A

autism speaks | MSSNG

Sm

CNV Query

One Box CNV Query

All coordinates are **0-based** and use the **GRCh38/hg38** reference.

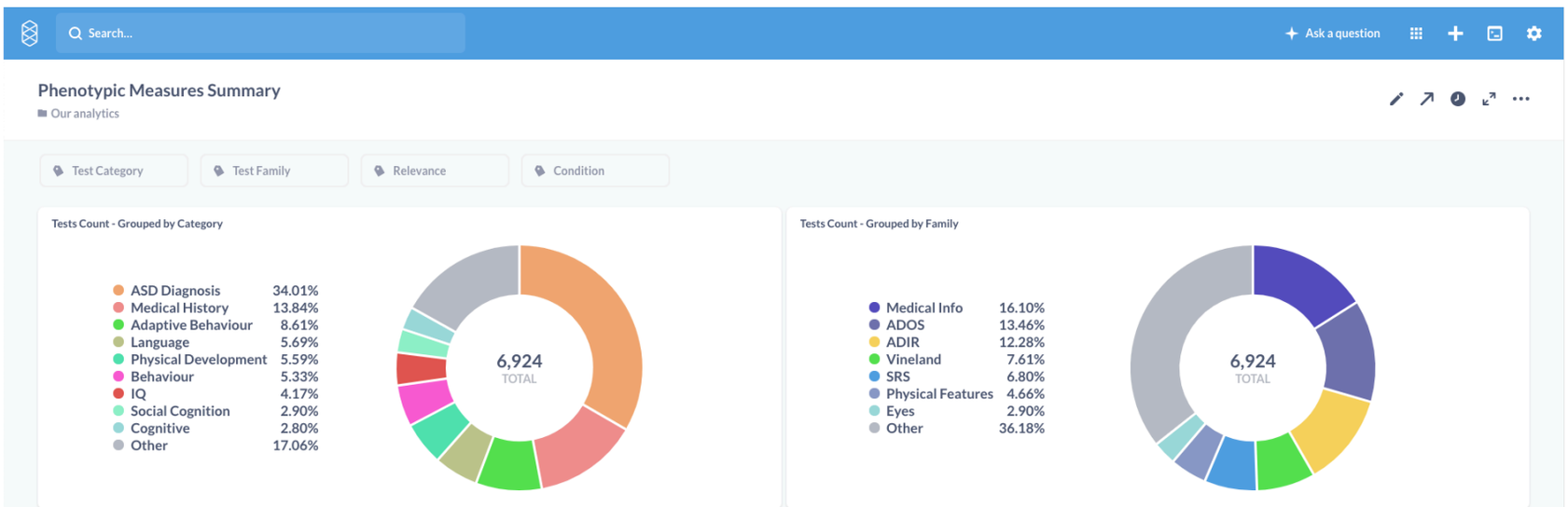
CNV Query History
Saved CNV Queries
Advanced CNV Query

What Can You Do?

With the one box CNV query, you can quickly make certain queries as shown in the table below.

Copy number variations for a specific gene symbol
LAMB2P1
Copy number variations for a genomic interval
chr2-50497000-50498000, chr2:50497000-50498000
Copy number variations for a specific subject
2-1116-003
Copy number variations for a specific family
FAM_1-0007-003

B



C

Query `subject_sample` data

The `subject_sample` table contains information about each subject's DNA sample, including:

- The source of the DNA
- The sequencing platform
- Predicted ancestry
- The IDs of the subject's relatives
- Quality control information

In [7]:

```
subject_sample_df = pd.read_gbq(f'''
    SELECT * FROM `{BQ_RELEASE_DATASET}.subject_sample`
''')
```

Display `subject_sample` data

Head

In [8]:

```
subject_sample_df.head()
```

Out[8]:

	SUBMITTEDID	INDEXID	DNASOURCE	PLATFORM	NIMHID	RUDCRID	COMMENTS	SOFTWARE_VERSION	PREDICTED_ANCESTRY	father_SUBMITTEDID	mother_SUBMITTEDID	sample_QC
0	AU3610201	AU3610201	Blood	Illumina HiSeqX	10C115445	05C48759	high het/hom ratio	None	AFR	0	0	QC_FAIL
1	AU1961303	AU1961303	Blood	Illumina HiSeqX	07C65590	08C78532	None	None	AFR	0	0	ok
2	AU1995201	AU1995201	Cell line	Illumina HiSeqX	07C69088	08C78918	None	None	AFR	0	0	ok
3	AU2103301	AU2103301	Blood	Illumina HiSeqX	07C71054	08C76270	None	None	AFR	0	0	ok
4	AU2107302	AU2107302	Blood	Illumina HiSeqX	08C72389	08C76392	None	None	AFR	0	0	ok