PerkinElmer
For the Better

HUMAN HEALTH | ENVIRONMENTAL HEALTH

The PerkinElmer Omics Laboratory

Todd Smith
PerkinElmer | Geospiza

SFAF June 5, 2012

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PerkinElmer: dedicated to improving human & environmental health…

…for a healthier today and an even better tomorrow

Products / Applications for Life Science Research and Medicine

75 Years of Analytical Chemistry and Instrumentation Experience

Cellular research

Cancer research

GPCRs

Protein:protein

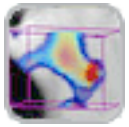
Epigenetics

Kinases

Immuno assays

Label free assays

High throughput screening


In Vivo

Screening technologies

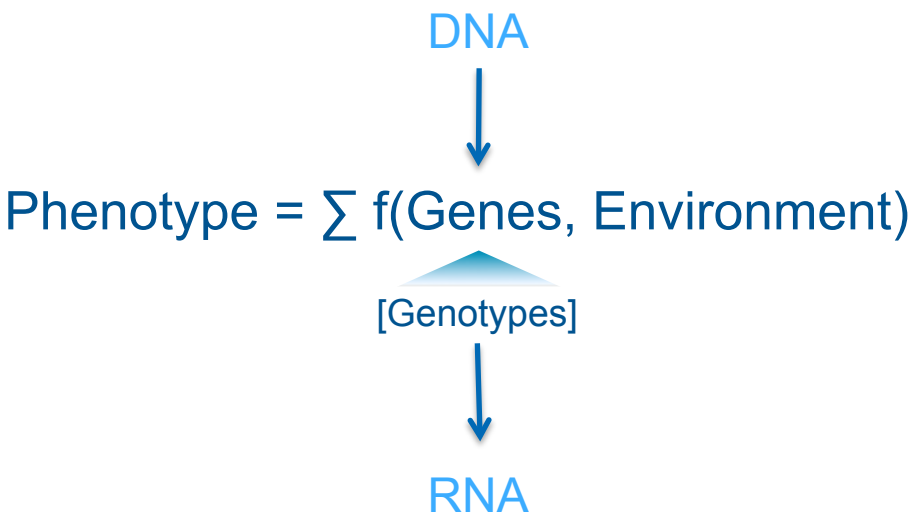
SPA “generic” assays

Biotherapeutics

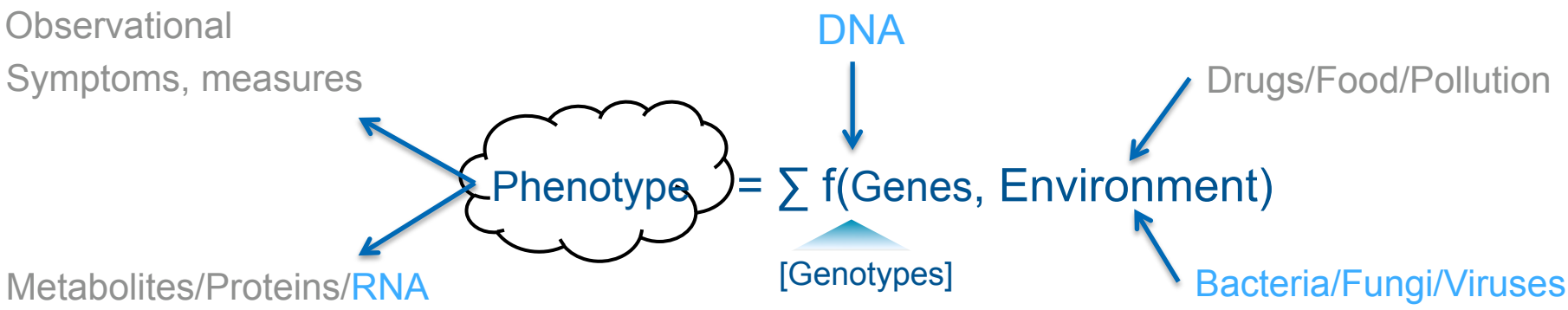
Radioligand binding

Laboratory automation

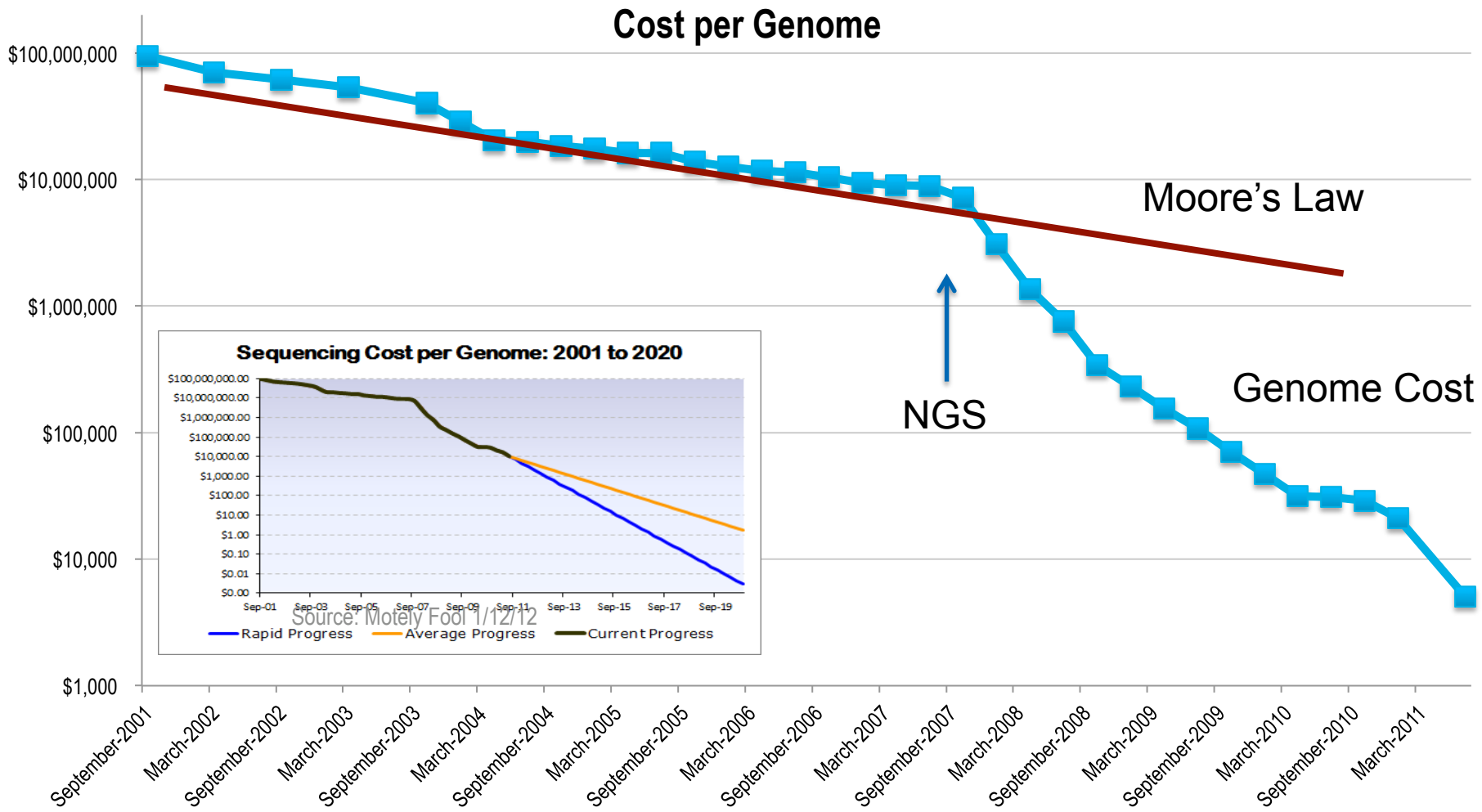
Genomics is Foundational in Omics



The Phenotype/Genotype Relationship: It's Complicated

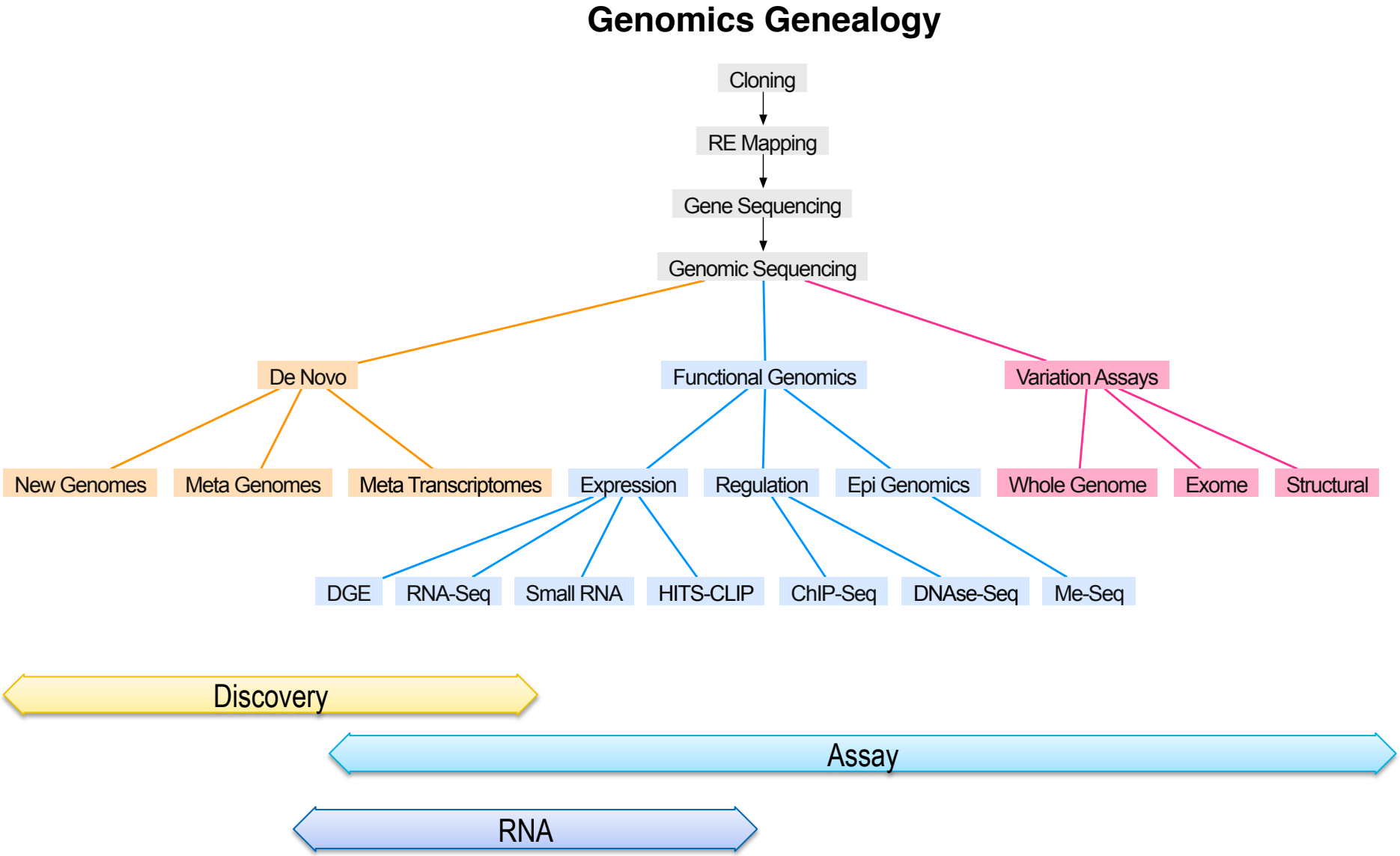


Increasing Access to Cheap Data



Source: NHGRI

Cheap Sequence Data Drives Nucleotide-based Omics Applications



http://finchtalk.geospiza.com/2010/09/genomics-genealogy.html

PerkinElmer and Next Generation Sequencing

January 2011

- Geospiza is selected to provide LIMS and analysis support PerkinElmer's DNA services

May 2011

- PerkinElmer acquires Geospiza

November 2011

- PerkinElmer acquires Caliper Life Sciences

Two bottlenecks: Sample Prep and Informatics

Omics Applications Demand Automation and Informatics

