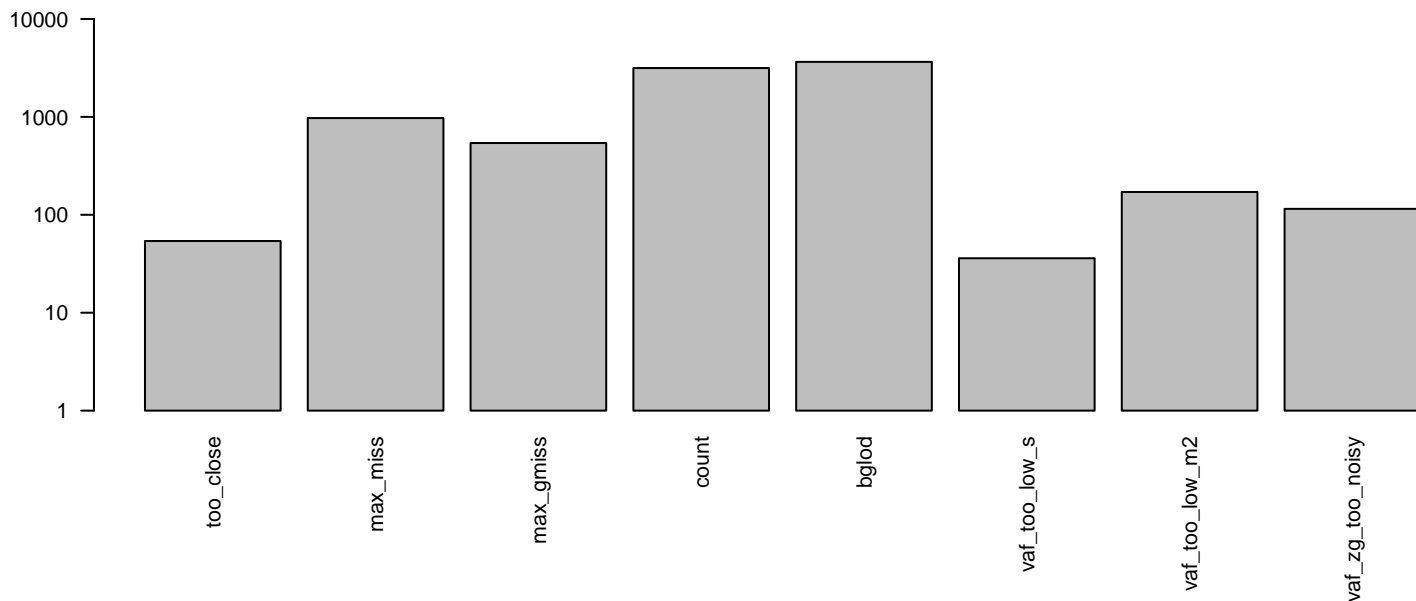


**PD6629: INDEL : VAF Distribution at Germline [Based on the Matched Normal] sites called in Pindel**

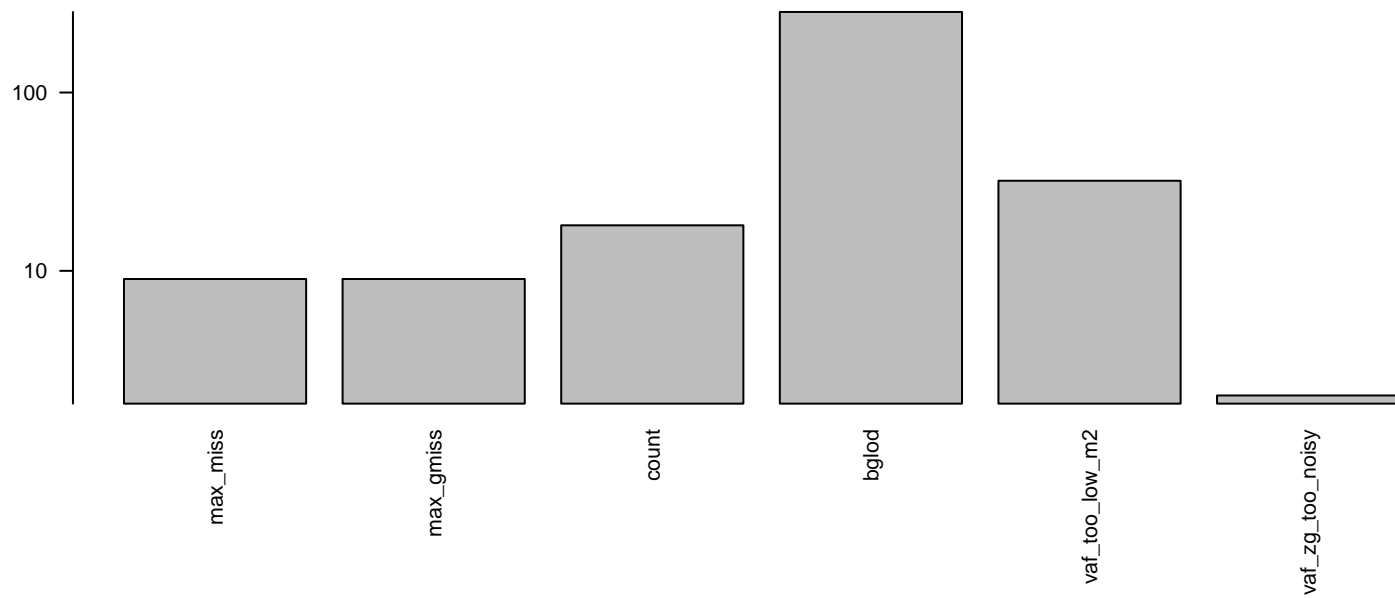




PD6629: INDEL: No. Sites removed by each filter



PD6629: INDEL: No. Sites UNIQUELY removed by each filter

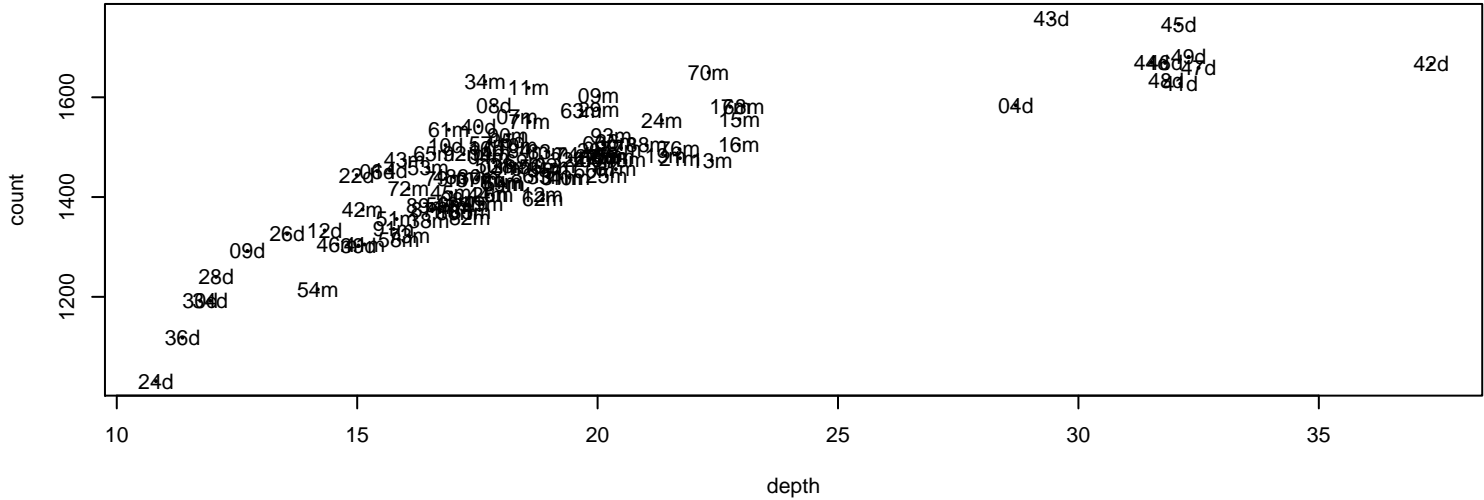


PD6646 : SNVs

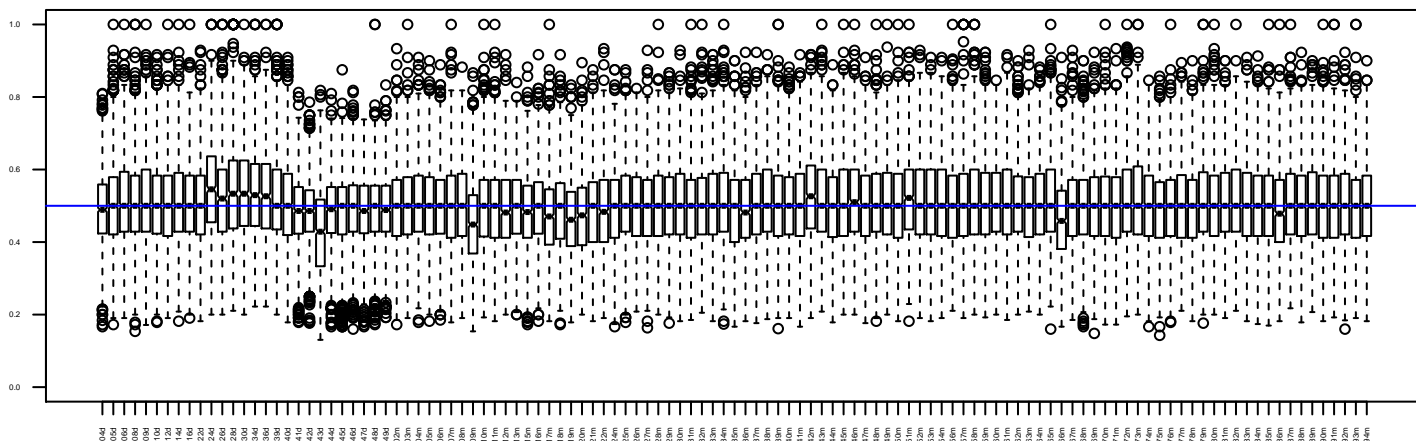
SNV:Pairwise Filter Overlap (% Filtered Variants):Total Fail=36723/Pass=57353

	near_indel	too_close	max_miss	max_gmiss	count	bgld	vaf_too_low_s	vaf_too_low_m2	vaf_zg_too_noisy	manual_exclude	
near_indel	0.1	0.0	0.0	0.1	0.0	0.1	0.1	0.1	0.1	0.0	
too_close	0.0	2.0	0.0	0.0	1.0	1.0	0.0	0.1	0.1	0.0	
max_miss	0.0	0.0	0.2	0.1	0.1	0.1	0.0	0.0	0.0	0.0	
max_gmiss	0.1	0.0	0.1	0.7	0.1	0.2	0.4	0.6	0.5	0.0	
count	0.0	1.0	0.1	0.1	92.1	90.3	0.8	1.1	0.8	0.0	
bgld	0.1	1.0	0.1	0.2	90.3	95.7	0.3	0.4	0.4	0.0	
vaf_too_low_s	0.1	0.0	0.0	0.4	0.8	0.3	1.5	1.5	1.3	0.0	
vaf_too_low_m2	0.1	0.1	0.0	0.6	1.1	0.4	1.5	2.9	1.6	0.0	
vaf_zg_too_noisy	0.1	0.1	0.0	0.5	0.8	0.4	1.3	1.6	1.7	0.0	
manual_exclude	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	

