ISO 9001 :2015

LABORATORY REPORT

Redcliffe labs

Patient Name:		**CRM ID:**	
Age:		**Sample Type:**	
Sex:		**Samplecollection date:**	
Referring Clinician:		**Samplereceiving date:**	
Test Requested:	Hereditary Breast& Ovarian Cancer Syndrome (HBOC) Extended Panel	**Reportingdate:**	

HEREDITARY BREAST & OVARIAN CANCER SYNDROME (HBOC) EXTENDED PANEL

CLINICAL INDICATION/DIAGNOSIS

Status: Affected
Type of cancer: Right breast cancer
Investigations: HER2 Neu by FISH - Spiculated heterogeneous mass in right breast with axillary LAP, minimal free fluid in pelvis

TESTRESULT SUMMARY

NO SIGNIFICANT PATHOGENIC/LIKELY PATHOGENIC VARIANT RELATED TO HBOC PHENOTYPE DETECTED

KEY FINDINGS

Genes & Transcript	Exon/ locus	Variant& depth	Zygosity/ Inheritance	OMIM Phenotype	ACMG Classification
		Not Detected			

*Genetic test results are reported based on the recommendations of ACMG guidelines.

Variant Interpretation & Clinical correlation

Genesassociated withmentioneddisorderswere evaluated.

Gene panels used for analysis: Cancer comprehensive gene panel; HBOC panel Ultrararevariantswitha gnomADfrequencyof <0.01were evaluated.

RECOMMENDATION

✓ Please MLPA is recommended for deletion/duplicationanalysis of BRCA1 and BRCA2 genes

Test Information

1. Clinical correlation as well as reverse phenotyping is recommended for all reports.
2. Genetic counseling for accurate interpretation of test results is recommended.
3. The reported findings are based on NGS analysis.
4. Analysis includes both single nucleotide (SNV) as well as copy number variant analysis (CNV).
5. Copy number variants when detected are included in the report.
6. Since CNV analysis is performed on a comparative basis, a negative result does not exclude the presence of a CNV.
7. The CNV pipeline is not validated for >3 exon copy number variants wherein detection is influenced by the underlying gene region and structure.
8. Variant calling (SNV and CNV) may be limited in low covered regions as well as in regions of low complexity and in pseudogenes.
9. Synonymous variants (not affecting splice site) as well as intronic variants are usually not reported.
10. Analysis and reporting is focussed on the provided phenotype and based on relevant HPO (Human Phenotype Ontology) terms as well as on genes associated with provided phenotype.
11. A genotype based analysis is also performed when the above yields negative results but reporting is limited to genes wherein current available evidence suggests a possible association with the provided phenotype.

12. It may not be possible to fully resolve certain details about variants, such as mosaicism, phasing, or mapping ambiguity
13. The test methodology currently does not detect large deletions/duplications, triplet repeat expansions and epigenetic changes. The test also does not include analysis of predictors for multifactorial, polygenic and/or complex diseases.
14. Phenotype variability may be due to modifying genetic/non-genetic factors and is not a part of the current analysis.
15. Candidate genes and genes with limited evidence are designated as genes of uncertain significance and all variants detected therein are classified as variants of uncertain significance.
16. Typically only variants at a depth of >/= 10X are reported. Lower depth variants may be false positives.
17. Detected variants in low complexity regions as well as variants at low depth and relatively low VAF should be reconfirmed by an alternate methodology.
18. CNV confirmation via MLPA or Exon array is recommended for copy number variants involving a single gene as well as for CNV <400kb. Only large constitutional CNV can be tested via other array platforms.
19. Variant depth/Total depth has been mentioned in summary of the variants.
20. Parental/Maternal testing as applicable is recommended for variants when detected for phasing (where applicable)
21. Segregation analysis (testing of multiple affected as well as unaffected members) of detected variants (if any) is recommended. Variant classification is subject to change after segregation.
22. ACMG secondary findings as well as carrier status of variants are only provided when requested.
23. Within carrier screening risk factors/alleles as well as hypomorphic variants may not be included
24. Interobserver as well as inter-laboratory variation is known with respect to variant classification due to the subjective nature of the provided criteria. Though the laboratory follows the updated recommendations provided by the ClinGen SVI as well as ACMG, independent assessment of variant classification by the referring clinician is recommended before decision making.
25. For prenatal samples analysis is limited to provided clinical phenotypes utilizing relevant HPO terms. Typically variants of uncertain significance are only introduced if the respective gene has been associated with the observed fetal phenotype. In solo fetal exomes, variants of uncertain deemed to be disease causing based on genotype characteristics may be included for further evaluation by the referring clinician. In prenatal scenarios trio fetal testing is strongly recommended to allow better interpretation of detected variants.
26. If the above results do not correlate completely with patient phenotype, additional testing is advised based on clinician's discretion.
27. Typically, heterozygous variants of uncertain significance in genes associated with autosomal recessive disorder are not reported in the proband. Such variants are included if relevant to phenotype in carrier screening.
28. A negative report does not exclude a genetic disorder due to inherent limitations of the assay design.
29. On the background of whole exome sequencing, analysis is limited to provided indications/ requested testing. Hence analysis is limited to a single gene if the same has been requested.
30. As a part of knowledge sharing initiative, all reported variants are submitted in de-identified form in the ClinVar database.
31. Extracted DNA if available after requisitioned testing will be stored as per recommendations. Please note that DNA may degrade over time and this may affect the quality of the stored sample.
32. Collected blood samples are not stored
33. Prenatal samples (AF/CVS/cord blood) are not stored. Extracted DNA if available is stored as acknowledged above.
34. As per PCPNDT fetal gender is not revealed.
35. Discrepant maternal cell contamination results may rise with use of donor gamete and hence information regarding the
36. same should be provided to the laboratory.
37. Maternal cell contamination is recommended for prenatal and POC (product of conception) to ensure accuracy of test results. The same is performed only when requested and on the availability of the maternal sample.
38. Reproductive decision making is not recommended based on variants of uncertain significance.
39. Raw data can be transferred on request and after due consent/assent from the involved patient/ family. Additional charges will be applicable for the same.
40. The test performed by the laboratory with the assumption that the sample belongs to the person herewith mentioned in the requisition form and appropriate consent as well as prenatal counseling including test information has been provided by the referring clinician.
41. Repeat sampling may be required in case of gender discrepancy (unless the same can be attributed to an underlying scientific reason) as well as in rare cases where DNA/data quality prevents further analysis.
42. Reanalysis of data is recommended as deemed necessary by the referring clinician. Additional charges will be applicable for the same.

Technical Notes

Methodology- Massively Parallel Sequencing (Next Generation Sequencing): Genomic DNA from the submitted specimen was enriched for the complete codingregions and splice site junctionsof genes listed below using acustom bait- capture system. Paired End Sequencing was performed with 2x100/2x150 chemistry. Reads were assembled and were aligned to reference sequences based on NCBI RefSeq transcripts and human genomebuild GRCh37/UCSC hg19. Datawas filtered and analyzed to identify variants of interest and interpreted in the context of asingle most damaging, clinically relevant transcript for the purpose of the report, indicated as apartof variant details. Enrichment and analysis focus on the coding sequence of the indicated transcripts, 5-10bp of flankingintronic sequence, and other specific genomic regions demonstrated to be causativeof diseaseat the time of assay design. Deletion and duplication analysis is performed in cases when indicated butdetected variations need to be confirmed by analternate methodology. Sequence and copy number variants are reported according to the Human Genome Variation Society (HGVS).

Laboratory reporting protocol: Laboratory reporting protocol: The analysis is based on the provided phenotype: relevant HPO terms, curated gene panels and relevant literature is assessed for phenotype based analysis. Variant reporting is limited to exon regions and upto 10 basepairs within exon intron boundaries. Previously reported deep intronic and non coding variants will be included when detected at a depth more than 10X . Variant reporting is performed at a minimum depth of 10X. The gnomAD variant frequency reflects the liftover of hg38 to hg19.

