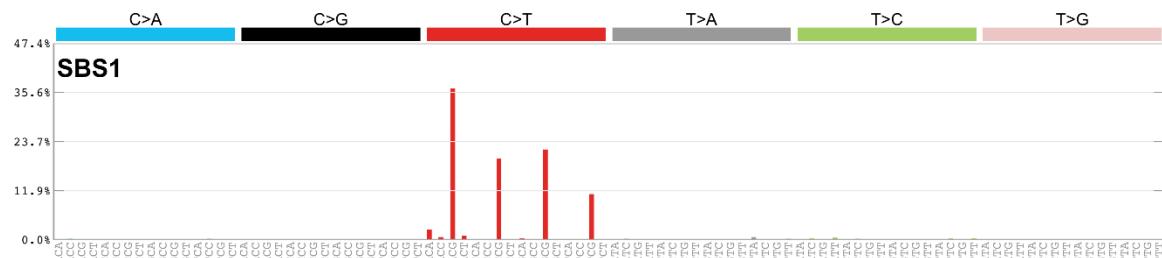


Mutational Signatures Vignettes Draft

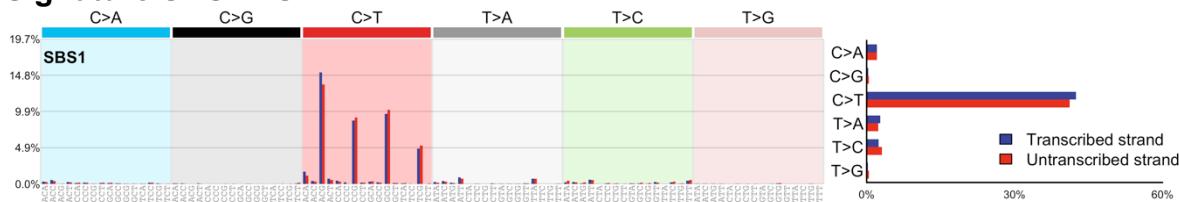
Single Base Substitution (SBS) Signatures

20 March 2018

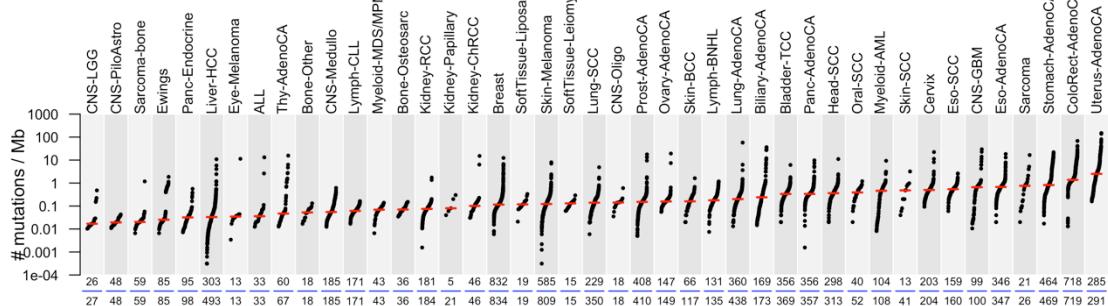
Signature SBS1 (v3.0)



Signature SBS1-TSB



Cancer types in which the signature is found



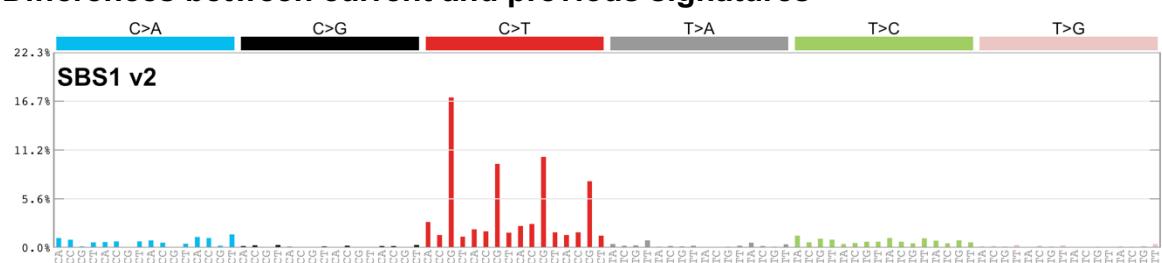
Proposed aetiology

An endogenous mutational process initiated by spontaneous or enzymatic deamination of 5-methylcytosine to thymine which generates G:T mismatches in double stranded DNA. Failure to detect and remove these mismatches prior to DNA replication results in fixation of the T substitution for C.

Associated mutation classes and signatures

The activity of signature SBS1 is closely correlated with the activity of signature SBS5 in many types of human cancer.

Differences between current and previous signatures

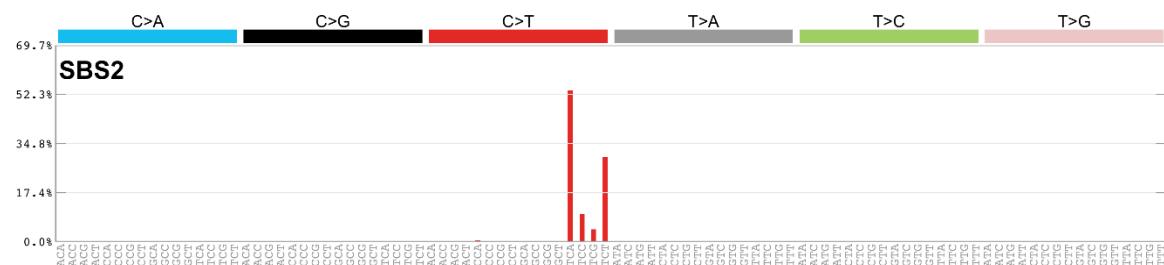


The contribution of C>T mutations not at NCG trinucleotides and of mutations other than C>T has diminished markedly compared to previous versions which were likely more contaminated by Signature SBS5 and other signatures. The cosine similarity between the prior and current versions of signature SBS1 is 0.95.

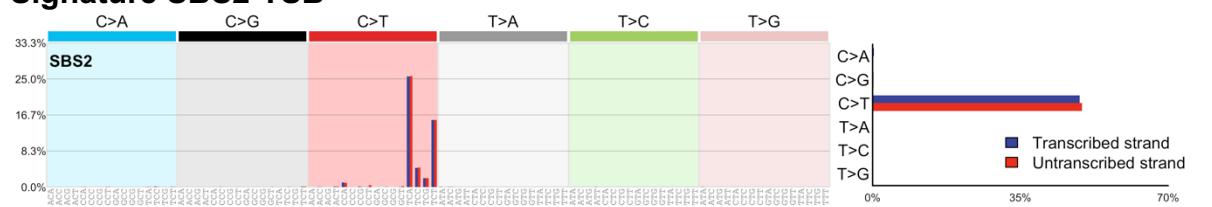
Comments

Signature SBS1 is clock-like in that the number of mutations in most cancers and normal cells correlates with the age of the individual. Rates of acquisition of Signature SBS1 mutations over time differ markedly between different cancer types and different normal cell types. These differences correlate with estimated rates of stem cell division in different tissues and Signature SBS1 may therefore be a cell division/mitotic clock.

Signature SBS2 (v3.0)

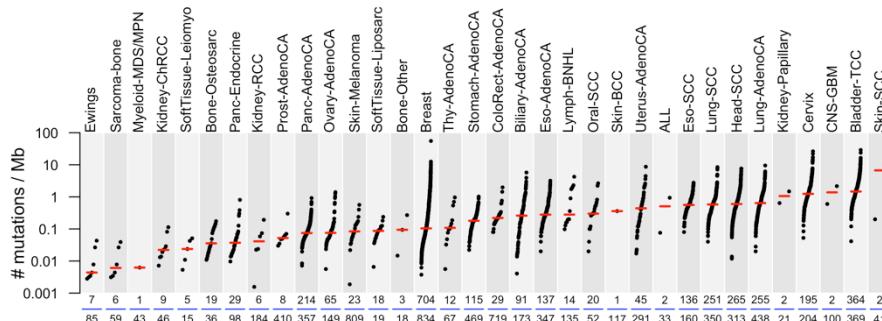


Signature SBS2-TSB



Transcriptional strand bias of mutations in exons (not shown) which is not present or is weaker in introns.

Cancer types in which the signature is found



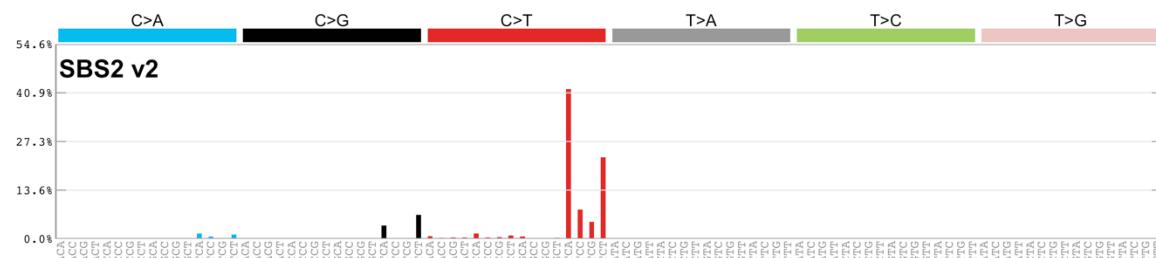
Proposed aetiology

Attributed to activity of the AID/APOBEC family of cytidine deaminases on the basis of similarities in the sequence context of cytosine mutations caused by APOBEC enzymes in experimental systems. APOBEC3A is probably responsible for most mutations in human cancer, although APOBEC3B may also contribute (these differ in the sequence context two bases 5' to the mutated cytosine, see 1,536 mutation classification signature extraction). Signature SBS2 mutations may be generated directly by DNA replication across uracil or by error prone polymerases replicating across abasic sites generated by base excision repair removal of uracil.

Associated mutation classes and signatures

Signature SBS2 is closely associated with signature SBS13. Signature SBS2 is associated with doublet base substitution mutational signature DBS11, which is characterised predominantly by CC>TT doublet base substitutions as well as other CC>NN doublet base substitutions.

Differences between current and previous profiles

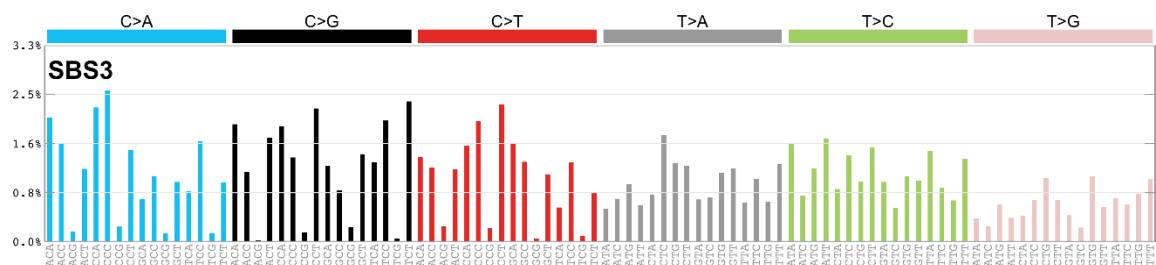


The contributions of C>G and C>A mutations at TCN trinucleotides have diminished markedly compared to previous profiles indicating reduced contamination by Signature SBS13. The cosine similarity between the prior and current versions of signature SBS2 is 0.99.

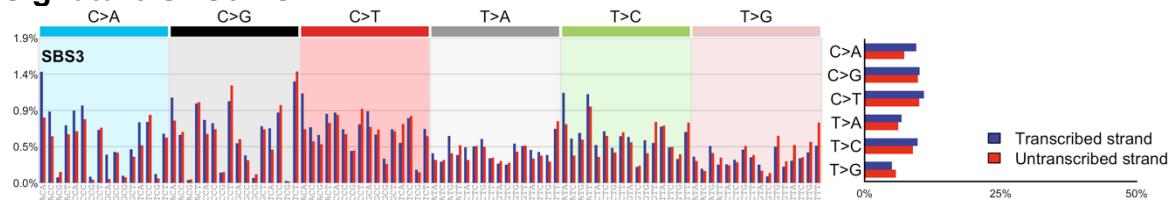
Comments

Signature SBS2 is usually found in the same samples as signature SBS13. It has been proposed that activation of AID/APOBEC cytidine deaminases in cancer may be due to previous viral infection, retrotransposon jumping, or tissue inflammation. Currently, there is limited evidence to support these hypotheses. Germline polymorphisms involving APOBEC3A and APOBEC3B are associated with predisposition to breast and bladder cancer as well as with mutation burdens of signatures SBS2 and SBS13. Mutations of similar patterns to signatures SBS2 and SBS13 are commonly found in the phenomenon of local hypermutation present in some cancers, known as kataegis, implicating AID/APOBEC enzymes in this process as well.

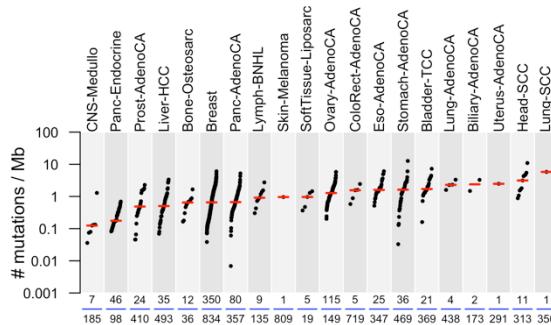
Signature SBS3 (v3.0)



Signature SBS3-TSB



Cancer types in which the signature is found



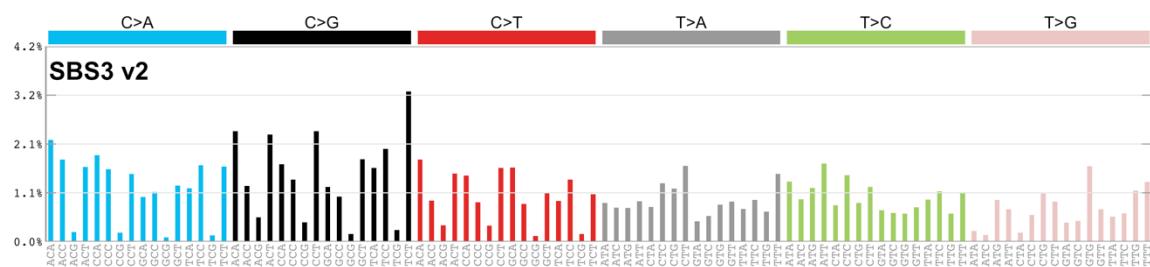
Proposed aetiology

Defective homologous recombination-based DNA damage repair which manifests predominantly as small indels and genome rearrangements due to abnormal double strand break repair but also in the form of this base substitution signature.

Associated mutation classes and signatures

Associated with small deletions of >5bp with extended stretches of overlapping microhomology at breakpoint junctions. Also associated with multiple genome rearrangement mutational signatures; short tandem duplications (1-10kb); longer tandem duplications (>100kb); deletions (1-10kb). Signature SBS3 is associated with indel signature ID6.

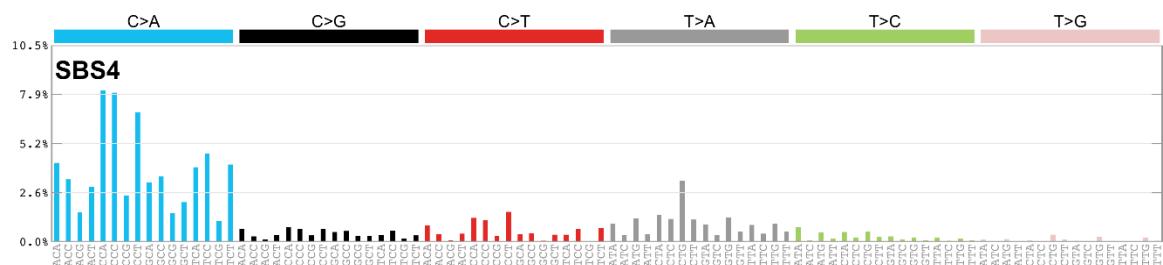
Differences between current and previous profiles



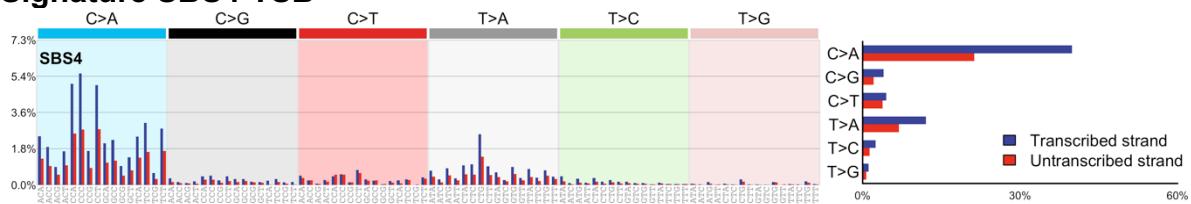
Comments

Signature 3 is strongly associated with germline and somatic *BRCA1* and *BRCA2* mutations and *BRCA1* promoter methylation in breast, pancreatic, and ovarian cancers. In pancreatic cancer, responders to platinum therapy usually exhibit signature 3 mutations. Together with associated indel and rearrangement signatures, signature 3 has been proposed as a predictor of defective homologous recombination-based repair and thus of response to therapies exploiting this repair defect. The cosine similarity between the prior and current versions of signature SBS3 is 0.96.

Signature SBS4 (v3.0)

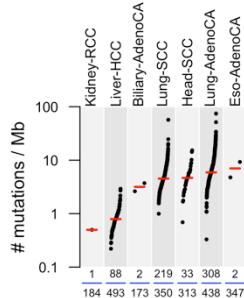


Signature SBS4-TSB



Signature 4 exhibits transcriptional strand bias for C>A (and also T>A mutations) with more mutated G than C bases on the untranscribed strands of genes consistent with damage to guanine and activity of transcription-coupled nucleotide excision repair and/or DNA damage.

Cancer types in which the signature is found



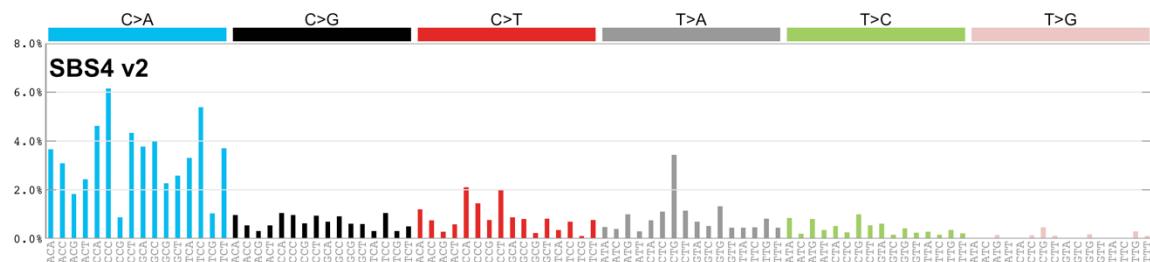
Proposed aetiology

Associated with tobacco smoking. Its profile is similar to the mutational spectrum observed in experimental systems exposed to tobacco carcinogens such as benzo[a]pyrene. Signature 4 is, therefore, likely due to direct DNA damage by tobacco smoke mutagens.

Associated mutation classes and signatures

Associated with indel signature ID3 characterised by single base deletions of predominantly C. Also, associated with doublet base substitution signature DBS2 characterised predominantly by CC>AA mutations.

Differences between current and previous profiles

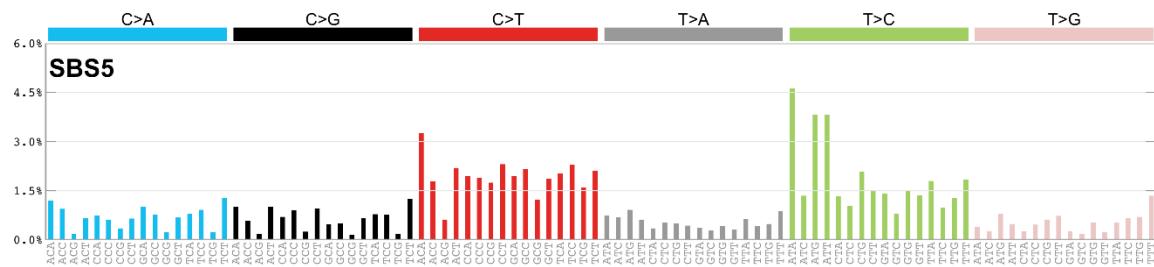


The cosine similarity between the prior and current versions of signature SBS4 is 0.94.

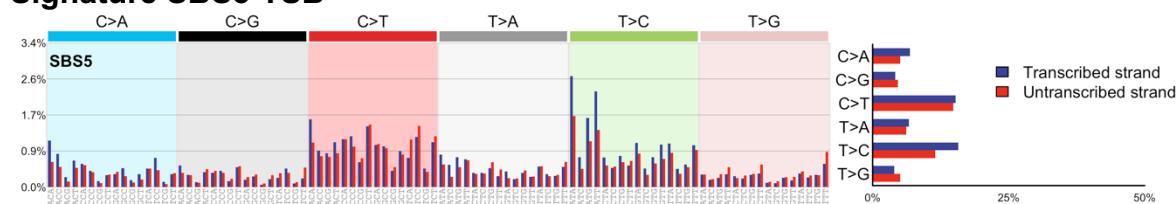
Comments

Although tobacco smoking causes multiple cancer types in addition to lung and head and neck, signature SBS4 has not been detected in many of these. Signature SBS29 is found in cancers associated with tobacco chewing and appears different from signature SBS4.

Signature SBS5 (v3.0)

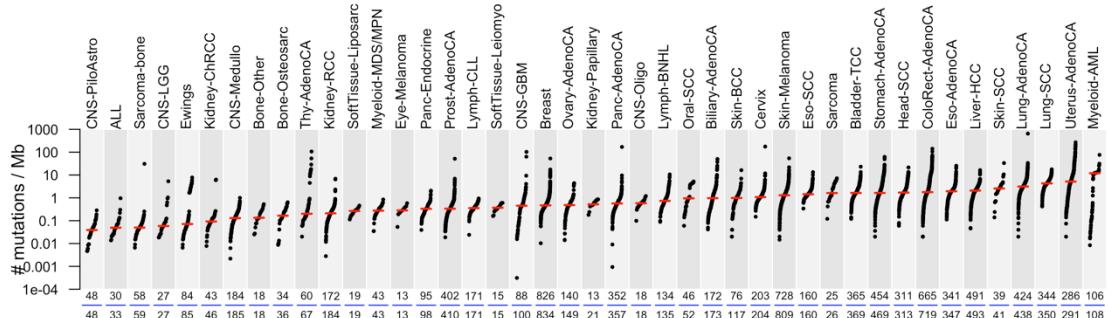


Signature SBS5-TSB



Transcriptional strand bias for T>C substitutions at ATN context with more mutated A than T bases on the untranscribed strands of genes compatible with damage to adenine and activity of transcription-coupled nucleotide excision repair and/or DNA damage.

Cancer types in which the signature is found



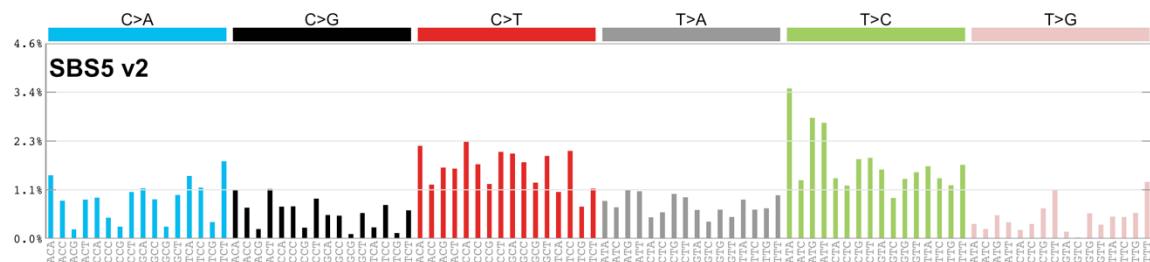
Proposed aetiology

Unknown. Signature SBS5 mutational burden is enriched in bladder cancer samples with ERCC5 mutations. The rate of signature SBS5 can be elevated due to tobacco smoking in many cancer types.

Associated mutation classes and signatures

N/A

Differences between current and previous profiles

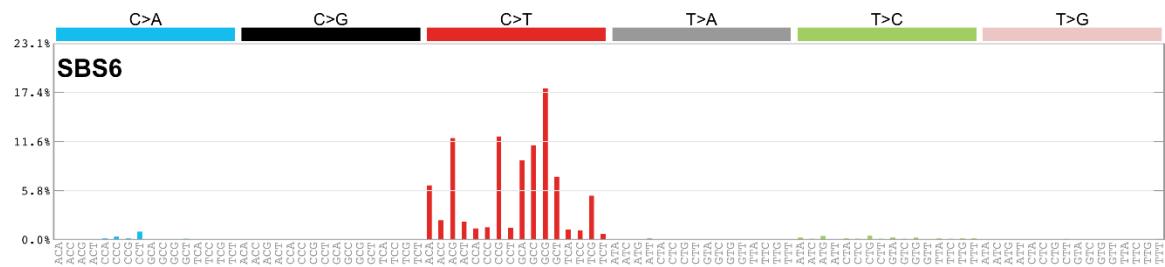


The pattern of signature SBS5 exhibits less contamination by signature SBS1. The cosine similarity between the prior and current versions of signature SBS5 is 0.96.

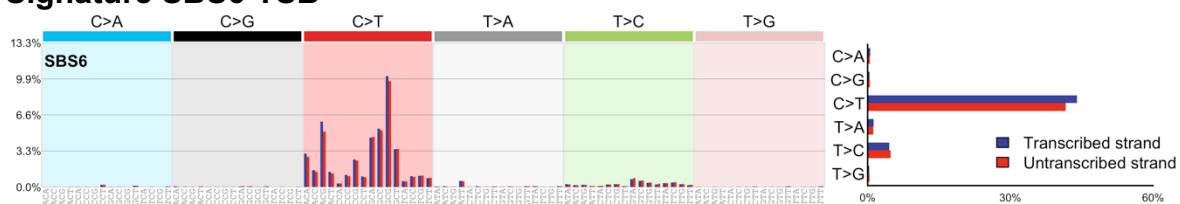
Comments

Clock-like in that the number of mutations in most cancers and normal cells correlates with the age of the individual. Rates of acquisition of signature SBS5 mutations over time differ between different cancer types and different normal cell types. These differences do not clearly correlate with estimated rates of stem cell division in different tissues nor with signature SBS1 mutation rates.

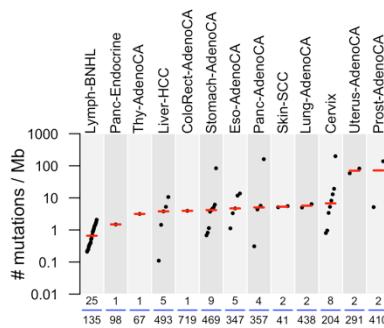
Signature SBS6 (v3.0)



Signature SBS6-TSB



Cancer types in which the signature is found



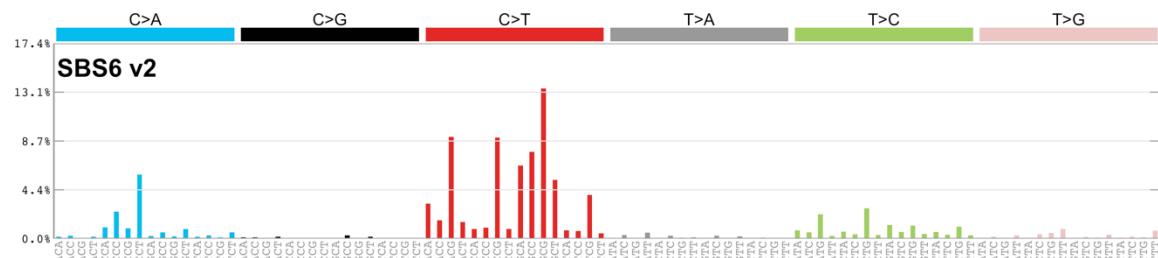
Proposed aetiology

Signature SBS6 is associated with defective DNA mismatch repair and is found in microsatellite unstable tumours.

Associated mutation classes and signatures

Signature SBS6 is associated with large numbers of small (usually 1bp) insertions and deletions at mono/polynucleotide repeats and particularly with indel signatures ID1 and ID2.

