

Research Tools Completeness Score Report

NF-OSI

2025-11-07

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Executive Summary

This report provides a comprehensive analysis of the completeness scores for research tools and biobanks in the NF-OSI database. The scoring system evaluates resources across multiple dimensions:

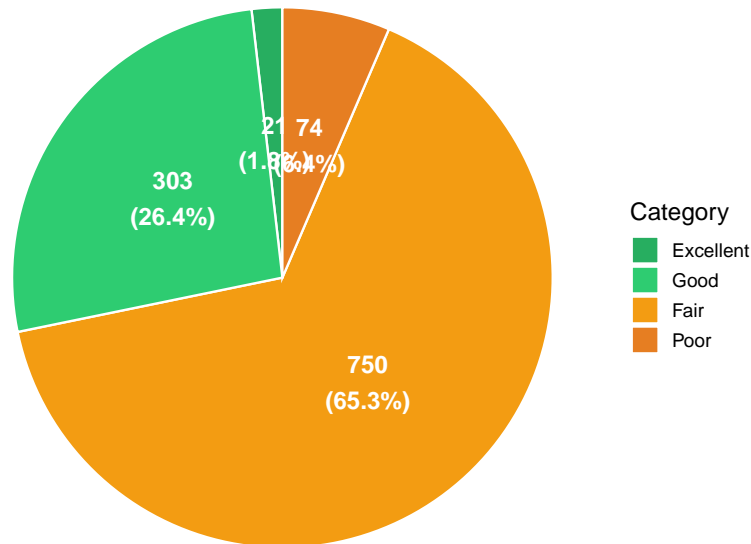
- **Availability** (30 points): Biobank URL, vendor/developer info, RRID, and DOI
- **Critical Info** (30 points): Type-specific essential fields
- **Other Info** (15 points): Type-specific additional fields
- **Observations** (25 points): Scientific characterizations with DOI weighting

