```
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", "?"]
```

```
/home/patryk/.local/lib/python3.10/site-packages/pyranges/methods/init.py:45: FutureWarning: The defaul
t of observed=False is deprecated and will be changed to True in a future version of pandas. Pass obser
ved=False to retain current behavior or observed=True to adopt the future default and silence this warn
ing.
  return {k: v for k, v in df.groupby(grpby_key)}
/home/patryk/.local/lib/python3.10/site-packages/pyranges/methods/init.py:45: FutureWarning: The defaul
t of observed=False is deprecated and will be changed to True in a future version of pandas. Pass obser
ved=False to retain current behavior or observed=True to adopt the future default and silence this warn
ing.
  return {k: v for k, v in df.groupby(grpby_key)}
```

```
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	152
mean	8.023923e+07	8.024604e+07	8.056954e+07	8.057634e+07	49.292851	14.441595	13.730485	
std	5.562852e+07	5.562856e+07	5.563722e+07	5.563726e+07	26.412381	11.156909	10.798754	
min	1.150000e+05	1.200000e+05	1.800000e+05	1.850000e+05	11.000000	0.012426	0.011332	
25%	3.606000e+07	3.607000e+07	3.628000e+07	3.628500e+07	30.000000	6.784028	6.482804	
50%	7.008500e+07	7.009000e+07	7.048000e+07	7.049000e+07	43.000000	11.354755	10.619547	
