Per patient initial QC assessment plots prior to 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 <=7. Colonies corresponding to filled red or grey boxes were subsequently excluded.

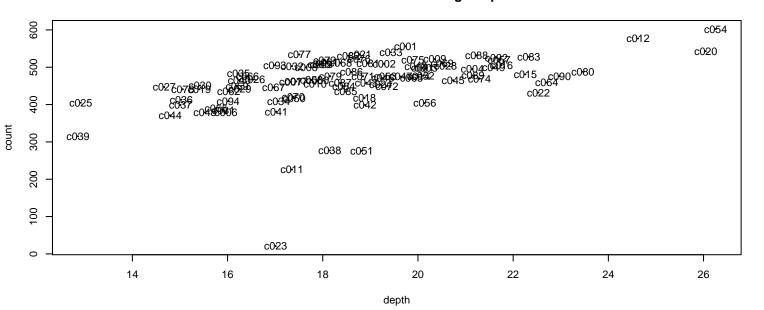
Page 3) Upper panel- Number of loci failing each filter on a log scale. Lower panel- Number of loci that uniquely fail each filter on a log scale. This measures the effect of removing a single filter.

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

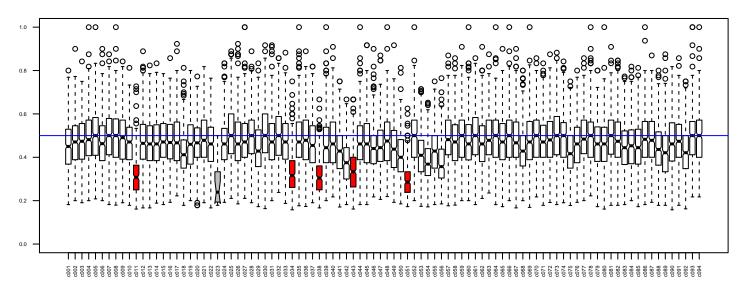
SNV:Pairwise Filter Overlap (% Filtered Variants):Total Fail=37573/Pass=40307

PD7271: SNVs

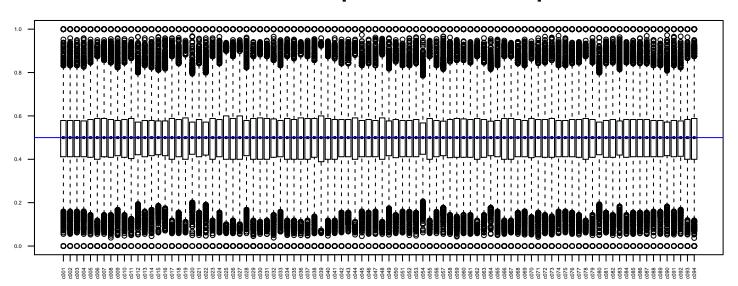
											丄
	near_indel	too_close	max_miss	max_gmiss	count	bglod	vaf_too_low_s	vaf_too_low_mv	af_zg_too_nois	ganual_exclude	
near_indel	0.1	0.0	0.0	0.1	0.0	0.0	0.0	0.1	0.1	0.0	
too_close	0.0	1.5	0.0	0.0	1.0	1.0	0.0	0.1	0.0	0.0	
max_miss	0.0	0.0	0.1	0.0	0.1	0.1	0.0	0.0	0.0	0.0	
max_gmiss	0.1	0.0	0.0	0.5	0.1	0.2	0.3	0.4	0.4	0.0	
count	0.0	1.0	0.1	0.1	95.7	94.4	0.7	1.0	0.8	0.0	
bglod	0.0	1.0	0.1	0.2	94.4	97.6	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	2 0.1	0.1	0.0	0.4	1.0	0.4	1.1	1.8	1.3	0.0	
vaf_zg_too_nois	y 0.1	0.0	0.0	0.4	0.8	0.4	1.0	1.3	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	



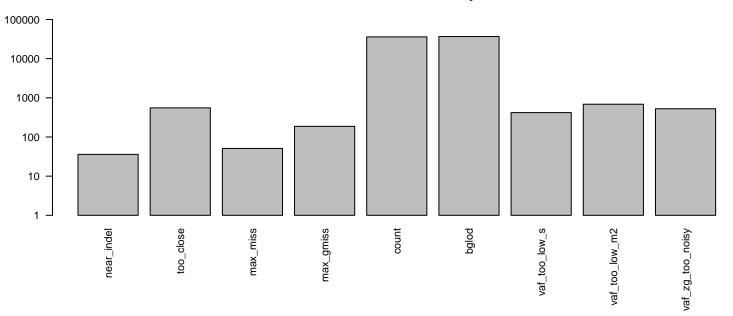
PD7271: SNV: VAF Distribution at Somatic (pass all filters) sites called in Caveman



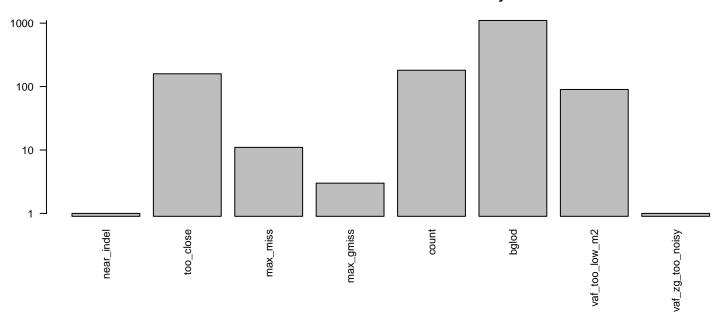
PD7271: SNV: VAF Distribution at Germline [Based on the Matched Normal] sites called in Caveman



PD7271: SNV: No. Sites removed by each filter



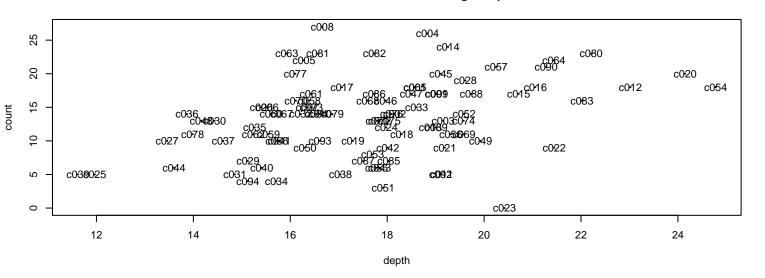
PD7271: SNV: No. Sites UNIQUELY removed by each filter



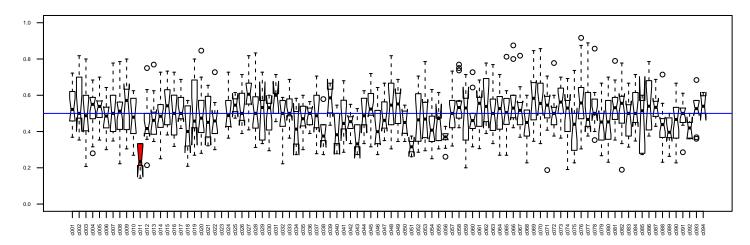
Indels:Pairwise Filter Overlap (% Filtered Variants):Total Fail=5588/Pass=1116

PD7271 : Indels

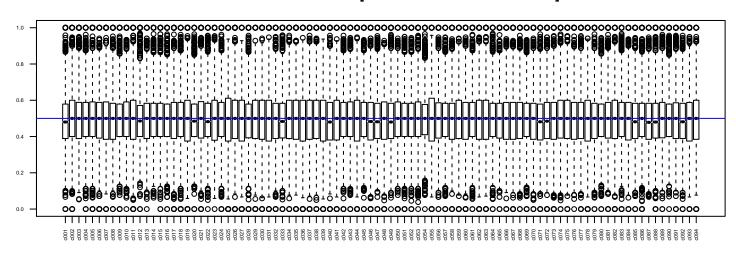
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	too_close	max_miss	max_gmiss	count	bglod	vaf_too_low_s	vaf_too_low_m2	af_zg_too_nois	manual_exclude	3
too_close	3.8	2.6	1.5	2.2	2.9	0.1	0.4	0.4	0.0	
max_miss	2.6	25.0	9.0	15.9	21.9	0.0	0.0	0.0	0.0	
max_gmiss	1.5	9.0	14.1	2.9	8.4	1.8	4.1	3.3	0.0	
count	2.2	15.9	2.9	72.8	70.1	0.5	1.8	1.3	0.0	
bglod	2.9	21.9	8.4	70.1	85.8	0.8	1.7	1.3	0.0	
vaf_too_low_s	0.1	0.0	1.8	0.5	0.8	2.6	2.6	2.5	0.0	
vaf_too_low_m2	0.4	0.0	4.1	1.8	1.7	2.6	12.1	9.0	0.0	
vaf_zg_too_noisy	0.4	0.0	3.3	1.3	1.3	2.5	9.0	9.2	0.0	
manual_exclude	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	



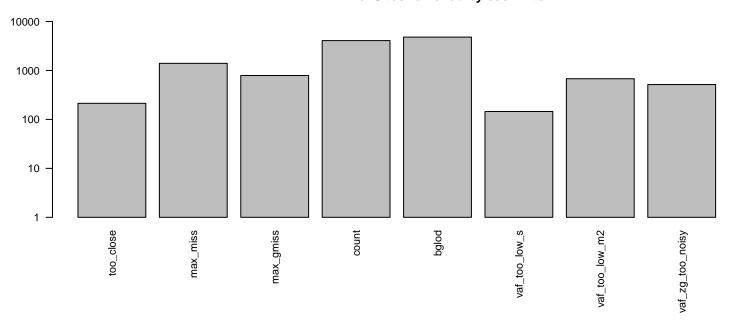
PD7271: INDEL: VAF Distribution at Somatic (pass all filters) sites called in Pindel



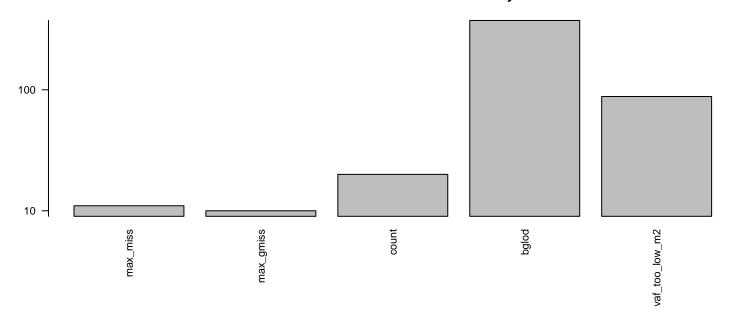
PD7271: INDEL: VAF Distribution at Germline [Based on the Matched Normal] sites called in Pindel



PD7271: INDEL: No. Sites removed by each filter



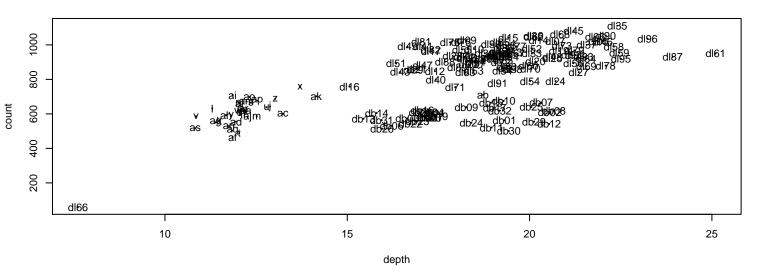
PD7271: INDEL: No. Sites UNIQUELY removed by each filter



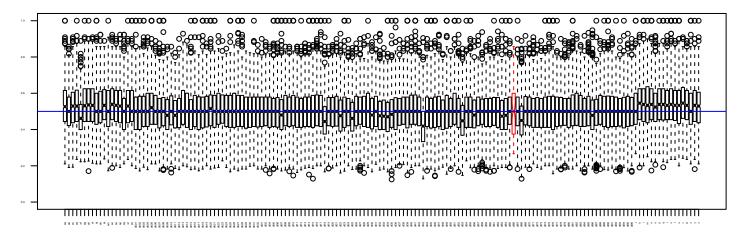
PD5182 : SNVs

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	near_indel	too_close	max_miss	max_gmiss	count	bglod	vaf_too_low_s	raf_too_low_mv	af_zg_too_nois	yanual_exclud	ē
near_indel	0.2	0.0	0.0	0.1	0.0	0.1	0.1	0.1	0.1	0.0	Γ
too_close	0.0	2.6	0.0	0.0	0.8	0.9	0.0	0.0	0.0	0.0	Γ
max_miss	0.0	0.0	0.7	0.2	0.2	0.4	0.0	0.0	0.0	0.0	Γ
max_gmiss	0.1	0.0	0.2	0.9	0.1	0.3	0.5	0.6	0.6	0.0	Γ
count	0.0	0.8	0.2	0.1	87.3	85.4	0.6	0.9	0.7	0.0	Γ
bglod	0.1	0.9	0.4	0.3	85.4	94.9	0.3	0.5	0.5	0.0	Γ
vaf_too_low_s	0.1	0.0	0.0	0.5	0.6	0.3	1.4	1.4	1.2	0.0	
vaf_too_low_m2	0.1	0.0	0.0	0.6	0.9	0.5	1.4	2.5	1.6	0.0	
vaf_zg_too_nois	у 0.1	0.0	0.0	0.6	0.7	0.5	1.2	1.6	1.7	0.0	Γ
manual_exclude	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	

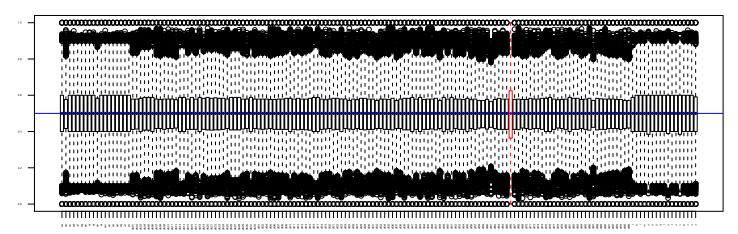
SNV:Pairwise Filter Overlap (% Filtered Variants):Total Fail=39385/Pass=101726



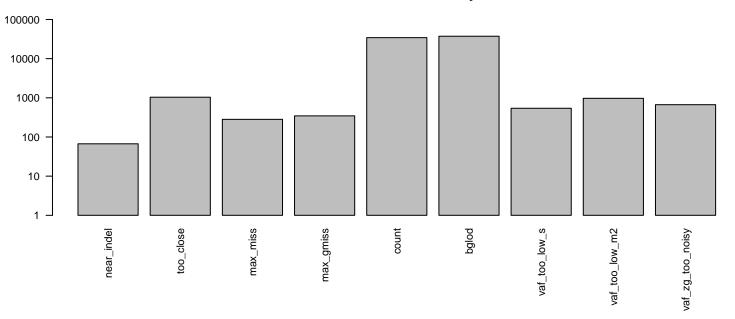
PD5182: SNV: VAF Distribution at Somatic (pass all filters) sites called in Caveman



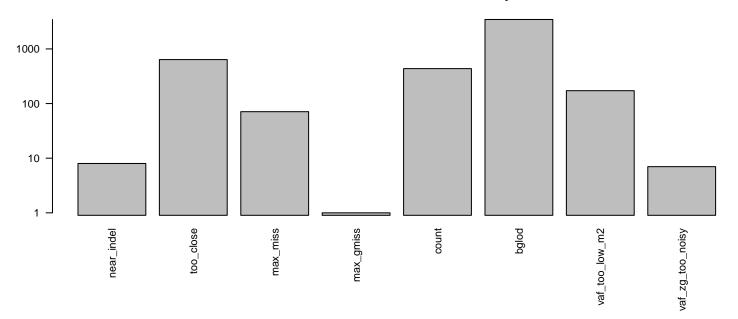
PD5182: SNV: VAF Distribution at Germline [Based on the Matched Normal] sites called in Caveman



