Comrad: detection of expressed rearrangements by integrated analysis of RNA-Seq and low coverage genome sequence data

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ABSTRACT

Motivation: Comrad is a novel algorithmic framework for the integrated analysis of RNA-Seq and whole genome shotgun sequencing (WGSS) data for the purposes of discovering genomic rearrangements and aberrant transcripts. The Comrad framework leverages the advantages of both RNA-Seq and WGSS data, providing accurate classification of rearrangements as expressed or not expressed and accurate classification of the genomic or non-genomic origin of aberrant transcripts. A major benefit of Comrad is its ability to accurately identify aberrant transcripts and associated rearrangements using low coverage genome data. As a result, a Comrad analysis can be performed at a cost comparable to that of two RNA-Seq experiments, significantly lower than an analysis requiring high coverage genome data.

Results: We have applied Comrad to the discovery of gene fusions and read-throughs in prostate cancer cell line C4-2, a derivative of the LNCaP cell line with androgen-independent characteristics. As a proof of concept, we have rediscovered in the C4-2 data 4 of the 6 fusions previously identified in LNCaP. We also identified six novel fusion transcripts and associated genomic breakpoints, and verified their existence in LNCaP, suggesting that Comrad may be more sensitive than previous methods that have been applied to fusion discovery in LNCaP. We show that many of the gene fusions discovered using Comrad would be difficult to identify using currently available techniques.

Availability: A C++ and Perl implementation of the method demonstrated in this article is available at http://compbio.cs.sfu.ca/.

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Supplementary information: Supplementary data are available at Bioinformatics online.

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1 INTRODUCTION

High-throughput sequencing of cDNA (RNA-Seq) is rapidly accelerating our understanding of the sequence content of the human transcriptome. RNA-Seq can be used for high-throughput quantification of transcript abundance as has been done previously using microarrays. However, microarray-based approaches require pre-existing knowledge of the transcriptome sequence. RNA-Seq, in contrast, can be used for de novo characterization of the transcriptome including unbiased discovery and nucleotide level characterization of novel transcripts. Compared to previous, Sanger sequencing-based approaches for discovering novel transcripts, RNA-Seq is higher throughput for lower cost (Wang et al., 2009).

Applied to cancer genomics, RNA-Seq can be employed for the discovery of novel aberrant transcripts with implications for cancer biology. Maher et al. (2009a, b) used RNA-Seq to rediscover known gene fusions in chronic myelogenous leukaemia (CML) and prostate cell lines, and also discovered novel gene fusions in prostate tumours. Similarly, Berger et al. (2010) applied RNA-Seq to the discovery of gene fusions in melanoma. Pflueger et al. (2011) used a newly developed method called FusionSeq (Sboner et al., 2010) to discover gene fusions in RNA-Seq data from prostate tumours, and Hu et al. (2010) developed PERAlign and used it to discover gene fusions in breast cancer cell lines. The general methodology used by all of these studies was the ‘paired end’ method: (i) RNA-Seq is used to sequence both ends of a set of cDNA fragments; (ii) the resulting sequence pairs are aligned to the reference genome or transcriptome; (iii) a chimeric transcript will produce chimeric fragments and those chimeric fragments will produce a pair of sequences (paired end reads) that align to different genes, thus, any paired end read for which one end aligns to one gene and the other end aligns to another gene is considered potential evidence of a gene fusion.