Total Maximum Score: 100 points

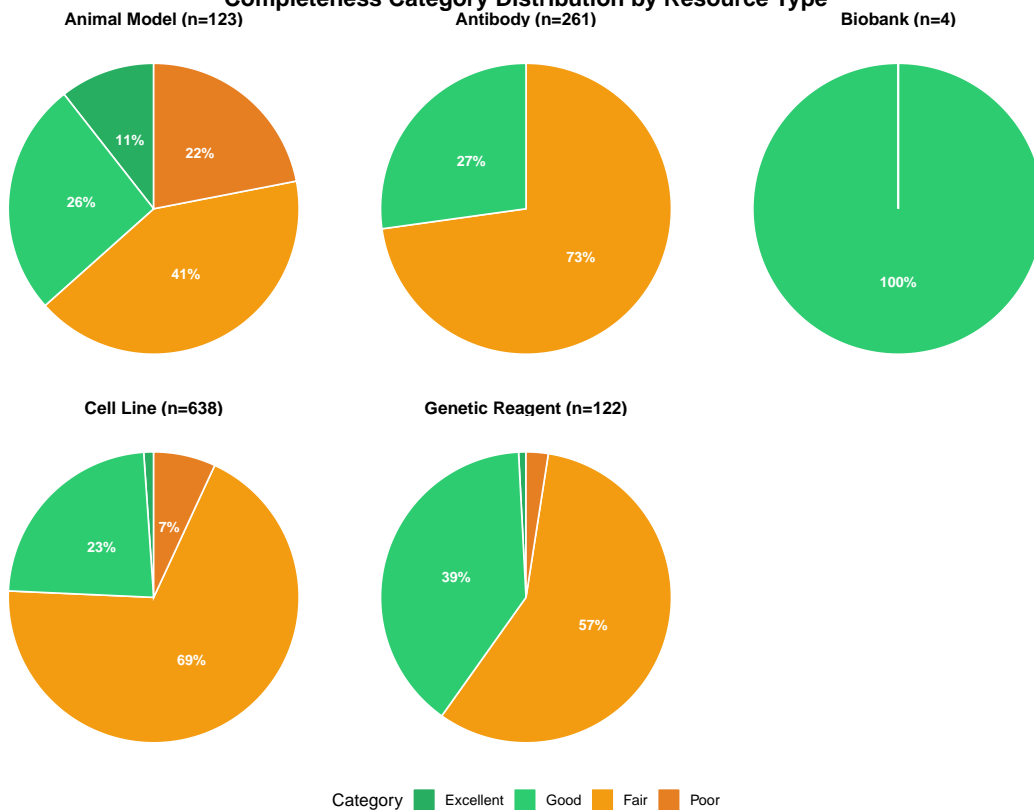
Completeness Category Distribution

Overall Distribution of Completeness Categories