PD5182: SNV: No. Sites removed by each filter



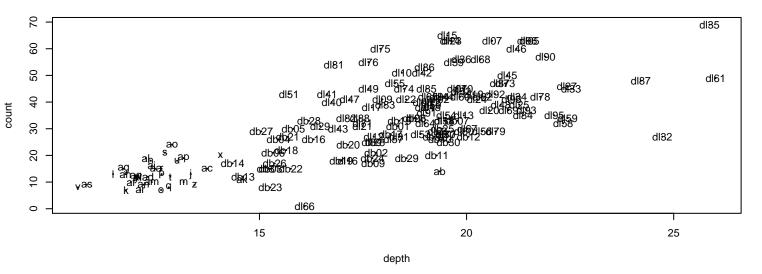
PD5182: SNV: No. Sites UNIQUELY removed by each filter



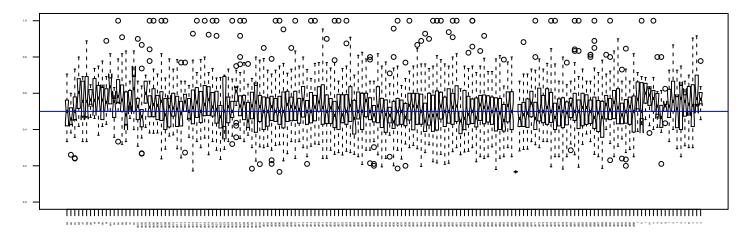
PD5182 : Indels

Indels:Pairwise Filter Overlap (% Filtered Variants):Total Fail=7816/Pass=3679

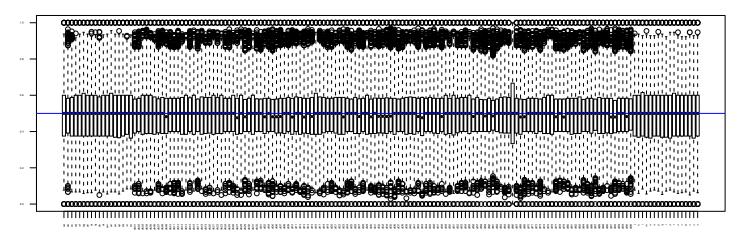
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	too_close	max_miss	max_gmiss	count	bglod	vaf_too_low_s	vaf_too_low_m2	raf_zg_too_nois	manual_exclude	
too_close	6.3	5.2	2.5	3.4	5.1	0.2	0.4	0.4	0.0	
max_miss	5.2	32.3	14.0	16.4	28.0	0.0	0.2	0.3	0.0	
max_gmiss	2.5	14.0	19.9	2.6	12.3	3.0	5.3	4.9	0.0	
count	3.4	16.4	2.6	55.5	52.0	0.3	3.0	1.8	0.0	
bglod	5.1	28.0	12.3	52.0	76.5	1.5	2.4	2.6	0.0	
vaf_too_low_s	0.2	0.0	3.0	0.3	1.5	4.7	4.7	4.5	0.0	
vaf_too_low_m2	0.4	0.2	5.3	3.0	2.4	4.7	21.2	15.7	0.0	
vaf_zg_too_noisy	0.4	0.3	4.9	1.8	2.6	4.5	15.7	16.3	0.0	
manual_exclude	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	
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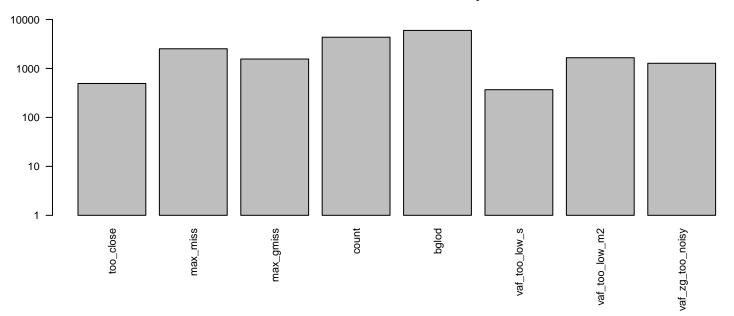
PD5182: INDEL: VAF Distribution at Somatic (pass all filters) sites called in Pindel



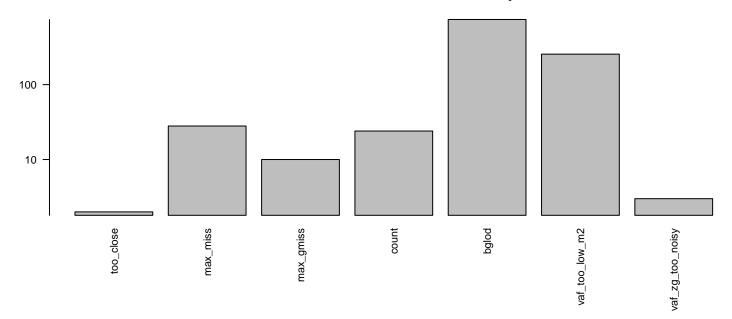
PD5182: INDEL: VAF Distribution at Germline [Based on the Matched Normal] sites called in Pindel



PD5182: INDEL: No. Sites removed by each filter



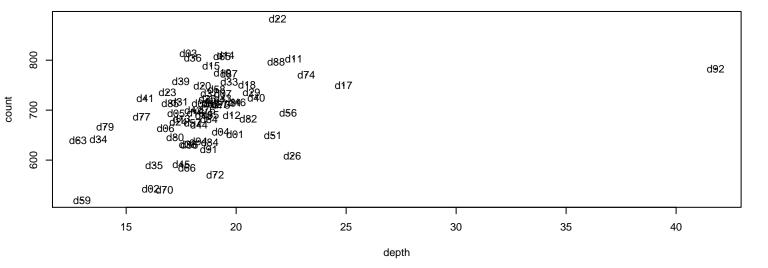
PD5182: INDEL: No. Sites UNIQUELY removed by each filter



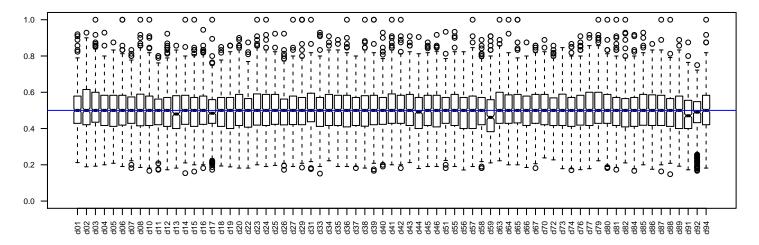
PD5163 : SNVs

SNV:Pairwise Filter Overlap (% Filtered Variants):Total Fail=86606/Pass=45323

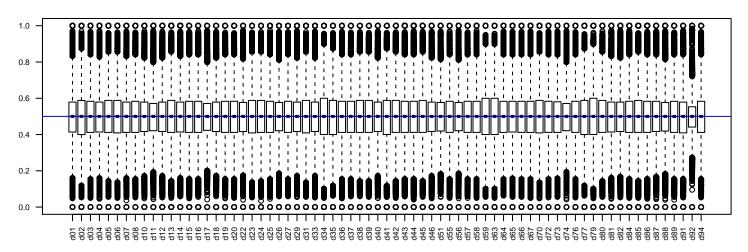
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	near_indel	too_close	max_miss	max_gmiss	count	bglod	vaf_too_low_s	af_too_low_m	af_zg_too_nois	yanual_exclud	ŧ
near_indel	0.1	0.0	0.0	0.1	0.0	0.0	0.0	0.1	0.1	0.0	
too_close	0.0	1.4	0.0	0.0	1.0	1.1	0.0	0.0	0.0	0.0	Ī
max_miss	0.0	0.0	0.1	0.1	0.1	0.1	0.0	0.0	0.0	0.0	Γ
max_gmiss	0.1	0.0	0.1	0.5	0.2	0.2	0.3	0.4	0.4	0.0	Γ
count	0.0	1.0	0.1	0.2	95.2	94.1	0.9	1.1	0.9	0.0	Γ
bglod	0.0	1.1	0.1	0.2	94.1	98.2	0.3	0.4	0.3	0.0	Ī
vaf_too_low_s	0.0	0.0	0.0	0.3	0.9	0.3	1.2	1.2	1.1	0.0	Γ
vaf_too_low_m2	0.1	0.0	0.0	0.4	1.1	0.4	1.2	1.7	1.3	0.0	Γ
vaf_zg_too_nois	y 0.1	0.0	0.0	0.4	0.9	0.3	1.1	1.3	1.3	0.0	Γ
manual_exclude	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	



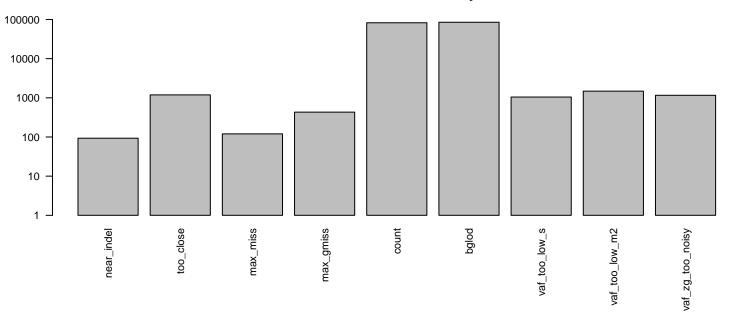
PD5163: SNV: VAF Distribution at Somatic (pass all filters) sites called in Caveman



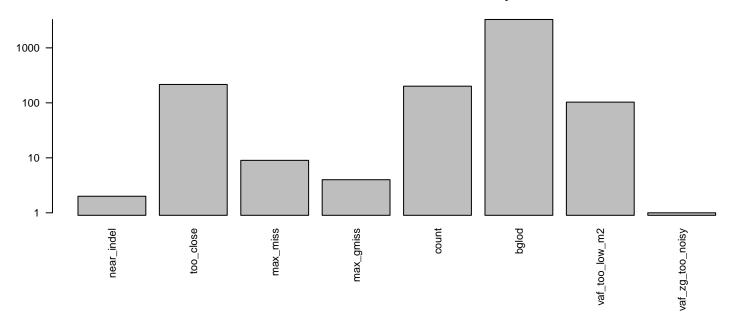
PD5163: SNV: VAF Distribution at Germline [Based on the Matched Normal] sites called in Caveman



PD5163: SNV: No. Sites removed by each filter

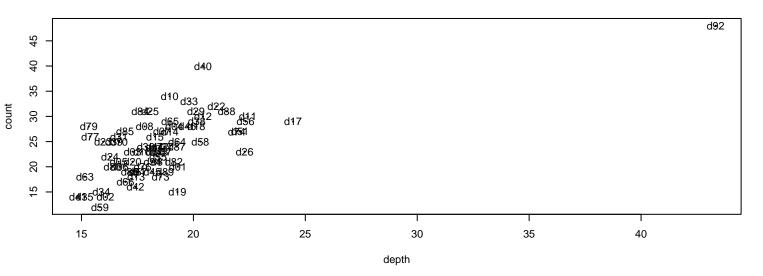


PD5163: SNV: No. Sites UNIQUELY removed by each filter

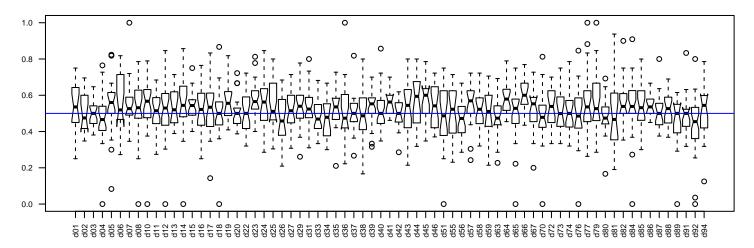


PD5163 : Indels
Indels:Pairwise Filter Overlap (% Filtered Variants):Total Fail=10558/Pass=1493

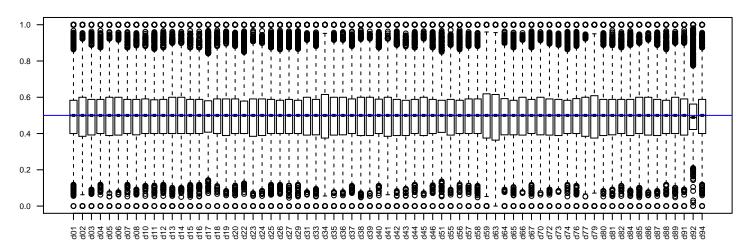
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	too_close	max_miss	max_gmiss	count	bglod	vaf_too_low_s	vaf_too_low_m2	af_zg_too_nois	manual_exclude	4
too_close	3.6	2.3	1.0	2.5	2.9	0.1	0.2	0.1	0.0	
max_miss	2.3	16.1	5.1	10.9	14.2	0.0	0.0	0.0	0.0	
max_gmiss	1.0	5.1	8.6	2.0	5.3	1.4	2.6	2.0	0.0	
count	2.5	10.9	2.0	80.5	77.2	0.9	2.5	1.8	0.0	
bglod	2.9	14.2	5.3	77.2	90.3	0.9	1.6	1.2	0.0	
vaf_too_low_s	0.1	0.0	1.4	0.9	0.9	2.7	2.7	2.5	0.0	
vaf_too_low_m2	0.2	0.0	2.6	2.5	1.6	2.7	8.4	6.1	0.0	
vaf_zg_too_noisy	0.1	0.0	2.0	1.8	1.2	2.5	6.1	6.4	0.0	
manual_exclude	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	



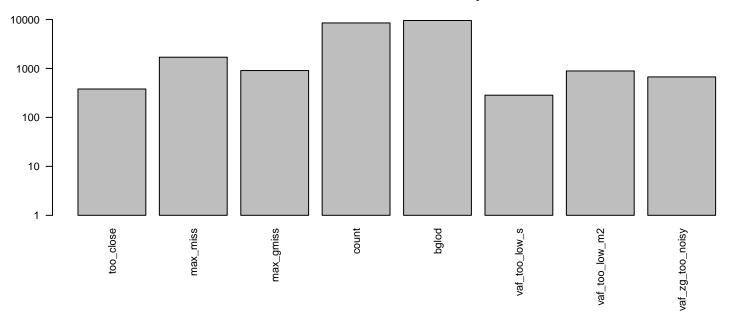
PD5163: INDEL: VAF Distribution at Somatic (pass all filters) sites called in Pindel



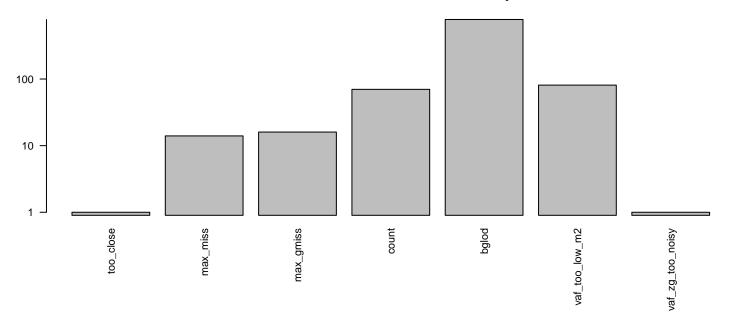
PD5163: INDEL: VAF Distribution at Germline [Based on the Matched Normal] sites called in Pindel



PD5163: INDEL: No. Sites removed by each filter



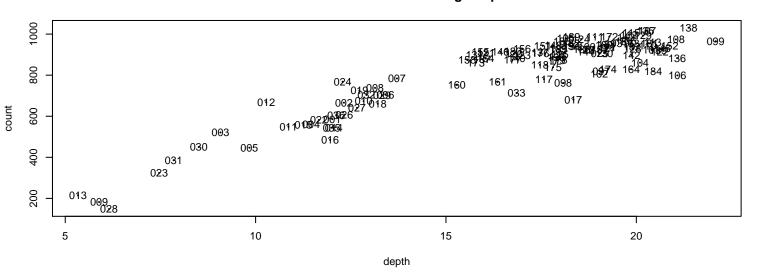
PD5163: INDEL: No. Sites UNIQUELY removed by each filter