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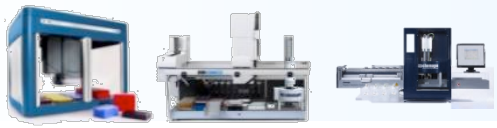
Geospiza LIMS and Analysis

Isolate Sample	Fragment & Sizing	Generate Library	Quantify Sample	Sequence	Analyze
MBW JANUS & chemagen	DS	XT	GX	NGS	XT	GX	NGSW	Geospiza

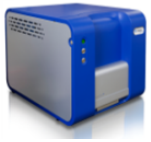


Zephyr Molecular Biology Workstation (MBW)
JANUS Solutions and chemagen • Nucleic Acid Extraction

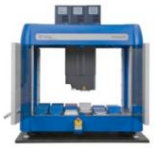
LabChip DS System • UV-Vis DNA/RNA Quantification

Sequencing Service

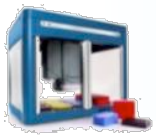
LabChip XT System • Automated DNA Fractionation and Sizing



LabChip GX System • HT Bioanalyzer-like QC for DNA and RNA



Sciclone NGS Workstation • Automated High-throughput Sequencing Sample Preparation



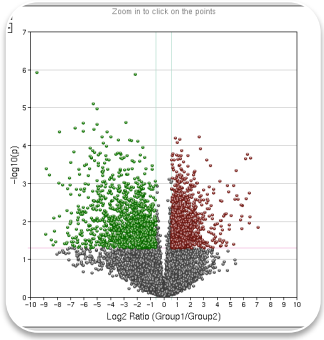
Zephyr NGS Workstation (NGSW) • Post PCR Workstation

Smaller samples, better quality & reduced PCR bias, higher throughput & productivity with lower costs, informatics correlation linkages

Geospiza® Products

GeneSifter® Lab Edition

- Comprehensive web-based LIMS for genomics
- Scalable, flexible, adaptable
- Unique in accounting, and linkage with data analysis



GeneSifter® Analysis Edition

- Comprehensive web-based data analysis
- From microarrays to NGS
- Unique in completeness for creating new knowledge

… and FinchTV

Edit View Insert Format Tools Data Window Help

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allSnps.12_25_2011.wReseqMAFjoined.xls

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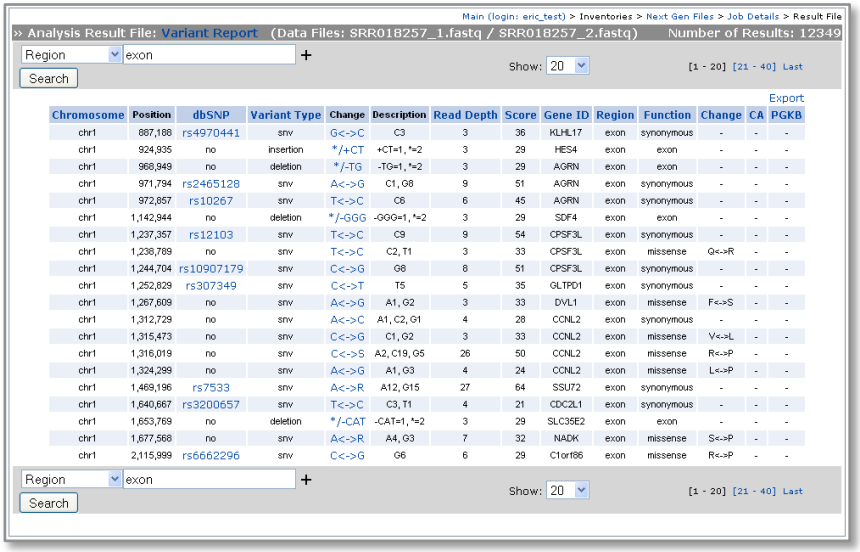
Sheets Charts SmartArt Graphics WordArt