Differences between current and previous profiles

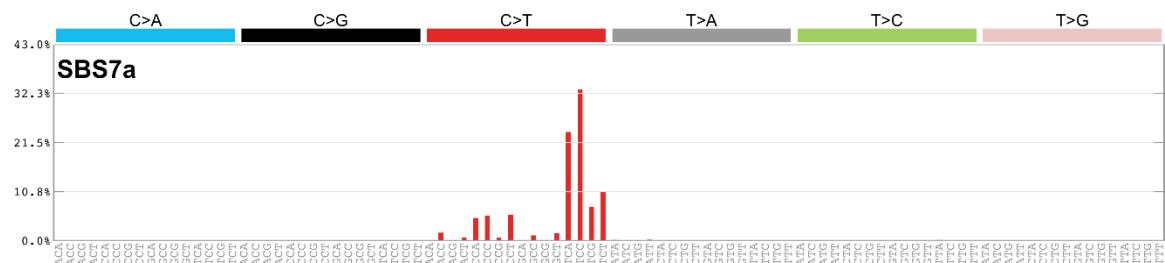


The pattern of signature SBS6 exhibits less contamination by other DNA mismatch repair deficiency signatures. The cosine similarity between the prior and current versions of signature SBS6 is 0.95.

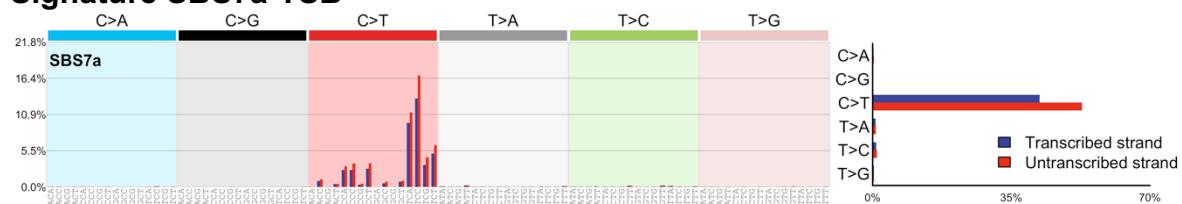
Comments

Comments
Signature SBS6 is one of seven mutational signatures associated with defective DNA mismatch repair (MSI) and is often found in the same samples as other MSI associated signatures: signatures SBS14, SBS15, SBS20, SBS21, SBS26, and SBS44.

Signature SBS7a (v3.0)

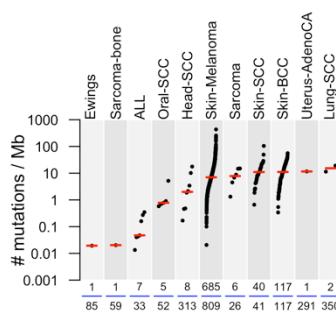


Signature SBS7a-TSB



Transcriptional strand bias with more mutated C than G bases on untranscribed strands of genes compatible with damage to cytosine and activity of transcription-coupled nucleotide excision repair and/or DNA damage.

Cancer types in which the signature is found



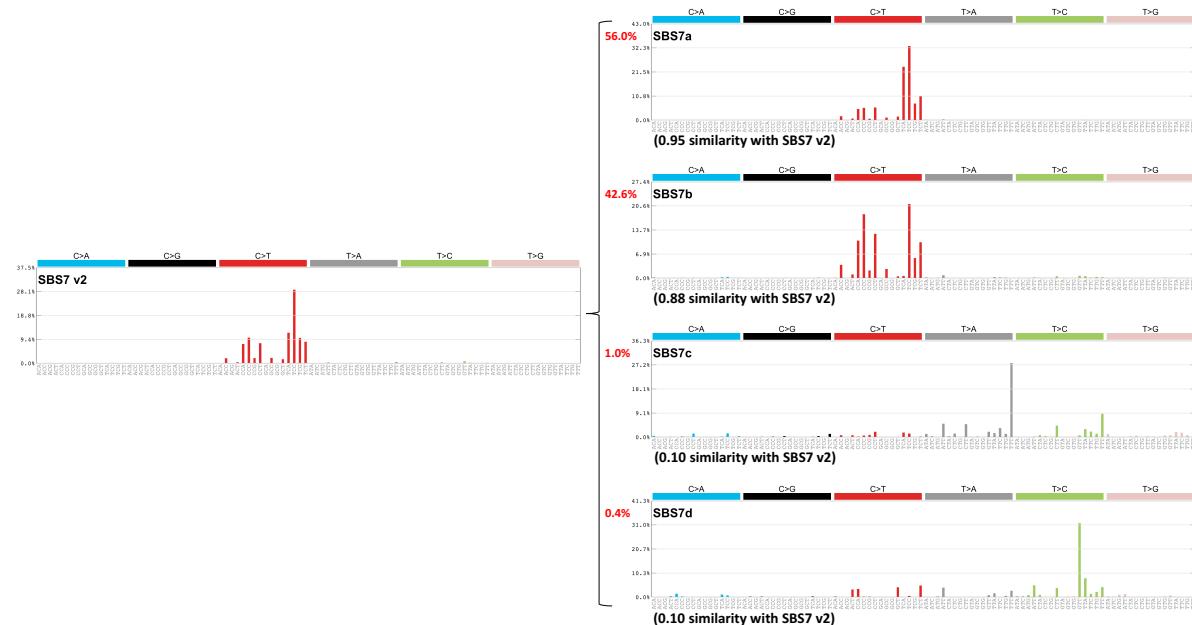
Proposed aetiology

Signatures SBS7a/b/c/d are found in cancers of the skin from sun exposed areas, therefore, these are likely to be due to exposure to ultraviolet light. Signature SBS 7a may possibly be the consequence of just one of the two major known UV photoproducts, cyclobutane pyrimidine dimers or 6-4 photoproducts, although there is no evidence for this hypothesis and it is unclear which of these photoproducts may be responsible.

Associated mutation classes and signatures

Signature SBS7a is associated with signature SBS7b/c/d and these signatures are commonly found in the same samples. Signature SBS7a is associated with doublet base nucleotide signature DBS1, which exhibits predominately CC>TT mutations. Signature SBS7a is also associated with indel signature ID13, which predominately generates single base thymine deletions.

Differences between current and previous profiles

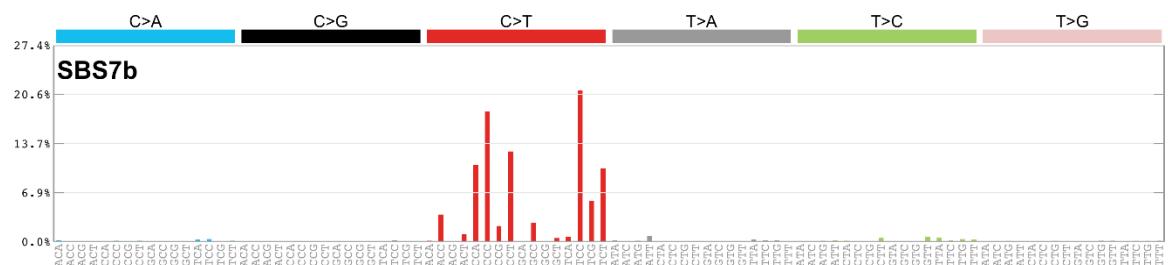


The larger number of analysed samples allow splitting of signature SBS7 into four distinct components, termed, signatures SBS7a/b/c/d, that almost ideally recapitulate the prior pattern signature SBS7.

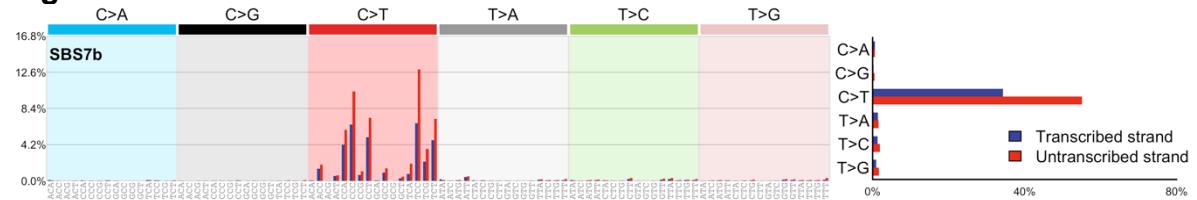
Comments

N/A

Signature SBS7b (v3.0)

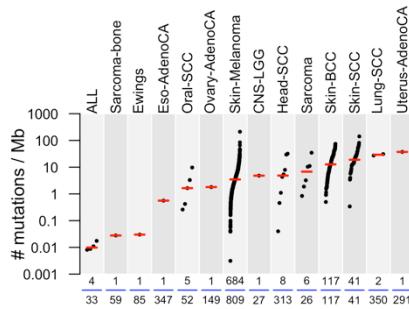


Signature SBS7b-TSB



Transcriptional strand bias with more mutated C than G bases on untranscribed strands of genes compatible with damage to cytosine and activity of transcription-coupled nucleotide excision repair and/or DNA damage.

Cancer types in which the signature is found



Proposed aetiology

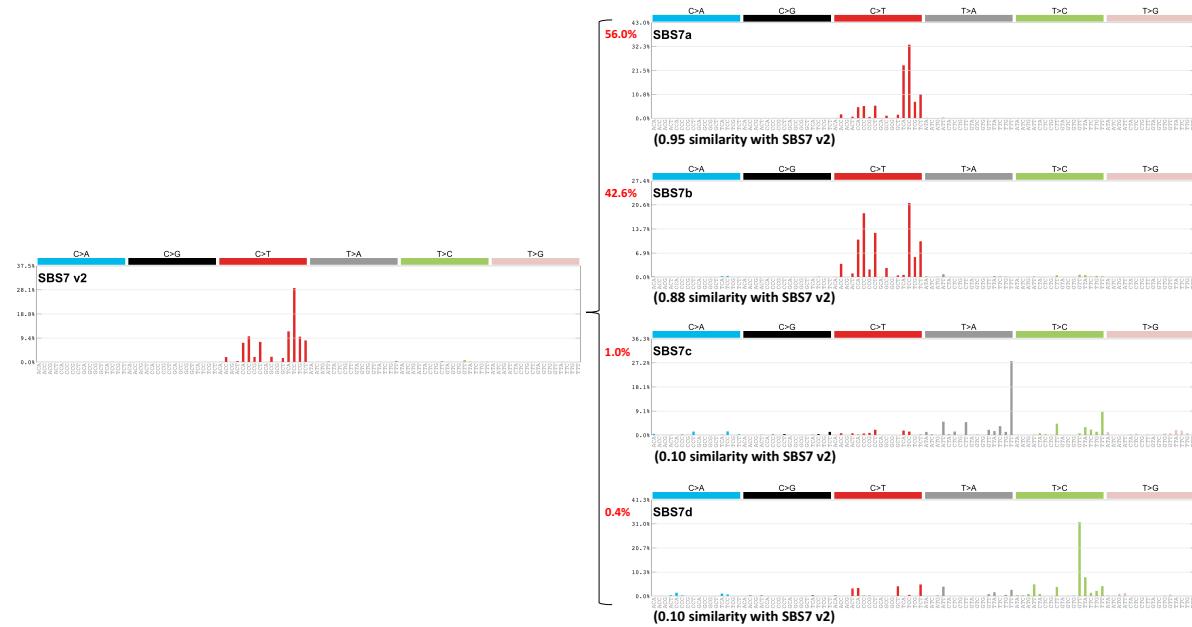
Signatures SBS7a/b/c/d are found in cancers of the skin from sun exposed areas, therefore, these are likely to be due to exposure to ultraviolet light. Signature SBS7b may possibly be the consequence of just one of the two major known UV photoproducts, cyclobutane pyrimidine dimers or 6-4 photoproducts, although there is no evidence for this hypothesis and it is unclear which of these photoproducts may be responsible.

Associated mutation classes and signatures

Signature SBS7b is associated with signature SBS7a/c/d and these signatures are commonly found in the same samples. Signature SBS7b is associated with doublet base nucleotide signature DBS1, which exhibits predominately CC>TT mutations.

Signature SBS7b is also associated with indel signature ID13, which predominately generates single base thymine deletions.

Differences between current and previous profiles

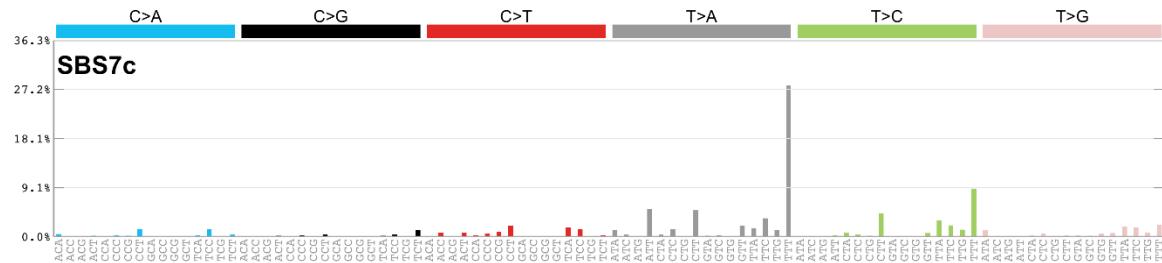


The larger number of analysed samples allow splitting of signature SBS7 into four distinct components, termed, signatures SBS7a/b/c/d, that almost ideally recapitulate the prior pattern signature SBS7.

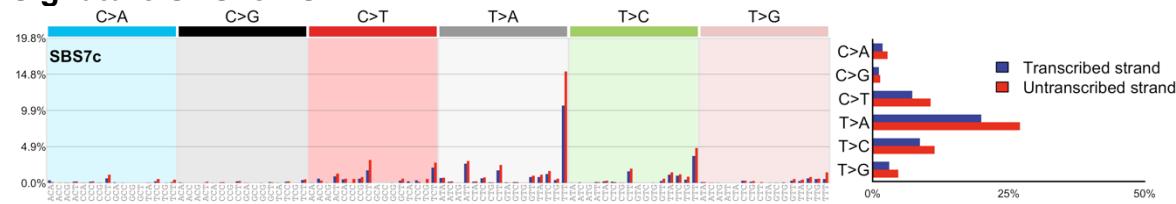
Comments

N/A

Signature SBS7c (v3.0)

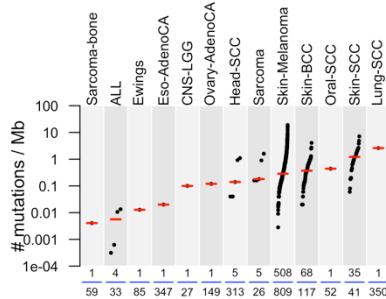


Signature SBS7c-TSB



Transcriptional strand bias with more mutated T than A bases on untranscribed strands compatible with damage to thymidine and activity of transcription-coupled nucleotide excision repair and/or DNA damage.

Cancer types in which the signature is found



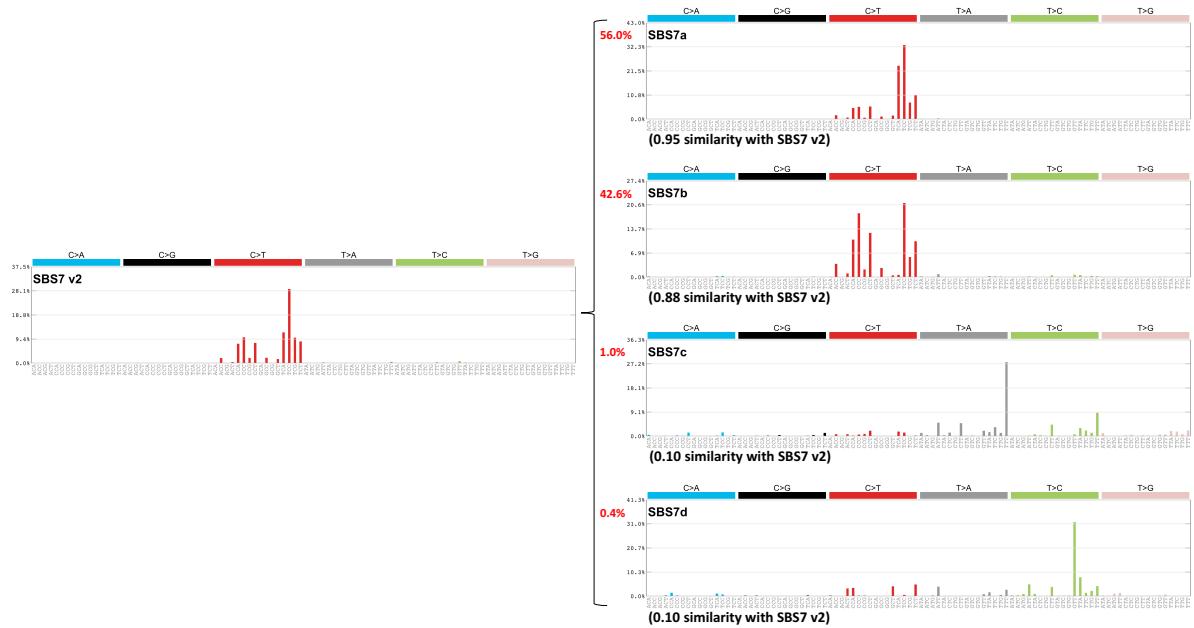
Proposed aetiology

Signatures SBS7a/b/c/d are found in cancers of the skin from sun exposed areas, therefore, these are likely to be due to exposure to ultraviolet light. Signature SBS7c is possibly the consequence of translesion DNA synthesis by enzymes with propensity to insert T, rather than A, opposite ultraviolet induced thymidine and cytidine photodimers. The preponderance of T>A rather than T>C mutations may reflect the heavier burden of thymidine compared to cytidine dimers induced by UV light.

Associated mutation classes and signatures

Signature SBS7c is associated with signature SBS7a/b/d and these signatures are commonly found in the same samples.

Differences between current and previous profiles

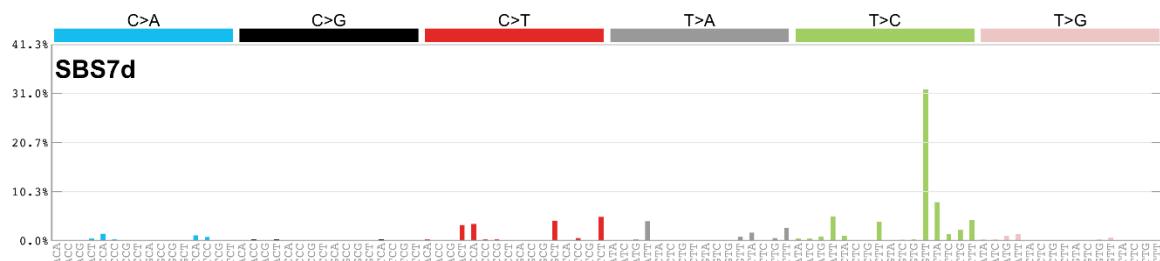


The larger number of analysed samples allow splitting of signature SBS7 into four distinct components, termed, signatures SBS7a/b/c/d, that almost ideally recapitulate the prior pattern signature SBS7.

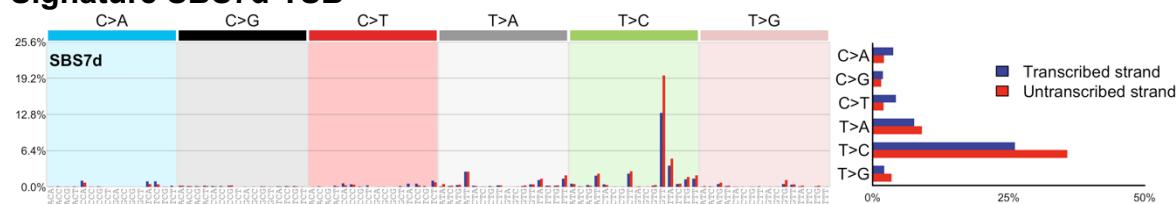
Comments

N/A

Signature SBS7d (v3.0)

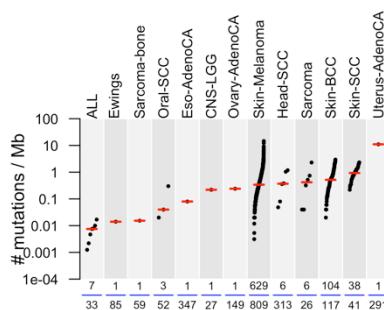


Signature SBS7d-TSB



Transcriptional strand bias with more mutated T than A on untranscribed strands of genes compatible with damage to thymidine and activity of transcription-coupled nucleotide excision repair and/or DNA damage.

Cancer types in which the signature is found



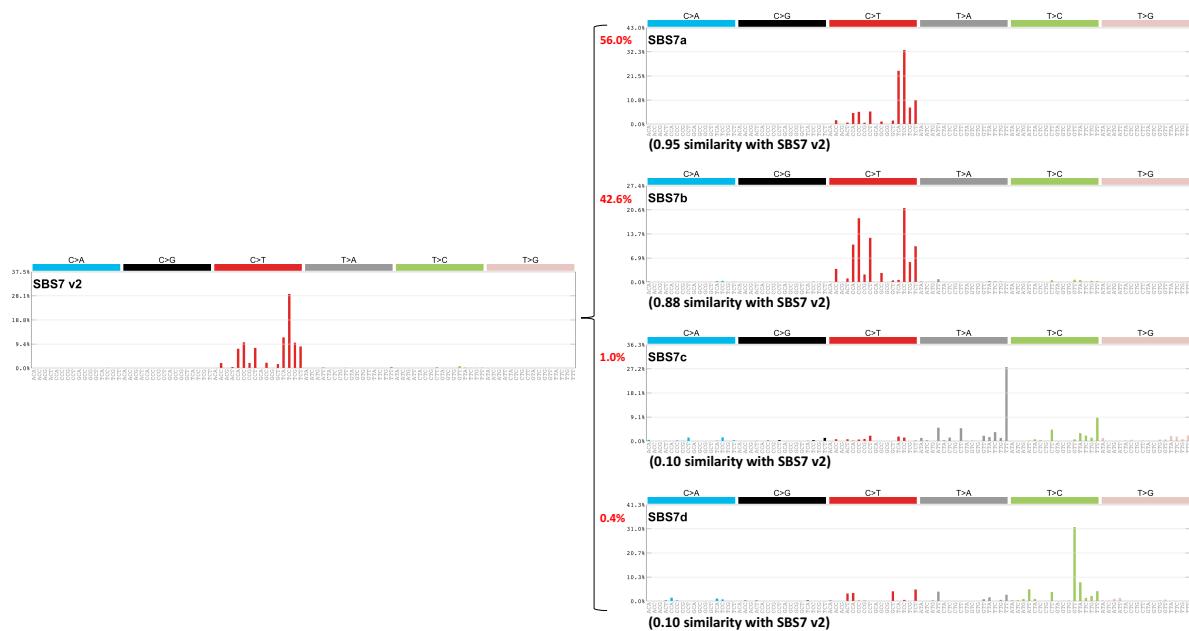
Proposed aetiology

Signatures SBS7a/b/c/d are found in cancers of the skin from sun exposed areas, therefore, these are likely to be due to exposure to ultraviolet light. Signature SBS7d is possibly the consequence of translesion DNA synthesis by error-prone polymerases with greater propensity to insert G, rather than A, opposite UV light induced thymidine and cytidine photodimers.

Associated mutation classes and signatures

Signature SBS7d is associated with signature SBS7a/b/c and these signatures are commonly found in the same samples.

Differences between current and previous profiles

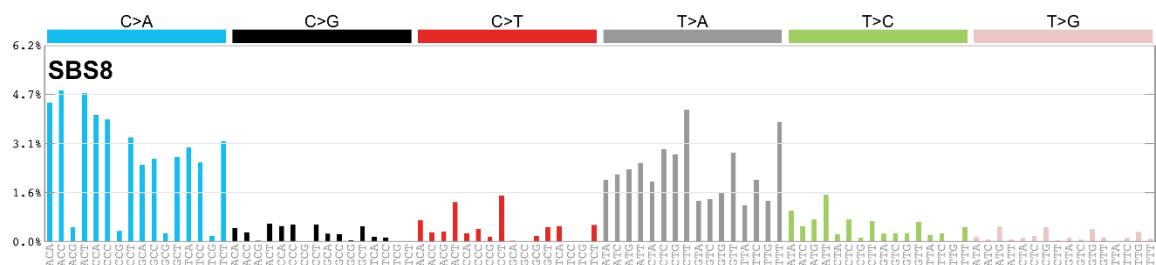


The larger number of analysed samples allow splitting of signature SBS7 into four distinct components, termed, signatures SBS7a/b/c/d, that almost ideally recapitulate the prior pattern signature SBS7.

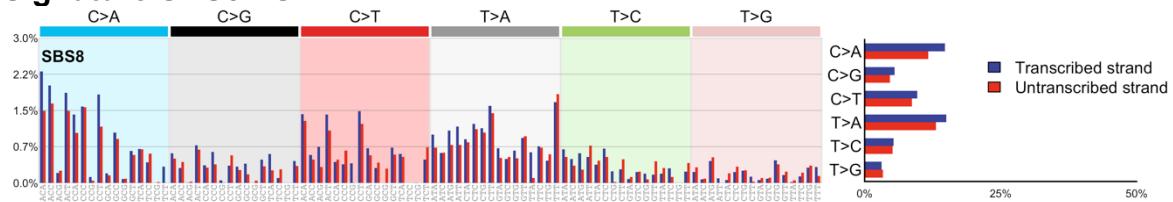
Comments

N/A

Signature SBS8 (v3.0)

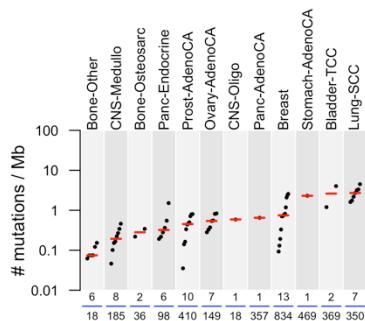


Signature SBS8-TSB



Transcriptional strand bias for C>A substitutions with more mutated G than C on the untranscribed strand, compatible with damage to guanine and activity of transcription-coupled nucleotide excision repair and/or DNA damage.

Cancer types in which the signature is found



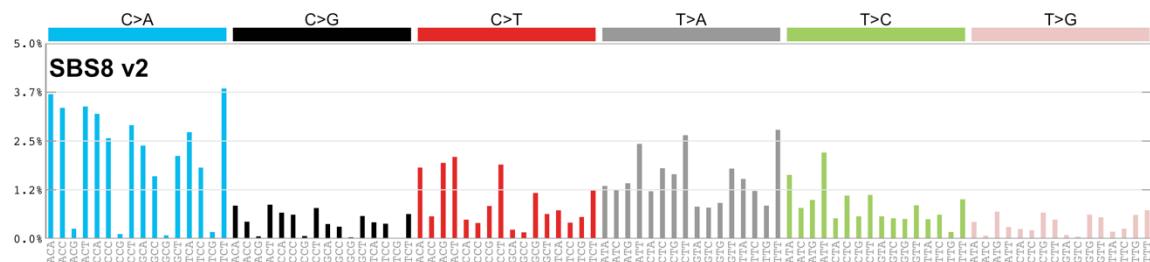
Proposed aetiology

Unknown.

Associated mutation classes and signatures

Signature SBS8 is associated with doublet base substitution signature DBS2 characterised predominantly by CC>AA mutations.

Differences between current and previous profiles

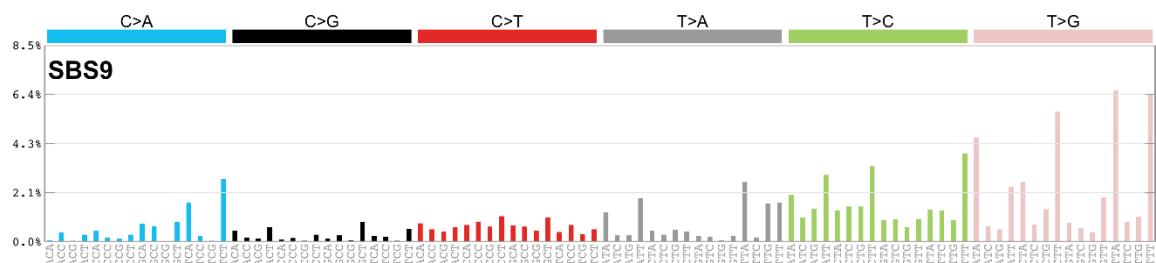


The pattern of signature SBS8 exhibits smaller contributions of C>T and T>C mutations, possibly reflecting greater separation between signatures SBS3 and SBS8. The cosine similarity between the prior and current versions of signature SBS8 is 0.94.

