

Supplementary Information for

Extraordinary expansion of a *Sorangium cellulosum* genome from an
alkaline milieu

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Supporting Text

Genome sequencing, assembly and annotation

A combined strategy of next-generation and traditional Sanger sequencing methodologies was applied. Seven libraries were constructed from the So0157 2 genomic DNA, with average insertion lengths ranging from 242 to 6000 bp. Assembly of the Solexa® sequenced libraries yielded 5749 Mb of clean data, 400 contigs and 41 scaffolds (Supplementary Table S6). Further co-assembly of an additional 2.5× 454 reads produced one scaffold with a 385-fold average depth of coverage. All of the regions with less than 3-fold coverage were validated by PCR and Sanger sequencing. Ultimately, we obtained the complete 14,782,125 bp circular genome sequence of *S. cellulosum* So0157-2, which is now the largest reported prokaryotic genome, being 1.75 Mb larger than the *S. cellulosum* so ce56 genome (13.03 Mb) ¹.

The GC content of So0157-2 genome is 72.1% and it contains 11,599 predicted protein-coding sequences (CDSs). Of these CDSs, 5,175 (44.6%) were annotated for hypothetical proteins through the RAST pipeline. Circles 2 & 4 in Fig. 2A show the final map of the chromosome numbered beginning from the *dnaA* gene. The *S. cellulosum* So0157-2 and So ce56 genomes are largely collinear (Fig. 2B), and approximately two-thirds of the total CDSs in the So0157-2 genome (8224) have homologues in So ce56 (Supplementary Table S7). The remaining one third of the sequences are unique to So0157-2, and approximately 1,000 of its 9,367 CDSs are unique to So ce56 (Supplementary Table S8 & S9). As in So ce56, the GC-skew inversion (Fig. 2A, circle 3), which is the hallmark of a bacterial chromosome replication origin, is absent in So0157-2, and thus, the location of *oriC* cannot be determined.

Genome characteristics

Non-coding RNA. A total of 74 non-coding RNAs, including 62 tRNAs and 12 rRNAs, were identified in the So0157-2 genome. Similar to other myxobacterial genomes, the rRNA genes of So0157-2 are located in four operons. However, only one of the operons presents the typical 5S-16S-23S structure, whereas two are atypical: one either lacks or contains a duplicated 5S rRNA gene, and one is interrupted ([Supplementary Table S10](#)). In the genome of the So ce56 strain, the 23S rRNA gene was not interrupted. Two inverted repeat sequences—the “calling cards” of transposons—were identified downstream of the operon containing three consecutive 5S rRNAs. In the interrupted operon, the 23S rRNA gene was replaced with an isoquinoline 1-oxidoreductase beta subunit and a hypothetical protein, which were both encoded by the complementary strand. There were no obvious sequence features suggesting that these two genes resulted from transposition or insertion.

Polysaccharide-degrading enzymes. The So0157-2 strain can effectively degrade a range of polysaccharides, including xylan, starch, mannan, lichenan, avicel, chitin and artificial carboxymethylcellulose. Surprisingly, a total of 557 ORFs, accounting for 7.95% (1,175,488 bp) of the total So0157-2 genome, were predicted to encode proteins involved in polysaccharide degradation, and nearly half of them were predicted to function in cellulose degradation. These polysaccharide degradation related enzymes, which included glycoside hydrolases (GHs), glycosyltransferases (GTs), polysaccharide lyases (PLs) and carbohydrate esterases (CEs), belonged to 112 families, 85 of which had more than one homolog ([Supplementary Fig. S3](#)). A total of 220 carbohydrate-binding modules (CBMs) were distributed across 22 families. Five families comprised 161 of the CBMs, with 56,

20, 51, 18 and 14 CBMs identified in the CBM2, CBM6, CBM13, CBM48 and CBM50 families, respectively. These five CBM families were predicted to function in the degradation of amorphous cellulose (CBM6), chitin (CBM2, CBM50), xylan (CBM2, CBM6, CBM13), glycogen (CBM48) and peptidoglycan (CBM13, CBM50). Smaller families contained genes involved in the degradation of various other polysaccharides, such as starch, mannan, arabinofuranose and fucose.

In comparison, only 226 ORFs in the *So ce56* genome were predicted to encode proteins responsible for polysaccharide degradation, *i.e.*, 114 GHs, 72 GTs, 11 PLs and 29 CEs. Most of these ORFs had homologues in *So0157-2*. Although each genome contained similar enzyme families, the number of enzymes was much greater in *So0157-2* ([Supplementary Fig. S3](#); [Supplementary Table S11](#)). Furthermore, although the composition ratios of the four enzyme classes (GH, GT, PL and CE) were rather consistent in *So0157-2* and *So ce56*, the CBM compositions (161 vs. 40) were significantly divergent in these two strains. The richness and diversity of the ORFs related to polysaccharide degradation may explain the bacteria's excellent ability to degrade various polysaccharides, and also implies that it has adapted to its dwelling environments.

Motility-related genes. Myxobacterial cells move on solid surfaces by gliding in swarms, which are coordinated by two distinct, independent mechanisms: the social motility (S-motility) and adventurous motility (A-motility) systems ². In the well-studied myxobacterium *Myxococcus xanthus* DK1622, S-motility is determined by three components: the molecular pulling motor type IV pilus (TFP), exopolysaccharide (EPS) and lipopolysaccharide (LPS). A-motility may be driven by polyelectrolyte secretion at

the lagging cell pole ³ and/or multiple focal adhesion complexes distributed along the cell body ⁴. Each system comprises many genes in *M. xanthus* DK1622. All of the related biosynthetic and regulatory genes were extracted from the *S. cellulosum* So0157-2 genome ([Supplementary Table S12](#)) for comparison. As previously reported in *S. cellulosum* So ce56 ⁵, LPS-related gene clusters, including those encoding lipid A, core oligosaccharide and O-polysaccharide, were partially absent in *S. cellulosum* So0157-2 ([Supplementary Table S12](#)). Former research shows that a 28-gene cluster is directly responsible for EPS biosynthesis and regulation in *M. xanthus* DK1622 ⁶. In the *S. cellulosum* So0157-2 genome, with the exception of two transposases, one glycosyltransferase and nine hypothetical proteins, all of these EPS genes were present. However, unlike their proximal distribution in the DK1622 genome, these EPS biosynthetic and regulatory genes were scattered across the *S. cellulosum* So0157-2 genome, which may, if functional, require much more complicated regulation. Furthermore, some TFP biosynthesis genes that had clear functions in *M. xanthus* DK1622 (e.g., *pilN*) ⁷ were also atypical in *S. cellulosum* So0157-2. However, *pilT*, a gene responsible for twitching motility ⁸, was present in five copies in the So0157-2 genome.

More than 35 genes or genome regions are involved in the function and regulation of A-motility in *M. xanthus* DK1622 ⁹. In the So0157-2 and So ce56 genomes, with the exception of *mgIA* (encoding a Ras-like protein) and the affiliated *mgIB* gene, none of the A-motility-related genes have counterparts. These data suggests that the A-motility mechanisms differ between myxobacterial groups.

Chemotaxis systems. In *Myxococcus xanthus* DK1622, there are eight chemotaxis-like

gene clusters defining eight chemosensory pathways. Most of these chemosensory pathways play roles in controlling motility, and at least two pathways regulate gene expression during development ¹⁰. In So0157-2, although all of the defined chemotaxis systems were present, they were each incomplete ([Supplementary Table S13](#)). For example, in the well-studied Frz system, only a methyltransferase (CheR) and two regulatory proteins (CheY and CheA) were annotated. A similar result was observed in the Dif system, where only CheA and CheY were annotated. The Che4 and Che5 systems in So0157-2 were structurally similar to the Frz system. The Che3, Che7 and Che8 systems exhibited included MCP (methyl-accepting chemotaxis protein), CheA, CheY, CheR, and an adaptor protein (CheW). In each of the eight chemotaxis systems, at least one histidine kinase (CheA) was annotated in the *S. cellulosum* So0157-2 genome. However, many copies of the components of the chemotaxis system were annotated in So0157-2. For example, 20 CheA proteins were annotated in the Che3 system and 10 CheA proteins were annotated in the Frz system. Notably, in contrast to the clustered chemotaxis systems observed in DK1622, only the Che6 and Che8 systems were organized in clusters, whereas the other systems were scattered throughout the So0157-2 genome.

Secondary metabolism. Myxobacteria can produce diverse bioactive compounds, and *Sorangium* strains contribute nearly half of the compounds produced by myxobacteria ¹¹. In the So0157-2 genome, we identified, 18 non-ribosomal peptide synthetase (NRPS) and polyketide synthase (PKS) gene clusters (420 kb, approximately 3% of the genome, [Fig. 2A, circle 18](#); [Supplementary Table S14](#)) and a number of clusters responsible for the biosynthesis of molecules such as terpenes, indoles, and bacteriocin (approximately 7%

of the genome) (Fig. 2A, circle 18). The 18 NRPS/PKS clusters are organized into three types: 6 with PKS only, 5 with NRPS only and 8 with a mixed distribution of NRPS/PKS. Two PKS clusters exhibited a classical modular structure and may function iteratively; three were single module clusters, with features typical of type II PKS; and one contained 12 modules without an AT domain, which is responsible for substrate identification and specificity. Of the five NRPS clusters, four had typical modular structures that function sequentially or iteratively, and one was atypical in that it contained only one module, which may be functionally irregular. The PKS/NRPS hybrids, including the epothilone biosynthetic gene cluster, represent a significant feature, endowing these compounds with unique bioactivity in myxobacteria ¹².

Electron transfer chain. Myxobacteria phylogenetically fall within the δ -proteobacteria, in which most members are strictly anaerobic ¹³. An analysis of *M. xanthus* DK1622 shows a chimeric Complex VI electron transfer chain ¹⁴. In *S. cellulosum* So0157-2, two electron transfer systems likely exist (Supplementary Table S15). The genes responsible for electron transfer were divided into several gene clusters surrounded by a series of hypothetical proteins. There was no evidence to suggest that these genes may have resulted from duplication events. *S. cellulosum* So0157-2 and So ce56 shared almost all of their electron transfer chain genes, suggesting that these strains share an early common ancestor. In the *S. cellulosum* genome, the two complete sets of genes responsible for electron transfer to the final acceptor were identified, suggesting that these genes were functional within bacterial cells. In the sequenced myxobacteria, two sets of Complex II succinate dehydrogenase genes. One of these genes arose from the Firmicutes group, but the other was homologous to the corresponding gene in high GC-content Gram-positive

bacteria. Interestingly, *Anaeromyxobacter* and *Sorangium* possess both types of succinate dehydrogenase, whereas *Myxococcus*, *Stigmatella*, and *Coralloccoccus* have only one type. Two sets of In Complex I NADH dehydrogenases were also identified in the So0157-2 genome. One complete set, comprising 15 components clustered in four groups, was detected; however, the second gene set was incomplete. These two Complex I gene sets originated from proteobacteria and bacteroidetes, respectively. Similar to Complex II, the complete set was common among myxobacteria species, whereas the incomplete set was only present in the anaerobic myxobacterial species and *Sorangium*. The Complex IV is relatively conserved among myxobacteria, and it mainly comprises two sets of heme-copper cytochrome *c* oxidases, one set of cytochrome *bd* quinol oxidases and an alternative *cbb₃*-type cytochrome *c* oxidase. However, the *cbb₃*-type cytochrome *c* oxidase was generally missing in the respiratory chain of *S. cellulosum*.

Phage invasion. Microbial genomics has revealed that a substantial number of bacterial genomes include prophage or virus sequences¹⁵. In So0157-2, 423 putative prophage CDSs and 62 viral CDSs were detected (Fig. 2A, circle 12 & 13). Of the annotated prophage-origin genes, 55 genes were hypothetical, and 367 genes were assigned specific functions. This ratio (367/422) is extremely high. Of the annotated serine/threonine protein kinase CDSs, 63 were predicted to have originated from prophages. Additionally, ATP-dependent proteases (13 CDSs), transcriptional regulators (8 CDSs) and some CDSs related to DNA/RNA metabolism also originated from phages. Putative virus CDSs were scattered throughout the So0157-2 genome. These CDSs included virus structural genes, DNA/RNA metabolism-related genes (*e.g.*, the 3'-to-5' exoribonuclease RNase R, poly(A) polymerase, ribonucleotide reductase, RNA-2',3'-PO₄:RNA-5'-OH ligase, and a single-

stranded-DNA-specific exonuclease), and four CDSs of unknown function. Finally, several PKS-related genes had viral homologues. However, none of the prophage or virus sequences was active in the So0157-2 genome.

Insert sequence (IS) elements. IS elements are represented as an open box including the terminal IRs and a single open reading frame encoding the transposase ¹⁶. There were 67 putative IS elements in the So0157-2 genome, like its close relative, So ce56, only one element was longer than 1 kb. The 66 short putative IS sites contained a number of known inverted repeats, but none of the intervening sequences showed significant similarity to any of the available database sequences. Furthermore, 37 predicted transposases were identified in the So0157-2 genome, a finding that is in accordance with presence of the putative IS sites (left and right inverted repeats). These results suggest that there are additional, specific linear insert sequence structures that may contain novel insertion sequence patterns.

Supplementary Methods

Genome assembly and feature annotation

Two independent assemblies of the bacterial genome were obtained using the 454[®] sequencing reads and the Solexa[®] reads. The assemblies were generated with SOAPdenovo ¹⁷, ABySS ¹⁸, and Velvet ¹⁹, with the default parameters being employed in all programs. For each assembly, all vs. all alignments were performed using the MUMmer package ²⁰ with a minimum overlap of 100 bp. A new consensus assembly of the hybrid sequences was generated with SOAPdenovo and manually curated. MUMmer alignments of the assembled sequence and the *Sorangium cellulosum* so ce56 genome

were used to assess the orientation and synteny conservation of the newly assembled fragments.

Gene prediction was performed with Glimmer v3.02²¹ and GeneMark.hmm for prokaryotes²². This analysis was followed with the application of an automatic annotation pipeline carried out with the RAST²³ and Blast2Go programs²⁴, which retrieve sequence information from SWISS PROT, InterPro, Pfam, PROSITE, COG, GO, KEGG, NCBI NR, and other databases. Transfer RNAs were detected with tRNAscan-SE²⁵. Annotations were checked manually, and frameshift corrections were performed with GenePRIMP²⁶ using the original reads. Extra annotation of small (<100 bp) ORFs of known function was performed manually. Sequence manipulation, parsing, and statistical features, such as genome size, %GC, codon usage, and Codon Adaptation Index (CAI), were determined using the EMBOSS 6.40 package²⁷ and related scripts. Schematic features of the genome were constructed by Circos²⁸.

A whole-genome BLAST search against the CAZy database was conducted to annotate putative polysaccharide-degrading enzymes in the So0157-2 genome²⁹.

Secondary metabolite pathway analysis

Annotation of PKS/NRPS gene clusters was carried out using ClustScan and related databases³⁰. Prediction of the amino acid usage for each module of non-ribosomal peptide synthetase (NRPS) was conducted with NRPSpredictor2³¹. Additional gene cluster analysis for secondary metabolites was conducted with antiSMASH³².

Analysis and mapping of paralogous genes

An all-against-all BLAST search of proteome was conducted with the BLASTP program (NCBI Blast+ 2.26 package) ³³ using an E-value threshold of 1e-10. All of the sequence pairs identified as reciprocal better or best hits were extracted. The average taxa weight based on all paralogous pairs was calculated. All pairs were clustered into independent groups with the MCL program ³⁴. The paralogous map was drawn by the Circos program ²⁸.

Annotation of mobile genetic elements

The Insertion Sequence (IS) database was downloaded from the IS finder website ³⁵. The Prophage database from the ACLAME website was also used, which contains prophage, virus and integrated plasmid gene annotations ³⁶. The ICEberg database was downloaded to annotate integrated and conjugative elements in the So0157-2 genome ³⁷. The predicted So0157-2 proteome dataset was subjected to BLAST searches against the above dataset (BLASTP). An E-value threshold of 1e-30 was used, and the top 10 hits, when possible, were parsed for subsequent manual validation. The genes were further examined for GC content and codon usage biases, and an additional phylogenetic analysis was applied to identify other sources of horizontally transferred genes.

Restriction and modification system analysis

The full set of protein sequences from all of the experimentally confirmed restriction and modification systems was obtained from REBASE ³⁸. A BLASTP search was conducted using the predicted So0157-2 proteome dataset against the REBASE database. The E-value cutoff was set to 1e-30. Only the top hit was parsed for follow-up analysis.

Annotation Clustered Regularly Interspaced Short Palindromic Repeats (CRISPR)

Whole-genome scanning for CRISPR sequences was conducted with PILER-CR v.1.06³⁹. The result was filtered using the following parameters: minimum array ≥ 10 , minimum conservation > 0.9 , repeat length 16-64 bp, and spacer length 8-64 bp. The CRISPR-associated genes were annotated via BLASTP searches against CRISPR/Cas profiles obtained from NCBI (ftp://ftp.ncbi.nih.gov/pub/wolf/_suppl/CRISPRclass/crisprPro.html) with an E-value threshold of $\leq 1e-30$.

Annotation sigma factors, transcriptional factors and protein kinase

The sigma factors, transcriptional factors and components of two component system were annotated by P2CS (<http://www.p2cs.org/>)⁴⁰ and P2TF (<http://www.p2tf.org/>) database. Genes encoding eukaryotic-like kinase in the prokaryotes were identified by BLASTP analysis of complete proteome using the Pfam matrix for protein kinases (Pkinase, PF00069; Pkinase_C, PF00433; Pkinase_tyr, PF07714). All sequences obtained with an E-value $\leq 1e-10$ were back-searched against Pfam and Prosite (<http://expasy.org/prosite/>) to verify unequivocally which proteins matched to the kinase domain.

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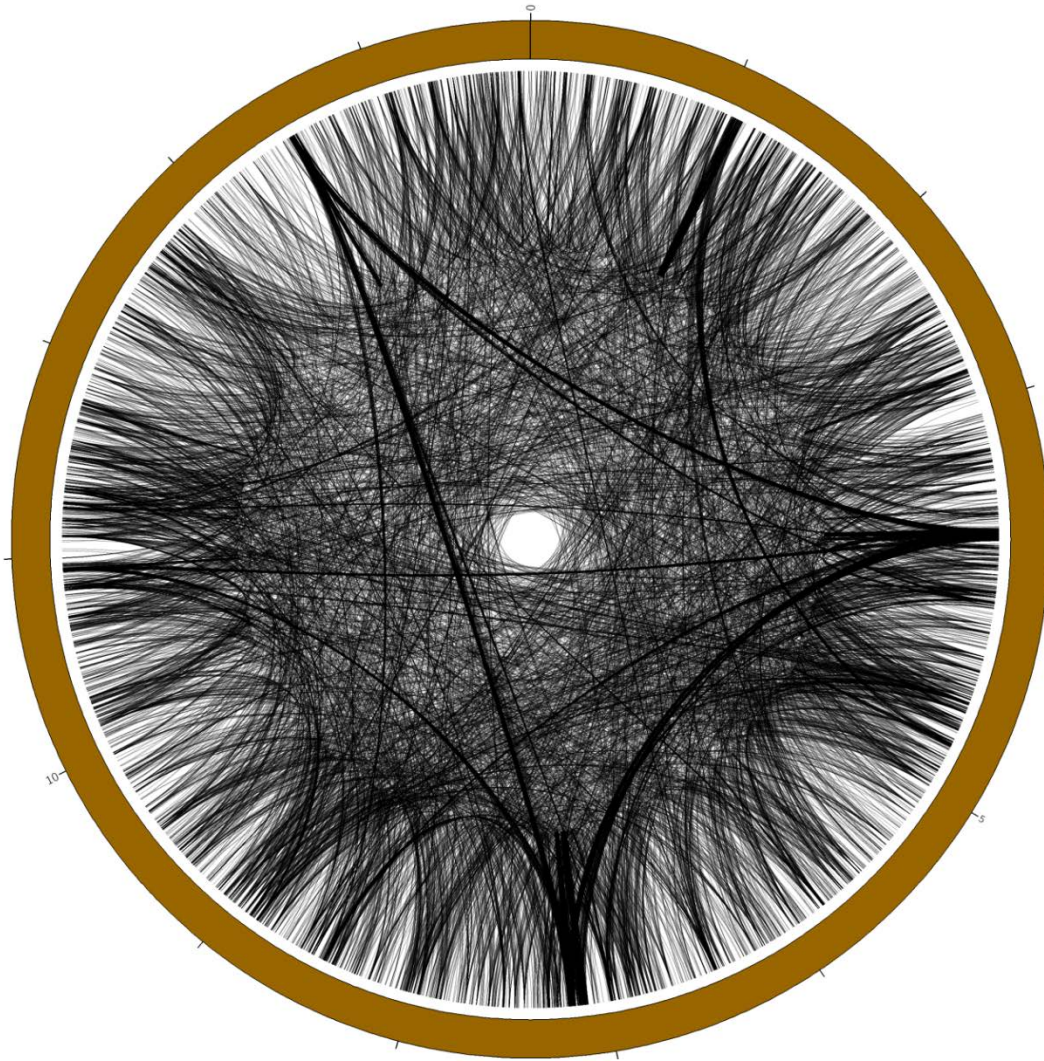
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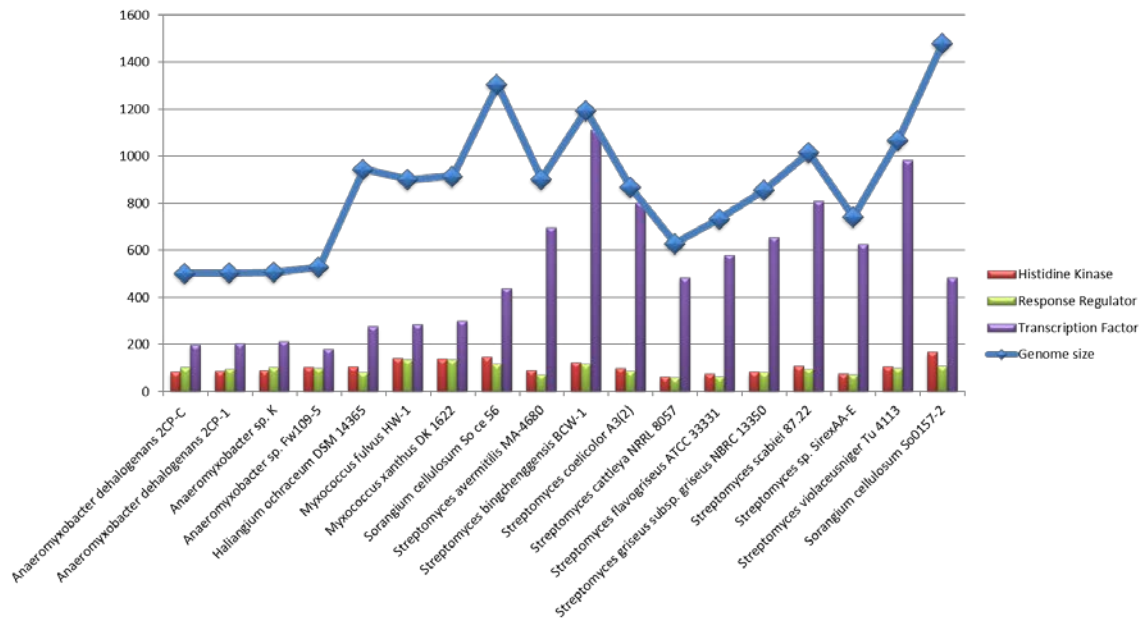
Supplementary Fig. S1.



chr1

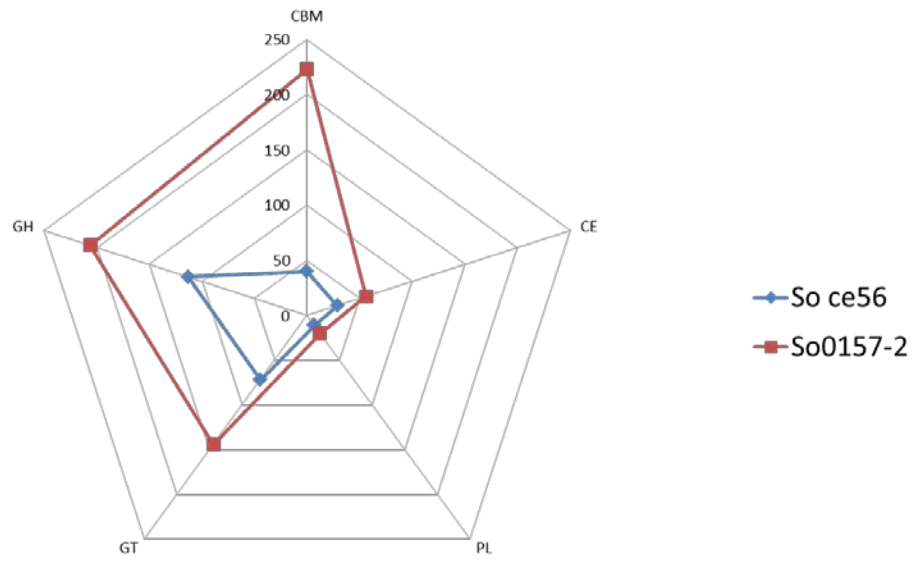
A schematic representation of genome sequence duplication in So0157-2.

Supplementary Fig. S2



The expansion of the regulatory network as an expansion of the genome.

Supplementary Fig. S3



A schematic representation of the abundance of polysaccharide-related families and CMB in two sequenced *Sorangium* genomes, So0157-2 and So ce56.

Supplementary Table S1. Annotations of eukaryotic-like kinases in So0157-2

| Locus tag | Database* ID | Identity | Alignment length | Q. start | Q. end | D. start | D. end | E-value | Bit score |
|-------------|----------------------|----------|------------------|----------|--------|----------|--------|-----------|-----------|
| SCE1572_2 | A9GHT8_SORC5/9-291 | 96.47 | 283 | 9 | 291 | 1 | 283 | 1.00E-161 | 566 |
| SCE1572_22 | A9GHZ6_SORC5/16-280 | 100 | 265 | 16 | 280 | 1 | 265 | 6.00E-150 | 526 |
| SCE1572_38 | A9GKW5_SORC5/18-287 | 97.78 | 270 | 18 | 287 | 1 | 270 | 1.00E-155 | 545 |
| SCE1572_45 | A9GKX5_SORC5/32-304 | 90.11 | 273 | 43 | 315 | 1 | 273 | 4.00E-142 | 500 |
| SCE1572_50 | B9RTW7_RICCO | 36.27 | 193 | 5 | 193 | 38 | 225 | 1.00E-19 | 93.6 |
| SCE1572_58 | A9G3F0_SORC5/15-286 | 79.04 | 272 | 15 | 286 | 1 | 272 | 4.00E-128 | 454 |
| SCE1572_72 | A9GL24_SORC5/17-279 | 91.63 | 263 | 17 | 279 | 1 | 263 | 6.00E-144 | 506 |
| SCE1572_157 | A9FXD2_SORC5/32-294 | 80.23 | 263 | 32 | 294 | 1 | 263 | 1.00E-118 | 422 |
| SCE1572_159 | A9FXC4_SORC5/66-318 | 92.49 | 253 | 66 | 318 | 1 | 253 | 5.00E-130 | 461 |
| SCE1572_221 | B5DPB6_DROPS | 31.68 | 202 | 266 | 457 | 758 | 958 | 2.00E-18 | 90.9 |
| SCE1572_301 | D0LG85_HALO1/9-288 | 38.23 | 327 | 27 | 351 | 1 | 280 | 4.00E-47 | 186 |
| SCE1572_324 | A6G4E4_9DELTA | 33.51 | 385 | 943 | 1296 | 900 | 1260 | 1.00E-35 | 149 |
| SCE1572_368 | A9GLX4_SORC5/38-301 | 83.71 | 264 | 24 | 286 | 1 | 264 | 4.00E-128 | 455 |
| SCE1572_418 | A6G4E4_9DELTA | 29.12 | 656 | 1080 | 1709 | 613 | 1219 | 1.00E-49 | 196 |
| SCE1572_430 | A9G5P3_SORC5/10-271 | 86.69 | 263 | 27 | 289 | 1 | 262 | 3.00E-134 | 474 |
| SCE1572_433 | A9GM76_SORC5/21-287 | 89.89 | 267 | 21 | 284 | 1 | 267 | 1.00E-137 | 486 |
| SCE1572_498 | A9FA64_SORC5/37-294 | 69.83 | 232 | 1 | 232 | 29 | 258 | 7.00E-89 | 325 |
| SCE1572_510 | A9GQH3_SORC5/6-269 | 90.53 | 264 | 6 | 268 | 1 | 264 | 4.00E-141 | 497 |
| SCE1572_515 | B9RTW7_RICCO | 31.98 | 197 | 50 | 238 | 38 | 225 | 2.00E-12 | 69.7 |
| SCE1572_535 | A9GQL8_SORC5/11-242 | 94.02 | 234 | 11 | 244 | 1 | 232 | 7.00E-112 | 401 |
| SCE1572_540 | A9GQM9_SORC5/13-268 | 91.27 | 252 | 2 | 253 | 5 | 256 | 5.00E-130 | 461 |
| SCE1572_587 | A9GQX2_SORC5/13-284 | 80.51 | 272 | 13 | 282 | 1 | 272 | 4.00E-126 | 447 |
| SCE1572_596 | A9GQY7_SORC5/22-296 | 92 | 275 | 22 | 296 | 1 | 275 | 4.00E-152 | 533 |
| SCE1572_602 | A9GQZ9_SORC5/222-494 | 93.04 | 273 | 507 | 779 | 1 | 273 | 1.00E-146 | 516 |
| SCE1572_648 | A9GR88_SORC5/43-313 | 95.2 | 271 | 43 | 313 | 1 | 271 | 3.00E-150 | 528 |

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|--------------|----------------------|-------|------|-----|------|------|------|-----------|------|
| SCE1572_669 | B4KV63_DROMO | 32.82 | 262 | 138 | 398 | 701 | 958 | 7.00E-31 | 132 |
| SCE1572_671 | A9GRD4_SORC5/21-295 | 86.79 | 280 | 21 | 300 | 1 | 275 | 5.00E-137 | 483 |
| SCE1572_686 | A9GU97_SORC5/162-331 | 92.35 | 170 | 144 | 313 | 1 | 170 | 5.00E-87 | 318 |
| SCE1572_728 | A9GUI6_SORC5/43-307 | 87.55 | 265 | 13 | 277 | 1 | 265 | 1.00E-134 | 475 |
| SCE1572_743 | D8LQ15_ECTSI | 35.44 | 206 | 110 | 307 | 612 | 816 | 1.00E-20 | 97.4 |
| SCE1572_745 | A9GUM9_SORC5/30-300 | 98.89 | 271 | 29 | 299 | 1 | 271 | 5.00E-159 | 556 |
| SCE1572_805 | A9G2M3_SORC5/18-300 | 72.79 | 283 | 19 | 301 | 1 | 283 | 2.00E-100 | 362 |
| SCE1572_810 | B8LDL2_THAPS | 24.32 | 588 | 151 | 718 | 953 | 1477 | 1.00E-35 | 149 |
| SCE1572_824 | A9FS91_SORC5/8-267 | 60.94 | 256 | 20 | 273 | 6 | 260 | 5.00E-79 | 293 |
| SCE1572_844 | A9GV94_SORC5/20-278 | 96.15 | 260 | 20 | 279 | 1 | 259 | 2.00E-140 | 495 |
| SCE1572_872 | E9C274_9EUKA | 48.11 | 212 | 317 | 528 | 1539 | 1748 | 7.00E-56 | 214 |
| SCE1572_894 | D3BLW9_POLPA | 37.04 | 135 | 4 | 137 | 1564 | 1697 | 7.00E-18 | 88.6 |
| SCE1572_910 | A9FP27_SORC5/11-267 | 84.82 | 257 | 11 | 267 | 1 | 257 | 6.00E-112 | 402 |
| SCE1572_928 | A9GVM0_SORC5/29-281 | 81.35 | 252 | 29 | 280 | 1 | 252 | 1.00E-103 | 372 |
| SCE1572_939 | A9EMV5_SORC5/25-308 | 86.01 | 286 | 24 | 309 | 1 | 284 | 1.00E-123 | 439 |
| SCE1572_940 | A9EMV8_SORC5/15-289 | 93.09 | 275 | 17 | 291 | 1 | 275 | 8.00E-158 | 553 |
| SCE1572_962 | F2UKF9_9EUKA | 54.45 | 696 | 5 | 695 | 9 | 704 | 0 | 766 |
| SCE1572_977 | A9EN27_SORC5/21-272 | 99.6 | 252 | 21 | 272 | 1 | 252 | 2.00E-149 | 525 |
| SCE1572_993 | B9RTW7_RICCO | 35.35 | 198 | 5 | 194 | 43 | 234 | 3.00E-16 | 82.4 |
| SCE1572_1008 | D3BJS3_POLPA | 26.92 | 442 | 7 | 437 | 815 | 1249 | 5.00E-32 | 135 |
| SCE1572_1013 | A9ENB1_SORC5/68-351 | 91.9 | 284 | 68 | 351 | 1 | 284 | 1.00E-143 | 506 |
| SCE1572_1015 | D0LZ14_HALO1 | 38.29 | 935 | 103 | 1019 | 163 | 1078 | 3.00E-148 | 523 |
| SCE1572_1041 | A9EU91_SORC5/223-477 | 58.1 | 253 | 342 | 594 | 1 | 253 | 7.00E-79 | 291 |
| SCE1572_1051 | B9RTW7_RICCO | 32.98 | 188 | 65 | 243 | 38 | 219 | 1.00E-13 | 73.9 |
| SCE1572_1054 | A9FFW3_SORC5/24-336 | 88.82 | 313 | 16 | 328 | 1 | 313 | 1.00E-165 | 578 |
| SCE1572_1075 | A9VA90_MONBE | 29.45 | 292 | 72 | 342 | 320 | 591 | 3.00E-13 | 73.2 |
| SCE1572_1098 | D0LZ14_HALO1 | 37.95 | 1199 | 105 | 1286 | 175 | 1345 | 1.00E-161 | 568 |
| SCE1572_1168 | F2EE39_HORVD | 32.08 | 293 | 308 | 555 | 23 | 312 | 1.00E-24 | 112 |

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|--------------|-----------------------|-------|-----|------|------|-----|------|-----------|------|
| SCE1572_1184 | A9F932_SORC5/34-318 | 71.58 | 285 | 68 | 352 | 1 | 285 | 3.00E-117 | 419 |
| SCE1572_1197 | A9FYH6_SORC5/7-273 | 74.16 | 267 | 16 | 274 | 1 | 267 | 4.00E-110 | 396 |
| SCE1572_1229 | A9EQJ9_SORC5/6-267 | 50.38 | 264 | 5 | 266 | 1 | 262 | 7.00E-60 | 228 |
| SCE1572_1230 | A6G4E4_9DELT | 30.17 | 633 | 1063 | 1634 | 589 | 1209 | 7.00E-50 | 196 |
| SCE1572_1255 | B8LDL2_THAPS | 27.16 | 567 | 26 | 584 | 997 | 1484 | 2.00E-51 | 201 |
| SCE1572_1256 | Q9FF29_ARATH | 26.35 | 296 | 189 | 471 | 14 | 250 | 3.00E-14 | 76.3 |
| SCE1572_1294 | A9EPH9_SORC5/19-285 | 91.79 | 268 | 19 | 286 | 1 | 267 | 1.00E-143 | 505 |
| SCE1572_1295 | A9EPI2_SORC5/10-279 | 88.52 | 270 | 10 | 279 | 1 | 270 | 9.00E-133 | 468 |
| SCE1572_1308 | F2UKF9_9EUKA | 43.1 | 710 | 2 | 703 | 4 | 696 | 1.00E-153 | 540 |
| SCE1572_1316 | A9ETG2_SORC5/740-1011 | 97.43 | 272 | 381 | 652 | 1 | 272 | 1.00E-159 | 560 |
| SCE1572_1319 | A9ETG8_SORC5/12-270 | 93.05 | 259 | 12 | 270 | 1 | 259 | 3.00E-139 | 491 |
| SCE1572_1322 | A9FE17_SORC5/11-267 | 51.89 | 264 | 1 | 264 | 12 | 254 | 4.00E-67 | 252 |
| SCE1572_1337 | A9ETI8_SORC5/40-302 | 96.2 | 263 | 40 | 301 | 1 | 263 | 3.00E-145 | 511 |
| SCE1572_1380 | Q75J39_ORYSJ | 31.4 | 293 | 362 | 624 | 51 | 315 | 3.00E-24 | 110 |
| SCE1572_1389 | E3X4G0_ANODA | 35.16 | 256 | 39 | 287 | 40 | 283 | 2.00E-25 | 113 |
| SCE1572_1402 | D8LHV1_ECTSI | 31.6 | 231 | 103 | 332 | 87 | 306 | 2.00E-12 | 71.6 |
| SCE1572_1421 | D0LYB2_HALO1 | 39.25 | 879 | 4 | 821 | 2 | 842 | 1.00E-122 | 437 |
| SCE1572_1422 | D0LYB2_HALO1 | 38.18 | 571 | 7 | 524 | 8 | 557 | 2.00E-76 | 283 |
| SCE1572_1447 | D7TTD5_VITVI | 25.32 | 233 | 122 | 340 | 688 | 901 | 9.00E-12 | 68.2 |
| SCE1572_1516 | F2UKF9_9EUKA | 40.94 | 149 | 2 | 145 | 8 | 156 | 8.00E-23 | 105 |
| SCE1572_1525 | A9EUD9_SORC5/28-288 | 99.6 | 250 | 1 | 250 | 12 | 261 | 4.00E-144 | 507 |
| SCE1572_1539 | A9EUI2_SORC5/20-285 | 95.49 | 266 | 20 | 285 | 1 | 266 | 2.00E-148 | 521 |
| SCE1572_1569 | B9RTW7_RICCO | 32.45 | 188 | 19 | 197 | 44 | 219 | 1.00E-12 | 70.5 |
| SCE1572_1610 | A9EVB6_SORC5/189-453 | 97.74 | 265 | 189 | 453 | 1 | 265 | 1.00E-151 | 531 |
| SCE1572_1633 | A9EZT1_SORC5/15-309 | 87.8 | 295 | 15 | 300 | 1 | 295 | 4.00E-135 | 477 |
| SCE1572_1649 | D7FZX4_ECTSI | 31.08 | 399 | 160 | 494 | 106 | 497 | 2.00E-28 | 123 |
| SCE1572_1699 | A9F066_SORC5/60-323 | 96.59 | 264 | 59 | 322 | 1 | 264 | 9.00E-152 | 532 |
| SCE1572_1705 | A9F084_SORC5/63-328 | 98.5 | 266 | 160 | 425 | 1 | 266 | 1.00E-155 | 545 |

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|--------------|---------------------|-------|------|-----|------|------|------|-----------|------|
| SCE1572_1715 | A9V4U4_MONBE | 34.27 | 143 | 4 | 136 | 944 | 1080 | 4.00E-12 | 66.6 |
| SCE1572_1733 | E9CI33_9EUKA | 47.8 | 205 | 206 | 408 | 70 | 265 | 9.00E-39 | 157 |
| SCE1572_1768 | D7FZX4_ECTSI | 27.12 | 413 | 105 | 476 | 106 | 499 | 3.00E-18 | 90.1 |
| SCE1572_1860 | D7SRK5_VITVI | 28.21 | 234 | 75 | 294 | 47 | 276 | 7.00E-13 | 72 |
| SCE1572_1869 | A9F1G8_SORC5/19-291 | 92.67 | 273 | 19 | 291 | 1 | 273 | 1.00E-144 | 508 |
| SCE1572_1882 | A9F694_SORC5/14-257 | 84.43 | 244 | 22 | 265 | 1 | 244 | 4.00E-112 | 402 |
| SCE1572_1884 | A9EV86_SORC5/15-281 | 67.42 | 267 | 11 | 273 | 1 | 267 | 1.00E-97 | 352 |
| SCE1572_1889 | B8LDL2_THAPS | 22.43 | 437 | 196 | 598 | 1445 | 1868 | 2.00E-17 | 88.2 |
| SCE1572_1903 | F2UKF9_9EUKA | 29.67 | 701 | 9 | 701 | 12 | 700 | 5.00E-91 | 332 |
| SCE1572_1906 | A9F6G8_SORC5/45-306 | 87.02 | 262 | 41 | 302 | 1 | 262 | 8.00E-126 | 446 |
| SCE1572_1928 | A9F6S1_SORC5/13-277 | 83.66 | 257 | 1 | 257 | 9 | 265 | 4.00E-126 | 446 |
| SCE1572_1936 | A9FE17_SORC5/11-267 | 55.81 | 258 | 13 | 270 | 1 | 255 | 5.00E-73 | 272 |
| SCE1572_1936 | D0LZ14_HALO1 | 34.97 | 1384 | 6 | 1321 | 9 | 1346 | 2.00E-179 | 626 |
| SCE1572_1940 | D7FKP6_ECTSI | 54.43 | 237 | 2 | 233 | 121 | 353 | 4.00E-63 | 240 |
| SCE1572_1941 | D7FKP6_ECTSI | 46.47 | 269 | 24 | 278 | 93 | 356 | 6.00E-54 | 207 |
| SCE1572_2073 | A9F816_SORC5/16-240 | 91.56 | 225 | 16 | 237 | 1 | 225 | 3.00E-109 | 392 |
| SCE1572_2143 | E9C274_9EUKA | 29.73 | 185 | 412 | 596 | 1568 | 1745 | 2.00E-20 | 97.4 |
| SCE1572_2170 | A9FRK3_SORC5/74-345 | 95.22 | 272 | 97 | 368 | 1 | 272 | 5.00E-150 | 526 |
| SCE1572_2171 | A9FRJ9_SORC5/22-280 | 93.05 | 259 | 22 | 280 | 1 | 259 | 1.00E-139 | 492 |
| SCE1572_2183 | D0LYB2_HALO1 | 36.51 | 641 | 185 | 779 | 182 | 807 | 2.00E-73 | 274 |
| SCE1572_2196 | A9FUH6_SORC5/44-314 | 91.88 | 271 | 91 | 361 | 1 | 271 | 1.00E-145 | 512 |
| SCE1572_2197 | A9GRQ7_SORC5/16-276 | 88.12 | 261 | 16 | 274 | 1 | 261 | 1.00E-129 | 461 |
| SCE1572_2206 | B9RTW7_RICCO | 31.98 | 197 | 3 | 192 | 38 | 219 | 3.00E-15 | 78.6 |
| SCE1572_2220 | A9F1G8_SORC5/19-291 | 75.09 | 273 | 19 | 291 | 1 | 273 | 2.00E-114 | 407 |
| SCE1572_2238 | A9FDG9_SORC5/21-281 | 96.92 | 260 | 20 | 279 | 1 | 260 | 2.00E-150 | 529 |
| SCE1572_2239 | A9FDH1_SORC5/20-281 | 88.55 | 262 | 20 | 281 | 1 | 262 | 3.00E-136 | 481 |
| SCE1572_2241 | A9FDG9_SORC5/21-281 | 60.62 | 259 | 7 | 264 | 1 | 259 | 1.00E-87 | 320 |
| SCE1572_2242 | A9FDJ3_SORC5/13-278 | 80.83 | 266 | 13 | 278 | 1 | 266 | 9.00E-119 | 422 |

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|--------------|----------------------|-------|------|-----|------|------|------|-----------|------|
| SCE1572_2258 | D0LZ14_HALO1 | 39.5 | 1395 | 2 | 1329 | 7 | 1346 | 0 | 800 |
| SCE1572_2283 | B5DPB6_DROPS | 38.39 | 224 | 166 | 385 | 731 | 950 | 6.00E-36 | 149 |
| SCE1572_2326 | B9RTW7_RICCO | 34.69 | 196 | 31 | 215 | 43 | 234 | 1.00E-20 | 97.1 |
| SCE1572_2359 | A9FIP5_SORC5/20-288 | 89.22 | 269 | 20 | 287 | 1 | 269 | 3.00E-125 | 443 |
| SCE1572_2371 | E9C274_9EUKA | 37.04 | 162 | 245 | 406 | 1568 | 1721 | 8.00E-18 | 88.6 |
| SCE1572_2410 | E3PW85_CLOSD | 38.69 | 168 | 140 | 304 | 1406 | 1570 | 1.00E-27 | 120 |
| SCE1572_2441 | A9FJE9_SORC5/231-472 | 92.56 | 242 | 231 | 472 | 1 | 242 | 2.00E-130 | 461 |
| SCE1572_2487 | A9FNZ9_SORC5/14-281 | 82.84 | 268 | 11 | 278 | 1 | 268 | 5.00E-131 | 464 |
| SCE1572_2490 | D7TTD5_VITVI | 33.8 | 213 | 223 | 432 | 256 | 460 | 4.00E-26 | 115 |
| SCE1572_2518 | A9GT67_SORC5/13-276 | 71.1 | 263 | 13 | 273 | 1 | 263 | 4.00E-104 | 374 |
| SCE1572_2519 | D7TTD5_VITVI | 26.39 | 341 | 107 | 429 | 121 | 458 | 6.00E-25 | 112 |
| SCE1572_2544 | A6G4E4_9DELT | 31.65 | 752 | 717 | 1426 | 537 | 1260 | 9.00E-69 | 259 |
| SCE1572_2588 | D0LZ14_HALO1 | 39.93 | 1212 | 103 | 1290 | 163 | 1346 | 0 | 670 |
| SCE1572_2590 | Q097E7_STIAU/1-261 | 54.98 | 291 | 32 | 322 | 1 | 261 | 1.00E-77 | 288 |
| SCE1572_2647 | A9G8I3_SORC5/10-268 | 73.96 | 265 | 10 | 273 | 1 | 259 | 2.00E-111 | 399 |
| SCE1572_2652 | B8HVH1_CYAP4/7-265 | 54.92 | 264 | 7 | 266 | 1 | 259 | 4.00E-83 | 306 |
| SCE1572_2679 | B9RTW7_RICCO | 28.14 | 231 | 4 | 216 | 36 | 262 | 6.00E-15 | 77.8 |
| SCE1572_2690 | A9FJE9_SORC5/231-472 | 64.56 | 237 | 221 | 456 | 1 | 237 | 2.00E-82 | 303 |
| SCE1572_2701 | D0LZ14_HALO1 | 38.18 | 1362 | 2 | 1303 | 7 | 1346 | 0 | 731 |
| SCE1572_2715 | A9FQS5_SORC5/56-333 | 95.68 | 278 | 56 | 333 | 1 | 278 | 6.00E-145 | 510 |
| SCE1572_2749 | A9FUX8_SORC5/6-235 | 92.14 | 229 | 116 | 344 | 1 | 229 | 4.00E-125 | 444 |
| SCE1572_2826 | B9RTW7_RICCO | 33.16 | 196 | 7 | 195 | 42 | 229 | 1.00E-15 | 79.7 |
| SCE1572_2832 | A9VA07_MONBE | 45.29 | 340 | 13 | 342 | 596 | 930 | 3.00E-69 | 259 |
| SCE1572_2934 | A9G0Y5_SORC5/28-295 | 86.94 | 268 | 61 | 328 | 1 | 268 | 6.00E-134 | 473 |
| SCE1572_2963 | A9G147_SORC5/98-359 | 96.95 | 262 | 98 | 359 | 1 | 262 | 3.00E-144 | 507 |
| SCE1572_2966 | C0WK81_9CORY/14-268 | 39.31 | 262 | 33 | 290 | 1 | 255 | 7.00E-39 | 158 |
| SCE1572_2987 | A9G170_SORC5/33-336 | 95.07 | 304 | 33 | 336 | 1 | 304 | 7.00E-163 | 570 |
| SCE1572_2996 | A9G190_SORC5/32-292 | 84.91 | 265 | 44 | 308 | 1 | 261 | 2.00E-119 | 426 |

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|--------------|---------------------|-------|------|-----|------|------|------|-----------|------|
| SCE1572_3033 | Q23ZG6_TETTH | 24.95 | 457 | 13 | 440 | 495 | 944 | 4.00E-37 | 153 |
| SCE1572_3041 | B4KV63_DROMO | 34.03 | 191 | 479 | 661 | 756 | 941 | 3.00E-14 | 77.4 |
| SCE1572_3114 | F2UAL0_9EUKA | 40.45 | 89 | 28 | 116 | 1280 | 1366 | 1.00E-10 | 64.7 |
| SCE1572_3137 | D0LZ14_HALO1 | 37.6 | 1367 | 1 | 1297 | 12 | 1344 | 0 | 713 |
| SCE1572_3141 | A9GTU1_SORC5/18-277 | 56.15 | 260 | 7 | 266 | 1 | 260 | 1.00E-81 | 301 |
| SCE1572_3158 | D0LZ14_HALO1 | 36.94 | 1367 | 2 | 1297 | 7 | 1344 | 0 | 668 |
| SCE1572_3180 | A9VA07_MONBE | 42.66 | 354 | 63 | 406 | 596 | 944 | 1.00E-69 | 260 |
| SCE1572_3183 | A9V4U4_MONBE | 41.98 | 131 | 9 | 137 | 954 | 1084 | 4.00E-28 | 121 |
| SCE1572_3267 | A9G5X1_SORC5/59-323 | 95.47 | 265 | 93 | 357 | 1 | 265 | 8.00E-146 | 513 |
| SCE1572_3271 | A9G5Y1_SORC5/47-312 | 98.12 | 266 | 26 | 291 | 1 | 266 | 3.00E-151 | 531 |
| SCE1572_3291 | A9F8N6_SORC5/25-290 | 55.35 | 271 | 19 | 287 | 1 | 266 | 8.00E-79 | 290 |
| SCE1572_3371 | D3BJS3_POLPA | 29.08 | 447 | 4 | 433 | 830 | 1268 | 9.00E-43 | 171 |
| SCE1572_3400 | A9G6S7_SORC5/13-281 | 96.64 | 268 | 13 | 280 | 1 | 268 | 4.00E-152 | 534 |
| SCE1572_3426 | Q15300_HUMAN | 33.33 | 90 | 370 | 459 | 155 | 239 | 2.00E-11 | 67.8 |
| SCE1572_3444 | B2J8F9_NOSP7/7-265 | 49.8 | 247 | 7 | 253 | 13 | 259 | 3.00E-69 | 259 |
| SCE1572_3509 | A9GA77_SORC5/13-209 | 90.86 | 197 | 13 | 209 | 1 | 197 | 9.00E-97 | 351 |
| SCE1572_3555 | D0LZ14_HALO1 | 40.06 | 1358 | 2 | 1297 | 7 | 1346 | 0 | 799 |
| SCE1572_3557 | B9SC01_RICCO | 29.83 | 295 | 232 | 509 | 61 | 332 | 4.00E-19 | 93.2 |
| SCE1572_3564 | D0LZ14_HALO1 | 37.98 | 1364 | 2 | 1294 | 9 | 1346 | 0 | 655 |
| SCE1572_3565 | A9FE17_SORC5/11-267 | 61.66 | 253 | 9 | 261 | 1 | 253 | 1.00E-84 | 309 |
| SCE1572_3568 | D0LZ14_HALO1 | 37.21 | 1360 | 2 | 1295 | 9 | 1346 | 0 | 656 |
| SCE1572_3602 | A9GN95_SORC5/15-286 | 60.44 | 273 | 57 | 329 | 1 | 272 | 2.00E-81 | 299 |
| SCE1572_3611 | D0LYB2_HALO1 | 37.44 | 844 | 7 | 818 | 3 | 808 | 1.00E-119 | 428 |
| SCE1572_3648 | A9EWS2_SORC5/19-281 | 90.87 | 263 | 24 | 286 | 1 | 263 | 2.00E-137 | 484 |
| SCE1572_3687 | D7TTD5_VITVI | 26.56 | 384 | 59 | 419 | 95 | 470 | 7.00E-23 | 105 |
| SCE1572_3742 | Q7UX63_RHOBA/29-285 | 38.61 | 259 | 48 | 301 | 1 | 257 | 2.00E-37 | 154 |
| SCE1572_3748 | A9GAS9_SORC5/19-278 | 93.9 | 246 | 1 | 246 | 15 | 260 | 3.00E-128 | 456 |
| SCE1572_3762 | A9GAU7_SORC5/11-280 | 97.04 | 270 | 11 | 280 | 1 | 270 | 5.00E-150 | 528 |

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|--------------|-----------------------|-------|-----|-----|------|------|------|-----------|------|
| SCE1572_3765 | B4KV63_DROMO | 36.52 | 230 | 139 | 367 | 716 | 941 | 3.00E-36 | 149 |
| SCE1572_3771 | A9GAX7_SORC5/14-273 | 86.54 | 260 | 226 | 485 | 1 | 260 | 9.00E-123 | 436 |
| SCE1572_3808 | A9GB51_SORC5/18-289 | 93.01 | 272 | 18 | 289 | 1 | 272 | 2.00E-143 | 504 |
| SCE1572_3832 | A9GB92_SORC5/15-298 | 91.55 | 284 | 15 | 298 | 1 | 284 | 1.00E-151 | 531 |
| SCE1572_3852 | A9GBB7_SORC5/15-282 | 92.91 | 268 | 15 | 282 | 1 | 268 | 2.00E-139 | 491 |
| SCE1572_3872 | E3PW85_CLOSD | 35 | 160 | 164 | 323 | 1415 | 1571 | 2.00E-24 | 109 |
| SCE1572_3891 | A9GEK8_SORC5/15-277 | 95.44 | 263 | 41 | 303 | 1 | 263 | 2.00E-138 | 488 |
| SCE1572_3909 | A9VA07_MONBE | 30.82 | 717 | 34 | 703 | 601 | 1247 | 7.00E-70 | 262 |
| SCE1572_3923 | A9GEU8_SORC5/15-246 | 82.88 | 222 | 15 | 233 | 1 | 222 | 2.00E-87 | 320 |
| SCE1572_3948 | A9GF00_SORC5/16-284 | 97.4 | 269 | 21 | 289 | 1 | 269 | 3.00E-157 | 550 |
| SCE1572_3949 | A9GF02_SORC5/17-290 | 90.15 | 274 | 17 | 290 | 1 | 274 | 2.00E-133 | 473 |
| SCE1572_3968 | A9GF27_SORC5/18-299 | 93.62 | 282 | 18 | 299 | 1 | 282 | 3.00E-153 | 538 |
| SCE1572_3971 | A9GF34_SORC5/16-292 | 97.47 | 277 | 16 | 292 | 1 | 277 | 5.00E-158 | 554 |
| SCE1572_3980 | F2E4N3_HORVD | 25.66 | 339 | 46 | 358 | 34 | 367 | 4.00E-18 | 89 |
| SCE1572_4022 | D3BJS3_POLPA | 26.42 | 405 | 37 | 422 | 829 | 1222 | 9.00E-28 | 121 |
| SCE1572_4043 | A9GFI8_SORC5/49-315 | 98.13 | 267 | 49 | 315 | 1 | 267 | 4.00E-154 | 540 |
| SCE1572_4045 | A9GFJ3_SORC5/905-1172 | 96.64 | 268 | 898 | 1165 | 1 | 268 | 1.00E-152 | 536 |
| SCE1572_4065 | A9GFN9_SORC5/14-285 | 90.16 | 244 | 1 | 244 | 29 | 272 | 9.00E-130 | 459 |
| SCE1572_4072 | A9GFQ7_SORC5/31-302 | 98.9 | 272 | 26 | 297 | 1 | 272 | 3.00E-162 | 568 |
| SCE1572_4101 | D7TTD5_VITVI | 26.14 | 352 | 123 | 446 | 121 | 468 | 3.00E-16 | 83.2 |
| SCE1572_4129 | D3BJS3_POLPA | 24.69 | 401 | 8 | 401 | 829 | 1223 | 5.00E-24 | 108 |
| SCE1572_4162 | B9RTW7_RICCO | 34.36 | 195 | 4 | 191 | 38 | 224 | 5.00E-13 | 71.2 |
| SCE1572_4165 | B9RTW7_RICCO | 31.9 | 232 | 5 | 226 | 38 | 258 | 8.00E-15 | 77 |
| SCE1572_4185 | A9GIL2_SORC5/14-269 | 93.75 | 256 | 14 | 269 | 1 | 256 | 4.00E-133 | 472 |
| SCE1572_4342 | A9GJC9_SORC5/88-343 | 92.97 | 256 | 83 | 338 | 1 | 256 | 3.00E-130 | 462 |
| SCE1572_4349 | A9G8J3_SORC5/18-265 | 42.86 | 189 | 80 | 262 | 60 | 248 | 1.00E-34 | 145 |
| SCE1572_4350 | D0LZ14_HALO1 | 41 | 944 | 2 | 870 | 7 | 930 | 3.00E-151 | 533 |
| SCE1572_4364 | C3XWU6_BRAFL | 33.71 | 353 | 92 | 439 | 785 | 1109 | 9.00E-41 | 164 |

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|--------------|----------------------|-------|------|------|------|-----|------|-----------|------|
| SCE1572_4372 | D8LQ15_ECTSI | 45.68 | 243 | 83 | 318 | 597 | 839 | 3.00E-49 | 194 |
| SCE1572_4375 | A9FDB2_SORC5/22-188 | 65.81 | 155 | 17 | 170 | 1 | 155 | 4.00E-54 | 209 |
| SCE1572_4463 | A9GQ42_SORC5/62-327 | 75.57 | 262 | 50 | 308 | 1 | 262 | 3.00E-107 | 385 |
| SCE1572_4493 | A9G1R5_SORC5/6-275 | 87.78 | 270 | 157 | 426 | 1 | 270 | 9.00E-136 | 479 |
| SCE1572_4540 | A9GJS7_SORC5/31-311 | 76.16 | 281 | 44 | 322 | 1 | 281 | 1.00E-122 | 436 |
| SCE1572_4558 | A9GN95_SORC5/15-286 | 93.75 | 272 | 13 | 284 | 1 | 272 | 3.00E-142 | 500 |
| SCE1572_4582 | A9VA07_MONBE | 44.32 | 352 | 829 | 1169 | 596 | 942 | 3.00E-77 | 287 |
| SCE1572_4600 | A9GNJ1_SORC5/16-306 | 91.75 | 291 | 16 | 306 | 1 | 291 | 7.00E-152 | 532 |
| SCE1572_4662 | D0LZ14_HALO1 | 39.48 | 1388 | 10 | 1337 | 15 | 1335 | 0 | 723 |
| SCE1572_4675 | A9GRN8_SORC5/20-297 | 88.85 | 269 | 20 | 288 | 1 | 269 | 1.00E-138 | 489 |
| SCE1572_4692 | A9F8N6_SORC5/25-290 | 56 | 275 | 316 | 588 | 1 | 266 | 2.00E-75 | 280 |
| SCE1572_4725 | B4D5D6_9BACT | 30.86 | 175 | 412 | 585 | 886 | 1055 | 6.00E-11 | 66.2 |
| SCE1572_4741 | A9GRY1_SORC5/11-278 | 94.03 | 268 | 11 | 278 | 1 | 268 | 1.00E-114 | 409 |
| SCE1572_4758 | A6GDW6_9DELT | 26.42 | 318 | 625 | 927 | 580 | 893 | 9.00E-12 | 69.7 |
| SCE1572_4776 | A9GS33_SORC5/10-280 | 95.94 | 271 | 10 | 280 | 1 | 271 | 3.00E-156 | 547 |
| SCE1572_4809 | A9GSA1_SORC5/16-290 | 93.45 | 275 | 16 | 288 | 1 | 275 | 7.00E-152 | 532 |
| SCE1572_4846 | D3BJS3_POLPA | 25.78 | 419 | 9 | 411 | 815 | 1197 | 8.00E-16 | 82 |
| SCE1572_4847 | A9GSI1_SORC5/16-296 | 90.04 | 281 | 16 | 296 | 1 | 281 | 3.00E-139 | 490 |
| SCE1572_4851 | A6G4E4_9DELT | 30.9 | 631 | 1089 | 1658 | 590 | 1209 | 1.00E-52 | 206 |
| SCE1572_4861 | D0LZ14_HALO1 | 39.69 | 1018 | 2 | 961 | 7 | 993 | 6.00E-163 | 571 |
| SCE1572_4879 | A9GSP6_SORC5/10-277 | 95.52 | 268 | 53 | 320 | 1 | 268 | 4.00E-145 | 511 |
| SCE1572_4900 | A9FJE9_SORC5/231-472 | 63.33 | 240 | 220 | 458 | 1 | 240 | 3.00E-82 | 302 |
| SCE1572_4916 | A9GVU5_SORC5/13-275 | 87.83 | 263 | 45 | 307 | 1 | 263 | 1.00E-132 | 469 |
| SCE1572_4960 | A9GW43_SORC5/19-293 | 89.09 | 275 | 19 | 292 | 1 | 275 | 4.00E-136 | 480 |
| SCE1572_4965 | A9GJS7_SORC5/31-311 | 69.74 | 271 | 1 | 269 | 12 | 281 | 1.00E-103 | 373 |
| SCE1572_4984 | A9GW92_SORC5/236-501 | 95.49 | 266 | 236 | 501 | 1 | 266 | 1.00E-149 | 525 |
| SCE1572_5016 | A9GWG4_SORC5/16-292 | 88.45 | 277 | 16 | 292 | 1 | 277 | 2.00E-146 | 515 |
| SCE1572_5032 | A9GWK1_SORC5/51-315 | 94.34 | 265 | 51 | 315 | 1 | 265 | 4.00E-145 | 510 |

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|--------------|---------------------|-------|-----|------|------|------|------|-----------|------|
| SCE1572_5053 | A9GS33_SORC5/10-280 | 58.15 | 270 | 10 | 279 | 1 | 270 | 6.00E-90 | 326 |
| SCE1572_5061 | E5SP72_TRISP | 56.04 | 91 | 19 | 109 | 678 | 768 | 2.00E-25 | 109 |
| SCE1572_5065 | A9GWP7_SORC5/9-264 | 94.53 | 256 | 30 | 285 | 1 | 256 | 2.00E-141 | 497 |
| SCE1572_5069 | A6GDW6_9DELT | 45.99 | 274 | 606 | 879 | 660 | 933 | 7.00E-50 | 196 |
| SCE1572_5098 | A9GWX6_SORC5/13-270 | 94.26 | 244 | 1 | 244 | 15 | 258 | 7.00E-139 | 489 |
| SCE1572_5105 | F2UKF9_9EUKA | 39.86 | 148 | 2 | 143 | 8 | 148 | 3.00E-19 | 94 |
| SCE1572_5119 | A9GX30_SORC5/18-287 | 93.7 | 270 | 18 | 287 | 1 | 270 | 1.00E-148 | 523 |
| SCE1572_5149 | A6GDW6_9DELT | 37.87 | 301 | 1013 | 1313 | 657 | 951 | 2.00E-29 | 128 |
| SCE1572_5183 | B9RTW7_RICCO | 29.29 | 198 | 1 | 192 | 34 | 225 | 2.00E-11 | 65.9 |
| SCE1572_5199 | B9RTW7_RICCO | 29.95 | 197 | 14 | 205 | 35 | 226 | 5.00E-12 | 68.2 |
| SCE1572_5213 | A9EPX8_SORC5/14-320 | 89.25 | 307 | 5 | 311 | 1 | 307 | 5.00E-152 | 533 |
| SCE1572_5222 | A9EPZ6_SORC5/98-351 | 91.34 | 254 | 98 | 351 | 1 | 254 | 1.00E-127 | 454 |
| SCE1572_5251 | A9EQ70_SORC5/13-281 | 95.54 | 269 | 13 | 281 | 1 | 269 | 3.00E-152 | 534 |
| SCE1572_5254 | A9EQ76_SORC5/30-377 | 84.44 | 347 | 30 | 375 | 1 | 347 | 2.00E-158 | 555 |
| SCE1572_5259 | A9EQ83_SORC5/28-318 | 88.7 | 292 | 40 | 331 | 1 | 291 | 6.00E-138 | 486 |
| SCE1572_5269 | A9EQA5_SORC5/46-335 | 97.24 | 290 | 22 | 311 | 1 | 290 | 1.00E-165 | 578 |
| SCE1572_5318 | B9RTW7_RICCO | 27.89 | 190 | 6 | 186 | 40 | 225 | 1.00E-11 | 66.6 |
| SCE1572_5332 | A9EQJ9_SORC5/6-267 | 85.88 | 262 | 6 | 267 | 1 | 262 | 2.00E-126 | 450 |
| SCE1572_5348 | A9EQM0_SORC5/13-276 | 85.98 | 264 | 13 | 276 | 1 | 264 | 1.00E-132 | 469 |
| SCE1572_5352 | E9C1L0_9EUKA | 31.53 | 222 | 421 | 641 | 935 | 1146 | 2.00E-20 | 98.2 |
| SCE1572_5363 | A9FX47_SORC5/11-274 | 59.47 | 264 | 42 | 303 | 1 | 264 | 5.00E-76 | 282 |
| SCE1572_5365 | A9G2X2_SORC5/56-320 | 66.42 | 265 | 31 | 292 | 1 | 265 | 1.00E-88 | 322 |
| SCE1572_5389 | A9EQW7_SORC5/16-262 | 91.9 | 247 | 9 | 255 | 1 | 247 | 1.00E-133 | 474 |
| SCE1572_5405 | A9ER29_SORC5/14-284 | 88.56 | 271 | 37 | 307 | 1 | 271 | 1.00E-126 | 449 |
| SCE1572_5420 | A9EVM0_SORC5/14-277 | 88.26 | 264 | 14 | 277 | 1 | 264 | 9.00E-141 | 496 |
| SCE1572_5425 | A9GS33_SORC5/10-280 | 55.56 | 270 | 55 | 322 | 1 | 270 | 6.00E-86 | 313 |
| SCE1572_5440 | A5BDW0_VITVI | 26.29 | 251 | 3 | 213 | 1116 | 1365 | 4.00E-16 | 82 |
| SCE1572_5449 | D3BJS3_POLPA | 24.01 | 404 | 26 | 420 | 829 | 1222 | 5.00E-27 | 119 |

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|--------------|---------------------|-------|-----|-----|-----|-----|------|-----------|------|
| SCE1572_5468 | A9GTU1_SORC5/18-277 | 55.77 | 260 | 4 | 263 | 1 | 260 | 7.00E-81 | 298 |
| SCE1572_5480 | A9GTU1_SORC5/18-277 | 90 | 260 | 7 | 266 | 1 | 260 | 7.00E-139 | 491 |
| SCE1572_5495 | B4KV63_DROMO | 33.16 | 190 | 488 | 668 | 756 | 940 | 8.00E-16 | 82.4 |
| SCE1572_5590 | A9FDG9_SORC5/21-281 | 48.08 | 260 | 20 | 279 | 1 | 259 | 6.00E-63 | 237 |
| SCE1572_5597 | E3X4G0_ANODA | 30.61 | 330 | 20 | 334 | 7 | 321 | 3.00E-35 | 146 |
| SCE1572_5606 | A9EWN7_SORC5/34-297 | 91.29 | 264 | 64 | 327 | 1 | 264 | 3.00E-129 | 457 |
| SCE1572_5640 | A9F619_SORC5/13-273 | 79.31 | 261 | 9 | 267 | 1 | 261 | 8.00E-112 | 401 |
| SCE1572_5644 | A9F619_SORC5/13-273 | 80.25 | 81 | 1 | 81 | 138 | 218 | 5.00E-35 | 142 |
| SCE1572_5645 | A9F619_SORC5/13-273 | 71.43 | 84 | 9 | 92 | 1 | 84 | 1.00E-28 | 120 |
| SCE1572_5647 | D0LZ14_HALO1 | 43.91 | 476 | 32 | 506 | 435 | 899 | 7.00E-106 | 380 |
| SCE1572_5658 | A9EWZ2_SORC5/22-300 | 88.17 | 279 | 40 | 315 | 1 | 279 | 2.00E-140 | 496 |
| SCE1572_5689 | A9EX99_SORC5/14-287 | 90.91 | 275 | 28 | 302 | 1 | 274 | 2.00E-133 | 471 |
| SCE1572_5727 | A9F1W2_SORC5/19-315 | 95.29 | 297 | 98 | 394 | 1 | 297 | 5.00E-154 | 540 |
| SCE1572_5800 | A9F2K1_SORC5/24-292 | 95.91 | 269 | 24 | 292 | 1 | 269 | 6.00E-153 | 536 |
| SCE1572_5808 | A9F2M6_SORC5/7-264 | 97.29 | 258 | 7 | 264 | 1 | 258 | 1.00E-139 | 491 |
| SCE1572_5809 | C1A3Y3_GEMAT/13-268 | 30.84 | 214 | 71 | 284 | 68 | 256 | 7.00E-14 | 75.9 |
| SCE1572_5837 | A9F2U6_SORC5/16-277 | 91.6 | 262 | 16 | 277 | 1 | 262 | 1.00E-137 | 486 |
| SCE1572_5839 | A9FDG9_SORC5/21-281 | 54.75 | 263 | 37 | 299 | 1 | 259 | 3.00E-74 | 275 |
| SCE1572_5876 | A9F2Y6_SORC5/28-293 | 78.73 | 268 | 23 | 290 | 1 | 266 | 3.00E-115 | 411 |
| SCE1572_5963 | B5DPB6_DROPS | 31.91 | 257 | 178 | 428 | 700 | 944 | 1.00E-20 | 97.8 |
| SCE1572_5967 | A6G4E4_9DELTA | 32.77 | 528 | 47 | 565 | 829 | 1260 | 2.00E-43 | 174 |
| SCE1572_5997 | A9F3J7_SORC5/16-278 | 88.97 | 263 | 16 | 278 | 1 | 263 | 2.00E-135 | 478 |
| SCE1572_6031 | D3BJS3_POLPA | 25.62 | 402 | 78 | 468 | 844 | 1223 | 2.00E-24 | 110 |
| SCE1572_6038 | A9F865_SORC5/77-280 | 93.63 | 204 | 228 | 431 | 1 | 204 | 4.00E-104 | 374 |
| SCE1572_6062 | A9F8E9_SORC5/10-280 | 95.94 | 271 | 10 | 280 | 1 | 271 | 7.00E-153 | 536 |
| SCE1572_6075 | D3BJS3_POLPA | 25.81 | 465 | 18 | 473 | 816 | 1274 | 3.00E-36 | 149 |
| SCE1572_6092 | A9EVM0_SORC5/14-277 | 49.8 | 255 | 1 | 252 | 12 | 264 | 4.00E-63 | 237 |
| SCE1572_6096 | A9GRQ7_SORC5/16-276 | 46.8 | 250 | 10 | 254 | 15 | 261 | 1.00E-51 | 201 |

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|--------------|---------------------|-------|------|-----|------|------|------|-----------|------|
| SCE1572_6098 | A9F8N6_SORC5/25-290 | 90.23 | 266 | 95 | 360 | 1 | 266 | 4.00E-139 | 491 |
| SCE1572_6122 | A9F8W3_SORC5/41-296 | 97.27 | 256 | 41 | 296 | 1 | 256 | 5.00E-148 | 520 |
| SCE1572_6127 | A9F8Y3_SORC5/32-301 | 92.96 | 270 | 32 | 301 | 1 | 270 | 5.00E-143 | 503 |
| SCE1572_6128 | B9G748_ORYSJ | 35.36 | 362 | 47 | 393 | 45 | 404 | 4.00E-53 | 205 |
| SCE1572_6133 | A9F900_SORC5/96-359 | 97.73 | 264 | 66 | 329 | 1 | 264 | 2.00E-152 | 534 |
| SCE1572_6155 | A9F950_SORC5/52-318 | 86.14 | 267 | 52 | 318 | 1 | 267 | 3.00E-133 | 470 |
| SCE1572_6158 | A9F9F8_SORC5/44-308 | 85.66 | 265 | 46 | 308 | 1 | 265 | 2.00E-118 | 421 |
| SCE1572_6159 | A9F9G1_SORC5/55-317 | 80.08 | 266 | 46 | 311 | 1 | 263 | 6.00E-100 | 361 |
| SCE1572_6164 | A9F9M5_SORC5/12-288 | 84.64 | 280 | 12 | 291 | 1 | 277 | 5.00E-122 | 433 |
| SCE1572_6165 | D0LZ14_HALO1 | 38.07 | 935 | 2 | 867 | 7 | 923 | 8.00E-144 | 508 |
| SCE1572_6166 | A9F9N0_SORC5/11-276 | 92.59 | 270 | 11 | 280 | 1 | 266 | 2.00E-145 | 511 |
| SCE1572_6182 | A9GBB7_SORC5/15-282 | 54.28 | 269 | 19 | 281 | 1 | 267 | 8.00E-71 | 264 |
| SCE1572_6183 | C3XWU6_BRAFL | 34.08 | 358 | 305 | 653 | 840 | 1194 | 3.00E-49 | 193 |
| SCE1572_6194 | A9GS33_SORC5/10-280 | 53.33 | 270 | 10 | 279 | 1 | 270 | 1.00E-80 | 295 |
| SCE1572_6202 | D0LZ14_HALO1 | 42.3 | 1357 | 2 | 1291 | 7 | 1346 | 0 | 870 |
| SCE1572_6203 | B9RTW7_RICCO | 40.17 | 234 | 8 | 236 | 39 | 266 | 4.00E-36 | 148 |
| SCE1572_6277 | B9RTW7_RICCO | 36.36 | 198 | 4 | 192 | 38 | 229 | 3.00E-18 | 88.6 |
| SCE1572_6322 | E5SP72_TRISP | 49.45 | 91 | 64 | 153 | 678 | 767 | 2.00E-15 | 79 |
| SCE1572_6323 | C3ZQY6_BRAFL | 27.31 | 249 | 50 | 291 | 69 | 316 | 2.00E-15 | 80.1 |
| SCE1572_6324 | A9FF01_SORC5/27-278 | 97.22 | 252 | 27 | 278 | 1 | 252 | 1.00E-138 | 488 |
| SCE1572_6382 | D0LZ14_HALO1 | 39.71 | 1365 | 2 | 1286 | 7 | 1346 | 0 | 806 |
| SCE1572_6384 | A9FFI9_SORC5/13-292 | 86.43 | 280 | 13 | 292 | 1 | 280 | 9.00E-141 | 494 |
| SCE1572_6462 | A9GQX2_SORC5/13-284 | 52.81 | 267 | 3 | 266 | 6 | 272 | 4.00E-75 | 278 |
| SCE1572_6468 | E4YNA2_OIKDI | 29.39 | 228 | 135 | 349 | 1287 | 1511 | 7.00E-15 | 79 |
| SCE1572_6475 | D7TTD5_VITVI | 26.24 | 343 | 70 | 391 | 121 | 460 | 5.00E-22 | 102 |
| SCE1572_6504 | B9RTW7_RICCO | 30.48 | 187 | 9 | 194 | 38 | 219 | 3.00E-15 | 79 |
| SCE1572_6512 | D7TTD5_VITVI | 24.85 | 326 | 67 | 373 | 121 | 441 | 5.00E-20 | 95.5 |
| SCE1572_6547 | A9FS91_SORC5/8-267 | 53.19 | 188 | 21 | 208 | 75 | 260 | 2.00E-50 | 198 |

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|--------------|---------------------|-------|------|------|------|------|------|-----------|------|
| SCE1572_6563 | B9RTW7_RICCO | 33.85 | 192 | 17 | 199 | 38 | 225 | 3.00E-21 | 99 |
| SCE1572_6585 | A9GTY9_SORC5/10-268 | 47.43 | 175 | 1 | 165 | 93 | 259 | 1.00E-37 | 155 |
| SCE1572_6594 | E9CI33_9EUKA | 45.15 | 206 | 236 | 440 | 36 | 241 | 6.00E-39 | 158 |
| SCE1572_6634 | A6G4E4_9DELT | 33.76 | 702 | 1567 | 2237 | 537 | 1219 | 8.00E-68 | 256 |
| SCE1572_6638 | A9GS33_SORC5/10-280 | 57.92 | 259 | 1 | 258 | 12 | 269 | 7.00E-83 | 303 |
| SCE1572_6657 | A6FAX0_9GAMM/20-314 | 54.55 | 286 | 41 | 326 | 1 | 286 | 3.00E-87 | 320 |
| SCE1572_6664 | B7P9G7_IXOSC | 29.79 | 235 | 137 | 362 | 578 | 798 | 1.00E-13 | 74.3 |
| SCE1572_6688 | A9F932_SORC5/34-318 | 73.33 | 285 | 377 | 661 | 1 | 285 | 8.00E-117 | 418 |
| SCE1572_6735 | D3BJS3_POLPA | 28.33 | 466 | 74 | 514 | 822 | 1276 | 2.00E-37 | 154 |
| SCE1572_6742 | A9FL39_SORC5/55-319 | 89.33 | 253 | 69 | 319 | 1 | 253 | 4.00E-125 | 444 |
| SCE1572_6800 | A9FLI0_SORC5/13-287 | 94.18 | 275 | 35 | 309 | 1 | 275 | 5.00E-154 | 540 |
| SCE1572_6833 | A9FR17_SORC5/15-284 | 88.15 | 270 | 15 | 284 | 1 | 270 | 3.00E-137 | 484 |
| SCE1572_6862 | A9FRA7_SORC5/27-289 | 92.4 | 263 | 82 | 344 | 1 | 263 | 4.00E-144 | 507 |
| SCE1572_6872 | A9FRE2_SORC5/13-279 | 89.14 | 267 | 13 | 279 | 1 | 267 | 5.00E-130 | 460 |
| SCE1572_6887 | D0LZ14_HALO1 | 38.34 | 193 | 3 | 192 | 1157 | 1346 | 1.00E-12 | 68.9 |
| SCE1572_6892 | D0LZ14_HALO1 | 39.38 | 833 | 2 | 775 | 7 | 828 | 1.00E-138 | 490 |
| SCE1572_6893 | D0LZ14_HALO1 | 39.13 | 1362 | 2 | 1294 | 7 | 1346 | 0 | 779 |
| SCE1572_6894 | D0LZ14_HALO1 | 38.68 | 1352 | 2 | 1291 | 7 | 1346 | 0 | 758 |
| SCE1572_6921 | A9FP27_SORC5/11-267 | 95.33 | 257 | 11 | 267 | 1 | 257 | 3.00E-126 | 449 |
| SCE1572_6948 | A9GQV1_SORC5/7-266 | 57.09 | 261 | 7 | 267 | 1 | 260 | 2.00E-80 | 297 |
| SCE1572_6974 | D0LZ14_HALO1 | 40.34 | 932 | 4 | 868 | 9 | 917 | 3.00E-156 | 549 |
| SCE1572_6983 | A9FRW7_SORC5/16-282 | 90.26 | 267 | 74 | 340 | 1 | 267 | 7.00E-139 | 491 |
| SCE1572_7026 | B9G748_ORYSJ | 29.65 | 226 | 277 | 498 | 70 | 286 | 3.00E-15 | 79.7 |
| SCE1572_7035 | A9FS85_SORC5/37-352 | 84.15 | 347 | 37 | 383 | 1 | 316 | 6.00E-137 | 484 |
| SCE1572_7045 | A5D1B0_PELTS/10-265 | 38.52 | 257 | 53 | 306 | 1 | 255 | 4.00E-49 | 192 |
| SCE1572_7065 | A9GS33_SORC5/10-280 | 54.44 | 270 | 10 | 279 | 1 | 270 | 2.00E-83 | 305 |
| SCE1572_7076 | A9FSE5_SORC5/14-280 | 91.39 | 267 | 14 | 280 | 1 | 267 | 6.00E-139 | 491 |
| SCE1572_7098 | A9F7S7_SORC5/16-279 | 86.74 | 264 | 16 | 279 | 1 | 264 | 2.00E-127 | 451 |

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|--------------|---------------------|-------|-----|-----|-----|-----|-----|-----------|------|
| SCE1572_7229 | A9FX40_SORC5/39-310 | 90.81 | 272 | 121 | 392 | 1 | 272 | 3.00E-142 | 501 |
| SCE1572_7235 | A9FX47_SORC5/11-274 | 81.82 | 264 | 42 | 304 | 1 | 264 | 2.00E-115 | 413 |
| SCE1572_7236 | A9FX52_SORC5/61-318 | 94.19 | 258 | 64 | 321 | 1 | 258 | 1.00E-139 | 492 |
| SCE1572_7241 | A9GRQ7_SORC5/16-276 | 53.64 | 261 | 55 | 313 | 1 | 261 | 2.00E-72 | 270 |
| SCE1572_7268 | A9FXC4_SORC5/66-318 | 82.68 | 254 | 63 | 316 | 1 | 253 | 2.00E-112 | 403 |
| SCE1572_7270 | A9FXD2_SORC5/32-294 | 88.21 | 263 | 31 | 293 | 1 | 263 | 2.00E-131 | 464 |
| SCE1572_7299 | A9GA96_SORC5/7-269 | 84.03 | 263 | 7 | 266 | 1 | 263 | 9.00E-126 | 447 |
| SCE1572_7311 | A9FYH6_SORC5/7-273 | 78.65 | 267 | 7 | 265 | 1 | 267 | 2.00E-117 | 420 |
| SCE1572_7326 | A9FYJ4_SORC5/24-284 | 88.51 | 261 | 85 | 345 | 1 | 261 | 7.00E-130 | 459 |
| SCE1572_7338 | A9FYM0_SORC5/12-281 | 95.93 | 246 | 2 | 247 | 25 | 270 | 8.00E-138 | 486 |
| SCE1572_7353 | E9CJ13_9EUKA | 44.54 | 119 | 75 | 191 | 315 | 431 | 2.00E-23 | 107 |
| SCE1572_7354 | A9VAH9_MONBE | 28.92 | 325 | 366 | 674 | 68 | 374 | 9.00E-22 | 102 |
| SCE1572_7360 | A9G2H5_SORC5/75-335 | 95.02 | 261 | 75 | 335 | 1 | 261 | 8.00E-146 | 513 |
| SCE1572_7397 | A9G2M3_SORC5/18-300 | 92.58 | 283 | 9 | 291 | 1 | 283 | 3.00E-133 | 471 |
| SCE1572_7413 | D7FZX4_ECTSI | 30.58 | 399 | 171 | 505 | 106 | 497 | 5.00E-27 | 119 |
| SCE1572_7427 | A9F932_SORC5/34-318 | 62.93 | 294 | 84 | 377 | 1 | 285 | 2.00E-101 | 367 |
| SCE1572_7443 | A9FKG8_SORC5/47-312 | 55.81 | 267 | 38 | 300 | 1 | 266 | 1.00E-69 | 260 |
| SCE1572_7456 | A9G394_SORC5/21-294 | 90.88 | 274 | 21 | 294 | 1 | 274 | 2.00E-145 | 511 |
| SCE1572_7473 | A9G3H0_SORC5/24-196 | 96.53 | 173 | 24 | 196 | 1 | 173 | 4.00E-88 | 321 |
| SCE1572_7501 | A9G3U5_SORC5/23-287 | 93.58 | 265 | 23 | 287 | 1 | 265 | 1.00E-144 | 509 |
| SCE1572_7543 | D7TTD5_VITVI | 22.72 | 471 | 29 | 481 | 34 | 480 | 2.00E-17 | 87.4 |
| SCE1572_7579 | A9G7V5_SORC5/54-335 | 96.45 | 282 | 54 | 335 | 1 | 282 | 3.00E-160 | 560 |
| SCE1572_7601 | A9G814_SORC5/50-310 | 91.57 | 261 | 49 | 309 | 1 | 261 | 5.00E-132 | 466 |
| SCE1572_7612 | D0LJH9_HALO1 | 30.22 | 460 | 173 | 613 | 529 | 917 | 3.00E-21 | 100 |
| SCE1572_7621 | B9RTW7_RICCO | 32.49 | 197 | 23 | 216 | 35 | 224 | 3.00E-15 | 79.3 |
| SCE1572_7637 | E3X4G0_ANODA | 32.77 | 296 | 1 | 291 | 14 | 293 | 5.00E-30 | 128 |
| SCE1572_7641 | A9G8A9_SORC5/19-269 | 99.2 | 251 | 19 | 269 | 1 | 251 | 4.00E-148 | 520 |
| SCE1572_7643 | A9G8B3_SORC5/33-299 | 92.88 | 267 | 48 | 314 | 1 | 267 | 5.00E-151 | 530 |

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|--------------|---------------------|-------|------|-----|------|------|------|-----------|------|
| SCE1572_7669 | B9L1Q1_THERP/10-268 | 41.73 | 266 | 336 | 592 | 1 | 258 | 3.00E-38 | 156 |
| SCE1572_7697 | A9G8G3_SORC5/22-297 | 93.12 | 276 | 40 | 315 | 1 | 276 | 2.00E-152 | 535 |
| SCE1572_7707 | A9G8K4_SORC5/15-290 | 93.09 | 275 | 15 | 289 | 1 | 275 | 9.00E-151 | 529 |
| SCE1572_7865 | A9GC13_SORC5/22-332 | 89.51 | 305 | 1 | 303 | 7 | 311 | 2.00E-138 | 488 |
| SCE1572_7872 | A9GC29_SORC5/7-277 | 96.31 | 271 | 7 | 277 | 1 | 271 | 3.00E-151 | 530 |
| SCE1572_7879 | D3BJS3_POLPA | 28.68 | 401 | 5 | 397 | 825 | 1222 | 4.00E-42 | 169 |
| SCE1572_7916 | B9S6C8_RICCO | 24.15 | 414 | 78 | 474 | 29 | 352 | 4.00E-13 | 73.2 |
| SCE1572_7931 | A9GCF7_SORC5/32-301 | 93.36 | 271 | 32 | 302 | 1 | 270 | 1.00E-144 | 508 |
| SCE1572_7938 | A9GCH4_SORC5/10-276 | 93.26 | 267 | 10 | 276 | 1 | 267 | 2.00E-147 | 518 |
| SCE1572_7942 | Q23ZG6_TETTH | 23 | 213 | 137 | 334 | 625 | 835 | 4.00E-13 | 73.9 |
| SCE1572_7955 | A9GCK3_SORC5/48-322 | 85.82 | 275 | 15 | 289 | 1 | 275 | 2.00E-139 | 491 |
| SCE1572_7984 | A9GCS7_SORC5/22-306 | 92.28 | 285 | 22 | 306 | 1 | 285 | 3.00E-147 | 518 |
| SCE1572_8190 | A6G4E4_9DELTA | 27.34 | 578 | 602 | 1160 | 648 | 1216 | 4.00E-37 | 154 |
| SCE1572_8240 | A9GGJ5_SORC5/9-279 | 82.33 | 283 | 9 | 291 | 1 | 271 | 3.00E-124 | 440 |
| SCE1572_8250 | F2UKF9_9EUKA | 27.89 | 484 | 6 | 457 | 9 | 474 | 3.00E-38 | 156 |
| SCE1572_8287 | A9GGW8_SORC5/20-305 | 94.41 | 286 | 20 | 305 | 1 | 286 | 3.00E-150 | 526 |
| SCE1572_8288 | B0VGL8_CLOAI | 27.39 | 376 | 123 | 456 | 251 | 592 | 3.00E-16 | 83.2 |
| SCE1572_8321 | A9GH81_SORC5/34-292 | 94.21 | 259 | 38 | 296 | 1 | 259 | 3.00E-136 | 481 |
| SCE1572_8378 | A9GJX9_SORC5/10-273 | 87.5 | 264 | 5 | 268 | 1 | 264 | 2.00E-123 | 437 |
| SCE1572_8383 | C8RRI2_CORJE/14-279 | 30.83 | 266 | 9 | 256 | 1 | 264 | 1.00E-22 | 103 |
| SCE1572_8391 | D0LZ14_HALO1 | 39.99 | 1353 | 2 | 1278 | 7 | 1344 | 0 | 758 |
| SCE1572_8403 | E4XBZ6_OIKDI | 28.65 | 192 | 105 | 292 | 1678 | 1869 | 4.00E-16 | 80.1 |
| SCE1572_8417 | A9GKG4_SORC5/22-288 | 88.76 | 267 | 22 | 288 | 1 | 267 | 1.00E-128 | 455 |
| SCE1572_8429 | D7TTD5_VITVI | 26.49 | 302 | 142 | 426 | 179 | 480 | 3.00E-15 | 79.7 |
| SCE1572_8434 | A9GKK0_SORC5/84-246 | 92.41 | 158 | 84 | 239 | 1 | 158 | 1.00E-67 | 254 |
| SCE1572_8448 | A9GJS7_SORC5/31-311 | 79.36 | 281 | 104 | 382 | 1 | 281 | 4.00E-129 | 458 |
| SCE1572_8495 | D0LZ14_HALO1 | 37.09 | 1146 | 24 | 1103 | 7 | 1141 | 2.00E-171 | 600 |
| SCE1572_8496 | D0LZ14_HALO1 | 39.91 | 847 | 94 | 932 | 176 | 1015 | 4.00E-142 | 503 |

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|--------------|----------------------|-------|------|-----|------|-----|------|-----------|------|
| SCE1572_8499 | D0LZ14_HALO1 | 37.51 | 909 | 2 | 802 | 7 | 905 | 7.00E-128 | 454 |
| SCE1572_8524 | A9GNU1_SORC5/8-279 | 91.57 | 261 | 1 | 261 | 12 | 272 | 4.00E-140 | 494 |
| SCE1572_8533 | A9GNW1_SORC5/30-305 | 95.65 | 276 | 9 | 284 | 1 | 276 | 3.00E-153 | 537 |
| SCE1572_8597 | D7FZX4_ECTSI | 43.19 | 426 | 65 | 476 | 106 | 521 | 2.00E-70 | 264 |
| SCE1572_8679 | B9RTW7_RICCO | 30.92 | 207 | 2 | 199 | 40 | 242 | 1.00E-16 | 83.6 |
| SCE1572_8698 | D0LZ14_HALO1 | 40.28 | 1003 | 13 | 950 | 7 | 981 | 0 | 630 |
| SCE1572_8739 | A9GT67_SORC5/13-276 | 87.12 | 264 | 35 | 298 | 1 | 264 | 4.00E-136 | 480 |
| SCE1572_8749 | B4CYY7_9BACT | 27.67 | 253 | 91 | 302 | 722 | 951 | 3.00E-14 | 76.6 |
| SCE1572_8762 | D0LZ14_HALO1 | 39.16 | 835 | 2 | 775 | 7 | 827 | 3.00E-135 | 479 |
| SCE1572_8765 | A9F6M3_SORC5 | 55.01 | 349 | 1 | 336 | 1 | 347 | 4.00E-91 | 332 |
| SCE1572_8775 | D0LZ14_HALO1 | 28.75 | 546 | 9 | 528 | 825 | 1346 | 4.00E-34 | 142 |
| SCE1572_8822 | B9RTW7_RICCO | 32.84 | 204 | 1 | 198 | 34 | 224 | 7.00E-15 | 77.4 |
| SCE1572_8834 | A9GC88_SORC5/32-303 | 66.18 | 272 | 138 | 408 | 1 | 272 | 4.00E-100 | 362 |
| SCE1572_8876 | B8LDL2_THAPS | 26.43 | 488 | 77 | 556 | 997 | 1431 | 1.00E-48 | 192 |
| SCE1572_8886 | A9GTY0_SORC5/11-268 | 96.9 | 258 | 11 | 268 | 1 | 258 | 1.00E-142 | 503 |
| SCE1572_8903 | E9C7Z1_9EUKA | 31.51 | 219 | 156 | 354 | 271 | 485 | 9.00E-14 | 74.7 |
| SCE1572_8954 | A9GX99_SORC5/49-311 | 90.11 | 263 | 9 | 271 | 1 | 263 | 1.00E-138 | 489 |
| SCE1572_8968 | D0LYB2_HALO1 | 35.9 | 493 | 43 | 512 | 349 | 814 | 1.00E-44 | 178 |
| SCE1572_8987 | A9GXH6_SORC5/24-319 | 82.83 | 297 | 24 | 320 | 1 | 296 | 2.00E-135 | 478 |
| SCE1572_9027 | A9GXN7_SORC5/42-300 | 88.46 | 260 | 43 | 302 | 1 | 259 | 8.00E-127 | 450 |
| SCE1572_9056 | A9VAH9_MONBE | 31.42 | 662 | 45 | 678 | 81 | 733 | 1.00E-59 | 228 |
| SCE1572_9060 | A6G4E4_9DELT | 27.73 | 815 | 523 | 1227 | 506 | 1260 | 3.00E-38 | 157 |
| SCE1572_9064 | A9VAH9_MONBE | 32.48 | 391 | 69 | 446 | 76 | 466 | 4.00E-32 | 135 |
| SCE1572_9065 | Q7PTP9_ANOGA | 32.27 | 220 | 344 | 559 | 818 | 1030 | 2.00E-18 | 90.9 |
| SCE1572_9071 | A9GXY7_SORC5/124-394 | 94.96 | 258 | 128 | 385 | 14 | 271 | 1.00E-142 | 503 |
| SCE1572_9073 | A9VA81_MONBE | 34.14 | 249 | 130 | 366 | 130 | 353 | 3.00E-21 | 100 |
| SCE1572_9075 | A9GJS7_SORC5/31-311 | 80 | 285 | 103 | 387 | 1 | 281 | 9.00E-132 | 467 |
| SCE1572_9112 | A9GYC7_SORC5/46-317 | 91.94 | 273 | 44 | 316 | 1 | 272 | 1.00E-140 | 495 |

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|--------------|----------------------|-------|-----|-----|-----|------|------|-----------|------|
| SCE1572_9177 | A9ERD0_SORC5/20-276 | 85.99 | 257 | 20 | 276 | 1 | 257 | 5.00E-124 | 441 |
| SCE1572_9204 | A9ERQ0_SORC5/24-283 | 90 | 260 | 47 | 306 | 1 | 260 | 2.00E-135 | 478 |
| SCE1572_9234 | Q098I7_STIAU/99-355 | 71.21 | 257 | 105 | 360 | 1 | 257 | 3.00E-100 | 362 |
| SCE1572_9273 | A9ES80_SORC5/13-299 | 81.47 | 313 | 26 | 338 | 1 | 287 | 3.00E-130 | 460 |
| SCE1572_9274 | A9ES85_SORC5/18-279 | 91.98 | 262 | 18 | 279 | 1 | 262 | 1.00E-136 | 482 |
| SCE1572_9286 | A9ESD5_SORC5/69-334 | 92.11 | 266 | 11 | 276 | 1 | 266 | 4.00E-143 | 503 |
| SCE1572_9290 | A9ESE9_SORC5/19-289 | 98.44 | 257 | 1 | 257 | 15 | 271 | 6.00E-149 | 524 |
| SCE1572_9346 | A9ESY9_SORC5/122-403 | 95.74 | 282 | 122 | 403 | 1 | 282 | 7.00E-151 | 530 |
| SCE1572_9383 | B4KV63_DROMO | 33.91 | 230 | 160 | 388 | 714 | 940 | 5.00E-36 | 149 |
| SCE1572_9387 | A9EXL8_SORC5/33-306 | 99.27 | 274 | 33 | 306 | 1 | 274 | 4.00E-165 | 577 |
| SCE1572_9440 | A9EY93_SORC5/26-264 | 94.14 | 239 | 14 | 252 | 1 | 239 | 4.00E-128 | 454 |
| SCE1572_9453 | A9FX52_SORC5/61-318 | 52.71 | 258 | 47 | 304 | 1 | 258 | 5.00E-75 | 277 |
| SCE1572_9454 | A9FX47_SORC5/11-274 | 56.32 | 261 | 46 | 301 | 4 | 264 | 4.00E-69 | 259 |
| SCE1572_9464 | A9EYF1_SORC5/26-299 | 95.26 | 274 | 24 | 297 | 1 | 274 | 2.00E-139 | 491 |
| SCE1572_9490 | A9EYQ5_SORC5/13-322 | 92.26 | 310 | 16 | 325 | 1 | 310 | 2.00E-166 | 581 |
| SCE1572_9503 | A5BUK4_VITVI | 38.36 | 73 | 5 | 77 | 38 | 110 | 4.00E-11 | 63.5 |
| SCE1572_9529 | A9EZ28_SORC5/20-279 | 93.85 | 260 | 20 | 279 | 1 | 260 | 7.00E-142 | 500 |
| SCE1572_9534 | A9EZ47_SORC5/30-295 | 86.84 | 266 | 26 | 286 | 1 | 266 | 2.00E-123 | 439 |
| SCE1572_9543 | E9CFQ5_9EUKA | 32.68 | 205 | 167 | 344 | 231 | 433 | 5.00E-20 | 95.5 |
| SCE1572_9561 | Q099F0_STIAU/22-311 | 55.81 | 301 | 53 | 347 | 1 | 290 | 1.00E-76 | 284 |
| SCE1572_9570 | A9GTY9_SORC5/10-268 | 47.69 | 260 | 12 | 271 | 1 | 259 | 4.00E-61 | 233 |
| SCE1572_9627 | B8LDL2_THAPS | 23.81 | 483 | 1 | 472 | 1038 | 1467 | 2.00E-32 | 139 |
| SCE1572_9635 | E5SP72_TRISP | 41.23 | 114 | 204 | 313 | 653 | 765 | 8.00E-13 | 71.2 |
| SCE1572_9698 | A9F548_SORC5/73-334 | 90.84 | 262 | 88 | 349 | 1 | 262 | 8.00E-134 | 472 |
| SCE1572_9699 | A9F553_SORC5/15-290 | 89.86 | 276 | 15 | 290 | 1 | 276 | 7.00E-142 | 499 |
| SCE1572_9718 | E9C1L0_9EUKA | 32.08 | 212 | 210 | 421 | 955 | 1155 | 7.00E-22 | 101 |
| SCE1572_9733 | A9F5E0_SORC5/14-276 | 93.16 | 263 | 14 | 276 | 1 | 263 | 1.00E-146 | 515 |
| SCE1572_9768 | A9F5P2_SORC5/100-253 | 81.82 | 154 | 100 | 250 | 1 | 154 | 3.00E-62 | 234 |

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|---------------|----------------------|-------|-----|-----|------|------|------|-----------|------|
| SCE1572_9776 | A9F5R7_SORC5/10-285 | 89.49 | 276 | 37 | 312 | 1 | 276 | 2.00E-137 | 485 |
| SCE1572_9812 | A9FA64_SORC5/37-294 | 73.66 | 262 | 16 | 277 | 1 | 258 | 8.00E-110 | 395 |
| SCE1572_9849 | A9FAC8_SORC5/14-277 | 93.94 | 264 | 14 | 277 | 1 | 264 | 1.00E-149 | 525 |
| SCE1572_9893 | A6G4E4_9DELTA | 30.84 | 454 | 508 | 955 | 788 | 1197 | 3.00E-36 | 151 |
| SCE1572_9895 | A9FAX2_SORC5/29-287 | 95.75 | 259 | 29 | 287 | 1 | 259 | 2.00E-143 | 505 |
| SCE1572_9959 | A6GDW6_9DELTA | 42.6 | 986 | 90 | 1024 | 29 | 1004 | 3.00E-140 | 496 |
| SCE1572_10034 | A9FG39_SORC5/21-290 | 90 | 270 | 25 | 294 | 1 | 270 | 7.00E-143 | 503 |
| SCE1572_10048 | A9FG77_SORC5/27-293 | 94.38 | 267 | 27 | 293 | 1 | 267 | 7.00E-151 | 529 |
| SCE1572_10051 | A9FG88_SORC5/13-278 | 96.62 | 266 | 77 | 342 | 1 | 266 | 2.00E-149 | 525 |
| SCE1572_10155 | A9FH30_SORC5/261-495 | 94.89 | 235 | 256 | 490 | 1 | 235 | 9.00E-116 | 413 |
| SCE1572_10170 | A9FH69_SORC5/13-277 | 93.21 | 265 | 13 | 276 | 1 | 265 | 3.00E-139 | 491 |
| SCE1572_10242 | A9F6M3_SORC5 | 57.64 | 314 | 1 | 303 | 1 | 313 | 2.00E-90 | 329 |
| SCE1572_10268 | Q23ZG6_TETTH | 26.18 | 359 | 145 | 466 | 619 | 964 | 1.00E-22 | 105 |
| SCE1572_10276 | E3PW85_CLOSD | 39.24 | 158 | 141 | 298 | 1414 | 1569 | 7.00E-28 | 120 |
| SCE1572_10294 | E4YNA2_OIKDI | 28.27 | 329 | 8 | 289 | 1152 | 1458 | 1.00E-16 | 84.7 |
| SCE1572_10347 | A9FHU2_SORC5/67-328 | 94.66 | 262 | 66 | 327 | 1 | 262 | 2.00E-145 | 511 |
| SCE1572_10352 | A6G4E4_9DELTA | 29.35 | 293 | 26 | 308 | 926 | 1213 | 3.00E-12 | 69.3 |
| SCE1572_10373 | D7SRK5_VITVI | 30.12 | 259 | 50 | 289 | 24 | 276 | 7.00E-16 | 82 |
| SCE1572_10391 | D7TV01_VITVI | 30.98 | 410 | 70 | 471 | 488 | 869 | 9.00E-39 | 157 |
| SCE1572_10405 | E7F1M5_DANRE | 38.58 | 197 | 182 | 325 | 98 | 294 | 3.00E-12 | 69.7 |
| SCE1572_10476 | A9V9Z1_MONBE | 31.82 | 286 | 1 | 263 | 948 | 1214 | 3.00E-22 | 102 |
| SCE1572_10484 | A9FMI8_SORC5/61-326 | 92.08 | 265 | 35 | 298 | 1 | 265 | 6.00E-141 | 496 |
| SCE1572_10529 | B4KV63_DROMO | 27.74 | 274 | 403 | 663 | 677 | 939 | 1.00E-13 | 75.1 |
| SCE1572_10654 | A9FNS6_SORC5/28-292 | 98.11 | 265 | 18 | 282 | 1 | 265 | 2.00E-147 | 517 |
| SCE1572_10719 | E3PW85_CLOSD | 35.47 | 172 | 541 | 712 | 1413 | 1578 | 4.00E-26 | 116 |
| SCE1572_10740 | B9RTW7_RICCO | 33.5 | 203 | 1 | 198 | 34 | 224 | 1.00E-14 | 76.6 |
| SCE1572_10785 | A9FU56_SORC5/23-293 | 92.99 | 271 | 23 | 293 | 1 | 271 | 6.00E-152 | 533 |
| SCE1572_10787 | A9FU59_SORC5/20-287 | 91.04 | 268 | 59 | 326 | 1 | 268 | 2.00E-144 | 508 |

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|---------------|---------------------|-------|------|-----|------|------|------|-----------|------|
| SCE1572_10800 | A9G0Y5_SORC5/28-295 | 63.16 | 266 | 28 | 293 | 1 | 266 | 3.00E-93 | 338 |
| SCE1572_10832 | C3ZSQ8_BRAFL | 40.32 | 124 | 498 | 621 | 1640 | 1761 | 3.00E-18 | 90.1 |
| SCE1572_10834 | Q23ZG6_TETTH | 18.88 | 466 | 126 | 518 | 578 | 1032 | 3.00E-11 | 67.8 |
| SCE1572_10838 | D7FZX4_ECTSI | 29.47 | 397 | 146 | 480 | 106 | 496 | 1.00E-19 | 94.7 |
| SCE1572_10868 | E9IEB9_SOLIN | 39.81 | 103 | 228 | 329 | 237 | 337 | 1.00E-10 | 66.6 |
| SCE1572_10892 | A9FYY9_SORC5/32-312 | 93.59 | 281 | 32 | 312 | 1 | 281 | 4.00E-156 | 548 |
| SCE1572_10919 | B9RTW7_RICCO | 30.9 | 233 | 2 | 230 | 34 | 258 | 6.00E-15 | 77.8 |
| SCE1572_10924 | A9FZ90_SORC5/7-269 | 89.74 | 273 | 7 | 279 | 1 | 263 | 5.00E-142 | 502 |
| SCE1572_10928 | A9FZ94_SORC5/32-347 | 91.77 | 316 | 32 | 347 | 1 | 316 | 2.00E-172 | 601 |
| SCE1572_10995 | A9G0J1_SORC5/93-365 | 88.64 | 273 | 16 | 288 | 1 | 273 | 4.00E-146 | 513 |
| SCE1572_11043 | A9G4G1_SORC5/11-269 | 92.66 | 259 | 11 | 269 | 1 | 259 | 3.00E-140 | 495 |
| SCE1572_11046 | A9G4G4_SORC5/74-341 | 83.08 | 260 | 74 | 333 | 1 | 259 | 1.00E-112 | 404 |
| SCE1572_11048 | A9G4H1_SORC5/35-296 | 94.44 | 234 | 1 | 234 | 27 | 260 | 3.00E-126 | 447 |
| SCE1572_11102 | B9RTW7_RICCO | 30.89 | 191 | 3 | 189 | 38 | 224 | 1.00E-11 | 67 |
| SCE1572_11141 | A9V7M5_MONBE | 29.36 | 327 | 404 | 717 | 71 | 382 | 4.00E-13 | 73.6 |
| SCE1572_11143 | B9RTW7_RICCO | 32.12 | 193 | 6 | 192 | 38 | 224 | 3.00E-11 | 65.1 |
| SCE1572_11169 | D8LHV1_ECTSI | 27.61 | 326 | 246 | 567 | 31 | 320 | 4.00E-13 | 73.2 |
| SCE1572_11185 | B9RTW7_RICCO | 30.41 | 194 | 6 | 195 | 39 | 225 | 3.00E-12 | 69.3 |
| SCE1572_11206 | D0LZ14_HALO1 | 39.67 | 1220 | 103 | 1304 | 163 | 1344 | 0 | 723 |
| SCE1572_11215 | A9GJS7_SORC5/31-311 | 64.34 | 286 | 85 | 369 | 1 | 280 | 2.00E-97 | 352 |
| SCE1572_11281 | A9G9I7_SORC5/19-323 | 86.56 | 305 | 65 | 369 | 1 | 305 | 3.00E-141 | 499 |
| SCE1572_11313 | D7U846_VITVI | 53.25 | 169 | 3 | 171 | 657 | 825 | 4.00E-45 | 177 |
| SCE1572_11364 | A9GD46_SORC5/12-271 | 89.62 | 260 | 12 | 271 | 1 | 260 | 3.00E-135 | 479 |
| SCE1572_11382 | A9GD84_SORC5/84-356 | 95.6 | 273 | 60 | 332 | 1 | 273 | 4.00E-149 | 523 |
| SCE1572_11384 | A9GD87_SORC5/29-299 | 97.42 | 271 | 29 | 299 | 1 | 271 | 1.00E-158 | 555 |
| SCE1572_11385 | D0LYB2_HALO1 | 24.13 | 630 | 395 | 986 | 345 | 937 | 9.00E-13 | 73.2 |
| SCE1572_11393 | A9GDB7_SORC5/16-307 | 93.14 | 277 | 31 | 306 | 16 | 292 | 6.00E-148 | 521 |
| SCE1572_11400 | A9GDD6_SORC5/1-262 | 93.89 | 262 | 27 | 288 | 1 | 262 | 2.00E-144 | 508 |

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|---------------|----------------------|-------|-----|-----|-----|-----|------|-----------|-----|
| SCE1572_11413 | D3BJS3_POLPA | 27.9 | 405 | 23 | 419 | 822 | 1222 | 6.00E-40 | 162 |
| SCE1572_11432 | A9GDN2_SORC5/49-311 | 92.02 | 263 | 49 | 311 | 1 | 263 | 1.00E-137 | 485 |
| SCE1572_11467 | A9GS33_SORC5/10-280 | 65.93 | 270 | 10 | 278 | 1 | 270 | 5.00E-104 | 374 |
| SCE1572_11561 | A9GS33_SORC5/10-280 | 56.83 | 271 | 10 | 279 | 1 | 270 | 1.00E-84 | 309 |
| SCE1572_11581 | A9GHH8_SORC5/49-320 | 91.54 | 272 | 49 | 320 | 1 | 272 | 8.00E-134 | 472 |
| SCE1572_11582 | A9GHI1_SORC5/382-646 | 80.68 | 264 | 382 | 645 | 1 | 264 | 2.00E-108 | 389 |
| SCE1572_11584 | A9GHP7_SORC5/10-312 | 83.61 | 305 | 15 | 315 | 1 | 303 | 5.00E-127 | 450 |

* Blasting against three Pfam families, PF00069, PF00433 and PF07714 with a cutoff 1e-10

Supplementary Table S2. CRISPR statistics in Myxobacteria.

| Strains | Genome size(bp) | Convincing CRISPR structure | Length (bp)* |
|--|-----------------|-----------------------------|--------------|
| <i>Coralloccoccus coralloides</i> DSM 2259 | 10,080,619 | 7 | 2805 |
| <i>Anaeromyxobacter dehalogenans</i> 2CP-1 | 5,029,329 | 2 | 2131 |
| <i>Anaeromyxobacter dehalogenans</i> 2CP-C | 5,013,479 | 0 | 0 |
| <i>Anaeromyxobacter</i> sp. Fw109-5 | 5,277,990 | 0 | 0 |
| <i>Anaeromyxobacter</i> sp. K | 5,061,632 | 2 | 4507 |
| <i>Haliangium ochraceum</i> DSM 14365 | 9,446,314 | 3 | 58594 |
| <i>Myxococcus fulvus</i> HW-1 | 9,003,593 | 4 | 5903 |
| <i>Myxococcus xanthus</i> DK 1622 | 9,139,763 | 4 | 10137 |
| <i>Sorangium cellulosum</i> 'So ce 56' | 13,033,779 | 5 | 12726 |
| <i>Stigmatella aurantiaca</i> DW4/3-1 | 10,260,756 | 1 | 176 |
| <i>Sorangium cellulosum</i> So0157-2 | 14,782,435 | 3 | 6572 |

* Just statistics of convincing CRISPR structure.

Supplementary Table S3 Primer and statistical results of qPCR experiment.

| Locus tag | Product name | Forward primer (5'-3') | Reverse primer (5'-3') | RNA-Seq Reads* (pH7.0/pH9.0) | logFC (RNA-Seq)** | $\Delta\Delta Ct$ (qPCR) #1 | $\Delta\Delta Ct$ (qPCR) #2 |
|-----------------------------|--|---------------------------|--------------------------|------------------------------|-------------------|-----------------------------|-----------------------------|
| SCE1572_3207 | gliding motility protein MglA | GGCATCGTGTTTCGTC AGC | GGAACGGGTTCAA CATCG | 91/439 | -3.54 | -1.03 | -1.44 |
| SCE1572_3710 | RNA-binding protein | CGTCTTTACGTCGGC AATC | GCCTCGTTGACCT TGAGC | 89/85 | -5.05 | -1.20 | -1.97 |
| SCE1572_6018 | RNA polymerase sigma factor RpoD | GTGCGGAAGGTCCTG AAG | CGAGATCACGCTC TTGTCC | 2640/712 | 0.62 | 0.3 | 0.61 |
| SCE1572_6365 | Macrolide-specific efflux protein MacA | GGTGGAGAAGGGGAC GCT | GACCACGCCCTGG AACAC | 108/500 | -3.48 | -3.54 | -2.7 |
| SCE1572_7438 | Cell division protein FtsZ | CCTCCCCAAGGACCA GTG | AAGCCGAGGTAG CCGAAG | 347/1317 | -3.20 | -0.47 | -2.57 |
| SCE1572_7464 (reference) | Urea ABC transporter, ATPase protein UrtD | GGACGGGCTCGACTT CTC | CACCTCCGTGGAA CACCA | 412/162 | 0.08 | NA | NA |
| SCE1572_7815 | Heat shock protein 60 family chaperone GroEL | AGGGCAAGGACTCGT TCG | TCGGTGGTGAGCA TCAGG | 3485/17984 | -3.64 | -1.62 | -3.02 |
| SCE1572_8437 | Outer membrane protein A precursor | GTGGAGCACAACATC AAGCTG | TCGTCGTTTCGTGA AGCAGA | 153/25 | 1.34 | 0.04 | -2 |

NA: Not applicable.

*These reads were produced by Illumina Sequencer directly.

** The logarithm values of fold-change (FC) were calculated from the reads after they were normalized by Fragments Per Kilobase of transcript per Million mapped reads (FPKM) using the edgeR program (Reference 53 in the text).

Supplementary Table S5. Statistics of big genome in prokaryote.

| Organisms | Genome sizes | Genes | GC content | Niche | Accession |
|---|--------------|-------|------------|--|-------------|
| <i>Sorangium cellulosum</i> So0157-2 | 14.87 | 11599 | 0.721 | Soil | CP003969 |
| <i>Sorangium cellulosum</i> So ce 56 | 13.03 | 9384 | 0.714 | Soil | AM746676 |
| <i>Streptomyces bingchenggensis</i> BCW-1 | 11.94 | 10022 | 0.708 | Soil | CP002047 |
| <i>Streptomyces violaceusniger</i> Tü 4113 | 10.66 | 8482 | 0.709 | Soil | CP002994 |
| <i>Streptosporangium roseum</i> DSM 43021 | 10.34 | 8945 | 0.7086 | Vegetable garden soil | CP001814 |
| <i>Stigmatella aurantiaca</i> DW4/3-1 | 10.26 | 8352 | 0.675 | Soil | CP002271 |
| <i>Amycolatopsis mediterranei</i> S699 | 10.24 | 9575 | 0.713 | Pine arboretum soil | CP002896 |
| <i>Amycolatopsis mediterranei</i> U32 | 10.24 | 9228 | 0.713 | Soil | CP002000 |
| <i>Catenulispora acidiphila</i> DSM 44928 | 10.17 | 8914 | 0.6977 | Forest soil, acidophilic | CP001700 |
| <i>Streptomyces hygrosopicus</i> subsp. <i>jinggangensis</i> 5008 | 10.15 | 8849 | 0.719 | Soil | CP003275 |
| <i>Streptomyces scabiei</i> 87.22 | 10.15 | 8809 | 0.7 | Deep-pitted scab lesion on a potato | FN554889 |
| <i>Corallocooccus coralloides</i> DSM 2259 | 10.08 | 8033 | 0.699 | Soil | CP003389 |
| <i>Solibacter usitatus</i> Ellin6076 | 9.97 | 7826 | 0.619 | Soil | CP000473 |
| <i>Streptomyces davawensis</i> JCM 4913 | 9.47 | 8503 | 0.7058 | Soil, near Davao Air Port, Mindanao, the Philippines | PRJEB184 |
| <i>Haliangium ochraceum</i> DSM 14365 | 9.45 | 6719 | 0.69 | Sea grass samples | CP001804 |
| <i>Nocardia brasiliensis</i> ATCC 700358 HUJEG-1 | 9.44 | 8414 | 0.68 | Human mycetoma | AIHV0000000 |
| <i>Saccharothrix espanaensis</i> DSM 44229 | 9.36 | 8427 | 0.7219 | Soil | HE804045 |
| <i>Actinoplanes</i> species SE50/110 | 9.24 | 8247 | 0.7132 | Soil | CP003170 |
| <i>Bradyrhizobium japonicum</i> USDA 6 | 9.21 | 8829 | 0.64 | Glycine max, a soybean plant | AP012206 |
| <i>Myxococcus xanthus</i> DK 1622 | 9.14 | 7331 | 0.689 | Soil | CP000113 |
| <i>Chitinophaga pinensis</i> DSM 2588 | 9.13 | 7192 | 0.4523 | Infusion of litter from | CP001699 |

| | | | | | |
|---|------|------|--------|---|----------|
| <i>Bradyrhizobium japonicum</i> USDA 110 | 9.11 | 8317 | 0.64 | the base of a pine tree Glycine max, a soybean plant | BA000040 |
| <i>Niastella koreensis</i> GR20-10 | 9.03 | 7174 | 0.45 | Korean ginseng soil | CP003178 |
| <i>Streptomyces avermitilis</i> MA-4680 | 9.03 | 7580 | 0.707 | Soil | BA000030 |
| <i>Myxococcus fulvus</i> HW-1 | 9 | 7284 | 0.706 | Marine | CP002830 |
| <i>Frankia</i> species EAN1pec | 8.98 | 7191 | 0.71 | Soybean plant | CP000820 |
| <i>Frankia</i> species Eu11c | 8.82 | 7083 | 0.72 | Soybean plant | CP002299 |
| <i>Kitasatospora setae</i> KM-6054 | 8.78 | 7569 | 0.742 | Soil | AP010968 |
| <i>Actinoplanes missouriensis</i> 431 | 8.77 | 8125 | 0.71 | Soil | AP012319 |
| <i>Paenibacillus mucilaginosus</i> K02 | 8.77 | 7253 | 0.58 | Soil | CP003422 |
| <i>Paenibacillus mucilaginosus</i> 3016 | 8.74 | 7057 | 0.583 | Rhizosphere soil | CP003235 |
| <i>Streptomyces coelicolor</i> A3(2) | 8.67 | 7825 | 0.721 | Soil | AL645882 |
| <i>Paenibacillus mucilaginosus</i> KNP414 | 8.66 | 7804 | 0.58 | Soil | CP002869 |
| <i>Streptomyces griseus</i> subsp. <i>griseus</i> NBRC 13350 | 8.55 | 7138 | 0.722 | Soil | AP009493 |
| <i>Haliscomenobacter hydrossis</i> DSM 1100 | 8.37 | 6451 | 0.471 | Activated sludge samples | CP002691 |
| <i>Bradyrhizobium</i> species BTAi1 | 8.26 | 7394 | 0.65 | Soybean plant | CP000494 |
| <i>Actinosynnema mirum</i> DSM 43827 | 8.25 | 6916 | 0.7371 | Grass blade | CP001630 |
| <i>Nostoc punctiforme</i> PCC 73102 | 8.23 | 6087 | 0.41 | Symbiotic association with the gymnosperm cycad <i>Macrozamia</i> sp. | CP001037 |
| <i>Streptomyces venezuelae</i> ATCC 10712 | 8.23 | 7453 | 0.724 | Soil | FR845719 |
| <i>Saccharopolyspora erythraea</i> NRRL 2338 (UCambridge) | 8.21 | 7198 | 0.7129 | Soil | AM420293 |
| <i>Spirosoma linguale</i> DSM 74 | 8.08 | 6524 | 0.5015 | Laboratory water bath | CP001769 |
| <i>Burkholderia xenovorans</i> LB400 | 9.73 | 9059 | 0.63 | PCB (polychlorinated biphenyl)-containing landfill | CP000270 |
| <i>Rhodococcus jostii</i> RHA1 | 9.7 | 9242 | 0.67 | Lindane-contaminated | CP000431 |

| | | | | | |
|--|------|------|------|---|----------|
| <i>Streptomyces sviveus</i> ATCC 29083 | 9.31 | 8275 | 0.7 | soil | CM000951 |
| <i>Streptomyces clavuligerus</i> ATCC 27064 | 9.13 | 7680 | 0.72 | Soil | CM001015 |
| <i>Burkholderia gladioli</i> BSR3 | 9.05 | 7493 | 0.67 | Diseased rice sheath | CP002600 |
| <i>Burkholderia phymatum</i> STM815 | 8.68 | 7574 | 0.62 | Soybean plant | CP001043 |
| <i>Burkholderia cepacia</i> 383 | 8.68 | 7828 | 0.66 | Forest soil | CP000152 |
| <i>Cupriavidus necator</i> N-1, ATCC 43291 | 8.48 | 7967 | 0.65 | Soil, described as a nonobligate predator of soil bacteria and fungi and resistance against heavy metal | CP002878 |
| <i>Burkholderia vietnamiensis</i> G4 | 8.39 | 7880 | 0.66 | Hazardous environmental contaminants in groundwaters | CP000616 |
| <i>Acaryochloris marina</i> MBIC11017 | 8.36 | 8488 | 0.47 | Marine | CP000828 |
| <i>Burkholderia phytofirmans</i> PsJN | 8.21 | 7487 | 0.62 | Glomus vesiculiferum-infected onion roots | CP001053 |
| <i>Streptomyces pristinaespiralis</i> ATCC 25486 | 8.13 | 6937 | 0.71 | Soil | CM000950 |
| <i>Streptomyces cattleya</i> DSM 46488 | 8.09 | 7650 | 0.73 | Soil | CP003219 |
| <i>Streptomyces cattleya</i> NRRL 8057 | 8.09 | 7585 | 0.73 | Soil | FQ859185 |
| <i>Burkholderia cenocepacia</i> J2315 | 8.05 | 7229 | 0.67 | Lungs of cystic fibrosis (CF) patients | AM747722 |

Supplementary Table S6. The sequencing library used for assembly of the So0157-2 genome.

| Sample ID | Fragment length(bp) | Raw data(Mb) | Clean Data(Mb) | Pair-end type |
|-----------|---------------------|--------------|----------------|---------------|
| So0157-2 | 274 | 2,022 | 869 | (75;75) |
| So0157-2 | 491 | 1,862 | 1,102 | (75;75) |
| So0157-2 | 242 | 376 | 353 | (44;44) |
| So0157-2 | 6000 | 1,810 | 649 | (44;44) |
| So0157-2 | 250 | 2,386 | 973 | (70;70) |
| So0157-2 | 350 | 2,830 | 1,278 | (44;44) |
| So0157-2 | 2500 | 679 | 525 | (70;70) |

Supplementary Table S10. The structure of the ribosomal RNA operon in So0157-2 and So ce56.

| | <i>Sorangium cellulosum</i> So ce56 | | | | <i>S. cellulosum</i> So0157-2 | | | |
|---|-------------------------------------|-----------------------------------|-------------------------------------|---|-------------------------------|---------------------------------------|-----------------------------|------------------------|
| RNA operon Structure | 16S rRNA→ 23S rRNA | 16S rRNA→ 23S rRNA→ 5S rRNA | 16S rRNA →23S rRNA→5S rRNA | 16S rRNA→ 23S rRNA→ 5S rRNA | 16S rRNA →23S rRNA | 16S rRNA→ 23S rRNA→ 5S rRNA(×3) | 16SRNA→ 23SRNA→ 5SRNA | 16S rRNA→5S rRNA |
| tRNA | — | tRNA-Ile- GAT,tRNA- Ala-TGC | — | tRNA-Ile- GAT | — | tRNA-Ile- GAT, tRNA- Ala-TGC | — | tRNA-Ile-GAT |
| interruption or duplication repeat | Absence of 5S rRNA | — | — | — | Absence of 5S rRNA | — 5S rRNA repeat | — | Absence of 23S rRNA |

Supplementary Table S12. BLAST analysis comparing the *E. coli* K12 strain's LPS gene cluster with the So0157-2 database.

| Gene ID | Gene symbol | Source | E-value* | Hits |
|----------------------|--|------------------|----------|------|
| lipid A | | | | |
| lpxA | UDP-N-acetylglucosamine acetyltransferase | <i>E. coli</i> + | 4.00E-05 | 1 |
| lpxB | tetraacyldisaccharide-1-P synthase | <i>E. coli</i> - | | |
| lpxC | UDP-3-O-acyl N-acetylglucosamine deacetylase | <i>E. coli</i> - | | |
| lpxD | UDP-3-O-(3-hydroxymyristoyl)-glucosamine N-acyltransferase | <i>E. coli</i> - | | |
| lpxH | UDP-2,3-diacylglucosamine pyrophosphatase | <i>E. coli</i> - | | |
| lpxK | lipid A 4kinase | <i>E. coli</i> - | | |
| lpxL | lauryl-acyl carrier protein (ACP)-dependent acyltransferase carrier | <i>E. coli</i> - | | |
| lpxM | myristoyl-acyl carrier protein (ACP)-dependent acyltransferase carrier | <i>E. coli</i> - | | |
| lpxP | palmitoleoyl-acyl carrier protein (ACP)-dependent acyltransferase carrier | <i>E. coli</i> - | | |
| core oligosaccharide | | | | |
| rfaB | UDP-D-galactose:(glucosyl)lipopolysaccharide-1,6-D-galactosyltransferase | <i>E. coli</i> + | 4.00E-10 | 7 |
| rfaC | ADP-heptose:LPS heptosyl transferase I | <i>E. coli</i> - | | |
| rfaD | ADP-L-glycero-D-mannoheptose-6-epimerase, NAD(P)-binding | <i>E. coli</i> + | 7.00E-13 | 8 |
| rfaE | fused heptose 7-phosphate kinase and heptose 1-phosphate adenylyltransferase | <i>E. coli</i> + | 5.00E-09 | 2 |
| rfaF | ADP-heptose:LPS heptosyltransferase II | <i>E. coli</i> - | | |
| rfaG | glucosyltransferase I | <i>E. coli</i> + | 8.00E-12 | 11 |
| rfaH | DNA-binding transcriptional antiterminator | <i>E. coli</i> - | | |
| rfaI | UDP-D-galactose:(glucosyl)lipopolysaccharide-alpha-1,3-D-galactosyltransferase | <i>E. coli</i> - | | |
| rfaJ | UDP-D-glucose:(galactosyl)lipopolysaccharide glucosyltransferase | <i>E. coli</i> - | | |
| rfaK | lipopolysaccharide core biosynthesis | <i>E. coli</i> - | | |
| rfaL | O-antigen ligase | <i>E. coli</i> - | | |
| rfaP | kinase that phosphorylates core heptose of lipopolysaccharide | <i>E. coli</i> - | | |
| rfaQ | lipopolysaccharide core biosynthesis protein | <i>E. coli</i> - | | |

| | | | | | |
|------------------|---|----------------|---|----------|----|
| rfaS | lipopolysaccharide core biosynthesis protein | <i>E. coli</i> | - | | |
| rfaY | lipopolysaccharide core biosynthesis protein | <i>E. coli</i> | - | | |
| rfaZ | lipopolysaccharide core biosynthesis protein | <i>E. coli</i> | - | | |
| <hr/> | | | | | |
| O polysaccharide | | | | | |
| rfbX | predicted polisoprenol-linked O-antigen transporter | <i>E. coli</i> | - | | |
| rfbC | dTDP-4-deoxyrhamnose-3,5-epimerase | <i>E. coli</i> | - | | |
| rfbA | glucose-1-phosphate thymidyltransferase | <i>E. coli</i> | + | 6.00E-14 | 2 |
| rfbD | dTDP-4-dehydrorhamnose reductase subunit, NAD(P)-binding, of dTDP-L-rhamnose synthase | <i>E. coli</i> | + | 7.00E-20 | 1 |
| rfbB | dTDP-glucose 4,6 dehydratase, NAD(P)-binding | <i>E. coli</i> | + | 3.00E-31 | 17 |

*cutoff of Blast is 0.0001

Supplementary Table S13. Chemotaxis in *Sorangium cellulosum* So157-2.

| Query ID | Subject ID | E-value* | Bit score | Family |
|---------------|------------|----------|-----------|---------------|
| SCE1572_4806 | MXAN_2682 | 1.00E-24 | 103 | Che4 |
| SCE1572_7946 | MXAN_2682 | 1.00E-24 | 103 | Che4 |
| SCE1572_4577 | MXAN_2682 | 7.00E-26 | 106 | Che4 |
| SCE1572_7810 | MXAN_2684 | 1.00E-13 | 64.7 | Che4 |
| SCE1572_9390 | MXAN_2684 | 2.00E-13 | 65.1 | Che4 |
| SCE1572_10471 | MXAN_2684 | 4.00E-14 | 68.6 | Che4 |
| SCE1572_411 | MXAN_2684 | 2.00E-14 | 69.7 | Che4 |
| SCE1572_2795 | MXAN_2684 | 1.00E-18 | 79.7 | Che4 |
| SCE1572_3799 | MXAN_2689 | 1.00E-27 | 112 | Che4 |
| SCE1572_5466 | MXAN_2689 | 1.00E- | 370 | Che4 |
| | | 105 | | |
| SCE1572_1358 | MXAN_2689 | 2.00E- | 446 | Che4 |
| | | 128 | | |
| SCE1572_2376 | MXAN_4138 | 2.00E-24 | 102 | Frz (Che1) |
| SCE1572_7523 | MXAN_4140 | 7.00E-11 | 58.2 | Frz (Che1) |
| SCE1572_3185 | MXAN_4140 | 4.00E-11 | 58.5 | Frz (Che1) |
| SCE1572_10862 | MXAN_4140 | 1.00E-12 | 63.5 | Frz (Che1) |
| SCE1572_6546 | MXAN_4140 | 9.00E-14 | 66.2 | Frz (Che1) |
| SCE1572_9886 | MXAN_4140 | 1.00E-13 | 67 | Frz (Che1) |
| SCE1572_6923 | MXAN_4140 | 4.00E-16 | 75.5 | Frz (Che1) |
| SCE1572_9628 | MXAN_4140 | 1.00E-16 | 75.9 | Frz (Che1) |
| SCE1572_4879 | MXAN_4140 | 5.00E-17 | 78.2 | Frz (Che1) |
| SCE1572_4349 | MXAN_4140 | 2.00E-17 | 80.1 | Frz (Che1) |
| SCE1572_1207 | MXAN_4140 | 8.00E-42 | 159 | Frz (Che1) |
| SCE1572_1851 | MXAN_4144 | 3.00E-12 | 59.3 | Frz (Che1) |
| SCE1572_7738 | MXAN_4149 | 6.00E-13 | 64.7 | Frz (Che1) |
| SCE1572_9885 | MXAN_4751 | 2.00E-15 | 70.9 | Che8 |
| SCE1572_5352 | MXAN_4751 | 2.00E-17 | 79 | Che8 |

| | | | | |
|---------------|-----------|----------|------|------|
| SCE1572_2409 | MXAN_4751 | 8.00E-31 | 120 | Che8 |
| SCE1572_5882 | MXAN_4752 | 2.00E-12 | 60.5 | Che8 |
| SCE1572_2235 | MXAN_4752 | 1.00E-71 | 258 | Che8 |
| SCE1572_5865 | MXAN_4753 | 4.00E-32 | 128 | Che8 |
| SCE1572_2234 | MXAN_4753 | 5.00E-63 | 229 | Che8 |
| SCE1572_2798 | MXAN_4756 | 1.00E-10 | 54.3 | Che8 |
| SCE1572_2232 | MXAN_4756 | 2.00E-12 | 59.7 | Che8 |
| SCE1572_2231 | MXAN_4757 | 4.00E-14 | 65.5 | Che8 |
| SCE1572_1252 | MXAN_4758 | 2.00E-28 | 115 | Che8 |
| SCE1572_2230 | MXAN_4758 | 7.00E-39 | 150 | Che8 |
| SCE1572_2797 | MXAN_4758 | 6.00E-55 | 202 | Che8 |
| SCE1572_2230 | MXAN_4758 | 3.00E- | 357 | Che8 |
| | | 101 | | |
| SCE1572_1887 | MXAN_4759 | 5.00E-12 | 60.8 | Che8 |
| SCE1572_9096 | MXAN_4759 | 5.00E-19 | 81.6 | Che8 |
| SCE1572_2229 | MXAN_4759 | 3.00E-25 | 102 | Che8 |
| SCE1572_1205 | MXAN_5144 | 2.00E-18 | 81.3 | Che3 |
| SCE1572_5867 | MXAN_5145 | 8.00E-25 | 102 | Che3 |
| SCE1572_4573 | MXAN_5145 | 9.00E-59 | 215 | Che3 |
| SCE1572_9153 | MXAN_5147 | 7.00E-11 | 54.7 | Che3 |
| SCE1572_4252 | MXAN_5147 | 2.00E-11 | 56.2 | Che3 |
| SCE1572_2742 | MXAN_5147 | 1.00E-11 | 57.8 | Che3 |
| SCE1572_10639 | MXAN_5147 | 3.00E-11 | 57.8 | Che3 |
| SCE1572_11082 | MXAN_5147 | 1.00E-11 | 57.8 | Che3 |
| SCE1572_10447 | MXAN_5147 | 3.00E-11 | 58.5 | Che3 |
| SCE1572_9669 | MXAN_5147 | 2.00E-12 | 60.5 | Che3 |
| SCE1572_6975 | MXAN_5147 | 2.00E-12 | 60.8 | Che3 |
| SCE1572_6485 | MXAN_5147 | 6.00E-13 | 62 | Che3 |
| SCE1572_7521 | MXAN_5147 | 3.00E-13 | 62 | Che3 |
| SCE1572_3835 | MXAN_5147 | 2.00E-12 | 62.4 | Che3 |
| SCE1572_6394 | MXAN_5147 | 2.00E-13 | 62.8 | Che3 |
| SCE1572_10286 | MXAN_5147 | 2.00E-13 | 63.5 | Che3 |
| SCE1572_2296 | MXAN_5147 | 5.00E-13 | 63.9 | Che3 |
| SCE1572_933 | MXAN_5147 | 7.00E-13 | 64.3 | Che3 |
| SCE1572_1254 | MXAN_5147 | 7.00E-14 | 64.3 | Che3 |
| SCE1572_9214 | MXAN_5147 | 5.00E-13 | 64.7 | Che3 |
| SCE1572_11146 | MXAN_5147 | 3.00E-13 | 64.7 | Che3 |
| SCE1572_1850 | MXAN_5147 | 2.00E-13 | 65.9 | Che3 |
| SCE1572_8842 | MXAN_5147 | 5.00E-14 | 66.2 | Che3 |
| SCE1572_3496 | MXAN_5147 | 1.00E-13 | 67 | Che3 |
| SCE1572_3496 | MXAN_5147 | 3.00E-14 | 68.9 | Che3 |
| SCE1572_6547 | MXAN_5147 | 5.00E-14 | 68.9 | Che3 |
| SCE1572_3872 | MXAN_5147 | 2.00E-15 | 71.6 | Che3 |

| | | | | |
|---------------|-----------|----------|------|------|
| SCE1572_1238 | MXAN_5147 | 5.00E-16 | 72.4 | Che3 |
| SCE1572_6251 | MXAN_5147 | 2.00E-15 | 72.8 | Che3 |
| SCE1572_6606 | MXAN_5147 | 3.00E-16 | 74.3 | Che3 |
| SCE1572_6664 | MXAN_5147 | 4.00E-17 | 77 | Che3 |
| SCE1572_4572 | MXAN_5147 | 1.00E-17 | 78.6 | Che3 |
| SCE1572_8841 | MXAN_5147 | 5.00E-18 | 81.3 | Che3 |
| SCE1572_1208 | MXAN_5148 | 5.00E-33 | 130 | Che3 |
| SCE1572_9692 | MXAN_5153 | 3.00E-12 | 59.7 | Che3 |
| SCE1572_9926 | MXAN_5153 | 7.00E-13 | 61.2 | Che3 |
| SCE1572_8613 | MXAN_5153 | 6.00E-13 | 62.4 | Che3 |
| SCE1572_8913 | MXAN_5153 | 4.00E-14 | 65.1 | Che3 |
| SCE1572_2647 | MXAN_5153 | 4.00E-14 | 67.8 | Che3 |
| SCE1572_3367 | MXAN_5153 | 8.00E-15 | 69.7 | Che3 |
| SCE1572_430 | MXAN_5153 | 3.00E-16 | 74.7 | Che3 |
| SCE1572_1974 | MXAN_5153 | 2.00E-18 | 79.7 | Che3 |
| SCE1572_10567 | MXAN_5153 | 2.00E-26 | 108 | Che3 |
| SCE1572_3150 | MXAN_5153 | 2.00E-28 | 114 | Che3 |
| SCE1572_3873 | MXAN_5153 | 1.00E-28 | 115 | Che3 |
| SCE1572_1470 | MXAN_5153 | 6.00E-29 | 117 | Che3 |
| SCE1572_1939 | MXAN_5153 | 2.00E-29 | 118 | Che3 |
| SCE1572_11212 | MXAN_5153 | 5.00E-35 | 136 | Che3 |
| SCE1572_9209 | MXAN_5153 | 2.00E-35 | 138 | Che3 |
| SCE1572_6814 | MXAN_5153 | 2.00E-36 | 141 | Che3 |
| SCE1572_3740 | MXAN_5153 | 7.00E-37 | 143 | Che3 |
| SCE1572_2589 | MXAN_5153 | 4.00E-37 | 144 | Che3 |
| SCE1572_8957 | MXAN_5153 | 5.00E-38 | 146 | Che3 |
| SCE1572_4341 | MXAN_5153 | 4.00E-39 | 150 | Che3 |
| SCE1572_7059 | MXAN_5153 | 3.00E-39 | 150 | Che3 |
| SCE1572_8480 | MXAN_5153 | 2.00E-39 | 151 | Che3 |
| SCE1572_8199 | MXAN_5153 | 1.00E-39 | 152 | Che3 |
| SCE1572_10539 | MXAN_5153 | 8.00E-40 | 153 | Che3 |
| SCE1572_6839 | MXAN_5153 | 2.00E-40 | 154 | Che3 |
| SCE1572_5366 | MXAN_5153 | 8.00E-41 | 155 | Che3 |
| SCE1572_8888 | MXAN_5153 | 6.00E-41 | 155 | Che3 |
| SCE1572_9233 | MXAN_5153 | 1.00E-42 | 162 | Che3 |
| SCE1572_432 | MXAN_5153 | 5.00E-43 | 163 | Che3 |
| SCE1572_6162 | MXAN_5153 | 1.00E-43 | 165 | Che3 |
| SCE1572_3179 | MXAN_5153 | 2.00E-44 | 167 | Che3 |
| SCE1572_5537 | MXAN_5153 | 4.00E-45 | 170 | Che3 |
| SCE1572_5925 | MXAN_5153 | 2.00E-45 | 171 | Che3 |
| SCE1572_3259 | MXAN_5153 | 1.00E-45 | 172 | Che3 |
| SCE1572_10720 | MXAN_5153 | 6.00E-47 | 176 | Che3 |
| SCE1572_701 | MXAN_5153 | 3.00E-47 | 177 | Che3 |

| | | | | |
|---------------|-----------|----------|-----|------|
| SCE1572_1018 | MXAN_5153 | 3.00E-48 | 180 | Che3 |
| SCE1572_3063 | MXAN_5153 | 3.00E-48 | 180 | Che3 |
| SCE1572_3661 | MXAN_5153 | 1.00E-48 | 181 | Che3 |
| SCE1572_6637 | MXAN_5153 | 2.00E-48 | 181 | Che3 |
| SCE1572_7037 | MXAN_5153 | 1.00E-48 | 181 | Che3 |
| SCE1572_5058 | MXAN_5153 | 7.00E-49 | 182 | Che3 |
| SCE1572_9084 | MXAN_5153 | 1.00E-48 | 182 | Che3 |
| SCE1572_3607 | MXAN_5153 | 2.00E-49 | 184 | Che3 |
| SCE1572_383 | MXAN_5153 | 1.00E-50 | 188 | Che3 |
| SCE1572_4536 | MXAN_5153 | 2.00E-50 | 188 | Che3 |
| SCE1572_11280 | MXAN_5153 | 1.00E-50 | 188 | Che3 |
| SCE1572_2644 | MXAN_5153 | 1.00E-50 | 189 | Che3 |
| SCE1572_3040 | MXAN_5153 | 1.00E-51 | 192 | Che3 |
| SCE1572_8245 | MXAN_5153 | 7.00E-52 | 192 | Che3 |
| SCE1572_5021 | MXAN_5153 | 2.00E-52 | 194 | Che3 |
| SCE1572_5602 | MXAN_5153 | 2.00E-52 | 194 | Che3 |
| SCE1572_4565 | MXAN_5153 | 2.00E-52 | 195 | Che3 |
| SCE1572_7337 | MXAN_5153 | 4.00E-53 | 196 | Che3 |
| SCE1572_2072 | MXAN_5153 | 2.00E-55 | 204 | Che3 |
| SCE1572_11300 | MXAN_5153 | 2.00E-55 | 204 | Che3 |
| SCE1572_3798 | MXAN_5153 | 1.00E-55 | 205 | Che3 |
| SCE1572_9960 | MXAN_5153 | 7.00E-56 | 206 | Che3 |
| SCE1572_3571 | MXAN_5153 | 1.00E-56 | 208 | Che3 |
| SCE1572_7435 | MXAN_5153 | 2.00E-57 | 210 | Che3 |
| SCE1572_1966 | MXAN_5153 | 4.00E-58 | 213 | Che3 |
| SCE1572_1420 | MXAN_5153 | 1.00E-58 | 215 | Che3 |
| SCE1572_9989 | MXAN_5153 | 1.00E-58 | 215 | Che3 |
| SCE1572_4441 | MXAN_5153 | 3.00E-59 | 217 | Che3 |
| SCE1572_5776 | MXAN_5153 | 2.00E-59 | 218 | Che3 |
| SCE1572_5412 | MXAN_5153 | 7.00E-60 | 219 | Che3 |
| SCE1572_990 | MXAN_5153 | 5.00E-60 | 220 | Che3 |
| SCE1572_3609 | MXAN_5153 | 3.00E-60 | 220 | Che3 |
| SCE1572_3923 | MXAN_5153 | 8.00E-60 | 220 | Che3 |
| SCE1572_2120 | MXAN_5153 | 6.00E-61 | 223 | Che3 |
| SCE1572_535 | MXAN_5153 | 5.00E-61 | 224 | Che3 |
| SCE1572_429 | MXAN_5153 | 2.00E-63 | 231 | Che3 |
| SCE1572_6987 | MXAN_5153 | 3.00E-63 | 231 | Che3 |
| SCE1572_7038 | MXAN_5153 | 3.00E-66 | 240 | Che3 |
| SCE1572_8695 | MXAN_5153 | 1.00E-66 | 241 | Che3 |
| SCE1572_9357 | MXAN_5153 | 5.00E-70 | 253 | Che3 |
| SCE1572_4010 | MXAN_5153 | 2.00E-70 | 254 | Che3 |
| SCE1572_4397 | MXAN_5153 | 7.00E-73 | 262 | Che3 |
| SCE1572_7927 | MXAN_5153 | 5.00E-76 | 272 | Che3 |

| | | | | |
|---------------|-----------|----------|------|---------------|
| SCE1572_9037 | MXAN_5153 | 3.00E-76 | 273 | Che3 |
| SCE1572_10380 | MXAN_5153 | 1.00E-76 | 275 | Che3 |
| SCE1572_11034 | MXAN_5153 | 2.00E-79 | 284 | Che3 |
| SCE1572_9916 | MXAN_5153 | 2.00E-80 | 287 | Che3 |
| SCE1572_7624 | MXAN_5153 | 1.00E-80 | 288 | Che3 |
| SCE1572_6927 | MXAN_5153 | 4.00E-82 | 293 | Che3 |
| SCE1572_2291 | MXAN_5153 | 3.00E-84 | 300 | Che3 |
| SCE1572_3905 | MXAN_5153 | 2.00E-85 | 304 | Che3 |
| SCE1572_2333 | MXAN_5153 | 1.00E-90 | 321 | Che3 |
| SCE1572_4820 | MXAN_5153 | 4.00E-96 | 339 | Che3 |
| SCE1572_3384 | MXAN_5153 | 2.00E-96 | 340 | Che3 |
| SCE1572_11450 | MXAN_5153 | 1.00E-96 | 341 | Che3 |
| SCE1572_6665 | MXAN_6029 | 1.00E-13 | 65.1 | Che5 |
| SCE1572_4205 | MXAN_6031 | 5.00E-16 | 72.8 | Che5 |
| SCE1572_10949 | MXAN_6032 | 2.00E-11 | 55.8 | Che5 |
| SCE1572_7680 | MXAN_6032 | 1.00E-11 | 57.8 | Che5 |
| SCE1572_6666 | MXAN_6032 | 4.00E-11 | 58.2 | Che5 |
| SCE1572_3219 | MXAN_6032 | 4.00E-12 | 58.9 | Che5 |
| SCE1572_5331 | MXAN_6032 | 1.00E-13 | 65.5 | Che5 |
| SCE1572_10791 | MXAN_6032 | 6.00E-15 | 69.7 | Che5 |
| SCE1572_1281 | MXAN_6032 | 4.00E-18 | 81.6 | Che5 |
| SCE1572_3493 | MXAN_6033 | 1.00E-11 | 60.1 | Che5 |
| SCE1572_1276 | MXAN_6692 | 4.00E-21 | 91.3 | Dif (Che2) |
| SCE1572_12 | MXAN_6693 | 5.00E-11 | 56.2 | Dif (Che2) |
| SCE1572_6549 | MXAN_6693 | 2.00E-13 | 63.5 | Dif (Che2) |
| SCE1572_910 | MXAN_6693 | 2.00E-15 | 73.9 | Dif (Che2) |
| SCE1572_9627 | MXAN_6693 | 5.00E-17 | 79 | Dif (Che2) |
| SCE1572_4575 | MXAN_6950 | 1.00E-26 | 108 | Che6 |
| SCE1572_2800 | MXAN_6950 | 6.00E-31 | 123 | Che6 |
| SCE1572_10164 | MXAN_6951 | 1.00E-11 | 56.6 | Che6 |
| SCE1572_9924 | MXAN_6951 | 8.00E-13 | 64.3 | Che6 |
| SCE1572_6860 | MXAN_6951 | 1.00E-13 | 67.4 | Che6 |
| SCE1572_1227 | MXAN_6951 | 1.00E-14 | 68.6 | Che6 |
| SCE1572_4574 | MXAN_6951 | 3.00E-32 | 128 | Che6 |
| SCE1572_3503 | MXAN_6959 | 2.00E-79 | 283 | Che6 |
| SCE1572_2799 | MXAN_6960 | 2.00E-19 | 84.7 | Che6 |
| SCE1572_3502 | MXAN_6960 | 5.00E-81 | 288 | Che6 |
| SCE1572_11255 | MXAN_6962 | 7.00E-25 | 103 | Che6 |
| SCE1572_3500 | MXAN_6962 | 3.00E-80 | 288 | Che6 |

| | | | | |
|--------------|-----------|----------|------|------|
| SCE1572_3499 | MXAN_6963 | 8.00E-36 | 137 | Che6 |
| SCE1572_3498 | MXAN_6964 | 3.00E- | 447 | Che6 |
| | | 128 | | |
| SCE1572_9923 | MXAN_6965 | 9.00E-11 | 57 | Che6 |
| SCE1572_4071 | MXAN_6965 | 4.00E-12 | 58.5 | Che6 |
| SCE1572_6853 | MXAN_6965 | 2.00E-11 | 58.9 | Che6 |
| SCE1572_3987 | MXAN_6965 | 5.00E-14 | 65.1 | Che6 |
| SCE1572_7522 | MXAN_6965 | 1.00E-15 | 71.6 | Che6 |
| SCE1572_198 | MXAN_6965 | 4.00E-16 | 74.7 | Che6 |
| SCE1572_3497 | MXAN_6965 | 4.00E-46 | 171 | Che6 |

* Blastp analysis against experiment identified Che systems in *Myxococcus xanthus* DK1622. E-value cutoff 1e-5.

Supplementary Table S14. NRPS/PKS statistics in *Sorangium cellulosum* So0157-2.

| ID | Type | Function | Modification domain | Number of modules | TE domian | Construction |
|----|----------------|-------------|---------------------|--------------------------|-----------|-------------------------------|
| 1 | NRPS | Unknown | no | 12 | yes | linear |
| 2 | NRPS-PKShybrid | Epithilones | Glycosylation | 10 (1 NRPS module) | yes | linear |
| 3 | PKS | Unknown | no | 1 | no | Nonmodular PKS |
| 4 | NRPS-PKShybrid | Unknown | no | 6 | yes | linear |
| 5 | PKS | Unknown | no | 5 | yes | linear |
| 6 | NRPS | Unknown | no | 4 | yes | linear |
| 7 | NRPS-PKShybrid | Unknown | Methylation | 15 | yes | linear |
| 8 | NRPS | Unknown | no | 2 | yes | linear or iterative |
| 9 | PKS | Unknown | no | 2 | no | Type II PKS or nonmodular PKS |
| 10 | PKS | Unknown | Methylation | 12, absence of AT domain | yes | linear |
| 11 | NRPS | Unknown | no | 1 | no | Unknown |
| 12 | NRPS-PKShybrid | Unknown | Epimerization | 9 | yes | linear |
| 13 | NRPS | Unknown | Methylation | 3 | yes | linear or iterative |

| | | | | | | |
|----|----------------|---------|---------------|---|-----|---------------------|
| 14 | NRPS-PKShybrid | Unknown | Epimerization | 2 | no | Unknown |
| 15 | PKS | Unknown | no | 5 | yes | iterative or linear |
| 16 | NRPS-PKShybrid | Unknown | Epimerization | 2 | no | Unknown |
| 17 | NRPS-PKShybrid | Unknown | no | 3 | yes | iterative or linear |
| 18 | PKS | Unknown | no | 1 | no | Unknown |

Supplementary Table S15. BLAST analysis of the electron transfer chain sequences against the *Myxococcus xanthus* DK1622 database.

| Gene Symbol | exist or not in 0157-2 | E-value* | Hits |
|---|------------------------|----------|------------------------------|
| succinate dehydrogenase cytochrome b558 subunit | + | 6.00E-20 | SCE1572_10673 |
| NADH dehydrogenase I, N subunit | + | 8.00E-95 | 12 SCE1572_5698 SCE1572_9714 |
| NADH dehydrogenase I, M subunit | + | e-121 | 13 SCE1572_5699 SCE1572_9713 |
| NADH dehydrogenase I, L subunit | + | e-138 | 15 SCE1572_5699 SCE1572_9716 |
| NADH dehydrogenase I, K subunit | + | 8.00E-24 | 2 SCE1572_5700 SCE1572_10173 |
| NADH dehydrogenase I, J subunit | + | 4.00E-26 | 2 SCE1572_5701 SCE1572_10174 |
| NADH dehydrogenase I, F subunit | + | e-105 | SCE1572_5702 |
| NADH dehydrogenase I, E subunit | + | 1.00E-28 | SCE1572_5703 |
| putative NADH dehydrogenase | + | e-148 | 3 SCE1572_4082 |
| NADH dehydrogenase I, I subunit | + | 4.00E-43 | 3 SCE1572_800 |
| putative NADH dehydrogenase I, H subunit | + | 1.00E-73 | 2 SCE1572_799 SCE1572_9661 |
| putative NADH dehydrogenase I, G subunit | + | | SCE1572_798 |
| NADH dehydrogenase I, D subunit | + | e-127 | 2 SCE1572_797 SCE1572_11340 |
| NADH dehydrogenase I, C subunit | + | 6.00E-30 | 2 SCE1572_796 SCE1572_11339 |
| sulfatase domain protein | + | 5.00E-17 | 7 SCE1572_4838 |
| NADH dehydrogenase I, B subunit | + | 4.00E-60 | 2 SCE1572_795 SCE1572_11337 |
| putative NADH dehydrogenase I, A subunit | + | 5.00E-29 | 2 SCE1572_794 SCE1572_11335 |
| succinate dehydrogenase, flavoprotein subunit | + | 0 | 3 SCE1572_10674 |
| succinate dehydrogenase, iron-sulfur protein | + | 2.00E-82 | 2 SCE1572_10675 SCE1572_8615 |
| putative cytochrome c oxidase, subunit IV | + | 2.00E-11 | 2 SCE1572_6126 SCE1572_9693 |
| cytochrome c oxidase, subunit III | + | 1.00E-51 | 2 SCE1572_6125 SCE1572_9692 |
| cytochrome c oxidase, subunit I | + | 0 | 2 SCE1572_6124 SCE1572_9691 |
| cytochrome c oxidase, subunit II | + | 4.00E-93 | 2 SCE1572_6123 SCE1572_9690 |
| cytochrome c oxidase accessory protein FixG | - | | |
| cytochrome c oxidase, cbb3-type, subunit III | - | | |
| cytochrome c oxidase, cbb3-type, CcoQ subunit | - | | |
| cytochrome c oxidase, cbb3-type, subunit I/II | + | 8.00E-09 | 3 SCE1572_1868 |

| | | | | | |
|---|---|----------|---|--------------|--------------|
| putative cytochrome oxidase maturation protein, cbb3-type | - | | | | |
| cytochrome c oxidase, subunit II | + | 2.00E-83 | 2 | SCE1572_6123 | SCE1572_9690 |
| cytochrome c oxidase, subunit I | + | 0 | 2 | SCE1572_6124 | SCE1572_9691 |
| cytochrome c oxidase, subunit III | + | 2.00E-52 | 3 | SCE1572_6125 | SCE1572_9692 |
| putative cytochrome c oxidase, subunit IV | + | 7.00E-12 | 3 | SCE1572_6126 | SCE1572_9693 |
| cytochrome d ubiquinol oxidase, subunit II | + | e-111 | | SCE1572_3243 | |
| cytochrome d ubiquinol oxidase, subunit I | + | e-161 | | SCE1572_3240 | |

*Cutoff of Blast is 0.0001.

Additional Dataset 1 Supplementary table S4 (separate file)

Transcripts detected under different pH conditions.

Additional Dataset 2 Supplementary table S7 (separate file)

Homologous genes in So0157-2 and So ce56.

Additional Dataset 3 Supplementary table S8 (separate file)

A comparison of KEGG categories for So0157-2 and So ce56.

Additional Dataset 4 Supplementary table S9 (separate file)

A comparison of sequence similarity for So0157-2 and So ce56.

Additional Dataset 5 Supplementary table S11 (separate file)

All annotated polysaccharide-degrading enzymes and related CBM motifs in So0157-2.

TableS4 Transcripts detected under different pH conditions (FPKM)

| Locus tag | pH 7.0 | pH 10.0 |
|---------------|--------|---------|
| SCE1572_5566 | 71.77 | 105.81 |
| SCE1572_4403 | 38.14 | 132.09 |
| SCE1572_3237 | 0 | 0 |
| SCE1572_7422 | 9.94 | 0 |
| SCE1572_6423 | 81.04 | 28.07 |
| SCE1572_5465 | 26.48 | 9.02 |
| SCE1572_5888 | 23.63 | 336.49 |
| SCE1572_1430 | 30.11 | 7.76 |
| SCE1572_9058 | 43.32 | 17.38 |
| SCE1572_8947 | 36.41 | 54.77 |
| SCE1572_1415 | 12.9 | 3.11 |
| SCE1572_9953 | 71.59 | 42.4 |
| SCE1572_8357 | 29.97 | 4.24 |
| SCE1572_5736 | 79.25 | 843.19 |
| SCE1572_963 | 269.73 | 219.45 |
| SCE1572_9431 | 35.04 | 34.06 |
| SCE1572_6979 | 24.38 | 11 |
| SCE1572_5559 | 0 | 0 |
| SCE1572_1203 | 104.74 | 41.78 |
| SCE1572_926 | 57.15 | 29.56 |
| SCE1572_6927 | 39.78 | 63.33 |
| SCE1572_4079 | 45.01 | 0 |
| SCE1572_1922 | 37.01 | 17.24 |
| SCE1572_10118 | 78.33 | 331.47 |
| SCE1572_8912 | 22.01 | 0 |
| SCE1572_7208 | 19.85 | 5.79 |
| SCE1572_6891 | 17.94 | 11.14 |
| SCE1572_10120 | 119.57 | 514.25 |
| SCE1572_8105 | 0 | 0 |
| SCE1572_5207 | 54.29 | 184.85 |
| SCE1572_4631 | 36.49 | 16.55 |
| SCE1572_211 | 42.7 | 19.92 |
| SCE1572_9167 | 79.6 | 4.56 |
| SCE1572_3914 | 75.5 | 22.34 |
| SCE1572_7224 | 84.4 | 141.1 |
| SCE1572_8249 | 32.33 | 48.34 |
| SCE1572_8904 | 10.14 | 0.77 |
| SCE1572_5794 | 118.68 | 247.38 |
| SCE1572_3433 | 17.2 | 117.65 |
| SCE1572_4684 | 100.06 | 99.12 |
| SCE1572_9858 | 4.65 | 0 |
| SCE1572_9695 | 0 | 0 |
| SCE1572_1899 | 29 | 9.52 |
| SCE1572_1005 | 80.17 | 22.87 |
| SCE1572_7497 | 0 | 0 |
| SCE1572_5550 | 27.01 | 7.36 |

| | | |
|---------------|--------|---------|
| SCE1572_10517 | 42.01 | 20.52 |
| SCE1572_5396 | 41.45 | 20.5 |
| SCE1572_11501 | 12.43 | 0 |
| SCE1572_3334 | 0 | 0 |
| SCE1572_10265 | 39.08 | 11.29 |
| SCE1572_11111 | 89.02 | 52.73 |
| SCE1572_6453 | 0 | 0 |
| SCE1572_816 | 84.42 | 27.99 |
| SCE1572_2624 | 73.08 | 29.22 |
| SCE1572_6657 | 45.53 | 106.94 |
| SCE1572_1590 | 32 | 30.03 |
| SCE1572_4855 | 38.4 | 9.48 |
| SCE1572_8348 | 109.01 | 92.49 |
| SCE1572_4967 | 22.74 | 188.85 |
| SCE1572_7617 | 140.23 | 738.5 |
| SCE1572_8843 | 53.38 | 31.44 |
| SCE1572_2650 | 18.43 | 12.67 |
| SCE1572_1513 | 44.99 | 4.45 |
| SCE1572_10034 | 54.06 | 37.85 |
| SCE1572_9206 | 78.58 | 54.16 |
| SCE1572_1573 | 33.65 | 20.93 |
| SCE1572_9449 | 65.11 | 39.45 |
| SCE1572_3515 | 12.87 | 47.05 |
| SCE1572_7608 | 3.45 | 0 |
| SCE1572_6365 | 39.46 | 439.67 |
| SCE1572_7454 | 41.35 | 77.75 |
| SCE1572_3975 | 14.44 | 17.38 |
| SCE1572_3071 | 74.22 | 43.87 |
| SCE1572_3042 | 16.92 | 3.92 |
| SCE1572_5691 | 18.81 | 7.7 |
| SCE1572_1404 | 86.89 | 15.87 |
| SCE1572_49 | 43.2 | 7.85 |
| SCE1572_8002 | 67.23 | 15.37 |
| SCE1572_2278 | 42.7 | 283 |
| SCE1572_4137 | 0 | 0 |
| SCE1572_1345 | 63.88 | 465.15 |
| SCE1572_8495 | 19.53 | 10.07 |
| SCE1572_5018 | 89.68 | 125.86 |
| SCE1572_830 | 17.14 | 19.04 |
| SCE1572_187 | 45.85 | 2032.88 |
| SCE1572_6610 | 12.57 | 14.24 |
| SCE1572_4114 | 32.99 | 47.3 |
| SCE1572_306 | 19.03 | 9.6 |
| SCE1572_7613 | 35.93 | 397.78 |
| SCE1572_1606 | 61.55 | 17.96 |
| SCE1572_10395 | 22.97 | 3.69 |
| SCE1572_9894 | 8.42 | 0 |
| SCE1572_9491 | 0 | 0 |

| | | |
|---------------|--------|---------|
| SCE1572_11230 | 157.52 | 170.44 |
| SCE1572_8955 | 2.71 | 0 |
| SCE1572_6436 | 47.38 | 21.29 |
| SCE1572_5448 | 50.73 | 20.81 |
| SCE1572_3105 | 47 | 68.9 |
| SCE1572_1366 | 64.08 | 175.7 |
| SCE1572_8601 | 47.77 | 149.97 |
| SCE1572_4069 | 0 | 0 |
| SCE1572_5880 | 0 | 0 |
| SCE1572_8037 | 0 | 0 |
| SCE1572_6726 | 23.23 | 23.29 |
| SCE1572_3543 | 0 | 0 |
| SCE1572_7367 | 124.16 | 3591.04 |
| SCE1572_248 | 95.24 | 16.45 |
| SCE1572_10623 | 20.92 | 24.32 |
| SCE1572_9768 | 22.51 | 135.47 |
| SCE1572_10652 | 15.57 | 87.97 |
| SCE1572_7802 | 33.59 | 221.2 |
| SCE1572_5985 | 14.85 | 4.7 |
| SCE1572_9841 | 0 | 0 |
| SCE1572_9963 | 92.7 | 27.57 |
| SCE1572_7577 | 17.3 | 4.9 |
| SCE1572_10612 | 66.3 | 105.45 |
| SCE1572_7663 | 15.74 | 3.99 |
| SCE1572_11224 | 66.43 | 42.03 |
| SCE1572_9408 | 41.42 | 32.07 |
| SCE1572_4376 | 32.88 | 8.79 |
| SCE1572_9362 | 53.14 | 326.55 |
| SCE1572_5731 | 11.78 | 205.49 |
| SCE1572_10286 | 172.62 | 1300.13 |
| SCE1572_7845 | 129.01 | 389.1 |
| SCE1572_4842 | 19.59 | 147.61 |
| SCE1572_8798 | 77.18 | 17.13 |
| SCE1572_7521 | 54.58 | 29.19 |
| SCE1572_2463 | 82.27 | 22.93 |
| SCE1572_7211 | 41.03 | 33.49 |
| SCE1572_4203 | 61.18 | 299.62 |
| SCE1572_782 | 17.84 | 17.89 |
| SCE1572_5176 | 23.13 | 17.52 |
| SCE1572_1742 | 31.71 | 31.73 |
| SCE1572_11206 | 25.38 | 28.88 |
| SCE1572_9567 | 2.11 | 0 |
| SCE1572_2193 | 26.87 | 4.62 |
| SCE1572_3990 | 35.57 | 62.58 |
| SCE1572_2460 | 20.67 | 0 |
| SCE1572_5137 | 8.27 | 11.06 |
| SCE1572_4098 | 8.85 | 5.33 |
| SCE1572_282 | 11.52 | 4.62 |

| | | |
|---------------|--------|--------|
| SCE1572_88 | 56.13 | 117.43 |
| SCE1572_8438 | 18.01 | 12.58 |
| SCE1572_6296 | 39.48 | 194.17 |
| SCE1572_1380 | 112.48 | 28.3 |
| SCE1572_2438 | 20.55 | 74.74 |
| SCE1572_2504 | 25.79 | 19.86 |
| SCE1572_6900 | 13.38 | 16.1 |
| SCE1572_2791 | 117.92 | 226.39 |
| SCE1572_80 | 79.94 | 213.65 |
| SCE1572_1472 | 63.67 | 47.4 |
| SCE1572_9104 | 52.91 | 23.91 |
| SCE1572_1624 | 45.84 | 26.87 |
| SCE1572_3362 | 41.83 | 52.43 |
| SCE1572_2168 | 2.37 | 0 |
| SCE1572_7856 | 34.27 | 13.68 |
| SCE1572_4773 | 21.73 | 18.91 |
| SCE1572_754 | 42.67 | 56.79 |
| SCE1572_6951 | 26.93 | 13.12 |
| SCE1572_10444 | 48.49 | 101.42 |
| SCE1572_9667 | 49.17 | 280.38 |
| SCE1572_10984 | 82.35 | 570.29 |
| SCE1572_8110 | 5.14 | 0 |
| SCE1572_5079 | 33.47 | 80.57 |
| SCE1572_8041 | 34.11 | 9.12 |
| SCE1572_2242 | 36.16 | 30.95 |
| SCE1572_1372 | 62.57 | 628.48 |
| SCE1572_8433 | 6.83 | 6.58 |
| SCE1572_5813 | 35.56 | 35.4 |
| SCE1572_700 | 2.92 | 0 |
| SCE1572_2010 | 59.77 | 15.79 |
| SCE1572_11149 | 7.64 | 15.33 |
| SCE1572_10976 | 250.29 | 0 |
| SCE1572_7217 | 40.64 | 50.96 |
| SCE1572_5719 | 26.64 | 11.51 |
| SCE1572_11292 | 86.24 | 628.48 |
| SCE1572_11053 | 73.26 | 228.87 |
| SCE1572_6650 | 27.16 | 27.23 |
| SCE1572_8277 | 40.65 | 29.5 |
| SCE1572_9473 | 56.5 | 125.8 |
| SCE1572_3550 | 24.25 | 15.36 |
| SCE1572_5232 | 30.32 | 70.9 |
| SCE1572_10529 | 19.96 | 29.64 |
| SCE1572_9606 | 2.14 | 0 |
| SCE1572_7979 | 101.62 | 30.08 |
| SCE1572_8021 | 50.54 | 20.7 |
| SCE1572_7030 | 32.49 | 14.48 |
| SCE1572_4972 | 36.82 | 195.49 |
| SCE1572_7997 | 43.36 | 4.15 |

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| SCE1572_3219 | 116.05 | 1470.95 |
| SCE1572_180 | 0 | 0 |
| SCE1572_1340 | 28.54 | 30.05 |
| SCE1572_9934 | 0 | 0 |
| SCE1572_7895 | 2.92 | 0 |
| SCE1572_7063 | 28.91 | 12.24 |
| SCE1572_1569 | 31.07 | 58.03 |
| SCE1572_8410 | 97.8 | 696.42 |
| SCE1572_1140 | 11.72 | 16.38 |
| SCE1572_11212 | 20.49 | 13.66 |
| SCE1572_5996 | 89.56 | 64.5 |
| SCE1572_4989 | 26.47 | 52.13 |
| SCE1572_8108 | 53.61 | 13.88 |
| SCE1572_2995 | 29.03 | 8.59 |
| SCE1572_9626 | 36.16 | 10.38 |
| SCE1572_525 | 70.68 | 101.52 |
| SCE1572_8183 | 42.61 | 5.54 |
| SCE1572_4091 | 39.43 | 18.08 |
| SCE1572_5859 | 25.4 | 15.28 |
| SCE1572_8465 | 6.79 | 0 |
| SCE1572_1858 | 37.1 | 7.76 |
| SCE1572_745 | 99.37 | 421.31 |
| SCE1572_739 | 15.46 | 6.8 |
| SCE1572_3507 | 27.49 | 16.04 |
| SCE1572_6096 | 41.19 | 22.1 |
| SCE1572_4152 | 23.33 | 1306.86 |
| SCE1572_1557 | 7.46 | 0 |
| SCE1572_1102 | 30.1 | 17.13 |
| SCE1572_8406 | 37.9 | 28.88 |
| SCE1572_10274 | 48.95 | 71.94 |
| SCE1572_5523 | 29.46 | 14.6 |
| SCE1572_1752 | 13.64 | 5.05 |
| SCE1572_7397 | 15.75 | 9.2 |
| SCE1572_6604 | 62.25 | 148.34 |
| SCE1572_520 | 43.45 | 20.03 |
| SCE1572_3861 | 108.86 | 369 |
| SCE1572_5452 | 36.88 | 10.65 |
| SCE1572_1479 | 45.06 | 30.41 |
| SCE1572_4183 | 19.53 | 13.82 |
| SCE1572_4277 | 56.44 | 26.77 |
| SCE1572_4055 | 20.71 | 64.08 |
| SCE1572_7277 | 0 | 0 |
| SCE1572_273 | 124.1 | 360.6 |
| SCE1572_4726 | 21.74 | 11.66 |
| SCE1572_4367 | 61.14 | 30.31 |
| SCE1572_10239 | 71.88 | 17.9 |
| SCE1572_5862 | 40.9 | 13.75 |
| SCE1572_5269 | 57.96 | 271.71 |

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| SCE1572_5003 | 35.13 | 211.39 |
| SCE1572_8270 | 29.15 | 19.03 |
| SCE1572_5742 | 84.48 | 67.08 |
| SCE1572_5688 | 43.32 | 21.24 |
| SCE1572_6380 | 63.75 | 45.62 |
| SCE1572_4251 | 11.58 | 12.67 |
| SCE1572_7555 | 9.69 | 2.74 |
| SCE1572_4451 | 0 | 0 |
| SCE1572_3700 | 39.48 | 35.73 |
| SCE1572_11134 | 50.1 | 25.39 |
| SCE1572_5330 | 32.53 | 11.36 |
| SCE1572_11 | 26.06 | 50.18 |
| SCE1572_6894 | 25.03 | 18.63 |
| SCE1572_2819 | 41.66 | 19.24 |
| SCE1572_10713 | 22.83 | 19.78 |
| SCE1572_10510 | 20.24 | 13.81 |
| SCE1572_1136 | 0 | 0 |
| SCE1572_1154 | 12.82 | 0 |
| SCE1572_9848 | 23.75 | 4.4 |
| SCE1572_588 | 7.28 | 7.67 |
| SCE1572_2092 | 54.64 | 9.26 |
| SCE1572_9341 | 71.44 | 694.4 |
| SCE1572_6101 | 63.96 | 22.81 |
| SCE1572_4552 | 40.93 | 14.07 |
| SCE1572_2039 | 14.88 | 69.4 |
| SCE1572_1691 | 133.09 | 318.29 |
| SCE1572_9088 | 11.09 | 0 |
| SCE1572_10912 | 32.65 | 79.69 |
| SCE1572_3654 | 46 | 250.12 |
| SCE1572_839 | 10.77 | 34.55 |
| SCE1572_3022 | 35.28 | 9.18 |
| SCE1572_5237 | 106.32 | 174.67 |
| SCE1572_1358 | 219.3 | 1779.1 |
| SCE1572_6327 | 13.04 | 3.92 |
| SCE1572_10525 | 28.18 | 29.61 |
| SCE1572_3380 | 17.28 | 20.8 |
| SCE1572_10676 | 83.55 | 69.26 |
| SCE1572_4713 | 24.9 | 12.93 |
| SCE1572_3785 | 183.78 | 453.39 |
| SCE1572_5601 | 52.44 | 20.85 |
| SCE1572_973 | 46.65 | 104.8 |
| SCE1572_8005 | 24.05 | 33.92 |
| SCE1572_10203 | 33.13 | 104.59 |
| SCE1572_6265 | 67.61 | 118.35 |
| SCE1572_8051 | 48.73 | 16.29 |
| SCE1572_6388 | 18.51 | 104.71 |
| SCE1572_1686 | 18.54 | 9.19 |
| SCE1572_5026 | 28.43 | 22.81 |

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| SCE1572_5838 | 17.47 | 6.78 |
| SCE1572_10160 | 63.73 | 102.42 |
| SCE1572_405 | 36.17 | 39.64 |
| SCE1572_6510 | 0 | 0 |
| SCE1572_4060 | 16.62 | 79.98 |
| SCE1572_1251 | 44.4 | 20.39 |
| SCE1572_8928 | 0 | 0 |
| SCE1572_10836 | 37.16 | 19.08 |
| SCE1572_8643 | 41.94 | 48.14 |
| SCE1572_7375 | 12 | 7.88 |
| SCE1572_335 | 47.29 | 23.46 |
| SCE1572_5510 | 32.6 | 34.87 |
| SCE1572_4130 | 107.97 | 175.55 |
| SCE1572_4475 | 1210.73 | 2314.91 |
| SCE1572_9498 | 291.66 | 1885.9 |
| SCE1572_2046 | 13.94 | 0 |
| SCE1572_11302 | 26.91 | 36.91 |
| SCE1572_5889 | 34.46 | 71.88 |
| SCE1572_8859 | 24.96 | 17.93 |
| SCE1572_5112 | 19.4 | 36.32 |
| SCE1572_4954 | 21.66 | 0 |
| SCE1572_6232 | 72.26 | 19.51 |
| SCE1572_295 | 8.15 | 262.9 |
| SCE1572_1892 | 20.75 | 21.17 |
| SCE1572_5495 | 25.1 | 8.99 |
| SCE1572_5462 | 30.64 | 13.41 |
| SCE1572_9142 | 15.81 | 6.06 |
| SCE1572_8918 | 28.79 | 424.97 |
| SCE1572_3926 | 58.34 | 284.55 |
| SCE1572_364 | 10.63 | 0.85 |
| SCE1572_3150 | 18.77 | 66.43 |
| SCE1572_995 | 51.58 | 9.41 |
| SCE1572_8751 | 38.33 | 11.99 |
| SCE1572_1718 | 30.32 | 46.25 |
| SCE1572_4925 | 37.45 | 76.99 |
| SCE1572_4641 | 37.84 | 19.11 |
| SCE1572_11128 | 0 | 0 |
| SCE1572_1355 | 14.9 | 20.62 |
| SCE1572_6588 | 41.73 | 41.22 |
| SCE1572_6193 | 0 | 0 |
| SCE1572_4588 | 45.69 | 391.58 |
| SCE1572_2258 | 20.9 | 9.29 |
| SCE1572_2030 | 58.45 | 13.19 |
| SCE1572_6967 | 55.26 | 34.91 |
| SCE1572_9748 | 19.58 | 14.14 |
| SCE1572_6884 | 46.39 | 18.98 |
| SCE1572_3659 | 21.16 | 25.46 |
| SCE1572_1935 | 0 | 0 |

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| SCE1572_5064 | 56.46 | 89.73 |
| SCE1572_1118 | 30.44 | 15.2 |
| SCE1572_11174 | 55.81 | 34.93 |
| SCE1572_8966 | 98.21 | 138.88 |
| SCE1572_2390 | 44.31 | 113.11 |
| SCE1572_4929 | 34.02 | 71.84 |
| SCE1572_10200 | 22.62 | 50.4 |
| SCE1572_6628 | 32.34 | 83.88 |
| SCE1572_4486 | 43.32 | 345.37 |
| SCE1572_8117 | 35.58 | 11.17 |
| SCE1572_8212 | 5.53 | 10.65 |
| SCE1572_8911 | 14.46 | 12.35 |
| SCE1572_3389 | 22.59 | 12.88 |
| SCE1572_886 | 1003.33 | 1367.59 |
| SCE1572_9295 | 41.49 | 84.75 |
| SCE1572_8415 | 33.96 | 17.92 |
| SCE1572_3294 | 10.87 | 4.13 |
| SCE1572_146 | 44.38 | 19.28 |
| SCE1572_4930 | 41.35 | 48.49 |
| SCE1572_7638 | 18.36 | 22.61 |
| SCE1572_7202 | 26.63 | 2.62 |
| SCE1572_3557 | 43.32 | 15.99 |
| SCE1572_8921 | 1.26 | 0 |
| SCE1572_8562 | 134.36 | 290.75 |
| SCE1572_6723 | 26.73 | 91.54 |
| SCE1572_5457 | 39.21 | 12.53 |
| SCE1572_4784 | 11.03 | 0 |
| SCE1572_4677 | 6.93 | 12.51 |
| SCE1572_1188 | 52.45 | 13.84 |
| SCE1572_5655 | 39 | 26.44 |
| SCE1572_7814 | 673.08 | 5319.02 |
| SCE1572_11271 | 28.66 | 90.09 |
| SCE1572_1595 | 40.99 | 45.42 |
| SCE1572_474 | 216.19 | 1006.92 |
| SCE1572_5185 | 59.12 | 2406.04 |
| SCE1572_3746 | 21.25 | 10.23 |
| SCE1572_4708 | 0 | 0 |
| SCE1572_7138 | 47.12 | 85.07 |
| SCE1572_5293 | 24.44 | 41.44 |
| SCE1572_4193 | 532.45 | 2482.71 |
| SCE1572_3754 | 22.8 | 2.74 |
| SCE1572_3251 | 10.83 | 0 |
| SCE1572_11044 | 28.64 | 37.84 |
| SCE1572_6377 | 23.94 | 15.37 |
| SCE1572_7353 | 61.91 | 16.61 |
| SCE1572_11193 | 30.95 | 16.73 |
| SCE1572_11325 | 90.2 | 92.08 |
| SCE1572_6854 | 64.3 | 3.82 |

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| SCE1572_2692 | 25.57 | 68.15 |
| SCE1572_6470 | 31.73 | 12.73 |
| SCE1572_2699 | 2.17 | 0 |
| SCE1572_9192 | 41.56 | 24.14 |
| SCE1572_9930 | 18.84 | 35.02 |
| SCE1572_4230 | 10.93 | 13.15 |
| SCE1572_7287 | 26.68 | 40.87 |
| SCE1572_8364 | 57.94 | 31.77 |
| SCE1572_2466 | 17.96 | 6.05 |
| SCE1572_5680 | 127.03 | 254.29 |
| SCE1572_8608 | 38.99 | 146.79 |
| SCE1572_6164 | 38.73 | 25.78 |
| SCE1572_2371 | 57.49 | 91.23 |
| SCE1572_6829 | 4.53 | 0 |
| SCE1572_6398 | 23.82 | 89.3 |
| SCE1572_7344 | 0 | 0 |
| SCE1572_2395 | 21.74 | 79.87 |
| SCE1572_2310 | 54.12 | 197.07 |
| SCE1572_1423 | 121.95 | 79.94 |
| SCE1572_6673 | 23.42 | 19.28 |
| SCE1572_6462 | 57.12 | 58.11 |
| SCE1572_11167 | 53.91 | 198.68 |
| SCE1572_11454 | 55.05 | 109.88 |
| SCE1572_8786 | 15.88 | 157.62 |
| SCE1572_6986 | 0 | 0 |
| SCE1572_3877 | 0 | 0 |
| SCE1572_6944 | 3.26 | 0 |
| SCE1572_7420 | 74.59 | 52.69 |
| SCE1572_9276 | 82.81 | 72.21 |
| SCE1572_2560 | 10.72 | 14.74 |
| SCE1572_7449 | 195.08 | 765.83 |
| SCE1572_10805 | 65.96 | 20.95 |
| SCE1572_9214 | 35.88 | 20.3 |
| SCE1572_76 | 15.27 | 0 |
| SCE1572_10657 | 55.29 | 49.9 |
| SCE1572_9705 | 48.48 | 19.86 |
| SCE1572_1218 | 84.78 | 26.99 |
| SCE1572_6972 | 44.82 | 18.25 |
| SCE1572_2301 | 8.99 | 58.76 |
| SCE1572_10659 | 22.25 | 26.49 |
| SCE1572_5475 | 26.4 | 90.78 |
| SCE1572_3148 | 26.48 | 8.73 |
| SCE1572_7037 | 23.19 | 51.52 |
| SCE1572_2635 | 37.56 | 83.79 |
| SCE1572_9712 | 0 | 0 |
| SCE1572_327 | 3.23 | 0 |
| SCE1572_10834 | 44.58 | 10.65 |
| SCE1572_1000 | 76.56 | 146.11 |

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| SCE1572_8502 | 40.87 | 14.88 |
| SCE1572_2544 | 35.87 | 15.24 |
| SCE1572_7769 | 9.03 | 8.15 |
| SCE1572_4048 | 29 | 72 |
| SCE1572_10216 | 78.25 | 35.32 |
| SCE1572_9534 | 22.24 | 16.53 |
| SCE1572_2376 | 40.25 | 67.54 |
| SCE1572_11510 | 49.59 | 25.58 |
| SCE1572_847 | 287.59 | 1460.46 |
| SCE1572_6631 | 2.08 | 0 |
| SCE1572_8509 | 95.8 | 47.64 |
| SCE1572_7626 | 50.54 | 20.56 |
| SCE1572_4490 | 28.64 | 14.26 |
| SCE1572_581 | 35.67 | 37.33 |
| SCE1572_485 | 25.87 | 10.38 |
| SCE1572_1261 | 41.57 | 57.68 |
| SCE1572_4297 | 0 | 0 |
| SCE1572_6486 | 6.51 | 0 |
| SCE1572_2598 | 0 | 0 |
| SCE1572_1028 | 2.41 | 0 |
| SCE1572_122 | 23.11 | 7.79 |
| SCE1572_5213 | 28.05 | 14.72 |
| SCE1572_387 | 40.72 | 104.05 |
| SCE1572_3452 | 53.09 | 16.53 |
| SCE1572_4140 | 19.39 | 45.62 |
| SCE1572_5841 | 39.82 | 16.96 |
| SCE1572_132 | 174 | 312.9 |
| SCE1572_10225 | 8.66 | 0 |
| SCE1572_6014 | 15.87 | 665.29 |
| SCE1572_6912 | 42.45 | 8.59 |
| SCE1572_5620 | 69.23 | 19.97 |
| SCE1572_11342 | 21.6 | 26.96 |
| SCE1572_10406 | 50.35 | 62.3 |
| SCE1572_6694 | 56.98 | 24.41 |
| SCE1572_7840 | 25.64 | 30.86 |
| SCE1572_10968 | 31.31 | 26.59 |
| SCE1572_10605 | 0 | 0 |
| SCE1572_9668 | 67.94 | 405.8 |
| SCE1572_9334 | 26.98 | 87.12 |
| SCE1572_9444 | 29.32 | 22.18 |
| SCE1572_422 | 21.09 | 58.12 |
| SCE1572_576 | 45.21 | 189.29 |
| SCE1572_8155 | 30.32 | 5.92 |
| SCE1572_3533 | 65.51 | 20.27 |
| SCE1572_2657 | 204.37 | 66.99 |
| SCE1572_7433 | 40.92 | 82.35 |
| SCE1572_5916 | 194.93 | 144.55 |
| SCE1572_6281 | 58.22 | 126.79 |

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| SCE1572_11368 | 7.22 | 0 |
| SCE1572_9369 | 0 | 0 |
| SCE1572_7400 | 58.94 | 57.39 |
| SCE1572_7108 | 0 | 0 |
| SCE1572_5275 | 3.61 | 4.34 |
| SCE1572_10825 | 159.45 | 219.3 |
| SCE1572_6075 | 63.01 | 59.55 |
| SCE1572_2478 | 58.89 | 64.52 |
| SCE1572_6270 | 19.56 | 19.13 |
| SCE1572_3199 | 75.81 | 478.68 |
| SCE1572_9190 | 45.78 | 24.33 |
| SCE1572_6401 | 0 | 0 |
| SCE1572_4153 | 0 | 0 |
| SCE1572_4285 | 32.58 | 31.06 |
| SCE1572_3442 | 36.62 | 36.49 |
| SCE1572_4159 | 13.12 | 21.47 |
| SCE1572_9908 | 33.8 | 33.26 |
| SCE1572_7128 | 59.75 | 36.44 |
| SCE1572_10661 | 38.52 | 58.15 |
| SCE1572_4343 | 103.37 | 35.73 |
| SCE1572_3613 | 54.65 | 135.79 |
| SCE1572_2215 | 20.02 | 34.8 |
| SCE1572_2433 | 15.62 | 18.11 |
| SCE1572_5403 | 45.27 | 17.98 |
| SCE1572_1865 | 23.26 | 9.33 |
| SCE1572_9881 | 52.93 | 53.98 |
| SCE1572_941 | 26.27 | 3.33 |
| SCE1572_6312 | 20.3 | 280.64 |
| SCE1572_7884 | 48.56 | 28.51 |
| SCE1572_11309 | 14.38 | 2.16 |
| SCE1572_3284 | 12.58 | 1.68 |
| SCE1572_4383 | 55.59 | 22.71 |
| SCE1572_9118 | 89.79 | 56.94 |
| SCE1572_5972 | 34.53 | 0 |
| SCE1572_5898 | 10.11 | 6.95 |
| SCE1572_5586 | 20.07 | 0 |
| SCE1572_5391 | 130.47 | 112.95 |
| SCE1572_4579 | 3.3 | 0 |
| SCE1572_7151 | 63.58 | 65.59 |
| SCE1572_1458 | 0 | 0 |
| SCE1572_3670 | 23.41 | 8.39 |
| SCE1572_11379 | 19.24 | 44.46 |
| SCE1572_6415 | 28.25 | 10 |
| SCE1572_4236 | 42.96 | 166.24 |
| SCE1572_10117 | 13.93 | 21.52 |
| SCE1572_10591 | 46.88 | 31.29 |
| SCE1572_9516 | 24.12 | 111.96 |
| SCE1572_98 | 41.51 | 26.07 |

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| SCE1572_1098 | 27.92 | 17.3 |
| SCE1572_3177 | 33.17 | 142.26 |
| SCE1572_1123 | 28.22 | 8.69 |
| SCE1572_10692 | 14.97 | 64.21 |
| SCE1572_10577 | 33.93 | 25.52 |
| SCE1572_4083 | 18.77 | 27.8 |
| SCE1572_2595 | 44.17 | 32.64 |
| SCE1572_7586 | 30.1 | 598.37 |
| SCE1572_2893 | 18.73 | 7.34 |
| SCE1572_6222 | 27.99 | 11.23 |
| SCE1572_4600 | 23.65 | 39.41 |
| SCE1572_643 | 129.82 | 307.79 |
| SCE1572_2336 | 18.29 | 23.21 |
| SCE1572_8892 | 99.58 | 119.06 |
| SCE1572_7056 | 14.02 | 14.77 |
| SCE1572_3741 | 94.98 | 73.4 |
| SCE1572_9871 | 11.72 | 5.81 |
| SCE1572_5596 | 77.64 | 76.69 |
| SCE1572_5514 | 128.49 | 24.74 |
| SCE1572_5978 | 30.99 | 19.49 |
| SCE1572_2864 | 0 | 0 |
| SCE1572_2177 | 31.95 | 4.71 |
| SCE1572_4654 | 27.71 | 42.09 |
| SCE1572_9307 | 46.48 | 141.17 |
| SCE1572_6432 | 20.43 | 6.47 |
| SCE1572_7483 | 73.13 | 49.76 |
| SCE1572_4469 | 63.22 | 25.98 |
| SCE1572_8401 | 67.06 | 46.01 |
| SCE1572_4848 | 12.69 | 9.08 |
| SCE1572_6871 | 23.19 | 20.42 |
| SCE1572_1739 | 33.09 | 5.79 |
| SCE1572_2453 | 44.13 | 39.37 |
| SCE1572_9263 | 17.66 | 35.43 |
| SCE1572_4939 | 54.96 | 94.59 |
| SCE1572_8763 | 0 | 0 |
| SCE1572_3449 | 38.71 | 13.2 |
| SCE1572_10729 | 22.01 | 38.26 |
| SCE1572_2535 | 24.07 | 26.07 |
| SCE1572_9795 | 47 | 3.65 |
| SCE1572_5717 | 134.38 | 242.87 |
| SCE1572_10197 | 0 | 0 |
| SCE1572_1190 | 65.38 | 79.59 |
| SCE1572_10580 | 24.92 | 27.49 |
| SCE1572_10640 | 136.2 | 840.61 |
| SCE1572_4935 | 69.98 | 314.39 |
| SCE1572_10865 | 173.05 | 437.04 |
| SCE1572_5438 | 0 | 0 |
| SCE1572_5141 | 34.79 | 22.12 |

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| SCE1572_8764 | 0.04 | 0.12 |
| SCE1572_7461 | 381.31 | 1249.12 |
| SCE1572_9651 | 45.44 | 14.31 |
| SCE1572_289 | 124.94 | 20.32 |
| SCE1572_4033 | 0 | 0 |
| SCE1572_2921 | 92.95 | 22.97 |
| SCE1572_9552 | 15.67 | 7.14 |
| SCE1572_9434 | 174.82 | 677.9 |
| SCE1572_2977 | 45.05 | 15.5 |
| SCE1572_10464 | 14.02 | 53.74 |
| SCE1572_7671 | 124.92 | 7.71 |
| SCE1572_10650 | 1383.5 | 2642.43 |
| SCE1572_6239 | 0 | 0 |
| SCE1572_9900 | 126.25 | 428.14 |
| SCE1572_9241 | 0 | 0 |
| SCE1572_8166 | 8.12 | 0 |
| SCE1572_3264 | 24.35 | 217 |
| SCE1572_10436 | 43.8 | 63.52 |
| SCE1572_213 | 60.56 | 24.83 |
| SCE1572_4017 | 17.84 | 7.16 |
| SCE1572_5956 | 51.49 | 34.43 |
| SCE1572_10495 | 19.87 | 45.62 |
| SCE1572_8129 | 0 | 0 |
| SCE1572_8633 | 43.26 | 54.74 |
| SCE1572_5723 | 3.47 | 0 |
| SCE1572_6662 | 51.35 | 47.22 |
| SCE1572_1224 | 29.24 | 30.27 |
| SCE1572_9736 | 71.71 | 13.15 |
| SCE1572_7762 | 38.07 | 138.25 |
| SCE1572_8826 | 63.13 | 15.78 |
| SCE1572_3128 | 37.32 | 67.37 |
| SCE1572_7086 | 43.2 | 14.27 |
| SCE1572_3479 | 25.27 | 0 |
| SCE1572_5942 | 27.3 | 9.57 |
| SCE1572_224 | 35.88 | 26.46 |
| SCE1572_4323 | 20.91 | 9.27 |
| SCE1572_1220 | 40.9 | 22.07 |
| SCE1572_1227 | 44.79 | 16.81 |
| SCE1572_8933 | 13.09 | 10.5 |
| SCE1572_2813 | 39.47 | 47.5 |
| SCE1572_7724 | 56.01 | 87.18 |
| SCE1572_11578 | 10.74 | 4.31 |
| SCE1572_10845 | 57.74 | 30.76 |
| SCE1572_1377 | 19.01 | 7.81 |
| SCE1572_11406 | 32.43 | 10.55 |
| SCE1572_5097 | 21.2 | 24.4 |
| SCE1572_4441 | 19.46 | 9.09 |
| SCE1572_2801 | 58.28 | 553.27 |

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| SCE1572_10786 | 22.11 | 13.94 |
| SCE1572_10241 | 17.59 | 9.15 |
| SCE1572_9923 | 32.19 | 105.48 |
| SCE1572_5 | 64.46 | 221.03 |
| SCE1572_25 | 45.68 | 54.97 |
| SCE1572_2025 | 37.18 | 83.34 |
| SCE1572_567 | 22.98 | 27.23 |
| SCE1572_3812 | 9.3 | 33.58 |
| SCE1572_490 | 94.96 | 255.5 |
| SCE1572_4841 | 41.03 | 291.31 |
| SCE1572_7331 | 2.53 | 0 |
| SCE1572_9992 | 0 | 0 |
| SCE1572_9282 | 901.24 | 946.41 |
| SCE1572_469 | 89.44 | 861.11 |
| SCE1572_2613 | 56.71 | 27.86 |
| SCE1572_460 | 4.44 | 0 |
| SCE1572_2075 | 46.96 | 8.07 |
| SCE1572_5525 | 37.42 | 17.58 |
| SCE1572_4430 | 6.71 | 4.31 |
| SCE1572_373 | 27.84 | 25.13 |
| SCE1572_9389 | 36.18 | 166.7 |
| SCE1572_3631 | 18.33 | 12.03 |
| SCE1572_6881 | 69.27 | 39.32 |
| SCE1572_5253 | 0 | 0 |
| SCE1572_6575 | 18.77 | 17.38 |
| SCE1572_3030 | 28.03 | 9.95 |
| SCE1572_2760 | 102.04 | 582.84 |
| SCE1572_10053 | 19.27 | 60.48 |
| SCE1572_9017 | 0 | 0 |
| SCE1572_824 | 28.06 | 16.99 |
| SCE1572_3986 | 95.51 | 1422.86 |
| SCE1572_8613 | 32.22 | 13.99 |
| SCE1572_4293 | 30.66 | 22.08 |
| SCE1572_4008 | 42.33 | 16.67 |
| SCE1572_11548 | 84.75 | 327.49 |
| SCE1572_1170 | 55.88 | 24.25 |
| SCE1572_7849 | 83.15 | 70.41 |
| SCE1572_8997 | 22.7 | 16.39 |
| SCE1572_516 | 0 | 0 |
| SCE1572_8182 | 45.75 | 12.96 |
| SCE1572_5534 | 46.28 | 15.91 |
| SCE1572_7759 | 32.2 | 175.2 |
| SCE1572_241 | 63.31 | 43.01 |
| SCE1572_8379 | 19.44 | 16.37 |
| SCE1572_9703 | 20.01 | 23.36 |
| SCE1572_3937 | 89.59 | 73.46 |
| SCE1572_1898 | 17.47 | 21.78 |
| SCE1572_8028 | 5.62 | 0 |

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| SCE1572_1564 | 20.64 | 35.98 |
| SCE1572_5419 | 13.78 | 46.9 |
| SCE1572_8802 | 93.43 | 67.79 |
| SCE1572_4763 | 28.46 | 138.05 |
| SCE1572_9370 | 10.83 | 6.95 |
| SCE1572_6322 | 46.01 | 47.2 |
| SCE1572_8818 | 41.6 | 21.08 |
| SCE1572_8073 | 39.23 | 18.08 |
| SCE1572_773 | 13.11 | 16.83 |
| SCE1572_6206 | 41.98 | 31.54 |
| SCE1572_5345 | 18.01 | 10.84 |
| SCE1572_2267 | 33.97 | 56.14 |
| SCE1572_7927 | 46.3 | 46.3 |
| SCE1572_78 | 78.78 | 27.43 |
| SCE1572_5801 | 28.36 | 87.05 |
| SCE1572_6229 | 23.63 | 10.43 |
| SCE1572_6481 | 16.37 | 1.71 |
| SCE1572_4456 | 28.64 | 61.83 |
| SCE1572_2928 | 26.73 | 10.02 |
| SCE1572_8205 | 12.13 | 38.93 |
| SCE1572_7876 | 34.31 | 27.97 |
| SCE1572_8485 | 17.37 | 10.33 |
| SCE1572_6370 | 35.29 | 23.89 |
| SCE1572_2723 | 34.43 | 42.16 |
| SCE1572_2517 | 0 | 0 |
| SCE1572_8536 | 25.94 | 12.41 |
| SCE1572_6642 | 89.14 | 40.1 |
| SCE1572_4965 | 29.14 | 19.46 |
| SCE1572_11461 | 3.09 | 0 |
| SCE1572_7444 | 0 | 0 |
| SCE1572_8708 | 21.87 | 35.89 |
| SCE1572_9950 | 46.48 | 21.09 |
| SCE1572_4168 | 24.66 | 4.4 |
| SCE1572_9545 | 43.37 | 55.43 |
| SCE1572_6509 | 38.16 | 12.41 |
| SCE1572_6593 | 31.59 | 79.07 |
| SCE1572_987 | 17.55 | 15.28 |
| SCE1572_8569 | 93.22 | 18.92 |
| SCE1572_7693 | 148.98 | 502.43 |
| SCE1572_10000 | 98.35 | 456.97 |
| SCE1572_2770 | 56.86 | 623.41 |
| SCE1572_1249 | 11.03 | 9.95 |
| SCE1572_4439 | 14.74 | 5.52 |
| SCE1572_3673 | 42.73 | 49.1 |
| SCE1572_5156 | 95.13 | 17.89 |
| SCE1572_59 | 25.87 | 16.39 |
| SCE1572_876 | 348.72 | 235.8 |
| SCE1572_4609 | 278.18 | 53.95 |

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| SCE1572_10011 | 354.36 | 1321.08 |
| SCE1572_5369 | 15.58 | 4.85 |
| SCE1572_1917 | 16.1 | 5.42 |
| SCE1572_7121 | 0 | 0 |
| SCE1572_42 | 46.95 | 39.83 |
| SCE1572_6958 | 56.86 | 12.67 |
| SCE1572_5592 | 46.87 | 37.35 |
| SCE1572_1284 | 89.6 | 2903.67 |
| SCE1572_10007 | 15.92 | 10.45 |
| SCE1572_8972 | 29.08 | 3467.6 |
| SCE1572_8899 | 4.74 | 0 |
| SCE1572_6358 | 39.74 | 15.59 |
| SCE1572_9234 | 63.5 | 98.07 |
| SCE1572_4819 | 56 | 249.22 |
| SCE1572_5354 | 19.16 | 27.67 |
| SCE1572_10416 | 6.64 | 8.72 |
| SCE1572_1169 | 42.32 | 19.25 |
| SCE1572_5788 | 198.75 | 820.05 |
| SCE1572_120 | 28.53 | 5.39 |
| SCE1572_1282 | 19.69 | 72.67 |
| SCE1572_8236 | 64.08 | 579.97 |
| SCE1572_11492 | 58.11 | 159.31 |
| SCE1572_8269 | 32.79 | 11.36 |
| SCE1572_5201 | 10.83 | 8.41 |
| SCE1572_799 | 49.6 | 231.27 |
| SCE1572_2826 | 18.02 | 13.46 |
| SCE1572_3346 | 196.12 | 142.52 |
| SCE1572_9481 | 58.04 | 50.61 |
| SCE1572_2713 | 36.97 | 92.84 |
| SCE1572_7036 | 59.56 | 189.91 |
| SCE1572_3277 | 0 | 0 |
| SCE1572_10917 | 12.86 | 17.99 |
| SCE1572_6636 | 108.15 | 29.77 |
| SCE1572_3948 | 78.84 | 189.76 |
| SCE1572_7775 | 38.99 | 13.9 |
| SCE1572_10398 | 36.54 | 39.98 |
| SCE1572_2997 | 18.78 | 3.23 |
| SCE1572_7476 | 488.25 | 0 |
| SCE1572_4514 | 143.38 | 425.74 |
| SCE1572_7348 | 38.11 | 15.61 |
| SCE1572_2571 | 47.44 | 49.65 |
| SCE1572_6502 | 26.35 | 24.72 |
| SCE1572_4056 | 25.9 | 61.32 |
| SCE1572_1323 | 12.31 | 20.8 |
| SCE1572_3575 | 45.42 | 15.51 |
| SCE1572_10575 | 0 | 0 |
| SCE1572_4412 | 2.94 | 0 |
| SCE1572_7650 | 27.57 | 0 |

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| SCE1572_5117 | 14.2 | 34.17 |
| SCE1572_9310 | 102.87 | 453.42 |
| SCE1572_4918 | 43.72 | 45.09 |
| SCE1572_1957 | 45.22 | 33.29 |
| SCE1572_4696 | 59.18 | 36.31 |
| SCE1572_1138 | 26.34 | 7.73 |
| SCE1572_10372 | 60.93 | 23.87 |
| SCE1572_6408 | 24.33 | 11.26 |
| SCE1572_2206 | 58.48 | 504.37 |
| SCE1572_10148 | 47.79 | 59.5 |
| SCE1572_9399 | 45.85 | 37.62 |
| SCE1572_4914 | 24.75 | 9.58 |
| SCE1572_11408 | 21.41 | 12.37 |
| SCE1572_9189 | 53.19 | 20.6 |
| SCE1572_8985 | 34.29 | 73.35 |
| SCE1572_6768 | 93.98 | 153.81 |
| SCE1572_8635 | 24.5 | 16.59 |
| SCE1572_6615 | 46.72 | 27.54 |
| SCE1572_5614 | 27.57 | 7.04 |
| SCE1572_2122 | 3.97 | 1.59 |
| SCE1572_3903 | 69.48 | 104.36 |
| SCE1572_1970 | 44.63 | 18.76 |
| SCE1572_1791 | 20.31 | 4.07 |
| SCE1572_11444 | 27.47 | 26.44 |
| SCE1572_3957 | 6.5 | 0 |
| SCE1572_889 | 29.09 | 8.67 |
| SCE1572_10709 | 20.37 | 0 |
| SCE1572_4321 | 103.9 | 52.89 |
| SCE1572_8395 | 23.78 | 530.39 |
| SCE1572_4561 | 0 | 0 |
| SCE1572_4024 | 229.96 | 201.85 |
| SCE1572_3510 | 22.55 | 114.6 |
| SCE1572_2330 | 86.07 | 58.92 |
| SCE1572_1822 | 99.69 | 22.5 |
| SCE1572_10500 | 49.67 | 576.75 |
| SCE1572_6994 | 11.89 | 14.31 |
| SCE1572_3299 | 41.76 | 43.7 |
| SCE1572_10924 | 75.72 | 1698.06 |
| SCE1572_10744 | 44.5 | 17.6 |
| SCE1572_3069 | 21.78 | 48.31 |
| SCE1572_6627 | 48.83 | 80.41 |
| SCE1572_4993 | 26.37 | 15.87 |
| SCE1572_611 | 9.38 | 46.4 |
| SCE1572_2103 | 41.41 | 60.36 |
| SCE1572_11032 | 0 | 0 |
| SCE1572_6467 | 34.48 | 8.49 |
| SCE1572_10694 | 39.48 | 0 |
| SCE1572_1077 | 55.07 | 36 |

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| SCE1572_6139 | 24.75 | 52.13 |
| SCE1572_9983 | 36.02 | 15.67 |
| SCE1572_5634 | 49.33 | 17.46 |
| SCE1572_8870 | 39.85 | 29.77 |
| SCE1572_10928 | 33.36 | 33.9 |
| SCE1572_7198 | 366.5 | 871.61 |
| SCE1572_9413 | 20.14 | 77.69 |
| SCE1572_3589 | 2.76 | 0 |
| SCE1572_3272 | 0 | 0 |
| SCE1572_1995 | 67.77 | 21.43 |
| SCE1572_6788 | 92.63 | 34.03 |
| SCE1572_3551 | 10.42 | 8.36 |
| SCE1572_9010 | 23.1 | 9.98 |
| SCE1572_4827 | 37.7 | 22.2 |
| SCE1572_9692 | 20.16 | 79.58 |
| SCE1572_6603 | 23.45 | 38.56 |
| SCE1572_8519 | 24.3 | 334.28 |
| SCE1572_4359 | 8.74 | 9.01 |
| SCE1572_10827 | 38.82 | 17.68 |
| SCE1572_7752 | 20.28 | 14.42 |
| SCE1572_1771 | 57.19 | 27.17 |
| SCE1572_5192 | 45.69 | 369.92 |
| SCE1572_2369 | 67.61 | 14.79 |
| SCE1572_6275 | 51 | 147.35 |
| SCE1572_2706 | 53.57 | 35.98 |
| SCE1572_10131 | 19.36 | 19.97 |
| SCE1572_10380 | 38.23 | 34.02 |
| SCE1572_437 | 22.48 | 12.3 |
| SCE1572_2935 | 9.41 | 2.52 |
| SCE1572_7502 | 25.95 | 42.74 |
| SCE1572_5909 | 87.65 | 647.17 |
| SCE1572_5347 | 27.42 | 15.53 |
| SCE1572_9752 | 0 | 0 |
| SCE1572_2677 | 10.21 | 166.39 |
| SCE1572_9153 | 245.89 | 208.19 |
| SCE1572_860 | 134.98 | 854.45 |
| SCE1572_3992 | 26.82 | 140.35 |
| SCE1572_6526 | 26.58 | 10.18 |
| SCE1572_8624 | 37.41 | 0 |
| SCE1572_8497 | 68.21 | 26.2 |
| SCE1572_2587 | 5.7 | 2.74 |
| SCE1572_11471 | 25.27 | 18.88 |
| SCE1572_10550 | 24.3 | 19.5 |
| SCE1572_11459 | 65.38 | 154 |
| SCE1572_3224 | 17.75 | 1.88 |
| SCE1572_2417 | 15.25 | 13.63 |
| SCE1572_10811 | 0 | 0 |
| SCE1572_3624 | 35.77 | 8.2 |

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| SCE1572_6114 | 87.18 | 15.21 |
| SCE1572_6566 | 21.35 | 21.15 |
| SCE1572_4572 | 45.48 | 11.52 |
| SCE1572_3845 | 77.73 | 24.25 |
| SCE1572_9723 | 30.17 | 13.03 |
| SCE1572_4549 | 35.03 | 11.47 |
| SCE1572_1068 | 38.83 | 0 |
| SCE1572_2855 | 16.39 | 5.44 |
| SCE1572_10383 | 16.13 | 8.63 |
| SCE1572_2774 | 33.46 | 23.86 |
| SCE1572_40 | 51.57 | 33.1 |
| SCE1572_1615 | 44.87 | 197.77 |
| SCE1572_11434 | 29.43 | 18.13 |
| SCE1572_7786 | 21.07 | 30.32 |
| SCE1572_7176 | 51.96 | 102.31 |
| SCE1572_7737 | 17.72 | 28.44 |
| SCE1572_7491 | 32.34 | 34.06 |
| SCE1572_6429 | 14.97 | 5.48 |
| SCE1572_9155 | 67.68 | 116.35 |
| SCE1572_1426 | 240.32 | 549.65 |
| SCE1572_3309 | 16.62 | 4.8 |
| SCE1572_4542 | 0 | 0 |
| SCE1572_7967 | 22.97 | 0 |
| SCE1572_5083 | 42.74 | 148.17 |
| SCE1572_3411 | 20.8 | 34.49 |
| SCE1572_2829 | 42.91 | 9.18 |
| SCE1572_1785 | 61.06 | 128.64 |
| SCE1572_1643 | 80.27 | 25.74 |
| SCE1572_5106 | 73.64 | 1454.48 |
| SCE1572_10944 | 77.29 | 78.71 |
| SCE1572_3581 | 40.16 | 22.96 |
| SCE1572_5770 | 270.86 | 4013.51 |
| SCE1572_501 | 37.23 | 16.8 |
| SCE1572_3819 | 48.22 | 27.26 |
| SCE1572_9092 | 26.7 | 17.85 |
| SCE1572_7113 | 35.21 | 23.5 |
| SCE1572_5629 | 13.96 | 0 |
| SCE1572_8642 | 6.06 | 4.87 |
| SCE1572_9878 | 23.28 | 8.62 |
| SCE1572_9437 | 254.1 | 344.65 |
| SCE1572_6134 | 33.93 | 45.93 |
| SCE1572_2666 | 35.1 | 51.63 |
| SCE1572_5645 | 6 | 3.61 |
| SCE1572_7716 | 19.74 | 0 |
| SCE1572_539 | 2.6 | 0 |
| SCE1572_4215 | 382.12 | 843.07 |
| SCE1572_1827 | 10.23 | 2.9 |
| SCE1572_982 | 55.28 | 47.43 |

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| SCE1572_6140 | 12.82 | 6.35 |
| SCE1572_5646 | 2.61 | 0 |
| SCE1572_11160 | 26.16 | 179.23 |
| SCE1572_7025 | 2.81 | 0 |
| SCE1572_4187 | 98.48 | 144.99 |
| SCE1572_2404 | 40.34 | 299.14 |
| SCE1572_7512 | 0 | 0 |
| SCE1572_4799 | 43.01 | 48.71 |
| SCE1572_10388 | 24.4 | 67.11 |
| SCE1572_8742 | 27.19 | 28.84 |
| SCE1572_6149 | 102.56 | 93.91 |
| SCE1572_2468 | 34.64 | 61.72 |
| SCE1572_862 | 74.89 | 267.1 |
| SCE1572_5146 | 20.67 | 9.6 |
| SCE1572_11073 | 3.47 | 181.42 |
| SCE1572_2019 | 29.79 | 14.82 |
| SCE1572_3084 | 32.11 | 9.66 |
| SCE1572_8145 | 17.4 | 105.69 |
| SCE1572_8884 | 42.98 | 3.76 |
| SCE1572_11500 | 40.29 | 96.98 |
| SCE1572_321 | 45.33 | 3.76 |
| SCE1572_11313 | 140.73 | 1973.81 |
| SCE1572_8833 | 21.81 | 11.25 |
| SCE1572_8663 | 53.2 | 22.41 |
| SCE1572_3045 | 6.11 | 0 |
| SCE1572_4864 | 21.49 | 9.24 |
| SCE1572_4484 | 27.14 | 34.08 |
| SCE1572_2547 | 21.57 | 23.32 |
| SCE1572_1849 | 45.69 | 27.99 |
| SCE1572_11387 | 172.74 | 312.95 |
| SCE1572_11553 | 40.98 | 29.59 |
| SCE1572_4266 | 30.32 | 32.44 |
| SCE1572_3602 | 12.25 | 30.79 |
| SCE1572_10342 | 20.22 | 32.44 |
| SCE1572_9526 | 58.75 | 637.47 |
| SCE1572_8053 | 25.89 | 11.13 |
| SCE1572_9179 | 46.6 | 18.96 |
| SCE1572_10934 | 33.19 | 16.44 |
| SCE1572_8734 | 27.57 | 28.75 |
| SCE1572_8332 | 129.96 | 131.78 |
| SCE1572_563 | 21.5 | 57.06 |
| SCE1572_1333 | 12.06 | 0 |
| SCE1572_11083 | 8.92 | 21.47 |
| SCE1572_6518 | 43.1 | 9.26 |
| SCE1572_2733 | 16.97 | 43.47 |
| SCE1572_1312 | 683.04 | 1949.94 |
| SCE1572_2020 | 26.45 | 38.82 |
| SCE1572_10304 | 64.44 | 97.89 |

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| SCE1572_8446 | 9.72 | 4.68 |
| SCE1572_4508 | 14.65 | 29.84 |
| SCE1572_9464 | 24.11 | 13.19 |
| SCE1572_752 | 20.81 | 0 |
| SCE1572_8686 | 65.12 | 9.8 |
| SCE1572_6742 | 24.16 | 5.11 |
| SCE1572_47 | 20.65 | 7.91 |
| SCE1572_8292 | 32.31 | 17.95 |
| SCE1572_6316 | 0 | 0 |
| SCE1572_2235 | 60.06 | 184.99 |
| SCE1572_7169 | 45.32 | 55.97 |
| SCE1572_7132 | 34.66 | 10.43 |
| SCE1572_1526 | 182.79 | 2697.39 |
| SCE1572_8534 | 59.45 | 255.11 |
| SCE1572_8936 | 8.27 | 0 |
| SCE1572_10531 | 2.23 | 0 |
| SCE1572_2115 | 35.67 | 16.28 |
| SCE1572_1740 | 19.28 | 3.2 |
| SCE1572_7328 | 25.27 | 4.34 |
| SCE1572_9071 | 99.07 | 252.2 |
| SCE1572_4818 | 7.22 | 0 |
| SCE1572_2697 | 72.94 | 31.35 |
| SCE1572_2135 | 2.57 | 0 |
| SCE1572_2683 | 46.09 | 328.92 |
| SCE1572_1809 | 10.47 | 25.2 |
| SCE1572_2323 | 23.65 | 82.13 |
| SCE1572_3494 | 22.68 | 2.87 |
| SCE1572_7260 | 97 | 1000.09 |
| SCE1572_7377 | 47.5 | 72.45 |
| SCE1572_8282 | 70.95 | 251.71 |
| SCE1572_9596 | 15.64 | 792.11 |
| SCE1572_3885 | 73.84 | 22.69 |
| SCE1572_2068 | 21.66 | 14.89 |
| SCE1572_2063 | 40.73 | 34.25 |
| SCE1572_2101 | 63.79 | 240.31 |
| SCE1572_7000 | 0 | 0 |
| SCE1572_9688 | 121.9 | 229.91 |
| SCE1572_4257 | 19.14 | 0 |
| SCE1572_9028 | 35.7 | 109.26 |
| SCE1572_11581 | 29.25 | 37.68 |
| SCE1572_11232 | 22.54 | 12.82 |
| SCE1572_2299 | 138.29 | 699.77 |
| SCE1572_8339 | 47.9 | 42.79 |
| SCE1572_8957 | 34.63 | 114.09 |
| SCE1572_10186 | 41.86 | 95.84 |
| SCE1572_2217 | 5.32 | 0 |
| SCE1572_9384 | 14.03 | 9.8 |
| SCE1572_8749 | 26.52 | 28.53 |

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| SCE1572_4612 | 35.5 | 5.34 |
| SCE1572_3795 | 26.97 | 18.69 |
| SCE1572_8487 | 7.58 | 3.65 |
| SCE1572_9356 | 29.62 | 140.35 |
| SCE1572_4354 | 27.3 | 18.18 |
| SCE1572_10322 | 33.93 | 505.28 |
| SCE1572_6052 | 317.8 | 431.27 |
| SCE1572_3663 | 21.78 | 6.31 |
| SCE1572_7624 | 42.76 | 66.35 |
| SCE1572_4738 | 24.89 | 46.3 |
| SCE1572_2493 | 83.77 | 50.24 |
| SCE1572_10218 | 47.87 | 70.56 |
| SCE1572_990 | 43.82 | 41.74 |
| SCE1572_596 | 215.32 | 828.27 |
| SCE1572_11452 | 27.47 | 7.35 |
| SCE1572_3857 | 15.93 | 41.84 |
| SCE1572_2273 | 22.4 | 47.69 |
| SCE1572_11099 | 30.54 | 28.37 |
| SCE1572_4881 | 10.11 | 4.87 |
| SCE1572_2555 | 27.34 | 13.16 |
| SCE1572_263 | 2.66 | 0 |
| SCE1572_3116 | 82.65 | 45.62 |
| SCE1572_2747 | 30.78 | 34.86 |
| SCE1572_4362 | 2.45 | 0 |
| SCE1572_1105 | 37.08 | 21.51 |
| SCE1572_805 | 70.25 | 60.46 |
| SCE1572_3943 | 568.8 | 1236.47 |
| SCE1572_11155 | 72.22 | 145.97 |
| SCE1572_11479 | 6.89 | 0 |
| SCE1572_8504 | 18.7 | 5.75 |
| SCE1572_6550 | 56.98 | 46.49 |
| SCE1572_8775 | 35.62 | 20.58 |
| SCE1572_9000 | 117.1 | 223.19 |
| SCE1572_699 | 14.38 | 2.88 |
| SCE1572_9009 | 0 | 0 |
| SCE1572_7519 | 38.15 | 242.5 |
| SCE1572_4311 | 32.42 | 14.75 |
| SCE1572_4040 | 134.98 | 71.2 |
| SCE1572_3193 | 85.88 | 90.31 |
| SCE1572_2455 | 37.53 | 80.3 |
| SCE1572_1948 | 18.58 | 944.33 |
| SCE1572_11377 | 20.74 | 63.69 |
| SCE1572_532 | 44.27 | 16.67 |
| SCE1572_4876 | 25.35 | 17.09 |
| SCE1572_5264 | 76.88 | 370.06 |
| SCE1572_8573 | 15.68 | 0 |
| SCE1572_3523 | 81.98 | 116.23 |
| SCE1572_1730 | 23.69 | 37.06 |

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| SCE1572_1852 | 33.06 | 89.11 |
| SCE1572_2762 | 0 | 0 |
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| SCE1572_3633 | 28.38 | 11.71 |
| SCE1572_1121 | 40.09 | 19.59 |
| SCE1572_3531 | 39.28 | 7.56 |
| SCE1572_1777 | 61.4 | 20.12 |
| SCE1572_1754 | 31.52 | 22.55 |
| SCE1572_854 | 211.76 | 693.65 |
| SCE1572_6001 | 132.15 | 387.11 |
| SCE1572_103 | 55.63 | 17.66 |
| SCE1572_6348 | 0 | 0 |
| SCE1572_4341 | 20.11 | 24.2 |
| SCE1572_7308 | 0 | 0 |
| SCE1572_4593 | 78.75 | 129.32 |
| SCE1572_2443 | 2.71 | 0 |
| SCE1572_11592 | 34.61 | 19.83 |
| SCE1572_10298 | 43.96 | 46.12 |
| SCE1572_8690 | 53.45 | 10.5 |
| SCE1572_2866 | 106.21 | 31.03 |
| SCE1572_5506 | 47.13 | 15.13 |
| SCE1572_446 | 26.73 | 13.44 |
| SCE1572_3504 | 26.76 | 51.88 |
| SCE1572_767 | 11.66 | 3.69 |
| SCE1572_11077 | 10.17 | 109.03 |
| SCE1572_9066 | 80.38 | 22.02 |
| SCE1572_4106 | 19.58 | 12.12 |
| SCE1572_8733 | 55.06 | 27.85 |
| SCE1572_6437 | 97.57 | 30.71 |
| SCE1572_2522 | 37.14 | 68.88 |
| SCE1572_5702 | 34.6 | 54.95 |
| SCE1572_4399 | 39.31 | 6.76 |
| SCE1572_2004 | 17.12 | 0 |
| SCE1572_5982 | 11.34 | 3.41 |
| SCE1572_2280 | 59.69 | 37.75 |
| SCE1572_5937 | 25.81 | 5.18 |
| SCE1572_907 | 25.27 | 9.5 |
| SCE1572_1019 | 0 | 0 |
| SCE1572_4462 | 0 | 0 |
| SCE1572_2914 | 42.41 | 12.65 |
| SCE1572_1026 | 11.66 | 519.31 |
| SCE1572_6747 | 0 | 0 |
| SCE1572_3715 | 102.14 | 147.89 |
| SCE1572_10463 | 85.76 | 320.38 |
| SCE1572_10456 | 68.57 | 13.63 |
| SCE1572_7170 | 38.06 | 63.07 |
| SCE1572_10867 | 26.76 | 17.89 |

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| SCE1572_6781 | 43.32 | 466.29 |
| SCE1572_8271 | 24.97 | 90.68 |
| SCE1572_7746 | 56.61 | 63.16 |
| SCE1572_7501 | 39.02 | 226.06 |
| SCE1572_9785 | 25.27 | 10.58 |
| SCE1572_10379 | 0 | 0 |
| SCE1572_7156 | 36.96 | 72.38 |
| SCE1572_10564 | 66.49 | 27.18 |
| SCE1572_4873 | 178.65 | 472.42 |
| SCE1572_2476 | 55.42 | 13.8 |
| SCE1572_3851 | 30.94 | 372.37 |
| SCE1572_1722 | 39.16 | 38.19 |
| SCE1572_10270 | 48.81 | 339.93 |
| SCE1572_1863 | 29.93 | 8.61 |
| SCE1572_9554 | 45.78 | 107.33 |
| SCE1572_4161 | 0 | 0 |
| SCE1572_1982 | 0 | 0 |
| SCE1572_6044 | 11.54 | 289.56 |
| SCE1572_5967 | 22.9 | 5.07 |
| SCE1572_10300 | 57.4 | 328.88 |
| SCE1572_7582 | 181.61 | 683.01 |
| SCE1572_522 | 27.63 | 34.1 |
| SCE1572_7473 | 36.4 | 100.07 |
| SCE1572_8194 | 32.98 | 6.78 |
| SCE1572_6049 | 33.63 | 188.07 |
| SCE1572_2032 | 50.22 | 29.18 |
| SCE1572_1920 | 27.52 | 29.87 |
| SCE1572_5324 | 46.04 | 110.82 |
| SCE1572_2426 | 323.75 | 703.78 |
| SCE1572_6490 | 61.21 | 24.93 |
| SCE1572_1929 | 14.03 | 29.56 |
| SCE1572_3483 | 89.11 | 122.71 |
| SCE1572_8518 | 24.33 | 169.7 |
| SCE1572_3738 | 6.42 | 5.79 |
| SCE1572_3246 | 136.04 | 433.01 |
| SCE1572_11563 | 22.61 | 12.2 |
| SCE1572_4036 | 11.36 | 0.85 |
| SCE1572_11241 | 61.62 | 60.82 |
| SCE1572_9560 | 47.57 | 37.46 |
| SCE1572_933 | 47.5 | 97.6 |
| SCE1572_2196 | 36.73 | 574.26 |
| SCE1572_3350 | 25.2 | 14.39 |
| SCE1572_7245 | 67.67 | 101.02 |
| SCE1572_2355 | 24.34 | 29.29 |
| SCE1572_3647 | 18.21 | 89.86 |
| SCE1572_9304 | 57.83 | 158.76 |
| SCE1572_218 | 32.91 | 110.33 |
| SCE1572_1484 | 71.43 | 36.6 |

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| SCE1572_1038 | 14.96 | 4.8 |
| SCE1572_8793 | 13.1 | 0 |
| SCE1572_5488 | 74.43 | 17.06 |
| SCE1572_36 | 38.17 | 65.88 |
| SCE1572_5827 | 25.12 | 19.76 |
| SCE1572_5049 | 31.18 | 57.39 |
| SCE1572_7939 | 8.66 | 29.19 |
| SCE1572_2833 | 53.16 | 298.57 |
| SCE1572_3374 | 97.78 | 3741.94 |
| SCE1572_114 | 44.28 | 9.69 |
| SCE1572_4240 | 37.78 | 24.57 |
| SCE1572_2970 | 30.9 | 50.47 |
| SCE1572_6536 | 66.42 | 134.6 |
| SCE1572_4634 | 43.88 | 17.13 |
| SCE1572_1638 | 15.45 | 9.3 |
| SCE1572_7781 | 14.91 | 0 |
| SCE1572_137 | 26.21 | 16.22 |
| SCE1572_6304 | 40.3 | 101.62 |
| SCE1572_3829 | 28.39 | 237.91 |
| SCE1572_2629 | 34.09 | 18 |
| SCE1572_2532 | 34.37 | 223.09 |
| SCE1572_8479 | 53.97 | 364.92 |
| SCE1572_3863 | 14.15 | 6.09 |
| SCE1572_9466 | 38.75 | 60.72 |
| SCE1572_913 | 13.26 | 21.94 |
| SCE1572_8869 | 46.92 | 23.77 |
| SCE1572_174 | 25.76 | 12.68 |
| SCE1572_7822 | 90.97 | 563.02 |
| SCE1572_10818 | 43.25 | 47.15 |
| SCE1572_158 | 146.17 | 1011.29 |
| SCE1572_8343 | 18.27 | 4.4 |
| SCE1572_6081 | 26.44 | 0 |
| SCE1572_3007 | 20.36 | 20.27 |
| SCE1572_7142 | 60.45 | 85.18 |
| SCE1572_8850 | 16.79 | 33.89 |
| SCE1572_1499 | 30.65 | 7.76 |
| SCE1572_4970 | 35.86 | 9.86 |
| SCE1572_3033 | 49.44 | 70.98 |
| SCE1572_11487 | 20.29 | 2.76 |
| SCE1572_3895 | 23.02 | 42.03 |
| SCE1572_1297 | 47.88 | 495.1 |
| SCE1572_8394 | 96.99 | 193.84 |
| SCE1572_832 | 14.54 | 10 |
| SCE1572_6684 | 28.45 | 82.35 |
| SCE1572_2646 | 0 | 0 |
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| SCE1572_2880 | 23.45 | 45.15 |
| SCE1572_737 | 63.95 | 44.97 |

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| SCE1572_11026 | 17.08 | 15.42 |
| SCE1572_8584 | 0 | 0 |
| SCE1572_9851 | 37.9 | 16.89 |
| SCE1572_300 | 22.74 | 16.94 |
| SCE1572_1462 | 19.78 | 0 |
| SCE1572_9135 | 10.46 | 5.03 |
| SCE1572_3843 | 7.58 | 0 |
| SCE1572_9223 | 462.99 | 95.52 |
| SCE1572_7790 | 0 | 0 |
| SCE1572_4905 | 47.96 | 932.79 |
| SCE1572_235 | 5.41 | 8.69 |
| SCE1572_6411 | 24.61 | 19.11 |
| SCE1572_346 | 62.19 | 24.58 |
| SCE1572_3217 | 33.15 | 21.28 |
| SCE1572_4895 | 25.95 | 16.44 |
| SCE1572_5062 | 55.02 | 149.61 |
| SCE1572_11600 | 12.29 | 1.97 |
| SCE1572_1706 | 44.96 | 75.04 |
| SCE1572_1442 | 40.62 | 17.42 |
| SCE1572_1395 | 51.02 | 3252.69 |
| SCE1572_1762 | 151.2 | 27 |
| SCE1572_10141 | 8.34 | 29.52 |
| SCE1572_7863 | 34.24 | 3.92 |
| SCE1572_9319 | 20.37 | 5.45 |
| SCE1572_4398 | 15.54 | 14.82 |
| SCE1572_5775 | 62.53 | 57.51 |
| SCE1572_11182 | 33.82 | 10.85 |
| SCE1572_3597 | 0 | 0 |
| SCE1572_333 | 43.72 | 50.57 |
| SCE1572_3240 | 5.14 | 0 |
| SCE1572_7435 | 33.3 | 6.22 |
| SCE1572_3733 | 0 | 0 |
| SCE1572_2577 | 40.55 | 18.67 |
| SCE1572_6127 | 41.9 | 167.14 |
| SCE1572_394 | 29.39 | 48.68 |
| SCE1572_11023 | 55.54 | 177.11 |
| SCE1572_6499 | 22.56 | 24.98 |
| SCE1572_11516 | 14.8 | 7.7 |
| SCE1572_8327 | 61.88 | 40.62 |
| SCE1572_5040 | 40.55 | 160.83 |
| SCE1572_7568 | 142.17 | 84.6 |
| SCE1572_499 | 30.05 | 18.35 |
| SCE1572_662 | 367.48 | 1028.16 |
| SCE1572_1570 | 69.22 | 128.25 |
| SCE1572_4042 | 38.99 | 31.28 |
| SCE1572_4667 | 0 | 0 |
| SCE1572_5851 | 0 | 0 |
| SCE1572_1904 | 10.24 | 0 |

