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Abstract

Recent studies suggest that oncogenic processes (from precancerous lesions to metastatic cancers) are widespread in wild animal species, but their importance for ecosystem functioning is still underestimated by evolutionary biologists and animal ecologists. Similar to what has been observed in humans, environmental modifications that often place wild organisms into an evolutionary trap and/or exposes them to a cocktail of mutagenic and carcinogenic pollutants might favor cancer emergence and progression, if animals do not up-regulate their defenses against these pathologies. Here, we compared, for the first time, the expression of 59 tumor-suppressor genes in blood and liver tissues of urban and rural great tits (*Parus major*); urban conditions being known to favor cancer progression due to, among other things, exposure to chemical or light pollution. Contrary to earlier indications, once we aligned the transcriptome to the great tit genome, we found negligible differences in the expression of anti-cancer defenses between urban and rural birds in blood and liver. Our results indicate the higher expression of a single caretaker gene (i.e. BRCA1) in livers of rural compared to urban birds. We conclude that, while urban birds might be exposed to an environment favoring the development of oncogenic processes, they seem to not upregulate their cancer defenses accordingly and future studies should confirm this result by assessing more markers of cancer defenses. This may result in a mismatch that might predispose urban birds to higher cancer risk and future studies in urban ecology should take into account this, so far completely ignored, hazard.

Introduction

Over the last century, the size of urban centres has drastically increased all over the world with considerable effects on natural ecosystems (Marzluff et al., 2008). Consequently, many wild species are now experiencing extreme changes in their habitats with, among other things, an increased exposure to a mixture of mutagenic pollutants, changes in habitat temperature (i.e. heat-island effect) and/or access to novel types of food items through human waste or intentional feeding. As these environmental modifications, as well as other characteristics of our modern world, have increased cancer prevalence in humans (Kloog et al., 2010), similar effects can also be expected in wild animals living in human-modified habitats, and especially in urban environments (Giraudeau et al., 2018; Sepp et al., 2019). In line with this hypothesis, it has now been shown that most animal species can develop cancer (Madsen et al., 2017), and several studies proposed that, even if invasive metastatic cancer might be rare in wild animals, most metazoan organisms should start to host early stages of oncogenic processes early in life and thus host them for months, years or decades with some effects on their health and vigour and an impact on intra- and inter-specific relationships (Vittecoq et al., 2013, Thomas et al. 2017). In addition, evidence is starting to accumulate showing that exposure to pollution might strongly affect neoplasia development in wild populations (Martineau et al., 2002). However, while cancer is one of the leading causes of mortality in humans and a research topic of prime importance for scientists and funding agencies worldwide, our understanding of oncogenic processes in wild populations is extremely limited due to the methodological difficulties of measuring this pathology in wild animals. Even more important in terms of conservation, the ability of wild organisms to limit cancer progression in "oncogenic environments" (i.e. habitats that favour neoplasia development such as those polluted with chemicals or artificial light at night) has never been studied in the field. In addition, longer lifespan has been linked with higher cancer-related mortality in humans, and age is considered

to be one of the major risk factors for cancer (White et al., 2014). As it has been suggested that many wild species also experience lower predation rates and increased survival to older age in urban environments (e.g. see Sepp et al., 2018)), age-related increase in cancer risk in wild animals in urban environment should also be considered.

To fill this gap, we used a recently published transcriptome analysis which compared gene expression levels between urban and rural great tits and focused our analysis on the expression of 59 well-known tumour suppressor genes. In addition, the previous analyses published by Watson et al. (2017) aligned the transcriptome to the best available genome at the time of their publication (i.e. zebra finch). In order to perform a more accurate scrutiny of differential expression of tumor-suppressor genes, we re-aligned the above transcriptomes to the great tit genome and re-analysed the latter. Given that urban great tits up-regulate the expression of genes related to immune activity, detoxification and repair machinery (Watson et al., 2017), we predicted that they might also up-regulate the activity of genes related to cancer defences.