For Mitochondrial Genome Sequencing (if requested): Only phenotype-related Pathogenic and Likely Pathogenic variations reported in the MitoMap database as well as literature are reported. Haplogroups are not analyzed. A list of variants other than the above are available on request. Analyzed genes include:MT-ND1, MT-ND2, MT-ND3, MT-ND4L, MT-ND4, MT-ND5, MT-ND6, MT-CYB, MT-CO1, MT-CO2, MT-CO3, MT-ATP6, MT-ATP8, MT-RNR2, MT-RNR1, MT-RNR2, MT-TA, MT-TR, MT-TN, MT-TD, MT-TC, MT-TE, MT-TQ, MT-TG, MT-TH, MT-TI, MTTL1, MT-TL2, MT-TK, MT-TM, MT-TF, MT-TP, MT-TS1, MT-TS2, MT-TT, MT-TW, MT-TY, MT-TV.

Tools and Databases employed for analysis: Clinvar, OMIM, HGMD, UCSC genome browser, Uniprot, Ensembl, dbSNP, gnomAD, ExAC, Pubmed, Dgap, icgc, Kaviar, various bioinformatics analysis, predictive tools and disease specific databases used as available and appropriate. Such tools/databases would be mentioned wherever used.

REVEL: The REVEL score for an individual missense variant can range from 0 to 1, with higher scores reflecting greater likelihood that the variant is disease-causing.

CADD: The variants with scores above 20 are predicted to be among the 1.0% most deleterious possible substitutions in the human genome.

Bioinformatics pipeline version: 15.10.8

Gene Coverage

Indication Based Analysis:

Gene	Coverage	Gene	Coverage	Gene	Coverage	Gene	Coverage
A1CF	100%	AAAS	100%	AAGAB	100%	AARS1	100%
AARS2	100%	ABAT	100%	ABCA12	100%	ABCA3	100%
ABCA4	100%	ABCB11	100%	ABCB4	100%	ABCB7	100%
ABCC2	100%	ABCC6	100%	ABCC8	100%	ABCC9	100%
ABCD1	100%	ABCD4	100%	ABHD12	100%	ABHD5	100%
ABL1	100%	ABL2	100%	ABRAXAS1	100%	ACACA	100%
ACAD8	100%	ACAD9	100%	ACADM	100%	ACADS	100%
ACADVL	100%	ACAT1	100%	ACD	100%	ACE	100%
ACO2	100%	ACOD1	100%	ACOX1	100%	ACOX2	100%
ACP4	100%	ACP5	100%	ACSL4	100%	ACTA1	100%
ACTA2	100%	ACTB	100%	ACTC1	100%	ACTL6B	100%

ACTN1	100%	ACTN2	100%	ACVR1	100%	ACVR1B	100%
ACVRL1	100%	ACY1	100%	ADA	100%	ADAM10	100%
ADAM22	100%	ADAM29	100%	ADAM9	100%	ADAMTS10	100%
ADAMTS13	98.5%	ADAMTS17	100%	ADAMTS18	100%	ADAMTS2	100%
ADAMTS3	100%	ADAMTSL2	100%	ADAMTSL4	100%	ADAR	100%
ADCY5	98.5%	ADCY6	100%	ADD3	100%	ADGRG1	100%
ADGRG6	100%	ADGRV1	100%	ADK	100%	ADNP	100%
ADPRS	100%	ADSL	100%	ADSS1	100%	AEBP1	100%
AFDN	100%	AFF2	100%	AFF4	100%	AFG3L2	100%
AFP	100%	AGA	100%	AGBL1	100%	AGBL5	100%
AGK	100%	AGL	100%	AGPAT2	100%	AGPS	100%
AGRN	100%	AGT	100%	AGTPBP1	100%	AGTR1	100%
AGXT	100%	AHCY	100%	AHI1	100%	AICDA	100%
AIFM1	100%	AIMP1	100%	AIMP2	100%	AIP	100%
AJUBA	100%	AK1	100%	AK2	100%	AKR1B1	100%
AKR1C2	100%	AKR1D1	100%	AKT1	100%	AKT2	100%
AKT3	100%	ALAD	100%	ALAS2	100%	ALB	100%
ALDH18A1	100%	ALDH1A3	100%	ALDH3A2	100%	ALDH4A1	100%
ALDH5A1	100%	ALDH6A1	100%	ALDH7A1	100%	ALDOA	100%
ALDOB	100%	ALG1	100%	ALG11	100%	ALG12	100%
ALG13	100%	ALG14	100%	ALG2	100%	ALG3	100%
ALG6	100%	ALG8	100%	ALG9	99.9%	ALK	100%
ALKBH8	100%	ALMS1	100%	ALOX12B	100%	ALOXE3	100%
ALPK3	100%	ALPL	100%	ALX1	100%	ALX3	100%
ALX4	100%	AMACR	100%	AMBN	100%	AMELX	100%
AMER1	100%	AMMECR1	100%	AMN	100%	AMPD1	100%
AMPD2	100%	AMT	100%	AMTN	100%	ANAPC1	100%
ANAPC2	99%	ANGPT2	100%	ANGPTL3	100%	ANK1	100%
ANK2	100%	ANK3	100%	ANKH	100%	ANKLE2	99.8%
ANKRD17	100%	ANKRD26	99.3%	ANKS1A	100%	ANKS6	98.2%
ANLN	100%	ANO10	100%	ANO3	100%	ANO5	100%

ANO6	100%	ANOS1	100%	ANTXR1	99.1%	ANTXR2	100%
ANXA11	100%	AP1B1	100%	AP1S1	100%	AP1S2	100%
AP2S1	100%	AP3B1	100%	AP3B2	100%	AP3D1	100%
AP4B1	100%	AP4E1	100%	AP4M1	100%	AP4S1	100%
AP5Z1	100%	APC	100%	APC2	100%	APCDD1	100%
APEX1	100%	APEX2	100%	APOB	100%	APOC2	100%
APOE	100%	APP	100%	APTX	100%	AQP2	100%
AQP5	100%	AR	100%	ARAF	100%	ARCN1	100%
AREG	100%	ARFGEF1	100%	ARFGEF2	100%	ARFRP1	100%
ARG1	100%	ARHGAP31	100%	ARHGDIA	100%	ARHGEF12	100%
ARHGEF18	100%	ARHGEF2	100%	ARHGEF7	100%	ARHGEF9	100%
ARID1A	100%	ARID1B	97.3%	ARID2	100%	ARL13B	100%
ARL2BP	100%	ARL3	100%	ARL6	100%	ARL6IP1	100%
ARMC2	100%	ARMC9	100%	ARPC1B	100%	ARPC4	100%
ARR3	100%	ARSA	100%	ARSB	100%	ARSG	100%
ARSL	100%	ARTN	100%	ARV1	100%	ARX	89.1%
ASAH1	100%	ASH1L	100%	ASL	100%	ASNS	100%
ASPA	100%	ASPH	100%	ASPM	100%	ASPSCR1	100%
ASS1	100%	ASXL1	100%	ASXL3	100%	ATAD1	100%
ATAD3A	98.7%	ATAT1	99.3%	ATCAY	100%	ATF6	100%
ATG2B	100%	ATIC	100%	ATM	100%	ATN1	100%
ATOH7	100%	ATP11C	100%	ATP13A2	100%	ATP1A1	100%
ATP1A2	100%	ATP1A3	100%	ATP1A4	100%	ATP2A1	100%
ATP2A2	100%	ATP2B3	100%	ATP2C1	100%	ATP5F1A	100%
ATP5F1D	100%	ATP5MC3	100%	ATP6AP1	100%	ATP6AP2	100%
ATP6V0A1	100%	ATP6V0A2	100%	ATP6V0A4	100%	ATP6V1A	100%
ATP6V1B1	100%	ATP6V1E1	100%	ATP6V1G3	100%	ATP7A	100%
ATP7B	100%	ATP8A2	100%	ATP8B1	100%	ATPAF2	100%
ATR	100%	ATRX	100%	AURKA	100%	AURKAIP1	100%
AURKB	100%	AURKC	100%	AVIL	100%	AVP	100%
AVPR2	100%	AXIN1	100%	AXIN2	100%	AXL	100%