1	2	3	4	5	6	7	8	9	10	11	12	13	14	15	16	17	18	19	20	21
			hg18										calculated from the 1000	individuals who have	the alternative allele in the	RD+Reseq	European American poulation			
		chr	pos	ref	alt	hm	ht	type	aa	loc	severity	inDB	ceuMAF	Reseq freq	Reseq MAF	Combined MAF	EVS (Seattle) MAF	Polyphen prediction	PhastCons	CompiGen
COBL		chr7	51051798	C	A	2	9	utr-3	none	NA	NA	dbSNP_1000Genomes	0.191666666666667				NA			0.529 (n=34)
		chr7	51051815	T	C	19	5	utr-3	none	NA	NA	dbSNP_1000Genomes	0.841666666666667				NA			0.888 (n=134)
		chr7	51060507	A	T	18	3	coding-synonymous	none	1187/1262	N/A	dbSNP_1000Genomes	0.95				0.0630 (0.8772 hm, 0.1197 ht)	unknown	0	0.948 (n=134)
		chr7	51060543	C	T	0	1	coding-synonymous	none	1175/1262	N/A	none	0.0166666666666667		0.00555555555555556	0.0087719298245614	NA			NA (n=0)
	X	chr7	51061763	G	A	0	5	missense	HIS,TYR	1160/1262	DAMAGING *W	dbSNP	0.0416666666666667	0.075 (1hm, 6ht)	0.043010752688172	0.0555555555555556	0.0798 (0.0071 hm, 0.1453 ht)	probably-damaging	0.891	0.500 (n=10)
		chr7	51063433	C	G	0	1	missense	GLY,ARG	952/1262	TOLERATED	none	-1				NA			NA (n=0)
		chr7	51063530	G	C	2	8	missense	HIS,GLN	919/1262	TOLERATED	dbSNP_1000Genomes	0.175	0.2 (2hm, 17ht)	0.110526315789474	0.138655462184874	0.1746 (0.0276 hm, 0.2940 ht)	benign	0.002	0.500 (n=32)
		chr7	51063641	A	G	0	3	coding-synonymous	none	882/1262	N/A	dbSNP	0.05		0.0368421052631579	0.0420168067226891	0.0593 (0.0048 hm, 0.1068 ht)	unknown	0	0.500 (n=28)
	X	chr7	51064324	C	G	0	1	missense	ALA,PRO	655/1262	DAMAGING *W	none	-1	0.092 (2hm, 6ht)	0.0602409638554217	0.0514018691588785	NA			0.500 (n=16)
	X	chr7	51064407	G	A	0	1	missense	THR,MET	627/1262	DAMAGING *W	none	-1	0.094 (1hm, 7ht)	0.0555555555555556	0.0476190476190476	NA			0.500 (n=2)
		chr7	51064468	C	T	8	12	missense	VAL,ILE	607/1262	TOLERATED	dbSNP_1000Genomes	0.65		0.629411764705882	0.619266055045872	0.3309 (0.4487 hm, 0.4407 ht)	benign	0	0.703 (n=118)
		chr7	51064557	T	G	21	2	missense	ASP,ALA	577/1262	TOLERATED	dbSNP_1000Genomes	0.933333333333333				0.0429 (0.9157 hm, 0.0829 ht)	benign	0.011	0.993 (n=138)
		chr7	51064710	G	A	0	4	missense	PRO,LEU	526/1262	TOLERATED	dbSNP_1000Genomes	0.141666666666667		0.094117647058235	0.0917431192660551	0.1242 (0.0194 hm, 0.2097 ht)	benign	0.004	0.500 (n=34)
	X	chr7	51066067	T	A	0	2	missense	GLU,ASP	480/1262	TOLERATED	dbSNP_1000Genomes	-1	-1			NA			NA (n=0)
		chr7	51254964	A	G	13	10	coding-synonymous	none	71/1262	N/A	dbSNP_1000Genomes	0.75		0.869318181818182	0.84375	0.2543 (0.5595 hm, 0.3724 ht)	unknown	0.941	0.836 (n=122)
	N	chr7	51096986? (hg19)	G	A			missense	ALA, THR	603/1262				0.024 (2ht)	0.0117647058823529		NA			
	N	chr7	51096990 (hg19)	C	T			missense (syn in EVS)	HIS,TYR	601/1262				0.024 (2ht)	0.0117647058823529		0.0000 (0.0000 hm, 0.0000 ht)	unknown	0	
	N	chr7	51097255 (hg19)	C	T			missense	SER, PHE	513/1262				0.011 (1ht)	0.00588235294117647		0.0120 (0.0000 hm, 0.0239 ht)	possibly-damaging	0.007	
		chr	pos	ref	alt	hm	ht	type	aa	loc	severity	inDB	ceuFreq	Reseq freq	Reseq MAF	Combined MAF	EVS MAF (proportion ht,hm)	Polyphen prediction	PhastCons	CompiGen
CELSR1		chr22	45135497	C	T	1	2	utr-3	none	NA	NA	dbSNP_1000Genomes	0.133333333333333				NA			0.659 (n=44)
		chr22	45136995	G	A	0	1	utr-3	none	NA	NA	none	-1				NA			NA (n=0)
		chr22	45136997	C	A	0	1	utr-3	none	NA	NA	dbSNP	-1				NA			0.500 (n=2)
		chr22	45137237	G	T	0	3	utr-3	none	NA	NA	dbSNP_1000Genomes	0.175				NA			0.568 (n=44)
		chr22	45137399	G	A	0	1	utr-3	none	NA	NA	dbSNP	-1				NA			NA (n=0)
		chr22	45138613	G	A	0	1	coding-synonymous	none	2993/3015	N/A	none	-1				NA			NA (n=0)
		chr22	45139145	C	G	0	5	missense	GLU,GLN	2903/3015	TOLERATED	dbSNP_1000Genomes	0.233333333333333	0.298 (0hm,28ht)	0.148936170212766	0.139830508474576	0.2439 (0.0536 hm, 0.3806 ht)	possibly-damaging	0	0.585 (n=53)
		chr22	45140161	C	G	0	2	missense	CYS,SER	2797/3015	TOLERATED	dbSNP_1000Genomes	0.216666666666667	0.263 (0hm,25ht)	0.131578947368421	0.113445378151261	0.2025 (0.0384 hm, 0.3283 ht)	benign	0.029	0.672 (n=64)
		chr22	45140965	G	A	0	1	missense	SER,LEU	2761/3015	DAMAGING *W	none	-1				NA			1.000 (n=1)
		chr22	45142335	A	G	0	6	coding-synonymous	none	2678/3015	N/A	dbSNP	0.075	0.141 (0hm,13ht)	0.0706521739130435	0.0818965517241379	0.1225 (0.0151 hm, 0.2148 ht)	unknown	0.215	0.597 (n=62)
		chr22	45147475	G	A	1	1	coding-synonymous	none	2576/3015	N/A	dbSNP	0.0333333333333333	0.058 (0hm,5ht)	0.0290697674418605	0.0363636363636364	0.0623 (0.0031 hm, 0.1182 ht)	unknown	0.974	0.500 (n=4)
		chr22	45156481	G	A	0	1	coding-synonymous	none	2338/3015	N/A	none	-1	0.047 (0hm,4ht)	0.0235294117647059	0.0229357798165138	NA			NA (n=0)
		chr22	45156556	C	T	0	3	coding-synonymous	none	2313/3015	N/A	dbSNP	0.0583333333333333	0.07 (0hm,6ht)	0.0348837209302326	0.0409090909090909	0.0472 (0.0024 hm, 0.0897 ht)	unknown	0	0.429 (n=7)
	X	chr22	45159185	T	C	1	4	missense	THR,ALA	2268/3015	TOLERATED	dbSNP_1000Genomes	0.2	0.177 (1hm,16ht)	0.09375	0.1	0.1536 (0.0182 hm, 0.2707 ht)	benign	0	0.621 (n=58)
		chr22	45159237	G	A	0	1	coding-synonymous	none	2250/3015	N/A	none	-1				NA			NA (n=0)
	X	chr22	45161046	C	T	0	3	missense	ARG,HIS	2219/3015	TOLERATED	dbSNP	0.075	0.077 (0hm,7ht)	0.0384615384615385	0.0434782608695652	0.0636 (0.0046 hm, 0.1180 ht)	benign	0	0.500 (n=8)
		chr22	45163965	C	T	1	1	coding-synonymous	none	2147/3015	N/A	dbSNP_1000Genomes	0.15	0.086 (1hm,5ht)	0.05	0.0531914893617021	0.0869 (0.0066 hm, 0.1607 ht)	unknown	0.055	0.500 (n=8)
		chr22	45164979	T	C	1	3	missense	ILE,VAL	2107/3015	TOLERATED	dbSNP_1000Genomes	0.233333333333333	0.183 (0hm,17ht)	0.0913978494623656	0.094017094017094	0.1604 (0.0211 hm, 0.2787 ht)	benign	0	0.613 (n=62)
		chr22	45166358	A	G	1	3	missense	LEU,PRO	1995/3015	TOLERATED	dbSNP_1000Genomes	0.191666666666667	0.159 (0hm,14ht)	0.0804597701149425	0.0855855855855856	0.1380 (0.0179 hm, 0.2402 ht)	benign	0.72	0.621 (n=58)
		chr22	45166361	A	G	1	3	missense	LEU,PRO	1994/3015	TOLERATED	dbSNP_1000Genomes	0.2	0.159 (0hm,14ht)	0.0795454545454545	0.0848214285714286	0.1338 (0.0177 hm, 0.2322 ht)	benign	0.978	0.548 (n=42)
		chr22	45173139	T	C	0	2	coding-synonymous	none	1824/3015	N/A	dbSNP	0.0583333333333333	0.093 (0hm,8ht)	0.0465116279069767	0.0454545454545455	0.0476 (0.0020 hm, 0.0912 ht)	unknown	0.08	0.500 (n=6)
		chr22	45183671	G	A	0	1	coding-synonymous	none	1704/3015	N/A	dbSNP_1000Genomes	0.1	0.045 (4hm,0ht)	0.0421052631578947	0.037815126050420	0.0564 (0.0026 hm, 0.1077 ht)	unknown	1	0.500 (n=24)
	X	chr22	45184436	C	T	0	3	missense	ALA,THR	1647/3015	DAMAGING	dbSNP_1000Genomes	0.0333333333333333	0.053 (0hm,5ht)	0.0265957446808511	0.0338983050847458	0.0346 (0.0023 hm, 0.0647 ht)	benign	0.033	0.500 (n=2)
		chr22	45186174	G	A	0	1	coding-synonymous	none	1586/3015	N/A	dbSNP	0.0333333333333333	0.065 (0hm,6ht)	0.0326086956521739	0.0301724137931034	0.0321 (0.0011 hm, 0.0618 ht)	unknown	0.358	0.500 (n=2)
		chr22	45213928	C	T	0	1	missense	GLY,ARG	1410/3015	TOLERATED	none	-1				NA			NA (n=0)
		chr22	45308356	A	G	20	3	missense	CYS,ARG	1126/3015	TOLERATED	dbSNP_1000Genomes	0.95	1 (78hm,9ht)	0.877659574468085	0.919491525423729	0.0657 (0.8732 hm, 0.1222 ht)	benign	1	0.920 (n=137)
		chr22	45308877	C	A	0	1	missense	ALA,SER	1019/3015	TOLERATED	dbSNP	-1	0.105 (2hm,7ht)	0.0632183908045977	0.0855855855855856	0.0023 (0.0000 hm, 0.0046 ht)	probably-damaging	0.993	0.500 (n=2)
		chr22	45308771	C	T	0	8	coding-synonymous	none	987/3015	N/A	dbSNP_1000Genomes	0.191666666666667	0.33 (4hm,26ht)	0.180851063829787	0.288135593220339	0.2427 (0.0587 hm, 0.3681 ht)	unknown	0.945	0.550 (n=40)
		chr22	45309741	G	C	16	3	missense	SER,TRP	664/3015	DAMAGING	dbSNP	0.908333333333333				0.0640 (0.8765 hm, 0.1189 ht)	probably-damaging	0.975	0.856 (n=132)
		chr22	45310066	G	C	0	2	missense	LEU,VAL	556/3015	TOLERATED	dbSNP_1000Genomes	0.05	0.038 (3hm,0ht)	0.0375	0.0384615384615385	0.0326 (0.0014 hm, 0.0624 ht)	benign	1	0.500 (n=6)
		chr22	45310457	G	C	19	3	coding-synonymous	none	425/3015	N/A	dbSNP_1000Genomes	0.941666666666667	0.492 (29hm,2ht)	0.476190476190476	0.591954022988506	0.0651 (0.8746 hm, 0.1205 ht)	unknown	1	0.917 (n=132)
		chr22	45310502	G	A	19	3	coding-synonymous	none	410/3015	N/A	dbSNP_1000Genomes	0.95	1 (96hm,0ht)	1	0.970833333333333	0.0659 (0.8731 hm, 0.1220 ht)	unknown	0.998	0.855 (n=131)
		chr22	45311076	G	A	0	1	missense	PRO,LEU	219/3015	TOLERATED	none	-1				NA			NA (n=0)
		chr22	45311423	G	A	0	1	coding-synonymous	none	103/3015	N/A	none	-1				NA			NA (n=0)
	N							missense	SER,GLY	p.G2948GS				0.152 (0hm,14ht)	0.0760869565217391		0.1437 (0.0188 hm, 0.2497 ht)	benign	0.252	
	N							missense	SER,GLY	p.G2862GS				0.011 (0hm,1ht)	0.00531914893617021		0.0006 (0.0000 hm, 0.0011 ht)	benign	0.062	
	N							missense		p.A2202AV				0.011 (0hm,1ht)	0.00549450549450549		NA			
	N							missense		p.A2156AV				0.014 (0hm,1ht)	0.00714285714285714		NA			
	N							missense	SER,ASN	p.N1884NS				0.022 (0hm,2ht)	0.0108695652173913		0.0044 (0.0000 hm, 0.0088 ht)	benign	0.303	
	N							missense	MET,VAL	p.V1821VL				0.012 (0hm,1ht)	0.00581395348837209		0.0003 (0.0000 hm, 0.0006 ht)	benign	0	
	N							missense	TRP,ARG	p.R72RW				0.011 (0hm,1ht)	0.00561797752808989		0.0000 (0.0000 hm, 0.0000 ht)	unknown	0.007	
	N							missense		p.C139CR				0.011 (0hm,1ht)	0.00531914893617021		NA			
	N							missense		p.T875TN				0.236 (0hm,21ht)	0.117977528089888		NA			
	N							missense		p.A1023AG				0.012 (0hm,1ht)	0.00537634408602151		NA			
	N							missense		p.I1124IM				0.011 (0hm,1ht)	0.00609756097560976		NA			
		chr	pos	ref	alt	hm	ht	type	aa	loc	severity	inDB	ceuFreq	Reseq freq	Reseq MAF	Combined MAF	EVS (Seattle) MAF	Polyphen prediction	PhastCons	CompiGen

