Medicare Advisory Panel on Clinical Diagnostic Laboratory Tests Meeting
July 22-23, 2019

2020 Clinical Laboratory Fee Schedule FACA Panel Voting Results
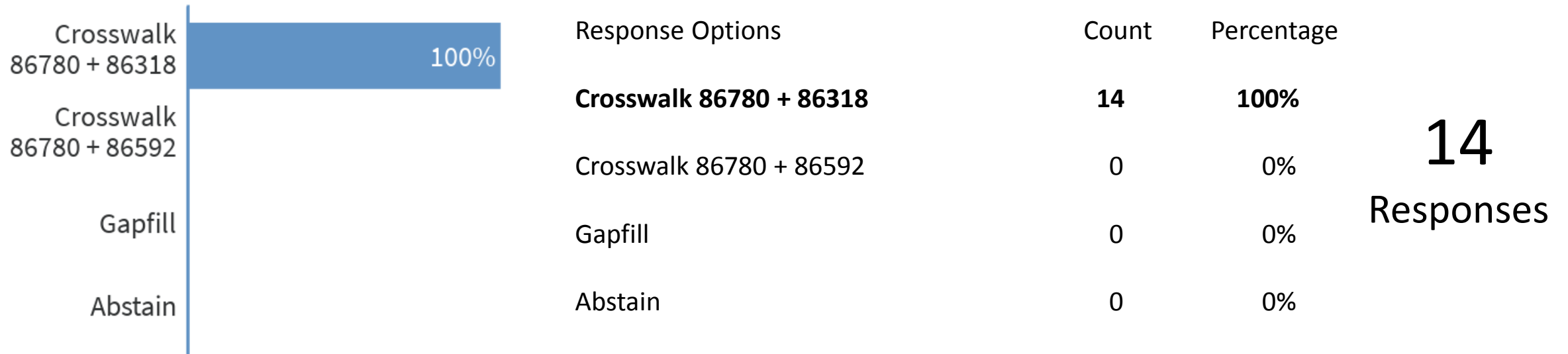
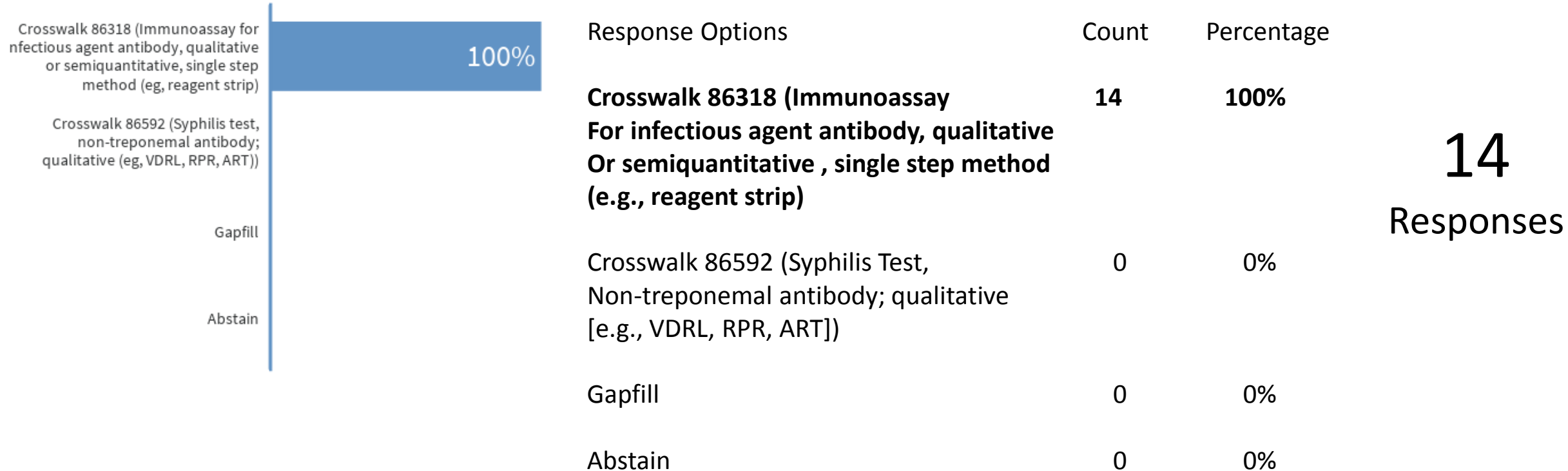# Voting Results Overview

90
Polls

14 Participants (#1-36)
13 Participants (#37-90)

1. 0064U: Antibody, Treponema Pallidum, Total and Rapid Plasma Reagin (RPR), Immunoassay Qualitative

Response Options	Count	Percentage
Crosswalk 86780 + 86318	**14**	**100%**
Crosswalk 86780 + 86592	0	0%
Gapfill	0	0%
Abstain	0	0%

14
Responses

2. 0065U: Syphilis Test , Non-treponemal antibody, Immunoassay, Qualitative (RPR)

Response Options	Count	Percentage
Crosswalk 86318 (Immunoassay For infectious agent antibody, qualitative Or semiquantitative , single step method (e.g., reagent strip)	**14**	**100%**
Crosswalk 86592 (Syphilis Test, Non-treponemal antibody; qualitative [e.g., VDRL, RPR, ART])	0	0%
Gapfill	0	0%
Abstain	0	0%

14
Responses

3. 0068U: Candida species panel (C. albicans, C. glabrata, C. parapsilosis, C. kruseii, C. tropicalis, and C. auris), amplified probe technique with qualitative report of the presence or absence of each species
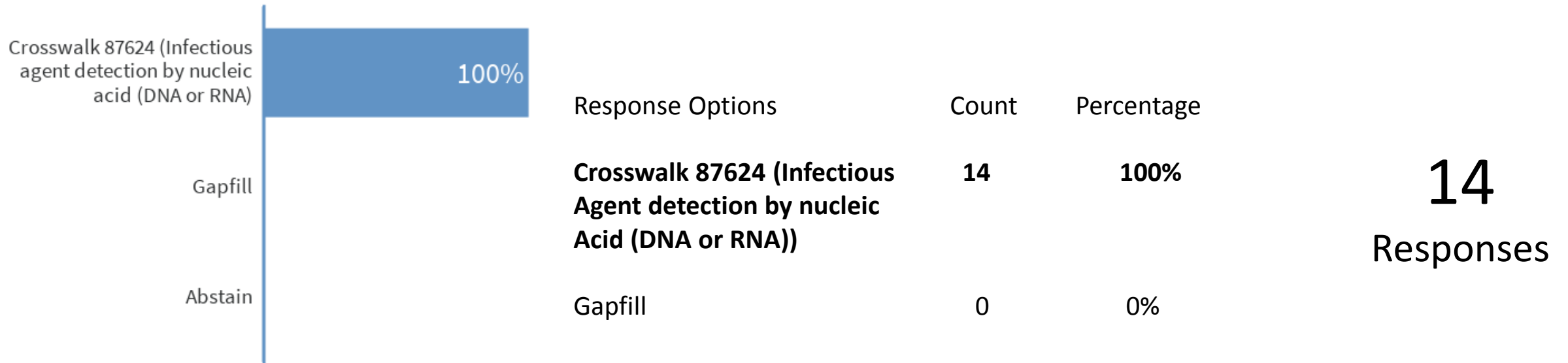
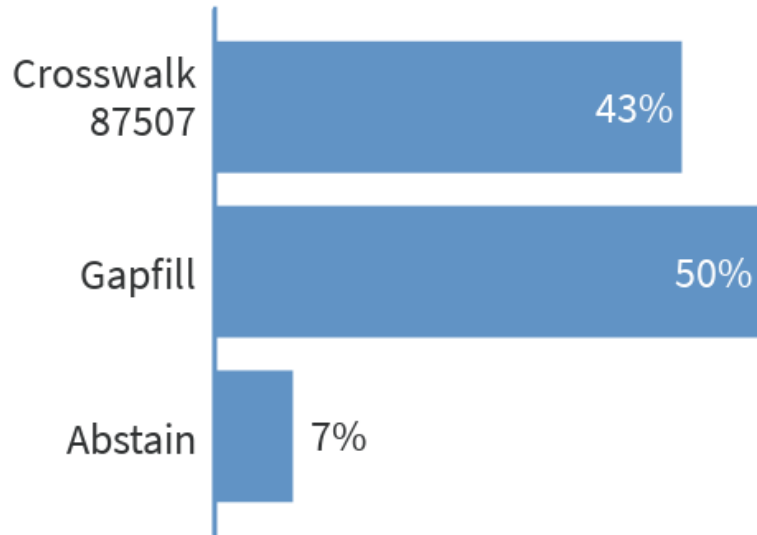| Response Options	Count	Percentage
Crosswalk 87632	**14**	**100%**
Gapfill	0	0%
Abstain	0	0%

14 Responses

4. 0086U: Infectious disease (bacterial and fungal), organism identification, blood culture, using rRNA FISH, 6 or more organism targets, reported as positive or negative with phenotypic minimum inhibitory concentration (MIC)-based antimicrobial susceptibility

Response Options	Count	Percentage
Gapfill	**13**	**93%**
Abstain	1	7%

Gapfill 93%

Abstain 7%

14 Responses

5. 0096U: Human papillomavirus (HPV), high-risk types (ie, 16, 18, 31, 33, 35, 39, 45, 51, 52, 56, 58, 59, 66, 68), male urine

Response Options	Count	Percentage
Crosswalk 87624 (Infectious Agent detection by nucleic Acid (DNA or RNA))	**14**	**100%**
Gapfill	0	0%

14
Responses

6. 0097U: Gastrointestinal Pathogen, Multiplex Reverse Transcription and Multiplex Amplified Probe Technique, Multiple Types or Subtypes, 22 Targets

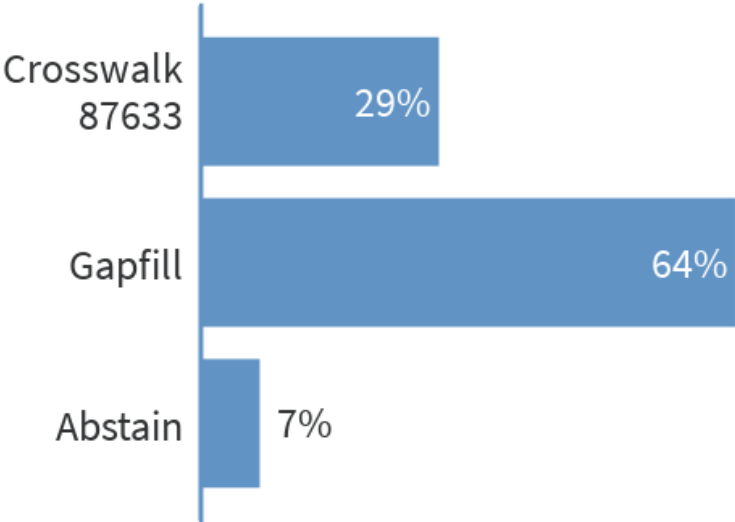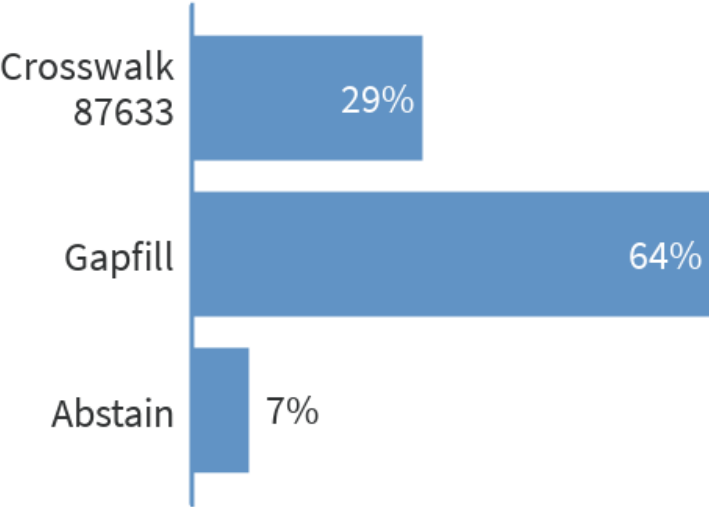| Response Options	Count	Percentage
Crosswalk 87507	6	43%
Gapfill	7	50%
Abstain	1	7%

14
Responses

7. 0098U: Respiratory Pathogen, Multiplex Reverse Transcription and Multiplex Amplified Probe Technique, Multiple Types or Subtypes, 14 Targets

Response Options	Count	Percentage
Crosswalk 87633	4	29%
Gapfill	**9**	**64%**
Abstain	1	7%

14
Responses

8. 0099U: Respiratory Pathogen, Multiplex Reverse Transcription and Multiple Amplified Probe Technique, Multiple Types or Subtypes, 20 Targets

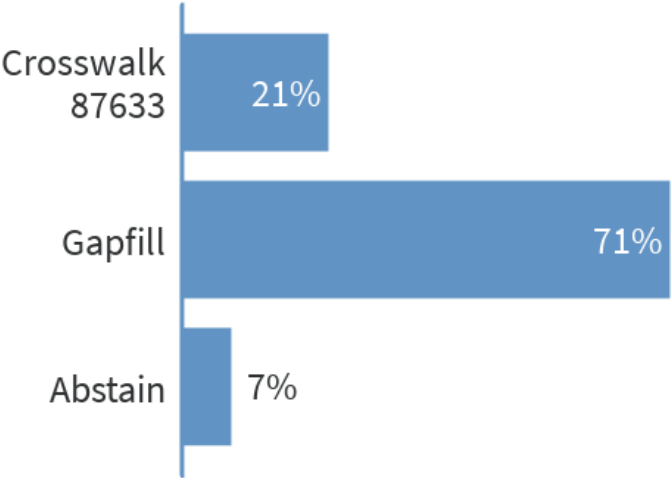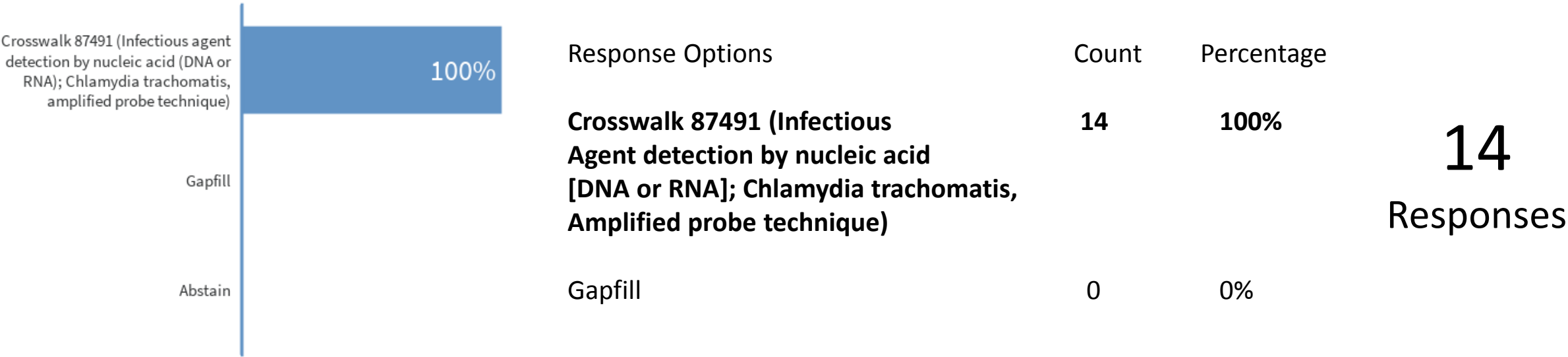| Response Options	Count	Percentage
Crosswalk 87633	4	29%
Gapfill	**9**	**64%**
Abstain	1	7%

14
Responses

9. 0100U: Respiratory Pathogen, Multiplex Reverse Transcription and Multiple Amplified Probe Technique, Multiple Types or Subtypes, 20 Targets
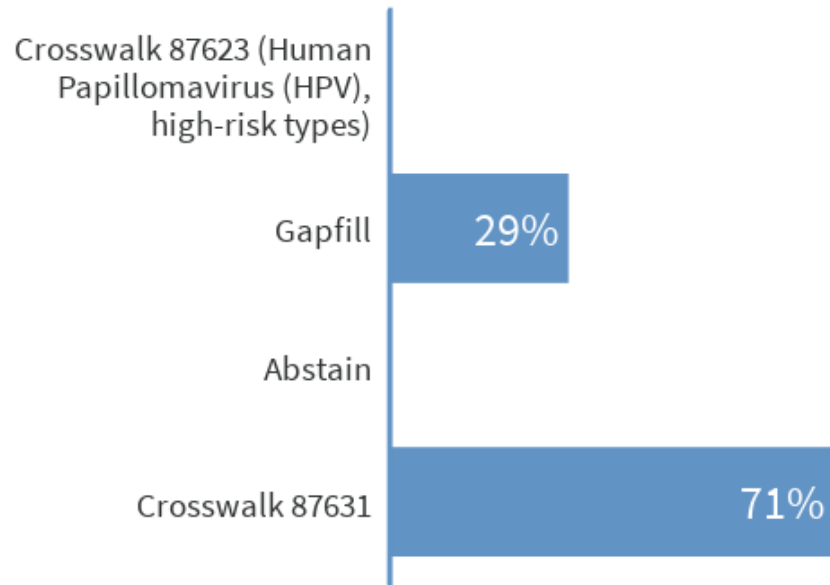

Response Options	Count	Percentage
Crosswalk 87633	3	21%
Gapfill	10	71%
Abstain	1	7%

14 Responses

10. 8XXXX: Infectious Agent Detection by Nucleic Acid (DNA or RNA); Mycoplasma Genitalium , Amplified Probe Technique

Response Options	Count	Percentage
Crosswalk 87491 (Infectious Agent detection by nucleic acid [DNA or RNA]; Chlamydia trachomatis, Amplified probe technique)	**14**	**100%**
Gapfill	0	0%

14
Responses

11. 0109U: Infectious Disease (Aspergillus Species) Real-time PCR for Detection of DNA from 4 Species