Methods

Field and laboratory methods have been previously described in (Watson et al., 2017). Briefly, six urban male great tits (Malmö, 55°35′N 12°59′E) and six rural great tits (Vombs fure located 35 km northeast of Malmö, 55°39′N 13°33′E), were captured in late winter 2014. At capture, birds were transported to the laboratory in Lund where biometrics were recorded, and a blood sample was collected and immediately transferred to storage at −80 °C. Birds were then euthanized and liver tissues were collected and transferred to storage at −80°C within 5 min of death. RNA was isolated and sequenced using 100 bp paired-end RNA-seq on Illumina HiSeq 2000. For the present study, we focused on the re-analysis of 59 tumor-

suppressor genes including 31 gatekeeper genes and 28 caretaker genes, following (Caulin and Maley, 2011). By limiting DNA damage and being involved in DNA repair, caretaker genes help to maintain genome integrity and thus limit cancer initiation. Gatekeeper genes are involved in the control of cells at risk for neoplastic transformation in order to stop their propagation (Caulin and Maley, 2011).

Read quality was first assessed using FastQC 0.11.5 (https://www.bioinformatics.babraham.ac.uk/projects/fastqc/), and quality trimming and filtering were performed to remove low-quality reads and adapter contamination using Trimmomatic (Bolger et al., 2014). Clean reads were aligned to the annotated regions of the great tit genome (Parus_major1.1 RefSeq assembly accession GCF_001522545.2) using HiSat2 2.1.0 (Kim et al., 2015) and sorted with SAMtools 1.5 (Li et al., 2009). Counts were made using StringTie 1.3.3 (Pertea et al., 2015) in accordance with the protocol described by Pertea et al. (Pertea et al., 2016). Counts were extracted for the 59 target genes. Following (Watson et al., 2017), one rural bird was removed from the analysis of reads from blood, since PCA revealed it to be an extreme outlier. All raw reads have been deposited in NCBI's Sequence Read Archive (PRJNA314210).

Statistical analyses

Analyses of differences in the expression of various genes between urban and rural great tits were performed separately for counts originating from blood and liver tissue, using the edgeR 3.24.3 package (Robinson et al., 2009) in R 3.5.2 (R Core Team 2018). Only genes with expression greater than one count per million (CPM) in at least two samples were considered for the differential expression analyses in order to filter out weakly expressed genes. As such, a total of 52 and 51 genes were tested for differential expression in liver and blood respectively (see Table S1 for the list of genes tested and excluded). Six of the target genes

have not been annotated in the great tit genome and there was no detectable expression of PHOX2B. P-values obtained from the differential expression analyses were corrected for multiple comparisons using the Benjamini–Hochberg (BH) procedure and only genes determined to have a false discovery rate (FDR) < 0.05 were considered to be significant.

In order to visualize the expression profiles of the sampled individuals, we generated heatmaps (see ESM) of the regularized log-transformed count data using the "pheatmap" function (R., 2019). Counts of gene expression were clustered for the genes according to the similarity of expression profiles across different samples.

This study was carried out in accordance with Swedish legislation and approved by the Malmö-Lund animal ethics committee (Dnr M454 12:1).

Results

None of the 51 genes on which our analysis was focused were differentially expressed in blood and only one gene (BRCA1) was differentially expressed among the 52 genes tested in liver tissue between urban and rural great tits following p-value adjustment (see Table 1a and 1b, respectively, for the differential expression statistics of each of these genes). BRCA1 was expressed at significantly higher levels in rural, compared with urban birds in liver, but not blood tissues.

Discussion

Despite the increasing occurrence of epizootics of cancer observed in wild species (McAloose and Newton, 2009) and the broad distribution of oncogenic processes along the tree of life (Athena Aktipis et al., 2015), wildlife cancer is, for the moment, a largely unexplored topic (except for a few emblematic species such as the Tasmanian devil

(*Sarcophilus harrisii* (Ujvari et al., 2016)) or the sea turtle (*Chelonia mydas* (Duffy et al., 2018)). This lack of interest from the scientific community is explained by the misconception shared by many ecologists and evolutionary biologists until recently that only late-stage visually detectable cancers affect wild organisms, mostly after the end of the reproductive period. Many articles published over the last few years have challenged this view, and it is now admitted that the first cancerous cells appear early in life and that the community of cancer cells (i.e. oncobiota) is a major actor of evolutionary processes influencing host life-history traits and strategies (Vittecoq et al., 2013, Thomas et al., 2017, Pesavento et al., 2018, Giraudeau et al., 2018).