Despite the aforementioned methodological advances and associated discoveries, accurate prediction of gene fusions from RNA-Seq data remains a difficult problem. The large amount of sequence data produced by high-throughput sequencing and the complexity of the transcriptome make RNA-Seq data difficult to interpret. High expression levels combined with sequencing errors and novel splicing produce many sequence pairs that appear to have been produced from chimeric fragments (Shomer et al., 2010). Furthermore, the reverse transcription step used to produce cDNA has been shown to produce chimeric fragments via the process of template switching (Houseley and Tollervey, 2010). Previous studies dealt with false positives produced by ‘false’ chimeric fragments with the application of heuristic filters (Berger et al., 2010; Maher et al., 2009a, b; Pflueger et al., 2011; Sboner et al., 2010). Another common practise was to discard paired end reads with multiple
mappings to the genome (multi-map reads) (Berger et al., 2010; Maher et al., 2009a, b; Pfueger et al., 2011; Shomer et al., 2010). Although discarding multi-map reads and applying heuristic filters may reduce the false positive rate, the effects of these practises on the false negative rate have not been properly quantified. Assuming successful prediction of fusion transcripts from RNA-Seq data, the significance of those transcripts may still depend on the discovery of an underlying genomic rearrangement. Fusions between adjacent genes not associated with a genomic rearrangement are a distinct class of fusion transcript known as transcription-induced chimeras (TICs) or read-throughs. Though a significant amount of recent work has identified tissue and tumour-specific read-throughs (Brooks et al., 2009; Kato et al., 2003; Rickman et al., 2009; Wang et al., 2007), the mechanisms for their heritability remain unclear, and their ubiquity in normal tissue (Akvila et al., 2006; Parva et al., 2006) impedes assessment of their functional significance in cancer. RNA-Seq alone cannot distinguish a read-through from a small deletion that brings together two genes. Instead of RNA-Seq, some investigators have sought to discover gene fusions using whole genome shotgun sequencing (WGSS) (Bashir et al., 2008; Pleasance et al., 2010). However, results produced from WGSS data suffer from the reverse problem, that is, the significance of any fusion discovered using WGSS data is difficult to determine without an understanding of its effects on expression and without knowing whether it produces a fusion transcript. Furthermore, the unfocused nature of whole genome sequencing makes this method expensive at coverage levels required to accurately predict genomic rearrangements. A natural progression, given the complementarity of genomic and transcriptomic data, would be an analysis that combine these two data types. For example, the study by Berger et al. (2010) combined RNA-Seq data with copy number data to identify gene fusions associated with deletions and unbalanced rearrangements. Unfortunately, copy number data is ineffective for the discovery of balanced rearrangements such as the reciprocal translocation that creates the BCR–ABL gene fusion associated with CML (Rowley, 1973). In contrast, WGSS data can effectively discover balanced and unbalanced rearrangements. However, there are currently no methods that combine whole genome sequence data with RNA-Seq data for the purposes of gene fusion detection.

The availability of methods for predicting gene fusions in RNA-Seq and rearrangements in WGSS data makes it conceivable that these existing methods could be combined for a joint analysis of RNA-Seq and WGSS data for accurate gene fusion prediction. However, as we demonstrate in this article, applying each tool independently and then combining the results would be inaccurate. All methods for analysis of either RNA-Seq or WGSS data use heuristic filters to discard low confidence predictions supported by marginal amounts of evidence in order to attain a reasonable true positive rate. Thus, any true fusion supported by only a marginal amount of evidence in either one or both datasets will be missed by independent analysis. We find that a joint analysis produces a limited number of results supported by both datasets, partially obviating the need for thresholding when searching for aberrant transcripts associated with genomic rearrangements. Similarly, the actual mapping location of multi-map reads may be difficult to resolve with an independent analysis of each dataset, even when using methods that effectively leverage multi-map reads, such as MoDIL (Lee et al., 2009) or VariationHunter (Hajirasouliha et al., 2010; Hormozdiari et al., 2009, 2010) for WGSS analysis, and deFuse (McPherson et al., 2011) or ShortFuse (KimseIl et al., 2011) for RNA-Seq analysis. We show that an analysis that simultaneously considers all reads from both datasets is better able to resolve the alignment location of multi-map reads.

2 APPROACH
Conrad is a novel algorithmic framework for the integrated analysis of RNA-Seq and WGSS data for the purposes of discovering genomic rearrangements and aberrant transcripts. Conrad builds on the COMMON-LAW framework first proposed in related work by Hormozdiari et al. (2011) on structural variation discovery in multiple sequenced genomes. The Conrad method leverages the advantages of both methods to accurately classify rearrangements as expressed or not expressed and accurate classification of the genomic or non-genomic origin of aberrant transcripts. A major benefit of Conrad is its ability to accurately predict fusion transcripts and their associated genome rearrangements using low coverage WGSS data. As a result, a Conrad analysis can be performed at a cost comparable to that of two RNA-Seq experiments, significantly lower than an analysis requiring high coverage genome data. The algorithmic basis of Conrad, provided in detail in this article, is an integer programming formulation which can be solved exactly using branch and bound or approximately using the relaxation of the linear program. For larger datasets, Conrad provides the option of using a greedy algorithm that can yield efficient solutions with reasonable running times.