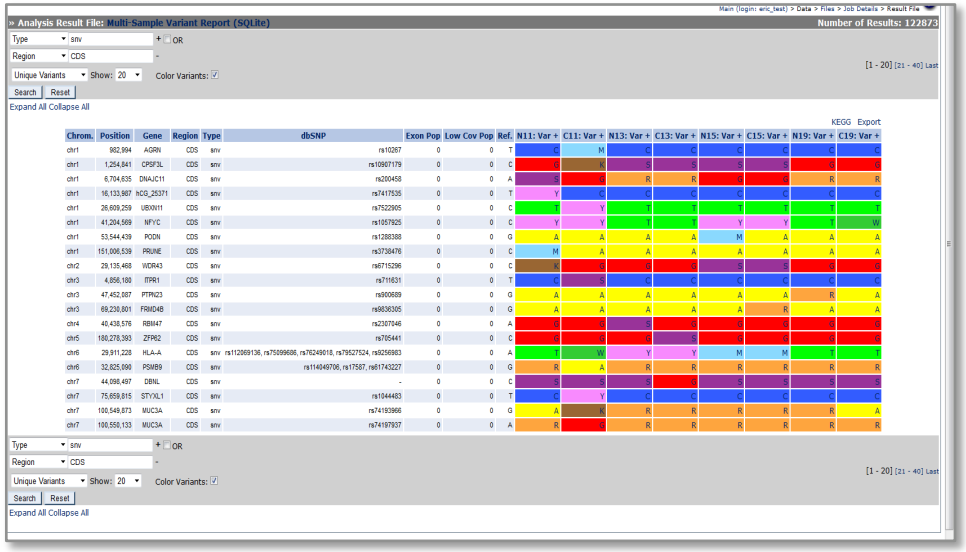
A Better Way

PerkinElmer
For the Better

Single sample

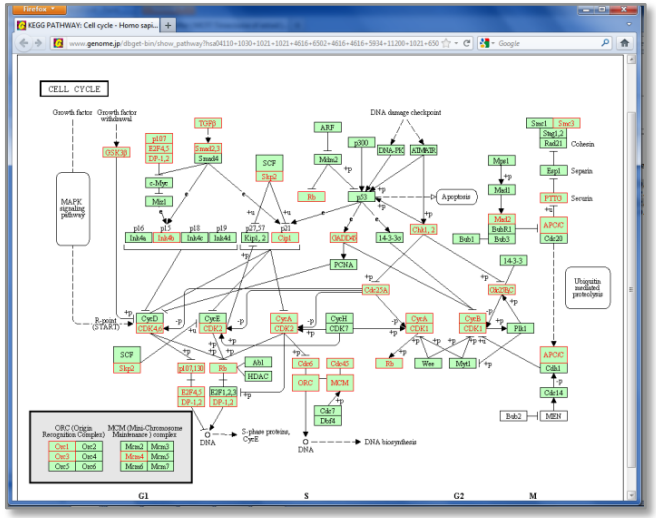


Many samples



Base level

Pathways



Geospiza® NGS Data Analysis Workflow

PerkinElmer
For the Better

Primary

Collect – Instrument Specific

Sequences +
Quality values

Secondary

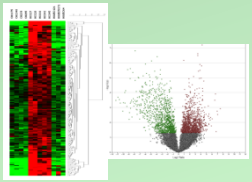
Individual Samples

Reduce – Application Specific

- Alignments
- Mapping to gene model
- Gene list
- Variant list
- Visualization

Multiple Data sets

Compare – Experiment Specific



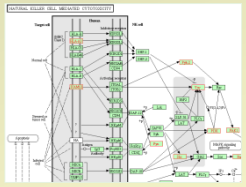
- Comparison statistics
- Clustering
- Splicing analysis
- Allele frequency
- Tumor specific mutations

Reiterative Process

Tertiary

Genes, variants, isoforms of interest

Discover – Experiment Specific



- Pathways
- Ontologies
- Networks
- Annotation

GeneSifter®

What do you See in Your Experiment?