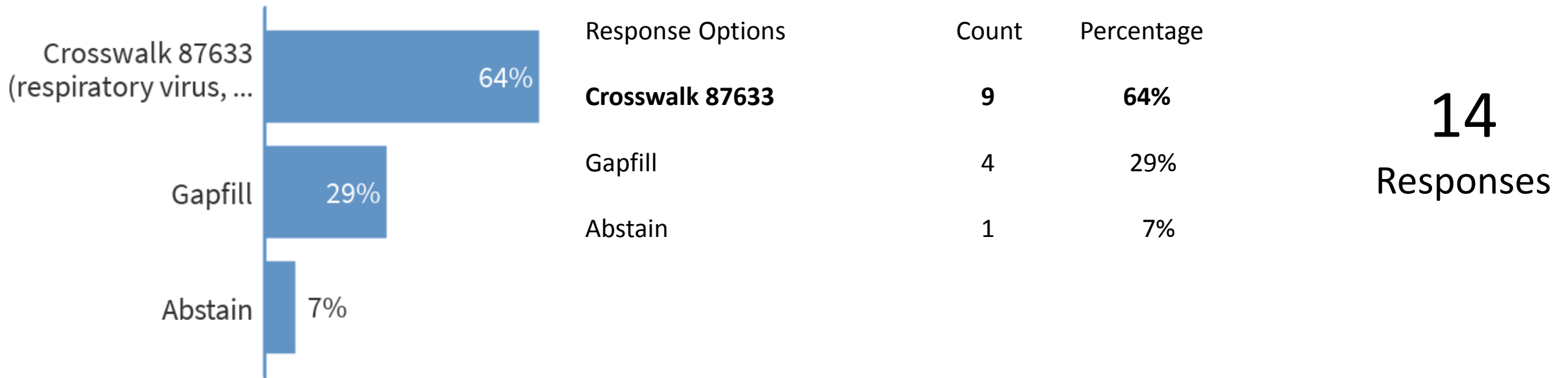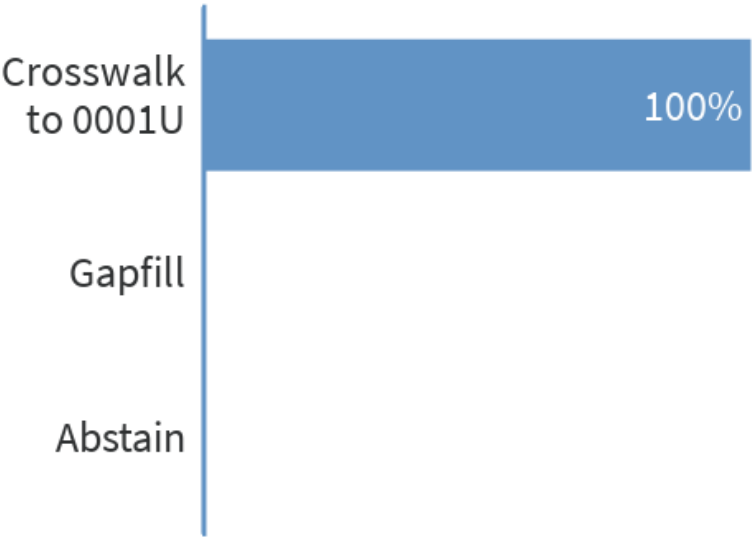| Response Options	Count	Percentage
Gapfill	4	29%
Crosswalk 87631	**10**	**71%**
Crosswalk 87623	0	0%

14
Responses

12. 0115U: Respiratory infectious agent detection by nucleic acid (DNA and RNA), 18 viral types and subtypes and 2 bacterial targets, amplified probe technique, including multiplex reverse transcription for RNA targets, each analyte reported as detected or not detected
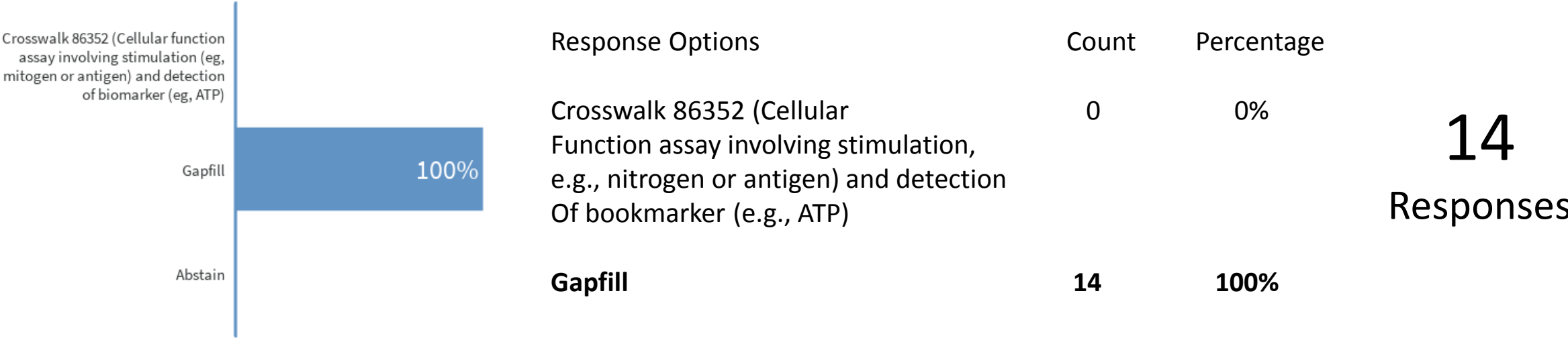

Response Options	Count	Percentage
Crosswalk 87633	**9**	**64%**
Gapfill	4	29%
Abstain	1	7%

14
Responses

13. 0084U: Red blood cell antigen typing, DNA, genotyping of 10 blood groups with phenotype prediction of 37 red blood cell antigens

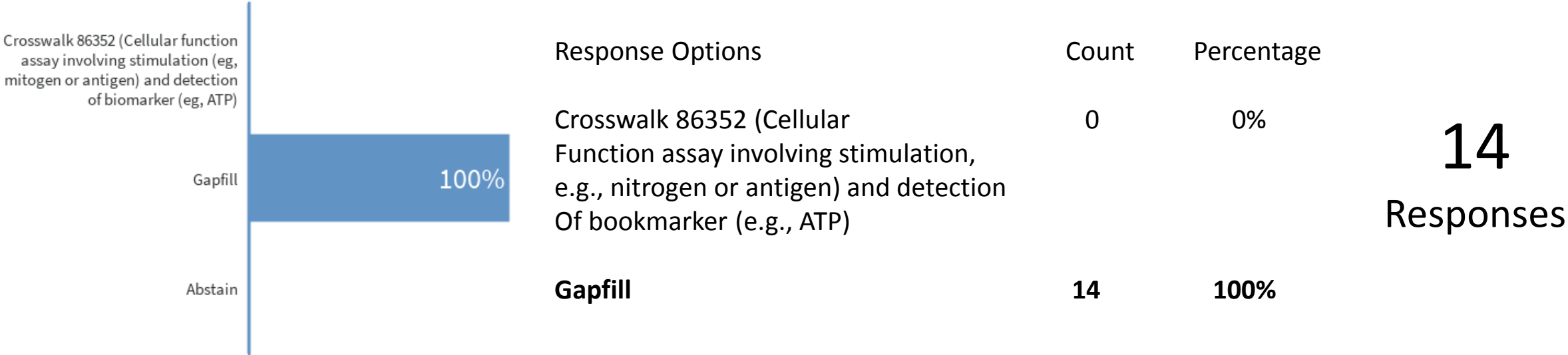| Response Options	Count	Percentage
Crosswalk to 0001U	**14**	**100%**
Gapfill	0	0%

14
Responses

14. 0121U: Sickle Cell Disease, Microfluidic Flow Adhesion (VCAM-1), Whole Blood

Response Options	Count	Percentage
Crosswalk 86352 (Cellular Function assay involving stimulation, e.g., nitrogen or antigen) and detection Of bookmarker (e.g., ATP)	0	0%
Gapfill	**14**	**100%**

14 Responses

15. 0122U: Sickle cell disease, microfluidic flow adhesion (P-Selectin), whole blood

Response Options	Count	Percentage
Crosswalk 86352 (Cellular Function assay involving stimulation, e.g., nitrogen or antigen) and detection Of bookmarker (e.g., ATP)	0	0%
Gapfill	**14**	**100%**

14
Responses

16. 0123U: Mechanical Fragility, RBC, Shear Stress and Spectral Analysis Profiling

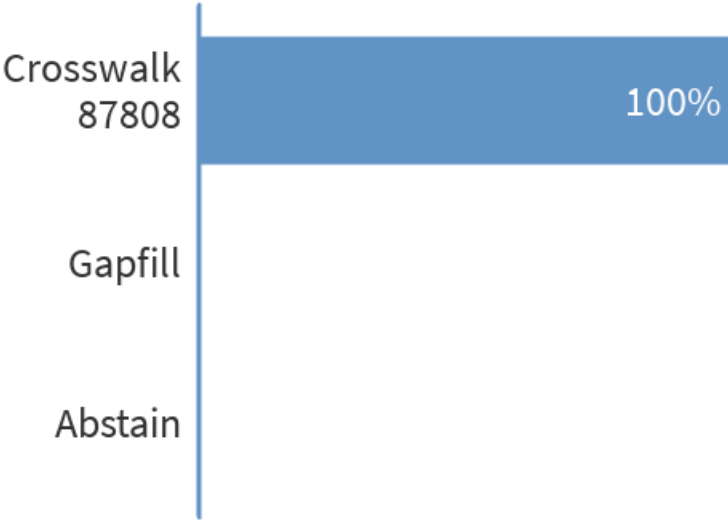| Response Options	Count	Percentage
Crosswalk 86352 (Cellular Function assay involving stimulation, e.g., nitrogen or antigen) and detection Of bookmarker (e.g., ATP)	0	0%
Gapfill	**14**	**100%**

14
Responses

17. 0062U: Autoimmune (System Lupus Erythematosus), IgG and IgM Analysis of 80 Biomarkers, Utilizing Serum, Algorithm Reported with a Risk Score

Response Options	Count	Percentage
Gapfill	**14**	**100%**

14
Responses

18. 0063U: Neurology (autism), 32 amines by LC-MS/MS, using plasma, algorithm reported as metabolic signature associated with autism spectrum disorder
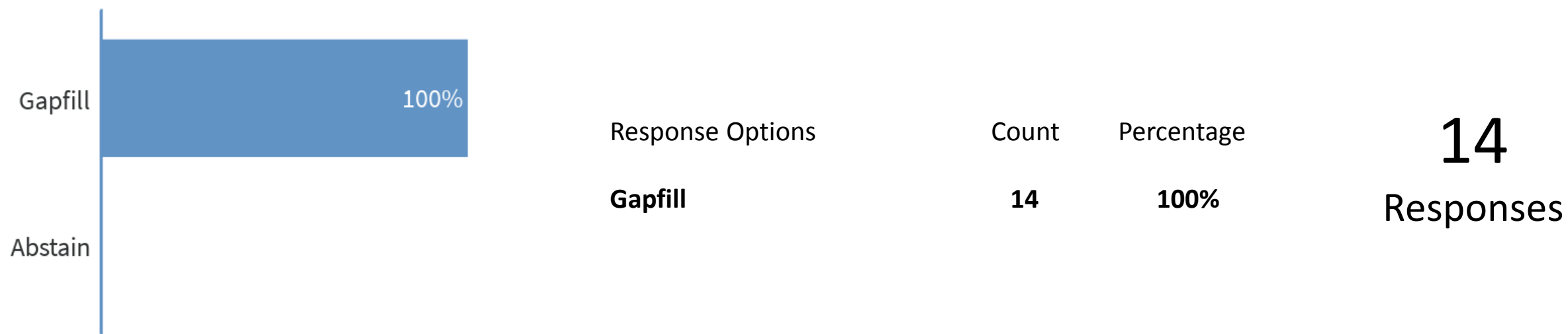

Response Options	Count	Percentage
Crosswalk 0003U	0	0%
Gapfill	**14**	**100%**

14
Responses

19. 0066U: Placenta Alpha-micro Globlulin-1 (PAMG-1) Immunoassay with Direct Optical Observation, Cervico-vaginal Fluid, Each Specimen
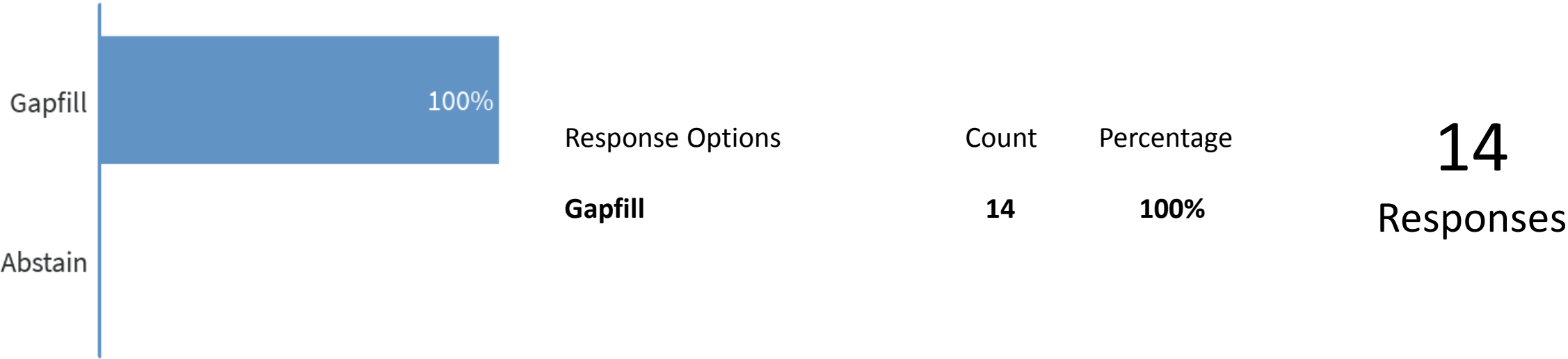

Response Options	Count	Percentage
Crosswalk 87808	**14**	**100%**
Gapfill	0	0%

14
Responses

20. 0067U: Oncology (Breast) Immunohistochemistry Protein Expression Profiling of 4 Biomarkers

Response Options	Count	Percentage
Gapfill	**14**	**100%**

14
Responses

21. 0077U: Immunoglobulin Paraprotein (M-protein), Qualitative, Immunoprecipitation and Mass Spectrometry, Blood or Urine, Including Isotype

Response Options	Count	Percentage
Gapfill	**14**	**100%**

14
Responses

22. 0082U: Drug test(s), definitive, 90 or more drugs or substances, definitive chromatography with mass spectrometry, and presumptive, any number of drug classes, by instrument chemistry analyzer (utilizing immunoassay), urine, report of presence or absence of each drug, drug metabolite or substance with description and severity of significant interactions per date of service

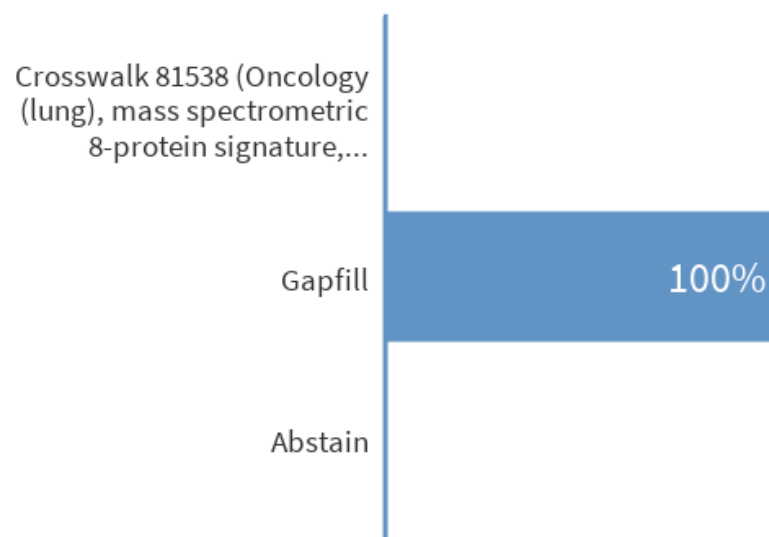| Response Options	Count	Percentage
Gapfill	**13**	**93%**
Abstain	1	7%

14
Responses

23. 0085U: Cytolethal Distending Toxin B (CdtB) and Vinculin IgG Antibodies by Immunoassay (i.e., ELISA)

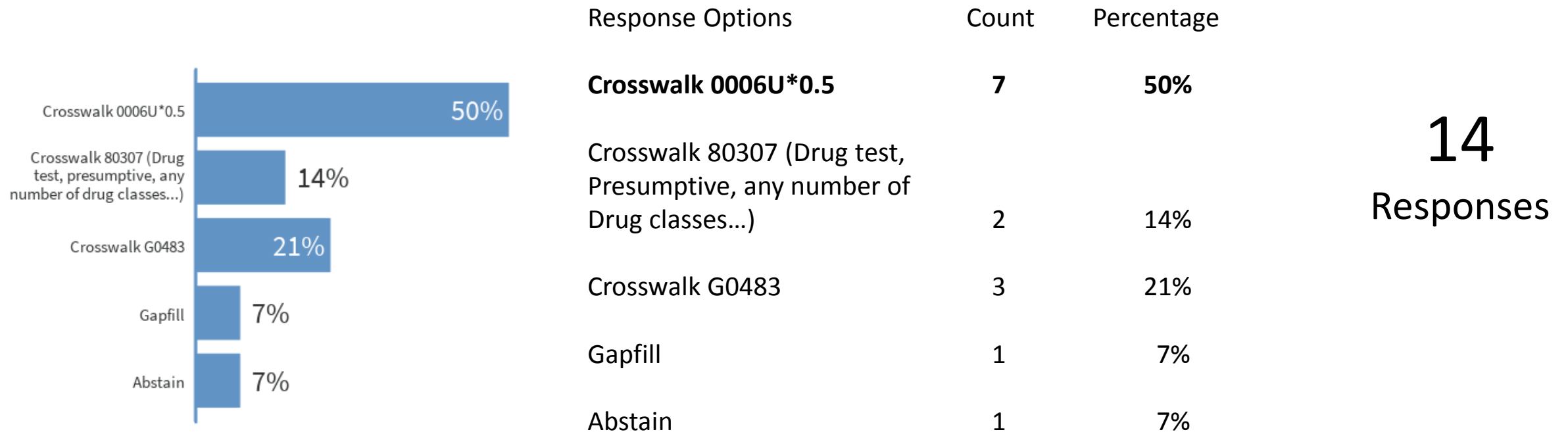| Response Options	Count	Percentage
Abstain	0	0%
Gapfill	**14**	**100%**

14
Responses

24. 0092U: Oncology (lung), three protein biomarkers, immunoassay using magnetic nanosensor technology, plasma, algorithm reported as risk score for likelihood of malignancy
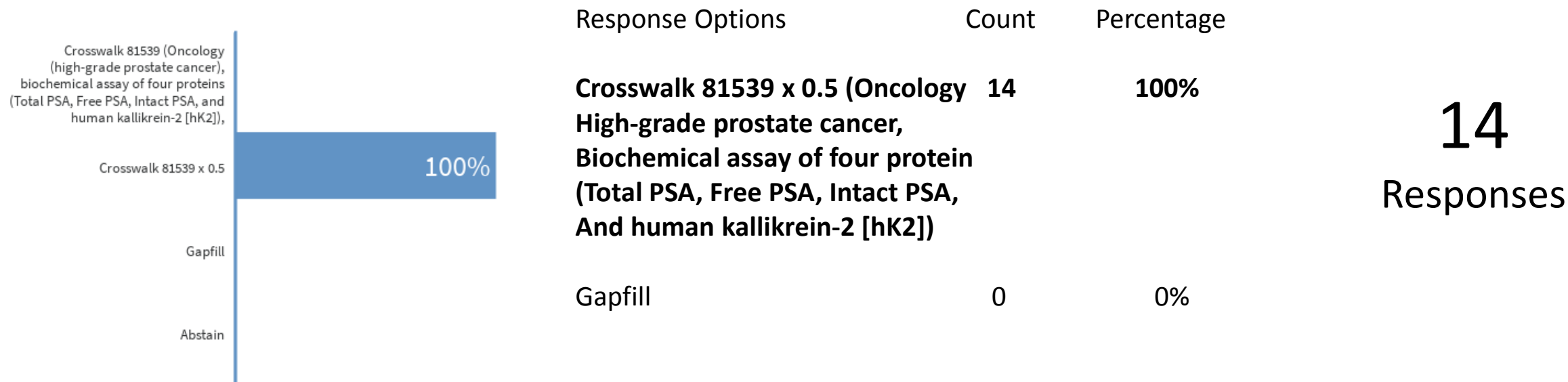