We have applied Conrad to the discovery of gene fusions and read-throughs in prostate cancer cell line C4-2, a derivative of the LNCap cell line with androgen-independent characteristics. As proof of concept, we have used Conrad to rediscover 4 out of 5 fusions previously described in LNCap and known to also exist in C4-2. We have also used Conrad to identify six novel fusion transcripts and associated genomic rearrangements. A simple extension to the Conrad framework has allowed us to discover reciprocal rearrangement breakpoints for the two translocations found in the C4-2 data, making Conrad the first method to allow for the systematic discovery of reciprocal rearrangements. Furthermore, since Conrad is not biased towards canonical fusion splice junctions or fusions between known exons, we are able to use Conrad to discover fusions exhibiting non-canonical splicing. Some of the fusions we identify are supported by multi-map reads, showing that Conrad can effectively leverage multi-map reads for fusion discovery. Finally, some of the rearrangement breakpoints discovered by Conrad have as few as one read of supporting evidence, showing that Conrad is effective at discovering fusion evidence in low coverage genome data.

3 METHODS
The Conrad method begins by enumerating all rearrangement breakpoints implied by the WGSS reads and all gene fusion splices implied by the RNA-Seq reads. Some of these breakpoints and fusion splices will be supported by multi-map reads, but a read can only originate from at most one genomic location. Thus, we require a robust method for determining the most likely origin for each read given the greater context of the alignments of all WGSS and RNA-Seq reads. Most rearrangements and gene fusions are specific to individual cell lineages, i.e. they occur at low levels of recurrence (Mitelman et al., 2007). Furthermore, since the RNA-Seq and WGSS data originate from independent and then combining the results would be inaccurate.
Analysis of the WGSS data begins by enumerating all rearrangement breakpoints implied by the WGSS reads, and forming clusters of WGSS reads that support each rearrangement breakpoint. WGSS reads are aligned to the genome (NCBI36). Concordantly, aligning reads are used to estimate the minimum and maximum DNA fragment length \( L_{\text{min}} \) and \( L_{\text{max}} \) (Berger et al., 2010, Maher et al., 2009a), and are subsequently discarded. All alignments of the remaining discordant reads are retained for further analysis. We then use an existing algorithm (Hormozdiari et al., 2009, McPherson et al., 2011) to identify all clusters of discordant alignments, where each cluster is a maximal set of reads that could be explained by a single pair of breakpoints.

Similar to the analysis of the WGSS data, analysis of the RNA-Seq data begins by enumerating all fusion splices implied by the RNA-Seq reads, and forming clusters of RNA-Seq reads that support each fusion splice. RNA-Seq reads are aligned to spliced transcript sequences and unspliced gene sequences as annotated by Ensembl (version 54) (Bengtsson et al., 2008). Aligning to all splice variants of each gene and also the unspliced gene sequence enables Conrad to handle alternative splicing in a natural way. Multiple alignments of RNA-Seq data will arise because of homology between genes and redundant inclusion of the same exons in multiple splice variants of the same gene. Selecting the most parsimonious set of unique alignments for RNA-Seq data, as described later, will select not only the most likely partner of genes involved in a fusion event, but also the most likely partner of splice variants for each gene. Maximal sets of discordant RNA-Seq alignments corroborating the same fusion splice are enumerated using analogous conditions and the same algorithm as described for WGSS alignments.

### 3.2 Corroborating rearrangement breakpoints and fusion splices

RNA-Seq and WGSS alignments corroborate the same rearrangement if there exists at least one plausible genomic breakpoint at each locus that could explain both the RNA-Seq and WGSS alignments. Splicing confounds this problem because it often results in RNA-Seq reads that align to the genome many kilobases from the corresponding rearrangement breakpoints. Thus, to accurately establish corroboration between RNA-Seq and WGSS data, the effects of splicing must be considered. We describe two conditions for corroboration that afford efficient computation and ensure the existence of rearrangement breakpoints that would explain the RNA-Seq and genome sequencing alignments.

From one end of a given set of RNA-Seq alignments, we define the projected intron as the \( I_{\text{proj}} \) sized region starting at the most downstream genomic position of those alignments (Fig. 1). A set of RNA-Seq alignments is said to be corroborated by a set of WGSS alignments if the projected introns for the RNA-Seq alignments overlap with the breakpoint regions for the WGSS alignments. Thus, the overlapping intron condition is the condition that the pair of projected introns for RNA-Seq alignments must overlap with the pairs of breakpoint regions for the WGSS alignments.

We also define the intron region as the portion of the projected intron of a set of RNA-Seq alignments that is upstream from and including the breakpoint regions of a set of WGSS alignments (Fig. 1). The non-conflicting intron condition is the condition that the two intron regions for a potentially corroborating set of RNA-Seq and WGSS alignments cannot overlap. The overlapping intron condition and the non-conflicting intron condition are the two conditions that are required for RNA-Seq alignments and genome sequencing alignments to be considered evidence of the same rearrangement. The projected introns of the RNA-Seq alignments must overlap with the breakpoint regions of the genomic alignments, and the two intron regions must not overlap.