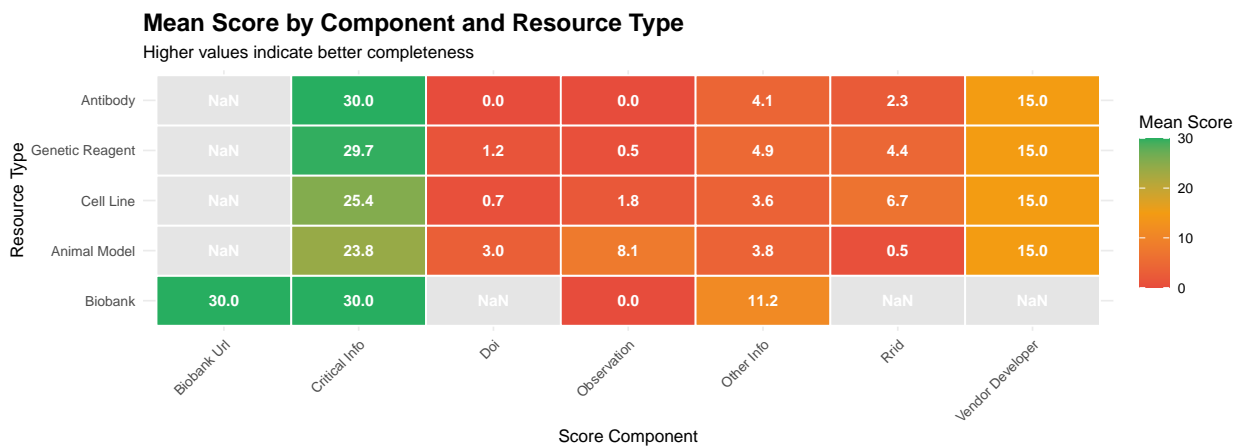
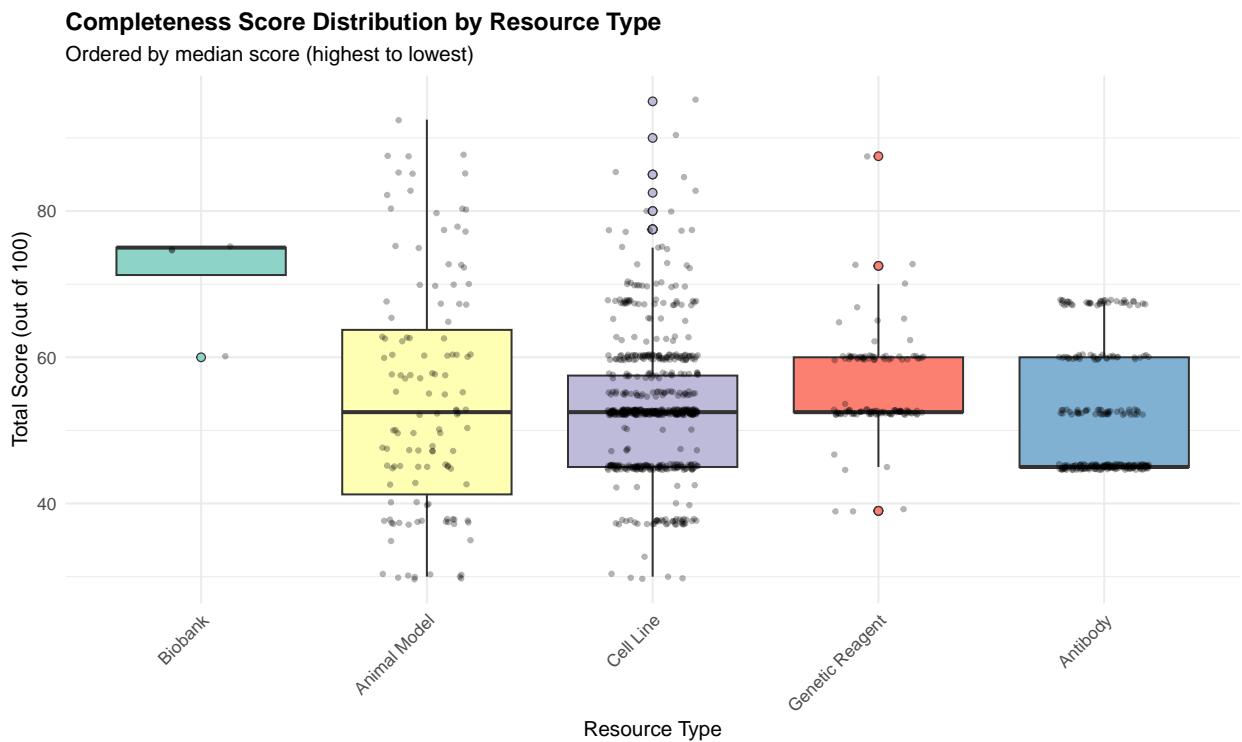
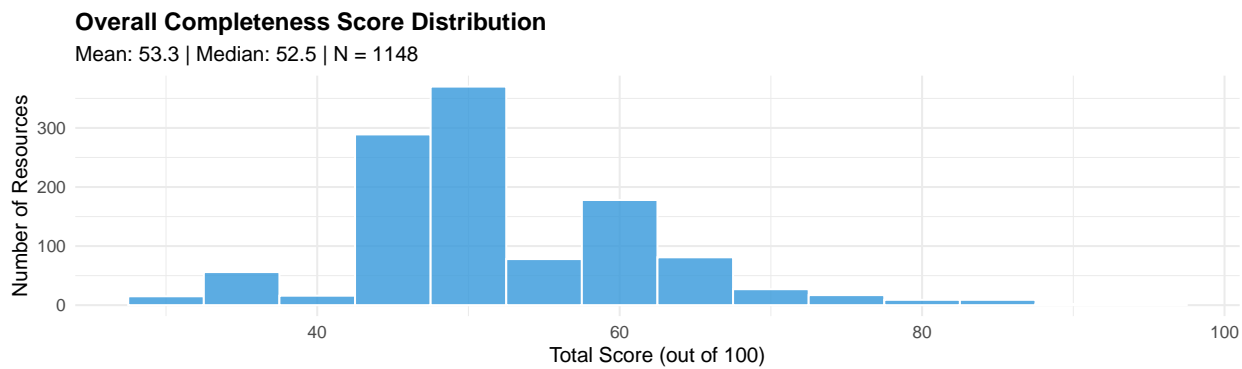
Total: 1148 resources