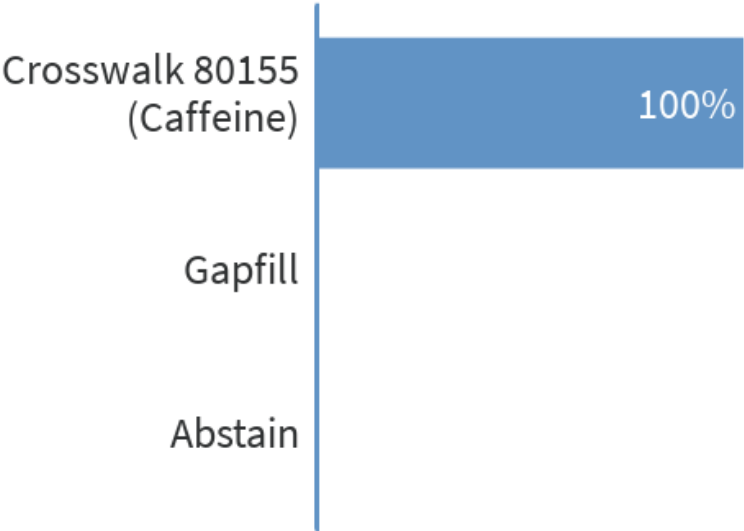| Response Options	Count	Percentage
Crosswalk 81538 (Oncology [lung], mass spec 8-protein signature…	0	0%
Gapfill	**14**	**100%**

14
Responses

25. 0093U: Prescription drug monitoring, evaluation of 65 common drugs by LC-MS/MS, urine, each drug reported detected or not detected

Response Options	Count	Percentage
Crosswalk 0006U*0.5	**7**	**50%**
Crosswalk 80307 (Drug test, Presumptive, any number of Drug classes…)	2	14%
Crosswalk G0483	3	21%
Gapfill	1	7%
Abstain	1	7%

14
Responses

26. 0095U: Inflammation (eosinophilic esophagitis), ELISA analysis of eotaxin-3 (CCL26 [C-C motif chemokine ligand 26]) and major basic protein (PRG2 [proteoglycan 2, pro eosinophil major basic protein]), specimen obtained by swallowed nylon string, algorithm reported as predictive probability index for active eosinophilic esophagitis
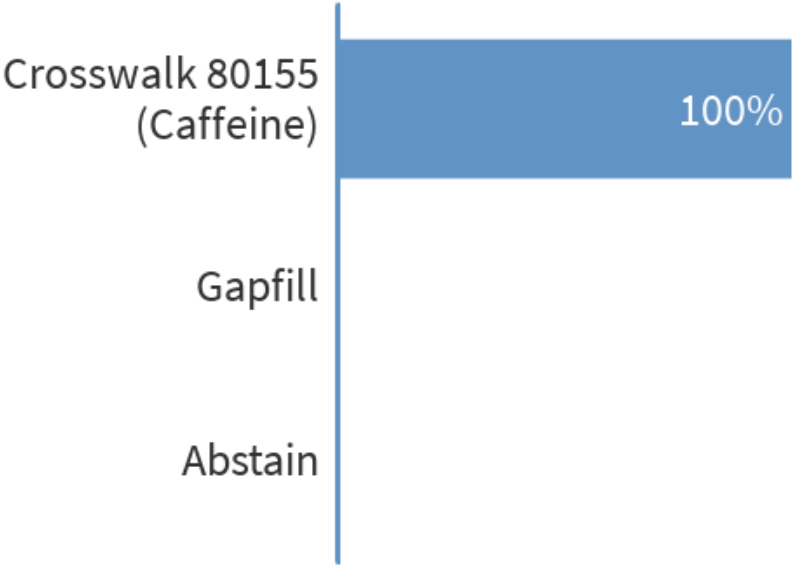
Response Options	Count	Percentage
Crosswalk 81539 x 0.5 (Oncology High-grade prostate cancer, Biochemical assay of four protein (Total PSA, Free PSA, Intact PSA, And human kallikrein-2 [hK2])	**14**	**100%**
Gapfill	0	0%

14 Responses

27. 80XX0: Adalimumab

Response Options	Count	Percentage
Crosswalk 80155 (Caffeine)	**14**	**100%**
Gapfill	0	0%

14
Responses

28. 80XX1: Infliximab

Response Options	Count	Percentage
Crosswalk 80155 (Caffeine)	**14**	**100%**
Gapfill	0	0%

14
Responses

29. 80XX2: Lacosamide

Response Options	Count	Percentage
Crosswalk 80199 (Tiagabine)	**14**	**100%**
Gapfill	0	0%

14
Responses

30. 802X0: Posaconazole

Response Options	Count	Percentage
Crosswalk 80199 (Tiagabine)	**14**	**100%**
Gapfill	0	0%

14
Responses

31. 802XX: Vedolizumab

Response Options	Count	Percentage
Crosswalk 80155 (Caffeine)	**14**	**100%**
Gapfill	0	0%

14
Responses

32. 802X1: Voriconazole

Response Options	Count	Percentage
Crosswalk 80199 (Tiagabine)	**14**	**100%**
Gapfill	0	0%

14
Responses

33. 0105U: Nephrology (chronic kidney disease), multiplex electrochemiluminescent immunoassay (ECLIA) of tumor necrosis factor receptor 1A, receptor superfamily 2 (TNFR1, TNFR2), and kidney injury molecule-1 (KIM-1) combined with longitudinal clinical data, including APOL1 genotype if available, and plasma (isolated fresh or frozen), algorithm reported as probability score for rapid kidney function decline (RKFD)
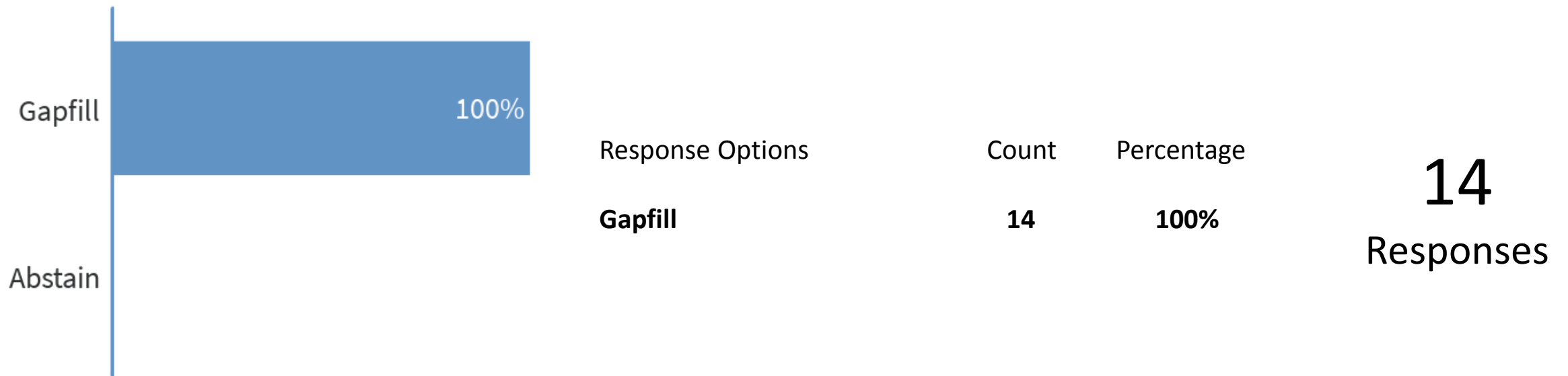
Response Options	Count	Percentage
Crosswalk 0003U (Oncology (ovarian biochemical assays of Five proteins...)	**13**	**93%**
Gapfill	1	7%

14 Responses

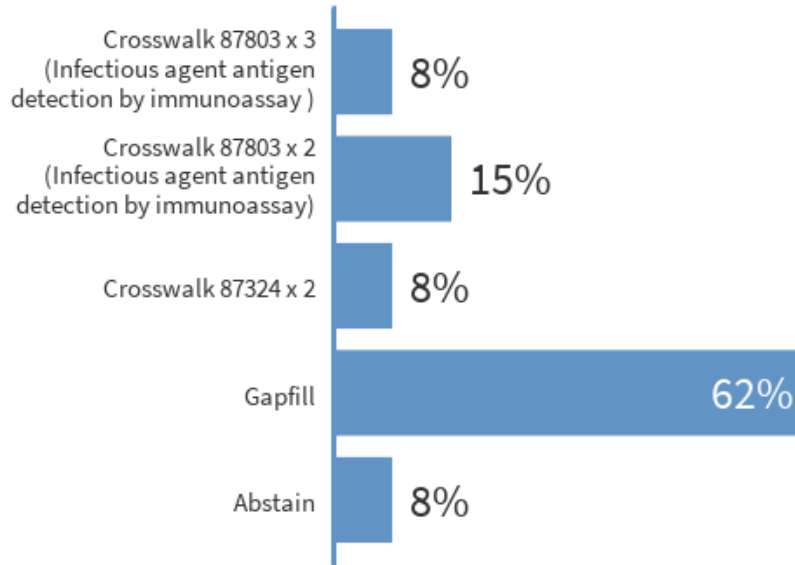Crosswalk 0003U (Oncology (ovarian) biochemical assays of five proteins...) — 93%
Gapfill — 7%
Abstain

34. 0106U: Gastric emptying, serial collection of 7 timed breath specimens, non-radioisotope carbon-13 (^{13}C) spirulina substrate, analysis of each specimen by gas isotope ratio mass spectrometry, reported as rate of $^{13}CO2$ excretion

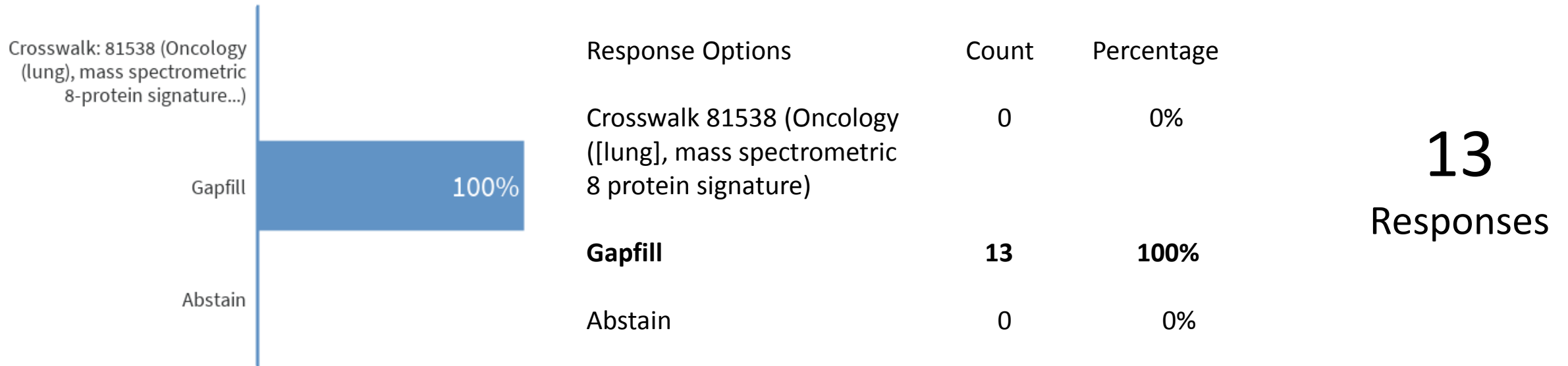| Response Options	Count	Percentage
Gapfill	**14**	**100%**

14
Responses

35. 0107U: Clostridium difficile toxin(s) antigen detection by immunoassay technique, stool, qualitative, multiple-step method

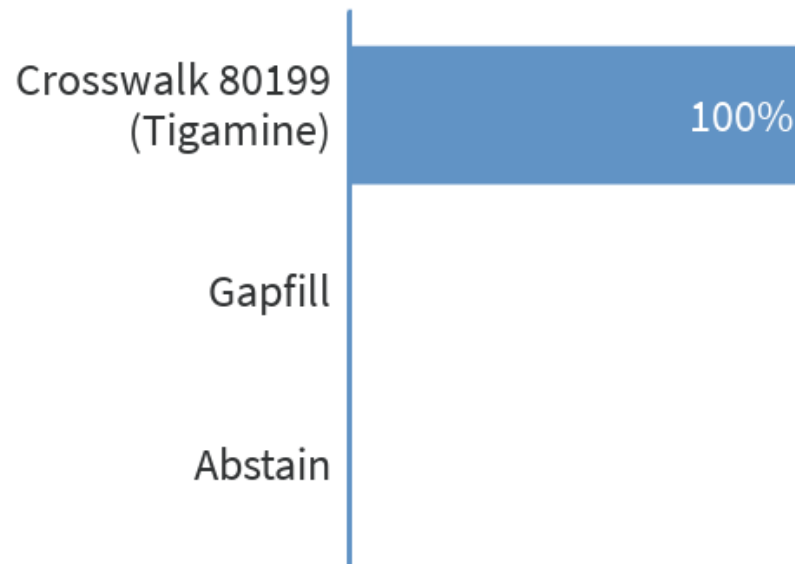| Response Options	Count	Percentage
Crosswalk 87803 x 3 (Infectious agent antigen Detection by immunoassay)	1	8%
Crosswalk 87803x 2 (Infection agent antigen detection by immunoassay)	2	15%
Crosswalk 87324 x 2	1	8%
Gapfill	**8**	**62%**
Abstain	1	8%

13
Responses

36. 0108U: Gastroenterology (Barrett's esophagus), whole slide–digital imaging, including morphometric analysis, computer-assisted quantitative immunolabeling of 9 protein biomarkers

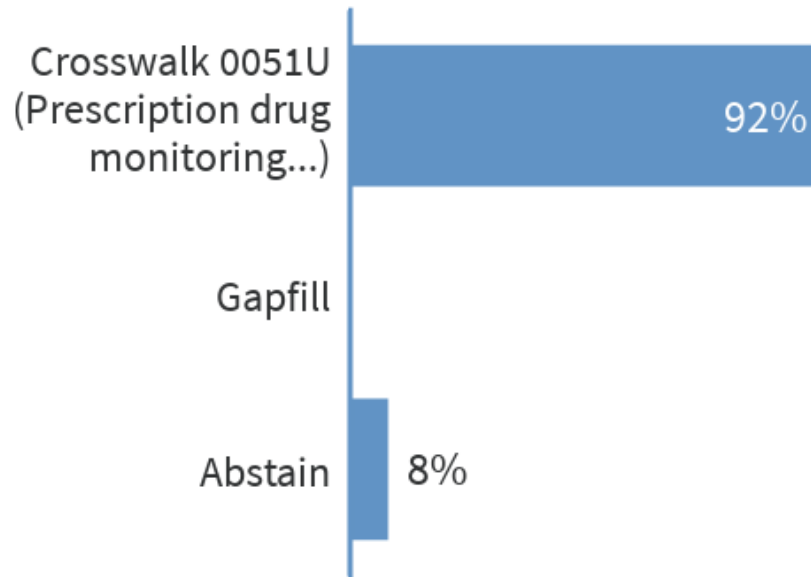| Response Options	Count	Percentage
Crosswalk 81538 (Oncology ([lung], mass spectrometric 8 protein signature)	0	0%
Gapfill	**13**	**100%**
Abstain	0	0%

13
Responses

37. 0110U: Prescription drug monitoring, one or more oral oncology drug(s) and substances, definitive tandem mass spectrometry with chromatography, serum or plasma from capillary blood or venous blood, quantitative report with steady-state range for the prescribed drug(s) when detected

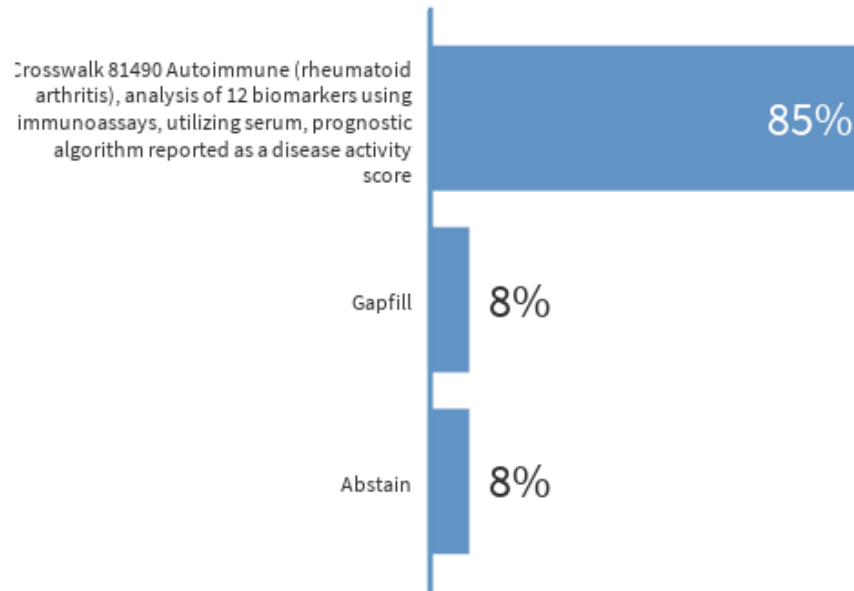| Response Options	Count	Percentage
Crosswalk 80199 (Tiagabine)	**13**	**100%**
Gapfill	0	0%

13 Responses

38. 0116U: Prescription drug monitoring, enzyme immunoassay of 35 or more drugs confirmed with LC-MS/MS, oral fluid, algorithm results reported as a patient-compliance measurement with risk of drug to drug interactions for prescribed medications

Response Options	Count	Percentage
Crosswalk 0051U (Prescription drug monitoring...)	**12**	**92%**
Gapfill	0	0%
Abstain	1	8%

