

Welcome to FL Variant!

Thank you for using our service.

The following pages contain your filtered data report:

Page 1: Filtered Data Table

Page 2: Analysis of Data

Page 3: Dashboard Screenshot

filters:

- CHROM:
- TYPE:
- IMPACT: LOW,HIGH
- GENE:

CHROM	POS	REF	ALT	TYPE	IMPACT	GENE
2	47635523	CT	C	splice region variant & intron variant	LOW	MSH2
2	48032740	AT	A	splice region variant & intron variant	LOW	MSH6
5	112111309	TA	T	splice region variant & intron variant	LOW	APC
6	163899919	T	TA	frameshift variant & splice region variant	HIGH	QKI
7	6037057	GA	G	splice region variant & intron variant	LOW	PMS2
10	89623860	CT	C	splice acceptor variant & splice donor variant & intron variant	HIGH	PTEN

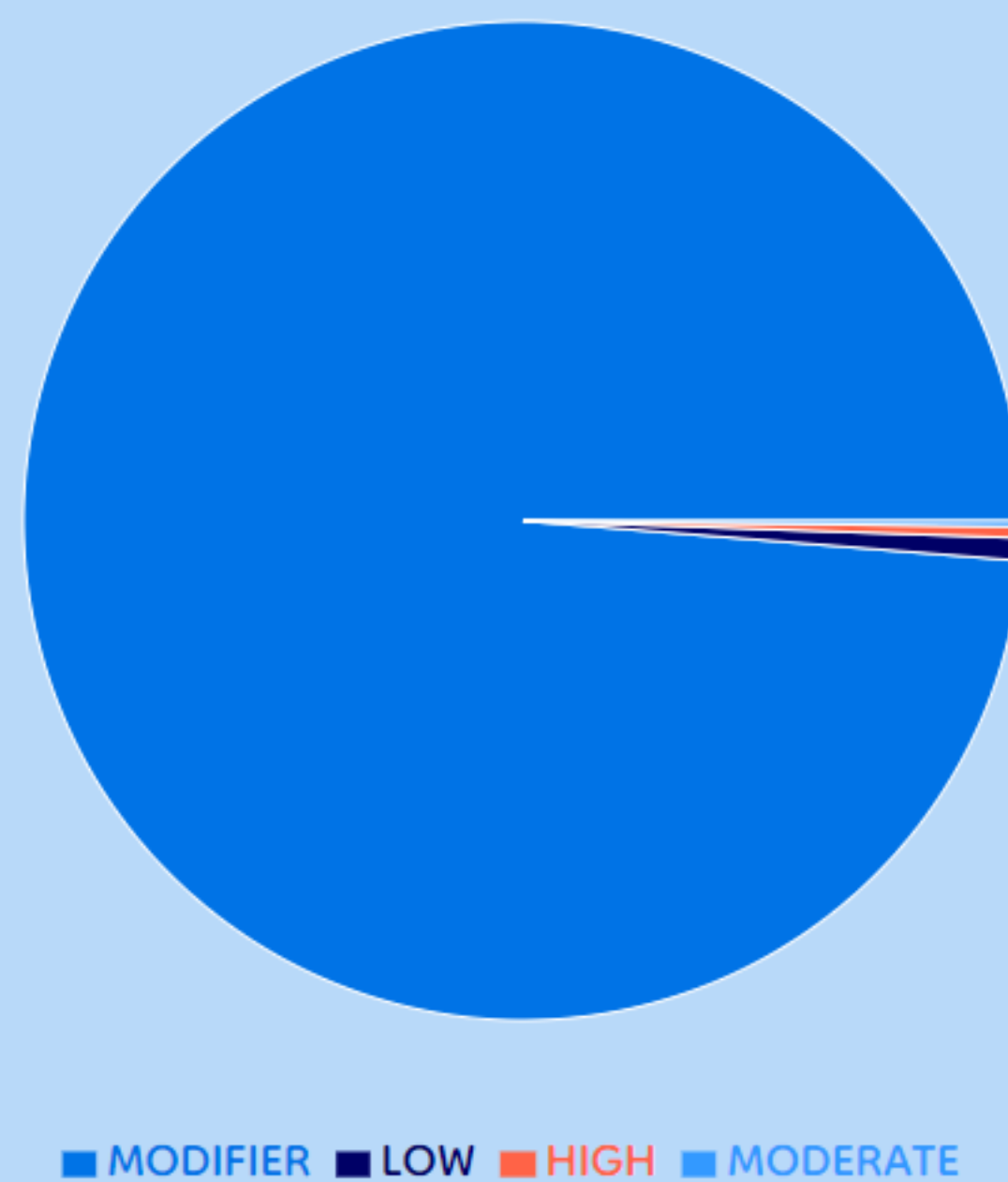
Analysis data:

