

```

import pandas as pd
import numpy as np
import pyranges
import pickle
import os.path
import seaborn as sns
import matplotlib.pyplot as plt

```

```

hicLoops = pd.read_csv("./Dataset/merged_loops.bedpe", delimiter="\t")
ctcfPeaks = pyranges.read_bed("./Dataset/ENCFF356LIU.bed").df
chiaPetLoops = pd.read_csv("./Dataset/4DNFIS9CCN6R.bedpe", delimiter="\t", header=None)
rad21Peaks = pyranges.read_bed("./Dataset/ENCFF834GOT.bed").df

hicLoops = hicLoops[1:]
chiaPetLoops.columns = ["#chr1", "x1", "x2", "chr2", "y1", "y2", "?"]

```

hicLoops.describe()

	x1	x2	y1	y2	observed	expectedBL	expectedDonut	e
count	1.523300e+04	1.523300e+04	1.523300e+04	1.523300e+04	15233.000000	15233.000000	15233.000000	15233.000000
mean	8.023923e+07	8.024604e+07	8.056954e+07	8.057634e+07	49.292851	14.441595	13.730485	13.730485
std	5.562852e+07	5.562856e+07	5.563722e+07	5.563726e+07	26.412381	11.156909	10.798754	10.798754
min	1.150000e+05	1.200000e+05	1.800000e+05	1.850000e+05	11.000000	0.012426	0.011332	0.011332
25%	3.606000e+07	3.607000e+07	3.628000e+07	3.628500e+07	30.000000	6.784028	6.482804	6.482804
50%	7.008500e+07	7.009000e+07	7.048000e+07	7.049000e+07	43.000000	11.354755	10.619547	10.619547
75%	1.158700e+08	1.158800e+08	1.162300e+08	1.162400e+08	61.000000	18.363478	17.439386	17.439386
max	2.474400e+08	2.474450e+08	2.475700e+08	2.475800e+08	271.000000	98.571365	92.682210	1

ctcfPeaks.describe()

	Start	End	Score	ThickStart	ThickEnd	ItemRGB	BlockCount
count	4.094900e+04	4.094900e+04	40949.000000	40949.000000	40949.0	40949.000000	40949.000000
mean	7.831949e+07	7.831980e+07	961.238834	73.253416	-1.0	4.246728	154.052187
std	5.596081e+07	5.596081e+07	103.619231	56.206305	0.0	0.924962	40.835497
min	1.144400e+04	1.179400e+04	537.000000	3.891950	-1.0	-0.142540	1.000000
25%	3.378754e+07	3.378769e+07	1000.000000	26.886680	-1.0	4.252250	175.000000
50%	6.739370e+07	6.739406e+07	1000.000000	56.959440	-1.0	4.690030	175.000000
75%	1.155417e+08	1.155420e+08	1000.000000	108.935150	-1.0	4.690030	175.000000
max	2.489248e+08	2.489251e+08	1000.000000	493.698390	-1.0	4.690030	460.000000

chiaPetLoops.describe()

	x1	x2	y1	y2	?
count	5.815083e+06	5.815083e+06	5.815083e+06	5.815083e+06	5.815083e+06
mean	7.780002e+07	7.780060e+07	8.380769e+07	8.380828e+07	1.223357e+00
std	5.542503e+07	5.542503e+07	5.649045e+07	5.649044e+07	1.361738e+00
min	0.000000e+00	1.320000e+02	7.642000e+03	8.559000e+03	1.000000e+00
25%	3.330289e+07	3.330345e+07	3.827097e+07	3.827151e+07	1.000000e+00
50%	6.742149e+07	6.742206e+07	7.406263e+07	7.406324e+07	1.000000e+00
75%	1.134992e+08	1.134999e+08	1.209587e+08	1.209593e+08	1.000000e+00
max	2.489168e+08	2.489174e+08	2.489342e+08	2.489348e+08	1.898000e+03

```
rad21Peaks.describe()
```

	Start	End	Score	ThickStart	ThickEnd	ItemRGB	BlockCount
count	3.462300e+04	3.462300e+04	34623.000000	34623.000000	34623.0	34623.000000	34623.000000
mean	7.850383e+07	7.850407e+07	944.956849	61.054135	-1.0	3.738735	118.721255
std	5.574411e+07	5.574411e+07	122.152293	48.439246	0.0	0.878939	28.875827
min	1.870400e+04	1.896800e+04	540.000000	4.231500	-1.0	-0.015850	1.000000
25%	3.396428e+07	3.396454e+07	1000.000000	22.078885	-1.0	3.313005	132.000000
50%	6.820523e+07	6.820550e+07	1000.000000	44.551970	-1.0	3.827920	132.000000
75%	1.144681e+08	1.144683e+08	1000.000000	88.545570	-1.0	4.491820	132.000000
max	2.489248e+08	2.489250e+08	1000.000000	334.213290	-1.0	4.491820	164.000000

```
ctcfPeaks["Chromosome"] = ctcfPeaks["Chromosome"].apply(lambda x: x.removeprefix("chr"))
rad21Peaks["Chromosome"] = rad21Peaks["Chromosome"].apply(
    lambda x: x.removeprefix("chr"))
)
chiaPetLoops["#chr1"] = chiaPetLoops["#chr1"].apply(lambda x: x.removeprefix("chr"))
chiaPetLoops["chr2"] = chiaPetLoops["chr2"].apply(lambda x: x.removeprefix("chr"))
```

```
print(ctcfPeaks.head())
print(rad21Peaks.head())
print(chiaPetLoops.head())
print(hicLoops.head())
```

Chromosome	Start	End	Name	Score	Strand	ThickStart	ThickEnd	\
0	1	177429483	177429833	.	611	.	3.96905	-1.0
1	1	84224251	84224601	.	855	.	3.99064	-1.0
2	1	236425556	236425906	.	668	.	4.03628	-1.0
3	1	6634797	6635147	.	1000	.	4.17682	-1.0
4	1	154478854	154479204	.	1000	.	4.18657	-1.0

ItemRGB BlockCount

0	-0.12232	175
1	-0.11580	175
2	-0.12009	175
3	-0.12427	175
4	-0.12400	175

Chromosome	Start	End	Name	Score	Strand	ThickStart	ThickEnd	\
0	1	93814064	93814272	.	1000	.	267.49725	-1.0
1	1	119367581	119367784	.	1000	.	256.48546	-1.0
2	1	23544795	23544995	.	1000	.	253.97355	-1.0
3	1	11037696	11037897	.	1000	.	245.81208	-1.0
4	1	93629577	93629769	.	1000	.	245.43445	-1.0

ItemRGB BlockCount

0	4.49182	111
1	4.49182	111
2	4.49182	113
3	4.49182	86
4	4.49182	93

#chr1	x1	x2	chr2	y1	y2	?	
0	10	49043	49694	10	1596907	1597444	1
1	10	49291	49814	10	71061105	71061664	1
2	10	50096	50747	10	19437275	19437902	2
3	10	52377	52917	10	78536	79151	1
4	10	52428	53079	10	806777	807334	1

#chr1	x1	x2	chr2	y1	y2	name	score	\
1	10	60880000.0	60890000.0	10	60960000.0	60970000.0	.	.
2	10	131900000.0	131910000.0	10	131980000.0	131990000.0	.	.
3	10	71720000.0	71730000.0	10	71810000.0	71820000.0	.	.
4	10	62610000.0	62620000.0	10	62730000.0	62740000.0	.	.
5	10	26780000.0	26790000.0	10	26850000.0	26860000.0	.	.