B2M	100%	B3GALNT2	100%	B3GALT6	82.2%	B3GAT3	100%
B3GLCT	97.9%	B4GALNT1	100%	B4GALT1	100%	B4GALT7	100%
B4GAT1	100%	B9D1	100%	B9D2	100%	BACH1	100%
BAG3	100%	BANF1	100%	BAP1	100%	BARD1	100%
BAX	100%	BBIP1	100%	BBS1	100%	BBS10	100%
BBS12	100%	BBS2	100%	BBS4	100%	BBS5	100%
BBS7	100%	BBS9	100%	BCAP31	100%	BCAR1	100%
BCHE	100%	BCKDHA	100%	BCKDHB	100%	BCL11A	100%
BCL11B	100%	BCL2	100%	BCL2L1	100%	BCL6	100%
BCOR	100%	BCORL1	100%	BCR	100%	BCS1L	100%
BEST1	100%	BFSP1	100%	BFSP2	100%	BGN	100%
BHLHA9	100%	BICRA	95.1%	BIN1	100%	BLM	100%
BLOC1S3	100%	BLVRA	100%	BMP1	100%	BMP15	100%
BMP2	100%	BMP6	100%	BMPER	100%	BMPR1A	100%
BMPR1B	100%	BNC1	97.5%	BOLA3	100%	BPGM	100%
BPNT2	100%	BRAF	100%	BRCA1	100%	BRCA2	100%
BRD4	97%	BRF1	100%	BRIP1	100%	BRWD3	100%
BSCL2	100%	BSND	100%	BTD	100%	BTK	100%
BTNL2	100%	BUB1	100%	BUB1B	100%	BUB3	100%
BVES	100%	C18orf32	100%	C1QA	100%	C1QBP	100%
C2	100%	C2CD3	100%	C3	100%	C4A	99.4%
C8A	100%	C8B	100%	CA12	100%	CA2	100%
CA5A	100%	CA8	100%	CABP2	100%	CABP4	100%
CACNA1B	100%	CACNA1C	100%	CACNA1F	100%	CACNA1S	100%
CACNA2D2	98.1%	CACNA2D4	100%	CACNB2	100%	CAD	100%
CADM3	100%	CALM1	100%	CALM2	100%	CALM3	100%
CAMK2A	100%	CANT1	100%	CAPN1	100%	CAPN3	100%
CAPN9	100%	CARD11	100%	CARD9	100%	CARMIL2	100%
CARS1	100%	CARS2	100%	CASK	100%	CASP10	100%
CASP14	100%	CASP8	100%	CASQ2	100%	CASR	100%
CAST	100%	CATSPER1	100%	CAV1	100%	CAV3	100%

CAVIN1	100%	CBFA2T3	100%	CBFB	100%	CBL	100%
CBLB	100%	CBLIF	100%	CBS	100%	CC2D1A	100%
CC2D2A	100%	CCBE1	100%	CCDC103	100%	CCDC115	100%
CCDC141	100%	CCDC174	95.8%	CCDC22	100%	CCDC39	100%
CCDC40	100%	CCDC47	100%	CCDC50	100%	CCDC65	100%
CCDC88C	100%	CCM2	100%	CCN6	100%	CCND1	100%
CCND2	100%	CCND3	100%	CCNI	100%	CCNO	100%
CCNQ	100%	CCSER1	100%	CCT5	100%	CD14	100%
CD151	100%	CD19	100%	CD27	100%	CD274	100%
CD36	100%	CD3D	100%	CD3E	100%	CD3G	100%
CD40	100%	CD40LG	100%	CD55	100%	CD59	100%
CD70	100%	CD79A	100%	CD79B	100%	CD81	98.3%
CD82	100%	CD8A	100%	CD96	100%	CDAN1	100%
CDC14A	100%	CDC42	100%	CDC42BPB	100%	CDC45	100%
CDC6	100%	CDC73	100%	CDCA7	100%	CDH1	100%
CDH11	100%	CDH2	100%	CDH23	100%	CDIN1	100%
CDK10	100%	CDK12	100%	CDK13	100%	CDK19	100%
CDK4	100%	CDK5RAP2	100%	CDK6	100%	CDK8	100%
CDKL5	100%	CDKN1A	100%	CDKN1B	100%	CDKN1C	100%
CDKN2A	100%	CDKN2B	100%	CDKN2C	100%	CDS1	100%
CDSN	100%	CDT1	86.1%	CDX1	100%	CDX2	100%
CEACAM16	100%	CEBPA	100%	CEBPE	100%	CEL	95.2%
CELF2	100%	CENPF	100%	CENPJ	100%	CEP120	100%
CEP135	100%	CEP164	100%	CEP19	100%	CEP250	100%
CEP290	100%	CEP41	100%	CEP55	100%	CEP57	100%
CEP78	100%	CEP83	100%	CERKL	100%	CERS1	95.5%
CERS3	100%	CERT1	100%	CFAP251	100%	CFAP298	100%
CFAP300	100%	CFAP44	100%	CFAP47	100%	CFAP53	100%
CFAP69	100%	CFD	100%	CFH	100%	CFI	100%
CFL2	100%	CFP	100%	CFTR	100%	CHAMP1	100%
CHAT	100%	CHD2	100%	CHD4	100%	CHD7	100%

CHEK1	100%	CHEK2	100%	CHIT1	100%	CHKB	100%
CHM	100%	CHMP1A	100%	CHN1	100%	CHRDL1	100%
CHRM3	100%	CHRNA1	100%	CHRNB1	100%	CHRND	100%
CHRNE	100%	CHRNG	100%	CHST14	100%	CHST3	100%
CHST6	100%	CHSY1	97%	CILK1	100%	CISD2	100%
CIT	100%	CKAP2L	100%	CLCF1	100%	CLCN1	100%
CLCN4	100%	CLCN5	100%	CLCNKA	100%	CLCNKB	100%
CLDN1	100%	CLDN10	100%	CLDN14	100%	CLDN16	100%
CLDN19	100%	CLDN2	100%	CLEC12B	100%	CLEC7A	100%
CLIC2	100%	CLMP	100%	CLN3	100%	CLN5	100%
CLN6	100%	CLN8	100%	CLP1	100%	CLPP	100%
CLRN1	100%	CNGA1	100%	CNGA3	100%	CNGB1	100%
CNGB3	100%	CNKSR2	100%	CNNM4	100%	CNPY3	100%
COA7	100%	COASY	100%	COG1	100%	COG4	100%
COG5	100%	COG6	100%	COG7	100%	COG8	100%
COL12A1	100%	COL14A1	100%	COL17A1	100%	COL2A1	100%
COL3A1	100%	COL4A5	100%	COL4A6	100%	COL7A1	100%
COL8A2	100%	COLEC10	100%	COLEC11	100%	COLEC12	100%
COPB2	100%	COQ2	100%	COQ6	100%	COQ7	100%
COQ8A	100%	COQ8B	100%	COQ9	100%	COX15	100%
COX20	100%	COX4I2	100%	COX6A1	100%	COX6A2	100%
COX6B1	100%	COX7B	100%	CP	100%	CPA1	100%
CPE	100%	CPLX1	100%	CPS1	100%	CPT1A	100%
CPT2	100%	CREBBP	100%	CRLF2	100%	CRPPA	100%
CRYAB	100%	CRYBA1	100%	CRYBA2	100%	CRYBB2	100%
CRYGB	100%	CRYGC	100%	CRYGD	100%	CRYGS	100%
CSF1R	100%	CSMD1	100%	CSMD2	100%	CSMD3	100%
CSPP1	100%	CSRP3	100%	CSTA	100%	CTBP1	100%
CTC1	100%	CTCF	100%	CTNNA1	100%	CTNNA2	100%
CTNNA3	100%	CTNNB1	100%	CTNND1	100%	CTNS	100%
CTRC	100%	CTSA	100%	CTSC	100%	CTSF	100%