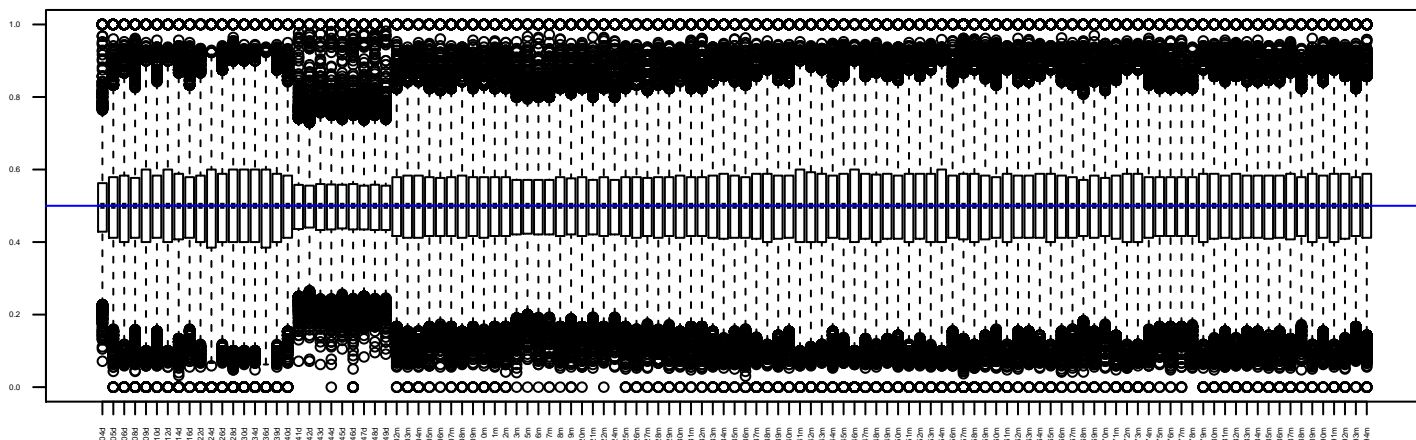
Called SNV Count vs Average Depth



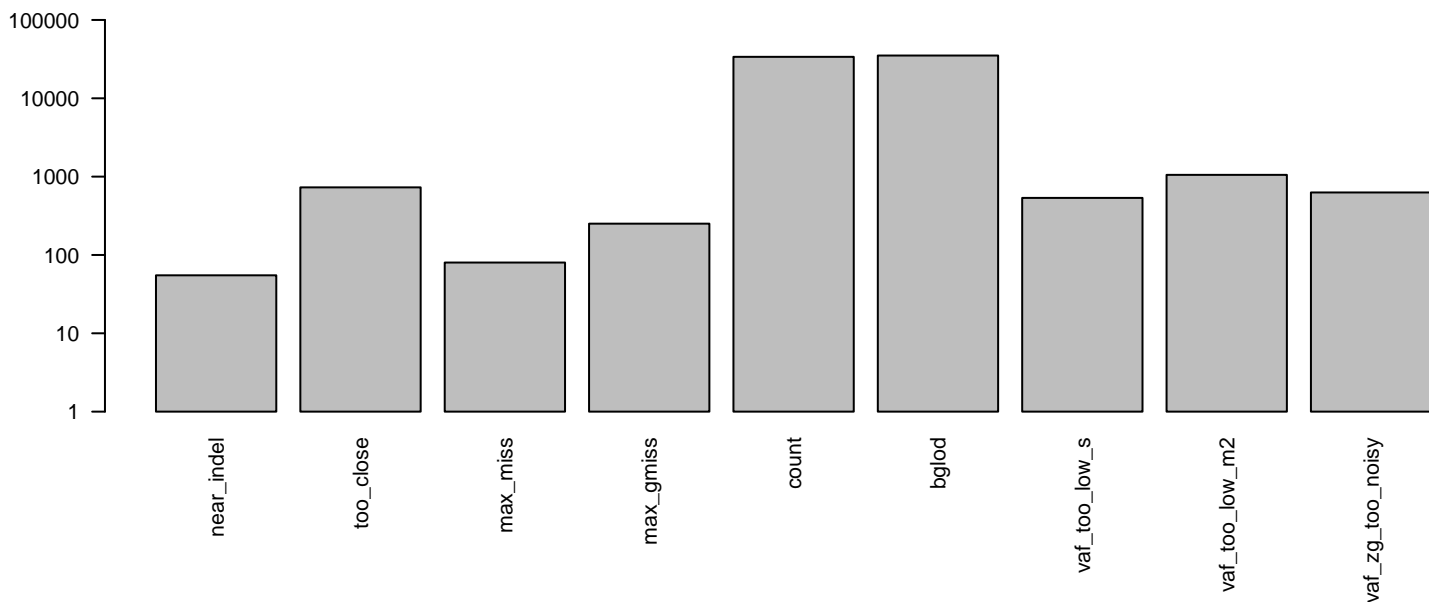
PD6646: SNV : VAF Distribution at Somatic (pass all filters) sites called in Caveman



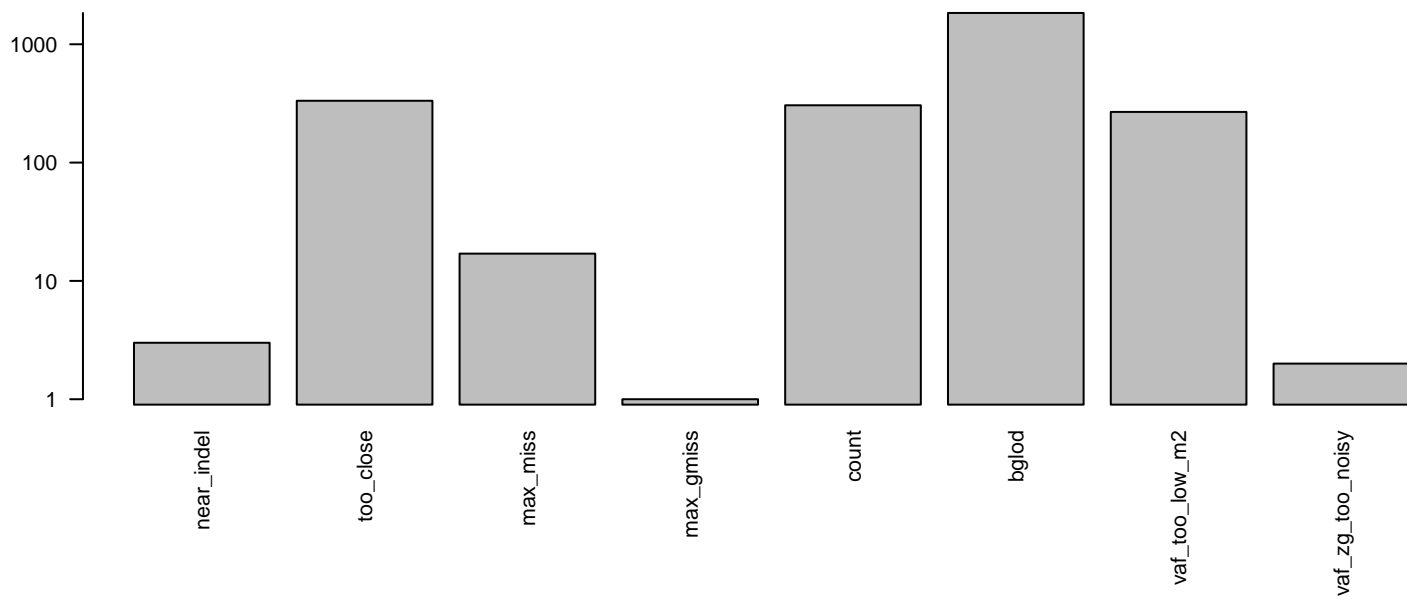
PD6646: SNV : VAF Distribution at Germline [Based on the Matched Normal] sites called in Caveman



PD6646: SNV: No. Sites removed by each filter



PD6646: SNV: No. Sites UNIQUELY removed by each filter

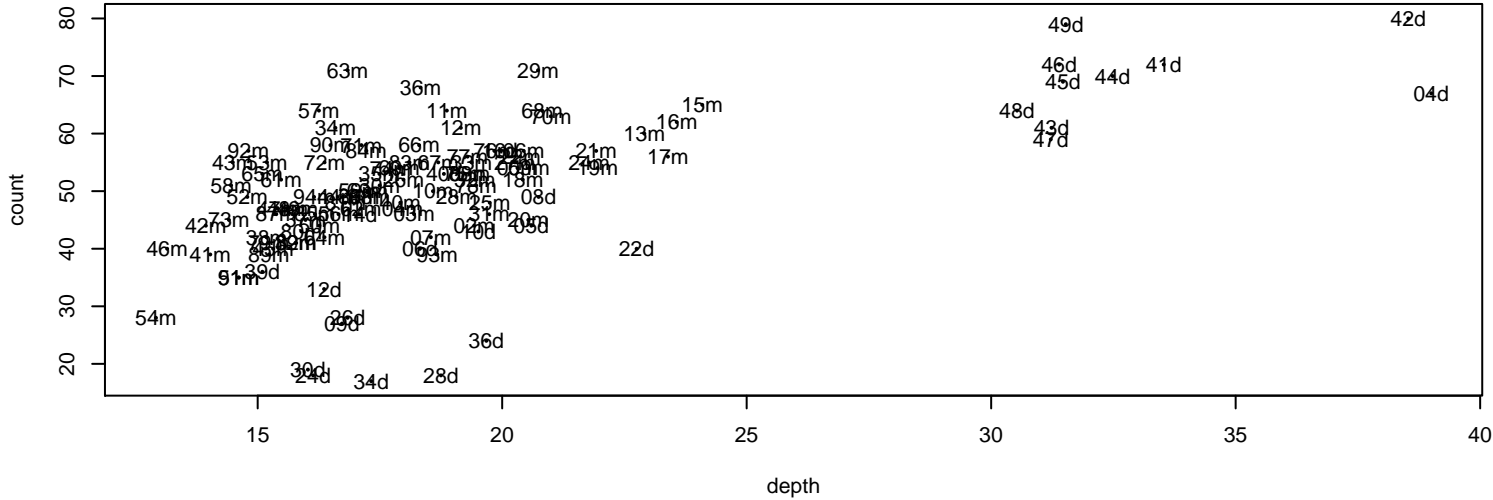


PD6646 : Indels

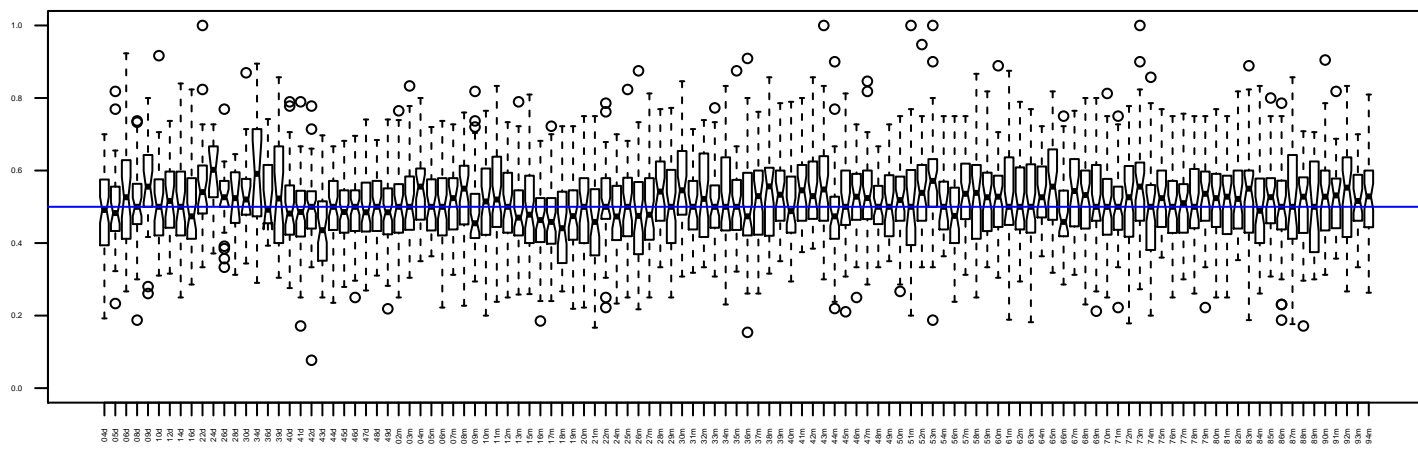
Indels:Pairwise Filter Overlap (% Filtered Variants):Total Fail=7207/Pass=1901

	too_close	max_miss	max_gmiss	count	bgld	vaf_too_low_s	vaf_too_low_m2	vaf_zg_too_noisy	manual_exclude	
too_close	4.9	3.6	1.8	2.6	3.9	0.0	0.3	0.2	0.0	
max_miss	3.6	27.5	11.2	15.1	22.7	0.0	0.2	0.0	0.0	
max_gmiss	1.8	11.2	16.9	2.6	9.4	2.8	4.9	3.9	0.0	
count	2.6	15.1	2.6	61.0	56.5	0.7	2.9	1.8	0.0	
bgld	3.9	22.7	9.4	56.5	77.0	1.6	2.5	2.4	0.0	
vaf_too_low_s	0.0	0.0	2.8	0.7	1.6	4.4	4.4	4.2	0.0	
vaf_too_low_m2	0.3	0.2	4.9	2.9	2.5	4.4	20.0	14.1	0.0	
vaf_zg_too_noisy	0.2	0.0	3.9	1.8	2.4	4.2	14.1	14.7	0.0	
manual_exclude	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	

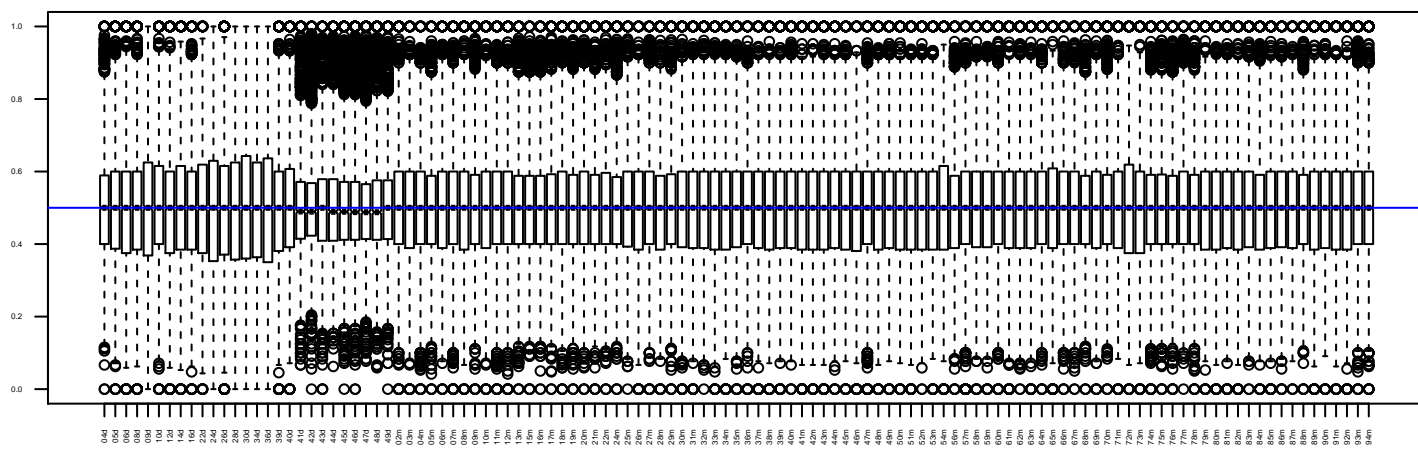
Called INDEL Count vs Average Depth



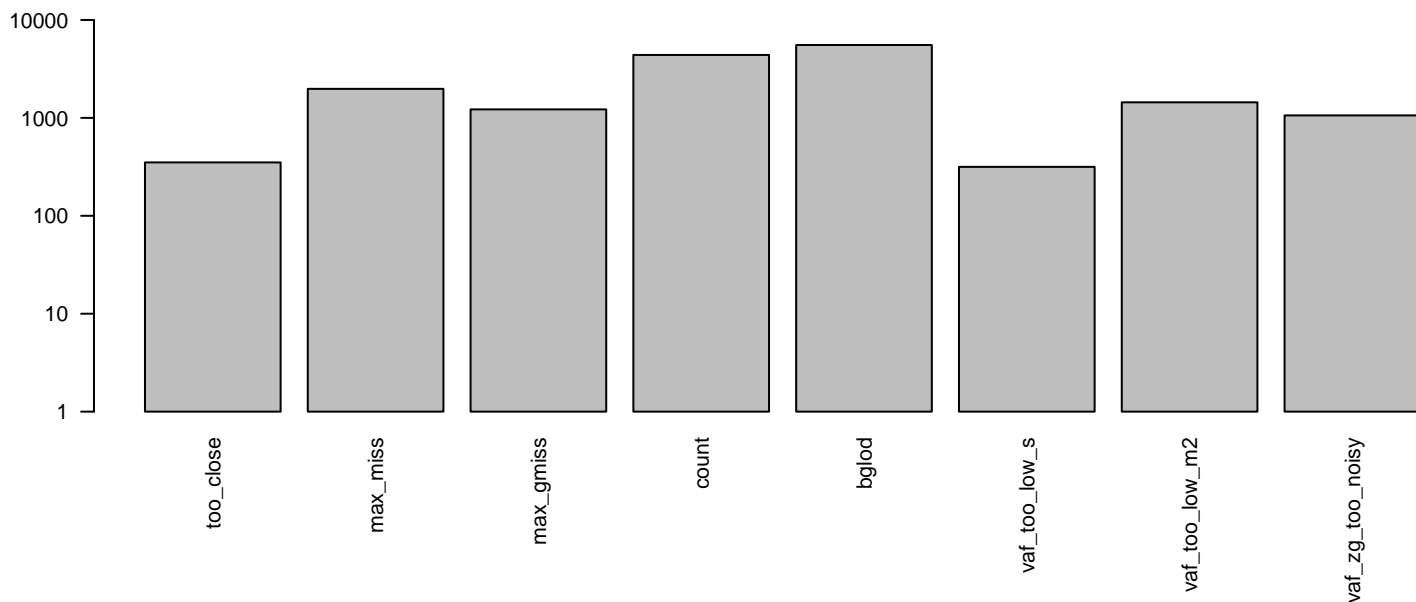
PD6646: INDEL : VAF Distribution at Somatic (pass all filters) sites called in Pindel