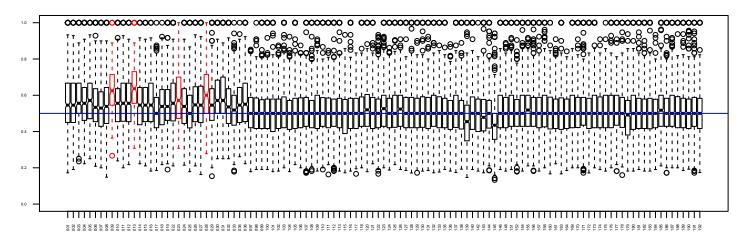
PD5847 : SNVs

		I	1	I	l	I	I	I	I	I	ı
	near_indel	too_close	max_miss	max_gmiss	count	bglod	vaf_too_low_s	raf_too_low_mv	af_zg_too_nois	yanual_exclud	ŧ
near_indel	0.1	0.0	0.0	0.0	0.0	0.0	0.0	0.1	0.0	0.0	
too_close	0.0	1.5	0.0	0.0	0.8	1.0	0.0	0.1	0.0	0.0	
max_miss	0.0	0.0	0.8	0.3	0.3	0.5	0.0	0.0	0.0	0.0	
max_gmiss	0.0	0.0	0.3	0.8	0.1	0.3	0.4	0.5	0.5	0.0	
count	0.0	0.8	0.3	0.1	84.3	83.3	0.5	0.6	0.6	0.0	
bglod	0.0	1.0	0.5	0.3	83.3	97.2	0.2	0.4	0.3	0.0	
vaf_too_low_s	0.0	0.0	0.0	0.4	0.5	0.2	1.2	1.2	1.1	0.0	
vaf_too_low_m2	0.1	0.1	0.0	0.5	0.6	0.4	1.2	1.9	1.4	0.0	
vaf_zg_too_nois	у 0.0	0.0	0.0	0.5	0.6	0.3	1.1	1.4	1.5	0.0	
manual_exclude	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	

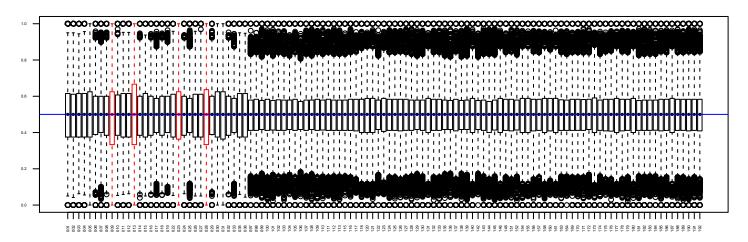
SNV:Pairwise Filter Overlap (% Filtered Variants):Total Fail=38207/Pass=35164



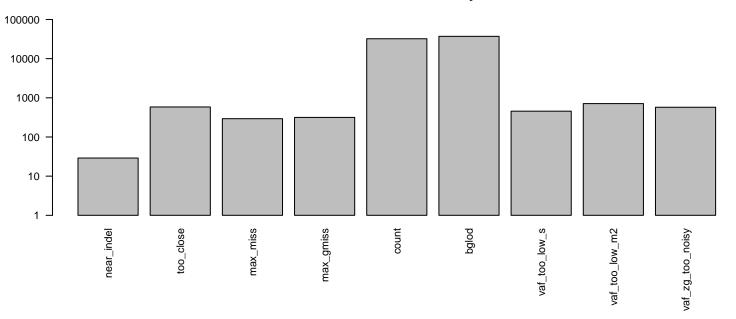
PD5847: SNV: VAF Distribution at Somatic (pass all filters) sites called in Caveman



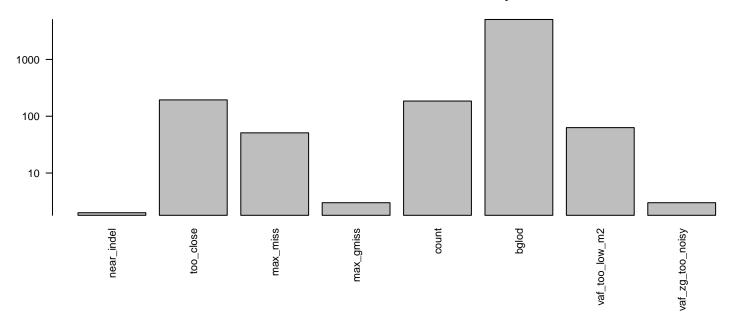
PD5847: SNV: VAF Distribution at Germline [Based on the Matched Normal] sites called in Caveman



PD5847: SNV: No. Sites removed by each filter

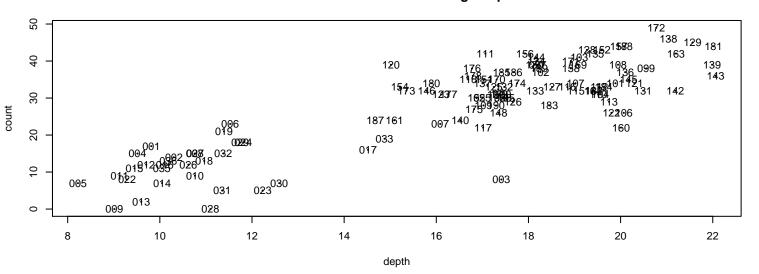


PD5847: SNV: No. Sites UNIQUELY removed by each filter

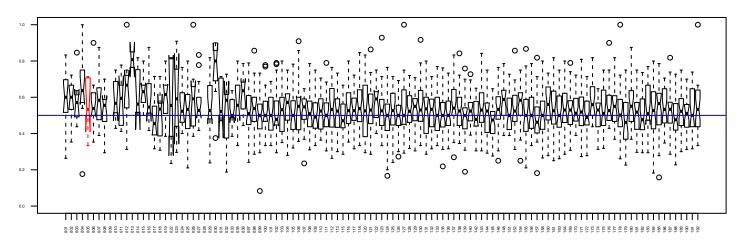


PD5847 : Indels
Indels:Pairwise Filter Overlap (% Filtered Variants):Total Fail=5913/Pass=1226

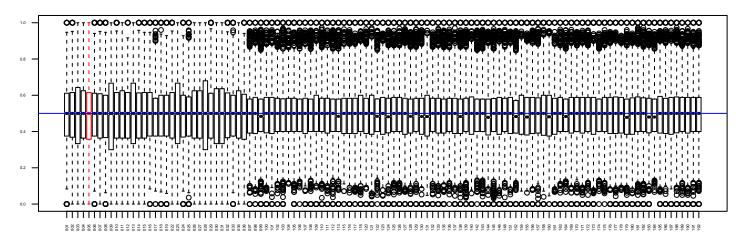
ı		1	I	I	I	I	I	I	1	ı
	too_close	max_miss	max_gmiss	count	bglod	vaf_too_low_s	vaf_too_low_m2	af_zg_too_nois	manual_exclude	
too_close	4.4	3.3	1.5	2.7	3.5	0.1	0.3	0.2	0.0	
max_miss	3.3	29.8	12.1	17.4	25.2	0.0	0.1	0.1	0.0	
max_gmiss	1.5	12.1	16.7	3.6	9.8	2.0	3.8	3.1	0.0	
count	2.7	17.4	3.6	58.9	55.9	0.2	1.5	0.9	0.0	
bglod	3.5	25.2	9.8	55.9	83.5	0.9	1.8	1.5	0.0	
vaf_too_low_s	0.1	0.0	2.0	0.2	0.9	3.1	3.1	2.9	0.0	
vaf_too_low_m2	0.3	0.1	3.8	1.5	1.8	3.1	13.1	9.1	0.0	
vaf_zg_too_noisy	0.2	0.1	3.1	0.9	1.5	2.9	9.1	9.4	0.0	
manual_exclude	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	
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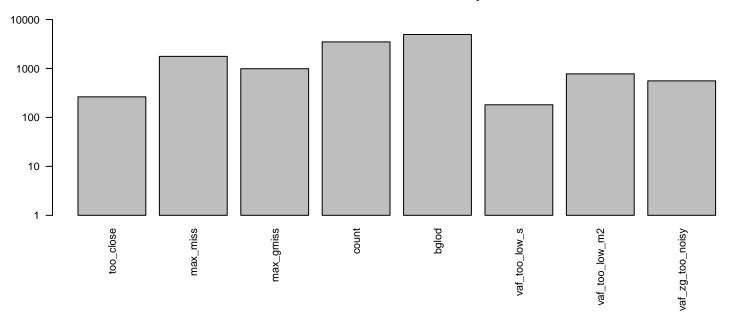
PD5847: INDEL: VAF Distribution at Somatic (pass all filters) sites called in Pindel



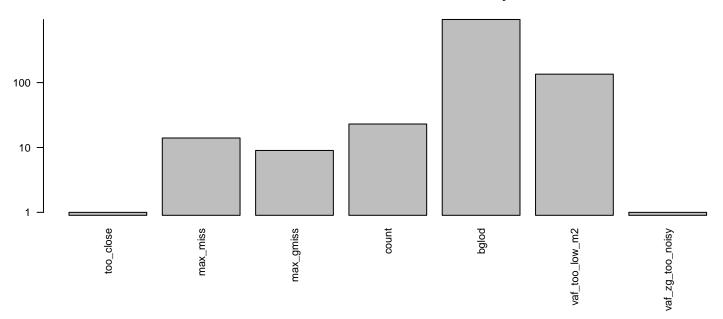
PD5847: INDEL: VAF Distribution at Germline [Based on the Matched Normal] sites called in Pindel



PD5847: INDEL: No. Sites removed by each filter



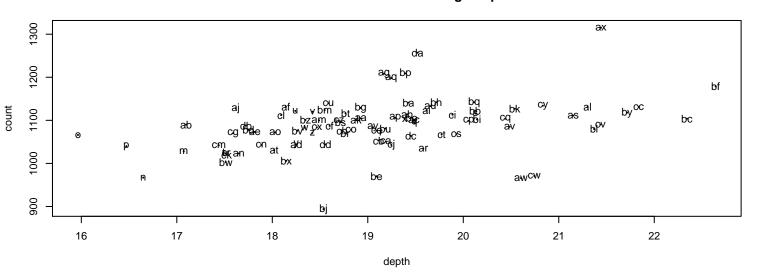
PD5847: INDEL: No. Sites UNIQUELY removed by each filter



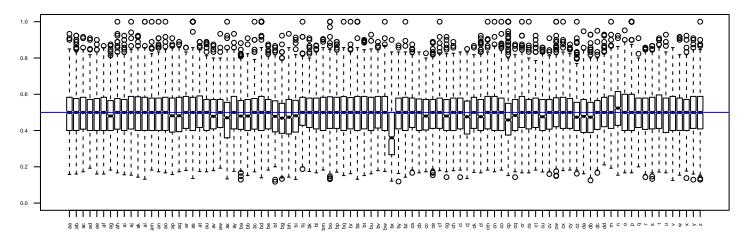
PD5179 : SNVs

SNV:Pairwise Filter Overlap (% Filtered Variants):Total Fail=38811/Pass=37325

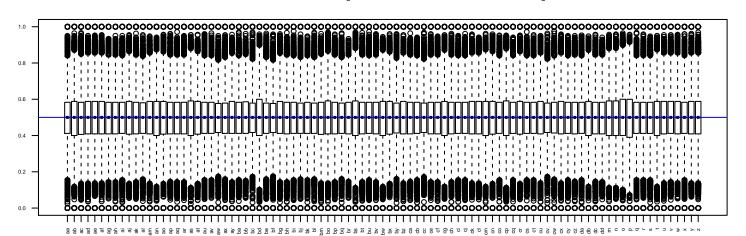
near_indel too_close max_miss max_gmiss count bglod vaf_too_low_slaf_too_low_maf_zg_too_noisyanual_exc near_indel 0.2 0.0 0.0 0.1 0.0 0.1 0.1 0.1 0.1 0.0 too_close 0.0 1.9 0.0 0.0 1.0 1.0 0.0 0.0 0.0 0.0 max_miss 0.0 0.0 0.2 0.1 0.1 0.1 0.0 0.0 0.0 0.0 max_gmiss 0.1 0.0 0.1 0.6 0.2 0.3 0.4 0.5 0.5 0.0 count 0.0 1.0 0.1 0.2 93.9 91.5 0.7 1.0 0.9 0.0 bglod 0.1 1.0 0.1 0.3 91.5 96.2 0.3 0.4 0.4 0.0 vaf_too_low_s 0.1 0.0 0.0 0.4 0.7 0.3 1.1 1.1 1.0 0.0												丄
too_close 0.0 1.9 0.0 0.0 1.0 1.0 0.0 0.0 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 0.3 0.4 0.5 0.5 0.0 count 0.0 1.0 0.1 0.2 93.9 91.5 0.7 1.0 0.9 0.0 bglod 0.1 1.0 0.1 0.3 91.5 96.2 0.3 0.4 0.4 0.0 vaf_too_low_s 0.1 0.0 0.0 0.4 0.7 0.3 1.1 1.1 1.0 0.0 vaf_too_low_m² 0.1 0.0 0.0 0.5 1.0 0.4 1.1 1.7 1.3 0.0 vaf_too_low_n² 0.1 0.0 0.0 0.5 0.9 0.4 1.0 1.3 1.5 0.0 <td></td> <td>near_indel</td> <td>too_close</td> <td>max_miss</td> <td>max_gmiss</td> <td>count</td> <td>bglod</td> <td>vaf_too_low_s</td> <td>af_too_low_m</td> <td>af_zg_too_nois</td> <td>yanual_exclud</td> <td>e</td>		near_indel	too_close	max_miss	max_gmiss	count	bglod	vaf_too_low_s	af_too_low_m	af_zg_too_nois	yanual_exclud	e
max_miss 0.0 0.0 0.2 0.1 0.1 0.0 0.0 0.0 0.0 max_gmiss 0.1 0.0 0.1 0.6 0.2 0.3 0.4 0.5 0.5 0.0 count 0.0 1.0 0.1 0.2 93.9 91.5 0.7 1.0 0.9 0.0 bglod 0.1 1.0 0.1 0.3 91.5 96.2 0.3 0.4 0.4 0.0 vaf_too_low_s 0.1 0.0 0.0 0.4 0.7 0.3 1.1 1.1 1.0 0.0 vaf_too_low_m² 0.1 0.0 0.0 0.5 1.0 0.4 1.1 1.7 1.3 0.0 vaf_zg_too_noisy 0.1 0.0 0.0 0.5 0.9 0.4 1.0 1.3 1.5 0.0	near_indel	0.2	0.0	0.0	0.1	0.0	0.1	0.1	0.1	0.1	0.0	
max_gmiss 0.1 0.0 0.1 0.6 0.2 0.3 0.4 0.5 0.5 0.0 count 0.0 1.0 0.1 0.2 93.9 91.5 0.7 1.0 0.9 0.0 bglod 0.1 1.0 0.1 0.3 91.5 96.2 0.3 0.4 0.4 0.0 vaf_too_low_s 0.1 0.0 0.0 0.4 0.7 0.3 1.1 1.1 1.0 0.0 vaf_too_low_m² 0.1 0.0 0.0 0.5 1.0 0.4 1.1 1.7 1.3 0.0 vaf_zg_too_noisy 0.1 0.0 0.0 0.5 0.9 0.4 1.0 1.3 1.5 0.0	too_close	0.0	1.9	0.0	0.0	1.0	1.0	0.0	0.0	0.0	0.0	Ī
count 0.0 1.0 0.1 0.2 93.9 91.5 0.7 1.0 0.9 0.0 bglod 0.1 1.0 0.1 0.3 91.5 96.2 0.3 0.4 0.4 0.0 vaf_too_low_s 0.1 0.0 0.0 0.4 0.7 0.3 1.1 1.1 1.0 0.0 vaf_too_low_m² 0.1 0.0 0.0 0.5 1.0 0.4 1.1 1.7 1.3 0.0 vaf_zg_too_noisy 0.1 0.0 0.0 0.5 0.9 0.4 1.0 1.3 1.5 0.0	max_miss	0.0	0.0	0.2	0.1	0.1	0.1	0.0	0.0	0.0	0.0	Γ
bglod 0.1 1.0 0.1 0.3 91.5 96.2 0.3 0.4 0.4 0.0 vaf_too_low_s 0.1 0.0 0.0 0.4 0.7 0.3 1.1 1.1 1.0 0.0 vaf_too_low_m² 0.1 0.0 0.0 0.5 1.0 0.4 1.1 1.7 1.3 0.0 vaf_zg_too_noisy 0.1 0.0 0.0 0.5 0.9 0.4 1.0 1.3 1.5 0.0	max_gmiss	0.1	0.0	0.1	0.6	0.2	0.3	0.4	0.5	0.5	0.0	Γ
vaf_too_low_s 0.1 0.0 0.0 0.4 0.7 0.3 1.1 1.1 1.0 0.0 vaf_too_low_m² 0.1 0.0 0.0 0.5 1.0 0.4 1.1 1.7 1.3 0.0 vaf_zg_too_noisy 0.1 0.0 0.0 0.5 0.9 0.4 1.0 1.3 1.5 0.0	count	0.0	1.0	0.1	0.2	93.9	91.5	0.7	1.0	0.9	0.0	Γ
vaf_too_low_m² 0.1 0.0 0.0 0.5 1.0 0.4 1.1 1.7 1.3 0.0 vaf_zg_too_noisy 0.1 0.0 0.0 0.5 0.9 0.4 1.0 1.3 1.5 0.0	bglod	0.1	1.0	0.1	0.3	91.5	96.2	0.3	0.4	0.4	0.0	Ī
vaf_zg_too_noisy 0.1 0.0 0.0 0.5 0.9 0.4 1.0 1.3 1.5 0.0	vaf_too_low_s	0.1	0.0	0.0	0.4	0.7	0.3	1.1	1.1	1.0	0.0	Γ
	vaf_too_low_m2	0.1	0.0	0.0	0.5	1.0	0.4	1.1	1.7	1.3	0.0	Γ
manual exclude 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.	vaf_zg_too_nois	у 0.1	0.0	0.0	0.5	0.9	0.4	1.0	1.3	1.5	0.0	Γ
1.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0	manual_exclude	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	Ī