strand1	strand2	...	expectedH	expectedV	fdrBL	fdrDonut	\
1	.	.	29.857151	34.565178	5.510599e-06	3.417617e-03	
2	.	.	47.551224	38.399870	4.084538e-06	5.531278e-03	
3	.	.	56.117943	43.748466	2.594937e-06	2.825991e-06	
4	.	.	72.266400	52.050930	6.261819e-07	7.079455e-07	
5	.	.	65.557430	90.107475	3.840393e-07	4.753292e-07	

fdrH	fdrV	numCollapsed	centroid1	centroid2	radius	
1	6.518073e-06	4.352302e-03	1.0	60885000.0	60965000.0	0.0
2	6.420658e-03	5.203196e-06	2.0	131905000.0	131980000.0	5000.0
3	8.173968e-03	3.346481e-06	2.0	71715000.0	71815000.0	10000.0
4	5.628446e-03	7.618980e-07	1.0	62615000.0	62735000.0	0.0
5	5.291055e-07	9.047872e-03	1.0	26785000.0	26855000.0	0.0

[5 rows x 24 columns]

- Given a loop, consider chr1, x1, x2, chr2, y1, y2
- For each row check whether a matching peak has an anchor in chr1 or chr2 or both

```
def getAnchors(loops, peaks):
    bothAnchorsIndexes = []
    singleAnchorCount = 0
    for i, loop in loops.iterrows():
        anchor1 = False
        anchor2 = False
```

```

sameChromosome = peaks[peaks["Chromosome"] == loop["#chr1"]]

x1 = sameChromosome[sameChromosome["Start"] >= loop["x1"]]
x2 = x1[x1["Start"] <= loop["x2"]]

x1 = x2[x2["End"] >= loop["x1"]]
x2 = x1[x1["End"] <= loop["x2"]]

if len(x2) > 0:

    anchor1 = True
    """ else:
        x1=sameChromosome[sameChromosome['End']>=loop['x1']]
        x2=x1[x1['End']<=loop['x2']]
        if len(x2) > 0:
            anchor1=True """
    """

sameChromosome = peaks[peaks["Chromosome"] == loop["chr2"]]

x1 = sameChromosome[sameChromosome["Start"] >= loop["y1"]]
x2 = x1[x1["Start"] <= loop["y2"]]

x1 = x2[x2["End"] >= loop["y1"]]
x2 = x1[x1["End"] <= loop["y2"]]

if len(x2) > 0:
    anchor2 = True
    """ else:
        x1=sameChromosome[sameChromosome['End']>=loop['y1']]
        x2=x1[x1['End']<=loop['y2']]
        if len(x2) > 0:
            anchor2=True
    """
    """

if anchor1 == True and anchor2 == True:
    bothAnchorsIndexes.append(i)
    singleAnchorCount += 1
elif anchor1 == True or anchor2 == True:
    singleAnchorCount += 1
return bothAnchorsIndexes, singleAnchorCount

```

```

peakLoopHicLCtcfPPairs, peakLoopHicLCtcfPSingleAnchorCount = getAnchors(
    hicLoops, ctcfPeaks
)
with open("peakLoopHicLCtcfPPairs", "wb") as f:
    pickle.dump(peakLoopHicLCtcfPPairs, f)
with open("peakLoopHicLCtcfPSingleAnchorCount", "wb") as f:
    pickle.dump(peakLoopHicLCtcfPSingleAnchorCount, f)

```

```
print(len(peakLoopHicLCtcfPPairs))
```

8374

```

peakLoopHicLRad21PPairs, peakLoopHicLRad21PSingleAnchorCount = getAnchors(
    hicLoops, rad21Peaks
)
with open("peakLoopHicLRad21PPairs", "wb") as f:
    pickle.dump(peakLoopHicLRad21PPairs, f)
with open("peakLoopHicLRad21PSingleAnchorCount", "wb") as f:
    pickle.dump(peakLoopHicLRad21PSingleAnchorCount, f)

```

```
print(len(peakLoopHicLRad21PPairs))
```

8377

```

peakLoopChiaLCtcfPPairs, peakLoopChiaLCtcfPSingleAnchorCount = getAnchors(
    chiaPetLoops, ctcfPeaks
)

```

```
)  
with open("peakLoopChiaLCtcfPPairs", "wb") as f:  
    pickle.dump(peakLoopChiaLCtcfPPairs, f)  
with open("peakLoopChiaLCtcfPSingleAnchorCount", "wb") as f:  
    pickle.dump(peakLoopChiaLCtcfPSingleAnchorCount, f)
```

```
print(len(peakLoopChiaLCtcfPPairs))
```

```
9520
```

```
peakLoopChiaLRad21PPairs, peakLoopChiaLRad21PSingleAnchorCount = getAnchors(  
    chiaPetLoops, rad21Peaks  
)  
with open("peakLoopChiaLRad21PPairs", "wb") as f:  
    pickle.dump(peakLoopChiaLRad21PPairs, f)  
with open("peakLoopChiaLRad21PSingleAnchorCount", "wb") as f:  
    pickle.dump(peakLoopChiaLRad21PSingleAnchorCount, f)
```

```
print(len(peakLoopChiaLRad21PPairs))
```

```
9756
```

Perform 4 comparisons between datasets. for two compared datasets (A and B) calculate how many loops from A match (**) some loop from B, and how many loops from B match some loop from A. You can present the result as a 2x2 table showing counts of total and matched loops for datasets.

```
with open(r"peakLoopChiaLCtcfPPairs", "rb") as input_file: # Chia Ctcf  
    peakLoopChiaLCtcfPPairs = pickle.load(input_file)  
  
with open(r"peakLoopHicLCtcfPPairs", "rb") as input_file: # HIC Ctcf  
    peakLoopHicLCtcfPPairs = pickle.load(input_file)  
  
with open(r"peakLoopChiaLRad21PPairs", "rb") as input_file: # CHIA Rad  
    peakLoopChiaLRad21PPairs = pickle.load(input_file)  
  
with open(r"peakLoopHicLRad21PPairs", "rb") as input_file: # Hic Rad  
    peakLoopHicLRad21PPairs = pickle.load(input_file)
```

```
# Adjust index positions  
peakLoopChiaLCtcfPPairs = [x - 1 for x in peakLoopChiaLCtcfPPairs]  
peakLoopHicLCtcfPPairs = [x - 1 for x in peakLoopHicLCtcfPPairs]  
peakLoopChiaLRad21PPairs = [x - 1 for x in peakLoopChiaLRad21PPairs]  
peakLoopHicLRad21PPairs = [x - 1 for x in peakLoopHicLRad21PPairs]
```

```
pairsIndexes = [  
    {  
        "loopDataset1": hicLoops,  
        "loopDataset2": hicLoops,  
        "filteredIndexes1": peakLoopHicLCtcfPPairs,  
        "filteredIndexes2": peakLoopHicLRad21PPairs,  
        "filename": "hicLcHicRadIndex",  
    },  
    {  
        "loopDataset1": chiaPetLoops,  
        "loopDataset2": chiaPetLoops,  
        "filteredIndexes1": peakLoopChiaLCtcfPPairs,  
        "filteredIndexes2": peakLoopChiaLRad21PPairs,  
        "filename": "chiaLcChiaRadCount",  
    },  
    {  
        "loopDataset1": chiaPetLoops,  
        "loopDataset2": hicLoops,  
        "filteredIndexes1": peakLoopChiaLCtcfPPairs,  
        "filteredIndexes2": peakLoopHicLCtcfPPairs,  
    }]
```

```

        "filename": "chiaLcHicLcCount",
    },
    {
        "loopDataset1": chiaPetLoops,
        "loopDataset2": hicLoops,
        "filteredIndexes1": peakLoopChiaLRad21PPPairs,
        "filteredIndexes2": peakLoopHicLCtcfPPairs,
        "filename": "chiaRadHicLdCount",
    },
    {
        "loopDataset1": chiaPetLoops,
        "loopDataset2": hicLoops,
        "filteredIndexes1": peakLoopChiaLRad21PPPairs,
        "filteredIndexes2": peakLoopHicLRad21PPPairs,
        "filename": "chiaLcRadHicRadCount",
    },
],
]