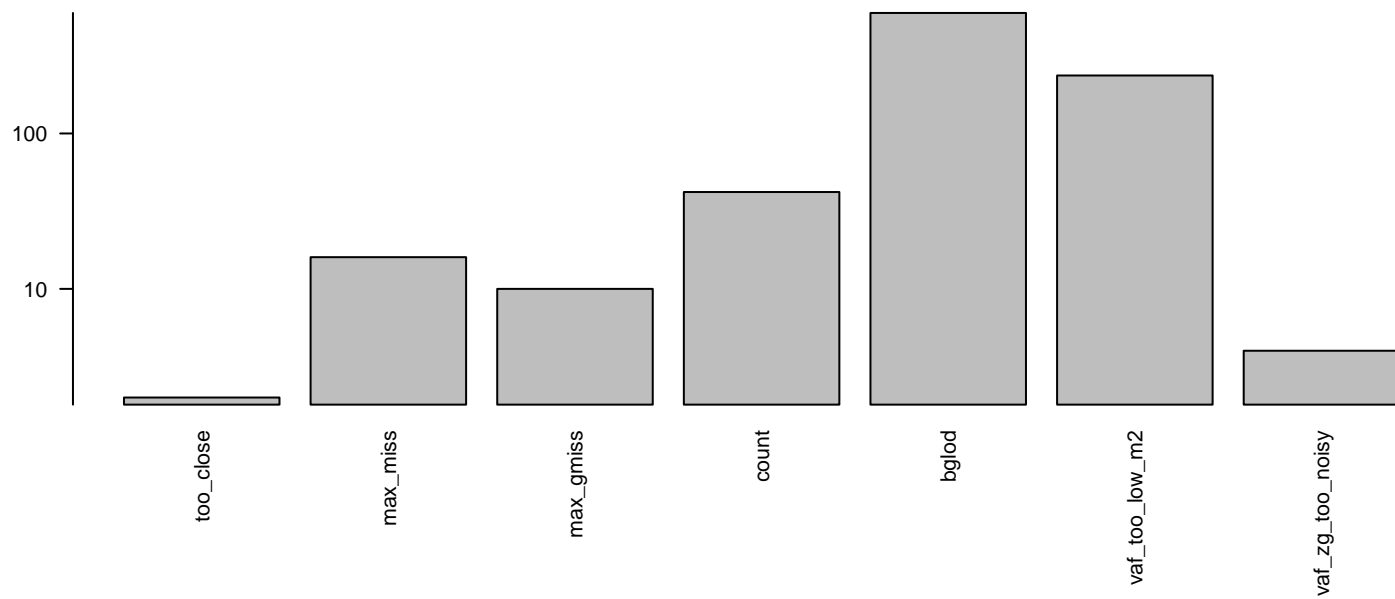
PD6646: INDEL : VAF Distribution at Germline [Based on the Matched Normal] sites called in Pindel



PD6646: INDEL: No. Sites removed by each filter



PD6646: INDEL: No. Sites UNIQUELY removed by each filter

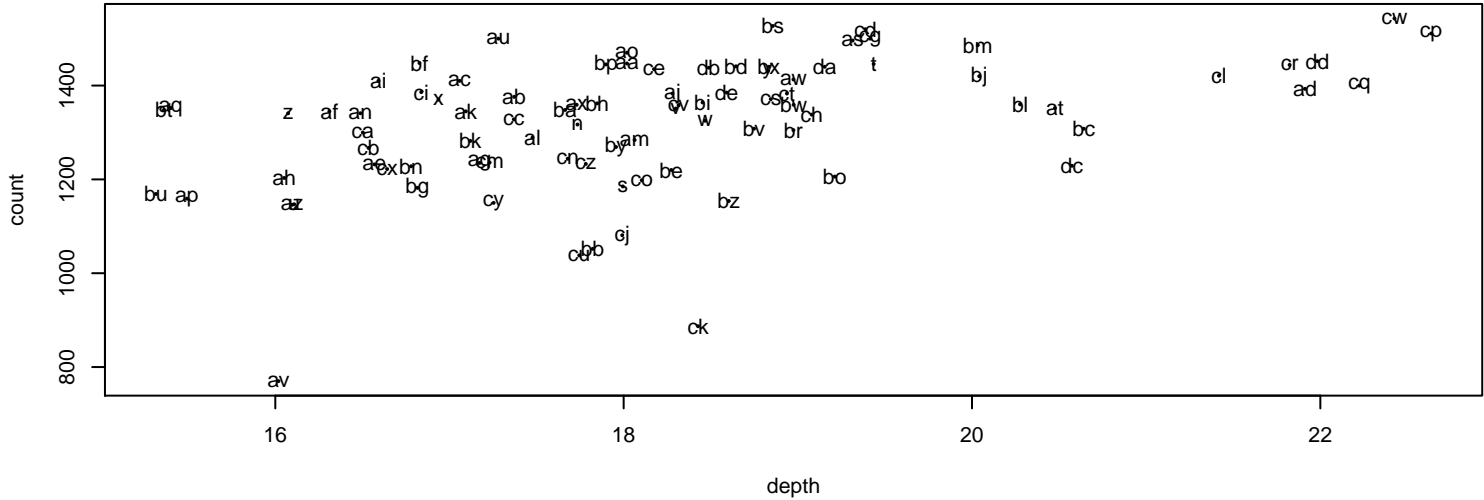


PD5117 : SNVs

SNV:Pairwise Filter Overlap (% Filtered Variants):Total Fail=38675/Pass=91827

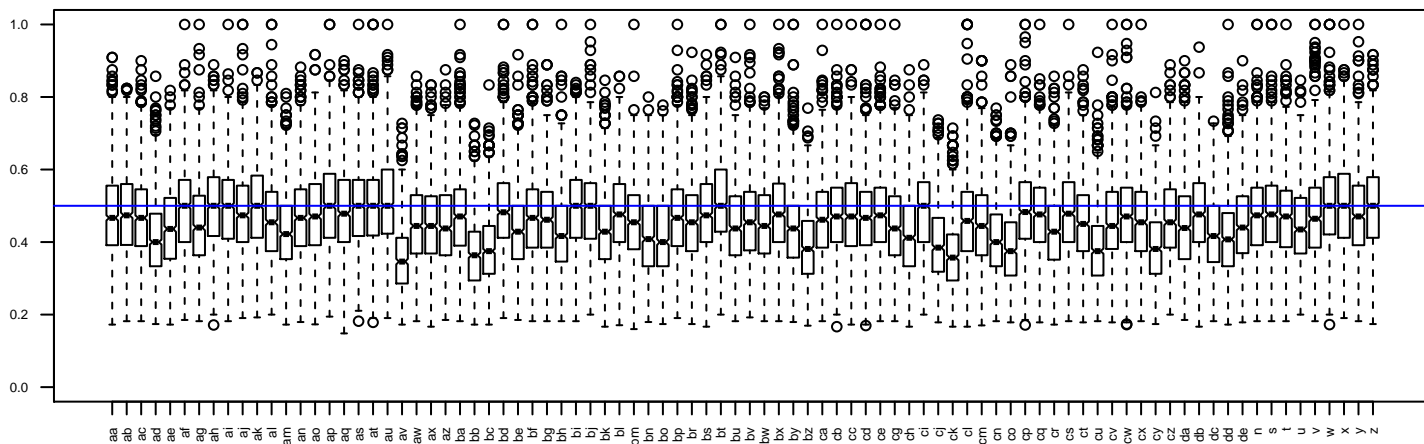
	near_indel	too_close	max_miss	max_gmiss	count	bglod	vaf_too_low_s	vaf_too_low_m2	vaf_zg_too_noisy	manual_exclude	
near_indel	0.1	0.0	0.0	0.1	0.0	0.1	0.0	0.1	0.0	0.0	
too_close	0.0	2.5	0.0	0.0	1.1	1.2	0.1	0.1	0.0	0.0	
max_miss	0.0	0.0	0.2	0.1	0.1	0.1	0.0	0.0	0.0	0.0	
max_gmiss	0.1	0.0	0.1	0.6	0.2	0.2	0.3	0.5	0.4	0.0	
count	0.0	1.1	0.1	0.2	94.4	93.0	0.8	1.0	0.8	0.0	
bglod	0.1	1.2	0.1	0.2	93.0	96.7	0.3	0.5	0.4	0.0	
vaf_too_low_s	0.0	0.1	0.0	0.3	0.8	0.3	1.1	1.1	1.0	0.0	
vaf_too_low_m2	0.1	0.1	0.0	0.5	1.0	0.5	1.1	1.8	1.2	0.0	
vaf_zg_too_noisy	0.0	0.0	0.0	0.4	0.8	0.4	1.0	1.2	1.3	0.0	
manual_exclude	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	

Called SNV Count vs Average Depth

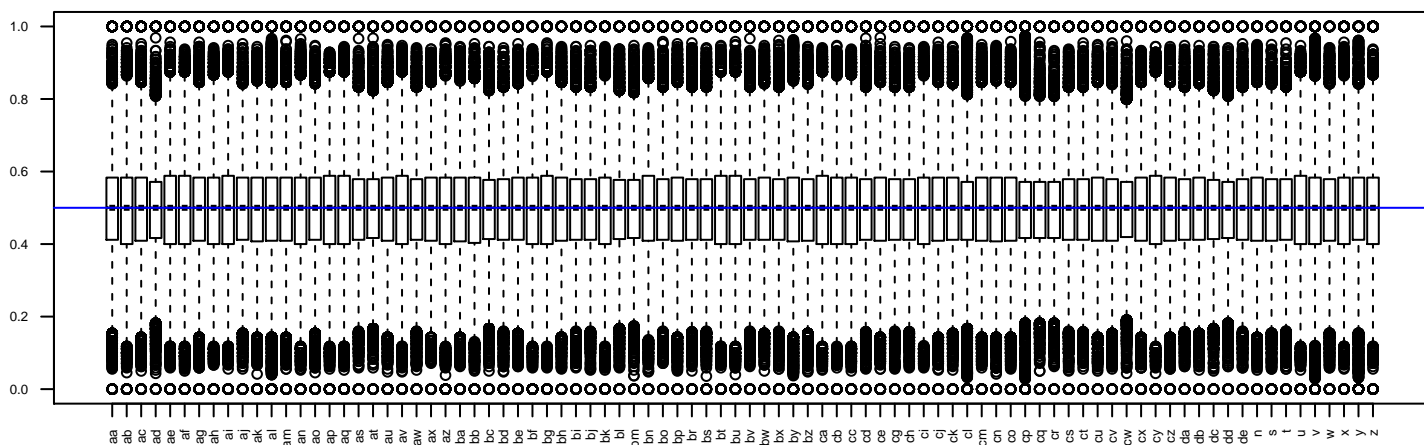




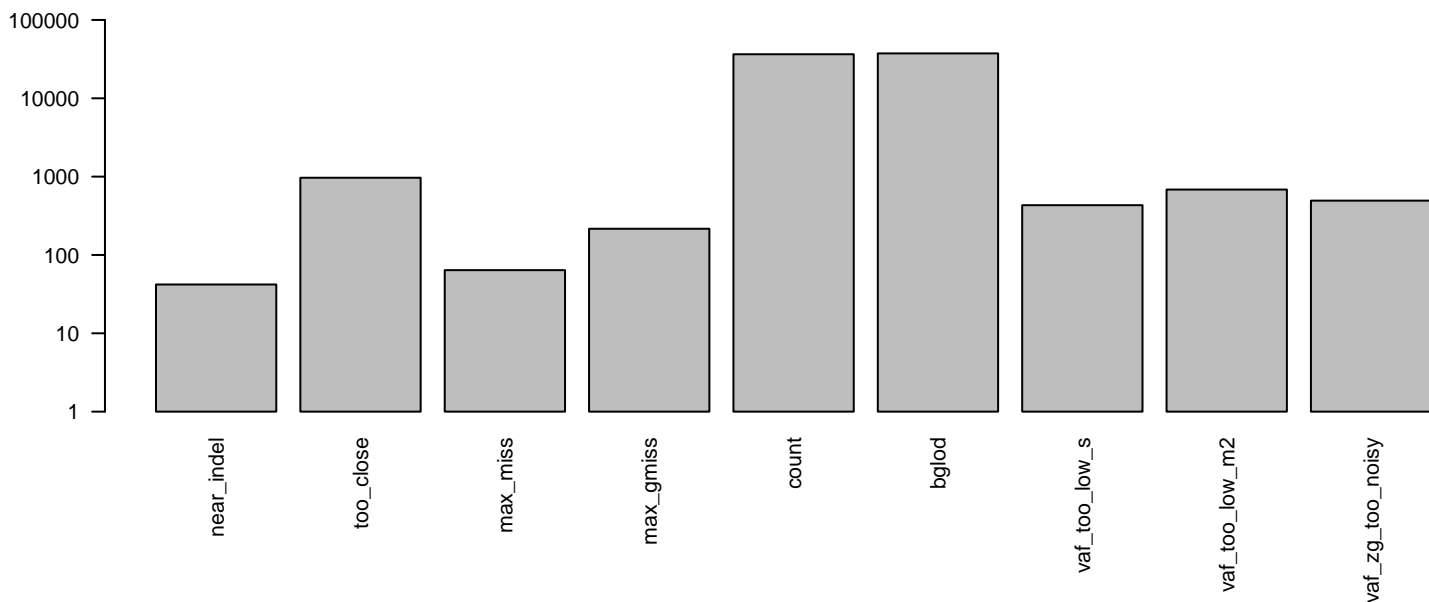
PD5117: SNV : VAF Distribution at Somatic (pass all filters) sites called in Caveman