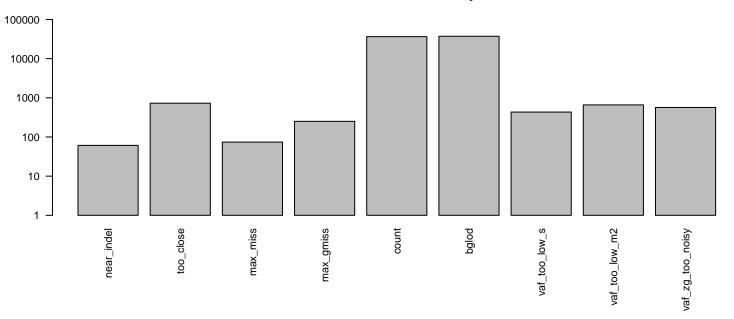
PD5179: SNV: VAF Distribution at Somatic (pass all filters) sites called in Caveman



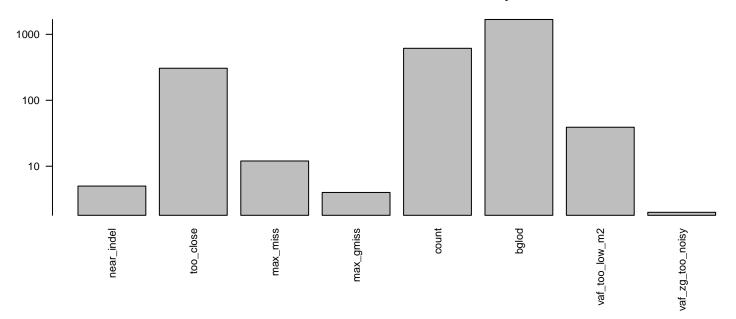
PD5179: SNV: VAF Distribution at Germline [Based on the Matched Normal] sites called in Caveman



PD5179: SNV: No. Sites removed by each filter



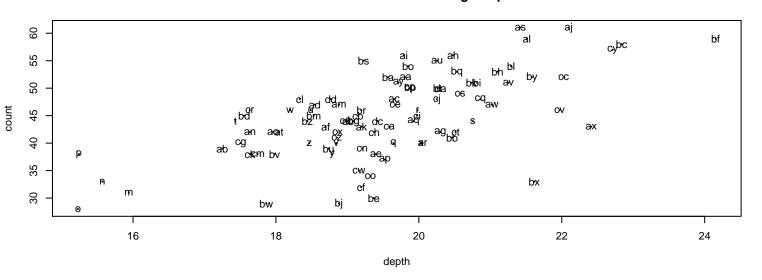
PD5179: SNV: No. Sites UNIQUELY removed by each filter



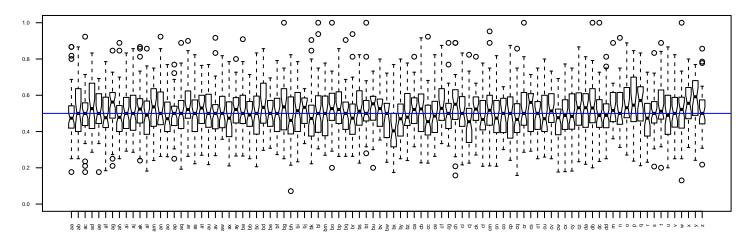
PD5179 : Indels

Indels:Pairwise Filter Overlap (% Filtered Variants):Total Fail=7119/Pass=1327

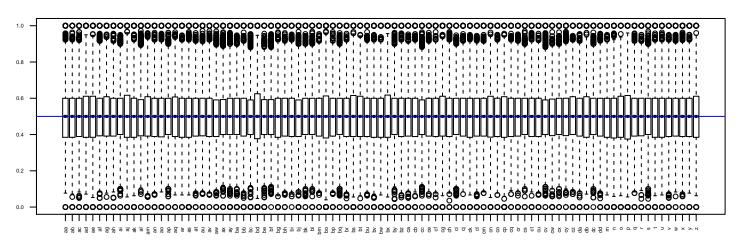
	too_close	max_miss	max_gmiss	count	bglod	vaf_too_low_s	vaf_too_low_m2	raf_zg_too_nois	manual_exclude
too_close	4.9	2.9	1.5	2.9	2.9	0.1	0.3	0.3	0.0
max_miss	2.9	22.2	8.0	13.5	15.2	0.0	0.0	0.2	0.0
max_gmiss	1.5	8.0	14.2	1.9	4.9	2.3	4.3	3.8	0.0
count	2.9	13.5	1.9	67.8	61.5	0.7	3.7	2.7	0.0
bglod	2.9	15.2	4.9	61.5	74.1	1.0	2.0	2.3	0.0
vaf_too_low_s	0.1	0.0	2.3	0.7	1.0	3.9	3.9	3.8	0.0
vaf_too_low_m2	0.3	0.0	4.3	3.7	2.0	3.9	18.3	13.4	0.0
vaf_zg_too_noisy	0.3	0.2	3.8	2.7	2.3	3.8	13.4	14.4	0.0
manual_exclude	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0



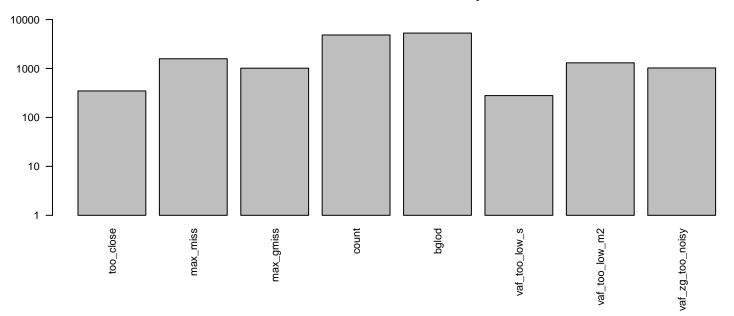
PD5179: INDEL: VAF Distribution at Somatic (pass all filters) sites called in Pindel



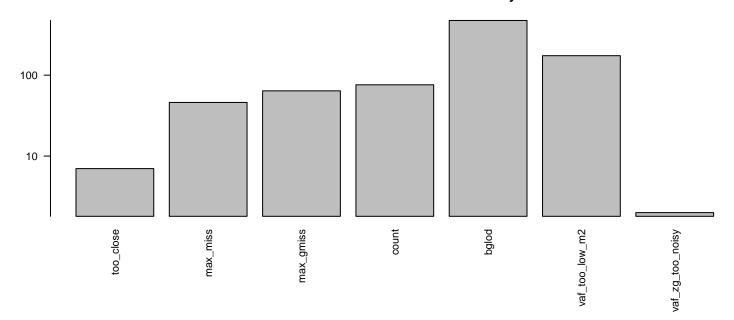
PD5179: INDEL: VAF Distribution at Germline [Based on the Matched Normal] sites called in Pindel



PD5179: INDEL: No. Sites removed by each filter

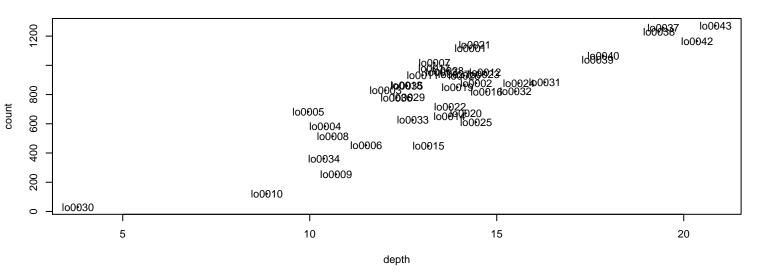


PD5179: INDEL: No. Sites UNIQUELY removed by each filter

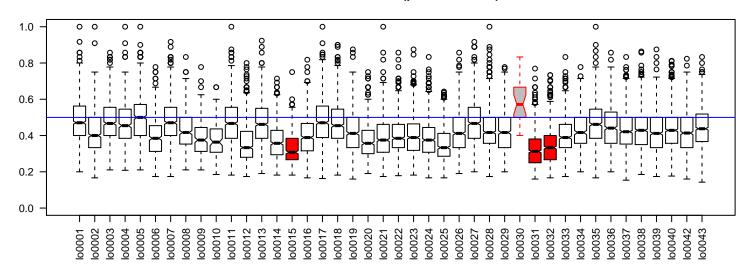


PD6634 : SNVs
SNV:Pairwise Filter Overlap (% Filtered Variants):Total Fail=36365/Pass=18717

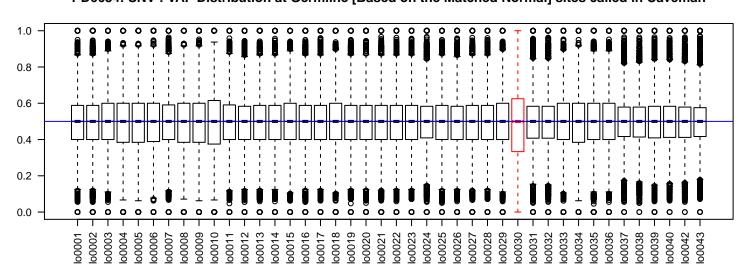
		l			l				l	1	L
	near_indel	too_close	max_miss	max_gmiss	count	bglod	vaf_too_low_s	raf_too_low_mv	af_zg_too_nois	yanual_exclud	e
near_indel	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	
too_close	0.0	1.3	0.0	0.0	0.9	0.9	0.0	0.0	0.0	0.0	
max_miss	0.0	0.0	1.5	0.4	1.0	1.2	0.0	0.0	0.0	0.0	
max_gmiss	0.0	0.0	0.4	0.9	0.4	0.3	0.3	0.4	0.3	0.0	Г
count	0.0	0.9	1.0	0.4	93.9	92.3	0.5	0.6	0.5	0.0	
bglod	0.0	0.9	1.2	0.3	92.3	97.2	0.0	0.1	0.0	0.0	
vaf_too_low_s	0.0	0.0	0.0	0.3	0.5	0.0	0.7	0.7	0.6	0.0	
vaf_too_low_m2	0.0	0.0	0.0	0.4	0.6	0.1	0.7	1.1	0.7	0.0	
vaf_zg_too_nois	у 0.0	0.0	0.0	0.3	0.5	0.0	0.6	0.7	0.8	0.0	Γ
manual_exclude	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	
		I	ı	1	I	ı	I	I	I	I	1



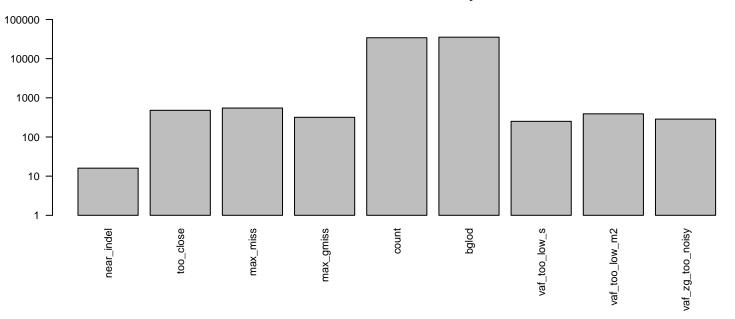
PD6634: SNV: VAF Distribution at Somatic (pass all filters) sites called in Caveman



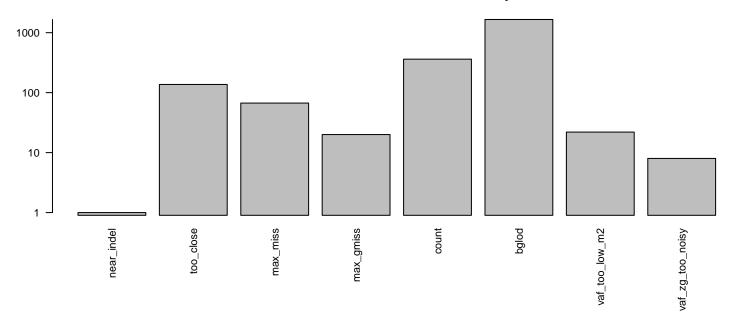
PD6634: SNV: VAF Distribution at Germline [Based on the Matched Normal] sites called in Caveman



PD6634: SNV: No. Sites removed by each filter



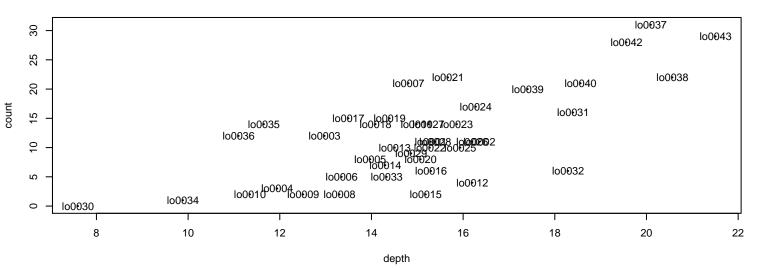
PD6634: SNV: No. Sites UNIQUELY removed by each filter



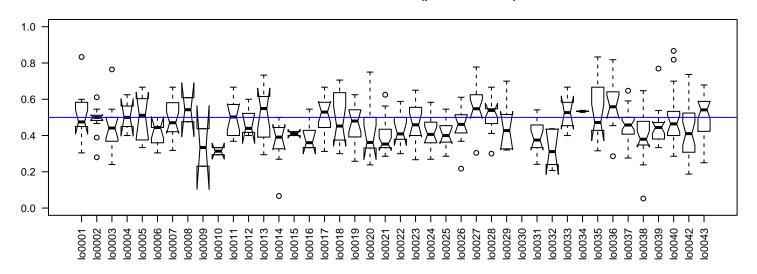
Indels:Pairwise Filter Overlap (% Filtered Variants):Total Fail=3455/Pass=303

