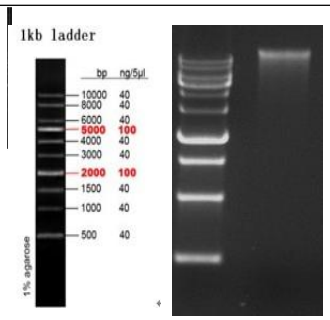
CERTIFICATE OF ANALYSIS
Panel-Ref® HRR-Related-28 Gene Cocktail

Product information

Name	Panel-Ref® HRR-Related-28 Gene Cocktail
Catalog No.	CBP90021
Lot No.	CBD45352727
Format	Genomic DNA
Buffer	Tris-EDTA
Storage Conditions	-20℃
Date of Manufacture	Sep.-03-2020
Expiry	36 months from the date of manufacture

Quality Control

Test Items	Standard	Results	Passed
Quantity	1ug/vial*1vial	1ug/vial*1vial	√
Concentration	Qubit 3.0	40 ng/uL±10%	√
OD_{260}/OD_{280}	1.7~2.0	1.76	√
DNA electrophoresis	No Degradation	 M 1 M: Marker 1: Panel-Ref® HRR-Related-28 Gene Cocktail	√

Allele Frequency(AF) and Genotype: DdPCR &NGS

Gene	Protein Change	CDS Change	%AF	Clinical significance
ATM	p.N625Ifs*10	c.1873_1874insT	21.57	Pathogenic
ATM	p.N1983S	c.5948A>G	99.85	Benign
ATM	p.K236Nfs*10	c.708delA	1.61	Uncertain Significance
ATM	p.A2843V	c.8528C>T	21.45	Likely Pathogenic
ATR	p.R2425Q	c.7274G>A	24.38	Benign
ATR	N/A	c.6552+5A>G	5.7	Uncertain Significance
ATR	N/A	c.4153-11_4153-10delTT	20.97	Uncertain Significance

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ATR	p.I774Yfs*5	c.2320delA	19.835	Uncertain Significance
ATR	p.L711F	c.2131C>T	3.39	Likely Benign
ATR	p.D564=	c.1692T>C	24.62	Likely Benign
BARD1	p.A724T	c.2170G>A	8.135	Uncertain Significance
BARD1	p.V507M	c.1519G>A	56.205	Benign
BARD1	p.H506=	c.1518T>C	70.16	Benign
BARD1	p.R378S	c.1134G>C	57.365	Benign
BARD1	p.P24S	c.70C>T	56.915	Benign
BLM	p.A603V	c.1808C>T	20.905	Uncertain Significance
BLM	p.Q615=	c.1845A>G	21.985	Likely Benign
BLM	p.H660Qfs*2	c.1979dupA	21.585	Pathogenic
BLM	p.G921=	c.2763C>T	22.105	Likely Benign
BLM	p.T1034=	c.3102G>A	31.655	Benign
BLM	p.A1177=	c.3531C>A	36.99	Benign
BLM	p.L1315=	c.3945C>T	34.21	Benign
BRCA1	p.S1634G	c.4900A>G	46.035	Benign
BRCA1	p.S1436=	c.4308T>C	48.82	Benign
BRCA1	p.K1183R	c.3548A>G	47.325	Benign
BRCA1	p.E1038G	c.3113A>G	46.345	Benign
BRCA1	p.P871L	c.2612C>T	63.68	Benign
BRCA1	p.L771=	c.2311T>C	48.71	Benign
BRCA1	p.S694=	c.2082C>T	47.16	Benign
BRCA2	p.N289H	c.865A>C	29.71	Benign
BRCA2	p.S455=	c.1365A>G	35.89	Benign
BRCA2	N/A	c.1909+2T>C	18.955	Pathogenic
BRCA2	p.H743=	c.2229T>C	34.535	Benign
BRCA2	p.N991D	c.2971A>G	34.72	Benign
BRCA2	p.N1287Ifs*6	c.3860delA	19.925	Pathogenic
BRCA2	p.D1476G	c.4427A>G	20.89	Likely Pathogenic
BRCA2	p.L1521=	c.4563A>G	99.94	Benign
BRCA2	p.V2014E	c.6041T>A	23.005	Likely Pathogenic
BRCA2	p.V2171=	c.6513G>C	99.93	Benign
BRCA2	p.V2466A	c.7397T>C	99.895	Benign
BRCA2	p.Q2934*	c.8800C>T	23.2	Pathogenic
BRIP1	p.N933I	c.2798A>T	18.63	Uncertain Significance
BRIP1	p.E879=	c.2637A>G	99.595	Benign
CDK12	p.R300K	c.899G>A	21.325	Uncertain Significance
CDK12	p.I873N	c.2618T>A	17.705	Uncertain Significance

