My methodology:

1) Obtain your state's Natural Heritage "tracked species" list.
2) organize list by S ranking, followed by Species Name alphabetically (see attached Excel spreadsheet).
3) Determine the number of taxa (in my case 208) that have the S1 designation.
4) Go to Random.org, and use the random integer set generator (see screen shot document attached). You need one set with 10 unique random integers. I selected integers between (and including) 2 and 209, since line 1 of my spreadsheet was the headings. Also, use the default settings, which provides the numbers in sequential order.
5) Random.org will give 10 unique randomly generated values (see page 2 of attached screen shot document).
6) Highlight the lines in spreadsheet that represent the randomly selected taxa.
7) Make an alphabetical list of the 10 taxa (also attached).

This exercise make me think about something important (here is where I'm throwing the wrench into the works). S1 taxa are often found from a single location or two. They are rare, and at the state-level exceedingly so. I wonder if we would not be better served by also (or instead) doing the same analysis on S2 taxa, which are known from a handful or dozen or two dozen locations within a state. The reason this may be important is that for the ultra-rare taxa, we are biasing our sample such that no herbaria within the state can have unique collections. That is if a plant species is known from a single location within a state, the options are for that taxon to be represented in only one collection in the state or more than one collection in the state. In either case, the vouchers will be from the single location, and if represented in more than one collection, these will represent redundancies without any unique information across collections. If we are arguing that small collections make important back-ups for larger collections, then this will be ok, but if we are interested in what unique vouchers small collections may have, then S2 collections may provide enough site locations in the states that show which collections have redundancies, and which provide unique information. It seems to me that S1 and S2 may tell different stories, which makes me think we should include both in our analysis, but that doubles our numbers from 10 to 20 just for "rare" taxa.

Best,

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