Tutorial 12: Using SAM through ArrayTrack

SAM-Test

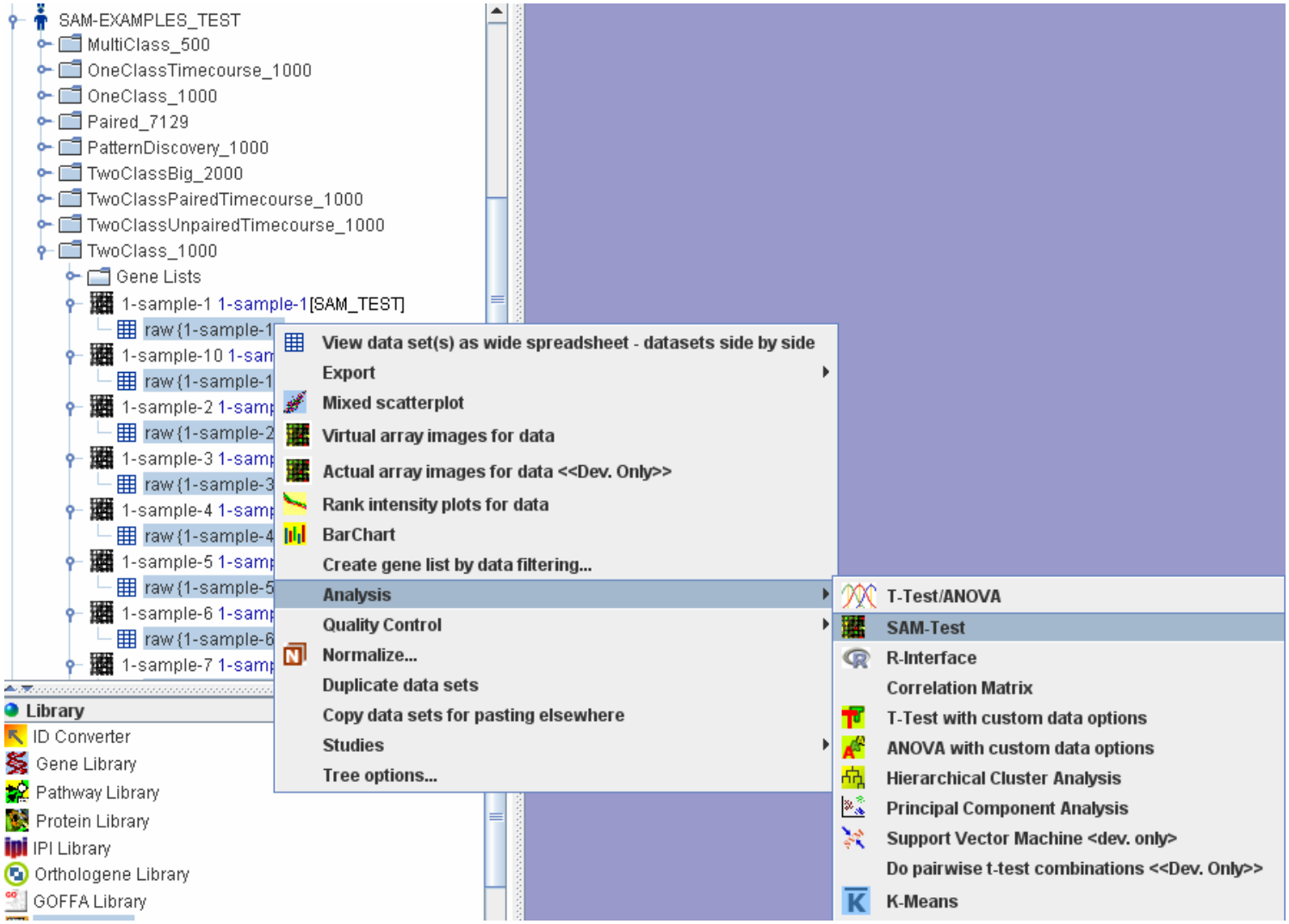
SAM (Significance Analysis of Microarrays) is an analysis tool for Identifying statistical significant genes in a set of microarray experiments.
http://www-stat.stanford.edu/~tibs/SAM/

Before using SAM-test tool in ArrayTrack, users should read SAM manual
http://www-stat.stanford.edu/~tibs/SAM/sam.pdf

The SAM tool in ArrayTrack includes following analysis types:

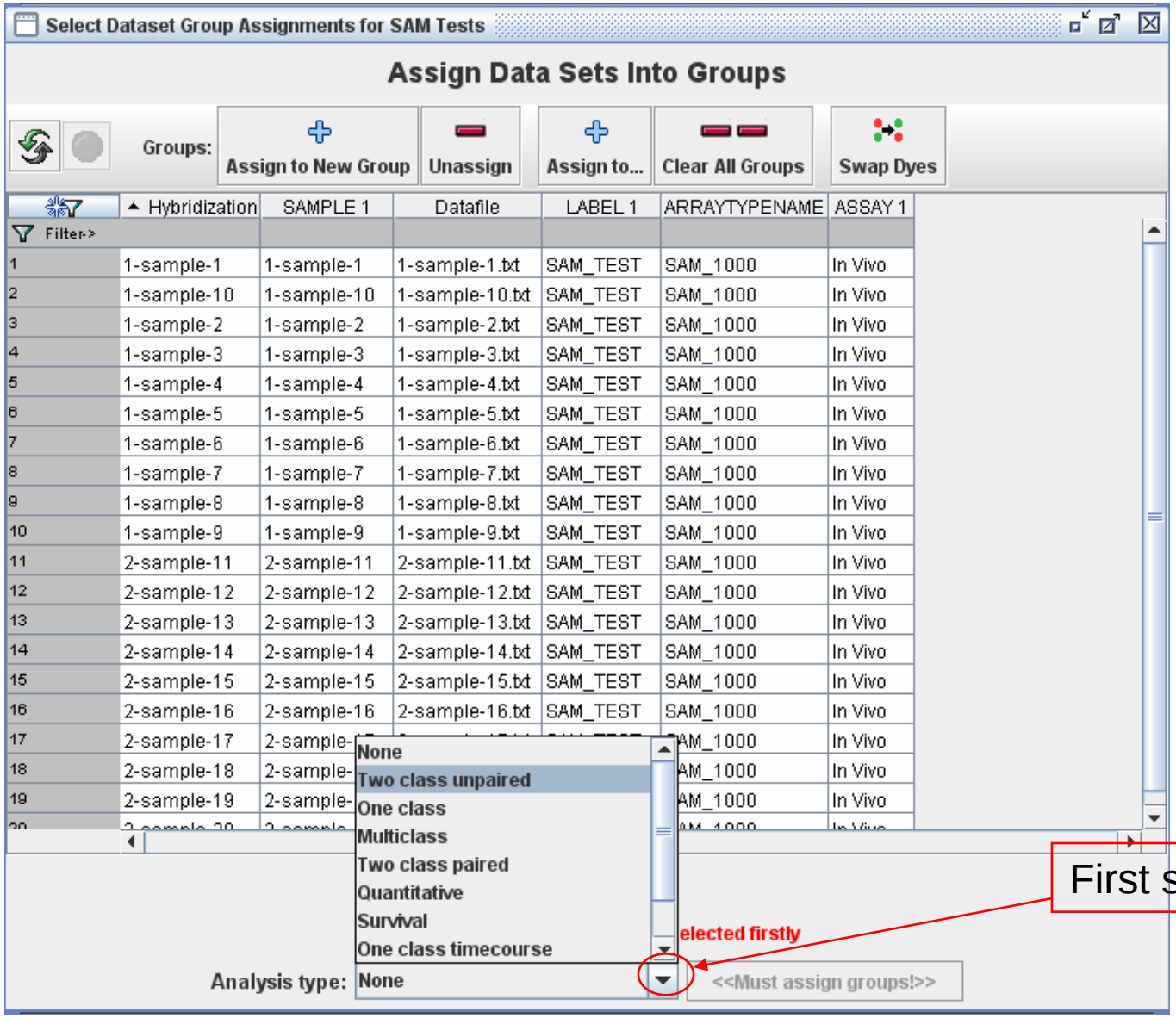
- Two class paired
- Two class unpaired
- One class
- Multi class
- Survival
- One class timecourse
- Two class unpaired timecourse
- Two class paired timecourse

SAM-Test: two class unpaired



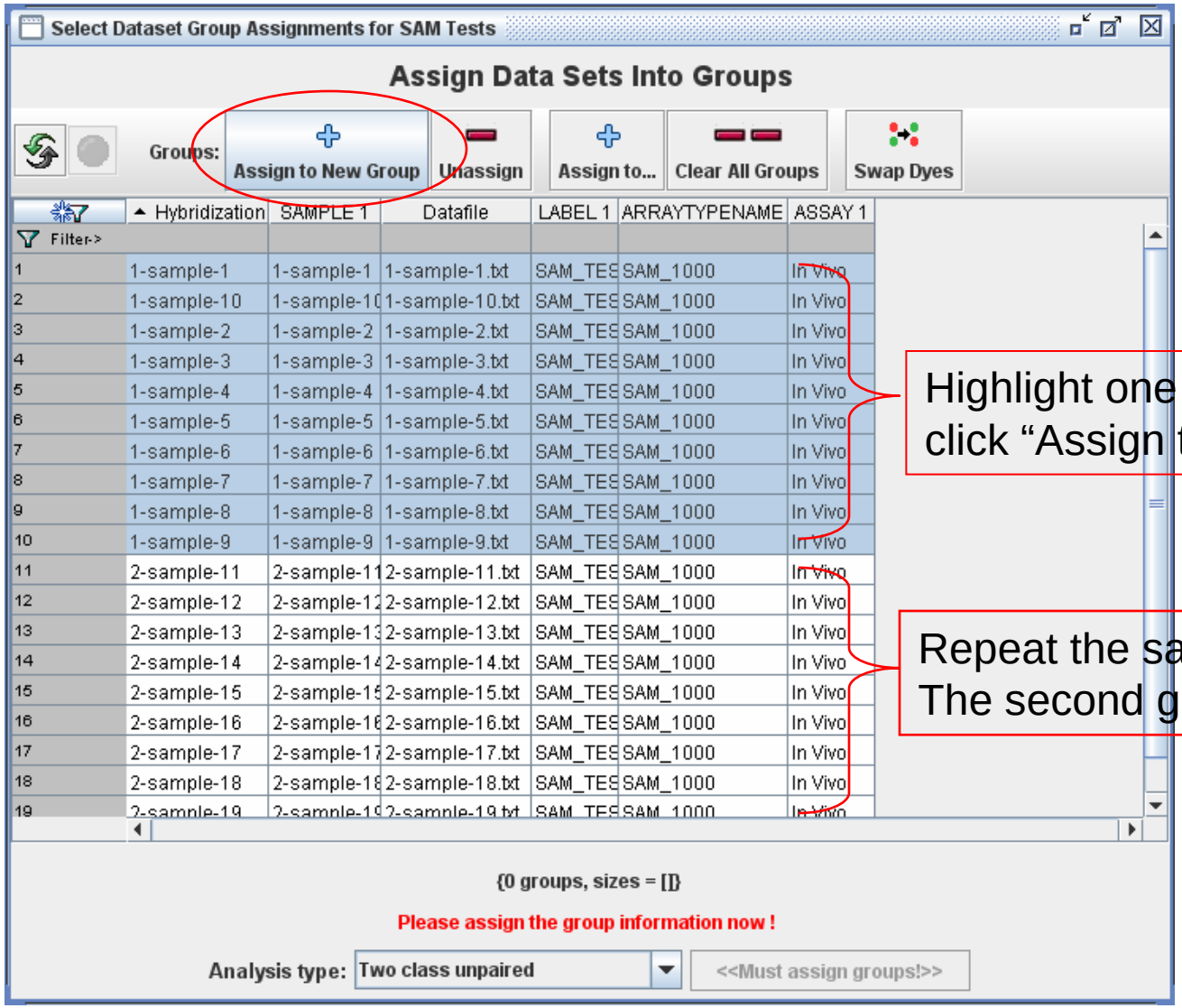
Select all the data, right-click, choose “Analysis -> SAM-Test”

SAM-Test: two class unpaired



First select analysis type

SAM-Test: two class unpaired

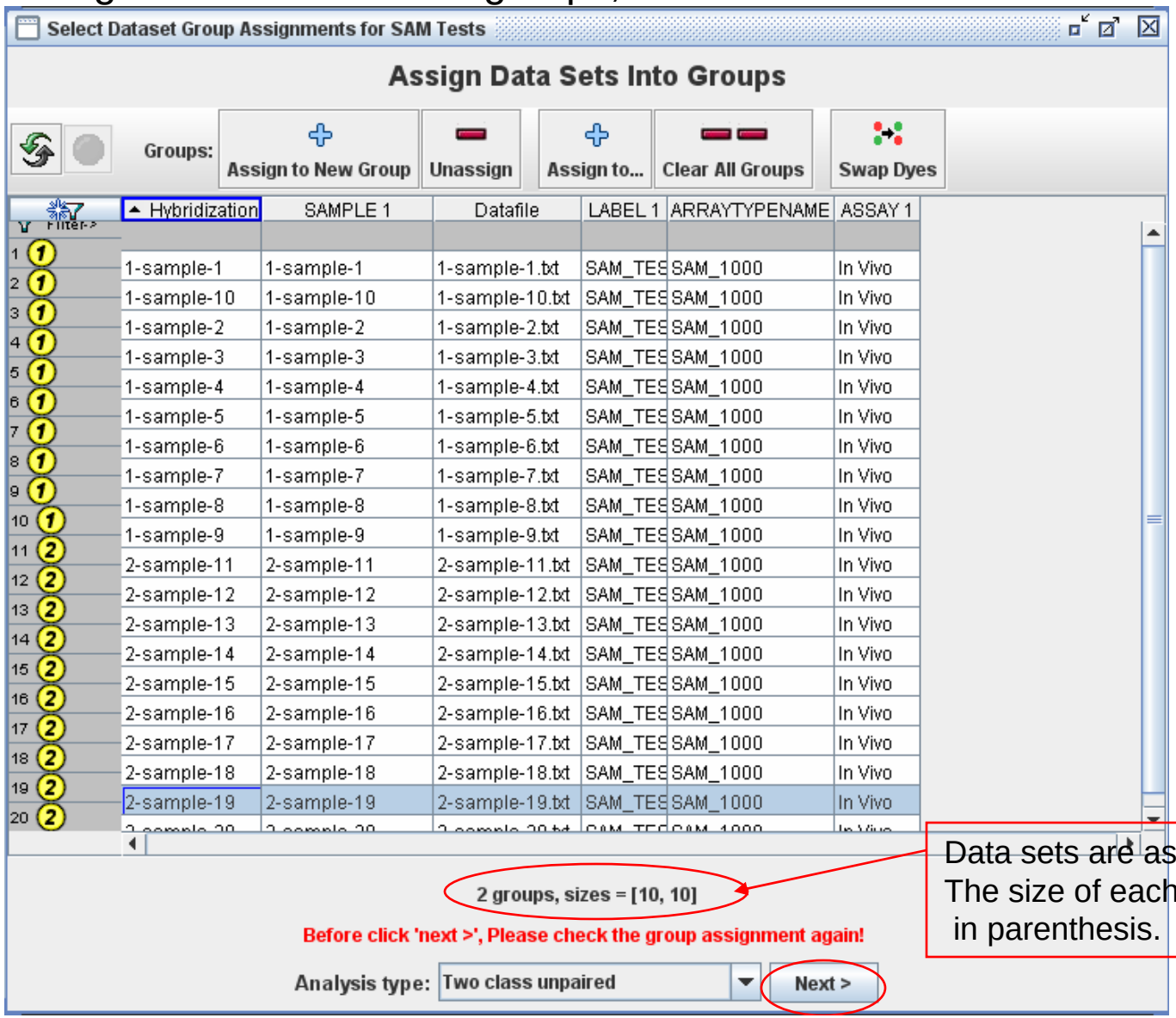


Highlight one group of data, then click “Assign to New Group” button.

Repeat the same step for assigning The second group.

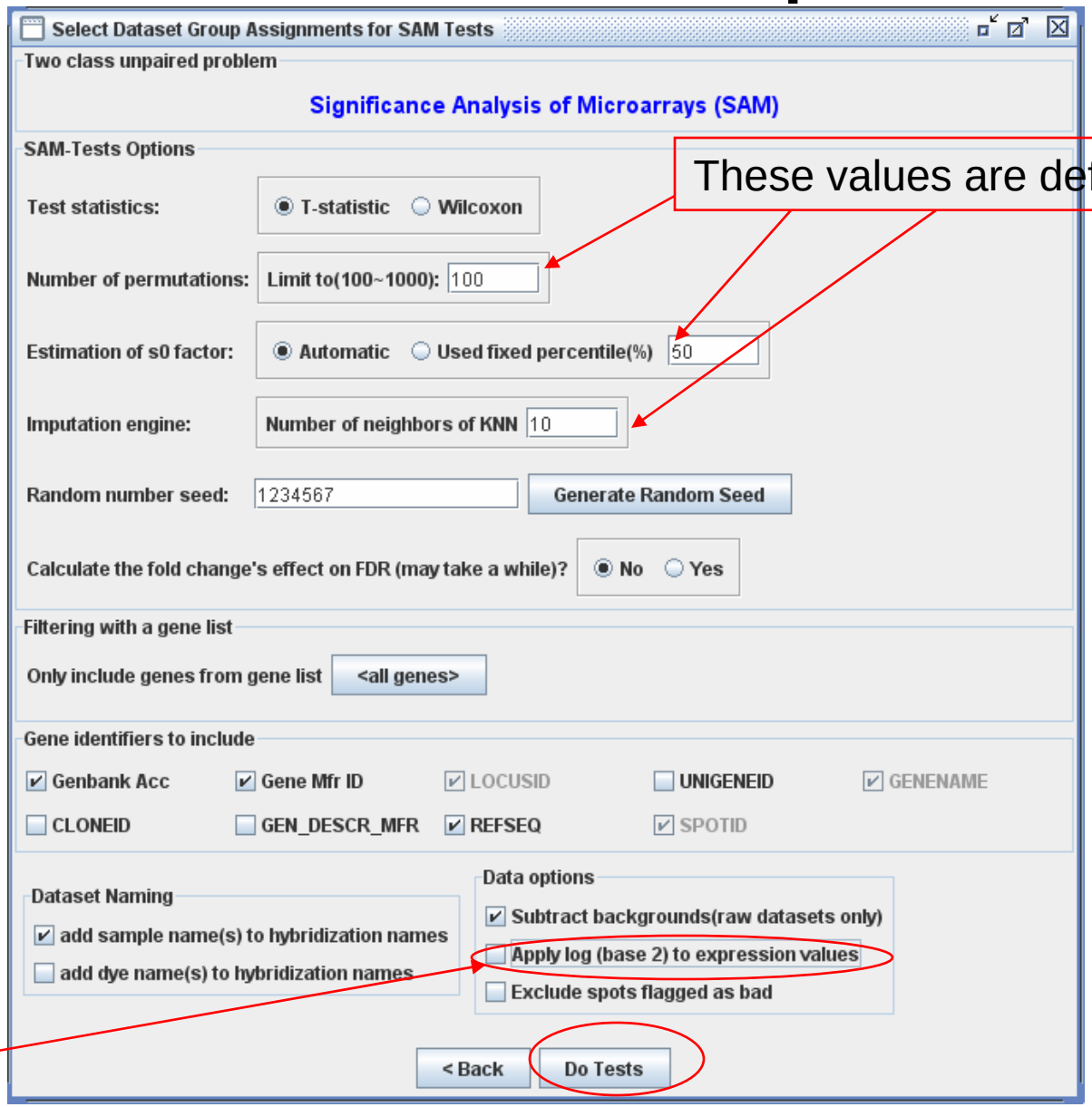
SAM-Test: two class unpaired

After assign data sets into two groups, click “Next” button.



Data sets are assigned to 2 groups. The size of each group is presented in parenthesis.

SAM-Test: two class unpaired



These values are default

If you use the sample data to compare with the SAM results in Excel, make sure “apply log…” is Unchecked.