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| SCE1572_5389 | 47.81 | 148.82 |
| SCE1572_1111 | 54.82 | 8.25 |
| SCE1572_8090 | 24.92 | 5.06 |
| SCE1572_1869 | 34.28 | 212.68 |
| SCE1572_6325 | 35.38 | 152.05 |
| SCE1572_10884 | 17.73 | 14.94 |
| SCE1572_2956 | 9.27 | 5.82 |
| SCE1572_481 | 59.04 | 15.92 |
| SCE1572_9264 | 77.29 | 113.05 |
| SCE1572_6309 | 36 | 47.26 |
| SCE1572_415 | 38.53 | 98.76 |
| SCE1572_6452 | 54.97 | 22.5 |
| SCE1572_2108 | 28.34 | 138.61 |
| SCE1572_9106 | 70.18 | 8.34 |
| SCE1572_8175 | 11.97 | 0 |
| SCE1572_2383 | 19.88 | 20.64 |
| SCE1572_11103 | 11.26 | 21.9 |
| SCE1572_1043 | 32.41 | 80.53 |
| SCE1572_9634 | 33.91 | 43.19 |
| SCE1572_10138 | 0 | 0 |
| SCE1572_10471 | 13.6 | 20.66 |
| SCE1572_3076 | 96.4 | 88.59 |
| SCE1572_10026 | 160.71 | 890.41 |
| SCE1572_7314 | 34.54 | 15.75 |
| SCE1572_5623 | 34.96 | 118.49 |
| SCE1572_2961 | 79.47 | 624.95 |
| SCE1572_9505 | 10.67 | 8.56 |
| SCE1572_1966 | 51.32 | 416.39 |
| SCE1572_9229 | 3.53 | 0 |
| SCE1572_4801 | 18.31 | 44.08 |
| SCE1572_8879 | 27.72 | 9.1 |
| SCE1572_8308 | 301.48 | 872.23 |
| SCE1572_1144 | 22.32 | 20.54 |
| SCE1572_7834 | 2.3 | 0 |
| SCE1572_9325 | 0 | 0 |
| SCE1572_3132 | 14.52 | 10.23 |
| SCE1572_476 | 66.64 | 182.46 |
| SCE1572_6066 | 6.46 | 1.35 |
| SCE1572_5036 | 7.15 | 13.77 |
| SCE1572_8367 | 32.25 | 10.88 |
| SCE1572_8457 | 95 | 167.32 |
| SCE1572_6832 | 20.03 | 8.51 |
| SCE1572_4530 | 19.16 | 6.15 |
| SCE1572_8350 | 28.41 | 0 |
| SCE1572_11485 | 149.52 | 184.98 |
| SCE1572_670 | 35.49 | 113.15 |
| SCE1572_10991 | 38.14 | 45.33 |
| SCE1572_5285 | 26.66 | 44.11 |

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| SCE1572_7685 | 19.24 | 11.11 |
| SCE1572_5289 | 24.77 | 4.77 |
| SCE1572_9226 | 35.2 | 20.64 |
| SCE1572_2887 | 15.55 | 2.34 |
| SCE1572_3146 | 23.33 | 8.02 |
| SCE1572_3317 | 53.85 | 362.43 |
| SCE1572_1466 | 89.65 | 22.21 |
| SCE1572_8346 | 52.91 | 19.8 |
| SCE1572_1278 | 46 | 26.65 |
| SCE1572_928 | 45.26 | 42.66 |
| SCE1572_8133 | 68.61 | 12.23 |
| SCE1572_7010 | 40.07 | 32.9 |
| SCE1572_2785 | 10.22 | 10.82 |
| SCE1572_784 | 31.75 | 7.9 |
| SCE1572_6738 | 15.91 | 35.89 |
| SCE1572_10751 | 45.41 | 18.16 |
| SCE1572_8429 | 36.79 | 45.04 |
| SCE1572_6844 | 28.21 | 48.6 |
| SCE1572_5382 | 22.94 | 8.42 |
| SCE1572_9078 | 20.19 | 1.91 |
| SCE1572_7185 | 35.41 | 13.11 |
| SCE1572_5166 | 8.27 | 8.85 |
| SCE1572_2630 | 40.26 | 11.8 |
| SCE1572_6459 | 35.76 | 6.89 |
| SCE1572_11262 | 23.41 | 55.45 |
| SCE1572_724 | 85.98 | 25.59 |
| SCE1572_11189 | 65.09 | 22.94 |
| SCE1572_7093 | 17.29 | 15.26 |
| SCE1572_11120 | 18.05 | 14.48 |
| SCE1572_5728 | 37.46 | 46.68 |
| SCE1572_7075 | 14.67 | 23.54 |
| SCE1572_1205 | 14.23 | 2.94 |
| SCE1572_8470 | 29.01 | 34.25 |
| SCE1572_1662 | 105.95 | 360.53 |
| SCE1572_11042 | 323.03 | 77.61 |
| SCE1572_2558 | 17.19 | 8.8 |
| SCE1572_2157 | 49.07 | 151.61 |
| SCE1572_9046 | 226.22 | 79.1 |
| SCE1572_6447 | 7.82 | 15.05 |
| SCE1572_6174 | 43.21 | 57.38 |
| SCE1572_7598 | 16.54 | 86.25 |
| SCE1572_11258 | 17.26 | 47.47 |
| SCE1572_3463 | 48.57 | 33.4 |
| SCE1572_10058 | 256.96 | 1741.67 |
| SCE1572_10900 | 46.8 | 200.48 |
| SCE1572_11197 | 58.31 | 59.88 |
| SCE1572_4979 | 37.9 | 235.68 |
| SCE1572_10368 | 15.05 | 5.57 |

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| SCE1572_2806 | 60.35 | 24.46 |
| SCE1572_7869 | 103.88 | 186.97 |
| SCE1572_5991 | 49.01 | 60.21 |
| SCE1572_11046 | 19.59 | 9.48 |
| SCE1572_2227 | 55.33 | 179.26 |
| SCE1572_6255 | 37.47 | 45.09 |
| SCE1572_10762 | 49.02 | 48.47 |
| SCE1572_6248 | 24.53 | 48.3 |
| SCE1572_1766 | 10.74 | 2.07 |
| SCE1572_5698 | 36.14 | 106.69 |
| SCE1572_694 | 9.39 | 19.11 |
| SCE1572_6195 | 50.54 | 12.58 |
| SCE1572_9258 | 14.11 | 9.86 |
| SCE1572_1671 | 36.53 | 515.66 |
| SCE1572_1239 | 9.49 | 3.51 |
| SCE1572_5092 | 0 | 0 |
| SCE1572_10963 | 28.43 | 22.81 |
| SCE1572_10065 | 292.4 | 1985.35 |
| SCE1572_11064 | 17.01 | 21.22 |
| SCE1572_1796 | 32.81 | 81.26 |
| SCE1572_9126 | 8.51 | 7.68 |
| SCE1572_3562 | 21.09 | 10.58 |
| SCE1572_5365 | 14.38 | 24.83 |
| SCE1572_4529 | 21.73 | 11.89 |
| SCE1572_605 | 37.5 | 94.17 |
| SCE1572_11141 | 47.63 | 17.24 |
| SCE1572_7402 | 11.8 | 1131.69 |
| SCE1572_7767 | 0 | 0 |
| SCE1572_2584 | 52.35 | 10.33 |
| SCE1572_2078 | 86.33 | 57.14 |
| SCE1572_7591 | 65.42 | 38.06 |
| SCE1572_6023 | 50.35 | 61.05 |
| SCE1572_3685 | 12.36 | 2.63 |
| SCE1572_1559 | 23.06 | 8.41 |
| SCE1572_9817 | 30.32 | 28.67 |
| SCE1572_6707 | 0 | 0 |
| SCE1572_1271 | 48.2 | 26.77 |
| SCE1572_10484 | 71.14 | 29.44 |
| SCE1572_9989 | 21.66 | 13.43 |
| SCE1572_10752 | 107.56 | 103.17 |
| SCE1572_10872 | 50.39 | 32.91 |
| SCE1572_2637 | 24.64 | 18.9 |
| SCE1572_1652 | 16.24 | 0 |
| SCE1572_11118 | 105.67 | 1200.19 |
| SCE1572_11411 | 46.59 | 22.06 |
| SCE1572_3424 | 103.35 | 50.64 |
| SCE1572_3824 | 34.29 | 83.44 |
| SCE1572_4838 | 154.86 | 122.51 |

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| SCE1572_4728 | 106.07 | 46.01 |
| SCE1572_1550 | 36.1 | 20.85 |
| SCE1572_1308 | 172.48 | 2455.07 |
| SCE1572_1055 | 53.66 | 22.15 |
| SCE1572_4302 | 49.36 | 29.7 |
| SCE1572_425 | 68.54 | 914.81 |
| SCE1572_9861 | 22.26 | 15.07 |
| SCE1572_554 | 30.1 | 69.76 |
| SCE1572_8554 | 40.91 | 135.4 |
| SCE1572_4070 | 220.29 | 656.86 |
| SCE1572_11060 | 26.46 | 41.64 |
| SCE1572_1049 | 13.1 | 4.51 |
| SCE1572_3183 | 21.58 | 31.44 |
| SCE1572_8659 | 501.81 | 1427.4 |
| SCE1572_6233 | 59.55 | 58.04 |
| SCE1572_3355 | 80.67 | 26.83 |
| SCE1572_2909 | 30.52 | 26.07 |
| SCE1572_7327 | 53.69 | 25 |
| SCE1572_1199 | 0 | 0 |
| SCE1572_7951 | 82.61 | 414.05 |
| SCE1572_11350 | 0 | 0 |
| SCE1572_4775 | 0 | 0 |
| SCE1572_2341 | 20.94 | 34.75 |
| SCE1572_6960 | 58.62 | 22.24 |
| SCE1572_10535 | 40.99 | 331.12 |
| SCE1572_9173 | 15.73 | 6.89 |
| SCE1572_7303 | 45.42 | 35.46 |
| SCE1572_3290 | 13.15 | 4.22 |
| SCE1572_2562 | 19.26 | 18.46 |
| SCE1572_6812 | 44.72 | 10.5 |
| SCE1572_7294 | 30.19 | 60.3 |
| SCE1572_6156 | 21.85 | 8.22 |
| SCE1572_10423 | 31.26 | 126.03 |
| SCE1572_1798 | 43.18 | 191.7 |
| SCE1572_867 | 34.18 | 64.31 |
| SCE1572_9426 | 44.13 | 42.83 |
| SCE1572_618 | 80.81 | 617.19 |
| SCE1572_4790 | 28.82 | 54.11 |
| SCE1572_10478 | 56.01 | 60.66 |
| SCE1572_1538 | 19 | 17.28 |
| SCE1572_7321 | 31.73 | 8.81 |
| SCE1572_5318 | 50.91 | 20.2 |
| SCE1572_4426 | 96.02 | 2123.5 |
| SCE1572_9961 | 52.31 | 10.95 |
| SCE1572_3399 | 22.33 | 17.5 |
| SCE1572_2271 | 23.3 | 21.86 |
| SCE1572_3322 | 3.37 | 0 |
| SCE1572_8670 | 17.6 | 149.88 |

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| SCE1572_2240 | 20.27 | 35.85 |
| SCE1572_9774 | 42.49 | 89.65 |
| SCE1572_6094 | 111.22 | 25.13 |
| SCE1572_1081 | 34.35 | 22.81 |
| SCE1572_10555 | 63.65 | 12.68 |
| SCE1572_6107 | 42.39 | 15.7 |
| SCE1572_2084 | 38.42 | 157.8 |
| SCE1572_11575 | 32.33 | 208.21 |
| SCE1572_3778 | 34.18 | 28 |
| SCE1572_10625 | 129.22 | 62.2 |
| SCE1572_6937 | 25.7 | 27.83 |
| SCE1572_10455 | 20.87 | 8.86 |
| SCE1572_9644 | 13.89 | 58.5 |
| SCE1572_3000 | 50.63 | 17.8 |
| SCE1572_2608 | 29.09 | 17.13 |
| SCE1572_7957 | 282.1 | 2485.79 |
| SCE1572_8526 | 70.36 | 128.8 |
| SCE1572_5398 | 59 | 27.48 |
| SCE1572_9133 | 5.41 | 2.61 |
| SCE1572_4520 | 63.47 | 161.24 |
| SCE1572_10802 | 14.72 | 5.97 |
| SCE1572_8383 | 32.38 | 18.73 |
| SCE1572_2984 | 122.35 | 85.95 |
| SCE1572_9913 | 0 | 0 |
| SCE1572_7941 | 59.16 | 167.85 |
| SCE1572_11333 | 65.87 | 85.37 |
| SCE1572_5311 | 69.72 | 71.92 |
| SCE1572_5915 | 126.07 | 159.28 |
| SCE1572_2604 | 17.79 | 14.27 |
| SCE1572_11523 | 10.94 | 15.05 |
| SCE1572_7730 | 14.5 | 2.83 |
| SCE1572_5304 | 63.96 | 82.68 |
| SCE1572_5342 | 12.07 | 10.89 |
| SCE1572_1301 | 35.35 | 18.98 |
| SCE1572_5180 | 26.42 | 968.48 |
| SCE1572_10879 | 59.15 | 188.32 |
| SCE1572_11359 | 58.39 | 38.53 |
| SCE1572_1659 | 27.53 | 25.48 |
| SCE1572_2143 | 17.69 | 21.29 |
| SCE1572_9587 | 36.87 | 78.2 |
| SCE1572_5128 | 141.46 | 623.57 |
| SCE1572_10672 | 6.82 | 8.69 |
| SCE1572_11172 | 18.17 | 10.56 |
| SCE1572_7183 | 48.09 | 21.79 |
| SCE1572_884 | 178.96 | 197.42 |
| SCE1572_10854 | 36.54 | 36.39 |
| SCE1572_10047 | 66.71 | 189.76 |
| SCE1572_11214 | 63.08 | 24.05 |

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| SCE1572_492 | 0 | 0 |
| SCE1572_5377 | 24.96 | 10.23 |
| SCE1572_10758 | 47.03 | 33.17 |
| SCE1572_7893 | 625.74 | 24527.11 |
| SCE1572_2937 | 92.53 | 952.56 |
| SCE1572_8412 | 57.64 | 63.15 |
| SCE1572_7674 | 57.3 | 15.04 |
| SCE1572_7385 | 37.19 | 17.21 |
| SCE1572_2347 | 2225.14 | 24547.25 |
| SCE1572_5239 | 8.87 | 13.87 |
| SCE1572_9085 | 21.66 | 17.38 |
| SCE1572_5234 | 205.94 | 2928.5 |
| SCE1572_4208 | 43.03 | 116.82 |
| SCE1572_2254 | 26.91 | 4.11 |
| SCE1572_10983 | 22.8 | 39.19 |
| SCE1572_6349 | 39.24 | 48 |
| SCE1572_154 | 53.3 | 76.98 |
| SCE1572_5751 | 142.82 | 147.32 |
| SCE1572_251 | 38.83 | 3.8 |
| SCE1572_9002 | 272.06 | 296.71 |
| SCE1572_10974 | 3.41 | 4.1 |
| SCE1572_9471 | 17.63 | 12.73 |
| SCE1572_10276 | 403.8 | 225.04 |
| SCE1572_8275 | 53.83 | 99.23 |
| SCE1572_107 | 52.99 | 88.57 |
| SCE1572_2037 | 35.11 | 222.79 |
| SCE1572_2027 | 0 | 0 |
| SCE1572_9580 | 57.4 | 28.53 |
| SCE1572_722 | 46.65 | 13.72 |
| SCE1572_790 | 0 | 0 |
| SCE1572_10678 | 44.29 | 229.49 |
| SCE1572_9628 | 44.98 | 20.03 |
| SCE1572_6344 | 43.19 | 38.89 |
| SCE1572_4279 | 47.75 | 60.48 |
| SCE1572_6372 | 0 | 0 |
| SCE1572_7358 | 32.99 | 68.25 |
| SCE1572_5332 | 33.56 | 37.47 |
| SCE1572_8119 | 72.83 | 178.28 |
| SCE1572_3827 | 69.19 | 235.12 |
| SCE1572_3017 | 25.07 | 30.17 |
| SCE1572_5871 | 23.54 | 23.53 |
| SCE1572_8940 | 50.74 | 172.03 |
| SCE1572_3039 | 84.42 | 12.44 |
| SCE1572_10237 | 34.72 | 16.92 |
| SCE1572_6956 | 45.86 | 2.25 |
| SCE1572_5857 | 0 | 0 |
| SCE1572_2754 | 52.57 | 52.46 |
| SCE1572_10904 | 28.82 | 439.85 |

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| SCE1572_11090 | 48.17 | 89.33 |
| SCE1572_10466 | 36.47 | 25.63 |
| SCE1572_5725 | 19.75 | 0 |
| SCE1572_1181 | 12.25 | 0 |
| SCE1572_1583 | 48.73 | 4.65 |
| SCE1572_4974 | 95.83 | 1450.21 |
| SCE1572_10847 | 52.21 | 22.38 |
| SCE1572_6622 | 43.32 | 32.41 |
| SCE1572_9086 | 59.17 | 14.83 |
| SCE1572_1509 | 58.9 | 15.94 |
| SCE1572_7548 | 53.95 | 17.91 |
| SCE1572_7427 | 31.66 | 19.53 |
| SCE1572_5843 | 21.84 | 6.19 |
| SCE1572_1156 | 0 | 0 |
| SCE1572_3387 | 19.52 | 3.13 |
| SCE1572_1721 | 9.12 | 0 |
| SCE1572_8857 | 63.08 | 149.17 |
| SCE1572_4982 | 36.81 | 6.33 |
| SCE1572_6479 | 30.58 | 180.52 |
| SCE1572_1439 | 23.14 | 8.64 |
| SCE1572_5552 | 3.23 | 11.65 |
| SCE1572_9144 | 18.58 | 7.21 |
| SCE1572_819 | 46.21 | 27.8 |
| SCE1572_2742 | 25.16 | 47.81 |
| SCE1572_5765 | 45.06 | 140.64 |
| SCE1572_8185 | 100.3 | 5.61 |
| SCE1572_1519 | 60.42 | 35.5 |
| SCE1572_5777 | 54.25 | 512.23 |
| SCE1572_10680 | 0 | 0 |
| SCE1572_3867 | 49.01 | 217.48 |
| SCE1572_10169 | 94.2 | 874.52 |
| SCE1572_1315 | 25.71 | 95.43 |
| SCE1572_9968 | 21.89 | 7.08 |
| SCE1572_3736 | 38.47 | 50.83 |
| SCE1572_810 | 33.85 | 24.49 |
| SCE1572_7909 | 37.37 | 72.64 |
| SCE1572_2256 | 24.47 | 14.54 |
| SCE1572_8214 | 53.91 | 44.75 |
| SCE1572_3020 | 66.8 | 20.63 |
| SCE1572_6906 | 0 | 0 |
| SCE1572_6577 | 17.27 | 15.01 |
| SCE1572_3489 | 19.69 | 6.32 |
| SCE1572_6965 | 21.74 | 16.97 |
| SCE1572_1831 | 0 | 0 |
| SCE1572_8681 | 44.59 | 11.45 |
| SCE1572_3756 | 35.45 | 9.82 |
| SCE1572_5868 | 98.83 | 82.74 |
| SCE1572_3928 | 85.48 | 90.1 |

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| SCE1572_4724 | 54.26 | 26.87 |
| SCE1572_1444 | 17.04 | 21.18 |
| SCE1572_7487 | 42.95 | 23.42 |
| SCE1572_7528 | 33.37 | 30.47 |
| SCE1572_6488 | 11.43 | 4.34 |
| SCE1572_7581 | 556.71 | 1523.64 |
| SCE1572_11247 | 22.46 | 16.89 |
| SCE1572_4786 | 338.42 | 4659.99 |
| SCE1572_297 | 48.31 | 28.45 |
| SCE1572_6386 | 31.98 | 9.5 |
| SCE1572_9944 | 3.3 | 0 |
| SCE1572_3357 | 0 | 0 |
| SCE1572_10508 | 74.24 | 352.34 |
| SCE1572_2044 | 3.16 | 0 |
| SCE1572_5255 | 4.67 | 0 |
| SCE1572_4405 | 28.84 | 7.12 |
| SCE1572_4497 | 37.54 | 103.11 |
| SCE1572_6970 | 10.24 | 180 |
| SCE1572_6083 | 38.14 | 9.36 |
| SCE1572_8916 | 28.63 | 130.15 |
| SCE1572_6801 | 35.38 | 28.38 |
| SCE1572_1160 | 23.8 | 12.63 |
| SCE1572_703 | 24.68 | 12.73 |
| SCE1572_658 | 512 | 746.69 |
| SCE1572_3891 | 41.38 | 54.77 |
| SCE1572_9614 | 92.99 | 0 |
| SCE1572_9589 | 32.37 | 74.6 |
| SCE1572_5653 | 54.26 | 331.89 |
| SCE1572_6562 | 18.18 | 15.58 |
| SCE1572_10996 | 36.73 | 18.81 |
| SCE1572_8164 | 16.44 | 17.59 |
| SCE1572_7116 | 62.12 | 129.24 |
| SCE1572_633 | 19.28 | 33.75 |
| SCE1572_6992 | 64.7 | 22.58 |
| SCE1572_5512 | 55.88 | 94.74 |
| SCE1572_1502 | 57.05 | 222.51 |
| SCE1572_145 | 28.24 | 23.25 |
| SCE1572_433 | 41.69 | 32.21 |
| SCE1572_7636 | 363.24 | 7582.13 |
| SCE1572_1909 | 0 | 0 |
| SCE1572_11261 | 131.08 | 57.02 |
| SCE1572_6529 | 31.7 | 33.06 |
| SCE1572_4675 | 22.82 | 16.53 |
| SCE1572_11512 | 364.07 | 1268.22 |
| SCE1572_6191 | 27.4 | 76.94 |
| SCE1572_5454 | 26.22 | 13.72 |
| SCE1572_6379 | 21.05 | 0 |
| SCE1572_8907 | 42.92 | 44.27 |

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| SCE1572_1482 | 51.24 | 21.96 |
| SCE1572_9810 | 28.25 | 34.99 |
| SCE1572_8771 | 0 | 0 |
| SCE1572_9442 | 11.66 | 2.25 |
| SCE1572_4746 | 37.28 | 18.98 |
| SCE1572_4706 | 49.35 | 46.02 |
| SCE1572_11442 | 39.52 | 43.67 |
| SCE1572_9347 | 37.04 | 12.44 |
| SCE1572_4991 | 8.62 | 6.92 |
| SCE1572_3699 | 31.41 | 5.21 |
| SCE1572_4956 | 35.44 | 59.42 |
| SCE1572_7881 | 27.55 | 26.16 |
| SCE1572_2392 | 95.58 | 258.82 |
| SCE1572_8417 | 22.06 | 17.02 |
| SCE1572_6319 | 34.1 | 31.57 |
| SCE1572_8197 | 20.26 | 10.09 |
| SCE1572_10418 | 36.24 | 50.49 |
| SCE1572_10515 | 103.94 | 195.63 |
| SCE1572_4360 | 65.52 | 119.28 |
| SCE1572_8900 | 161.12 | 160.07 |
| SCE1572_8949 | 11.78 | 22.44 |
| SCE1572_9208 | 15.16 | 16.68 |
| SCE1572_527 | 25.64 | 58.18 |
| SCE1572_2191 | 93.5 | 1067.07 |
| SCE1572_7236 | 27.59 | 83.89 |
| SCE1572_366 | 82.15 | 279.72 |
| SCE1572_7615 | 23.92 | 19.02 |
| SCE1572_5493 | 0 | 0 |
| SCE1572_9244 | 7.34 | 0 |
| SCE1572_4756 | 43.85 | 22.89 |
| SCE1572_3258 | 21.41 | 98.83 |
| SCE1572_8621 | 43.59 | 155.84 |
| SCE1572_1347 | 147.92 | 618.88 |
| SCE1572_6545 | 64.6 | 282.42 |
| SCE1572_3973 | 21.78 | 72.58 |
| SCE1572_874 | 160.97 | 78.09 |
| SCE1572_3435 | 52.85 | 69.39 |
| SCE1572_10544 | 15.55 | 3.12 |
| SCE1572_4418 | 19.36 | 15.53 |
| SCE1572_2618 | 0 | 0 |
| SCE1572_732 | 41.71 | 21.98 |
| SCE1572_5028 | 30.13 | 23.65 |
| SCE1572_3336 | 40.48 | 501.97 |
| SCE1572_5055 | 33.72 | 19.83 |
| SCE1572_11503 | 39.74 | 16.08 |
| SCE1572_6659 | 60.16 | 72.39 |
| SCE1572_4969 | 26.76 | 8.59 |
| SCE1572_8161 | 25.72 | 2.77 |

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| SCE1572_10952 | 0 | 0 |
| SCE1572_4633 | 36.23 | 31.22 |
| SCE1572_5749 | 25.45 | 18.71 |
| SCE1572_5678 | 81.32 | 256.66 |
| SCE1572_2652 | 54.9 | 27.67 |
| SCE1572_7229 | 25.81 | 134.42 |
| SCE1572_7105 | 36.87 | 17.04 |
| SCE1572_6520 | 26.12 | 25.83 |
| SCE1572_1768 | 70.5 | 23.28 |
| SCE1572_6860 | 45.56 | 22.92 |
| SCE1572_3239 | 19.12 | 13.15 |
| SCE1572_7215 | 34.9 | 64.32 |
| SCE1572_2622 | 38.57 | 3.2 |
| SCE1572_3088 | 28.64 | 24.33 |
| SCE1572_10855 | 46.34 | 31.76 |
| SCE1572_8845 | 20.67 | 9.33 |
| SCE1572_5306 | 426.08 | 1492.86 |
| SCE1572_9360 | 35.57 | 327.21 |
| SCE1572_278 | 16.69 | 6.7 |
| SCE1572_10036 | 16.74 | 6.72 |
| SCE1572_4164 | 48.26 | 18.77 |
| SCE1572_3242 | 17.27 | 0 |
| SCE1572_1413 | 18.81 | 14.14 |
| SCE1572_8541 | 17.89 | 239.86 |
| SCE1572_5886 | 41.9 | 19.74 |
| SCE1572_1843 | 48.06 | 22.81 |
| SCE1572_8862 | 48.88 | 12 |
| SCE1572_6516 | 11.87 | 2.86 |
| SCE1572_3162 | 47.88 | 151 |
| SCE1572_11169 | 27.74 | 7.03 |
| SCE1572_11019 | 51.47 | 147.31 |
| SCE1572_9160 | 39.51 | 110.53 |
| SCE1572_5205 | 47.96 | 48.97 |
| SCE1572_3871 | 41.52 | 94.32 |
| SCE1572_5020 | 24.36 | 18.32 |
| SCE1572_4232 | 16.8 | 4.49 |
| SCE1572_258 | 40.66 | 61.16 |
| SCE1572_1062 | 120.23 | 14.71 |
| SCE1572_10598 | 0 | 0 |
| SCE1572_9707 | 196.21 | 64.4 |
| SCE1572_7718 | 30.8 | 12.43 |
| SCE1572_10089 | 40.98 | 103.56 |
| SCE1572_10080 | 275.77 | 1102.7 |
| SCE1572_3706 | 58.62 | 47.03 |
| SCE1572_5803 | 21.26 | 24.24 |
| SCE1572_6893 | 25.62 | 11.26 |
| SCE1572_6999 | 57.9 | 7.34 |
| SCE1572_9679 | 144.72 | 484.35 |

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| SCE1572_3513 | 40.06 | 309.94 |
| SCE1572_9856 | 28.93 | 16.81 |
| SCE1572_583 | 19.37 | 68.93 |
| SCE1572_2113 | 54.24 | 50.33 |
| SCE1572_8355 | 39.11 | 15.97 |
| SCE1572_1368 | 37.23 | 75.68 |
| SCE1572_801 | 28.29 | 24.41 |
| SCE1572_7222 | 30.39 | 585.22 |
| SCE1572_7452 | 33.52 | 53.78 |
| SCE1572_2659 | 54.32 | 40.98 |
| SCE1572_3275 | 284.77 | 533.1 |
| SCE1572_7534 | 5.83 | 0 |
| SCE1572_404 | 61.03 | 65.41 |
| SCE1572_10619 | 73.31 | 45.62 |
| SCE1572_3921 | 48.88 | 54.47 |
| SCE1572_4488 | 66.43 | 32.09 |
| SCE1572_5095 | 41.23 | 139.9 |
| SCE1572_8847 | 0 | 0 |
| SCE1572_4835 | 126.98 | 102.63 |
| SCE1572_2724 | 36.85 | 157.02 |
| SCE1572_628 | 15.16 | 28.75 |
| SCE1572_9309 | 0 | 0 |
| SCE1572_6455 | 2.14 | 0 |
| SCE1572_2575 | 25.17 | 12.7 |
| SCE1572_7573 | 30.1 | 224.57 |
| SCE1572_3003 | 18.47 | 57.42 |
| SCE1572_5671 | 60.19 | 31.44 |
| SCE1572_202 | 52.2 | 45.27 |
| SCE1572_3455 | 19.27 | 6.14 |
| SCE1572_11332 | 33.97 | 87.74 |
| SCE1572_7804 | 67.35 | 58.56 |
| SCE1572_10718 | 15.29 | 52.13 |
| SCE1572_4686 | 49.1 | 248.77 |
| SCE1572_4249 | 2.14 | 0 |
| SCE1572_6869 | 22.5 | 15.47 |
| SCE1572_10052 | 28.7 | 84.71 |
| SCE1572_1709 | 56.12 | 42.78 |
| SCE1572_969 | 42.35 | 121.15 |
| SCE1572_5229 | 31.52 | 72.26 |
| SCE1572_5143 | 70.11 | 10.55 |
| SCE1572_1711 | 62.9 | 45.11 |
| SCE1572_7843 | 80.57 | 342.01 |
| SCE1572_10230 | 49.74 | 16.41 |
| SCE1572_6294 | 20.44 | 342.37 |
| SCE1572_3338 | 203.96 | 3041.02 |
| SCE1572_1012 | 37.19 | 5.51 |
| SCE1572_4844 | 37.35 | 68.75 |
| SCE1572_10282 | 35.11 | 126.76 |

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| SCE1572_6288 | 34.18 | 12.66 |
| SCE1572_189 | 48.78 | 57.12 |
| SCE1572_1058 | 5.09 | 2.45 |
| SCE1572_1728 | 54.03 | 32.51 |
| SCE1572_8474 | 14.17 | 13.57 |
| SCE1572_2423 | 127.03 | 355.06 |
| SCE1572_9406 | 21.19 | 51.01 |
| SCE1572_2502 | 0 | 0 |
| SCE1572_6413 | 126.19 | 77.06 |
| SCE1572_5023 | 0 | 0 |
| SCE1572_5220 | 25.82 | 73.38 |
| SCE1572_4411 | 24.52 | 6.89 |
| SCE1572_4015 | 90.58 | 144.57 |
| SCE1572_1094 | 30.72 | 14.47 |
| SCE1572_10263 | 56.94 | 33.46 |
| SCE1572_5869 | 19.33 | 198.38 |
| SCE1572_7228 | 82.13 | 1060.98 |
| SCE1572_9169 | 38.78 | 18.3 |
| SCE1572_651 | 69.16 | 0 |
| SCE1572_198 | 32.06 | 80.28 |
| SCE1572_8376 | 7.64 | 0 |
| SCE1572_5934 | 16.11 | 3.53 |
| SCE1572_5030 | 133.21 | 902.2 |
| SCE1572_11284 | 24.61 | 36.73 |
| SCE1572_11299 | 42.57 | 15.44 |
| SCE1572_9896 | 9.13 | 0 |
| SCE1572_5005 | 42.96 | 0 |
| SCE1572_6878 | 186 | 40.13 |
| SCE1572_10973 | 50.65 | 242.2 |
| SCE1572_5136 | 22.41 | 21.22 |
| SCE1572_5958 | 50.86 | 46.19 |
| SCE1572_459 | 13.04 | 3.92 |
| SCE1572_8758 | 74.79 | 340.31 |
| SCE1572_7972 | 16.44 | 89.4 |
| SCE1572_10646 | 72.64 | 34.69 |
| SCE1572_9661 | 262.85 | 1816.64 |
| SCE1572_5734 | 48.49 | 104.38 |
| SCE1572_3619 | 38.35 | 14.27 |
| SCE1572_10393 | 80.71 | 32.68 |
| SCE1572_1211 | 30.51 | 24.48 |
| SCE1572_86 | 0 | 0 |
| SCE1572_7210 | 4.84 | 1.94 |
| SCE1572_11560 | 45.35 | 24.66 |
| SCE1572_3286 | 27.03 | 16.97 |
| SCE1572_10040 | 28.6 | 40.6 |
| SCE1572_3521 | 52.86 | 60.82 |
| SCE1572_3611 | 23.63 | 24.18 |
| SCE1572_11208 | 84.16 | 135.29 |

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| SCE1572_3545 | 0 | 0 |
| SCE1572_3472 | 37.09 | 7.81 |
| SCE1572_9902 | 21.87 | 24.56 |
| SCE1572_7735 | 536.4 | 3430.82 |
| SCE1572_8529 | 48.51 | 31.46 |
| SCE1572_7764 | 10.24 | 4.93 |
| SCE1572_5218 | 51.52 | 24.8 |
| SCE1572_1547 | 24.63 | 35.2 |
| SCE1572_3390 | 59.33 | 150.73 |
| SCE1572_6109 | 40.43 | 6.49 |
| SCE1572_3202 | 131.4 | 3207.09 |
| SCE1572_7550 | 65.64 | 22.85 |
| SCE1572_5119 | 28.5 | 61.68 |
| SCE1572_11180 | 7.29 | 2.63 |
| SCE1572_6852 | 0 | 0 |
| SCE1572_9921 | 59.69 | 82.86 |
| SCE1572_10245 | 50.26 | 14.11 |
| SCE1572_10707 | 0 | 0 |
| SCE1572_182 | 119.89 | 128.74 |
| SCE1572_7084 | 132.93 | 71.1 |
| SCE1572_9288 | 709.78 | 1088.31 |
| SCE1572_565 | 105.14 | 367.59 |
| SCE1572_8684 | 16.9 | 28.36 |
| SCE1572_5174 | 7.19 | 1.73 |
| SCE1572_6598 | 51.8 | 39.53 |
| SCE1572_9036 | 28.98 | 18.32 |
| SCE1572_354 | 24.5 | 14.74 |
| SCE1572_8789 | 38.24 | 95.29 |
| SCE1572_4433 | 56.42 | 19.4 |
| SCE1572_2202 | 54.73 | 487.75 |
| SCE1572_2051 | 62.4 | 19.76 |
| SCE1572_2519 | 57.96 | 20.49 |
| SCE1572_8808 | 16.77 | 8.77 |
| SCE1572_8126 | 23.66 | 10.17 |
| SCE1572_11395 | 102.3 | 621.39 |
| SCE1572_4291 | 16.9 | 26.73 |
| SCE1572_11162 | 26.27 | 57.97 |
| SCE1572_7847 | 52.97 | 48.36 |
| SCE1572_621 | 36.63 | 22.65 |
| SCE1572_1871 | 49.98 | 48.92 |
| SCE1572_5664 | 13.89 | 29.51 |
| SCE1572_3668 | 41.66 | 18.08 |
| SCE1572_1247 | 26.36 | 7.61 |
| SCE1572_3344 | 102.52 | 356 |
| SCE1572_10570 | 87.74 | 150.83 |
| SCE1572_778 | 30.67 | 41.52 |
| SCE1572_6834 | 0 | 0 |
| SCE1572_10181 | 17.98 | 24.04 |

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| SCE1572_3625 | 46.21 | 13.9 |
| SCE1572_3676 | 117.75 | 183.94 |
| SCE1572_3462 | 1.67 | 72.18 |
| SCE1572_8015 | 18.3 | 229.65 |
| SCE1572_5240 | 7.75 | 23.97 |
| SCE1572_4519 | 34.33 | 214.59 |
| SCE1572_52 | 6.15 | 0 |
| SCE1572_4220 | 31.64 | 38.08 |
| SCE1572_10248 | 52.02 | 21.4 |
| SCE1572_2641 | 65.36 | 57.47 |
| SCE1572_8560 | 32.64 | 22.7 |
| SCE1572_3814 | 53.78 | 66.81 |
| SCE1572_1870 | 5.78 | 1.07 |
| SCE1572_10720 | 43.25 | 17.35 |
| SCE1572_8318 | 9.97 | 4.8 |
| SCE1572_4287 | 25.09 | 7.49 |
| SCE1572_27 | 715.39 | 1257.74 |
| SCE1572_5573 | 39.33 | 21.85 |
| SCE1572_271 | 167.6 | 1088.58 |
| SCE1572_7575 | 48.77 | 115.87 |
| SCE1572_3477 | 0 | 0 |
| SCE1572_10788 | 65.34 | 45.46 |
| SCE1572_7831 | 40.43 | 116.35 |
| SCE1572_6019 | 34.53 | 25.29 |
| SCE1572_8926 | 35.22 | 57.6 |
| SCE1572_10949 | 42.51 | 10.23 |
| SCE1572_6619 | 31.81 | 15.31 |
| SCE1572_4002 | 113.52 | 1573.84 |
| SCE1572_1375 | 43.66 | 43.45 |
| SCE1572_1455 | 61.79 | 36.03 |
| SCE1572_11589 | 15.72 | 24.41 |
| SCE1572_3806 | 26.37 | 0 |
| SCE1572_8656 | 81.86 | 917.16 |
| SCE1572_11546 | 39.03 | 4.32 |
| SCE1572_1548 | 51.71 | 25.11 |
| SCE1572_6700 | 10.13 | 4.48 |
| SCE1572_4268 | 50.25 | 14.6 |
| SCE1572_2899 | 71.26 | 20.72 |
| SCE1572_9243 | 70.24 | 57.13 |
| SCE1572_6640 | 61.97 | 20.64 |
| SCE1572_3939 | 12.16 | 15.49 |
| SCE1572_6596 | 19.42 | 3.9 |
| SCE1572_7541 | 29.11 | 49.63 |
| SCE1572_826 | 40.9 | 12.54 |
| SCE1572_3816 | 0 | 0 |
| SCE1572_3748 | 34.91 | 61.51 |
| SCE1572_5350 | 416.44 | 380.74 |
| SCE1572_7442 | 19.07 | 7.84 |

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| SCE1572_6919 | 39.52 | 29.4 |
| SCE1572_6028 | 22.17 | 157.92 |
| SCE1572_7870 | 71.79 | 77.45 |
| SCE1572_7692 | 120.13 | 199.44 |
| SCE1572_10068 | 254.23 | 1070.29 |
| SCE1572_9887 | 32.75 | 40.69 |
| SCE1572_4132 | 65.46 | 134.18 |
| SCE1572_3136 | 43.16 | 17.31 |
| SCE1572_5594 | 30.74 | 23.83 |
| SCE1572_1393 | 22.3 | 17.89 |
| SCE1572_11191 | 60.58 | 88.67 |
| SCE1572_7697 | 33.04 | 44.5 |
| SCE1572_9746 | 51.04 | 41.91 |
| SCE1572_2483 | 29.42 | 16.34 |
| SCE1572_9880 | 19.19 | 18.48 |
| SCE1572_3058 | 32.22 | 13.68 |
| SCE1572_5360 | 0 | 0 |
| SCE1572_4853 | 20.31 | 8.73 |
| SCE1572_4477 | 45.12 | 12.72 |
| SCE1572_8241 | 24.44 | 91 |
| SCE1572_5922 | 8.78 | 19.21 |
| SCE1572_10321 | 35.18 | 108.87 |
| SCE1572_7701 | 40.05 | 6.89 |
| SCE1572_7504 | 35.24 | 17.61 |
| SCE1572_5322 | 72.65 | 83.63 |
| SCE1572_3839 | 60.97 | 25.97 |
| SCE1572_8727 | 53.45 | 19.25 |
| SCE1572_10878 | 59.1 | 14.43 |
| SCE1572_9496 | 52.1 | 160.52 |
| SCE1572_5410 | 0 | 0 |
| SCE1572_771 | 42.41 | 47.42 |
| SCE1572_9681 | 138.2 | 385.91 |
| SCE1572_7838 | 22.99 | 6.3 |
| SCE1572_3751 | 41.06 | 30.41 |
| SCE1572_6463 | 0 | 0 |
| SCE1572_6330 | 41.89 | 141.37 |
| SCE1572_6320 | 13.31 | 12.46 |
| SCE1572_11550 | 20.87 | 18.51 |
| SCE1572_129 | 5.91 | 0 |
| SCE1572_7099 | 31.42 | 3.29 |
| SCE1572_5918 | 0 | 0 |
| SCE1572_6070 | 10.2 | 21.05 |
| SCE1572_1566 | 23.68 | 8.88 |
| SCE1572_2510 | 51.8 | 54.49 |
| SCE1572_5590 | 67.54 | 22.48 |
| SCE1572_10261 | 97.42 | 91.09 |
| SCE1572_2710 | 37.44 | 21.02 |
| SCE1572_9562 | 11.23 | 0 |

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| SCE1572_7925 | 22.24 | 7.3 |
| SCE1572_350 | 51.23 | 1825.44 |
| SCE1572_6753 | 57.65 | 39.91 |
| SCE1572_8567 | 48.69 | 46.77 |
| SCE1572_4212 | 2.61 | 0 |
| SCE1572_5584 | 37.61 | 15.09 |
| SCE1572_83 | 27.7 | 29.89 |
| SCE1572_3126 | 29.42 | 177.01 |
| SCE1572_4546 | 26.64 | 8.22 |
| SCE1572_9280 | 15.76 | 6.54 |
| SCE1572_2144 | 14.7 | 49.65 |
| SCE1572_7877 | 72.46 | 16.12 |
| SCE1572_11112 | 21.19 | 18.13 |
| SCE1572_5536 | 38.08 | 37 |
| SCE1572_4629 | 56.9 | 136.96 |
| SCE1572_4239 | 80.18 | 354.86 |
| SCE1572_9675 | 38.75 | 92.72 |
| SCE1572_4943 | 74.27 | 430.91 |
| SCE1572_9639 | 0 | 0 |
| SCE1572_9236 | 30.52 | 14.22 |
| SCE1572_2690 | 27.92 | 17.27 |
| SCE1572_9536 | 84.92 | 38.37 |
| SCE1572_4765 | 15.54 | 10.59 |
| SCE1572_1222 | 34.51 | 17.8 |
| SCE1572_6185 | 37.54 | 19.95 |
| SCE1572_1174 | 16.24 | 0 |
| SCE1572_4948 | 20.84 | 12.11 |
| SCE1572_2891 | 8.79 | 0 |
| SCE1572_8890 | 208.85 | 71.16 |
| SCE1572_8668 | 15.96 | 2.4 |
| SCE1572_10820 | 110.27 | 201.42 |
| SCE1572_2878 | 61.3 | 79.05 |
| SCE1572_2056 | 33.22 | 4.51 |
| SCE1572_7258 | 51.03 | 29.52 |
| SCE1572_487 | 59.58 | 74.46 |
| SCE1572_201 | 3.94 | 0 |
| SCE1572_11034 | 109.43 | 1709.33 |
| SCE1572_4620 | 17.96 | 34.33 |
| SCE1572_392 | 60.79 | 7.57 |
| SCE1572_6204 | 30.72 | 64.3 |
| SCE1572_845 | 0 | 0 |
| SCE1572_57 | 67.53 | 20.44 |
| SCE1572_5473 | 14.03 | 22.08 |
| SCE1572_441 | 473.54 | 202.46 |
| SCE1572_7206 | 23.33 | 6.24 |
| SCE1572_5821 | 28.54 | 36.26 |
| SCE1572_5599 | 98.35 | 51.68 |
| SCE1572_4280 | 33.69 | 21.47 |

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| SCE1572_4142 | 0 | 0 |
| SCE1572_30 | 180.68 | 513.49 |
| SCE1572_9216 | 57.78 | 95.37 |
| SCE1572_5900 | 13.65 | 18.77 |
| SCE1572_2316 | 15.56 | 9.55 |
| SCE1572_8546 | 48.24 | 17.56 |
| SCE1572_4035 | 41.44 | 32.85 |
| SCE1572_4566 | 14.01 | 13.8 |
| SCE1572_7285 | 91.83 | 84.95 |
| SCE1572_4659 | 46.98 | 59.62 |
| SCE1572_6695 | 12.86 | 10.67 |
| SCE1572_7588 | 48.77 | 392.72 |
| SCE1572_3693 | 48.48 | 18.7 |
| SCE1572_10959 | 28.77 | 12.22 |
| SCE1572_9959 | 13.81 | 17.68 |
| SCE1572_9932 | 62.98 | 5.61 |
| SCE1572_7641 | 98.47 | 1032.43 |
| SCE1572_11517 | 21.09 | 15.31 |
| SCE1572_9714 | 44.28 | 1401.56 |
| SCE1572_6942 | 35.27 | 16.69 |
| SCE1572_763 | 41.35 | 21.11 |
| SCE1572_9828 | 34.13 | 19.95 |
| SCE1572_3221 | 42.29 | 105.64 |
| SCE1572_11381 | 18.89 | 46.59 |
| SCE1572_6166 | 58.27 | 196.07 |
| SCE1572_10999 | 58.48 | 5.21 |
| SCE1572_1266 | 927.38 | 11063.23 |
| SCE1572_8247 | 29.5 | 16.51 |
| SCE1572_7600 | 52.75 | 79.76 |
| SCE1572_11321 | 32.25 | 24.51 |
| SCE1572_4077 | 25.27 | 72.59 |
| SCE1572_2870 | 16.03 | 8.04 |
| SCE1572_8362 | 0 | 0 |
| SCE1572_10940 | 22.4 | 13.82 |
| SCE1572_951 | 111.57 | 158.36 |
| SCE1572_10832 | 50.05 | 283.05 |
| SCE1572_1389 | 20.34 | 233.18 |
| SCE1572_2542 | 71.92 | 9.36 |
| SCE1572_9514 | 90.97 | 724.5 |
| SCE1572_3304 | 8.16 | 5.61 |
| SCE1572_3912 | 11.43 | 33.01 |
| SCE1572_1370 | 60.98 | 220.16 |
| SCE1572_4295 | 38.41 | 14.6 |
| SCE1572_10566 | 60.38 | 26.35 |
| SCE1572_8421 | 23.87 | 28.72 |
| SCE1572_1080 | 28.02 | 20.75 |
| SCE1572_5339 | 45.75 | 31.46 |
| SCE1572_4656 | 25.39 | 69.84 |

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| SCE1572_3040 | 22.31 | 10.07 |
| SCE1572_10227 | 29.71 | 9.86 |
| SCE1572_7147 | 39.36 | 109.8 |
| SCE1572_6168 | 14.53 | 17.02 |
| SCE1572_1674 | 90.97 | 257.27 |
| SCE1572_8000 | 57.69 | 25.84 |
| SCE1572_6925 | 12.06 | 8.29 |
| SCE1572_11373 | 121.19 | 754.67 |
| SCE1572_10654 | 33.06 | 212.19 |
| SCE1572_11526 | 84.61 | 31.44 |
| SCE1572_9522 | 7.29 | 3.51 |
| SCE1572_3414 | 87.28 | 128.66 |
| SCE1572_1896 | 0 | 0 |
| SCE1572_4602 | 35.91 | 103.23 |
| SCE1572_6798 | 27.52 | 30.22 |
| SCE1572_4080 | 37.73 | 206 |
| SCE1572_4046 | 0 | 0 |
| SCE1572_5246 | 305.03 | 1077.49 |
| SCE1572_3212 | 18.4 | 30.11 |
| SCE1572_4694 | 32.58 | 30.41 |
| SCE1572_7983 | 168.22 | 209.1 |
| SCE1572_6665 | 31.31 | 141.8 |
| SCE1572_5568 | 18.12 | 15.17 |
| SCE1572_3144 | 15.16 | 2.81 |
| SCE1572_1125 | 54.28 | 19.71 |
| SCE1572_8778 | 41.17 | 16.32 |
| SCE1572_2334 | 0 | 0 |
| SCE1572_518 | 0 | 0 |
| SCE1572_10208 | 37.04 | 16.08 |
| SCE1572_7369 | 8.29 | 2.85 |
| SCE1572_10494 | 61.94 | 490.61 |
| SCE1572_9621 | 35.79 | 16.25 |
| SCE1572_8071 | 62.8 | 38.87 |
| SCE1572_4448 | 22.13 | 10.65 |
| SCE1572_6161 | 39.63 | 21.77 |
| SCE1572_4937 | 33.57 | 80.8 |
| SCE1572_8953 | 28.74 | 9.15 |
| SCE1572_5974 | 0 | 0 |
| SCE1572_5370 | 0 | 0 |
| SCE1572_3855 | 45.53 | 26.5 |
| SCE1572_3029 | 17.27 | 0 |
| SCE1572_9805 | 27.09 | 18.49 |
| SCE1572_10892 | 30.68 | 74.46 |
| SCE1572_2766 | 79.86 | 68.25 |
| SCE1572_11187 | 5.23 | 3.15 |
| SCE1572_10505 | 47.44 | 21.19 |
| SCE1572_1289 | 0 | 0 |
| SCE1572_1035 | 28.57 | 22.74 |

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| SCE1572_6310 | 25.43 | 302.53 |
| SCE1572_5179 | 5.86 | 94.76 |
| SCE1572_2537 | 8.14 | 24.92 |
| SCE1572_6910 | 43.03 | 15.26 |
| SCE1572_3403 | 17.15 | 42.62 |
| SCE1572_5182 | 12.9 | 432.21 |
| SCE1572_9377 | 14.73 | 16.25 |
| SCE1572_6223 | 29.64 | 16.46 |
| SCE1572_6314 | 17.18 | 0 |
| SCE1572_7551 | 106.22 | 86.59 |
| SCE1572_5715 | 42.15 | 39.37 |
| SCE1572_3608 | 73.85 | 858.83 |
| SCE1572_8766 | 48.27 | 16.42 |
| SCE1572_5000 | 100.39 | 118.35 |
| SCE1572_10593 | 3.09 | 0 |
| SCE1572_8597 | 56.63 | 18.53 |
| SCE1572_3179 | 38.12 | 6.19 |
| SCE1572_3 | 101.32 | 282.07 |
| SCE1572_1100 | 40.98 | 58.08 |
| SCE1572_11340 | 29.9 | 11.36 |
| SCE1572_8296 | 22.74 | 68.01 |
| SCE1572_389 | 11.03 | 8.29 |
| SCE1572_381 | 40.53 | 10.84 |
| SCE1572_11253 | 93.61 | 1304.73 |
| SCE1572_2597 | 1.63 | 10.47 |
| SCE1572_9019 | 4.8 | 3.85 |
| SCE1572_4089 | 33.56 | 93.78 |
| SCE1572_3529 | 83.35 | 823.04 |
| SCE1572_4481 | 36.81 | 10.49 |
| SCE1572_2321 | 79.47 | 420.29 |
| SCE1572_9332 | 0 | 0 |
| SCE1572_10122 | 62.4 | 22.32 |
| SCE1572_6896 | 55.77 | 202.01 |
| SCE1572_3372 | 23.57 | 34.71 |
| SCE1572_3247 | 67.38 | 238.6 |
| SCE1572_10434 | 49.09 | 48.06 |
| SCE1572_10137 | 43.74 | 19.09 |
| SCE1572_9031 | 58.11 | 40.29 |
| SCE1572_7481 | 31.01 | 0 |
| SCE1572_9653 | 64.68 | 22.86 |
| SCE1572_7057 | 29.58 | 0 |
| SCE1572_10190 | 67.21 | 194.73 |
| SCE1572_11014 | 53.86 | 33.82 |
| SCE1572_130 | 42.4 | 15.41 |
| SCE1572_2927 | 25.07 | 5.75 |
| SCE1572_215 | 41.63 | 33.75 |
| SCE1572_7903 | 9.72 | 11.7 |
| SCE1572_5295 | 15.38 | 3.53 |

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| SCE1572_8261 | 78.55 | 334.15 |
| SCE1572_8648 | 54.93 | 8.26 |
| SCE1572_6591 | 32.37 | 14.27 |
| SCE1572_191 | 44.61 | 21.41 |
| SCE1572_9062 | 53.07 | 29.86 |
| SCE1572_10663 | 86.64 | 130.69 |
| SCE1572_4467 | 21.72 | 6.54 |
| SCE1572_4201 | 21.32 | 19.96 |
| SCE1572_7106 | 19.78 | 7.93 |
| SCE1572_11226 | 42.92 | 21.47 |
| SCE1572_9212 | 42.33 | 54.06 |
| SCE1572_483 | 20.43 | 12.29 |
| SCE1572_3536 | 19.98 | 5.66 |
| SCE1572_2471 | 19.48 | 5.7 |
| SCE1572_2431 | 72.15 | 542.99 |
| SCE1572_1981 | 0 | 0 |
| SCE1572_3743 | 20.86 | 24.49 |
| SCE1572_1737 | 40.01 | 15.21 |
| SCE1572_8103 | 28.7 | 38.97 |
| SCE1572_5541 | 40.95 | 159.39 |
| SCE1572_10124 | 123.56 | 47.4 |
| SCE1572_9576 | 30.99 | 7.99 |
| SCE1572_4814 | 176.18 | 476.43 |
| SCE1572_287 | 40.99 | 61.22 |
| SCE1572_939 | 34.52 | 13.71 |
| SCE1572_10096 | 38.39 | 95.98 |
| SCE1572_5471 | 40.06 | 17.02 |
| SCE1572_3832 | 31.79 | 98.1 |
| SCE1572_3170 | 39.34 | 90.43 |
| SCE1572_2094 | 17.08 | 33.41 |
| SCE1572_7854 | 27.44 | 66.05 |
| SCE1572_10582 | 12.4 | 13.27 |
| SCE1572_9196 | 47.08 | 21.13 |
| SCE1572_6709 | 43.7 | 88.01 |
| SCE1572_4933 | 37.9 | 136.85 |
| SCE1572_11276 | 59.64 | 31.63 |
| SCE1572_8615 | 47.05 | 35.46 |
| SCE1572_5393 | 155.3 | 73.49 |
| SCE1572_5405 | 11.72 | 19.39 |
| SCE1572_10589 | 16.85 | 4.51 |
| SCE1572_2451 | 0 | 0 |
| SCE1572_8320 | 10.46 | 16.78 |
| SCE1572_1091 | 53.2 | 10.47 |
| SCE1572_5467 | 41.45 | 16.18 |
| SCE1572_7463 | 87.23 | 322.93 |
| SCE1572_11039 | 27.46 | 22.26 |
| SCE1572_7653 | 14.56 | 16.49 |
| SCE1572_641 | 54.05 | 87.26 |

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| SCE1572_5148 | 31.43 | 2.97 |
| SCE1572_10288 | 90.25 | 70.3 |
| SCE1572_9654 | 24.51 | 7.51 |
| SCE1572_10579 | 26.5 | 7.09 |
| SCE1572_578 | 5.27 | 0 |
| SCE1572_8086 | 19.22 | 0 |
| SCE1572_711 | 67.27 | 313.52 |
| SCE1572_6873 | 46.1 | 368.62 |
| SCE1572_3209 | 43.38 | 41.77 |
| SCE1572_3922 | 46.36 | 21.11 |
| SCE1572_9978 | 42.06 | 6.25 |
| SCE1572_7478 | 58.22 | 163.49 |
| SCE1572_11264 | 33.81 | 118.35 |
| SCE1572_5499 | 18.99 | 5.9 |
| SCE1572_7404 | 8.75 | 152.99 |
| SCE1572_6332 | 65.51 | 40.69 |
| SCE1572_1334 | 6.05 | 0 |
| SCE1572_3315 | 21.08 | 37.08 |
| SCE1572_7994 | 58.31 | 0 |
| SCE1572_6977 | 8.01 | 0 |
| SCE1572_7278 | 28.03 | 9.2 |
| SCE1572_11421 | 38.79 | 40.46 |
| SCE1572_11450 | 35.09 | 60.43 |
| SCE1572_9619 | 76.64 | 46.17 |
| SCE1572_6744 | 15.47 | 2.98 |
| SCE1572_7390 | 14.47 | 13.63 |
| SCE1572_3313 | 33.69 | 10.46 |
| SCE1572_11234 | 20.73 | 9.78 |
| SCE1572_11398 | 47.64 | 267.36 |
| SCE1572_3609 | 26.52 | 6.01 |
| SCE1572_7167 | 0 | 0 |
| SCE1572_5902 | 53.57 | 15.27 |
| SCE1572_10184 | 13.78 | 64.4 |
| SCE1572_6649 | 80.37 | 4.4 |
| SCE1572_3427 | 43.07 | 35.72 |
| SCE1572_8532 | 36.65 | 0 |
| SCE1572_6125 | 21.28 | 61.46 |
| SCE1572_8938 | 10.83 | 19.55 |
| SCE1572_4767 | 109.93 | 195 |
| SCE1572_1234 | 16.73 | 7.43 |
| SCE1572_10344 | 799.46 | 6126.12 |
| SCE1572_10932 | 21.03 | 37.97 |
| SCE1572_7134 | 46.24 | 20.7 |
| SCE1572_543 | 24.45 | 16.05 |
| SCE1572_8986 | 2.33 | 0 |
| SCE1572_8489 | 83.46 | 97.47 |
| SCE1572_997 | 18.55 | 24.24 |
| SCE1572_9488 | 55.13 | 70.63 |

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| SCE1572_10993 | 0 | 0 |
| SCE1572_9594 | 22.55 | 445.76 |
| SCE1572_3883 | 20.73 | 12.48 |
| SCE1572_9994 | 82.56 | 29.47 |
| SCE1572_11081 | 36.86 | 134.86 |
| SCE1572_769 | 31.19 | 8.34 |
| SCE1572_594 | 15.01 | 3.61 |
| SCE1572_7655 | 23.55 | 8.86 |
| SCE1572_7399 | 21.46 | 26.66 |
| SCE1572_127 | 28.1 | 15.73 |
| SCE1572_1979 | 1404.97 | 4309.83 |
| SCE1572_6129 | 152.42 | 390.44 |
| SCE1572_265 | 42.06 | 21.69 |
| SCE1572_6030 | 21.46 | 19.78 |
| SCE1572_1946 | 47.43 | 31.19 |
| SCE1572_1436 | 31.08 | 18.13 |
| SCE1572_992 | 128.55 | 262.62 |
| SCE1572_891 | 34.1 | 84.65 |
| SCE1572_7262 | 31.35 | 32.05 |
| SCE1572_10310 | 11.22 | 6.14 |
| SCE1572_9761 | 10.66 | 19.96 |
| SCE1572_6003 | 52 | 726.83 |
| SCE1572_6242 | 18.57 | 13.68 |
| SCE1572_7526 | 0 | 0 |
| SCE1572_5928 | 68.16 | 73.65 |
| SCE1572_11303 | 33.06 | 33.66 |
| SCE1572_413 | 27.92 | 11.77 |
| SCE1572_1641 | 53.22 | 16.92 |
| SCE1572_2061 | 27.24 | 15.3 |
| SCE1572_7240 | 50.69 | 83.13 |
| SCE1572_9710 | 52.88 | 132.13 |
| SCE1572_7050 | 0 | 0 |
| SCE1572_2769 | 17.44 | 16.32 |
| SCE1572_760 | 1124.53 | 486.8 |
| SCE1572_311 | 27.44 | 24.48 |
| SCE1572_10401 | 34.42 | 74.96 |
| SCE1572_9201 | 63.17 | 25.73 |
| SCE1572_11401 | 46.78 | 25.23 |
| SCE1572_6779 | 9.17 | 6.79 |
| SCE1572_7985 | 32.95 | 72.69 |
| SCE1572_4812 | 64.32 | 60.82 |
| SCE1572_4155 | 17.71 | 51.94 |
| SCE1572_2358 | 65.87 | 95.63 |
| SCE1572_8550 | 38.45 | 117.3 |
| SCE1572_807 | 49.35 | 39.19 |
| SCE1572_9738 | 30.86 | 6.4 |
| SCE1572_8444 | 24.68 | 19.09 |
| SCE1572_2745 | 31.88 | 70.82 |

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| SCE1572_4334 | 28.57 | 7.93 |
| SCE1572_4191 | 36.01 | 39.6 |
| SCE1572_5248 | 26.34 | 53.43 |
| SCE1572_3195 | 53.86 | 0 |
| SCE1572_10492 | 63.37 | 229.77 |
| SCE1572_9528 | 97.7 | 184.03 |
| SCE1572_10296 | 221.97 | 4072.53 |
| SCE1572_1469 | 6.52 | 11.77 |
| SCE1572_11108 | 34.93 | 36.32 |
| SCE1572_10211 | 47.62 | 40.94 |
| SCE1572_6176 | 95.09 | 146.22 |
| SCE1572_8250 | 57.96 | 125.08 |
| SCE1572_8777 | 29.56 | 22.4 |
| SCE1572_3502 | 37.77 | 39.52 |
| SCE1572_9683 | 51.04 | 270.98 |
| SCE1572_2219 | 0 | 0 |
| SCE1572_10483 | 47.77 | 31.66 |
| SCE1572_5786 | 40.58 | 39.71 |
| SCE1572_7447 | 3.53 | 0 |
| SCE1572_10272 | 43.65 | 509.6 |
| SCE1572_1596 | 55.02 | 8.83 |
| SCE1572_9116 | 97.72 | 297.03 |
| SCE1572_6500 | 29.83 | 59.82 |
| SCE1572_3302 | 101.08 | 121.03 |
| SCE1572_9358 | 39.7 | 110.8 |
| SCE1572_7955 | 41.86 | 71.86 |
| SCE1572_7171 | 29.42 | 0 |
| SCE1572_1807 | 12.92 | 37.84 |
| SCE1572_105 | 36.48 | 0 |
| SCE1572_1756 | 7.13 | 0 |
| SCE1572_11477 | 41.78 | 8.69 |
| SCE1572_494 | 41.86 | 12.71 |
| SCE1572_6346 | 20.1 | 25.24 |
| SCE1572_7313 | 39.98 | 23.87 |
| SCE1572_1293 | 19.98 | 11.03 |
| SCE1572_2688 | 12.88 | 19.73 |
| SCE1572_9911 | 24.87 | 17.27 |
| SCE1572_5190 | 59.69 | 189.8 |
| SCE1572_10507 | 129.96 | 186.81 |
| SCE1572_5266 | 33.47 | 107.11 |
| SCE1572_8701 | 24.2 | 30.75 |
| SCE1572_11210 | 61.77 | 29.73 |
| SCE1572_7269 | 202.72 | 1120.45 |
| SCE1572_4506 | 34.52 | 13.03 |
| SCE1572_7009 | 73.58 | 24.82 |
| SCE1572_9754 | 21.37 | 28.57 |
| SCE1572_529 | 10.03 | 0 |
| SCE1572_10361 | 25.84 | 901.94 |

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| SCE1572_10256 | 58.8 | 24.26 |
| SCE1572_8571 | 15.59 | 6.82 |
| SCE1572_2843 | 7.82 | 7.52 |
| SCE1572_11203 | 34.57 | 62.4 |
| SCE1572_677 | 48.25 | 27.72 |
| SCE1572_9640 | 541.37 | 1262.76 |
| SCE1572_5508 | 1.64 | 0 |
| SCE1572_8228 | 21.24 | 6.1 |
| SCE1572_9462 | 22.42 | 43.9 |
| SCE1572_3950 | 0 | 0 |
| SCE1572_1201 | 37.9 | 15.46 |
| SCE1572_11085 | 52.67 | 138.29 |
| SCE1572_1773 | 0 | 0 |
| SCE1572_9068 | 16.44 | 16.95 |
| SCE1572_721 | 46.73 | 34.03 |
| SCE1572_1811 | 34.33 | 24.59 |
| SCE1572_5554 | 89.53 | 92.97 |
| SCE1572_3666 | 41.47 | 3.27 |
| SCE1572_7163 | 49.59 | 80.71 |
| SCE1572_10533 | 36.23 | 81.84 |
| SCE1572_4583 | 0 | 0 |
| SCE1572_2681 | 95.6 | 16.22 |
| SCE1572_10353 | 2042.3 | 2793.71 |
| SCE1572_9061 | 26.72 | 13.74 |
| SCE1572_2907 | 53.07 | 549.04 |
| SCE1572_208 | 10.64 | 3.2 |
| SCE1572_6667 | 100.73 | 100.2 |
| SCE1572_6091 | 31.59 | 8.69 |
| SCE1572_11278 | 19.69 | 0 |
| SCE1572_909 | 66.44 | 32.63 |
| SCE1572_9352 | 29.96 | 175.1 |
| SCE1572_3711 | 91.96 | 0 |
| SCE1572_2182 | 13.69 | 6.34 |
| SCE1572_4111 | 31.52 | 9.03 |
| SCE1572_9379 | 15.36 | 5.55 |
| SCE1572_4591 | 13.87 | 13.35 |
| SCE1572_7188 | 43.75 | 113.48 |
| SCE1572_3725 | 261.64 | 4918.72 |
| SCE1572_2282 | 30.94 | 74.47 |
| SCE1572_6761 | 6.08 | 5.57 |
| SCE1572_1732 | 48.75 | 28.37 |
| SCE1572_7905 | 62.26 | 22.92 |
| SCE1572_3717 | 65.33 | 89.4 |
| SCE1572_2524 | 26.01 | 27.97 |
| SCE1572_8294 | 35.26 | 30.55 |
| SCE1572_4533 | 23.11 | 5.85 |
| SCE1572_10665 | 71.07 | 323.58 |
| SCE1572_14 | 23.39 | 24.5 |

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| SCE1572_5578 | 22.74 | 0 |
| SCE1572_9847 | 22 | 11.07 |
| SCE1572_10377 | 57.59 | 12.73 |
| SCE1572_9556 | 28.36 | 60.7 |
| SCE1572_1473 | 45.62 | 21.53 |
| SCE1572_11281 | 20.36 | 5.17 |
| SCE1572_361 | 3.99 | 0 |
| SCE1572_6749 | 10.7 | 4.29 |
| SCE1572_3443 | 30.99 | 6.05 |
| SCE1572_6552 | 0 | 0 |
| SCE1572_4369 | 54.58 | 92.45 |
| SCE1572_5603 | 37.43 | 58.02 |
| SCE1572_2066 | 70 | 59.73 |
| SCE1572_4568 | 12.78 | 2.12 |
| SCE1572_10094 | 59.65 | 0 |
| SCE1572_900 | 40.61 | 22.51 |
| SCE1572_4871 | 31.59 | 30.41 |
| SCE1572_10177 | 44.07 | 140.03 |
| SCE1572_7046 | 12.63 | 7.6 |
| SCE1572_1854 | 0 | 0 |
| SCE1572_8528 | 48.15 | 82.05 |
| SCE1572_8280 | 13.21 | 3.61 |
| SCE1572_5700 | 7.43 | 0 |
| SCE1572_5199 | 50.54 | 48.38 |
| SCE1572_4364 | 49.52 | 19.98 |
| SCE1572_2949 | 13.96 | 0 |
| SCE1572_11079 | 178.17 | 1896.77 |
| SCE1572_1182 | 0 | 0 |
| SCE1572_7820 | 108.69 | 525.8 |
| SCE1572_11286 | 59.68 | 126.45 |
| SCE1572_5636 | 30.51 | 71.15 |
| SCE1572_561 | 109.44 | 966.68 |
| SCE1572_10396 | 16.32 | 14.73 |
| SCE1572_1280 | 61.33 | 19.68 |
| SCE1572_9521 | 0 | 0 |
| SCE1572_11552 | 46.52 | 24.88 |
| SCE1572_4920 | 30.8 | 5.7 |
| SCE1572_6984 | 13.54 | 13.03 |
| SCE1572_8267 | 71.32 | 85.34 |
| SCE1572_7722 | 117.43 | 110.91 |
| SCE1572_10926 | 0 | 0 |
| SCE1572_10919 | 20.22 | 14.31 |
| SCE1572_5662 | 14.15 | 34.06 |
| SCE1572_556 | 13.24 | 4.78 |
| SCE1572_11245 | 33.28 | 14.83 |
| SCE1572_820 | 60.94 | 60.82 |
| SCE1572_911 | 20.83 | 15.16 |
| SCE1572_7259 | 0 | 0 |

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| SCE1572_5811 | 31.07 | 18.81 |
| SCE1572_1902 | 108.97 | 32.87 |
| SCE1572_1072 | 21.35 | 9.12 |
| SCE1572_989 | 63.36 | 155.23 |
| SCE1572_9543 | 46.16 | 19.46 |
| SCE1572_3959 | 9.72 | 6.18 |
| SCE1572_8238 | 63.33 | 465.39 |
| SCE1572_2552 | 28.22 | 30.51 |
| SCE1572_1529 | 17.12 | 13.96 |
| SCE1572_10829 | 31.15 | 15 |
| SCE1572_8221 | 25.7 | 7.17 |
| SCE1572_3640 | 14.33 | 99.85 |
| SCE1572_6613 | 65.56 | 45.37 |
| SCE1572_11154 | 50.54 | 129.75 |
| SCE1572_4916 | 50.44 | 479.74 |
| SCE1572_280 | 61.97 | 31.86 |
| SCE1572_4893 | 57.76 | 57.92 |
| SCE1572_3086 | 49.38 | 15.07 |
| SCE1572_10942 | 138.01 | 60.15 |
| SCE1572_5113 | 5.67 | 6.21 |
| SCE1572_9800 | 36.12 | 28.7 |
| SCE1572_5769 | 331.14 | 2884.68 |
| SCE1572_2675 | 15.98 | 100.17 |
| SCE1572_2246 | 38.51 | 38.72 |
| SCE1572_5313 | 20.67 | 9.22 |
| SCE1572_1079 | 0 | 0 |
| SCE1572_237 | 97.14 | 30.59 |
| SCE1572_6783 | 13.55 | 53.01 |
| SCE1572_3013 | 21.39 | 22.39 |
| SCE1572_2925 | 60.98 | 31.64 |
| SCE1572_6057 | 116.06 | 271.8 |
| SCE1572_5387 | 36.41 | 52.44 |
| SCE1572_9719 | 32.07 | 445.63 |
| SCE1572_3905 | 124.23 | 675.19 |
| SCE1572_1554 | 71.37 | 42.02 |
| SCE1572_7750 | 31.82 | 4.51 |
| SCE1572_10742 | 46.97 | 33.58 |
| SCE1572_8964 | 41.59 | 82.35 |
| SCE1572_5672 | 0 | 0 |
| SCE1572_4792 | 25.27 | 4.05 |
| SCE1572_8289 | 21.35 | 28.27 |
| SCE1572_11357 | 50.54 | 26.44 |
| SCE1572_10800 | 28.74 | 30.05 |
| SCE1572_8860 | 40.64 | 11.29 |
| SCE1572_8490 | 17.33 | 39.39 |
| SCE1572_1325 | 32.82 | 7.52 |
| SCE1572_5216 | 17.43 | 40.55 |
| SCE1572_4308 | 0 | 0 |

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| SCE1572_2772 | 11.06 | 7.6 |
| SCE1572_8720 | 10.16 | 10.19 |
| SCE1572_3369 | 90.91 | 197.47 |
| SCE1572_9137 | 13.54 | 16.29 |
| SCE1572_5709 | 33.69 | 45.75 |
| SCE1572_243 | 10.91 | 2.63 |
| SCE1572_3226 | 53.58 | 20.52 |
| SCE1572_11056 | 8.25 | 24.82 |
| SCE1572_5548 | 32.72 | 13.31 |
| SCE1572_2821 | 100.94 | 87.13 |
| SCE1572_390 | 35.28 | 13.77 |
| SCE1572_5538 | 45.25 | 60.51 |
| SCE1572_5500 | 44.92 | 25.68 |
| SCE1572_6469 | 31.18 | 7.5 |
| SCE1572_2233 | 12.78 | 9.38 |
| SCE1572_10157 | 27.34 | 42.54 |
| SCE1572_616 | 33.78 | 125.55 |
| SCE1572_8797 | 64.18 | 14.6 |
| SCE1572_3270 | 25.2 | 172.86 |
| SCE1572_7969 | 8.52 | 2.05 |
| SCE1572_8257 | 65.49 | 183.32 |
| SCE1572_8831 | 110.81 | 386.13 |
| SCE1572_8665 | 42.36 | 16.1 |
| SCE1572_669 | 28.94 | 17.86 |
| SCE1572_5792 | 19.88 | 37.89 |
| SCE1572_4820 | 27.51 | 33.11 |
| SCE1572_9075 | 37.68 | 14.28 |
| SCE1572_8341 | 29.16 | 24.56 |
| SCE1572_4869 | 11.72 | 16.93 |
| SCE1572_8729 | 11.54 | 15.87 |
| SCE1572_2137 | 29.11 | 16.54 |
| SCE1572_4544 | 38.12 | 31.28 |
| SCE1572_2415 | 65.83 | 14.4 |
| SCE1572_8699 | 44.46 | 21.4 |
| SCE1572_5648 | 33.92 | 15.83 |
| SCE1572_10813 | 38.93 | 54.25 |
| SCE1572_9351 | 329.55 | 1299.85 |
| SCE1572_439 | 251.3 | 56.14 |
| SCE1572_2912 | 42.5 | 13.66 |
| SCE1572_9411 | 55.31 | 295.59 |
| SCE1572_3051 | 32.87 | 1.61 |
| SCE1572_7699 | 17.84 | 15.74 |
| SCE1572_8124 | 50.82 | 30.58 |
| SCE1572_1919 | 45.36 | 34.37 |
| SCE1572_2857 | 24.64 | 6.84 |
| SCE1572_6772 | 15.47 | 0 |
| SCE1572_5995 | 67.97 | 58.72 |
| SCE1572_4181 | 12.95 | 14.79 |

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| SCE1572_8499 | 19.89 | 7.68 |
| SCE1572_4550 | 40.18 | 14.63 |
| SCE1572_11534 | 34.82 | 13.52 |
| SCE1572_1824 | 22.31 | 33.84 |
| SCE1572_4744 | 14.3 | 192.79 |
| SCE1572_1829 | 236.36 | 860.14 |
| SCE1572_10078 | 415.02 | 971.06 |
| SCE1572_2402 | 29.71 | 120.82 |
| SCE1572_5879 | 16.67 | 5.2 |
| SCE1572_5920 | 28.61 | 62.54 |
| SCE1572_3092 | 66.33 | 0 |
| SCE1572_9458 | 60.29 | 70.42 |
| SCE1572_5625 | 3.39 | 4.08 |
| SCE1572_5273 | 9.6 | 4.62 |
| SCE1572_10523 | 41.96 | 4.59 |
| SCE1572_9469 | 104.21 | 188.11 |
| SCE1572_8740 | 35.64 | 22.96 |
| SCE1572_7115 | 24.5 | 4.91 |
| SCE1572_5846 | 14.82 | 29.72 |
| SCE1572_6638 | 36.27 | 17.72 |
| SCE1572_507 | 41.16 | 13.21 |
| SCE1572_4570 | 40.28 | 16.62 |
| SCE1572_8738 | 52.88 | 40.55 |
| SCE1572_9124 | 29.56 | 20.92 |
| SCE1572_9699 | 29.32 | 23.15 |
| SCE1572_140 | 10.11 | 8.69 |
| SCE1572_7733 | 38.88 | 188.31 |
| SCE1572_8886 | 26.66 | 10.15 |
| SCE1572_11436 | 67.93 | 66.58 |
| SCE1572_7629 | 27.52 | 82.45 |
| SCE1572_6187 | 72.78 | 87.58 |
| SCE1572_6151 | 22.52 | 4.54 |
| SCE1572_8888 | 7.86 | 3.15 |
| SCE1572_6608 | 16.85 | 62.66 |
| SCE1572_5352 | 68.61 | 156.6 |
| SCE1572_2672 | 44.9 | 58.95 |
| SCE1572_10107 | 156.98 | 939.76 |
| SCE1572_2381 | 54.98 | 165.57 |
| SCE1572_3850 | 28.43 | 76.57 |
| SCE1572_9076 | 36.98 | 19.07 |
| SCE1572_11040 | 57.07 | 42.98 |
| SCE1572_2719 | 39.73 | 27.68 |
| SCE1572_10385 | 18.38 | 6.45 |
| SCE1572_9885 | 33.97 | 58.06 |
| SCE1572_1778 | 39.63 | 22.71 |
| SCE1572_864 | 122.32 | 204.5 |
| SCE1572_6147 | 21.87 | 7.26 |
| SCE1572_7729 | 49.13 | 121.64 |

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| SCE1572_4512 | 0 | 0 |
| SCE1572_6564 | 0 | 0 |
| SCE1572_6116 | 50.28 | 19.96 |
| SCE1572_3043 | 0 | 0 |
| SCE1572_7023 | 0 | 0 |
| SCE1572_150 | 28.57 | 20.32 |
| SCE1572_9312 | 110.5 | 168.54 |
| SCE1572_9151 | 32.05 | 11.87 |
| SCE1572_1613 | 533.81 | 129.24 |
| SCE1572_6031 | 41.3 | 40.7 |
| SCE1572_2668 | 16.36 | 26.25 |
| SCE1572_3698 | 42.28 | 42.11 |
| SCE1572_2125 | 46.4 | 25.61 |
| SCE1572_2150 | 21.06 | 4.34 |
| SCE1572_9301 | 36.03 | 177.04 |
| SCE1572_4754 | 49.44 | 70.52 |
| SCE1572_6506 | 2.81 | 0 |
| SCE1572_10499 | 22.39 | 484.93 |
| SCE1572_4577 | 16.91 | 7.72 |
| SCE1572_4356 | 24.92 | 20 |
| SCE1572_2704 | 75.81 | 268.33 |
| SCE1572_9604 | 10.34 | 1.46 |
| SCE1572_2155 | 41.17 | 23.36 |
| SCE1572_2958 | 74.34 | 49.01 |
| SCE1572_8378 | 23.87 | 36.41 |
| SCE1572_5429 | 46.59 | 90.72 |
| SCE1572_1626 | 35.7 | 95.97 |
| SCE1572_2275 | 126.99 | 825.49 |
| SCE1572_4121 | 81.38 | 220.09 |
| SCE1572_2397 | 56.6 | 1771.09 |
| SCE1572_7065 | 60.65 | 59.14 |
| SCE1572_893 | 35.41 | 72.11 |
| SCE1572_4104 | 43.44 | 11.84 |
| SCE1572_9819 | 54.25 | 16.74 |
| SCE1572_1273 | 30.51 | 17.12 |
| SCE1572_3453 | 31.42 | 13.7 |
| SCE1572_11179 | 29.57 | 34.83 |
| SCE1572_5380 | 15.04 | 4.22 |
| SCE1572_1744 | 56.05 | 62.26 |
| SCE1572_1758 | 67.02 | 20.33 |
| SCE1572_2412 | 21.35 | 13.19 |
| SCE1572_8135 | 20.71 | 6.15 |
| SCE1572_60 | 47.34 | 39.29 |
| SCE1572_9048 | 8.27 | 9.95 |
| SCE1572_8925 | 1.26 | 0 |
| SCE1572_6917 | 21.79 | 31.93 |
| SCE1572_1783 | 59.82 | 141.5 |
| SCE1572_8472 | 32.36 | 875.53 |

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| SCE1572_3343 | 140.48 | 330.66 |
| SCE1572_1237 | 14.59 | 15.42 |
| SCE1572_2425 | 164.33 | 310.57 |
| SCE1572_1937 | 2.53 | 0 |
| SCE1572_8467 | 33.14 | 8.49 |
| SCE1572_1017 | 20.79 | 402.46 |
| SCE1572_5168 | 48.05 | 135.6 |
| SCE1572_5090 | 36.73 | 52.13 |
| SCE1572_6021 | 76.83 | 101.09 |
| SCE1572_7293 | 0 | 0 |
| SCE1572_9772 | 28.04 | 72.48 |
| SCE1572_4527 | 58.73 | 208.21 |
| SCE1572_4862 | 3.32 | 0 |
| SCE1572_10366 | 44.14 | 9.24 |
| SCE1572_3971 | 26.32 | 21.32 |
| SCE1572_7122 | 91.21 | 113.44 |
| SCE1572_8650 | 32.15 | 12.55 |
| SCE1572_2041 | 27.78 | 170.04 |
| SCE1572_10961 | 41.92 | 100.89 |
| SCE1572_3185 | 47.6 | 16.97 |
| SCE1572_67 | 60.5 | 23.68 |
| SCE1572_10252 | 0 | 0 |
| SCE1572_10038 | 66.65 | 140.15 |
| SCE1572_4428 | 16.95 | 29.47 |
| SCE1572_9210 | 40.04 | 27.66 |
| SCE1572_4770 | 53.51 | 161 |
| SCE1572_8552 | 102.84 | 176.11 |
| SCE1572_2632 | 48.22 | 20.99 |
| SCE1572_10063 | 625.56 | 4775.6 |
| SCE1572_2804 | 44.48 | 35.82 |
| SCE1572_5108 | 132.3 | 126.81 |
| SCE1572_10898 | 9.52 | 64.13 |
| SCE1572_5420 | 33.43 | 70.4 |
| SCE1572_3364 | 36.44 | 67.35 |
| SCE1572_8442 | 9.78 | 10.46 |
| SCE1572_10906 | 2.9 | 0 |
| SCE1572_6514 | 11.02 | 2.79 |
| SCE1572_3994 | 89.93 | 36.67 |
| SCE1572_11201 | 53.39 | 123.66 |
| SCE1572_6054 | 22.06 | 70.39 |
| SCE1572_5039 | 18.19 | 48.66 |
| SCE1572_2910 | 48.88 | 18.52 |
| SCE1572_6449 | 190.51 | 57.12 |
| SCE1572_11480 | 82.97 | 107.78 |
| SCE1572_8130 | 43.47 | 21.69 |
| SCE1572_10902 | 35.11 | 30.73 |
| SCE1572_11066 | 23.8 | 21.92 |
| SCE1572_4808 | 24.82 | 143.36 |

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| SCE1572_3687 | 62.8 | 15.03 |
| SCE1572_8334 | 0 | 0 |
| SCE1572_3793 | 54.66 | 135.27 |
| SCE1572_7593 | 46.63 | 47.01 |
| SCE1572_6258 | 7.11 | 8.55 |
| SCE1572_3426 | 69.84 | 22.99 |
| SCE1572_1535 | 22.49 | 44.11 |
| SCE1572_11356 | 31.59 | 66.52 |
| SCE1572_8676 | 57.12 | 62.96 |
| SCE1572_3822 | 20.99 | 44.91 |
| SCE1572_10642 | 52.91 | 217.95 |
| SCE1572_9052 | 55.69 | 56.77 |
| SCE1572_3232 | 30.53 | 91.02 |
| SCE1572_1468 | 0 | 0 |
| SCE1572_921 | 29.72 | 15.23 |
| SCE1572_4643 | 31.94 | 25.62 |
| SCE1572_2850 | 44.83 | 206 |
| SCE1572_2986 | 0 | 0 |
| SCE1572_10005 | 12.2 | 12.58 |
| SCE1572_4829 | 13.82 | 60.38 |
| SCE1572_9428 | 152.45 | 257.65 |
| SCE1572_5799 | 29.82 | 24.33 |
| SCE1572_1698 | 24.32 | 175.58 |
| SCE1572_3765 | 32.71 | 38.74 |
| SCE1572_3587 | 310.28 | 277.23 |
| SCE1572_9251 | 57.15 | 28.07 |
| SCE1572_4028 | 84.81 | 158.98 |
| SCE1572_8158 | 72.47 | 18.36 |
| SCE1572_10453 | 22.8 | 15.55 |
| SCE1572_7796 | 44.99 | 29.16 |
| SCE1572_2602 | 67.25 | 21.02 |
| SCE1572_4836 | 39.65 | 123.51 |
| SCE1572_256 | 23.58 | 4.05 |
| SCE1572_4420 | 0 | 0 |
| SCE1572_11143 | 37.14 | 43.97 |
| SCE1572_9987 | 78.79 | 25.63 |
| SCE1572_6814 | 27.49 | 36.09 |
| SCE1572_3945 | 396.81 | 795.06 |
| SCE1572_8206 | 38.46 | 71.05 |
| SCE1572_2963 | 65.37 | 812.15 |
| SCE1572_7852 | 0 | 0 |
| SCE1572_6158 | 12.42 | 10.73 |
| SCE1572_1794 | 20.09 | 568.63 |
| SCE1572_3577 | 39.68 | 81.25 |
| SCE1572_2606 | 43.89 | 6.4 |
| SCE1572_10793 | 8.64 | 5.67 |
| SCE1572_3134 | 19.05 | 7.64 |
| SCE1572_9397 | 28.23 | 56.29 |

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| SCE1572_1649 | 38.34 | 11.99 |
| SCE1572_6373 | 46.92 | 30.3 |
| SCE1572_1664 | 25.35 | 70.59 |
| SCE1572_8714 | 92.37 | 150.1 |
| SCE1572_7688 | 76.63 | 18.21 |
| SCE1572_1053 | 41.17 | 85.11 |
| SCE1572_7937 | 8.21 | 5.2 |
| SCE1572_3841 | 70.11 | 34.8 |
| SCE1572_9439 | 31.46 | 39.37 |
| SCE1572_2082 | 36.86 | 40.32 |
| SCE1572_10822 | 46.8 | 46.55 |
| SCE1572_10537 | 0 | 0 |
| SCE1572_11062 | 49.35 | 28.8 |
| SCE1572_3984 | 31.15 | 96.23 |
| SCE1572_6842 | 28.84 | 21.03 |
| SCE1572_6559 | 50.01 | 74.26 |
| SCE1572_2290 | 311.92 | 1957.1 |
| SCE1572_11310 | 36.26 | 11.9 |
| SCE1572_3002 | 7.26 | 3.88 |
| SCE1572_1883 | 0 | 0 |
| SCE1572_5379 | 42.47 | 14.23 |
| SCE1572_4777 | 35.47 | 139.48 |
| SCE1572_7459 | 172.01 | 420.41 |
| SCE1572_5980 | 440.23 | 298.97 |
| SCE1572_5763 | 0 | 0 |
| SCE1572_11463 | 91.29 | 169.23 |
| SCE1572_11573 | 0 | 0 |
| SCE1572_325 | 21.34 | 5.41 |
| SCE1572_7539 | 68.21 | 20.79 |
| SCE1572_2445 | 20.05 | 7.62 |
| SCE1572_3967 | 118.49 | 78.39 |
| SCE1572_4559 | 11.58 | 34.21 |
| SCE1572_1536 | 62.4 | 34.25 |
| SCE1572_4636 | 111.72 | 22.41 |
| SCE1572_7683 | 17.84 | 4.91 |
| SCE1572_7144 | 48.84 | 105.31 |
| SCE1572_9646 | 98.91 | 132.36 |
| SCE1572_7783 | 0 | 0 |
| SCE1572_5187 | 18.78 | 1332.13 |
| SCE1572_2353 | 6.51 | 20.15 |
| SCE1572_4242 | 18.01 | 3.61 |
| SCE1572_1984 | 0 | 0 |
| SCE1572_10408 | 38.97 | 56.27 |
| SCE1572_9822 | 12.86 | 8.85 |
| SCE1572_10685 | 12.68 | 9.46 |
| SCE1572_11135 | 38.48 | 45.38 |
| SCE1572_6530 | 25.77 | 33.76 |
| SCE1572_8196 | 27.39 | 15.33 |

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| SCE1572_2648 | 49.15 | 24.06 |
| SCE1572_2378 | 39.83 | 507.18 |
| SCE1572_1402 | 55.96 | 17.68 |
| SCE1572_1708 | 36.1 | 0 |
| SCE1572_2171 | 111.94 | 58.48 |
| SCE1572_7247 | 0 | 0 |
| SCE1572_1496 | 20.13 | 9.69 |
| SCE1572_7252 | 33.11 | 10.19 |
| SCE1572_1147 | 52.64 | 69.72 |
| SCE1572_2953 | 20.09 | 0 |
| SCE1572_2204 | 29.13 | 205.51 |
| SCE1572_8657 | 9.78 | 133.41 |
| SCE1572_4171 | 52.51 | 60.25 |
| SCE1572_5486 | 77.65 | 19.01 |
| SCE1572_11122 | 37.24 | 10.73 |
| SCE1572_2189 | 29.03 | 80.23 |
| SCE1572_2835 | 12.23 | 0 |
| SCE1572_2210 | 42.34 | 227.11 |
| SCE1572_4396 | 15.29 | 21.47 |
| SCE1572_1491 | 0 | 0 |
| SCE1572_1497 | 32.78 | 13.12 |
| SCE1572_11489 | 0 | 0 |
| SCE1572_681 | 16.01 | 7.23 |
| SCE1572_3297 | 8.94 | 6.59 |
| SCE1572_4139 | 12.48 | 4.51 |
| SCE1572_5158 | 7.84 | 0 |
| SCE1572_9829 | 22.01 | 0 |
| SCE1572_4903 | 46.72 | 70.53 |
| SCE1572_3215 | 147.14 | 480.98 |
| SCE1572_302 | 16.53 | 5.19 |
| SCE1572_8791 | 80.27 | 400.7 |
| SCE1572_4326 | 24.68 | 15.76 |
| SCE1572_4271 | 30.44 | 25.78 |
| SCE1572_735 | 79.37 | 40.41 |
| SCE1572_6882 | 0 | 0 |
| SCE1572_1955 | 15.08 | 18.15 |
| SCE1572_3009 | 15.9 | 23.54 |
| SCE1572_4038 | 48.83 | 58.35 |
| SCE1572_5070 | 23.13 | 35.05 |
| SCE1572_7619 | 69.98 | 338.13 |
| SCE1572_5016 | 73.45 | 1054.07 |
| SCE1572_9981 | 51.01 | 29.72 |
| SCE1572_1464 | 45.53 | 19.57 |
| SCE1572_5290 | 52.43 | 21.51 |
| SCE1572_4668 | 7.98 | 4.8 |
| SCE1572_2589 | 41.43 | 70.46 |
| SCE1572_1295 | 65.84 | 37.53 |
| SCE1572_10199 | 73.69 | 73.1 |

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| SCE1572_663 | 0 | 0 |
| SCE1572_3352 | 21.09 | 8.92 |
| SCE1572_1764 | 39.71 | 12.16 |
| SCE1572_2106 | 87.86 | 241.13 |
| SCE1572_11315 | 259.58 | 460.76 |
| SCE1572_8867 | 47.15 | 24.5 |
| SCE1572_10697 | 75.16 | 167.47 |
| SCE1572_9838 | 0 | 0 |
| SCE1572_787 | 66.41 | 280.74 |
| SCE1572_1900 | 13.35 | 6.89 |
| SCE1572_135 | 33.55 | 18.88 |
| SCE1572_8516 | 83.27 | 13.24 |
| SCE1572_11583 | 44.84 | 118.44 |
| SCE1572_7865 | 28.34 | 17.05 |
| SCE1572_1023 | 23.69 | 17.11 |
| SCE1572_8097 | 25.08 | 15.32 |
| SCE1572_11101 | 37.49 | 44.11 |
| SCE1572_717 | 18.14 | 6.98 |
| SCE1572_8392 | 0 | 0 |
| SCE1572_7194 | 0 | 0 |
| SCE1572_2780 | 49.17 | 6.58 |
| SCE1572_10882 | 40.11 | 303.6 |
| SCE1572_10324 | 21.1 | 32.65 |
| SCE1572_5282 | 94.71 | 113.49 |
| SCE1572_3645 | 209.13 | 424.24 |
| SCE1572_1802 | 43.82 | 44.3 |
| SCE1572_8877 | 3.09 | 0 |
| SCE1572_2885 | 25.93 | 15.01 |
| SCE1572_8306 | 124.05 | 8.29 |
| SCE1572_6497 | 40.91 | 7.72 |
| SCE1572_8173 | 22.26 | 5.79 |
| SCE1572_4605 | 121.41 | 819.98 |
| SCE1572_9266 | 26.87 | 47.79 |
| SCE1572_1258 | 37.9 | 3.65 |
| SCE1572_10336 | 11.84 | 9.5 |
| SCE1572_3074 | 27.5 | 11.88 |
| SCE1572_6306 | 16.3 | 9.51 |
| SCE1572_3491 | 29.41 | 54.01 |
| SCE1572_1517 | 3.3 | 0 |
| SCE1572_3773 | 59.26 | 24.59 |
| SCE1572_7948 | 128.14 | 207.18 |
| SCE1572_440 | 173.68 | 56.55 |
| SCE1572_9897 | 9.33 | 7.67 |
| SCE1572_10446 | 11.81 | 7.48 |
| SCE1572_10772 | 32.88 | 30.78 |
| SCE1572_8068 | 42.78 | 11.8 |
| SCE1572_7643 | 92.65 | 115.85 |
| SCE1572_5561 | 47.15 | 23.29 |

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| SCE1572_11006 | 0 | 0 |
| SCE1572_7005 | 10.78 | 3.24 |
| SCE1572_8544 | 76.47 | 60.29 |
| SCE1572_1041 | 57.61 | 24.52 |
| SCE1572_6676 | 48.27 | 31.09 |
| SCE1572_4226 | 29.96 | 48.56 |
| SCE1572_11561 | 35.09 | 58.67 |
| SCE1572_3595 | 20.29 | 2.76 |
| SCE1572_9292 | 22.12 | 42.03 |
| SCE1572_7915 | 2.53 | 0 |
| SCE1572_4661 | 12.63 | 6.61 |
| SCE1572_3103 | 20.04 | 8.39 |
| SCE1572_2360 | 69.56 | 450.79 |
| SCE1572_9812 | 52.02 | 17.54 |
| SCE1572_2735 | 26.56 | 20.66 |
| SCE1572_3709 | 0 | 0 |
| SCE1572_7784 | 13.75 | 66.79 |
| SCE1572_7103 | 0 | 0 |
| SCE1572_10087 | 0 | 0 |
| SCE1572_11021 | 34.77 | 26.34 |
| SCE1572_9503 | 582.37 | 1943.03 |
| SCE1572_3731 | 25.15 | 11.08 |
| SCE1572_2327 | 63.75 | 34.27 |
| SCE1572_7437 | 43.76 | 14.09 |
| SCE1572_168 | 20.2 | 8.38 |
| SCE1572_9867 | 37.38 | 75.81 |
| SCE1572_6718 | 0 | 0 |
| SCE1572_8838 | 0 | 0 |
| SCE1572_6218 | 37.35 | 12.84 |
| SCE1572_9323 | 26.86 | 42.4 |
| SCE1572_8995 | 22.56 | 9.77 |
| SCE1572_3897 | 27.21 | 42.63 |
| SCE1572_6803 | 38.45 | 61.11 |
| SCE1572_9394 | 11.74 | 2.42 |
| SCE1572_8746 | 25.66 | 28.07 |
| SCE1572_3062 | 18.53 | 4.05 |
| SCE1572_230 | 109.04 | 47.49 |
| SCE1572_10307 | 20.22 | 4.42 |
| SCE1572_11418 | 69.19 | 62.95 |
| SCE1572_4644 | 49.39 | 36.24 |
| SCE1572_456 | 35.13 | 11.87 |
| SCE1572_9569 | 0 | 0 |
| SCE1572_8459 | 43.32 | 49.46 |
| SCE1572_8365 | 39.2 | 17.8 |
| SCE1572_4198 | 20.67 | 0 |
| SCE1572_10020 | 46.39 | 19.64 |
| SCE1572_9633 | 45.4 | 14.28 |
| SCE1572_5580 | 31.66 | 32.08 |

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| SCE1572_5772 | 24.43 | 15.87 |
| SCE1572_2488 | 4.27 | 0 |
| SCE1572_10761 | 0 | 0 |
| SCE1572_371 | 19.69 | 194.31 |
| SCE1572_2300 | 26.87 | 139.73 |
| SCE1572_8258 | 37.38 | 224.05 |
| SCE1572_9448 | 42.05 | 28.51 |
| SCE1572_4622 | 79.68 | 1877.88 |
| SCE1572_6355 | 0 | 0 |
| SCE1572_11495 | 120.27 | 22.81 |
| SCE1572_937 | 13.46 | 10.23 |
| SCE1572_11432 | 24.29 | 19.15 |
| SCE1572_9012 | 32.8 | 28.47 |
| SCE1572_2314 | 35.92 | 59.76 |
| SCE1572_917 | 17.91 | 46.34 |
| SCE1572_5479 | 45.24 | 21.54 |
| SCE1572_4888 | 22.24 | 14.15 |
| SCE1572_2591 | 40.73 | 23.97 |
| SCE1572_3379 | 68.72 | 19.61 |
| SCE1572_9513 | 18.21 | 16.31 |
| SCE1572_384 | 0 | 0 |
| SCE1572_10785 | 48.08 | 76.46 |
| SCE1572_7800 | 52.27 | 101.65 |
| SCE1572_10808 | 8.6 | 0 |
| SCE1572_843 | 55.34 | 299.42 |
| SCE1572_603 | 11.66 | 4.16 |
| SCE1572_4960 | 27.09 | 47.87 |
| SCE1572_1488 | 0 | 0 |
| SCE1572_6395 | 0 | 0 |
| SCE1572_9656 | 41.09 | 22.29 |
| SCE1572_6000 | 37.9 | 125.2 |
| SCE1572_8688 | 154.01 | 241.36 |
| SCE1572_3370 | 17.44 | 271.27 |
| SCE1572_11256 | 28.71 | 48.58 |
| SCE1572_9716 | 20.37 | 187.91 |
| SCE1572_414 | 43.22 | 31.37 |
| SCE1572_6691 | 2.33 | 0 |
| SCE1572_8628 | 47.46 | 132.02 |
| SCE1572_8342 | 29.62 | 16.42 |
| SCE1572_9709 | 51.73 | 83.49 |
| SCE1572_1639 | 25.95 | 39.45 |
| SCE1572_464 | 40.53 | 415.51 |
| SCE1572_6209 | 27.69 | 4.57 |
| SCE1572_7871 | 19.51 | 13.09 |
| SCE1572_7765 | 35.91 | 32.01 |
| SCE1572_5363 | 16.18 | 4.71 |
| SCE1572_3073 | 16.7 | 6.43 |
| SCE1572_55 | 73.31 | 23.11 |

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| SCE1572_7602 | 63.91 | 56.22 |
| SCE1572_1427 | 3.45 | 0 |
| SCE1572_5297 | 53.16 | 61.61 |
| SCE1572_7922 | 33.33 | 19.57 |
| SCE1572_6071 | 0 | 0 |
| SCE1572_7480 | 45.41 | 66.99 |
| SCE1572_3906 | 87.52 | 94.55 |
| SCE1572_3487 | 27.17 | 6.99 |
| SCE1572_260 | 57.68 | 14.93 |
| SCE1572_10541 | 56.17 | 58.63 |
| SCE1572_6202 | 28.99 | 19.77 |
| SCE1572_5845 | 45.71 | 42.18 |
| SCE1572_573 | 207.66 | 389.75 |
| SCE1572_4478 | 26.63 | 32.04 |
| SCE1572_8694 | 24.87 | 10.69 |
| SCE1572_3873 | 12.71 | 10.67 |
| SCE1572_10433 | 20.05 | 15.08 |
| SCE1572_10972 | 22.25 | 93.91 |
| SCE1572_4166 | 40.61 | 19.55 |
| SCE1572_9271 | 28.43 | 45.62 |
| SCE1572_1265 | 305.7 | 11633.01 |
| SCE1572_10077 | 380.89 | 893.02 |
| SCE1572_7523 | 34.41 | 15.31 |
| SCE1572_9338 | 28.31 | 41.77 |
| SCE1572_4282 | 31.04 | 2.87 |
| SCE1572_2540 | 46.95 | 25.11 |
| SCE1572_7904 | 14.52 | 5.18 |
| SCE1572_8543 | 52.96 | 1087.57 |
| SCE1572_6697 | 16.22 | 74.16 |
| SCE1572_10313 | 48.29 | 22.98 |
| SCE1572_9199 | 19.84 | 3.67 |
| SCE1572_9670 | 43.79 | 154.11 |
| SCE1572_7559 | 42.46 | 28.81 |
| SCE1572_10994 | 37.25 | 53.48 |
| SCE1572_6862 | 24.74 | 7.58 |
| SCE1572_6976 | 42.94 | 13.54 |
| SCE1572_10339 | 40.56 | 25.57 |
| SCE1572_10725 | 17.1 | 7.55 |
| SCE1572_2247 | 38.55 | 12.37 |
| SCE1572_11279 | 31.22 | 128.8 |
| SCE1572_5328 | 50.64 | 42.85 |
| SCE1572_2 | 28.63 | 53.01 |
| SCE1572_519 | 41.96 | 43.61 |
| SCE1572_1306 | 220.18 | 8947.52 |
| SCE1572_7465 | 125.05 | 207.41 |
| SCE1572_468 | 22.44 | 71.66 |
| SCE1572_1609 | 20.1 | 18.67 |
| SCE1572_9821 | 65.51 | 27.97 |

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| SCE1572_5498 | 25.34 | 23.72 |
| SCE1572_6235 | 30.96 | 32.12 |
| SCE1572_2260 | 26.41 | 26.65 |
| SCE1572_1004 | 18.65 | 18.51 |
| SCE1572_10341 | 35.93 | 13.19 |
| SCE1572_1645 | 63.69 | 116.67 |
| SCE1572_10050 | 63.33 | 124.05 |
| SCE1572_7411 | 40.08 | 29.36 |
| SCE1572_2539 | 21.06 | 25.8 |
| SCE1572_6203 | 31.98 | 160.57 |
| SCE1572_4010 | 30.06 | 14.47 |
| SCE1572_3249 | 43.2 | 61.99 |
| SCE1572_8263 | 40.78 | 124.28 |
| SCE1572_2188 | 184.21 | 334.23 |
| SCE1572_10032 | 23.15 | 68.95 |
| SCE1572_8102 | 15.39 | 77.34 |
| SCE1572_118 | 184.04 | 849.19 |
| SCE1572_7340 | 121.62 | 258.6 |
| SCE1572_5461 | 24.59 | 5.92 |
| SCE1572_8599 | 0 | 0 |
| SCE1572_3172 | 20.73 | 11.75 |
| SCE1572_624 | 3.3 | 0 |
| SCE1572_4825 | 100.61 | 111.5 |
| SCE1572_3475 | 19.06 | 46.89 |
| SCE1572_10522 | 13.56 | 20.77 |
| SCE1572_11397 | 6.19 | 0 |
| SCE1572_4584 | 88.74 | 32.1 |
| SCE1572_11138 | 9.6 | 0 |
| SCE1572_11392 | 65.21 | 133.41 |
| SCE1572_3206 | 72.41 | 60.66 |
| SCE1572_9392 | 33.21 | 128.18 |
| SCE1572_1963 | 45.43 | 17.8 |
| SCE1572_10947 | 3.79 | 3.04 |
| SCE1572_3482 | 39.63 | 9.98 |
| SCE1572_1681 | 32.16 | 296.73 |
| SCE1572_5780 | 35.77 | 51.4 |
| SCE1572_11190 | 0 | 0 |
| SCE1572_3801 | 107.83 | 70.25 |
| SCE1572_8760 | 82.8 | 84.83 |
| SCE1572_8159 | 5.88 | 0 |
| SCE1572_7380 | 45.55 | 18.79 |
| SCE1572_5032 | 79.32 | 791.51 |
| SCE1572_10823 | 54.23 | 40.02 |
| SCE1572_6825 | 0 | 0 |
| SCE1572_9572 | 12.79 | 17.59 |
| SCE1572_8610 | 48.65 | 27.32 |
| SCE1572_3405 | 53.99 | 24.95 |
| SCE1572_4358 | 54.62 | 18.93 |

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| SCE1572_5684 | 58.45 | 178.06 |
| SCE1572_10774 | 130.94 | 497.62 |
| SCE1572_8704 | 11.44 | 41.31 |
| SCE1572_7976 | 19.85 | 5.08 |
| SCE1572_10584 | 157.31 | 660.38 |
| SCE1572_9865 | 27.12 | 25.54 |
| SCE1572_10957 | 40.11 | 49.09 |
| SCE1572_4495 | 35.07 | 24.62 |
| SCE1572_227 | 13.09 | 6.52 |
| SCE1572_5430 | 107.68 | 134.11 |
| SCE1572_9630 | 44.22 | 15.21 |
| SCE1572_4515 | 51.98 | 45.18 |
| SCE1572_252 | 0 | 0 |
| SCE1572_8174 | 10.53 | 2.53 |
| SCE1572_6859 | 17.69 | 4.56 |
| SCE1572_1943 | 41.95 | 24.33 |
| SCE1572_220 | 42.96 | 93.66 |
| SCE1572_2726 | 73.68 | 1023.15 |
| SCE1572_6163 | 30.4 | 10.73 |
| SCE1572_3593 | 37.15 | 15.99 |
| SCE1572_7003 | 67.61 | 16.91 |
| SCE1572_10015 | 26.62 | 67.59 |
| SCE1572_3982 | 38.54 | 97.86 |
| SCE1572_11475 | 32.76 | 19.36 |
| SCE1572_1288 | 104.57 | 104.04 |
| SCE1572_21 | 46.93 | 26.07 |
| SCE1572_1941 | 104.6 | 17.8 |
| SCE1572_7013 | 20.92 | 0 |
| SCE1572_2053 | 61.81 | 58.11 |
| SCE1572_6690 | 36.45 | 63.81 |
| SCE1572_3830 | 30.07 | 144.76 |
| SCE1572_2530 | 0 | 0 |
| SCE1572_2268 | 21.9 | 10.67 |
| SCE1572_3037 | 30.61 | 12.87 |
| SCE1572_11593 | 69.05 | 514.87 |
| SCE1572_9956 | 42.62 | 25.23 |
| SCE1572_3194 | 51.06 | 63.79 |
| SCE1572_10183 | 69.98 | 282.19 |
| SCE1572_8730 | 78.97 | 54.3 |
| SCE1572_10876 | 51.14 | 46.07 |
| SCE1572_11164 | 21.16 | 28.29 |
| SCE1572_5374 | 54.09 | 53.23 |
| SCE1572_9574 | 15.96 | 3.84 |
| SCE1572_10010 | 31.3 | 21.19 |
| SCE1572_3524 | 27.97 | 23.28 |
| SCE1572_3307 | 111.16 | 2481.68 |
| SCE1572_6078 | 2.78 | 0 |
| SCE1572_4347 | 51.94 | 20.27 |

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| SCE1572_2512 | 45.21 | 989.31 |
| SCE1572_972 | 63.17 | 170.95 |
| SCE1572_9232 | 3.49 | 0 |
| SCE1572_3125 | 42.05 | 47.95 |
| SCE1572_8216 | 25.57 | 13.03 |
| SCE1572_6010 | 165.24 | 1795.91 |
| SCE1572_7415 | 11.23 | 3.38 |
| SCE1572_5530 | 99.89 | 52.13 |
| SCE1572_3766 | 22.92 | 86.15 |
| SCE1572_7079 | 20.22 | 236.33 |
| SCE1572_8209 | 38.64 | 40.24 |
| SCE1572_2389 | 13.71 | 23.29 |
| SCE1572_5577 | 28.43 | 0 |
| SCE1572_777 | 11.71 | 2.25 |
| SCE1572_1733 | 70.87 | 31.16 |
| SCE1572_7676 | 37.9 | 5.37 |
| SCE1572_10756 | 28.2 | 23.52 |
| SCE1572_9799 | 6.89 | 6.63 |
| SCE1572_504 | 14.15 | 6.49 |
| SCE1572_7307 | 17.63 | 3.39 |
| SCE1572_7082 | 28.45 | 16.34 |
| SCE1572_5123 | 23.92 | 7.43 |
| SCE1572_1267 | 0 | 0 |
| SCE1572_10049 | 55.33 | 48.83 |
| SCE1572_958 | 19.43 | 22.81 |
| SCE1572_6458 | 51.4 | 47.82 |
| SCE1572_5518 | 15.23 | 5.72 |
| SCE1572_8645 | 0 | 0 |
| SCE1572_11151 | 28.21 | 19.8 |
| SCE1572_4388 | 24.97 | 17.17 |
| SCE1572_6092 | 41.4 | 4.8 |
| SCE1572_1223 | 21.66 | 52.13 |
| SCE1572_6553 | 0 | 0 |
| SCE1572_10682 | 11.87 | 11.64 |
| SCE1572_8229 | 9.71 | 5.56 |
| SCE1572_5408 | 31.92 | 24.33 |
| SCE1572_1913 | 0 | 0 |
| SCE1572_8125 | 186.4 | 30.05 |
| SCE1572_7878 | 29.16 | 14.04 |
| SCE1572_6594 | 68.82 | 106.61 |
| SCE1572_9252 | 5.95 | 3.58 |
| SCE1572_2749 | 59.96 | 186.91 |
| SCE1572_91 | 258.42 | 2622.77 |
| SCE1572_1877 | 0 | 0 |
| SCE1572_6268 | 63.22 | 34.64 |
| SCE1572_6180 | 35.4 | 19.18 |
| SCE1572_6816 | 64.16 | 20.59 |
| SCE1572_9097 | 10 | 4.01 |

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| SCE1572_7253 | 44.9 | 15.94 |
| SCE1572_5349 | 77.69 | 15.08 |
| SCE1572_4650 | 58.77 | 152.15 |
| SCE1572_2930 | 49.17 | 14.25 |
| SCE1572_5639 | 11.46 | 5.3 |
| SCE1572_10950 | 41.92 | 18.5 |
| SCE1572_11018 | 0 | 0 |
| SCE1572_3234 | 47.3 | 27.66 |
| SCE1572_2475 | 50.13 | 42.45 |
| SCE1572_9538 | 82.77 | 21.7 |
| SCE1572_3782 | 22.03 | 51.25 |
| SCE1572_8935 | 9.76 | 5.87 |
| SCE1572_6317 | 0 | 0 |
| SCE1572_6940 | 17.1 | 21.95 |
| SCE1572_6017 | 86.3 | 296.43 |
| SCE1572_7621 | 24.83 | 16.01 |
| SCE1572_3418 | 32.07 | 26.51 |
| SCE1572_6259 | 14.95 | 12.85 |
| SCE1572_9375 | 0 | 0 |
| SCE1572_6261 | 15.92 | 5.47 |
| SCE1572_7243 | 38.42 | 62.6 |
| SCE1572_1620 | 54.58 | 300.7 |
| SCE1572_8809 | 81.85 | 12.92 |
| SCE1572_2185 | 81.59 | 24.55 |
| SCE1572_3692 | 24.41 | 23.73 |
| SCE1572_10083 | 192.46 | 868.37 |
| SCE1572_1676 | 20.33 | 46.52 |
| SCE1572_10460 | 45.35 | 141.26 |
| SCE1572_2939 | 17.84 | 54.64 |
| SCE1572_9790 | 99.41 | 175.11 |
| SCE1572_8013 | 23.4 | 64.9 |
| SCE1572_714 | 30.86 | 3.23 |
| SCE1572_6067 | 13.66 | 11.75 |
| SCE1572_4003 | 53.7 | 144.45 |
| SCE1572_9531 | 22.53 | 33.33 |
| SCE1572_690 | 41.78 | 30.17 |
| SCE1572_2639 | 67.02 | 31.32 |
| SCE1572_5912 | 37.37 | 67.45 |
| SCE1572_11580 | 36.98 | 1.78 |
| SCE1572_8523 | 38.44 | 0 |
| SCE1572_9794 | 20.12 | 22.46 |
| SCE1572_6823 | 55.86 | 180.54 |
| SCE1572_2058 | 6.15 | 0 |
| SCE1572_9108 | 47.51 | 65.69 |
| SCE1572_4435 | 24.51 | 39.33 |
| SCE1572_3933 | 103.28 | 262.14 |
| SCE1572_9616 | 2.92 | 0 |
| SCE1572_1939 | 28.08 | 96.65 |

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| SCE1572_705 | 20.57 | 21.3 |
| SCE1572_7734 | 16.58 | 0 |
| SCE1572_5784 | 56.48 | 145.97 |
| SCE1572_4436 | 34.47 | 25.31 |
| SCE1572_4945 | 24.11 | 56.45 |
| SCE1572_3995 | 17.11 | 16.84 |
| SCE1572_11587 | 1.97 | 4.75 |
| SCE1572_9926 | 78.39 | 779.49 |
| SCE1572_5903 | 17.19 | 13.79 |
| SCE1572_5271 | 24.95 | 13.86 |
| SCE1572_9802 | 23.42 | 20.03 |
| SCE1572_7705 | 0 | 0 |
| SCE1572_1543 | 539.61 | 367.8 |
| SCE1572_8349 | 77.2 | 6.72 |
| SCE1572_10017 | 66.61 | 282.37 |
| SCE1572_3918 | 25.91 | 73.91 |
| SCE1572_1634 | 129.32 | 692.95 |
| SCE1572_2580 | 0 | 0 |
| SCE1572_6482 | 79.17 | 65.5 |
| SCE1572_8895 | 44.21 | 48.36 |
| SCE1572_6982 | 12.43 | 0 |
| SCE1572_73 | 34.21 | 142.09 |
| SCE1572_11338 | 70.04 | 8.54 |
| SCE1572_6750 | 22.04 | 16.97 |
| SCE1572_1560 | 2.49 | 0 |
| SCE1572_1546 | 64.88 | 31.01 |
| SCE1572_2873 | 90.31 | 65.81 |
| SCE1572_9756 | 13.78 | 8.29 |
| SCE1572_3753 | 78.19 | 292.92 |
| SCE1572_550 | 0 | 0 |
| SCE1572_11365 | 15.79 | 7.6 |
| SCE1572_9246 | 0 | 0 |
| SCE1572_11268 | 40.64 | 47.98 |
| SCE1572_851 | 60.74 | 183.33 |
| SCE1572_3635 | 27.39 | 16.48 |
| SCE1572_9 | 26.32 | 33.05 |
| SCE1572_6505 | 36.21 | 30.22 |
| SCE1572_4681 | 21.31 | 13.81 |
| SCE1572_5572 | 28.03 | 14.47 |
| SCE1572_1376 | 26.83 | 15.31 |
| SCE1572_6791 | 6.67 | 6.89 |
| SCE1572_11514 | 53.27 | 36.99 |
| SCE1572_6955 | 47.77 | 12.35 |
| SCE1572_1931 | 46.31 | 16.46 |
| SCE1572_10042 | 474.9 | 1500.24 |
| SCE1572_1162 | 38.3 | 12.8 |
| SCE1572_5732 | 65.16 | 208.09 |
| SCE1572_10988 | 59.85 | 787.46 |

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| SCE1572_5953 | 49.51 | 31.64 |
| SCE1572_7719 | 65.32 | 28.85 |
| SCE1572_430 | 56.43 | 39.82 |
| SCE1572_11036 | 13.38 | 136.85 |
| SCE1572_10037 | 21.23 | 45.25 |
| SCE1572_10631 | 36.03 | 0 |
| SCE1572_1687 | 38.61 | 13.6 |
| SCE1572_1714 | 70.05 | 57.74 |
| SCE1572_5308 | 31.15 | 44.99 |
| SCE1572_8874 | 110.44 | 25.95 |
| SCE1572_5211 | 47.63 | 68.97 |
| SCE1572_9383 | 592.45 | 2352.03 |
| SCE1572_1576 | 35.96 | 16.95 |
| SCE1572_11557 | 35.02 | 20.9 |
| SCE1572_8435 | 70.97 | 3.88 |
| SCE1572_6888 | 39.76 | 11.48 |
| SCE1572_11205 | 3.74 | 13.52 |
| SCE1572_1344 | 11.13 | 6.35 |
| SCE1572_3721 | 2.57 | 0 |
| SCE1572_10449 | 20.57 | 97 |
| SCE1572_368 | 45.46 | 50.97 |
| SCE1572_9970 | 8.58 | 4.92 |
| SCE1572_6990 | 2.3 | 0 |
| SCE1572_1159 | 44.13 | 18.75 |
| SCE1572_7974 | 29.97 | 28.85 |
| SCE1572_5058 | 22.66 | 9.99 |
| SCE1572_2346 | 37.9 | 687.41 |
| SCE1572_10367 | 16.51 | 8.64 |
| SCE1572_276 | 43.49 | 22.63 |
| SCE1572_9320 | 34.43 | 45.77 |
| SCE1572_7537 | 7.46 | 1.99 |
| SCE1572_45 | 27.06 | 120.86 |
| SCE1572_1840 | 20.67 | 42.39 |
| SCE1572_1360 | 62.14 | 194.21 |
| SCE1572_9698 | 21.75 | 8.47 |
| SCE1572_8950 | 59.03 | 24.53 |
| SCE1572_10700 | 0 | 0 |
| SCE1572_2362 | 36.63 | 58.57 |
| SCE1572_11438 | 52.54 | 33.24 |
| SCE1572_5022 | 50.7 | 242.89 |
| SCE1572_3331 | 33.69 | 337.89 |
| SCE1572_4207 | 49.4 | 135.31 |
| SCE1572_10602 | 75.31 | 36.97 |
| SCE1572_183 | 149.84 | 366.14 |
| SCE1572_160 | 68.57 | 37.7 |
| SCE1572_11057 | 35.08 | 18.1 |
| SCE1572_6374 | 40.16 | 11.24 |
| SCE1572_6914 | 14.93 | 11.06 |

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| SCE1572_5562 | 94.99 | 48.36 |
| SCE1572_7485 | 105.29 | 284.5 |
| SCE1572_7450 | 9.86 | 50.44 |
| SCE1572_6892 | 36.27 | 37.43 |
| SCE1572_6522 | 72.27 | 122.78 |
| SCE1572_6422 | 35.21 | 44.73 |
| SCE1572_9611 | 53.44 | 8.97 |
| SCE1572_4264 | 31.33 | 10.56 |
| SCE1572_5167 | 0 | 0 |
| SCE1572_6675 | 45.31 | 16.78 |
| SCE1572_10135 | 19.87 | 16.36 |
| SCE1572_1245 | 6.04 | 4.85 |
| SCE1572_8829 | 0 | 0 |
| SCE1572_7196 | 2.68 | 0 |
| SCE1572_8323 | 36.03 | 42.55 |
| SCE1572_7810 | 113.28 | 209.31 |
| SCE1572_5160 | 28.11 | 20.5 |
| SCE1572_3547 | 0 | 0 |
| SCE1572_4921 | 7.07 | 9.28 |
| SCE1572_9327 | 265.63 | 580.96 |
| SCE1572_4692 | 19.18 | 18.65 |
| SCE1572_4373 | 23.94 | 25.99 |
| SCE1572_5611 | 6.67 | 4.59 |
| SCE1572_4064 | 0 | 0 |
| SCE1572_7806 | 38.14 | 34.43 |
| SCE1572_4289 | 43.62 | 66.58 |
| SCE1572_2292 | 102.28 | 124.54 |
| SCE1572_9764 | 35.43 | 33.96 |
| SCE1572_443 | 29.82 | 8.09 |
| SCE1572_10656 | 74.74 | 143.06 |
| SCE1572_3155 | 91.57 | 184.27 |
| SCE1572_2382 | 9.34 | 3.46 |
| SCE1572_4908 | 59.65 | 105.12 |
| SCE1572_1213 | 0 | 0 |
| SCE1572_6733 | 37.9 | 231.59 |
| SCE1572_6427 | 12.26 | 10.73 |
| SCE1572_5433 | 47.38 | 10.53 |
| SCE1572_6997 | 23.23 | 11.77 |
| SCE1572_5086 | 163.28 | 50.53 |
| SCE1572_8419 | 8.92 | 0 |
| SCE1572_5286 | 89.09 | 35.6 |
| SCE1572_1320 | 15.09 | 36.33 |
| SCE1572_812 | 0 | 0 |
| SCE1572_7072 | 58.44 | 87.61 |
| SCE1572_3256 | 31.14 | 16.29 |
| SCE1572_4688 | 0 | 0 |
| SCE1572_6297 | 12.2 | 88.08 |
| SCE1572_11287 | 80.79 | 466.14 |

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| SCE1572_10411 | 27.73 | 28.93 |
| SCE1572_10206 | 70.75 | 31.47 |
| SCE1572_5134 | 20.22 | 43.79 |
| SCE1572_8605 | 75.42 | 102.1 |
| SCE1572_6363 | 39.7 | 333.07 |
| SCE1572_10269 | 11.53 | 6.94 |
| SCE1572_3519 | 15.72 | 11.13 |
| SCE1572_2654 | 24.26 | 9.73 |
| SCE1572_429 | 41.11 | 66.35 |
| SCE1572_2758 | 61.09 | 183.23 |
| SCE1572_653 | 527.66 | 1742.14 |
| SCE1572_6600 | 36.93 | 33.99 |
| SCE1572_9999 | 24.5 | 238.09 |
| SCE1572_8006 | 5.14 | 0 |
| SCE1572_7667 | 190.47 | 40.24 |
| SCE1572_786 | 12.79 | 4.4 |
| SCE1572_9967 | 36.44 | 24.19 |
| SCE1572_403 | 19.61 | 34.47 |
| SCE1572_6439 | 26.8 | 20.37 |
| SCE1572_1974 | 0 | 0.69 |
| SCE1572_8924 | 0 | 0 |
| SCE1572_7387 | 54.4 | 98.2 |
| SCE1572_10628 | 22.8 | 67.84 |
| SCE1572_8908 | 22.22 | 12.58 |
| SCE1572_8469 | 136.63 | 163.37 |
| SCE1572_448 | 20.14 | 21.15 |
| SCE1572_10488 | 97.42 | 1263.39 |
| SCE1572_10108 | 23.04 | 68.32 |
| SCE1572_4147 | 23.18 | 1385.31 |
| SCE1572_5939 | 32.53 | 8.41 |
| SCE1572_10192 | 17.58 | 5.29 |
| SCE1572_1489 | 36.87 | 10 |
| SCE1572_10097 | 18.08 | 118.85 |
| SCE1572_7571 | 26.26 | 101.05 |
| SCE1572_943 | 112.48 | 34.09 |
| SCE1572_9807 | 297.4 | 1178.98 |
| SCE1572_1926 | 100.79 | 762.23 |
| SCE1572_113 | 35.65 | 28.29 |
| SCE1572_8109 | 45.05 | 26.44 |
| SCE1572_3288 | 31.93 | 72.98 |
| SCE1572_4228 | 16.41 | 9.41 |
| SCE1572_6729 | 8.42 | 28.38 |
| SCE1572_637 | 14.19 | 34.16 |
| SCE1572_6713 | 28.14 | 48.38 |
| SCE1572_5767 | 112.2 | 681.88 |
| SCE1572_8959 | 0 | 0 |
| SCE1572_2164 | 6.45 | 3.88 |
| SCE1572_2795 | 44.38 | 62.3 |

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| SCE1572_955 | 0 | 0 |
| SCE1572_11505 | 191.13 | 1191.82 |
| SCE1572_7290 | 13.54 | 6.52 |
| SCE1572_6020 | 118.79 | 160.91 |
| SCE1572_8273 | 24.7 | 43.05 |
| SCE1572_3459 | 3913.89 | 1122.72 |
| SCE1572_932 | 0 | 0 |
| SCE1572_3837 | 52.12 | 21.99 |
| SCE1572_11297 | 55.55 | 77.55 |
| SCE1572_3979 | 32.74 | 47.69 |
| SCE1572_10090 | 49.26 | 98.68 |
| SCE1572_10503 | 9.83 | 28.72 |
| SCE1572_377 | 85.7 | 33.28 |
| SCE1572_9898 | 36.62 | 8.81 |
| SCE1572_3586 | 28.04 | 22.5 |
| SCE1572_457 | 13.9 | 17.53 |
| SCE1572_10126 | 4.15 | 0 |
| SCE1572_8430 | 51.93 | 98.53 |
| SCE1572_10044 | 675.22 | 2732.67 |
| SCE1572_4059 | 11.08 | 12.63 |
| SCE1572_10668 | 0 | 0 |
| SCE1572_9110 | 16.36 | 14.6 |
| SCE1572_1096 | 52.89 | 99.72 |
| SCE1572_7220 | 45.08 | 1134.22 |
| SCE1572_4094 | 10.06 | 5.85 |
| SCE1572_8491 | 24.62 | 19.96 |
| SCE1572_343 | 47.11 | 49.45 |
| SCE1572_10616 | 34.99 | 53.02 |
| SCE1572_7651 | 76.85 | 24.99 |
| SCE1572_5945 | 24.67 | 18.1 |
| SCE1572_7779 | 14.52 | 7.76 |
| SCE1572_3016 | 1.7 | 0 |
| SCE1572_9404 | 22.89 | 216.89 |
| SCE1572_7227 | 117.63 | 3768.77 |
| SCE1572_5540 | 15.11 | 34.03 |
| SCE1572_4417 | 15.55 | 12.48 |
| SCE1572_9700 | 44.43 | 49.8 |
| SCE1572_5184 | 17.7 | 1257.56 |
| SCE1572_1024 | 37.49 | 10.03 |
| SCE1572_1349 | 18.72 | 279.32 |
| SCE1572_5547 | 39.92 | 11.24 |
| SCE1572_3094 | 23.04 | 48.8 |
| SCE1572_11012 | 51.74 | 62.81 |
| SCE1572_1046 | 20.9 | 14.49 |
| SCE1572_6384 | 34.37 | 27.98 |
| SCE1572_8697 | 2.57 | 0 |
| SCE1572_3027 | 54.06 | 106.19 |
| SCE1572_9845 | 66.92 | 12.58 |

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| SCE1572_3384 | 66.02 | 270.65 |
| SCE1572_968 | 99.52 | 510.89 |
| SCE1572_2035 | 0 | 0 |
| SCE1572_4563 | 7.22 | 13.03 |
| SCE1572_10852 | 84.28 | 52.92 |
| SCE1572_8083 | 13.99 | 9.43 |
| SCE1572_1131 | 14.8 | 3.69 |
| SCE1572_7891 | 98.96 | 3730.07 |
| SCE1572_524 | 16.8 | 21.28 |
| SCE1572_4716 | 37.37 | 17.99 |
| SCE1572_3503 | 23.59 | 38.91 |
| SCE1572_11124 | 25.63 | 3.43 |
| SCE1572_7906 | 50.54 | 22.22 |
| SCE1572_8316 | 49.22 | 65.92 |
| SCE1572_4073 | 51.07 | 552.8 |
| SCE1572_4718 | 30.18 | 22.48 |
| SCE1572_6850 | 10.21 | 7.56 |
| SCE1572_1581 | 29.92 | 38.41 |
| SCE1572_9346 | 46.35 | 56.57 |
| SCE1572_8480 | 24.38 | 90.02 |
| SCE1572_1015 | 13.8 | 5.07 |
| SCE1572_10326 | 31.73 | 11.32 |
| SCE1572_2752 | 33.33 | 65.57 |
| SCE1572_5962 | 0 | 0 |
| SCE1572_3758 | 51.8 | 26.32 |
| SCE1572_8066 | 154.01 | 56.69 |
| SCE1572_6285 | 43.22 | 48.02 |
| SCE1572_2456 | 431.95 | 357.47 |
| SCE1572_1150 | 121.29 | 1426.57 |
| SCE1572_3662 | 20.14 | 0.95 |
| SCE1572_1185 | 41.65 | 9.01 |
| SCE1572_740 | 8.86 | 2.37 |
| SCE1572_3970 | 31.22 | 76.66 |
| SCE1572_10440 | 52.64 | 5.07 |
| SCE1572_7159 | 37.17 | 15.62 |
| SCE1572_8246 | 36.24 | 89.51 |
| SCE1572_706 | 10.42 | 2.28 |
| SCE1572_3109 | 70.38 | 16.73 |
| SCE1572_7123 | 11.54 | 3.97 |
| SCE1572_5650 | 2.92 | 0 |
| SCE1572_4647 | 0 | 0 |
| SCE1572_10110 | 35.67 | 118.6 |
| SCE1572_1507 | 67.23 | 24.77 |
| SCE1572_750 | 27.6 | 9.02 |
| SCE1572_10167 | 21.35 | 28.98 |
| SCE1572_7564 | 22.79 | 7.62 |
| SCE1572_5335 | 38.39 | 83.7 |
| SCE1572_1433 | 0 | 0 |

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| SCE1572_8147 | 39.55 | 18.63 |
| SCE1572_4995 | 35.89 | 72.28 |
| SCE1572_3262 | 11.66 | 15.49 |
| SCE1572_7282 | 45.6 | 31.55 |
| SCE1572_8653 | 22.09 | 16.31 |
| SCE1572_3610 | 0 | 0 |
| SCE1572_7496 | 0 | 0 |
| SCE1572_9946 | 34.99 | 0 |
| SCE1572_2991 | 30.36 | 22.14 |
| SCE1572_5226 | 24.43 | 59.81 |
| SCE1572_5383 | 45.2 | 16.62 |
| SCE1572_6686 | 9.48 | 9.12 |
| SCE1572_4050 | 74.9 | 195.29 |
| SCE1572_7446 | 21.16 | 0 |
| SCE1572_4363 | 86.45 | 19.21 |
| SCE1572_3658 | 8.6 | 2.3 |
| SCE1572_9942 | 36.74 | 20.15 |
| SCE1572_7324 | 0 | 0 |
| SCE1572_152 | 36.22 | 38.41 |
| SCE1572_7354 | 51.87 | 15.14 |
| SCE1572_6807 | 21.57 | 14.83 |
| SCE1572_8815 | 4.46 | 0 |
| SCE1572_3429 | 25.4 | 5.15 |
| SCE1572_5303 | 14.94 | 9.32 |
| SCE1572_7187 | 36.04 | 24.14 |
| SCE1572_3437 | 25.99 | 9.12 |
| SCE1572_7273 | 1.78 | 0 |
| SCE1572_5569 | 40.86 | 29.62 |
| SCE1572_9904 | 24.9 | 19.39 |
| SCE1572_858 | 806.81 | 26391.7 |
| SCE1572_4985 | 9.02 | 0 |
| SCE1572_2786 | 16.93 | 59.28 |
| SCE1572_4722 | 52.52 | 122.01 |
| SCE1572_6654 | 84.9 | 390.17 |
| SCE1572_11145 | 70.61 | 91.23 |
| SCE1572_8386 | 86.21 | 40.16 |
| SCE1572_792 | 138.88 | 205.46 |
| SCE1572_1408 | 15.29 | 1.99 |
| SCE1572_10235 | 32.88 | 16.96 |
| SCE1572_6625 | 22.61 | 25.61 |
| SCE1572_5746 | 24.78 | 51.83 |
| SCE1572_4134 | 64.49 | 21.89 |
| SCE1572_8009 | 364.94 | 21246.12 |
| SCE1572_2951 | 0 | 0 |
| SCE1572_4702 | 101.27 | 49.73 |
| SCE1572_1986 | 45.44 | 628.86 |
| SCE1572_9084 | 20.57 | 47.38 |
| SCE1572_5412 | 14.31 | 8.79 |

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| SCE1572_7403 | 67.76 | 2009.33 |
| SCE1572_3250 | 178.09 | 379.4 |
| SCE1572_1018 | 26.86 | 139.73 |
| SCE1572_9494 | 649.64 | 725.01 |
| SCE1572_8477 | 61.51 | 29.39 |
| SCE1572_683 | 49.31 | 35.6 |
| SCE1572_584 | 26.47 | 126.49 |
| SCE1572_5444 | 38.21 | 8.76 |
| SCE1572_5189 | 16.51 | 261.95 |
| SCE1572_514 | 69.92 | 56.72 |
| SCE1572_1319 | 21.79 | 8.36 |
| SCE1572_5132 | 42.94 | 85.04 |
| SCE1572_8640 | 42.94 | 216.91 |
| SCE1572_5659 | 38.41 | 46.98 |
| SCE1572_1418 | 68.68 | 96.69 |
| SCE1572_2496 | 17.07 | 4.83 |
| SCE1572_4704 | 85.66 | 22.68 |
| SCE1572_1833 | 38.32 | 28.62 |
| SCE1572_6337 | 45.33 | 68.97 |
| SCE1572_9743 | 153.51 | 1043.45 |
| SCE1572_3026 | 17.68 | 22.75 |
| SCE1572_6755 | 55.02 | 35.32 |
| SCE1572_10679 | 182.32 | 954.27 |
| SCE1572_7993 | 21.97 | 7.05 |
| SCE1572_5006 | 76.64 | 496.25 |
| SCE1572_11457 | 122.63 | 137.47 |
| SCE1572_1746 | 58.2 | 36.67 |
| SCE1572_5712 | 26.76 | 4.77 |
| SCE1572_6899 | 25.89 | 126.09 |
| SCE1572_8962 | 31.1 | 22.46 |
| SCE1572_8150 | 27.96 | 8.92 |
| SCE1572_5320 | 34.36 | 90.57 |
| SCE1572_10767 | 31.07 | 13.82 |
| SCE1572_8062 | 0 | 0 |
| SCE1572_6273 | 13.88 | 21.62 |
| SCE1572_999 | 41.84 | 37.07 |
| SCE1572_10862 | 20.55 | 128.42 |
| SCE1572_749 | 64.03 | 88.82 |
| SCE1572_1351 | 61.16 | 105.15 |
| SCE1572_2846 | 27.85 | 7.45 |
| SCE1572_8725 | 48.7 | 18.43 |
| SCE1572_9331 | 288.61 | 2595.21 |
| SCE1572_10987 | 18.32 | 106.01 |
| SCE1572_11170 | 62.46 | 55.08 |
| SCE1572_11556 | 1.56 | 0 |
| SCE1572_3490 | 19.14 | 56.69 |
| SCE1572_7135 | 24.09 | 19.33 |
| SCE1572_9928 | 22.94 | 43.21 |

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| SCE1572_8120 | 55.13 | 15.31 |
| SCE1572_10546 | 4.74 | 3.8 |
| SCE1572_2013 | 60.23 | 17.23 |
| SCE1572_5157 | 10.04 | 4.16 |
| SCE1572_8780 | 54.55 | 75.3 |
| SCE1572_11569 | 17.78 | 168.95 |
| SCE1572_10981 | 54.54 | 228.23 |
| SCE1572_7703 | 16.02 | 63.79 |
| SCE1572_1859 | 26.37 | 3.97 |
| SCE1572_1195 | 2.71 | 0 |
| SCE1572_3925 | 103.44 | 107.4 |
| SCE1572_2252 | 42.36 | 41.89 |
| SCE1572_8033 | 0 | 0 |
| SCE1572_7034 | 85.34 | 83.75 |
| SCE1572_81 | 5.05 | 8.11 |
| SCE1572_11535 | 46.45 | 52.03 |
| SCE1572_10674 | 62.64 | 178.94 |
| SCE1572_4788 | 68.1 | 72.16 |
| SCE1572_9349 | 135.18 | 402.29 |
| SCE1572_8114 | 42.25 | 17.95 |
| SCE1572_4406 | 71.52 | 18.36 |
| SCE1572_8856 | 27.43 | 113.69 |
| SCE1572_4022 | 19.73 | 58.33 |
| SCE1572_1176 | 51.07 | 39.37 |
| SCE1572_11389 | 218.67 | 377.66 |
| SCE1572_8915 | 23.94 | 543.27 |
| SCE1572_5276 | 16.85 | 0 |
| SCE1572_1906 | 21.17 | 153.97 |
| SCE1572_835 | 42.34 | 13.15 |
| SCE1572_3214 | 0 | 0 |
| SCE1572_5491 | 37.11 | 24.25 |
| SCE1572_6635 | 3.05 | 0 |
| SCE1572_7125 | 50.79 | 40.75 |
| SCE1572_10891 | 67.11 | 129.62 |
| SCE1572_10719 | 30.98 | 14.91 |
| SCE1572_3010 | 18.05 | 5.21 |
| SCE1572_8224 | 12.06 | 8.29 |
| SCE1572_6715 | 21.45 | 12.91 |
| SCE1572_2550 | 55.24 | 31.12 |
| SCE1572_733 | 29.06 | 11.08 |
| SCE1572_9315 | 14.78 | 13.24 |
| SCE1572_8744 | 56.31 | 29.75 |
| SCE1572_5385 | 76.73 | 50.4 |
| SCE1572_509 | 35.5 | 19.1 |
| SCE1572_3456 | 57.02 | 14.89 |
| SCE1572_1800 | 7.88 | 9.48 |
| SCE1572_6576 | 30.02 | 9.63 |
| SCE1572_7028 | 62.57 | 101.37 |

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| SCE1572_632 | 117.98 | 344.4 |
| SCE1572_4638 | 10.61 | 2.43 |
| SCE1572_4759 | 70.97 | 45.29 |
| SCE1572_7682 | 87.14 | 14.68 |
| SCE1572_8952 | 20.78 | 9.09 |
| SCE1572_2567 | 130.01 | 262.67 |
| SCE1572_2702 | 46.99 | 75.13 |
| SCE1572_6540 | 10.93 | 0 |
| SCE1572_4850 | 78.87 | 66.35 |
| SCE1572_9255 | 17.93 | 11.26 |
| SCE1572_4899 | 13.63 | 10.93 |
| SCE1572_10777 | 183.81 | 200.93 |
| SCE1572_2644 | 28.48 | 22.23 |
| SCE1572_8390 | 2.92 | 0 |
| SCE1572_3735 | 55.39 | 20.44 |
| SCE1572_7059 | 32.7 | 50.92 |
| SCE1572_2153 | 38.53 | 50.4 |
| SCE1572_1115 | 15.96 | 19.21 |
| SCE1572_3048 | 7.44 | 1.05 |
| SCE1572_3643 | 0 | 0 |
| SCE1572_3359 | 51.63 | 23.59 |
| SCE1572_178 | 33.86 | 18.52 |
| SCE1572_2823 | 20.15 | 7.27 |
| SCE1572_5484 | 24.29 | 4.38 |
| SCE1572_6085 | 35.76 | 35.57 |
| SCE1572_9940 | 0 | 0 |
| SCE1572_10112 | 75.81 | 0 |
| SCE1572_5582 | 19.56 | 11.77 |
| SCE1572_9523 | 82.47 | 174.44 |
| SCE1572_3960 | 60.34 | 57.72 |
| SCE1572_9581 | 26.2 | 41.08 |
| SCE1572_2250 | 152.16 | 147.3 |
| SCE1572_2043 | 22.02 | 278.61 |
| SCE1572_5668 | 4.71 | 0 |
| SCE1572_7826 | 39.53 | 44.25 |
| SCE1572_4890 | 275.46 | 450.47 |
| SCE1572_8711 | 65.56 | 39.45 |
| SCE1572_4177 | 67.25 | 21.02 |
| SCE1572_11518 | 59.31 | 29.79 |
| SCE1572_8047 | 34.73 | 12.23 |
| SCE1572_7770 | 21.89 | 25.79 |
| SCE1572_11022 | 41.14 | 30.86 |
| SCE1572_1446 | 33.51 | 12.1 |
| SCE1572_8326 | 39.78 | 39.54 |
| SCE1572_9139 | 0 | 0 |
| SCE1572_728 | 28 | 81.9 |
| SCE1572_5088 | 35.41 | 58.75 |
| SCE1572_9365 | 58.05 | 76.29 |

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| SCE1572_2326 | 11.9 | 52.31 |
| SCE1572_4097 | 24.26 | 10.95 |
| SCE1572_8111 | 49.62 | 13.72 |
| SCE1572_6064 | 35.75 | 11.15 |
| SCE1572_8040 | 72.84 | 44.85 |
| SCE1572_10573 | 27.99 | 39.3 |
| SCE1572_10146 | 160.67 | 192.97 |
| SCE1572_6532 | 37.62 | 14.78 |
| SCE1572_1908 | 33.82 | 54.26 |
| SCE1572_8375 | 28.78 | 143.49 |
| SCE1572_5516 | 2.71 | 0 |
| SCE1572_9300 | 78.41 | 161.43 |
| SCE1572_10152 | 289.85 | 1348.78 |
| SCE1572_11572 | 46.34 | 195.19 |
| SCE1572_101 | 6.59 | 0 |
| SCE1572_674 | 215.97 | 435.81 |
| SCE1572_4503 | 28.61 | 19.97 |
| SCE1572_9583 | 28.61 | 17.22 |
| SCE1572_8865 | 92.09 | 97.39 |
| SCE1572_6494 | 9.36 | 9.01 |
| SCE1572_11376 | 40.65 | 54.11 |
| SCE1572_3004 | 7.08 | 0 |
| SCE1572_454 | 34.94 | 14.92 |
| SCE1572_1305 | 31.37 | 15.1 |
| SCE1572_5214 | 94.46 | 42.03 |
| SCE1572_5564 | 11.84 | 0 |
| SCE1572_9065 | 41.86 | 14.86 |
| SCE1572_6466 | 27.63 | 3.24 |
| SCE1572_9551 | 42.55 | 23.08 |
| SCE1572_10420 | 78.32 | 132.49 |
| SCE1572_10695 | 21.42 | 11.9 |
| SCE1572_2212 | 12.94 | 22.25 |
| SCE1572_1882 | 33.94 | 16.08 |
| SCE1572_4901 | 31.35 | 18.26 |
| SCE1572_1033 | 42.78 | 19.55 |
| SCE1572_10275 | 30.32 | 94.04 |
| SCE1572_8153 | 74.43 | 13.27 |
| SCE1572_5042 | 24.3 | 57.27 |
| SCE1572_8372 | 78.8 | 91.23 |
| SCE1572_3142 | 33.31 | 29.46 |
| SCE1572_2628 | 49.65 | 17.07 |
| SCE1572_4458 | 18.31 | 16.28 |
| SCE1572_5435 | 31.45 | 14.42 |
| SCE1572_10609 | 42.79 | 237.75 |
| SCE1572_6443 | 2.92 | 10.53 |
| SCE1572_4136 | 44.16 | 15.34 |
| SCE1572_6513 | 0 | 0 |
| SCE1572_1087 | 11.23 | 22.53 |

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| SCE1572_2836 | 14.6 | 40.55 |
| SCE1572_9197 | 100.21 | 54.82 |
| SCE1572_2952 | 13.46 | 4.05 |
| SCE1572_4575 | 37.36 | 12.63 |
| SCE1572_5159 | 38.51 | 44.41 |
| SCE1572_1862 | 45.76 | 10.3 |
| SCE1572_6702 | 84.1 | 20.44 |
| SCE1572_4547 | 87.24 | 16.09 |
| SCE1572_31 | 11.47 | 16.87 |
| SCE1572_4272 | 39.67 | 74.69 |
| SCE1572_4076 | 21.23 | 0 |
| SCE1572_5076 | 35.59 | 147.55 |
| SCE1572_10022 | 15.15 | 4.51 |
| SCE1572_7642 | 19.2 | 9.43 |
| SCE1572_1208 | 37.83 | 24.14 |
| SCE1572_3899 | 65.61 | 26.44 |
| SCE1572_2429 | 106.24 | 157.16 |
| SCE1572_4752 | 16.39 | 59.18 |
| SCE1572_5694 | 19.74 | 3.59 |
| SCE1572_8514 | 51.85 | 0 |
| SCE1572_1533 | 5.19 | 8.03 |
| SCE1572_9649 | 39.31 | 7.72 |
| SCE1572_4663 | 0 | 0 |
| SCE1572_11423 | 33.86 | 14.82 |
| SCE1572_5169 | 29.26 | 0 |
| SCE1572_7830 | 82.43 | 60.23 |
| SCE1572_4173 | 46.52 | 54 |
| SCE1572_10498 | 19.87 | 28.52 |
| SCE1572_11107 | 42.03 | 76.43 |
| SCE1572_6308 | 50.36 | 20.2 |
| SCE1572_5529 | 29.86 | 29.55 |
| SCE1572_1490 | 30.63 | 7.37 |
| SCE1572_8820 | 30.31 | 13.15 |
| SCE1572_5876 | 38.14 | 334.32 |
| SCE1572_1384 | 78.57 | 28.41 |
| SCE1572_2306 | 48.93 | 149.29 |
| SCE1572_3060 | 51.06 | 7.56 |
| SCE1572_3707 | 21.38 | 28.07 |
| SCE1572_8578 | 86.21 | 40.16 |
| SCE1572_9777 | 36.8 | 687.33 |
| SCE1572_8475 | 315.38 | 255.98 |
| SCE1572_3445 | 79.39 | 51.29 |
| SCE1572_8941 | 39.34 | 91.23 |
| SCE1572_7368 | 326.84 | 2636.53 |
| SCE1572_398 | 13.24 | 3.98 |
| SCE1572_7049 | 14.42 | 4.79 |
| SCE1572_93 | 83.07 | 41.52 |
| SCE1572_10027 | 32.69 | 26.68 |

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| SCE1572_8922 | 35.22 | 57.6 |
| SCE1572_6539 | 49.05 | 7.16 |
| SCE1572_1126 | 0 | 0 |
| SCE1572_7913 | 23.69 | 10.69 |
| SCE1572_10880 | 83.47 | 406.31 |
| SCE1572_9884 | 27.97 | 19.12 |
| SCE1572_9038 | 28.97 | 48.81 |
| SCE1572_7119 | 35.53 | 74.12 |
| SCE1572_3229 | 252.69 | 141.5 |
| SCE1572_8354 | 55.54 | 10.84 |
| SCE1572_4087 | 14.53 | 6.56 |
| SCE1572_10250 | 49.07 | 13.22 |
| SCE1572_4244 | 80.03 | 915.69 |
| SCE1572_4394 | 37.1 | 13.23 |
| SCE1572_5926 | 133.97 | 19.6 |
| SCE1572_5067 | 137.66 | 355.65 |
| SCE1572_8187 | 4.74 | 2.28 |
| SCE1572_688 | 96.51 | 249.6 |
| SCE1572_10796 | 0 | 0 |
| SCE1572_3157 | 28.06 | 36.93 |
| SCE1572_8451 | 40.31 | 346.1 |
| SCE1572_6025 | 31.19 | 37.53 |
| SCE1572_10699 | 51.1 | 1273.17 |
| SCE1572_4538 | 75.81 | 26.53 |
| SCE1572_15 | 24.32 | 79.18 |
| SCE1572_7431 | 33.69 | 6.54 |
| SCE1572_9322 | 111.95 | 95.47 |
| SCE1572_6155 | 33.61 | 33.26 |
| SCE1572_6389 | 29.46 | 40.34 |
| SCE1572_9422 | 152.89 | 466.12 |
| SCE1572_9186 | 117.21 | 43.16 |
| SCE1572_7661 | 46.97 | 8.6 |
| SCE1572_5741 | 32.26 | 19.97 |
| SCE1572_541 | 100.86 | 51.68 |
| SCE1572_3420 | 35.18 | 146.9 |
| SCE1572_7639 | 27.63 | 40.75 |
| SCE1572_1813 | 16.75 | 8.06 |
| SCE1572_1354 | 23.66 | 4.81 |
| SCE1572_4328 | 20.45 | 8.56 |
| SCE1572_9329 | 0 | 0 |
| SCE1572_11254 | 29.61 | 64.94 |
| SCE1572_8253 | 14.28 | 13.09 |
| SCE1572_6677 | 44.7 | 68.85 |
| SCE1572_11228 | 19.06 | 207.39 |
| SCE1572_2088 | 52.88 | 35.8 |
| SCE1572_9813 | 22.68 | 11.49 |
| SCE1572_7097 | 27.61 | 20.04 |
| SCE1572_4524 | 64.11 | 14.6 |

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| SCE1572_5101 | 35.95 | 23.51 |
| SCE1572_3526 | 18.05 | 2111.34 |
| SCE1572_9225 | 2.61 | 0 |
| SCE1572_7594 | 23.58 | 32.44 |
| SCE1572_10849 | 40.84 | 16.73 |
| SCE1572_10428 | 43.04 | 20.01 |
| SCE1572_8440 | 177.4 | 233.35 |
| SCE1572_7744 | 35.23 | 1162.87 |
| SCE1572_5361 | 44.29 | 139.41 |
| SCE1572_6376 | 23.29 | 1.25 |
| SCE1572_5911 | 35.4 | 60.28 |
| SCE1572_9745 | 20.75 | 15.37 |
| SCE1572_9045 | 60.31 | 25.65 |
| SCE1572_5254 | 15.54 | 3.68 |
| SCE1572_357 | 57.91 | 64.44 |
| SCE1572_1660 | 117.82 | 418.38 |
| SCE1572_2765 | 52.5 | 70.72 |
| SCE1572_8756 | 162.83 | 74.03 |
| SCE1572_6849 | 12.24 | 1.69 |
| SCE1572_1254 | 55.35 | 23.17 |
| SCE1572_2789 | 37.13 | 37.24 |
| SCE1572_3681 | 7.32 | 5.29 |
| SCE1572_232 | 6.79 | 0 |
| SCE1572_7052 | 19.71 | 0 |
| SCE1572_6722 | 56.99 | 191.52 |
| SCE1572_5056 | 37.15 | 28.79 |
| SCE1572_4557 | 26.82 | 12.16 |
| SCE1572_2348 | 22.84 | 8.19 |
| SCE1572_6012 | 36.74 | 76.12 |
| SCE1572_3808 | 43.54 | 107.55 |
| SCE1572_9770 | 43.32 | 23.97 |
| SCE1572_8137 | 35.64 | 15.99 |
| SCE1572_3140 | 72.1 | 136.5 |
| SCE1572_4735 | 174.58 | 8302.36 |
| SCE1572_3342 | 167.91 | 416.63 |
| SCE1572_10921 | 45.84 | 50.92 |
| SCE1572_3186 | 51.73 | 157.42 |
| SCE1572_6080 | 57.48 | 31.76 |
| SCE1572_4526 | 34.39 | 17.56 |
| SCE1572_11098 | 39.68 | 39.97 |
| SCE1572_5904 | 20.47 | 23.72 |
| SCE1572_4332 | 18.23 | 20.79 |
| SCE1572_11272 | 17.65 | 11.58 |
| SCE1572_8449 | 24.03 | 39.88 |
| SCE1572_1326 | 2.33 | 5.61 |
| SCE1572_1232 | 28.61 | 13.77 |
| SCE1572_239 | 14.21 | 0 |
| SCE1572_5657 | 13.74 | 23.7 |

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| SCE1572_411 | 39.51 | 21.52 |
| SCE1572_3392 | 161.48 | 224.74 |
| SCE1572_5959 | 67.69 | 59.02 |
| SCE1572_11441 | 24.82 | 38.75 |
| SCE1572_6802 | 178.17 | 805.1 |
| SCE1572_5120 | 107.91 | 1085.06 |
| SCE1572_7817 | 33.6 | 62.2 |
| SCE1572_9418 | 281.42 | 3254.31 |
| SCE1572_9854 | 149.3 | 51.79 |
| SCE1572_8203 | 19.25 | 0 |
| SCE1572_3468 | 21.06 | 3.38 |
| SCE1572_8559 | 27.61 | 28.48 |
| SCE1572_1164 | 119.25 | 192.71 |
| SCE1572_6170 | 20.72 | 68 |
| SCE1572_961 | 135.09 | 481.88 |
| SCE1572_895 | 10.71 | 2.06 |
| SCE1572_175 | 20.15 | 2.42 |
| SCE1572_6680 | 26.58 | 26.17 |
| SCE1572_4470 | 22.9 | 5.7 |
| SCE1572_10645 | 64.84 | 92.07 |
| SCE1572_9427 | 15.72 | 0 |
| SCE1572_6661 | 32.17 | 43.4 |
| SCE1572_65 | 31.1 | 220.56 |
| SCE1572_2686 | 0 | 0 |
| SCE1572_5161 | 505.39 | 5279.97 |
| SCE1572_5855 | 50 | 27.18 |
| SCE1572_7894 | 1682.69 | 0 |
| SCE1572_7953 | 20.97 | 11.54 |
| SCE1572_11403 | 19.56 | 35.32 |
| SCE1572_9147 | 25.49 | 157.29 |
| SCE1572_10474 | 29.71 | 36.76 |
| SCE1572_4446 | 0 | 0 |
| SCE1572_3969 | 64.86 | 266.6 |
| SCE1572_536 | 163.54 | 413.12 |
| SCE1572_601 | 53.44 | 83.49 |
| SCE1572_11185 | 30.96 | 14.25 |
| SCE1572_1291 | 45.39 | 32.54 |
| SCE1572_2988 | 17.55 | 13.52 |
| SCE1572_10332 | 95.91 | 27.83 |
| SCE1572_8078 | 0 | 0 |
| SCE1572_2507 | 0 | 0 |
| SCE1572_8303 | 18.02 | 76.56 |
| SCE1572_1391 | 47.41 | 60.62 |
| SCE1572_923 | 91.65 | 159.58 |
| SCE1572_10749 | 62.9 | 589.49 |
| SCE1572_1694 | 44.46 | 14.94 |
| SCE1572_1654 | 23.85 | 12.94 |
| SCE1572_6840 | 18.57 | 50.27 |

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| SCE1572_8587 | 0 | 0 |
| SCE1572_675 | 79.01 | 10.28 |
| SCE1572_5761 | 44.54 | 31.4 |
| SCE1572_10351 | 48.16 | 34.29 |
| SCE1572_4223 | 53.83 | 69.1 |
| SCE1572_8409 | 0 | 0 |
| SCE1572_4423 | 1.33 | 0 |
| SCE1572_7180 | 15.64 | 5.79 |
| SCE1572_417 | 8.03 | 4.29 |
| SCE1572_7918 | 43.71 | 15.51 |
| SCE1572_11215 | 31.79 | 14.8 |
| SCE1572_11318 | 24.83 | 32.6 |
| SCE1572_3584 | 6 | 0 |
| SCE1572_10481 | 62.36 | 64.73 |
| SCE1572_2388 | 0 | 0 |
| SCE1572_7007 | 0 | 0 |
| SCE1572_11067 | 33.17 | 45.62 |
| SCE1572_9549 | 47.97 | 22.81 |
| SCE1572_11559 | 41.58 | 21.39 |
| SCE1572_8132 | 14.49 | 5.68 |
| SCE1572_1667 | 16.45 | 22.38 |
| SCE1572_4419 | 47.27 | 14.16 |
| SCE1572_7044 | 943.07 | 7059.24 |
| SCE1572_423 | 44.45 | 177.68 |
| SCE1572_8841 | 35.04 | 18.25 |
| SCE1572_11177 | 33.99 | 67.53 |
| SCE1572_2400 | 74.32 | 757.67 |
| SCE1572_8425 | 23.84 | 158.36 |
| SCE1572_1148 | 16.99 | 40.88 |
| SCE1572_259 | 15.55 | 12.48 |
| SCE1572_2520 | 76.3 | 36.73 |
| SCE1572_5482 | 59.26 | 84.08 |
| SCE1572_2783 | 24.79 | 48.2 |
| SCE1572_10840 | 34.51 | 71.2 |
| SCE1572_11115 | 61.9 | 64.45 |
| SCE1572_809 | 74.51 | 168.43 |
| SCE1572_7647 | 83.26 | 24.95 |
| SCE1572_5969 | 42.54 | 15.4 |
| SCE1572_472 | 44.66 | 251.77 |
| SCE1572_2447 | 49.44 | 15.87 |
| SCE1572_6153 | 0 | 0 |
| SCE1572_2965 | 27.24 | 6.19 |
| SCE1572_983 | 66.89 | 269.46 |
| SCE1572_7346 | 0 | 0 |
| SCE1572_4205 | 34.36 | 64.32 |
| SCE1572_1421 | 18.72 | 6.19 |
| SCE1572_5884 | 43.75 | 43.15 |
| SCE1572_6571 | 26.43 | 7.49 |

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| SCE1572_11465 | 34.08 | 20.37 |
| SCE1572_10155 | 13.74 | 10.67 |
| SCE1572_7777 | 18.14 | 15.71 |
| SCE1572_2969 | 52.28 | 6 |
| SCE1572_5358 | 45.94 | 137.54 |
| SCE1572_5805 | 53.2 | 685.03 |
| SCE1572_9565 | 41.4 | 19.36 |
| SCE1572_7795 | 19.37 | 23.87 |
| SCE1572_4598 | 52.25 | 142.14 |
| SCE1572_8170 | 46.65 | 9.36 |
| SCE1572_3868 | 116.29 | 55.68 |
| SCE1572_11348 | 33.3 | 42.19 |
| SCE1572_9601 | 91.3 | 254.26 |
| SCE1572_5754 | 26.94 | 54.67 |
| SCE1572_3267 | 28.63 | 94 |
| SCE1572_6382 | 18.36 | 9.07 |
| SCE1572_3430 | 51.08 | 148.31 |
| SCE1572_7457 | 9.2 | 1.17 |
| SCE1572_1275 | 15.49 | 29.3 |
| SCE1572_3567 | 32.02 | 7.93 |
| SCE1572_3761 | 77.04 | 45.08 |
| SCE1572_8232 | 19.16 | 29.07 |
| SCE1572_5670 | 168.62 | 78.38 |
| SCE1572_9678 | 26.44 | 12.99 |
| SCE1572_7460 | 21.49 | 19.57 |
| SCE1572_4870 | 10.83 | 98.25 |
| SCE1572_11355 | 46.11 | 27.99 |
| SCE1572_4510 | 97.99 | 97.05 |
| SCE1572_599 | 26.14 | 16.36 |
| SCE1572_11585 | 18.66 | 0 |
| SCE1572_5933 | 19.49 | 7.9 |
| SCE1572_5895 | 104.41 | 20.99 |
| SCE1572_4020 | 29.42 | 72.62 |
| SCE1572_7021 | 48.2 | 18.91 |
| SCE1572_6036 | 16.85 | 0 |
| SCE1572_3325 | 69.77 | 199.5 |
| SCE1572_1241 | 17.81 | 22.08 |
| SCE1572_3080 | 43.42 | 223.93 |
| SCE1572_1009 | 22.85 | 13.57 |
| SCE1572_2993 | 124.86 | 123.43 |
| SCE1572_2922 | 44.89 | 16.81 |
| SCE1572_9354 | 93.65 | 98.74 |
| SCE1572_629 | 42.95 | 129.4 |
| SCE1572_4365 | 71.89 | 18.04 |
| SCE1572_6283 | 11.2 | 27.92 |
| SCE1572_7532 | 7.59 | 4.81 |
| SCE1572_4124 | 38.47 | 32.68 |
| SCE1572_4794 | 327.2 | 728.67 |

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| SCE1572_5575 | 11.66 | 21.05 |
| SCE1572_5649 | 120.78 | 157.44 |
| SCE1572_6271 | 5.35 | 15.03 |
| SCE1572_7174 | 0 | 0 |
| SCE1572_7110 | 0 | 0 |
| SCE1572_3535 | 29.24 | 7.58 |
| SCE1572_8335 | 0 | 0 |
| SCE1572_11595 | 362.1 | 1311.64 |
| SCE1572_10281 | 76.14 | 364.92 |
| SCE1572_5840 | 30.82 | 2.97 |
| SCE1572_163 | 37.18 | 19.35 |
| SCE1572_2869 | 13.69 | 68.42 |
| SCE1572_7712 | 15.05 | 18.56 |
| SCE1572_6404 | 8.32 | 0 |
| SCE1572_821 | 30.32 | 12.16 |
| SCE1572_4386 | 22.48 | 8.49 |
| SCE1572_6800 | 233.94 | 467.08 |
| SCE1572_3900 | 71.97 | 95.37 |
| SCE1572_7363 | 89.29 | 80.67 |
| SCE1572_192 | 3.61 | 0 |
| SCE1572_7756 | 16.06 | 6.19 |
| SCE1572_2778 | 23.68 | 32.99 |
| SCE1572_2434 | 43.19 | 32.79 |
| SCE1572_2662 | 42.18 | 170.11 |
| SCE1572_4053 | 42.94 | 177.62 |
| SCE1572_622 | 0 | 0 |
| SCE1572_2852 | 0 | 0 |
| SCE1572_9130 | 17.8 | 8.29 |
| SCE1572_6059 | 102.76 | 874.44 |
| SCE1572_1602 | 19.03 | 11.45 |
| SCE1572_8024 | 11.34 | 10.23 |
| SCE1572_5686 | 34.91 | 64.82 |
| SCE1572_4832 | 0 | 0 |
| SCE1572_2919 | 34.39 | 32.6 |
| SCE1572_10578 | 0 | 0 |
| SCE1572_382 | 20.22 | 6.08 |
| SCE1572_718 | 16.49 | 10.69 |
| SCE1572_4531 | 26.77 | 17.77 |
| SCE1572_10909 | 62.49 | 67.62 |
| SCE1572_8795 | 28.47 | 30.28 |
| SCE1572_5630 | 77.63 | 263.17 |
| SCE1572_11566 | 53.75 | 44.41 |
| SCE1572_4742 | 24.96 | 71.2 |
| SCE1572_3164 | 55.64 | 21.58 |
| SCE1572_7041 | 31.92 | 6.78 |
| SCE1572_8616 | 67.58 | 46.68 |
| SCE1572_4867 | 0 | 0 |
| SCE1572_9129 | 20.17 | 12.55 |

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| SCE1572_7963 | 36.88 | 147.08 |
| SCE1572_4026 | 54.16 | 157.03 |
| SCE1572_7506 | 43.51 | 13.56 |
| SCE1572_6606 | 35.05 | 17.15 |
| SCE1572_5618 | 69.29 | 23.54 |
| SCE1572_2118 | 19.56 | 8.83 |
| SCE1572_9150 | 51.71 | 330.98 |
| SCE1572_2419 | 293.81 | 1695.41 |
| SCE1572_3907 | 12.06 | 4.15 |
| SCE1572_11094 | 55.98 | 28.07 |
| SCE1572_2947 | 0 | 0 |
| SCE1572_6872 | 23.7 | 38.03 |
| SCE1572_4315 | 35.38 | 9.73 |
| SCE1572_3997 | 56.18 | 210.81 |
| SCE1572_11049 | 53.05 | 47.64 |
| SCE1572_2669 | 58.73 | 28.64 |
| SCE1572_7720 | 34.87 | 194.54 |
| SCE1572_7999 | 7.86 | 2.7 |
| SCE1572_5759 | 9.5 | 0 |
| SCE1572_3113 | 61.71 | 15.82 |
| SCE1572_11430 | 100.56 | 366.42 |
| SCE1572_6145 | 26.79 | 8.51 |
| SCE1572_10621 | 17.41 | 17.21 |
| SCE1572_3064 | 74.85 | 26.18 |
| SCE1572_6764 | 31.03 | 65.09 |
| SCE1572_9159 | 23.69 | 7.6 |
| SCE1572_9486 | 10.73 | 17.5 |
| SCE1572_5442 | 30.62 | 15.71 |
| SCE1572_2008 | 55.57 | 9.28 |
| SCE1572_557 | 36.56 | 49.25 |
| SCE1572_9456 | 0 | 0 |
| SCE1572_6793 | 43.83 | 142.84 |
| SCE1572_4262 | 43.86 | 22.12 |
| SCE1572_6618 | 16.59 | 12.2 |
| SCE1572_1256 | 46.58 | 37.88 |
| SCE1572_8662 | 19.27 | 14.95 |
| SCE1572_762 | 102.04 | 32.43 |
| SCE1572_7237 | 103.21 | 1123.89 |
| SCE1572_668 | 26.47 | 26.65 |
| SCE1572_7162 | 43.05 | 28.16 |
| SCE1572_8168 | 26.52 | 8.33 |
| SCE1572_7192 | 58.48 | 5.21 |
| SCE1572_1073 | 48.45 | 27.59 |
| SCE1572_1588 | 10.94 | 5.18 |
| SCE1572_9119 | 36.84 | 11.94 |
| SCE1572_8095 | 9.73 | 1.38 |
| SCE1572_4337 | 0 | 0 |
| SCE1572_4305 | 21.69 | 13.36 |

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| SCE1572_10387 | 26.24 | 19.09 |
| SCE1572_10705 | 29.23 | 6.59 |
| SCE1572_9122 | 103.59 | 46.24 |
| SCE1572_2943 | 5.76 | 0 |
| SCE1572_3119 | 10.05 | 56.45 |
| SCE1572_4445 | 35.97 | 113.52 |
| SCE1572_4339 | 36.36 | 20.48 |
| SCE1572_11008 | 22.91 | 49.88 |
| SCE1572_1611 | 10.11 | 164.68 |
| SCE1572_7632 | 345.12 | 3112.79 |
| SCE1572_11416 | 22.87 | 47.86 |
| SCE1572_10734 | 31.55 | 18.52 |
| SCE1572_6646 | 22.7 | 11.71 |
| SCE1572_548 | 52.42 | 18.12 |
| SCE1572_337 | 54.46 | 26.7 |
| SCE1572_7634 | 94.71 | 860.11 |
| SCE1572_11544 | 57.44 | 17.44 |
| SCE1572_517 | 61.58 | 40.55 |
| SCE1572_11266 | 305.88 | 1693.75 |
| SCE1572_7518 | 100.51 | 555.61 |
| SCE1572_10371 | 17.21 | 16.75 |
| SCE1572_1510 | 42.17 | 20.56 |
| SCE1572_11248 | 21.95 | 11.56 |
| SCE1572_7946 | 62.85 | 38.65 |
| SCE1572_9918 | 58.21 | 28.24 |
| SCE1572_8508 | 32.31 | 43.07 |
| SCE1572_11322 | 12.79 | 12.54 |
| SCE1572_592 | 24.78 | 65.32 |
| SCE1572_2482 | 13.66 | 21.81 |
| SCE1572_9831 | 15.23 | 10 |
| SCE1572_9511 | 2.49 | 0 |
| SCE1572_2897 | 5.99 | 0 |
| SCE1572_4860 | 13.13 | 0 |
| SCE1572_3775 | 26.76 | 27.32 |
| SCE1572_1636 | 27.42 | 308.63 |
| SCE1572_3274 | 23.82 | 16.38 |
| SCE1572_8521 | 0 | 0 |
| SCE1572_1805 | 12.85 | 12.37 |
| SCE1572_9975 | 21.11 | 13.48 |
| SCE1572_1618 | 21.97 | 24.93 |
| SCE1572_7805 | 47.68 | 61.39 |
| SCE1572_8981 | 0 | 0 |
| SCE1572_6774 | 45.7 | 27.94 |
| SCE1572_2676 | 16.5 | 191.15 |
| SCE1572_3305 | 67.42 | 97.05 |
| SCE1572_10105 | 24.45 | 23.54 |
| SCE1572_7727 | 41.96 | 100.5 |
| SCE1572_4565 | 25.33 | 58.2 |

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| SCE1572_841 | 47.12 | 80.31 |
| SCE1572_11383 | 71.63 | 77.58 |
| SCE1572_6426 | 33.08 | 8.85 |
| SCE1572_2527 | 186.22 | 36.34 |
| SCE1572_9090 | 23.45 | 4.03 |
| SCE1572_6179 | 65.86 | 1384.42 |
| SCE1572_11087 | 20.96 | 90.81 |
| SCE1572_6244 | 27.88 | 6.99 |
| SCE1572_5351 | 22.15 | 12.3 |
| SCE1572_142 | 19.41 | 3.78 |
| SCE1572_341 | 62.37 | 40.64 |
| SCE1572_4823 | 29.35 | 50.45 |
| SCE1572_348 | 22.86 | 183.43 |
| SCE1572_315 | 52.03 | 20.77 |
| SCE1572_6118 | 33.61 | 7.19 |
| SCE1572_8493 | 9.51 | 4.29 |
| SCE1572_7392 | 6.22 | 0 |
| SCE1572_8286 | 24.74 | 69.14 |
| SCE1572_6226 | 28.39 | 34.42 |
| SCE1572_1521 | 27.86 | 9.36 |
| SCE1572_7130 | 45.72 | 28.77 |
| SCE1572_3878 | 92.57 | 74.91 |
| SCE1572_10316 | 0 | 0 |
| SCE1572_2127 | 12.63 | 3.38 |
| SCE1572_5661 | 19.61 | 15.73 |
| SCE1572_1456 | 26.95 | 13.52 |
| SCE1572_2410 | 87.26 | 163.1 |
| SCE1572_11345 | 121.95 | 341.12 |
| SCE1572_4877 | 15.98 | 13.81 |
| SCE1572_4213 | 285.6 | 1054.03 |
| SCE1572_7136 | 37.25 | 10.87 |
| SCE1572_8988 | 11.44 | 0 |
| SCE1572_205 | 20.6 | 10.34 |
| SCE1572_9181 | 34.27 | 15.66 |
| SCE1572_298 | 26.84 | 32.3 |
| SCE1572_6033 | 166.75 | 260.19 |
| SCE1572_882 | 81.71 | 88.24 |
| SCE1572_8638 | 69.89 | 191.52 |
| SCE1572_7990 | 0 | 0 |
| SCE1572_9024 | 79.25 | 725.7 |
| SCE1572_3605 | 238.67 | 130.66 |
| SCE1572_2717 | 62.49 | 32.05 |
| SCE1572_9697 | 11.98 | 17.75 |
| SCE1572_125 | 33.77 | 13.84 |
| SCE1572_10294 | 62.09 | 198.8 |
| SCE1572_1924 | 79.42 | 170.88 |
| SCE1572_6334 | 22.89 | 8.58 |
| SCE1572_3881 | 16.17 | 4.87 |

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| SCE1572_6131 | 129.47 | 881.55 |
| SCE1572_6113 | 21.5 | 46.44 |
| SCE1572_4805 | 32.63 | 26.18 |
| SCE1572_1575 | 21.08 | 20.49 |
| SCE1572_43 | 10 | 6.68 |
| SCE1572_3789 | 695.72 | 6152.73 |
| SCE1572_10966 | 40.82 | 18.05 |
| SCE1572_10795 | 6.69 | 21.47 |
| SCE1572_7698 | 27.8 | 16.95 |
| SCE1572_199 | 32.56 | 56.08 |
| SCE1572_7177 | 29.53 | 24.97 |
| SCE1572_6433 | 14.21 | 9.12 |
| SCE1572_11236 | 20.05 | 7.62 |
| SCE1572_9237 | 116.13 | 46.59 |
| SCE1572_6343 | 31.01 | 103.67 |
| SCE1572_5677 | 31.59 | 46.78 |
| SCE1572_1789 | 18.01 | 0 |
| SCE1572_4761 | 0 | 0 |
| SCE1572_8979 | 0 | 0 |
| SCE1572_7019 | 114.77 | 75.28 |
| SCE1572_2368 | 14.19 | 3.9 |
| SCE1572_2370 | 13.32 | 32.07 |
| SCE1572_7987 | 27.09 | 42.64 |
| SCE1572_9020 | 0 | 0 |
| SCE1572_312 | 35.63 | 17.95 |
| SCE1572_3178 | 6.59 | 0 |
| SCE1572_8881 | 61.82 | 30.16 |
| SCE1572_8898 | 3.18 | 0 |
| SCE1572_6789 | 71.72 | 34.83 |
| SCE1572_5993 | 68.16 | 62.86 |
| SCE1572_9470 | 71.6 | 448.04 |
| SCE1572_7241 | 31.55 | 26.75 |
| SCE1572_2130 | 5.77 | 0.99 |
| SCE1572_5425 | 53.47 | 84.58 |
| SCE1572_5877 | 52.48 | 87.02 |
| SCE1572_3555 | 22.53 | 10.11 |
| SCE1572_267 | 47.48 | 27.12 |
| SCE1572_6048 | 102.03 | 225.68 |
| SCE1572_3890 | 13.47 | 8.24 |
| SCE1572_9684 | 125.22 | 403.05 |
| SCE1572_9726 | 13.02 | 11.19 |
| SCE1572_3791 | 40.09 | 33.37 |
| SCE1572_1316 | 23.39 | 20.13 |
| SCE1572_9290 | 39.33 | 159.84 |
| SCE1572_2067 | 32.02 | 34 |
| SCE1572_9111 | 37.15 | 5.47 |
| SCE1572_9175 | 622.11 | 944.12 |
| SCE1572_1769 | 38.64 | 14.09 |

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| SCE1572_5609 | 11.09 | 2.85 |
| SCE1572_695 | 6.27 | 22.65 |
| SCE1572_609 | 0 | 0 |
| SCE1572_3230 | 41.01 | 121.14 |
| SCE1572_6477 | 20.76 | 10.86 |
| SCE1572_7230 | 57.83 | 52.67 |
| SCE1572_3395 | 30.63 | 7.37 |
| SCE1572_8667 | 34.69 | 24.74 |
| SCE1572_4517 | 14.96 | 7.55 |
| SCE1572_9299 | 158.38 | 1676.74 |
| SCE1572_3570 | 31.5 | 13.43 |
| SCE1572_1449 | 24.59 | 27.62 |
| SCE1572_2862 | 5.95 | 0 |
| SCE1572_6930 | 15.59 | 0 |
| SCE1572_3947 | 142.99 | 329.19 |
| SCE1572_2696 | 40.49 | 27.2 |
| SCE1572_7426 | 40.89 | 131.21 |
| SCE1572_7477 | 13.71 | 52.41 |
| SCE1572_5831 | 31.95 | 34.68 |
| SCE1572_1552 | 58.17 | 44.68 |
| SCE1572_8276 | 58.71 | 63.67 |
| SCE1572_7264 | 63.33 | 29.26 |
| SCE1572_6743 | 10.83 | 3.72 |
| SCE1572_6005 | 27.2 | 57.62 |
| SCE1572_10690 | 38.48 | 62.68 |
| SCE1572_323 | 24.96 | 28.46 |
| SCE1572_5125 | 46.62 | 9.44 |
| SCE1572_2111 | 32.06 | 144.53 |
| SCE1572_9054 | 24.33 | 12.78 |
| SCE1572_4997 | 22.97 | 34.88 |
| SCE1572_9874 | 34.72 | 15.3 |
| SCE1572_8770 | 4.1 | 0 |
| SCE1572_3886 | 40.68 | 27.97 |
| SCE1572_5333 | 11.23 | 11.58 |
| SCE1572_743 | 20.12 | 15.77 |
| SCE1572_3719 | 30.51 | 492.87 |
| SCE1572_106 | 72.47 | 18.56 |
| SCE1572_3509 | 18.23 | 10.24 |
| SCE1572_977 | 88.44 | 1141.35 |
| SCE1572_6974 | 16.47 | 12.26 |
| SCE1572_3826 | 68.41 | 44.29 |
| SCE1572_7546 | 49.95 | 47.81 |
| SCE1572_9781 | 9.86 | 0 |
| SCE1572_1696 | 26.91 | 12.45 |
| SCE1572_9203 | 31.49 | 36.49 |
| SCE1572_2139 | 23.3 | 6.43 |
| SCE1572_8297 | 101.2 | 205.67 |
| SCE1572_3181 | 55.25 | 379.7 |

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| SCE1572_8530 | 29.48 | 44.98 |
| SCE1572_2902 | 19.58 | 9.43 |
| SCE1572_8679 | 25.63 | 21 |
| SCE1572_4102 | 1.88 | 0 |
| SCE1572_10346 | 41.96 | 50.92 |
| SCE1572_5260 | 29.82 | 415.54 |
| SCE1572_3727 | 35.86 | 13.33 |
| SCE1572_5247 | 91.89 | 42.02 |
| SCE1572_5196 | 14.38 | 3.15 |
| SCE1572_1998 | 62.52 | 21.32 |
| SCE1572_6581 | 29.37 | 32.65 |
| SCE1572_11329 | 199.23 | 491.59 |
| SCE1572_1945 | 28.3 | 17.52 |
| SCE1572_3415 | 57.28 | 450.07 |
| SCE1572_2859 | 15.63 | 7.52 |
| SCE1572_9218 | 38.65 | 32.2 |
| SCE1572_6939 | 34.13 | 8.21 |
| SCE1572_10888 | 24.89 | 0 |
| SCE1572_1173 | 48.82 | 13.56 |
| SCE1572_11455 | 130.76 | 86.82 |
| SCE1572_10358 | 72.51 | 32.95 |
| SCE1572_1647 | 67.18 | 114.44 |
| SCE1572_9985 | 16.71 | 11.49 |
| SCE1572_903 | 41.35 | 12.95 |
| SCE1572_2128 | 85.19 | 29.54 |
| SCE1572_2221 | 10.11 | 0 |
| SCE1572_7407 | 0 | 0 |
| SCE1572_10560 | 2.14 | 0 |
| SCE1572_5115 | 27.23 | 51.37 |
| SCE1572_7332 | 73.3 | 36.17 |
| SCE1572_5951 | 28.36 | 15.75 |
| SCE1572_1438 | 16.46 | 10.8 |
| SCE1572_4911 | 69.98 | 162.11 |
| SCE1572_1598 | 67.28 | 26.89 |
| SCE1572_11312 | 0 | 0 |
| SCE1572_4615 | 35.4 | 29.27 |
| SCE1572_11428 | 59.27 | 29.86 |
| SCE1572_9642 | 13.46 | 30.23 |
| SCE1572_5706 | 38.96 | 129.93 |
| SCE1572_9622 | 15.37 | 12.09 |
| SCE1572_10175 | 533.77 | 1039.78 |
| SCE1572_7334 | 100.76 | 602.78 |
| SCE1572_1889 | 43.73 | 386.06 |
| SCE1572_10254 | 0 | 0 |
| SCE1572_1133 | 22.68 | 28.73 |
| SCE1572_3664 | 23.88 | 5.13 |
| SCE1572_4150 | 26.37 | 31.07 |
| SCE1572_1651 | 60.8 | 7.23 |

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| SCE1572_5208 | 7.09 | 0 |
| SCE1572_1328 | 51.7 | 9.79 |
| SCE1572_2895 | 19.02 | 27.47 |
| SCE1572_2974 | 0 | 0 |
| SCE1572_9702 | 28.85 | 14.98 |
| SCE1572_2454 | 73.36 | 238.64 |
| SCE1572_7382 | 0 | 0 |
| SCE1572_4006 | 35.17 | 32.52 |
| SCE1572_4235 | 40.65 | 15.87 |
| SCE1572_9936 | 73.15 | 203.27 |
| SCE1572_837 | 26.39 | 27.03 |
| SCE1572_4652 | 46.2 | 51.82 |
| SCE1572_1420 | 15.09 | 24.97 |
| SCE1572_7080 | 22.81 | 112.22 |
| SCE1572_8652 | 40.25 | 137.67 |
| SCE1572_4188 | 37.43 | 134.82 |
| SCE1572_7204 | 22.3 | 0 |
| SCE1572_9373 | 54.95 | 17.53 |
| SCE1572_849 | 45.83 | 108.96 |
| SCE1572_1875 | 56.13 | 37.79 |
| SCE1572_9284 | 0 | 0 |
| SCE1572_5372 | 109.82 | 1473.72 |
| SCE1572_5178 | 16.68 | 13.73 |
| SCE1572_2073 | 9.79 | 1.68 |
| SCE1572_8706 | 35.67 | 54.49 |
| SCE1572_6592 | 55.52 | 149.05 |
| SCE1572_7836 | 17.78 | 38.53 |
| SCE1572_11591 | 52.51 | 45.81 |
| SCE1572_8539 | 15.12 | 15.87 |
| SCE1572_3835 | 34.41 | 14.05 |
| SCE1572_6830 | 7 | 0 |
| SCE1572_11030 | 47.38 | 98.07 |
| SCE1572_3266 | 43.9 | 105.66 |
| SCE1572_5948 | 58.03 | 36.04 |
| SCE1572_148 | 16.95 | 9.07 |
| SCE1572_23 | 21.04 | 66.23 |
| SCE1572_5947 | 28.54 | 19.24 |
| SCE1572_948 | 38.14 | 15.71 |
| SCE1572_2338 | 21.97 | 88.85 |
| SCE1572_4224 | 15.16 | 0 |
| SCE1572_7888 | 13.62 | 15.05 |
| SCE1572_1562 | 42.73 | 16.59 |
| SCE1572_5532 | 44.98 | 22.06 |
| SCE1572_10132 | 29.35 | 23.32 |
| SCE1572_775 | 163.48 | 317.32 |
| SCE1572_2070 | 75.81 | 13.68 |
| SCE1572_9183 | 27.44 | 13.46 |
| SCE1572_6949 | 36.87 | 16.95 |

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| SCE1572_5121 | 14.08 | 7.09 |
| SCE1572_1874 | 14.1 | 11.88 |
| SCE1572_8937 | 832.84 | 7173.44 |
| SCE1572_6818 | 16.28 | 7.35 |
| SCE1572_10945 | 34.55 | 32.25 |
| SCE1572_3281 | 18.06 | 27.45 |
| SCE1572_5527 | 38.09 | 26.59 |
| SCE1572_4618 | 32.31 | 24.8 |
| SCE1572_3833 | 33.6 | 11.55 |
| SCE1572_11166 | 31.13 | 86.03 |
| SCE1572_1477 | 51.12 | 25.81 |
| SCE1572_8127 | 46.1 | 22.19 |
| SCE1572_8824 | 7.32 | 102.91 |
| SCE1572_7061 | 0 | 0 |
| SCE1572_2817 | 0 | 0 |
| SCE1572_9804 | 0 | 0 |
| SCE1572_871 | 88.44 | 175.16 |
| SCE1572_6585 | 66.64 | 137.14 |
| SCE1572_4607 | 11.59 | 16.27 |
| SCE1572_9906 | 117.52 | 94.29 |
| SCE1572_8011 | 35.12 | 102.42 |
| SCE1572_7417 | 19.19 | 24.02 |
| SCE1572_7349 | 36.37 | 17.71 |
| SCE1572_9032 | 35.1 | 21.47 |
| SCE1572_7874 | 29.99 | 46.12 |
| SCE1572_6923 | 24.57 | 14.79 |
| SCE1572_6015 | 153.66 | 44.38 |
| SCE1572_7429 | 29.86 | 11.06 |
| SCE1572_4005 | 25.92 | 43.67 |
| SCE1572_1787 | 31.7 | 14.93 |
| SCE1572_2514 | 17.58 | 0 |
| SCE1572_5459 | 26.47 | 9.1 |
| SCE1572_3630 | 34.14 | 59.96 |
| SCE1572_8769 | 151.17 | 51.68 |
| SCE1572_3935 | 13.39 | 9.91 |
| SCE1572_5414 | 23.28 | 10.25 |
| SCE1572_11016 | 7.11 | 0 |
| SCE1572_7544 | 15.06 | 0 |
| SCE1572_6671 | 25.5 | 9.95 |
| SCE1572_7073 | 138.98 | 45.62 |
| SCE1572_6329 | 34.53 | 28.66 |
| SCE1572_64 | 50.22 | 83.68 |
| SCE1572_5977 | 27.98 | 17.23 |
| SCE1572_8807 | 41.18 | 4.51 |
| SCE1572_6839 | 13.6 | 4.71 |
| SCE1572_7760 | 71.71 | 68.33 |
| SCE1572_4711 | 40.25 | 34.45 |
| SCE1572_3348 | 32.75 | 20.44 |

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| SCE1572_1029 | 20.22 | 120.12 |
| SCE1572_462 | 38.33 | 50.19 |
| SCE1572_11038 | 0 | 0 |
| SCE1572_10520 | 32.73 | 23.81 |
| SCE1572_5154 | 28.83 | 20.15 |
| SCE1572_6555 | 49.64 | 22.45 |
| SCE1572_6123 | 19.45 | 29.68 |
| SCE1572_5496 | 62.1 | 37.36 |
| SCE1572_3450 | 26.93 | 10.97 |
| SCE1572_4001 | 43.17 | 708.73 |
| SCE1572_1269 | 41.28 | 35.29 |
| SCE1572_4463 | 20.26 | 10.39 |
| SCE1572_2265 | 53.86 | 108.04 |
| SCE1572_1933 | 29 | 108.47 |
| SCE1572_8218 | 37.43 | 21.73 |
| SCE1572_1243 | 33.82 | 84.21 |
| SCE1572_7233 | 30.99 | 19.98 |
| SCE1572_5140 | 29.32 | 18.93 |
| SCE1572_3120 | 32.31 | 17.95 |
| SCE1572_8811 | 18.16 | 4.37 |
| SCE1572_7929 | 55.78 | 142.87 |
| SCE1572_8672 | 47.43 | 52.4 |
| SCE1572_10059 | 627.87 | 4216.06 |
| SCE1572_2486 | 48.68 | 77.79 |
| SCE1572_5570 | 32.59 | 18.14 |
| SCE1572_1716 | 0 | 0 |
| SCE1572_7296 | 27.7 | 35.09 |
| SCE1572_1286 | 49.97 | 835.53 |
| SCE1572_4143 | 42.72 | 24.19 |
| SCE1572_10838 | 27.76 | 28.64 |
| SCE1572_11467 | 60.08 | 160.29 |
| SCE1572_3123 | 67.22 | 34.16 |
| SCE1572_3810 | 65.47 | 38.7 |
| SCE1572_1374 | 28.18 | 59.25 |
| SCE1572_5194 | 13.96 | 14.4 |
| SCE1572_11300 | 22.65 | 45.8 |
| SCE1572_8122 | 30.32 | 10.07 |
| SCE1572_3637 | 0 | 0 |
| SCE1572_2420 | 367.54 | 1325.91 |
| SCE1572_8093 | 31.23 | 12.53 |
| SCE1572_7376 | 30.55 | 26.11 |
| SCE1572_5072 | 27.77 | 23.01 |
| SCE1572_6105 | 35.88 | 0 |
| SCE1572_9149 | 127.01 | 361.1 |
| SCE1572_6795 | 80.01 | 135.94 |
| SCE1572_11116 | 11.93 | 11.83 |
| SCE1572_9809 | 19.84 | 34.1 |
| SCE1572_1541 | 0 | 0 |

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| SCE1572_8590 | 202.74 | 708.63 |
| SCE1572_4120 | 89.32 | 965.34 |
| SCE1572_4617 | 36.81 | 4.22 |
| SCE1572_1565 | 84.94 | 84.07 |
| SCE1572_9165 | 0 | 0 |
| SCE1572_4976 | 138.8 | 1498.24 |
| SCE1572_3465 | 0 | 0 |
| SCE1572_11582 | 42.76 | 45.68 |
| SCE1572_10816 | 21.84 | 7.22 |
| SCE1572_2694 | 17.77 | 98.36 |
| SCE1572_6704 | 60.03 | 188.94 |
| SCE1572_2207 | 33.22 | 16.4 |
| SCE1572_3780 | 18.74 | 49.2 |
| SCE1572_7 | 156.05 | 608.2 |
| SCE1572_5340 | 26.74 | 34.53 |
| SCE1572_11554 | 52.74 | 7.93 |
| SCE1572_71 | 28.11 | 16.64 |
| SCE1572_7096 | 62.97 | 29.66 |
| SCE1572_3671 | 35.33 | 46.06 |
| SCE1572_8200 | 56.15 | 9.01 |
| SCE1572_1544 | 99.77 | 40.02 |
| SCE1572_970 | 71.72 | 91.78 |
| SCE1572_6418 | 83.7 | 1053.18 |
| SCE1572_1379 | 33.01 | 13.47 |
| SCE1572_10013 | 33.78 | 11.34 |
| SCE1572_7317 | 9.19 | 3.69 |
| SCE1572_915 | 5 | 4.01 |
| SCE1572_8692 | 0 | 0 |
| SCE1572_5477 | 23.35 | 286.56 |
| SCE1572_795 | 170.33 | 322.57 |
| SCE1572_11497 | 28.54 | 0 |
| SCE1572_1571 | 27.44 | 10.43 |
| SCE1572_4127 | 0 | 0 |
| SCE1572_9636 | 96.15 | 130.84 |
| SCE1572_8368 | 23.04 | 4.03 |
| SCE1572_4962 | 22.8 | 100.61 |
| SCE1572_4857 | 33.93 | 21.69 |
| SCE1572_11183 | 62.43 | 119.4 |
| SCE1572_9518 | 56.03 | 115.03 |
| SCE1572_11306 | 36.71 | 89.45 |
| SCE1572_8265 | 50.91 | 78.58 |
| SCE1572_4350 | 18.09 | 8.71 |
| SCE1572_4031 | 1147.07 | 1218.61 |
| SCE1572_6200 | 68.83 | 110.06 |
| SCE1572_4401 | 10.9 | 0 |
| SCE1572_1229 | 18.95 | 19.63 |
| SCE1572_2408 | 122.99 | 718.67 |
| SCE1572_2593 | 0 | 0 |

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| SCE1572_6038 | 8.76 | 7.3 |
| SCE1572_10076 | 321.83 | 846.9 |
| SCE1572_10543 | 0 | 0 |
| SCE1572_9672 | 39.9 | 108.84 |
| SCE1572_575 | 2.76 | 0 |
| SCE1572_8018 | 12.2 | 12.58 |
| SCE1572_10896 | 5.12 | 0 |
| SCE1572_5710 | 12.25 | 1.4 |
| SCE1572_2223 | 48.33 | 197.16 |
| SCE1572_10586 | 0 | 0 |
| SCE1572_1362 | 113.78 | 519.02 |
| SCE1572_8990 | 94.62 | 1865.86 |
| SCE1572_10806 | 111.86 | 27.72 |
| SCE1572_3669 | 0 | 0 |
| SCE1572_1578 | 39.74 | 16.19 |
| SCE1572_8503 | 62.27 | 10.86 |
| SCE1572_9446 | 86.97 | 104.67 |
| SCE1572_7700 | 35.02 | 10.67 |
| SCE1572_570 | 74.73 | 224.33 |
| SCE1572_9127 | 28.64 | 47.3 |
| SCE1572_5203 | 33.82 | 214.34 |
| SCE1572_788 | 56.49 | 69.22 |
| SCE1572_10755 | 34.47 | 16.85 |
| SCE1572_4690 | 34.65 | 53.67 |
| SCE1572_5820 | 76.42 | 71.44 |
| SCE1572_195 | 2.23 | 8.05 |
| SCE1572_7850 | 47.92 | 73.81 |
| SCE1572_5356 | 0 | 0 |
| SCE1572_4298 | 101.08 | 78.2 |
| SCE1572_7842 | 157.74 | 261.71 |
| SCE1572_9792 | 12.69 | 3.39 |
| SCE1572_4389 | 98.39 | 27.18 |
| SCE1572_2190 | 52.09 | 158.95 |
| SCE1572_9862 | 37.9 | 30.98 |
| SCE1572_9955 | 51.23 | 20.05 |
| SCE1572_4771 | 28.21 | 14.4 |
| SCE1572_2841 | 30.32 | 19.46 |
| SCE1572_4815 | 22.4 | 103.78 |
| SCE1572_4105 | 20.07 | 7.51 |
| SCE1572_648 | 64.18 | 98.53 |
| SCE1572_2865 | 5.76 | 0 |
| SCE1572_10221 | 82.13 | 29.28 |
| SCE1572_8152 | 13.78 | 0 |
| SCE1572_4625 | 18.47 | 8.27 |
| SCE1572_11307 | 34.85 | 74.66 |
| SCE1572_4678 | 7.15 | 0 |
| SCE1572_3680 | 27.86 | 8.78 |
| SCE1572_4846 | 19.09 | 43.21 |

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| SCE1572_7342 | 50 | 282.84 |
| SCE1572_10731 | 49.22 | 76.42 |
| SCE1572_10431 | 46.31 | 32.36 |
| SCE1572_6886 | 16.85 | 14.1 |
| SCE1572_339 | 17.09 | 18.58 |
| SCE1572_351 | 30.79 | 82.49 |
| SCE1572_2303 | 21.25 | 64.8 |
| SCE1572_11009 | 37.39 | 36.62 |
| SCE1572_2477 | 86.27 | 20.56 |
| SCE1572_386 | 4.1 | 4.93 |
| SCE1572_3916 | 94.09 | 98.35 |
| SCE1572_10223 | 37.74 | 56.26 |
| SCE1572_9273 | 56.12 | 69.56 |
| SCE1572_10315 | 13.34 | 37.95 |
| SCE1572_2197 | 41.85 | 38.34 |
| SCE1572_7677 | 20.44 | 6.05 |
| SCE1572_6353 | 53.96 | 37.11 |
| SCE1572_5847 | 50.54 | 63.77 |
| SCE1572_7645 | 26.46 | 21.47 |
| SCE1572_396 | 0 | 0 |
| SCE1572_1263 | 47.79 | 759.36 |
| SCE1572_8930 | 166.23 | 164.88 |
| SCE1572_8718 | 40.23 | 55.04 |
| SCE1572_646 | 0 | 0 |
| SCE1572_116 | 42.06 | 72.32 |
| SCE1572_4107 | 16.48 | 9.7 |
| SCE1572_7978 | 45.01 | 35.42 |
| SCE1572_5941 | 32.78 | 11.66 |
| SCE1572_1961 | 64.68 | 19.56 |
| SCE1572_1002 | 24.02 | 5.42 |
| SCE1572_9336 | 14.73 | 29.19 |
| SCE1572_3473 | 138.2 | 90.72 |
| SCE1572_10099 | 44.2 | 76.83 |
| SCE1572_9650 | 38.64 | 16.91 |
| SCE1572_5825 | 30.94 | 29.49 |
| SCE1572_9924 | 120.05 | 354.9 |
| SCE1572_5598 | 39.74 | 116.55 |
| SCE1572_5299 | 34.68 | 13.12 |
| SCE1572_3541 | 0 | 0 |
| SCE1572_10403 | 30.26 | 62.59 |
| SCE1572_7289 | 60.52 | 17.82 |
| SCE1572_6165 | 18.06 | 35.1 |
| SCE1572_3066 | 21.18 | 10.19 |
| SCE1572_8619 | 39.83 | 25.23 |
| SCE1572_4157 | 5.8 | 3.99 |
| SCE1572_1084 | 15.5 | 11.66 |
| SCE1572_2081 | 77.69 | 35.44 |
| SCE1572_4493 | 29.79 | 52.46 |

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| SCE1572_8762 | 36.76 | 19.25 |
| SCE1572_10438 | 20.64 | 25.7 |
| SCE1572_7493 | 58.17 | 22.05 |
| SCE1572_2465 | 30.78 | 40.75 |
| SCE1572_466 | 49.01 | 36.86 |
| SCE1572_3197 | 11.2 | 7.19 |
| SCE1572_6827 | 41.6 | 220.55 |
| SCE1572_6934 | 63.96 | 148.47 |
| SCE1572_7467 | 45.67 | 36.94 |
| SCE1572_2244 | 48.22 | 32.41 |
| SCE1572_7579 | 62.31 | 72.21 |
| SCE1572_5545 | 25.27 | 21.96 |
| SCE1572_10693 | 32.4 | 21.83 |
| SCE1572_8314 | 89.65 | 99.64 |
| SCE1572_2311 | 136.42 | 262.98 |
| SCE1572_8612 | 40.4 | 11.03 |
| SCE1572_11147 | 35.92 | 12.64 |
| SCE1572_3204 | 75.37 | 102.18 |
| SCE1572_6189 | 42.24 | 34.82 |
| SCE1572_11522 | 50.77 | 20.37 |
| SCE1572_626 | 40.49 | 43.07 |
| SCE1572_7092 | 13.62 | 50.26 |
| SCE1572_8149 | 30.01 | 15.21 |
| SCE1572_157 | 73.23 | 439.46 |
| SCE1572_6805 | 50.41 | 47.64 |
| SCE1572_5015 | 223.58 | 6096.05 |
| SCE1572_246 | 7.98 | 7.68 |
| SCE1572_6876 | 17.36 | 39 |
| SCE1572_6947 | 32.37 | 18.18 |
| SCE1572_4648 | 57.17 | 29.91 |
| SCE1572_3300 | 35.64 | 14.98 |
| SCE1572_4322 | 31 | 11.76 |
| SCE1572_7413 | 36.53 | 57.73 |
| SCE1572_345 | 25.7 | 9.9 |
| SCE1572_3174 | 46.61 | 77.06 |
| SCE1572_1032 | 39.14 | 32.56 |
| SCE1572_3024 | 42.13 | 20.68 |
| SCE1572_4045 | 16.41 | 13.37 |
| SCE1572_10955 | 142.7 | 391.27 |
| SCE1572_10092 | 74.6 | 59.02 |
| SCE1572_6989 | 14.88 | 15.67 |
| SCE1572_7126 | 165.09 | 75.69 |
| SCE1572_6902 | 63.63 | 11.34 |
| SCE1572_11542 | 75.53 | 18.44 |
| SCE1572_10244 | 8.03 | 0 |
| SCE1572_1039 | 24.28 | 4.77 |
| SCE1572_11361 | 28.89 | 39.85 |
| SCE1572_5394 | 212.95 | 99.52 |

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| SCE1572_7001 | 40.88 | 38.74 |
| SCE1572_1928 | 107.28 | 247.67 |
| SCE1572_9659 | 62.12 | 86.39 |
| SCE1572_10292 | 153.1 | 228.97 |
| SCE1572_11372 | 41.48 | 161.7 |
| SCE1572_10501 | 39.31 | 70.96 |
| SCE1572_10469 | 31.78 | 113.14 |
| SCE1572_7153 | 91.92 | 26.23 |
| SCE1572_5337 | 63.83 | 28.23 |
| SCE1572_4586 | 168.22 | 323.39 |
| SCE1572_10442 | 19.1 | 6.11 |
| SCE1572_1867 | 85.28 | 56.42 |
| SCE1572_4092 | 61.59 | 24.71 |
| SCE1572_3522 | 0 | 0 |
| SCE1572_9718 | 63.12 | 212.18 |
| SCE1572_8100 | 26.34 | 34.75 |
| SCE1572_11051 | 42.96 | 336.03 |
| SCE1572_5416 | 24.24 | 6.78 |
| SCE1572_4826 | 68.01 | 88.36 |
| SCE1572_1192 | 44.51 | 27.62 |
| SCE1572_3500 | 51.32 | 47.07 |
| SCE1572_10115 | 39.22 | 57.14 |
| SCE1572_3036 | 38.52 | 8.88 |
| SCE1572_3078 | 43.16 | 47.36 |
| SCE1572_2318 | 15.11 | 0 |
| SCE1572_9823 | 79.16 | 20.19 |
| SCE1572_1406 | 72.97 | 119.45 |
| SCE1572_7068 | 16.91 | 10.18 |
| SCE1572_5314 | 0 | 0 |
| SCE1572_10715 | 42.59 | 31.51 |
| SCE1572_2090 | 14.74 | 0 |
| SCE1572_11243 | 16.33 | 37.43 |
| SCE1572_4940 | 179.18 | 2116.55 |
| SCE1572_4118 | 28.61 | 3541.81 |
| SCE1572_1558 | 40.45 | 15.89 |
| SCE1572_5224 | 43.63 | 70.88 |
| SCE1572_10858 | 275.39 | 449.06 |
| SCE1572_7747 | 52.42 | 70.54 |
| SCE1572_11219 | 48.41 | 28 |
| SCE1572_6498 | 60.49 | 222.58 |
| SCE1572_10173 | 74.3 | 75.12 |
| SCE1572_4019 | 31.62 | 38.51 |
| SCE1572_8116 | 0 | 0 |
| SCE1572_9140 | 30.84 | 13.61 |
| SCE1572_2259 | 116.72 | 35.8 |
| SCE1572_10910 | 88.82 | 19.31 |
| SCE1572_10689 | 14.15 | 14.6 |
| SCE1572_7190 | 45.53 | 55.96 |

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| SCE1572_9344 | 31.69 | 91.75 |
| SCE1572_3439 | 24.2 | 18.69 |
| SCE1572_10231 | 80.64 | 29.08 |
| SCE1572_8189 | 34.24 | 26.16 |
| SCE1572_10129 | 27.46 | 2.87 |
| SCE1572_5468 | 43.07 | 18.18 |
| SCE1572_8592 | 64.54 | 65.67 |
| SCE1572_6688 | 27.4 | 8.78 |
| SCE1572_2262 | 17.4 | 11.39 |
| SCE1572_1587 | 51.32 | 0 |
| SCE1572_8244 | 354.59 | 1253.68 |
| SCE1572_4709 | 37.61 | 6.32 |
| SCE1572_3382 | 9.45 | 27.69 |
| SCE1572_8088 | 56.78 | 14.04 |
| SCE1572_8813 | 0 | 0 |
| SCE1572_7356 | 100 | 102.66 |
| SCE1572_8655 | 211.69 | 2161.99 |
| SCE1572_7819 | 120.41 | 442.48 |
| SCE1572_8227 | 21.41 | 77.31 |
| SCE1572_7669 | 23.11 | 6.89 |
| SCE1572_3496 | 34.95 | 48.31 |
| SCE1572_3695 | 26.87 | 110.86 |
| SCE1572_2549 | 0 | 0 |
| SCE1572_8482 | 18.27 | 131.9 |
| SCE1572_975 | 340.72 | 5457.79 |
| SCE1572_7695 | 17.3 | 22.04 |
| SCE1572_1331 | 50.54 | 34.17 |
| SCE1572_3107 | 15.08 | 13.1 |
| SCE1572_9343 | 140.27 | 1218.32 |
| SCE1572_5259 | 13.59 | 11.15 |
| SCE1572_7280 | 19.64 | 7.27 |
| SCE1572_4987 | 68.86 | 87.23 |
| SCE1572_5451 | 49.15 | 21.58 |
| SCE1572_2033 | 78.43 | 160.9 |
| SCE1572_11425 | 51.27 | 72.01 |
| SCE1572_7365 | 66.5 | 148.99 |
| SCE1572_1748 | 49.09 | 43.8 |
| SCE1572_8081 | 4.97 | 0 |
| SCE1572_10527 | 42.64 | 40.73 |
| SCE1572_8038 | 66.83 | 18.41 |
| SCE1572_407 | 51.02 | 383.95 |
| SCE1572_9948 | 73.64 | 20.85 |
| SCE1572_4473 | 41.35 | 88.47 |
| SCE1572_7898 | 37.04 | 93.91 |
| SCE1572_1451 | 23.98 | 5.87 |
| SCE1572_6098 | 31.29 | 32.22 |
| SCE1572_6719 | 49.55 | 364.92 |
| SCE1572_10233 | 21.66 | 6.13 |

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| SCE1572_3295 | 12.89 | 14.77 |
| SCE1572_3787 | 76.85 | 121.64 |
| SCE1572_586 | 38.48 | 31.25 |
| SCE1572_8388 | 26.59 | 10.89 |
| SCE1572_11126 | 27.07 | 21.26 |
| SCE1572_2579 | 66.74 | 35.7 |
| SCE1572_1505 | 38.13 | 10.67 |
| SCE1572_11598 | 85.7 | 1010.9 |
| SCE1572_3401 | 26.44 | 12.73 |
| SCE1572_856 | 0 | 0 |
| SCE1572_11157 | 87.16 | 35.66 |
| SCE1572_1363 | 177.76 | 926.99 |
| SCE1572_4700 | 26.97 | 12.98 |
| SCE1572_5008 | 195.95 | 629.54 |
| SCE1572_4923 | 14.17 | 6.82 |
| SCE1572_6864 | 2.11 | 0 |
| SCE1572_4952 | 9.85 | 0.85 |
| SCE1572_1629 | 6.42 | 3.09 |
| SCE1572_8056 | 0 | 0 |
| SCE1572_2998 | 85.55 | 75.59 |
| SCE1572_1338 | 24.35 | 17.45 |
| SCE1572_534 | 0 | 0 |
| SCE1572_5084 | 83.57 | 1490.47 |
| SCE1572_10864 | 25.27 | 79.53 |
| SCE1572_4670 | 31.37 | 9.56 |
| SCE1572_4408 | 45.91 | 12.85 |
| SCE1572_7960 | 41.14 | 77.02 |
| SCE1572_7920 | 66.8 | 32.93 |
| SCE1572_6928 | 34.36 | 37 |
| SCE1572_11482 | 40.68 | 151.31 |
| SCE1572_5130 | 51.9 | 95.34 |
| SCE1572_8999 | 164.86 | 784.03 |
| SCE1572_6207 | 40.64 | 8.87 |
| SCE1572_747 | 34.06 | 12.06 |
| SCE1572_7318 | 22.99 | 19.25 |
| SCE1572_5697 | 43.71 | 89.03 |
| SCE1572_2626 | 25.72 | 28.37 |
| SCE1572_8713 | 62.36 | 39.4 |
| SCE1572_3408 | 91.3 | 143.84 |
| SCE1572_6211 | 50.54 | 9.5 |
| SCE1572_4720 | 54.12 | 20.88 |
| SCE1572_5782 | 17.76 | 32.88 |
| SCE1572_8210 | 13.04 | 20.17 |
| SCE1572_8460 | 16.01 | 70.26 |
| SCE1572_9741 | 41.77 | 214.73 |
| SCE1572_1894 | 46.65 | 19.81 |
| SCE1572_10738 | 60.03 | 29.1 |
| SCE1572_9990 | 24.76 | 21.9 |

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| SCE1572_1915 | 88.7 | 41.38 |
| SCE1572_7209 | 33.27 | 45.62 |
| SCE1572_6968 | 42.87 | 223.99 |
| SCE1572_5729 | 32.19 | 35.68 |
| SCE1572_8852 | 39.89 | 19.69 |
| SCE1572_3618 | 0 | 0 |
| SCE1572_9891 | 43.77 | 1.88 |
| SCE1572_1847 | 61.77 | 25.34 |
| SCE1572_781 | 10.75 | 11.62 |
| SCE1572_1724 | 58.18 | 277.39 |
| SCE1572_5230 | 64.35 | 356.64 |
| SCE1572_4683 | 76.41 | 49.63 |
| SCE1572_9081 | 75.81 | 10.58 |
| SCE1572_5280 | 66.56 | 97.91 |
| SCE1572_7658 | 0 | 0 |
| SCE1572_6961 | 0 | 0 |
| SCE1572_8854 | 25.96 | 116.23 |
| SCE1572_5807 | 24.5 | 18.43 |
| SCE1572_1152 | 17.65 | 17.5 |
| SCE1572_10165 | 24.12 | 11.85 |
| SCE1572_5520 | 24.12 | 35.94 |
| SCE1572_11499 | 24.24 | 13.79 |
| SCE1572_4959 | 0 | 0 |
| SCE1572_2116 | 24.45 | 5.89 |
| SCE1572_11538 | 43.03 | 650.94 |
| SCE1572_8060 | 70.26 | 4.45 |
| SCE1572_7558 | 17.97 | 0.76 |
| SCE1572_5864 | 18.01 | 18.07 |
| SCE1572_3367 | 63.89 | 1156.57 |
| SCE1572_6339 | 15.82 | 45.94 |
| SCE1572_8893 | 0 | 0 |
| SCE1572_11490 | 0 | 13.81 |
| SCE1572_11323 | 35.72 | 103.9 |
| SCE1572_1167 | 12.4 | 56.4 |
| SCE1572_5367 | 12.63 | 22.12 |
| SCE1572_2151 | 41.81 | 8.13 |
| SCE1572_9082 | 24.68 | 0 |
| SCE1572_8945 | 161.13 | 811.67 |
| SCE1572_10487 | 251.38 | 8122.2 |
| SCE1572_9834 | 51.79 | 22.67 |
| SCE1572_8804 | 27.71 | 172.27 |
| SCE1572_8902 | 31.31 | 16.99 |
| SCE1572_1310 | 233.26 | 2150.94 |
| SCE1572_8191 | 51.46 | 21.52 |
| SCE1572_8064 | 30.32 | 0 |
| SCE1572_3333 | 70.02 | 148.08 |
| SCE1572_8031 | 73.36 | 55.99 |
| SCE1572_8256 | 21.96 | 40.93 |

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| SCE1572_708 | 59.7 | 100.21 |
| SCE1572_10649 | 27.27 | 3.86 |
| SCE1572_5833 | 46.74 | 97.42 |
| SCE1572_4727 | 25.09 | 13.01 |
| SCE1572_7808 | 122.85 | 99.32 |
| SCE1572_10039 | 11.54 | 15.15 |
| SCE1572_254 | 0 | 0 |
| SCE1572_6367 | 27.34 | 130.12 |
| SCE1572_7707 | 34.64 | 23.59 |
| SCE1572_11059 | 67.23 | 15.37 |
| SCE1572_2556 | 0 | 0 |
| SCE1572_89 | 98.94 | 119.59 |
| SCE1572_823 | 32.44 | 10.89 |
| SCE1572_10365 | 41.9 | 122.86 |
| SCE1572_1486 | 61.64 | 90.38 |
| SCE1572_5720 | 22.66 | 11.69 |
| SCE1572_274 | 0 | 0 |
| SCE1572_8359 | 0 | 0 |
| SCE1572_5250 | 44.55 | 220.51 |
| SCE1572_9204 | 36.67 | 61.61 |
| SCE1572_6460 | 62.71 | 28.16 |
| SCE1572_7225 | 110.77 | 92.65 |
| SCE1572_3279 | 41.94 | 68.77 |
| SCE1572_3254 | 9.28 | 20.61 |
| SCE1572_1215 | 44.63 | 3.41 |
| SCE1572_6980 | 24.4 | 11.53 |
| SCE1572_10061 | 1251.91 | 7965.73 |
| SCE1572_4971 | 0 | 0 |
| SCE1572_10259 | 20.81 | 7.16 |
| SCE1572_8835 | 50.75 | 16.8 |
| SCE1572_5955 | 0 | 0 |
| SCE1572_1198 | 99.48 | 33.9 |
| SCE1572_8437 | 1.56 | 22.57 |
| SCE1572_4927 | 18.1 | 0 |
| SCE1572_2096 | 20.86 | 65.28 |
| SCE1572_6905 | 30.93 | 9.08 |
| SCE1572_5882 | 41.2 | 37.02 |
| SCE1572_6445 | 26.1 | 12.03 |
| SCE1572_8555 | 15.73 | 192.79 |
| SCE1572_9163 | 12.26 | 1.55 |
| SCE1572_9120 | 18 | 15.97 |
| SCE1572_10711 | 9.63 | 0 |
| SCE1572_2277 | 55.46 | 447.14 |
| SCE1572_5730 | 0 | 0 |
| SCE1572_8432 | 6.65 | 1.69 |
| SCE1572_1342 | 195.25 | 673.4 |
| SCE1572_1108 | 55.22 | 15.25 |
| SCE1572_7530 | 39.19 | 30.49 |

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| SCE1572_111 | 39.55 | 23.8 |
| SCE1572_3770 | 0 | 0 |
| SCE1572_5024 | 52.75 | 34.82 |
| SCE1572_6420 | 43.65 | 58.31 |
| SCE1572_11221 | 9.94 | 0 |
| SCE1572_5053 | 64.33 | 47.34 |
| SCE1572_965 | 6.37 | 0 |
| SCE1572_10626 | 17.44 | 45.21 |
| SCE1572_2393 | 49.52 | 290.04 |
| SCE1572_5914 | 30.23 | 92.08 |
| SCE1572_9533 | 28.17 | 29.88 |
| SCE1572_9014 | 130.89 | 528.85 |
| SCE1572_10970 | 99.98 | 270.71 |
| SCE1572_10600 | 16.5 | 8.99 |
| SCE1572_10085 | 86.82 | 245.84 |
| SCE1572_3100 | 18.22 | 6.45 |
| SCE1572_6821 | 45.75 | 14.16 |
| SCE1572_7628 | 17.53 | 15.82 |
| SCE1572_5037 | 33.54 | 241.44 |
| SCE1572_7740 | 38.41 | 71.04 |
| SCE1572_2737 | 17.04 | 23.63 |
| SCE1572_6735 | 42.44 | 149.35 |
| SCE1572_1425 | 47.79 | 57.51 |
| SCE1572_4733 | 28.93 | 39 |
| SCE1572_2700 | 7.98 | 2.95 |
| SCE1572_1842 | 49.71 | 7.49 |
| SCE1572_9618 | 15.16 | 15.78 |
| SCE1572_5865 | 36.27 | 22.79 |
| SCE1572_5756 | 44.65 | 16.25 |
| SCE1572_162 | 36.26 | 20.82 |
| SCE1572_10519 | 25.02 | 13.21 |
| SCE1572_7513 | 10.17 | 3.16 |
| SCE1572_432 | 34.15 | 155.06 |
| SCE1572_10985 | 2945.68 | 8445.35 |
| SCE1572_11399 | 34.54 | 56.53 |
| SCE1572_8397 | 26.31 | 14.48 |
| SCE1572_3236 | 74.8 | 559.55 |
| SCE1572_569 | 73.36 | 115.36 |
| SCE1572_6712 | 58.11 | 247.57 |
| SCE1572_980 | 21.17 | 17.9 |
| SCE1572_945 | 74.53 | 14.72 |
| SCE1572_4483 | 42.72 | 66.66 |
| SCE1572_5744 | 42.18 | 32.53 |
| SCE1572_11289 | 0 | 0 |
| SCE1572_9402 | 297.4 | 1405.3 |
| SCE1572_6728 | 12.29 | 32.41 |
| SCE1572_5674 | 33.28 | 13.35 |
| SCE1572_503 | 12.57 | 3.78 |

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| SCE1572_1048 | 18.49 | 32.64 |
| SCE1572_1604 | 65.42 | 42.61 |
| SCE1572_10512 | 164.34 | 387.89 |
| SCE1572_3977 | 59.9 | 40.83 |
| SCE1572_10201 | 20.55 | 43.48 |
| SCE1572_7535 | 527.12 | 153.08 |
| SCE1572_10684 | 49.17 | 14.79 |
| SCE1572_6602 | 10.22 | 6.83 |
| SCE1572_2793 | 15.55 | 1.65 |
| SCE1572_4253 | 1.46 | 0 |
| SCE1572_10871 | 48.13 | 18.42 |
| SCE1572_1622 | 31.24 | 196.21 |
| SCE1572_8321 | 31.55 | 23.2 |
| SCE1572_185 | 31.99 | 6.7 |
| SCE1572_650 | 756.41 | 1310.03 |
| SCE1572_9797 | 25.57 | 30.78 |
| SCE1572_1637 | 10.47 | 8.94 |
| SCE1572_6215 | 44.59 | 16.36 |
| SCE1572_2615 | 20.35 | 20.54 |
| SCE1572_7611 | 35.35 | 98.51 |
| SCE1572_475 | 25.49 | 268.97 |
| SCE1572_2656 | 47.6 | 26.16 |
| SCE1572_9436 | 587.4 | 1828.88 |
| SCE1572_635 | 153.03 | 966.7 |
| SCE1572_10267 | 31.69 | 52.8 |
| SCE1572_1632 | 36.53 | 48.36 |
| SCE1572_5284 | 27.32 | 65.76 |
| SCE1572_4057 | 1.85 | 0 |
| SCE1572_1470 | 56.74 | 49.76 |
| SCE1572_2756 | 3.37 | 0 |
| SCE1572_400 | 26.85 | 22.81 |
| SCE1572_5013 | 43.54 | 93.7 |
| SCE1572_6953 | 22.58 | 14.23 |
| SCE1572_5556 | 60.58 | 94.96 |
| SCE1572_10859 | 141.54 | 405.11 |
| SCE1572_1658 | 24.78 | 8.77 |
| SCE1572_4932 | 232.98 | 956.72 |
| SCE1572_9965 | 0 | 0 |
| SCE1572_6542 | 54.65 | 87.68 |
| SCE1572_359 | 46.33 | 27.44 |
| SCE1572_7774 | 7.71 | 0 |
| SCE1572_401 | 49.62 | 42.02 |
| SCE1572_11549 | 26.67 | 15.83 |
| SCE1572_8023 | 16.33 | 0 |
| SCE1572_8404 | 20.34 | 4.45 |
| SCE1572_3422 | 38.04 | 49.4 |
| SCE1572_6475 | 97.54 | 560.57 |
| SCE1572_10727 | 80.37 | 53.5 |

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| SCE1572_11507 | 24.09 | 9.9 |
| SCE1572_953 | 43.18 | 43.5 |
| SCE1572_5930 | 0 | 0 |
| SCE1572_7214 | 32.23 | 104.88 |
| SCE1572_6073 | 2.92 | 0 |
| SCE1572_3803 | 46.29 | 16.15 |
| SCE1572_2166 | 62.72 | 23.02 |
| SCE1572_6391 | 0 | 0 |
| SCE1572_1683 | 10.22 | 434.63 |
| SCE1572_206 | 0 | 0 |
| SCE1572_4345 | 20.89 | 22.99 |
| SCE1572_11295 | 13.42 | 32.29 |
| SCE1572_11150 | 28.99 | 41.44 |
| SCE1572_1022 | 43.89 | 20.58 |
| SCE1572_284 | 14.76 | 16.15 |
| SCE1572_8043 | 0 | 0 |
| SCE1572_1013 | 19.17 | 9.74 |
| SCE1572_6360 | 68.75 | 253.86 |
| SCE1572_1702 | 22.05 | 23.7 |
| SCE1572_5589 | 53.8 | 42.56 |
| SCE1572_3554 | 6.97 | 2.1 |
| SCE1572_6361 | 86.74 | 48.43 |
| SCE1572_9962 | 3.09 | 0 |
| SCE1572_375 | 44.02 | 14.13 |
| SCE1572_3360 | 15.18 | 12.42 |
| SCE1572_1382 | 3.61 | 0 |
| SCE1572_496 | 33.51 | 32.26 |
| SCE1572_4906 | 30.12 | 39.99 |
| SCE1572_10279 | 9.32 | 0 |
| SCE1572_7742 | 43.19 | 73.72 |
| SCE1572_1958 | 71.95 | 89.07 |
| SCE1572_2484 | 143.1 | 262.42 |
| SCE1572_5543 | 58.2 | 7.37 |
| SCE1572_11096 | 43.62 | 24.96 |
| SCE1572_3840 | 35.18 | 12.1 |
| SCE1572_11175 | 52.15 | 114.5 |
| SCE1572_9050 | 45.79 | 52.39 |
| SCE1572_4536 | 19.88 | 84.95 |
| SCE1572_2141 | 23.78 | 1.43 |
| SCE1572_363 | 28.39 | 9.62 |
| SCE1572_2979 | 54 | 20 |
| SCE1572_6042 | 85.32 | 3260.6 |
| SCE1572_139 | 12.63 | 30.41 |
| SCE1572_10363 | 42.26 | 140.8 |
| SCE1572_2086 | 44.94 | 60.67 |
| SCE1572_7149 | 11.95 | 50.87 |
| SCE1572_2884 | 39.53 | 56.04 |
| SCE1572_7256 | 41.23 | 84.47 |

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| SCE1572_7012 | 0 | 0 |
| SCE1572_10071 | 851.58 | 1529.63 |
| SCE1572_9429 | 11.96 | 8.06 |
| SCE1572_6087 | 32.22 | 36.49 |
| SCE1572_1454 | 22.3 | 12.38 |
| SCE1572_5163 | 0 | 0 |
| SCE1572_2811 | 114.59 | 8.49 |
| SCE1572_6963 | 46.4 | 123.63 |
| SCE1572_11528 | 20.61 | 4.41 |
| SCE1572_2771 | 3.49 | 0 |
| SCE1572_8139 | 17.63 | 53.75 |
| SCE1572_8427 | 67.11 | 8.97 |
| SCE1572_6847 | 11.39 | 0.68 |
| SCE1572_18 | 55.2 | 188.91 |
| SCE1572_9852 | 47.96 | 57.72 |
| SCE1572_8582 | 43.08 | 29.91 |
| SCE1572_3980 | 53.8 | 93.19 |
| SCE1572_1717 | 17.81 | 55.42 |
| SCE1572_713 | 47.21 | 61.62 |
| SCE1572_4522 | 46.4 | 20.22 |
| SCE1572_3892 | 48.29 | 89.2 |
| SCE1572_1887 | 54.15 | 126.24 |
| SCE1572_2458 | 48.76 | 160.76 |
| SCE1572_3340 | 97.22 | 5100.43 |
| SCE1572_2148 | 58.18 | 16.94 |
| SCE1572_559 | 37.9 | 1148.83 |
| SCE1572_2023 | 46.52 | 48.33 |
| SCE1572_4729 | 36.93 | 23.39 |
| SCE1572_10328 | 59.23 | 17.04 |
| SCE1572_11069 | 56.94 | 54.03 |
| SCE1572_5035 | 27.06 | 19.64 |
| SCE1572_8484 | 27.72 | 56.61 |
| SCE1572_10964 | 34.38 | 19.14 |
| SCE1572_3188 | 13.33 | 2.76 |
| SCE1572_10046 | 59.71 | 427.35 |
| SCE1572_660 | 343.25 | 992.62 |
| SCE1572_5654 | 37.87 | 434.93 |
| SCE1572_7637 | 56.04 | 795.44 |
| SCE1572_10703 | 36.14 | 173.95 |
| SCE1572_3683 | 33.32 | 7.02 |
| SCE1572_2729 | 22.59 | 16.15 |
| SCE1572_7670 | 17.33 | 5.21 |
| SCE1572_6172 | 3.23 | 0 |
| SCE1572_10213 | 11.66 | 0 |
| SCE1572_5060 | 67.26 | 179.78 |
| SCE1572_3517 | 57.93 | 21.82 |
| SCE1572_2945 | 0 | 0 |
| SCE1572_2730 | 30.92 | 22.43 |

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| SCE1572_10334 | 25.42 | 24.04 |
| SCE1572_8557 | 18.46 | 9 |
| SCE1572_2343 | 54.15 | 39.1 |
| SCE1572_7160 | 17.37 | 9.04 |
| SCE1572_2076 | 38.12 | 41.99 |
| SCE1572_7855 | 61.19 | 105.52 |
| SCE1572_4309 | 23.11 | 9.14 |
| SCE1572_1238 | 22.37 | 11.96 |
| SCE1572_7792 | 24.48 | 9.07 |
| SCE1572_1398 | 74.42 | 35.29 |
| SCE1572_7799 | 2.57 | 0 |
| SCE1572_552 | 22.88 | 110.14 |
| SCE1572_11352 | 21.66 | 0 |
| SCE1572_8589 | 17.38 | 4.65 |
| SCE1572_4555 | 50.45 | 23.38 |
| SCE1572_8548 | 42.54 | 17.73 |
| SCE1572_8291 | 57.95 | 23.7 |
| SCE1572_6757 | 32.52 | 43.37 |
| SCE1572_685 | 0 | 0 |
| SCE1572_5480 | 39.88 | 19.24 |
| SCE1572_7732 | 11 | 28.07 |
| SCE1572_9613 | 15.35 | 0 |
| SCE1572_8301 | 89.89 | 1300.69 |
| SCE1572_171 | 39.24 | 68.69 |
| SCE1572_1880 | 44.62 | 30.03 |
| SCE1572_3629 | 15.9 | 5.1 |
| SCE1572_6786 | 91.57 | 160.78 |
| SCE1572_6227 | 9.69 | 3.01 |
| SCE1572_4580 | 53.27 | 24.28 |
| SCE1572_11419 | 0 | 0 |
| SCE1572_2279 | 81.56 | 122.16 |
| SCE1572_2386 | 78.92 | 104.26 |
| SCE1572_9171 | 16.98 | 10.97 |
| SCE1572_1656 | 12.55 | 53.46 |
| SCE1572_10893 | 34.36 | 58.93 |
| SCE1572_10557 | 25.41 | 10.87 |
| SCE1572_4317 | 18.8 | 2.89 |
| SCE1572_1303 | 18.89 | 89.69 |
| SCE1572_925 | 68.56 | 128.8 |
| SCE1572_5437 | 0 | 0 |
| SCE1572_8974 | 34.51 | 22.25 |
| SCE1572_6549 | 42.62 | 92.49 |
| SCE1572_1493 | 4.46 | 0 |
| SCE1572_234 | 66.33 | 43.08 |
| SCE1572_6573 | 50.07 | 15.17 |
| SCE1572_8782 | 43.09 | 231.87 |
| SCE1572_7749 | 82.7 | 28.75 |
| SCE1572_759 | 1398.15 | 940.17 |

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| SCE1572_7301 | 0 | 0 |
| SCE1572_4425 | 16.07 | 79.22 |
| SCE1572_3091 | 151.62 | 102.8 |
| SCE1572_3569 | 11.17 | 3.84 |
| SCE1572_2509 | 42.45 | 79.24 |
| SCE1572_8045 | 36.53 | 11.99 |
| SCE1572_1040 | 8.64 | 0 |
| SCE1572_2867 | 0 | 0 |
| SCE1572_7311 | 38.49 | 15.35 |
| SCE1572_1412 | 15.76 | 61.38 |
| SCE1572_8723 | 18.27 | 13.19 |
| SCE1572_10277 | 11.38 | 10.47 |
| SCE1572_613 | 59.49 | 41.9 |
| SCE1572_8076 | 84.34 | 26.99 |
| SCE1572_10633 | 42.71 | 259.39 |
| SCE1572_3763 | 29.9 | 35.98 |
| SCE1572_7561 | 25.52 | 18.07 |
| SCE1572_5892 | 39.13 | 150.09 |
| SCE1572_470 | 67.38 | 187.43 |
| SCE1572_2449 | 24.97 | 6.44 |
| SCE1572_11092 | 37.65 | 146.21 |
| SCE1572_11217 | 20.01 | 25.93 |
| SCE1572_1277 | 0 | 0 |
| SCE1572_3432 | 70.22 | 225.83 |
| SCE1572_8180 | 20.78 | 5.86 |
| SCE1572_2967 | 0.92 | 0 |
| SCE1572_10009 | 41.4 | 30.01 |
| SCE1572_9257 | 67.83 | 9.6 |
| SCE1572_10056 | 17.93 | 141.26 |
| SCE1572_9388 | 89.72 | 135.59 |
| SCE1572_4596 | 97.79 | 574.75 |
| SCE1572_9424 | 74.58 | 43.4 |
| SCE1572_7857 | 37.83 | 29.61 |
| SCE1572_10178 | 75.81 | 243.28 |
| SCE1572_9815 | 38.36 | 21.29 |
| SCE1572_2440 | 31.05 | 25.39 |
| SCE1572_6435 | 36.6 | 8.99 |
| SCE1572_3582 | 27.66 | 12.33 |
| SCE1572_1524 | 128.29 | 135.68 |
| SCE1572_9381 | 27.19 | 50.24 |
| SCE1572_5893 | 17.54 | 9.38 |
| SCE1572_3866 | 75.01 | 875.81 |
| SCE1572_2238 | 69.3 | 479.21 |
| SCE1572_10002 | 69.96 | 233.89 |
| SCE1572_6324 | 57.78 | 195.22 |
| SCE1572_10873 | 100.92 | 24.86 |
| SCE1572_10781 | 10.46 | 0 |
| SCE1572_8134 | 52.57 | 15.82 |