CTSK	100%	CUBN	100%	CUL3	100%	CUL4B	100%
CYB5A	100%	CYBA	100%	CYBB	100%	CYC1	100%
CYLD	100%	CYP11A1	100%	CYP11B1	100%	CYP11B2	100%
CYP17A1	100%	CYP19A1	100%	CYP21A2	99.8%	CYP24A1	100%
CYP27A1	100%	CYP27B1	100%	CYP2U1	100%	CYP4F22	100%
DAG1	100%	DARS2	100%	DAXX	100%	DBT	100%
DCAF8	100%	DCC	100%	DCLRE1C	100%	DCN	100%
DCX	100%	DDB1	100%	DDB2	100%	DDHD1	100%
DDHD2	100%	DDOST	100%	DDR2	100%	DDX10	100%
DDX3X	100%	DDX41	100%	DDX6	100%	DEF6	100%
DEGS1	100%	DES	100%	DFFB	100%	DGAT1	100%
DGCR8	100%	DGKE	100%	DGUOK	100%	DHCR24	100%
DHCR7	100%	DHDDS	100%	DHODH	100%	DHTKD1	99.7%
DHX37	100%	DIAPH3	100%	DICER1	100%	DIS3L2	100%
DKC1	100%	DLAT	99.9%	DLC1	100%	DLD	100%
DLG3	100%	DLK1	100%	DLST	100%	DMC1	100%

Gene	Coverage	Gene	Coverage	Gene	Coverage	Gene	Coverage
DMD	100%	DMGDH	100%	DNA2	100%	DNAAF6	100%
DNAH5	100%	DNAH7	100%	DNAI1	100%	DNAI2	100%
DNAJC21	100%	DNAJC5	100%	DNM1L	100%	DNM2	100%
DNMT3A	100%	DNMT3B	100%	DOK7	100%	DOLK	100%
DOT1L	100%	DPAGT1	100%	DPF2	100%	DPH3	100%
DPM1	100%	DPM2	100%	DPM3	100%	DPP10	100%
DPYD	100%	DPYS	100%	DPYSL5	100%	DROSHA	100%
DSC2	100%	DSC3	100%	DSCAM	99.3%	DSE	100%
DSG1	100%	DSG2	100%	DSG4	100%	DSP	100%
DSPP	100%	DST	100%	DSTYK	100%	DTD1	100%
DUSP6	100%	DYM	100%	DYNC1H1	100%	DYNC2H1	100%
DYNC2I1	100%	DYNC2I2	100%	DYRK1A	100%	DYSF	100%
EARS2	100%	EBF3	100%	EBP	100%	EDA	100%
EDARADD	100%	EDNRB	100%	EED	100%	EEF1A2	100%
EFEMP1	100%	EFL1	100%	EFNA1	100%	EFNB1	100%
EGFL7	100%	EGFR	100%	EGLN1	100%	EGR2	100%
EIF2S3	100%	EIF3A	100%	EIF4A2	100%	EIF5A	100%
EIF6	100%	ELAC2	100%	ELANE	100%	ELF4	100%
ELN	100%	ELOVL1	100%	ELOVL4	100%	ELOVL5	100%
ELP1	100%	EMC1	100%	EMD	100%	EME1	100%
EME2	100%	EMSY	100%	ENG	100%	ENPP1	97.6%
EOGT	100%	EP300	100%	EPAS1	100%	EPCAM	100%
EPHA10	100%	EPHA2	100%	EPHA3	100%	EPHB1	100%
EPHB4	100%	EPM2A	100%	ERAL1	100%	ERBB2	100%
ERBB3	100%	ERBB4	100%	ERC2	100%	ERCC1	100%

Gene	Coverage	Gene	Coverage	Gene	Coverage	Gene	Coverage
ERCC2	100%	ERCC3	100%	ERCC4	100%	ERCC5	100%
ERCC6	100%	ERCC6L2	100%	ERCC8	100%	ERF	100%
ERG	100%	ERMARD	100%	ERRFI1	100%	ESCO2	100%
ESR1	100%	ESR2	100%	ETF1	100%	ETFA	100%
ETFB	100%	ETFDH	100%	ETHE1	100%	ETV1	100%
ETV4	100%	ETV6	100%	EVC	99.8%	EVC2	100%
EXO1	100%	EXOC2	100%	EXOSC3	100%	EXPH5	100%
EXT1	100%	EXT2	100%	EXTL3	100%	EYS	100%
EZH2	100%	F11	100%	F12	100%	F2	100%
F3	100%	F5	100%	F8	100%	F9	100%
FA2H	100%	FAAP24	100%	FABP2	100%	FAH	100%
FAM111B	100%	FAM135B	100%	FAM161A	100%	FAM3A	100%
FAM50A	100%	FAM83H	100%	FAN1	100%	FANCA	100%
FANCB	100%	FANCC	100%	FANCD2	100%	FANCE	100%
FANCF	100%	FANCG	100%	FANCI	100%	FANCL	100%
FANCM	100%	FAP	100%	FAR1	100%	FAS	100%
FASLG	100%	FASN	100%	FASTKD2	100%	FAT1	100%
FAT2	100%	FAT3	100%	FAT4	100%	FBN1	100%
FBP1	100%	FBXL4	100%	FBXO24	100%	FBXO28	100%
FBXW7	100%	FCSK	100%	FDFT1	100%	FDXR	100%
FERMT1	100%	FEZF1	100%	FGF10	100%	FGF13	100%
FGF14	100%	FGF16	100%	FGF17	100%	FGF23	100%
FGF3	100%	FGF4	100%	FGF6	100%	FGF8	100%
FGFR1	100%	FGFR2	100%	FGFR3	100%	FGFR4	100%
FGFRL1	100%	FH	100%	FHIT	100%	FHL1	100%
FIG4	100%	FKRP	100%	FKTN	100%	FLAD1	100%
FLCN	100%	FLNA	100%	FLNC	100%	FLRT3	100%
FLT1	100%	FLT3	100%	FLT4	100%	FMO3	100%
FMR1	100%	FOXA2	100%	FOXC1	100%	FOXF1	100%

FOXJ1	100%	FOXL2	100%	FOXP3	100%	FRAS1	100%
FREM2	100%	FRMD7	100%	FRMPD4	100%	FSCN1	100%
FSHB	100%	FSHR	100%	FTCD	100%	FTL	100%
FTSJ1	100%	FUCA1	100%	FUT8	100%	FXN	100%
FZD6	100%	FZR1	100%	G6PC3	100%	G6PD	100%
GAA	100%	GABRA1	100%	GABRA2	100%	GABRA3	100%
GABRA5	100%	GABRB2	100%	GABRG1	100%	GALC	100%
GALE	100%	GALK1	100%	GALNS	100%	GALNT12	100%
GALNT14	100%	GALNT3	100%	GALT	100%	GATA1	100%
GATA2	100%	GATA3	100%	GATA4	100%	GATA5	100%
GATA6	100%	GBA2	100%	GBE1	100%	GBF1	100%
GCDH	100%	GCK	100%	GCLC	100%	GCNA	100%
GDAP1	100%	GDF1	100%	GDF11	100%	GDF5	100%
GDI1	100%	GEN1	100%	GFAP	100%	GFER	100%
GFI1	100%	GFM1	100%	GFM2	100%	GFPT1	100%
GGCX	100%	GJA3	100%	GJA5	100%	GJA8	100%
GJB1	100%	GJB2	100%	GJB6	100%	GJC2	98.8%
GK	100%	GLA	100%	GLB1	100%	GLDC	100%
GLE1	100%	GLI1	100%	GLI2	100%	GLI3	100%
GLMN	100%	GLRA2	100%	GLRX5	100%	GLUD1	100%
GLUL	100%	GM2A	100%	GMNN	100%	GMPPA	100%
GMPPB	100%	GNA11	100%	GNA13	100%	GNAI3	100%
GNAL	100%	GNAO1	100%	GNAQ	100%	GNAS	100%
GNB2	100%	GNB4	100%	GNE	100%	GNMT	100%
GNPAT	100%	GNPDA1	100%	GNPTAB	100%	GNPTG	100%
GNRH1	100%	GNRHR	100%	GNS	100%	GORAB	100%
GPC3	100%	GPC4	100%	GPD1L	100%	GPHN	100%
GPI	100%	GPIHBP1	100%	GPR101	100%	GPR143	100%
GPR161	100%	GPRASP2	100%	GPRIN1	100%	GPX4	100%
GREM1	100%	GRHPR	100%	GRIA3	100%	GRIN1	100%