SAM-Test: two class unpaired

SAM-Tests Results

File Selected-Spot All-Spots

	Genbank Acc	Gene Mfr ID	LOCUSID	GENENAME	REFSEQ	SPOTID	Observed s...	P value	Numerator(r)	Denominat...	Fold Change	q
1		GENE703				4661482	-0.0454	0.9194	-0.0565	1.2451	0.8345	89
2		GENE704				4661483	-0.1482	0.6589	-0.1534	1.0353	0.9822	84
3		GENE705				4661484	0.761	0.0832	0.9029	1.1864	2.2999	45
4		GENE706				4661485	-0.3265	0.4395	-0.3862	1.1827	0.7524	75
5		GENE707				4661486	0.0143	0.9672	0.0151	1.0555	0.9252	92
6		GENE708				4661487	0.5624	0.1804	0.651	1.1576	1.1782	86
7		GENE709				4661488	0.3802	0.3629	0.4447	1.1698	1.4819	91
8		GENE710				4661489	0.1115	0.7359	0.1147	1.029	1.0886	92
9		GENE711				4661490	-0.3565	0.3319	-0.3835	1.0757	0.8565	75
10		GENE712				4661491	0.1968	0.6172	0.2226	1.1314	1.1666	91
11		GENE713				4661492	0.1229	0.7774	0.1493	1.2145	1.0299	92
12		GENE714				4661493	-2.927	0	-3.4858	1.1909	0.0855	0
13		GENE715				4661494	-0.5412	0.1842	-0.6168	1.1398	0.5658	63
14		GENE716				4661495	-0.6519	0.0836	-0.7026	1.0778	0.6399	58
15		GENE717				4661496	-0.0329	0.9406	-0.0405	1.2304	1.0624	90
16		GENE718				4661497	-0.0177	0.9649	-0.0204	1.1509	1.1047	90
17		GENE719				4661498	-0.159	0.7136	-0.1913	1.2032	0.6056	84
18		GENE720				4661499	-0.5584	0.1313	-0.5993	1.0732	0.6625	63
19		GENE721				4661500	-0.5336	0.2539	-0.6746	1.2642	0.4535	63
20		GENE722				4661501	0.3128	0.4216	0.3501	1.1193	1.3825	91
21		GENE723				4661502	-0.6569	0.1064	-0.7384	1.124	0.5101	58
22		GENE724				4661503	0.2127	0.638	0.2648	1.2449	1.5199	91
23		GENE725				4661504	0.0909	0.8039	0.0987	1.0859	1.0696	92
24		GENE726				4661505	-1.6399	0.0006	-1.7439	1.0634	0.375	0
25		GENE727				4661506	0.3239	0.353	0.3405	1.0513	1.2123	91
26		GENE728				4661507	-0.2093	0.6108	-0.2434	1.1631	0.9654	80
27		GENE729				4661508	0.329	0.4524	0.3995	1.2143	1.4442	91
28		GENE730				4661509	0.0478	0.9102	0.0569	1.1914	1.1592	92

1000 genes

Significance Filtering

Target False Discovery Rate (FDR): Delta =

Select # genes by largest SAM absolute score

Mean Channel Intensities > Bad Flags <=

Abs Fold Change >

Apply Filters Clear Filters

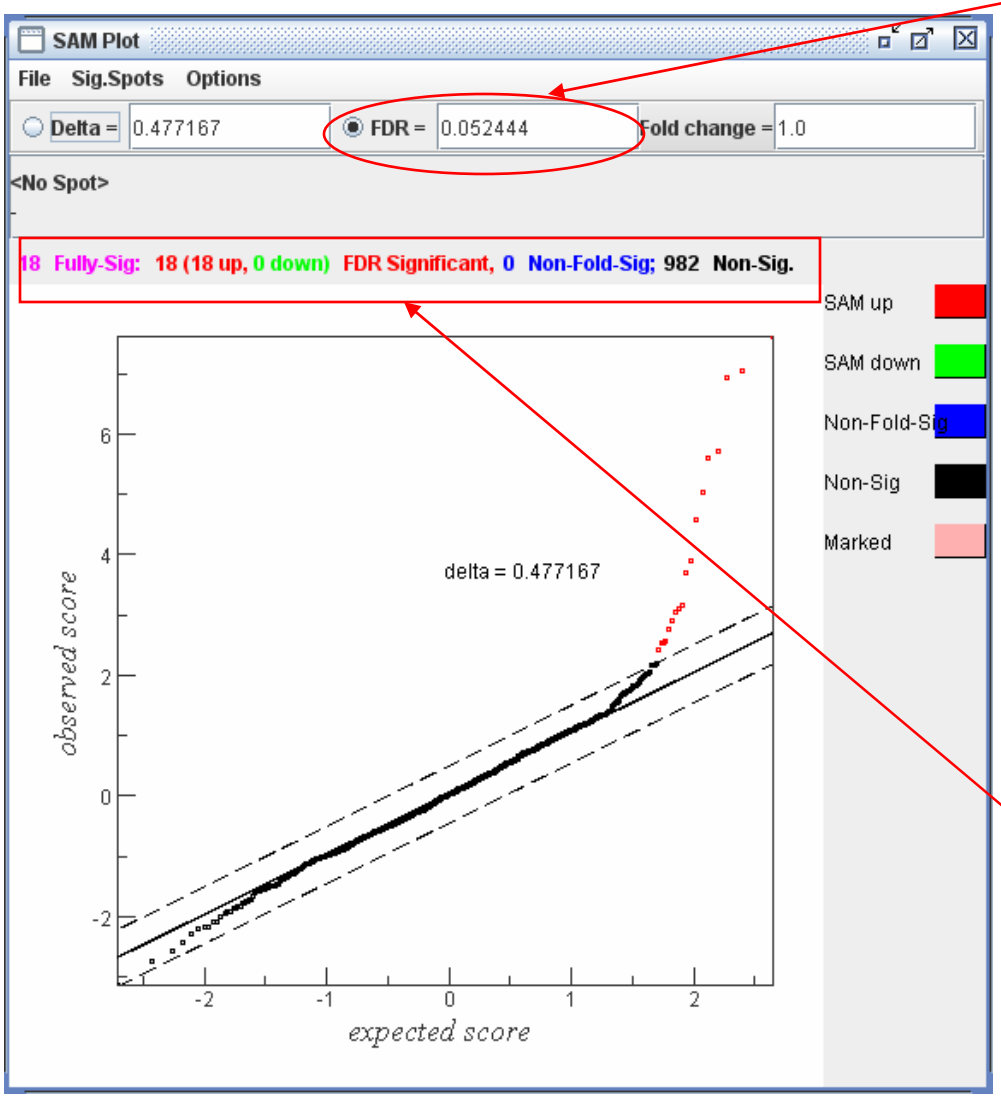
Create Sig. Gene List HCA PCA K-Means SAM Plot

Click SAM Plot button

SAM-Test: two class unpaired

This is the SAM plot

The default FDR <0.05.

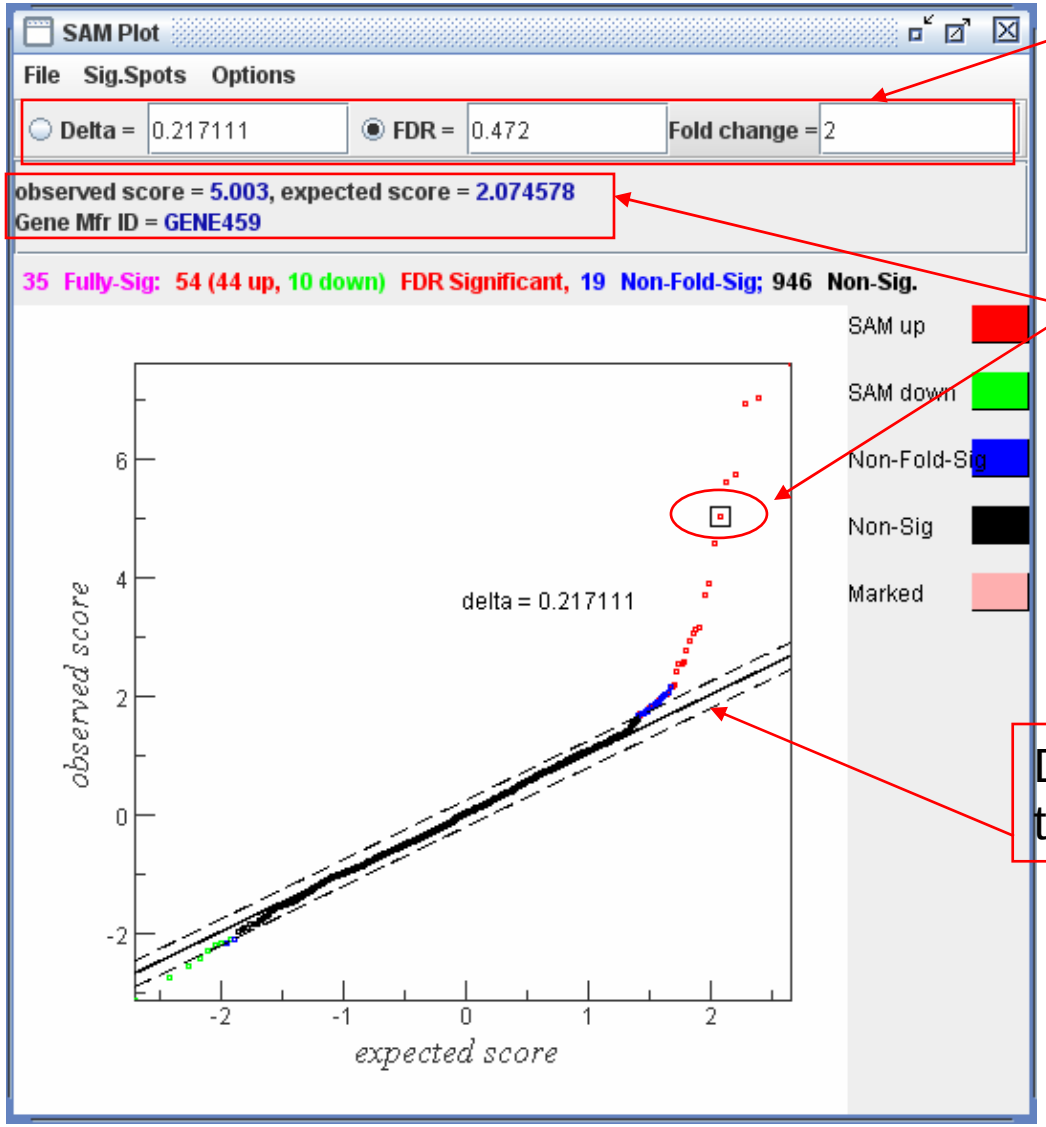


Color legend:
Red – SAM up
Green – SAM down
Blue – non fold significant
Black – non significant
Pink - marked

Display the numbers for significant genes according to the current delta, FDR and fold change values.

SAM-Test: two class unpaired

SAM Plot

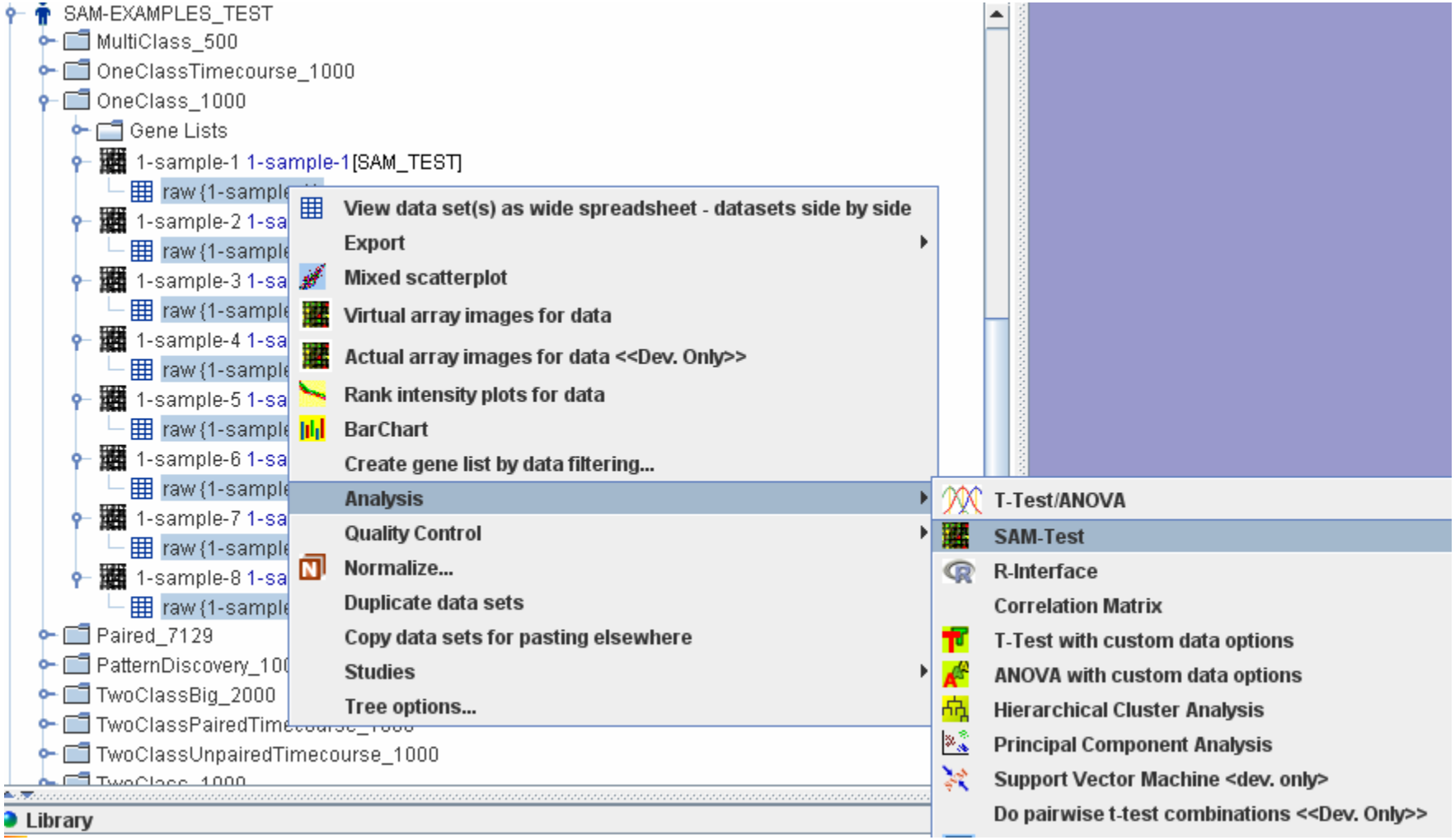


Users can type in numbers for Delta, FDR and fold change

Move mouse over a spot, the score value and gene name will be shown.

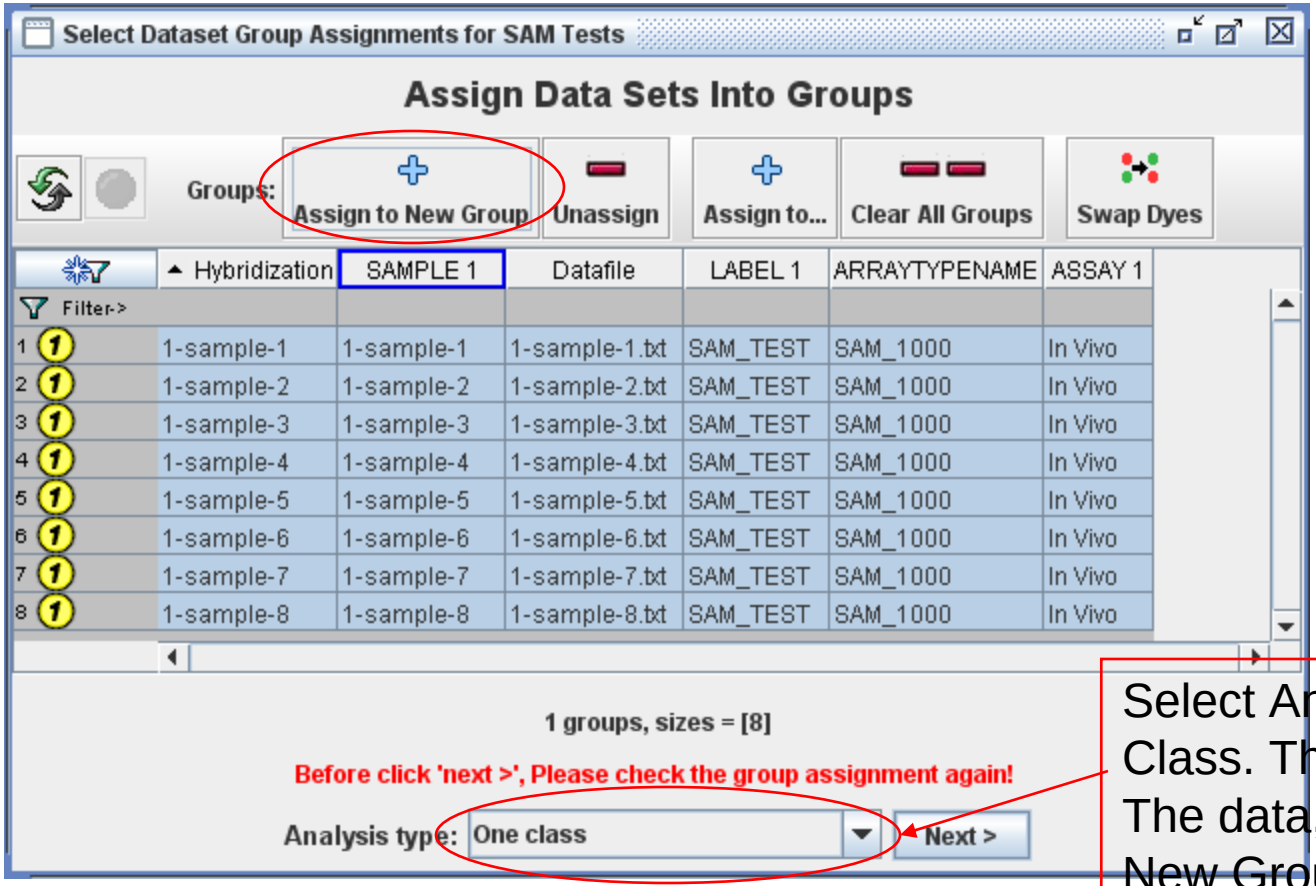
Dragging the dash line will change the delta, FDR value.

SAM-test: One class



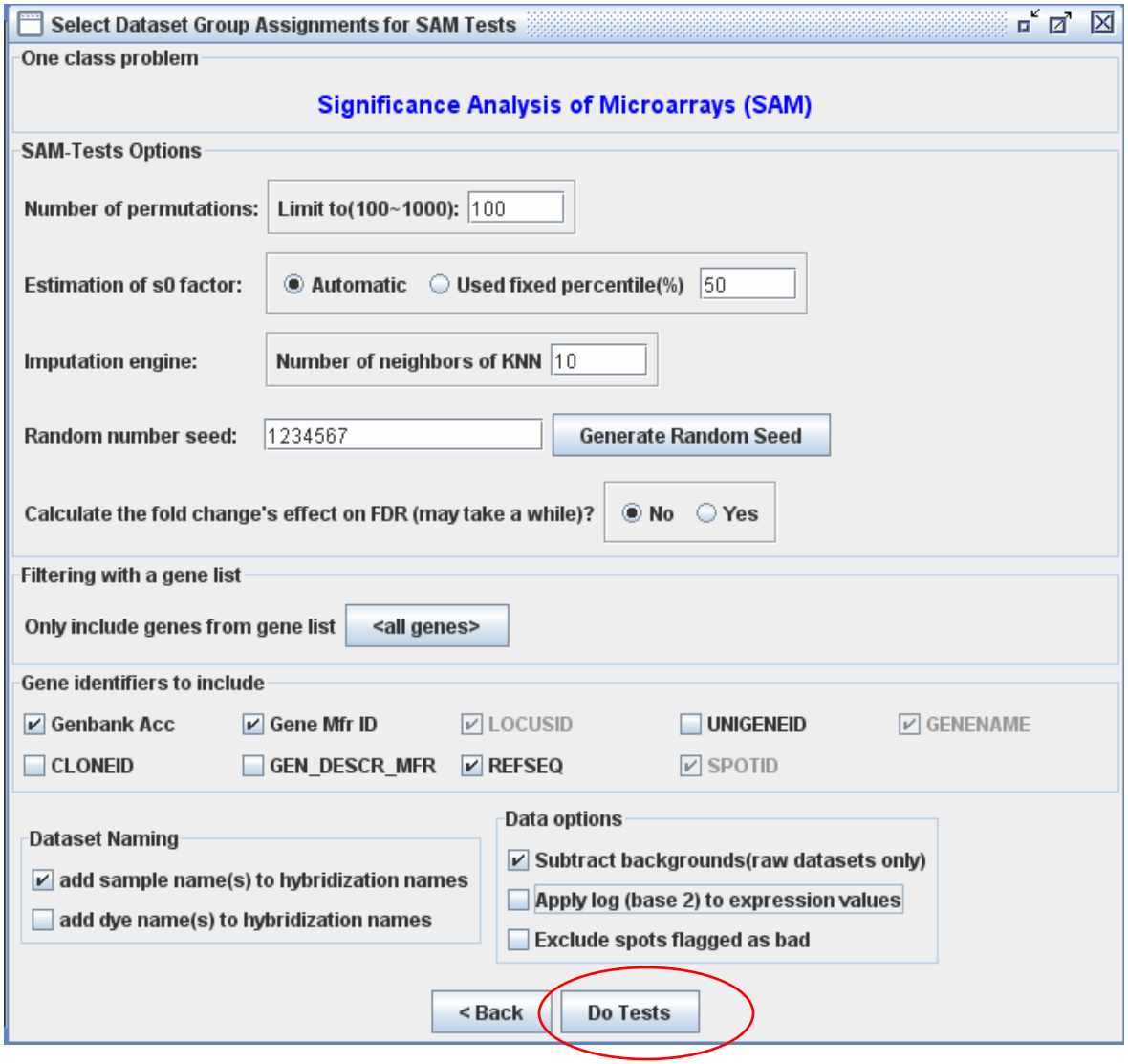
Right-click the selected data set, choose “Analysis” -> SAM-Test.