An intriguing question in this emerging field of study, with consequences for the conservation of wild species, concerns the ability of wild organisms inhabiting environments impacted by human activities to adjust their level of defenses against this pathology whose progression should be stimulated by, among other things, exposure to many carcinogenic pollutants (Vittecoq et al., 2018). Our study constitutes a first attempt to study this question in wild urban birds, in a population known to be exposed to higher levels of urban pollutant (i.e. nitric oxide, a marker of traffic-related air pollution) (Salmón et al., 2018a) known to be associated with cancer in humans (Cohen et al. 2019). While examining the expression of a large number of tumor-suppressor genes, we found negligible differences in the expression of tumor-suppressor genes between urban and rural great tits examined in blood and liver tissues. The only gene differentially expressed was BRCA1, with reduced levels of expression in urban birds. BRCA1 is involved in the maintenance of genome integrity by repairing damaged DNA and has been mainly associated with breast and prostate cancers so far in humans (Gorodetska *et al.* 2019). Given our limited knowledge on the consequences of a reduced expression of BRCA1 in liver, especially in wild birds, it's difficult to draw any conclusion based on this

result. However, we can hypothesize that this reduced expression might favor the development of oncogenic processes in urban birds.

One can argue that the sample size used in this study was too small to detect differences between populations, but due to the terminal nature of our sampling to get the liver samples and for obvious ethical reasons, we preferred to limit the number of individuals euthanized for this study. In addition, the sample size used here is common for this kind of study and (Watson et al., 2017) found large differences in the expression of genes related to immune activity, detoxification and repair machinery using the same transcriptome data and thus the same sample size. We can also exclude the hypothesis that rural birds were exposed to mutagenic substances, such as pesticides to explain the absence of significant differences observed in our study since our rural site was a water reserve area without any agricultural activity nearby.

Avian antitumor defenses have been mainly described in poultry, with a focus on commercially relevant diseases like the avian leucosis virus, which induces various neoplasias in chickens (Sironi et al., 2006). In this model system, transcriptome analyses have indicated a significant decrease of the expression of genes related to both immune defenses and antitumor pathways in spleens and tumors of susceptible birds (Zhang et al., 2016, Qiu et al., 2018), indicating that both mechanisms play an important role in avian cancer defenses. While in our study, antitumor genes were not expressed in higher levels in birds living in a potentially oncogenic environment, the role of increased expression of immune-related genes shown in the same individuals (Watson et al., 2017) could act as a first line of defense against the effects of oncogenic stressors. In accordance with life-history theory, in a short-lived animal such as the great tit, selection should favor investment in physiological defenses that increase short-term survival, at the expense of later-life performance and survival (Stearns, 2006). Additionally, in other studies of the same population (but with larger sample size) reveal

increased antioxidant defenses (Salmón et al., 2018a, 2018b), shorter telomeres of developing nestlings and selective disappearance of birds with short telomeres during their first year of life (Salmón et al., 2016, 2017). Together, these results provide evidence that the present urban environment is physiologically challenging and that only individuals with a "strong" physiological response survive. However, whether this also protect the surviving urban birds from developing cancer or if resources have been allocated to combat current physiological threats rather than to more long-term anti-cancer defenses, requires further studies.

Unfortunately, we do not know the movements between the studied populations and their surroundings. Thus, we cannot exclude that bird immigration influence the present findings and thereby prevent local adaptation against the proliferation of neoplasia.

In any cases, given that lifespan of urban birds can be prolonged due to reduced predation (Sepp et al., 2018), the lack of anti-cancer responses may be a greater cause of death in the future than previously acknowledged.

While future studies should confirm our results with more tumor-suppressor genes (and thus more anti-cancer mechanisms) examined and other tissues sampled (for example the kidney due to its important contribution in detoxification or the spleen for its role in the production of immune agents), our results suggest that wild birds do not up-regulate their anti-cancer defenses in urban environments. As repeatedly suggested over the last few years (Thomas et al. 2017, Vittecoq et al., 2018, Giraudeau et al., 2018, Sepp et al., 2019), this supports the idea that wild animals living in human impacted habitats might be at higher risk of developing oncogenic processes. An important methodological step allowing the detection of this pathology in non-terminal samples is now urgently needed to confirm this hypothesis and measure the potential unexplored consequences of pollution on wildlife cancer. Collaborative projects between different fields (medicine, animal ecology, evolution) appear to be the

necessary approach to use the extensive knowledge accumulated in human oncology in order to develop new cancer biomarkers usable with wild animals.

