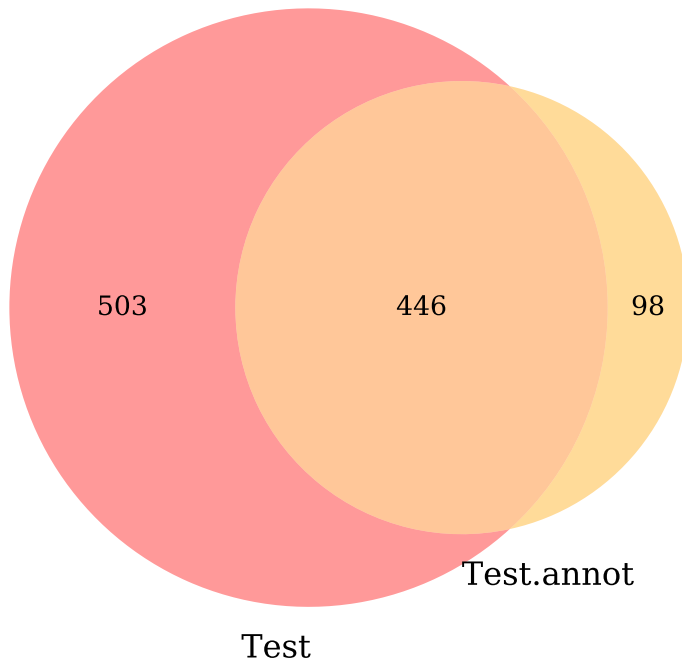


	Type	Positions	SNPs	INDELs
0	Test	949	426	522
1	Test.annot	544	104	439

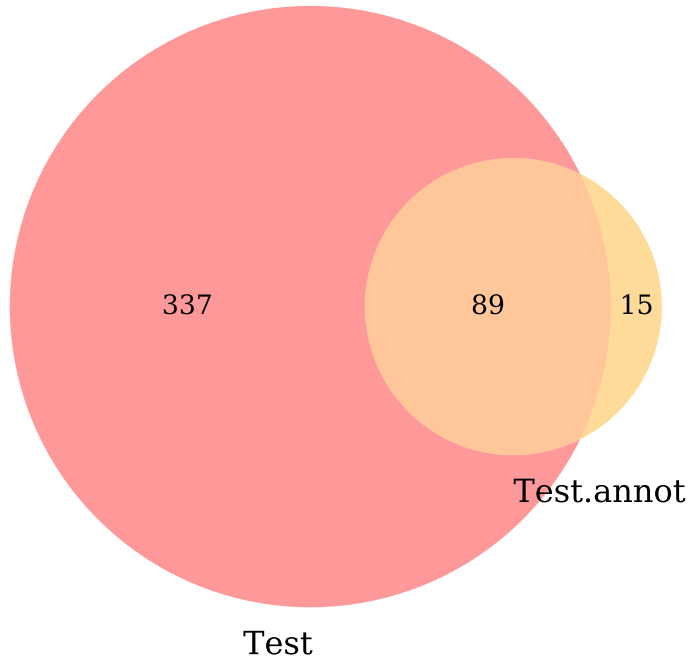
	Type	Positions
0	Test	949
1	Test.annot	544
2	Common_Positions	446

# Positions [SNPs + Indels]



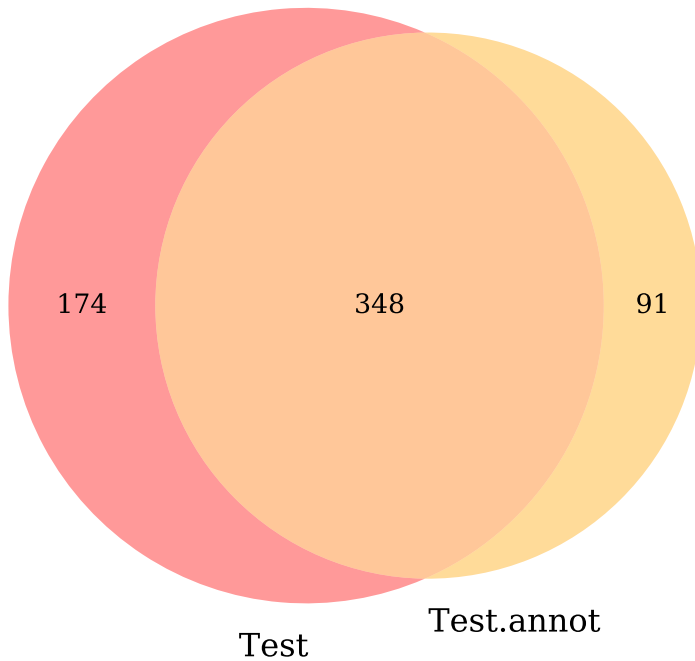
	Type	Positions
0	Test	426
1	Test.annot	104
2	Common_SNPs	89