PD6634: Indels

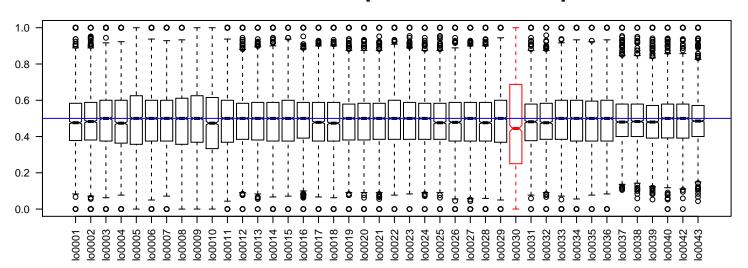
										丰
	too_close	max_miss	max_gmiss	count	bglod	vaf_too_low_s	vaf_too_low_m2	raf_zg_too_nois	manual_exclude	3
too_close	0.6	0.2	0.1	0.3	0.5	0.0	0.0	0.0	0.0	
max_miss	0.2	14.9	6.3	9.7	13.6	0.0	0.0	0.0	0.0	
max_gmiss	0.1	6.3	8.4	3.4	6.0	0.2	1.3	0.8	0.0	Γ
count	0.3	9.7	3.4	80.6	79.5	0.4	0.9	0.6	0.0	Γ
bglod	0.5	13.6	6.0	79.5	95.6	0.3	0.7	0.4	0.0	Γ
vaf_too_low_s	0.0	0.0	0.2	0.4	0.3	0.8	0.8	0.6	0.0	Γ
vaf_too_low_m2	0.0	0.0	1.3	0.9	0.7	0.8	3.2	1.9	0.0	Γ
vaf_zg_too_noisy	0.0	0.0	0.8	0.6	0.4	0.6	1.9	2.0	0.0	Γ
manual_exclude	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	Ī



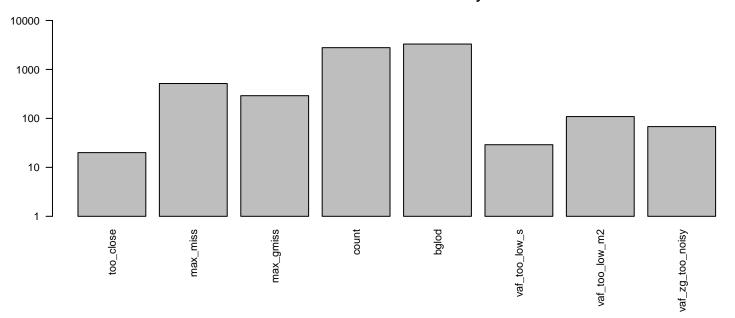
PD6634: INDEL: VAF Distribution at Somatic (pass all filters) sites called in Pindel



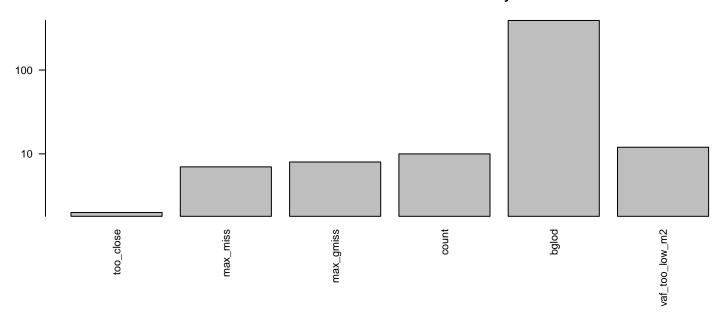
PD6634: INDEL: VAF Distribution at Germline [Based on the Matched Normal] sites called in Pindel



PD6634: INDEL: No. Sites removed by each filter



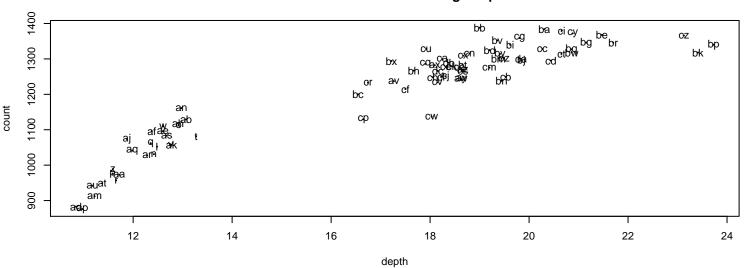
PD6634: INDEL: No. Sites UNIQUELY removed by each filter



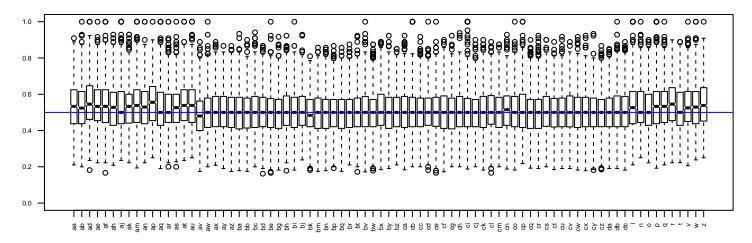
PD9478 : SNVs

SNV:Pairwise Filter Overlap (% Filtered Variants):Total Fail=36942/Pass=33705

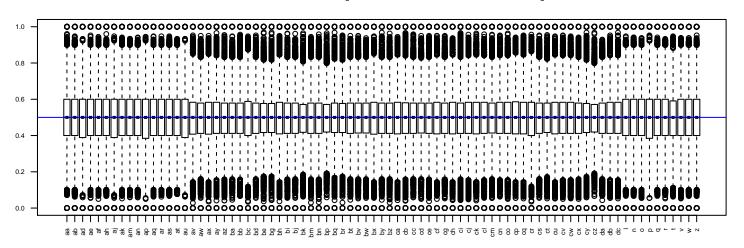
											L
	near_indel	too_close	max_miss	max_gmiss	count	bglod	vaf_too_low_s	raf_too_low_m/	af_zg_too_nois	yanual_exclude	₽
near_indel	0.1	0.0	0.0	0.1	0.0	0.0	0.0	0.1	0.0	0.0	
too_close	0.0	1.5	0.0	0.0	0.9	1.0	0.0	0.0	0.0	0.0	
max_miss	0.0	0.0	0.6	0.2	0.3	0.4	0.0	0.0	0.0	0.0	Г
max_gmiss	0.1	0.0	0.2	0.7	0.2	0.3	0.4	0.5	0.4	0.0	Г
count	0.0	0.9	0.3	0.2	92.8	91.6	0.6	0.7	0.6	0.0	Γ
bglod	0.0	1.0	0.4	0.3	91.6	97.6	0.2	0.3	0.2	0.0	Г
vaf_too_low_s	0.0	0.0	0.0	0.4	0.6	0.2	1.0	1.0	0.9	0.0	Г
vaf_too_low_m2	2 0.1	0.0	0.0	0.5	0.7	0.3	1.0	1.5	1.2	0.0	
vaf_zg_too_nois	у 0.0	0.0	0.0	0.4	0.6	0.2	0.9	1.2	1.2	0.0	Γ
manual_exclude	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	Γ
		l	l			l	1	l	l		



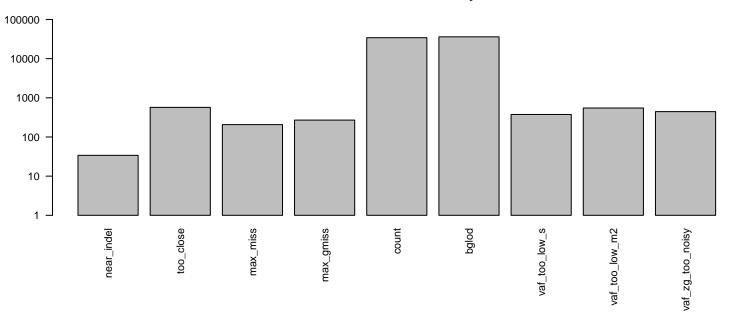
PD9478: SNV: VAF Distribution at Somatic (pass all filters) sites called in Caveman



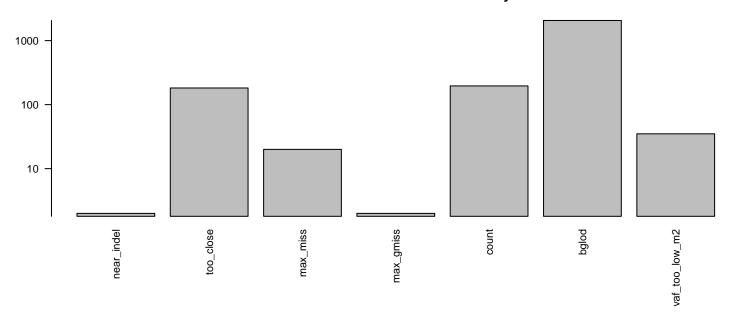
PD9478: SNV: VAF Distribution at Germline [Based on the Matched Normal] sites called in Caveman



PD9478: SNV: No. Sites removed by each filter



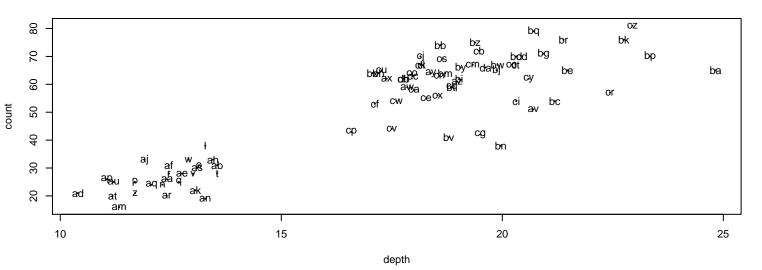
PD9478: SNV: No. Sites UNIQUELY removed by each filter



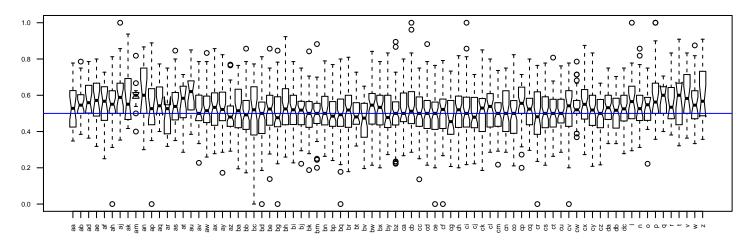
PD9478 : Indels

Indels:Pairwise Filter Overlap (% Filtered Variants):Total Fail=5885/Pass=1299

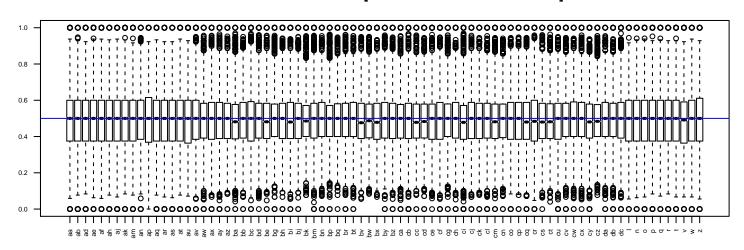
					<u> </u>				ļ	Ш
	too_close	max_miss	max_gmiss	count	bglod	vaf_too_low_s	vaf_too_low_m2	af_zg_too_nois	manual_exclude	2
too_close	3.1	2.4	1.3	1.8	2.0	0.0	0.2	0.1	0.0	
max_miss	2.4	28.5	12.6	17.6	20.5	0.1	0.2	0.1	0.0	
max_gmiss	1.3	12.6	17.8	4.7	7.7	1.5	4.2	3.2	0.0	
count	1.8	17.6	4.7	68.9	63.2	0.5	2.9	1.6	0.0	Г
bglod	2.0	20.5	7.7	63.2	77.1	0.7	1.7	1.2	0.0	Г
vaf_too_low_s	0.0	0.1	1.5	0.5	0.7	2.5	2.5	2.4	0.0	
vaf_too_low_m2	0.2	0.2	4.2	2.9	1.7	2.5	15.4	9.8	0.0	
vaf_zg_too_noisy	0.1	0.1	3.2	1.6	1.2	2.4	9.8	10.0	0.0	Г
manual_exclude	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	



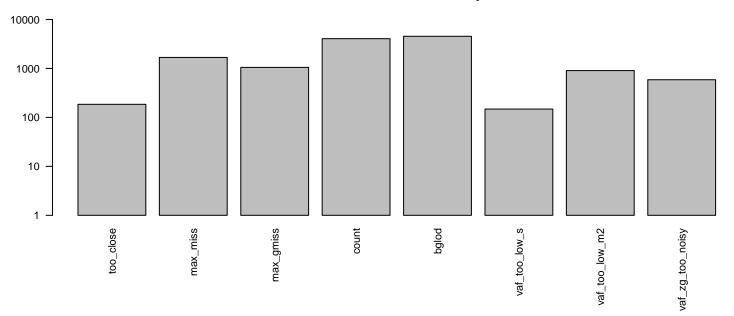
PD9478: INDEL: VAF Distribution at Somatic (pass all filters) sites called in Pindel



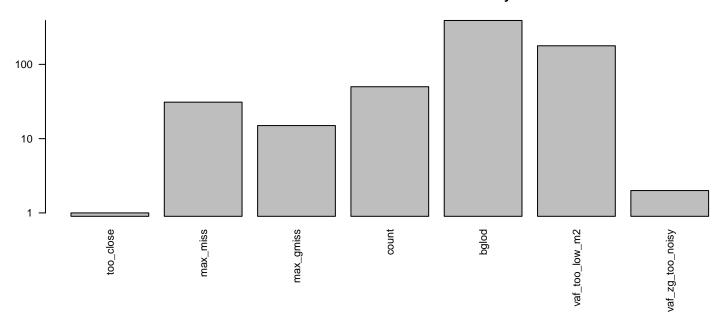
PD9478: INDEL: VAF Distribution at Germline [Based on the Matched Normal] sites called in Pindel



PD9478: INDEL: No. Sites removed by each filter



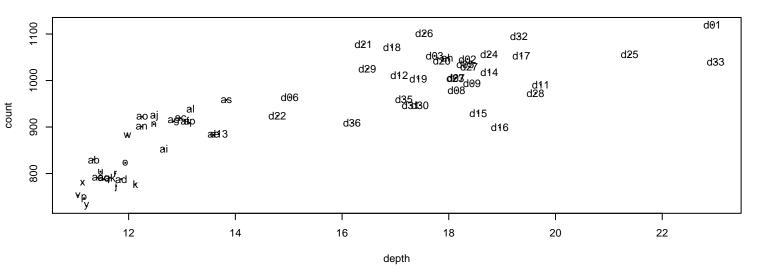
PD9478: INDEL: No. Sites UNIQUELY removed by each filter



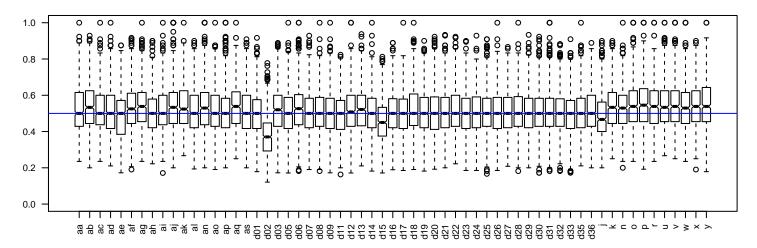
PD6629 : SNVs

SNV:Pairwise Filter Overlap (% Filtered Variants):Total Fail=34532/Pass=31547

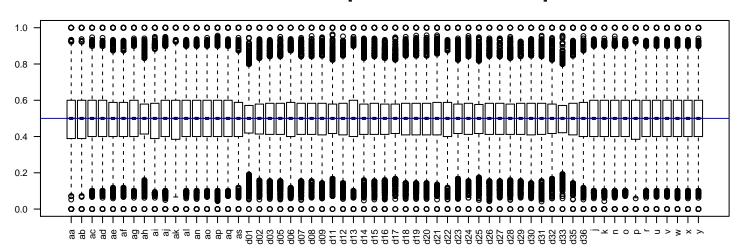
		.				L				 	+
	near_indel	too_close	max_miss	max_gmiss	count	bglod	vaf_too_low_s	raf_too_low_m	at_zg_too_nois	granual_exclud	<u></u>
near_indel	0.1	0.0	0.0	0.1	0.0	0.0	0.0	0.1	0.1	0.0	
too_close	0.0	1.5	0.0	0.0	0.9	1.0	0.0	0.0	0.0	0.0	
max_miss	0.0	0.0	1.1	0.3	0.7	0.8	0.0	0.0	0.0	0.0	
max_gmiss	0.1	0.0	0.3	0.8	0.2	0.3	0.3	0.4	0.4	0.0	
count	0.0	0.9	0.7	0.2	92.7	91.2	0.6	0.8	0.6	0.0	
bglod	0.0	1.0	0.8	0.3	91.2	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	1.0	1.0	0.9	0.0	
vaf_too_low_m2	2 0.1	0.0	0.0	0.4	0.8	0.2	1.0	1.4	1.0	0.0	Г
vaf_zg_too_nois	y 0.1	0.0	0.0	0.4	0.6	0.1	0.9	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	