### 3.3 Selecting the most parsimonious set of alignments for ambiguously aligning reads

The relationship between WGSS reads, rearrangement breakpoints, RNA-Seq reads and fusion splices can be depicted in the rearrangement support graph as shown in Figure 2. The rearrangement support graph is formed by connecting WGSS reads to rearrangement breakpoints supported by those reads, and connecting RNA-Seq reads to fusion splices supported by those reads. Fusion splices and rearrangements breakpoints are connected based on the corroboration indicated by the overlapping intron condition and the non-conflicting intron condition.

The rearrangement support graph encodes the ambiguity of WGSS and RNA-Seq reads with multiple alignments. Since at most one alignment for each read is valid, we seek a transformation of the graph that removes edges such that the transformed graph has exactly one edge incident with each read. Given only RNA-Seq data, we previously attempted to produce a maximum parsimony solution with a minimum number of predicted fusions (McPherson et al., 2011). More recently, we introduced combinatorial formulations to identify structural variation events in several donor genomes by means of minimizing a weighted sum of structural differences between the donor genomes as well as one reference genome (Hormozdiari et al., 2011). Expanding on this principle, we now attempt to select a set of alignments...
Let $X^S$ be the set of all rearrangement breakpoints and let $X^T$ be the set of all fusion splices. Let $\delta^S$ be the set of all rearrangement breakpoint/fusion splice pairs $(x^S, x^T) \in X^S \times X^T$ that satisfy both conditions of corroboration. For each rearrangement breakpoint $x^S \in X^S$, let $\delta^S_{k} \in \delta^S$ be a corresponding indicator variable, such that $\delta^S_{x^S} = 1$ if and only if at least one alignment has been selected that supports $x^S$. In other words, $\delta^S_{x^S} = 1$ if and only if the corresponding rearrangement breakpoint vertex has at least one incident alignment edge in the transformed graph. Define fusion splice indicator variables, $\delta^T_{k} \in \Delta^T$, similarly.

We are now in a position to give precise definitions of the three types of differences being considered. For a given set of selected alignments, each $\delta^S_{x^S} \in \delta^S$ implies a single difference between the WGS data and the reference. Similarly, each $\delta^T_{k} \in \Delta^T$ implies a single difference between the RNA-Seq data and the reference. Fully enumerating the differences between the WGS data and the RNA-Seq data would require assembly of at least one of these datasets, a method we do not consider here. Instead, we define a difference between the WGS data and the RNA-Seq data as a difference found between one dataset and the reference that is not corroborated by a difference between the other dataset and the reference.

First define a corroboration indicator variable $\delta^C_{x^S}$ for each rearrangement breakpoint $x^S$ that indicates whether a fusion splice has been selected that corroborates $x^S$. More formally, $\delta^C_{x^S}$ is 1 if and only if there exists a $\delta^S_{x^T} \in \delta^S$ for each fusion splice $x^T$ such that $\delta^S_{x^T} \in \delta^S$ and the reference not corroborated by a difference between the WGS data and the reference is given by $\delta^C_{x^S} = (1 - \delta^S_{x^T})$. Conversely, an uncorroborated difference between the RNA-Seq data and the reference is given by $\delta^C_{x^S} = (1 - \delta^S_{x^T})$. Let $\Delta^C$ be the full set of alignments considered and let $\Delta^C \subseteq \Delta^T$, be any valid subset, that is, a set of alignments for which each read is aligned to exactly one mapping location. We seek to minimize the objective function $f(M)$ that calculates the total number of differences implied by $M$ (Equation (1)).

$$f(M) = \sum_{x^S} \delta^S_{x^S} + \sum_{x^T} \delta^T_{x^T} + \sum_{x^S} \delta^C_{x^S} + \sum_{x^T} \delta^C_{x^T}$$

We seek an efficient algorithm that minimizes this objective function by reducing the rearrangement support graph. We propose two algorithms for solving this problem, an ILP formulation for use with an ILP solver and an approximate algorithm based on weight set cover.