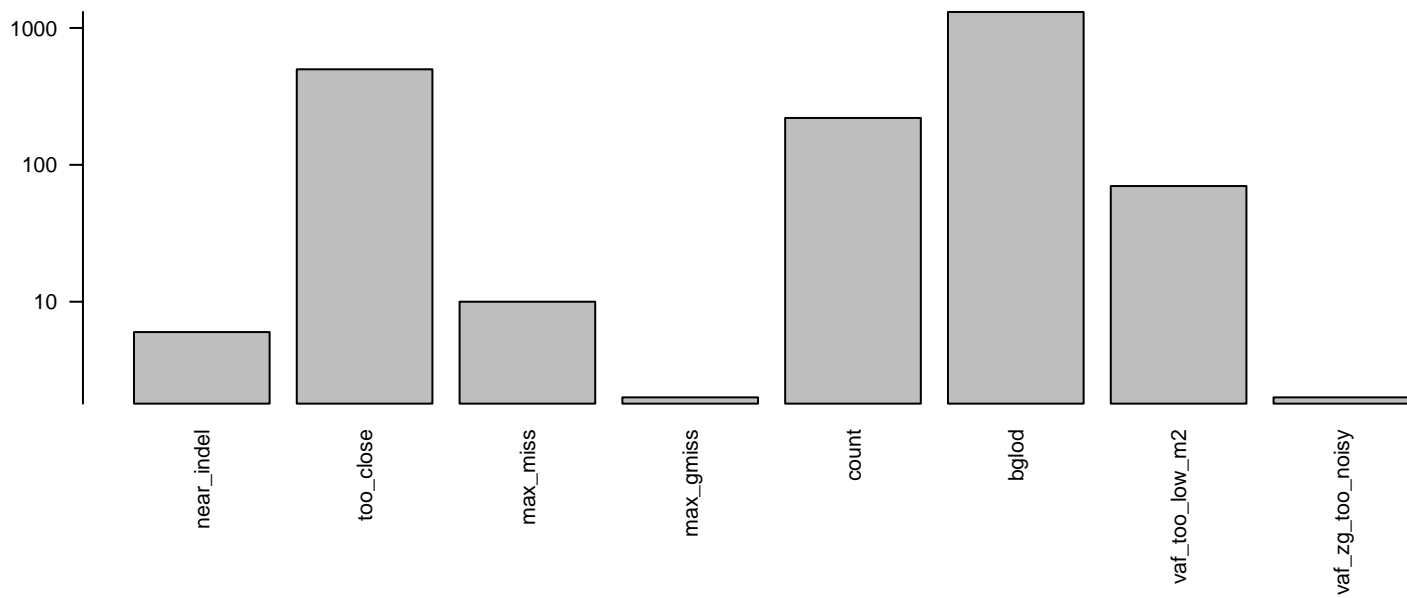
PD5117: SNV : VAF Distribution at Germline [Based on the Matched Normal] sites called in Caveman



PD5117: SNV: No. Sites removed by each filter



PD5117: SNV: No. Sites UNIQUELY removed by each filter

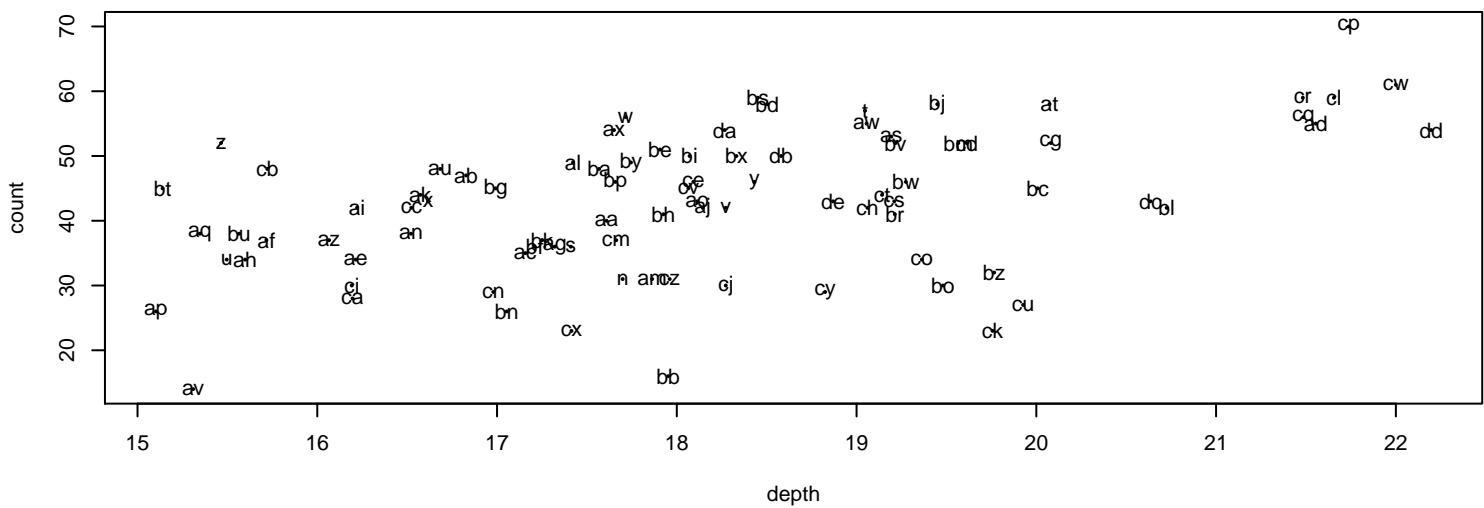


PD5117 : Indels

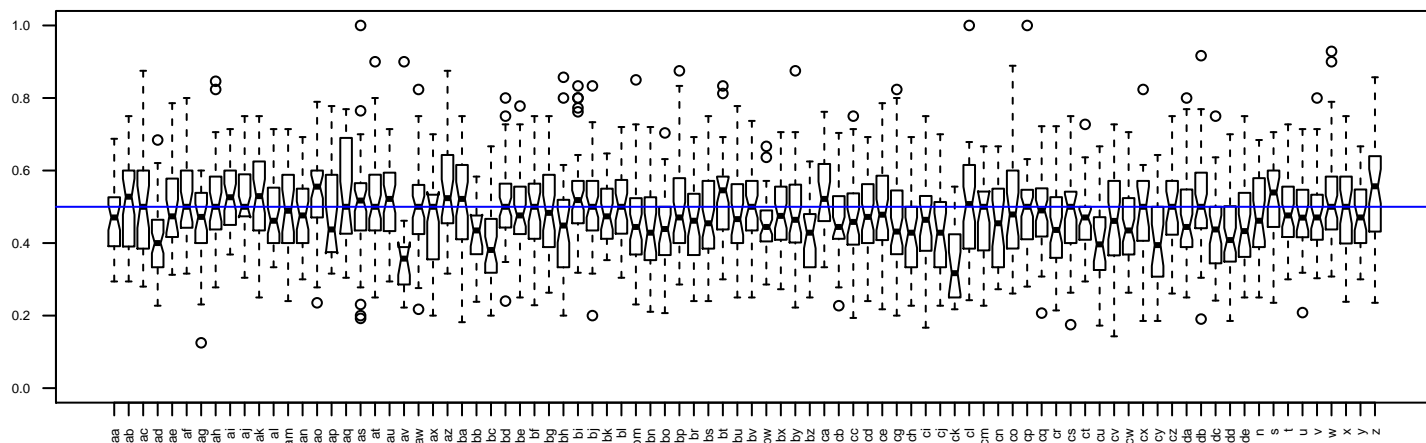
Indels:Pairwise Filter Overlap (% Filtered Variants):Total Fail=6409/Pass=2668

	too_close	max_miss	max_gmiss	count	bgld	vaf_too_low_s	vaf_too_low_m2	vaf_zg_too_noisy	manual_exclude	
too_close	3.8	2.6	1.4	2.3	2.9	0.0	0.2	0.1	0.0	
max_miss	2.6	22.9	8.1	14.2	20.5	0.0	0.0	0.0	0.0	
max_gmiss	1.4	8.1	13.7	2.3	8.4	1.9	4.3	3.5	0.0	
count	2.3	14.2	2.3	69.5	65.9	0.6	2.8	1.5	0.0	
bgld	2.9	20.5	8.4	65.9	81.6	0.9	1.8	1.5	0.0	
vaf_too_low_s	0.0	0.0	1.9	0.6	0.9	2.9	2.9	2.7	0.0	
vaf_too_low_m2	0.2	0.0	4.3	2.8	1.8	2.9	16.7	11.6	0.0	
vaf_zg_too_noisy	0.1	0.0	3.5	1.5	1.5	2.7	11.6	11.8	0.0	
manual_exclude	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	

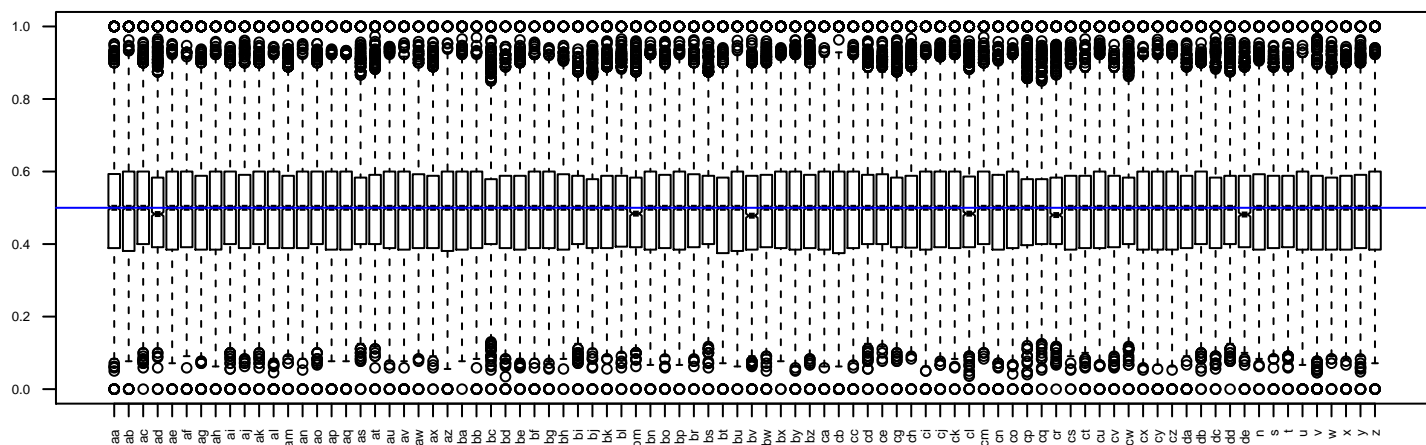
Called INDEL Count vs Average Depth



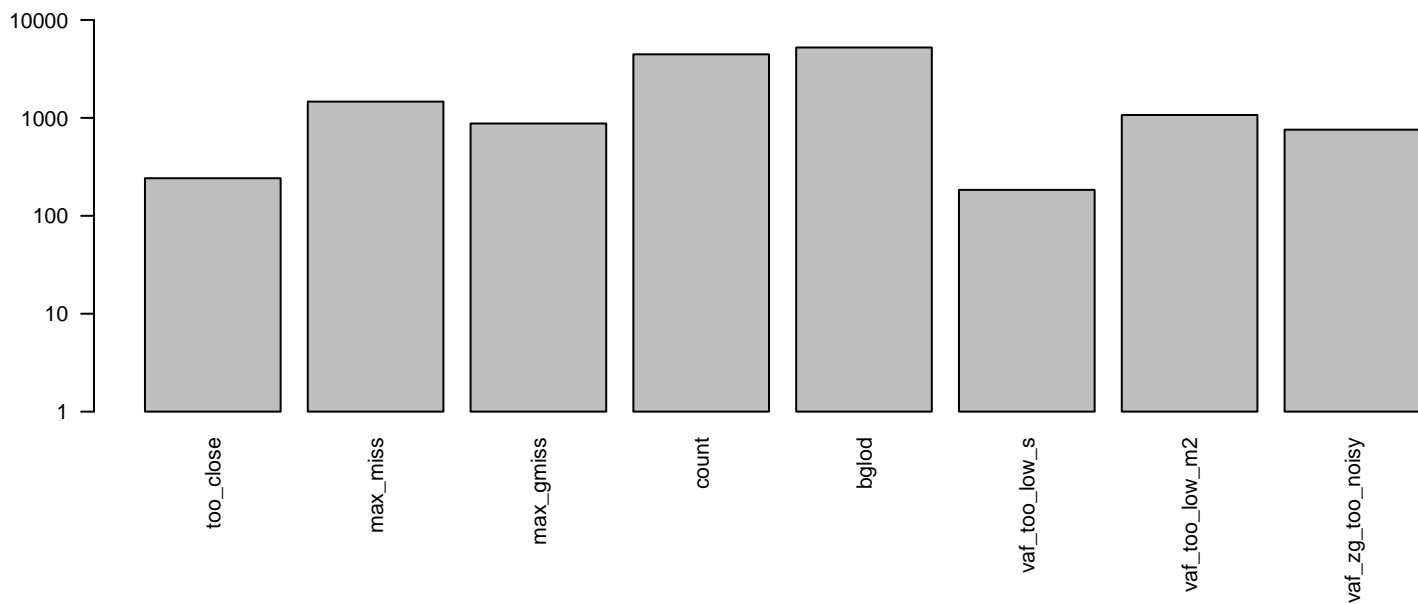
PD5117: INDEL : VAF Distribution at Somatic (pass all filters) sites called in Pindel