SAM-test: One class



Select Analysis type – One Class. Then highlight all The data, click “Assign to New Group” button.

SAM-test: One class



The value in the text boxes are default. Click “Do Tests” button.

SAM-test: One class

SAM-Tests Results

File Selected-Spot All-Spots

	Gene Mfr ID	Observed score (d)	P value	Numerator(r)	Denominat...	GEN...	q-value(%)	REF...	SPOTID
1	GENE703	-0.3922		-0.5909	1.5068		5.9055		4661482
2	GENE704	-0.4424	0.1608	-0.6147	1.3895		5.9055		4661483
3	GENE705	-0.2094	0.5751	-0.2568	1.2264		10.9112		4661484
4	GENE706	-0.468	0.3963	-0.741	1.5833		5.9055		4661485
5	GENE707	-0.1579		-0.1847	1.17		10.9112		4661486
6	GENE708	-0.7139	0.1181	-1.2662	1.7738		1.4605		4661487
7	GENE709	-0.5778	0.0789	-0.8629	1.4934		2.496		4661488
8	GENE710	-0.2387	0.6411	-0.3496	1.4643		10.334		4661489
9	GENE711	-0.4595	0.2318	-0.7098	1.5445		5.9055		4661490
10	GENE712	0.283	0.0852	0.3731	1.3186		14.253		4661491
11	GENE713	-0.1933		-0.2218	1.1474		10.9112		4661492
12	GENE714	-0.4287	0.3627	-0.6128	1.4294		5.9055		4661493
13	GENE715	-0.5146	0.2931	-0.9513	1.8486		3.1854		4661494
14	GENE716	-0.4829	0.1603	-0.7646	1.5834		3.1854		4661495
15	GENE717	0.4599	0.0169	0.6108	1.3282		12.4867		4661496
16	GENE718	-0.5346	0.3272	-1.0246	1.9166		3.1854		4661497
17	GENE719	0.0668	0.5303	0.0971	1.454		14.253		4661498
18	GENE720	-0.8768	0.1351	-1.6637	1.8975		0		4661499
19	GENE721	-0.3551		-0.494	1.3915		6.6517		4661500

1000 genes

Significance Filtering

Target False Discovery Rate (FDR): Delta =

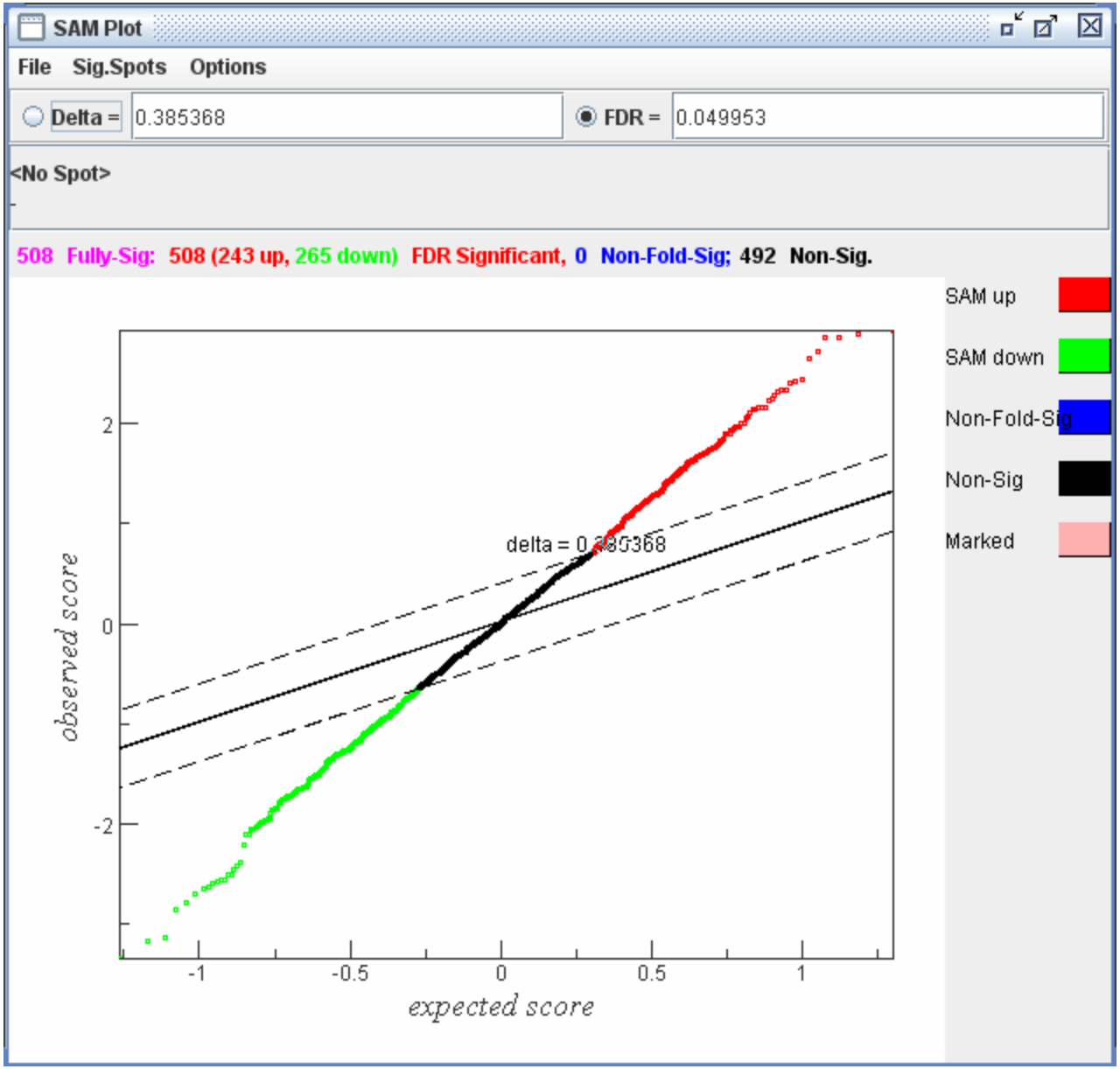
Select # genes by largest SAM absolute score

Mean Channel Intensities > Bad Flags <=

Apply Filters Clear Filters

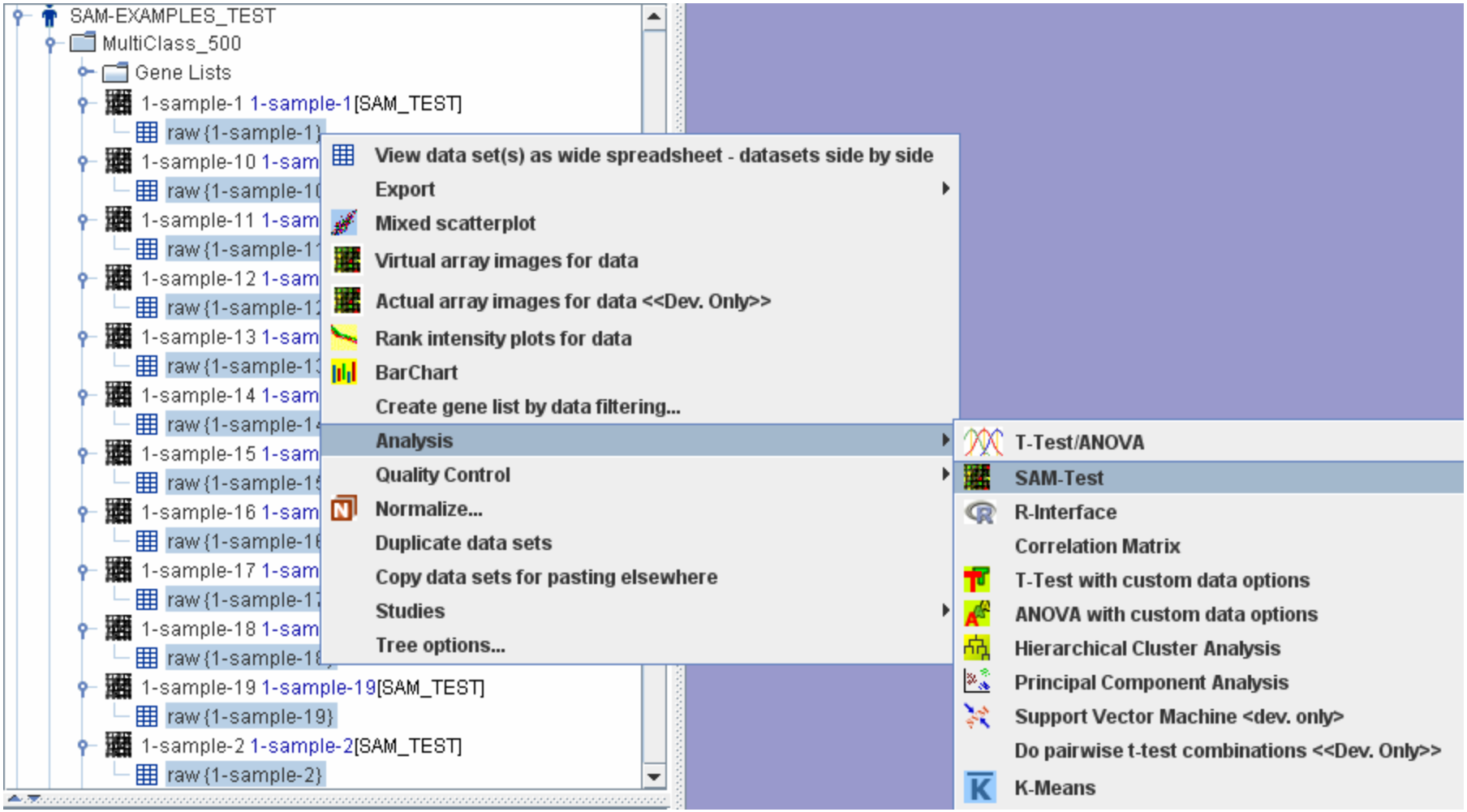
Create Sig. Gene List HCA PCA K-Means SAM Plot

SAM-test: One class

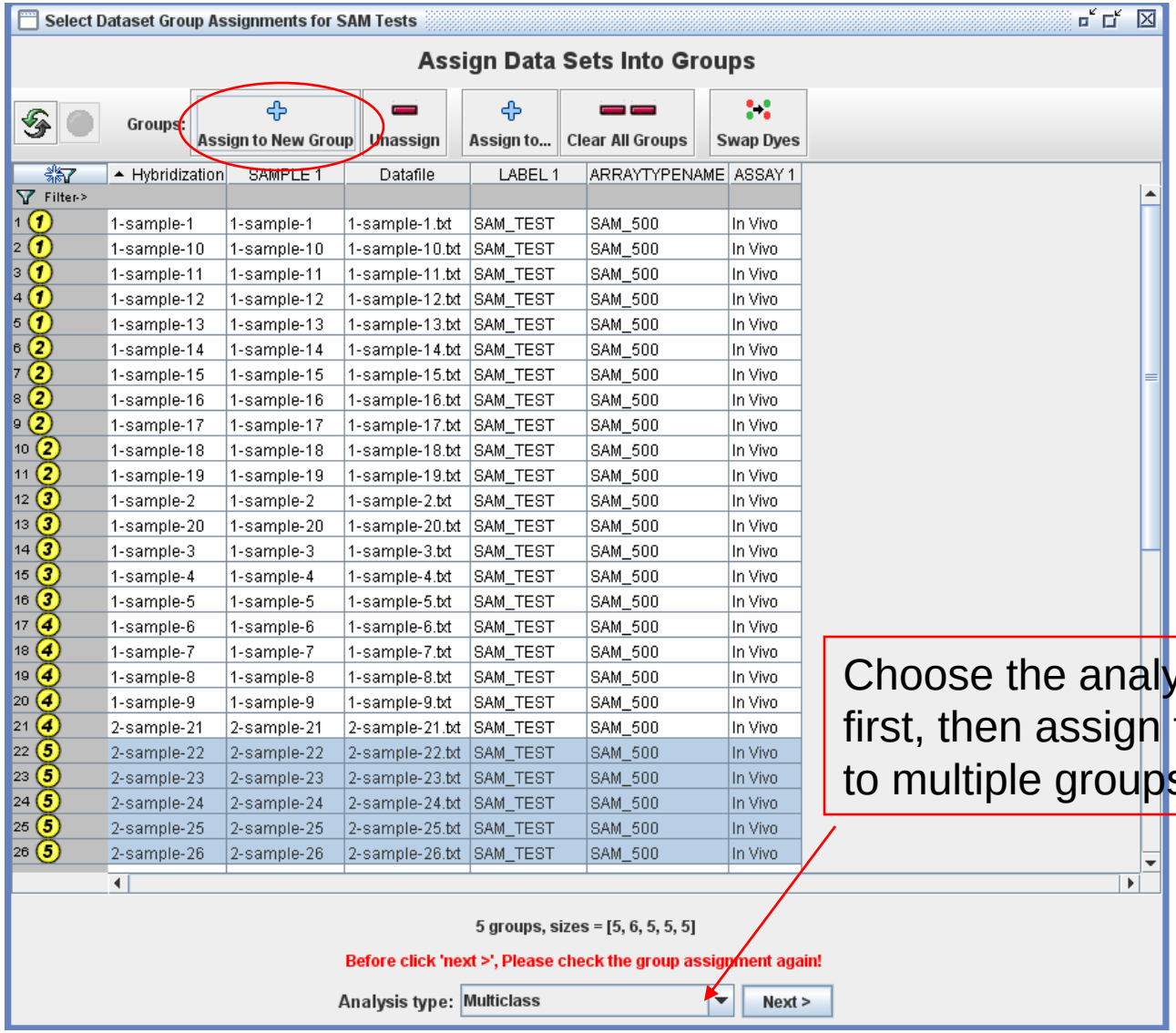


SAM-test: MultiClass

Right-click the selected data set, choose “Analysis” ->SAM-Test



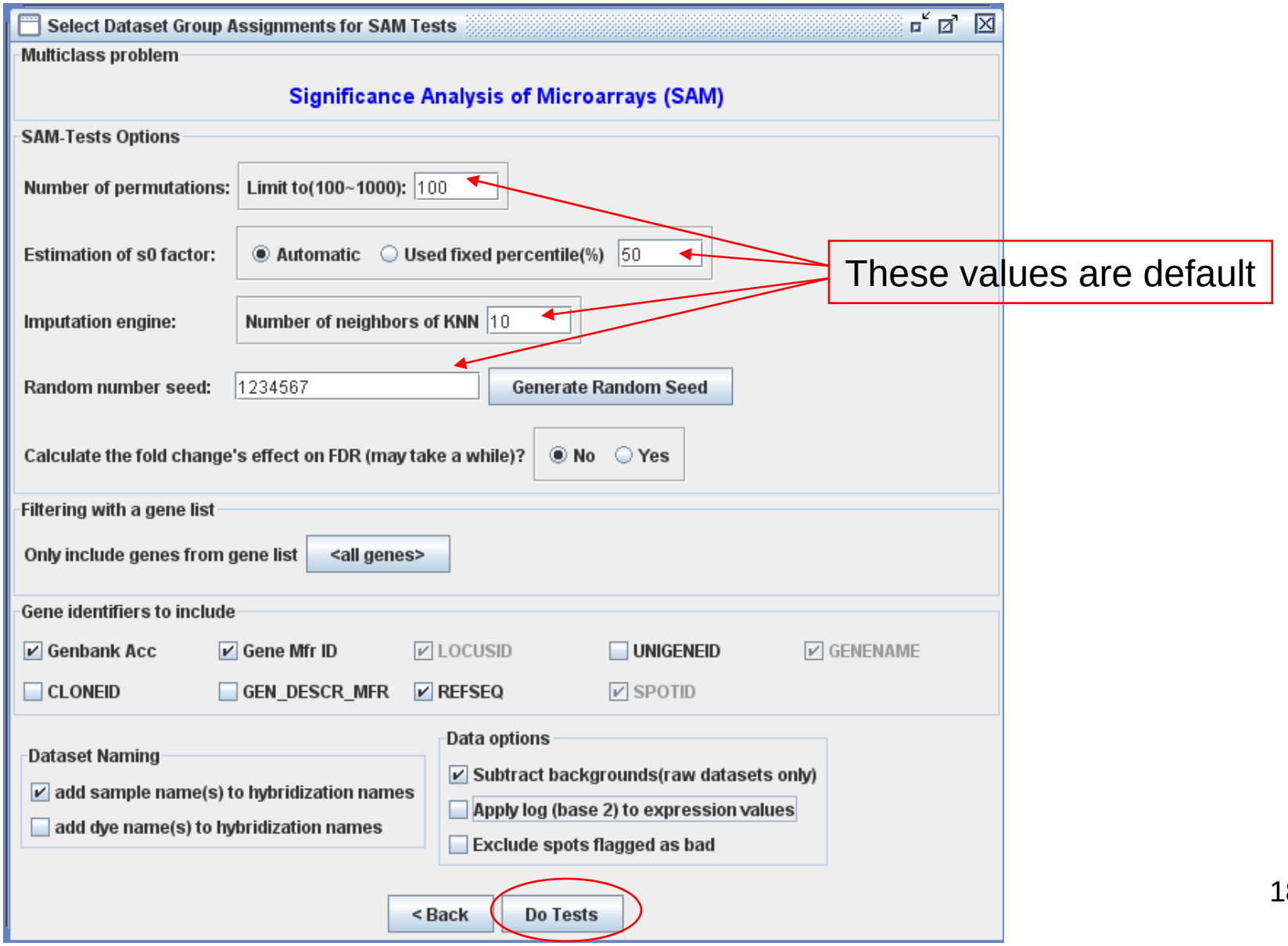
SAM-test: MultiClass



		Hybridization	SAMPLE 1	Datafile	LABEL 1	ARRAYTYPENAME	ASSAY 1
1	1	1-sample-1	1-sample-1	1-sample-1.txt	SAM_TEST	SAM_500	In Vivo
2	1	1-sample-10	1-sample-10	1-sample-10.txt	SAM_TEST	SAM_500	In Vivo
3	1	1-sample-11	1-sample-11	1-sample-11.txt	SAM_TEST	SAM_500	In Vivo
4	1	1-sample-12	1-sample-12	1-sample-12.txt	SAM_TEST	SAM_500	In Vivo
5	1	1-sample-13	1-sample-13	1-sample-13.txt	SAM_TEST	SAM_500	In Vivo
6	2	1-sample-14	1-sample-14	1-sample-14.txt	SAM_TEST	SAM_500	In Vivo
7	2	1-sample-15	1-sample-15	1-sample-15.txt	SAM_TEST	SAM_500	In Vivo
8	2	1-sample-16	1-sample-16	1-sample-16.txt	SAM_TEST	SAM_500	In Vivo
9	2	1-sample-17	1-sample-17	1-sample-17.txt	SAM_TEST	SAM_500	In Vivo
10	2	1-sample-18	1-sample-18	1-sample-18.txt	SAM_TEST	SAM_500	In Vivo
11	2	1-sample-19	1-sample-19	1-sample-19.txt	SAM_TEST	SAM_500	In Vivo
12	3	1-sample-2	1-sample-2	1-sample-2.txt	SAM_TEST	SAM_500	In Vivo
13	3	1-sample-20	1-sample-20	1-sample-20.txt	SAM_TEST	SAM_500	In Vivo
14	3	1-sample-3	1-sample-3	1-sample-3.txt	SAM_TEST	SAM_500	In Vivo
15	3	1-sample-4	1-sample-4	1-sample-4.txt	SAM_TEST	SAM_500	In Vivo
16	3	1-sample-5	1-sample-5	1-sample-5.txt	SAM_TEST	SAM_500	In Vivo
17	4	1-sample-6	1-sample-6	1-sample-6.txt	SAM_TEST	SAM_500	In Vivo
18	4	1-sample-7	1-sample-7	1-sample-7.txt	SAM_TEST	SAM_500	In Vivo
19	4	1-sample-8	1-sample-8	1-sample-8.txt	SAM_TEST	SAM_500	In Vivo
20	4	1-sample-9	1-sample-9	1-sample-9.txt	SAM_TEST	SAM_500	In Vivo
21	4	2-sample-21	2-sample-21	2-sample-21.txt	SAM_TEST	SAM_500	In Vivo
22	5	2-sample-22	2-sample-22	2-sample-22.txt	SAM_TEST	SAM_500	In Vivo
23	5	2-sample-23	2-sample-23	2-sample-23.txt	SAM_TEST	SAM_500	In Vivo
24	5	2-sample-24	2-sample-24	2-sample-24.txt	SAM_TEST	SAM_500	In Vivo
25	5	2-sample-25	2-sample-25	2-sample-25.txt	SAM_TEST	SAM_500	In Vivo
26	5	2-sample-26	2-sample-26	2-sample-26.txt	SAM_TEST	SAM_500	In Vivo

Choose the analysis type first, then assign the data set to multiple groups.