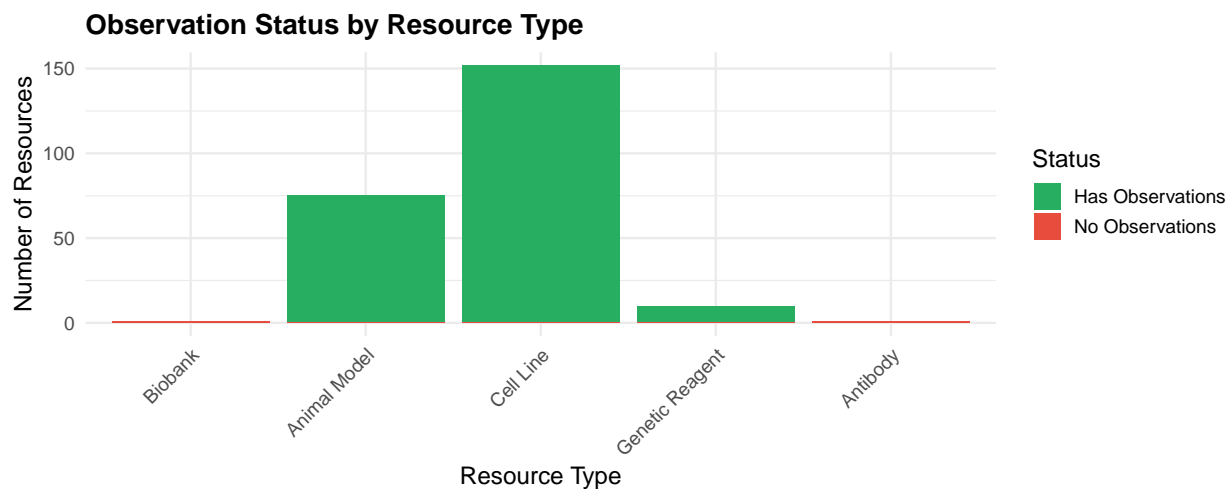
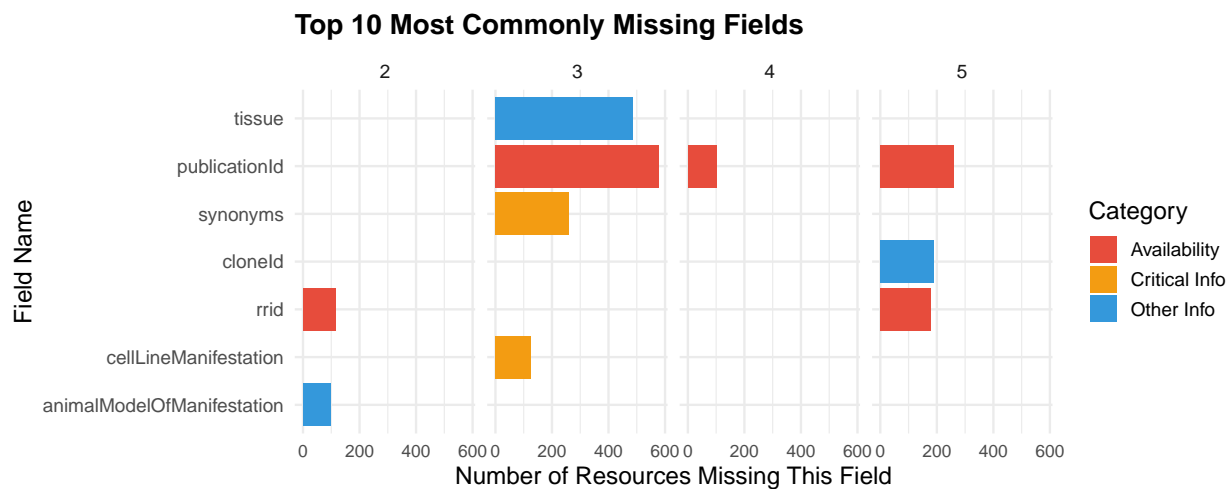
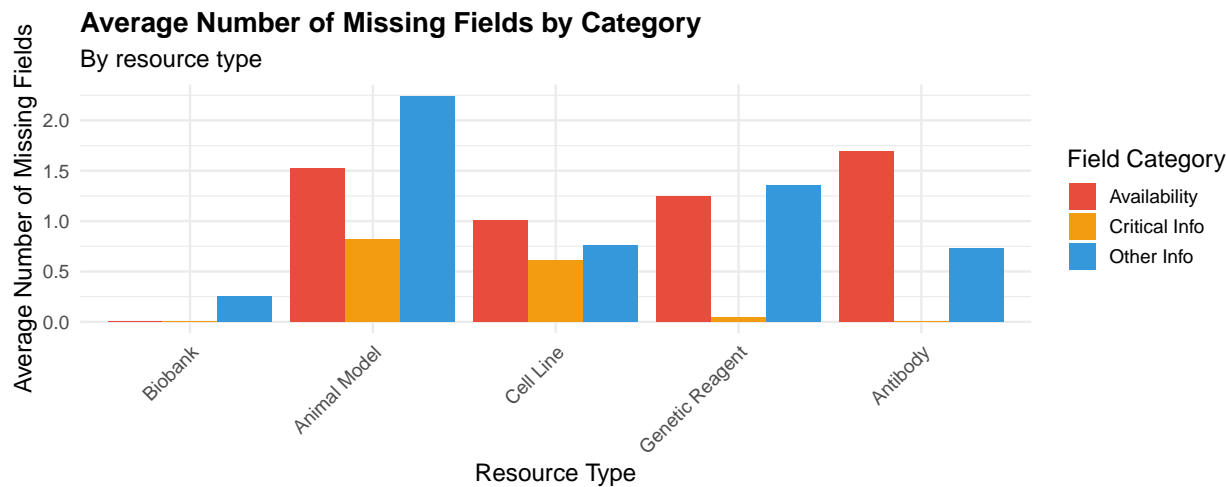
Completeness Category Distribution by Resource Type