```

```

descriptions = [
    {"loop1": "Hic", "peak1": "Ctcf", "loop2": "Hic", "peak2": "Rad21"}, 
    {"loop1": "ChiaPet", "peak1": "Ctcf", "loop2": "ChiaPet", "peak2": "Rad21"}, 
    {"loop1": "ChiaPet", "peak1": "Ctcf", "loop2": "Hic", "peak2": "Ctcf"}, 
    {"loop1": "ChiaPet", "peak1": "Rad21", "loop2": "Hic", "peak2": "Ctcf"}, 
    {"loop1": "ChiaPet", "peak1": "Rad21", "loop2": "Hic", "peak2": "Rad21"}, 
]

```

```

def compareFilteredLoops(
    loopDataset1, loopDataset2, filteredIndexes1, filteredIndexes2, filename, threshold
):
    countOfMatchedLoopsBothAnchors = 0
    countOfMatchedLoopsAtLeastSingleAnchor = 0
    for index1 in filteredIndexes1:
        for index2 in filteredIndexes2:
            if (
                loopDataset1.iloc[index1]["#chr1"] == loopDataset2.iloc[index2]["#chr1"]
                and loopDataset1.iloc[index1]["chr2"]
                == loopDataset2.iloc[index2]["chr2"]
            ):
                middleX1 = (
                    abs(
                        loopDataset1.iloc[index1]["x1"]
                        + loopDataset1.iloc[index1]["x2"]
                    )
                    / 2
                )
                middleY1 = (
                    abs(
                        loopDataset1.iloc[index1]["y1"]
                        + loopDataset1.iloc[index1]["y2"]
                    )
                    / 2
                )
                middleX2 = (
                    abs(
                        loopDataset2.iloc[index2]["x1"]
                        + loopDataset2.iloc[index2]["x2"]
                    )
                    / 2
                )
                middleY2 = (
                    abs(
                        loopDataset2.iloc[index2]["y1"]
                        + loopDataset2.iloc[index2]["y2"]
                    )
                    / 2
                )
                if (
                    abs(middleX1 - middleX2) <= threshold
                    and abs(middleY1 - middleY2) <= threshold
                ):
                    countOfMatchedLoopsBothAnchors += 1
                else:
                    countOfMatchedLoopsAtLeastSingleAnchor += 1
    print(f"Number of matched loops with both anchors: {countOfMatchedLoopsBothAnchors}")
    print(f"Number of matched loops with at least one anchor: {countOfMatchedLoopsAtLeastSingleAnchor}")
    with open(filename, "w") as f:
        f.write(f"Number of matched loops with both anchors: {countOfMatchedLoopsBothAnchors}\n")
        f.write(f"Number of matched loops with at least one anchor: {countOfMatchedLoopsAtLeastSingleAnchor}\n")

```

```

        )
        if abs(middleX1 - middleX2) <= threshold:
            countOfMatchedLoopsAtLeastSingleAnchor += 1
            if abs(middleY1 - middleY2) <= threshold:
                countOfMatchedLoopsBothAnchors += 1
        elif abs(middleY2 - middleY1) <= threshold:
            countOfMatchedLoopsAtLeastSingleAnchor += 1
    with open(r"" + str(filename) + "-" + str(threshold), "wb") as input_file:
        pickle.dump(countOfMatchedLoopsBothAnchors, input_file)
    with open(r"single-" + str(filename) + "-" + str(threshold), "wb") as input_file:
        pickle.dump(countOfMatchedLoopsAtLeastSingleAnchor, input_file)
    return countOfMatchedLoopsAtLeastSingleAnchor, countOfMatchedLoopsBothAnchors

```

```
thresholds = [5000, 10000]
```

```

results = []

for threshold in thresholds:
    for pairIndex in pairsIndexes:
        atLeastSingleAnchorCount, bothAnchorsCount = compareFilteredLoops(
            **pairIndex, threshold=threshold
        )
        results.append([atLeastSingleAnchorCount, bothAnchorsCount])
        print(
            "Finished: "
            + str(pairIndex["filename"])
            + ", with threshold: "
            + str(threshold)
        )

```

```

Finished: hicLcHicRadIndex, with threshold: 5000
Finished: chiaLcChiaRadCount, with threshold: 5000
Finished: chiaLcHicLcCount, with threshold: 5000
Finished: chiaRadHicLdCount, with threshold: 5000
Finished: chiaLcRadHicRadCount, with threshold: 5000
Finished: hicLcHicRadIndex, with threshold: 10000
Finished: chiaLcChiaRadCount, with threshold: 10000
Finished: chiaLcHicLcCount, with threshold: 10000
Finished: chiaRadHicLdCount, with threshold: 10000
Finished: chiaLcRadHicRadCount, with threshold: 10000

```

```

results = []
for threshold in thresholds:
    for i, pairIndex in enumerate(pairsIndexes):
        with open(
            pairIndex["filename"] + "-" + str(threshold), "rb"
        ) as input_file: # Chia Rad Hic Rad
            result = pickle.load(input_file)
        with open(
            "single-" + pairIndex["filename"] + "-" + str(threshold), "rb"
        ) as input_file: # Chia Rad Hic Rad
            single = pickle.load(input_file)

        results.append(
            [
                result,
                len(pairIndex["filteredIndexes1"]),
                len(pairIndex["filteredIndexes2"]),
                descriptions[i]["loop1"],
                descriptions[i]["loop2"],
                descriptions[i]["peak1"],
                descriptions[i]["peak2"],
                threshold,
                single,

```

```
        ]
    )

resultsDf = pd.DataFrame(
    results,
    columns=[
        "matched",
        "count1",
        "count2",
        "loop1",
        "loop2",
        "peak1",
        "peak2",
        "threshold",
        "single",
    ],
)
```

```
for i, result in resultsDf.iterrows():
    print(
        result["loop1"]
        + " filtered by "
        + result["peak1"]
        + " vs "
        + result["loop2"]
        + " filtered by "
        + result["peak2"]
    )
    print(
        "\t"
        + result["loop1"]
        + " filtered by "
        + result["peak1"]
        + " total: "
        + str(result["count1"])
    )
    print(
        "\t"
        + result["loop2"]
        + " filtered by "
        + result["peak2"]
        + " total: "
        + str(result["count2"])
    )
    print("\tMatched: " + str(result["matched"]))
    print("\tMatched (at least one anchor): " + str(result["single"]))
    print("\n")
```

Hic filtered by Ctcf vs Hic filtered by Rad21
Hic filtered by Ctcf total: 8374
Hic filtered by Rad21 total: 8377
Matched: 7707
Matched (at least one anchor): 18817

ChiaPet filtered by Ctcf vs ChiaPet filtered by Rad21
ChiaPet filtered by Ctcf total: 9520
ChiaPet filtered by Rad21 total: 9756
Matched: 7910
Matched (at least one anchor): 21377

ChiaPet filtered by Ctcf vs Hic filtered by Ctcf
ChiaPet filtered by Ctcf total: 9520
Hic filtered by Ctcf total: 8374
Matched: 1661
Matched (at least one anchor): 9671