SAM-test: MultiClass



SAM-test: MultiClass

SAM-Tests Results

File Selected-Spot All-Spots

	Gene Mfr ID	SPOTID	Observed score (d)	P value	Numerator(r)	Denominat...	contrast-1	contrast
1	GENE199	4660478	0.0684	0.9532	0.0826	1.2088	0.6396	-0.1507
2	GENE200	4660479	0.1082	0.6209	0.1897	1.7535	0.2063	0.5882
3	GENE201	4660480	0.0632	0.9577	0.1119	1.7695	0.0768	-0.3344
4	GENE202	4660481	0.0548		0.0973	1.7752	0.2543	0.1381
5	GENE203	4660482	0.1619	0.1716	0.2372	1.4648	1.0482	0.0642
6	GENE204	4660483	0.071	0.8664	0.1442	2.0316	-0.0939	0.1011
7	GENE205	4660484	0.1747	0.1109	0.2407	1.3779	0.4285	0.4524
8	GENE206	4660485	0.087	0.6966	0.1474	1.6948	-0.0446	0.045
9	GENE207	4660486	0.1188	0.1882	0.1727	1.4537	0.0569	-0.0524
10	GENE208	4660487	0.1523	0.1006	0.2093	1.3743	0.3434	-0.6046
11	GENE209	4660488	0.105	0.4709	0.2001	1.9061	-0.4153	0.2514
12	GENE210	4660489	0.0902	0.7682	0.1677	1.8595	-0.3386	0.0254
13	GENE211	4660490	0.1079	0.6225	0.1816	1.6826	0.1645	0.428
14	GENE212	4660491	0.1174	0.3474	0.2096	1.7856	0.2178	-0.7163
15	GENE213	4660492	0.1563	0.1057	0.2266	1.4495	-0.2053	0.786
16	GENE214	4660493	0.0683		0.1305	1.9108	0.0806	0.1939
17	GENE215	4660494	0.2033	0.019	0.3867	1.9027	0.1648	0.3296
18	GENE216	4660495	0.1884		0.2603	1.3816	-1.5802	0.5408
19	GENE217	4660496	0.1153	0.664	0.1646	1.4273	0.2295	0.4566

500 genes

Significance Filtering

Target False Discovery Rate (FDR): Delta =

Select # genes by largest SAM absolute score

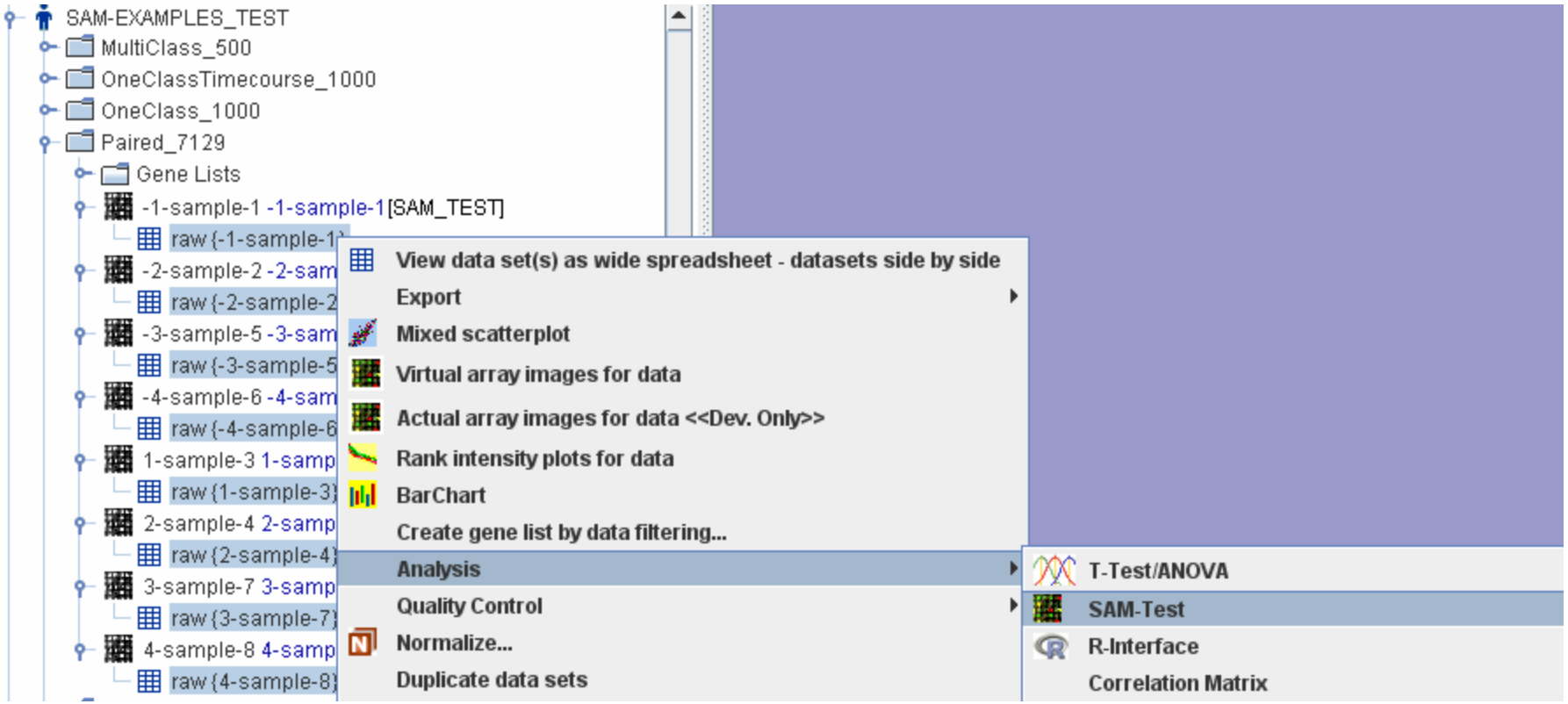
Mean Channel Intensities > Bad Flags <=

Apply Filters Clear Filters

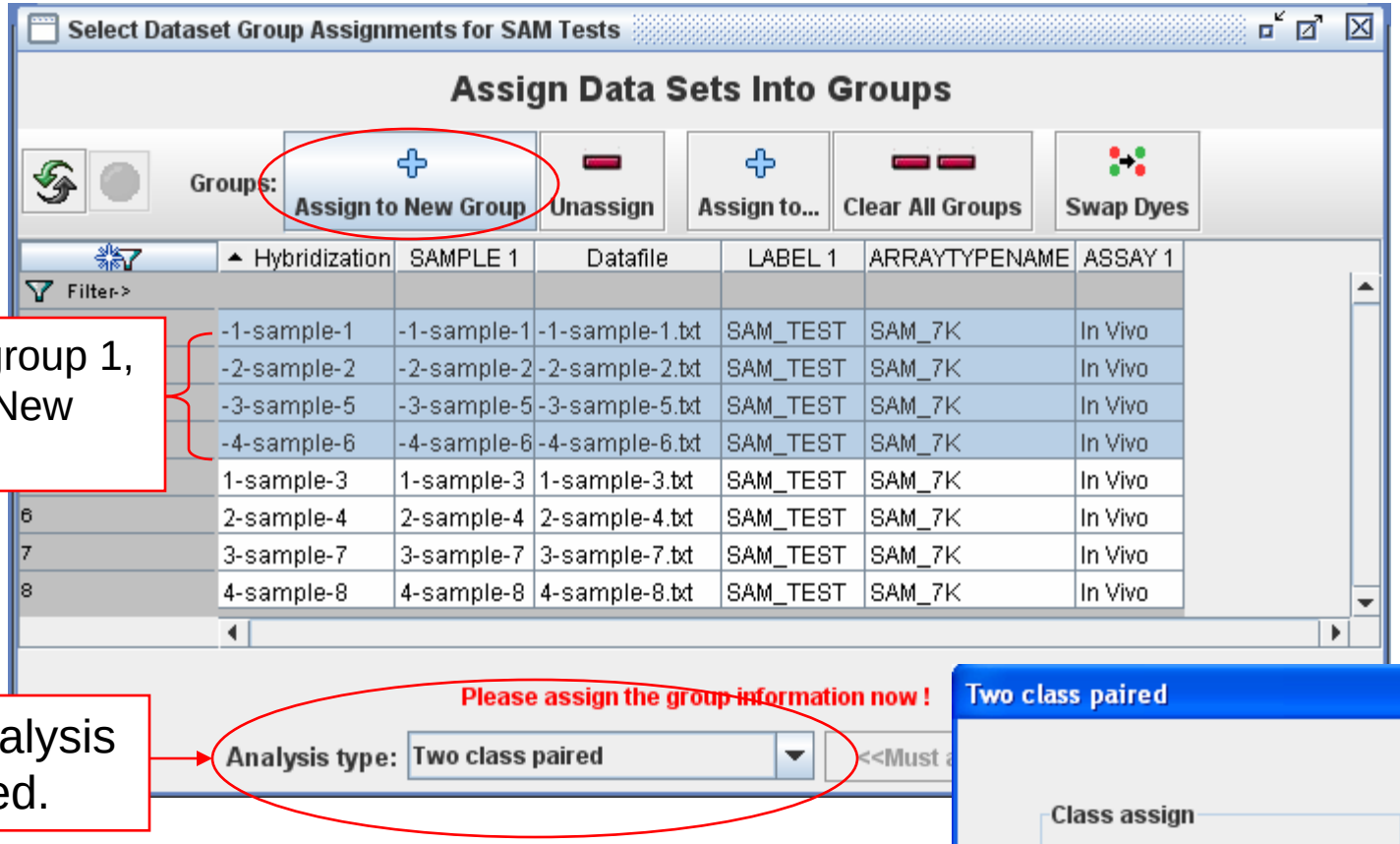
Create Sig. Gene List HCA PCA K-Means SAM Plot

SAM-Test: two class paired

Right-click the selected data set, choose “Analysis” ->SAM-Test.

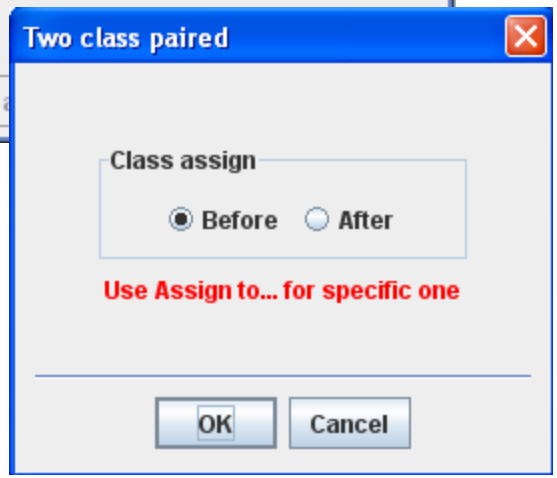


SAM-Test: two class paired



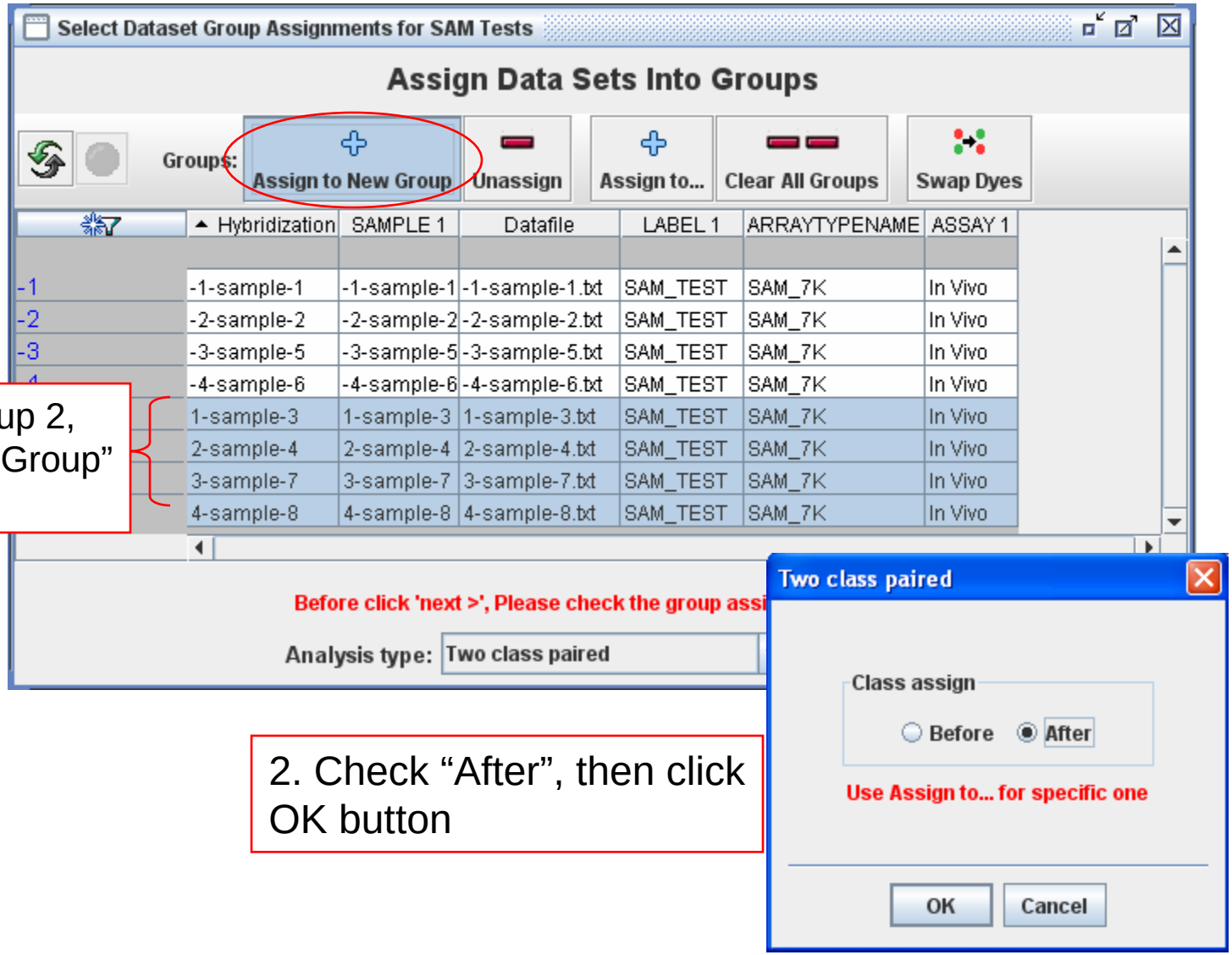
2 Select data for group 1, click “Assign to New Group” button.

1 Make sure analysis type is selected.



3 Check “Before”, then click OK button

SAM-Test: two class paired

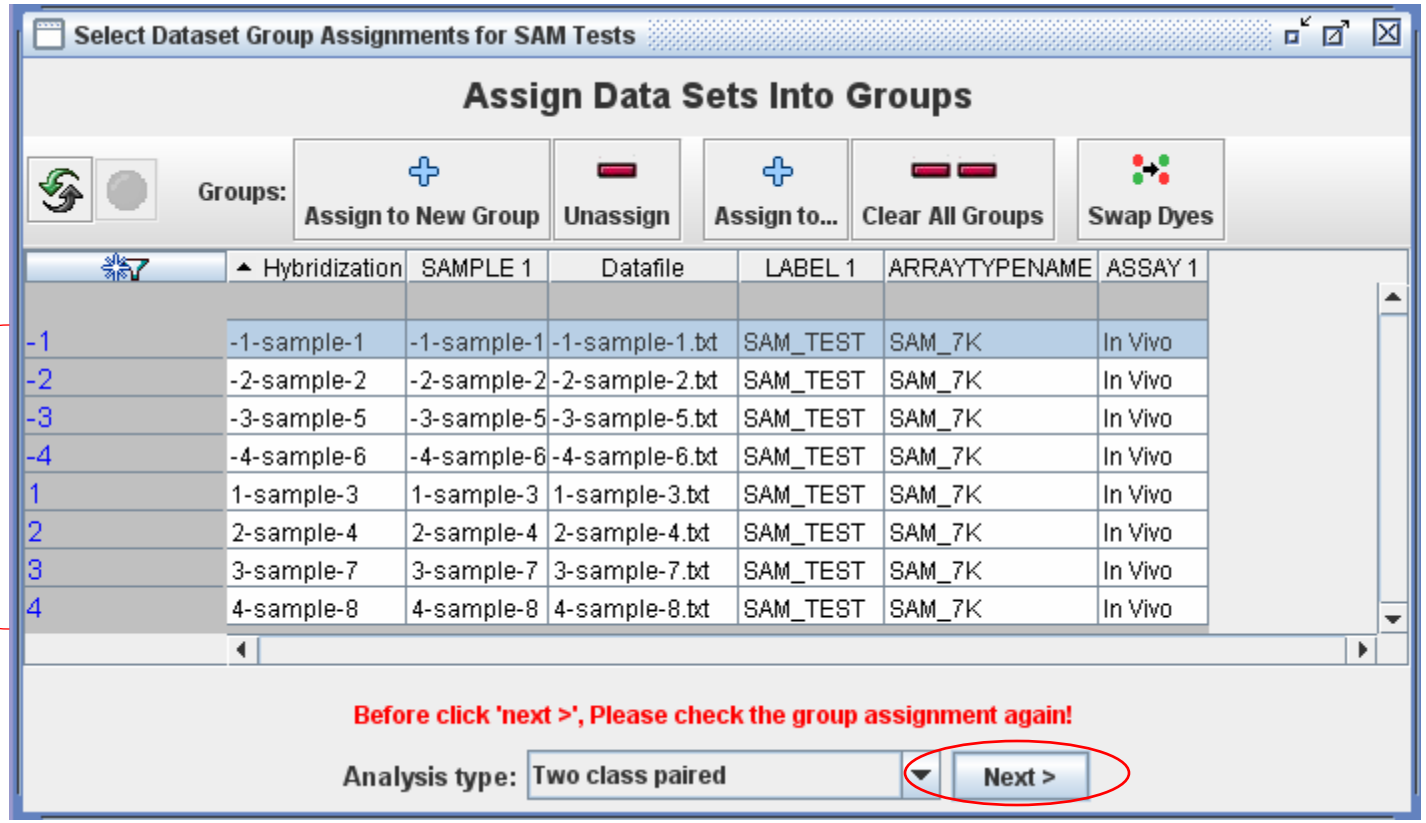


1. Select data for group 2, Click “Assign to New Group” Button.

2. Check “After”, then click OK button

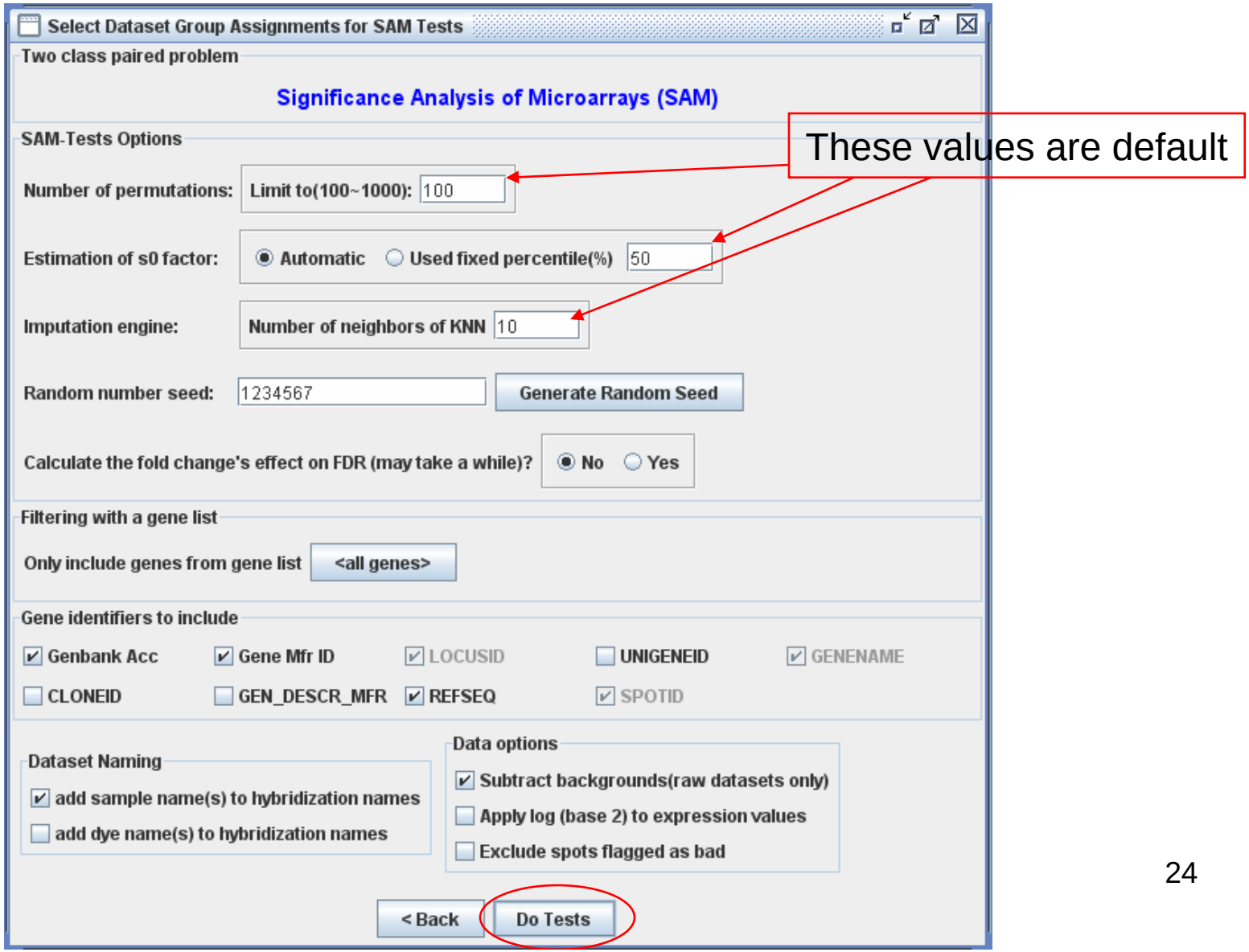
SAM-Test: two class paired

Data are assigned
In pairs



Click “Next” button.