Score Distribution



Missing Fields Analysis



Summary Statistics Tables

Table 1: Overall Summary Statistics

| Metric | Value |
|-----------------|---------|
| Total Resources | 1148.00 |
| Mean Score | 53.29 |
| Median Score | 52.50 |
| Std Dev | 9.70 |
| Min Score | 30.00 |
| Max Score | 95.00 |
| Range | 65.00 |

Table 2: Summary Statistics by Resource Type

| Resource Type | Count | Mean | Median | Std Dev | Min | Max |
|-----------------|-------|-------|--------|---------|-----|------|
| Biobank | 4 | 71.25 | 75.0 | 7.50 | 60 | 75.0 |
| Genetic Reagent | 122 | 55.75 | 52.5 | 6.30 | 39 | 87.5 |
| Animal Model | 123 | 54.35 | 52.5 | 15.98 | 30 | 92.5 |
| Cell Line | 638 | 53.26 | 52.5 | 8.91 | 30 | 95.0 |
| Antibody | 261 | 51.41 | 45.0 | 8.35 | 45 | 67.5 |

Table 3: Top 10 Most Complete Resources

| Resource Name | Type | RRID | Score | Category |
|---------------------------------|-----------------|---------------------|-------|-----------|
| SK-N-AS | Cell Line | rrid:CVCL_1700 | 95.0 | Excellent |
| Nf14F/4F;CAGGCre-ERTM | Animal Model | NA | 92.5 | Excellent |
| GI-ME-N | Cell Line | rrid:CVCL_1232 | 90.0 | Excellent |
| NF1flox4/Arg681*;Dhh-Cre | Animal Model | NA | 87.5 | Excellent |
| Nf1+/-GFAPCKO | Animal Model | NA | 87.5 | Excellent |
| NF1fl/fl;Dhh-Cre | Animal Model | NA | 87.5 | Excellent |
| pAMP-CY1_NF1 T1 (+minintr, KDR) | Genetic Reagent | rrid:Addgene_119200 | 87.5 | Excellent |
| 2XSB | Cell Line | rrid:CVCL_A7NI | 85.0 | Excellent |
| Capan-1 | Cell Line | rrid:CVCL_0237 | 85.0 | Excellent |
| Nf1tm1.1Kest | Animal Model | NA | 85.0 | Excellent |

Table 4: Resources Needing Improvement (N = 74)

| Resource Name | Type | Score | Category |
|---|--------------|-------|----------|
| Dh5 alpha | Cell Line | 30.0 | Poor |
| ELK-TAD Luciferase Reporter HEK293 Stable | Cell Line | 30.0 | Poor |
| c.1149C > A NF1-mutant hiPSCs | Cell Line | 30.0 | Poor |
| c.3431-32_dupGT NF1-mutant hiPSCs | Cell Line | 30.0 | Poor |
| U87-NF1-419 | Cell Line | 30.0 | Poor |
| Krox20;Nf1flox/- | Animal Model | 30.0 | Poor |
| MPNST-Nf1-001 | Animal Model | 30.0 | Poor |