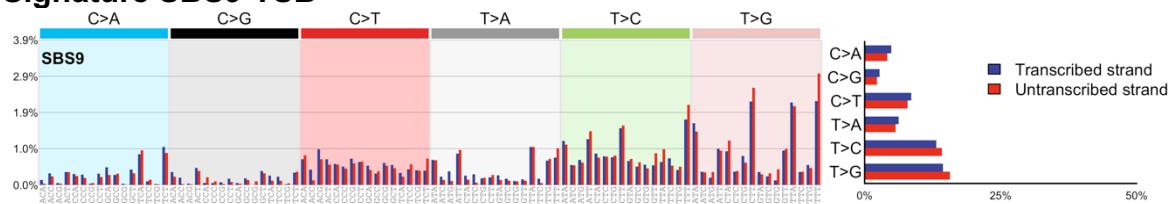
Comments

N/A

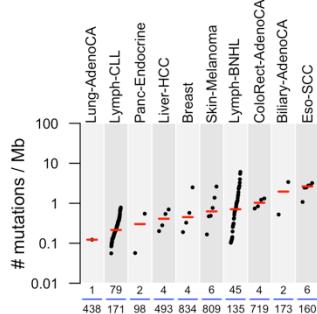
Signature SBS9 (v3.0)



Signature SBS9-TSB



Cancer types in which the signature is found



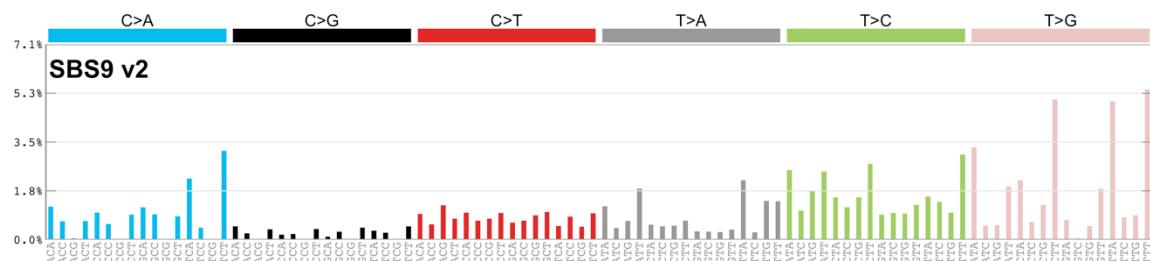
Proposed aetiology

Attributed to mutations induced during replication by polymerase η across lesions induced by activation induced cytidine deaminase as part of somatic hypermutation.

Associated mutation classes and signatures

N/A

Differences between current and previous profiles

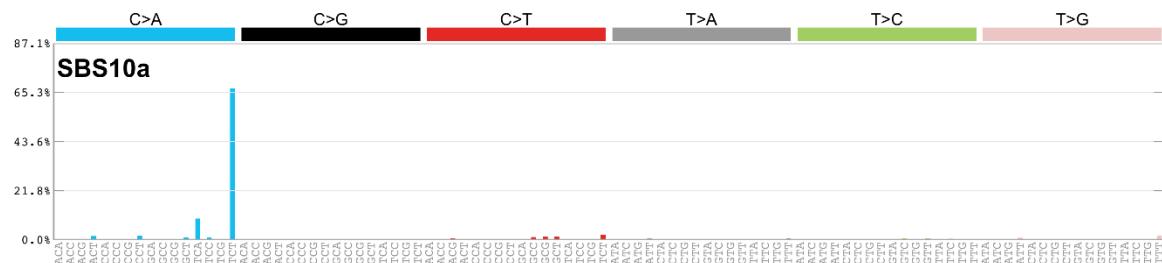


The pattern of SBS9 has been quite stable. The cosine similarity between the prior and current versions of signature SBS9 is 0.98.

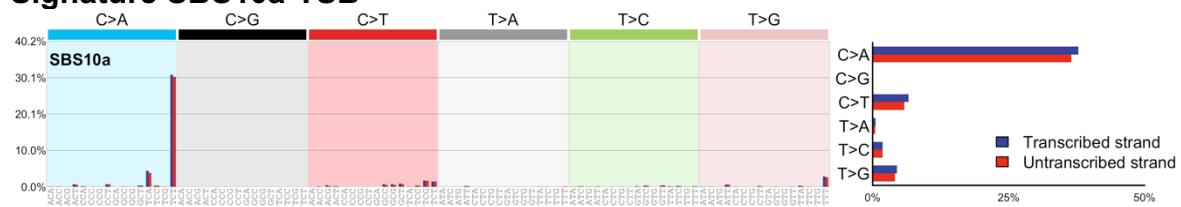
Comments

Comments
Chronic lymphocytic leukaemias that possess immunoglobulin gene hypermutation (IGHV-mutated) have elevated numbers of mutations attributed to Signature 9 compared to those that do not have immunoglobulin gene hypermutation.

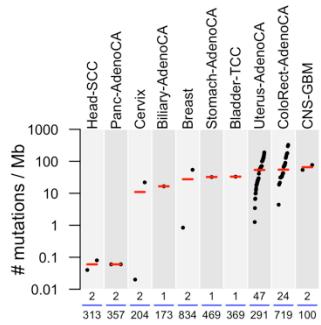
Signature SBS10a (v3.0)



Signature SBS10a-TSB



Cancer types in which the signature is found



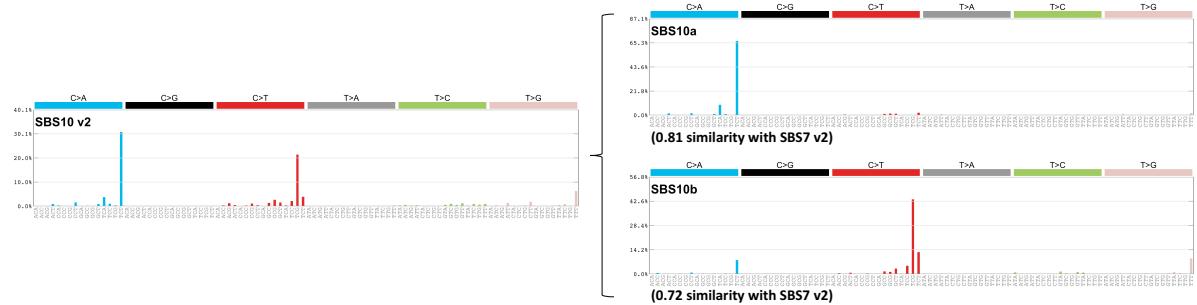
Proposed aetiology

Polymerase epsilon exonuclease domain mutations.

Associated mutation classes and signatures

Signature SBS10a is associated with signature SBS10b and these signatures are commonly found in the same samples.

Differences between current and previous profiles

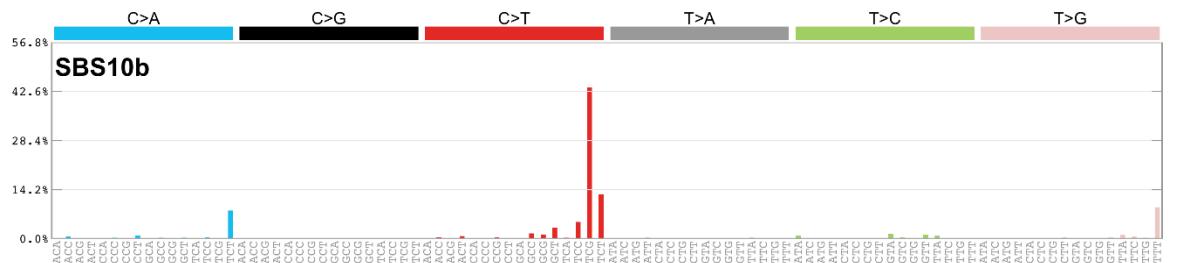


The larger number of analysed samples allow splitting of signature SBS10 into two distinct components, termed, signatures SBS10a/b. Further, signature SBS28 is also found in most samples with signatures SBS10a/b potentially accounting for the T>G component of the previous signature SBS10.

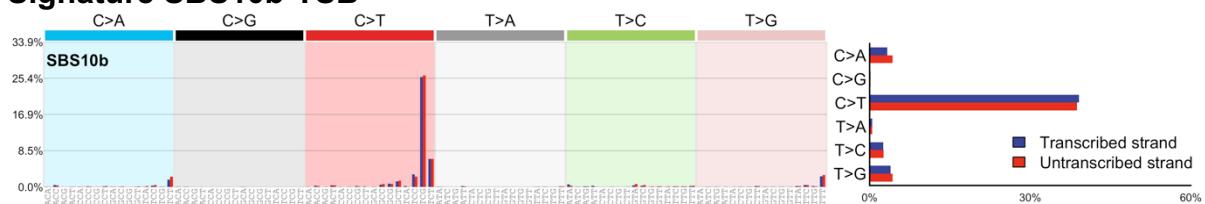
Comments

Signature SBS10a/b usually generate large numbers of somatic mutations (>100 mutations per MB) and samples with these signatures have been termed ultra-hypermutators.

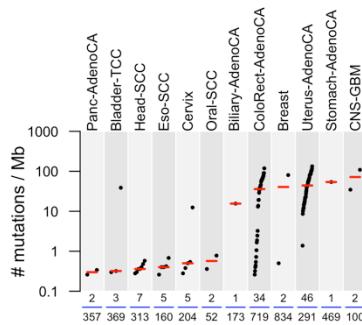
Signature SBS10b (v3.0)



Signature SBS10b-TSB



Cancer types in which the signature is found



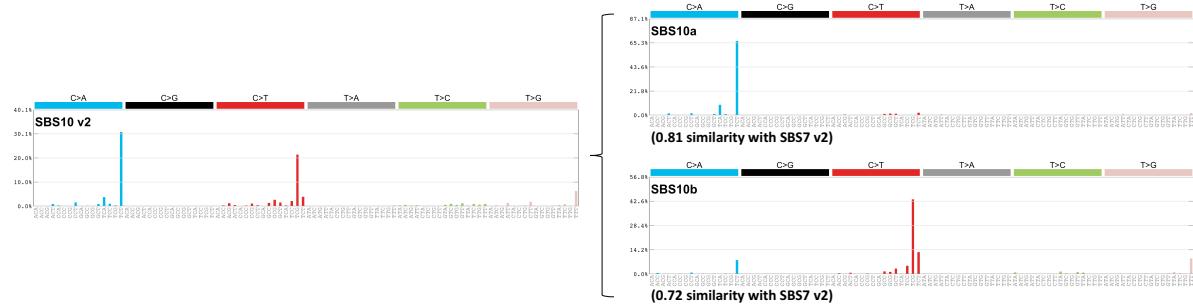
Proposed aetiology

Polymerase epsilon exonuclease domain mutations.

Associated mutation classes and signatures

Signature SBS10b is associated with signature SBS10a and these signatures are commonly found in the same samples.

Differences between current and previous profiles

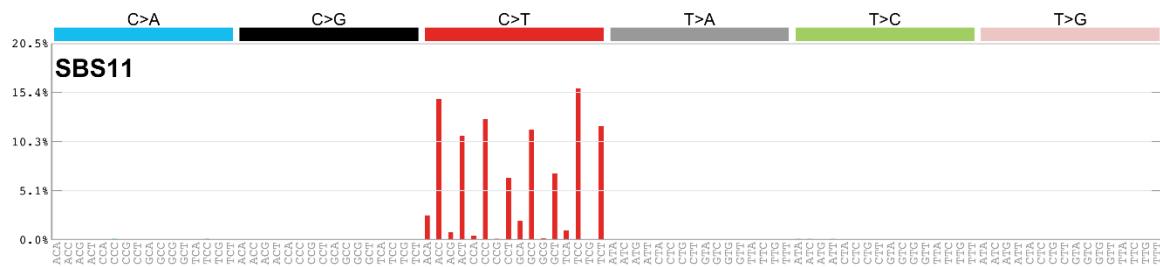


The larger number of analysed samples allow splitting of signature SBS10 into two distinct components, termed, signatures SBS10a/b. Further, signature SBS28 is also found in most samples with signatures SBS10a/b potentially accounting for the T>G component of the previous signature SBS10.

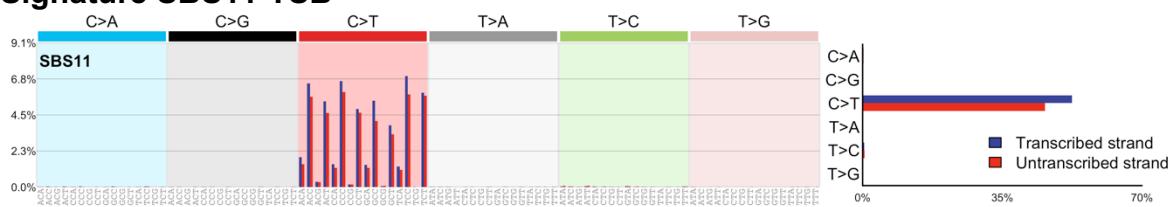
Comments

Signature SBS10a/b usually generate large numbers of somatic mutations (>100 mutations per MB) and samples with these signatures have been termed ultra-hypermutators.

Signature SBS11 (v3.0)

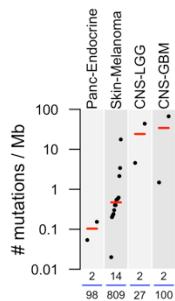


Signature SBS11-TSB



Signature SBS11 exhibits a very weak transcriptional strand-bias with more mutations of G than C on the untranscribed strands of genes consistent with damage to guanine and repair by transcription-coupled nucleotide excision repair and/or DNA damage.

Cancer types in which the signature is found



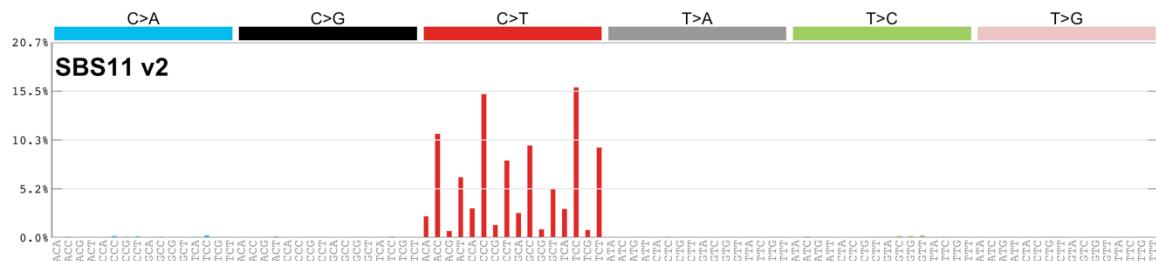
Proposed aetiology

Signature SBS11 exhibits a mutational pattern resembling that of alkylating agents. Patient histories indicate an association between previous treatment with the alkylating agent temozolomide and Signature SBS11 mutations.

Associated mutation classes and signatures

N/A

Differences between current and previous profiles

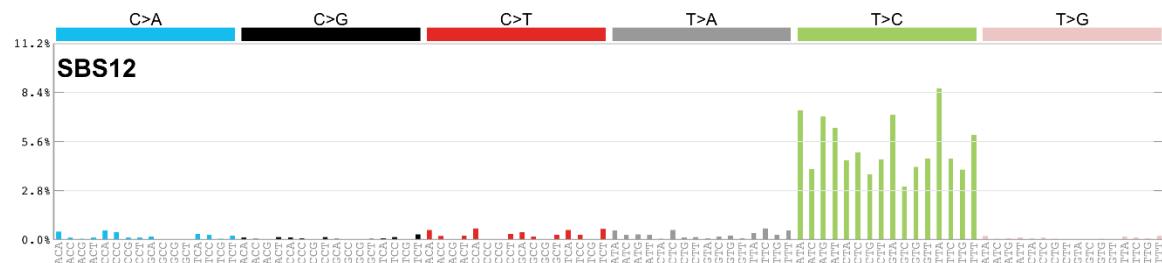


The pattern of SBS11 has been quite stable. The cosine similarity between the prior and current versions of signature SBS11 is 0.97.

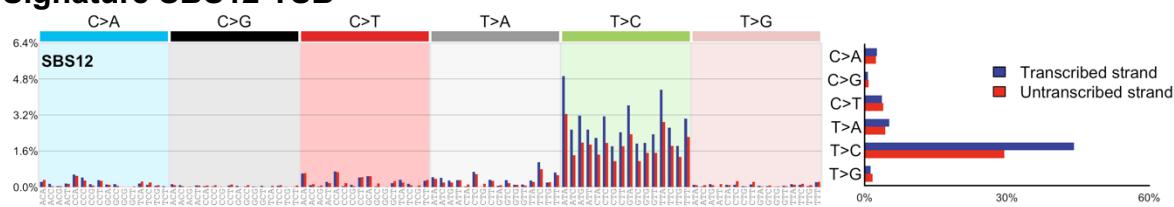
Comments

Signature SBS11 usually generated large numbers of somatic mutations (>10 mutations per MB).

Signature SBS12 (v3.0)

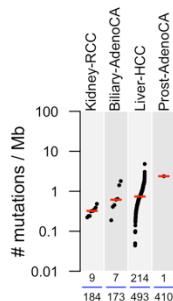


Signature SBS12-TSB



Transcriptional strand-bias for T>C substitutions with more mutations of A than T on the untranscribed strands of genes consistent with damage to adenine and repair by transcription-coupled nucleotide excision repair and/or DNA damage.

Cancer types in which the signature is found



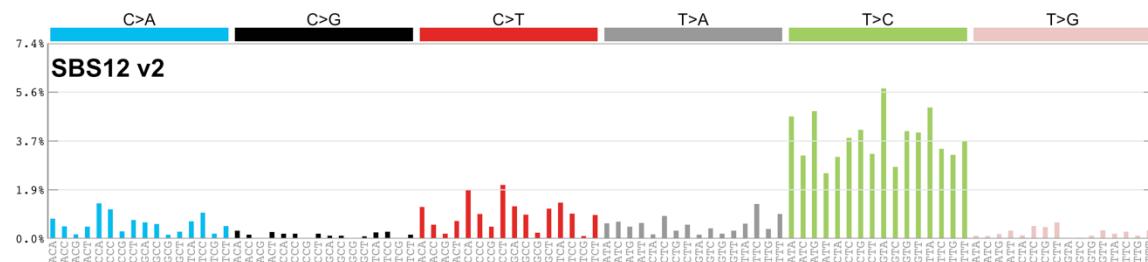
Proposed aetiology

Unknown.

Associated mutation classes and signatures

N/A

Differences between current and previous profiles

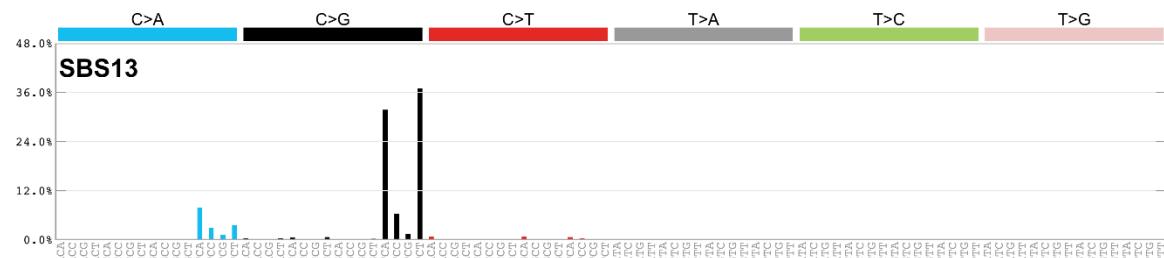


Smaller contributions from C>T and C>A mutations probably reflecting less contamination by other mutational signatures. The cosine similarity between the prior and current versions of signature SBS12 is 0.94.

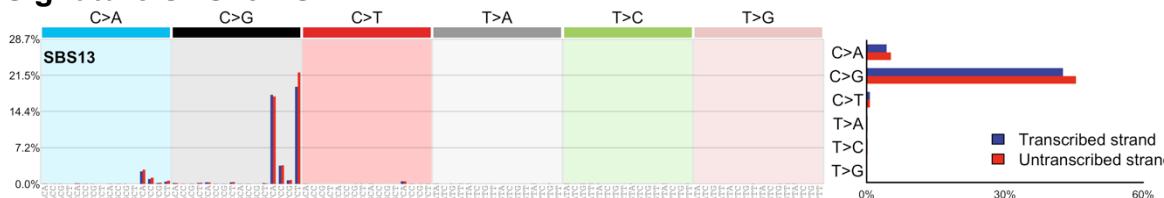
Comments:

Signature 12 usually contributes a small percentage (<20%) of the mutations observed in liver cancer samples.

Signature SBS13 (v3.0)

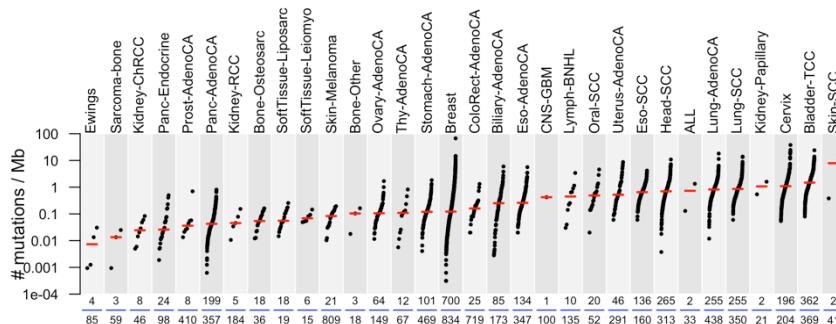


Signature SBS13-TSB



Transcriptional strand bias of mutations in exons (not shown) which is not present or is weaker in introns.

Cancer types in which the signature is found



Proposed aetiology

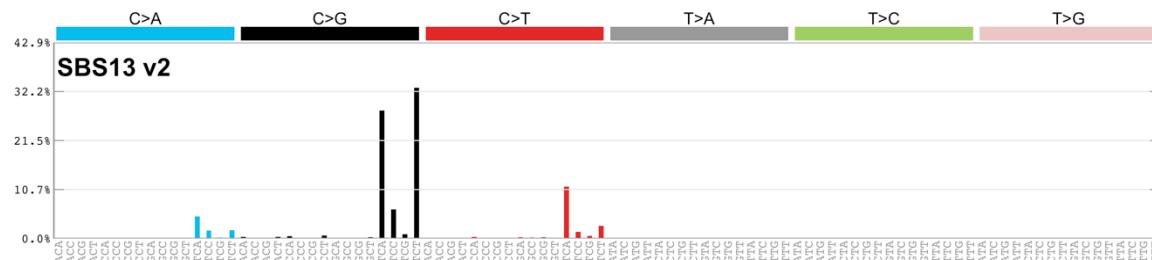
Attributed to activity of the AID/APOBEC family of cytidine deaminases on the basis of similarities in the sequence context of cytosine mutations caused by APOBEC enzymes in experimental systems. APOBEC3A is probably responsible for most mutations in human cancer, although APOBEC3B may also contribute (these differ in the sequence context two bases 5' to the mutated cytosine, see 1536 mutation classification signature extraction). Signature SBS13 mutations are likely generated by error prone polymerases (such as REV1) replicating across abasic sites generated by base excision repair removal of uracil.

Associated mutation classes and signatures

Signature SBS13 is closely associated with signature SBS2. Signature SBS13 is associated with doublet base substitution mutational signature DBS11, which is

characterised predominantly by CC>TT doublet base substitutions as well as other CC>>NN doublet base substitutions.

Differences between current and previous profiles

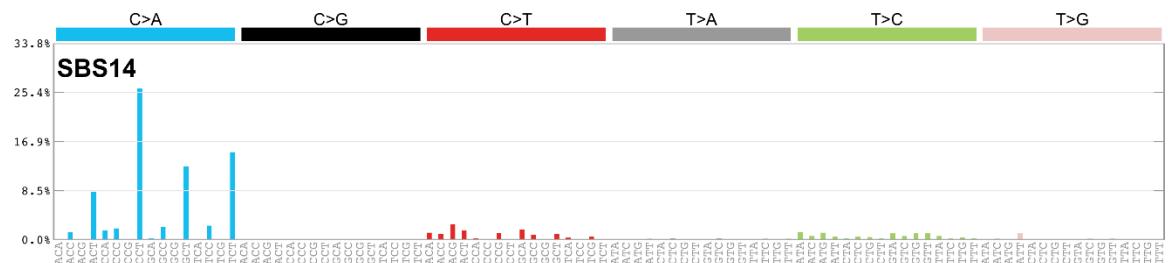


The contribution of C>T mutations at TCN trinucleotides has diminished markedly compared to previous profiles indicating reduced contamination by Signature SBS2. The cosine similarity between the prior and current versions of signature SBS13 is 0.97.

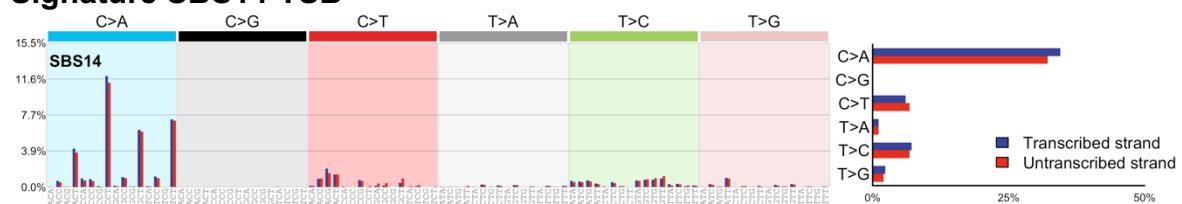
Comments

Signature SBS13 is usually found in the same samples as signature SBS2. It has been proposed that activation of AID/APOBEC cytidine deaminases in cancer may be due to previous viral infection, retrotransposon jumping, or tissue inflammation. Currently, there is limited evidence to support these hypotheses. Germline polymorphisms involving APOBEC3A and APOBEC3B are associated with predisposition to breast and bladder cancer as well as with mutation burdens of signatures SBS2 and SBS13. Mutations of similar patterns to signatures SBS2 and SBS13 are commonly found in the phenomenon of local hypermutation present in some cancers, known as kataegis, implicating AID/APOBEC enzymes in this process as well.

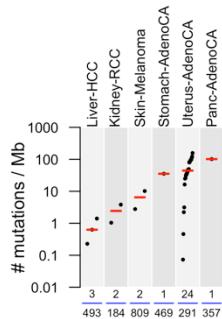
Signature SBS14 (v3.0)



Signature SBS14-TSB



Cancer types in which the signature is found



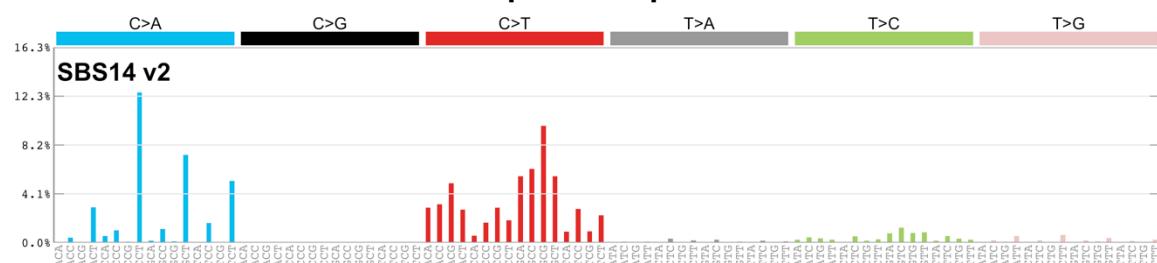
Proposed aetiology

Defective DNA mismatch repair.