ChiaPet filtered by Rad21 vs Hic filtered by Ctcf
ChiaPet filtered by Rad21 total: 9756
Hic filtered by Ctcf total: 8374
Matched: 1720
Matched (at least one anchor): 10110

ChiaPet filtered by Rad21 vs Hic filtered by Rad21
ChiaPet filtered by Rad21 total: 9756
Hic filtered by Rad21 total: 8377
Matched: 1799
Matched (at least one anchor): 10312

Hic filtered by Ctcf vs Hic filtered by Rad21
Hic filtered by Ctcf total: 8374
Hic filtered by Rad21 total: 8377
Matched: 7707
Matched (at least one anchor): 19351

ChiaPet filtered by Ctcf vs ChiaPet filtered by Rad21
ChiaPet filtered by Ctcf total: 9520
ChiaPet filtered by Rad21 total: 9756
Matched: 8898
Matched (at least one anchor): 24882

ChiaPet filtered by Ctcf vs Hic filtered by Ctcf
ChiaPet filtered by Ctcf total: 9520
Hic filtered by Ctcf total: 8374
Matched: 2316
Matched (at least one anchor): 11399

ChiaPet filtered by Rad21 vs Hic filtered by Ctcf
ChiaPet filtered by Rad21 total: 9756
Hic filtered by Ctcf total: 8374
Matched: 2374
Matched (at least one anchor): 11850

ChiaPet filtered by Rad21 vs Hic filtered by Rad21
ChiaPet filtered by Rad21 total: 9756
Hic filtered by Rad21 total: 8377

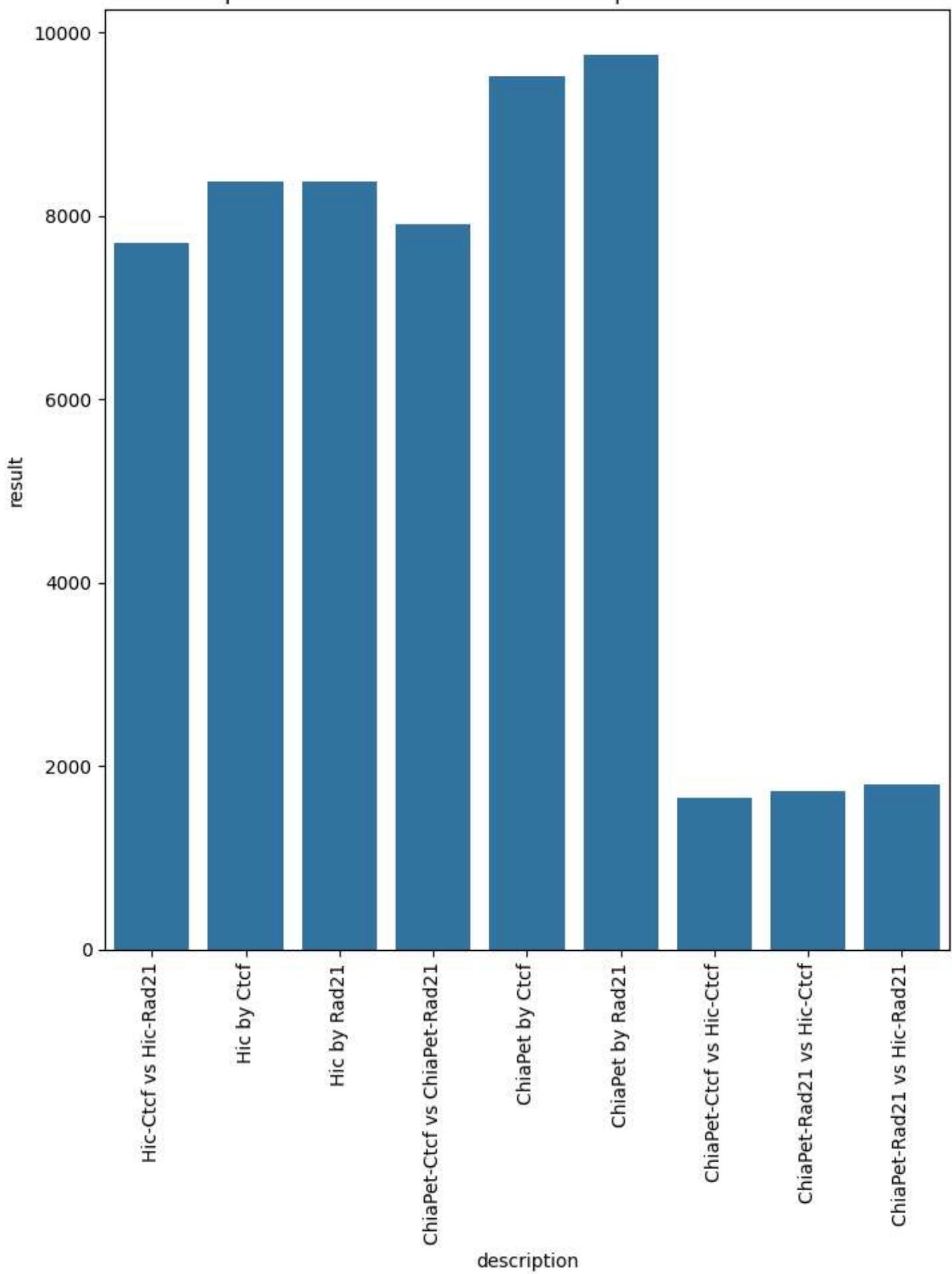
```
Matched: 2469  
Matched (at least one anchor): 12083
```

```
resultsBar = []  
for i, result in enumerate(results):  
    resultsBar.append(  
        [  
            result[3] + "-" + result[5] + " vs " + result[4] + "-" + result[6],  
            result[0],  
            i,  
            result[7],  
        ]  
    )  
    resultsBar.append([result[3] + " by " + result[5], result[1], i, result[7]])  
    resultsBar.append([result[4] + " by " + result[6], result[2], i, result[7]])
```