13
Responses

39. 0117U: Pain Management, Analysis of 11 Endogenous Analytes

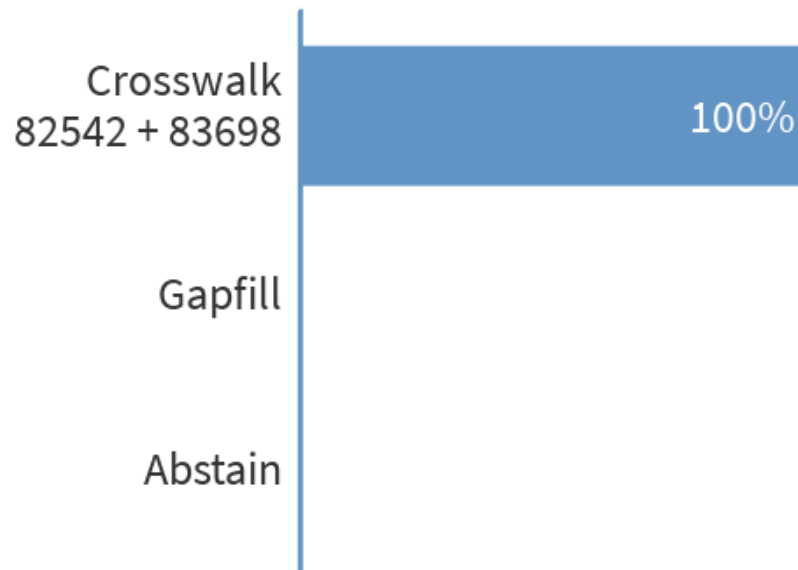| Response Options	Count	Percentage
Crosswalk 81490 Autoimmune (rheumatoid arthritis), analysis of 12 biomarkers using immunoassays. Utilizing serum, prognostic algorithm reported As a disease activity score	**11**	**85%**
Gapfill	1	8%
Abstain	1	8%

13 Responses

40. 0119U: Cardiology, ceramides by liquid chromatography–tandem mass spectrometry, plasma, quantitative report with risk score for major cardiovascular events

Response Options	Count	Percentage
Crosswalk 82542 + 83698	**13**	**100%**
Gapfill	0	0%

13
Responses
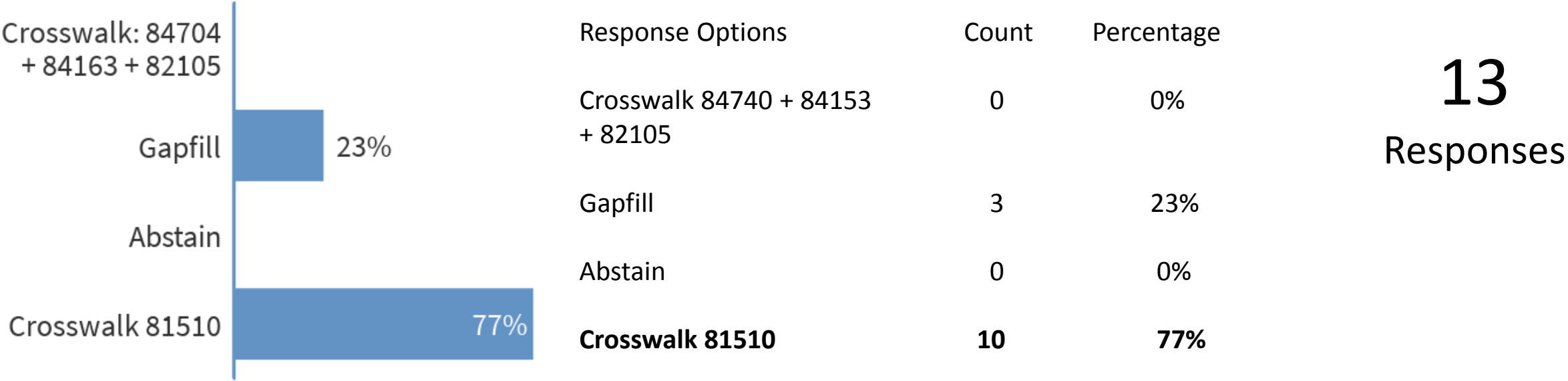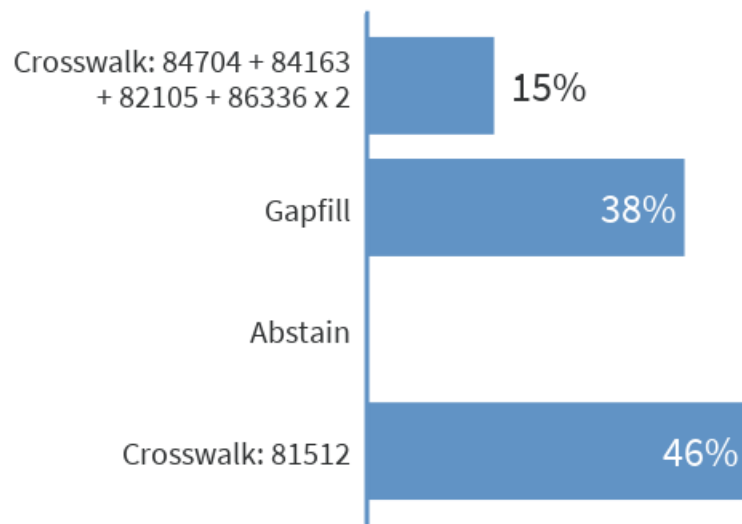
41. 0124U: Fetal congenital abnormalities, biochemical assays of 3 analytes (free beta-hCG, PAPP-A, AFP), time-resolved fluorescence immunoassay, maternal dried-blood spot, algorithm reported as risk scores for fetal trisomies 13/18 and 21

Response Options	Count	Percentage
Crosswalk 84740 + 84153 + 82105	0	0%
Gapfill	3	23%
Abstain	0	0%
Crosswalk 81510	**10**	**77%**

13
Responses

42. 0125U: Fetal congenital abnormalities and perinatal complications, biochemical assays of 5 analytes (free beta-hCG, PAPP-A, AFP, placental growth factor, and inhibin-A), time-resolved fluorescence immunoassay, maternal serum, algorithm reported as risk scores for fetal trisomies 13/18, 21, and preeclampsia

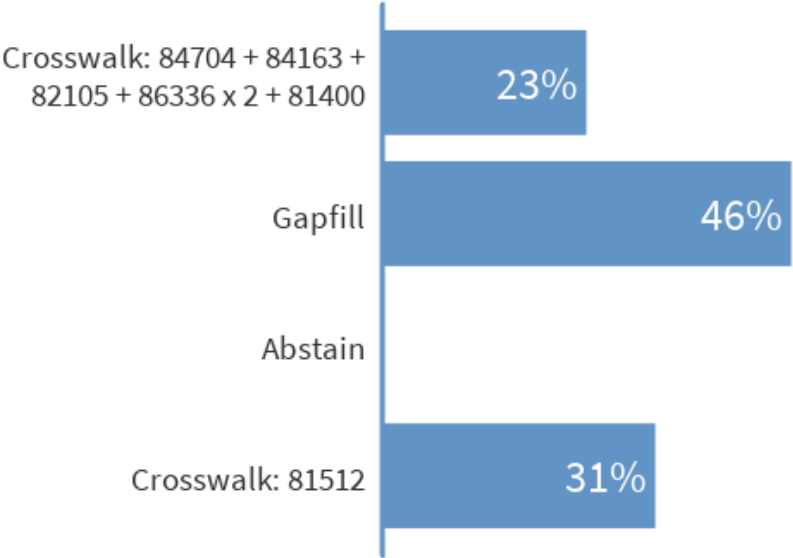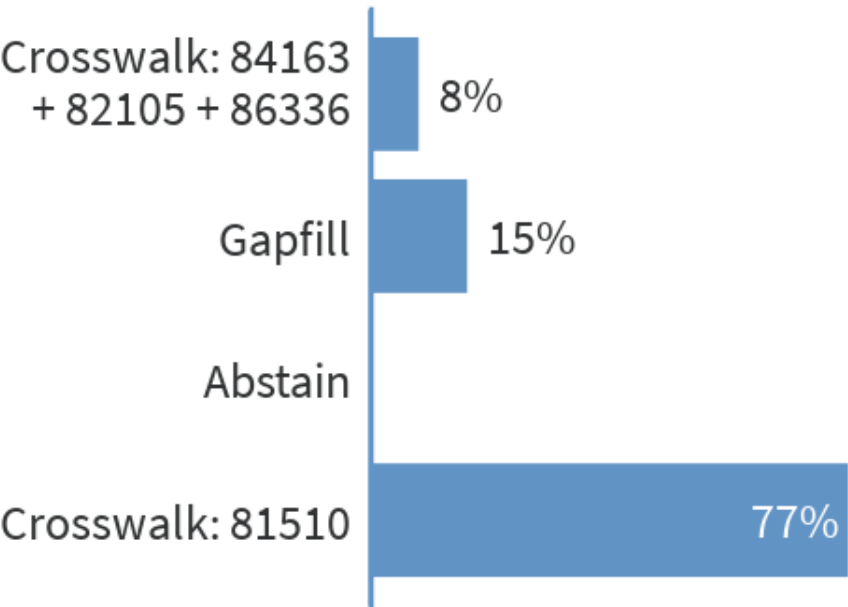| Response Options	Count	Percentage
Crosswalk 84704 + 84163 + 82105 + 86336 x 2	2	15%
Gapfill	5	38%
Abstain	0	0%
Crosswalk 81512	**6**	**46%**

13
Responses

43. 0126U: Fetal congenital abnormalities and perinatal complications, biochemical assays of 5 analytes (free beta-hCG, PAPP-A, AFP, placental growth factor, and inhibin-A), time-resolved fluorescence immunoassay, includes qualitative assessment of Y chromosome in cell-free fetal DNA, maternal serum and plasma, predictive algorithm reported as a risk scores for fetal trisomies 13/18, 21, and preeclampsia

Response Options	Count	Percentage
Crosswalk 84704 + 84163 + 82105 + 86336 x 2 + 81400	3	23%
Gapfill	**6**	**46%**
Abstain	0	0%
Crosswalk 81510	4	31%

13
Responses

44. 0127U: Obstetrics (preeclampsia), biochemical assays of 3 analytes (PAPP-A, AFP, and placental growth factor), time-resolved fluorescence immunoassay, maternal serum, predictive algorithm reported as a risk score for preeclampsia

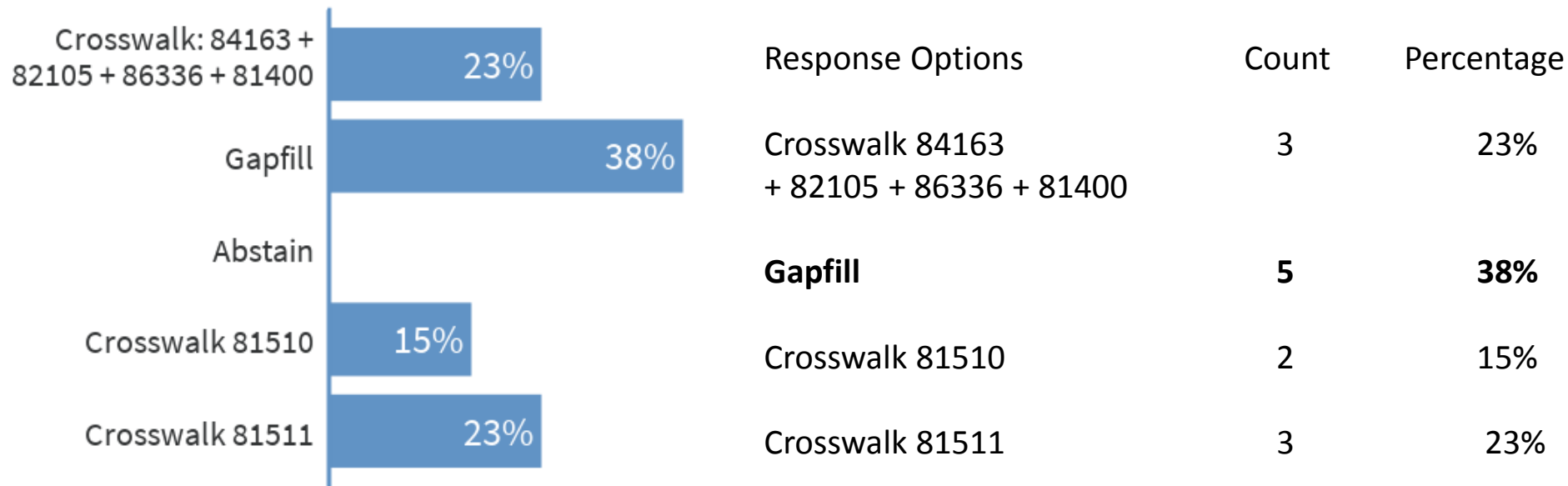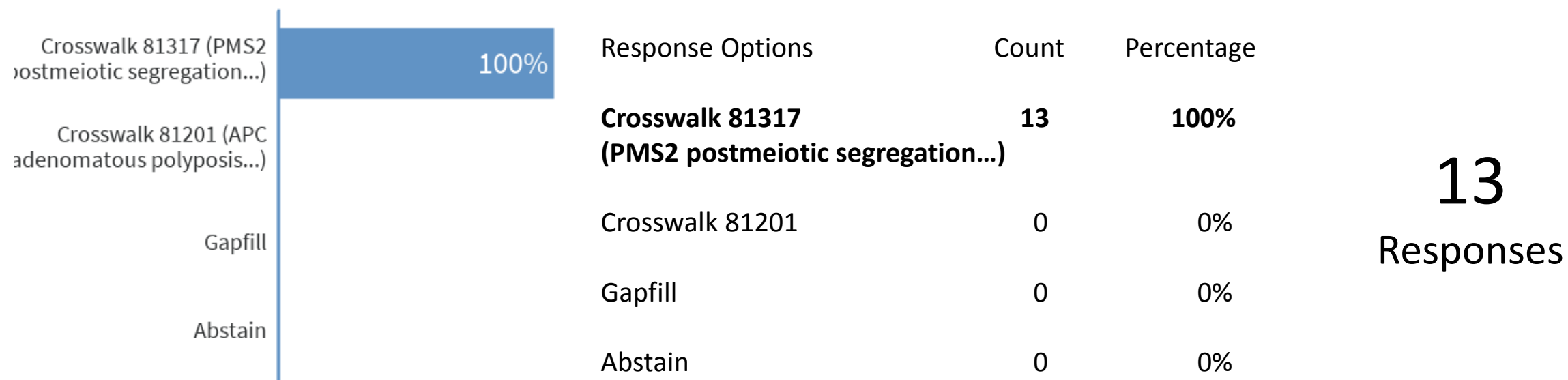| Response Options	Count	Percentage
Crosswalk 84163 + 82105 + 86336	1	8%
Gapfill	2	15%
Crosswalk 81510	**10**	**77%**

13
Responses

45. 0128U: Obstetrics (preeclampsia), biochemical assays of 3 analytes (PAPP-A, AFP, and placental growth factor), time-resolved fluorescence immunoassay, includes qualitative assessment of Y chromosome in cell-free fetal DNA, maternal serum and plasma, predictive algorithm reported as a risk score for preeclampsia
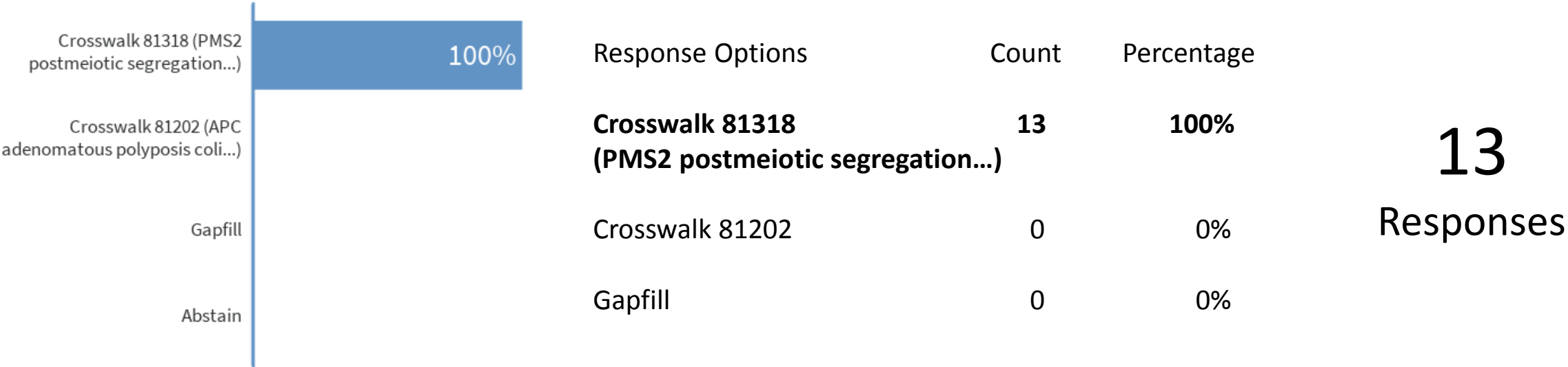

Response Options	Count	Percentage
Crosswalk 84163 + 82105 + 86336 + 81400	3	23%
Gapfill	**5**	**38%**
Crosswalk 81510	2	15%
Crosswalk 81511	3	23%

13
Responses

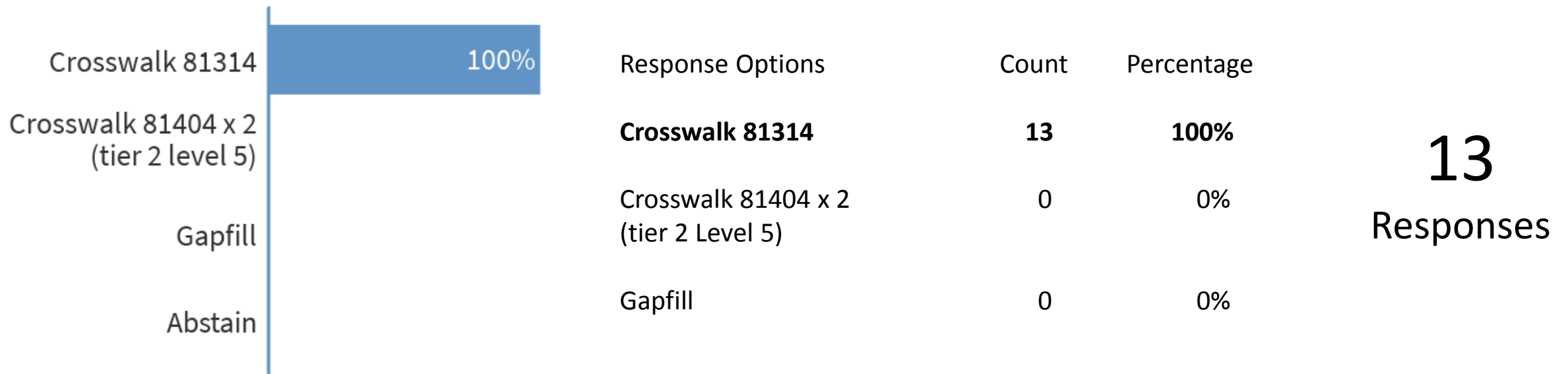# 46. 813X1: PALB2 (partner and localizer of BRCA2) (eg, breast and pancreatic cancer) gene analysis; full gene sequence