Associated mutation classes and signatures

N/A

Differences between current and previous profiles

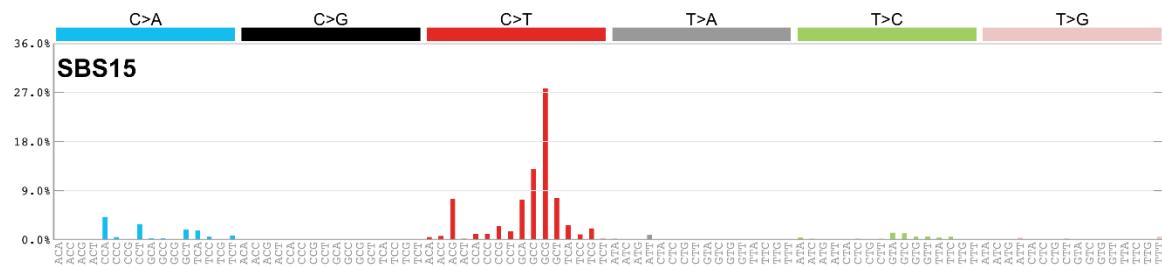


The pattern of SBS14 has changed extensively with C>A mutations separating from C>T mutations. Please note that the pattern of C>T mutations in the prior version of SBS14 was most likely a contamination from signature SBS6. The cosine similarity between the prior and current versions of signature SBS14 is 0.74.

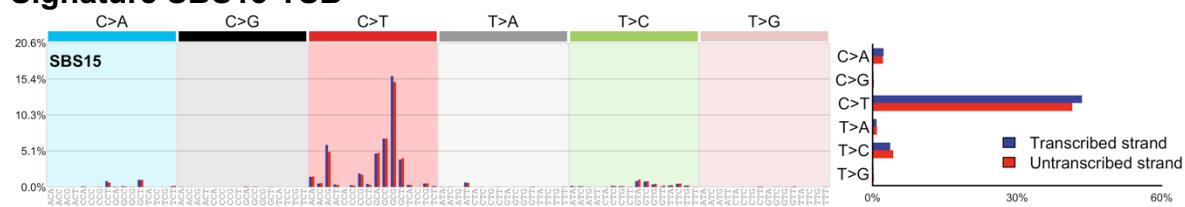
Comments

Signature SBS14 mutations are present in very high numbers in all samples in which it has been observed. Signature SBS14 is one of seven mutational signatures associated with defective DNA mismatch repair (MSI) and is often found in the same samples as other MSI associated signatures: signatures SBS6, SBS15, SBS20, SBS21, SBS26, and SBS44.

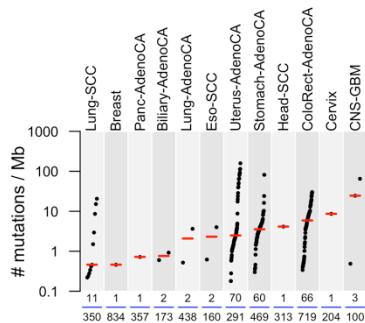
Signature SBS15 (v3.0)



Signature SBS15-TSB



Cancer types in which the signature is found



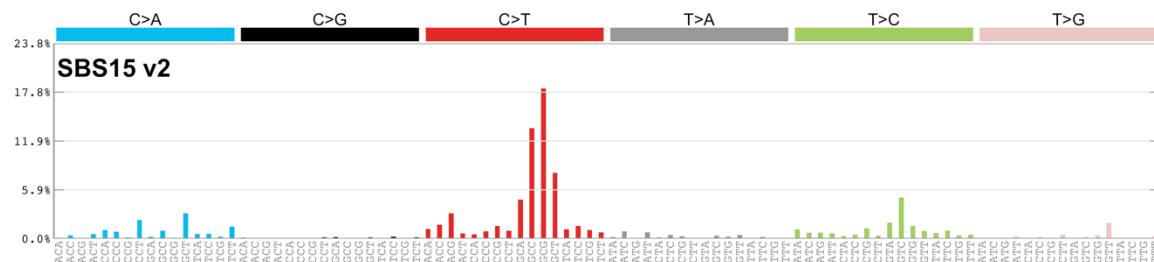
Proposed aetiology

Defective DNA mismatch repair.

Associated mutation classes and signatures

Signature SBS15 is associated with high numbers of small (shorter than 3bp) insertions and deletions at mono/polynucleotide repeats. Signature SBS15 is associated indel signatures ID1 and ID2.

Differences between current and previous profiles

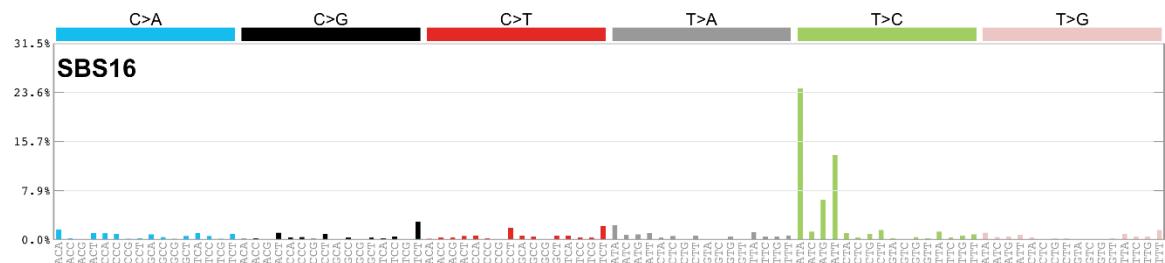


Smaller contributions of C>A and T>C mutations indicating less contamination by other DNA mismatch repair deficiency signatures. The cosine similarity between the prior and current versions of signature SBS15 is 0.94.

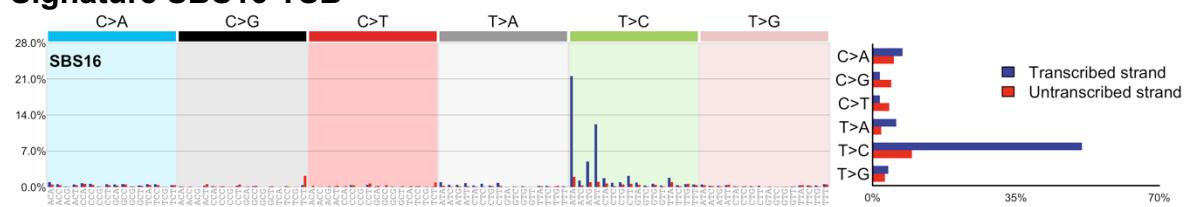
Comments

Signature SBS15 is one of seven mutational signatures associated with defective DNA mismatch repair (MSI) and is often found in the same samples as other MSI associated signatures: signatures SBS6, SBS14, SBS20, SBS21, SBS26, and SBS44.

Signature SBS16 (v3.0)

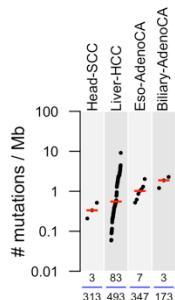


Signature SBS16-TSB



Extremely strong transcriptional strand bias of T>C mutations at ATN trinucleotides with more mutations of A than T on the untranscribed strands of genes consistent with damage to adenine and repair by transcription coupled nucleotide excision repair and/or DNA damage.

Cancer types in which the signature is found



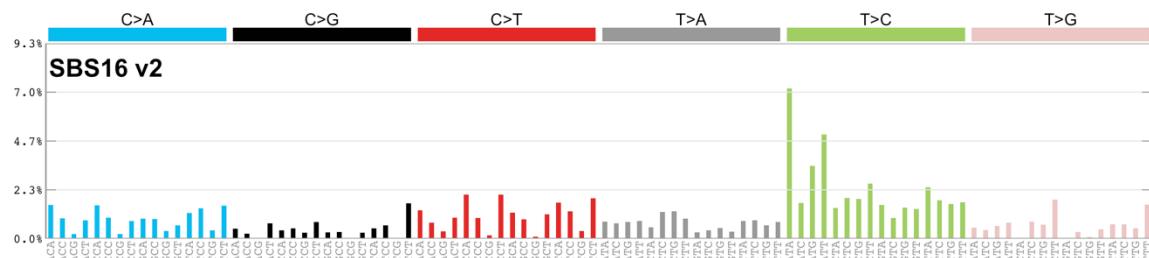
Proposed aetiology

Unknown.

Associated mutation classes and signatures

N/A

Differences between current and previous profiles

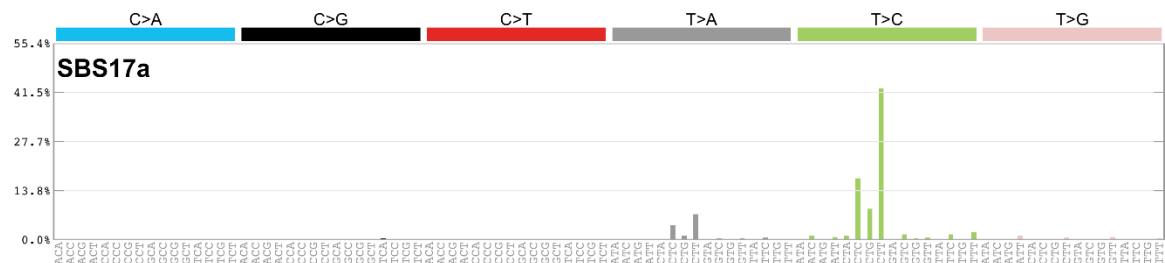


The pattern of signature SBS16 exhibits less contamination by other mutation signatures, notably signatures SBS5 and SBS12. The cosine similarity between the prior and current versions of signature SBS5 is 0.79.

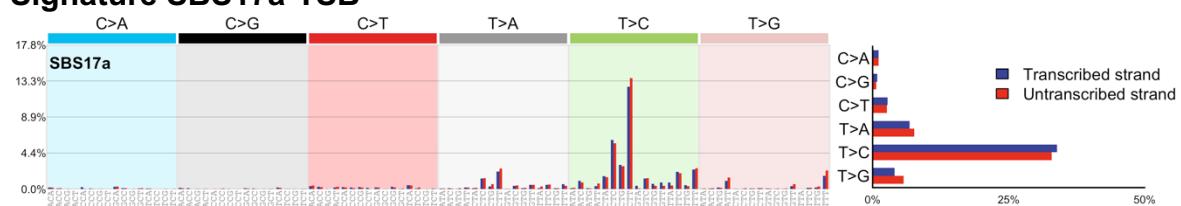
Comments

In addition to lower levels of nucleotide excision repair on the untranscribed strands of genes, elevated levels DNA damage on untranscribed strands, compared to the remainder of the genome, may contribute to signature SBS16. Contamination by signature SBS16 may still be present in the current version of signature SBS5.

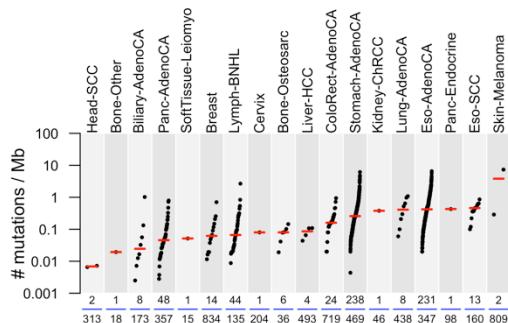
Signature SBS17a (v3.0)



Signature SBS17a-TSB



Cancer types in which the signature is found



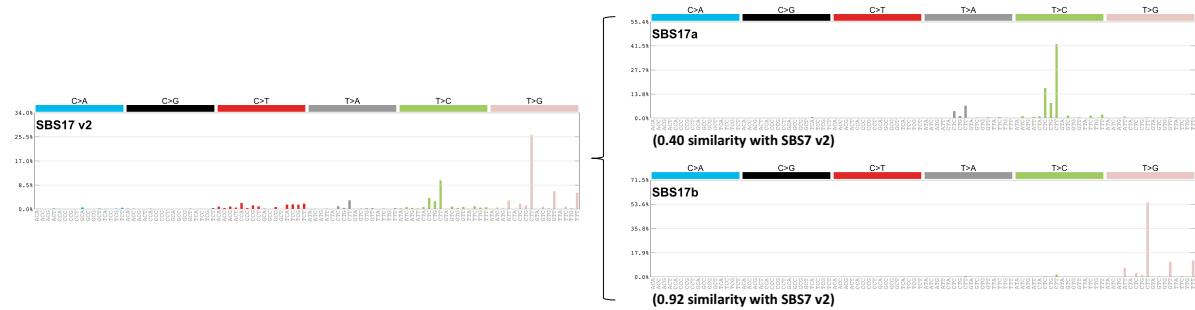
Proposed aetiology

Unknown.

Associated mutation classes and signatures

Signature SBS17a is associated with signature SBS17b and these signatures are commonly found in the same samples.

Differences between current and previous profiles

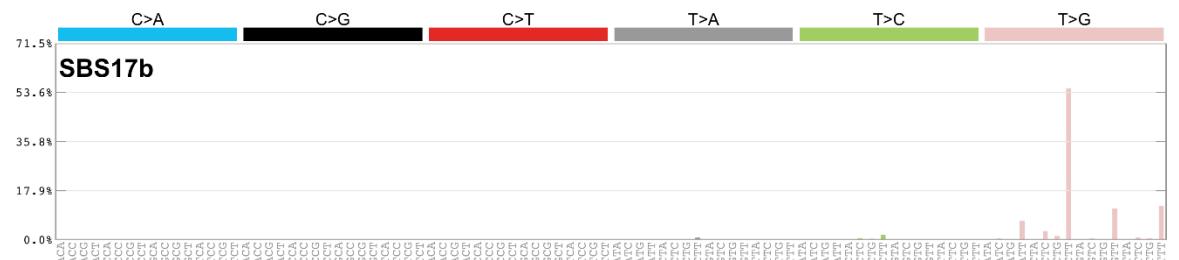


The larger number of analysed samples allow splitting of signature SBS17 into two distinct components, termed, signatures SBS17a/b, that almost perfectly recapitulate the original signature.

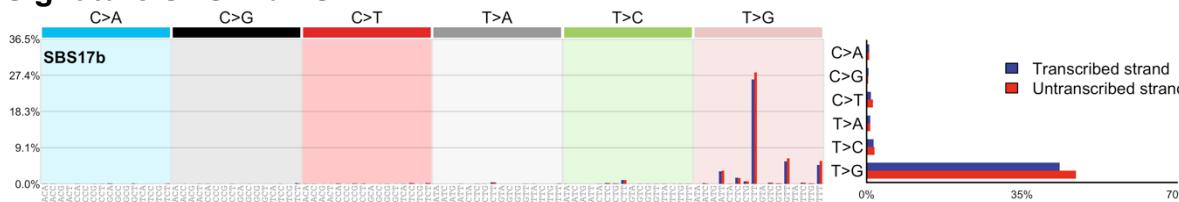
Comments

Signature SBS17b has similarities to signature SBS28 and these two signatures can be mistaken to one another.

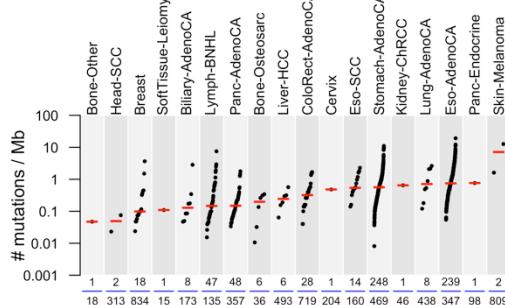
Signature SBS17b (v3.0)



Signature SBS17b-TSB



Cancer types in which the signature is found



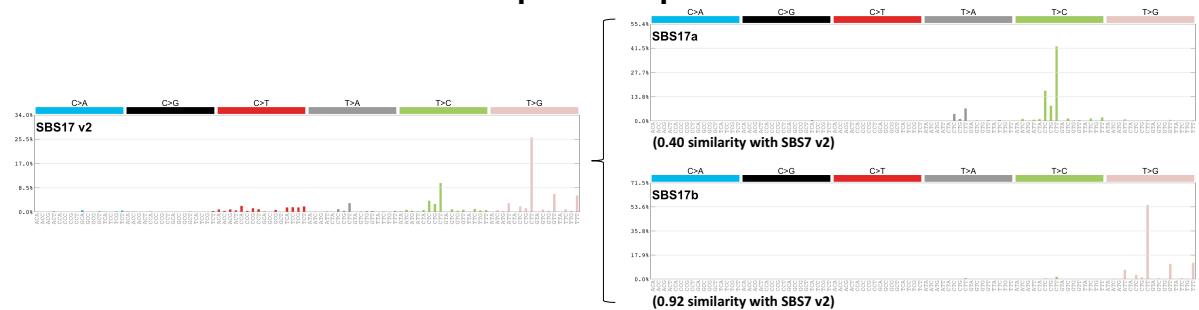
Proposed aetiology

Unknown.

Associated mutation classes and signatures

Signature SBS17b is associated with signature SBS17a and these signatures are commonly found in the same samples.

Differences between current and previous profiles

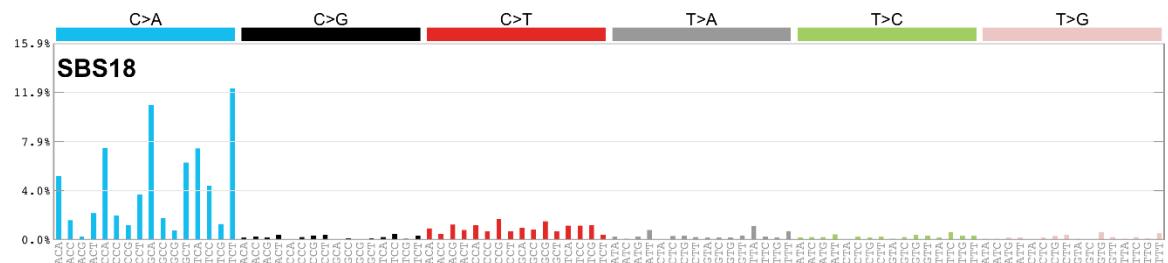


The larger number of analysed samples allow splitting of signature SBS17 into two distinct components, termed, signatures SBS17a/b, that almost perfectly recapitulate the original signature.

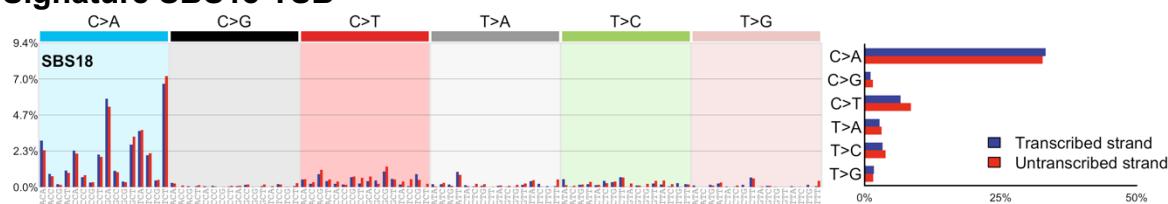
Comments

N/A

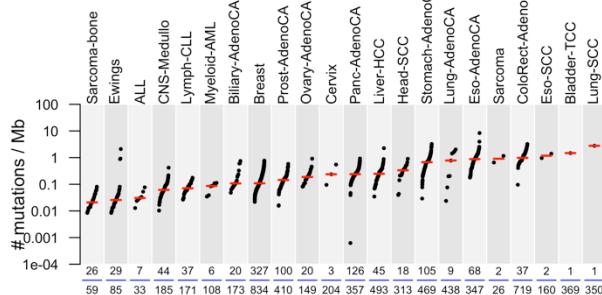
Signature SBS18 (v3.0)



Signature SBS18-TSB



Cancer types in which the signature is found



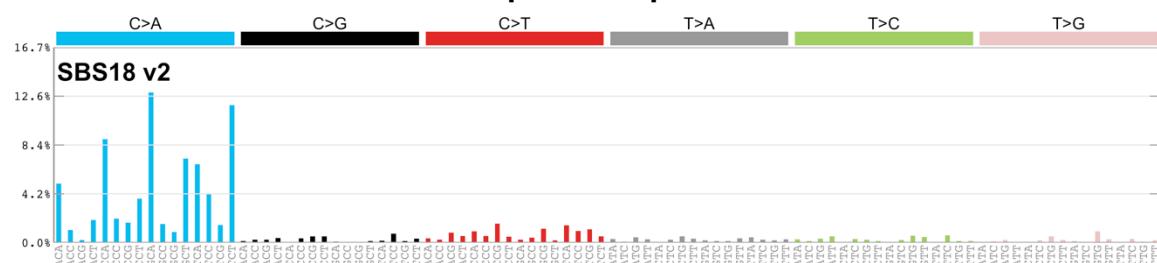
Proposed aetiology

Possibly damage by reactive oxygen species.

Associated mutation classes and signatures

N/A

Differences between current and previous profiles

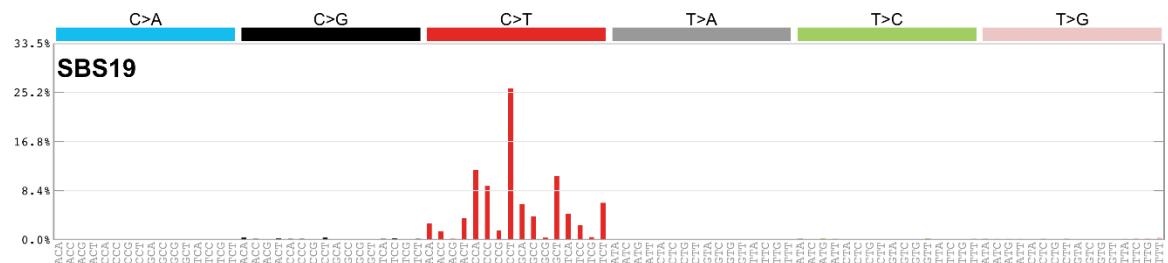


The cosine similarity between the prior and current versions of signature SBS18 is 0.99.

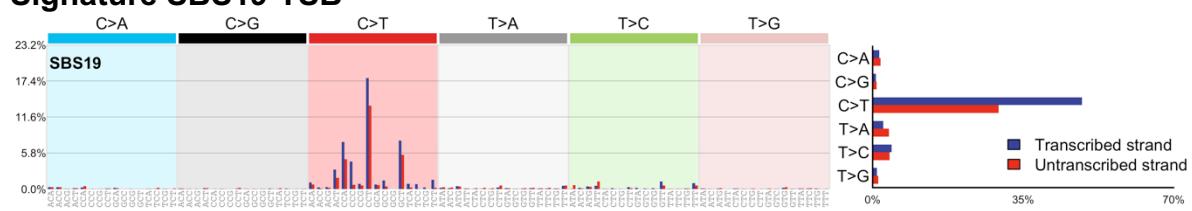
Comments

Similar in profile to signature SBS36 which is associated with defective base excision repair due to MUTYH mutations.

Signature SBS19 (v3.0)

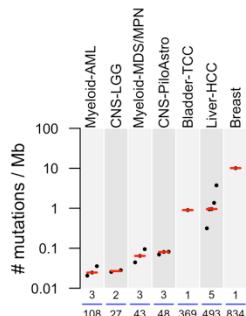


Signature SBS19-TSB



Transcriptional strand bias of C>T mutations with more mutations of G than C on the untranscribed strands of genes consistent with damage to guanine and repair by transcription coupled nucleotide excision repair and/or DNA damage.

Cancer types in which the signature is found



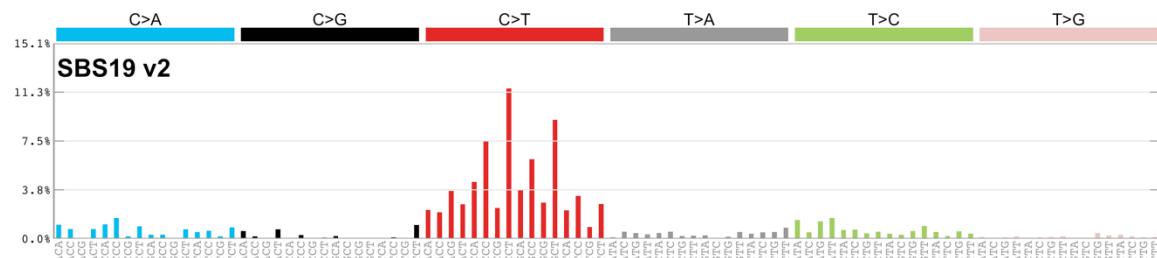
Proposed aetiology

Unknown.

Associated mutation classes and signatures

N/A

Differences between current and previous profiles

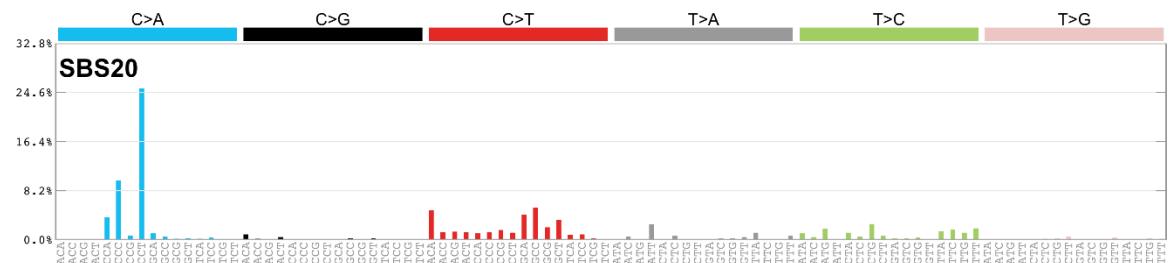


Reduced contamination by other mutational signatures especially signatures SBS1 and SBS5. The cosine similarity between the prior and current versions of signature SBS19 is 0.89.

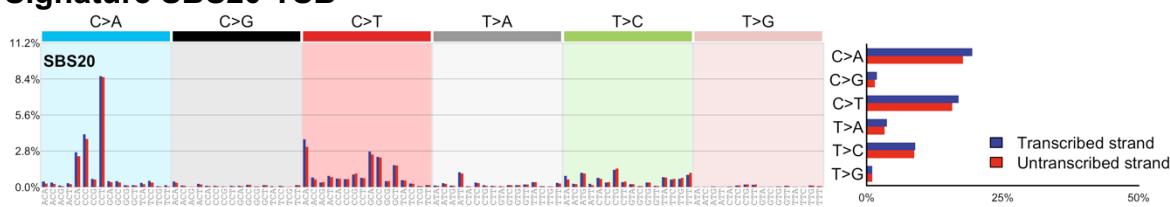
Comments

N/A

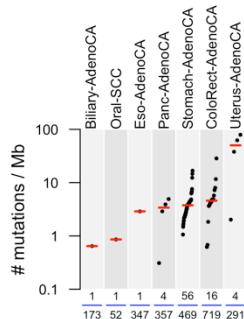
Signature SBS20 (v3.0)



Signature SBS20-TSB



Cancer types in which the signature is found



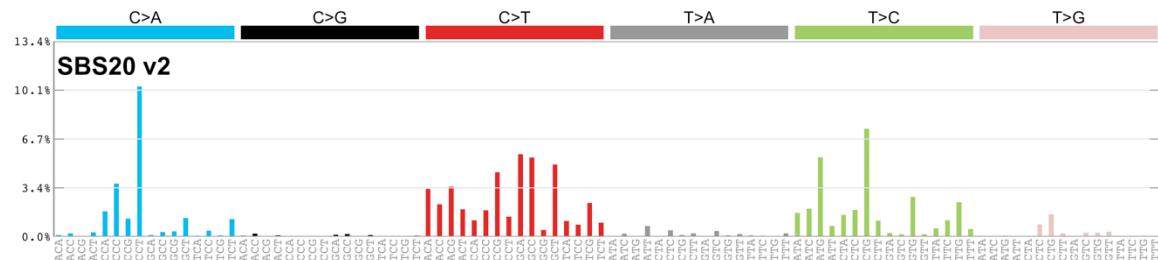
Proposed aetiology

Unknown.

Associated mutation classes and signatures

Signature SBS20 is associated with high numbers of small (shorter than 3bp) insertions and deletions at mono/polynucleotide repeats. Signature SBS20 is associated indel signatures ID1 and ID2.

Differences between current and previous profiles

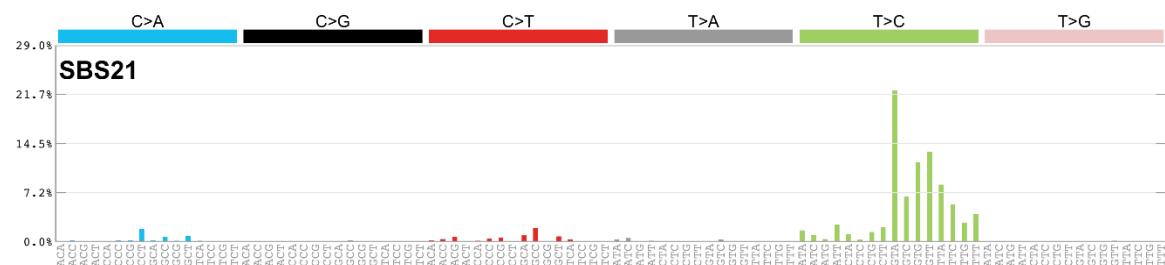


Reduced contamination by other DNA mismatch deficiency signatures. The cosine similarity between the prior and current versions of signature SBS20 is 0.78.