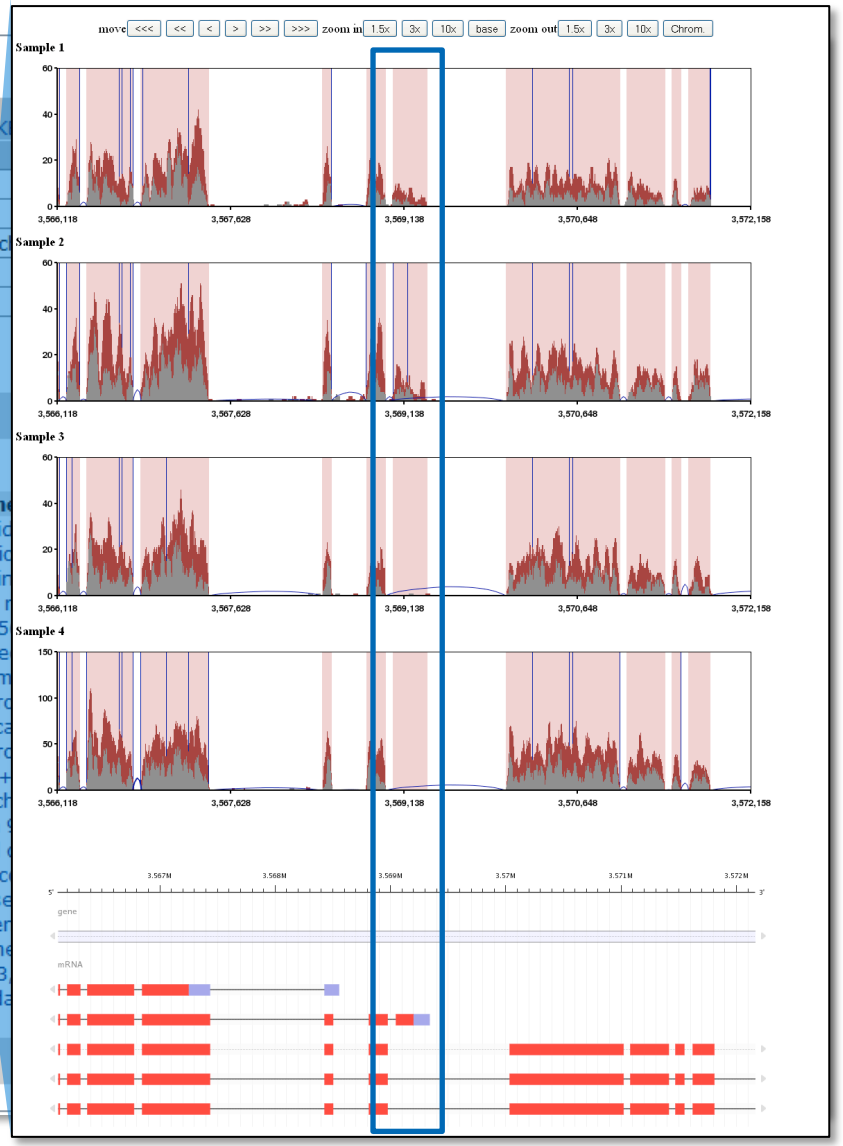
Pairwise Analysis: Prostate Cancer GSE22260 [Reports: Ontology | K

	Group 1
Conditions:	Normal
Experiments:	87527, 87534
Significance:	1.5 - 5, edgeR, Benjamini and Hoc
Normalization:	Mapped reads
Quality Cutoff:	5
Data Transformation:	None

Show: 20 p Cutoff: 0.05 raw p Fold Change: 1.5 Upper: 5

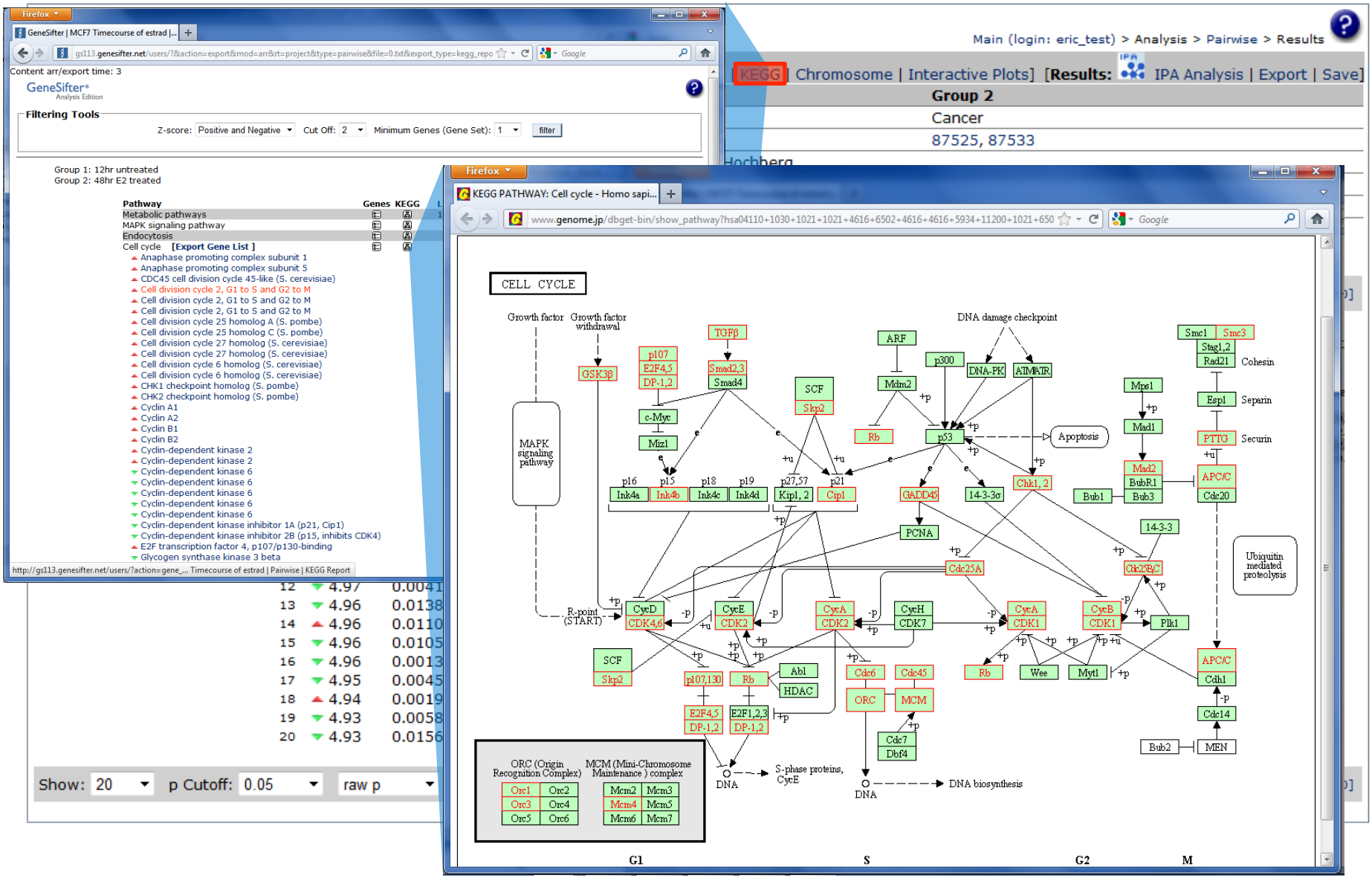
No.	Ratio	p-value	adj. p	Identifier	Gene Name
1	▼ 5.00	0.00995	0.22520	NOXO1	NADPH oxid
2	▼ 5.00	0.00168	0.10977	NKD2	Naked cutic
3	▼ 5.00	0.00406	0.15943	TEAD4	TEA domain
4	▼ 4.99	0.00410	0.16005	DRD4	Dopamine r
5	▲ 4.99	0.00678	0.19776	693153	microRNA 5
6	▲ 4.99	0.00841	0.21368	SNORD22	Small nucle
7	▼ 4.99	0.01309	0.25318	TRIM50	Tripartite m
8	▼ 4.98	0.00616	0.18936	DOK3	Docking pro
9	▲ 4.98	0.00704	0.19956	100190940	hypothetica
10	▲ 4.98	0.02006	0.29120	PTPN20A	Protein tyro
11	▼ 4.97	0.03240	0.33877	ATP6V0A4	ATPase, H+
12	▼ 4.97	0.00419	0.16153	LINGO3	Leucine rich
13	▼ 4.96	0.01384	0.25751	AQP9	Aquaporin 9
14	▲ 4.96	0.01105	0.23526	CCDC138	Coiled-coil (
15	▼ 4.96	0.01052	0.22893	GPR25	G protein-c
16	▼ 4.96	0.00130	0.10153	POLD1	Polymerase
17	▼ 4.95	0.00454	0.16602	CFD	Complemer
18	▲ 4.94	0.00198	0.11731	RAB27B	RAB27B, me
19	▼ 4.93	0.00587	0.18458	CDH3	Cadherin 3,
20	▼ 4.93	0.01562	0.26742	SLA	Src-like-ada