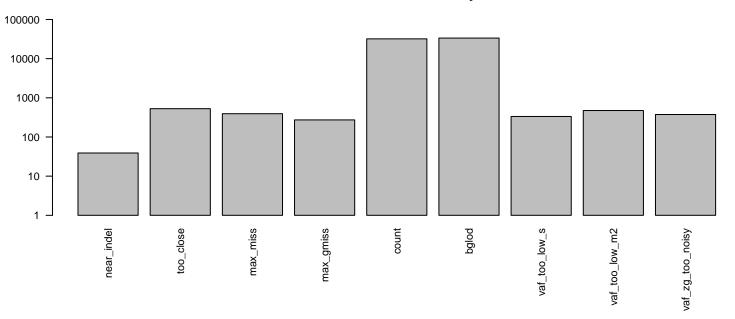
PD6629: SNV: VAF Distribution at Somatic (pass all filters) sites called in Caveman



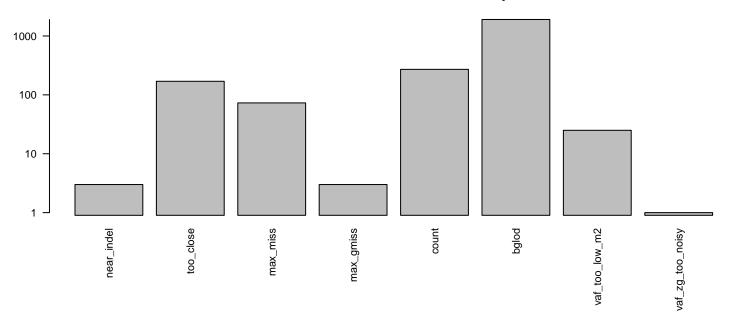
PD6629: SNV: VAF Distribution at Germline [Based on the Matched Normal] sites called in Caveman



PD6629: SNV: No. Sites removed by each filter



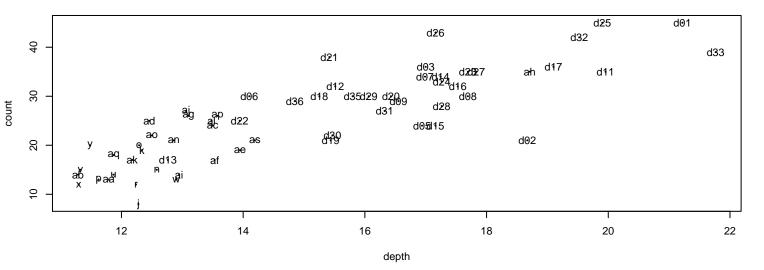
PD6629: SNV: No. Sites UNIQUELY removed by each filter



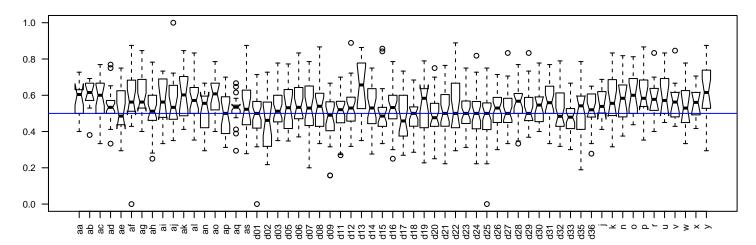
PD6629 : Indels

Indels:Pairwise Filter Overlap (% Filtered Variants):Total Fail=3924/Pass=928

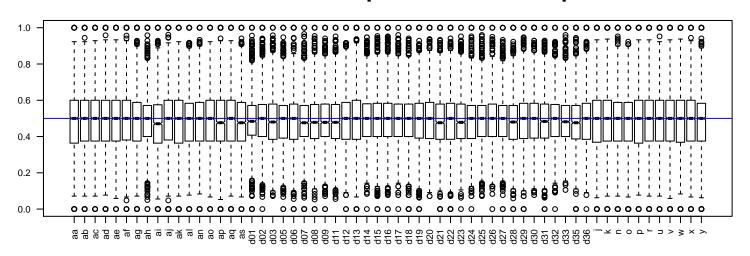
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	too_close	max_miss	max_gmiss	count	bglod	vaf_too_low_s	vaf_too_low_m2	raf_zg_too_nois	manual_exclude	_
too_close	1.4	1.1	0.6	0.9	1.0	0.0	0.0	0.0	0.0	
max_miss	1.1	24.5	10.6	16.3	22.1	0.0	0.1	0.2	0.0	
max_gmiss	0.6	10.6	12.9	4.8	9.5	0.5	1.6	1.4	0.0	Г
count	0.9	16.3	4.8	80.5	78.5	0.3	1.1	1.0	0.0	Г
bglod	1.0	22.1	9.5	78.5	93.3	0.3	0.8	0.7	0.0	Г
vaf_too_low_s	0.0	0.0	0.5	0.3	0.3	1.0	1.0	0.9	0.0	Г
vaf_too_low_m2	0.0	0.1	1.6	1.1	0.8	1.0	4.4	2.7	0.0	Г
vaf_zg_too_noisy	0.0	0.2	1.4	1.0	0.7	0.9	2.7	3.0	0.0	
manual_exclude	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	



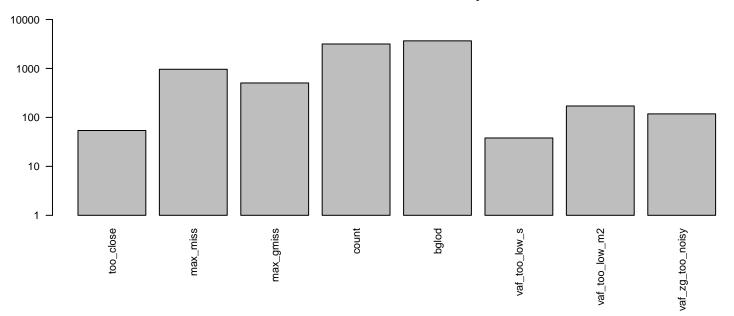
PD6629: INDEL: VAF Distribution at Somatic (pass all filters) sites called in Pindel



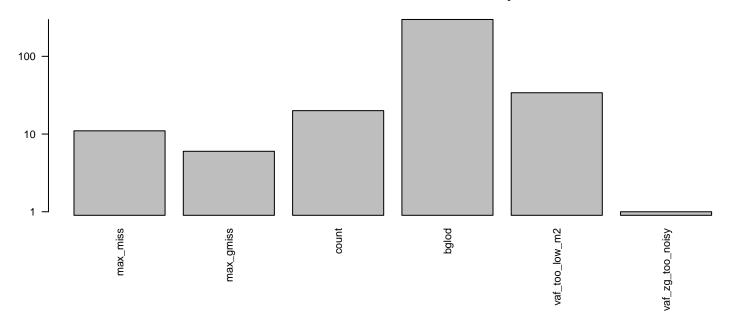
PD6629: INDEL: VAF Distribution at Germline [Based on the Matched Normal] sites called in Pindel



PD6629: INDEL: No. Sites removed by each filter



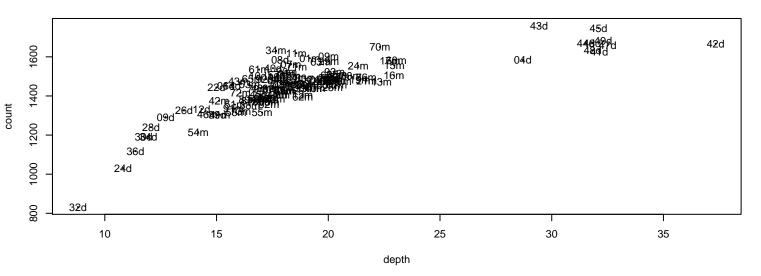
PD6629: INDEL: No. Sites UNIQUELY removed by each filter



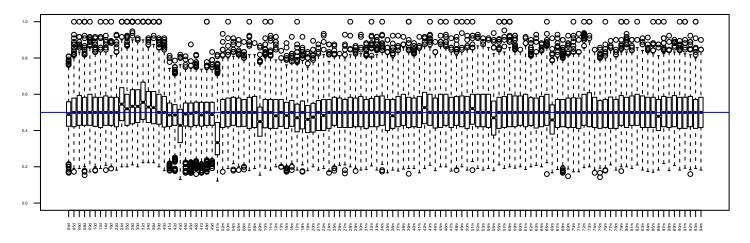
PD6646 : SNVs

SNV:Pairwise Filter Overlap (% Filtered Variants):Total Fail=36766/Pass=58247

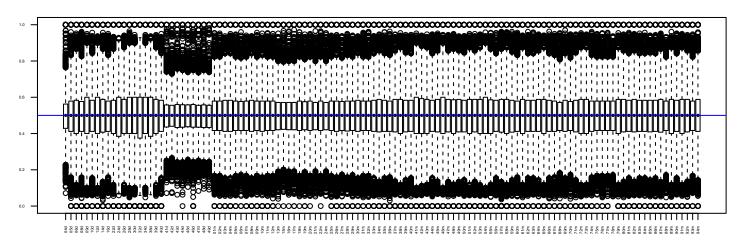
										l	丄
	near_indel	too_close	max_miss	max_gmiss	count	bglod	vaf_too_low_s	af_too_low_m	af_zg_too_nois	yanual_exclud	e
near_indel	0.1	0.0	0.0	0.1	0.0	0.1	0.1	0.1	0.1	0.0	
too_close	0.0	2.0	0.0	0.0	1.0	1.0	0.0	0.1	0.1	0.0	
max_miss	0.0	0.0	0.2	0.1	0.1	0.1	0.0	0.0	0.0	0.0	
max_gmiss	0.1	0.0	0.1	0.7	0.1	0.2	0.4	0.6	0.5	0.0	
count	0.0	1.0	0.1	0.1	91.6	89.8	0.7	1.1	0.8	0.0	Π
bglod	0.1	1.0	0.1	0.2	89.8	95.6	0.3	0.4	0.4	0.0	
vaf_too_low_s	0.1	0.0	0.0	0.4	0.7	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	Π
vaf_zg_too_nois	у 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	



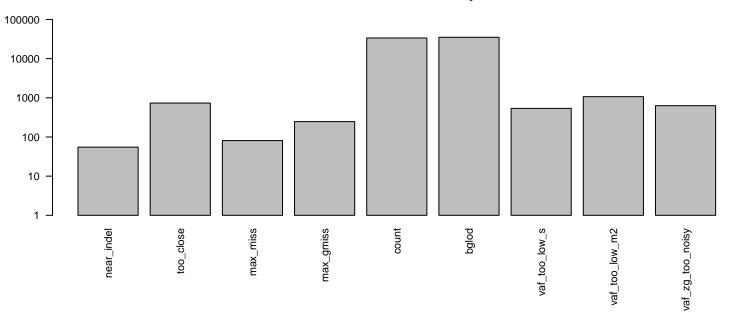
PD6646: SNV: VAF Distribution at Somatic (pass all filters) sites called in Caveman



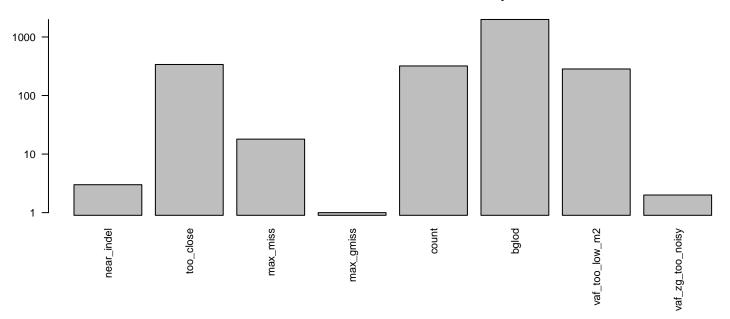
PD6646: SNV: VAF Distribution at Germline [Based on the Matched Normal] sites called in Caveman



PD6646: SNV: No. Sites removed by each filter

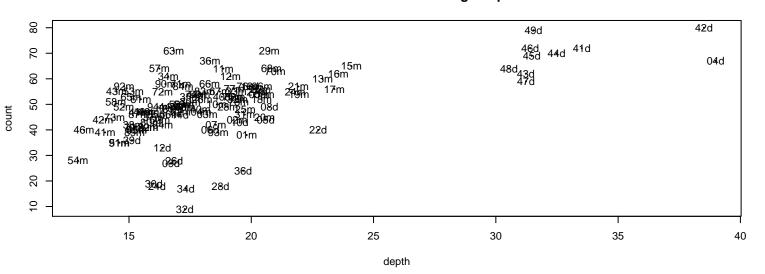


PD6646: SNV: No. Sites UNIQUELY removed by each filter

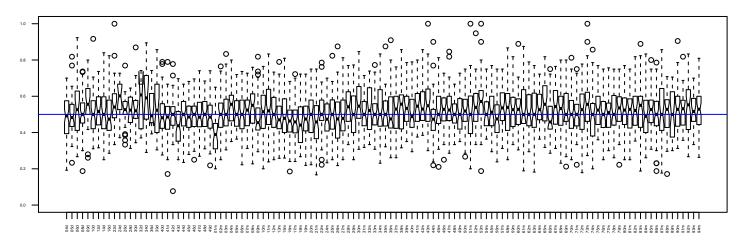


PD6646 : Indels
Indels:Pairwise Filter Overlap (% Filtered Variants):Total Fail=7337/Pass=1917

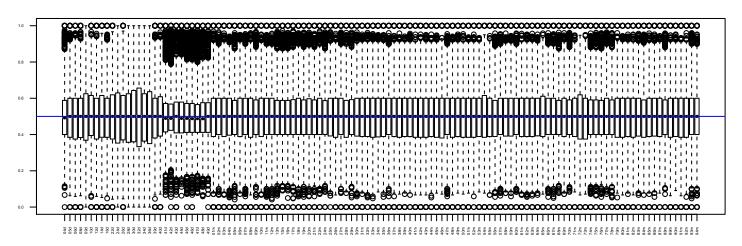
I		I				I	l	I		1
	too_close	max_miss	max_gmiss	count	bglod	vaf_too_low_s	vaf_too_low_m2	af_zg_too_nois	manual_exclude	
too_close	4.9	3.6	1.8	2.6	4.0	0.0	0.3	0.2	0.0	
max_miss	3.6	28.1	11.6	15.5	23.2	0.0	0.2	0.0	0.0	
max_gmiss	1.8	11.6	17.2	2.8	9.6	2.7	4.7	3.8	0.0	
count	2.6	15.5	2.8	59.6	55.2	0.6	2.8	1.7	0.0	
bglod	4.0	23.2	9.6	55.2	76.8	1.5	2.6	2.4	0.0	
vaf_too_low_s	0.0	0.0	2.7	0.6	1.5	4.4	4.4	4.2	0.0	
vaf_too_low_m2	0.3	0.2	4.7	2.8	2.6	4.4	20.1	14.3	0.0	
vaf_zg_too_noisy	0.2	0.0	3.8	1.7	2.4	4.2	14.3	14.9	0.0	
manual_exclude	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	
		I	ı	ı	ı	I	I	I	I	i