SAM-Test: two class paired



SAM-Test: two class paired

SAM-Tests Results

File Selected-Spot All-Spots

	Gene Mfr ID	SPOTID	Observed score (d)	Numerator(r)	Denominat...	Fold Change	q-value(%)	localfdr
1	GENE870	4654020	0.4245	0.7516	1.7706	4.9263	80.8766	94.0522
2	GENE871	4654021	0.0677	0.1264	1.8682	3.0871	94.3878	100
3	GENE872	4654022	-0.2398	-0.4027	1.6793	0.8102	86.4446	94.1904
4	GENE873	4654023	-0.0792	-0.1556	1.9641	1.3397	91.078	99.4605
5	GENE874	4654024	0.0535	0.1033	1.9306	1.7484	94.3878	100
6	GENE875	4654025	-0.2488	-0.5128	2.0609	1.1078	86.4446	93.8744
7	GENE876	4654026	-0.2298	-0.3941	1.715	0.823	86.4446	94.5365
8	GENE877	4654027	-0.6001	-1.0456	1.7423	0.4787	77.8565	80.77
9	GENE878	4654028	-0.3534	-0.605	1.712	0.6823	86.4446	89.5737
10	GENE826	4653976	-0.0168	-0.0245	1.4572	1.0481	92.688	100
11	GENE827	4653977	-0.2985	-0.4591	1.5381	0.7289	86.4446	92.0149
12	GENE828	4653978	-0.1136	-0.2142	1.8858	1.3896	89.6273	98.399
13	GENE829	4653979	0.3222	0.5884	1.826	3.588	86.3568	95.7861
14	GENE830	4653980	0.0323	0.0533	1.6476	1.2171	94.3878	100
15	GENE831	4653981	0.0076	0.0122	1.5909	1.1026	94.3878	100
16	GENE832	4653982	-0.0855	-0.1446	1.6914	1.2943	91.078	99.2674
17	GENE833	4653983	0.3023	0.4876	1.6128	2.1278	86.4309	96.1364

7129 genes

Significance Filtering

Target False Discovery Rate (FDR): Delta =

Select # genes by largest SAM absolute score

Mean Channel Intensities > Bad Flags <=

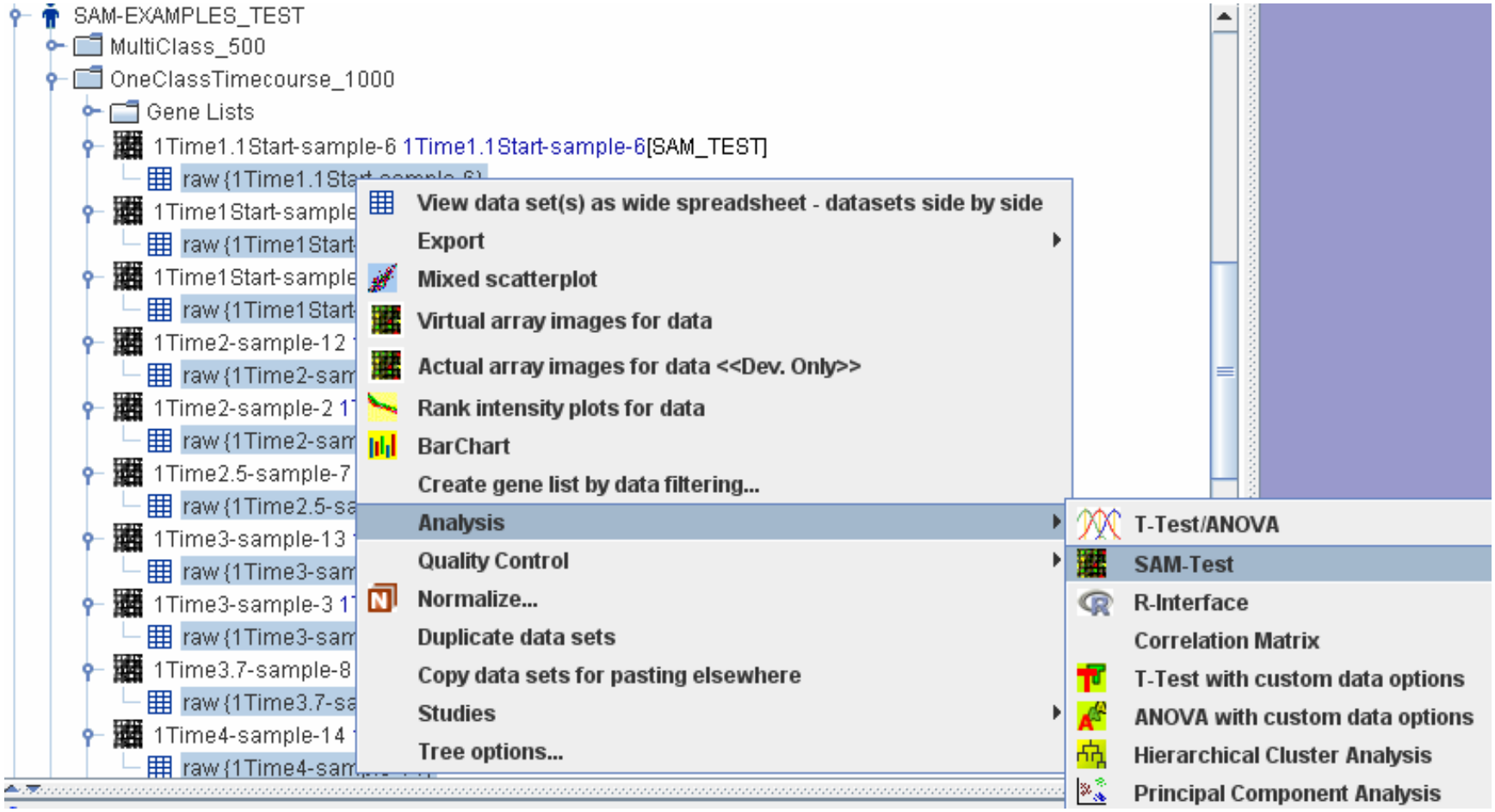
Abs Fold Change >

Apply Filters Clear Filters

Create Sig. Gene List HCA PCA K-Means SAM Plot

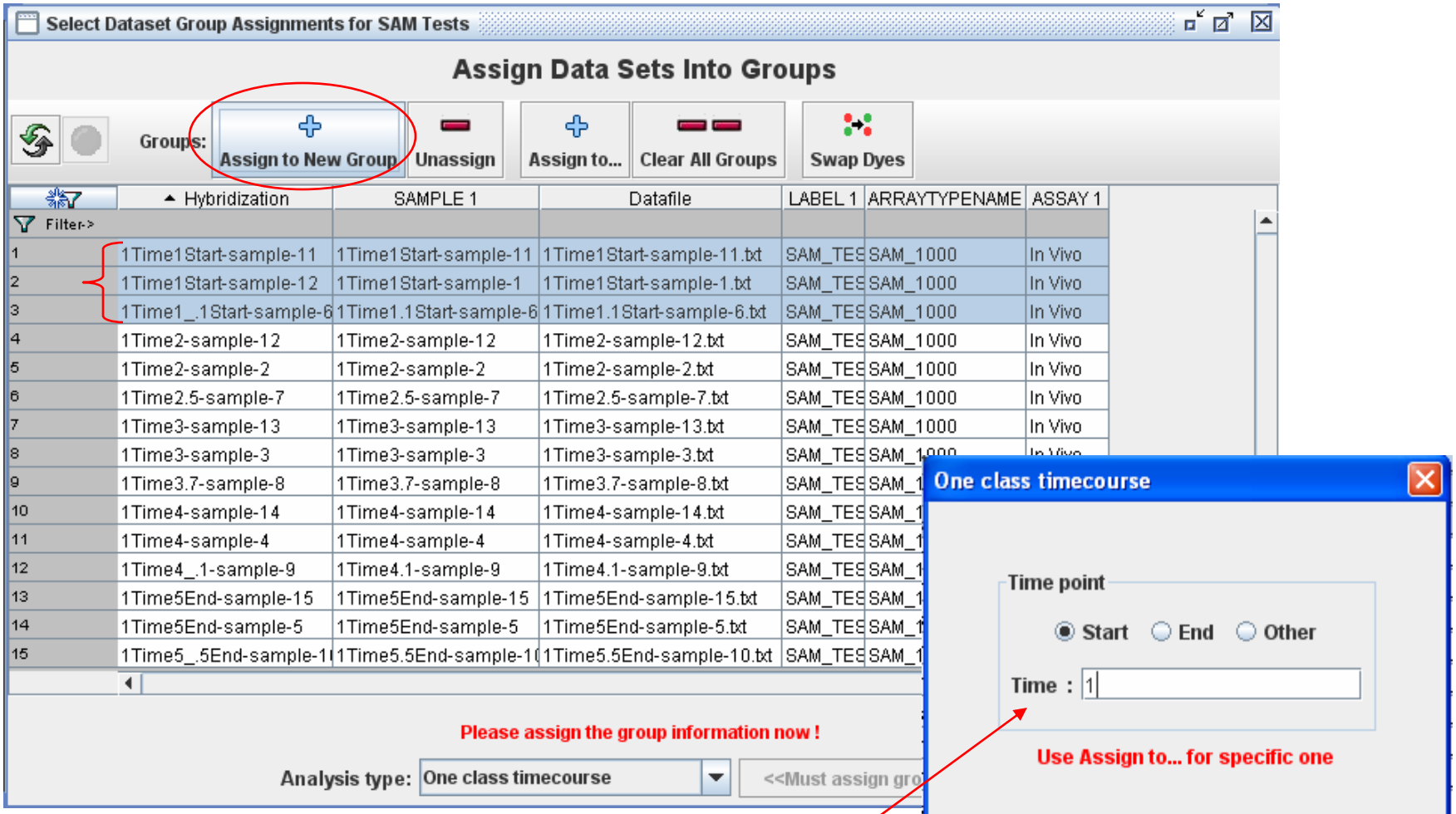
SAM-Test: Timecourse

One class timecourse



SAM-Test: one class timecourse

Highlight the first group, click “Assign to New Group” button.

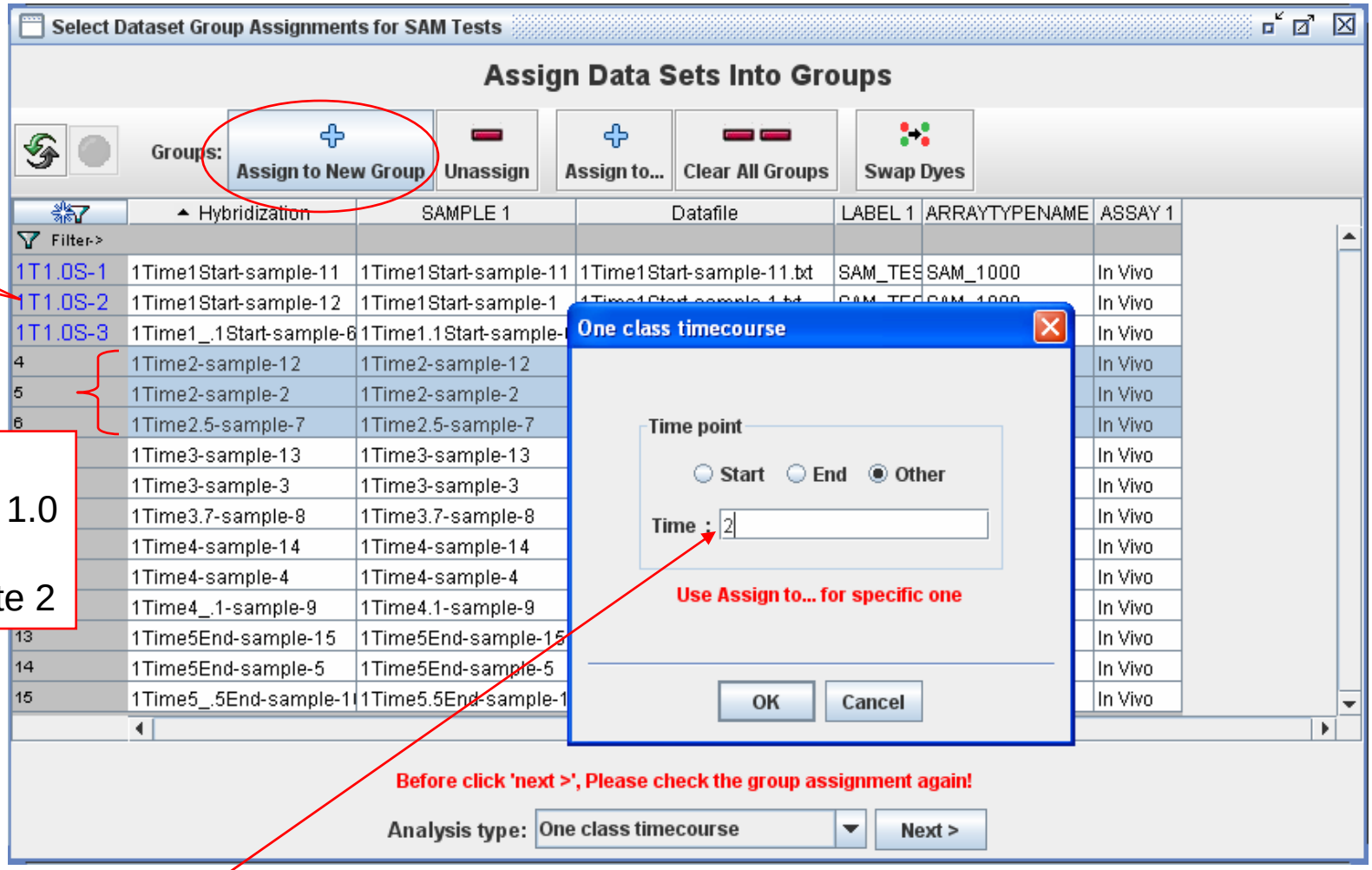


Check “Start” radio button, type in number “1” in the time text box. Click OK button.

SAM-Test: One Class Timecourse

1T1.0S-2

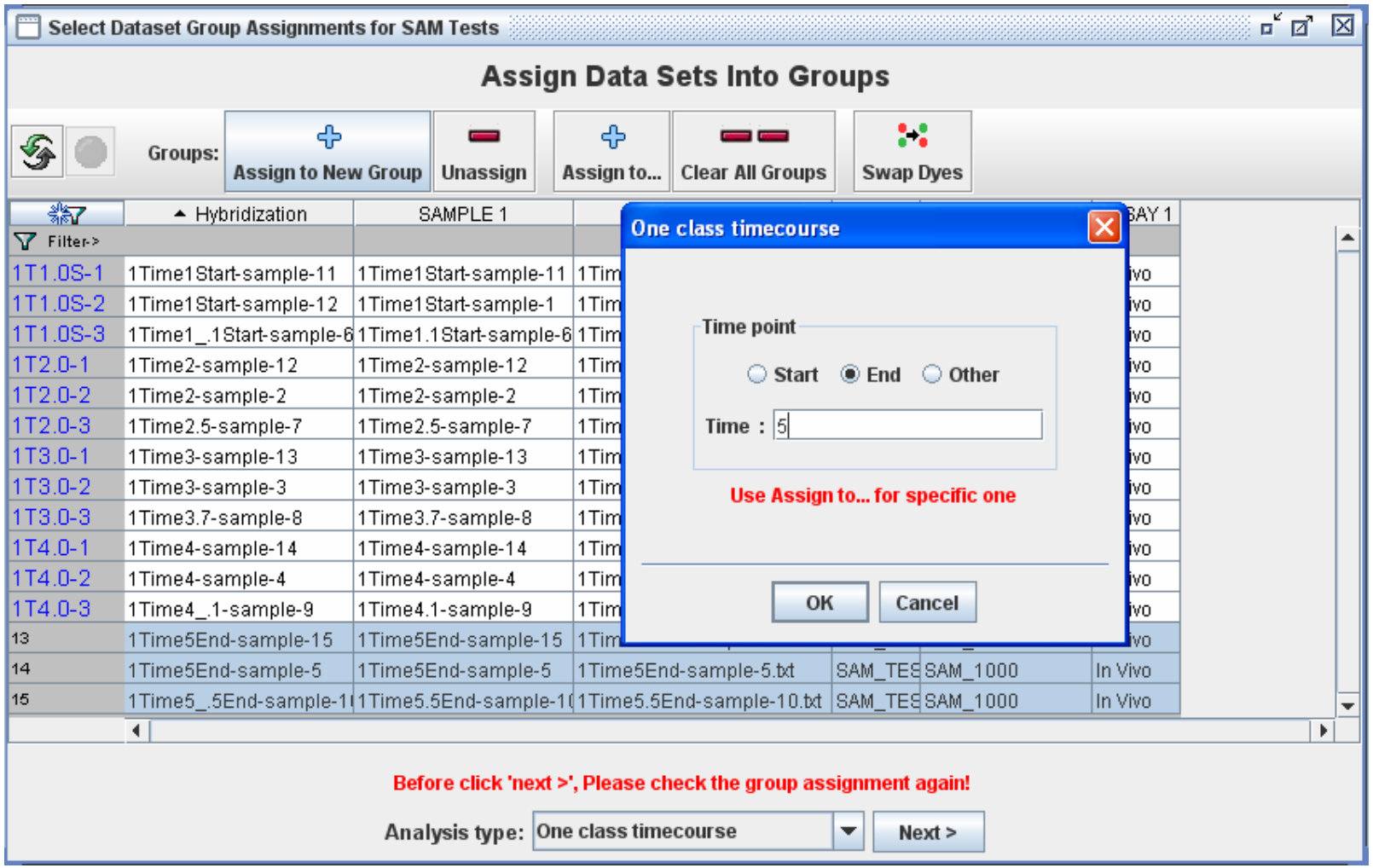
1 means class 1.
T1.0 means time 1.0
S means start
-2 means replicate 2



For second group, check “Other” radio button and type in number “2” for time course.

SAM-Test: One Class Timecourse

Repeat the previous steps for assigning the other groups. For the last group, check "End" radio button and type in the time. Click OK button.



SAM-Test: One Class Timecourse

This is what looks like after assigning all the groups.