It is now admitted that oncogenic processes are widespread among metazoan species with potential consequences on their life history strategies and, in some cases, on their population dynamics as well as on ecosystem functioning. The worldwide modifications of natural environments and in particular the release of mutagenic pollutants might exacerbate this process, and wildlife neoplasia should thus be considered as an important player in the reorganization of ecosystems currently happening under the pressure of human activities.

Data accessibility. All data are available in Dryad.

Authors' contributions. H.W., C.I., T.S. and M.G. conceived and designed the study. C.I. and H.W. performed post-mortems and H.W. isolated RNA. D.P. carried out the alignment and generation of read counts. H.W. and O.V. carried out downstream analyses. M.G. wrote the manuscript with input from all other authors. All authors gave final approval for publication.

Competing interests. We declare we have no competing interests.

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Table 1 Results of differential expression analyses of tumor suppressor genes in liver (A) and blood (B) tissues of urban and rural great tits. LogFC = log2 fold-change (negative values indicate higehr expression in rural birds), LogCPM = average log counts per million; LR = likelihood ratio statistic; P-value = unadjusted P value; FDR = false discovery rate, Mean Expr. = average expression level in urban and rural birds respectively. Genes with missing data were either not included in the annotated gene set or had no mapped reads. Genes marked in italics are differentially expressed following p-value adjustment.

Table 1A.

Gene	**Classification**	**logFC**	**LR**	**P-Value**	**FDR**	**Mean Expr. urban**	**Mean Expr. rural**
BRCA1	***Caretaker***	***-1.41***	***12.52***	***0.0004***	***0.0210***	***419.00***	***1093.17***
FLT3	Gatekeeper	1.23	6.26	0.0124	0.3212	1120.33	467.17
BLM	Caretaker	0.66	2.75	0.0970	0.8653	1209.17	738.00
BMPR1A	Gatekeeper	-0.45	1.70	0.1922	0.8653	888.33	1314.83
BRCA2	Caretaker	-0.32	1.26	0.2613	0.8653	1169.33	1480.00
CEBPA	Gatekeeper	0.27	1.66	0.1976	0.8653	9966.33	8444.33
ERCC4	Caretaker	-0.35	1.06	0.3034	0.8653	833.67	1095.50
EXT1	Gatekeeper	-0.33	1.01	0.3149	0.8653	1117.50	1408.50
EXT2	Gatekeeper	-0.27	0.62	0.4319	0.8653	5197.50	6708.00
FANCC	Caretaker	0.46	0.62	0.4299	0.8653	119.50	87.17
FANCD2	Caretaker	0.64	0.78	0.3777	0.8653	73.83	45.50
FANCE	Caretaker	0.36	1.03	0.3112	0.8653	3818.83	2979.67
FANCF	Caretaker	-0.85	2.40	0.1215	0.8653	73.00	130.33
FANCG	Caretaker	0.57	1.04	0.3075	0.8653	181.17	118.17
FH	Gatekeeper	0.54	2.43	0.1193	0.8653	23016.33	17341.00
GATA1	Gatekeeper	0.49	0.60	0.4383	0.8653	232.00	161.33
KLF6	Gatekeeper	1.02	1.87	0.1719	0.8653	669.17	388.00
NBN	Caretaker	0.36	1.46	0.2277	0.8653	1628.67	1267.83
NF1	Gatekeeper	0.46	1.21	0.2705	0.8653	3703.50	2694.17
NF2	Gatekeeper	0.28	0.53	0.4659	0.8653	843.00	691.33