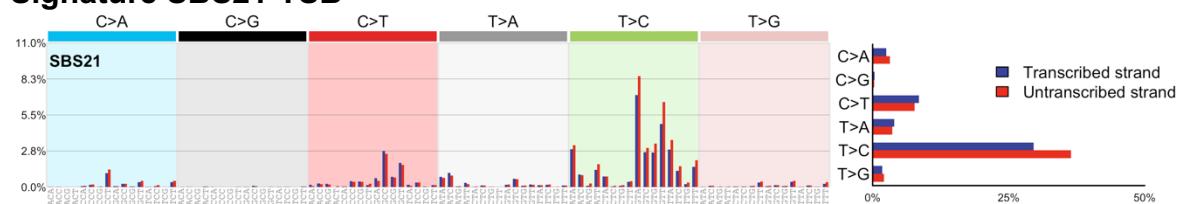
Comments

Signature SBS20 is one of seven mutational signatures associated with defective DNA mismatch repair (MSI) and is often found in the same samples as other MSI associated signatures: signatures SBS6, SBS14, SBS15, SBS21, SBS26, and SBS44.

Signature SBS21 (v3.0)

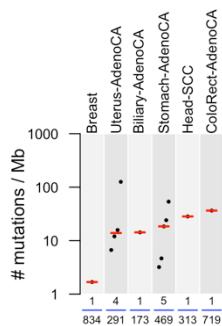


Signature SBS21-TSB



Transcriptional strand bias with more mutated T than A on untranscribed strands of genes compatible with damage to thymidine and activity of transcription-coupled nucleotide excision repair and/or DNA damage.

Cancer types in which the signature is found



Proposed aetiology

DNA mismatch repair deficiency.

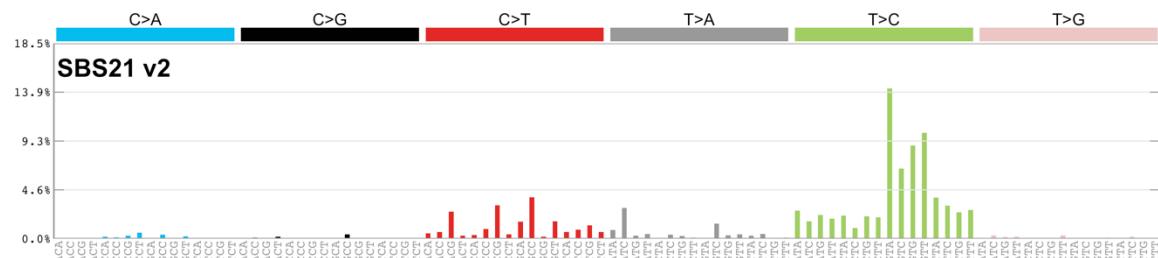
Proposed aetiology

Unknown.

Associated mutation classes and signatures

Signature SBS21 is associated with high numbers of small (shorter than 3bp) insertions and deletions at mono/polynucleotide repeats. Signature SBS20 is associated indel signatures ID1 and ID2.

Differences between current and previous profile

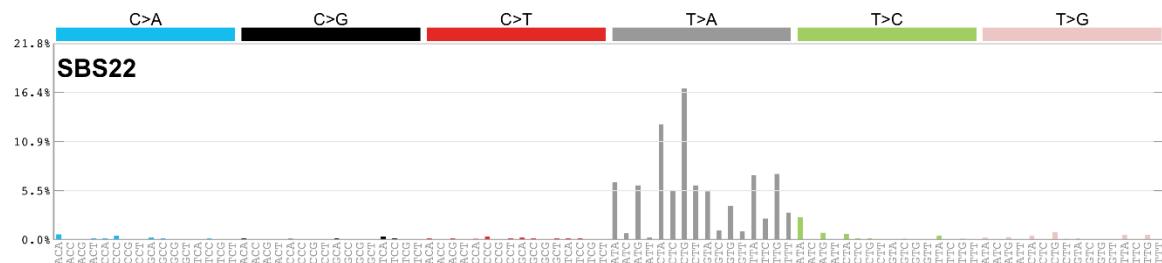


Reduced contamination by other signatures of DNA mismatch repair deficiency. The cosine similarity between the prior and current versions of signature SBS21 is 0.95.

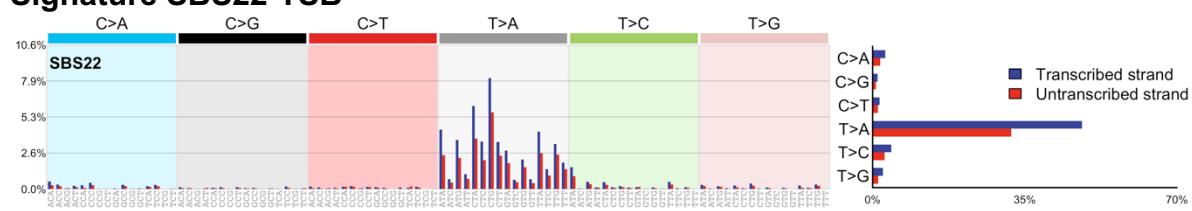
Comments

Signature SBS21 is one of seven mutational signatures associated with defective DNA mismatch repair (MSI) and is often found in the same samples as other MSI associated signatures: signatures SBS6, SBS14, SBS15, SBS20, SBS26, and SBS44.

Signature SBS22 (v3.0)

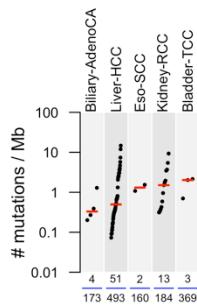


Signature SBS22-TSB



Signature SBS22 exhibits strong transcriptional strand bias for T>A mutations with more mutations of A than T on the untranscribed strands of genes consistent with damage to adenine and repair by transcription-coupled nucleotide excision repair and/or DNA damage.

Cancer types in which the signature is found



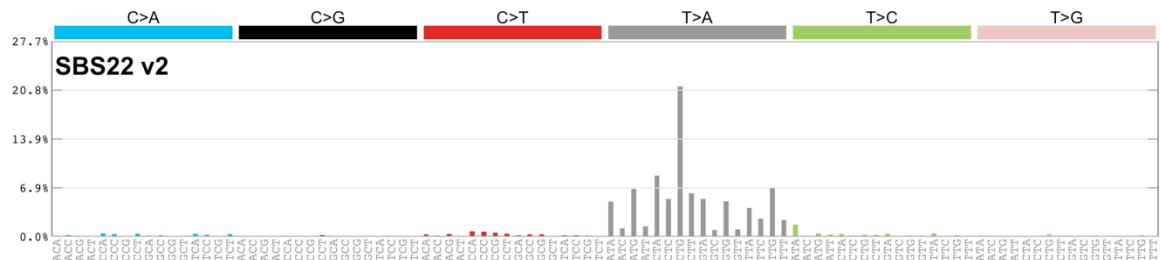
Proposed aetiology

Aristolochic acid exposure. Found in cancer samples with known exposures to aristolochic acid and the pattern of mutations exhibited by the signature is consistent with that observed in experimental systems of aristolochic acid exposure.

Associated mutation classes and signatures

N/A

Differences between current and previous profiles

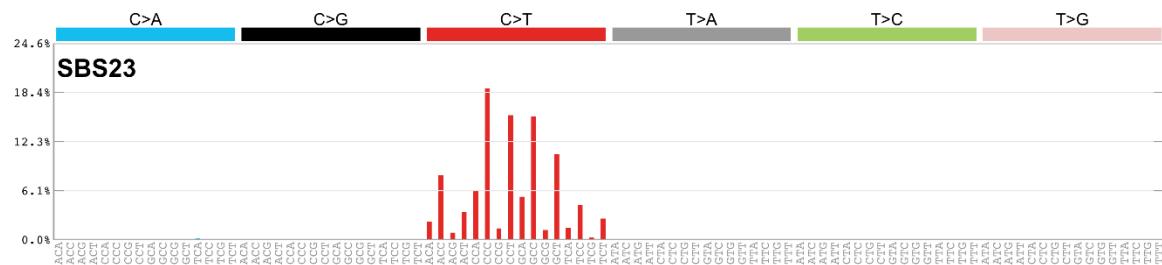


The cosine similarity between the prior and current versions of signature SBS22 is 0.96.

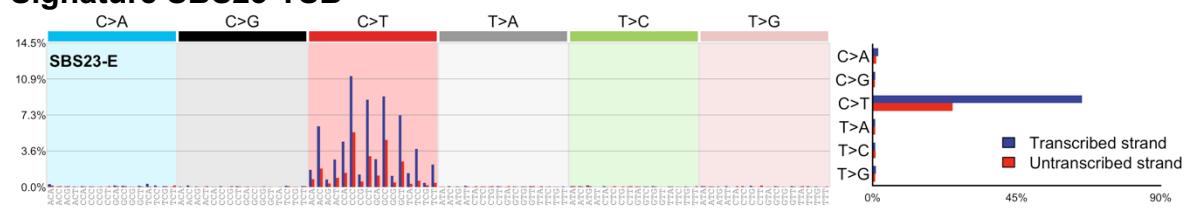
Comments

N/A

Signature SBS23 (v3.0)

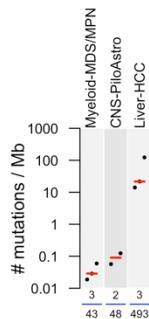


Signature SBS23-TSB



Signature SBS23 exhibits strong transcriptional strand bias for C>T mutations with more mutations of G than C on the untranscribed strands of genes consistent with damage to guanine and repair by transcription coupled nucleotide excision repair and/or DNA damage. Please note that signature SBS23 has only been found in exome sequencing data and, as such, the transcriptional strand bias reflects the one observed in the coding regions of the genome.

Cancer types in which the signature is found



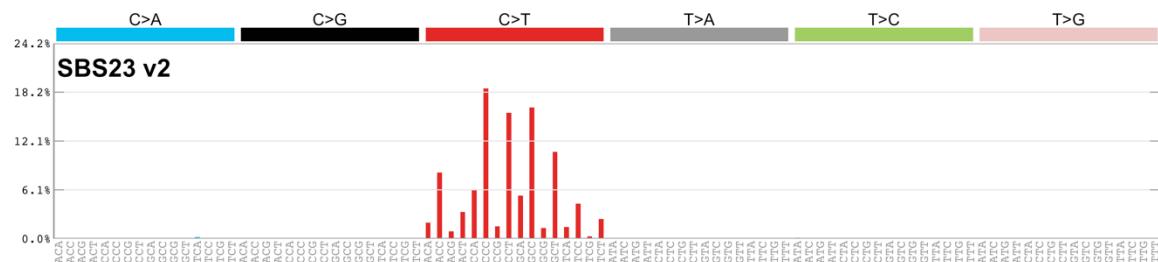
Proposed aetiology

Unknown.

Associated mutation classes and signatures

N/A

Differences between current and previous profiles

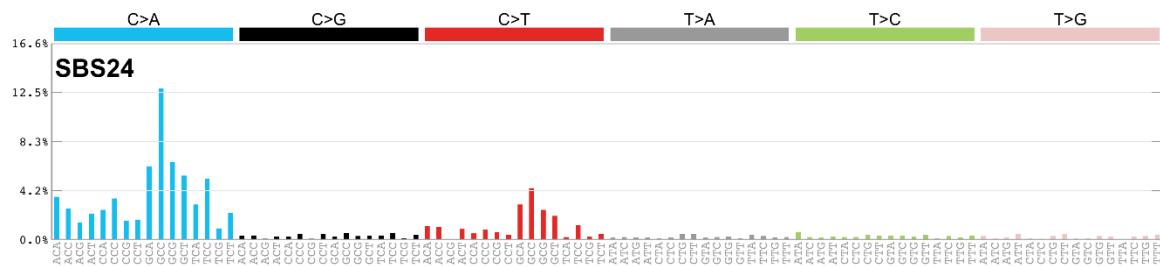


The cosine similarity between the prior and current versions of signature SBS23 is 1.00.

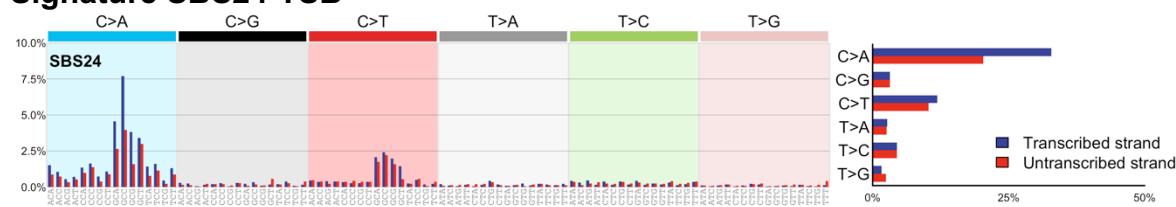
Comments

N/A

Signature SBS24 (v3.0)

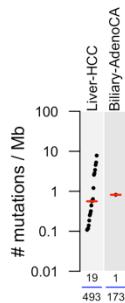


Signature SBS24-TSB



Signature SBS24 exhibits strong transcriptional strand bias for C>A mutations with more mutations of G than C on the untranscribed strands of genes consistent with damage to guanine and repair by transcription-coupled nucleotide excision repair and/or DNA damage.

Cancer types in which the signature is found



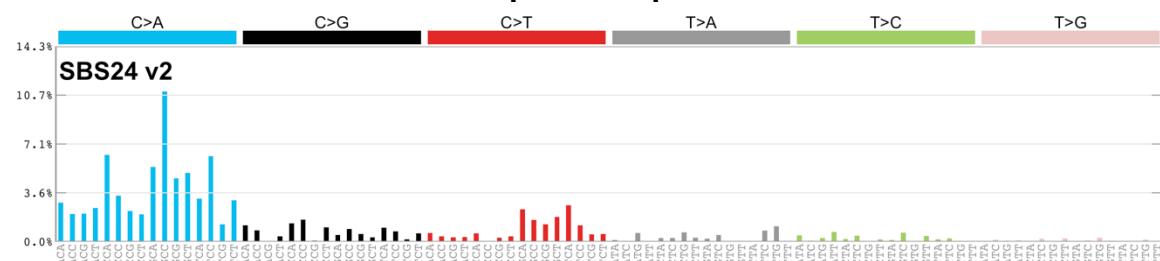
Proposed aetiology

Aflatoxin exposure. Signature SBS24 has been found in cancer samples with known exposures to aflatoxin and the pattern of mutations exhibited by the signature is consistent with that observed in experimental systems exposed to aflatoxin.

Associated mutation classes and signatures

N/A

Differences between current and previous profiles

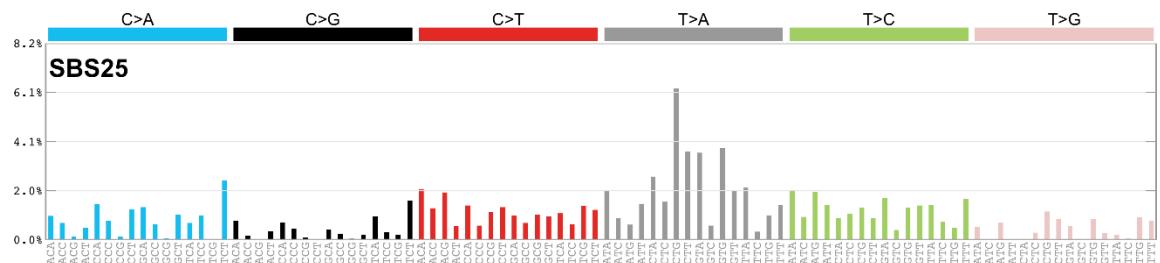


The cosine similarity between the prior and current versions of signature SBS24 is 0.94.

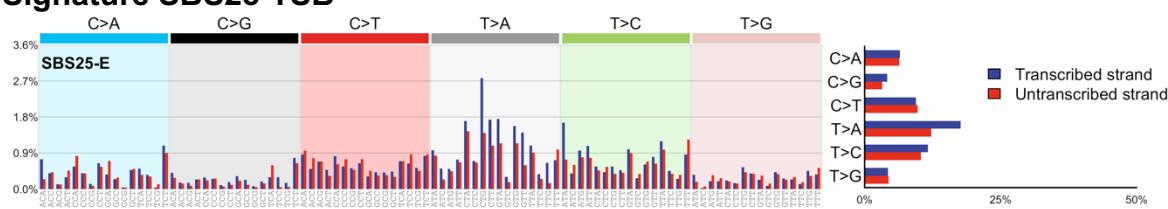
Comments

N/A

Signature SBS25 (v3.0)



Signature SBS25-TSB



Transcriptional strand bias for T>A mutations with more mutations of A than T on the untranscribed strands of genes consistent with damage to adenine and repair by transcription coupled nucleotide excision repair and/or DNA damage. Please note that signature SBS25 has only been found in exome sequencing data and, as such, the transcriptional strand bias reflects the one observed in the coding regions of the genome.

Cancer types in which the signature is found

N/A

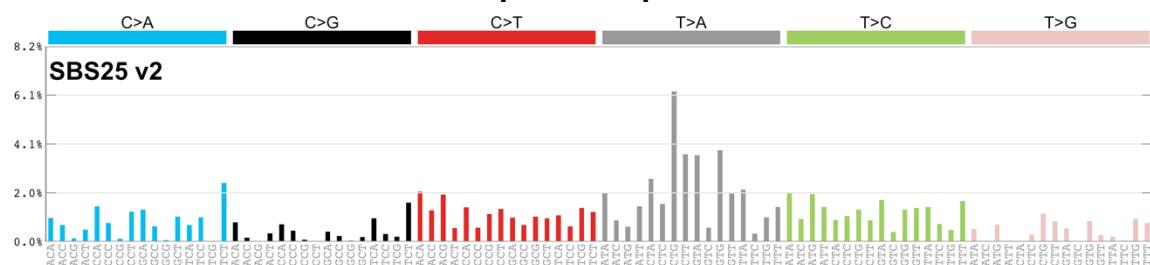
Proposed aetiology

Unknown. However, some Hodgkin's cell line samples in which the signature has been found were from patients exposed to chemotherapy.

Associated mutation classes and signatures

N/A

Differences between current and previous profiles

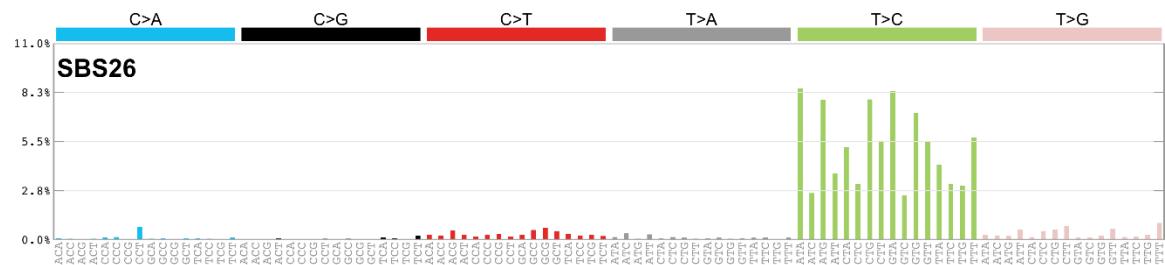


The cosine similarity between the prior and current versions of signature SBS25 is 1.00.

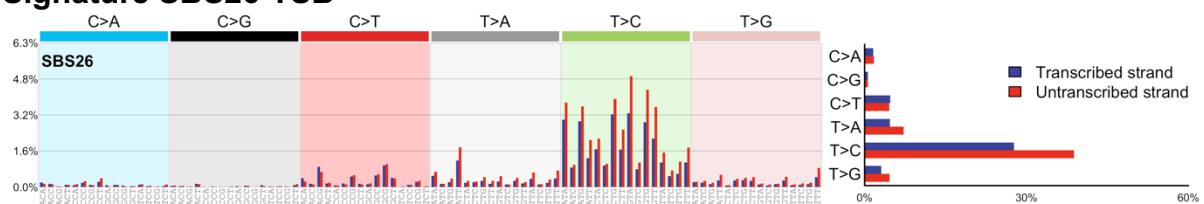
Comments

This signature has only been identified in Hodgkin's cell lines. Data is not available from primary Hodgkin lymphomas.

Signature SBS26 (v3.0)

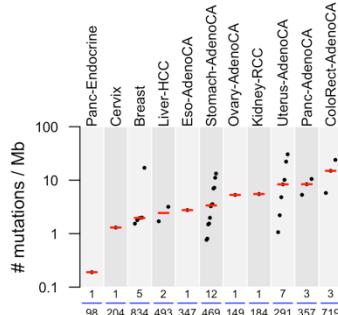


Signature SBS26-TSB



Transcriptional strand bias with more mutated T than A on untranscribed strands of genes compatible with damage to thymidine and activity of transcription-coupled nucleotide excision repair and/or DNA damage.

Cancer types in which the signature is found



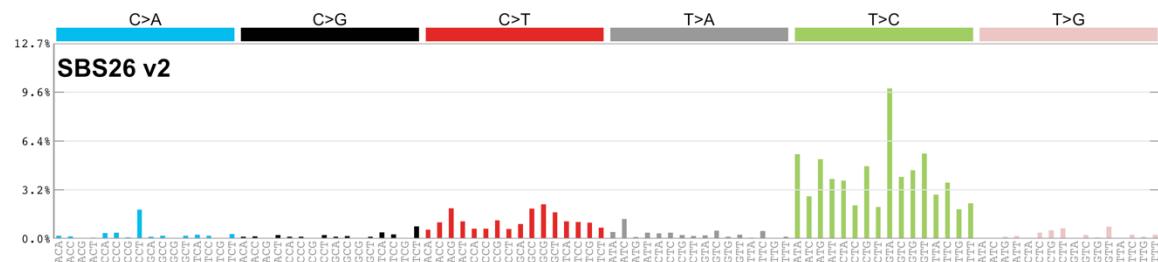
Proposed aetiology

Defective DNA mismatch repair.

Associated mutation classes and signatures

Signature SBS26 is associated with high numbers of small (shorter than 3bp) insertions and deletions at mono/polynucleotide repeats. Signature SBS26 is associated indel signatures ID1 and ID2.

Differences between current and previous profiles

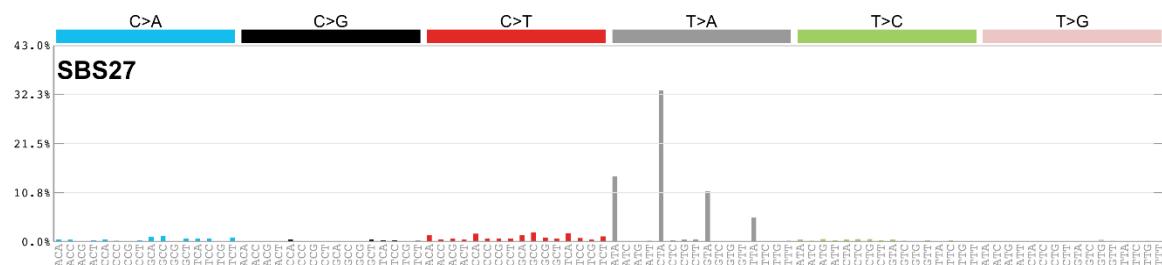


Reduced contamination by other signatures of defective DNA mismatch repair. The cosine similarity between the prior and current versions of signature SBS26 is 0.92.

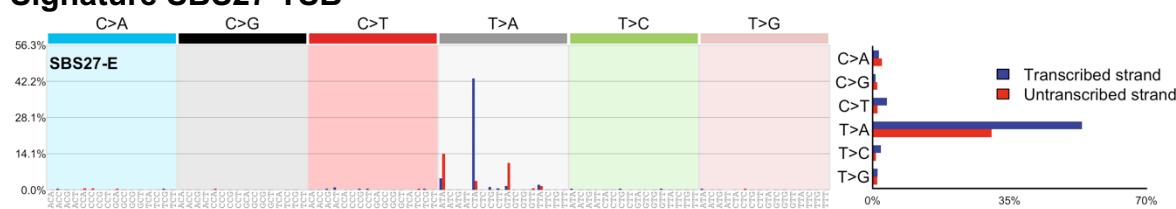
Comments

Signature SBS26 is one of seven mutational signatures associated with defective DNA mismatch repair (MSI) and is often found in the same samples as other MSI associated signatures: signatures SBS6, SBS14, SBS15, SBS20, SBS21, and SBS44.

Signature SBS27 (v3.0)

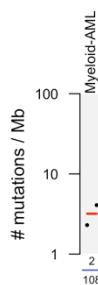


Signature SBS27-TSB



Signature 27 exhibits strong transcriptional strand bias for T>A mutations with more mutations of A than T on the untranscribed strands of genes consistent with damage to adenine and repair by transcription couple nucleotide excision repair and/or DNA damage. However, the transcriptional strand bias is inconsistent across trinucleotide contexts. Please note that signature SBS27 has only been found in exome sequencing data and, as such, the transcriptional strand bias reflects the one observed in the coding regions of the genome.

Cancer types in which the signature is found



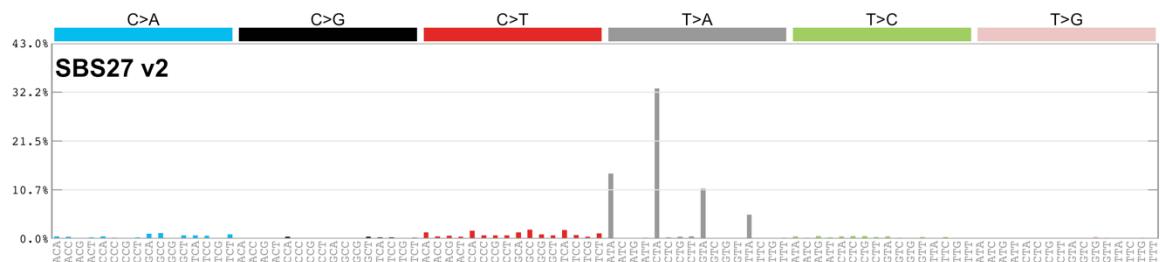
Proposed aetiology

Possible sequencing artefact.

Associated mutation classes and signatures

N/A

Differences between current and previous profiles

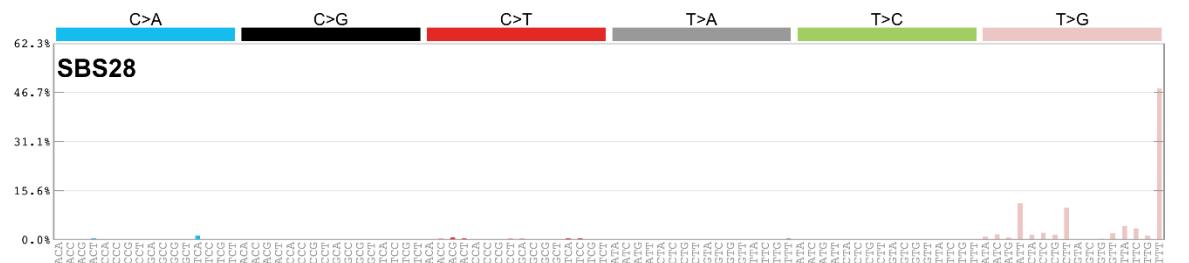


The cosine similarity between the prior and current versions of signature SBS27 is 1.00.