Select Dataset Group Assignments for SAM Tests

Assign Data Sets Into Groups

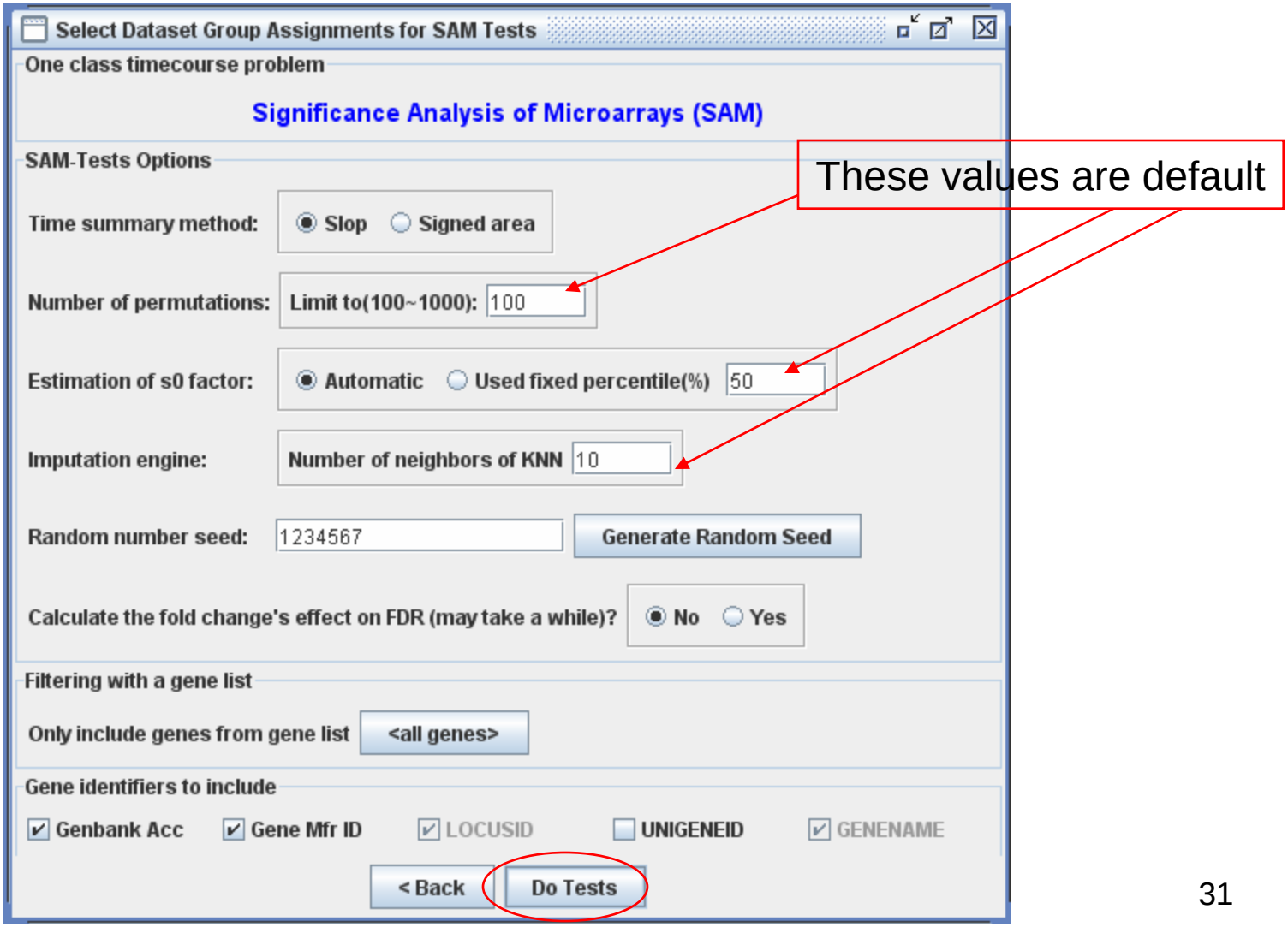
Groups: Assign to New Group | Unassign | Assign to... | Clear All Groups | Swap Dyes

	Hybridization	SAMPLE 1	Datafile	LABEL 1	ARRAYTYPENAME	ASSAY 1
Filter->						
Time 1 Start: 1T1.0S-1	1Time1Start-sample-11	1Time1Start-sample-11	1Time1Start-sample-11.txt	SAM_TEST	SAM_1000	In Vivo
1T1.0S-2	1Time1Start-sample-12	1Time1Start-sample-1	1Time1Start-sample-1.txt	SAM_TEST	SAM_1000	In Vivo
1T1.0S-3	1Time1_.1Start-sample-6	1Time1.1Start-sample-6	1Time1.1Start-sample-6.txt	SAM_TEST	SAM_1000	In Vivo
Time 2: 1T2.0-1	1Time2-sample-12	1Time2-sample-12	1Time2-sample-12.txt	SAM_TEST	SAM_1000	In Vivo
1T2.0-2	1Time2-sample-2	1Time2-sample-2	1Time2-sample-2.txt	SAM_TEST	SAM_1000	In Vivo
1T2.0-3	1Time2.5-sample-7	1Time2.5-sample-7	1Time2.5-sample-7.txt	SAM_TEST	SAM_1000	In Vivo
Time 3: 1T3.0-1	1Time3-sample-13	1Time3-sample-13	1Time3-sample-13.txt	SAM_TEST	SAM_1000	In Vivo
1T3.0-2	1Time3-sample-3	1Time3-sample-3	1Time3-sample-3.txt	SAM_TEST	SAM_1000	In Vivo
1T3.0-3	1Time3.7-sample-8	1Time3.7-sample-8	1Time3.7-sample-8.txt	SAM_TEST	SAM_1000	In Vivo
Time 4: 1T4.0-1	1Time4-sample-14	1Time4-sample-14	1Time4-sample-14.txt	SAM_TEST	SAM_1000	In Vivo
1T4.0-2	1Time4-sample-4	1Time4-sample-4	1Time4-sample-4.txt	SAM_TEST	SAM_1000	In Vivo
1T4.0-3	1Time4_.1-sample-9	1Time4.1-sample-9	1Time4.1-sample-9.txt	SAM_TEST	SAM_1000	In Vivo
Time 5 End: 1T5.0E-1	1Time5End-sample-15	1Time5End-sample-15	1Time5End-sample-15.txt	SAM_TEST	SAM_1000	In Vivo
1T5.0E-2	1Time5End-sample-5	1Time5End-sample-5	1Time5End-sample-5.txt	SAM_TEST	SAM_1000	In Vivo
1T5.0E-3	1Time5_.5End-sample-1	1Time5.5End-sample-1	1Time5.5End-sample-10.txt	SAM_TEST	SAM_1000	In Vivo

Before click 'next >', Please check the group assignment again!

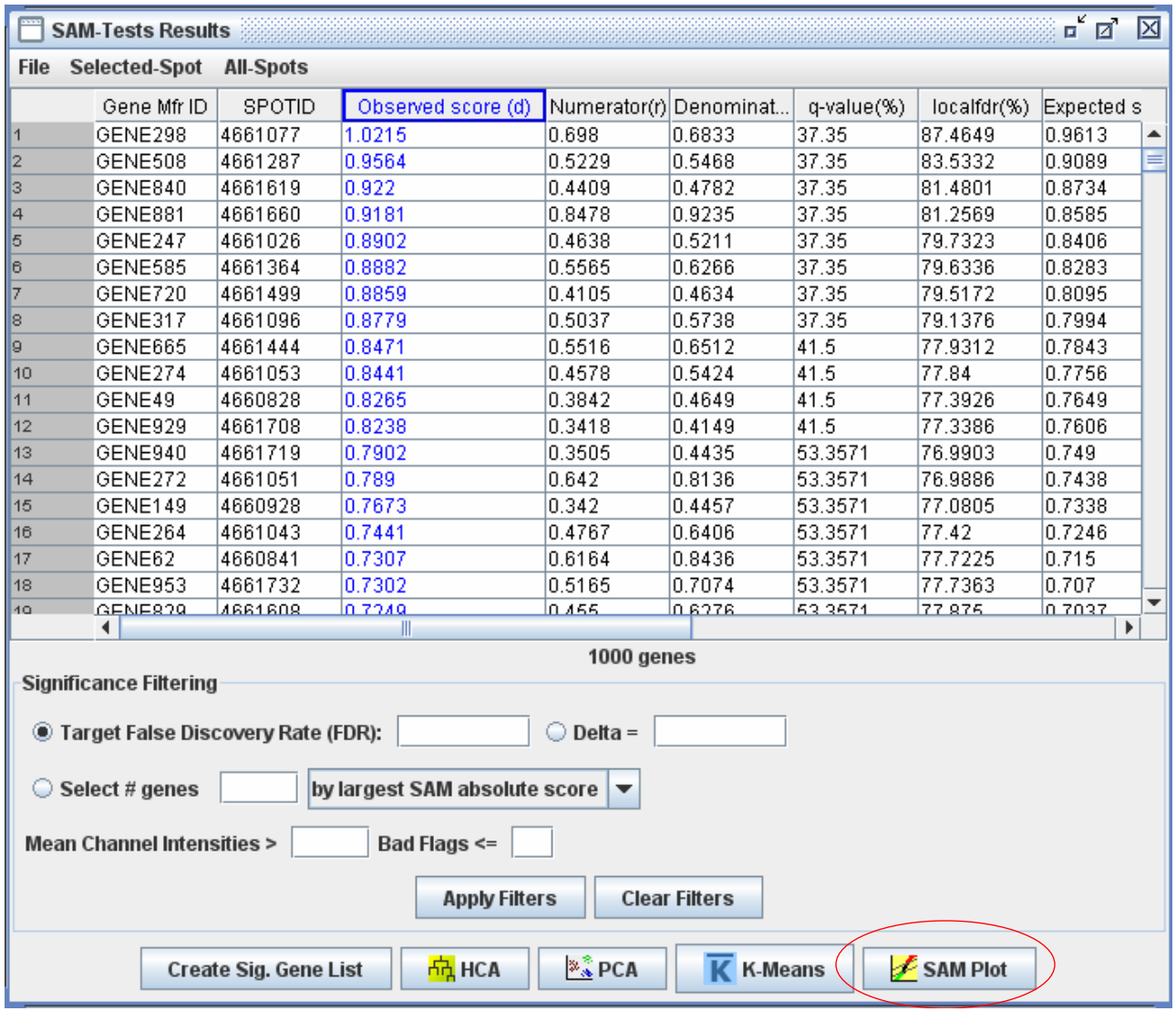
Analysis type: One class timecourse | Next >

SAM-Test: One Class Timecourse



SAM-Test: One Class Timecourse

One class time course result:



SAM-Tests Results

File Selected-Spot All-Spots

	Gene Mfr ID	SPOTID	Observed score (d)	Numerator(r)	Denominat...	q-value(%)	localfdr(%)	Expected s
1	GENE298	4661077	1.0215	0.698	0.6833	37.35	87.4649	0.9613
2	GENE508	4661287	0.9564	0.5229	0.5468	37.35	83.5332	0.9089
3	GENE840	4661619	0.922	0.4409	0.4782	37.35	81.4801	0.8734
4	GENE881	4661660	0.9181	0.8478	0.9235	37.35	81.2569	0.8585
5	GENE247	4661026	0.8902	0.4638	0.5211	37.35	79.7323	0.8406
6	GENE585	4661364	0.8882	0.5565	0.6266	37.35	79.6336	0.8283
7	GENE720	4661499	0.8859	0.4105	0.4634	37.35	79.5172	0.8095
8	GENE317	4661096	0.8779	0.5037	0.5738	37.35	79.1376	0.7994
9	GENE665	4661444	0.8471	0.5516	0.6512	41.5	77.9312	0.7843
10	GENE274	4661053	0.8441	0.4578	0.5424	41.5	77.84	0.7756
11	GENE49	4660828	0.8265	0.3842	0.4649	41.5	77.3926	0.7649
12	GENE929	4661708	0.8238	0.3418	0.4149	41.5	77.3386	0.7606
13	GENE940	4661719	0.7902	0.3505	0.4435	53.3571	76.9903	0.749
14	GENE272	4661051	0.789	0.642	0.8136	53.3571	76.9886	0.7438
15	GENE149	4660928	0.7673	0.342	0.4457	53.3571	77.0805	0.7338
16	GENE264	4661043	0.7441	0.4767	0.6406	53.3571	77.42	0.7246
17	GENE62	4660841	0.7307	0.6164	0.8436	53.3571	77.7225	0.715
18	GENE953	4661732	0.7302	0.5165	0.7074	53.3571	77.7363	0.707
19	GENE829	4661608	0.7249	0.455	0.6276	53.3571	77.875	0.7037

1000 genes

Significance Filtering

Target False Discovery Rate (FDR): Delta =

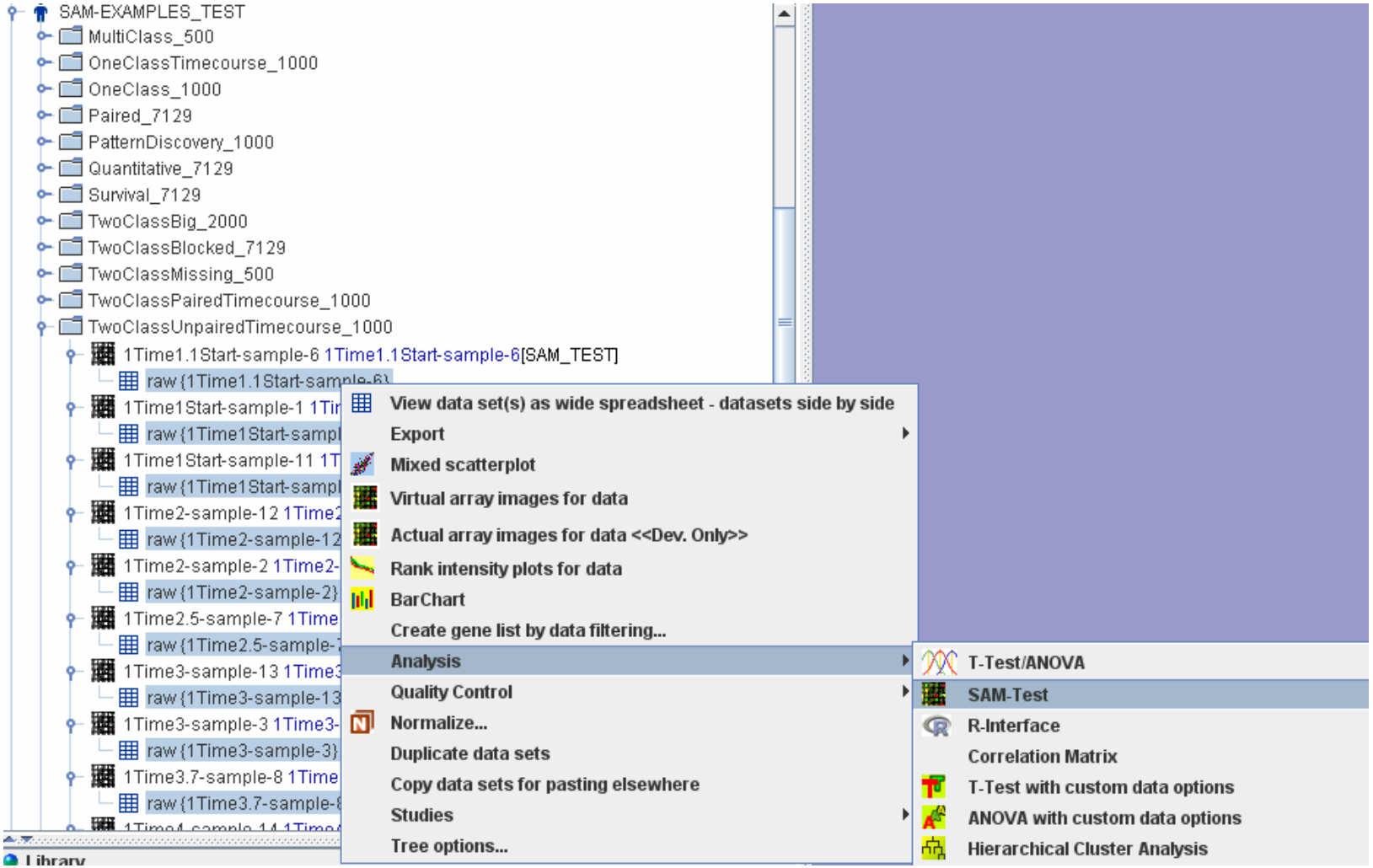
Select # genes by largest SAM absolute score

Mean Channel Intensities > Bad Flags <=

Apply Filters Clear Filters

Create Sig. Gene List HCA PCA K-Means SAM Plot

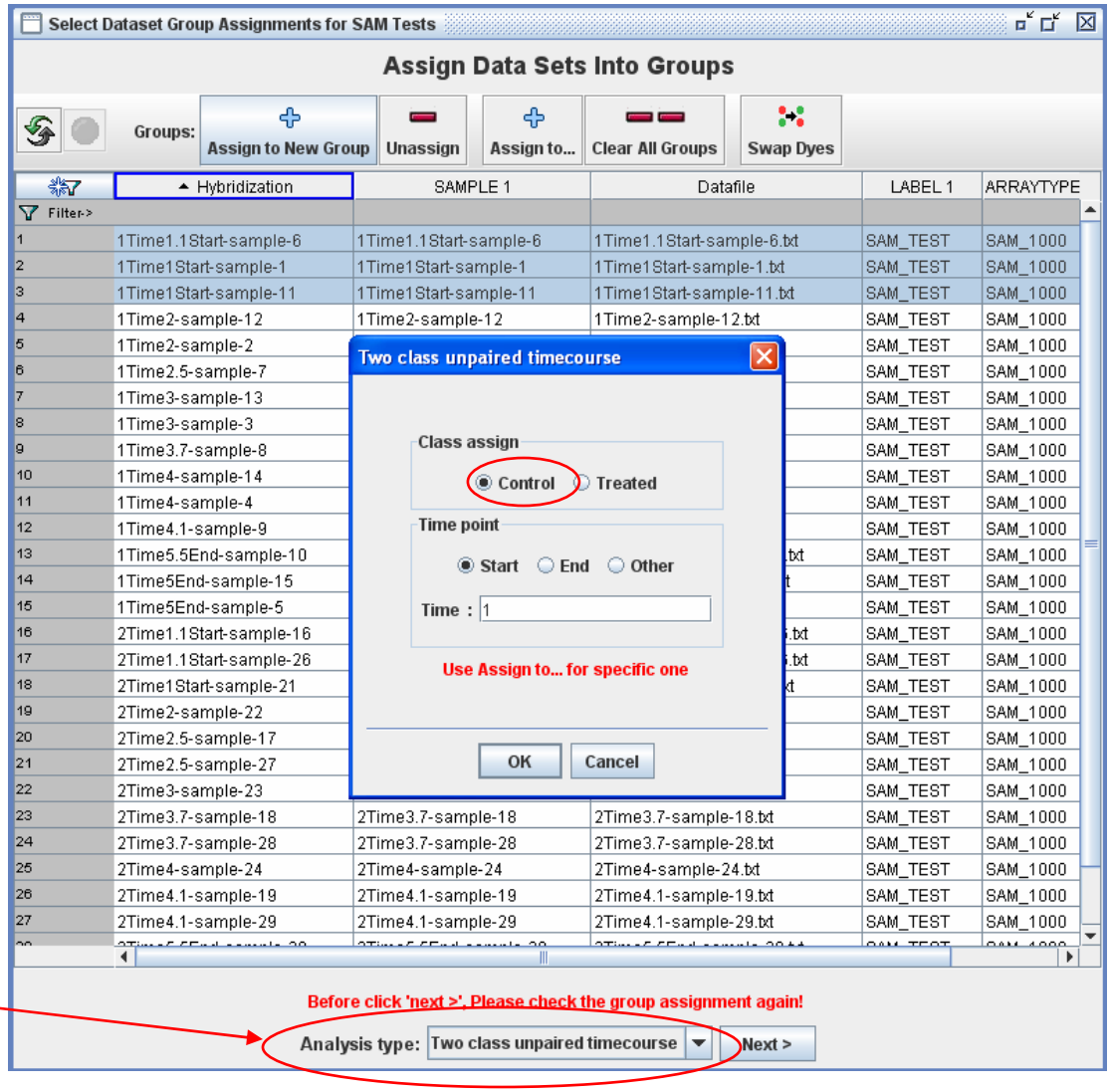
SAM-Test: Two Class Unpaired Timecourse



Right-click the selected data set, choose “Analysis” ->SAM-Test.

SAM-Test: Two Class Unpaired Timecourse

Here the steps are similar as one class time course. User assign start time point, middle point and end time point for class one. And then repeat the steps for class two. Just remember if class one is control group, then class two will be treated group.