| Resource Name | Type | Score | Category |
|---|--------------|-------|----------|
| MPNST-Nf1-002 | Animal Model | 30.0 | Poor |
| MPNST-SP-001 | Animal Model | 30.0 | Poor |
| MPSNT-SP-002 | Animal Model | 30.0 | Poor |
| Nf1 GEM | Animal Model | 30.0 | Poor |
| Nf1-/- Drosophila | Animal Model | 30.0 | Poor |
| Nf1Fcr | Animal Model | 30.0 | Poor |
| Prx1-Cre+/- Nf1flox/+ | Animal Model | 30.0 | Poor |
| HS-PSS | Cell Line | 32.5 | Poor |
| miR-155 +/-;Nf1flox/+ | Animal Model | 35.0 | Poor |
| Nf1bdelta55 zebrafish | Animal Model | 35.0 | Poor |
| HEK293 NF1 -/- with R1306X mNf1 cDNA | Cell Line | 37.5 | Poor |
| WT ES | Cell Line | 37.5 | Poor |
| HEK293 NF1 -/- Exon 47 insT #14 | Cell Line | 37.5 | Poor |
| HEK293 NF1 -/- with R1947X mNf1 cDNA | Cell Line | 37.5 | Poor |
| Dhh-Cre; NF1Arg681*/flox Schwann Cells | Cell Line | 37.5 | Poor |
| Schwann cell NF1 -/- (iPN97.4 #24) | Cell Line | 37.5 | Poor |
| ELK-TAD Luciferase Reporter HEK293 Stable NF1 -/- | Cell Line | 37.5 | Poor |
| Schwann cell NF1 -/- with R816X mNf1 cDNA | Cell Line | 37.5 | Poor |
| Schwann cell NF1 -/- with WT tagged mNf1 cDNA | Cell Line | 37.5 | Poor |
| HEK293 NF1 -/- with R461X mNf1 cDNA | Cell Line | 37.5 | Poor |
| Nf1-/- HEK 293 | Cell Line | 37.5 | Poor |
| iPSC NF1 WT | Cell Line | 37.5 | Poor |
| Nf1Arg681*/+ ES | Cell Line | 37.5 | Poor |
| Nf1Arg681/Arg681 ES | Cell Line | 37.5 | Poor |
| Nf1-/- Epithelial lung cells | Cell Line | 37.5 | Poor |
| HEK293 NF1 -/- Exon 52 R2550X #5 | Cell Line | 37.5 | Poor |
| NF1-R68X Embryonic cells | Cell Line | 37.5 | Poor |
| iPSC NF1 +/- BJFF.6 bkgd | Cell Line | 37.5 | Poor |
| HEK293 NF1 -/- with R2550X mNf1 cDNA | Cell Line | 37.5 | Poor |
| HEK293 NF1 -/- Exon 17 #A15 G629R cryptic splice | Cell Line | 37.5 | Poor |
| ScienCell Schwann cells | Cell Line | 37.5 | Poor |
| HEK293 NF1 -/- with R816X mNf1 cDNA | Cell Line | 37.5 | Poor |
| Schwann cell NF1 -/- with R681X mNf1 cDNA | Cell Line | 37.5 | Poor |
| HEK293 NF1 -/- with R192X mNf1 cDNA | Cell Line | 37.5 | Poor |
| SIGTR ES cell line AA0320 | Cell Line | 37.5 | Poor |
| CPTC-NF1-1 | Cell Line | 37.5 | Poor |
| CPTC-NF1-2 | Cell Line | 37.5 | Poor |
| CPTC-NF1-3 | Cell Line | 37.5 | Poor |
| FMS-1 | Cell Line | 37.5 | Poor |
| MCF10A_NF1_1 | Cell Line | 37.5 | Poor |
| MCF10A_NF1_7A1 | Cell Line | 37.5 | Poor |
| MCF10A_NF1_7B2 | Cell Line | 37.5 | Poor |
| MPNST-90 | Cell Line | 37.5 | Poor |
| MPNST-91 | Cell Line | 37.5 | Poor |
| MPNST-92 | Cell Line | 37.5 | Poor |
| NFS-1 | Cell Line | 37.5 | Poor |
| NMS-2PC | Cell Line | 37.5 | Poor |
| XL110 | Cell Line | 37.5 | Poor |
| B6;CBA-Nf1/Flmg | Animal Model | 37.5 | Poor |
| C57BL/6JSmoc-Nf1em1Smoc | Animal Model | 37.5 | Poor |
| C57BL/6JSmoc-Nf1tm1(flox)Smoc | Animal Model | 37.5 | Poor |
| Nf1-/- | Animal Model | 37.5 | Poor |

| Resource Name | Type | Score | Category |
|--|-----------------|-------|----------|
| CisNf1+/-; p53+/- | Animal Model | 37.5 | Poor |
| Nf1 flox/+; DhhCre/+ | Animal Model | 37.5 | Poor |
| Nf1P1/Nf1E1 Drosophila | Animal Model | 37.5 | Poor |
| Nf1-/-MyoD | Animal Model | 37.5 | Poor |
| Nf1:p53 | Animal Model | 37.5 | Poor |
| Nf1+/Arg681 | Animal Model | 37.5 | Poor |
| Nf1flox/-;P0A-Cre- | Animal Model | 37.5 | Poor |
| Nf1flox/+;P0A-Cre(+) | Animal Model | 37.5 | Poor |
| Nf1flox/flox;P0A-cre- | Animal Model | 37.5 | Poor |
| Nf1flox/mut | Animal Model | 37.5 | Poor |
| Nf1P1 Drosophila | Animal Model | 37.5 | Poor |
| Nf1tm1a(KOMP)Wtsi | Animal Model | 37.5 | Poor |
| Neurofibromin CRISPR Plasmids (h) | Genetic Reagent | 39.0 | Poor |
| Neurofibromin CRISPR Plasmids (m) | Genetic Reagent | 39.0 | Poor |
| Neurofibromin siRNA and shRNA Plasmids | Genetic Reagent | 39.0 | Poor |

Recommendations

Based on the analysis above, here are key recommendations for improving resource completeness:

1. **Focus on Low-Scoring Components:** Identify which score components (availability, critical info, other info, observations) have the lowest average scores across resource types and prioritize filling those fields.
2. **Resource Type Priorities:** Target resource types with lower median scores for systematic improvement efforts.
3. **Observation Documentation:** Encourage researchers to submit observations with publication DOIs, as these contribute more points (7.5 vs 2.5) to the completeness score.
4. **RRID Registration:** Ensure all resources have registered RRIDs to improve findability and citation.
5. **Vendor/Developer Information:** Complete vendor or developer information for resources to improve availability scores.