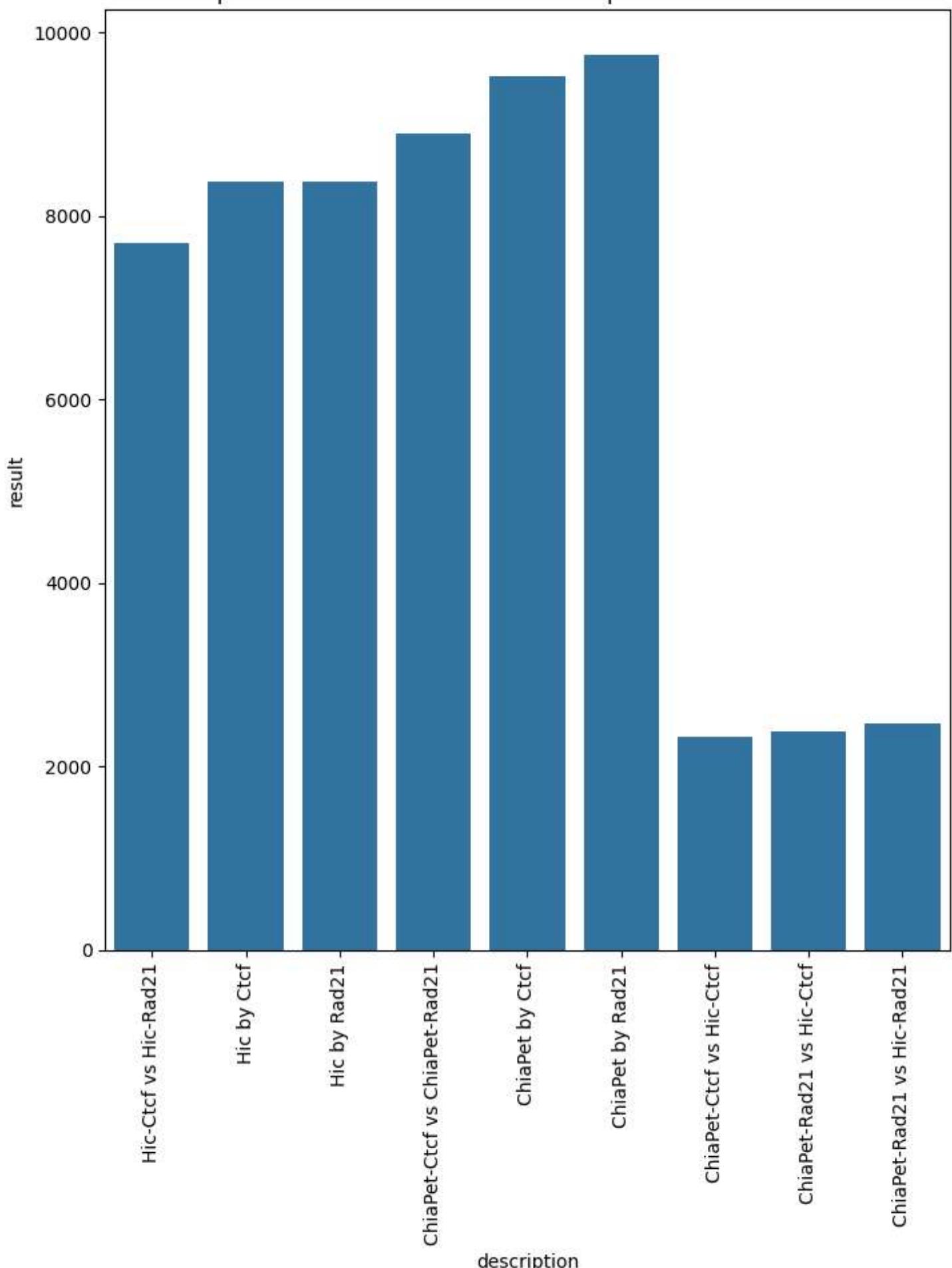
```
resultsBarDf = pd.DataFrame(  
    resultsBar, columns=["description", "result", "series", "threshold"]  
)
```

```
plt.figure(figsize=(8, 8))  
plt.title("Comparison of matched and filtered loops for threshold of 5000")  
  
sns.barplot(  
    data=resultsBarDf[resultsBarDf["threshold"] == 5000],  
    x="description",  
    y="result",  
)  
plt.tight_layout()  
plt.xticks(rotation=90)  
plt.show()  
  
plt.figure(figsize=(8, 8))  
plt.title("Comparison of matched and filtered loops for threshold of 10000")  
  
sns.barplot(  
    data=resultsBarDf[resultsBarDf["threshold"] == 10000],  
    x="description",  
    y="result",  
)  
plt.tight_layout()  
plt.xticks(rotation=90)  
plt.show()
```

Comparison of matched and filtered loops for threshold of 5000

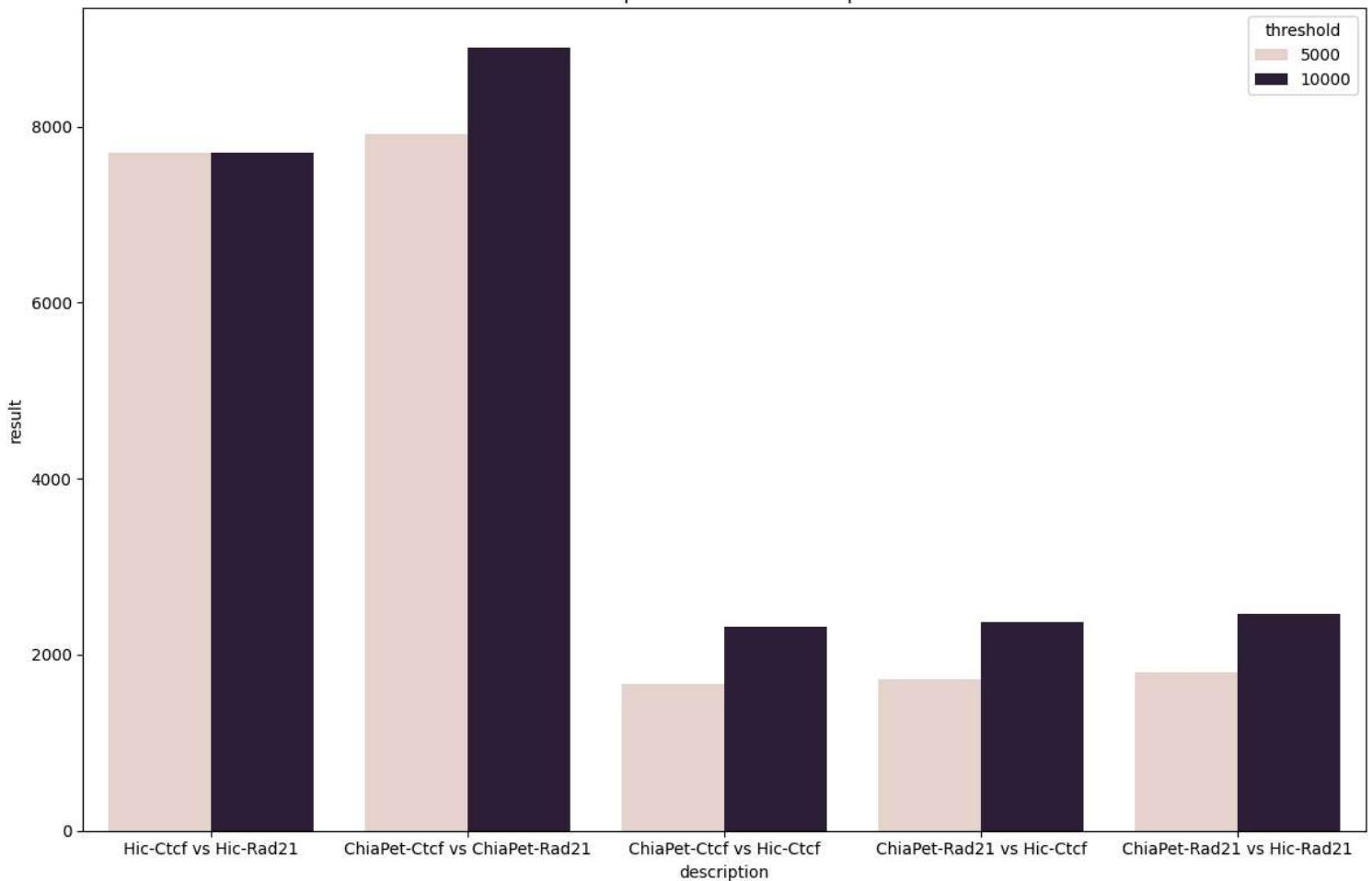


Comparison of matched and filtered loops for threshold of 10000



```
plt.figure(figsize=(12, 8))
plt.title("Comparison of matched loops")
filteredData = resultsBarDf[resultsBarDf["description"].str.contains("vs", na=False)]
sns.barplot(data=filteredData, x="description", y="result", hue="threshold")
plt.tight_layout()
plt.show()
```