75%	1.158700e+08	1.158800e+08	1.162300e+08	1.162400e+08	61.000000	18.363478	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]
```

1. Given a loop, consider chr1, x1, x2, chr2, y1, y2
2. 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": peakLoopChiaLRad21PPairs,
        "filteredIndexes2": peakLoopHicLCtcfPPairs,
        "filename": "chiaRadHicLdCount",
    },
    {
        "loopDataset1": chiaPetLoops,
        "loopDataset2": hicLoops,
        "filteredIndexes1": peakLoopChiaLRad21PPairs,
        "filteredIndexes2": peakLoopHicLRad21PPairs,
        "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:
                    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")
```

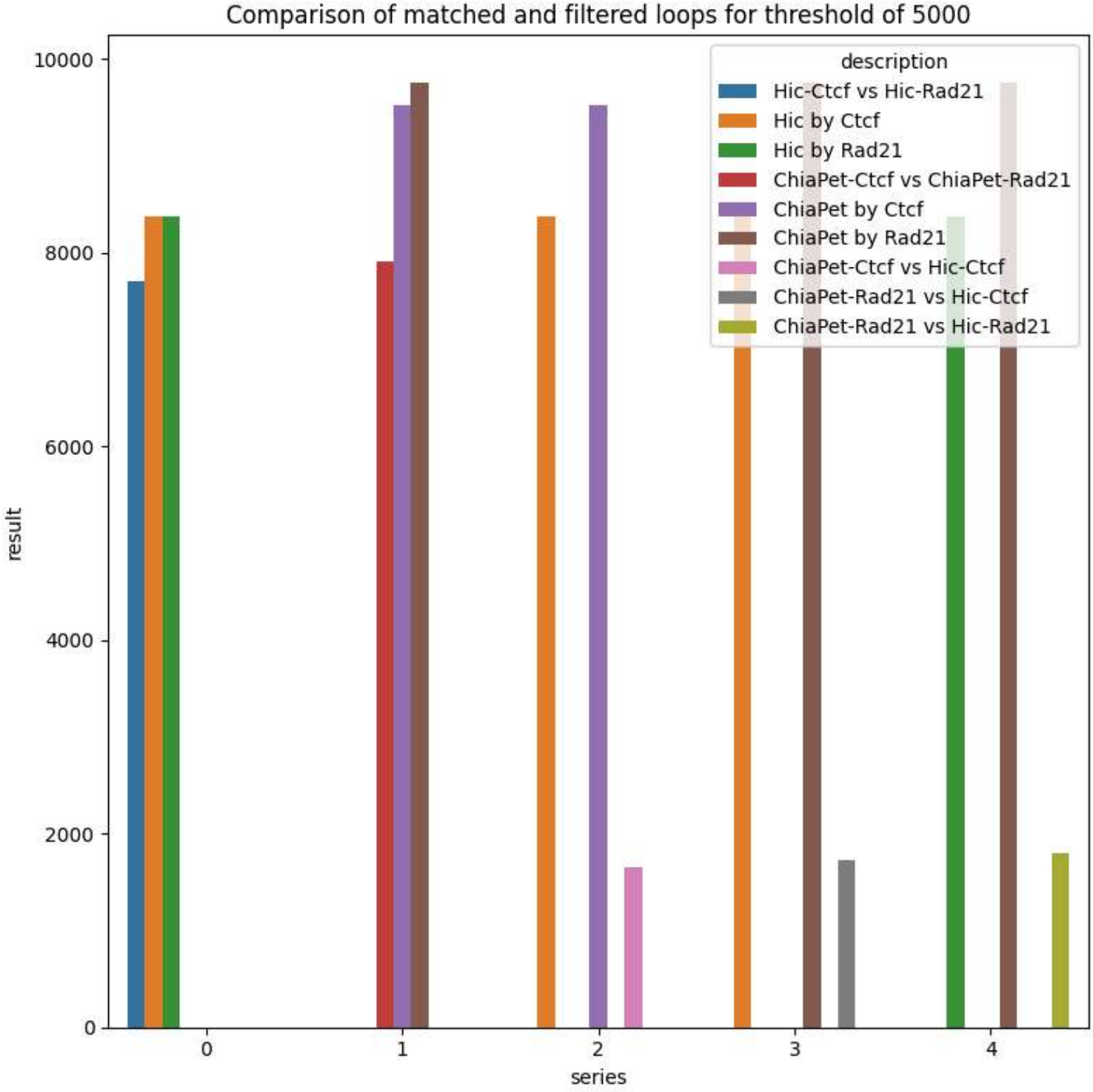
```
Hic filtered by Ctcf vs Hic filtered by Rad21
        Hic filtered by Ctcf total: 8374
        Hic filtered by Rad21 total: 8377
        Matched: 7707
        Matched (at least one anchor): 18817


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
```

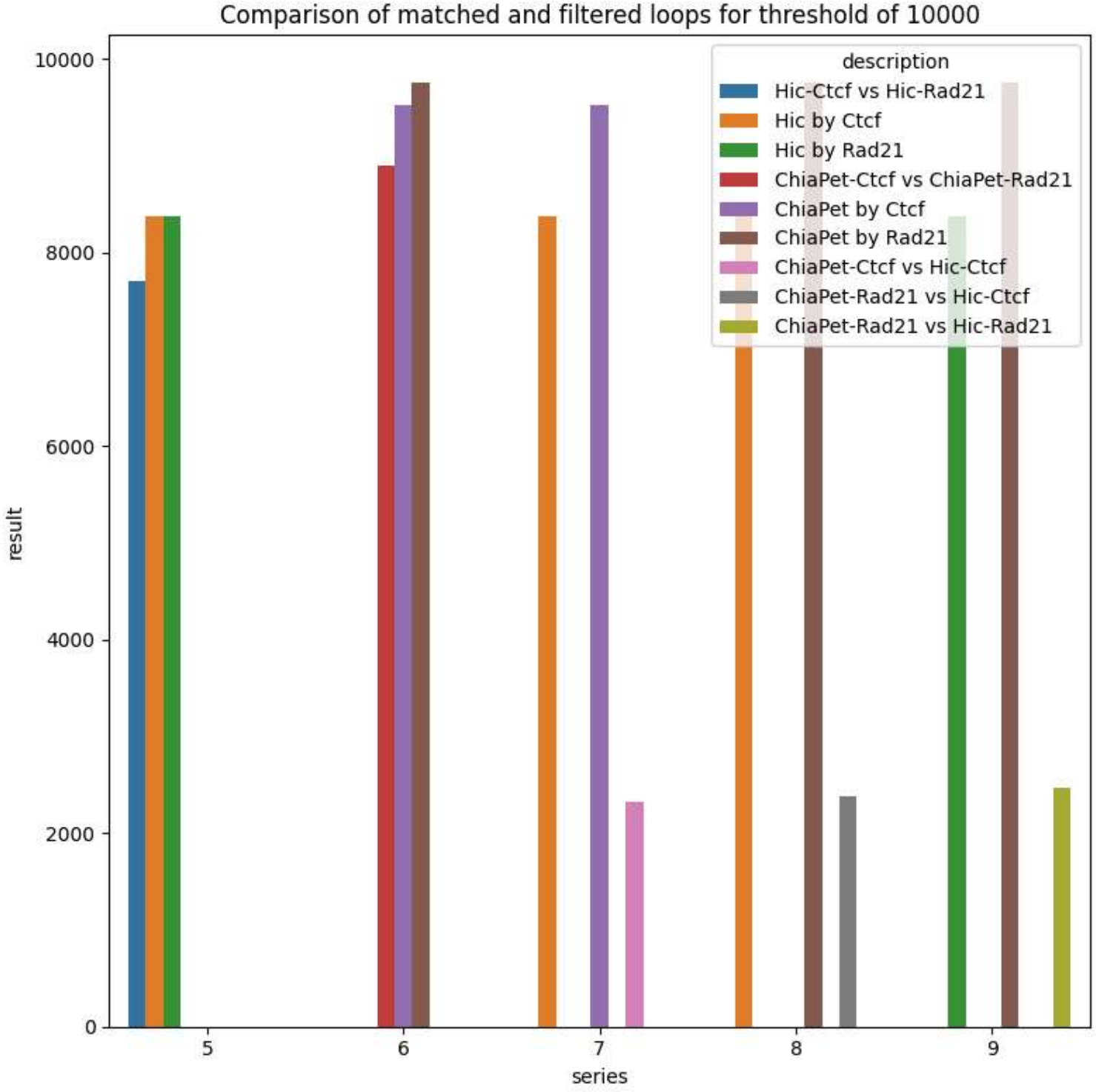
```
Matched: 2469
Matched (at least one anchor): 12083
```

```
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]])
```

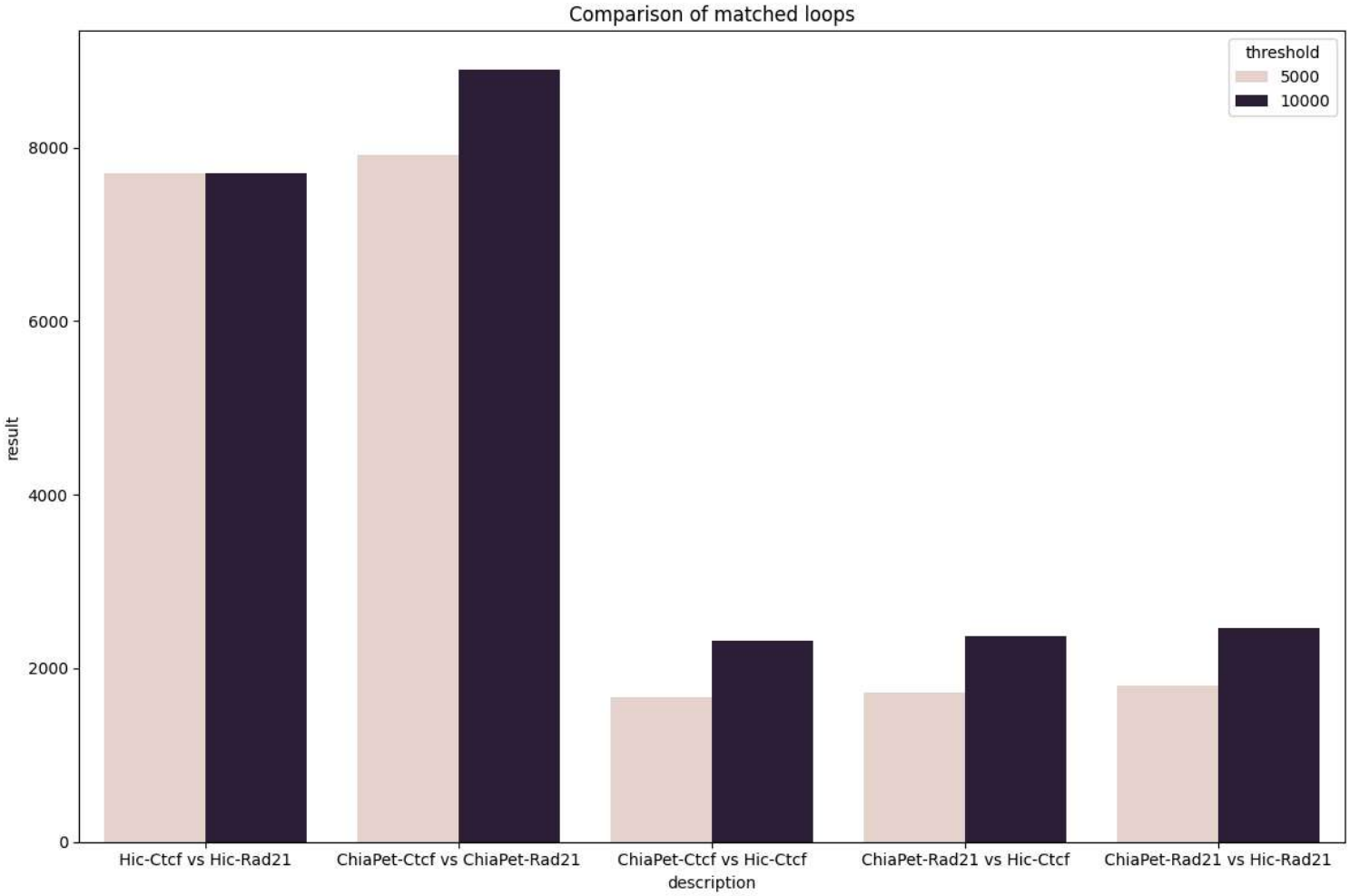
```
resultsBarDf = pd.DataFrame(