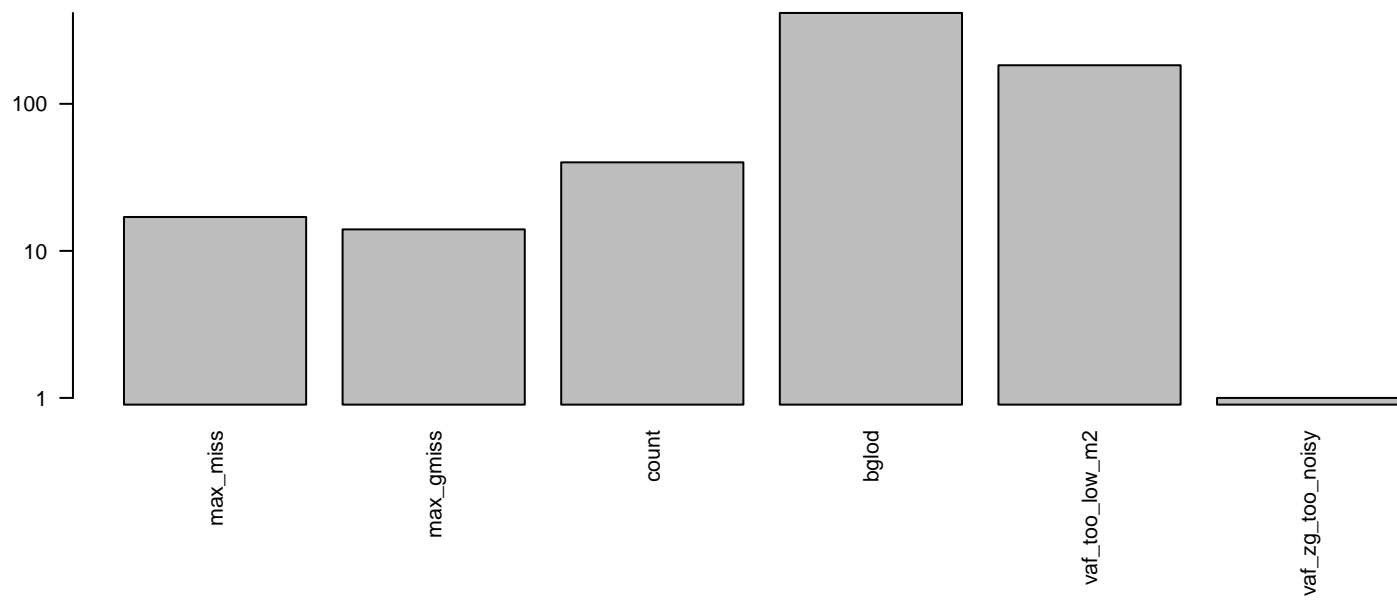
PD5117: INDEL : VAF Distribution at Germline [Based on the Matched Normal] sites called in Pindel



PD5117: INDEL: No. Sites removed by each filter



PD5117: INDEL: No. Sites UNIQUELY removed by each filter

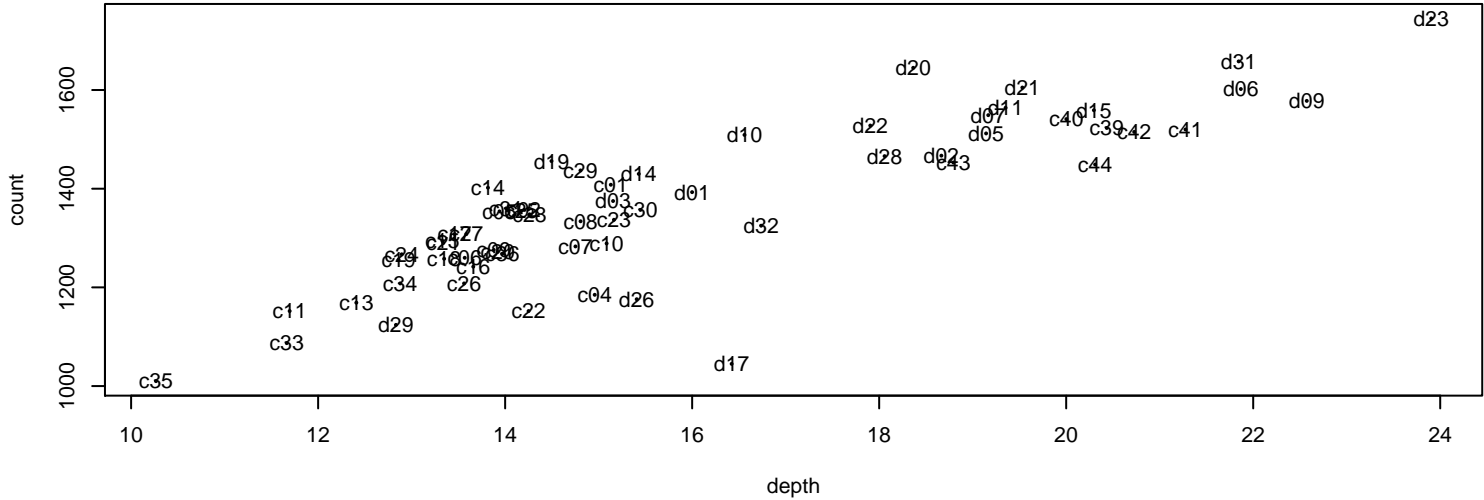


PD4781 : SNVs

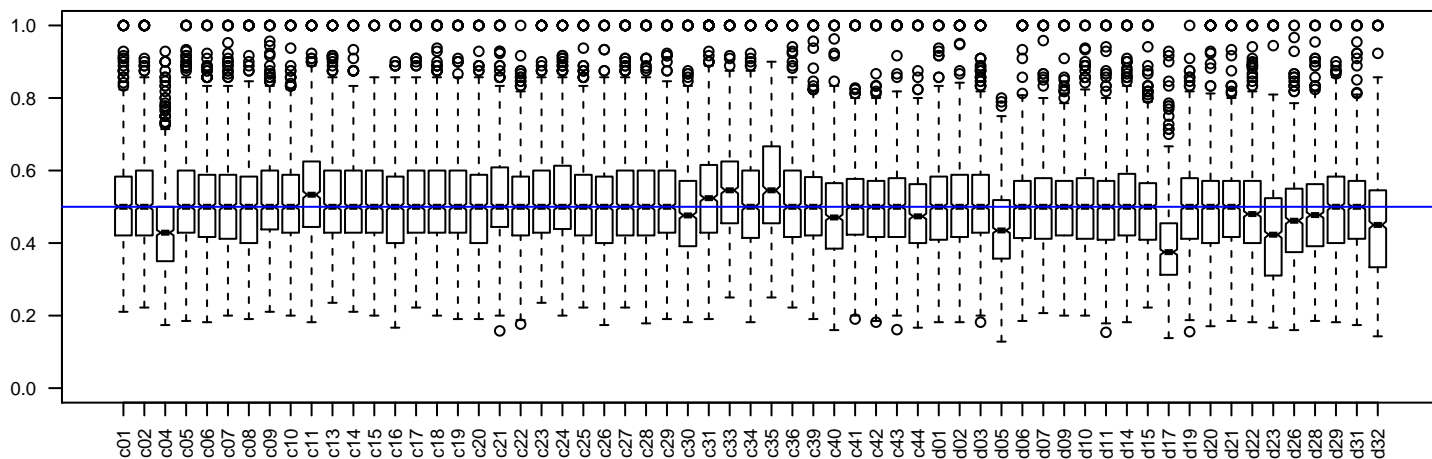
SNV:Pairwise Filter Overlap (% Filtered Variants):Total Fail=35233/Pass=22889

	near_indel	too_close	max_miss	max_gmiss	count	bglod	vaf_too_low_s	vaf_too_low_m2	vaf_zg_too_noisy	manual_exclude	
near_indel	<b>0.1</b>	0.0	0.0	0.1	0.0	0.0	0.0	0.1	0.1	0.0	
too_close	0.0	<b>1.4</b>	0.0	0.0	0.9	1.0	0.0	0.0	0.0	0.0	
max_miss	0.0	0.0	<b>2.4</b>	0.7	1.0	1.8	0.0	0.0	0.0	0.0	
max_gmiss	0.1	0.0	0.7	<b>1.4</b>	0.2	0.8	0.3	0.5	0.4	0.0	
count	0.0	0.9	1.0	0.2	<b>90.6</b>	89.6	0.6	0.7	0.6	0.0	
bglod	0.0	1.0	1.8	0.8	89.6	<b>97.5</b>	0.2	0.3	0.2	0.0	
vaf_too_low_s	0.0	0.0	0.0	0.3	0.6	0.2	<b>1.0</b>	1.0	0.9	0.0	
vaf_too_low_m2	0.1	0.0	0.0	0.5	0.7	0.3	1.0	<b>1.3</b>	1.0	0.0	
vaf_zg_too_noisy	0.1	0.0	0.0	0.4	0.6	0.2	0.9	1.0	<b>1.1</b>	0.0	
manual_exclude	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	<b>0.0</b>	

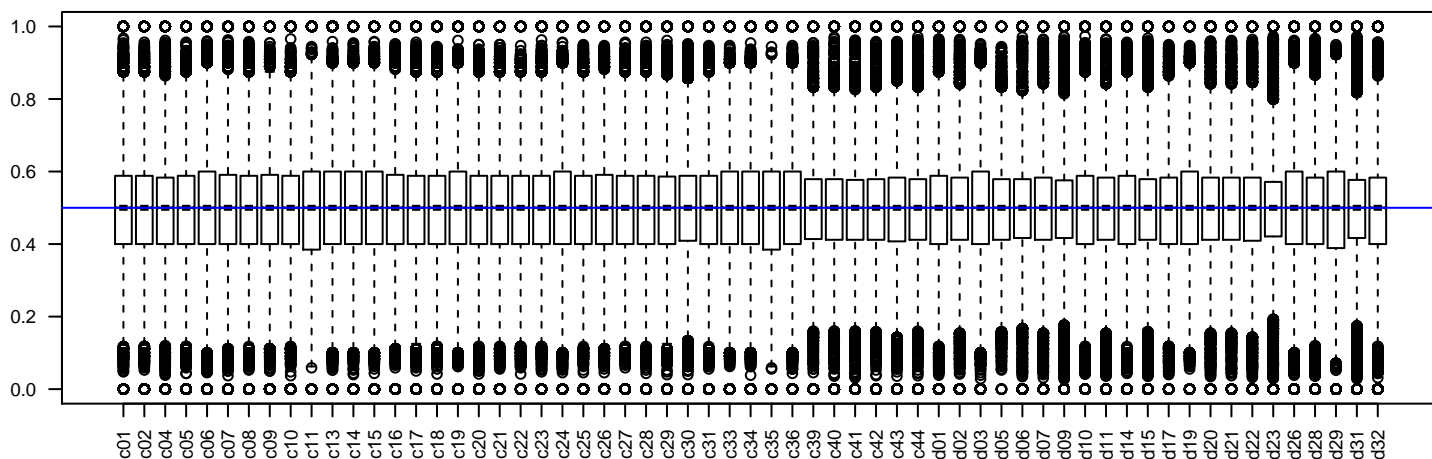
Called SNV Count vs Average Depth



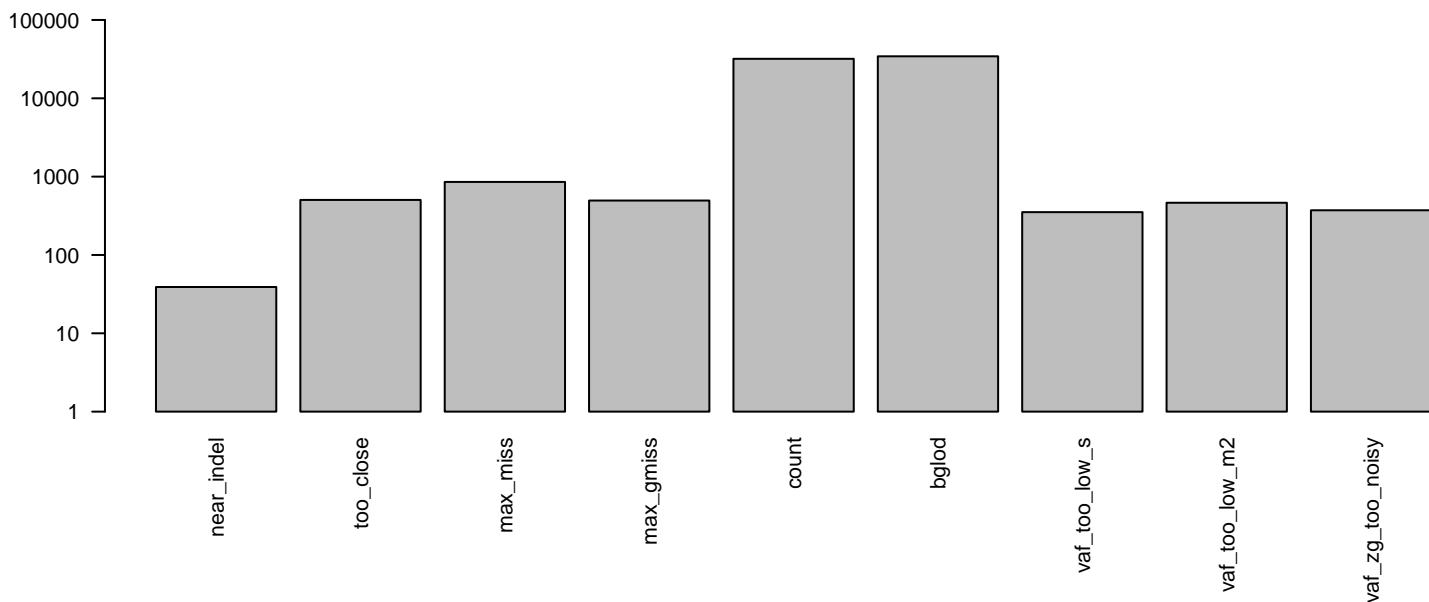
PD4781: SNV : VAF Distribution at Somatic (pass all filters) sites called in Caveman