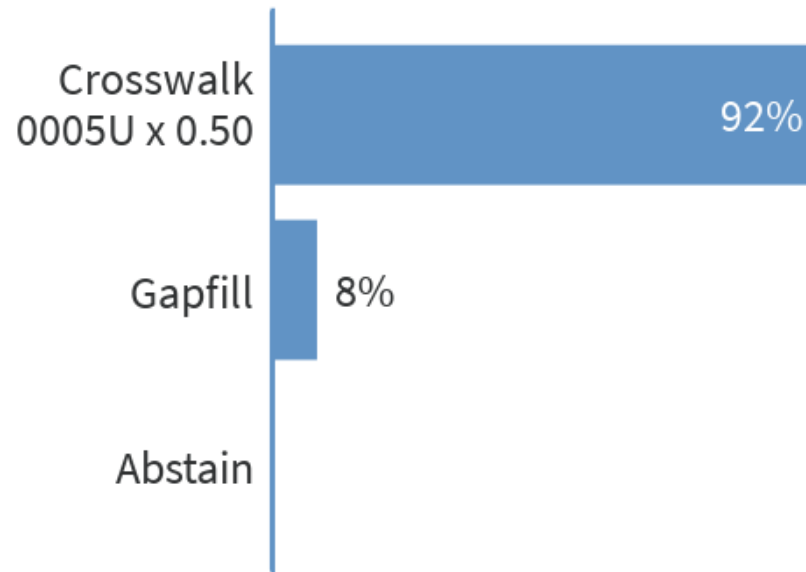| Response Options	Count	Percentage
Crosswalk 81317 (PMS2 postmeiotic segregation...)	**13**	**100%**
Crosswalk 81201	0	0%
Gapfill	0	0%
Abstain	0	0%

13
Responses

47. 813X2: PALB2 (partner and localizer of BRCA2) (eg, breast and pancreatic cancer) gene analysis; known familial variant

Response Options	Count	Percentage
Crosswalk 81318 (PMS2 postmeiotic segregation…)	**13**	**100%**
Crosswalk 81202	0	0%
Gapfill	0	0%

13
Responses

48. 8XX01: PIK3CA (phosphatidylinositol-4, 5-biphosphate 3-kinase, catalytic subunit alpha) (eg, colorectal and breast cancer) gene analysis, targeted sequence analysis (eg, exons 7, 9, and 20)

Response Options	Count	Percentage
Crosswalk 81314	**13**	**100%**
Crosswalk 81404 x 2 (tier 2 Level 5)	0	0%
Gapfill	0	0%

13 Responses

49. 0069U: Oncology (colorectal), microRNA, RT-PCR expression profiling of miR-31-3p, formalin-fixed paraffin-embedded tissue, algorithm reported as an expression score

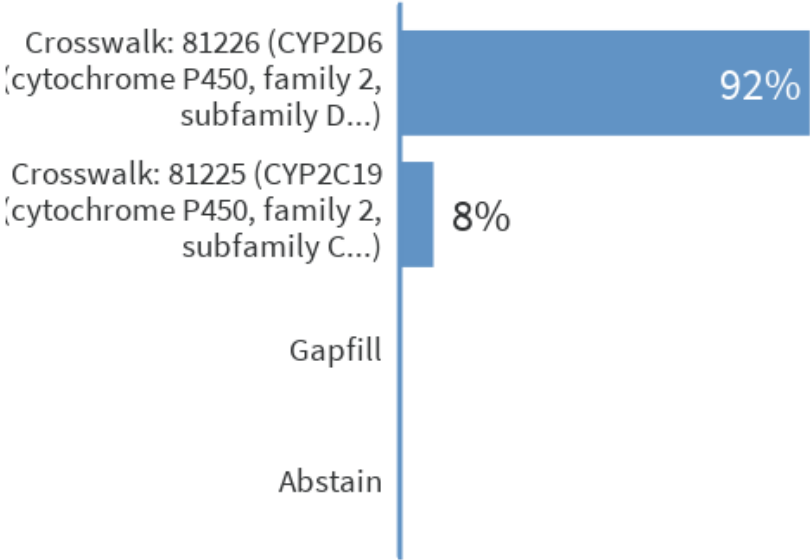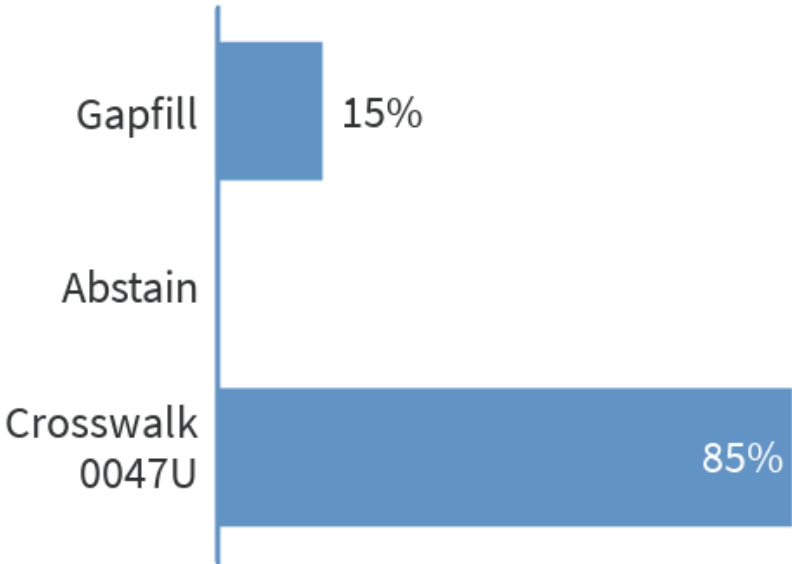| Response Options	Count	Percentage
Crosswalk 0005U x 0.50	**12**	**92%**
Gapfill	1	8%

13
Responses

50. 0078U: Pain management (opioid-use disorder) genotyping panel, 16 common variants (ie, ABCB1, COMT, DAT1, DBH, DOR, DRD1, DRD2, DRD4, GABA, GAL, HTR2A, HTTLPR, MTHFR, MUOR, OPRK1, OPRM1), buccal swab or other germline tissue sample, algorithm reported as positive or negative risk of opioid-use disorder

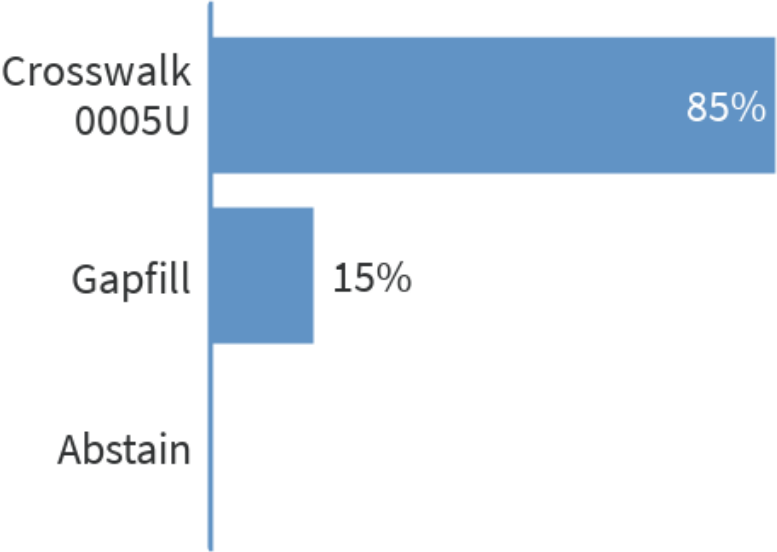| Response Options	Count	Percentage
Crosswalk 81226 (CYP2D6 [cytochrome P450, Family 2 , subfamily D...)	**12**	**92%**
Crosswalk 81225 (CYP2C19 cytochrome P450, Family 2, subfamily C...)	1	8%
Gapfill	0	0%

13
Responses

51. 0081U: Oncology (uveal melanoma), mRNA, gene-expression profiling by real-time RT-PCR of 15 genes (12 content and 3 housekeeping genes), utilizing fine needle aspirate or formalin-fixed paraffin-embedded tissue, algorithm reported as risk of metastasis

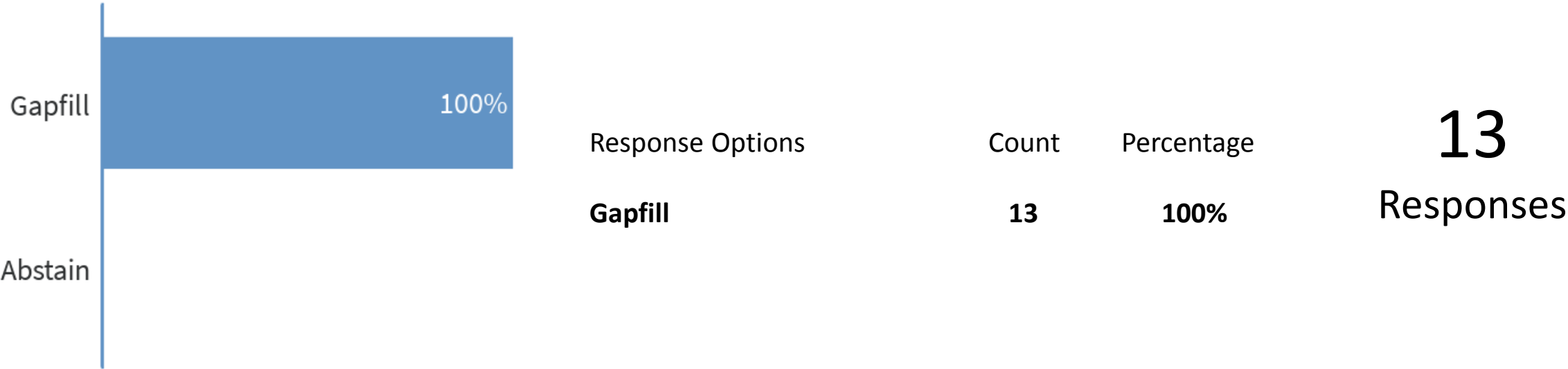| Response Options	Count	Percentage
Gapfill	2	15%
Abstain	0	0%
Crosswalk 0047U	**11**	**85%**

13
Responses

52. 0089U: Oncology (melanoma), gene expression profiling by RTqPCR, PRAME and LINC00518, superficial collection using adhesive patch(es)
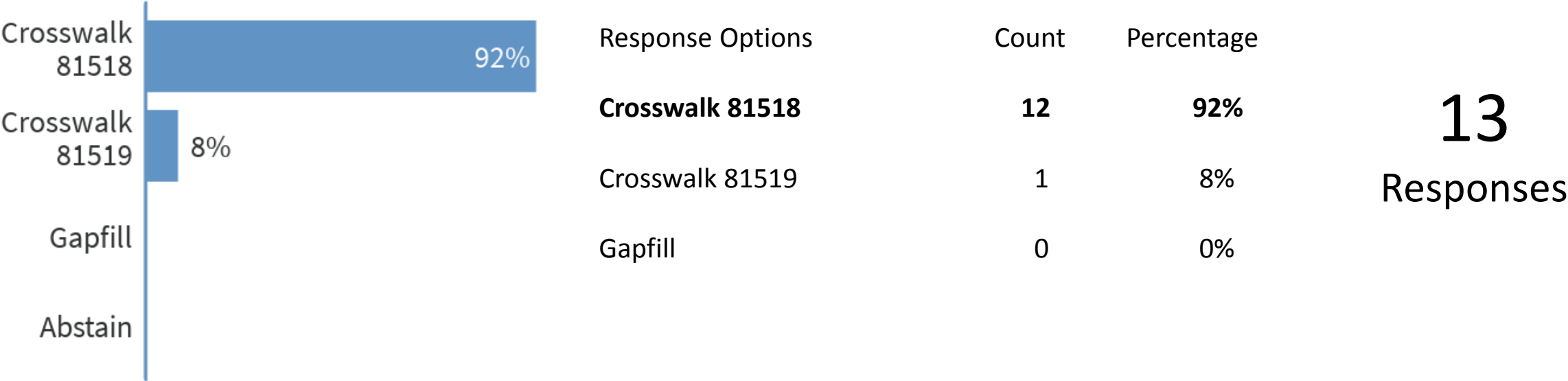

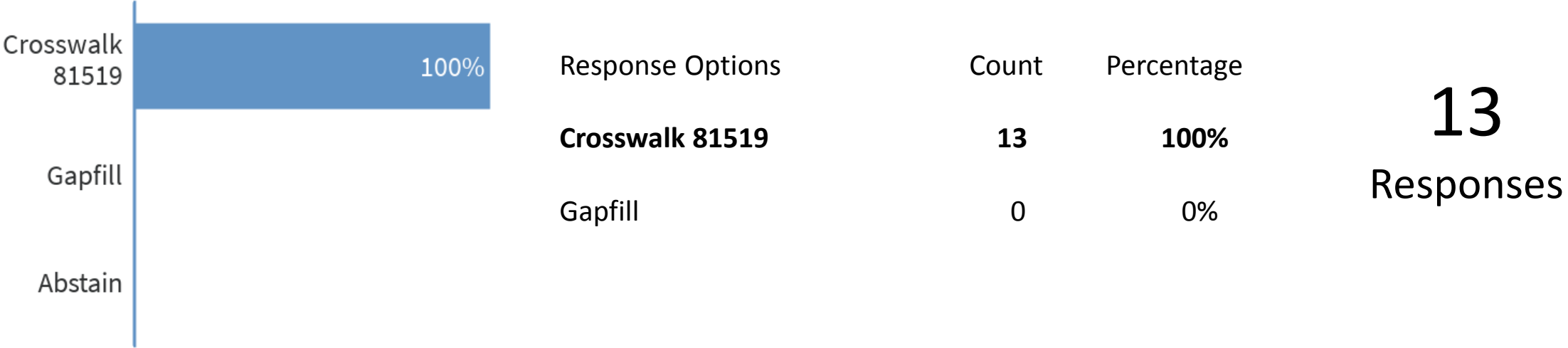| Response Options	Count	Percentage
Crosswalk 0005U	**11**	**85%**
Gapfill	2	15%

13
Responses

53. 0090U: Oncology (cutaneous melanoma), mRNA gene expression profiling by RT-PCR of 23 genes (14 content and 9 housekeeping), utilizing formalin-fixed paraffin-embedded tissue, algorithm reported as a categorical result (ie, benign, indeterminate, malignant)

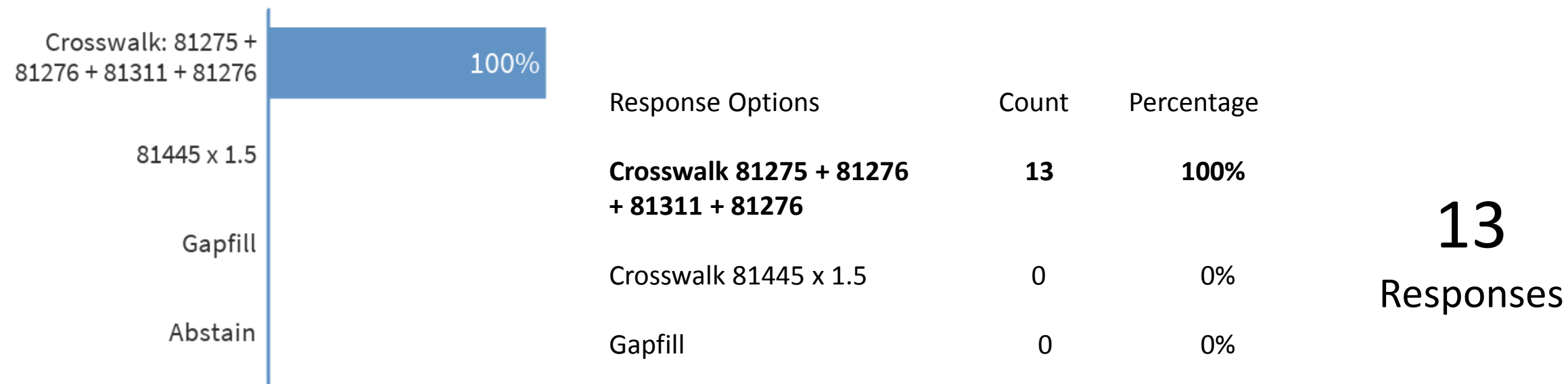| Response Options	Count	Percentage
Gapfill	**13**	**100%**

13 Responses

54. 815X0: Oncology (breast), mRNA gene expression profiling by RT-PCR of 12 genes (8 content and 4 housekeeping), utilizing formalin-fixed paraffin-embedded tissue, algorithm reported as recurrence risk score
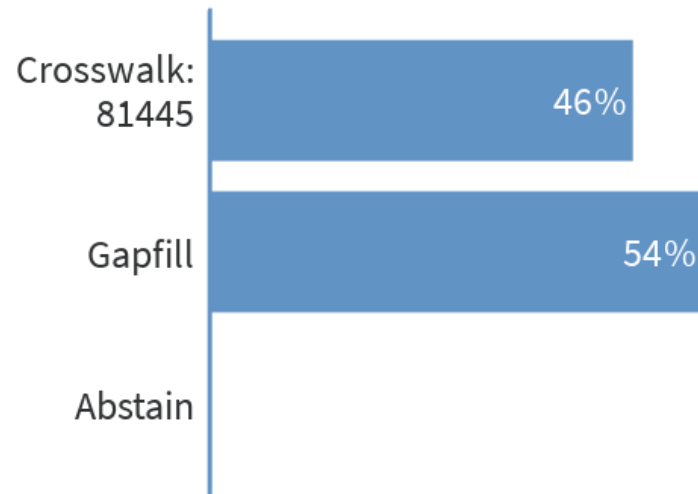

Response Options	Count	Percentage
Crosswalk 81518	**12**	**92%**
Crosswalk 81519	1	8%
Gapfill	0	0%

13
Responses

55. 815XX: Oncology (prostate), mRNA microarray gene expression profiling of 22 content genes, utilizing formalin-fixed paraffin-embedded tissue, algorithm reported as metastasis risk score

Response Options	Count	Percentage
Crosswalk 81519	**13**	**100%**
Gapfill	0	0%

13
Responses

56. 0111U: Oncology (colon cancer), targeted KRAS (codons 12, 13, and 61) and NRAS (codons 12, 13, and 61) gene analysis, utilizing formalin-fixed paraffin-embedded tissue

Response Options	Count	Percentage
Crosswalk 81275 + 81276 + 81311 + 81276	**13**	**100%**
Crosswalk 81445 x 1.5	0	0%
Gapfill	0	0%

13
Responses

57. 0112U: Infectious agent detection and identification, targeted sequence analysis (16S and 18S rRNA genes) with drug-resistance gene