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| SCE1572_6157 | 48.54 | 28.81 |
| SCE1572_5316 | 40.99 | 19.02 |
| SCE1572_3320 | 33.46 | 47.01 |
| SCE1572_11047 | 26.51 | 23.51 |
| SCE1572_8178 | 1.52 | 0 |
| SCE1572_11448 | 9.24 | 4.45 |
| SCE1572_7680 | 31.76 | 21.64 |
| SCE1572_3006 | 2.41 | 0 |
| SCE1572_3728 | 55.27 | 14.13 |
| SCE1572_6511 | 11.37 | 7.82 |
| SCE1572_2838 | 67.23 | 15.37 |
| SCE1572_930 | 78.84 | 639.02 |
| SCE1572_2214 | 0 | 0 |
| SCE1572_630 | 69.88 | 689.3 |
| SCE1572_607 | 73.19 | 767.6 |
| SCE1572_4392 | 35.75 | 13.35 |
| SCE1572_1670 | 109.92 | 691.07 |
| SCE1572_1760 | 0 | 0 |
| SCE1572_7772 | 18.42 | 17.09 |
| SCE1572_11335 | 0 | 0 |
| SCE1572_672 | 26.15 | 75.72 |
| SCE1572_2364 | 5.89 | 0 |
| SCE1572_8352 | 19.36 | 7.76 |
| SCE1572_5257 | 26.51 | 14.04 |
| SCE1572_4202 | 26.86 | 31.97 |
| SCE1572_9274 | 49.4 | 181.09 |
| SCE1572_4757 | 33.57 | 18.25 |
| SCE1572_2529 | 42.45 | 36.49 |
| SCE1572_2799 | 32.75 | 12.96 |
| SCE1572_7911 | 47.78 | 6.63 |
| SCE1572_5853 | 27.96 | 15.73 |
| SCE1572_7885 | 31.34 | 34.89 |
| SCE1572_7140 | 0 | 0 |
| SCE1572_3909 | 21.26 | 8.27 |
| SCE1572_3622 | 80.88 | 17.24 |
| SCE1572_3549 | 82.01 | 28.57 |
| SCE1572_10842 | 4.13 | 6.63 |
| SCE1572_10422 | 34.74 | 66.89 |
| SCE1572_1704 | 16.85 | 0 |
| SCE1572_2200 | 67.33 | 100.86 |
| SCE1572_9269 | 63.55 | 72.26 |
| SCE1572_7607 | 266.03 | 43.93 |
| SCE1572_6278 | 40.15 | 92.08 |
| SCE1572_11270 | 113.13 | 178.76 |
| SCE1572_3641 | 34.72 | 20.1 |
| SCE1572_1448 | 10.99 | 7.05 |
| SCE1572_8222 | 28.08 | 21.83 |
| SCE1572_6668 | 34.67 | 31.91 |

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| SCE1572_10391 | 44.65 | 17.78 |
| SCE1572_3723 | 19.58 | 346.29 |
| SCE1572_5401 | 19.88 | 0 |
| SCE1572_2209 | 17.41 | 8.11 |
| SCE1572_5051 | 53.45 | 31.5 |
| SCE1572_2294 | 42.16 | 40 |
| SCE1572_2739 | 27.86 | 41.42 |
| SCE1572_9260 | 15.14 | 16.54 |
| SCE1572_6238 | 36.57 | 11.87 |
| SCE1572_2175 | 14.44 | 22.59 |
| SCE1572_10144 | 32.13 | 16.34 |
| SCE1572_1793 | 2.66 | 0 |
| SCE1572_8299 | 28.27 | 6.19 |
| SCE1572_5044 | 14.3 | 14.4 |
| SCE1572_11579 | 61.01 | 36.16 |
| SCE1572_3989 | 9.08 | 14.13 |
| SCE1572_3448 | 31.5 | 29.53 |
| SCE1572_2473 | 131.4 | 756.04 |
| SCE1572_3614 | 24.69 | 14.6 |
| SCE1572_4179 | 39.16 | 14.33 |
| SCE1572_217 | 21.01 | 20.88 |
| SCE1572_3012 | 27.69 | 7.93 |
| SCE1572_7604 | 13.32 | 9.16 |
| SCE1572_5446 | 52.99 | 19.49 |
| SCE1572_6629 | 23.17 | 124.87 |
| SCE1572_11570 | 23.73 | 577.53 |
| SCE1572_3537 | 58.71 | 23.29 |
| SCE1572_2564 | 25.27 | 13.22 |
| SCE1572_7053 | 68.38 | 28.62 |
| SCE1572_3293 | 44.4 | 30.24 |
| SCE1572_6213 | 27.69 | 17.45 |
| SCE1572_5011 | 20.18 | 44.84 |
| SCE1572_3067 | 38.61 | 31.44 |
| SCE1572_10740 | 24.78 | 14.2 |
| SCE1572_9132 | 69.81 | 58.86 |
| SCE1572_3161 | 26.37 | 63.46 |
| SCE1572_2882 | 33.24 | 36.49 |
| SCE1572_726 | 18.59 | 7.3 |
| SCE1572_4371 | 37.66 | 16.27 |
| SCE1572_7824 | 16.77 | 6.34 |
| SCE1572_8143 | 10.03 | 0 |
| SCE1572_2954 | 52.31 | 23.61 |
| SCE1572_5103 | 60.52 | 414.99 |
| SCE1572_9826 | 42.96 | 15.21 |
| SCE1572_3579 | 46.65 | 158.08 |
| SCE1572_9507 | 33.28 | 28.19 |
| SCE1572_1085 | 75.81 | 30.6 |
| SCE1572_7861 | 5.32 | 0 |

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| SCE1572_6231 | 25.48 | 14.07 |
| SCE1572_11414 | 33.91 | 43.11 |
| SCE1572_6492 | 26.41 | 26.7 |
| SCE1572_1886 | 7.36 | 3.54 |
| SCE1572_4664 | 94.76 | 15.61 |
| SCE1572_9500 | 19.27 | 13.43 |
| SCE1572_838 | 17.96 | 23.12 |
| SCE1572_4803 | 31.73 | 30.54 |
| SCE1572_5874 | 37.56 | 43.52 |
| SCE1572_11531 | 24.23 | 11.66 |
| SCE1572_8455 | 16.39 | 87.78 |
| SCE1572_6926 | 31.98 | 5.7 |
| SCE1572_9780 | 57.14 | 37.9 |
| SCE1572_3260 | 143.26 | 224.13 |
| SCE1572_3777 | 16.28 | 12.25 |
| SCE1572_6220 | 40.57 | 8.57 |
| SCE1572_1142 | 32.23 | 10.34 |
| SCE1572_8822 | 21.83 | 5.68 |
| SCE1572_7566 | 10.83 | 37.91 |
| SCE1572_3604 | 95.2 | 64.86 |
| SCE1572_10374 | 53.4 | 57.38 |
| SCE1572_9914 | 1.92 | 0 |
| SCE1572_4802 | 17.71 | 49.35 |
| SCE1572_8785 | 16.19 | 130.19 |
| SCE1572_4750 | 45.76 | 80.1 |
| SCE1572_4672 | 41.03 | 22.9 |
| SCE1572_3768 | 32.68 | 45.09 |
| SCE1572_8251 | 32.59 | 23.87 |
| SCE1572_2809 | 30.25 | 19.04 |
| SCE1572_9608 | 51.69 | 42.85 |
| SCE1572_11139 | 19.33 | 10.18 |
| SCE1572_2017 | 44.65 | 17 |
| SCE1572_7047 | 23.94 | 15.37 |
| SCE1572_7038 | 32.61 | 26.96 |
| SCE1572_4149 | 38.57 | 17.14 |
| SCE1572_7596 | 77.74 | 190.5 |
| SCE1572_10029 | 16.46 | 26.19 |
| SCE1572_5074 | 490.01 | 179.82 |
| SCE1572_2225 | 39.73 | 14.04 |
| SCE1572_11002 | 15.44 | 13.52 |
| SCE1572_9094 | 62.61 | 632.7 |
| SCE1572_3159 | 319.19 | 1263.45 |
| SCE1572_2634 | 69.43 | 28.26 |
| SCE1572_11028 | 33.23 | 5 |
| SCE1572_6136 | 75.17 | 59.28 |
| SCE1572_4496 | 29.36 | 38.55 |
| SCE1572_3130 | 39.21 | 19.92 |
| SCE1572_8453 | 19.2 | 60.82 |

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| SCE1572_2427 | 388.3 | 511.32 |
| SCE1572_8943 | 89.69 | 25.7 |
| SCE1572_6301 | 55.26 | 85.96 |
| SCE1572_4897 | 51.52 | 51.37 |
| SCE1572_8863 | 20.79 | 7.3 |
| SCE1572_3705 | 0 | 0 |
| SCE1572_10023 | 25.75 | 19.85 |
| SCE1572_7336 | 43.39 | 31.57 |
| SCE1572_1113 | 7.4 | 22.25 |
| SCE1572_2889 | 26.03 | 10.94 |
| SCE1572_5818 | 55.63 | 18.4 |
| SCE1572_7916 | 122.41 | 324.75 |
| SCE1572_5727 | 26.99 | 99.99 |
| SCE1572_2352 | 45.63 | 280.45 |
| SCE1572_764 | 30.55 | 12.49 |
| SCE1572_2372 | 49.74 | 137.01 |
| SCE1572_9220 | 54.16 | 23.71 |
| SCE1572_8603 | 36.43 | 50.95 |
| SCE1572_10779 | 81.57 | 27.74 |
| SCE1572_2831 | 31.72 | 21.38 |
| SCE1572_7868 | 77.13 | 261.93 |
| SCE1572_4175 | 88.48 | 20.64 |
| SCE1572_1591 | 54.42 | 69.65 |
| SCE1572_10318 | 77.93 | 52.55 |
| SCE1572_1416 | 37.99 | 24.27 |
| SCE1572_3031 | 5.83 | 0 |
| SCE1572_9916 | 36.76 | 26.07 |
| SCE1572_7640 | 28.02 | 85.28 |
| SCE1572_229 | 100.22 | 510.27 |
| SCE1572_5600 | 74.17 | 46.27 |
| SCE1572_8512 | 118.23 | 52.62 |
| SCE1572_1206 | 6.83 | 1.17 |
| SCE1572_8369 | 19.17 | 20.39 |
| SCE1572_4246 | 77.26 | 55.78 |
| SCE1572_10798 | 28.43 | 11.4 |
| SCE1572_9317 | 238.32 | 1187.64 |
| SCE1572_7389 | 2.71 | 0 |
| SCE1572_7409 | 31.95 | 16.94 |
| SCE1572_6745 | 71.27 | 299.42 |
| SCE1572_4875 | 54.56 | 30.41 |
| SCE1572_3319 | 40.36 | 54.47 |
| SCE1572_865 | 36.21 | 81.7 |
| SCE1572_4211 | 203.23 | 528.84 |
| SCE1572_3632 | 41.01 | 29.1 |
| SCE1572_9026 | 15.01 | 326.02 |
| SCE1572_803 | 3.09 | 0 |
| SCE1572_222 | 31.78 | 18.81 |
| SCE1572_1836 | 20.49 | 49.31 |

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| SCE1572_313 | 32.25 | 7.14 |
| SCE1572_3591 | 0 | 0 |
| SCE1572_7031 | 54.58 | 33.36 |
| SCE1572_9686 | 86.33 | 133.76 |
| SCE1572_9177 | 23.79 | 6.42 |
| SCE1572_5427 | 31.18 | 62.11 |
| SCE1572_4749 | 62.47 | 34.84 |
| SCE1572_7017 | 0 | 0 |
| SCE1572_3530 | 35.47 | 30.94 |
| SCE1572_11195 | 17.59 | 13.1 |
| SCE1572_994 | 52.12 | 27.37 |
| SCE1572_5607 | 26.07 | 42.62 |
| SCE1572_8574 | 6.32 | 10.14 |
| SCE1572_9624 | 44.47 | 41.59 |
| SCE1572_4453 | 34.38 | 48.8 |
| SCE1572_3702 | 43.44 | 24.8 |
| SCE1572_11274 | 69.11 | 242.42 |
| SCE1572_9889 | 14.74 | 26.36 |
| SCE1572_1850 | 57.6 | 43.25 |
| SCE1572_6557 | 35.4 | 6.89 |
| SCE1572_2001 | 33.37 | 19.21 |
| SCE1572_11105 | 10.18 | 16.34 |
| SCE1572_1432 | 5.51 | 4.42 |
| SCE1572_2121 | 8.33 | 0 |
| SCE1572_697 | 61.88 | 47.88 |
| SCE1572_6143 | 6.74 | 0 |
| SCE1572_2065 | 22.18 | 21 |
| SCE1572_6776 | 228.46 | 69.22 |
| SCE1572_5970 | 7.58 | 0 |
| SCE1572_2751 | 54.23 | 40.44 |
| SCE1572_8576 | 24.4 | 6.37 |
| SCE1572_6740 | 21.21 | 76.86 |
| SCE1572_8716 | 39.2 | 80.1 |
| SCE1572_11251 | 33.49 | 11.52 |
| SCE1572_4275 | 40.49 | 46.56 |
| SCE1572_10552 | 0 | 0 |
| SCE1572_269 | 48.07 | 22.25 |
| SCE1572_293 | 4.53 | 0 |
| SCE1572_5558 | 44.28 | 59.22 |
| SCE1572_2491 | 113.33 | 33.17 |
| SCE1572_6291 | 9.26 | 9.39 |
| SCE1572_11385 | 106.53 | 867.44 |
| SCE1572_10764 | 139.15 | 0 |
| SCE1572_9238 | 27.07 | 18.25 |
| SCE1572_9193 | 11.12 | 1.41 |
| SCE1572_10936 | 0 | 0 |
| SCE1572_11469 | 35.14 | 86.14 |
| SCE1572_8617 | 38.04 | 6.73 |

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| SCE1572_9540 | 36.05 | 12.98 |
| SCE1572_1968 | 29.63 | 46.14 |
| SCE1572_3853 | 2.76 | 0 |
| SCE1572_6246 | 29.76 | 6.78 |
| SCE1572_9721 | 77.57 | 796.52 |
| SCE1572_8165 | 0 | 0 |
| SCE1572_6336 | 69.47 | 39.81 |
| SCE1572_3572 | 0 | 0 |
| SCE1572_1815 | 14.85 | 3.14 |
| SCE1572_6007 | 44.24 | 89.61 |
| SCE1572_4255 | 151.62 | 350.78 |
| SCE1572_2981 | 24.72 | 54.21 |
| SCE1572_2170 | 60.58 | 82.48 |
| SCE1572_5696 | 77.48 | 55.32 |
| SCE1572_1751 | 29.68 | 42.48 |
| SCE1572_6198 | 83.59 | 16.65 |
| SCE1572_7944 | 46.03 | 26.07 |
| SCE1572_5924 | 24.73 | 18.79 |
| SCE1572_10451 | 39.03 | 379.37 |
| SCE1572_5522 | 21.96 | 19.31 |
| SCE1572_4883 | 23.16 | 38.01 |
| SCE1572_9188 | 25.85 | 18.23 |
| SCE1572_10162 | 39 | 12.66 |
| SCE1572_108 | 116.13 | 336.19 |
| SCE1572_9728 | 37.3 | 47.8 |
| SCE1572_11393 | 30.35 | 32.24 |
| SCE1572_3129 | 21.14 | 14.04 |
| SCE1572_3652 | 22.54 | 19.15 |
| SCE1572_3190 | 9.57 | 0 |
| SCE1572_7274 | 24.44 | 8.02 |
| SCE1572_11370 | 31.19 | 9.5 |
| SCE1572_5704 | 97.59 | 104.86 |
| SCE1572_1988 | 61.39 | 20.9 |
| SCE1572_4608 | 80.24 | 140.45 |
| SCE1572_1075 | 39.21 | 32.36 |
| SCE1572_10405 | 55.96 | 69.7 |
| SCE1572_4731 | 24.26 | 7.3 |
| SCE1572_3712 | 25.61 | 1848.48 |
| SCE1572_10747 | 22.48 | 11.51 |
| SCE1572_6932 | 74 | 1116.49 |
| SCE1572_9057 | 2.81 | 0 |
| SCE1572_10886 | 134.56 | 34.21 |
| SCE1572_310 | 14.28 | 8.18 |
| SCE1572_757 | 115.52 | 26.86 |
| SCE1572_11405 | 22.57 | 9.73 |
| SCE1572_7090 | 0 | 0 |
| SCE1572_9731 | 64.42 | 57.18 |
| SCE1572_9585 | 26.23 | 21.7 |

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| SCE1572_8284 | 44.47 | 4.87 |
| SCE1572_10150 | 21.29 | 122.34 |
| SCE1572_7339 | 39.65 | 800.02 |
| SCE1572_10291 | 23.23 | 35.32 |
| SCE1572_7901 | 43.48 | 8.94 |
| SCE1572_1171 | 45.86 | 24.67 |
| SCE1572_2132 | 43.54 | 14.71 |
| SCE1572_11238 | 15.16 | 7.3 |
| SCE1572_10496 | 55.55 | 80.78 |
| SCE1572_2048 | 17.78 | 35.23 |
| SCE1572_905 | 38.29 | 12.1 |
| SCE1572_8631 | 111.02 | 75.78 |
| SCE1572_7424 | 13.83 | 33.29 |
| SCE1572_11132 | 10.31 | 4.38 |
| SCE1572_526 | 43.85 | 110.46 |
| SCE1572_11075 | 50.54 | 444.69 |
| SCE1572_8669 | 14.61 | 0 |
| SCE1572_7989 | 95.65 | 168.17 |
| SCE1572_10938 | 20.64 | 12.16 |
| SCE1572_9286 | 50.12 | 87.18 |
| SCE1572_798 | 143.53 | 149.21 |
| SCE1572_10348 | 49.45 | 17.5 |
| SCE1572_9787 | 26.37 | 9.92 |
| SCE1572_9547 | 49.33 | 19.67 |
| SCE1572_7350 | 13.86 | 2.09 |
| SCE1572_9007 | 24.92 | 32.49 |
| SCE1572_7471 | 0 | 0 |
| SCE1572_9758 | 61.03 | 127.23 |
| SCE1572_8772 | 78.6 | 163.68 |
| SCE1572_11453 | 20.14 | 22.81 |
| SCE1572_3397 | 23.44 | 16.97 |
| SCE1572_6121 | 11.14 | 7.31 |
| SCE1572_10302 | 36.29 | 7.18 |
| SCE1572_10472 | 67.06 | 173.44 |
| SCE1572_1059 | 42.06 | 18.83 |
| SCE1572_1186 | 12.09 | 12.12 |
| SCE1572_8319 | 62.4 | 99.37 |
| SCE1572_2287 | 44.09 | 144.93 |
| SCE1572_9113 | 14.36 | 55.7 |
| SCE1572_10458 | 87.14 | 61.52 |
| SCE1572_5613 | 45.02 | 14.32 |
| SCE1572_2900 | 7.68 | 9.24 |
| SCE1572_7933 | 0 | 0 |
| SCE1572_2289 | 23.49 | 179.89 |
| SCE1572_7330 | 43.4 | 19.5 |
| SCE1572_7266 | 0 | 0 |
| SCE1572_1135 | 6.79 | 0 |
| SCE1572_2972 | 46.52 | 30.65 |

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| SCE1572_10562 | 74.45 | 32.39 |
| SCE1572_2848 | 27.72 | 10.04 |
| SCE1572_8564 | 36.1 | 61.79 |
| SCE1572_985 | 54.26 | 49.09 |
| SCE1572_8058 | 38.51 | 0 |
| SCE1572_5245 | 24.68 | 12.73 |
| SCE1572_4999 | 108.74 | 583.33 |
| SCE1572_10538 | 25.45 | 5.33 |
| SCE1572_4304 | 26.11 | 9.92 |
| SCE1572_8977 | 11.2 | 3.6 |
| SCE1572_421 | 10.83 | 39.1 |
| SCE1572_4115 | 57.76 | 63.72 |
| SCE1572_1952 | 25.2 | 12.34 |
| SCE1572_10717 | 14.57 | 8.35 |
| SCE1572_8677 | 34.51 | 60.4 |
| SCE1572_2002 | 29.74 | 66.53 |
| SCE1572_480 | 28.01 | 21.98 |
| SCE1572_1991 | 51.3 | 15.3 |
| SCE1572_53 | 67 | 26.31 |
| SCE1572_2160 | 43.71 | 18.65 |
| SCE1572_3055 | 16.02 | 0 |
| SCE1572_5262 | 0 | 0 |
| SCE1572_1052 | 105.64 | 535.24 |
| SCE1572_7370 | 43.93 | 24.33 |
| SCE1572_6484 | 18.95 | 7.84 |
| SCE1572_8753 | 28.39 | 7.74 |
| SCE1572_11089 | 22.19 | 42.52 |
| SCE1572_9475 | 55.45 | 116.92 |
| SCE1572_5081 | 3337.38 | 4102.08 |
| SCE1572_6583 | 34.9 | 31.67 |
| SCE1572_8969 | 18.65 | 70.96 |
| SCE1572_7158 | 36.41 | 39.24 |
| SCE1572_4491 | 31.72 | 172.11 |
| SCE1572_11343 | 31.66 | 156.4 |
| SCE1572_10356 | 52.63 | 357.36 |
| SCE1572_5222 | 39.43 | 27.77 |
| SCE1572_1514 | 29.27 | 7.36 |
| SCE1572_8982 | 29.01 | 17.13 |
| SCE1572_6069 | 86.29 | 390.16 |
| SCE1572_7323 | 4.94 | 0 |
| SCE1572_4100 | 23.74 | 24.12 |
| SCE1572_5965 | 21.4 | 20.39 |
| SCE1572_9041 | 247.77 | 1838.83 |
| SCE1572_3329 | 85.79 | 570.82 |
| SCE1572_4500 | 21.16 | 5.66 |
| SCE1572_6568 | 20.89 | 70.4 |
| SCE1572_11446 | 94.34 | 131.08 |
| SCE1572_9590 | 50.32 | 402.73 |

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| SCE1572_1972 | 28.41 | 105.2 |
| SCE1572_4980 | 27.64 | 98.83 |
| SCE1572_5643 | 0 | 0 |
| SCE1572_4284 | 53.53 | 22.53 |
| SCE1572_9468 | 23.84 | 54.79 |
| SCE1572_6148 | 42.33 | 12.97 |
| SCE1572_9306 | 40.6 | 78.9 |
| SCE1572_8337 | 45.13 | 44.72 |
| SCE1572_5632 | 18.28 | 40.79 |
| SCE1572_9599 | 40.32 | 22 |
| SCE1572_11353 | 3.37 | 0 |
| SCE1572_7109 | 30.98 | 19.62 |
| SCE1572_9570 | 58.97 | 20.03 |
| SCE1572_3955 | 63.58 | 28.98 |
| SCE1572_3798 | 22.57 | 31.57 |
| SCE1572_2689 | 82.51 | 237.62 |
| SCE1572_5344 | 45.75 | 21.59 |
| SCE1572_3999 | 255.23 | 525.36 |
| SCE1572_590 | 37.25 | 18.11 |
| SCE1572_4501 | 52.34 | 232.46 |
| SCE1572_3817 | 60.09 | 694.53 |
| SCE1572_878 | 83.62 | 485.31 |
| SCE1572_731 | 6.46 | 4.79 |
| SCE1572_3940 | 335.21 | 662.17 |
| SCE1572_2815 | 29.16 | 44.66 |
| SCE1572_4126 | 62.77 | 23.24 |
| SCE1572_8960 | 55.89 | 32.91 |
| SCE1572_11282 | 34.28 | 80.27 |
| SCE1572_4414 | 35.48 | 19.41 |
| SCE1572_2231 | 13.55 | 93.78 |
| SCE1572_165 | 21.91 | 7.54 |
| SCE1572_3744 | 52.07 | 114.27 |
| SCE1572_4195 | 35.62 | 74.14 |
| SCE1572_307 | 0 | 0 |
| SCE1572_7379 | 32.08 | 13.63 |
| SCE1572_3327 | 289.1 | 2603.94 |
| SCE1572_10635 | 65.08 | 168.69 |
| SCE1572_5796 | 27.42 | 27.18 |
| SCE1572_3902 | 20.42 | 98.31 |
| SCE1572_7754 | 44.15 | 114.65 |
| SCE1572_5504 | 31.72 | 27 |
| SCE1572_546 | 0 | 0 |
| SCE1572_10082 | 134.06 | 1006.42 |
| SCE1572_7516 | 18.95 | 30.41 |
| SCE1572_7231 | 52.48 | 94.42 |
| SCE1572_3082 | 24.21 | 19.42 |
| SCE1572_8537 | 26.59 | 26.75 |
| SCE1572_8141 | 28.17 | 8.65 |

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| SCE1572_3560 | 53.47 | 13.68 |
| SCE1572_3847 | 25.07 | 9.73 |
| SCE1572_2740 | 14.08 | 9.97 |
| SCE1572_7965 | 14.56 | 23.36 |
| SCE1572_8234 | 0 | 0 |
| SCE1572_6760 | 112.7 | 120.79 |
| SCE1572_3166 | 48.93 | 30.99 |
| SCE1572_6766 | 0 | 0 |
| SCE1572_9459 | 0 | 0 |
| SCE1572_34 | 58.78 | 217.83 |
| SCE1572_7554 | 10.38 | 2 |
| SCE1572_303 | 33.19 | 13.7 |
| SCE1572_6874 | 116.57 | 1750.22 |
| SCE1572_10915 | 0 | 0 |
| SCE1572_6341 | 57.15 | 22.74 |
| SCE1572_2105 | 157.27 | 812.91 |
| SCE1572_2664 | 201.98 | 1877.65 |
| SCE1572_9443 | 21.85 | 42.74 |
| SCE1572_2920 | 44.66 | 11.27 |
| SCE1572_2183 | 14.75 | 8.13 |
| SCE1572_2854 | 0 | 0 |
| SCE1572_6406 | 14.63 | 105.64 |
| SCE1572_5666 | 11.73 | 7.6 |
| SCE1572_10594 | 52.4 | 23.69 |
| SCE1572_2917 | 10.4 | 4.81 |
| SCE1572_10354 | 15.64 | 11.58 |
| SCE1572_10143 | 39.11 | 159.29 |
| SCE1572_1066 | 37.74 | 14.1 |
| SCE1572_9553 | 42.35 | 17.73 |
| SCE1572_4886 | 4.27 | 0 |
| SCE1572_6352 | 55.82 | 54.47 |
| SCE1572_9157 | 96.06 | 76.05 |
| SCE1572_3310 | 18.31 | 6.15 |
| SCE1572_9478 | 103.59 | 778.58 |
| SCE1572_2776 | 0 | 0 |
| SCE1572_2331 | 46.27 | 30.84 |
| SCE1572_2714 | 44.56 | 58.86 |
| SCE1572_2941 | 33.6 | 22.81 |
| SCE1572_9484 | 179.73 | 778.94 |
| SCE1572_3096 | 3.39 | 2.72 |
| SCE1572_5987 | 15.34 | 12.21 |
| SCE1572_10614 | 27.05 | 5.92 |
| SCE1572_4465 | 42.08 | 61.85 |
| SCE1572_193 | 31.7 | 46.2 |
| SCE1572_2093 | 31.26 | 33.86 |
| SCE1572_6253 | 38.08 | 221.37 |
| SCE1572_9454 | 21.08 | 12.55 |
| SCE1572_1820 | 21.78 | 30.24 |

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| SCE1572_1810 | 27.31 | 22.81 |
| SCE1572_10923 | 239.67 | 19913.2 |
| SCE1572_2498 | 0 | 0 |
| SCE1572_8754 | 72.03 | 21.67 |
| SCE1572_1803 | 20.53 | 15.21 |
| SCE1572_7630 | 50.94 | 297.78 |
| SCE1572_10548 | 40.91 | 14.45 |
| SCE1572_489 | 16.04 | 8.18 |
| SCE1572_10189 | 20.34 | 49.92 |
| SCE1572_4865 | 34.04 | 81.92 |
| SCE1572_7981 | 27.27 | 39.38 |
| SCE1572_2674 | 22.97 | 125.33 |
| SCE1572_3115 | 32.96 | 15.87 |
| SCE1572_5906 | 57.3 | 335.37 |
| SCE1572_11071 | 69.94 | 75.81 |
| SCE1572_10102 | 31.15 | 115.98 |
| SCE1572_5099 | 21.52 | 4.78 |
| SCE1572_3962 | 33.01 | 24.54 |
| SCE1572_7714 | 50.28 | 179.71 |
| SCE1572_2871 | 0 | 0 |
| SCE1572_8872 | 35.42 | 16.45 |
| SCE1572_6663 | 15.57 | 9.71 |
| SCE1572_11473 | 47.58 | 32.06 |
| SCE1572_4831 | 62.25 | 114.64 |
| SCE1572_8580 | 202.8 | 88.75 |
| SCE1572_8506 | 19.51 | 7.23 |
| SCE1572_4740 | 52.47 | 80.13 |
| SCE1572_9775 | 0 | 0 |
| SCE1572_4067 | 41.75 | 50.24 |
| SCE1572_10732 | 62.5 | 32.02 |
| SCE1572_7508 | 40.78 | 15.18 |
| SCE1572_9665 | 22.89 | 91.8 |
| SCE1572_10647 | 23.94 | 65.3 |
| SCE1572_5069 | 24.24 | 20.97 |
| SCE1572_2406 | 31.03 | 229.73 |
| SCE1572_10074 | 154.06 | 0 |
| SCE1572_2825 | 17.49 | 14.04 |
| SCE1572_9558 | 0 | 0 |
| SCE1572_6182 | 26.77 | 8.36 |
| SCE1572_156 | 62.12 | 191.33 |
| SCE1572_1825 | 14.59 | 9.16 |
| SCE1572_7739 | 6.41 | 0 |
| SCE1572_4260 | 34.84 | 33.13 |
| SCE1572_5621 | 65.42 | 27.39 |
| SCE1572_1774 | 27.47 | 7.93 |
| SCE1572_2860 | 42.22 | 13.86 |
| SCE1572_7088 | 38.78 | 14.68 |
| SCE1572_6424 | 0 | 0 |

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| SCE1572_6175 | 53.09 | 88.47 |
| SCE1572_6616 | 25.31 | 10.05 |
| SCE1572_8736 | 21.55 | 16.67 |
| SCE1572_2720 | 90.17 | 20.54 |
| SCE1572_2055 | 19.16 | 25.78 |
| SCE1572_6778 | 260.44 | 111.83 |
| SCE1572_9517 | 62.25 | 103.44 |
| SCE1572_1616 | 9.88 | 40.24 |
| SCE1572_7100 | 10.71 | 28.37 |
| SCE1572_449 | 19.28 | 16.01 |
| SCE1572_4443 | 28.43 | 108.34 |
| SCE1572_9766 | 27.67 | 69.26 |
| SCE1572_6644 | 2.53 | 0 |
| SCE1572_331 | 55.57 | 157.72 |
| SCE1572_10569 | 122.34 | 211.37 |
| SCE1572_4335 | 42.39 | 23.35 |
| SCE1572_4796 | 148.17 | 77.41 |
| SCE1572_10791 | 56.95 | 78.73 |
| SCE1572_2679 | 24.19 | 638.97 |
| SCE1572_4217 | 32.49 | 45.79 |
| SCE1572_9525 | 9.05 | 25.42 |
| SCE1572_9072 | 31.5 | 47.6 |
| SCE1572_41 | 59.81 | 45.75 |
| SCE1572_1128 | 30.04 | 26.07 |
| SCE1572_1523 | 32.59 | 11.27 |
| SCE1572_5212 | 40.15 | 81.38 |
| SCE1572_9882 | 74.59 | 60.5 |
| SCE1572_3480 | 44.13 | 50.01 |
| SCE1572_9973 | 62.4 | 239.05 |
| SCE1572_11074 | 7 | 0 |
| SCE1572_6681 | 13.61 | 74.57 |
| SCE1572_1122 | 71.3 | 15.05 |
| SCE1572_5346 | 3.42 | 5.49 |
| SCE1572_11532 | 0 | 0 |
| SCE1572_4573 | 20.67 | 15.55 |
| SCE1572_9154 | 39.34 | 138.92 |
| SCE1572_2707 | 31.17 | 10.14 |
| SCE1572_10551 | 29.48 | 11.26 |
| SCE1572_8774 | 129.51 | 297.39 |
| SCE1572_1851 | 59.42 | 36.99 |
| SCE1572_8666 | 19.11 | 1.48 |
| SCE1572_2665 | 58.14 | 439.32 |
| SCE1572_5604 | 41.09 | 48.86 |
| SCE1572_8623 | 72.09 | 228.59 |
| SCE1572_8259 | 125.04 | 368.07 |
| SCE1572_861 | 49.98 | 743.36 |
| SCE1572_2416 | 114.57 | 137.19 |
| SCE1572_8975 | 14.66 | 9.07 |

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| SCE1572_7268 | 37.14 | 76.18 |
| SCE1572_1614 | 46.92 | 126 |
| SCE1572_7725 | 33.69 | 31.81 |
| SCE1572_2596 | 82.69 | 94.85 |
| SCE1572_9387 | 73.1 | 152.74 |
| SCE1572_7112 | 0 | 0 |
| SCE1572_6111 | 18.63 | 51.03 |
| SCE1572_167 | 73 | 21.63 |
| SCE1572_2678 | 20.59 | 272.57 |
| SCE1572_6643 | 172.05 | 176.15 |
| SCE1572_6637 | 35 | 40.08 |
| SCE1572_8288 | 13.24 | 38.69 |
| SCE1572_2929 | 0 | 0 |
| SCE1572_3951 | 32.87 | 44.9 |
| SCE1572_9480 | 34.17 | 41.12 |
| SCE1572_7250 | 44.21 | 17.69 |
| SCE1572_4312 | 41.27 | 14.49 |
| SCE1572_9416 | 109.5 | 2275.13 |
| SCE1572_3621 | 20.91 | 3.15 |
| SCE1572_2024 | 14.16 | 5.38 |
| SCE1572_5793 | 127.43 | 220.52 |
| SCE1572_6115 | 71.31 | 20.19 |
| SCE1572_9350 | 114.93 | 509.88 |
| SCE1572_5673 | 25.57 | 31.48 |
| SCE1572_2856 | 23.43 | 8.85 |
| SCE1572_3499 | 35.48 | 49.17 |
| SCE1572_2469 | 10.69 | 7.45 |
| SCE1572_804 | 0 | 0 |
| SCE1572_10588 | 13.18 | 3.53 |
| SCE1572_4913 | 19.87 | 10.07 |
| SCE1572_1784 | 29.08 | 10 |
| SCE1572_9077 | 33.97 | 16.22 |
| SCE1572_8235 | 30.32 | 44.6 |
| SCE1572_10176 | 126.83 | 77.2 |
| SCE1572_4817 | 164.5 | 1485.93 |
| SCE1572_10596 | 51.71 | 19.8 |
| SCE1572_6146 | 59.76 | 35.96 |
| SCE1572_1779 | 52.71 | 72.04 |
| SCE1572_7045 | 24.79 | 124.32 |
| SCE1572_3412 | 25.73 | 85.37 |
| SCE1572_3708 | 0 | 0 |
| SCE1572_11508 | 20.67 | 9.22 |
| SCE1572_11472 | 8.53 | 0 |
| SCE1572_5983 | 6.67 | 8.76 |
| SCE1572_7511 | 46.69 | 23.17 |
| SCE1572_8462 | 67.01 | 667.34 |
| SCE1572_5626 | 11.52 | 4.38 |
| SCE1572_1916 | 7 | 0 |

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| SCE1572_10664 | 50.77 | 369.88 |
| SCE1572_3580 | 37.46 | 16.33 |
| SCE1572_2405 | 29.55 | 239.61 |
| SCE1572_10352 | 28.24 | 19.87 |
| SCE1572_6056 | 148.87 | 465.05 |
| SCE1572_1248 | 82.91 | 181.78 |
| SCE1572_9995 | 41.57 | 21.34 |
| SCE1572_564 | 59.87 | 1338.82 |
| SCE1572_797 | 97.04 | 157.99 |
| SCE1572_7026 | 43.62 | 18.83 |
| SCE1572_8144 | 35.05 | 7.85 |
| SCE1572_3413 | 50.09 | 58.65 |
| SCE1572_8743 | 4.33 | 0 |
| SCE1572_2098 | 46.65 | 110.2 |
| SCE1572_4455 | 122.5 | 126.36 |
| SCE1572_9751 | 39.14 | 24.73 |
| SCE1572_11358 | 45.73 | 28 |
| SCE1572_9520 | 51 | 147.35 |
| SCE1572_9879 | 32.88 | 63.02 |
| SCE1572_2996 | 18.1 | 9.14 |
| SCE1572_5082 | 82.81 | 159.75 |
| SCE1572_9776 | 19.99 | 28.07 |
| SCE1572_3796 | 8.93 | 1.57 |
| SCE1572_6769 | 324.79 | 4879.58 |
| SCE1572_2572 | 50.28 | 17.16 |
| SCE1572_8883 | 56.86 | 25.78 |
| SCE1572_4798 | 60.35 | 683.79 |
| SCE1572_10929 | 55.24 | 39.6 |
| SCE1572_179 | 15.3 | 11.54 |
| SCE1572_10389 | 36.73 | 49.41 |
| SCE1572_4016 | 112.63 | 93.84 |
| SCE1572_6138 | 32.2 | 48.44 |
| SCE1572_2731 | 61.2 | 58.32 |
| SCE1572_2712 | 267.07 | 865.74 |
| SCE1572_10072 | 402.87 | 1115.62 |
| SCE1572_10194 | 27 | 14.04 |
| SCE1572_4329 | 22.28 | 24.48 |
| SCE1572_6407 | 17.14 | 55.59 |
| SCE1572_7776 | 47.68 | 245 |
| SCE1572_9769 | 11.04 | 19.33 |
| SCE1572_6501 | 35.11 | 19.21 |
| SCE1572_10399 | 58.06 | 70.72 |
| SCE1572_10992 | 6.42 | 12.37 |
| SCE1572_9398 | 28.91 | 71.13 |
| SCE1572_10415 | 18.83 | 38.53 |
| SCE1572_5310 | 22.66 | 33.56 |
| SCE1572_1335 | 26.49 | 10.99 |
| SCE1572_4267 | 0 | 0 |

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| SCE1572_2142 | 34.44 | 9.4 |
| SCE1572_6177 | 51.47 | 68.68 |
| SCE1572_1014 | 45.35 | 32.58 |
| SCE1572_9544 | 65.8 | 18.93 |
| SCE1572_9324 | 644.51 | 1002.74 |
| SCE1572_4324 | 30.16 | 21.58 |
| SCE1572_26 | 39.32 | 58.14 |
| SCE1572_2978 | 21.42 | 3.97 |
| SCE1572_9034 | 27.09 | 18.04 |
| SCE1572_10100 | 47.83 | 26.94 |
| SCE1572_11460 | 187.27 | 464.54 |
| SCE1572_1322 | 10.85 | 3.07 |
| SCE1572_10149 | 27.36 | 7.12 |
| SCE1572_5118 | 54.15 | 161.61 |
| SCE1572_10916 | 39.01 | 31.46 |
| SCE1572_988 | 33.46 | 85.51 |
| SCE1572_8428 | 21.96 | 17.05 |
| SCE1572_3011 | 37.05 | 8.76 |
| SCE1572_484 | 38.08 | 24.84 |
| SCE1572_7809 | 0 | 0 |
| SCE1572_7723 | 40.86 | 53.06 |
| SCE1572_10305 | 43.32 | 29.41 |
| SCE1572_6737 | 116.01 | 728.37 |
| SCE1572_6717 | 86.92 | 254.82 |
| SCE1572_544 | 53.51 | 52.13 |
| SCE1572_6710 | 109.15 | 91.89 |
| SCE1572_11584 | 31.47 | 16.75 |
| SCE1572_9489 | 39.08 | 26.52 |
| SCE1572_11244 | 25.17 | 57.62 |
| SCE1572_10290 | 25.87 | 13.84 |
| SCE1572_5615 | 51.04 | 12.16 |
| SCE1572_10069 | 136.01 | 21.47 |
| SCE1572_10708 | 47.6 | 29.7 |
| SCE1572_6 | 18.37 | 24.81 |
| SCE1572_6441 | 11.66 | 0 |
| SCE1572_7982 | 33.35 | 20.81 |
| SCE1572_9735 | 92.13 | 161.08 |
| SCE1572_3511 | 39.47 | 65.84 |
| SCE1572_9452 | 153.4 | 84.43 |
| SCE1572_9305 | 26.79 | 48.02 |
| SCE1572_2708 | 109.44 | 27.68 |
| SCE1572_2915 | 35.69 | 10.9 |
| SCE1572_3956 | 34.63 | 12.04 |
| SCE1572_766 | 13.02 | 3.69 |
| SCE1572_1106 | 38.21 | 7.83 |
| SCE1572_3949 | 27.24 | 142.37 |
| SCE1572_1396 | 15.67 | 187.33 |
| SCE1572_3068 | 46.78 | 108.53 |

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| SCE1572_4440 | 55.86 | 32.57 |
| SCE1572_4413 | 9.7 | 0 |
| SCE1572_9837 | 106.5 | 238.65 |
| SCE1572_102 | 21.79 | 7.98 |
| SCE1572_10925 | 0 | 0 |
| SCE1572_2380 | 21.19 | 19.12 |
| SCE1572_4904 | 28.93 | 402.53 |
| SCE1572_4333 | 7 | 3.74 |
| SCE1572_11140 | 30.63 | 24.99 |
| SCE1572_6648 | 4.56 | 0 |
| SCE1572_8330 | 33.55 | 210.2 |
| SCE1572_8223 | 10.01 | 13.77 |
| SCE1572_5191 | 51.14 | 182.94 |
| SCE1572_6614 | 77.79 | 42.03 |
| SCE1572_11443 | 117.02 | 78.37 |
| SCE1572_1947 | 71.48 | 45.62 |
| SCE1572_3059 | 10.46 | 1.8 |
| SCE1572_3271 | 40.92 | 443.79 |
| SCE1572_1838 | 81.58 | 401.32 |
| SCE1572_8965 | 37.9 | 66.26 |
| SCE1572_691 | 13.39 | 4.2 |
| SCE1572_10574 | 105.75 | 129.87 |
| SCE1572_11233 | 109.92 | 290.11 |
| SCE1572_3598 | 75.57 | 23.52 |
| SCE1572_8510 | 37.47 | 16.78 |
| SCE1572_4747 | 91.06 | 30.41 |
| SCE1572_9693 | 44.46 | 856.97 |
| SCE1572_4081 | 16.68 | 22.81 |
| SCE1572_9482 | 15.26 | 29.39 |
| SCE1572_1078 | 31.57 | 19.44 |
| SCE1572_853 | 42.33 | 199.05 |
| SCE1572_7931 | 64.56 | 54.14 |
| SCE1572_7300 | 125.13 | 57.16 |
| SCE1572_6196 | 16.72 | 6.94 |
| SCE1572_3634 | 31.17 | 17.8 |
| SCE1572_1994 | 47.28 | 17.4 |
| SCE1572_7958 | 99.73 | 292.72 |
| SCE1572_6350 | 35.06 | 43.24 |
| SCE1572_9487 | 36.18 | 55.98 |
| SCE1572_10210 | 104.24 | 19.77 |
| SCE1572_10728 | 26.44 | 63.63 |
| SCE1572_3321 | 54.31 | 98.48 |
| SCE1572_3552 | 53.07 | 20.85 |
| SCE1572_10375 | 67.31 | 17.05 |
| SCE1572_6785 | 0 | 0 |
| SCE1572_6347 | 38.96 | 42.81 |
| SCE1572_6126 | 21.9 | 95.11 |
| SCE1572_9117 | 59.41 | 34.14 |

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| SCE1572_1992 | 0 | 0 |
| SCE1572_5265 | 0 | 0 |
| SCE1572_8832 | 9.72 | 9.36 |
| SCE1572_10721 | 92.9 | 41.14 |
| SCE1572_1452 | 0 | 0 |
| SCE1572_9722 | 576.27 | 5983.35 |
| SCE1572_7961 | 32.16 | 0 |
| SCE1572_10299 | 28.4 | 89.68 |
| SCE1572_9069 | 45.43 | 250.12 |
| SCE1572_7864 | 57.55 | 72.98 |
| SCE1572_1776 | 23.81 | 12.06 |
| SCE1572_3052 | 35.8 | 10.14 |
| SCE1572_10792 | 41.35 | 65.02 |
| SCE1572_8700 | 35.16 | 27.5 |
| SCE1572_1025 | 44.44 | 1113.64 |
| SCE1572_7309 | 54.26 | 17.29 |
| SCE1572_2283 | 21.02 | 10.84 |
| SCE1572_2775 | 39.47 | 118.76 |
| SCE1572_5505 | 1.6 | 7.68 |
| SCE1572_7166 | 27.42 | 7.95 |
| SCE1572_3093 | 159.48 | 129.75 |
| SCE1572_680 | 11.06 | 22.81 |
| SCE1572_5535 | 39.3 | 12.43 |
| SCE1572_3846 | 26.99 | 6.91 |
| SCE1572_4351 | 34.95 | 11.65 |
| SCE1572_11084 | 15.07 | 47.6 |
| SCE1572_1219 | 15.79 | 12.35 |
| SCE1572_209 | 9.9 | 5.62 |
| SCE1572_2003 | 124.3 | 56.35 |
| SCE1572_219 | 29.11 | 105.1 |
| SCE1572_2523 | 2.57 | 0 |
| SCE1572_5317 | 5.62 | 0 |
| SCE1572_8583 | 85.65 | 35.05 |
| SCE1572_8252 | 36.54 | 107.08 |
| SCE1572_5936 | 18.07 | 12.66 |
| SCE1572_128 | 9.48 | 0 |
| SCE1572_7787 | 80.27 | 0 |
| SCE1572_3486 | 84.07 | 42.11 |
| SCE1572_1137 | 76.39 | 35.87 |
| SCE1572_8272 | 15.16 | 22.59 |
| SCE1572_9391 | 40.34 | 25.11 |
| SCE1572_6400 | 30.56 | 111.46 |
| SCE1572_4145 | 50.79 | 155.38 |
| SCE1572_3398 | 178.37 | 42.93 |
| SCE1572_9008 | 9.83 | 3.64 |
| SCE1572_9888 | 35.95 | 20.78 |
| SCE1572_7155 | 26.49 | 13.42 |
| SCE1572_8527 | 20.44 | 0 |

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| SCE1572_7583 | 190.36 | 1212.19 |
| SCE1572_6741 | 61.48 | 29.55 |
| SCE1572_9788 | 74.01 | 64.78 |
| SCE1572_7745 | 1308.39 | 6305.05 |
| SCE1572_7322 | 18.76 | 3.66 |
| SCE1572_5966 | 14.84 | 8.69 |
| SCE1572_4513 | 3.79 | 4.56 |
| SCE1572_6135 | 36.4 | 66.35 |
| SCE1572_8735 | 0 | 0 |
| SCE1572_223 | 16.28 | 3.67 |
| SCE1572_6921 | 38.33 | 32.44 |
| SCE1572_11078 | 22.01 | 11.77 |
| SCE1572_3316 | 43.36 | 44.44 |
| SCE1572_1866 | 17.71 | 17.05 |
| SCE1572_4730 | 27.96 | 16.53 |
| SCE1572_8279 | 26.71 | 8.29 |
| SCE1572_7474 | 102.54 | 221.48 |
| SCE1572_9979 | 51.69 | 20.14 |
| SCE1572_3714 | 80.07 | 153.76 |
| SCE1572_908 | 12.09 | 6.72 |
| SCE1572_1630 | 109.82 | 44.45 |
| SCE1572_6032 | 34.24 | 58.86 |
| SCE1572_11080 | 34.51 | 400.52 |
| SCE1572_8535 | 65.55 | 40.95 |
| SCE1572_8293 | 20.28 | 12.2 |
| SCE1572_912 | 47.03 | 144.23 |
| SCE1572_1313 | 836.9 | 3508.26 |
| SCE1572_998 | 39.11 | 70.89 |
| SCE1572_8054 | 11.03 | 6.63 |
| SCE1572_2492 | 61.54 | 35.58 |
| SCE1572_10933 | 42.12 | 0 |
| SCE1572_3046 | 12.2 | 2.26 |
| SCE1572_11451 | 13.86 | 7.85 |
| SCE1572_3223 | 9.68 | 2.59 |
| SCE1572_4307 | 29.5 | 25.96 |
| SCE1572_7788 | 0 | 0 |
| SCE1572_4699 | 24.64 | 11.4 |
| SCE1572_10343 | 21.31 | 121.25 |
| SCE1572_6041 | 85.38 | 133.48 |
| SCE1572_5665 | 15.78 | 8.44 |
| SCE1572_897 | 68.14 | 32.8 |
| SCE1572_9027 | 35.79 | 59.84 |
| SCE1572_4286 | 0 | 0 |
| SCE1572_10669 | 77.23 | 332.12 |
| SCE1572_2546 | 48.52 | 26.27 |
| SCE1572_2671 | 111.35 | 205.52 |
| SCE1572_7345 | 18.74 | 4.1 |
| SCE1572_10565 | 64.31 | 27.21 |

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| SCE1572_3559 | 26.04 | 31.34 |
| SCE1572_8242 | 51.6 | 198.7 |
| SCE1572_1504 | 52.53 | 73.62 |
| SCE1572_4861 | 10 | 4.89 |
| SCE1572_5771 | 3.3 | 0 |
| SCE1572_314 | 26.28 | 10.95 |
| SCE1572_2324 | 19.72 | 38.57 |
| SCE1572_6762 | 0 | 0 |
| SCE1572_890 | 20.05 | 39.21 |
| SCE1572_10301 | 30.19 | 12.78 |
| SCE1572_11388 | 297.79 | 529.61 |
| SCE1572_6519 | 28.64 | 7.66 |
| SCE1572_2069 | 42.5 | 18.5 |
| SCE1572_2746 | 25.75 | 2.3 |
| SCE1572_11196 | 47.72 | 46.83 |
| SCE1572_1821 | 13.92 | 17.63 |
| SCE1572_2114 | 194.39 | 176.14 |
| SCE1572_9211 | 9.36 | 15.03 |
| SCE1572_11349 | 0 | 0 |
| SCE1572_2554 | 27.16 | 12.06 |
| SCE1572_3858 | 22.18 | 64.27 |
| SCE1572_9070 | 27.78 | 22.05 |
| SCE1572_10187 | 11.82 | 5.02 |
| SCE1572_5923 | 61.9 | 76.38 |
| SCE1572_5708 | 39.78 | 34.19 |
| SCE1572_9711 | 54.53 | 220.56 |
| SCE1572_5421 | 22.3 | 119.4 |
| SCE1572_597 | 91.92 | 285.9 |
| SCE1572_10639 | 43.27 | 259.97 |
| SCE1572_2583 | 13.78 | 3.32 |
| SCE1572_6089 | 7.82 | 47.65 |
| SCE1572_9597 | 35.03 | 1735.56 |
| SCE1572_2134 | 0 | 0 |
| SCE1572_7261 | 0 | 0 |
| SCE1572_2060 | 18.95 | 22.81 |
| SCE1572_5979 | 12.8 | 37.3 |
| SCE1572_1770 | 44.12 | 21.24 |
| SCE1572_9335 | 33.44 | 150.91 |
| SCE1572_4256 | 35.74 | 216.52 |
| SCE1572_4992 | 34.99 | 116.29 |
| SCE1572_10969 | 74.48 | 150.81 |
| SCE1572_9281 | 147.21 | 553.35 |
| SCE1572_8675 | 34.31 | 26.64 |
| SCE1572_2687 | 28.22 | 30.19 |
| SCE1572_689 | 12.78 | 19.57 |
| SCE1572_4192 | 25.41 | 68.42 |
| SCE1572_9689 | 137.05 | 240.63 |
| SCE1572_4611 | 16.26 | 10.58 |

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| SCE1572_7971 | 6.05 | 8.32 |
| SCE1572_7479 | 45.69 | 38.09 |
| SCE1572_1071 | 30.43 | 13.65 |
| SCE1572_6228 | 67.7 | 25.53 |
| SCE1572_9172 | 38.53 | 14.11 |
| SCE1572_8447 | 20.34 | 0 |
| SCE1572_7751 | 42.47 | 20.56 |
| SCE1572_3231 | 31.94 | 115.87 |
| SCE1572_319 | 40.18 | 14.4 |
| SCE1572_4349 | 40.46 | 19.29 |
| SCE1572_7623 | 33.04 | 45.75 |
| SCE1572_11025 | 38.84 | 64.72 |
| SCE1572_4122 | 35.73 | 34.87 |
| SCE1572_9586 | 33.72 | 61.03 |
| SCE1572_6002 | 17.33 | 96.97 |
| SCE1572_1410 | 41.19 | 20.11 |
| SCE1572_372 | 32.54 | 160.08 |
| SCE1572_10142 | 31.34 | 64.4 |
| SCE1572_10883 | 25.49 | 280.96 |
| SCE1572_9053 | 66.45 | 26.52 |
| SCE1572_1112 | 7.15 | 8.61 |
| SCE1572_6833 | 18.4 | 19.69 |
| SCE1572_8752 | 34.07 | 12.3 |
| SCE1572_4129 | 63.34 | 191.15 |
| SCE1572_8594 | 17.38 | 29.13 |
| SCE1572_2888 | 29.29 | 13.17 |
| SCE1572_8728 | 48.48 | 22.28 |
| SCE1572_8069 | 24.91 | 3.07 |
| SCE1572_10323 | 26.7 | 53.94 |
| SCE1572_9265 | 31.38 | 43.2 |
| SCE1572_8305 | 35.08 | 22.62 |
| SCE1572_10479 | 56.47 | 57.72 |
| SCE1572_6326 | 18.01 | 10.84 |
| SCE1572_3686 | 19.05 | 0 |
| SCE1572_5835 | 475.64 | 703.96 |
| SCE1572_4669 | 72.81 | 14.43 |
| SCE1572_4828 | 84.83 | 34.75 |
| SCE1572_262 | 65.06 | 25.87 |
| SCE1572_8142 | 14.95 | 2.57 |
| SCE1572_5288 | 18.73 | 15.62 |
| SCE1572_9477 | 0 | 0 |
| SCE1572_2442 | 83.58 | 458.49 |
| SCE1572_8581 | 101.3 | 25.59 |
| SCE1572_9227 | 20.48 | 23.67 |
| SCE1572_734 | 25.08 | 11.79 |
| SCE1572_8091 | 6.65 | 0 |
| SCE1572_11486 | 35.99 | 64.51 |
| SCE1572_4043 | 51.07 | 305.37 |

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| SCE1572_8393 | 44.13 | 38.28 |
| SCE1572_2342 | 38.19 | 139.28 |
| SCE1572_3732 | 16.55 | 15.93 |
| SCE1572_3772 | 59.44 | 78.78 |
| SCE1572_6517 | 12.57 | 62.4 |
| SCE1572_3354 | 40.9 | 42.76 |
| SCE1572_4528 | 0 | 0 |
| SCE1572_11181 | 35.35 | 54 |
| SCE1572_3077 | 38.04 | 17.11 |
| SCE1572_8553 | 32.3 | 420.45 |
| SCE1572_11102 | 44.48 | 84.44 |
| SCE1572_7609 | 32.75 | 43.79 |
| SCE1572_4553 | 17.6 | 1.63 |
| SCE1572_5388 | 106.6 | 443.8 |
| SCE1572_8283 | 17 | 3.23 |
| SCE1572_661 | 0 | 0 |
| SCE1572_8098 | 16.29 | 678.57 |
| SCE1572_3301 | 22.34 | 20.59 |
| SCE1572_1983 | 0 | 0 |
| SCE1572_6855 | 17.07 | 38.67 |
| SCE1572_7914 | 28.05 | 17.61 |
| SCE1572_1145 | 17.05 | 4.32 |
| SCE1572_3147 | 33.5 | 4.24 |
| SCE1572_7329 | 19.17 | 2.1 |
| SCE1572_6250 | 0 | 0 |
| SCE1572_7315 | 12.22 | 6.92 |
| SCE1572_7938 | 20.14 | 62.72 |
| SCE1572_11420 | 39.52 | 39.08 |
| SCE1572_9869 | 120.41 | 540.51 |
| SCE1572_1089 | 44.64 | 30.19 |
| SCE1572_7606 | 61.39 | 51.43 |
| SCE1572_6451 | 37.04 | 18.6 |
| SCE1572_4199 | 16.44 | 46.16 |
| SCE1572_4800 | 52.77 | 1243.24 |
| SCE1572_9860 | 48.93 | 34.75 |
| SCE1572_6247 | 14.41 | 9.08 |
| SCE1572_3133 | 71.39 | 44.77 |
| SCE1572_8456 | 40.08 | 434.65 |
| SCE1572_11417 | 50.98 | 41.43 |
| SCE1572_1204 | 0 | 0 |
| SCE1572_1030 | 37.11 | 188.84 |
| SCE1572_1146 | 139.39 | 94.17 |
| SCE1572_9504 | 12.36 | 3.22 |
| SCE1572_11484 | 8.15 | 0 |
| SCE1572_8195 | 52.34 | 48.99 |
| SCE1572_1921 | 0 | 0 |
| SCE1572_1699 | 43.75 | 111.35 |
| SCE1572_3245 | 35.72 | 26.52 |

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| SCE1572_3852 | 38.61 | 67.58 |
| SCE1572_10844 | 13.33 | 8.02 |
| SCE1572_4227 | 23.15 | 26.19 |
| SCE1572_10073 | 161.95 | 682.85 |
| SCE1572_4666 | 37.33 | 5.5 |
| SCE1572_8839 | 22.46 | 0 |
| SCE1572_8366 | 39.51 | 8.99 |
| SCE1572_7833 | 43.72 | 64.92 |
| SCE1572_7436 | 6.38 | 4.72 |
| SCE1572_8213 | 37.11 | 49.23 |
| SCE1572_9311 | 81.67 | 371.97 |
| SCE1572_7567 | 17.94 | 8.22 |
| SCE1572_1082 | 20.52 | 3.61 |
| SCE1572_5537 | 38.52 | 26.49 |
| SCE1572_6535 | 30.78 | 22.12 |
| SCE1572_934 | 42.58 | 177.96 |
| SCE1572_11564 | 6.47 | 5.19 |
| SCE1572_11263 | 22.61 | 53.35 |
| SCE1572_11020 | 9.72 | 6.93 |
| SCE1572_2533 | 19.22 | 336.65 |
| SCE1572_5489 | 0 | 0 |
| SCE1572_4809 | 56.5 | 52.24 |
| SCE1572_33 | 408.2 | 2198.17 |
| SCE1572_6300 | 75.06 | 277.27 |
| SCE1572_9607 | 14.86 | 4.77 |
| SCE1572_11524 | 23.42 | 11.87 |
| SCE1572_10753 | 35.33 | 7.79 |
| SCE1572_115 | 31.15 | 11.66 |
| SCE1572_6102 | 28.11 | 8.2 |
| SCE1572_6410 | 0 | 0 |
| SCE1572_8792 | 46.54 | 56.01 |
| SCE1572_610 | 44.78 | 72.37 |
| SCE1572_1973 | 0 | 0 |
| SCE1572_2828 | 0 | 0 |
| SCE1572_136 | 36.48 | 11.64 |
| SCE1572_3375 | 20.24 | 67.08 |
| SCE1572_5690 | 26.65 | 41.34 |
| SCE1572_2172 | 58.62 | 4.87 |
| SCE1572_6082 | 60.92 | 9.77 |
| SCE1572_5041 | 126.86 | 441.26 |
| SCE1572_10895 | 93.23 | 179.06 |
| SCE1572_5325 | 27.83 | 33.49 |
| SCE1572_9645 | 74.04 | 1005.66 |
| SCE1572_7780 | 14.89 | 6.52 |
| SCE1572_1037 | 2.61 | 0 |
| SCE1572_1903 | 90.24 | 29.03 |
| SCE1572_5816 | 21.1 | 10.33 |
| SCE1572_7143 | 31.59 | 9.68 |

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| SCE1572_11435 | 39.94 | 30.86 |
| SCE1572_2732 | 45.87 | 90.82 |
| SCE1572_11223 | 21.66 | 13.9 |
| SCE1572_4830 | 34.99 | 52.93 |
| SCE1572_452 | 9.7 | 67.15 |
| SCE1572_1556 | 43.7 | 70.12 |
| SCE1572_159 | 39.1 | 70.43 |
| SCE1572_4894 | 55.32 | 21.37 |
| SCE1572_4109 | 19.42 | 8.09 |
| SCE1572_5852 | 112 | 118.35 |
| SCE1572_6473 | 124.78 | 248.31 |
| SCE1572_3648 | 28.55 | 137.42 |
| SCE1572_1719 | 68.57 | 89.86 |
| SCE1572_2205 | 20.31 | 202.01 |
| SCE1572_606 | 60.38 | 108.44 |
| SCE1572_2179 | 22.71 | 68.75 |
| SCE1572_4041 | 123.12 | 1594.3 |
| SCE1572_2563 | 34.19 | 17.33 |
| SCE1572_12 | 94.23 | 335.78 |
| SCE1572_1252 | 23.77 | 10.44 |
| SCE1572_1460 | 15.47 | 11.17 |
| SCE1572_10773 | 22.92 | 27.58 |
| SCE1572_2216 | 40.26 | 216.44 |
| SCE1572_2645 | 5.27 | 0 |
| SCE1572_147 | 21.45 | 19.8 |
| SCE1572_3844 | 52.82 | 293.99 |
| SCE1572_4030 | 182.21 | 422.31 |
| SCE1572_1461 | 44.74 | 25.03 |
| SCE1572_2588 | 27.24 | 10.6 |
| SCE1572_7646 | 37.47 | 51.7 |
| SCE1572_725 | 24.48 | 23.78 |
| SCE1572_4884 | 12.09 | 27.77 |
| SCE1572_7828 | 45.94 | 118.88 |
| SCE1572_6491 | 8.92 | 0 |
| SCE1572_4037 | 11.21 | 17.04 |
| SCE1572_1414 | 57.34 | 21.05 |
| SCE1572_4502 | 96.71 | 39.45 |
| SCE1572_1298 | 153.66 | 64.11 |
| SCE1572_1705 | 82.83 | 97.96 |
| SCE1572_664 | 84.12 | 279.17 |
| SCE1572_3423 | 8.58 | 0 |
| SCE1572_3008 | 50.54 | 27.31 |
| SCE1572_3034 | 69.22 | 174.53 |
| SCE1572_3823 | 24.16 | 44.11 |
| SCE1572_10890 | 45.75 | 34.6 |
| SCE1572_1498 | 88.95 | 19.48 |
| SCE1572_7798 | 9.02 | 11.99 |
| SCE1572_2603 | 20.29 | 2.76 |

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| SCE1572_2181 | 45.41 | 29.64 |
| SCE1572_2079 | 19.44 | 13.1 |
| SCE1572_4839 | 59.3 | 126.51 |
| SCE1572_10006 | 17.84 | 21.47 |
| SCE1572_9960 | 24.17 | 12.21 |
| SCE1572_6292 | 40.86 | 24.59 |
| SCE1572_1231 | 44.07 | 182.13 |
| SCE1572_617 | 175.56 | 775.94 |
| SCE1572_6587 | 44.65 | 29.44 |
| SCE1572_3757 | 38.97 | 12.49 |
| SCE1572_1551 | 25 | 10.68 |
| SCE1572_5046 | 0 | 0 |
| SCE1572_6159 | 8.58 | 0.32 |
| SCE1572_1801 | 33.23 | 284.94 |
| SCE1572_4739 | 139.32 | 32.05 |
| SCE1572_6496 | 25.46 | 10.1 |
| SCE1572_5907 | 1111.85 | 1060.98 |
| SCE1572_7900 | 40.31 | 28.96 |
| SCE1572_3864 | 8.13 | 3.15 |
| SCE1572_6811 | 89.24 | 62.46 |
| SCE1572_10812 | 21.86 | 9.19 |
| SCE1572_10554 | 43.19 | 15.91 |
| SCE1572_1799 | 20.58 | 234.42 |
| SCE1572_2241 | 35.52 | 24.17 |
| SCE1572_1585 | 63.17 | 330.93 |
| SCE1572_10534 | 55.38 | 253.48 |
| SCE1572_8384 | 17.12 | 7.85 |
| SCE1572_1270 | 51.85 | 185.9 |
| SCE1572_2499 | 59.91 | 29.43 |
| SCE1572_8329 | 36.79 | 24.28 |
| SCE1572_1592 | 83.89 | 97.58 |
| SCE1572_3563 | 74.82 | 43.33 |
| SCE1572_9465 | 6.69 | 0 |
| SCE1572_3991 | 199.47 | 1821.29 |
| SCE1572_2879 | 66.04 | 125.61 |
| SCE1572_3182 | 51.7 | 247.67 |
| SCE1572_3568 | 35.27 | 9.23 |
| SCE1572_553 | 71.07 | 117.84 |
| SCE1572_1365 | 104.39 | 2627.74 |
| SCE1572_4509 | 42 | 113.42 |
| SCE1572_10424 | 64.32 | 24.33 |
| SCE1572_5073 | 58.24 | 596.62 |
| SCE1572_4429 | 24.78 | 47.46 |
| SCE1572_9101 | 23.73 | 59.68 |
| SCE1572_9859 | 46.55 | 44.01 |
| SCE1572_6936 | 8.78 | 4.6 |
| SCE1572_10057 | 56.86 | 47.58 |
| SCE1572_9773 | 28.93 | 30.85 |

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| SCE1572_5078 | 43.66 | 291.36 |
| SCE1572_10819 | 34.82 | 66.9 |
| SCE1572_7599 | 1892.17 | 4688.52 |
| SCE1572_2049 | 27.47 | 69.93 |
| SCE1572_8939 | 27.34 | 340.99 |
| SCE1572_3985 | 42.44 | 127.92 |
| SCE1572_334 | 27.57 | 62.2 |
| SCE1572_1884 | 30.16 | 74.55 |
| SCE1572_10746 | 10.55 | 3.17 |
| SCE1572_6106 | 20.11 | 6.54 |
| SCE1572_5105 | 120.08 | 1460.3 |
| SCE1572_11334 | 126.22 | 277.86 |
| SCE1572_11412 | 59.29 | 209.36 |
| SCE1572_7394 | 16.02 | 1.71 |
| SCE1572_13 | 50.09 | 30.41 |
| SCE1572_9423 | 41.65 | 56.14 |
| SCE1572_10803 | 17.2 | 10.35 |
| SCE1572_10429 | 44.26 | 15.87 |
| SCE1572_1812 | 31.22 | 14.57 |
| SCE1572_11576 | 25.89 | 51.18 |
| SCE1572_2607 | 28.67 | 18.29 |
| SCE1572_1525 | 86.64 | 428.42 |
| SCE1572_8651 | 15.05 | 2.59 |
| SCE1572_5999 | 34.51 | 315.85 |
| SCE1572_11259 | 57.26 | 556.62 |
| SCE1572_4917 | 10.63 | 3.34 |
| SCE1572_10130 | 24.67 | 20.11 |
| SCE1572_4485 | 25.48 | 110.4 |
| SCE1572_1530 | 0 | 0 |
| SCE1572_2805 | 20.44 | 20.83 |
| SCE1572_428 | 36.28 | 92.53 |
| SCE1572_8471 | 160.93 | 458.62 |
| SCE1572_870 | 12.88 | 33.39 |
| SCE1572_4449 | 2.23 | 0 |
| SCE1572_11041 | 64.51 | 78.1 |
| SCE1572_3616 | 35.63 | 17.95 |
| SCE1572_3464 | 57.35 | 27.32 |
| SCE1572_5397 | 31.36 | 15.98 |
| SCE1572_6024 | 76.28 | 73.44 |
| SCE1572_3335 | 27.97 | 61.28 |
| SCE1572_5644 | 25.6 | 2.37 |
| SCE1572_11121 | 53.25 | 26.07 |
| SCE1572_2195 | 79.64 | 81.09 |
| SCE1572_4103 | 39.9 | 16.01 |
| SCE1572_2973 | 2.97 | 0 |
| SCE1572_785 | 39.04 | 48.35 |
| SCE1572_5699 | 19.76 | 96.04 |
| SCE1572_6767 | 16.68 | 7.3 |

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| SCE1572_4685 | 59.58 | 80.18 |
| SCE1572_7768 | 97.11 | 93.97 |
| SCE1572_1465 | 28.9 | 13.43 |
| SCE1572_9093 | 9.23 | 1.06 |
| SCE1572_2489 | 6.93 | 0 |
| SCE1572_4170 | 0 | 0 |
| SCE1572_5381 | 27.44 | 9.91 |
| SCE1572_6448 | 95.43 | 44.71 |
| SCE1572_9476 | 15.58 | 4.33 |
| SCE1572_10901 | 16.22 | 25.37 |
| SCE1572_4534 | 29.13 | 30.56 |
| SCE1572_2834 | 336.38 | 3757.74 |
| SCE1572_8658 | 60.34 | 352.21 |
| SCE1572_8707 | 54.66 | 43.44 |
| SCE1572_7018 | 31.54 | 9.8 |
| SCE1572_5990 | 77.92 | 55.92 |
| SCE1572_9156 | 56.53 | 144.84 |
| SCE1572_2959 | 69.89 | 31.06 |
| SCE1572_7094 | 0 | 0 |
| SCE1572_11529 | 33.13 | 10.27 |
| SCE1572_2226 | 46.85 | 16.47 |
| SCE1572_5235 | 31.76 | 322.4 |
| SCE1572_7076 | 18.29 | 20.69 |
| SCE1572_2296 | 48.09 | 130.8 |
| SCE1572_9566 | 0 | 0 |
| SCE1572_5890 | 29.58 | 21.73 |
| SCE1572_4942 | 15.96 | 90.79 |
| SCE1572_4978 | 50.4 | 720.59 |
| SCE1572_1441 | 39.7 | 15.05 |
| SCE1572_10905 | 159.95 | 232.59 |
| SCE1572_11109 | 92.91 | 105.64 |
| SCE1572_10066 | 180.66 | 847.51 |
| SCE1572_11275 | 80.21 | 403.53 |
| SCE1572_7592 | 32.73 | 27.07 |
| SCE1572_7821 | 33.22 | 187.55 |
| SCE1572_1492 | 52.61 | 21.5 |
| SCE1572_8871 | 67.76 | 52.48 |
| SCE1572_8300 | 64.64 | 8.49 |
| SCE1572_10641 | 17.01 | 19.88 |
| SCE1572_1763 | 47.51 | 3.4 |
| SCE1572_1797 | 45.27 | 35.48 |
| SCE1572_2559 | 40.95 | 25.3 |
| SCE1572_4138 | 37.02 | 12.73 |
| SCE1572_4270 | 56.02 | 20.52 |
| SCE1572_9125 | 12.88 | 10.73 |
| SCE1572_11171 | 30.59 | 3.2 |
| SCE1572_7791 | 14.18 | 2.35 |
| SCE1572_927 | 19.65 | 7.72 |

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| SCE1572_10962 | 100.86 | 37.59 |
| SCE1572_9003 | 186.76 | 775.76 |
| SCE1572_9136 | 19.04 | 5.09 |
| SCE1572_6706 | 565.79 | 1973.7 |
| SCE1572_292 | 10.11 | 82.11 |
| SCE1572_10485 | 55.9 | 257.48 |
| SCE1572_5093 | 97.59 | 1157.68 |
| SCE1572_1272 | 7.71 | 12.37 |
| SCE1572_5100 | 27.26 | 47.15 |
| SCE1572_9178 | 162.76 | 456.15 |
| SCE1572_11063 | 26.34 | 19.73 |
| SCE1572_305 | 42.51 | 22.17 |
| SCE1572_2112 | 2.45 | 0 |
| SCE1572_10394 | 0 | 0 |
| SCE1572_10835 | 89.66 | 27.88 |
| SCE1572_10624 | 44.59 | 136.31 |
| SCE1572_9740 | 77.7 | 403.88 |
| SCE1572_7372 | 16.93 | 22.49 |
| SCE1572_1677 | 3.72 | 2.24 |
| SCE1572_9363 | 26.03 | 65.78 |
| SCE1572_8905 | 9.1 | 3.65 |
| SCE1572_11129 | 54.25 | 62.61 |
| SCE1572_5860 | 0 | 0 |
| SCE1572_5283 | 33.08 | 18.58 |
| SCE1572_4071 | 31.13 | 140.17 |
| SCE1572_3936 | 0 | 0 |
| SCE1572_7455 | 36.93 | 240.94 |
| SCE1572_6725 | 34.73 | 57.87 |
| SCE1572_1844 | 31.93 | 19.36 |
| SCE1572_2505 | 13.98 | 9.06 |
| SCE1572_6563 | 30.55 | 32.08 |
| SCE1572_1296 | 0 | 0 |
| SCE1572_652 | 560.76 | 2315.25 |
| SCE1572_6730 | 356.06 | 5485.43 |
| SCE1572_7453 | 50.59 | 368.95 |
| SCE1572_1672 | 15.52 | 16.19 |
| SCE1572_5689 | 30.03 | 14.22 |
| SCE1572_8439 | 35.93 | 29.53 |
| SCE1572_1736 | 58.43 | 28.48 |
| SCE1572_6290 | 0 | 0 |
| SCE1572_79 | 49.78 | 28.59 |
| SCE1572_3291 | 14.06 | 16.62 |
| SCE1572_4084 | 36.95 | 10.73 |
| SCE1572_5366 | 33.95 | 542.12 |
| SCE1572_5844 | 30.96 | 24.84 |
| SCE1572_6293 | 54.09 | 60.82 |
| SCE1572_4200 | 37.03 | 107.19 |
| SCE1572_4776 | 69.19 | 363.72 |

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| SCE1572_2158 | 0 | 0 |
| SCE1572_6797 | 49 | 135.73 |
| SCE1572_1960 | 59.75 | 12.16 |
| SCE1572_10613 | 13.27 | 12.29 |
| SCE1572_8382 | 15.41 | 2.97 |
| SCE1572_5135 | 49.93 | 389.99 |
| SCE1572_2011 | 27.01 | 1.14 |
| SCE1572_10528 | 8.81 | 0 |
| SCE1572_1934 | 82.81 | 151.58 |
| SCE1572_11207 | 0 | 0 |
| SCE1572_1743 | 53.46 | 30.73 |
| SCE1572_5718 | 21.06 | 26.19 |
| SCE1572_9134 | 27.63 | 13.48 |
| SCE1572_1625 | 56.22 | 27.37 |
| SCE1572_1381 | 20.06 | 15.87 |
| SCE1572_2085 | 24.6 | 22.32 |
| SCE1572_4014 | 0 | 0 |
| SCE1572_4560 | 12.13 | 4.87 |
| SCE1572_4649 | 43.98 | 17.38 |
| SCE1572_3779 | 15.98 | 13.92 |
| SCE1572_7107 | 51.29 | 32.3 |
| SCE1572_11562 | 0 | 0 |
| SCE1572_3755 | 27.74 | 7.57 |
| SCE1572_5138 | 0 | 0 |
| SCE1572_11283 | 30.12 | 41.78 |
| SCE1572_10088 | 0 | 0 |
| SCE1572_2807 | 8.91 | 0 |
| SCE1572_10266 | 60.85 | 167.57 |
| SCE1572_9441 | 50.87 | 429.18 |
| SCE1572_8799 | 7 | 0 |
| SCE1572_4843 | 28.12 | 33.49 |
| SCE1572_3612 | 46.78 | 19.67 |
| SCE1572_1710 | 25 | 38.82 |
| SCE1572_3363 | 40.16 | 74.96 |
| SCE1572_7352 | 40.35 | 14.71 |
| SCE1572_1471 | 0 | 0 |
| SCE1572_309 | 37.06 | 11.58 |
| SCE1572_9103 | 44.81 | 56.3 |
| SCE1572_5305 | 0 | 0 |
| SCE1572_1350 | 38.5 | 42.76 |
| SCE1572_8020 | 43.16 | 23.67 |
| SCE1572_5984 | 44.75 | 41.83 |
| SCE1572_3079 | 0 | 0 |
| SCE1572_9249 | 38.37 | 12.43 |
| SCE1572_6950 | 11.66 | 0 |
| SCE1572_7522 | 34.46 | 12.44 |
| SCE1572_701 | 34.99 | 352.09 |
| SCE1572_6820 | 22.92 | 5.66 |

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| SCE1572_8389 | 57.97 | 21.47 |
| SCE1572_11293 | 119.89 | 409.55 |
| SCE1572_5739 | 117.59 | 97.91 |
| SCE1572_2790 | 16.32 | 7.6 |
| SCE1572_5209 | 8.99 | 6.19 |
| SCE1572_7219 | 132.43 | 2315.68 |
| SCE1572_8163 | 30.63 | 17.82 |
| SCE1572_1300 | 49.7 | 13 |
| SCE1572_491 | 366.86 | 346.86 |
| SCE1572_5455 | 26.16 | 8.36 |
| SCE1572_7184 | 0 | 0 |
| SCE1572_5233 | 18.76 | 127.91 |
| SCE1572_8913 | 62.23 | 24.51 |
| SCE1572_4278 | 65.13 | 39.06 |
| SCE1572_8414 | 44.35 | 29.19 |
| SCE1572_3238 | 36.47 | 22.77 |
| SCE1572_8464 | 170.83 | 426.6 |
| SCE1572_8496 | 39.46 | 14.72 |
| SCE1572_10606 | 31.12 | 24.7 |
| SCE1572_5404 | 11.49 | 11.06 |
| SCE1572_744 | 98.21 | 103.67 |
| SCE1572_10856 | 118.46 | 452.16 |
| SCE1572_964 | 97.19 | 534.91 |
| SCE1572_10846 | 15.28 | 12.51 |
| SCE1572_4640 | 154.05 | 91.52 |
| SCE1572_947 | 64.32 | 8.58 |
| SCE1572_6924 | 2.86 | 0 |
| SCE1572_4090 | 25.64 | 13.42 |
| SCE1572_8405 | 30.76 | 134.86 |
| SCE1572_7549 | 71.87 | 21.24 |
| SCE1572_6454 | 81.68 | 88.47 |
| SCE1572_9207 | 45.64 | 37.83 |
| SCE1572_8087 | 61.51 | 12.8 |
| SCE1572_3098 | 0 | 0 |
| SCE1572_9972 | 72.16 | 340.11 |
| SCE1572_210 | 30.23 | 10.86 |
| SCE1572_5524 | 31.54 | 20.82 |
| SCE1572_5357 | 51.99 | 29.1 |
| SCE1572_5795 | 48.59 | 37.43 |
| SCE1572_10257 | 31.74 | 27.14 |
| SCE1572_3514 | 60.28 | 395.7 |
| SCE1572_5887 | 19.56 | 14.39 |
| SCE1572_8946 | 118.93 | 489.73 |
| SCE1572_11502 | 18.78 | 1.67 |
| SCE1572_7205 | 74.16 | 94.09 |
| SCE1572_9694 | 716.09 | 4340.34 |
| SCE1572_1141 | 15.26 | 8.29 |
| SCE1572_2623 | 3.45 | 0 |

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| SCE1572_7419 | 13.78 | 3.9 |
| SCE1572_6656 | 49.02 | 136.27 |
| SCE1572_2270 | 109.58 | 614.95 |
| SCE1572_3151 | 36.9 | 422.85 |
| SCE1572_7614 | 20.3 | 15.76 |
| SCE1572_4679 | 50.43 | 15.17 |
| SCE1572_5206 | 54.75 | 136.12 |
| SCE1572_6611 | 28.51 | 9.36 |
| SCE1572_6287 | 44.16 | 72.63 |
| SCE1572_11290 | 331.89 | 518.12 |
| SCE1572_196 | 17.58 | 0 |
| SCE1572_6478 | 34.49 | 13.84 |
| SCE1572_3070 | 23.8 | 21.27 |
| SCE1572_9515 | 38.89 | 113.44 |
| SCE1572_10283 | 30.21 | 136.18 |
| SCE1572_11540 | 25.14 | 11.34 |
| SCE1572_10033 | 64.45 | 473.58 |
| SCE1572_5802 | 66.89 | 128.8 |
| SCE1572_9492 | 39.43 | 21.52 |
| SCE1572_7064 | 42.92 | 18.56 |
| SCE1572_8345 | 0 | 0 |
| SCE1572_582 | 12.96 | 6.93 |
| SCE1572_1346 | 19.7 | 35.92 |
| SCE1572_4569 | 37.9 | 31.73 |
| SCE1572_655 | 1052.09 | 1472.02 |
| SCE1572_3021 | 11.74 | 2.35 |
| SCE1572_5587 | 21.03 | 9.49 |
| SCE1572_8858 | 50.03 | 42.11 |
| SCE1572_4983 | 246.42 | 511.21 |
| SCE1572_11173 | 25.58 | 30.03 |
| SCE1572_6366 | 14.8 | 206.45 |
| SCE1572_11004 | 24.88 | 41.97 |
| SCE1572_6897 | 0 | 0 |
| SCE1572_2818 | 45.99 | 31.63 |
| SCE1572_9818 | 20.54 | 21.19 |
| SCE1572_5567 | 45.05 | 148.07 |
| SCE1572_11298 | 62.59 | 201.29 |
| SCE1572_3929 | 41.83 | 71.1 |
| SCE1572_831 | 0 | 0 |
| SCE1572_772 | 13.46 | 8.64 |
| SCE1572_5837 | 29.07 | 60.68 |
| SCE1572_3974 | 13.22 | 53.04 |
| SCE1572_8074 | 17.28 | 5.67 |
| SCE1572_7618 | 157.08 | 300.81 |
| SCE1572_6387 | 26.25 | 73.55 |
| SCE1572_4377 | 44.91 | 29.4 |
| SCE1572_7664 | 39.79 | 13.34 |
| SCE1572_6885 | 46.78 | 98.99 |

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| SCE1572_5511 | 87.54 | 73.85 |
| SCE1572_1891 | 53.07 | 7.3 |
| SCE1572_4955 | 23.65 | 8.4 |
| SCE1572_3104 | 21.46 | 9.89 |
| SCE1572_10163 | 51.71 | 22.63 |
| SCE1572_9407 | 23.38 | 32.23 |
| SCE1572_2576 | 25.37 | 7.45 |
| SCE1572_1057 | 23.31 | 9.8 |
| SCE1572_3041 | 13.78 | 1.56 |
| SCE1572_3894 | 16.79 | 7.35 |
| SCE1572_9509 | 16.85 | 10.81 |
| SCE1572_1729 | 21.81 | 94.98 |
| SCE1572_10171 | 10.15 | 3.7 |
| SCE1572_11043 | 31.15 | 25.83 |
| SCE1572_1117 | 11.62 | 19.46 |
| SCE1572_2373 | 41.14 | 14.14 |
| SCE1572_188 | 23.15 | 288.44 |
| SCE1572_6957 | 0 | 0 |
| SCE1572_9168 | 29.53 | 17.77 |
| SCE1572_7074 | 48.88 | 67.22 |
| SCE1572_2983 | 14.41 | 38.85 |
| SCE1572_6866 | 55.16 | 30.35 |
| SCE1572_7234 | 61.93 | 60.82 |
| SCE1572_6806 | 23.35 | 17.34 |
| SCE1572_8920 | 62.19 | 93.8 |
| SCE1572_8919 | 29.73 | 787.09 |
| SCE1572_117 | 37.35 | 286.91 |
| SCE1572_7702 | 48.77 | 16.36 |
| SCE1572_1503 | 38.22 | 102.63 |
| SCE1572_5774 | 35.56 | 3 |
| SCE1572_1512 | 10.01 | 13.77 |
| SCE1572_5065 | 27.14 | 90.1 |
| SCE1572_3749 | 37.59 | 286.51 |
| SCE1572_7921 | 2.61 | 0 |
| SCE1572_11396 | 215.8 | 660.44 |
| SCE1572_2257 | 53.71 | 43.3 |
| SCE1572_4926 | 45.05 | 13.99 |
| SCE1572_9141 | 14.23 | 4.72 |
| SCE1572_6890 | 42.88 | 7.37 |
| SCE1572_7139 | 0 | 0 |
| SCE1572_10736 | 28.92 | 53.69 |
| SCE1572_4587 | 92.51 | 217.45 |
| SCE1572_473 | 33.33 | 259.54 |
| SCE1572_9660 | 351.78 | 834.95 |
| SCE1572_5186 | 37.65 | 1252.14 |
| SCE1572_4194 | 499.81 | 939.36 |
| SCE1572_8894 | 38.94 | 29.12 |
| SCE1572_8906 | 70.19 | 67.58 |

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| SCE1572_3388 | 11.1 | 0.92 |
| SCE1572_6857 | 24.32 | 6.83 |
| SCE1572_11148 | 22.02 | 37.86 |
| SCE1572_10658 | 1164.39 | 996.69 |
| SCE1572_9615 | 0 | 0 |
| SCE1572_10048 | 35.5 | 155.48 |
| SCE1572_4370 | 27.07 | 14.89 |
| SCE1572_1483 | 80.18 | 30.79 |
| SCE1572_8118 | 33.13 | 104.59 |
| SCE1572_11491 | 25.97 | 18.38 |
| SCE1572_5830 | 41.78 | 22.71 |
| SCE1572_996 | 55.42 | 27.63 |
| SCE1572_5897 | 30.07 | 15.08 |
| SCE1572_702 | 63.68 | 32.84 |
| SCE1572_2960 | 40.03 | 31.44 |
| SCE1572_7942 | 29.21 | 16.91 |
| SCE1572_4707 | 17.84 | 37.28 |
| SCE1572_1967 | 15.86 | 19.08 |
| SCE1572_4676 | 45.48 | 29.47 |
| SCE1572_815 | 30.32 | 14.79 |
| SCE1572_3168 | 64.03 | 34.02 |
| SCE1572_4990 | 98.91 | 670.76 |
| SCE1572_6378 | 34.35 | 9.98 |
| SCE1572_11371 | 207.4 | 225.23 |
| SCE1572_1594 | 38.43 | 60.99 |
| SCE1572_9191 | 23.53 | 18.88 |
| SCE1572_9059 | 18.69 | 15 |
| SCE1572_10443 | 22.97 | 6.63 |
| SCE1572_3127 | 16.28 | 41.64 |
| SCE1572_7996 | 56.42 | 25.54 |
| SCE1572_6471 | 16.18 | 10.25 |
| SCE1572_3243 | 43.62 | 22.5 |
| SCE1572_528 | 46.45 | 164.53 |
| SCE1572_2255 | 21.23 | 5.47 |
| SCE1572_5711 | 230.03 | 532.5 |
| SCE1572_5870 | 33.14 | 57.83 |
| SCE1572_3001 | 19.12 | 8.22 |
| SCE1572_181 | 28.9 | 16.36 |
| SCE1572_4973 | 239.89 | 2367.1 |
| SCE1572_9432 | 27.76 | 20.97 |
| SCE1572_2263 | 128.9 | 807.41 |
| SCE1572_5494 | 85.92 | 20.27 |
| SCE1572_738 | 18.19 | 15.99 |
| SCE1572_10712 | 22.68 | 30.66 |
| SCE1572_10975 | 491.55 | 6726.09 |
| SCE1572_1753 | 33.94 | 108.93 |
| SCE1572_4250 | 30.72 | 77.07 |
| SCE1572_5439 | 48.89 | 15.9 |

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| SCE1572_4551 | 32.83 | 5.75 |
| SCE1572_8107 | 35.08 | 13.57 |
| SCE1572_7499 | 55.33 | 26.64 |
| SCE1572_2026 | 63.39 | 50.15 |
| SCE1572_3377 | 48.63 | 25.64 |
| SCE1572_6978 | 16.78 | 1.5 |
| SCE1572_1855 | 46.69 | 16.53 |
| SCE1572_3220 | 140.88 | 258.35 |
| SCE1572_3600 | 66.75 | 52.79 |
| SCE1572_498 | 49.81 | 25.4 |
| SCE1572_7276 | 39.07 | 5.6 |
| SCE1572_6901 | 129.47 | 1312.08 |
| SCE1572_10 | 28.75 | 83.89 |
| SCE1572_10204 | 2.81 | 0 |
| SCE1572_3869 | 28.43 | 30.41 |
| SCE1572_8184 | 2.17 | 0 |
| SCE1572_434 | 254.32 | 235.43 |
| SCE1572_5268 | 14.86 | 50.09 |
| SCE1572_5027 | 26.42 | 212.6 |
| SCE1572_35 | 15.03 | 65.75 |
| SCE1572_4988 | 63.73 | 126.17 |
| SCE1572_10524 | 49.21 | 20.81 |
| SCE1572_6861 | 12.49 | 6.44 |
| SCE1572_4630 | 71.08 | 20.48 |
| SCE1572_6095 | 24.06 | 16.39 |
| SCE1572_8115 | 20.18 | 2.49 |
| SCE1572_8121 | 62.74 | 24.5 |
| SCE1572_7359 | 7.38 | 4.74 |
| SCE1572_5463 | 29.32 | 11.14 |
| SCE1572_9340 | 631.12 | 14657.71 |
| SCE1572_10913 | 71.45 | 230.7 |
| SCE1572_8039 | 53.62 | 19.21 |
| SCE1572_3651 | 44.81 | 48.91 |
| SCE1572_7556 | 0 | 0 |
| SCE1572_3259 | 42.96 | 142.05 |
| SCE1572_478 | 18.78 | 20.95 |
| SCE1572_1403 | 2.97 | 0 |
| SCE1572_9836 | 92.59 | 30.64 |
| SCE1572_1179 | 16.97 | 7.99 |
| SCE1572_5228 | 52.64 | 150.1 |
| SCE1572_9089 | 43.53 | 17.34 |
| SCE1572_6589 | 118.02 | 30.59 |
| SCE1572_7533 | 0 | 0 |
| SCE1572_3383 | 50.89 | 505.08 |
| SCE1572_4498 | 25.44 | 45.92 |
| SCE1572_10670 | 11.49 | 0 |
| SCE1572_6100 | 32.76 | 6.87 |
| SCE1572_5861 | 38.56 | 0 |

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| SCE1572_7527 | 49.48 | 16.2 |
| SCE1572_1050 | 26.44 | 14.85 |
| SCE1572_9842 | 0 | 0 |
| SCE1572_8036 | 16.85 | 4.51 |
| SCE1572_10675 | 74.37 | 61.44 |
| SCE1572_10599 | 25.67 | 3.59 |
| SCE1572_4113 | 35.42 | 31.83 |
| SCE1572_7859 | 74.4 | 149.6 |
| SCE1572_8602 | 43.74 | 26.58 |
| SCE1572_8967 | 23.02 | 74.51 |
| SCE1572_1357 | 53.4 | 149.22 |
| SCE1572_3544 | 53.75 | 18.37 |
| SCE1572_4402 | 12.89 | 57.62 |
| SCE1572_1155 | 41.48 | 30.54 |
| SCE1572_2031 | 56.98 | 13.95 |
| SCE1572_5019 | 14.71 | 36.61 |
| SCE1572_5449 | 39.12 | 25.54 |
| SCE1572_8004 | 9.19 | 3.69 |
| SCE1572_1692 | 7.03 | 0 |
| SCE1572_5122 | 14.13 | 131.46 |
| SCE1572_8358 | 54.22 | 23.8 |
| SCE1572_7223 | 184.53 | 715.64 |
| SCE1572_3218 | 8.05 | 0 |
| SCE1572_5223 | 117.44 | 199.84 |
| SCE1572_8721 | 53.1 | 47.09 |
| SCE1572_589 | 6.64 | 2.66 |
| SCE1572_9849 | 37.73 | 38.61 |
| SCE1572_936 | 18.81 | 1.33 |
| SCE1572_8819 | 21.94 | 12 |
| SCE1572_3626 | 33.74 | 10.51 |
| SCE1572_3821 | 51.32 | 42.06 |
| SCE1572_6371 | 9.19 | 5.53 |
| SCE1572_7542 | 47.78 | 247.7 |
| SCE1572_4382 | 16.84 | 3.55 |
| SCE1572_97 | 20.99 | 11.23 |
| SCE1572_6282 | 7.34 | 0 |
| SCE1572_3198 | 12.78 | 139.41 |
| SCE1572_8156 | 37.2 | 15.35 |
| SCE1572_10159 | 6.74 | 8.11 |
| SCE1572_2432 | 48.44 | 121.25 |
| SCE1572_7672 | 6.63 | 0 |
| SCE1572_9825 | 7.61 | 19.48 |
| SCE1572_2479 | 12.63 | 43.44 |
| SCE1572_4578 | 7.4 | 8.9 |
| SCE1572_7152 | 20.17 | 10.3 |
| SCE1572_10378 | 37.51 | 16.07 |
| SCE1572_10430 | 54.69 | 43.15 |
| SCE1572_9909 | 52.61 | 29.93 |

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| SCE1572_11367 | 18.38 | 7.74 |
| SCE1572_1191 | 25.1 | 10.07 |
| SCE1572_7552 | 10.86 | 0 |
| SCE1572_6414 | 14 | 2.81 |
| SCE1572_6544 | 68.97 | 190.32 |
| SCE1572_9016 | 0 | 0 |
| SCE1572_8260 | 83.58 | 340.59 |
| SCE1572_4507 | 26.84 | 12.47 |
| SCE1572_6240 | 90.69 | 26.46 |
| SCE1572_2080 | 34.26 | 27.76 |
| SCE1572_9806 | 50.16 | 74.76 |
| SCE1572_4154 | 2.17 | 0 |
| SCE1572_5144 | 0 | 0 |
| SCE1572_577 | 0 | 0 |
| SCE1572_288 | 20.5 | 83.11 |
| SCE1572_2057 | 21.17 | 17.67 |
| SCE1572_1605 | 66.48 | 26.01 |
| SCE1572_5973 | 37.33 | 8.87 |
| SCE1572_10826 | 0 | 0 |
| SCE1572_7926 | 17.1 | 49.39 |
| SCE1572_7883 | 47.38 | 9.77 |
| SCE1572_10437 | 27.52 | 24.99 |
| SCE1572_8956 | 31.22 | 0 |
| SCE1572_7875 | 46.82 | 48.3 |
| SCE1572_10012 | 34.39 | 110.37 |
| SCE1572_2932 | 28.3 | 15.35 |
| SCE1572_4964 | 28.33 | 68.19 |
| SCE1572_6759 | 40.76 | 15.49 |
| SCE1572_10590 | 54.57 | 23.8 |
| SCE1572_10191 | 66.33 | 63.35 |
| SCE1572_5542 | 32.62 | 14.81 |
| SCE1572_7055 | 65.88 | 16.59 |
| SCE1572_6392 | 55.2 | 100.9 |
| SCE1572_9870 | 22.97 | 25.8 |
| SCE1572_10136 | 24.83 | 34.6 |
| SCE1572_5327 | 82.87 | 1921.6 |
| SCE1572_482 | 34.72 | 21.17 |
| SCE1572_9720 | 20.33 | 157.99 |
| SCE1572_9262 | 31.04 | 34.48 |
| SCE1572_8741 | 24.72 | 7.93 |
| SCE1572_10726 | 12.98 | 3.35 |
| SCE1572_9895 | 28.05 | 39.31 |
| SCE1572_6782 | 4.48 | 46.74 |
| SCE1572_9674 | 33.48 | 76.94 |
| SCE1572_2691 | 109.32 | 201.26 |
| SCE1572_10691 | 55.59 | 0 |
| SCE1572_8501 | 2.25 | 0.39 |
| SCE1572_7585 | 343.99 | 753.39 |

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| SCE1572_1457 | 18.82 | 7.55 |
| SCE1572_6708 | 24.86 | 95.62 |
| SCE1572_7853 | 68.45 | 219.66 |
| SCE1572_10581 | 47.38 | 22.81 |
| SCE1572_1097 | 36.52 | 31.96 |
| SCE1572_3805 | 40.75 | 196.16 |
| SCE1572_3044 | 15.59 | 0.94 |
| SCE1572_4032 | 1331.03 | 311.14 |
| SCE1572_5716 | 183.33 | 505.87 |
| SCE1572_6186 | 3.74 | 0 |
| SCE1572_6402 | 21.03 | 7.56 |
| SCE1572_4628 | 1.96 | 0 |
| SCE1572_5155 | 67.84 | 75.84 |
| SCE1572_887 | 156.12 | 363.72 |
| SCE1572_5533 | 40.18 | 16.49 |
| SCE1572_10770 | 35.28 | 56 |
| SCE1572_8765 | 51.51 | 22.41 |
| SCE1572_5789 | 56.22 | 202.99 |
| SCE1572_8547 | 27.13 | 6.72 |
| SCE1572_2178 | 30.69 | 24.13 |
| SCE1572_10545 | 24.57 | 15.21 |
| SCE1572_4093 | 17.62 | 3.35 |
| SCE1572_2797 | 56.76 | 21.81 |
| SCE1572_2534 | 0 | 0 |
| SCE1572_1918 | 39.83 | 30.93 |
| SCE1572_7257 | 20.15 | 25.41 |
| SCE1572_5513 | 41.51 | 56.48 |
| SCE1572_2863 | 36.12 | 13.47 |
| SCE1572_7494 | 35.67 | 56.59 |
| SCE1572_10196 | 53.37 | 5.84 |
| SCE1572_212 | 42.63 | 13.01 |
| SCE1572_7129 | 41.45 | 46.38 |
| SCE1572_2452 | 35.1 | 19.43 |
| SCE1572_3740 | 44.14 | 17.71 |
| SCE1572_2074 | 14.38 | 11.01 |
| SCE1572_4627 | 10.19 | 1.97 |
| SCE1572_9080 | 13.48 | 0 |
| SCE1572_9555 | 49.51 | 469.19 |
| SCE1572_7462 | 84.17 | 267.28 |
| SCE1572_2335 | 37.72 | 385 |
| SCE1572_502 | 19.06 | 4.17 |
| SCE1572_2021 | 9.78 | 0 |
| SCE1572_942 | 73.61 | 21.12 |
| SCE1572_7024 | 46.97 | 27.58 |
| SCE1572_10943 | 65.77 | 19.32 |
| SCE1572_8787 | 29.09 | 122.3 |
| SCE1572_8312 | 89.32 | 211.37 |
| SCE1572_3964 | 41.59 | 25.74 |

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| SCE1572_5822 | 0 | 0 |
| SCE1572_1217 | 7.71 | 0 |
| SCE1572_5474 | 12.45 | 10.89 |
| SCE1572_3368 | 106.69 | 370.16 |
| SCE1572_4543 | 38.6 | 23.56 |
| SCE1572_3089 | 44.51 | 354.88 |
| SCE1572_8634 | 0 | 0 |
| SCE1572_11341 | 40.8 | 17.59 |
| SCE1572_249 | 0 | 0 |
| SCE1572_4269 | 31.28 | 27.19 |
| SCE1572_255 | 30.68 | 13.03 |
| SCE1572_2894 | 59.53 | 25.7 |
| SCE1572_5703 | 40.01 | 281.86 |
| SCE1572_7286 | 49.22 | 214.72 |
| SCE1572_6689 | 6.69 | 0 |
| SCE1572_9296 | 43.59 | 108.56 |
| SCE1572_4849 | 68 | 92.12 |
| SCE1572_9215 | 16.22 | 13.66 |
| SCE1572_123 | 15.42 | 0 |
| SCE1572_6315 | 30.11 | 16.59 |
| SCE1572_5292 | 26.16 | 376.23 |
| SCE1572_8649 | 47.09 | 24.93 |
| SCE1572_9463 | 11.66 | 0 |
| SCE1572_2684 | 57.93 | 575.27 |
| SCE1572_4601 | 12.01 | 12.04 |
| SCE1572_9935 | 19.04 | 6.55 |
| SCE1572_6630 | 19.05 | 645.49 |
| SCE1572_10530 | 21.66 | 56.96 |
| SCE1572_2636 | 56.29 | 20.42 |
| SCE1572_8044 | 26.29 | 14.77 |
| SCE1572_1378 | 37.48 | 17.43 |
| SCE1572_8685 | 60.01 | 26.07 |
| SCE1572_486 | 39.08 | 11.29 |
| SCE1572_365 | 32.49 | 15.4 |
| SCE1572_2302 | 67.31 | 198.19 |
| SCE1572_121 | 11 | 11.14 |
| SCE1572_4296 | 36.83 | 31.84 |
| SCE1572_6971 | 72.45 | 14.38 |
| SCE1572_3694 | 34.74 | 20.49 |
| SCE1572_4725 | 54.07 | 55.38 |
| SCE1572_6397 | 28.79 | 88.69 |
| SCE1572_5241 | 23.48 | 29.06 |
| SCE1572_10462 | 54.5 | 519.64 |
| SCE1572_11380 | 11.16 | 96.27 |
| SCE1572_9357 | 65.18 | 592.65 |
| SCE1572_9527 | 46.96 | 96.88 |
| SCE1572_8625 | 48.73 | 56.79 |
| SCE1572_5551 | 41.12 | 12.05 |

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| SCE1572_846 | 61.1 | 91.23 |
| SCE1572_9993 | 75.01 | 27.63 |
| SCE1572_90 | 61.46 | 133.03 |
| SCE1572_2350 | 957.45 | 1778.64 |
| SCE1572_3225 | 17.73 | 10.83 |
| SCE1572_3534 | 0 | 0 |
| SCE1572_2545 | 62.24 | 11.52 |
| SCE1572_410 | 17.45 | 595.95 |
| SCE1572_9283 | 61.25 | 251.34 |
| SCE1572_8748 | 6.41 | 1.84 |
| SCE1572_2722 | 42.32 | 107.47 |
| SCE1572_5560 | 30 | 18.5 |
| SCE1572_133 | 80.23 | 143.15 |
| SCE1572_10953 | 14.69 | 26.87 |
| SCE1572_3674 | 64.31 | 546.64 |
| SCE1572_7200 | 33.76 | 36.49 |
| SCE1572_328 | 9.78 | 1.96 |
| SCE1572_10226 | 45.94 | 12.9 |
| SCE1572_2561 | 240.62 | 575.41 |
| SCE1572_3145 | 5.69 | 4.56 |
| SCE1572_9123 | 66.19 | 48.16 |
| SCE1572_5681 | 155.99 | 80.7 |
| SCE1572_6693 | 0 | 0 |
| SCE1572_10637 | 13.07 | 6.29 |
| SCE1572_8691 | 31.17 | 20.36 |
| SCE1572_8927 | 9.63 | 5.79 |
| SCE1572_9958 | 32.83 | 9.3 |
| SCE1572_10833 | 0 | 0 |
| SCE1572_1262 | 49.25 | 195.86 |
| SCE1572_9669 | 29.2 | 106.19 |
| SCE1572_6487 | 26.49 | 2.71 |
| SCE1572_6995 | 93.56 | 20.11 |
| SCE1572_69 | 98.45 | 41.07 |
| SCE1572_3623 | 81.57 | 18.48 |
| SCE1572_5392 | 74.44 | 59.28 |
| SCE1572_9704 | 50.54 | 76.96 |
| SCE1572_7443 | 27.32 | 19.73 |
| SCE1572_6913 | 50.4 | 14.51 |
| SCE1572_2264 | 43 | 727.12 |
| SCE1572_5908 | 133.52 | 331.66 |
| SCE1572_9749 | 54.46 | 79.72 |
| SCE1572_8709 | 17.02 | 7.45 |
| SCE1572_11324 | 79.65 | 1121.67 |
| SCE1572_4344 | 7.46 | 0 |
| SCE1572_4460 | 26.04 | 11.06 |
| SCE1572_5200 | 24.34 | 17.41 |
| SCE1572_9011 | 26.17 | 33.34 |
| SCE1572_388 | 42.71 | 43.69 |

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| SCE1572_5274 | 29.16 | 18.71 |
| SCE1572_1817 | 108.59 | 98.63 |
| SCE1572_5745 | 20.49 | 167.67 |
| SCE1572_4712 | 67.74 | 55.29 |
| SCE1572_6918 | 49.08 | 65.63 |
| SCE1572_3283 | 62.73 | 21.67 |
| SCE1572_6264 | 47.59 | 9.45 |
| SCE1572_6525 | 37.64 | 30.2 |
| SCE1572_8486 | 46.12 | 16.61 |
| SCE1572_11462 | 107.87 | 186.07 |
| SCE1572_7570 | 12.26 | 18.63 |
| SCE1572_3874 | 49.67 | 57.41 |
| SCE1572_8016 | 255.71 | 49.02 |
| SCE1572_3149 | 25.14 | 22.09 |
| SCE1572_4682 | 53.67 | 12.92 |
| SCE1572_242 | 31.43 | 45.24 |
| SCE1572_8810 | 73.26 | 26.94 |
| SCE1572_7272 | 65.54 | 37.67 |
| SCE1572_8240 | 14.32 | 10.7 |
| SCE1572_8561 | 32.17 | 30.49 |
| SCE1572_1914 | 52.11 | 30.48 |
| SCE1572_2516 | 30.8 | 19.01 |
| SCE1572_5258 | 6.89 | 0 |
| SCE1572_8204 | 2.61 | 0 |
| SCE1572_4438 | 16.86 | 8.44 |
| SCE1572_5809 | 20.34 | 25.66 |
| SCE1572_9378 | 0 | 0 |
| SCE1572_4764 | 18.85 | 12.55 |
| SCE1572_3913 | 53.88 | 138.17 |
| SCE1572_5323 | 35.56 | 51.81 |
| SCE1572_8400 | 25.11 | 50.36 |
| SCE1572_2095 | 34.57 | 35.09 |
| SCE1572_5652 | 27.76 | 317.2 |
| SCE1572_2594 | 40.34 | 43.38 |
| SCE1572_8568 | 9.96 | 4.37 |
| SCE1572_1872 | 18.04 | 92.18 |
| SCE1572_4160 | 25.81 | 27.18 |
| SCE1572_62 | 29.99 | 0 |
| SCE1572_7837 | 70.64 | 62.2 |
| SCE1572_2926 | 14.13 | 4.53 |
| SCE1572_6074 | 85.22 | 317.18 |
| SCE1572_6508 | 1.97 | 0 |
| SCE1572_1283 | 0 | 0 |
| SCE1572_4167 | 16.91 | 10.5 |
| SCE1572_4476 | 18.29 | 17.38 |
| SCE1572_2711 | 60.26 | 177.38 |
| SCE1572_6835 | 26.3 | 260.66 |
| SCE1572_5628 | 36.57 | 10.73 |

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| SCE1572_6987 | 21.13 | 5.3 |
| SCE1572_10093 | 436.13 | 1265.97 |
| SCE1572_1950 | 16.07 | 16.73 |
| SCE1572_9931 | 50.54 | 207.05 |
| SCE1572_70 | 84.05 | 45.53 |
| SCE1572_8973 | 11.18 | 17.94 |
| SCE1572_9579 | 70.87 | 27.18 |
| SCE1572_892 | 0 | 0 |
| SCE1572_9037 | 42.13 | 77.59 |
| SCE1572_10413 | 3.03 | 0 |
| SCE1572_612 | 36.57 | 232.08 |
| SCE1572_10019 | 47.47 | 81.49 |
| SCE1572_1281 | 40.4 | 10.1 |
| SCE1572_5173 | 13.07 | 0 |
| SCE1572_10262 | 31.51 | 20.52 |
| SCE1572_2511 | 70.89 | 360.18 |
| SCE1572_5595 | 0 | 0 |
| SCE1572_10001 | 14.52 | 5.14 |
| SCE1572_3831 | 22.9 | 28.66 |
| SCE1572_9877 | 0 | 0 |
| SCE1572_8805 | 24.07 | 7.72 |
| SCE1572_6141 | 36.76 | 19.9 |
| SCE1572_825 | 52.28 | 16.52 |
| SCE1572_880 | 216.7 | 841.12 |
| SCE1572_1225 | 19.46 | 8.07 |
| SCE1572_9901 | 1.67 | 0 |
| SCE1572_8551 | 56 | 59.6 |
| SCE1572_3786 | 203.86 | 303.99 |
| SCE1572_4697 | 0 | 0 |
| SCE1572_7890 | 662.62 | 28158.49 |
| SCE1572_8891 | 109.16 | 46.04 |
| SCE1572_5591 | 37.38 | 10.1 |
| SCE1572_9240 | 0 | 0 |
| SCE1572_10866 | 13.91 | 13.39 |
| SCE1572_2877 | 132.88 | 229.61 |
| SCE1572_4655 | 0 | 0 |
| SCE1572_4186 | 22.89 | 16.63 |
| SCE1572_8825 | 35.91 | 48.02 |
| SCE1572_5526 | 25.66 | 23.39 |
| SCE1572_11054 | 10.73 | 7.5 |
| SCE1572_2167 | 69.34 | 19.67 |
| SCE1572_7503 | 47.73 | 64.2 |
| SCE1572_9629 | 30.06 | 10.34 |
| SCE1572_8844 | 0 | 0 |
| SCE1572_7384 | 203.37 | 160.5 |
| SCE1572_3987 | 122.93 | 3866.2 |
| SCE1572_11577 | 15.98 | 5.98 |
| SCE1572_8317 | 15.25 | 92.34 |

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| SCE1572_10787 | 41.35 | 61.85 |
| SCE1572_3263 | 311.97 | 3461.2 |
| SCE1572_1008 | 55.81 | 30.6 |
| SCE1572_875 | 93.17 | 72.32 |
| SCE1572_5096 | 74.69 | 86.76 |
| SCE1572_5943 | 34.63 | 11.91 |
| SCE1572_710 | 118.4 | 107.74 |
| SCE1572_2802 | 32.82 | 26.86 |
| SCE1572_5378 | 49.12 | 11.56 |
| SCE1572_2976 | 22.32 | 3.88 |
| SCE1572_755 | 17.84 | 10.02 |
| SCE1572_2236 | 49.98 | 48.2 |
| SCE1572_7813 | 6.45 | 0 |
| SCE1572_51 | 52.88 | 16.46 |
| SCE1572_10242 | 35.52 | 9.04 |
| SCE1572_1388 | 30.95 | 51.86 |
| SCE1572_6108 | 57.2 | 17.79 |
| SCE1572_3811 | 30.64 | 10.17 |
| SCE1572_6359 | 23.03 | 9.24 |
| SCE1572_1890 | 33.45 | 65.63 |
| SCE1572_3053 | 28.98 | 11.35 |
| SCE1572_11192 | 18.12 | 15.1 |
| SCE1572_2761 | 44.27 | 256.18 |
| SCE1572_9706 | 126.35 | 111.5 |
| SCE1572_10247 | 0 | 0 |
| SCE1572_3471 | 7.58 | 0 |
| SCE1572_976 | 0 | 0 |
| SCE1572_761 | 20.05 | 16.48 |
| SCE1572_7364 | 42.98 | 82.42 |
| SCE1572_10054 | 54.5 | 269.66 |
| SCE1572_1221 | 49.29 | 8.99 |
| SCE1572_6311 | 26.09 | 1091.21 |
| SCE1572_10215 | 2.61 | 0 |
| SCE1572_959 | 32.96 | 65.23 |
| SCE1572_1330 | 54.27 | 16.59 |
| SCE1572_5145 | 18.79 | 22.23 |
| SCE1572_9951 | 15.11 | 13.02 |
| SCE1572_7085 | 25.99 | 14.99 |
| SCE1572_2162 | 17.58 | 5.29 |
| SCE1572_9798 | 21.97 | 0 |
| SCE1572_11547 | 22.06 | 3.53 |
| SCE1572_5635 | 102.81 | 74.41 |
| SCE1572_3451 | 28.91 | 5.68 |
| SCE1572_9499 | 399.18 | 3232.98 |
| SCE1572_353 | 22.69 | 9.3 |
| SCE1572_4594 | 60.92 | 53.22 |
| SCE1572_568 | 15.72 | 111.26 |
| SCE1572_11407 | 30.09 | 16.71 |

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| SCE1572_3137 | 27.47 | 51.89 |
| SCE1572_855 | 69.64 | 450.88 |
| SCE1572_11031 | 35.28 | 151.48 |
| SCE1572_8422 | 105.05 | 844.53 |
| SCE1572_7761 | 16.62 | 5 |
| SCE1572_9733 | 155.33 | 65.29 |
| SCE1572_7696 | 147.85 | 86.7 |
| SCE1572_3235 | 603.78 | 487.46 |
| SCE1572_4007 | 53.14 | 131.24 |
| SCE1572_10745 | 32.99 | 24.58 |
| SCE1572_7709 | 237.11 | 3596.25 |
| SCE1572_4292 | 30.79 | 16.78 |
| SCE1572_5750 | 20.24 | 2.87 |
| SCE1572_4854 | 15.45 | 11.02 |
| SCE1572_981 | 57.04 | 20.42 |
| SCE1572_1808 | 12.04 | 31.62 |
| SCE1572_9022 | 26.08 | 43.93 |
| SCE1572_379 | 25.38 | 115.67 |
| SCE1572_3993 | 24.04 | 66.75 |
| SCE1572_104 | 22.52 | 2.41 |
| SCE1572_1780 | 33.42 | 65.54 |
| SCE1572_11427 | 30.61 | 27.8 |
| SCE1572_7302 | 116.11 | 32.33 |
| SCE1572_9641 | 71.27 | 51.53 |
| SCE1572_5423 | 31.96 | 13.77 |
| SCE1572_3505 | 85.65 | 30.81 |
| SCE1572_493 | 35.25 | 5.14 |
| SCE1572_5997 | 15.95 | 31.68 |
| SCE1572_6565 | 17.27 | 10.39 |
| SCE1572_1450 | 8.03 | 21.6 |
| SCE1572_7448 | 29.64 | 44.12 |
| SCE1572_360 | 108.91 | 133.63 |
| SCE1572_7164 | 30.43 | 10.1 |
| SCE1572_9278 | 3.46 | 0 |
| SCE1572_1755 | 36.5 | 157.68 |
| SCE1572_6911 | 57.55 | 18.15 |
| SCE1572_2904 | 41.89 | 4.8 |
| SCE1572_5507 | 3.3 | 0 |
| SCE1572_9457 | 52.03 | 17.61 |
| SCE1572_10643 | 73.04 | 247.72 |
| SCE1572_9461 | 51.01 | 77.3 |
| SCE1572_3393 | 21.02 | 3.61 |
| SCE1572_5994 | 45.53 | 46.17 |
| SCE1572_9724 | 30.64 | 18.81 |
| SCE1572_3303 | 20.8 | 30.81 |
| SCE1572_9648 | 61.82 | 102.75 |
| SCE1572_8230 | 20.75 | 39.37 |
| SCE1572_7175 | 70.61 | 212.28 |

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| SCE1572_1597 | 56.34 | 26.7 |
| SCE1572_1772 | 64.02 | 18.92 |
| SCE1572_9230 | 38.75 | 10.49 |
| SCE1572_2218 | 33.69 | 49.42 |
| SCE1572_3856 | 59.95 | 30.53 |
| SCE1572_131 | 10.99 | 26.44 |
| SCE1572_2322 | 11.37 | 39.53 |
| SCE1572_10255 | 37.98 | 19.93 |
| SCE1572_7968 | 46.07 | 51.58 |
| SCE1572_8636 | 8.35 | 13.39 |
| SCE1572_4582 | 35.09 | 18.94 |
| SCE1572_6194 | 39.29 | 70.49 |
| SCE1572_9359 | 36.06 | 46.73 |
| SCE1572_11153 | 148.16 | 1377.82 |
| SCE1572_5701 | 15.49 | 69.26 |
| SCE1572_10506 | 0 | 0 |
| SCE1572_3061 | 4.3 | 0 |
| SCE1572_5502 | 22.33 | 8.49 |
| SCE1572_7785 | 2.81 | 0 |
| SCE1572_8732 | 0 | 0 |
| SCE1572_6043 | 0 | 0 |
| SCE1572_3710 | 2516.82 | 83355.21 |
| SCE1572_6345 | 18.1 | 9.08 |
| SCE1572_5267 | 41.74 | 143.08 |
| SCE1572_9886 | 33.04 | 101.21 |
| SCE1572_471 | 17.14 | 34.91 |
| SCE1572_10559 | 12.63 | 11.4 |
| SCE1572_7470 | 71.37 | 70.14 |
| SCE1572_5319 | 72.02 | 27.37 |
| SCE1572_322 | 37.74 | 21.56 |
| SCE1572_2285 | 13.1 | 189.22 |
| SCE1572_3656 | 21.57 | 29.67 |
| SCE1572_5509 | 10.17 | 5.83 |
| SCE1572_6039 | 11.86 | 41.04 |
| SCE1572_3446 | 0 | 0 |
| SCE1572_9213 | 96.22 | 23.06 |
| SCE1572_8647 | 63.68 | 18.25 |
| SCE1572_1183 | 35.03 | 23.1 |
| SCE1572_549 | 0 | 0 |
| SCE1572_5579 | 34.61 | 21.47 |
| SCE1572_9783 | 33.17 | 45.62 |
| SCE1572_11086 | 36.29 | 74.95 |
| SCE1572_4567 | 68.47 | 58.86 |
| SCE1572_521 | 10.98 | 6.6 |
| SCE1572_9592 | 31.06 | 381.39 |
| SCE1572_8281 | 17.72 | 23.7 |
| SCE1572_4119 | 44.59 | 8840.42 |
| SCE1572_48 | 30.32 | 8.42 |

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| SCE1572_2892 | 29.57 | 15.51 |
| SCE1572_3724 | 22.83 | 438.19 |
| SCE1572_1474 | 45.48 | 12.16 |
| SCE1572_506 | 8.66 | 2.61 |
| SCE1572_7475 | 107.21 | 503.72 |
| SCE1572_1911 | 50.39 | 30.32 |
| SCE1572_3323 | 0 | 0 |
| SCE1572_11347 | 31.14 | 48.33 |
| SCE1572_9730 | 49.87 | 90.27 |
| SCE1572_9786 | 71.09 | 19.14 |
| SCE1572_2948 | 36.22 | 20.27 |
| SCE1572_4450 | 17.33 | 20.85 |
| SCE1572_5165 | 83.33 | 577.07 |
| SCE1572_4889 | 14.81 | 13.17 |
| SCE1572_901 | 36.23 | 18.78 |
| SCE1572_9353 | 48.06 | 150.63 |
| SCE1572_7189 | 54.93 | 32.38 |
| SCE1572_8641 | 35.2 | 15.73 |
| SCE1572_1814 | 15.89 | 4.78 |
| SCE1572_11280 | 30.82 | 218.06 |
| SCE1572_6133 | 61.11 | 441.27 |
| SCE1572_10760 | 18.74 | 393.62 |
| SCE1572_7355 | 89.55 | 76.78 |
| SCE1572_9941 | 20.26 | 23.59 |
| SCE1572_9029 | 62.56 | 21.71 |
| SCE1572_8331 | 57.54 | 251.71 |
| SCE1572_3312 | 29.98 | 36.6 |
| SCE1572_7168 | 87.65 | 224.82 |
| SCE1572_10801 | 0 | 0 |
| SCE1572_5901 | 43.67 | 26.27 |
| SCE1572_11265 | 91.53 | 274.89 |
| SCE1572_3314 | 20.08 | 18.21 |
| SCE1572_6845 | 93.24 | 417.49 |
| SCE1572_8800 | 47.54 | 3.09 |
| SCE1572_5637 | 47.36 | 22.97 |
| SCE1572_6046 | 97.17 | 201.9 |
| SCE1572_3087 | 24.64 | 18.25 |
| SCE1572_1642 | 25.27 | 22.41 |
| SCE1572_2744 | 59.43 | 502.13 |
| SCE1572_1090 | 21.77 | 8.27 |
| SCE1572_3961 | 116.3 | 167.65 |
| SCE1572_2570 | 40.98 | 0 |
| SCE1572_5773 | 0 | 0 |
| SCE1572_9200 | 0 | 0 |
| SCE1572_7656 | 4.08 | 4.21 |
| SCE1572_2844 | 8.29 | 0 |
| SCE1572_6331 | 70.54 | 544.85 |
| SCE1572_10931 | 19.83 | 14.04 |

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| SCE1572_3942 | 696.98 | 870.64 |
| SCE1572_6051 | 21.89 | 56.51 |
| SCE1572_10185 | 76.27 | 60.45 |
| SCE1572_6058 | 10.74 | 38.31 |
| SCE1572_9595 | 23.94 | 689.03 |
| SCE1572_8739 | 35.41 | 11 |
| SCE1572_3923 | 14.06 | 5.89 |
| SCE1572_595 | 42.22 | 12.7 |
| SCE1572_899 | 34.4 | 19.87 |
| SCE1572_8987 | 20.22 | 40.55 |
| SCE1572_4892 | 62.26 | 97.13 |
| SCE1572_11327 | 10.47 | 19.98 |
| SCE1572_1435 | 30.75 | 35.06 |
| SCE1572_3601 | 13.27 | 12.29 |
| SCE1572_5929 | 78.36 | 25.11 |
| SCE1572_9060 | 37.69 | 19.73 |
| SCE1572_11363 | 28.99 | 17.52 |
| SCE1572_141 | 32.6 | 5.12 |
| SCE1572_8533 | 51.1 | 26.7 |
| SCE1572_126 | 13.96 | 7.25 |
| SCE1572_6276 | 44.5 | 201.52 |
| SCE1572_8026 | 2.49 | 0 |
| SCE1572_7299 | 84.26 | 50.4 |
| SCE1572_4599 | 11.37 | 0 |
| SCE1572_991 | 0 | 0 |
| SCE1572_1139 | 34.41 | 23.29 |
| SCE1572_10070 | 476.72 | 1198.25 |
| SCE1572_806 | 0 | 0 |
| SCE1572_4994 | 48.41 | 25.28 |
| SCE1572_8445 | 31.29 | 26.07 |
| SCE1572_10567 | 38.4 | 25.33 |
| SCE1572_8520 | 5.82 | 0.5 |
| SCE1572_10369 | 51.06 | 21.17 |
| SCE1572_10311 | 5.62 | 1.35 |
| SCE1572_2005 | 82.03 | 576.47 |
| SCE1572_4882 | 46.34 | 32.29 |
| SCE1572_1555 | 0 | 0 |
| SCE1572_317 | 28.49 | 23.22 |
| SCE1572_445 | 68.82 | 28.47 |
| SCE1572_979 | 0 | 0 |
| SCE1572_7172 | 82.97 | 50.83 |
| SCE1572_1996 | 34.39 | 8.28 |
| SCE1572_6128 | 200.69 | 2087.29 |
| SCE1572_7133 | 48.37 | 21.11 |
| SCE1572_4811 | 25.27 | 60.16 |
| SCE1572_9762 | 12.79 | 21.62 |
| SCE1572_9982 | 32.07 | 19.49 |
| SCE1572_6171 | 23.01 | 16.29 |

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| SCE1572_8673 | 32.63 | 7.7 |
| SCE1572_3457 | 0 | 0 |
| SCE1572_5921 | 0 | 0 |
| SCE1572_9030 | 71.18 | 34.82 |
| SCE1572_7051 | 20 | 2.63 |
| SCE1572_2298 | 60.65 | 105.7 |
| SCE1572_264 | 37.9 | 44.5 |
| SCE1572_4590 | 9.19 | 0 |
| SCE1572_10212 | 48 | 23.75 |
| SCE1572_6004 | 38.54 | 122.05 |
| SCE1572_753 | 35.75 | 40.05 |
| SCE1572_7410 | 0 | 0 |
| SCE1572_5249 | 28.3 | 55.47 |
| SCE1572_9385 | 17.06 | 36.49 |
| SCE1572_9115 | 257.24 | 656.04 |
| SCE1572_7995 | 65.75 | 13.03 |
| SCE1572_6124 | 18.27 | 48.36 |
| SCE1572_11409 | 20.7 | 13.9 |
| SCE1572_2768 | 6.36 | 2.55 |
| SCE1572_7263 | 18.87 | 12.53 |
| SCE1572_50 | 19.47 | 4.46 |
| SCE1572_11533 | 24.22 | 10.14 |
| SCE1572_1765 | 15.38 | 1.72 |
| SCE1572_11082 | 44.41 | 76.34 |
| SCE1572_1741 | 72.8 | 79.84 |
| SCE1572_11488 | 67.25 | 21.02 |
| SCE1572_4447 | 39.03 | 24.06 |
| SCE1572_9371 | 36.43 | 42.65 |
| SCE1572_5386 | 36.82 | 24.77 |
| SCE1572_6626 | 31.81 | 43.38 |
| SCE1572_11525 | 24.71 | 14.87 |
| SCE1572_2136 | 39.25 | 5.56 |
| SCE1572_6787 | 52.25 | 51.78 |
| SCE1572_4190 | 20.36 | 34.02 |
| SCE1572_6664 | 34.44 | 26.82 |
| SCE1572_6784 | 96.54 | 61.07 |
| SCE1572_6752 | 10.63 | 9.43 |
| SCE1572_2705 | 10.48 | 11.65 |
| SCE1572_6641 | 34.99 | 24.33 |
| SCE1572_10376 | 58.43 | 12.12 |
| SCE1572_4902 | 16.41 | 10.4 |
| SCE1572_5791 | 32.88 | 38.58 |
| SCE1572_3153 | 0 | 0 |
| SCE1572_2163 | 15.62 | 8.85 |
| SCE1572_10382 | 30.32 | 28.89 |
| SCE1572_370 | 31.76 | 30.29 |
| SCE1572_2667 | 61.75 | 27.35 |
| SCE1572_2414 | 94.13 | 69.94 |

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| SCE1572_10814 | 11.66 | 14.04 |
| SCE1572_3057 | 46.88 | 12 |
| SCE1572_1897 | 11.09 | 8.9 |
| SCE1572_9753 | 58.1 | 13.64 |
| SCE1572_5089 | 13.71 | 21.35 |
| SCE1572_1294 | 42.35 | 24.9 |
| SCE1572_6144 | 0 | 0 |
| SCE1572_10140 | 26.31 | 28.98 |
| SCE1572_7114 | 52.15 | 32.54 |
| SCE1572_1279 | 78.84 | 29.19 |
| SCE1572_8887 | 22.61 | 0 |
| SCE1572_1823 | 30.66 | 77.9 |
| SCE1572_2123 | 32.94 | 47.76 |
| SCE1572_3187 | 11.23 | 0 |
| SCE1572_11415 | 20.99 | 11.23 |
| SCE1572_10345 | 25.33 | 17.78 |
| SCE1572_2913 | 25.47 | 7.53 |
| SCE1572_8498 | 0 | 0 |
| SCE1572_4505 | 2.41 | 0 |
| SCE1572_6241 | 23.24 | 23.77 |
| SCE1572_4745 | 20.12 | 49 |
| SCE1572_5622 | 30.37 | 52.73 |
| SCE1572_4859 | 32.7 | 9.52 |
| SCE1572_1619 | 224.93 | 3085.56 |
| SCE1572_9074 | 95.68 | 23.21 |
| SCE1572_4182 | 9.15 | 5.87 |
| SCE1572_6428 | 24.41 | 4.45 |
| SCE1572_1200 | 38.13 | 11.74 |
| SCE1572_2403 | 26.31 | 24.99 |
| SCE1572_169 | 50.96 | 119.63 |
| SCE1572_2147 | 77.84 | 27.96 |
| SCE1572_2858 | 77.83 | 195.57 |
| SCE1572_4319 | 43.09 | 6.6 |
| SCE1572_6771 | 10.22 | 16.4 |
| SCE1572_1600 | 31.06 | 32.04 |
| SCE1572_4320 | 49.28 | 30.41 |
| SCE1572_6639 | 38.36 | 13.19 |
| SCE1572_4314 | 36.51 | 11.68 |
| SCE1572_10287 | 272.38 | 459.82 |
| SCE1572_8750 | 0 | 0 |
| SCE1572_9152 | 30.37 | 39.14 |
| SCE1572_10723 | 30.86 | 35.43 |
| SCE1572_10154 | 82.83 | 564.28 |
| SCE1572_4874 | 679.2 | 2181.1 |
| SCE1572_7924 | 21.82 | 20.61 |
| SCE1572_9638 | 28.94 | 122.75 |
| SCE1572_8698 | 22.04 | 19.47 |
| SCE1572_2124 | 58.37 | 18.08 |

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| SCE1572_10576 | 80.88 | 31.65 |
| SCE1572_7635 | 603.14 | 6212.34 |
| SCE1572_3774 | 28.87 | 10.53 |
| SCE1572_3716 | 154.35 | 54.79 |
| SCE1572_6299 | 22.22 | 22.02 |
| SCE1572_7686 | 10.11 | 0 |
| SCE1572_1274 | 14.21 | 3.8 |
| SCE1572_6252 | 64.94 | 92.87 |
| SCE1572_6609 | 43.54 | 37.43 |
| SCE1572_8885 | 1.74 | 0 |
| SCE1572_9557 | 32.06 | 273.36 |
| SCE1572_1612 | 14.07 | 24.04 |
| SCE1572_4571 | 27.41 | 21.05 |
| SCE1572_9830 | 0 | 0 |
| SCE1572_3278 | 17.91 | 61.24 |
| SCE1572_7391 | 51.86 | 21.67 |
| SCE1572_1209 | 50.02 | 9.41 |
| SCE1572_4821 | 32.96 | 5.05 |
| SCE1572_8572 | 0 | 0 |
| SCE1572_10330 | 0 | 0 |
| SCE1572_5988 | 0 | 0 |
| SCE1572_1259 | 17.04 | 4.1 |
| SCE1572_10106 | 195.86 | 924.38 |
| SCE1572_6438 | 2.45 | 0 |
| SCE1572_10783 | 45.7 | 27.94 |
| SCE1572_5617 | 49.39 | 20.73 |
| SCE1572_11470 | 25.08 | 20.58 |
| SCE1572_5981 | 41.83 | 69.21 |
| SCE1572_863 | 40.41 | 123.18 |
| SCE1572_531 | 27.24 | 200.01 |
| SCE1572_5798 | 58.72 | 21.09 |
| SCE1572_1124 | 37.43 | 12.87 |
| SCE1572_4062 | 58.87 | 434.43 |
| SCE1572_2718 | 46.15 | 16.66 |
| SCE1572_5647 | 24.63 | 12 |
| SCE1572_6612 | 21.32 | 11.4 |
| SCE1572_1527 | 32.23 | 91.95 |
| SCE1572_10927 | 47.32 | 168.75 |
| SCE1572_9542 | 11.12 | 7.3 |
| SCE1572_10666 | 53.92 | 168.6 |
| SCE1572_6060 | 166.06 | 178.12 |
| SCE1572_6409 | 9.13 | 0 |
| SCE1572_1104 | 49.1 | 124.41 |
| SCE1572_11551 | 5.14 | 0 |
| SCE1572_7721 | 41.62 | 243.28 |
| SCE1572_7035 | 16.72 | 5.15 |
| SCE1572_1782 | 16.54 | 102.84 |
| SCE1572_8268 | 3.7 | 0 |

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| SCE1572_2600 | 10.18 | 12.25 |
| SCE1572_555 | 44.84 | 34.49 |
| SCE1572_3953 | 35.05 | 47.54 |
| SCE1572_6219 | 23.02 | 11.82 |
| SCE1572_3345 | 260.59 | 1772.86 |
| SCE1572_3497 | 291.39 | 1485.35 |
| SCE1572_3958 | 19.34 | 27.33 |
| SCE1572_10381 | 30.14 | 19.05 |
| SCE1572_3882 | 22.31 | 3.98 |
| SCE1572_8984 | 11.34 | 0.68 |
| SCE1572_10397 | 35.15 | 65.66 |
| SCE1572_281 | 13.31 | 10.89 |
| SCE1572_5312 | 64.66 | 35.51 |
| SCE1572_7361 | 4.33 | 9.12 |
| SCE1572_3675 | 0 | 0 |
| SCE1572_9396 | 53.78 | 129.15 |
| SCE1572_7738 | 47.35 | 48.06 |
| SCE1572_562 | 85.85 | 495.42 |
| SCE1572_6150 | 19.49 | 0 |
| SCE1572_7984 | 42.76 | 122.63 |
| SCE1572_8237 | 47.92 | 293.62 |
| SCE1572_542 | 38.16 | 3.67 |
| SCE1572_4936 | 20.7 | 36.64 |
| SCE1572_5663 | 26.49 | 6.26 |
| SCE1572_7736 | 22.83 | 60.59 |
| SCE1572_4300 | 32.07 | 17.72 |
| SCE1572_2611 | 19.24 | 11.23 |
| SCE1572_6117 | 19.01 | 16.34 |
| SCE1572_2682 | 37.27 | 25.46 |
| SCE1572_3574 | 27.14 | 14.2 |
| SCE1572_6739 | 2.76 | 0 |
| SCE1572_391 | 0 | 0 |
| SCE1572_8796 | 13.63 | 0.8 |
| SCE1572_7199 | 33.63 | 152.28 |
| SCE1572_9737 | 23.18 | 33.17 |
| SCE1572_3351 | 18.93 | 21.35 |
| SCE1572_3110 | 31.22 | 11.3 |
| SCE1572_9145 | 18.71 | 46.19 |
| SCE1572_3117 | 52.84 | 171.26 |
| SCE1572_4361 | 60.65 | 15.64 |
| SCE1572_9450 | 42.83 | 24.88 |
| SCE1572_4265 | 27.79 | 7.04 |
| SCE1572_5693 | 13.78 | 6.32 |
| SCE1572_9495 | 34.01 | 60.97 |
| SCE1572_9180 | 32.49 | 9.31 |
| SCE1572_10743 | 54.71 | 60.19 |
| SCE1572_2245 | 85.62 | 69.88 |
| SCE1572_3425 | 20.11 | 11.77 |

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| SCE1572_6412 | 39.93 | 14.66 |
| SCE1572_2924 | 61.81 | 28.36 |
| SCE1572_4915 | 170.83 | 1989.08 |
| SCE1572_9529 | 30.18 | 45.27 |
| SCE1572_9691 | 24.59 | 140.19 |
| SCE1572_1324 | 15.87 | 8.49 |
| SCE1572_4025 | 52.13 | 81.01 |
| SCE1572_2232 | 8.37 | 15.1 |
| SCE1572_8014 | 23.48 | 14.3 |
| SCE1572_9414 | 126.05 | 1997.66 |
| SCE1572_4791 | 42.52 | 32.47 |
| SCE1572_1212 | 25.86 | 21.47 |
| SCE1572_1130 | 0 | 0 |
| SCE1572_9997 | 92.28 | 192.17 |
| SCE1572_11055 | 41.06 | 137.61 |
| SCE1572_2436 | 13.66 | 70.48 |
| SCE1572_10706 | 26.9 | 27.82 |
| SCE1572_9771 | 26.47 | 20.27 |
| SCE1572_3241 | 45.57 | 14.62 |
| SCE1572_3565 | 0 | 0 |
| SCE1572_6551 | 8.12 | 1.09 |
| SCE1572_7797 | 49.67 | 41.53 |
| SCE1572_2047 | 0 | 0 |
| SCE1572_2638 | 64.29 | 35.27 |
| SCE1572_4737 | 32.82 | 170.96 |
| SCE1572_7326 | 26.89 | 51.78 |
| SCE1572_11410 | 18.3 | 8.39 |
| SCE1572_2962 | 3.7 | 0 |
| SCE1572_7866 | 170.13 | 841.27 |
| SCE1572_10452 | 27.35 | 92.65 |
| SCE1572_3192 | 62.74 | 69.69 |
| SCE1572_4075 | 43.58 | 124.55 |
| SCE1572_4837 | 103.01 | 253.5 |
| SCE1572_10618 | 65.55 | 63.83 |
| SCE1572_10698 | 36.3 | 155.91 |
| SCE1572_7161 | 31.12 | 17.29 |
| SCE1572_4645 | 68.24 | 119.97 |
| SCE1572_20 | 35.98 | 307.71 |
| SCE1572_3596 | 67.25 | 21.02 |
| SCE1572_2803 | 22.46 | 69.27 |
| SCE1572_1042 | 0 | 0 |
| SCE1572_4039 | 44.76 | 6.95 |
| SCE1572_257 | 54.64 | 19.73 |
| SCE1572_6813 | 111.55 | 45.72 |
| SCE1572_9420 | 38.12 | 224.25 |
| SCE1572_4325 | 21.54 | 10.16 |
| SCE1572_4781 | 184.12 | 240.13 |
| SCE1572_9250 | 66.48 | 19.54 |

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| SCE1572_7950 | 65.08 | 99.15 |
| SCE1572_6192 | 29.77 | 27.87 |
| SCE1572_10920 | 17 | 40.91 |
| SCE1572_1731 | 74.94 | 29.89 |
| SCE1572_2107 | 69.07 | 140.11 |
| SCE1572_2605 | 11.63 | 4.66 |
| SCE1572_9055 | 35.57 | 11.21 |
| SCE1572_9209 | 30.44 | 100.3 |
| SCE1572_8759 | 70.27 | 232.29 |
| SCE1572_9245 | 12.2 | 0 |
| SCE1572_11065 | 2.81 | 13.52 |
| SCE1572_5198 | 0 | 0 |
| SCE1572_6931 | 12.63 | 0 |
| SCE1572_4783 | 178.16 | 85.2 |
| SCE1572_11061 | 534.74 | 1520.14 |
| SCE1572_9485 | 36.98 | 66.75 |
| SCE1572_8830 | 52.43 | 178.71 |
| SCE1572_8374 | 38.65 | 83.48 |
| SCE1572_68 | 58.63 | 126.3 |
| SCE1572_11142 | 0 | 16.78 |
| SCE1572_6652 | 26.47 | 10.8 |
| SCE1572_7077 | 0 | 0 |
| SCE1572_2640 | 214.79 | 129.52 |
| SCE1572_2725 | 39.31 | 42.93 |
| SCE1572_3014 | 31.29 | 8.97 |
| SCE1572_450 | 29.28 | 19.31 |
| SCE1572_1795 | 46.45 | 180.13 |
| SCE1572_4101 | 110.55 | 1968.3 |
| SCE1572_8747 | 20.22 | 0 |
| SCE1572_5301 | 19.44 | 24.95 |
| SCE1572_1337 | 30.26 | 86.39 |
| SCE1572_11123 | 43.76 | 21.76 |
| SCE1572_2601 | 0 | 0 |
| SCE1572_3983 | 13.97 | 14.95 |
| SCE1572_3966 | 10.57 | 34.33 |
| SCE1572_4421 | 0 | 0 |
| SCE1572_5048 | 26.84 | 5.24 |
| SCE1572_5111 | 343.34 | 1015.94 |
| SCE1572_7320 | 14.03 | 4.12 |
| SCE1572_7500 | 12.15 | 16.71 |
| SCE1572_6916 | 20.77 | 21.25 |
| SCE1572_9912 | 56.68 | 17.05 |
| SCE1572_10536 | 93.04 | 453.39 |
| SCE1572_4331 | 10.04 | 3.81 |
| SCE1572_1539 | 35.79 | 44.64 |
| SCE1572_8220 | 95.87 | 85.86 |
| SCE1572_4487 | 50.35 | 78.58 |
| SCE1572_11000 | 27.7 | 10.53 |

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| SCE1572_8702 | 54.09 | 229.22 |
| SCE1572_9568 | 33.14 | 20.84 |
| SCE1572_10051 | 71.12 | 109.73 |
| SCE1572_10004 | 34.07 | 14.35 |
| SCE1572_9977 | 79.78 | 37.36 |
| SCE1572_336 | 25.61 | 16.22 |
| SCE1572_11574 | 31.81 | 36.49 |
| SCE1572_4822 | 0 | 0 |
| SCE1572_4353 | 131.55 | 258.67 |
| SCE1572_4919 | 43.23 | 10.87 |
| SCE1572_6558 | 29.62 | 19.33 |
| SCE1572_10821 | 0 | 0 |
| SCE1572_2291 | 123.77 | 386.72 |
| SCE1572_7956 | 27.29 | 120.95 |
| SCE1572_9425 | 33.37 | 22.7 |
| SCE1572_7896 | 3031.15 | 118712 |
| SCE1572_2971 | 52.71 | 23.95 |
| SCE1572_4511 | 67.32 | 39.41 |
| SCE1572_426 | 31.3 | 266.04 |
| SCE1572_6790 | 15.77 | 2.92 |
| SCE1572_5428 | 19.19 | 36.95 |
| SCE1572_7525 | 96.48 | 117.62 |
| SCE1572_9049 | 33.33 | 21.36 |
| SCE1572_512 | 22.85 | 0 |
| SCE1572_3862 | 50.93 | 94.4 |
| SCE1572_6090 | 33.19 | 718.95 |
| SCE1572_9185 | 21.46 | 0 |
| SCE1572_4637 | 24.7 | 18.75 |
| SCE1572_7396 | 120.65 | 94.72 |
| SCE1572_10907 | 98.68 | 717.17 |
| SCE1572_3257 | 26.48 | 12.5 |
| SCE1572_929 | 36.85 | 73.49 |
| SCE1572_5896 | 35.56 | 8.56 |
| SCE1572_11331 | 36.45 | 67.8 |
| SCE1572_10064 | 0 | 0 |
| SCE1572_3484 | 23.73 | 15.87 |
| SCE1572_8715 | 95.65 | 97.1 |
| SCE1572_9419 | 69.61 | 789.52 |
| SCE1572_5091 | 122.69 | 285.2 |
| SCE1572_8637 | 33.6 | 33.3 |
| SCE1572_6507 | 59.1 | 29.79 |
| SCE1572_10407 | 43.18 | 62.83 |
| SCE1572_9222 | 66.71 | 62.04 |
| SCE1572_1467 | 277.67 | 480.97 |
| SCE1572_2398 | 72.97 | 1120.35 |
| SCE1572_7251 | 0 | 0 |
| SCE1572_5399 | 0 | 0 |
| SCE1572_10400 | 36.55 | 299.55 |

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| SCE1572_4243 | 24.27 | 13.66 |
| SCE1572_2424 | 136.03 | 243.91 |
| SCE1572_294 | 0 | 0 |
| SCE1572_8473 | 135.66 | 53.35 |
| SCE1572_8162 | 3.23 | 11.65 |
| SCE1572_4395 | 0 | 0 |
| SCE1572_8868 | 43.23 | 17.82 |
| SCE1572_2685 | 0 | 0 |
| SCE1572_7221 | 10.16 | 85.62 |
| SCE1572_1197 | 41.12 | 11.67 |
| SCE1572_11198 | 24.43 | 21.47 |
| SCE1572_2631 | 41.3 | 24.14 |
| SCE1572_10139 | 0 | 0 |
| SCE1572_9005 | 24.21 | 9.2 |
| SCE1572_8391 | 16.64 | 6.82 |
| SCE1572_8136 | 16.13 | 7.76 |
| SCE1572_10769 | 16.05 | 12.88 |
| SCE1572_4632 | 34.41 | 15.47 |
| SCE1572_5107 | 84.66 | 129.19 |
| SCE1572_10960 | 8.39 | 6.21 |
| SCE1572_10903 | 78.2 | 30.73 |
| SCE1572_4613 | 46.19 | 25.38 |
| SCE1572_5029 | 51.48 | 202.89 |
| SCE1572_10967 | 34.99 | 16.04 |
| SCE1572_4385 | 19.58 | 8.78 |
| SCE1572_7560 | 32.18 | 13.41 |
| SCE1572_7401 | 13.32 | 1109.56 |
| SCE1572_8207 | 22.54 | 28 |
| SCE1572_4532 | 0 | 0 |
| SCE1572_3216 | 47.15 | 75.11 |
| SCE1572_6303 | 1.8 | 0 |
| SCE1572_2040 | 49.77 | 315.71 |
| SCE1572_7043 | 92.86 | 1446 |
| SCE1572_6022 | 0 | 0 |
| SCE1572_8344 | 36.5 | 9.01 |
| SCE1572_1011 | 17.35 | 5.97 |
| SCE1572_10174 | 0 | 0 |
| SCE1572_1063 | 13.15 | 8.33 |
| SCE1572_8443 | 6.11 | 2.94 |
| SCE1572_9138 | 39.31 | 5.41 |
| SCE1572_615 | 4.21 | 0 |
| SCE1572_10350 | 7.98 | 5.24 |
| SCE1572_3165 | 38.58 | 14.39 |
| SCE1572_3794 | 43.51 | 25.39 |
| SCE1572_5150 | 39.82 | 5.53 |
| SCE1572_6257 | 35.18 | 20.16 |
| SCE1572_9988 | 24.08 | 11.86 |
| SCE1572_894 | 57.4 | 90.86 |

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| SCE1572_9474 | 92.16 | 1144.85 |
| SCE1572_8585 | 19.23 | 12.46 |
| SCE1572_10426 | 12.06 | 16.59 |
| SCE1572_5071 | 60.1 | 98.39 |
| SCE1572_2272 | 36.69 | 62.98 |
| SCE1572_10750 | 15.93 | 21.47 |
| SCE1572_8515 | 15.84 | 12.53 |
| SCE1572_6029 | 40.43 | 130.29 |
| SCE1572_5278 | 21.58 | 11.69 |
| SCE1572_2156 | 7.78 | 21.83 |
| SCE1572_2015 | 5.57 | 5.37 |
| SCE1572_3849 | 29.26 | 2.13 |
| SCE1572_4604 | 43.25 | 58.21 |
| SCE1572_2987 | 36.98 | 110.66 |
| SCE1572_2329 | 47.11 | 28.14 |
| SCE1572_3356 | 14.48 | 3.67 |
| SCE1572_10308 | 36.3 | 5.14 |
| SCE1572_7715 | 16.34 | 1.23 |
| SCE1572_7644 | 37.35 | 32.16 |
| SCE1572_10325 | 39.22 | 55.37 |
| SCE1572_7438 | 132.86 | 1213.64 |
| SCE1572_2526 | 19.06 | 4.27 |
| SCE1572_8878 | 20.07 | 8.59 |
| SCE1572_8837 | 18.95 | 13.03 |
| SCE1572_6249 | 14.52 | 3.88 |
| SCE1572_9174 | 77.57 | 83.65 |
| SCE1572_11119 | 69.75 | 271.13 |
| SCE1572_2585 | 46.72 | 12.73 |
| SCE1572_10735 | 8.61 | 9.56 |
| SCE1572_3646 | 63.69 | 119.38 |
| SCE1572_416 | 29.21 | 14.51 |
| SCE1572_6683 | 47.83 | 265.92 |
| SCE1572_9588 | 32.77 | 33.94 |
| SCE1572_3135 | 9.48 | 14.66 |
| SCE1572_9400 | 11.09 | 35.6 |
| SCE1572_8328 | 0 | 0 |
| SCE1572_3492 | 0 | 0 |
| SCE1572_393 | 23.76 | 10.89 |
| SCE1572_9850 | 0 | 0 |
| SCE1572_1697 | 111.82 | 118.6 |
| SCE1572_11007 | 16.68 | 31.04 |
| SCE1572_6234 | 26.04 | 18.66 |
| SCE1572_10360 | 25.53 | 32.64 |
| SCE1572_3075 | 43.7 | 27.44 |
| SCE1572_9632 | 193.25 | 508.5 |
| SCE1572_8067 | 23.65 | 13.39 |
| SCE1572_3639 | 18.95 | 32.2 |
| SCE1572_11024 | 138.53 | 372.8 |

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| SCE1572_4518 | 47.54 | 70.12 |
| SCE1572_9313 | 78.39 | 68.42 |
| SCE1572_9105 | 44.15 | 76.9 |
| SCE1572_5778 | 40.5 | 50.06 |
| SCE1572_8545 | 22.85 | 17.19 |
| SCE1572_2328 | 26.29 | 24.86 |
| SCE1572_4660 | 66.39 | 1075.33 |
| SCE1572_2886 | 31.11 | 24.72 |
| SCE1572_6515 | 13.61 | 2.98 |
| SCE1572_716 | 40.3 | 17.86 |
| SCE1572_11100 | 58.16 | 145.65 |
| SCE1572_10532 | 0 | 0 |
| SCE1572_10470 | 37.9 | 45.62 |
| SCE1572_7912 | 111.53 | 13.37 |
| SCE1572_10337 | 20.49 | 0 |
| SCE1572_7947 | 27 | 0 |
| SCE1572_2083 | 3.16 | 0 |
| SCE1572_1110 | 3.37 | 0 |
| SCE1572_8827 | 16.31 | 0 |
| SCE1572_2194 | 35.26 | 21.22 |
| SCE1572_10030 | 28.88 | 9.27 |
| SCE1572_3730 | 0 | 0 |
| SCE1572_8507 | 17.87 | 3.91 |
| SCE1572_2461 | 55.64 | 0 |
| SCE1572_6034 | 51.74 | 92.38 |
| SCE1572_95 | 16.34 | 3.15 |
| SCE1572_2784 | 38.47 | 9.34 |
| SCE1572_8157 | 41.14 | 3.67 |
| SCE1572_10079 | 120.4 | 21.47 |
| SCE1572_9866 | 21.46 | 35.8 |
| SCE1572_8146 | 63.58 | 61.8 |
| SCE1572_10516 | 79.06 | 39.59 |
| SCE1572_4218 | 43.17 | 182.46 |
| SCE1572_9367 | 28.33 | 10.85 |
| SCE1572_4778 | 26.26 | 87.66 |
| SCE1572_1635 | 19.36 | 20.7 |
| SCE1572_10025 | 24.09 | 39.6 |
| SCE1572_5114 | 82.6 | 245.13 |
| SCE1572_10477 | 34.89 | 106.57 |
| SCE1572_455 | 34.94 | 27.08 |
| SCE1572_420 | 13.56 | 10.49 |
| SCE1572_8500 | 29.56 | 2.3 |
| SCE1572_2734 | 749.92 | 1406.35 |
| SCE1572_1309 | 1818.76 | 13320.88 |
| SCE1572_3739 | 3.74 | 0 |
| SCE1572_10881 | 0 | 0 |
| SCE1572_5343 | 88.61 | 82.15 |
| SCE1572_10119 | 34.21 | 30.04 |

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| SCE1572_4197 | 31.46 | 30.68 |
| SCE1572_6065 | 0 | 0 |
| SCE1572_10447 | 39.08 | 49.74 |
| SCE1572_919 | 69.81 | 115.51 |
| SCE1572_7846 | 2.31 | 1.85 |
| SCE1572_10622 | 22.97 | 17.27 |
| SCE1572_8994 | 37.54 | 62.19 |
| SCE1572_7248 | 31.1 | 9.36 |
| SCE1572_7569 | 24.07 | 21.49 |
| SCE1572_11422 | 37.9 | 37.63 |
| SCE1572_7070 | 2.81 | 0 |
| SCE1572_11586 | 19.89 | 46.58 |
| SCE1572_910 | 48.18 | 28.96 |
| SCE1572_1202 | 34.76 | 11.54 |
| SCE1572_11136 | 42.1 | 57.4 |
| SCE1572_7782 | 0 | 0 |
| SCE1572_1236 | 82.54 | 91.75 |
| SCE1572_9647 | 148.17 | 181.31 |
| SCE1572_1985 | 161.07 | 7565.41 |
| SCE1572_7882 | 32.36 | 51.96 |
| SCE1572_7145 | 55.49 | 37.62 |
| SCE1572_2384 | 61.9 | 113.83 |
| SCE1572_236 | 7.71 | 0 |
| SCE1572_2647 | 52.89 | 47.52 |
| SCE1572_1819 | 37.15 | 20.14 |
| SCE1572_2377 | 23.01 | 136.85 |
| SCE1572_7936 | 30.21 | 12.58 |
| SCE1572_2356 | 55.92 | 198.91 |
| SCE1572_9303 | 117.92 | 683.06 |
| SCE1572_5814 | 15.57 | 7.14 |
| SCE1572_1463 | 35.94 | 52.26 |
| SCE1572_10889 | 27.36 | 42.34 |
| SCE1572_1495 | 0 | 0 |
| SCE1572_1663 | 0 | 0 |
| SCE1572_11029 | 4.79 | 0 |
| SCE1572_1707 | 591.8 | 139.55 |
| SCE1572_9228 | 0 | 0 |
| SCE1572_153 | 33.39 | 19.55 |
| SCE1572_2861 | 0 | 0 |
| SCE1572_723 | 36.31 | 12.27 |
| SCE1572_2308 | 37.5 | 99.6 |
| SCE1572_604 | 53.17 | 154.91 |
| SCE1572_679 | 88.27 | 89.98 |
| SCE1572_10686 | 24.71 | 119.68 |
| SCE1572_1971 | 15.27 | 21.79 |
| SCE1572_10373 | 49.89 | 60.82 |
| SCE1572_4806 | 38.58 | 124.07 |
| SCE1572_5487 | 61.77 | 43.25 |

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| SCE1572_1965 | 40.31 | 13.03 |
| SCE1572_5539 | 43.13 | 102.72 |
| SCE1572_10759 | 5.76 | 13.86 |
| SCE1572_173 | 11.66 | 0 |
| SCE1572_6537 | 29.43 | 20.05 |
| SCE1572_10794 | 26.6 | 33.61 |
| SCE1572_3764 | 33.16 | 17.05 |
| SCE1572_6084 | 39.23 | 45.93 |
| SCE1572_693 | 56.12 | 41.07 |
| SCE1572_666 | 85.4 | 351.06 |
| SCE1572_1978 | 47.03 | 501.52 |
| SCE1572_3896 | 88.44 | 585.59 |
| SCE1572_10251 | 2.3 | 0 |
| SCE1572_5291 | 10.34 | 11.06 |
| SCE1572_1394 | 23.17 | 83.29 |
| SCE1572_4340 | 44.1 | 16.64 |
| SCE1572_10897 | 18.54 | 39.67 |
| SCE1572_682 | 36.47 | 8.73 |
| SCE1572_7292 | 13.16 | 6.03 |
| SCE1572_9259 | 30.85 | 19.09 |
| SCE1572_8790 | 63.69 | 79.15 |
| SCE1572_7469 | 38.68 | 42.45 |
| SCE1572_6260 | 85.84 | 43.79 |
| SCE1572_1956 | 6.63 | 2.28 |
| SCE1572_2918 | 14.88 | 13.43 |
| SCE1572_2174 | 38.14 | 11.33 |
| SCE1572_6393 | 189.98 | 353.2 |
| SCE1572_8176 | 57.58 | 15.09 |
| SCE1572_3842 | 23.27 | 24.01 |
| SCE1572_9839 | 0 | 0 |
| SCE1572_9291 | 23.69 | 114.04 |
| SCE1572_2569 | 16.58 | 17.11 |
| SCE1572_5878 | 42.62 | 30.57 |
| SCE1572_6621 | 25.27 | 16.97 |
| SCE1572_1250 | 20.95 | 21.61 |
| SCE1572_2481 | 220.87 | 1254.7 |
| SCE1572_1443 | 57.24 | 24.19 |
| SCE1572_9605 | 6.54 | 0 |
| SCE1572_2851 | 22.58 | 5.18 |
| SCE1572_4807 | 70.04 | 106.39 |
| SCE1572_5850 | 54.33 | 28.38 |
| SCE1572_11390 | 47.79 | 40.99 |
| SCE1572_3588 | 109.57 | 24.53 |
| SCE1572_11314 | 432.17 | 594.79 |
| SCE1572_9561 | 40.88 | 14.73 |
| SCE1572_10297 | 16.18 | 34.62 |
| SCE1572_2444 | 7.22 | 8.69 |
| SCE1572_5692 | 15.45 | 13.34 |

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| SCE1572_134 | 0 | 0 |
| SCE1572_2911 | 46.95 | 21.77 |
| SCE1572_6578 | 38.81 | 21.72 |
| SCE1572_8029 | 45.94 | 84.78 |
| SCE1572_10161 | 32.68 | 43.7 |
| SCE1572_7405 | 52.8 | 67.17 |
| SCE1572_9112 | 18.44 | 20.66 |
| SCE1572_4674 | 54.35 | 34.43 |
| SCE1572_7949 | 63.98 | 141.86 |
| SCE1572_2574 | 13.57 | 13.44 |
| SCE1572_8803 | 14.61 | 54.96 |
| SCE1572_4714 | 42.24 | 18.16 |
| SCE1572_1901 | 10.07 | 59.25 |
| SCE1572_4723 | 73.46 | 75.24 |
| SCE1572_6809 | 97.52 | 593 |
| SCE1572_10509 | 22.93 | 70.53 |
| SCE1572_2391 | 99.75 | 2855.36 |
| SCE1572_2743 | 27.93 | 45.62 |
| SCE1572_6907 | 27.07 | 11.17 |
| SCE1572_5152 | 0 | 0 |
| SCE1572_5867 | 37.21 | 13.27 |
| SCE1572_1846 | 33.17 | 17.11 |
| SCE1572_5743 | 19.09 | 147.25 |
| SCE1572_1734 | 15.04 | 6.03 |
| SCE1572_9620 | 12.38 | 7.45 |
| SCE1572_8600 | 6.59 | 5.29 |
| SCE1572_6169 | 0 | 0 |
| SCE1572_828 | 18.45 | 4.16 |
| SCE1572_8034 | 33.06 | 21.95 |
| SCE1572_742 | 38.45 | 79.76 |
| SCE1572_1727 | 66.03 | 52.97 |
| SCE1572_11246 | 73.1 | 17.11 |
| SCE1572_5776 | 25.46 | 58.5 |
| SCE1572_8817 | 0 | 0 |
| SCE1572_10285 | 8.37 | 18.88 |
| SCE1572_8917 | 33.48 | 97.31 |
| SCE1572_2543 | 30.28 | 14.01 |
| SCE1572_8198 | 2.49 | 0 |
| SCE1572_7195 | 61.07 | 20.56 |
| SCE1572_10630 | 71.79 | 28.37 |
| SCE1572_1356 | 112.39 | 642.7 |
| SCE1572_1508 | 66.09 | 18.71 |
| SCE1572_6883 | 96.38 | 78.68 |
| SCE1572_7908 | 0 | 0 |
| SCE1572_7578 | 43.52 | 253.42 |
| SCE1572_3102 | 14.1 | 38.19 |
| SCE1572_7803 | 2.81 | 0 |
| SCE1572_9840 | 92.41 | 0 |

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| SCE1572_11005 | 37.41 | 42.34 |
| SCE1572_9430 | 20.43 | 8.85 |
| SCE1572_7844 | 176.89 | 5392.11 |
| SCE1572_11045 | 41.73 | 16.74 |
| SCE1572_1832 | 31.37 | 34.6 |
| SCE1572_8052 | 55.28 | 5.7 |
| SCE1572_7489 | 14.21 | 125.44 |
| SCE1572_6724 | 38.1 | 49.24 |
| SCE1572_6093 | 24.31 | 9.75 |
| SCE1572_1386 | 0 | 0 |
| SCE1572_2617 | 58.96 | 552.45 |
| SCE1572_6804 | 42.62 | 19.05 |
| SCE1572_8992 | 42.59 | 68.34 |
| SCE1572_87 | 37.19 | 39.59 |
| SCE1572_9864 | 11.66 | 6.6 |
| SCE1572_2985 | 19.07 | 17.66 |
| SCE1572_1161 | 31.15 | 6.67 |
| SCE1572_10306 | 34.83 | 115.89 |
| SCE1572_2006 | 16.03 | 67.36 |
| SCE1572_3636 | 73.45 | 16.22 |
| SCE1572_5221 | 40.43 | 52.13 |
| SCE1572_9747 | 23.65 | 42.33 |
| SCE1572_6651 | 6.5 | 20.85 |
| SCE1572_6908 | 58.07 | 11.09 |
| SCE1572_7666 | 8.36 | 11.49 |
| SCE1572_10489 | 58.6 | 639.05 |
| SCE1572_214 | 68.51 | 13.52 |
| SCE1572_6837 | 51.49 | 105.58 |
| SCE1572_4950 | 48.21 | 33.59 |
| SCE1572_5054 | 16.46 | 14.6 |
| SCE1572_5492 | 26.03 | 20.67 |
| SCE1572_11260 | 134.66 | 150.05 |
| SCE1572_7117 | 74.68 | 44.26 |
| SCE1572_4705 | 11.31 | 10.89 |
| SCE1572_7616 | 72.65 | 104.75 |
| SCE1572_8172 | 27.26 | 10.93 |
| SCE1572_1056 | 32.01 | 23.07 |
| SCE1572_3252 | 156.56 | 110.5 |
| SCE1572_7940 | 135.8 | 240.3 |
| SCE1572_5188 | 28.54 | 761.07 |
| SCE1572_1119 | 26.01 | 6.85 |
| SCE1572_7815 | 973.08 | 12086.12 |
| SCE1572_7580 | 14.18 | 53.11 |
| SCE1572_3920 | 93.74 | 29.59 |
| SCE1572_9293 | 18.48 | 47.9 |
| SCE1572_5832 | 22.81 | 39.64 |
| SCE1572_1481 | 39.84 | 21.17 |
| SCE1572_3558 | 9.24 | 0 |

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| SCE1572_3828 | 65.08 | 224.95 |
| SCE1572_1419 | 6.79 | 0 |
| SCE1572_419 | 20.71 | 40.26 |
| SCE1572_1501 | 0 | 0 |
| SCE1572_144 | 41.35 | 29.49 |
| SCE1572_5131 | 11.04 | 7.25 |
| SCE1572_6385 | 0 | 0 |
| SCE1572_4172 | 58.41 | 56.81 |
| SCE1572_10688 | 98.52 | 1160.35 |
| SCE1572_4452 | 20.11 | 9.31 |
| SCE1572_8416 | 89.96 | 218.04 |
| SCE1572_3628 | 28.27 | 18.56 |
| SCE1572_3546 | 64.98 | 9.07 |
| SCE1572_5752 | 225.17 | 528.92 |
| SCE1572_5127 | 20.24 | 15.53 |
| SCE1572_620 | 46.83 | 73.53 |
| SCE1572_10809 | 4.94 | 11.9 |
| SCE1572_5722 | 18.66 | 17.97 |
| SCE1572_4957 | 3.07 | 2.47 |
| SCE1572_2253 | 200.97 | 258.98 |
| SCE1572_5957 | 31.33 | 41.36 |
| SCE1572_538 | 24.96 | 52.9 |
| SCE1572_4404 | 0 | 0 |
| SCE1572_11568 | 138.51 | 935.97 |
| SCE1572_8646 | 116.02 | 63.46 |
| SCE1572_10264 | 61.34 | 28.79 |
| SCE1572_5960 | 20.14 | 10.77 |
| SCE1572_3436 | 25.57 | 58.67 |
| SCE1572_9409 | 41.48 | 431.19 |
| SCE1572_10671 | 17.3 | 3.97 |
| SCE1572_9235 | 24.04 | 4.82 |
| SCE1572_8910 | 41.51 | 21.72 |
| SCE1572_1180 | 15.62 | 23.49 |
| SCE1572_1006 | 99.04 | 248.68 |
| SCE1572_8278 | 26.2 | 18.61 |
| SCE1572_10454 | 0 | 0 |
| SCE1572_8689 | 40.76 | 36.62 |
| SCE1572_8458 | 80.51 | 635.34 |
| SCE1572_2038 | 20.77 | 33.74 |
| SCE1572_3222 | 44.74 | 110.07 |
| SCE1572_1189 | 37.99 | 59.53 |
| SCE1572_347 | 39.97 | 90.09 |
| SCE1572_8846 | 15.74 | 25.25 |
| SCE1572_10979 | 31.22 | 39.02 |
| SCE1572_1401 | 20.43 | 16.39 |
| SCE1572_10677 | 16.04 | 48.27 |
| SCE1572_4966 | 16.39 | 26.3 |
| SCE1572_3038 | 65.62 | 20.83 |

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| SCE1572_957 | 51.71 | 169.43 |
| SCE1572_7710 | 22.63 | 65.36 |
| SCE1572_272 | 0 | 0 |
| SCE1572_4163 | 56.9 | 24.33 |
| SCE1572_5331 | 37.33 | 77.64 |
| SCE1572_1157 | 17.11 | 8.01 |
| SCE1572_2781 | 6.63 | 9.12 |
| SCE1572_920 | 3.3 | 0 |
| SCE1572_6623 | 36.91 | 24.61 |
| SCE1572_1314 | 416.94 | 3959.41 |
| SCE1572_9289 | 15.87 | 25.46 |
| SCE1572_4184 | 53 | 221.03 |
| SCE1572_1720 | 18.95 | 53.67 |
| SCE1572_5858 | 3.7 | 0 |
| SCE1572_3386 | 2.61 | 0 |
| SCE1572_1582 | 76.67 | 22.03 |
| SCE1572_3888 | 46.41 | 12.86 |
| SCE1572_9063 | 91.15 | 20.64 |
| SCE1572_8540 | 18.24 | 10.79 |
| SCE1572_3381 | 33.91 | 41.28 |
| SCE1572_8614 | 86.92 | 130.55 |
| SCE1572_10445 | 23.33 | 19.75 |
| SCE1572_2994 | 2.53 | 0 |
| SCE1572_3607 | 23.14 | 15 |
| SCE1572_3653 | 11.97 | 0 |
| SCE1572_9497 | 49.05 | 75.64 |
| SCE1572_2494 | 27.18 | 16.35 |
| SCE1572_3280 | 24.68 | 39.26 |
| SCE1572_5348 | 160.57 | 225.94 |
| SCE1572_8186 | 0 | 0 |
| SCE1572_10651 | 69.58 | 177.47 |
| SCE1572_2649 | 27.83 | 18.51 |
| SCE1572_9087 | 61.99 | 22.81 |
| SCE1572_4975 | 346.74 | 2597.64 |
| SCE1572_10757 | 32.75 | 32.31 |
| SCE1572_6868 | 11.23 | 3.38 |
| SCE1572_1518 | 31.44 | 23.4 |
| SCE1572_5017 | 38.67 | 41.25 |
| SCE1572_818 | 12.13 | 4.87 |
| SCE1572_791 | 61.63 | 280.86 |
| SCE1572_6863 | 55.75 | 20.27 |
| SCE1572_9922 | 0 | 0 |
| SCE1572_7428 | 18.02 | 8.23 |
| SCE1572_4034 | 217.26 | 205.03 |
| SCE1572_10238 | 73.83 | 31.73 |
| SCE1572_6815 | 51.9 | 22.71 |
| SCE1572_5764 | 79.86 | 41.96 |
| SCE1572_1690 | 14.21 | 7.6 |

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| SCE1572_2755 | 102.49 | 72.76 |
| SCE1572_7694 | 25.16 | 33.31 |
| SCE1572_10853 | 82.07 | 36.83 |
| SCE1572_1712 | 17.39 | 8.19 |
| SCE1572_2500 | 33.41 | 8.25 |
| SCE1572_627 | 29 | 36.63 |
| SCE1572_1093 | 16.28 | 22.04 |
| SCE1572_10611 | 17.95 | 43.21 |
| SCE1572_4248 | 24.87 | 69.56 |
| SCE1572_7066 | 58.04 | 14.25 |
| SCE1572_1044 | 14.64 | 22.65 |
| SCE1572_2109 | 58.42 | 462.01 |
| SCE1572_1679 | 40.88 | 127.76 |
| SCE1572_8848 | 54.4 | 30.31 |
| SCE1572_3688 | 63.63 | 21.56 |
| SCE1572_203 | 44.26 | 42.86 |
| SCE1572_2045 | 25.18 | 30.3 |
| SCE1572_9969 | 16.2 | 26.51 |
| SCE1572_4029 | 166.86 | 183.43 |
| SCE1572_7212 | 2.45 | 0 |
| SCE1572_5431 | 23.07 | 15.87 |
| SCE1572_2059 | 69.09 | 15.71 |
| SCE1572_2503 | 64.86 | 25.37 |
| SCE1572_3784 | 26.14 | 1184.42 |
| SCE1572_6732 | 38.18 | 162.77 |
| SCE1572_2309 | 14.27 | 49.37 |
| SCE1572_657 | 848.88 | 707.17 |
| SCE1572_5021 | 68.24 | 271.68 |
| SCE1572_8215 | 18.14 | 3.12 |
| SCE1572_190 | 29.23 | 18.76 |
| SCE1572_7492 | 20.09 | 12.09 |
| SCE1572_4131 | 41.69 | 54.74 |
| SCE1572_7851 | 43.4 | 78.68 |
| SCE1572_10848 | 26.14 | 15.49 |
| SCE1572_4642 | 91.15 | 31.97 |
| SCE1572_4834 | 0 | 0 |
| SCE1572_9966 | 9.23 | 6.35 |
| SCE1572_2169 | 25.27 | 18.8 |
| SCE1572_10410 | 38.94 | 55.65 |
| SCE1572_654 | 0 | 0 |
| SCE1572_11296 | 19.85 | 20.09 |
| SCE1572_9302 | 70.89 | 113.74 |
| SCE1572_8085 | 0 | 0 |
| SCE1572_6190 | 51.36 | 19.47 |
| SCE1572_11209 | 20.62 | 22.06 |
| SCE1572_5737 | 118.49 | 143.27 |
| SCE1572_11285 | 47.29 | 1103.14 |
| SCE1572_3339 | 266.23 | 4016.62 |

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| SCE1572_4082 | 0 | 0 |
| SCE1572_4785 | 35.55 | 41.32 |
| SCE1572_1210 | 2.23 | 0 |
| SCE1572_8377 | 0 | 0 |
| SCE1572_7706 | 16.8 | 17.75 |
| SCE1572_5872 | 81.68 | 78.87 |
| SCE1572_3520 | 13.58 | 0 |
| SCE1572_4410 | 0 | 0 |
| SCE1572_9490 | 48.6 | 72.49 |
| SCE1572_10860 | 446.87 | 746.31 |
| SCE1572_340 | 36.39 | 11.35 |
| SCE1572_6879 | 73.66 | 136.91 |
| SCE1572_11213 | 13.78 | 12.44 |
| SCE1572_4258 | 57.99 | 218.08 |
| SCE1572_4845 | 20.96 | 26.33 |
| SCE1572_8954 | 21.77 | 27.74 |
| SCE1572_4687 | 16.1 | 10 |
| SCE1572_6528 | 15.42 | 9.28 |
| SCE1572_10392 | 14.44 | 13.9 |
| SCE1572_1745 | 56.92 | 23.71 |
| SCE1572_4099 | 26.95 | 38.93 |
| SCE1572_197 | 53.84 | 233.62 |
| SCE1572_1627 | 189.78 | 168.95 |
| SCE1572_2875 | 25.8 | 36.75 |
| SCE1572_9368 | 9.59 | 1.44 |
| SCE1572_9294 | 39.57 | 348.87 |
| SCE1572_1923 | 23.74 | 17.51 |
| SCE1572_380 | 25.91 | 4.62 |
| SCE1572_7520 | 9.97 | 12.63 |
| SCE1572_11231 | 32.04 | 16.28 |
| SCE1572_3337 | 332.73 | 5135.07 |
| SCE1572_8876 | 55.9 | 17.42 |
| SCE1572_7182 | 52.27 | 15.87 |
| SCE1572_7246 | 46.29 | 41.78 |
| SCE1572_885 | 161.38 | 42.06 |
| SCE1572_5133 | 13.78 | 16.59 |
| SCE1572_8059 | 0 | 0 |
| SCE1572_6870 | 73.32 | 230.94 |
| SCE1572_3163 | 82.37 | 44.41 |
| SCE1572_3876 | 27.71 | 15.7 |
| SCE1572_639 | 46.04 | 45.17 |
| SCE1572_9447 | 0 | 0 |
| SCE1572_5748 | 27.4 | 34.32 |
| SCE1572_9472 | 136.51 | 107.59 |
| SCE1572_7104 | 49.41 | 23.78 |
| SCE1572_5464 | 33.54 | 14.53 |
| SCE1572_8622 | 44.22 | 40.55 |
| SCE1572_8517 | 30.42 | 14.64 |

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| SCE1572_11504 | 10.34 | 3.32 |
| SCE1572_10604 | 30.92 | 26.9 |
| SCE1572_4468 | 9.75 | 10.56 |
| SCE1572_8003 | 95.68 | 36.92 |
| SCE1572_1572 | 55.22 | 33.83 |
| SCE1572_949 | 147.43 | 149.77 |
| SCE1572_8434 | 16.17 | 13.26 |
| SCE1572_6546 | 101.96 | 67.39 |
| SCE1572_7498 | 26.89 | 8.93 |
| SCE1572_7218 | 50.93 | 80.31 |
| SCE1572_7235 | 16.72 | 23.43 |
| SCE1572_8407 | 14.33 | 31.61 |
| SCE1572_10121 | 104.29 | 225.9 |
| SCE1572_3919 | 18.59 | 6.14 |
| SCE1572_510 | 24.9 | 24.68 |
| SCE1572_5307 | 39.9 | 43.21 |
| SCE1572_1103 | 131.76 | 114.69 |
| SCE1572_9013 | 2.49 | 0 |
| SCE1572_10273 | 83.14 | 184.42 |
| SCE1572_3972 | 129.96 | 238.94 |
| SCE1572_4635 | 43.86 | 20.66 |
| SCE1572_2651 | 56.9 | 19.3 |
| SCE1572_1936 | 36.83 | 31.64 |
| SCE1572_250 | 18.01 | 21.68 |
| SCE1572_10209 | 0 | 0 |
| SCE1572_10514 | 30.12 | 37.46 |
| SCE1572_5679 | 98.82 | 265 |
| SCE1572_4755 | 25.22 | 21.79 |
| SCE1572_2621 | 42.65 | 28.17 |
| SCE1572_8106 | 90.54 | 16.45 |
| SCE1572_4793 | 13.1 | 31.54 |
| SCE1572_3184 | 7.11 | 0 |
| SCE1572_1685 | 14.66 | 2.58 |
| SCE1572_2192 | 0 | 0 |
| SCE1572_8466 | 88.21 | 200.71 |
| SCE1572_2513 | 61.37 | 198.1 |
| SCE1572_1976 | 42.29 | 315.08 |
| SCE1572_4241 | 43.07 | 31.1 |
| SCE1572_1767 | 49.85 | 38.06 |
| SCE1572_5406 | 4.7 | 4.24 |
| SCE1572_3276 | 19.29 | 65.86 |
| SCE1572_6605 | 18.36 | 198.84 |
| SCE1572_8948 | 11.26 | 10.43 |
| SCE1572_1669 | 14.15 | 104.61 |
| SCE1572_1759 | 27.38 | 10.14 |
| SCE1572_5687 | 0 | 0 |
| SCE1572_3018 | 46.43 | 16.81 |
| SCE1572_3512 | 15.09 | 14.52 |

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| SCE1572_5204 | 90.97 | 214.01 |
| SCE1572_9161 | 11.94 | 24.99 |
| SCE1572_4968 | 21.17 | 5.99 |
| SCE1572_10035 | 18.95 | 8.29 |
| SCE1572_296 | 28.92 | 67.72 |
| SCE1572_4054 | 50.95 | 155.54 |
| SCE1572_3454 | 34.08 | 24.91 |
| SCE1572_1061 | 33.43 | 100.57 |
| SCE1572_5885 | 33.79 | 16.49 |
| SCE1572_6456 | 21.41 | 8.25 |
| SCE1572_833 | 126.49 | 225.21 |
| SCE1572_4078 | 28.83 | 15.55 |
| SCE1572_7601 | 41.35 | 39.4 |
| SCE1572_3269 | 31.05 | 172.94 |
| SCE1572_2599 | 42.65 | 24.82 |
| SCE1572_8901 | 12.59 | 17.21 |
| SCE1572_817 | 0 | 0 |
| SCE1572_7083 | 30.15 | 153.65 |
| SCE1572_2199 | 49.73 | 28.29 |
| SCE1572_9857 | 59.68 | 126.17 |
| SCE1572_3701 | 42.17 | 26.58 |
| SCE1572_6670 | 36.15 | 2.42 |
| SCE1572_6658 | 371.67 | 293.97 |
| SCE1572_10168 | 24.66 | 10.99 |
| SCE1572_5804 | 32.35 | 53.44 |
| SCE1572_7717 | 10.69 | 2.03 |
| SCE1572_38 | 94.09 | 323.66 |
| SCE1572_8169 | 57.59 | 14.14 |
| SCE1572_3365 | 7.25 | 2.42 |
| SCE1572_1367 | 43.32 | 91.8 |
| SCE1572_279 | 0 | 0 |
| SCE1572_4061 | 17.56 | 43.3 |
| SCE1572_7510 | 3.94 | 0 |
| SCE1572_4397 | 21.85 | 12.75 |
| SCE1572_1348 | 195.46 | 885.68 |
| SCE1572_4852 | 16.24 | 24.2 |
| SCE1572_5272 | 40.86 | 16.39 |
| SCE1572_11252 | 0 | 0 |
| SCE1572_6027 | 11.05 | 10.34 |
| SCE1572_1680 | 88.86 | 628.25 |
| SCE1572_8123 | 10.64 | 0 |
| SCE1572_1895 | 26.76 | 11.56 |
| SCE1572_9617 | 30.32 | 20.01 |
| SCE1572_7691 | 23.33 | 62.75 |
| SCE1572_6076 | 0 | 0 |
| SCE1572_2145 | 19.98 | 82.24 |
| SCE1572_3285 | 43.05 | 49.5 |
| SCE1572_4947 | 20 | 41.81 |

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| SCE1572_8660 | 16.48 | 15.87 |
| SCE1572_10870 | 48.1 | 8.79 |
| SCE1572_2773 | 145.02 | 66.31 |
| SCE1572_4342 | 16.57 | 10.46 |
| SCE1572_1653 | 70.22 | 0 |
| SCE1572_5418 | 19.68 | 21.77 |
| SCE1572_9043 | 11.9 | 16.63 |
| SCE1572_5658 | 55.57 | 24.46 |
| SCE1572_7704 | 17.29 | 19.21 |
| SCE1572_1673 | 48.43 | 180.81 |
| SCE1572_4592 | 17.69 | 41.97 |
| SCE1572_8970 | 35.52 | 535.91 |
| SCE1572_8861 | 54.72 | 18.97 |
| SCE1572_1429 | 23.2 | 50.65 |
| SCE1572_5147 | 19.46 | 0.76 |
| SCE1572_4009 | 45.29 | 21.27 |
| SCE1572_1476 | 53.73 | 16.65 |
| SCE1572_3800 | 0 | 0 |
| SCE1572_6561 | 27.77 | 5.42 |
| SCE1572_10320 | 13.48 | 2.03 |
| SCE1572_6480 | 32.91 | 37.6 |
| SCE1572_1860 | 44.78 | 68.52 |
| SCE1572_3911 | 147.23 | 1628.44 |
| SCE1572_704 | 57.31 | 233.97 |
| SCE1572_6224 | 41.48 | 154.92 |
| SCE1572_9405 | 25.92 | 10.26 |
| SCE1572_10067 | 335.4 | 884.71 |
| SCE1572_5102 | 45.32 | 178.05 |
| SCE1572_644 | 83.27 | 158.71 |
| SCE1572_9563 | 31.07 | 13.97 |
| SCE1572_3441 | 19.07 | 55.52 |
| SCE1572_5585 | 57.34 | 10.62 |
| SCE1572_4407 | 24.26 | 9.73 |
| SCE1572_5353 | 75.51 | 139.91 |
| SCE1572_9099 | 356.26 | 4709.09 |
| SCE1572_10918 | 12.31 | 65.5 |
| SCE1572_873 | 20.22 | 0 |
| SCE1572_3330 | 42.64 | 590.15 |
| SCE1572_10877 | 75.59 | 39.28 |
| SCE1572_834 | 101.08 | 281.03 |
| SCE1572_1424 | 23.57 | 100.13 |
| SCE1572_2366 | 51.3 | 34.96 |
| SCE1572_4162 | 72.2 | 50.68 |
| SCE1572_7374 | 10.36 | 11.33 |
| SCE1572_7347 | 24.45 | 8.83 |
| SCE1572_8566 | 45.7 | 143.18 |
| SCE1572_200 | 20.75 | 18.35 |
| SCE1572_10095 | 21.79 | 395.51 |

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| SCE1572_9680 | 104.71 | 327.77 |
| SCE1572_5376 | 42.8 | 15.97 |
| SCE1572_7098 | 34.46 | 24.88 |
| SCE1572_10260 | 23.43 | 12.53 |
| SCE1572_6966 | 27.23 | 20.55 |
| SCE1572_3201 | 47.73 | 0 |
| SCE1572_4589 | 20.94 | 12.1 |
| SCE1572_7758 | 13.28 | 1.33 |
| SCE1572_5944 | 48.6 | 23.57 |
| SCE1572_11326 | 25.71 | 7.58 |
| SCE1572_5031 | 400.75 | 3340.84 |
| SCE1572_2228 | 94.91 | 125.6 |
| SCE1572_8696 | 0 | 0 |
| SCE1572_7015 | 18.28 | 18.12 |
| SCE1572_6009 | 137.18 | 369.27 |
| SCE1572_9577 | 2.23 | 1.79 |
| SCE1572_5917 | 68.83 | 230.54 |
| SCE1572_7441 | 118.29 | 18.05 |
| SCE1572_8402 | 68.25 | 35.11 |
| SCE1572_10156 | 68.63 | 169.02 |
| SCE1572_2266 | 29.1 | 30.69 |
| SCE1572_1392 | 19.02 | 5.09 |
| SCE1572_2203 | 31.37 | 207.14 |
| SCE1572_5593 | 21.9 | 8.69 |
| SCE1572_11493 | 25.22 | 9.74 |
| SCE1572_7386 | 53.36 | 22.43 |
| SCE1572_4294 | 36.73 | 22.67 |
| SCE1572_9195 | 47.98 | 27.72 |
| SCE1572_4766 | 59.51 | 73.33 |
| SCE1572_2518 | 58.15 | 54.97 |
| SCE1572_3697 | 14.84 | 12.42 |
| SCE1572_2050 | 45.05 | 29.15 |
| SCE1572_1549 | 37.9 | 71.88 |
| SCE1572_9662 | 116.39 | 653.67 |
| SCE1572_10246 | 0 | 0 |
| SCE1572_974 | 0 | 0 |
| SCE1572_2234 | 43 | 25.05 |
| SCE1572_7973 | 8.68 | 0 |
| SCE1572_10465 | 63.99 | 30.53 |
| SCE1572_9903 | 23.69 | 27.56 |
| SCE1572_5219 | 5.29 | 4.24 |
| SCE1572_6062 | 59.09 | 155.4 |
| SCE1572_7305 | 62.67 | 24.33 |
| SCE1572_6945 | 9.36 | 0 |
| SCE1572_3931 | 435.54 | 1413.22 |
| SCE1572_6985 | 22.49 | 1.87 |
| SCE1572_4238 | 0 | 0 |
| SCE1572_1568 | 44.76 | 32.79 |

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| SCE1572_1246 | 13.38 | 2.3 |
| SCE1572_1839 | 11.15 | 5.37 |
| SCE1572_9277 | 30.23 | 18.74 |
| SCE1572_4206 | 41.47 | 114.06 |
| SCE1572_3665 | 0 | 0 |
| SCE1572_11161 | 42.21 | 24.88 |
| SCE1572_436 | 31.7 | 25.17 |
| SCE1572_5171 | 48.59 | 252.31 |
| SCE1572_6461 | 36.9 | 29.06 |
| SCE1572_566 | 48.23 | 35.27 |
| SCE1572_8932 | 26.93 | 39.21 |
| SCE1572_2698 | 23.96 | 6.96 |
| SCE1572_1857 | 0 | 0 |
| SCE1572_7679 | 66.83 | 248.74 |
| SCE1572_5236 | 47.05 | 77.07 |
| SCE1572_9535 | 0 | 0 |
| SCE1572_4657 | 33.11 | 157.29 |
| SCE1572_75 | 10.46 | 5.59 |
| SCE1572_10868 | 13.46 | 3.36 |
| SCE1572_2028 | 102.47 | 405.02 |
| SCE1572_3815 | 441.13 | 3721.49 |
| SCE1572_9242 | 11.66 | 5.61 |
| SCE1572_1158 | 15.35 | 5.6 |
| SCE1572_2820 | 73.22 | 189.53 |
| SCE1572_3461 | 42.92 | 13.33 |
| SCE1572_1879 | 25.4 | 29.64 |
| SCE1572_3813 | 0 | 0 |
| SCE1572_3478 | 26.92 | 92.08 |
| SCE1572_6799 | 72.04 | 20.4 |
| SCE1572_3391 | 13.4 | 20.16 |
| SCE1572_2767 | 23.94 | 34.57 |
| SCE1572_7451 | 31.26 | 69.6 |
| SCE1572_10217 | 17.59 | 114.3 |
| SCE1572_6266 | 22.05 | 33.17 |
| SCE1572_29 | 47.51 | 77.36 |
| SCE1572_9708 | 27.55 | 60.74 |
| SCE1572_2375 | 8.99 | 18.56 |
| SCE1572_5935 | 38.58 | 12.43 |
| SCE1572_11374 | 79.6 | 991.68 |
| SCE1572_1528 | 55.25 | 54.47 |
| SCE1572_10869 | 48.46 | 11.73 |
| SCE1572_4221 | 81.41 | 631.87 |
| SCE1572_9361 | 0 | 0 |
| SCE1572_10240 | 0 | 0 |
| SCE1572_2658 | 249.19 | 189.45 |
| SCE1572_4290 | 19.09 | 38.26 |
| SCE1572_8488 | 67.93 | 31.97 |
| SCE1572_6013 | 20.07 | 38.52 |

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| SCE1572_9376 | 5.41 | 0 |
| SCE1572_2248 | 80.87 | 28.38 |
| SCE1572_5910 | 44.06 | 114.36 |
| SCE1572_2800 | 79.2 | 29.38 |
| SCE1572_9713 | 16.05 | 290.51 |
| SCE1572_244 | 39.13 | 17.21 |
| SCE1572_11033 | 56.1 | 25.54 |
| SCE1572_7763 | 0 | 0 |
| SCE1572_11545 | 43.14 | 22.18 |
| SCE1572_5094 | 47.11 | 239.16 |
| SCE1572_4 | 129.85 | 501.53 |
| SCE1572_3677 | 26.93 | 16.81 |
| SCE1572_10789 | 49.73 | 125.53 |
| SCE1572_5002 | 199.22 | 1413.85 |
| SCE1572_5338 | 24.59 | 6.58 |
| SCE1572_8420 | 137.74 | 51.4 |
| SCE1572_1332 | 26.7 | 6.89 |
| SCE1572_7540 | 60.03 | 149.44 |
| SCE1572_4695 | 7.62 | 6.67 |
| SCE1572_3139 | 17.42 | 983.81 |
| SCE1572_4288 | 17.41 | 33.4 |
| SCE1572_6701 | 60.41 | 19.11 |
| SCE1572_8411 | 44.8 | 78.79 |
| SCE1572_2642 | 42.52 | 24.81 |
| SCE1572_355 | 48.86 | 16.97 |
| SCE1572_827 | 23.77 | 9.28 |
| SCE1572_1665 | 97.07 | 182.98 |
| SCE1572_1567 | 8.61 | 0 |
| SCE1572_3737 | 51.15 | 13.19 |
| SCE1572_7464 | 176.46 | 167 |
| SCE1572_5470 | 75.81 | 13.34 |
| SCE1572_11478 | 119.76 | 162.08 |
| SCE1572_3248 | 6.55 | 2.25 |
| SCE1572_4938 | 3.94 | 0 |
| SCE1572_11188 | 1.94 | 0 |
| SCE1572_5975 | 15.96 | 20.04 |
| SCE1572_5472 | 47.2 | 19.42 |
| SCE1572_9938 | 4.59 | 0 |
| SCE1572_4480 | 16.8 | 13.48 |
| SCE1572_2450 | 22.95 | 1.45 |
| SCE1572_5787 | 25.91 | 154.75 |
| SCE1572_11113 | 12.42 | 2.03 |
| SCE1572_5043 | 30.54 | 131.27 |
| SCE1572_5553 | 40.31 | 17.38 |
| SCE1572_2614 | 23.91 | 26.94 |
| SCE1572_9018 | 65.94 | 44.77 |
| SCE1572_286 | 29.66 | 0 |
| SCE1572_7649 | 41.45 | 19.57 |

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| SCE1572_5411 | 22.86 | 11.58 |
| SCE1572_7484 | 28.23 | 28.94 |
| SCE1572_77 | 18.81 | 8.31 |
| SCE1572_3938 | 177.23 | 190.01 |
| SCE1572_3904 | 0 | 0 |
| SCE1572_579 | 20.59 | 216.25 |
| SCE1572_10435 | 23.54 | 38.41 |
| SCE1572_1036 | 52.63 | 15.13 |
| SCE1572_7825 | 15.74 | 11.36 |
| SCE1572_1099 | 34.67 | 143.76 |
| SCE1572_4237 | 28.94 | 27.03 |
| SCE1572_7366 | 117.74 | 1821.63 |
| SCE1572_6590 | 8.2 | 16.44 |
| SCE1572_2430 | 41.2 | 67.43 |
| SCE1572_6633 | 71.34 | 20.17 |
| SCE1572_7587 | 139.99 | 1619.34 |
| SCE1572_5899 | 31.52 | 16.26 |
| SCE1572_6205 | 91.52 | 23.84 |
| SCE1572_4375 | 14.9 | 19.27 |
| SCE1572_1607 | 29.92 | 8.54 |
| SCE1572_3649 | 17.94 | 10.8 |
| SCE1572_3742 | 16.97 | 13.05 |
| SCE1572_6313 | 36.39 | 14.6 |
| SCE1572_11304 | 47.47 | 116.81 |
| SCE1572_8776 | 78.62 | 13.52 |
| SCE1572_10592 | 25.97 | 4.36 |
| SCE1572_3404 | 20.86 | 28.46 |
| SCE1572_4384 | 28.4 | 11.57 |
| SCE1572_9933 | 30.95 | 22.69 |
| SCE1572_9333 | 33.32 | 368.93 |
| SCE1572_2934 | 39.69 | 137.85 |
| SCE1572_4545 | 50.11 | 8.32 |
| SCE1572_8596 | 20.67 | 4.15 |
| SCE1572_11211 | 72.93 | 29.79 |
| SCE1572_5515 | 49.85 | 20.7 |
| SCE1572_6464 | 22.48 | 7.34 |
| SCE1572_7902 | 30.16 | 7.64 |
| SCE1572_3208 | 68.39 | 442.57 |
| SCE1572_11277 | 14.62 | 34.36 |
| SCE1572_9652 | 45.7 | 37.01 |
| SCE1572_5294 | 41.89 | 15.34 |
| SCE1572_7505 | 31.48 | 18.61 |
| SCE1572_3528 | 25.51 | 3442.32 |
| SCE1572_9676 | 9.36 | 13.52 |
| SCE1572_1980 | 169.51 | 1086.39 |
| SCE1572_11369 | 36.24 | 4.59 |
| SCE1572_4012 | 27.22 | 20.78 |
| SCE1572_9876 | 9.33 | 2.81 |

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| SCE1572_11225 | 33.91 | 22.81 |
| SCE1572_8295 | 62.05 | 159.21 |
| SCE1572_8767 | 18.12 | 4.59 |
| SCE1572_4540 | 44.38 | 20.36 |
| SCE1572_4209 | 49.53 | 157.09 |
| SCE1572_5210 | 6.94 | 2.79 |
| SCE1572_1644 | 19.35 | 18.41 |
| SCE1572_2536 | 74.74 | 73.24 |
| SCE1572_5640 | 44.95 | 16.63 |
| SCE1572_6431 | 95.79 | 50.59 |
| SCE1572_5829 | 22.72 | 3.77 |
| SCE1572_3444 | 54.06 | 18.59 |
| SCE1572_10583 | 13.27 | 0 |
| SCE1572_500 | 27.32 | 0 |
| SCE1572_5602 | 16.88 | 57.37 |
| SCE1572_9796 | 122.79 | 59.11 |
| SCE1572_5714 | 17.76 | 29.01 |
| SCE1572_6184 | 26.76 | 8.35 |
| SCE1572_6357 | 16.02 | 8.46 |
| SCE1572_10271 | 41.38 | 18.89 |
| SCE1572_1713 | 27.07 | 40.96 |
| SCE1572_4934 | 227.88 | 439.86 |
| SCE1572_3171 | 97.74 | 453.84 |
| SCE1572_8683 | 31.12 | 65.36 |
| SCE1572_8262 | 16.76 | 12.53 |
| SCE1572_10998 | 26.12 | 81.26 |
| SCE1572_1878 | 33.11 | 41.95 |
| SCE1572_4432 | 51.74 | 12.11 |
| SCE1572_844 | 67.12 | 230.69 |
| SCE1572_4621 | 48.22 | 230.92 |
| SCE1572_8363 | 87.59 | 28.9 |
| SCE1572_11511 | 34.2 | 32.05 |
| SCE1572_8042 | 47.7 | 16.4 |
| SCE1572_7547 | 49.1 | 23.84 |
| SCE1572_1092 | 0 | 0 |
| SCE1572_10941 | 51.26 | 11.69 |
| SCE1572_8315 | 44.77 | 34.48 |
| SCE1572_10547 | 19.38 | 11.66 |
| SCE1572_4603 | 106.66 | 556.86 |
| SCE1572_11320 | 27.15 | 3.19 |
| SCE1572_2525 | 18.38 | 11.8 |
| SCE1572_10571 | 67.28 | 150.82 |
| SCE1572_11013 | 27.96 | 31.91 |
| SCE1572_1361 | 38.34 | 146.81 |
| SCE1572_5355 | 26.37 | 31.73 |
| SCE1572_291 | 0 | 0 |
| SCE1572_8049 | 49.83 | 5.14 |
| SCE1572_3227 | 24.05 | 4.14 |

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| SCE1572_8072 | 32.78 | 14.09 |
| SCE1572_768 | 58.18 | 69.2 |
| SCE1572_2315 | 99.97 | 497.26 |
| SCE1572_4049 | 35.39 | 263.62 |
| SCE1572_4281 | 33.9 | 20.4 |
| SCE1572_952 | 12.63 | 34.75 |
| SCE1572_9603 | 16.34 | 3.15 |
| SCE1572_10831 | 53.09 | 34.85 |
| SCE1572_2906 | 66.44 | 15.38 |
| SCE1572_28 | 29.88 | 53.93 |
| SCE1572_5440 | 63.17 | 41.36 |
| SCE1572_4431 | 13.42 | 5.7 |
| SCE1572_9827 | 38.84 | 37.7 |
| SCE1572_9217 | 48.24 | 91.72 |
| SCE1572_634 | 49.48 | 171.9 |
| SCE1572_4944 | 17.37 | 40.19 |
| SCE1572_6167 | 49.6 | 15.77 |
| SCE1572_11168 | 21.63 | 15.58 |
| SCE1572_2814 | 40.71 | 227.23 |
| SCE1572_8310 | 36.23 | 16.09 |
| SCE1572_3176 | 38.53 | 49.41 |
| SCE1572_4231 | 80.41 | 38.95 |
| SCE1572_6527 | 0 | 0 |
| SCE1572_9945 | 764.19 | 1400.89 |
| SCE1572_225 | 0 | 0 |
| SCE1572_11382 | 38.31 | 241.66 |
| SCE1572_367 | 32.7 | 71.55 |
| SCE1572_488 | 93.15 | 72.33 |
| SCE1572_770 | 47.25 | 100.14 |
| SCE1572_7848 | 39.25 | 45.21 |
| SCE1572_4169 | 53.66 | 150.34 |
| SCE1572_10951 | 33.38 | 37.94 |
| SCE1572_2439 | 11.08 | 21.34 |
| SCE1572_2333 | 50.65 | 116.36 |
| SCE1572_4141 | 18.84 | 10.55 |
| SCE1572_572 | 22.11 | 22.81 |
| SCE1572_3660 | 37.4 | 48.66 |
| SCE1572_6574 | 40.22 | 20.05 |
| SCE1572_10828 | 46.2 | 28.51 |
| SCE1572_515 | 78.11 | 20.89 |
| SCE1572_4768 | 28.46 | 15.72 |
| SCE1572_8079 | 22.63 | 0 |
| SCE1572_5243 | 10.53 | 0 |
| SCE1572_7954 | 184.73 | 16.78 |
| SCE1572_7832 | 41.83 | 264.25 |
| SCE1572_7312 | 25.04 | 16.29 |
| SCE1572_9143 | 45.68 | 32.28 |
| SCE1572_7284 | 28.16 | 1.74 |

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| SCE1572_7150 | 15.48 | 11.73 |
| SCE1572_6399 | 47.83 | 427.57 |
| SCE1572_3211 | 3.63 | 0 |
| SCE1572_10493 | 79.28 | 410.24 |
| SCE1572_4156 | 14.66 | 16.88 |
| SCE1572_6489 | 24.75 | 29.79 |
| SCE1572_10228 | 31.52 | 0 |
| SCE1572_6280 | 14.71 | 298.71 |
| SCE1572_1260 | 49.14 | 19.18 |
| SCE1572_5432 | 57.61 | 14.6 |
| SCE1572_5824 | 16.77 | 20.18 |
| SCE1572_8779 | 30.58 | 162.53 |
| SCE1572_7146 | 62.84 | 38.41 |
| SCE1572_11400 | 47.99 | 164.8 |
| SCE1572_6993 | 17.48 | 7.21 |
| SCE1572_10958 | 31.31 | 23.68 |
| SCE1572_8607 | 97.13 | 350.26 |
| SCE1572_3143 | 34 | 18.78 |
| SCE1572_5252 | 41.58 | 399.29 |
| SCE1572_58 | 36.8 | 34.01 |
| SCE1572_1861 | 67.28 | 59.3 |
| SCE1572_10475 | 29.89 | 46.99 |
| SCE1572_11424 | 17.1 | 100.71 |
| SCE1572_2881 | 44.72 | 32.82 |
| SCE1572_2787 | 35.21 | 166.51 |
| SCE1572_602 | 54.43 | 67.28 |
| SCE1572_2955 | 2.49 | 0 |
| SCE1572_2839 | 42.71 | 27.24 |
| SCE1572_585 | 23.36 | 30.46 |
| SCE1572_11199 | 10.43 | 0 |
| SCE1572_2792 | 29.55 | 11.85 |
| SCE1572_3776 | 50 | 50.47 |
| SCE1572_9198 | 27.93 | 16.81 |
| SCE1572_1987 | 14.83 | 7.93 |
| SCE1572_8450 | 30.03 | 10.02 |
| SCE1572_5012 | 18.51 | 83.95 |
| SCE1572_10687 | 10.96 | 17.59 |
| SCE1572_8304 | 46.28 | 32.65 |
| SCE1572_1701 | 73.42 | 122.21 |
| SCE1572_3769 | 47.63 | 406.9 |
| SCE1572_8505 | 15.72 | 14.29 |
| SCE1572_1494 | 37.67 | 20.4 |
| SCE1572_1881 | 36.88 | 7.89 |
| SCE1572_4958 | 23.02 | 3.61 |
| SCE1572_6216 | 57.8 | 27.82 |
| SCE1572_8710 | 28.21 | 25.46 |
| SCE1572_10894 | 18.95 | 36.49 |
| SCE1572_6547 | 35.9 | 42.16 |

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| SCE1572_2506 | 40.85 | 17.02 |
| SCE1572_2016 | 48.9 | 22.47 |
| SCE1572_5434 | 34.48 | 17.84 |
| SCE1572_6465 | 3.73 | 2.69 |
| SCE1572_10608 | 24.23 | 111.59 |
| SCE1572_4665 | 8.71 | 2.1 |
| SCE1572_8513 | 15.15 | 4.51 |
| SCE1572_2305 | 16.01 | 67.24 |
| SCE1572_4548 | 43.62 | 0 |
| SCE1572_2883 | 78.84 | 531.33 |
| SCE1572_10409 | 24.19 | 58.23 |
| SCE1572_5624 | 0 | 0 |
| SCE1572_2470 | 8.57 | 0.94 |
| SCE1572_6909 | 54.87 | 0 |
| SCE1572_4872 | 6.7 | 4.36 |
| SCE1572_369 | 17.92 | 3.32 |
| SCE1572_730 | 13.84 | 13.44 |
| SCE1572_1276 | 19.89 | 9.77 |
| SCE1572_8171 | 48.5 | 17.2 |
| SCE1572_5875 | 7.02 | 6.76 |
| SCE1572_1149 | 616.74 | 2322.51 |
| SCE1572_3358 | 14.53 | 6.08 |
| SCE1572_5823 | 32.39 | 4.98 |
| SCE1572_2428 | 120.18 | 244.76 |
| SCE1572_9564 | 14.84 | 10.87 |
| SCE1572_5077 | 145.41 | 638.08 |
| SCE1572_1257 | 31.45 | 104.38 |
| SCE1572_5441 | 58.18 | 33.95 |
| SCE1572_6756 | 32.98 | 25.77 |
| SCE1572_5321 | 39.36 | 38.6 |
| SCE1572_8199 | 32.29 | 15.24 |
| SCE1572_7648 | 45.77 | 24.48 |
| SCE1572_7662 | 23.45 | 5.64 |
| SCE1572_10193 | 29.36 | 9.68 |
| SCE1572_8309 | 38.5 | 105.33 |
| SCE1572_32 | 21.29 | 10.87 |
| SCE1572_1194 | 41.96 | 57.23 |
| SCE1572_10317 | 20.04 | 13.61 |
| SCE1572_8724 | 34.35 | 19.96 |
| SCE1572_1907 | 26.4 | 76.57 |
| SCE1572_4174 | 9.28 | 9.31 |
| SCE1572_2441 | 48.61 | 39.54 |
| SCE1572_6154 | 54.15 | 7.45 |
| SCE1572_10733 | 15.55 | 152.83 |
| SCE1572_684 | 27.94 | 12.86 |
| SCE1572_9039 | 23.05 | 29.88 |
| SCE1572_10797 | 17.22 | 14.72 |
| SCE1572_11413 | 45.71 | 23.52 |

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| SCE1572_9508 | 18.09 | 9.01 |
| SCE1572_9890 | 54.25 | 24.48 |
| SCE1572_9501 | 135.27 | 395.33 |
| SCE1572_10790 | 214.86 | 771.95 |
| SCE1572_4216 | 215.66 | 406.2 |
| SCE1572_7406 | 25.11 | 17.91 |
| SCE1572_530 | 70.53 | 40.18 |
| SCE1572_10776 | 137.95 | 197.95 |
| SCE1572_2201 | 64.54 | 539.57 |
| SCE1572_10062 | 433.82 | 1307.86 |
| SCE1572_1453 | 86.21 | 40.16 |
| SCE1572_2736 | 15.41 | 30.08 |
| SCE1572_4804 | 53.49 | 22.05 |
| SCE1572_6225 | 41.35 | 26.86 |
| SCE1572_7432 | 43.46 | 55.78 |
| SCE1572_10491 | 68.92 | 213.02 |
| SCE1572_11449 | 118.49 | 391.87 |
| SCE1572_4273 | 64.48 | 42.99 |
| SCE1572_5581 | 43.69 | 170.89 |
| SCE1572_2553 | 10.52 | 4.68 |
| SCE1572_100 | 23.29 | 14.45 |
| SCE1572_1445 | 39.93 | 30.3 |
| SCE1572_2251 | 73.5 | 60.65 |
| SCE1572_7687 | 19.99 | 14.08 |
| SCE1572_7148 | 66.48 | 294.74 |
| SCE1572_2131 | 20.95 | 11.92 |
| SCE1572_5485 | 37.41 | 16.6 |
| SCE1572_9899 | 84.46 | 453.09 |
| SCE1572_2104 | 100.62 | 926.68 |
| SCE1572_8361 | 30.73 | 4.93 |
| SCE1572_4909 | 4.97 | 0 |
| SCE1572_10636 | 13.38 | 0 |
| SCE1572_5707 | 11.81 | 16.5 |
| SCE1572_7910 | 10.42 | 2.28 |
| SCE1572_2916 | 49.46 | 12.94 |
| SCE1572_7778 | 21.66 | 16.82 |
| SCE1572_7249 | 42.32 | 14.09 |
| SCE1572_9321 | 13.43 | 6.93 |
| SCE1572_7124 | 42.07 | 65.05 |
| SCE1572_2446 | 42.54 | 27.3 |
| SCE1572_4023 | 61.76 | 645.82 |
| SCE1572_10364 | 20.38 | 72.59 |
| SCE1572_4898 | 32.1 | 14.79 |
| SCE1572_3428 | 24.63 | 33.39 |
| SCE1572_3880 | 30.43 | 21.91 |
| SCE1572_6086 | 2.37 | 0 |
| SCE1572_6531 | 33.18 | 30.33 |
| SCE1572_9268 | 41.09 | 62.53 |

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| SCE1572_11048 | 27.19 | 41.11 |
| SCE1572_3729 | 11.66 | 4.68 |
| SCE1572_9100 | 49.9 | 680.65 |
| SCE1572_3207 | 32.01 | 371.7 |
| SCE1572_2154 | 28.43 | 13.68 |
| SCE1572_6617 | 43.8 | 5.41 |
| SCE1572_2159 | 0 | 0 |
| SCE1572_2568 | 48.73 | 36.49 |
| SCE1572_614 | 20.33 | 15.38 |
| SCE1572_8179 | 0 | 0 |
| SCE1572_4013 | 38.53 | 97.26 |
| SCE1572_5812 | 72.99 | 50.89 |
| SCE1572_10280 | 28.96 | 263.1 |
| SCE1572_715 | 0 | 0 |
| SCE1572_11567 | 0 | 0 |
| SCE1572_10696 | 16 | 18.95 |
| SCE1572_665 | 28.16 | 29.54 |
| SCE1572_9855 | 61.7 | 27.92 |
| SCE1572_5007 | 633.92 | 1507.1 |
| SCE1572_8923 | 9.63 | 5.79 |
| SCE1572_10476 | 40.58 | 96.32 |
| SCE1572_3527 | 26.47 | 10309.6 |
| SCE1572_9064 | 69.59 | 22.66 |
| SCE1572_4851 | 35.87 | 20.85 |
| SCE1572_2401 | 91.91 | 340.34 |
| SCE1572_4721 | 86.57 | 231.52 |
| SCE1572_2357 | 38.36 | 101.12 |
| SCE1572_1792 | 16.48 | 38.08 |
| SCE1572_9582 | 62.63 | 45.04 |
| SCE1572_216 | 76.77 | 217.11 |
| SCE1572_8325 | 53.93 | 122.6 |
| SCE1572_10327 | 26.14 | 5.03 |
| SCE1572_729 | 26.04 | 86.62 |
| SCE1572_7325 | 137.8 | 770.71 |
| SCE1572_1695 | 0 | 0 |
| SCE1572_8070 | 20.14 | 9.69 |
| SCE1572_11601 | 33.27 | 137.83 |
| SCE1572_1074 | 2.81 | 0 |
| SCE1572_4047 | 31.46 | 11.86 |
| SCE1572_1132 | 22.74 | 5.61 |
| SCE1572_6716 | 103.07 | 254.01 |
| SCE1572_5856 | 24.97 | 4.29 |
| SCE1572_10147 | 25.59 | 74.46 |
| SCE1572_7563 | 66.08 | 31.23 |
| SCE1572_4178 | 20.29 | 2.76 |
| SCE1572_5563 | 57.98 | 63 |
| SCE1572_4891 | 3.09 | 0 |
| SCE1572_9364 | 89.8 | 86.08 |

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| SCE1572_2176 | 23.17 | 8.12 |
| SCE1572_10572 | 27.12 | 41.85 |
| SCE1572_10899 | 9.6 | 0 |
| SCE1572_453 | 35.58 | 12.07 |
| SCE1572_9131 | 7.67 | 8.2 |
| SCE1572_6836 | 21.84 | 157.72 |
| SCE1572_8084 | 0 | 0 |
| SCE1572_8371 | 21 | 15.8 |
| SCE1572_9682 | 130.97 | 342.2 |
| SCE1572_11330 | 84.33 | 386.52 |
| SCE1572_362 | 39.51 | 22.54 |
| SCE1572_8077 | 49.57 | 9.77 |
| SCE1572_7562 | 21.18 | 4.02 |
| SCE1572_3860 | 24.95 | 48.5 |
| SCE1572_3627 | 35.38 | 10.43 |
| SCE1572_11429 | 30.64 | 21.89 |
| SCE1572_5109 | 43.07 | 124.41 |
| SCE1572_2521 | 17.03 | 5.52 |
| SCE1572_720 | 6.32 | 3.8 |
| SCE1572_537 | 62.13 | 142.96 |
| SCE1572_10482 | 42.08 | 15.71 |
| SCE1572_5104 | 61.64 | 179.05 |
| SCE1572_2399 | 531.19 | 3524.18 |
| SCE1572_8558 | 10.7 | 2.92 |
| SCE1572_2365 | 160.17 | 353.95 |
| SCE1572_8993 | 75.17 | 240.73 |
| SCE1572_2029 | 52.45 | 23.96 |
| SCE1572_5952 | 5.41 | 0 |
| SCE1572_4471 | 43.28 | 32 |
| SCE1572_6444 | 25.27 | 18.25 |
| SCE1572_9455 | 23.42 | 69.72 |
| SCE1572_2345 | 37.68 | 99.14 |
| SCE1572_5407 | 0 | 0 |
| SCE1572_1666 | 17.15 | 12.8 |
| SCE1572_11402 | 7.49 | 4.51 |
| SCE1572_4259 | 2.41 | 0 |
| SCE1572_435 | 50.91 | 146.68 |
| SCE1572_2653 | 47.43 | 28.54 |
| SCE1572_1693 | 7.64 | 3.07 |
| SCE1572_3720 | 26.52 | 23.08 |
| SCE1572_6011 | 32.78 | 68.33 |
| SCE1572_4148 | 64.98 | 440.75 |
| SCE1572_4671 | 0 | 0 |
| SCE1572_3585 | 40.82 | 14.04 |
| SCE1572_5961 | 32.99 | 37.82 |
| SCE1572_3460 | 47.41 | 52.75 |
| SCE1572_11114 | 78.22 | 273.91 |
| SCE1572_7919 | 48.9 | 12.39 |

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| SCE1572_11202 | 53.56 | 1031.35 |
| SCE1572_896 | 0 | 0 |
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| SCE1572_2764 | 11.49 | 0 |
| SCE1572_4222 | 74.57 | 47.86 |
| SCE1572_3576 | 26.89 | 9.64 |
| SCE1572_37 | 15.21 | 23.19 |
| SCE1572_1537 | 13.6 | 30.74 |
| SCE1572_11558 | 44.66 | 21.37 |
| SCE1572_6178 | 38.97 | 218.27 |
| SCE1572_2413 | 46.91 | 217.74 |
| SCE1572_1116 | 0 | 0 |
| SCE1572_10539 | 46.08 | 28.84 |
| SCE1572_3760 | 75.93 | 3.58 |
| SCE1572_2485 | 49.23 | 126.38 |
| SCE1572_10459 | 17.18 | 70.55 |
| SCE1572_9732 | 74.49 | 22.17 |
| SCE1572_8586 | 34.83 | 10.16 |
| SCE1572_7610 | 72.05 | 232.22 |
| SCE1572_9779 | 0 | 0 |
| SCE1572_8639 | 24.24 | 82.97 |
| SCE1572_6026 | 38.32 | 80.2 |
| SCE1572_6560 | 0 | 0 |
| SCE1572_1735 | 66.33 | 40.47 |
| SCE1572_3968 | 26.04 | 12.9 |
| SCE1572_9537 | 79.35 | 242.14 |
| SCE1572_5359 | 19.23 | 205.6 |
| SCE1572_3019 | 23.44 | 12.66 |
| SCE1572_1655 | 0 | 0 |
| SCE1572_1304 | 54.84 | 109.29 |
| SCE1572_11255 | 72.87 | 139.43 |
| SCE1572_5968 | 4.16 | 1.43 |
| SCE1572_9254 | 15 | 6.08 |
| SCE1572_5151 | 1.02 | 0 |
| SCE1572_5753 | 0 | 0 |
| SCE1572_10425 | 43.32 | 52.13 |
| SCE1572_5894 | 21.19 | 3.19 |
| SCE1572_7458 | 18.83 | 14.5 |
| SCE1572_2091 | 14.01 | 0 |
| SCE1572_3820 | 44.5 | 29.05 |
| SCE1572_6570 | 31.79 | 27.96 |
| SCE1572_2387 | 21.23 | 13.93 |
| SCE1572_7595 | 66.81 | 361.83 |
| SCE1572_2968 | 24 | 52.96 |
| SCE1572_5483 | 37.76 | 7.87 |
| SCE1572_9919 | 28.54 | 12.88 |
| SCE1572_5362 | 25.45 | 46.61 |
| SCE1572_1977 | 861.59 | 20858.47 |

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| SCE1572_4327 | 17.72 | 7.9 |
| SCE1572_16 | 52.23 | 107.92 |
| SCE1572_10289 | 140.56 | 157.75 |
| SCE1572_3564 | 29.34 | 10.17 |
| SCE1572_11366 | 23.79 | 9.32 |
| SCE1572_9382 | 0 | 0 |
| SCE1572_4422 | 11 | 5.67 |
| SCE1572_4204 | 22.11 | 391.53 |
| SCE1572_3538 | 16.24 | 7.82 |
| SCE1572_3470 | 30.13 | 12.48 |
| SCE1572_11519 | 57.45 | 28.17 |
| SCE1572_631 | 80.56 | 135.49 |
| SCE1572_10172 | 53.19 | 57.39 |
| SCE1572_11527 | 46 | 25.63 |
| SCE1572_11537 | 70.97 | 241.8 |
| SCE1572_8757 | 17.41 | 13.52 |
| SCE1572_5631 | 27.57 | 17.69 |
| SCE1572_7048 | 0 | 0 |
| SCE1572_4523 | 13.96 | 0 |
| SCE1572_66 | 32.89 | 54.06 |
| SCE1572_2703 | 218.37 | 122.55 |
| SCE1572_7743 | 134.12 | 643.08 |
| SCE1572_5819 | 31.98 | 15.21 |
| SCE1572_6375 | 53.1 | 10.15 |
| SCE1572_3893 | 14.55 | 5.53 |
| SCE1572_3210 | 11.46 | 30.82 |
| SCE1572_3138 | 78.42 | 1029.33 |
| SCE1572_330 | 37.41 | 33.46 |
| SCE1572_751 | 65.3 | 68.65 |
| SCE1572_10219 | 45.81 | 40.15 |
| SCE1572_8481 | 34.21 | 28.93 |
| SCE1572_356 | 56.22 | 12.3 |
| SCE1572_11229 | 12.63 | 13.03 |
| SCE1572_2643 | 73.81 | 35.32 |
| SCE1572_17 | 18 | 57.02 |
| SCE1572_6848 | 11.96 | 0.71 |
| SCE1572_3734 | 52.66 | 6.81 |
| SCE1572_5066 | 193.01 | 354.85 |
| SCE1572_7398 | 40.64 | 187.14 |
| SCE1572_3141 | 36.5 | 13.77 |
| SCE1572_2822 | 22.64 | 20.27 |
| SCE1572_5919 | 36.94 | 83.74 |
| SCE1572_2089 | 18.25 | 9.76 |
| SCE1572_8441 | 52.33 | 108.72 |
| SCE1572_8661 | 14.27 | 6.25 |
| SCE1572_673 | 135.25 | 1081.64 |
| SCE1572_9051 | 72.78 | 29.19 |
| SCE1572_3495 | 61.33 | 36.9 |

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| SCE1572_3981 | 25.58 | 23.73 |
| SCE1572_2495 | 112.86 | 50.73 |
| SCE1572_10667 | 13.54 | 7.24 |
| SCE1572_6666 | 39.91 | 189.36 |
| SCE1572_9541 | 14.36 | 5.9 |
| SCE1572_1888 | 66.89 | 762.04 |
| SCE1572_3287 | 35.67 | 0 |
| SCE1572_10134 | 26.57 | 11.29 |
| SCE1572_5162 | 0 | 0 |
| SCE1572_779 | 34.56 | 37.69 |
| SCE1572_2293 | 32.34 | 41.84 |
| SCE1572_4525 | 27.66 | 12.8 |
| SCE1572_5768 | 131.18 | 917.47 |
| SCE1572_2007 | 19.7 | 27.67 |
| SCE1572_9808 | 405.36 | 1193.6 |
| SCE1572_5244 | 20.97 | 43.86 |
| SCE1572_1387 | 54.64 | 31.42 |
| SCE1572_5656 | 20.86 | 6.03 |
| SCE1572_5038 | 243.09 | 2406.68 |
| SCE1572_10939 | 186.45 | 244.1 |
| SCE1572_9417 | 194.11 | 2963.59 |
| SCE1572_6053 | 111.96 | 565.63 |
| SCE1572_3807 | 47.07 | 70.73 |
| SCE1572_2759 | 34.67 | 181.75 |
| SCE1572_2980 | 117.04 | 1702.97 |
| SCE1572_3682 | 63.17 | 3.04 |
| SCE1572_7089 | 30.66 | 27.29 |
| SCE1572_4662 | 14.41 | 3.79 |
| SCE1572_10402 | 41.14 | 85.64 |
| SCE1572_8138 | 34.85 | 15.25 |
| SCE1572_4736 | 77.58 | 629.54 |
| SCE1572_5610 | 30.06 | 1.61 |
| SCE1572_7507 | 32.52 | 10.93 |
| SCE1572_9121 | 28.12 | 7.96 |
| SCE1572_2340 | 0 | 0 |
| SCE1572_11093 | 41.3 | 24.25 |
| SCE1572_5217 | 82.82 | 27.47 |
| SCE1572_170 | 20.89 | 7.45 |
| SCE1572_10739 | 28.83 | 12.85 |
| SCE1572_7945 | 11.4 | 0 |
| SCE1572_11097 | 26.96 | 24.43 |
| SCE1572_9148 | 58.49 | 310.23 |
| SCE1572_231 | 1.68 | 0 |
| SCE1572_8875 | 20.66 | 0 |
| SCE1572_8333 | 242.27 | 402.54 |
| SCE1572_4558 | 26.44 | 68.18 |
| SCE1572_176 | 21.37 | 4.9 |
| SCE1572_765 | 17.63 | 101.84 |

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| SCE1572_2670 | 38.83 | 10.07 |
| SCE1572_10384 | 13.46 | 1.71 |
| SCE1572_1938 | 12.09 | 15.87 |
| SCE1572_6061 | 676.97 | 1874.17 |
| SCE1572_10704 | 34.93 | 145.2 |
| SCE1572_8298 | 161.28 | 101.02 |
| SCE1572_9182 | 24.92 | 12.76 |
| SCE1572_719 | 37.79 | 42.79 |
| SCE1572_3112 | 5.17 | 0 |
| SCE1572_2876 | 32.19 | 44.15 |
| SCE1572_4306 | 15.62 | 9.4 |
| SCE1572_10103 | 23.33 | 50.88 |
| SCE1572_3097 | 26.02 | 8.64 |
| SCE1572_1868 | 21.04 | 102.45 |
| SCE1572_9980 | 16.7 | 41.8 |
| SCE1572_1516 | 84.59 | 239.31 |
| SCE1572_11070 | 31.59 | 76.03 |
| SCE1572_5848 | 36.83 | 23.16 |
| SCE1572_9875 | 42.81 | 90.16 |
| SCE1572_1648 | 28.7 | 9.28 |
| SCE1572_10648 | 37.42 | 93.54 |
| SCE1572_3944 | 149.72 | 387.73 |
| SCE1572_2989 | 100.11 | 60.94 |
| SCE1572_4338 | 22.43 | 7.6 |
| SCE1572_6773 | 26.23 | 24.09 |
| SCE1572_9107 | 15.78 | 48.52 |
| SCE1572_904 | 29.8 | 30.2 |
| SCE1572_9832 | 13.55 | 3.11 |
| SCE1572_9412 | 34.49 | 121.06 |
| SCE1572_8096 | 6.67 | 4.59 |
| SCE1572_7757 | 14.84 | 8.93 |
| SCE1572_2409 | 93.86 | 747.22 |
| SCE1572_3952 | 18.51 | 12.04 |
| SCE1572_9548 | 20.91 | 0 |
| SCE1572_7755 | 39.05 | 49.76 |
| SCE1572_7468 | 29.57 | 32.76 |
| SCE1572_5758 | 14.64 | 22.81 |
| SCE1572_3228 | 62.43 | 126.65 |
| SCE1572_7118 | 133.61 | 67.11 |
| SCE1572_2138 | 25.7 | 0 |
| SCE1572_9739 | 0 | 0 |
| SCE1572_3118 | 0 | 0 |
| SCE1572_2942 | 39.99 | 38.1 |
| SCE1572_4263 | 41.38 | 21.59 |
| SCE1572_7288 | 63.86 | 116.93 |
| SCE1572_7631 | 67.77 | 724.32 |
| SCE1572_4066 | 43.75 | 117.01 |
| SCE1572_6068 | 16.22 | 1.59 |

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| SCE1572_8889 | 27.71 | 22.23 |
| SCE1572_7022 | 84.06 | 26.1 |
| SCE1572_290 | 0 | 0 |
| SCE1572_5195 | 60.38 | 46.68 |
| SCE1572_6763 | 57.48 | 84.05 |
| SCE1572_6647 | 31.92 | 4.8 |
| SCE1572_1633 | 27.51 | 65.46 |
| SCE1572_8167 | 0 | 0 |
| SCE1572_1826 | 35.83 | 11.25 |
| SCE1572_7986 | 61.37 | 36.2 |
| SCE1572_1775 | 34.66 | 0 |
| SCE1572_2903 | 0 | 0 |
| SCE1572_5797 | 16.99 | 4.54 |
| SCE1572_9637 | 92.03 | 1287.21 |
| SCE1572_8057 | 0 | 0 |
| SCE1572_7102 | 58.82 | 69.21 |
| SCE1572_4330 | 70.66 | 38.97 |
| SCE1572_7633 | 439.08 | 712.33 |
| SCE1572_6112 | 54.86 | 37.21 |
| SCE1572_2126 | 63.34 | 24.01 |
| SCE1572_9690 | 129.96 | 281.06 |
| SCE1572_808 | 29.21 | 10.86 |
| SCE1572_7517 | 62.48 | 119.64 |
| SCE1572_3111 | 24.74 | 8.87 |
| SCE1572_1127 | 28.71 | 12.96 |
| SCE1572_2716 | 38.84 | 52.22 |
| SCE1572_4858 | 42.82 | 25.34 |
| SCE1572_9073 | 56.7 | 38.66 |
| SCE1572_9623 | 28.45 | 14.61 |
| SCE1572_2673 | 31.88 | 167.63 |
| SCE1572_1511 | 89.93 | 670.81 |
| SCE1572_3416 | 25.92 | 20.8 |
| SCE1572_9974 | 45.88 | 36.81 |
| SCE1572_9957 | 18.13 | 3.97 |
| SCE1572_7728 | 0 | 0 |
| SCE1572_1207 | 17.45 | 11.13 |
| SCE1572_2249 | 34.82 | 25.61 |
| SCE1572_6632 | 45.3 | 182.91 |
| SCE1572_2528 | 1.64 | 1.97 |
| SCE1572_9765 | 26.01 | 31.31 |
| SCE1572_9042 | 43.2 | 186.39 |
| SCE1572_9091 | 28.51 | 9.36 |
| SCE1572_8160 | 13.83 | 4.44 |
| SCE1572_9750 | 16.55 | 23.9 |
| SCE1572_11001 | 17.63 | 4.24 |
| SCE1572_4444 | 33.45 | 85.4 |
| SCE1572_10104 | 38.81 | 105.1 |
| SCE1572_2992 | 57.76 | 52.13 |