GRIN2A	100%	GRIN2B	100%	GRIP1	100%	GRM3	100%
GRN	100%	GSK3B	100%	GSKIP	100%	GSN	100%
GSR	100%	GSS	100%	GTF2E2	100%	GTF2H1	100%
GTF2H2	100%	GTF2H3	100%	GTF2H4	100%	GTF2H5	100%
GTPBP3	100%	GUCY2C	100%	GUSB	100%	GYG1	100%
GYS1	100%	GYS2	100%	H3-3A	100%	H3-3B	100%
H4C9	100%	HAAO	100%	HACD1	100%	HADH	100%
HADHA	100%	HADHB	100%	HAMP	100%	HARS1	100%
HARS2	100%	HAVCR2	100%	HAX1	100%	HBA1	100%
HBA2	100%	HBB	100%	HCCS	100%	HCFC1	100%
HCK	100%	HCN1	100%	HCN4	100%	HDAC4	100%
HDAC8	100%	HERPUD1	100%	HESX1	100%	HEXA	100%
HEXB	100%	HEXIM1	100%	HFE	100%	HGD	100%
HGF	100%	HGSNAT	100%	HID1	100%	HJV	100%
HK1	100%	HLCS	97.7%	HMGCL	100%	HMGCS2	100%
HMMR	100%	HMOX1	100%	HNF1A	100%	HNF1B	100%
HNRNPC	100%	HNRNPH2	100%	HNRNPK	100%	HOGA1	100%
HOOK1	100%	HOXB13	100%	HPGD	100%	HPRT1	100%
HPS1	100%	HPS3	100%	HRAS	100%	HS2ST1	100%
HS6ST1	100%	HS6ST2	100%	HSD11B1	100%	HSD17B10	100%
HSD17B3	100%	HSD17B4	100%	HSD3B2	100%	HSF4	100%
HSP90AA1	100%	HSPA9	100%	HSPD1	100%	HUWE1	100%
HYAL1	100%	HYLS1	100%	IARS2	100%	IBA57	100%
IDH1	100%	IDH2	100%	IDH3B	100%	IDS	100%
IDUA	100%	IFNAR1	100%	IFT122	100%	IFT140	100%
IFT172	100%	IFT43	100%	IFT52	100%	IFT80	100%
IFT81	100%	IGBP1	100%	IGF1R	100%	IGF2	100%
IGFALS	100%	IGSF1	100%	IHH	100%	IKBKE	100%
IKBKG	100%	IKZF1	100%	IL17RD	100%	IL1RAPL1	100%
IL1RN	100%	IL2RG	100%	IL6	100%	IL7R	100%

INHBA	100%	INPP5E	100%	INPP5K	100%	INPPL1	100%
INS	100%	INSL3	100%	INSR	100%	INTU	100%
INVS	100%	IQSEC2	97.6%	IRF1	100%	IRF2	100%
IRF2BP2	100%	IRF4	100%	IRS2	100%	IRS4	100%
ISCA1	100%	ISCA2	100%	ITGA3	100%	ITGA6	100%
ITGB4	100%	ITIH2	100%	ITPR1	100%	ITPR3	100%
IVD	100%	JAGN1	100%	JAK1	100%	JAK2	100%
JAK3	100%	JARID2	100%	JUN	100%	JUP	100%
KANK2	100%	KANSL1	100%	KAT6A	100%	KAT6B	100%
KATNB1	100%	KCNA2	100%	KCNA4	100%	KCNA5	100%
KCNB1	100%	KCNC2	100%	KCNE1	100%	KCNE2	100%
KCNH2	100%	KCNJ1	100%	KCNJ11	100%	KCNJ2	100%
KCNN4	100%	KCNQ1	100%	KCNT1	100%	KCTD1	99.6%
KCTD11	100%	KCTD17	100%	KCTD7	100%	KDELR2	100%
KDF1	100%	KDM1A	100%	KDM3B	100%	KDM5B	100%
KDM5C	100%	KDM6A	100%	KDM6B	99.8%	KDR	100%
KDSR	100%	KEAP1	100%	KEL	100%	KIAA0586	100%
KIF14	100%	KIF15	99.1%	KIF1A	100%	KIF1B	100%
KIF1C	100%	KIF23	100%	KIF2A	100%	KIF4A	100%
KIF5C	100%	KIF7	100%	KIFBP	100%	KISS1	100%
KISS1R	100%	KIT	100%	KITLG	100%	KLF5	98.4%
KLF6	100%	KLHL15	100%	KLHL24	100%	KLHL40	100%
KLHL41	100%	KLHL6	100%	KLHL7	100%	KLLN	100%
KMT2A	99.6%	KMT2B	98.8%	KMT2C	100%	KMT2D	100%
KNSTRN	100%	KRAS	100%	KRT1	100%	KRT10	100%
KRT14	100%	KRT16	100%	KRT17	100%	KRT5	100%
KRT6A	100%	KRT6B	100%	KRT6C	100%	KRT76	100%
KRT8	100%	KRT9	100%	KYNU	100%	L1CAM	100%
L2HGDH	100%	LAGE3	100%	LAMA2	100%	LAMA3	100%
LAMA4	100%	LAMA5	100%	LAMB2	100%	LAMB3	100%

LAMB4	100%	LAMC1	99.5%	LAMC2	100%	LAMP2	100%
LARGE1	100%	LARS2	100%	LAS1L	100%	LBR	100%
LCAT	100%	LCP1	100%	LCT	100%	LDHA	100%
LDHD	100%	LDLR	100%	LDLRAP1	100%	LEMD3	100%
LEP	100%	LEPR	100%	LETM1	100%	LFNG	83.5%
LGALS12	100%	LGR4	100%	LHB	100%	LHX4	100%
LIAS	100%	LIFR	100%	LIG4	100%	LIPA	100%
LIPC	100%	LIPE	100%	LIPH	100%	LIPN	100%
LIPT1	100%	LIPT2	100%	LITAF	100%	LMBR1	100%
LMBRD1	98.2%	LMBRD2	100%	LMF1	100%	LMNA	100%
LMNB2	99.8%	LMO1	100%	LOC112694756	100%	LONP1	100%
LORICRIN	100%	LOX	100%	LOXHD1	100%	LOXL2	100%
LPAR6	100%	LPIN1	100%	LPIN2	100%	LPL	100%
LRP1B	100%	LRP2	100%	LRP5	98.1%	LRPPRC	100%
LSP1	100%	LSS	100%	LTC4S	100%	LYN	100%
LYRM7	77.2%	LZTR1	100%	MAB21L1	100%	MAD2L2	100%
MADD	100%	MAF	82.6%	MAFB	100%	MAGED2	100%
MAGI1	100%	MAGI2	97%	MAGT1	100%	MAMLD1	100%
MAN1B1	100%	MAN2B1	100%	MANBA	100%	MAOA	100%
MAP2K1	100%	MAP2K2	100%	MAP2K4	100%	MAP3K1	100%
MAP3K6	100%	MAP3K9	100%	MAP4K2	100%	MAPKAPK3	100%
MAPRE2	100%	MARS2	100%	MASP1	100%	MAST3	100%
MAT1A	100%	MATR3	100%	MAX	100%	MBD4	100%
MBOAT7	100%	MBTPS2	100%	MC1R	100%	MCAT	100%
MCC	100%	MCCC1	100%	MCCC2	100%	MCEE	100%
MCL1	100%	MCM2	100%	MCOLN1	100%	MCPH1	100%
MDH2	100%	MDM2	100%	MDM4	100%	MECOM	100%
MECP2	100%	MECR	100%	MED12	100%	MED17	100%
MEFV	100%	MEGF8	99.9%	MEIS2	100%	MEN1	100%
MESP2	100%	MET	100%	MFAP5	100%	MFF	100%

