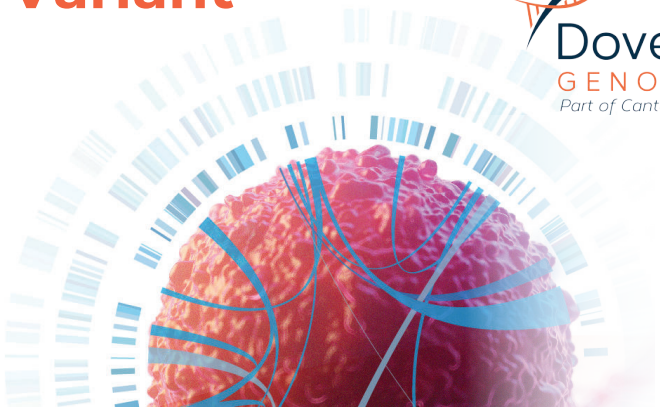
Improved Whole Genome Variant Discovery with Dovetail® LinkPrep™ Technology

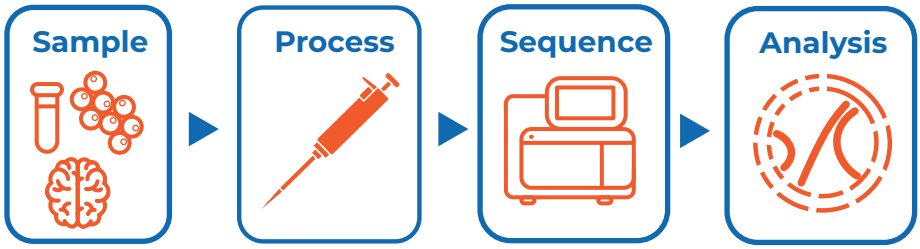
Dovetail GENOMICS
Part of Cantata Bio, LLC

Do more with your short reads - high sensitivity detection of SVs while capturing SNVs, InDels, and CNVs in one NGS assay.



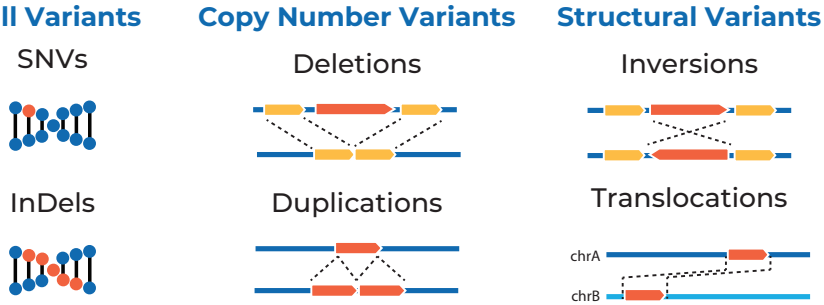
How LinkPrep Works

A NGS solution for genetic variation
Through a few simple steps, generate NGS data that can be processed using standard NGS bioinformic tools with no specialized training or equipment required.



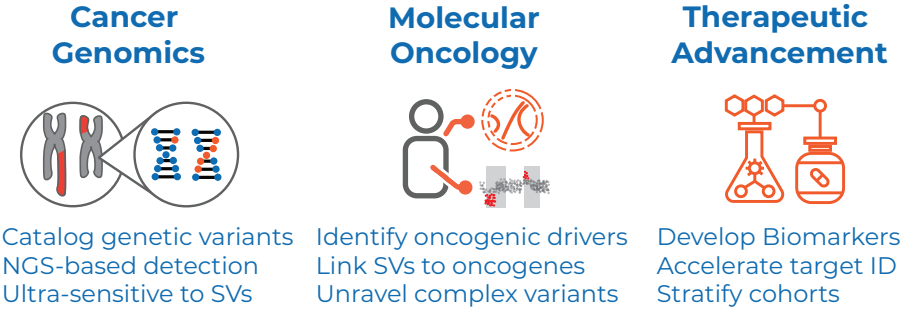
What LinkPrep Provides

Catalog all genetic variants in one assay
Capture the full spectrum of genetic variants including SNVs, InDels, CNVs, and SVs in a single NGS library. Retain WGS-like capabilities for SNV, InDel, and CNV, while enabling ultra-high sensitivity for SVs.



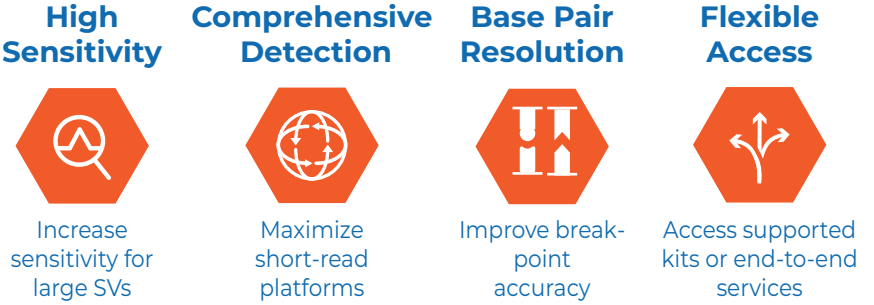
Who LinkPrep Is For

A new view into the cancer genome
Whether you are cataloging all genetic variants in a cancer genome or refining a list of candidate driver mutations, the need for variant detection is a critical component that is uniquely addressed with LinkPrep technology.