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| SCE1572_1617 | 11.45 | 10.86 |
| SCE1572_9755 | 22.02 | 10.19 |
| SCE1572_9524 | 30.67 | 34.82 |
| SCE1572_11464 | 179.9 | 60.91 |
| SCE1572_3879 | 24.56 | 68.21 |
| SCE1572_984 | 42.36 | 106.26 |
| SCE1572_6119 | 201.39 | 147.44 |
| SCE1572_9598 | 107.5 | 1940.22 |
| SCE1572_1235 | 76.02 | 23.38 |
| SCE1572_3324 | 40.5 | 155.86 |
| SCE1572_4753 | 89.91 | 258.84 |
| SCE1572_1287 | 33.54 | 452.37 |
| SCE1572_7531 | 33.9 | 172.08 |
| SCE1572_9811 | 0 | 0 |
| SCE1572_776 | 9.63 | 0 |
| SCE1572_11588 | 15.62 | 15.72 |
| SCE1572_7042 | 25.94 | 11.1 |
| SCE1572_7371 | 21.56 | 8.37 |
| SCE1572_3353 | 0 | 0 |
| SCE1572_11476 | 10.55 | 41.25 |
| SCE1572_7684 | 0 | 0 |
| SCE1572_9445 | 30.81 | 20 |
| SCE1572_11354 | 10.33 | 6.54 |
| SCE1572_3620 | 18.41 | 5.21 |
| SCE1572_4123 | 89.31 | 29.99 |
| SCE1572_2798 | 49.17 | 11.84 |
| SCE1572_8731 | 19.13 | 6.82 |
| SCE1572_9814 | 40.91 | 217.22 |
| SCE1572_6403 | 82.58 | 61.91 |
| SCE1572_866 | 43.32 | 26.07 |
| SCE1572_3005 | 6.89 | 0 |
| SCE1572_4052 | 44.74 | 305.1 |
| SCE1572_10295 | 31.46 | 148.28 |
| SCE1572_4390 | 52.57 | 26.59 |
| SCE1572_10568 | 82.63 | 205.02 |
| SCE1572_4196 | 41.8 | 54.3 |
| SCE1572_696 | 8.31 | 0 |
| SCE1572_1240 | 61.32 | 18.11 |
| SCE1572_3606 | 24.09 | 3.41 |
| SCE1572_7029 | 39.37 | 25.18 |
| SCE1572_1603 | 0 | 0 |
| SCE1572_8336 | 86.21 | 40.16 |
| SCE1572_6342 | 26.66 | 43.31 |
| SCE1572_8880 | 29.06 | 9.12 |
| SCE1572_10839 | 3.94 | 0 |
| SCE1572_5676 | 11.45 | 4.75 |
| SCE1572_1292 | 26.21 | 12.76 |
| SCE1572_4833 | 88.22 | 942.18 |

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| SCE1572_560 | 215.71 | 3594.96 |
| SCE1572_5050 | 12.9 | 0 |
| SCE1572_5619 | 18.46 | 28.28 |
| SCE1572_2779 | 85.91 | 302.53 |
| SCE1572_5375 | 27.98 | 16.29 |
| SCE1572_4868 | 19.14 | 12.65 |
| SCE1572_2418 | 20.3 | 67.78 |
| SCE1572_8025 | 0 | 0 |
| SCE1572_1534 | 28 | 14.51 |
| SCE1572_4313 | 0 | 0 |
| SCE1572_1010 | 45.94 | 20.73 |
| SCE1572_8961 | 10.39 | 5.89 |
| SCE1572_7238 | 42.77 | 179.18 |
| SCE1572_5057 | 113.5 | 484.5 |
| SCE1572_2186 | 2.41 | 0 |
| SCE1572_1788 | 4.59 | 3.69 |
| SCE1572_8356 | 15.31 | 5.26 |
| SCE1572_3081 | 9.53 | 45.85 |
| SCE1572_6181 | 51.69 | 59.71 |
| SCE1572_2847 | 45.97 | 49.54 |
| SCE1572_2946 | 23.38 | 11.58 |
| SCE1572_3200 | 101.27 | 488.86 |
| SCE1572_2435 | 24.23 | 45.62 |
| SCE1572_3996 | 3.35 | 2.02 |
| SCE1572_6607 | 0 | 0 |
| SCE1572_5932 | 18.29 | 18.79 |
| SCE1572_204 | 56.86 | 34.21 |
| SCE1572_5616 | 0 | 0 |
| SCE1572_800 | 0 | 0 |
| SCE1572_3469 | 33.57 | 12.57 |
| SCE1572_320 | 38.03 | 12.2 |
| SCE1572_3049 | 7.44 | 2.11 |
| SCE1572_1700 | 90.69 | 145.53 |
| SCE1572_1268 | 76.31 | 71.52 |
| SCE1572_8794 | 25.03 | 11.37 |
| SCE1572_109 | 37.28 | 41.88 |
| SCE1572_5641 | 7.31 | 0 |
| SCE1572_301 | 16.39 | 15.78 |
| SCE1572_1640 | 26.33 | 15.37 |
| SCE1572_4316 | 56.13 | 14.83 |
| SCE1572_7962 | 62.78 | 617.87 |
| SCE1572_2837 | 70.48 | 61.81 |
| SCE1572_11316 | 357.31 | 715.02 |
| SCE1572_6217 | 7.31 | 13.19 |
| SCE1572_4576 | 2.38 | 0 |
| SCE1572_8231 | 44.57 | 32.49 |
| SCE1572_10198 | 54.88 | 21.79 |
| SCE1572_5695 | 49.33 | 13.97 |

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| SCE1572_7425 | 7.87 | 130.82 |
| SCE1572_10922 | 300.57 | 32336.89 |
| SCE1572_2715 | 45.39 | 104.13 |
| SCE1572_2110 | 37.06 | 386.93 |
| SCE1572_922 | 10.23 | 15.67 |
| SCE1572_9483 | 89.1 | 230.67 |
| SCE1572_10561 | 0 | 0 |
| SCE1572_2741 | 25.27 | 13.03 |
| SCE1572_11131 | 18.27 | 7.69 |
| SCE1572_11200 | 41.9 | 151.29 |
| SCE1572_7858 | 55.9 | 63.28 |
| SCE1572_6554 | 19.88 | 0 |
| SCE1572_9202 | 17.76 | 22.19 |
| SCE1572_7265 | 14.63 | 12.14 |
| SCE1572_6975 | 34.71 | 13.19 |
| SCE1572_2840 | 40.17 | 29.28 |
| SCE1572_6122 | 60.75 | 172.52 |
| SCE1572_6045 | 256.73 | 1042.1 |
| SCE1572_2680 | 33.69 | 9.54 |
| SCE1572_3792 | 4.89 | 0 |
| SCE1572_6580 | 18.8 | 3.02 |
| SCE1572_326 | 33.55 | 35.78 |
| SCE1572_8570 | 5.05 | 0 |
| SCE1572_5126 | 25.14 | 43.49 |
| SCE1572_3898 | 30.69 | 94.35 |
| SCE1572_5950 | 73.19 | 17.62 |
| SCE1572_5986 | 9.83 | 0 |
| SCE1572_3180 | 27.59 | 60.61 |
| SCE1572_4539 | 26.62 | 25.29 |
| SCE1572_978 | 37.35 | 54.21 |
| SCE1572_7934 | 49.47 | 3.84 |
| SCE1572_8050 | 48.32 | 9.36 |
| SCE1572_10887 | 46.34 | 68.85 |
| SCE1572_11237 | 21.39 | 6.43 |
| SCE1572_9395 | 27.76 | 25.7 |
| SCE1572_3889 | 12.15 | 6.36 |
| SCE1572_1553 | 21.42 | 13.22 |
| SCE1572_3825 | 24.72 | 11.9 |
| SCE1572_3713 | 134.71 | 237.77 |
| SCE1572_8773 | 72.27 | 78.47 |
| SCE1572_8048 | 33.44 | 10.94 |
| SCE1572_1054 | 62.08 | 76.86 |
| SCE1572_10359 | 28.36 | 28.88 |
| SCE1572_3788 | 53.3 | 98.36 |
| SCE1572_9986 | 14.83 | 10.71 |
| SCE1572_3311 | 24.68 | 10.61 |
| SCE1572_9663 | 32.12 | 213.72 |
| SCE1572_3781 | 77.09 | 675.42 |

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| SCE1572_7304 | 59.81 | 15.62 |
| SCE1572_3678 | 19.87 | 47.82 |
| SCE1572_3056 | 7.8 | 2.61 |
| SCE1572_2220 | 32.96 | 92.93 |
| SCE1572_9784 | 29.4 | 4.42 |
| SCE1572_10521 | 23.02 | 23.35 |
| SCE1572_9355 | 95.7 | 292.46 |
| SCE1572_10220 | 39.27 | 47.63 |
| SCE1572_3594 | 12.72 | 2.45 |
| SCE1572_1437 | 39.02 | 16.1 |
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| SCE1572_1997 | 17.08 | 5.14 |
| SCE1572_5261 | 68.69 | 786.3 |
| SCE1572_155 | 52.06 | 102.24 |
| SCE1572_5242 | 33.1 | 7.71 |
| SCE1572_5762 | 10.7 | 4.48 |
| SCE1572_7393 | 22.99 | 2.13 |
| SCE1572_2036 | 225.44 | 2511.52 |
| SCE1572_10370 | 26.03 | 9.31 |
| SCE1572_11088 | 35.82 | 52.13 |
| SCE1572_5116 | 29.45 | 32.54 |
| SCE1572_6130 | 17.46 | 115.01 |
| SCE1572_9021 | 7.35 | 7.74 |
| SCE1572_2042 | 63.05 | 248.1 |
| SCE1572_4303 | 60.65 | 10.68 |
| SCE1572_11249 | 15.65 | 69.45 |
| SCE1572_3273 | 26.39 | 137.64 |
| SCE1572_3063 | 49.29 | 95.74 |
| SCE1572_6938 | 34.58 | 10.24 |
| SCE1572_11267 | 403.05 | 2452.46 |
| SCE1572_1953 | 46.93 | 65.16 |
| SCE1572_1329 | 37.63 | 122.53 |
| SCE1572_6538 | 43.57 | 25.17 |
| SCE1572_5927 | 124.86 | 36.06 |
| SCE1572_6152 | 59.22 | 53.58 |
| SCE1572_4996 | 8.92 | 10.73 |
| SCE1572_9677 | 29.67 | 14.51 |
| SCE1572_4614 | 61.88 | 25.53 |
| SCE1572_11339 | 19.18 | 12.98 |
| SCE1572_3394 | 92.11 | 162.84 |
| SCE1572_4393 | 16.05 | 9.04 |
| SCE1572_2239 | 61.86 | 54.01 |
| SCE1572_10182 | 30.32 | 86.02 |
| SCE1572_9643 | 62.2 | 82.66 |
| SCE1572_1599 | 0 | 0 |
| SCE1572_4910 | 3.09 | 0 |
| SCE1572_8745 | 6.23 | 0 |

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| SCE1572_508 | 31.27 | 6.39 |
| SCE1572_6279 | 47.7 | 1976.32 |
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| SCE1572_9910 | 27.99 | 17.97 |
| SCE1572_1954 | 22.01 | 25.51 |
| SCE1572_9298 | 86.45 | 177.03 |
| SCE1572_3930 | 230.69 | 957.38 |
| SCE1572_6035 | 22.91 | 36.37 |
| SCE1572_3726 | 80.14 | 1866.32 |
| SCE1572_3865 | 28.88 | 10.43 |
| SCE1572_5781 | 73.77 | 256.85 |
| SCE1572_8522 | 88.38 | 170.78 |
| SCE1572_299 | 44.62 | 30.82 |
| SCE1572_9760 | 25.94 | 56.69 |
| SCE1572_10028 | 12.98 | 2.23 |
| SCE1572_11375 | 0 | 0 |
| SCE1572_7991 | 51.39 | 203.28 |
| SCE1572_7335 | 34 | 108.37 |
| SCE1572_8971 | 73.09 | 203.98 |
| SCE1572_4479 | 10.78 | 19.25 |
| SCE1572_4887 | 57.76 | 20.85 |
| SCE1572_8579 | 0 | 0 |
| SCE1572_6746 | 40.17 | 65.5 |
| SCE1572_4639 | 18.73 | 2.91 |
| SCE1572_5608 | 53.9 | 22 |
| SCE1572_9023 | 548.85 | 1260.84 |
| SCE1572_2229 | 33.6 | 680.08 |
| SCE1572_11481 | 31.57 | 14.98 |
| SCE1572_4245 | 26.27 | 92.06 |
| SCE1572_1475 | 0 | 0 |
| SCE1572_1925 | 0 | 0 |
| SCE1572_1500 | 24.39 | 21.87 |
| SCE1572_4597 | 0 | 0 |
| SCE1572_3556 | 12.85 | 0 |
| SCE1572_4880 | 122.83 | 320.58 |
| SCE1572_3571 | 24.36 | 22.37 |
| SCE1572_6843 | 22.66 | 20.78 |
| SCE1572_1781 | 11.16 | 12.2 |
| SCE1572_8287 | 36.29 | 112.58 |
| SCE1572_593 | 51.37 | 92.39 |
| SCE1572_399 | 28.64 | 16.22 |
| SCE1572_6254 | 35.19 | 42.35 |
| SCE1572_318 | 25.04 | 3.35 |
| SCE1572_11596 | 48.58 | 528.23 |
| SCE1572_9725 | 5.27 | 17.45 |
| SCE1572_2274 | 43.18 | 9.24 |
| SCE1572_1520 | 45.48 | 16.42 |

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| SCE1572_4355 | 28.93 | 28.81 |
| SCE1572_3167 | 23.49 | 34.27 |
| SCE1572_3872 | 63.44 | 157.49 |
| SCE1572_6333 | 20.25 | 72.55 |
| SCE1572_4366 | 36.27 | 32.3 |
| SCE1572_6243 | 26.86 | 7.36 |
| SCE1572_2064 | 32.93 | 29.49 |
| SCE1572_8264 | 44.74 | 144.77 |
| SCE1572_5424 | 28.13 | 28.9 |
| SCE1572_678 | 31.59 | 45.62 |
| SCE1572_338 | 36.86 | 23.8 |
| SCE1572_9602 | 40.18 | 12.96 |
| SCE1572_9187 | 27.09 | 47.65 |
| SCE1572_7178 | 74.51 | 48.48 |
| SCE1572_2320 | 55.47 | 748.92 |
| SCE1572_1969 | 41.12 | 26.8 |
| SCE1572_9098 | 37.9 | 12 |
| SCE1572_7006 | 0 | 0 |
| SCE1572_5501 | 18.37 | 14.34 |
| SCE1572_1317 | 34.58 | 63.93 |
| SCE1572_5061 | 57.89 | 265.4 |
| SCE1572_7016 | 0 | 0 |
| SCE1572_1610 | 78.97 | 60.94 |
| SCE1572_4879 | 60.04 | 105.86 |
| SCE1572_2661 | 45.48 | 60.82 |
| SCE1572_6305 | 24.65 | 13.35 |
| SCE1572_5669 | 24.24 | 8.01 |
| SCE1572_8989 | 97.78 | 241.3 |
| SCE1572_5992 | 39.17 | 62.85 |
| SCE1572_6142 | 23.35 | 16.93 |
| SCE1572_3298 | 12.58 | 10.09 |
| SCE1572_5549 | 31.94 | 13.13 |
| SCE1572_3189 | 9.58 | 0 |
| SCE1572_10965 | 50.31 | 26.82 |
| SCE1572_11106 | 41.71 | 53.14 |
| SCE1572_6132 | 0 | 0 |
| SCE1572_8531 | 24.52 | 30.86 |
| SCE1572_143 | 12.63 | 30.41 |
| SCE1572_349 | 21.54 | 74.78 |
| SCE1572_5839 | 39.13 | 14.66 |
| SCE1572_9685 | 57.4 | 123.4 |
| SCE1572_3508 | 26.46 | 17.14 |
| SCE1572_238 | 30.32 | 4.87 |
| SCE1572_1065 | 71.79 | 18.13 |
| SCE1572_5296 | 40.13 | 17.89 |
| SCE1572_10153 | 20.18 | 95.74 |
| SCE1572_8978 | 30.08 | 28 |
| SCE1572_9593 | 46.86 | 843.54 |

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| SCE1572_8866 | 48.37 | 28.13 |
| SCE1572_2728 | 14.53 | 11.65 |
| SCE1572_2284 | 10.42 | 9.12 |
| SCE1572_2149 | 43.15 | 70.68 |
| SCE1572_1845 | 6.74 | 4.05 |
| SCE1572_6476 | 79.32 | 902.17 |
| SCE1572_5329 | 67.56 | 19.48 |
| SCE1572_7242 | 52.66 | 68.49 |
| SCE1572_10930 | 50.54 | 40.21 |
| SCE1572_6251 | 42.72 | 18.94 |
| SCE1572_5940 | 25.16 | 10.5 |
| SCE1572_4516 | 18.59 | 14.13 |
| SCE1572_6160 | 16.11 | 17.63 |
| SCE1572_7574 | 57.33 | 316.81 |
| SCE1572_11391 | 54.44 | 36.74 |
| SCE1572_7466 | 77.74 | 439.3 |
| SCE1572_6236 | 47.74 | 17.68 |
| SCE1572_8695 | 14.74 | 21.6 |
| SCE1572_4494 | 34.43 | 24.72 |
| SCE1572_266 | 40.96 | 13.84 |
| SCE1572_9393 | 20.52 | 12.35 |
| SCE1572_7545 | 63.54 | 48.3 |
| SCE1572_3173 | 38.13 | 22.12 |
| SCE1572_8687 | 24.3 | 13.1 |
| SCE1572_1101 | 30.72 | 11.25 |
| SCE1572_11137 | 44.41 | 311.47 |
| SCE1572_8598 | 0 | 0 |
| SCE1572_11017 | 66.39 | 178.88 |
| SCE1572_9996 | 28.84 | 21.99 |
| SCE1572_2695 | 20.06 | 110.06 |
| SCE1572_4769 | 22.74 | 100.35 |
| SCE1572_8897 | 43.73 | 85.75 |
| SCE1572_1747 | 68.34 | 56.61 |
| SCE1572_7829 | 26.25 | 104.45 |
| SCE1572_8313 | 14.85 | 10.43 |
| SCE1572_7360 | 30.83 | 56.42 |
| SCE1572_7482 | 0 | 0 |
| SCE1572_8101 | 60.47 | 547.91 |
| SCE1572_2319 | 36.97 | 246.29 |
| SCE1572_10031 | 68.71 | 62.87 |
| SCE1572_1003 | 60.23 | 26.99 |
| SCE1572_10125 | 0.87 | 0 |
| SCE1572_2422 | 23.46 | 13.03 |
| SCE1572_5785 | 46.03 | 128.16 |
| SCE1572_1601 | 5.41 | 0 |
| SCE1572_3718 | 0 | 0 |
| SCE1572_623 | 176.46 | 1527.49 |
| SCE1572_352 | 24.29 | 33.66 |

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| SCE1572_8217 | 68.46 | 21.97 |
| SCE1572_5546 | 37.47 | 12.39 |
| SCE1572_1031 | 52.93 | 289.35 |
| SCE1572_2394 | 12.49 | 12.19 |
| SCE1572_8148 | 40.72 | 21 |
| SCE1572_5001 | 115.82 | 587.93 |
| SCE1572_3783 | 15.55 | 9.36 |
| SCE1572_5413 | 3.33 | 0 |
| SCE1572_4787 | 240.94 | 1721.36 |
| SCE1572_6991 | 41.77 | 10.24 |
| SCE1572_10347 | 40.47 | 116.61 |
| SCE1572_9573 | 72.28 | 10.61 |
| SCE1572_10997 | 53.69 | 234.46 |
| SCE1572_7381 | 26.95 | 18.92 |
| SCE1572_285 | 83.47 | 22.12 |
| SCE1572_2339 | 25.36 | 147.87 |
| SCE1572_7412 | 29.99 | 105.72 |
| SCE1572_1175 | 25.87 | 145.28 |
| SCE1572_4658 | 40.28 | 82.14 |
| SCE1572_6483 | 36.78 | 12.96 |
| SCE1572_245 | 18.42 | 4.95 |
| SCE1572_3205 | 43.95 | 120.33 |
| SCE1572_11513 | 55.07 | 112.41 |
| SCE1572_7430 | 58.11 | 21.3 |
| SCE1572_8591 | 77.46 | 20.94 |
| SCE1572_5517 | 39.25 | 16.82 |
| SCE1572_4946 | 2.92 | 0 |
| SCE1572_9219 | 23.89 | 4.55 |
| SCE1572_6006 | 13.42 | 49.42 |
| SCE1572_2173 | 9.65 | 6.63 |
| SCE1572_226 | 28.61 | 13.77 |
| SCE1572_467 | 33.57 | 71.23 |
| SCE1572_342 | 141.65 | 853.2 |
| SCE1572_1608 | 17.96 | 12.04 |
| SCE1572_2464 | 66.81 | 18.33 |
| SCE1572_10585 | 186.47 | 71.31 |
| SCE1572_9824 | 16.42 | 5.61 |
| SCE1572_9440 | 22.08 | 28.13 |
| SCE1572_6875 | 239.22 | 97.31 |
| SCE1572_7977 | 0 | 0 |
| SCE1572_10775 | 43.67 | 20.94 |
| SCE1572_5478 | 31.43 | 26.54 |
| SCE1572_6858 | 40.41 | 23.15 |
| SCE1572_1307 | 696.27 | 10545.56 |
| SCE1572_3406 | 54.46 | 23.62 |
| SCE1572_2538 | 12.18 | 18.84 |
| SCE1572_3466 | 20.32 | 27.59 |
| SCE1572_9701 | 37.28 | 0 |

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| SCE1572_3213 | 39.16 | 63.44 |
| SCE1572_4623 | 31.64 | 193.95 |
| SCE1572_5422 | 11.23 | 0 |
| SCE1572_2515 | 16.13 | 23.29 |
| SCE1572_3650 | 18.15 | 11.27 |
| SCE1572_3690 | 2.89 | 0 |
| SCE1572_85 | 41.12 | 89.55 |
| SCE1572_6356 | 32.92 | 17.72 |
| SCE1572_836 | 30.73 | 32.11 |
| SCE1572_4824 | 41.4 | 82.11 |
| SCE1572_2313 | 21.72 | 36.11 |
| SCE1572_7899 | 42.65 | 65.77 |
| SCE1572_11494 | 13.12 | 4.28 |
| SCE1572_9954 | 46.39 | 28.53 |
| SCE1572_9671 | 43.41 | 358.68 |
| SCE1572_8104 | 34.29 | 24.98 |
| SCE1572_2590 | 18.61 | 21.14 |
| SCE1572_9267 | 16.62 | 0 |
| SCE1572_574 | 37.36 | 139.45 |
| SCE1572_872 | 32.77 | 30.18 |
| SCE1572_1021 | 57.35 | 16.81 |
| SCE1572_383 | 35.33 | 39.51 |
| SCE1572_2890 | 43.19 | 16.22 |
| SCE1572_4624 | 121.72 | 408.61 |
| SCE1572_1574 | 41.83 | 17.62 |
| SCE1572_11431 | 44.11 | 27.49 |
| SCE1572_7004 | 5.79 | 1.44 |
| SCE1572_10982 | 37.29 | 32.37 |
| SCE1572_842 | 10.19 | 6.13 |
| SCE1572_7659 | 25.97 | 16.42 |
| SCE1572_918 | 28.17 | 31.81 |
| SCE1572_7490 | 60.41 | 62.72 |
| SCE1572_3152 | 78.82 | 68.42 |
| SCE1572_6521 | 29.86 | 0 |
| SCE1572_8248 | 8.81 | 10.6 |
| SCE1572_9512 | 70.1 | 277.34 |
| SCE1572_7708 | 37.62 | 13.72 |
| SCE1572_4646 | 23.87 | 15.96 |
| SCE1572_9502 | 24.2 | 48.83 |
| SCE1572_2354 | 55.72 | 728.29 |
| SCE1572_3617 | 33.69 | 9.67 |
| SCE1572_1478 | 37.9 | 15.21 |
| SCE1572_2097 | 18.64 | 565.33 |
| SCE1572_4357 | 47.81 | 20.55 |
| SCE1572_7589 | 49.6 | 419.19 |
| SCE1572_4489 | 34.51 | 50.44 |
| SCE1572_10166 | 0 | 0 |
| SCE1572_3072 | 25.42 | 14.77 |

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| SCE1572_2211 | 75.05 | 123.27 |
| SCE1572_10312 | 85.46 | 60.82 |
| SCE1572_6915 | 29.98 | 11.61 |
| SCE1572_7627 | 25.1 | 23.17 |
| SCE1572_3870 | 99.08 | 76.83 |
| SCE1572_8542 | 82.26 | 533.8 |
| SCE1572_3488 | 16.75 | 11.98 |
| SCE1572_7889 | 35.31 | 1837.08 |
| SCE1572_10971 | 2.14 | 10.28 |
| SCE1572_9270 | 0 | 0 |
| SCE1572_2312 | 164.52 | 2703.92 |
| SCE1572_7524 | 15.42 | 58.76 |
| SCE1572_2187 | 25.86 | 14.01 |
| SCE1572_10331 | 58.7 | 27.05 |
| SCE1572_5779 | 20.75 | 16.32 |
| SCE1572_6696 | 21.97 | 7.74 |
| SCE1572_3696 | 117.92 | 229.77 |
| SCE1572_9905 | 0 | 0 |
| SCE1572_56 | 70.17 | 6.03 |
| SCE1572_7283 | 17.4 | 9.31 |
| SCE1572_5638 | 24.77 | 19.87 |
| SCE1572_11305 | 6.79 | 0 |
| SCE1572_10540 | 73.04 | 25.45 |
| SCE1572_3378 | 62.32 | 24.63 |
| SCE1572_3498 | 30.32 | 51.34 |
| SCE1572_10782 | 33.44 | 12.13 |
| SCE1572_2853 | 48.21 | 26.57 |
| SCE1572_1621 | 129.64 | 1012.79 |
| SCE1572_8001 | 151.82 | 53.52 |
| SCE1572_9015 | 0 | 0 |
| SCE1572_3790 | 15.8 | 5.34 |
| SCE1572_9939 | 31.25 | 9.6 |
| SCE1572_7081 | 19.27 | 80.02 |
| SCE1572_6933 | 12.25 | 44.23 |
| SCE1572_1675 | 33.57 | 78.1 |
| SCE1572_10338 | 54.19 | 270.06 |
| SCE1572_7988 | 30.1 | 5.37 |
| SCE1572_3349 | 32.49 | 22.81 |
| SCE1572_7622 | 74.7 | 160.08 |
| SCE1572_5172 | 42.88 | 75.56 |
| SCE1572_6964 | 36.37 | 35.01 |
| SCE1572_10417 | 1.8 | 0 |
| SCE1572_3417 | 56.52 | 328.11 |
| SCE1572_7071 | 22.97 | 24.33 |
| SCE1572_11328 | 119.25 | 196.81 |
| SCE1572_5976 | 39.98 | 24.64 |
| SCE1572_5826 | 21.96 | 16.78 |
| SCE1572_5571 | 6.45 | 2.96 |

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| SCE1572_9763 | 22.33 | 32.53 |
| SCE1572_2541 | 0 | 0 |
| SCE1572_4693 | 71.01 | 138.06 |
| SCE1572_5300 | 43.32 | 17.66 |
| SCE1572_6504 | 51.71 | 60.82 |
| SCE1572_5497 | 56.63 | 113.88 |
| SCE1572_9374 | 49.65 | 18.14 |
| SCE1572_9287 | 205.05 | 886.35 |
| SCE1572_4949 | 16.91 | 10.18 |
| SCE1572_10018 | 45.61 | 31.51 |
| SCE1572_4760 | 45.54 | 21.64 |
| SCE1572_1589 | 0 | 0 |
| SCE1572_4434 | 58.05 | 39 |
| SCE1572_5149 | 25.66 | 12.98 |
| SCE1572_8012 | 2.37 | 0 |
| SCE1572_8027 | 12.21 | 14.69 |
| SCE1572_8094 | 41.56 | 12.68 |
| SCE1572_4409 | 16.67 | 12.94 |
| SCE1572_6018 | 625.42 | 405.98 |
| SCE1572_1910 | 55.42 | 22.65 |
| SCE1572_1373 | 41.21 | 177.46 |
| SCE1572_3481 | 15.68 | 6.29 |
| SCE1572_11364 | 51.37 | 29.09 |
| SCE1572_5270 | 39.9 | 8023.49 |
| SCE1572_1244 | 0 | 0 |
| SCE1572_879 | 100.56 | 548.01 |
| SCE1572_3809 | 26.08 | 51.09 |
| SCE1572_950 | 7.12 | 25.12 |
| SCE1572_10243 | 23.63 | 0 |
| SCE1572_8761 | 21.66 | 30.95 |
| SCE1572_5033 | 122.14 | 2489.29 |
| SCE1572_5946 | 21.74 | 11.16 |
| SCE1572_667 | 6.68 | 7.78 |
| SCE1572_2180 | 48.06 | 20.42 |
| SCE1572_6751 | 83.19 | 84.7 |
| SCE1572_3767 | 13.32 | 48.1 |
| SCE1572_8201 | 111.84 | 35.38 |
| SCE1572_74 | 28.98 | 55.14 |
| SCE1572_1522 | 32.28 | 30.61 |
| SCE1572_6794 | 17.03 | 26.44 |
| SCE1572_8565 | 26.13 | 53.03 |
| SCE1572_6983 | 26.54 | 13.17 |
| SCE1572_4299 | 68.07 | 28.31 |
| SCE1572_2936 | 36.98 | 13.35 |
| SCE1572_9927 | 64.6 | 140.7 |
| SCE1572_7835 | 39.73 | 183.44 |
| SCE1572_9530 | 35.79 | 35.5 |
| SCE1572_2052 | 0 | 0 |

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| SCE1572_2437 | 6.76 | 9.03 |
| SCE1572_6831 | 60.21 | 97.61 |
| SCE1572_7181 | 31.43 | 27.6 |
| SCE1572_2581 | 26.76 | 55.81 |
| SCE1572_5685 | 47.8 | 238.15 |
| SCE1572_7291 | 9.72 | 0 |
| SCE1572_9631 | 69.24 | 42.19 |
| SCE1572_3124 | 18.52 | 5.57 |
| SCE1572_11050 | 40.29 | 71.98 |
| SCE1572_10617 | 118.59 | 43.36 |
| SCE1572_6440 | 40.49 | 14.51 |
| SCE1572_6419 | 39.5 | 41.91 |
| SCE1572_2874 | 29.77 | 16.86 |
| SCE1572_8674 | 20.57 | 86.19 |
| SCE1572_11543 | 84.79 | 36.19 |
| SCE1572_124 | 50.14 | 5.75 |
| SCE1572_463 | 53.29 | 1958.15 |
| SCE1572_2269 | 76.86 | 649.12 |
| SCE1572_2014 | 39.38 | 7.97 |
| SCE1572_11362 | 26.49 | 6.94 |
| SCE1572_8089 | 18.34 | 8.61 |
| SCE1572_10875 | 61.27 | 32.49 |
| SCE1572_2905 | 25.5 | 239.93 |
| SCE1572_1343 | 13.86 | 9.81 |
| SCE1572_1942 | 0 | 0 |
| SCE1572_3306 | 20.91 | 296.13 |
| SCE1572_1228 | 18.55 | 32.79 |
| SCE1572_1940 | 96.51 | 25.11 |
| SCE1572_1682 | 247.37 | 2473.79 |
| SCE1572_698 | 22.46 | 105.42 |
| SCE1572_3802 | 41.57 | 35.32 |
| SCE1572_9575 | 1.08 | 0 |
| SCE1572_6582 | 15.29 | 46 |
| SCE1572_1327 | 0 | 0 |
| SCE1572_11011 | 0 | 0 |
| SCE1572_4689 | 61.2 | 336.7 |
| SCE1572_1876 | 66.12 | 95.49 |
| SCE1572_4210 | 5.51 | 0 |
| SCE1572_5576 | 49.31 | 20.77 |
| SCE1572_2071 | 6.93 | 7.41 |
| SCE1572_8403 | 66.91 | 47.28 |
| SCE1572_4074 | 125.89 | 997.37 |
| SCE1572_8413 | 23.37 | 7.21 |
| SCE1572_971 | 54.6 | 42.11 |
| SCE1572_4779 | 0 | 0 |
| SCE1572_5177 | 47.74 | 26.32 |
| SCE1572_11035 | 17.64 | 185.61 |
| SCE1572_2898 | 20.37 | 5.45 |

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| SCE1572_6077 | 3.89 | 18.71 |
| SCE1572_6599 | 33.05 | 59.66 |
| SCE1572_8208 | 60.21 | 47.6 |
| SCE1572_10807 | 43.41 | 34.31 |
| SCE1572_9801 | 61.25 | 24.17 |
| SCE1572_10016 | 9.43 | 90.76 |
| SCE1572_8705 | 0 | 0 |
| SCE1572_6104 | 39.82 | 9.22 |
| SCE1572_149 | 38.81 | 122.74 |
| SCE1572_4348 | 43.85 | 12.72 |
| SCE1572_4459 | 45.54 | 18.71 |
| SCE1572_6653 | 23.94 | 0 |
| SCE1572_22 | 39.34 | 76.22 |
| SCE1572_3838 | 0 | 0 |
| SCE1572_859 | 265.77 | 7725.62 |
| SCE1572_4472 | 18.28 | 3.88 |
| SCE1572_883 | 0 | 0 |
| SCE1572_8703 | 21.66 | 52.13 |
| SCE1572_852 | 84.98 | 309.89 |
| SCE1572_10841 | 22.64 | 5.84 |
| SCE1572_4651 | 46.16 | 63.2 |
| SCE1572_10180 | 38.03 | 122.47 |
| SCE1572_6267 | 21.66 | 22.34 |
| SCE1572_9253 | 12.26 | 3.97 |
| SCE1572_10558 | 49.02 | 19.21 |
| SCE1572_9033 | 20.72 | 12.16 |
| SCE1572_6099 | 39.66 | 57.79 |
| SCE1572_270 | 35.84 | 28.2 |
| SCE1572_4144 | 51.53 | 234.93 |
| SCE1572_10722 | 115.71 | 38.41 |
| SCE1572_4387 | 23.38 | 23.87 |
| SCE1572_7440 | 22.03 | 15.59 |
| SCE1572_4606 | 21.06 | 162.19 |
| SCE1572_7298 | 60.1 | 13.95 |
| SCE1572_2146 | 39.72 | 11.23 |
| SCE1572_5409 | 2.23 | 0 |
| SCE1572_10003 | 10.83 | 10.43 |
| SCE1572_11163 | 31 | 211.03 |
| SCE1572_8801 | 0 | 0 |
| SCE1572_5724 | 0 | 0 |
| SCE1572_8768 | 21.09 | 15.87 |
| SCE1572_8717 | 18.38 | 5.53 |
| SCE1572_5373 | 30.61 | 478 |
| SCE1572_7416 | 79.38 | 415.37 |
| SCE1572_6597 | 96.06 | 61.28 |
| SCE1572_9793 | 24.46 | 18.59 |
| SCE1572_8644 | 29.45 | 21.41 |
| SCE1572_3691 | 118.05 | 24.59 |

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| SCE1572_7388 | 20.01 | 12.97 |
| SCE1572_5004 | 20.49 | 66.57 |
| SCE1572_5238 | 74.3 | 79.24 |
| SCE1572_7254 | 10.87 | 0.67 |
| SCE1572_3476 | 42.1 | 115.24 |
| SCE1572_4108 | 64.72 | 32.99 |
| SCE1572_10084 | 43.9 | 99.52 |
| SCE1572_10610 | 16.62 | 5 |
| SCE1572_2612 | 16.63 | 10.3 |
| SCE1572_4900 | 28.55 | 9.56 |
| SCE1572_6579 | 32.54 | 24.99 |
| SCE1572_8909 | 30.94 | 14.89 |
| SCE1572_4133 | 7.24 | 5.45 |
| SCE1572_8468 | 25.43 | 55.38 |
| SCE1572_11178 | 0 | 0 |
| SCE1572_8008 | 92.65 | 1943.36 |
| SCE1572_11440 | 44.22 | 30.41 |
| SCE1572_10681 | 24.26 | 26.27 |
| SCE1572_10109 | 40.37 | 125.59 |
| SCE1572_4743 | 30.93 | 32.11 |
| SCE1572_659 | 68.23 | 0 |
| SCE1572_11288 | 45.6 | 374.65 |
| SCE1572_8408 | 38.9 | 35.11 |
| SCE1572_11317 | 110.01 | 143.42 |
| SCE1572_10412 | 10.51 | 7.23 |
| SCE1572_9435 | 175.54 | 856.5 |
| SCE1572_458 | 31.4 | 17.51 |
| SCE1572_8424 | 58.1 | 85.26 |
| SCE1572_1975 | 37.18 | 136.26 |
| SCE1572_3518 | 12 | 3.94 |
| SCE1572_1964 | 23.82 | 6.99 |
| SCE1572_402 | 47.75 | 14.11 |
| SCE1572_505 | 7.89 | 2.71 |
| SCE1572_1064 | 45.48 | 17.58 |
| SCE1572_5014 | 62.31 | 367.28 |
| SCE1572_2931 | 0 | 0 |
| SCE1572_6421 | 27.28 | 4.31 |
| SCE1572_11152 | 21.66 | 14.48 |
| SCE1572_7357 | 15.39 | 19.09 |
| SCE1572_7060 | 71.19 | 25.39 |
| SCE1572_4051 | 158.14 | 829.9 |
| SCE1572_6721 | 79.05 | 377.4 |
| SCE1572_5139 | 40.27 | 19.96 |
| SCE1572_9366 | 9.15 | 1.38 |
| SCE1572_8998 | 99.25 | 597.7 |
| SCE1572_3050 | 21.34 | 2.7 |
| SCE1572_9162 | 177.1 | 6.13 |
| SCE1572_4088 | 47.18 | 56.59 |

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| SCE1572_3638 | 59.73 | 24.88 |
| SCE1572_112 | 10.11 | 0 |
| SCE1572_944 | 82.87 | 26.54 |
| SCE1572_8781 | 42.68 | 903.01 |
| SCE1572_8255 | 56.86 | 80.17 |
| SCE1572_10114 | 21.13 | 2.76 |
| SCE1572_378 | 36.5 | 36.04 |
| SCE1572_6474 | 30.52 | 92.42 |
| SCE1572_1151 | 13.78 | 47.39 |
| SCE1572_3373 | 45.16 | 19.41 |
| SCE1572_707 | 67.17 | 518.51 |
| SCE1572_10043 | 53.42 | 1212.94 |
| SCE1572_5806 | 44.14 | 120.1 |
| SCE1572_8629 | 25.75 | 94.67 |
| SCE1572_789 | 0 | 0 |
| SCE1572_7654 | 19.14 | 12.9 |
| SCE1572_11227 | 52.62 | 47.23 |
| SCE1572_9610 | 25.43 | 13.6 |
| SCE1572_3759 | 25.87 | 29.07 |
| SCE1572_8431 | 48.37 | 22.59 |
| SCE1572_6394 | 636.02 | 241.22 |
| SCE1572_4813 | 34.42 | 241.52 |
| SCE1572_956 | 0 | 0 |
| SCE1572_9964 | 51.72 | 18.99 |
| SCE1572_3095 | 40.97 | 75.56 |
| SCE1572_1045 | 34.41 | 42.7 |
| SCE1572_9929 | 23.49 | 0 |
| SCE1572_4715 | 41.19 | 107.84 |
| SCE1572_4466 | 30.51 | 15.3 |
| SCE1572_5790 | 22.3 | 60.1 |
| SCE1572_10673 | 12.67 | 22.45 |
| SCE1572_5555 | 44.12 | 51.6 |
| SCE1572_4416 | 43.62 | 13.22 |
| SCE1572_1095 | 34.92 | 234.43 |
| SCE1572_1561 | 24.78 | 12.87 |
| SCE1572_11536 | 29.69 | 59.56 |
| SCE1572_931 | 320.25 | 6326.56 |
| SCE1572_10824 | 143.36 | 273.07 |
| SCE1572_10989 | 14.39 | 32.94 |
| SCE1572_10632 | 0 | 0 |
| SCE1572_8849 | 25.91 | 16.36 |
| SCE1572_1369 | 51.29 | 97.46 |
| SCE1572_8873 | 42.46 | 10.98 |
| SCE1572_7841 | 26.46 | 14.69 |
| SCE1572_6954 | 25.18 | 10.32 |
| SCE1572_6734 | 32.45 | 78.11 |
| SCE1572_277 | 48.05 | 28.02 |
| SCE1572_6792 | 26.28 | 158.96 |

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| SCE1572_1930 | 72.5 | 131.33 |
| SCE1572_6904 | 61.19 | 10.99 |
| SCE1572_8436 | 83.03 | 61.39 |
| SCE1572_5740 | 23.75 | 43.97 |
| SCE1572_2501 | 21.41 | 55.67 |
| SCE1572_6364 | 26.72 | 321.55 |
| SCE1572_6853 | 46.81 | 47.9 |
| SCE1572_6998 | 48.38 | 35.5 |
| SCE1572_5197 | 8.83 | 0 |
| SCE1572_2307 | 18.76 | 13.55 |
| SCE1572_442 | 40.82 | 39.77 |
| SCE1572_5755 | 60.84 | 197.51 |
| SCE1572_1506 | 46.07 | 15.07 |
| SCE1572_5989 | 0 | 4.65 |
| SCE1572_5735 | 33.8 | 70.89 |
| SCE1572_748 | 8.1 | 92.12 |
| SCE1572_2480 | 15.16 | 5.21 |
| SCE1572_4219 | 38.23 | 36.6 |
| SCE1572_84 | 14.67 | 87.11 |
| SCE1572_1353 | 38.42 | 24.66 |
| SCE1572_9971 | 54.55 | 403.17 |
| SCE1572_3015 | 44.66 | 15.92 |
| SCE1572_1688 | 11.08 | 16.84 |
| SCE1572_5883 | 42.07 | 53.5 |
| SCE1572_46 | 82.91 | 167.58 |
| SCE1572_8942 | 47.2 | 36.72 |
| SCE1572_6298 | 25.01 | 53.51 |
| SCE1572_10480 | 27.44 | 86.89 |
| SCE1572_358 | 41.99 | 29.76 |
| SCE1572_9328 | 54.04 | 70.06 |
| SCE1572_11506 | 33.47 | 34.12 |
| SCE1572_1422 | 18.11 | 17.56 |
| SCE1572_7771 | 31.89 | 148.12 |
| SCE1572_10041 | 27.8 | 0 |
| SCE1572_3400 | 36.15 | 209.88 |
| SCE1572_4564 | 32.49 | 29.79 |
| SCE1572_7216 | 58.81 | 20.78 |
| SCE1572_8620 | 32.21 | 168.28 |
| SCE1572_7538 | 75.62 | 40.35 |
| SCE1572_3101 | 10.6 | 63.8 |
| SCE1572_7310 | 23.01 | 18.79 |
| SCE1572_1841 | 127.3 | 929.52 |
| SCE1572_8951 | 0 | 0 |
| SCE1572_1109 | 0 | 0 |
| SCE1572_4233 | 11.4 | 6.04 |
| SCE1572_5651 | 0 | 0 |
| SCE1572_6824 | 141.07 | 341.12 |
| SCE1572_4772 | 26.8 | 6.53 |

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| SCE1572_10701 | 0 | 0 |
| SCE1572_2548 | 25.46 | 9.29 |
| SCE1572_8226 | 13.66 | 18.79 |
| SCE1572_6678 | 173.63 | 680.63 |
| SCE1572_9976 | 0 | 0 |
| SCE1572_10309 | 72.58 | 2.59 |
| SCE1572_10850 | 35.4 | 15.04 |
| SCE1572_2619 | 18.11 | 8.96 |
| SCE1572_10448 | 23.53 | 39.85 |
| SCE1572_9314 | 64.15 | 76.61 |
| SCE1572_10513 | 0 | 0 |
| SCE1572_3255 | 13 | 88.62 |
| SCE1572_447 | 29.98 | 23.15 |
| SCE1572_5309 | 26.59 | 35.4 |
| SCE1572_4922 | 60.65 | 12.16 |
| SCE1572_10111 | 63.78 | 462.44 |
| SCE1572_10948 | 45.01 | 45.28 |
| SCE1572_10603 | 0 | 0 |
| SCE1572_9947 | 10.95 | 12.16 |
| SCE1572_8828 | 14.77 | 6.89 |
| SCE1572_4063 | 49.51 | 75.54 |
| SCE1572_7816 | 29.81 | 198.86 |
| SCE1572_11439 | 80.5 | 39.33 |
| SCE1572_5087 | 63.28 | 521.75 |
| SCE1572_10390 | 50.14 | 24.99 |
| SCE1572_4984 | 63.45 | 21.82 |
| SCE1572_962 | 270.34 | 133.7 |
| SCE1572_6731 | 0 | 0 |
| SCE1572_6274 | 112.52 | 651.81 |
| SCE1572_9403 | 78.4 | 45.72 |
| SCE1572_811 | 14.52 | 7.76 |
| SCE1572_2950 | 3.03 | 0 |
| SCE1572_7992 | 58.01 | 5.78 |
| SCE1572_4011 | 87.27 | 246.3 |
| SCE1572_6865 | 40.12 | 30.23 |
| SCE1572_184 | 17.84 | 0 |
| SCE1572_3282 | 13.3 | 6.4 |
| SCE1572_902 | 58.07 | 15.53 |
| SCE1572_4283 | 13 | 20.85 |
| SCE1572_6898 | 50.44 | 126.98 |
| SCE1572_3025 | 37.28 | 13.16 |
| SCE1572_6173 | 32.72 | 145.97 |
| SCE1572_10123 | 182.83 | 168.66 |
| SCE1572_4703 | 36.39 | 10.7 |
| SCE1572_8151 | 37.46 | 15.03 |
| SCE1572_5490 | 73.74 | 31.91 |
| SCE1572_8063 | 8.75 | 0 |
| SCE1572_2627 | 60.01 | 23.57 |

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| SCE1572_7197 | 49.63 | 26.13 |
| SCE1572_1417 | 133.83 | 65.33 |
| SCE1572_1725 | 33.98 | 68.69 |
| SCE1572_1628 | 53.67 | 94.73 |
| SCE1572_1088 | 34.99 | 5.61 |
| SCE1572_8112 | 40.87 | 12.58 |
| SCE1572_4165 | 45.91 | 13.08 |
| SCE1572_8032 | 0 | 0 |
| SCE1572_4701 | 62.29 | 46.95 |
| SCE1572_9146 | 0 | 0 |
| SCE1572_7488 | 45.24 | 79.46 |
| SCE1572_11458 | 73.33 | 126.41 |
| SCE1572_8606 | 1.99 | 0 |
| SCE1572_6672 | 0 | 0 |
| SCE1572_2497 | 51.5 | 36.41 |
| SCE1572_1834 | 9.87 | 8.64 |
| SCE1572_5445 | 36.26 | 17.45 |
| SCE1572_6338 | 29.13 | 80.89 |
| SCE1572_4951 | 13.46 | 6.82 |
| SCE1572_1853 | 62.95 | 19.4 |
| SCE1572_8353 | 336.53 | 1797.9 |
| SCE1572_3978 | 35.29 | 26.32 |
| SCE1572_6754 | 109.25 | 30.72 |
| SCE1572_1385 | 24.36 | 20.22 |
| SCE1572_8476 | 118.2 | 98.43 |
| SCE1572_10644 | 87.78 | 1943.24 |
| SCE1572_9231 | 29.48 | 4.05 |
| SCE1572_8190 | 39.93 | 13.57 |
| SCE1572_2845 | 42.42 | 0 |
| SCE1572_11599 | 11.54 | 4.51 |
| SCE1572_10978 | 349.64 | 1176.69 |
| SCE1572_1715 | 37.35 | 44.95 |
| SCE1572_8492 | 134.28 | 252.83 |
| SCE1572_10207 | 24.02 | 28.9 |
| SCE1572_7058 | 38.55 | 12.37 |
| SCE1572_10278 | 10.61 | 1.82 |
| SCE1572_3458 | 91.54 | 20.66 |
| SCE1572_9348 | 56.93 | 51.73 |
| SCE1572_4112 | 37.04 | 11.14 |
| SCE1572_8726 | 48.4 | 22.27 |
| SCE1572_4380 | 18.06 | 6.72 |
| SCE1572_1848 | 69.72 | 34.37 |
| SCE1572_2087 | 0 | 0 |
| SCE1572_3332 | 0 | 0 |
| SCE1572_649 | 0 | 0 |
| SCE1572_7681 | 20.42 | 15.13 |
| SCE1572_10768 | 6.79 | 0 |
| SCE1572_3366 | 21.43 | 373.95 |

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| SCE1572_642 | 68.64 | 146.85 |
| SCE1572_495 | 0 | 0 |
| SCE1572_8682 | 19.84 | 51.16 |
| SCE1572_10830 | 14.26 | 7.63 |
| SCE1572_7033 | 49.34 | 17.38 |
| SCE1572_9004 | 19.01 | 5.58 |
| SCE1572_6210 | 47.36 | 26.45 |
| SCE1572_1318 | 11.72 | 3.53 |
| SCE1572_10861 | 373.22 | 1467.88 |
| SCE1572_5279 | 86.3 | 66.97 |
| SCE1572_1757 | 47.32 | 24.64 |
| SCE1572_11216 | 29.87 | 27.23 |
| SCE1572_1196 | 24.73 | 37.53 |
| SCE1572_10504 | 39.69 | 46.99 |
| SCE1572_5466 | 45.41 | 21.02 |
| SCE1572_3924 | 33.69 | 243.28 |
| SCE1572_8855 | 103.99 | 252.64 |
| SCE1572_2551 | 23.11 | 13.35 |
| SCE1572_5458 | 27.97 | 7.81 |
| SCE1572_6620 | 31.88 | 20.59 |
| SCE1572_8188 | 0 | 0 |
| SCE1572_7975 | 15.94 | 2.07 |
| SCE1572_7279 | 3.16 | 0 |
| SCE1572_4931 | 62.08 | 39.32 |
| SCE1572_1311 | 219.41 | 2356.21 |
| SCE1572_11144 | 28.74 | 20.75 |
| SCE1572_5963 | 34.14 | 17.72 |
| SCE1572_6383 | 32.75 | 0 |
| SCE1572_829 | 30.82 | 14.04 |
| SCE1572_5384 | 14.24 | 15.12 |
| SCE1572_1487 | 123.09 | 61.42 |
| SCE1572_8840 | 66.75 | 27.54 |
| SCE1572_523 | 39.98 | 63.74 |
| SCE1572_3667 | 10.01 | 1.85 |
| SCE1572_7557 | 25.41 | 10.19 |
| SCE1572_1166 | 43.41 | 23.31 |
| SCE1572_11125 | 17.99 | 16.49 |
| SCE1572_1184 | 40.03 | 18.19 |
| SCE1572_7067 | 85.18 | 4.1 |
| SCE1572_5834 | 11.87 | 237.99 |
| SCE1572_1163 | 14.01 | 22.88 |
| SCE1572_4018 | 27.76 | 23.38 |
| SCE1572_7445 | 69.34 | 36.78 |
| SCE1572_1434 | 67.94 | 37.89 |
| SCE1572_9655 | 19.52 | 2.56 |
| SCE1572_7673 | 52.99 | 14.22 |
| SCE1572_8245 | 24.34 | 37.83 |
| SCE1572_4717 | 18.95 | 10.95 |

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| SCE1572_1580 | 30.43 | 13.32 |
| SCE1572_5583 | 41.59 | 24.76 |
| SCE1572_6541 | 16.61 | 11.61 |
| SCE1572_9920 | 58.05 | 25.93 |
| SCE1572_9846 | 37.56 | 6.7 |
| SCE1572_1577 | 28.43 | 9.65 |
| SCE1572_5334 | 128.04 | 398.19 |
| SCE1572_6943 | 10.83 | 2.61 |
| SCE1572_3108 | 34.73 | 18.58 |
| SCE1572_9279 | 13.71 | 10.68 |
| SCE1572_6286 | 7.13 | 0 |
| SCE1572_8816 | 38.41 | 10.95 |
| SCE1572_8082 | 0 | 0 |
| SCE1572_3655 | 17.58 | 0 |
| SCE1572_10716 | 55.13 | 12.06 |
| SCE1572_11235 | 19.83 | 8.95 |
| SCE1572_9715 | 9 | 5.41 |
| SCE1572_11294 | 18.55 | 3.88 |
| SCE1572_7203 | 0 | 0 |
| SCE1572_8035 | 23.03 | 15.44 |
| SCE1572_6584 | 68.23 | 173.34 |
| SCE1572_8461 | 104.05 | 110.91 |
| SCE1572_1336 | 27.66 | 91.23 |
| SCE1572_793 | 206.04 | 275.1 |
| SCE1572_7665 | 72.43 | 8.86 |
| SCE1572_2794 | 6.41 | 0 |
| SCE1572_6889 | 67.87 | 20.85 |
| SCE1572_9744 | 34.46 | 147.21 |
| SCE1572_3750 | 31.81 | 11.04 |
| SCE1572_4096 | 18.49 | 0 |
| SCE1572_2359 | 24.16 | 58.16 |
| SCE1572_8788 | 0 | 0 |
| SCE1572_6826 | 16.85 | 83.12 |
| SCE1572_3548 | 30.32 | 15.81 |
| SCE1572_11159 | 19.53 | 33.58 |
| SCE1572_408 | 20.99 | 20.03 |
| SCE1572_5227 | 4.1 | 0 |
| SCE1572_11130 | 39.46 | 22.46 |
| SCE1572_10467 | 67.08 | 141.11 |
| SCE1572_3438 | 0 | 0 |
| SCE1572_6817 | 71.65 | 10 |
| SCE1572_7186 | 23.94 | 11.82 |
| SCE1572_96 | 27.62 | 26.87 |
| SCE1572_6495 | 9.05 | 0 |
| SCE1572_8418 | 29.69 | 16.24 |
| SCE1572_7341 | 46.34 | 125.53 |
| SCE1572_7078 | 0 | 0 |
| SCE1572_10851 | 23.71 | 48.6 |

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| SCE1572_7495 | 48.77 | 17.86 |
| SCE1572_1364 | 604.14 | 3379.26 |
| SCE1572_8373 | 62.77 | 128.4 |
| SCE1572_1409 | 113.54 | 33.02 |
| SCE1572_8385 | 39.63 | 17.03 |
| SCE1572_3261 | 28.98 | 47.15 |
| SCE1572_10236 | 132.6 | 82.75 |
| SCE1572_511 | 44.03 | 37.68 |
| SCE1572_4374 | 34.24 | 0 |
| SCE1572_5181 | 34.21 | 1118.16 |
| SCE1572_151 | 16.73 | 7.55 |
| SCE1572_9345 | 23.92 | 47.83 |
| SCE1572_9339 | 179.35 | 1426.31 |
| SCE1572_3679 | 29.91 | 14.89 |
| SCE1572_2753 | 22.82 | 7.85 |
| SCE1572_409 | 25.75 | 13.77 |
| SCE1572_8963 | 50.79 | 34.16 |
| SCE1572_5866 | 40.03 | 37.95 |
| SCE1572_9943 | 151.62 | 513.51 |
| SCE1572_6922 | 24.21 | 205.46 |
| SCE1572_7576 | 10.88 | 10.97 |
| SCE1572_10653 | 318.25 | 2652.83 |
| SCE1572_3540 | 113.26 | 39.57 |
| SCE1572_6624 | 21.73 | 24.96 |
| SCE1572_1407 | 13.74 | 12.8 |
| SCE1572_7668 | 15.37 | 11.31 |
| SCE1572_11058 | 59.77 | 64.33 |
| SCE1572_11351 | 72.08 | 31.48 |
| SCE1572_4301 | 60.45 | 18.64 |
| SCE1572_11186 | 28.18 | 4.31 |
| SCE1572_4581 | 26.93 | 12 |
| SCE1572_7793 | 49.5 | 29.08 |
| SCE1572_10556 | 0 | 0 |
| SCE1572_4424 | 31.42 | 11.11 |
| SCE1572_6548 | 0 | 0 |
| SCE1572_11520 | 36.18 | 12.44 |
| SCE1572_9256 | 610.73 | 806.94 |
| SCE1572_2808 | 72.05 | 27.6 |
| SCE1572_5481 | 10.83 | 4.34 |
| SCE1572_1399 | 16.14 | 12.49 |
| SCE1572_3976 | 45.11 | 60.32 |
| SCE1572_11220 | 35.25 | 13.95 |
| SCE1572_5675 | 17.91 | 25.06 |
| SCE1572_8046 | 7.78 | 0 |
| SCE1572_3532 | 37.03 | 13.45 |
| SCE1572_497 | 25.27 | 3.5 |
| SCE1572_5045 | 36.01 | 52.46 |
| SCE1572_7862 | 53.92 | 269.3 |

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| SCE1572_10457 | 0 | 0 |
| SCE1572_3988 | 33.32 | 42.11 |
| SCE1572_4427 | 40.37 | 7.91 |
| SCE1572_2966 | 48.29 | 24.91 |
| SCE1572_1302 | 17.42 | 135.1 |
| SCE1572_2224 | 20.72 | 8.31 |
| SCE1572_3722 | 69.24 | 3187.94 |
| SCE1572_8483 | 9.79 | 12.04 |
| SCE1572_868 | 45.34 | 99.76 |
| SCE1572_6323 | 26.9 | 34.33 |
| SCE1572_2738 | 12.93 | 5.19 |
| SCE1572_551 | 33.82 | 53.33 |
| SCE1572_2777 | 28.51 | 10.72 |
| SCE1572_10497 | 58.36 | 40.55 |
| SCE1572_3054 | 14.21 | 0 |
| SCE1572_9102 | 0 | 0 |
| SCE1572_8755 | 87.42 | 19.73 |
| SCE1572_418 | 102.88 | 25.6 |
| SCE1572_2763 | 32.92 | 13.36 |
| SCE1572_2782 | 28.3 | 22.7 |
| SCE1572_8075 | 22.32 | 28.02 |
| SCE1572_8351 | 20.81 | 9.54 |
| SCE1572_3440 | 87.04 | 34.46 |
| SCE1572_5891 | 50.87 | 76.83 |
| SCE1572_687 | 42.45 | 12.51 |
| SCE1572_8834 | 43.26 | 26.51 |
| SCE1572_8177 | 26.21 | 12.9 |
| SCE1572_207 | 0 | 0 |
| SCE1572_3032 | 16.92 | 17.92 |
| SCE1572_10055 | 246.13 | 500.8 |
| SCE1572_3818 | 19.67 | 62.63 |
| SCE1572_5068 | 140.69 | 163.56 |
| SCE1572_8131 | 24.63 | 14.82 |
| SCE1572_2508 | 37.24 | 20.63 |
| SCE1572_10008 | 16.29 | 9.31 |
| SCE1572_374 | 35.85 | 14.83 |
| SCE1572_1856 | 30.28 | 12.33 |
| SCE1572_4912 | 25.27 | 30.41 |
| SCE1572_9600 | 125.52 | 696.94 |
| SCE1572_7917 | 200.63 | 339.93 |
| SCE1572_10874 | 33.9 | 22.67 |
| SCE1572_11091 | 39.13 | 57.55 |
| SCE1572_186 | 52.74 | 34.17 |
| SCE1572_9095 | 46.3 | 95.52 |
| SCE1572_9559 | 29.07 | 39.71 |
| SCE1572_6572 | 27.19 | 36.17 |
| SCE1572_9421 | 51.59 | 392.16 |
| SCE1572_1864 | 0 | 0 |

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| SCE1572_332 | 33.23 | 84.98 |
| SCE1572_7794 | 5.69 | 10.28 |
| SCE1572_1172 | 24.61 | 22.21 |
| SCE1572_275 | 147.88 | 62.92 |
| SCE1572_2385 | 41.77 | 65.66 |
| SCE1572_3762 | 35.55 | 89.51 |
| SCE1572_3689 | 11.93 | 18.52 |
| SCE1572_1411 | 39.04 | 11.8 |
| SCE1572_7456 | 29.04 | 15.46 |
| SCE1572_8588 | 34.66 | 24.76 |
| SCE1572_3566 | 33.65 | 12.68 |
| SCE1572_8290 | 57.83 | 19.57 |
| SCE1572_10780 | 42.59 | 49.2 |
| SCE1572_7008 | 0 | 0 |
| SCE1572_7731 | 23.78 | 10.73 |
| SCE1572_324 | 24.82 | 20.66 |
| SCE1572_2609 | 48.58 | 40.32 |
| SCE1572_9401 | 28.99 | 56.35 |
| SCE1572_8525 | 80.77 | 98.9 |
| SCE1572_9917 | 59.75 | 27.83 |
| SCE1572_9467 | 22.48 | 26.59 |
| SCE1572_1069 | 46.82 | 10.34 |
| SCE1572_3292 | 46.34 | 162.41 |
| SCE1572_3169 | 33.29 | 73.72 |
| SCE1572_5164 | 13.63 | 295.22 |
| SCE1572_10170 | 34.1 | 46.11 |
| SCE1572_4247 | 51.48 | 52.89 |
| SCE1572_6962 | 33.3 | 56.27 |
| SCE1572_6846 | 41.49 | 314.99 |
| SCE1572_7255 | 100.66 | 631.85 |
| SCE1572_2472 | 58.42 | 1710.78 |
| SCE1572_9380 | 6.45 | 3.88 |
| SCE1572_608 | 66.49 | 107.77 |
| SCE1572_1253 | 22.02 | 10.19 |
| SCE1572_10490 | 20.86 | 28.17 |
| SCE1572_3421 | 20.99 | 27 |
| SCE1572_7373 | 38.56 | 20.45 |
| SCE1572_10214 | 61.22 | 75.98 |
| SCE1572_2349 | 43.73 | 53.77 |
| SCE1572_2276 | 67.09 | 368.74 |
| SCE1572_2721 | 307.56 | 243.28 |
| SCE1572_7020 | 35.7 | 6.52 |
| SCE1572_19 | 49.86 | 238.81 |
| SCE1572_7011 | 95.48 | 64.11 |
| SCE1572_2701 | 26.91 | 12.51 |
| SCE1572_7597 | 58.75 | 260.01 |
| SCE1572_2824 | 34.7 | 25.85 |
| SCE1572_5544 | 31.6 | 7.7 |

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| SCE1572_1255 | 43 | 32.12 |
| SCE1572_8202 | 76.27 | 20.46 |
| SCE1572_11095 | 33.06 | 13.72 |
| SCE1572_6634 | 22.17 | 8.36 |
| SCE1572_11539 | 33.1 | 7.97 |
| SCE1572_7590 | 59.2 | 77.71 |
| SCE1572_2982 | 0 | 0 |
| SCE1572_3642 | 70.68 | 28.23 |
| SCE1572_4673 | 23.48 | 28.61 |
| SCE1572_8381 | 32.45 | 31.06 |
| SCE1572_3684 | 34 | 4.42 |
| SCE1572_11068 | 46.49 | 78.83 |
| SCE1572_5215 | 83.52 | 203.59 |
| SCE1572_9176 | 0 | 0 |
| SCE1572_7660 | 37.83 | 10.93 |
| SCE1572_2295 | 13.78 | 0 |
| SCE1572_1951 | 41.84 | 14.39 |
| SCE1572_10914 | 20.14 | 19.24 |
| SCE1572_3771 | 31.98 | 42.05 |
| SCE1572_4734 | 32.67 | 45.29 |
| SCE1572_9248 | 32.85 | 44.31 |
| SCE1572_9044 | 37.18 | 28.23 |
| SCE1572_7753 | 16.85 | 10.14 |
| SCE1572_2459 | 47.09 | 43.07 |
| SCE1572_619 | 10.8 | 23 |
| SCE1572_2208 | 18.38 | 11.06 |
| SCE1572_6685 | 37.1 | 21.47 |
| SCE1572_8140 | 20.99 | 117.1 |
| SCE1572_2100 | 1.58 | 3.8 |
| SCE1572_7943 | 31.8 | 131.73 |
| SCE1572_3561 | 24.79 | 8.95 |
| SCE1572_2812 | 48.32 | 52.28 |
| SCE1572_2616 | 29.81 | 87.09 |
| SCE1572_11378 | 20.79 | 169.95 |
| SCE1572_7741 | 46.32 | 40.06 |
| SCE1572_2788 | 47.69 | 32.37 |
| SCE1572_10737 | 36.96 | 63.93 |
| SCE1572_7952 | 174.17 | 512.03 |
| SCE1572_8556 | 49.82 | 129.22 |
| SCE1572_6446 | 8.83 | 3.54 |
| SCE1572_7823 | 103.13 | 466.8 |
| SCE1572_2620 | 55.94 | 34.43 |
| SCE1572_3539 | 38.48 | 16.7 |
| SCE1572_4863 | 43.32 | 44.68 |
| SCE1572_758 | 8.92 | 8.35 |
| SCE1572_2022 | 130.46 | 1284.31 |
| SCE1572_1531 | 18.05 | 14.22 |
| SCE1572_3493 | 36.88 | 15.3 |

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| SCE1572_9001 | 555.93 | 932.58 |
| SCE1572_3160 | 78.97 | 65.89 |
| SCE1572_6856 | 68.77 | 45.86 |
| SCE1572_8396 | 43.01 | 183.76 |
| SCE1572_7565 | 18.95 | 8.4 |
| SCE1572_10607 | 36.47 | 68.85 |
| SCE1572_4457 | 43.32 | 56.36 |
| SCE1572_6302 | 78.25 | 1121.52 |
| SCE1572_686 | 20.33 | 6.22 |
| SCE1572_9609 | 88.78 | 339.95 |
| SCE1572_6534 | 42.62 | 9.86 |
| SCE1572_1067 | 39.81 | 11.62 |
| SCE1572_8549 | 36.26 | 15.87 |
| SCE1572_10335 | 109.19 | 266.16 |
| SCE1572_6230 | 24.22 | 28.07 |
| SCE1572_8511 | 41.64 | 34.69 |
| SCE1572_3376 | 19.44 | 163.75 |
| SCE1572_9056 | 45.62 | 18.77 |
| SCE1572_6493 | 24.75 | 18.62 |
| SCE1572_6929 | 22.38 | 5.77 |
| SCE1572_7439 | 11.97 | 0 |
| SCE1572_1885 | 14.26 | 61.8 |
| SCE1572_1143 | 35.5 | 60.52 |
| SCE1572_5873 | 36.36 | 25.9 |
| SCE1572_10362 | 35.24 | 368.92 |
| SCE1572_935 | 55.34 | 187.43 |
| SCE1572_8154 | 31.74 | 6.84 |
| SCE1572_5588 | 25.36 | 9.29 |
| SCE1572_5557 | 41.17 | 94.97 |
| SCE1572_10329 | 39.77 | 49.85 |
| SCE1572_9506 | 24.59 | 9.35 |
| SCE1572_1129 | 33.5 | 15.51 |
| SCE1572_10473 | 73.97 | 491.81 |
| SCE1572_9261 | 53.01 | 15.31 |
| SCE1572_11027 | 47.53 | 31.56 |
| SCE1572_10021 | 95.36 | 40.64 |
| SCE1572_5766 | 232.33 | 1234.76 |
| SCE1572_8864 | 51.02 | 0 |
| SCE1572_8784 | 23.71 | 120.71 |
| SCE1572_3341 | 217.9 | 478.59 |
| SCE1572_8426 | 19.72 | 0 |
| SCE1572_3308 | 11.44 | 1.38 |
| SCE1572_5817 | 7.78 | 0 |
| SCE1572_8452 | 27.04 | 230.11 |
| SCE1572_11319 | 65.98 | 16.89 |
| SCE1572_11590 | 14.09 | 10.53 |
| SCE1572_638 | 33.88 | 47 |
| SCE1572_676 | 21 | 7.62 |

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| SCE1572_924 | 152.75 | 620.91 |
| SCE1572_477 | 13.65 | 12.11 |
| SCE1572_5854 | 7.4 | 0 |
| SCE1572_8399 | 53.38 | 65.42 |
| SCE1572_9778 | 57.71 | 241.71 |
| SCE1572_10799 | 77.25 | 68.95 |
| SCE1572_6307 | 68.88 | 78.39 |
| SCE1572_9318 | 257.91 | 396.74 |
| SCE1572_8454 | 18.08 | 41.29 |
| SCE1572_10319 | 52.91 | 85.53 |
| SCE1572_11003 | 106.45 | 236.81 |
| SCE1572_2102 | 24.64 | 84.39 |
| SCE1572_9742 | 46.85 | 67.24 |
| SCE1572_11176 | 22.61 | 144.05 |
| SCE1572_9915 | 110.61 | 57.58 |
| SCE1572_3158 | 25.95 | 14.56 |
| SCE1572_1959 | 1.92 | 0 |
| SCE1572_11222 | 64.34 | 27.61 |
| SCE1572_1390 | 54.9 | 173.82 |
| SCE1572_8976 | 10.99 | 2.64 |
| SCE1572_9109 | 7.9 | 7.6 |
| SCE1572_8307 | 848.7 | 43.62 |
| SCE1572_5075 | 4.17 | 1.67 |
| SCE1572_5368 | 19.93 | 10.28 |
| SCE1572_4535 | 55.25 | 24.74 |
| SCE1572_1060 | 0 | 0 |
| SCE1572_10024 | 29.24 | 19.56 |
| SCE1572_7131 | 19.65 | 3.38 |
| SCE1572_3131 | 25.98 | 13.49 |
| SCE1572_9820 | 116.44 | 97.24 |
| SCE1572_9221 | 51.99 | 36.99 |
| SCE1572_2830 | 21.9 | 4.05 |
| SCE1572_8737 | 50.22 | 23.24 |
| SCE1572_397 | 40.43 | 30.41 |
| SCE1572_8722 | 28.66 | 9.08 |
| SCE1572_6430 | 33.59 | 34.75 |
| SCE1572_10990 | 57.68 | 63.46 |
| SCE1572_2957 | 145.5 | 81.49 |
| SCE1572_2633 | 45.96 | 3.5 |
| SCE1572_2152 | 25.63 | 34.27 |
| SCE1572_8609 | 37.41 | 21.69 |
| SCE1572_2351 | 36.14 | 450.55 |
| SCE1572_4214 | 0 | 0 |
| SCE1572_10179 | 60.75 | 280.34 |
| SCE1572_4310 | 68.39 | 21.15 |
| SCE1572_2901 | 0 | 0 |
| SCE1572_4780 | 40.27 | 67.51 |
| SCE1572_2325 | 13.1 | 69.1 |

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| SCE1572_5726 | 32.24 | 250.12 |
| SCE1572_4085 | 37.34 | 12.58 |
| SCE1572_10771 | 28.77 | 18.65 |
| SCE1572_4758 | 77.5 | 42.65 |
| SCE1572_5256 | 41.35 | 16.59 |
| SCE1572_1299 | 48.8 | 23.49 |
| SCE1572_5810 | 5204.42 | 6531.47 |
| SCE1572_6758 | 26.84 | 14.84 |
| SCE1572_4391 | 33.01 | 13.05 |
| SCE1572_9224 | 49.19 | 10.6 |
| SCE1572_5469 | 78.37 | 16.48 |
| SCE1572_9835 | 17.62 | 30.84 |
| SCE1572_8593 | 0 | 0 |
| SCE1572_11483 | 217.75 | 302.81 |
| SCE1572_1668 | 35.31 | 28.99 |
| SCE1572_1459 | 47.25 | 17.79 |
| SCE1572_3583 | 30.05 | 16.94 |
| SCE1572_412 | 15.64 | 16.36 |
| SCE1572_600 | 1.65 | 0 |
| SCE1572_9438 | 27.02 | 52.39 |
| SCE1572_2566 | 27.99 | 0 |
| SCE1572_9883 | 42.41 | 51.04 |
| SCE1572_6088 | 25.65 | 65.96 |
| SCE1572_2140 | 41.26 | 19.86 |
| SCE1572_10421 | 30.32 | 13.84 |
| SCE1572_177 | 14.1 | 4.24 |
| SCE1572_10303 | 85.02 | 50.68 |
| SCE1572_8851 | 10.7 | 103.04 |
| SCE1572_9275 | 49.25 | 59.03 |
| SCE1572_7141 | 27.49 | 8.02 |
| SCE1572_5063 | 7.34 | 5.89 |
| SCE1572_1703 | 80.79 | 89.02 |
| SCE1572_10427 | 7.22 | 4.34 |
| SCE1572_4378 | 179.18 | 20.42 |
| SCE1572_9816 | 13.91 | 21.2 |
| SCE1572_5436 | 64.98 | 25.32 |
| SCE1572_7434 | 20.61 | 88.57 |
| SCE1572_8193 | 25.51 | 8.77 |
| SCE1572_2565 | 41.77 | 116.95 |
| SCE1572_2288 | 37.46 | 54.38 |
| SCE1572_3407 | 98.32 | 255.81 |
| SCE1572_451 | 13.45 | 25.01 |
| SCE1572_10258 | 25.27 | 4.34 |
| SCE1572_10908 | 47.69 | 85.34 |
| SCE1572_6533 | 86 | 10.67 |
| SCE1572_9584 | 23.34 | 24.8 |
| SCE1572_11239 | 30.59 | 11.91 |
| SCE1572_6703 | 25.2 | 16.11 |

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| SCE1572_11426 | 44.96 | 65.43 |
| SCE1572_11433 | 74.79 | 148.25 |
| SCE1572_7054 | 24.09 | 23.87 |
| SCE1572_10145 | 192.69 | 309.49 |
| SCE1572_6669 | 15.66 | 16.59 |
| SCE1572_424 | 30.44 | 171.4 |
| SCE1572_7603 | 23.74 | 7.37 |
| SCE1572_5010 | 86.45 | 506.08 |
| SCE1572_8712 | 33.18 | 13.52 |
| SCE1572_1532 | 37.38 | 134.97 |
| SCE1572_4541 | 79.68 | 24.22 |
| SCE1572_11156 | 43.14 | 44.5 |
| SCE1572_2923 | 73.76 | 35.75 |
| SCE1572_8324 | 66.21 | 23.9 |
| SCE1572_4907 | 38.29 | 63.89 |
| SCE1572_1086 | 40.6 | 51.18 |
| SCE1572_138 | 30.32 | 38.41 |
| SCE1572_3447 | 48.87 | 78.41 |
| SCE1572_11404 | 26.57 | 18.81 |
| SCE1572_3467 | 49.52 | 25.01 |
| SCE1572_2077 | 30.88 | 41.04 |
| SCE1572_1034 | 52.4 | 18.06 |
| SCE1572_9949 | 69.89 | 20.7 |
| SCE1572_6714 | 100.06 | 244.5 |
| SCE1572_10060 | 0 | 0 |
| SCE1572_1650 | 12.38 | 7.45 |
| SCE1572_3244 | 108.91 | 241.57 |
| SCE1572_2213 | 32.17 | 71.37 |
| SCE1572_1321 | 36.61 | 81.41 |
| SCE1572_11242 | 95.72 | 48.77 |
| SCE1572_727 | 38.21 | 8.9 |
| SCE1572_1447 | 34.18 | 13.13 |
| SCE1572_3859 | 52.83 | 83.66 |
| SCE1572_7886 | 24.99 | 112.28 |
| SCE1572_10741 | 21.76 | 32.1 |
| SCE1572_5400 | 13.51 | 7.23 |
| SCE1572_11565 | 31.42 | 65.75 |
| SCE1572_6214 | 13.24 | 4.4 |
| SCE1572_6468 | 29.98 | 9.71 |
| SCE1572_10937 | 31.05 | 99.92 |
| SCE1572_8931 | 17.01 | 7.23 |
| SCE1572_5964 | 13.78 | 12.76 |
| SCE1572_8632 | 23.24 | 90.56 |
| SCE1572_3887 | 32.88 | 116.37 |
| SCE1572_7678 | 35.2 | 420.31 |
| SCE1572_2009 | 49.6 | 13.57 |
| SCE1572_4732 | 16.93 | 12.97 |
| SCE1572_9734 | 29.6 | 86.89 |

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| SCE1572_7472 | 71.02 | 121 |
| SCE1572_3191 | 0 | 0 |
| SCE1572_5760 | 18.34 | 9.81 |
| SCE1572_558 | 44.47 | 324.38 |
| SCE1572_645 | 5.41 | 18.25 |
| SCE1572_11076 | 13.28 | 251.53 |
| SCE1572_7111 | 24.08 | 23.19 |
| SCE1572_8934 | 12.09 | 5.6 |
| SCE1572_6047 | 9.94 | 149.56 |
| SCE1572_7091 | 34.49 | 28.54 |
| SCE1572_9453 | 21.31 | 42.5 |
| SCE1572_2237 | 90.44 | 70.42 |
| SCE1572_8524 | 44.49 | 262.15 |
| SCE1572_10151 | 39 | 271.04 |
| SCE1572_3396 | 79.17 | 74.06 |
| SCE1572_9789 | 12.52 | 9.77 |
| SCE1572_10660 | 6.87 | 0 |
| SCE1572_906 | 43.21 | 0 |
| SCE1572_7351 | 15.49 | 6.07 |
| SCE1572_1804 | 2.27 | 0 |
| SCE1572_7529 | 34.66 | 15.64 |
| SCE1572_7789 | 0 | 0 |
| SCE1572_10748 | 21.14 | 43.86 |
| SCE1572_1989 | 0 | 4.62 |
| SCE1572_1949 | 4.81 | 0 |
| SCE1572_6237 | 27.07 | 11.73 |
| SCE1572_9782 | 36.05 | 25.52 |
| SCE1572_7306 | 6.69 | 0 |
| SCE1572_2281 | 36.07 | 16.19 |
| SCE1572_7964 | 31.73 | 29.7 |
| SCE1572_7423 | 83.99 | 133.89 |
| SCE1572_5667 | 3.89 | 0 |
| SCE1572_10563 | 38.42 | 28.45 |
| SCE1572_7275 | 71.78 | 27.18 |
| SCE1572_11133 | 38.35 | 24.69 |
| SCE1572_9114 | 3.65 | 0 |
| SCE1572_7239 | 0 | 0 |
| SCE1572_4027 | 41.66 | 111.12 |
| SCE1572_5905 | 0 | 0 |
| SCE1572_7267 | 58.09 | 18.76 |
| SCE1572_2133 | 61.57 | 16.08 |
| SCE1572_10810 | 84.47 | 185.07 |
| SCE1572_4116 | 12.84 | 1.72 |
| SCE1572_5080 | 164.77 | 1102.68 |
| SCE1572_8448 | 36.22 | 12.35 |
| SCE1572_7157 | 60.19 | 22.88 |
| SCE1572_2129 | 23.78 | 16.1 |
| SCE1572_794 | 170.99 | 241.14 |

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| SCE1572_4368 | 31.92 | 120.04 |
| SCE1572_11311 | 47.72 | 22.16 |
| SCE1572_11337 | 18.08 | 10.04 |
| SCE1572_9843 | 33.13 | 104.59 |
| SCE1572_2222 | 30.09 | 25.07 |
| SCE1572_5124 | 42.18 | 4.12 |
| SCE1572_1070 | 19.47 | 1.12 |
| SCE1572_1187 | 41.94 | 2.59 |
| SCE1572_545 | 21.62 | 4.79 |
| SCE1572_2849 | 0 | 0 |
| SCE1572_2230 | 50.74 | 171.07 |
| SCE1572_1076 | 25.27 | 53.67 |
| SCE1572_3932 | 765.83 | 4832.6 |
| SCE1572_7165 | 80.59 | 19.73 |
| SCE1572_10357 | 37.04 | 350.66 |
| SCE1572_1051 | 24.24 | 18.03 |
| SCE1572_7137 | 35.56 | 8.07 |
| SCE1572_3023 | 37.9 | 16.19 |
| SCE1572_7337 | 58.24 | 234.93 |
| SCE1572_11344 | 71.16 | 275.42 |
| SCE1572_11394 | 82.43 | 308.24 |
| SCE1572_11594 | 80.74 | 505.02 |
| SCE1572_3525 | 57.76 | 793.34 |
| SCE1572_3917 | 123.47 | 76.08 |
| SCE1572_7408 | 23.87 | 128.4 |
| SCE1572_7932 | 18.08 | 12.76 |
| SCE1572_3065 | 18.19 | 20.44 |
| SCE1572_1835 | 42.64 | 38.77 |
| SCE1572_5417 | 72.31 | 97.69 |
| SCE1572_6263 | 20.14 | 18.71 |
| SCE1572_2908 | 33.43 | 46.78 |
| SCE1572_4998 | 16.8 | 34.96 |
| SCE1572_5705 | 53.7 | 66.52 |
| SCE1572_11269 | 33.33 | 41.68 |
| SCE1572_10778 | 50.97 | 44.26 |
| SCE1572_1114 | 38.53 | 158.6 |
| SCE1572_1515 | 18.09 | 49.76 |
| SCE1572_10885 | 30.99 | 16.84 |
| SCE1572_6780 | 0 | 0 |
| SCE1572_4885 | 39.74 | 20.08 |
| SCE1572_329 | 24.48 | 52.72 |
| SCE1572_7039 | 36.83 | 15.46 |
| SCE1572_2000 | 4.07 | 0 |
| SCE1572_9025 | 63.17 | 243.28 |
| SCE1572_4176 | 90.69 | 39.69 |
| SCE1572_3506 | 90.21 | 266.39 |
| SCE1572_6256 | 28.55 | 12.21 |
| SCE1572_5642 | 9.89 | 10.58 |

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| SCE1572_2374 | 149.17 | 1268.4 |
| SCE1572_5660 | 33.34 | 8.51 |
| SCE1572_7032 | 37.31 | 17.92 |
| SCE1572_4616 | 8.61 | 4.15 |
| SCE1572_10293 | 0 | 0 |
| SCE1572_8577 | 0 | 0 |
| SCE1572_3910 | 81.13 | 155.25 |
| SCE1572_1431 | 4.97 | 0 |
| SCE1572_4795 | 45.1 | 122.41 |
| SCE1572_316 | 49.19 | 26.02 |
| SCE1572_5633 | 30.72 | 22.02 |
| SCE1572_3703 | 26.91 | 11.88 |
| SCE1572_4595 | 12.42 | 11.21 |
| SCE1572_10587 | 39.43 | 12.03 |
| SCE1572_10763 | 2.71 | 0 |
| SCE1572_10935 | 15.98 | 13.42 |
| SCE1572_4963 | 109.81 | 427.13 |
| SCE1572_6137 | 10.78 | 13.84 |
| SCE1572_6748 | 37.67 | 22.12 |
| SCE1572_5606 | 12.38 | 10.43 |
| SCE1572_9687 | 138.22 | 301.61 |
| SCE1572_2832 | 20.02 | 35.44 |
| SCE1572_1818 | 19.23 | 24.51 |
| SCE1572_4454 | 22.24 | 14.6 |
| SCE1572_221 | 54.64 | 58.54 |
| SCE1572_6037 | 9.63 | 0 |
| SCE1572_11273 | 54.75 | 236.95 |
| SCE1572_6277 | 56.93 | 65.54 |
| SCE1572_3590 | 16.08 | 0 |
| SCE1572_9591 | 45.94 | 606.7 |
| SCE1572_6556 | 31.63 | 10.07 |
| SCE1572_9625 | 20.85 | 15.37 |
| SCE1572_4274 | 53 | 272.95 |
| SCE1572_3501 | 15.43 | 13 |
| SCE1572_10414 | 37.03 | 50.45 |
| SCE1572_5925 | 27.6 | 41.2 |
| SCE1572_11104 | 10.83 | 72.98 |
| SCE1572_3573 | 11.14 | 0.96 |
| SCE1572_9635 | 68.39 | 69.07 |
| SCE1572_9194 | 31.22 | 49.37 |
| SCE1572_2062 | 94.25 | 64.11 |
| SCE1572_1990 | 41.88 | 22.4 |
| SCE1572_9006 | 48.42 | 68.47 |
| SCE1572_4254 | 8.92 | 3.07 |
| SCE1572_6660 | 38.97 | 37.26 |
| SCE1572_6434 | 136.98 | 37.03 |
| SCE1572_9096 | 37.9 | 101.96 |
| SCE1572_11386 | 102.18 | 417.2 |

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| SCE1572_5521 | 42.93 | 47.56 |
| SCE1572_2842 | 8.29 | 0 |
| SCE1572_10730 | 17.97 | 4.05 |
| SCE1572_2286 | 14.28 | 34.36 |
| SCE1572_11466 | 32.62 | 22.69 |
| SCE1572_1440 | 38.96 | 46.88 |
| SCE1572_9727 | 25.97 | 15.12 |
| SCE1572_5503 | 41.54 | 37.99 |
| SCE1572_10188 | 49.73 | 86.83 |
| SCE1572_3854 | 36.37 | 37.78 |
| SCE1572_9729 | 45.94 | 51.04 |
| SCE1572_888 | 36.71 | 3.84 |
| SCE1572_8618 | 44.06 | 31.19 |
| SCE1572_7014 | 14.44 | 2.9 |
| SCE1572_7244 | 0 | 0 |
| SCE1572_1233 | 43.54 | 14.86 |
| SCE1572_9239 | 55.13 | 24.88 |
| SCE1572_2490 | 42.53 | 17.19 |
| SCE1572_61 | 35.39 | 73.49 |
| SCE1572_6335 | 26.43 | 4.73 |
| SCE1572_6765 | 97.37 | 30.13 |
| SCE1572_9170 | 7.84 | 0 |
| SCE1572_268 | 0 | 0 |
| SCE1572_3927 | 174.8 | 279.06 |
| SCE1572_993 | 18.34 | 37.66 |
| SCE1572_8575 | 95.49 | 16.07 |
| SCE1572_11250 | 21.06 | 0 |
| SCE1572_2748 | 35.56 | 50.1 |
| SCE1572_6245 | 15.46 | 3.54 |
| SCE1572_10450 | 23.85 | 4.1 |
| SCE1572_44 | 32.3 | 47.5 |
| SCE1572_4878 | 9.52 | 4.58 |
| SCE1572_1646 | 0 | 0 |
| SCE1572_7509 | 0 | 0 |
| SCE1572_6008 | 60.29 | 597.53 |
| SCE1572_8285 | 44.09 | 83.78 |
| SCE1572_5281 | 49.24 | 41.38 |
| SCE1572_7812 | 140.01 | 1230.68 |
| SCE1572_10549 | 39.02 | 20.63 |
| SCE1572_172 | 143.42 | 59.18 |
| SCE1572_2944 | 70.19 | 28.72 |
| SCE1572_2332 | 76.18 | 70.21 |
| SCE1572_9460 | 24.33 | 8.28 |
| SCE1572_194 | 0 | 0 |
| SCE1572_4556 | 30.1 | 12.37 |
| SCE1572_11456 | 46.76 | 23.87 |
| SCE1572_869 | 0 | 0 |
| SCE1572_1905 | 7.29 | 0 |

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| SCE1572_7101 | 141.39 | 405.31 |
| SCE1572_11474 | 51.13 | 14.6 |
| SCE1572_5193 | 34.62 | 174.96 |
| SCE1572_5443 | 53.02 | 17.91 |
| SCE1572_4741 | 24.76 | 13.39 |
| SCE1572_10553 | 0 | 0 |
| SCE1572_3114 | 68.32 | 22.36 |
| SCE1572_4068 | 28.91 | 43.69 |
| SCE1572_11072 | 57.88 | 130.68 |
| SCE1572_9767 | 69.36 | 584.26 |
| SCE1572_756 | 0 | 0 |
| SCE1572_4464 | 84.71 | 27.41 |
| SCE1572_7980 | 38.62 | 30.98 |
| SCE1572_6512 | 36.27 | 12.58 |
| SCE1572_9297 | 112.18 | 426.09 |
| SCE1572_5574 | 58.44 | 40.19 |
| SCE1572_6775 | 0 | 0 |
| SCE1572_9184 | 29.76 | 16.22 |
| SCE1572_3090 | 86.98 | 84.21 |
| SCE1572_2940 | 19.85 | 40.18 |
| SCE1572_1007 | 63.26 | 163.65 |
| SCE1572_10101 | 14.53 | 7.65 |
| SCE1572_9664 | 32.31 | 167.51 |
| SCE1572_4521 | 12.94 | 4.45 |
| SCE1572_9451 | 0 | 0 |
| SCE1572_10349 | 0 | 0 |
| SCE1572_6063 | 9.19 | 0 |
| SCE1572_7711 | 32.27 | 84 |
| SCE1572_6040 | 145.2 | 224.62 |
| SCE1572_7295 | 83.18 | 95.55 |
| SCE1572_5612 | 56.76 | 110.41 |
| SCE1572_914 | 78.11 | 213.79 |
| SCE1572_7338 | 23.01 | 200.71 |
| SCE1572_9546 | 34.48 | 57.49 |
| SCE1572_2361 | 59.52 | 104.84 |
| SCE1572_10081 | 574.3 | 3500.73 |
| SCE1572_6425 | 40.68 | 10.01 |
| SCE1572_7087 | 40.32 | 17.28 |
| SCE1572_3122 | 62.01 | 24.28 |
| SCE1572_10629 | 37.57 | 146.47 |
| SCE1572_6183 | 44.99 | 13.54 |
| SCE1572_2407 | 77.91 | 313.22 |
| SCE1572_9479 | 109.09 | 121.27 |
| SCE1572_3946 | 330.25 | 346.86 |
| SCE1572_2018 | 14.29 | 13.37 |
| SCE1572_7193 | 36.12 | 44.33 |
| SCE1572_8678 | 16.04 | 10.53 |
| SCE1572_6295 | 40.55 | 237.62 |

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| SCE1572_4225 | 36.82 | 7.82 |
| SCE1572_9757 | 21.45 | 16.81 |
| SCE1572_2709 | 59.3 | 21.68 |
| SCE1572_1134 | 23.83 | 20.85 |
| SCE1572_5682 | 22.26 | 95.42 |
| SCE1572_6996 | 32.54 | 21.36 |
| SCE1572_4442 | 44.67 | 27.34 |
| SCE1572_10956 | 19.92 | 65.5 |
| SCE1572_3745 | 12.69 | 3.92 |
| SCE1572_4336 | 91.79 | 17.38 |
| SCE1572_3099 | 17.26 | 3.93 |
| SCE1572_11336 | 9.05 | 5.45 |
| SCE1572_1216 | 3.89 | 0 |
| SCE1572_535 | 24.19 | 64.43 |
| SCE1572_9158 | 58.69 | 31.39 |
| SCE1572_166 | 25.08 | 65.85 |
| SCE1572_3410 | 9.94 | 0 |
| SCE1572_2161 | 32.18 | 11.79 |
| SCE1572_3908 | 17.92 | 3.32 |
| SCE1572_6777 | 6.85 | 5.5 |
| SCE1572_6645 | 26.86 | 16.44 |
| SCE1572_3965 | 25.16 | 21.2 |
| SCE1572_4261 | 48.13 | 25.43 |
| SCE1572_2344 | 67.43 | 382.21 |
| SCE1572_6770 | 2.79 | 4.48 |
| SCE1572_1828 | 33.28 | 11.87 |
| SCE1572_5426 | 69.7 | 52.29 |
| SCE1572_7726 | 20.56 | 507.18 |
| SCE1572_598 | 23.45 | 13.17 |
| SCE1572_3901 | 35.71 | 81.43 |
| SCE1572_8478 | 6.13 | 0 |
| SCE1572_10284 | 40.07 | 147.9 |
| SCE1572_11240 | 32.66 | 31.81 |
| SCE1572_4461 | 201.41 | 21.55 |
| SCE1572_10638 | 19.56 | 0 |
| SCE1572_3799 | 64.44 | 220.36 |
| SCE1572_1786 | 39.15 | 73.91 |
| SCE1572_10158 | 21.02 | 12.04 |
| SCE1572_8338 | 74.65 | 51.95 |
| SCE1572_8980 | 73.3 | 24.17 |
| SCE1572_3954 | 30.96 | 21.42 |
| SCE1572_6417 | 0 | 0 |
| SCE1572_9079 | 0 | 0 |
| SCE1572_3083 | 33.21 | 7.36 |
| SCE1572_10595 | 55.11 | 14.81 |
| SCE1572_3328 | 137.1 | 392.1 |
| SCE1572_3434 | 73.01 | 136.28 |
| SCE1572_9984 | 72.32 | 35.93 |

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| SCE1572_8968 | 21.47 | 14.09 |
| SCE1572_39 | 34.71 | 29.24 |
| SCE1572_2411 | 62.39 | 244.78 |
| SCE1572_1999 | 10.86 | 5.23 |
| SCE1572_3318 | 9.93 | 30.2 |
| SCE1572_10817 | 27.66 | 20.49 |
| SCE1572_9696 | 50.39 | 125.01 |
| SCE1572_6524 | 120.64 | 122.81 |
| SCE1572_6569 | 15.99 | 95.57 |
| SCE1572_7689 | 0 | 0 |
| SCE1572_6110 | 46.96 | 19.38 |
| SCE1572_7027 | 37.87 | 52.19 |
| SCE1572_2816 | 83.72 | 36.49 |
| SCE1572_5263 | 0 | 0 |
| SCE1572_2933 | 0 | 0 |
| SCE1572_6272 | 35.59 | 58.97 |
| SCE1572_7271 | 27.57 | 9.76 |
| SCE1572_4318 | 44.97 | 8.62 |
| SCE1572_8239 | 40.9 | 111.64 |
| SCE1572_2660 | 0 | 0 |
| SCE1572_4415 | 29.23 | 6.59 |
| SCE1572_11571 | 27.71 | 1391.15 |
| SCE1572_308 | 30.14 | 69.19 |
| SCE1572_3326 | 31.48 | 65.81 |
| SCE1572_4125 | 18.45 | 7.67 |
| SCE1572_7515 | 26.55 | 30.93 |
| SCE1572_6405 | 30.11 | 39.42 |
| SCE1572_802 | 32.25 | 45.18 |
| SCE1572_9326 | 409.36 | 583.88 |
| SCE1572_4981 | 50.93 | 188.16 |
| SCE1572_7173 | 38.98 | 160.3 |
| SCE1572_8233 | 13.81 | 23.75 |
| SCE1572_10355 | 25.11 | 167.91 |
| SCE1572_8626 | 76.35 | 49.88 |
| SCE1572_822 | 5.83 | 0 |
| SCE1572_2586 | 9.18 | 3.22 |
| SCE1572_1120 | 35.94 | 13.71 |
| SCE1572_10702 | 12.85 | 142.26 |
| SCE1572_9415 | 3.3 | 0 |
| SCE1572_6120 | 64 | 57.66 |
| SCE1572_3047 | 24.02 | 12.85 |
| SCE1572_1540 | 21.04 | 46.23 |
| SCE1572_7232 | 55.31 | 22.03 |
| SCE1572_3848 | 15.45 | 9.64 |
| SCE1572_7998 | 25.73 | 12.25 |
| SCE1572_8882 | 0 | 0 |
| SCE1572_4751 | 44.2 | 178.74 |
| SCE1572_6050 | 0 | 0 |

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| SCE1572_10386 | 57.77 | 26.78 |
| SCE1572_9410 | 91.01 | 1580.21 |
| SCE1572_3578 | 9.99 | 32.78 |
| SCE1572_9550 | 160.39 | 108.57 |
| SCE1572_6199 | 4.15 | 0 |
| SCE1572_4504 | 56.07 | 30.41 |
| SCE1572_7179 | 25.63 | 15.42 |
| SCE1572_7040 | 12.55 | 0 |
| SCE1572_4185 | 29.75 | 50.92 |
| SCE1572_2868 | 37.18 | 33.7 |
| SCE1572_304 | 78.61 | 22.36 |
| SCE1572_11445 | 58.57 | 83.87 |
| SCE1572_4021 | 31.03 | 45.09 |
| SCE1572_4574 | 23.51 | 14.28 |
| SCE1572_2367 | 0 | 0 |
| SCE1572_1750 | 39.93 | 37.61 |
| SCE1572_986 | 99.98 | 372.81 |
| SCE1572_7378 | 8.59 | 7.39 |
| SCE1572_1790 | 21.1 | 5.9 |
| SCE1572_2796 | 23.16 | 22.81 |
| SCE1572_2184 | 55.55 | 18.09 |
| SCE1572_2119 | 54.1 | 111.36 |
| SCE1572_6351 | 64.54 | 19.32 |
| SCE1572_8494 | 6.49 | 0 |
| SCE1572_8812 | 41.85 | 16.51 |
| SCE1572_898 | 18.28 | 11.65 |
| SCE1572_11468 | 51.52 | 152.35 |
| SCE1572_6079 | 0 | 0 |
| SCE1572_8680 | 21.04 | 17.87 |
| SCE1572_3347 | 159.06 | 85.59 |
| SCE1572_6055 | 117.56 | 171.88 |
| SCE1572_5153 | 36.18 | 10.76 |
| SCE1572_119 | 82.41 | 223.79 |
| SCE1572_8896 | 65.51 | 322.12 |
| SCE1572_1242 | 59.85 | 64.75 |
| SCE1572_3419 | 63.59 | 79.36 |
| SCE1572_9666 | 2.31 | 16.67 |
| SCE1572_2487 | 34.28 | 133.9 |
| SCE1572_1264 | 0 | 0 |
| SCE1572_5098 | 59.33 | 254.61 |
| SCE1572_2474 | 43.16 | 295.06 |
| SCE1572_3592 | 16.01 | 13.6 |
| SCE1572_1830 | 37.72 | 38.07 |
| SCE1572_5597 | 82.17 | 300.16 |
| SCE1572_7095 | 61.94 | 22.69 |
| SCE1572_10249 | 0 | 0 |
| SCE1572_4482 | 75.5 | 182.21 |
| SCE1572_161 | 34.44 | 9.91 |

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| SCE1572_4585 | 30.55 | 40.1 |
| SCE1572_63 | 28.54 | 25.34 |
| SCE1572_2872 | 25.86 | 18.76 |
| SCE1572_2379 | 22.92 | 100.42 |
| SCE1572_6262 | 24.11 | 14.95 |
| SCE1572_5456 | 11.43 | 4.23 |
| SCE1572_8360 | 16.51 | 3.61 |
| SCE1572_7880 | 34.24 | 35.32 |
| SCE1572_6935 | 48.48 | 48.41 |
| SCE1572_6679 | 48.52 | 40.14 |
| SCE1572_3121 | 38.44 | 64.86 |
| SCE1572_4352 | 0 | 0 |
| SCE1572_1623 | 0 | 0 |
| SCE1572_8671 | 13.78 | 4.74 |
| SCE1572_10766 | 62.82 | 3112.93 |
| SCE1572_4866 | 23.94 | 220 |
| SCE1572_1285 | 93.23 | 1921.58 |
| SCE1572_9791 | 0 | 0 |
| SCE1572_24 | 35.91 | 47.06 |
| SCE1572_9539 | 41.18 | 9.01 |
| SCE1572_3941 | 648.03 | 891.46 |
| SCE1572_6796 | 66.96 | 127.72 |
| SCE1572_9330 | 334.31 | 1053.97 |
| SCE1572_1657 | 39.51 | 33.17 |
| SCE1572_3963 | 63.31 | 19.25 |
| SCE1572_7879 | 53.99 | 46.69 |
| SCE1572_5175 | 33.88 | 17.97 |
| SCE1572_8423 | 92.88 | 60.82 |
| SCE1572_4437 | 0 | 0 |
| SCE1572_2421 | 20.39 | 33.01 |
| SCE1572_6988 | 22.28 | 3.92 |
| SCE1572_11010 | 29.03 | 144.07 |
| SCE1572_5170 | 54.88 | 683.28 |
| SCE1572_8563 | 74.48 | 464.16 |
| SCE1572_3747 | 0 | 0 |
| SCE1572_3998 | 28.74 | 52.28 |
| SCE1572_4977 | 59.38 | 991.07 |
| SCE1572_6959 | 2.57 | 0 |
| SCE1572_1684 | 48.48 | 63.3 |
| SCE1572_7333 | 0 | 0 |
| SCE1572_3804 | 18.48 | 7.6 |
| SCE1572_9627 | 52.96 | 19.9 |
| SCE1572_7297 | 48.88 | 24.01 |
| SCE1572_3672 | 28.19 | 17.38 |
| SCE1572_1107 | 63.63 | 14.18 |
| SCE1572_11117 | 33.19 | 21.79 |
| SCE1572_11541 | 24.26 | 2.43 |
| SCE1572_10815 | 13.48 | 9.93 |

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| SCE1572_11555 | 33.59 | 14.63 |
| SCE1572_7690 | 33.13 | 104.59 |
| SCE1572_6318 | 13.15 | 8.33 |
| SCE1572_6941 | 24.49 | 10.4 |
| SCE1572_8 | 75.18 | 78.85 |
| SCE1572_9759 | 44.12 | 17.38 |
| SCE1572_7657 | 39.68 | 26.94 |
| SCE1572_6851 | 7.26 | 4.37 |
| SCE1572_7002 | 0 | 0 |
| SCE1572_9166 | 55.81 | 15.67 |
| SCE1572_2975 | 35.64 | 7.09 |
| SCE1572_4128 | 23.33 | 25.52 |
| SCE1572_2261 | 37.23 | 119.46 |
| SCE1572_4234 | 40.5 | 12.5 |
| SCE1572_461 | 16.68 | 7.3 |
| SCE1572_9873 | 18.38 | 14.74 |
| SCE1572_9372 | 41.12 | 25.77 |
| SCE1572_72 | 42.15 | 57.19 |
| SCE1572_228 | 24.86 | 0 |
| SCE1572_82 | 0 | 0 |
| SCE1572_5341 | 39.42 | 44.14 |
| SCE1572_10486 | 18.95 | 34.21 |
| SCE1572_6682 | 46.65 | 303.68 |
| SCE1572_9571 | 17.2 | 18.58 |
| SCE1572_9040 | 26.68 | 171.25 |
| SCE1572_11052 | 59.33 | 684.75 |
| SCE1572_11360 | 125.74 | 569.24 |
| SCE1572_5202 | 16.77 | 26.07 |
| SCE1572_6880 | 2.26 | 0 |
| SCE1572_4610 | 16.04 | 14.48 |
| SCE1572_7675 | 58.7 | 15.1 |
| SCE1572_1661 | 52.43 | 155.75 |
| SCE1572_7892 | 492.21 | 22628.64 |
| SCE1572_9047 | 5.14 | 0 |
| SCE1572_5277 | 0 | 0 |
| SCE1572_5998 | 30.12 | 58.98 |
| SCE1572_8266 | 156.42 | 118.06 |
| SCE1572_938 | 20.22 | 20.85 |
| SCE1572_7383 | 140.14 | 51.29 |
| SCE1572_2457 | 2.81 | 0 |
| SCE1572_2054 | 100 | 143.64 |
| SCE1572_571 | 0 | 0 |
| SCE1572_4856 | 44.2 | 12.77 |
| SCE1572_591 | 103.15 | 156.24 |
| SCE1572_4653 | 71.56 | 33.37 |
| SCE1572_3661 | 28.72 | 5.67 |
| SCE1572_10229 | 14.21 | 11.4 |
| SCE1572_6595 | 0 | 0 |

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| SCE1572_10091 | 80.53 | 462.5 |
| SCE1572_4346 | 0 | 0 |
| SCE1572_2896 | 42.03 | 10.84 |
| SCE1572_692 | 20.22 | 24.33 |
| SCE1572_881 | 75.1 | 109.82 |
| SCE1572_4474 | 0 | 0 |
| SCE1572_7801 | 68.98 | 112.6 |
| SCE1572_6981 | 105.01 | 9.46 |
| SCE1572_2582 | 52.61 | 28.47 |
| SCE1572_5949 | 37.77 | 20.52 |
| SCE1572_6269 | 13.87 | 40.05 |
| SCE1572_11015 | 10.11 | 9.73 |
| SCE1572_5129 | 0 | 0 |
| SCE1572_1584 | 44.8 | 215.64 |
| SCE1572_427 | 29.45 | 338.67 |
| SCE1572_857 | 85.62 | 1850.37 |
| SCE1572_3371 | 28.11 | 15.31 |
| SCE1572_6197 | 3.76 | 3.02 |
| SCE1572_640 | 9.88 | 16.64 |
| SCE1572_9128 | 33.69 | 192.6 |
| SCE1572_1193 | 35.91 | 62.74 |
| SCE1572_5713 | 118.13 | 62.69 |
| SCE1572_7201 | 25.96 | 22.09 |
| SCE1572_11346 | 25.45 | 105.89 |
| SCE1572_11037 | 34.96 | 166.78 |
| SCE1572_7343 | 42.74 | 48.98 |
| SCE1572_8128 | 31.22 | 0 |
| SCE1572_1226 | 46.75 | 14.72 |
| SCE1572_513 | 35.22 | 17.76 |
| SCE1572_5913 | 7.37 | 3.73 |
| SCE1572_1944 | 54.87 | 18.15 |
| SCE1572_2663 | 29.78 | 19.55 |
| SCE1572_4762 | 66.68 | 1070.27 |
| SCE1572_3875 | 49.53 | 100.32 |
| SCE1572_9233 | 39.69 | 174.56 |
| SCE1572_3797 | 38.64 | 55.42 |
| SCE1572_9285 | 13.43 | 16.16 |
| SCE1572_11165 | 33.69 | 5.59 |
| SCE1572_9532 | 62.53 | 973.13 |
| SCE1572_8340 | 0 | 0 |
| SCE1572_9803 | 22.16 | 35.16 |
| SCE1572_8719 | 29.54 | 16.73 |
| SCE1572_7418 | 0 | 0 |
| SCE1572_4619 | 0 | 0 |
| SCE1572_3836 | 16.85 | 0 |
| SCE1572_1873 | 17.89 | 8.2 |
| SCE1572_7970 | 24.24 | 37.24 |
| SCE1572_3265 | 0 | 0 |

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| SCE1572_7069 | 54.44 | 207.34 |
| SCE1572_8463 | 111.48 | 491.29 |
| SCE1572_7553 | 25.08 | 13.72 |
| SCE1572_11110 | 58.96 | 170.52 |
| SCE1572_3915 | 8.39 | 0 |
| SCE1572_5528 | 52.99 | 27.33 |
| SCE1572_6920 | 43.32 | 0 |
| SCE1572_9578 | 44.36 | 16.22 |
| SCE1572_8019 | 0 | 0.01 |
| SCE1572_8538 | 33.65 | 28.58 |
| SCE1572_10597 | 64.98 | 17.38 |
| SCE1572_3834 | 3.7 | 0 |
| SCE1572_261 | 33.17 | 10.26 |
| SCE1572_877 | 222.04 | 449.68 |
| SCE1572_7620 | 21.32 | 19.86 |
| SCE1572_8823 | 40.3 | 25.41 |
| SCE1572_10432 | 38.98 | 24.38 |
| SCE1572_3485 | 44.59 | 33.6 |
| SCE1572_9925 | 222.8 | 704.88 |
| SCE1572_736 | 36.15 | 26.58 |
| SCE1572_7536 | 65.42 | 17.24 |
| SCE1572_9893 | 22.83 | 12.7 |
| SCE1572_3474 | 24.22 | 10.6 |
| SCE1572_4680 | 4.15 | 0 |
| SCE1572_5298 | 24.42 | 23.23 |
| SCE1572_940 | 53.04 | 14.8 |
| SCE1572_8983 | 4.94 | 0 |
| SCE1572_6162 | 31.72 | 43.52 |
| SCE1572_11509 | 27.99 | 19.34 |
| SCE1572_9247 | 35.26 | 7.64 |
| SCE1572_8387 | 112.31 | 23.65 |
| SCE1572_10404 | 30.85 | 25.17 |
| SCE1572_7127 | 3.16 | 0 |
| SCE1572_7652 | 68.11 | 27.32 |
| SCE1572_1001 | 0 | 0 |
| SCE1572_3203 | 32.87 | 391.72 |
| SCE1572_2243 | 61.24 | 34.79 |
| SCE1572_10340 | 29.61 | 9.38 |
| SCE1572_4698 | 6.77 | 3.26 |
| SCE1572_92 | 89.36 | 198.98 |
| SCE1572_547 | 13.91 | 14.62 |
| SCE1572_8219 | 28.43 | 30.41 |
| SCE1572_4004 | 0 | 0 |
| SCE1572_4774 | 41.81 | 0 |
| SCE1572_5326 | 0 | 0 |
| SCE1572_6895 | 0 | 0 |
| SCE1572_6208 | 0 | 0 |
| SCE1572_6946 | 29.09 | 16.38 |

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| SCE1572_406 | 3.37 | 0 |
| SCE1572_6188 | 14.88 | 10.07 |
| SCE1572_5364 | 12.43 | 0 |
| SCE1572_3196 | 48.42 | 136.93 |
| SCE1572_3934 | 0 | 0 |
| SCE1572_8611 | 32.87 | 12.92 |
| SCE1572_6810 | 197.42 | 543.58 |
| SCE1572_8806 | 0 | 0 |
| SCE1572_4158 | 64.98 | 34.09 |
| SCE1572_625 | 0 | 0 |
| SCE1572_9337 | 83.96 | 251.67 |
| SCE1572_9717 | 95.36 | 1145.26 |
| SCE1572_848 | 59.17 | 42.73 |
| SCE1572_9658 | 16.98 | 35.54 |
| SCE1572_6828 | 16.68 | 13.21 |
| SCE1572_7207 | 9.24 | 28.19 |
| SCE1572_5783 | 24.59 | 46.62 |
| SCE1572_7362 | 18.49 | 4.45 |
| SCE1572_6948 | 29.55 | 24.36 |
| SCE1572_6328 | 37.74 | 67.35 |
| SCE1572_5971 | 82.64 | 157.8 |
| SCE1572_11515 | 6.2 | 6.78 |
| SCE1572_9998 | 16.6 | 3.77 |
| SCE1572_7827 | 159.43 | 466.5 |
| SCE1572_11498 | 0 | 0 |
| SCE1572_8627 | 23.22 | 14.82 |
| SCE1572_6396 | 13.27 | 44.85 |
| SCE1572_1816 | 18.66 | 5.61 |
| SCE1572_1689 | 34.99 | 47.72 |
| SCE1572_540 | 29.26 | 18.76 |
| SCE1572_4847 | 41.19 | 69.61 |
| SCE1572_54 | 28.73 | 14.89 |
| SCE1572_2120 | 51.89 | 85.78 |
| SCE1572_1480 | 64.59 | 20.95 |
| SCE1572_3175 | 47.89 | 87.95 |
| SCE1572_6472 | 15.5 | 2.33 |
| SCE1572_5395 | 0 | 0 |
| SCE1572_7930 | 109.01 | 50.42 |
| SCE1572_6485 | 17.57 | 23.49 |
| SCE1572_2317 | 14.21 | 9.12 |
| SCE1572_11521 | 27.57 | 10.3 |
| SCE1572_6877 | 77.71 | 187.42 |
| SCE1572_2337 | 17.4 | 9.97 |
| SCE1572_9657 | 26.5 | 26.27 |
| SCE1572_99 | 29.08 | 15 |
| SCE1572_10461 | 44 | 198.87 |
| SCE1572_2610 | 23.85 | 41 |
| SCE1572_2693 | 13.36 | 5.8 |

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| SCE1572_5047 | 36.94 | 48.16 |
| SCE1572_465 | 41.95 | 99.2 |
| SCE1572_1806 | 21.83 | 14.6 |
| SCE1572_1545 | 37.9 | 28.17 |
| SCE1572_10098 | 21.79 | 88.16 |
| SCE1572_783 | 51.08 | 20.7 |
| SCE1572_9872 | 51.27 | 243.28 |
| SCE1572_1542 | 11.37 | 29.65 |
| SCE1572_6838 | 89.19 | 47.7 |
| SCE1572_283 | 41.09 | 32.97 |
| SCE1572_4492 | 33.69 | 27.47 |
| SCE1572_850 | 52.08 | 176.1 |
| SCE1572_3599 | 25.27 | 44.82 |
| SCE1572_9433 | 136.62 | 180.46 |
| SCE1572_1837 | 73.88 | 139.06 |
| SCE1572_10439 | 194.26 | 713.55 |
| SCE1572_10075 | 901.55 | 1765.8 |
| SCE1572_10995 | 42.06 | 28.49 |
| SCE1572_5183 | 23.82 | 457.2 |
| SCE1572_10468 | 12.81 | 5.14 |
| SCE1572_10502 | 43.55 | 33.89 |
| SCE1572_1563 | 20.77 | 0 |
| SCE1572_8311 | 7.17 | 1.26 |
| SCE1572_3752 | 75.25 | 145.97 |
| SCE1572_4381 | 18.06 | 8.21 |
| SCE1572_164 | 21.6 | 13.48 |
| SCE1572_2810 | 4.79 | 0 |
| SCE1572_4276 | 43.84 | 24.43 |
| SCE1572_5476 | 32.92 | 843.63 |
| SCE1572_10133 | 13.3 | 10.06 |
| SCE1572_11496 | 72.29 | 20.02 |
| SCE1572_3154 | 11.05 | 11.82 |
| SCE1572_10954 | 76.64 | 22.72 |
| SCE1572_11204 | 63.75 | 141.64 |
| SCE1572_6699 | 23.72 | 11.58 |
| SCE1572_6692 | 6.23 | 0 |
| SCE1572_2592 | 0 | 0 |
| SCE1572_11437 | 39.98 | 61.73 |
| SCE1572_4044 | 23.58 | 61.63 |
| SCE1572_4691 | 38.81 | 65.69 |
| SCE1572_5415 | 44.23 | 12.45 |
| SCE1572_4748 | 86.18 | 42.25 |
| SCE1572_7421 | 23.33 | 9.36 |
| SCE1572_5627 | 43.8 | 6.08 |
| SCE1572_6284 | 40.96 | 81.29 |
| SCE1572_6442 | 71.5 | 40.55 |
| SCE1572_916 | 0 | 0 |
| SCE1572_240 | 19.77 | 0 |

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| SCE1572_11184 | 20.96 | 4.45 |
| SCE1572_6705 | 567.87 | 2153.41 |
| SCE1572_4810 | 0 | 0 |
| SCE1572_2750 | 41.87 | 62.59 |
| SCE1572_5828 | 16.52 | 9.23 |
| SCE1572_7923 | 9.37 | 2.05 |
| SCE1572_7154 | 14.56 | 9.67 |
| SCE1572_9510 | 9.3 | 0 |
| SCE1572_7887 | 79.1 | 393.68 |
| SCE1572_9937 | 17.33 | 0 |
| SCE1572_4961 | 22.81 | 96.88 |
| SCE1572_8370 | 30.89 | 10.3 |
| SCE1572_2727 | 26.49 | 13.19 |
| SCE1572_8092 | 16.07 | 2.42 |
| SCE1572_8693 | 45.12 | 9.78 |
| SCE1572_2531 | 20.49 | 0 |
| SCE1572_746 | 35.05 | 51.33 |
| SCE1572_2099 | 20.11 | 12.41 |
| SCE1572_5565 | 78.24 | 58.54 |
| SCE1572_10542 | 80.2 | 53.54 |
| SCE1572_9272 | 37.06 | 35.68 |
| SCE1572_7316 | 0 | 0 |
| SCE1572_8991 | 11.17 | 23.05 |
| SCE1572_9863 | 56.46 | 21.82 |
| SCE1572_5231 | 61.79 | 235.7 |
| SCE1572_840 | 40.85 | 102.1 |
| SCE1572_11308 | 24.93 | 5.75 |
| SCE1572_2198 | 0 | 0 |
| SCE1572_10222 | 21.92 | 36.64 |
| SCE1572_4626 | 146.64 | 260.35 |
| SCE1572_11257 | 47.93 | 77.69 |
| SCE1572_10224 | 144.92 | 96.68 |
| SCE1572_6698 | 19.53 | 20.15 |
| SCE1572_580 | 16.48 | 37.02 |
| SCE1572_6523 | 2.37 | 0 |
| SCE1572_5519 | 0 | 0 |
| SCE1572_8347 | 51.48 | 54.21 |
| SCE1572_10511 | 0 | 0 |
| SCE1572_444 | 27.27 | 7.88 |
| SCE1572_5371 | 63.77 | 83.72 |
| SCE1572_7543 | 17.02 | 72.24 |
| SCE1572_7928 | 93.1 | 73.17 |
| SCE1572_6072 | 34.19 | 14.31 |
| SCE1572_6289 | 11.35 | 25.72 |
| SCE1572_7872 | 94.81 | 299.73 |
| SCE1572_7766 | 19.86 | 7.59 |
| SCE1572_7584 | 20.13 | 0 |
| SCE1572_2304 | 67.56 | 194.56 |

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| SCE1572_10314 | 30.72 | 4.77 |
| SCE1572_6450 | 55.03 | 42.87 |
| SCE1572_9907 | 38.53 | 62.5 |
| SCE1572_385 | 2.76 | 0 |
| SCE1572_10765 | 32.54 | 270.58 |
| SCE1572_647 | 0 | 0 |
| SCE1572_8929 | 32.26 | 116.46 |
| SCE1572_6354 | 10.16 | 3.76 |
| SCE1572_5287 | 38.29 | 243.28 |
| SCE1572_6201 | 45.24 | 20.74 |
| SCE1572_9991 | 52.67 | 15.39 |
| SCE1572_395 | 38.2 | 54.41 |
| SCE1572_9673 | 36.31 | 119.6 |
| SCE1572_774 | 63.97 | 153.09 |
| SCE1572_10195 | 16.68 | 5.47 |
| SCE1572_796 | 83.72 | 163.41 |
| SCE1572_1428 | 23.47 | 7.17 |
| SCE1572_1400 | 15.32 | 15.53 |
| SCE1572_2573 | 34.13 | 9.39 |
| SCE1572_5836 | 27.07 | 26.07 |
| SCE1572_11301 | 21.02 | 57.81 |
| SCE1572_2655 | 29.85 | 21.43 |
| SCE1572_4710 | 14.94 | 8.46 |
| SCE1572_479 | 36.74 | 11.18 |
| SCE1572_5447 | 54.65 | 19.8 |
| SCE1572_6103 | 15.09 | 6.92 |
| SCE1572_3603 | 168.43 | 104.26 |
| SCE1572_4110 | 20.33 | 4.98 |
| SCE1572_813 | 26.3 | 12.1 |
| SCE1572_8604 | 14.18 | 29.49 |
| SCE1572_8055 | 20.14 | 17.11 |
| SCE1572_5747 | 6.1 | 1.83 |
| SCE1572_1893 | 3.74 | 38.29 |
| SCE1572_2990 | 8.42 | 0 |
| SCE1572_3542 | 0 | 0 |
| SCE1572_5938 | 14.21 | 3.8 |
| SCE1572_1912 | 27.13 | 0 |
| SCE1572_10333 | 0 | 0 |
| SCE1572_967 | 0 | 0 |
| SCE1572_11447 | 64.18 | 61.45 |
| SCE1572_8007 | 54.01 | 1130.54 |
| SCE1572_780 | 23.58 | 8.11 |
| SCE1572_10863 | 31.11 | 362.81 |
| SCE1572_6841 | 90.88 | 116.16 |
| SCE1572_9493 | 0 | 0 |
| SCE1572_10754 | 35.69 | 14.81 |
| SCE1572_6212 | 67.53 | 26.98 |
| SCE1572_1405 | 17.15 | 11.56 |

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| SCE1572_5390 | 0 | 0 |
| SCE1572_7572 | 77.12 | 177.72 |
| SCE1572_8821 | 9.52 | 22.91 |
| SCE1572_1339 | 21.25 | 105.18 |
| SCE1572_4924 | 32.34 | 51.9 |
| SCE1572_7839 | 30.96 | 42.4 |
| SCE1572_533 | 14.13 | 49.48 |
| SCE1572_6340 | 27.77 | 23.34 |
| SCE1572_1485 | 43.58 | 36.99 |
| SCE1572_6969 | 49.29 | 442.22 |
| SCE1572_4180 | 8.37 | 17.62 |
| SCE1572_6543 | 94.08 | 115.67 |
| SCE1572_7713 | 22.74 | 10.14 |
| SCE1572_1020 | 28.36 | 100.03 |
| SCE1572_1352 | 43.37 | 62.15 |
| SCE1572_6221 | 59.17 | 31.15 |
| SCE1572_4928 | 3.94 | 0 |
| SCE1572_11194 | 33.49 | 168.54 |
| SCE1572_8274 | 18.84 | 32.07 |
| SCE1572_7612 | 43.5 | 88.07 |
| SCE1572_8192 | 28.25 | 13.88 |
| SCE1572_2938 | 44.56 | 84.21 |
| SCE1572_1723 | 9.92 | 6.82 |
| SCE1572_10164 | 44.66 | 14.14 |
| SCE1572_10441 | 14.39 | 42.62 |
| SCE1572_10980 | 9.48 | 16.67 |
| SCE1572_3704 | 41.35 | 193.94 |
| SCE1572_2165 | 85.65 | 47.38 |
| SCE1572_2117 | 62.68 | 105.05 |
| SCE1572_4941 | 15.33 | 23.92 |
| SCE1572_8030 | 61.42 | 51.71 |
| SCE1572_6903 | 51.13 | 12.09 |
| SCE1572_4896 | 5.93 | 4.08 |
| SCE1572_7270 | 118.57 | 95.13 |
| SCE1572_7226 | 40.89 | 149.66 |
| SCE1572_6720 | 5434.99 | 20079.31 |
| SCE1572_9067 | 26.33 | 17.48 |
| SCE1572_8853 | 5.83 | 3.51 |
| SCE1572_3409 | 30.98 | 18.31 |
| SCE1572_4072 | 50.16 | 134.85 |
| SCE1572_1230 | 31.96 | 39.31 |
| SCE1572_9833 | 31.07 | 10.32 |
| SCE1572_4537 | 24.51 | 10.34 |
| SCE1572_5721 | 66.41 | 68.36 |
| SCE1572_11218 | 30.09 | 22.5 |
| SCE1572_4782 | 59.03 | 47.86 |
| SCE1572_10205 | 60.04 | 14.7 |
| SCE1572_5110 | 34.42 | 311.44 |

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| SCE1572_4953 | 41.05 | 25.11 |
| SCE1572_4499 | 57.15 | 43.94 |
| SCE1572_5453 | 44.98 | 14.6 |
| SCE1572_1383 | 0 | 0 |
| SCE1572_10128 | 2.08 | 0 |
| SCE1572_3035 | 15.05 | 6.19 |
| SCE1572_3385 | 39.14 | 40.74 |
| SCE1572_2578 | 22.33 | 4.09 |
| SCE1572_8254 | 37.3 | 1859.59 |
| SCE1572_10620 | 28.12 | 22.56 |
| SCE1572_4986 | 16.9 | 43.07 |
| SCE1572_6819 | 33.41 | 4.64 |
| SCE1572_7748 | 11.73 | 1.13 |
| SCE1572_1165 | 41.5 | 46.29 |
| SCE1572_6381 | 24.19 | 139.76 |
| SCE1572_3296 | 0 | 0 |
| SCE1572_5450 | 46.61 | 44.38 |
| SCE1572_7191 | 183.26 | 425.21 |
| SCE1572_2557 | 58.89 | 28.13 |
| SCE1572_3615 | 43.49 | 14.14 |
| SCE1572_10857 | 105.29 | 66.69 |
| SCE1572_4117 | 14.63 | 2131.91 |
| SCE1572_6867 | 191.38 | 182.46 |
| SCE1572_8380 | 17.84 | 18.4 |
| SCE1572_1761 | 61.48 | 16.82 |
| SCE1572_10234 | 15.04 | 0 |
| SCE1572_10232 | 58.31 | 12.96 |
| SCE1572_1579 | 23.18 | 25.57 |
| SCE1572_5315 | 21.94 | 33.61 |
| SCE1572_4151 | 27.96 | 251.34 |
| SCE1572_3657 | 13.24 | 14.29 |
| SCE1572_10615 | 54.18 | 32.83 |
| SCE1572_1341 | 54.93 | 342.45 |
| SCE1572_8243 | 113.07 | 261.01 |
| SCE1572_7414 | 10.29 | 1.65 |
| SCE1572_10911 | 3.92 | 0 |
| SCE1572_5225 | 204.22 | 610.69 |
| SCE1572_2396 | 9.83 | 25.64 |
| SCE1572_4400 | 18.31 | 9.04 |
| SCE1572_8842 | 38.6 | 55.97 |
| SCE1572_10419 | 88.97 | 43.7 |
| SCE1572_7959 | 14.01 | 24.53 |
| SCE1572_1153 | 43.96 | 133.98 |
| SCE1572_5336 | 25.93 | 16.01 |
| SCE1572_4719 | 28.43 | 9.02 |
| SCE1572_6586 | 241.25 | 55.08 |
| SCE1572_7897 | 17.56 | 38.41 |
| SCE1572_11158 | 50.28 | 47.83 |

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|---------------|--------|---------|
| SCE1572_3884 | 38.88 | 14.04 |
| SCE1572_8080 | 25.54 | 3.84 |
| SCE1572_3106 | 56.57 | 103.49 |
| SCE1572_8814 | 23.07 | 11.38 |
| SCE1572_5302 | 48.38 | 12.48 |
| SCE1572_8654 | 411.33 | 2273.81 |
| SCE1572_10843 | 19.25 | 0 |
| SCE1572_7605 | 39.96 | 22.63 |
| SCE1572_1593 | 45.39 | 83.68 |
| SCE1572_11127 | 43.76 | 29.67 |
| SCE1572_6369 | 43.48 | 42.04 |
| SCE1572_741 | 17.2 | 27.23 |
| SCE1572_1749 | 41.06 | 32.31 |
| SCE1572_11146 | 35.84 | 75.75 |
| SCE1572_6097 | 32.07 | 54.39 |
| SCE1572_7486 | 18.42 | 14.43 |
| SCE1572_10655 | 77.86 | 601.63 |
| SCE1572_4816 | 2.61 | 0 |
| SCE1572_2034 | 64.65 | 113.42 |
| SCE1572_1214 | 21.41 | 12.37 |
| SCE1572_10804 | 56.12 | 20.16 |
| SCE1572_4252 | 62.5 | 22.29 |
| SCE1572_11597 | 68.88 | 813.26 |
| SCE1572_6887 | 16.41 | 3.76 |
| SCE1572_7811 | 18.44 | 4.93 |
| SCE1572_1359 | 61.74 | 193.19 |
| SCE1572_10714 | 37.78 | 10.36 |
| SCE1572_5251 | 65.33 | 273.36 |
| SCE1572_7395 | 21.56 | 3.46 |
| SCE1572_587 | 28.34 | 12.87 |
| SCE1572_6808 | 97.31 | 380.45 |
| SCE1572_2363 | 20.07 | 10.73 |
| SCE1572_9844 | 13.24 | 28.96 |
| SCE1572_10526 | 24.72 | 11.9 |
| SCE1572_9342 | 211.46 | 2837.75 |
| SCE1572_4146 | 25.94 | 9.76 |
| SCE1572_7281 | 14.52 | 67.11 |
| SCE1572_4372 | 49.84 | 18.75 |
| SCE1572_814 | 16.4 | 6.4 |
| SCE1572_5025 | 23.6 | 16.71 |
| SCE1572_1083 | 31.13 | 4.83 |
| SCE1572_6457 | 23.66 | 12.27 |
| SCE1572_3233 | 31.11 | 20.49 |
| SCE1572_671 | 23.92 | 79.72 |
| SCE1572_4379 | 16.24 | 6.17 |
| SCE1572_10683 | 88.3 | 196.98 |
| SCE1572_1027 | 29.71 | 746.96 |
| SCE1572_1631 | 39.24 | 8.59 |

| | | |
|---------------|--------|---------|
| SCE1572_8958 | 22 | 39.82 |
| SCE1572_7873 | 75.81 | 264.33 |
| SCE1572_233 | 14.36 | 34.57 |
| SCE1572_10045 | 590.27 | 6756.38 |
| SCE1572_344 | 59.95 | 18.04 |
| SCE1572_5842 | 65.03 | 17.92 |
| SCE1572_5402 | 31.45 | 20.34 |
| SCE1572_10627 | 38.24 | 122.28 |
| SCE1572_1 | 78.06 | 479.35 |
| SCE1572_5460 | 25.62 | 1.26 |
| SCE1572_5738 | 178.92 | 188.51 |
| SCE1572_5815 | 13 | 13.21 |
| SCE1572_6362 | 114.77 | 84.32 |
| SCE1572_247 | 92.48 | 22.52 |
| SCE1572_2757 | 32.34 | 20.42 |
| SCE1572_8113 | 32.41 | 9.75 |
| SCE1572_6567 | 32.64 | 57.67 |
| SCE1572_3516 | 20.66 | 84.43 |
| SCE1572_10268 | 42.08 | 28.88 |
| SCE1572_4095 | 24.93 | 20.61 |
| SCE1572_6711 | 55.01 | 96.88 |
| SCE1572_7319 | 30.99 | 40.32 |
| SCE1572_8996 | 22.93 | 32.49 |
| SCE1572_10202 | 78.2 | 30.23 |
| SCE1572_4229 | 37.35 | 25.9 |
| SCE1572_10113 | 21.02 | 45.77 |
| SCE1572_3289 | 44.63 | 26.07 |
| SCE1572_5800 | 55.13 | 154.08 |
| SCE1572_2827 | 32.9 | 6.89 |
| SCE1572_10116 | 25.56 | 49.5 |
| SCE1572_8211 | 49.29 | 63.61 |
| SCE1572_6952 | 45.21 | 11.72 |
| SCE1572_1962 | 54.18 | 20.22 |
| SCE1572_9390 | 33.3 | 61.39 |
| SCE1572_960 | 52.66 | 96.15 |
| SCE1572_10946 | 51.87 | 23.63 |
| SCE1572_2999 | 13.86 | 5.89 |
| SCE1572_1927 | 30.61 | 57.39 |
| SCE1572_9035 | 25.99 | 12.74 |
| SCE1572_10724 | 0 | 0 |
| SCE1572_4058 | 16.13 | 10.35 |
| SCE1572_6655 | 24.99 | 12.3 |
| SCE1572_438 | 0 | 0 |
| SCE1572_5849 | 22.07 | 4.62 |
| SCE1572_6601 | 100.27 | 115.95 |
| SCE1572_8322 | 24.83 | 91.23 |
| SCE1572_10662 | 44.4 | 34 |
| SCE1572_10127 | 12.03 | 5.79 |

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|---------------|--------|---------|
| SCE1572_3361 | 22.58 | 0 |
| SCE1572_5931 | 11.76 | 6.53 |
| SCE1572_7120 | 60.96 | 32.95 |
| SCE1572_8914 | 22.13 | 7.99 |
| SCE1572_7213 | 112.71 | 16.15 |
| SCE1572_5808 | 56.18 | 23.15 |
| SCE1572_1738 | 32.49 | 0 |
| SCE1572_1178 | 43.75 | 16.68 |
| SCE1572_5531 | 55.79 | 0 |
| SCE1572_3085 | 0 | 0 |
| SCE1572_4189 | 26.14 | 63.28 |
| SCE1572_1290 | 22.64 | 16.45 |
| SCE1572_6503 | 6.85 | 0 |
| SCE1572_7966 | 34.33 | 15.49 |
| SCE1572_7867 | 11.73 | 91.23 |
| SCE1572_10986 | 743.08 | 13966.3 |
| SCE1572_8302 | 99.79 | 282.65 |
| SCE1572_712 | 5.36 | 1.84 |
| SCE1572_1371 | 69.58 | 63.46 |
| SCE1572_10014 | 17.8 | 6.9 |
| SCE1572_8836 | 0 | 0 |
| SCE1572_4135 | 31.84 | 10.95 |
| SCE1572_9308 | 351.96 | 2140.32 |
| SCE1572_7860 | 61.5 | 92.95 |
| SCE1572_11530 | 47.38 | 28.17 |
| SCE1572_1168 | 86.01 | 38.63 |
| SCE1572_3268 | 127.94 | 1735.08 |
| SCE1572_5142 | 71.15 | 24.57 |
| SCE1572_954 | 4.36 | 2.63 |
| SCE1572_6321 | 6.62 | 6.67 |
| SCE1572_9892 | 0 | 0 |
| SCE1572_8065 | 140.33 | 32.25 |
| SCE1572_8022 | 22.81 | 25.84 |
| SCE1572_1397 | 40.05 | 77.46 |
| SCE1572_6727 | 63.14 | 137.49 |
| SCE1572_946 | 55.84 | 19.09 |
| SCE1572_2467 | 37.38 | 27.75 |
| SCE1572_1047 | 50.72 | 16.7 |
| SCE1572_4000 | 24.5 | 51.84 |
| SCE1572_7773 | 88.75 | 133.51 |
| SCE1572_2072 | 27.61 | 12.82 |
| SCE1572_6390 | 56.2 | 142.31 |
| SCE1572_1177 | 47.09 | 48.57 |
| SCE1572_8664 | 41.12 | 8.25 |
| SCE1572_5863 | 29.48 | 16.69 |
| SCE1572_10634 | 32.74 | 77.59 |
| SCE1572_3028 | 0 | 0 |
| SCE1572_1678 | 13.93 | 36.75 |

| | | |
|---------------|--------|--------|
| SCE1572_376 | 32.34 | 11.68 |
| SCE1572_4086 | 45.87 | 23.39 |
| SCE1572_4789 | 40.95 | 355.16 |
| SCE1572_9083 | 10.67 | 0.89 |
| SCE1572_8181 | 27 | 5 |
| SCE1572_94 | 180.22 | 130.82 |
| SCE1572_8595 | 0 | 0 |
| SCE1572_4562 | 75.81 | 98.53 |
| SCE1572_6368 | 23.87 | 139.98 |
| SCE1572_7514 | 0 | 0 |
| SCE1572_709 | 0 | 0 |
| SCE1572_10710 | 21.95 | 10 |
| SCE1572_3553 | 3.37 | 0 |
| SCE1572_253 | 52.15 | 20.92 |
| SCE1572_8944 | 9.78 | 0 |
| SCE1572_6674 | 13.9 | 24.33 |
| SCE1572_6736 | 60.55 | 312.13 |
| SCE1572_2448 | 14.8 | 7.7 |
| SCE1572_11291 | 125.25 | 105.77 |
| SCE1572_5059 | 54.63 | 75.13 |
| SCE1572_3156 | 16.71 | 16.68 |
| SCE1572_1016 | 0 | 0 |
| SCE1572_10518 | 45.57 | 28.36 |
| SCE1572_7907 | 224.67 | 1334.9 |
| SCE1572_1586 | 26.82 | 46.35 |
| SCE1572_10977 | 115.94 | 182.46 |
| SCE1572_6973 | 3.09 | 0 |
| SCE1572_9853 | 76.43 | 29.83 |
| SCE1572_1932 | 69.88 | 19.79 |
| SCE1572_9952 | 9.97 | 8 |
| SCE1572_5881 | 51.04 | 45.5 |
| SCE1572_5954 | 39 | 27.26 |
| SCE1572_110 | 100.98 | 331.62 |
| SCE1572_6687 | 11.15 | 18.78 |
| SCE1572_8903 | 56.1 | 11.86 |
| SCE1572_5683 | 101.19 | 315.56 |
| SCE1572_8061 | 6.5 | 0 |
| SCE1572_2297 | 29.8 | 109.16 |
| SCE1572_9316 | 29.77 | 65.05 |
| SCE1572_7818 | 15.37 | 19.14 |
| SCE1572_9386 | 7.16 | 9.4 |
| SCE1572_4554 | 29.06 | 6.08 |
| SCE1572_2012 | 39.76 | 17.88 |
| SCE1572_3431 | 172.24 | 451.81 |
| SCE1572_8225 | 63.79 | 33.38 |
| SCE1572_9164 | 53.91 | 16.22 |
| SCE1572_3644 | 44.12 | 22.2 |
| SCE1572_966 | 28.46 | 53.54 |

| | | |
|---------------|--------|---------|
| SCE1572_9205 | 31.4 | 36.86 |
| SCE1572_2462 | 29.31 | 45.41 |
| SCE1572_5733 | 104.04 | 870.41 |
| SCE1572_636 | 151.27 | 443.3 |
| SCE1572_10837 | 37.16 | 56.54 |
| SCE1572_8783 | 45.07 | 264.02 |
| SCE1572_5757 | 59.86 | 64.91 |
| SCE1572_5085 | 0 | 0 |
| SCE1572_9612 | 8.42 | 0 |
| SCE1572_5009 | 256.41 | 397.12 |
| SCE1572_5052 | 34.94 | 19.72 |
| SCE1572_6416 | 34.75 | 7.6 |
| SCE1572_2625 | 0 | 0 |
| SCE1572_5034 | 39.51 | 13.27 |
| SCE1572_7625 | 57.32 | 98.87 |
| SCE1572_3253 | 26.1 | 19.44 |
| SCE1572_8099 | 21.2 | 176.7 |
| SCE1572_4840 | 58.67 | 436.32 |
| SCE1572_431 | 44.38 | 26.7 |
| SCE1572_4065 | 22.45 | 11.77 |
| SCE1572_10086 | 294.71 | 1283.38 |
| SCE1572_8010 | 45.01 | 245.18 |
| SCE1572_7807 | 220.41 | 173.2 |
| SCE1572_4797 | 70.36 | 244.47 |
| SCE1572_10784 | 50.13 | 51.11 |
| SCE1572_3402 | 24.56 | 92.52 |
| SCE1572_10601 | 31.1 | 10.92 |
| SCE1572_6016 | 153.25 | 459.1 |
| SCE1572_6822 | 131.67 | 1569.17 |
| SCE1572_656 | 642.29 | 1382.7 |
| SCE1572_8398 | 52.6 | 32.02 |
| SCE1572_7062 | 0 | 0 |
| SCE1572_9868 | 33.55 | 71.79 |

TableS3 Transcripts detected under different pH conditions(Original reads)

| Locus tag | pH 7.0 | pH 10.0 |
|---------------|--------|---------|
| SCE1572_5566 | 240 | 147 |
| SCE1572_4403 | 41 | 59 |
| SCE1572_3237 | 0 | 0 |
| SCE1572_7422 | 4 | 0 |
| SCE1572_6423 | 271 | 39 |
| SCE1572_5465 | 106 | 15 |
| SCE1572_5888 | 12 | 71 |
| SCE1572_1430 | 56 | 6 |
| SCE1572_9058 | 138 | 23 |
| SCE1572_8947 | 128 | 80 |
| SCE1572_1415 | 20 | 2 |
| SCE1572_9953 | 382 | 94 |
| SCE1572_8357 | 17 | 1 |
| SCE1572_5736 | 69 | 305 |
| SCE1572_963 | 781 | 264 |
| SCE1572_9431 | 52 | 21 |
| SCE1572_6979 | 32 | 6 |
| SCE1572_5559 | 0 | 0 |
| SCE1572_1203 | 181 | 30 |
| SCE1572_926 | 121 | 26 |
| SCE1572_6927 | 127 | 84 |
| SCE1572_4079 | 19 | 0 |
| SCE1572_1922 | 93 | 18 |
| SCE1572_10118 | 124 | 218 |
| SCE1572_8912 | 9 | 0 |
| SCE1572_7208 | 33 | 4 |
| SCE1572_6891 | 31 | 8 |
| SCE1572_10120 | 291 | 520 |
| SCE1572_8105 | 0 | 0 |
| SCE1572_5207 | 82 | 116 |
| SCE1572_4631 | 207 | 39 |
| SCE1572_211 | 98 | 19 |
| SCE1572_9167 | 42 | 1 |
| SCE1572_3914 | 122 | 15 |
| SCE1572_7224 | 167 | 116 |
| SCE1572_8249 | 132 | 82 |
| SCE1572_8904 | 63 | 2 |
| SCE1572_5794 | 209 | 181 |
| SCE1572_3433 | 38 | 108 |
| SCE1572_4684 | 328 | 135 |
| SCE1572_9858 | 13 | 0 |
| SCE1572_9695 | 0 | 0 |
| SCE1572_1899 | 66 | 9 |
| SCE1572_1005 | 294.01 | 34.85 |
| SCE1572_7497 | 0 | 0 |
| SCE1572_5550 | 106 | 12 |

| | | |
|---------------|-------|------|
| SCE1572_10517 | 69 | 14 |
| SCE1572_5396 | 73 | 15 |
| SCE1572_11501 | 5 | 0 |
| SCE1572_3334 | 0 | 0 |
| SCE1572_10265 | 50 | 6 |
| SCE1572_11111 | 256 | 63 |
| SCE1572_6453 | 0 | 0 |
| SCE1572_816 | 196 | 27 |
| SCE1572_2624 | 295 | 49 |
| SCE1572_6657 | 415 | 405 |
| SCE1572_1590 | 118 | 46 |
| SCE1572_4855 | 39 | 4 |
| SCE1572_8348 | 261 | 92 |
| SCE1572_4967 | 60 | 207 |
| SCE1572_7617 | 234 | 512 |
| SCE1572_8843 | 94 | 23 |
| SCE1572_2650 | 35 | 10 |
| SCE1572_1513 | 73 | 3 |
| SCE1572_10034 | 220 | 64 |
| SCE1572_9206 | 227 | 65 |
| SCE1572_1573 | 89 | 23 |
| SCE1572_9449 | 143 | 36 |
| SCE1572_3515 | 27 | 41 |
| SCE1572_7608 | 1 | 0 |
| SCE1572_6365 | 108 | 500 |
| SCE1572_7454 | 96 | 75 |
| SCE1572_3975 | 16 | 8 |
| SCE1572_3071 | 281 | 69 |
| SCE1572_3042 | 104 | 10 |
| SCE1572_5691 | 100 | 17 |
| SCE1572_1404 | 145 | 11 |
| SCE1572_49 | 53 | 4 |
| SCE1572_8002 | 205.3 | 19.5 |
| SCE1572_2278 | 69 | 190 |
| SCE1572_4137 | 0 | 0 |
| SCE1572_1345 | 158 | 478 |
| SCE1572_8495 | 168 | 36 |
| SCE1572_5018 | 307 | 179 |
| SCE1572_830 | 39 | 18 |
| SCE1572_187 | 62 | 1142 |
| SCE1572_6610 | 17 | 8 |
| SCE1572_4114 | 47 | 28 |
| SCE1572_306 | 62 | 13 |
| SCE1572_7613 | 50 | 230 |
| SCE1572_1606 | 231 | 28 |
| SCE1572_10395 | 15 | 1 |
| SCE1572_9894 | 3 | 0 |
| SCE1572_9491 | 0 | 0 |

| | | |
|---------------|--------|--------|
| SCE1572_11230 | 347 | 156 |
| SCE1572_8955 | 1 | 0 |
| SCE1572_6436 | 75 | 14 |
| SCE1572_5448 | 88 | 15 |
| SCE1572_3105 | 133 | 81 |
| SCE1572_1366 | 194 | 221 |
| SCE1572_8601 | 46 | 60 |
| SCE1572_4069 | 0 | 0 |
| SCE1572_5880 | 0 | 0 |
| SCE1572_8037 | 0 | 0 |
| SCE1572_6726 | 36 | 15 |
| SCE1572_3543 | 0 | 0 |
| SCE1572_7367 | 416 | 4999 |
| SCE1572_248 | 223 | 16 |
| SCE1572_10623 | 368.73 | 178.08 |
| SCE1572_9768 | 64 | 160 |
| SCE1572_10652 | 23 | 54 |
| SCE1572_7802 | 72 | 197 |
| SCE1572_5985 | 38 | 5 |
| SCE1572_9841 | 0 | 0 |
| SCE1572_9963 | 601.01 | 74.26 |
| SCE1572_7577 | 17 | 2 |
| SCE1572_10612 | 115 | 76 |
| SCE1572_7663 | 19 | 2 |
| SCE1572_11224 | 83.68 | 22 |
| SCE1572_9408 | 115 | 37 |
| SCE1572_4376 | 18 | 2 |
| SCE1572_9362 | 170 | 434 |
| SCE1572_5731 | 8 | 58 |
| SCE1572_10286 | 263 | 823 |
| SCE1572_7845 | 411 | 515 |
| SCE1572_4842 | 23 | 72 |
| SCE1572_8798 | 141 | 13 |
| SCE1572_7521 | 45 | 10 |
| SCE1572_2463 | 106.9 | 12.38 |
| SCE1572_7211 | 115 | 39 |
| SCE1572_4203 | 115 | 234 |
| SCE1572_782 | 24 | 10 |
| SCE1572_5176 | 54 | 17 |
| SCE1572_1742 | 178 | 74 |
| SCE1572_11206 | 220 | 104 |
| SCE1572_9567 | 1 | 0 |
| SCE1572_2193 | 28 | 2 |
| SCE1572_3990 | 355.64 | 259.98 |
| SCE1572_2460 | 18 | 0 |
| SCE1572_5137 | 18 | 10 |
| SCE1572_4098 | 8 | 2 |
| SCE1572_282 | 6 | 1 |

| | | |
|---------------|-------|------|
| SCE1572_88 | 107 | 93 |
| SCE1572_8438 | 31 | 9 |
| SCE1572_6296 | 69 | 141 |
| SCE1572_1380 | 641 | 67 |
| SCE1572_2438 | 45 | 68 |
| SCE1572_2504 | 25 | 8 |
| SCE1572_6900 | 6 | 3 |
| SCE1572_2791 | 252 | 201 |
| SCE1572_80 | 145 | 161 |
| SCE1572_1472 | 236 | 73 |
| SCE1572_9104 | 245 | 46 |
| SCE1572_1624 | 78 | 19 |
| SCE1572_3362 | 96 | 50 |
| SCE1572_2168 | 1 | 0 |
| SCE1572_7856 | 205 | 34 |
| SCE1572_4773 | 47 | 17 |
| SCE1572_754 | 85 | 47 |
| SCE1572_6951 | 84 | 17 |
| SCE1572_10444 | 252 | 219 |
| SCE1572_9667 | 84 | 199 |
| SCE1572_10984 | 359 | 1033 |
| SCE1572_8110 | 2 | 0 |
| SCE1572_5079 | 34 | 34 |
| SCE1572_8041 | 63 | 7 |
| SCE1572_2242 | 135 | 48 |
| SCE1572_1372 | 52 | 217 |
| SCE1572_8433 | 5 | 2 |
| SCE1572_5813 | 133 | 55 |
| SCE1572_700 | 1 | 0 |
| SCE1572_2010 | 82 | 9 |
| SCE1572_11149 | 6 | 5 |
| SCE1572_10976 | 104 | 0 |
| SCE1572_7217 | 119 | 62 |
| SCE1572_5719 | 39 | 7 |
| SCE1572_11292 | 215 | 651 |
| SCE1572_11053 | 359 | 466 |
| SCE1572_6650 | 60 | 25 |
| SCE1572_8277 | 63 | 19 |
| SCE1572_9473 | 120 | 111 |
| SCE1572_3550 | 95 | 25 |
| SCE1572_5232 | 35 | 34 |
| SCE1572_10529 | 94 | 58 |
| SCE1572_9606 | 5 | 0 |
| SCE1572_7979 | 374 | 46 |
| SCE1572_8021 | 47 | 8 |
| SCE1572_7030 | 27 | 5 |
| SCE1572_4972 | 34 | 75 |
| SCE1572_7997 | 77.79 | 3.09 |

| | | |
|---------------|-------|-------|
| SCE1572_3219 | 124 | 653 |
| SCE1572_180 | 0 | 0 |
| SCE1572_1340 | 48 | 21 |
| SCE1572_9934 | 0 | 0 |
| SCE1572_7895 | 1 | 0 |
| SCE1572_7063 | 290 | 51 |
| SCE1572_1569 | 58 | 45 |
| SCE1572_8410 | 169 | 500 |
| SCE1572_1140 | 31 | 18 |
| SCE1572_11212 | 65 | 18 |
| SCE1572_5996 | 127 | 38 |
| SCE1572_4989 | 33 | 27 |
| SCE1572_8108 | 186 | 20 |
| SCE1572_2995 | 179 | 22 |
| SCE1572_9626 | 87.06 | 10.38 |
| SCE1572_525 | 62 | 37 |
| SCE1572_8183 | 111 | 6 |
| SCE1572_4091 | 84 | 16 |
| SCE1572_5859 | 96 | 24 |
| SCE1572_8465 | 3 | 0 |
| SCE1572_1858 | 46 | 4 |
| SCE1572_745 | 369 | 650 |
| SCE1572_739 | 93 | 17 |
| SCE1572_3507 | 33 | 8 |
| SCE1572_6096 | 480 | 107 |
| SCE1572_4152 | 36 | 838 |
| SCE1572_1557 | 3 | 0 |
| SCE1572_1102 | 55 | 13 |
| SCE1572_8406 | 199 | 63 |
| SCE1572_10274 | 113 | 69 |
| SCE1572_5523 | 68 | 14 |
| SCE1572_1752 | 26 | 4 |
| SCE1572_7397 | 70 | 17 |
| SCE1572_6604 | 101 | 100 |
| SCE1572_520 | 47 | 9 |
| SCE1572_3861 | 578 | 814 |
| SCE1572_5452 | 225 | 27 |
| SCE1572_1479 | 107 | 30 |
| SCE1572_4183 | 17 | 5 |
| SCE1572_4277 | 274 | 54 |
| SCE1572_4055 | 84 | 108 |
| SCE1572_7277 | 0 | 0 |
| SCE1572_273 | 415 | 501 |
| SCE1572_4726 | 157 | 35 |
| SCE1572_4367 | 369 | 76 |
| SCE1572_10239 | 174 | 18 |
| SCE1572_5862 | 222 | 31 |
| SCE1572_5269 | 229 | 446 |

| | | |
|---------------|--------|--------|
| SCE1572_5003 | 38 | 95 |
| SCE1572_8270 | 129 | 35 |
| SCE1572_5742 | 344.91 | 113.79 |
| SCE1572_5688 | 54 | 11 |
| SCE1572_6380 | 37 | 11 |
| SCE1572_4251 | 11 | 5 |
| SCE1572_7555 | 17 | 2 |
| SCE1572_4451 | 0 | 0 |
| SCE1572_3700 | 125 | 47 |
| SCE1572_11134 | 114 | 24 |
| SCE1572_5330 | 62 | 9 |
| SCE1572_11 | 55 | 44 |
| SCE1572_6894 | 213.43 | 66 |
| SCE1572_2819 | 172 | 33 |
| SCE1572_10713 | 25 | 9 |
| SCE1572_10510 | 67 | 19 |
| SCE1572_1136 | 0 | 0 |
| SCE1572_1154 | 12.85 | 0 |
| SCE1572_9848 | 13 | 1 |
| SCE1572_588 | 16 | 7 |
| SCE1572_2092 | 71 | 5 |
| SCE1572_9341 | 131 | 529 |
| SCE1572_6101 | 189 | 28 |
| SCE1572_4552 | 98 | 14 |
| SCE1572_2039 | 16 | 31 |
| SCE1572_1691 | 158 | 157 |
| SCE1572_9088 | 9 | 0 |
| SCE1572_10912 | 143 | 145 |
| SCE1572_3654 | 54 | 122 |
| SCE1572_839 | 12 | 16 |
| SCE1572_3022 | 37 | 4 |
| SCE1572_5237 | 230 | 157 |
| SCE1572_1358 | 661 | 2228 |
| SCE1572_6327 | 8 | 1 |
| SCE1572_10525 | 71 | 31 |
| SCE1572_3380 | 22 | 11 |
| SCE1572_10676 | 151 | 52 |
| SCE1572_4713 | 102 | 22 |
| SCE1572_3785 | 120 | 123 |
| SCE1572_5601 | 230 | 38 |
| SCE1572_973 | 60 | 56 |
| SCE1572_8005 | 99 | 58 |
| SCE1572_10203 | 46.55 | 61.05 |
| SCE1572_6265 | 99 | 72 |
| SCE1572_8051 | 72 | 10 |
| SCE1572_6388 | 57 | 134 |
| SCE1572_1686 | 34 | 7 |
| SCE1572_5026 | 45 | 15 |

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| SCE1572_5838 | 31 | 5 |
| SCE1572_10160 | 641 | 428 |
| SCE1572_405 | 224 | 102 |
| SCE1572_6510 | 0 | 0 |
| SCE1572_4060 | 16 | 32 |
| SCE1572_1251 | 152 | 29 |
| SCE1572_8928 | 0 | 0 |
| SCE1572_10836 | 75 | 16 |
| SCE1572_8643 | 65 | 31 |
| SCE1572_7375 | 22 | 6 |
| SCE1572_335 | 131 | 27 |
| SCE1572_5510 | 63 | 28 |
| SCE1572_4130 | 188 | 127 |
| SCE1572_4475 | 4416 | 3508 |
| SCE1572_9498 | 252 | 677 |
| SCE1572_2046 | 24 | 0 |
| SCE1572_11302 | 93 | 53 |
| SCE1572_5889 | 30 | 26 |
| SCE1572_8859 | 67 | 20 |
| SCE1572_5112 | 54 | 42 |
| SCE1572_4954 | 12 | 0 |
| SCE1572_6232 | 214 | 24 |
| SCE1572_295 | 5 | 67 |
| SCE1572_1892 | 59 | 25 |
| SCE1572_5495 | 121 | 18 |
| SCE1572_5462 | 77 | 14 |
| SCE1572_9142 | 31.38 | 5 |
| SCE1572_8918 | 30 | 184 |
| SCE1572_3926 | 152 | 308 |
| SCE1572_364 | 30 | 1 |
| SCE1572_3150 | 51 | 75 |
| SCE1572_995 | 66 | 5 |
| SCE1572_8751 | 585 | 76 |
| SCE1572_1718 | 101 | 64 |
| SCE1572_4925 | 144 | 123 |
| SCE1572_4641 | 143 | 30 |
| SCE1572_11128 | 0 | 0 |
| SCE1572_1355 | 40 | 23 |
| SCE1572_6588 | 480 | 197 |
| SCE1572_6193 | 0 | 0 |
| SCE1572_4588 | 66 | 235 |
| SCE1572_2258 | 184 | 34 |
| SCE1572_2030 | 64 | 6 |
| SCE1572_6967 | 160 | 42 |
| SCE1572_9748 | 70 | 21 |
| SCE1572_6884 | 153 | 26 |
| SCE1572_3659 | 18 | 9 |
| SCE1572_1935 | 0 | 0 |

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| SCE1572_5064 | 159 | 105 |
| SCE1572_1118 | 429 | 89 |
| SCE1572_11174 | 300 | 78 |
| SCE1572_8966 | 160 | 94 |
| SCE1572_2390 | 346 | 367 |
| SCE1572_4929 | 57 | 50 |
| SCE1572_10200 | 27 | 25 |
| SCE1572_6628 | 90 | 97 |
| SCE1572_4486 | 48 | 159 |
| SCE1572_8117 | 23 | 3 |
| SCE1572_8212 | 5 | 4 |
| SCE1572_8911 | 31 | 11 |
| SCE1572_3389 | 38 | 9 |
| SCE1572_886 | 3461 | 1960 |
| SCE1572_9295 | 185 | 157 |
| SCE1572_8415 | 114 | 25 |
| SCE1572_3294 | 19 | 3 |
| SCE1572_146 | 216 | 39 |
| SCE1572_4930 | 78 | 38 |
| SCE1572_7638 | 43 | 22 |
| SCE1572_7202 | 49 | 2 |
| SCE1572_3557 | 150 | 23 |
| SCE1572_8921 | 0.5 | 0 |
| SCE1572_8562 | 327 | 294 |
| SCE1572_6723 | 104 | 148 |
| SCE1572_5457 | 113 | 15 |
| SCE1572_4784 | 4 | 0 |
| SCE1572_4677 | 8 | 6 |
| SCE1572_1188 | 73 | 8 |
| SCE1572_5655 | 142 | 40 |
| SCE1572_7814 | 586 | 1924 |
| SCE1572_11271 | 121 | 158 |
| SCE1572_1595 | 63 | 29 |
| SCE1572_474 | 154 | 298 |
| SCE1572_5185 | 163 | 2756 |
| SCE1572_3746 | 30 | 6 |
| SCE1572_4708 | 0 | 0 |
| SCE1572_7138 | 92 | 69 |
| SCE1572_5293 | 44 | 31 |
| SCE1572_4193 | 1036 | 2007 |
| SCE1572_3754 | 20 | 1 |
| SCE1572_3251 | 4 | 0 |
| SCE1572_11044 | 51 | 28 |
| SCE1572_6377 | 45 | 12 |
| SCE1572_7353 | 269.08 | 30 |
| SCE1572_11193 | 49 | 11 |
| SCE1572_11325 | 257 | 109 |
| SCE1572_6854 | 81 | 2 |

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| SCE1572_2692 | 28 | 31 |
| SCE1572_6470 | 54 | 9 |
| SCE1572_2699 | 1 | 0 |
| SCE1572_9192 | 145 | 35 |
| SCE1572_9930 | 123 | 95 |
| SCE1572_4230 | 16 | 8 |
| SCE1572_7287 | 22 | 14 |
| SCE1572_8364 | 180 | 41 |
| SCE1572_2466 | 50 | 7 |
| SCE1572_5680 | 713 | 593 |
| SCE1572_8608 | 296 | 463 |
| SCE1572_6164 | 94 | 26 |
| SCE1572_2371 | 182 | 120 |
| SCE1572_6829 | 2 | 0 |
| SCE1572_6398 | 52 | 81 |
| SCE1572_7344 | 0 | 0 |
| SCE1572_2395 | 76 | 116 |
| SCE1572_2310 | 156 | 236 |
| SCE1572_1423 | 481 | 131 |
| SCE1572_6673 | 38 | 13 |
| SCE1572_6462 | 220 | 93 |
| SCE1572_11167 | 32 | 49 |
| SCE1572_11454 | 293 | 243 |
| SCE1572_8786 | 40 | 165 |
| SCE1572_6986 | 0 | 0 |
| SCE1572_3877 | 0 | 0 |
| SCE1572_6944 | 2 | 0 |
| SCE1572_7420 | 184 | 54 |
| SCE1572_9276 | 207 | 75 |
| SCE1572_2560 | 7 | 4 |
| SCE1572_7449 | 561 | 915 |
| SCE1572_10805 | 144 | 19 |
| SCE1572_9214 | 217 | 51 |
| SCE1572_76 | 28 | 0 |
| SCE1572_10657 | 128 | 48 |
| SCE1572_9705 | 47 | 8 |
| SCE1572_1218 | 189 | 25 |
| SCE1572_6972 | 201 | 34 |
| SCE1572_2301 | 7 | 19 |
| SCE1572_10659 | 91 | 45 |
| SCE1572_5475 | 35 | 50 |
| SCE1572_3148 | 73 | 10 |
| SCE1572_7037 | 78 | 72 |
| SCE1572_2635 | 82 | 76 |
| SCE1572_9712 | 0 | 0 |
| SCE1572_327 | 2 | 0 |
| SCE1572_10834 | 252 | 25 |
| SCE1572_1000 | 512 | 406 |

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| SCE1572_8502 | 238 | 36 |
| SCE1572_2544 | 340 | 60 |
| SCE1572_7769 | 24 | 9 |
| SCE1572_4048 | 127 | 131 |
| SCE1572_10216 | 48 | 9 |
| SCE1572_9534 | 136 | 42 |
| SCE1572_2376 | 274 | 191 |
| SCE1572_11510 | 70 | 15 |
| SCE1572_847 | 901 | 1901 |
| SCE1572_6631 | 1 | 0 |
| SCE1572_8509 | 271.07 | 56 |
| SCE1572_7626 | 71 | 12 |
| SCE1572_4490 | 58 | 12 |
| SCE1572_581 | 92 | 40 |
| SCE1572_485 | 114 | 19 |
| SCE1572_1261 | 85 | 49 |
| SCE1572_4297 | 0 | 0 |
| SCE1572_6486 | 10 | 0 |
| SCE1572_2598 | 0 | 0 |
| SCE1572_1028 | 1 | 0 |
| SCE1572_122 | 50 | 7 |
| SCE1572_5213 | 133 | 29 |
| SCE1572_387 | 65 | 69 |
| SCE1572_3452 | 201 | 26 |
| SCE1572_4140 | 44 | 43 |
| SCE1572_5841 | 130 | 23 |
| SCE1572_132 | 1586 | 1185 |
| SCE1572_10225 | 4 | 0 |
| SCE1572_6014 | 29 | 505 |
| SCE1572_6912 | 119 | 10 |
| SCE1572_5620 | 242.01 | 29 |
| SCE1572_11342 | 54 | 28 |
| SCE1572_10406 | 177 | 91 |
| SCE1572_6694 | 118 | 21 |
| SCE1572_7840 | 114 | 57 |
| SCE1572_10968 | 51 | 18 |
| SCE1572_10605 | 0 | 0 |
| SCE1572_9668 | 164 | 407 |
| SCE1572_9334 | 79 | 106 |
| SCE1572_9444 | 105 | 33 |
| SCE1572_422 | 69 | 79 |
| SCE1572_576 | 215 | 374 |
| SCE1572_8155 | 74 | 6 |
| SCE1572_3533 | 210 | 27 |
| SCE1572_2657 | 492 | 67 |
| SCE1572_7433 | 61 | 51 |
| SCE1572_5916 | 198 | 61 |
| SCE1572_6281 | 299.53 | 271 |

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| SCE1572_11368 | 3 | 0 |
| SCE1572_9369 | 0 | 0 |
| SCE1572_7400 | 131 | 53 |
| SCE1572_7108 | 0 | 0 |
| SCE1572_5275 | 2 | 1 |
| SCE1572_10825 | 224 | 128 |
| SCE1572_6075 | 219 | 86 |
| SCE1572_2478 | 134 | 61 |
| SCE1572_6270 | 32 | 13 |
| SCE1572_3199 | 162 | 425 |
| SCE1572_9190 | 77 | 17 |
| SCE1572_6401 | 0 | 0 |
| SCE1572_4153 | 0 | 0 |
| SCE1572_4285 | 101 | 40 |
| SCE1572_3442 | 128 | 53 |
| SCE1572_4159 | 25 | 17 |
| SCE1572_9908 | 181 | 74 |
| SCE1572_7128 | 292 | 74 |
| SCE1572_10661 | 110 | 69 |
| SCE1572_4343 | 195 | 28 |
| SCE1572_3613 | 62 | 64 |
| SCE1572_2215 | 54 | 39 |
| SCE1572_2433 | 27 | 13 |
| SCE1572_5403 | 103 | 17 |
| SCE1572_1865 | 54 | 9 |
| SCE1572_9881 | 118 | 50 |
| SCE1572_941 | 57 | 3 |
| SCE1572_6312 | 51 | 293 |
| SCE1572_7884 | 123 | 30 |
| SCE1572_11309 | 48 | 3 |
| SCE1572_3284 | 36 | 2 |
| SCE1572_4383 | 165 | 28 |
| SCE1572_9118 | 167 | 44 |
| SCE1572_5972 | 23 | 0 |
| SCE1572_5898 | 7 | 2 |
| SCE1572_5586 | 18 | 0 |
| SCE1572_5391 | 253 | 91 |
| SCE1572_4579 | 1 | 0 |
| SCE1572_7151 | 91 | 39 |
| SCE1572_1458 | 0 | 0 |
| SCE1572_3670 | 40.3 | 6 |
| SCE1572_11379 | 50 | 48 |
| SCE1572_6415 | 68 | 10 |
| SCE1572_4236 | 102 | 164 |
| SCE1572_10117 | 67 | 43 |
| SCE1572_10591 | 256 | 71 |
| SCE1572_9516 | 28 | 54 |
| SCE1572_98 | 23 | 6 |

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| SCE1572_1098 | 237 | 61 |
| SCE1572_3177 | 142 | 253 |
| SCE1572_1123 | 86 | 11 |
| SCE1572_10692 | 23 | 41 |
| SCE1572_10577 | 32 | 10 |
| SCE1572_4083 | 39 | 24 |
| SCE1572_2595 | 215 | 66 |
| SCE1572_7586 | 54 | 446 |
| SCE1572_2893 | 43 | 7 |
| SCE1572_6222 | 108 | 18 |
| SCE1572_4600 | 78 | 54 |
| SCE1572_643 | 268 | 264 |
| SCE1572_2336 | 55 | 29 |
| SCE1572_8892 | 155 | 77 |
| SCE1572_7056 | 16 | 7 |
| SCE1572_3741 | 109 | 35 |
| SCE1572_9871 | 34 | 7 |
| SCE1572_5596 | 212 | 87 |
| SCE1572_5514 | 100 | 8 |
| SCE1572_5978 | 111 | 29 |
| SCE1572_2864 | 0 | 0 |
| SCE1572_2177 | 98 | 6 |
| SCE1572_4654 | 122.99 | 77.63 |
| SCE1572_9307 | 126 | 159 |
| SCE1572_6432 | 38 | 5 |
| SCE1572_7483 | 382 | 108 |
| SCE1572_4469 | 369 | 63 |
| SCE1572_8401 | 207 | 59 |
| SCE1572_4848 | 74 | 22 |
| SCE1572_6871 | 41 | 15 |
| SCE1572_1739 | 55 | 4 |
| SCE1572_2453 | 170 | 63 |
| SCE1572_9263 | 12 | 10 |
| SCE1572_4939 | 207 | 148 |
| SCE1572_8763 | 0 | 0 |
| SCE1572_3449 | 120 | 17 |
| SCE1572_10729 | 36 | 26 |
| SCE1572_2535 | 20 | 9 |
| SCE1572_9795 | 31 | 1 |
| SCE1572_5717 | 265 | 199 |
| SCE1572_10197 | 0 | 0 |
| SCE1572_1190 | 348 | 176 |
| SCE1572_10580 | 24 | 11 |
| SCE1572_10640 | 583 | 1495 |
| SCE1572_4935 | 120 | 224 |
| SCE1572_10865 | 670 | 703 |
| SCE1572_5438 | 0 | 0 |
| SCE1572_5141 | 159 | 42 |

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| SCE1572_8764 | 0.15 | 0.18 |
| SCE1572_7461 | 1094 | 1489 |
| SCE1572_9651 | 107 | 14 |
| SCE1572_289 | 651 | 44 |
| SCE1572_4033 | 0 | 0 |
| SCE1572_2921 | 263 | 27 |
| SCE1572_9552 | 37 | 7 |
| SCE1572_9434 | 324 | 522 |
| SCE1572_2977 | 76.95 | 11 |
| SCE1572_10464 | 27 | 43 |
| SCE1572_7671 | 117 | 3 |
| SCE1572_10650 | 1022 | 811 |
| SCE1572_6239 | 0 | 0 |
| SCE1572_9900 | 423 | 596 |
| SCE1572_9241 | 0 | 0 |
| SCE1572_8166 | 3 | 0 |
| SCE1572_3264 | 84 | 311 |
| SCE1572_10436 | 78 | 47 |
| SCE1572_213 | 135 | 23 |
| SCE1572_4017 | 30 | 5 |
| SCE1572_5956 | 54 | 15 |
| SCE1572_10495 | 130 | 124 |
| SCE1572_8129 | 0 | 0 |
| SCE1572_8633 | 97 | 51 |
| SCE1572_5723 | 3 | 0 |
| SCE1572_6662 | 212 | 81 |
| SCE1572_1224 | 86 | 37 |
| SCE1572_9736 | 105 | 8 |
| SCE1572_7762 | 57 | 86 |
| SCE1572_8826 | 148.64 | 15.44 |
| SCE1572_3128 | 32 | 24 |
| SCE1572_7086 | 51 | 7 |
| SCE1572_3479 | 16 | 0 |
| SCE1572_5942 | 103 | 15 |
| SCE1572_224 | 62 | 19 |
| SCE1572_4323 | 76 | 14 |
| SCE1572_1220 | 58 | 13 |
| SCE1572_1227 | 109 | 17 |
| SCE1572_8933 | 24 | 8 |
| SCE1572_2813 | 44 | 22 |
| SCE1572_7724 | 133 | 86 |
| SCE1572_11578 | 18 | 3 |
| SCE1572_10845 | 131 | 29 |
| SCE1572_1377 | 41 | 7 |
| SCE1572_11406 | 37 | 5 |
| SCE1572_5097 | 46 | 22 |
| SCE1572_4441 | 67 | 13 |
| SCE1572_2801 | 143 | 564 |

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| SCE1572_10786 | 42 | 11 |
| SCE1572_10241 | 37 | 8 |
| SCE1572_9923 | 155 | 211 |
| SCE1572_5 | 179 | 255 |
| SCE1572_25 | 94 | 47 |
| SCE1572_2025 | 102 | 95 |
| SCE1572_567 | 132 | 65 |
| SCE1572_3812 | 10 | 15 |
| SCE1572_490 | 86.43 | 96.62 |
| SCE1572_4841 | 220 | 649 |
| SCE1572_7331 | 1 | 0 |
| SCE1572_9992 | 0 | 0 |
| SCE1572_9282 | 1813 | 791 |
| SCE1572_469 | 164 | 656 |
| SCE1572_2613 | 49 | 10 |
| SCE1572_460 | 7 | 0 |
| SCE1572_2075 | 70 | 5 |
| SCE1572_5525 | 292 | 57 |
| SCE1572_4430 | 15 | 4 |
| SCE1572_373 | 56 | 21 |
| SCE1572_9389 | 105 | 201 |
| SCE1572_3631 | 44 | 12 |
| SCE1572_6881 | 318 | 75 |
| SCE1572_5253 | 0 | 0 |
| SCE1572_6575 | 13 | 5 |
| SCE1572_3030 | 61 | 9 |
| SCE1572_2760 | 142 | 337 |
| SCE1572_10053 | 46 | 60 |
| SCE1572_9017 | 0 | 0 |
| SCE1572_824 | 318 | 80 |
| SCE1572_3986 | 206 | 1275 |
| SCE1572_8613 | 61 | 11 |
| SCE1572_4293 | 127 | 38 |
| SCE1572_4008 | 55 | 9 |
| SCE1572_11548 | 109 | 175 |
| SCE1572_1170 | 122 | 22 |
| SCE1572_7849 | 793 | 279 |
| SCE1572_8997 | 50 | 15 |
| SCE1572_516 | 0 | 0 |
| SCE1572_8182 | 102 | 12 |
| SCE1572_5534 | 406 | 58 |
| SCE1572_7759 | 96 | 217 |
| SCE1572_241 | 489 | 138 |
| SCE1572_8379 | 40 | 14 |
| SCE1572_9703 | 33 | 16 |
| SCE1572_3937 | 182 | 62 |
| SCE1572_1898 | 56 | 29 |
| SCE1572_8028 | 2 | 0 |

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| SCE1572_1564 | 29 | 21 |
| SCE1572_5419 | 29 | 41 |
| SCE1572_8802 | 554 | 167 |
| SCE1572_4763 | 64 | 129 |
| SCE1572_9370 | 30 | 8 |
| SCE1572_6322 | 61 | 26 |
| SCE1572_8818 | 76 | 16 |
| SCE1572_8073 | 141 | 27 |
| SCE1572_773 | 30 | 16 |
| SCE1572_6206 | 157 | 49 |
| SCE1572_5345 | 24 | 6 |
| SCE1572_2267 | 67 | 46 |
| SCE1572_7927 | 142 | 59 |
| SCE1572_78 | 159 | 23 |
| SCE1572_5801 | 98 | 125 |
| SCE1572_6229 | 60 | 11 |
| SCE1572_6481 | 23 | 1 |
| SCE1572_4456 | 68 | 61 |
| SCE1572_2928 | 122 | 19 |
| SCE1572_8205 | 12 | 16 |
| SCE1572_7876 | 62 | 21 |
| SCE1572_8485 | 89 | 22 |
| SCE1572_6370 | 64 | 18 |
| SCE1572_2723 | 57 | 29 |
| SCE1572_2517 | 0 | 0 |
| SCE1572_8536 | 85.73 | 17.04 |
| SCE1572_6642 | 107 | 20 |
| SCE1572_4965 | 173 | 48 |
| SCE1572_11461 | 1 | 0 |
| SCE1572_7444 | 0 | 0 |
| SCE1572_8708 | 44 | 30 |
| SCE1572_9950 | 122 | 23 |
| SCE1572_4168 | 27 | 2 |
| SCE1572_9545 | 113 | 60 |
| SCE1572_6509 | 37 | 5 |
| SCE1572_6593 | 25 | 26 |
| SCE1572_987 | 47 | 17 |
| SCE1572_8569 | 83 | 7 |
| SCE1572_7693 | 339 | 475 |
| SCE1572_10000 | 72 | 139 |
| SCE1572_2770 | 36 | 164 |
| SCE1572_1249 | 8 | 3 |
| SCE1572_4439 | 45 | 7 |
| SCE1572_3673 | 155 | 74 |
| SCE1572_5156 | 64 | 5 |
| SCE1572_59 | 57 | 15 |
| SCE1572_876 | 299 | 84 |
| SCE1572_4609 | 211 | 17 |

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| SCE1572_10011 | 603 | 934 |
| SCE1572_5369 | 85 | 11 |
| SCE1572_1917 | 50 | 7 |
| SCE1572_7121 | 0 | 0 |
| SCE1572_42 | 122 | 43 |
| SCE1572_6958 | 54 | 5 |
| SCE1572_5592 | 145 | 48 |
| SCE1572_1284 | 302 | 4066 |
| SCE1572_10007 | 44 | 12 |
| SCE1572_8972 | 84 | 4162 |
| SCE1572_8899 | 2 | 0 |
| SCE1572_6358 | 135 | 22 |
| SCE1572_9234 | 508 | 326 |
| SCE1572_4819 | 106 | 196 |
| SCE1572_5354 | 35 | 21 |
| SCE1572_10416 | 11 | 6 |
| SCE1572_1169 | 127 | 24 |
| SCE1572_5788 | 350 | 600 |
| SCE1572_120 | 51 | 4 |
| SCE1572_1282 | 30 | 46 |
| SCE1572_8236 | 71 | 267 |
| SCE1572_11492 | 151 | 172 |
| SCE1572_8269 | 125 | 18 |
| SCE1572_5201 | 31 | 10 |
| SCE1572_799 | 159 | 308 |
| SCE1572_2826 | 29 | 9 |
| SCE1572_3346 | 520 | 157 |
| SCE1572_9481 | 276 | 100 |
| SCE1572_2713 | 69 | 72 |
| SCE1572_7036 | 77 | 102 |
| SCE1572_3277 | 0 | 0 |
| SCE1572_10917 | 43 | 25 |
| SCE1572_6636 | 306 | 35 |
| SCE1572_3948 | 286 | 286 |
| SCE1572_7775 | 27 | 4 |
| SCE1572_10398 | 121 | 55 |
| SCE1572_2997 | 14 | 1 |
| SCE1572_7476 | 190 | 0 |
| SCE1572_4514 | 261 | 322 |
| SCE1572_7348 | 94 | 16 |
| SCE1572_2571 | 138 | 60 |
| SCE1572_6502 | 118 | 46 |
| SCE1572_4056 | 62 | 61 |
| SCE1572_1323 | 47 | 33 |
| SCE1572_3575 | 148 | 21 |
| SCE1572_10575 | 0 | 0 |
| SCE1572_4412 | 2 | 0 |
| SCE1572_7650 | 12 | 0 |

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| SCE1572_5117 | 25 | 25 |
| SCE1572_9310 | 249 | 456 |
| SCE1572_4918 | 126 | 54 |
| SCE1572_1957 | 85 | 26 |
| SCE1572_4696 | 153 | 39 |
| SCE1572_1138 | 41 | 5 |
| SCE1572_10372 | 86 | 14 |
| SCE1572_6408 | 52 | 10 |
| SCE1572_2206 | 108 | 387 |
| SCE1572_10148 | 29 | 15 |
| SCE1572_9399 | 88 | 30 |
| SCE1572_4914 | 56 | 9 |
| SCE1572_11408 | 25 | 6 |
| SCE1572_9189 | 174 | 28 |
| SCE1572_8985 | 45 | 40 |
| SCE1572_6768 | 75 | 51 |
| SCE1572_8635 | 32 | 9 |
| SCE1572_6615 | 49 | 12 |
| SCE1572_5614 | 66 | 7 |
| SCE1572_2122 | 6 | 1 |
| SCE1572_3903 | 258 | 161 |
| SCE1572_1970 | 126 | 22 |
| SCE1572_1791 | 60 | 5 |
| SCE1572_11444 | 25 | 10 |
| SCE1572_3957 | 3 | 0 |
| SCE1572_889 | 113 | 14 |
| SCE1572_10709 | 18 | 0 |
| SCE1572_4321 | 331 | 70 |
| SCE1572_8395 | 64 | 593 |
| SCE1572_4561 | 0 | 0 |
| SCE1572_4024 | 1042 | 380 |
| SCE1572_3510 | 36 | 76 |
| SCE1572_2330 | 218 | 62 |
| SCE1572_1822 | 192 | 18 |
| SCE1572_10500 | 57 | 275 |
| SCE1572_6994 | 24 | 12 |
| SCE1572_3299 | 92 | 40 |
| SCE1572_10924 | 828 | 7715 |
| SCE1572_10744 | 140 | 23 |
| SCE1572_3069 | 51 | 47 |
| SCE1572_6627 | 38 | 26 |
| SCE1572_4993 | 48 | 12 |
| SCE1572_611 | 18 | 37 |
| SCE1572_2103 | 180 | 109 |
| SCE1572_11032 | 0 | 0 |
| SCE1572_6467 | 88 | 9 |
| SCE1572_10694 | 25 | 0 |
| SCE1572_1077 | 162 | 44 |

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| SCE1572_6139 | 120 | 105 |
| SCE1572_9983 | 177 | 32 |
| SCE1572_5634 | 68 | 10 |
| SCE1572_8870 | 87 | 27 |
| SCE1572_10928 | 180 | 76 |
| SCE1572_7198 | 336 | 332 |
| SCE1572_9413 | 68 | 109 |
| SCE1572_3589 | 1 | 0 |
| SCE1572_3272 | 0 | 0 |
| SCE1572_1995 | 236 | 31 |
| SCE1572_6788 | 190 | 29 |
| SCE1572_3551 | 9 | 3 |
| SCE1572_9010 | 39 | 7 |
| SCE1572_4827 | 139 | 34 |
| SCE1572_9692 | 25 | 41 |
| SCE1572_6603 | 60 | 41 |
| SCE1572_8519 | 21 | 120 |
| SCE1572_4359 | 14 | 6 |
| SCE1572_10827 | 74 | 14 |
| SCE1572_7752 | 44 | 13 |
| SCE1572_1771 | 152 | 30 |
| SCE1572_5192 | 66 | 222 |
| SCE1572_2369 | 33 | 3 |
| SCE1572_6275 | 239.5 | 287.5 |
| SCE1572_2706 | 430 | 120 |
| SCE1572_10131 | 42 | 18 |
| SCE1572_10380 | 119 | 44 |
| SCE1572_437 | 110 | 25 |
| SCE1572_2935 | 9 | 1 |
| SCE1572_7502 | 57 | 39 |
| SCE1572_5909 | 74 | 227 |
| SCE1572_5347 | 51 | 12 |
| SCE1572_9752 | 0 | 0 |
| SCE1572_2677 | 13 | 88 |
| SCE1572_9153 | 253 | 89 |
| SCE1572_860 | 73 | 192 |
| SCE1572_3992 | 23 | 50 |
| SCE1572_6526 | 44 | 7 |
| SCE1572_8624 | 19 | 0 |
| SCE1572_8497 | 539 | 86 |
| SCE1572_2587 | 5 | 1 |
| SCE1572_11471 | 58 | 18 |
| SCE1572_10550 | 21 | 7 |
| SCE1572_11459 | 47 | 46 |
| SCE1572_3224 | 68 | 3 |
| SCE1572_2417 | 35 | 13 |
| SCE1572_10811 | 0 | 0 |
| SCE1572_3624 | 21 | 2 |

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| SCE1572_6114 | 138 | 10 |
| SCE1572_6566 | 68 | 28 |
| SCE1572_4572 | 114 | 12 |
| SCE1572_3845 | 162 | 21 |
| SCE1572_9723 | 39 | 7 |
| SCE1572_4549 | 125 | 17 |
| SCE1572_1068 | 21 | 0 |
| SCE1572_2855 | 28.64 | 3.95 |
| SCE1572_10383 | 45 | 10 |
| SCE1572_2774 | 81 | 24 |
| SCE1572_40 | 150 | 40 |
| SCE1572_1615 | 261 | 478 |
| SCE1572_11434 | 125 | 32 |
| SCE1572_7786 | 40.16 | 24.01 |
| SCE1572_7176 | 110 | 90 |
| SCE1572_7737 | 18 | 12 |
| SCE1572_7491 | 32 | 14 |
| SCE1572_6429 | 46 | 7 |
| SCE1572_9155 | 154 | 110 |
| SCE1572_1426 | 382 | 363 |
| SCE1572_3309 | 50 | 6 |
| SCE1572_4542 | 0 | 0 |
| SCE1572_7967 | 20 | 0 |
| SCE1572_5083 | 84 | 121 |
| SCE1572_3411 | 45 | 31 |
| SCE1572_2829 | 45 | 4 |
| SCE1572_1785 | 329.01 | 288 |
| SCE1572_1643 | 728 | 97 |
| SCE1572_5106 | 34 | 279 |
| SCE1572_10944 | 52 | 22 |
| SCE1572_3581 | 80 | 19 |
| SCE1572_5770 | 1029 | 6335 |
| SCE1572_501 | 96 | 18 |
| SCE1572_3819 | 166 | 39 |
| SCE1572_9092 | 252 | 70 |
| SCE1572_7113 | 137 | 38 |
| SCE1572_5629 | 7 | 0 |
| SCE1572_8642 | 3 | 1 |
| SCE1572_9878 | 39 | 6 |
| SCE1572_9437 | 181 | 102 |
| SCE1572_6134 | 32 | 18 |
| SCE1572_2666 | 72 | 44 |
| SCE1572_5645 | 4 | 1 |
| SCE1572_7716 | 47 | 0 |
| SCE1572_539 | 3 | 0 |
| SCE1572_4215 | 1056 | 968 |
| SCE1572_1827 | 17 | 2 |
| SCE1572_982 | 101 | 36 |

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| SCE1572_6140 | 68 | 14 |
| SCE1572_5646 | 1 | 0 |
| SCE1572_11160 | 39 | 111 |
| SCE1572_7025 | 1 | 0 |
| SCE1572_4187 | 291 | 178 |
| SCE1572_2404 | 62 | 191 |
| SCE1572_7512 | 0 | 0 |
| SCE1572_4799 | 238 | 112 |
| SCE1572_10388 | 14 | 16 |
| SCE1572_8742 | 59 | 26 |
| SCE1572_6149 | 92 | 35 |
| SCE1572_2468 | 77 | 57 |
| SCE1572_862 | 164 | 243 |
| SCE1572_5146 | 57 | 11 |
| SCE1572_11073 | 4 | 87 |
| SCE1572_2019 | 179 | 37 |
| SCE1572_3084 | 72 | 9 |
| SCE1572_8145 | 21 | 53 |
| SCE1572_8884 | 55 | 2 |
| SCE1572_11500 | 97 | 97 |
| SCE1572_321 | 29 | 1 |
| SCE1572_11313 | 168 | 979 |
| SCE1572_8833 | 42 | 9 |
| SCE1572_8663 | 80 | 14 |
| SCE1572_3045 | 5 | 0 |
| SCE1572_4864 | 56 | 10 |
| SCE1572_4484 | 46 | 24 |
| SCE1572_2547 | 69 | 31 |
| SCE1572_1849 | 220 | 56 |
| SCE1572_11387 | 368 | 277 |
| SCE1572_11553 | 140 | 42 |
| SCE1572_4266 | 27 | 12 |
| SCE1572_3602 | 45 | 47 |
| SCE1572_10342 | 48 | 32 |
| SCE1572_9526 | 124 | 559 |
| SCE1572_8053 | 28 | 5 |
| SCE1572_9179 | 71 | 12 |
| SCE1572_10934 | 102 | 21 |
| SCE1572_8734 | 30 | 13 |
| SCE1572_8332 | 216 | 91 |
| SCE1572_563 | 39 | 43 |
| SCE1572_1333 | 7 | 0 |
| SCE1572_11083 | 7 | 7 |
| SCE1572_6518 | 56 | 5 |
| SCE1572_2733 | 31 | 33 |
| SCE1572_1312 | 446 | 529 |
| SCE1572_2020 | 41 | 25 |
| SCE1572_10304 | 431 | 272 |

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| SCE1572_8446 | 10 | 2 |
| SCE1572_4508 | 26 | 22 |
| SCE1572_9464 | 66 | 15 |
| SCE1572_752 | 14 | 0 |
| SCE1572_8686 | 64 | 4 |
| SCE1572_6742 | 91 | 8 |
| SCE1572_47 | 44 | 7 |
| SCE1572_8292 | 91 | 21 |
| SCE1572_6316 | 0 | 0 |
| SCE1572_2235 | 143 | 183 |
| SCE1572_7169 | 191 | 98 |
| SCE1572_7132 | 40 | 5 |
| SCE1572_1526 | 985 | 6039 |
| SCE1572_8534 | 129 | 230 |
| SCE1572_8936 | 3 | 0 |
| SCE1572_10531 | 6 | 0 |
| SCE1572_2115 | 116 | 22 |
| SCE1572_1740 | 29 | 2 |
| SCE1572_7328 | 28 | 2 |
| SCE1572_9071 | 624 | 660 |
| SCE1572_4818 | 5 | 0 |
| SCE1572_2697 | 140 | 25 |
| SCE1572_2135 | 1 | 0 |
| SCE1572_2683 | 114 | 338 |
| SCE1572_1809 | 25 | 25 |
| SCE1572_2323 | 61 | 88 |
| SCE1572_3494 | 19 | 1 |
| SCE1572_7260 | 254 | 1088 |
| SCE1572_7377 | 172 | 109 |
| SCE1572_8282 | 270 | 398 |
| SCE1572_9596 | 26 | 547 |
| SCE1572_3885 | 94 | 12 |
| SCE1572_2068 | 14 | 4 |
| SCE1572_2063 | 83 | 29 |
| SCE1572_2101 | 69 | 108 |
| SCE1572_7000 | 0 | 0 |
| SCE1572_9688 | 439 | 344 |
| SCE1572_4257 | 13 | 0 |
| SCE1572_9028 | 81 | 103 |
| SCE1572_11581 | 71 | 38 |
| SCE1572_11232 | 55 | 13 |
| SCE1572_2299 | 166 | 349 |
| SCE1572_8339 | 97 | 36 |
| SCE1572_8957 | 103 | 141 |
| SCE1572_10186 | 82 | 78 |
| SCE1572_2217 | 2 | 0 |
| SCE1572_9384 | 31 | 9 |
| SCE1572_8749 | 85 | 38 |

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| SCE1572_4612 | 48 | 3 |
| SCE1572_3795 | 66 | 19 |
| SCE1572_8487 | 5 | 1 |
| SCE1572_9356 | 160 | 315 |
| SCE1572_4354 | 47 | 13 |
| SCE1572_10322 | 32 | 198 |
| SCE1572_6052 | 807 | 455 |
| SCE1572_3663 | 133 | 16 |
| SCE1572_7624 | 152 | 98 |
| SCE1572_4738 | 22 | 17 |
| SCE1572_2493 | 305 | 76 |
| SCE1572_10218 | 209 | 128 |
| SCE1572_990 | 187 | 74 |
| SCE1572_596 | 774 | 1237 |
| SCE1572_11452 | 27 | 3 |
| SCE1572_3857 | 66 | 72 |
| SCE1572_2273 | 26 | 23 |
| SCE1572_11099 | 57 | 22 |
| SCE1572_4881 | 5 | 1 |
| SCE1572_2555 | 55 | 11 |
| SCE1572_263 | 1 | 0 |
| SCE1572_3116 | 157 | 36 |
| SCE1572_2747 | 68 | 32 |
| SCE1572_4362 | 1 | 0 |
| SCE1572_1105 | 112 | 27 |
| SCE1572_805 | 316 | 113 |
| SCE1572_3943 | 1797 | 1623 |
| SCE1572_11155 | 131 | 110 |
| SCE1572_11479 | 3 | 0 |
| SCE1572_8504 | 47 | 6 |
| SCE1572_6550 | 118 | 40 |
| SCE1572_8775 | 125 | 30 |
| SCE1572_9000 | 173 | 137 |
| SCE1572_699 | 48 | 4 |
| SCE1572_9009 | 0 | 0 |
| SCE1572_7519 | 39 | 103 |
| SCE1572_4311 | 164 | 31 |
| SCE1572_4040 | 73 | 16 |
| SCE1572_3193 | 618 | 270 |
| SCE1572_2455 | 126 | 112 |
| SCE1572_1948 | 44 | 929 |
| SCE1572_11377 | 29 | 37 |
| SCE1572_532 | 294 | 46 |
| SCE1572_4876 | 150 | 42 |
| SCE1572_5264 | 108 | 216 |
| SCE1572_8573 | 6 | 0 |
| SCE1572_3523 | 73 | 43 |
| SCE1572_1730 | 20 | 13 |

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| SCE1572_1852 | 75 | 84 |
| SCE1572_2762 | 0 | 0 |
| SCE1572_5605 | 39 | 5 |
| SCE1572_1993 | 29 | 32 |
| SCE1572_3633 | 35 | 6 |
| SCE1572_1121 | 133 | 27 |
| SCE1572_3531 | 50 | 4 |
| SCE1572_1777 | 213 | 29 |
| SCE1572_1754 | 37 | 11 |
| SCE1572_854 | 169 | 230 |
| SCE1572_6001 | 129 | 157 |
| SCE1572_103 | 91 | 12 |
| SCE1572_6348 | 0 | 0 |
| SCE1572_4341 | 76 | 38 |
| SCE1572_7308 | 0 | 0 |
| SCE1572_4593 | 107 | 73 |
| SCE1572_2443 | 1 | 0 |
| SCE1572_11592 | 21 | 5 |
| SCE1572_10298 | 78 | 34 |
| SCE1572_8690 | 49 | 4 |
| SCE1572_2866 | 552 | 67 |
| SCE1572_5506 | 60 | 8 |
| SCE1572_446 | 67 | 14 |
| SCE1572_3504 | 72 | 58 |
| SCE1572_767 | 38 | 5 |
| SCE1572_11077 | 11 | 49 |
| SCE1572_9066 | 246 | 28 |
| SCE1572_4106 | 35 | 9 |
| SCE1572_8733 | 138 | 29 |
| SCE1572_6437 | 130 | 17 |
| SCE1572_2522 | 61 | 47 |
| SCE1572_5702 | 97 | 64 |
| SCE1572_4399 | 42 | 3 |
| SCE1572_2004 | 7 | 0 |
| SCE1572_5982 | 16 | 2 |
| SCE1572_2280 | 137 | 36 |
| SCE1572_5937 | 72 | 6 |
| SCE1572_907 | 32 | 5 |
| SCE1572_1019 | 0 | 0 |
| SCE1572_4462 | 0 | 0 |
| SCE1572_2914 | 1949.98 | 241.72 |
| SCE1572_1026 | 10 | 185 |
| SCE1572_6747 | 0 | 0 |
| SCE1572_3715 | 256 | 154 |
| SCE1572_10463 | 519.27 | 805.96 |
| SCE1572_10456 | 109 | 9 |
| SCE1572_7170 | 122 | 84 |
| SCE1572_10867 | 36 | 10 |

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| SCE1572_6781 | 36 | 161 |
| SCE1572_8271 | 55 | 83 |
| SCE1572_7746 | 466 | 216 |
| SCE1572_7501 | 140 | 337 |
| SCE1572_9785 | 23 | 4 |
| SCE1572_10379 | 0 | 0 |
| SCE1572_7156 | 59 | 48 |
| SCE1572_10564 | 371 | 63 |
| SCE1572_4873 | 304 | 334 |
| SCE1572_2476 | 87 | 9 |
| SCE1572_3851 | 40 | 200 |
| SCE1572_1722 | 311 | 126 |
| SCE1572_10270 | 94 | 272 |
| SCE1572_1863 | 92 | 11 |
| SCE1572_9554 | 77 | 75 |
| SCE1572_4161 | 0 | 0 |
| SCE1572_1982 | 0 | 0 |
| SCE1572_6044 | 7 | 73 |
| SCE1572_5967 | 87 | 8 |
| SCE1572_10300 | 92 | 219 |
| SCE1572_7582 | 224 | 350 |
| SCE1572_522 | 39 | 20 |
| SCE1572_7473 | 176 | 201 |
| SCE1572_8194 | 82 | 7 |
| SCE1572_6049 | 65 | 151 |
| SCE1572_2032 | 118.59 | 28.63 |
| SCE1572_1920 | 51 | 23 |
| SCE1572_5324 | 157 | 157 |
| SCE1572_2426 | 568 | 513 |
| SCE1572_6490 | 65 | 11 |
| SCE1572_1929 | 56 | 49 |
| SCE1572_3483 | 201 | 115 |
| SCE1572_8518 | 39 | 113 |
| SCE1572_3738 | 16 | 6 |
| SCE1572_3246 | 428 | 566 |
| SCE1572_11563 | 58 | 13 |
| SCE1572_4036 | 32 | 1 |
| SCE1572_11241 | 139 | 57 |
| SCE1572_9560 | 107 | 35 |
| SCE1572_933 | 287 | 245 |
| SCE1572_2196 | 125 | 812 |
| SCE1572_3350 | 59 | 14 |
| SCE1572_7245 | 79 | 49 |
| SCE1572_2355 | 48 | 24 |
| SCE1572_3647 | 40 | 82 |
| SCE1572_9304 | 185 | 211 |
| SCE1572_218 | 28 | 39 |
| SCE1572_1484 | 155 | 33 |

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| SCE1572_1038 | 15 | 2 |
| SCE1572_8793 | 7 | 0 |
| SCE1572_5488 | 189 | 18 |
| SCE1572_36 | 106 | 76 |
| SCE1572_5827 | 111.16 | 36.34 |
| SCE1572_5049 | 51 | 39 |
| SCE1572_7939 | 20 | 28 |
| SCE1572_2833 | 27 | 63 |
| SCE1572_3374 | 198 | 3148 |
| SCE1572_114 | 33 | 3 |
| SCE1572_4240 | 74 | 20 |
| SCE1572_2970 | 19.16 | 13 |
| SCE1572_6536 | 329 | 277 |
| SCE1572_4634 | 222 | 36 |
| SCE1572_1638 | 16 | 4 |
| SCE1572_7781 | 6 | 0 |
| SCE1572_137 | 70 | 18 |
| SCE1572_6304 | 21 | 22 |
| SCE1572_3829 | 106 | 369 |
| SCE1572_2629 | 100.27 | 22 |
| SCE1572_2532 | 56 | 151 |
| SCE1572_8479 | 110 | 309 |
| SCE1572_3863 | 123 | 22 |
| SCE1572_9466 | 149 | 97 |
| SCE1572_913 | 16 | 11 |
| SCE1572_8869 | 95 | 20 |
| SCE1572_174 | 44 | 9 |
| SCE1572_7822 | 189 | 486 |
| SCE1572_10818 | 170 | 77 |
| SCE1572_158 | 295 | 848 |
| SCE1572_8343 | 10 | 1 |
| SCE1572_6081 | 15 | 0 |
| SCE1572_3007 | 29 | 12 |
| SCE1572_7142 | 151.9 | 88.93 |
| SCE1572_8850 | 31 | 26 |
| SCE1572_1499 | 19 | 2 |
| SCE1572_4970 | 35 | 4 |
| SCE1572_3033 | 285 | 170 |
| SCE1572_11487 | 13.25 | 0.75 |
| SCE1572_3895 | 29 | 22 |
| SCE1572_1297 | 54 | 232 |
| SCE1572_8394 | 277 | 230 |
| SCE1572_832 | 7 | 2 |
| SCE1572_6684 | 79 | 95 |
| SCE1572_2646 | 0 | 0 |
| SCE1572_7935 | 115 | 26 |
| SCE1572_2880 | 15 | 12 |
| SCE1572_737 | 89 | 26 |

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| SCE1572_11026 | 16 | 6 |
| SCE1572_8584 | 0 | 0 |
| SCE1572_9851 | 27 | 5 |
| SCE1572_300 | 42 | 13 |
| SCE1572_1462 | 9 | 0 |
| SCE1572_9135 | 30 | 6 |
| SCE1572_3843 | 3 | 0 |
| SCE1572_9223 | 455 | 39 |
| SCE1572_7790 | 0 | 0 |
| SCE1572_4905 | 62 | 501 |
| SCE1572_235 | 3 | 2 |
| SCE1572_6411 | 31 | 10 |
| SCE1572_346 | 201 | 33 |
| SCE1572_3217 | 150 | 40 |
| SCE1572_4895 | 57 | 15 |
| SCE1572_5062 | 131 | 148 |
| SCE1572_11600 | 15 | 1 |
| SCE1572_1706 | 137 | 95 |
| SCE1572_1442 | 101 | 18 |
| SCE1572_1395 | 140 | 3707.96 |
| SCE1572_1762 | 447.76 | 33.22 |
| SCE1572_10141 | 17 | 25 |
| SCE1572_7863 | 42 | 2 |
| SCE1572_9319 | 9 | 1 |
| SCE1572_4398 | 53 | 21 |
| SCE1572_5775 | 212 | 81 |
| SCE1572_11182 | 60 | 8 |
| SCE1572_3597 | 0 | 0 |
| SCE1572_333 | 77 | 37 |
| SCE1572_3240 | 2 | 0 |
| SCE1572_7435 | 103 | 8 |
| SCE1572_3733 | 0 | 0 |
| SCE1572_2577 | 115 | 22 |
| SCE1572_6127 | 181 | 300 |
| SCE1572_394 | 234 | 161 |
| SCE1572_11023 | 200 | 265 |
| SCE1572_6499 | 50 | 23 |
| SCE1572_11516 | 37 | 8 |
| SCE1572_8327 | 220 | 60 |
| SCE1572_5040 | 88 | 145 |
| SCE1572_7568 | 271 | 67 |
| SCE1572_499 | 67 | 17 |
| SCE1572_662 | 3466 | 4029 |
| SCE1572_1570 | 126 | 97 |
| SCE1572_4042 | 18 | 6 |
| SCE1572_4667 | 0 | 0 |
| SCE1572_5851 | 0 | 0 |
| SCE1572_1904 | 5 | 0 |

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| SCE1572_5389 | 532 | 688 |
| SCE1572_1111 | 64 | 4 |
| SCE1572_8090 | 83 | 7 |
| SCE1572_1869 | 71 | 183 |
| SCE1572_6325 | 42 | 75 |
| SCE1572_10884 | 40 | 14 |
| SCE1572_2956 | 23 | 6 |
| SCE1572_481 | 125 | 14 |
| SCE1572_9264 | 130 | 79 |
| SCE1572_6309 | 66 | 36 |
| SCE1572_415 | 77 | 82 |
| SCE1572_6452 | 399.88 | 68 |
| SCE1572_2108 | 63 | 128 |
| SCE1572_9106 | 81 | 4 |
| SCE1572_8175 | 6 | 0 |
| SCE1572_2383 | 51 | 22 |
| SCE1572_11103 | 26 | 21 |
| SCE1572_1043 | 31 | 32 |
| SCE1572_9634 | 206 | 109 |
| SCE1572_10138 | 0 | 0 |
| SCE1572_10471 | 103 | 65 |
| SCE1572_3076 | 110 | 42 |
| SCE1572_10026 | 159 | 366 |
| SCE1572_7314 | 95 | 18 |
| SCE1572_5623 | 98 | 138 |
| SCE1572_2961 | 217 | 709 |
| SCE1572_9505 | 33 | 11 |
| SCE1572_1966 | 132 | 445 |
| SCE1572_9229 | 1 | 0 |
| SCE1572_4801 | 61 | 61 |
| SCE1572_8879 | 66 | 9 |
| SCE1572_8308 | 688 | 827 |
| SCE1572_1144 | 68 | 26 |
| SCE1572_7834 | 1 | 0 |
| SCE1572_9325 | 0 | 0 |
| SCE1572_3132 | 41 | 12 |
| SCE1572_476 | 80 | 91 |
| SCE1572_6066 | 23 | 2 |
| SCE1572_5036 | 5 | 4 |
| SCE1572_8367 | 107 | 15 |
| SCE1572_8457 | 302 | 221 |
| SCE1572_6832 | 51 | 9 |
| SCE1572_4530 | 45 | 6 |
| SCE1572_8350 | 15.55 | 0 |
| SCE1572_11485 | 714 | 367 |
| SCE1572_670 | 114 | 151 |
| SCE1572_10991 | 81 | 40 |
| SCE1572_5285 | 16 | 11 |

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| SCE1572_7685 | 25 | 6 |
| SCE1572_5289 | 25 | 2 |
| SCE1572_9226 | 78 | 19 |
| SCE1572_2887 | 16 | 1 |
| SCE1572_3146 | 28 | 4 |
| SCE1572_3317 | 260 | 727 |
| SCE1572_1466 | 136 | 14 |
| SCE1572_8346 | 193 | 30 |
| SCE1572_1278 | 54 | 13 |
| SCE1572_928 | 143 | 56 |
| SCE1572_8133 | 81 | 6 |
| SCE1572_7010 | 96.72 | 33 |
| SCE1572_2785 | 25 | 11 |
| SCE1572_784 | 58 | 6 |
| SCE1572_6738 | 32 | 30 |
| SCE1572_10751 | 325 | 54 |
| SCE1572_8429 | 116 | 59 |
| SCE1572_6844 | 88 | 63 |
| SCE1572_5382 | 59 | 9 |
| SCE1572_9078 | 51 | 2 |
| SCE1572_7185 | 39 | 6 |
| SCE1572_5166 | 9 | 4 |
| SCE1572_2630 | 174.21 | 21.22 |
| SCE1572_6459 | 75 | 6 |
| SCE1572_11262 | 63 | 62 |
| SCE1572_724 | 186 | 23 |
| SCE1572_11189 | 956 | 140 |
| SCE1572_7093 | 30 | 11 |
| SCE1572_11120 | 15 | 5 |
| SCE1572_5728 | 85 | 44 |
| SCE1572_7075 | 33 | 22 |
| SCE1572_1205 | 35 | 3 |
| SCE1572_8470 | 106 | 52 |
| SCE1572_1662 | 58 | 82 |
| SCE1572_11042 | 571 | 57 |
| SCE1572_2558 | 94 | 20 |
| SCE1572_2157 | 67 | 86 |
| SCE1572_9046 | 943 | 137 |
| SCE1572_6447 | 5 | 4 |
| SCE1572_6174 | 116 | 64 |
| SCE1572_7598 | 18 | 39 |
| SCE1572_11258 | 14 | 16 |
| SCE1572_3463 | 189 | 54 |
| SCE1572_10058 | 261 | 735 |
| SCE1572_10900 | 50 | 89 |
| SCE1572_11197 | 75 | 32 |
| SCE1572_4979 | 24 | 62 |
| SCE1572_10368 | 13 | 2 |

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| SCE1572_2806 | 174.74 | 29.43 |
| SCE1572_7869 | 222 | 166 |
| SCE1572_5991 | 96 | 49 |
| SCE1572_11046 | 184 | 37 |
| SCE1572_2227 | 104 | 140 |
| SCE1572_6255 | 108 | 54 |
| SCE1572_10762 | 129 | 53 |
| SCE1572_6248 | 22 | 18 |
| SCE1572_1766 | 25 | 2 |
| SCE1572_5698 | 47.19 | 57.89 |
| SCE1572_694 | 13 | 11 |
| SCE1572_6195 | 58 | 6 |
| SCE1572_9258 | 31 | 9 |
| SCE1572_1671 | 140 | 821 |
| SCE1572_1239 | 39 | 6 |
| SCE1572_5092 | 0 | 0 |
| SCE1572_10963 | 48 | 16 |
| SCE1572_10065 | 162 | 457 |
| SCE1572_11064 | 115.64 | 59.95 |
| SCE1572_1796 | 103 | 106 |
| SCE1572_9126 | 16 | 6 |
| SCE1572_3562 | 48 | 10 |
| SCE1572_5365 | 46 | 33 |
| SCE1572_4529 | 44 | 10 |
| SCE1572_605 | 46 | 48 |
| SCE1572_11141 | 246 | 37 |
| SCE1572_7402 | 20 | 797 |
| SCE1572_7767 | 0 | 0 |
| SCE1572_2584 | 183 | 15 |
| SCE1572_2078 | 160 | 44 |
| SCE1572_7591 | 211 | 51 |
| SCE1572_6023 | 266 | 134 |
| SCE1572_3685 | 34 | 3 |
| SCE1572_1559 | 33 | 5 |
| SCE1572_9817 | 56 | 22 |
| SCE1572_6707 | 0 | 0 |
| SCE1572_1271 | 117 | 27 |
| SCE1572_10484 | 221 | 38 |
| SCE1572_9989 | 66 | 17 |
| SCE1572_10752 | 271 | 108 |
| SCE1572_10872 | 339 | 92 |
| SCE1572_2637 | 91 | 29 |
| SCE1572_1652 | 15 | 0 |
| SCE1572_11118 | 345 | 1628 |
| SCE1572_11411 | 122 | 24 |
| SCE1572_3424 | 167 | 34 |
| SCE1572_3824 | 90 | 91 |
| SCE1572_4838 | 143 | 47 |

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| SCE1572_4728 | 566 | 102 |
| SCE1572_1550 | 50 | 12 |
| SCE1572_1308 | 802 | 4743 |
| SCE1572_1055 | 309 | 53 |
| SCE1572_4302 | 84 | 21 |
| SCE1572_425 | 99 | 549 |
| SCE1572_9861 | 32 | 9 |
| SCE1572_554 | 27 | 26 |
| SCE1572_8554 | 272 | 374 |
| SCE1572_4070 | 247 | 306 |
| SCE1572_11060 | 26 | 17 |
| SCE1572_1049 | 7 | 1 |
| SCE1572_3183 | 38 | 23 |
| SCE1572_8659 | 374 | 442 |
| SCE1572_6233 | 163 | 66 |
| SCE1572_3355 | 398 | 55 |
| SCE1572_2909 | 62 | 22 |
| SCE1572_7327 | 579 | 112 |
| SCE1572_1199 | 0 | 0 |
| SCE1572_7951 | 85 | 177 |
| SCE1572_11350 | 0 | 0 |
| SCE1572_4775 | 0 | 0 |
| SCE1572_2341 | 29 | 20 |
| SCE1572_6960 | 203 | 32 |
| SCE1572_10535 | 143 | 480 |
| SCE1572_9173 | 11 | 2 |
| SCE1572_7303 | 74 | 24 |
| SCE1572_3290 | 30 | 4 |
| SCE1572_2562 | 108 | 43 |
| SCE1572_6812 | 41 | 4 |
| SCE1572_7294 | 47 | 39 |
| SCE1572_6156 | 32 | 5 |
| SCE1572_10423 | 40 | 67 |
| SCE1572_1798 | 45 | 83 |
| SCE1572_867 | 55 | 43 |
| SCE1572_9426 | 62 | 25 |
| SCE1572_618 | 202 | 641 |
| SCE1572_4790 | 50 | 39 |
| SCE1572_10478 | 140 | 63 |
| SCE1572_1538 | 45 | 17 |
| SCE1572_7321 | 104 | 12 |
| SCE1572_5318 | 91 | 15 |
| SCE1572_4426 | 133 | 1222 |
| SCE1572_9961 | 69 | 6 |
| SCE1572_3399 | 43 | 14 |
| SCE1572_2271 | 59 | 23 |
| SCE1572_3322 | 1 | 0 |
| SCE1572_8670 | 13 | 46 |

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| SCE1572_2240 | 98 | 72 |
| SCE1572_9774 | 162 | 142 |
| SCE1572_6094 | 245 | 23 |
| SCE1572_1081 | 29 | 8 |
| SCE1572_10555 | 157 | 13 |
| SCE1572_6107 | 104 | 16 |
| SCE1572_2084 | 75 | 128 |
| SCE1572_11575 | 71 | 190 |
| SCE1572_3778 | 94 | 32 |
| SCE1572_10625 | 75 | 15 |
| SCE1572_6937 | 20 | 9 |
| SCE1572_10455 | 68 | 12 |
| SCE1572_9644 | 24 | 42 |
| SCE1572_3000 | 356 | 52 |
| SCE1572_2608 | 94 | 23 |
| SCE1572_7957 | 534 | 1955 |
| SCE1572_8526 | 71 | 54 |
| SCE1572_5398 | 93 | 18 |
| SCE1572_9133 | 5 | 1 |
| SCE1572_4520 | 108 | 114 |
| SCE1572_10802 | 89 | 15 |
| SCE1572_8383 | 104 | 25 |
| SCE1572_2984 | 209 | 61 |
| SCE1572_9913 | 0 | 0 |
| SCE1572_7941 | 151 | 178 |
| SCE1572_11333 | 169 | 91 |
| SCE1572_5311 | 63 | 27 |
| SCE1572_5915 | 301 | 158 |
| SCE1572_2604 | 21 | 7 |
| SCE1572_11523 | 7 | 4 |
| SCE1572_7730 | 37 | 3 |
| SCE1572_5304 | 54 | 29 |
| SCE1572_5342 | 16 | 6 |
| SCE1572_1301 | 121 | 27 |
| SCE1572_5180 | 73 | 1112 |
| SCE1572_10879 | 158 | 209 |
| SCE1572_11359 | 62 | 17 |
| SCE1572_1659 | 65 | 25 |
| SCE1572_2143 | 70 | 35 |
| SCE1572_9587 | 143 | 126 |
| SCE1572_5128 | 362 | 663 |
| SCE1572_10672 | 17 | 9 |
| SCE1572_11172 | 29 | 7 |
| SCE1572_7183 | 85 | 16 |
| SCE1572_884 | 216 | 99 |
| SCE1572_10854 | 87 | 36 |
| SCE1572_10047 | 44 | 52 |
| SCE1572_11214 | 322 | 51 |

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| SCE1572_492 | 0 | 0 |
| SCE1572_5377 | 94 | 16 |
| SCE1572_10758 | 116 | 34 |
| SCE1572_7893 | 487 | 7931 |
| SCE1572_2937 | 296 | 1266 |
| SCE1572_8412 | 268 | 122 |
| SCE1572_7674 | 174.22 | 19 |
| SCE1572_7385 | 78 | 15 |
| SCE1572_2347 | 2583 | 11839 |
| SCE1572_5239 | 20 | 13 |
| SCE1572_9085 | 33 | 11 |
| SCE1572_5234 | 163 | 963 |
| SCE1572_4208 | 86 | 97 |
| SCE1572_2254 | 63 | 4 |
| SCE1572_10983 | 63 | 45 |
| SCE1572_6349 | 183 | 93 |
| SCE1572_154 | 90 | 54 |
| SCE1572_5751 | 406 | 174 |
| SCE1572_251 | 114.99 | 4.68 |
| SCE1572_9002 | 192 | 87 |
| SCE1572_10974 | 2 | 1 |
| SCE1572_9471 | 10 | 3 |
| SCE1572_10276 | 799 | 185 |
| SCE1572_8275 | 158 | 121 |
| SCE1572_107 | 72 | 50 |
| SCE1572_2037 | 44 | 116 |
| SCE1572_2027 | 0 | 0 |
| SCE1572_9580 | 92 | 19 |
| SCE1572_722 | 40.92 | 5 |
| SCE1572_790 | 0 | 0 |
| SCE1572_10678 | 85 | 183 |
| SCE1572_9628 | 199.96 | 37 |
| SCE1572_6344 | 139 | 52 |
| SCE1572_4279 | 57 | 30 |
| SCE1572_6372 | 0 | 0 |
| SCE1572_7358 | 57 | 49 |
| SCE1572_5332 | 444 | 206 |
| SCE1572_8119 | 125.38 | 127.51 |
| SCE1572_3827 | 68 | 96 |
| SCE1572_3017 | 126 | 63 |
| SCE1572_5871 | 118 | 49 |
| SCE1572_8940 | 164 | 231 |
| SCE1572_3039 | 98 | 6 |
| SCE1572_10237 | 158 | 32 |
| SCE1572_6956 | 49 | 1 |
| SCE1572_5857 | 0 | 0 |
| SCE1572_2754 | 164 | 68 |
| SCE1572_10904 | 50 | 317 |

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| SCE1572_11090 | 122 | 94 |
| SCE1572_10466 | 185 | 54 |
| SCE1572_5725 | 19.28 | 0 |
| SCE1572_1181 | 16 | 0 |
| SCE1572_1583 | 126 | 5 |
| SCE1572_4974 | 146 | 918 |
| SCE1572_10847 | 146 | 26 |
| SCE1572_6622 | 74 | 23 |
| SCE1572_9086 | 48 | 5 |
| SCE1572_1509 | 169 | 19 |
| SCE1572_7548 | 116 | 16 |
| SCE1572_7427 | 359 | 92 |
| SCE1572_5843 | 17 | 2 |
| SCE1572_1156 | 0 | 0 |
| SCE1572_3387 | 30 | 2 |
| SCE1572_1721 | 8 | 0 |
| SCE1572_8857 | 57 | 56 |
| SCE1572_4982 | 42 | 3 |
| SCE1572_6479 | 95 | 233 |
| SCE1572_1439 | 58 | 9 |
| SCE1572_5552 | 2 | 3 |
| SCE1572_9144 | 31 | 5 |
| SCE1572_819 | 64 | 16 |
| SCE1572_2742 | 38 | 30 |
| SCE1572_5765 | 118 | 153 |
| SCE1572_8185 | 43 | 1 |
| SCE1572_1519 | 381 | 93 |
| SCE1572_5777 | 39 | 153 |
| SCE1572_10680 | 0 | 0 |
| SCE1572_3867 | 64 | 118 |
| SCE1572_10169 | 105 | 405 |
| SCE1572_1315 | 59 | 91 |
| SCE1572_9968 | 67 | 9 |
| SCE1572_3736 | 51 | 28 |
| SCE1572_810 | 336 | 101 |
| SCE1572_7909 | 52 | 42 |
| SCE1572_2256 | 231 | 57 |
| SCE1572_8214 | 261 | 90 |
| SCE1572_3020 | 304 | 39 |
| SCE1572_6906 | 0 | 0 |
| SCE1572_6577 | 36 | 13 |
| SCE1572_3489 | 30 | 4 |
| SCE1572_6965 | 37 | 12 |
| SCE1572_1831 | 0 | 0 |
| SCE1572_8681 | 75 | 8 |
| SCE1572_3756 | 445.41 | 51.28 |
| SCE1572_5868 | 161 | 56 |
| SCE1572_3928 | 274 | 120 |

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| SCE1572_4724 | 175 | 36 |
| SCE1572_1444 | 60 | 31 |
| SCE1572_7487 | 234 | 53 |
| SCE1572_7528 | 116 | 44 |
| SCE1572_6488 | 19 | 3 |
| SCE1572_7581 | 2137 | 2430 |
| SCE1572_11247 | 32 | 10 |
| SCE1572_4786 | 1154 | 6602 |
| SCE1572_297 | 94 | 23 |
| SCE1572_6386 | 81 | 10 |
| SCE1572_9944 | 1 | 0 |
| SCE1572_3357 | 0 | 0 |
| SCE1572_10508 | 71 | 140 |
| SCE1572_2044 | 1 | 0 |
| SCE1572_5255 | 2 | 0 |
| SCE1572_4405 | 39 | 4 |
| SCE1572_4497 | 78 | 89 |
| SCE1572_6970 | 10 | 73 |
| SCE1572_6083 | 206 | 21 |
| SCE1572_8916 | 27 | 51 |
| SCE1572_6801 | 63 | 21 |
| SCE1572_1160 | 127 | 28 |
| SCE1572_703 | 14 | 3 |
| SCE1572_658 | 439 | 266 |
| SCE1572_3891 | 140 | 77 |
| SCE1572_9614 | 46 | 0 |
| SCE1572_9589 | 472 | 452 |
| SCE1572_5653 | 170 | 432 |
| SCE1572_6562 | 59 | 21 |
| SCE1572_10996 | 47 | 10 |
| SCE1572_8164 | 9 | 4 |
| SCE1572_7116 | 59 | 51 |
| SCE1572_633 | 44 | 32 |
| SCE1572_6992 | 131 | 19 |
| SCE1572_5512 | 230 | 162 |
| SCE1572_1502 | 108 | 175 |
| SCE1572_145 | 76 | 26 |
| SCE1572_433 | 377 | 121 |
| SCE1572_7636 | 678 | 5880 |
| SCE1572_1909 | 0 | 0 |
| SCE1572_11261 | 83 | 15 |
| SCE1572_6529 | 60 | 26 |
| SCE1572_4675 | 93 | 28 |
| SCE1572_11512 | 1167 | 1689 |
| SCE1572_6191 | 30 | 35 |
| SCE1572_5454 | 46 | 10 |
| SCE1572_6379 | 54 | 0 |
| SCE1572_8907 | 77 | 33 |

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| SCE1572_1482 | 146 | 26 |
| SCE1572_9810 | 68 | 35 |
| SCE1572_8771 | 0 | 0 |
| SCE1572_9442 | 25 | 2 |
| SCE1572_4746 | 208 | 44 |
| SCE1572_4706 | 111 | 43 |
| SCE1572_11442 | 61 | 28 |
| SCE1572_9347 | 43 | 6 |
| SCE1572_4991 | 12 | 4 |
| SCE1572_3699 | 29 | 2 |
| SCE1572_4956 | 122 | 85 |
| SCE1572_7881 | 147 | 58 |
| SCE1572_2392 | 232 | 261 |
| SCE1572_8417 | 78 | 25 |
| SCE1572_6319 | 65 | 25 |
| SCE1572_8197 | 29 | 6 |
| SCE1572_10418 | 38 | 22 |
| SCE1572_10515 | 133 | 104 |
| SCE1572_4360 | 156 | 118 |
| SCE1572_8900 | 407 | 168 |
| SCE1572_8949 | 24 | 19 |
| SCE1572_9208 | 35 | 16 |
| SCE1572_527 | 35 | 33 |
| SCE1572_2191 | 325 | 1541 |
| SCE1572_7236 | 95 | 120 |
| SCE1572_366 | 123 | 174 |
| SCE1572_7615 | 115 | 38 |
| SCE1572_5493 | 0 | 0 |
| SCE1572_9244 | 3 | 0 |
| SCE1572_4756 | 83 | 18 |
| SCE1572_3258 | 61 | 117 |
| SCE1572_8621 | 136 | 202 |
| SCE1572_1347 | 600 | 1043 |
| SCE1572_6545 | 196 | 356 |
| SCE1572_3973 | 52 | 72 |
| SCE1572_874 | 258 | 52 |
| SCE1572_3435 | 99 | 54 |
| SCE1572_10544 | 12 | 1 |
| SCE1572_4418 | 18 | 6 |
| SCE1572_2618 | 0 | 0 |
| SCE1572_732 | 137 | 30 |
| SCE1572_5028 | 92 | 30 |
| SCE1572_3336 | 118 | 608 |
| SCE1572_5055 | 131 | 32 |
| SCE1572_11503 | 119 | 20 |
| SCE1572_6659 | 98 | 49 |
| SCE1572_4969 | 60 | 8 |
| SCE1572_8161 | 67 | 3 |

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| SCE1572_10952 | 0 | 0 |
| SCE1572_4633 | 81 | 29 |
| SCE1572_5749 | 72 | 22 |
| SCE1572_5678 | 273 | 358 |
| SCE1572_2652 | 659 | 138 |
| SCE1572_7229 | 128 | 277 |
| SCE1572_7105 | 125 | 24 |
| SCE1572_6520 | 56 | 23 |
| SCE1572_1768 | 226 | 31 |
| SCE1572_6860 | 531 | 111 |
| SCE1572_3239 | 56 | 16 |
| SCE1572_7215 | 64 | 49 |
| SCE1572_2622 | 29 | 1 |
| SCE1572_3088 | 17 | 6 |
| SCE1572_10855 | 158 | 45 |
| SCE1572_8845 | 48 | 9 |
| SCE1572_5306 | 711 | 1035 |
| SCE1572_9360 | 84 | 321 |
| SCE1572_278 | 12 | 2 |
| SCE1572_10036 | 18 | 3 |
| SCE1572_4164 | 99 | 16 |
| SCE1572_3242 | 18 | 0 |
| SCE1572_1413 | 16 | 5 |
| SCE1572_8541 | 21 | 117 |
| SCE1572_5886 | 286 | 56 |
| SCE1572_1843 | 71 | 14 |
| SCE1572_8862 | 49 | 5 |
| SCE1572_6516 | 180 | 18 |
| SCE1572_3162 | 174 | 228 |
| SCE1572_11169 | 114 | 12 |
| SCE1572_11019 | 37 | 44 |
| SCE1572_9160 | 117 | 136 |
| SCE1572_5205 | 99 | 42 |
| SCE1572_3871 | 89 | 84 |
| SCE1572_5020 | 80 | 25 |
| SCE1572_4232 | 90 | 10 |
| SCE1572_258 | 48 | 30 |
| SCE1572_1062 | 295 | 15 |
| SCE1572_10598 | 0 | 0 |
| SCE1572_9707 | 132 | 18 |
| SCE1572_7718 | 167 | 28 |
| SCE1572_10089 | 60 | 63 |
| SCE1572_10080 | 251 | 417 |
| SCE1572_3706 | 87 | 29 |
| SCE1572_5803 | 38 | 18 |
| SCE1572_6893 | 219 | 40 |
| SCE1572_6999 | 76 | 4 |
| SCE1572_9679 | 210 | 292 |

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| SCE1572_3513 | 121 | 389 |
| SCE1572_9856 | 58 | 14 |
| SCE1572_583 | 46 | 68 |
| SCE1572_2113 | 83 | 32 |
| SCE1572_8355 | 116.84 | 19.83 |
| SCE1572_1368 | 206 | 174 |
| SCE1572_801 | 53 | 19 |
| SCE1572_7222 | 87 | 696 |
| SCE1572_7452 | 21 | 14 |
| SCE1572_2659 | 134 | 42 |
| SCE1572_3275 | 216 | 168 |
| SCE1572_7534 | 2 | 0 |
| SCE1572_404 | 128 | 57 |
| SCE1572_10619 | 147 | 38 |
| SCE1572_3921 | 108 | 50 |
| SCE1572_4488 | 174.39 | 35 |
| SCE1572_5095 | 183 | 258 |
| SCE1572_8847 | 0 | 0 |
| SCE1572_4835 | 134 | 45 |
| SCE1572_2724 | 61 | 108 |
| SCE1572_628 | 33 | 26 |
| SCE1572_9309 | 0 | 0 |
| SCE1572_6455 | 1 | 0 |
| SCE1572_2575 | 124 | 26 |
| SCE1572_7573 | 80 | 248 |
| SCE1572_3003 | 24 | 31 |
| SCE1572_5671 | 106 | 23 |
| SCE1572_202 | 136 | 49 |
| SCE1572_3455 | 68 | 9 |
| SCE1572_11332 | 41 | 44 |
| SCE1572_7804 | 418 | 151 |
| SCE1572_10718 | 12 | 17 |
| SCE1572_4686 | 87.77 | 184.74 |
| SCE1572_4249 | 1 | 0 |
| SCE1572_6869 | 42 | 12 |
| SCE1572_10052 | 106 | 130 |
| SCE1572_1709 | 161 | 51 |
| SCE1572_969 | 69 | 82 |
| SCE1572_5229 | 21 | 20 |
| SCE1572_5143 | 80 | 5 |
| SCE1572_1711 | 151 | 45 |
| SCE1572_7843 | 237 | 418 |
| SCE1572_10230 | 160.76 | 22.04 |
| SCE1572_6294 | 24 | 167 |
| SCE1572_3338 | 113 | 700 |
| SCE1572_1012 | 65 | 4 |
| SCE1572_4844 | 85 | 65 |
| SCE1572_10282 | 22 | 33 |

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| SCE1572_6288 | 39 | 6 |
| SCE1572_189 | 74 | 36 |
| SCE1572_1058 | 5 | 1 |
| SCE1572_1728 | 196 | 49 |
| SCE1572_8474 | 93 | 37 |
| SCE1572_2423 | 124 | 144 |
| SCE1572_9406 | 13 | 13 |
| SCE1572_2502 | 0 | 0 |
| SCE1572_6413 | 134 | 34 |
| SCE1572_5023 | 0 | 0 |
| SCE1572_5220 | 94 | 111 |
| SCE1572_4411 | 60 | 7 |
| SCE1572_4015 | 187 | 124 |
| SCE1572_1094 | 46 | 9 |
| SCE1572_10263 | 86 | 21 |
| SCE1572_5869 | 38 | 162 |
| SCE1572_7228 | 117 | 628 |
| SCE1572_9169 | 129.41 | 25.37 |
| SCE1572_651 | 26 | 0 |
| SCE1572_198 | 148 | 154 |
| SCE1572_8376 | 6 | 0 |
| SCE1572_5934 | 22 | 2 |
| SCE1572_5030 | 666 | 1874 |
| SCE1572_11284 | 50 | 31 |
| SCE1572_11299 | 73 | 11 |
| SCE1572_9896 | 13 | 0 |
| SCE1572_5005 | 17 | 0 |
| SCE1572_6878 | 357 | 32 |
| SCE1572_10973 | 301 | 598 |
| SCE1572_5136 | 89 | 35 |
| SCE1572_5958 | 53 | 20 |
| SCE1572_459 | 24 | 3 |
| SCE1572_8758 | 256 | 484 |
| SCE1572_7972 | 27 | 61 |
| SCE1572_10646 | 126 | 25 |
| SCE1572_9661 | 397 | 1140 |
| SCE1572_5734 | 142 | 127 |
| SCE1572_3619 | 194 | 30 |
| SCE1572_10393 | 321 | 54 |
| SCE1572_1211 | 33 | 11 |
| SCE1572_86 | 0 | 0 |
| SCE1572_7210 | 6 | 1 |
| SCE1572_11560 | 427.69 | 96.63 |
| SCE1572_3286 | 46 | 12 |
| SCE1572_10040 | 156 | 92 |
| SCE1572_3521 | 228 | 109 |
| SCE1572_3611 | 207 | 88 |
| SCE1572_11208 | 277 | 185 |