This table contains 13 INDEL made up of the following types:

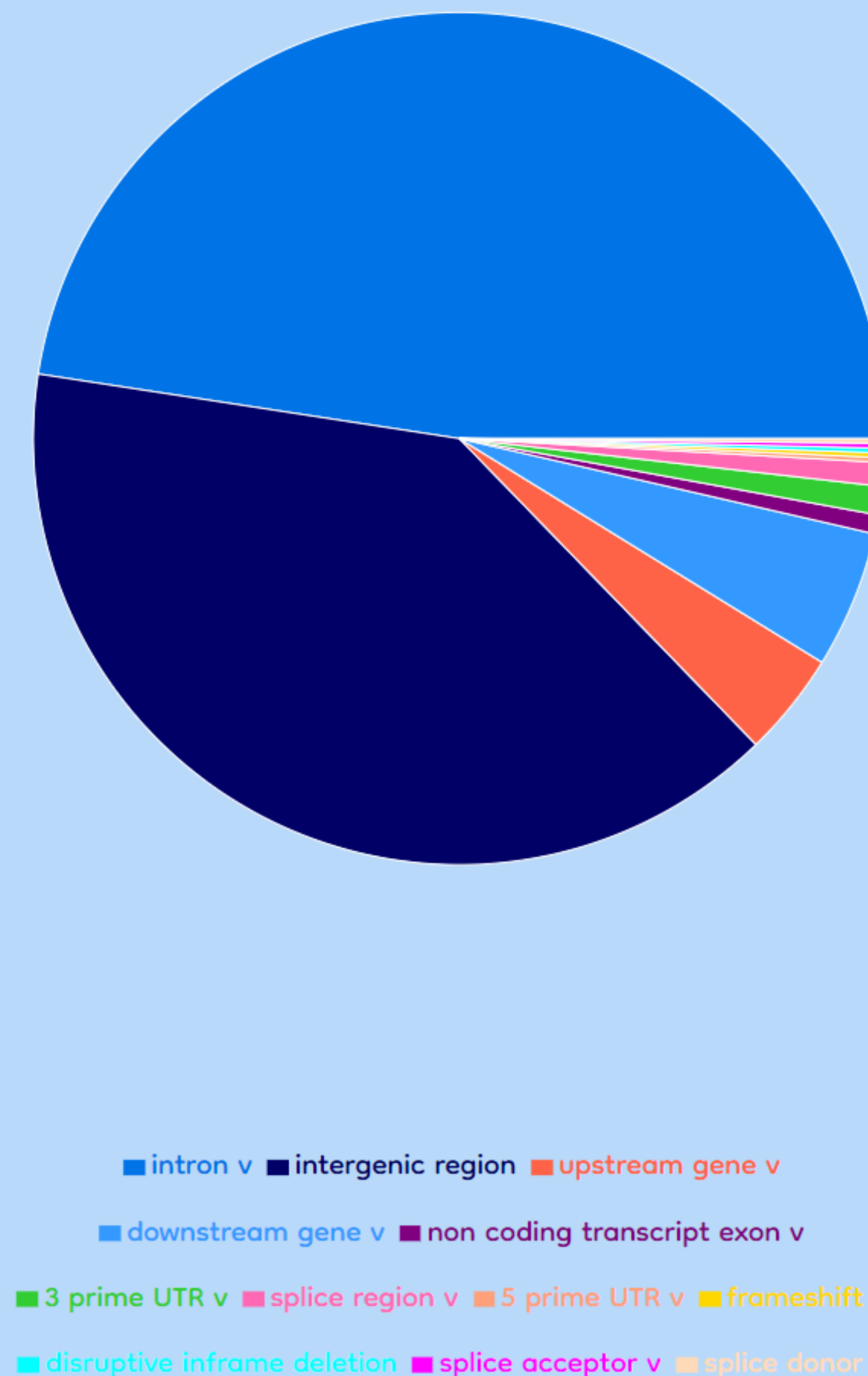
- splice region variant: 5
- intron variant: 5
- frameshift variant: 1
- splice acceptor variant: 1
- splice donor variant: 1