3.3.1 ILP formulation For each RNA-Seq read $x^S \in X^S$, a 0-1 integer variable $\delta^S_{x^S}$ indicates whether the edge between $x^S$ and $x^T$ is present in the transformed graph. Similarly, 0-1 integer variable $\delta^T_{x^T}$ represents whether the edge between $x^T$ and $x^S$ is present in the transformed graph. The ILP formulation for reducing the rearrangement support graph attempts to find a valid assignment for variables $\delta^S_{x^S}$ and $\delta^T_{x^T}$ that minimizes the objective function given in Equation (1). As described above, 0-1 integer variable $\delta^C_{x^S}$ and $\delta^C_{x^T}$ represent whether at least one read has been assigned to the respective rearrangement breakpoint $x^S$ and fusion splice $x^T$. Let $\delta^C_{x^S} = \delta^S_{x^T}$ and $\delta^C_{x^T} = \delta^T_{x^S}$. Also, let $\delta^C_{x^S} = 1$ if $\delta^C_{x^S}$ and $\delta^C_{x^T}$ are both in $\Delta^C$, otherwise $\delta^C_{x^S} = 0$. The objective function for this ILP is given as in Equation (1), and the constraints are given below in Equations (2)–(9).

$$\forall x^S \in X^S : \sum_{x^S} \delta^S_{x^S} = 1$$

$$\forall x^T \in X^T : \sum_{x^T} \delta^T_{x^T} = 1$$

$$\forall j \in R^T : \sum_{x^S} \delta^C_{x^S} = 0$$

$$\forall i \in R^C : \sum_{x^T} \delta^C_{x^T} = 1$$

$$\forall r \in R^T : \delta^C_{x^S} = 0$$

$$\forall r \in R^C : \delta^C_{x^T} = 0$$

$$\forall r \in R^T : \delta^C_{x^S} = \delta^T_{x^S}$$

$$\forall r \in R^C : \delta^C_{x^T} = \delta^S_{x^T}$$

$$\forall r \in R^T : \delta^C_{x^S} = \delta^C_{x^T}$$

Constraints 2 and 3 ensure that each read is assigned to exactly one cluster in the transformed graph. Constraints 4 and 5 ensure that a cluster is considered as selected if at least one read has been assigned to that cluster. The constraint given by Equation (6) ensures that $\delta^C_{x^S} = 1$ only if $\delta^C_{x^T} = 1$, a consequence of defining $\delta^C_{x^S} = \delta^C_{x^T} = \delta^C_{x^T}$. The constraint given by Equation (8) ensures that $\delta^C_{x^S}$ is 1 only if there exists a $k$ such that $\delta^S_{k} = 1$ and $\delta^C_{x^T} = 1$, that is, $\delta^C_{x^S}$ is 1 for rearrangement breakpoint $k$ only if a corroborating fusion splice has been selected. The constraints given by Equations (7) and (9) are analogous constraints for $\delta^C_{x^T}$.
We explored one other possibility. Given a rearrangement breakpoint \( x_j \) and a fusion splice \( x_{k+} \), we calculate the pair of genes potentially affected by the events represented by those clusters. We then define \( C^{ST} \) as:
\[
C^{ST} = \{(x_j, x_{k+}) : \text{genepair}(x_j) \neq \text{genepair}(x_{k+})\}
\]
We show in the Section 4 that this alternative corroborative relationship allows us to discover reciprocal translocations.

### 3.5 Assembling a prediction sequence
For each fusion splice and each rearrangement breakpoint, Conrad assembles a prediction sequence. Suppose a set of reads implies a fusion splice (or rearrangement breakpoint) between transcript A and B (or genomic loci A and B). Let \((\overrightarrow{x}_1, \overrightarrow{x}_2)\) and \((\overrightarrow{x}'_1, \overrightarrow{x}'_2)\) be the start and end positions for the alignments to A and B, respectively. Let \(S_x\) be the sequence in A in the range \([\min(\overrightarrow{x}_1), \max(\overrightarrow{x}_2)]\), and let \(S_y\) be the sequence in B in the range \([\min(\overrightarrow{x}'_1), \max(\overrightarrow{x}'_2)]\). If the alignments are to the \(\pm\) strand of gene A and the \(\pm\) strand of gene B (\(\mp\) orientation), then the prediction sequence is \(S_y \cdot S_x \) For \(\overrightarrow{\pm}\), \(\overrightarrow{\pm}\) and \(\overrightarrow{\mp}\) orientations, the predicted sequence is \(rc(S_x) \cdot rc(S_y)\) and \(rc(S_y) \cdot rc(S_x)\), respectively, where \(rc()\) is reverse complementation.

### 3.6 Heuristic filtering
The heuristic filtering used by Conrad can be categorized as pre-filtering or post-filtering. Pre-filtering is applied before the application of the above algorithms, and is intended to remove reads that are unlikely to inform a gene fusion analysis. Post-filtering is applied to the results of the above algorithms in an attempt to remove predictions that are likely to be false positives or are unlikely to be novel.