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| SCE1572_3545 | 0 | 0 |
| SCE1572_3472 | 80 | 7 |
| SCE1572_9902 | 60 | 28 |
| SCE1572_7735 | 467 | 1241 |
| SCE1572_8529 | 167 | 45 |
| SCE1572_7764 | 5 | 1 |
| SCE1572_5218 | 35 | 7 |
| SCE1572_1547 | 32 | 19 |
| SCE1572_3390 | 54 | 57 |
| SCE1572_6109 | 60 | 4 |
| SCE1572_3202 | 299 | 3032 |
| SCE1572_7550 | 242 | 35 |
| SCE1572_5119 | 278 | 250 |
| SCE1572_11180 | 20 | 3 |
| SCE1572_6852 | 0 | 0 |
| SCE1572_9921 | 163 | 94 |
| SCE1572_10245 | 60 | 7 |
| SCE1572_10707 | 0 | 0 |
| SCE1572_182 | 325 | 145 |
| SCE1572_7084 | 441 | 98 |
| SCE1572_9288 | 529 | 337 |
| SCE1572_565 | 95 | 138 |
| SCE1572_8684 | 33 | 23 |
| SCE1572_5174 | 10 | 1 |
| SCE1572_6598 | 82 | 26 |
| SCE1572_9036 | 99 | 26 |
| SCE1572_354 | 48 | 12 |
| SCE1572_8789 | 85 | 88 |
| SCE1572_4433 | 147 | 21 |
| SCE1572_2202 | 74 | 274 |
| SCE1572_2051 | 114 | 15 |
| SCE1572_2519 | 177 | 26 |
| SCE1572_8808 | 23 | 5 |
| SCE1572_8126 | 140 | 25 |
| SCE1572_11395 | 336 | 848 |
| SCE1572_4291 | 35 | 23 |
| SCE1572_11162 | 96 | 88 |
| SCE1572_7847 | 29 | 11 |
| SCE1572_621 | 144 | 37 |
| SCE1572_1871 | 150 | 61 |
| SCE1572_5664 | 34 | 30 |
| SCE1572_3668 | 61 | 11 |
| SCE1572_1247 | 125 | 15 |
| SCE1572_3344 | 332 | 479 |
| SCE1572_10570 | 217 | 155 |
| SCE1572_778 | 160 | 90 |
| SCE1572_6834 | 0 | 0 |
| SCE1572_10181 | 90 | 50 |

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| SCE1572_3625 | 64 | 8 |
| SCE1572_3676 | 286.57 | 186 |
| SCE1572_3462 | 1 | 18 |
| SCE1572_8015 | 14 | 73 |
| SCE1572_5240 | 7 | 9 |
| SCE1572_4519 | 72 | 187 |
| SCE1572_52 | 3 | 0 |
| SCE1572_4220 | 24 | 12 |
| SCE1572_10248 | 117 | 20 |
| SCE1572_2641 | 219 | 80 |
| SCE1572_8560 | 45 | 13 |
| SCE1572_3814 | 155 | 80 |
| SCE1572_1870 | 13 | 1 |
| SCE1572_10720 | 168 | 28 |
| SCE1572_8318 | 25 | 5 |
| SCE1572_4287 | 137 | 17 |
| SCE1572_27 | 486 | 355 |
| SCE1572_5573 | 117 | 27 |
| SCE1572_271 | 490.82 | 1324.47 |
| SCE1572_7575 | 156 | 154 |
| SCE1572_3477 | 0 | 0 |
| SCE1572_10788 | 128 | 37 |
| SCE1572_7831 | 92 | 110 |
| SCE1572_6019 | 23 | 7 |
| SCE1572_8926 | 92 | 62.5 |
| SCE1572_10949 | 30 | 3 |
| SCE1572_6619 | 30 | 6 |
| SCE1572_4002 | 450 | 2592 |
| SCE1572_1375 | 237 | 98 |
| SCE1572_1455 | 194 | 47 |
| SCE1572_11589 | 31 | 20 |
| SCE1572_3806 | 16 | 0 |
| SCE1572_8656 | 142 | 661 |
| SCE1572_11546 | 141.59 | 6.51 |
| SCE1572_1548 | 352 | 71 |
| SCE1572_6700 | 24.98 | 4.59 |
| SCE1572_4268 | 348 | 42 |
| SCE1572_2899 | 149 | 18 |
| SCE1572_9243 | 145 | 49 |
| SCE1572_6640 | 224 | 31 |
| SCE1572_3939 | 17 | 9 |
| SCE1572_6596 | 72 | 6 |
| SCE1572_7541 | 24 | 17 |
| SCE1572_826 | 157 | 20 |
| SCE1572_3816 | 0 | 0 |
| SCE1572_3748 | 388 | 284 |
| SCE1572_5350 | 824 | 313 |
| SCE1572_7442 | 41 | 7 |

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| SCE1572_6919 | 55 | 17 |
| SCE1572_6028 | 25 | 74 |
| SCE1572_7870 | 116 | 52 |
| SCE1572_7692 | 332 | 229 |
| SCE1572_10068 | 275 | 481 |
| SCE1572_9887 | 62 | 32 |
| SCE1572_4132 | 155 | 132 |
| SCE1572_3136 | 78 | 13 |
| SCE1572_5594 | 59 | 19 |
| SCE1572_1393 | 60 | 20 |
| SCE1572_11191 | 171 | 104 |
| SCE1572_7697 | 134 | 75 |
| SCE1572_9746 | 170 | 58 |
| SCE1572_2483 | 26 | 6 |
| SCE1572_9880 | 20 | 8 |
| SCE1572_3058 | 153 | 27 |
| SCE1572_5360 | 0 | 0 |
| SCE1572_4853 | 28 | 5 |
| SCE1572_4477 | 111 | 13 |
| SCE1572_8241 | 64 | 99 |
| SCE1572_5922 | 22 | 20 |
| SCE1572_10321 | 42 | 54 |
| SCE1572_7701 | 28 | 2 |
| SCE1572_7504 | 53 | 11 |
| SCE1572_5322 | 69 | 33 |
| SCE1572_3839 | 113 | 20 |
| SCE1572_8727 | 147 | 22 |
| SCE1572_10878 | 69 | 7 |
| SCE1572_9496 | 100 | 128 |
| SCE1572_5410 | 0 | 0 |
| SCE1572_771 | 127 | 59 |
| SCE1572_9681 | 412 | 478 |
| SCE1572_7838 | 79 | 9 |
| SCE1572_3751 | 52 | 16 |
| SCE1572_6463 | 0 | 0 |
| SCE1572_6330 | 92 | 129 |
| SCE1572_6320 | 18 | 7 |
| SCE1572_11550 | 38 | 14 |
| SCE1572_129 | 3 | 0 |
| SCE1572_7099 | 23 | 1 |
| SCE1572_5918 | 0 | 0 |
| SCE1572_6070 | 14 | 12 |
| SCE1572_1566 | 77 | 12 |
| SCE1572_2510 | 151 | 66 |
| SCE1572_5590 | 188 | 26 |
| SCE1572_10261 | 417 | 162 |
| SCE1572_2710 | 60 | 14 |
| SCE1572_9562 | 4 | 0 |

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| SCE1572_7925 | 22 | 3 |
| SCE1572_350 | 149 | 2206 |
| SCE1572_6753 | 73 | 21 |
| SCE1572_8567 | 228 | 91 |
| SCE1572_4212 | 1 | 0 |
| SCE1572_5584 | 96 | 16 |
| SCE1572_83 | 43.84 | 19.66 |
| SCE1572_3126 | 26 | 65 |
| SCE1572_4546 | 39 | 5 |
| SCE1572_9280 | 29 | 5 |
| SCE1572_2144 | 57 | 80 |
| SCE1572_7877 | 119 | 11 |
| SCE1572_11112 | 45 | 16 |
| SCE1572_5536 | 109 | 44 |
| SCE1572_4629 | 301 | 301 |
| SCE1572_4239 | 211 | 388 |
| SCE1572_9675 | 172 | 171 |
| SCE1572_4943 | 363 | 875 |
| SCE1572_9639 | 0 | 0 |
| SCE1572_9236 | 31 | 6 |
| SCE1572_2690 | 144 | 37 |
| SCE1572_9536 | 261 | 49 |
| SCE1572_4765 | 53 | 15 |
| SCE1572_1222 | 56 | 12 |
| SCE1572_6185 | 154 | 34 |
| SCE1572_1174 | 6 | 0 |
| SCE1572_4948 | 58 | 14 |
| SCE1572_2891 | 4 | 0 |
| SCE1572_8890 | 551 | 78 |
| SCE1572_8668 | 16 | 1 |
| SCE1572_10820 | 112 | 85 |
| SCE1572_2878 | 321 | 172 |
| SCE1572_2056 | 71 | 4 |
| SCE1572_7258 | 104 | 25 |
| SCE1572_487 | 156 | 81 |
| SCE1572_201 | 2 | 0 |
| SCE1572_11034 | 345 | 2239 |
| SCE1572_4620 | 34 | 27 |
| SCE1572_392 | 174 | 9 |
| SCE1572_6204 | 46 | 40 |
| SCE1572_845 | 0 | 0 |
| SCE1572_57 | 159 | 20 |
| SCE1572_5473 | 26 | 17 |
| SCE1572_441 | 456 | 81 |
| SCE1572_7206 | 54 | 6 |
| SCE1572_5821 | 84.33 | 44.51 |
| SCE1572_5599 | 297.73 | 65 |
| SCE1572_4280 | 34 | 9 |

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| SCE1572_4142 | 0 | 0 |
| SCE1572_30 | 1206 | 1424 |
| SCE1572_9216 | 210 | 144 |
| SCE1572_5900 | 28 | 16 |
| SCE1572_2316 | 51 | 13 |
| SCE1572_8546 | 119 | 18 |
| SCE1572_4035 | 85 | 28 |
| SCE1572_4566 | 22 | 9 |
| SCE1572_7285 | 255 | 98 |
| SCE1572_4659 | 110 | 58 |
| SCE1572_6695 | 29 | 10 |
| SCE1572_7588 | 266 | 890 |
| SCE1572_3693 | 181 | 29 |
| SCE1572_10959 | 85 | 15 |
| SCE1572_9959 | 94 | 50 |
| SCE1572_9932 | 27 | 1 |
| SCE1572_7641 | 365 | 1590 |
| SCE1572_11517 | 63 | 19 |
| SCE1572_9714 | 33 | 434 |
| SCE1572_6942 | 117 | 23 |
| SCE1572_763 | 33 | 7 |
| SCE1572_9828 | 70 | 17 |
| SCE1572_3221 | 53 | 55 |
| SCE1572_11381 | 41 | 42 |
| SCE1572_6166 | 201 | 281 |
| SCE1572_10999 | 27 | 1 |
| SCE1572_1266 | 734 | 3638 |
| SCE1572_8247 | 43 | 10 |
| SCE1572_7600 | 191 | 120 |
| SCE1572_11321 | 57 | 18 |
| SCE1572_4077 | 31 | 37 |
| SCE1572_2870 | 24 | 5 |
| SCE1572_8362 | 0 | 0 |
| SCE1572_10940 | 39 | 10 |
| SCE1572_951 | 78 | 46 |
| SCE1572_10832 | 206 | 484 |
| SCE1572_1389 | 42 | 200 |
| SCE1572_2542 | 74 | 4 |
| SCE1572_9514 | 123 | 407 |
| SCE1572_3304 | 7 | 2 |
| SCE1572_3912 | 15 | 18 |
| SCE1572_1370 | 146 | 219 |
| SCE1572_4295 | 57 | 9 |
| SCE1572_10566 | 182 | 33 |
| SCE1572_8421 | 68 | 34 |
| SCE1572_1080 | 39 | 12 |
| SCE1572_5339 | 35 | 10 |
| SCE1572_4656 | 35 | 40 |

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| SCE1572_3040 | 64 | 12 |
| SCE1572_10227 | 29 | 4 |
| SCE1572_7147 | 88 | 102 |
| SCE1572_6168 | 37 | 18 |
| SCE1572_1674 | 240 | 282 |
| SCE1572_8000 | 43 | 8 |
| SCE1572_6925 | 14 | 4 |
| SCE1572_11373 | 235 | 608 |
| SCE1572_10654 | 87 | 232 |
| SCE1572_11526 | 149 | 23 |
| SCE1572_9522 | 5 | 1 |
| SCE1572_3414 | 449 | 275 |
| SCE1572_1896 | 0 | 0 |
| SCE1572_4602 | 36 | 43 |
| SCE1572_6798 | 114 | 52 |
| SCE1572_4080 | 108 | 245 |
| SCE1572_4046 | 0 | 0 |
| SCE1572_5246 | 340 | 499 |
| SCE1572_3212 | 25 | 17 |
| SCE1572_4694 | 49 | 19 |
| SCE1572_7983 | 304 | 157 |
| SCE1572_6665 | 76 | 143 |
| SCE1572_5568 | 46 | 16 |
| SCE1572_3144 | 26 | 2 |
| SCE1572_1125 | 232 | 35 |
| SCE1572_8778 | 85 | 14 |
| SCE1572_2334 | 0 | 0 |
| SCE1572_518 | 0 | 0 |
| SCE1572_10208 | 183 | 33 |
| SCE1572_7369 | 14 | 2 |
| SCE1572_10494 | 172 | 566 |
| SCE1572_9621 | 106 | 20 |
| SCE1572_8071 | 70 | 18 |
| SCE1572_4448 | 20 | 4 |
| SCE1572_6161 | 149 | 34 |
| SCE1572_4937 | 186 | 186 |
| SCE1572_8953 | 60.46 | 8 |
| SCE1572_5974 | 0 | 0 |
| SCE1572_5370 | 0 | 0 |
| SCE1572_3855 | 91 | 22 |
| SCE1572_3029 | 9 | 0 |
| SCE1572_9805 | 67 | 19 |
| SCE1572_10892 | 241 | 243 |
| SCE1572_2766 | 138 | 49 |
| SCE1572_11187 | 4 | 1 |
| SCE1572_10505 | 97 | 18 |
| SCE1572_1289 | 0 | 0 |
| SCE1572_1035 | 130 | 43 |

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| SCE1572_6310 | 52 | 257 |
| SCE1572_5179 | 7 | 47 |
| SCE1572_2537 | 11 | 14 |
| SCE1572_6910 | 441 | 65 |
| SCE1572_3403 | 31 | 32 |
| SCE1572_5182 | 24 | 334 |
| SCE1572_9377 | 24 | 11 |
| SCE1572_6223 | 52 | 12 |
| SCE1572_6314 | 17 | 0 |
| SCE1572_7551 | 124 | 42 |
| SCE1572_5715 | 67 | 26 |
| SCE1572_3608 | 226 | 1092 |
| SCE1572_8766 | 92 | 13 |
| SCE1572_5000 | 49 | 24 |
| SCE1572_10593 | 1 | 0 |
| SCE1572_8597 | 434 | 59 |
| SCE1572_3179 | 89 | 6 |
| SCE1572_3 | 415 | 480 |
| SCE1572_1100 | 90 | 53 |
| SCE1572_11340 | 57 | 9 |
| SCE1572_8296 | 33 | 41 |
| SCE1572_389 | 16 | 5 |
| SCE1572_381 | 27 | 3 |
| SCE1572_11253 | 807 | 4673 |
| SCE1572_2597 | 2.21 | 5.91 |
| SCE1572_9019 | 9 | 3 |
| SCE1572_4089 | 87 | 101 |
| SCE1572_3529 | 409 | 1678 |
| SCE1572_4481 | 76 | 9 |
| SCE1572_2321 | 76 | 167 |
| SCE1572_9332 | 0 | 0 |
| SCE1572_10122 | 249 | 37 |
| SCE1572_6896 | 103 | 155 |
| SCE1572_3372 | 67 | 41 |
| SCE1572_3247 | 104 | 153 |
| SCE1572_10434 | 531 | 216 |
| SCE1572_10137 | 375 | 68 |
| SCE1572_9031 | 243 | 70 |
| SCE1572_7481 | 18 | 0 |
| SCE1572_9653 | 325.08 | 47.73 |
| SCE1572_7057 | 8 | 0 |
| SCE1572_10190 | 211 | 254 |
| SCE1572_11014 | 92 | 24 |
| SCE1572_130 | 106 | 16 |
| SCE1572_2927 | 21 | 2 |
| SCE1572_215 | 95 | 32 |
| SCE1572_7903 | 10 | 5 |
| SCE1572_5295 | 42 | 4 |

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| SCE1572_8261 | 172 | 304 |
| SCE1572_8648 | 96 | 6 |
| SCE1572_6591 | 76.44 | 14 |
| SCE1572_191 | 336 | 67 |
| SCE1572_9062 | 154 | 36 |
| SCE1572_10663 | 292 | 183 |
| SCE1572_4467 | 48 | 6 |
| SCE1572_4201 | 18 | 7 |
| SCE1572_7106 | 18 | 3 |
| SCE1572_11226 | 77 | 16 |
| SCE1572_9212 | 98 | 52 |
| SCE1572_483 | 76 | 19 |
| SCE1572_3536 | 17 | 2 |
| SCE1572_2471 | 74 | 9 |
| SCE1572_2431 | 79 | 247 |
| SCE1572_1981 | 0 | 0 |
| SCE1572_3743 | 41 | 20 |
| SCE1572_1737 | 38 | 6 |
| SCE1572_8103 | 39 | 22 |
| SCE1572_5541 | 47 | 76 |
| SCE1572_10124 | 458 | 73 |
| SCE1572_9576 | 28 | 3 |
| SCE1572_4814 | 502 | 564 |
| SCE1572_287 | 166 | 103 |
| SCE1572_939 | 97 | 16 |
| SCE1572_10096 | 258 | 268 |
| SCE1572_5471 | 51 | 9 |
| SCE1572_3832 | 78 | 100 |
| SCE1572_3170 | 89 | 85 |
| SCE1572_2094 | 16 | 13 |
| SCE1572_7854 | 61 | 61 |
| SCE1572_10582 | 9 | 4 |
| SCE1572_9196 | 118 | 22 |
| SCE1572_6709 | 98 | 82 |
| SCE1572_4933 | 18 | 27 |
| SCE1572_11276 | 59 | 13 |
| SCE1572_8615 | 198 | 62 |
| SCE1572_5393 | 295 | 58 |
| SCE1572_5405 | 48 | 33 |
| SCE1572_10589 | 9 | 1 |
| SCE1572_2451 | 0 | 0 |
| SCE1572_8320 | 12 | 8 |
| SCE1572_1091 | 171.22 | 14 |
| SCE1572_5467 | 111 | 18 |
| SCE1572_7463 | 210 | 323 |
| SCE1572_11039 | 98 | 33 |
| SCE1572_7653 | 17 | 8 |
| SCE1572_641 | 82 | 55 |

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| SCE1572_5148 | 51 | 2 |
| SCE1572_10288 | 275 | 89 |
| SCE1572_9654 | 39.29 | 5 |
| SCE1572_10579 | 18 | 2 |
| SCE1572_578 | 4 | 0 |
| SCE1572_8086 | 9 | 0 |
| SCE1572_711 | 63 | 122 |
| SCE1572_6873 | 90 | 299 |
| SCE1572_3209 | 95 | 38 |
| SCE1572_3922 | 74 | 14 |
| SCE1572_9978 | 81 | 5 |
| SCE1572_7478 | 48 | 56 |
| SCE1572_11264 | 33 | 48 |
| SCE1572_5499 | 62 | 8 |
| SCE1572_7404 | 15 | 109 |
| SCE1572_6332 | 124 | 32 |
| SCE1572_1334 | 17 | 0 |
| SCE1572_3315 | 26 | 19 |
| SCE1572_7994 | 25 | 0 |
| SCE1572_6977 | 16 | 0 |
| SCE1572_7278 | 22 | 3 |
| SCE1572_11421 | 120 | 52 |
| SCE1572_11450 | 109 | 78 |
| SCE1572_9619 | 963 | 241 |
| SCE1572_6744 | 25 | 2 |
| SCE1572_7390 | 23 | 9 |
| SCE1572_3313 | 62 | 8 |
| SCE1572_11234 | 51 | 10 |
| SCE1572_11398 | 181 | 422 |
| SCE1572_3609 | 85 | 8 |
| SCE1572_7167 | 0 | 0 |
| SCE1572_5902 | 760 | 90 |
| SCE1572_10184 | 17 | 33 |
| SCE1572_6649 | 44 | 1 |
| SCE1572_3427 | 174.15 | 60 |
| SCE1572_8532 | 22 | 0 |
| SCE1572_6125 | 40 | 48 |
| SCE1572_8938 | 8 | 6 |
| SCE1572_4767 | 327 | 241 |
| SCE1572_1234 | 65 | 12 |
| SCE1572_10344 | 2357 | 7504 |
| SCE1572_10932 | 24 | 18 |
| SCE1572_7134 | 43 | 8 |
| SCE1572_543 | 55 | 15 |
| SCE1572_8986 | 1 | 0 |
| SCE1572_8489 | 169 | 82 |
| SCE1572_997 | 35 | 19 |
| SCE1572_9488 | 124 | 66 |

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| SCE1572_10993 | 0 | 0 |
| SCE1572_9594 | 47 | 386 |
| SCE1572_3883 | 32 | 8 |
| SCE1572_9994 | 263 | 39 |
| SCE1572_11081 | 123 | 187 |
| SCE1572_769 | 36 | 4 |
| SCE1572_594 | 10 | 1 |
| SCE1572_7655 | 32 | 5 |
| SCE1572_7399 | 31 | 16 |
| SCE1572_127 | 43 | 10 |
| SCE1572_1979 | 1807 | 2303 |
| SCE1572_6129 | 762 | 811 |
| SCE1572_265 | 210 | 45 |
| SCE1572_6030 | 47 | 18 |
| SCE1572_1946 | 183 | 50 |
| SCE1572_1436 | 33 | 8 |
| SCE1572_992 | 496 | 421 |
| SCE1572_891 | 159 | 164 |
| SCE1572_7262 | 73 | 31 |
| SCE1572_10310 | 53.58 | 12.18 |
| SCE1572_9761 | 9 | 7 |
| SCE1572_6003 | 83 | 482 |
| SCE1572_6242 | 49 | 15 |
| SCE1572_7526 | 0 | 0 |
| SCE1572_5928 | 147 | 66 |
| SCE1572_11303 | 208 | 88 |
| SCE1572_413 | 137 | 24 |
| SCE1572_1641 | 53 | 7 |
| SCE1572_2061 | 30 | 7 |
| SCE1572_7240 | 113 | 77 |
| SCE1572_9710 | 263 | 273 |
| SCE1572_7050 | 0 | 0 |
| SCE1572_2769 | 36 | 14 |
| SCE1572_760 | 3842 | 691 |
| SCE1572_311 | 116 | 43 |
| SCE1572_10401 | 42 | 38 |
| SCE1572_9201 | 130 | 22 |
| SCE1572_11401 | 58 | 13 |
| SCE1572_6779 | 26 | 8 |
| SCE1572_7985 | 108 | 99 |
| SCE1572_4812 | 84 | 33 |
| SCE1572_4155 | 32 | 39 |
| SCE1572_2358 | 126 | 76 |
| SCE1572_8550 | 71 | 90 |
| SCE1572_807 | 97 | 32 |
| SCE1572_9738 | 58 | 5 |
| SCE1572_8444 | 28 | 9 |
| SCE1572_2745 | 78 | 72 |

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| SCE1572_4334 | 52 | 6 |
| SCE1572_4191 | 162 | 74 |
| SCE1572_5248 | 70 | 59 |
| SCE1572_3195 | 27 | 0 |
| SCE1572_10492 | 79 | 119 |
| SCE1572_9528 | 299 | 234 |
| SCE1572_10296 | 183 | 1395 |
| SCE1572_1469 | 4 | 3 |
| SCE1572_11108 | 48.61 | 21 |
| SCE1572_10211 | 98 | 35 |
| SCE1572_6176 | 180 | 115 |
| SCE1572_8250 | 203 | 182 |
| SCE1572_8777 | 54 | 17 |
| SCE1572_3502 | 69 | 30 |
| SCE1572_9683 | 68 | 150 |
| SCE1572_2219 | 0 | 0 |
| SCE1572_10483 | 69 | 19 |
| SCE1572_5786 | 91 | 37 |
| SCE1572_7447 | 1 | 0 |
| SCE1572_10272 | 114 | 553 |
| SCE1572_1596 | 45 | 3 |
| SCE1572_9116 | 388 | 490 |
| SCE1572_6500 | 36 | 30 |
| SCE1572_3302 | 398 | 198 |
| SCE1572_9358 | 94 | 109 |
| SCE1572_7955 | 143 | 102 |
| SCE1572_7171 | 13 | 0 |
| SCE1572_1807 | 23 | 28 |
| SCE1572_105 | 32 | 0 |
| SCE1572_1756 | 4 | 0 |
| SCE1572_11477 | 34.72 | 3 |
| SCE1572_494 | 111 | 14 |
| SCE1572_6346 | 46 | 24 |
| SCE1572_7313 | 125 | 31 |
| SCE1572_1293 | 61 | 14 |
| SCE1572_2688 | 22 | 14 |
| SCE1572_9911 | 52 | 15 |
| SCE1572_5190 | 137 | 181 |
| SCE1572_10507 | 144 | 86 |
| SCE1572_5266 | 85 | 113 |
| SCE1572_8701 | 72 | 38 |
| SCE1572_11210 | 55 | 11 |
| SCE1572_7269 | 361 | 829 |
| SCE1572_4506 | 51 | 8 |
| SCE1572_7009 | 264 | 37 |
| SCE1572_9754 | 63 | 35 |
| SCE1572_529 | 9 | 0 |
| SCE1572_10361 | 30 | 435 |

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| SCE1572_10256 | 140 | 24 |
| SCE1572_8571 | 11 | 2 |
| SCE1572_2843 | 5 | 2 |
| SCE1572_11203 | 44 | 33 |
| SCE1572_677 | 176 | 42 |
| SCE1572_9640 | 2071 | 2007.01 |
| SCE1572_5508 | 5 | 0 |
| SCE1572_8228 | 109 | 13 |
| SCE1572_9462 | 59 | 48 |
| SCE1572_3950 | 0 | 0 |
| SCE1572_1201 | 59 | 10 |
| SCE1572_11085 | 99 | 108 |
| SCE1572_1773 | 0 | 0 |
| SCE1572_9068 | 49 | 21 |
| SCE1572_721 | 59.48 | 18 |
| SCE1572_1811 | 84 | 25 |
| SCE1572_5554 | 248 | 107 |
| SCE1572_3666 | 61 | 2 |
| SCE1572_7163 | 105 | 71 |
| SCE1572_10533 | 65 | 61 |
| SCE1572_4583 | 0 | 0 |
| SCE1572_2681 | 227 | 16 |
| SCE1572_10353 | 2034 | 1156 |
| SCE1572_9061 | 117 | 25 |
| SCE1572_2907 | 77 | 331 |
| SCE1572_208 | 8 | 1 |
| SCE1572_6667 | 196 | 81 |
| SCE1572_6091 | 35 | 4 |
| SCE1572_11278 | 10 | 0 |
| SCE1572_909 | 294.04 | 60 |
| SCE1572_9352 | 49 | 119 |
| SCE1572_3711 | 37 | 0 |
| SCE1572_2182 | 26 | 5 |
| SCE1572_4111 | 42 | 5 |
| SCE1572_9379 | 100 | 15 |
| SCE1572_4591 | 15 | 6 |
| SCE1572_7188 | 129 | 139 |
| SCE1572_3725 | 692 | 5405 |
| SCE1572_2282 | 50 | 50 |
| SCE1572_6761 | 21 | 8 |
| SCE1572_1732 | 91 | 22 |
| SCE1572_7905 | 85 | 13 |
| SCE1572_3717 | 343 | 195 |
| SCE1572_2524 | 47 | 21 |
| SCE1572_8294 | 50 | 18 |
| SCE1572_4533 | 57 | 6 |
| SCE1572_10665 | 120 | 227 |
| SCE1572_14 | 85 | 37 |

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| SCE1572_5578 | 12 | 0 |
| SCE1572_9847 | 110 | 23 |
| SCE1572_10377 | 98 | 9 |
| SCE1572_9556 | 289 | 257 |
| SCE1572_1473 | 102 | 20 |
| SCE1572_11281 | 199 | 21 |
| SCE1572_361 | 2 | 0 |
| SCE1572_6749 | 6 | 1 |
| SCE1572_3443 | 37 | 3 |
| SCE1572_6552 | 0 | 0 |
| SCE1572_4369 | 189 | 133 |
| SCE1572_5603 | 59 | 38 |
| SCE1572_2066 | 488 | 173 |
| SCE1572_4568 | 29 | 2 |
| SCE1572_10094 | 24 | 0 |
| SCE1572_900 | 165 | 38 |
| SCE1572_4871 | 40 | 16 |
| SCE1572_10177 | 50 | 66 |
| SCE1572_7046 | 8 | 2 |
| SCE1572_1854 | 0 | 0 |
| SCE1572_8528 | 202 | 143 |
| SCE1572_8280 | 44 | 5 |
| SCE1572_5700 | 10 | 0 |
| SCE1572_5199 | 88 | 35 |
| SCE1572_4364 | 179 | 30 |
| SCE1572_2949 | 7 | 0 |
| SCE1572_11079 | 208 | 920 |
| SCE1572_1182 | 0 | 0 |
| SCE1572_7820 | 200 | 402 |
| SCE1572_11286 | 209 | 184 |
| SCE1572_5636 | 64 | 62 |
| SCE1572_561 | 218 | 800 |
| SCE1572_10396 | 24 | 9 |
| SCE1572_1280 | 180 | 24 |
| SCE1572_9521 | 0 | 0 |
| SCE1572_11552 | 189 | 42 |
| SCE1572_4920 | 26 | 2 |
| SCE1572_6984 | 10 | 4 |
| SCE1572_8267 | 175 | 87 |
| SCE1572_7722 | 158 | 62 |
| SCE1572_10926 | 0 | 0 |
| SCE1572_10919 | 34 | 10 |
| SCE1572_5662 | 7 | 7 |
| SCE1572_556 | 20 | 3 |
| SCE1572_11245 | 27 | 5 |
| SCE1572_820 | 41 | 17 |
| SCE1572_911 | 43 | 13 |
| SCE1572_7259 | 0 | 0 |

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| SCE1572_5811 | 167 | 42 |
| SCE1572_1902 | 391 | 49 |
| SCE1572_1072 | 107 | 19 |
| SCE1572_989 | 56 | 57 |
| SCE1572_9543 | 137 | 24 |
| SCE1572_3959 | 53 | 14 |
| SCE1572_8238 | 132 | 403 |
| SCE1572_2552 | 118 | 53 |
| SCE1572_1529 | 62 | 21 |
| SCE1572_10829 | 45 | 9 |
| SCE1572_8221 | 69 | 8 |
| SCE1572_3640 | 19 | 55 |
| SCE1572_6613 | 80 | 23 |
| SCE1572_11154 | 30 | 32 |
| SCE1572_4916 | 166 | 656 |
| SCE1572_280 | 103 | 22 |
| SCE1572_4893 | 144 | 60 |
| SCE1572_3086 | 71 | 9 |
| SCE1572_10942 | 497 | 90 |
| SCE1572_5113 | 11 | 5 |
| SCE1572_9800 | 106 | 35 |
| SCE1572_5769 | 712 | 2577 |
| SCE1572_2675 | 43 | 112 |
| SCE1572_2246 | 79 | 33 |
| SCE1572_5313 | 27 | 5 |
| SCE1572_1079 | 0 | 0 |
| SCE1572_237 | 107 | 14 |
| SCE1572_6783 | 16 | 26 |
| SCE1572_3013 | 23 | 10 |
| SCE1572_2925 | 399 | 86 |
| SCE1572_6057 | 111 | 108 |
| SCE1572_5387 | 122 | 73 |
| SCE1572_9719 | 44 | 254 |
| SCE1572_3905 | 372 | 840 |
| SCE1572_1554 | 233 | 57 |
| SCE1572_7750 | 34 | 2 |
| SCE1572_10742 | 101 | 30 |
| SCE1572_8964 | 62 | 51 |
| SCE1572_5672 | 0 | 0 |
| SCE1572_4792 | 15 | 1 |
| SCE1572_8289 | 20 | 11 |
| SCE1572_11357 | 92 | 20 |
| SCE1572_10800 | 145 | 63 |
| SCE1572_8860 | 26 | 3 |
| SCE1572_8490 | 36 | 34 |
| SCE1572_1325 | 21 | 2 |
| SCE1572_5216 | 30 | 29 |
| SCE1572_4308 | 0 | 0 |

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| SCE1572_2772 | 14 | 4 |
| SCE1572_8720 | 12 | 5 |
| SCE1572_3369 | 328 | 296 |
| SCE1572_9137 | 10 | 5 |
| SCE1572_5709 | 78 | 44 |
| SCE1572_243 | 10 | 1 |
| SCE1572_3226 | 88 | 14 |
| SCE1572_11056 | 8 | 10 |
| SCE1572_5548 | 142 | 24 |
| SCE1572_2821 | 237 | 85 |
| SCE1572_390 | 37 | 6 |
| SCE1572_5538 | 234 | 130 |
| SCE1572_5500 | 842 | 200 |
| SCE1572_6469 | 80 | 8 |
| SCE1572_2233 | 59 | 18 |
| SCE1572_10157 | 99 | 64 |
| SCE1572_616 | 90 | 139 |
| SCE1572_8797 | 127 | 12 |
| SCE1572_3270 | 60 | 171 |
| SCE1572_7969 | 10 | 1 |
| SCE1572_8257 | 92 | 107 |
| SCE1572_8831 | 239 | 346 |
| SCE1572_8665 | 57 | 9 |
| SCE1572_669 | 117 | 30 |
| SCE1572_5792 | 24 | 19 |
| SCE1572_4820 | 92 | 46 |
| SCE1572_9075 | 254 | 40 |
| SCE1572_8341 | 20 | 7 |
| SCE1572_4869 | 15 | 9 |
| SCE1572_8729 | 21 | 12 |
| SCE1572_2137 | 72 | 17 |
| SCE1572_4544 | 88 | 30 |
| SCE1572_2415 | 33 | 3 |
| SCE1572_8699 | 190 | 38 |
| SCE1572_5648 | 98 | 19 |
| SCE1572_10813 | 19 | 11 |
| SCE1572_9351 | 263 | 431 |
| SCE1572_439 | 905 | 84 |
| SCE1572_2912 | 1027.07 | 137.17 |
| SCE1572_9411 | 190.42 | 422.82 |
| SCE1572_3051 | 49 | 1 |
| SCE1572_7699 | 30 | 11 |
| SCE1572_8124 | 60 | 15 |
| SCE1572_1919 | 108 | 34 |
| SCE1572_2857 | 26 | 3 |
| SCE1572_6772 | 10 | 0 |
| SCE1572_5995 | 156 | 56 |
| SCE1572_4181 | 59 | 28 |

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| SCE1572_8499 | 106 | 17 |
| SCE1572_4550 | 119 | 18 |
| SCE1572_11534 | 62 | 10 |
| SCE1572_1824 | 73 | 46 |
| SCE1572_4744 | 10 | 56 |
| SCE1572_1829 | 692.18 | 1046.53 |
| SCE1572_10078 | 323 | 314 |
| SCE1572_2402 | 29 | 49 |
| SCE1572_5879 | 54 | 7 |
| SCE1572_5920 | 87 | 79 |
| SCE1572_3092 | 28 | 0 |
| SCE1572_9458 | 68 | 33 |
| SCE1572_5625 | 4 | 2 |
| SCE1572_5273 | 5 | 1 |
| SCE1572_10523 | 44 | 2 |
| SCE1572_9469 | 244 | 183 |
| SCE1572_8740 | 71 | 19 |
| SCE1572_7115 | 48 | 4 |
| SCE1572_5846 | 108 | 90 |
| SCE1572_6638 | 133 | 27 |
| SCE1572_507 | 60 | 8 |
| SCE1572_4570 | 140 | 24 |
| SCE1572_8738 | 113 | 36 |
| SCE1572_9124 | 85 | 25 |
| SCE1572_9699 | 64 | 21 |
| SCE1572_140 | 14 | 5 |
| SCE1572_7733 | 80 | 161 |
| SCE1572_8886 | 227.51 | 36 |
| SCE1572_11436 | 194 | 79 |
| SCE1572_7629 | 49 | 61 |
| SCE1572_6187 | 84 | 42 |
| SCE1572_6151 | 179 | 15 |
| SCE1572_8888 | 18 | 3 |
| SCE1572_6608 | 11 | 17 |
| SCE1572_5352 | 348 | 330 |
| SCE1572_2672 | 77 | 42 |
| SCE1572_10107 | 117 | 291 |
| SCE1572_2381 | 235 | 294 |
| SCE1572_3850 | 42 | 47 |
| SCE1572_9076 | 70 | 15 |
| SCE1572_11040 | 163 | 51 |
| SCE1572_2719 | 38 | 11 |
| SCE1572_10385 | 48 | 7 |
| SCE1572_9885 | 69 | 49 |
| SCE1572_1778 | 63 | 15 |
| SCE1572_864 | 334 | 232 |
| SCE1572_6147 | 29 | 4 |
| SCE1572_7729 | 70 | 72 |

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| SCE1572_4512 | 0 | 0 |
| SCE1572_6564 | 0 | 0 |
| SCE1572_6116 | 194 | 32 |
| SCE1572_3043 | 0 | 0 |
| SCE1572_7023 | 0 | 0 |
| SCE1572_150 | 88 | 26 |
| SCE1572_9312 | 172 | 109 |
| SCE1572_9151 | 26 | 4 |
| SCE1572_1613 | 338 | 34 |
| SCE1572_6031 | 149 | 61 |
| SCE1572_2668 | 15 | 10 |
| SCE1572_3698 | 58 | 24 |
| SCE1572_2125 | 157 | 36 |
| SCE1572_2150 | 35 | 3 |
| SCE1572_9301 | 24 | 49 |
| SCE1572_4754 | 135 | 80 |
| SCE1572_6506 | 1 | 0 |
| SCE1572_10499 | 22 | 198 |
| SCE1572_4577 | 58 | 11 |
| SCE1572_4356 | 36 | 12 |
| SCE1572_2704 | 187 | 275 |
| SCE1572_9604 | 51 | 3 |
| SCE1572_2155 | 123 | 29 |
| SCE1572_2958 | 303 | 83 |
| SCE1572_8378 | 71 | 45 |
| SCE1572_5429 | 110 | 89 |
| SCE1572_1626 | 77 | 86 |
| SCE1572_2275 | 294 | 794 |
| SCE1572_4121 | 380 | 427 |
| SCE1572_2397 | 28 | 364 |
| SCE1572_7065 | 232 | 94 |
| SCE1572_893 | 39 | 33 |
| SCE1572_4104 | 53 | 6 |
| SCE1572_9819 | 78 | 10 |
| SCE1572_1273 | 163 | 38 |
| SCE1572_3453 | 149 | 27 |
| SCE1572_11179 | 94 | 46 |
| SCE1572_5380 | 60 | 7 |
| SCE1572_1744 | 156 | 72 |
| SCE1572_1758 | 484 | 61 |
| SCE1572_2412 | 148 | 38 |
| SCE1572_8135 | 81 | 10 |
| SCE1572_60 | 232 | 80 |
| SCE1572_9048 | 6 | 3 |
| SCE1572_8925 | 0.5 | 0 |
| SCE1572_6917 | 23 | 14 |
| SCE1572_1783 | 58 | 57 |
| SCE1572_8472 | 54 | 607 |

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| SCE1572_3343 | 227 | 222 |
| SCE1572_1237 | 41 | 18 |
| SCE1572_2425 | 866 | 680 |
| SCE1572_1937 | 1 | 0 |
| SCE1572_8467 | 47 | 5 |
| SCE1572_1017 | 24 | 193 |
| SCE1572_5168 | 58 | 68 |
| SCE1572_5090 | 78 | 46 |
| SCE1572_6021 | 450 | 246 |
| SCE1572_7293 | 0 | 0 |
| SCE1572_9772 | 27 | 29 |
| SCE1572_4527 | 129 | 190 |
| SCE1572_4862 | 11 | 0 |
| SCE1572_10366 | 23 | 2 |
| SCE1572_3971 | 205 | 69 |
| SCE1572_7122 | 598 | 309 |
| SCE1572_8650 | 74 | 12 |
| SCE1572_2041 | 35 | 89 |
| SCE1572_10961 | 47 | 47 |
| SCE1572_3185 | 324 | 48 |
| SCE1572_67 | 166 | 27 |
| SCE1572_10252 | 0 | 0 |
| SCE1572_10038 | 182 | 159 |
| SCE1572_4428 | 18 | 13 |
| SCE1572_9210 | 108 | 31 |
| SCE1572_4770 | 48 | 60 |
| SCE1572_8552 | 156 | 111 |
| SCE1572_2632 | 146.94 | 26.57 |
| SCE1572_10063 | 524 | 1662 |
| SCE1572_2804 | 269 | 90 |
| SCE1572_5108 | 226 | 90 |
| SCE1572_10898 | 15 | 42 |
| SCE1572_5420 | 112 | 98 |
| SCE1572_3364 | 56 | 43 |
| SCE1572_8442 | 18 | 8 |
| SCE1572_10906 | 3 | 0 |
| SCE1572_6514 | 38 | 4 |
| SCE1572_3994 | 242 | 41 |
| SCE1572_11201 | 106 | 102 |
| SCE1572_6054 | 86 | 114 |
| SCE1572_5039 | 9 | 10 |
| SCE1572_2910 | 108 | 17 |
| SCE1572_6449 | 578 | 72 |
| SCE1572_11480 | 365 | 197 |
| SCE1572_8130 | 82 | 17 |
| SCE1572_10902 | 22 | 8 |
| SCE1572_11066 | 81 | 31 |
| SCE1572_4808 | 55 | 132 |

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| SCE1572_3687 | 181 | 18 |
| SCE1572_8334 | 0 | 0 |
| SCE1572_3793 | 177 | 182 |
| SCE1572_7593 | 191 | 80 |
| SCE1572_6258 | 6 | 3 |
| SCE1572_3426 | 234 | 32 |
| SCE1572_1535 | 27 | 22 |
| SCE1572_11356 | 40 | 35 |
| SCE1572_8676 | 107 | 49 |
| SCE1572_3822 | 18 | 16 |
| SCE1572_10642 | 253 | 433 |
| SCE1572_9052 | 82.65 | 35 |
| SCE1572_3232 | 88 | 109 |
| SCE1572_1468 | 0 | 0 |
| SCE1572_921 | 108 | 23 |
| SCE1572_4643 | 99 | 33 |
| SCE1572_2850 | 55 | 105 |
| SCE1572_2986 | 0 | 0 |
| SCE1572_10005 | 14 | 6 |
| SCE1572_4829 | 38 | 69 |
| SCE1572_9428 | 366 | 257 |
| SCE1572_5799 | 59 | 20 |
| SCE1572_1698 | 17 | 51 |
| SCE1572_3765 | 126 | 62 |
| SCE1572_3587 | 264 | 98 |
| SCE1572_9251 | 245 | 50 |
| SCE1572_4028 | 113 | 88 |
| SCE1572_8158 | 76 | 8 |
| SCE1572_10453 | 60 | 17 |
| SCE1572_7796 | 468 | 126 |
| SCE1572_2602 | 147.7 | 19.18 |
| SCE1572_4836 | 51 | 66 |
| SCE1572_256 | 14 | 1 |
| SCE1572_4420 | 0 | 0 |
| SCE1572_11143 | 61 | 30 |
| SCE1572_9987 | 185 | 25 |
| SCE1572_6814 | 99 | 54 |
| SCE1572_3945 | 2065 | 1719 |
| SCE1572_8206 | 86 | 66 |
| SCE1572_2963 | 216 | 1115 |
| SCE1572_7852 | 0 | 0 |
| SCE1572_6158 | 39 | 14 |
| SCE1572_1794 | 33 | 388 |
| SCE1572_3577 | 67 | 57 |
| SCE1572_2606 | 33 | 2 |
| SCE1572_10793 | 22 | 6 |
| SCE1572_3134 | 102 | 17 |
| SCE1572_9397 | 35 | 29 |

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| SCE1572_1649 | 128.72 | 16.73 |
| SCE1572_6373 | 82 | 22 |
| SCE1572_1664 | 51 | 59 |
| SCE1572_8714 | 237 | 160 |
| SCE1572_7688 | 233 | 23 |
| SCE1572_1053 | 85 | 73 |
| SCE1572_7937 | 19 | 5 |
| SCE1572_3841 | 160 | 33 |
| SCE1572_9439 | 50 | 26 |
| SCE1572_2082 | 44 | 20 |
| SCE1572_10822 | 75 | 31 |
| SCE1572_10537 | 0 | 0 |
| SCE1572_11062 | 264 | 64 |
| SCE1572_3984 | 60 | 77 |
| SCE1572_6842 | 66 | 20 |
| SCE1572_6559 | 94 | 58 |
| SCE1572_2290 | 323 | 842 |
| SCE1572_11310 | 110 | 15 |
| SCE1572_3002 | 9 | 2 |
| SCE1572_1883 | 0 | 0 |
| SCE1572_5379 | 79 | 11 |
| SCE1572_4777 | 142 | 232 |
| SCE1572_7459 | 194 | 197 |
| SCE1572_5980 | 1205 | 340 |
| SCE1572_5763 | 0 | 0 |
| SCE1572_11463 | 731 | 563 |
| SCE1572_11573 | 0 | 0 |
| SCE1572_325 | 19 | 2 |
| SCE1572_7539 | 229 | 29 |
| SCE1572_2445 | 57 | 9 |
| SCE1572_3967 | 211 | 58 |
| SCE1572_4559 | 22 | 27 |
| SCE1572_1536 | 114 | 26 |
| SCE1572_4636 | 84 | 7 |
| SCE1572_7683 | 70 | 8 |
| SCE1572_7144 | 48 | 43 |
| SCE1572_9646 | 259 | 144 |
| SCE1572_7783 | 0 | 0 |
| SCE1572_5187 | 28 | 825 |
| SCE1572_2353 | 7 | 9 |
| SCE1572_4242 | 12 | 1 |
| SCE1572_1984 | 0 | 0 |
| SCE1572_10408 | 55 | 33 |
| SCE1572_9822 | 28 | 8 |
| SCE1572_10685 | 71 | 22 |
| SCE1572_11135 | 100 | 49 |
| SCE1572_6530 | 68 | 37 |
| SCE1572_8196 | 43 | 10 |

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| SCE1572_2648 | 59 | 12 |
| SCE1572_2378 | 31 | 164 |
| SCE1572_1402 | 358 | 47 |
| SCE1572_1708 | 15 | 0 |
| SCE1572_2171 | 364 | 79 |
| SCE1572_7247 | 0 | 0 |
| SCE1572_1496 | 15 | 3 |
| SCE1572_7252 | 133 | 17 |
| SCE1572_1147 | 318 | 175 |
| SCE1572_2953 | 11 | 0 |
| SCE1572_2204 | 73 | 214 |
| SCE1572_8657 | 6 | 34 |
| SCE1572_4171 | 258 | 123 |
| SCE1572_5486 | 295 | 30 |
| SCE1572_11122 | 167 | 20 |
| SCE1572_2189 | 27 | 31 |
| SCE1572_2835 | 5 | 0 |
| SCE1572_2210 | 105 | 234 |
| SCE1572_4396 | 12 | 7 |
| SCE1572_1491 | 0 | 0 |
| SCE1572_1497 | 44.75 | 7.44 |
| SCE1572_11489 | 0 | 0 |
| SCE1572_681 | 32 | 6 |
| SCE1572_3297 | 49 | 15 |
| SCE1572_4139 | 40 | 6 |
| SCE1572_5158 | 3 | 0 |
| SCE1572_9829 | 9 | 0 |
| SCE1572_4903 | 110 | 69 |
| SCE1572_3215 | 592 | 804 |
| SCE1572_302 | 46 | 6 |
| SCE1572_8791 | 108 | 224 |
| SCE1572_4326 | 49 | 13 |
| SCE1572_4271 | 54 | 19 |
| SCE1572_735 | 156 | 33 |
| SCE1572_6882 | 0 | 0 |
| SCE1572_1955 | 18 | 9 |
| SCE1572_3009 | 13 | 8 |
| SCE1572_4038 | 143 | 71 |
| SCE1572_5070 | 54 | 34 |
| SCE1572_7619 | 132 | 265 |
| SCE1572_5016 | 265 | 1580 |
| SCE1572_9981 | 252 | 61 |
| SCE1572_1464 | 112 | 20 |
| SCE1572_5290 | 176 | 30 |
| SCE1572_4668 | 4 | 1 |
| SCE1572_2589 | 150 | 106 |
| SCE1572_1295 | 152 | 36 |
| SCE1572_10199 | 296 | 122 |

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| SCE1572_663 | 0 | 0 |
| SCE1572_3352 | 74 | 13 |
| SCE1572_1764 | 55 | 7 |
| SCE1572_2106 | 164 | 187 |
| SCE1572_11315 | 1017 | 750 |
| SCE1572_8867 | 88 | 19 |
| SCE1572_10697 | 175 | 162 |
| SCE1572_9838 | 0 | 0 |
| SCE1572_787 | 431 | 757 |
| SCE1572_1900 | 14 | 3 |
| SCE1572_135 | 77 | 18 |
| SCE1572_8516 | 106 | 7 |
| SCE1572_11583 | 236 | 259 |
| SCE1572_7865 | 80 | 20 |
| SCE1572_1023 | 30 | 9 |
| SCE1572_8097 | 67 | 17 |
| SCE1572_11101 | 45 | 22 |
| SCE1572_717 | 25 | 4 |
| SCE1572_8392 | 0 | 0 |
| SCE1572_7194 | 0 | 0 |
| SCE1572_2780 | 36 | 2 |
| SCE1572_10882 | 159 | 500 |
| SCE1572_10324 | 70 | 45 |
| SCE1572_5282 | 233 | 116 |
| SCE1572_3645 | 280 | 236 |
| SCE1572_1802 | 50 | 21 |
| SCE1572_8877 | 1 | 0 |
| SCE1572_2885 | 79 | 19 |
| SCE1572_8306 | 72 | 2 |
| SCE1572_6497 | 51 | 4 |
| SCE1572_8173 | 37 | 4 |
| SCE1572_4605 | 201 | 564 |
| SCE1572_9266 | 134 | 99 |
| SCE1572_1258 | 50 | 2 |
| SCE1572_10336 | 36 | 12 |
| SCE1572_3074 | 39 | 7 |
| SCE1572_6306 | 33 | 8 |
| SCE1572_3491 | 97 | 74 |
| SCE1572_1517 | 1 | 0 |
| SCE1572_3773 | 145 | 25 |
| SCE1572_7948 | 131 | 88 |
| SCE1572_440 | 1094 | 148 |
| SCE1572_9897 | 41 | 14 |
| SCE1572_10446 | 19 | 5 |
| SCE1572_10772 | 36 | 14 |
| SCE1572_8068 | 150.4 | 17.23 |
| SCE1572_7643 | 385 | 200 |
| SCE1572_5561 | 570 | 117 |

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| SCE1572_11006 | 0 | 0 |
| SCE1572_7005 | 16 | 2 |
| SCE1572_8544 | 58 | 19 |
| SCE1572_1041 | 345 | 61 |
| SCE1572_6676 | 71 | 19 |
| SCE1572_4226 | 49 | 33 |
| SCE1572_11561 | 131 | 91 |
| SCE1572_3595 | 13.25 | 0.75 |
| SCE1572_9292 | 76 | 60 |
| SCE1572_7915 | 1 | 0 |
| SCE1572_4661 | 23 | 5 |
| SCE1572_3103 | 23 | 4 |
| SCE1572_2360 | 39 | 105 |
| SCE1572_9812 | 621 | 87 |
| SCE1572_2735 | 65 | 21 |
| SCE1572_3709 | 0 | 0 |
| SCE1572_7784 | 32.02 | 64.61 |
| SCE1572_7103 | 0 | 0 |
| SCE1572_10087 | 0 | 0 |
| SCE1572_11021 | 108 | 34 |
| SCE1572_9503 | 580 | 804 |
| SCE1572_3731 | 142 | 26 |
| SCE1572_2327 | 394 | 88 |
| SCE1572_7437 | 142 | 19 |
| SCE1572_168 | 87 | 15 |
| SCE1572_9867 | 89 | 75 |
| SCE1572_6718 | 0 | 0 |
| SCE1572_8838 | 0 | 0 |
| SCE1572_6218 | 84 | 12 |
| SCE1572_9323 | 93 | 61 |
| SCE1572_8995 | 50 | 9 |
| SCE1572_3897 | 63 | 41 |
| SCE1572_6803 | 53 | 35 |
| SCE1572_9394 | 35 | 3 |
| SCE1572_8746 | 22 | 10 |
| SCE1572_3062 | 22 | 2 |
| SCE1572_230 | 105 | 19 |
| SCE1572_10307 | 44 | 4 |
| SCE1572_11418 | 209 | 79 |
| SCE1572_4644 | 187 | 57 |
| SCE1572_456 | 57 | 8 |
| SCE1572_9569 | 0 | 0 |
| SCE1572_8459 | 78 | 37 |
| SCE1572_8365 | 53 | 10 |
| SCE1572_4198 | 15 | 0 |
| SCE1572_10020 | 108 | 19 |
| SCE1572_9633 | 153 | 20 |
| SCE1572_5580 | 76 | 32 |

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| SCE1572_5772 | 126 | 34 |
| SCE1572_2488 | 2 | 0 |
| SCE1572_10761 | 0 | 0 |
| SCE1572_371 | 30 | 123 |
| SCE1572_2300 | 56 | 121 |
| SCE1572_8258 | 53 | 132 |
| SCE1572_9448 | 142 | 40 |
| SCE1572_4622 | 144 | 1410 |
| SCE1572_6355 | 0 | 0 |
| SCE1572_11495 | 165 | 13 |
| SCE1572_937 | 19 | 6 |
| SCE1572_11432 | 58 | 19 |
| SCE1572_9012 | 61 | 22 |
| SCE1572_2314 | 68 | 47 |
| SCE1572_917 | 187 | 201 |
| SCE1572_5479 | 91 | 18 |
| SCE1572_4888 | 87 | 23 |
| SCE1572_2591 | 90 | 22 |
| SCE1572_3379 | 194 | 23 |
| SCE1572_9513 | 43 | 16 |
| SCE1572_384 | 0 | 0 |
| SCE1572_10785 | 280 | 185 |
| SCE1572_7800 | 151 | 122 |
| SCE1572_10808 | 8 | 0 |
| SCE1572_843 | 242 | 544 |
| SCE1572_603 | 27 | 4 |
| SCE1572_4960 | 94 | 69 |
| SCE1572_1488 | 0 | 0 |
| SCE1572_6395 | 0 | 0 |
| SCE1572_9656 | 71 | 16 |
| SCE1572_6000 | 94 | 129 |
| SCE1572_8688 | 321 | 209 |
| SCE1572_3370 | 13 | 84 |
| SCE1572_11256 | 64 | 45 |
| SCE1572_9716 | 18 | 69 |
| SCE1572_414 | 63 | 19 |
| SCE1572_6691 | 1 | 0 |
| SCE1572_8628 | 77 | 89 |
| SCE1572_8342 | 117.22 | 27 |
| SCE1572_9709 | 173 | 116 |
| SCE1572_1639 | 38 | 24 |
| SCE1572_464 | 27 | 115 |
| SCE1572_6209 | 44.01 | 3.02 |
| SCE1572_7871 | 61 | 17 |
| SCE1572_7765 | 27 | 10 |
| SCE1572_5363 | 149 | 18 |
| SCE1572_3073 | 25 | 4 |
| SCE1572_55 | 794 | 104 |

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| SCE1572_7602 | 145 | 53 |
| SCE1572_1427 | 2 | 0 |
| SCE1572_5297 | 54 | 26 |
| SCE1572_7922 | 82 | 20 |
| SCE1572_6071 | 0 | 0 |
| SCE1572_7480 | 62 | 38 |
| SCE1572_3906 | 254 | 114 |
| SCE1572_3487 | 131 | 14 |
| SCE1572_260 | 121.36 | 13.05 |
| SCE1572_10541 | 113 | 49 |
| SCE1572_6202 | 247 | 70 |
| SCE1572_5845 | 120 | 46 |
| SCE1572_573 | 604 | 471 |
| SCE1572_4478 | 36 | 18 |
| SCE1572_8694 | 84 | 15 |
| SCE1572_3873 | 43 | 15 |
| SCE1572_10433 | 48 | 15 |
| SCE1572_10972 | 65 | 114 |
| SCE1572_4166 | 60 | 12 |
| SCE1572_9271 | 33 | 22 |
| SCE1572_1265 | 248 | 3921 |
| SCE1572_10077 | 309 | 301 |
| SCE1572_7523 | 276 | 51 |
| SCE1572_9338 | 31 | 19 |
| SCE1572_4282 | 26 | 1 |
| SCE1572_2540 | 144 | 32 |
| SCE1572_7904 | 27 | 4 |
| SCE1572_8543 | 124 | 1058 |
| SCE1572_6697 | 20 | 38 |
| SCE1572_10313 | 86 | 17 |
| SCE1572_9199 | 39 | 3 |
| SCE1572_9670 | 132 | 193 |
| SCE1572_7559 | 149 | 42 |
| SCE1572_10994 | 57 | 34 |
| SCE1572_6862 | 110 | 14 |
| SCE1572_6976 | 145 | 19 |
| SCE1572_10339 | 42 | 11 |
| SCE1572_10725 | 60 | 11 |
| SCE1572_2247 | 30 | 4 |
| SCE1572_11279 | 28 | 48 |
| SCE1572_5328 | 165 | 58 |
| SCE1572_2 | 247 | 190 |
| SCE1572_519 | 44 | 19 |
| SCE1572_1306 | 957 | 16158 |
| SCE1572_7465 | 193 | 133 |
| SCE1572_468 | 49 | 65 |
| SCE1572_1609 | 57 | 22 |
| SCE1572_9821 | 124 | 22 |

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| SCE1572_5498 | 180 | 70 |
| SCE1572_6235 | 58 | 25 |
| SCE1572_2260 | 31 | 13 |
| SCE1572_1004 | 55.24 | 22.78 |
| SCE1572_10341 | 59 | 9 |
| SCE1572_1645 | 339 | 258 |
| SCE1572_10050 | 274 | 223 |
| SCE1572_7411 | 69 | 21 |
| SCE1572_2539 | 55 | 28 |
| SCE1572_6203 | 58 | 121 |
| SCE1572_4010 | 115 | 23 |
| SCE1572_3249 | 104 | 62 |
| SCE1572_8263 | 124 | 157 |
| SCE1572_2188 | 130 | 98 |
| SCE1572_10032 | 80 | 99 |
| SCE1572_8102 | 34 | 71 |
| SCE1572_118 | 193 | 370 |
| SCE1572_7340 | 223 | 197 |
| SCE1572_5461 | 60 | 6 |
| SCE1572_8599 | 0 | 0 |
| SCE1572_3172 | 569 | 134 |
| SCE1572_624 | 1 | 0 |
| SCE1572_4825 | 215 | 99 |
| SCE1572_3475 | 45 | 46 |
| SCE1572_10522 | 11 | 7 |
| SCE1572_11397 | 2 | 0 |
| SCE1572_4584 | 326 | 49 |
| SCE1572_11138 | 5 | 0 |
| SCE1572_11392 | 160 | 136 |
| SCE1572_3206 | 181 | 63 |
| SCE1572_9392 | 53 | 85 |
| SCE1572_1963 | 86 | 14 |
| SCE1572_10947 | 6 | 2 |
| SCE1572_3482 | 86 | 9 |
| SCE1572_1681 | 42 | 161 |
| SCE1572_5780 | 67 | 40 |
| SCE1572_11190 | 0 | 0 |
| SCE1572_3801 | 266 | 72 |
| SCE1572_8760 | 296 | 126 |
| SCE1572_8159 | 5 | 0 |
| SCE1572_7380 | 140 | 24 |
| SCE1572_5032 | 226 | 937 |
| SCE1572_10823 | 137 | 42 |
| SCE1572_6825 | 0 | 0 |
| SCE1572_9572 | 7 | 4 |
| SCE1572_8610 | 120 | 28 |
| SCE1572_3405 | 125 | 24 |
| SCE1572_4358 | 125 | 18 |

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| SCE1572_5684 | 64 | 81 |
| SCE1572_10774 | 209 | 330 |
| SCE1572_8704 | 16 | 24 |
| SCE1572_7976 | 47 | 5 |
| SCE1572_10584 | 387 | 675 |
| SCE1572_9865 | 115 | 45 |
| SCE1572_10957 | 59 | 30 |
| SCE1572_4495 | 96 | 28 |
| SCE1572_227 | 29 | 6 |
| SCE1572_5430 | 804 | 416 |
| SCE1572_9630 | 63 | 9 |
| SCE1572_4515 | 36 | 13 |
| SCE1572_252 | 0 | 0 |
| SCE1572_8174 | 10 | 1 |
| SCE1572_6859 | 28 | 3 |
| SCE1572_1943 | 83 | 20 |
| SCE1572_220 | 85 | 77 |
| SCE1572_2726 | 104 | 600 |
| SCE1572_6163 | 75 | 11 |
| SCE1572_3593 | 123 | 22 |
| SCE1572_7003 | 231 | 24 |
| SCE1572_10015 | 145 | 153 |
| SCE1572_3982 | 91 | 96 |
| SCE1572_11475 | 102.19 | 25.1 |
| SCE1572_1288 | 329 | 136 |
| SCE1572_21 | 65 | 15 |
| SCE1572_1941 | 198 | 14 |
| SCE1572_7013 | 11.45 | 0 |
| SCE1572_2053 | 64 | 25 |
| SCE1572_6690 | 44 | 32 |
| SCE1572_3830 | 48 | 96 |
| SCE1572_2530 | 0 | 0 |
| SCE1572_2268 | 79 | 16 |
| SCE1572_3037 | 63 | 11 |
| SCE1572_11593 | 92 | 285 |
| SCE1572_9956 | 61 | 15 |
| SCE1572_3194 | 131 | 68 |
| SCE1572_10183 | 114 | 191 |
| SCE1572_8730 | 175 | 50 |
| SCE1572_10876 | 171 | 64 |
| SCE1572_11164 | 18 | 10 |
| SCE1572_5374 | 203 | 83 |
| SCE1572_9574 | 10 | 1 |
| SCE1572_10010 | 32 | 9 |
| SCE1572_3524 | 81 | 28 |
| SCE1572_3307 | 261 | 2421 |
| SCE1572_6078 | 2 | 0 |
| SCE1572_4347 | 37 | 6 |

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| SCE1572_2512 | 65 | 591 |
| SCE1572_972 | 185 | 208 |
| SCE1572_9232 | 2 | 0 |
| SCE1572_3125 | 38 | 18 |
| SCE1572_8216 | 85 | 18 |
| SCE1572_6010 | 97 | 438 |
| SCE1572_7415 | 24 | 3 |
| SCE1572_5530 | 309 | 67 |
| SCE1572_3766 | 57 | 89 |
| SCE1572_7079 | 14 | 68 |
| SCE1572_8209 | 342 | 148 |
| SCE1572_2389 | 17 | 12 |
| SCE1572_5577 | 12 | 0 |
| SCE1572_777 | 75 | 6 |
| SCE1572_1733 | 208 | 38 |
| SCE1572_7676 | 51 | 3 |
| SCE1572_10756 | 101 | 35 |
| SCE1572_9799 | 5 | 2 |
| SCE1572_504 | 21 | 4 |
| SCE1572_7307 | 25 | 2 |
| SCE1572_7082 | 88 | 21 |
| SCE1572_5123 | 62 | 8 |
| SCE1572_1267 | 0 | 0 |
| SCE1572_10049 | 150 | 55 |
| SCE1572_958 | 41 | 20 |
| SCE1572_6458 | 119 | 46 |
| SCE1572_5518 | 109 | 17 |
| SCE1572_8645 | 0 | 0 |
| SCE1572_11151 | 48 | 14 |
| SCE1572_4388 | 28 | 8 |
| SCE1572_6092 | 83 | 4 |
| SCE1572_1223 | 11 | 11 |
| SCE1572_6553 | 0 | 0 |
| SCE1572_10682 | 27 | 11 |
| SCE1572_8229 | 21 | 5 |
| SCE1572_5408 | 60 | 19 |
| SCE1572_1913 | 0 | 0 |
| SCE1572_8125 | 209 | 14 |
| SCE1572_7878 | 65 | 13 |
| SCE1572_6594 | 202 | 130 |
| SCE1572_9252 | 4 | 1 |
| SCE1572_2749 | 227 | 294 |
| SCE1572_91 | 346 | 1459 |
| SCE1572_1877 | 0 | 0 |
| SCE1572_6268 | 123 | 28 |
| SCE1572_6180 | 311 | 70 |
| SCE1572_6816 | 435 | 58 |
| SCE1572_9097 | 6 | 1 |

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| SCE1572_7253 | 61 | 9 |
| SCE1572_5349 | 62 | 5 |
| SCE1572_4650 | 119 | 128 |
| SCE1572_2930 | 108 | 13 |
| SCE1572_5639 | 26 | 5 |
| SCE1572_10950 | 120 | 22 |
| SCE1572_11018 | 0 | 0 |
| SCE1572_3234 | 107 | 26 |
| SCE1572_2475 | 162 | 57 |
| SCE1572_9538 | 101 | 11 |
| SCE1572_3782 | 60 | 58 |
| SCE1572_8935 | 24 | 6 |
| SCE1572_6317 | 0 | 0 |
| SCE1572_6940 | 15 | 8 |
| SCE1572_6017 | 370 | 528 |
| SCE1572_7621 | 56 | 15 |
| SCE1572_3418 | 99 | 34 |
| SCE1572_6259 | 14 | 5 |
| SCE1572_9375 | 0 | 0 |
| SCE1572_6261 | 21 | 3 |
| SCE1572_7243 | 130 | 88 |
| SCE1572_1620 | 45 | 103 |
| SCE1572_8809 | 122 | 8 |
| SCE1572_2185 | 240 | 30 |
| SCE1572_3692 | 52 | 21 |
| SCE1572_10083 | 311 | 583 |
| SCE1572_1676 | 81 | 77 |
| SCE1572_10460 | 102 | 132 |
| SCE1572_2939 | 22 | 28 |
| SCE1572_9790 | 179 | 131 |
| SCE1572_8013 | 92 | 106 |
| SCE1572_714 | 23 | 1 |
| SCE1572_6067 | 42 | 15 |
| SCE1572_4003 | 51 | 57 |
| SCE1572_9531 | 96 | 59 |
| SCE1572_690 | 70 | 21 |
| SCE1572_2639 | 103 | 20 |
| SCE1572_5912 | 52 | 39 |
| SCE1572_11580 | 50 | 1 |
| SCE1572_8523 | 18 | 0 |
| SCE1572_9794 | 69 | 32 |
| SCE1572_6823 | 140 | 188 |
| SCE1572_2058 | 3 | 0 |
| SCE1572_9108 | 47 | 27 |
| SCE1572_4435 | 27 | 18 |
| SCE1572_3933 | 312 | 329 |
| SCE1572_9616 | 1 | 0 |
| SCE1572_1939 | 93.71 | 134.01 |

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| SCE1572_705 | 86 | 37 |
| SCE1572_7734 | 7 | 0 |
| SCE1572_5784 | 95 | 102 |
| SCE1572_4436 | 118 | 36 |
| SCE1572_4945 | 73 | 71 |
| SCE1572_3995 | 66 | 27 |
| SCE1572_11587 | 6 | 6 |
| SCE1572_9926 | 76 | 314 |
| SCE1572_5903 | 33 | 11 |
| SCE1572_5271 | 13 | 3 |
| SCE1572_9802 | 76 | 27 |
| SCE1572_7705 | 0 | 0 |
| SCE1572_1543 | 452 | 128 |
| SCE1572_8349 | 83 | 3 |
| SCE1572_10017 | 134 | 236 |
| SCE1572_3918 | 27 | 32 |
| SCE1572_1634 | 464 | 1033 |
| SCE1572_2580 | 0 | 0 |
| SCE1572_6482 | 224 | 77 |
| SCE1572_8895 | 121 | 55 |
| SCE1572_6982 | 10 | 0 |
| SCE1572_73 | 102 | 176 |
| SCE1572_11338 | 79 | 4 |
| SCE1572_6750 | 50 | 16 |
| SCE1572_1560 | 5 | 0 |
| SCE1572_1546 | 282 | 56 |
| SCE1572_2873 | 109 | 33 |
| SCE1572_9756 | 16 | 4 |
| SCE1572_3753 | 115 | 179 |
| SCE1572_550 | 0 | 0 |
| SCE1572_11365 | 10 | 2 |
| SCE1572_9246 | 0 | 0 |
| SCE1572_11268 | 212 | 104 |
| SCE1572_851 | 1775 | 2226 |
| SCE1572_3635 | 28 | 7 |
| SCE1572_9 | 46 | 24 |
| SCE1572_6505 | 75 | 26 |
| SCE1572_4681 | 26 | 7 |
| SCE1572_5572 | 595.59 | 127.72 |
| SCE1572_1376 | 63.36 | 15.02 |
| SCE1572_6791 | 7 | 3 |
| SCE1572_11514 | 156 | 45 |
| SCE1572_6955 | 121 | 13 |
| SCE1572_1931 | 325 | 48 |
| SCE1572_10042 | 1184 | 1554 |
| SCE1572_1162 | 72 | 10 |
| SCE1572_5732 | 153 | 203 |
| SCE1572_10988 | 60 | 328 |

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| SCE1572_5953 | 177 | 47 |
| SCE1572_7719 | 109 | 20 |
| SCE1572_430 | 249 | 73 |
| SCE1572_11036 | 12 | 51 |
| SCE1572_10037 | 35 | 31 |
| SCE1572_10631 | 24 | 0 |
| SCE1572_1687 | 41 | 6 |
| SCE1572_1714 | 73 | 25 |
| SCE1572_5308 | 60 | 36 |
| SCE1572_8874 | 338 | 33 |
| SCE1572_5211 | 251 | 151 |
| SCE1572_9383 | 2536 | 4183 |
| SCE1572_1576 | 97 | 19 |
| SCE1572_11557 | 177.37 | 43.99 |
| SCE1572_8435 | 44 | 1 |
| SCE1572_6888 | 75 | 9 |
| SCE1572_11205 | 2 | 3 |
| SCE1572_1344 | 59 | 14 |
| SCE1572_3721 | 1 | 0 |
| SCE1572_10449 | 73 | 143 |
| SCE1572_368 | 322 | 150 |
| SCE1572_9970 | 21 | 5 |
| SCE1572_6990 | 1 | 0 |
| SCE1572_1159 | 85 | 15 |
| SCE1572_7974 | 85 | 34 |
| SCE1572_5058 | 71 | 13 |
| SCE1572_2346 | 43 | 324 |
| SCE1572_10367 | 92 | 20 |
| SCE1572_276 | 37 | 8 |
| SCE1572_9320 | 67 | 37 |
| SCE1572_7537 | 9 | 1 |
| SCE1572_45 | 83 | 154 |
| SCE1572_1840 | 54 | 46 |
| SCE1572_1360 | 191 | 248 |
| SCE1572_9698 | 68 | 11 |
| SCE1572_8950 | 139 | 24 |
| SCE1572_10700 | 0 | 0 |
| SCE1572_2362 | 137 | 91 |
| SCE1572_11438 | 175 | 46 |
| SCE1572_5022 | 105 | 209 |
| SCE1572_3331 | 42 | 175 |
| SCE1572_4207 | 116 | 132 |
| SCE1572_10602 | 152 | 31 |
| SCE1572_183 | 591 | 600 |
| SCE1572_160 | 232 | 53 |
| SCE1572_11057 | 28 | 6 |
| SCE1572_6374 | 129 | 15 |
| SCE1572_6914 | 26 | 8 |

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| SCE1572_5562 | 884 | 187 |
| SCE1572_7485 | 375 | 421 |
| SCE1572_7450 | 8 | 17 |
| SCE1572_6892 | 214.57 | 92 |
| SCE1572_6522 | 51 | 36 |
| SCE1572_6422 | 36 | 19 |
| SCE1572_9611 | 43 | 3 |
| SCE1572_4264 | 50 | 7 |
| SCE1572_5167 | 0 | 0 |
| SCE1572_6675 | 26 | 4 |
| SCE1572_10135 | 38 | 13 |
| SCE1572_1245 | 12 | 4 |
| SCE1572_8829 | 0 | 0 |
| SCE1572_7196 | 0.83 | 0 |
| SCE1572_8323 | 53 | 26 |
| SCE1572_7810 | 198 | 152 |
| SCE1572_5160 | 66 | 20 |
| SCE1572_3547 | 0 | 0 |
| SCE1572_4921 | 11 | 6 |
| SCE1572_9327 | 219 | 199 |
| SCE1572_4692 | 104 | 42 |
| SCE1572_4373 | 51 | 23 |
| SCE1572_5611 | 7 | 2 |
| SCE1572_4064 | 0 | 0 |
| SCE1572_7806 | 80 | 30 |
| SCE1572_4289 | 82 | 52 |
| SCE1572_2292 | 85 | 43 |
| SCE1572_9764 | 118 | 47 |
| SCE1572_443 | 71 | 8 |
| SCE1572_10656 | 210 | 167 |
| SCE1572_3155 | 122 | 102 |
| SCE1572_2382 | 26 | 4 |
| SCE1572_4908 | 168 | 123 |
| SCE1572_1213 | 0 | 0 |
| SCE1572_6733 | 78 | 198 |
| SCE1572_6427 | 11 | 4 |
| SCE1572_5433 | 65 | 6 |
| SCE1572_6997 | 19 | 4 |
| SCE1572_5086 | 70 | 9 |
| SCE1572_8419 | 4 | 0 |
| SCE1572_5286 | 265 | 44 |
| SCE1572_1320 | 45 | 45 |
| SCE1572_812 | 0 | 0 |
| SCE1572_7072 | 175 | 109 |
| SCE1572_3256 | 46 | 10 |
| SCE1572_4688 | 0 | 0 |
| SCE1572_6297 | 14 | 42 |
| SCE1572_11287 | 73 | 175 |

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| SCE1572_10411 | 30 | 13 |
| SCE1572_10206 | 1065.38 | 196.87 |
| SCE1572_5134 | 10 | 9 |
| SCE1572_8605 | 96 | 54 |
| SCE1572_6363 | 105 | 366 |
| SCE1572_10269 | 20 | 5 |
| SCE1572_3519 | 17 | 5 |
| SCE1572_2654 | 36 | 6 |
| SCE1572_429 | 173 | 116 |
| SCE1572_2758 | 191 | 238 |
| SCE1572_653 | 616 | 845 |
| SCE1572_6600 | 217 | 83 |
| SCE1572_9999 | 53 | 214 |
| SCE1572_8006 | 2 | 0 |
| SCE1572_7667 | 648.22 | 56.9 |
| SCE1572_786 | 7 | 1 |
| SCE1572_9967 | 87 | 24 |
| SCE1572_403 | 63 | 46 |
| SCE1572_6439 | 38 | 12 |
| SCE1572_1974 | 0 | 0.24 |
| SCE1572_8924 | 0 | 0 |
| SCE1572_7387 | 108 | 81 |
| SCE1572_10628 | 237 | 293 |
| SCE1572_8908 | 17 | 4 |
| SCE1572_8469 | 155 | 77 |
| SCE1572_448 | 55 | 24 |
| SCE1572_10488 | 559 | 3012 |
| SCE1572_10108 | 69 | 85 |
| SCE1572_4147 | 24 | 596 |
| SCE1572_5939 | 121 | 13 |
| SCE1572_10192 | 16 | 2 |
| SCE1572_1489 | 71 | 8 |
| SCE1572_10097 | 26 | 71 |
| SCE1572_7571 | 132 | 211 |
| SCE1572_943 | 225.53 | 28.4 |
| SCE1572_9807 | 255 | 420 |
| SCE1572_1926 | 472 | 1483 |
| SCE1572_113 | 91 | 30 |
| SCE1572_8109 | 82 | 20 |
| SCE1572_3288 | 199 | 189 |
| SCE1572_4228 | 63 | 15 |
| SCE1572_6729 | 5 | 7 |
| SCE1572_637 | 19 | 19 |
| SCE1572_6713 | 49 | 35 |
| SCE1572_5767 | 259 | 654 |
| SCE1572_8959 | 0 | 0 |
| SCE1572_2164 | 4 | 1 |
| SCE1572_2795 | 36 | 21 |

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| SCE1572_955 | 0 | 0 |
| SCE1572_11505 | 237 | 614 |
| SCE1572_7290 | 30 | 6 |
| SCE1572_6020 | 199 | 112 |
| SCE1572_8273 | 29 | 21 |
| SCE1572_3459 | 6402 | 763 |
| SCE1572_932 | 0 | 0 |
| SCE1572_3837 | 154 | 27 |
| SCE1572_11297 | 281 | 163 |
| SCE1572_3979 | 76 | 46 |
| SCE1572_10090 | 199.17 | 165.77 |
| SCE1572_10503 | 14 | 17 |
| SCE1572_377 | 173.53 | 28 |
| SCE1572_9898 | 50 | 5 |
| SCE1572_3586 | 27 | 9 |
| SCE1572_457 | 21 | 11 |
| SCE1572_10126 | 2 | 0 |
| SCE1572_8430 | 137 | 108 |
| SCE1572_10044 | 383 | 644 |
| SCE1572_4059 | 38 | 18 |
| SCE1572_10668 | 0 | 0 |
| SCE1572_9110 | 89 | 33 |
| SCE1572_1096 | 60 | 47 |
| SCE1572_7220 | 33 | 345 |
| SCE1572_4094 | 29 | 7 |
| SCE1572_8491 | 95 | 32 |
| SCE1572_343 | 133 | 58 |
| SCE1572_10616 | 54 | 34 |
| SCE1572_7651 | 185 | 25 |
| SCE1572_5945 | 82 | 25 |
| SCE1572_7779 | 9 | 2 |
| SCE1572_3016 | 1 | 0 |
| SCE1572_9404 | 32 | 126 |
| SCE1572_7227 | 135 | 1797 |
| SCE1572_5540 | 31 | 29 |
| SCE1572_4417 | 12 | 4 |
| SCE1572_9700 | 131 | 61 |
| SCE1572_5184 | 39 | 1151 |
| SCE1572_1024 | 45 | 5 |
| SCE1572_1349 | 10 | 62 |
| SCE1572_5547 | 94 | 11 |
| SCE1572_3094 | 50 | 44 |
| SCE1572_11012 | 115 | 58 |
| SCE1572_1046 | 59 | 17 |
| SCE1572_6384 | 68 | 23 |
| SCE1572_8697 | 1 | 0 |
| SCE1572_3027 | 87 | 71 |
| SCE1572_9845 | 128 | 10 |

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| SCE1572_3384 | 209 | 356 |
| SCE1572_968 | 128 | 273 |
| SCE1572_2035 | 0 | 0 |
| SCE1572_4563 | 4 | 3 |
| SCE1572_10852 | 184 | 48 |
| SCE1572_8083 | 25 | 7 |
| SCE1572_1131 | 29 | 3 |
| SCE1572_7891 | 109 | 1707 |
| SCE1572_524 | 38 | 20 |
| SCE1572_4716 | 35 | 7 |
| SCE1572_3503 | 54 | 37 |
| SCE1572_11124 | 36 | 2 |
| SCE1572_7906 | 219 | 40 |
| SCE1572_8316 | 124 | 69 |
| SCE1572_4073 | 159 | 715 |
| SCE1572_4718 | 42 | 13 |
| SCE1572_6850 | 13 | 4 |
| SCE1572_1581 | 45 | 24 |
| SCE1572_9346 | 280 | 142 |
| SCE1572_8480 | 73 | 112 |
| SCE1572_1015 | 118 | 18 |
| SCE1572_10326 | 27 | 4 |
| SCE1572_2752 | 93 | 76 |
| SCE1572_5962 | 0 | 0 |
| SCE1572_3758 | 359.09 | 75.81 |
| SCE1572_8066 | 1092 | 167 |
| SCE1572_6285 | 65 | 30 |
| SCE1572_2456 | 698 | 240 |
| SCE1572_1150 | 520 | 2541 |
| SCE1572_3662 | 51 | 1 |
| SCE1572_1185 | 89 | 8 |
| SCE1572_740 | 18 | 2 |
| SCE1572_3970 | 49 | 50 |
| SCE1572_10440 | 25 | 1 |
| SCE1572_7159 | 63 | 11 |
| SCE1572_8246 | 38 | 39 |
| SCE1572_706 | 11 | 1 |
| SCE1572_3109 | 162 | 16 |
| SCE1572_7123 | 7 | 1 |
| SCE1572_5650 | 1 | 0 |
| SCE1572_4647 | 0 | 0 |
| SCE1572_10110 | 47.05 | 65 |
| SCE1572_1507 | 294 | 45 |
| SCE1572_750 | 81 | 11 |
| SCE1572_10167 | 188 | 106 |
| SCE1572_7564 | 72 | 10 |
| SCE1572_5335 | 138 | 125 |
| SCE1572_1433 | 0 | 0 |

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| SCE1572_8147 | 138 | 27 |
| SCE1572_4995 | 49 | 41 |
| SCE1572_3262 | 29 | 16 |
| SCE1572_7282 | 80 | 23 |
| SCE1572_8653 | 88 | 27 |
| SCE1572_3610 | 0 | 0 |
| SCE1572_7496 | 0 | 0 |
| SCE1572_9946 | 15 | 0 |
| SCE1572_2991 | 165 | 50 |
| SCE1572_5226 | 58 | 59 |
| SCE1572_5383 | 144 | 22 |
| SCE1572_6686 | 5 | 2 |
| SCE1572_4050 | 288 | 312 |
| SCE1572_7446 | 12 | 0 |
| SCE1572_4363 | 65 | 6 |
| SCE1572_3658 | 54 | 6 |
| SCE1572_9942 | 79 | 18 |
| SCE1572_7324 | 0 | 0 |
| SCE1572_152 | 59 | 26 |
| SCE1572_7354 | 230.92 | 28 |
| SCE1572_6807 | 35 | 10 |
| SCE1572_8815 | 2 | 0 |
| SCE1572_3429 | 95 | 8 |
| SCE1572_5303 | 27 | 7 |
| SCE1572_7187 | 309 | 86 |
| SCE1572_3437 | 48 | 7 |
| SCE1572_7273 | 1 | 0 |
| SCE1572_5569 | 83 | 25 |
| SCE1572_9904 | 34 | 11 |
| SCE1572_858 | 596 | 8100 |
| SCE1572_4985 | 5 | 0 |
| SCE1572_2786 | 22 | 32 |
| SCE1572_4722 | 115 | 111 |
| SCE1572_6654 | 1036 | 1978 |
| SCE1572_11145 | 95 | 51 |
| SCE1572_8386 | 307.05 | 59.43 |
| SCE1572_792 | 109 | 67 |
| SCE1572_1408 | 37 | 2 |
| SCE1572_10235 | 115.6 | 24.77 |
| SCE1572_6625 | 51 | 24 |
| SCE1572_5746 | 84 | 73 |
| SCE1572_4134 | 305 | 43 |
| SCE1572_8009 | 621 | 15021 |
| SCE1572_2951 | 0 | 0 |
| SCE1572_4702 | 348 | 71 |
| SCE1572_1986 | 157.03 | 903 |
| SCE1572_9084 | 70 | 67 |
| SCE1572_5412 | 47 | 12 |

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| SCE1572_7403 | 181 | 2230 |
| SCE1572_3250 | 148 | 131 |
| SCE1572_1018 | 87 | 188 |
| SCE1572_9494 | 647 | 300 |
| SCE1572_8477 | 413 | 82 |
| SCE1572_683 | 40 | 12 |
| SCE1572_584 | 70 | 139 |
| SCE1572_5444 | 63 | 6 |
| SCE1572_5189 | 44 | 290 |
| SCE1572_514 | 89 | 30 |
| SCE1572_1319 | 69 | 11 |
| SCE1572_5132 | 96 | 79 |
| SCE1572_8640 | 81 | 170 |
| SCE1572_5659 | 246 | 125 |
| SCE1572_1418 | 53 | 31 |
| SCE1572_2496 | 17 | 2 |
| SCE1572_4704 | 100 | 11 |
| SCE1572_1833 | 116 | 36 |
| SCE1572_6337 | 87 | 55 |
| SCE1572_9743 | 324 | 915 |
| SCE1572_3026 | 43.03 | 23 |
| SCE1572_6755 | 45 | 12 |
| SCE1572_10679 | 481 | 1046 |
| SCE1572_7993 | 60 | 8 |
| SCE1572_5006 | 184 | 495 |
| SCE1572_11457 | 715 | 333 |
| SCE1572_1746 | 233 | 61 |
| SCE1572_5712 | 27 | 2 |
| SCE1572_6899 | 42 | 85 |
| SCE1572_8962 | 40 | 12 |
| SCE1572_8150 | 83 | 11 |
| SCE1572_5320 | 63 | 69 |
| SCE1572_10767 | 92 | 17 |
| SCE1572_8062 | 0 | 0 |
| SCE1572_6273 | 51 | 33 |
| SCE1572_999 | 383 | 141 |
| SCE1572_10862 | 124 | 322 |
| SCE1572_749 | 144 | 83 |
| SCE1572_1351 | 119 | 85 |
| SCE1572_2846 | 18 | 2 |
| SCE1572_8725 | 159 | 25 |
| SCE1572_9331 | 375 | 1401 |
| SCE1572_10987 | 47 | 113 |
| SCE1572_11170 | 131 | 48 |
| SCE1572_11556 | 1 | 0 |
| SCE1572_3490 | 39 | 48 |
| SCE1572_7135 | 51 | 17 |
| SCE1572_9928 | 23 | 18 |

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| SCE1572_8120 | 52 | 6 |
| SCE1572_10546 | 3 | 1 |
| SCE1572_2013 | 143 | 17 |
| SCE1572_5157 | 64 | 11 |
| SCE1572_8780 | 68 | 39 |
| SCE1572_11569 | 19 | 75 |
| SCE1572_10981 | 218 | 379 |
| SCE1572_7703 | 26 | 43 |
| SCE1572_1859 | 32 | 2 |
| SCE1572_1195 | 1 | 0 |
| SCE1572_3925 | 204 | 88 |
| SCE1572_2252 | 202 | 83 |
| SCE1572_8033 | 0 | 0 |
| SCE1572_7034 | 103 | 42 |
| SCE1572_81 | 3 | 2 |
| SCE1572_11535 | 159 | 74 |
| SCE1572_10674 | 107 | 127 |
| SCE1572_4788 | 159 | 70 |
| SCE1572_9349 | 148 | 183 |
| SCE1572_8114 | 68 | 12 |
| SCE1572_4406 | 75 | 8 |
| SCE1572_8856 | 36 | 62 |
| SCE1572_4022 | 70 | 86 |
| SCE1572_1176 | 128 | 41 |
| SCE1572_11389 | 1487 | 1067 |
| SCE1572_8915 | 21 | 198 |
| SCE1572_5276 | 9 | 0 |
| SCE1572_1906 | 93 | 281 |
| SCE1572_835 | 31 | 4 |
| SCE1572_3214 | 0 | 0 |
| SCE1572_5491 | 151 | 41 |
| SCE1572_6635 | 3 | 0 |
| SCE1572_7125 | 135 | 45 |
| SCE1572_10891 | 81 | 65 |
| SCE1572_10719 | 170 | 34 |
| SCE1572_3010 | 25 | 3 |
| SCE1572_8224 | 7 | 2 |
| SCE1572_6715 | 88 | 22 |
| SCE1572_2550 | 47 | 11 |
| SCE1572_733 | 101 | 16 |
| SCE1572_9315 | 43 | 16 |
| SCE1572_8744 | 205 | 45 |
| SCE1572_5385 | 458 | 125 |
| SCE1572_509 | 85 | 19 |
| SCE1572_3456 | 129 | 14 |
| SCE1572_1800 | 4 | 2 |
| SCE1572_6576 | 60 | 8 |
| SCE1572_7028 | 52 | 35 |

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| SCE1572_632 | 249 | 302 |
| SCE1572_4638 | 21 | 2 |
| SCE1572_4759 | 132 | 35 |
| SCE1572_7682 | 100 | 7 |
| SCE1572_8952 | 44 | 8 |
| SCE1572_2567 | 355 | 298 |
| SCE1572_2702 | 137 | 91 |
| SCE1572_6540 | 8 | 0 |
| SCE1572_4850 | 103 | 36 |
| SCE1572_9255 | 46 | 12 |
| SCE1572_4899 | 24 | 8 |
| SCE1572_10777 | 491 | 223 |
| SCE1572_2644 | 111 | 36 |
| SCE1572_8390 | 1 | 0 |
| SCE1572_3735 | 137 | 21 |
| SCE1572_7059 | 102 | 66 |
| SCE1572_2153 | 46 | 25 |
| SCE1572_1115 | 16 | 8 |
| SCE1572_3048 | 34 | 2 |
| SCE1572_3643 | 0 | 0 |
| SCE1572_3359 | 237 | 45 |
| SCE1572_178 | 44 | 10 |
| SCE1572_2823 | 40 | 6 |
| SCE1572_5484 | 65.53 | 4.91 |
| SCE1572_6085 | 75 | 31 |
| SCE1572_9940 | 0 | 0 |
| SCE1572_10112 | 34 | 0 |
| SCE1572_5582 | 48 | 12 |
| SCE1572_9523 | 99 | 87 |
| SCE1572_3960 | 78 | 31 |
| SCE1572_9581 | 66 | 43 |
| SCE1572_2250 | 551.97 | 222 |
| SCE1572_2043 | 35 | 184 |
| SCE1572_5668 | 5 | 0 |
| SCE1572_7826 | 200 | 93 |
| SCE1572_4890 | 496 | 337 |
| SCE1572_8711 | 64 | 16 |
| SCE1572_4177 | 147.7 | 19.18 |
| SCE1572_11518 | 115 | 24 |
| SCE1572_8047 | 41 | 6 |
| SCE1572_7770 | 96 | 47 |
| SCE1572_11022 | 292 | 91 |
| SCE1572_1446 | 40 | 6 |
| SCE1572_8326 | 138 | 57 |
| SCE1572_9139 | 0 | 0 |
| SCE1572_728 | 65 | 79 |
| SCE1572_5088 | 103 | 71 |
| SCE1572_9365 | 152 | 83 |

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| SCE1572_2326 | 23 | 42 |
| SCE1572_4097 | 16 | 3 |
| SCE1572_8111 | 235 | 27 |
| SCE1572_6064 | 54 | 7 |
| SCE1572_8040 | 172 | 44 |
| SCE1572_10573 | 24 | 14 |
| SCE1572_10146 | 497 | 248 |
| SCE1572_6532 | 98 | 16 |
| SCE1572_1908 | 60 | 40 |
| SCE1572_8375 | 56 | 116 |
| SCE1572_5516 | 1 | 0 |
| SCE1572_9300 | 166 | 142 |
| SCE1572_10152 | 195 | 377 |
| SCE1572_11572 | 92 | 161 |
| SCE1572_101 | 3 | 0 |
| SCE1572_674 | 198 | 166 |
| SCE1572_4503 | 100 | 29 |
| SCE1572_9583 | 144 | 36 |
| SCE1572_8865 | 198 | 87 |
| SCE1572_6494 | 25 | 10 |
| SCE1572_11376 | 85 | 47 |
| SCE1572_3004 | 5 | 0 |
| SCE1572_454 | 62 | 11 |
| SCE1572_1305 | 30 | 6 |
| SCE1572_5214 | 119 | 22 |
| SCE1572_5564 | 5 | 0 |
| SCE1572_9065 | 156 | 23 |
| SCE1572_6466 | 41 | 2 |
| SCE1572_9551 | 71 | 16 |
| SCE1572_10420 | 249 | 175 |
| SCE1572_10695 | 26 | 6 |
| SCE1572_2212 | 28 | 20 |
| SCE1572_1882 | 381 | 75 |
| SCE1572_4901 | 219 | 53 |
| SCE1572_1033 | 79 | 15 |
| SCE1572_10275 | 52 | 67 |
| SCE1572_8153 | 81 | 6 |
| SCE1572_5042 | 96 | 94 |
| SCE1572_8372 | 79 | 38 |
| SCE1572_3142 | 49 | 18 |
| SCE1572_2628 | 168 | 24 |
| SCE1572_4458 | 46 | 17 |
| SCE1572_5435 | 84 | 16 |
| SCE1572_10609 | 298 | 688 |
| SCE1572_6443 | 2 | 3 |
| SCE1572_4136 | 97 | 14 |
| SCE1572_6513 | 0 | 0 |
| SCE1572_1087 | 6 | 5 |

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| SCE1572_2836 | 13 | 15 |
| SCE1572_9197 | 154 | 35 |
| SCE1572_2952 | 7.99 | 1 |
| SCE1572_4575 | 121 | 17 |
| SCE1572_5159 | 48 | 23 |
| SCE1572_1862 | 246 | 23 |
| SCE1572_6702 | 208 | 21 |
| SCE1572_4547 | 248 | 19 |
| SCE1572_31 | 18 | 11 |
| SCE1572_4272 | 101 | 79 |
| SCE1572_4076 | 7 | 0 |
| SCE1572_5076 | 173 | 298 |
| SCE1572_10022 | 24.68 | 3.05 |
| SCE1572_7642 | 49 | 10 |
| SCE1572_1208 | 132 | 35 |
| SCE1572_3899 | 209 | 35 |
| SCE1572_2429 | 96 | 59 |
| SCE1572_4752 | 8 | 12 |
| SCE1572_5694 | 53 | 4 |
| SCE1572_8514 | 73.19 | 0 |
| SCE1572_1533 | 14 | 9 |
| SCE1572_9649 | 49 | 4 |
| SCE1572_4663 | 0 | 0 |
| SCE1572_11423 | 44 | 8 |
| SCE1572_5169 | 11 | 0 |
| SCE1572_7830 | 280 | 85 |
| SCE1572_4173 | 282 | 136 |
| SCE1572_10498 | 57 | 34 |
| SCE1572_11107 | 135 | 102 |
| SCE1572_6308 | 96 | 16 |
| SCE1572_5529 | 90 | 37 |
| SCE1572_1490 | 20 | 2 |
| SCE1572_8820 | 66.58 | 12 |
| SCE1572_5876 | 162 | 590 |
| SCE1572_1384 | 426 | 64 |
| SCE1572_2306 | 142 | 180 |
| SCE1572_3060 | 65 | 4 |
| SCE1572_3707 | 44 | 24 |
| SCE1572_8578 | 307.05 | 59.43 |
| SCE1572_9777 | 25 | 194 |
| SCE1572_8475 | 857 | 289 |
| SCE1572_3445 | 488 | 131 |
| SCE1572_8941 | 82 | 79 |
| SCE1572_7368 | 623 | 2088 |
| SCE1572_398 | 104 | 13 |
| SCE1572_7049 | 29 | 4 |
| SCE1572_93 | 183 | 38 |
| SCE1572_10027 | 91.41 | 31 |

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| SCE1572_8922 | 92 | 62.5 |
| SCE1572_6539 | 33 | 2 |
| SCE1572_1126 | 0 | 0 |
| SCE1572_7913 | 80 | 15 |
| SCE1572_10880 | 267 | 540 |
| SCE1572_9884 | 81 | 23 |
| SCE1572_9038 | 30 | 21 |
| SCE1572_7119 | 45 | 39 |
| SCE1572_3229 | 245 | 57 |
| SCE1572_8354 | 37 | 3 |
| SCE1572_4087 | 32 | 6 |
| SCE1572_10250 | 134 | 15 |
| SCE1572_4244 | 256 | 1217 |
| SCE1572_4394 | 81 | 12 |
| SCE1572_5926 | 691 | 42 |
| SCE1572_5067 | 286 | 307 |
| SCE1572_8187 | 5 | 1 |
| SCE1572_688 | 282 | 303 |
| SCE1572_10796 | 0 | 0 |
| SCE1572_3157 | 139 | 76 |
| SCE1572_8451 | 67 | 239 |
| SCE1572_6025 | 36 | 18 |
| SCE1572_10699 | 91 | 942 |
| SCE1572_4538 | 337 | 49 |
| SCE1572_15 | 17 | 23 |
| SCE1572_7431 | 62 | 5 |
| SCE1572_9322 | 127 | 45 |
| SCE1572_6155 | 90 | 37 |
| SCE1572_6389 | 116 | 66 |
| SCE1572_9422 | 120 | 152 |
| SCE1572_9186 | 804 | 123 |
| SCE1572_7661 | 92 | 7 |
| SCE1572_5741 | 70 | 18 |
| SCE1572_541 | 155 | 33 |
| SCE1572_3420 | 200 | 347 |
| SCE1572_7639 | 111 | 68 |
| SCE1572_1813 | 20 | 4 |
| SCE1572_1354 | 71 | 6 |
| SCE1572_4328 | 46 | 8 |
| SCE1572_9329 | 0 | 0 |
| SCE1572_11254 | 124 | 113 |
| SCE1572_8253 | 42 | 16 |
| SCE1572_6677 | 125 | 80 |
| SCE1572_11228 | 23 | 104 |
| SCE1572_2088 | 128 | 36 |
| SCE1572_9813 | 19 | 4 |
| SCE1572_7097 | 63 | 19 |
| SCE1572_4524 | 148 | 14 |

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| SCE1572_5101 | 92 | 25 |
| SCE1572_3526 | 25 | 1215 |
| SCE1572_9225 | 1 | 0 |
| SCE1572_7594 | 14 | 8 |
| SCE1572_10849 | 94 | 16 |
| SCE1572_10428 | 88 | 17 |
| SCE1572_8440 | 344 | 188 |
| SCE1572_7744 | 66 | 905 |
| SCE1572_5361 | 78 | 102 |
| SCE1572_6376 | 45 | 1 |
| SCE1572_5911 | 106 | 75 |
| SCE1572_9745 | 26 | 8 |
| SCE1572_9045 | 249 | 44 |
| SCE1572_5254 | 61 | 6 |
| SCE1572_357 | 186 | 86 |
| SCE1572_1660 | 244 | 360 |
| SCE1572_2765 | 134 | 75 |
| SCE1572_8756 | 450 | 85 |
| SCE1572_6849 | 87 | 5 |
| SCE1572_1254 | 46 | 8 |
| SCE1572_2789 | 36 | 15 |
| SCE1572_3681 | 10 | 3 |
| SCE1572_232 | 3 | 0 |
| SCE1572_7052 | 13 | 0 |
| SCE1572_6722 | 53 | 74 |
| SCE1572_5056 | 441 | 142 |
| SCE1572_4557 | 69 | 13 |
| SCE1572_2348 | 47 | 7 |
| SCE1572_6012 | 79 | 68 |
| SCE1572_3808 | 114 | 117 |
| SCE1572_9770 | 174 | 40 |
| SCE1572_8137 | 59 | 11 |
| SCE1572_3140 | 253 | 199 |
| SCE1572_4735 | 555 | 10966 |
| SCE1572_3342 | 680 | 701 |
| SCE1572_10921 | 117 | 54 |
| SCE1572_3186 | 87 | 110 |
| SCE1572_6080 | 196 | 45 |
| SCE1572_4526 | 66 | 14 |
| SCE1572_11098 | 184 | 77 |
| SCE1572_5904 | 27 | 13 |
| SCE1572_4332 | 38 | 18 |
| SCE1572_11272 | 44 | 12 |
| SCE1572_8449 | 29 | 20 |
| SCE1572_1326 | 1 | 1 |
| SCE1572_1232 | 30 | 6 |
| SCE1572_239 | 6 | 0 |
| SCE1572_5657 | 53 | 38 |

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| SCE1572_411 | 296 | 67 |
| SCE1572_3392 | 524 | 303 |
| SCE1572_5959 | 196 | 71 |
| SCE1572_11441 | 37 | 24 |
| SCE1572_6802 | 416 | 781 |
| SCE1572_5120 | 321 | 1341 |
| SCE1572_7817 | 39 | 30 |
| SCE1572_9418 | 271 | 1302 |
| SCE1572_9854 | 451 | 65 |
| SCE1572_8203 | 8 | 0 |
| SCE1572_3468 | 30 | 2 |
| SCE1572_8559 | 63 | 27 |
| SCE1572_1164 | 70 | 47 |
| SCE1572_6170 | 22 | 30 |
| SCE1572_961 | 139 | 206 |
| SCE1572_895 | 25 | 2 |
| SCE1572_175 | 40 | 2 |
| SCE1572_6680 | 44 | 18 |
| SCE1572_4470 | 29 | 3 |
| SCE1572_10645 | 139 | 82 |
| SCE1572_9427 | 14 | 0 |
| SCE1572_6661 | 157 | 88 |
| SCE1572_65 | 56 | 165 |
| SCE1572_2686 | 0 | 0 |
| SCE1572_5161 | 640 | 2778 |
| SCE1572_5855 | 62 | 14 |
| SCE1572_7894 | 677 | 0 |
| SCE1572_7953 | 105 | 24 |
| SCE1572_11403 | 28 | 21 |
| SCE1572_9147 | 39 | 100 |
| SCE1572_10474 | 107 | 55 |
| SCE1572_4446 | 0 | 0 |
| SCE1572_3969 | 308 | 526 |
| SCE1572_536 | 343 | 360 |
| SCE1572_601 | 399 | 259 |
| SCE1572_11185 | 68 | 13 |
| SCE1572_1291 | 94 | 28 |
| SCE1572_2988 | 25 | 8 |
| SCE1572_10332 | 365 | 44 |
| SCE1572_8078 | 0 | 0 |
| SCE1572_2507 | 0 | 0 |
| SCE1572_8303 | 17 | 30 |
| SCE1572_1391 | 96 | 51 |
| SCE1572_923 | 188 | 136 |
| SCE1572_10749 | 151 | 588 |
| SCE1572_1694 | 351 | 49 |
| SCE1572_1654 | 173 | 39 |
| SCE1572_6840 | 24 | 27 |

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| SCE1572_8587 | 0 | 0 |
| SCE1572_675 | 74 | 4 |
| SCE1572_5761 | 99 | 29 |
| SCE1572_10351 | 142 | 42 |
| SCE1572_4223 | 60 | 32 |
| SCE1572_8409 | 0 | 0 |
| SCE1572_4423 | 1 | 0 |
| SCE1572_7180 | 26 | 4 |
| SCE1572_417 | 18 | 4 |
| SCE1572_7918 | 190 | 28 |
| SCE1572_11215 | 212 | 41 |
| SCE1572_11318 | 132 | 72 |
| SCE1572_3584 | 4 | 0 |
| SCE1572_10481 | 160 | 69 |
| SCE1572_2388 | 0 | 0 |
| SCE1572_7007 | 0 | 0 |
| SCE1572_11067 | 35 | 20 |
| SCE1572_9549 | 81 | 16 |
| SCE1572_11559 | 210.63 | 45.01 |
| SCE1572_8132 | 43 | 7 |
| SCE1572_1667 | 23 | 13 |
| SCE1572_4419 | 241 | 30 |
| SCE1572_7044 | 1300 | 4043 |
| SCE1572_423 | 56 | 93 |
| SCE1572_8841 | 208 | 45 |
| SCE1572_11177 | 63 | 52 |
| SCE1572_2400 | 225 | 953 |
| SCE1572_8425 | 25 | 69 |
| SCE1572_1148 | 81 | 81 |
| SCE1572_259 | 12 | 4 |
| SCE1572_2520 | 155 | 31 |
| SCE1572_5482 | 324 | 191 |
| SCE1572_2783 | 52 | 42 |
| SCE1572_10840 | 28 | 24 |
| SCE1572_11115 | 178 | 77 |
| SCE1572_809 | 460 | 432 |
| SCE1572_7647 | 257 | 32 |
| SCE1572_5969 | 133 | 20 |
| SCE1572_472 | 38 | 89 |
| SCE1572_2447 | 60 | 8 |
| SCE1572_6153 | 0 | 0 |
| SCE1572_2965 | 53 | 5 |
| SCE1572_983 | 285 | 477 |
| SCE1572_7346 | 0 | 0 |
| SCE1572_4205 | 63 | 49 |
| SCE1572_1421 | 160 | 22 |
| SCE1572_5884 | 144 | 59 |
| SCE1572_6571 | 13.25 | 1.56 |

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| SCE1572_11465 | 145 | 36 |
| SCE1572_10155 | 62 | 20 |
| SCE1572_7777 | 25 | 9 |
| SCE1572_2969 | 184.81 | 8.81 |
| SCE1572_5358 | 160 | 199 |
| SCE1572_5805 | 40 | 214 |
| SCE1572_9565 | 139 | 27 |
| SCE1572_7795 | 41 | 21 |
| SCE1572_4598 | 315 | 356 |
| SCE1572_8170 | 84 | 7 |
| SCE1572_3868 | 372 | 74 |
| SCE1572_11348 | 38 | 20 |
| SCE1572_9601 | 554 | 641 |
| SCE1572_5754 | 51 | 43 |
| SCE1572_3267 | 118 | 161 |
| SCE1572_6382 | 156 | 32 |
| SCE1572_3430 | 63 | 76 |
| SCE1572_7457 | 19 | 1 |
| SCE1572_1275 | 14 | 11 |
| SCE1572_3567 | 68 | 7 |
| SCE1572_3761 | 218 | 53 |
| SCE1572_8232 | 46 | 29 |
| SCE1572_5670 | 466 | 90 |
| SCE1572_9678 | 49 | 10 |
| SCE1572_7460 | 37 | 14 |
| SCE1572_4870 | 13 | 49 |
| SCE1572_11355 | 111 | 28 |
| SCE1572_4510 | 243 | 100 |
| SCE1572_599 | 50 | 13 |
| SCE1572_11585 | 8 | 0 |
| SCE1572_5933 | 95 | 16 |
| SCE1572_5895 | 407 | 34 |
| SCE1572_4020 | 39 | 40 |
| SCE1572_7021 | 50.55 | 8.24 |
| SCE1572_6036 | 7 | 0 |
| SCE1572_3325 | 335 | 398 |
| SCE1572_1241 | 33 | 17 |
| SCE1572_3080 | 63 | 135 |
| SCE1572_1009 | 77 | 19 |
| SCE1572_2993 | 224 | 92 |
| SCE1572_2922 | 90 | 14 |
| SCE1572_9354 | 105 | 46 |
| SCE1572_629 | 151 | 189 |
| SCE1572_4365 | 211 | 22 |
| SCE1572_6283 | 28 | 29 |
| SCE1572_7532 | 13.02 | 3.43 |
| SCE1572_4124 | 34 | 12 |
| SCE1572_4794 | 1338 | 1238 |

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| SCE1572_5575 | 8 | 6 |
| SCE1572_5649 | 517 | 280 |
| SCE1572_6271 | 6 | 7 |
| SCE1572_7174 | 0 | 0 |
| SCE1572_7110 | 0 | 0 |
| SCE1572_3535 | 65 | 7 |
| SCE1572_8335 | 0 | 0 |
| SCE1572_11595 | 1507 | 2268 |
| SCE1572_10281 | 113 | 225 |
| SCE1572_5840 | 25 | 1 |
| SCE1572_163 | 296 | 64 |
| SCE1572_2869 | 13 | 27 |
| SCE1572_7712 | 41 | 21 |
| SCE1572_6404 | 9 | 0 |
| SCE1572_821 | 18 | 3 |
| SCE1572_4386 | 51 | 8 |
| SCE1572_6800 | 915 | 759 |
| SCE1572_3900 | 178 | 98 |
| SCE1572_7363 | 626 | 235 |
| SCE1572_192 | 1 | 0 |
| SCE1572_7756 | 25 | 4 |
| SCE1572_2778 | 57 | 33 |
| SCE1572_2434 | 149 | 47 |
| SCE1572_2662 | 37 | 62 |
| SCE1572_4053 | 128 | 220 |
| SCE1572_622 | 0 | 0 |
| SCE1572_2852 | 0 | 0 |
| SCE1572_9130 | 31 | 6 |
| SCE1572_6059 | 467 | 1651 |
| SCE1572_1602 | 60 | 15 |
| SCE1572_8024 | 8 | 3 |
| SCE1572_5686 | 35 | 27 |
| SCE1572_4832 | 0 | 0 |
| SCE1572_2919 | 66 | 26 |
| SCE1572_10578 | 0 | 0 |
| SCE1572_382 | 16 | 2 |
| SCE1572_718 | 26 | 7 |
| SCE1572_4531 | 116 | 32 |
| SCE1572_10909 | 129 | 58 |
| SCE1572_8795 | 43 | 19 |
| SCE1572_5630 | 213 | 300 |
| SCE1572_11566 | 134 | 46 |
| SCE1572_4742 | 27 | 32 |
| SCE1572_3164 | 211 | 34 |
| SCE1572_7041 | 68 | 6 |
| SCE1572_8616 | 115 | 33 |
| SCE1572_4867 | 0 | 0 |
| SCE1572_9129 | 116 | 30 |

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| SCE1572_7963 | 207 | 343 |
| SCE1572_4026 | 264 | 318 |
| SCE1572_7506 | 338.88 | 43.87 |
| SCE1572_6606 | 123 | 25 |
| SCE1572_5618 | 85 | 12 |
| SCE1572_2118 | 16 | 3 |
| SCE1572_9150 | 44 | 117 |
| SCE1572_2419 | 717 | 1719 |
| SCE1572_3907 | 28 | 4 |
| SCE1572_11094 | 168 | 35 |
| SCE1572_2947 | 0 | 0 |
| SCE1572_6872 | 78 | 52 |
| SCE1572_4315 | 35 | 4 |
| SCE1572_3997 | 186 | 290 |
| SCE1572_11049 | 134 | 50 |
| SCE1572_2669 | 153 | 31 |
| SCE1572_7720 | 66 | 153 |
| SCE1572_7999 | 7 | 1 |
| SCE1572_5759 | 28 | 0 |
| SCE1572_3113 | 291 | 31 |
| SCE1572_11430 | 323 | 489 |
| SCE1572_6145 | 53 | 7 |
| SCE1572_10621 | 168 | 69 |
| SCE1572_3064 | 117 | 17 |
| SCE1572_6764 | 140 | 122 |
| SCE1572_9159 | 45 | 6 |
| SCE1572_9486 | 31 | 21 |
| SCE1572_5442 | 61 | 13 |
| SCE1572_2008 | 173 | 12 |
| SCE1572_557 | 109 | 61 |
| SCE1572_9456 | 0 | 0 |
| SCE1572_6793 | 209 | 283 |
| SCE1572_4262 | 105 | 22 |
| SCE1572_6618 | 36 | 11 |
| SCE1572_1256 | 145 | 49 |
| SCE1572_8662 | 90 | 29 |
| SCE1572_762 | 568 | 75 |
| SCE1572_7237 | 435 | 1968 |
| SCE1572_668 | 55 | 23 |
| SCE1572_7162 | 92 | 25 |
| SCE1572_8168 | 46 | 6 |
| SCE1572_7192 | 27 | 1 |
| SCE1572_1073 | 93 | 22 |
| SCE1572_1588 | 24.39 | 4.8 |
| SCE1572_9119 | 52 | 7 |
| SCE1572_8095 | 17 | 1 |
| SCE1572_4337 | 0 | 0 |
| SCE1572_4305 | 211 | 54 |

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| SCE1572_10387 | 86 | 26 |
| SCE1572_10705 | 32 | 3 |
| SCE1572_9122 | 399 | 74 |
| SCE1572_2943 | 3 | 0 |
| SCE1572_3119 | 12 | 28 |
| SCE1572_4445 | 135 | 177 |
| SCE1572_4339 | 47 | 11 |
| SCE1572_11008 | 21 | 19 |
| SCE1572_1611 | 13 | 88 |
| SCE1572_7632 | 1821 | 6824 |
| SCE1572_11416 | 46 | 40 |
| SCE1572_10734 | 41 | 10 |
| SCE1572_6646 | 28 | 6 |
| SCE1572_548 | 195 | 28 |
| SCE1572_337 | 162 | 33 |
| SCE1572_7634 | 238 | 898 |
| SCE1572_11544 | 111 | 14 |
| SCE1572_517 | 106 | 29 |
| SCE1572_11266 | 692 | 1592 |
| SCE1572_7518 | 647 | 1486 |
| SCE1572_10371 | 47 | 19 |
| SCE1572_1510 | 79 | 16 |
| SCE1572_11248 | 64 | 14 |
| SCE1572_7946 | 548 | 140 |
| SCE1572_9918 | 129 | 26 |
| SCE1572_8508 | 65 | 36 |
| SCE1572_11322 | 27 | 11 |
| SCE1572_592 | 42 | 46 |
| SCE1572_2482 | 101 | 67 |
| SCE1572_9831 | 22 | 6 |
| SCE1572_9511 | 1 | 0 |
| SCE1572_2897 | 13 | 0 |
| SCE1572_4860 | 31 | 0 |
| SCE1572_3775 | 33 | 14 |
| SCE1572_1636 | 34 | 159 |
| SCE1572_3274 | 63 | 18 |
| SCE1572_8521 | 0 | 0 |
| SCE1572_1805 | 15 | 6 |
| SCE1572_9975 | 98 | 26 |
| SCE1572_1618 | 70 | 33 |
| SCE1572_7805 | 200 | 107 |
| SCE1572_8981 | 0 | 0 |
| SCE1572_6774 | 63 | 16 |
| SCE1572_2676 | 32 | 154 |
| SCE1572_3305 | 209 | 125 |
| SCE1572_10105 | 25 | 10 |
| SCE1572_7727 | 207 | 206 |
| SCE1572_4565 | 132 | 126 |

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| SCE1572_841 | 161 | 114 |
| SCE1572_11383 | 60 | 27 |
| SCE1572_6426 | 36 | 4 |
| SCE1572_2527 | 296 | 24 |
| SCE1572_9090 | 28 | 2 |
| SCE1572_6179 | 139 | 1214 |
| SCE1572_11087 | 30 | 54 |
| SCE1572_6244 | 48 | 5 |
| SCE1572_5351 | 13 | 3 |
| SCE1572_142 | 37.13 | 3 |
| SCE1572_341 | 181 | 49 |
| SCE1572_4823 | 42 | 30 |
| SCE1572_348 | 57 | 190 |
| SCE1572_315 | 627 | 104 |
| SCE1572_6118 | 45 | 4 |
| SCE1572_8493 | 16 | 3 |
| SCE1572_7392 | 6.93 | 0 |
| SCE1572_8286 | 31 | 36 |
| SCE1572_6226 | 135 | 68 |
| SCE1572_1521 | 43 | 6 |
| SCE1572_7130 | 218 | 57 |
| SCE1572_3878 | 232 | 78 |
| SCE1572_10316 | 0 | 0 |
| SCE1572_2127 | 9 | 1 |
| SCE1572_5661 | 15 | 5 |
| SCE1572_1456 | 24 | 5 |
| SCE1572_2410 | 179 | 139 |
| SCE1572_11345 | 111 | 129 |
| SCE1572_4877 | 39 | 14 |
| SCE1572_4213 | 405 | 621 |
| SCE1572_7136 | 99 | 12 |
| SCE1572_8988 | 4 | 0 |
| SCE1572_205 | 139 | 29 |
| SCE1572_9181 | 158 | 30 |
| SCE1572_298 | 54 | 27 |
| SCE1572_6033 | 617 | 400 |
| SCE1572_882 | 263 | 118 |
| SCE1572_8638 | 65 | 74 |
| SCE1572_7990 | 0 | 0 |
| SCE1572_9024 | 46 | 175 |
| SCE1572_3605 | 743 | 169 |
| SCE1572_2717 | 61 | 13 |
| SCE1572_9697 | 26 | 16 |
| SCE1572_125 | 94 | 16 |
| SCE1572_10294 | 215 | 286 |
| SCE1572_1924 | 198 | 177 |
| SCE1572_6334 | 167 | 26 |
| SCE1572_3881 | 24 | 3 |

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| SCE1572_6131 | 76 | 215 |
| SCE1572_6113 | 39 | 35 |
| SCE1572_4805 | 51 | 17 |
| SCE1572_1575 | 52 | 21 |
| SCE1572_43 | 18 | 5 |
| SCE1572_3789 | 1216 | 4468 |
| SCE1572_10966 | 49 | 9 |
| SCE1572_10795 | 3 | 4 |
| SCE1572_7698 | 75 | 19 |
| SCE1572_199 | 102 | 73 |
| SCE1572_7177 | 37 | 13 |
| SCE1572_6433 | 15 | 4 |
| SCE1572_11236 | 57 | 9 |
| SCE1572_9237 | 72 | 12 |
| SCE1572_6343 | 108 | 150 |
| SCE1572_5677 | 65 | 40 |
| SCE1572_1789 | 12 | 0 |
| SCE1572_4761 | 0 | 0 |
| SCE1572_8979 | 0 | 0 |
| SCE1572_7019 | 433 | 118 |
| SCE1572_2368 | 35 | 4 |
| SCE1572_2370 | 58 | 58 |
| SCE1572_7987 | 52 | 34 |
| SCE1572_9020 | 0 | 0 |
| SCE1572_312 | 86 | 18 |
| SCE1572_3178 | 3 | 0 |
| SCE1572_8881 | 148 | 30 |
| SCE1572_8898 | 3 | 0 |
| SCE1572_6789 | 228 | 46 |
| SCE1572_5993 | 107 | 41 |
| SCE1572_9470 | 85 | 221 |
| SCE1572_7241 | 423 | 149 |
| SCE1572_2130 | 14 | 1 |
| SCE1572_5425 | 213 | 140 |
| SCE1572_5877 | 45 | 31 |
| SCE1572_3555 | 193 | 36 |
| SCE1572_267 | 434 | 103 |
| SCE1572_6048 | 358 | 329 |
| SCE1572_3890 | 63 | 16 |
| SCE1572_9684 | 332 | 444 |
| SCE1572_9726 | 14 | 5 |
| SCE1572_3791 | 133 | 46 |
| SCE1572_1316 | 151 | 54 |
| SCE1572_9290 | 228 | 385 |
| SCE1572_2067 | 68 | 30 |
| SCE1572_9111 | 49 | 3 |
| SCE1572_9175 | 1153 | 727 |
| SCE1572_1769 | 66 | 10 |

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| SCE1572_5609 | 75 | 8 |
| SCE1572_695 | 6 | 9 |
| SCE1572_609 | 0 | 0 |
| SCE1572_3230 | 66 | 81 |
| SCE1572_6477 | 23 | 5 |
| SCE1572_7230 | 37 | 14 |
| SCE1572_3395 | 20 | 2 |
| SCE1572_8667 | 54 | 16 |
| SCE1572_4517 | 105 | 22 |
| SCE1572_9299 | 281 | 1236 |
| SCE1572_3570 | 96 | 17 |
| SCE1572_1449 | 30 | 14 |
| SCE1572_2862 | 4 | 0 |
| SCE1572_6930 | 18 | 0 |
| SCE1572_3947 | 3631 | 3473 |
| SCE1572_2696 | 43 | 12 |
| SCE1572_7426 | 48 | 64 |
| SCE1572_7477 | 34 | 54 |
| SCE1572_5831 | 51 | 23 |
| SCE1572_1552 | 94 | 30 |
| SCE1572_8276 | 91 | 41 |
| SCE1572_7264 | 99 | 19 |
| SCE1572_6743 | 7 | 1 |
| SCE1572_6005 | 75 | 66 |
| SCE1572_10690 | 133 | 90 |
| SCE1572_323 | 95 | 45 |
| SCE1572_5125 | 107 | 9 |
| SCE1572_2111 | 118 | 221 |
| SCE1572_9054 | 142 | 31 |
| SCE1572_4997 | 65 | 41 |
| SCE1572_9874 | 71 | 13 |
| SCE1572_8770 | 2 | 0 |
| SCE1572_3886 | 77 | 22 |
| SCE1572_5333 | 28 | 12 |
| SCE1572_743 | 43 | 14 |
| SCE1572_3719 | 66 | 443 |
| SCE1572_106 | 141 | 15 |
| SCE1572_3509 | 227 | 53 |
| SCE1572_977 | 329 | 1764 |
| SCE1572_6974 | 97 | 30 |
| SCE1572_3826 | 342 | 92 |
| SCE1572_7546 | 171 | 68 |
| SCE1572_9781 | 16 | 0 |
| SCE1572_1696 | 52 | 10 |
| SCE1572_9203 | 54 | 26 |
| SCE1572_2139 | 61 | 7 |
| SCE1572_8297 | 803 | 678 |
| SCE1572_3181 | 387 | 1105 |

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| SCE1572_8530 | 112 | 71 |
| SCE1572_2902 | 35 | 7 |
| SCE1572_8679 | 47 | 16 |
| SCE1572_4102 | 2 | 0 |
| SCE1572_10346 | 119 | 60 |
| SCE1572_5260 | 95 | 550 |
| SCE1572_3727 | 123 | 19 |
| SCE1572_5247 | 100 | 19 |
| SCE1572_5196 | 11 | 1 |
| SCE1572_1998 | 120 | 17 |
| SCE1572_6581 | 184 | 85 |
| SCE1572_11329 | 159 | 163 |
| SCE1572_1945 | 70 | 18 |
| SCE1572_3415 | 68 | 222 |
| SCE1572_2859 | 10 | 2 |
| SCE1572_9218 | 26 | 9 |
| SCE1572_6939 | 70 | 7 |
| SCE1572_10888 | 11 | 0 |
| SCE1572_1173 | 104 | 12 |
| SCE1572_11455 | 232 | 64 |
| SCE1572_10358 | 143 | 27 |
| SCE1572_1647 | 170.15 | 120.42 |
| SCE1572_9985 | 14 | 4 |
| SCE1572_903 | 123 | 16 |
| SCE1572_2128 | 236 | 34 |
| SCE1572_2221 | 3 | 0 |
| SCE1572_7407 | 0 | 0 |
| SCE1572_10560 | 1 | 0 |
| SCE1572_5115 | 74 | 58 |
| SCE1572_7332 | 278 | 57 |
| SCE1572_5951 | 26 | 6 |
| SCE1572_1438 | 33 | 9 |
| SCE1572_4911 | 240 | 231 |
| SCE1572_1598 | 84.31 | 14 |
| SCE1572_11312 | 0 | 0 |
| SCE1572_4615 | 131 | 45 |
| SCE1572_11428 | 43 | 9 |
| SCE1572_9642 | 15 | 14 |
| SCE1572_5706 | 83 | 115 |
| SCE1572_9622 | 52 | 17 |
| SCE1572_10175 | 257 | 208 |
| SCE1572_7334 | 313 | 778 |
| SCE1572_1889 | 244 | 895 |
| SCE1572_10254 | 0 | 0 |
| SCE1572_1133 | 19 | 10 |
| SCE1572_3664 | 112 | 10 |
| SCE1572_4150 | 96 | 47 |
| SCE1572_1651 | 81 | 4 |

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| SCE1572_5208 | 8 | 0 |
| SCE1572_1328 | 89 | 7 |
| SCE1572_2895 | 35 | 21 |
| SCE1572_2974 | 0 | 0 |
| SCE1572_9702 | 51 | 11 |
| SCE1572_2454 | 165 | 223 |
| SCE1572_7382 | 0 | 0 |
| SCE1572_4006 | 164 | 63 |
| SCE1572_4235 | 37 | 6 |
| SCE1572_9936 | 110 | 127 |
| SCE1572_837 | 47 | 20 |
| SCE1572_4652 | 103 | 48 |
| SCE1572_1420 | 64 | 44 |
| SCE1572_7080 | 68 | 139 |
| SCE1572_8652 | 133 | 189 |
| SCE1572_4188 | 139 | 208 |
| SCE1572_7204 | 10 | 0 |
| SCE1572_9373 | 83 | 11 |
| SCE1572_849 | 1804 | 1782 |
| SCE1572_1875 | 261 | 73 |
| SCE1572_9284 | 0 | 0 |
| SCE1572_5372 | 339 | 1890 |
| SCE1572_5178 | 76 | 26 |
| SCE1572_2073 | 56 | 4 |
| SCE1572_8706 | 52 | 33 |
| SCE1572_6592 | 52 | 58 |
| SCE1572_7836 | 40 | 36 |
| SCE1572_11591 | 160 | 58 |
| SCE1572_8539 | 39 | 17 |
| SCE1572_3835 | 165 | 28 |
| SCE1572_6830 | 3 | 0 |
| SCE1572_11030 | 50 | 43 |
| SCE1572_3266 | 97 | 97 |
| SCE1572_5948 | 155 | 40 |
| SCE1572_148 | 18 | 4 |
| SCE1572_23 | 39 | 51 |
| SCE1572_5947 | 125 | 35 |
| SCE1572_948 | 165.53 | 28.33 |
| SCE1572_2338 | 50 | 84 |
| SCE1572_4224 | 14 | 0 |
| SCE1572_7888 | 98 | 45 |
| SCE1572_1562 | 31 | 5 |
| SCE1572_5532 | 54 | 11 |
| SCE1572_10132 | 103 | 34 |
| SCE1572_775 | 124 | 100 |
| SCE1572_2070 | 40 | 3 |
| SCE1572_9183 | 162 | 33 |
| SCE1572_6949 | 89 | 17 |

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| SCE1572_5121 | 86 | 18 |
| SCE1572_1874 | 20 | 7 |
| SCE1572_8937 | 3175 | 11362 |
| SCE1572_6818 | 16 | 3 |
| SCE1572_10945 | 49 | 19 |
| SCE1572_3281 | 38 | 24 |
| SCE1572_5527 | 262 | 76 |
| SCE1572_4618 | 185 | 59 |
| SCE1572_3833 | 84 | 12 |
| SCE1572_11166 | 54 | 62 |
| SCE1572_1477 | 205 | 43 |
| SCE1572_8127 | 305 | 61 |
| SCE1572_8824 | 22.78 | 133.1 |
| SCE1572_7061 | 0 | 0 |
| SCE1572_2817 | 0 | 0 |
| SCE1572_9804 | 0 | 0 |
| SCE1572_871 | 350 | 288 |
| SCE1572_6585 | 614 | 525 |
| SCE1572_4607 | 24 | 14 |
| SCE1572_9906 | 162 | 54 |
| SCE1572_8011 | 85 | 103 |
| SCE1572_7417 | 100 | 52 |
| SCE1572_7349 | 89 | 18 |
| SCE1572_9032 | 122 | 31 |
| SCE1572_7874 | 36 | 23 |
| SCE1572_6923 | 212 | 53 |
| SCE1572_6015 | 75 | 9 |
| SCE1572_7429 | 91 | 14 |
| SCE1572_4005 | 20 | 14 |
| SCE1572_1787 | 46 | 9 |
| SCE1572_2514 | 8 | 0 |
| SCE1572_5459 | 77 | 11 |
| SCE1572_3630 | 111 | 81 |
| SCE1572_8769 | 683 | 97 |
| SCE1572_3935 | 52 | 16 |
| SCE1572_5414 | 82 | 15 |
| SCE1572_11016 | 3 | 0 |
| SCE1572_7544 | 30 | 0 |
| SCE1572_6671 | 74 | 12 |
| SCE1572_7073 | 132 | 18 |
| SCE1572_6329 | 87 | 30 |
| SCE1572_64 | 104 | 72 |
| SCE1572_5977 | 43 | 11 |
| SCE1572_8807 | 22 | 1 |
| SCE1572_6839 | 47 | 6.76 |
| SCE1572_7760 | 245 | 97 |
| SCE1572_4711 | 180 | 64 |
| SCE1572_3348 | 27 | 7 |

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| SCE1572_1029 | 32 | 79 |
| SCE1572_462 | 68 | 37 |
| SCE1572_11038 | 0 | 0 |
| SCE1572_10520 | 182 | 55 |
| SCE1572_5154 | 31 | 9 |
| SCE1572_6555 | 314 | 59 |
| SCE1572_6123 | 224 | 142 |
| SCE1572_5496 | 120 | 30 |
| SCE1572_3450 | 65 | 11 |
| SCE1572_4001 | 123 | 839 |
| SCE1572_1269 | 107 | 38 |
| SCE1572_4463 | 122 | 26 |
| SCE1572_2265 | 108 | 90 |
| SCE1572_1933 | 83 | 129 |
| SCE1572_8218 | 199 | 48 |
| SCE1572_1243 | 58 | 60 |
| SCE1572_7233 | 56 | 15 |
| SCE1572_5140 | 41 | 11 |
| SCE1572_3120 | 39 | 9 |
| SCE1572_8811 | 20 | 2 |
| SCE1572_7929 | 78 | 83 |
| SCE1572_8672 | 61 | 28 |
| SCE1572_10059 | 1437 | 4009 |
| SCE1572_2486 | 122 | 81 |
| SCE1572_5570 | 1223.25 | 282.83 |
| SCE1572_1716 | 0 | 0 |
| SCE1572_7296 | 57 | 30 |
| SCE1572_1286 | 907 | 6301 |
| SCE1572_4143 | 51 | 12 |
| SCE1572_10838 | 91 | 39 |
| SCE1572_11467 | 212 | 235 |
| SCE1572_3123 | 180 | 38 |
| SCE1572_3810 | 57 | 14 |
| SCE1572_1374 | 158 | 138 |
| SCE1572_5194 | 7 | 3 |
| SCE1572_11300 | 75 | 63 |
| SCE1572_8122 | 29 | 4 |
| SCE1572_3637 | 0 | 0 |
| SCE1572_2420 | 1263 | 1893 |
| SCE1572_8093 | 90 | 15 |
| SCE1572_7376 | 107 | 38 |
| SCE1572_5072 | 61 | 21 |
| SCE1572_6105 | 31 | 0 |
| SCE1572_9149 | 160 | 189 |
| SCE1572_6795 | 238 | 168 |
| SCE1572_11116 | 17 | 7 |
| SCE1572_9809 | 28 | 20 |
| SCE1572_1541 | 0 | 0 |

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| SCE1572_8590 | 115 | 167 |
| SCE1572_4120 | 681 | 3058 |
| SCE1572_4617 | 42 | 2 |
| SCE1572_1565 | 107 | 44 |
| SCE1572_9165 | 0 | 0 |
| SCE1572_4976 | 520 | 2332 |
| SCE1572_3465 | 0 | 0 |
| SCE1572_11582 | 196 | 87 |
| SCE1572_10816 | 51 | 7 |
| SCE1572_2694 | 30 | 69 |
| SCE1572_6704 | 78 | 102 |
| SCE1572_2207 | 39 | 8 |
| SCE1572_3780 | 11 | 12 |
| SCE1572_7 | 176 | 285 |
| SCE1572_5340 | 82 | 44 |
| SCE1572_11554 | 112 | 7 |
| SCE1572_71 | 61 | 15 |
| SCE1572_7096 | 184 | 36 |
| SCE1572_3671 | 24 | 13 |
| SCE1572_8200 | 30 | 2 |
| SCE1572_1544 | 102 | 17 |
| SCE1572_970 | 79 | 42 |
| SCE1572_6418 | 281 | 1469 |
| SCE1572_1379 | 59 | 10 |
| SCE1572_10013 | 43 | 6 |
| SCE1572_7317 | 12 | 2 |
| SCE1572_915 | 3 | 1 |
| SCE1572_8692 | 0 | 0 |
| SCE1572_5477 | 71 | 362 |
| SCE1572_795 | 455 | 358 |
| SCE1572_11497 | 16 | 0 |
| SCE1572_1571 | 19 | 3 |
| SCE1572_4127 | 0 | 0 |
| SCE1572_9636 | 260 | 147 |
| SCE1572_8368 | 55 | 4 |
| SCE1572_4962 | 60 | 110 |
| SCE1572_4857 | 64 | 17 |
| SCE1572_11183 | 112 | 89 |
| SCE1572_9518 | 102 | 87 |
| SCE1572_11306 | 161 | 163 |
| SCE1572_8265 | 92 | 59 |
| SCE1572_4350 | 155 | 31 |
| SCE1572_4031 | 1672 | 738 |
| SCE1572_6200 | 143 | 95 |
| SCE1572_4401 | 11 | 0 |
| SCE1572_1229 | 172 | 74 |
| SCE1572_2408 | 159 | 386 |
| SCE1572_2593 | 0 | 0 |

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| SCE1572_6038 | 26 | 9 |
| SCE1572_10076 | 225 | 246 |
| SCE1572_10543 | 0 | 0 |
| SCE1572_9672 | 105 | 119 |
| SCE1572_575 | 1 | 0 |
| SCE1572_8018 | 14 | 6 |
| SCE1572_10896 | 5 | 0 |
| SCE1572_5710 | 21 | 1 |
| SCE1572_2223 | 95 | 161 |
| SCE1572_10586 | 0 | 0 |
| SCE1572_1362 | 391 | 741 |
| SCE1572_8990 | 254 | 2081 |
| SCE1572_10806 | 709 | 73 |
| SCE1572_3669 | 0 | 0 |
| SCE1572_1578 | 65 | 11 |
| SCE1572_8503 | 69 | 5 |
| SCE1572_9446 | 74 | 37 |
| SCE1572_7700 | 79 | 10 |
| SCE1572_570 | 174 | 217 |
| SCE1572_9127 | 51 | 35 |
| SCE1572_5203 | 60 | 158 |
| SCE1572_788 | 332 | 169 |
| SCE1572_10755 | 128 | 26 |
| SCE1572_4690 | 101 | 65 |
| SCE1572_5820 | 380.57 | 147.8 |
| SCE1572_195 | 2 | 3 |
| SCE1572_7850 | 250 | 160 |
| SCE1572_5356 | 0 | 0 |
| SCE1572_4298 | 112 | 36 |
| SCE1572_7842 | 206 | 142 |
| SCE1572_9792 | 18 | 2 |
| SCE1572_4389 | 61 | 7 |
| SCE1572_2190 | 56 | 71 |
| SCE1572_9862 | 53 | 18 |
| SCE1572_9955 | 123 | 20 |
| SCE1572_4771 | 99 | 21 |
| SCE1572_2841 | 15 | 4 |
| SCE1572_4815 | 159 | 306 |
| SCE1572_4105 | 45 | 7 |
| SCE1572_648 | 254 | 162 |
| SCE1572_2865 | 3 | 0 |
| SCE1572_10221 | 351 | 52 |
| SCE1572_8152 | 7 | 0 |
| SCE1572_4625 | 43 | 8 |
| SCE1572_11307 | 100 | 89 |
| SCE1572_4678 | 5 | 0 |
| SCE1572_3680 | 53.48 | 7 |
| SCE1572_4846 | 67 | 63 |

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| SCE1572_7342 | 217 | 510 |
| SCE1572_10731 | 62 | 40 |
| SCE1572_10431 | 124 | 36 |
| SCE1572_6886 | 23 | 8 |
| SCE1572_339 | 31 | 14 |
| SCE1572_351 | 53 | 59 |
| SCE1572_2303 | 75 | 95 |
| SCE1572_11009 | 145 | 59 |
| SCE1572_2477 | 202 | 20 |
| SCE1572_386 | 2 | 1 |
| SCE1572_3916 | 175 | 76 |
| SCE1572_10223 | 176 | 109 |
| SCE1572_9273 | 134 | 69 |
| SCE1572_10315 | 11 | 13 |
| SCE1572_2197 | 557 | 212 |
| SCE1572_7677 | 122 | 15 |
| SCE1572_6353 | 84 | 24 |
| SCE1572_5847 | 103 | 54 |
| SCE1572_7645 | 89 | 30 |
| SCE1572_396 | 0 | 0 |
| SCE1572_1263 | 226 | 1492 |
| SCE1572_8930 | 512 | 211 |
| SCE1572_8718 | 95 | 54 |
| SCE1572_646 | 0 | 0 |
| SCE1572_116 | 91 | 65 |
| SCE1572_4107 | 45 | 11 |
| SCE1572_7978 | 263 | 86 |
| SCE1572_5941 | 88 | 13 |
| SCE1572_1961 | 183 | 23 |
| SCE1572_1002 | 32 | 3 |
| SCE1572_9336 | 17 | 14 |
| SCE1572_3473 | 484 | 132 |
| SCE1572_10099 | 72 | 52 |
| SCE1572_9650 | 66 | 12 |
| SCE1572_5825 | 101 | 40 |
| SCE1572_9924 | 1008.79 | 1239 |
| SCE1572_5598 | 119 | 145 |
| SCE1572_5299 | 140 | 22 |
| SCE1572_3541 | 0 | 0 |
| SCE1572_10403 | 178 | 153 |
| SCE1572_7289 | 188 | 23 |
| SCE1572_6165 | 109 | 88 |
| SCE1572_3066 | 25 | 5 |
| SCE1572_8619 | 57 | 15 |
| SCE1572_4157 | 7 | 2 |
| SCE1572_1084 | 32 | 10 |
| SCE1572_2081 | 248 | 47 |
| SCE1572_4493 | 123 | 90 |

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| SCE1572_8762 | 216 | 47 |
| SCE1572_10438 | 29 | 15 |
| SCE1572_7493 | 127 | 20 |
| SCE1572_2465 | 40 | 22 |
| SCE1572_466 | 96 | 30 |
| SCE1572_3197 | 30 | 8 |
| SCE1572_6827 | 138 | 304 |
| SCE1572_6934 | 197 | 190 |
| SCE1572_7467 | 122 | 41 |
| SCE1572_2244 | 111 | 31 |
| SCE1572_7579 | 270 | 130 |
| SCE1572_5545 | 36 | 13 |
| SCE1572_10693 | 100 | 28 |
| SCE1572_8314 | 327 | 151 |
| SCE1572_2311 | 437 | 350 |
| SCE1572_8612 | 97 | 11 |
| SCE1572_11147 | 294 | 43 |
| SCE1572_3204 | 87 | 49 |
| SCE1572_6189 | 73 | 25 |
| SCE1572_11522 | 72 | 12 |
| SCE1572_626 | 43 | 19 |
| SCE1572_7092 | 15 | 23 |
| SCE1572_8149 | 38 | 8 |
| SCE1572_157 | 227 | 566 |
| SCE1572_6805 | 135 | 53 |
| SCE1572_5015 | 320 | 3625 |
| SCE1572_246 | 5 | 2 |
| SCE1572_6876 | 15 | 14 |
| SCE1572_6947 | 60 | 14 |
| SCE1572_4648 | 46 | 10 |
| SCE1572_3300 | 63 | 11 |
| SCE1572_4322 | 165 | 26 |
| SCE1572_7413 | 125.28 | 82.27 |
| SCE1572_345 | 50 | 8 |
| SCE1572_3174 | 99 | 68 |
| SCE1572_1032 | 29.69 | 10.26 |
| SCE1572_3024 | 152 | 31 |
| SCE1572_4045 | 130 | 44 |
| SCE1572_10955 | 704 | 802 |
| SCE1572_10092 | 216 | 71 |
| SCE1572_6989 | 16 | 7 |
| SCE1572_7126 | 147 | 28 |
| SCE1572_6902 | 162 | 12 |
| SCE1572_11542 | 138 | 14 |
| SCE1572_10244 | 8 | 0 |
| SCE1572_1039 | 49 | 4 |
| SCE1572_11361 | 89 | 51 |
| SCE1572_5394 | 618 | 120 |

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| SCE1572_7001 | 254 | 100 |
| SCE1572_1928 | 196 | 188 |
| SCE1572_9659 | 270 | 156 |
| SCE1572_10292 | 103 | 64 |
| SCE1572_11372 | 113 | 183 |
| SCE1572_10501 | 28 | 21 |
| SCE1572_10469 | 48 | 71 |
| SCE1572_7153 | 194 | 23 |
| SCE1572_5337 | 381 | 70 |
| SCE1572_4586 | 780 | 623 |
| SCE1572_10442 | 128 | 17 |
| SCE1572_1867 | 171 | 47 |
| SCE1572_4092 | 78 | 13 |
| SCE1572_3522 | 0 | 0 |
| SCE1572_9718 | 184 | 257 |
| SCE1572_8100 | 135 | 74 |
| SCE1572_11051 | 136 | 442 |
| SCE1572_5416 | 43 | 5 |
| SCE1572_4826 | 628 | 339 |
| SCE1572_1192 | 128 | 33 |
| SCE1572_3500 | 286 | 109 |
| SCE1572_10115 | 196.6 | 119 |
| SCE1572_3036 | 94 | 9 |
| SCE1572_3078 | 193 | 88 |
| SCE1572_2318 | 27 | 0 |
| SCE1572_9823 | 519 | 55 |
| SCE1572_1406 | 347 | 236 |
| SCE1572_7068 | 88 | 22 |
| SCE1572_5314 | 0 | 0 |
| SCE1572_10715 | 257 | 79 |
| SCE1572_2090 | 7 | 0 |
| SCE1572_11243 | 21 | 20 |
| SCE1572_4940 | 260 | 1276 |
| SCE1572_4118 | 50 | 2572 |
| SCE1572_1558 | 147 | 24 |
| SCE1572_5224 | 80 | 54 |
| SCE1572_10858 | 1355 | 918 |
| SCE1572_7747 | 93 | 52 |
| SCE1572_11219 | 129 | 31 |
| SCE1572_6498 | 225 | 344 |
| SCE1572_10173 | 419 | 176 |
| SCE1572_4019 | 83 | 42 |
| SCE1572_8116 | 0 | 0 |
| SCE1572_9140 | 60 | 11 |
| SCE1572_2259 | 204 | 26 |
| SCE1572_10910 | 221.43 | 20 |
| SCE1572_10689 | 7 | 3 |
| SCE1572_7190 | 94 | 48 |

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| SCE1572_9344 | 74 | 89 |
| SCE1572_3439 | 53 | 17 |
| SCE1572_10231 | 267 | 40 |
| SCE1572_8189 | 63 | 20 |
| SCE1572_10129 | 23 | 1 |
| SCE1572_5468 | 496 | 87 |
| SCE1572_8592 | 272 | 115 |
| SCE1572_6688 | 368 | 49 |
| SCE1572_2262 | 136 | 37 |
| SCE1572_1587 | 22 | 0 |
| SCE1572_8244 | 435 | 639 |
| SCE1572_4709 | 129 | 9 |
| SCE1572_3382 | 23 | 28 |
| SCE1572_8088 | 185 | 19 |
| SCE1572_8813 | 0 | 0 |
| SCE1572_7356 | 279 | 119 |
| SCE1572_8655 | 592 | 2512 |
| SCE1572_7819 | 355 | 542 |
| SCE1572_8227 | 62 | 93 |
| SCE1572_7669 | 121 | 15 |
| SCE1572_3496 | 195 | 112 |
| SCE1572_3695 | 14 | 24 |
| SCE1572_2549 | 0 | 0 |
| SCE1572_8482 | 10 | 30 |
| SCE1572_975 | 409 | 2722 |
| SCE1572_7695 | 34 | 18 |
| SCE1572_1331 | 89 | 25 |
| SCE1572_3107 | 36 | 13 |
| SCE1572_9343 | 235 | 848 |
| SCE1572_5259 | 44 | 15 |
| SCE1572_7280 | 39 | 6 |
| SCE1572_4987 | 228 | 120 |
| SCE1572_5451 | 296 | 54 |
| SCE1572_2033 | 279.35 | 238.09 |
| SCE1572_11425 | 305 | 178 |
| SCE1572_7365 | 318 | 296 |
| SCE1572_1748 | 383 | 142 |
| SCE1572_8081 | 2 | 0 |
| SCE1572_10527 | 63 | 25 |
| SCE1572_8038 | 201 | 23 |
| SCE1572_407 | 71 | 222 |
| SCE1572_9948 | 153 | 18 |
| SCE1572_4473 | 36 | 32 |
| SCE1572_7898 | 75 | 79 |
| SCE1572_1451 | 59 | 6 |
| SCE1572_6098 | 194 | 83 |
| SCE1572_6719 | 100 | 306 |
| SCE1572_10233 | 17 | 2 |

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| SCE1572_3295 | 21 | 10 |
| SCE1572_3787 | 111 | 73 |
| SCE1572_586 | 166 | 56 |
| SCE1572_8388 | 47 | 8 |
| SCE1572_11126 | 95 | 31 |
| SCE1572_2579 | 81 | 18 |
| SCE1572_1505 | 43 | 5 |
| SCE1572_11598 | 91 | 446 |
| SCE1572_3401 | 15 | 3 |
| SCE1572_856 | 0 | 0 |
| SCE1572_11157 | 123.03 | 20.91 |
| SCE1572_1363 | 102 | 221 |
| SCE1572_4700 | 45 | 9 |
| SCE1572_5008 | 221 | 295 |
| SCE1572_4923 | 30 | 6 |
| SCE1572_6864 | 1 | 0 |
| SCE1572_4952 | 28 | 1 |
| SCE1572_1629 | 5 | 1 |
| SCE1572_8056 | 0 | 0 |
| SCE1572_2998 | 79 | 29 |
| SCE1572_1338 | 225 | 67 |
| SCE1572_534 | 0 | 0 |
| SCE1572_5084 | 183 | 1356 |
| SCE1572_10864 | 26 | 34 |
| SCE1572_4670 | 150 | 19 |
| SCE1572_4408 | 43 | 5 |
| SCE1572_7960 | 108 | 84 |
| SCE1572_7920 | 293 | 60 |
| SCE1572_6928 | 114 | 51 |
| SCE1572_11482 | 77 | 119 |
| SCE1572_5130 | 38 | 29 |
| SCE1572_8999 | 249 | 492 |
| SCE1572_6207 | 36.19 | 3.28 |
| SCE1572_747 | 102 | 15 |
| SCE1572_7318 | 69 | 24 |
| SCE1572_5697 | 371 | 314 |
| SCE1572_2626 | 48 | 22 |
| SCE1572_8713 | 160 | 42 |
| SCE1572_3408 | 165 | 108 |
| SCE1572_6211 | 64 | 5 |
| SCE1572_4720 | 156 | 25 |
| SCE1572_5782 | 13 | 10 |
| SCE1572_8210 | 70 | 45 |
| SCE1572_8460 | 34 | 62 |
| SCE1572_9741 | 162 | 346 |
| SCE1572_1894 | 136 | 24 |
| SCE1572_10738 | 293 | 59 |
| SCE1572_9990 | 49 | 18 |

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| SCE1572_1915 | 485 | 94 |
| SCE1572_7209 | 79 | 45 |
| SCE1572_6968 | 82 | 178 |
| SCE1572_5729 | 76 | 35 |
| SCE1572_8852 | 156 | 32 |
| SCE1572_3618 | 0 | 0 |
| SCE1572_9891 | 56 | 1 |
| SCE1572_1847 | 176 | 30 |
| SCE1572_781 | 49 | 22 |
| SCE1572_1724 | 104 | 206 |
| SCE1572_5230 | 542 | 1248 |
| SCE1572_4683 | 252 | 68 |
| SCE1572_9081 | 69 | 4 |
| SCE1572_5280 | 108 | 66 |
| SCE1572_7658 | 0 | 0 |
| SCE1572_6961 | 0 | 0 |
| SCE1572_8854 | 50 | 93 |
| SCE1572_5807 | 32 | 10 |
| SCE1572_1152 | 17 | 7 |
| SCE1572_10165 | 49 | 10 |
| SCE1572_5520 | 42 | 26 |
| SCE1572_11499 | 55 | 13 |
| SCE1572_4959 | 0 | 0 |
| SCE1572_2116 | 20 | 2 |
| SCE1572_11538 | 63 | 396 |
| SCE1572_8060 | 38 | 1 |
| SCE1572_7558 | 57 | 1 |
| SCE1572_5864 | 12 | 5 |
| SCE1572_3367 | 209 | 1572 |
| SCE1572_6339 | 29 | 35 |
| SCE1572_8893 | 0 | 0 |
| SCE1572_11490 | 0 | 10.33 |
| SCE1572_11323 | 168 | 203 |
| SCE1572_1167 | 9 | 17 |
| SCE1572_5367 | 22 | 16 |
| SCE1572_2151 | 99 | 8 |
| SCE1572_9082 | 35 | 0 |
| SCE1572_8945 | 237 | 496 |
| SCE1572_10487 | 1469 | 19720 |
| SCE1572_9834 | 110 | 20 |
| SCE1572_8804 | 36 | 93 |
| SCE1572_8902 | 102 | 23 |
| SCE1572_1310 | 160 | 613 |
| SCE1572_8191 | 374 | 65 |
| SCE1572_8064 | 19 | 0 |
| SCE1572_3333 | 272 | 239 |
| SCE1572_8031 | 315.48 | 100.04 |
| SCE1572_8256 | 31 | 24 |

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| SCE1572_708 | 76 | 53 |
| SCE1572_10649 | 34 | 2 |
| SCE1572_5833 | 209 | 181 |
| SCE1572_4727 | 116 | 25 |
| SCE1572_7808 | 521 | 175 |
| SCE1572_10039 | 22 | 12 |
| SCE1572_254 | 0 | 0 |
| SCE1572_6367 | 44 | 87 |
| SCE1572_7707 | 159 | 45 |
| SCE1572_11059 | 205.3 | 19.5 |
| SCE1572_2556 | 0 | 0 |
| SCE1572_89 | 928 | 466 |
| SCE1572_823 | 43 | 6 |
| SCE1572_10365 | 110 | 134 |
| SCE1572_1486 | 87 | 53 |
| SCE1572_5720 | 42 | 9 |
| SCE1572_274 | 0 | 0 |
| SCE1572_8359 | 0 | 0 |
| SCE1572_5250 | 248 | 510 |
| SCE1572_9204 | 149 | 104 |
| SCE1572_6460 | 134 | 25 |
| SCE1572_7225 | 282 | 98 |
| SCE1572_3279 | 91 | 62 |
| SCE1572_3254 | 26 | 24 |
| SCE1572_1215 | 63 | 2 |
| SCE1572_6980 | 56 | 11 |
| SCE1572_10061 | 1734 | 4584 |
| SCE1572_4971 | 0 | 0 |
| SCE1572_10259 | 21 | 3 |
| SCE1572_8835 | 80 | 11 |
| SCE1572_5955 | 0 | 0 |
| SCE1572_1198 | 332 | 47 |
| SCE1572_8437 | 1 | 6 |
| SCE1572_4927 | 8 | 0 |
| SCE1572_2096 | 30 | 39 |
| SCE1572_6905 | 41 | 5 |
| SCE1572_5882 | 75 | 28 |
| SCE1572_6445 | 47 | 9 |
| SCE1572_8555 | 11 | 56 |
| SCE1572_9163 | 19 | 1 |
| SCE1572_9120 | 19 | 7 |
| SCE1572_10711 | 20 | 0 |
| SCE1572_2277 | 263 | 881 |
| SCE1572_5730 | 0 | 0 |
| SCE1572_8432 | 19 | 2 |
| SCE1572_1342 | 358 | 513 |
| SCE1572_1108 | 122 | 14 |
| SCE1572_7530 | 99 | 32 |

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| SCE1572_111 | 84 | 21 |
| SCE1572_3770 | 0 | 0 |
| SCE1572_5024 | 175 | 48 |
| SCE1572_6420 | 391 | 217 |
| SCE1572_11221 | 4 | 0 |
| SCE1572_5053 | 157 | 48 |
| SCE1572_965 | 15 | 0 |
| SCE1572_10626 | 91 | 98 |
| SCE1572_2393 | 113 | 275 |
| SCE1572_5914 | 64 | 81 |
| SCE1572_9533 | 118 | 52 |
| SCE1572_9014 | 221 | 371 |
| SCE1572_10970 | 424 | 477 |
| SCE1572_10600 | 53 | 12 |
| SCE1572_10085 | 272 | 320 |
| SCE1572_3100 | 34 | 5 |
| SCE1572_6821 | 70 | 9 |
| SCE1572_7628 | 40 | 15 |
| SCE1572_5037 | 219 | 655 |
| SCE1572_7740 | 95 | 73 |
| SCE1572_2737 | 59 | 34 |
| SCE1572_6735 | 145 | 212 |
| SCE1572_1425 | 110 | 55 |
| SCE1572_4733 | 25 | 14 |
| SCE1572_2700 | 13 | 2 |
| SCE1572_1842 | 127.88 | 8 |
| SCE1572_9618 | 37 | 16 |
| SCE1572_5865 | 272 | 71 |
| SCE1572_5756 | 86 | 13 |
| SCE1572_162 | 88 | 21 |
| SCE1572_10519 | 187 | 41 |
| SCE1572_7513 | 31 | 4 |
| SCE1572_432 | 132 | 249 |
| SCE1572_10985 | 1496 | 1782 |
| SCE1572_11399 | 100 | 68 |
| SCE1572_8397 | 210 | 48 |
| SCE1572_3236 | 296 | 920 |
| SCE1572_569 | 75 | 49 |
| SCE1572_6712 | 174 | 308 |
| SCE1572_980 | 37 | 13 |
| SCE1572_945 | 185.33 | 15.21 |
| SCE1572_4483 | 91 | 59 |
| SCE1572_5744 | 259 | 83 |
| SCE1572_11289 | 0 | 0 |
| SCE1572_9402 | 816 | 1602 |
| SCE1572_6728 | 21 | 23 |
| SCE1572_5674 | 18 | 3 |
| SCE1572_503 | 16 | 2 |

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| SCE1572_1048 | 30 | 22 |
| SCE1572_1604 | 85 | 23 |
| SCE1572_10512 | 155 | 152 |
| SCE1572_3977 | 113 | 32 |
| SCE1572_10201 | 58 | 51 |
| SCE1572_7535 | 1641 | 198 |
| SCE1572_10684 | 24 | 3 |
| SCE1572_6602 | 18 | 5 |
| SCE1572_2793 | 68 | 3 |
| SCE1572_4253 | 1 | 0 |
| SCE1572_10871 | 713.92 | 113.51 |
| SCE1572_1622 | 41 | 107 |
| SCE1572_8321 | 180 | 55 |
| SCE1572_185 | 69 | 6 |
| SCE1572_650 | 1980.64 | 1425.18 |
| SCE1572_9797 | 14 | 7 |
| SCE1572_1637 | 31 | 11 |
| SCE1572_6215 | 105 | 16 |
| SCE1572_2615 | 93 | 39 |
| SCE1572_7611 | 38 | 44 |
| SCE1572_475 | 117 | 513 |
| SCE1572_2656 | 254 | 58 |
| SCE1572_9436 | 1325 | 1714 |
| SCE1572_635 | 325 | 853 |
| SCE1572_10267 | 130 | 90 |
| SCE1572_1632 | 40 | 22 |
| SCE1572_5284 | 51 | 51 |
| SCE1572_4057 | 1 | 0 |
| SCE1572_1470 | 222.29 | 80.99 |
| SCE1572_2756 | 1 | 0 |
| SCE1572_400 | 17 | 6 |
| SCE1572_5013 | 85 | 76 |
| SCE1572_6953 | 42 | 11 |
| SCE1572_5556 | 1261.75 | 821.75 |
| SCE1572_10859 | 534 | 635 |
| SCE1572_1658 | 34 | 5 |
| SCE1572_4932 | 524 | 894 |
| SCE1572_9965 | 0 | 0 |
| SCE1572_6542 | 102 | 68 |
| SCE1572_359 | 191 | 47 |
| SCE1572_7774 | 3 | 0 |
| SCE1572_401 | 54 | 19 |
| SCE1572_11549 | 73 | 18 |
| SCE1572_8023 | 7 | 0 |
| SCE1572_8404 | 22 | 2 |
| SCE1572_3422 | 139 | 75 |
| SCE1572_6475 | 276 | 659 |
| SCE1572_10727 | 141 | 39 |

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| SCE1572_11507 | 41 | 7 |
| SCE1572_953 | 43 | 18 |
| SCE1572_5930 | 0 | 0 |
| SCE1572_7214 | 54 | 73 |
| SCE1572_6073 | 1 | 0 |
| SCE1572_3803 | 138 | 20 |
| SCE1572_2166 | 400 | 61 |
| SCE1572_6391 | 0 | 0 |
| SCE1572_1683 | 6 | 106 |
| SCE1572_206 | 0 | 0 |
| SCE1572_4345 | 35 | 16 |
| SCE1572_11295 | 10 | 10 |
| SCE1572_11150 | 96 | 57 |
| SCE1572_1022 | 77 | 15 |
| SCE1572_284 | 22 | 10 |
| SCE1572_8043 | 0 | 0 |
| SCE1572_1013 | 109 | 23 |
| SCE1572_6360 | 73 | 112 |
| SCE1572_1702 | 56 | 25 |
| SCE1572_5589 | 143 | 47 |
| SCE1572_3554 | 16 | 2 |
| SCE1572_6361 | 250 | 58 |
| SCE1572_9962 | 1 | 0 |
| SCE1572_375 | 45 | 6 |
| SCE1572_3360 | 100 | 34 |
| SCE1572_1382 | 2 | 0 |
| SCE1572_496 | 80 | 32 |
| SCE1572_4906 | 29 | 16 |
| SCE1572_10279 | 23 | 0 |
| SCE1572_7742 | 141 | 100 |
| SCE1572_1958 | 140 | 72 |
| SCE1572_2484 | 84 | 64 |
| SCE1572_5543 | 38 | 2 |
| SCE1572_11096 | 143 | 34 |
| SCE1572_3840 | 42 | 6 |
| SCE1572_11175 | 205 | 187 |
| SCE1572_9050 | 61 | 29 |
| SCE1572_4536 | 80 | 142 |
| SCE1572_2141 | 40 | 1 |
| SCE1572_363 | 135 | 19 |
| SCE1572_2979 | 52 | 8 |
| SCE1572_6042 | 130 | 2064 |
| SCE1572_139 | 27 | 27 |
| SCE1572_10363 | 177 | 245 |
| SCE1572_2086 | 123 | 69 |
| SCE1572_7149 | 13 | 23 |
| SCE1572_2884 | 73 | 43 |
| SCE1572_7256 | 121 | 103 |

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| SCE1572_7012 | 0 | 0 |
| SCE1572_10071 | 674 | 503 |
| SCE1572_9429 | 25 | 7 |
| SCE1572_6087 | 170 | 80 |
| SCE1572_1454 | 65 | 15 |
| SCE1572_5163 | 0 | 0 |
| SCE1572_2811 | 65 | 2 |
| SCE1572_6963 | 112 | 124 |
| SCE1572_11528 | 45 | 4 |
| SCE1572_2771 | 2 | 0 |
| SCE1572_8139 | 30 | 38 |
| SCE1572_8427 | 54 | 3 |
| SCE1572_6847 | 81 | 2 |
| SCE1572_18 | 237 | 337 |
| SCE1572_9852 | 62 | 31 |
| SCE1572_8582 | 52 | 15 |
| SCE1572_3980 | 132 | 95 |
| SCE1572_1717 | 41 | 53 |
| SCE1572_713 | 142 | 77 |
| SCE1572_4522 | 127 | 23 |
| SCE1572_3892 | 86 | 66 |
| SCE1572_1887 | 255 | 247 |
| SCE1572_2458 | 119 | 163 |
| SCE1572_3340 | 386 | 8414 |
| SCE1572_2148 | 181.89 | 22 |
| SCE1572_559 | 27 | 340 |
| SCE1572_2023 | 139 | 60 |
| SCE1572_4729 | 38 | 10 |
| SCE1572_10328 | 159 | 19 |
| SCE1572_11069 | 175 | 69 |
| SCE1572_5035 | 63 | 19 |
| SCE1572_8484 | 66 | 56 |
| SCE1572_10964 | 134 | 31 |
| SCE1572_3188 | 93 | 8 |
| SCE1572_10046 | 343 | 1020 |
| SCE1572_660 | 3122 | 3751 |
| SCE1572_5654 | 263 | 1255 |
| SCE1572_7637 | 146 | 861 |
| SCE1572_10703 | 92 | 184 |
| SCE1572_3683 | 80 | 7 |
| SCE1572_2729 | 101 | 30 |
| SCE1572_7670 | 8 | 1 |
| SCE1572_6172 | 1 | 0 |
| SCE1572_10213 | 9 | 0 |
| SCE1572_5060 | 181 | 201 |
| SCE1572_3517 | 115 | 18 |
| SCE1572_2945 | 0 | 0 |
| SCE1572_2730 | 73 | 22 |

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| SCE1572_10334 | 56 | 22 |
| SCE1572_8557 | 79 | 16 |
| SCE1572_2343 | 50 | 15 |
| SCE1572_7160 | 37 | 8 |
| SCE1572_2076 | 177 | 81 |
| SCE1572_7855 | 67 | 48 |
| SCE1572_4309 | 73 | 12 |
| SCE1572_1238 | 36 | 8 |
| SCE1572_7792 | 26 | 4 |
| SCE1572_1398 | 401 | 79 |
| SCE1572_7799 | 1 | 0 |
| SCE1572_552 | 91 | 182 |
| SCE1572_11352 | 9 | 0 |
| SCE1572_8589 | 18 | 2 |
| SCE1572_4555 | 187 | 36 |
| SCE1572_8548 | 179 | 31 |
| SCE1572_8291 | 206 | 35 |
| SCE1572_6757 | 74 | 41 |
| SCE1572_685 | 0 | 0 |
| SCE1572_5480 | 444 | 89 |
| SCE1572_7732 | 33 | 35 |
| SCE1572_9613 | 8 | 0 |
| SCE1572_8301 | 249 | 1497 |
| SCE1572_171 | 22 | 16 |
| SCE1572_1880 | 211 | 59 |
| SCE1572_3629 | 15 | 2 |
| SCE1572_6786 | 122 | 89 |
| SCE1572_6227 | 31 | 4 |
| SCE1572_4580 | 169 | 32 |
| SCE1572_11419 | 0 | 0 |
| SCE1572_2279 | 376 | 234 |
| SCE1572_2386 | 583 | 320 |
| SCE1572_9171 | 41 | 11 |
| SCE1572_1656 | 13 | 23 |
| SCE1572_10893 | 80 | 57 |
| SCE1572_10557 | 90 | 16 |
| SCE1572_4317 | 40.43 | 2.58 |
| SCE1572_1303 | 37 | 73 |
| SCE1572_925 | 123 | 96 |
| SCE1572_5437 | 0 | 0 |
| SCE1572_8974 | 56 | 15 |
| SCE1572_6549 | 61 | 55 |
| SCE1572_1493 | 2 | 0 |
| SCE1572_234 | 63 | 17 |
| SCE1572_6573 | 143 | 18 |
| SCE1572_8782 | 106 | 237 |
| SCE1572_7749 | 90 | 13 |
| SCE1572_759 | 1872 | 523 |

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| SCE1572_7301 | 0 | 0 |
| SCE1572_4425 | 62 | 127 |
| SCE1572_3091 | 71 | 20 |
| SCE1572_3569 | 7 | 1 |
| SCE1572_2509 | 49 | 38 |
| SCE1572_8045 | 220 | 30 |
| SCE1572_1040 | 11 | 0 |
| SCE1572_2867 | 0 | 0 |
| SCE1572_7311 | 507 | 84 |
| SCE1572_1412 | 34 | 55 |
| SCE1572_8723 | 10 | 3 |
| SCE1572_10277 | 34 | 13 |
| SCE1572_613 | 82 | 24 |
| SCE1572_8076 | 88.45 | 11.76 |
| SCE1572_10633 | 151 | 381 |
| SCE1572_3763 | 28 | 14 |
| SCE1572_7561 | 17 | 5 |
| SCE1572_5892 | 32 | 51 |
| SCE1572_470 | 212 | 245 |
| SCE1572_2449 | 28 | 3 |
| SCE1572_11092 | 75 | 121 |
| SCE1572_11217 | 52 | 28 |
| SCE1572_1277 | 0 | 0 |
| SCE1572_3432 | 113 | 151 |
| SCE1572_8180 | 111 | 13 |
| SCE1572_2967 | 2 | 0 |
| SCE1572_10009 | 83 | 25 |
| SCE1572_9257 | 34 | 2 |
| SCE1572_10056 | 11 | 36 |
| SCE1572_9388 | 129 | 81 |
| SCE1572_4596 | 258 | 630 |
| SCE1572_9424 | 91 | 22 |
| SCE1572_7857 | 123 | 40 |
| SCE1572_10178 | 114 | 152 |
| SCE1572_9815 | 30.36 | 7 |
| SCE1572_2440 | 103 | 35 |
| SCE1572_6435 | 49 | 5 |
| SCE1572_3582 | 27 | 5 |
| SCE1572_1524 | 66 | 29 |
| SCE1572_9381 | 99 | 76 |
| SCE1572_5893 | 45 | 10 |
| SCE1572_3866 | 141 | 684 |
| SCE1572_2238 | 378 | 1086 |
| SCE1572_10002 | 257 | 357 |
| SCE1572_6324 | 109 | 153 |
| SCE1572_10873 | 215 | 22 |
| SCE1572_10781 | 4 | 0 |
| SCE1572_8134 | 216 | 27 |

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| SCE1572_6157 | 73 | 18 |
| SCE1572_5316 | 83 | 16 |
| SCE1572_3320 | 209 | 122 |
| SCE1572_11047 | 57 | 21 |
| SCE1572_8178 | 1 | 0 |
| SCE1572_11448 | 5 | 1 |
| SCE1572_7680 | 53 | 15 |
| SCE1572_3006 | 1 | 0 |
| SCE1572_3728 | 226 | 24 |
| SCE1572_6511 | 21 | 6 |
| SCE1572_2838 | 205.3 | 19.5 |
| SCE1572_930 | 117 | 394 |
| SCE1572_2214 | 0 | 0 |
| SCE1572_630 | 112 | 459 |
| SCE1572_607 | 42 | 183 |
| SCE1572_4392 | 116 | 18 |
| SCE1572_1670 | 348 | 909 |
| SCE1572_1760 | 0 | 0 |
| SCE1572_7772 | 96 | 37 |
| SCE1572_11335 | 0 | 0 |
| SCE1572_672 | 69 | 83 |
| SCE1572_2364 | 4 | 0 |
| SCE1572_8352 | 18 | 3 |
| SCE1572_5257 | 50 | 11 |
| SCE1572_4202 | 93 | 46 |
| SCE1572_9274 | 174 | 265 |
| SCE1572_4757 | 62 | 14 |
| SCE1572_2529 | 42 | 15 |
| SCE1572_2799 | 73 | 12 |
| SCE1572_7911 | 52 | 3 |
| SCE1572_5853 | 21.39 | 5 |
| SCE1572_7885 | 80 | 37 |
| SCE1572_7140 | 0 | 0 |
| SCE1572_3909 | 99 | 16 |
| SCE1572_3622 | 271 | 24 |
| SCE1572_3549 | 304 | 44 |
| SCE1572_10842 | 3 | 2 |
| SCE1572_10422 | 255 | 204 |
| SCE1572_1704 | 7 | 0 |
| SCE1572_2200 | 143 | 89 |
| SCE1572_9269 | 254 | 120 |
| SCE1572_7607 | 379 | 26 |
| SCE1572_6278 | 85 | 81 |
| SCE1572_11270 | 294 | 193 |
| SCE1572_3641 | 79 | 19 |
| SCE1572_1448 | 15 | 4 |
| SCE1572_8222 | 65 | 21 |
| SCE1572_6668 | 102 | 39 |

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| SCE1572_10391 | 139 | 23 |
| SCE1572_3723 | 43 | 316 |
| SCE1572_5401 | 24 | 0 |
| SCE1572_2209 | 31 | 6 |
| SCE1572_5051 | 98 | 24 |
| SCE1572_2294 | 104 | 41 |
| SCE1572_2739 | 102 | 63 |
| SCE1572_9260 | 130 | 59 |
| SCE1572_6238 | 89 | 12 |
| SCE1572_2175 | 20 | 13 |
| SCE1572_10144 | 71 | 15 |
| SCE1572_1793 | 1 | 0 |
| SCE1572_8299 | 44 | 4 |
| SCE1572_5044 | 43 | 18 |
| SCE1572_11579 | 134 | 33 |
| SCE1572_3989 | 17 | 11 |
| SCE1572_3448 | 172 | 67 |
| SCE1572_2473 | 169 | 404 |
| SCE1572_3614 | 57 | 14 |
| SCE1572_4179 | 125 | 19 |
| SCE1572_217 | 46 | 19 |
| SCE1572_3012 | 42 | 5 |
| SCE1572_7604 | 21 | 6 |
| SCE1572_5446 | 72 | 11 |
| SCE1572_6629 | 46 | 103 |
| SCE1572_11570 | 18 | 182 |
| SCE1572_3537 | 91 | 15 |
| SCE1572_2564 | 23 | 5 |
| SCE1572_7053 | 46 | 8 |
| SCE1572_3293 | 53 | 15 |
| SCE1572_6213 | 42 | 11 |
| SCE1572_5011 | 39 | 36 |
| SCE1572_3067 | 68 | 23 |
| SCE1572_10740 | 42 | 10 |
| SCE1572_9132 | 157 | 55 |
| SCE1572_3161 | 20 | 20 |
| SCE1572_2882 | 57 | 26 |
| SCE1572_726 | 147 | 24 |
| SCE1572_4371 | 78 | 14 |
| SCE1572_7824 | 70 | 11 |
| SCE1572_8143 | 9 | 0 |
| SCE1572_2954 | 128 | 24 |
| SCE1572_5103 | 192 | 547 |
| SCE1572_9826 | 34 | 5 |
| SCE1572_3579 | 76 | 107 |
| SCE1572_9507 | 54 | 19 |
| SCE1572_1085 | 161 | 27 |
| SCE1572_7861 | 2 | 0 |

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| SCE1572_6231 | 61 | 14 |
| SCE1572_11414 | 106 | 56 |
| SCE1572_6492 | 50 | 21 |
| SCE1572_1886 | 5 | 1 |
| SCE1572_4664 | 190 | 13 |
| SCE1572_9500 | 76 | 22 |
| SCE1572_838 | 43 | 23 |
| SCE1572_4803 | 95 | 38 |
| SCE1572_5874 | 27 | 13 |
| SCE1572_11531 | 35 | 7 |
| SCE1572_8455 | 40 | 89 |
| SCE1572_6926 | 27 | 2 |
| SCE1572_9780 | 127 | 35 |
| SCE1572_3260 | 120 | 78 |
| SCE1572_3777 | 32 | 10 |
| SCE1572_6220 | 57 | 5 |
| SCE1572_1142 | 135 | 18 |
| SCE1572_8822 | 37 | 4 |
| SCE1572_7566 | 11 | 16 |
| SCE1572_3604 | 491 | 139 |
| SCE1572_10374 | 56 | 25 |
| SCE1572_9914 | 1 | 0 |
| SCE1572_4802 | 57 | 66 |
| SCE1572_8785 | 41 | 137 |
| SCE1572_4750 | 99 | 72 |
| SCE1572_4672 | 69 | 16 |
| SCE1572_3768 | 75 | 43 |
| SCE1572_8251 | 46 | 14 |
| SCE1572_2809 | 31.92 | 8.35 |
| SCE1572_9608 | 90 | 31 |
| SCE1572_11139 | 32 | 7 |
| SCE1572_2017 | 215 | 34 |
| SCE1572_7047 | 15 | 4 |
| SCE1572_7038 | 131 | 45 |
| SCE1572_4149 | 130 | 24 |
| SCE1572_7596 | 221 | 225 |
| SCE1572_10029 | 118 | 78 |
| SCE1572_5074 | 223 | 34 |
| SCE1572_2225 | 109 | 16 |
| SCE1572_11002 | 11 | 4 |
| SCE1572_9094 | 121 | 508 |
| SCE1572_3159 | 920 | 1513 |
| SCE1572_2634 | 272 | 46 |
| SCE1572_11028 | 16 | 1 |
| SCE1572_6136 | 293 | 96 |
| SCE1572_4496 | 55 | 30 |
| SCE1572_3130 | 90 | 19 |
| SCE1572_8453 | 19 | 25 |

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| SCE1572_2427 | 881 | 482 |
| SCE1572_8943 | 84 | 10 |
| SCE1572_6301 | 164 | 106 |
| SCE1572_4897 | 70 | 29 |
| SCE1572_8863 | 48 | 7 |
| SCE1572_3705 | 0 | 0 |
| SCE1572_10023 | 36.35 | 11.64 |
| SCE1572_7336 | 172 | 52 |
| SCE1572_1113 | 4 | 5 |
| SCE1572_2889 | 63 | 11 |
| SCE1572_5818 | 131 | 18 |
| SCE1572_7916 | 440 | 485 |
| SCE1572_5727 | 102 | 157 |
| SCE1572_2352 | 65 | 166 |
| SCE1572_764 | 106 | 18 |
| SCE1572_2372 | 187 | 214 |
| SCE1572_9220 | 1442.33 | 262.39 |
| SCE1572_8603 | 74 | 43 |
| SCE1572_10779 | 92 | 13 |
| SCE1572_2831 | 50 | 14 |
| SCE1572_7868 | 146 | 206 |
| SCE1572_4175 | 227 | 22 |
| SCE1572_1591 | 173 | 92 |
| SCE1572_10318 | 257 | 72 |
| SCE1572_1416 | 211 | 56 |
| SCE1572_3031 | 2 | 0 |
| SCE1572_9916 | 112 | 33 |
| SCE1572_7640 | 34 | 43 |
| SCE1572_229 | 78 | 165 |
| SCE1572_5600 | 280.79 | 72.78 |
| SCE1572_8512 | 248.76 | 46 |
| SCE1572_1206 | 14 | 1 |
| SCE1572_8369 | 43 | 19 |
| SCE1572_4246 | 80 | 24 |
| SCE1572_10798 | 24 | 4 |
| SCE1572_9317 | 525 | 1087 |
| SCE1572_7389 | 1 | 0 |
| SCE1572_7409 | 59 | 13 |
| SCE1572_6745 | 55 | 96 |
| SCE1572_4875 | 95 | 22 |
| SCE1572_3319 | 107 | 60 |
| SCE1572_865 | 32 | 30 |
| SCE1572_4211 | 567 | 613 |
| SCE1572_3632 | 139.83 | 41.23 |
| SCE1572_9026 | 39 | 352 |
| SCE1572_803 | 1 | 0 |
| SCE1572_222 | 61 | 15 |
| SCE1572_1836 | 10 | 10 |

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| SCE1572_313 | 87 | 8 |
| SCE1572_3591 | 0 | 0 |
| SCE1572_7031 | 63 | 16 |
| SCE1572_9686 | 160 | 103 |
| SCE1572_9177 | 214 | 24 |
| SCE1572_5427 | 29 | 24 |
| SCE1572_4749 | 82 | 19 |
| SCE1572_7017 | 0 | 0 |
| SCE1572_3530 | 80 | 29 |
| SCE1572_11195 | 42 | 13 |
| SCE1572_994 | 55 | 12 |
| SCE1572_5607 | 293 | 199 |
| SCE1572_8574 | 3 | 2 |
| SCE1572_9624 | 193 | 75 |
| SCE1572_4453 | 78 | 46 |
| SCE1572_3702 | 253 | 60 |
| SCE1572_11274 | 129 | 188 |
| SCE1572_9889 | 35 | 26 |
| SCE1572_1850 | 359 | 112 |
| SCE1572_6557 | 99 | 8 |
| SCE1572_2001 | 46 | 11 |
| SCE1572_11105 | 18 | 12 |
| SCE1572_1432 | 6 | 2 |
| SCE1572_2121 | 5 | 0 |
| SCE1572_697 | 140 | 45 |
| SCE1572_6143 | 4 | 0 |
| SCE1572_2065 | 61 | 24 |
| SCE1572_6776 | 993 | 125 |
| SCE1572_5970 | 3 | 0 |
| SCE1572_2751 | 142 | 44 |
| SCE1572_8576 | 88.36 | 9.58 |
| SCE1572_6740 | 87 | 131 |
| SCE1572_8716 | 106 | 90 |
| SCE1572_11251 | 112 | 16 |
| SCE1572_4275 | 90 | 43 |
| SCE1572_10552 | 0 | 0 |
| SCE1572_269 | 26 | 5 |
| SCE1572_293 | 2 | 0 |
| SCE1572_5558 | 1887.95 | 1049.22 |
| SCE1572_2491 | 74 | 9 |
| SCE1572_6291 | 19 | 8 |
| SCE1572_11385 | 723 | 2446 |
| SCE1572_10764 | 67 | 0 |
| SCE1572_9238 | 25 | 7 |
| SCE1572_9193 | 19 | 1 |
| SCE1572_10936 | 0 | 0 |
| SCE1572_11469 | 54 | 55 |
| SCE1572_8617 | 68 | 5 |

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| SCE1572_9540 | 107 | 16 |
| SCE1572_1968 | 17 | 11 |
| SCE1572_3853 | 2 | 0 |
| SCE1572_6246 | 74 | 7 |
| SCE1572_9721 | 154 | 657 |
| SCE1572_8165 | 0 | 0 |
| SCE1572_6336 | 252 | 60 |
| SCE1572_3572 | 0 | 0 |
| SCE1572_1815 | 57 | 5 |
| SCE1572_6007 | 82 | 69 |
| SCE1572_4255 | 129 | 124 |
| SCE1572_2981 | 45 | 41 |
| SCE1572_2170 | 175 | 99 |
| SCE1572_5696 | 209 | 62 |
| SCE1572_1751 | 37 | 22 |
| SCE1572_6198 | 145 | 12 |
| SCE1572_7944 | 68 | 16 |
| SCE1572_5924 | 38 | 12 |
| SCE1572_10451 | 26 | 105 |
| SCE1572_5522 | 52 | 19 |
| SCE1572_4883 | 22 | 15 |
| SCE1572_9188 | 157 | 46 |
| SCE1572_10162 | 89 | 12 |
| SCE1572_108 | 360 | 433 |
| SCE1572_9728 | 77 | 41 |
| SCE1572_11393 | 256 | 113 |
| SCE1572_3129 | 29 | 8 |
| SCE1572_3652 | 51 | 18 |
| SCE1572_3190 | 13 | 0 |
| SCE1572_7274 | 44 | 6 |
| SCE1572_11370 | 79 | 10 |
| SCE1572_5704 | 168 | 75 |
| SCE1572_1988 | 396 | 56 |
| SCE1572_4608 | 154 | 112 |
| SCE1572_1075 | 105 | 36 |
| SCE1572_10405 | 172 | 89 |
| SCE1572_4731 | 56 | 7 |
| SCE1572_3712 | 62 | 1859 |
| SCE1572_10747 | 47 | 10 |
| SCE1572_6932 | 82 | 514 |
| SCE1572_9057 | 1 | 0 |
| SCE1572_10886 | 426 | 45 |
| SCE1572_310 | 21 | 5 |
| SCE1572_757 | 176 | 17 |
| SCE1572_11405 | 67 | 12 |
| SCE1572_7090 | 0 | 0 |
| SCE1572_9731 | 263 | 97 |
| SCE1572_9585 | 64 | 22 |

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| SCE1572_8284 | 22 | 1 |
| SCE1572_10150 | 49 | 117 |
| SCE1572_7339 | 34 | 285 |
| SCE1572_10291 | 19 | 12 |
| SCE1572_7901 | 117 | 10 |
| SCE1572_1171 | 85 | 19 |
| SCE1572_2132 | 114 | 16 |
| SCE1572_11238 | 40 | 8 |
| SCE1572_10496 | 48 | 29 |
| SCE1572_2048 | 17 | 14 |
| SCE1572_905 | 99 | 13 |
| SCE1572_8631 | 134 | 38 |
| SCE1572_7424 | 27 | 27 |
| SCE1572_11132 | 34 | 6 |
| SCE1572_526 | 107 | 112 |
| SCE1572_11075 | 61 | 223 |
| SCE1572_8669 | 8 | 0 |
| SCE1572_7989 | 282 | 206 |
| SCE1572_10938 | 49 | 12 |
| SCE1572_9286 | 119 | 86 |
| SCE1572_798 | 213 | 92 |
| SCE1572_10348 | 136 | 20 |
| SCE1572_9787 | 64 | 10 |
| SCE1572_9547 | 163 | 27 |
| SCE1572_7350 | 32 | 2 |
| SCE1572_9007 | 24 | 13 |
| SCE1572_7471 | 0 | 0 |
| SCE1572_9758 | 254 | 220 |
| SCE1572_8772 | 141 | 122 |
| SCE1572_11453 | 17 | 8 |
| SCE1572_3397 | 276 | 83 |
| SCE1572_6121 | 44 | 12 |
| SCE1572_10302 | 73 | 6 |
| SCE1572_10472 | 161 | 173 |
| SCE1572_1059 | 43 | 8 |
| SCE1572_1186 | 24 | 10 |
| SCE1572_8319 | 263 | 174 |
| SCE1572_2287 | 41 | 56 |
| SCE1572_9113 | 36 | 58 |
| SCE1572_10458 | 150 | 44 |
| SCE1572_5613 | 174 | 23 |
| SCE1572_2900 | 4 | 2 |
| SCE1572_7933 | 0 | 0 |
| SCE1572_2289 | 11 | 35 |
| SCE1572_7330 | 150 | 28 |
| SCE1572_7266 | 0 | 0 |
| SCE1572_1135 | 3 | 0 |
| SCE1572_2972 | 274 | 75 |

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| SCE1572_10562 | 437 | 79 |
| SCE1572_2848 | 113 | 17 |
| SCE1572_8564 | 315 | 224 |
| SCE1572_985 | 141 | 53 |
| SCE1572_8058 | 16 | 0 |
| SCE1572_5245 | 42 | 9 |
| SCE1572_4999 | 870 | 1939 |
| SCE1572_10538 | 23 | 2 |
| SCE1572_4304 | 57 | 9 |
| SCE1572_8977 | 15 | 2 |
| SCE1572_421 | 14 | 21 |
| SCE1572_4115 | 144 | 66 |
| SCE1572_1952 | 59 | 12 |
| SCE1572_10717 | 42 | 10 |
| SCE1572_8677 | 33 | 24 |
| SCE1572_2002 | 71 | 66 |
| SCE1572_480 | 46 | 15 |
| SCE1572_1991 | 113 | 14 |
| SCE1572_53 | 331 | 54 |
| SCE1572_2160 | 79 | 14 |
| SCE1572_3055 | 15 | 0 |
| SCE1572_5262 | 0 | 0 |
| SCE1572_1052 | 733 | 1543 |
| SCE1572_7370 | 113 | 26 |
| SCE1572_6484 | 64 | 11 |
| SCE1572_8753 | 53 | 6 |
| SCE1572_11089 | 54 | 43 |
| SCE1572_9475 | 113 | 99 |
| SCE1572_5081 | 1827 | 933 |
| SCE1572_6583 | 61 | 23 |
| SCE1572_8969 | 31 | 49 |
| SCE1572_7158 | 67 | 30 |
| SCE1572_4491 | 59 | 133 |
| SCE1572_11343 | 38 | 78 |
| SCE1572_10356 | 67 | 189 |
| SCE1572_5222 | 458 | 134 |
| SCE1572_1514 | 67 | 7 |
| SCE1572_8982 | 53 | 13 |
| SCE1572_6069 | 107 | 201 |
| SCE1572_7323 | 3 | 0 |
| SCE1572_4100 | 109 | 46 |
| SCE1572_5965 | 48 | 19 |
| SCE1572_9041 | 755 | 2328 |
| SCE1572_3329 | 348 | 962 |
| SCE1572_4500 | 36 | 4 |
| SCE1572_6568 | 35 | 49 |
| SCE1572_11446 | 369 | 213 |
| SCE1572_9590 | 157 | 522 |

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| SCE1572_1972 | 104 | 160 |
| SCE1572_4980 | 70 | 104 |
| SCE1572_5643 | 0 | 0 |
| SCE1572_4284 | 143 | 25 |
| SCE1572_9468 | 111 | 106 |
| SCE1572_6148 | 55 | 7 |
| SCE1572_9306 | 109 | 88 |
| SCE1572_8337 | 261.32 | 107.59 |
| SCE1572_5632 | 41 | 38 |
| SCE1572_9599 | 75 | 17 |
| SCE1572_11353 | 1 | 0 |
| SCE1572_7109 | 19 | 5 |
| SCE1572_9570 | 737 | 104 |
| SCE1572_3955 | 169 | 32 |
| SCE1572_3798 | 74 | 43 |
| SCE1572_2689 | 117 | 140 |
| SCE1572_5344 | 51 | 10 |
| SCE1572_3999 | 739 | 632 |
| SCE1572_590 | 99 | 20 |
| SCE1572_4501 | 97 | 179 |
| SCE1572_3817 | 86 | 413 |
| SCE1572_878 | 107 | 258 |
| SCE1572_731 | 13 | 4 |
| SCE1572_3940 | 608 | 499 |
| SCE1572_2815 | 55 | 35 |
| SCE1572_4126 | 65 | 10 |
| SCE1572_8960 | 94 | 23 |
| SCE1572_11282 | 111 | 108 |
| SCE1572_4414 | 22 | 5 |
| SCE1572_2231 | 16 | 46 |
| SCE1572_165 | 49 | 7 |
| SCE1572_3744 | 68 | 62 |
| SCE1572_4195 | 74 | 64 |
| SCE1572_307 | 0 | 0 |
| SCE1572_7379 | 51 | 9 |
| SCE1572_3327 | 225 | 842 |
| SCE1572_10635 | 182 | 196 |
| SCE1572_5796 | 51 | 21 |
| SCE1572_3902 | 33 | 66 |
| SCE1572_7754 | 76 | 82 |
| SCE1572_5504 | 82 | 29 |
| SCE1572_546 | 0 | 0 |
| SCE1572_10082 | 84 | 262 |
| SCE1572_7516 | 30 | 20 |
| SCE1572_7231 | 99 | 74 |
| SCE1572_3082 | 57 | 19 |
| SCE1572_8537 | 67 | 28 |
| SCE1572_8141 | 47 | 6 |

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| SCE1572_3560 | 207 | 22 |
| SCE1572_3847 | 62 | 10 |
| SCE1572_2740 | 17 | 5 |
| SCE1572_7965 | 12 | 8 |
| SCE1572_8234 | 0 | 0 |
| SCE1572_6760 | 530 | 236 |
| SCE1572_3166 | 152 | 40 |
| SCE1572_6766 | 0 | 0 |
| SCE1572_9459 | 0 | 0 |
| SCE1572_34 | 126 | 194 |
| SCE1572_7554 | 25 | 2 |
| SCE1572_303 | 204 | 35 |
| SCE1572_6874 | 479 | 2988 |
| SCE1572_10915 | 0 | 0 |
| SCE1572_6341 | 121 | 20 |
| SCE1572_2105 | 278 | 597 |
| SCE1572_2664 | 385 | 1487 |
| SCE1572_9443 | 32 | 26 |
| SCE1572_2920 | 124 | 13 |
| SCE1572_2183 | 96 | 22 |
| SCE1572_2854 | 0 | 0 |
| SCE1572_6406 | 22 | 66 |
| SCE1572_5666 | 26 | 7 |
| SCE1572_10594 | 197 | 37 |
| SCE1572_2917 | 26 | 5 |
| SCE1572_10354 | 13 | 4 |
| SCE1572_10143 | 65 | 110 |
| SCE1572_1066 | 58 | 9 |
| SCE1572_9553 | 69 | 12 |
| SCE1572_4886 | 2 | 0 |
| SCE1572_6352 | 74 | 30 |
| SCE1572_9157 | 453 | 149 |
| SCE1572_3310 | 43 | 6 |
| SCE1572_9478 | 220 | 687 |
| SCE1572_2776 | 0 | 0 |
| SCE1572_2331 | 65 | 18 |
| SCE1572_2714 | 82 | 45 |
| SCE1572_2941 | 39 | 11 |
| SCE1572_9484 | 326 | 587 |
| SCE1572_3096 | 3 | 1 |
| SCE1572_5987 | 60 | 19.84 |
| SCE1572_10614 | 33 | 3 |
| SCE1572_4465 | 262 | 160 |
| SCE1572_193 | 147 | 89 |
| SCE1572_2093 | 80 | 36 |
| SCE1572_6253 | 53 | 128 |
| SCE1572_9454 | 186 | 46 |
| SCE1572_1820 | 26 | 15 |

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| SCE1572_1810 | 49 | 17 |
| SCE1572_10923 | 509 | 17571 |
| SCE1572_2498 | 0 | 0 |
| SCE1572_8754 | 200 | 25 |
| SCE1572_1803 | 13 | 4 |
| SCE1572_7630 | 42 | 102 |
| SCE1572_10548 | 109 | 16 |
| SCE1572_489 | 71.1 | 15.07 |
| SCE1572_10189 | 101 | 103 |
| SCE1572_4865 | 44 | 44 |
| SCE1572_7981 | 25 | 15 |
| SCE1572_2674 | 75 | 170 |
| SCE1572_3115 | 50 | 10 |
| SCE1572_5906 | 308 | 749 |
| SCE1572_11071 | 131 | 59 |
| SCE1572_10102 | 53 | 82 |
| SCE1572_5099 | 65 | 6 |
| SCE1572_3962 | 123 | 38 |
| SCE1572_7714 | 66 | 98 |
| SCE1572_2871 | 0 | 0 |
| SCE1572_8872 | 114 | 22 |
| SCE1572_6663 | 27 | 7 |
| SCE1572_11473 | 75 | 21 |
| SCE1572_4831 | 264 | 202 |
| SCE1572_8580 | 737 | 134 |
| SCE1572_8506 | 26 | 4 |
| SCE1572_4740 | 145 | 92 |
| SCE1572_9775 | 0 | 0 |
| SCE1572_4067 | 38 | 19 |
| SCE1572_10732 | 202 | 43 |
| SCE1572_7508 | 183.42 | 28.37 |
| SCE1572_9665 | 24 | 40 |
| SCE1572_10647 | 30 | 34 |
| SCE1572_5069 | 153 | 55 |
| SCE1572_2406 | 79 | 243 |
| SCE1572_10074 | 63 | 0 |
| SCE1572_2825 | 36 | 12 |
| SCE1572_9558 | 0 | 0 |
| SCE1572_6182 | 131 | 17 |
| SCE1572_156 | 118 | 151 |
| SCE1572_1825 | 23 | 6 |
| SCE1572_7739 | 3 | 0 |
| SCE1572_4260 | 324 | 128 |
| SCE1572_5621 | 229.99 | 40 |
| SCE1572_1774 | 50 | 6 |
| SCE1572_2860 | 44 | 6 |
| SCE1572_7088 | 89 | 14 |
| SCE1572_6424 | 0 | 0 |

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| SCE1572_6175 | 104 | 72 |
| SCE1572_6616 | 103 | 17 |
| SCE1572_8736 | 28 | 9 |
| SCE1572_2720 | 317 | 30 |
| SCE1572_2055 | 34 | 19 |
| SCE1572_6778 | 426 | 76 |
| SCE1572_9517 | 365 | 252 |
| SCE1572_1616 | 26 | 44 |
| SCE1572_7100 | 20 | 22 |
| SCE1572_449 | 29 | 10 |
| SCE1572_4443 | 24 | 38 |
| SCE1572_9766 | 75 | 78 |
| SCE1572_6644 | 1 | 0 |
| SCE1572_331 | 173 | 204 |
| SCE1572_10569 | 326 | 234 |
| SCE1572_4335 | 118 | 27 |
| SCE1572_4796 | 129 | 28 |
| SCE1572_10791 | 148 | 85 |
| SCE1572_2679 | 41 | 450 |
| SCE1572_4217 | 111 | 65 |
| SCE1572_9525 | 12 | 14 |
| SCE1572_9072 | 43 | 27 |
| SCE1572_41 | 129 | 41 |
| SCE1572_1128 | 86 | 31 |
| SCE1572_1523 | 181 | 26 |
| SCE1572_5212 | 76 | 64 |
| SCE1572_9882 | 92 | 31 |
| SCE1572_3480 | 172 | 81 |
| SCE1572_9973 | 284 | 452 |
| SCE1572_11074 | 6 | 0 |
| SCE1572_6681 | 29 | 66 |
| SCE1572_1122 | 593 | 52 |
| SCE1572_5346 | 3 | 2 |
| SCE1572_11532 | 0 | 0 |
| SCE1572_4573 | 48 | 15 |
| SCE1572_9154 | 137 | 201 |
| SCE1572_2707 | 37 | 5 |
| SCE1572_10551 | 63 | 10 |
| SCE1572_8774 | 457 | 436 |
| SCE1572_1851 | 58 | 15 |
| SCE1572_8666 | 31 | 1 |
| SCE1572_2665 | 79 | 248 |
| SCE1572_5604 | 419 | 207 |
| SCE1572_8623 | 126 | 166 |
| SCE1572_8259 | 287 | 351 |
| SCE1572_861 | 89 | 550 |
| SCE1572_2416 | 201 | 100 |
| SCE1572_8975 | 35 | 9 |

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| SCE1572_7268 | 328 | 279.52 |
| SCE1572_1614 | 164 | 183 |
| SCE1572_7725 | 130 | 51 |
| SCE1572_2596 | 141.25 | 67.32 |
| SCE1572_9387 | 364 | 316 |
| SCE1572_7112 | 0 | 0 |
| SCE1572_6111 | 29 | 33 |
| SCE1572_167 | 65 | 8 |
| SCE1572_2678 | 22 | 121 |
| SCE1572_6643 | 623 | 265 |
| SCE1572_6637 | 119.82 | 57 |
| SCE1572_8288 | 42 | 51 |
| SCE1572_2929 | 0 | 0 |
| SCE1572_3951 | 111 | 63 |
| SCE1572_9480 | 48 | 24 |
| SCE1572_7250 | 403 | 67 |
| SCE1572_4312 | 144 | 21 |
| SCE1572_9416 | 117 | 1010 |
| SCE1572_3621 | 16 | 1 |
| SCE1572_2024 | 38 | 6 |
| SCE1572_5793 | 274 | 197 |
| SCE1572_6115 | 119 | 14 |
| SCE1572_9350 | 708 | 1305 |
| SCE1572_5673 | 43 | 22 |
| SCE1572_2856 | 51 | 8 |
| SCE1572_3499 | 33 | 19 |
| SCE1572_2469 | 38 | 11 |
| SCE1572_804 | 0 | 0 |
| SCE1572_10588 | 18 | 2 |
| SCE1572_4913 | 19 | 4 |
| SCE1572_1784 | 14 | 2 |
| SCE1572_9077 | 121 | 24 |
| SCE1572_8235 | 18 | 11 |
| SCE1572_10176 | 87 | 22 |
| SCE1572_4817 | 166 | 623 |
| SCE1572_10596 | 88 | 14 |
| SCE1572_6146 | 188 | 47 |
| SCE1572_1779 | 81 | 46 |
| SCE1572_7045 | 156 | 325 |
| SCE1572_3412 | 37 | 51 |
| SCE1572_3708 | 0 | 0 |
| SCE1572_11508 | 27 | 5 |
| SCE1572_11472 | 18 | 0 |
| SCE1572_5983 | 11 | 6 |
| SCE1572_7511 | 97 | 20 |
| SCE1572_8462 | 80 | 331 |
| SCE1572_5626 | 19 | 3 |
| SCE1572_1916 | 3 | 0 |

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| SCE1572_10664 | 74 | 224 |
| SCE1572_3580 | 276 | 50 |
| SCE1572_2405 | 84 | 283 |
| SCE1572_10352 | 65 | 19 |
| SCE1572_6056 | 705 | 915 |
| SCE1572_1248 | 146 | 133 |
| SCE1572_9995 | 136 | 29 |
| SCE1572_564 | 62 | 576 |
| SCE1572_797 | 377 | 255 |
| SCE1572_7026 | 145 | 26 |
| SCE1572_8144 | 43 | 4 |
| SCE1572_3413 | 37 | 18 |
| SCE1572_8743 | 3 | 0 |
| SCE1572_2098 | 108 | 106 |
| SCE1572_4455 | 854 | 366 |
| SCE1572_9751 | 221 | 58 |
| SCE1572_11358 | 114 | 29 |
| SCE1572_9520 | 239.5 | 287.5 |
| SCE1572_9879 | 54 | 43 |
| SCE1572_2996 | 162 | 34 |
| SCE1572_5082 | 136 | 109 |
| SCE1572_9776 | 96 | 56 |
| SCE1572_3796 | 41 | 3 |
| SCE1572_6769 | 934 | 5830 |
| SCE1572_2572 | 261 | 37 |
| SCE1572_8883 | 69 | 13 |
| SCE1572_4798 | 41 | 193 |
| SCE1572_10929 | 47 | 14 |
| SCE1572_179 | 67 | 21 |
| SCE1572_10389 | 102 | 57 |
| SCE1572_4016 | 78 | 27 |
| SCE1572_6138 | 48 | 30 |
| SCE1572_2731 | 245 | 97 |
| SCE1572_2712 | 421 | 567 |
| SCE1572_10072 | 558 | 642 |
| SCE1572_10194 | 125 | 27 |
| SCE1572_4329 | 46 | 21 |
| SCE1572_6407 | 46 | 62 |
| SCE1572_7776 | 111 | 237 |
| SCE1572_9769 | 11 | 8 |
| SCE1572_6501 | 44 | 10 |
| SCE1572_10399 | 247 | 125 |
| SCE1572_10992 | 5 | 4 |
| SCE1572_9398 | 45 | 46 |
| SCE1572_10415 | 40 | 34 |
| SCE1572_5310 | 26 | 16 |
| SCE1572_1335 | 29 | 5 |
| SCE1572_4267 | 0 | 0 |

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| SCE1572_2142 | 97 | 11 |
| SCE1572_6177 | 92 | 51 |
| SCE1572_1014 | 67 | 20 |
| SCE1572_9544 | 92 | 11 |
| SCE1572_9324 | 3388 | 2190 |
| SCE1572_4324 | 37 | 11 |
| SCE1572_26 | 153 | 94 |
| SCE1572_2978 | 13 | 1 |
| SCE1572_9034 | 47 | 13 |
| SCE1572_10100 | 94 | 22 |
| SCE1572_11460 | 914 | 942 |
| SCE1572_1322 | 85 | 10 |
| SCE1572_10149 | 37 | 4 |
| SCE1572_5118 | 50 | 62 |
| SCE1572_10916 | 194 | 65 |
| SCE1572_988 | 81 | 86 |
| SCE1572_8428 | 62 | 20 |
| SCE1572_3011 | 173 | 17 |
| SCE1572_484 | 107 | 29 |
| SCE1572_7809 | 0 | 0 |
| SCE1572_7723 | 76 | 41 |
| SCE1572_10305 | 78 | 22 |
| SCE1572_6737 | 189 | 493 |
| SCE1572_6717 | 133 | 162 |
| SCE1572_544 | 42 | 17 |
| SCE1572_6710 | 892 | 312 |
| SCE1572_11584 | 104 | 23 |
| SCE1572_9489 | 149 | 42 |
| SCE1572_11244 | 41 | 39 |
| SCE1572_10290 | 36 | 8 |
| SCE1572_5615 | 101 | 10 |
| SCE1572_10069 | 61 | 4 |
| SCE1572_10708 | 27 | 7 |
| SCE1572_6 | 98 | 55 |
| SCE1572_6441 | 5 | 0 |
| SCE1572_7982 | 108 | 28 |
| SCE1572_9735 | 223 | 162 |
| SCE1572_3511 | 101 | 70 |
| SCE1572_9452 | 258 | 59 |
| SCE1572_9305 | 47 | 35 |
| SCE1572_2708 | 314 | 33 |
| SCE1572_2915 | 1151 | 146 |
| SCE1572_3956 | 180 | 26 |
| SCE1572_766 | 17 | 2 |
| SCE1572_1106 | 94 | 8 |
| SCE1572_3949 | 233 | 506 |
| SCE1572_1396 | 31 | 154 |
| SCE1572_3068 | 83 | 80 |

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| SCE1572_4440 | 161 | 39 |
| SCE1572_4413 | 8 | 0 |
| SCE1572_9837 | 203 | 189 |
| SCE1572_102 | 46 | 7 |
| SCE1572_10925 | 0 | 0 |
| SCE1572_2380 | 32 | 12 |
| SCE1572_4904 | 50 | 289 |
| SCE1572_4333 | 9 | 2 |
| SCE1572_11140 | 59 | 20 |
| SCE1572_6648 | 4 | 0 |
| SCE1572_8330 | 131 | 341 |
| SCE1572_8223 | 7 | 4 |
| SCE1572_5191 | 255 | 379 |
| SCE1572_6614 | 196 | 44 |
| SCE1572_11443 | 115 | 32 |
| SCE1572_1947 | 132 | 35 |
| SCE1572_3059 | 14 | 1 |
| SCE1572_3271 | 251 | 1131 |
| SCE1572_1838 | 205 | 419 |
| SCE1572_8965 | 95 | 69 |
| SCE1572_691 | 46 | 6 |
| SCE1572_10574 | 196 | 100 |
| SCE1572_11233 | 145 | 159 |
| SCE1572_3598 | 317 | 41 |
| SCE1572_8510 | 43 | 8 |
| SCE1572_4747 | 209 | 29 |
| SCE1572_9693 | 117 | 937 |
| SCE1572_4081 | 44 | 25 |
| SCE1572_9482 | 15 | 12 |
| SCE1572_1078 | 86 | 22 |
| SCE1572_853 | 129 | 252 |
| SCE1572_7931 | 155 | 54 |
| SCE1572_7300 | 137 | 26 |
| SCE1572_6196 | 29 | 5 |
| SCE1572_3634 | 59 | 14 |
| SCE1572_1994 | 242 | 37 |
| SCE1572_7958 | 246 | 300 |
| SCE1572_6350 | 80 | 41 |
| SCE1572_9487 | 42 | 27 |
| SCE1572_10210 | 165 | 13 |
| SCE1572_10728 | 34 | 34 |
| SCE1572_3321 | 365 | 275 |
| SCE1572_3552 | 147 | 24 |
| SCE1572_10375 | 95 | 10 |
| SCE1572_6785 | 0 | 0 |
| SCE1572_6347 | 46 | 21 |
| SCE1572_6126 | 51 | 92 |
| SCE1572_9117 | 201 | 48 |

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| SCE1572_1992 | 0 | 0 |
| SCE1572_5265 | 0 | 0 |
| SCE1572_8832 | 5 | 2 |
| SCE1572_10721 | 1348 | 248 |
| SCE1572_1452 | 0 | 0 |
| SCE1572_9722 | 1813 | 7821 |
| SCE1572_7961 | 14 | 0 |
| SCE1572_10299 | 77 | 101 |
| SCE1572_9069 | 80 | 183 |
| SCE1572_7864 | 93 | 49 |
| SCE1572_1776 | 76 | 16 |
| SCE1572_3052 | 85 | 10 |
| SCE1572_10792 | 150 | 98 |
| SCE1572_8700 | 80 | 26 |
| SCE1572_1025 | 34 | 354 |
| SCE1572_7309 | 204 | 27 |
| SCE1572_2283 | 84 | 18 |
| SCE1572_2775 | 44 | 55 |
| SCE1572_5505 | 1 | 2 |
| SCE1572_7166 | 83 | 10 |
| SCE1572_3093 | 142 | 48 |
| SCE1572_680 | 14 | 12 |
| SCE1572_5535 | 274 | 36 |
| SCE1572_3846 | 47 | 5 |
| SCE1572_4351 | 65 | 9 |
| SCE1572_11084 | 16 | 21 |
| SCE1572_1219 | 40 | 13 |
| SCE1572_209 | 72 | 17 |
| SCE1572_2003 | 223 | 42 |
| SCE1572_219 | 24 | 36 |
| SCE1572_2523 | 1 | 0 |
| SCE1572_5317 | 3 | 0 |
| SCE1572_8583 | 1688 | 287 |
| SCE1572_8252 | 147 | 179 |
| SCE1572_5936 | 79 | 23 |
| SCE1572_128 | 4 | 0 |
| SCE1572_7787 | 27 | 0 |
| SCE1572_3486 | 346 | 72 |
| SCE1572_1137 | 148.64 | 29 |
| SCE1572_8272 | 21 | 13 |
| SCE1572_9391 | 58 | 15 |
| SCE1572_6400 | 130 | 197 |
| SCE1572_4145 | 133 | 169.04 |
| SCE1572_3398 | 80 | 8 |
| SCE1572_9008 | 52 | 8 |
| SCE1572_9888 | 179 | 43 |
| SCE1572_7155 | 76 | 16 |
| SCE1572_8527 | 12 | 0 |

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| SCE1572_7583 | 398 | 1053 |
| SCE1572_6741 | 676 | 135 |
| SCE1572_9788 | 165 | 60 |
| SCE1572_7745 | 932 | 1866 |
| SCE1572_7322 | 37 | 3 |
| SCE1572_5966 | 37 | 9 |
| SCE1572_4513 | 2 | 1 |
| SCE1572_6135 | 103 | 78 |
| SCE1572_8735 | 0 | 0 |
| SCE1572_223 | 32 | 3 |
| SCE1572_6921 | 467.98 | 164.53 |
| SCE1572_11078 | 18 | 4 |
| SCE1572_3316 | 155 | 66 |
| SCE1572_1866 | 25 | 10 |
| SCE1572_4730 | 162.85 | 40 |
| SCE1572_8279 | 31 | 4 |
| SCE1572_7474 | 117 | 105 |
| SCE1572_9979 | 105 | 17 |
| SCE1572_3714 | 94 | 75 |
| SCE1572_908 | 13 | 3 |
| SCE1572_1630 | 113 | 19 |
| SCE1572_6032 | 21 | 15 |
| SCE1572_11080 | 56 | 270 |
| SCE1572_8535 | 131 | 34 |
| SCE1572_8293 | 40 | 10 |
| SCE1572_912 | 456 | 581 |
| SCE1572_1313 | 1529 | 2663 |
| SCE1572_998 | 81 | 61 |
| SCE1572_8054 | 8 | 2 |
| SCE1572_2492 | 179 | 43 |
| SCE1572_10933 | 15 | 0 |
| SCE1572_3046 | 26 | 2 |
| SCE1572_11451 | 17 | 4 |
| SCE1572_3223 | 9 | 1 |
| SCE1572_4307 | 93 | 34 |
| SCE1572_7788 | 0 | 0 |
| SCE1572_4699 | 52 | 10 |
| SCE1572_10343 | 44 | 104 |
| SCE1572_6041 | 214 | 139 |
| SCE1572_5665 | 36 | 8 |
| SCE1572_897 | 80 | 16 |
| SCE1572_9027 | 190 | 132 |
| SCE1572_4286 | 0 | 0 |
| SCE1572_10669 | 136 | 243 |
| SCE1572_2546 | 120 | 27 |
| SCE1572_2671 | 459 | 352 |
| SCE1572_7345 | 11 | 1 |
| SCE1572_10565 | 165 | 29 |

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| SCE1572_3559 | 152 | 76 |
| SCE1572_8242 | 65 | 104 |
| SCE1572_1504 | 158 | 92 |
| SCE1572_4861 | 64 | 13 |
| SCE1572_5771 | 1 | 0 |
| SCE1572_314 | 52 | 9 |
| SCE1572_2324 | 16 | 13 |
| SCE1572_6762 | 0 | 0 |
| SCE1572_890 | 48 | 39 |
| SCE1572_10301 | 91 | 16 |
| SCE1572_11388 | 383 | 283 |
| SCE1572_6519 | 99 | 11 |
| SCE1572_2069 | 199 | 36 |
| SCE1572_2746 | 27 | 1 |
| SCE1572_11196 | 130 | 53 |
| SCE1572_1821 | 19 | 10 |
| SCE1572_2114 | 517.97 | 195 |
| SCE1572_9211 | 21 | 14 |
| SCE1572_11349 | 0 | 0 |
| SCE1572_2554 | 168 | 31 |
| SCE1572_3858 | 49 | 59 |
| SCE1572_9070 | 94 | 31 |
| SCE1572_10187 | 17 | 3 |
| SCE1572_5923 | 158 | 81 |
| SCE1572_5708 | 154 | 55 |
| SCE1572_9711 | 310 | 521 |
| SCE1572_5421 | 40 | 89 |
| SCE1572_597 | 154 | 199 |
| SCE1572_10639 | 129 | 322 |
| SCE1572_2583 | 10 | 1 |
| SCE1572_6089 | 15 | 38 |
| SCE1572_9597 | 232 | 4775 |
| SCE1572_2134 | 0 | 0 |
| SCE1572_7261 | 0 | 0 |
| SCE1572_2060 | 14 | 7 |
| SCE1572_5979 | 19 | 23 |
| SCE1572_1770 | 55 | 11 |
| SCE1572_9335 | 88 | 165 |
| SCE1572_4256 | 120 | 302 |
| SCE1572_4992 | 21 | 29 |
| SCE1572_10969 | 252 | 212 |
| SCE1572_9281 | 267 | 417 |
| SCE1572_8675 | 62 | 20 |
| SCE1572_2687 | 126 | 56 |
| SCE1572_689 | 44 | 28 |
| SCE1572_4192 | 118 | 132 |
| SCE1572_9689 | 207 | 151 |
| SCE1572_4611 | 37 | 10 |

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| SCE1572_7971 | 14 | 8 |
| SCE1572_7479 | 179 | 62 |
| SCE1572_1071 | 59 | 11 |
| SCE1572_6228 | 217 | 34 |
| SCE1572_9172 | 46 | 7 |
| SCE1572_8447 | 11 | 0 |
| SCE1572_7751 | 179 | 36 |
| SCE1572_3231 | 71 | 107 |
| SCE1572_319 | 141 | 21 |
| SCE1572_4349 | 530 | 105 |
| SCE1572_7623 | 73 | 42 |
| SCE1572_11025 | 260 | 180 |
| SCE1572_4122 | 37 | 15 |
| SCE1572_9586 | 129 | 97 |
| SCE1572_6002 | 40 | 93 |
| SCE1572_1410 | 69 | 14 |
| SCE1572_372 | 91 | 186 |
| SCE1572_10142 | 123 | 105 |
| SCE1572_10883 | 19 | 87 |
| SCE1572_9053 | 1218.35 | 202 |
| SCE1572_1112 | 10 | 5 |
| SCE1572_6833 | 63 | 28 |
| SCE1572_8752 | 60 | 9 |
| SCE1572_4129 | 193 | 242 |
| SCE1572_8594 | 79 | 55 |
| SCE1572_2888 | 91 | 17 |
| SCE1572_8728 | 110 | 21 |
| SCE1572_8069 | 19.55 | 1 |
| SCE1572_10323 | 56 | 47 |
| SCE1572_9265 | 278 | 159 |
| SCE1572_8305 | 56 | 15 |
| SCE1572_10479 | 73 | 31 |
| SCE1572_6326 | 12 | 3 |
| SCE1572_3686 | 24 | 0 |
| SCE1572_5835 | 1327 | 816 |
| SCE1572_4669 | 85 | 7 |
| SCE1572_4828 | 47 | 8 |
| SCE1572_262 | 115 | 19 |
| SCE1572_8142 | 14 | 1 |
| SCE1572_5288 | 202 | 70 |
| SCE1572_9477 | 0 | 0 |
| SCE1572_2442 | 129 | 294 |
| SCE1572_8581 | 1294.22 | 135.84 |
| SCE1572_9227 | 49.97 | 24 |
| SCE1572_734 | 87 | 17 |
| SCE1572_8091 | 5 | 0 |
| SCE1572_11486 | 94 | 70 |
| SCE1572_4043 | 194 | 482 |

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| SCE1572_8393 | 172 | 62 |
| SCE1572_2342 | 33 | 50 |
| SCE1572_3732 | 55 | 22 |
| SCE1572_3772 | 158 | 87 |
| SCE1572_6517 | 16 | 33 |
| SCE1572_3354 | 99 | 43 |
| SCE1572_4528 | 0 | 0 |
| SCE1572_11181 | 52 | 33 |
| SCE1572_3077 | 214 | 40 |
| SCE1572_8553 | 49 | 265 |
| SCE1572_11102 | 71 | 56 |
| SCE1572_7609 | 27 | 15 |
| SCE1572_4553 | 26 | 1 |
| SCE1572_5388 | 270 | 467 |
| SCE1572_8283 | 38 | 3 |
| SCE1572_661 | 0 | 0 |
| SCE1572_8098 | 13 | 225 |
| SCE1572_3301 | 47 | 18 |
| SCE1572_1983 | 0 | 0 |
| SCE1572_6855 | 17 | 16 |
| SCE1572_7914 | 69 | 18 |
| SCE1572_1145 | 19 | 2 |
| SCE1572_3147 | 19 | 1 |
| SCE1572_7329 | 22 | 1 |
| SCE1572_6250 | 0 | 0 |
| SCE1572_7315 | 17 | 4 |
| SCE1572_7938 | 68 | 88 |
| SCE1572_11420 | 202 | 83 |
| SCE1572_9869 | 274 | 511 |
| SCE1572_1089 | 121 | 34 |
| SCE1572_7606 | 181 | 63 |
| SCE1572_6451 | 276.76 | 57.74 |
| SCE1572_4199 | 36 | 42 |
| SCE1572_4800 | 71 | 695 |
| SCE1572_9860 | 183 | 54 |
| SCE1572_6247 | 42 | 11 |
| SCE1572_3133 | 380 | 99 |
| SCE1572_8456 | 83 | 374 |
| SCE1572_11417 | 77 | 26 |
| SCE1572_1204 | 0 | 0 |
| SCE1572_1030 | 35 | 74 |
| SCE1572_1146 | 171 | 48 |
| SCE1572_9504 | 37 | 4 |
| SCE1572_11484 | 35 | 0 |
| SCE1572_8195 | 126 | 49 |
| SCE1572_1921 | 0 | 0 |
| SCE1572_1699 | 174 | 184 |
| SCE1572_3245 | 94 | 29 |

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| SCE1572_3852 | 110 | 80 |
| SCE1572_10844 | 8 | 2 |
| SCE1572_4227 | 100 | 47 |
| SCE1572_10073 | 141 | 247 |
| SCE1572_4666 | 49 | 3 |
| SCE1572_8839 | 12 | 0 |
| SCE1572_8366 | 74 | 7 |
| SCE1572_7833 | 188 | 116 |
| SCE1572_7436 | 13 | 4 |
| SCE1572_8213 | 176 | 97 |
| SCE1572_9311 | 223 | 422 |
| SCE1572_7567 | 42 | 8 |
| SCE1572_1082 | 41 | 3 |
| SCE1572_5537 | 126 | 36 |
| SCE1572_6535 | 67 | 20 |
| SCE1572_934 | 91 | 158 |
| SCE1572_11564 | 12 | 4 |
| SCE1572_11263 | 51 | 50 |
| SCE1572_11020 | 27 | 8 |
| SCE1572_2533 | 18 | 131 |
| SCE1572_5489 | 0 | 0 |
| SCE1572_4809 | 177 | 68 |
| SCE1572_33 | 1365 | 3054 |
| SCE1572_6300 | 101 | 155 |
| SCE1572_9607 | 30 | 4 |
| SCE1572_11524 | 19 | 4 |
| SCE1572_10753 | 120 | 11 |
| SCE1572_115 | 45 | 7 |
| SCE1572_6102 | 33 | 4 |
| SCE1572_6410 | 0 | 0 |
| SCE1572_8792 | 66 | 33 |
| SCE1572_610 | 70 | 47 |
| SCE1572_1973 | 0 | 0 |
| SCE1572_2828 | 0 | 0 |
| SCE1572_136 | 83 | 11 |
| SCE1572_3375 | 61 | 84 |
| SCE1572_5690 | 45 | 29 |
| SCE1572_2172 | 29 | 1 |
| SCE1572_6082 | 45 | 3 |
| SCE1572_5041 | 164 | 237 |
| SCE1572_10895 | 99 | 79 |
| SCE1572_5325 | 58 | 29 |
| SCE1572_9645 | 42 | 237 |
| SCE1572_7780 | 11 | 2 |
| SCE1572_1037 | 1 | 0 |
| SCE1572_1903 | 419 | 56 |
| SCE1572_5816 | 59 | 12 |
| SCE1572_7143 | 55 | 7 |

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| SCE1572_11435 | 162 | 52 |
| SCE1572_2732 | 203 | 167 |
| SCE1572_11223 | 15 | 4 |
| SCE1572_4830 | 105 | 66 |
| SCE1572_452 | 8 | 23 |
| SCE1572_1556 | 66 | 44 |
| SCE1572_159 | 344 | 257.48 |
| SCE1572_4894 | 81 | 13 |
| SCE1572_4109 | 52 | 9 |
| SCE1572_5852 | 82 | 36 |
| SCE1572_6473 | 358 | 296 |
| SCE1572_3648 | 90 | 180 |
| SCE1572_1719 | 180 | 98 |
| SCE1572_2205 | 15 | 62 |
| SCE1572_606 | 323 | 241 |
| SCE1572_2179 | 31 | 39 |
| SCE1572_4041 | 579 | 3115 |
| SCE1572_2563 | 76 | 16 |
| SCE1572_12 | 179 | 265 |
| SCE1572_1252 | 148 | 27 |
| SCE1572_1460 | 10 | 3 |
| SCE1572_10773 | 26 | 13 |
| SCE1572_2216 | 77 | 172 |
| SCE1572_2645 | 4 | 0 |
| SCE1572_147 | 73 | 28 |
| SCE1572_3844 | 285 | 659 |
| SCE1572_4030 | 405 | 390 |
| SCE1572_1461 | 185 | 43 |
| SCE1572_2588 | 235 | 38 |
| SCE1572_7646 | 300 | 172 |
| SCE1572_725 | 57 | 23 |
| SCE1572_4884 | 22 | 21 |
| SCE1572_7828 | 80 | 86 |
| SCE1572_6491 | 4 | 0 |
| SCE1572_4037 | 19 | 12 |
| SCE1572_1414 | 59 | 9 |
| SCE1572_4502 | 118 | 20 |
| SCE1572_1298 | 75 | 13 |
| SCE1572_1705 | 348 | 171 |
| SCE1572_664 | 425 | 586 |
| SCE1572_3423 | 3 | 0 |
| SCE1572_3008 | 49 | 11 |
| SCE1572_3034 | 147 | 154 |
| SCE1572_3823 | 29 | 22 |
| SCE1572_10890 | 70 | 22 |
| SCE1572_1498 | 102.67 | 9.34 |
| SCE1572_7798 | 38 | 21 |
| SCE1572_2603 | 13.25 | 0.75 |

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| SCE1572_2181 | 59 | 16 |
| SCE1572_2079 | 25 | 7 |
| SCE1572_4839 | 176 | 156 |
| SCE1572_10006 | 12 | 6 |
| SCE1572_9960 | 81 | 17 |
| SCE1572_6292 | 76 | 19 |
| SCE1572_1231 | 159 | 273 |
| SCE1572_617 | 220 | 404 |
| SCE1572_6587 | 533 | 146 |
| SCE1572_3757 | 338 | 45 |
| SCE1572_1551 | 62 | 11 |
| SCE1572_5046 | 0 | 0 |
| SCE1572_6159 | 65 | 1 |
| SCE1572_1801 | 32 | 114 |
| SCE1572_4739 | 136 | 13 |
| SCE1572_6496 | 91 | 15 |
| SCE1572_5907 | 792 | 314 |
| SCE1572_7900 | 67 | 20 |
| SCE1572_3864 | 56 | 9 |
| SCE1572_6811 | 196 | 57 |
| SCE1572_10812 | 63 | 11 |
| SCE1572_10554 | 98 | 15 |
| SCE1572_1799 | 41 | 194 |
| SCE1572_2241 | 145 | 41 |
| SCE1572_1585 | 85 | 185 |
| SCE1572_10534 | 61 | 116 |
| SCE1572_8384 | 21 | 4 |
| SCE1572_1270 | 145 | 216 |
| SCE1572_2499 | 196 | 40 |
| SCE1572_8329 | 124 | 34 |
| SCE1572_1592 | 358 | 173 |
| SCE1572_3563 | 453 | 109 |
| SCE1572_9465 | 3 | 0 |
| SCE1572_3991 | 867 | 3289 |
| SCE1572_2879 | 267 | 211 |
| SCE1572_3182 | 208 | 414 |
| SCE1572_3568 | 301.97 | 32.84 |
| SCE1572_553 | 45 | 31 |
| SCE1572_1365 | 168 | 1757 |
| SCE1572_4509 | 41 | 46 |
| SCE1572_10424 | 70 | 11 |
| SCE1572_5073 | 121 | 515 |
| SCE1572_4429 | 93 | 74 |
| SCE1572_9101 | 67 | 70 |
| SCE1572_9859 | 140 | 55 |
| SCE1572_6936 | 23 | 5 |
| SCE1572_10057 | 279 | 97 |
| SCE1572_9773 | 79 | 35 |

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| SCE1572_5078 | 110 | 305 |
| SCE1572_10819 | 124 | 99 |
| SCE1572_7599 | 1560 | 1606 |
| SCE1572_2049 | 52 | 55 |
| SCE1572_8939 | 33 | 171 |
| SCE1572_3985 | 103 | 129 |
| SCE1572_334 | 48 | 45 |
| SCE1572_1884 | 74 | 76 |
| SCE1572_10746 | 8 | 1 |
| SCE1572_6106 | 37 | 5 |
| SCE1572_5105 | 476 | 2405 |
| SCE1572_11334 | 164 | 150 |
| SCE1572_11412 | 122 | 179 |
| SCE1572_7394 | 45 | 2 |
| SCE1572_13 | 333 | 84 |
| SCE1572_9423 | 25 | 14 |
| SCE1572_10803 | 16 | 4 |
| SCE1572_10429 | 47 | 7 |
| SCE1572_1812 | 98 | 19 |
| SCE1572_11576 | 28 | 23 |
| SCE1572_2607 | 83 | 22 |
| SCE1572_1525 | 312 | 641 |
| SCE1572_8651 | 14 | 1 |
| SCE1572_5999 | 66 | 251 |
| SCE1572_11259 | 179 | 723 |
| SCE1572_4917 | 23 | 3 |
| SCE1572_10130 | 62 | 21 |
| SCE1572_4485 | 40 | 72 |
| SCE1572_1530 | 0 | 0 |
| SCE1572_2805 | 113.36 | 48 |
| SCE1572_428 | 67 | 71 |
| SCE1572_8471 | 864 | 1023 |
| SCE1572_870 | 26 | 28 |
| SCE1572_4449 | 1 | 0 |
| SCE1572_11041 | 334 | 168 |
| SCE1572_3616 | 43 | 9 |
| SCE1572_3464 | 480 | 95 |
| SCE1572_5397 | 85 | 18 |
| SCE1572_6024 | 325 | 130 |
| SCE1572_3335 | 145 | 132 |
| SCE1572_5644 | 26 | 1 |
| SCE1572_11121 | 59 | 12 |
| SCE1572_2195 | 104 | 44 |
| SCE1572_4103 | 90 | 15 |
| SCE1572_2973 | 1 | 0 |
| SCE1572_785 | 103 | 53 |
| SCE1572_5699 | 25.81 | 52.11 |
| SCE1572_6767 | 11 | 2 |

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| SCE1572_4685 | 279 | 156 |
| SCE1572_7768 | 490 | 197 |
| SCE1572_1465 | 57 | 11 |
| SCE1572_9093 | 21 | 1 |
| SCE1572_2489 | 8 | 0 |
| SCE1572_4170 | 0 | 0 |
| SCE1572_5381 | 80 | 12 |
| SCE1572_6448 | 411 | 80 |
| SCE1572_9476 | 26 | 3 |
| SCE1572_10901 | 40 | 26 |
| SCE1572_4534 | 78 | 34 |
| SCE1572_2834 | 761 | 3532 |
| SCE1572_8658 | 80 | 194 |
| SCE1572_8707 | 106 | 35 |
| SCE1572_7018 | 31 | 4 |
| SCE1572_5990 | 332 | 99 |
| SCE1572_9156 | 217 | 231 |
| SCE1572_2959 | 65 | 12 |
| SCE1572_7094 | 0 | 0 |
| SCE1572_11529 | 132 | 17 |
| SCE1572_2226 | 89 | 13 |
| SCE1572_5235 | 133 | 561 |
| SCE1572_7076 | 134 | 63 |
| SCE1572_2296 | 177 | 200 |
| SCE1572_9566 | 0 | 0 |
| SCE1572_5890 | 95 | 29 |
| SCE1572_4942 | 22 | 52 |
| SCE1572_4978 | 118 | 701 |
| SCE1572_1441 | 127 | 20 |
| SCE1572_10905 | 192 | 116 |
| SCE1572_11109 | 93.15 | 44 |
| SCE1572_10066 | 255 | 497 |
| SCE1572_11275 | 155 | 324 |
| SCE1572_7592 | 163 | 56 |
| SCE1572_7821 | 55 | 129 |
| SCE1572_1492 | 155.1 | 26.33 |
| SCE1572_8871 | 202 | 65 |
| SCE1572_8300 | 55 | 3 |
| SCE1572_10641 | 70 | 34 |
| SCE1572_1763 | 172.99 | 5.15 |
| SCE1572_1797 | 43 | 14 |
| SCE1572_2559 | 74 | 19 |
| SCE1572_4138 | 105 | 15 |
| SCE1572_4270 | 92 | 14 |
| SCE1572_9125 | 26 | 9 |
| SCE1572_11171 | 23 | 1 |
| SCE1572_7791 | 29 | 2 |
| SCE1572_927 | 49 | 8 |