PMS1	Caretaker	-0.32	0.93	0.3344	0.8653	2027.33	2692.83
PTEN	Gatekeeper	0.20	0.56	0.4552	0.8653	5434.83	4997.67
SDHB	Gatekeeper	0.22	0.82	0.3645	0.8653	3362.33	3018.67
SMARCB1	Gatekeeper	0.27	1.11	0.2926	0.8653	1986.17	1667.00
VHL	Gatekeeper	-0.20	0.56	0.4533	0.8653	5943.50	7199.83
WRN	Caretaker	0.34	1.44	0.2309	0.8653	1692.00	1330.17
XPA	Caretaker	-0.32	2.08	0.1496	0.8653	8957.50	11491.33
XPC	Caretaker	-0.16	0.63	0.4276	0.8653	3895.00	4426.50
APC	Gatekeeper	0.08	0.06	0.8040	0.9162	1400.00	1349.33
ATM	Caretaker	-0.18	0.43	0.5140	0.9162	1556.50	1802.17
CDH1	Gatekeeper	0.06	0.08	0.7805	0.9162	13177.50	13069.50
CHEK2	Caretaker	0.06	0.03	0.8709	0.9162	494.00	465.17
CYLD	Gatekeeper	0.09	0.16	0.6876	0.9162	2308.67	2173.00
DDB2	Caretaker	-0.08	0.02	0.8810	0.9162	406.33	414.67
ERCC3	Caretaker	0.06	0.07	0.7890	0.9162	2242.33	2166.33
FANCA	Caretaker	0.25	0.09	0.7669	0.9162	64.17	51.33
FLT4	Gatekeeper	-0.10	0.10	0.7541	0.9162	869.33	967.00
HNF1A	Gatekeeper	0.04	0.03	0.8615	0.9162	2428.00	2390.00
MAP2K4	Gatekeeper	-0.13	0.22	0.6419	0.9162	2903.00	3309.50
MEN1	Gatekeeper	0.21	0.33	0.5678	0.9162	624.83	527.67
MLH1	Caretaker	0.06	0.05	0.8229	0.9162	2089.33	2006.83
MSH2	Caretaker	0.19	0.37	0.5411	0.9162	721.33	651.00
MSH6	Caretaker	-0.06	0.02	0.8777	0.9162	238.17	245.67
MUTYH	Caretaker	-0.11	0.05	0.8156	0.9162	358.00	385.33
PMS2	Caretaker	-0.10	0.08	0.7726	0.9162	763.50	829.67
RB1	Gatekeeper	-0.14	0.16	0.6870	0.9162	4156.17	5007.67
SBDS	Gatekeeper	-0.12	0.21	0.6497	0.9162	3361.67	3856.17
SDHD	Gatekeeper	-0.13	0.31	0.5776	0.9162	19594.17	22325.83
SMAD4	Gatekeeper	0.34	0.15	0.6981	0.9162	123.67	96.17
STK11	Gatekeeper	0.24	0.23	0.6342	0.9162	775.17	637.00

GPC3	Gatekeeper	-0.01	0.00	0.9865	0.9865	120.67	123.33
SUFU	Gatekeeper	-0.01	0.00	0.9708	0.9865	1089.17	1097.50
CDKN2A	Gatekeeper	NA	NA	NA	NA	NA	NA
ERCC2	Caretaker	NA	NA	NA	NA	NA	NA
ERCC5	Caretaker	NA	NA	NA	NA	NA	NA
PHOX2B	Gatekeeper	NA	NA	NA	NA	0.00	0.00
RECQL4	Caretaker	NA	NA	NA	NA	NA	NA
SDHC	Gatekeeper	NA	NA	NA	NA	NA	NA
TP53	Caretaker	NA	NA	NA	NA	NA	NA

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Row.names	**Classification**	**logFC**	**LR**	**P-Value**	**FDR**	**Mean Expr. urban**	**Mean Expr. rural**
KLF6	Gatekeeper	1.32	6.83	0.0090	0.4573	7514.83	2699.00
ATM	Caretaker	0.54	1.63	0.2023	0.7723	326.00	199.20
CDH1	Gatekeeper	-2.21	3.86	0.0494	0.7723	74.67	347.40
CYLD	Gatekeeper	0.67	3.01	0.0826	0.7723	1027.33	569.40
ERCC4	Caretaker	0.64	2.16	0.1419	0.7723	219.17	121.60
EXT1	Gatekeeper	1.12	2.83	0.0926	0.7723	139.00	50.80
FANCA	Caretaker	1.12	1.46	0.2272	0.7723	14.33	5.40
FANCC	Caretaker	1.42	1.73	0.1882	0.7723	14.00	5.00
FH	Gatekeeper	-0.63	2.33	0.1266	0.7723	880.17	1324.80
FLT4	Gatekeeper	0.86	2.55	0.1103	0.7723	140.17	69.60
HNF1A	Gatekeeper	-0.61	2.52	0.1127	0.7723	249.50	364.40
MSH2	Caretaker	1.00	1.85	0.1742	0.7723	77.83	36.60
MSH6	Caretaker	0.74	1.54	0.2140	0.7723	33.67	17.80
NBN	Caretaker	0.53	1.96	0.1615	0.7723	484.00	291.60
PMS2	Caretaker	0.69	2.45	0.1178	0.7723	297.50	156.00
CHEK2	Caretaker	0.47	1.31	0.2525	0.8048	567.17	354.40
FANCF	Caretaker	-0.78	1.20	0.2738	0.8214	9.00	15.40
APC	Gatekeeper	0.33	0.99	0.3208	0.8739	3033.00	2056.40