#### 3.6.1 Pre-filtering
The pre-filtering used by Conrad involves aligning reads to a specific set of sequences using bowtie (Langmead et al., 2009) and removing those reads from further consideration if their alignments satisfy a given criteria. RNA-Seq reads are aligned to the genome and Unigene clusters (Kayers et al., 2011) and reads with concordant alignments are discarded. RNA-Seq data are often contaminated by a significant amount of ribosomal RNA (rRNA) (Shoster et al., 2010). Thus, RNA-Seq reads are also aligned to ensembl annotated rRNA, and any read with one or both ends aligning to any rRNA is discarded. Conrad is not intended as a method for reconstructing immunoglobulin (IG) rearrangements. Thus, any RNA-Seq read that aligns with one end to one IG gene, and the other end to any other IG gene is discarded. Finally, Conrad discards RNA-Seq and WGS reads for which each end aligns to a repeat region in the genome, and those repeat regions are of the same type.

#### 3.6.2 False positive post-filtering
False positive post-filtering attempts to remove predictions that are most likely to be false positives produced by spurious alignment artifacts. The sequence concordance filter aligns each prediction sequence to the appropriate reference sequences using blat (Kent, 2002). Fusion splices are aligned to spliced and unspliced gene sequences and rearrangement breakpoints are aligned to the genome. A prediction sequence is discarded if that sequence aligns to the reference with \( \geq 80\% \) identity. The read concordance filter uses blat to align all reads suggestive of an event to the appropriate reference (see above). A prediction is discarded if \( \geq 10\% \) of the supporting reads align concordantly to that reference..Genomic fusions require at least one supporting WGS read and five supporting RNA-Seq reads to be considered in this study.

#### 3.6.3 Novelty post-filtering
Novelty post-filtering attempts to remove predictions that are unlikely to be novel. The sequence concordance filter is used to remove fusion splice predictions with significant alignments to ESTs (EST database retrieved from UCSC genome browser (Rhead et al., 2010)). The EST island filter begins by aligning fusion splice prediction sequences to the genome using blat and allowing for a spliced alignment. Fusion splices are discarded if their prediction sequence aligns entirely within a region of the genome suggested as co-transcribed by clusters of overlapping EST alignments (Rhead et al., 2010).

### 4 RESULTS
We analyzed RNA-Seq and WGS data produced from the C4-2 cell line, a derivative of the LNCaP prostate cell line. As a result of the close relationship between C4-2 and LNCaP, we hypothesized that fusions previously discovered in LNCaP would be useful as positive controls to be searched for in the C4-2 data. We also sought to use the C4-2 data as a proxy for discovering novel gene fusions in LNCaP. The WGS and RNA-Seq data for C4-2 each consisted of \( \geq 84 \) million 50 bp \( \times \) 50 bp paired end reads. With an approximate fragment length of 500 bp, the WGS data provide 7x physical coverage of a diploid human genome. Given that the LNCaP genome is tetraploid (Beheshti et al., 2000), the physical coverage for C4-2 is more likely closer to 3.5x.

Previous analysis of LNCaP resulted in the discovery of six fusion transcripts (Maher et al., 2009a, b), DLEU2-PSPC1, RERE-PIK3CD, MIPOL1-DGKB, MRPS10-HPR, C19orf25-APC2 and SLC45A3-ELK4. We used PCR to confirm five of these fusion transcripts as present in C4-2; DLEU2-PSPC1 could not be confirmed in C4-2. The five confirmed fusion transcripts serve as positive control fusion transcripts to be discovered by Conrad in the C4-2 data. Both C19orf25-APC2 and SLC45A3-ELK4 involve adjacent genes, and are thus potential read-through events, a possibility that was confirmed for SLC45A3-ELK4 in a more recent study (Rickman et al., 2009). Conrad found only RNA-Seq evidence of SLC45A3-ELK4 in C4-2, providing further evidence that SLC45A3-ELK4 is not associated with chromosomal rearrangement. No RNA-Seq or WGS evidence was found for C19orf25-APC2. A targeted search did not identify any RNA-Seq reads supporting a C19orf25-APC2 fusion transcript, suggesting that C19orf25-APC2 expression is less than that required for detection at the sequencing depth provided by the C4-2 RNA-Seq data. The remaining three fusions, RERE-PIK3CD, MIPOL1-DGKB and MRPS10-HPR involve distant genes and are thus potentially caused by underlying genomic rearrangement. Conrad successfully identified the previously described (Tomlins et al., 2007) rearrangement breakpoint for MIPOL1-DGKB and also identified rearrangement breakpoints for RERE-PIK3CD and MRPS10-HPR. The novel rearrangement breakpoints for RERE-PIK3CD and MRPS10-HPR were confirmed by PCR for both C4-2 and LNCaP.