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| SCE1572_10962 | 155 | 24 |
| SCE1572_9003 | 186 | 321 |
| SCE1572_9136 | 27 | 3 |
| SCE1572_6706 | 612 | 887 |
| SCE1572_292 | 8 | 27 |
| SCE1572_10485 | 139 | 266 |
| SCE1572_5093 | 56 | 276 |
| SCE1572_1272 | 6 | 4 |
| SCE1572_5100 | 32 | 23 |
| SCE1572_9178 | 146 | 170 |
| SCE1572_11063 | 90 | 28 |
| SCE1572_305 | 60 | 13 |
| SCE1572_2112 | 1 | 0 |
| SCE1572_10394 | 0 | 0 |
| SCE1572_10835 | 178 | 23 |
| SCE1572_10624 | 100 | 127 |
| SCE1572_9740 | 144 | 311 |
| SCE1572_7372 | 87 | 48 |
| SCE1572_1677 | 4 | 1 |
| SCE1572_9363 | 40 | 42 |
| SCE1572_8905 | 12 | 2 |
| SCE1572_11129 | 73 | 35 |
| SCE1572_5860 | 0 | 0 |
| SCE1572_5283 | 60 | 14 |
| SCE1572_4071 | 31 | 58 |
| SCE1572_3936 | 0 | 0 |
| SCE1572_7455 | 76 | 206 |
| SCE1572_6725 | 52 | 36 |
| SCE1572_1844 | 135 | 34 |
| SCE1572_2505 | 26 | 7 |
| SCE1572_6563 | 55 | 24 |
| SCE1572_1296 | 0 | 0 |
| SCE1572_652 | 773 | 1326 |
| SCE1572_6730 | 1921 | 12296 |
| SCE1572_7453 | 302 | 915 |
| SCE1572_1672 | 30 | 13 |
| SCE1572_5689 | 61 | 12 |
| SCE1572_8439 | 82 | 28 |
| SCE1572_1736 | 158 | 32 |
| SCE1572_6290 | 0 | 0 |
| SCE1572_79 | 88 | 21 |
| SCE1572_3291 | 55 | 27 |
| SCE1572_4084 | 58 | 7 |
| SCE1572_5366 | 101 | 670 |
| SCE1572_5844 | 39 | 13 |
| SCE1572_6293 | 137 | 64 |
| SCE1572_4200 | 74 | 89 |
| SCE1572_4776 | 277 | 605 |

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| SCE1572_2158 | 0 | 0 |
| SCE1572_6797 | 106 | 122 |
| SCE1572_1960 | 201 | 17 |
| SCE1572_10613 | 26 | 10 |
| SCE1572_8382 | 25 | 2 |
| SCE1572_5135 | 163 | 529 |
| SCE1572_2011 | 57 | 1 |
| SCE1572_10528 | 5 | 0 |
| SCE1572_1934 | 71 | 54 |
| SCE1572_11207 | 0 | 0 |
| SCE1572_1743 | 67 | 16 |
| SCE1572_5718 | 60 | 31 |
| SCE1572_9134 | 74 | 15 |
| SCE1572_1625 | 89 | 18 |
| SCE1572_1381 | 70 | 23 |
| SCE1572_2085 | 61 | 23 |
| SCE1572_4014 | 0 | 0 |
| SCE1572_4560 | 6 | 1 |
| SCE1572_4649 | 134 | 22 |
| SCE1572_3779 | 163 | 59 |
| SCE1572_7107 | 409 | 107 |
| SCE1572_11562 | 0 | 0 |
| SCE1572_3755 | 694.59 | 78.72 |
| SCE1572_5138 | 0 | 0 |
| SCE1572_11283 | 59 | 34 |
| SCE1572_10088 | 0 | 0 |
| SCE1572_2807 | 4.64 | 0 |
| SCE1572_10266 | 118 | 135 |
| SCE1572_9441 | 101 | 354 |
| SCE1572_8799 | 3 | 0 |
| SCE1572_4843 | 97 | 48 |
| SCE1572_3612 | 166 | 29 |
| SCE1572_1710 | 31 | 20 |
| SCE1572_3363 | 49 | 38 |
| SCE1572_7352 | 66 | 10 |
| SCE1572_1471 | 0 | 0 |
| SCE1572_309 | 77 | 10 |
| SCE1572_9103 | 159 | 83 |
| SCE1572_5305 | 0 | 0 |
| SCE1572_1350 | 65 | 30 |
| SCE1572_8020 | 158 | 36 |
| SCE1572_5984 | 121 | 47 |
| SCE1572_3079 | 0 | 0 |
| SCE1572_9249 | 104 | 14 |
| SCE1572_6950 | 5 | 0 |
| SCE1572_7522 | 80 | 12 |
| SCE1572_701 | 105 | 439 |
| SCE1572_6820 | 39 | 4 |

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| SCE1572_8389 | 78 | 12 |
| SCE1572_11293 | 291 | 413 |
| SCE1572_5739 | 159 | 55 |
| SCE1572_2790 | 31 | 6 |
| SCE1572_5209 | 7 | 2 |
| SCE1572_7219 | 283 | 2056 |
| SCE1572_8163 | 120 | 29 |
| SCE1572_1300 | 138 | 15 |
| SCE1572_491 | 965.44 | 379.25 |
| SCE1572_5455 | 113 | 15 |
| SCE1572_7184 | 0 | 0 |
| SCE1572_5233 | 12 | 34 |
| SCE1572_8913 | 55 | 9 |
| SCE1572_4278 | 317 | 79 |
| SCE1572_8414 | 117 | 32 |
| SCE1572_3238 | 293 | 76 |
| SCE1572_8464 | 80 | 83 |
| SCE1572_8496 | 329 | 51 |
| SCE1572_10606 | 94 | 31 |
| SCE1572_5404 | 10 | 4 |
| SCE1572_744 | 57 | 25 |
| SCE1572_10856 | 268 | 425 |
| SCE1572_964 | 150 | 343 |
| SCE1572_10846 | 50 | 17 |
| SCE1572_4640 | 316 | 78 |
| SCE1572_947 | 158.67 | 8.79 |
| SCE1572_6924 | 1 | 0 |
| SCE1572_4090 | 46 | 10 |
| SCE1572_8405 | 28 | 51 |
| SCE1572_7549 | 228 | 28 |
| SCE1572_6454 | 160 | 72 |
| SCE1572_9207 | 90 | 31 |
| SCE1572_8087 | 185 | 16 |
| SCE1572_3098 | 0 | 0 |
| SCE1572_9972 | 168 | 329 |
| SCE1572_210 | 67 | 10 |
| SCE1572_5524 | 62 | 17 |
| SCE1572_5357 | 215 | 50 |
| SCE1572_5795 | 75 | 24 |
| SCE1572_10257 | 76 | 27 |
| SCE1572_3514 | 132 | 360 |
| SCE1572_5887 | 36 | 11 |
| SCE1572_8946 | 422 | 722 |
| SCE1572_11502 | 27 | 1 |
| SCE1572_7205 | 203 | 107 |
| SCE1572_9694 | 2626 | 6613 |
| SCE1572_1141 | 31 | 7 |
| SCE1572_2623 | 2 | 0 |

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| SCE1572_7419 | 17 | 2 |
| SCE1572_6656 | 129 | 149 |
| SCE1572_2270 | 769 | 1793 |
| SCE1572_3151 | 46 | 219 |
| SCE1572_7614 | 62 | 20 |
| SCE1572_4679 | 152 | 19 |
| SCE1572_5206 | 91 | 94 |
| SCE1572_6611 | 22 | 3 |
| SCE1572_6287 | 60 | 41 |
| SCE1572_11290 | 1679 | 1089 |
| SCE1572_196 | 8 | 0 |
| SCE1572_6478 | 48 | 8 |
| SCE1572_3070 | 35 | 13 |
| SCE1572_9515 | 118 | 143 |
| SCE1572_10283 | 55 | 103 |
| SCE1572_11540 | 32 | 6 |
| SCE1572_10033 | 227 | 693 |
| SCE1572_5802 | 150 | 120 |
| SCE1572_9492 | 194 | 44 |
| SCE1572_7064 | 167 | 30 |
| SCE1572_8345 | 0 | 0 |
| SCE1572_582 | 36 | 8 |
| SCE1572_1346 | 33 | 25 |
| SCE1572_4569 | 92 | 32 |
| SCE1572_655 | 1027 | 597 |
| SCE1572_3021 | 12 | 1 |
| SCE1572_5587 | 48 | 9 |
| SCE1572_8858 | 163 | 57 |
| SCE1572_4983 | 746 | 643 |
| SCE1572_11173 | 41 | 20 |
| SCE1572_6366 | 49 | 284 |
| SCE1572_11004 | 117 | 82 |
| SCE1572_6897 | 0 | 0 |
| SCE1572_2818 | 91 | 26 |
| SCE1572_9818 | 21 | 9 |
| SCE1572_5567 | 93 | 127 |
| SCE1572_11298 | 116 | 155 |
| SCE1572_3929 | 160 | 113 |
| SCE1572_831 | 0 | 0 |
| SCE1572_772 | 60 | 16 |
| SCE1572_5837 | 241 | 209 |
| SCE1572_3974 | 15 | 25 |
| SCE1572_8074 | 22 | 3 |
| SCE1572_7618 | 230 | 183 |
| SCE1572_6387 | 67 | 78 |
| SCE1572_4377 | 125 | 34 |
| SCE1572_7664 | 79 | 11 |
| SCE1572_6885 | 58 | 51 |

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| SCE1572_5511 | 97 | 34 |
| SCE1572_1891 | 35 | 2 |
| SCE1572_4955 | 61 | 9 |
| SCE1572_3104 | 47 | 9 |
| SCE1572_10163 | 176 | 32 |
| SCE1572_9407 | 124 | 71 |
| SCE1572_2576 | 41 | 5 |
| SCE1572_1057 | 103 | 18 |
| SCE1572_3041 | 64 | 3 |
| SCE1572_3894 | 33 | 6 |
| SCE1572_9509 | 15 | 4 |
| SCE1572_1729 | 21 | 38 |
| SCE1572_10171 | 33 | 5 |
| SCE1572_11043 | 270 | 93 |
| SCE1572_1117 | 23 | 16 |
| SCE1572_2373 | 35 | 5 |
| SCE1572_188 | 51 | 264 |
| SCE1572_6957 | 0 | 0 |
| SCE1572_9168 | 52 | 13 |
| SCE1572_7074 | 49 | 28 |
| SCE1572_2983 | 25 | 28 |
| SCE1572_6866 | 175 | 40 |
| SCE1572_7234 | 125 | 51 |
| SCE1572_6806 | 81 | 25 |
| SCE1572_8920 | 233 | 146 |
| SCE1572_8919 | 20 | 220 |
| SCE1572_117 | 68 | 217 |
| SCE1572_7702 | 165 | 23 |
| SCE1572_1503 | 121 | 135 |
| SCE1572_5774 | 57 | 2 |
| SCE1572_1512 | 21 | 12 |
| SCE1572_5065 | 87 | 120 |
| SCE1572_3749 | 30 | 95 |
| SCE1572_7921 | 1 | 0 |
| SCE1572_11396 | 232 | 295 |
| SCE1572_2257 | 209 | 70 |
| SCE1572_4926 | 93 | 12 |
| SCE1572_9141 | 29 | 4 |
| SCE1572_6890 | 28 | 2 |
| SCE1572_7139 | 0 | 0 |
| SCE1572_10736 | 70 | 54 |
| SCE1572_4587 | 385 | 376 |
| SCE1572_473 | 51 | 165 |
| SCE1572_9660 | 1297 | 1279 |
| SCE1572_5186 | 186 | 2570 |
| SCE1572_4194 | 1045 | 816 |
| SCE1572_8894 | 206 | 64 |
| SCE1572_8906 | 75 | 30 |

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| SCE1572_3388 | 29 | 1 |
| SCE1572_6857 | 60 | 7 |
| SCE1572_11148 | 35 | 25 |
| SCE1572_10658 | 1943 | 691 |
| SCE1572_9615 | 0 | 0 |
| SCE1572_10048 | 133 | 242 |
| SCE1572_4370 | 70 | 16 |
| SCE1572_1483 | 257 | 41 |
| SCE1572_8118 | 46.55 | 61.05 |
| SCE1572_11491 | 68 | 20 |
| SCE1572_5830 | 62 | 14 |
| SCE1572_996 | 140 | 29 |
| SCE1572_5897 | 24 | 5 |
| SCE1572_702 | 42 | 9 |
| SCE1572_2960 | 141 | 46 |
| SCE1572_7942 | 158 | 38 |
| SCE1572_4707 | 38 | 33 |
| SCE1572_1967 | 16 | 8 |
| SCE1572_4676 | 78 | 21 |
| SCE1572_815 | 74 | 15 |
| SCE1572_3168 | 231 | 51 |
| SCE1572_4990 | 137 | 386 |
| SCE1572_6378 | 58 | 7 |
| SCE1572_11371 | 461 | 208 |
| SCE1572_1594 | 91 | 60 |
| SCE1572_9191 | 18 | 6 |
| SCE1572_9059 | 18 | 6 |
| SCE1572_10443 | 50 | 6 |
| SCE1572_3127 | 16 | 17 |
| SCE1572_7996 | 111.64 | 21 |
| SCE1572_6471 | 38 | 10 |
| SCE1572_3243 | 168 | 36 |
| SCE1572_528 | 53 | 78 |
| SCE1572_2255 | 28 | 3 |
| SCE1572_5711 | 707 | 680 |
| SCE1572_5870 | 40 | 29 |
| SCE1572_3001 | 28 | 5 |
| SCE1572_181 | 85 | 20 |
| SCE1572_4973 | 943 | 3866 |
| SCE1572_9432 | 102 | 32 |
| SCE1572_2263 | 244 | 635 |
| SCE1572_5494 | 51 | 5 |
| SCE1572_738 | 63 | 23 |
| SCE1572_10712 | 130 | 73 |
| SCE1572_10975 | 308 | 1751 |
| SCE1572_1753 | 30 | 40 |
| SCE1572_4250 | 94 | 98 |
| SCE1572_5439 | 148 | 20 |

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| SCE1572_4551 | 55 | 4 |
| SCE1572_8107 | 56 | 9 |
| SCE1572_7499 | 50 | 10 |
| SCE1572_2026 | 143 | 47 |
| SCE1572_3377 | 178 | 39 |
| SCE1572_6978 | 27 | 1 |
| SCE1572_1855 | 170 | 25 |
| SCE1572_3220 | 105 | 80 |
| SCE1572_3600 | 70 | 23 |
| SCE1572_498 | 524 | 111 |
| SCE1572_7276 | 84 | 5 |
| SCE1572_6901 | 76 | 320 |
| SCE1572_10 | 66 | 80 |
| SCE1572_10204 | 1 | 0 |
| SCE1572_3869 | 36 | 16 |
| SCE1572_8184 | 1 | 0 |
| SCE1572_434 | 156 | 60 |
| SCE1572_5268 | 20 | 28 |
| SCE1572_5027 | 96 | 321 |
| SCE1572_35 | 33 | 60 |
| SCE1572_4988 | 79.02 | 65 |
| SCE1572_10524 | 74 | 13 |
| SCE1572_6861 | 14 | 3 |
| SCE1572_4630 | 376 | 45 |
| SCE1572_6095 | 53 | 15 |
| SCE1572_8115 | 39 | 2 |
| SCE1572_8121 | 228 | 37 |
| SCE1572_7359 | 15 | 4 |
| SCE1572_5463 | 76 | 12 |
| SCE1572_9340 | 1024 | 9881 |
| SCE1572_10913 | 41 | 55 |
| SCE1572_8039 | 168 | 25 |
| SCE1572_3651 | 86 | 39 |
| SCE1572_7556 | 0 | 0 |
| SCE1572_3259 | 206 | 283 |
| SCE1572_478 | 41 | 19 |
| SCE1572_1403 | 1 | 0 |
| SCE1572_9836 | 160 | 22 |
| SCE1572_1179 | 46 | 9 |
| SCE1572_5228 | 92 | 109 |
| SCE1572_9089 | 145 | 24 |
| SCE1572_6589 | 130 | 14 |
| SCE1572_7533 | 0 | 0 |
| SCE1572_3383 | 97 | 400 |
| SCE1572_4498 | 76 | 57 |
| SCE1572_10670 | 5 | 0 |
| SCE1572_6100 | 218 | 19 |
| SCE1572_5861 | 44 | 0 |

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| SCE1572_7527 | 125 | 17 |
| SCE1572_1050 | 30 | 7 |
| SCE1572_9842 | 0 | 0 |
| SCE1572_8036 | 9 | 1 |
| SCE1572_10675 | 335 | 115 |
| SCE1572_10599 | 86 | 5 |
| SCE1572_4113 | 75 | 28 |
| SCE1572_7859 | 79 | 66 |
| SCE1572_8602 | 103 | 26 |
| SCE1572_8967 | 29 | 39 |
| SCE1572_1357 | 174 | 202 |
| SCE1572_3544 | 162 | 23 |
| SCE1572_4402 | 21 | 39 |
| SCE1572_1155 | 65.39 | 20 |
| SCE1572_2031 | 59 | 6 |
| SCE1572_5019 | 29 | 30 |
| SCE1572_5449 | 129 | 35 |
| SCE1572_8004 | 6 | 1 |
| SCE1572_1692 | 7 | 0 |
| SCE1572_5122 | 15 | 58 |
| SCE1572_8358 | 175.24 | 31.96 |
| SCE1572_7223 | 813 | 1310 |
| SCE1572_3218 | 17 | 0 |
| SCE1572_5223 | 488 | 345 |
| SCE1572_8721 | 152 | 56 |
| SCE1572_589 | 6 | 1 |
| SCE1572_9849 | 167 | 71 |
| SCE1572_936 | 34 | 1 |
| SCE1572_8819 | 22 | 5 |
| SCE1572_3626 | 85 | 11 |
| SCE1572_3821 | 373 | 127 |
| SCE1572_6371 | 8 | 2 |
| SCE1572_7542 | 52 | 112 |
| SCE1572_4382 | 171 | 15 |
| SCE1572_97 | 27 | 6 |
| SCE1572_6282 | 3 | 0 |
| SCE1572_3198 | 15 | 68 |
| SCE1572_8156 | 210 | 36 |
| SCE1572_10159 | 4 | 2 |
| SCE1572_2432 | 100 | 104 |
| SCE1572_7672 | 2.8 | 0 |
| SCE1572_9825 | 17.92 | 19.06 |
| SCE1572_2479 | 14 | 20 |
| SCE1572_4578 | 6 | 3 |
| SCE1572_7152 | 33 | 7 |
| SCE1572_10378 | 191 | 34 |
| SCE1572_10430 | 180 | 59 |
| SCE1572_9909 | 110 | 26 |

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| SCE1572_11367 | 40 | 7 |
| SCE1572_1191 | 24 | 4 |
| SCE1572_7552 | 25 | 0 |
| SCE1572_6414 | 12 | 1 |
| SCE1572_6544 | 560 | 642 |
| SCE1572_9016 | 0 | 0 |
| SCE1572_8260 | 215 | 364 |
| SCE1572_4507 | 57 | 11 |
| SCE1572_6240 | 396 | 48 |
| SCE1572_2080 | 101 | 34 |
| SCE1572_9806 | 218 | 135 |
| SCE1572_4154 | 1 | 0 |
| SCE1572_5144 | 0 | 0 |
| SCE1572_577 | 0 | 0 |
| SCE1572_288 | 38 | 64 |
| SCE1572_2057 | 49 | 17 |
| SCE1572_1605 | 203 | 33 |
| SCE1572_5973 | 81 | 8 |
| SCE1572_10826 | 0 | 0 |
| SCE1572_7926 | 15 | 18 |
| SCE1572_7883 | 70 | 6 |
| SCE1572_10437 | 53 | 20 |
| SCE1572_8956 | 14 | 0 |
| SCE1572_7875 | 84 | 36 |
| SCE1572_10012 | 93 | 124 |
| SCE1572_2932 | 182 | 41 |
| SCE1572_4964 | 37 | 37 |
| SCE1572_6759 | 57 | 9 |
| SCE1572_10590 | 149 | 27 |
| SCE1572_10191 | 63 | 25 |
| SCE1572_5542 | 159 | 30 |
| SCE1572_7055 | 478 | 50 |
| SCE1572_6392 | 79 | 60 |
| SCE1572_9870 | 30 | 14 |
| SCE1572_10136 | 19 | 11 |
| SCE1572_5327 | 364 | 3507 |
| SCE1572_482 | 229 | 58 |
| SCE1572_9720 | 70 | 226 |
| SCE1572_9262 | 26 | 12 |
| SCE1572_8741 | 60 | 8 |
| SCE1572_10726 | 28 | 3 |
| SCE1572_9895 | 170 | 99 |
| SCE1572_6782 | 6 | 26 |
| SCE1572_9674 | 155 | 148 |
| SCE1572_2691 | 336 | 257 |
| SCE1572_10691 | 22 | 0 |
| SCE1572_8501 | 14 | 1 |
| SCE1572_7585 | 211 | 192 |

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| SCE1572_1457 | 18 | 3 |
| SCE1572_6708 | 92 | 147 |
| SCE1572_7853 | 93 | 124 |
| SCE1572_10581 | 90 | 18 |
| SCE1572_1097 | 132 | 48 |
| SCE1572_3805 | 68 | 136 |
| SCE1572_3044 | 40 | 1 |
| SCE1572_4032 | 1668 | 162 |
| SCE1572_5716 | 1318 | 1511 |
| SCE1572_6186 | 2 | 0 |
| SCE1572_6402 | 67 | 10 |
| SCE1572_4628 | 2 | 0 |
| SCE1572_5155 | 183 | 85 |
| SCE1572_887 | 312 | 302 |
| SCE1572_5533 | 393 | 67 |
| SCE1572_10770 | 47 | 31 |
| SCE1572_8765 | 177 | 32 |
| SCE1572_5789 | 178 | 267 |
| SCE1572_8547 | 68 | 7 |
| SCE1572_2178 | 202 | 66 |
| SCE1572_10545 | 35 | 9 |
| SCE1572_4093 | 38 | 3 |
| SCE1572_2797 | 213 | 34 |
| SCE1572_2534 | 0 | 0 |
| SCE1572_1918 | 62 | 20 |
| SCE1572_7257 | 42 | 22 |
| SCE1572_5513 | 23 | 13 |
| SCE1572_2863 | 71 | 11 |
| SCE1572_7494 | 44 | 29 |
| SCE1572_10196 | 44 | 2 |
| SCE1572_212 | 142 | 18 |
| SCE1572_7129 | 114 | 53 |
| SCE1572_2452 | 100 | 23 |
| SCE1572_3740 | 168 | 28 |
| SCE1572_2074 | 22 | 7 |
| SCE1572_4627 | 87 | 7 |
| SCE1572_9080 | 12 | 0 |
| SCE1572_9555 | 64 | 252 |
| SCE1572_7462 | 166 | 219 |
| SCE1572_2335 | 104 | 441 |
| SCE1572_502 | 22 | 2 |
| SCE1572_2021 | 4 | 0 |
| SCE1572_942 | 151 | 18 |
| SCE1572_7024 | 123 | 30 |
| SCE1572_10943 | 213 | 26 |
| SCE1572_8787 | 71 | 124 |
| SCE1572_8312 | 119 | 117 |
| SCE1572_3964 | 175 | 45 |

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| SCE1572_5822 | 0 | 0 |
| SCE1572_1217 | 3 | 0 |
| SCE1572_5474 | 22 | 8 |
| SCE1572_3368 | 539 | 777 |
| SCE1572_4543 | 209 | 53 |
| SCE1572_3089 | 32 | 106 |
| SCE1572_8634 | 0 | 0 |
| SCE1572_11341 | 67 | 12 |
| SCE1572_249 | 0 | 0 |
| SCE1572_4269 | 72 | 26 |
| SCE1572_255 | 17 | 3 |
| SCE1572_2894 | 223 | 40 |
| SCE1572_5703 | 109 | 319 |
| SCE1572_7286 | 112 | 203 |
| SCE1572_6689 | 3 | 0 |
| SCE1572_9296 | 115 | 119 |
| SCE1572_4849 | 183 | 103 |
| SCE1572_9215 | 20 | 7 |
| SCE1572_123 | 6 | 0 |
| SCE1572_6315 | 83 | 19 |
| SCE1572_5292 | 39 | 233 |
| SCE1572_8649 | 50 | 11 |
| SCE1572_9463 | 16 | 0 |
| SCE1572_2684 | 175 | 722 |
| SCE1572_4601 | 24 | 10 |
| SCE1572_9935 | 28 | 4 |
| SCE1572_6630 | 25 | 352 |
| SCE1572_10530 | 54 | 59 |
| SCE1572_2636 | 199 | 30 |
| SCE1572_8044 | 30 | 7 |
| SCE1572_1378 | 88 | 17 |
| SCE1572_8685 | 133 | 24 |
| SCE1572_486 | 25 | 3 |
| SCE1572_365 | 66 | 13 |
| SCE1572_2302 | 309 | 378 |
| SCE1572_121 | 19 | 8 |
| SCE1572_4296 | 103 | 37 |
| SCE1572_6971 | 194 | 16 |
| SCE1572_3694 | 151 | 37 |
| SCE1572_4725 | 235 | 100 |
| SCE1572_6397 | 75 | 96 |
| SCE1572_5241 | 35 | 18 |
| SCE1572_10462 | 156 | 618 |
| SCE1572_11380 | 12 | 43 |
| SCE1572_9357 | 279 | 1054 |
| SCE1572_9527 | 35 | 30 |
| SCE1572_8625 | 126 | 61 |
| SCE1572_5551 | 115 | 14 |

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| SCE1572_846 | 108 | 67 |
| SCE1572_9993 | 254.78 | 39 |
| SCE1572_90 | 246.87 | 222 |
| SCE1572_2350 | 802 | 619 |
| SCE1572_3225 | 67 | 17 |
| SCE1572_3534 | 0 | 0 |
| SCE1572_2545 | 39 | 3 |
| SCE1572_410 | 16 | 227 |
| SCE1572_9283 | 61 | 104 |
| SCE1572_8748 | 42 | 5 |
| SCE1572_2722 | 127 | 134 |
| SCE1572_5560 | 163.05 | 41.78 |
| SCE1572_133 | 329.13 | 244 |
| SCE1572_10953 | 25 | 19 |
| SCE1572_3674 | 207 | 731 |
| SCE1572_7200 | 236 | 106 |
| SCE1572_328 | 12 | 1 |
| SCE1572_10226 | 60 | 7 |
| SCE1572_2561 | 465 | 462 |
| SCE1572_3145 | 3 | 1 |
| SCE1572_9123 | 86 | 26 |
| SCE1572_5681 | 107 | 23 |
| SCE1572_6693 | 0 | 0 |
| SCE1572_10637 | 10 | 2 |
| SCE1572_8691 | 140 | 38 |
| SCE1572_8927 | 8 | 2 |
| SCE1572_9958 | 34 | 4 |
| SCE1572_10833 | 0 | 0 |
| SCE1572_1262 | 115 | 190 |
| SCE1572_9669 | 47 | 71 |
| SCE1572_6487 | 47 | 2 |
| SCE1572_6995 | 224 | 20 |
| SCE1572_69 | 150 | 26 |
| SCE1572_3623 | 85 | 8 |
| SCE1572_5392 | 136 | 45 |
| SCE1572_9704 | 147 | 93 |
| SCE1572_7443 | 120 | 36 |
| SCE1572_6913 | 117 | 14 |
| SCE1572_2264 | 38 | 267 |
| SCE1572_5908 | 686 | 708 |
| SCE1572_9749 | 74 | 45 |
| SCE1572_8709 | 33 | 6 |
| SCE1572_11324 | 114 | 667 |
| SCE1572_4344 | 6 | 0 |
| SCE1572_4460 | 17 | 3 |
| SCE1572_5200 | 74 | 22 |
| SCE1572_9011 | 34 | 18 |
| SCE1572_388 | 40 | 17 |

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| SCE1572_5274 | 15 | 4 |
| SCE1572_1817 | 159 | 60 |
| SCE1572_5745 | 15 | 51 |
| SCE1572_4712 | 575 | 195 |
| SCE1572_6918 | 45 | 25 |
| SCE1572_3283 | 223 | 32 |
| SCE1572_6264 | 97 | 8 |
| SCE1572_6525 | 36 | 12 |
| SCE1572_8486 | 254 | 38 |
| SCE1572_11462 | 180 | 129 |
| SCE1572_7570 | 19 | 12 |
| SCE1572_3874 | 152 | 73 |
| SCE1572_8016 | 113 | 9 |
| SCE1572_3149 | 63 | 23 |
| SCE1572_4682 | 80 | 8 |
| SCE1572_242 | 102 | 61 |
| SCE1572_8810 | 72 | 11 |
| SCE1572_7272 | 67 | 16 |
| SCE1572_8240 | 29 | 9 |
| SCE1572_8561 | 160 | 63 |
| SCE1572_1914 | 144 | 35 |
| SCE1572_2516 | 39 | 10 |
| SCE1572_5258 | 3 | 0 |
| SCE1572_8204 | 1 | 0 |
| SCE1572_4438 | 101 | 21 |
| SCE1572_5809 | 145 | 76 |
| SCE1572_9378 | 0 | 0 |
| SCE1572_4764 | 47 | 13 |
| SCE1572_3913 | 183 | 195 |
| SCE1572_5323 | 38 | 23 |
| SCE1572_8400 | 78 | 65 |
| SCE1572_2095 | 83 | 35 |
| SCE1572_5652 | 91 | 432 |
| SCE1572_2594 | 141 | 63 |
| SCE1572_8568 | 13.01 | 2.37 |
| SCE1572_1872 | 57 | 121 |
| SCE1572_4160 | 48 | 21 |
| SCE1572_62 | 18 | 0 |
| SCE1572_7837 | 41 | 15 |
| SCE1572_2926 | 15 | 2 |
| SCE1572_6074 | 421 | 651 |
| SCE1572_6508 | 1 | 0 |
| SCE1572_1283 | 0 | 0 |
| SCE1572_4167 | 31 | 8 |
| SCE1572_4476 | 38 | 15 |
| SCE1572_2711 | 157 | 192 |
| SCE1572_6835 | 34 | 140 |
| SCE1572_5628 | 41 | 5 |

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| SCE1572_6987 | 96 | 10 |
| SCE1572_10093 | 233 | 281 |
| SCE1572_1950 | 37 | 16 |
| SCE1572_9931 | 47 | 80 |
| SCE1572_70 | 311 | 70 |
| SCE1572_8973 | 57 | 38 |
| SCE1572_9579 | 251 | 40 |
| SCE1572_892 | 0 | 0 |
| SCE1572_9037 | 132 | 101 |
| SCE1572_10413 | 1 | 0 |
| SCE1572_612 | 55 | 145 |
| SCE1572_10019 | 129 | 92 |
| SCE1572_1281 | 231 | 24 |
| SCE1572_5173 | 10 | 0 |
| SCE1572_10262 | 85 | 23 |
| SCE1572_2511 | 144 | 304 |
| SCE1572_5595 | 0 | 0 |
| SCE1572_10001 | 34 | 5 |
| SCE1572_3831 | 50 | 26 |
| SCE1572_9877 | 0 | 0 |
| SCE1572_8805 | 30 | 4 |
| SCE1572_6141 | 40 | 9 |
| SCE1572_825 | 160 | 21 |
| SCE1572_880 | 839 | 1353 |
| SCE1572_1225 | 29 | 5 |
| SCE1572_9901 | 1 | 0 |
| SCE1572_8551 | 147 | 65 |
| SCE1572_3786 | 757 | 469 |
| SCE1572_4697 | 0 | 0 |
| SCE1572_7890 | 590 | 10417 |
| SCE1572_8891 | 234 | 41 |
| SCE1572_5591 | 196 | 22 |
| SCE1572_9240 | 0 | 0 |
| SCE1572_10866 | 20 | 8 |
| SCE1572_2877 | 78 | 56 |
| SCE1572_4655 | 0 | 0 |
| SCE1572_4186 | 53 | 16 |
| SCE1572_8825 | 18 | 10 |
| SCE1572_5526 | 66 | 25 |
| SCE1572_11054 | 31 | 9 |
| SCE1572_2167 | 90.1 | 10.62 |
| SCE1572_7503 | 170 | 95 |
| SCE1572_9629 | 182 | 26 |
| SCE1572_8844 | 0 | 0 |
| SCE1572_7384 | 613 | 201 |
| SCE1572_3987 | 120 | 1568 |
| SCE1572_11577 | 45 | 7 |
| SCE1572_8317 | 33 | 83 |

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| SCE1572_10787 | 177 | 110 |
| SCE1572_3263 | 607 | 2798 |
| SCE1572_1008 | 180 | 41 |
| SCE1572_875 | 338 | 109 |
| SCE1572_5096 | 201 | 97 |
| SCE1572_5943 | 98 | 14 |
| SCE1572_710 | 82 | 31 |
| SCE1572_2802 | 150 | 51 |
| SCE1572_5378 | 184 | 18 |
| SCE1572_2976 | 13.84 | 1 |
| SCE1572_755 | 30 | 7 |
| SCE1572_2236 | 297 | 119 |
| SCE1572_7813 | 2 | 0 |
| SCE1572_51 | 263 | 34 |
| SCE1572_10242 | 123 | 13 |
| SCE1572_1388 | 79 | 55 |
| SCE1572_6108 | 209 | 27 |
| SCE1572_3811 | 58 | 8 |
| SCE1572_6359 | 36 | 6 |
| SCE1572_1890 | 92 | 75 |
| SCE1572_3053 | 43 | 7 |
| SCE1572_11192 | 52 | 18 |
| SCE1572_2761 | 146 | 351 |
| SCE1572_9706 | 270 | 99 |
| SCE1572_10247 | 0 | 0 |
| SCE1572_3471 | 4 | 0 |
| SCE1572_976 | 0 | 0 |
| SCE1572_761 | 41 | 14 |
| SCE1572_7364 | 182 | 145 |
| SCE1572_10054 | 252 | 518 |
| SCE1572_1221 | 132 | 10 |
| SCE1572_6311 | 53 | 921 |
| SCE1572_10215 | 1 | 0 |
| SCE1572_959 | 90 | 74 |
| SCE1572_1330 | 189 | 24 |
| SCE1572_5145 | 59 | 29 |
| SCE1572_9951 | 134 | 48 |
| SCE1572_7085 | 96 | 23 |
| SCE1572_2162 | 40 | 5 |
| SCE1572_9798 | 10 | 0 |
| SCE1572_11547 | 22.41 | 1.49 |
| SCE1572_5635 | 868 | 261 |
| SCE1572_3451 | 98 | 8 |
| SCE1572_9499 | 337 | 1134 |
| SCE1572_353 | 47 | 8 |
| SCE1572_4594 | 135 | 49 |
| SCE1572_568 | 17 | 50 |
| SCE1572_11407 | 78 | 18 |

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| SCE1572_3137 | 237 | 186 |
| SCE1572_855 | 429 | 1154 |
| SCE1572_11031 | 37 | 66 |
| SCE1572_8422 | 194 | 648 |
| SCE1572_7761 | 16 | 2 |
| SCE1572_9733 | 418 | 73 |
| SCE1572_7696 | 275 | 67 |
| SCE1572_3235 | 2704 | 907 |
| SCE1572_4007 | 191 | 196 |
| SCE1572_10745 | 42 | 13 |
| SCE1572_7709 | 2607 | 16428 |
| SCE1572_4292 | 53 | 12 |
| SCE1572_5750 | 51 | 3 |
| SCE1572_4854 | 27 | 8 |
| SCE1572_981 | 269 | 40 |
| SCE1572_1808 | 22 | 24 |
| SCE1572_9022 | 70 | 49 |
| SCE1572_379 | 75 | 142 |
| SCE1572_3993 | 13 | 15 |
| SCE1572_104 | 45 | 2 |
| SCE1572_1780 | 54 | 44 |
| SCE1572_11427 | 106 | 40 |
| SCE1572_7302 | 121 | 14 |
| SCE1572_9641 | 283 | 85 |
| SCE1572_5423 | 257 | 46 |
| SCE1572_3505 | 174 | 26 |
| SCE1572_493 | 132.07 | 8 |
| SCE1572_5997 | 63 | 52 |
| SCE1572_6565 | 36 | 9 |
| SCE1572_1450 | 17 | 19 |
| SCE1572_7448 | 131 | 81 |
| SCE1572_360 | 102 | 52 |
| SCE1572_7164 | 58 | 8 |
| SCE1572_9278 | 7 | 0 |
| SCE1572_1755 | 39 | 70 |
| SCE1572_6911 | 290 | 38 |
| SCE1572_2904 | 21 | 1 |
| SCE1572_5507 | 3 | 0 |
| SCE1572_9457 | 128 | 18 |
| SCE1572_10643 | 198 | 279 |
| SCE1572_9461 | 108 | 68 |
| SCE1572_3393 | 14 | 1 |
| SCE1572_5994 | 197 | 83 |
| SCE1572_9724 | 98 | 25 |
| SCE1572_3303 | 52 | 32 |
| SCE1572_9648 | 42 | 29 |
| SCE1572_8230 | 52 | 41 |
| SCE1572_7175 | 285 | 356 |

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| SCE1572_1597 | 259 | 51 |
| SCE1572_1772 | 171 | 21 |
| SCE1572_9230 | 80 | 9 |
| SCE1572_2218 | 256 | 156 |
| SCE1572_3856 | 293 | 62 |
| SCE1572_131 | 10 | 10 |
| SCE1572_2322 | 18 | 26 |
| SCE1572_10255 | 133 | 29 |
| SCE1572_7968 | 86 | 40 |
| SCE1572_8636 | 6 | 4 |
| SCE1572_4582 | 330 | 74 |
| SCE1572_6194 | 106 | 79 |
| SCE1572_9359 | 78 | 42 |
| SCE1572_11153 | 257 | 993 |
| SCE1572_5701 | 14 | 26 |
| SCE1572_10506 | 0 | 0 |
| SCE1572_3061 | 8 | 0 |
| SCE1572_5502 | 19 | 3 |
| SCE1572_7785 | 1 | 0 |
| SCE1572_8732 | 0 | 0 |
| SCE1572_6043 | 0 | 0 |
| SCE1572_3710 | 1743 | 23984 |
| SCE1572_6345 | 48 | 10 |
| SCE1572_5267 | 125 | 178 |
| SCE1572_9886 | 231 | 294 |
| SCE1572_471 | 39 | 33 |
| SCE1572_10559 | 8 | 3 |
| SCE1572_7470 | 169 | 69 |
| SCE1572_5319 | 133 | 21 |
| SCE1572_322 | 59 | 14 |
| SCE1572_2285 | 7 | 42 |
| SCE1572_3656 | 35 | 20 |
| SCE1572_5509 | 21 | 5 |
| SCE1572_6039 | 32 | 46 |
| SCE1572_3446 | 0 | 0 |
| SCE1572_9213 | 231 | 23 |
| SCE1572_8647 | 42 | 5 |
| SCE1572_1183 | 73 | 20 |
| SCE1572_549 | 0 | 0 |
| SCE1572_5579 | 163 | 42 |
| SCE1572_9783 | 105 | 60 |
| SCE1572_11086 | 169 | 145 |
| SCE1572_4567 | 112 | 40 |
| SCE1572_521 | 16 | 4 |
| SCE1572_9592 | 59 | 301 |
| SCE1572_8281 | 45 | 25 |
| SCE1572_4119 | 60 | 4942 |
| SCE1572_48 | 52 | 6 |

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| SCE1572_2892 | 78 | 17 |
| SCE1572_3724 | 39 | 311 |
| SCE1572_1474 | 45 | 5 |
| SCE1572_506 | 8 | 1 |
| SCE1572_7475 | 396 | 773 |
| SCE1572_1911 | 112 | 28 |
| SCE1572_3323 | 0 | 0 |
| SCE1572_11347 | 76 | 49 |
| SCE1572_9730 | 125 | 94 |
| SCE1572_9786 | 143 | 16 |
| SCE1572_2948 | 43 | 10 |
| SCE1572_4450 | 16 | 8 |
| SCE1572_5165 | 277 | 797 |
| SCE1572_4889 | 46 | 17 |
| SCE1572_901 | 65 | 14 |
| SCE1572_9353 | 129 | 168 |
| SCE1572_7189 | 196 | 48 |
| SCE1572_8641 | 140 | 26 |
| SCE1572_1814 | 48 | 6 |
| SCE1572_11280 | 100 | 294 |
| SCE1572_6133 | 210 | 630 |
| SCE1572_10760 | 11 | 96 |
| SCE1572_7355 | 466 | 166 |
| SCE1572_9941 | 31 | 15 |
| SCE1572_9029 | 111 | 16 |
| SCE1572_8331 | 137 | 249 |
| SCE1572_3312 | 69 | 35 |
| SCE1572_7168 | 259 | 276 |
| SCE1572_10801 | 0 | 0 |
| SCE1572_5901 | 144 | 36 |
| SCE1572_11265 | 230 | 287 |
| SCE1572_3314 | 138 | 52 |
| SCE1572_6845 | 222 | 413 |
| SCE1572_8800 | 37 | 1 |
| SCE1572_5637 | 129 | 26 |
| SCE1572_6046 | 373 | 322 |
| SCE1572_3087 | 13 | 4 |
| SCE1572_1642 | 19 | 7 |
| SCE1572_2744 | 49 | 172 |
| SCE1572_1090 | 57 | 9 |
| SCE1572_3961 | 359 | 215 |
| SCE1572_2570 | 20 | 0 |
| SCE1572_5773 | 0 | 0 |
| SCE1572_9200 | 0 | 0 |
| SCE1572_7656 | 7 | 3 |
| SCE1572_2844 | 3.5 | 0 |
| SCE1572_6331 | 67 | 215 |
| SCE1572_10931 | 34 | 10 |

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| SCE1572_3942 | 5898 | 3061 |
| SCE1572_6051 | 55 | 59 |
| SCE1572_10185 | 82 | 27 |
| SCE1572_6058 | 27 | 40 |
| SCE1572_9595 | 24 | 287 |
| SCE1572_8739 | 124 | 16 |
| SCE1572_3923 | 138 | 24 |
| SCE1572_595 | 88 | 11 |
| SCE1572_899 | 125 | 30 |
| SCE1572_8987 | 72 | 60 |
| SCE1572_4892 | 108 | 70 |
| SCE1572_11327 | 29 | 23 |
| SCE1572_1435 | 57 | 27 |
| SCE1572_3601 | 26 | 10 |
| SCE1572_5929 | 368 | 49 |
| SCE1572_9060 | 308 | 67 |
| SCE1572_11363 | 227 | 57 |
| SCE1572_141 | 46.02 | 3 |
| SCE1572_8533 | 152 | 33 |
| SCE1572_126 | 51 | 11 |
| SCE1572_6276 | 59 | 111 |
| SCE1572_8026 | 1 | 0 |
| SCE1572_7299 | 1002 | 249 |
| SCE1572_4599 | 6 | 0 |
| SCE1572_991 | 0 | 0 |
| SCE1572_1139 | 96 | 27 |
| SCE1572_10070 | 632 | 660 |
| SCE1572_806 | 0 | 0 |
| SCE1572_4994 | 106 | 23 |
| SCE1572_8445 | 26 | 9 |
| SCE1572_10567 | 135 | 37 |
| SCE1572_8520 | 28 | 1 |
| SCE1572_10369 | 389 | 67 |
| SCE1572_10311 | 10 | 1 |
| SCE1572_2005 | 112 | 327 |
| SCE1572_4882 | 114 | 33 |
| SCE1572_1555 | 0 | 0 |
| SCE1572_317 | 62 | 21 |
| SCE1572_445 | 128 | 22 |
| SCE1572_979 | 0 | 0 |
| SCE1572_7172 | 110 | 28 |
| SCE1572_1996 | 110 | 11 |
| SCE1572_6128 | 548 | 2368 |
| SCE1572_7133 | 193 | 35 |
| SCE1572_4811 | 92 | 91 |
| SCE1572_9762 | 47 | 33 |
| SCE1572_9982 | 99 | 25 |
| SCE1572_6171 | 102 | 30 |

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| SCE1572_8673 | 51 | 5 |
| SCE1572_3457 | 0 | 0 |
| SCE1572_5921 | 0 | 0 |
| SCE1572_9030 | 123 | 25 |
| SCE1572_7051 | 55 | 3 |
| SCE1572_2298 | 58 | 42 |
| SCE1572_264 | 41 | 20 |
| SCE1572_4590 | 4 | 0 |
| SCE1572_10212 | 107 | 22 |
| SCE1572_6004 | 76 | 100 |
| SCE1572_753 | 58 | 27 |
| SCE1572_7410 | 0 | 0 |
| SCE1572_5249 | 140 | 114 |
| SCE1572_9385 | 9 | 8 |
| SCE1572_9115 | 151 | 160 |
| SCE1572_7995 | 85 | 7 |
| SCE1572_6124 | 20 | 22 |
| SCE1572_11409 | 43 | 12 |
| SCE1572_2768 | 6 | 1 |
| SCE1572_7263 | 29 | 8 |
| SCE1572_50 | 42 | 4 |
| SCE1572_11533 | 69 | 12 |
| SCE1572_1765 | 43 | 2 |
| SCE1572_11082 | 70 | 50 |
| SCE1572_1741 | 327 | 149 |
| SCE1572_11488 | 147.7 | 19.18 |
| SCE1572_4447 | 164 | 42 |
| SCE1572_9371 | 37 | 18 |
| SCE1572_5386 | 93 | 26 |
| SCE1572_6626 | 60 | 34 |
| SCE1572_11525 | 52 | 13 |
| SCE1572_2136 | 51 | 3 |
| SCE1572_6787 | 102 | 42 |
| SCE1572_4190 | 121 | 84 |
| SCE1572_6664 | 102 | 33 |
| SCE1572_6784 | 312 | 82 |
| SCE1572_6752 | 19 | 7 |
| SCE1572_2705 | 13 | 6 |
| SCE1572_6641 | 90 | 26 |
| SCE1572_10376 | 116 | 10 |
| SCE1572_4902 | 38 | 10 |
| SCE1572_5791 | 121 | 59 |
| SCE1572_3153 | 0 | 0 |
| SCE1572_2163 | 34 | 8 |
| SCE1572_10382 | 48 | 19 |
| SCE1572_370 | 53 | 21 |
| SCE1572_2667 | 413 | 76 |
| SCE1572_2414 | 298 | 92 |

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| SCE1572_10814 | 46 | 23 |
| SCE1572_3057 | 47 | 5 |
| SCE1572_1897 | 6 | 2 |
| SCE1572_9753 | 41 | 4 |
| SCE1572_5089 | 17 | 11 |
| SCE1572_1294 | 131 | 32 |
| SCE1572_6144 | 0 | 0 |
| SCE1572_10140 | 59 | 27 |
| SCE1572_7114 | 108 | 28 |
| SCE1572_1279 | 104 | 16 |
| SCE1572_8887 | 17 | 0 |
| SCE1572_1823 | 18 | 19 |
| SCE1572_2123 | 88 | 53 |
| SCE1572_3187 | 4 | 0 |
| SCE1572_11415 | 45 | 10 |
| SCE1572_10345 | 72 | 21 |
| SCE1572_2913 | 773.95 | 95.11 |
| SCE1572_8498 | 0 | 0 |
| SCE1572_4505 | 1 | 0 |
| SCE1572_6241 | 40 | 17 |
| SCE1572_4745 | 84 | 85 |
| SCE1572_5622 | 122 | 88 |
| SCE1572_4859 | 124 | 15 |
| SCE1572_1619 | 316 | 1801 |
| SCE1572_9074 | 248 | 25 |
| SCE1572_4182 | 30 | 8 |
| SCE1572_6428 | 66 | 5 |
| SCE1572_1200 | 86 | 11 |
| SCE1572_2403 | 38 | 15 |
| SCE1572_169 | 122 | 119 |
| SCE1572_2147 | 134 | 20 |
| SCE1572_2858 | 250 | 261 |
| SCE1572_4319 | 110 | 7 |
| SCE1572_6771 | 6 | 4 |
| SCE1572_1600 | 83.99 | 36 |
| SCE1572_4320 | 156 | 40 |
| SCE1572_6639 | 21 | 3 |
| SCE1572_4314 | 98.48 | 13.09 |
| SCE1572_10287 | 1430 | 1003 |
| SCE1572_8750 | 0 | 0 |
| SCE1572_9152 | 127 | 68 |
| SCE1572_10723 | 174 | 83 |
| SCE1572_10154 | 177 | 501 |
| SCE1572_4874 | 775 | 1034 |
| SCE1572_7924 | 79 | 31 |
| SCE1572_9638 | 42 | 74 |
| SCE1572_8698 | 139 | 51 |
| SCE1572_2124 | 303 | 39 |

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| SCE1572_10576 | 861 | 140 |
| SCE1572_7635 | 2180 | 9329 |
| SCE1572_3774 | 99 | 15 |
| SCE1572_3716 | 339 | 50 |
| SCE1572_6299 | 17 | 7 |
| SCE1572_7686 | 4 | 0 |
| SCE1572_1274 | 18 | 2 |
| SCE1572_6252 | 239 | 142 |
| SCE1572_6609 | 56 | 20 |
| SCE1572_8885 | 1 | 0 |
| SCE1572_9557 | 59 | 209 |
| SCE1572_1612 | 31 | 22 |
| SCE1572_4571 | 47 | 15 |
| SCE1572_9830 | 0 | 0 |
| SCE1572_3278 | 69 | 98 |
| SCE1572_7391 | 144 | 25 |
| SCE1572_1209 | 64 | 5 |
| SCE1572_4821 | 110 | 7 |
| SCE1572_8572 | 0 | 0 |
| SCE1572_10330 | 0 | 0 |
| SCE1572_5988 | 0 | 0 |
| SCE1572_1259 | 10 | 1 |
| SCE1572_10106 | 332 | 651 |
| SCE1572_6438 | 1 | 0 |
| SCE1572_10783 | 126 | 32 |
| SCE1572_5617 | 172 | 30 |
| SCE1572_11470 | 44 | 15 |
| SCE1572_5981 | 32 | 22 |
| SCE1572_863 | 105 | 133 |
| SCE1572_531 | 99 | 302 |
| SCE1572_5798 | 134 | 20 |
| SCE1572_1124 | 98 | 14 |
| SCE1572_4062 | 106 | 325 |
| SCE1572_2718 | 199.98 | 30 |
| SCE1572_5647 | 84 | 17 |
| SCE1572_6612 | 18 | 4 |
| SCE1572_1527 | 27 | 32 |
| SCE1572_10927 | 191 | 283 |
| SCE1572_9542 | 11 | 3 |
| SCE1572_10666 | 117 | 152 |
| SCE1572_6060 | 92 | 41 |
| SCE1572_6409 | 10 | 0 |
| SCE1572_1104 | 57 | 60 |
| SCE1572_11551 | 2 | 0 |
| SCE1572_7721 | 28 | 68 |
| SCE1572_7035 | 172 | 22 |
| SCE1572_1782 | 12 | 31 |
| SCE1572_8268 | 1 | 0 |

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| SCE1572_2600 | 10 | 5 |
| SCE1572_555 | 97 | 31 |
| SCE1572_3953 | 126 | 71 |
| SCE1572_6219 | 75 | 16 |
| SCE1572_3345 | 715 | 2021 |
| SCE1572_3497 | 246 | 521 |
| SCE1572_3958 | 63 | 37 |
| SCE1572_10381 | 99 | 26 |
| SCE1572_3882 | 54 | 4 |
| SCE1572_8984 | 40 | 1 |
| SCE1572_10397 | 67 | 52 |
| SCE1572_281 | 100 | 34 |
| SCE1572_5312 | 206 | 47 |
| SCE1572_7361 | 8 | 7 |
| SCE1572_3675 | 0 | 0 |
| SCE1572_9396 | 431 | 430 |
| SCE1572_7738 | 332 | 140 |
| SCE1572_562 | 171 | 410 |
| SCE1572_6150 | 9 | 0 |
| SCE1572_7984 | 209 | 249 |
| SCE1572_8237 | 55 | 140 |
| SCE1572_542 | 75 | 3 |
| SCE1572_4936 | 34 | 25 |
| SCE1572_5663 | 112 | 11 |
| SCE1572_7736 | 39 | 43 |
| SCE1572_4300 | 257 | 59 |
| SCE1572_2611 | 66 | 16 |
| SCE1572_6117 | 42 | 15 |
| SCE1572_2682 | 74 | 21 |
| SCE1572_3574 | 46 | 10 |
| SCE1572_6739 | 1 | 0 |
| SCE1572_391 | 0 | 0 |
| SCE1572_8796 | 41 | 1 |
| SCE1572_7199 | 59 | 111 |
| SCE1572_9737 | 74 | 44 |
| SCE1572_3351 | 111 | 52 |
| SCE1572_3110 | 133 | 20 |
| SCE1572_9145 | 39 | 40 |
| SCE1572_3117 | 176 | 237 |
| SCE1572_4361 | 28 | 3 |
| SCE1572_9450 | 87 | 21 |
| SCE1572_4265 | 57 | 6 |
| SCE1572_5693 | 21 | 4 |
| SCE1572_9495 | 94 | 70 |
| SCE1572_9180 | 42 | 5 |
| SCE1572_10743 | 35 | 16 |
| SCE1572_2245 | 265.41 | 90 |
| SCE1572_3425 | 37 | 9 |

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| SCE1572_6412 | 59 | 9 |
| SCE1572_2924 | 320 | 61 |
| SCE1572_4915 | 240 | 1161 |
| SCE1572_9529 | 130 | 81 |
| SCE1572_9691 | 84 | 199 |
| SCE1572_1324 | 18 | 4 |
| SCE1572_4025 | 175 | 113 |
| SCE1572_2232 | 8 | 6 |
| SCE1572_8014 | 83 | 21 |
| SCE1572_9414 | 419 | 2759 |
| SCE1572_4791 | 145 | 46 |
| SCE1572_1212 | 29 | 10 |
| SCE1572_1130 | 0 | 0 |
| SCE1572_9997 | 423 | 366 |
| SCE1572_11055 | 130 | 181 |
| SCE1572_2436 | 21 | 45 |
| SCE1572_10706 | 121 | 52 |
| SCE1572_9771 | 22 | 7 |
| SCE1572_3241 | 165 | 22 |
| SCE1572_3565 | 0 | 0 |
| SCE1572_6551 | 36 | 2 |
| SCE1572_7797 | 95 | 33 |
| SCE1572_2047 | 0 | 0 |
| SCE1572_2638 | 215 | 49 |
| SCE1572_4737 | 79 | 171 |
| SCE1572_7326 | 80 | 64 |
| SCE1572_11410 | 63 | 12 |
| SCE1572_2962 | 1 | 0 |
| SCE1572_7866 | 441 | 906 |
| SCE1572_10452 | 81 | 114 |
| SCE1572_3192 | 156 | 72 |
| SCE1572_4075 | 48 | 57 |
| SCE1572_4837 | 178 | 182 |
| SCE1572_10618 | 131 | 53 |
| SCE1572_10698 | 51 | 91 |
| SCE1572_7161 | 39 | 9 |
| SCE1572_4645 | 230 | 168 |
| SCE1572_20 | 112 | 398 |
| SCE1572_3596 | 147.7 | 19.18 |
| SCE1572_2803 | 32 | 41 |
| SCE1572_1042 | 0 | 0 |
| SCE1572_4039 | 31 | 2 |
| SCE1572_257 | 40 | 6 |
| SCE1572_6813 | 323 | 55 |
| SCE1572_9420 | 45 | 110 |
| SCE1572_4325 | 51 | 10 |
| SCE1572_4781 | 1218 | 660 |
| SCE1572_9250 | 303 | 37 |

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| SCE1572_7950 | 188 | 119 |
| SCE1572_6192 | 54 | 21 |
| SCE1572_10920 | 25 | 25 |
| SCE1572_1731 | 519 | 86 |
| SCE1572_2107 | 159 | 134 |
| SCE1572_2605 | 24 | 4 |
| SCE1572_9055 | 84 | 11 |
| SCE1572_9209 | 103 | 141 |
| SCE1572_8759 | 241 | 331 |
| SCE1572_9245 | 7 | 0 |
| SCE1572_11065 | 2 | 4 |
| SCE1572_5198 | 0 | 0 |
| SCE1572_6931 | 6 | 0 |
| SCE1572_4783 | 557 | 110.67 |
| SCE1572_11061 | 3142.49 | 3711.59 |
| SCE1572_9485 | 60 | 45 |
| SCE1572_8830 | 185 | 262 |
| SCE1572_8374 | 39 | 35 |
| SCE1572_68 | 505 | 452 |
| SCE1572_11142 | 0 | 4 |
| SCE1572_6652 | 59 | 10 |
| SCE1572_7077 | 0 | 0 |
| SCE1572_2640 | 459 | 115 |
| SCE1572_2725 | 119 | 54 |
| SCE1572_3014 | 84 | 10 |
| SCE1572_450 | 73 | 20 |
| SCE1572_1795 | 144 | 232 |
| SCE1572_4101 | 350 | 2589 |
| SCE1572_8747 | 8 | 0 |
| SCE1572_5301 | 15 | 8 |
| SCE1572_1337 | 188 | 223 |
| SCE1572_11123 | 213 | 44 |
| SCE1572_2601 | 0 | 0 |
| SCE1572_3983 | 27 | 12 |
| SCE1572_3966 | 20 | 27 |
| SCE1572_4421 | 0 | 0 |
| SCE1572_5048 | 37 | 3 |
| SCE1572_5111 | 933 | 1147 |
| SCE1572_7320 | 41 | 5 |
| SCE1572_7500 | 21 | 12 |
| SCE1572_6916 | 40 | 17 |
| SCE1572_9912 | 40 | 5 |
| SCE1572_10536 | 81 | 164 |
| SCE1572_4331 | 19 | 3 |
| SCE1572_1539 | 110 | 57 |
| SCE1572_8220 | 172 | 64 |
| SCE1572_4487 | 91 | 59 |
| SCE1572_11000 | 19 | 3 |

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| SCE1572_8702 | 71 | 125 |
| SCE1572_9568 | 134 | 35 |
| SCE1572_10051 | 273 | 175 |
| SCE1572_10004 | 40 | 7 |
| SCE1572_9977 | 221 | 43 |
| SCE1572_336 | 76 | 20 |
| SCE1572_11574 | 107 | 51 |
| SCE1572_4822 | 0 | 0 |
| SCE1572_4353 | 295 | 241 |
| SCE1572_4919 | 67 | 7 |
| SCE1572_6558 | 59 | 16 |
| SCE1572_10821 | 0 | 0 |
| SCE1572_2291 | 369 | 479 |
| SCE1572_7956 | 63 | 116 |
| SCE1572_9425 | 46 | 13 |
| SCE1572_7896 | 2599 | 42290 |
| SCE1572_2971 | 90.05 | 17 |
| SCE1572_4511 | 111 | 27 |
| SCE1572_426 | 32 | 113 |
| SCE1572_6790 | 13 | 1 |
| SCE1572_5428 | 20 | 16 |
| SCE1572_7525 | 308 | 156 |
| SCE1572_9049 | 184 | 49 |
| SCE1572_512 | 11 | 0 |
| SCE1572_3862 | 87 | 67 |
| SCE1572_6090 | 44 | 396 |
| SCE1572_9185 | 15 | 0 |
| SCE1572_4637 | 130 | 41 |
| SCE1572_7396 | 187 | 61 |
| SCE1572_10907 | 356 | 1075 |
| SCE1572_3257 | 51 | 10 |
| SCE1572_929 | 105 | 87 |
| SCE1572_5896 | 110 | 11 |
| SCE1572_11331 | 44 | 34 |
| SCE1572_10064 | 0 | 0 |
| SCE1572_3484 | 36 | 10 |
| SCE1572_8715 | 147 | 62 |
| SCE1572_9419 | 73 | 344 |
| SCE1572_5091 | 263 | 254 |
| SCE1572_8637 | 119 | 49 |
| SCE1572_6507 | 191 | 40 |
| SCE1572_10407 | 43 | 26 |
| SCE1572_9222 | 88 | 34 |
| SCE1572_1467 | 478 | 344 |
| SCE1572_2398 | 103 | 657 |
| SCE1572_7251 | 0 | 0 |
| SCE1572_5399 | 0 | 0 |
| SCE1572_10400 | 74 | 252 |

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| SCE1572_4243 | 77 | 18 |
| SCE1572_2424 | 349 | 260 |
| SCE1572_294 | 0 | 0 |
| SCE1572_8473 | 153 | 25 |
| SCE1572_8162 | 2 | 3 |
| SCE1572_4395 | 0 | 0 |
| SCE1572_8868 | 146 | 25 |
| SCE1572_2685 | 0 | 0 |
| SCE1572_7221 | 12 | 42 |
| SCE1572_1197 | 543 | 64 |
| SCE1572_11198 | 63 | 23 |
| SCE1572_2631 | 140 | 34 |
| SCE1572_10139 | 0 | 0 |
| SCE1572_9005 | 19 | 3 |
| SCE1572_8391 | 141 | 24 |
| SCE1572_8136 | 10 | 2 |
| SCE1572_10769 | 9 | 3 |
| SCE1572_4632 | 91 | 17 |
| SCE1572_5107 | 153 | 97 |
| SCE1572_10960 | 13 | 4 |
| SCE1572_10903 | 49 | 8 |
| SCE1572_4613 | 92 | 21 |
| SCE1572_5029 | 91 | 149 |
| SCE1572_10967 | 63 | 12 |
| SCE1572_4385 | 376 | 70 |
| SCE1572_7560 | 104 | 18 |
| SCE1572_7401 | 13 | 450 |
| SCE1572_8207 | 62 | 32 |
| SCE1572_4532 | 0 | 0 |
| SCE1572_3216 | 139 | 92 |
| SCE1572_6303 | 1 | 0 |
| SCE1572_2040 | 129 | 340 |
| SCE1572_7043 | 49 | 317 |
| SCE1572_6022 | 0 | 0 |
| SCE1572_8344 | 39 | 4 |
| SCE1572_1011 | 42 | 6 |
| SCE1572_10174 | 0 | 0 |
| SCE1572_1063 | 19 | 5 |
| SCE1572_8443 | 10 | 2 |
| SCE1572_9138 | 35 | 2 |
| SCE1572_615 | 2 | 0 |
| SCE1572_10350 | 11 | 3 |
| SCE1572_3165 | 200 | 31 |
| SCE1572_3794 | 33 | 8 |
| SCE1572_5150 | 52 | 3 |
| SCE1572_6257 | 42 | 10 |
| SCE1572_9988 | 44 | 9 |
| SCE1572_894 | 184 | 121 |

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| SCE1572_9474 | 217 | 1120 |
| SCE1572_8585 | 26 | 7 |
| SCE1572_10426 | 7 | 4 |
| SCE1572_5071 | 197 | 134 |
| SCE1572_2272 | 143 | 102 |
| SCE1572_10750 | 25 | 14 |
| SCE1572_8515 | 48.38 | 15.9 |
| SCE1572_6029 | 180 | 241 |
| SCE1572_5278 | 40 | 9 |
| SCE1572_2156 | 6 | 7 |
| SCE1572_2015 | 5 | 2 |
| SCE1572_3849 | 66 | 2 |
| SCE1572_4604 | 93 | 52 |
| SCE1572_2987 | 181 | 225 |
| SCE1572_2329 | 133 | 33 |
| SCE1572_3356 | 19 | 2 |
| SCE1572_10308 | 51 | 3 |
| SCE1572_7715 | 32 | 1 |
| SCE1572_7644 | 218 | 78 |
| SCE1572_10325 | 104 | 61 |
| SCE1572_7438 | 347 | 1317 |
| SCE1572_2526 | 43 | 4 |
| SCE1572_8878 | 45 | 8 |
| SCE1572_8837 | 14 | 4 |
| SCE1572_6249 | 9 | 1 |
| SCE1572_9174 | 154 | 69 |
| SCE1572_11119 | 426 | 688 |
| SCE1572_2585 | 53 | 6 |
| SCE1572_10735 | 13 | 6 |
| SCE1572_3646 | 113 | 88 |
| SCE1572_416 | 126 | 26 |
| SCE1572_6683 | 100 | 231 |
| SCE1572_9588 | 402 | 173 |
| SCE1572_3135 | 14 | 9 |
| SCE1572_9400 | 9 | 12 |
| SCE1572_8328 | 0 | 0 |
| SCE1572_3492 | 0 | 0 |
| SCE1572_393 | 42 | 8 |
| SCE1572_9850 | 0 | 0 |
| SCE1572_1697 | 59 | 26 |
| SCE1572_11007 | 282 | 218 |
| SCE1572_6234 | 84 | 25 |
| SCE1572_10360 | 145 | 77 |
| SCE1572_3075 | 115 | 30 |
| SCE1572_9632 | 311 | 340 |
| SCE1572_8067 | 17 | 4 |
| SCE1572_3639 | 17 | 12 |
| SCE1572_11024 | 127 | 142 |

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| SCE1572_4518 | 248 | 152 |
| SCE1572_9313 | 91 | 33 |
| SCE1572_9105 | 76 | 55 |
| SCE1572_5778 | 74 | 38 |
| SCE1572_8545 | 112 | 35 |
| SCE1572_2328 | 56 | 22 |
| SCE1572_4660 | 74 | 498 |
| SCE1572_2886 | 103 | 34 |
| SCE1572_6515 | 22 | 2 |
| SCE1572_716 | 315 | 58 |
| SCE1572_11100 | 173 | 180 |
| SCE1572_10532 | 0 | 0 |
| SCE1572_10470 | 22 | 11 |
| SCE1572_7912 | 281 | 14 |
| SCE1572_10337 | 15 | 0 |
| SCE1572_7947 | 13 | 0 |
| SCE1572_2083 | 1 | 0 |
| SCE1572_1110 | 1 | 0 |
| SCE1572_8827 | 23.45 | 0 |
| SCE1572_2194 | 20 | 5 |
| SCE1572_10030 | 60 | 8 |
| SCE1572_3730 | 0 | 0 |
| SCE1572_8507 | 33 | 3 |
| SCE1572_2461 | 43.67 | 0 |
| SCE1572_6034 | 244 | 181 |
| SCE1572_95 | 25 | 2 |
| SCE1572_2784 | 119 | 12 |
| SCE1572_8157 | 54 | 2 |
| SCE1572_10079 | 54 | 4 |
| SCE1572_9866 | 75 | 52 |
| SCE1572_8146 | 52 | 21 |
| SCE1572_10516 | 947 | 197 |
| SCE1572_4218 | 41 | 72 |
| SCE1572_9367 | 88 | 14 |
| SCE1572_4778 | 31 | 43 |
| SCE1572_1635 | 18 | 8 |
| SCE1572_10025 | 41 | 28 |
| SCE1572_5114 | 395 | 487 |
| SCE1572_10477 | 26 | 33 |
| SCE1572_455 | 59 | 19 |
| SCE1572_420 | 28 | 9 |
| SCE1572_8500 | 31 | 1 |
| SCE1572_2734 | 643 | 501 |
| SCE1572_1309 | 4762.36 | 14491.82 |
| SCE1572_3739 | 2 | 0 |
| SCE1572_10881 | 0 | 0 |
| SCE1572_5343 | 135 | 52 |
| SCE1572_10119 | 74 | 27 |

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| SCE1572_4197 | 116 | 47 |
| SCE1572_6065 | 0 | 0 |
| SCE1572_10447 | 208 | 110 |
| SCE1572_919 | 64 | 44 |
| SCE1572_7846 | 3 | 1 |
| SCE1572_10622 | 317 | 99 |
| SCE1572_8994 | 77 | 53 |
| SCE1572_7248 | 16 | 2 |
| SCE1572_7569 | 124 | 46 |
| SCE1572_11422 | 80 | 33 |
| SCE1572_7070 | 1 | 0 |
| SCE1572_11586 | 223 | 217 |
| SCE1572_910 | 665.17 | 166.09 |
| SCE1572_1202 | 58 | 8 |
| SCE1572_11136 | 143 | 81 |
| SCE1572_7782 | 0 | 0 |
| SCE1572_1236 | 288 | 133 |
| SCE1572_9647 | 773 | 393 |
| SCE1572_1985 | 562 | 10967 |
| SCE1572_7882 | 69.57 | 46.42 |
| SCE1572_7145 | 142 | 40 |
| SCE1572_2384 | 89 | 68 |
| SCE1572_236 | 3 | 0 |
| SCE1572_2647 | 225 | 84 |
| SCE1572_1819 | 111 | 25 |
| SCE1572_2377 | 34 | 84 |
| SCE1572_7936 | 52 | 9 |
| SCE1572_2356 | 180 | 266 |
| SCE1572_9303 | 182 | 438 |
| SCE1572_5814 | 84 | 16 |
| SCE1572_1463 | 96 | 58 |
| SCE1572_10889 | 98 | 63 |
| SCE1572_1495 | 0 | 0 |
| SCE1572_1663 | 0 | 0 |
| SCE1572_11029 | 3 | 0 |
| SCE1572_1707 | 1776 | 174 |
| SCE1572_9228 | 0 | 0 |
| SCE1572_153 | 37 | 9 |
| SCE1572_2861 | 0 | 0 |
| SCE1572_723 | 57 | 8 |
| SCE1572_2308 | 116 | 128 |
| SCE1572_604 | 209 | 253 |
| SCE1572_679 | 85 | 36 |
| SCE1572_10686 | 81 | 163 |
| SCE1572_1971 | 27 | 16 |
| SCE1572_10373 | 154 | 78 |
| SCE1572_4806 | 369 | 493 |
| SCE1572_5487 | 110 | 32 |

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| SCE1572_1965 | 67 | 9 |
| SCE1572_5539 | 192 | 190 |
| SCE1572_10759 | 6 | 6 |
| SCE1572_173 | 14 | 0 |
| SCE1572_6537 | 53 | 15 |
| SCE1572_10794 | 40 | 21 |
| SCE1572_3764 | 206 | 44 |
| SCE1572_6084 | 37 | 18 |
| SCE1572_693 | 171 | 52 |
| SCE1572_666 | 178 | 304 |
| SCE1572_1978 | 58 | 257 |
| SCE1572_3896 | 273 | 751 |
| SCE1572_10251 | 1 | 0 |
| SCE1572_5291 | 9 | 4 |
| SCE1572_1394 | 79 | 118 |
| SCE1572_4340 | 185 | 29 |
| SCE1572_10897 | 45 | 40 |
| SCE1572_682 | 191 | 19 |
| SCE1572_7292 | 21 | 4 |
| SCE1572_9259 | 70 | 18 |
| SCE1572_8790 | 184 | 95 |
| SCE1572_7469 | 125 | 57 |
| SCE1572_6260 | 184 | 39 |
| SCE1572_1956 | 14 | 2 |
| SCE1572_2918 | 16 | 6 |
| SCE1572_2174 | 81 | 10 |
| SCE1572_6393 | 312 | 241 |
| SCE1572_8176 | 248 | 27 |
| SCE1572_3842 | 35 | 15 |
| SCE1572_9839 | 0 | 0 |
| SCE1572_9291 | 30 | 60 |
| SCE1572_2569 | 14 | 6 |
| SCE1572_5878 | 104 | 31 |
| SCE1572_6621 | 43 | 12 |
| SCE1572_1250 | 21 | 9 |
| SCE1572_2481 | 472 | 1114 |
| SCE1572_1443 | 205 | 36 |
| SCE1572_9605 | 10 | 0 |
| SCE1572_2851 | 21 | 2 |
| SCE1572_4807 | 328 | 207 |
| SCE1572_5850 | 129 | 28 |
| SCE1572_11390 | 87 | 31 |
| SCE1572_3588 | 86 | 8 |
| SCE1572_11314 | 362 | 207 |
| SCE1572_9561 | 354 | 53 |
| SCE1572_10297 | 27 | 24 |
| SCE1572_2444 | 14 | 7 |
| SCE1572_5692 | 92 | 33 |

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| SCE1572_134 | 0 | 0 |
| SCE1572_2911 | 109 | 21 |
| SCE1572_6578 | 86 | 20 |
| SCE1572_8029 | 90 | 69 |
| SCE1572_10161 | 72 | 40 |
| SCE1572_7405 | 70 | 37 |
| SCE1572_9112 | 58 | 27 |
| SCE1572_4674 | 38 | 10 |
| SCE1572_7949 | 165 | 152 |
| SCE1572_2574 | 17 | 7 |
| SCE1572_8803 | 16 | 25 |
| SCE1572_4714 | 56 | 10 |
| SCE1572_1901 | 18 | 44 |
| SCE1572_4723 | 47 | 20 |
| SCE1572_6809 | 988 | 2496 |
| SCE1572_10509 | 36 | 46 |
| SCE1572_2391 | 75 | 892 |
| SCE1572_2743 | 84 | 57 |
| SCE1572_6907 | 70 | 12 |
| SCE1572_5152 | 0 | 0 |
| SCE1572_5867 | 81 | 12 |
| SCE1572_1846 | 28 | 6 |
| SCE1572_5743 | 29.09 | 93.21 |
| SCE1572_1734 | 12 | 2 |
| SCE1572_9620 | 8 | 2 |
| SCE1572_8600 | 3 | 1 |
| SCE1572_6169 | 0 | 0 |
| SCE1572_828 | 32 | 3 |
| SCE1572_8034 | 29 | 8 |
| SCE1572_742 | 123 | 106 |
| SCE1572_1727 | 243 | 81 |
| SCE1572_11246 | 216 | 21 |
| SCE1572_5776 | 110 | 105 |
| SCE1572_8817 | 0 | 0 |
| SCE1572_10285 | 16 | 15 |
| SCE1572_8917 | 53 | 64 |
| SCE1572_2543 | 130 | 25 |
| SCE1572_8198 | 1 | 0 |
| SCE1572_7195 | 143 | 20 |
| SCE1572_10630 | 134 | 22 |
| SCE1572_1356 | 149 | 354 |
| SCE1572_1508 | 85 | 10 |
| SCE1572_6883 | 171 | 58 |
| SCE1572_7908 | 0 | 0 |
| SCE1572_7578 | 31 | 75 |
| SCE1572_3102 | 8 | 9 |
| SCE1572_7803 | 1 | 0 |
| SCE1572_9840 | 64 | 0 |

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| SCE1572_11005 | 151 | 71 |
| SCE1572_9430 | 50 | 9 |
| SCE1572_7844 | 224 | 2837 |
| SCE1572_11045 | 30 | 5 |
| SCE1572_1832 | 24 | 11 |
| SCE1572_8052 | 70 | 3 |
| SCE1572_7489 | 9 | 33 |
| SCE1572_6724 | 95 | 51 |
| SCE1572_6093 | 72 | 12 |
| SCE1572_1386 | 0 | 0 |
| SCE1572_2617 | 56 | 218 |
| SCE1572_6804 | 70 | 13 |
| SCE1572_8992 | 75 | 50 |
| SCE1572_87 | 52 | 23 |
| SCE1572_9864 | 17 | 4 |
| SCE1572_2985 | 39 | 15 |
| SCE1572_1161 | 45 | 4 |
| SCE1572_10306 | 34 | 47 |
| SCE1572_2006 | 59 | 103 |
| SCE1572_3636 | 109 | 10 |
| SCE1572_5221 | 28 | 15 |
| SCE1572_9747 | 39 | 29 |
| SCE1572_6651 | 3 | 4 |
| SCE1572_6908 | 126 | 10 |
| SCE1572_7666 | 7 | 4 |
| SCE1572_10489 | 160 | 725 |
| SCE1572_214 | 61 | 5 |
| SCE1572_6837 | 54 | 46 |
| SCE1572_4950 | 76 | 22 |
| SCE1572_5054 | 19 | 7 |
| SCE1572_5492 | 97 | 32 |
| SCE1572_11260 | 270 | 125 |
| SCE1572_7117 | 199 | 49 |
| SCE1572_4705 | 25 | 10 |
| SCE1572_7616 | 207 | 124 |
| SCE1572_8172 | 48 | 8 |
| SCE1572_1056 | 106.42 | 31.86 |
| SCE1572_3252 | 665 | 195 |
| SCE1572_7940 | 438 | 322 |
| SCE1572_5188 | 77 | 853 |
| SCE1572_1119 | 64 | 7 |
| SCE1572_7815 | 3485 | 17984 |
| SCE1572_7580 | 45 | 70 |
| SCE1572_3920 | 183 | 24 |
| SCE1572_9293 | 78 | 84 |
| SCE1572_5832 | 54 | 39 |
| SCE1572_1481 | 77 | 17 |
| SCE1572_3558 | 10 | 0 |

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| SCE1572_3828 | 94 | 135 |
| SCE1572_1419 | 3 | 0 |
| SCE1572_419 | 78 | 63 |
| SCE1572_1501 | 0 | 0 |
| SCE1572_144 | 27 | 8 |
| SCE1572_5131 | 11 | 3 |
| SCE1572_6385 | 0 | 0 |
| SCE1572_4172 | 292 | 118 |
| SCE1572_10688 | 141 | 690 |
| SCE1572_4452 | 26 | 5 |
| SCE1572_8416 | 143 | 144 |
| SCE1572_3628 | 33 | 9 |
| SCE1572_3546 | 69 | 4 |
| SCE1572_5752 | 499 | 487 |
| SCE1572_5127 | 69 | 22 |
| SCE1572_620 | 164 | 107 |
| SCE1572_10809 | 3 | 3 |
| SCE1572_5722 | 40 | 16 |
| SCE1572_4957 | 3 | 1 |
| SCE1572_2253 | 452 | 242 |
| SCE1572_5957 | 31 | 17 |
| SCE1572_538 | 67 | 59 |
| SCE1572_4404 | 0 | 0 |
| SCE1572_11568 | 317 | 890 |
| SCE1572_8646 | 88 | 20 |
| SCE1572_10264 | 159 | 31 |
| SCE1572_5960 | 36 | 8 |
| SCE1572_3436 | 43 | 41 |
| SCE1572_9409 | 354 | 1529 |
| SCE1572_10671 | 21 | 2 |
| SCE1572_9235 | 36 | 3 |
| SCE1572_8910 | 92 | 20 |
| SCE1572_1180 | 24 | 15 |
| SCE1572_1006 | 162 | 169 |
| SCE1572_8278 | 61 | 18 |
| SCE1572_10454 | 0 | 0 |
| SCE1572_8689 | 75 | 28 |
| SCE1572_8458 | 488 | 1600 |
| SCE1572_2038 | 40 | 27 |
| SCE1572_3222 | 90 | 92 |
| SCE1572_1189 | 106 | 69 |
| SCE1572_347 | 63 | 59 |
| SCE1572_8846 | 30 | 20 |
| SCE1572_10979 | 104 | 54 |
| SCE1572_1401 | 69 | 23 |
| SCE1572_10677 | 20 | 25 |
| SCE1572_4966 | 12 | 8 |
| SCE1572_3038 | 235 | 31 |

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| SCE1572_957 | 191 | 260 |
| SCE1572_7710 | 30 | 36 |
| SCE1572_272 | 0 | 0 |
| SCE1572_4163 | 152 | 27 |
| SCE1572_5331 | 81 | 70 |
| SCE1572_1157 | 36 | 7 |
| SCE1572_2781 | 7 | 4 |
| SCE1572_920 | 1 | 0 |
| SCE1572_6623 | 148 | 41 |
| SCE1572_1314 | 275 | 1085 |
| SCE1572_9289 | 18 | 12 |
| SCE1572_4184 | 86 | 149 |
| SCE1572_1720 | 34 | 40 |
| SCE1572_5858 | 1 | 0 |
| SCE1572_3386 | 1 | 0 |
| SCE1572_1582 | 134 | 16 |
| SCE1572_3888 | 165 | 19 |
| SCE1572_9063 | 202 | 19 |
| SCE1572_8540 | 118 | 29 |
| SCE1572_3381 | 87 | 44 |
| SCE1572_8614 | 133 | 83 |
| SCE1572_10445 | 54 | 19 |
| SCE1572_2994 | 1 | 0 |
| SCE1572_3607 | 78 | 21 |
| SCE1572_3653 | 6 | 0 |
| SCE1572_9497 | 231 | 148 |
| SCE1572_2494 | 76 | 19 |
| SCE1572_3280 | 118 | 78 |
| SCE1572_5348 | 520 | 304 |
| SCE1572_8186 | 0 | 0 |
| SCE1572_10651 | 218 | 231 |
| SCE1572_2649 | 76 | 21 |
| SCE1572_9087 | 157 | 24 |
| SCE1572_4975 | 773 | 2406 |
| SCE1572_10757 | 100 | 41 |
| SCE1572_6868 | 24 | 3 |
| SCE1572_1518 | 152 | 47 |
| SCE1572_5017 | 88 | 39 |
| SCE1572_818 | 6 | 1 |
| SCE1572_791 | 150 | 284 |
| SCE1572_6863 | 139 | 21 |
| SCE1572_9922 | 0 | 0 |
| SCE1572_7428 | 58 | 11 |
| SCE1572_4034 | 278 | 109 |
| SCE1572_10238 | 56 | 10 |
| SCE1572_6815 | 165 | 30 |
| SCE1572_5764 | 197 | 43 |
| SCE1572_1690 | 18 | 4 |

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| SCE1572_2755 | 217 | 64 |
| SCE1572_7694 | 120 | 66 |
| SCE1572_10853 | 177 | 33 |
| SCE1572_1712 | 92 | 18 |
| SCE1572_2500 | 78 | 8 |
| SCE1572_627 | 101 | 53 |
| SCE1572_1093 | 32 | 18 |
| SCE1572_10611 | 9 | 9 |
| SCE1572_4248 | 105 | 122 |
| SCE1572_7066 | 147 | 15 |
| SCE1572_1044 | 14 | 9 |
| SCE1572_2109 | 42 | 138 |
| SCE1572_1679 | 134 | 174 |
| SCE1572_8848 | 216 | 50 |
| SCE1572_3688 | 277 | 39 |
| SCE1572_203 | 87 | 35 |
| SCE1572_2045 | 94 | 47 |
| SCE1572_9969 | 25 | 17 |
| SCE1572_4029 | 208 | 95 |
| SCE1572_7212 | 1 | 0 |
| SCE1572_5431 | 42 | 12 |
| SCE1572_2059 | 180 | 17 |
| SCE1572_2503 | 160 | 26 |
| SCE1572_3784 | 40 | 753 |
| SCE1572_6732 | 70 | 124 |
| SCE1572_2309 | 32 | 46 |
| SCE1572_657 | 991 | 343 |
| SCE1572_5021 | 266 | 440 |
| SCE1572_8215 | 14 | 1 |
| SCE1572_190 | 75 | 20 |
| SCE1572_7492 | 44 | 11 |
| SCE1572_4131 | 22 | 12 |
| SCE1572_7851 | 77 | 58 |
| SCE1572_10848 | 65 | 16 |
| SCE1572_4642 | 199 | 29 |
| SCE1572_4834 | 0 | 0 |
| SCE1572_9966 | 14 | 4 |
| SCE1572_2169 | 55 | 17 |
| SCE1572_10410 | 160 | 95 |
| SCE1572_654 | 0 | 0 |
| SCE1572_11296 | 88 | 37 |
| SCE1572_9302 | 36 | 24 |
| SCE1572_8085 | 0 | 0 |
| SCE1572_6190 | 146 | 23 |
| SCE1572_11209 | 54 | 24 |
| SCE1572_5737 | 211 | 106 |
| SCE1572_11285 | 68 | 659 |
| SCE1572_3339 | 518 | 3247 |

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| SCE1572_4082 | 0 | 0 |
| SCE1572_4785 | 147 | 71 |
| SCE1572_1210 | 2 | 0 |
| SCE1572_8377 | 0 | 0 |
| SCE1572_7706 | 41 | 18 |
| SCE1572_5872 | 501 | 201 |
| SCE1572_3520 | 6 | 0 |
| SCE1572_4410 | 0 | 0 |
| SCE1572_9490 | 142 | 88 |
| SCE1572_10860 | 392 | 272 |
| SCE1572_340 | 54 | 7 |
| SCE1572_6879 | 360 | 278 |
| SCE1572_11213 | 8 | 3 |
| SCE1572_4258 | 96 | 150 |
| SCE1572_4845 | 69 | 36 |
| SCE1572_8954 | 85 | 45 |
| SCE1572_4687 | 31 | 8 |
| SCE1572_6528 | 36 | 9 |
| SCE1572_10392 | 20 | 8 |
| SCE1572_1745 | 104 | 18 |
| SCE1572_4099 | 40 | 24 |
| SCE1572_197 | 76 | 137 |
| SCE1572_1627 | 930 | 344 |
| SCE1572_2875 | 49 | 29 |
| SCE1572_9368 | 16 | 1 |
| SCE1572_9294 | 89 | 326 |
| SCE1572_1923 | 62 | 19 |
| SCE1572_380 | 27 | 2 |
| SCE1572_7520 | 19 | 10 |
| SCE1572_11231 | 161.01 | 34 |
| SCE1572_3337 | 643 | 4123 |
| SCE1572_8876 | 556 | 72 |
| SCE1572_7182 | 111 | 14 |
| SCE1572_7246 | 80 | 30 |
| SCE1572_885 | 314 | 34 |
| SCE1572_5133 | 34 | 17 |
| SCE1572_8059 | 0 | 0 |
| SCE1572_6870 | 162 | 212 |
| SCE1572_3163 | 433 | 97 |
| SCE1572_3876 | 17 | 4 |
| SCE1572_639 | 157 | 64 |
| SCE1572_9447 | 0 | 0 |
| SCE1572_5748 | 73 | 38 |
| SCE1572_9472 | 226 | 74 |
| SCE1572_7104 | 175 | 35 |
| SCE1572_5464 | 100 | 18 |
| SCE1572_8622 | 105 | 40 |
| SCE1572_8517 | 65 | 13 |

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| SCE1572_11504 | 15 | 2 |
| SCE1572_10604 | 83 | 30 |
| SCE1572_4468 | 20 | 9 |
| SCE1572_8003 | 1111.32 | 178.16 |
| SCE1572_1572 | 275 | 70 |
| SCE1572_949 | 369.5 | 155.96 |
| SCE1572_8434 | 91 | 31 |
| SCE1572_6546 | 386 | 106 |
| SCE1572_7498 | 58 | 8 |
| SCE1572_7218 | 87 | 57 |
| SCE1572_7235 | 146 | 85 |
| SCE1572_8407 | 12 | 11 |
| SCE1572_10121 | 130 | 117 |
| SCE1572_3919 | 51 | 7 |
| SCE1572_510 | 102 | 42 |
| SCE1572_5307 | 60 | 27 |
| SCE1572_1103 | 365 | 132 |
| SCE1572_9013 | 1 | 0 |
| SCE1572_10273 | 153 | 141 |
| SCE1572_3972 | 72 | 55 |
| SCE1572_4635 | 46 | 9 |
| SCE1572_2651 | 149 | 21 |
| SCE1572_1936 | 325 | 116 |
| SCE1572_250 | 24 | 12 |
| SCE1572_10209 | 0 | 0 |
| SCE1572_10514 | 60 | 31 |
| SCE1572_5679 | 438 | 488 |
| SCE1572_4755 | 78 | 28 |
| SCE1572_2621 | 164 | 45 |
| SCE1572_8106 | 212 | 16 |
| SCE1572_4793 | 14 | 14 |
| SCE1572_3184 | 3 | 0 |
| SCE1572_1685 | 41 | 3 |
| SCE1572_2192 | 0 | 0 |
| SCE1572_8466 | 128 | 121 |
| SCE1572_2513 | 85 | 114 |
| SCE1572_1976 | 241 | 746 |
| SCE1572_4241 | 50 | 15 |
| SCE1572_1767 | 145 | 46 |
| SCE1572_5406 | 8 | 3 |
| SCE1572_3276 | 43 | 61 |
| SCE1572_6605 | 58 | 261 |
| SCE1572_8948 | 13 | 5 |
| SCE1572_1669 | 14 | 43 |
| SCE1572_1759 | 13 | 2 |
| SCE1572_5687 | 0 | 0 |
| SCE1572_3018 | 113 | 17 |
| SCE1572_3512 | 40 | 16 |

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| SCE1572_5204 | 177 | 173 |
| SCE1572_9161 | 23 | 20 |
| SCE1572_4968 | 68 | 8 |
| SCE1572_10035 | 11 | 2 |
| SCE1572_296 | 37 | 36 |
| SCE1572_4054 | 82 | 104 |
| SCE1572_3454 | 75.75 | 23 |
| SCE1572_1061 | 112 | 140 |
| SCE1572_5885 | 74 | 15 |
| SCE1572_6456 | 25 | 4 |
| SCE1572_833 | 146 | 108 |
| SCE1572_4078 | 58 | 13 |
| SCE1572_7601 | 96 | 38 |
| SCE1572_3269 | 51 | 118 |
| SCE1572_2599 | 182 | 44 |
| SCE1572_8901 | 44 | 25 |
| SCE1572_817 | 0 | 0 |
| SCE1572_7083 | 34 | 72 |
| SCE1572_2199 | 165 | 39 |
| SCE1572_9857 | 222 | 195 |
| SCE1572_3701 | 42 | 11 |
| SCE1572_6670 | 36 | 1 |
| SCE1572_6658 | 353 | 116 |
| SCE1572_10168 | 27 | 5 |
| SCE1572_5804 | 51 | 35 |
| SCE1572_7717 | 38 | 3 |
| SCE1572_38 | 247 | 353 |
| SCE1572_8169 | 98 | 10 |
| SCE1572_3365 | 36 | 5 |
| SCE1572_1367 | 92 | 81 |
| SCE1572_279 | 0 | 0 |
| SCE1572_4061 | 41 | 42 |
| SCE1572_7510 | 2 | 0 |
| SCE1572_4397 | 66 | 16 |
| SCE1572_1348 | 477 | 898 |
| SCE1572_4852 | 21 | 13 |
| SCE1572_5272 | 114 | 19 |
| SCE1572_11252 | 0 | 0 |
| SCE1572_6027 | 18 | 7 |
| SCE1572_1680 | 160 | 470 |
| SCE1572_8123 | 4 | 0 |
| SCE1572_1895 | 39 | 7 |
| SCE1572_9617 | 62 | 17 |
| SCE1572_7691 | 34 | 38 |
| SCE1572_6076 | 0 | 0 |
| SCE1572_2145 | 107 | 183 |
| SCE1572_3285 | 90 | 43 |
| SCE1572_4947 | 38 | 33 |

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| SCE1572_8660 | 10 | 4 |
| SCE1572_10870 | 79 | 6 |
| SCE1572_2773 | 879 | 167 |
| SCE1572_4342 | 122 | 32 |
| SCE1572_1653 | 44 | 0 |
| SCE1572_5418 | 37 | 17 |
| SCE1572_9043 | 31 | 18 |
| SCE1572_5658 | 339 | 62 |
| SCE1572_7704 | 13 | 6 |
| SCE1572_1673 | 176 | 273 |
| SCE1572_4592 | 70 | 69 |
| SCE1572_8970 | 82 | 514 |
| SCE1572_8861 | 1305 | 188 |
| SCE1572_1429 | 43 | 39 |
| SCE1572_5147 | 62 | 1 |
| SCE1572_4009 | 164 | 32 |
| SCE1572_1476 | 101 | 13 |
| SCE1572_3800 | 0 | 0 |
| SCE1572_6561 | 37 | 3 |
| SCE1572_10320 | 16 | 1 |
| SCE1572_6480 | 158 | 75 |
| SCE1572_1860 | 140 | 89 |
| SCE1572_3911 | 168 | 772 |
| SCE1572_704 | 158 | 268 |
| SCE1572_6224 | 87 | 135 |
| SCE1572_9405 | 73 | 12 |
| SCE1572_10067 | 980 | 1074 |
| SCE1572_5102 | 136 | 222 |
| SCE1572_644 | 173 | 137 |
| SCE1572_9563 | 91 | 17 |
| SCE1572_3441 | 62 | 75 |
| SCE1572_5585 | 104 | 8 |
| SCE1572_4407 | 12 | 2 |
| SCE1572_5353 | 126 | 97 |
| SCE1572_9099 | 860 | 4723 |
| SCE1572_10918 | 19 | 42 |
| SCE1572_873 | 12 | 0 |
| SCE1572_3330 | 36 | 207 |
| SCE1572_10877 | 176 | 38 |
| SCE1572_834 | 58 | 67 |
| SCE1572_1424 | 51 | 90 |
| SCE1572_2366 | 226 | 64 |
| SCE1572_4162 | 120 | 35 |
| SCE1572_7374 | 11 | 5 |
| SCE1572_7347 | 20 | 3 |
| SCE1572_8566 | 63 | 82 |
| SCE1572_200 | 49 | 18 |
| SCE1572_10095 | 24 | 181 |

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| SCE1572_9680 | 692 | 900 |
| SCE1572_5376 | 129 | 20 |
| SCE1572_7098 | 110 | 33 |
| SCE1572_10260 | 36 | 8 |
| SCE1572_6966 | 67 | 21 |
| SCE1572_3201 | 17 | 0 |
| SCE1572_4589 | 25 | 6 |
| SCE1572_7758 | 24 | 1 |
| SCE1572_5944 | 134 | 27 |
| SCE1572_11326 | 49 | 6 |
| SCE1572_5031 | 563 | 1950 |
| SCE1572_2228 | 231 | 127 |
| SCE1572_8696 | 0 | 0 |
| SCE1572_7015 | 17 | 7 |
| SCE1572_6009 | 76 | 85 |
| SCE1572_9577 | 3 | 1 |
| SCE1572_5917 | 143 | 199 |
| SCE1572_7441 | 142 | 9 |
| SCE1572_8402 | 131 | 28 |
| SCE1572_10156 | 43 | 44 |
| SCE1572_2266 | 105 | 46 |
| SCE1572_1392 | 36 | 4 |
| SCE1572_2203 | 78 | 214 |
| SCE1572_5593 | 91 | 15 |
| SCE1572_11493 | 81 | 13 |
| SCE1572_7386 | 126 | 22 |
| SCE1572_4294 | 273 | 70 |
| SCE1572_9195 | 75 | 18 |
| SCE1572_4766 | 168 | 86 |
| SCE1572_2518 | 247 | 97 |
| SCE1572_3697 | 23 | 8 |
| SCE1572_2050 | 93 | 25 |
| SCE1572_1549 | 99 | 78 |
| SCE1572_9662 | 228 | 532 |
| SCE1572_10246 | 0 | 0 |
| SCE1572_974 | 0 | 0 |
| SCE1572_2234 | 95 | 23 |
| SCE1572_7973 | 13 | 0 |
| SCE1572_10465 | 111 | 22 |
| SCE1572_9903 | 120 | 58 |
| SCE1572_5219 | 3 | 1 |
| SCE1572_6062 | 205 | 224 |
| SCE1572_7305 | 155 | 25 |
| SCE1572_6945 | 5 | 0 |
| SCE1572_3931 | 767 | 1034 |
| SCE1572_6985 | 58 | 2 |
| SCE1572_4238 | 0 | 0 |
| SCE1572_1568 | 230 | 70 |

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| SCE1572_1246 | 42 | 3 |
| SCE1572_1839 | 5 | 1 |
| SCE1572_9277 | 66 | 17 |
| SCE1572_4206 | 259 | 296 |
| SCE1572_3665 | 0 | 0 |
| SCE1572_11161 | 147 | 36 |
| SCE1572_436 | 97 | 32 |
| SCE1572_5171 | 108 | 233 |
| SCE1572_6461 | 110 | 36 |
| SCE1572_566 | 181 | 55 |
| SCE1572_8932 | 81 | 49 |
| SCE1572_2698 | 58 | 7 |
| SCE1572_1857 | 0 | 0 |
| SCE1572_7679 | 108 | 167 |
| SCE1572_5236 | 216 | 147 |
| SCE1572_9535 | 0 | 0 |
| SCE1572_4657 | 38 | 75 |
| SCE1572_75 | 18 | 4 |
| SCE1572_10868 | 164 | 17 |
| SCE1572_2028 | 123 | 202 |
| SCE1572_3815 | 1190 | 4171 |
| SCE1572_9242 | 5 | 1 |
| SCE1572_1158 | 33 | 5 |
| SCE1572_2820 | 212 | 228 |
| SCE1572_3461 | 62 | 8 |
| SCE1572_1879 | 33 | 16 |
| SCE1572_3813 | 0 | 0 |
| SCE1572_3478 | 76 | 108 |
| SCE1572_6799 | 153 | 18 |
| SCE1572_3391 | 16 | 10 |
| SCE1572_2767 | 30 | 18 |
| SCE1572_7451 | 40 | 37 |
| SCE1572_10217 | 50 | 135 |
| SCE1572_6266 | 16 | 10 |
| SCE1572_29 | 68 | 46 |
| SCE1572_9708 | 131 | 120 |
| SCE1572_2375 | 7 | 6 |
| SCE1572_5935 | 142 | 19 |
| SCE1572_11374 | 210 | 1087 |
| SCE1572_1528 | 293 | 120 |
| SCE1572_10869 | 179 | 18 |
| SCE1572_4221 | 138 | 445 |
| SCE1572_9361 | 0 | 0 |
| SCE1572_10240 | 0 | 0 |
| SCE1572_2658 | 687 | 217 |
| SCE1572_4290 | 15.61 | 13 |
| SCE1572_8488 | 358 | 70 |
| SCE1572_6013 | 74 | 59 |

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| SCE1572_9376 | 2 | 0 |
| SCE1572_2248 | 288.03 | 42 |
| SCE1572_5910 | 102 | 110 |
| SCE1572_2800 | 292 | 45 |
| SCE1572_9713 | 27 | 203 |
| SCE1572_244 | 54.71 | 10 |
| SCE1572_11033 | 37 | 7 |
| SCE1572_7763 | 0 | 0 |
| SCE1572_11545 | 103 | 22 |
| SCE1572_5094 | 165 | 348 |
| SCE1572_4 | 167 | 268 |
| SCE1572_3677 | 27 | 7 |
| SCE1572_10789 | 82 | 86 |
| SCE1572_5002 | 272 | 802 |
| SCE1572_5338 | 18 | 2 |
| SCE1572_8420 | 129 | 20 |
| SCE1572_1332 | 28 | 3 |
| SCE1572_7540 | 175 | 181 |
| SCE1572_4695 | 11 | 4 |
| SCE1572_3139 | 17 | 399 |
| SCE1572_4288 | 33.87 | 27 |
| SCE1572_6701 | 251 | 33 |
| SCE1572_8411 | 52 | 38 |
| SCE1572_2642 | 99 | 24 |
| SCE1572_355 | 97 | 14 |
| SCE1572_827 | 37 | 6 |
| SCE1572_1665 | 226 | 177 |
| SCE1572_1567 | 5 | 0 |
| SCE1572_3737 | 56 | 6 |
| SCE1572_7464 | 412 | 162 |
| SCE1572_5470 | 301 | 22 |
| SCE1572_11478 | 297 | 167 |
| SCE1572_3248 | 7 | 1 |
| SCE1572_4938 | 2 | 0 |
| SCE1572_11188 | 1 | 0 |
| SCE1572_5975 | 46 | 24 |
| SCE1572_5472 | 193 | 33 |
| SCE1572_9938 | 2 | 0 |
| SCE1572_4480 | 42 | 14 |
| SCE1572_2450 | 38 | 1 |
| SCE1572_5787 | 27 | 67 |
| SCE1572_11113 | 59 | 4 |
| SCE1572_5043 | 28 | 50 |
| SCE1572_5553 | 67 | 12 |
| SCE1572_2614 | 47 | 22 |
| SCE1572_9018 | 117 | 33 |
| SCE1572_286 | 18 | 0 |
| SCE1572_7649 | 158 | 31 |

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| SCE1572_5411 | 19 | 4 |
| SCE1572_7484 | 54 | 23 |
| SCE1572_77 | 49 | 9 |
| SCE1572_3938 | 339 | 151 |
| SCE1572_3904 | 0 | 0 |
| SCE1572_579 | 22 | 96 |
| SCE1572_10435 | 59 | 40 |
| SCE1572_1036 | 67 | 8 |
| SCE1572_7825 | 30 | 9 |
| SCE1572_1099 | 83 | 143 |
| SCE1572_4237 | 67 | 26 |
| SCE1572_7366 | 285 | 1832 |
| SCE1572_6590 | 6 | 5 |
| SCE1572_2430 | 125 | 85 |
| SCE1572_6633 | 1294 | 152 |
| SCE1572_7587 | 325 | 1562 |
| SCE1572_5899 | 42 | 9 |
| SCE1572_6205 | 268 | 29 |
| SCE1572_4375 | 147 | 79 |
| SCE1572_1607 | 59 | 7 |
| SCE1572_3649 | 20 | 5 |
| SCE1572_3742 | 119 | 38 |
| SCE1572_6313 | 102 | 17 |
| SCE1572_11304 | 134 | 137 |
| SCE1572_8776 | 70 | 5 |
| SCE1572_10592 | 43 | 3 |
| SCE1572_3404 | 30 | 17 |
| SCE1572_4384 | 65 | 11 |
| SCE1572_9933 | 197 | 60 |
| SCE1572_9333 | 40 | 184 |
| SCE1572_2934 | 167 | 241 |
| SCE1572_4545 | 116 | 8 |
| SCE1572_8596 | 12 | 1 |
| SCE1572_11211 | 165 | 28 |
| SCE1572_5515 | 458 | 79 |
| SCE1572_6464 | 59 | 8 |
| SCE1572_7902 | 38 | 4 |
| SCE1572_3208 | 106 | 285 |
| SCE1572_11277 | 43 | 42 |
| SCE1572_9652 | 107 | 36 |
| SCE1572_5294 | 92 | 14 |
| SCE1572_7505 | 114 | 28 |
| SCE1572_3528 | 54 | 3028 |
| SCE1572_9676 | 5 | 3 |
| SCE1572_1980 | 341 | 908 |
| SCE1572_11369 | 38 | 2 |
| SCE1572_4012 | 186 | 59 |
| SCE1572_9876 | 8 | 1 |

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| SCE1572_11225 | 68 | 19 |
| SCE1572_8295 | 106 | 113 |
| SCE1572_8767 | 19 | 2 |
| SCE1572_4540 | 278.1 | 53 |
| SCE1572_4209 | 148 | 195 |
| SCE1572_5210 | 6 | 1 |
| SCE1572_1644 | 43 | 17 |
| SCE1572_2536 | 140 | 57 |
| SCE1572_5640 | 566 | 87 |
| SCE1572_6431 | 278 | 61 |
| SCE1572_5829 | 58 | 4 |
| SCE1572_3444 | 588 | 84 |
| SCE1572_10583 | 7 | 0 |
| SCE1572_500 | 20 | 0 |
| SCE1572_5602 | 51 | 72 |
| SCE1572_9796 | 230 | 46 |
| SCE1572_5714 | 28 | 19 |
| SCE1572_6184 | 54 | 7 |
| SCE1572_6357 | 41 | 9 |
| SCE1572_10271 | 116 | 22 |
| SCE1572_1713 | 35 | 22 |
| SCE1572_4934 | 505 | 405 |
| SCE1572_3171 | 127 | 245 |
| SCE1572_8683 | 55 | 48 |
| SCE1572_8262 | 103 | 32 |
| SCE1572_10998 | 41 | 53 |
| SCE1572_1878 | 19 | 10 |
| SCE1572_4432 | 144 | 14 |
| SCE1572_844 | 278 | 397 |
| SCE1572_4621 | 97 | 193 |
| SCE1572_8363 | 175.04 | 24 |
| SCE1572_11511 | 113 | 44 |
| SCE1572_8042 | 56 | 8 |
| SCE1572_7547 | 114 | 23 |
| SCE1572_1092 | 0 | 0 |
| SCE1572_10941 | 95 | 9 |
| SCE1572_8315 | 75 | 24 |
| SCE1572_10547 | 40 | 10 |
| SCE1572_4603 | 325 | 705 |
| SCE1572_11320 | 41 | 2 |
| SCE1572_2525 | 60 | 16 |
| SCE1572_10571 | 481 | 448 |
| SCE1572_11013 | 97 | 46 |
| SCE1572_1361 | 154 | 245 |
| SCE1572_5355 | 36 | 18 |
| SCE1572_291 | 0 | 0 |
| SCE1572_8049 | 140 | 6 |
| SCE1572_3227 | 56 | 4 |

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| SCE1572_8072 | 56 | 10 |
| SCE1572_768 | 170 | 84 |
| SCE1572_2315 | 60 | 124 |
| SCE1572_4049 | 74 | 229 |
| SCE1572_4281 | 36 | 9 |
| SCE1572_952 | 7 | 8 |
| SCE1572_9603 | 25 | 2 |
| SCE1572_10831 | 132 | 36 |
| SCE1572_2906 | 312 | 30 |
| SCE1572_28 | 40 | 30 |
| SCE1572_5440 | 125 | 34 |
| SCE1572_4431 | 17 | 3 |
| SCE1572_9827 | 62 | 25 |
| SCE1572_9217 | 119 | 94 |
| SCE1572_634 | 203 | 293 |
| SCE1572_4944 | 26 | 25 |
| SCE1572_6167 | 53 | 7 |
| SCE1572_11168 | 117 | 35 |
| SCE1572_2814 | 116 | 269 |
| SCE1572_8310 | 103 | 19 |
| SCE1572_3176 | 107 | 57 |
| SCE1572_4231 | 323 | 65 |
| SCE1572_6527 | 0 | 0 |
| SCE1572_9945 | 2878 | 2192 |
| SCE1572_225 | 0 | 0 |
| SCE1572_11382 | 95 | 249 |
| SCE1572_367 | 55 | 50 |
| SCE1572_488 | 75.57 | 24.38 |
| SCE1572_770 | 67 | 59 |
| SCE1572_7848 | 117 | 56 |
| SCE1572_4169 | 195 | 227 |
| SCE1572_10951 | 144 | 68 |
| SCE1572_2439 | 25 | 20 |
| SCE1572_2333 | 154 | 147 |
| SCE1572_4141 | 43 | 10 |
| SCE1572_572 | 14 | 6 |
| SCE1572_3660 | 37 | 20 |
| SCE1572_6574 | 169 | 35 |
| SCE1572_10828 | 39 | 10 |
| SCE1572_515 | 153 | 17 |
| SCE1572_4768 | 61 | 14 |
| SCE1572_8079 | 10 | 0 |
| SCE1572_5243 | 5 | 0 |
| SCE1572_7954 | 106 | 4 |
| SCE1572_7832 | 48 | 126 |
| SCE1572_7312 | 37 | 10 |
| SCE1572_9143 | 532.64 | 156.41 |
| SCE1572_7284 | 39 | 1 |

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| SCE1572_7150 | 54 | 17 |
| SCE1572_6399 | 147 | 546 |
| SCE1572_3211 | 7 | 0 |
| SCE1572_10493 | 400 | 860 |
| SCE1572_4156 | 161 | 77 |
| SCE1572_6489 | 32 | 16 |
| SCE1572_10228 | 21 | 0 |
| SCE1572_6280 | 23 | 194 |
| SCE1572_1260 | 222 | 36 |
| SCE1572_5432 | 209 | 22 |
| SCE1572_5824 | 24 | 12 |
| SCE1572_8779 | 24 | 53 |
| SCE1572_7146 | 63 | 16 |
| SCE1572_11400 | 157 | 224 |
| SCE1572_6993 | 70 | 12 |
| SCE1572_10958 | 70 | 22 |
| SCE1572_8607 | 271 | 406 |
| SCE1572_3143 | 61 | 14 |
| SCE1572_5252 | 99 | 395 |
| SCE1572_58 | 125 | 48 |
| SCE1572_1861 | 71 | 26 |
| SCE1572_10475 | 124 | 81 |
| SCE1572_11424 | 38 | 93 |
| SCE1572_2881 | 82 | 25 |
| SCE1572_2787 | 85 | 167 |
| SCE1572_602 | 294 | 151 |
| SCE1572_2955 | 1 | 0 |
| SCE1572_2839 | 200 | 53 |
| SCE1572_585 | 96 | 52 |
| SCE1572_11199 | 13 | 0 |
| SCE1572_2792 | 84 | 14 |
| SCE1572_3776 | 186 | 78 |
| SCE1572_9198 | 56 | 14 |
| SCE1572_1987 | 9 | 2 |
| SCE1572_8450 | 101 | 14 |
| SCE1572_5012 | 26 | 49 |
| SCE1572_10687 | 6 | 4 |
| SCE1572_8304 | 58 | 17 |
| SCE1572_1701 | 308 | 213 |
| SCE1572_3769 | 71 | 252 |
| SCE1572_8505 | 45 | 17 |
| SCE1572_1494 | 120 | 27 |
| SCE1572_1881 | 45 | 4 |
| SCE1572_4958 | 46 | 3 |
| SCE1572_6216 | 130 | 26 |
| SCE1572_8710 | 24 | 9 |
| SCE1572_10894 | 20 | 16 |
| SCE1572_6547 | 457 | 223 |

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| SCE1572_2506 | 104 | 18 |
| SCE1572_2016 | 199 | 38 |
| SCE1572_5434 | 214 | 46 |
| SCE1572_6465 | 10 | 3 |
| SCE1572_10608 | 58 | 111 |
| SCE1572_4665 | 20 | 2 |
| SCE1572_8513 | 24.68 | 3.05 |
| SCE1572_2305 | 47 | 82 |
| SCE1572_4548 | 21 | 0 |
| SCE1572_2883 | 65 | 182 |
| SCE1572_10409 | 86 | 86 |
| SCE1572_5624 | 0 | 0 |
| SCE1572_2470 | 22 | 1 |
| SCE1572_6909 | 38 | 0 |
| SCE1572_4872 | 37 | 10 |
| SCE1572_369 | 13 | 1 |
| SCE1572_730 | 62 | 25 |
| SCE1572_1276 | 98 | 20 |
| SCE1572_8171 | 190 | 28 |
| SCE1572_5875 | 5 | 2 |
| SCE1572_1149 | 480 | 751 |
| SCE1572_3358 | 23 | 4 |
| SCE1572_5823 | 47 | 3 |
| SCE1572_2428 | 130 | 110 |
| SCE1572_9564 | 23 | 7 |
| SCE1572_5077 | 164 | 299 |
| SCE1572_1257 | 95 | 131 |
| SCE1572_5441 | 165 | 40 |
| SCE1572_6756 | 77 | 25 |
| SCE1572_5321 | 81 | 33 |
| SCE1572_8199 | 102 | 20 |
| SCE1572_7648 | 243 | 54 |
| SCE1572_7662 | 60 | 6 |
| SCE1572_10193 | 73 | 10 |
| SCE1572_8309 | 161 | 183 |
| SCE1572_32 | 33 | 7 |
| SCE1572_1194 | 150 | 85 |
| SCE1572_10317 | 39 | 11 |
| SCE1572_8724 | 116 | 28 |
| SCE1572_1907 | 78 | 94 |
| SCE1572_4174 | 12 | 5 |
| SCE1572_2441 | 219 | 74 |
| SCE1572_6154 | 70 | 4 |
| SCE1572_10733 | 12 | 49 |
| SCE1572_684 | 68 | 13 |
| SCE1572_9039 | 52 | 28 |
| SCE1572_10797 | 107 | 38 |
| SCE1572_11413 | 145 | 31 |

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| SCE1572_9508 | 58 | 12 |
| SCE1572_9890 | 224 | 42 |
| SCE1572_9501 | 546 | 663 |
| SCE1572_10790 | 479 | 715 |
| SCE1572_4216 | 1182 | 925 |
| SCE1572_7406 | 54 | 16 |
| SCE1572_530 | 207 | 49 |
| SCE1572_10776 | 525 | 312.99 |
| SCE1572_2201 | 169 | 587 |
| SCE1572_10062 | 392 | 491 |
| SCE1572_1453 | 307.05 | 59.43 |
| SCE1572_2736 | 37 | 30 |
| SCE1572_4804 | 181 | 31 |
| SCE1572_6225 | 63 | 17 |
| SCE1572_7432 | 45 | 24 |
| SCE1572_10491 | 380 | 488 |
| SCE1572_11449 | 254 | 349 |
| SCE1572_4273 | 148 | 41 |
| SCE1572_5581 | 200 | 325 |
| SCE1572_2553 | 157 | 29 |
| SCE1572_100 | 194 | 50 |
| SCE1572_1445 | 222 | 70 |
| SCE1572_2251 | 175 | 60 |
| SCE1572_7687 | 41 | 12 |
| SCE1572_7148 | 114 | 210 |
| SCE1572_2131 | 55 | 13 |
| SCE1572_5485 | 917 | 169 |
| SCE1572_9899 | 166 | 370 |
| SCE1572_2104 | 219 | 838 |
| SCE1572_8361 | 30 | 2 |
| SCE1572_4909 | 4 | 0 |
| SCE1572_10636 | 6 | 0 |
| SCE1572_5707 | 31 | 18 |
| SCE1572_7910 | 11 | 1 |
| SCE1572_2916 | 92 | 10 |
| SCE1572_7778 | 31 | 10 |
| SCE1572_7249 | 441 | 61 |
| SCE1572_9321 | 14 | 3 |
| SCE1572_7124 | 495 | 318 |
| SCE1572_2446 | 195 | 52 |
| SCE1572_4023 | 299 | 1299 |
| SCE1572_10364 | 25 | 37 |
| SCE1572_4898 | 47 | 9 |
| SCE1572_3428 | 24.85 | 14 |
| SCE1572_3880 | 117 | 35 |
| SCE1572_6086 | 1 | 0 |
| SCE1572_6531 | 79 | 30 |
| SCE1572_9268 | 87 | 55 |

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| SCE1572_11048 | 78 | 49 |
| SCE1572_3729 | 6 | 1 |
| SCE1572_9100 | 105 | 595 |
| SCE1572_3207 | 91 | 439 |
| SCE1572_2154 | 45 | 9 |
| SCE1572_6617 | 39 | 2 |
| SCE1572_2159 | 0 | 0 |
| SCE1572_2568 | 45 | 14 |
| SCE1572_614 | 35 | 11 |
| SCE1572_8179 | 0 | 0 |
| SCE1572_4013 | 123 | 129 |
| SCE1572_5812 | 466 | 135 |
| SCE1572_10280 | 102 | 385 |
| SCE1572_715 | 0 | 0 |
| SCE1572_11567 | 0 | 0 |
| SCE1572_10696 | 63 | 31 |
| SCE1572_665 | 39 | 17 |
| SCE1572_9855 | 234 | 44 |
| SCE1572_5007 | 1062 | 1049 |
| SCE1572_8923 | 8 | 2 |
| SCE1572_10476 | 72 | 71 |
| SCE1572_3527 | 59 | 9549 |
| SCE1572_9064 | 207 | 28 |
| SCE1572_4851 | 410 | 99 |
| SCE1572_2401 | 117 | 180 |
| SCE1572_4721 | 189 | 210 |
| SCE1572_2357 | 42 | 46 |
| SCE1572_1792 | 25 | 24 |
| SCE1572_9582 | 164 | 49 |
| SCE1572_216 | 80 | 94 |
| SCE1572_8325 | 180 | 170 |
| SCE1572_10327 | 25 | 2 |
| SCE1572_729 | 34 | 47 |
| SCE1572_7325 | 349 | 811 |
| SCE1572_1695 | 0 | 0 |
| SCE1572_8070 | 15.01 | 3 |
| SCE1572_11601 | 61 | 105 |
| SCE1572_1074 | 1 | 0 |
| SCE1572_4047 | 83 | 13 |
| SCE1572_1132 | 39 | 4 |
| SCE1572_6716 | 293 | 300 |
| SCE1572_5856 | 14 | 1 |
| SCE1572_10147 | 67 | 81 |
| SCE1572_7563 | 275 | 54 |
| SCE1572_4178 | 13.25 | 0.75 |
| SCE1572_5563 | 556 | 251 |
| SCE1572_4891 | 1 | 0 |
| SCE1572_9364 | 231 | 92 |

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| SCE1572_2176 | 103 | 15 |
| SCE1572_10572 | 39 | 25 |
| SCE1572_10899 | 5 | 0 |
| SCE1572_453 | 149 | 21 |
| SCE1572_9131 | 9 | 4 |
| SCE1572_6836 | 17 | 51 |
| SCE1572_8084 | 0 | 0 |
| SCE1572_8371 | 32 | 10 |
| SCE1572_9682 | 222 | 241 |
| SCE1572_11330 | 94 | 179 |
| SCE1572_362 | 135 | 32 |
| SCE1572_8077 | 36.62 | 3 |
| SCE1572_7562 | 38 | 3 |
| SCE1572_3860 | 52 | 42 |
| SCE1572_3627 | 98 | 12 |
| SCE1572_11429 | 155 | 46 |
| SCE1572_5109 | 75 | 90 |
| SCE1572_2521 | 52 | 7 |
| SCE1572_720 | 4 | 1 |
| SCE1572_537 | 159 | 152 |
| SCE1572_10482 | 58 | 9 |
| SCE1572_5104 | 87 | 105 |
| SCE1572_2399 | 501 | 1381 |
| SCE1572_8558 | 53 | 6 |
| SCE1572_2365 | 281 | 258 |
| SCE1572_8993 | 236 | 314 |
| SCE1572_2029 | 137 | 26 |
| SCE1572_5952 | 2 | 0 |
| SCE1572_4471 | 153 | 47 |
| SCE1572_6444 | 30 | 9 |
| SCE1572_9455 | 38 | 47 |
| SCE1572_2345 | 43 | 47 |
| SCE1572_5407 | 0 | 0 |
| SCE1572_1666 | 100 | 31 |
| SCE1572_11402 | 8 | 2 |
| SCE1572_4259 | 1 | 0 |
| SCE1572_435 | 137 | 164 |
| SCE1572_2653 | 112 | 28 |
| SCE1572_1693 | 6 | 1 |
| SCE1572_3720 | 177 | 64 |
| SCE1572_6011 | 112 | 97 |
| SCE1572_4148 | 33 | 93 |
| SCE1572_4671 | 0 | 0 |
| SCE1572_3585 | 56 | 8 |
| SCE1572_5961 | 42 | 20 |
| SCE1572_3460 | 106 | 49 |
| SCE1572_11114 | 211 | 307 |
| SCE1572_7919 | 209 | 22 |

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| SCE1572_11202 | 124 | 992 |
| SCE1572_896 | 0 | 0 |
| SCE1572_2964 | 135 | 1500 |
| SCE1572_2764 | 5 | 0 |
| SCE1572_4222 | 150 | 40 |
| SCE1572_3576 | 47 | 7 |
| SCE1572_37 | 30 | 19 |
| SCE1572_1537 | 33 | 31 |
| SCE1572_11558 | 243.31 | 48.37 |
| SCE1572_6178 | 55 | 128 |
| SCE1572_2413 | 56 | 108 |
| SCE1572_1116 | 0 | 0 |
| SCE1572_10539 | 200 | 52 |
| SCE1572_3760 | 51.08 | 1 |
| SCE1572_2485 | 75 | 80 |
| SCE1572_10459 | 17 | 29 |
| SCE1572_9732 | 283 | 35 |
| SCE1572_8586 | 99 | 12 |
| SCE1572_7610 | 115 | 154 |
| SCE1572_9779 | 0 | 0 |
| SCE1572_8639 | 90 | 128 |
| SCE1572_6026 | 69 | 60 |
| SCE1572_6560 | 0 | 0 |
| SCE1572_1735 | 217 | 55 |
| SCE1572_3968 | 204 | 42 |
| SCE1572_9537 | 56 | 71 |
| SCE1572_5359 | 52 | 231 |
| SCE1572_3019 | 49 | 11 |
| SCE1572_1655 | 0 | 0 |
| SCE1572_1304 | 285 | 236 |
| SCE1572_11255 | 322 | 256 |
| SCE1572_5968 | 7 | 1 |
| SCE1572_9254 | 95 | 16 |
| SCE1572_5151 | 1 | 0 |
| SCE1572_5753 | 0 | 0 |
| SCE1572_10425 | 28 | 14 |
| SCE1572_5894 | 32 | 2 |
| SCE1572_7458 | 75 | 24 |
| SCE1572_2091 | 11 | 0 |
| SCE1572_3820 | 118 | 32 |
| SCE1572_6570 | 52 | 19 |
| SCE1572_2387 | 77 | 21 |
| SCE1572_7595 | 156 | 351 |
| SCE1572_2968 | 60 | 55 |
| SCE1572_5483 | 127 | 11 |
| SCE1572_9919 | 64 | 12 |
| SCE1572_5362 | 46 | 35 |
| SCE1572_1977 | 1182 | 11889 |

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| SCE1572_4327 | 27 | 5 |
| SCE1572_16 | 113 | 97 |
| SCE1572_10289 | 178 | 83 |
| SCE1572_3564 | 251.03 | 36.16 |
| SCE1572_11366 | 43 | 7 |
| SCE1572_9382 | 0 | 0 |
| SCE1572_4422 | 14 | 3 |
| SCE1572_4204 | 14 | 103 |
| SCE1572_3538 | 30 | 6 |
| SCE1572_3470 | 93 | 16 |
| SCE1572_11519 | 108 | 22 |
| SCE1572_631 | 322 | 225 |
| SCE1572_10172 | 87 | 39 |
| SCE1572_11527 | 108 | 25 |
| SCE1572_11537 | 154 | 218 |
| SCE1572_8757 | 31 | 10 |
| SCE1572_5631 | 30 | 8 |
| SCE1572_7048 | 0 | 0 |
| SCE1572_4523 | 14 | 0 |
| SCE1572_66 | 123 | 84 |
| SCE1572_2703 | 193 | 45 |
| SCE1572_7743 | 253 | 504 |
| SCE1572_5819 | 81 | 16 |
| SCE1572_6375 | 214 | 17 |
| SCE1572_3893 | 19 | 3 |
| SCE1572_3210 | 17 | 19 |
| SCE1572_3138 | 75 | 409 |
| SCE1572_330 | 113 | 42 |
| SCE1572_751 | 87 | 38 |
| SCE1572_10219 | 184 | 67 |
| SCE1572_8481 | 37 | 13 |
| SCE1572_356 | 33 | 3 |
| SCE1572_11229 | 7 | 3 |
| SCE1572_2643 | 166 | 33 |
| SCE1572_17 | 19 | 25 |
| SCE1572_6848 | 81 | 2 |
| SCE1572_3734 | 149 | 8 |
| SCE1572_5066 | 415 | 317 |
| SCE1572_7398 | 115 | 220 |
| SCE1572_3141 | 402 | 63 |
| SCE1572_2822 | 43 | 16 |
| SCE1572_5919 | 86 | 81 |
| SCE1572_2089 | 36 | 8 |
| SCE1572_8441 | 117 | 101 |
| SCE1572_8661 | 313 | 57 |
| SCE1572_673 | 124 | 412 |
| SCE1572_9051 | 72 | 12 |
| SCE1572_3495 | 72 | 18 |

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| SCE1572_3981 | 83 | 32 |
| SCE1572_2495 | 166 | 31 |
| SCE1572_10667 | 36 | 8 |
| SCE1572_6666 | 209 | 412 |
| SCE1572_9541 | 41 | 7 |
| SCE1572_1888 | 30 | 142 |
| SCE1572_3287 | 24 | 0 |
| SCE1572_10134 | 17 | 3 |
| SCE1572_5162 | 0 | 0 |
| SCE1572_779 | 181 | 82 |
| SCE1572_2293 | 80 | 43 |
| SCE1572_4525 | 52 | 10 |
| SCE1572_5768 | 520 | 1511 |
| SCE1572_2007 | 36 | 21 |
| SCE1572_9808 | 1155 | 1413 |
| SCE1572_5244 | 61 | 53 |
| SCE1572_1387 | 293 | 70 |
| SCE1572_5656 | 75 | 9 |
| SCE1572_5038 | 194 | 798 |
| SCE1572_10939 | 364 | 198 |
| SCE1572_9417 | 539 | 3419 |
| SCE1572_6053 | 192 | 403 |
| SCE1572_3807 | 402 | 251 |
| SCE1572_2759 | 118 | 257 |
| SCE1572_2980 | 176 | 1064 |
| SCE1572_3682 | 50 | 1 |
| SCE1572_7089 | 73 | 27 |
| SCE1572_4662 | 128 | 14 |
| SCE1572_10402 | 474 | 410 |
| SCE1572_8138 | 77 | 14 |
| SCE1572_4736 | 175 | 590 |
| SCE1572_5610 | 45 | 1 |
| SCE1572_7507 | 82.36 | 11.5 |
| SCE1572_9121 | 51 | 6 |
| SCE1572_2340 | 0 | 0 |
| SCE1572_11093 | 164 | 40 |
| SCE1572_5217 | 254 | 35 |
| SCE1572_170 | 27 | 4 |
| SCE1572_10739 | 27 | 5 |
| SCE1572_7945 | 10 | 0 |
| SCE1572_11097 | 85 | 32 |
| SCE1572_9148 | 157 | 346 |
| SCE1572_231 | 1 | 0 |
| SCE1572_8875 | 10.49 | 0 |
| SCE1572_8333 | 155 | 107 |
| SCE1572_4558 | 98 | 105 |
| SCE1572_176 | 21 | 2 |
| SCE1572_765 | 15 | 36 |

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| SCE1572_2670 | 167 | 18 |
| SCE1572_10384 | 19 | 1 |
| SCE1572_1938 | 11 | 6 |
| SCE1572_6061 | 1085 | 1248 |
| SCE1572_10704 | 44 | 76 |
| SCE1572_8298 | 684 | 178 |
| SCE1572_9182 | 47 | 10 |
| SCE1572_719 | 87.98 | 41.39 |
| SCE1572_3112 | 3 | 0 |
| SCE1572_2876 | 86 | 49 |
| SCE1572_4306 | 24 | 6 |
| SCE1572_10103 | 32 | 29 |
| SCE1572_3097 | 87 | 12 |
| SCE1572_1868 | 44 | 89 |
| SCE1572_9980 | 25 | 26 |
| SCE1572_1516 | 342 | 402 |
| SCE1572_11070 | 65 | 65 |
| SCE1572_5848 | 111 | 29 |
| SCE1572_9875 | 48 | 42 |
| SCE1572_1648 | 67 | 9 |
| SCE1572_10648 | 78 | 81 |
| SCE1572_3944 | 79 | 85 |
| SCE1572_2989 | 344 | 87 |
| SCE1572_4338 | 71 | 10 |
| SCE1572_6773 | 283 | 108 |
| SCE1572_9107 | 18 | 23 |
| SCE1572_904 | 57 | 24 |
| SCE1572_9832 | 21 | 2 |
| SCE1572_9412 | 96 | 140 |
| SCE1572_8096 | 7 | 2 |
| SCE1572_7757 | 32 | 8 |
| SCE1572_2409 | 78 | 258 |
| SCE1572_3952 | 37 | 10 |
| SCE1572_9548 | 20 | 0 |
| SCE1572_7755 | 51 | 27 |
| SCE1572_7468 | 63 | 29 |
| SCE1572_5758 | 17 | 11 |
| SCE1572_3228 | 70 | 59 |
| SCE1572_7118 | 230 | 48 |
| SCE1572_2138 | 10 | 0 |
| SCE1572_9739 | 0 | 0 |
| SCE1572_3118 | 0 | 0 |
| SCE1572_2942 | 96 | 38 |
| SCE1572_4263 | 143 | 31 |
| SCE1572_7288 | 163 | 124 |
| SCE1572_7631 | 59 | 262 |
| SCE1572_4066 | 144 | 160 |
| SCE1572_6068 | 49 | 2 |

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| SCE1572_8889 | 72 | 24 |
| SCE1572_7022 | 306.06 | 39.48 |
| SCE1572_290 | 0 | 0 |
| SCE1572_5195 | 137 | 44 |
| SCE1572_6763 | 265 | 161 |
| SCE1572_6647 | 32 | 2 |
| SCE1572_1633 | 88 | 87 |
| SCE1572_8167 | 0 | 0 |
| SCE1572_1826 | 69 | 9 |
| SCE1572_7986 | 102 | 25 |
| SCE1572_1775 | 16 | 0 |
| SCE1572_2903 | 0 | 0 |
| SCE1572_5797 | 54 | 6 |
| SCE1572_9637 | 122 | 709 |
| SCE1572_8057 | 0 | 0 |
| SCE1572_7102 | 180 | 88 |
| SCE1572_4330 | 144 | 33 |
| SCE1572_7633 | 724 | 488 |
| SCE1572_6112 | 110 | 31 |
| SCE1572_2126 | 127 | 20 |
| SCE1572_9690 | 138 | 124 |
| SCE1572_808 | 110 | 17 |
| SCE1572_7517 | 225 | 179 |
| SCE1572_3111 | 47 | 7 |
| SCE1572_1127 | 32 | 6 |
| SCE1572_2716 | 145 | 81 |
| SCE1572_4858 | 61 | 15 |
| SCE1572_9073 | 233 | 66 |
| SCE1572_9623 | 225 | 48 |
| SCE1572_2673 | 119 | 260 |
| SCE1572_1511 | 121 | 375 |
| SCE1572_3416 | 33 | 11 |
| SCE1572_9974 | 69 | 23 |
| SCE1572_9957 | 11 | 1 |
| SCE1572_7728 | 0 | 0 |
| SCE1572_1207 | 83 | 22 |
| SCE1572_2249 | 78.54 | 24 |
| SCE1572_6632 | 121 | 203 |
| SCE1572_2528 | 2 | 1 |
| SCE1572_9765 | 64 | 32 |
| SCE1572_9042 | 53 | 95 |
| SCE1572_9091 | 22 | 3 |
| SCE1572_8160 | 30 | 4 |
| SCE1572_9750 | 75 | 45 |
| SCE1572_11001 | 20 | 2 |
| SCE1572_4444 | 214 | 227 |
| SCE1572_10104 | 32 | 36 |
| SCE1572_2992 | 48 | 18 |

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| SCE1572_1617 | 33 | 13 |
| SCE1572_9755 | 26 | 5 |
| SCE1572_9524 | 53 | 25 |
| SCE1572_11464 | 846 | 119 |
| SCE1572_3879 | 52 | 60 |
| SCE1572_984 | 95 | 99 |
| SCE1572_6119 | 263 | 80 |
| SCE1572_9598 | 329 | 2467 |
| SCE1572_1235 | 180 | 23 |
| SCE1572_3324 | 207 | 331 |
| SCE1572_4753 | 102 | 122 |
| SCE1572_1287 | 48 | 269 |
| SCE1572_7531 | 55 | 116 |
| SCE1572_9811 | 0 | 0 |
| SCE1572_776 | 4 | 0 |
| SCE1572_11588 | 55 | 23 |
| SCE1572_7042 | 45 | 8 |
| SCE1572_7371 | 31 | 5 |
| SCE1572_3353 | 0 | 0 |
| SCE1572_11476 | 8 | 13 |
| SCE1572_7684 | 0 | 0 |
| SCE1572_9445 | 89 | 24 |
| SCE1572_11354 | 19 | 5 |
| SCE1572_3620 | 17 | 2 |
| SCE1572_4123 | 43 | 6 |
| SCE1572_2798 | 60 | 6 |
| SCE1572_8731 | 27 | 4 |
| SCE1572_9814 | 68 | 150 |
| SCE1572_6403 | 122 | 38 |
| SCE1572_866 | 36 | 9 |
| SCE1572_3005 | 10 | 0 |
| SCE1572_4052 | 108 | 306 |
| SCE1572_10295 | 72 | 141 |
| SCE1572_4390 | 138 | 29 |
| SCE1572_10568 | 454 | 468 |
| SCE1572_4196 | 126 | 68 |
| SCE1572_696 | 4 | 0 |
| SCE1572_1240 | 383 | 47 |
| SCE1572_3606 | 17 | 1 |
| SCE1572_7029 | 214.47 | 57 |
| SCE1572_1603 | 0 | 0 |
| SCE1572_8336 | 307.05 | 59.43 |
| SCE1572_6342 | 80 | 54 |
| SCE1572_8880 | 92 | 12 |
| SCE1572_10839 | 2 | 0 |
| SCE1572_5676 | 29 | 5 |
| SCE1572_1292 | 84 | 17 |
| SCE1572_4833 | 199 | 883 |

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| SCE1572_560 | 488 | 3379 |
| SCE1572_5050 | 8 | 0 |
| SCE1572_5619 | 33 | 21 |
| SCE1572_2779 | 285 | 417 |
| SCE1572_5375 | 62 | 15 |
| SCE1572_4868 | 102 | 28 |
| SCE1572_2418 | 62 | 86 |
| SCE1572_8025 | 0 | 0 |
| SCE1572_1534 | 65 | 14 |
| SCE1572_4313 | 0 | 0 |
| SCE1572_1010 | 160 | 30 |
| SCE1572_8961 | 17 | 4 |
| SCE1572_7238 | 235 | 409 |
| SCE1572_5057 | 265 | 470 |
| SCE1572_2186 | 1 | 0 |
| SCE1572_1788 | 3 | 1 |
| SCE1572_8356 | 21 | 3 |
| SCE1572_3081 | 24 | 48 |
| SCE1572_6181 | 75 | 36 |
| SCE1572_2847 | 67 | 30 |
| SCE1572_2946 | 68 | 14 |
| SCE1572_3200 | 177 | 355 |
| SCE1572_2435 | 78 | 61 |
| SCE1572_3996 | 4 | 1 |
| SCE1572_6607 | 0 | 0 |
| SCE1572_5932 | 232 | 99 |
| SCE1572_204 | 108 | 27 |
| SCE1572_5616 | 0 | 0 |
| SCE1572_800 | 0 | 0 |
| SCE1572_3469 | 302 | 47 |
| SCE1572_320 | 75 | 10 |
| SCE1572_3049 | 34 | 4 |
| SCE1572_1700 | 198 | 132 |
| SCE1572_1268 | 226 | 88 |
| SCE1572_8794 | 53 | 10 |
| SCE1572_109 | 75 | 35 |
| SCE1572_5641 | 4 | 0 |
| SCE1572_301 | 145 | 58 |
| SCE1572_1640 | 66 | 16 |
| SCE1572_4316 | 164 | 18 |
| SCE1572_7962 | 224 | 916 |
| SCE1572_2837 | 258 | 94 |
| SCE1572_11316 | 1044 | 868 |
| SCE1572_6217 | 4 | 3 |
| SCE1572_4576 | 3 | 0 |
| SCE1572_8231 | 142 | 43 |
| SCE1572_10198 | 97 | 16 |
| SCE1572_5695 | 68 | 8 |

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| SCE1572_7425 | 11 | 76 |
| SCE1572_10922 | 789 | 35268 |
| SCE1572_2715 | 235 | 224 |
| SCE1572_2110 | 77 | 334 |
| SCE1572_922 | 11 | 7 |
| SCE1572_9483 | 238 | 256 |
| SCE1572_10561 | 0 | 0 |
| SCE1572_2741 | 14 | 3 |
| SCE1572_11131 | 40 | 7 |
| SCE1572_11200 | 110 | 165 |
| SCE1572_7858 | 219 | 103 |
| SCE1572_6554 | 8 | 0 |
| SCE1572_9202 | 52 | 27 |
| SCE1572_7265 | 58 | 20 |
| SCE1572_6975 | 57 | 9 |
| SCE1572_2840 | 142 | 43 |
| SCE1572_6122 | 228 | 269 |
| SCE1572_6045 | 657 | 1108 |
| SCE1572_2680 | 34 | 4 |
| SCE1572_3792 | 2 | 0 |
| SCE1572_6580 | 30 | 2 |
| SCE1572_326 | 79 | 35 |
| SCE1572_8570 | 2 | 0 |
| SCE1572_5126 | 32 | 23 |
| SCE1572_3898 | 83 | 106 |
| SCE1572_5950 | 70 | 7 |
| SCE1572_5986 | 7 | 0 |
| SCE1572_3180 | 103 | 94 |
| SCE1572_4539 | 59.35 | 23.42 |
| SCE1572_978 | 68 | 41 |
| SCE1572_7934 | 31 | 1 |
| SCE1572_8050 | 87 | 7 |
| SCE1572_10887 | 81 | 50 |
| SCE1572_11237 | 56 | 7 |
| SCE1572_9395 | 26 | 10 |
| SCE1572_3889 | 23 | 5 |
| SCE1572_1553 | 39 | 10 |
| SCE1572_3825 | 15 | 3 |
| SCE1572_3713 | 255 | 187 |
| SCE1572_8773 | 184 | 83 |
| SCE1572_8048 | 103 | 14 |
| SCE1572_1054 | 208 | 107 |
| SCE1572_10359 | 52 | 22 |
| SCE1572_3788 | 90 | 69 |
| SCE1572_9986 | 40 | 12 |
| SCE1572_3311 | 28 | 5 |
| SCE1572_9663 | 68 | 188 |
| SCE1572_3781 | 150 | 546 |

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| SCE1572_7304 | 129 | 14 |
| SCE1572_3678 | 19 | 19 |
| SCE1572_3056 | 36 | 5 |
| SCE1572_2220 | 70 | 82 |
| SCE1572_9784 | 64 | 4 |
| SCE1572_10521 | 121 | 51 |
| SCE1572_9355 | 89 | 113 |
| SCE1572_10220 | 129 | 65 |
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| SCE1572_1437 | 35 | 6 |
| SCE1572_10253 | 0 | 0 |
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| SCE1572_5261 | 82 | 390 |
| SCE1572_155 | 239 | 195 |
| SCE1572_5242 | 31 | 3 |
| SCE1572_5762 | 23 | 4 |
| SCE1572_7393 | 52 | 2 |
| SCE1572_2036 | 455 | 2106 |
| SCE1572_10370 | 74 | 11 |
| SCE1572_11088 | 43 | 26 |
| SCE1572_5116 | 61 | 28 |
| SCE1572_6130 | 19 | 52 |
| SCE1572_9021 | 16 | 7 |
| SCE1572_2042 | 126 | 206 |
| SCE1572_4303 | 82 | 6 |
| SCE1572_11249 | 32 | 59 |
| SCE1572_3273 | 90 | 195 |
| SCE1572_3063 | 151.18 | 122 |
| SCE1572_6938 | 65 | 8 |
| SCE1572_11267 | 428 | 1082 |
| SCE1572_1953 | 52 | 30 |
| SCE1572_1329 | 34 | 46 |
| SCE1572_6538 | 75 | 18 |
| SCE1572_5927 | 350 | 42 |
| SCE1572_6152 | 141 | 53 |
| SCE1572_4996 | 12 | 6 |
| SCE1572_9677 | 64 | 13 |
| SCE1572_4614 | 140 | 24 |
| SCE1572_11339 | 32 | 9 |
| SCE1572_3394 | 113 | 83 |
| SCE1572_4393 | 47 | 11 |
| SCE1572_2239 | 204 | 74 |
| SCE1572_10182 | 140 | 165 |
| SCE1572_9643 | 297 | 164 |
| SCE1572_1599 | 0 | 0 |
| SCE1572_4910 | 2 | 0 |
| SCE1572_8745 | 3 | 0 |

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| SCE1572_508 | 106 | 9 |
| SCE1572_6279 | 56 | 964 |
| SCE1572_1726 | 97 | 24 |
| SCE1572_11384 | 725 | 612 |
| SCE1572_9910 | 60 | 16 |
| SCE1572_1954 | 27 | 13 |
| SCE1572_9298 | 134 | 114 |
| SCE1572_3930 | 388 | 669 |
| SCE1572_6035 | 141 | 93 |
| SCE1572_3726 | 74 | 716 |
| SCE1572_3865 | 20 | 3 |
| SCE1572_5781 | 253 | 366 |
| SCE1572_8522 | 355 | 285 |
| SCE1572_299 | 108 | 31 |
| SCE1572_9760 | 141 | 128 |
| SCE1572_10028 | 28 | 2 |
| SCE1572_11375 | 0 | 0 |
| SCE1572_7991 | 101 | 166 |
| SCE1572_7335 | 37 | 49 |
| SCE1572_8971 | 188 | 218 |
| SCE1572_4479 | 31 | 23 |
| SCE1572_4887 | 40 | 6 |
| SCE1572_8579 | 0 | 0 |
| SCE1572_6746 | 31 | 21 |
| SCE1572_4639 | 31 | 2 |
| SCE1572_5608 | 171 | 29 |
| SCE1572_9023 | 2458 | 2346 |
| SCE1572_2229 | 39 | 328 |
| SCE1572_11481 | 71 | 14 |
| SCE1572_4245 | 57 | 83 |
| SCE1572_1475 | 0 | 0 |
| SCE1572_1925 | 0 | 0 |
| SCE1572_1500 | 51 | 19 |
| SCE1572_4597 | 0 | 0 |
| SCE1572_3556 | 5 | 0 |
| SCE1572_4880 | 320 | 347 |
| SCE1572_3571 | 76 | 29 |
| SCE1572_6843 | 42 | 16 |
| SCE1572_1781 | 22 | 10 |
| SCE1572_8287 | 90 | 116 |
| SCE1572_593 | 186 | 139 |
| SCE1572_399 | 17 | 4 |
| SCE1572_6254 | 162 | 81 |
| SCE1572_318 | 18 | 1 |
| SCE1572_11596 | 58 | 262 |
| SCE1572_9725 | 8 | 11 |
| SCE1572_2274 | 45 | 4 |
| SCE1572_1520 | 60 | 9 |

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| SCE1572_4355 | 29 | 12 |
| SCE1572_3167 | 33 | 20 |
| SCE1572_3872 | 159 | 164 |
| SCE1572_6333 | 45 | 67 |
| SCE1572_4366 | 100 | 37 |
| SCE1572_6243 | 79 | 9 |
| SCE1572_2064 | 43 | 16 |
| SCE1572_8264 | 90 | 121 |
| SCE1572_5424 | 82 | 35 |
| SCE1572_678 | 85 | 51 |
| SCE1572_338 | 123 | 33 |
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| SCE1572_9187 | 52 | 38 |
| SCE1572_7178 | 344 | 93 |
| SCE1572_2320 | 105 | 589 |
| SCE1572_1969 | 48 | 13 |
| SCE1572_9098 | 38 | 5 |
| SCE1572_7006 | 0 | 0 |
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| SCE1572_1317 | 125 | 96 |
| SCE1572_5061 | 42 | 80 |
| SCE1572_7016 | 0 | 0 |
| SCE1572_1610 | 262 | 84 |
| SCE1572_4879 | 415 | 304 |
| SCE1572_2661 | 72 | 40 |
| SCE1572_6305 | 40 | 9 |
| SCE1572_5669 | 51 | 7 |
| SCE1572_8989 | 356 | 365 |
| SCE1572_5992 | 93 | 62 |
| SCE1572_6142 | 83 | 25 |
| SCE1572_3298 | 18 | 6 |
| SCE1572_5549 | 281 | 48 |
| SCE1572_3189 | 6 | 0 |
| SCE1572_10965 | 149 | 33 |
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| SCE1572_8531 | 65 | 34 |
| SCE1572_143 | 6 | 6 |
| SCE1572_349 | 52 | 75 |
| SCE1572_5839 | 167 | 26 |
| SCE1572_9685 | 131 | 117 |
| SCE1572_3508 | 26 | 7 |
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| SCE1572_5296 | 27 | 5 |
| SCE1572_10153 | 35 | 69 |
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| SCE1572_9593 | 123 | 920 |

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| SCE1572_8866 | 149 | 36 |
| SCE1572_2728 | 48 | 16 |
| SCE1572_2284 | 11 | 4 |
| SCE1572_2149 | 72 | 49 |
| SCE1572_1845 | 4 | 1 |
| SCE1572_6476 | 226 | 1068 |
| SCE1572_5329 | 217 | 26 |
| SCE1572_7242 | 124 | 67 |
| SCE1572_10930 | 121 | 40 |
| SCE1572_6251 | 304 | 56 |
| SCE1572_5940 | 75 | 13 |
| SCE1572_4516 | 38 | 12 |
| SCE1572_6160 | 22 | 10 |
| SCE1572_7574 | 152 | 349 |
| SCE1572_11391 | 107 | 30 |
| SCE1572_7466 | 161 | 378 |
| SCE1572_6236 | 91 | 14 |
| SCE1572_8695 | 46 | 28 |
| SCE1572_4494 | 57 | 17 |
| SCE1572_266 | 57 | 8 |
| SCE1572_9393 | 36 | 9 |
| SCE1572_7545 | 171 | 54 |
| SCE1572_3173 | 83 | 20 |
| SCE1572_8687 | 67 | 15 |
| SCE1572_1101 | 46 | 7 |
| SCE1572_11137 | 58 | 169 |
| SCE1572_8598 | 0 | 0 |
| SCE1572_11017 | 67 | 75 |
| SCE1572_9996 | 101 | 32 |
| SCE1572_2695 | 25 | 57 |
| SCE1572_4769 | 12 | 22 |
| SCE1572_8897 | 394 | 321 |
| SCE1572_1747 | 215 | 74 |
| SCE1572_7829 | 49 | 81 |
| SCE1572_8313 | 48 | 14 |
| SCE1572_7360 | 121 | 92 |
| SCE1572_7482 | 0 | 0 |
| SCE1572_8101 | 276 | 1039 |
| SCE1572_2319 | 69 | 191 |
| SCE1572_10031 | 242 | 92 |
| SCE1572_1003 | 145 | 27 |
| SCE1572_10125 | 1 | 0 |
| SCE1572_2422 | 13 | 3 |
| SCE1572_5785 | 51 | 59 |
| SCE1572_1601 | 11 | 0 |
| SCE1572_3718 | 0 | 0 |
| SCE1572_623 | 1328 | 4776 |
| SCE1572_352 | 33 | 19 |

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| SCE1572_8217 | 270 | 36 |
| SCE1572_5546 | 131 | 18 |
| SCE1572_1031 | 59 | 134 |
| SCE1572_2394 | 74 | 30 |
| SCE1572_8148 | 112 | 24 |
| SCE1572_5001 | 275 | 580 |
| SCE1572_3783 | 12 | 3 |
| SCE1572_5413 | 2 | 0 |
| SCE1572_4787 | 410 | 1217 |
| SCE1572_6991 | 108 | 11 |
| SCE1572_10347 | 142 | 170 |
| SCE1572_9573 | 82 | 5 |
| SCE1572_10997 | 210 | 381 |
| SCE1572_7381 | 24 | 7 |
| SCE1572_285 | 109 | 12 |
| SCE1572_2339 | 45 | 109 |
| SCE1572_7412 | 71 | 104 |
| SCE1572_1175 | 36 | 84 |
| SCE1572_4658 | 72 | 61 |
| SCE1572_6483 | 41 | 6 |
| SCE1572_245 | 26.85 | 3 |
| SCE1572_3205 | 189 | 215 |
| SCE1572_11513 | 158 | 134 |
| SCE1572_7430 | 197 | 30 |
| SCE1572_8591 | 187 | 21 |
| SCE1572_5517 | 146 | 26 |
| SCE1572_4946 | 1 | 0 |
| SCE1572_9219 | 101 | 8 |
| SCE1572_6006 | 17 | 26 |
| SCE1572_2173 | 7 | 2 |
| SCE1572_226 | 40 | 8 |
| SCE1572_467 | 828 | 730 |
| SCE1572_342 | 199 | 498 |
| SCE1572_1608 | 79 | 22 |
| SCE1572_2464 | 193 | 22 |
| SCE1572_10585 | 107 | 17 |
| SCE1572_9824 | 36.61 | 5.2 |
| SCE1572_9440 | 68 | 36 |
| SCE1572_6875 | 142 | 24 |
| SCE1572_7977 | 0 | 0 |
| SCE1572_10775 | 246 | 49 |
| SCE1572_5478 | 57 | 20 |
| SCE1572_6858 | 105 | 25 |
| SCE1572_1307 | 721 | 4537 |
| SCE1572_3406 | 111 | 20 |
| SCE1572_2538 | 42 | 27 |
| SCE1572_3466 | 39 | 22 |
| SCE1572_9701 | 15 | 0 |

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| SCE1572_3213 | 156 | 105 |
| SCE1572_4623 | 53 | 135 |
| SCE1572_5422 | 6 | 0 |
| SCE1572_2515 | 10 | 6 |
| SCE1572_3650 | 31 | 8 |
| SCE1572_3690 | 2 | 0 |
| SCE1572_85 | 147 | 133 |
| SCE1572_6356 | 76 | 17 |
| SCE1572_836 | 76 | 33 |
| SCE1572_4824 | 142 | 117 |
| SCE1572_2313 | 55 | 38 |
| SCE1572_7899 | 128 | 82 |
| SCE1572_11494 | 59 | 8 |
| SCE1572_9954 | 317 | 81 |
| SCE1572_9671 | 67 | 230 |
| SCE1572_8104 | 109 | 33 |
| SCE1572_2590 | 161 | 76 |
| SCE1572_9267 | 8 | 0 |
| SCE1572_574 | 69 | 107 |
| SCE1572_872 | 115 | 44 |
| SCE1572_1021 | 230 | 28 |
| SCE1572_383 | 127 | 59 |
| SCE1572_2890 | 141 | 22 |
| SCE1572_4624 | 114 | 159 |
| SCE1572_1574 | 80 | 14 |
| SCE1572_11431 | 112 | 29 |
| SCE1572_7004 | 29 | 3 |
| SCE1572_10982 | 61 | 22 |
| SCE1572_842 | 8 | 2 |
| SCE1572_7659 | 99 | 26 |
| SCE1572_918 | 356 | 167 |
| SCE1572_7490 | 153 | 66 |
| SCE1572_3152 | 366 | 132 |
| SCE1572_6521 | 13 | 0 |
| SCE1572_8248 | 32 | 16 |
| SCE1572_9512 | 393 | 646 |
| SCE1572_7708 | 33 | 5 |
| SCE1572_4646 | 54 | 15 |
| SCE1572_9502 | 68 | 57 |
| SCE1572_2354 | 86 | 467 |
| SCE1572_3617 | 218 | 26 |
| SCE1572_1478 | 60 | 10 |
| SCE1572_2097 | 15 | 189 |
| SCE1572_4357 | 140 | 25 |
| SCE1572_7589 | 88 | 309 |
| SCE1572_4489 | 112 | 68 |
| SCE1572_10166 | 0 | 0 |
| SCE1572_3072 | 29 | 7 |

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| SCE1572_2211 | 148 | 101 |
| SCE1572_10312 | 416 | 123 |
| SCE1572_6915 | 87 | 14 |
| SCE1572_7627 | 73 | 28 |
| SCE1572_3870 | 149 | 48 |
| SCE1572_8542 | 102 | 275 |
| SCE1572_3488 | 37 | 11 |
| SCE1572_7889 | 75 | 1621 |
| SCE1572_10971 | 1 | 2 |
| SCE1572_9270 | 0 | 0 |
| SCE1572_2312 | 408 | 2786 |
| SCE1572_7524 | 12 | 19 |
| SCE1572_2187 | 80 | 18 |
| SCE1572_10331 | 235 | 45 |
| SCE1572_5779 | 101 | 33 |
| SCE1572_6696 | 41 | 6 |
| SCE1572_3696 | 84 | 68 |
| SCE1572_9905 | 0 | 0 |
| SCE1572_56 | 56 | 2 |
| SCE1572_7283 | 63 | 14 |
| SCE1572_5638 | 33 | 11 |
| SCE1572_11305 | 3 | 0 |
| SCE1572_10540 | 753 | 109 |
| SCE1572_3378 | 134 | 22 |
| SCE1572_3498 | 145 | 102 |
| SCE1572_10782 | 73 | 11 |
| SCE1572_2853 | 131 | 30 |
| SCE1572_1621 | 118 | 383 |
| SCE1572_8001 | 699.92 | 102.52 |
| SCE1572_9015 | 0 | 0 |
| SCE1572_3790 | 57 | 8 |
| SCE1572_9939 | 47 | 6 |
| SCE1572_7081 | 91 | 157 |
| SCE1572_6933 | 8 | 12 |
| SCE1572_1675 | 60 | 58 |
| SCE1572_10338 | 269.47 | 558 |
| SCE1572_7988 | 54 | 4 |
| SCE1572_3349 | 48 | 14 |
| SCE1572_7622 | 237 | 211 |
| SCE1572_5172 | 56 | 41 |
| SCE1572_6964 | 130 | 52 |
| SCE1572_10417 | 1 | 0 |
| SCE1572_3417 | 85 | 205 |
| SCE1572_7071 | 25 | 11 |
| SCE1572_11328 | 70 | 48 |
| SCE1572_5976 | 82 | 21 |
| SCE1572_5826 | 63 | 20 |
| SCE1572_5571 | 186.16 | 35.44 |

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| SCE1572_9763 | 38 | 23 |
| SCE1572_2541 | 0 | 0 |
| SCE1572_4693 | 281 | 227 |
| SCE1572_5300 | 124 | 21 |
| SCE1572_6504 | 88 | 43 |
| SCE1572_5497 | 158 | 132 |
| SCE1572_9374 | 112 | 17 |
| SCE1572_9287 | 637 | 1144 |
| SCE1572_4949 | 28 | 7 |
| SCE1572_10018 | 108 | 31 |
| SCE1572_4760 | 76 | 15 |
| SCE1572_1589 | 0 | 0 |
| SCE1572_4434 | 171.91 | 47.98 |
| SCE1572_5149 | 238 | 50 |
| SCE1572_8012 | 1 | 0 |
| SCE1572_8027 | 12 | 6 |
| SCE1572_8094 | 71 | 9 |
| SCE1572_4409 | 31 | 10 |
| SCE1572_6018 | 2640 | 712 |
| SCE1572_1910 | 53 | 9 |
| SCE1572_1373 | 109 | 195 |
| SCE1572_3481 | 12 | 2 |
| SCE1572_11364 | 578 | 136 |
| SCE1572_5270 | 20 | 1671 |
| SCE1572_1244 | 0 | 0 |
| SCE1572_879 | 193 | 437 |
| SCE1572_3809 | 43 | 35 |
| SCE1572_950 | 3.99 | 5.85 |
| SCE1572_10243 | 12 | 0 |
| SCE1572_8761 | 32 | 19 |
| SCE1572_5033 | 203 | 1719 |
| SCE1572_5946 | 75 | 16 |
| SCE1572_667 | 31 | 15 |
| SCE1572_2180 | 136 | 24 |
| SCE1572_6751 | 383 | 162 |
| SCE1572_3767 | 42 | 63 |
| SCE1572_8201 | 388 | 51 |
| SCE1572_74 | 43 | 34 |
| SCE1572_1522 | 66 | 26 |
| SCE1572_6794 | 31 | 20 |
| SCE1572_8565 | 893 | 753 |
| SCE1572_6983 | 257 | 53 |
| SCE1572_4299 | 625 | 108 |
| SCE1572_2936 | 40 | 6 |
| SCE1572_9927 | 242 | 219 |
| SCE1572_7835 | 49 | 94 |
| SCE1572_9530 | 148 | 61 |
| SCE1572_2052 | 0 | 0 |

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| SCE1572_2437 | 9 | 5 |
| SCE1572_6831 | 193 | 130 |
| SCE1572_7181 | 74 | 27 |
| SCE1572_2581 | 30 | 26 |
| SCE1572_5685 | 157 | 325 |
| SCE1572_7291 | 5 | 0 |
| SCE1572_9631 | 79 | 20 |
| SCE1572_3124 | 16 | 2 |
| SCE1572_11050 | 97 | 72 |
| SCE1572_10617 | 79 | 12 |
| SCE1572_6440 | 47 | 7 |
| SCE1572_6419 | 93 | 41 |
| SCE1572_2874 | 119 | 28 |
| SCE1572_8674 | 27 | 47 |
| SCE1572_11543 | 203 | 36 |
| SCE1572_124 | 42 | 2 |
| SCE1572_463 | 97 | 1481 |
| SCE1572_2269 | 220 | 772 |
| SCE1572_2014 | 107 | 9 |
| SCE1572_11362 | 101 | 11 |
| SCE1572_8089 | 41 | 8 |
| SCE1572_10875 | 59 | 13 |
| SCE1572_2905 | 55 | 215 |
| SCE1572_1343 | 17 | 5 |
| SCE1572_1942 | 0 | 0 |
| SCE1572_3306 | 60 | 353 |
| SCE1572_1228 | 64 | 47 |
| SCE1572_1940 | 592 | 64 |
| SCE1572_1682 | 465 | 1932 |
| SCE1572_698 | 20 | 39 |
| SCE1572_3802 | 51 | 18 |
| SCE1572_9575 | 1 | 0 |
| SCE1572_6582 | 24 | 30 |
| SCE1572_1327 | 0 | 0 |
| SCE1572_11011 | 0 | 0 |
| SCE1572_4689 | 202.23 | 462.26 |
| SCE1572_1876 | 215 | 129 |
| SCE1572_4210 | 2 | 0 |
| SCE1572_5576 | 40 | 7 |
| SCE1572_2071 | 9 | 4 |
| SCE1572_8403 | 218 | 64 |
| SCE1572_4074 | 504 | 1659 |
| SCE1572_8413 | 39 | 5 |
| SCE1572_971 | 103 | 33 |
| SCE1572_4779 | 0 | 0 |
| SCE1572_5177 | 131 | 30 |
| SCE1572_11035 | 27 | 118 |
| SCE1572_2898 | 9 | 1 |

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| SCE1572_6077 | 2 | 4 |
| SCE1572_6599 | 80 | 60 |
| SCE1572_8208 | 137 | 45 |
| SCE1572_10807 | 134 | 44 |
| SCE1572_9801 | 61 | 10 |
| SCE1572_10016 | 12 | 48 |
| SCE1572_8705 | 0 | 0 |
| SCE1572_6104 | 104 | 10 |
| SCE1572_149 | 85.25 | 112 |
| SCE1572_4348 | 83 | 10 |
| SCE1572_4459 | 82 | 14 |
| SCE1572_6653 | 12 | 0 |
| SCE1572_22 | 164 | 132 |
| SCE1572_3838 | 0 | 0 |
| SCE1572_859 | 596 | 7198 |
| SCE1572_4472 | 34 | 3 |
| SCE1572_883 | 0 | 0 |
| SCE1572_8703 | 35 | 35 |
| SCE1572_852 | 565 | 856 |
| SCE1572_10841 | 56 | 6 |
| SCE1572_4651 | 109 | 62 |
| SCE1572_10180 | 74 | 99 |
| SCE1572_6267 | 21 | 9 |
| SCE1572_9253 | 52 | 7 |
| SCE1572_10558 | 43 | 7 |
| SCE1572_9033 | 41 | 10 |
| SCE1572_6099 | 147 | 89 |
| SCE1572_270 | 52 | 17 |
| SCE1572_4144 | 104 | 197 |
| SCE1572_10722 | 116 | 16 |
| SCE1572_4387 | 66 | 28 |
| SCE1572_7440 | 17 | 5 |
| SCE1572_4606 | 20 | 64 |
| SCE1572_7298 | 197 | 19 |
| SCE1572_2146 | 68.11 | 8 |
| SCE1572_5409 | 1 | 0 |
| SCE1572_10003 | 35 | 14 |
| SCE1572_11163 | 64 | 181 |
| SCE1572_8801 | 0 | 0 |
| SCE1572_5724 | 0 | 0 |
| SCE1572_8768 | 16 | 5 |
| SCE1572_8717 | 8 | 1 |
| SCE1572_5373 | 43 | 279 |
| SCE1572_7416 | 178 | 387 |
| SCE1572_6597 | 83 | 22 |
| SCE1572_9793 | 76 | 24 |
| SCE1572_8644 | 149 | 45 |
| SCE1572_3691 | 647 | 56 |

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| SCE1572_7388 | 52 | 14 |
| SCE1572_5004 | 20 | 27 |
| SCE1572_5238 | 246 | 109 |
| SCE1572_7254 | 39 | 1 |
| SCE1572_3476 | 153 | 174 |
| SCE1572_4108 | 75.55 | 16 |
| SCE1572_10084 | 86 | 81 |
| SCE1572_10610 | 8 | 1 |
| SCE1572_2612 | 70 | 18 |
| SCE1572_4900 | 151 | 21 |
| SCE1572_6579 | 47 | 15 |
| SCE1572_8909 | 80 | 16 |
| SCE1572_4133 | 16 | 5 |
| SCE1572_8468 | 105 | 95 |
| SCE1572_11178 | 0 | 0 |
| SCE1572_8008 | 231 | 2013 |
| SCE1572_11440 | 70 | 20 |
| SCE1572_10681 | 40 | 18 |
| SCE1572_10109 | 41 | 53 |
| SCE1572_4743 | 51 | 22 |
| SCE1572_659 | 27 | 0 |
| SCE1572_11288 | 203 | 693 |
| SCE1572_8408 | 176 | 66 |
| SCE1572_11317 | 312 | 169 |
| SCE1572_10412 | 7 | 2 |
| SCE1572_9435 | 477 | 967 |
| SCE1572_458 | 82 | 19 |
| SCE1572_8424 | 41 | 25 |
| SCE1572_1975 | 153 | 233 |
| SCE1572_3518 | 22 | 3 |
| SCE1572_1964 | 41 | 5 |
| SCE1572_402 | 57 | 7 |
| SCE1572_505 | 14 | 2 |
| SCE1572_1064 | 330 | 53 |
| SCE1572_5014 | 127 | 311 |
| SCE1572_2931 | 0 | 0 |
| SCE1572_6421 | 61 | 4 |
| SCE1572_11152 | 18 | 5 |
| SCE1572_7357 | 33 | 17 |
| SCE1572_7060 | 108 | 16 |
| SCE1572_4051 | 194 | 423 |
| SCE1572_6721 | 61 | 121 |
| SCE1572_5139 | 34 | 7 |
| SCE1572_9366 | 16 | 1 |
| SCE1572_8998 | 235 | 588 |
| SCE1572_3050 | 19 | 1 |
| SCE1572_9162 | 139 | 2 |
| SCE1572_4088 | 309 | 154 |

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| SCE1572_3638 | 52 | 9 |
| SCE1572_112 | 20.47 | 0 |
| SCE1572_944 | 186.94 | 24.87 |
| SCE1572_8781 | 105 | 923 |
| SCE1572_8255 | 297 | 174 |
| SCE1572_10114 | 18.4 | 1 |
| SCE1572_378 | 39 | 16 |
| SCE1572_6474 | 31 | 39 |
| SCE1572_1151 | 7 | 10 |
| SCE1572_3373 | 28 | 5 |
| SCE1572_707 | 140 | 449 |
| SCE1572_10043 | 99 | 934 |
| SCE1572_5806 | 23 | 26 |
| SCE1572_8629 | 36 | 55 |
| SCE1572_789 | 0 | 0 |
| SCE1572_7654 | 25 | 7 |
| SCE1572_11227 | 118 | 44 |
| SCE1572_9610 | 27 | 6 |
| SCE1572_3759 | 163.12 | 76.15 |
| SCE1572_8431 | 67 | 13 |
| SCE1572_6394 | 495 | 78 |
| SCE1572_4813 | 94 | 274 |
| SCE1572_956 | 0 | 0 |
| SCE1572_9964 | 1007.99 | 153.74 |
| SCE1572_3095 | 107 | 82 |
| SCE1572_1045 | 64 | 33 |
| SCE1572_9929 | 11 | 0 |
| SCE1572_4715 | 91 | 99 |
| SCE1572_4466 | 96 | 20 |
| SCE1572_5790 | 50 | 56 |
| SCE1572_10673 | 53 | 39 |
| SCE1572_5555 | 710 | 345 |
| SCE1572_4416 | 143 | 18 |
| SCE1572_1095 | 38 | 106 |
| SCE1572_1561 | 51 | 11 |
| SCE1572_11536 | 66 | 55 |
| SCE1572_931 | 414 | 3398 |
| SCE1572_10824 | 139 | 110 |
| SCE1572_10989 | 41 | 39 |
| SCE1572_10632 | 0 | 0 |
| SCE1572_8849 | 61 | 16 |
| SCE1572_1369 | 114 | 90 |
| SCE1572_8873 | 149 | 16 |
| SCE1572_7841 | 52 | 12 |
| SCE1572_6954 | 47 | 8 |
| SCE1572_6734 | 64 | 64 |
| SCE1572_277 | 161 | 39 |
| SCE1572_6792 | 74 | 186 |

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| SCE1572_1930 | 186 | 140 |
| SCE1572_6904 | 67 | 5 |
| SCE1572_8436 | 293 | 90 |
| SCE1572_5740 | 26 | 20 |
| SCE1572_2501 | 25 | 27 |
| SCE1572_6364 | 43 | 215 |
| SCE1572_6853 | 247 | 105 |
| SCE1572_6998 | 82 | 25 |
| SCE1572_5197 | 6 | 0 |
| SCE1572_2307 | 50 | 15 |
| SCE1572_442 | 84 | 34 |
| SCE1572_5755 | 321 | 433 |
| SCE1572_1506 | 103 | 14 |
| SCE1572_5989 | 0 | 1.16 |
| SCE1572_5735 | 109 | 95 |
| SCE1572_748 | 11 | 52 |
| SCE1572_2480 | 7 | 1 |
| SCE1572_4219 | 88 | 35 |
| SCE1572_84 | 15 | 37 |
| SCE1572_1353 | 75 | 20 |
| SCE1572_9971 | 127 | 390 |
| SCE1572_3015 | 81 | 12 |
| SCE1572_1688 | 19 | 12 |
| SCE1572_5883 | 53 | 28 |
| SCE1572_46 | 181 | 152 |
| SCE1572_8942 | 99 | 32 |
| SCE1572_6298 | 81 | 72 |
| SCE1572_10480 | 19 | 25 |
| SCE1572_358 | 180 | 53 |
| SCE1572_9328 | 453 | 244 |
| SCE1572_11506 | 85 | 36 |
| SCE1572_1422 | 67 | 27 |
| SCE1572_7771 | 57 | 110 |
| SCE1572_10041 | 11 | 0 |
| SCE1572_3400 | 165 | 398 |
| SCE1572_4564 | 63 | 24 |
| SCE1572_7216 | 109 | 16 |
| SCE1572_8620 | 41 | 89 |
| SCE1572_7538 | 203 | 45 |
| SCE1572_3101 | 10 | 25 |
| SCE1572_7310 | 56 | 19 |
| SCE1572_1841 | 89 | 270 |
| SCE1572_8951 | 0 | 0 |
| SCE1572_1109 | 0 | 0 |
| SCE1572_4233 | 50 | 11 |
| SCE1572_5651 | 0 | 0 |
| SCE1572_6824 | 214 | 215 |
| SCE1572_4772 | 79 | 8 |

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| SCE1572_10701 | 0 | 0 |
| SCE1572_2548 | 66 | 10 |
| SCE1572_8226 | 21 | 12 |
| SCE1572_6678 | 552 | 899 |
| SCE1572_9976 | 0 | 0 |
| SCE1572_10309 | 135 | 2 |
| SCE1572_10850 | 85 | 15 |
| SCE1572_2619 | 73 | 15 |
| SCE1572_10448 | 27 | 19 |
| SCE1572_9314 | 264 | 131 |
| SCE1572_10513 | 0 | 0 |
| SCE1572_3255 | 18 | 51 |
| SCE1572_447 | 53 | 17 |
| SCE1572_5309 | 47 | 26 |
| SCE1572_4922 | 132 | 11 |
| SCE1572_10111 | 244 | 735 |
| SCE1572_10948 | 244 | 102 |
| SCE1572_10603 | 0 | 0 |
| SCE1572_9947 | 13 | 6 |
| SCE1572_8828 | 20.65 | 4 |
| SCE1572_4063 | 224 | 142 |
| SCE1572_7816 | 35 | 97 |
| SCE1572_11439 | 266 | 54 |
| SCE1572_5087 | 101 | 346 |
| SCE1572_10390 | 169 | 35 |
| SCE1572_4984 | 231 | 33 |
| SCE1572_962 | 1241 | 255 |
| SCE1572_6731 | 0 | 0 |
| SCE1572_6274 | 118 | 284 |
| SCE1572_9403 | 227 | 55 |
| SCE1572_811 | 9 | 2 |
| SCE1572_2950 | 1 | 0 |
| SCE1572_7992 | 145 | 6 |
| SCE1572_4011 | 255 | 299 |
| SCE1572_6865 | 131 | 41 |
| SCE1572_184 | 10 | 0 |
| SCE1572_3282 | 10 | 2 |
| SCE1572_902 | 36 | 4 |
| SCE1572_4283 | 15 | 10 |
| SCE1572_6898 | 326 | 341 |
| SCE1572_3025 | 75 | 11 |
| SCE1572_6173 | 41 | 76 |
| SCE1572_10123 | 287 | 110 |
| SCE1572_4703 | 90 | 11 |
| SCE1572_8151 | 42 | 7 |
| SCE1572_5490 | 89 | 16 |
| SCE1572_8063 | 3 | 0 |
| SCE1572_2627 | 190 | 31 |

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| SCE1572_7197 | 128 | 28 |
| SCE1572_1417 | 143 | 29 |
| SCE1572_1725 | 331 | 278 |
| SCE1572_1628 | 120 | 88 |
| SCE1572_1088 | 15 | 1 |
| SCE1572_8112 | 86 | 11 |
| SCE1572_4165 | 76 | 9 |
| SCE1572_8032 | 0 | 0 |
| SCE1572_4701 | 182 | 57 |
| SCE1572_9146 | 0 | 0 |
| SCE1572_7488 | 37 | 27 |
| SCE1572_11458 | 148 | 106 |
| SCE1572_8606 | 1 | 0 |
| SCE1572_6672 | 0 | 0 |
| SCE1572_2497 | 160 | 47 |
| SCE1572_1834 | 11 | 4 |
| SCE1572_5445 | 55 | 11 |
| SCE1572_6338 | 39 | 45 |
| SCE1572_4951 | 19 | 4 |
| SCE1572_1853 | 164 | 21 |
| SCE1572_8353 | 1425 | 3163 |
| SCE1572_3978 | 71 | 22 |
| SCE1572_6754 | 214 | 25 |
| SCE1572_1385 | 58 | 20 |
| SCE1572_8476 | 237 | 82 |
| SCE1572_10644 | 187 | 1720 |
| SCE1572_9231 | 35 | 2 |
| SCE1572_8190 | 340 | 48 |
| SCE1572_2845 | 48.68 | 0 |
| SCE1572_11599 | 37 | 6 |
| SCE1572_10978 | 452 | 632 |
| SCE1572_1715 | 34 | 17 |
| SCE1572_8492 | 395 | 309 |
| SCE1572_10207 | 32 | 16 |
| SCE1572_7058 | 30 | 4 |
| SCE1572_10278 | 28 | 2 |
| SCE1572_3458 | 96 | 9 |
| SCE1572_9348 | 196 | 74 |
| SCE1572_4112 | 128 | 16 |
| SCE1572_8726 | 68 | 13 |
| SCE1572_4380 | 220 | 34 |
| SCE1572_1848 | 166 | 34 |
| SCE1572_2087 | 0 | 0 |
| SCE1572_3332 | 0 | 0 |
| SCE1572_649 | 0 | 0 |
| SCE1572_7681 | 52 | 16 |
| SCE1572_10768 | 3 | 0 |
| SCE1572_3366 | 40 | 290 |

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| SCE1572_642 | 225 | 200 |
| SCE1572_495 | 0 | 0 |
| SCE1572_8682 | 28 | 30 |
| SCE1572_10830 | 54 | 12 |
| SCE1572_7033 | 41 | 6 |
| SCE1572_9004 | 41 | 5 |
| SCE1572_6210 | 544.12 | 126.28 |
| SCE1572_1318 | 16 | 2 |
| SCE1572_10861 | 2085 | 3407 |
| SCE1572_5279 | 303.95 | 98 |
| SCE1572_1757 | 319 | 69 |
| SCE1572_11216 | 66 | 25 |
| SCE1572_1196 | 46 | 29 |
| SCE1572_10504 | 61 | 30 |
| SCE1572_5466 | 130 | 25 |
| SCE1572_3924 | 54 | 162 |
| SCE1572_8855 | 107 | 108 |
| SCE1572_2551 | 75 | 18 |
| SCE1572_5458 | 69 | 8 |
| SCE1572_6620 | 41 | 11 |
| SCE1572_8188 | 0 | 0 |
| SCE1572_7975 | 37 | 2 |
| SCE1572_7279 | 1 | 0 |
| SCE1572_4931 | 95 | 25 |
| SCE1572_1311 | 301 | 1343 |
| SCE1572_11144 | 40 | 12 |
| SCE1572_5963 | 102 | 22 |
| SCE1572_6383 | 27 | 0 |
| SCE1572_829 | 37 | 7 |
| SCE1572_5384 | 34 | 15 |
| SCE1572_1487 | 82 | 17 |
| SCE1572_8840 | 210 | 36 |
| SCE1572_523 | 77 | 51 |
| SCE1572_3667 | 26 | 2 |
| SCE1572_7557 | 30 | 5 |
| SCE1572_1166 | 130 | 29 |
| SCE1572_11125 | 21 | 8 |
| SCE1572_1184 | 429 | 81 |
| SCE1572_7067 | 50 | 1 |
| SCE1572_5834 | 9 | 75 |
| SCE1572_1163 | 28 | 19 |
| SCE1572_4018 | 80 | 28 |
| SCE1572_7445 | 118 | 26 |
| SCE1572_1434 | 587 | 136 |
| SCE1572_9655 | 27.29 | 1.49 |
| SCE1572_7673 | 125.11 | 13.95 |
| SCE1572_8245 | 79 | 51 |
| SCE1572_4717 | 25 | 6 |

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| SCE1572_1580 | 55 | 10 |
| SCE1572_5583 | 93 | 23 |
| SCE1572_6541 | 31 | 9 |
| SCE1572_9920 | 291 | 54 |
| SCE1572_9846 | 27 | 2 |
| SCE1572_1577 | 78 | 11 |
| SCE1572_5334 | 315 | 407 |
| SCE1572_6943 | 10 | 1 |
| SCE1572_3108 | 63 | 14 |
| SCE1572_9279 | 34 | 11 |
| SCE1572_6286 | 12 | 0 |
| SCE1572_8816 | 76 | 9 |
| SCE1572_8082 | 0 | 0 |
| SCE1572_3655 | 8 | 0 |
| SCE1572_10716 | 44 | 4 |
| SCE1572_11235 | 48 | 9 |
| SCE1572_9715 | 20 | 5 |
| SCE1572_11294 | 23 | 2 |
| SCE1572_7203 | 0 | 0 |
| SCE1572_8035 | 89.78 | 25 |
| SCE1572_6584 | 54 | 57 |
| SCE1572_8461 | 70 | 31 |
| SCE1572_1336 | 54 | 74 |
| SCE1572_793 | 265 | 147 |
| SCE1572_7665 | 118 | 6 |
| SCE1572_2794 | 3 | 0 |
| SCE1572_6889 | 47 | 6 |
| SCE1572_9744 | 80 | 142 |
| SCE1572_3750 | 111 | 16 |
| SCE1572_4096 | 10 | 0 |
| SCE1572_2359 | 51 | 51 |
| SCE1572_8788 | 0 | 0 |
| SCE1572_6826 | 20 | 41 |
| SCE1572_3548 | 60 | 13 |
| SCE1572_11159 | 21 | 15 |
| SCE1572_408 | 58 | 23 |
| SCE1572_5227 | 2 | 0 |
| SCE1572_11130 | 241 | 57 |
| SCE1572_10467 | 246 | 215 |
| SCE1572_3438 | 0 | 0 |
| SCE1572_6817 | 69 | 4 |
| SCE1572_7186 | 78 | 16 |
| SCE1572_96 | 47 | 19 |
| SCE1572_6495 | 4 | 0 |
| SCE1572_8418 | 66 | 15 |
| SCE1572_7341 | 287 | 323 |
| SCE1572_7078 | 0 | 0 |
| SCE1572_10851 | 58.02 | 49.41 |

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| SCE1572_7495 | 46 | 7 |
| SCE1572_1364 | 781 | 1815 |
| SCE1572_8373 | 313 | 266 |
| SCE1572_1409 | 331 | 40 |
| SCE1572_8385 | 257.75 | 46.02 |
| SCE1572_3261 | 142 | 96 |
| SCE1572_10236 | 1346 | 349 |
| SCE1572_511 | 374 | 133 |
| SCE1572_4374 | 14 | 0 |
| SCE1572_5181 | 88 | 1195 |
| SCE1572_151 | 16 | 3 |
| SCE1572_9345 | 65 | 54 |
| SCE1572_9339 | 194 | 641 |
| SCE1572_3679 | 87 | 18 |
| SCE1572_2753 | 14 | 2 |
| SCE1572_409 | 54 | 12 |
| SCE1572_8963 | 68 | 19 |
| SCE1572_5866 | 33 | 13 |
| SCE1572_9943 | 167 | 235 |
| SCE1572_6922 | 19 | 67 |
| SCE1572_7576 | 43 | 18 |
| SCE1572_10653 | 911 | 3155 |
| SCE1572_3540 | 310 | 45 |
| SCE1572_6624 | 44 | 21 |
| SCE1572_1407 | 31 | 12 |
| SCE1572_7668 | 31.63 | 9.67 |
| SCE1572_11058 | 246 | 110 |
| SCE1572_11351 | 821 | 149 |
| SCE1572_4301 | 242 | 31 |
| SCE1572_11186 | 63 | 4 |
| SCE1572_4581 | 27 | 5 |
| SCE1572_7793 | 254 | 62 |
| SCE1572_10556 | 0 | 0 |
| SCE1572_4424 | 143 | 21 |
| SCE1572_6548 | 0 | 0 |
| SCE1572_11520 | 21 | 3 |
| SCE1572_9256 | 286 | 157 |
| SCE1572_2808 | 89.34 | 14.22 |
| SCE1572_5481 | 6 | 1 |
| SCE1572_1399 | 28 | 9 |
| SCE1572_3976 | 72 | 40 |
| SCE1572_11220 | 73 | 12 |
| SCE1572_5675 | 43 | 25 |
| SCE1572_8046 | 4 | 0 |
| SCE1572_3532 | 106 | 16 |
| SCE1572_497 | 87 | 5 |
| SCE1572_5045 | 114 | 69 |
| SCE1572_7862 | 133 | 276 |

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| SCE1572_10457 | 0 | 0 |
| SCE1572_3988 | 40 | 21 |
| SCE1572_4427 | 86 | 7 |
| SCE1572_2966 | 322 | 69 |
| SCE1572_1302 | 27 | 87 |
| SCE1572_2224 | 66 | 11 |
| SCE1572_3722 | 211 | 4036 |
| SCE1572_8483 | 45 | 23 |
| SCE1572_868 | 128 | 117 |
| SCE1572_6323 | 66 | 35 |
| SCE1572_2738 | 18 | 3 |
| SCE1572_551 | 58 | 38 |
| SCE1572_2777 | 160 | 25 |
| SCE1572_10497 | 97 | 28 |
| SCE1572_3054 | 6 | 0 |
| SCE1572_9102 | 0 | 0 |
| SCE1572_8755 | 64 | 6 |
| SCE1572_418 | 1180 | 122 |
| SCE1572_2763 | 261 | 44 |
| SCE1572_2782 | 162 | 54 |
| SCE1572_8075 | 94.94 | 49.52 |
| SCE1572_8351 | 21 | 4 |
| SCE1572_3440 | 310 | 51 |
| SCE1572_5891 | 51 | 32 |
| SCE1572_687 | 49 | 6 |
| SCE1572_8834 | 487 | 124 |
| SCE1572_8177 | 88 | 18 |
| SCE1572_207 | 0 | 0 |
| SCE1572_3032 | 25 | 11 |
| SCE1572_10055 | 763 | 645 |
| SCE1572_3818 | 192 | 254 |
| SCE1572_5068 | 412 | 199 |
| SCE1572_8131 | 32 | 8 |
| SCE1572_2508 | 113 | 26 |
| SCE1572_10008 | 59 | 14 |
| SCE1572_374 | 192 | 33 |
| SCE1572_1856 | 130 | 22 |
| SCE1572_4912 | 18 | 9 |
| SCE1572_9600 | 101 | 233 |
| SCE1572_7917 | 483 | 340 |
| SCE1572_10874 | 72 | 20 |
| SCE1572_11091 | 72 | 44 |
| SCE1572_186 | 104 | 28 |
| SCE1572_9095 | 91 | 78 |
| SCE1572_9559 | 37 | 21 |
| SCE1572_6572 | 28.33 | 15.66 |
| SCE1572_9421 | 228 | 720 |
| SCE1572_1864 | 0 | 0 |

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| SCE1572_332 | 48 | 51 |
| SCE1572_7794 | 8 | 6 |
| SCE1572_1172 | 56 | 21 |
| SCE1572_275 | 198 | 35 |
| SCE1572_2385 | 173 | 113 |
| SCE1572_3762 | 348 | 364 |
| SCE1572_3689 | 31 | 20 |
| SCE1572_1411 | 207 | 26 |
| SCE1572_7456 | 113 | 25 |
| SCE1572_8588 | 64 | 19 |
| SCE1572_3566 | 83 | 13 |
| SCE1572_8290 | 505 | 71 |
| SCE1572_10780 | 25 | 12 |
| SCE1572_7008 | 0 | 0 |
| SCE1572_7731 | 16 | 3 |
| SCE1572_324 | 214 | 74 |
| SCE1572_2609 | 58 | 20 |
| SCE1572_9401 | 26 | 21 |
| SCE1572_8525 | 57 | 29 |
| SCE1572_9917 | 93 | 18 |
| SCE1572_9467 | 59 | 29 |
| SCE1572_1069 | 109 | 10 |
| SCE1572_3292 | 114 | 166 |
| SCE1572_3169 | 175 | 161 |
| SCE1572_5164 | 16 | 144 |
| SCE1572_10170 | 124.6 | 70 |
| SCE1572_4247 | 164 | 70 |
| SCE1572_6962 | 47 | 33 |
| SCE1572_6846 | 52 | 164 |
| SCE1572_7255 | 403 | 1051 |
| SCE1572_2472 | 42 | 511 |
| SCE1572_9380 | 12 | 3 |
| SCE1572_608 | 346 | 233 |
| SCE1572_1253 | 26 | 5 |
| SCE1572_10490 | 41 | 23 |
| SCE1572_3421 | 58 | 31 |
| SCE1572_7373 | 59 | 13 |
| SCE1572_10214 | 128 | 66 |
| SCE1572_2349 | 92 | 47 |
| SCE1572_2276 | 254 | 580 |
| SCE1572_2721 | 426 | 140 |
| SCE1572_7020 | 26.37 | 2 |
| SCE1572_19 | 197 | 392 |
| SCE1572_7011 | 233 | 65 |
| SCE1572_2701 | 233 | 45 |
| SCE1572_7597 | 62 | 114 |
| SCE1572_2824 | 84 | 26 |
| SCE1572_5544 | 79 | 8 |

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| SCE1572_1255 | 348 | 108 |
| SCE1572_8202 | 332 | 37 |
| SCE1572_11095 | 58 | 10 |
| SCE1572_6634 | 332 | 52 |
| SCE1572_11539 | 50 | 5 |
| SCE1572_7590 | 253 | 138 |
| SCE1572_2982 | 0 | 0 |
| SCE1572_3642 | 241 | 40 |
| SCE1572_4673 | 81 | 41 |
| SCE1572_8381 | 269 | 107 |
| SCE1572_3684 | 37 | 2 |
| SCE1572_11068 | 176 | 124 |
| SCE1572_5215 | 214.85 | 217.58 |
| SCE1572_9176 | 0 | 0 |
| SCE1572_7660 | 125 | 15 |
| SCE1572_2295 | 6 | 0 |
| SCE1572_1951 | 77 | 11 |
| SCE1572_10914 | 68 | 27 |
| SCE1572_3771 | 108 | 59 |
| SCE1572_4734 | 92 | 53 |
| SCE1572_9248 | 91 | 51 |
| SCE1572_9044 | 168 | 53 |
| SCE1572_7753 | 24 | 6 |
| SCE1572_2459 | 100 | 38 |
| SCE1572_619 | 26 | 23 |
| SCE1572_2208 | 12 | 3 |
| SCE1572_6685 | 104 | 25 |
| SCE1572_8140 | 63 | 146 |
| SCE1572_2100 | 1 | 1 |
| SCE1572_7943 | 43 | 74 |
| SCE1572_3561 | 60 | 9 |
| SCE1572_2812 | 109 | 49 |
| SCE1572_2616 | 117 | 142 |
| SCE1572_11378 | 58 | 197 |
| SCE1572_7741 | 128 | 46 |
| SCE1572_2788 | 39 | 11 |
| SCE1572_10737 | 167 | 120 |
| SCE1572_7952 | 587 | 717 |
| SCE1572_8556 | 116 | 125 |
| SCE1572_6446 | 12 | 2 |
| SCE1572_7823 | 134 | 252 |
| SCE1572_2620 | 176 | 45 |
| SCE1572_3539 | 183 | 33 |
| SCE1572_4863 | 70 | 30 |
| SCE1572_758 | 18 | 7 |
| SCE1572_2022 | 709 | 2900 |
| SCE1572_1531 | 55 | 18 |
| SCE1572_3493 | 261 | 45 |

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| SCE1572_9001 | 660 | 460 |
| SCE1572_3160 | 75 | 26 |
| SCE1572_6856 | 83 | 23 |
| SCE1572_8396 | 40 | 71 |
| SCE1572_7565 | 38 | 7 |
| SCE1572_10607 | 51 | 40 |
| SCE1572_4457 | 74 | 40 |
| SCE1572_6302 | 352 | 2096 |
| SCE1572_686 | 173 | 22 |
| SCE1572_9609 | 154 | 245 |
| SCE1572_6534 | 52 | 5 |
| SCE1572_1067 | 99 | 12 |
| SCE1572_8549 | 88 | 16 |
| SCE1572_10335 | 157 | 159 |
| SCE1572_6230 | 27 | 13 |
| SCE1572_8511 | 78 | 27 |
| SCE1572_3376 | 30 | 105 |
| SCE1572_9056 | 275 | 47 |
| SCE1572_6493 | 48 | 15 |
| SCE1572_6929 | 84 | 9 |
| SCE1572_7439 | 6 | 0 |
| SCE1572_1885 | 35 | 63 |
| SCE1572_1143 | 48 | 34 |
| SCE1572_5873 | 223 | 66 |
| SCE1572_10362 | 106 | 461 |
| SCE1572_935 | 100.74 | 141.76 |
| SCE1572_8154 | 67 | 6 |
| SCE1572_5588 | 46 | 7 |
| SCE1572_5557 | 192.25 | 184.25 |
| SCE1572_10329 | 48 | 25 |
| SCE1572_9506 | 133 | 21 |
| SCE1572_1129 | 78 | 15 |
| SCE1572_10473 | 181 | 500 |
| SCE1572_9261 | 50 | 6 |
| SCE1572_11027 | 58 | 16 |
| SCE1572_10021 | 198.75 | 35.19 |
| SCE1572_5766 | 711 | 1570 |
| SCE1572_8864 | 35 | 0 |
| SCE1572_8784 | 61 | 129 |
| SCE1572_3341 | 526 | 480 |
| SCE1572_8426 | 16 | 0 |
| SCE1572_3308 | 20 | 1 |
| SCE1572_5817 | 4 | 0 |
| SCE1572_8452 | 28 | 99 |
| SCE1572_11319 | 47 | 5 |
| SCE1572_11590 | 29 | 9 |
| SCE1572_638 | 59 | 34 |
| SCE1572_676 | 73 | 11 |

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| SCE1572_924 | 135 | 228 |
| SCE1572_477 | 19 | 7 |
| SCE1572_5854 | 4 | 0 |
| SCE1572_8399 | 163 | 83 |
| SCE1572_9778 | 177 | 308 |
| SCE1572_10799 | 267 | 99 |
| SCE1572_6307 | 184 | 87 |
| SCE1572_9318 | 956 | 611 |
| SCE1572_8454 | 39 | 37 |
| SCE1572_10319 | 134 | 90 |
| SCE1572_11003 | 264 | 244 |
| SCE1572_2102 | 52 | 74 |
| SCE1572_9742 | 161 | 96 |
| SCE1572_11176 | 17 | 45 |
| SCE1572_9915 | 356 | 77 |
| SCE1572_3158 | 223 | 52 |
| SCE1572_1959 | 1 | 0 |
| SCE1572_11222 | 129 | 23 |
| SCE1572_1390 | 130 | 171 |
| SCE1572_8976 | 20 | 2 |
| SCE1572_9109 | 10 | 4 |
| SCE1572_8307 | 1920 | 41 |
| SCE1572_5075 | 6 | 1 |
| SCE1572_5368 | 28 | 6 |
| SCE1572_4535 | 43 | 8 |
| SCE1572_1060 | 0 | 0 |
| SCE1572_10024 | 93.52 | 26 |
| SCE1572_7131 | 14 | 1 |
| SCE1572_3131 | 153 | 33 |
| SCE1572_9820 | 245 | 85 |
| SCE1572_9221 | 908.67 | 268.61 |
| SCE1572_2830 | 13 | 1 |
| SCE1572_8737 | 104 | 20 |
| SCE1572_397 | 32 | 10 |
| SCE1572_8722 | 38 | 5 |
| SCE1572_6430 | 107 | 46 |
| SCE1572_10990 | 35 | 16 |
| SCE1572_2957 | 1070 | 249 |
| SCE1572_2633 | 140.06 | 4.43 |
| SCE1572_2152 | 36 | 20 |
| SCE1572_8609 | 191 | 46 |
| SCE1572_2351 | 128 | 663 |
| SCE1572_4214 | 0 | 0 |
| SCE1572_10179 | 121 | 232 |
| SCE1572_4310 | 249 | 32 |
| SCE1572_2901 | 0 | 0 |
| SCE1572_4780 | 247.26 | 172.24 |
| SCE1572_2325 | 26 | 57 |

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| SCE1572_5726 | 363 | 1170 |
| SCE1572_4085 | 50 | 7 |
| SCE1572_10771 | 26 | 7 |
| SCE1572_4758 | 503 | 115 |
| SCE1572_5256 | 24 | 4 |
| SCE1572_1299 | 150 | 30 |
| SCE1572_5810 | 9783 | 5101 |
| SCE1572_6758 | 74 | 17 |
| SCE1572_4391 | 140 | 23 |
| SCE1572_9224 | 134 | 12 |
| SCE1572_5469 | 229 | 20 |
| SCE1572_9835 | 33 | 24 |
| SCE1572_8593 | 0 | 0 |
| SCE1572_11483 | 270 | 156 |
| SCE1572_1668 | 85 | 29 |
| SCE1572_1459 | 698.67 | 109.32 |
| SCE1572_3583 | 111 | 26 |
| SCE1572_412 | 23 | 10 |
| SCE1572_600 | 1 | 0 |
| SCE1572_9438 | 36 | 29 |
| SCE1572_2566 | 12 | 0 |
| SCE1572_9883 | 40 | 20 |
| SCE1572_6088 | 102 | 109 |
| SCE1572_2140 | 40 | 8 |
| SCE1572_10421 | 58 | 11 |
| SCE1572_177 | 8 | 1 |
| SCE1572_10303 | 323 | 80 |
| SCE1572_8851 | 6 | 24 |
| SCE1572_9275 | 243 | 121 |
| SCE1572_7141 | 33 | 4 |
| SCE1572_5063 | 9 | 3 |
| SCE1572_1703 | 308 | 141 |
| SCE1572_10427 | 4 | 1 |
| SCE1572_4378 | 169 | 8 |
| SCE1572_9816 | 30 | 19 |
| SCE1572_5436 | 105 | 17 |
| SCE1572_7434 | 14 | 25 |
| SCE1572_8193 | 210 | 30 |
| SCE1572_2565 | 343 | 399 |
| SCE1572_2288 | 63 | 38 |
| SCE1572_3407 | 321 | 347 |
| SCE1572_451 | 22 | 17 |
| SCE1572_10258 | 14 | 1 |
| SCE1572_10908 | 117 | 87 |
| SCE1572_6533 | 97 | 5 |
| SCE1572_9584 | 111 | 49 |
| SCE1572_11239 | 68 | 11 |
| SCE1572_6703 | 64 | 17 |

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| SCE1572_11426 | 43 | 26 |
| SCE1572_11433 | 221 | 182 |
| SCE1572_7054 | 17 | 7 |
| SCE1572_10145 | 502 | 335 |
| SCE1572_6669 | 25 | 11 |
| SCE1572_424 | 53 | 124 |
| SCE1572_7603 | 93 | 12 |
| SCE1572_5010 | 199 | 484 |
| SCE1572_8712 | 65 | 11 |
| SCE1572_1532 | 36 | 54 |
| SCE1572_4541 | 483 | 61 |
| SCE1572_11156 | 35 | 15 |
| SCE1572_2923 | 144 | 29 |
| SCE1572_8324 | 100 | 15 |
| SCE1572_4907 | 75 | 52 |
| SCE1572_1086 | 147 | 77 |
| SCE1572_138 | 19 | 10 |
| SCE1572_3447 | 39 | 26 |
| SCE1572_11404 | 51 | 15 |
| SCE1572_3467 | 81 | 17 |
| SCE1572_2077 | 67 | 37 |
| SCE1572_1034 | 175.58 | 25.14 |
| SCE1572_9949 | 65 | 8 |
| SCE1572_6714 | 592 | 601 |
| SCE1572_10060 | 0 | 0 |
| SCE1572_1650 | 24 | 6 |
| SCE1572_3244 | 102 | 94 |
| SCE1572_2213 | 115 | 106 |
| SCE1572_1321 | 92 | 85 |
| SCE1572_11242 | 274 | 58 |
| SCE1572_727 | 31 | 3 |
| SCE1572_1447 | 94 | 15 |
| SCE1572_3859 | 231 | 152 |
| SCE1572_7886 | 30 | 56 |
| SCE1572_10741 | 31 | 19 |
| SCE1572_5400 | 63 | 14 |
| SCE1572_11565 | 23 | 20 |
| SCE1572_6214 | 29 | 4 |
| SCE1572_6468 | 104 | 14 |
| SCE1572_10937 | 86 | 115 |
| SCE1572_8931 | 34 | 6 |
| SCE1572_5964 | 13 | 5 |
| SCE1572_8632 | 21 | 34 |
| SCE1572_3887 | 85 | 125 |
| SCE1572_7678 | 26 | 129 |
| SCE1572_2009 | 88 | 10 |
| SCE1572_4732 | 22 | 7 |
| SCE1572_9734 | 41 | 50 |

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| SCE1572_7472 | 89 | 63 |
| SCE1572_3191 | 0 | 0 |
| SCE1572_5760 | 45 | 10 |
| SCE1572_558 | 66 | 200 |
| SCE1572_645 | 5 | 7 |
| SCE1572_11076 | 31 | 244 |
| SCE1572_7111 | 115 | 46 |
| SCE1572_8934 | 26 | 5 |
| SCE1572_6047 | 8 | 50 |
| SCE1572_7091 | 96 | 33 |
| SCE1572_9453 | 70 | 58 |
| SCE1572_2237 | 68 | 22 |
| SCE1572_8524 | 174 | 426 |
| SCE1572_10151 | 62 | 179 |
| SCE1572_3396 | 247 | 96 |
| SCE1572_9789 | 37 | 12 |
| SCE1572_10660 | 12 | 0 |
| SCE1572_906 | 59 | 0 |
| SCE1572_7351 | 43 | 7 |
| SCE1572_1804 | 1.99 | 0 |
| SCE1572_7529 | 48 | 9 |
| SCE1572_7789 | 0 | 0 |
| SCE1572_10748 | 58 | 50 |
| SCE1572_1989 | 0 | 1 |
| SCE1572_1949 | 2 | 0 |
| SCE1572_6237 | 50 | 9 |
| SCE1572_9782 | 34 | 10 |
| SCE1572_7306 | 3 | 0 |
| SCE1572_2281 | 59 | 11 |
| SCE1572_7964 | 18 | 7 |
| SCE1572_7423 | 77 | 51 |
| SCE1572_5667 | 5 | 0 |
| SCE1572_10563 | 130 | 40 |
| SCE1572_7275 | 89 | 14 |
| SCE1572_11133 | 86 | 23 |
| SCE1572_9114 | 2 | 0 |
| SCE1572_7239 | 0 | 0 |
| SCE1572_4027 | 305 | 338 |
| SCE1572_5905 | 0 | 0 |
| SCE1572_7267 | 313 | 42 |
| SCE1572_2133 | 387 | 42 |
| SCE1572_10810 | 78 | 71 |
| SCE1572_4116 | 36 | 2 |
| SCE1572_5080 | 451 | 1254 |
| SCE1572_8448 | 232.9 | 33 |
| SCE1572_7157 | 133 | 21 |
| SCE1572_2129 | 32 | 9 |
| SCE1572_794 | 256 | 150 |

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| SCE1572_4368 | 48 | 75 |
| SCE1572_11311 | 254 | 49 |
| SCE1572_11337 | 39 | 9 |
| SCE1572_9843 | 46.55 | 61.05 |
| SCE1572_2222 | 26 | 9 |
| SCE1572_5124 | 74 | 3 |
| SCE1572_1070 | 42 | 1 |
| SCE1572_1187 | 39 | 1 |
| SCE1572_545 | 76 | 7 |
| SCE1572_2849 | 0 | 0 |
| SCE1572_2230 | 252 | 353 |
| SCE1572_1076 | 102 | 90 |
| SCE1572_3932 | 1581 | 4145 |
| SCE1572_7165 | 177 | 18 |
| SCE1572_10357 | 75 | 295 |
| SCE1572_1051 | 55 | 17 |
| SCE1572_7137 | 53 | 5 |
| SCE1572_3023 | 62 | 11 |
| SCE1572_7337 | 179 | 300 |
| SCE1572_11344 | 421 | 677 |
| SCE1572_11394 | 56 | 87 |
| SCE1572_11594 | 172 | 447 |
| SCE1572_3525 | 208 | 1187 |
| SCE1572_3917 | 250 | 64 |
| SCE1572_7408 | 34 | 76 |
| SCE1572_7932 | 75 | 22 |
| SCE1572_3065 | 15 | 7 |
| SCE1572_1835 | 45 | 17 |
| SCE1572_5417 | 155 | 87 |
| SCE1572_6263 | 57 | 22 |
| SCE1572_2908 | 43 | 25 |
| SCE1572_4998 | 37 | 32 |
| SCE1572_5705 | 68 | 35 |
| SCE1572_11269 | 102 | 53 |
| SCE1572_10778 | 158 | 57 |
| SCE1572_1114 | 138 | 236 |
| SCE1572_1515 | 21 | 24 |
| SCE1572_10885 | 93 | 21 |
| SCE1572_6780 | 0 | 0 |
| SCE1572_4885 | 81 | 17 |
| SCE1572_329 | 57 | 51 |
| SCE1572_7039 | 86 | 15 |
| SCE1572_2000 | 9 | 0 |
| SCE1572_9025 | 105 | 168 |
| SCE1572_4176 | 198 | 36 |
| SCE1572_3506 | 119 | 146 |
| SCE1572_6256 | 45 | 8 |
| SCE1572_5642 | 9 | 4 |

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| SCE1572_2374 | 122 | 431 |
| SCE1572_5660 | 65.96 | 7 |
| SCE1572_7032 | 205.46 | 41 |
| SCE1572_4616 | 5 | 1 |
| SCE1572_10293 | 0 | 0 |
| SCE1572_8577 | 0 | 0 |
| SCE1572_3910 | 122 | 97 |
| SCE1572_1431 | 4 | 0 |
| SCE1572_4795 | 47 | 53 |
| SCE1572_316 | 182 | 40 |
| SCE1572_5633 | 47 | 14 |
| SCE1572_3703 | 60 | 11 |
| SCE1572_4595 | 24 | 9 |
| SCE1572_10587 | 71 | 9 |
| SCE1572_10763 | 1 | 0 |
| SCE1572_10935 | 43 | 15 |
| SCE1572_4963 | 633 | 1023 |
| SCE1572_6137 | 15 | 8 |
| SCE1572_6748 | 41 | 10 |
| SCE1572_5606 | 40 | 14 |
| SCE1572_9687 | 289 | 262 |
| SCE1572_2832 | 87 | 64 |
| SCE1572_1818 | 17 | 9 |
| SCE1572_4454 | 33 | 9 |
| SCE1572_221 | 173 | 77 |
| SCE1572_6037 | 4 | 0 |
| SCE1572_11273 | 104 | 187 |
| SCE1572_6277 | 92 | 44 |
| SCE1572_3590 | 14 | 0 |
| SCE1572_9591 | 343 | 1882 |
| SCE1572_6556 | 68 | 9 |
| SCE1572_9625 | 111 | 34 |
| SCE1572_4274 | 43 | 92 |
| SCE1572_3501 | 80 | 28 |
| SCE1572_10414 | 53 | 30 |
| SCE1572_5925 | 79 | 49 |
| SCE1572_11104 | 15 | 42 |
| SCE1572_3573 | 28 | 1 |
| SCE1572_9635 | 143 | 60 |
| SCE1572_9194 | 35 | 23 |
| SCE1572_2062 | 92 | 26 |
| SCE1572_1990 | 108 | 24 |
| SCE1572_9006 | 160 | 94 |
| SCE1572_4254 | 7 | 1 |
| SCE1572_6660 | 73 | 29 |
| SCE1572_6434 | 365 | 41 |
| SCE1572_9096 | 34 | 38 |
| SCE1572_11386 | 494 | 838 |

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| SCE1572_5521 | 252 | 116 |
| SCE1572_2842 | 3.5 | 0 |
| SCE1572_10730 | 32 | 3 |
| SCE1572_2286 | 21 | 21 |
| SCE1572_11466 | 128 | 37 |
| SCE1572_1440 | 176 | 88 |
| SCE1572_9727 | 62 | 15 |
| SCE1572_5503 | 100 | 38 |
| SCE1572_10188 | 102 | 74 |
| SCE1572_3854 | 95 | 41 |
| SCE1572_9729 | 130 | 60 |
| SCE1572_888 | 23 | 1 |
| SCE1572_8618 | 102 | 30 |
| SCE1572_7014 | 12 | 1 |
| SCE1572_7244 | 0 | 0 |
| SCE1572_1233 | 141 | 20 |
| SCE1572_9239 | 48 | 9 |
| SCE1572_2490 | 131 | 22 |
| SCE1572_61 | 102 | 88 |
| SCE1572_6335 | 175 | 13 |
| SCE1572_6765 | 140 | 18 |
| SCE1572_9170 | 3 | 0 |
| SCE1572_268 | 0 | 0 |
| SCE1572_3927 | 98 | 65 |
| SCE1572_993 | 34 | 29 |
| SCE1572_8575 | 149.9 | 10.48 |
| SCE1572_11250 | 10 | 0 |
| SCE1572_2748 | 205 | 120 |
| SCE1572_6245 | 42 | 4 |
| SCE1572_10450 | 14 | 1 |
| SCE1572_44 | 72 | 44 |
| SCE1572_4878 | 30 | 6 |
| SCE1572_1646 | 0 | 0 |
| SCE1572_7509 | 0 | 0 |
| SCE1572_6008 | 68 | 280 |
| SCE1572_8285 | 57 | 45 |
| SCE1572_5281 | 63 | 22 |
| SCE1572_7812 | 181 | 661 |
| SCE1572_10549 | 100.36 | 22.05 |
| SCE1572_172 | 140 | 24 |
| SCE1572_2944 | 100 | 17 |
| SCE1572_2332 | 224.59 | 86 |
| SCE1572_9460 | 99 | 14 |
| SCE1572_194 | 0 | 0 |
| SCE1572_4556 | 82 | 14 |
| SCE1572_11456 | 33 | 7 |
| SCE1572_869 | 0 | 0 |
| SCE1572_1905 | 5 | 0 |

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| SCE1572_7101 | 691 | 823 |
| SCE1572_11474 | 248.87 | 29.53 |
| SCE1572_5193 | 50 | 105 |
| SCE1572_5443 | 114 | 16 |
| SCE1572_4741 | 89 | 20 |
| SCE1572_10553 | 0 | 0 |
| SCE1572_3114 | 228 | 31 |
| SCE1572_4068 | 86 | 54 |
| SCE1572_11072 | 113 | 106 |
| SCE1572_9767 | 86 | 301 |
| SCE1572_756 | 0 | 0 |
| SCE1572_4464 | 238 | 32 |
| SCE1572_7980 | 27 | 9 |
| SCE1572_6512 | 111 | 16 |
| SCE1572_9297 | 128 | 202 |
| SCE1572_5574 | 175 | 50 |
| SCE1572_6775 | 0 | 0 |
| SCE1572_9184 | 53 | 12 |
| SCE1572_3090 | 179 | 72 |
| SCE1572_2940 | 44 | 37 |
| SCE1572_1007 | 174 | 187 |
| SCE1572_10101 | 32 | 7 |
| SCE1572_9664 | 26 | 56 |
| SCE1572_4521 | 28 | 4 |
| SCE1572_9451 | 0 | 0 |
| SCE1572_10349 | 0 | 0 |
| SCE1572_6063 | 4 | 0 |
| SCE1572_7711 | 86 | 93 |
| SCE1572_6040 | 543 | 349 |
| SCE1572_7295 | 220 | 105 |
| SCE1572_5612 | 73 | 59 |
| SCE1572_914 | 51 | 58 |
| SCE1572_7338 | 85 | 308 |
| SCE1572_9546 | 166 | 115 |
| SCE1572_2361 | 179 | 131 |
| SCE1572_10081 | 875 | 2216 |
| SCE1572_6425 | 88 | 9 |
| SCE1572_7087 | 146 | 26 |
| SCE1572_3122 | 209 | 34 |
| SCE1572_10629 | 451.27 | 730.92 |
| SCE1572_6183 | 200 | 25 |
| SCE1572_2407 | 185 | 309 |
| SCE1572_9479 | 236 | 109 |
| SCE1572_3946 | 660 | 288 |
| SCE1572_2018 | 18 | 7 |
| SCE1572_7193 | 143.17 | 73 |
| SCE1572_8678 | 33 | 9 |
| SCE1572_6295 | 92 | 224 |

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| SCE1572_4225 | 136 | 12 |
| SCE1572_9757 | 43 | 14 |
| SCE1572_2709 | 79 | 12 |
| SCE1572_1134 | 22 | 8 |
| SCE1572_5682 | 32 | 57 |
| SCE1572_6996 | 44 | 12 |
| SCE1572_4442 | 236 | 60 |
| SCE1572_10956 | 41 | 56 |
| SCE1572_3745 | 39 | 5 |
| SCE1572_4336 | 267 | 21 |
| SCE1572_3099 | 74 | 7 |
| SCE1572_11336 | 8 | 2 |
| SCE1572_1216 | 2 | 0 |
| SCE1572_535 | 253 | 280 |
| SCE1572_9158 | 108 | 24 |
| SCE1572_166 | 22 | 24 |
| SCE1572_3410 | 4 | 0 |
| SCE1572_2161 | 545 | 83 |
| SCE1572_3908 | 13 | 1 |
| SCE1572_6777 | 15 | 5 |
| SCE1572_6645 | 59 | 15 |
| SCE1572_3965 | 40 | 14 |
| SCE1572_4261 | 246 | 54 |
| SCE1572_2344 | 169 | 398 |
| SCE1572_6770 | 3 | 2 |
| SCE1572_1828 | 81 | 12 |
| SCE1572_5426 | 154 | 48 |
| SCE1572_7726 | 16 | 164 |
| SCE1572_598 | 30 | 7 |
| SCE1572_3901 | 57 | 54 |
| SCE1572_8478 | 7 | 0 |
| SCE1572_10284 | 60 | 92 |
| SCE1572_11240 | 42 | 17 |
| SCE1572_4461 | 360 | 16 |
| SCE1572_10638 | 12 | 0 |
| SCE1572_3799 | 221 | 314 |
| SCE1572_1786 | 102 | 80 |
| SCE1572_10158 | 42 | 10 |
| SCE1572_8338 | 321.52 | 92.96 |
| SCE1572_8980 | 73 | 10 |
| SCE1572_3954 | 87 | 25 |
| SCE1572_6417 | 0 | 0 |
| SCE1572_9079 | 0 | 0 |
| SCE1572_3083 | 76 | 7 |
| SCE1572_10595 | 197 | 22 |
| SCE1572_3328 | 170 | 202 |
| SCE1572_3434 | 352 | 273 |
| SCE1572_9984 | 218 | 45 |

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| SCE1572_8968 | 143 | 39 |
| SCE1572_39 | 220 | 77 |
| SCE1572_2411 | 100 | 163 |
| SCE1572_1999 | 25 | 5 |
| SCE1572_3318 | 19 | 24 |
| SCE1572_10817 | 104 | 32 |
| SCE1572_9696 | 228 | 235 |
| SCE1572_6524 | 331 | 140 |
| SCE1572_6569 | 31 | 77 |
| SCE1572_7689 | 0 | 0 |
| SCE1572_6110 | 35 | 6 |
| SCE1572_7027 | 206.07 | 118 |
| SCE1572_2816 | 127 | 23 |
| SCE1572_5263 | 0 | 0 |
| SCE1572_2933 | 0 | 0 |
| SCE1572_6272 | 77 | 53 |
| SCE1572_7271 | 34 | 5 |
| SCE1572_4318 | 113 | 9 |
| SCE1572_8239 | 82 | 93 |
| SCE1572_2660 | 0 | 0 |
| SCE1572_4415 | 32 | 3 |
| SCE1572_11571 | 36 | 751 |
| SCE1572_308 | 65 | 62 |
| SCE1572_3326 | 76 | 66 |
| SCE1572_4125 | 110 | 19 |
| SCE1572_7515 | 31 | 15 |
| SCE1572_6405 | 57 | 31 |
| SCE1572_802 | 244 | 142 |
| SCE1572_9326 | 324 | 192 |
| SCE1572_4981 | 43 | 66 |
| SCE1572_7173 | 127 | 217 |
| SCE1572_8233 | 42 | 30 |
| SCE1572_10355 | 54 | 150 |
| SCE1572_8626 | 70 | 19 |
| SCE1572_822 | 2 | 0 |
| SCE1572_2586 | 27.44 | 4 |
| SCE1572_1120 | 183 | 29 |
| SCE1572_10702 | 15 | 69 |
| SCE1572_9415 | 1 | 0 |
| SCE1572_6120 | 187 | 70 |
| SCE1572_3047 | 45 | 10 |
| SCE1572_1540 | 92 | 84 |
| SCE1572_7232 | 139 | 23 |
| SCE1572_3848 | 27 | 7 |
| SCE1572_7998 | 76.72 | 15.17 |
| SCE1572_8882 | 0 | 0 |
| SCE1572_4751 | 100 | 168 |
| SCE1572_6050 | 0 | 0 |

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| SCE1572_10386 | 405 | 78 |
| SCE1572_9410 | 458 | 3304 |
| SCE1572_3578 | 11 | 15 |
| SCE1572_9550 | 128 | 36 |
| SCE1572_6199 | 2 | 0 |
| SCE1572_4504 | 213 | 48 |
| SCE1572_7179 | 60 | 15 |
| SCE1572_7040 | 12 | 0 |
| SCE1572_4185 | 270 | 192 |
| SCE1572_2868 | 77 | 29 |
| SCE1572_304 | 533 | 63 |
| SCE1572_11445 | 158 | 94 |
| SCE1572_4021 | 53 | 32 |
| SCE1572_4574 | 107 | 27 |
| SCE1572_2367 | 0 | 0 |
| SCE1572_1750 | 69 | 27 |
| SCE1572_986 | 488 | 756 |
| SCE1572_7378 | 14 | 5 |
| SCE1572_1790 | 43 | 5 |
| SCE1572_2796 | 22 | 9 |
| SCE1572_2184 | 340 | 46 |
| SCE1572_2119 | 76 | 65 |
| SCE1572_6351 | 209 | 26 |
| SCE1572_8494 | 17 | 0 |
| SCE1572_8812 | 61 | 10 |
| SCE1572_898 | 34 | 9 |
| SCE1572_11468 | 70 | 86 |
| SCE1572_6079 | 0 | 0 |
| SCE1572_8680 | 34 | 12 |
| SCE1572_3347 | 577 | 129 |
| SCE1572_6055 | 321 | 195 |
| SCE1572_5153 | 89 | 11 |
| SCE1572_119 | 156 | 176 |
| SCE1572_8896 | 70 | 143 |
| SCE1572_1242 | 287 | 129 |
| SCE1572_3419 | 216 | 112 |
| SCE1572_9666 | 3 | 9 |
| SCE1572_2487 | 175 | 284 |
| SCE1572_1264 | 0 | 0 |
| SCE1572_5098 | 189 | 337 |
| SCE1572_2474 | 113 | 321 |
| SCE1572_3592 | 17 | 6 |
| SCE1572_1830 | 155 | 65 |
| SCE1572_5597 | 226 | 343 |
| SCE1572_7095 | 230 | 35 |
| SCE1572_10249 | 0 | 0 |
| SCE1572_4482 | 366 | 367 |
| SCE1572_161 | 92 | 11 |

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| SCE1572_4585 | 55 | 30 |
| SCE1572_63 | 122 | 45 |
| SCE1572_2872 | 73 | 22 |
| SCE1572_2379 | 39 | 71 |
| SCE1572_6262 | 66 | 17 |
| SCE1572_5456 | 26 | 4 |
| SCE1572_8360 | 11 | 1 |
| SCE1572_7880 | 28 | 12 |
| SCE1572_6935 | 94 | 39 |
| SCE1572_6679 | 64 | 22 |
| SCE1572_3121 | 107 | 75 |
| SCE1572_4352 | 0 | 0 |
| SCE1572_1623 | 0 | 0 |
| SCE1572_8671 | 7 | 1 |
| SCE1572_10766 | 75 | 1544 |
| SCE1572_4866 | 33 | 126 |
| SCE1572_1285 | 1458 | 12485 |
| SCE1572_9791 | 0 | 0 |
| SCE1572_24 | 90 | 49 |
| SCE1572_9539 | 66 | 6 |
| SCE1572_3941 | 2432 | 1390 |
| SCE1572_6796 | 53 | 42 |
| SCE1572_9330 | 355 | 465 |
| SCE1572_1657 | 43 | 15 |
| SCE1572_3963 | 190 | 24 |
| SCE1572_7879 | 167 | 60 |
| SCE1572_5175 | 59 | 13 |
| SCE1572_8423 | 272 | 74 |
| SCE1572_4437 | 0 | 0 |
| SCE1572_2421 | 55 | 37 |
| SCE1572_6988 | 41 | 3 |
| SCE1572_11010 | 81 | 167 |
| SCE1572_5170 | 295 | 1526 |
| SCE1572_8563 | 56 | 145 |
| SCE1572_3747 | 0 | 0 |
| SCE1572_3998 | 131 | 99 |
| SCE1572_4977 | 215 | 1491 |
| SCE1572_6959 | 1 | 0 |
| SCE1572_1684 | 94 | 51 |
| SCE1572_7333 | 0 | 0 |
| SCE1572_3804 | 117 | 20 |
| SCE1572_9627 | 614.79 | 96 |
| SCE1572_7297 | 49 | 10 |
| SCE1572_3672 | 19.52 | 5 |
| SCE1572_1107 | 162 | 15 |
| SCE1572_11117 | 44 | 12 |
| SCE1572_11541 | 24 | 1 |
| SCE1572_10815 | 49 | 15 |

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| SCE1572_11555 | 105 | 19 |
| SCE1572_7690 | 46.55 | 61.05 |
| SCE1572_6318 | 38 | 10 |
| SCE1572_6941 | 68 | 12 |
| SCE1572_8 | 179 | 78 |
| SCE1572_9759 | 110 | 18 |
| SCE1572_7657 | 78 | 22 |
| SCE1572_6851 | 8 | 2 |
| SCE1572_7002 | 0 | 0 |
| SCE1572_9166 | 60 | 7 |
| SCE1572_2975 | 111.19 | 9.19 |
| SCE1572_4128 | 22 | 10 |
| SCE1572_2261 | 96 | 128 |
| SCE1572_4234 | 78 | 10 |
| SCE1572_461 | 11 | 2 |
| SCE1572_9873 | 24 | 8 |
| SCE1572_9372 | 96 | 25 |
| SCE1572_72 | 149 | 84 |
| SCE1572_228 | 10 | 0 |
| SCE1572_82 | 0 | 0 |
| SCE1572_5341 | 273 | 127 |
| SCE1572_10486 | 48 | 36 |
| SCE1572_6682 | 44 | 119 |
| SCE1572_9571 | 49 | 22 |
| SCE1572_9040 | 63 | 168 |
| SCE1572_11052 | 171 | 820 |
| SCE1572_11360 | 277 | 521 |
| SCE1572_5202 | 48 | 31 |
| SCE1572_6880 | 1 | 0 |
| SCE1572_4610 | 40 | 15 |
| SCE1572_7675 | 823.86 | 88.05 |
| SCE1572_1661 | 111 | 137 |
| SCE1572_7892 | 685 | 13084 |
| SCE1572_9047 | 2 | 0 |
| SCE1572_5277 | 0 | 0 |
| SCE1572_5998 | 59 | 48 |
| SCE1572_8266 | 456 | 143 |
| SCE1572_938 | 14 | 6 |
| SCE1572_7383 | 171 | 26 |
| SCE1572_2457 | 1 | 0 |
| SCE1572_2054 | 186 | 111 |
| SCE1572_571 | 0 | 0 |
| SCE1572_4856 | 100 | 12 |
| SCE1572_591 | 232 | 146 |
| SCE1572_4653 | 160 | 31 |
| SCE1572_3661 | 61 | 5 |
| SCE1572_10229 | 9 | 3 |
| SCE1572_6595 | 0 | 0 |

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| SCE1572_10091 | 290 | 692 |
| SCE1572_4346 | 0 | 0 |
| SCE1572_2896 | 28 | 3 |
| SCE1572_692 | 12 | 6 |
| SCE1572_881 | 158 | 96 |
| SCE1572_4474 | 0 | 0 |
| SCE1572_7801 | 202 | 137 |
| SCE1572_6981 | 187 | 7 |
| SCE1572_2582 | 169 | 38 |
| SCE1572_5949 | 350 | 79 |
| SCE1572_6269 | 15 | 18 |
| SCE1572_11015 | 5 | 2 |
| SCE1572_5129 | 0 | 0 |
| SCE1572_1584 | 52 | 104 |
| SCE1572_427 | 54 | 258 |
| SCE1572_857 | 48 | 431 |
| SCE1572_3371 | 84 | 19 |
| SCE1572_6197 | 3 | 1 |
| SCE1572_640 | 20 | 14 |
| SCE1572_9128 | 32 | 76 |
| SCE1572_1193 | 135 | 98 |
| SCE1572_5713 | 127 | 28 |
| SCE1572_7201 | 82 | 29 |
| SCE1572_11346 | 118 | 204 |
| SCE1572_11037 | 110 | 218 |
| SCE1572_7343 | 126 | 60 |
| SCE1572_8128 | 14 | 0 |
| SCE1572_1226 | 107 | 14 |
| SCE1572_513 | 105 | 22 |
| SCE1572_5913 | 19 | 4 |
| SCE1572_1944 | 131 | 18 |
| SCE1572_2663 | 33 | 9 |
| SCE1572_4762 | 190 | 1267 |
| SCE1572_3875 | 82 | 69 |
| SCE1572_9233 | 139 | 254 |
| SCE1572_3797 | 198 | 118 |
| SCE1572_9285 | 52 | 26 |
| SCE1572_11165 | 58 | 4 |
| SCE1572_9532 | 73 | 472 |
| SCE1572_8340 | 0 | 0 |
| SCE1572_9803 | 44 | 29 |
| SCE1572_8719 | 68 | 16 |
| SCE1572_7418 | 0 | 0 |
| SCE1572_4619 | 0 | 0 |
| SCE1572_3836 | 7 | 0 |
| SCE1572_1873 | 21 | 4 |
| SCE1572_7970 | 47 | 30 |
| SCE1572_3265 | 0 | 0 |

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| SCE1572_7069 | 79 | 125 |
| SCE1572_8463 | 775 | 1419 |
| SCE1572_7553 | 22 | 5 |
| SCE1572_11110 | 117.44 | 141.12 |
| SCE1572_3915 | 15 | 0 |
| SCE1572_5528 | 238 | 51 |
| SCE1572_6920 | 18 | 0 |
| SCE1572_9578 | 79 | 12 |
| SCE1572_8019 | 0 | 0.02 |
| SCE1572_8538 | 85 | 30 |
| SCE1572_10597 | 45 | 5 |
| SCE1572_3834 | 1 | 0 |
| SCE1572_261 | 70 | 9 |
| SCE1572_877 | 227 | 191 |
| SCE1572_7620 | 62 | 24 |
| SCE1572_8823 | 42 | 11 |
| SCE1572_10432 | 254 | 66 |
| SCE1572_3485 | 115 | 36 |
| SCE1572_9925 | 279.21 | 367 |
| SCE1572_736 | 72 | 22 |
| SCE1572_7536 | 274 | 30 |
| SCE1572_9893 | 173 | 40 |
| SCE1572_3474 | 77 | 14 |
| SCE1572_4680 | 2 | 0 |
| SCE1572_5298 | 43 | 17 |
| SCE1572_940 | 276 | 32 |
| SCE1572_8983 | 3 | 0 |
| SCE1572_6162 | 100 | 57 |
| SCE1572_11509 | 216 | 62 |
| SCE1572_9247 | 100 | 9 |
| SCE1572_8387 | 80 | 7 |
| SCE1572_10404 | 118 | 40 |
| SCE1572_7127 | 1 | 0 |
| SCE1572_7652 | 252 | 42 |
| SCE1572_1001 | 0 | 0 |
| SCE1572_3203 | 62 | 307 |
| SCE1572_2243 | 224.59 | 53 |
| SCE1572_10340 | 190 | 25 |
| SCE1572_4698 | 5 | 1 |
| SCE1572_92 | 267 | 247 |
| SCE1572_547 | 71 | 31 |
| SCE1572_8219 | 18 | 8 |
| SCE1572_4004 | 0 | 0 |
| SCE1572_4774 | 75 | 0 |
| SCE1572_5326 | 0 | 0 |
| SCE1572_6895 | 0 | 0 |
| SCE1572_6208 | 0 | 0 |
| SCE1572_6946 | 47 | 11 |

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| SCE1572_406 | 1 | 0 |
| SCE1572_6188 | 32 | 9 |
| SCE1572_5364 | 5 | 0 |
| SCE1572_3196 | 183 | 215 |
| SCE1572_3934 | 0 | 0 |
| SCE1572_8611 | 98 | 16 |
| SCE1572_6810 | 625 | 715 |
| SCE1572_8806 | 0 | 0 |
| SCE1572_4158 | 78 | 17 |
| SCE1572_625 | 0 | 0 |
| SCE1572_9337 | 546 | 680 |
| SCE1572_9717 | 200 | 998 |
| SCE1572_848 | 1913 | 574 |
| SCE1572_9658 | 69 | 60 |
| SCE1572_6828 | 79 | 26 |
| SCE1572_7207 | 15 | 19 |
| SCE1572_5783 | 66 | 52 |
| SCE1572_7362 | 10 | 1 |
| SCE1572_6948 | 327 | 112 |
| SCE1572_6328 | 58 | 43 |
| SCE1572_5971 | 121 | 96 |
| SCE1572_11515 | 11 | 5 |
| SCE1572_9998 | 53 | 5 |
| SCE1572_7827 | 102 | 124 |
| SCE1572_11498 | 0 | 0 |
| SCE1572_8627 | 49 | 13 |
| SCE1572_6396 | 47 | 66 |
| SCE1572_1816 | 32 | 4 |
| SCE1572_1689 | 30 | 17 |
| SCE1572_540 | 199 | 53 |
| SCE1572_4847 | 141 | 99 |
| SCE1572_54 | 65 | 14 |
| SCE1572_2120 | 166 | 114 |
| SCE1572_1480 | 141 | 19 |
| SCE1572_3175 | 211 | 161 |
| SCE1572_6472 | 32 | 2 |
| SCE1572_5395 | 0 | 0 |
| SCE1572_7930 | 307 | 59 |
| SCE1572_6485 | 27 | 15 |
| SCE1572_2317 | 30 | 8 |
| SCE1572_11521 | 58 | 9 |
| SCE1572_6877 | 471 | 472 |
| SCE1572_2337 | 21 | 5 |
| SCE1572_9657 | 68 | 28 |
| SCE1572_99 | 14 | 3 |
| SCE1572_10461 | 213 | 400 |
| SCE1572_2610 | 42 | 30 |
| SCE1572_2693 | 61 | 11 |