MFN2	100%	MFSD2A	100%	MFSD8	100%	MGAT2	100%
MGME1	100%	MGMT	100%	MICOS13	100%	MICU1	100%
MID1	100%	MID2	100%	MIP	100%	MIPEP	100%
MITF	100%	MKKS	100%	MKRN3	100%	MKS1	100%
MLC1	100%	MLH1	100%	MLH3	100%	MLLT1	98.9%
MLLT6	100%	MMAA	100%	MMAB	100%	MMACHC	100%
MMADHC	100%	MME	100%	MMP1	100%	MMP14	100%
MMP19	100%	MMP2	100%	MMS19	100%	MMUT	100%
MN1	100%	MNAT1	100%	MNX1	77.5%	MOCOS	100%
MOCS1	100%	MOCS2	100%	MOGAT2	100%	MOGS	100%
MORC2	100%	MPC1	100%	MPDU1	100%	MPG	100%
MPI	100%	MPL	100%	MPLKIP	100%	MPP3	100%
MPV17	100%	MPZ	100%	MRAS	100%	MRE11	100%
MRPL23	100%	MRPL3	100%	MRPL36	100%	MRPL44	100%
MRPS16	100%	MRPS2	100%	MRPS22	100%	MRPS34	100%
MSH2	100%	MSH3	100%	MSH4	100%	MSH5	100%
MSH6	100%	MSI2	100%	MSL3	100%	MSMO1	100%
MSN	100%	MSR1	100%	MST1R	100%	MSTO1	100%
MTAP	100%	MTFMT	100%	MTHFR	100%	MTM1	100%
MTMR2	100%	MTO1	100%	MTOR	100%	MTR	100%
MTRR	100%	MUC16	100%	MUS81	100%	MUSK	100%
MUTYH	100%	MVK	100%	MX2	100%	MXI1	100%
MYB	100%	MYBPC1	100%	MYBPC3	100%	MYC	100%
MYCL	100%	MYCN	100%	MYD88	100%	MYH11	100%
MYH3	100%	MYH7	100%	MYL1	100%	MYL2	100%
MYL3	100%	MYL4	100%	MYLK	100%	MYLK2	100%
MYO7A	100%	MYOZ2	100%	MYPN	100%	MYSM1	100%
NAA10	100%	NAF1	100%	NAGA	100%	NAGLU	100%
NAGS	100%	NALCN	100%	NANP	100%	NANS	100%
NARS2	99.4%	NAT8	100%	NAXD	100%	NAXE	100%

NBAS	100%	NBN	100%	NCOA2	100%	NCSTN	100%
NDNF	100%	NDP	100%	NDUFA1	100%	NDUFA10	100%
NDUFA11	100%	NDUFA12	100%	NDUFA2	100%	NDUFA6	100%
NDUFA9	100%	NDUFAF1	100%	NDUFAF2	100%	NDUFAF3	100%
NDUFAF4	100%	NDUFAF5	100%	NDUFAF6	100%	NDUFB11	100%
NDUFB3	100%	NDUFB8	100%	NDUFS1	100%	NDUFS2	100%
NDUFS4	100%	NDUFS6	100%	NDUFS7	100%	NDUFS8	100%
NDUFV1	100%	NEB	100%	NECTIN1	100%	NEFH	100%
NEIL1	100%	NEIL2	100%	NEIL3	100%	NEK10	100%
NEK11	100%	NEK2	100%	NEK4	100%	NEK9	100%
NELFA	100%	NEU1	100%	NEXMIF	100%	NEXN	100%
NF1	100%	NF2	100%	NFE2L2	100%	NFIA	100%
NFIX	98.2%	NFKBIA	100%	NFU1	100%	NGLY1	100%
NHEJ1	100%	NHLH2	100%	NHLRC1	100%	NHP2	100%
NHS	100%	NIN	100%	NIPAL4	100%	NIPBL	100%
NKAP	100%	NKX2-1	100%	NKX2-5	100%	NLGN4X	100%
NLRC4	100%	NLRP1	100%	NLRP3	100%	NME1	100%
NMNAT1	100%	NOD2	100%	NONO	100%	NOP10	100%
NOTCH1	100%	NOTCH2	100%	NOTCH3	100%	NPC1	100%
NPC2	100%	NPHP3	100%	NPHS1	100%	NPHS2	100%
NPM1	100%	NPR2	100%	NPRL2	100%	NQO2	100%
NR0B1	100%	NR0B2	100%	NR2E3	99.9%	NR2F1	98%
NR2F2	100%	NR5A1	100%	NRAS	100%	NSD1	100%
NSD2	99.7%	NSDHL	100%	NSF	100%	NSMCE3	100%
NSMF	100%	NSUN2	100%	NT5C3A	100%	NTHL1	100%
NTRK1	100%	NTRK2	100%	NTRK3	100%	NUDT19	100%
NUMA1	100%	NUP107	100%	NUP188	100%	NUP88	100%
NUP93	100%	NUS1	100%	NYNRIN	100%	NYX	100%
OAT	100%	OCA2	100%	OCRL	100%	ODC1	100%
OFD1	100%	OGG1	100%	OGT	100%	OPA1	100%

OPA3	100%	OPHN1	100%	OPN1LW	100%	OPN1MW	97.9%
OPN1SW	100%	ORC1	100%	ORC4	100%	ORC6	100%
OSMR	100%	OTC	100%	OTUD5	100%	OTX2	100%
OVOL2	100%	OXCT1	100%	P4HB	100%	PACS1	100%
PAH	100%	PAK2	100%	PAK3	100%	PALB2	100%
PALLD	100%	PAM16	100%	PANK2	100%	PANK3	99.9%
PAPSS2	100%	PARN	100%	PARP1	100%	PARP2	100%
PARP3	100%	PARS2	100%	PAX3	100%	PAX5	100%
PAX7	100%	PBRM1	100%	PBX1	100%	PC	100%
PCCA	100%	PCCB	100%	PCDH10	100%	PCDH15	100%
PCDH19	100%	PCDH9	100%	PCK1	100%	PCK2	100%
PCSK9	100%	PCYT1A	100%	PDCD10	100%	PDCD6	100%
PDE11A	100%	PDE4D	100%	PDE6H	100%	PDGFB	100%
PDGFRA	100%	PDGFRB	100%	PDGFRL	100%	PDHA1	100%
PDHX	100%	PDP1	100%	PDSS1	100%	PDSS2	100%
PDX1	100%	PEPD	100%	PER2	100%	PET100	100%
PEX1	100%	PEX10	100%	PEX11B	100%	PEX12	100%
PEX13	100%	PEX14	100%	PEX16	100%	PEX19	100%
PEX2	100%	PEX26	100%	PEX3	100%	PEX6	100%
PEX7	100%	PFKM	100%	PGAM2	100%	PGAP1	100%
PGAP2	100%	PGAP3	100%	PGK1	100%	PGR	100%
PHEX	100%	PHF6	100%	PHF8	100%	PHGDH	100%
PHIP	99.7%	PHKA1	100%	PHKA2	100%	PHOX2B	100%
PHYH	100%	PIEZO2	100%	PIGA	100%	PIGG	100%
PIGL	100%	PIGN	100%	PIGO	100%	PIGT	100%
PIGV	100%	PIGW	100%	PIGY	100%	PIK3C2B	100%
PIK3CA	100%	PIK3CB	100%	PIK3CD	100%	PIK3CG	100%
PIK3R1	100%	PIK3R2	99.2%	PIKFYVE	100%	PINK1	100%
PITPNM3	100%	PKD1	99.3%	PKD2	100%	PKHD1	100%
PKP1	100%	PKP2	100%	PLA2G2A	100%	PLA2G6	100%