Comrad predicted an additional 10 novel genomic fusions for C4-2 (Supplementary Table S1). We attempted to validate 9 of the 10 predictions, excluding AMACR-GUSBL1 as a likely read-through associated with a small 600 bp deletion. Of the nine novel Conrad predictions, six were validated in C4-2 by PCR and sanger sequencing. We also validated all six novel Conrad predictions in LNCaP, thereby showing that Conrad is more sensitive than previous methods that have been applied to fusion discovery in LNCaP. Evidence for the six previously identified fusion transcripts and the six novel Conrad predictions is shown in Table 1.

To identify potential false negatives, we also analyzed the C4-2 RNA-Seq data using deFuse, a method for identifying fusion transcripts in RNA-Seq data alone. The deFuse analysis produced 31 predictions, 8 of which are predicted to be interchromosomal or long-range intrachromosomal fusions (Supplementary Table S4).
Table 1. Known and novel fusions predicted by Comrad in C4-2 and validated in both LNCaP and C4-2

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<tr>
<td>FAM190B</td>
<td>CYP21C9</td>
<td>Transcript</td>
<td>RNA-Seq</td>
<td>20</td>
<td>20</td>
</tr>
<tr>
<td></td>
<td></td>
<td>Deletion</td>
<td>RNA-Seq</td>
<td>2</td>
<td>2</td>
</tr>
</tbody>
</table>

The number of reads supporting each event is provided, in addition to how many of those reads multi-map to the genome. The first six fusions have been previously described.

Genomic evidence was identified by Comrad for 7 of these 8 fusions; genomic evidence for the single remaining fusion transcript, ZDHHC20-TNFRSF19, could not be identified by Comrad. The predicted ZDHHC20-TNFRSF19 sequence exhibits canonical GT-AG splicing at the fusion boundary and is thus not likely to be the product of template switching during reverse transcriptase (Houseley and Tollervey, 2010). The lack of genomic evidence for ZDHHC20-TNFRSF19 makes this fusion a candidate trans-splicing event (Chen et al., 2009; Hormozdiari et al., 2009). Alternatively, ZDHHC20-TNFRSF19, could represent a false negative for Comrad.

4.1 Accurate discovery of gene fusions

Analysis of WGSS data for evidence of genomic rearrangement is made difficult by the repetitive nature of the genome, and the large amount of coverage required to reliably predict rearrangements (Chen et al., 2009; Hormozdiari et al., 2009). Conversely, RNA-Seq produces many spurious chimeric reads by at least two mechanisms: template switching during reverse transcriptase (Houseley and Tollervey, 2010) and the combined effect of read errors and high gene expression (Shomer et al., 2010). Given RNA-Seq and WGSS data from the same sample, an integrated analysis using Comrad provides the ability to more accurately resolve multi-map reads, and more confidently identify real events even where those events have relatively little evidence.

Comrad accurately identifies WGSS evidence for gene fusions, even when the evidence consists of only a small number of reads. Five of the validated genomic breakpoints are supported by two or less WGSS reads (Table 1). The breakpoint for DGKB-MIPOL1, arguably the most biologically important fusion in the dataset, is supported by one read. An independent analysis of WGSS data using a threshold of one read would result in the prediction of 20 675 fusions between the genes considered in this study. Considering only uniquely aligned reads results in the prediction of 9949 fusions supported by at least one WGSS read.

The existence of 9949 fusions would indicate that C4-2 is very highly rearranged, especially since these 9949 fusions represent rearrangements involving genomic regions only. However, aCGH data does not indicate this level of genomic rearrangement as only 41 copy number change points are predicted across the genome (Supplementary Table S5). Additionally, previous spectral karyotype results identified only nine structural aberrations (per diploid cell) for LNCaP (Beheshti et al., 2000). Thus, it is likely that many of the 9949 fusions are either false positives or represent transposable elements as opposed to large-scale structural aberrations. Clearly, identification of true positives from this set of fusions would be difficult if not impossible, rendering a single discordant WGSS read unreliable in an independent analysis of WGSS data. However, that single discordant WGSS read could be used to identify an important rearrangement breakpoint when considered in conjunction with RNA-Seq data as is done by Comrad.