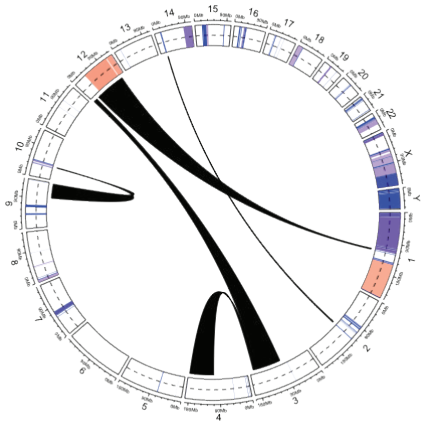
LinkPrep Benefits

Unparalleled access to genetic variation
The LinkPrep technology priotizes sensitivity and accuracy, while providing the most comprehensive view to genetic variation. The LinkPrep™ solution is flexible and available through kits and services with access to best-in-class customer support.



Summarize genetic variation with clear, actionable reporting

Genomic Summary



Actionable Variants 2	**Structural Variants** 7
Coding SNVs 143	**Coding Indels** 78
Putative Gene Fusions 3	**Affected Oncogenes** 3

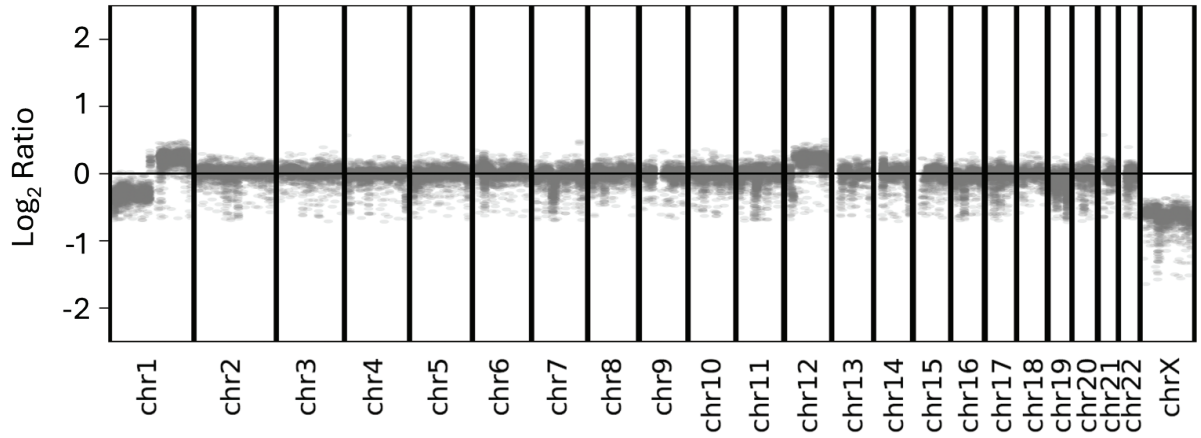
SNV/INDEL

Gene	Chromosome	Position	Ref	Alt	Type	HGVS	VAF
EP300	chr22	41150065	A	G	missense_variant	p.Gln895Arg	33.3 (18)
KRAS	chr12	25245350	C	A	missense_variant	p.Gly12Val	46.4 (56)
EMSY	chr11	76513400	A	C	missense_variant	p.Thr475Pro	53.3 (45)
BRD3	chr9	134041896	G	A	missense_variant	p.Ala424Val	11.1 (9)
ARID1A	chr1	26780022-26780031	GCTGCAACAA	-	frameshift_variant	p.Ser2042LysfsTer90	60 (5)
MAPK3	chr16	30118414	C	T	missense_variant	p.Ala160Thr	66.7 (6)
CBFA2T3	chr16	88876999	G	A	missense_variant	p.Pro647Ser	60 (5)
TERT	chr5	1293616	C	T	missense_variant	p.Gly424Ser	60 (5)
CDKN1A	chr6	36684357	C	T	missense_variant	p.Arg86Trp	60 (5)
PTPRS	chr19	5274342	G	A	missense_variant	p.Pro32Ser	75 (8)

Structural Variants

Chrom1	Start1	End1	Strand1	Chrom1	Start1	End1	Strand1	Score
chr9	9.20e+07	1.38e+08	-	chr10	4.10e+07	4.20e+07	-	280.298
chr2	1.29e+08	1.32e+08	+	chr14	1.90e+07	2.00e+07	-	210.707
chr3	1.69e+08	1.86e+08	+	chr4	1.09e+08	1.87e+08	+	1639.700
chr3	9.40e+07	1.70e+08	+	chr12	2.00e+06	1.40e+07	+	5026.490
chr1	1.17e+08	1.20e+08	+	chr12	2.30e+07	1.21e+08	-	3316.350

Copy Number Variation



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