BMPR1A	Gatekeeper	-0.68	0.88	0.3483	0.8739	26.33	42.40
BRCA2	Caretaker	0.35	0.80	0.3708	0.8739	528.33	351.80
CEBPA	Gatekeeper	-0.41	0.66	0.4158	0.8739	269.67	336.00
FANCE	Caretaker	0.37	0.61	0.4355	0.8739	4627.17	3468.40
FANCG	Caretaker	0.27	0.51	0.4768	0.8739	907.50	741.80
GATA1	Gatekeeper	-0.20	0.43	0.5140	0.8739	17552.17	19833.20
MAP2K4	Gatekeeper	0.29	0.46	0.4987	0.8739	1504.67	1278.60
MLH1	Caretaker	0.36	0.57	0.4509	0.8739	567.50	411.20
NF1	Gatekeeper	-0.31	0.64	0.4237	0.8739	4124.83	4798.00
SMAD4	Gatekeeper	-0.45	0.77	0.3791	0.8739	344.83	436.40
STK11	Gatekeeper	-0.22	0.45	0.5003	0.8739	3353.00	3806.20
SUFU	Gatekeeper	-0.30	0.94	0.3315	0.8739	4010.83	4664.80
BLM	Caretaker	-0.16	0.22	0.6378	0.9393	5363.17	5824.00
ERCC3	Caretaker	0.15	0.28	0.5984	0.9393	4039.00	3470.40
FANCD2	Caretaker	-0.25	0.21	0.6499	0.9393	183.83	211.00
FLT3	Gatekeeper	0.27	0.19	0.6630	0.9393	58.67	45.00
SDHB	Gatekeeper	0.17	0.21	0.6470	0.9393	625.67	542.60
XPA	Caretaker	0.12	0.22	0.6389	0.9393	9170.33	7879.60
BRCA1	Caretaker	-0.19	0.14	0.7048	0.9715	121.50	121.00
DDB2	Caretaker	-0.05	0.01	0.9048	0.9950	471.00	439.00
EXT2	Gatekeeper	0.08	0.05	0.8291	0.9950	1278.83	1063.60
MEN1	Gatekeeper	0.07	0.02	0.8870	0.9950	191.50	158.20
MUTYH	Caretaker	0.06	0.01	0.9130	0.9950	88.00	71.60
NF2	Gatekeeper	0.15	0.11	0.7420	0.9950	169.83	134.60
PMS1	Caretaker	-0.04	0.01	0.9231	0.9950	274.50	252.40
PTEN	Gatekeeper	-0.07	0.07	0.7928	0.9950	4607.33	4593.00
RB1	Gatekeeper	0.02	0.01	0.9400	0.9950	9445.00	8756.80
SBDS	Gatekeeper	0.00	0.00	0.9950	0.9950	6287.00	6347.20
SDHD	Gatekeeper	0.06	0.03	0.8650	0.9950	4422.50	4121.80

SMARCB1	Gatekeeper	-0.01	0.00	0.9715	0.9950	1879.50	1788.80
VHL	Gatekeeper	0.06	0.05	0.8214	0.9950	8967.33	8265.60
WRN	Caretaker	0.06	0.04	0.8475	0.9950	2787.67	2467.40
XPC	Caretaker	-0.01	0.00	0.9757	0.9950	2009.33	1908.40
CDKN2A	Gatekeeper	NA	NA	NA	NA	NA	NA
ERCC2	Caretaker	NA	NA	NA	NA	NA	NA
ERCC5	Caretaker	NA	NA	NA	NA	NA	NA
GPC3	Gatekeeper	NA	NA	NA	NA	0.00	1.60
PHOX2B	Gatekeeper	NA	NA	NA	NA	0.00	0.00
RECQL4	Caretaker	NA	NA	NA	NA	NA	NA
SDHC	Gatekeeper	NA	NA	NA	NA	NA	NA
TP53	Caretaker	NA	NA	NA	NA	NA	NA