PLAAT3	100%	PLCE1	100%	PLCG2	100%	PLEC	100%
PLK2	100%	PLN	100%	PLP1	100%	PLPP6	100%
PLS3	100%	PLXND1	99.5%	PMM2	100%	PMP2	100%
PMP22	100%	PMPCA	100%	PMPCB	100%	PMS1	100%
PMS2	100%	PNKP	100%	PNPLA1	100%	PNPLA6	100%
POC1A	100%	PODXL	100%	POF1B	100%	POFUT1	100%
POGLUT1	100%	POLA1	100%	POLD1	100%	POLE	100%
POLG	100%	POLH	100%	POLK	100%	POLR1A	100%
POLR1G	100%	POLR3A	100%	POLR3H	100%	POMGNT1	100%
POMGNT2	100%	POMP	100%	PORCN	100%	POT1	100%
POU1F1	100%	POU3F4	100%	POU4F1	75.2%	POU6F2	100%
PPARG	100%	PPM1D	100%	PPP1CB	100%	PPP2R1A	100%
PPP2R2A	100%	PPP2R5D	100%	PPP3CA	100%	PPT1	100%
PQBP1	100%	PRDM1	100%	PRDX6	100%	PREX2	100%
PRF1	100%	PRKAG2	97.8%	PRKAR1A	100%	PRKD1	100%
PRKD2	100%	PRKDC	100%	PRKG1	100%	PRKG2	100%
PRKN	100%	PRLR	100%	PRNP	100%	PROC	100%
PROK2	100%	PROKR2	100%	PROP1	100%	PROSER2	100%
PRPS1	100%	PRPS1L1	100%	PRSS1	100%	PRSS58	100%
PRSS8	100%	PRX	100%	PSAT1	100%	PSEN2	100%
PSENEN	100%	PSMB8	100%	PSMC3IP	100%	PTCH1	100%
PTEN	100%	PTGES2	100%	PTGS2	100%	PTHLH	100%
PTPN11	100%	PTPN6	100%	PTPRD	100%	PTPRF	100%
PTS	100%	PUS1	100%	PXMP2	100%	PYGM	100%
PZP	100%	RAB18	100%	RAB39B	100%	RAB3GAP2	100%
RAB40AL	100%	RAB43	100%	RAB7A	100%	RABL3	100%
RAC1	100%	RAD17	100%	RAD21	100%	RAD50	100%
RAD51	100%	RAD51B	97.6%	RAD51C	100%	RAD51D	100%
RAD52	100%	RAD54B	100%	RAD54L	100%	RAF1	100%
RAG1	100%	RAG2	100%	RAI1	100%	RANBP2	100%

RAPSN	100%	RARA	100%	RARS2	100%	RASA1	100%
RASA2	100%	RASAL1	100%	RASEF	100%	RB1	98.9%
RB1CC1	100%	RBBP8	100%	RBM10	100%	RBM15	100%
RBM20	100%	RBM28	100%	RBMX	100%	RECQL	100%
RECQL4	100%	REEP1	100%	RELA	100%	REN	100%
RERE	97.1%	REST	100%	RET	100%	REV3L	100%
RFC1	100%	RFT1	100%	RFWD3	100%	RHBDF2	100%
RICTOR	100%	RIMS1	100%	RINT1	100%	RIPK1	100%
RIPK4	100%	RIT1	100%	RLIM	100%	RNASE1	100%
RNASE3	100%	RNASEH2B	100%	RNASEL	100%	RNF113A	100%
RNF170	100%	RNF2	100%	RNF216	100%	RNF4	100%
RNF43	100%	RNMT	100%	ROBO4	100%	ROR2	100%
RORA	100%	ROS1	100%	RP2	100%	RPA1	100%
RPE65	100%	RPGR	100%	RPL10	100%	RPL11	100%
RPL15	100%	RPL17	100%	RPL23	100%	RPL26	100%
RPL27	100%	RPL31	100%	RPL35A	100%	RPL5	100%
RPL9	100%	RPS10	100%	RPS17	100%	RPS19	100%
RPS20	100%	RPS23	100%	RPS24	100%	RPS26	87.2%
RPS27	100%	RPS28	100%	RPS29	100%	RPS6KA3	100%
RPS7	100%	RPSA	100%	RPTOR	100%	RRAS	100%
RRAS2	100%	RS1	100%	RSC1A1	100%	RSPO1	100%
RSPO2	100%	RTEL1	100%	RTL1	100%	RUNDC1	100%
RUNX1	100%	RUNX1T1	100%	RYR1	99.9%	RYR2	100%
SACS	100%	SAMD9	100%	SAMD9L	100%	SASH1	100%
SASH3	100%	SBDS	100%	SBF1	100%	SBF2	100%
SCGB1D1	100%	SCN1B	100%	SCN2A	100%	SCN2B	100%
SCN3B	100%	SCN4A	100%	SCN4B	100%	SCN5A	100%
SCN8A	100%	SCNN1G	100%	SCO2	100%	SDHA	100%
SDHAF2	100%	SDHB	100%	SDHC	100%	SDHD	100%
SEC23B	100%	SEMA3A	100%	SEMA3E	100%	SEMA4A	100%

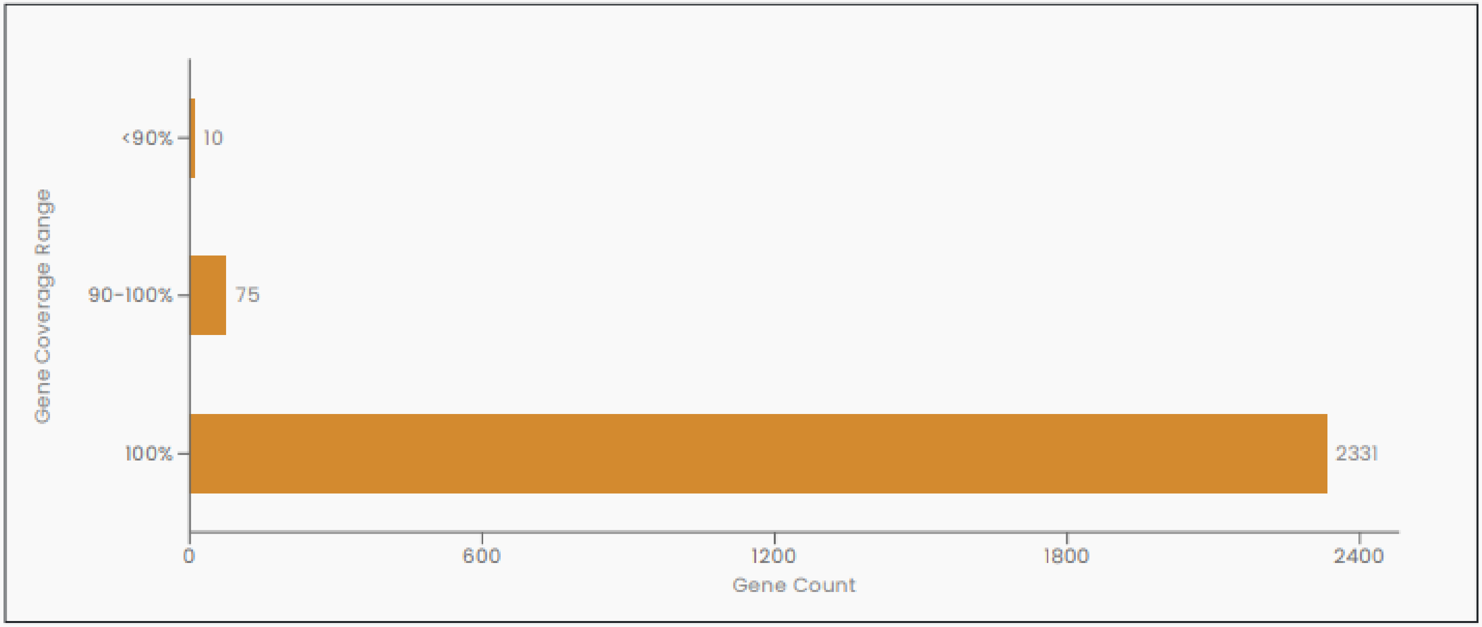
SEPSECS	100%	SERPINA1	100%	SERPINB7	100%	SERPINB8	100%
SET	100%	SETBP1	100%	SETD1B	97%	SETD2	100%
SF3B1	100%	SF3B2	100%	SF3B4	100%	SGCA	100%
SGCB	100%	SGCD	100%	SGCE	100%	SGCG	100%
SGMS2	100%	SGSH	100%	SH2D1A	100%	SH2D3C	100%
SH3BP2	100%	SH3D19	100%	SH3PXD2B	100%	SHH	100%
SHOC2	100%	SIAH1	100%	SIK1	100%	SIX1	100%
SIX2	100%	SLC11A2	100%	SLC12A3	100%	SLC12A6	100%
SLC16A1	100%	SLC16A12	100%	SLC16A2	100%	SLC17A5	100%
SLC19A1	100%	SLC19A3	100%	SLC1A2	100%	SLC20A2	100%
SLC22A18	100%	SLC22A5	100%	SLC25A11	100%	SLC25A15	100%
SLC25A20	100%	SLC25A21	100%	SLC25A22	100%	SLC25A23	100%
SLC25A24	100%	SLC25A26	100%	SLC25A38	100%	SLC25A46	100%
SLC26A2	100%	SLC26A4	100%	SLC29A3	100%	SLC2A1	100%
SLC2A10	100%	SLC34A2	100%	SLC35A2	100%	SLC35A3	100%
SLC37A4	99.9%	SLC38A3	100%	SLC39A4	100%	SLC45A1	100%
SLC45A2	100%	SLC4A10	100%	SLC6A17	100%	SLC6A8	100%
SLC9A6	100%	SLC9A7	100%	SLCO2A1	100%	SLFN14	100%
SLIT2	100%	SLPI	100%	SLURP1	100%	SLX4	100%
SMAD2	100%	SMAD3	100%	SMAD4	100%	SMAD7	100%
SMAD9	100%	SMARCA2	100%	SMARCA4	100%	SMARCAD1	100%
SMARCB1	100%	SMARCC2	100%	SMARCD1	100%	SMARCE1	100%
SMC1A	100%	SMC3	100%	SMC5	100%	SMCHD1	100%
SMIM6	100%	SMN1	100%	SMO	100%	SMOX	100%
SMPD1	100%	SMPD4	100%	SMPX	100%	SMS	100%
SMUG1	100%	SNCA	100%	SNCAIP	100%	SNCB	100%
SOAT1	100%	SOCS1	100%	SON	100%	SORD	100%
SORT1	100%	SOS1	100%	SOS2	100%	SOX10	100%
SOX2	100%	SOX3	100%	SOX4	100%	SOX5	100%
SOX6	100%	SOX9	100%	SP6	100%	SP8	100%