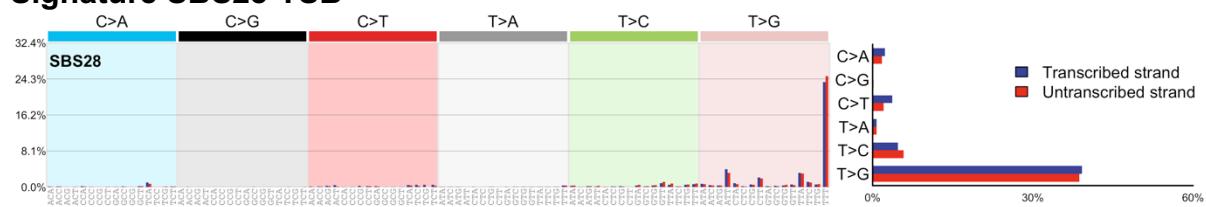
Comments

N/A

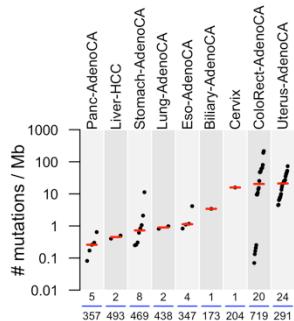
Signature SBS28 (v3.0)



Signature SBS28-TSB



Cancer types in which the signature is found



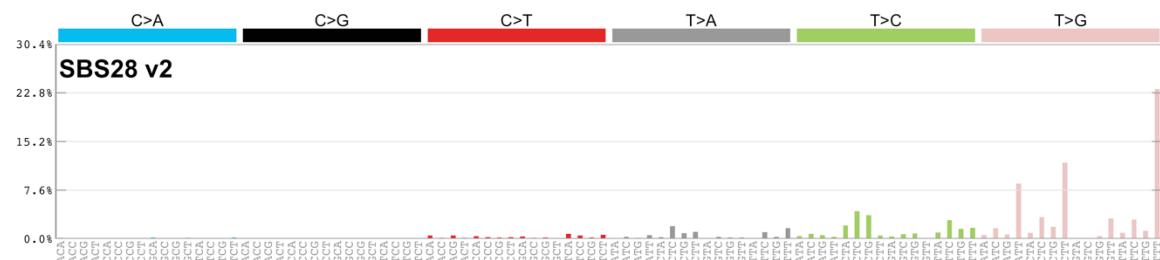
Proposed aetiology

Unknown.

Associated mutation classes and signatures

Signature SBS28 is found in most samples with signature 10a/b.

Differences between current and previous profiles

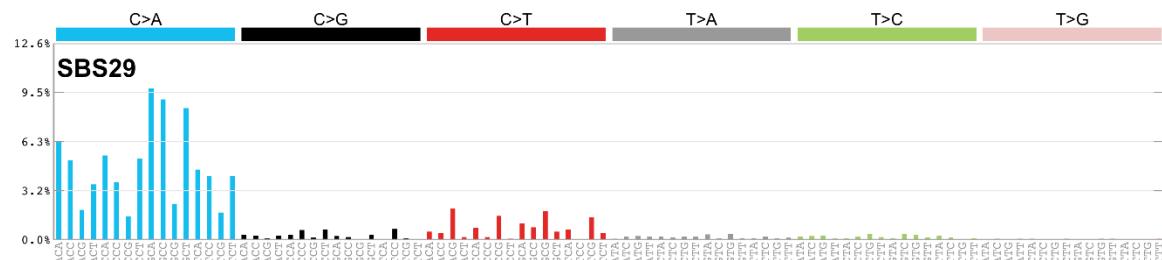


The cosine similarity between the prior and current versions of signature SBS28 is 0.92.

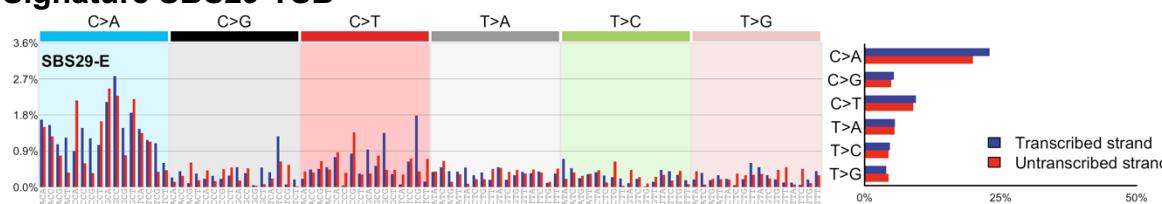
Comments

Signature SBS28 has similarities to signature SBS17b and these two signatures can be mistaken to one another. Signature SBS28 is found in most samples with signatures SBS10a/b where it contributes very high numbers of mutations. In contrast, SBS28 contributes much smaller number of mutations in samples lacking signatures SBS10a/b.

Signature SBS29 (v3.0)

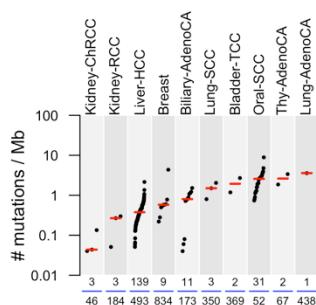


Signature SBS29-TSB



Signature 29 exhibits weak transcriptional strand bias for C>A mutations indicating guanine damage that is most likely repaired by transcription-coupled nucleotide excision repair and/or DNA damage. Please note that signature SBS29 has only been found in exome sequencing data and, as such, the transcriptional strand bias reflects the one observed in the coding regions of the genome.

Cancer types in which the signature is found



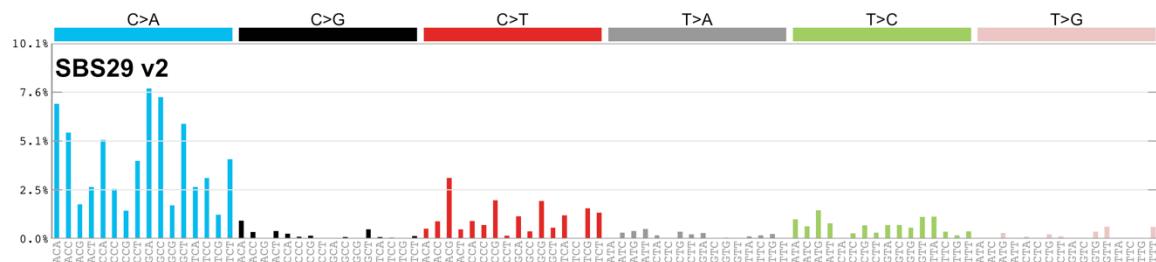
Proposed aetiology

Signature SBS29 has been found in cancer samples from individuals with a tobacco chewing habit.

Associated mutation classes and signatures

N/A

Differences between current and previous profiles

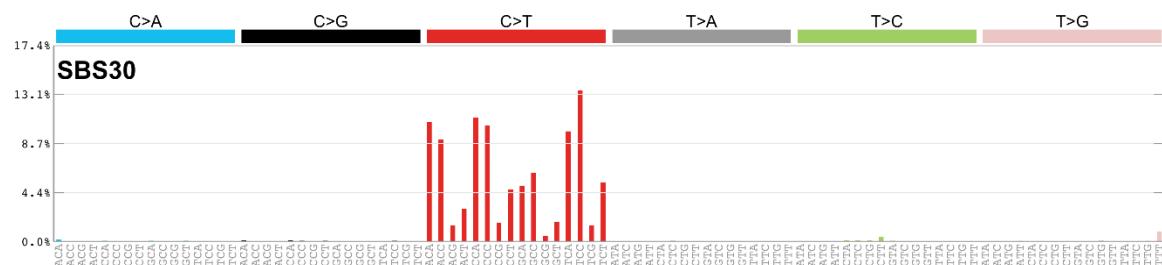


The cosine similarity between the prior and current versions of signature SBS29 is 0.97.

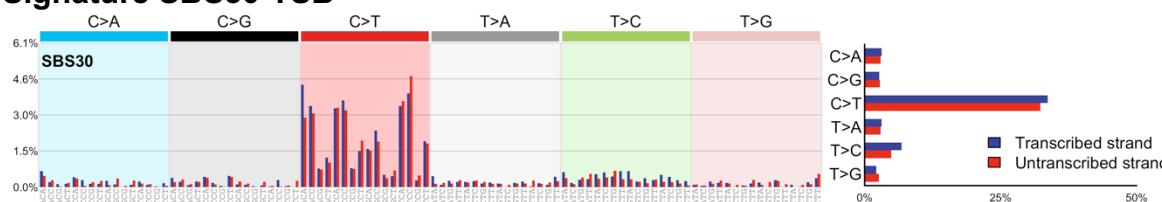
Comments

The pattern of C>A mutations in signature SBS29 appears different from the pattern of mutations due to tobacco smoking reflected by signature SBS4.

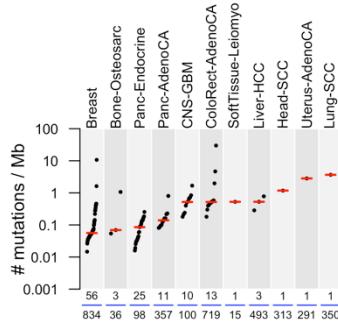
Signature SBS30(v3.0)



Signature SBS30-TSB



Cancer types in which the signature is found



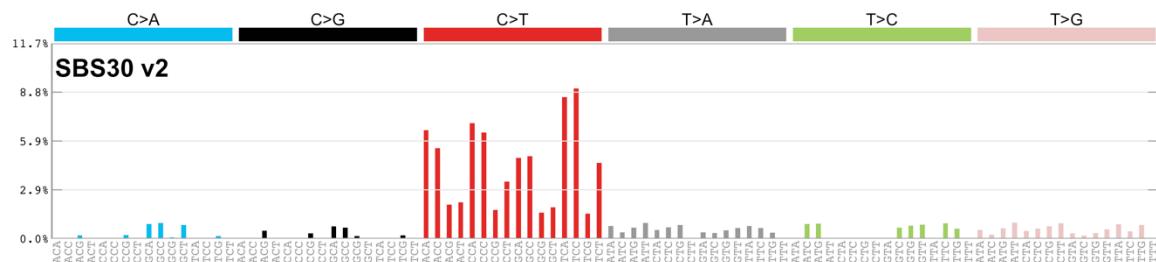
Proposed aetiology

Signature SBS30 is due to deficiency in base excision repair and, more specifically, to inactivating mutations in NTHL1.

Associated mutation classes and signatures

N/A

Differences between current and previous profiles

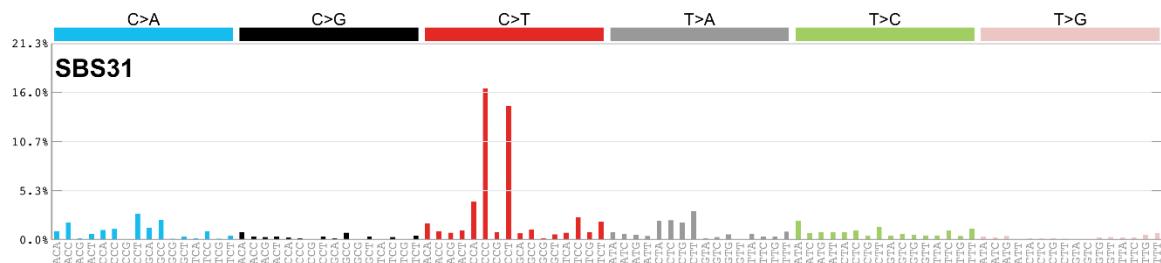


The cosine similarity between the prior and current versions of signature SBS30 is 0.96.

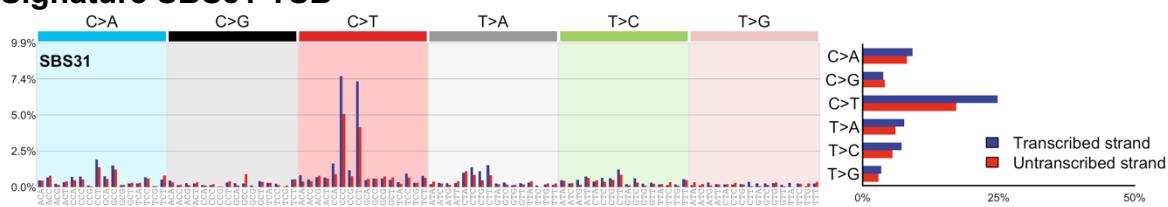
Comments

N/A

Signature SBS31 (v3.0)

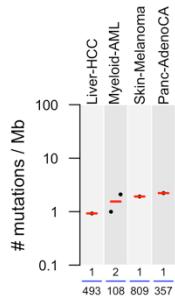


Signature SBS31-TSB



Transcriptional strand bias of C>T mutations with more G than C mutations on the untranscribed strands of genes consistent with damage to guanine and repair by transcription coupled nucleotide excision repair and/or DNA damage.

Cancer types in which the signature is found



Proposed aetiology

Prior chemotherapy treatment with platinum drugs.

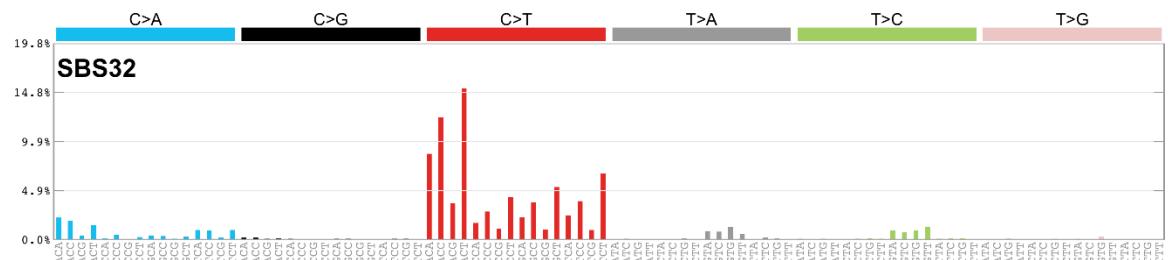
Associated mutation classes and signatures

Signature SBS31 is associated with doublet nucleotide signature DBS5, which is predominantly characterized with CT>AA mutations.

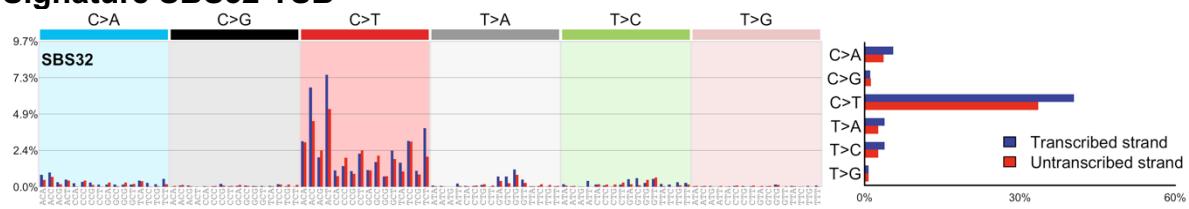
Comments

Signature SBS31 exhibits a pattern of mutations similar to components of signature SBS35 and both may be due to platinum drug treatment.

Signature SBS32 (v3.0)

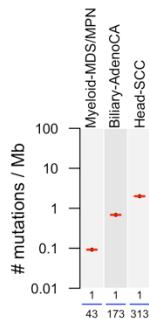


Signature SBS32-TSB



Transcriptional strand bias of C>T mutations with more G than C mutations on the untranscribed strands of genes consistent with damage to guanine and repair by transcription coupled nucleotide excision repair and/or DNA damage.

Cancer types in which the signature is found



Proposed aetiology

Prior treatment with azathioprine to induce immunosuppression.

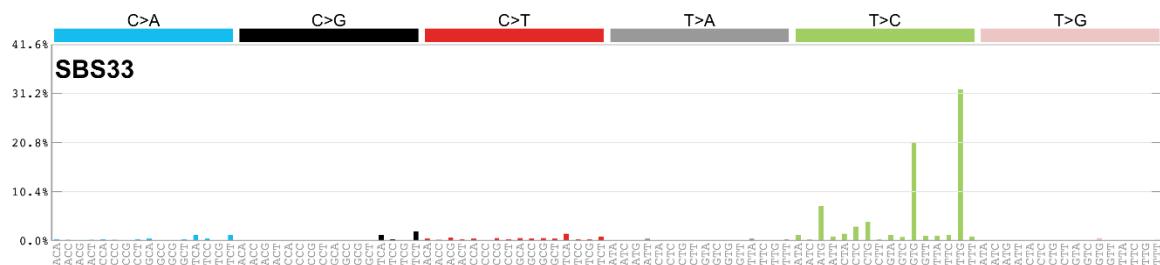
Associated mutation classes and signatures

N/A

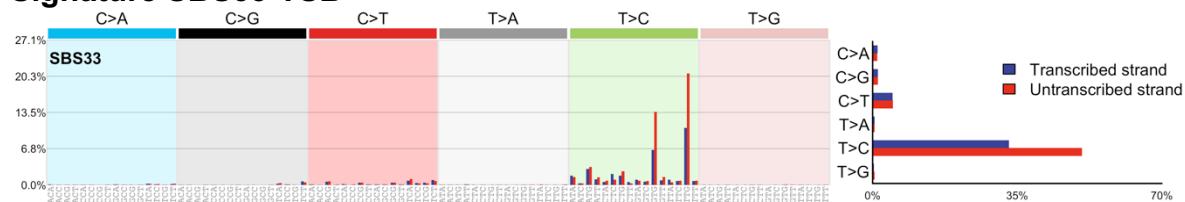
Comments

N/A

Signature SBS33 (v3.0)

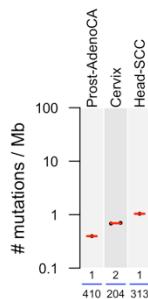


Signature SBS33-TSB



Transcriptional strand bias of T>C mutations with more T than A mutations on untranscribed strands of gene consistent with damage to thymidine and transcriptional coupled nucleotide excision repair and/or DNA damage.

Cancer types in which the signature is found



Proposed aetiology

Unknown.

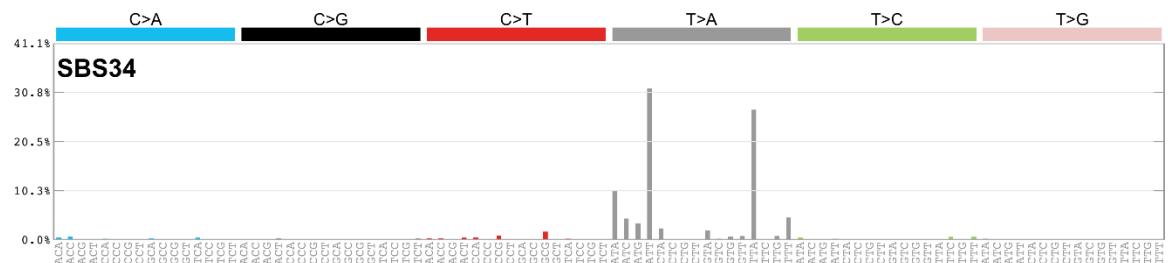
Associated mutation classes and signatures

N/A

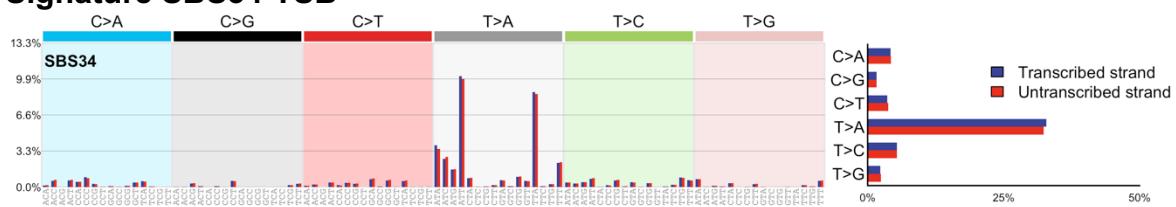
Comments

N/A

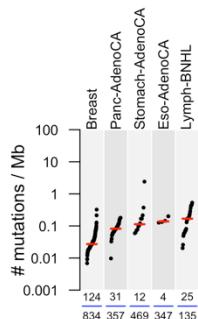
Signature SBS34 (v3.0)



Signature SBS34-TSB



Cancer types in which the signature is found



Proposed aetiology

Unknown.

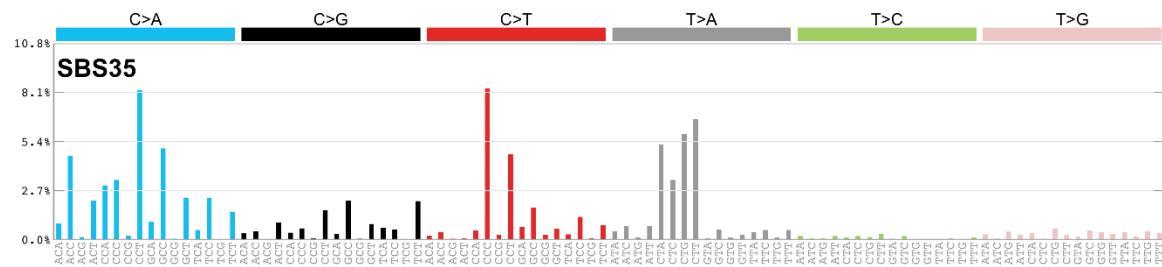
Associated mutation classes and signatures

N/A

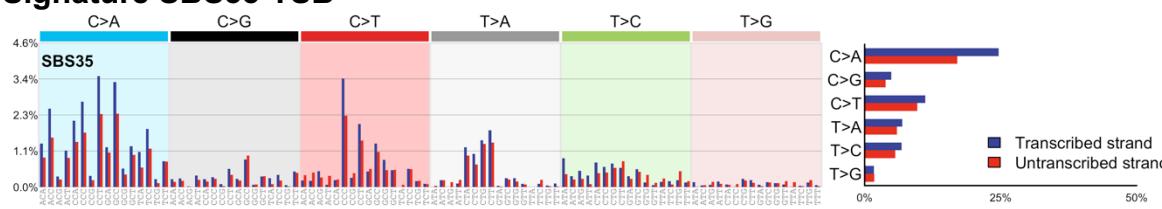
Comments

N/A

Signature SBS35 (v3.0)

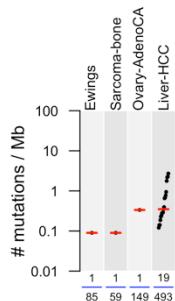


Signature SBS35-TSB



Transcriptional strand bias of C>A and C>T mutations with more G than C mutations on the untranscribed strands of genes consistent with damage to guanine and repair by transcription coupled nucleotide excision repair and/or DNA damage.

Cancer types in which the signature is found



Proposed aetiology

Prior chemotherapy treatment with platinum drugs.

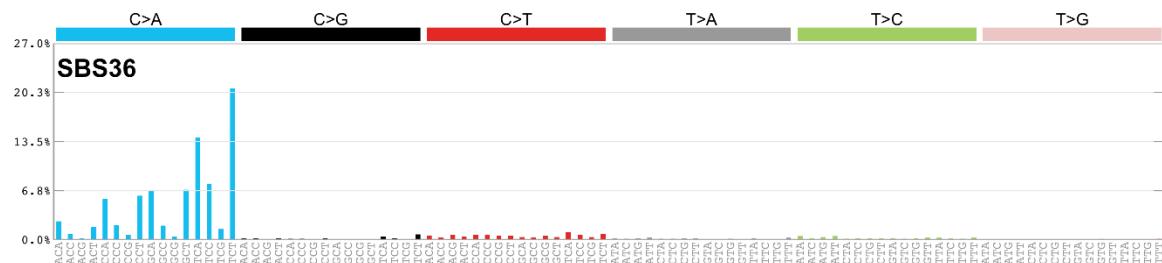
Associated mutation classes and signatures

Signature SBS35 is associated with doublet nucleotide signature DBS5, which is predominantly characterized with CT>AA mutations.

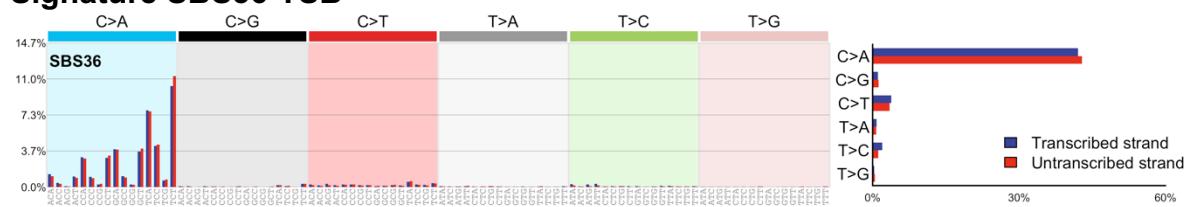
Comments

Signature SBS35 exhibits a pattern of mutations that encompasses signature SBS31 and both may be due to platinum drug treatment.

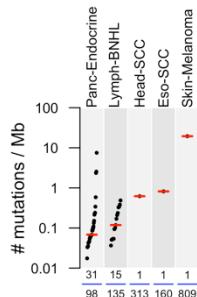
Signature SBS36 (v3.0)



Signature SBS36-TSB



Cancer types in which the signature is found



Proposed aetiology

Defective base excision repair, including DNA damage due to reactive oxygen species, due to biallelic germline or somatic MUTYH mutations.

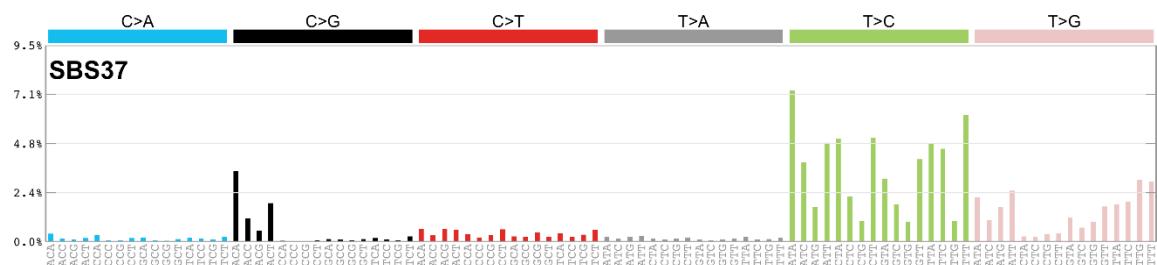
Associated mutation classes and signatures

N/A

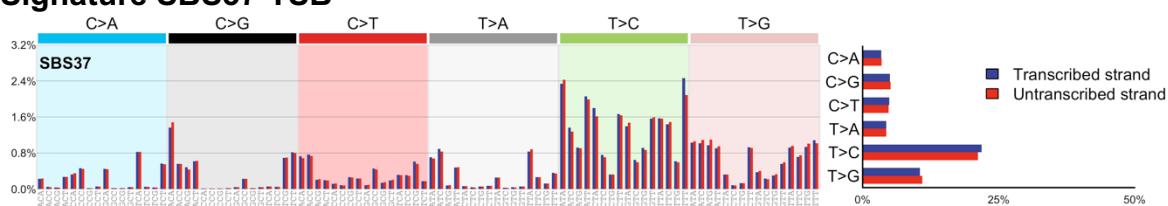
Comments

Similar to signature SBS18 which has been proposed to be due to reactive oxygen species DNA damage.

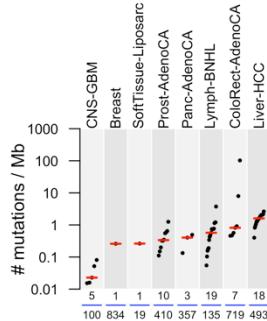
Signature SBS37 (v3.0)



Signature SBS37-TSB



Cancer types in which the signature is found



Proposed aetiology

Unknown.

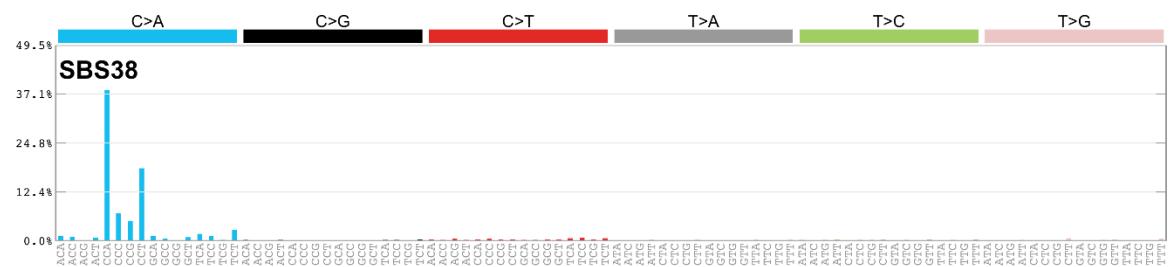
Associated mutation classes and signatures

N/A

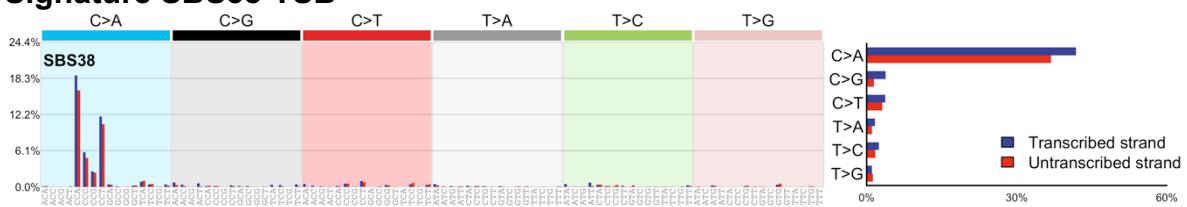
Comments

N/A

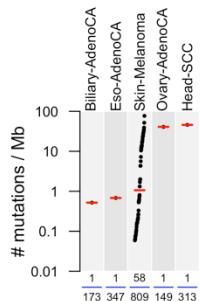
Signature SBS38 (v3.0)



Signature SBS38-TSB



Cancer types in which the signature is found



Proposed aetiology

Unknown. Found only in ultraviolet light associated melanomas suggesting a potential indirect damage from UV-light.