Show: 20 p Cutoff: 0.05 raw p Fold Change: 1.5 Upper: 5

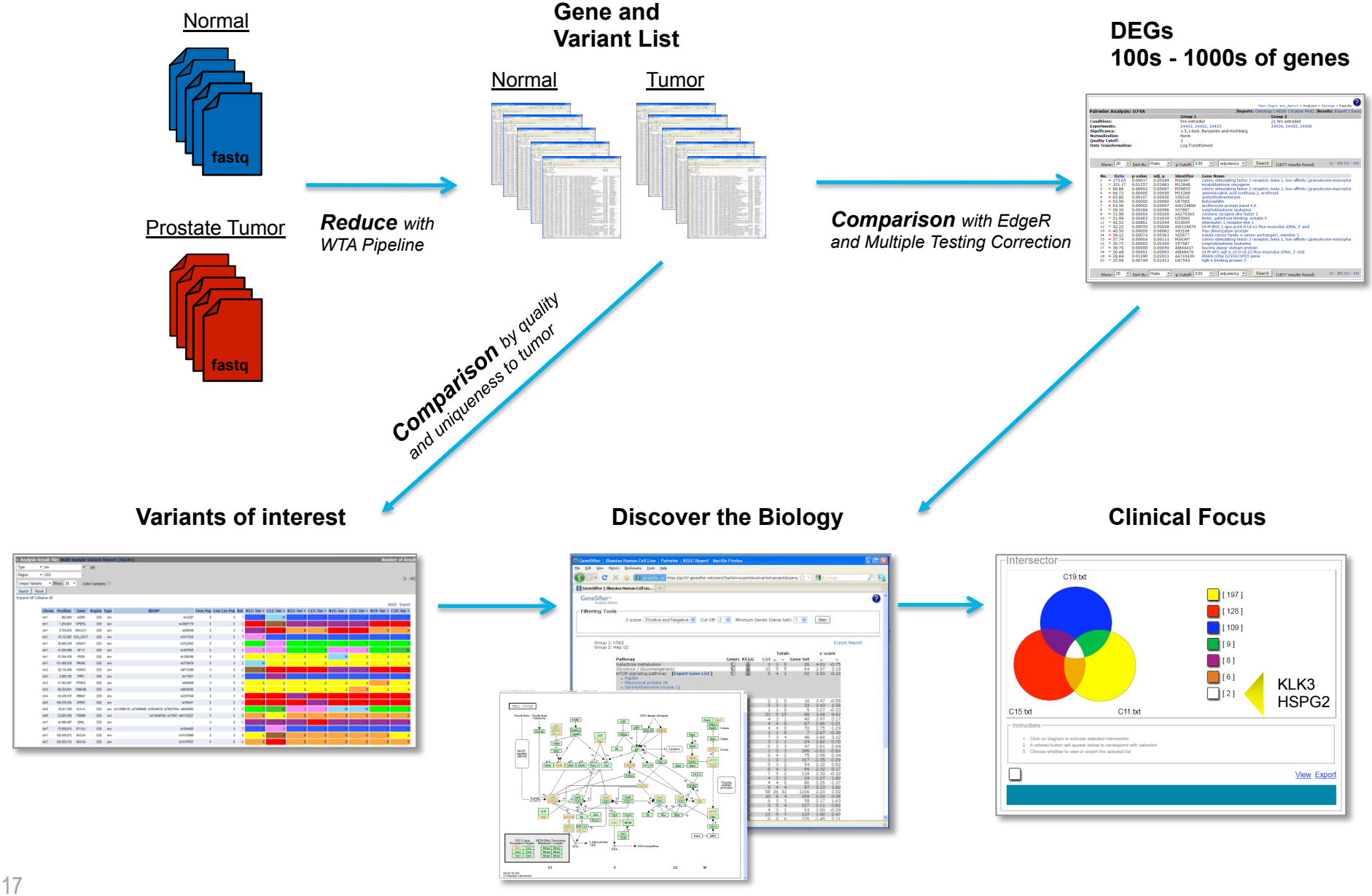


GeneSifter® Analysis Edition

Discover Complex Relationships



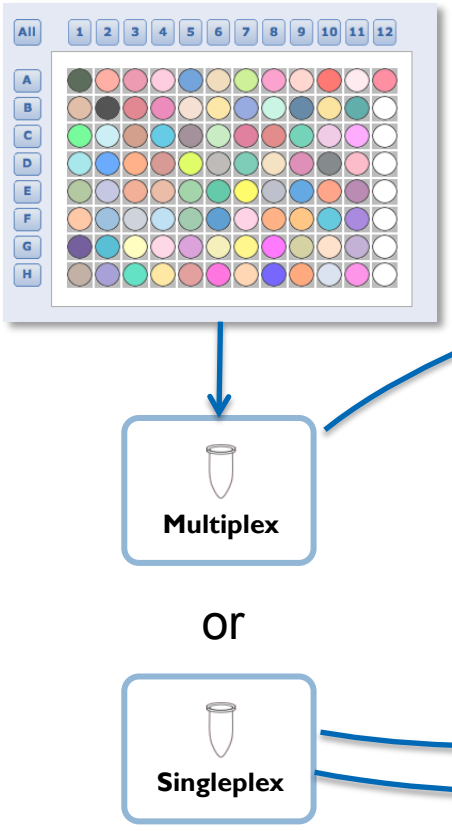
Reduce, Compare, Discover



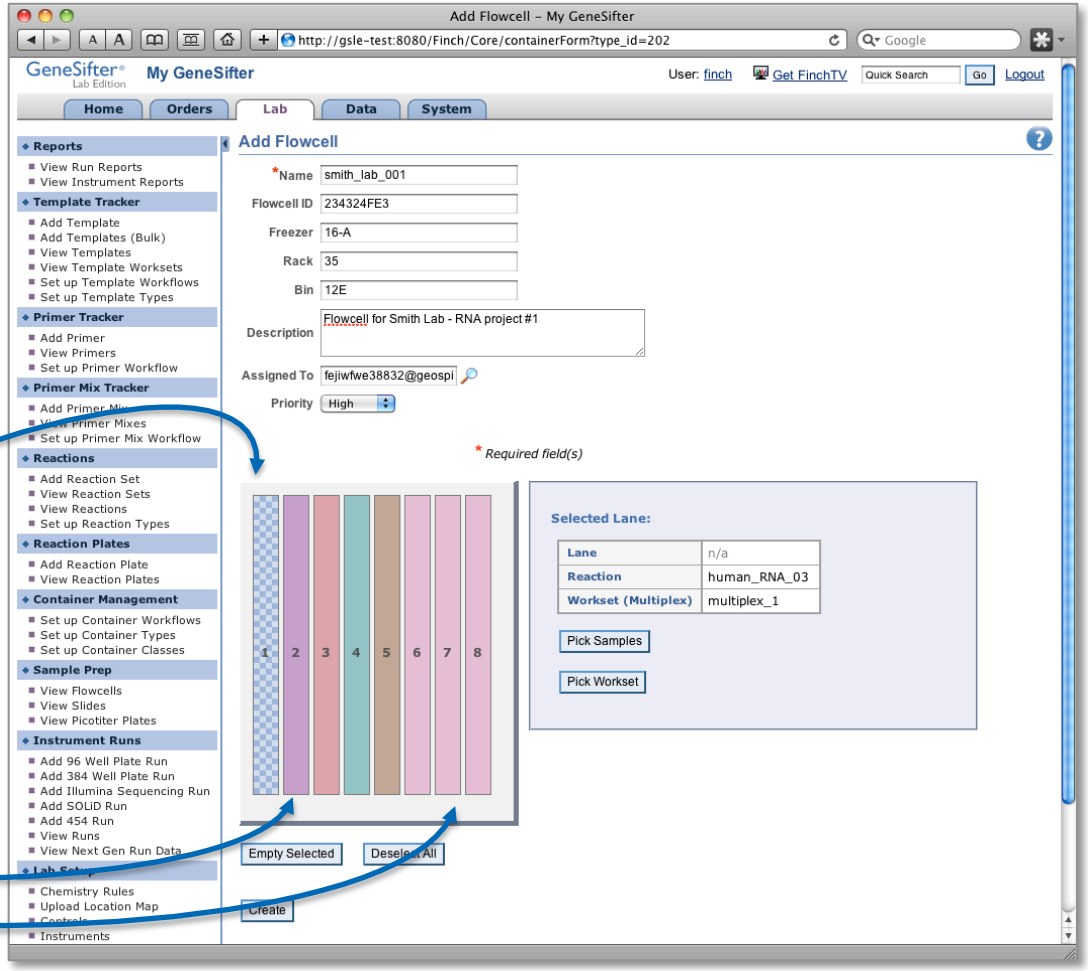
Focus on the Process:
GeneSifter Lab Edition