CHEK1	p.Y390=	c.1170T>C	22.57	Likely Benign
CHEK1	p.I471V	c.1411A>G	100	Benign
CHEK2	N/A	c.721+2T>C	22.06	Pathogenic
CHEK2	p.R188W	c.562C>T	13.165	Pathogenic
FANCA	p.P1218=	c.3654A>G	24.475	Benign
FANCA	N/A	c.3067-4T>C	23.625	Benign
FANCA	p.S967=	c.2901C>T	21.5	Benign
FANCA	N/A	c.2779-7T>C	22.005	Benign
FANCA	p.P643A	c.1927C>G	18.555	Benign
FANCA	p.G501S	c.1501G>A	66.755	Benign
FANCA	p.T381=	c.1143G>T	24.555	Benign
FANCA	N/A	c.894-8A>G	24.575	Benign
FANCA	p.S208L	c.623C>T	24.47	Uncertain Significance
FANCC	p.G307V	c.920G>T	19.015	Uncertain Significance
FANCC	p.A158V	c.473C>T	16.975	Likely Benign
FANCC	p.S156=	c.468A>G	16.285	Likely Benign
FANCD2	p.Y425=	c.1275C>T	14.935	Likely Benign
FANCD2	N/A	c.1278+3_1278+6delAAGT	13.87	Uncertain Significance
FANCF	p.L111=	c.331C>T	2.375	Likely Benign
FANCI	p.K849=	c.2547G>A	99.9	Benign
FANCL	p.A299T	c.895G>A	21.065	Likely Benign
FANCL	N/A	c.791-10delT	25.73	Uncertain Significance
FANCM	p.L42=	c.126G>A	2.01	Likely Benign
FANCM	N/A	c.1788+6T>C	22.375	Uncertain Significance
FANCM	p.V878L	c.2632G>T	39.685	Benign
FANCM	p.Q1333Tfs*11	c.3996_3997insA	18.86	Likely Benign
FANCM	p.S1949T	c.5845T>A	19.725	Uncertain Significance
FANCM	p.M2010V	c.6028A>G	20.895	Uncertain Significance
MRE11A	N/A	c.1867+6T>C	17.2	Uncertain Significance
MRE11A	N/A	c.315-5_315-4delTT	27.945	Uncertain Significance
NBN	N/A	c.1398-10delT	19.56	Uncertain Significance
NBN	p.L34=	p.102G>A	34.07	Benign
NBN	N/A	c.38-10_38-9insA	17.625	Uncertain Significance
PALB2	p.G808*	c.2422G>T	15.005	hogenic
PPP2R2A	p.C249Y	c.746G>A	16.335	Uncertain Significance
RAD50	p.K722Rfs*14	c.2165delA	20.43	Pathogenic
RAD51B	p.R348G	c.1042A>G	25.77	Likely Benign
RAD51C	p.T287A	c.859A>G	10.79	Benign

RAD51D	p.V66=	c.198G>T	21.21	Likely Benign
RAD52	p.R253C	c.757C>T	22.585	Uncertain Significance
RAD52	N/A	c.348+7_348+8insA	34.44	Uncertain Significance
RAD54L	p.R587W	c.1759C>T	12.65	Likely Benign
RPA1	p.A128V	c.383C>T	22.53	Uncertain Significance
RPA1	p.S352=	c.1056C>T	43.09	Benign
RPA1	p.E363Kfs*60	c.1087delG	19.995	Pathogenic
RPA1	p.S535=	c.1605T>C	39.92	Benign
To get the complete informations of 1000x WES, please contact us.				

Caution:
For research use only.
If you have any questions about the Certificate of Analysis, please contact us.

Certified by: Date:****