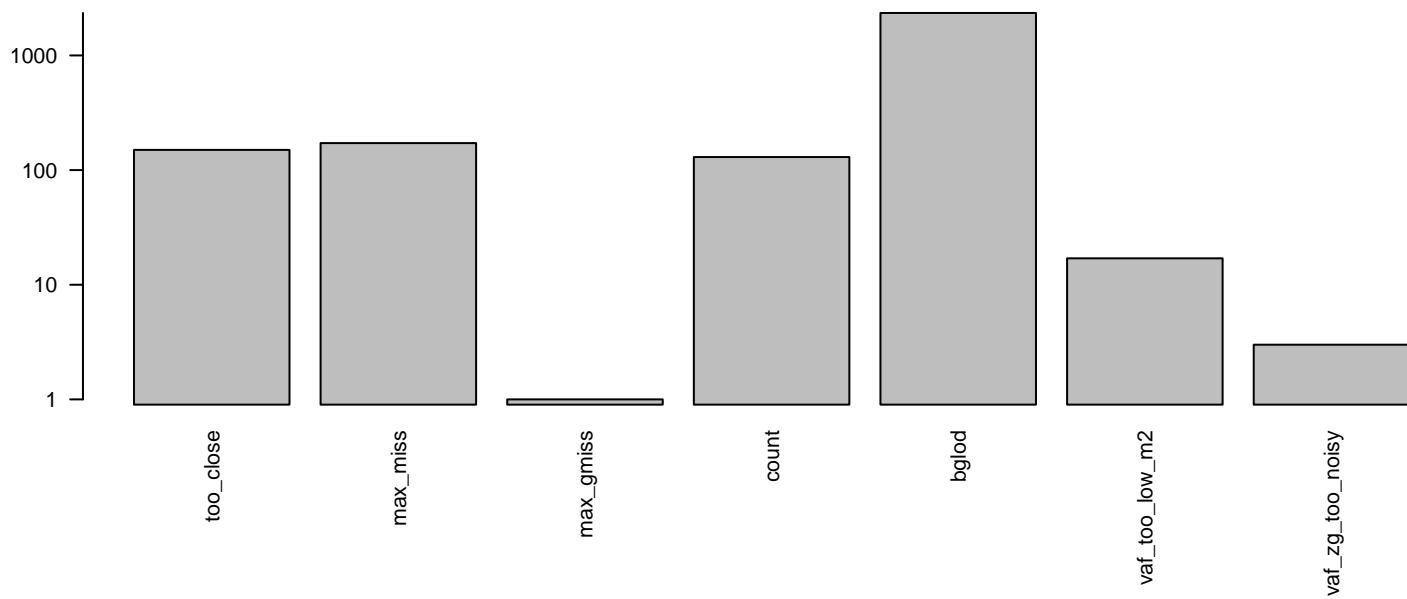
PD4781: SNV : VAF Distribution at Germline [Based on the Matched Normal] sites called in Caveman



**PD4781: SNV: No. Sites removed by each filter**



**PD4781: SNV: No. Sites UNIQUELY removed by each filter**



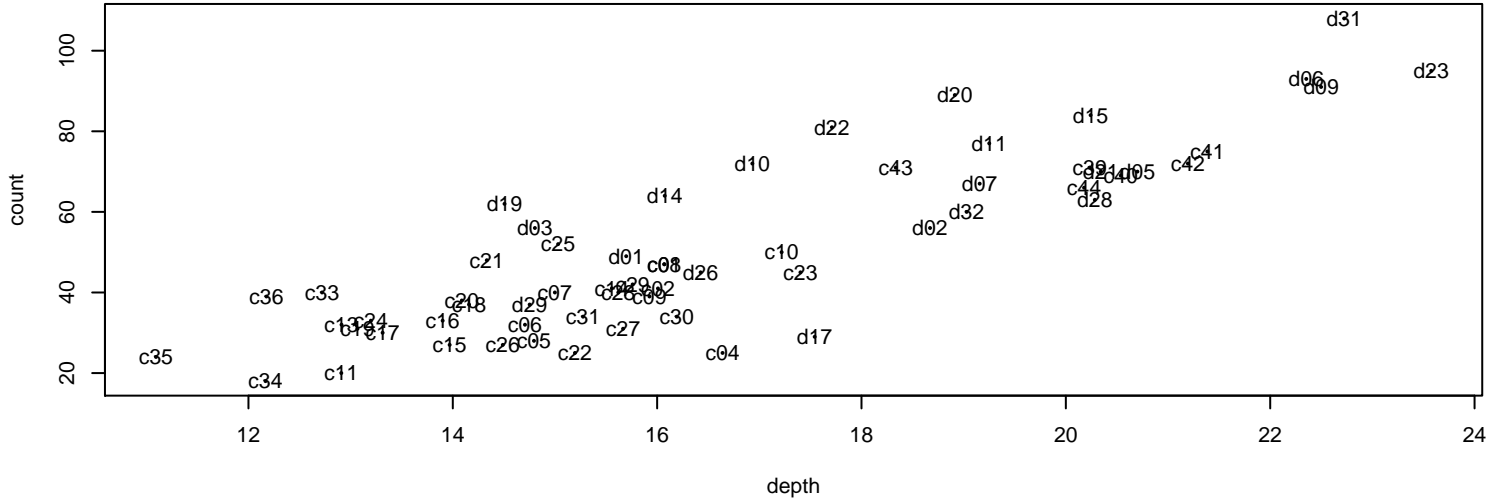


PD4781 : Indels

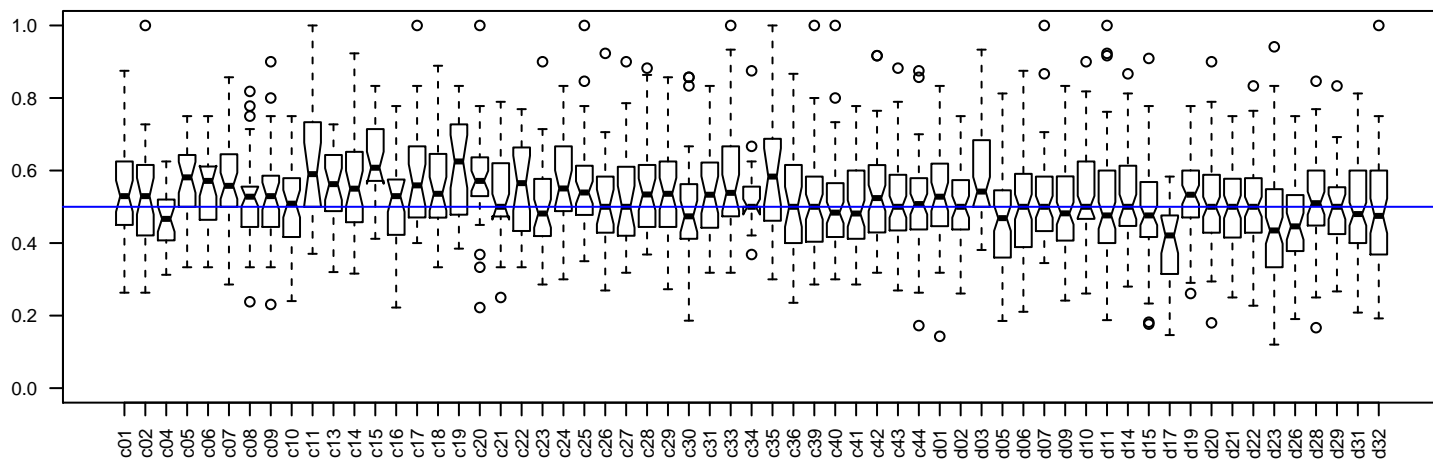
Indels:Pairwise Filter Overlap (% Filtered Variants):Total Fail=4626/Pass=875

	too_close	max_miss	max_gmiss	count	bgld	vaf_too_low_s	vaf_too_low_m2	vaf_zg_too_noisy	manual_exclude	
too_close	2.0	1.6	1.0	1.1	1.6	0.0	0.1	0.1	0.0	
max_miss	1.6	28.1	12.3	17.9	24.1	0.0	0.1	0.0	0.0	
max_gmiss	1.0	12.3	16.7	4.9	10.3	0.8	3.4	2.4	0.0	
count	1.1	17.9	4.9	72.5	69.6	0.6	1.8	1.3	0.0	
bgld	1.6	24.1	10.3	69.6	87.0	0.6	1.3	1.0	0.0	
vaf_too_low_s	0.0	0.0	0.8	0.6	0.6	1.7	1.7	1.5	0.0	
vaf_too_low_m2	0.1	0.1	3.4	1.8	1.3	1.7	9.3	5.7	0.0	
vaf_zg_too_noisy	0.1	0.0	2.4	1.3	1.0	1.5	5.7	5.8	0.0	
manual_exclude	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	

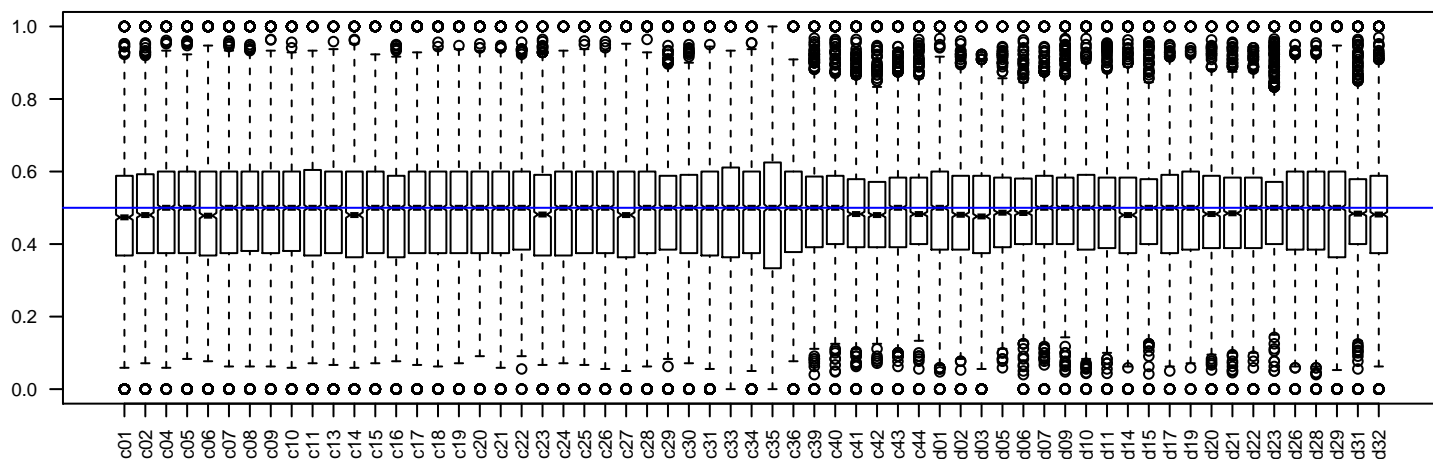
Called INDEL Count vs Average Depth



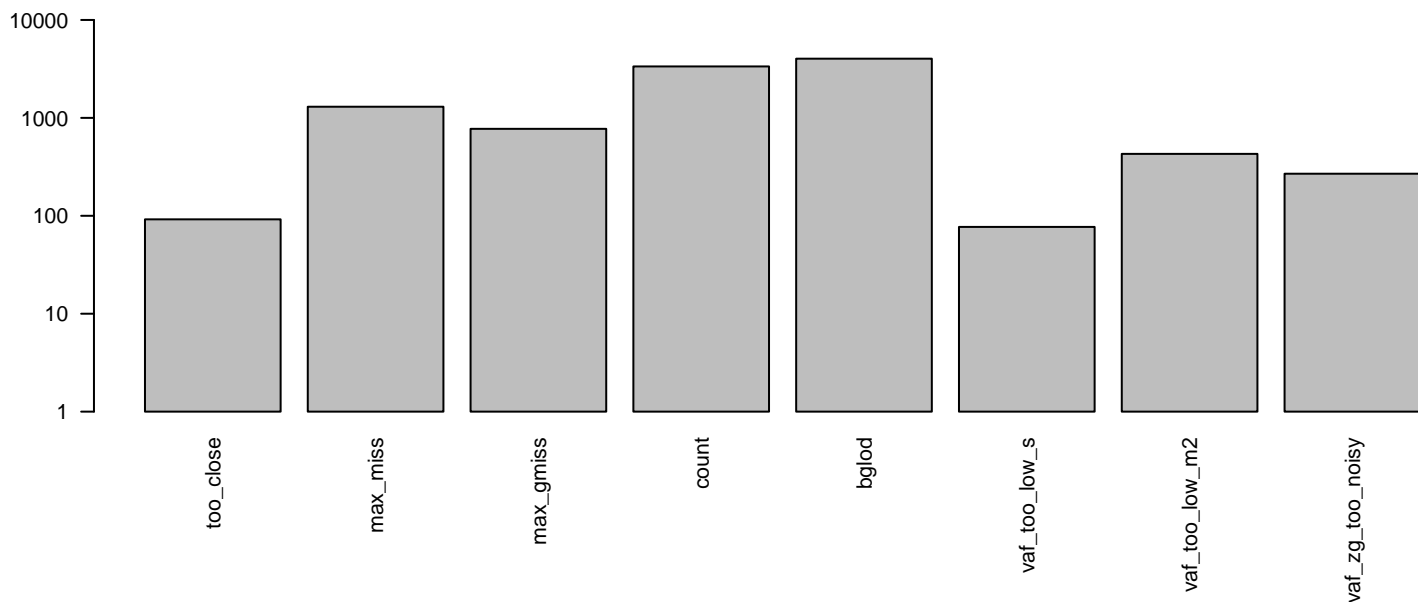
**PD4781: INDEL : VAF Distribution at Somatic (pass all filters) sites called in Pindel**