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| SCE1572_5047 | 48 | 26 |
| SCE1572_465 | 57 | 56 |
| SCE1572_1806 | 36 | 10 |
| SCE1572_1545 | 285 | 88 |
| SCE1572_10098 | 47 | 79 |
| SCE1572_783 | 190 | 32 |
| SCE1572_9872 | 70 | 138 |
| SCE1572_1542 | 12 | 13 |
| SCE1572_6838 | 90 | 20 |
| SCE1572_283 | 87 | 29 |
| SCE1572_4492 | 62 | 21 |
| SCE1572_850 | 2315 | 3252 |
| SCE1572_3599 | 19 | 14 |
| SCE1572_9433 | 82 | 45 |
| SCE1572_1837 | 211 | 165 |
| SCE1572_10439 | 287 | 438 |
| SCE1572_10075 | 1439 | 1171 |
| SCE1572_10995 | 167 | 47 |
| SCE1572_5183 | 41 | 327 |
| SCE1572_10468 | 6 | 1 |
| SCE1572_10502 | 133 | 43 |
| SCE1572_1563 | 10 | 0 |
| SCE1572_8311 | 41 | 3 |
| SCE1572_3752 | 201 | 162 |
| SCE1572_4381 | 180 | 34 |
| SCE1572_164 | 54 | 14 |
| SCE1572_2810 | 3 | 0 |
| SCE1572_4276 | 216 | 50 |
| SCE1572_5476 | 195 | 2076 |
| SCE1572_10133 | 35 | 11 |
| SCE1572_11496 | 113 | 13 |
| SCE1572_3154 | 18 | 8 |
| SCE1572_10954 | 138 | 17 |
| SCE1572_11204 | 156 | 144 |
| SCE1572_6699 | 69 | 14 |
| SCE1572_6692 | 3 | 0 |
| SCE1572_2592 | 0 | 0 |
| SCE1572_11437 | 53 | 34 |
| SCE1572_4044 | 35 | 38 |
| SCE1572_4691 | 64 | 45 |
| SCE1572_5415 | 479 | 56 |
| SCE1572_4748 | 270 | 55 |
| SCE1572_7421 | 12 | 2 |
| SCE1572_5627 | 52 | 3 |
| SCE1572_6284 | 57 | 47 |
| SCE1572_6442 | 191 | 45 |
| SCE1572_916 | 0 | 0 |
| SCE1572_240 | 27.64 | 0 |

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| SCE1572_11184 | 34 | 3 |
| SCE1572_6705 | 1854 | 2921 |
| SCE1572_4810 | 0 | 0 |
| SCE1572_2750 | 95 | 59 |
| SCE1572_5828 | 56 | 13 |
| SCE1572_7923 | 11 | 1 |
| SCE1572_7154 | 29 | 8 |
| SCE1572_9510 | 10 | 0 |
| SCE1572_7887 | 192 | 397 |
| SCE1572_9937 | 8 | 0 |
| SCE1572_4961 | 34 | 60 |
| SCE1572_8370 | 65 | 9 |
| SCE1572_2727 | 58 | 12 |
| SCE1572_8092 | 16 | 1 |
| SCE1572_8693 | 111 | 10 |
| SCE1572_2531 | 15 | 0 |
| SCE1572_746 | 166 | 101 |
| SCE1572_2099 | 39 | 10 |
| SCE1572_5565 | 193 | 60 |
| SCE1572_10542 | 137 | 38 |
| SCE1572_9272 | 55 | 22 |
| SCE1572_7316 | 0 | 0 |
| SCE1572_8991 | 7 | 6 |
| SCE1572_9863 | 604 | 97 |
| SCE1572_5231 | 183 | 290 |
| SCE1572_840 | 208 | 216 |
| SCE1572_11308 | 73 | 7 |
| SCE1572_2198 | 0 | 0 |
| SCE1572_10222 | 36 | 25 |
| SCE1572_4626 | 324 | 239 |
| SCE1572_11257 | 49 | 33 |
| SCE1572_10224 | 736 | 204 |
| SCE1572_6698 | 42 | 18 |
| SCE1572_580 | 30 | 28 |
| SCE1572_6523 | 1 | 0 |
| SCE1572_5519 | 0 | 0 |
| SCE1572_8347 | 128 | 56 |
| SCE1572_10511 | 0 | 0 |
| SCE1572_444 | 25 | 3 |
| SCE1572_5371 | 286 | 156 |
| SCE1572_7543 | 55 | 97 |
| SCE1572_7928 | 245 | 80 |
| SCE1572_6072 | 46 | 8 |
| SCE1572_6289 | 17 | 16 |
| SCE1572_7872 | 252 | 331 |
| SCE1572_7766 | 63 | 10 |
| SCE1572_7584 | 15 | 0 |
| SCE1572_2304 | 168 | 201 |

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| SCE1572_10314 | 31 | 2 |
| SCE1572_6450 | 380 | 123 |
| SCE1572_9907 | 92 | 62 |
| SCE1572_385 | 1 | 0 |
| SCE1572_10765 | 88 | 304 |
| SCE1572_647 | 0 | 0 |
| SCE1572_8929 | 20 | 30 |
| SCE1572_6354 | 13 | 2 |
| SCE1572_5287 | 25 | 66 |
| SCE1572_6201 | 168 | 32 |
| SCE1572_9991 | 140 | 17 |
| SCE1572_395 | 98 | 58 |
| SCE1572_9673 | 57 | 78 |
| SCE1572_774 | 173 | 172 |
| SCE1572_10195 | 22 | 3 |
| SCE1572_796 | 312 | 253 |
| SCE1572_1428 | 63 | 8 |
| SCE1572_1400 | 19 | 8 |
| SCE1572_2573 | 70 | 8 |
| SCE1572_5836 | 15 | 6 |
| SCE1572_11301 | 28 | 32 |
| SCE1572_2655 | 114 | 34 |
| SCE1572_4710 | 34 | 8 |
| SCE1572_479 | 87 | 11 |
| SCE1572_5447 | 93 | 14 |
| SCE1572_6103 | 21 | 4 |
| SCE1572_3603 | 521 | 134 |
| SCE1572_4110 | 59 | 6 |
| SCE1572_813 | 68 | 13 |
| SCE1572_8604 | 59 | 51 |
| SCE1572_8055 | 17 | 6 |
| SCE1572_5747 | 8 | 1 |
| SCE1572_1893 | 4 | 17 |
| SCE1572_2990 | 4 | 0 |
| SCE1572_3542 | 0 | 0 |
| SCE1572_5938 | 18 | 2 |
| SCE1572_1912 | 17 | 0 |
| SCE1572_10333 | 0 | 0 |
| SCE1572_967 | 0 | 0 |
| SCE1572_11447 | 367 | 146 |
| SCE1572_8007 | 109 | 948 |
| SCE1572_780 | 14 | 2 |
| SCE1572_10863 | 71 | 344 |
| SCE1572_6841 | 386 | 205 |
| SCE1572_9493 | 0 | 0 |
| SCE1572_10754 | 145 | 25 |
| SCE1572_6212 | 253 | 42 |
| SCE1572_1405 | 50 | 14 |

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| SCE1572_5390 | 0 | 0 |
| SCE1572_7572 | 78.33 | 75 |
| SCE1572_8821 | 14 | 14 |
| SCE1572_1339 | 88 | 181 |
| SCE1572_4924 | 48 | 32 |
| SCE1572_7839 | 58 | 33 |
| SCE1572_533 | 11 | 16 |
| SCE1572_6340 | 63 | 22 |
| SCE1572_1485 | 190 | 67 |
| SCE1572_6969 | 66 | 246 |
| SCE1572_4180 | 8 | 7 |
| SCE1572_6543 | 139 | 71 |
| SCE1572_7713 | 27 | 5 |
| SCE1572_1020 | 50.31 | 73.74 |
| SCE1572_1352 | 131 | 78 |
| SCE1572_6221 | 64 | 14 |
| SCE1572_4928 | 2 | 0 |
| SCE1572_11194 | 55 | 115 |
| SCE1572_8274 | 41 | 29 |
| SCE1572_7612 | 315 | 265 |
| SCE1572_8192 | 49 | 10 |
| SCE1572_2938 | 149 | 117 |
| SCE1572_1723 | 7 | 2 |
| SCE1572_10164 | 38 | 5 |
| SCE1572_10441 | 13 | 16 |
| SCE1572_10980 | 26 | 19 |
| SCE1572_3704 | 39 | 76 |
| SCE1572_2165 | 161 | 37 |
| SCE1572_2117 | 191 | 133 |
| SCE1572_4941 | 54 | 35 |
| SCE1572_8030 | 355.68 | 124.41 |
| SCE1572_6903 | 173 | 17 |
| SCE1572_4896 | 7 | 2 |
| SCE1572_7270 | 366 | 122 |
| SCE1572_7226 | 96 | 146 |
| SCE1572_6720 | 6094 | 9354 |
| SCE1572_9067 | 58 | 16 |
| SCE1572_8853 | 4 | 1 |
| SCE1572_3409 | 57 | 14 |
| SCE1572_4072 | 265 | 296 |
| SCE1572_1230 | 360 | 184 |
| SCE1572_9833 | 58 | 8 |
| SCE1572_4537 | 54.65 | 9.58 |
| SCE1572_5721 | 166 | 71 |
| SCE1572_11218 | 131.99 | 41 |
| SCE1572_4782 | 95 | 32 |
| SCE1572_10205 | 130.69 | 13.29 |
| SCE1572_5110 | 79 | 297 |

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| SCE1572_4953 | 303 | 77 |
| SCE1572_4499 | 72 | 23 |
| SCE1572_5453 | 89 | 12 |
| SCE1572_1383 | 0 | 0 |
| SCE1572_10128 | 1 | 0 |
| SCE1572_3035 | 41 | 7 |
| SCE1572_3385 | 111 | 48 |
| SCE1572_2578 | 105 | 8 |
| SCE1572_8254 | 77 | 1595 |
| SCE1572_10620 | 87 | 29 |
| SCE1572_4986 | 34 | 36 |
| SCE1572_6819 | 52 | 3 |
| SCE1572_7748 | 25 | 1 |
| SCE1572_1165 | 205 | 95 |
| SCE1572_6381 | 15 | 36 |
| SCE1572_3296 | 0 | 0 |
| SCE1572_5450 | 91 | 36 |
| SCE1572_7191 | 278 | 268 |
| SCE1572_2557 | 388 | 77 |
| SCE1572_3615 | 111 | 15 |
| SCE1572_10857 | 273.61 | 72 |
| SCE1572_4117 | 22 | 1332 |
| SCE1572_6867 | 1083 | 429 |
| SCE1572_8380 | 28 | 12 |
| SCE1572_1761 | 88 | 10 |
| SCE1572_10234 | 6.45 | 0 |
| SCE1572_10232 | 65 | 6 |
| SCE1572_1579 | 24 | 11 |
| SCE1572_5315 | 22 | 14 |
| SCE1572_4151 | 64 | 239 |
| SCE1572_3657 | 29 | 13 |
| SCE1572_10615 | 139 | 35 |
| SCE1572_1341 | 100 | 259 |
| SCE1572_8243 | 220 | 211 |
| SCE1572_7414 | 30 | 2 |
| SCE1572_10911 | 3 | 0 |
| SCE1572_5225 | 132 | 164 |
| SCE1572_2396 | 24 | 26 |
| SCE1572_4400 | 39 | 8 |
| SCE1572_8842 | 83 | 50 |
| SCE1572_10419 | 98 | 20 |
| SCE1572_7959 | 11 | 8 |
| SCE1572_1153 | 87.56 | 110.88 |
| SCE1572_5336 | 39 | 10 |
| SCE1572_4719 | 129 | 17 |
| SCE1572_6586 | 253 | 24 |
| SCE1572_7897 | 11 | 10 |
| SCE1572_11158 | 86.55 | 34.21 |

| | | |
|---------------|-------|------|
| SCE1572_3884 | 40 | 6 |
| SCE1572_8080 | 16 | 1 |
| SCE1572_3106 | 50 | 38 |
| SCE1572_8814 | 68.31 | 14 |
| SCE1572_5302 | 112 | 12 |
| SCE1572_8654 | 1210 | 2779 |
| SCE1572_10843 | 8 | 0 |
| SCE1572_7605 | 68 | 16 |
| SCE1572_1593 | 47 | 36 |
| SCE1572_11127 | 71 | 20 |
| SCE1572_6369 | 117 | 47 |
| SCE1572_741 | 38 | 25 |
| SCE1572_1749 | 52 | 17 |
| SCE1572_11146 | 156 | 137 |
| SCE1572_6097 | 44 | 31 |
| SCE1572_7486 | 43 | 14 |
| SCE1572_10655 | 38 | 122 |
| SCE1572_4816 | 1 | 0 |
| SCE1572_2034 | 391 | 285 |
| SCE1572_1214 | 25 | 6 |
| SCE1572_10804 | 67 | 10 |
| SCE1572_4252 | 54 | 8 |
| SCE1572_11597 | 159 | 780 |
| SCE1572_6887 | 21 | 2 |
| SCE1572_7811 | 27 | 3 |
| SCE1572_1359 | 270 | 351 |
| SCE1572_10714 | 79 | 9 |
| SCE1572_5251 | 237 | 412 |
| SCE1572_7395 | 30 | 2 |
| SCE1572_587 | 106 | 20 |
| SCE1572_6808 | 181 | 294 |
| SCE1572_2363 | 18 | 4 |
| SCE1572_9844 | 11 | 10 |
| SCE1572_10526 | 15 | 3 |
| SCE1572_9342 | 106 | 591 |
| SCE1572_4146 | 32 | 5 |
| SCE1572_7281 | 25 | 48 |
| SCE1572_4372 | 307 | 48 |
| SCE1572_814 | 37 | 6 |
| SCE1572_5025 | 85 | 25 |
| SCE1572_1083 | 31 | 2 |
| SCE1572_6457 | 130 | 28 |
| SCE1572_3233 | 95 | 26 |
| SCE1572_671 | 65 | 90 |
| SCE1572_4379 | 95 | 15 |
| SCE1572_10683 | 205 | 190 |
| SCE1572_1027 | 117 | 1222 |
| SCE1572_1631 | 22 | 2 |

| | | |
|---------------|--------|-------|
| SCE1572_8958 | 121 | 91 |
| SCE1572_7873 | 78 | 113 |
| SCE1572_233 | 9 | 9 |
| SCE1572_10045 | 401 | 1907 |
| SCE1572_344 | 312 | 39 |
| SCE1572_5842 | 166 | 19 |
| SCE1572_5402 | 67 | 18 |
| SCE1572_10627 | 143 | 190 |
| SCE1572_1 | 243 | 620 |
| SCE1572_5460 | 49 | 1 |
| SCE1572_5738 | 249 | 109 |
| SCE1572_5815 | 45 | 19 |
| SCE1572_6362 | 190 | 58 |
| SCE1572_247 | 193.36 | 19.56 |
| SCE1572_2757 | 61 | 16 |
| SCE1572_8113 | 56 | 7 |
| SCE1572_6567 | 79 | 58 |
| SCE1572_3516 | 53 | 90 |
| SCE1572_10268 | 242 | 69 |
| SCE1572_4095 | 99 | 34 |
| SCE1572_6711 | 82 | 60 |
| SCE1572_7319 | 37 | 20 |
| SCE1572_8996 | 124 | 73 |
| SCE1572_10202 | 160.93 | 25.85 |
| SCE1572_4229 | 118 | 34 |
| SCE1572_10113 | 42 | 38 |
| SCE1572_3289 | 136 | 33 |
| SCE1572_5800 | 180 | 209 |
| SCE1572_2827 | 23 | 2 |
| SCE1572_10116 | 87 | 70 |
| SCE1572_8211 | 276 | 148 |
| SCE1572_6952 | 65 | 7 |
| SCE1572_1962 | 129 | 20 |
| SCE1572_9390 | 94 | 72 |
| SCE1572_960 | 58 | 44 |
| SCE1572_10946 | 391 | 74 |
| SCE1572_2999 | 51 | 9 |
| SCE1572_1927 | 86 | 67 |
| SCE1572_9035 | 54 | 11 |
| SCE1572_10724 | 0 | 0 |
| SCE1572_4058 | 30 | 8 |
| SCE1572_6655 | 44 | 9 |
| SCE1572_438 | 0 | 0 |
| SCE1572_5849 | 46 | 4 |
| SCE1572_6601 | 537 | 258 |
| SCE1572_8322 | 38 | 58 |
| SCE1572_10662 | 176 | 56 |
| SCE1572_10127 | 10 | 2 |

| | | |
|---------------|-------|-------|
| SCE1572_3361 | 7 | 0 |
| SCE1572_5931 | 65 | 15 |
| SCE1572_7120 | 236 | 53 |
| SCE1572_8914 | 40 | 6 |
| SCE1572_7213 | 84 | 5 |
| SCE1572_5808 | 146 | 25 |
| SCE1572_1738 | 36 | 0 |
| SCE1572_1178 | 101 | 16 |
| SCE1572_5531 | 46 | 0 |
| SCE1572_3085 | 0 | 0 |
| SCE1572_4189 | 166 | 167 |
| SCE1572_1290 | 53 | 16 |
| SCE1572_6503 | 16 | 0 |
| SCE1572_7966 | 48 | 9 |
| SCE1572_7867 | 13 | 42 |
| SCE1572_10986 | 1784 | 13931 |
| SCE1572_8302 | 181 | 213 |
| SCE1572_712 | 7 | 1 |
| SCE1572_1371 | 190 | 72 |
| SCE1572_10014 | 180 | 29 |
| SCE1572_8836 | 0 | 0 |
| SCE1572_4135 | 63 | 9 |
| SCE1572_9308 | 1618 | 4088 |
| SCE1572_7860 | 43 | 27 |
| SCE1572_11530 | 85 | 21 |
| SCE1572_1168 | 493 | 92 |
| SCE1572_3268 | 227 | 1279 |
| SCE1572_5142 | 237 | 34 |
| SCE1572_954 | 4 | 1 |
| SCE1572_6321 | 19.12 | 8 |
| SCE1572_9892 | 0 | 0 |
| SCE1572_8065 | 199 | 19 |
| SCE1572_8022 | 17 | 8 |
| SCE1572_1397 | 56 | 45 |
| SCE1572_6727 | 147 | 133 |
| SCE1572_946 | 200 | 28.41 |
| SCE1572_2467 | 107 | 33 |
| SCE1572_1047 | 95 | 13 |
| SCE1572_4000 | 58 | 51 |
| SCE1572_7773 | 72 | 45 |
| SCE1572_2072 | 114 | 22 |
| SCE1572_6390 | 96 | 101 |
| SCE1572_1177 | 91 | 39 |
| SCE1572_8664 | 48 | 4 |
| SCE1572_5863 | 153 | 36 |
| SCE1572_10634 | 195 | 192 |
| SCE1572_3028 | 0 | 0 |
| SCE1572_1678 | 52 | 57 |

| | | |
|---------------|-------|-------|
| SCE1572_376 | 80 | 12 |
| SCE1572_4086 | 203 | 43 |
| SCE1572_4789 | 111 | 400 |
| SCE1572_9083 | 29 | 1 |
| SCE1572_8181 | 13 | 1 |
| SCE1572_94 | 126 | 38 |
| SCE1572_8595 | 0 | 0 |
| SCE1572_4562 | 100 | 54 |
| SCE1572_6368 | 71 | 173 |
| SCE1572_7514 | 0 | 0 |
| SCE1572_709 | 0 | 0 |
| SCE1572_10710 | 42.28 | 8 |
| SCE1572_3553 | 4 | 0 |
| SCE1572_253 | 54 | 9 |
| SCE1572_8944 | 4 | 0 |
| SCE1572_6674 | 22 | 16 |
| SCE1572_6736 | 127 | 272 |
| SCE1572_2448 | 37 | 8 |
| SCE1572_11291 | 57 | 20 |
| SCE1572_5059 | 98 | 56 |
| SCE1572_3156 | 41 | 17 |
| SCE1572_1016 | 0 | 0 |
| SCE1572_10518 | 437 | 113 |
| SCE1572_7907 | 286 | 706 |
| SCE1572_1586 | 82.08 | 58.94 |
| SCE1572_10977 | 104 | 68 |
| SCE1572_6973 | 1 | 0 |
| SCE1572_9853 | 185 | 30 |
| SCE1572_1932 | 289 | 34 |
| SCE1572_9952 | 24 | 8 |
| SCE1572_5881 | 135 | 50 |
| SCE1572_5954 | 62 | 18 |
| SCE1572_110 | 343 | 468 |
| SCE1572_6687 | 10 | 7 |
| SCE1572_8903 | 148 | 13 |
| SCE1572_5683 | 301 | 390 |
| SCE1572_8061 | 3 | 0 |
| SCE1572_2297 | 138 | 210 |
| SCE1572_9316 | 65 | 59 |
| SCE1572_7818 | 29 | 15 |
| SCE1572_9386 | 22 | 12 |
| SCE1572_4554 | 23 | 2 |
| SCE1572_2012 | 91 | 17 |
| SCE1572_3431 | 167 | 182 |
| SCE1572_8225 | 138 | 30 |
| SCE1572_9164 | 128 | 16 |
| SCE1572_3644 | 110 | 23 |
| SCE1572_966 | 174 | 136 |

| | | |
|---------------|--------|-------|
| SCE1572_9205 | 41 | 20 |
| SCE1572_2462 | 87 | 56 |
| SCE1572_5733 | 269 | 935 |
| SCE1572_636 | 432 | 526 |
| SCE1572_10837 | 87 | 55 |
| SCE1572_8783 | 129 | 314 |
| SCE1572_5757 | 182 | 82 |
| SCE1572_5085 | 0 | 0 |
| SCE1572_9612 | 4 | 0 |
| SCE1572_5009 | 230 | 148 |
| SCE1572_5052 | 119.36 | 27.99 |
| SCE1572_6416 | 44 | 4 |
| SCE1572_2625 | 0 | 0 |
| SCE1572_5034 | 86 | 12 |
| SCE1572_7625 | 307 | 220 |
| SCE1572_3253 | 42 | 13 |
| SCE1572_8099 | 93 | 322 |
| SCE1572_4840 | 89 | 275 |
| SCE1572_431 | 168 | 42 |
| SCE1572_4065 | 101 | 22 |
| SCE1572_10086 | 346 | 626 |
| SCE1572_8010 | 76 | 172 |
| SCE1572_7807 | 487 | 159 |
| SCE1572_4797 | 142 | 205 |
| SCE1572_10784 | 406 | 172 |
| SCE1572_3402 | 46 | 72 |
| SCE1572_10601 | 48 | 7 |
| SCE1572_6016 | 188 | 234 |
| SCE1572_6822 | 165 | 817 |
| SCE1572_656 | 1004 | 898 |
| SCE1572_8398 | 170 | 43 |
| SCE1572_7062 | 0 | 0 |
| SCE1572_9868 | 81 | 72 |

TableS3 Transcripts detected under different pH conditions (edgeR)

| Locus tag | logFoldChange | logConc | PValue | FDR |
|---------------|---------------|----------|----------|----------|
| SCE1572_3527 | -8.60991438 | -11.1416 | 6.37E-21 | 6.70E-17 |
| SCE1572_4119 | -7.635412187 | -11.6046 | 5.55E-18 | 2.92E-14 |
| SCE1572_5270 | -7.65599141 | -13.1793 | 2.74E-17 | 9.62E-14 |
| SCE1572_3528 | -7.080685475 | -12.034 | 2.68E-16 | 7.05E-13 |
| SCE1572_4117 | -7.191370235 | -13.2741 | 4.49E-16 | 9.19E-13 |
| SCE1572_8972 | -6.902167314 | -11.4858 | 5.67E-16 | 9.19E-13 |
| SCE1572_4118 | -6.956242225 | -12.2072 | 6.11E-16 | 9.19E-13 |
| SCE1572_10922 | -6.753614141 | -8.32851 | 7.99E-16 | 1.05E-12 |
| SCE1572_3526 | -6.874307896 | -13.2482 | 3.11E-15 | 3.63E-12 |
| SCE1572_10923 | -6.380810321 | -9.14727 | 1.06E-14 | 1.12E-11 |
| SCE1572_7894 | 38.08986581 | -30.9711 | 1.97E-14 | 1.88E-11 |
| SCE1572_7402 | -6.587931306 | -13.7133 | 3.93E-14 | 3.44E-11 |
| SCE1572_3712 | -6.177538232 | -12.2862 | 1.03E-13 | 8.32E-11 |
| SCE1572_1395 | -5.998550436 | -11.2006 | 1.93E-13 | 1.36E-10 |
| SCE1572_5184 | -6.154693386 | -12.9665 | 1.94E-13 | 1.36E-10 |
| SCE1572_8009 | -5.86766727 | -9.11692 | 3.30E-13 | 1.99E-10 |
| SCE1572_7401 | -6.38476496 | -14.4364 | 3.32E-13 | 1.99E-10 |
| SCE1572_5187 | -6.152318874 | -13.4457 | 3.40E-13 | 1.99E-10 |
| SCE1572_3340 | -5.717542553 | -9.87797 | 9.41E-13 | 5.21E-10 |
| SCE1572_9597 | -5.63472751 | -10.6539 | 1.82E-12 | 9.20E-10 |
| SCE1572_4147 | -5.905629507 | -13.7914 | 1.91E-12 | 9.20E-10 |
| SCE1572_7889 | -5.705273172 | -12.2477 | 1.92E-12 | 9.20E-10 |
| SCE1572_4152 | -5.812304919 | -13.2531 | 2.09E-12 | 9.56E-10 |
| SCE1572_4735 | -5.575829284 | -9.42494 | 2.33E-12 | 1.02E-09 |
| SCE1572_1985 | -5.55787848 | -9.41583 | 2.66E-12 | 1.12E-09 |
| SCE1572_10766 | -5.635061834 | -12.2829 | 3.08E-12 | 1.21E-09 |
| SCE1572_7892 | -5.526979353 | -9.14575 | 3.18E-12 | 1.21E-09 |
| SCE1572_8254 | -5.643977655 | -12.2404 | 3.23E-12 | 1.21E-09 |
| SCE1572_1948 | -5.671526655 | -13.034 | 3.92E-12 | 1.37E-09 |
| SCE1572_3722 | -5.529034757 | -10.8436 | 3.92E-12 | 1.37E-09 |
| SCE1572_11571 | -5.654167583 | -13.3322 | 5.97E-12 | 2.03E-09 |
| SCE1572_7890 | -5.413504577 | -9.41788 | 6.90E-12 | 2.27E-09 |
| SCE1572_3139 | -5.824205582 | -14.3296 | 9.21E-12 | 2.94E-09 |
| SCE1572_1306 | -5.349009388 | -8.75232 | 1.01E-11 | 3.12E-09 |
| SCE1572_187 | -5.474574112 | -12.6377 | 1.13E-11 | 3.30E-09 |
| SCE1572_9596 | -5.666380792 | -13.7956 | 1.13E-11 | 3.30E-09 |
| SCE1572_7896 | -5.295711508 | -7.3376 | 1.34E-11 | 3.82E-09 |
| SCE1572_5185 | -5.351055506 | -11.3049 | 1.39E-11 | 3.84E-09 |
| SCE1572_7893 | -5.296932593 | -9.75296 | 1.50E-11 | 4.04E-09 |
| SCE1572_3784 | -5.506001447 | -13.2543 | 1.59E-11 | 4.17E-09 |
| SCE1572_6311 | -5.390560379 | -12.906 | 2.18E-11 | 5.59E-09 |
| SCE1572_3374 | -5.262286692 | -11.0687 | 2.24E-11 | 5.59E-09 |
| SCE1572_6279 | -5.376957901 | -12.8334 | 2.29E-11 | 5.59E-09 |
| SCE1572_1265 | -5.254233103 | -10.7479 | 2.34E-11 | 5.59E-09 |
| SCE1572_6042 | -5.260282929 | -11.6767 | 2.86E-11 | 6.68E-09 |
| SCE1572_7891 | -5.240486505 | -11.9408 | 3.38E-11 | 7.72E-09 |

| | | | | |
|---------------|--------------|----------|----------|----------|
| SCE1572_463 | -5.20386657 | -12.1274 | 4.41E-11 | 9.86E-09 |
| SCE1572_350 | -5.159472042 | -11.5303 | 5.09E-11 | 1.11E-08 |
| SCE1572_6014 | -5.39358207 | -13.7744 | 5.69E-11 | 1.22E-08 |
| SCE1572_5180 | -5.200540001 | -12.5391 | 5.85E-11 | 1.23E-08 |
| SCE1572_3710 | -5.053851301 | -8.03492 | 6.64E-11 | 1.37E-08 |
| SCE1572_858 | -5.035961159 | -9.59205 | 8.35E-11 | 1.67E-08 |
| SCE1572_10487 | -5.018176738 | -8.29949 | 8.41E-11 | 1.67E-08 |
| SCE1572_5186 | -5.05981732 | -11.2601 | 9.13E-11 | 1.78E-08 |
| SCE1572_1284 | -5.022413248 | -10.5796 | 9.84E-11 | 1.88E-08 |
| SCE1572_7227 | -5.005982584 | -11.7494 | 1.46E-10 | 2.73E-08 |
| SCE1572_7744 | -5.04880335 | -12.7604 | 1.56E-10 | 2.87E-08 |
| SCE1572_5181 | -5.034786771 | -12.3524 | 1.59E-10 | 2.89E-08 |
| SCE1572_3987 | -4.979242736 | -11.9327 | 1.76E-10 | 3.15E-08 |
| SCE1572_7844 | -4.934219 | -11.0547 | 1.90E-10 | 3.32E-08 |
| SCE1572_10361 | -5.129404482 | -13.8576 | 2.33E-10 | 4.01E-08 |
| SCE1572_8098 | -5.38476496 | -14.9364 | 2.41E-10 | 4.08E-08 |
| SCE1572_859 | -4.865635354 | -9.67721 | 2.54E-10 | 4.14E-08 |
| SCE1572_7403 | -4.894405595 | -11.3822 | 2.55E-10 | 4.14E-08 |
| SCE1572_1026 | -5.480876853 | -15.2668 | 2.56E-10 | 4.14E-08 |
| SCE1572_7367 | -4.858407581 | -10.1996 | 2.78E-10 | 4.44E-08 |
| SCE1572_6630 | -5.086998916 | -14.1418 | 4.57E-10 | 7.15E-08 |
| SCE1572_5182 | -5.070165279 | -14.2092 | 4.62E-10 | 7.15E-08 |
| SCE1572_5015 | -4.773260672 | -10.6206 | 5.03E-10 | 7.67E-08 |
| SCE1572_9714 | -4.9885806 | -13.7905 | 5.13E-10 | 7.70E-08 |
| SCE1572_2391 | -4.843504696 | -12.6786 | 5.58E-10 | 8.26E-08 |
| SCE1572_2964 | -4.745354675 | -11.8797 | 7.89E-10 | 1.15E-07 |
| SCE1572_2397 | -4.971863205 | -14.0359 | 8.06E-10 | 1.16E-07 |
| SCE1572_2472 | -4.876285545 | -13.4987 | 8.30E-10 | 1.18E-07 |
| SCE1572_410 | -5.097971974 | -14.7802 | 9.56E-10 | 1.34E-07 |
| SCE1572_5476 | -4.683683902 | -11.38 | 9.76E-10 | 1.34E-07 |
| SCE1572_559 | -4.925926921 | -14.1113 | 9.81E-10 | 1.34E-07 |
| SCE1572_5188 | -4.741038878 | -12.6919 | 1.19E-09 | 1.61E-07 |
| SCE1572_1365 | -4.65800454 | -11.6079 | 1.24E-09 | 1.65E-07 |
| SCE1572_1977 | -4.60174892 | -8.82131 | 1.32E-09 | 1.73E-07 |
| SCE1572_3202 | -4.613475851 | -10.7985 | 1.40E-09 | 1.80E-07 |
| SCE1572_8472 | -4.762088691 | -13.1933 | 1.40E-09 | 1.80E-07 |
| SCE1572_1027 | -4.656087337 | -12.1308 | 1.43E-09 | 1.81E-07 |
| SCE1572_1794 | -4.82694221 | -13.8713 | 1.46E-09 | 1.83E-07 |
| SCE1572_9595 | -4.851367913 | -14.3186 | 1.88E-09 | 2.33E-07 |
| SCE1572_9340 | -4.541864828 | -9.05827 | 1.95E-09 | 2.38E-07 |
| SCE1572_10699 | -4.643212096 | -12.4998 | 1.98E-09 | 2.39E-07 |
| SCE1572_2679 | -4.727652674 | -13.6078 | 2.00E-09 | 2.39E-07 |
| SCE1572_5327 | -4.539650562 | -10.5516 | 2.18E-09 | 2.58E-07 |
| SCE1572_7476 | 36.2567094 | -31.8877 | 2.49E-09 | 2.91E-07 |
| SCE1572_4622 | -4.562977933 | -11.8778 | 2.53E-09 | 2.92E-07 |
| SCE1572_10924 | -4.491386971 | -9.39002 | 2.73E-09 | 3.13E-07 |
| SCE1572_3307 | -4.484904854 | -11.0588 | 3.35E-09 | 3.79E-07 |
| SCE1572_10644 | -4.472721877 | -11.5459 | 3.85E-09 | 4.31E-07 |

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|---------------|--------------|----------|----------|----------|
| SCE1572_4800 | -4.562545535 | -12.8982 | 3.91E-09 | 4.33E-07 |
| SCE1572_3726 | -4.545785899 | -12.8469 | 4.25E-09 | 4.63E-07 |
| SCE1572_10043 | -4.509345607 | -12.4452 | 4.32E-09 | 4.63E-07 |
| SCE1572_7220 | -4.657481919 | -13.9561 | 4.32E-09 | 4.63E-07 |
| SCE1572_11285 | -4.548095301 | -12.9677 | 4.39E-09 | 4.67E-07 |
| SCE1572_4426 | -4.471169621 | -12.0383 | 4.74E-09 | 4.98E-07 |
| SCE1572_1683 | -5.414381441 | -16.037 | 4.78E-09 | 4.98E-07 |
| SCE1572_1025 | -4.651566196 | -13.916 | 4.88E-09 | 5.03E-07 |
| SCE1572_2097 | -4.926775316 | -14.9589 | 5.13E-09 | 5.24E-07 |
| SCE1572_7636 | -4.387882464 | -9.73012 | 5.33E-09 | 5.39E-07 |
| SCE1572_1285 | -4.369556684 | -8.63465 | 5.58E-09 | 5.59E-07 |
| SCE1572_8008 | -4.394805903 | -11.28 | 6.23E-09 | 6.18E-07 |
| SCE1572_8395 | -4.483311782 | -13.0875 | 6.38E-09 | 6.27E-07 |
| SCE1572_6179 | -4.398035121 | -12.0112 | 6.80E-09 | 6.58E-07 |
| SCE1572_564 | -4.487152178 | -13.1314 | 6.82E-09 | 6.58E-07 |
| SCE1572_11073 | -5.714366983 | -16.472 | 7.55E-09 | 7.22E-07 |
| SCE1572_8919 | -4.730855106 | -14.6418 | 7.71E-09 | 7.30E-07 |
| SCE1572_2512 | -4.456069994 | -13.0788 | 8.02E-09 | 7.50E-07 |
| SCE1572_8781 | -4.407364807 | -12.4113 | 8.09E-09 | 7.50E-07 |
| SCE1572_8007 | -4.391982411 | -12.365 | 8.13E-09 | 7.50E-07 |
| SCE1572_9416 | -4.381198345 | -12.2682 | 8.23E-09 | 7.53E-07 |
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| SCE1572_1127 | 1.143614012 | -16.901 | 0.25882 | 0.433897 |
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| SCE1572_6249 | 1.898501514 | -19.1085 | 0.372947 | 0.546103 |
| SCE1572_2898 | 1.898501514 | -19.1085 | 0.372947 | 0.546103 |
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| SCE1572_6615 | 0.758323856 | -16.0937 | 0.37369 | 0.546566 |
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| SCE1572_8249 | -0.584581372 | -13.9925 | 0.410148 | 0.582261 |
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| SCE1572_4435 | -0.686460986 | -16.2311 | 0.410207 | 0.582261 |
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| SCE1572_3820 | 0.611219562 | -14.7522 | 0.41158 | 0.583816 |
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| SCE1572_10218 | -0.564064355 | -13.3398 | 0.411647 | 0.583833 |
| SCE1572_2050 | 0.623879134 | -15.102 | 0.411745 | 0.583893 |
| SCE1572_10318 | 0.564276061 | -13.6057 | 0.412037 | 0.584229 |
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| SCE1572_3120 | 0.84405373 | -16.4658 | 0.413309 | 0.585716 |
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| SCE1572_11337 | 0.84405373 | -16.4658 | 0.413309 | 0.585716 |
| SCE1572_241 | 0.553742711 | -12.6724 | 0.414036 | 0.586668 |
| SCE1572_10292 | -0.58492296 | -14.3502 | 0.414588 | 0.58737 |
| SCE1572_4965 | 0.57824224 | -14.1837 | 0.41505 | 0.587946 |
| SCE1572_8270 | 0.610520751 | -14.6232 | 0.415387 | 0.588053 |
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| SCE1572_4068 | -0.600046235 | -14.6029 | 0.415387 | 0.588053 |
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| SCE1572_2607 | 0.644184326 | -15.2763 | 0.415664 | 0.588053 |
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| SCE1572_164 | 0.676109093 | -15.9124 | 0.419933 | 0.592151 |
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| SCE1572_881 | -0.55260524 | -13.7491 | 0.420444 | 0.592635 |
| SCE1572_5202 | -0.640657297 | -15.4239 | 0.420445 | 0.592635 |
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| SCE1572_3072 | 0.779202586 | -16.8608 | 0.421156 | 0.593239 |
| SCE1572_2739 | -0.576278069 | -14.3686 | 0.421407 | 0.593513 |
| SCE1572_1824 | -0.605160884 | -14.8368 | 0.422202 | 0.594554 |
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| SCE1572_9486 | -0.709544599 | -16.0202 | 0.42351 | 0.595837 |
| SCE1572_6746 | -0.709544599 | -16.0202 | 0.42351 | 0.595837 |
| SCE1572_792 | -0.569328353 | -14.2764 | 0.423827 | 0.596203 |
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| SCE1572_3715 | -0.538210028 | -13.0601 | 0.424825 | 0.597128 |
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| SCE1572_5309 | -0.417274354 | -15.566 | 0.615458 | 0.757654 |
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| SCE1572_3942 | -0.32520071 | -8.64059 | 0.619789 | 0.761647 |
| SCE1572_697 | 0.366006434 | -14.3829 | 0.619883 | 0.761674 |
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| SCE1572_4607 | -0.493815908 | -16.4973 | 0.622031 | 0.763868 |
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| SCE1572_11144 | 0.465542107 | -16.24 | 0.623263 | 0.764558 |
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| SCE1572_9472 | 0.33930211 | -13.6787 | 0.623594 | 0.764558 |
| SCE1572_7396 | 0.344733635 | -13.9547 | 0.623751 | 0.764558 |
| SCE1572_2152 | -0.42342658 | -15.9476 | 0.623857 | 0.764558 |
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| SCE1572_2169 | 0.422473385 | -15.7591 | 0.624149 | 0.764558 |
| SCE1572_1051 | 0.422473385 | -15.7591 | 0.624149 | 0.764558 |
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| SCE1572_4122 | 0.031139283 | -16.1353 | 1 | 1 |
| SCE1572_2394 | 0.031139283 | -15.1353 | 1 | 1 |
| SCE1572_10944 | -0.030415388 | -15.6136 | 1 | 1 |
| SCE1572_2195 | -0.030415388 | -14.6136 | 1 | 1 |
| SCE1572_10359 | -0.030415388 | -15.6136 | 1 | 1 |
| SCE1572_6270 | 0.028136795 | -16.3433 | 1 | 1 |
| SCE1572_5815 | -0.027497904 | -15.8236 | 1 | 1 |
| SCE1572_5786 | 0.026917788 | -14.8349 | 1 | 1 |
| SCE1572_4100 | -0.026801118 | -14.5476 | 1 | 1 |
| SCE1572_8715 | -0.025947453 | -14.1166 | 1 | 1 |
| SCE1572_11009 | 0.025842554 | -14.1622 | 1 | 1 |
| SCE1572_2536 | 0.024969516 | -14.2124 | 1 | 1 |
| SCE1572_10682 | 0.024032396 | -16.5863 | 1 | 1 |
| SCE1572_11322 | 0.024032396 | -16.5863 | 1 | 1 |
| SCE1572_6291 | -0.023495974 | -17.0695 | 1 | 1 |
| SCE1572_121 | -0.023495974 | -17.0695 | 1 | 1 |
| SCE1572_904 | -0.023495974 | -15.4846 | 1 | 1 |
| SCE1572_1400 | -0.023495974 | -17.0695 | 1 | 1 |
| SCE1572_639 | 0.023197262 | -14.0462 | 1 | 1 |
| SCE1572_7234 | 0.021935456 | -14.3744 | 1 | 1 |
| SCE1572_11296 | -0.021445234 | -14.859 | 1 | 1 |
| SCE1572_1802 | -0.01988472 | -15.6754 | 1 | 1 |
| SCE1572_6492 | -0.01988472 | -15.6754 | 1 | 1 |
| SCE1572_9908 | 0.018969034 | -13.8388 | 1 | 1 |
| SCE1572_9635 | -0.018442746 | -14.1601 | 1 | 1 |
| SCE1572_3995 | 0.01808313 | -15.2938 | 1 | 1 |
| SCE1572_4566 | 0.01808313 | -16.8788 | 1 | 1 |
| SCE1572_6680 | 0.01808313 | -15.8788 | 1 | 1 |
| SCE1572_2796 | 0.01808313 | -16.8788 | 1 | 1 |
| SCE1572_2260 | -0.017666895 | -16.3662 | 1 | 1 |
| SCE1572_3776 | -0.017666895 | -13.7812 | 1 | 1 |
| SCE1572_1830 | -0.017666895 | -14.0442 | 1 | 1 |
| SCE1572_6031 | 0.017007696 | -14.1185 | 1 | 1 |
| SCE1572_5884 | 0.015858465 | -14.1672 | 1 | 1 |
| SCE1572_953 | -0.015083734 | -15.8954 | 1 | 1 |

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|---------------|--------------|----------|---|---|
| SCE1572_5044 | -0.015083734 | -15.8954 | 1 | 1 |
| SCE1572_7576 | -0.015083734 | -15.8954 | 1 | 1 |
| SCE1572_10757 | 0.014880698 | -14.6928 | 1 | 1 |
| SCE1572_11241 | 0.014627572 | -14.2176 | 1 | 1 |
| SCE1572_6321 | -0.014412869 | -17.065 | 1 | 1 |
| SCE1572_378 | 0.013978732 | -16.0508 | 1 | 1 |
| SCE1572_668 | -0.01362573 | -15.541 | 1 | 1 |
| SCE1572_11588 | -0.01362573 | -15.541 | 1 | 1 |
| SCE1572_8537 | -0.012689219 | -15.2568 | 1 | 1 |
| SCE1572_6520 | 0.012369479 | -15.528 | 1 | 1 |
| SCE1572_2246 | -0.012036858 | -15.0194 | 1 | 1 |
| SCE1572_10762 | 0.011883314 | -14.3239 | 1 | 1 |
| SCE1572_2252 | 0.011748564 | -13.6769 | 1 | 1 |
| SCE1572_11420 | 0.011748564 | -13.6769 | 1 | 1 |
| SCE1572_5529 | 0.010976244 | -14.8428 | 1 | 1 |
| SCE1572_6155 | 0.010976244 | -14.8428 | 1 | 1 |
| SCE1572_6566 | 0.008684432 | -15.2461 | 1 | 1 |
| SCE1572_11116 | 0.008684432 | -17.2461 | 1 | 1 |
| SCE1572_1152 | 0.008684432 | -17.2461 | 1 | 1 |
| SCE1572_5796 | 0.008684432 | -15.6611 | 1 | 1 |
| SCE1572_6299 | 0.008684432 | -17.2461 | 1 | 1 |
| SCE1572_2574 | 0.008684432 | -17.2461 | 1 | 1 |
| SCE1572_7015 | 0.008684432 | -17.2461 | 1 | 1 |
| SCE1572_7054 | 0.008684432 | -17.2461 | 1 | 1 |
| SCE1572_9657 | 0.008684432 | -15.2461 | 1 | 1 |
| SCE1572_8637 | 0.008684432 | -14.4387 | 1 | 1 |
| SCE1572_6726 | -0.008389081 | -16.1551 | 1 | 1 |
| SCE1572_4893 | -0.008389081 | -14.1551 | 1 | 1 |
| SCE1572_8720 | -0.008389081 | -17.74 | 1 | 1 |
| SCE1572_2789 | -0.008389081 | -16.1551 | 1 | 1 |
| SCE1572_5864 | -0.008389081 | -17.74 | 1 | 1 |
| SCE1572_4174 | -0.008389081 | -17.74 | 1 | 1 |
| SCE1572_6650 | -0.008389081 | -15.4181 | 1 | 1 |
| SCE1572_10199 | 0.007292541 | -13.1234 | 1 | 1 |
| SCE1572_9530 | 0.007292541 | -14.1234 | 1 | 1 |
| SCE1572_1004 | 0.006522085 | -15.5448 | 1 | 1 |
| SCE1572_11422 | 0.006110488 | -15.0103 | 1 | 1 |
| SCE1572_1742 | -0.005143422 | -13.8509 | 1 | 1 |
| SCE1572_8326 | 0.004210956 | -14.2228 | 1 | 1 |
| SCE1572_217 | 0.004210956 | -15.8077 | 1 | 1 |
| SCE1572_5871 | -0.003490282 | -14.4448 | 1 | 1 |
| SCE1572_6667 | 0.003436354 | -13.7162 | 1 | 1 |
| SCE1572_10822 | 0.003198893 | -15.102 | 1 | 1 |
| SCE1572_6085 | 0.003198893 | -15.102 | 1 | 1 |
| SCE1572_1288 | 0.003057445 | -12.9688 | 1 | 1 |
| SCE1572_1375 | 0.002609918 | -13.4418 | 1 | 1 |
| SCE1572_5813 | 0.002499235 | -14.2752 | 1 | 1 |
| SCE1572_3007 | 0.001595007 | -16.472 | 1 | 1 |

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|---------------|--------------|----------|---|---|
| SCE1572_10854 | 0.001595007 | -14.8871 | 1 | 1 |
| SCE1572_3698 | 0.001595007 | -15.472 | 1 | 1 |
| SCE1572_4355 | 0.001595007 | -16.472 | 1 | 1 |
| SCE1572_2754 | -0.001334324 | -13.971 | 1 | 1 |
| SCE1572_820 | -0.001334324 | -15.971 | 1 | 1 |
| SCE1572_3156 | -0.001334324 | -15.971 | 1 | 1 |
| SCE1572_3442 | 0.000656058 | -14.3295 | 1 | 1 |
| SCE1572_4897 | -0.000121465 | -15.1999 | 1 | 1 |

TableS7 Homologous genes in So0157-2 and So ce56

| <i>Sorangium cellulosum</i> So0157-2 | <i>Sorangium cellulosum</i> So ce56 | E-value (So0157-2 vs So ce56) | E-value (So ce56 vs So0157-2) |
|--------------------------------------|-------------------------------------|-------------------------------|-------------------------------|
| SCE1572_1 | sce_1 | 0.00E+00 | 0.00E+00 |
| SCE1572_10 | sce_10 | 9.00E-171 | 3.00E-166 |
| SCE1572_100 | sce_87 | 0.00E+00 | 0.00E+00 |
| SCE1572_10000 | sce_8822 | 2.00E-55 | 2.00E-55 |
| SCE1572_10002 | sce_8823 | 0.00E+00 | 0.00E+00 |
| SCE1572_10003 | sce_8824 | 1.00E-148 | 1.00E-149 |
| SCE1572_10006 | sce_8830 | 6.00E-49 | 6.00E-49 |
| SCE1572_10007 | sce_8831 | 4.00E-139 | 2.00E-121 |
| SCE1572_10008 | sce_8832 | 4.00E-77 | 3.00E-91 |
| SCE1572_10009 | sce_8833 | 8.00E-122 | 3.00E-120 |
| SCE1572_10010 | sce_8834 | 8.00E-30 | 2.00E-23 |
| SCE1572_10011 | sce_8835 | 9.00E-151 | 9.00E-151 |
| SCE1572_10012 | sce_8836 | 2.00E-144 | 4.00E-136 |
| SCE1572_10013 | sce_8837 | 2.00E-80 | 2.00E-79 |
| SCE1572_10014 | sce_8838 | 0.00E+00 | 0.00E+00 |
| SCE1572_10015 | sce_8839 | 0.00E+00 | 0.00E+00 |
| SCE1572_10015 | sce_10220 | 0.00E+00 | 0.00E+00 |
| SCE1572_10016 | sce_8840 | 3.00E-07 | 1.00E-11 |
| SCE1572_10017 | sce_8841 | 1.00E-136 | 6.00E-145 |
| SCE1572_10018 | sce_9498 | 2.00E-172 | 2.00E-172 |
| SCE1572_10019 | sce_9499 | 0.00E+00 | 0.00E+00 |
| SCE1572_1002 | sce_757 | 1.00E-79 | 7.00E-80 |
| SCE1572_10020 | sce_9500 | 1.00E-111 | 1.00E-127 |
| SCE1572_10024 | sce_10364 | 2.00E-148 | 2.00E-128 |
| SCE1572_10026 | sce_8842 | 2.00E-48 | 6.00E-54 |
| SCE1572_10027 | sce_8843 | 6.00E-60 | 1.00E-68 |
| SCE1572_10028 | sce_8844 | 4.00E-107 | 5.00E-115 |
| SCE1572_10029 | sce_8845 | 0.00E+00 | 0.00E+00 |
| SCE1572_1003 | sce_758 | 7.00E-175 | 7.00E-172 |
| SCE1572_10030 | sce_8846 | 2.00E-107 | 4.00E-111 |
| SCE1572_10033 | sce_8847 | 0.00E+00 | 0.00E+00 |
| SCE1572_10034 | sce_8851 | 6.00E-172 | 3.00E-177 |
| SCE1572_10036 | sce_8852 | 4.00E-54 | 3.00E-46 |
| SCE1572_10037 | sce_8853 | 4.00E-89 | 2.00E-103 |
| SCE1572_10038 | sce_8854 | 5.00E-176 | 3.00E-167 |
| SCE1572_1004 | sce_5158 | 0.00E+00 | 0.00E+00 |
| SCE1572_1004 | sce_1116 | 0.00E+00 | 0.00E+00 |
| SCE1572_1004 | sce_7318 | 0.00E+00 | 0.00E+00 |
| SCE1572_10040 | sce_8856 | 0.00E+00 | 0.00E+00 |
| SCE1572_10042 | sce_8858 | 0.00E+00 | 0.00E+00 |
| SCE1572_10043 | sce_8859 | 5.00E-147 | 5.00E-147 |
| SCE1572_10044 | sce_8860 | 3.00E-36 | 3.00E-36 |
| SCE1572_10045 | sce_8861 | 3.00E-40 | 3.00E-39 |
| SCE1572_10046 | sce_8862 | 0.00E+00 | 0.00E+00 |
| SCE1572_10047 | sce_8863 | 2.00E-43 | 2.00E-43 |
| SCE1572_10048 | sce_8864 | 0.00E+00 | 0.00E+00 |
| SCE1572_10049 | sce_8865 | 2.00E-179 | 7.00E-175 |
| SCE1572_1005 | sce_1115 | 0.00E+00 | 0.00E+00 |
| SCE1572_1005 | sce_5159 | 0.00E+00 | 0.00E+00 |
| SCE1572_10050 | sce_8866 | 0.00E+00 | 0.00E+00 |
| SCE1572_10051 | sce_8868 | 0.00E+00 | 0.00E+00 |
| SCE1572_10052 | sce_8869 | 0.00E+00 | 0.00E+00 |
| SCE1572_10053 | sce_8870 | 1.00E-165 | 1.00E-169 |
| SCE1572_10054 | sce_8871 | 0.00E+00 | 0.00E+00 |
| SCE1572_10055 | sce_8872 | 0.00E+00 | 0.00E+00 |
| SCE1572_10056 | sce_8873 | 3.00E-47 | 3.00E-47 |
| SCE1572_10057 | sce_8874 | 1.00E-161 | 3.00E-149 |
| SCE1572_10058 | sce_8875 | 8.00E-65 | 5.00E-65 |
| SCE1572_10059 | sce_8876 | 0.00E+00 | 0.00E+00 |
| SCE1572_1006 | sce_759 | 2.00E-114 | 6.00E-126 |
| SCE1572_10061 | sce_8878 | 1.00E-118 | 5.00E-109 |
| SCE1572_10062 | sce_8879 | 2.00E-49 | 1.00E-49 |
| SCE1572_10063 | sce_8880 | 3.00E-66 | 3.00E-66 |
| SCE1572_10064 | sce_8881 | 2.00E-09 | 2.00E-09 |
| SCE1572_10065 | sce_8882 | 3.00E-42 | 3.00E-42 |
| SCE1572_10066 | sce_8883 | 9.00E-113 | 9.00E-113 |
| SCE1572_10067 | sce_8884 | 0.00E+00 | 0.00E+00 |
| SCE1572_10068 | sce_8885 | 4.00E-55 | 3.00E-65 |
| SCE1572_10069 | sce_8886 | 6.00E-24 | 1.00E-21 |
| SCE1572_1007 | sce_760 | 0.00E+00 | 0.00E+00 |
| SCE1572_10070 | sce_8887 | 5.00E-83 | 7.00E-91 |
| SCE1572_10071 | sce_8888 | 1.00E-63 | 1.00E-63 |
| SCE1572_10072 | sce_8889 | 1.00E-96 | 3.00E-102 |
| SCE1572_10073 | sce_8890 | 7.00E-60 | 7.00E-60 |

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|---------------|----------|-----------|-----------|
| SCE1572_10074 | sce_8891 | 4.00E-30 | 4.00E-30 |
| SCE1572_10075 | sce_8892 | 3.00E-104 | 5.00E-105 |
| SCE1572_10076 | sce_8893 | 3.00E-52 | 3.00E-52 |
| SCE1572_10077 | sce_8894 | 2.00E-64 | 2.00E-64 |
| SCE1572_10078 | sce_8895 | 7.00E-43 | 9.00E-43 |
| SCE1572_10079 | sce_8896 | 2.00E-22 | 2.00E-22 |
| SCE1572_1008 | sce_761 | 0.00E+00 | 0.00E+00 |
| SCE1572_10080 | sce_8897 | 2.00E-75 | 2.00E-75 |
| SCE1572_10081 | sce_8898 | 5.00E-132 | 5.00E-132 |
| SCE1572_10082 | sce_8899 | 2.00E-49 | 2.00E-49 |
| SCE1572_10083 | sce_8901 | 3.00E-65 | 2.00E-58 |
| SCE1572_10084 | sce_8902 | 2.00E-143 | 2.00E-143 |
| SCE1572_10085 | sce_8903 | 0.00E+00 | 0.00E+00 |
| SCE1572_10086 | sce_8904 | 4.00E-39 | 2.00E-40 |
| SCE1572_10089 | sce_8905 | 6.00E-95 | 2.00E-97 |
| SCE1572_1009 | sce_763 | 0.00E+00 | 0.00E+00 |
| SCE1572_10090 | sce_8907 | 3.00E-180 | 1.00E-180 |
| SCE1572_10091 | sce_8909 | 0.00E+00 | 0.00E+00 |
| SCE1572_10092 | sce_8910 | 0.00E+00 | 0.00E+00 |
| SCE1572_10093 | sce_8911 | 8.00E-21 | 8.00E-21 |
| SCE1572_10095 | sce_8913 | 3.00E-63 | 8.00E-65 |
| SCE1572_10096 | sce_8914 | 0.00E+00 | 0.00E+00 |
| SCE1572_10097 | sce_8915 | 3.00E-59 | 2.00E-54 |
| SCE1572_10098 | sce_8916 | 4.00E-142 | 3.00E-130 |
| SCE1572_10099 | sce_8917 | 3.00E-117 | 5.00E-117 |
| SCE1572_10100 | sce_8918 | 2.00E-114 | 4.00E-105 |
| SCE1572_10101 | sce_8919 | 2.00E-125 | 9.00E-139 |
| SCE1572_10102 | sce_8920 | 6.00E-128 | 5.00E-128 |
| SCE1572_10103 | sce_8921 | 3.00E-85 | 6.00E-87 |
| SCE1572_10104 | sce_8922 | 2.00E-31 | 1.00E-47 |
| SCE1572_10105 | sce_8923 | 8.00E-36 | 2.00E-48 |
| SCE1572_10106 | sce_8924 | 3.00E-137 | 4.00E-137 |
| SCE1572_10107 | sce_8925 | 4.00E-41 | 4.00E-41 |
| SCE1572_10108 | sce_8926 | 0.00E+00 | 0.00E+00 |
| SCE1572_10109 | sce_8927 | 5.00E-60 | 1.00E-53 |
| SCE1572_1011 | sce_9659 | 3.00E-45 | 7.00E-46 |
| SCE1572_10111 | sce_8928 | 0.00E+00 | 0.00E+00 |
| SCE1572_10115 | sce_8930 | 0.00E+00 | 0.00E+00 |
| SCE1572_10117 | sce_8934 | 1.00E-95 | 1.00E-93 |
| SCE1572_10118 | sce_8935 | 2.00E-110 | 4.00E-113 |
| SCE1572_10119 | sce_8937 | 3.00E-144 | 7.00E-144 |
| SCE1572_10120 | sce_8938 | 0.00E+00 | 2.00E-177 |
| SCE1572_10121 | sce_8939 | 2.00E-76 | 1.00E-81 |
| SCE1572_10122 | sce_8940 | 0.00E+00 | 0.00E+00 |
| SCE1572_10123 | sce_8941 | 2.00E-48 | 1.00E-48 |
| SCE1572_1013 | sce_768 | 0.00E+00 | 0.00E+00 |
| SCE1572_10130 | sce_8942 | 4.00E-116 | 2.00E-118 |
| SCE1572_1014 | sce_769 | 3.00E-76 | 3.00E-76 |
| SCE1572_10141 | sce_8944 | 2.00E-119 | 2.00E-119 |
| SCE1572_10142 | sce_8945 | 0.00E+00 | 0.00E+00 |
| SCE1572_10143 | sce_8946 | 4.00E-121 | 3.00E-120 |
| SCE1572_10144 | sce_8947 | 2.00E-149 | 3.00E-159 |
| SCE1572_10145 | sce_8948 | 0.00E+00 | 0.00E+00 |
| SCE1572_10146 | sce_8949 | 0.00E+00 | 0.00E+00 |
| SCE1572_10147 | sce_8950 | 2.00E-153 | 4.00E-164 |
| SCE1572_10148 | sce_8951 | 1.00E-47 | 1.00E-47 |
| SCE1572_10149 | sce_8952 | 3.00E-33 | 1.00E-55 |
| SCE1572_1015 | sce_3750 | 0.00E+00 | 0.00E+00 |
| SCE1572_1015 | sce_5229 | 0.00E+00 | 0.00E+00 |
| SCE1572_1015 | sce_6712 | 0.00E+00 | 0.00E+00 |
| SCE1572_1015 | sce_5226 | 0.00E+00 | 0.00E+00 |
| SCE1572_1015 | sce_9954 | 0.00E+00 | 0.00E+00 |
| SCE1572_10150 | sce_8953 | 3.00E-98 | 4.00E-106 |
| SCE1572_10151 | sce_8954 | 8.00E-64 | 9.00E-66 |
| SCE1572_10152 | sce_8955 | 1.00E-51 | 1.00E-51 |
| SCE1572_10153 | sce_8956 | 3.00E-65 | 7.00E-79 |
| SCE1572_10154 | sce_8957 | 4.00E-123 | 4.00E-133 |
| SCE1572_10155 | sce_8958 | 4.00E-154 | 1.00E-170 |
| SCE1572_10156 | sce_8959 | 9.00E-24 | 1.00E-24 |
| SCE1572_10157 | sce_8960 | 0.00E+00 | 0.00E+00 |
| SCE1572_10159 | sce_8961 | 1.00E-13 | 3.00E-11 |
| SCE1572_10160 | sce_8962 | 0.00E+00 | 0.00E+00 |
| SCE1572_10161 | sce_8963 | 2.00E-176 | 2.00E-169 |
| SCE1572_10165 | sce_8964 | 2.00E-149 | 8.00E-159 |
| SCE1572_10167 | sce_8966 | 0.00E+00 | 0.00E+00 |
| SCE1572_10168 | sce_8967 | 6.00E-68 | 1.00E-67 |

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|---------------|----------|-----------|-----------|
| SCE1572_10169 | sce_8968 | 1.00E-55 | 5.00E-48 |
| SCE1572_1017 | sce_772 | 4.00E-45 | 2.00E-45 |
| SCE1572_10170 | sce_8969 | 2.00E-143 | 1.00E-134 |
| SCE1572_10172 | sce_8970 | 8.00E-134 | 8.00E-134 |
| SCE1572_10173 | sce_8972 | 5.00E-55 | 2.00E-50 |
| SCE1572_10175 | sce_8974 | 7.00E-33 | 6.00E-31 |
| SCE1572_10176 | sce_8975 | 2.00E-37 | 4.00E-29 |
| SCE1572_10177 | sce_8976 | 1.00E-53 | 4.00E-63 |
| SCE1572_10178 | sce_8977 | 8.00E-113 | 3.00E-113 |
| SCE1572_10179 | sce_8978 | 2.00E-126 | 3.00E-123 |
| SCE1572_10180 | sce_8979 | 8.00E-146 | 3.00E-145 |
| SCE1572_10181 | sce_8980 | 7.00E-89 | 2.00E-74 |
| SCE1572_10182 | sce_8981 | 0.00E+00 | 0.00E+00 |
| SCE1572_10183 | sce_9845 | 9.00E-94 | 4.00E-102 |
| SCE1572_10184 | sce_9844 | 3.00E-84 | 4.00E-83 |
| SCE1572_10186 | sce_8992 | 2.00E-147 | 4.00E-151 |
| SCE1572_10187 | sce_8993 | 3.00E-62 | 3.00E-52 |
| SCE1572_10188 | sce_8994 | 9.00E-130 | 2.00E-123 |
| SCE1572_10189 | sce_8995 | 0.00E+00 | 0.00E+00 |
| SCE1572_10190 | sce_8996 | 0.00E+00 | 0.00E+00 |
| SCE1572_10191 | sce_8997 | 6.00E-45 | 6.00E-45 |
| SCE1572_10192 | sce_8998 | 6.00E-46 | 6.00E-46 |
| SCE1572_10193 | sce_8999 | 4.00E-147 | 3.00E-161 |
| SCE1572_10194 | sce_9000 | 0.00E+00 | 0.00E+00 |
| SCE1572_10195 | sce_9001 | 7.00E-63 | 7.00E-63 |
| SCE1572_10198 | sce_9003 | 1.00E-33 | 2.00E-17 |
| SCE1572_10199 | sce_9004 | 0.00E+00 | 0.00E+00 |
| SCE1572_102 | sce_88 | 2.00E-78 | 5.00E-70 |
| SCE1572_10200 | sce_9005 | 1.00E-73 | 1.00E-73 |
| SCE1572_10201 | sce_9006 | 3.00E-112 | 1.00E-125 |
| SCE1572_10206 | sce_8592 | 0.00E+00 | 0.00E+00 |
| SCE1572_10206 | sce_3937 | 0.00E+00 | 0.00E+00 |
| SCE1572_10208 | sce_9676 | 0.00E+00 | 0.00E+00 |
| SCE1572_10210 | sce_9675 | 9.00E-127 | 9.00E-127 |
| SCE1572_10212 | sce_9674 | 3.00E-129 | 2.00E-119 |
| SCE1572_10213 | sce_9673 | 4.00E-20 | 1.00E-17 |
| SCE1572_10214 | sce_9672 | 1.00E-143 | 9.00E-153 |
| SCE1572_10216 | sce_9670 | 4.00E-26 | 4.00E-25 |
| SCE1572_10217 | sce_9669 | 0.00E+00 | 0.00E+00 |
| SCE1572_10218 | sce_9668 | 0.00E+00 | 0.00E+00 |
| SCE1572_10219 | sce_9667 | 0.00E+00 | 0.00E+00 |
| SCE1572_1022 | sce_6293 | 8.00E-39 | 3.00E-40 |
| SCE1572_10220 | sce_9666 | 0.00E+00 | 0.00E+00 |
| SCE1572_10221 | sce_2358 | 0.00E+00 | 0.00E+00 |
| SCE1572_10222 | sce_9656 | 9.00E-118 | 7.00E-126 |
| SCE1572_10223 | sce_9655 | 0.00E+00 | 0.00E+00 |
| SCE1572_10231 | sce_7445 | 6.00E-98 | 4.00E-84 |
| SCE1572_10231 | sce_4534 | 6.00E-98 | 4.00E-84 |
| SCE1572_10235 | sce_7404 | 0.00E+00 | 0.00E+00 |
| SCE1572_10239 | sce_6868 | 8.00E-132 | 6.00E-129 |
| SCE1572_10242 | sce_1432 | 1.00E-89 | 8.00E-88 |
| SCE1572_10245 | sce_6866 | 2.00E-86 | 2.00E-86 |
| SCE1572_10248 | sce_7083 | 2.00E-55 | 9.00E-56 |
| SCE1572_10250 | sce_5192 | 6.00E-122 | 8.00E-117 |
| SCE1572_10256 | sce_1659 | 8.00E-172 | 6.00E-161 |
| SCE1572_10257 | sce_8036 | 0.00E+00 | 2.00E-180 |
| SCE1572_10257 | sce_6864 | 0.00E+00 | 5.00E-178 |
| SCE1572_10259 | sce_9277 | 3.00E-14 | 1.00E-08 |
| SCE1572_10260 | sce_9652 | 5.00E-76 | 9.00E-77 |
| SCE1572_10261 | sce_9651 | 0.00E+00 | 0.00E+00 |
| SCE1572_10262 | sce_9650 | 0.00E+00 | 0.00E+00 |
| SCE1572_10265 | sce_9648 | 6.00E-85 | 1.00E-84 |
| SCE1572_10266 | sce_9647 | 4.00E-110 | 2.00E-114 |
| SCE1572_10267 | sce_9646 | 0.00E+00 | 0.00E+00 |
| SCE1572_10268 | sce_9645 | 0.00E+00 | 0.00E+00 |
| SCE1572_10269 | sce_9644 | 9.00E-127 | 2.00E-125 |
| SCE1572_10270 | sce_2619 | 3.00E-34 | 2.00E-37 |
| SCE1572_10271 | sce_9643 | 4.00E-147 | 2.00E-154 |
| SCE1572_10272 | sce_9642 | 0.00E+00 | 0.00E+00 |
| SCE1572_10273 | sce_9641 | 9.00E-100 | 5.00E-96 |
| SCE1572_10274 | sce_9639 | 1.00E-174 | 1.00E-175 |
| SCE1572_10275 | sce_9638 | 3.00E-136 | 3.00E-136 |
| SCE1572_10276 | sce_9637 | 4.00E-167 | 3.00E-167 |
| SCE1572_10277 | sce_9636 | 6.00E-177 | 0.00E+00 |
| SCE1572_10278 | sce_9635 | 1.00E-158 | 3.00E-150 |
| SCE1572_10279 | sce_9634 | 3.00E-84 | 5.00E-83 |

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|---------------|-----------|-----------|-----------|
| SCE1572_10280 | sce_9633 | 0.00E+00 | 0.00E+00 |
| SCE1572_10281 | sce_9631 | 1.00E-68 | 3.00E-69 |
| SCE1572_10282 | sce_9630 | 2.00E-38 | 4.00E-38 |
| SCE1572_10283 | sce_9629 | 9.00E-141 | 3.00E-133 |
| SCE1572_10284 | sce_9628 | 1.00E-106 | 5.00E-108 |
| SCE1572_10285 | sce_9627 | 8.00E-65 | 1.00E-82 |
| SCE1572_10286 | sce_9626 | 1.00E-109 | 9.00E-110 |
| SCE1572_10287 | sce_9625 | 0.00E+00 | 0.00E+00 |
| SCE1572_10287 | sce_5292 | 0.00E+00 | 0.00E+00 |
| SCE1572_10287 | sce_5639 | 0.00E+00 | 0.00E+00 |
| SCE1572_10287 | sce_6281 | 0.00E+00 | 0.00E+00 |
| SCE1572_10288 | sce_9624 | 0.00E+00 | 0.00E+00 |
| SCE1572_10289 | sce_9623 | 4.00E-58 | 2.00E-58 |
| SCE1572_10290 | sce_9622 | 5.00E-75 | 2.00E-62 |
| SCE1572_10291 | sce_9621 | 7.00E-63 | 7.00E-63 |
| SCE1572_10292 | sce_9620 | 4.00E-54 | 4.00E-54 |
| SCE1572_10294 | sce_9619 | 0.00E+00 | 0.00E+00 |
| SCE1572_10295 | sce_9617 | 2.00E-134 | 1.00E-142 |
| SCE1572_10296 | sce_9616 | 1.00E-63 | 1.00E-56 |
| SCE1572_10297 | sce_9615 | 1.00E-140 | 1.00E-140 |
| SCE1572_10298 | sce_9614 | 5.00E-138 | 4.00E-132 |
| SCE1572_10299 | sce_9613 | 9.00E-142 | 1.00E-143 |
| SCE1572_103 | sce_89 | 2.00E-120 | 2.00E-122 |
| SCE1572_1030 | sce_6285 | 7.00E-57 | 1.00E-65 |
| SCE1572_10300 | sce_9612 | 7.00E-77 | 4.00E-64 |
| SCE1572_10301 | sce_9611 | 0.00E+00 | 0.00E+00 |
| SCE1572_10301 | sce_9956 | 0.00E+00 | 0.00E+00 |
| SCE1572_10302 | sce_9610 | 2.00E-37 | 1.00E-51 |
| SCE1572_10303 | sce_9609 | 0.00E+00 | 0.00E+00 |
| SCE1572_10304 | sce_9607 | 0.00E+00 | 0.00E+00 |
| SCE1572_10304 | sce_4238 | 0.00E+00 | 0.00E+00 |
| SCE1572_10305 | sce_9606 | 1.00E-139 | 8.00E-145 |
| SCE1572_10306 | sce_9605 | 2.00E-57 | 4.00E-57 |
| SCE1572_10307 | sce_9604 | 2.00E-46 | 2.00E-55 |
| SCE1572_10308 | sce_9603 | 3.00E-88 | 6.00E-88 |
| SCE1572_10309 | sce_9602 | 3.00E-61 | 1.00E-62 |
| SCE1572_10311 | sce_9601 | 5.00E-70 | 9.00E-90 |
| SCE1572_10312 | sce_9600 | 0.00E+00 | 0.00E+00 |
| SCE1572_10313 | sce_9007 | 9.00E-69 | 6.00E-62 |
| SCE1572_10314 | sce_9008 | 7.00E-32 | 2.00E-39 |
| SCE1572_10315 | sce_9009 | 3.00E-26 | 3.00E-26 |
| SCE1572_10317 | sce_9010 | 3.00E-127 | 3.00E-133 |
| SCE1572_10318 | sce_9011 | 0.00E+00 | 0.00E+00 |
| SCE1572_10319 | sce_9012 | 4.00E-149 | 3.00E-160 |
| SCE1572_10320 | sce_9013 | 2.00E-55 | 4.00E-57 |
| SCE1572_10321 | sce_9015 | 2.00E-63 | 6.00E-62 |
| SCE1572_10322 | sce_9016 | 5.00E-18 | 3.00E-16 |
| SCE1572_10323 | sce_9017 | 3.00E-121 | 6.00E-138 |
| SCE1572_10325 | sce_9018 | 0.00E+00 | 0.00E+00 |
| SCE1572_10326 | sce_9019 | 6.00E-32 | 1.00E-26 |
| SCE1572_10329 | sce_9020 | 1.00E-98 | 1.00E-98 |
| SCE1572_1033 | sce_9382 | 9.00E-53 | 7.00E-49 |
| SCE1572_10331 | sce_9022 | 0.00E+00 | 0.00E+00 |
| SCE1572_10332 | sce_9023 | 0.00E+00 | 0.00E+00 |
| SCE1572_10335 | sce_9025 | 6.00E-49 | 5.00E-37 |
| SCE1572_10336 | sce_9027 | 7.00E-124 | 2.00E-127 |
| SCE1572_10338 | sce_1108 | 0.00E+00 | 0.00E+00 |
| SCE1572_10338 | sce_9028 | 0.00E+00 | 0.00E+00 |
| SCE1572_10339 | sce_9029 | 5.00E-68 | 4.00E-68 |
| SCE1572_1034 | sce_778 | 0.00E+00 | 0.00E+00 |
| SCE1572_10340 | sce_9030 | 0.00E+00 | 0.00E+00 |
| SCE1572_10341 | sce_9031 | 6.00E-90 | 1.00E-75 |
| SCE1572_10342 | sce_9032 | 0.00E+00 | 2.00E-154 |
| SCE1572_10343 | sce_9033 | 2.00E-148 | 2.00E-139 |
| SCE1572_10344 | sce_9034 | 1.00E-167 | 2.00E-169 |
| SCE1572_10345 | sce_9035 | 1.00E-134 | 1.00E-133 |
| SCE1572_10346 | sce_9037 | 0.00E+00 | 0.00E+00 |
| SCE1572_10347 | sce_9038 | 0.00E+00 | 0.00E+00 |
| SCE1572_1035 | sce_10117 | 0.00E+00 | 0.00E+00 |
| SCE1572_10353 | sce_8066 | 1.00E-13 | 7.00E-24 |
| SCE1572_10354 | sce_9218 | 3.00E-25 | 3.00E-25 |
| SCE1572_1036 | sce_7392 | 9.00E-19 | 4.00E-18 |
| SCE1572_10367 | sce_4494 | 0.00E+00 | 0.00E+00 |
| SCE1572_10368 | sce_9055 | 1.00E-45 | 1.00E-49 |
| SCE1572_10369 | sce_9056 | 0.00E+00 | 0.00E+00 |
| SCE1572_10370 | sce_9057 | 0.00E+00 | 0.00E+00 |

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| SCE1572_10371 | sce_9058 | 3.00E-134 | 4.00E-155 |
| SCE1572_10372 | sce_9059 | 1.00E-82 | 2.00E-85 |
| SCE1572_10373 | sce_9061 | 0.00E+00 | 0.00E+00 |
| SCE1572_10374 | sce_9062 | 2.00E-50 | 2.00E-51 |
| SCE1572_10375 | sce_9065 | 4.00E-103 | 1.00E-103 |
| SCE1572_10376 | sce_9066 | 5.00E-159 | 6.00E-159 |
| SCE1572_10378 | sce_9067 | 0.00E+00 | 0.00E+00 |
| SCE1572_1038 | sce_6088 | 1.00E-12 | 3.00E-16 |
| SCE1572_10380 | sce_9069 | 0.00E+00 | 0.00E+00 |
| SCE1572_10381 | sce_9070 | 0.00E+00 | 0.00E+00 |
| SCE1572_10382 | sce_9071 | 4.00E-114 | 2.00E-99 |
| SCE1572_10383 | sce_9072 | 4.00E-132 | 3.00E-121 |
| SCE1572_10384 | sce_9073 | 2.00E-69 | 5.00E-81 |
| SCE1572_10385 | sce_9074 | 2.00E-131 | 9.00E-140 |
| SCE1572_10386 | sce_9075 | 0.00E+00 | 0.00E+00 |
| SCE1572_10391 | sce_9046 | 1.00E-146 | 7.00E-145 |
| SCE1572_10393 | sce_3027 | 0.00E+00 | 0.00E+00 |
| SCE1572_10394 | sce_9047 | 9.00E-09 | 9.00E-09 |
| SCE1572_10397 | sce_9216 | 2.00E-131 | 3.00E-141 |
| SCE1572_10398 | sce_9215 | 0.00E+00 | 0.00E+00 |
| SCE1572_10399 | sce_9214 | 0.00E+00 | 0.00E+00 |
| SCE1572_104 | sce_90 | 3.00E-41 | 4.00E-71 |
| SCE1572_1040 | sce_775 | 2.00E-51 | 3.00E-52 |
| SCE1572_10400 | sce_9209 | 6.00E-172 | 6.00E-172 |
| SCE1572_10402 | sce_2173 | 2.00E-13 | 1.00E-11 |
| SCE1572_10435 | sce_9076 | 6.00E-107 | 1.00E-101 |
| SCE1572_10436 | sce_9077 | 5.00E-139 | 2.00E-144 |
| SCE1572_10437 | sce_9078 | 2.00E-121 | 3.00E-119 |
| SCE1572_10438 | sce_9079 | 5.00E-48 | 2.00E-55 |
| SCE1572_10439 | sce_9080 | 7.00E-124 | 7.00E-124 |
| SCE1572_1044 | sce_780 | 1.00E-54 | 1.00E-54 |
| SCE1572_10441 | sce_9082 | 1.00E-44 | 7.00E-29 |
| SCE1572_10442 | sce_9083 | 0.00E+00 | 0.00E+00 |
| SCE1572_10443 | sce_9084 | 2.00E-92 | 4.00E-110 |
| SCE1572_10444 | sce_9085 | 0.00E+00 | 0.00E+00 |
| SCE1572_10446 | sce_9086 | 5.00E-68 | 7.00E-80 |
| SCE1572_10447 | sce_9087 | 0.00E+00 | 0.00E+00 |
| SCE1572_10448 | sce_9088 | 5.00E-89 | 5.00E-89 |
| SCE1572_10449 | sce_9089 | 0.00E+00 | 0.00E+00 |
| SCE1572_1045 | sce_781 | 7.00E-66 | 1.00E-66 |
| SCE1572_10451 | sce_9093 | 8.00E-35 | 1.00E-34 |
| SCE1572_10452 | sce_9094 | 2.00E-121 | 4.00E-112 |
| SCE1572_10453 | sce_9095 | 3.00E-175 | 8.00E-178 |
| SCE1572_10455 | sce_9096 | 8.00E-150 | 4.00E-162 |
| SCE1572_10456 | sce_9097 | 3.00E-59 | 1.00E-67 |
| SCE1572_10459 | sce_9098 | 7.00E-65 | 5.00E-68 |
| SCE1572_1046 | sce_782 | 0.00E+00 | 0.00E+00 |
| SCE1572_10460 | sce_9099 | 5.00E-148 | 4.00E-153 |
| SCE1572_10461 | sce_9100 | 0.00E+00 | 0.00E+00 |
| SCE1572_10462 | sce_9101 | 0.00E+00 | 0.00E+00 |
| SCE1572_10463 | sce_9102 | 0.00E+00 | 0.00E+00 |
| SCE1572_10464 | sce_9103 | 5.00E-96 | 1.00E-80 |
| SCE1572_10465 | sce_9104 | 1.00E-58 | 4.00E-67 |
| SCE1572_10466 | sce_9105 | 0.00E+00 | 0.00E+00 |
| SCE1572_10469 | sce_9115 | 4.00E-90 | 2.00E-93 |
| SCE1572_1047 | sce_784 | 1.00E-125 | 8.00E-129 |
| SCE1572_10471 | sce_9116 | 0.00E+00 | 0.00E+00 |
| SCE1572_10472 | sce_9117 | 0.00E+00 | 0.00E+00 |
| SCE1572_10473 | sce_9118 | 3.00E-174 | 0.00E+00 |
| SCE1572_10474 | sce_9119 | 0.00E+00 | 0.00E+00 |
| SCE1572_10475 | sce_9120 | 0.00E+00 | 0.00E+00 |
| SCE1572_10476 | sce_9121 | 2.00E-124 | 2.00E-124 |
| SCE1572_10477 | sce_9122 | 1.00E-50 | 1.00E-50 |
| SCE1572_10478 | sce_9123 | 2.00E-82 | 7.00E-82 |
| SCE1572_10479 | sce_9124 | 2.00E-68 | 6.00E-69 |
| SCE1572_1048 | sce_785 | 4.00E-97 | 7.00E-102 |
| SCE1572_10480 | sce_9125 | 2.00E-41 | 1.00E-35 |
| SCE1572_10481 | sce_9126 | 9.00E-144 | 4.00E-134 |
| SCE1572_10482 | sce_9127 | 9.00E-69 | 1.00E-63 |
| SCE1572_10483 | sce_9128 | 3.00E-99 | 8.00E-89 |
| SCE1572_10484 | sce_9129 | 2.00E-163 | 2.00E-165 |
| SCE1572_10485 | sce_9130 | 0.00E+00 | 0.00E+00 |
| SCE1572_10486 | sce_9131 | 0.00E+00 | 5.00E-163 |
| SCE1572_10487 | sce_9133 | 0.00E+00 | 0.00E+00 |
| SCE1572_10488 | sce_9135 | 0.00E+00 | 0.00E+00 |
| SCE1572_10489 | sce_9136 | 0.00E+00 | 0.00E+00 |

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|---------------|----------|-----------|-----------|
| SCE1572_1049 | sce_786 | 4.00E-40 | 4.00E-40 |
| SCE1572_10490 | sce_9137 | 2.00E-118 | 3.00E-117 |
| SCE1572_10491 | sce_9138 | 1.00E-167 | 6.00E-160 |
| SCE1572_10492 | sce_9140 | 1.00E-65 | 9.00E-69 |
| SCE1572_10493 | sce_9141 | 0.00E+00 | 0.00E+00 |
| SCE1572_10494 | sce_9142 | 0.00E+00 | 0.00E+00 |
| SCE1572_10495 | sce_9143 | 0.00E+00 | 0.00E+00 |
| SCE1572_10496 | sce_9144 | 2.00E-58 | 2.00E-58 |
| SCE1572_10497 | sce_9145 | 2.00E-134 | 2.00E-134 |
| SCE1572_10498 | sce_9146 | 3.00E-179 | 4.00E-174 |
| SCE1572_10499 | sce_9147 | 3.00E-69 | 3.00E-69 |
| SCE1572_105 | sce_91 | 2.00E-21 | 2.00E-21 |
| SCE1572_10500 | sce_9148 | 6.00E-94 | 5.00E-86 |
| SCE1572_10501 | sce_9149 | 1.00E-45 | 1.00E-45 |
| SCE1572_10502 | sce_9150 | 0.00E+00 | 0.00E+00 |
| SCE1572_10503 | sce_9151 | 4.00E-75 | 2.00E-71 |
| SCE1572_10504 | sce_9152 | 2.00E-102 | 2.00E-102 |
| SCE1572_10507 | sce_9156 | 3.00E-84 | 3.00E-84 |
| SCE1572_10508 | sce_9157 | 2.00E-73 | 2.00E-73 |
| SCE1572_10509 | sce_9159 | 3.00E-60 | 5.00E-68 |
| SCE1572_1051 | sce_3616 | 6.00E-131 | 1.00E-137 |
| SCE1572_10510 | sce_9160 | 1.00E-142 | 4.00E-164 |
| SCE1572_10516 | sce_2347 | 1.00E-13 | 4.00E-13 |
| SCE1572_10518 | sce_2335 | 5.00E-10 | 1.00E-12 |
| SCE1572_10519 | sce_2334 | 5.00E-21 | 1.00E-20 |
| SCE1572_1052 | sce_8827 | 0.00E+00 | 0.00E+00 |
| SCE1572_10520 | sce_2333 | 2.00E-30 | 2.00E-38 |
| SCE1572_10521 | sce_2332 | 5.00E-28 | 1.00E-27 |
| SCE1572_10522 | sce_2331 | 6.00E-14 | 2.00E-11 |
| SCE1572_10524 | sce_2329 | 6.00E-27 | 4.00E-27 |
| SCE1572_10526 | sce_2327 | 1.00E-10 | 1.00E-10 |
| SCE1572_10527 | sce_2326 | 1.00E-18 | 1.00E-18 |
| SCE1572_10529 | sce_2324 | 6.00E-65 | 4.00E-65 |
| SCE1572_1053 | sce_8826 | 2.00E-109 | 8.00E-118 |
| SCE1572_10534 | sce_2320 | 8.00E-52 | 9.00E-52 |
| SCE1572_1054 | sce_8825 | 2.00E-177 | 2.00E-177 |
| SCE1572_1055 | sce_4687 | 0.00E+00 | 0.00E+00 |
| SCE1572_1056 | sce_778 | 0.00E+00 | 0.00E+00 |
| SCE1572_10564 | sce_9181 | 2.00E-122 | 3.00E-124 |
| SCE1572_10565 | sce_9180 | 3.00E-11 | 2.00E-15 |
| SCE1572_10566 | sce_9179 | 7.00E-52 | 7.00E-52 |
| SCE1572_10567 | sce_9178 | 5.00E-51 | 5.00E-51 |
| SCE1572_1057 | sce_792 | 0.00E+00 | 0.00E+00 |
| SCE1572_1058 | sce_793 | 7.00E-49 | 3.00E-37 |
| SCE1572_10585 | sce_3805 | 7.00E-47 | 7.00E-47 |
| SCE1572_10586 | sce_3806 | 6.00E-16 | 6.00E-16 |
| SCE1572_1059 | sce_4898 | 3.00E-70 | 3.00E-70 |
| SCE1572_10591 | sce_9173 | 6.00E-08 | 4.00E-08 |
| SCE1572_10594 | sce_7746 | 0.00E+00 | 0.00E+00 |
| SCE1572_10595 | sce_7745 | 0.00E+00 | 0.00E+00 |
| SCE1572_10595 | sce_142 | 0.00E+00 | 0.00E+00 |
| SCE1572_10595 | sce_3777 | 0.00E+00 | 0.00E+00 |
| SCE1572_10596 | sce_7744 | 2.00E-107 | 6.00E-112 |
| SCE1572_10597 | sce_7743 | 2.00E-38 | 3.00E-38 |
| SCE1572_10600 | sce_7488 | 3.00E-15 | 5.00E-11 |
| SCE1572_10604 | sce_9219 | 0.00E+00 | 2.00E-180 |
| SCE1572_10607 | sce_9220 | 1.00E-96 | 1.00E-96 |
| SCE1572_10608 | sce_9221 | 1.00E-131 | 8.00E-129 |
| SCE1572_10609 | sce_9222 | 0.00E+00 | 0.00E+00 |
| SCE1572_10609 | sce_1814 | 0.00E+00 | 0.00E+00 |
| SCE1572_10609 | sce_3148 | 0.00E+00 | 0.00E+00 |
| SCE1572_1061 | sce_794 | 2.00E-151 | 3.00E-150 |
| SCE1572_10610 | sce_9042 | 2.00E-28 | 2.00E-28 |
| SCE1572_10615 | sce_9224 | 1.00E-164 | 6.00E-162 |
| SCE1572_10616 | sce_9225 | 2.00E-85 | 1.00E-83 |
| SCE1572_10620 | sce_9228 | 0.00E+00 | 0.00E+00 |
| SCE1572_10621 | sce_9229 | 0.00E+00 | 0.00E+00 |
| SCE1572_10622 | sce_9230 | 0.00E+00 | 0.00E+00 |
| SCE1572_10622 | sce_9231 | 0.00E+00 | 0.00E+00 |
| SCE1572_10622 | sce_389 | 0.00E+00 | 0.00E+00 |
| SCE1572_10623 | sce_9231 | 0.00E+00 | 0.00E+00 |
| SCE1572_10623 | sce_9237 | 0.00E+00 | 0.00E+00 |
| SCE1572_10623 | sce_9230 | 0.00E+00 | 0.00E+00 |
| SCE1572_10624 | sce_9232 | 5.00E-136 | 5.00E-138 |
| SCE1572_10625 | sce_9233 | 2.00E-34 | 2.00E-34 |
| SCE1572_10626 | sce_9234 | 0.00E+00 | 0.00E+00 |

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| SCE1572_10627 | sce_9235 | 0.00E+00 | 0.00E+00 |
| SCE1572_10628 | sce_9236 | 0.00E+00 | 0.00E+00 |
| SCE1572_10628 | sce_389 | 0.00E+00 | 0.00E+00 |
| SCE1572_10629 | sce_9237 | 0.00E+00 | 0.00E+00 |
| SCE1572_10629 | sce_9231 | 0.00E+00 | 0.00E+00 |
| SCE1572_10629 | sce_2666 | 0.00E+00 | 0.00E+00 |
| SCE1572_10629 | sce_389 | 0.00E+00 | 0.00E+00 |
| SCE1572_10629 | sce_7637 | 0.00E+00 | 0.00E+00 |
| SCE1572_10633 | sce_9240 | 0.00E+00 | 0.00E+00 |
| SCE1572_10634 | sce_9238 | 0.00E+00 | 0.00E+00 |
| SCE1572_10634 | sce_4347 | 0.00E+00 | 0.00E+00 |
| SCE1572_10635 | sce_9239 | 5.00E-162 | 5.00E-180 |
| SCE1572_10637 | sce_9241 | 9.00E-06 | 1.00E-12 |
| SCE1572_10638 | sce_9242 | 5.00E-15 | 3.00E-13 |
| SCE1572_10639 | sce_9244 | 0.00E+00 | 0.00E+00 |
| SCE1572_10640 | sce_9245 | 0.00E+00 | 0.00E+00 |
| SCE1572_10641 | sce_9246 | 8.00E-150 | 1.00E-161 |
| SCE1572_10642 | sce_9247 | 0.00E+00 | 0.00E+00 |
| SCE1572_10643 | sce_9248 | 5.00E-157 | 6.00E-157 |
| SCE1572_10644 | sce_9249 | 2.00E-173 | 1.00E-173 |
| SCE1572_10645 | sce_9250 | 7.00E-147 | 9.00E-146 |
| SCE1572_10646 | sce_9251 | 2.00E-119 | 1.00E-131 |
| SCE1572_10647 | sce_9252 | 2.00E-91 | 2.00E-91 |
| SCE1572_10648 | sce_9253 | 1.00E-160 | 1.00E-158 |
| SCE1572_1065 | sce_9451 | 2.00E-117 | 2.00E-117 |
| SCE1572_10650 | sce_9254 | 3.00E-57 | 3.00E-57 |
| SCE1572_10651 | sce_9255 | 0.00E+00 | 0.00E+00 |
| SCE1572_10652 | sce_9256 | 9.00E-97 | 1.00E-104 |
| SCE1572_10653 | sce_9257 | 0.00E+00 | 0.00E+00 |
| SCE1572_10654 | sce_9258 | 0.00E+00 | 5.00E-175 |
| SCE1572_10655 | sce_9259 | 1.00E-34 | 1.00E-34 |
| SCE1572_10656 | sce_9260 | 0.00E+00 | 0.00E+00 |
| SCE1572_10657 | sce_9261 | 4.00E-166 | 5.00E-166 |
| SCE1572_10658 | sce_9263 | 8.00E-41 | 9.00E-37 |
| SCE1572_10659 | sce_9264 | 0.00E+00 | 0.00E+00 |
| SCE1572_1066 | sce_9453 | 2.00E-120 | 2.00E-119 |
| SCE1572_10660 | sce_9265 | 7.00E-61 | 2.00E-61 |
| SCE1572_10661 | sce_9266 | 0.00E+00 | 0.00E+00 |
| SCE1572_10662 | sce_9267 | 0.00E+00 | 0.00E+00 |
| SCE1572_10663 | sce_9271 | 0.00E+00 | 0.00E+00 |
| SCE1572_10664 | sce_9272 | 6.00E-123 | 6.00E-123 |
| SCE1572_10665 | sce_9273 | 9.00E-132 | 1.00E-131 |
| SCE1572_10666 | sce_9274 | 8.00E-160 | 4.00E-160 |
| SCE1572_10667 | sce_9275 | 4.00E-121 | 2.00E-92 |
| SCE1572_10669 | sce_9279 | 2.00E-149 | 2.00E-149 |
| SCE1572_1067 | sce_9454 | 0.00E+00 | 0.00E+00 |
| SCE1572_10671 | sce_9283 | 7.00E-35 | 1.00E-55 |
| SCE1572_10672 | sce_9284 | 1.00E-109 | 2.00E-99 |
| SCE1572_10673 | sce_9285 | 0.00E+00 | 0.00E+00 |
| SCE1572_10674 | sce_9286 | 4.00E-115 | 1.00E-115 |
| SCE1572_10675 | sce_9287 | 0.00E+00 | 0.00E+00 |
| SCE1572_10676 | sce_9288 | 1.00E-143 | 2.00E-149 |
| SCE1572_10677 | sce_9289 | 1.00E-59 | 1.00E-64 |
| SCE1572_10678 | sce_9290 | 1.00E-137 | 3.00E-137 |
| SCE1572_10679 | sce_9291 | 0.00E+00 | 0.00E+00 |
| SCE1572_10681 | sce_9292 | 3.00E-110 | 1.00E-110 |
| SCE1572_10682 | sce_9293 | 1.00E-102 | 9.00E-91 |
| SCE1572_10683 | sce_9294 | 5.00E-149 | 2.00E-146 |
| SCE1572_10685 | sce_9295 | 0.00E+00 | 0.00E+00 |
| SCE1572_10686 | sce_9296 | 0.00E+00 | 0.00E+00 |
| SCE1572_10687 | sce_9297 | 3.00E-40 | 3.00E-40 |
| SCE1572_10688 | sce_9298 | 9.00E-116 | 9.00E-116 |
| SCE1572_10692 | sce_9299 | 7.00E-94 | 3.00E-96 |
| SCE1572_10693 | sce_9300 | 0.00E+00 | 0.00E+00 |
| SCE1572_10695 | sce_9306 | 7.00E-89 | 7.00E-89 |
| SCE1572_10696 | sce_9307 | 2.00E-136 | 5.00E-61 |
| SCE1572_10697 | sce_9308 | 0.00E+00 | 0.00E+00 |
| SCE1572_10698 | sce_9309 | 1.00E-92 | 5.00E-78 |
| SCE1572_10699 | sce_9310 | 7.00E-130 | 2.00E-118 |
| SCE1572_107 | sce_95 | 2.00E-107 | 2.00E-107 |
| SCE1572_10702 | sce_9311 | 4.00E-33 | 4.00E-36 |
| SCE1572_10703 | sce_9312 | 1.00E-140 | 2.00E-144 |
| SCE1572_10704 | sce_9313 | 1.00E-80 | 1.00E-71 |
| SCE1572_10710 | sce_9505 | 1.00E-83 | 4.00E-76 |
| SCE1572_10711 | sce_9314 | 7.00E-90 | 8.00E-77 |
| SCE1572_10712 | sce_9315 | 0.00E+00 | 0.00E+00 |

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| SCE1572_10713 | sce_9316 | 1.00E-86 | 1.00E-86 |
| SCE1572_10717 | sce_9370 | 3.00E-120 | 4.00E-118 |
| SCE1572_10718 | sce_9378 | 3.00E-31 | 2.00E-42 |
| SCE1572_10719 | sce_9379 | 0.00E+00 | 0.00E+00 |
| SCE1572_1072 | sce_795 | 0.00E+00 | 0.00E+00 |
| SCE1572_10725 | sce_9383 | 5.00E-143 | 8.00E-149 |
| SCE1572_10728 | sce_9384 | 5.00E-100 | 5.00E-100 |
| SCE1572_10729 | sce_9385 | 8.00E-111 | 3.00E-113 |
| SCE1572_10730 | sce_9387 | 7.00E-102 | 3.00E-100 |
| SCE1572_10731 | sce_9388 | 1.00E-31 | 8.00E-22 |
| SCE1572_10732 | sce_9390 | 0.00E+00 | 0.00E+00 |
| SCE1572_10733 | sce_9391 | 1.00E-39 | 8.00E-38 |
| SCE1572_10735 | sce_9393 | 3.00E-83 | 7.00E-80 |
| SCE1572_10736 | sce_9394 | 0.00E+00 | 0.00E+00 |
| SCE1572_10737 | sce_9395 | 0.00E+00 | 0.00E+00 |
| SCE1572_10738 | sce_9396 | 0.00E+00 | 0.00E+00 |
| SCE1572_10745 | sce_10010 | 1.00E-91 | 1.00E-91 |
| SCE1572_10747 | sce_9992 | 6.00E-139 | 4.00E-156 |
| SCE1572_10748 | sce_9993 | 5.00E-92 | 1.00E-124 |
| SCE1572_10749 | sce_10027 | 3.00E-158 | 3.00E-158 |
| SCE1572_10750 | sce_10004 | 1.00E-65 | 1.00E-65 |
| SCE1572_10751 | sce_827 | 0.00E+00 | 0.00E+00 |
| SCE1572_10752 | sce_5142 | 1.00E-113 | 3.00E-114 |
| SCE1572_10753 | sce_6048 | 0.00E+00 | 0.00E+00 |
| SCE1572_10754 | sce_1347 | 1.00E-74 | 2.00E-83 |
| SCE1572_10755 | sce_10007 | 0.00E+00 | 0.00E+00 |
| SCE1572_10756 | sce_9959 | 0.00E+00 | 0.00E+00 |
| SCE1572_10757 | sce_9958 | 0.00E+00 | 0.00E+00 |
| SCE1572_10758 | sce_10009 | 7.00E-47 | 2.00E-49 |
| SCE1572_10762 | sce_10003 | 0.00E+00 | 0.00E+00 |
| SCE1572_10765 | sce_10018 | 0.00E+00 | 0.00E+00 |
| SCE1572_10767 | sce_10013 | 3.00E-171 | 2.00E-159 |
| SCE1572_10768 | sce_8396 | 8.00E-28 | 7.00E-28 |
| SCE1572_10769 | sce_8395 | 1.00E-33 | 1.00E-33 |
| SCE1572_1077 | sce_5210 | 1.00E-105 | 5.00E-82 |
| SCE1572_10772 | sce_10029 | 7.00E-83 | 1.00E-75 |
| SCE1572_10773 | sce_10030 | 9.00E-81 | 5.00E-81 |
| SCE1572_10774 | sce_10031 | 2.00E-93 | 1.00E-93 |
| SCE1572_10776 | sce_9407 | 0.00E+00 | 0.00E+00 |
| SCE1572_10776 | sce_3765 | 0.00E+00 | 0.00E+00 |
| SCE1572_10776 | sce_8451 | 0.00E+00 | 0.00E+00 |
| SCE1572_10776 | sce_4817 | 0.00E+00 | 0.00E+00 |
| SCE1572_10777 | sce_9040 | 4.00E-162 | 5.00E-160 |
| SCE1572_10778 | sce_2922 | 0.00E+00 | 0.00E+00 |
| SCE1572_1078 | sce_5665 | 9.00E-177 | 9.00E-177 |
| SCE1572_10782 | sce_9409 | 4.00E-132 | 8.00E-155 |
| SCE1572_10783 | sce_9410 | 0.00E+00 | 0.00E+00 |
| SCE1572_10784 | sce_9411 | 0.00E+00 | 0.00E+00 |
| SCE1572_10785 | sce_9412 | 0.00E+00 | 0.00E+00 |
| SCE1572_10787 | sce_9413 | 7.00E-176 | 7.00E-174 |
| SCE1572_10789 | sce_9414 | 7.00E-73 | 4.00E-73 |
| SCE1572_10790 | sce_9415 | 5.00E-110 | 2.00E-110 |
| SCE1572_10791 | sce_9416 | 9.00E-169 | 2.00E-159 |
| SCE1572_10792 | sce_9417 | 0.00E+00 | 0.00E+00 |
| SCE1572_10793 | sce_9418 | 4.00E-97 | 7.00E-105 |
| SCE1572_10794 | sce_9419 | 9.00E-61 | 5.00E-57 |
| SCE1572_10795 | sce_9420 | 1.00E-12 | 1.00E-12 |
| SCE1572_10797 | sce_9422 | 3.00E-149 | 3.00E-158 |
| SCE1572_10798 | sce_9424 | 1.00E-56 | 1.00E-56 |
| SCE1572_108 | sce_96 | 0.00E+00 | 0.00E+00 |
| SCE1572_1080 | sce_796 | 6.00E-70 | 2.00E-64 |
| SCE1572_10802 | sce_9425 | 0.00E+00 | 0.00E+00 |
| SCE1572_10805 | sce_4489 | 8.00E-140 | 3.00E-148 |
| SCE1572_10807 | sce_2093 | 0.00E+00 | 0.00E+00 |
| SCE1572_10808 | sce_9441 | 3.00E-41 | 2.00E-37 |
| SCE1572_1081 | sce_798 | 4.00E-44 | 4.00E-48 |
| SCE1572_10810 | sce_9443 | 2.00E-55 | 1.00E-55 |
| SCE1572_10812 | sce_9444 | 9.00E-49 | 3.00E-51 |
| SCE1572_10813 | sce_9446 | 2.00E-22 | 4.00E-22 |
| SCE1572_10814 | sce_9447 | 4.00E-174 | 7.00E-174 |
| SCE1572_10815 | sce_9448 | 3.00E-158 | 6.00E-169 |
| SCE1572_10816 | sce_9449 | 5.00E-84 | 7.00E-90 |
| SCE1572_10817 | sce_2995 | 0.00E+00 | 0.00E+00 |
| SCE1572_10818 | sce_2996 | 0.00E+00 | 0.00E+00 |
| SCE1572_10819 | sce_2998 | 0.00E+00 | 0.00E+00 |
| SCE1572_1082 | sce_799 | 3.00E-95 | 1.00E-107 |

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| SCE1572_10820 | sce_9459 | 8.00E-84 | 8.00E-84 |
| SCE1572_10822 | sce_9460 | 2.00E-113 | 2.00E-124 |
| SCE1572_10823 | sce_6965 | 1.00E-139 | 1.00E-132 |
| SCE1572_10824 | sce_8729 | 3.00E-45 | 3.00E-45 |
| SCE1572_10825 | sce_8728 | 5.00E-52 | 3.00E-63 |
| SCE1572_10827 | sce_3440 | 1.00E-155 | 4.00E-148 |
| SCE1572_10828 | sce_3441 | 2.00E-58 | 2.00E-58 |
| SCE1572_1083 | sce_800 | 1.00E-54 | 2.00E-54 |
| SCE1572_10830 | sce_3442 | 0.00E+00 | 0.00E+00 |
| SCE1572_10831 | sce_2163 | 1.00E-160 | 3.00E-156 |
| SCE1572_10834 | sce_1601 | 0.00E+00 | 0.00E+00 |
| SCE1572_10834 | sce_6742 | 0.00E+00 | 0.00E+00 |
| SCE1572_10838 | sce_9473 | 1.00E-174 | 0.00E+00 |
| SCE1572_1084 | sce_801 | 2.00E-133 | 3.00E-112 |
| SCE1572_10840 | sce_5249 | 2.00E-23 | 2.00E-23 |
| SCE1572_10841 | sce_9475 | 3.00E-113 | 6.00E-120 |
| SCE1572_10842 | sce_9476 | 2.00E-26 | 4.00E-27 |
| SCE1572_10846 | sce_1385 | 0.00E+00 | 0.00E+00 |
| SCE1572_10847 | sce_1384 | 0.00E+00 | 0.00E+00 |
| SCE1572_10848 | sce_1383 | 5.00E-175 | 0.00E+00 |
| SCE1572_10849 | sce_1382 | 1.00E-153 | 5.00E-159 |
| SCE1572_10850 | sce_1381 | 5.00E-161 | 2.00E-166 |
| SCE1572_10852 | sce_2474 | 6.00E-179 | 6.00E-179 |
| SCE1572_10853 | sce_2473 | 1.00E-123 | 1.00E-110 |
| SCE1572_10854 | sce_2472 | 6.00E-144 | 2.00E-161 |
| SCE1572_10855 | sce_2471 | 0.00E+00 | 0.00E+00 |
| SCE1572_10856 | sce_2470 | 2.00E-155 | 8.00E-163 |
| SCE1572_10857 | sce_5146 | 1.00E-154 | 3.00E-155 |
| SCE1572_10858 | sce_9486 | 0.00E+00 | 0.00E+00 |
| SCE1572_10859 | sce_9487 | 0.00E+00 | 0.00E+00 |
| SCE1572_1086 | sce_802 | 0.00E+00 | 0.00E+00 |
| SCE1572_10860 | sce_9488 | 6.00E-57 | 6.00E-57 |
| SCE1572_10861 | sce_9489 | 0.00E+00 | 0.00E+00 |
| SCE1572_10862 | sce_9491 | 0.00E+00 | 0.00E+00 |
| SCE1572_10863 | sce_9492 | 5.00E-130 | 4.00E-120 |
| SCE1572_10865 | sce_3077 | 1.00E-68 | 2.00E-68 |
| SCE1572_10867 | sce_9494 | 6.00E-69 | 6.00E-74 |
| SCE1572_10868 | sce_9495 | 0.00E+00 | 0.00E+00 |
| SCE1572_10869 | sce_9496 | 0.00E+00 | 0.00E+00 |
| SCE1572_10871 | sce_3937 | 0.00E+00 | 0.00E+00 |
| SCE1572_10871 | sce_8592 | 0.00E+00 | 0.00E+00 |
| SCE1572_10879 | sce_9509 | 2.00E-170 | 1.00E-172 |
| SCE1572_10880 | sce_9510 | 0.00E+00 | 0.00E+00 |
| SCE1572_10882 | sce_9511 | 1.00E-141 | 8.00E-145 |
| SCE1572_10883 | sce_9512 | 3.00E-23 | 1.00E-23 |
| SCE1572_10884 | sce_9513 | 6.00E-103 | 3.00E-114 |
| SCE1572_10885 | sce_9514 | 0.00E+00 | 0.00E+00 |
| SCE1572_10886 | sce_9515 | 2.00E-158 | 3.00E-142 |
| SCE1572_10887 | sce_9517 | 5.00E-134 | 2.00E-128 |
| SCE1572_10889 | sce_9521 | 0.00E+00 | 0.00E+00 |
| SCE1572_10890 | sce_9522 | 1.00E-71 | 6.00E-90 |
| SCE1572_10892 | sce_9524 | 7.00E-154 | 7.00E-172 |
| SCE1572_10893 | sce_9525 | 9.00E-173 | 1.00E-180 |
| SCE1572_10894 | sce_9529 | 2.00E-52 | 4.00E-44 |
| SCE1572_10897 | sce_9530 | 2.00E-99 | 5.00E-99 |
| SCE1572_10898 | sce_9531 | 1.00E-74 | 3.00E-79 |
| SCE1572_109 | sce_97 | 2.00E-121 | 7.00E-130 |
| SCE1572_10901 | sce_9534 | 2.00E-168 | 9.00E-159 |
| SCE1572_10904 | sce_9537 | 5.00E-81 | 7.00E-84 |
| SCE1572_10905 | sce_9539 | 4.00E-96 | 4.00E-96 |
| SCE1572_10906 | sce_9540 | 1.00E-20 | 9.00E-25 |
| SCE1572_10907 | sce_9541 | 0.00E+00 | 0.00E+00 |
| SCE1572_10908 | sce_9542 | 4.00E-111 | 1.00E-111 |
| SCE1572_10912 | sce_9548 | 0.00E+00 | 0.00E+00 |
| SCE1572_10913 | sce_9550 | 3.00E-30 | 3.00E-30 |
| SCE1572_10914 | sce_8717 | 5.00E-161 | 4.00E-168 |
| SCE1572_10916 | sce_9551 | 0.00E+00 | 0.00E+00 |
| SCE1572_10917 | sce_9552 | 0.00E+00 | 0.00E+00 |
| SCE1572_10919 | sce_9553 | 1.00E-108 | 5.00E-107 |
| SCE1572_10920 | sce_9554 | 4.00E-99 | 2.00E-92 |
| SCE1572_10921 | sce_8693 | 6.00E-51 | 7.00E-48 |
| SCE1572_10922 | sce_9555 | 6.00E-140 | 8.00E-154 |
| SCE1572_10923 | sce_9556 | 3.00E-125 | 5.00E-128 |
| SCE1572_10924 | sce_9557 | 0.00E+00 | 0.00E+00 |
| SCE1572_10924 | sce_10204 | 0.00E+00 | 0.00E+00 |
| SCE1572_10924 | sce_5835 | 0.00E+00 | 0.00E+00 |

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| SCE1572_10924 | sce_388 | 0.00E+00 | 0.00E+00 |
| SCE1572_10924 | sce_7640 | 0.00E+00 | 0.00E+00 |
| SCE1572_10924 | sce_4513 | 0.00E+00 | 0.00E+00 |
| SCE1572_10924 | sce_6535 | 0.00E+00 | 0.00E+00 |
| SCE1572_10924 | sce_3003 | 0.00E+00 | 0.00E+00 |
| SCE1572_10924 | sce_9920 | 0.00E+00 | 0.00E+00 |
| SCE1572_10924 | sce_3085 | 0.00E+00 | 0.00E+00 |
| SCE1572_10924 | sce_7661 | 0.00E+00 | 0.00E+00 |
| SCE1572_10924 | sce_7109 | 0.00E+00 | 0.00E+00 |
| SCE1572_10924 | sce_3917 | 0.00E+00 | 0.00E+00 |
| SCE1572_10924 | sce_6107 | 0.00E+00 | 0.00E+00 |
| SCE1572_10924 | sce_6095 | 0.00E+00 | 0.00E+00 |
| SCE1572_10924 | sce_6093 | 0.00E+00 | 0.00E+00 |
| SCE1572_10924 | sce_6092 | 0.00E+00 | 0.00E+00 |
| SCE1572_10924 | sce_6094 | 0.00E+00 | 0.00E+00 |
| SCE1572_10924 | sce_8618 | 0.00E+00 | 0.00E+00 |
| SCE1572_10924 | sce_2065 | 0.00E+00 | 0.00E+00 |
| SCE1572_10927 | sce_9558 | 0.00E+00 | 0.00E+00 |
| SCE1572_10928 | sce_9559 | 4.00E-164 | 0.00E+00 |
| SCE1572_10929 | sce_2568 | 2.00E-16 | 5.00E-12 |
| SCE1572_10940 | sce_8783 | 4.00E-52 | 2.00E-52 |
| SCE1572_10941 | sce_6032 | 1.00E-14 | 3.00E-22 |
| SCE1572_10947 | sce_9423 | 7.00E-38 | 2.00E-45 |
| SCE1572_10949 | sce_9560 | 3.00E-49 | 3.00E-49 |
| SCE1572_1095 | sce_5295 | 2.00E-64 | 2.00E-60 |
| SCE1572_10951 | sce_9561 | 0.00E+00 | 0.00E+00 |
| SCE1572_10955 | sce_9564 | 0.00E+00 | 0.00E+00 |
| SCE1572_10956 | sce_9569 | 2.00E-131 | 4.00E-130 |
| SCE1572_10957 | sce_9570 | 1.00E-67 | 9.00E-64 |
| SCE1572_10958 | sce_9572 | 7.00E-153 | 3.00E-159 |
| SCE1572_10959 | sce_9573 | 0.00E+00 | 0.00E+00 |
| SCE1572_10960 | sce_9574 | 1.00E-53 | 6.00E-57 |
| SCE1572_10961 | sce_9575 | 2.00E-51 | 2.00E-54 |
| SCE1572_10964 | sce_9678 | 0.00E+00 | 0.00E+00 |
| SCE1572_10965 | sce_9679 | 0.00E+00 | 0.00E+00 |
| SCE1572_10966 | sce_9680 | 6.00E-63 | 1.00E-61 |
| SCE1572_10967 | sce_9681 | 8.00E-91 | 2.00E-91 |
| SCE1572_10968 | sce_9682 | 4.00E-97 | 1.00E-97 |
| SCE1572_10969 | sce_9683 | 0.00E+00 | 0.00E+00 |
| SCE1572_10970 | sce_9684 | 0.00E+00 | 0.00E+00 |
| SCE1572_10971 | sce_9685 | 3.00E-18 | 8.00E-11 |
| SCE1572_10972 | sce_9686 | 7.00E-155 | 3.00E-148 |
| SCE1572_10973 | sce_9687 | 0.00E+00 | 0.00E+00 |
| SCE1572_10973 | sce_9694 | 0.00E+00 | 0.00E+00 |
| SCE1572_10975 | sce_9696 | 2.00E-41 | 2.00E-41 |
| SCE1572_10976 | sce_9697 | 2.00E-10 | 4.00E-15 |
| SCE1572_10977 | sce_9698 | 2.00E-63 | 2.00E-62 |
| SCE1572_10978 | sce_9699 | 4.00E-80 | 3.00E-80 |
| SCE1572_10979 | sce_9701 | 0.00E+00 | 0.00E+00 |
| SCE1572_1098 | sce_3750 | 0.00E+00 | 0.00E+00 |
| SCE1572_1098 | sce_5229 | 0.00E+00 | 0.00E+00 |
| SCE1572_1098 | sce_6712 | 0.00E+00 | 0.00E+00 |
| SCE1572_1098 | sce_5226 | 0.00E+00 | 0.00E+00 |
| SCE1572_10980 | sce_9702 | 1.00E-110 | 9.00E-107 |
| SCE1572_10981 | sce_9703 | 0.00E+00 | 0.00E+00 |
| SCE1572_10982 | sce_9704 | 1.00E-130 | 1.00E-130 |
| SCE1572_10983 | sce_9705 | 0.00E+00 | 0.00E+00 |
| SCE1572_10984 | sce_9706 | 0.00E+00 | 0.00E+00 |
| SCE1572_10985 | sce_9707 | 3.00E-38 | 3.00E-38 |
| SCE1572_10986 | sce_9708 | 1.00E-175 | 1.00E-163 |
| SCE1572_10987 | sce_9709 | 2.00E-110 | 4.00E-113 |
| SCE1572_10988 | sce_9710 | 4.00E-69 | 1.00E-61 |
| SCE1572_10989 | sce_9711 | 4.00E-165 | 5.00E-153 |
| SCE1572_10990 | sce_9712 | 4.00E-45 | 4.00E-45 |
| SCE1572_10991 | sce_9713 | 3.00E-124 | 6.00E-136 |
| SCE1572_10992 | sce_9714 | 3.00E-34 | 1.00E-21 |
| SCE1572_10994 | sce_9715 | 8.00E-97 | 9.00E-109 |
| SCE1572_10995 | sce_9716 | 0.00E+00 | 0.00E+00 |
| SCE1572_10997 | sce_9718 | 0.00E+00 | 0.00E+00 |
| SCE1572_10998 | sce_9719 | 6.00E-88 | 3.00E-105 |
| SCE1572_10999 | sce_9721 | 1.00E-22 | 1.00E-22 |
| SCE1572_11 | sce_11 | 4.00E-148 | 6.00E-152 |
| SCE1572_110 | sce_98 | 0.00E+00 | 0.00E+00 |
| SCE1572_11000 | sce_9722 | 3.00E-30 | 4.00E-30 |
| SCE1572_11001 | sce_9723 | 2.00E-36 | 1.00E-27 |
| SCE1572_11002 | sce_9724 | 1.00E-20 | 2.00E-13 |

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|---------------|----------|-----------|-----------|
| SCE1572_11003 | sce_9725 | 8.00E-158 | 2.00E-154 |
| SCE1572_11004 | sce_9726 | 0.00E+00 | 0.00E+00 |
| SCE1572_11005 | sce_9727 | 0.00E+00 | 0.00E+00 |
| SCE1572_11007 | sce_9729 | 0.00E+00 | 0.00E+00 |
| SCE1572_11009 | sce_9730 | 0.00E+00 | 0.00E+00 |
| SCE1572_11010 | sce_9731 | 7.00E-142 | 3.00E-139 |
| SCE1572_11019 | sce_9732 | 1.00E-40 | 7.00E-30 |
| SCE1572_11020 | sce_9733 | 8.00E-77 | 4.00E-68 |
| SCE1572_11021 | sce_9734 | 5.00E-118 | 2.00E-138 |
| SCE1572_11022 | sce_9735 | 0.00E+00 | 0.00E+00 |
| SCE1572_11022 | sce_3075 | 0.00E+00 | 0.00E+00 |
| SCE1572_11023 | sce_9737 | 0.00E+00 | 0.00E+00 |
| SCE1572_11024 | sce_9738 | 2.00E-66 | 2.00E-66 |
| SCE1572_11025 | sce_9739 | 0.00E+00 | 0.00E+00 |
| SCE1572_11027 | sce_9741 | 1.00E-54 | 2.00E-46 |
| SCE1572_11028 | sce_9742 | 4.00E-27 | 2.00E-19 |
| SCE1572_11029 | sce_9743 | 1.00E-23 | 7.00E-23 |
| SCE1572_11030 | sce_9744 | 2.00E-72 | 7.00E-66 |
| SCE1572_11033 | sce_9745 | 6.00E-08 | 7.00E-07 |
| SCE1572_11034 | sce_9746 | 0.00E+00 | 0.00E+00 |
| SCE1572_11035 | sce_9747 | 7.00E-80 | 5.00E-71 |
| SCE1572_11036 | sce_9748 | 7.00E-42 | 6.00E-42 |
| SCE1572_11037 | sce_9749 | 0.00E+00 | 0.00E+00 |
| SCE1572_11038 | sce_9750 | 2.00E-15 | 2.00E-15 |
| SCE1572_11039 | sce_9751 | 0.00E+00 | 0.00E+00 |
| SCE1572_11040 | sce_9752 | 0.00E+00 | 0.00E+00 |
| SCE1572_11041 | sce_9754 | 8.00E-26 | 6.00E-27 |
| SCE1572_11042 | sce_9755 | 5.00E-101 | 6.00E-101 |
| SCE1572_11043 | sce_9757 | 0.00E+00 | 0.00E+00 |
| SCE1572_11043 | sce_3883 | 0.00E+00 | 0.00E+00 |
| SCE1572_11043 | sce_5226 | 0.00E+00 | 0.00E+00 |
| SCE1572_11043 | sce_5403 | 0.00E+00 | 0.00E+00 |
| SCE1572_11043 | sce_5751 | 0.00E+00 | 0.00E+00 |
| SCE1572_11043 | sce_9665 | 0.00E+00 | 0.00E+00 |
| SCE1572_11043 | sce_7154 | 0.00E+00 | 0.00E+00 |
| SCE1572_11043 | sce_7969 | 0.00E+00 | 0.00E+00 |
| SCE1572_11043 | sce_9954 | 0.00E+00 | 0.00E+00 |
| SCE1572_11043 | sce_5746 | 0.00E+00 | 0.00E+00 |
| SCE1572_11043 | sce_6712 | 0.00E+00 | 0.00E+00 |
| SCE1572_11043 | sce_2053 | 0.00E+00 | 0.00E+00 |
| SCE1572_11043 | sce_3750 | 0.00E+00 | 0.00E+00 |
| SCE1572_11043 | sce_5229 | 0.00E+00 | 0.00E+00 |
| SCE1572_11044 | sce_7609 | 7.00E-81 | 2.00E-75 |
| SCE1572_11046 | sce_9758 | 0.00E+00 | 0.00E+00 |
| SCE1572_11046 | sce_5980 | 0.00E+00 | 0.00E+00 |
| SCE1572_11047 | sce_9760 | 6.00E-86 | 3.00E-85 |
| SCE1572_11048 | sce_9761 | 2.00E-177 | 0.00E+00 |
| SCE1572_11049 | sce_9762 | 0.00E+00 | 0.00E+00 |
| SCE1572_11050 | sce_9763 | 2.00E-93 | 3.00E-87 |
| SCE1572_11051 | sce_9765 | 1.00E-93 | 1.00E-108 |
| SCE1572_11052 | sce_9766 | 1.00E-150 | 5.00E-146 |
| SCE1572_11053 | sce_9767 | 0.00E+00 | 0.00E+00 |
| SCE1572_11054 | sce_9771 | 7.00E-117 | 2.00E-124 |
| SCE1572_11055 | sce_9772 | 0.00E+00 | 0.00E+00 |
| SCE1572_11056 | sce_9773 | 6.00E-50 | 9.00E-50 |
| SCE1572_11062 | sce_4581 | 0.00E+00 | 0.00E+00 |
| SCE1572_11062 | sce_9106 | 0.00E+00 | 0.00E+00 |
| SCE1572_11064 | sce_9779 | 0.00E+00 | 0.00E+00 |
| SCE1572_11066 | sce_9780 | 0.00E+00 | 0.00E+00 |
| SCE1572_11068 | sce_9813 | 0.00E+00 | 0.00E+00 |
| SCE1572_11069 | sce_9814 | 0.00E+00 | 0.00E+00 |
| SCE1572_11070 | sce_9815 | 8.00E-98 | 1.00E-101 |
| SCE1572_11072 | sce_9822 | 4.00E-122 | 5.00E-131 |
| SCE1572_11073 | sce_9823 | 4.00E-35 | 2.00E-28 |
| SCE1572_11074 | sce_9824 | 1.00E-08 | 2.00E-12 |
| SCE1572_11075 | sce_9825 | 7.00E-42 | 1.00E-54 |
| SCE1572_11076 | sce_9826 | 2.00E-54 | 8.00E-74 |
| SCE1572_11077 | sce_9827 | 1.00E-79 | 1.00E-79 |
| SCE1572_11078 | sce_7074 | 1.00E-09 | 8.00E-09 |
| SCE1572_11079 | sce_9829 | 2.00E-56 | 1.00E-45 |
| SCE1572_11080 | sce_9830 | 4.00E-92 | 1.00E-93 |
| SCE1572_11081 | sce_9831 | 3.00E-167 | 3.00E-174 |
| SCE1572_11082 | sce_9832 | 6.00E-112 | 4.00E-119 |
| SCE1572_11083 | sce_9833 | 6.00E-37 | 3.00E-45 |
| SCE1572_11090 | sce_9835 | 0.00E+00 | 0.00E+00 |
| SCE1572_11091 | sce_9836 | 8.00E-120 | 6.00E-122 |

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|---------------|-----------|-----------|-----------|
| SCE1572_11093 | sce_9837 | 0.00E+00 | 0.00E+00 |
| SCE1572_11094 | sce_9838 | 0.00E+00 | 0.00E+00 |
| SCE1572_11096 | sce_9839 | 2.00E-151 | 8.00E-157 |
| SCE1572_11097 | sce_9840 | 0.00E+00 | 0.00E+00 |
| SCE1572_11098 | sce_9841 | 0.00E+00 | 0.00E+00 |
| SCE1572_11099 | sce_9842 | 3.00E-119 | 6.00E-123 |
| SCE1572_111 | sce_99 | 5.00E-139 | 1.00E-149 |
| SCE1572_11102 | sce_9843 | 3.00E-112 | 2.00E-117 |
| SCE1572_11103 | sce_6096 | 7.00E-52 | 2.00E-53 |
| SCE1572_11104 | sce_6097 | 1.00E-64 | 1.00E-71 |
| SCE1572_11105 | sce_6098 | 2.00E-15 | 1.00E-26 |
| SCE1572_11106 | sce_6099 | 4.00E-79 | 8.00E-88 |
| SCE1572_11111 | sce_311 | 4.00E-130 | 2.00E-122 |
| SCE1572_11112 | sce_1119 | 4.00E-54 | 1.00E-51 |
| SCE1572_11113 | sce_9847 | 0.00E+00 | 0.00E+00 |
| SCE1572_11114 | sce_7062 | 9.00E-71 | 2.00E-71 |
| SCE1572_11117 | sce_6854 | 2.00E-54 | 2.00E-55 |
| SCE1572_11118 | sce_8356 | 0.00E+00 | 0.00E+00 |
| SCE1572_11119 | sce_8357 | 0.00E+00 | 0.00E+00 |
| SCE1572_11119 | sce_225 | 0.00E+00 | 0.00E+00 |
| SCE1572_11119 | sce_6235 | 0.00E+00 | 0.00E+00 |
| SCE1572_11119 | sce_2161 | 0.00E+00 | 0.00E+00 |
| SCE1572_11119 | sce_5276 | 0.00E+00 | 0.00E+00 |
| SCE1572_11120 | sce_6777 | 1.00E-41 | 2.00E-43 |
| SCE1572_11121 | sce_6778 | 6.00E-85 | 6.00E-85 |
| SCE1572_11123 | sce_1320 | 0.00E+00 | 0.00E+00 |
| SCE1572_11125 | sce_3466 | 2.00E-61 | 1.00E-71 |
| SCE1572_11126 | sce_9853 | 0.00E+00 | 0.00E+00 |
| SCE1572_11130 | sce_3722 | 0.00E+00 | 0.00E+00 |
| SCE1572_11131 | sce_3725 | 4.00E-109 | 1.00E-112 |
| SCE1572_11132 | sce_3724 | 0.00E+00 | 0.00E+00 |
| SCE1572_11133 | sce_3723 | 3.00E-148 | 1.00E-152 |
| SCE1572_11134 | sce_8378 | 2.00E-142 | 3.00E-140 |
| SCE1572_11137 | sce_8625 | 3.00E-59 | 1.00E-57 |
| SCE1572_1114 | sce_7128 | 2.00E-27 | 1.00E-27 |
| SCE1572_11145 | sce_9872 | 6.00E-101 | 6.00E-101 |
| SCE1572_11151 | sce_9873 | 1.00E-110 | 2.00E-114 |
| SCE1572_11152 | sce_9874 | 1.00E-23 | 9.00E-16 |
| SCE1572_11153 | sce_8393 | 1.00E-72 | 6.00E-63 |
| SCE1572_11156 | sce_7817 | 6.00E-22 | 1.00E-19 |
| SCE1572_11159 | sce_9876 | 9.00E-38 | 1.00E-30 |
| SCE1572_11160 | sce_9877 | 6.00E-99 | 6.00E-90 |
| SCE1572_11161 | sce_9887 | 0.00E+00 | 0.00E+00 |
| SCE1572_11162 | sce_9888 | 6.00E-178 | 0.00E+00 |
| SCE1572_11163 | sce_9890 | 3.00E-166 | 4.00E-166 |
| SCE1572_11165 | sce_9891 | 2.00E-87 | 1.00E-96 |
| SCE1572_11166 | sce_9892 | 2.00E-116 | 7.00E-112 |
| SCE1572_11167 | sce_8358 | 1.00E-26 | 1.00E-19 |
| SCE1572_11170 | sce_10020 | 3.00E-150 | 6.00E-163 |
| SCE1572_11171 | sce_10021 | 2.00E-44 | 2.00E-44 |
| SCE1572_11172 | sce_9911 | 8.00E-107 | 2.00E-100 |
| SCE1572_11173 | sce_9912 | 9.00E-111 | 7.00E-111 |
| SCE1572_11174 | sce_9913 | 0.00E+00 | 0.00E+00 |
| SCE1572_11175 | sce_9914 | 0.00E+00 | 0.00E+00 |
| SCE1572_11177 | sce_9915 | 8.00E-104 | 3.00E-103 |
| SCE1572_11179 | sce_9922 | 6.00E-169 | 3.00E-169 |
| SCE1572_11180 | sce_9924 | 2.00E-79 | 6.00E-81 |
| SCE1572_11181 | sce_9925 | 4.00E-107 | 4.00E-107 |
| SCE1572_11182 | sce_9926 | 5.00E-63 | 5.00E-78 |
| SCE1572_11183 | sce_9927 | 8.00E-131 | 8.00E-131 |
| SCE1572_11189 | sce_2238 | 0.00E+00 | 0.00E+00 |
| SCE1572_11191 | sce_9930 | 0.00E+00 | 0.00E+00 |
| SCE1572_11192 | sce_9931 | 3.00E-156 | 9.00E-150 |
| SCE1572_11193 | sce_9932 | 2.00E-84 | 3.00E-84 |
| SCE1572_11194 | sce_9933 | 2.00E-102 | 3.00E-92 |
| SCE1572_11195 | sce_9948 | 2.00E-79 | 5.00E-83 |
| SCE1572_11196 | sce_9947 | 4.00E-152 | 2.00E-180 |
| SCE1572_11198 | sce_9949 | 0.00E+00 | 0.00E+00 |
| SCE1572_11199 | sce_9950 | 1.00E-66 | 2.00E-58 |
| SCE1572_11200 | sce_9951 | 0.00E+00 | 7.00E-175 |
| SCE1572_11201 | sce_9952 | 7.00E-59 | 9.00E-68 |
| SCE1572_11202 | sce_9953 | 2.00E-152 | 3.00E-147 |
| SCE1572_11206 | sce_9954 | 0.00E+00 | 0.00E+00 |
| SCE1572_11206 | sce_5226 | 0.00E+00 | 0.00E+00 |
| SCE1572_11206 | sce_7154 | 0.00E+00 | 0.00E+00 |
| SCE1572_11206 | sce_5403 | 0.00E+00 | 0.00E+00 |

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|---------------|-----------|-----------|-----------|
| SCE1572_11206 | sce_1803 | 0.00E+00 | 0.00E+00 |
| SCE1572_11206 | sce_3750 | 0.00E+00 | 0.00E+00 |
| SCE1572_11206 | sce_6712 | 0.00E+00 | 0.00E+00 |
| SCE1572_11206 | sce_7969 | 0.00E+00 | 0.00E+00 |
| SCE1572_11206 | sce_5751 | 0.00E+00 | 0.00E+00 |
| SCE1572_11206 | sce_9665 | 0.00E+00 | 0.00E+00 |
| SCE1572_11206 | sce_5746 | 0.00E+00 | 0.00E+00 |
| SCE1572_11206 | sce_2053 | 0.00E+00 | 0.00E+00 |
| SCE1572_11206 | sce_5229 | 0.00E+00 | 0.00E+00 |
| SCE1572_11206 | sce_9757 | 0.00E+00 | 0.00E+00 |
| SCE1572_11206 | sce_4073 | 0.00E+00 | 0.00E+00 |
| SCE1572_11206 | sce_3491 | 0.00E+00 | 0.00E+00 |
| SCE1572_11206 | sce_7465 | 0.00E+00 | 0.00E+00 |
| SCE1572_11206 | sce_7657 | 0.00E+00 | 0.00E+00 |
| SCE1572_11208 | sce_9956 | 0.00E+00 | 0.00E+00 |
| SCE1572_11209 | sce_9957 | 3.00E-118 | 9.00E-147 |
| SCE1572_11210 | sce_9963 | 5.00E-51 | 5.00E-51 |
| SCE1572_11211 | sce_9964 | 2.00E-144 | 2.00E-141 |
| SCE1572_11215 | sce_3793 | 0.00E+00 | 0.00E+00 |
| SCE1572_11215 | sce_7069 | 0.00E+00 | 0.00E+00 |
| SCE1572_11215 | sce_5085 | 0.00E+00 | 0.00E+00 |
| SCE1572_11215 | sce_5086 | 0.00E+00 | 0.00E+00 |
| SCE1572_11215 | sce_6701 | 0.00E+00 | 0.00E+00 |
| SCE1572_11217 | sce_9972 | 3.00E-142 | 7.00E-142 |
| SCE1572_11218 | sce_9973 | 0.00E+00 | 0.00E+00 |
| SCE1572_11218 | sce_9974 | 0.00E+00 | 0.00E+00 |
| SCE1572_11225 | sce_2399 | 3.00E-161 | 1.00E-161 |
| SCE1572_11226 | sce_2398 | 4.00E-121 | 1.00E-122 |
| SCE1572_11227 | sce_2397 | 3.00E-156 | 2.00E-156 |
| SCE1572_11228 | sce_2396 | 1.00E-81 | 8.00E-82 |
| SCE1572_11230 | sce_4485 | 3.00E-120 | 4.00E-120 |
| SCE1572_11231 | sce_9974 | 0.00E+00 | 0.00E+00 |
| SCE1572_11231 | sce_9973 | 0.00E+00 | 0.00E+00 |
| SCE1572_11231 | sce_8694 | 0.00E+00 | 0.00E+00 |
| SCE1572_11231 | sce_2645 | 0.00E+00 | 0.00E+00 |
| SCE1572_11232 | sce_9975 | 2.00E-131 | 5.00E-134 |
| SCE1572_11233 | sce_9976 | 3.00E-65 | 2.00E-62 |
| SCE1572_11235 | sce_9977 | 9.00E-148 | 1.00E-151 |
| SCE1572_11236 | sce_9978 | 0.00E+00 | 0.00E+00 |
| SCE1572_11237 | sce_9979 | 6.00E-141 | 1.00E-134 |
| SCE1572_11238 | sce_9980 | 4.00E-171 | 2.00E-163 |
| SCE1572_11239 | sce_9981 | 3.00E-164 | 4.00E-168 |
| SCE1572_11240 | sce_3744 | 4.00E-65 | 1.00E-65 |
| SCE1572_11242 | sce_1013 | 0.00E+00 | 0.00E+00 |
| SCE1572_11243 | sce_4521 | 1.00E-71 | 1.00E-78 |
| SCE1572_11244 | sce_10033 | 9.00E-100 | 7.00E-100 |
| SCE1572_11246 | sce_5205 | 9.00E-137 | 7.00E-131 |
| SCE1572_11249 | sce_10035 | 4.00E-61 | 1.00E-70 |
| SCE1572_11253 | sce_10036 | 0.00E+00 | 0.00E+00 |
| SCE1572_11253 | sce_5546 | 0.00E+00 | 0.00E+00 |
| SCE1572_11254 | sce_10037 | 0.00E+00 | 0.00E+00 |
| SCE1572_11255 | sce_10038 | 0.00E+00 | 0.00E+00 |
| SCE1572_11256 | sce_10039 | 3.00E-96 | 2.00E-106 |
| SCE1572_11257 | sce_10040 | 1.00E-58 | 6.00E-58 |
| SCE1572_11258 | sce_10041 | 3.00E-62 | 3.00E-62 |
| SCE1572_11259 | sce_10042 | 0.00E+00 | 0.00E+00 |
| SCE1572_11260 | sce_10043 | 6.00E-171 | 6.00E-171 |
| SCE1572_11261 | sce_10044 | 4.00E-37 | 4.00E-37 |
| SCE1572_11262 | sce_10045 | 2.00E-163 | 0.00E+00 |
| SCE1572_11263 | sce_10046 | 3.00E-148 | 2.00E-153 |
| SCE1572_11264 | sce_10047 | 7.00E-67 | 7.00E-67 |
| SCE1572_11265 | sce_10048 | 0.00E+00 | 0.00E+00 |
| SCE1572_11266 | sce_10049 | 3.00E-173 | 3.00E-173 |
| SCE1572_11267 | sce_10050 | 6.00E-91 | 6.00E-91 |
| SCE1572_11268 | sce_10051 | 0.00E+00 | 0.00E+00 |
| SCE1572_11269 | sce_10052 | 4.00E-108 | 7.00E-112 |
| SCE1572_11270 | sce_10053 | 0.00E+00 | 0.00E+00 |
| SCE1572_11271 | sce_10054 | 0.00E+00 | 0.00E+00 |
| SCE1572_11272 | sce_10055 | 6.00E-119 | 2.00E-133 |
| SCE1572_11273 | sce_10056 | 2.00E-157 | 2.00E-149 |
| SCE1572_11274 | sce_10057 | 2.00E-148 | 2.00E-148 |
| SCE1572_11275 | sce_10058 | 2.00E-149 | 2.00E-157 |
| SCE1572_11276 | sce_10060 | 1.00E-63 | 1.00E-63 |
| SCE1572_11277 | sce_10061 | 0.00E+00 | 0.00E+00 |
| SCE1572_11279 | sce_10062 | 4.00E-73 | 4.00E-73 |
| SCE1572_1128 | sce_808 | 0.00E+00 | 0.00E+00 |

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| SCE1572_11280 | sce_10063 | 0.00E+00 | 0.00E+00 |
| SCE1572_11281 | sce_10064 | 0.00E+00 | 0.00E+00 |
| SCE1572_11282 | sce_10065 | 3.00E-156 | 1.00E-160 |
| SCE1572_11283 | sce_10067 | 2.00E-88 | 9.00E-82 |
| SCE1572_11284 | sce_10068 | 5.00E-131 | 4.00E-133 |
| SCE1572_11285 | sce_10069 | 8.00E-109 | 8.00E-109 |
| SCE1572_11286 | sce_1373 | 1.00E-106 | 7.00E-119 |
| SCE1572_11287 | sce_10070 | 4.00E-71 | 5.00E-67 |
| SCE1572_11288 | sce_10071 | 0.00E+00 | 0.00E+00 |
| SCE1572_11290 | sce_10072 | 0.00E+00 | 0.00E+00 |
| SCE1572_11291 | sce_10074 | 7.00E-35 | 7.00E-35 |
| SCE1572_11292 | sce_10075 | 4.00E-164 | 0.00E+00 |
| SCE1572_11293 | sce_10076 | 2.00E-173 | 1.00E-169 |
| SCE1572_11294 | sce_10077 | 2.00E-32 | 3.00E-36 |
| SCE1572_11295 | sce_10078 | 1.00E-56 | 3.00E-47 |
| SCE1572_11296 | sce_10079 | 0.00E+00 | 0.00E+00 |
| SCE1572_11297 | sce_10080 | 0.00E+00 | 1.00E-150 |
| SCE1572_11298 | sce_10081 | 2.00E-130 | 1.00E-130 |
| SCE1572_11299 | sce_10082 | 1.00E-135 | 1.00E-135 |
| SCE1572_113 | sce_101 | 1.00E-164 | 9.00E-166 |
| SCE1572_11300 | sce_10083 | 0.00E+00 | 0.00E+00 |
| SCE1572_11301 | sce_10084 | 2.00E-40 | 3.00E-41 |
| SCE1572_11302 | sce_10085 | 0.00E+00 | 0.00E+00 |
| SCE1572_11303 | sce_10086 | 0.00E+00 | 0.00E+00 |
| SCE1572_11304 | sce_10087 | 0.00E+00 | 0.00E+00 |
| SCE1572_11306 | sce_10088 | 0.00E+00 | 0.00E+00 |
| SCE1572_11307 | sce_10089 | 3.00E-139 | 9.00E-139 |
| SCE1572_11308 | sce_10090 | 0.00E+00 | 2.00E-163 |
| SCE1572_11309 | sce_10091 | 0.00E+00 | 4.00E-161 |
| SCE1572_11313 | sce_10092 | 6.00E-95 | 7.00E-95 |
| SCE1572_11315 | sce_10095 | 0.00E+00 | 0.00E+00 |
| SCE1572_11316 | sce_10096 | 0.00E+00 | 0.00E+00 |
| SCE1572_11317 | sce_10097 | 0.00E+00 | 0.00E+00 |
| SCE1572_11318 | sce_10098 | 0.00E+00 | 0.00E+00 |
| SCE1572_1132 | sce_809 | 8.00E-69 | 1.00E-69 |
| SCE1572_11320 | sce_10100 | 2.00E-75 | 3.00E-84 |
| SCE1572_11321 | sce_4678 | 6.00E-137 | 4.00E-144 |
| SCE1572_11322 | sce_10101 | 2.00E-128 | 2.00E-119 |
| SCE1572_11323 | sce_10102 | 0.00E+00 | 0.00E+00 |
| SCE1572_11324 | sce_10103 | 1.00E-87 | 4.00E-86 |
| SCE1572_11325 | sce_10105 | 3.00E-166 | 3.00E-170 |
| SCE1572_11326 | sce_10106 | 1.00E-122 | 1.00E-127 |
| SCE1572_11327 | sce_10107 | 1.00E-151 | 7.00E-134 |
| SCE1572_1133 | sce_810 | 2.00E-10 | 3.00E-08 |
| SCE1572_11330 | sce_10110 | 9.00E-69 | 1.00E-70 |
| SCE1572_11331 | sce_10111 | 1.00E-103 | 1.00E-103 |
| SCE1572_11332 | sce_10112 | 1.00E-86 | 2.00E-86 |
| SCE1572_11333 | sce_10113 | 0.00E+00 | 0.00E+00 |
| SCE1572_11334 | sce_10114 | 3.00E-40 | 6.00E-34 |
| SCE1572_11336 | sce_10135 | 8.00E-07 | 5.00E-07 |
| SCE1572_1134 | sce_8742 | 2.00E-25 | 2.00E-25 |
| SCE1572_11340 | sce_10140 | 5.00E-135 | 2.00E-142 |
| SCE1572_11342 | sce_10141 | 5.00E-163 | 7.00E-163 |
| SCE1572_11343 | sce_10142 | 2.00E-83 | 1.00E-91 |
| SCE1572_11344 | sce_10143 | 0.00E+00 | 0.00E+00 |
| SCE1572_11345 | sce_10144 | 2.00E-57 | 5.00E-57 |
| SCE1572_11346 | sce_10145 | 0.00E+00 | 0.00E+00 |
| SCE1572_11347 | sce_10146 | 6.00E-142 | 4.00E-142 |
| SCE1572_11348 | sce_10147 | 9.00E-25 | 3.00E-25 |
| SCE1572_11351 | sce_3937 | 0.00E+00 | 0.00E+00 |
| SCE1572_11351 | sce_8592 | 0.00E+00 | 0.00E+00 |
| SCE1572_11354 | sce_10188 | 4.00E-105 | 3.00E-118 |
| SCE1572_11355 | sce_8736 | 5.00E-30 | 9.00E-34 |
| SCE1572_11356 | sce_10189 | 1.00E-72 | 3.00E-78 |
| SCE1572_11360 | sce_10195 | 1.00E-178 | 7.00E-165 |
| SCE1572_11361 | sce_10196 | 0.00E+00 | 0.00E+00 |
| SCE1572_11362 | sce_10202 | 2.00E-178 | 5.00E-176 |
| SCE1572_11363 | sce_10203 | 0.00E+00 | 0.00E+00 |
| SCE1572_11363 | sce_2733 | 0.00E+00 | 0.00E+00 |
| SCE1572_11364 | sce_10204 | 0.00E+00 | 0.00E+00 |
| SCE1572_11364 | sce_5835 | 0.00E+00 | 0.00E+00 |
| SCE1572_11364 | sce_4513 | 0.00E+00 | 0.00E+00 |
| SCE1572_11364 | sce_388 | 0.00E+00 | 0.00E+00 |
| SCE1572_11364 | sce_7640 | 0.00E+00 | 0.00E+00 |
| SCE1572_11364 | sce_7661 | 0.00E+00 | 0.00E+00 |
| SCE1572_11364 | sce_3085 | 0.00E+00 | 0.00E+00 |

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| SCE1572_11364 | sce_9557 | 0.00E+00 | 0.00E+00 |
| SCE1572_11364 | sce_7109 | 0.00E+00 | 0.00E+00 |
| SCE1572_11364 | sce_6535 | 0.00E+00 | 0.00E+00 |
| SCE1572_11364 | sce_9920 | 0.00E+00 | 0.00E+00 |
| SCE1572_11364 | sce_3003 | 0.00E+00 | 0.00E+00 |
| SCE1572_11364 | sce_6092 | 0.00E+00 | 0.00E+00 |
| SCE1572_11364 | sce_6093 | 0.00E+00 | 0.00E+00 |
| SCE1572_11364 | sce_6095 | 0.00E+00 | 0.00E+00 |
| SCE1572_11364 | sce_2065 | 0.00E+00 | 0.00E+00 |
| SCE1572_11364 | sce_8618 | 0.00E+00 | 0.00E+00 |
| SCE1572_11364 | sce_3917 | 0.00E+00 | 0.00E+00 |
| SCE1572_1137 | sce_9398 | 1.00E-109 | 1.00E-134 |
| SCE1572_11370 | sce_10205 | 2.00E-121 | 7.00E-135 |
| SCE1572_11371 | sce_10206 | 1.00E-118 | 9.00E-129 |
| SCE1572_11372 | sce_10209 | 1.00E-156 | 2.00E-159 |
| SCE1572_11373 | sce_10210 | 2.00E-139 | 2.00E-139 |
| SCE1572_11374 | sce_10211 | 0.00E+00 | 0.00E+00 |
| SCE1572_11376 | sce_10212 | 2.00E-152 | 3.00E-152 |
| SCE1572_11377 | sce_10213 | 4.00E-111 | 4.00E-111 |
| SCE1572_11378 | sce_10214 | 0.00E+00 | 0.00E+00 |
| SCE1572_11379 | sce_10215 | 8.00E-145 | 3.00E-147 |
| SCE1572_11380 | sce_10216 | 2.00E-74 | 1.00E-74 |
| SCE1572_11381 | sce_10217 | 8.00E-138 | 2.00E-157 |
| SCE1572_11382 | sce_10218 | 0.00E+00 | 0.00E+00 |
| SCE1572_11384 | sce_10219 | 0.00E+00 | 0.00E+00 |
| SCE1572_11385 | sce_10220 | 0.00E+00 | 0.00E+00 |
| SCE1572_11385 | sce_8839 | 0.00E+00 | 0.00E+00 |
| SCE1572_11386 | sce_10221 | 0.00E+00 | 0.00E+00 |
| SCE1572_11387 | sce_10223 | 2.00E-146 | 2.00E-146 |
| SCE1572_11389 | sce_10228 | 0.00E+00 | 0.00E+00 |
| SCE1572_11389 | sce_2553 | 0.00E+00 | 0.00E+00 |
| SCE1572_11390 | sce_10229 | 3.00E-122 | 3.00E-131 |
| SCE1572_11391 | sce_10230 | 8.00E-133 | 6.00E-133 |
| SCE1572_11392 | sce_10231 | 0.00E+00 | 0.00E+00 |
| SCE1572_11393 | sce_10233 | 0.00E+00 | 0.00E+00 |
| SCE1572_11394 | sce_10235 | 2.00E-53 | 2.00E-53 |
| SCE1572_11395 | sce_10237 | 0.00E+00 | 0.00E+00 |
| SCE1572_11396 | sce_10238 | 5.00E-54 | 2.00E-55 |
| SCE1572_11398 | sce_10239 | 0.00E+00 | 0.00E+00 |
| SCE1572_11399 | sce_10240 | 0.00E+00 | 0.00E+00 |
| SCE1572_1140 | sce_814 | 8.00E-24 | 1.00E-27 |
| SCE1572_11400 | sce_10241 | 0.00E+00 | 0.00E+00 |
| SCE1572_11402 | sce_10242 | 5.00E-47 | 4.00E-51 |
| SCE1572_11404 | sce_10243 | 2.00E-115 | 1.00E-108 |
| SCE1572_11410 | sce_10267 | 1.00E-132 | 2.00E-142 |
| SCE1572_11412 | sce_10269 | 2.00E-55 | 2.00E-49 |
| SCE1572_11413 | sce_10270 | 0.00E+00 | 0.00E+00 |
| SCE1572_11414 | sce_10271 | 0.00E+00 | 0.00E+00 |
| SCE1572_11415 | sce_10272 | 1.00E-119 | 1.00E-119 |
| SCE1572_11416 | sce_10274 | 2.00E-107 | 3.00E-92 |
| SCE1572_1142 | sce_815 | 0.00E+00 | 0.00E+00 |
| SCE1572_11420 | sce_10275 | 0.00E+00 | 0.00E+00 |
| SCE1572_11421 | sce_10276 | 0.00E+00 | 0.00E+00 |
| SCE1572_11422 | sce_10277 | 3.00E-144 | 3.00E-156 |
| SCE1572_11424 | sce_10283 | 5.00E-106 | 1.00E-96 |
| SCE1572_11429 | sce_3038 | 2.00E-105 | 2.00E-97 |
| SCE1572_1143 | sce_816 | 3.00E-38 | 2.00E-33 |
| SCE1572_11430 | sce_10284 | 0.00E+00 | 0.00E+00 |
| SCE1572_11431 | sce_10285 | 0.00E+00 | 0.00E+00 |
| SCE1572_11432 | sce_10288 | 0.00E+00 | 2.00E-176 |
| SCE1572_11433 | sce_10289 | 0.00E+00 | 0.00E+00 |
| SCE1572_11435 | sce_10290 | 0.00E+00 | 0.00E+00 |
| SCE1572_11436 | sce_10291 | 5.00E-179 | 7.00E-175 |
| SCE1572_11437 | sce_10292 | 1.00E-66 | 9.00E-73 |
| SCE1572_11438 | sce_10293 | 0.00E+00 | 0.00E+00 |
| SCE1572_11439 | sce_10294 | 0.00E+00 | 0.00E+00 |
| SCE1572_11440 | sce_10295 | 3.00E-113 | 2.00E-113 |
| SCE1572_11441 | sce_10296 | 4.00E-78 | 5.00E-80 |
| SCE1572_11442 | sce_10297 | 8.00E-80 | 4.00E-85 |
| SCE1572_11443 | sce_10298 | 4.00E-48 | 5.00E-48 |
| SCE1572_11444 | sce_10299 | 2.00E-57 | 7.00E-58 |
| SCE1572_11445 | sce_10300 | 0.00E+00 | 0.00E+00 |
| SCE1572_11446 | sce_10301 | 0.00E+00 | 0.00E+00 |
| SCE1572_11447 | sce_10302 | 0.00E+00 | 0.00E+00 |
| SCE1572_11449 | sce_10304 | 2.00E-146 | 1.00E-152 |
| SCE1572_11450 | sce_10305 | 0.00E+00 | 0.00E+00 |

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| SCE1572_11451 | sce_10306 | 1.00E-85 | 1.00E-85 |
| SCE1572_11452 | sce_10307 | 6.00E-64 | 5.00E-64 |
| SCE1572_11453 | sce_10308 | 3.00E-57 | 3.00E-57 |
| SCE1572_11457 | sce_5222 | 0.00E+00 | 0.00E+00 |
| SCE1572_11457 | sce_5216 | 0.00E+00 | 0.00E+00 |
| SCE1572_11458 | sce_3037 | 5.00E-40 | 1.00E-35 |
| SCE1572_11459 | sce_5221 | 6.00E-25 | 2.00E-27 |
| SCE1572_1146 | sce_817 | 1.00E-72 | 7.00E-65 |
| SCE1572_11460 | sce_5222 | 0.00E+00 | 0.00E+00 |
| SCE1572_11460 | sce_5216 | 0.00E+00 | 0.00E+00 |
| SCE1572_11460 | sce_3035 | 0.00E+00 | 0.00E+00 |
| SCE1572_11462 | sce_1332 | 1.00E-14 | 1.00E-16 |
| SCE1572_11468 | sce_10309 | 7.00E-77 | 5.00E-70 |
| SCE1572_11469 | sce_10310 | 1.00E-94 | 2.00E-97 |
| SCE1572_1147 | sce_3880 | 0.00E+00 | 0.00E+00 |
| SCE1572_11470 | sce_10311 | 2.00E-103 | 1.00E-112 |
| SCE1572_11471 | sce_10312 | 1.00E-153 | 6.00E-147 |
| SCE1572_11474 | sce_9503 | 0.00E+00 | 0.00E+00 |
| SCE1572_11474 | sce_10365 | 0.00E+00 | 0.00E+00 |
| SCE1572_11474 | sce_9908 | 0.00E+00 | 0.00E+00 |
| SCE1572_11478 | sce_10313 | 6.00E-132 | 6.00E-131 |
| SCE1572_1148 | sce_3879 | 0.00E+00 | 0.00E+00 |
| SCE1572_11480 | sce_10315 | 0.00E+00 | 0.00E+00 |
| SCE1572_11481 | sce_10316 | 3.00E-129 | 1.00E-132 |
| SCE1572_11482 | sce_10317 | 4.00E-144 | 3.00E-144 |
| SCE1572_11483 | sce_10318 | 8.00E-103 | 8.00E-103 |
| SCE1572_11484 | sce_10319 | 2.00E-143 | 3.00E-146 |
| SCE1572_11485 | sce_10321 | 0.00E+00 | 0.00E+00 |
| SCE1572_11486 | sce_10322 | 3.00E-74 | 1.00E-75 |
| SCE1572_11491 | sce_10323 | 1.00E-180 | 6.00E-179 |
| SCE1572_11492 | sce_10324 | 0.00E+00 | 0.00E+00 |
| SCE1572_11493 | sce_10326 | 0.00E+00 | 0.00E+00 |
| SCE1572_11499 | sce_10332 | 4.00E-57 | 5.00E-54 |
| SCE1572_115 | sce_103 | 3.00E-71 | 2.00E-81 |
| SCE1572_11500 | sce_10333 | 7.00E-149 | 1.00E-140 |
| SCE1572_11502 | sce_10334 | 2.00E-42 | 3.00E-49 |
| SCE1572_11503 | sce_10335 | 7.00E-115 | 7.00E-103 |
| SCE1572_11505 | sce_10337 | 2.00E-82 | 1.00E-81 |
| SCE1572_11506 | sce_10338 | 2.00E-111 | 2.00E-114 |
| SCE1572_11507 | sce_10339 | 4.00E-133 | 4.00E-133 |
| SCE1572_11508 | sce_10340 | 1.00E-92 | 8.00E-92 |
| SCE1572_11509 | sce_10341 | 0.00E+00 | 0.00E+00 |
| SCE1572_11510 | sce_10342 | 3.00E-40 | 2.00E-45 |
| SCE1572_11511 | sce_10344 | 0.00E+00 | 0.00E+00 |
| SCE1572_11512 | sce_10345 | 6.00E-141 | 3.00E-144 |
| SCE1572_11513 | sce_10346 | 0.00E+00 | 0.00E+00 |
| SCE1572_11514 | sce_10347 | 0.00E+00 | 0.00E+00 |
| SCE1572_11515 | sce_10348 | 1.00E-88 | 9.00E-92 |
| SCE1572_11516 | sce_10349 | 5.00E-117 | 2.00E-139 |
| SCE1572_11517 | sce_10350 | 0.00E+00 | 0.00E+00 |
| SCE1572_11518 | sce_10351 | 8.00E-116 | 7.00E-116 |
| SCE1572_11519 | sce_10352 | 2.00E-124 | 8.00E-127 |
| SCE1572_11520 | sce_10353 | 8.00E-29 | 1.00E-36 |
| SCE1572_11523 | sce_7057 | 1.00E-15 | 6.00E-17 |
| SCE1572_11524 | sce_7056 | 1.00E-24 | 1.00E-20 |
| SCE1572_11525 | sce_7055 | 6.00E-95 | 2.00E-97 |
| SCE1572_11526 | sce_10265 | 6.00E-21 | 1.00E-21 |
| SCE1572_11529 | sce_10371 | 0.00E+00 | 0.00E+00 |
| SCE1572_11530 | sce_10372 | 3.00E-23 | 4.00E-23 |
| SCE1572_11531 | sce_10373 | 1.00E-70 | 1.00E-81 |
| SCE1572_11533 | sce_10380 | 1.00E-133 | 1.00E-122 |
| SCE1572_11534 | sce_10381 | 1.00E-119 | 4.00E-127 |
| SCE1572_11535 | sce_10384 | 0.00E+00 | 0.00E+00 |
| SCE1572_11536 | sce_10385 | 0.00E+00 | 0.00E+00 |
| SCE1572_11537 | sce_10386 | 5.00E-129 | 1.00E-121 |
| SCE1572_11538 | sce_10387 | 6.00E-92 | 2.00E-91 |
| SCE1572_11539 | sce_10388 | 5.00E-95 | 3.00E-99 |
| SCE1572_11540 | sce_10389 | 2.00E-91 | 5.00E-85 |
| SCE1572_11541 | sce_10390 | 2.00E-76 | 1.00E-68 |
| SCE1572_11542 | sce_10391 | 3.00E-125 | 2.00E-121 |
| SCE1572_11543 | sce_10392 | 6.00E-175 | 0.00E+00 |
| SCE1572_11544 | sce_10393 | 9.00E-131 | 1.00E-126 |
| SCE1572_11545 | sce_10394 | 0.00E+00 | 0.00E+00 |
| SCE1572_11546 | sce_10396 | 1.00E-130 | 6.00E-124 |
| SCE1572_11548 | sce_10397 | 3.00E-99 | 3.00E-99 |
| SCE1572_11549 | sce_10398 | 1.00E-156 | 2.00E-158 |

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| SCE1572_11553 | sce_10402 | 0.00E+00 | 0.00E+00 |
| SCE1572_11554 | sce_10403 | 3.00E-114 | 1.00E-117 |
| SCE1572_11555 | sce_6028 | 2.00E-173 | 0.00E+00 |
| SCE1572_11564 | sce_10405 | 2.00E-72 | 8.00E-69 |
| SCE1572_11565 | sce_8641 | 2.00E-06 | 2.00E-12 |
| SCE1572_11569 | sce_167 | 2.00E-79 | 3.00E-78 |
| SCE1572_11571 | sce_7925 | 5.00E-89 | 4.00E-101 |
| SCE1572_11574 | sce_9347 | 0.00E+00 | 0.00E+00 |
| SCE1572_11575 | sce_10410 | 3.00E-163 | 3.00E-163 |
| SCE1572_11576 | sce_8743 | 1.00E-77 | 1.00E-77 |
| SCE1572_11577 | sce_10411 | 2.00E-153 | 2.00E-145 |
| SCE1572_11578 | sce_10415 | 7.00E-62 | 3.00E-62 |
| SCE1572_11579 | sce_10416 | 4.00E-147 | 9.00E-133 |
| SCE1572_11580 | sce_10417 | 4.00E-64 | 2.00E-69 |
| SCE1572_11581 | sce_10418 | 8.00E-165 | 5.00E-158 |
| SCE1572_11582 | sce_10419 | 0.00E+00 | 0.00E+00 |
| SCE1572_11583 | sce_10447 | 0.00E+00 | 0.00E+00 |
| SCE1572_11584 | sce_10448 | 1.00E-149 | 3.00E-150 |
| SCE1572_11586 | sce_10450 | 0.00E+00 | 0.00E+00 |
| SCE1572_11588 | sce_10452 | 2.00E-150 | 2.00E-148 |
| SCE1572_11589 | sce_10454 | 3.00E-98 | 1.00E-106 |
| SCE1572_11590 | sce_10455 | 1.00E-153 | 1.00E-153 |
| SCE1572_11593 | sce_10456 | 1.00E-97 | 1.00E-97 |
| SCE1572_11594 | sce_10457 | 3.00E-133 | 7.00E-140 |
| SCE1572_11595 | sce_10458 | 0.00E+00 | 0.00E+00 |
| SCE1572_11596 | sce_10459 | 7.00E-83 | 7.00E-83 |
| SCE1572_11597 | sce_10460 | 1.00E-102 | 4.00E-104 |
| SCE1572_11598 | sce_10461 | 9.00E-76 | 1.00E-74 |
| SCE1572_11599 | sce_10462 | 4.00E-119 | 2.00E-134 |
| SCE1572_116 | sce_104 | 2.00E-145 | 1.00E-144 |
| SCE1572_11600 | sce_10463 | 1.00E-90 | 1.00E-90 |
| SCE1572_11601 | sce_10464 | 1.00E-111 | 4.00E-96 |
| SCE1572_1164 | sce_854 | 6.00E-32 | 2.00E-26 |
| SCE1572_1165 | sce_856 | 0.00E+00 | 0.00E+00 |
| SCE1572_1166 | sce_857 | 0.00E+00 | 0.00E+00 |
| SCE1572_1168 | sce_4696 | 0.00E+00 | 0.00E+00 |
| SCE1572_1169 | sce_858 | 0.00E+00 | 0.00E+00 |
| SCE1572_117 | sce_105 | 3.00E-135 | 4.00E-126 |
| SCE1572_1175 | sce_5251 | 3.00E-84 | 2.00E-84 |
| SCE1572_1176 | sce_2435 | 1.00E-86 | 4.00E-87 |
| SCE1572_1177 | sce_860 | 9.00E-128 | 1.00E-127 |
| SCE1572_1178 | sce_2432 | 9.00E-117 | 5.00E-104 |
| SCE1572_1179 | sce_2431 | 3.00E-132 | 6.00E-128 |
| SCE1572_118 | sce_106 | 6.00E-80 | 6.00E-80 |
| SCE1572_1180 | sce_2430 | 3.00E-88 | 2.00E-85 |
| SCE1572_1181 | sce_5268 | 1.00E-57 | 1.00E-55 |
| SCE1572_1184 | sce_5086 | 0.00E+00 | 0.00E+00 |
| SCE1572_1184 | sce_5085 | 0.00E+00 | 0.00E+00 |
| SCE1572_1184 | sce_6701 | 0.00E+00 | 0.00E+00 |
| SCE1572_1184 | sce_3793 | 0.00E+00 | 0.00E+00 |
| SCE1572_1185 | sce_2391 | 6.00E-104 | 3.00E-100 |
| SCE1572_1186 | sce_862 | 2.00E-121 | 2.00E-121 |
| SCE1572_1187 | sce_863 | 2.00E-35 | 9.00E-37 |
| SCE1572_1188 | sce_9528 | 3.00E-59 | 2.00E-63 |
| SCE1572_1189 | sce_202 | 1.00E-150 | 1.00E-151 |
| SCE1572_119 | sce_107 | 6.00E-150 | 6.00E-150 |
| SCE1572_1190 | sce_1118 | 0.00E+00 | 0.00E+00 |
| SCE1572_1192 | sce_866 | 0.00E+00 | 0.00E+00 |
| SCE1572_1193 | sce_867 | 0.00E+00 | 0.00E+00 |
| SCE1572_1197 | sce_3917 | 0.00E+00 | 0.00E+00 |
| SCE1572_1197 | sce_6092 | 0.00E+00 | 0.00E+00 |
| SCE1572_1197 | sce_6107 | 0.00E+00 | 0.00E+00 |
| SCE1572_1197 | sce_6093 | 0.00E+00 | 0.00E+00 |
| SCE1572_1197 | sce_6094 | 0.00E+00 | 0.00E+00 |
| SCE1572_1197 | sce_6095 | 0.00E+00 | 0.00E+00 |
| SCE1572_1197 | sce_7661 | 0.00E+00 | 0.00E+00 |
| SCE1572_1197 | sce_388 | 0.00E+00 | 0.00E+00 |
| SCE1572_1197 | sce_9920 | 0.00E+00 | 0.00E+00 |
| SCE1572_1197 | sce_6535 | 0.00E+00 | 0.00E+00 |
| SCE1572_1197 | sce_3003 | 0.00E+00 | 0.00E+00 |
| SCE1572_1197 | sce_2065 | 0.00E+00 | 0.00E+00 |
| SCE1572_1197 | sce_10204 | 0.00E+00 | 0.00E+00 |
| SCE1572_1197 | sce_8602 | 0.00E+00 | 0.00E+00 |
| SCE1572_1197 | sce_7640 | 0.00E+00 | 0.00E+00 |
| SCE1572_1197 | sce_9557 | 0.00E+00 | 0.00E+00 |
| SCE1572_1197 | sce_4513 | 0.00E+00 | 0.00E+00 |

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| SCE1572_1197 | sce_5835 | 0.00E+00 | 0.00E+00 |
| SCE1572_1198 | sce_868 | 0.00E+00 | 0.00E+00 |
| SCE1572_12 | sce_12 | 3.00E-103 | 9.00E-99 |
| SCE1572_120 | sce_108 | 3.00E-133 | 5.00E-138 |
| SCE1572_1200 | sce_837 | 4.00E-104 | 2.00E-99 |
| SCE1572_1202 | sce_869 | 1.00E-75 | 1.00E-78 |
| SCE1572_1203 | sce_870 | 6.00E-89 | 5.00E-69 |
| SCE1572_1207 | sce_871 | 0.00E+00 | 0.00E+00 |
| SCE1572_1208 | sce_872 | 0.00E+00 | 0.00E+00 |
| SCE1572_1209 | sce_873 | 2.00E-82 | 6.00E-77 |
| SCE1572_121 | sce_109 | 1.00E-105 | 5.00E-113 |
| SCE1572_1211 | sce_874 | 3.00E-56 | 2.00E-49 |
| SCE1572_1212 | sce_875 | 5.00E-51 | 3.00E-59 |
| SCE1572_1216 | sce_2569 | 5.00E-23 | 9.00E-22 |
| SCE1572_1219 | sce_879 | 6.00E-97 | 8.00E-95 |
| SCE1572_122 | sce_110 | 2.00E-167 | 3.00E-167 |
| SCE1572_1222 | sce_881 | 3.00E-34 | 3.00E-45 |
| SCE1572_1230 | sce_4062 | 0.00E+00 | 0.00E+00 |
| SCE1572_1230 | sce_9373 | 0.00E+00 | 0.00E+00 |
| SCE1572_1231 | sce_885 | 0.00E+00 | 0.00E+00 |
| SCE1572_1233 | sce_895 | 0.00E+00 | 0.00E+00 |
| SCE1572_1234 | sce_896 | 0.00E+00 | 0.00E+00 |
| SCE1572_1236 | sce_898 | 0.00E+00 | 0.00E+00 |
| SCE1572_1242 | sce_900 | 0.00E+00 | 0.00E+00 |
| SCE1572_1243 | sce_9368 | 1.00E-08 | 2.00E-15 |
| SCE1572_1245 | sce_5041 | 3.00E-29 | 3.00E-33 |
| SCE1572_1248 | sce_901 | 4.00E-76 | 2.00E-76 |
| SCE1572_125 | sce_125 | 7.00E-49 | 5.00E-50 |
| SCE1572_1250 | sce_1317 | 7.00E-17 | 8.00E-17 |
| SCE1572_1251 | sce_1318 | 1.00E-22 | 1.00E-28 |
| SCE1572_1252 | sce_902 | 0.00E+00 | 0.00E+00 |
| SCE1572_1253 | sce_903 | 2.00E-87 | 2.00E-87 |
| SCE1572_1254 | sce_904 | 2.00E-60 | 2.00E-60 |
| SCE1572_1255 | sce_7640 | 0.00E+00 | 0.00E+00 |
| SCE1572_1255 | sce_5835 | 0.00E+00 | 0.00E+00 |
| SCE1572_1255 | sce_388 | 0.00E+00 | 0.00E+00 |
| SCE1572_1255 | sce_10204 | 0.00E+00 | 0.00E+00 |
| SCE1572_1255 | sce_4513 | 0.00E+00 | 0.00E+00 |
| SCE1572_1257 | sce_846 | 0.00E+00 | 0.00E+00 |
| SCE1572_1258 | sce_1687 | 3.00E-90 | 3.00E-90 |
| SCE1572_1259 | sce_1688 | 7.00E-43 | 7.00E-43 |
| SCE1572_126 | sce_127 | 2.00E-153 | 4.00E-175 |
| SCE1572_1260 | sce_1689 | 0.00E+00 | 0.00E+00 |
| SCE1572_1261 | sce_1690 | 9.00E-159 | 3.00E-148 |
| SCE1572_1262 | sce_10368 | 5.00E-122 | 3.00E-106 |
| SCE1572_1263 | sce_909 | 0.00E+00 | 0.00E+00 |
| SCE1572_1265 | sce_910 | 5.00E-46 | 4.00E-46 |
| SCE1572_1266 | sce_911 | 7.00E-19 | 7.00E-19 |
| SCE1572_1268 | sce_916 | 4.00E-176 | 0.00E+00 |
| SCE1572_1269 | sce_917 | 4.00E-145 | 5.00E-150 |
| SCE1572_127 | sce_128 | 4.00E-80 | 4.00E-96 |
| SCE1572_1270 | sce_1557 | 2.00E-153 | 2.00E-162 |
| SCE1572_1271 | sce_1556 | 7.00E-170 | 3.00E-162 |
| SCE1572_1272 | sce_1553 | 4.00E-15 | 2.00E-06 |
| SCE1572_1273 | sce_1552 | 0.00E+00 | 0.00E+00 |
| SCE1572_1274 | sce_1551 | 8.00E-69 | 6.00E-62 |
| SCE1572_1275 | sce_1550 | 6.00E-67 | 6.00E-67 |
| SCE1572_1276 | sce_1549 | 0.00E+00 | 0.00E+00 |
| SCE1572_1280 | sce_1493 | 2.00E-147 | 2.00E-146 |
| SCE1572_1281 | sce_919 | 1.00E-178 | 0.00E+00 |
| SCE1572_1284 | sce_920 | 0.00E+00 | 0.00E+00 |
| SCE1572_1285 | sce_921 | 0.00E+00 | 0.00E+00 |
| SCE1572_1286 | sce_922 | 0.00E+00 | 0.00E+00 |
| SCE1572_1287 | sce_923 | 1.00E-74 | 5.00E-72 |
| SCE1572_1288 | sce_924 | 2.00E-154 | 1.00E-150 |
| SCE1572_1290 | sce_925 | 4.00E-131 | 6.00E-134 |
| SCE1572_1291 | sce_926 | 1.00E-97 | 2.00E-90 |
| SCE1572_1292 | sce_927 | 0.00E+00 | 0.00E+00 |
| SCE1572_1293 | sce_928 | 1.00E-165 | 5.00E-172 |
| SCE1572_1294 | sce_929 | 3.00E-126 | 7.00E-154 |
| SCE1572_1295 | sce_930 | 5.00E-142 | 3.00E-136 |
| SCE1572_1297 | sce_931 | 2.00E-64 | 1.00E-70 |
| SCE1572_1298 | sce_932 | 4.00E-27 | 4.00E-27 |
| SCE1572_1299 | sce_933 | 9.00E-142 | 4.00E-132 |
| SCE1572_13 | sce_13 | 0.00E+00 | 0.00E+00 |
| SCE1572_1300 | sce_934 | 7.00E-155 | 2.00E-155 |

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| SCE1572_1301 | sce_936 | 0.00E+00 | 0.00E+00 |
| SCE1572_1302 | sce_937 | 3.00E-81 | 4.00E-91 |
| SCE1572_1303 | sce_938 | 3.00E-98 | 4.00E-101 |
| SCE1572_1304 | sce_939 | 0.00E+00 | 0.00E+00 |
| SCE1572_1305 | sce_940 | 2.00E-31 | 2.00E-30 |
| SCE1572_1306 | sce_942 | 5.00E-72 | 5.00E-74 |
| SCE1572_1307 | sce_943 | 6.00E-80 | 6.00E-80 |
| SCE1572_1308 | sce_944 | 0.00E+00 | 0.00E+00 |
| SCE1572_1309 | sce_945 | 0.00E+00 | 0.00E+00 |
| SCE1572_1309 | sce_457 | 0.00E+00 | 0.00E+00 |
| SCE1572_131 | sce_129 | 4.00E-67 | 6.00E-62 |
| SCE1572_1310 | sce_946 | 1.00E-54 | 1.00E-54 |
| SCE1572_1311 | sce_947 | 2.00E-107 | 3.00E-99 |
| SCE1572_1312 | sce_948 | 8.00E-51 | 8.00E-51 |
| SCE1572_1313 | sce_949 | 1.00E-152 | 1.00E-152 |
| SCE1572_1314 | sce_950 | 1.00E-52 | 1.00E-44 |
| SCE1572_1315 | sce_951 | 2.00E-97 | 7.00E-113 |
| SCE1572_1316 | sce_952 | 0.00E+00 | 0.00E+00 |
| SCE1572_1318 | sce_953 | 1.00E-72 | 2.00E-71 |
| SCE1572_1319 | sce_954 | 4.00E-152 | 2.00E-136 |
| SCE1572_132 | sce_130 | 0.00E+00 | 0.00E+00 |
| SCE1572_1320 | sce_956 | 0.00E+00 | 0.00E+00 |
| SCE1572_1321 | sce_957 | 4.00E-159 | 2.00E-150 |
| SCE1572_1323 | sce_959 | 0.00E+00 | 8.00E-179 |
| SCE1572_1324 | sce_960 | 1.00E-76 | 3.00E-76 |
| SCE1572_1329 | sce_8257 | 9.00E-14 | 6.00E-18 |
| SCE1572_133 | sce_131 | 0.00E+00 | 0.00E+00 |
| SCE1572_1337 | sce_961 | 0.00E+00 | 0.00E+00 |
| SCE1572_1338 | sce_962 | 0.00E+00 | 0.00E+00 |
| SCE1572_1339 | sce_963 | 0.00E+00 | 0.00E+00 |
| SCE1572_1341 | sce_965 | 2.00E-138 | 2.00E-138 |
| SCE1572_1342 | sce_967 | 7.00E-164 | 7.00E-164 |
| SCE1572_1343 | sce_968 | 8.00E-65 | 1.00E-56 |
| SCE1572_1344 | sce_969 | 0.00E+00 | 7.00E-179 |
| SCE1572_1345 | sce_970 | 3.00E-180 | 0.00E+00 |
| SCE1572_1346 | sce_971 | 1.00E-83 | 5.00E-79 |
| SCE1572_1347 | sce_972 | 0.00E+00 | 0.00E+00 |
| SCE1572_1348 | sce_973 | 9.00E-166 | 8.00E-159 |
| SCE1572_135 | sce_9966 | 4.00E-120 | 3.00E-120 |
| SCE1572_1350 | sce_974 | 1.00E-64 | 4.00E-65 |
| SCE1572_1351 | sce_975 | 2.00E-166 | 2.00E-166 |
| SCE1572_1352 | sce_976 | 0.00E+00 | 0.00E+00 |
| SCE1572_1353 | sce_978 | 3.00E-113 | 2.00E-109 |
| SCE1572_1354 | sce_979 | 3.00E-146 | 6.00E-165 |
| SCE1572_1355 | sce_980 | 6.00E-156 | 8.00E-162 |
| SCE1572_1356 | sce_981 | 6.00E-102 | 2.00E-99 |
| SCE1572_1357 | sce_982 | 0.00E+00 | 0.00E+00 |
| SCE1572_1358 | sce_984 | 0.00E+00 | 0.00E+00 |
| SCE1572_1359 | sce_985 | 0.00E+00 | 0.00E+00 |
| SCE1572_136 | sce_9965 | 6.00E-152 | 1.00E-150 |
| SCE1572_1360 | sce_986 | 0.00E+00 | 0.00E+00 |
| SCE1572_1361 | sce_987 | 0.00E+00 | 0.00E+00 |
| SCE1572_1362 | sce_988 | 0.00E+00 | 0.00E+00 |
| SCE1572_1363 | sce_989 | 9.00E-43 | 9.00E-43 |
| SCE1572_1364 | sce_990 | 4.00E-97 | 4.00E-97 |
| SCE1572_1365 | sce_991 | 1.00E-122 | 3.00E-129 |
| SCE1572_1366 | sce_992 | 0.00E+00 | 0.00E+00 |
| SCE1572_1367 | sce_993 | 1.00E-151 | 9.00E-159 |
| SCE1572_1368 | sce_994 | 0.00E+00 | 0.00E+00 |
| SCE1572_1369 | sce_995 | 0.00E+00 | 0.00E+00 |
| SCE1572_137 | sce_133 | 0.00E+00 | 0.00E+00 |
| SCE1572_1370 | sce_996 | 0.00E+00 | 0.00E+00 |
| SCE1572_1371 | sce_998 | 0.00E+00 | 0.00E+00 |
| SCE1572_1372 | sce_999 | 1.00E-62 | 1.00E-62 |
| SCE1572_1374 | sce_1000 | 0.00E+00 | 0.00E+00 |
| SCE1572_1375 | sce_1002 | 0.00E+00 | 0.00E+00 |
| SCE1572_1377 | sce_5241 | 7.00E-63 | 1.00E-77 |
| SCE1572_1379 | sce_1428 | 1.00E-37 | 6.00E-38 |
| SCE1572_1380 | sce_4696 | 0.00E+00 | 0.00E+00 |
| SCE1572_1381 | sce_6188 | 0.00E+00 | 0.00E+00 |
| SCE1572_1384 | sce_8656 | 0.00E+00 | 0.00E+00 |
| SCE1572_1385 | sce_6414 | 4.00E-133 | 5.00E-132 |
| SCE1572_1387 | sce_9995 | 0.00E+00 | 0.00E+00 |
| SCE1572_1389 | sce_1692 | 2.00E-26 | 2.00E-26 |
| SCE1572_1390 | sce_4602 | 2.00E-163 | 1.00E-160 |
| SCE1572_1392 | sce_1004 | 8.00E-130 | 1.00E-132 |

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|--------------|-----------|-----------|-----------|
| SCE1572_1393 | sce_1005 | 3.00E-168 | 2.00E-178 |
| SCE1572_1394 | sce_6012 | 4.00E-39 | 2.00E-40 |
| SCE1572_1395 | sce_1006 | 2.00E-179 | 8.00E-172 |
| SCE1572_1396 | sce_1007 | 2.00E-93 | 7.00E-107 |
| SCE1572_1397 | sce_1333 | 2.00E-38 | 8.00E-42 |
| SCE1572_1398 | sce_1331 | 4.00E-53 | 1.00E-49 |
| SCE1572_1399 | sce_1330 | 6.00E-40 | 2.00E-41 |
| SCE1572_14 | sce_14 | 0.00E+00 | 0.00E+00 |
| SCE1572_1400 | sce_1341 | 1.00E-54 | 1.00E-65 |
| SCE1572_1401 | sce_1340 | 1.00E-135 | 7.00E-134 |
| SCE1572_1405 | sce_1339 | 1.00E-158 | 2.00E-128 |
| SCE1572_1406 | sce_1338 | 0.00E+00 | 0.00E+00 |
| SCE1572_1407 | sce_1337 | 1.00E-157 | 3.00E-157 |
| SCE1572_1408 | sce_1336 | 1.00E-80 | 4.00E-85 |
| SCE1572_1409 | sce_1335 | 0.00E+00 | 0.00E+00 |
| SCE1572_1410 | sce_1334 | 1.00E-111 | 9.00E-121 |
| SCE1572_1411 | sce_1008 | 0.00E+00 | 0.00E+00 |
| SCE1572_1412 | sce_1009 | 6.00E-140 | 1.00E-136 |
| SCE1572_1413 | sce_1010 | 3.00E-47 | 2.00E-48 |
| SCE1572_1414 | sce_1011 | 9.00E-30 | 5.00E-36 |
| SCE1572_1416 | sce_5962 | 0.00E+00 | 0.00E+00 |
| SCE1572_1417 | sce_4679 | 2.00E-39 | 3.00E-39 |
| SCE1572_1418 | sce_4680 | 2.00E-37 | 2.00E-37 |
| SCE1572_1423 | sce_1015 | 0.00E+00 | 0.00E+00 |
| SCE1572_1424 | sce_3601 | 1.00E-119 | 5.00E-113 |
| SCE1572_1425 | sce_3600 | 1.00E-150 | 8.00E-154 |
| SCE1572_1426 | sce_1017 | 1.00E-128 | 1.00E-128 |
| SCE1572_1428 | sce_1018 | 1.00E-158 | 2.00E-151 |
| SCE1572_1429 | sce_1019 | 2.00E-122 | 2.00E-122 |
| SCE1572_1430 | sce_1022 | 5.00E-122 | 2.00E-129 |
| SCE1572_1431 | sce_1023 | 2.00E-31 | 2.00E-31 |
| SCE1572_1432 | sce_1024 | 4.00E-30 | 1.00E-67 |
| SCE1572_1434 | sce_8817 | 0.00E+00 | 0.00E+00 |
| SCE1572_1434 | sce_10193 | 0.00E+00 | 0.00E+00 |
| SCE1572_1435 | sce_4560 | 2.00E-25 | 5.00E-29 |
| SCE1572_1437 | sce_6320 | 6.00E-68 | 6.00E-68 |
| SCE1572_1438 | sce_6321 | 1.00E-143 | 7.00E-148 |
| SCE1572_1439 | sce_6322 | 2.00E-161 | 4.00E-152 |
| SCE1572_144 | sce_1298 | 3.00E-11 | 3.00E-11 |
| SCE1572_1440 | sce_6323 | 0.00E+00 | 0.00E+00 |
| SCE1572_1441 | sce_6330 | 0.00E+00 | 0.00E+00 |
| SCE1572_1442 | sce_6326 | 2.00E-108 | 4.00E-106 |
| SCE1572_1443 | sce_1084 | 0.00E+00 | 0.00E+00 |
| SCE1572_1445 | sce_2350 | 0.00E+00 | 0.00E+00 |
| SCE1572_1447 | sce_6187 | 0.00E+00 | 0.00E+00 |
| SCE1572_1448 | sce_2658 | 7.00E-43 | 5.00E-49 |
| SCE1572_1449 | sce_2659 | 4.00E-48 | 4.00E-48 |
| SCE1572_145 | sce_6050 | 5.00E-46 | 6.00E-53 |
| SCE1572_1450 | sce_9885 | 3.00E-157 | 3.00E-157 |
| SCE1572_1451 | sce_9884 | 4.00E-149 | 5.00E-144 |
| SCE1572_1453 | sce_1676 | 0.00E+00 | 0.00E+00 |
| SCE1572_1455 | sce_7521 | 0.00E+00 | 0.00E+00 |
| SCE1572_1459 | sce_8592 | 0.00E+00 | 0.00E+00 |
| SCE1572_1459 | sce_3937 | 0.00E+00 | 0.00E+00 |
| SCE1572_146 | sce_6051 | 0.00E+00 | 0.00E+00 |
| SCE1572_1463 | sce_9794 | 3.00E-123 | 3.00E-127 |
| SCE1572_1464 | sce_9795 | 6.00E-115 | 1.00E-131 |
| SCE1572_1465 | sce_7514 | 6.00E-79 | 2.00E-82 |
| SCE1572_147 | sce_6052 | 0.00E+00 | 0.00E+00 |
| SCE1572_149 | sce_1469 | 4.00E-70 | 5.00E-62 |
| SCE1572_1492 | sce_7318 | 0.00E+00 | 0.00E+00 |
| SCE1572_1492 | sce_5158 | 0.00E+00 | 0.00E+00 |
| SCE1572_1492 | sce_1116 | 0.00E+00 | 0.00E+00 |
| SCE1572_1494 | sce_2498 | 0.00E+00 | 0.00E+00 |
| SCE1572_1496 | sce_8802 | 1.00E-60 | 3.00E-52 |
| SCE1572_1497 | sce_9879 | 1.00E-69 | 3.00E-68 |
| SCE1572_15 | sce_15 | 4.00E-25 | 1.00E-19 |
| SCE1572_150 | sce_138 | 8.00E-85 | 2.00E-97 |
| SCE1572_1504 | sce_10169 | 0.00E+00 | 0.00E+00 |
| SCE1572_1511 | sce_7061 | 5.00E-83 | 6.00E-73 |
| SCE1572_1512 | sce_9866 | 2.00E-141 | 6.00E-137 |
| SCE1572_1514 | sce_1037 | 2.00E-100 | 3.00E-121 |
| SCE1572_1515 | sce_1039 | 2.00E-16 | 1.00E-16 |
| SCE1572_1516 | sce_1040 | 0.00E+00 | 0.00E+00 |
| SCE1572_1518 | sce_1041 | 0.00E+00 | 0.00E+00 |
| SCE1572_1521 | sce_1044 | 5.00E-63 | 3.00E-58 |

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|--------------|----------|-----------|-----------|
| SCE1572_1523 | sce_1046 | 3.00E-106 | 3.00E-99 |
| SCE1572_1525 | sce_1047 | 0.00E+00 | 0.00E+00 |
| SCE1572_1526 | sce_1048 | 0.00E+00 | 0.00E+00 |
| SCE1572_1527 | sce_1049 | 3.00E-20 | 2.00E-20 |
| SCE1572_1528 | sce_1051 | 0.00E+00 | 0.00E+00 |
| SCE1572_1529 | sce_1052 | 0.00E+00 | 0.00E+00 |
| SCE1572_1532 | sce_1053 | 2.00E-59 | 4.00E-61 |
| SCE1572_1533 | sce_1054 | 1.00E-75 | 7.00E-92 |
| SCE1572_1534 | sce_1056 | 1.00E-119 | 3.00E-115 |
| SCE1572_1535 | sce_1057 | 4.00E-79 | 8.00E-93 |
| SCE1572_1538 | sce_1058 | 1.00E-152 | 7.00E-153 |
| SCE1572_1539 | sce_1059 | 5.00E-166 | 6.00E-163 |
| SCE1572_1540 | sce_1060 | 0.00E+00 | 0.00E+00 |
| SCE1572_1543 | sce_1061 | 7.00E-13 | 7.00E-18 |
| SCE1572_1544 | sce_1063 | 5.00E-79 | 5.00E-79 |
| SCE1572_1545 | sce_1065 | 0.00E+00 | 0.00E+00 |
| SCE1572_1546 | sce_1066 | 0.00E+00 | 0.00E+00 |
| SCE1572_1547 | sce_1071 | 2.00E-84 | 1.00E-84 |
| SCE1572_1548 | sce_1074 | 0.00E+00 | 0.00E+00 |
| SCE1572_1549 | sce_1075 | 4.00E-142 | 3.00E-140 |
| SCE1572_155 | sce_140 | 0.00E+00 | 0.00E+00 |
| SCE1572_1550 | sce_1076 | 6.00E-45 | 4.00E-46 |
| SCE1572_1551 | sce_1078 | 3.00E-163 | 7.00E-140 |
| SCE1572_1552 | sce_9982 | 9.00E-78 | 1.00E-97 |
| SCE1572_1553 | sce_1080 | 4.00E-52 | 3.00E-70 |
| SCE1572_1554 | sce_1081 | 0.00E+00 | 0.00E+00 |
| SCE1572_1556 | sce_4904 | 3.00E-52 | 5.00E-53 |
| SCE1572_1558 | sce_1087 | 0.00E+00 | 0.00E+00 |
| SCE1572_1559 | sce_1088 | 2.00E-58 | 2.00E-60 |
| SCE1572_156 | sce_141 | 4.00E-133 | 4.00E-133 |
| SCE1572_1560 | sce_1090 | 4.00E-112 | 1.00E-92 |
| SCE1572_1561 | sce_1091 | 2.00E-124 | 9.00E-126 |
| SCE1572_1562 | sce_1092 | 4.00E-49 | 2.00E-49 |
| SCE1572_1563 | sce_1094 | 4.00E-27 | 4.00E-27 |
| SCE1572_1564 | sce_1095 | 6.00E-71 | 1.00E-70 |
| SCE1572_1567 | sce_1096 | 3.00E-18 | 1.00E-16 |
| SCE1572_1568 | sce_1097 | 0.00E+00 | 0.00E+00 |
| SCE1572_1569 | sce_1098 | 6.00E-132 | 1.00E-132 |
| SCE1572_157 | sce_5982 | 0.00E+00 | 0.00E+00 |
| SCE1572_1571 | sce_1122 | 7.00E-26 | 2.00E-32 |
| SCE1572_1572 | sce_1123 | 0.00E+00 | 0.00E+00 |
| SCE1572_1573 | sce_1124 | 4.00E-176 | 2.00E-178 |
| SCE1572_1574 | sce_1125 | 1.00E-99 | 3.00E-99 |
| SCE1572_1575 | sce_1126 | 2.00E-150 | 4.00E-150 |
| SCE1572_1576 | sce_1127 | 2.00E-180 | 9.00E-160 |
| SCE1572_1577 | sce_1128 | 2.00E-152 | 5.00E-155 |
| SCE1572_158 | sce_5981 | 7.00E-84 | 1.00E-104 |
| SCE1572_1581 | sce_1132 | 2.00E-111 | 1.00E-110 |
| SCE1572_1582 | sce_1133 | 2.00E-121 | 2.00E-125 |
| SCE1572_1584 | sce_1604 | 8.00E-95 | 8.00E-95 |
| SCE1572_1585 | sce_7900 | 1.00E-95 | 1.00E-95 |
| SCE1572_159 | sce_5980 | 0.00E+00 | 0.00E+00 |
| SCE1572_16 | sce_16 | 6.00E-160 | 3.00E-162 |
| SCE1572_1600 | sce_8426 | 0.00E+00 | 0.00E+00 |
| SCE1572_1604 | sce_1140 | 1.00E-37 | 8.00E-46 |
| SCE1572_1605 | sce_1143 | 0.00E+00 | 0.00E+00 |
| SCE1572_1606 | sce_1144 | 0.00E+00 | 0.00E+00 |
| SCE1572_1607 | sce_1145 | 2.00E-108 | 7.00E-109 |
| SCE1572_1608 | sce_1146 | 0.00E+00 | 0.00E+00 |
| SCE1572_1609 | sce_1148 | 0.00E+00 | 0.00E+00 |
| SCE1572_161 | sce_8630 | 1.00E-133 | 1.00E-135 |
| SCE1572_1610 | sce_1149 | 0.00E+00 | 0.00E+00 |
| SCE1572_1612 | sce_1151 | 8.00E-99 | 3.00E-88 |
| SCE1572_1614 | sce_1152 | 0.00E+00 | 0.00E+00 |
| SCE1572_1615 | sce_1153 | 0.00E+00 | 0.00E+00 |
| SCE1572_1616 | sce_1154 | 1.00E-142 | 4.00E-128 |
| SCE1572_1617 | sce_1155 | 8.00E-137 | 1.00E-136 |
| SCE1572_1618 | sce_1156 | 0.00E+00 | 0.00E+00 |
| SCE1572_1619 | sce_1157 | 6.00E-105 | 6.00E-96 |
| SCE1572_162 | sce_8629 | 0.00E+00 | 0.00E+00 |
| SCE1572_1620 | sce_1158 | 1.00E-60 | 1.00E-60 |
| SCE1572_1621 | sce_1159 | 2.00E-60 | 3.00E-70 |
| SCE1572_1625 | sce_8406 | 5.00E-30 | 3.00E-31 |
| SCE1572_1626 | sce_1164 | 7.00E-83 | 1.00E-77 |
| SCE1572_1627 | sce_7633 | 0.00E+00 | 0.00E+00 |
| SCE1572_1628 | sce_1165 | 4.00E-145 | 7.00E-147 |

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| SCE1572_1629 | sce_1166 | 1.00E-51 | 1.00E-43 |
| SCE1572_1633 | sce_1167 | 0.00E+00 | 0.00E+00 |
| SCE1572_1634 | sce_1168 | 0.00E+00 | 0.00E+00 |
| SCE1572_1636 | sce_1170 | 2.00E-99 | 2.00E-99 |
| SCE1572_1640 | sce_9109 | 5.00E-28 | 7.00E-26 |
| SCE1572_1643 | sce_8347 | 0.00E+00 | 0.00E+00 |
| SCE1572_1645 | sce_4581 | 0.00E+00 | 0.00E+00 |
| SCE1572_1645 | sce_9106 | 0.00E+00 | 0.00E+00 |
| SCE1572_1649 | sce_6171 | 0.00E+00 | 0.00E+00 |
| SCE1572_165 | sce_147 | 8.00E-131 | 3.00E-154 |
| SCE1572_1651 | sce_5536 | 9.00E-51 | 4.00E-51 |
| SCE1572_1658 | sce_1173 | 4.00E-80 | 1.00E-80 |
| SCE1572_1659 | sce_1174 | 7.00E-153 | 4.00E-137 |
| SCE1572_1660 | sce_1175 | 7.00E-168 | 3.00E-166 |
| SCE1572_1661 | sce_1176 | 1.00E-177 | 1.00E-177 |
| SCE1572_1663 | sce_1177 | 1.00E-09 | 1.00E-08 |
| SCE1572_1664 | sce_1178 | 1.00E-167 | 1.00E-167 |
| SCE1572_1665 | sce_1180 | 1.00E-165 | 3.00E-169 |
| SCE1572_1666 | sce_1181 | 0.00E+00 | 0.00E+00 |
| SCE1572_1667 | sce_1183 | 3.00E-99 | 1.00E-92 |
| SCE1572_1668 | sce_1184 | 5.00E-175 | 2.00E-180 |
| SCE1572_1669 | sce_1185 | 9.00E-43 | 1.00E-51 |
| SCE1572_1670 | sce_1186 | 0.00E+00 | 0.00E+00 |
| SCE1572_1671 | sce_1187 | 0.00E+00 | 0.00E+00 |
| SCE1572_1672 | sce_1188 | 4.00E-78 | 5.00E-88 |
| SCE1572_1673 | sce_1189 | 0.00E+00 | 0.00E+00 |
| SCE1572_1674 | sce_1190 | 4.00E-161 | 2.00E-148 |
| SCE1572_1675 | sce_1191 | 3.00E-89 | 2.00E-85 |
| SCE1572_1677 | sce_1192 | 4.00E-18 | 1.00E-24 |
| SCE1572_1678 | sce_1193 | 0.00E+00 | 0.00E+00 |
| SCE1572_1679 | sce_1194 | 0.00E+00 | 0.00E+00 |
| SCE1572_168 | sce_148 | 6.00E-105 | 1.00E-107 |
| SCE1572_1680 | sce_1195 | 3.00E-153 | 3.00E-153 |
| SCE1572_1681 | sce_1196 | 1.00E-62 | 8.00E-72 |
| SCE1572_1682 | sce_1197 | 1.00E-116 | 1.00E-108 |
| SCE1572_1683 | sce_1198 | 3.00E-43 | 3.00E-43 |
| SCE1572_1684 | sce_1199 | 3.00E-144 | 3.00E-144 |
| SCE1572_1685 | sce_1200 | 9.00E-87 | 8.00E-100 |
| SCE1572_1686 | sce_1201 | 8.00E-24 | 1.00E-20 |
| SCE1572_1687 | sce_1202 | 9.00E-79 | 5.00E-72 |
| SCE1572_1688 | sce_1203 | 1.00E-69 | 3.00E-69 |
| SCE1572_169 | sce_149 | 1.00E-138 | 6.00E-133 |
| SCE1572_1690 | sce_1204 | 3.00E-56 | 4.00E-50 |
| SCE1572_1691 | sce_1205 | 8.00E-71 | 9.00E-71 |
| SCE1572_1692 | sce_1206 | 6.00E-14 | 2.00E-21 |
| SCE1572_1693 | sce_1207 | 1.00E-32 | 4.00E-10 |
| SCE1572_1696 | sce_1209 | 9.00E-116 | 1.00E-107 |
| SCE1572_1697 | sce_1210 | 2.00E-17 | 2.00E-26 |
| SCE1572_1698 | sce_1211 | 8.00E-33 | 8.00E-42 |
| SCE1572_1699 | sce_1212 | 0.00E+00 | 0.00E+00 |
| SCE1572_17 | sce_17 | 1.00E-49 | 6.00E-51 |
| SCE1572_170 | sce_151 | 9.00E-71 | 2.00E-71 |
| SCE1572_1700 | sce_1213 | 8.00E-159 | 4.00E-154 |
| SCE1572_1701 | sce_1214 | 0.00E+00 | 0.00E+00 |
| SCE1572_1702 | sce_1215 | 3.00E-105 | 8.00E-112 |
| SCE1572_1703 | sce_1216 | 0.00E+00 | 0.00E+00 |
| SCE1572_1705 | sce_1218 | 0.00E+00 | 0.00E+00 |
| SCE1572_1706 | sce_1219 | 0.00E+00 | 0.00E+00 |
| SCE1572_1707 | sce_1221 | 3.00E-169 | 6.00E-171 |
| SCE1572_1708 | sce_1222 | 2.00E-25 | 2.00E-25 |
| SCE1572_1709 | sce_1223 | 0.00E+00 | 0.00E+00 |
| SCE1572_171 | sce_152 | 7.00E-39 | 7.00E-39 |
| SCE1572_1710 | sce_1224 | 4.00E-43 | 2.00E-40 |
| SCE1572_1711 | sce_1225 | 2.00E-162 | 5.00E-169 |
| SCE1572_1712 | sce_1226 | 6.00E-149 | 3.00E-159 |
| SCE1572_1713 | sce_1227 | 2.00E-84 | 5.00E-85 |
| SCE1572_1717 | sce_1230 | 3.00E-154 | 5.00E-161 |
| SCE1572_1718 | sce_1231 | 0.00E+00 | 0.00E+00 |
| SCE1572_1719 | sce_1232 | 0.00E+00 | 0.00E+00 |
| SCE1572_1720 | sce_1233 | 3.00E-111 | 2.00E-103 |
| SCE1572_1722 | sce_1235 | 0.00E+00 | 0.00E+00 |
| SCE1572_1724 | sce_1236 | 5.00E-135 | 8.00E-135 |
| SCE1572_1725 | sce_1237 | 0.00E+00 | 0.00E+00 |
| SCE1572_1727 | sce_1238 | 0.00E+00 | 0.00E+00 |
| SCE1572_1728 | sce_1240 | 0.00E+00 | 6.00E-129 |
| SCE1572_173 | sce_153 | 2.00E-24 | 2.00E-35 |

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| SCE1572_1731 | sce_9222 | 0.00E+00 | 0.00E+00 |
| SCE1572_1731 | sce_1814 | 0.00E+00 | 0.00E+00 |
| SCE1572_1739 | sce_1242 | 3.00E-116 | 1.00E-104 |
| SCE1572_174 | sce_154 | 2.00E-98 | 4.00E-88 |
| SCE1572_1740 | sce_1243 | 1.00E-105 | 3.00E-121 |
| SCE1572_175 | sce_155 | 8.00E-118 | 1.00E-134 |
| SCE1572_176 | sce_156 | 8.00E-32 | 3.00E-32 |
| SCE1572_1761 | sce_1670 | 1.00E-107 | 1.00E-107 |
| SCE1572_1762 | sce_1116 | 0.00E+00 | 0.00E+00 |
| SCE1572_1762 | sce_5158 | 0.00E+00 | 0.00E+00 |
| SCE1572_1762 | sce_7318 | 0.00E+00 | 0.00E+00 |
| SCE1572_1763 | sce_1115 | 0.00E+00 | 0.00E+00 |
| SCE1572_1763 | sce_5159 | 0.00E+00 | 0.00E+00 |
| SCE1572_1768 | sce_5098 | 0.00E+00 | 0.00E+00 |
| SCE1572_177 | sce_7124 | 8.00E-38 | 4.00E-37 |
| SCE1572_1771 | sce_1085 | 5.00E-179 | 7.00E-180 |
| SCE1572_1772 | sce_1086 | 0.00E+00 | 0.00E+00 |
| SCE1572_1774 | sce_5484 | 1.00E-74 | 4.00E-76 |
| SCE1572_1775 | sce_5485 | 2.00E-09 | 4.00E-17 |
| SCE1572_1776 | sce_5486 | 0.00E+00 | 0.00E+00 |
| SCE1572_1776 | sce_1479 | 0.00E+00 | 0.00E+00 |
| SCE1572_1777 | sce_5487 | 0.00E+00 | 0.00E+00 |
| SCE1572_1777 | sce_1478 | 0.00E+00 | 0.00E+00 |
| SCE1572_1778 | sce_8627 | 1.00E-99 | 4.00E-104 |
| SCE1572_1780 | sce_1565 | 1.00E-124 | 1.00E-124 |
| SCE1572_1781 | sce_1564 | 1.00E-142 | 5.00E-152 |
| SCE1572_1782 | sce_7064 | 5.00E-53 | 5.00E-53 |
| SCE1572_1783 | sce_7065 | 2.00E-70 | 2.00E-70 |
| SCE1572_1785 | sce_7067 | 0.00E+00 | 0.00E+00 |
| SCE1572_179 | sce_159 | 0.00E+00 | 0.00E+00 |
| SCE1572_18 | sce_18 | 0.00E+00 | 0.00E+00 |
| SCE1572_1806 | sce_1266 | 2.00E-87 | 2.00E-89 |
| SCE1572_1807 | sce_1267 | 1.00E-78 | 9.00E-49 |
| SCE1572_1808 | sce_1268 | 2.00E-111 | 3.00E-105 |
| SCE1572_1809 | sce_1269 | 6.00E-138 | 5.00E-137 |
| SCE1572_181 | sce_1372 | 0.00E+00 | 0.00E+00 |
| SCE1572_1810 | sce_5174 | 7.00E-92 | 5.00E-97 |
| SCE1572_1811 | sce_5175 | 2.00E-176 | 2.00E-171 |
| SCE1572_1812 | sce_1270 | 1.00E-130 | 5.00E-146 |
| SCE1572_1813 | sce_1271 | 2.00E-84 | 5.00E-75 |
| SCE1572_1814 | sce_1272 | 2.00E-147 | 3.00E-157 |
| SCE1572_1815 | sce_1273 | 3.00E-143 | 4.00E-180 |
| SCE1572_1816 | sce_1275 | 3.00E-80 | 2.00E-79 |
| SCE1572_1818 | sce_9112 | 4.00E-22 | 4.00E-22 |
| SCE1572_1820 | sce_1284 | 1.00E-61 | 2.00E-66 |
| SCE1572_1824 | sce_2457 | 0.00E+00 | 0.00E+00 |
| SCE1572_1825 | sce_2458 | 7.00E-101 | 1.00E-96 |
| SCE1572_1829 | sce_6076 | 0.00E+00 | 0.00E+00 |
| SCE1572_183 | sce_9533 | 0.00E+00 | 0.00E+00 |
| SCE1572_1830 | sce_1292 | 0.00E+00 | 0.00E+00 |
| SCE1572_1832 | sce_1293 | 3.00E-30 | 3.00E-36 |
| SCE1572_1833 | sce_1294 | 0.00E+00 | 0.00E+00 |
| SCE1572_1834 | sce_1295 | 1.00E-39 | 1.00E-42 |
| SCE1572_1835 | sce_1296 | 9.00E-71 | 6.00E-78 |
| SCE1572_1836 | sce_1297 | 3.00E-25 | 4.00E-25 |
| SCE1572_1837 | sce_1299 | 0.00E+00 | 0.00E+00 |
| SCE1572_1838 | sce_1300 | 0.00E+00 | 0.00E+00 |
| SCE1572_1840 | sce_1302 | 1.00E-141 | 3.00E-152 |
| SCE1572_1841 | sce_1303 | 6.00E-45 | 7.00E-50 |
| SCE1572_1842 | sce_1304 | 0.00E+00 | 0.00E+00 |
| SCE1572_1843 | sce_1305 | 5.00E-93 | 5.00E-93 |
| SCE1572_1844 | sce_1306 | 1.00E-177 | 0.00E+00 |
| SCE1572_1846 | sce_1308 | 2.00E-50 | 1.00E-46 |
| SCE1572_1849 | sce_1492 | 0.00E+00 | 0.00E+00 |
| SCE1572_185 | sce_7864 | 1.00E-85 | 1.00E-96 |
| SCE1572_1850 | sce_1491 | 0.00E+00 | 0.00E+00 |
| SCE1572_1851 | sce_1490 | 6.00E-47 | 4.00E-47 |
| SCE1572_1852 | sce_1488 | 2.00E-136 | 7.00E-136 |
| SCE1572_1853 | sce_1487 | 2.00E-98 | 5.00E-99 |
| SCE1572_1855 | sce_1309 | 0.00E+00 | 0.00E+00 |
| SCE1572_1856 | sce_1310 | 0.00E+00 | 0.00E+00 |
| SCE1572_1858 | sce_1312 | 5.00E-51 | 5.00E-51 |
| SCE1572_1859 | sce_1313 | 2.00E-35 | 1.00E-47 |
| SCE1572_186 | sce_7863 | 6.00E-126 | 5.00E-136 |
| SCE1572_1860 | sce_1315 | 0.00E+00 | 0.00E+00 |
| SCE1572_1862 | sce_3679 | 2.00E-179 | 0.00E+00 |

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| SCE1572_1866 | sce_6298 | 7.00E-12 | 3.00E-08 |
| SCE1572_1869 | sce_1342 | 1.00E-157 | 3.00E-162 |
| SCE1572_1870 | sce_1344 | 1.00E-62 | 1.00E-87 |
| SCE1572_1871 | sce_3671 | 1.00E-93 | 3.00E-93 |
| SCE1572_1872 | sce_1345 | 0.00E+00 | 0.00E+00 |
| SCE1572_1874 | sce_1390 | 3.00E-87 | 2.00E-83 |
| SCE1572_1875 | sce_1391 | 0.00E+00 | 0.00E+00 |
| SCE1572_1876 | sce_1392 | 0.00E+00 | 0.00E+00 |
| SCE1572_1876 | sce_5578 | 0.00E+00 | 0.00E+00 |
| SCE1572_1878 | sce_1394 | 6.00E-15 | 4.00E-19 |
| SCE1572_1879 | sce_1395 | 9.00E-66 | 1.00E-66 |
| SCE1572_188 | sce_171 | 1.00E-117 | 9.00E-127 |
| SCE1572_1880 | sce_1396 | 0.00E+00 | 0.00E+00 |
| SCE1572_1881 | sce_1397 | 4.00E-71 | 8.00E-67 |
| SCE1572_1882 | sce_1398 | 0.00E+00 | 0.00E+00 |
| SCE1572_1882 | sce_7661 | 0.00E+00 | 0.00E+00 |
| SCE1572_1884 | sce_1399 | 3.00E-113 | 2.00E-102 |
| SCE1572_1885 | sce_1401 | 3.00E-128 | 5.00E-157 |
| SCE1572_1887 | sce_1402 | 0.00E+00 | 0.00E+00 |
| SCE1572_1889 | sce_1404 | 0.00E+00 | 0.00E+00 |
| SCE1572_189 | sce_172 | 5.00E-57 | 1.00E-53 |
| SCE1572_1891 | sce_1405 | 3.00E-06 | 6.00E-06 |
| SCE1572_1892 | sce_1406 | 4.00E-155 | 2.00E-159 |
| SCE1572_1893 | sce_1407 | 3.00E-70 | 4.00E-71 |
| SCE1572_1894 | sce_1408 | 0.00E+00 | 3.00E-180 |
| SCE1572_1895 | sce_1409 | 7.00E-67 | 5.00E-98 |
| SCE1572_1898 | sce_1410 | 0.00E+00 | 0.00E+00 |
| SCE1572_1899 | sce_1411 | 1.00E-148 | 1.00E-166 |
| SCE1572_19 | sce_19 | 0.00E+00 | 0.00E+00 |
| SCE1572_190 | sce_3728 | 5.00E-157 | 3.00E-167 |
| SCE1572_1902 | sce_1414 | 0.00E+00 | 0.00E+00 |
| SCE1572_1903 | sce_1415 | 0.00E+00 | 0.00E+00 |
| SCE1572_1905 | sce_1416 | 3.00E-34 | 9.00E-30 |
| SCE1572_1906 | sce_1417 | 0.00E+00 | 0.00E+00 |
| SCE1572_1907 | sce_1418 | 0.00E+00 | 0.00E+00 |
| SCE1572_1908 | sce_1419 | 6.00E-106 | 4.00E-106 |
| SCE1572_1914 | sce_1421 | 7.00E-128 | 2.00E-136 |
| SCE1572_1915 | sce_1422 | 0.00E+00 | 0.00E+00 |
| SCE1572_1917 | sce_1436 | 5.00E-94 | 6.00E-97 |
| SCE1572_1918 | sce_1437 | 2.00E-107 | 5.00E-100 |
| SCE1572_1919 | sce_1438 | 0.00E+00 | 0.00E+00 |
| SCE1572_1920 | sce_1439 | 9.00E-134 | 2.00E-143 |
| SCE1572_1922 | sce_1440 | 5.00E-132 | 7.00E-150 |
| SCE1572_1923 | sce_1441 | 0.00E+00 | 1.00E-174 |
| SCE1572_1924 | sce_1442 | 0.00E+00 | 0.00E+00 |
| SCE1572_1925 | sce_1443 | 9.00E-16 | 1.00E-15 |
| SCE1572_1926 | sce_1444 | 0.00E+00 | 0.00E+00 |
| SCE1572_1926 | sce_2656 | 0.00E+00 | 0.00E+00 |
| SCE1572_1927 | sce_1445 | 0.00E+00 | 0.00E+00 |
| SCE1572_1928 | sce_1446 | 9.00E-119 | 7.00E-125 |
| SCE1572_1929 | sce_1447 | 8.00E-140 | 0.00E+00 |
| SCE1572_1930 | sce_1448 | 0.00E+00 | 0.00E+00 |
| SCE1572_1931 | sce_2577 | 0.00E+00 | 0.00E+00 |
| SCE1572_1932 | sce_1449 | 0.00E+00 | 0.00E+00 |
| SCE1572_1934 | sce_1450 | 1.00E-67 | 1.00E-67 |
| SCE1572_1946 | sce_5198 | 3.00E-26 | 2.00E-23 |
| SCE1572_1948 | sce_1316 | 3.00E-79 | 7.00E-72 |
| SCE1572_1950 | sce_848 | 1.00E-89 | 9.00E-93 |
| SCE1572_1951 | sce_849 | 2.00E-57 | 7.00E-65 |
| SCE1572_1952 | sce_850 | 1.00E-60 | 4.00E-59 |
| SCE1572_1953 | sce_1455 | 5.00E-86 | 5.00E-86 |
| SCE1572_1954 | sce_6015 | 2.00E-90 | 2.00E-90 |
| SCE1572_1955 | sce_1456 | 9.00E-78 | 9.00E-78 |
| SCE1572_1956 | sce_1457 | 2.00E-81 | 1.00E-116 |
| SCE1572_1957 | sce_6060 | 2.00E-44 | 5.00E-38 |
| SCE1572_1958 | sce_2565 | 1.00E-115 | 8.00E-114 |
| SCE1572_1960 | sce_1462 | 0.00E+00 | 0.00E+00 |
| SCE1572_1961 | sce_1463 | 0.00E+00 | 0.00E+00 |
| SCE1572_1962 | sce_1464 | 0.00E+00 | 0.00E+00 |
| SCE1572_1963 | sce_1465 | 3.00E-112 | 4.00E-111 |
| SCE1572_1964 | sce_1466 | 5.00E-103 | 4.00E-103 |
| SCE1572_1965 | sce_1467 | 1.00E-132 | 1.00E-132 |
| SCE1572_1966 | sce_1468 | 1.00E-177 | 0.00E+00 |
| SCE1572_1967 | sce_1470 | 4.00E-55 | 2.00E-55 |
| SCE1572_1969 | sce_1471 | 4.00E-67 | 3.00E-71 |
| SCE1572_1971 | sce_1472 | 1.00E-83 | 4.00E-76 |

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| SCE1572_1972 | sce_1473 | 0.00E+00 | 0.00E+00 |
| SCE1572_1975 | sce_1474 | 0.00E+00 | 0.00E+00 |
| SCE1572_1976 | sce_1475 | 0.00E+00 | 0.00E+00 |
| SCE1572_199 | sce_173 | 0.00E+00 | 0.00E+00 |
| SCE1572_1993 | sce_1476 | 1.00E-117 | 4.00E-108 |
| SCE1572_1994 | sce_1477 | 0.00E+00 | 0.00E+00 |
| SCE1572_1995 | sce_1478 | 0.00E+00 | 0.00E+00 |
| SCE1572_1995 | sce_5487 | 0.00E+00 | 0.00E+00 |
| SCE1572_1996 | sce_1479 | 0.00E+00 | 0.00E+00 |
| SCE1572_1996 | sce_5486 | 0.00E+00 | 0.00E+00 |
| SCE1572_1997 | sce_1480 | 2.00E-14 | 8.00E-11 |
| SCE1572_1998 | sce_1481 | 1.00E-78 | 1.00E-80 |
| SCE1572_1999 | sce_1482 | 2.00E-57 | 6.00E-63 |
| SCE1572_2 | sce_2 | 0.00E+00 | 0.00E+00 |
| SCE1572_20 | sce_20 | 2.00E-158 | 0.00E+00 |
| SCE1572_200 | sce_6011 | 2.00E-59 | 8.00E-62 |
| SCE1572_2000 | sce_1483 | 2.00E-28 | 7.00E-29 |
| SCE1572_2001 | sce_1484 | 1.00E-92 | 8.00E-96 |
| SCE1572_2002 | sce_3672 | 5.00E-62 | 3.00E-61 |
| SCE1572_2003 | sce_1486 | 9.00E-65 | 1.00E-55 |
| SCE1572_2005 | sce_8025 | 2.00E-105 | 8.00E-98 |
| SCE1572_2009 | sce_1587 | 3.00E-16 | 1.00E-15 |
| SCE1572_2014 | sce_6082 | 1.00E-104 | 1.00E-85 |
| SCE1572_2016 | sce_1496 | 0.00E+00 | 0.00E+00 |
| SCE1572_2017 | sce_1497 | 0.00E+00 | 0.00E+00 |
| SCE1572_2018 | sce_1498 | 1.00E-74 | 3.00E-81 |
| SCE1572_2019 | sce_1499 | 0.00E+00 | 0.00E+00 |
| SCE1572_2020 | sce_1500 | 9.00E-88 | 1.00E-90 |
| SCE1572_2022 | sce_3705 | 0.00E+00 | 0.00E+00 |
| SCE1572_2023 | sce_5152 | 2.00E-133 | 7.00E-143 |
| SCE1572_2024 | sce_1510 | 0.00E+00 | 5.00E-176 |
| SCE1572_2025 | sce_1511 | 4.00E-168 | 4.00E-172 |
| SCE1572_2026 | sce_9276 | 9.00E-77 | 3.00E-75 |
| SCE1572_2028 | sce_1517 | 3.00E-75 | 3.00E-75 |
| SCE1572_2029 | sce_1512 | 2.00E-156 | 2.00E-156 |
| SCE1572_203 | sce_1460 | 6.00E-107 | 2.00E-108 |
| SCE1572_2030 | sce_8774 | 2.00E-14 | 3.00E-21 |
| SCE1572_2031 | sce_1513 | 4.00E-74 | 4.00E-74 |
| SCE1572_2032 | sce_1515 | 4.00E-54 | 7.00E-51 |
| SCE1572_2033 | sce_1676 | 0.00E+00 | 0.00E+00 |
| SCE1572_2036 | sce_1518 | 5.00E-49 | 7.00E-50 |
| SCE1572_2038 | sce_1519 | 8.00E-88 | 6.00E-91 |
| SCE1572_2039 | sce_1520 | 2.00E-35 | 2.00E-44 |
| SCE1572_2040 | sce_1521 | 5.00E-114 | 3.00E-114 |
| SCE1572_2041 | sce_1679 | 1.00E-70 | 6.00E-79 |
| SCE1572_2042 | sce_1522 | 3.00E-151 | 3.00E-137 |
| SCE1572_2043 | sce_1523 | 6.00E-103 | 1.00E-110 |
| SCE1572_2045 | sce_1527 | 0.00E+00 | 3.00E-174 |
| SCE1572_2046 | sce_1529 | 6.00E-131 | 9.00E-118 |
| SCE1572_2048 | sce_1530 | 1.00E-46 | 3.00E-55 |
| SCE1572_205 | sce_6005 | 0.00E+00 | 0.00E+00 |
| SCE1572_2054 | sce_1546 | 2.00E-127 | 1.00E-132 |
| SCE1572_2055 | sce_1567 | 7.00E-90 | 1.00E-75 |
| SCE1572_2059 | sce_1569 | 1.00E-138 | 3.00E-134 |
| SCE1572_2064 | sce_3848 | 2.00E-14 | 1.00E-14 |
| SCE1572_2065 | sce_1576 | 4.00E-173 | 2.00E-174 |
| SCE1572_2066 | sce_1577 | 0.00E+00 | 0.00E+00 |
| SCE1572_2067 | sce_1578 | 2.00E-156 | 8.00E-153 |
| SCE1572_2069 | sce_1579 | 0.00E+00 | 1.00E-141 |
| SCE1572_2071 | sce_1583 | 4.00E-25 | 3.00E-14 |
| SCE1572_2072 | sce_1588 | 0.00E+00 | 0.00E+00 |
| SCE1572_2074 | sce_1589 | 1.00E-71 | 1.00E-51 |
| SCE1572_2075 | sce_1590 | 1.00E-33 | 1.00E-31 |
| SCE1572_2076 | sce_1591 | 0.00E+00 | 0.00E+00 |
| SCE1572_2077 | sce_10225 | 3.00E-117 | 1.00E-127 |
| SCE1572_2078 | sce_7460 | 3.00E-128 | 3.00E-140 |
| SCE1572_2080 | sce_1592 | 7.00E-170 | 2.00E-177 |
| SCE1572_2081 | sce_1593 | 0.00E+00 | 0.00E+00 |
| SCE1572_2082 | sce_1594 | 1.00E-69 | 2.00E-66 |
| SCE1572_2086 | sce_1596 | 0.00E+00 | 0.00E+00 |
| SCE1572_2089 | sce_5892 | 7.00E-50 | 4.00E-45 |
| SCE1572_2092 | sce_7399 | 4.00E-55 | 9.00E-43 |
| SCE1572_2095 | sce_1609 | 4.00E-132 | 4.00E-133 |
| SCE1572_2096 | sce_1610 | 2.00E-53 | 5.00E-61 |
| SCE1572_2097 | sce_1611 | 1.00E-62 | 1.00E-62 |
| SCE1572_2098 | sce_1612 | 1.00E-113 | 7.00E-113 |

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| SCE1572_2099 | sce_1613 | 3.00E-140 | 1.00E-144 |
| SCE1572_21 | sce_22 | 2.00E-28 | 1.00E-31 |
| SCE1572_2100 | sce_1614 | 2.00E-18 | 1.00E-29 |
| SCE1572_2101 | sce_1617 | 4.00E-70 | 2.00E-65 |
| SCE1572_2102 | sce_1618 | 1.00E-137 | 2.00E-137 |
| SCE1572_2103 | sce_1619 | 0.00E+00 | 0.00E+00 |
| SCE1572_2104 | sce_1620 | 1.00E-170 | 3.00E-177 |
| SCE1572_2105 | sce_1621 | 2.00E-133 | 3.00E-133 |
| SCE1572_2106 | sce_1622 | 8.00E-137 | 1.00E-142 |
| SCE1572_2107 | sce_1623 | 0.00E+00 | 0.00E+00 |
| SCE1572_2108 | sce_1624 | 1.00E-122 | 1.00E-147 |
| SCE1572_2109 | sce_1625 | 2.00E-47 | 3.00E-47 |
| SCE1572_2110 | sce_1626 | 4.00E-163 | 9.00E-163 |
| SCE1572_2111 | sce_1627 | 0.00E+00 | 0.00E+00 |
| SCE1572_2114 | sce_1629 | 2.00E-131 | 6.00E-138 |
| SCE1572_2115 | sce_1630 | 0.00E+00 | 0.00E+00 |
| SCE1572_2117 | sce_1631 | 0.00E+00 | 0.00E+00 |
| SCE1572_2119 | sce_1632 | 2.00E-87 | 6.00E-73 |
| SCE1572_2120 | sce_1633 | 0.00E+00 | 0.00E+00 |
| SCE1572_2121 | sce_1634 | 3.00E-34 | 3.00E-34 |
| SCE1572_2123 | sce_1635 | 2.00E-164 | 5.00E-160 |
| SCE1572_2125 | sce_1645 | 0.00E+00 | 0.00E+00 |
| SCE1572_2126 | sce_1646 | 6.00E-19 | 1.00E-25 |
| SCE1572_2128 | sce_1647 | 7.00E-155 | 2.00E-149 |
| SCE1572_2129 | sce_1648 | 1.00E-74 | 1.00E-84 |
| SCE1572_2130 | sce_1649 | 1.00E-36 | 1.00E-35 |
| SCE1572_2131 | sce_1650 | 8.00E-13 | 7.00E-14 |
| SCE1572_2132 | sce_1652 | 4.00E-110 | 5.00E-117 |
| SCE1572_2136 | sce_1655 | 6.00E-93 | 8.00E-93 |
| SCE1572_2137 | sce_1656 | 1.00E-169 | 5.00E-147 |
| SCE1572_2139 | sce_7075 | 4.00E-99 | 5.00E-131 |
| SCE1572_214 | sce_2177 | 6.00E-49 | 2.00E-55 |
| SCE1572_2142 | sce_1658 | 0.00E+00 | 0.00E+00 |
| SCE1572_2143 | sce_1666 | 0.00E+00 | 0.00E+00 |
| SCE1572_2144 | sce_1667 | 0.00E+00 | 0.00E+00 |
| SCE1572_2145 | sce_1668 | 0.00E+00 | 0.00E+00 |
| SCE1572_2148 | sce_841 | 0.00E+00 | 0.00E+00 |
| SCE1572_215 | sce_6003 | 3.00E-179 | 3.00E-179 |
| SCE1572_2151 | sce_1719 | 1.00E-127 | 7.00E-131 |
| SCE1572_2152 | sce_1720 | 3.00E-105 | 4.00E-105 |
| SCE1572_2153 | sce_1721 | 3.00E-95 | 3.00E-95 |
| SCE1572_2154 | sce_1722 | 1.00E-100 | 3.00E-101 |
| SCE1572_2161 | sce_389 | 0.00E+00 | 0.00E+00 |
| SCE1572_2161 | sce_2666 | 0.00E+00 | 0.00E+00 |
| SCE1572_2161 | sce_7637 | 0.00E+00 | 0.00E+00 |
| SCE1572_2161 | sce_9237 | 0.00E+00 | 0.00E+00 |
| SCE1572_2163 | sce_175 | 3.00E-136 | 3.00E-145 |
| SCE1572_2170 | sce_5759 | 0.00E+00 | 0.00E+00 |
| SCE1572_2171 | sce_5758 | 0.00E+00 | 0.00E+00 |
| SCE1572_2174 | sce_764 | 6.00E-167 | 2.00E-166 |
| SCE1572_2176 | sce_1727 | 2.00E-66 | 2.00E-85 |
| SCE1572_2177 | sce_1728 | 6.00E-133 | 4.00E-128 |
| SCE1572_2178 | sce_10158 | 3.00E-40 | 3.00E-52 |
| SCE1572_2181 | sce_1323 | 8.00E-105 | 2.00E-104 |
| SCE1572_2184 | sce_6334 | 3.00E-22 | 2.00E-33 |
| SCE1572_2185 | sce_9438 | 0.00E+00 | 0.00E+00 |
| SCE1572_2187 | sce_7422 | 0.00E+00 | 0.00E+00 |
| SCE1572_219 | sce_5881 | 7.00E-64 | 7.00E-64 |
| SCE1572_2190 | sce_2564 | 8.00E-80 | 8.00E-80 |
| SCE1572_2191 | sce_7916 | 0.00E+00 | 0.00E+00 |
| SCE1572_2193 | sce_3807 | 1.00E-78 | 3.00E-78 |
| SCE1572_2195 | sce_176 | 3.00E-69 | 7.00E-77 |
| SCE1572_2196 | sce_9450 | 6.00E-155 | 1.00E-149 |
| SCE1572_2197 | sce_3917 | 0.00E+00 | 0.00E+00 |
| SCE1572_2197 | sce_6094 | 0.00E+00 | 0.00E+00 |
| SCE1572_2197 | sce_6092 | 0.00E+00 | 0.00E+00 |
| SCE1572_2197 | sce_6107 | 0.00E+00 | 0.00E+00 |
| SCE1572_2197 | sce_6093 | 0.00E+00 | 0.00E+00 |
| SCE1572_2197 | sce_6095 | 0.00E+00 | 0.00E+00 |
| SCE1572_2197 | sce_7661 | 0.00E+00 | 0.00E+00 |
| SCE1572_2197 | sce_388 | 0.00E+00 | 0.00E+00 |
| SCE1572_2197 | sce_6535 | 0.00E+00 | 0.00E+00 |
| SCE1572_2197 | sce_9920 | 0.00E+00 | 0.00E+00 |
| SCE1572_2197 | sce_8602 | 0.00E+00 | 0.00E+00 |
| SCE1572_2197 | sce_10204 | 0.00E+00 | 0.00E+00 |
| SCE1572_2197 | sce_4513 | 0.00E+00 | 0.00E+00 |