    resultsBar, columns=["description", "result", "series", "threshold"]
)
```

```
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="series",
    y="result",
    hue="description",
)
plt.tight_layout()
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="series",
    y="result",
    hue="description",
)
plt.tight_layout()
plt.show()
```

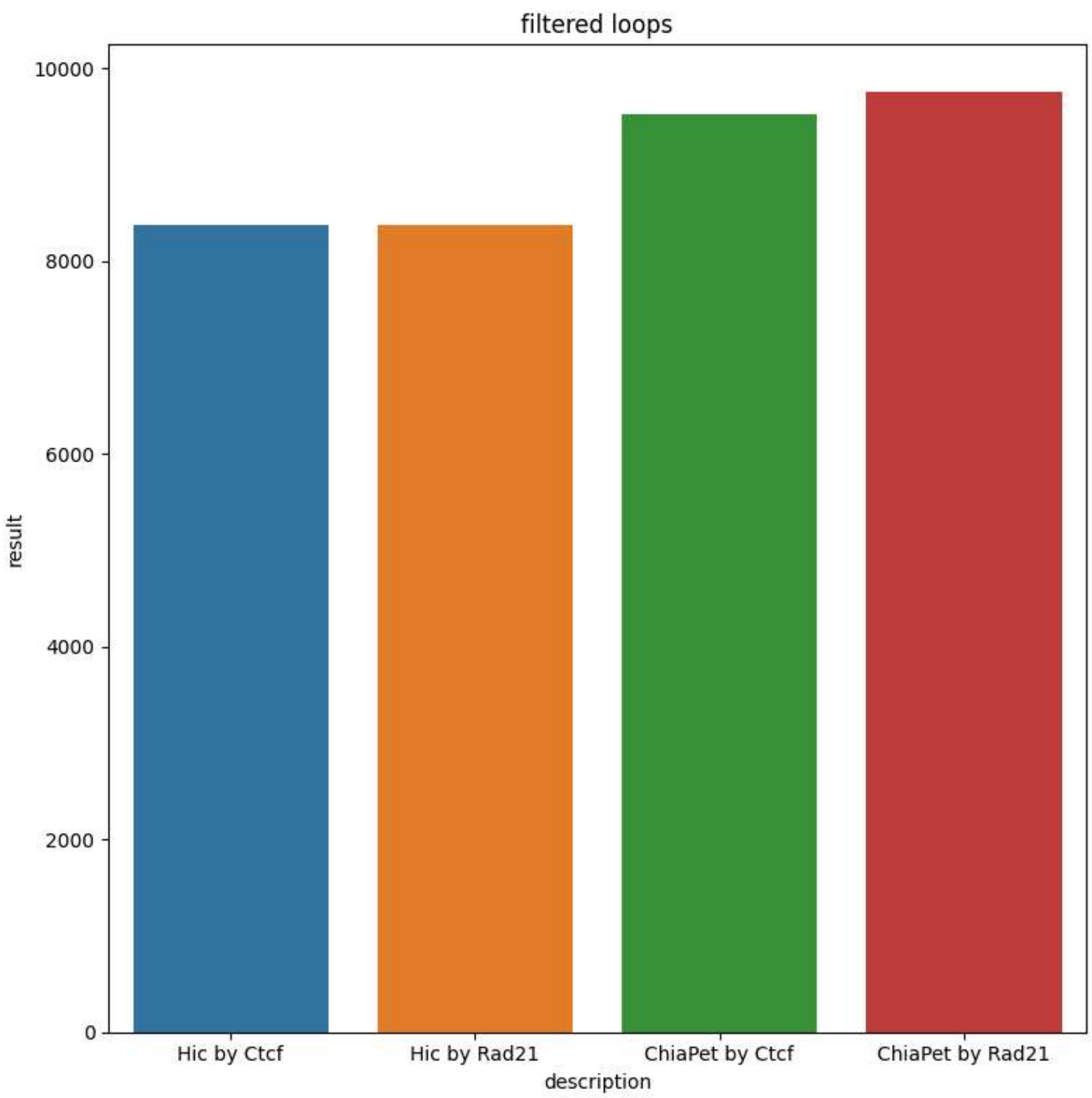

Comparison of matched and filtered loops for threshold of 5000
description
Hic-Ctcf vs Hic-Rad21
Hic by Ctcf
Hic by Rad21
ChiaPet-Ctcf vs ChiaPet-Rad21
ChiaPet by Ctcf
ChiaPet by Rad21
ChiaPet-Ctcf vs Hic-Ctcf
ChiaPet-Rad21 vs Hic-Ctcf
ChiaPet-Rad21 vs Hic-Rad21
result
series
0
2000
4000