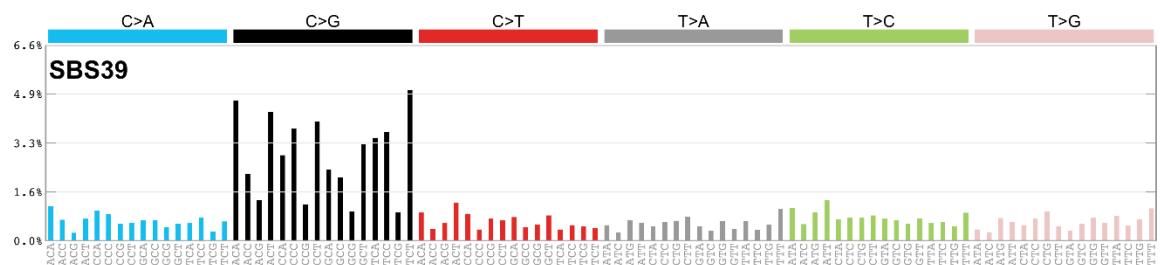
Associated mutation classes and signatures

N/A

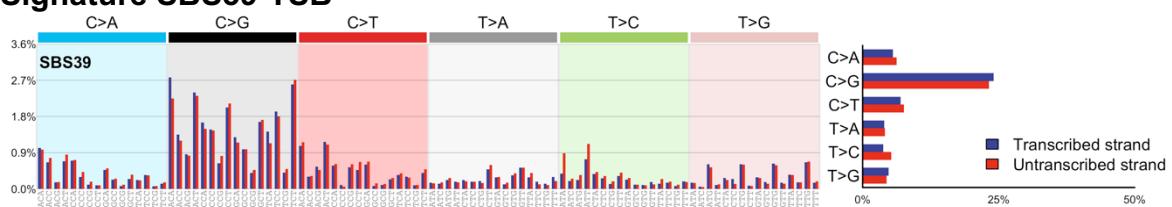
Comments

N/A

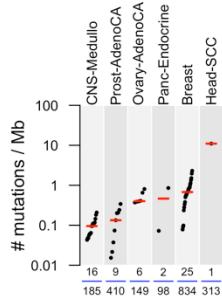
Signature SBS39 (v3.0)



Signature SBS39-TSB



Cancer types in which the signature is found



Proposed aetiology

Unknown.

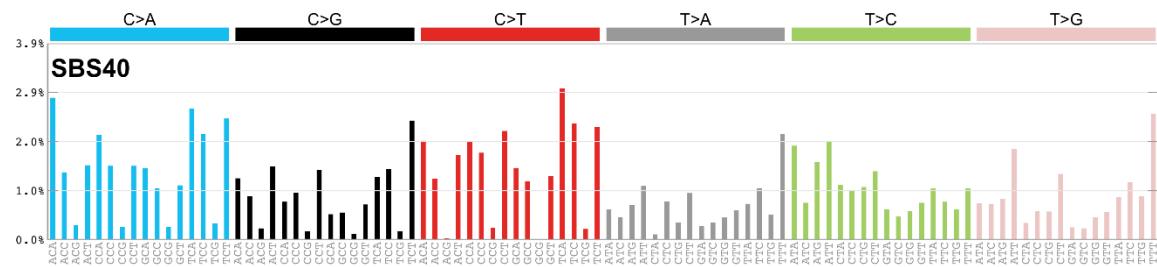
Associated mutation classes and signatures

N/A

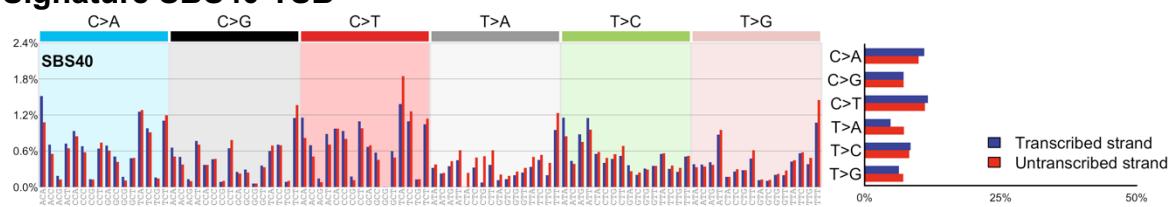
Comments

N/A

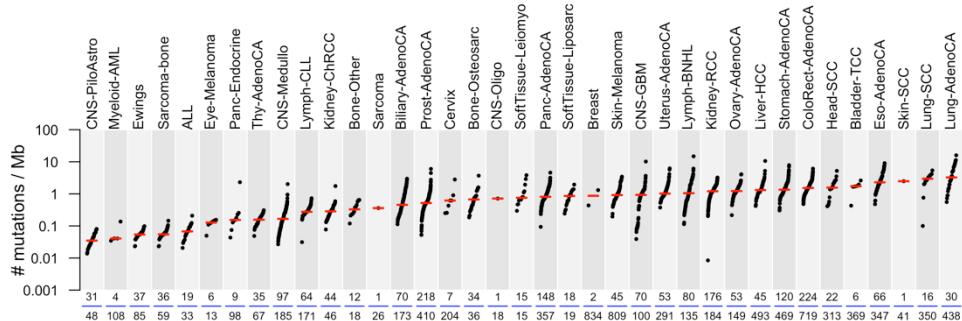
Signature SBS40 (v3.0)



Signature SBS40-TSB



Cancer types in which the signature is found



Proposed aetiology

Unknown.

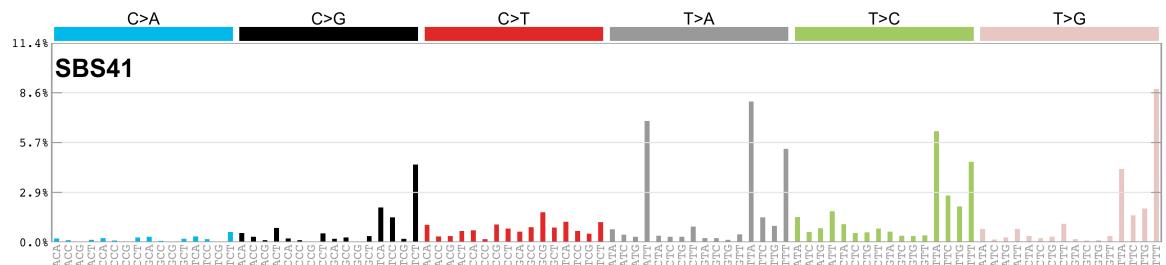
Associated mutation classes and signatures

N/A

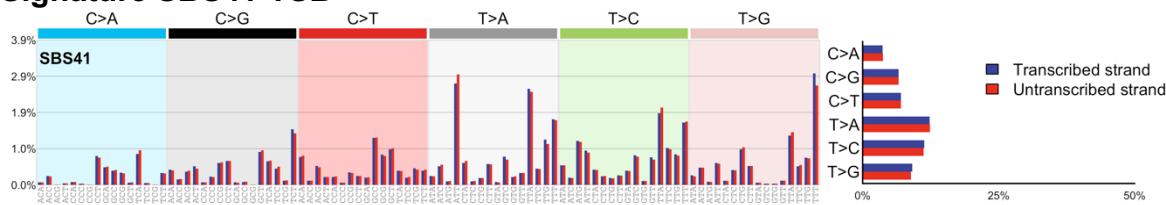
Comments

Numbers of mutations attributed to SBS40 are correlated with patients' ages for some types of human cancer.

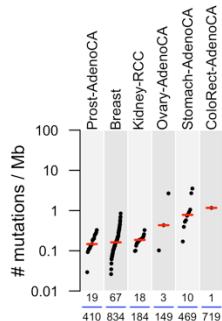
Signature SBS41 (v3.0)



Signature SBS41-TSB



Cancer types in which the signature is found



Proposed aetiology

Unknown

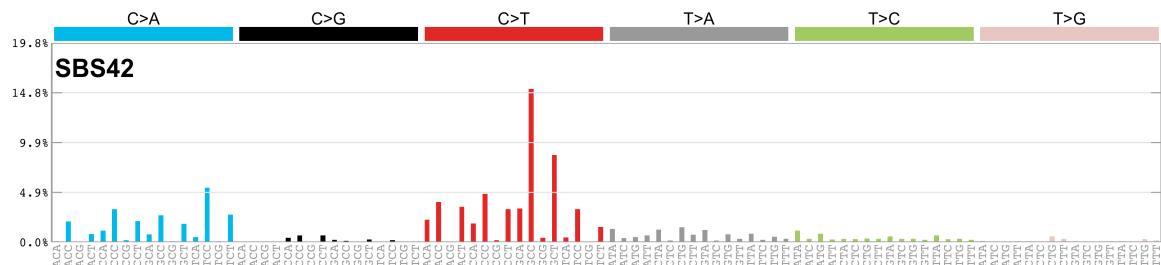
Associated mutation classes and signatures

N/A

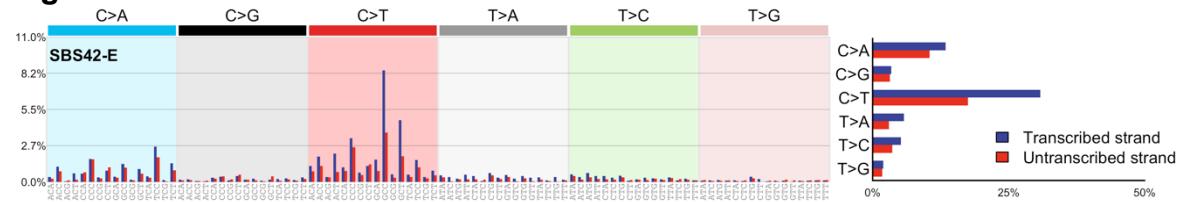
Comments

N/A

Signature SBS42 (v3.0)

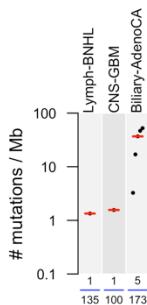


Signature SBS42-TSB



Transcriptional strand bias of C>A mutations with more G than C mutations on the untranscribed strands of genes consistent with damage to guanine and repair by transcription coupled nucleotide excision repair and/or DNA damage. Transcriptional strand bias of C>T mutations with more G than C mutations on the untranscribed strands of genes consistent with damage to guanine and repair by transcription coupled nucleotide excision repair and/or DNA damage. Please note that signature SBS42 has only been found in exome sequencing data and, as such, the transcriptional strand bias reflects the one observed in the coding regions of the genome.

Cancer types in which the signature is found



Proposed aetiology

Occupational exposure to haloalkanes.

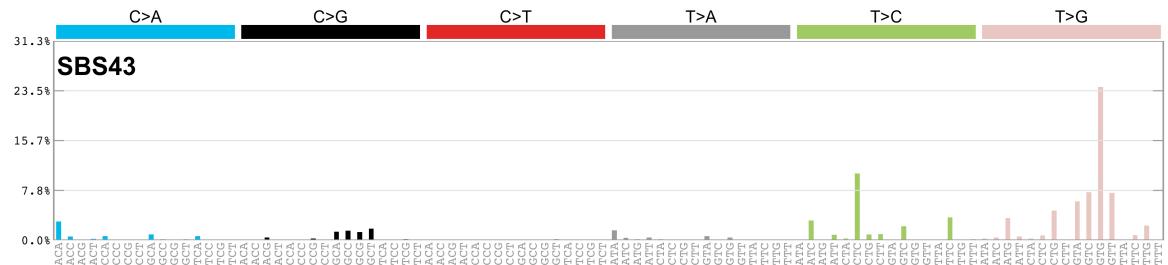
Associated mutation classes and signatures

N/A

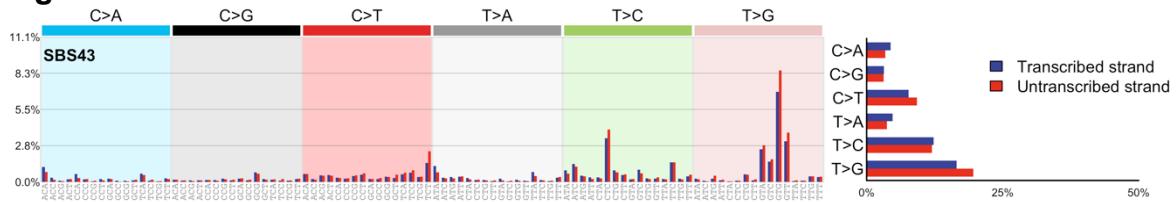
Comments

N/A

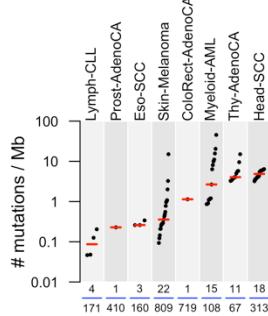
Signature SBS43 (v3.0)



Signature SBS43-TSB



Cancer types in which the signature is found



Proposed aetiology

Unknown. Possible sequencing artefact.

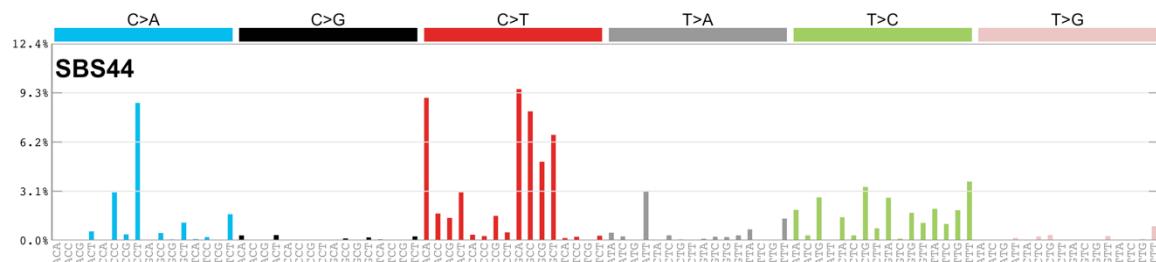
Associated mutation classes and signatures

N/A

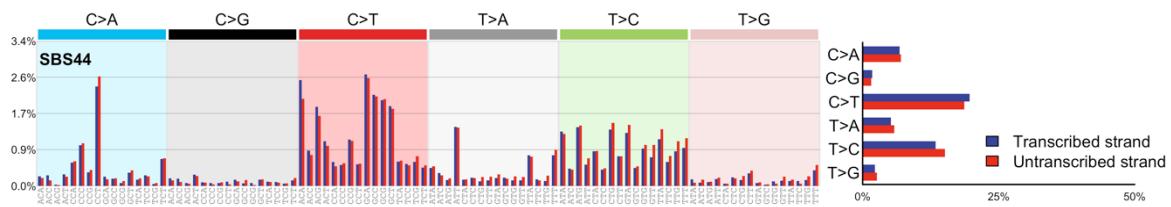
Comments

N/A

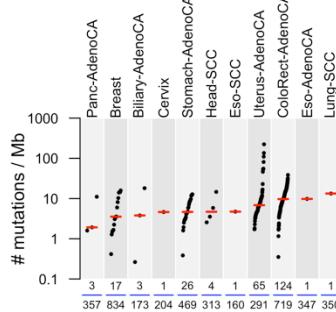
Signature SBS44



Signature SBS44-TSB



Cancer types in which the signature is found



Proposed aetiology

Defective DNA mismatch repair.

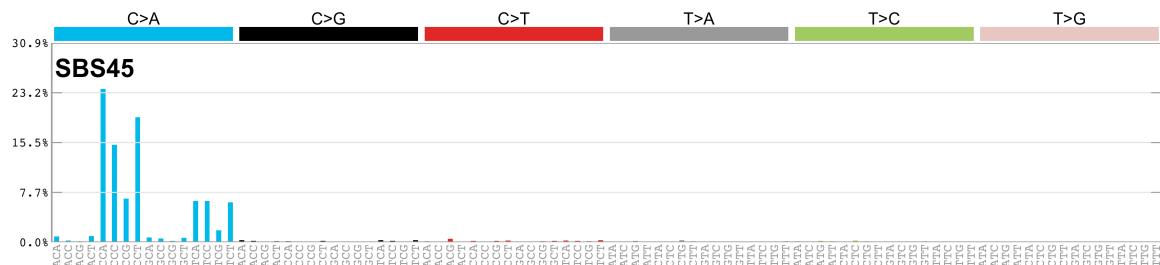
Associated mutation classes and signatures

Signature SBS44 is associated with high numbers of small (shorter than 3bp) insertions and deletions at mono/polynucleotide repeats. Signature SBS44 is associated with indel signatures ID1 and ID2.

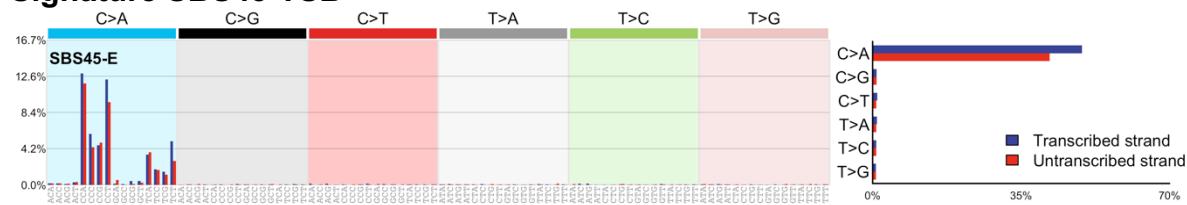
Comments

Signature SBS44 is one of seven mutational signatures associated with defective DNA mismatch repair (MSI) and is often found in the same samples as other MSI associated signatures: signatures SBS6, SBS14, SBS15, SBS20, SBS21, and SBS26.

Signature SBS45 (v3.0)

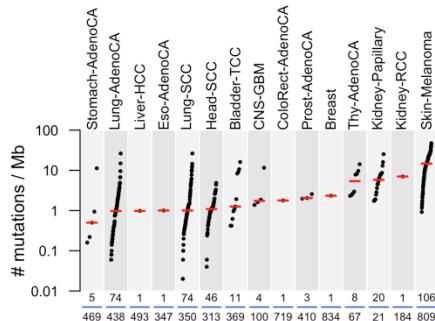


Signature SBS45-TSB



Weal transcriptional strand bias of C>A mutations with more G than C mutations on the untranscribed strands of genes consistent with damage to guanine and repair by transcription coupled nucleotide excision repair and/or DNA damage.

Cancer types in which the signature is found



Proposed aetiology

Likely artefact due to 8-oxo-guanine introduced during sequencing.

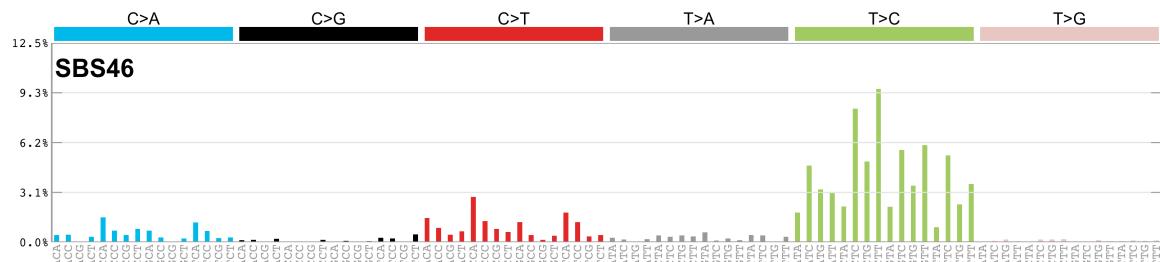
Associated mutation classes and signatures

N/A

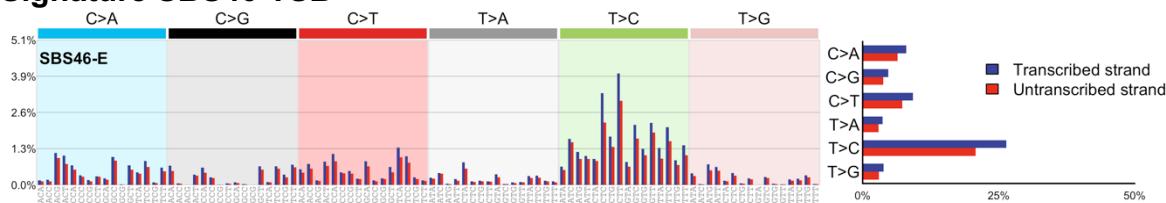
Comments

N/A

Signature SBS46

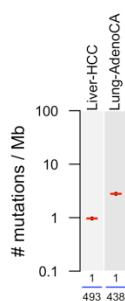


Signature SBS46-TSB



Transcriptional strand-bias for T>C substitutions with more mutations of A than T on the untranscribed strands of genes consistent with damage to adenine and repair by transcription-coupled nucleotide excision repair and/or DNA damage. Please note that signature SBS46 has only been found in exome sequencing data and, as such, the transcriptional strand bias reflects the one observed in the coding regions of the genome.

Cancer types in which the signature is found



Proposed aetiology

Likely sequencing artefact.

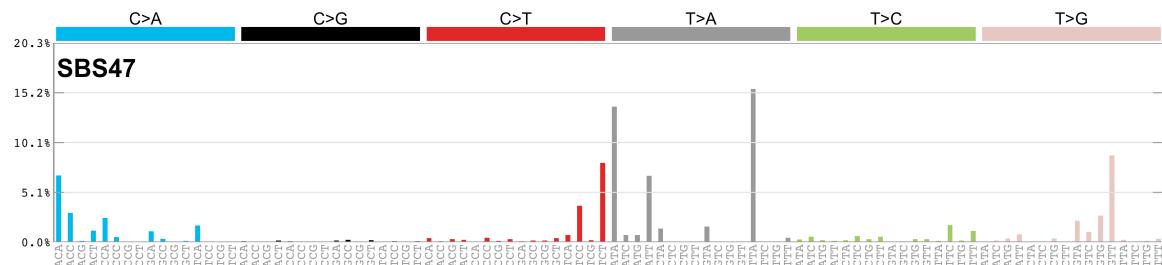
Associated mutation classes and signatures

N/A

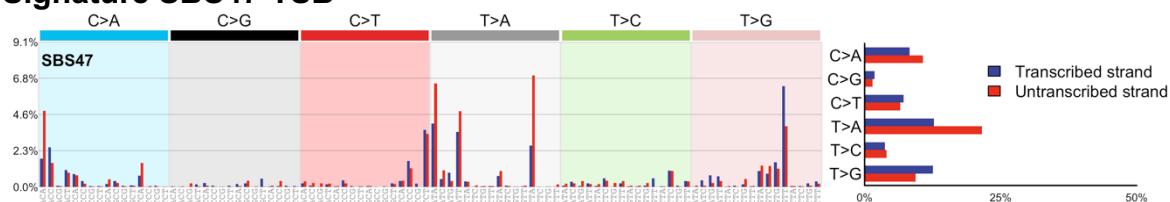
Comments

Signature SBS46 was found commonly in colorectal cancers from early releases of TCGA (data released prior 2013).

Signature SBS47 (v3.0)



Signature SBS47-TSB



Signature SBS47 exhibits inconsistent transcriptional strand bias. Transcriptional strand-bias for T>A substitutions with more mutations of T than A on the untranscribed strands of genes consistent with damage to thymine and repair by transcription-coupled nucleotide excision repair and/or DNA damage. Transcriptional strand-bias for T>G substitutions with more mutations of A than T on the untranscribed strands of genes consistent with damage to adenine and repair by transcription-coupled nucleotide excision repair and/or DNA damage.

Cancer types in which the signature is found

N/A

Proposed aetiology

Likely sequencing artefact

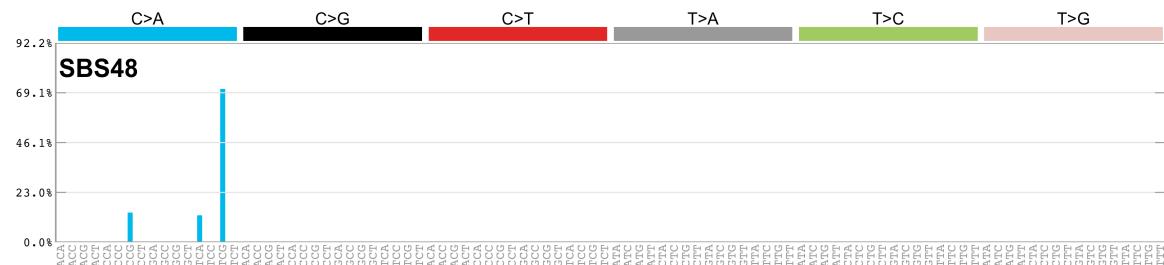
Associated mutation classes and signatures

N/A

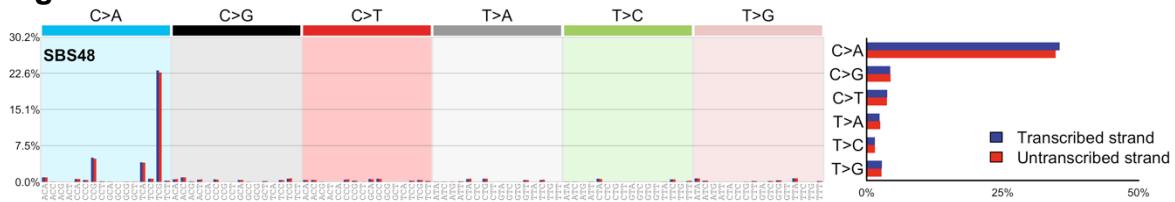
Comments

Signature SBS47 was found in cancer samples that were subsequently blacklisted for poor quality of sequencing data.

Signature SBS48 (v3.0)



Signature SBS48-TSB



Cancer types in which the signature is found

N/A

Proposed aetiology

Likely sequencing artefact

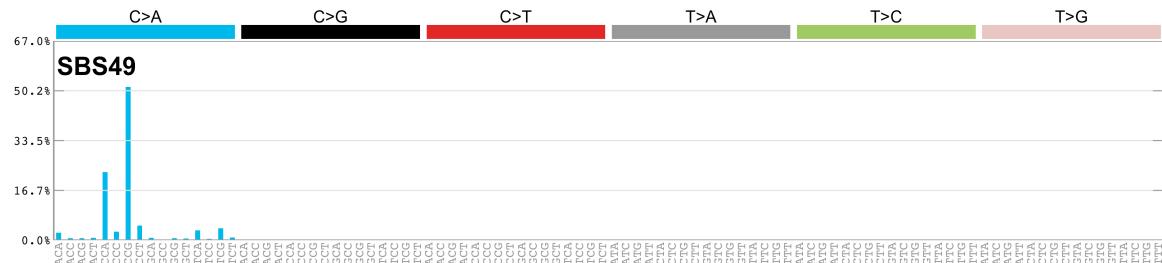
Associated mutation classes and signatures

N/A

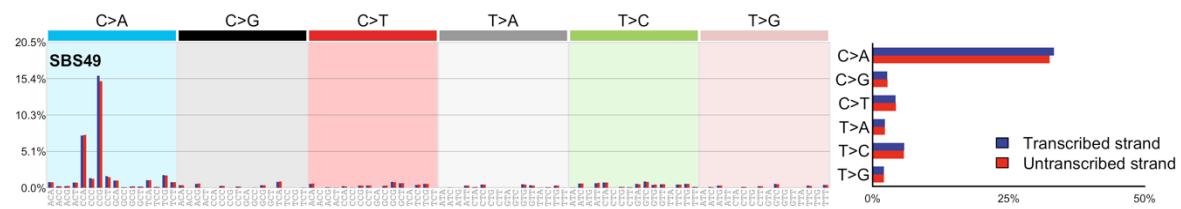
Comments

Signature SBS48 was found in cancer samples that were subsequently blacklisted for poor quality of sequencing data.