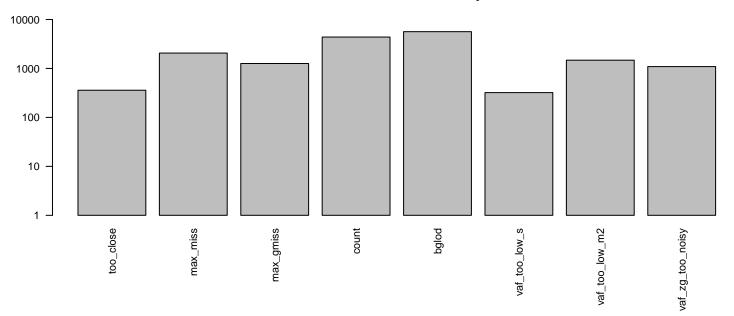
PD6646: INDEL: VAF Distribution at Somatic (pass all filters) sites called in Pindel



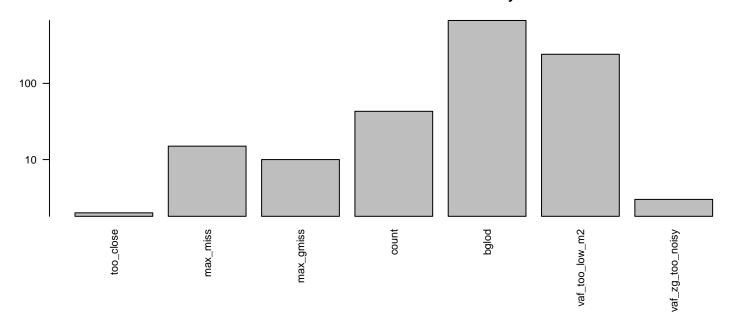
PD6646: INDEL: VAF Distribution at Germline [Based on the Matched Normal] sites called in Pindel



PD6646: INDEL: No. Sites removed by each filter



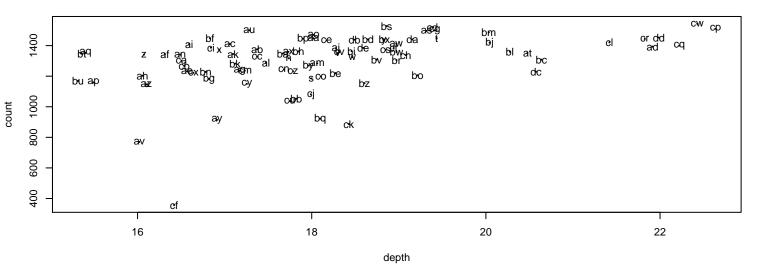
PD6646: INDEL: No. Sites UNIQUELY removed by each filter



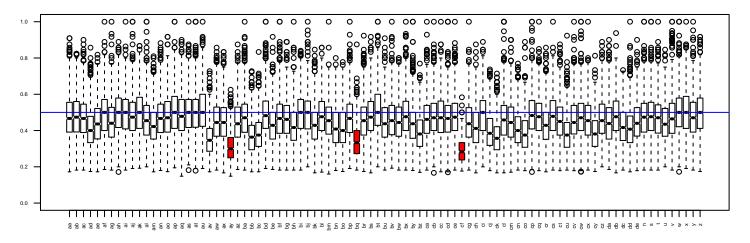
PD5117 : SNVs

SNV:Pairwise Filter Overlap (% Filtered Variants):Total Fail=38760/Pass=93884

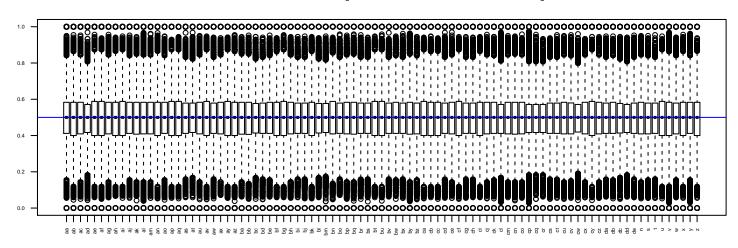
		<u> </u>				 				 	\vdash
	near_indel	too_close	max_miss	max_gmiss	count	bglod	vaf_too_low_s	raf_too_low_m	at_zg_too_nois	granual_exclud	<u>e</u>
near_indel	0.1	0.0	0.0	0.1	0.0	0.1	0.0	0.1	0.0	0.0	
too_close	0.0	2.5	0.0	0.0	1.1	1.2	0.1	0.1	0.1	0.0	
max_miss	0.0	0.0	0.2	0.1	0.1	0.1	0.0	0.0	0.0	0.0	
max_gmiss	0.1	0.0	0.1	0.5	0.1	0.2	0.3	0.4	0.3	0.0	
count	0.0	1.1	0.1	0.1	94.2	92.8	0.7	1.0	0.8	0.0	
bglod	0.1	1.2	0.1	0.2	92.8	96.6	0.3	0.5	0.4	0.0	
vaf_too_low_s	0.0	0.1	0.0	0.3	0.7	0.3	1.1	1.1	1.0	0.0	
vaf_too_low_m2	2 0.1	0.1	0.0	0.4	1.0	0.5	1.1	1.8	1.2	0.0	
vaf_zg_too_nois	y 0.0	0.1	0.0	0.3	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	



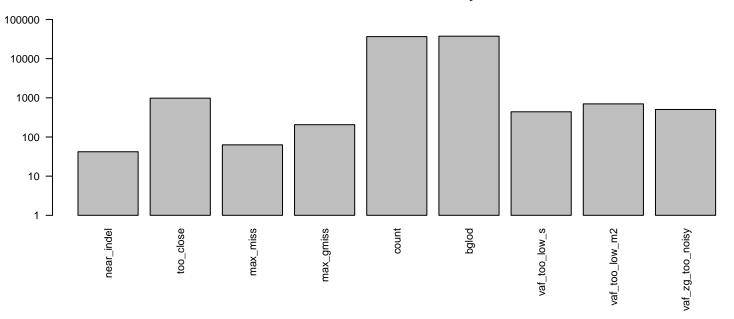
PD5117: SNV: VAF Distribution at Somatic (pass all filters) sites called in Caveman



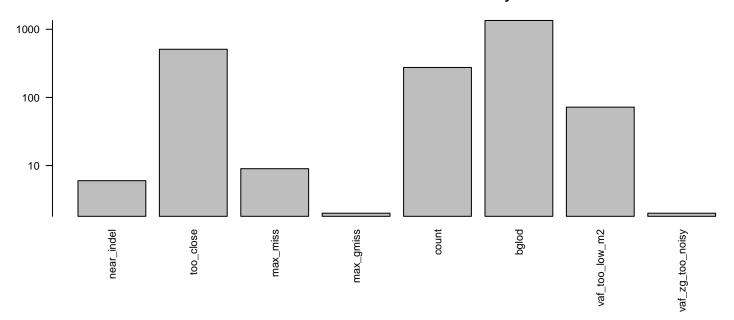
PD5117: SNV: VAF Distribution at Germline [Based on the Matched Normal] sites called in Caveman



PD5117: SNV: No. Sites removed by each filter

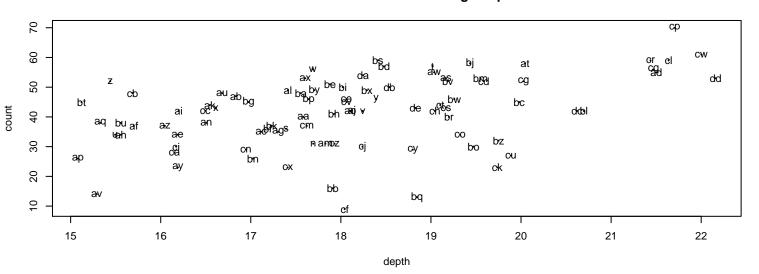


PD5117: SNV: No. Sites UNIQUELY removed by each filter

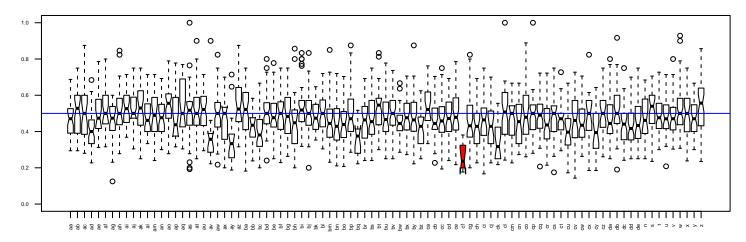


PD5117 : Indels
Indels:Pairwise Filter Overlap (% Filtered Variants):Total Fail=6643/Pass=2721

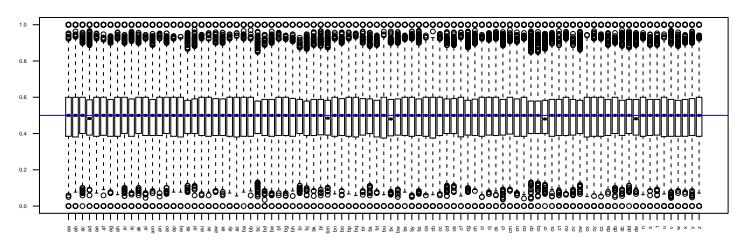
ı		I	I	I	I	I	I	I	I
	too_close	max_miss	max_gmiss	count	bglod	vaf_too_low_s	vaf_too_low_m2	af_zg_too_nois	manual_exclude
too_close	3.9	2.7	1.4	2.3	3.0	0.0	0.2	0.1	0.0
max_miss	2.7	24.3	8.6	15.2	21.6	0.0	0.0	0.0	0.0
max_gmiss	1.4	8.6	14.0	2.6	8.6	1.8	4.1	3.3	0.0
count	2.3	15.2	2.6	68.8	65.0	0.5	2.8	1.5	0.0
bglod	3.0	21.6	8.6	65.0	81.3	0.9	1.9	1.5	0.0
vaf_too_low_s	0.0	0.0	1.8	0.5	0.9	2.9	2.9	2.8	0.0
vaf_too_low_m2	0.2	0.0	4.1	2.8	1.9	2.9	16.7	11.6	0.0
vaf_zg_too_noisy	0.1	0.0	3.3	1.5	1.5	2.8	11.6	11.9	0.0
manual_exclude	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0
		1	1	1	1	1		l	



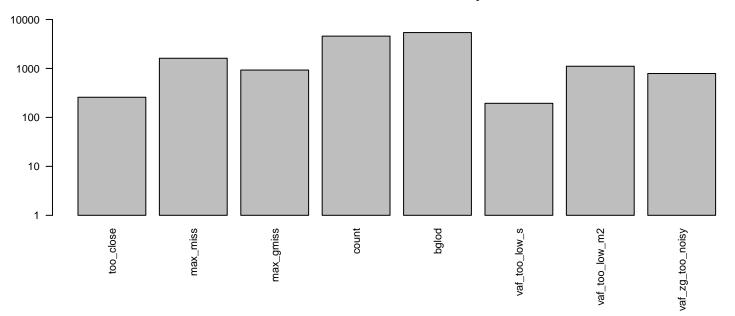
PD5117: INDEL: VAF Distribution at Somatic (pass all filters) sites called in Pindel



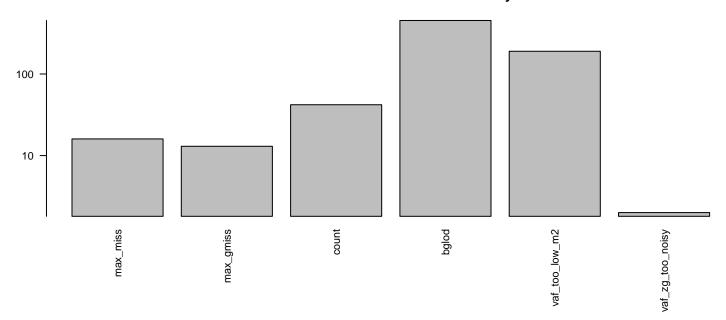
PD5117: INDEL: VAF Distribution at Germline [Based on the Matched Normal] sites called in Pindel



PD5117: INDEL: No. Sites removed by each filter



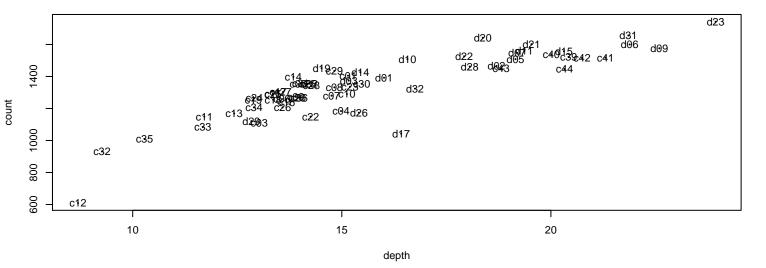
PD5117: INDEL: No. Sites UNIQUELY removed by each filter



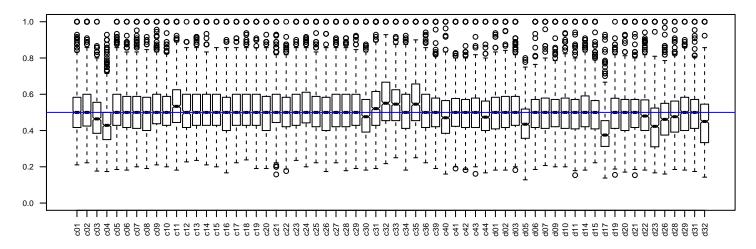
SNV:Pairwise Filter Overlap (% Filtered Variants):Total Fail=35310/Pass=24729

PD4781: SNVs

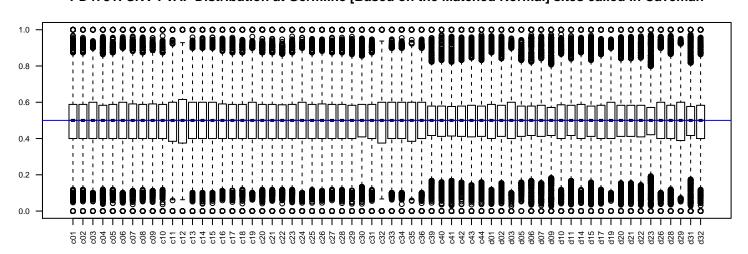
											\perp
	near_indel	too_close	max_miss	max_gmiss	count	bglod	vaf_too_low_s	raf_too_low_m/	af_zg_too_nois	yanual_exclud	e
near_indel	0.1	0.0	0.0	0.1	0.0	0.0	0.0	0.1	0.1	0.0	
too_close	0.0	1.4	0.0	0.0	0.9	1.0	0.0	0.0	0.0	0.0	Ī
max_miss	0.0	0.0	2.9	0.9	1.1	2.1	0.0	0.0	0.0	0.0	Γ
max_gmiss	0.1	0.0	0.9	1.6	0.3	1.0	0.4	0.5	0.5	0.0	Γ
count	0.0	0.9	1.1	0.3	89.5	88.6	0.6	0.7	0.6	0.0	Γ
bglod	0.0	1.0	2.1	1.0	88.6	97.3	0.2	0.3	0.2	0.0	Ī
vaf_too_low_s	0.0	0.0	0.0	0.4	0.6	0.2	1.0	1.0	0.9	0.0	Γ
vaf_too_low_m2	0.1	0.0	0.0	0.5	0.7	0.3	1.0	1.3	1.0	0.0	Γ
vaf_zg_too_nois	0.1	0.0	0.0	0.5	0.6	0.2	0.9	1.0	1.1	0.0	Γ
manual_exclude	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	Ī