Comparison of matched loops

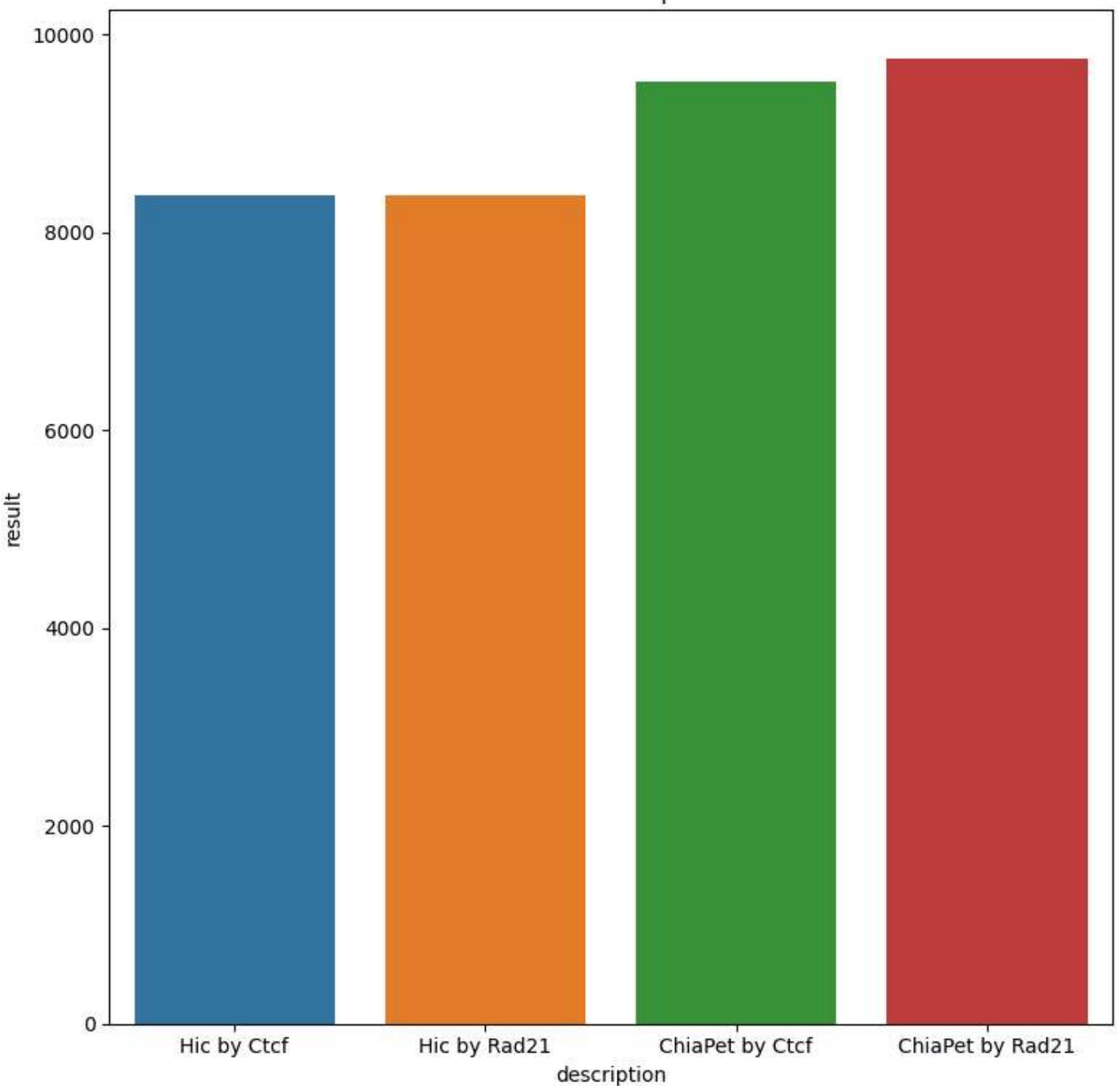


```

plt.figure(figsize=(8, 8))
plt.title("filtered loops")
filteredData = resultsBarDf[resultsBarDf["description"].str.contains("by", na=False)]
sns.barplot(
    data=filteredData[filteredData["threshold"] == 5000],
    x="description",
    y="result",
    hue="description",
)
plt.tight_layout()
plt.show()

```

filtered loops



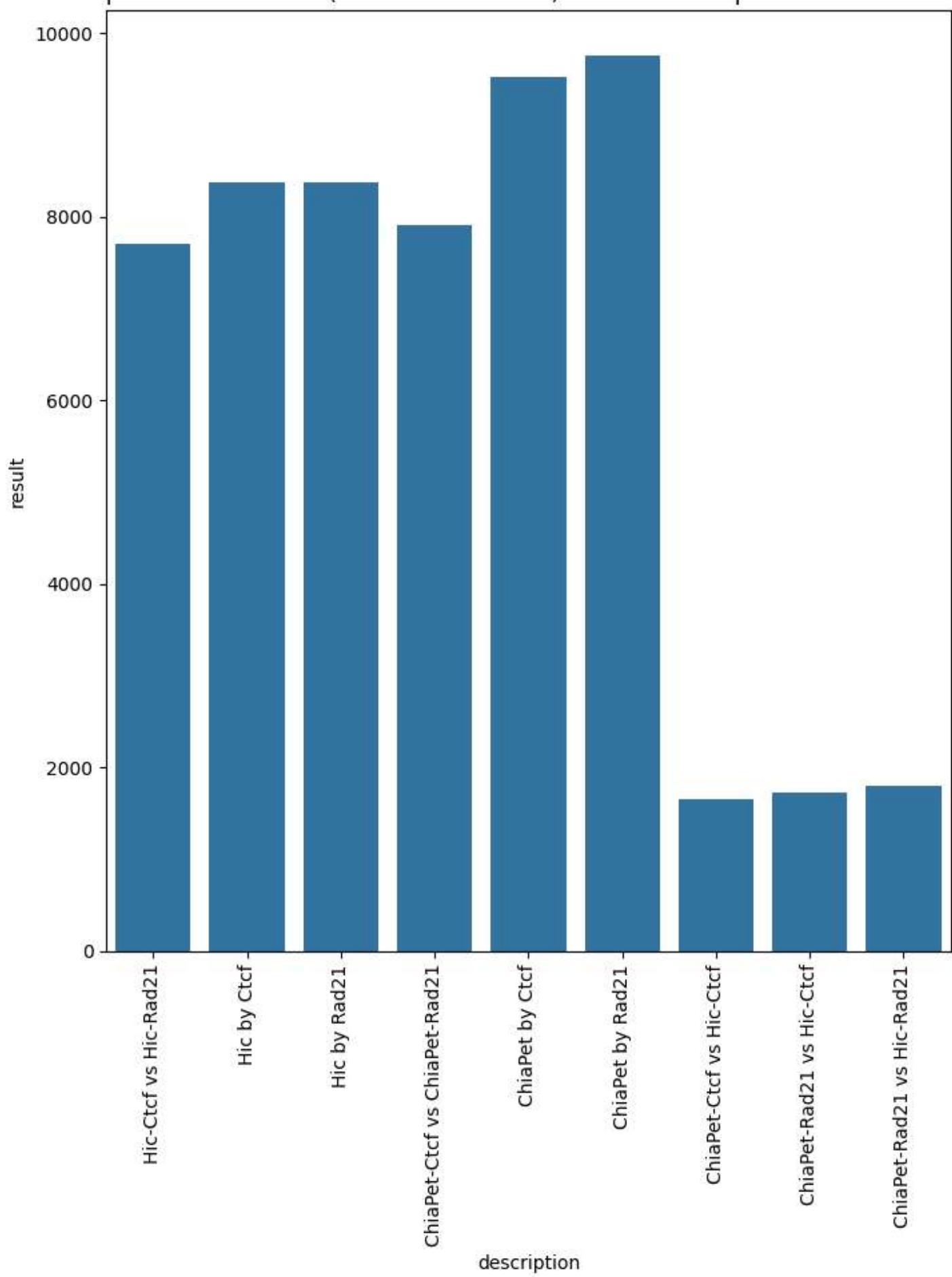
```
resultsBar = []
for i, result in enumerate(results):
    resultsBar.append(
        [
            result[3] + "-" + result[5] + " vs " + result[4] + "-" + result[6],
            result[8],
            i,
            result[7],
        ]
    )
resultsBar.append([result[3] + " by " + result[5], result[1], i, result[7]])
resultsBar.append([result[4] + " by " + result[6], result[2], i, result[7]])
```

```
resultsBarDf = pd.DataFrame(
    resultsBar, columns=["description", "result", "series", "threshold"]
)
```