In a Nutshell

Track samples, complex manipulations

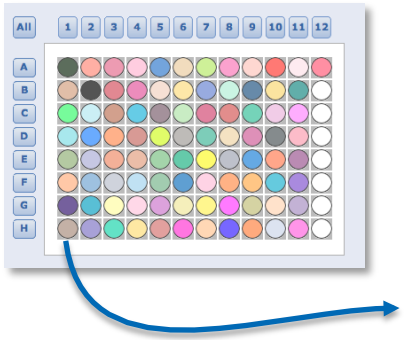


GeneSifter Slide Builder



collect, sort, and deliver

View Sample Details in an Easy to View Format



Template Details

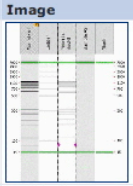
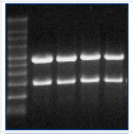
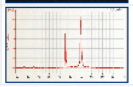
Next Step | Edit Template | Upload Attachment | Set to Archived | Delete

Sample QC	TruSeq Small RNA	Library Validation
1. Qubit Fluorometer	1. TruSeq Small RNA Kit Info	1. Qubit Fluorometer
2. LabChip GX	2. Ligate 3' Adapter	**2. LabChip GX**
	3. Ligate 5' Adapter	
	4. Reverse Transcribe and Amplify	
	5. PCR Amplification	
	6. Purify cDNA Construct	

Name	spleen_597	**Template Workset**	Cancer_Group_5
Template ID	3621	**Parent**	n/a
Template Type	Library Validation	**Volume (µL)**	50
Barcode	79521671	**Concentration (ng/µL)**	150
Archived	No	**Storage Location**	Freezer 2
Order Name	n/a	**MID**	n/a
Description	Created from Template spleen_597		

Related Links: Details, Workflow History, Results, Relationships, Attachments (3)

Template Attachments

Filename	File type	Image	File Size	Upload Step	Field Label	Uploaded By	Uploaded At
LabChip_GX_1.png	png file		135.9 kB	LabChip GX	LabChip File	LabManager	2012-01-24 14:11:30-08
Gel_Image.jpg	unknown		17.3 kB	Purify cDNA Construct	Gel Image	LabManager	2012-01-24 14:09:42-08
LabChip.png	png file		110.4 kB	LabChip GX	LabChip File	LabManager	2012-01-24 14:07:13-08

Workflow History

Workflow	Workflow Version	State	Step	Updated By	Updated At	Comment	Info
Library Validation	28-68058228	Ready	LabChip GX	LabManager	2012-01-24 14:11:30-08	n/a	**LabChip File**: LabChip_GX_1.png **LabChip GX**: --Select Chip--
TruSeq Small RNA	70-68058228	Ready	Purify cDNA Construct	LabManager	2012-01-24 14:09:42-08	n/a	**Novex Gel lot #**: 089085-12 **Gel Image**: Gel_Image.jpg
TruSeq Small RNA	70-68058228	Not Ready	Ligate 3' Adapter	LabManager	2012-01-24 14:08:37-08	n/a	**Total RNA (µg)**: 5 **Thermal Cycler**: Thermal Cycler #2
TruSeq Small RNA	70-68058228	Not Ready	TruSeq Small RNA Kit Info	LabManager	2012-01-24 14:07:56-08	n/a	**TruSeq kit lot #**: 324234-C
Sample QC	39-68058228	Ready	LabChip GX	LabManager	2012-01-24 14:07:13-08	n/a	**LabChip GX**: RNA-6000 **RIN value**: 9 **LabChip File**: LabChip.png

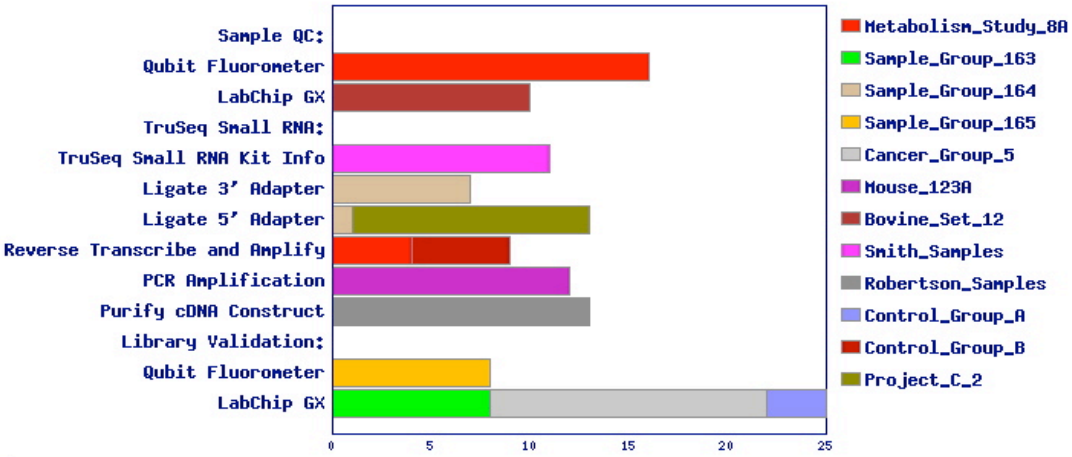
Also includes:
- Relationships
- Change log
- Links to data

To meet regulatory needs

Know Where Samples Are in the Process

GeneSifter
Protocol Viewer

Label	Illumina TruSeq Small RNA - LabChip	Archived	No
Created By	LabManager	Created At	2012-01-24 13:23:20.707987-08
Modified By	LabManager	Modified At	2012-01-24 13:37:04.809804-08
Component Workflows	Sample QC, TruSeq Small RNA, Library Validation		
Description	n/a		



The data browser below shows Templates and Template Worksets that have or need pending work.

Template Worksets (12) | Current Templates (124) | All Templates

Find: Label | CONTAINS | Go | Reset

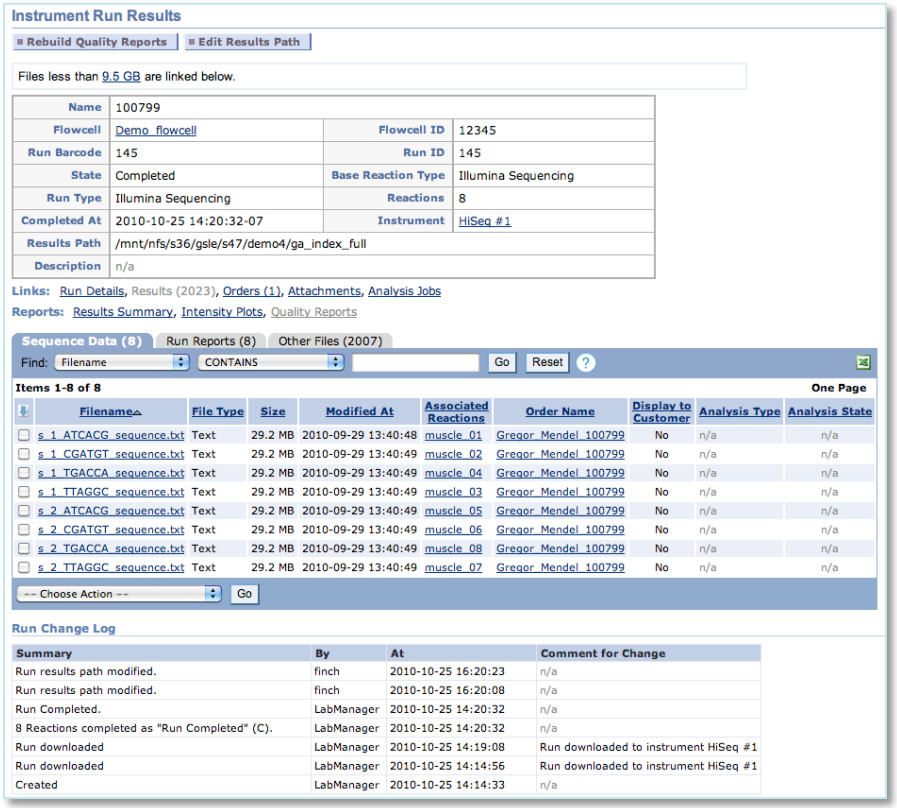
Items 1-12 of 12 — One Page

Label	Templates	Barcode	Storage_location	Assigned_to	Description
Smith_Samples	11	n/a	n/a	n/a	n/a
Sample_Group_165	8	n/a	n/a	n/a	n/a
Sample_Group_164	8	n/a	n/a	LabManager	n/a
Sample_Group_163	8	n/a	n/a	n/a	n/a
Robertson_Samples	13	n/a	n/a	n/a	n/a
Project_C_2	12	n/a	n/a	n/a	n/a
Mouse_123A	12	n/a	n/a	n/a	n/a
Metabolism_Study_8A	20	n/a	n/a	n/a	n/a
Control_Group_B	5	n/a	n/a	n/a	n/a
Control_Group_A	3	n/a	n/a	n/a	n/a
Cancer_Group_5	14	n/a	n/a	n/a	n/a
Bovine_Set_12	10	n/a	n/a	n/a	n/a

Review Data Quality

GeneSifter Run Reports

- Software routines link data to samples
- Vendor reports, and Geospiza reports are linked for review.
- Single-click distribution of lab data to collaborators



Instrument Run Results

Rebuild Quality Reports | Edit Results Path

Files less than 9.5 GB are linked below.

