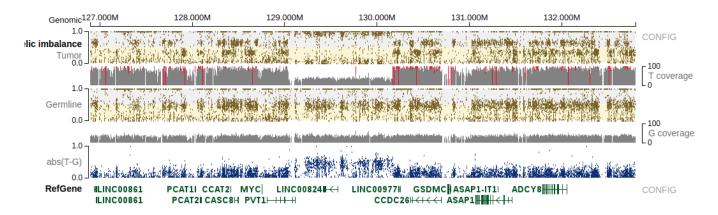
## Alcheck track format and usage

"aicheck" is a term coined by Xiaotu Ma, who also designed the visualization to show the allelic imbalance of the heterozygous SNP markers in a tumor genome as compared to this patient's germline genome, as a way of indicating loss-of-heterozygosity.



Live example: https://proteinpaint.stjude.org/?appcard=ai

The JSON definition for a aicheck track is:

```
"type": "aicheck",
    "file": "files/hg19/example/aicheck/SJBALL020340_D1_sorted.gz",
    "name": "SJBALL020340 tumor allelic imbalance"
}
```

Submit this JSON text to the custom track panel to make it work. See custom track guide for details.

Declare tracks as JSON text:



## Additional JSON parameters:

- coveragemax: Integer
  - Maximum Y-axis value for coverage tracks of both tumor and normal; default: 100.
- vafheight: Integer
  - Variant allele fraction track height for both tumor and normal; default: 50.
- coverageheight: Integer

- Coverage track height; default: 30.
- rowspace: Integer
  - Vertical spacing between rows; default: 5.

Following two optional parameters allow to filter markers.

- gtotalcutoff: Integer
  - Minimum total germline coverage. Markers with values below the cutoff will be excluded.
- gmafrestrict: float between 0 to 0.5
  - A limit on the germline B-allele fraction so as to only include markers with BAF close to 50%. E.g. by setting value 0.3 to this parameter, it will require 0.3 <= BAF <= 0.7. Markers with BAF outside this range will be excluded.

Aicheck track file has 6 columns, tab-separated. First line is a header, optional.

Chr	Pos	MinD	TinD	MinN	TinN
chr1	10003	3	38	0	23
chr1	10007	2	60	1	32
chr1	10009	3	58	1	32
chr1	10016	3	79	1	65
chr1	10019	1	94	2	76
chr1	10020	3	102	1	82
chr1	10025	2	127	1	91
chr1	10025	2	129	1	92

Each row is one germline heterozygous marker. All markers are from the same patient. Columns:

- 1. Chromosome name
- 2. Position of the SNP
- 3. Alternative allele read count in tumor DNA
- 4. Total read count of this SNP in tumor DNA
- 5. Alternative allele read count in germline DNA
- 6. Total read count of this SNP in germline DNA

After you assemble the marker data into a text file, do following to convert it to a track file:

```
$ sort -k1,1 -k2,2n input.file > input.sorted
$ bgzip input.sorted
$ tabix -c 'C' -s 1 -b 2 -e 2 input.sorted.gz
```

This generates two files "sorted.gz" and "sorted.gz.tbi". Put both of them in the same path.