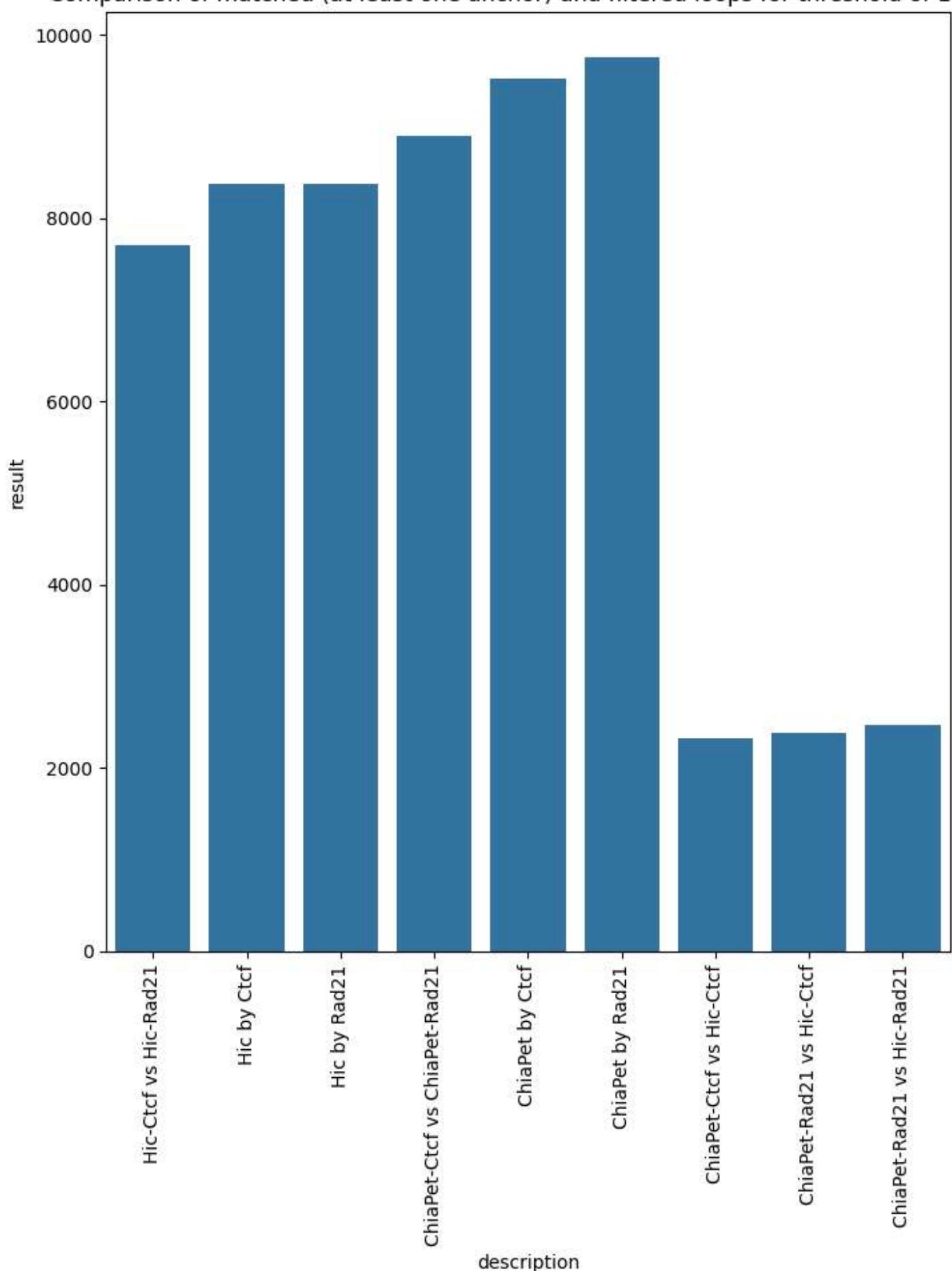
```
plt.figure(figsize=(8, 8))
plt.title(
    "Comparison of matched (at least one anchor) and filtered loops for threshold of 5000"
```

```
)  
sns.barplot(  
    data=resultsBarDf[resultsBarDf["threshold"] == 5000],  
    x="description",  
    y="result",  
)  
plt.tight_layout()  
plt.xticks(rotation=90)  
plt.show()  
  
plt.figure(figsize=(8, 8))  
plt.title(  
    "Comparison of matched (at least one anchor) and filtered loops for threshold of 10000"  
)  
  
sns.barplot(  
    data=resultsBarDf[resultsBarDf["threshold"] == 10000],  
    x="description",  
    y="result",  
)  
plt.tight_layout()  
plt.xticks(rotation=90)  
plt.show()
```

Comparison of matched (at least one anchor) and filtered loops for threshold of 5000