Resulting in 5 deletions and 1 insertions.

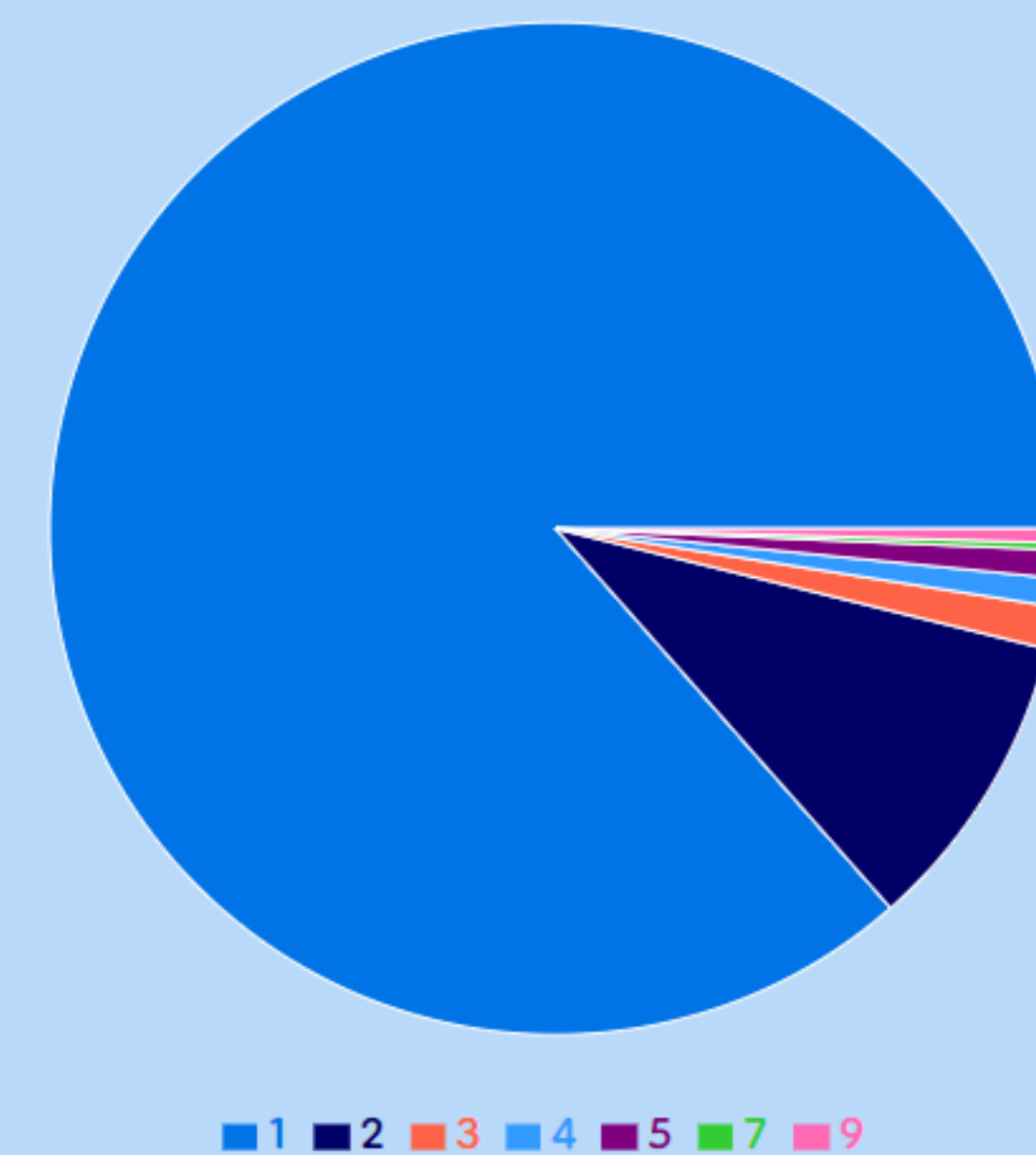
Impact distribution per mutation



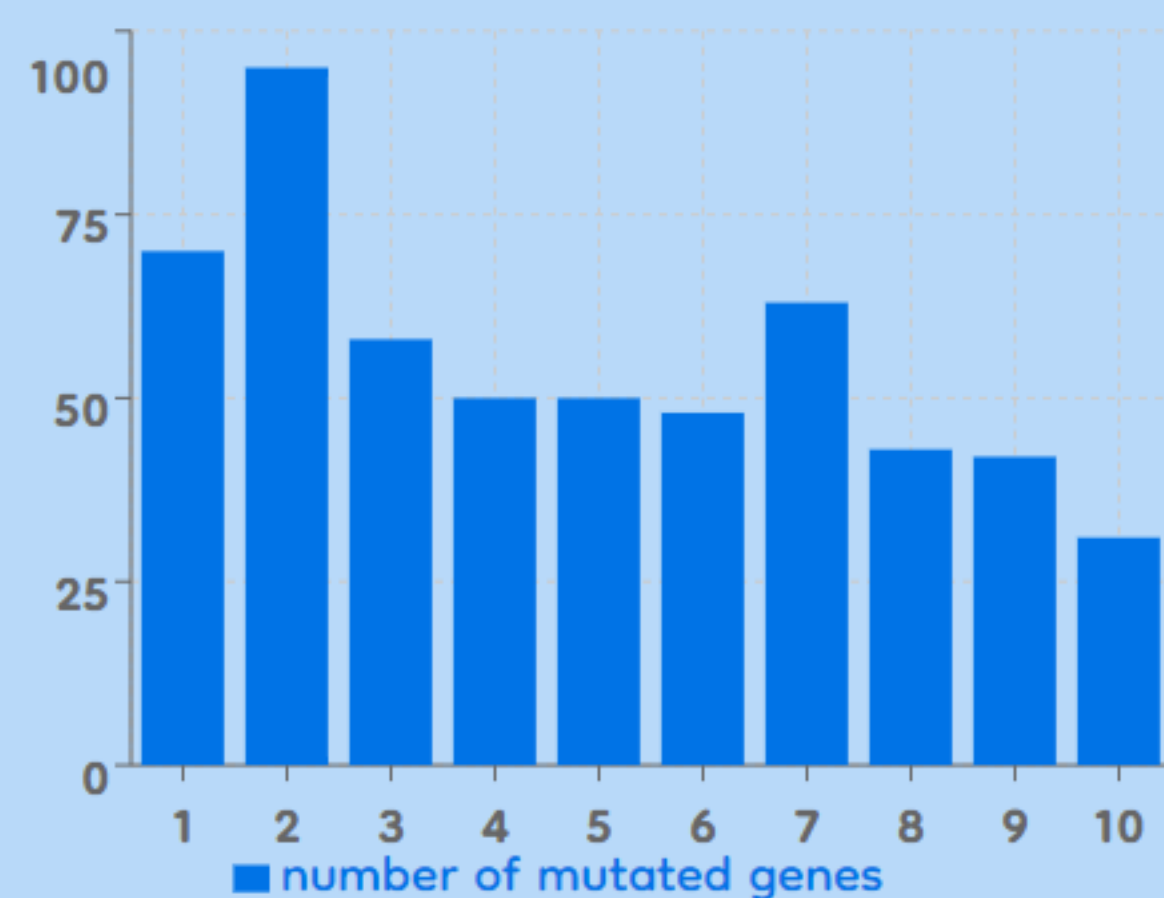
Distribution by mutation type



Number of mutations per impact per gene



Gene distribution by chromosome



Number of mutations per impact per chromosome