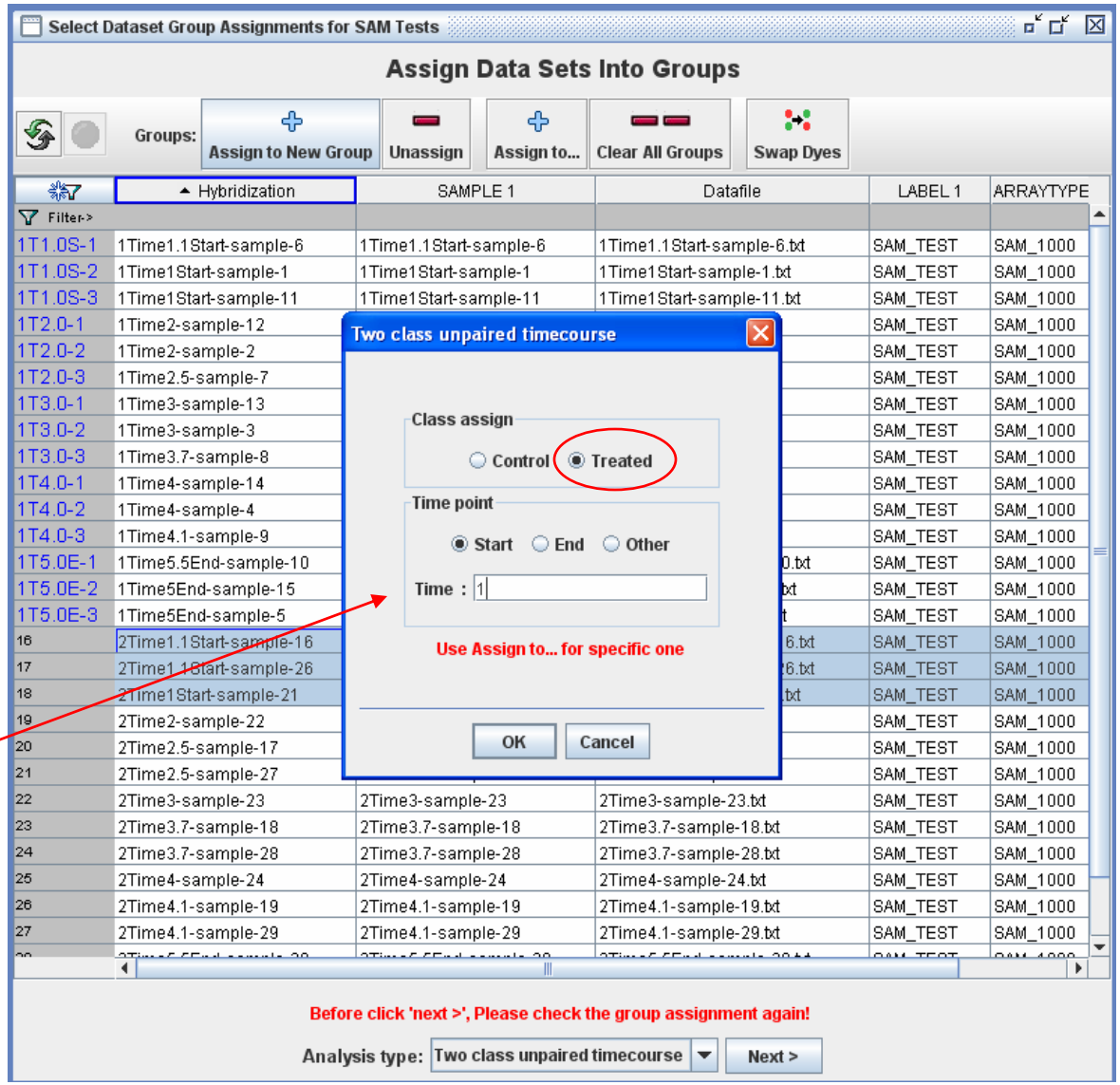


Make sure the analysis type is Selected before assigning class.

SAM-Test: Two Class Unpaired Timecourse

Class one from start to end time point.

Repeat the steps to assign class two. Class two is treated.



SAM-Test: Two Class Unpaired Timecourse

Here is what looks like after assigning.

Class one

Class two

Select Dataset Group Assignments for SAM Tests

Assign Data Sets Into Groups

Groups: Assign to New Group | Unassign | Assign to... | Clear All Groups | Swap Dyes

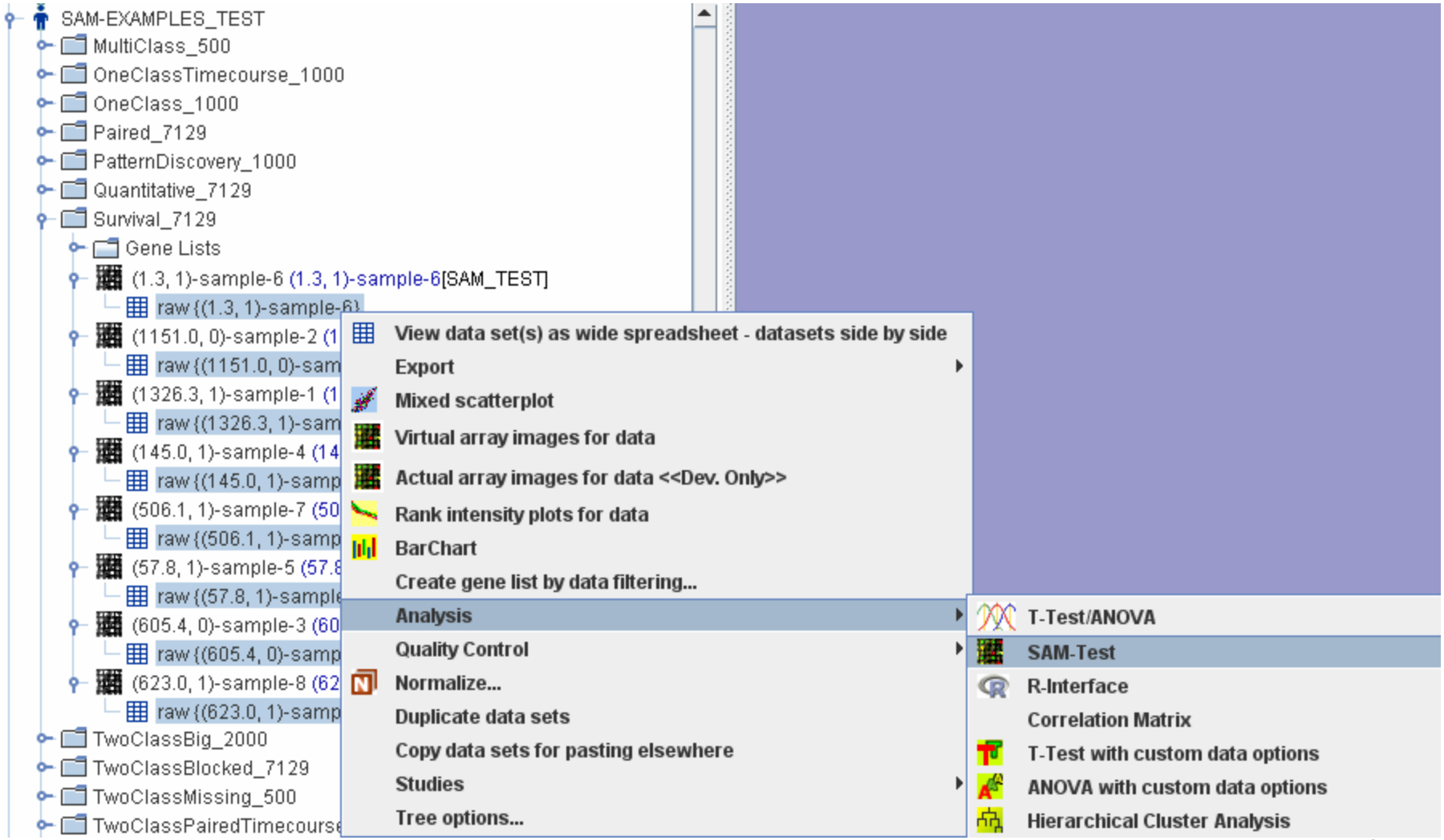
	Hybridization	SAMPLE 1	Datafile	LABEL 1	ARRAYTYPENAME	ASSAY 1
Filter->						
1T1.0S-1	1Time1.1Start-sample-6	1Time1.1Start-sample-6	1Time1.1Start-sample-6.txt	SAM_TEST	SAM_1000	In Vivo
1T1.0S-2	1Time1Start-sample-1	1Time1Start-sample-1	1Time1Start-sample-1.txt	SAM_TEST	SAM_1000	In Vivo
1T1.0S-3	1Time1Start-sample-11	1Time1Start-sample-11	1Time1Start-sample-11.txt	SAM_TEST	SAM_1000	In Vivo
1T2.0-1	1Time2-sample-12	1Time2-sample-12	1Time2-sample-12.txt	SAM_TEST	SAM_1000	In Vivo
1T2.0-2	1Time2-sample-2	1Time2-sample-2	1Time2-sample-2.txt	SAM_TEST	SAM_1000	In Vivo
1T2.0-3	1Time2.5-sample-7	1Time2.5-sample-7	1Time2.5-sample-7.txt	SAM_TEST	SAM_1000	In Vivo
1T3.0-1	1Time3-sample-13	1Time3-sample-13	1Time3-sample-13.txt	SAM_TEST	SAM_1000	In Vivo
1T3.0-2	1Time3-sample-3	1Time3-sample-3	1Time3-sample-3.txt	SAM_TEST	SAM_1000	In Vivo
1T3.0-3	1Time3.7-sample-8	1Time3.7-sample-8	1Time3.7-sample-8.txt	SAM_TEST	SAM_1000	In Vivo
1T4.0-1	1Time4-sample-14	1Time4-sample-14	1Time4-sample-14.txt	SAM_TEST	SAM_1000	In Vivo
1T4.0-2	1Time4-sample-4	1Time4-sample-4	1Time4-sample-4.txt	SAM_TEST	SAM_1000	In Vivo
1T4.0-3	1Time4.1-sample-9	1Time4.1-sample-9	1Time4.1-sample-9.txt	SAM_TEST	SAM_1000	In Vivo
1T5.0E-1	1Time5.5End-sample-10	1Time5.5End-sample-10	1Time5.5End-sample-10.txt	SAM_TEST	SAM_1000	In Vivo
1T5.0E-2	1Time5End-sample-15	1Time5End-sample-15	1Time5End-sample-15.txt	SAM_TEST	SAM_1000	In Vivo
1T5.0E-3	1Time5End-sample-5	1Time5End-sample-5	1Time5End-sample-5.txt	SAM_TEST	SAM_1000	In Vivo
2T1.0S-1	2Time1.1Start-sample-16	2Time1.1Start-sample-16	2Time1.1Start-sample-16.txt	SAM_TEST	SAM_1000	In Vivo
2T1.0S-2	2Time1.1Start-sample-26	2Time1.1Start-sample-26	2Time1.1Start-sample-26.txt	SAM_TEST	SAM_1000	In Vivo
2T1.0S-3	2Time1Start-sample-21	2Time1Start-sample-21	2Time1Start-sample-21.txt	SAM_TEST	SAM_1000	In Vivo
2T2.0-1	2Time2-sample-22	2Time2-sample-22	2Time2-sample-22.txt	SAM_TEST	SAM_1000	In Vivo
2T2.0-2	2Time2.5-sample-17	2Time2.5-sample-17	2Time2.5-sample-17.txt	SAM_TEST	SAM_1000	In Vivo
2T2.0-3	2Time2.5-sample-27	2Time2.5-sample-27	2Time2.5-sample-27.txt	SAM_TEST	SAM_1000	In Vivo
2T3.0-1	2Time3-sample-23	2Time3-sample-23	2Time3-sample-23.txt	SAM_TEST	SAM_1000	In Vivo
2T3.0-2	2Time3.7-sample-18	2Time3.7-sample-18	2Time3.7-sample-18.txt	SAM_TEST	SAM_1000	In Vivo
2T3.0-3	2Time3.7-sample-28	2Time3.7-sample-28	2Time3.7-sample-28.txt	SAM_TEST	SAM_1000	In Vivo
2T4.0-1	2Time4-sample-24	2Time4-sample-24	2Time4-sample-24.txt	SAM_TEST	SAM_1000	In Vivo
2T4.0-2	2Time4.1-sample-19	2Time4.1-sample-19	2Time4.1-sample-19.txt	SAM_TEST	SAM_1000	In Vivo
2T4.0-3	2Time4.1-sample-29	2Time4.1-sample-29	2Time4.1-sample-29.txt	SAM_TEST	SAM_1000	In Vivo
2T5.0E-1	2Time5.5End-sample-20	2Time5.5End-sample-20	2Time5.5End-sample-20.txt	SAM_TEST	SAM_1000	In Vivo
2T5.0E-2	2Time5.5End-sample-30	2Time5.5End-sample-30	2Time5.5End-sample-30.txt	SAM_TEST	SAM_1000	In Vivo
2T5.0E-3	2Time5End-sample-25	2Time5End-sample-25	2Time5End-sample-25.txt	SAM_TEST	SAM_1000	In Vivo

Before click 'next >', Please check the group assignment again!

Analysis type: Two class unpaired timecourse | Next >

Click Next button to get SAM-test

SAM-Test: Survival

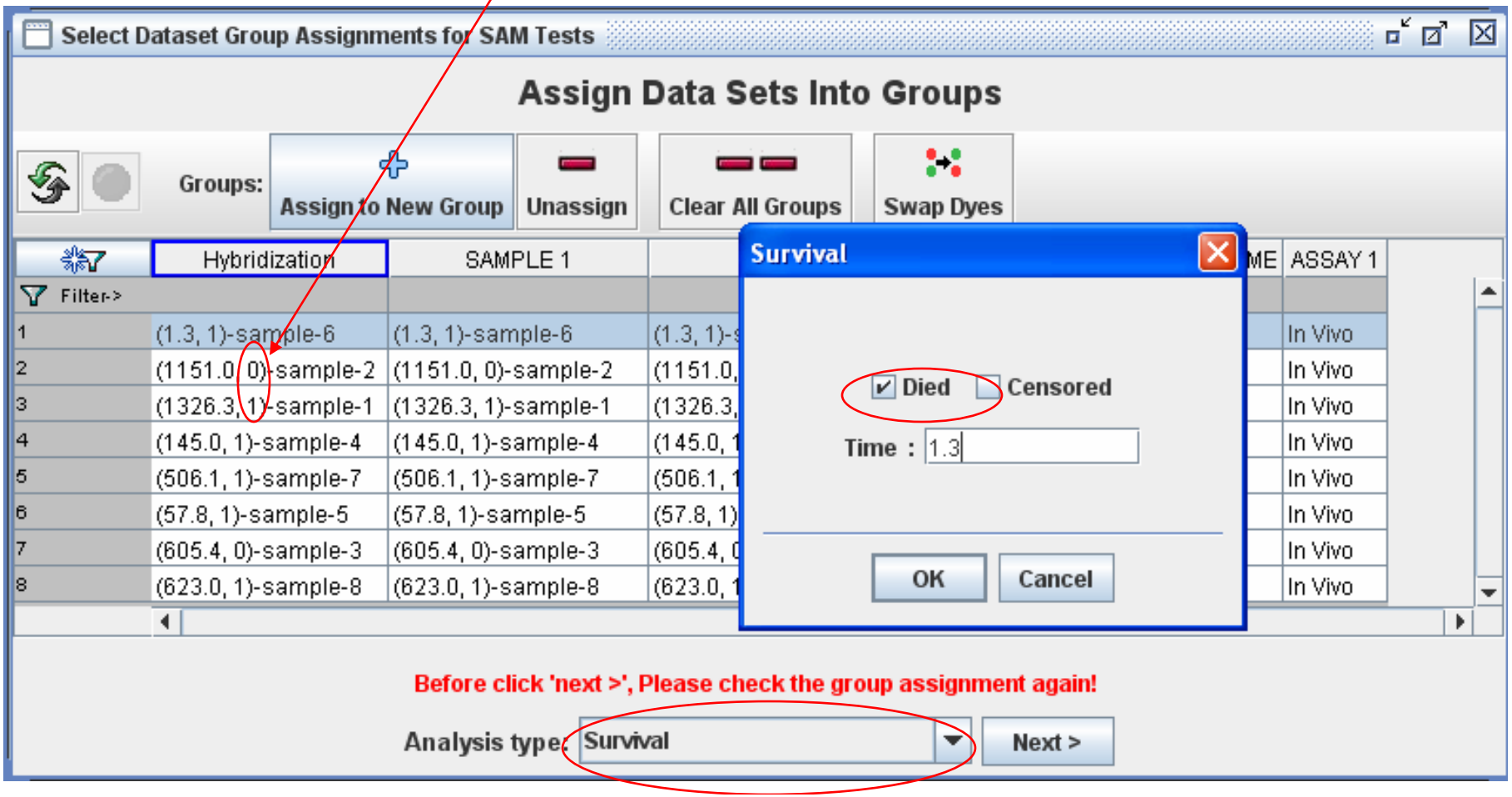


Right-click the selected data set, choose “Analysis” ->SAM-Test

SAM-Test: Survival

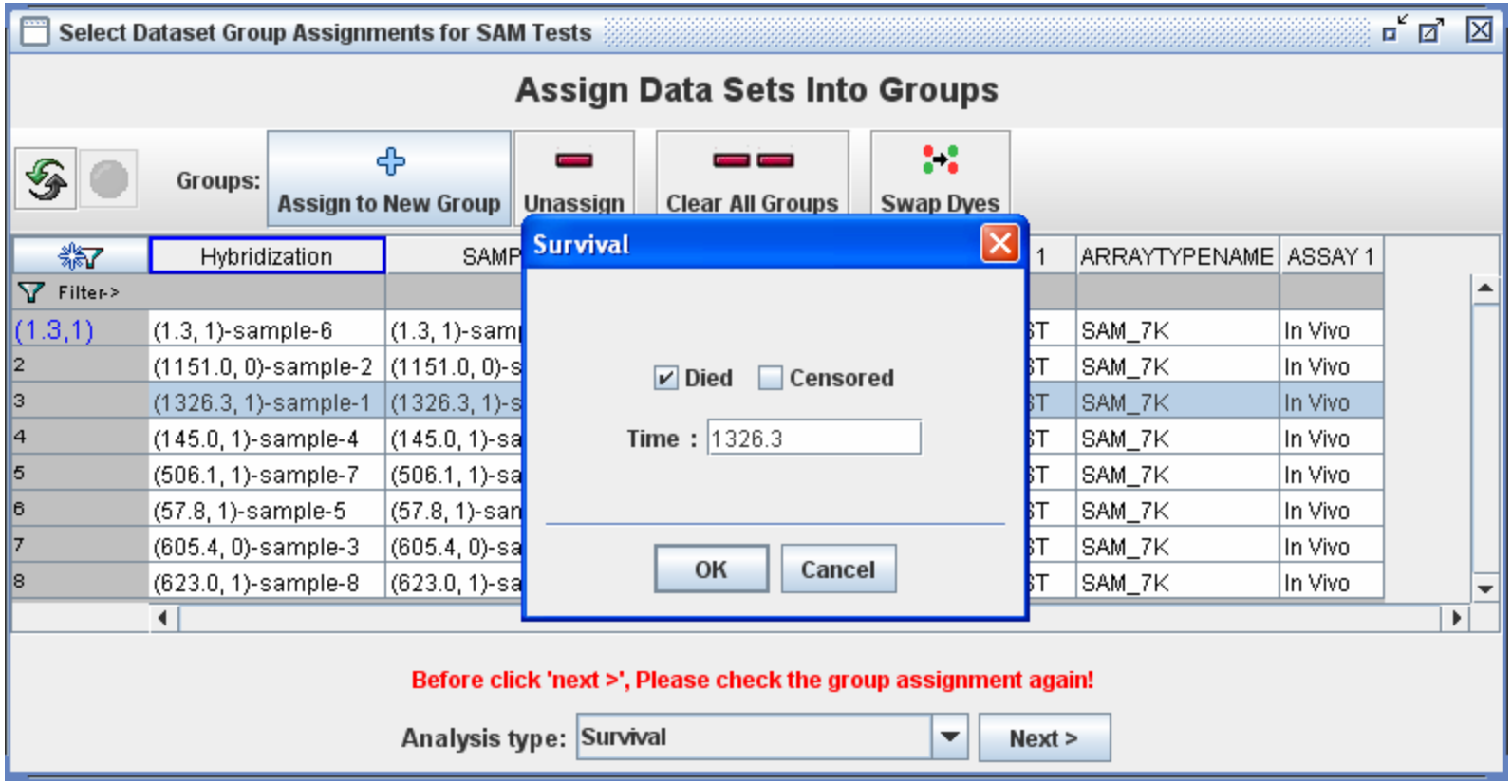
This data set has two groups. The first number in parenthesis represent time and the second number in parenthesis (1 or 0) represents “died” (1) or “censored”(0) group.

Select the first data – (1.3, 1)-sample-6, click “Assign to New Group” button. Type 1.3 in the time area.