6000
8000
10000
0
1
2
3
4




```
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()
```




```
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()
```

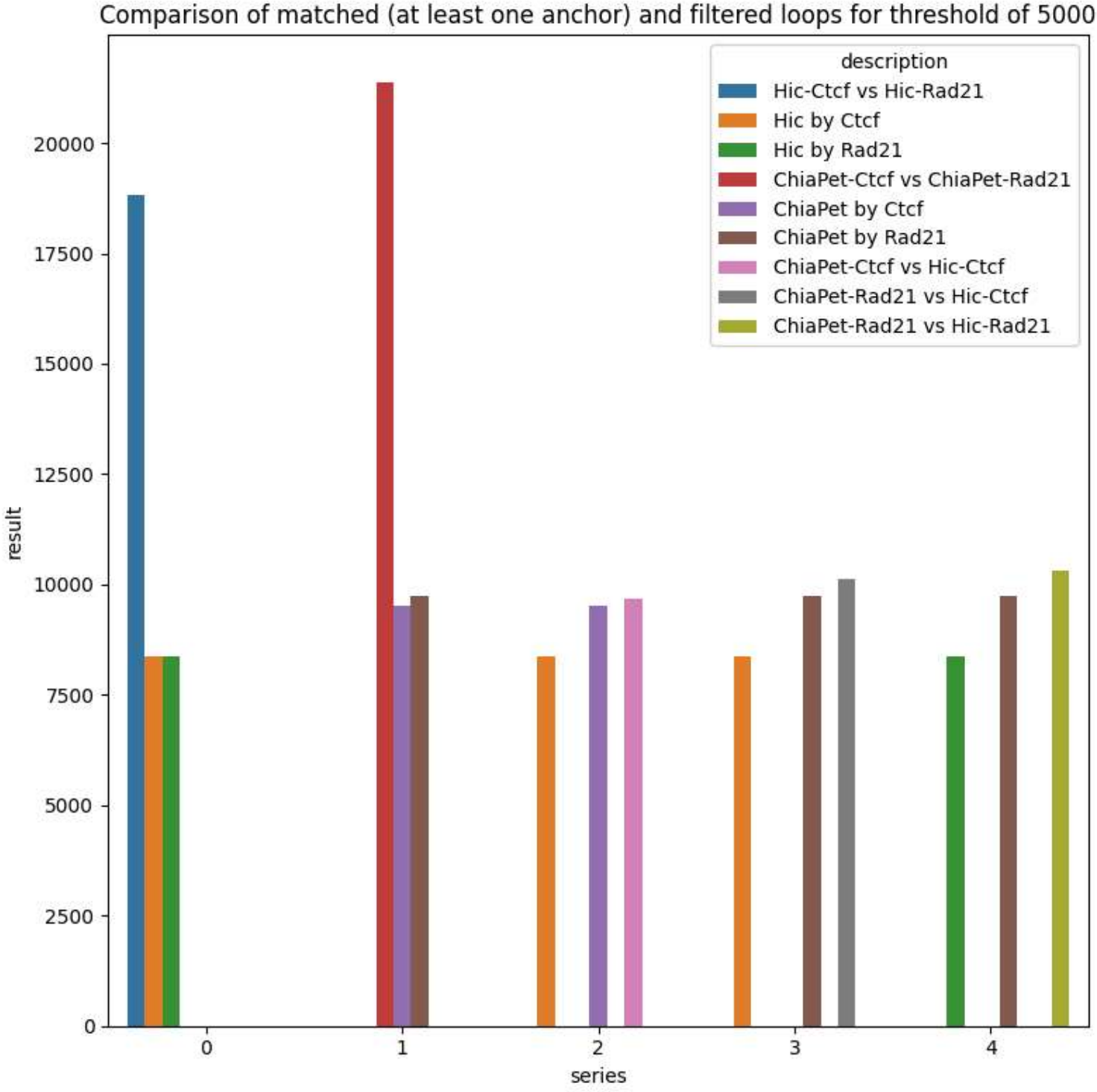


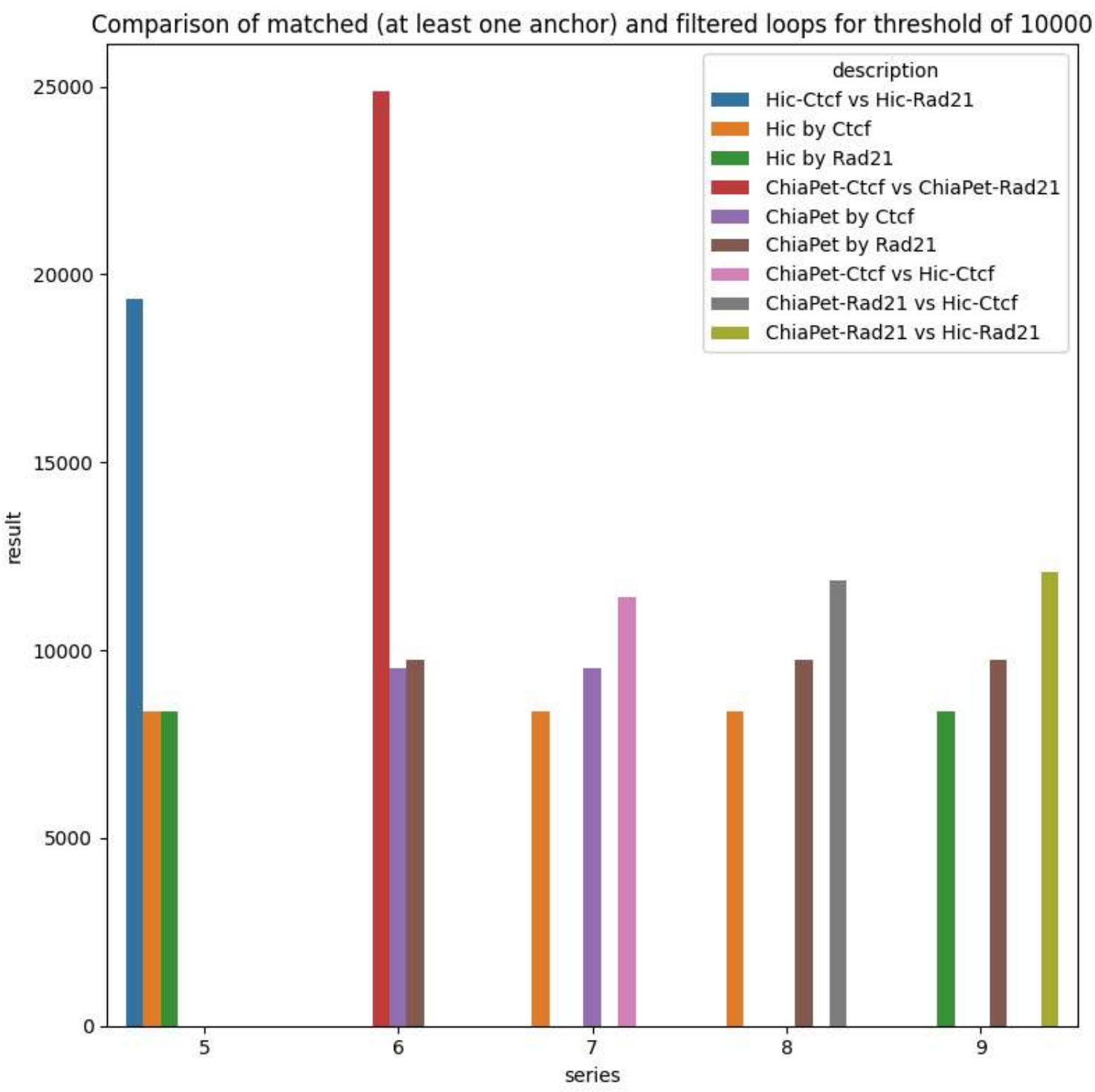

```
resultsBar = []
for i, result in enumerate(results):
    resultsBar.append(
        [
            result[3] + "-" + result[5] + " vs " + result[4] + "-" + result[6],
            result[8],
            i,
            result[7],
        ]
    )
    resultsBar.append([result[3] + " by " + result[5],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

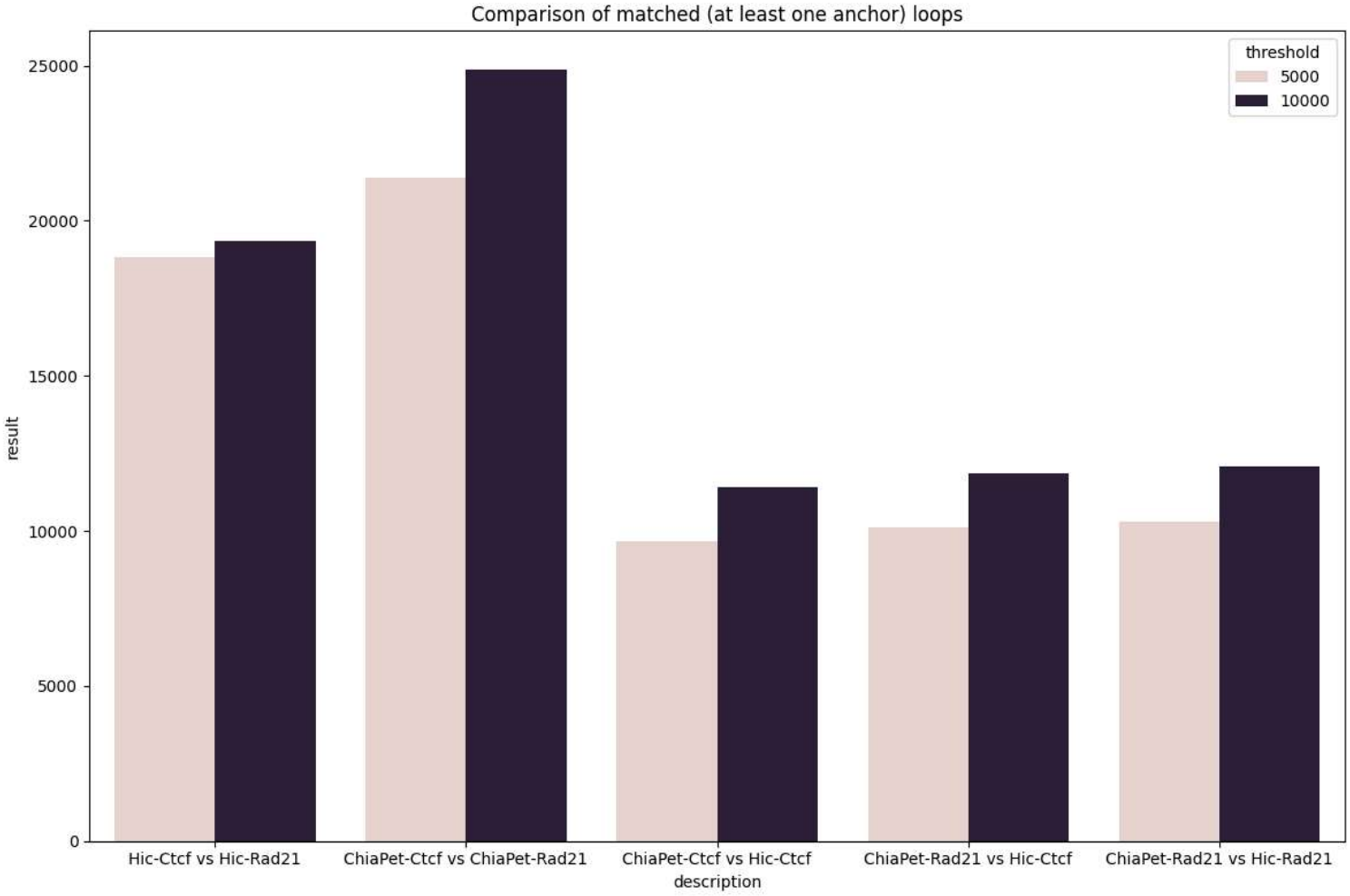
```