SNPs



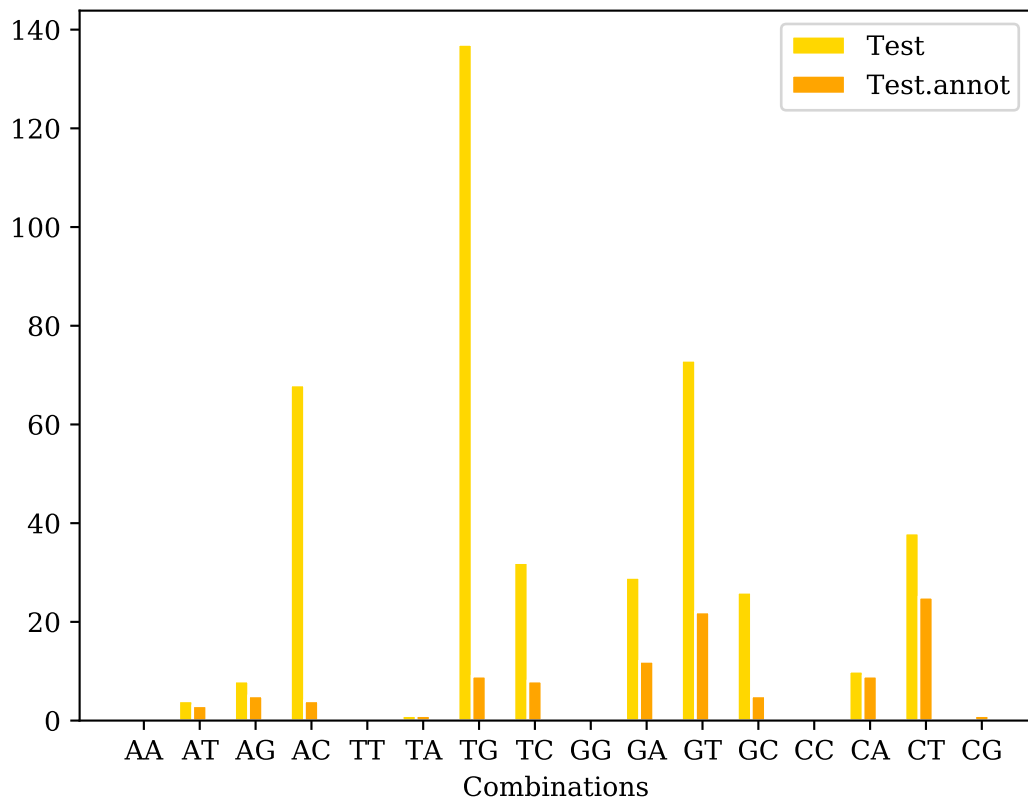
	Type	INDELs
0	Test	522
1	Test.annot	439
2	Common_SNPs	348