Comrad provides the ability to accurately identify fusions where evidence for those fusions does not map uniquely to the genome. For the 9 PCR confirmed genomic fusions, 38% of the RNA-Seq reads and 32% of the WGSS reads are multi-map reads. Removing these reads from the analysis would prevent the identification of the MRPS10-HPR and TFDPI-GRK1 fusion transcripts and would hinder our ability to properly identify the CYP21C9-FAM190B fusion transcript (14/20 multi-map reads) and both the forward and reciprocal rearrangement breakpoints for MRPS10-HPR (12/13 and 4/5 multi-map reads, respectively). The MRPS10-HPR and TFDPI-GRK1 fusion transcripts are supported entirely by multi-map RNA-Seq reads. Intron 2 of WDR32 contains a region of high sequence similarity to parts of MRPS10. As a result, the RNA-Seq evidence for MRPS10-HPR aligns to either a hypothetical WDR32-HPR fusion transcript or the MRPS10-HPR fusion transcript. Similarly, RNA-Seq evidence for TFDPI-GRK1 also supports a hypothetical BNX42568-GRK1 fusion transcript. TFDPI and BNX42568 have 96% sequence similarity over a region of 1234 bp, making the two possibilities, TFDPI-GRK1 or BNX42568-GRK1, equally likely without knowledge of the corroborating WGSS data identified by Comrad. Therefore, even an analysis of the RNA-Seq data using a method that considers multi-map reads could fail to correctly identify the MRPS10-HPR and TFDPI-GRK1 fusion transcripts. However, Comrad is able to resolve the correct alignment location of multi-map reads that support the MRPS10-HPR and TFDPI-GRK1 fusion transcripts by leveraging the relatively unambiguous WGSS evidence of associated rearrangement breakpoints.

4.2 MIPOL1-DGKB and MRPS10-HPR are caused by reciprocal exchanges in C4-2 and LNCaP

In order to search for multiple genomic breakpoints associated with gene fusions, we altered the breakpoint overlap function as described...
The MRPS10-HPR fusion activates a cryptic splice site in the 3′ region of RERE. The Comrad predictions include three validated fusion transcripts for the PIK3CD-RERE fusion include one for which an intronic splice site and an AG at the 3′ splice site sequences of the aberrant AT-AG intron of CCDC43-YBX2. RNA-Seq and WGSS reads supporting the fusion are shown at the bottom of the figure.

4.3 Genomic rearrangements create fusion transcripts with non-canonical splicing

The Comrad predictions include three validated fusion transcripts with non-canonical splicing in C4-2. The three transcripts predicted for the PIK3CD-RERE fusion include one for which an intronic region of RERE is not spliced out of the resulting transcript. The MRPS10-HPR fusion activates a cryptic splice site in the 3′...
10 novel genomic fusions nominated by Comrad. All six fusions were confirmed by PCR for both C4-2 and LNCaP, showing that Comrad is more sensitive to genomic fusions than previous methods that have been applied to LNCaP. Additionally, we used deFuse to identify fusion transcripts for which no genomic rearrangement is detected by Comrad, despite the fact that a genomic rearrangement is expected given the position and orientation of the genes involved. We identified and validated ZDHHC20-TNFRSF19, possibly a reciprocal evidence that this fusion could be the result of a reciprocal insertion. MIPOL1, a reciprocal was previously thought to be a result of genomic structural variation. We identified and validated ZDHHC20-TNFRSF19, possibly a reciprocal evidence of rearrangement breakpoints. The modified splice sites of the rearrangement-induced intron. We have also used a simple modification of the Comrad framework to identify reciprocal evidence of rearrangement breakpoints. The modified framework led to the discovery of reciprocal evidence for both interchromosomal fusions identified by Comrad. For one of these fusions, MRP510-HPR, the location of the reciprocal translocation coincides precisely with a translocation found in LNCaP by spectral karyotyping (Beheshti et al., 2000). The other fusion, DGBK-MIPOL1, a reciprocal was previously thought to be a result of an insertion (Tomlins et al., 2007); however, Comrad has provided evidence that this fusion could be the result of a reciprocal insertion. RNA-Seq has already proven to be a powerful tool for the discovery of aberrant transcripts, and WGSS has already proven its utility when searching for rearrangements. We find that an integrated analysis of RNA-Seq and WGSS data minimizes some of the limitations of analyzing either RNA-Seq or WGSS data alone, and yields greater insight than either of these data types can provide independently. Given the possible existence of rearrangement fusions occurring at low levels of recurrence in cancer, the increased accuracy and decreased cost associated with a Comrad analysis may be useful when searching for these rearrangement fusions in a large number of tumours. The identification of such rearrangement fusions would then hopefully assist in the classification of molecular subtypes and the development of targeted therapies.

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REFERENCES