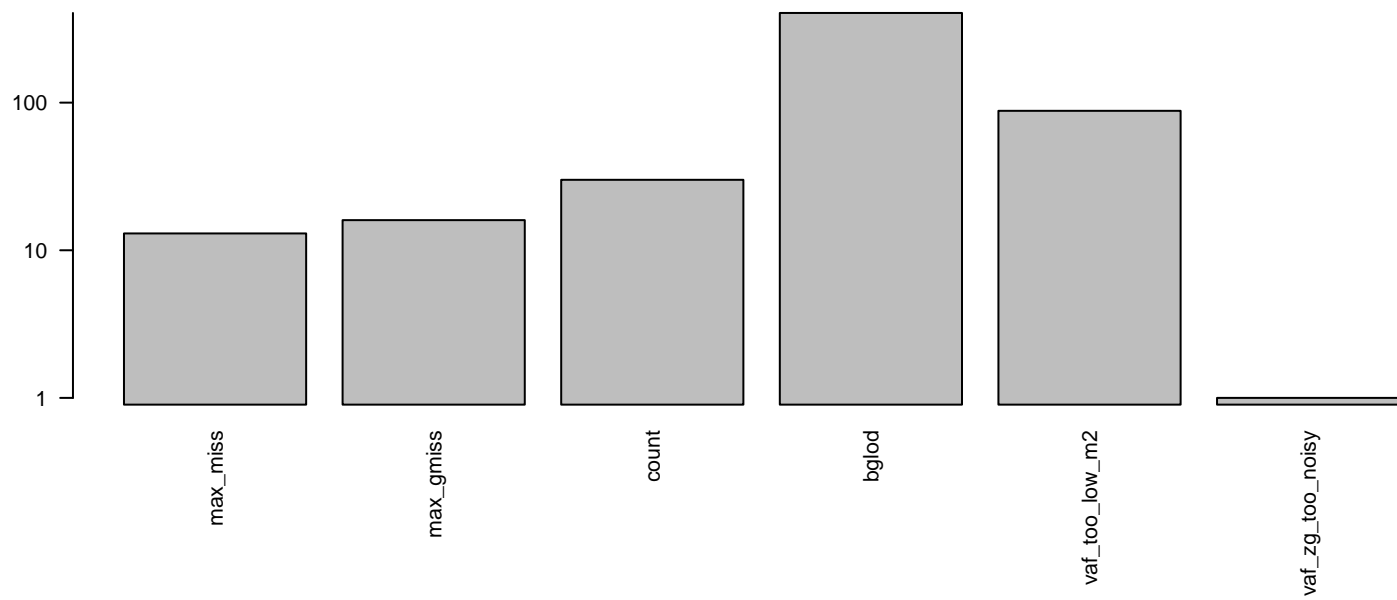
**PD4781: INDEL : VAF Distribution at Germline [Based on the Matched Normal] sites called in Pindel**



**PD4781: INDEL: No. Sites removed by each filter**



**PD4781: INDEL: No. Sites UNIQUELY removed by each filter**

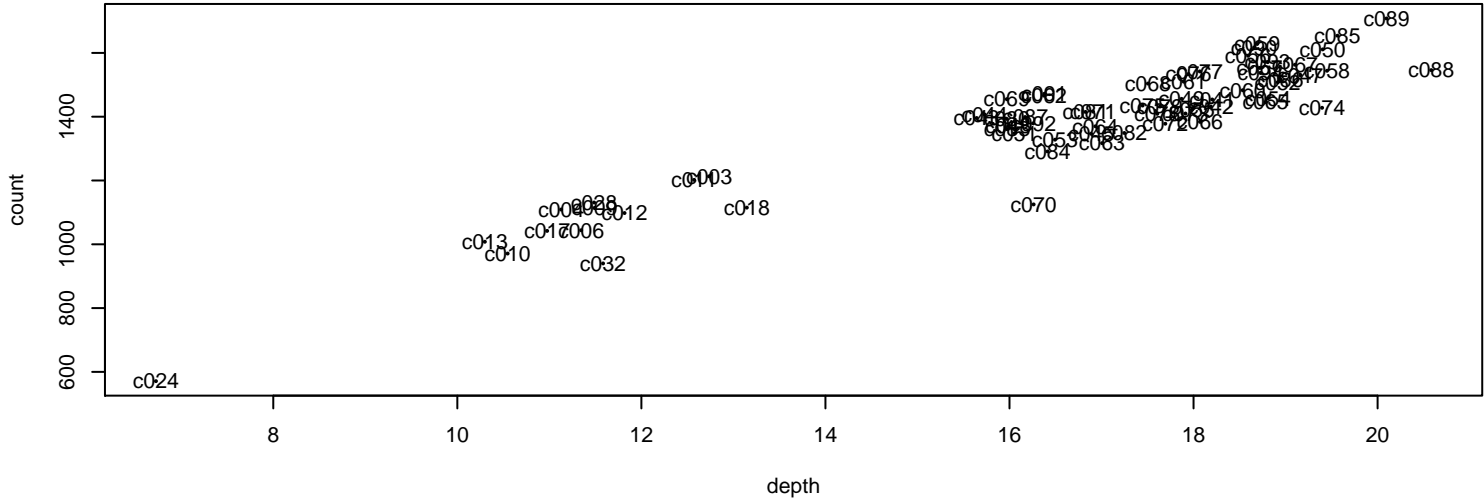


PD5147 : SNVs

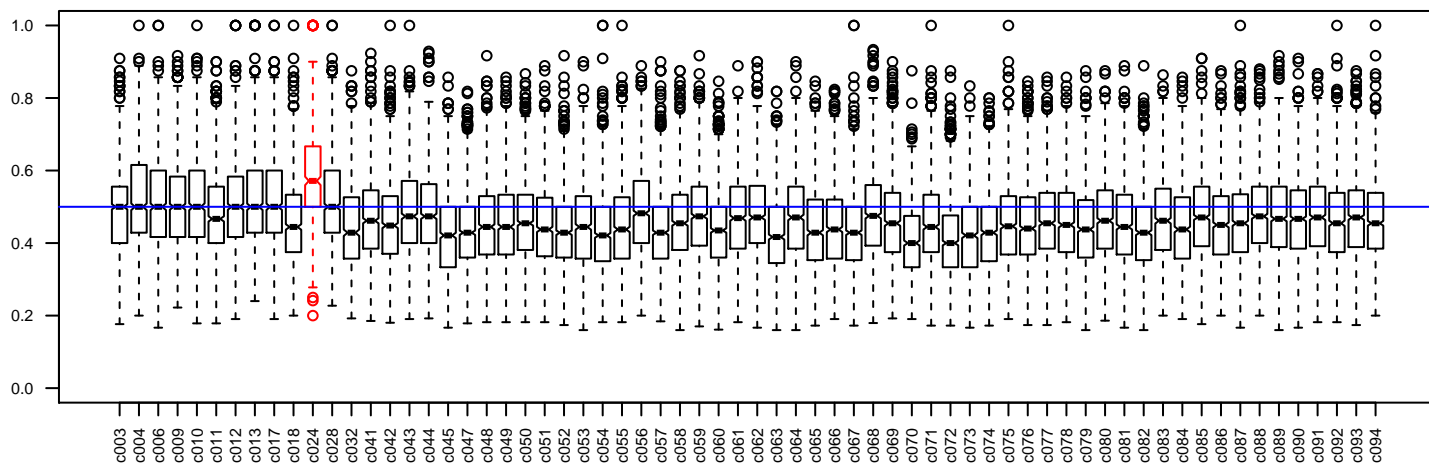
SNV:Pairwise Filter Overlap (% Filtered Variants):Total Fail=40657/Pass=51967

	near_indel	too_close	max_miss	max_gmiss	count	bglod	vaf_too_low_s	vaf_too_low_m2	vaf_zg_too_noisy	manual_exclude	
near_indel	<b>0.1</b>	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	
too_close	0.0	<b>1.6</b>	0.0	0.0	0.9	0.9	0.1	0.1	0.1	0.0	
max_miss	0.0	0.0	<b>0.4</b>	0.1	0.2	0.3	0.0	0.0	0.0	0.0	
max_gmiss	0.0	0.0	0.1	<b>1.1</b>	0.6	0.2	0.8	0.9	0.9	0.0	
count	0.0	0.9	0.2	0.6	<b>92.9</b>	82.2	4.4	6.0	4.5	0.0	
bglod	0.0	0.9	0.3	0.2	82.2	<b>86.8</b>	0.2	0.3	0.2	0.0	
vaf_too_low_s	0.0	0.1	0.0	0.8	4.4	0.2	<b>5.7</b>	5.7	5.5	0.0	
vaf_too_low_m2	0.0	0.1	0.0	0.9	6.0	0.3	5.7	<b>7.8</b>	5.8	0.0	
vaf_zg_too_noisy	0.0	0.1	0.0	0.9	4.5	0.2	5.5	5.8	<b>5.9</b>	0.0	
manual_exclude	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	<b>0.0</b>	

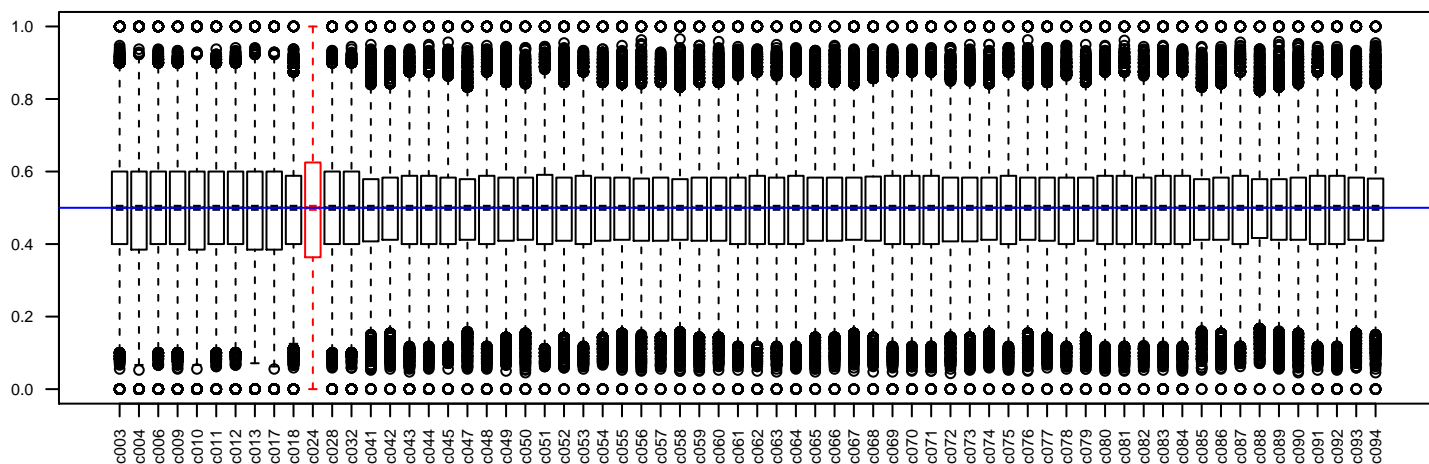
Called SNV Count vs Average Depth



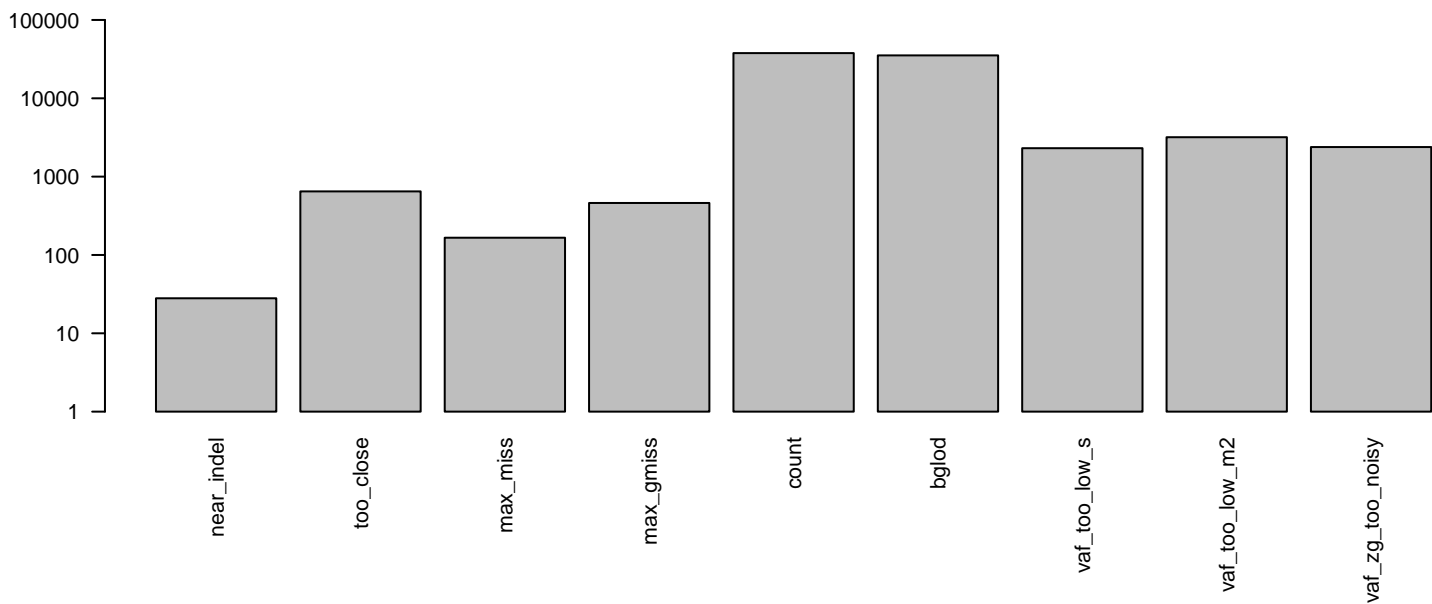
PD5147: SNV : VAF Distribution at Somatic (pass all filters) sites called in Caveman