INDELs

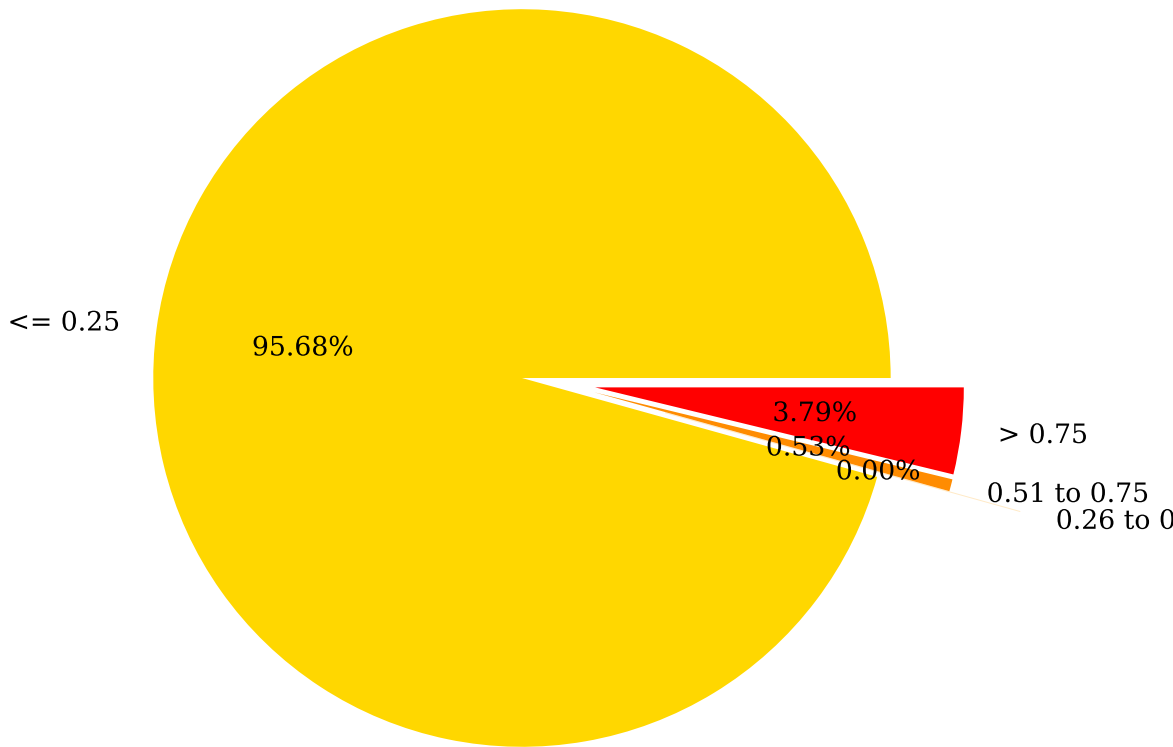


	REF	ALT	Test	Test.annot
0	A	A	0	0
1	A	T	4	3
2	A	G	8	5
3	A	C	68	4
4	T	T	0	0
5	T	A	1	1
6	T	G	137	9
7	T	C	32	8
8	G	G	0	0
9	G	A	29	12
10	G	T	73	22
11	G	C	26	5
12	C	C	0	0
13	C	A	10	9
14	C	T	38	25
15	C	G	0	1

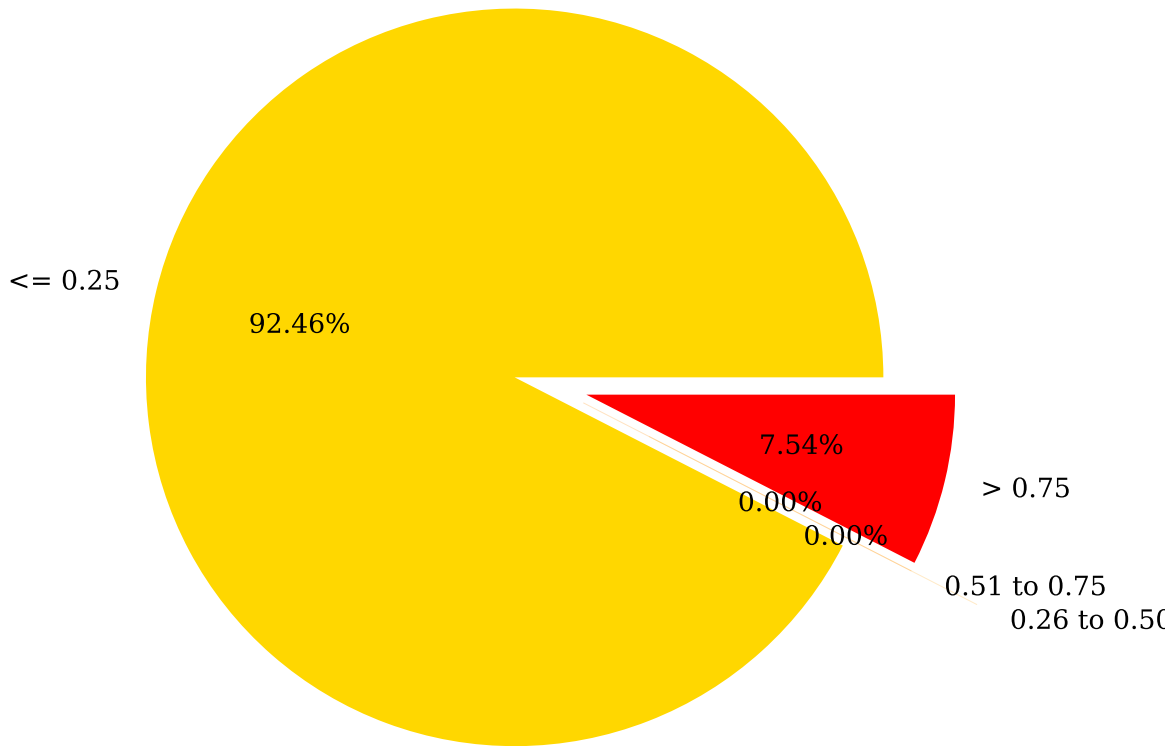




	Test_Allele_Frequency	Count
0	Less than 0.25	908
1	Between 0.25 to 0.50	0
2	Between 0.50 to 0.75	5
3	Above 0.75	36