Name	100799		
Flowcell	Demo_flowcell	Flowcell ID	12345
Run Barcode	145	Run ID	145
State	Completed	Base Reaction Type	Illumina Sequencing
Run Type	Illumina Sequencing	Reactions	8
Completed At	2010-10-25 14:20:32-07	Instrument	HiSeq #1
Results Path	/mnt/nfs/s36/gsle/s47/demo4/ga_index_full		
Description	n/a		

Links: Run Details, Results (2023), Orders (1), Attachments, Analysis Jobs

Reports: Results Summary, Intensity Plots, Quality Reports

Sequence Data (8) | Run Reports (8) | Other Files (2007)

Find: Filename CONTAINS Go Reset

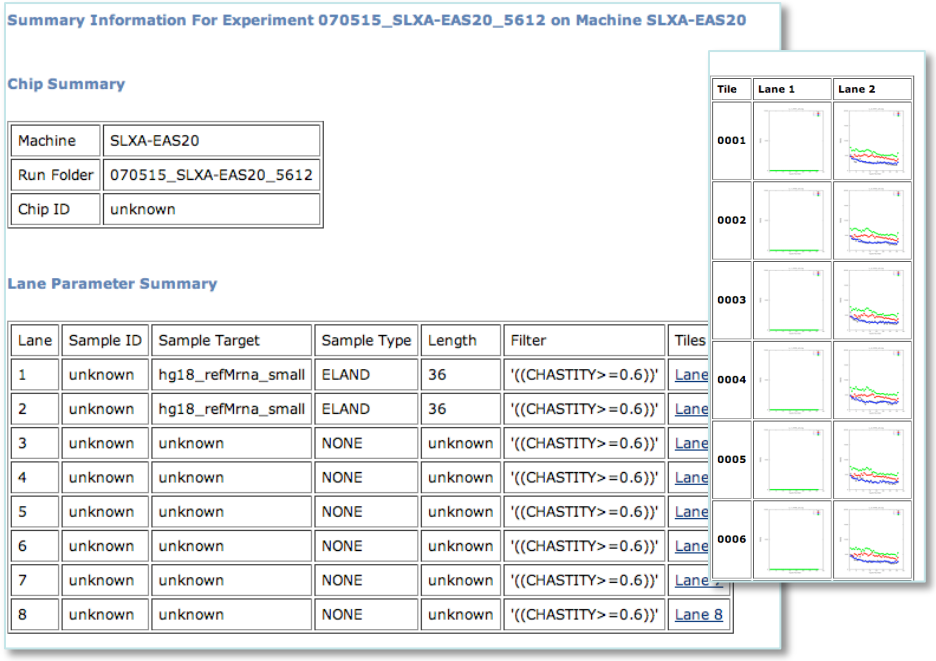
Items 1-8 of 8 — One Page

Filename	File Type	Size	Modified At	Associated Reactions	Order Name	Display to Customer	Analysis Type	Analysis State
s_1_ATCACG_sequence.txt	Text	29.2 MB	2010-09-29 13:40:48	muscle_01	Gregor_Mendel_100799	No	n/a	n/a
s_1_CGATGT_sequence.txt	Text	29.2 MB	2010-09-29 13:40:49	muscle_02	Gregor_Mendel_100799	No	n/a	n/a
s_1_TGACCA_sequence.txt	Text	29.2 MB	2010-09-29 13:40:49	muscle_04	Gregor_Mendel_100799	No	n/a	n/a
s_1_TTAGGC_sequence.txt	Text	29.2 MB	2010-09-29 13:40:49	muscle_03	Gregor_Mendel_100799	No	n/a	n/a
s_2_ATCACG_sequence.txt	Text	29.2 MB	2010-09-29 13:40:49	muscle_05	Gregor_Mendel_100799	No	n/a	n/a
s_2_CGATGT_sequence.txt	Text	29.2 MB	2010-09-29 13:40:49	muscle_06	Gregor_Mendel_100799	No	n/a	n/a
s_2_TGACCA_sequence.txt	Text	29.2 MB	2010-09-29 13:40:49	muscle_08	Gregor_Mendel_100799	No	n/a	n/a
s_2_TTAGGC_sequence.txt	Text	29.2 MB	2010-09-29 13:40:49	muscle_07	Gregor_Mendel_100799	No	n/a	n/a

-- Choose Action -- Go

Run Change Log

Summary	By	At	Comment for Change
Run results path modified.	finch	2010-10-25 16:20:23	n/a
Run results path modified.	finch	2010-10-25 16:20:08	n/a
Run Completed.	LabManager	2010-10-25 14:20:32	n/a
8 Reactions completed as "Run Completed" (C).	LabManager	2010-10-25 14:20:32	n/a
Run downloaded	LabManager	2010-10-25 14:19:08	Run downloaded to instrument HiSeq #1
Run downloaded	LabManager	2010-10-25 14:14:56	Run downloaded to instrument HiSeq #1
Created	LabManager	2010-10-25 14:14:33	n/a



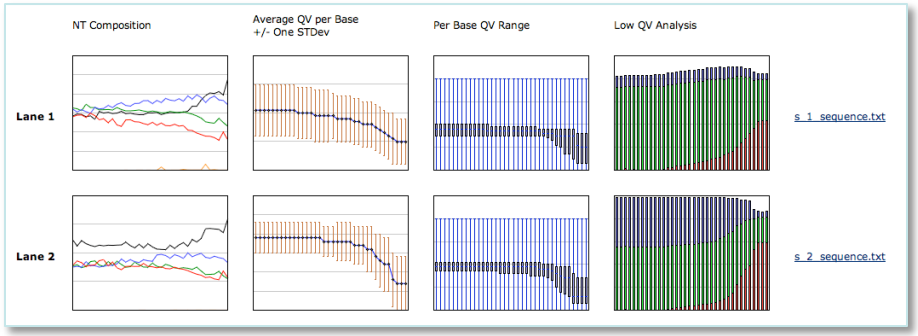
Summary Information For Experiment 070515_SLXA-EAS20_5612 on Machine SLXA-EAS20

Chip Summary

Machine	SLXA-EAS20
Run Folder	070515_SLXA-EAS20_5612
Chip ID	unknown

Lane Parameter Summary

Lane	Sample ID	Sample Target	Sample Type	Length	Filter	Tiles
1	unknown	hg18_refMrna_small	ELAND	36	'((CHASTITY>=0.6))'	Lane
2	unknown	hg18_refMrna_small	ELAND	36	'((CHASTITY>=0.6))'	Lane
3	unknown	unknown	NONE	unknown	'((CHASTITY>=0.6))'	Lane
4	unknown	unknown	NONE	unknown	'((CHASTITY>=0.6))'	Lane
5	unknown	unknown	NONE	unknown	'((CHASTITY>=0.6))'	Lane
6	unknown	unknown	NONE	unknown	'((CHASTITY>=0.6))'	Lane
7	unknown	unknown	NONE	unknown	'((CHASTITY>=0.6))'	Lane
8	unknown	unknown	NONE	unknown	'((CHASTITY>=0.6))'	Lane 8



Putting it Together

Scale up / Clinical

Research / Development

Caliper Automation

Geospiza LIMS

Geospiza Analysis

Project Design

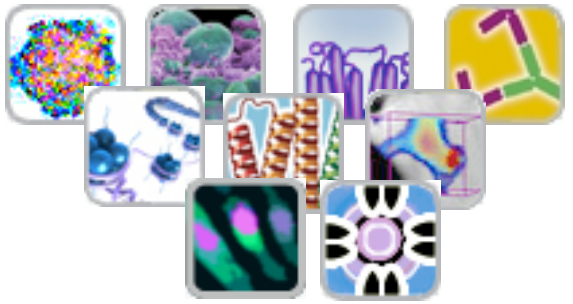
Sample Collection

Sequencing

Analysis

Validation

Clinical Correlation

Application

Geospiza Analysis