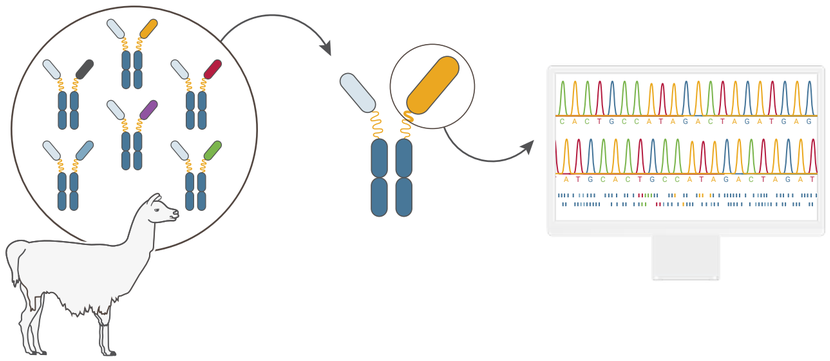
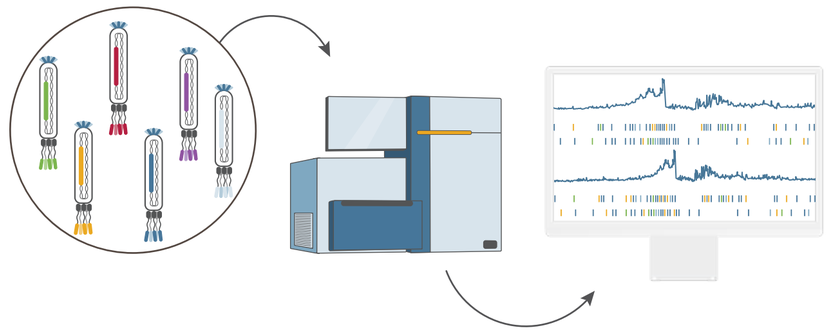
Harnessing the Power of NGS for **Nanobody Discovery and Development**

Challenges of Traditional Methods



- Nanobody sequences are analyzed and verified using Sanger sequencing
- Sanger sequencing is labor intensive with limited throughput, resulting in missed potential candidates
- Comparisons between libraries of different repertoires or biopanning rounds remain difficult

Benefits of NGS Methods



- Thorough analysis by sequencing tens of millions of sequences in parallel
- Mining the entire repertoire of phage display libraries across multiple rounds of selection
- Continuous monitoring of the gradual enrichment of sequences over multiple rounds of biopanning and selection
- Identifing even the lowest-abundance clones that become enriched throughout multiple rounds of biopanning
- Rapid identification of exceptional binder sequences with superior characteristics that may have been overlooked using traditional methods

Genedata Selector Solution

- Playbooks enable the automation of analysis workflows, without the need for bioinformatics expertise
- Transparent information management to track samples and generate reports in a GMP compliant environment
- Centralization of data management and processing
- Preservation of an organization’s memory
- Accelerated decision-making & speed-to-market
- Prerequisite for any centralized AI analysis or predictive work to discover new binders via NGS
- FAIRification of NGS data
- Compliance to regulatory requirements for GMP