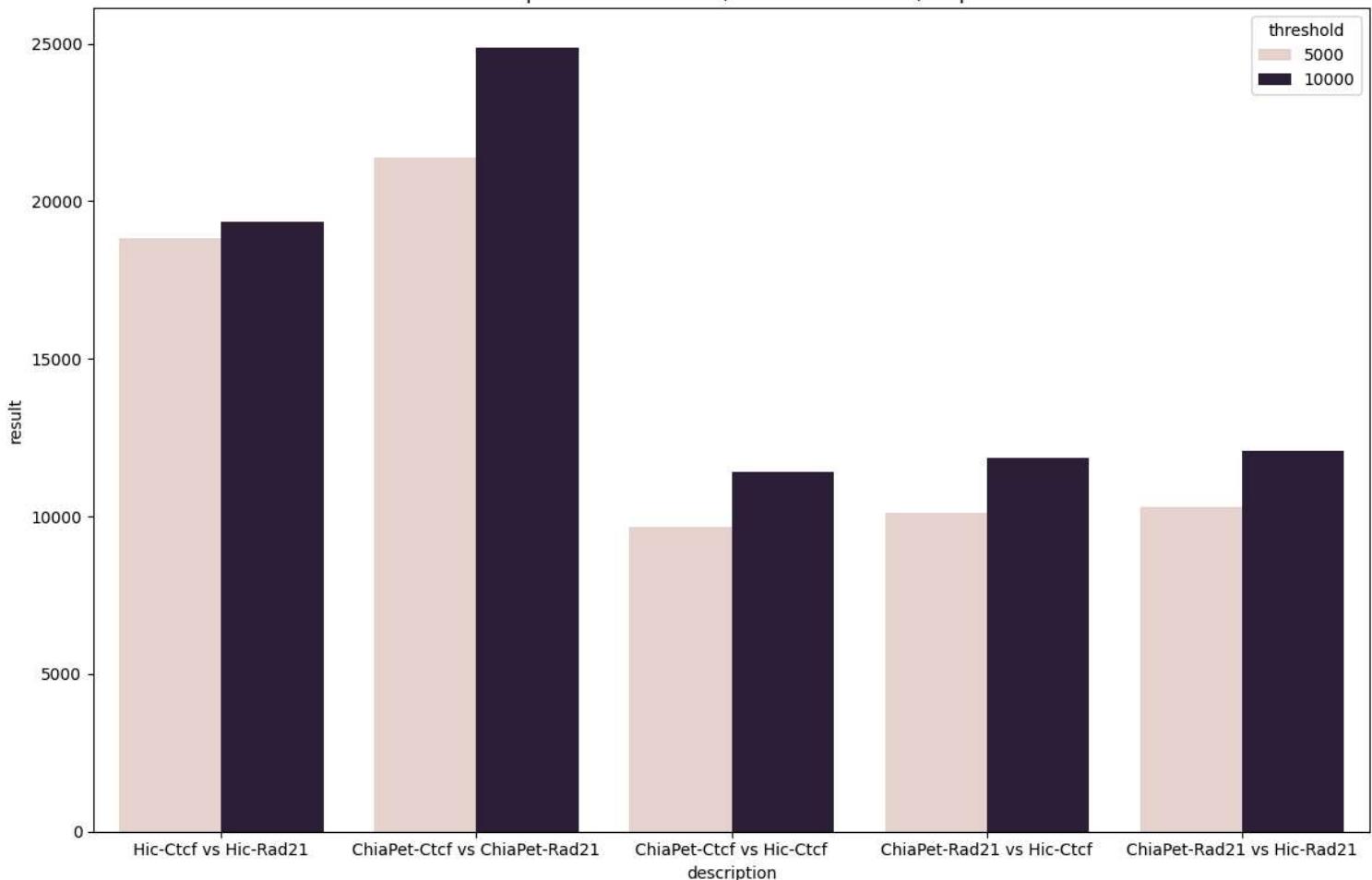


Comparison of matched (at least one anchor) and filtered loops for threshold of 10000



```
plt.figure(figsize=(12, 8))
plt.title("Comparison of matched (at least one anchor) loops")
filteredData = resultsBarDf[resultsBarDf["description"].str.contains("vs", na=False)]
sns.barplot(data=filteredData, x="description", y="result", hue="threshold")
plt.tight_layout()
plt.show()
```

Comparison of matched (at least one anchor) loops



```

resultsBar = []
for i, result in enumerate(results):

    resultsBar.append(
        [
            result[3] + "-" + result[5] + " vs " + result[4] + "-" + result[6],
            result[8],
            "single",
            i,
            result[7],
        ]
    )
    resultsBar.append(
        [
            result[3] + "-" + result[5] + " vs " + result[4] + "-" + result[6],
            result[7],
            "both",
            i,
            result[7],
        ]
    )
)

```

```

resultsBarDF = pd.DataFrame(
    resultsBar, columns=["description", "result", "type", "series", "threshold"]
)

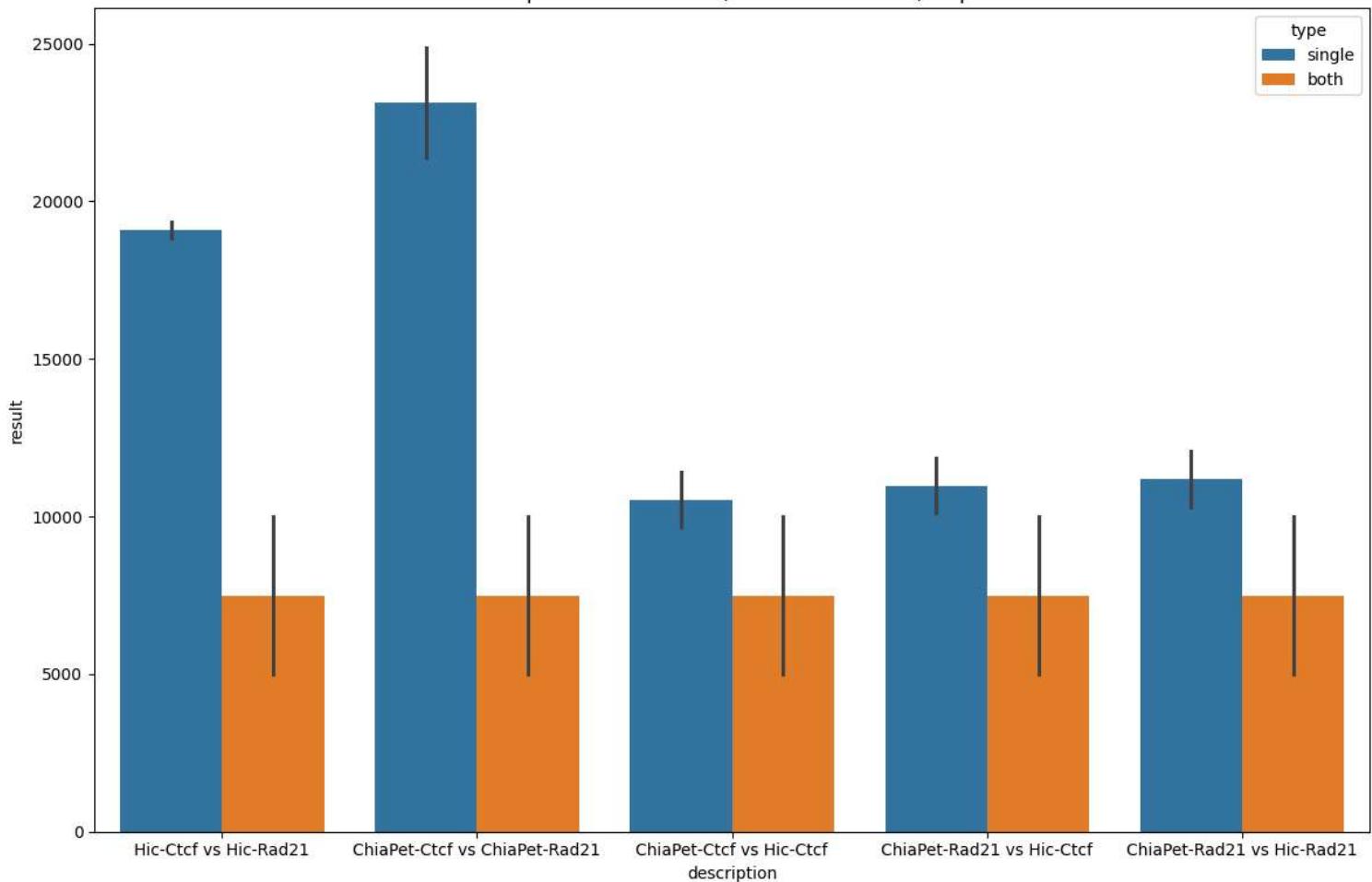
```

```

plt.figure(figsize=(12, 8))
plt.title("Comparison of matched (at least one anchor) loops")
filteredData = resultsBarDF[resultsBarDF["description"].str.contains("vs", na=False)]
sns.barplot(data=filteredData, x="description", y="result", hue="type")
plt.tight_layout()
plt.show()

```

Comparison of matched (at least one anchor) loops



Make a visualization of a selected region (e.g. in IGV), choose something that looks nicely, zoom in enough so that you can see the peak locations. You can also include the loops matched between 2 datasets.

```
chiaPetLoops.iloc[peakLoopChiaLCtcfPPairs[0]]
```

```
#chr1      10
x1      2927863
x2      2928484
chr2      10
y1      3036017
y2      3036561
?
Name: 5191, dtype: object
```