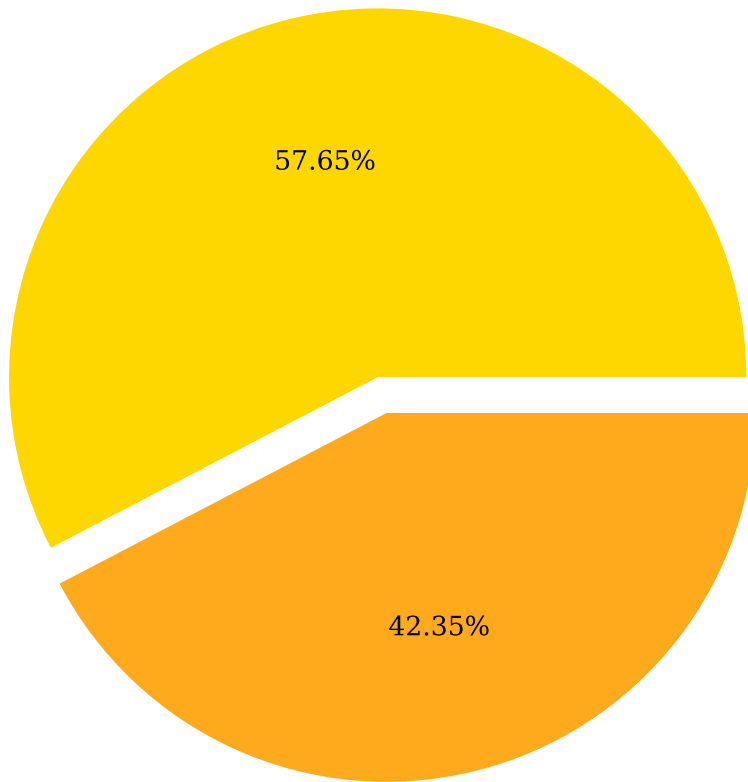


	Test.annot_Allele_Frequency	Count
0	Less than 0.25	503
1	Between 0.25 to 0.50	0
2	Between 0.50 to 0.75	0
3	Above 0.75	41



	Test_Read_Depth	Values
0	Minimum_Value	2292.000000
1	Maximum_Value	61546.000000
2	Mean_Value	17776.181243
3	Median_Value	15578.000000
4	SD_Value	8868.062457

Selected\_Count



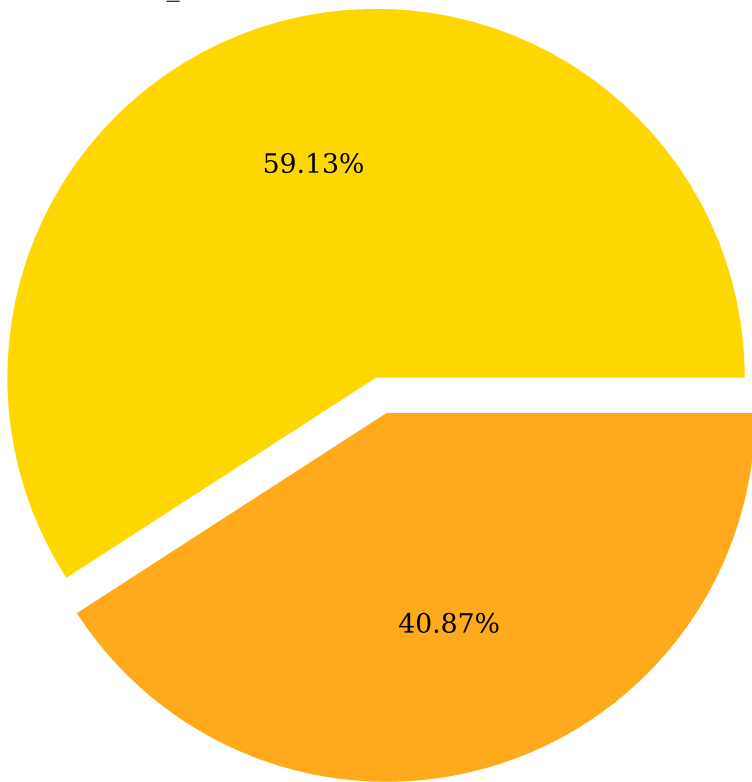
42.35%

Filtered\_Count

	Test.annot_Read_Depth	Values
0	Minimum_Value	876.000000
1	Maximum_Value	37351.000000
2	Mean_Value	13474.946691
3	Median_Value	11550.500000
4	SD_Value	7369.188181



Selected\_Count



Filtered\_Count

	Benchmarking	Count
0	Total	1068
1	True_Positive_ALTs	447
2	True_True_Positives_ALTs	436
3	True_False_Positives_ALTs	11
4	True_Negative_ALTs	0
5	False_Positives_ALTs	113
6	False_Negative_ALTs	508