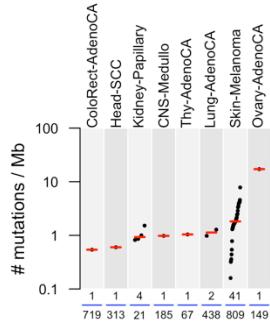
Signature SBS49 (v3.0)



Signature SBS49-TSB



Cancer types in which the signature is found



Proposed aetiology

Possible sequencing artefact.

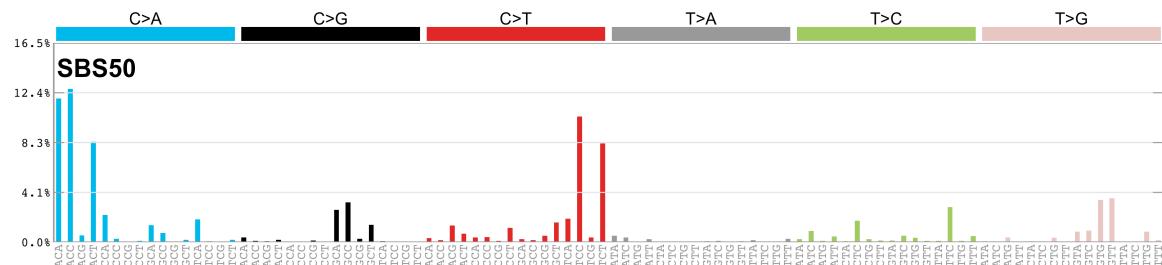
Associated mutation classes and signatures

N/A

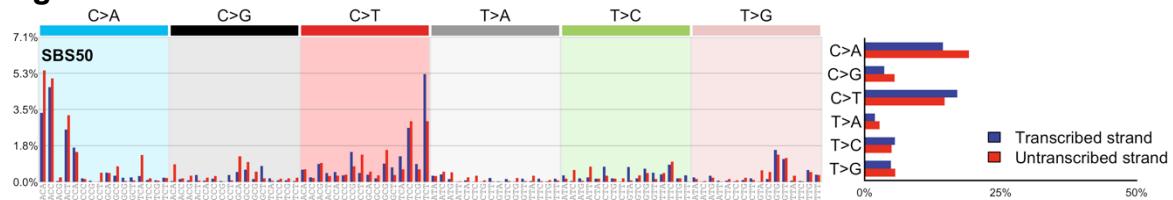
Comments

N/A

Signature SBS50 (v3.0)

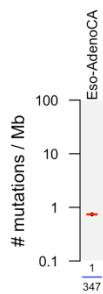


Signature SBS50-TSB



Signature SBS50 exhibits transcriptional strand-bias for C>A substitutions with more mutations of C than G on the untranscribed strands of genes consistent with damage to cytosine and repair by transcription-coupled nucleotide excision repair and/or DNA damage.

Cancer types in which the signature is found



Proposed aetiology

Likely sequencing artefact

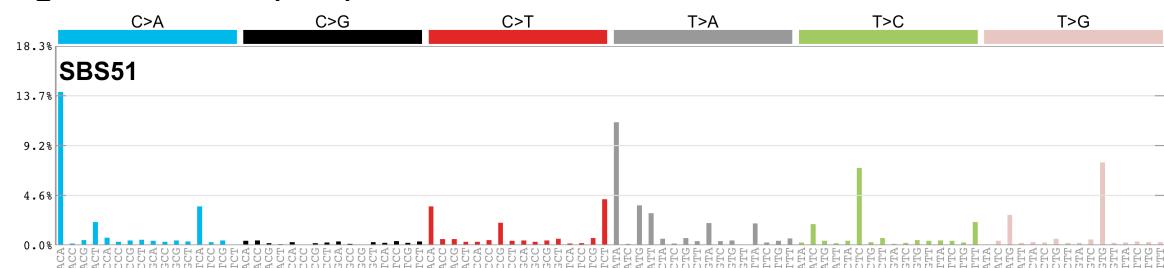
Associated mutation classes and signatures

N/A

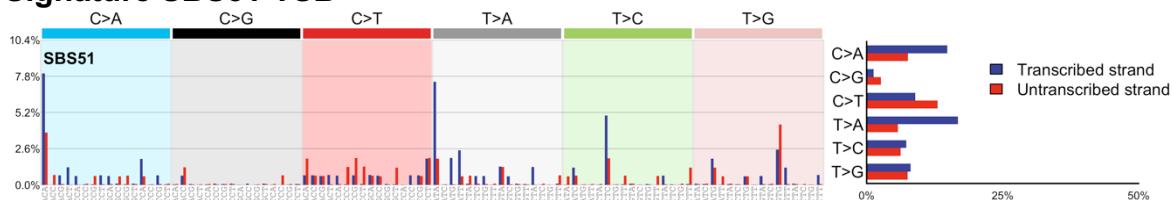
Comments

Signature SBS50 was found in cancer samples that were subsequently blacklisted for poor quality of sequencing data.

Signature SBS51 (v3.0)

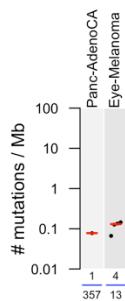


Signature SBS51-TSB



Signature SBS51 exhibits inconsistent transcriptional strand bias. Transcriptional strand-bias for C>A substitutions with more mutations of G than C on the untranscribed strands of genes consistent with damage to guanine and repair by transcription-coupled nucleotide excision repair and/or DNA damage. Transcriptional strand-bias for C>T substitutions with more mutations of C than G on the untranscribed strands of genes consistent with damage to cytosine and repair by transcription-coupled nucleotide excision repair and/or DNA damage. Transcriptional strand-bias for T>A substitutions with more mutations of A than T on the untranscribed strands of genes consistent with damage to adenine and repair by transcription-coupled nucleotide excision repair and/or DNA damage.

Cancer types in which the signature is found



Proposed aetiology

Possible sequencing artefact

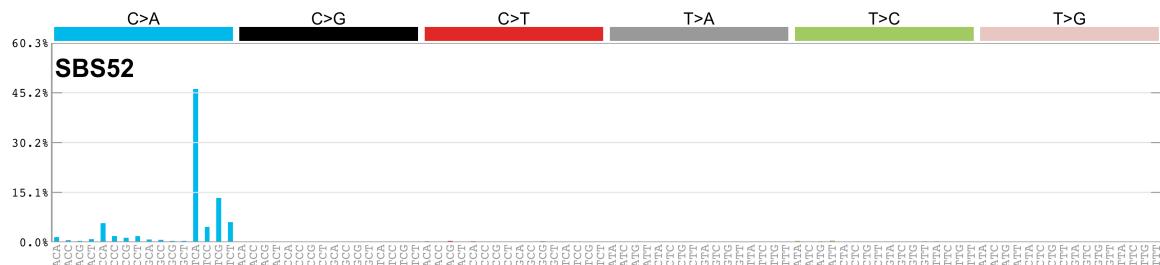
Associated mutation classes and signatures

N/A

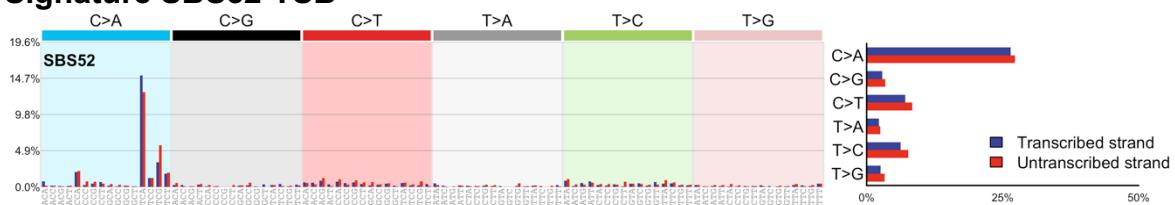
Comments

N/A

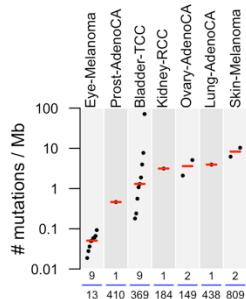
Signature SBS52 (v3.0)



Signature SBS52-TSB



Cancer types in which the signature is found



Proposed aetiology

Possible sequencing artefact

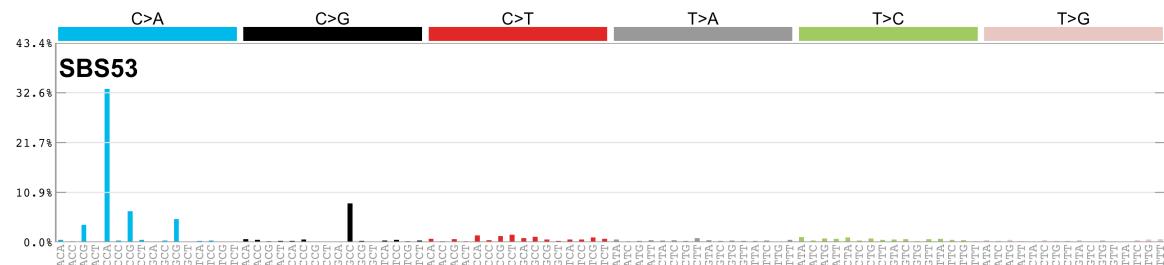
Associated mutation classes and signatures

N/A

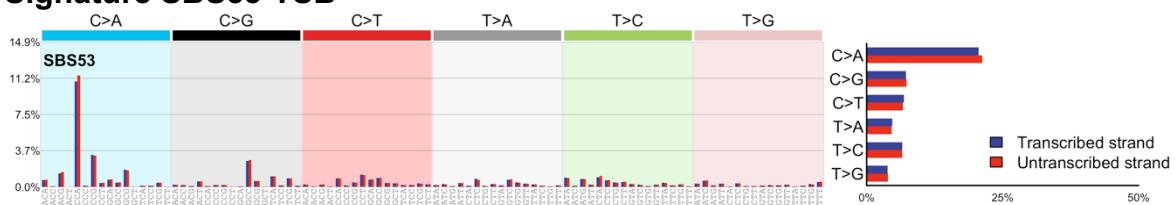
Comments

N/A

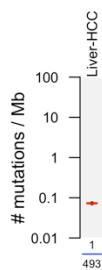
Signature SBS53 (v3.0)



Signature SBS53-TSB



Cancer types in which the signature is found



Proposed aetiology

Likely sequencing artefact

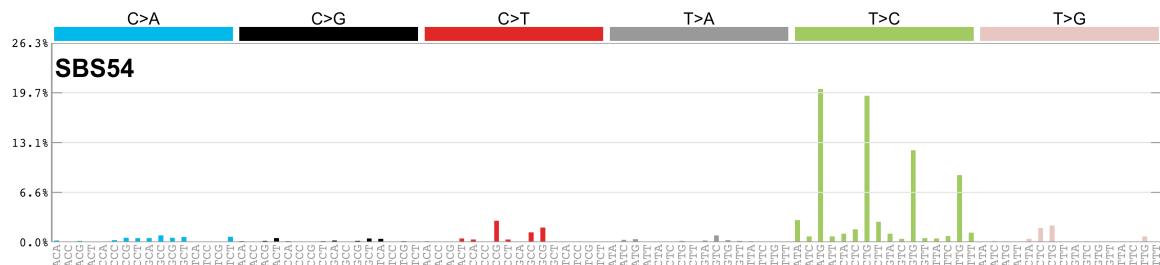
Associated mutation classes and signatures

N/A

Comments

Signature SBS53 was found in cancer samples that were subsequently blacklisted for poor quality of sequencing data.

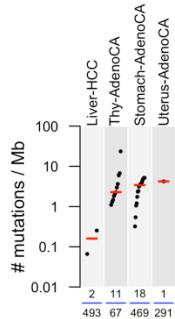
Signature SBS54 (v3.0)



Signature SBS54-TSB



Cancer types in which the signature is found



Proposed aetiology

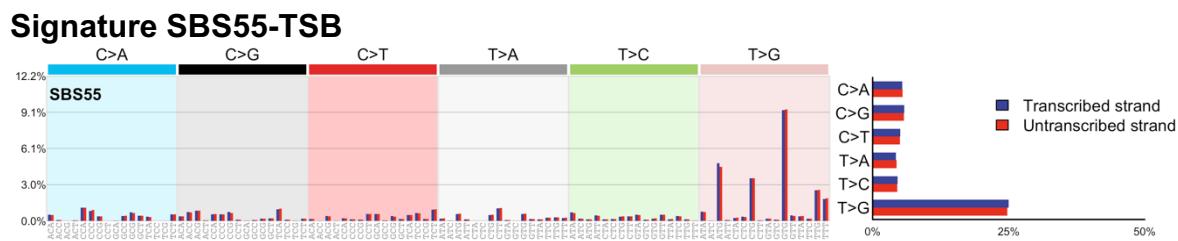
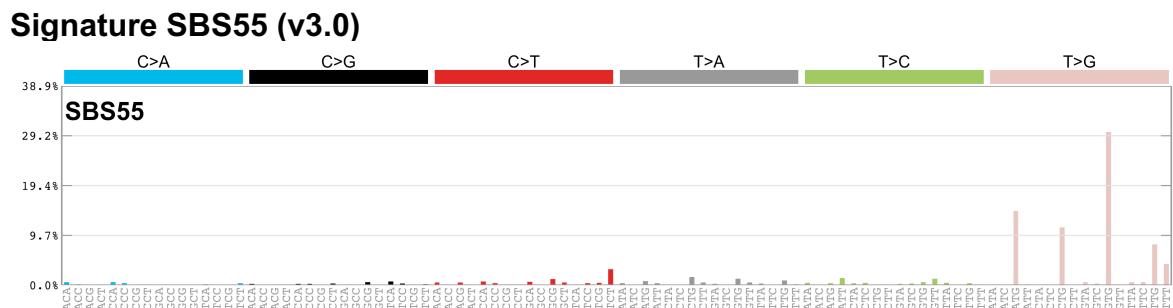
Potential sequencing artefact. Potential contamination with germline variants.

Associated mutation classes and signatures

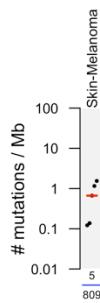
N/A

Comments

N/A



Cancer types in which the signature is found



Proposed aetiology

Potential sequencing artefact.

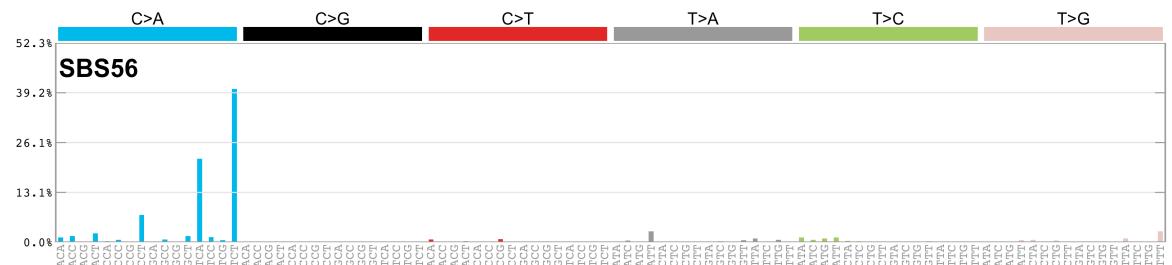
Associated mutation classes and signatures

N/A

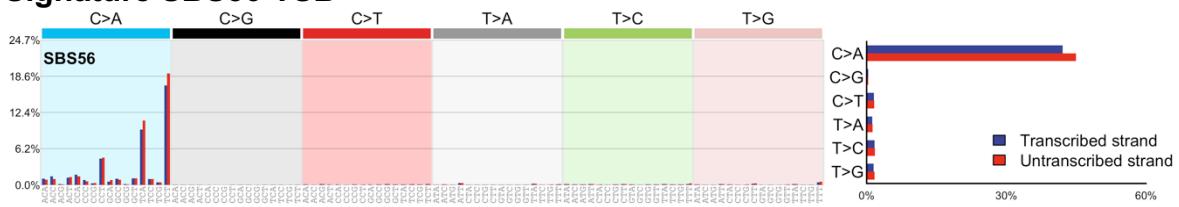
Comments

N/A

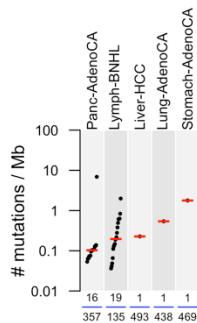
Signature SBS56 (v3.0)



Signature SBS56-TSB



Cancer types in which the signature is found



Proposed aetiology

Potential sequencing artefact.

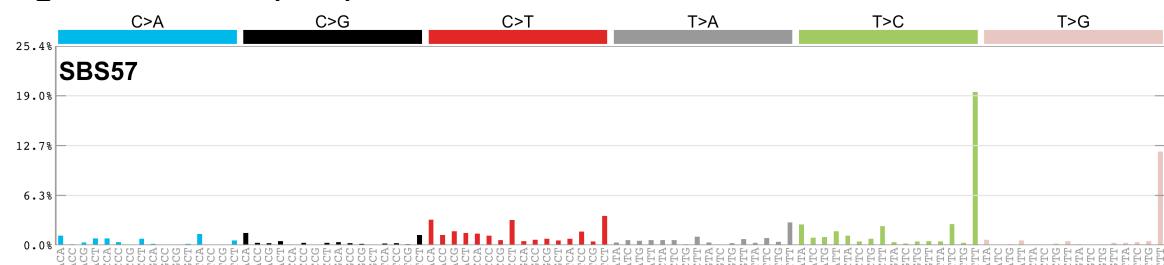
Associated mutation classes and signatures

N/A

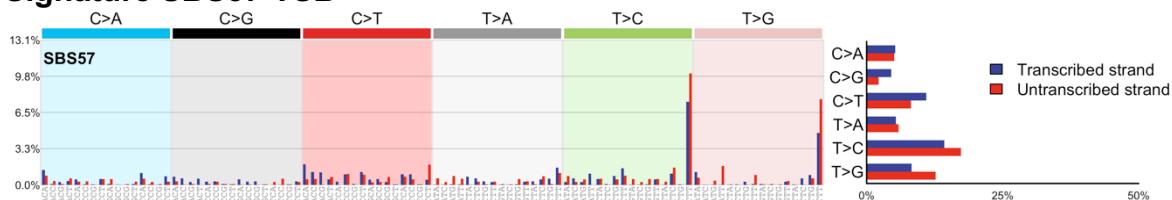
Comments

N/A

Signature SBS57 (v3.0)

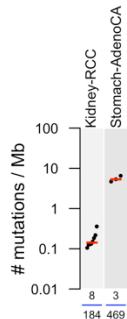


Signature SBS57-TSB



Transcriptional strand bias of T>C and T>G mutations with more A than T mutations on the untranscribed strands of genes consistent with damage to thymine and repair by transcription coupled nucleotide excision repair and/or DNA damage.

Cancer types in which the signature is found



Proposed aetiology

Potential sequencing artefact.

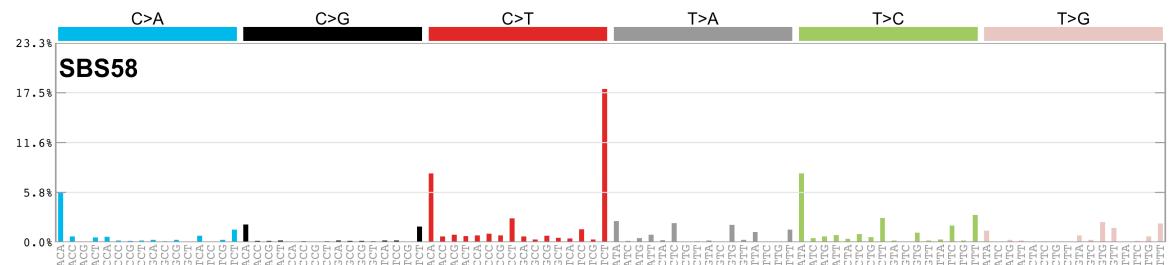
Associated mutation classes and signatures

N/A

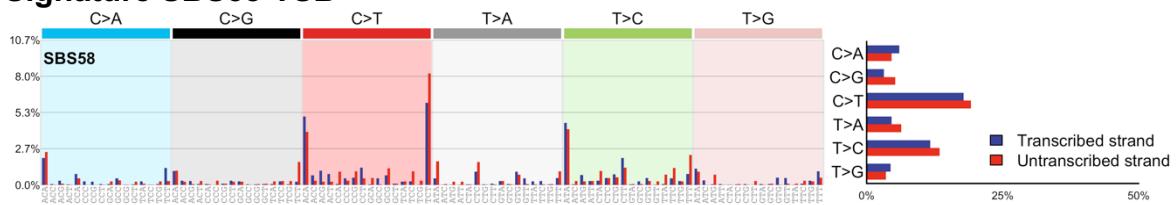
Comments

N/A

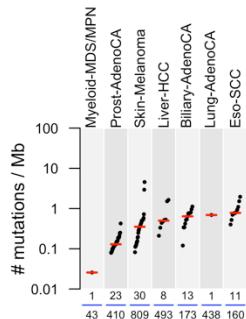
Signature SBS58 (v3.0)



Signature SBS58-TSB



Cancer types in which the signature is found



Proposed aetiology

Potential sequencing artefact.

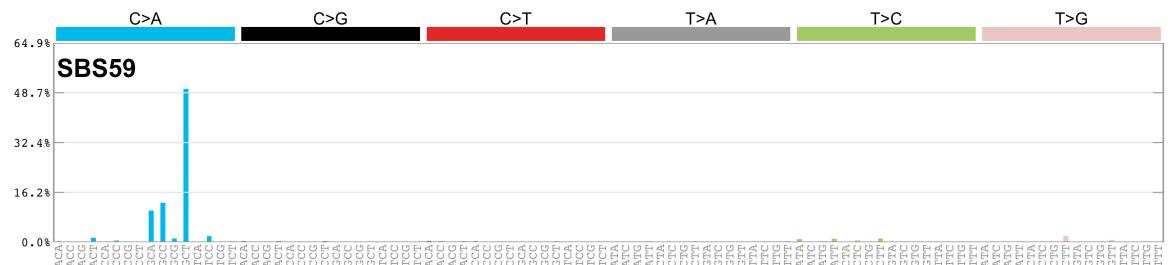
Associated mutation classes and signatures

N/A

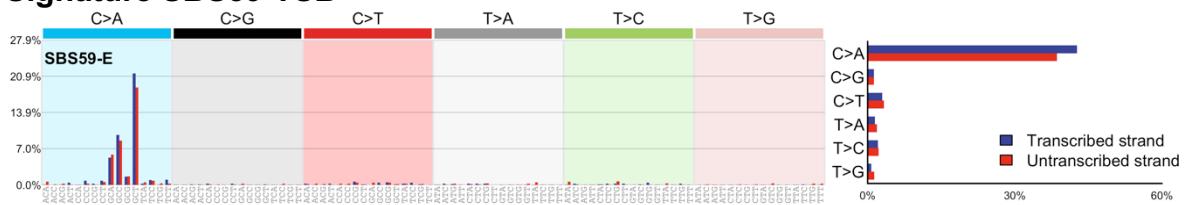
Comments

N/A

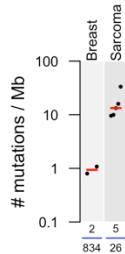
Signature SBS59 (v3.0)



Signature SBS59-TSB



Cancer types in which the signature is found



Proposed aetiology

Potential sequencing artefact.

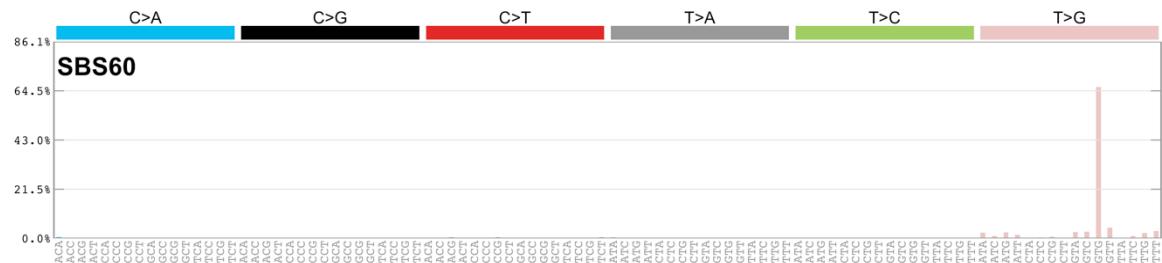
Associated mutation classes and signatures

N/A

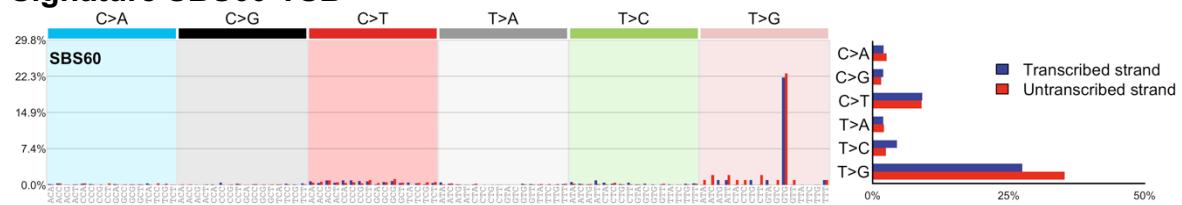
Comments

N/A

Signature SBS60

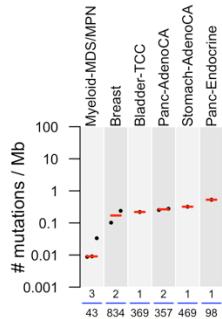


Signature SBS60-TSB



Transcriptional strand bias of T>G mutations with more A than T mutations on the untranscribed strands of genes consistent with damage to thymine and repair by transcription coupled nucleotide excision repair and/or DNA damage.

Cancer types in which the signature is found



Proposed aetiology

Known sequencing artefact.

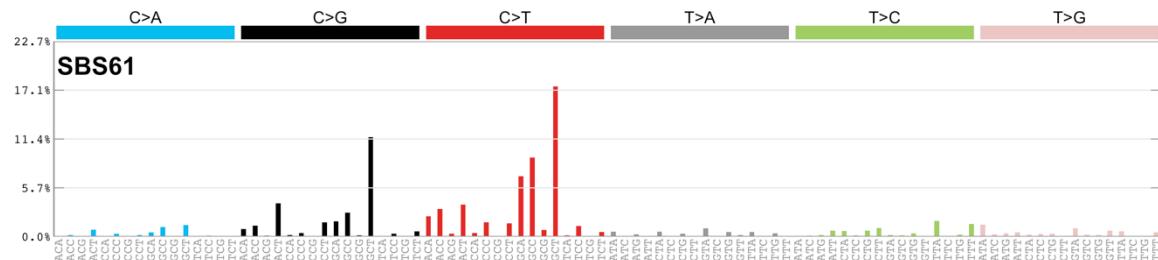
Associated mutation classes and signatures

N/A

Comments

N/A

Signature SBS61



Signature SBS61-TSB

ToDo

Cancer types in which the signature is found

ToDo

Proposed aetiology

Activity of AID

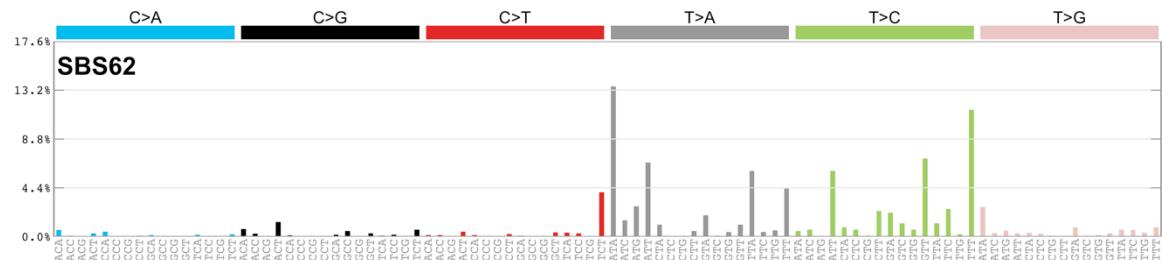
Associated mutation classes and signatures

ToDo

Comments

ToDo

Signature SBS62



Signature SBS62-TSB

ToDo

Cancer types in which the signature is found

ToDo

Proposed aetiology

ToDo

Associated mutation classes and signatures

ToDo

Comments

ToDo