SEQUENCE JUST ONCE

Say you're investigating colorectal cancer, targeting mutations in KRAS, NRAS, and BRAF genes — NGS makes analysis simple and efficient:

KRAS

qPCR

Exon 2 (codons 12 and 13) and Exon 3 (codon 61)

PYROSEQUENCING

Exon 3 (codon 59) and Exon 4 (codons 117 and 146)

NRAS

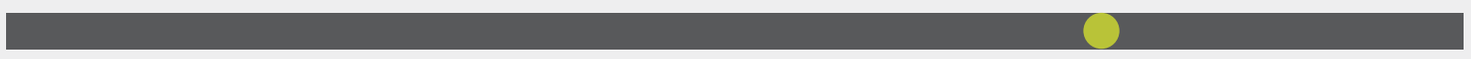
PYROSEQUENCING

Exon 2 (codons 12 and 13), Exon 3 (codons 59 and 61), and Exon 4 (codons 117 and 146)

BRAF

qPCR

V600E, D, K, and R



That's

18 REACTION MIXTURES

across 2 different technologies

KRAS, NRAS, AND BRAF

NGS covers all of the above codons

With NGS, you could assess everything with

2 REACTION MIXTURES

SAVE ON SAMPLE MATERIAL

This leaves more sample material available for further investigation, if necessary

qPCR + Pyrosequencing:

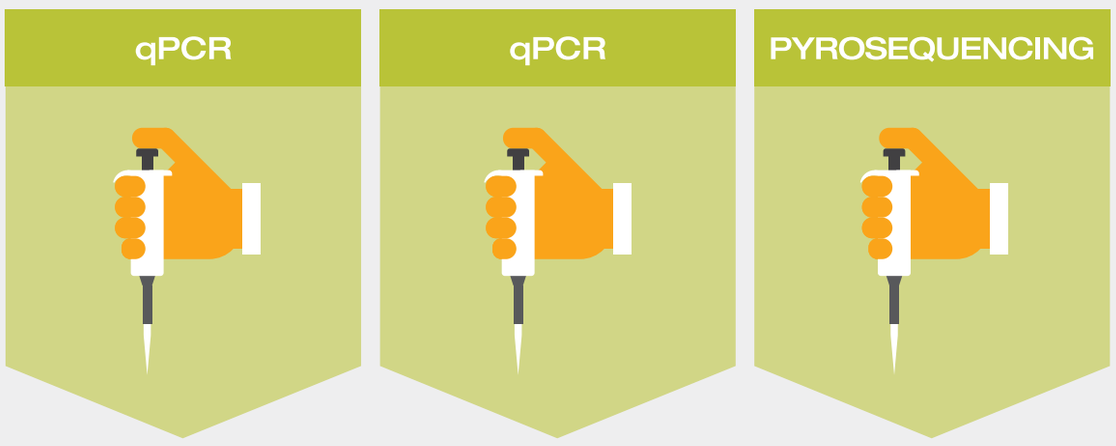
100ng

NGS:

20ng

MINIMIZE WORKFLOW PROTOCOLS

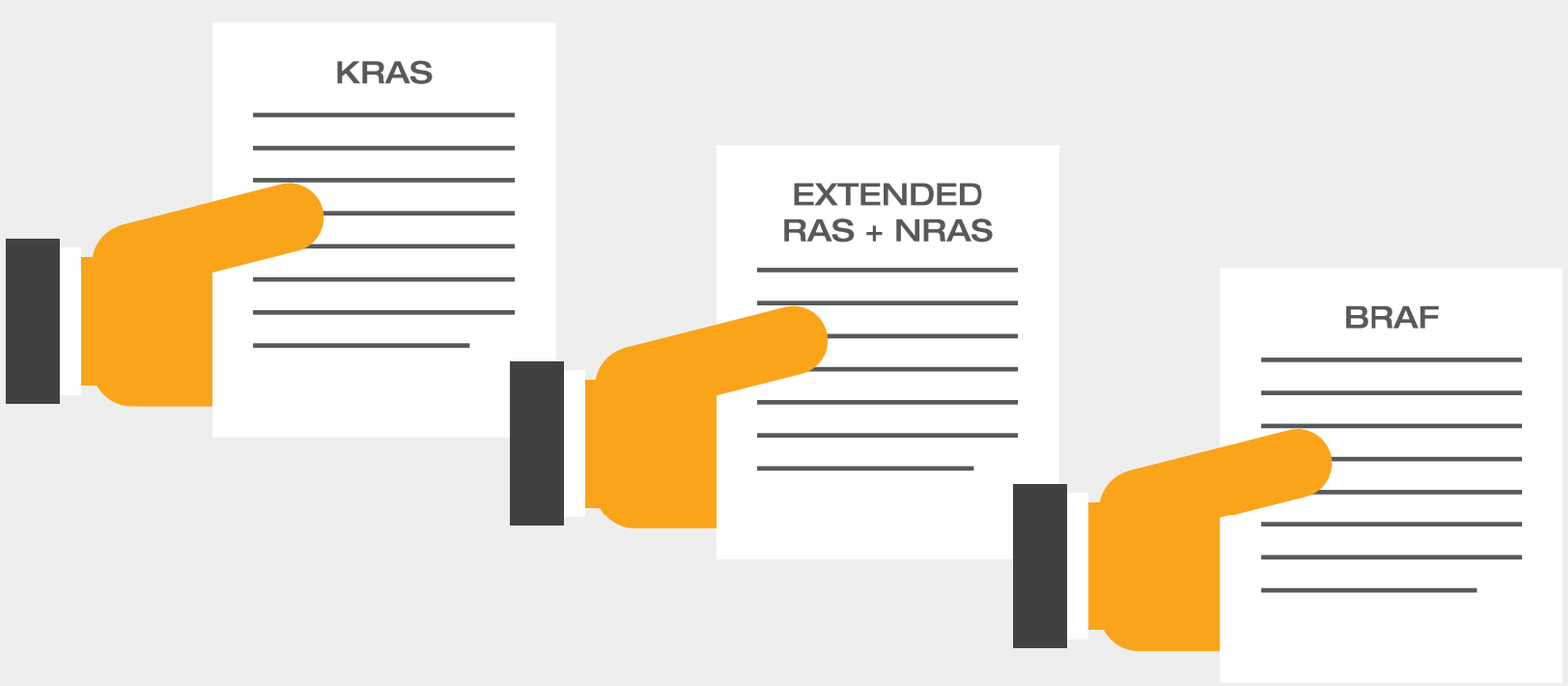
Non-NGS analysis would require maintaining 3 workflow protocols — 2 for qPCR and 1 for pyrosequencing



NGS would require maintaining only a single workflow protocol

SIMPLIFY REPORTING

Between qPCR and pyrosequencing, you would need to consolidate 3 different reports, one for each assessment



With NGS, you would get one report inclusive of all relevant genes