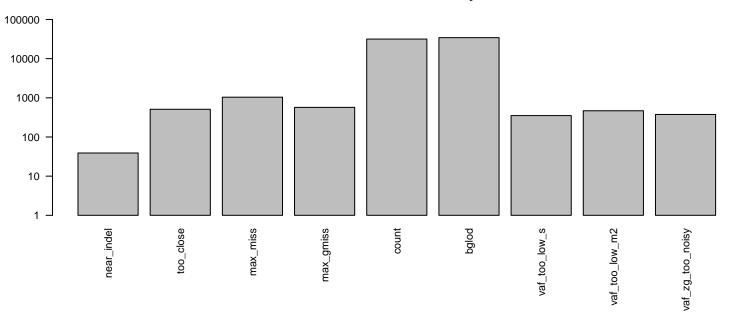
PD4781: SNV: VAF Distribution at Somatic (pass all filters) sites called in Caveman



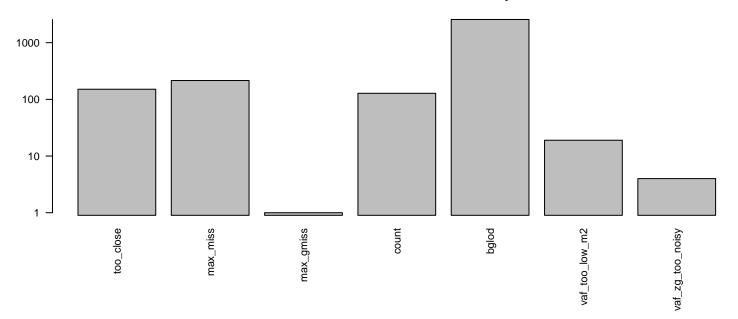
PD4781: SNV: VAF Distribution at Germline [Based on the Matched Normal] sites called in Caveman



PD4781: SNV: No. Sites removed by each filter



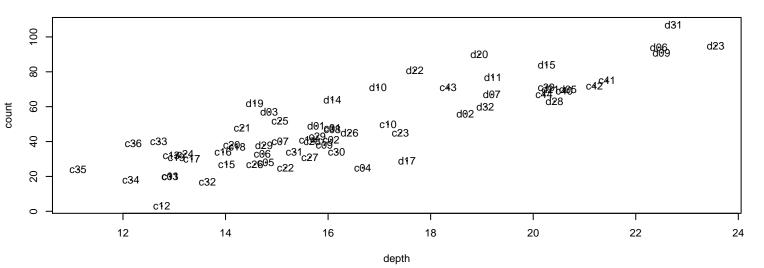
PD4781: SNV: No. Sites UNIQUELY removed by each filter



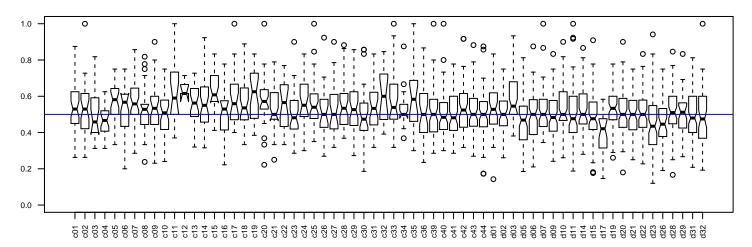
Indels:Pairwise Filter Overlap (% Filtered Variants):Total Fail=4739/Pass=899

PD4781 : Indels

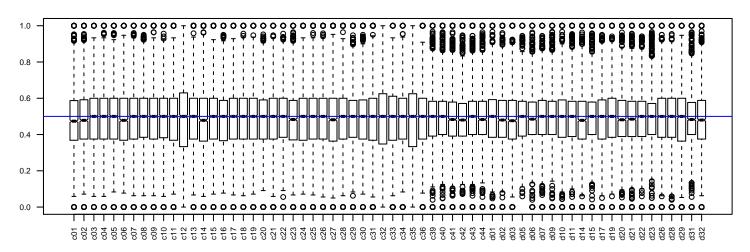
		<u> </u>					<u> </u>	ļ		Ш
	too_close	max_miss	max_gmiss	count	bglod	vaf_too_low_s	vaf_too_low_m2	af_zg_too_nois	manual_exclude	
too_close	2.0	1.6	1.0	1.1	1.6	0.0	0.1	0.1	0.0	
max_miss	1.6	30.6	15.3	19.7	25.9	0.0	0.1	0.0	0.0	
max_gmiss	1.0	15.3	19.9	7.0	12.5	0.8	3.8	2.7	0.0	
count	1.1	19.7	7.0	71.0	67.6	0.5	1.7	1.1	0.0	
bglod	1.6	25.9	12.5	67.6	86.5	0.5	1.2	1.0	0.0	
vaf_too_low_s	0.0	0.0	0.8	0.5	0.5	1.6	1.6	1.5	0.0	
vaf_too_low_m2	0.1	0.1	3.8	1.7	1.2	1.6	9.1	5.7	0.0	
vaf_zg_too_noisy	0.1	0.0	2.7	1.1	1.0	1.5	5.7	5.9	0.0	
manual_exclude	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	



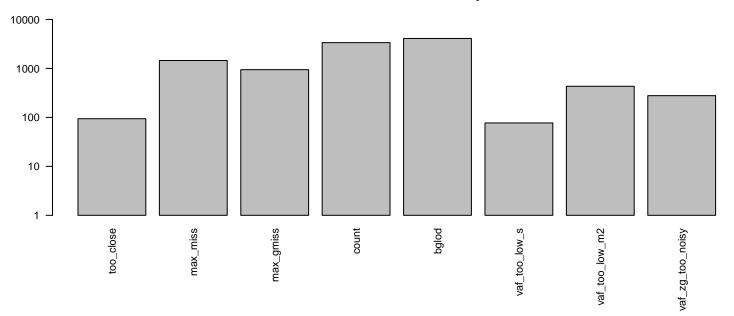
PD4781: INDEL: VAF Distribution at Somatic (pass all filters) sites called in Pindel



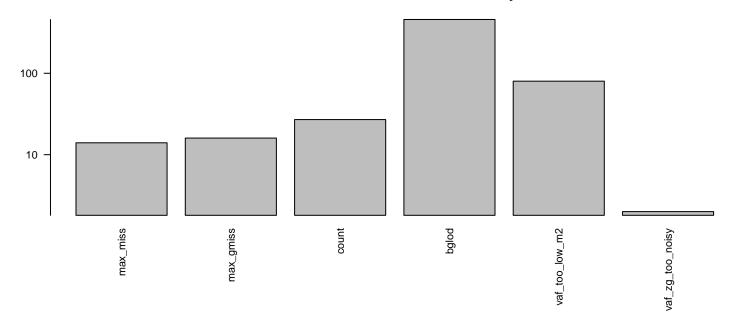
PD4781: INDEL: VAF Distribution at Germline [Based on the Matched Normal] sites called in Pindel



PD4781: INDEL: No. Sites removed by each filter



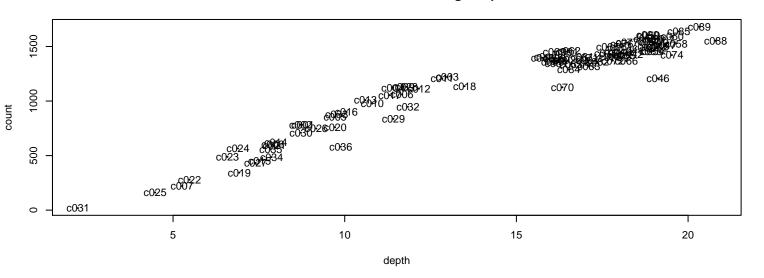
PD4781: INDEL: No. Sites UNIQUELY removed by each filter



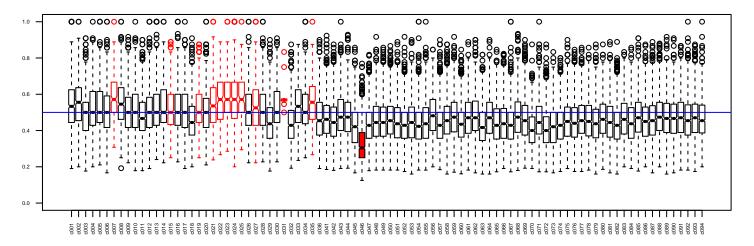
SNV:Pairwise Filter Overlap (% Filtered Variants):Total Fail=43193/Pass=57338

PD5147: SNVs

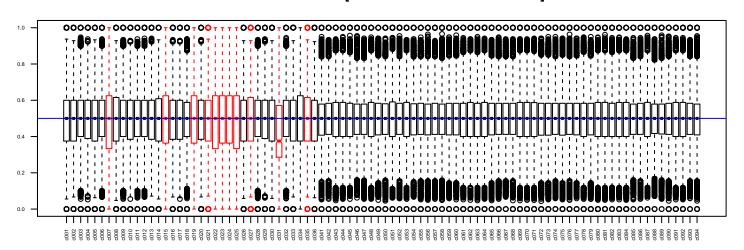
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	near_indel	too_close	max_miss	max_gmiss	count	bglod	vaf_too_low_s	raf_too_low_mv	af_zg_too_nois	ganual_exclude	ŧ
near_indel	0.1	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	
too_close	0.0	1.6	0.0	0.0	0.7	0.8	0.1	0.1	0.1	0.0	
max_miss	0.0	0.0	8.8	1.1	2.9	3.4	0.0	0.0	0.0	0.0	
max_gmiss	0.0	0.0	1.1	2.5	0.5	0.4	1.2	1.4	1.3	0.0	
count	0.0	0.7	2.9	0.5	79.4	70.9	2.2	3.7	2.3	0.0	
bglod	0.0	0.8	3.4	0.4	70.9	81.8	0.1	0.3	0.2	0.0	
vaf_too_low_s	0.0	0.1	0.0	1.2	2.2	0.1	5.3	5.3	5.3	0.0	
vaf_too_low_m2	0.0	0.1	0.0	1.4	3.7	0.3	5.3	7.6	5.5	0.0	
vaf_zg_too_nois	у 0.0	0.1	0.0	1.3	2.3	0.2	5.3	5.5	5.6	0.0	
manual_exclude	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	
		l	1	I		l		l	l		ı



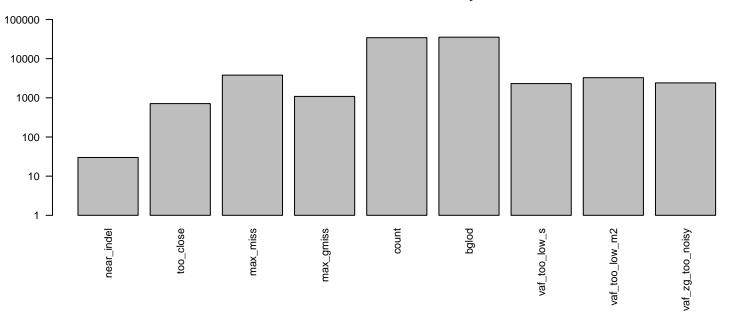
PD5147: SNV: VAF Distribution at Somatic (pass all filters) sites called in Caveman



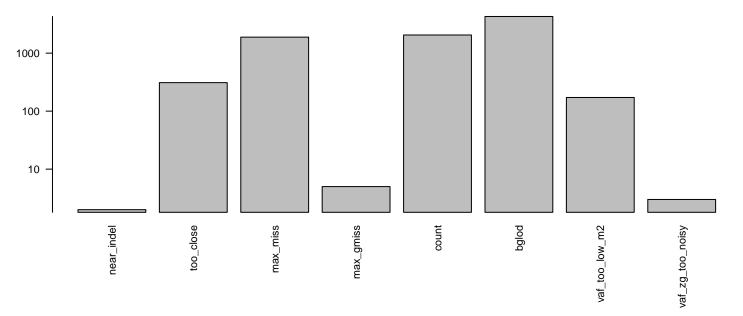
PD5147: SNV: VAF Distribution at Germline [Based on the Matched Normal] sites called in Caveman



PD5147: SNV: No. Sites removed by each filter



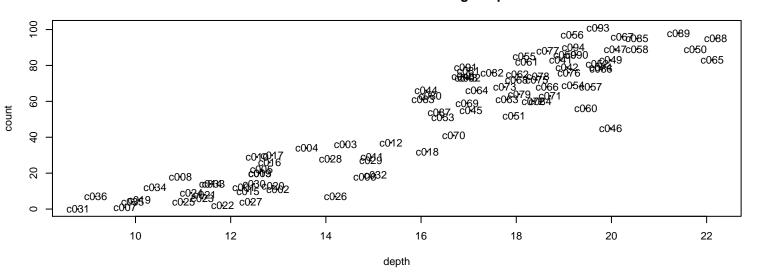
PD5147: SNV: No. Sites UNIQUELY removed by each filter



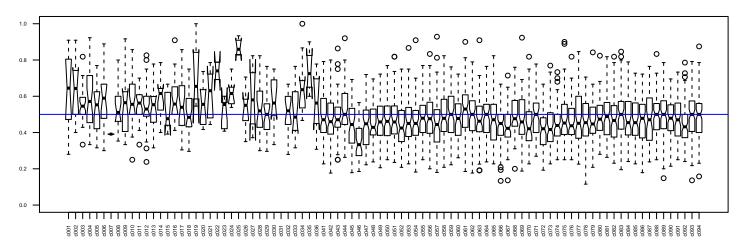
Indels:Pairwise Filter Overlap (% Filtered Variants):Total Fail=5997/Pass=2870

PD5147 : Indels

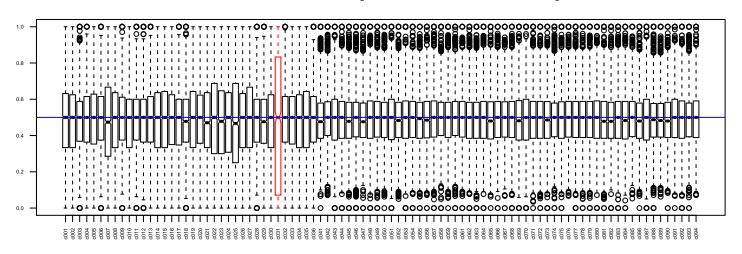
										上
	too_close	max_miss	max_gmiss	count	bglod	vaf_too_low_s	vaf_too_low_m2	af_zg_too_nois	manual_exclude	,
too_close	2.5	1.8	0.9	1.4	2.2	0.0	0.2	0.1	0.0	
max_miss	1.8	28.5	13.7	14.5	25.7	0.1	0.7	0.5	0.0	
max_gmiss	0.9	13.7	19.6	4.2	13.6	1.7	5.7	4.8	0.0	
count	1.4	14.5	4.2	46.2	41.5	0.6	3.4	2.1	0.0	
bglod	2.2	25.7	13.6	41.5	82.0	3.3	5.0	5.3	0.0	
vaf_too_low_s	0.0	0.1	1.7	0.6	3.3	5.0	5.0	4.8	0.0	
vaf_too_low_m2	0.2	0.7	5.7	3.4	5.0	5.0	18.8	13.2	0.0	
vaf_zg_too_noisy	0.1	0.5	4.8	2.1	5.3	4.8	13.2	13.8	0.0	Γ
manual_exclude	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	Γ
					l	1	l	l		



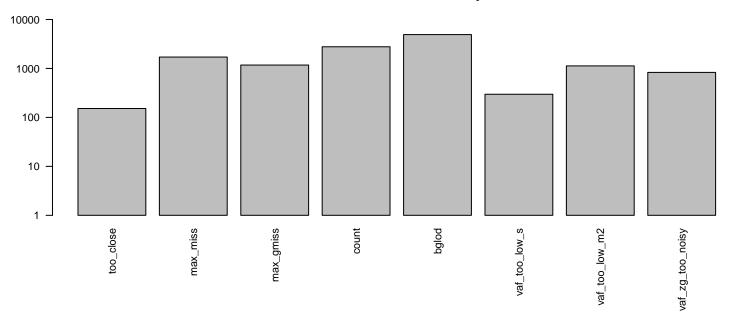
PD5147: INDEL: VAF Distribution at Somatic (pass all filters) sites called in Pindel



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