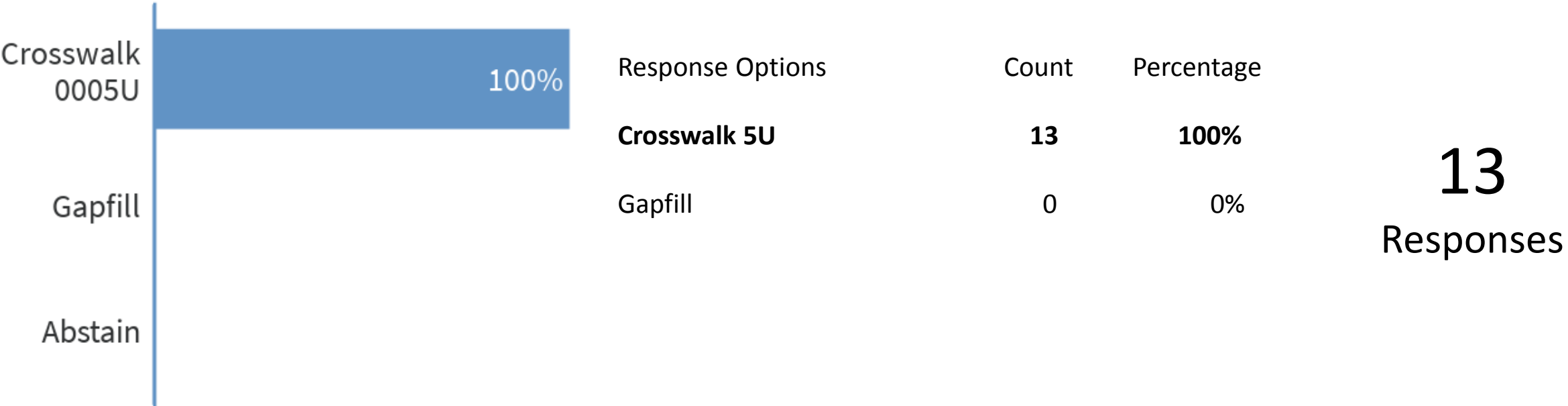| Response Options	Count	Percentage
Crosswalk 81445	6	46%
Gapfill	**7**	**54%**

13
Responses

58. 0113U: Oncology (Prostrate), Measurement of PCA3 and TMPRSS2-ERG in Urine and PSA

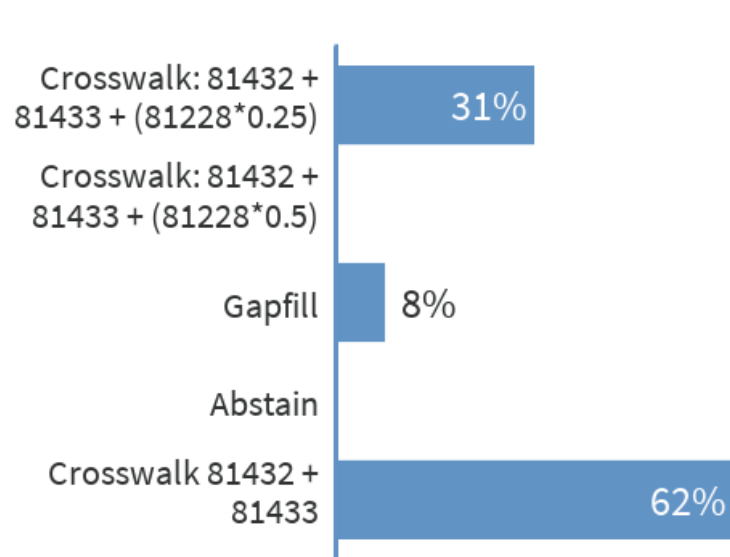| Response Options	Count	Percentage
Crosswalk 5U	**13**	**100%**
Gapfill	0	0%

13
Responses

59. 0114U: Gastroenterology (Barrett's esophagus), VIM and CCNA1 methylation analysis, esophageal cells, algorithm reported as likelihood for Barrett's esophagus

Response Options	Count	Percentage
Gapfill	**9**	**69%**
Crosswalk 81287 x 2	2	15%
Crosswalk 81288 x 2	2	15%
Crosswalk 81519	0	0%

13
Responses

60. 0120U: Oncology (B-cell lymphoma classification), mRNA, gene expression profiling by fluorescent probe hybridization of 58 genes (45 content and 13 housekeeping genes), formalin-fixed paraffin-embedded tissue, algorithm reported as likelihood for primary mediastinal B-cell lymphoma (PMBCL) and diffuse large B-cell lymphoma (DLBCL) with cell of origin subtyping in the latter

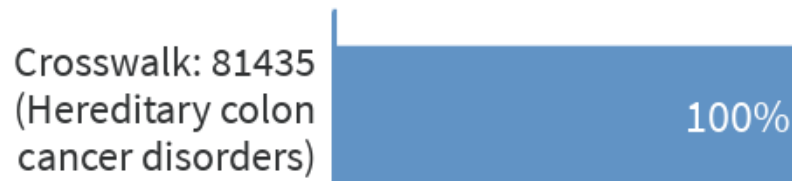| Response Options	Count	Percentage
Crosswalk 81520	**13**	**100%**
Gapfill	0	0%

13
Responses

61. 0129U: Hereditary breast cancer–related disorders (eg, hereditary breast cancer, hereditary ovarian cancer, hereditary endometrial cancer), genomic sequence analysis and deletion/duplication analysis panel (ATM, BRCA1, BRCA2, CDH1, CHEK2, PALB2, PTEN, and TP53)

Response Options	Count	Percentage
Crosswalk 81432 + 81433 + (81228*0.25)	4	31%
Crosswalk 81432 + 81433 + (81228*0.5)	0	0%
Gapfill	1	8%
Abstain	0	0%
Crosswalk 81432 + 81433	**8**	**62%**

13
Responses

62. 0130U: Hereditary colon cancer disorders (eg, Lynch syndrome, PTEN hamartoma syndrome, Cowden syndrome, familial adenomatosis polyposis), targeted mRNA sequence analysis panel (APC, CDH1, CHEK2, MLH1, MSH2, MSH6, MUTYH, PMS2, PTEN, and TP53)

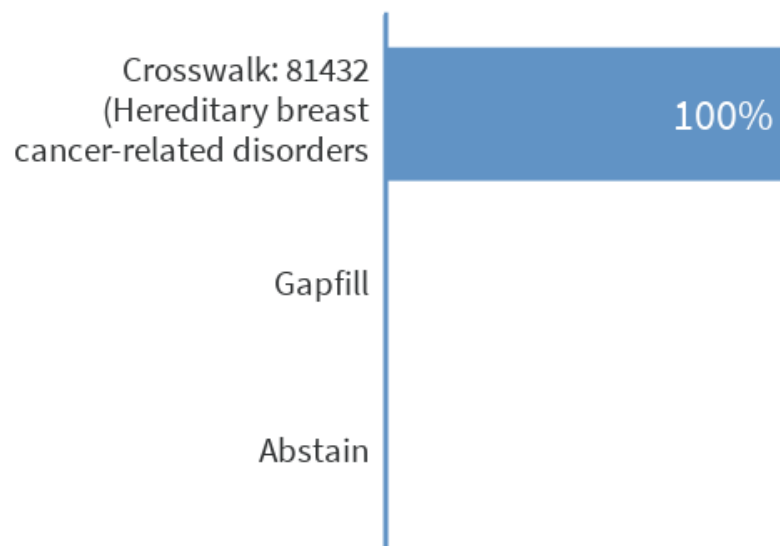| Response Options	Count	Percentage
Crosswalk 81435 (Hereditary colon cancer disorders)	**13**	**100%**
Gapfill	0	0%

13
Responses

63. 0131U: Hereditary breast cancer–related disorders (eg, hereditary breast cancer, hereditary ovarian cancer, hereditary endometrial cancer), targeted mRNA sequence analysis panel (13 genes)

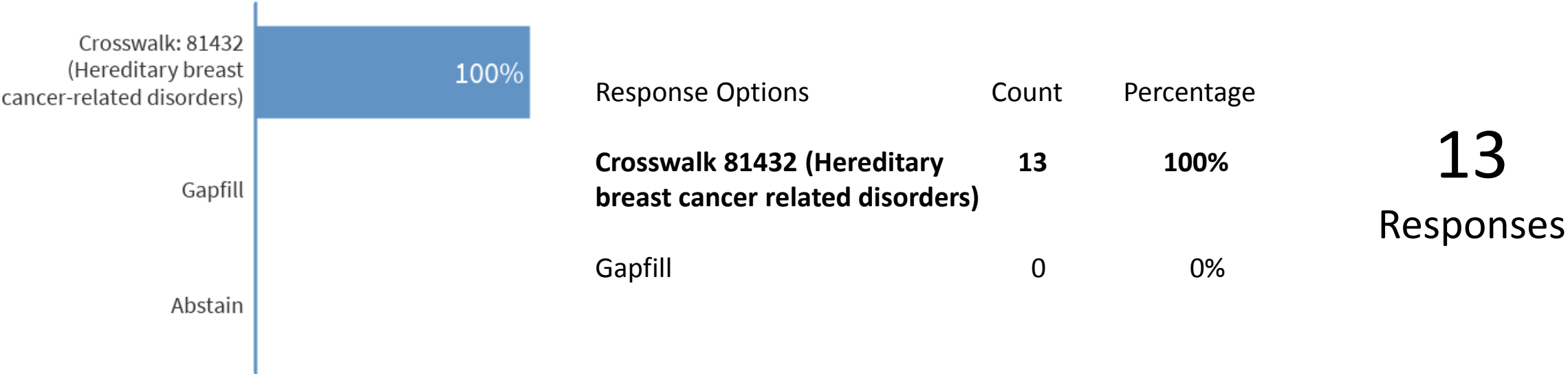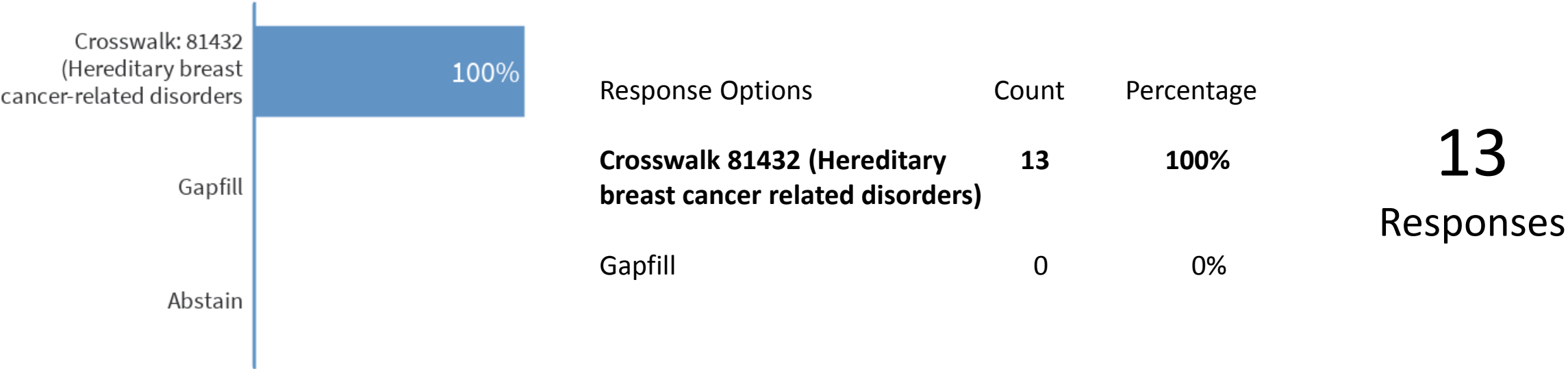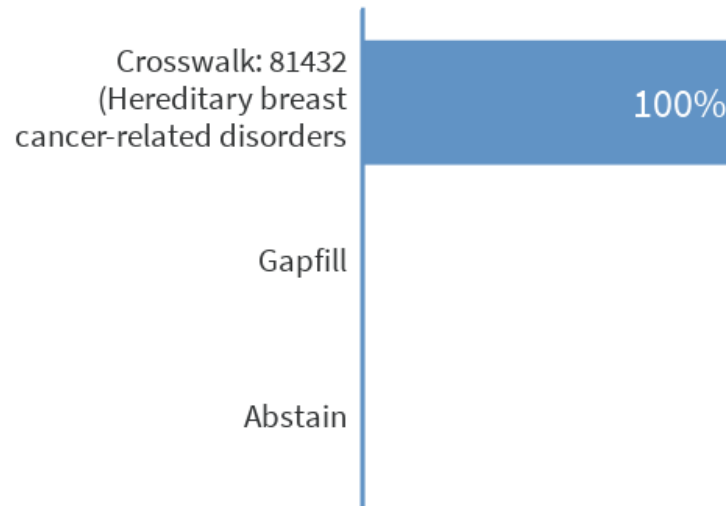| Response Options	Count	Percentage
Crosswalk 81432 (Hereditary breast cancer related disorders)	**13**	**100%**
Gapfill	0	0%

13
Responses

64. 0132U: Hereditary ovarian cancer–related disorders (eg, hereditary breast cancer, hereditary ovarian cancer, hereditary endometrial cancer), targeted mRNA sequence analysis panel (17 genes)

Response Options	Count	Percentage
Crosswalk 81432 (Hereditary breast cancer related disorders)	**13**	**100%**
Gapfill	0	0%

13 Responses

65. 0133U: Hereditary prostate cancer–related disorders, targeted mRNA sequence analysis panel (11 genes)

Response Options	Count	Percentage
Crosswalk 81432 (Hereditary breast cancer related disorders)	**13**	**100%**
Gapfill	0	0%

13
Responses

66. 0134U: Hereditary pan cancer (eg, hereditary breast and ovarian cancer, hereditary endometrial cancer, hereditary colorectal cancer), targeted mRNA sequence analysis panel (18 genes)

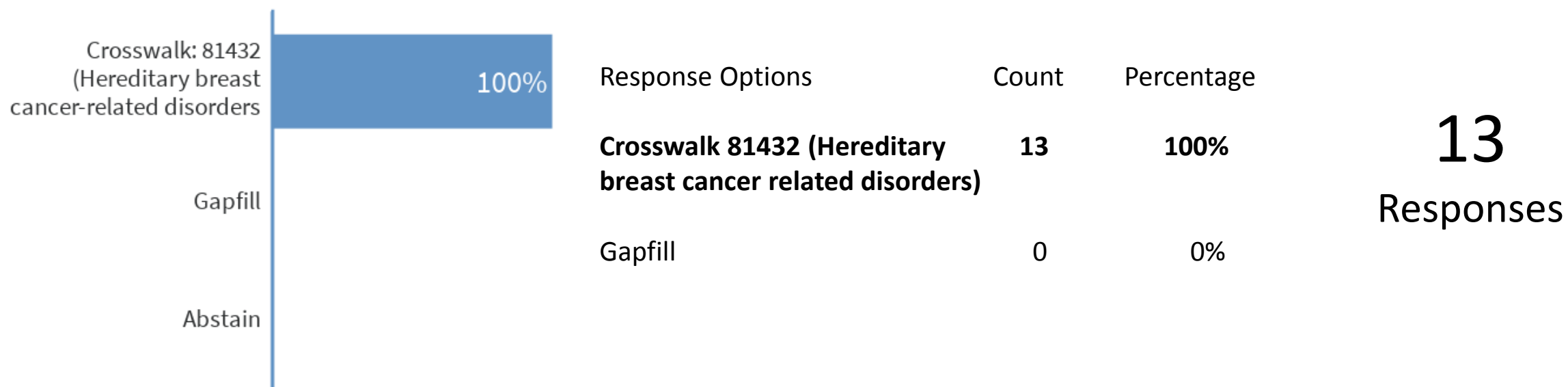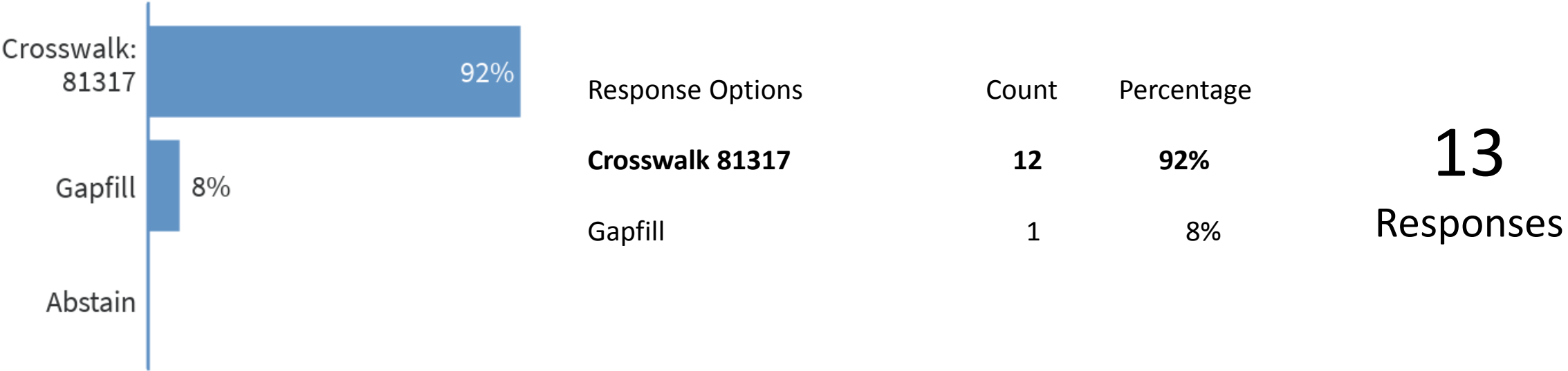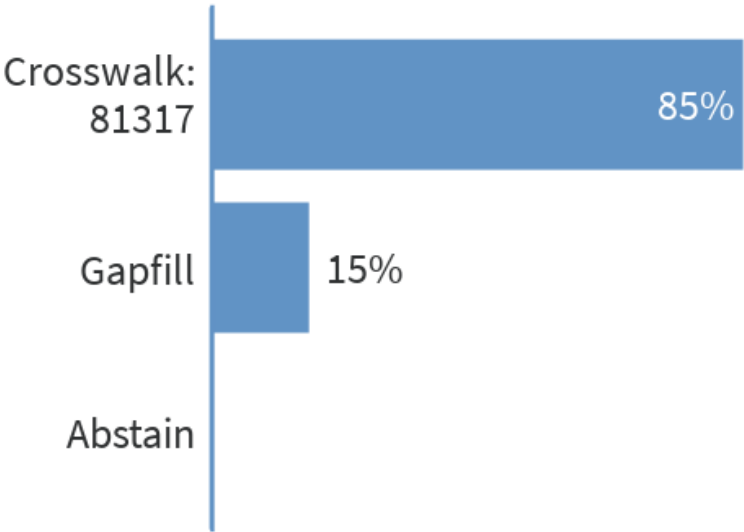| Response Options	Count	Percentage
Crosswalk 81432 (Hereditary breast cancer related disorders)	**13**	**100%**
Gapfill	0	0%

13
Responses

67. 0135U: Hereditary gynecological cancer (eg, hereditary breast and ovarian cancer, hereditary endometrial cancer, hereditary colorectal cancer), targeted mRNA sequence analysis panel (12 genes)

Response Options	Count	Percentage
Crosswalk 81432 (Hereditary breast cancer related disorders)	**13**	**100%**
Gapfill	0	0%

13
Responses

68. 0136U: ATM (ataxia telangiectasia mutated) (eg, ataxia telangiectasia) mRNA sequence analysis (List separately in addition to code for primary procedure)

