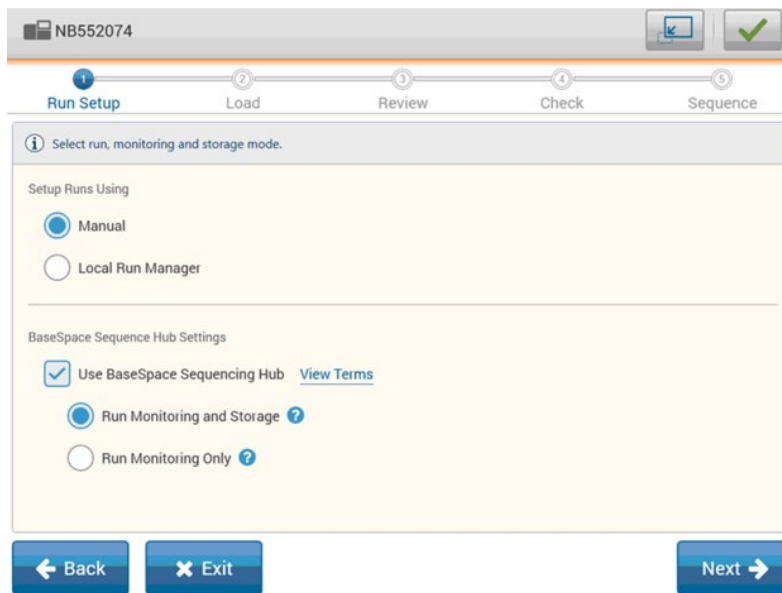


NextSeq (upgraded) run protocol:

- Home page



- To start a run, select **Sequence**



- Setup runs using: choose **Manual**
- Use BaseSpace Sequencing Hub:
 - Choose **Run Monitoring and Storage** or **Run Monitoring Only***

*If running Monitoring and Storage, you must upload a sample sheet in the next step. If you just want bcl files to be stored at BaseSpace, you may upload a fake sample sheet from a file located on the desktop. If you are not interested in storage, just want to monitor the run from BaseSpace, choose Run Monitoring Only.

- Select **Next**

- **Login** to BaseSpace
- **Select Next**

- Enter Run Name
- Enter Library ID (optional)
- Select Single Read or Paired End
- Enter read length for each read and indexes
- For Mars-seq: Read1 - 75, Read2 - 15, no indexes
- **Do not choose Custom Primers unless this is your design (not trivial)**
- Output should always be: [\\Stefan\nextseq_data\](#)
- Sample sheet: needs to be uploaded only if you chose Run Monitoring and Storage
- Purge consumables for this run - ✓
- **Select Next**

* Register the run (while sequencing is still on) in susanc as usual:

<https://ngs-pipeline.weizmann.ac.il/>

For more details see: <https://ngs-pipeline.weizmann.ac.il/ngsb/howto>