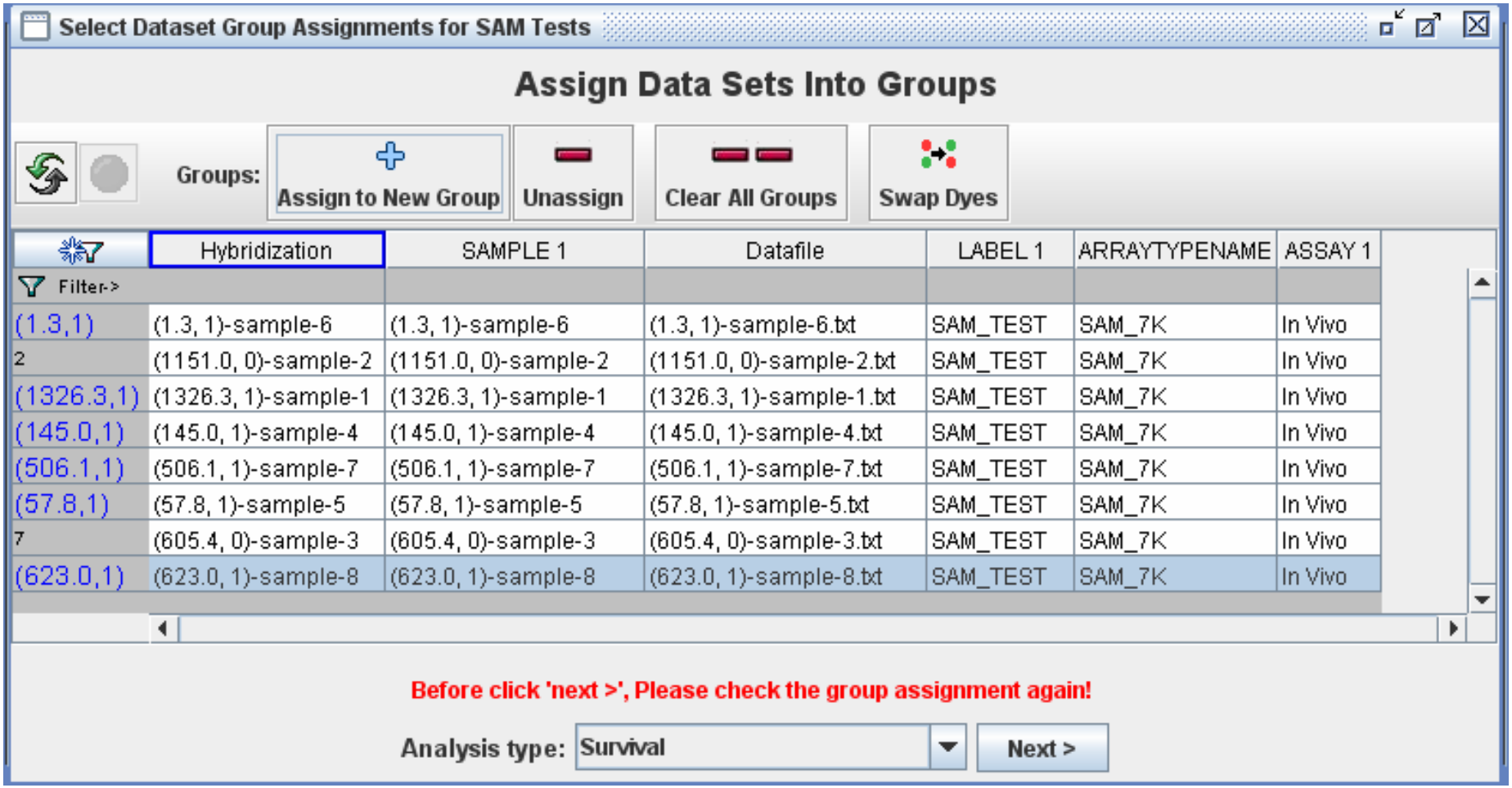
SAM-Test: Survival

Repeat the previous steps to assign the other data of group 1, type in the time.



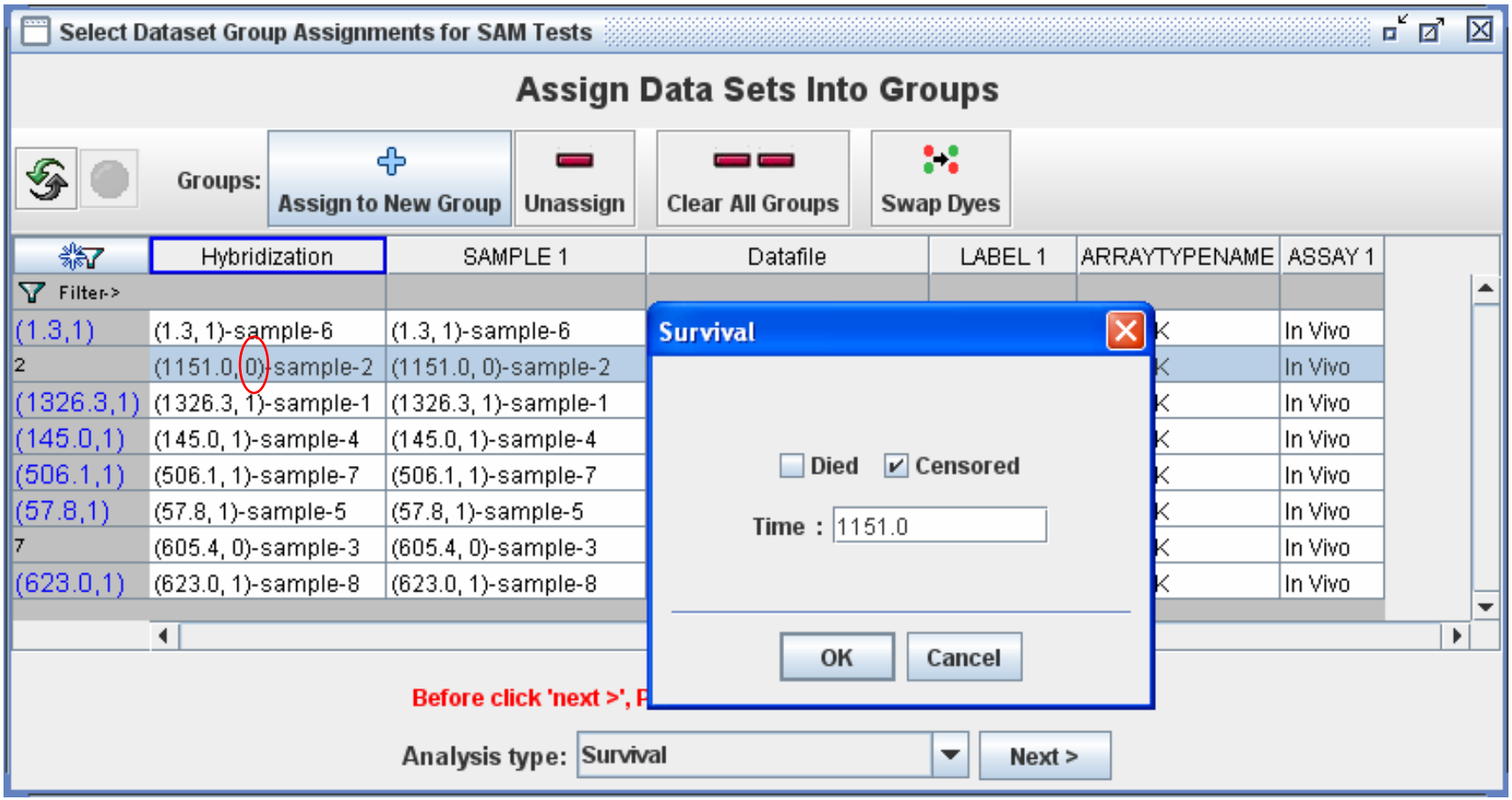
SAM-Test: Survival

This image shows all the data of group 1 has been assigned.



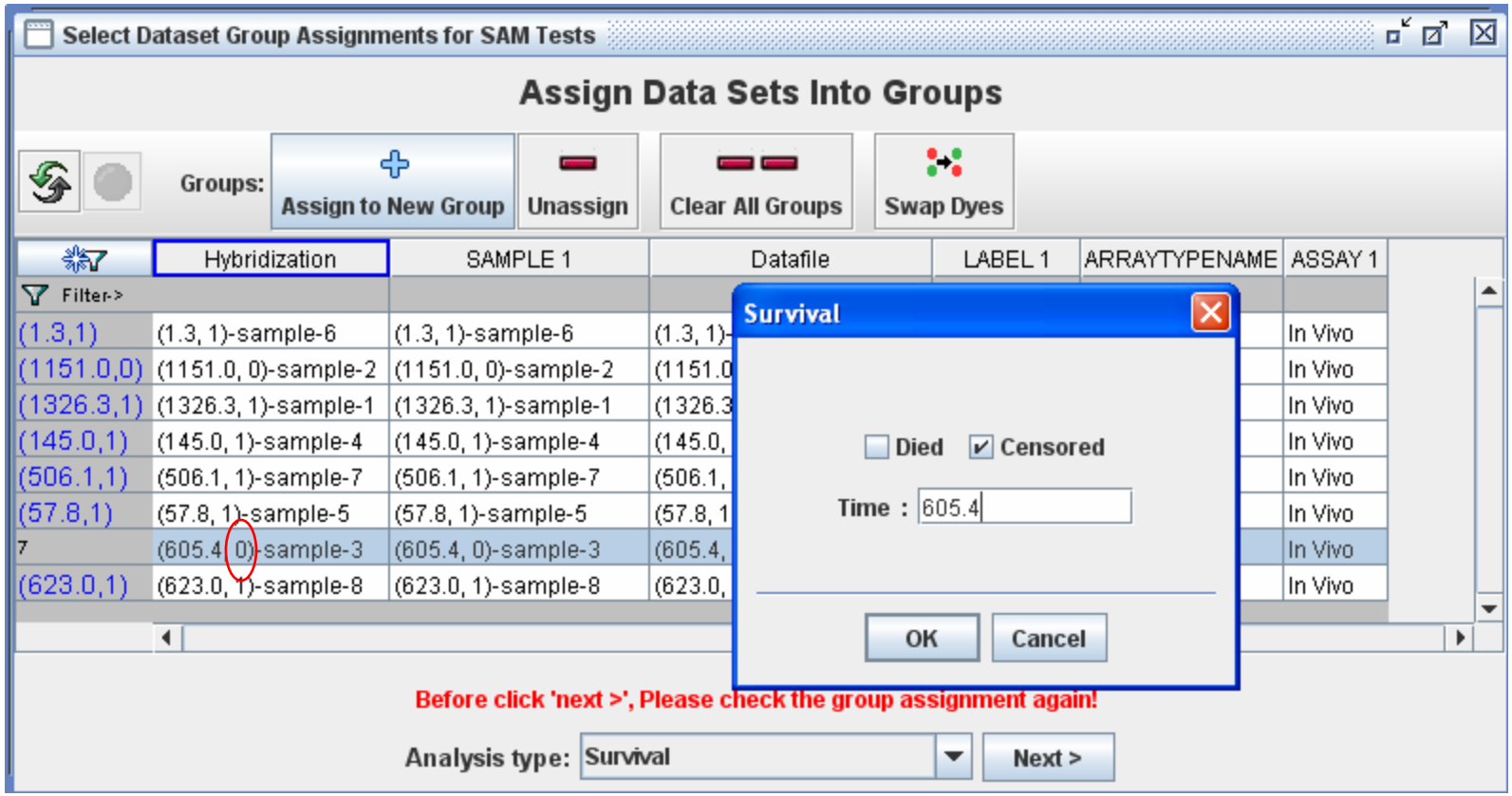
SAM-Test: Survival

Select the 2nd data which is in group 0, click “Assign to New Group” button. Check “Censored” check box and type in the time.



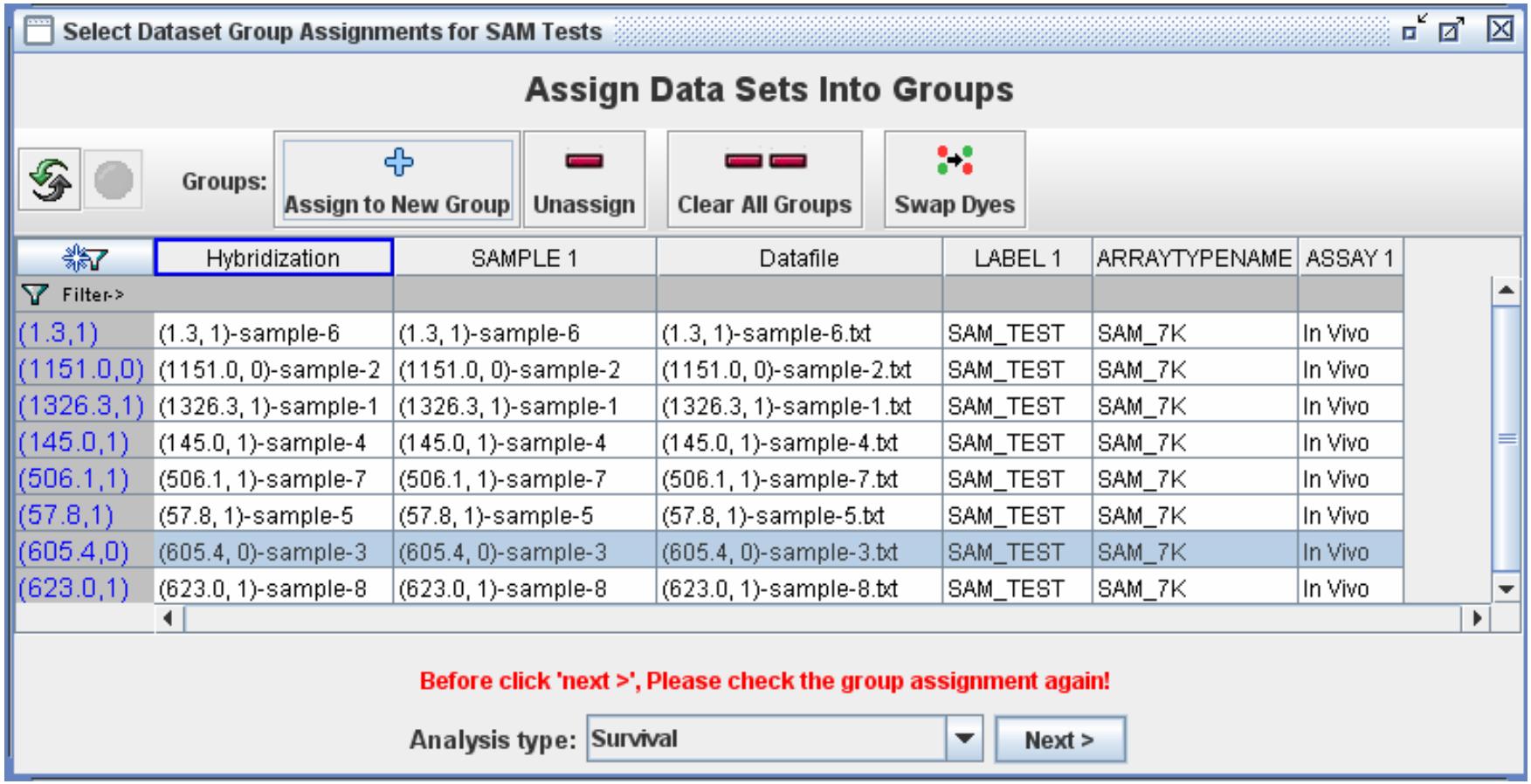
SAM-Test: Survival

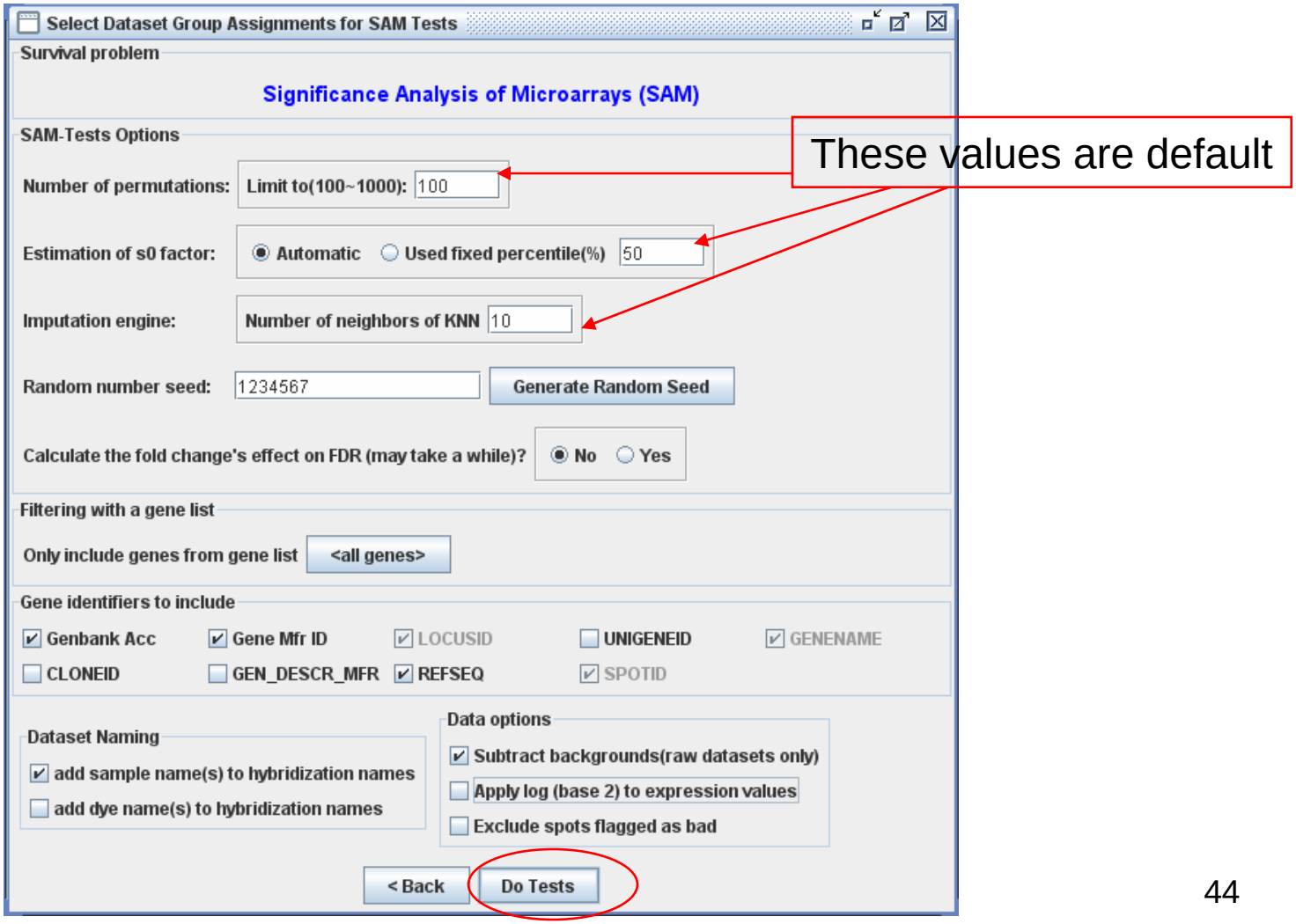
Do the same steps for the other data of group 0.



SAM-Test: Survival

Here is what looks like after assigning all the data. Click “Next” button.



	Hybridization	SAMPLE 1	Datafile	LABEL 1	ARRAYTYPENAME	ASSAY 1
(1.3,1)	(1.3, 1)-sample-6	(1.3, 1)-sample-6	(1.3, 1)-sample-6.txt	SAM_TEST	SAM_7K	In Vivo
(1151.0,0)	(1151.0, 0)-sample-2	(1151.0, 0)-sample-2	(1151.0, 0)-sample-2.txt	SAM_TEST	SAM_7K	In Vivo
(1326.3,1)	(1326.3, 1)-sample-1	(1326.3, 1)-sample-1	(1326.3, 1)-sample-1.txt	SAM_TEST	SAM_7K	In Vivo
(145.0,1)	(145.0, 1)-sample-4	(145.0, 1)-sample-4	(145.0, 1)-sample-4.txt	SAM_TEST	SAM_7K	In Vivo
(506.1,1)	(506.1, 1)-sample-7	(506.1, 1)-sample-7	(506.1, 1)-sample-7.txt	SAM_TEST	SAM_7K	In Vivo
(57.8,1)	(57.8, 1)-sample-5	(57.8, 1)-sample-5	(57.8, 1)-sample-5.txt	SAM_TEST	SAM_7K	In Vivo
(605.4,0)	(605.4, 0)-sample-3	(605.4, 0)-sample-3	(605.4, 0)-sample-3.txt	SAM_TEST	SAM_7K	In Vivo
(623.0,1)	(623.0, 1)-sample-8	(623.0, 1)-sample-8	(623.0, 1)-sample-8.txt	SAM_TEST	SAM_7K	In Vivo

SAM-Test: Survival