plt.figure(figsize=(8, 8))
plt.title(
    "Comparison of matched (at least one anchor) and filtered loops for threshold of 5000"
```

```
)

sns.barplot(
    data=resultsBarDf[resultsBarDf["threshold"] == 5000],
    x="series",
    y="result",
    hue="description",
)
plt.tight_layout()
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="series",
    y="result",
    hue="description",
)
plt.tight_layout()
plt.show()
```


Comparison of matched (at least one anchor) and filtered loops for threshold of 5000
description
Hic-Ctcf vs Hic-Rad21
Hic by Ctcf
Hic by Rad21
ChiaPet-Ctcf vs ChiaPet-Rad21
ChiaPet by Ctcf
ChiaPet by Rad21
ChiaPet-Ctcf vs Hic-Ctcf
ChiaPet-Rad21 vs Hic-Ctcf
ChiaPet-Rad21 vs Hic-Rad21
result
20000
17500
15000
12500
10000
7500
5000
2500
0
0
1
2
3
4
series



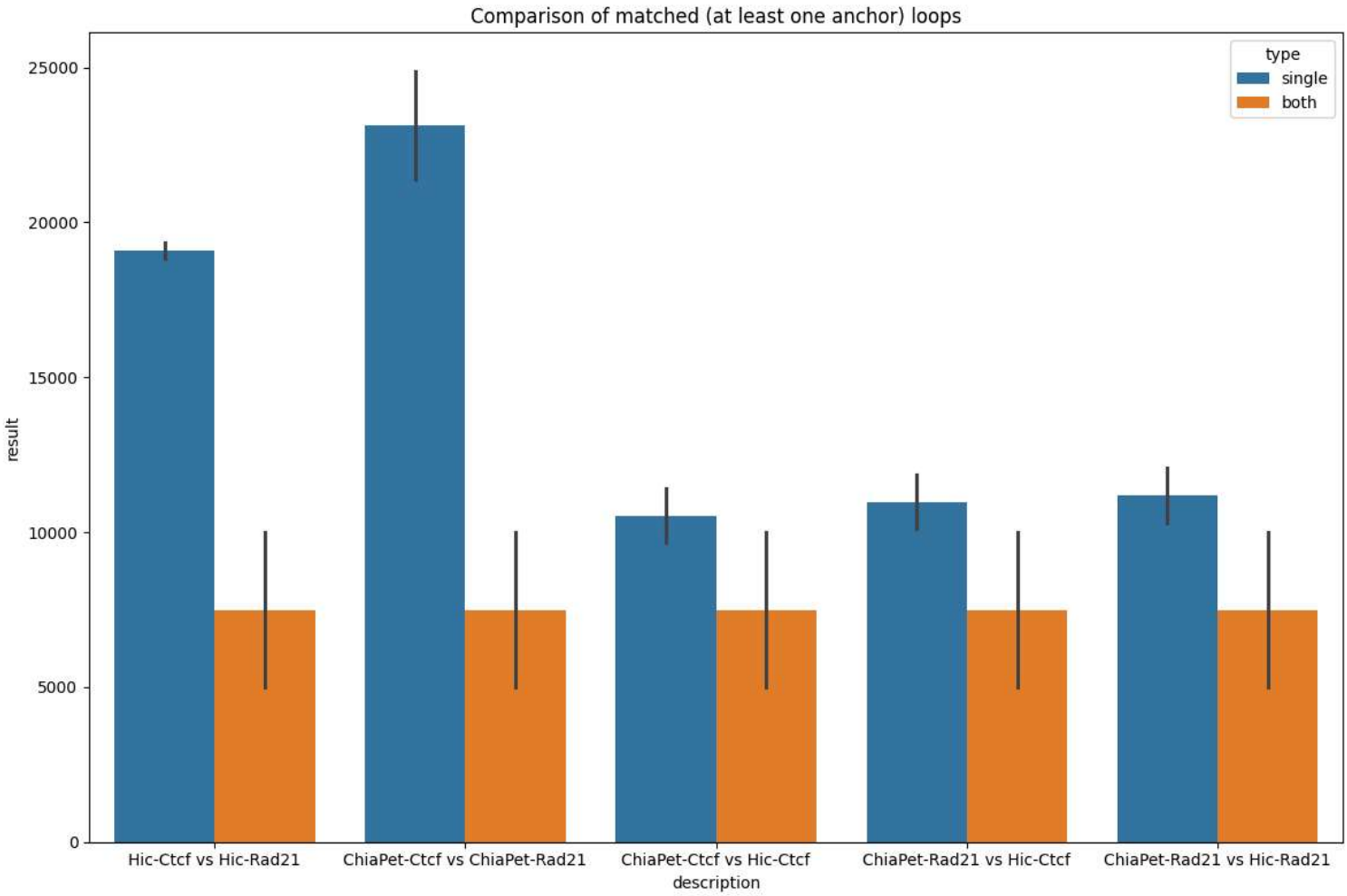

```
plt.figure(figsize=(12, 8))
plt.title("Comparison of matched (at least one anchor) loops")
filteredData = resultsBarDf[resultsBarDf["description"].str.contains("vs", na=False)]
sns.barplot(data=filteredData, x="description", y="result", hue="threshold")
plt.tight_layout()
plt.show()
```




```
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()
```



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
?              1
Name: 5191, dtype: object
```