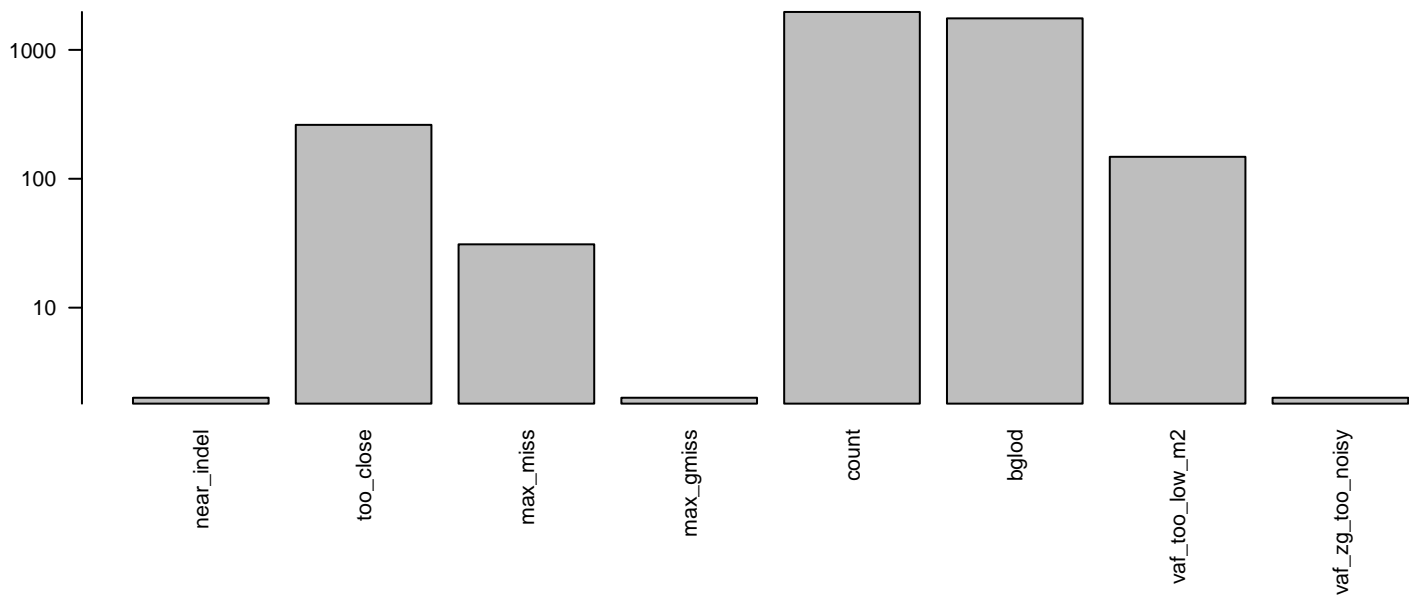
PD5147: SNV : VAF Distribution at Germline [Based on the Matched Normal] sites called in Caveman



PD5147: SNV: No. Sites removed by each filter



PD5147: SNV: No. Sites UNIQUELY removed by each filter

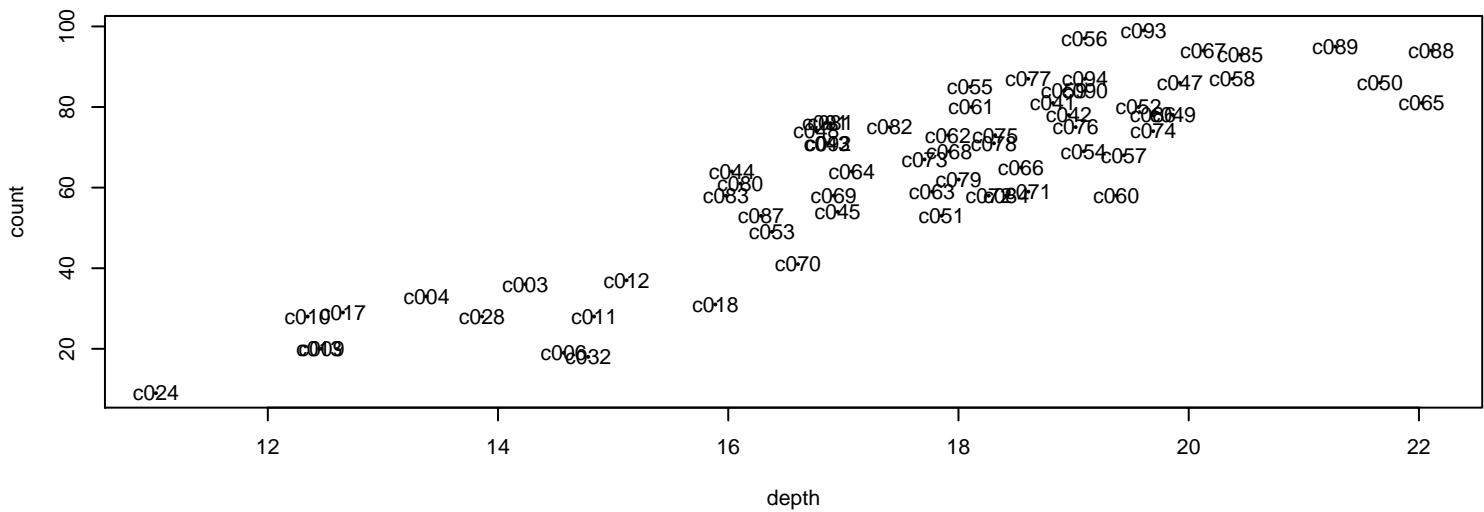


PD5147 : Indels

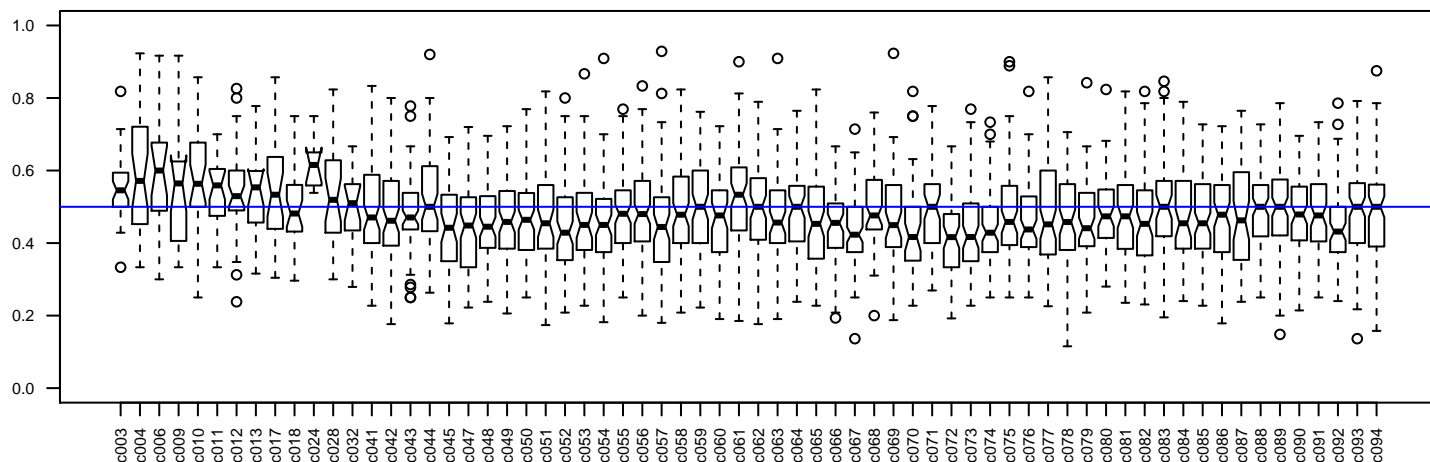
Indels:Pairwise Filter Overlap (% Filtered Variants):Total Fail=5774/Pass=2706

	too_close	max_miss	max_gmiss	count	bgld	vaf_too_low_s	vaf_too_low_m2	vaf_zg_too_noisy	manual_exclude	
too_close	2.5	1.6	0.6	1.9	2.1	0.0	0.2	0.1	0.0	
max_miss	1.6	20.4	7.6	12.7	18.7	0.0	0.1	0.1	0.0	
max_gmiss	0.6	7.6	12.8	2.5	8.6	1.7	4.3	3.5	0.0	
count	1.9	12.7	2.5	70.6	64.6	2.4	6.2	4.5	0.0	
bgld	2.1	18.7	8.6	64.6	82.6	3.4	5.0	4.8	0.0	
vaf_too_low_s	0.0	0.0	1.7	2.4	3.4	5.0	5.0	4.8	0.0	
vaf_too_low_m2	0.2	0.1	4.3	6.2	5.0	5.0	18.7	13.1	0.0	
vaf_zg_too_noisy	0.1	0.1	3.5	4.5	4.8	4.8	13.1	13.5	0.0	
manual_exclude	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	

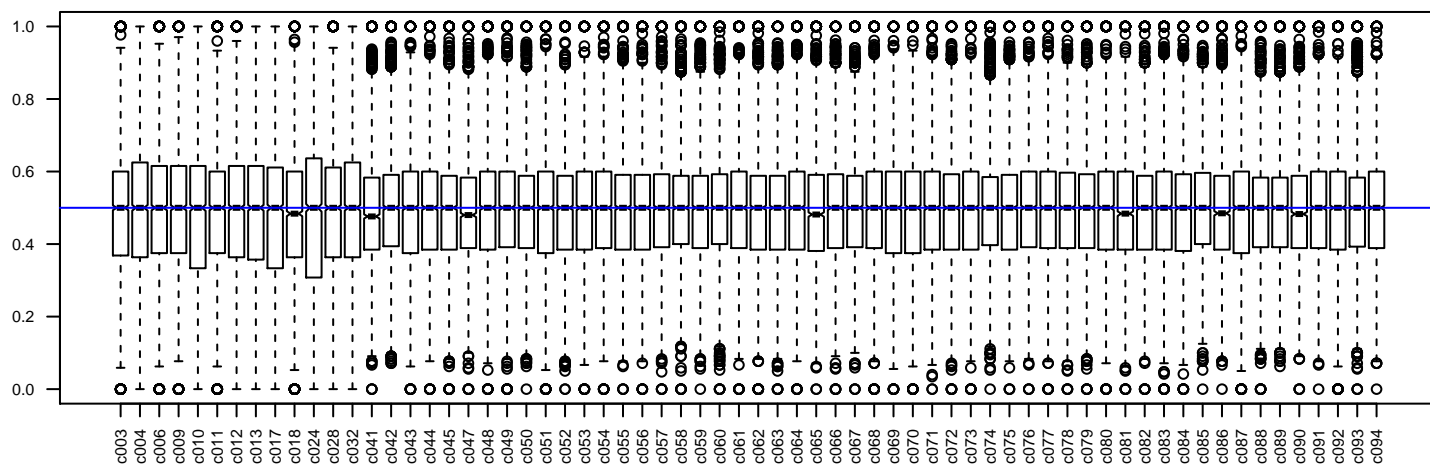
Called INDEL Count vs Average Depth



**PD5147: INDEL : VAF Distribution at Somatic (pass all filters) sites called in Pindel**

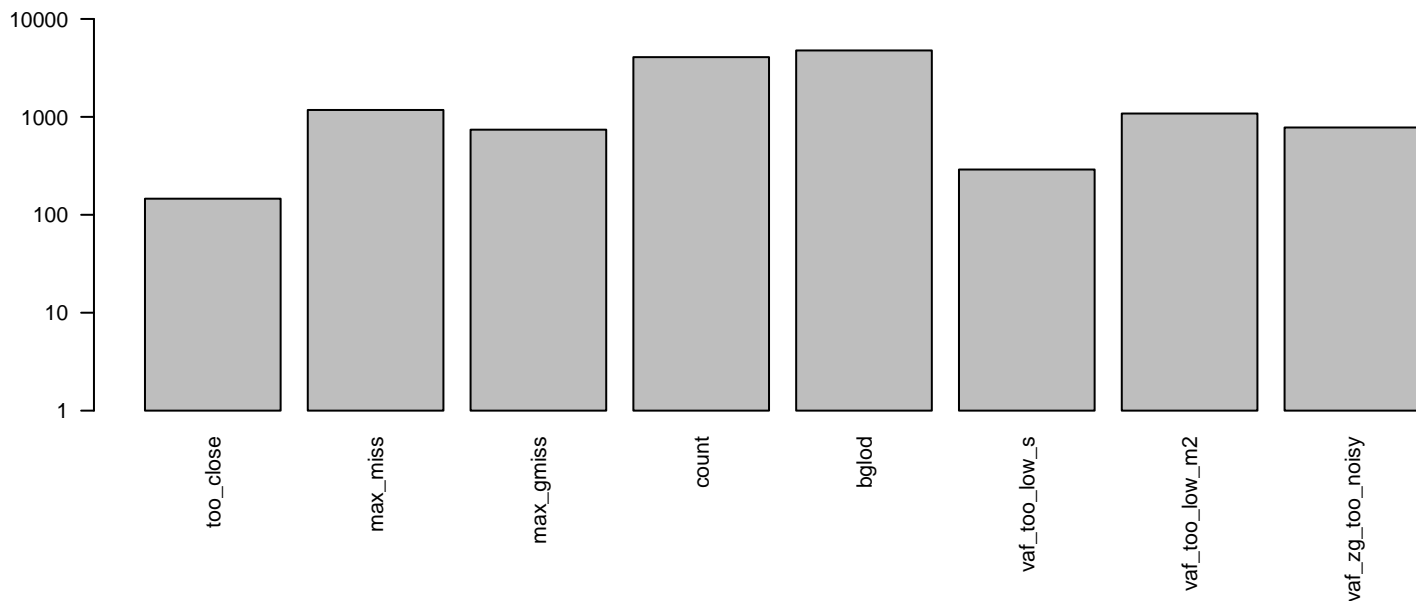


**PD5147: INDEL : VAF Distribution at Germline [Based on the Matched Normal] sites called in Pindel**





PD5147: INDEL: No. Sites removed by each filter



PD5147: INDEL: No. Sites UNIQUELY removed by each filter