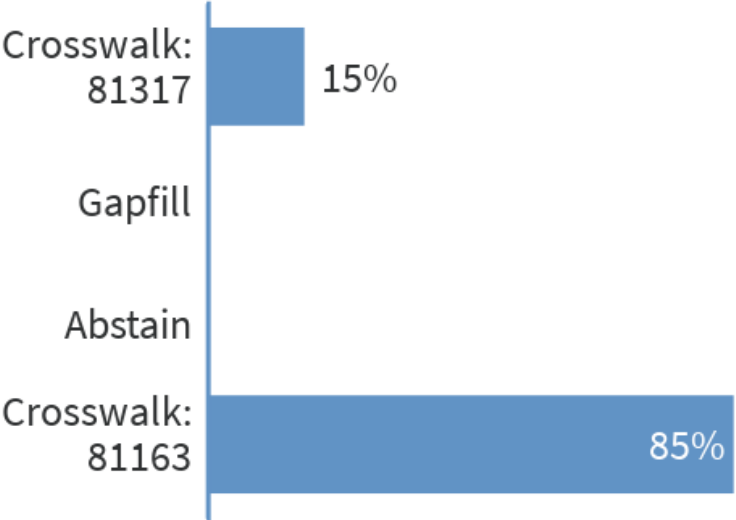| Response Options	Count	Percentage
Crosswalk 81317	**12**	**92%**
Gapfill	1	8%

13 Responses

69. 0137U: PALB2 (partner and localizer of BRCA2) (eg, breast and pancreatic cancer) mRNA sequence analysis (List separately in addition to code for primary procedure)

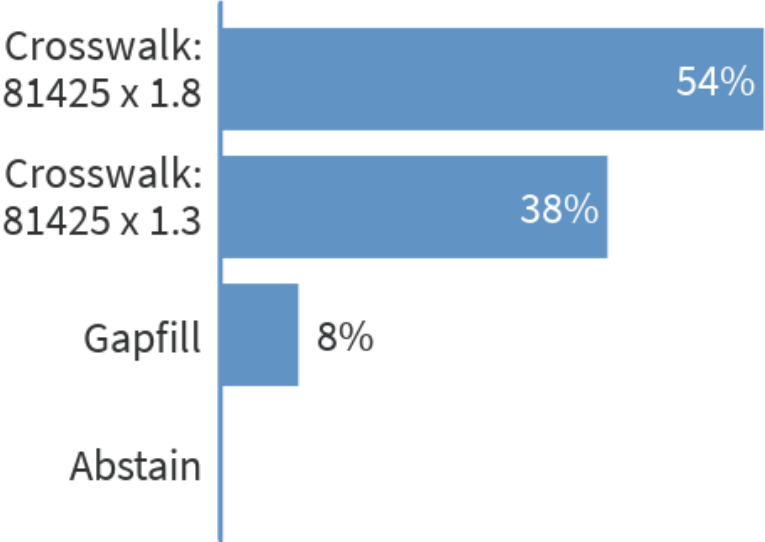| Response Options	Count	Percentage
Crosswalk 81317	**11**	**85%**
Gapfill	2	15%

13 Responses

70. 0138U: BRCA1 (BRCA1, DNA repair associated), BRCA2 (BRCA2, DNA repair associated) (eg, hereditary breast and ovarian cancer) mRNA sequence analysis (List separately in addition to code for primary procedure)

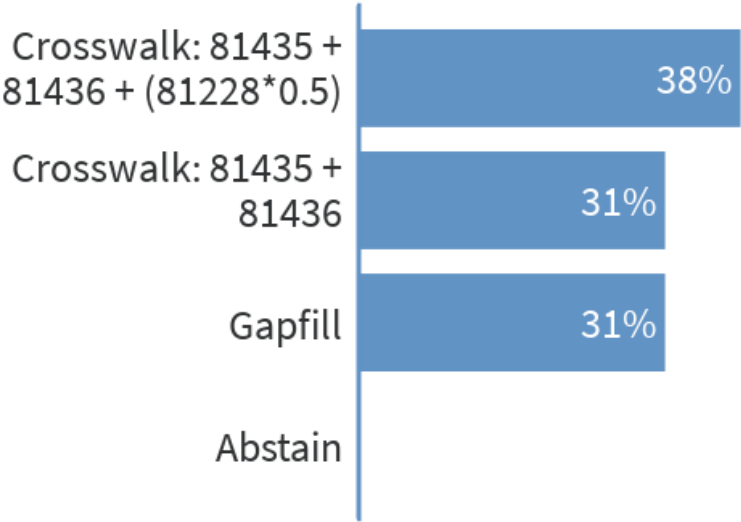| Response Options	Count	Percentage
Crosswalk 81317	2	15%
Gapfill	0	0%
Abstain	0	0%
Crosswalk 81163	**11**	**85%**

13
Responses

71. 0094U: Genome (e.g., Unexplained Constitutional or Heritable Disorder or Syndrome), Rapid Sequence Analysis

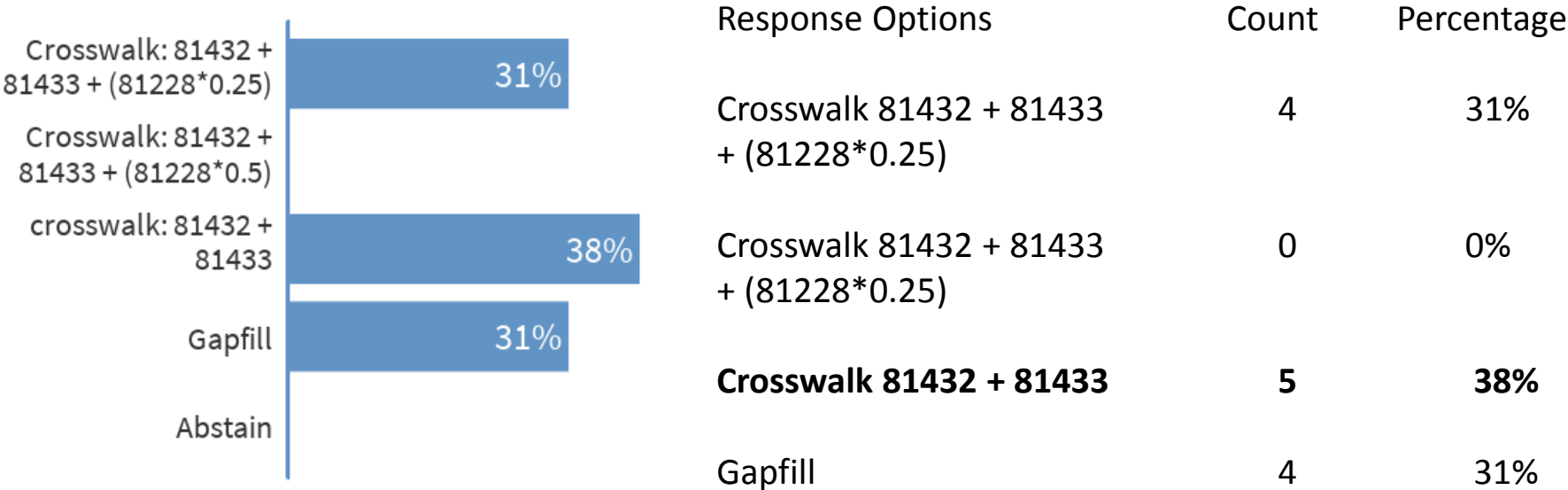| Response Options	Count	Percentage
Crosswalk 81425 x 1.8	**7**	**54%**
Crosswalk 81425 x 1.3	5	38%
Gapfill	1	8%

13 Responses

72. 0101U: Hereditary colon cancer disorders (eg, Lynch syndrome, PTEN hamartoma syndrome, Cowden syndrome, familial adenomatosis polyposis), genomic sequence analysis panel utilizing a combination of NGS, Sanger, MLPA, and array CGH, with MRNA analytics to resolve variants of unknown significance when indicated (15 genes [sequencing and deletion/duplication], EPCAM and GREM1 [deletion/duplication only])

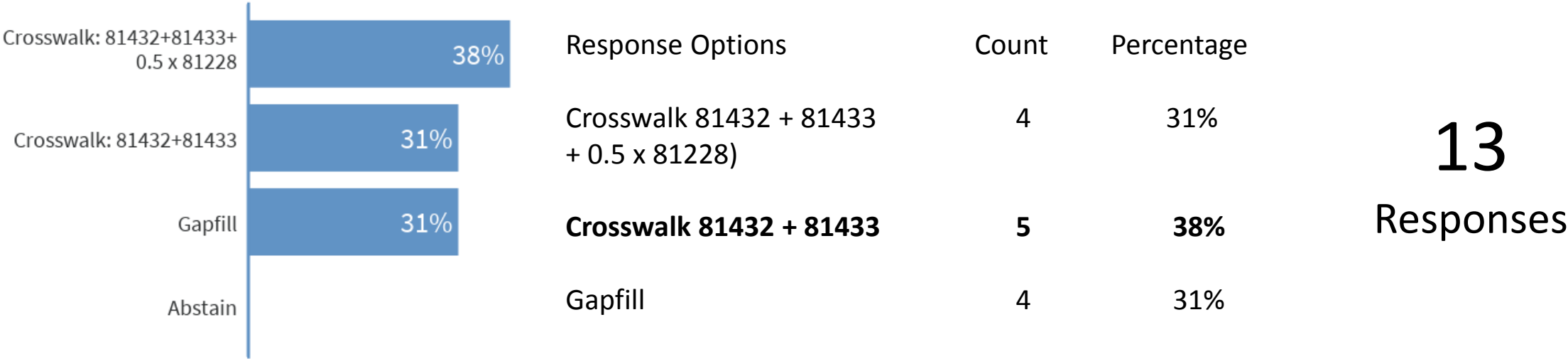| Response Options	Count	Percentage
Crosswalk 81435 + 81436 + (81228*0.5)	**5**	**38%**
Crosswalk 81435 + 81436	4	31%
Gapfill	4	31%
Abstain	0	0%

13
Responses

73. 0102U: Hereditary breast cancer-related disorders (eg, hereditary breast cancer, hereditary ovarian cancer, hereditary endometrial cancer), genomic sequence analysis panel utilizing a combination of NGS, Sanger, MLPA, and array CGH, with MRNA analytics to resolve variants of unknown significance when indicated (17 genes [sequencing and deletion/duplication])

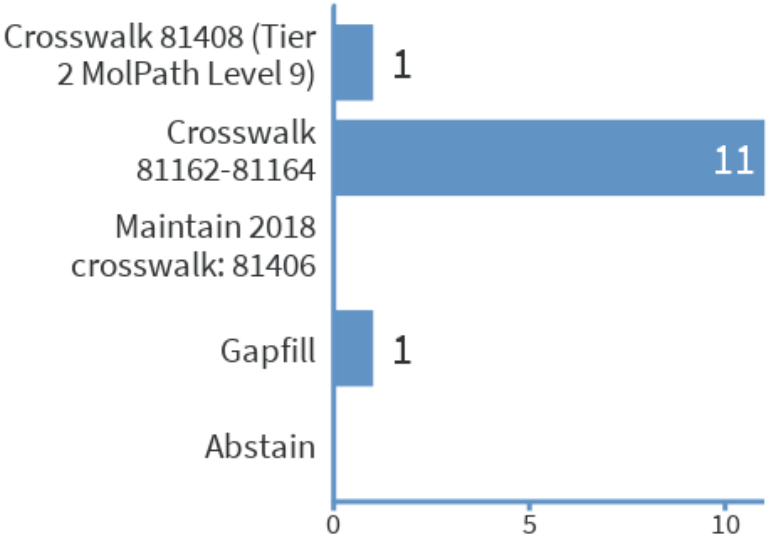| Response Options	Count	Percentage
Crosswalk 81432 + 81433 + (81228*0.25)	4	31%
Crosswalk 81432 + 81433 + (81228*0.25)	0	0%
Crosswalk 81432 + 81433	**5**	**38%**
Gapfill	4	31%

13
Responses

74. 0103U: Hereditary ovarian cancer (eg, hereditary ovarian cancer, hereditary endometrial cancer), genomic sequence analysis panel utilizing a combination of NGS, Sanger, MLPA, and array CGH, with MRNA analytics to resolve variants of unknown significance when indicated (24 genes [sequencing and deletion/duplication], EPCAM [deletion/duplication only])
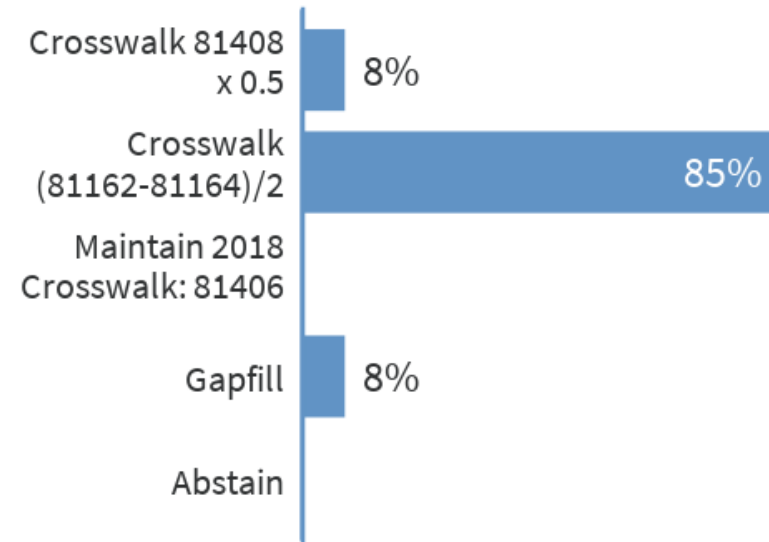

Response Options	Count	Percentage
Crosswalk 81432 + 81433 + 0.5 x 81228)	4	31%
Crosswalk 81432 + 81433	**5**	**38%**
Gapfill	4	31%

13
Responses

75. 81163: Gene Analysis (Breast Cancer 1 and 2) of Full Sequence

Response Options	Count	Percentage
Crosswalk 81408 (Tier 2 MolPath Level 9)	1	8%
Crosswalk 81162 – 81164	**11**	**85%**
Gapfill	1	8%
Abstain	0	0%

13 Responses

76. 81165: Gene Analysis (Breast Cancer 1) of Full Sequence

Response Options	Count	Percentage
Crosswalk 81408 x .0.5	1	8%
Crosswalk (81162 – 81164)/2	**11**	**85%**
Gapfill	1	8%
Abstain	0	0%

13
Responses

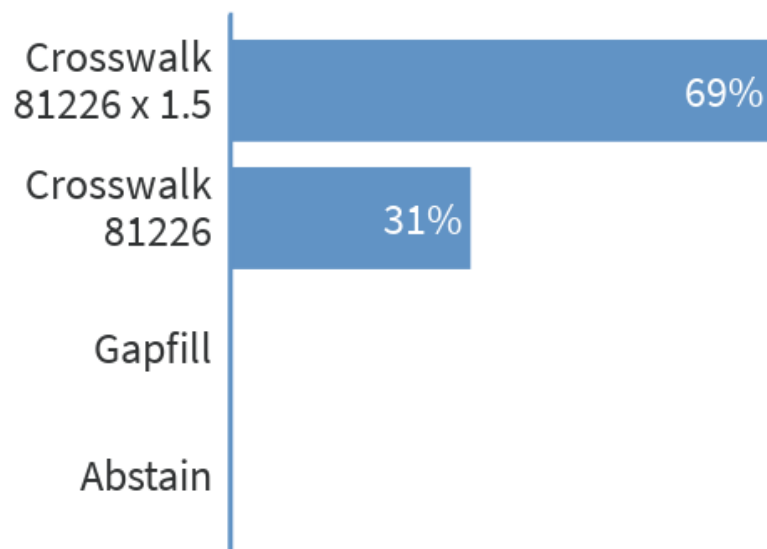# 77. 0046U: Gene Analysis (Fms-related Tyrosine Kinase 3) for Internal Tandem Duplication Variants

Response Options	Count	Percentage
Gapfill	**12**	**92%**
Abstain	0	0%
Maintain 2018 Crosswalk: 81245	1	8%

13 Responses

78. 0049U: Gene Analysis (Nucleophosmin)

Response Options	Count	Percentage
Gapfill	**12**	**92%**
Abstain	0	0%
Maintain 2018 Crosswalk: 81310	1	8%

13
Responses

79. 0070U: CYP2D6 (cytochrome P450, family 2, subfamily D, polypeptide 6) (eg, drug metabolism) gene analysis, common and select rare variants (ie, *2, *3, *4, *4N, *5, *6, *7, *8, *9, *10, *11, *12, *13, *14A, *14B, *15, *17, *29, *35, *36, *41, *57, *61, *63, *68, *83, *xN)

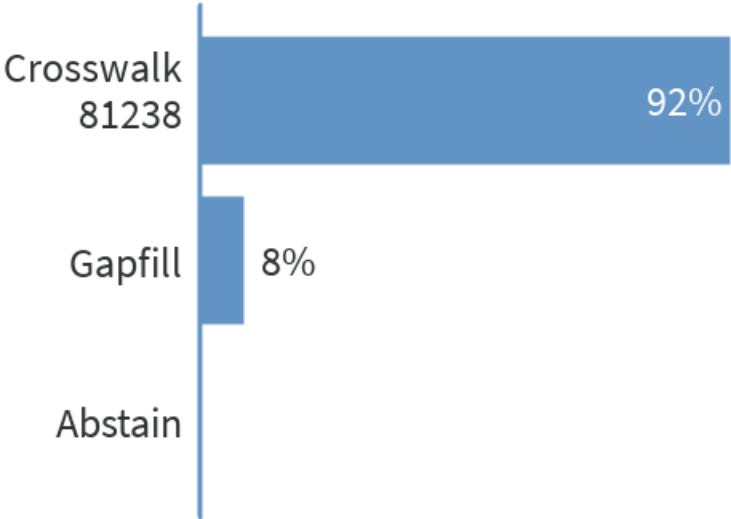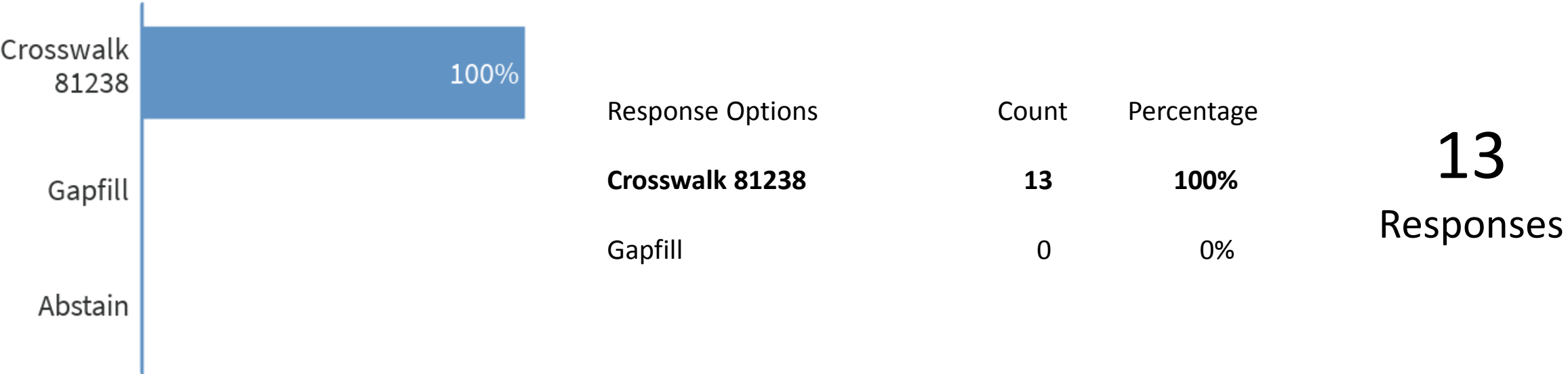| Response Options	Count	Percentage
Crosswalk 81226 X 1.5	**9**	**69%**
Crosswalk 81226	4	31%
Gapfill	0	0%