SPAG9	100%	SPAM1	100%	SPEN	100%	SPI1	100%
SPIDR	100%	SPIN4	100%	SPINK1	100%	SPOP	100%
SPRED1	100%	SPRED2	100%	SPRY4	100%	SPTA1	100%
SPTBN1	100%	SPTLC1	100%	SRA1	100%	SRC	100%
SRCAP	100%	SRD5A3	100%	SRP72	100%	SSR4	100%
SSX1	100%	STAG1	100%	STAG2	100%	STAT3	100%
STAT4	100%	STEAP3	100%	STEAP4	100%	STK11	100%
STOML3	100%	STS	100%	STT3A	100%	SUFU	100%
SULT2B1	100%	SUMF1	100%	SUZ12	100%	SYK	100%
SYN1	100%	SYNE1	100%	SYNGAP1	98.3%	SYP	100%
SYT1	100%	TAB2	100%	TAC3	100%	TAC4	100%
TACO1	100%	TACR3	100%	TAF1	100%	TAF4	73.5%
TANGO2	100%	TAOK1	100%	TARS1	100%	TARS2	100%
TAT	100%	TBC1D8B	100%	TBL1X	100%	TBL1XR1	100%
TBX18	100%	TBX22	100%	TBX3	100%	TBXAS1	100%
TCAP	100%	TCEAL1	100%	TCF20	100%	TCF4	100%
TCIRG1	100%	TECPR2	100%	TECTA	100%	TENT4A	95.1%
TERF1	100%	TERF2	100%	TERF2IP	100%	TERT	100%
TESC	100%	TET2	100%	TEX11	100%	TF	100%
TFAP2A	100%	TFAP2B	100%	TFE3	100%	TFR2	100%
TGFB1	100%	TGFB2	100%	TGFB3	100%	TGFBI	100%
TGFBR1	99.1%	TGFBR2	100%	TGM1	100%	TGM5	100%
TGM6	100%	TH	100%	THAP1	100%	THOC2	100%
THSD4	100%	TIMM50	100%	TIMM8A	100%	TIMP3	100%
TINAGL1	100%	TINF2	100%	TLL1	100%	TLR2	100%
TLR7	100%	TLR8	100%	TMC1	100%	TMC6	100%
TMCO1	100%	TMEM127	100%	TMEM216	100%	TMEM43	100%
TMEM53	100%	TMEM67	100%	TMEM94	100%	TMPRSS2	100%
TMPRSS3	100%	TMPRSS4	100%	TNFAIP3	100%	TNFRSF14	100%
TNIP1	100%	TNNC1	100%	TNNC2	100%	TNNI2	100%

TNNI3	100%	TNNI3K	100%	TNNT2	100%	TNPO1	100%
TNRC6B	100%	TNXB	100%	TOGARAM1	100%	TOP1	100%
TOP2A	100%	TOP2B	99.7%	TOX3	100%	TOX4	100%
TP53	100%	TP63	100%	TPI1	100%	TPM1	100%
TPM3	100%	TPP1	100%	TPSAB1	100%	TRAF7	100%
TRAPPC12	100%	TRAPPC2	100%	TRDN	94.7%	TRIM26	100%
TRIM28	98.4%	TRIM37	100%	TRIP11	100%	TRIP13	100%
TRIT1	100%	TRMT10C	100%	TRMU	100%	TRPV3	100%
TRRAP	99.9%	TSC1	100%	TSC2	100%	TSFM	100%
TSHR	100%	TSPAN7	100%	TSR2	100%	TTC5	100%
TTF2	100%	TTI1	100%	TTN	100%	TTPA	100%
TTR	100%	TUBA4A	100%	TUBB	100%	TUBB2A	100%
TUBB2B	100%	TUBB3	100%	TUBB4A	100%	TUBG1	100%
TWIST1	100%	TWIST2	100%	TWNK	100%	TYMP	100%
TYMS	100%	TYR	100%	TYRP1	100%	U2AF1	100%
UBA1	100%	UBA2	100%	UBE2A	100%	UBE2T	100%
UBIAD1	100%	UBL4A	100%	UBQLN2	100%	UBR1	100%
UNG	100%	UPF1	99.3%	UPF3B	100%	USF3	100%
USH1C	100%	USH2A	100%	USP26	100%	USP27X	100%
USP9X	100%	VAC14	100%	VAMP1	100%	VAMP7	100%
VARS1	100%	VARS2	100%	VCL	100%	VEGFA	100%
VHL	100%	VIM	100%	VMA21	100%	VPS13A	100%
VPS13B	100%	VPS16	100%	VPS35L	100%	VPS4A	100%
VPS53	100%	VRK1	100%	VSX2	100%	WAC	100%
WAS	100%	WASF1	100%	WASHC5	100%	WDFY3	100%
WDR11	100%	WDR19	100%	WDR37	100%	WDR45	100%
WLS	100%	WNK3	100%	WNT3	100%	WNT7A	100%
WRAP53	100%	WRN	100%	WRNIP1	100%	WT1	100%
WWOX	100%	XAB2	100%	XDH	100%	XIAP	100%
XIRP2	100%	XK	100%	XPA	100%	XPC	100%

XPO1	100%	XPR1	100%	XRCC1	100%	XRCC2	100%
XRCC3	100%	XRCC4	100%	XRCC5	100%	XRCC6	100%
YAP1	100%	YEATS2	100%	YY1	100%	ZBTB20	100%
ZC3H14	100%	ZC4H2	100%	ZCCHC8	100%	ZDHHC9	100%
ZEB2	100%	ZFHX3	100%	ZFP36L1	100%	ZFPM2	100%
ZFYVE26	100%	ZIC1	100%	ZIC3	100%	ZMYND11	100%
ZNF148	100%	ZNF160	100%	ZNF260	100%	ZNF395	100%
ZNF711	100%	ZNF750	100%	ZSWIM6	90.8%	ZSWIM7	100%

Gene Coverage Distribution



QC Metrics

Total aligned reads	99.95 %
Total reads	50.64 (M)
Total data generated	7.52 (Gb)
Total reads which passed mapping quality cutt-off	7.17 (Gb)

...........End of Report ......

Performed By
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