13
Responses

80. 0071U: CYP2D6 (Cytochrome P4506, Family 2, Subfamily D, Polypeptide 6) (e.g., Drug Metabolism) Gene Analysis , Full Gene Sequence
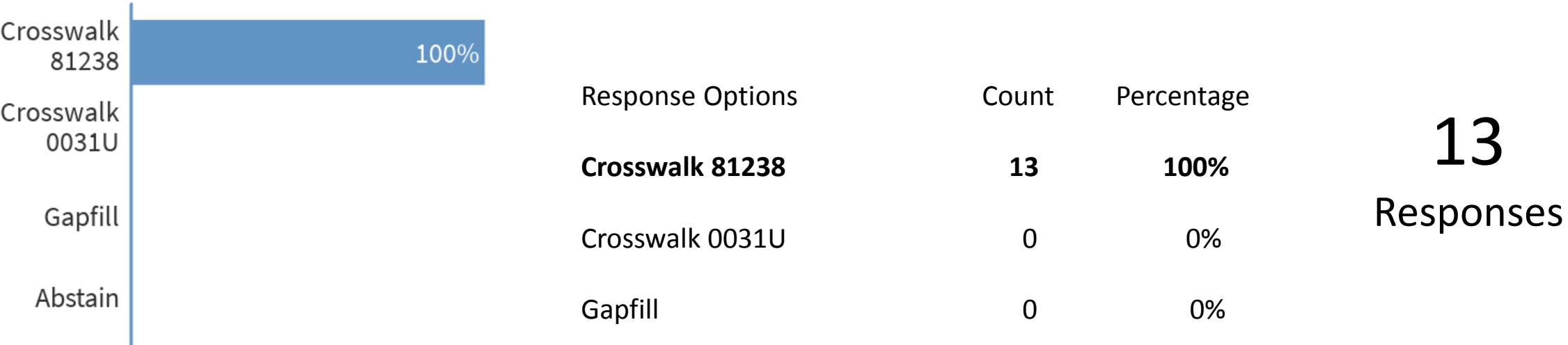

Response Options	Count	Percentage
Crosswalk 81238	**12**	**92%**
Gapfill	1	8%

13
Responses

81. 0072U: CYP2D6 (cytochrome P450, family 2, subfamily D, polypeptide 6) (eg, drug metabolism) gene analysis, targeted sequence analysis (ie, CYP2D6-2D7 hybrid gene)

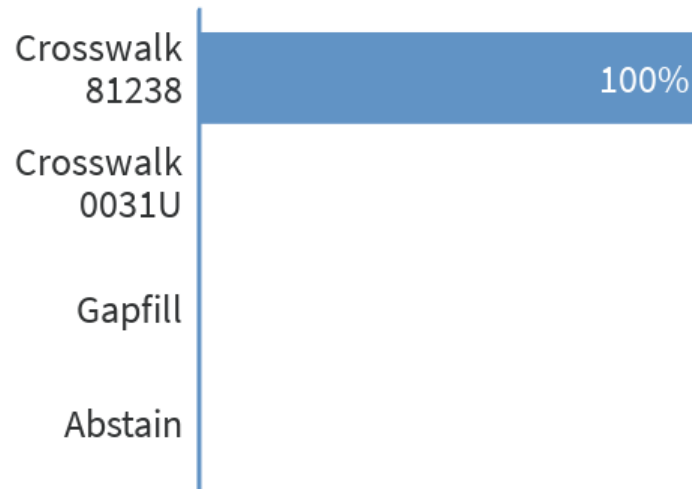| Response Options	Count	Percentage
Crosswalk 81238	**13**	**100%**
Gapfill	0	0%

13
Responses

82. 0073U: CYP2D6 (cytochrome P450, family 2, subfamily D, polypeptide 6) (eg, drug metabolism) gene analysis, targeted sequence analysis (ie, CYP2D7-2D6 hybrid gene)

Response Options	Count	Percentage
Crosswalk 81238	**13**	**100%**
Crosswalk 0031U	0	0%
Gapfill	0	0%

13
Responses

83. 0074U: CYP2D6 (cytochrome P450, family 2, subfamily D, polypeptide 6) (eg, drug metabolism) gene analysis, targeted sequence analysis (ie, non-duplicated gene when duplication/multiplication is trans)

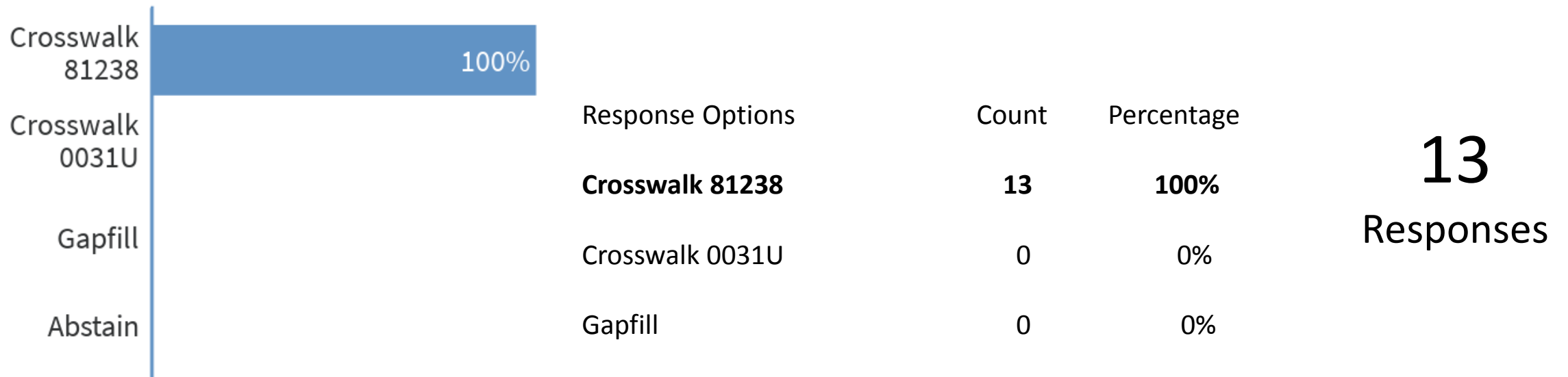| Response Options	Count	Percentage
Crosswalk 81238	13	100%
Crosswalk 0031U	0	0%
Gapfill	0	0%

13
Responses

84. 0075U: CYP2D6 (cytochrome P450, family 2, subfamily D, polypeptide 6) (eg, drug metabolism) gene analysis, targeted sequence analysis (ie, 5' gene duplication/multiplication)

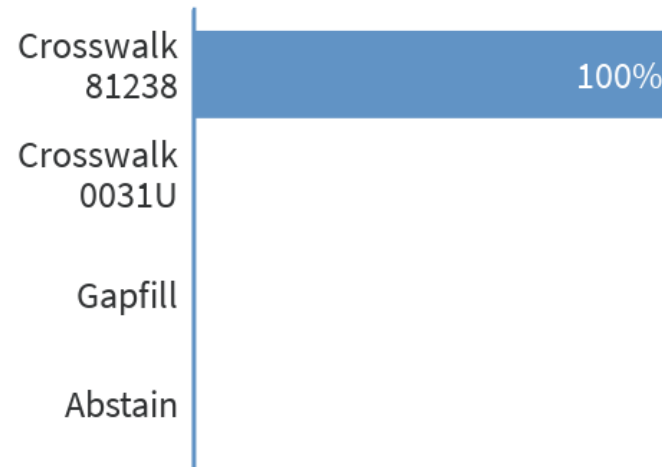| Response Options	Count	Percentage
Crosswalk 81238	**13**	**100%**
Crosswalk 0031U	0	0%
Gapfill	0	0%

13
Responses

85. 0076U: CYP2D6 (cytochrome P450, family 2, subfamily D, polypeptide 6) (eg, drug metabolism) gene analysis, targeted sequence analysis (ie, 3' gene duplication/ multiplication)

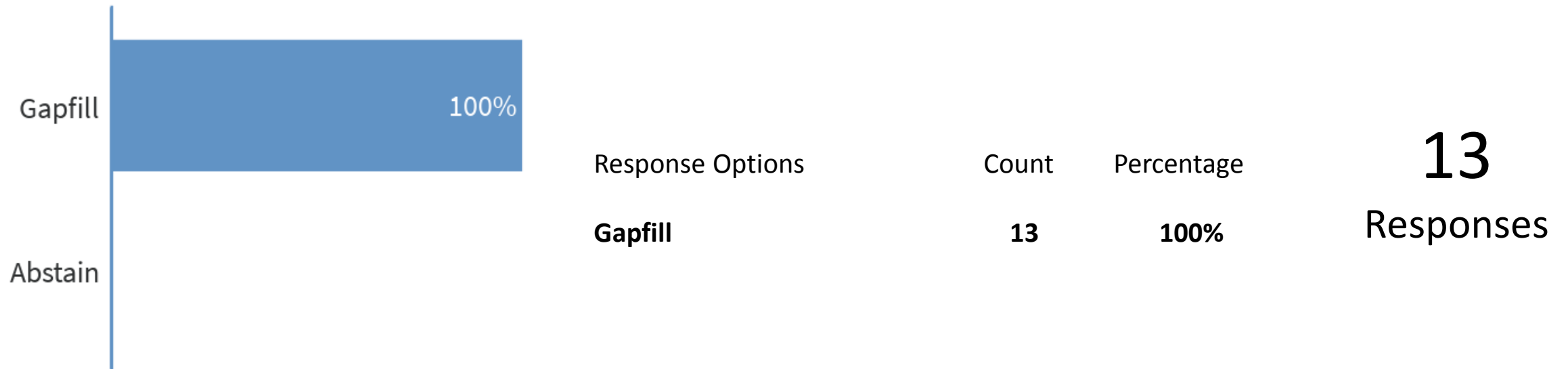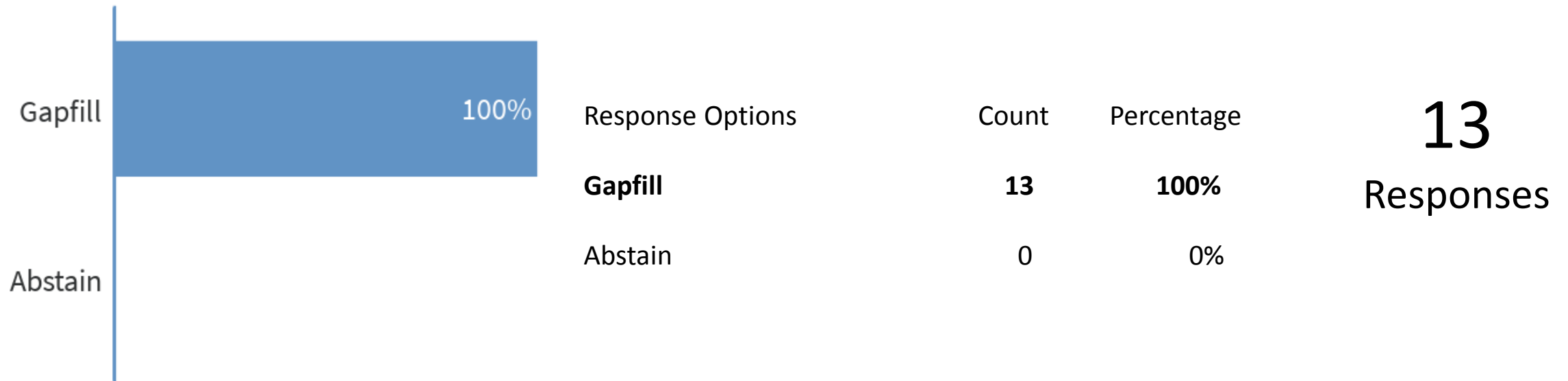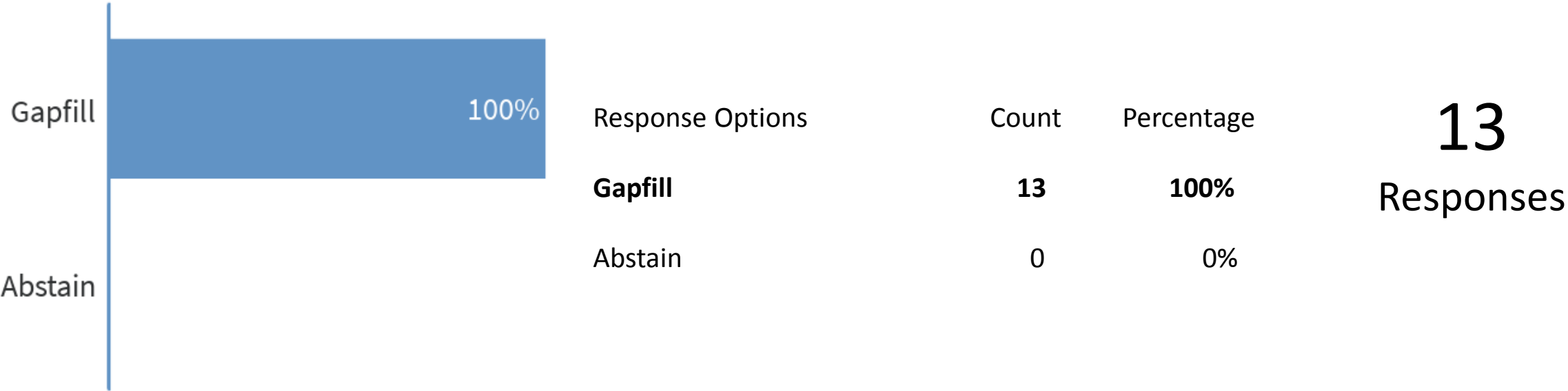| Response Options	Count	Percentage
Crosswalk 81238	**13**	**100%**
Crosswalk 0031U	0	0%
Gapfill	0	0%

13
Responses

86. 0083U: Oncology, response to chemotherapy drugs using motility contrast tomography, fresh or frozen tissue, reported as likelihood of sensitivity or resistance to drugs or drug combinations

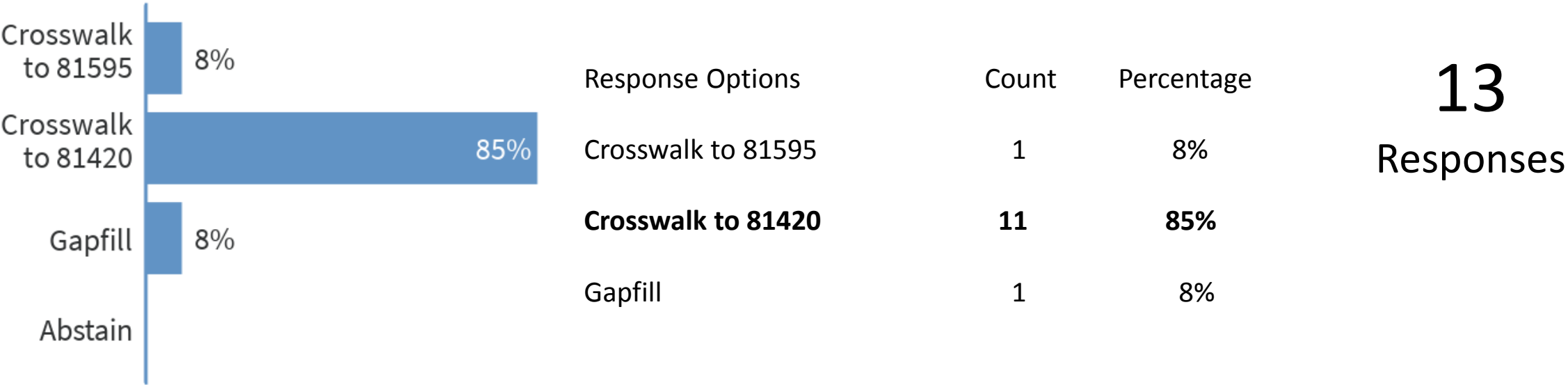| Response Options	Count	Percentage
Gapfill	**13**	**100%**

13
Responses

87. 0087U: Cardiology (heart transplant), mRNA gene expression profiling by microarray of 1283 genes, transplant biopsy tissue, allograft rejection and injury algorithm reported as a probability score

Response Options	Count	Percentage
Gapfill	**13**	**100%**
Abstain	0	0%

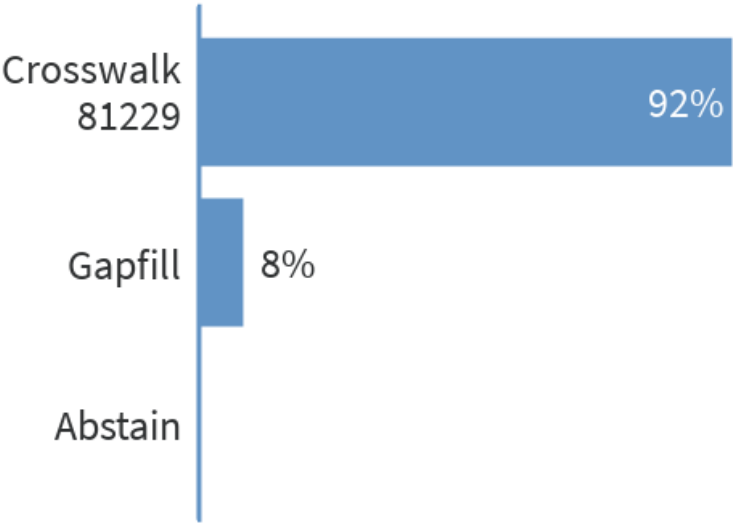Gapfill 100%

Abstain

13
Responses

88. 0088U: Transplantation medicine (kidney allograft rejection), microarray gene expression profiling of 1494 genes, utilizing transplant biopsy tissue, algorithm reported as a probability score for rejection

Response Options	Count	Percentage
Gapfill	**13**	**100%**
Abstain	0	0%

13
Responses

89. 0118U: Transplantation medicine, quantification of donor-derived cell-free DNA using whole genome next-generation sequencing, plasma, reported as percentage of donor-derived cell-free DNA in the total cell-free DNA

Response Options	Count	Percentage
Crosswalk to 81595	1	8%
Crosswalk to 81420	**11**	**85%**
Gapfill	1	8%

13 Responses

90. 8XX0X: Cytogenomic neoplasia (genome-wide) microarray analysis, interrogation of genomic regions for copy number and loss-of-heterozygosity variants for chromosomal abnormalities

Response Options	Count	Percentage
Crosswalk to 81229	**12**	**92%**
Gapfill	1	8%

13
Responses