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| SCE1572_2197 | sce_3003 | 0.00E+00 | 0.00E+00 |
| SCE1572_2197 | sce_7640 | 0.00E+00 | 0.00E+00 |
| SCE1572_2197 | sce_5835 | 0.00E+00 | 0.00E+00 |
| SCE1572_2197 | sce_9557 | 0.00E+00 | 0.00E+00 |
| SCE1572_2197 | sce_3085 | 0.00E+00 | 0.00E+00 |
| SCE1572_2199 | sce_1746 | 0.00E+00 | 0.00E+00 |
| SCE1572_22 | sce_23 | 0.00E+00 | 0.00E+00 |
| SCE1572_2200 | sce_1747 | 3.00E-175 | 3.00E-175 |
| SCE1572_2201 | sce_1748 | 0.00E+00 | 0.00E+00 |
| SCE1572_2202 | sce_1749 | 7.00E-74 | 6.00E-82 |
| SCE1572_2203 | sce_1750 | 4.00E-149 | 2.00E-151 |
| SCE1572_2204 | sce_1751 | 3.00E-137 | 3.00E-129 |
| SCE1572_2205 | sce_1752 | 3.00E-36 | 3.00E-36 |
| SCE1572_2206 | sce_1753 | 2.00E-148 | 2.00E-141 |
| SCE1572_2207 | sce_1754 | 2.00E-58 | 1.00E-56 |
| SCE1572_2209 | sce_1755 | 1.00E-115 | 2.00E-121 |
| SCE1572_2210 | sce_1586 | 6.00E-24 | 5.00E-29 |
| SCE1572_2212 | sce_1756 | 3.00E-85 | 2.00E-53 |
| SCE1572_2215 | sce_1759 | 2.00E-141 | 5.00E-165 |
| SCE1572_2216 | sce_1760 | 6.00E-115 | 9.00E-123 |
| SCE1572_2218 | sce_1762 | 0.00E+00 | 0.00E+00 |
| SCE1572_222 | sce_10163 | 2.00E-124 | 2.00E-124 |
| SCE1572_2222 | sce_1765 | 3.00E-36 | 2.00E-29 |
| SCE1572_2223 | sce_1766 | 3.00E-119 | 8.00E-121 |
| SCE1572_2226 | sce_1775 | 4.00E-76 | 2.00E-64 |
| SCE1572_2227 | sce_1103 | 1.00E-118 | 1.00E-115 |
| SCE1572_2228 | sce_1776 | 0.00E+00 | 0.00E+00 |
| SCE1572_2229 | sce_1777 | 2.00E-64 | 7.00E-65 |
| SCE1572_223 | sce_9852 | 6.00E-109 | 2.00E-117 |
| SCE1572_2230 | sce_1778 | 0.00E+00 | 0.00E+00 |
| SCE1572_2231 | sce_1779 | 4.00E-95 | 4.00E-95 |
| SCE1572_2232 | sce_1780 | 2.00E-65 | 2.00E-65 |
| SCE1572_2233 | sce_1781 | 0.00E+00 | 0.00E+00 |
| SCE1572_2234 | sce_1782 | 2.00E-150 | 5.00E-133 |
| SCE1572_2235 | sce_1783 | 0.00E+00 | 4.00E-178 |
| SCE1572_2236 | sce_1784 | 0.00E+00 | 0.00E+00 |
| SCE1572_2237 | sce_1785 | 8.00E-56 | 9.00E-56 |
| SCE1572_2238 | sce_1786 | 3.00E-163 | 2.00E-172 |
| SCE1572_2239 | sce_1787 | 3.00E-125 | 7.00E-136 |
| SCE1572_224 | sce_9851 | 3.00E-115 | 1.00E-123 |
| SCE1572_2242 | sce_1794 | 2.00E-104 | 5.00E-114 |
| SCE1572_2246 | sce_1793 | 8.00E-33 | 5.00E-32 |
| SCE1572_2249 | sce_1790 | 3.00E-62 | 1.00E-67 |
| SCE1572_2251 | sce_1796 | 2.00E-35 | 7.00E-32 |
| SCE1572_2252 | sce_1797 | 3.00E-163 | 2.00E-162 |
| SCE1572_2253 | sce_1798 | 5.00E-156 | 2.00E-165 |
| SCE1572_2254 | sce_1799 | 2.00E-122 | 2.00E-150 |
| SCE1572_2255 | sce_1800 | 2.00E-80 | 2.00E-80 |
| SCE1572_2256 | sce_1801 | 0.00E+00 | 0.00E+00 |
| SCE1572_2258 | sce_1803 | 0.00E+00 | 0.00E+00 |
| SCE1572_2258 | sce_5403 | 0.00E+00 | 0.00E+00 |
| SCE1572_2258 | sce_5226 | 0.00E+00 | 0.00E+00 |
| SCE1572_2258 | sce_7154 | 0.00E+00 | 0.00E+00 |
| SCE1572_2258 | sce_7969 | 0.00E+00 | 0.00E+00 |
| SCE1572_2258 | sce_4073 | 0.00E+00 | 0.00E+00 |
| SCE1572_2258 | sce_9665 | 0.00E+00 | 0.00E+00 |
| SCE1572_2258 | sce_5751 | 0.00E+00 | 0.00E+00 |
| SCE1572_2258 | sce_2053 | 0.00E+00 | 0.00E+00 |
| SCE1572_2258 | sce_9954 | 0.00E+00 | 0.00E+00 |
| SCE1572_2258 | sce_9757 | 0.00E+00 | 0.00E+00 |
| SCE1572_2258 | sce_5746 | 0.00E+00 | 0.00E+00 |
| SCE1572_2258 | sce_3491 | 0.00E+00 | 0.00E+00 |
| SCE1572_2259 | sce_1804 | 3.00E-106 | 2.00E-98 |
| SCE1572_226 | sce_2494 | 1.00E-54 | 9.00E-50 |
| SCE1572_2261 | sce_1805 | 0.00E+00 | 0.00E+00 |
| SCE1572_2262 | sce_1806 | 0.00E+00 | 0.00E+00 |
| SCE1572_2263 | sce_1807 | 1.00E-141 | 8.00E-133 |
| SCE1572_2264 | sce_1808 | 7.00E-71 | 8.00E-64 |
| SCE1572_2265 | sce_1809 | 4.00E-91 | 5.00E-84 |
| SCE1572_2266 | sce_1810 | 2.00E-172 | 0.00E+00 |
| SCE1572_2267 | sce_1811 | 5.00E-125 | 2.00E-134 |
| SCE1572_2268 | sce_1812 | 0.00E+00 | 0.00E+00 |
| SCE1572_2269 | sce_1813 | 1.00E-151 | 3.00E-163 |
| SCE1572_2270 | sce_1814 | 0.00E+00 | 0.00E+00 |
| SCE1572_2270 | sce_9222 | 0.00E+00 | 0.00E+00 |
| SCE1572_2270 | sce_3148 | 0.00E+00 | 0.00E+00 |

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|--------------|-----------|-----------|-----------|
| SCE1572_2271 | sce_1815 | 1.00E-163 | 4.00E-166 |
| SCE1572_2272 | sce_1817 | 0.00E+00 | 0.00E+00 |
| SCE1572_2273 | sce_1818 | 3.00E-45 | 5.00E-60 |
| SCE1572_2274 | sce_1819 | 8.00E-31 | 4.00E-39 |
| SCE1572_2275 | sce_1820 | 0.00E+00 | 0.00E+00 |
| SCE1572_2276 | sce_1821 | 0.00E+00 | 0.00E+00 |
| SCE1572_2277 | sce_1822 | 0.00E+00 | 0.00E+00 |
| SCE1572_2278 | sce_1823 | 4.00E-127 | 1.00E-134 |
| SCE1572_2279 | sce_1824 | 0.00E+00 | 0.00E+00 |
| SCE1572_2280 | sce_1826 | 0.00E+00 | 0.00E+00 |
| SCE1572_2281 | sce_1827 | 1.00E-100 | 5.00E-91 |
| SCE1572_2282 | sce_1828 | 1.00E-104 | 1.00E-108 |
| SCE1572_2283 | sce_1829 | 0.00E+00 | 0.00E+00 |
| SCE1572_2284 | sce_1831 | 4.00E-49 | 5.00E-49 |
| SCE1572_2285 | sce_1832 | 2.00E-38 | 2.00E-38 |
| SCE1572_2286 | sce_1833 | 4.00E-66 | 1.00E-65 |
| SCE1572_2287 | sce_1834 | 2.00E-68 | 2.00E-68 |
| SCE1572_2288 | sce_1835 | 6.00E-136 | 1.00E-126 |
| SCE1572_2289 | sce_1836 | 7.00E-27 | 7.00E-27 |
| SCE1572_2290 | sce_1837 | 3.00E-72 | 4.00E-82 |
| SCE1572_2291 | sce_1838 | 0.00E+00 | 0.00E+00 |
| SCE1572_2292 | sce_1840 | 2.00E-65 | 2.00E-65 |
| SCE1572_2293 | sce_1841 | 0.00E+00 | 2.00E-178 |
| SCE1572_2294 | sce_1842 | 0.00E+00 | 0.00E+00 |
| SCE1572_2296 | sce_1843 | 9.00E-162 | 2.00E-164 |
| SCE1572_2297 | sce_1844 | 3.00E-75 | 3.00E-48 |
| SCE1572_2298 | sce_1845 | 6.00E-71 | 5.00E-71 |
| SCE1572_2299 | sce_1846 | 2.00E-85 | 1.00E-85 |
| SCE1572_23 | sce_24 | 2.00E-130 | 2.00E-125 |
| SCE1572_230 | sce_3089 | 2.00E-21 | 1.00E-21 |
| SCE1572_2300 | sce_1847 | 9.00E-128 | 2.00E-122 |
| SCE1572_2301 | sce_1848 | 3.00E-32 | 3.00E-33 |
| SCE1572_2302 | sce_1849 | 0.00E+00 | 0.00E+00 |
| SCE1572_2303 | sce_1850 | 0.00E+00 | 0.00E+00 |
| SCE1572_2304 | sce_1851 | 5.00E-169 | 2.00E-170 |
| SCE1572_2305 | sce_1852 | 3.00E-168 | 2.00E-164 |
| SCE1572_2306 | sce_1853 | 5.00E-157 | 5.00E-162 |
| SCE1572_2307 | sce_1854 | 3.00E-118 | 1.00E-124 |
| SCE1572_2308 | sce_1855 | 0.00E+00 | 0.00E+00 |
| SCE1572_2309 | sce_1856 | 1.00E-121 | 1.00E-125 |
| SCE1572_2310 | sce_1857 | 0.00E+00 | 0.00E+00 |
| SCE1572_2311 | sce_1858 | 0.00E+00 | 0.00E+00 |
| SCE1572_2312 | sce_1859 | 5.00E-173 | 3.00E-173 |
| SCE1572_2313 | sce_1860 | 6.00E-138 | 5.00E-140 |
| SCE1572_2314 | sce_1861 | 6.00E-93 | 7.00E-89 |
| SCE1572_2315 | sce_1862 | 1.00E-15 | 1.00E-15 |
| SCE1572_2316 | sce_1863 | 6.00E-170 | 0.00E+00 |
| SCE1572_2317 | sce_1864 | 1.00E-63 | 6.00E-63 |
| SCE1572_2318 | sce_1865 | 2.00E-40 | 2.00E-40 |
| SCE1572_2319 | sce_1866 | 6.00E-101 | 9.00E-113 |
| SCE1572_2320 | sce_1867 | 2.00E-109 | 4.00E-129 |
| SCE1572_2321 | sce_1868 | 8.00E-61 | 7.00E-61 |
| SCE1572_2322 | sce_1869 | 6.00E-109 | 3.00E-119 |
| SCE1572_2323 | sce_1870 | 0.00E+00 | 0.00E+00 |
| SCE1572_2324 | sce_1871 | 1.00E-56 | 2.00E-56 |
| SCE1572_2325 | sce_1872 | 6.00E-138 | 1.00E-151 |
| SCE1572_2326 | sce_1873 | 1.00E-96 | 2.00E-103 |
| SCE1572_2327 | sce_1875 | 0.00E+00 | 0.00E+00 |
| SCE1572_2328 | sce_1877 | 3.00E-146 | 3.00E-151 |
| SCE1572_2329 | sce_1878 | 0.00E+00 | 0.00E+00 |
| SCE1572_2330 | sce_1879 | 0.00E+00 | 0.00E+00 |
| SCE1572_2331 | sce_10208 | 1.00E-41 | 6.00E-41 |
| SCE1572_2332 | sce_10207 | 5.00E-100 | 3.00E-104 |
| SCE1572_2333 | sce_1883 | 0.00E+00 | 0.00E+00 |
| SCE1572_2335 | sce_1885 | 1.00E-112 | 3.00E-128 |
| SCE1572_2336 | sce_1886 | 2.00E-158 | 0.00E+00 |
| SCE1572_2337 | sce_1887 | 7.00E-59 | 3.00E-45 |
| SCE1572_2338 | sce_1888 | 3.00E-120 | 5.00E-139 |
| SCE1572_2339 | sce_1889 | 3.00E-88 | 1.00E-90 |
| SCE1572_234 | sce_5301 | 4.00E-44 | 3.00E-45 |
| SCE1572_2341 | sce_1890 | 7.00E-69 | 5.00E-76 |
| SCE1572_2342 | sce_1891 | 2.00E-34 | 2.00E-34 |
| SCE1572_2343 | sce_1893 | 1.00E-72 | 1.00E-72 |
| SCE1572_2344 | sce_1894 | 0.00E+00 | 0.00E+00 |
| SCE1572_2345 | sce_1895 | 1.00E-80 | 2.00E-80 |
| SCE1572_2346 | sce_1896 | 7.00E-69 | 6.00E-69 |

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|--------------|-----------|-----------|-----------|
| SCE1572_2347 | sce_1897 | 9.00E-98 | 9.00E-98 |
| SCE1572_2348 | sce_1898 | 2.00E-125 | 6.00E-125 |
| SCE1572_2349 | sce_1899 | 1.00E-144 | 2.00E-142 |
| SCE1572_235 | sce_5302 | 4.00E-38 | 4.00E-38 |
| SCE1572_2351 | sce_1902 | 0.00E+00 | 0.00E+00 |
| SCE1572_2352 | sce_1903 | 1.00E-75 | 1.00E-78 |
| SCE1572_2353 | sce_1904 | 1.00E-37 | 3.00E-51 |
| SCE1572_2354 | sce_1905 | 2.00E-109 | 2.00E-109 |
| SCE1572_2355 | sce_1906 | 1.00E-128 | 2.00E-118 |
| SCE1572_2356 | sce_1907 | 0.00E+00 | 0.00E+00 |
| SCE1572_2357 | sce_1908 | 4.00E-91 | 4.00E-91 |
| SCE1572_2358 | sce_1909 | 6.00E-125 | 2.00E-125 |
| SCE1572_2359 | sce_1910 | 4.00E-121 | 2.00E-133 |
| SCE1572_2361 | sce_1912 | 0.00E+00 | 0.00E+00 |
| SCE1572_2362 | sce_1913 | 0.00E+00 | 0.00E+00 |
| SCE1572_2363 | sce_1914 | 7.00E-52 | 3.00E-60 |
| SCE1572_2364 | sce_1915 | 5.00E-16 | 1.00E-21 |
| SCE1572_2365 | sce_1916 | 2.00E-110 | 6.00E-94 |
| SCE1572_2366 | sce_1917 | 0.00E+00 | 0.00E+00 |
| SCE1572_2368 | sce_1918 | 1.00E-94 | 1.00E-98 |
| SCE1572_2369 | sce_1919 | 6.00E-27 | 1.00E-27 |
| SCE1572_237 | sce_5613 | 2.00E-23 | 1.00E-23 |
| SCE1572_2370 | sce_1920 | 2.00E-159 | 0.00E+00 |
| SCE1572_2371 | sce_1921 | 0.00E+00 | 0.00E+00 |
| SCE1572_2372 | sce_1922 | 0.00E+00 | 0.00E+00 |
| SCE1572_2373 | sce_1923 | 2.00E-41 | 5.00E-37 |
| SCE1572_2374 | sce_1925 | 2.00E-54 | 2.00E-54 |
| SCE1572_2375 | sce_1926 | 2.00E-45 | 2.00E-45 |
| SCE1572_2376 | sce_1927 | 0.00E+00 | 0.00E+00 |
| SCE1572_2377 | sce_1928 | 2.00E-32 | 6.00E-58 |
| SCE1572_2378 | sce_1929 | 2.00E-51 | 2.00E-51 |
| SCE1572_2379 | sce_1930 | 1.00E-91 | 3.00E-91 |
| SCE1572_238 | sce_5612 | 2.00E-12 | 2.00E-12 |
| SCE1572_2380 | sce_1931 | 1.00E-101 | 5.00E-88 |
| SCE1572_2381 | sce_1932 | 0.00E+00 | 0.00E+00 |
| SCE1572_2382 | sce_1933 | 2.00E-133 | 3.00E-136 |
| SCE1572_2383 | sce_1935 | 1.00E-143 | 1.00E-138 |
| SCE1572_2384 | sce_1937 | 8.00E-93 | 1.00E-93 |
| SCE1572_2385 | sce_1938 | 0.00E+00 | 0.00E+00 |
| SCE1572_2386 | sce_1939 | 0.00E+00 | 0.00E+00 |
| SCE1572_2387 | sce_1940 | 0.00E+00 | 0.00E+00 |
| SCE1572_2389 | sce_1941 | 9.00E-35 | 3.00E-31 |
| SCE1572_2390 | sce_1942 | 0.00E+00 | 0.00E+00 |
| SCE1572_2392 | sce_1945 | 0.00E+00 | 0.00E+00 |
| SCE1572_2393 | sce_1946 | 1.00E-155 | 3.00E-154 |
| SCE1572_2394 | sce_1947 | 0.00E+00 | 0.00E+00 |
| SCE1572_2395 | sce_1948 | 0.00E+00 | 0.00E+00 |
| SCE1572_2396 | sce_1950 | 4.00E-96 | 5.00E-119 |
| SCE1572_2397 | sce_1951 | 1.00E-24 | 1.00E-24 |
| SCE1572_2398 | sce_1952 | 2.00E-54 | 2.00E-49 |
| SCE1572_2399 | sce_1953 | 8.00E-78 | 8.00E-78 |
| SCE1572_24 | sce_25 | 0.00E+00 | 0.00E+00 |
| SCE1572_2400 | sce_1954 | 0.00E+00 | 0.00E+00 |
| SCE1572_2401 | sce_1955 | 2.00E-80 | 2.00E-79 |
| SCE1572_2402 | sce_1956 | 5.00E-70 | 5.00E-70 |
| SCE1572_2403 | sce_1957 | 2.00E-79 | 4.00E-78 |
| SCE1572_2404 | sce_1958 | 7.00E-94 | 2.00E-101 |
| SCE1572_2405 | sce_1959 | 0.00E+00 | 0.00E+00 |
| SCE1572_2406 | sce_1960 | 2.00E-150 | 4.00E-142 |
| SCE1572_2407 | sce_1961 | 4.00E-165 | 1.00E-160 |
| SCE1572_2408 | sce_1962 | 3.00E-108 | 1.00E-107 |
| SCE1572_2409 | sce_1963 | 3.00E-68 | 3.00E-68 |
| SCE1572_241 | sce_10193 | 0.00E+00 | 0.00E+00 |
| SCE1572_241 | sce_3499 | 0.00E+00 | 0.00E+00 |
| SCE1572_241 | sce_8817 | 0.00E+00 | 0.00E+00 |
| SCE1572_2410 | sce_1964 | 9.00E-174 | 9.00E-174 |
| SCE1572_2411 | sce_1965 | 3.00E-113 | 1.00E-118 |
| SCE1572_2412 | sce_1966 | 0.00E+00 | 0.00E+00 |
| SCE1572_2413 | sce_1967 | 3.00E-84 | 3.00E-84 |
| SCE1572_2414 | sce_1968 | 0.00E+00 | 0.00E+00 |
| SCE1572_2415 | sce_1969 | 2.00E-21 | 1.00E-24 |
| SCE1572_2416 | sce_1970 | 7.00E-17 | 2.00E-14 |
| SCE1572_2418 | sce_1971 | 2.00E-41 | 2.00E-39 |
| SCE1572_2419 | sce_1973 | 0.00E+00 | 0.00E+00 |
| SCE1572_2420 | sce_1974 | 0.00E+00 | 0.00E+00 |
| SCE1572_2421 | sce_1975 | 2.00E-113 | 4.00E-118 |

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|--------------|----------|-----------|-----------|
| SCE1572_2423 | sce_1976 | 2.00E-43 | 1.00E-43 |
| SCE1572_2424 | sce_1977 | 1.00E-159 | 2.00E-159 |
| SCE1572_2425 | sce_1978 | 0.00E+00 | 0.00E+00 |
| SCE1572_2426 | sce_1979 | 3.00E-146 | 3.00E-146 |
| SCE1572_2427 | sce_1980 | 0.00E+00 | 0.00E+00 |
| SCE1572_2428 | sce_1981 | 2.00E-69 | 3.00E-69 |
| SCE1572_2429 | sce_1982 | 3.00E-76 | 3.00E-76 |
| SCE1572_2430 | sce_1983 | 0.00E+00 | 0.00E+00 |
| SCE1572_2431 | sce_1985 | 7.00E-79 | 4.00E-67 |
| SCE1572_2432 | sce_1986 | 6.00E-169 | 7.00E-171 |
| SCE1572_2433 | sce_1987 | 4.00E-102 | 1.00E-104 |
| SCE1572_2434 | sce_1988 | 0.00E+00 | 0.00E+00 |
| SCE1572_2435 | sce_1989 | 7.00E-156 | 1.00E-153 |
| SCE1572_2436 | sce_1990 | 3.00E-88 | 6.00E-93 |
| SCE1572_2437 | sce_1991 | 2.00E-42 | 8.00E-45 |
| SCE1572_2438 | sce_1992 | 1.00E-136 | 1.00E-135 |
| SCE1572_2439 | sce_1993 | 3.00E-115 | 2.00E-127 |
| SCE1572_244 | sce_8398 | 5.00E-73 | 3.00E-82 |
| SCE1572_2440 | sce_1994 | 0.00E+00 | 0.00E+00 |
| SCE1572_2441 | sce_1995 | 0.00E+00 | 0.00E+00 |
| SCE1572_2442 | sce_1997 | 4.00E-81 | 2.00E-75 |
| SCE1572_2443 | sce_8759 | 3.00E-18 | 3.00E-17 |
| SCE1572_2444 | sce_1996 | 3.00E-112 | 7.00E-100 |
| SCE1572_2446 | sce_1998 | 0.00E+00 | 0.00E+00 |
| SCE1572_245 | sce_513 | 7.00E-52 | 3.00E-62 |
| SCE1572_2453 | sce_1999 | 0.00E+00 | 0.00E+00 |
| SCE1572_2454 | sce_2000 | 8.00E-148 | 2.00E-162 |
| SCE1572_2455 | sce_2001 | 5.00E-177 | 2.00E-180 |
| SCE1572_2456 | sce_2002 | 1.00E-60 | 2.00E-62 |
| SCE1572_2458 | sce_2003 | 4.00E-165 | 3.00E-169 |
| SCE1572_2459 | sce_2004 | 2.00E-100 | 2.00E-102 |
| SCE1572_2464 | sce_2005 | 0.00E+00 | 0.00E+00 |
| SCE1572_2466 | sce_2006 | 2.00E-162 | 4.00E-159 |
| SCE1572_2467 | sce_2007 | 0.00E+00 | 0.00E+00 |
| SCE1572_2468 | sce_2010 | 3.00E-148 | 3.00E-148 |
| SCE1572_2469 | sce_2011 | 9.00E-133 | 3.00E-112 |
| SCE1572_2471 | sce_2012 | 0.00E+00 | 0.00E+00 |
| SCE1572_2472 | sce_2013 | 4.00E-39 | 1.00E-52 |
| SCE1572_2473 | sce_2014 | 5.00E-75 | 1.00E-79 |
| SCE1572_2474 | sce_2015 | 1.00E-179 | 0.00E+00 |
| SCE1572_2475 | sce_2016 | 0.00E+00 | 0.00E+00 |
| SCE1572_2476 | sce_2017 | 1.00E-81 | 6.00E-89 |
| SCE1572_2477 | sce_2018 | 1.00E-137 | 1.00E-147 |
| SCE1572_2478 | sce_2019 | 7.00E-129 | 4.00E-118 |
| SCE1572_2479 | sce_2020 | 4.00E-69 | 4.00E-69 |
| SCE1572_2481 | sce_7593 | 3.00E-115 | 8.00E-109 |
| SCE1572_2482 | sce_2042 | 0.00E+00 | 0.00E+00 |
| SCE1572_2486 | sce_2056 | 1.00E-116 | 2.00E-132 |
| SCE1572_2487 | sce_2058 | 8.00E-129 | 3.00E-137 |
| SCE1572_2489 | sce_2059 | 3.00E-33 | 1.00E-37 |
| SCE1572_2490 | sce_2066 | 0.00E+00 | 0.00E+00 |
| SCE1572_2494 | sce_2073 | 4.00E-180 | 0.00E+00 |
| SCE1572_2495 | sce_2074 | 6.00E-113 | 5.00E-113 |
| SCE1572_2497 | sce_2075 | 0.00E+00 | 0.00E+00 |
| SCE1572_2499 | sce_2419 | 0.00E+00 | 0.00E+00 |
| SCE1572_25 | sce_27 | 5.00E-83 | 2.00E-69 |
| SCE1572_2500 | sce_2418 | 2.00E-134 | 9.00E-119 |
| SCE1572_2503 | sce_7548 | 2.00E-157 | 6.00E-161 |
| SCE1572_2504 | sce_3033 | 2.00E-69 | 2.00E-69 |
| SCE1572_2505 | sce_3034 | 3.00E-113 | 1.00E-113 |
| SCE1572_251 | sce_7318 | 0.00E+00 | 0.00E+00 |
| SCE1572_251 | sce_1116 | 0.00E+00 | 0.00E+00 |
| SCE1572_251 | sce_5158 | 0.00E+00 | 0.00E+00 |
| SCE1572_2510 | sce_2355 | 4.00E-13 | 4.00E-10 |
| SCE1572_2511 | sce_2094 | 4.00E-135 | 5.00E-139 |
| SCE1572_2517 | sce_8744 | 1.00E-10 | 1.00E-10 |
| SCE1572_2519 | sce_2437 | 0.00E+00 | 0.00E+00 |
| SCE1572_2520 | sce_2097 | 1.00E-150 | 2.00E-160 |
| SCE1572_2521 | sce_2098 | 9.00E-89 | 1.00E-98 |
| SCE1572_2522 | sce_2099 | 2.00E-93 | 2.00E-113 |
| SCE1572_2524 | sce_2100 | 9.00E-57 | 1.00E-79 |
| SCE1572_2525 | sce_2101 | 0.00E+00 | 0.00E+00 |
| SCE1572_2526 | sce_2102 | 2.00E-138 | 6.00E-117 |
| SCE1572_2527 | sce_3701 | 9.00E-99 | 9.00E-100 |
| SCE1572_253 | sce_5453 | 5.00E-44 | 7.00E-40 |
| SCE1572_2537 | sce_2104 | 2.00E-73 | 4.00E-67 |

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| SCE1572_2538 | sce_2118 | 0.00E+00 | 1.00E-179 |
| SCE1572_2539 | sce_2119 | 0.00E+00 | 0.00E+00 |
| SCE1572_2543 | sce_2126 | 8.00E-52 | 2.00E-61 |
| SCE1572_2544 | sce_5086 | 0.00E+00 | 0.00E+00 |
| SCE1572_2544 | sce_5085 | 0.00E+00 | 0.00E+00 |
| SCE1572_2544 | sce_6701 | 0.00E+00 | 0.00E+00 |
| SCE1572_2547 | sce_2128 | 0.00E+00 | 0.00E+00 |
| SCE1572_255 | sce_8414 | 2.00E-22 | 2.00E-26 |
| SCE1572_2551 | sce_2130 | 0.00E+00 | 0.00E+00 |
| SCE1572_2553 | sce_2131 | 0.00E+00 | 0.00E+00 |
| SCE1572_2554 | sce_2132 | 0.00E+00 | 0.00E+00 |
| SCE1572_2555 | sce_2133 | 3.00E-93 | 9.00E-101 |
| SCE1572_2557 | sce_8817 | 0.00E+00 | 0.00E+00 |
| SCE1572_256 | sce_8408 | 6.00E-15 | 3.00E-16 |
| SCE1572_2560 | sce_2134 | 2.00E-30 | 7.00E-40 |
| SCE1572_2561 | sce_2135 | 1.00E-147 | 8.00E-137 |
| SCE1572_2562 | sce_2136 | 0.00E+00 | 0.00E+00 |
| SCE1572_2563 | sce_2137 | 4.00E-122 | 1.00E-122 |
| SCE1572_2564 | sce_2138 | 9.00E-40 | 7.00E-35 |
| SCE1572_2567 | sce_2139 | 0.00E+00 | 0.00E+00 |
| SCE1572_2568 | sce_2140 | 5.00E-22 | 7.00E-31 |
| SCE1572_2570 | sce_2143 | 2.00E-23 | 2.00E-23 |
| SCE1572_2573 | sce_2144 | 8.00E-99 | 2.00E-104 |
| SCE1572_2574 | sce_2145 | 2.00E-74 | 8.00E-64 |
| SCE1572_2575 | sce_2146 | 0.00E+00 | 0.00E+00 |
| SCE1572_2577 | sce_2148 | 2.00E-159 | 8.00E-153 |
| SCE1572_2578 | sce_2156 | 0.00E+00 | 0.00E+00 |
| SCE1572_258 | sce_8407 | 6.00E-78 | 2.00E-75 |
| SCE1572_2581 | sce_2162 | 2.00E-58 | 3.00E-59 |
| SCE1572_2586 | sce_6226 | 0.00E+00 | 0.00E+00 |
| SCE1572_2587 | sce_6227 | 7.00E-29 | 1.00E-28 |
| SCE1572_2588 | sce_3750 | 0.00E+00 | 0.00E+00 |
| SCE1572_2588 | sce_6712 | 0.00E+00 | 0.00E+00 |
| SCE1572_2588 | sce_9954 | 0.00E+00 | 0.00E+00 |
| SCE1572_2588 | sce_5226 | 0.00E+00 | 0.00E+00 |
| SCE1572_2588 | sce_5751 | 0.00E+00 | 0.00E+00 |
| SCE1572_2589 | sce_6703 | 0.00E+00 | 0.00E+00 |
| SCE1572_259 | sce_8408 | 1.00E-15 | 3.00E-16 |
| SCE1572_2594 | sce_2174 | 0.00E+00 | 0.00E+00 |
| SCE1572_26 | sce_28 | 9.00E-157 | 0.00E+00 |
| SCE1572_260 | sce_6878 | 2.00E-87 | 8.00E-93 |
| SCE1572_2604 | sce_2186 | 1.00E-80 | 4.00E-74 |
| SCE1572_2605 | sce_2187 | 2.00E-137 | 1.00E-124 |
| SCE1572_2606 | sce_2188 | 1.00E-43 | 2.00E-42 |
| SCE1572_2608 | sce_2189 | 0.00E+00 | 0.00E+00 |
| SCE1572_2609 | sce_2190 | 7.00E-84 | 7.00E-84 |
| SCE1572_2610 | sce_2192 | 1.00E-124 | 1.00E-116 |
| SCE1572_2612 | sce_2195 | 0.00E+00 | 4.00E-125 |
| SCE1572_2613 | sce_2196 | 8.00E-63 | 3.00E-54 |
| SCE1572_2614 | sce_2199 | 1.00E-66 | 3.00E-55 |
| SCE1572_2615 | sce_2200 | 0.00E+00 | 0.00E+00 |
| SCE1572_2616 | sce_7835 | 1.00E-65 | 3.00E-49 |
| SCE1572_2617 | sce_2202 | 2.00E-38 | 1.00E-38 |
| SCE1572_2619 | sce_2204 | 0.00E+00 | 0.00E+00 |
| SCE1572_262 | sce_4682 | 2.00E-111 | 8.00E-96 |
| SCE1572_2620 | sce_3715 | 0.00E+00 | 0.00E+00 |
| SCE1572_2621 | sce_3716 | 0.00E+00 | 0.00E+00 |
| SCE1572_2624 | sce_5143 | 0.00E+00 | 0.00E+00 |
| SCE1572_2626 | sce_8582 | 2.00E-79 | 2.00E-83 |
| SCE1572_2627 | sce_5133 | 0.00E+00 | 0.00E+00 |
| SCE1572_2628 | sce_5134 | 0.00E+00 | 0.00E+00 |
| SCE1572_2629 | sce_5147 | 0.00E+00 | 0.00E+00 |
| SCE1572_2629 | sce_4662 | 0.00E+00 | 0.00E+00 |
| SCE1572_2630 | sce_4663 | 0.00E+00 | 0.00E+00 |
| SCE1572_2630 | sce_5148 | 0.00E+00 | 0.00E+00 |
| SCE1572_2631 | sce_5156 | 0.00E+00 | 0.00E+00 |
| SCE1572_2632 | sce_1664 | 0.00E+00 | 0.00E+00 |
| SCE1572_2632 | sce_5137 | 0.00E+00 | 0.00E+00 |
| SCE1572_2633 | sce_5137 | 0.00E+00 | 0.00E+00 |
| SCE1572_2633 | sce_1664 | 0.00E+00 | 0.00E+00 |
| SCE1572_2634 | sce_5138 | 0.00E+00 | 0.00E+00 |
| SCE1572_2634 | sce_1665 | 0.00E+00 | 0.00E+00 |
| SCE1572_2635 | sce_3717 | 1.00E-165 | 2.00E-162 |
| SCE1572_2636 | sce_3502 | 3.00E-97 | 1.00E-102 |
| SCE1572_2637 | sce_3712 | 0.00E+00 | 0.00E+00 |
| SCE1572_2638 | sce_3711 | 0.00E+00 | 0.00E+00 |

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| SCE1572_2639 | sce_3710 | 1.00E-124 | 1.00E-124 |
| SCE1572_264 | sce_1106 | 2.00E-39 | 1.00E-38 |
| SCE1572_2640 | sce_3709 | 2.00E-160 | 7.00E-155 |
| SCE1572_2641 | sce_3708 | 0.00E+00 | 0.00E+00 |
| SCE1572_2642 | sce_3707 | 4.00E-121 | 1.00E-135 |
| SCE1572_2643 | sce_3706 | 6.00E-129 | 2.00E-133 |
| SCE1572_2644 | sce_6530 | 0.00E+00 | 1.00E-174 |
| SCE1572_2647 | sce_6531 | 0.00E+00 | 0.00E+00 |
| SCE1572_2647 | sce_9918 | 0.00E+00 | 0.00E+00 |
| SCE1572_2647 | sce_894 | 0.00E+00 | 0.00E+00 |
| SCE1572_265 | sce_5651 | 1.00E-51 | 5.00E-55 |
| SCE1572_2652 | sce_9920 | 0.00E+00 | 0.00E+00 |
| SCE1572_2652 | sce_6535 | 0.00E+00 | 0.00E+00 |
| SCE1572_2652 | sce_3003 | 0.00E+00 | 0.00E+00 |
| SCE1572_2652 | sce_5835 | 0.00E+00 | 0.00E+00 |
| SCE1572_2652 | sce_10204 | 0.00E+00 | 0.00E+00 |
| SCE1572_2652 | sce_9557 | 0.00E+00 | 0.00E+00 |
| SCE1572_2652 | sce_7640 | 0.00E+00 | 0.00E+00 |
| SCE1572_2652 | sce_388 | 0.00E+00 | 0.00E+00 |
| SCE1572_2652 | sce_2065 | 0.00E+00 | 0.00E+00 |
| SCE1572_2652 | sce_4513 | 0.00E+00 | 0.00E+00 |
| SCE1572_2652 | sce_6092 | 0.00E+00 | 0.00E+00 |
| SCE1572_2652 | sce_7661 | 0.00E+00 | 0.00E+00 |
| SCE1572_2652 | sce_6107 | 0.00E+00 | 0.00E+00 |
| SCE1572_2652 | sce_8618 | 0.00E+00 | 0.00E+00 |
| SCE1572_2652 | sce_3085 | 0.00E+00 | 0.00E+00 |
| SCE1572_2652 | sce_6095 | 0.00E+00 | 0.00E+00 |
| SCE1572_2652 | sce_3917 | 0.00E+00 | 0.00E+00 |
| SCE1572_2653 | sce_2205 | 6.00E-110 | 5.00E-128 |
| SCE1572_2654 | sce_2206 | 3.00E-78 | 2.00E-84 |
| SCE1572_2655 | sce_2207 | 0.00E+00 | 0.00E+00 |
| SCE1572_2656 | sce_2208 | 0.00E+00 | 0.00E+00 |
| SCE1572_2656 | sce_3055 | 0.00E+00 | 6.00E-166 |
| SCE1572_2657 | sce_2209 | 5.00E-129 | 4.00E-137 |
| SCE1572_2658 | sce_2210 | 0.00E+00 | 0.00E+00 |
| SCE1572_2659 | sce_2212 | 0.00E+00 | 0.00E+00 |
| SCE1572_2661 | sce_2213 | 7.00E-105 | 1.00E-88 |
| SCE1572_2662 | sce_2214 | 6.00E-45 | 2.00E-44 |
| SCE1572_2663 | sce_2215 | 4.00E-30 | 3.00E-39 |
| SCE1572_2664 | sce_2216 | 4.00E-124 | 2.00E-124 |
| SCE1572_2665 | sce_2217 | 6.00E-107 | 6.00E-107 |
| SCE1572_2669 | sce_2218 | 0.00E+00 | 0.00E+00 |
| SCE1572_2670 | sce_2219 | 0.00E+00 | 0.00E+00 |
| SCE1572_2671 | sce_2220 | 4.00E-136 | 8.00E-132 |
| SCE1572_2672 | sce_2221 | 3.00E-96 | 4.00E-113 |
| SCE1572_2673 | sce_2222 | 0.00E+00 | 0.00E+00 |
| SCE1572_2674 | sce_2223 | 0.00E+00 | 0.00E+00 |
| SCE1572_2675 | sce_2224 | 2.00E-162 | 1.00E-156 |
| SCE1572_2676 | sce_2225 | 4.00E-112 | 2.00E-112 |
| SCE1572_2677 | sce_2226 | 1.00E-70 | 1.00E-72 |
| SCE1572_2678 | sce_2227 | 3.00E-41 | 6.00E-51 |
| SCE1572_2679 | sce_2228 | 1.00E-112 | 4.00E-102 |
| SCE1572_2688 | sce_2229 | 3.00E-54 | 4.00E-51 |
| SCE1572_2689 | sce_2230 | 4.00E-99 | 6.00E-99 |
| SCE1572_269 | sce_9355 | 7.00E-28 | 6.00E-28 |
| SCE1572_2691 | sce_2231 | 0.00E+00 | 0.00E+00 |
| SCE1572_2692 | sce_2232 | 2.00E-73 | 2.00E-73 |
| SCE1572_2693 | sce_2233 | 1.00E-140 | 0.00E+00 |
| SCE1572_2694 | sce_2234 | 1.00E-112 | 9.00E-107 |
| SCE1572_2695 | sce_2235 | 9.00E-76 | 4.00E-66 |
| SCE1572_27 | sce_29 | 8.00E-40 | 1.00E-39 |
| SCE1572_2700 | sce_1425 | 1.00E-20 | 4.00E-23 |
| SCE1572_2701 | sce_6712 | 0.00E+00 | 0.00E+00 |
| SCE1572_2701 | sce_3750 | 0.00E+00 | 0.00E+00 |
| SCE1572_2701 | sce_9954 | 0.00E+00 | 0.00E+00 |
| SCE1572_2701 | sce_5229 | 0.00E+00 | 0.00E+00 |
| SCE1572_2701 | sce_5226 | 0.00E+00 | 0.00E+00 |
| SCE1572_2701 | sce_9665 | 0.00E+00 | 0.00E+00 |
| SCE1572_2701 | sce_5403 | 0.00E+00 | 0.00E+00 |
| SCE1572_2701 | sce_5751 | 0.00E+00 | 0.00E+00 |
| SCE1572_2701 | sce_7154 | 0.00E+00 | 0.00E+00 |
| SCE1572_2702 | sce_2240 | 0.00E+00 | 0.00E+00 |
| SCE1572_2703 | sce_2241 | 4.00E-67 | 4.00E-67 |
| SCE1572_2704 | sce_2242 | 0.00E+00 | 0.00E+00 |
| SCE1572_2705 | sce_2243 | 5.00E-64 | 1.00E-56 |
| SCE1572_2706 | sce_2244 | 0.00E+00 | 0.00E+00 |

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| SCE1572_2706 | sce_2245 | 0.00E+00 | 0.00E+00 |
| SCE1572_2707 | sce_2246 | 4.00E-67 | 9.00E-66 |
| SCE1572_2708 | sce_2247 | 8.00E-148 | 3.00E-152 |
| SCE1572_2709 | sce_2248 | 2.00E-76 | 6.00E-87 |
| SCE1572_271 | sce_6076 | 0.00E+00 | 0.00E+00 |
| SCE1572_2710 | sce_2249 | 6.00E-75 | 8.00E-75 |
| SCE1572_2711 | sce_2250 | 1.00E-147 | 5.00E-151 |
| SCE1572_2712 | sce_2251 | 9.00E-65 | 3.00E-69 |
| SCE1572_2713 | sce_2252 | 2.00E-138 | 7.00E-133 |
| SCE1572_2714 | sce_2253 | 1.00E-94 | 2.00E-94 |
| SCE1572_2715 | sce_2254 | 0.00E+00 | 0.00E+00 |
| SCE1572_2716 | sce_2255 | 2.00E-126 | 6.00E-132 |
| SCE1572_2718 | sce_2256 | 0.00E+00 | 0.00E+00 |
| SCE1572_2719 | sce_2257 | 1.00E-53 | 1.00E-53 |
| SCE1572_2720 | sce_2258 | 0.00E+00 | 0.00E+00 |
| SCE1572_2721 | sce_2259 | 1.00E-82 | 4.00E-70 |
| SCE1572_2722 | sce_2260 | 0.00E+00 | 0.00E+00 |
| SCE1572_2723 | sce_2261 | 8.00E-67 | 1.00E-69 |
| SCE1572_2724 | sce_2262 | 4.00E-102 | 4.00E-122 |
| SCE1572_2725 | sce_2263 | 2.00E-160 | 1.00E-160 |
| SCE1572_2726 | sce_2264 | 3.00E-111 | 3.00E-111 |
| SCE1572_2727 | sce_2265 | 4.00E-114 | 2.00E-119 |
| SCE1572_2728 | sce_2266 | 3.00E-172 | 3.00E-176 |
| SCE1572_2729 | sce_2267 | 2.00E-149 | 2.00E-149 |
| SCE1572_273 | sce_9375 | 0.00E+00 | 0.00E+00 |
| SCE1572_2730 | sce_2268 | 2.00E-165 | 3.00E-177 |
| SCE1572_2731 | sce_2269 | 0.00E+00 | 0.00E+00 |
| SCE1572_2732 | sce_2270 | 8.00E-105 | 5.00E-106 |
| SCE1572_2733 | sce_2272 | 2.00E-92 | 3.00E-89 |
| SCE1572_2734 | sce_2273 | 2.00E-46 | 3.00E-46 |
| SCE1572_2735 | sce_2274 | 3.00E-107 | 2.00E-132 |
| SCE1572_2736 | sce_2275 | 1.00E-139 | 3.00E-134 |
| SCE1572_2737 | sce_2276 | 0.00E+00 | 0.00E+00 |
| SCE1572_2738 | sce_2277 | 2.00E-48 | 2.00E-43 |
| SCE1572_2739 | sce_2278 | 4.00E-139 | 2.00E-141 |
| SCE1572_2740 | sce_2279 | 2.00E-59 | 5.00E-67 |
| SCE1572_2741 | sce_2280 | 3.00E-21 | 1.00E-24 |
| SCE1572_2742 | sce_2281 | 2.00E-88 | 3.00E-88 |
| SCE1572_2743 | sce_2282 | 4.00E-163 | 4.00E-175 |
| SCE1572_2744 | sce_2283 | 4.00E-46 | 2.00E-52 |
| SCE1572_2745 | sce_2284 | 2.00E-116 | 6.00E-137 |
| SCE1572_2746 | sce_2285 | 8.00E-54 | 2.00E-62 |
| SCE1572_2747 | sce_2286 | 7.00E-72 | 6.00E-71 |
| SCE1572_2748 | sce_2287 | 0.00E+00 | 0.00E+00 |
| SCE1572_2749 | sce_2288 | 3.00E-153 | 7.00E-175 |
| SCE1572_275 | sce_8423 | 4.00E-111 | 4.00E-111 |
| SCE1572_2750 | sce_2289 | 1.00E-166 | 2.00E-166 |
| SCE1572_2751 | sce_2290 | 7.00E-144 | 5.00E-147 |
| SCE1572_2752 | sce_2291 | 1.00E-161 | 8.00E-157 |
| SCE1572_2754 | sce_2292 | 9.00E-81 | 4.00E-79 |
| SCE1572_2758 | sce_2304 | 0.00E+00 | 0.00E+00 |
| SCE1572_2759 | sce_2305 | 0.00E+00 | 0.00E+00 |
| SCE1572_2760 | sce_2306 | 3.00E-78 | 8.00E-70 |
| SCE1572_2761 | sce_2307 | 4.00E-103 | 1.00E-99 |
| SCE1572_2763 | sce_2308 | 0.00E+00 | 0.00E+00 |
| SCE1572_2765 | sce_2310 | 7.00E-51 | 4.00E-76 |
| SCE1572_2766 | sce_2311 | 3.00E-116 | 3.00E-116 |
| SCE1572_2767 | sce_2312 | 4.00E-56 | 7.00E-69 |
| SCE1572_2768 | sce_2313 | 2.00E-54 | 5.00E-55 |
| SCE1572_2769 | sce_2314 | 1.00E-38 | 7.00E-61 |
| SCE1572_2770 | sce_4153 | 3.00E-21 | 3.00E-19 |
| SCE1572_2771 | sce_7299 | 2.00E-25 | 1.00E-25 |
| SCE1572_2774 | sce_7302 | 6.00E-125 | 1.00E-119 |
| SCE1572_2777 | sce_10401 | 0.00E+00 | 0.00E+00 |
| SCE1572_2781 | sce_2367 | 2.00E-57 | 3.00E-54 |
| SCE1572_2782 | sce_2368 | 0.00E+00 | 0.00E+00 |
| SCE1572_2783 | sce_2369 | 2.00E-80 | 8.00E-83 |
| SCE1572_2784 | sce_5173 | 6.00E-157 | 3.00E-169 |
| SCE1572_2787 | sce_2372 | 8.00E-28 | 2.00E-29 |
| SCE1572_2788 | sce_2375 | 5.00E-48 | 5.00E-48 |
| SCE1572_2789 | sce_2376 | 7.00E-52 | 2.00E-49 |
| SCE1572_2790 | sce_2381 | 6.00E-75 | 3.00E-75 |
| SCE1572_2792 | sce_2439 | 0.00E+00 | 0.00E+00 |
| SCE1572_2795 | sce_2451 | 4.00E-48 | 4.00E-48 |
| SCE1572_2796 | sce_2449 | 2.00E-50 | 3.00E-46 |
| SCE1572_2797 | sce_1364 | 0.00E+00 | 0.00E+00 |

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| SCE1572_2798 | sce_1365 | 1.00E-71 | 2.00E-69 |
| SCE1572_2799 | sce_2462 | 5.00E-109 | 3.00E-111 |
| SCE1572_28 | sce_30 | 9.00E-74 | 5.00E-90 |
| SCE1572_2800 | sce_1367 | 0.00E+00 | 0.00E+00 |
| SCE1572_2803 | sce_6975 | 3.00E-82 | 2.00E-91 |
| SCE1572_2804 | sce_2463 | 0.00E+00 | 0.00E+00 |
| SCE1572_2805 | sce_2465 | 0.00E+00 | 0.00E+00 |
| SCE1572_2806 | sce_4688 | 4.00E-138 | 2.00E-130 |
| SCE1572_281 | sce_6002 | 0.00E+00 | 0.00E+00 |
| SCE1572_2813 | sce_10023 | 2.00E-86 | 2.00E-86 |
| SCE1572_2814 | sce_7618 | 0.00E+00 | 0.00E+00 |
| SCE1572_2815 | sce_4673 | 7.00E-128 | 2.00E-132 |
| SCE1572_2820 | sce_7859 | 9.00E-172 | 0.00E+00 |
| SCE1572_2821 | sce_7860 | 1.00E-177 | 2.00E-176 |
| SCE1572_2824 | sce_6417 | 0.00E+00 | 0.00E+00 |
| SCE1572_2825 | sce_1113 | 6.00E-147 | 8.00E-137 |
| SCE1572_2826 | sce_1112 | 3.00E-103 | 5.00E-98 |
| SCE1572_2827 | sce_1111 | 6.00E-39 | 8.00E-47 |
| SCE1572_2829 | sce_1110 | 1.00E-23 | 1.00E-23 |
| SCE1572_283 | sce_1702 | 9.00E-83 | 4.00E-80 |
| SCE1572_2835 | sce_521 | 2.00E-14 | 2.00E-14 |
| SCE1572_2836 | sce_520 | 3.00E-09 | 4.00E-09 |
| SCE1572_284 | sce_9986 | 5.00E-93 | 2.00E-98 |
| SCE1572_2846 | sce_514 | 6.00E-29 | 4.00E-35 |
| SCE1572_2848 | sce_10371 | 0.00E+00 | 0.00E+00 |
| SCE1572_2850 | sce_10151 | 1.00E-101 | 1.00E-101 |
| SCE1572_2858 | sce_10022 | 2.00E-126 | 6.00E-118 |
| SCE1572_2872 | sce_2416 | 3.00E-14 | 3.00E-31 |
| SCE1572_2873 | sce_1277 | 1.00E-68 | 5.00E-68 |
| SCE1572_2875 | sce_2477 | 6.00E-133 | 1.00E-129 |
| SCE1572_2876 | sce_2478 | 0.00E+00 | 0.00E+00 |
| SCE1572_2877 | sce_2483 | 2.00E-32 | 1.00E-30 |
| SCE1572_2878 | sce_2484 | 0.00E+00 | 0.00E+00 |
| SCE1572_288 | sce_6683 | 2.00E-53 | 3.00E-57 |
| SCE1572_2883 | sce_2505 | 6.00E-61 | 5.00E-61 |
| SCE1572_2884 | sce_2506 | 2.00E-139 | 2.00E-139 |
| SCE1572_2885 | sce_2507 | 3.00E-166 | 2.00E-174 |
| SCE1572_2886 | sce_2508 | 0.00E+00 | 0.00E+00 |
| SCE1572_2887 | sce_2510 | 1.00E-14 | 7.00E-25 |
| SCE1572_2888 | sce_2511 | 9.00E-166 | 2.00E-166 |
| SCE1572_2895 | sce_2512 | 7.00E-128 | 1.00E-118 |
| SCE1572_2897 | sce_2548 | 3.00E-91 | 4.00E-83 |
| SCE1572_2899 | sce_2549 | 6.00E-172 | 3.00E-159 |
| SCE1572_29 | sce_31 | 2.00E-106 | 2.00E-106 |
| SCE1572_2912 | sce_7637 | 0.00E+00 | 0.00E+00 |
| SCE1572_2912 | sce_389 | 0.00E+00 | 0.00E+00 |
| SCE1572_2912 | sce_2666 | 0.00E+00 | 0.00E+00 |
| SCE1572_2912 | sce_9231 | 0.00E+00 | 0.00E+00 |
| SCE1572_2912 | sce_9237 | 0.00E+00 | 0.00E+00 |
| SCE1572_2913 | sce_7637 | 0.00E+00 | 0.00E+00 |
| SCE1572_2913 | sce_9231 | 0.00E+00 | 0.00E+00 |
| SCE1572_2913 | sce_389 | 0.00E+00 | 0.00E+00 |
| SCE1572_2913 | sce_9230 | 0.00E+00 | 0.00E+00 |
| SCE1572_2913 | sce_2666 | 0.00E+00 | 0.00E+00 |
| SCE1572_2913 | sce_9237 | 0.00E+00 | 0.00E+00 |
| SCE1572_2914 | sce_7637 | 0.00E+00 | 0.00E+00 |
| SCE1572_2914 | sce_389 | 0.00E+00 | 0.00E+00 |
| SCE1572_2914 | sce_2666 | 0.00E+00 | 0.00E+00 |
| SCE1572_2914 | sce_9230 | 0.00E+00 | 0.00E+00 |
| SCE1572_2914 | sce_9237 | 0.00E+00 | 0.00E+00 |
| SCE1572_2914 | sce_9231 | 0.00E+00 | 0.00E+00 |
| SCE1572_2915 | sce_4641 | 0.00E+00 | 0.00E+00 |
| SCE1572_2916 | sce_6296 | 4.00E-128 | 7.00E-128 |
| SCE1572_2917 | sce_2550 | 5.00E-132 | 1.00E-109 |
| SCE1572_2926 | sce_6392 | 2.00E-36 | 2.00E-29 |
| SCE1572_2932 | sce_2553 | 0.00E+00 | 0.00E+00 |
| SCE1572_2934 | sce_2554 | 3.00E-129 | 6.00E-148 |
| SCE1572_2935 | sce_2555 | 2.00E-14 | 6.00E-10 |
| SCE1572_2936 | sce_2556 | 1.00E-35 | 6.00E-36 |
| SCE1572_2950 | sce_7501 | 6.00E-08 | 8.00E-08 |
| SCE1572_2954 | sce_3808 | 1.00E-69 | 1.00E-70 |
| SCE1572_2957 | sce_2577 | 0.00E+00 | 0.00E+00 |
| SCE1572_2960 | sce_5463 | 3.00E-141 | 4.00E-143 |
| SCE1572_2961 | sce_2578 | 0.00E+00 | 0.00E+00 |
| SCE1572_2963 | sce_2579 | 0.00E+00 | 0.00E+00 |
| SCE1572_297 | sce_8687 | 3.00E-118 | 4.00E-117 |

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|--------------|----------|-----------|-----------|
| SCE1572_2979 | sce_2583 | 7.00E-60 | 1.00E-66 |
| SCE1572_298 | sce_8686 | 1.00E-142 | 3.00E-132 |
| SCE1572_2980 | sce_2584 | 2.00E-101 | 2.00E-99 |
| SCE1572_2983 | sce_2585 | 3.00E-106 | 8.00E-109 |
| SCE1572_2984 | sce_2586 | 6.00E-50 | 7.00E-50 |
| SCE1572_2985 | sce_2587 | 5.00E-60 | 6.00E-60 |
| SCE1572_2987 | sce_2588 | 0.00E+00 | 0.00E+00 |
| SCE1572_299 | sce_9374 | 2.00E-110 | 2.00E-106 |
| SCE1572_2991 | sce_2589 | 0.00E+00 | 0.00E+00 |
| SCE1572_2991 | sce_5830 | 0.00E+00 | 0.00E+00 |
| SCE1572_2991 | sce_5824 | 0.00E+00 | 0.00E+00 |
| SCE1572_2991 | sce_5827 | 0.00E+00 | 0.00E+00 |
| SCE1572_2991 | sce_2940 | 0.00E+00 | 0.00E+00 |
| SCE1572_2992 | sce_2590 | 2.00E-52 | 2.00E-52 |
| SCE1572_2993 | sce_2591 | 3.00E-93 | 1.00E-93 |
| SCE1572_2995 | sce_2593 | 0.00E+00 | 5.00E-180 |
| SCE1572_2996 | sce_2596 | 0.00E+00 | 0.00E+00 |
| SCE1572_2998 | sce_2597 | 1.00E-70 | 1.00E-70 |
| SCE1572_3 | sce_3 | 0.00E+00 | 0.00E+00 |
| SCE1572_30 | sce_32 | 0.00E+00 | 0.00E+00 |
| SCE1572_3002 | sce_6068 | 2.00E-68 | 2.00E-60 |
| SCE1572_3003 | sce_9937 | 2.00E-73 | 1.00E-70 |
| SCE1572_3005 | sce_9938 | 7.00E-26 | 3.00E-25 |
| SCE1572_3007 | sce_2598 | 4.00E-55 | 6.00E-68 |
| SCE1572_3008 | sce_2600 | 2.00E-63 | 2.00E-63 |
| SCE1572_3009 | sce_6056 | 5.00E-40 | 4.00E-40 |
| SCE1572_3010 | sce_2938 | 2.00E-31 | 4.00E-23 |
| SCE1572_3011 | sce_2937 | 0.00E+00 | 0.00E+00 |
| SCE1572_3014 | sce_2467 | 3.00E-147 | 5.00E-149 |
| SCE1572_3015 | sce_2476 | 6.00E-105 | 1.00E-117 |
| SCE1572_3020 | sce_7521 | 0.00E+00 | 0.00E+00 |
| SCE1572_3023 | sce_6869 | 1.00E-96 | 9.00E-95 |
| SCE1572_3024 | sce_6870 | 9.00E-99 | 1.00E-114 |
| SCE1572_3032 | sce_2601 | 1.00E-112 | 1.00E-112 |
| SCE1572_3033 | sce_2602 | 0.00E+00 | 0.00E+00 |
| SCE1572_3034 | sce_2603 | 4.00E-110 | 5.00E-114 |
| SCE1572_3035 | sce_2604 | 4.00E-60 | 3.00E-71 |
| SCE1572_3036 | sce_2606 | 4.00E-157 | 5.00E-173 |
| SCE1572_3037 | sce_2607 | 2.00E-105 | 1.00E-129 |
| SCE1572_3061 | sce_7454 | 7.00E-30 | 7.00E-13 |
| SCE1572_3062 | sce_7455 | 3.00E-62 | 2.00E-53 |
| SCE1572_3063 | sce_5710 | 0.00E+00 | 0.00E+00 |
| SCE1572_3064 | sce_2609 | 3.00E-43 | 3.00E-43 |
| SCE1572_3065 | sce_2610 | 9.00E-42 | 7.00E-47 |
| SCE1572_3066 | sce_2611 | 7.00E-67 | 6.00E-68 |
| SCE1572_3067 | sce_2612 | 2.00E-110 | 7.00E-104 |
| SCE1572_3068 | sce_2614 | 2.00E-120 | 1.00E-97 |
| SCE1572_3069 | sce_7327 | 4.00E-13 | 2.00E-10 |
| SCE1572_3070 | sce_7328 | 7.00E-51 | 8.00E-51 |
| SCE1572_3071 | sce_7329 | 0.00E+00 | 0.00E+00 |
| SCE1572_3073 | sce_7330 | 2.00E-06 | 7.00E-12 |
| SCE1572_3074 | sce_7331 | 3.00E-65 | 4.00E-65 |
| SCE1572_3077 | sce_9583 | 0.00E+00 | 0.00E+00 |
| SCE1572_308 | sce_2028 | 2.00E-142 | 8.00E-133 |
| SCE1572_3080 | sce_157 | 7.00E-86 | 7.00E-86 |
| SCE1572_3082 | sce_1504 | 1.00E-55 | 2.00E-51 |
| SCE1572_3084 | sce_7092 | 7.00E-97 | 2.00E-87 |
| SCE1572_309 | sce_7865 | 2.00E-135 | 2.00E-132 |
| SCE1572_3093 | sce_2615 | 8.00E-65 | 8.00E-65 |
| SCE1572_3099 | sce_9462 | 5.00E-56 | 4.00E-73 |
| SCE1572_31 | sce_33 | 1.00E-72 | 4.00E-72 |
| SCE1572_310 | sce_7866 | 1.00E-91 | 5.00E-85 |
| SCE1572_3101 | sce_2618 | 2.00E-47 | 3.00E-59 |
| SCE1572_3103 | sce_2621 | 1.00E-72 | 1.00E-70 |
| SCE1572_3105 | sce_2481 | 2.00E-53 | 1.00E-43 |
| SCE1572_3107 | sce_2623 | 4.00E-147 | 4.00E-131 |
| SCE1572_3108 | sce_2624 | 1.00E-143 | 1.00E-143 |
| SCE1572_3109 | sce_2625 | 0.00E+00 | 0.00E+00 |
| SCE1572_311 | sce_9786 | 1.00E-58 | 5.00E-53 |
| SCE1572_3110 | sce_2626 | 0.00E+00 | 0.00E+00 |
| SCE1572_3111 | sce_2627 | 4.00E-118 | 6.00E-120 |
| SCE1572_3113 | sce_1386 | 0.00E+00 | 0.00E+00 |
| SCE1572_3114 | sce_1387 | 0.00E+00 | 0.00E+00 |
| SCE1572_3115 | sce_2628 | 2.00E-121 | 2.00E-121 |
| SCE1572_3116 | sce_2629 | 8.00E-112 | 4.00E-109 |
| SCE1572_3117 | sce_2630 | 0.00E+00 | 0.00E+00 |

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| SCE1572_3118 | sce_2631 | 4.00E-08 | 1.00E-08 |
| SCE1572_3119 | sce_2632 | 1.00E-54 | 5.00E-49 |
| SCE1572_312 | sce_9787 | 2.00E-26 | 1.00E-25 |
| SCE1572_3120 | sce_2633 | 1.00E-28 | 2.00E-26 |
| SCE1572_3124 | sce_2634 | 2.00E-49 | 3.00E-43 |
| SCE1572_3125 | sce_2636 | 4.00E-70 | 4.00E-70 |
| SCE1572_3126 | sce_2637 | 7.00E-57 | 2.00E-58 |
| SCE1572_3127 | sce_6335 | 2.00E-21 | 1.00E-24 |
| SCE1572_3131 | sce_6339 | 0.00E+00 | 0.00E+00 |
| SCE1572_3133 | sce_6341 | 0.00E+00 | 0.00E+00 |
| SCE1572_3137 | sce_3750 | 0.00E+00 | 0.00E+00 |
| SCE1572_3137 | sce_7657 | 0.00E+00 | 0.00E+00 |
| SCE1572_3137 | sce_6712 | 0.00E+00 | 0.00E+00 |
| SCE1572_3137 | sce_9954 | 0.00E+00 | 0.00E+00 |
| SCE1572_3137 | sce_3491 | 0.00E+00 | 0.00E+00 |
| SCE1572_3137 | sce_5226 | 0.00E+00 | 0.00E+00 |
| SCE1572_3137 | sce_9665 | 0.00E+00 | 0.00E+00 |
| SCE1572_3137 | sce_5751 | 0.00E+00 | 0.00E+00 |
| SCE1572_3137 | sce_7154 | 0.00E+00 | 0.00E+00 |
| SCE1572_3137 | sce_5403 | 0.00E+00 | 0.00E+00 |
| SCE1572_3137 | sce_5746 | 0.00E+00 | 0.00E+00 |
| SCE1572_3138 | sce_2638 | 4.00E-74 | 5.00E-74 |
| SCE1572_314 | sce_2561 | 2.00E-92 | 5.00E-93 |
| SCE1572_3140 | sce_1537 | 0.00E+00 | 0.00E+00 |
| SCE1572_3141 | sce_7640 | 0.00E+00 | 0.00E+00 |
| SCE1572_3141 | sce_388 | 0.00E+00 | 0.00E+00 |
| SCE1572_3141 | sce_5835 | 0.00E+00 | 0.00E+00 |
| SCE1572_3141 | sce_10204 | 0.00E+00 | 0.00E+00 |
| SCE1572_3141 | sce_3085 | 0.00E+00 | 0.00E+00 |
| SCE1572_3141 | sce_4513 | 0.00E+00 | 0.00E+00 |
| SCE1572_3141 | sce_7109 | 0.00E+00 | 0.00E+00 |
| SCE1572_3141 | sce_9557 | 0.00E+00 | 0.00E+00 |
| SCE1572_3141 | sce_3003 | 0.00E+00 | 0.00E+00 |
| SCE1572_3141 | sce_9920 | 0.00E+00 | 0.00E+00 |
| SCE1572_3141 | sce_7661 | 0.00E+00 | 0.00E+00 |
| SCE1572_3141 | sce_3917 | 0.00E+00 | 0.00E+00 |
| SCE1572_3141 | sce_6107 | 0.00E+00 | 0.00E+00 |
| SCE1572_3141 | sce_6093 | 0.00E+00 | 0.00E+00 |
| SCE1572_3141 | sce_6095 | 0.00E+00 | 0.00E+00 |
| SCE1572_3141 | sce_6094 | 0.00E+00 | 0.00E+00 |
| SCE1572_3141 | sce_2065 | 0.00E+00 | 0.00E+00 |
| SCE1572_3141 | sce_6535 | 0.00E+00 | 0.00E+00 |
| SCE1572_3141 | sce_4466 | 0.00E+00 | 0.00E+00 |
| SCE1572_3141 | sce_6092 | 0.00E+00 | 0.00E+00 |
| SCE1572_3149 | sce_5504 | 4.00E-173 | 0.00E+00 |
| SCE1572_315 | sce_616 | 0.00E+00 | 0.00E+00 |
| SCE1572_3151 | sce_2640 | 4.00E-77 | 1.00E-55 |
| SCE1572_3152 | sce_2641 | 0.00E+00 | 0.00E+00 |
| SCE1572_3152 | sce_5502 | 0.00E+00 | 0.00E+00 |
| SCE1572_3154 | sce_2642 | 1.00E-39 | 4.00E-15 |
| SCE1572_3155 | sce_2643 | 2.00E-89 | 5.00E-83 |
| SCE1572_3156 | sce_2644 | 5.00E-73 | 2.00E-72 |
| SCE1572_3157 | sce_2645 | 0.00E+00 | 0.00E+00 |
| SCE1572_3157 | sce_9974 | 0.00E+00 | 0.00E+00 |
| SCE1572_3157 | sce_9973 | 0.00E+00 | 0.00E+00 |
| SCE1572_3158 | sce_5229 | 0.00E+00 | 0.00E+00 |
| SCE1572_3158 | sce_6712 | 0.00E+00 | 0.00E+00 |
| SCE1572_3158 | sce_3750 | 0.00E+00 | 0.00E+00 |
| SCE1572_3158 | sce_9954 | 0.00E+00 | 0.00E+00 |
| SCE1572_3158 | sce_5403 | 0.00E+00 | 0.00E+00 |
| SCE1572_3158 | sce_5226 | 0.00E+00 | 0.00E+00 |
| SCE1572_3158 | sce_774 | 0.00E+00 | 0.00E+00 |
| SCE1572_3158 | sce_9665 | 0.00E+00 | 0.00E+00 |
| SCE1572_3159 | sce_2654 | 3.00E-176 | 3.00E-173 |
| SCE1572_316 | sce_619 | 0.00E+00 | 0.00E+00 |
| SCE1572_3160 | sce_10130 | 4.00E-08 | 5.00E-08 |
| SCE1572_3161 | sce_10131 | 5.00E-27 | 5.00E-27 |
| SCE1572_3162 | sce_2655 | 0.00E+00 | 0.00E+00 |
| SCE1572_3163 | sce_2656 | 0.00E+00 | 0.00E+00 |
| SCE1572_3163 | sce_1444 | 0.00E+00 | 0.00E+00 |
| SCE1572_3164 | sce_9942 | 0.00E+00 | 0.00E+00 |
| SCE1572_3165 | sce_9943 | 0.00E+00 | 0.00E+00 |
| SCE1572_3166 | sce_9944 | 0.00E+00 | 0.00E+00 |
| SCE1572_3169 | sce_5119 | 4.00E-116 | 1.00E-110 |
| SCE1572_317 | sce_620 | 5.00E-105 | 1.00E-101 |
| SCE1572_3172 | sce_389 | 0.00E+00 | 0.00E+00 |

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| SCE1572_3172 | sce_7637 | 0.00E+00 | 0.00E+00 |
| SCE1572_3172 | sce_9237 | 0.00E+00 | 0.00E+00 |
| SCE1572_3172 | sce_2666 | 0.00E+00 | 0.00E+00 |
| SCE1572_3172 | sce_9230 | 0.00E+00 | 0.00E+00 |
| SCE1572_3172 | sce_9231 | 0.00E+00 | 0.00E+00 |
| SCE1572_3173 | sce_2667 | 4.00E-79 | 2.00E-87 |
| SCE1572_3174 | sce_2668 | 2.00E-93 | 9.00E-101 |
| SCE1572_3181 | sce_2671 | 0.00E+00 | 0.00E+00 |
| SCE1572_3182 | sce_2672 | 0.00E+00 | 0.00E+00 |
| SCE1572_3183 | sce_2673 | 4.00E-123 | 4.00E-122 |
| SCE1572_3188 | sce_2679 | 0.00E+00 | 0.00E+00 |
| SCE1572_3189 | sce_2680 | 9.00E-21 | 3.00E-26 |
| SCE1572_3190 | sce_2681 | 1.00E-69 | 4.00E-72 |
| SCE1572_3191 | sce_2683 | 7.00E-20 | 7.00E-20 |
| SCE1572_3192 | sce_2684 | 6.00E-66 | 9.00E-66 |
| SCE1572_3193 | sce_2685 | 0.00E+00 | 0.00E+00 |
| SCE1572_3194 | sce_2686 | 0.00E+00 | 0.00E+00 |
| SCE1572_3196 | sce_2688 | 0.00E+00 | 0.00E+00 |
| SCE1572_3197 | sce_2689 | 4.00E-163 | 4.00E-175 |
| SCE1572_3198 | sce_2690 | 6.00E-57 | 8.00E-59 |
| SCE1572_3199 | sce_2692 | 6.00E-150 | 2.00E-149 |
| SCE1572_32 | sce_34 | 2.00E-86 | 3.00E-73 |
| SCE1572_3200 | sce_2694 | 3.00E-66 | 5.00E-71 |
| SCE1572_3201 | sce_2695 | 2.00E-25 | 2.00E-25 |
| SCE1572_3202 | sce_2696 | 0.00E+00 | 0.00E+00 |
| SCE1572_3203 | sce_2697 | 6.00E-123 | 1.00E-124 |
| SCE1572_3204 | sce_2698 | 1.00E-67 | 2.00E-70 |
| SCE1572_3205 | sce_2699 | 0.00E+00 | 0.00E+00 |
| SCE1572_3206 | sce_2700 | 0.00E+00 | 0.00E+00 |
| SCE1572_3207 | sce_2701 | 3.00E-167 | 1.00E-167 |
| SCE1572_3208 | sce_2702 | 7.00E-114 | 7.00E-114 |
| SCE1572_3209 | sce_2703 | 2.00E-110 | 8.00E-125 |
| SCE1572_3210 | sce_2704 | 9.00E-97 | 2.00E-103 |
| SCE1572_3211 | sce_2705 | 6.00E-19 | 2.00E-07 |
| SCE1572_3212 | sce_2706 | 1.00E-47 | 5.00E-44 |
| SCE1572_3213 | sce_2707 | 3.00E-125 | 4.00E-119 |
| SCE1572_3215 | sce_2708 | 0.00E+00 | 0.00E+00 |
| SCE1572_3216 | sce_2709 | 0.00E+00 | 4.00E-172 |
| SCE1572_3217 | sce_2710 | 0.00E+00 | 0.00E+00 |
| SCE1572_3218 | sce_2711 | 2.00E-13 | 5.00E-28 |
| SCE1572_3219 | sce_2712 | 2.00E-60 | 4.00E-62 |
| SCE1572_322 | sce_4699 | 3.00E-61 | 1.00E-68 |
| SCE1572_3220 | sce_2713 | 2.00E-42 | 2.00E-42 |
| SCE1572_3221 | sce_2714 | 9.00E-63 | 9.00E-58 |
| SCE1572_3222 | sce_2715 | 8.00E-122 | 7.00E-127 |
| SCE1572_3223 | sce_2716 | 4.00E-34 | 2.00E-38 |
| SCE1572_3225 | sce_2717 | 0.00E+00 | 0.00E+00 |
| SCE1572_3226 | sce_2718 | 1.00E-125 | 1.00E-136 |
| SCE1572_3227 | sce_2719 | 5.00E-113 | 1.00E-116 |
| SCE1572_3228 | sce_2720 | 3.00E-87 | 3.00E-87 |
| SCE1572_3229 | sce_2721 | 2.00E-42 | 2.00E-42 |
| SCE1572_3230 | sce_2722 | 6.00E-119 | 5.00E-119 |
| SCE1572_3231 | sce_2723 | 3.00E-151 | 3.00E-154 |
| SCE1572_3232 | sce_2724 | 3.00E-174 | 0.00E+00 |
| SCE1572_3233 | sce_2726 | 0.00E+00 | 0.00E+00 |
| SCE1572_3234 | sce_2727 | 2.00E-105 | 8.00E-99 |
| SCE1572_3235 | sce_2728 | 0.00E+00 | 0.00E+00 |
| SCE1572_3236 | sce_2732 | 0.00E+00 | 0.00E+00 |
| SCE1572_3238 | sce_2733 | 0.00E+00 | 0.00E+00 |
| SCE1572_3238 | sce_10203 | 0.00E+00 | 0.00E+00 |
| SCE1572_3239 | sce_2734 | 2.00E-166 | 1.00E-161 |
| SCE1572_3241 | sce_2735 | 0.00E+00 | 0.00E+00 |
| SCE1572_3243 | sce_2737 | 0.00E+00 | 0.00E+00 |
| SCE1572_3244 | sce_2738 | 6.00E-36 | 2.00E-35 |
| SCE1572_3245 | sce_2740 | 2.00E-175 | 2.00E-174 |
| SCE1572_3246 | sce_2741 | 0.00E+00 | 0.00E+00 |
| SCE1572_3247 | sce_2742 | 5.00E-82 | 1.00E-91 |
| SCE1572_3248 | sce_2744 | 5.00E-64 | 3.00E-64 |
| SCE1572_3249 | sce_2745 | 4.00E-167 | 8.00E-174 |
| SCE1572_3250 | sce_2746 | 2.00E-55 | 2.00E-54 |
| SCE1572_3252 | sce_2748 | 0.00E+00 | 0.00E+00 |
| SCE1572_3253 | sce_2749 | 1.00E-100 | 2.00E-103 |
| SCE1572_3254 | sce_2750 | 3.00E-153 | 7.00E-166 |
| SCE1572_3255 | sce_2751 | 1.00E-100 | 4.00E-100 |
| SCE1572_3256 | sce_2752 | 3.00E-82 | 4.00E-93 |
| SCE1572_3257 | sce_2753 | 5.00E-106 | 2.00E-111 |

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|--------------|----------|-----------|-----------|
| SCE1572_3259 | sce_2754 | 0.00E+00 | 0.00E+00 |
| SCE1572_3260 | sce_2755 | 7.00E-11 | 6.00E-06 |
| SCE1572_3261 | sce_2756 | 0.00E+00 | 0.00E+00 |
| SCE1572_3262 | sce_2757 | 1.00E-120 | 7.00E-129 |
| SCE1572_3263 | sce_2758 | 7.00E-167 | 7.00E-167 |
| SCE1572_3264 | sce_2759 | 0.00E+00 | 0.00E+00 |
| SCE1572_3266 | sce_2760 | 1.00E-160 | 2.00E-159 |
| SCE1572_3267 | sce_2761 | 0.00E+00 | 0.00E+00 |
| SCE1572_3268 | sce_2762 | 3.00E-89 | 1.00E-89 |
| SCE1572_3269 | sce_2764 | 5.00E-129 | 8.00E-137 |
| SCE1572_3270 | sce_2765 | 0.00E+00 | 0.00E+00 |
| SCE1572_3271 | sce_2766 | 0.00E+00 | 0.00E+00 |
| SCE1572_3273 | sce_2767 | 2.00E-118 | 1.00E-118 |
| SCE1572_3274 | sce_2768 | 9.00E-176 | 3.00E-172 |
| SCE1572_3275 | sce_2769 | 9.00E-58 | 9.00E-58 |
| SCE1572_3276 | sce_2770 | 5.00E-99 | 4.00E-111 |
| SCE1572_3278 | sce_2773 | 0.00E+00 | 3.00E-180 |
| SCE1572_3279 | sce_2774 | 6.00E-144 | 1.00E-137 |
| SCE1572_3280 | sce_2775 | 0.00E+00 | 0.00E+00 |
| SCE1572_3281 | sce_2776 | 7.00E-136 | 1.00E-130 |
| SCE1572_3283 | sce_2777 | 0.00E+00 | 0.00E+00 |
| SCE1572_3284 | sce_2784 | 2.00E-07 | 2.00E-08 |
| SCE1572_3285 | sce_2782 | 5.00E-166 | 5.00E-166 |
| SCE1572_3286 | sce_2778 | 8.00E-99 | 2.00E-100 |
| SCE1572_3288 | sce_2785 | 0.00E+00 | 0.00E+00 |
| SCE1572_3292 | sce_2786 | 0.00E+00 | 0.00E+00 |
| SCE1572_3293 | sce_2787 | 6.00E-83 | 2.00E-82 |
| SCE1572_3294 | sce_2788 | 2.00E-83 | 3.00E-74 |
| SCE1572_3297 | sce_2789 | 0.00E+00 | 0.00E+00 |
| SCE1572_3298 | sce_2790 | 6.00E-55 | 3.00E-67 |
| SCE1572_3299 | sce_2791 | 5.00E-166 | 1.00E-174 |
| SCE1572_33 | sce_35 | 0.00E+00 | 0.00E+00 |
| SCE1572_330 | sce_4328 | 0.00E+00 | 6.00E-168 |
| SCE1572_3300 | sce_2792 | 6.00E-101 | 8.00E-108 |
| SCE1572_3301 | sce_2793 | 7.00E-146 | 4.00E-134 |
| SCE1572_3302 | sce_2794 | 0.00E+00 | 0.00E+00 |
| SCE1572_3306 | sce_2797 | 0.00E+00 | 0.00E+00 |
| SCE1572_3307 | sce_2798 | 2.00E-180 | 0.00E+00 |
| SCE1572_3308 | sce_2799 | 7.00E-55 | 1.00E-41 |
| SCE1572_3309 | sce_2800 | 4.00E-90 | 1.00E-92 |
| SCE1572_331 | sce_4326 | 1.00E-159 | 3.00E-170 |
| SCE1572_3310 | sce_2801 | 1.00E-108 | 3.00E-108 |
| SCE1572_3311 | sce_2802 | 1.00E-58 | 4.00E-60 |
| SCE1572_3312 | sce_2804 | 1.00E-61 | 5.00E-70 |
| SCE1572_3313 | sce_2805 | 6.00E-74 | 1.00E-86 |
| SCE1572_3314 | sce_2807 | 0.00E+00 | 0.00E+00 |
| SCE1572_3315 | sce_2808 | 1.00E-37 | 2.00E-32 |
| SCE1572_3316 | sce_2811 | 0.00E+00 | 0.00E+00 |
| SCE1572_3317 | sce_2812 | 0.00E+00 | 0.00E+00 |
| SCE1572_3318 | sce_2813 | 2.00E-104 | 2.00E-105 |
| SCE1572_3319 | sce_2814 | 5.00E-134 | 2.00E-143 |
| SCE1572_332 | sce_180 | 1.00E-78 | 2.00E-76 |
| SCE1572_3320 | sce_2815 | 0.00E+00 | 0.00E+00 |
| SCE1572_3320 | sce_3653 | 0.00E+00 | 0.00E+00 |
| SCE1572_3321 | sce_2816 | 0.00E+00 | 0.00E+00 |
| SCE1572_3322 | sce_2817 | 3.00E-11 | 3.00E-11 |
| SCE1572_3324 | sce_2819 | 7.00E-149 | 5.00E-153 |
| SCE1572_3325 | sce_2820 | 0.00E+00 | 0.00E+00 |
| SCE1572_3326 | sce_2821 | 3.00E-73 | 5.00E-77 |
| SCE1572_3327 | sce_2822 | 2.00E-61 | 2.00E-61 |
| SCE1572_3328 | sce_2823 | 3.00E-69 | 2.00E-69 |
| SCE1572_3329 | sce_2824 | 0.00E+00 | 0.00E+00 |
| SCE1572_333 | sce_181 | 3.00E-135 | 2.00E-127 |
| SCE1572_3330 | sce_2826 | 7.00E-43 | 3.00E-50 |
| SCE1572_3331 | sce_2827 | 9.00E-45 | 1.00E-46 |
| SCE1572_3332 | sce_2828 | 1.00E-21 | 1.00E-21 |
| SCE1572_3333 | sce_2829 | 0.00E+00 | 0.00E+00 |
| SCE1572_3335 | sce_2831 | 0.00E+00 | 0.00E+00 |
| SCE1572_3336 | sce_2832 | 0.00E+00 | 0.00E+00 |
| SCE1572_3337 | sce_2833 | 4.00E-153 | 1.00E-164 |
| SCE1572_3338 | sce_2834 | 7.00E-40 | 7.00E-40 |
| SCE1572_3339 | sce_2835 | 2.00E-171 | 2.00E-171 |
| SCE1572_334 | sce_183 | 7.00E-111 | 1.00E-122 |
| SCE1572_3340 | sce_2836 | 0.00E+00 | 0.00E+00 |
| SCE1572_3341 | sce_2837 | 2.00E-145 | 1.00E-144 |
| SCE1572_3342 | sce_2838 | 0.00E+00 | 0.00E+00 |

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| SCE1572_3343 | sce_2839 | 1.00E-132 | 1.00E-132 |
| SCE1572_3344 | sce_2840 | 0.00E+00 | 0.00E+00 |
| SCE1572_3345 | sce_2841 | 0.00E+00 | 0.00E+00 |
| SCE1572_335 | sce_184 | 3.00E-166 | 3.00E-160 |
| SCE1572_3352 | sce_2846 | 0.00E+00 | 0.00E+00 |
| SCE1572_3358 | sce_2848 | 4.00E-50 | 2.00E-63 |
| SCE1572_3359 | sce_2849 | 0.00E+00 | 0.00E+00 |
| SCE1572_336 | sce_185 | 1.00E-78 | 7.00E-76 |
| SCE1572_3360 | sce_2850 | 0.00E+00 | 0.00E+00 |
| SCE1572_3363 | sce_2851 | 1.00E-76 | 1.00E-76 |
| SCE1572_3364 | sce_2853 | 5.00E-73 | 3.00E-73 |
| SCE1572_3365 | sce_2854 | 1.00E-91 | 2.00E-85 |
| SCE1572_3366 | sce_2855 | 3.00E-123 | 9.00E-113 |
| SCE1572_3367 | sce_2856 | 0.00E+00 | 0.00E+00 |
| SCE1572_3368 | sce_2857 | 0.00E+00 | 0.00E+00 |
| SCE1572_3369 | sce_2859 | 2.00E-123 | 1.00E-130 |
| SCE1572_337 | sce_187 | 0.00E+00 | 0.00E+00 |
| SCE1572_3370 | sce_2860 | 3.00E-52 | 3.00E-52 |
| SCE1572_3371 | sce_2861 | 0.00E+00 | 0.00E+00 |
| SCE1572_3372 | sce_2862 | 0.00E+00 | 0.00E+00 |
| SCE1572_3373 | sce_2863 | 1.00E-21 | 2.00E-20 |
| SCE1572_3374 | sce_2864 | 2.00E-128 | 7.00E-124 |
| SCE1572_3375 | sce_2865 | 2.00E-180 | 6.00E-179 |
| SCE1572_3376 | sce_2866 | 2.00E-93 | 7.00E-93 |
| SCE1572_3377 | sce_7568 | 4.00E-43 | 8.00E-48 |
| SCE1572_3378 | sce_7569 | 2.00E-22 | 2.00E-22 |
| SCE1572_3379 | sce_7570 | 2.00E-38 | 9.00E-42 |
| SCE1572_3380 | sce_2867 | 3.00E-94 | 3.00E-94 |
| SCE1572_3381 | sce_2868 | 3.00E-133 | 4.00E-133 |
| SCE1572_3382 | sce_2869 | 1.00E-136 | 4.00E-136 |
| SCE1572_3383 | sce_2870 | 5.00E-76 | 4.00E-73 |
| SCE1572_3384 | sce_2871 | 0.00E+00 | 0.00E+00 |
| SCE1572_3385 | sce_2872 | 4.00E-180 | 0.00E+00 |
| SCE1572_3387 | sce_2873 | 3.00E-42 | 8.00E-36 |
| SCE1572_3388 | sce_2874 | 3.00E-95 | 1.00E-84 |
| SCE1572_3389 | sce_2875 | 4.00E-49 | 3.00E-33 |
| SCE1572_339 | sce_7549 | 2.00E-108 | 6.00E-107 |
| SCE1572_3390 | sce_2876 | 4.00E-61 | 5.00E-61 |
| SCE1572_3391 | sce_2877 | 2.00E-67 | 4.00E-75 |
| SCE1572_3392 | sce_2878 | 0.00E+00 | 0.00E+00 |
| SCE1572_3393 | sce_2879 | 1.00E-39 | 1.00E-39 |
| SCE1572_3394 | sce_2880 | 8.00E-71 | 1.00E-71 |
| SCE1572_3395 | sce_2881 | 6.00E-15 | 4.00E-21 |
| SCE1572_3396 | sce_2882 | 9.00E-63 | 2.00E-54 |
| SCE1572_3397 | sce_2884 | 0.00E+00 | 0.00E+00 |
| SCE1572_3398 | sce_2885 | 4.00E-19 | 5.00E-19 |
| SCE1572_34 | sce_36 | 3.00E-145 | 4.00E-145 |
| SCE1572_340 | sce_7550 | 1.00E-97 | 2.00E-96 |
| SCE1572_3400 | sce_2887 | 0.00E+00 | 0.00E+00 |
| SCE1572_3402 | sce_2889 | 9.00E-116 | 2.00E-111 |
| SCE1572_3403 | sce_2890 | 5.00E-87 | 8.00E-92 |
| SCE1572_3404 | sce_2891 | 3.00E-118 | 3.00E-118 |
| SCE1572_3405 | sce_2892 | 0.00E+00 | 0.00E+00 |
| SCE1572_3406 | sce_2893 | 2.00E-172 | 2.00E-172 |
| SCE1572_3407 | sce_2894 | 0.00E+00 | 0.00E+00 |
| SCE1572_3408 | sce_2895 | 4.00E-144 | 4.00E-144 |
| SCE1572_3409 | sce_2896 | 1.00E-68 | 2.00E-97 |
| SCE1572_341 | sce_188 | 0.00E+00 | 0.00E+00 |
| SCE1572_3410 | sce_2897 | 2.00E-13 | 6.00E-16 |
| SCE1572_3411 | sce_2898 | 2.00E-82 | 7.00E-84 |
| SCE1572_3412 | sce_2899 | 7.00E-100 | 3.00E-101 |
| SCE1572_3414 | sce_2900 | 0.00E+00 | 0.00E+00 |
| SCE1572_3415 | sce_2901 | 5.00E-61 | 1.00E-63 |
| SCE1572_3416 | sce_2903 | 2.00E-59 | 2.00E-69 |
| SCE1572_3417 | sce_2904 | 2.00E-99 | 3.00E-107 |
| SCE1572_3418 | sce_2905 | 0.00E+00 | 2.00E-180 |
| SCE1572_3419 | sce_2906 | 0.00E+00 | 0.00E+00 |
| SCE1572_342 | sce_189 | 5.00E-120 | 5.00E-120 |
| SCE1572_3420 | sce_2907 | 0.00E+00 | 0.00E+00 |
| SCE1572_3421 | sce_2908 | 0.00E+00 | 0.00E+00 |
| SCE1572_3422 | sce_2909 | 0.00E+00 | 0.00E+00 |
| SCE1572_3423 | sce_2910 | 4.00E-09 | 6.00E-09 |
| SCE1572_3424 | sce_2911 | 3.00E-119 | 3.00E-119 |
| SCE1572_3425 | sce_2912 | 2.00E-20 | 1.00E-21 |
| SCE1572_3427 | sce_2913 | 0.00E+00 | 0.00E+00 |
| SCE1572_3429 | sce_2914 | 0.00E+00 | 0.00E+00 |

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| SCE1572_343 | sce_190 | 0.00E+00 | 0.00E+00 |
| SCE1572_3430 | sce_2915 | 9.00E-61 | 4.00E-61 |
| SCE1572_3431 | sce_2916 | 1.00E-31 | 9.00E-30 |
| SCE1572_3432 | sce_2917 | 6.00E-87 | 3.00E-81 |
| SCE1572_3433 | sce_2918 | 1.00E-101 | 8.00E-130 |
| SCE1572_3434 | sce_2919 | 0.00E+00 | 0.00E+00 |
| SCE1572_3435 | sce_2920 | 8.00E-112 | 1.00E-111 |
| SCE1572_3436 | sce_2925 | 3.00E-107 | 7.00E-106 |
| SCE1572_3437 | sce_2931 | 2.00E-117 | 3.00E-117 |
| SCE1572_3439 | sce_2932 | 1.00E-163 | 1.00E-163 |
| SCE1572_344 | sce_2552 | 6.00E-128 | 2.00E-116 |
| SCE1572_3441 | sce_2933 | 3.00E-99 | 3.00E-93 |
| SCE1572_3442 | sce_2934 | 0.00E+00 | 0.00E+00 |
| SCE1572_3443 | sce_2935 | 2.00E-57 | 3.00E-69 |
| SCE1572_3444 | sce_5835 | 0.00E+00 | 0.00E+00 |
| SCE1572_3444 | sce_7640 | 0.00E+00 | 0.00E+00 |
| SCE1572_3444 | sce_388 | 0.00E+00 | 0.00E+00 |
| SCE1572_3444 | sce_3085 | 0.00E+00 | 0.00E+00 |
| SCE1572_3444 | sce_10204 | 0.00E+00 | 0.00E+00 |
| SCE1572_3444 | sce_4513 | 0.00E+00 | 0.00E+00 |
| SCE1572_3444 | sce_9557 | 0.00E+00 | 0.00E+00 |
| SCE1572_3444 | sce_7109 | 0.00E+00 | 0.00E+00 |
| SCE1572_3444 | sce_9920 | 0.00E+00 | 0.00E+00 |
| SCE1572_3444 | sce_6535 | 0.00E+00 | 0.00E+00 |
| SCE1572_3444 | sce_3003 | 0.00E+00 | 0.00E+00 |
| SCE1572_3444 | sce_7661 | 0.00E+00 | 0.00E+00 |
| SCE1572_3444 | sce_3917 | 0.00E+00 | 0.00E+00 |
| SCE1572_3444 | sce_6093 | 0.00E+00 | 0.00E+00 |
| SCE1572_3444 | sce_6107 | 0.00E+00 | 0.00E+00 |
| SCE1572_3444 | sce_6094 | 0.00E+00 | 0.00E+00 |
| SCE1572_3444 | sce_6092 | 0.00E+00 | 0.00E+00 |
| SCE1572_3444 | sce_8618 | 0.00E+00 | 0.00E+00 |
| SCE1572_3444 | sce_7643 | 0.00E+00 | 0.00E+00 |
| SCE1572_3445 | sce_225 | 0.00E+00 | 0.00E+00 |
| SCE1572_3445 | sce_2161 | 0.00E+00 | 0.00E+00 |
| SCE1572_3445 | sce_6235 | 0.00E+00 | 0.00E+00 |
| SCE1572_3445 | sce_8357 | 0.00E+00 | 0.00E+00 |
| SCE1572_3445 | sce_5276 | 0.00E+00 | 0.00E+00 |
| SCE1572_3447 | sce_2939 | 4.00E-53 | 5.00E-53 |
| SCE1572_3448 | sce_2940 | 0.00E+00 | 0.00E+00 |
| SCE1572_3448 | sce_5830 | 0.00E+00 | 0.00E+00 |
| SCE1572_3448 | sce_5827 | 0.00E+00 | 0.00E+00 |
| SCE1572_3448 | sce_5824 | 0.00E+00 | 0.00E+00 |
| SCE1572_3448 | sce_2589 | 0.00E+00 | 0.00E+00 |
| SCE1572_3449 | sce_2941 | 0.00E+00 | 0.00E+00 |
| SCE1572_345 | sce_2359 | 3.00E-85 | 3.00E-90 |
| SCE1572_3450 | sce_2942 | 9.00E-172 | 6.00E-178 |
| SCE1572_3451 | sce_2943 | 0.00E+00 | 0.00E+00 |
| SCE1572_3452 | sce_2944 | 0.00E+00 | 0.00E+00 |
| SCE1572_3453 | sce_2945 | 0.00E+00 | 0.00E+00 |
| SCE1572_3455 | sce_2946 | 0.00E+00 | 0.00E+00 |
| SCE1572_3456 | sce_2947 | 7.00E-179 | 2.00E-178 |
| SCE1572_3458 | sce_2948 | 8.00E-82 | 1.00E-81 |
| SCE1572_3459 | sce_2952 | 2.00E-34 | 2.00E-38 |
| SCE1572_346 | sce_3609 | 0.00E+00 | 0.00E+00 |
| SCE1572_3460 | sce_2953 | 1.00E-35 | 5.00E-36 |
| SCE1572_3461 | sce_2954 | 3.00E-70 | 8.00E-71 |
| SCE1572_3462 | sce_2955 | 3.00E-21 | 5.00E-15 |
| SCE1572_3463 | sce_2956 | 0.00E+00 | 0.00E+00 |
| SCE1572_3464 | sce_2957 | 0.00E+00 | 0.00E+00 |
| SCE1572_3467 | sce_2958 | 7.00E-91 | 7.00E-97 |
| SCE1572_3468 | sce_2960 | 4.00E-56 | 7.00E-68 |
| SCE1572_3469 | sce_2962 | 0.00E+00 | 0.00E+00 |
| SCE1572_347 | sce_9865 | 9.00E-115 | 1.00E-114 |
| SCE1572_3470 | sce_2963 | 0.00E+00 | 0.00E+00 |
| SCE1572_3472 | sce_2964 | 1.00E-99 | 2.00E-96 |
| SCE1572_3473 | sce_2965 | 4.00E-69 | 5.00E-62 |
| SCE1572_3474 | sce_2966 | 0.00E+00 | 0.00E+00 |
| SCE1572_3475 | sce_2967 | 8.00E-68 | 8.00E-104 |
| SCE1572_3476 | sce_2969 | 0.00E+00 | 0.00E+00 |
| SCE1572_3480 | sce_2972 | 0.00E+00 | 0.00E+00 |
| SCE1572_3481 | sce_2973 | 7.00E-22 | 1.00E-26 |
| SCE1572_3483 | sce_2974 | 7.00E-146 | 8.00E-155 |
| SCE1572_3484 | sce_2975 | 2.00E-69 | 1.00E-68 |
| SCE1572_3490 | sce_1329 | 7.00E-83 | 5.00E-96 |
| SCE1572_3493 | sce_2976 | 0.00E+00 | 0.00E+00 |

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|--------------|-----------|-----------|-----------|
| SCE1572_3494 | sce_2977 | 2.00E-48 | 8.00E-49 |
| SCE1572_3496 | sce_2978 | 0.00E+00 | 0.00E+00 |
| SCE1572_3497 | sce_2980 | 2.00E-61 | 2.00E-61 |
| SCE1572_3498 | sce_2981 | 0.00E+00 | 0.00E+00 |
| SCE1572_3499 | sce_2982 | 3.00E-65 | 3.00E-65 |
| SCE1572_35 | sce_37 | 5.00E-127 | 2.00E-124 |
| SCE1572_350 | sce_9998 | 6.00E-159 | 0.00E+00 |
| SCE1572_3500 | sce_2983 | 0.00E+00 | 0.00E+00 |
| SCE1572_3501 | sce_2984 | 0.00E+00 | 0.00E+00 |
| SCE1572_3502 | sce_2985 | 7.00E-119 | 5.00E-127 |
| SCE1572_3503 | sce_2986 | 5.00E-135 | 2.00E-138 |
| SCE1572_3504 | sce_2987 | 1.00E-145 | 1.00E-153 |
| SCE1572_3505 | sce_2988 | 6.00E-144 | 6.00E-144 |
| SCE1572_3506 | sce_2989 | 1.00E-107 | 2.00E-107 |
| SCE1572_3507 | sce_2990 | 1.00E-52 | 4.00E-50 |
| SCE1572_3508 | sce_2991 | 8.00E-61 | 3.00E-68 |
| SCE1572_3509 | sce_2992 | 0.00E+00 | 0.00E+00 |
| SCE1572_3510 | sce_2993 | 2.00E-62 | 4.00E-72 |
| SCE1572_3511 | sce_2994 | 2.00E-125 | 7.00E-114 |
| SCE1572_3513 | sce_7498 | 0.00E+00 | 0.00E+00 |
| SCE1572_3514 | sce_7500 | 8.00E-136 | 6.00E-128 |
| SCE1572_3516 | sce_7492 | 9.00E-143 | 4.00E-145 |
| SCE1572_3517 | sce_8421 | 1.00E-46 | 1.00E-46 |
| SCE1572_352 | sce_193 | 6.00E-75 | 1.00E-69 |
| SCE1572_3521 | sce_1043 | 1.00E-139 | 6.00E-131 |
| SCE1572_3523 | sce_3138 | 2.00E-51 | 4.00E-60 |
| SCE1572_3525 | sce_7491 | 0.00E+00 | 0.00E+00 |
| SCE1572_3528 | sce_2106 | 7.00E-57 | 3.00E-52 |
| SCE1572_3529 | sce_7067 | 0.00E+00 | 0.00E+00 |
| SCE1572_353 | sce_194 | 2.00E-75 | 6.00E-78 |
| SCE1572_3533 | sce_7120 | 0.00E+00 | 0.00E+00 |
| SCE1572_3534 | sce_8653 | 1.00E-20 | 1.00E-20 |
| SCE1572_354 | sce_195 | 1.00E-142 | 4.00E-151 |
| SCE1572_3549 | sce_5143 | 0.00E+00 | 0.00E+00 |
| SCE1572_355 | sce_196 | 7.00E-149 | 1.00E-140 |
| SCE1572_3550 | sce_1370 | 0.00E+00 | 0.00E+00 |
| SCE1572_3552 | sce_6024 | 2.00E-46 | 6.00E-49 |
| SCE1572_3553 | sce_6183 | 7.00E-21 | 7.00E-28 |
| SCE1572_3554 | sce_10012 | 1.00E-108 | 1.00E-104 |
| SCE1572_3555 | sce_5751 | 0.00E+00 | 0.00E+00 |
| SCE1572_3555 | sce_5746 | 0.00E+00 | 0.00E+00 |
| SCE1572_3555 | sce_9665 | 0.00E+00 | 0.00E+00 |
| SCE1572_3555 | sce_5226 | 0.00E+00 | 0.00E+00 |
| SCE1572_3555 | sce_5403 | 0.00E+00 | 0.00E+00 |
| SCE1572_3555 | sce_7969 | 0.00E+00 | 0.00E+00 |
| SCE1572_3555 | sce_4073 | 0.00E+00 | 0.00E+00 |
| SCE1572_3555 | sce_7154 | 0.00E+00 | 0.00E+00 |
| SCE1572_3555 | sce_2053 | 0.00E+00 | 0.00E+00 |
| SCE1572_3555 | sce_9757 | 0.00E+00 | 0.00E+00 |
| SCE1572_3555 | sce_9954 | 0.00E+00 | 0.00E+00 |
| SCE1572_3555 | sce_6712 | 0.00E+00 | 0.00E+00 |
| SCE1572_3555 | sce_3750 | 0.00E+00 | 0.00E+00 |
| SCE1572_3555 | sce_1803 | 0.00E+00 | 0.00E+00 |
| SCE1572_3564 | sce_5229 | 0.00E+00 | 0.00E+00 |
| SCE1572_3564 | sce_6712 | 0.00E+00 | 0.00E+00 |
| SCE1572_3564 | sce_3750 | 0.00E+00 | 0.00E+00 |
| SCE1572_3564 | sce_9954 | 0.00E+00 | 0.00E+00 |
| SCE1572_3564 | sce_5403 | 0.00E+00 | 0.00E+00 |
| SCE1572_3564 | sce_774 | 0.00E+00 | 0.00E+00 |
| SCE1572_3564 | sce_9665 | 0.00E+00 | 0.00E+00 |
| SCE1572_3568 | sce_5229 | 0.00E+00 | 0.00E+00 |
| SCE1572_3568 | sce_6712 | 0.00E+00 | 0.00E+00 |
| SCE1572_3568 | sce_3750 | 0.00E+00 | 0.00E+00 |
| SCE1572_3568 | sce_9954 | 0.00E+00 | 0.00E+00 |
| SCE1572_3568 | sce_5403 | 0.00E+00 | 0.00E+00 |
| SCE1572_3568 | sce_9665 | 0.00E+00 | 0.00E+00 |
| SCE1572_3568 | sce_774 | 0.00E+00 | 0.00E+00 |
| SCE1572_3568 | sce_5226 | 0.00E+00 | 0.00E+00 |
| SCE1572_357 | sce_198 | 0.00E+00 | 0.00E+00 |
| SCE1572_3576 | sce_6709 | 3.00E-40 | 2.00E-40 |
| SCE1572_3577 | sce_170 | 6.00E-105 | 1.00E-104 |
| SCE1572_3579 | sce_6216 | 4.00E-49 | 3.00E-49 |
| SCE1572_358 | sce_199 | 0.00E+00 | 0.00E+00 |
| SCE1572_3581 | sce_4603 | 4.00E-90 | 1.00E-81 |
| SCE1572_3585 | sce_9857 | 2.00E-86 | 2.00E-86 |
| SCE1572_359 | sce_200 | 0.00E+00 | 0.00E+00 |

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| SCE1572_3592 | sce_7649 | 4.00E-63 | 8.00E-57 |
| SCE1572_3593 | sce_7648 | 0.00E+00 | 0.00E+00 |
| SCE1572_3594 | sce_7651 | 1.00E-117 | 4.00E-132 |
| SCE1572_3599 | sce_1701 | 3.00E-21 | 3.00E-21 |
| SCE1572_36 | sce_38 | 0.00E+00 | 0.00E+00 |
| SCE1572_360 | sce_201 | 2.00E-73 | 2.00E-73 |
| SCE1572_3604 | sce_1597 | 0.00E+00 | 0.00E+00 |
| SCE1572_3605 | sce_1598 | 0.00E+00 | 0.00E+00 |
| SCE1572_3605 | sce_1599 | 0.00E+00 | 0.00E+00 |
| SCE1572_3607 | sce_4487 | 0.00E+00 | 0.00E+00 |
| SCE1572_3608 | sce_3024 | 1.00E-148 | 9.00E-153 |
| SCE1572_3609 | sce_3025 | 0.00E+00 | 0.00E+00 |
| SCE1572_3614 | sce_6533 | 1.00E-22 | 4.00E-33 |
| SCE1572_3619 | sce_2155 | 0.00E+00 | 0.00E+00 |
| SCE1572_3620 | sce_2154 | 3.00E-60 | 1.00E-46 |
| SCE1572_3621 | sce_2153 | 6.00E-46 | 9.00E-46 |
| SCE1572_3622 | sce_2152 | 0.00E+00 | 0.00E+00 |
| SCE1572_3623 | sce_2151 | 2.00E-63 | 4.00E-63 |
| SCE1572_3624 | sce_2150 | 2.00E-30 | 2.00E-30 |
| SCE1572_3625 | sce_2149 | 5.00E-95 | 5.00E-95 |
| SCE1572_3626 | sce_6850 | 3.00E-158 | 1.00E-139 |
| SCE1572_3627 | sce_6851 | 3.00E-94 | 8.00E-108 |
| SCE1572_3628 | sce_1042 | 2.00E-63 | 2.00E-63 |
| SCE1572_3629 | sce_7856 | 1.00E-45 | 6.00E-44 |
| SCE1572_3630 | sce_6065 | 0.00E+00 | 0.00E+00 |
| SCE1572_3631 | sce_6047 | 3.00E-159 | 7.00E-166 |
| SCE1572_3632 | sce_6048 | 0.00E+00 | 0.00E+00 |
| SCE1572_3633 | sce_6046 | 7.00E-76 | 1.00E-72 |
| SCE1572_3634 | sce_2425 | 2.00E-140 | 2.00E-131 |
| SCE1572_3639 | sce_6070 | 1.00E-56 | 2.00E-56 |
| SCE1572_3641 | sce_6018 | 2.00E-161 | 4.00E-167 |
| SCE1572_3646 | sce_4691 | 2.00E-114 | 1.00E-105 |
| SCE1572_3647 | sce_4692 | 4.00E-102 | 8.00E-101 |
| SCE1572_3648 | sce_4693 | 4.00E-153 | 5.00E-154 |
| SCE1572_3650 | sce_2436 | 1.00E-76 | 8.00E-77 |
| SCE1572_3654 | sce_3043 | 7.00E-75 | 1.00E-74 |
| SCE1572_3656 | sce_5240 | 7.00E-16 | 1.00E-17 |
| SCE1572_3658 | sce_5238 | 2.00E-66 | 4.00E-101 |
| SCE1572_367 | sce_203 | 1.00E-93 | 9.00E-104 |
| SCE1572_3670 | sce_2337 | 7.00E-117 | 3.00E-118 |
| SCE1572_3675 | sce_8689 | 1.00E-09 | 1.00E-08 |
| SCE1572_3677 | sce_7357 | 9.00E-70 | 2.00E-58 |
| SCE1572_3678 | sce_7356 | 2.00E-71 | 2.00E-71 |
| SCE1572_368 | sce_204 | 0.00E+00 | 0.00E+00 |
| SCE1572_3680 | sce_6700 | 1.00E-20 | 9.00E-20 |
| SCE1572_3688 | sce_1325 | 0.00E+00 | 0.00E+00 |
| SCE1572_3689 | sce_3046 | 2.00E-115 | 7.00E-126 |
| SCE1572_3691 | sce_3794 | 0.00E+00 | 0.00E+00 |
| SCE1572_3696 | sce_3047 | 1.00E-06 | 6.00E-10 |
| SCE1572_37 | sce_39 | 5.00E-97 | 2.00E-90 |
| SCE1572_3700 | sce_3049 | 0.00E+00 | 0.00E+00 |
| SCE1572_3701 | sce_3051 | 6.00E-78 | 6.00E-78 |
| SCE1572_3702 | sce_3052 | 0.00E+00 | 0.00E+00 |
| SCE1572_3703 | sce_3053 | 2.00E-142 | 4.00E-150 |
| SCE1572_3704 | sce_10152 | 2.00E-27 | 1.00E-27 |
| SCE1572_3707 | sce_7655 | 4.00E-114 | 6.00E-113 |
| SCE1572_3710 | sce_8390 | 8.00E-40 | 8.00E-40 |
| SCE1572_3711 | sce_8388 | 7.00E-23 | 7.00E-23 |
| SCE1572_3712 | sce_3061 | 2.00E-137 | 3.00E-138 |
| SCE1572_3717 | sce_7923 | 2.00E-14 | 8.00E-16 |
| SCE1572_3719 | sce_3062 | 9.00E-125 | 1.00E-125 |
| SCE1572_3720 | sce_3065 | 0.00E+00 | 0.00E+00 |
| SCE1572_3722 | sce_3066 | 0.00E+00 | 0.00E+00 |
| SCE1572_3725 | sce_7838 | 3.00E-124 | 2.00E-121 |
| SCE1572_373 | sce_205 | 9.00E-126 | 2.00E-134 |
| SCE1572_3731 | sce_3071 | 0.00E+00 | 0.00E+00 |
| SCE1572_3732 | sce_3072 | 0.00E+00 | 0.00E+00 |
| SCE1572_3734 | sce_5891 | 3.00E-93 | 5.00E-101 |
| SCE1572_3738 | sce_3078 | 7.00E-62 | 2.00E-98 |
| SCE1572_374 | sce_206 | 0.00E+00 | 0.00E+00 |
| SCE1572_3745 | sce_3083 | 4.00E-57 | 2.00E-129 |
| SCE1572_3746 | sce_3084 | 6.00E-84 | 6.00E-83 |
| SCE1572_3748 | sce_3085 | 0.00E+00 | 0.00E+00 |
| SCE1572_3748 | sce_7640 | 0.00E+00 | 0.00E+00 |
| SCE1572_3748 | sce_388 | 0.00E+00 | 0.00E+00 |
| SCE1572_3748 | sce_5835 | 0.00E+00 | 0.00E+00 |

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| SCE1572_3748 | sce_10204 | 0.00E+00 | 0.00E+00 |
| SCE1572_3748 | sce_3003 | 0.00E+00 | 0.00E+00 |
| SCE1572_3748 | sce_9557 | 0.00E+00 | 0.00E+00 |
| SCE1572_3748 | sce_7109 | 0.00E+00 | 0.00E+00 |
| SCE1572_3748 | sce_7661 | 0.00E+00 | 0.00E+00 |
| SCE1572_3748 | sce_4513 | 0.00E+00 | 0.00E+00 |
| SCE1572_3748 | sce_9920 | 0.00E+00 | 0.00E+00 |
| SCE1572_3748 | sce_3917 | 0.00E+00 | 0.00E+00 |
| SCE1572_3748 | sce_6535 | 0.00E+00 | 0.00E+00 |
| SCE1572_3748 | sce_6093 | 0.00E+00 | 0.00E+00 |
| SCE1572_3749 | sce_3086 | 3.00E-48 | 2.00E-55 |
| SCE1572_3750 | sce_3087 | 4.00E-88 | 2.00E-90 |
| SCE1572_3752 | sce_9196 | 6.00E-49 | 6.00E-49 |
| SCE1572_3755 | sce_4641 | 0.00E+00 | 0.00E+00 |
| SCE1572_3758 | sce_8592 | 0.00E+00 | 0.00E+00 |
| SCE1572_3758 | sce_3937 | 0.00E+00 | 0.00E+00 |
| SCE1572_3759 | sce_8592 | 0.00E+00 | 0.00E+00 |
| SCE1572_3759 | sce_3937 | 0.00E+00 | 0.00E+00 |
| SCE1572_3761 | sce_3092 | 0.00E+00 | 0.00E+00 |
| SCE1572_3762 | sce_3093 | 0.00E+00 | 0.00E+00 |
| SCE1572_3763 | sce_3100 | 2.00E-51 | 1.00E-53 |
| SCE1572_3764 | sce_3101 | 2.00E-145 | 7.00E-149 |
| SCE1572_3765 | sce_3102 | 0.00E+00 | 0.00E+00 |
| SCE1572_3766 | sce_3103 | 5.00E-176 | 4.00E-164 |
| SCE1572_3767 | sce_3104 | 2.00E-126 | 1.00E-128 |
| SCE1572_3768 | sce_3105 | 6.00E-161 | 7.00E-163 |
| SCE1572_3769 | sce_3106 | 5.00E-50 | 3.00E-57 |
| SCE1572_3771 | sce_3107 | 5.00E-149 | 4.00E-159 |
| SCE1572_3772 | sce_3108 | 1.00E-159 | 1.00E-159 |
| SCE1572_3773 | sce_3109 | 0.00E+00 | 0.00E+00 |
| SCE1572_3774 | sce_3110 | 0.00E+00 | 0.00E+00 |
| SCE1572_3775 | sce_3111 | 2.00E-71 | 5.00E-72 |
| SCE1572_3776 | sce_3112 | 0.00E+00 | 0.00E+00 |
| SCE1572_3777 | sce_3113 | 3.00E-140 | 2.00E-154 |
| SCE1572_3778 | sce_3114 | 2.00E-173 | 9.00E-174 |
| SCE1572_3779 | sce_3115 | 0.00E+00 | 0.00E+00 |
| SCE1572_3780 | sce_3116 | 5.00E-41 | 5.00E-41 |
| SCE1572_3781 | sce_3117 | 2.00E-157 | 8.00E-149 |
| SCE1572_3782 | sce_3118 | 9.00E-156 | 9.00E-148 |
| SCE1572_3784 | sce_3119 | 8.00E-84 | 7.00E-74 |
| SCE1572_3785 | sce_3120 | 1.00E-48 | 1.00E-48 |
| SCE1572_3786 | sce_3121 | 0.00E+00 | 0.00E+00 |
| SCE1572_3786 | sce_6618 | 0.00E+00 | 0.00E+00 |
| SCE1572_3787 | sce_3122 | 1.00E-97 | 3.00E-91 |
| SCE1572_3788 | sce_3123 | 2.00E-143 | 2.00E-143 |
| SCE1572_3789 | sce_3124 | 9.00E-152 | 9.00E-152 |
| SCE1572_379 | sce_211 | 8.00E-173 | 3.00E-162 |
| SCE1572_3790 | sce_3126 | 0.00E+00 | 0.00E+00 |
| SCE1572_3791 | sce_3127 | 0.00E+00 | 0.00E+00 |
| SCE1572_3793 | sce_3129 | 0.00E+00 | 0.00E+00 |
| SCE1572_3794 | sce_3130 | 6.00E-53 | 4.00E-44 |
| SCE1572_3795 | sce_3131 | 1.00E-146 | 4.00E-155 |
| SCE1572_3796 | sce_3132 | 0.00E+00 | 0.00E+00 |
| SCE1572_3797 | sce_3133 | 0.00E+00 | 0.00E+00 |
| SCE1572_3798 | sce_3134 | 0.00E+00 | 0.00E+00 |
| SCE1572_3799 | sce_3135 | 0.00E+00 | 0.00E+00 |
| SCE1572_38 | sce_40 | 1.00E-179 | 0.00E+00 |
| SCE1572_3801 | sce_5620 | 1.00E-53 | 1.00E-53 |
| SCE1572_3803 | sce_3137 | 0.00E+00 | 0.00E+00 |
| SCE1572_3805 | sce_3139 | 1.00E-97 | 9.00E-75 |
| SCE1572_3807 | sce_5178 | 0.00E+00 | 0.00E+00 |
| SCE1572_3808 | sce_3140 | 3.00E-178 | 0.00E+00 |
| SCE1572_3809 | sce_3141 | 4.00E-56 | 2.00E-70 |
| SCE1572_381 | sce_6106 | 1.00E-16 | 2.00E-17 |
| SCE1572_3815 | sce_2107 | 1.00E-125 | 1.00E-123 |
| SCE1572_3817 | sce_4644 | 9.00E-87 | 1.00E-86 |
| SCE1572_3818 | sce_3145 | 0.00E+00 | 0.00E+00 |
| SCE1572_382 | sce_212 | 1.00E-47 | 8.00E-46 |
| SCE1572_3820 | sce_3147 | 7.00E-159 | 5.00E-141 |
| SCE1572_3821 | sce_3148 | 0.00E+00 | 0.00E+00 |
| SCE1572_3821 | sce_1814 | 0.00E+00 | 0.00E+00 |
| SCE1572_3821 | sce_9222 | 0.00E+00 | 0.00E+00 |
| SCE1572_3822 | sce_3149 | 3.00E-15 | 2.00E-12 |
| SCE1572_3823 | sce_3151 | 9.00E-61 | 8.00E-67 |
| SCE1572_3824 | sce_3152 | 1.00E-169 | 7.00E-158 |
| SCE1572_3826 | sce_3153 | 0.00E+00 | 0.00E+00 |

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| SCE1572_3827 | sce_3154 | 6.00E-19 | 9.00E-19 |
| SCE1572_3828 | sce_3155 | 3.00E-117 | 3.00E-117 |
| SCE1572_3829 | sce_3156 | 0.00E+00 | 4.00E-142 |
| SCE1572_383 | sce_7076 | 1.00E-144 | 2.00E-140 |
| SCE1572_3830 | sce_3157 | 2.00E-86 | 9.00E-87 |
| SCE1572_3831 | sce_3158 | 4.00E-101 | 1.00E-105 |
| SCE1572_3832 | sce_3159 | 2.00E-145 | 1.00E-150 |
| SCE1572_3833 | sce_3161 | 5.00E-126 | 2.00E-116 |
| SCE1572_3835 | sce_7642 | 2.00E-169 | 0.00E+00 |
| SCE1572_3839 | sce_3162 | 8.00E-152 | 8.00E-152 |
| SCE1572_3840 | sce_3163 | 2.00E-88 | 2.00E-88 |
| SCE1572_3841 | sce_3164 | 9.00E-177 | 0.00E+00 |
| SCE1572_3842 | sce_3165 | 2.00E-98 | 2.00E-98 |
| SCE1572_3846 | sce_2595 | 7.00E-20 | 8.00E-20 |
| SCE1572_3848 | sce_3166 | 9.00E-82 | 4.00E-82 |
| SCE1572_3849 | sce_3167 | 3.00E-82 | 1.00E-87 |
| SCE1572_3850 | sce_3168 | 6.00E-112 | 6.00E-112 |
| SCE1572_3851 | sce_3169 | 2.00E-109 | 2.00E-109 |
| SCE1572_3852 | sce_3170 | 3.00E-145 | 1.00E-145 |
| SCE1572_3854 | sce_3171 | 2.00E-132 | 2.00E-120 |
| SCE1572_3855 | sce_3172 | 2.00E-78 | 2.00E-85 |
| SCE1572_3856 | sce_3180 | 2.00E-83 | 4.00E-141 |
| SCE1572_3857 | sce_3181 | 0.00E+00 | 0.00E+00 |
| SCE1572_3858 | sce_3182 | 2.00E-109 | 5.00E-129 |
| SCE1572_3859 | sce_3183 | 0.00E+00 | 0.00E+00 |
| SCE1572_3860 | sce_3184 | 1.00E-102 | 3.00E-106 |
| SCE1572_3861 | sce_3185 | 0.00E+00 | 0.00E+00 |
| SCE1572_3861 | sce_5602 | 0.00E+00 | 0.00E+00 |
| SCE1572_3861 | sce_5033 | 0.00E+00 | 0.00E+00 |
| SCE1572_3863 | sce_3186 | 0.00E+00 | 0.00E+00 |
| SCE1572_3864 | sce_3187 | 0.00E+00 | 0.00E+00 |
| SCE1572_3866 | sce_3188 | 3.00E-86 | 2.00E-88 |
| SCE1572_3867 | sce_3189 | 2.00E-69 | 4.00E-65 |
| SCE1572_3868 | sce_3190 | 3.00E-153 | 2.00E-160 |
| SCE1572_3869 | sce_3191 | 2.00E-78 | 4.00E-76 |
| SCE1572_387 | sce_213 | 9.00E-20 | 3.00E-24 |
| SCE1572_3870 | sce_3192 | 1.00E-56 | 4.00E-66 |
| SCE1572_3871 | sce_3194 | 2.00E-104 | 6.00E-107 |
| SCE1572_3872 | sce_3195 | 0.00E+00 | 0.00E+00 |
| SCE1572_3873 | sce_3196 | 4.00E-151 | 7.00E-162 |
| SCE1572_3874 | sce_3197 | 0.00E+00 | 0.00E+00 |
| SCE1572_3875 | sce_3198 | 8.00E-89 | 7.00E-95 |
| SCE1572_3876 | sce_3199 | 6.00E-44 | 6.00E-44 |
| SCE1572_3877 | sce_3200 | 4.00E-11 | 2.00E-12 |
| SCE1572_3878 | sce_3201 | 0.00E+00 | 0.00E+00 |
| SCE1572_3879 | sce_3202 | 2.00E-174 | 2.00E-174 |
| SCE1572_388 | sce_214 | 8.00E-52 | 2.00E-56 |
| SCE1572_3880 | sce_3204 | 0.00E+00 | 0.00E+00 |
| SCE1572_3881 | sce_3205 | 2.00E-95 | 9.00E-94 |
| SCE1572_3882 | sce_3206 | 5.00E-119 | 1.00E-142 |
| SCE1572_3883 | sce_3207 | 2.00E-62 | 2.00E-69 |
| SCE1572_3884 | sce_3208 | 2.00E-86 | 2.00E-86 |
| SCE1572_3885 | sce_3209 | 2.00E-76 | 2.00E-76 |
| SCE1572_3886 | sce_3210 | 6.00E-101 | 1.00E-98 |
| SCE1572_3887 | sce_3211 | 0.00E+00 | 0.00E+00 |
| SCE1572_3888 | sce_3212 | 0.00E+00 | 0.00E+00 |
| SCE1572_3889 | sce_3213 | 4.00E-101 | 2.00E-105 |
| SCE1572_389 | sce_5187 | 8.00E-20 | 2.00E-19 |
| SCE1572_3890 | sce_3215 | 0.00E+00 | 0.00E+00 |
| SCE1572_3891 | sce_3216 | 0.00E+00 | 0.00E+00 |
| SCE1572_3892 | sce_3221 | 2.00E-133 | 5.00E-139 |
| SCE1572_3893 | sce_3222 | 3.00E-65 | 2.00E-60 |
| SCE1572_3894 | sce_3223 | 3.00E-86 | 2.00E-87 |
| SCE1572_3895 | sce_3224 | 2.00E-82 | 3.00E-81 |
| SCE1572_3896 | sce_3225 | 7.00E-135 | 3.00E-152 |
| SCE1572_3897 | sce_3226 | 1.00E-131 | 5.00E-144 |
| SCE1572_3898 | sce_3227 | 0.00E+00 | 0.00E+00 |
| SCE1572_3899 | sce_3228 | 0.00E+00 | 7.00E-178 |
| SCE1572_39 | sce_41 | 0.00E+00 | 0.00E+00 |
| SCE1572_39 | sce_370 | 0.00E+00 | 0.00E+00 |
| SCE1572_390 | sce_5188 | 9.00E-53 | 1.00E-56 |
| SCE1572_3900 | sce_3229 | 5.00E-102 | 3.00E-102 |
| SCE1572_3901 | sce_3230 | 8.00E-69 | 6.00E-78 |
| SCE1572_3903 | sce_3232 | 0.00E+00 | 0.00E+00 |
| SCE1572_3905 | sce_3234 | 0.00E+00 | 0.00E+00 |
| SCE1572_3906 | sce_3235 | 0.00E+00 | 0.00E+00 |

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|--------------|-----------|-----------|-----------|
| SCE1572_3907 | sce_3236 | 4.00E-118 | 1.00E-131 |
| SCE1572_3908 | sce_3238 | 1.00E-13 | 1.00E-22 |
| SCE1572_3909 | sce_3239 | 0.00E+00 | 0.00E+00 |
| SCE1572_3910 | sce_3240 | 4.00E-113 | 9.00E-111 |
| SCE1572_3911 | sce_3241 | 7.00E-86 | 7.00E-86 |
| SCE1572_3912 | sce_3242 | 9.00E-29 | 1.00E-14 |
| SCE1572_3913 | sce_3243 | 0.00E+00 | 0.00E+00 |
| SCE1572_3914 | sce_3245 | 7.00E-129 | 1.00E-136 |
| SCE1572_3915 | sce_3246 | 2.00E-103 | 3.00E-80 |
| SCE1572_3916 | sce_3247 | 1.00E-136 | 7.00E-148 |
| SCE1572_3917 | sce_3249 | 2.00E-127 | 2.00E-134 |
| SCE1572_3918 | sce_3250 | 2.00E-85 | 2.00E-85 |
| SCE1572_3919 | sce_3251 | 1.00E-68 | 5.00E-86 |
| SCE1572_392 | sce_215 | 1.00E-51 | 3.00E-57 |
| SCE1572_3920 | sce_3252 | 2.00E-119 | 9.00E-119 |
| SCE1572_3921 | sce_3254 | 1.00E-114 | 9.00E-98 |
| SCE1572_3922 | sce_3255 | 5.00E-90 | 6.00E-96 |
| SCE1572_3923 | sce_3256 | 0.00E+00 | 0.00E+00 |
| SCE1572_3924 | sce_3257 | 3.00E-84 | 1.00E-84 |
| SCE1572_3925 | sce_3258 | 9.00E-150 | 3.00E-159 |
| SCE1572_3926 | sce_3259 | 3.00E-142 | 6.00E-155 |
| SCE1572_3927 | sce_3260 | 3.00E-42 | 3.00E-42 |
| SCE1572_3928 | sce_3261 | 0.00E+00 | 0.00E+00 |
| SCE1572_3929 | sce_3262 | 0.00E+00 | 0.00E+00 |
| SCE1572_393 | sce_2460 | 1.00E-22 | 7.00E-20 |
| SCE1572_3930 | sce_3263 | 3.00E-115 | 7.00E-123 |
| SCE1572_3931 | sce_3264 | 3.00E-141 | 3.00E-141 |
| SCE1572_3932 | sce_3265 | 1.00E-140 | 1.00E-140 |
| SCE1572_3933 | sce_3267 | 9.00E-164 | 6.00E-167 |
| SCE1572_3935 | sce_3268 | 0.00E+00 | 0.00E+00 |
| SCE1572_3937 | sce_3270 | 7.00E-103 | 2.00E-94 |
| SCE1572_3938 | sce_3271 | 4.00E-128 | 5.00E-131 |
| SCE1572_3939 | sce_3272 | 2.00E-42 | 5.00E-38 |
| SCE1572_394 | sce_217 | 0.00E+00 | 0.00E+00 |
| SCE1572_3940 | sce_3273 | 6.00E-99 | 7.00E-99 |
| SCE1572_3941 | sce_3274 | 0.00E+00 | 0.00E+00 |
| SCE1572_3942 | sce_3275 | 0.00E+00 | 0.00E+00 |
| SCE1572_3943 | sce_3276 | 0.00E+00 | 0.00E+00 |
| SCE1572_3944 | sce_3277 | 3.00E-27 | 3.00E-22 |
| SCE1572_3945 | sce_3278 | 0.00E+00 | 0.00E+00 |
| SCE1572_3946 | sce_3279 | 3.00E-174 | 2.00E-166 |
| SCE1572_3947 | sce_3281 | 0.00E+00 | 0.00E+00 |
| SCE1572_3947 | sce_3280 | 0.00E+00 | 0.00E+00 |
| SCE1572_3948 | sce_3282 | 0.00E+00 | 0.00E+00 |
| SCE1572_3949 | sce_3283 | 0.00E+00 | 0.00E+00 |
| SCE1572_395 | sce_218 | 4.00E-149 | 1.00E-132 |
| SCE1572_3951 | sce_3285 | 0.00E+00 | 0.00E+00 |
| SCE1572_3952 | sce_3286 | 2.00E-101 | 5.00E-102 |
| SCE1572_3953 | sce_3287 | 2.00E-96 | 2.00E-93 |
| SCE1572_3958 | sce_8665 | 2.00E-07 | 3.00E-14 |
| SCE1572_3959 | sce_3289 | 0.00E+00 | 0.00E+00 |
| SCE1572_3960 | sce_2531 | 4.00E-25 | 9.00E-24 |
| SCE1572_3961 | sce_3291 | 2.00E-176 | 5.00E-177 |
| SCE1572_3962 | sce_3292 | 0.00E+00 | 0.00E+00 |
| SCE1572_3963 | sce_3293 | 0.00E+00 | 0.00E+00 |
| SCE1572_3964 | sce_3294 | 0.00E+00 | 0.00E+00 |
| SCE1572_3965 | sce_3295 | 2.00E-68 | 1.00E-64 |
| SCE1572_3967 | sce_10164 | 3.00E-101 | 1.00E-101 |
| SCE1572_3968 | sce_3296 | 0.00E+00 | 0.00E+00 |
| SCE1572_3969 | sce_3297 | 0.00E+00 | 0.00E+00 |
| SCE1572_3970 | sce_3299 | 8.00E-118 | 8.00E-118 |
| SCE1572_3971 | sce_3300 | 0.00E+00 | 0.00E+00 |
| SCE1572_3972 | sce_3301 | 2.00E-38 | 2.00E-38 |
| SCE1572_3973 | sce_3302 | 1.00E-171 | 7.00E-159 |
| SCE1572_3974 | sce_3303 | 2.00E-73 | 7.00E-74 |
| SCE1572_3975 | sce_3304 | 6.00E-62 | 1.00E-73 |
| SCE1572_3976 | sce_3305 | 2.00E-131 | 2.00E-131 |
| SCE1572_3977 | sce_3306 | 4.00E-137 | 2.00E-137 |
| SCE1572_3978 | sce_3307 | 1.00E-138 | 5.00E-132 |
| SCE1572_3979 | sce_3308 | 2.00E-145 | 8.00E-152 |
| SCE1572_398 | sce_219 | 0.00E+00 | 0.00E+00 |
| SCE1572_3980 | sce_3309 | 0.00E+00 | 0.00E+00 |
| SCE1572_3981 | sce_3310 | 0.00E+00 | 0.00E+00 |
| SCE1572_3982 | sce_3311 | 5.00E-118 | 6.00E-118 |
| SCE1572_3983 | sce_3314 | 4.00E-84 | 4.00E-91 |
| SCE1572_3984 | sce_3315 | 1.00E-124 | 2.00E-122 |

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| SCE1572_3985 | sce_3316 | 0.00E+00 | 0.00E+00 |
| SCE1572_3986 | sce_3317 | 7.00E-140 | 2.00E-136 |
| SCE1572_3987 | sce_3318 | 6.00E-72 | 5.00E-72 |
| SCE1572_3988 | sce_3319 | 5.00E-67 | 1.00E-71 |
| SCE1572_3989 | sce_3320 | 2.00E-111 | 7.00E-103 |
| SCE1572_3990 | sce_3321 | 0.00E+00 | 0.00E+00 |
| SCE1572_3991 | sce_3322 | 0.00E+00 | 0.00E+00 |
| SCE1572_3992 | sce_3323 | 4.00E-07 | 3.00E-06 |
| SCE1572_3993 | sce_3324 | 1.00E-22 | 3.00E-18 |
| SCE1572_3997 | sce_3327 | 0.00E+00 | 0.00E+00 |
| SCE1572_3998 | sce_3328 | 0.00E+00 | 0.00E+00 |
| SCE1572_3999 | sce_3329 | 0.00E+00 | 0.00E+00 |
| SCE1572_4 | sce_4 | 1.00E-76 | 1.00E-83 |
| SCE1572_400 | sce_8410 | 2.00E-45 | 5.00E-35 |
| SCE1572_4000 | sce_3330 | 2.00E-144 | 2.00E-136 |
| SCE1572_4001 | sce_3331 | 0.00E+00 | 0.00E+00 |
| SCE1572_4002 | sce_3332 | 0.00E+00 | 0.00E+00 |
| SCE1572_4003 | sce_3333 | 1.00E-77 | 1.00E-77 |
| SCE1572_4005 | sce_3335 | 2.00E-56 | 4.00E-56 |
| SCE1572_4006 | sce_3336 | 0.00E+00 | 0.00E+00 |
| SCE1572_4007 | sce_3337 | 0.00E+00 | 0.00E+00 |
| SCE1572_4008 | sce_3338 | 5.00E-49 | 5.00E-60 |
| SCE1572_4009 | sce_3339 | 0.00E+00 | 0.00E+00 |
| SCE1572_4010 | sce_3340 | 0.00E+00 | 0.00E+00 |
| SCE1572_4011 | sce_3341 | 8.00E-113 | 7.00E-111 |
| SCE1572_4012 | sce_3342 | 0.00E+00 | 0.00E+00 |
| SCE1572_4013 | sce_3343 | 6.00E-172 | 1.00E-155 |
| SCE1572_4015 | sce_3344 | 3.00E-51 | 5.00E-53 |
| SCE1572_4017 | sce_3345 | 9.00E-116 | 1.00E-113 |
| SCE1572_4018 | sce_3346 | 0.00E+00 | 0.00E+00 |
| SCE1572_4019 | sce_3347 | 2.00E-123 | 5.00E-111 |
| SCE1572_4020 | sce_3348 | 7.00E-95 | 1.00E-86 |
| SCE1572_4021 | sce_3349 | 2.00E-112 | 2.00E-112 |
| SCE1572_4022 | sce_3350 | 0.00E+00 | 0.00E+00 |
| SCE1572_4023 | sce_3351 | 5.00E-78 | 2.00E-80 |
| SCE1572_4024 | sce_3352 | 0.00E+00 | 0.00E+00 |
| SCE1572_4025 | sce_3353 | 2.00E-150 | 6.00E-138 |
| SCE1572_4026 | sce_3354 | 0.00E+00 | 0.00E+00 |
| SCE1572_4027 | sce_3355 | 0.00E+00 | 0.00E+00 |
| SCE1572_4028 | sce_3356 | 2.00E-108 | 2.00E-108 |
| SCE1572_4029 | sce_3357 | 1.00E-92 | 1.00E-92 |
| SCE1572_4030 | sce_3358 | 4.00E-116 | 5.00E-120 |
| SCE1572_4031 | sce_3360 | 1.00E-115 | 1.00E-115 |
| SCE1572_4032 | sce_3361 | 1.00E-97 | 1.00E-97 |
| SCE1572_4034 | sce_3362 | 2.00E-99 | 2.00E-99 |
| SCE1572_4035 | sce_3363 | 6.00E-165 | 5.00E-165 |
| SCE1572_4036 | sce_3364 | 8.00E-107 | 1.00E-119 |
| SCE1572_4037 | sce_3365 | 2.00E-65 | 3.00E-59 |
| SCE1572_4038 | sce_3366 | 0.00E+00 | 0.00E+00 |
| SCE1572_404 | sce_224 | 9.00E-155 | 9.00E-155 |
| SCE1572_4041 | sce_3368 | 0.00E+00 | 0.00E+00 |
| SCE1572_4043 | sce_3369 | 0.00E+00 | 0.00E+00 |
| SCE1572_4044 | sce_3370 | 4.00E-104 | 4.00E-96 |
| SCE1572_4045 | sce_3372 | 0.00E+00 | 0.00E+00 |
| SCE1572_4047 | sce_3374 | 9.00E-164 | 7.00E-158 |
| SCE1572_4048 | sce_5533 | 1.00E-66 | 7.00E-59 |
| SCE1572_4049 | sce_3375 | 9.00E-143 | 3.00E-143 |
| SCE1572_405 | sce_225 | 0.00E+00 | 0.00E+00 |
| SCE1572_405 | sce_2161 | 0.00E+00 | 0.00E+00 |
| SCE1572_405 | sce_6235 | 0.00E+00 | 0.00E+00 |
| SCE1572_405 | sce_8357 | 0.00E+00 | 0.00E+00 |
| SCE1572_405 | sce_5276 | 0.00E+00 | 0.00E+00 |
| SCE1572_4050 | sce_3376 | 0.00E+00 | 0.00E+00 |
| SCE1572_4050 | sce_5364 | 0.00E+00 | 0.00E+00 |
| SCE1572_4050 | sce_4711 | 0.00E+00 | 0.00E+00 |
| SCE1572_4051 | sce_3377 | 6.00E-95 | 6.00E-95 |
| SCE1572_4052 | sce_3378 | 9.00E-150 | 1.00E-157 |
| SCE1572_4053 | sce_3379 | 1.00E-173 | 5.00E-166 |
| SCE1572_4054 | sce_3380 | 4.00E-126 | 4.00E-126 |
| SCE1572_4055 | sce_3381 | 0.00E+00 | 0.00E+00 |
| SCE1572_4056 | sce_3382 | 1.00E-89 | 2.00E-107 |
| SCE1572_4058 | sce_3383 | 1.00E-99 | 1.00E-75 |
| SCE1572_4059 | sce_3384 | 2.00E-174 | 0.00E+00 |
| SCE1572_4060 | sce_3385 | 9.00E-75 | 9.00E-75 |
| SCE1572_4061 | sce_3386 | 1.00E-132 | 5.00E-137 |
| SCE1572_4062 | sce_3387 | 2.00E-124 | 1.00E-124 |

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| SCE1572_4063 | sce_3388 | 2.00E-119 | 2.00E-133 |
| SCE1572_4065 | sce_3390 | 0.00E+00 | 0.00E+00 |
| SCE1572_4066 | sce_3391 | 0.00E+00 | 0.00E+00 |
| SCE1572_4067 | sce_3392 | 2.00E-66 | 1.00E-65 |
| SCE1572_4068 | sce_3393 | 0.00E+00 | 0.00E+00 |
| SCE1572_407 | sce_226 | 4.00E-82 | 4.00E-82 |
| SCE1572_4070 | sce_3394 | 1.00E-79 | 2.00E-87 |
| SCE1572_4071 | sce_3396 | 2.00E-55 | 4.00E-50 |
| SCE1572_4072 | sce_3397 | 0.00E+00 | 0.00E+00 |
| SCE1572_4073 | sce_3398 | 0.00E+00 | 0.00E+00 |
| SCE1572_4074 | sce_3399 | 0.00E+00 | 0.00E+00 |
| SCE1572_4075 | sce_3401 | 4.00E-60 | 4.00E-47 |
| SCE1572_4077 | sce_3403 | 1.00E-70 | 1.00E-70 |
| SCE1572_4078 | sce_3404 | 2.00E-114 | 2.00E-122 |
| SCE1572_408 | sce_227 | 0.00E+00 | 0.00E+00 |
| SCE1572_4080 | sce_3406 | 0.00E+00 | 0.00E+00 |
| SCE1572_4084 | sce_3407 | 1.00E-94 | 1.00E-105 |
| SCE1572_4085 | sce_3410 | 1.00E-47 | 3.00E-48 |
| SCE1572_4086 | sce_3412 | 0.00E+00 | 0.00E+00 |
| SCE1572_4089 | sce_3415 | 2.00E-175 | 1.00E-170 |
| SCE1572_409 | sce_5625 | 2.00E-116 | 1.00E-121 |
| SCE1572_4090 | sce_3416 | 1.00E-126 | 4.00E-135 |
| SCE1572_4091 | sce_3417 | 2.00E-147 | 1.00E-151 |
| SCE1572_4092 | sce_3418 | 2.00E-92 | 2.00E-92 |
| SCE1572_4093 | sce_3419 | 2.00E-125 | 1.00E-138 |
| SCE1572_4095 | sce_3420 | 0.00E+00 | 0.00E+00 |
| SCE1572_4098 | sce_3422 | 9.00E-53 | 2.00E-52 |
| SCE1572_41 | sce_42 | 4.00E-62 | 1.00E-57 |
| SCE1572_410 | sce_228 | 2.00E-39 | 1.00E-48 |
| SCE1572_4100 | sce_3438 | 0.00E+00 | 0.00E+00 |
| SCE1572_4101 | sce_3439 | 0.00E+00 | 0.00E+00 |
| SCE1572_4105 | sce_3459 | 6.00E-135 | 6.00E-142 |
| SCE1572_411 | sce_229 | 0.00E+00 | 0.00E+00 |
| SCE1572_411 | sce_805 | 0.00E+00 | 0.00E+00 |
| SCE1572_4110 | sce_3461 | 1.00E-140 | 2.00E-141 |
| SCE1572_4111 | sce_3462 | 1.00E-102 | 1.00E-102 |
| SCE1572_4112 | sce_3463 | 2.00E-82 | 2.00E-95 |
| SCE1572_4113 | sce_3464 | 5.00E-122 | 6.00E-128 |
| SCE1572_4115 | sce_3465 | 4.00E-168 | 3.00E-157 |
| SCE1572_4116 | sce_7384 | 1.00E-67 | 1.00E-70 |
| SCE1572_4118 | sce_3468 | 2.00E-121 | 3.00E-124 |
| SCE1572_4119 | sce_3469 | 4.00E-103 | 4.00E-103 |
| SCE1572_412 | sce_230 | 8.00E-75 | 2.00E-83 |
| SCE1572_4122 | sce_3467 | 6.00E-74 | 2.00E-74 |
| SCE1572_4125 | sce_3471 | 1.00E-128 | 2.00E-180 |
| SCE1572_4128 | sce_3472 | 4.00E-65 | 5.00E-65 |
| SCE1572_4129 | sce_3473 | 0.00E+00 | 0.00E+00 |
| SCE1572_413 | sce_231 | 0.00E+00 | 0.00E+00 |
| SCE1572_4130 | sce_3474 | 6.00E-138 | 6.00E-138 |
| SCE1572_4131 | sce_3475 | 3.00E-21 | 5.00E-19 |
| SCE1572_4132 | sce_3476 | 0.00E+00 | 0.00E+00 |
| SCE1572_4133 | sce_3477 | 6.00E-73 | 2.00E-83 |
| SCE1572_4138 | sce_3483 | 2.00E-129 | 8.00E-139 |
| SCE1572_4139 | sce_3484 | 2.00E-105 | 7.00E-114 |
| SCE1572_414 | sce_232 | 6.00E-40 | 1.00E-46 |
| SCE1572_4140 | sce_3485 | 1.00E-178 | 1.00E-174 |
| SCE1572_4141 | sce_3486 | 7.00E-153 | 1.00E-139 |
| SCE1572_4147 | sce_7614 | 1.00E-82 | 1.00E-76 |
| SCE1572_4148 | sce_7615 | 2.00E-39 | 2.00E-39 |
| SCE1572_4151 | sce_3080 | 1.00E-173 | 2.00E-153 |
| SCE1572_4152 | sce_8359 | 1.00E-80 | 1.00E-73 |
| SCE1572_4155 | sce_2035 | 1.00E-104 | 6.00E-101 |
| SCE1572_4156 | sce_3492 | 0.00E+00 | 0.00E+00 |
| SCE1572_4158 | sce_2442 | 8.00E-66 | 2.00E-63 |
| SCE1572_4166 | sce_9855 | 2.00E-20 | 7.00E-18 |
| SCE1572_4171 | sce_3495 | 0.00E+00 | 0.00E+00 |
| SCE1572_4172 | sce_3496 | 0.00E+00 | 0.00E+00 |
| SCE1572_4173 | sce_3497 | 0.00E+00 | 0.00E+00 |
| SCE1572_4174 | sce_3498 | 3.00E-48 | 3.00E-54 |
| SCE1572_4179 | sce_3503 | 2.00E-44 | 9.00E-65 |
| SCE1572_418 | sce_9373 | 0.00E+00 | 0.00E+00 |
| SCE1572_418 | sce_4062 | 0.00E+00 | 0.00E+00 |
| SCE1572_4180 | sce_3504 | 5.00E-55 | 1.00E-51 |
| SCE1572_4181 | sce_3505 | 0.00E+00 | 0.00E+00 |
| SCE1572_4184 | sce_3506 | 4.00E-78 | 1.00E-78 |
| SCE1572_4185 | sce_3507 | 0.00E+00 | 0.00E+00 |

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| SCE1572_4186 | sce_3508 | 6.00E-57 | 9.00E-57 |
| SCE1572_4187 | sce_3509 | 0.00E+00 | 0.00E+00 |
| SCE1572_4188 | sce_3510 | 0.00E+00 | 0.00E+00 |
| SCE1572_4189 | sce_3511 | 0.00E+00 | 0.00E+00 |
| SCE1572_419 | sce_233 | 0.00E+00 | 0.00E+00 |
| SCE1572_4190 | sce_3512 | 0.00E+00 | 0.00E+00 |
| SCE1572_4191 | sce_3513 | 0.00E+00 | 0.00E+00 |
| SCE1572_4192 | sce_3514 | 0.00E+00 | 0.00E+00 |
| SCE1572_4193 | sce_3515 | 2.00E-131 | 3.00E-131 |
| SCE1572_4194 | sce_3516 | 9.00E-146 | 5.00E-139 |
| SCE1572_4195 | sce_3517 | 2.00E-120 | 4.00E-123 |
| SCE1572_4199 | sce_3518 | 6.00E-138 | 9.00E-126 |
| SCE1572_420 | sce_234 | 5.00E-101 | 7.00E-91 |
| SCE1572_4200 | sce_479 | 3.00E-85 | 9.00E-107 |
| SCE1572_4201 | sce_3519 | 1.00E-58 | 3.00E-49 |
| SCE1572_4202 | sce_3520 | 0.00E+00 | 0.00E+00 |
| SCE1572_4202 | sce_10425 | 0.00E+00 | 0.00E+00 |
| SCE1572_4202 | sce_7361 | 0.00E+00 | 0.00E+00 |
| SCE1572_4203 | sce_3521 | 2.00E-156 | 2.00E-156 |
| SCE1572_4204 | sce_3522 | 7.00E-37 | 6.00E-27 |
| SCE1572_4205 | sce_3523 | 3.00E-120 | 5.00E-114 |
| SCE1572_4206 | sce_3524 | 0.00E+00 | 0.00E+00 |
| SCE1572_4207 | sce_3525 | 4.00E-140 | 2.00E-139 |
| SCE1572_4208 | sce_3526 | 8.00E-136 | 9.00E-125 |
| SCE1572_4209 | sce_3527 | 2.00E-137 | 3.00E-136 |
| SCE1572_421 | sce_235 | 2.00E-72 | 6.00E-78 |
| SCE1572_4210 | sce_3528 | 5.00E-22 | 2.00E-15 |
| SCE1572_4211 | sce_3529 | 0.00E+00 | 0.00E+00 |
| SCE1572_4213 | sce_3531 | 2.00E-124 | 2.00E-124 |
| SCE1572_4215 | sce_3533 | 0.00E+00 | 0.00E+00 |
| SCE1572_4216 | sce_3534 | 0.00E+00 | 0.00E+00 |
| SCE1572_4217 | sce_3535 | 0.00E+00 | 0.00E+00 |
| SCE1572_4219 | sce_3536 | 1.00E-148 | 2.00E-152 |
| SCE1572_422 | sce_236 | 0.00E+00 | 0.00E+00 |
| SCE1572_4220 | sce_3537 | 1.00E-46 | 4.00E-50 |
| SCE1572_4221 | sce_3538 | 2.00E-108 | 2.00E-108 |
| SCE1572_4222 | sce_10449 | 2.00E-06 | 4.00E-08 |
| SCE1572_4223 | sce_3539 | 3.00E-62 | 3.00E-64 |
| SCE1572_4225 | sce_3540 | 0.00E+00 | 0.00E+00 |
| SCE1572_4227 | sce_3542 | 0.00E+00 | 0.00E+00 |
| SCE1572_4228 | sce_1020 | 2.00E-122 | 3.00E-126 |
| SCE1572_4229 | sce_118 | 1.00E-165 | 2.00E-148 |
| SCE1572_423 | sce_237 | 3.00E-71 | 6.00E-68 |
| SCE1572_4232 | sce_116 | 5.00E-110 | 2.00E-67 |
| SCE1572_4233 | sce_115 | 3.00E-50 | 3.00E-30 |
| SCE1572_4234 | sce_114 | 2.00E-26 | 2.00E-24 |
| SCE1572_4235 | sce_113 | 1.00E-29 | 1.00E-29 |
| SCE1572_4236 | sce_3543 | 4.00E-127 | 2.00E-130 |
| SCE1572_4237 | sce_3544 | 2.00E-173 | 3.00E-173 |
| SCE1572_4239 | sce_3545 | 6.00E-131 | 8.00E-123 |
| SCE1572_424 | sce_238 | 1.00E-137 | 1.00E-140 |
| SCE1572_4240 | sce_1034 | 2.00E-107 | 8.00E-113 |
| SCE1572_4244 | sce_3546 | 0.00E+00 | 0.00E+00 |
| SCE1572_4245 | sce_3547 | 4.00E-97 | 2.00E-82 |
| SCE1572_4246 | sce_3548 | 1.00E-38 | 4.00E-41 |
| SCE1572_4247 | sce_3549 | 1.00E-175 | 2.00E-175 |
| SCE1572_4248 | sce_3550 | 0.00E+00 | 0.00E+00 |
| SCE1572_425 | sce_7595 | 3.00E-110 | 3.00E-110 |
| SCE1572_4250 | sce_3551 | 0.00E+00 | 0.00E+00 |
| SCE1572_4251 | sce_3553 | 7.00E-53 | 6.00E-43 |
| SCE1572_4252 | sce_3554 | 2.00E-62 | 5.00E-67 |
| SCE1572_4255 | sce_3556 | 1.00E-32 | 2.00E-32 |
| SCE1572_4256 | sce_3557 | 7.00E-120 | 2.00E-119 |
| SCE1572_4258 | sce_3559 | 2.00E-114 | 5.00E-117 |
| SCE1572_426 | sce_7596 | 1.00E-59 | 4.00E-61 |
| SCE1572_4260 | sce_9165 | 0.00E+00 | 0.00E+00 |
| SCE1572_4268 | sce_4615 | 7.00E-28 | 6.00E-29 |
| SCE1572_427 | sce_7597 | 2.00E-105 | 2.00E-104 |
| SCE1572_4273 | sce_4652 | 1.00E-08 | 8.00E-08 |
| SCE1572_428 | sce_821 | 2.00E-64 | 2.00E-78 |
| SCE1572_4282 | sce_3583 | 1.00E-53 | 4.00E-53 |
| SCE1572_4284 | sce_4504 | 4.00E-114 | 4.00E-114 |
| SCE1572_4288 | sce_3587 | 1.00E-143 | 2.00E-150 |
| SCE1572_4289 | sce_2038 | 1.00E-99 | 2.00E-99 |
| SCE1572_429 | sce_9917 | 0.00E+00 | 0.00E+00 |
| SCE1572_4292 | sce_3630 | 7.00E-142 | 8.00E-142 |

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| SCE1572_4293 | sce_3631 | 0.00E+00 | 0.00E+00 |
| SCE1572_4294 | sce_3632 | 0.00E+00 | 0.00E+00 |
| SCE1572_4295 | sce_3633 | 2.00E-107 | 2.00E-113 |
| SCE1572_4296 | sce_3634 | 0.00E+00 | 0.00E+00 |
| SCE1572_4299 | sce_3635 | 0.00E+00 | 0.00E+00 |
| SCE1572_430 | sce_9918 | 0.00E+00 | 0.00E+00 |
| SCE1572_430 | sce_894 | 0.00E+00 | 0.00E+00 |
| SCE1572_430 | sce_6531 | 0.00E+00 | 0.00E+00 |
| SCE1572_4300 | sce_3636 | 0.00E+00 | 0.00E+00 |
| SCE1572_4301 | sce_3637 | 0.00E+00 | 0.00E+00 |
| SCE1572_4303 | sce_1742 | 3.00E-32 | 1.00E-31 |
| SCE1572_4304 | sce_6369 | 4.00E-60 | 2.00E-65 |
| SCE1572_4305 | sce_6370 | 1.00E-104 | 2.00E-102 |
| SCE1572_4306 | sce_6371 | 9.00E-63 | 4.00E-65 |
| SCE1572_4307 | sce_6372 | 9.00E-110 | 2.00E-118 |
| SCE1572_431 | sce_893 | 0.00E+00 | 0.00E+00 |
| SCE1572_4311 | sce_3642 | 0.00E+00 | 0.00E+00 |
| SCE1572_4312 | sce_3643 | 0.00E+00 | 0.00E+00 |
| SCE1572_4314 | sce_5479 | 0.00E+00 | 0.00E+00 |
| SCE1572_4315 | sce_5478 | 1.00E-54 | 4.00E-62 |
| SCE1572_4316 | sce_5477 | 0.00E+00 | 2.00E-177 |
| SCE1572_4317 | sce_5476 | 2.00E-168 | 7.00E-178 |
| SCE1572_4318 | sce_5475 | 0.00E+00 | 0.00E+00 |
| SCE1572_4318 | sce_6689 | 0.00E+00 | 0.00E+00 |
| SCE1572_4319 | sce_5474 | 8.00E-180 | 0.00E+00 |
| SCE1572_432 | sce_247 | 0.00E+00 | 0.00E+00 |
| SCE1572_432 | sce_2052 | 0.00E+00 | 0.00E+00 |
| SCE1572_4325 | sce_9304 | 4.00E-56 | 1.00E-61 |
| SCE1572_4326 | sce_1249 | 4.00E-48 | 2.00E-63 |
| SCE1572_4327 | sce_3613 | 2.00E-62 | 3.00E-60 |
| SCE1572_4328 | sce_3644 | 5.00E-158 | 1.00E-147 |
| SCE1572_4329 | sce_3645 | 2.00E-139 | 1.00E-139 |
| SCE1572_433 | sce_248 | 0.00E+00 | 0.00E+00 |
| SCE1572_433 | sce_3612 | 0.00E+00 | 0.00E+00 |
| SCE1572_433 | sce_886 | 0.00E+00 | 0.00E+00 |
| SCE1572_433 | sce_5797 | 0.00E+00 | 0.00E+00 |
| SCE1572_4331 | sce_1730 | 7.00E-126 | 6.00E-128 |
| SCE1572_4332 | sce_1731 | 5.00E-135 | 2.00E-141 |
| SCE1572_4334 | sce_1451 | 6.00E-101 | 9.00E-95 |
| SCE1572_4336 | sce_9941 | 3.00E-179 | 0.00E+00 |
| SCE1572_4338 | sce_3614 | 0.00E+00 | 0.00E+00 |
| SCE1572_4339 | sce_3615 | 3.00E-82 | 4.00E-90 |
| SCE1572_4340 | sce_3617 | 0.00E+00 | 0.00E+00 |
| SCE1572_4341 | sce_3618 | 2.00E-155 | 4.00E-169 |
| SCE1572_4342 | sce_3619 | 1.00E-155 | 0.00E+00 |
| SCE1572_4343 | sce_3620 | 6.00E-51 | 2.00E-51 |
| SCE1572_4345 | sce_6956 | 4.00E-50 | 9.00E-56 |
| SCE1572_4347 | sce_3647 | 1.00E-45 | 2.00E-45 |
| SCE1572_4348 | sce_3648 | 1.00E-131 | 8.00E-131 |
| SCE1572_435 | sce_9784 | 5.00E-124 | 2.00E-117 |
| SCE1572_4350 | sce_8789 | 0.00E+00 | 0.00E+00 |
| SCE1572_4351 | sce_8790 | 1.00E-116 | 2.00E-116 |
| SCE1572_4353 | sce_10400 | 1.00E-123 | 2.00E-123 |
| SCE1572_4357 | sce_4503 | 5.00E-180 | 2.00E-178 |
| SCE1572_4358 | sce_4502 | 1.00E-151 | 3.00E-152 |
| SCE1572_4359 | sce_3650 | 4.00E-72 | 6.00E-83 |
| SCE1572_436 | sce_9783 | 7.00E-107 | 2.00E-119 |
| SCE1572_4360 | sce_3651 | 0.00E+00 | 0.00E+00 |
| SCE1572_4366 | sce_3652 | 6.00E-85 | 5.00E-85 |
| SCE1572_4367 | sce_3653 | 0.00E+00 | 0.00E+00 |
| SCE1572_4367 | sce_2815 | 0.00E+00 | 0.00E+00 |
| SCE1572_4368 | sce_3654 | 2.00E-124 | 2.00E-124 |
| SCE1572_4369 | sce_3656 | 0.00E+00 | 0.00E+00 |
| SCE1572_437 | sce_251 | 0.00E+00 | 0.00E+00 |
| SCE1572_4372 | sce_1774 | 5.00E-138 | 1.00E-119 |
| SCE1572_4375 | sce_7552 | 1.00E-71 | 3.00E-141 |
| SCE1572_4378 | sce_7961 | 5.00E-28 | 3.00E-28 |
| SCE1572_4379 | sce_2664 | 3.00E-104 | 3.00E-113 |
| SCE1572_4380 | sce_9237 | 0.00E+00 | 0.00E+00 |
| SCE1572_4380 | sce_2666 | 0.00E+00 | 0.00E+00 |
| SCE1572_4381 | sce_9236 | 0.00E+00 | 0.00E+00 |
| SCE1572_4381 | sce_389 | 0.00E+00 | 0.00E+00 |
| SCE1572_4387 | sce_3657 | 0.00E+00 | 0.00E+00 |
| SCE1572_4388 | sce_5785 | 2.00E-67 | 1.00E-74 |
| SCE1572_4390 | sce_8231 | 3.00E-145 | 9.00E-150 |
| SCE1572_4391 | sce_3655 | 0.00E+00 | 0.00E+00 |

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| SCE1572_4392 | sce_7959 | 2.00E-175 | 0.00E+00 |
| SCE1572_4393 | sce_5977 | 2.00E-32 | 1.00E-52 |
| SCE1572_4394 | sce_5975 | 3.00E-102 | 1.00E-112 |
| SCE1572_4397 | sce_3659 | 0.00E+00 | 0.00E+00 |
| SCE1572_4398 | sce_3660 | 0.00E+00 | 0.00E+00 |
| SCE1572_44 | sce_43 | 3.00E-97 | 1.00E-104 |
| SCE1572_4400 | sce_3662 | 2.00E-126 | 3.00E-113 |
| SCE1572_4401 | sce_3663 | 2.00E-56 | 1.00E-57 |
| SCE1572_4424 | sce_3665 | 0.00E+00 | 0.00E+00 |
| SCE1572_4424 | sce_549 | 0.00E+00 | 0.00E+00 |
| SCE1572_4426 | sce_7566 | 5.00E-112 | 5.00E-112 |
| SCE1572_4427 | sce_7565 | 3.00E-156 | 2.00E-159 |
| SCE1572_4429 | sce_3666 | 3.00E-152 | 5.00E-153 |
| SCE1572_4430 | sce_3667 | 2.00E-147 | 7.00E-115 |
| SCE1572_4431 | sce_3668 | 1.00E-87 | 3.00E-79 |
| SCE1572_4434 | sce_7318 | 0.00E+00 | 0.00E+00 |
| SCE1572_4434 | sce_1116 | 0.00E+00 | 0.00E+00 |
| SCE1572_4434 | sce_5158 | 0.00E+00 | 0.00E+00 |
| SCE1572_4435 | sce_1685 | 2.00E-19 | 5.00E-19 |
| SCE1572_4438 | sce_5548 | 5.00E-09 | 3.00E-09 |
| SCE1572_4439 | sce_5547 | 2.00E-17 | 4.00E-18 |
| SCE1572_444 | sce_257 | 9.00E-64 | 1.00E-63 |
| SCE1572_4440 | sce_3676 | 0.00E+00 | 0.00E+00 |
| SCE1572_4441 | sce_3678 | 0.00E+00 | 0.00E+00 |
| SCE1572_4442 | sce_3679 | 0.00E+00 | 0.00E+00 |
| SCE1572_4443 | sce_6978 | 2.00E-31 | 2.00E-34 |
| SCE1572_4444 | sce_3689 | 0.00E+00 | 0.00E+00 |
| SCE1572_4445 | sce_3690 | 0.00E+00 | 0.00E+00 |
| SCE1572_4447 | sce_3691 | 0.00E+00 | 0.00E+00 |
| SCE1572_4448 | sce_3692 | 2.00E-61 | 1.00E-58 |
| SCE1572_4449 | sce_4170 | 4.00E-16 | 5.00E-18 |
| SCE1572_445 | sce_258 | 4.00E-148 | 4.00E-144 |
| SCE1572_4450 | sce_7444 | 3.00E-64 | 3.00E-64 |
| SCE1572_4450 | sce_4542 | 3.00E-64 | 3.00E-64 |
| SCE1572_4452 | sce_9472 | 1.00E-49 | 5.00E-50 |
| SCE1572_4453 | sce_3693 | 9.00E-113 | 9.00E-110 |
| SCE1572_4454 | sce_3694 | 5.00E-84 | 2.00E-94 |
| SCE1572_4455 | sce_3696 | 6.00E-147 | 2.00E-140 |
| SCE1572_4456 | sce_3699 | 8.00E-105 | 5.00E-98 |
| SCE1572_4458 | sce_3700 | 3.00E-169 | 2.00E-167 |
| SCE1572_4459 | sce_3702 | 1.00E-142 | 1.00E-142 |
| SCE1572_446 | sce_259 | 0.00E+00 | 0.00E+00 |
| SCE1572_4460 | sce_7662 | 2.00E-12 | 1.00E-11 |
| SCE1572_4461 | sce_7663 | 2.00E-54 | 3.00E-48 |
| SCE1572_4463 | sce_7475 | 0.00E+00 | 0.00E+00 |
| SCE1572_4466 | sce_3703 | 3.00E-171 | 2.00E-171 |
| SCE1572_4469 | sce_7563 | 0.00E+00 | 0.00E+00 |
| SCE1572_447 | sce_260 | 3.00E-136 | 3.00E-136 |
| SCE1572_4470 | sce_3713 | 4.00E-63 | 1.00E-63 |
| SCE1572_4471 | sce_3714 | 3.00E-172 | 0.00E+00 |
| SCE1572_4475 | sce_5993 | 0.00E+00 | 0.00E+00 |
| SCE1572_4476 | sce_1358 | 7.00E-39 | 6.00E-55 |
| SCE1572_4478 | sce_6103 | 2.00E-49 | 4.00E-48 |
| SCE1572_448 | sce_261 | 0.00E+00 | 0.00E+00 |
| SCE1572_4480 | sce_6105 | 3.00E-34 | 2.00E-24 |
| SCE1572_4486 | sce_7885 | 9.00E-75 | 6.00E-75 |
| SCE1572_4487 | sce_3726 | 5.00E-113 | 1.00E-121 |
| SCE1572_4489 | sce_3719 | 2.00E-124 | 6.00E-140 |
| SCE1572_449 | sce_262 | 9.00E-108 | 2.00E-107 |
| SCE1572_4490 | sce_7400 | 7.00E-114 | 7.00E-108 |
| SCE1572_4491 | sce_6061 | 8.00E-68 | 4.00E-74 |
| SCE1572_4493 | sce_2657 | 3.00E-149 | 6.00E-139 |
| SCE1572_4494 | sce_7608 | 1.00E-07 | 3.00E-06 |
| SCE1572_4495 | sce_3745 | 0.00E+00 | 0.00E+00 |
| SCE1572_4496 | sce_3746 | 5.00E-84 | 8.00E-89 |
| SCE1572_4497 | sce_3747 | 2.00E-143 | 2.00E-145 |
| SCE1572_4498 | sce_3748 | 5.00E-153 | 0.00E+00 |
| SCE1572_4499 | sce_3749 | 5.00E-99 | 5.00E-99 |
| SCE1572_45 | sce_44 | 6.00E-154 | 6.00E-156 |
| SCE1572_450 | sce_263 | 1.00E-179 | 2.00E-169 |
| SCE1572_4500 | sce_3763 | 7.00E-111 | 1.00E-109 |
| SCE1572_4501 | sce_3764 | 3.00E-56 | 1.00E-119 |
| SCE1572_4504 | sce_3765 | 0.00E+00 | 0.00E+00 |
| SCE1572_4504 | sce_9407 | 0.00E+00 | 0.00E+00 |
| SCE1572_4504 | sce_8451 | 0.00E+00 | 0.00E+00 |
| SCE1572_4504 | sce_4817 | 0.00E+00 | 0.00E+00 |

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| SCE1572_4507 | sce_3766 | 4.00E-141 | 1.00E-139 |
| SCE1572_4508 | sce_3767 | 2.00E-27 | 1.00E-25 |
| SCE1572_4509 | sce_3769 | 5.00E-78 | 4.00E-78 |
| SCE1572_451 | sce_267 | 6.00E-97 | 2.00E-88 |
| SCE1572_4510 | sce_3770 | 2.00E-107 | 6.00E-117 |
| SCE1572_4514 | sce_3771 | 9.00E-138 | 9.00E-138 |
| SCE1572_4515 | sce_3772 | 1.00E-41 | 1.00E-43 |
| SCE1572_4516 | sce_3773 | 1.00E-92 | 3.00E-89 |
| SCE1572_4517 | sce_3774 | 0.00E+00 | 5.00E-167 |
| SCE1572_4519 | sce_3778 | 2.00E-162 | 2.00E-162 |
| SCE1572_452 | sce_268 | 1.00E-53 | 3.00E-53 |
| SCE1572_4520 | sce_8632 | 1.00E-112 | 1.00E-112 |
| SCE1572_4521 | sce_3779 | 2.00E-123 | 8.00E-110 |
| SCE1572_4523 | sce_3782 | 4.00E-63 | 1.00E-63 |
| SCE1572_4524 | sce_3783 | 3.00E-142 | 7.00E-142 |
| SCE1572_4525 | sce_3784 | 6.00E-107 | 1.00E-95 |
| SCE1572_4526 | sce_3785 | 1.00E-87 | 6.00E-95 |
| SCE1572_4527 | sce_3787 | 3.00E-122 | 2.00E-125 |
| SCE1572_4529 | sce_3788 | 3.00E-126 | 2.00E-111 |
| SCE1572_453 | sce_269 | 0.00E+00 | 0.00E+00 |
| SCE1572_4530 | sce_3789 | 2.00E-135 | 6.00E-152 |
| SCE1572_4533 | sce_3790 | 3.00E-175 | 4.00E-175 |
| SCE1572_4534 | sce_3791 | 4.00E-144 | 3.00E-160 |
| SCE1572_4535 | sce_3792 | 1.00E-45 | 2.00E-42 |
| SCE1572_4536 | sce_9770 | 2.00E-150 | 5.00E-143 |
| SCE1572_4538 | sce_3794 | 0.00E+00 | 0.00E+00 |
| SCE1572_4539 | sce_3796 | 6.00E-99 | 8.00E-98 |
| SCE1572_4540 | sce_3793 | 0.00E+00 | 0.00E+00 |
| SCE1572_4540 | sce_7069 | 0.00E+00 | 0.00E+00 |
| SCE1572_4540 | sce_5086 | 0.00E+00 | 0.00E+00 |
| SCE1572_4541 | sce_3794 | 0.00E+00 | 0.00E+00 |
| SCE1572_4543 | sce_3797 | 0.00E+00 | 0.00E+00 |
| SCE1572_4544 | sce_3798 | 0.00E+00 | 0.00E+00 |
| SCE1572_4552 | sce_1380 | 0.00E+00 | 0.00E+00 |
| SCE1572_4553 | sce_1379 | 3.00E-88 | 5.00E-89 |
| SCE1572_4557 | sce_3799 | 3.00E-155 | 4.00E-155 |
| SCE1572_4558 | sce_3801 | 8.00E-163 | 9.00E-152 |
| SCE1572_4559 | sce_3802 | 1.00E-79 | 6.00E-75 |
| SCE1572_4563 | sce_3813 | 8.00E-38 | 8.00E-38 |
| SCE1572_4564 | sce_3814 | 2.00E-16 | 3.00E-17 |
| SCE1572_4565 | sce_3816 | 0.00E+00 | 0.00E+00 |
| SCE1572_4566 | sce_3818 | 3.00E-78 | 2.00E-83 |
| SCE1572_4567 | sce_3819 | 9.00E-139 | 9.00E-139 |
| SCE1572_4568 | sce_3820 | 2.00E-10 | 3.00E-11 |
| SCE1572_458 | sce_270 | 0.00E+00 | 0.00E+00 |
| SCE1572_4580 | sce_3097 | 1.00E-155 | 2.00E-154 |
| SCE1572_4582 | sce_3821 | 0.00E+00 | 0.00E+00 |
| SCE1572_4583 | sce_3822 | 7.00E-08 | 1.00E-07 |
| SCE1572_4584 | sce_3823 | 1.00E-142 | 1.00E-142 |
| SCE1572_4585 | sce_3824 | 3.00E-132 | 4.00E-126 |
| SCE1572_4586 | sce_3825 | 0.00E+00 | 0.00E+00 |
| SCE1572_4587 | sce_3826 | 0.00E+00 | 0.00E+00 |
| SCE1572_4588 | sce_3827 | 9.00E-60 | 2.00E-58 |
| SCE1572_4589 | sce_3828 | 8.00E-56 | 5.00E-54 |
| SCE1572_459 | sce_271 | 9.00E-112 | 3.00E-111 |
| SCE1572_4591 | sce_3829 | 3.00E-18 | 1.00E-18 |
| SCE1572_4592 | sce_3830 | 0.00E+00 | 0.00E+00 |
| SCE1572_4593 | sce_3831 | 5.00E-93 | 4.00E-93 |
| SCE1572_4594 | sce_3832 | 2.00E-150 | 2.00E-144 |
| SCE1572_4596 | sce_3833 | 0.00E+00 | 0.00E+00 |
| SCE1572_4598 | sce_3835 | 0.00E+00 | 0.00E+00 |
| SCE1572_46 | sce_45 | 8.00E-155 | 3.00E-146 |
| SCE1572_460 | sce_272 | 3.00E-08 | 5.00E-14 |
| SCE1572_4600 | sce_3837 | 2.00E-180 | 0.00E+00 |
| SCE1572_4602 | sce_3838 | 2.00E-75 | 1.00E-68 |
| SCE1572_4603 | sce_3839 | 0.00E+00 | 0.00E+00 |
| SCE1572_4604 | sce_3840 | 1.00E-103 | 4.00E-105 |
| SCE1572_4605 | sce_3841 | 5.00E-137 | 3.00E-130 |
| SCE1572_4606 | sce_3842 | 1.00E-69 | 7.00E-59 |
| SCE1572_4607 | sce_3843 | 2.00E-92 | 5.00E-92 |
| SCE1572_4608 | sce_3844 | 7.00E-124 | 1.00E-134 |
| SCE1572_4609 | sce_3845 | 3.00E-14 | 1.00E-14 |
| SCE1572_461 | sce_273 | 3.00E-25 | 1.00E-21 |
| SCE1572_4610 | sce_3846 | 2.00E-140 | 2.00E-136 |
| SCE1572_4611 | sce_3847 | 5.00E-140 | 1.00E-136 |
| SCE1572_4618 | sce_3850 | 0.00E+00 | 0.00E+00 |

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| SCE1572_462 | sce_274 | 2.00E-101 | 3.00E-108 |
| SCE1572_4623 | sce_3852 | 3.00E-64 | 2.00E-72 |
| SCE1572_4624 | sce_3853 | 3.00E-75 | 3.00E-75 |
| SCE1572_4625 | sce_3855 | 3.00E-64 | 1.00E-66 |
| SCE1572_4626 | sce_3856 | 6.00E-98 | 9.00E-92 |
| SCE1572_4627 | sce_3857 | 3.00E-40 | 2.00E-40 |
| SCE1572_4629 | sce_3859 | 0.00E+00 | 0.00E+00 |
| SCE1572_4629 | sce_3861 | 0.00E+00 | 0.00E+00 |
| SCE1572_463 | sce_277 | 1.00E-127 | 2.00E-125 |
| SCE1572_4630 | sce_6341 | 0.00E+00 | 0.00E+00 |
| SCE1572_4633 | sce_3860 | 0.00E+00 | 0.00E+00 |
| SCE1572_4634 | sce_3861 | 0.00E+00 | 0.00E+00 |
| SCE1572_4634 | sce_3859 | 0.00E+00 | 0.00E+00 |
| SCE1572_4637 | sce_3862 | 0.00E+00 | 0.00E+00 |
| SCE1572_4638 | sce_3863 | 1.00E-135 | 1.00E-132 |
| SCE1572_4639 | sce_3864 | 9.00E-72 | 2.00E-96 |
| SCE1572_4640 | sce_3865 | 2.00E-106 | 1.00E-104 |
| SCE1572_4644 | sce_10174 | 3.00E-105 | 1.00E-105 |
| SCE1572_4645 | sce_3868 | 0.00E+00 | 0.00E+00 |
| SCE1572_4646 | sce_3869 | 3.00E-123 | 4.00E-139 |
| SCE1572_4648 | sce_3870 | 3.00E-52 | 2.00E-49 |
| SCE1572_4650 | sce_3872 | 3.00E-172 | 1.00E-164 |
| SCE1572_4651 | sce_3873 | 2.00E-165 | 3.00E-168 |
| SCE1572_4652 | sce_3874 | 0.00E+00 | 0.00E+00 |
| SCE1572_4653 | sce_3875 | 0.00E+00 | 0.00E+00 |
| SCE1572_4654 | sce_3876 | 1.00E-89 | 7.00E-84 |
| SCE1572_4657 | sce_3877 | 7.00E-51 | 2.00E-59 |
| SCE1572_4658 | sce_3878 | 2.00E-147 | 2.00E-147 |
| SCE1572_4659 | sce_4570 | 2.00E-62 | 2.00E-69 |
| SCE1572_466 | sce_278 | 2.00E-161 | 4.00E-151 |
| SCE1572_4660 | sce_3881 | 6.00E-67 | 4.00E-67 |
| SCE1572_4661 | sce_3882 | 1.00E-97 | 5.00E-78 |
| SCE1572_4662 | sce_3883 | 0.00E+00 | 0.00E+00 |
| SCE1572_4662 | sce_9757 | 0.00E+00 | 0.00E+00 |
| SCE1572_4662 | sce_5226 | 0.00E+00 | 0.00E+00 |
| SCE1572_4662 | sce_5403 | 0.00E+00 | 0.00E+00 |
| SCE1572_4662 | sce_7154 | 0.00E+00 | 0.00E+00 |
| SCE1572_4664 | sce_3885 | 4.00E-156 | 6.00E-145 |
| SCE1572_4665 | sce_3886 | 6.00E-61 | 1.00E-56 |
| SCE1572_4666 | sce_3887 | 4.00E-34 | 9.00E-35 |
| SCE1572_467 | sce_279 | 0.00E+00 | 0.00E+00 |
| SCE1572_4670 | sce_7871 | 9.00E-124 | 5.00E-124 |
| SCE1572_4673 | sce_3906 | 0.00E+00 | 0.00E+00 |
| SCE1572_4674 | sce_3907 | 6.00E-49 | 6.00E-49 |
| SCE1572_4675 | sce_3910 | 1.00E-137 | 6.00E-130 |
| SCE1572_468 | sce_280 | 5.00E-127 | 2.00E-132 |
| SCE1572_4684 | sce_1283 | 0.00E+00 | 0.00E+00 |
| SCE1572_4685 | sce_1282 | 0.00E+00 | 0.00E+00 |
| SCE1572_4689 | sce_8439 | 3.00E-163 | 5.00E-154 |
| SCE1572_469 | sce_281 | 6.00E-118 | 6.00E-118 |
| SCE1572_4693 | sce_1662 | 0.00E+00 | 0.00E+00 |
| SCE1572_4696 | sce_7939 | 6.00E-137 | 8.00E-137 |
| SCE1572_4697 | sce_5765 | 1.00E-19 | 3.00E-25 |
| SCE1572_4699 | sce_3926 | 4.00E-112 | 2.00E-95 |
| SCE1572_47 | sce_46 | 1.00E-145 | 2.00E-149 |
| SCE1572_470 | sce_282 | 7.00E-137 | 1.00E-140 |
| SCE1572_4700 | sce_3927 | 2.00E-89 | 1.00E-84 |
| SCE1572_4701 | sce_5100 | 5.00E-16 | 8.00E-21 |
| SCE1572_4703 | sce_3929 | 3.00E-88 | 1.00E-98 |
| SCE1572_4704 | sce_3930 | 8.00E-86 | 9.00E-86 |
| SCE1572_4705 | sce_3931 | 4.00E-155 | 5.00E-145 |
| SCE1572_4706 | sce_3932 | 2.00E-133 | 3.00E-133 |
| SCE1572_4707 | sce_3933 | 2.00E-112 | 1.00E-112 |
| SCE1572_4709 | sce_9357 | 0.00E+00 | 0.00E+00 |
| SCE1572_4710 | sce_3935 | 3.00E-79 | 5.00E-82 |
| SCE1572_4711 | sce_8816 | 0.00E+00 | 0.00E+00 |
| SCE1572_4712 | sce_8817 | 0.00E+00 | 0.00E+00 |
| SCE1572_4712 | sce_10193 | 0.00E+00 | 0.00E+00 |
| SCE1572_4712 | sce_3499 | 0.00E+00 | 0.00E+00 |
| SCE1572_4713 | sce_3939 | 0.00E+00 | 0.00E+00 |
| SCE1572_4714 | sce_3940 | 3.00E-84 | 4.00E-93 |
| SCE1572_4716 | sce_3941 | 1.00E-59 | 7.00E-48 |
| SCE1572_4717 | sce_3942 | 1.00E-80 | 2.00E-86 |
| SCE1572_4718 | sce_3943 | 3.00E-78 | 5.00E-91 |
| SCE1572_4719 | sce_3945 | 0.00E+00 | 0.00E+00 |
| SCE1572_472 | sce_283 | 2.00E-55 | 6.00E-62 |

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| SCE1572_4720 | sce_3946 | 5.00E-129 | 6.00E-129 |
| SCE1572_4721 | sce_3947 | 4.00E-159 | 2.00E-162 |
| SCE1572_4722 | sce_3948 | 1.00E-160 | 2.00E-169 |
| SCE1572_4723 | sce_3949 | 3.00E-44 | 3.00E-44 |
| SCE1572_4724 | sce_3950 | 8.00E-37 | 1.00E-44 |
| SCE1572_4725 | sce_3951 | 0.00E+00 | 0.00E+00 |
| SCE1572_4726 | sce_3952 | 0.00E+00 | 0.00E+00 |
| SCE1572_4727 | sce_6342 | 1.00E-120 | 4.00E-122 |
| SCE1572_4728 | sce_6341 | 0.00E+00 | 0.00E+00 |
| SCE1572_4729 | sce_6340 | 6.00E-35 | 7.00E-28 |
| SCE1572_473 | sce_284 | 3.00E-118 | 3.00E-118 |
| SCE1572_4730 | sce_6339 | 0.00E+00 | 0.00E+00 |
| SCE1572_4731 | sce_6338 | 2.00E-146 | 8.00E-160 |
| SCE1572_4732 | sce_6337 | 3.00E-84 | 2.00E-63 |
| SCE1572_4733 | sce_6336 | 1.00E-59 | 1.00E-59 |
| SCE1572_4734 | sce_3954 | 8.00E-170 | 2.00E-173 |
| SCE1572_4735 | sce_3956 | 0.00E+00 | 0.00E+00 |
| SCE1572_4736 | sce_3957 | 2.00E-139 | 9.00E-138 |
| SCE1572_4738 | sce_3958 | 7.00E-51 | 7.00E-57 |
| SCE1572_474 | sce_285 | 2.00E-54 | 2.00E-54 |
| SCE1572_4740 | sce_3961 | 0.00E+00 | 0.00E+00 |
| SCE1572_4741 | sce_3962 | 6.00E-161 | 4.00E-175 |
| SCE1572_4742 | sce_3963 | 5.00E-74 | 4.00E-74 |
| SCE1572_4743 | sce_3965 | 4.00E-119 | 4.00E-109 |
| SCE1572_4744 | sce_3966 | 7.00E-42 | 2.00E-42 |
| SCE1572_4745 | sce_3967 | 0.00E+00 | 0.00E+00 |
| SCE1572_4746 | sce_3968 | 0.00E+00 | 0.00E+00 |
| SCE1572_4747 | sce_3969 | 1.00E-62 | 2.00E-63 |
| SCE1572_475 | sce_286 | 0.00E+00 | 0.00E+00 |
| SCE1572_4750 | sce_3971 | 1.00E-177 | 1.00E-177 |
| SCE1572_4751 | sce_3972 | 2.00E-178 | 9.00E-159 |
| SCE1572_4752 | sce_3974 | 2.00E-35 | 2.00E-35 |
| SCE1572_4754 | sce_7978 | 2.00E-119 | 2.00E-119 |
| SCE1572_4755 | sce_10127 | 2.00E-83 | 3.00E-91 |
| SCE1572_4758 | sce_3976 | 0.00E+00 | 0.00E+00 |
| SCE1572_476 | sce_287 | 3.00E-90 | 3.00E-90 |
| SCE1572_4762 | sce_3978 | 5.00E-154 | 4.00E-162 |
| SCE1572_4763 | sce_3979 | 3.00E-110 | 1.00E-111 |
| SCE1572_4764 | sce_3980 | 2.00E-89 | 8.00E-90 |
| SCE1572_4765 | sce_3981 | 5.00E-156 | 2.00E-146 |
| SCE1572_4766 | sce_3982 | 0.00E+00 | 0.00E+00 |
| SCE1572_4767 | sce_3983 | 8.00E-150 | 3.00E-140 |
| SCE1572_477 | sce_288 | 2.00E-91 | 3.00E-86 |
| SCE1572_4771 | sce_3987 | 4.00E-177 | 0.00E+00 |
| SCE1572_4772 | sce_3988 | 6.00E-166 | 2.00E-167 |
| SCE1572_4773 | sce_7233 | 3.00E-122 | 2.00E-125 |
| SCE1572_4774 | sce_3989 | 4.00E-25 | 1.00E-24 |
| SCE1572_4776 | sce_3991 | 0.00E+00 | 0.00E+00 |
| SCE1572_4777 | sce_3992 | 0.00E+00 | 0.00E+00 |
| SCE1572_478 | sce_289 | 5.00E-154 | 7.00E-145 |
| SCE1572_4780 | sce_3993 | 0.00E+00 | 0.00E+00 |
| SCE1572_4781 | sce_3995 | 2.00E-120 | 2.00E-112 |
| SCE1572_4782 | sce_3997 | 6.00E-27 | 1.00E-21 |
| SCE1572_4783 | sce_299 | 2.00E-121 | 7.00E-127 |
| SCE1572_4785 | sce_3999 | 0.00E+00 | 0.00E+00 |
| SCE1572_4786 | sce_4000 | 0.00E+00 | 0.00E+00 |
| SCE1572_4787 | sce_4001 | 9.00E-108 | 3.00E-110 |
| SCE1572_4788 | sce_4002 | 5.00E-135 | 2.00E-136 |
| SCE1572_4789 | sce_4004 | 0.00E+00 | 0.00E+00 |
| SCE1572_479 | sce_290 | 0.00E+00 | 0.00E+00 |
| SCE1572_4790 | sce_4005 | 4.00E-123 | 4.00E-121 |
| SCE1572_4791 | sce_4006 | 9.00E-96 | 1.00E-99 |
| SCE1572_4793 | sce_4007 | 6.00E-72 | 7.00E-72 |
| SCE1572_4794 | sce_4008 | 0.00E+00 | 0.00E+00 |
| SCE1572_4795 | sce_4010 | 7.00E-83 | 3.00E-73 |
| SCE1572_4796 | sce_4011 | 3.00E-70 | 2.00E-61 |
| SCE1572_4797 | sce_4012 | 5.00E-101 | 5.00E-113 |
| SCE1572_4798 | sce_4013 | 1.00E-45 | 1.00E-45 |
| SCE1572_4799 | sce_4014 | 0.00E+00 | 0.00E+00 |
| SCE1572_48 | sce_47 | 3.00E-119 | 1.00E-94 |
| SCE1572_480 | sce_291 | 9.00E-126 | 9.00E-126 |
| SCE1572_4800 | sce_4015 | 1.00E-90 | 1.00E-90 |
| SCE1572_4801 | sce_4016 | 3.00E-176 | 2.00E-173 |
| SCE1572_4802 | sce_4017 | 0.00E+00 | 0.00E+00 |
| SCE1572_4803 | sce_4018 | 0.00E+00 | 0.00E+00 |
| SCE1572_4807 | sce_4021 | 0.00E+00 | 0.00E+00 |

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| SCE1572_4808 | sce_4022 | 8.00E-132 | 6.00E-138 |
| SCE1572_4809 | sce_4023 | 0.00E+00 | 0.00E+00 |
| SCE1572_481 | sce_292 | 6.00E-147 | 1.00E-144 |
| SCE1572_4811 | sce_4025 | 8.00E-106 | 1.00E-100 |
| SCE1572_4812 | sce_4026 | 3.00E-61 | 5.00E-66 |
| SCE1572_4813 | sce_4027 | 0.00E+00 | 0.00E+00 |
| SCE1572_4814 | sce_4028 | 4.00E-147 | 4.00E-138 |
| SCE1572_4815 | sce_4029 | 0.00E+00 | 0.00E+00 |
| SCE1572_4817 | sce_4031 | 2.00E-83 | 2.00E-83 |
| SCE1572_4818 | sce_4032 | 4.00E-40 | 1.00E-37 |
| SCE1572_4819 | sce_4033 | 4.00E-122 | 5.00E-132 |
| SCE1572_482 | sce_293 | 0.00E+00 | 0.00E+00 |
| SCE1572_4820 | sce_4034 | 0.00E+00 | 0.00E+00 |
| SCE1572_4821 | sce_4035 | 0.00E+00 | 0.00E+00 |
| SCE1572_4823 | sce_4036 | 4.00E-99 | 9.00E-101 |
| SCE1572_4824 | sce_4037 | 0.00E+00 | 0.00E+00 |
| SCE1572_4825 | sce_4038 | 4.00E-133 | 6.00E-133 |
| SCE1572_4826 | sce_4039 | 0.00E+00 | 0.00E+00 |
| SCE1572_4827 | sce_4040 | 8.00E-86 | 5.00E-73 |
| SCE1572_4828 | sce_4041 | 1.00E-33 | 1.00E-33 |
| SCE1572_4829 | sce_4042 | 7.00E-136 | 8.00E-155 |
| SCE1572_483 | sce_294 | 0.00E+00 | 0.00E+00 |
| SCE1572_4830 | sce_4043 | 8.00E-132 | 5.00E-143 |
| SCE1572_4831 | sce_4045 | 4.00E-169 | 1.00E-169 |
| SCE1572_4833 | sce_4046 | 2.00E-171 | 2.00E-171 |
| SCE1572_4835 | sce_4047 | 9.00E-68 | 2.00E-67 |
| SCE1572_4836 | sce_4048 | 2.00E-85 | 1.00E-94 |
| SCE1572_4837 | sce_4049 | 1.00E-128 | 5.00E-128 |
| SCE1572_4838 | sce_4050 | 5.00E-73 | 5.00E-73 |
| SCE1572_4839 | sce_4051 | 0.00E+00 | 0.00E+00 |
| SCE1572_484 | sce_295 | 0.00E+00 | 0.00E+00 |
| SCE1572_4840 | sce_4052 | 3.00E-76 | 2.00E-80 |
| SCE1572_4841 | sce_4053 | 0.00E+00 | 0.00E+00 |
| SCE1572_4842 | sce_4054 | 1.00E-50 | 3.00E-50 |
| SCE1572_4843 | sce_4055 | 3.00E-178 | 2.00E-173 |
| SCE1572_4844 | sce_4056 | 7.00E-109 | 1.00E-108 |
| SCE1572_4845 | sce_4057 | 2.00E-121 | 9.00E-135 |
| SCE1572_4846 | sce_4058 | 0.00E+00 | 0.00E+00 |
| SCE1572_4847 | sce_4059 | 6.00E-157 | 4.00E-163 |
| SCE1572_4848 | sce_4060 | 0.00E+00 | 1.00E-175 |
| SCE1572_4849 | sce_3628 | 3.00E-16 | 3.00E-18 |
| SCE1572_485 | sce_296 | 4.00E-113 | 3.00E-113 |
| SCE1572_4851 | sce_4062 | 0.00E+00 | 0.00E+00 |
| SCE1572_4851 | sce_9373 | 0.00E+00 | 0.00E+00 |
| SCE1572_4853 | sce_4063 | 2.00E-38 | 4.00E-39 |
| SCE1572_4854 | sce_4066 | 2.00E-95 | 3.00E-107 |
| SCE1572_4855 | sce_4067 | 3.00E-52 | 3.00E-59 |
| SCE1572_4856 | sce_4069 | 2.00E-125 | 1.00E-139 |
| SCE1572_4857 | sce_6129 | 7.00E-43 | 6.00E-35 |
| SCE1572_4859 | sce_4071 | 5.00E-129 | 5.00E-149 |
| SCE1572_486 | sce_297 | 4.00E-39 | 5.00E-39 |
| SCE1572_4861 | sce_4073 | 0.00E+00 | 0.00E+00 |
| SCE1572_4861 | sce_5403 | 0.00E+00 | 0.00E+00 |
| SCE1572_4861 | sce_7154 | 0.00E+00 | 0.00E+00 |
| SCE1572_4862 | sce_4075 | 4.00E-65 | 8.00E-53 |
| SCE1572_4863 | sce_4077 | 7.00E-123 | 4.00E-124 |
| SCE1572_4864 | sce_4078 | 1.00E-105 | 2.00E-120 |
| SCE1572_4866 | sce_4080 | 1.00E-115 | 1.00E-115 |
| SCE1572_4868 | sce_4081 | 0.00E+00 | 0.00E+00 |
| SCE1572_4869 | sce_4082 | 7.00E-45 | 3.00E-57 |
| SCE1572_487 | sce_298 | 4.00E-118 | 5.00E-110 |
| SCE1572_4870 | sce_4083 | 3.00E-51 | 9.00E-60 |
| SCE1572_4871 | sce_4084 | 4.00E-96 | 5.00E-96 |
| SCE1572_4872 | sce_4086 | 0.00E+00 | 0.00E+00 |
| SCE1572_4873 | sce_4087 | 4.00E-104 | 1.00E-103 |
| SCE1572_4874 | sce_4088 | 9.00E-93 | 9.00E-93 |
| SCE1572_4875 | sce_4089 | 2.00E-143 | 2.00E-143 |
| SCE1572_4876 | sce_4090 | 0.00E+00 | 0.00E+00 |
| SCE1572_4877 | sce_4091 | 4.00E-105 | 2.00E-107 |
| SCE1572_4879 | sce_4092 | 0.00E+00 | 0.00E+00 |
| SCE1572_4880 | sce_4094 | 7.00E-177 | 0.00E+00 |
| SCE1572_4882 | sce_4095 | 0.00E+00 | 0.00E+00 |
| SCE1572_4883 | sce_4096 | 9.00E-58 | 1.00E-57 |
| SCE1572_4884 | sce_4097 | 2.00E-110 | 3.00E-115 |
| SCE1572_4889 | sce_4102 | 9.00E-123 | 8.00E-159 |
| SCE1572_4890 | sce_914 | 1.00E-141 | 1.00E-141 |

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| SCE1572_49 | sce_48 | 3.00E-92 | 3.00E-92 |
| SCE1572_4901 | sce_4861 | 0.00E+00 | 0.00E+00 |
| SCE1572_4901 | sce_4106 | 0.00E+00 | 0.00E+00 |
| SCE1572_4902 | sce_4107 | 2.00E-132 | 3.00E-140 |
| SCE1572_4903 | sce_4108 | 2.00E-147 | 7.00E-141 |
| SCE1572_4906 | sce_4116 | 2.00E-73 | 2.00E-73 |
| SCE1572_4907 | sce_4117 | 1.00E-86 | 3.00E-71 |
| SCE1572_4908 | sce_4118 | 2.00E-171 | 7.00E-173 |
| SCE1572_4911 | sce_4121 | 0.00E+00 | 0.00E+00 |
| SCE1572_4912 | sce_4122 | 2.00E-41 | 2.00E-41 |
| SCE1572_4913 | sce_4123 | 2.00E-43 | 2.00E-43 |
| SCE1572_4914 | sce_4124 | 9.00E-90 | 1.00E-79 |
| SCE1572_4916 | sce_4127 | 0.00E+00 | 0.00E+00 |
| SCE1572_4917 | sce_4128 | 2.00E-47 | 6.00E-72 |
| SCE1572_4918 | sce_4129 | 0.00E+00 | 0.00E+00 |
| SCE1572_4919 | sce_4130 | 2.00E-60 | 2.00E-51 |
| SCE1572_4920 | sce_4131 | 1.00E-45 | 3.00E-53 |
| SCE1572_4921 | sce_4132 | 4.00E-72 | 5.00E-66 |
| SCE1572_4922 | sce_4134 | 5.00E-80 | 4.00E-96 |
| SCE1572_4923 | sce_4135 | 5.00E-176 | 5.00E-176 |
| SCE1572_4924 | sce_4136 | 5.00E-103 | 2.00E-102 |
| SCE1572_4925 | sce_4137 | 0.00E+00 | 0.00E+00 |
| SCE1572_4926 | sce_4138 | 7.00E-113 | 2.00E-135 |
| SCE1572_4929 | sce_4140 | 1.00E-112 | 5.00E-113 |
| SCE1572_493 | sce_5846 | 1.00E-92 | 2.00E-68 |
| SCE1572_4930 | sce_4141 | 5.00E-143 | 1.00E-140 |
| SCE1572_4931 | sce_4142 | 5.00E-128 | 7.00E-121 |
| SCE1572_4932 | sce_4143 | 1.00E-167 | 7.00E-170 |
| SCE1572_4933 | sce_4144 | 3.00E-30 | 3.00E-30 |
| SCE1572_4934 | sce_4145 | 1.00E-76 | 8.00E-74 |
| SCE1572_4935 | sce_4146 | 8.00E-115 | 3.00E-113 |
| SCE1572_4936 | sce_4147 | 2.00E-131 | 2.00E-121 |
| SCE1572_4937 | sce_4149 | 8.00E-154 | 3.00E-142 |
| SCE1572_4939 | sce_4152 | 0.00E+00 | 0.00E+00 |
| SCE1572_494 | sce_5847 | 3.00E-38 | 7.00E-42 |
| SCE1572_4940 | sce_4154 | 1.00E-120 | 1.00E-120 |
| SCE1572_4941 | sce_4155 | 7.00E-133 | 2.00E-120 |
| SCE1572_4942 | sce_4156 | 2.00E-77 | 1.00E-75 |
| SCE1572_4943 | sce_4157 | 0.00E+00 | 0.00E+00 |
| SCE1572_4944 | sce_4158 | 8.00E-110 | 1.00E-88 |
| SCE1572_4945 | sce_4159 | 0.00E+00 | 0.00E+00 |
| SCE1572_4947 | sce_4161 | 8.00E-123 | 2.00E-112 |
| SCE1572_4949 | sce_4162 | 2.00E-71 | 2.00E-72 |
| SCE1572_4950 | sce_4899 | 8.00E-39 | 3.00E-34 |
| SCE1572_4951 | sce_4163 | 3.00E-88 | 3.00E-88 |
| SCE1572_4952 | sce_4164 | 9.00E-15 | 3.00E-11 |
| SCE1572_4953 | sce_1234 | 4.00E-23 | 6.00E-23 |
| SCE1572_4955 | sce_4165 | 4.00E-137 | 1.00E-142 |
| SCE1572_4956 | sce_4166 | 0.00E+00 | 0.00E+00 |
| SCE1572_4958 | sce_4167 | 2.00E-76 | 9.00E-70 |
| SCE1572_496 | sce_5848 | 1.00E-145 | 8.00E-146 |
| SCE1572_4960 | sce_4168 | 0.00E+00 | 5.00E-135 |
| SCE1572_4961 | sce_4169 | 2.00E-36 | 2.00E-37 |
| SCE1572_4962 | sce_4173 | 9.00E-39 | 9.00E-35 |
| SCE1572_4963 | sce_4174 | 0.00E+00 | 0.00E+00 |
| SCE1572_4964 | sce_4175 | 4.00E-74 | 2.00E-76 |
| SCE1572_4965 | sce_3793 | 0.00E+00 | 0.00E+00 |
| SCE1572_4965 | sce_7069 | 0.00E+00 | 0.00E+00 |
| SCE1572_4965 | sce_5086 | 0.00E+00 | 0.00E+00 |
| SCE1572_4965 | sce_6701 | 0.00E+00 | 0.00E+00 |
| SCE1572_4965 | sce_5085 | 0.00E+00 | 0.00E+00 |
| SCE1572_4967 | sce_4176 | 6.00E-180 | 0.00E+00 |
| SCE1572_4968 | sce_4177 | 0.00E+00 | 0.00E+00 |
| SCE1572_4969 | sce_4178 | 9.00E-94 | 1.00E-98 |
| SCE1572_497 | sce_2515 | 3.00E-42 | 3.00E-49 |
| SCE1572_4972 | sce_4181 | 8.00E-41 | 2.00E-46 |
| SCE1572_4973 | sce_4182 | 0.00E+00 | 0.00E+00 |
| SCE1572_4974 | sce_4183 | 2.00E-93 | 7.00E-94 |
| SCE1572_4975 | sce_4184 | 0.00E+00 | 0.00E+00 |
| SCE1572_4976 | sce_4185 | 0.00E+00 | 0.00E+00 |
| SCE1572_4977 | sce_4186 | 0.00E+00 | 0.00E+00 |
| SCE1572_4978 | sce_4187 | 2.00E-162 | 7.00E-167 |
| SCE1572_498 | sce_8618 | 0.00E+00 | 0.00E+00 |
| SCE1572_498 | sce_2065 | 0.00E+00 | 0.00E+00 |
| SCE1572_498 | sce_10204 | 0.00E+00 | 0.00E+00 |
| SCE1572_498 | sce_388 | 0.00E+00 | 0.00E+00 |

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| SCE1572_498 | sce_7640 | 0.00E+00 | 0.00E+00 |
| SCE1572_498 | sce_4513 | 0.00E+00 | 0.00E+00 |
| SCE1572_498 | sce_3003 | 0.00E+00 | 0.00E+00 |
| SCE1572_498 | sce_7109 | 0.00E+00 | 0.00E+00 |
| SCE1572_498 | sce_7661 | 0.00E+00 | 0.00E+00 |
| SCE1572_4984 | sce_4189 | 0.00E+00 | 0.00E+00 |
| SCE1572_4986 | sce_4190 | 6.00E-160 | 5.00E-150 |
| SCE1572_4987 | sce_4191 | 0.00E+00 | 0.00E+00 |
| SCE1572_4988 | sce_4192 | 2.00E-62 | 5.00E-69 |
| SCE1572_4989 | sce_4193 | 4.00E-80 | 5.00E-86 |
| SCE1572_4990 | sce_4194 | 2.00E-113 | 2.00E-113 |
| SCE1572_4991 | sce_4195 | 7.00E-31 | 3.00E-26 |
| SCE1572_4992 | sce_4196 | 6.00E-14 | 4.00E-23 |
| SCE1572_4993 | sce_4197 | 4.00E-96 | 1.00E-104 |
| SCE1572_4994 | sce_4198 | 2.00E-172 | 7.00E-163 |
| SCE1572_4995 | sce_4199 | 2.00E-110 | 7.00E-117 |
| SCE1572_4996 | sce_4200 | 5.00E-72 | 6.00E-67 |
| SCE1572_4998 | sce_4201 | 2.00E-111 | 6.00E-126 |
| SCE1572_4999 | sce_4202 | 0.00E+00 | 0.00E+00 |
| SCE1572_5 | sce_5 | 2.00E-174 | 2.00E-177 |
| SCE1572_50 | sce_49 | 1.00E-122 | 2.00E-128 |
| SCE1572_5001 | sce_4203 | 2.00E-150 | 3.00E-157 |
| SCE1572_5002 | sce_4204 | 1.00E-77 | 5.00E-77 |
| SCE1572_5003 | sce_4205 | 3.00E-65 | 8.00E-67 |
| SCE1572_5004 | sce_4206 | 2.00E-44 | 4.00E-46 |
| SCE1572_5005 | sce_4207 | 2.00E-26 | 7.00E-20 |
| SCE1572_5006 | sce_4208 | 0.00E+00 | 0.00E+00 |
| SCE1572_5007 | sce_4209 | 1.00E-121 | 2.00E-121 |
| SCE1572_5008 | sce_4210 | 2.00E-83 | 3.00E-90 |
| SCE1572_5009 | sce_4211 | 1.00E-61 | 1.00E-61 |
| SCE1572_5010 | sce_4212 | 0.00E+00 | 0.00E+00 |
| SCE1572_5011 | sce_4213 | 4.00E-118 | 3.00E-119 |
| SCE1572_5012 | sce_4214 | 4.00E-114 | 5.00E-114 |
| SCE1572_5013 | sce_4215 | 1.00E-140 | 2.00E-146 |
| SCE1572_5014 | sce_4216 | 2.00E-171 | 2.00E-171 |
| SCE1572_5015 | sce_4217 | 7.00E-86 | 2.00E-91 |
| SCE1572_5016 | sce_4218 | 0.00E+00 | 0.00E+00 |
| SCE1572_5017 | sce_4219 | 2.00E-85 | 1.00E-79 |
| SCE1572_5018 | sce_4220 | 0.00E+00 | 0.00E+00 |
| SCE1572_5019 | sce_4221 | 3.00E-108 | 4.00E-107 |
| SCE1572_5020 | sce_4222 | 0.00E+00 | 0.00E+00 |
| SCE1572_5021 | sce_4223 | 0.00E+00 | 0.00E+00 |
| SCE1572_5022 | sce_4225 | 9.00E-157 | 9.00E-157 |
| SCE1572_5024 | sce_4226 | 0.00E+00 | 0.00E+00 |
| SCE1572_5025 | sce_4227 | 9.00E-168 | 9.00E-179 |
| SCE1572_5026 | sce_4228 | 1.00E-82 | 3.00E-86 |
| SCE1572_5027 | sce_4229 | 0.00E+00 | 0.00E+00 |
| SCE1572_5028 | sce_4230 | 5.00E-112 | 4.00E-134 |
| SCE1572_5029 | sce_4231 | 3.00E-114 | 2.00E-114 |
| SCE1572_5030 | sce_4232 | 0.00E+00 | 0.00E+00 |
| SCE1572_5031 | sce_4233 | 2.00E-65 | 1.00E-67 |
| SCE1572_5032 | sce_4234 | 0.00E+00 | 0.00E+00 |
| SCE1572_5033 | sce_4235 | 7.00E-112 | 2.00E-119 |
| SCE1572_5034 | sce_4236 | 1.00E-146 | 2.00E-146 |
| SCE1572_5035 | sce_4237 | 1.00E-125 | 2.00E-132 |
| SCE1572_5037 | sce_4238 | 0.00E+00 | 0.00E+00 |
| SCE1572_5037 | sce_9607 | 0.00E+00 | 0.00E+00 |
| SCE1572_5038 | sce_4239 | 5.00E-63 | 5.00E-63 |
| SCE1572_5040 | sce_4240 | 1.00E-135 | 7.00E-145 |
| SCE1572_5041 | sce_4241 | 1.00E-91 | 4.00E-98 |
| SCE1572_5042 | sce_4242 | 0.00E+00 | 0.00E+00 |
| SCE1572_5043 | sce_4243 | 5.00E-58 | 9.00E-62 |
| SCE1572_5044 | sce_4244 | 3.00E-18 | 4.00E-14 |
| SCE1572_5045 | sce_4245 | 4.00E-93 | 1.00E-84 |
| SCE1572_5047 | sce_6904 | 8.00E-81 | 7.00E-72 |
| SCE1572_505 | sce_8661 | 7.00E-10 | 1.00E-06 |
| SCE1572_5052 | sce_522 | 7.00E-135 | 2.00E-126 |
| SCE1572_5056 | sce_7667 | 0.00E+00 | 0.00E+00 |
| SCE1572_5057 | sce_7841 | 3.00E-169 | 5.00E-175 |
| SCE1572_5058 | sce_4246 | 0.00E+00 | 0.00E+00 |
| SCE1572_5059 | sce_4247 | 6.00E-101 | 1.00E-98 |
| SCE1572_5060 | sce_4248 | 1.00E-171 | 1.00E-176 |
| SCE1572_5061 | sce_4250 | 4.00E-55 | 4.00E-55 |
| SCE1572_5062 | sce_4251 | 2.00E-139 | 5.00E-151 |
| SCE1572_5063 | sce_4252 | 1.00E-13 | 2.00E-21 |
| SCE1572_5064 | sce_4253 | 8.00E-143 | 2.00E-149 |

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| SCE1572_5065 | sce_4254 | 2.00E-167 | 2.00E-170 |
| SCE1572_5066 | sce_4255 | 9.00E-162 | 1.00E-164 |
| SCE1572_5067 | sce_4256 | 2.00E-172 | 2.00E-172 |
| SCE1572_5068 | sce_4257 | 1.00E-144 | 0.00E+00 |
| SCE1572_5069 | sce_4258 | 0.00E+00 | 0.00E+00 |
| SCE1572_507 | sce_1673 | 1.00E-57 | 2.00E-63 |
| SCE1572_5070 | sce_4259 | 2.00E-153 | 2.00E-144 |
| SCE1572_5071 | sce_4260 | 0.00E+00 | 0.00E+00 |
| SCE1572_5072 | sce_4261 | 8.00E-136 | 5.00E-144 |
| SCE1572_5073 | sce_4262 | 3.00E-128 | 5.00E-131 |
| SCE1572_5074 | sce_4263 | 1.00E-34 | 1.00E-34 |
| SCE1572_5076 | sce_4265 | 0.00E+00 | 0.00E+00 |
| SCE1572_5077 | sce_4266 | 3.00E-90 | 3.00E-90 |
| SCE1572_5078 | sce_4267 | 0.00E+00 | 2.00E-178 |
| SCE1572_5079 | sce_4268 | 2.00E-64 | 3.00E-64 |
| SCE1572_508 | sce_1674 | 0.00E+00 | 0.00E+00 |
| SCE1572_5080 | sce_4269 | 0.00E+00 | 0.00E+00 |
| SCE1572_5081 | sce_4270 | 3.00E-39 | 3.00E-39 |
| SCE1572_5082 | sce_4271 | 5.00E-119 | 2.00E-118 |
| SCE1572_5083 | sce_4272 | 7.00E-130 | 5.00E-131 |
| SCE1572_5084 | sce_4273 | 1.00E-163 | 8.00E-164 |
| SCE1572_5086 | sce_4274 | 9.00E-27 | 8.00E-27 |
| SCE1572_5087 | sce_4275 | 2.00E-86 | 1.00E-93 |
| SCE1572_5088 | sce_4276 | 7.00E-160 | 8.00E-170 |
| SCE1572_5089 | sce_4277 | 3.00E-89 | 2.00E-89 |
| SCE1572_509 | sce_312 | 6.00E-94 | 3.00E-95 |
| SCE1572_5090 | sce_4278 | 0.00E+00 | 2.00E-171 |
| SCE1572_5091 | sce_4279 | 1.00E-172 | 2.00E-167 |
| SCE1572_5093 | sce_4280 | 8.00E-43 | 8.00E-43 |
| SCE1572_5094 | sce_4281 | 0.00E+00 | 0.00E+00 |
| SCE1572_5095 | sce_4282 | 0.00E+00 | 0.00E+00 |
| SCE1572_5096 | sce_4283 | 3.00E-139 | 3.00E-137 |
| SCE1572_5097 | sce_4284 | 1.00E-110 | 9.00E-110 |
| SCE1572_5098 | sce_4285 | 4.00E-155 | 2.00E-169 |
| SCE1572_5099 | sce_4286 | 1.00E-99 | 2.00E-104 |
| SCE1572_510 | sce_313 | 1.00E-157 | 9.00E-155 |
| SCE1572_5100 | sce_4287 | 5.00E-49 | 2.00E-48 |
| SCE1572_5101 | sce_4288 | 2.00E-111 | 3.00E-122 |
| SCE1572_5102 | sce_4289 | 0.00E+00 | 0.00E+00 |
| SCE1572_5103 | sce_4290 | 0.00E+00 | 0.00E+00 |
| SCE1572_5104 | sce_4291 | 4.00E-76 | 8.00E-64 |
| SCE1572_5105 | sce_4292 | 0.00E+00 | 0.00E+00 |
| SCE1572_5106 | sce_4293 | 4.00E-28 | 4.00E-28 |
| SCE1572_5107 | sce_4294 | 2.00E-97 | 1.00E-97 |
| SCE1572_5108 | sce_4295 | 1.00E-101 | 7.00E-95 |
| SCE1572_511 | sce_315 | 0.00E+00 | 0.00E+00 |
| SCE1572_5110 | sce_4297 | 0.00E+00 | 0.00E+00 |
| SCE1572_5111 | sce_4298 | 0.00E+00 | 0.00E+00 |
| SCE1572_5112 | sce_4299 | 3.00E-178 | 0.00E+00 |
| SCE1572_5113 | sce_4300 | 1.00E-69 | 5.00E-63 |
| SCE1572_5114 | sce_4301 | 0.00E+00 | 0.00E+00 |
| SCE1572_5115 | sce_4303 | 0.00E+00 | 4.00E-170 |
| SCE1572_5116 | sce_4304 | 2.00E-131 | 6.00E-146 |
| SCE1572_5117 | sce_4305 | 6.00E-80 | 2.00E-88 |
| SCE1572_5118 | sce_4306 | 4.00E-73 | 1.00E-63 |
| SCE1572_5119 | sce_4307 | 0.00E+00 | 0.00E+00 |
| SCE1572_512 | sce_317 | 3.00E-15 | 2.00E-12 |
| SCE1572_5120 | sce_4308 | 1.00E-169 | 2.00E-173 |
| SCE1572_5121 | sce_4309 | 0.00E+00 | 0.00E+00 |
| SCE1572_5122 | sce_4310 | 1.00E-69 | 1.00E-60 |
| SCE1572_5123 | sce_4311 | 4.00E-132 | 6.00E-139 |
| SCE1572_5127 | sce_4314 | 1.00E-180 | 0.00E+00 |
| SCE1572_5128 | sce_4315 | 2.00E-164 | 7.00E-179 |
| SCE1572_513 | sce_318 | 3.00E-131 | 1.00E-132 |
| SCE1572_5130 | sce_4317 | 6.00E-54 | 6.00E-54 |
| SCE1572_5131 | sce_4318 | 2.00E-53 | 5.00E-49 |
| SCE1572_5132 | sce_4319 | 5.00E-147 | 4.00E-154 |
| SCE1572_5134 | sce_4320 | 1.00E-25 | 2.00E-33 |
| SCE1572_5135 | sce_4321 | 1.00E-160 | 8.00E-161 |
| SCE1572_5136 | sce_4322 | 3.00E-139 | 2.00E-134 |
| SCE1572_5137 | sce_4323 | 5.00E-128 | 4.00E-141 |
| SCE1572_514 | sce_319 | 9.00E-88 | 2.00E-96 |
| SCE1572_5141 | sce_4324 | 0.00E+00 | 0.00E+00 |
| SCE1572_5142 | sce_4325 | 0.00E+00 | 3.00E-173 |
| SCE1572_5145 | sce_1505 | 2.00E-121 | 9.00E-116 |
| SCE1572_5146 | sce_3919 | 2.00E-53 | 9.00E-40 |

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| SCE1572_5147 | sce_1503 | 4.00E-49 | 1.00E-69 |
| SCE1572_5148 | sce_4330 | 5.00E-95 | 6.00E-97 |
| SCE1572_515 | sce_321 | 5.00E-140 | 4.00E-140 |
| SCE1572_5150 | sce_4331 | 2.00E-86 | 3.00E-93 |
| SCE1572_5154 | sce_4332 | 4.00E-82 | 4.00E-82 |
| SCE1572_5157 | sce_4333 | 0.00E+00 | 0.00E+00 |
| SCE1572_5159 | sce_4334 | 1.00E-88 | 1.00E-88 |
| SCE1572_5160 | sce_4335 | 9.00E-132 | 6.00E-114 |
| SCE1572_5164 | sce_7843 | 2.00E-40 | 1.00E-37 |
| SCE1572_5170 | sce_4336 | 0.00E+00 | 0.00E+00 |
| SCE1572_5171 | sce_4337 | 7.00E-175 | 0.00E+00 |
| SCE1572_5177 | sce_4338 | 0.00E+00 | 0.00E+00 |
| SCE1572_5178 | sce_4339 | 0.00E+00 | 0.00E+00 |
| SCE1572_5180 | sce_4340 | 0.00E+00 | 0.00E+00 |
| SCE1572_5181 | sce_4342 | 4.00E-139 | 6.00E-142 |
| SCE1572_5182 | sce_4343 | 1.00E-112 | 9.00E-120 |
| SCE1572_5183 | sce_4344 | 4.00E-94 | 9.00E-94 |
| SCE1572_5184 | sce_4345 | 1.00E-114 | 5.00E-103 |
| SCE1572_5185 | sce_4346 | 5.00E-119 | 1.00E-119 |
| SCE1572_5186 | sce_4347 | 0.00E+00 | 0.00E+00 |
| SCE1572_519 | sce_2023 | 1.00E-68 | 3.00E-69 |
| SCE1572_520 | sce_322 | 6.00E-48 | 1.00E-50 |
| SCE1572_5200 | sce_4359 | 1.00E-39 | 6.00E-40 |
| SCE1572_5202 | sce_4360 | 2.00E-168 | 1.00E-167 |
| SCE1572_5203 | sce_4361 | 7.00E-21 | 5.00E-23 |
| SCE1572_5204 | sce_4362 | 2.00E-144 | 2.00E-154 |
| SCE1572_5205 | sce_4363 | 5.00E-137 | 2.00E-135 |
| SCE1572_5206 | sce_4364 | 1.00E-88 | 2.00E-94 |
| SCE1572_5207 | sce_4365 | 3.00E-86 | 6.00E-90 |
| SCE1572_5208 | sce_4366 | 3.00E-16 | 5.00E-26 |
| SCE1572_5209 | sce_4367 | 2.00E-15 | 9.00E-29 |
| SCE1572_521 | sce_323 | 2.00E-41 | 3.00E-43 |
| SCE1572_5211 | sce_4368 | 0.00E+00 | 0.00E+00 |
| SCE1572_5212 | sce_9054 | 3.00E-106 | 3.00E-106 |
| SCE1572_5213 | sce_4370 | 3.00E-162 | 2.00E-154 |
| SCE1572_5214 | sce_4371 | 3.00E-98 | 4.00E-90 |
| SCE1572_5215 | sce_4372 | 2.00E-142 | 2.00E-142 |
| SCE1572_5217 | sce_4373 | 0.00E+00 | 0.00E+00 |
| SCE1572_522 | sce_325 | 4.00E-103 | 4.00E-103 |
| SCE1572_5220 | sce_4374 | 3.00E-168 | 7.00E-86 |
| SCE1572_5221 | sce_4375 | 3.00E-25 | 1.00E-25 |
| SCE1572_5222 | sce_4377 | 0.00E+00 | 0.00E+00 |
| SCE1572_5223 | sce_4378 | 4.00E-173 | 6.00E-161 |
| SCE1572_5224 | sce_4379 | 3.00E-110 | 3.00E-101 |
| SCE1572_5225 | sce_4380 | 3.00E-11 | 1.00E-17 |
| SCE1572_5226 | sce_4381 | 2.00E-104 | 7.00E-105 |
| SCE1572_5227 | sce_4382 | 1.00E-07 | 1.00E-07 |
| SCE1572_5228 | sce_4383 | 7.00E-129 | 7.00E-129 |
| SCE1572_5229 | sce_4384 | 7.00E-49 | 7.00E-49 |
| SCE1572_523 | sce_326 | 2.00E-141 | 9.00E-141 |
| SCE1572_5230 | sce_4385 | 0.00E+00 | 0.00E+00 |
| SCE1572_5231 | sce_4386 | 0.00E+00 | 0.00E+00 |
| SCE1572_5232 | sce_4387 | 1.00E-70 | 1.00E-70 |
| SCE1572_5233 | sce_4388 | 3.00E-41 | 5.00E-41 |
| SCE1572_5234 | sce_4389 | 6.00E-63 | 6.00E-63 |
| SCE1572_5235 | sce_4390 | 0.00E+00 | 0.00E+00 |
| SCE1572_5236 | sce_4391 | 0.00E+00 | 0.00E+00 |
| SCE1572_5237 | sce_4392 | 1.00E-172 | 8.00E-173 |
| SCE1572_5238 | sce_4393 | 0.00E+00 | 0.00E+00 |
| SCE1572_5239 | sce_4394 | 2.00E-108 | 3.00E-124 |
| SCE1572_524 | sce_327 | 3.00E-91 | 1.00E-100 |
| SCE1572_5240 | sce_4395 | 5.00E-41 | 7.00E-45 |
| SCE1572_5241 | sce_4396 | 1.00E-69 | 3.00E-72 |
| SCE1572_5242 | sce_4397 | 3.00E-47 | 9.00E-48 |
| SCE1572_5243 | sce_4398 | 4.00E-24 | 5.00E-24 |
| SCE1572_5244 | sce_4399 | 3.00E-166 | 4.00E-170 |
| SCE1572_5245 | sce_4400 | 3.00E-93 | 6.00E-106 |
| SCE1572_5246 | sce_4402 | 2.00E-82 | 1.00E-82 |
| SCE1572_5247 | sce_4403 | 1.00E-54 | 2.00E-53 |
| SCE1572_5248 | sce_4404 | 2.00E-159 | 2.00E-172 |
| SCE1572_5249 | sce_4405 | 0.00E+00 | 0.00E+00 |
| SCE1572_525 | sce_328 | 4.00E-73 | 4.00E-73 |
| SCE1572_5250 | sce_4406 | 0.00E+00 | 0.00E+00 |
| SCE1572_5251 | sce_4407 | 4.00E-164 | 3.00E-170 |
| SCE1572_5252 | sce_4408 | 3.00E-116 | 1.00E-117 |
| SCE1572_5254 | sce_4409 | 1.00E-155 | 1.00E-173 |

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|--------------|----------|-----------|-----------|
| SCE1572_5255 | sce_4410 | 1.00E-09 | 2.00E-09 |
| SCE1572_5256 | sce_4411 | 6.00E-28 | 5.00E-31 |
| SCE1572_5257 | sce_4412 | 1.00E-98 | 2.00E-97 |
| SCE1572_5259 | sce_4413 | 3.00E-160 | 7.00E-163 |
| SCE1572_526 | sce_329 | 2.00E-172 | 3.00E-174 |
| SCE1572_5260 | sce_4415 | 7.00E-151 | 1.00E-162 |
| SCE1572_5261 | sce_4416 | 6.00E-71 | 6.00E-51 |
| SCE1572_5264 | sce_4418 | 4.00E-101 | 9.00E-102 |
| SCE1572_5266 | sce_4420 | 4.00E-163 | 4.00E-160 |
| SCE1572_5267 | sce_4421 | 0.00E+00 | 0.00E+00 |
| SCE1572_5268 | sce_4422 | 1.00E-50 | 6.00E-61 |
| SCE1572_5269 | sce_4423 | 0.00E+00 | 0.00E+00 |
| SCE1572_527 | sce_330 | 1.00E-76 | 2.00E-93 |
| SCE1572_5270 | sce_4424 | 2.00E-30 | 2.00E-30 |
| SCE1572_5273 | sce_4427 | 6.00E-23 | 2.00E-29 |
| SCE1572_5276 | sce_4428 | 1.00E-21 | 1.00E-18 |
| SCE1572_5278 | sce_4431 | 1.00E-133 | 2.00E-132 |
| SCE1572_5279 | sce_4432 | 0.00E+00 | 0.00E+00 |
| SCE1572_528 | sce_331 | 8.00E-74 | 1.00E-81 |
| SCE1572_5280 | sce_4433 | 2.00E-123 | 6.00E-126 |
| SCE1572_5283 | sce_4434 | 5.00E-100 | 5.00E-104 |
| SCE1572_5284 | sce_4435 | 6.00E-106 | 4.00E-106 |
| SCE1572_5285 | sce_4436 | 1.00E-21 | 3.00E-22 |
| SCE1572_5286 | sce_4439 | 1.00E-177 | 0.00E+00 |
| SCE1572_5287 | sce_4440 | 5.00E-24 | 5.00E-27 |
| SCE1572_5288 | sce_4441 | 0.00E+00 | 0.00E+00 |
| SCE1572_529 | sce_332 | 1.00E-20 | 2.00E-28 |
| SCE1572_5290 | sce_4444 | 0.00E+00 | 0.00E+00 |
| SCE1572_5292 | sce_4448 | 9.00E-76 | 2.00E-76 |
| SCE1572_5295 | sce_4451 | 7.00E-99 | 3.00E-104 |
| SCE1572_5296 | sce_9863 | 2.00E-20 | 2.00E-17 |
| SCE1572_5297 | sce_4452 | 6.00E-56 | 5.00E-49 |
| SCE1572_5298 | sce_4454 | 1.00E-106 | 3.00E-108 |
| SCE1572_5299 | sce_4455 | 0.00E+00 | 0.00E+00 |
| SCE1572_53 | sce_9404 | 0.00E+00 | 0.00E+00 |
| SCE1572_530 | sce_333 | 0.00E+00 | 0.00E+00 |
| SCE1572_5304 | sce_4456 | 6.00E-62 | 7.00E-62 |
| SCE1572_5306 | sce_1644 | 8.00E-125 | 8.00E-125 |
| SCE1572_5307 | sce_1643 | 1.00E-99 | 1.00E-99 |
| SCE1572_5308 | sce_1642 | 4.00E-139 | 6.00E-139 |
| SCE1572_5309 | sce_1641 | 1.00E-131 | 3.00E-132 |
| SCE1572_531 | sce_334 | 0.00E+00 | 0.00E+00 |
| SCE1572_5310 | sce_1640 | 1.00E-70 | 6.00E-64 |
| SCE1572_5311 | sce_1639 | 4.00E-63 | 3.00E-63 |
| SCE1572_5315 | sce_4457 | 4.00E-38 | 8.00E-37 |
| SCE1572_532 | sce_121 | 2.00E-98 | 4.00E-93 |
| SCE1572_5321 | sce_9369 | 4.00E-54 | 4.00E-54 |
| SCE1572_5324 | sce_4460 | 0.00E+00 | 0.00E+00 |
| SCE1572_5325 | sce_4462 | 6.00E-65 | 2.00E-64 |
| SCE1572_5327 | sce_4463 | 0.00E+00 | 0.00E+00 |
| SCE1572_533 | sce_339 | 2.00E-33 | 2.00E-36 |
| SCE1572_5331 | sce_4465 | 9.00E-130 | 3.00E-132 |
| SCE1572_5332 | sce_4466 | 0.00E+00 | 0.00E+00 |
| SCE1572_5332 | sce_7643 | 0.00E+00 | 0.00E+00 |
| SCE1572_5333 | sce_4467 | 1.00E-122 | 6.00E-147 |
| SCE1572_5334 | sce_2438 | 1.00E-164 | 6.00E-168 |
| SCE1572_5335 | sce_6710 | 0.00E+00 | 0.00E+00 |
| SCE1572_5336 | sce_4472 | 9.00E-97 | 2.00E-98 |
| SCE1572_5337 | sce_3082 | 0.00E+00 | 0.00E+00 |
| SCE1572_5339 | sce_3073 | 6.00E-32 | 1.00E-37 |
| SCE1572_5340 | sce_3074 | 0.00E+00 | 0.00E+00 |
| SCE1572_5341 | sce_3075 | 0.00E+00 | 0.00E+00 |
| SCE1572_5341 | sce_9735 | 0.00E+00 | 0.00E+00 |
| SCE1572_5342 | sce_3076 | 8.00E-63 | 3.00E-52 |
| SCE1572_5345 | sce_4471 | 1.00E-100 | 1.00E-100 |
| SCE1572_5346 | sce_4473 | 6.00E-25 | 9.00E-19 |
| SCE1572_5347 | sce_4474 | 6.00E-93 | 7.00E-102 |
| SCE1572_5348 | sce_4475 | 6.00E-153 | 1.00E-152 |
| SCE1572_535 | sce_341 | 0.00E+00 | 0.00E+00 |
| SCE1572_5352 | sce_4477 | 0.00E+00 | 0.00E+00 |
| SCE1572_5353 | sce_8197 | 4.00E-07 | 5.00E-07 |
| SCE1572_5354 | sce_4479 | 2.00E-81 | 7.00E-87 |
| SCE1572_5355 | sce_4481 | 3.00E-101 | 4.00E-101 |
| SCE1572_5359 | sce_4482 | 1.00E-79 | 8.00E-48 |
| SCE1572_536 | sce_342 | 2.00E-107 | 3.00E-101 |
| SCE1572_5361 | sce_4484 | 3.00E-141 | 3.00E-141 |

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| SCE1572_5362 | sce_6192 | 2.00E-32 | 3.00E-42 |
| SCE1572_5363 | sce_6193 | 2.00E-106 | 4.00E-168 |
| SCE1572_5365 | sce_6194 | 1.00E-100 | 6.00E-102 |
| SCE1572_5368 | sce_4493 | 1.00E-58 | 1.00E-39 |
| SCE1572_5369 | sce_4494 | 0.00E+00 | 0.00E+00 |
| SCE1572_537 | sce_343 | 0.00E+00 | 0.00E+00 |
| SCE1572_5371 | sce_4495 | 0.00E+00 | 0.00E+00 |
| SCE1572_5372 | sce_7583 | 0.00E+00 | 0.00E+00 |
| SCE1572_5373 | sce_7582 | 3.00E-73 | 2.00E-73 |
| SCE1572_5374 | sce_4496 | 0.00E+00 | 0.00E+00 |
| SCE1572_5375 | sce_7141 | 6.00E-33 | 1.00E-26 |
| SCE1572_5376 | sce_4498 | 0.00E+00 | 0.00E+00 |
| SCE1572_5377 | sce_4499 | 0.00E+00 | 0.00E+00 |
| SCE1572_5379 | sce_4505 | 6.00E-144 | 6.00E-144 |
| SCE1572_538 | sce_344 | 8.00E-170 | 1.00E-173 |
| SCE1572_5380 | sce_4506 | 6.00E-135 | 3.00E-122 |
| SCE1572_5381 | sce_4507 | 0.00E+00 | 1.00E-166 |
| SCE1572_5382 | sce_4508 | 6.00E-170 | 3.00E-160 |
| SCE1572_5384 | sce_2062 | 4.00E-35 | 5.00E-34 |
| SCE1572_5385 | sce_4509 | 0.00E+00 | 0.00E+00 |
| SCE1572_5386 | sce_4510 | 3.00E-177 | 6.00E-171 |
| SCE1572_5387 | sce_4511 | 0.00E+00 | 0.00E+00 |
| SCE1572_5388 | sce_4512 | 1.00E-166 | 1.00E-163 |
| SCE1572_5389 | sce_4513 | 0.00E+00 | 0.00E+00 |
| SCE1572_5389 | sce_10204 | 0.00E+00 | 0.00E+00 |
| SCE1572_5389 | sce_388 | 0.00E+00 | 0.00E+00 |
| SCE1572_5389 | sce_5835 | 0.00E+00 | 0.00E+00 |
| SCE1572_5389 | sce_7640 | 0.00E+00 | 0.00E+00 |
| SCE1572_5389 | sce_3085 | 0.00E+00 | 0.00E+00 |
| SCE1572_5389 | sce_9557 | 0.00E+00 | 0.00E+00 |
| SCE1572_5389 | sce_7109 | 0.00E+00 | 0.00E+00 |
| SCE1572_5389 | sce_6535 | 0.00E+00 | 0.00E+00 |
| SCE1572_5389 | sce_3003 | 0.00E+00 | 0.00E+00 |
| SCE1572_5389 | sce_6093 | 0.00E+00 | 0.00E+00 |
| SCE1572_5389 | sce_6095 | 0.00E+00 | 0.00E+00 |
| SCE1572_5389 | sce_9920 | 0.00E+00 | 0.00E+00 |
| SCE1572_5389 | sce_6107 | 0.00E+00 | 0.00E+00 |
| SCE1572_5389 | sce_3917 | 0.00E+00 | 0.00E+00 |
| SCE1572_5389 | sce_6092 | 0.00E+00 | 0.00E+00 |
| SCE1572_5389 | sce_7661 | 0.00E+00 | 0.00E+00 |
| SCE1572_5389 | sce_8618 | 0.00E+00 | 0.00E+00 |
| SCE1572_539 | sce_345 | 4.00E-56 | 3.00E-50 |
| SCE1572_5391 | sce_4516 | 2.00E-162 | 2.00E-162 |
| SCE1572_5392 | sce_4517 | 3.00E-138 | 3.00E-138 |
| SCE1572_5393 | sce_4518 | 7.00E-149 | 7.00E-149 |
| SCE1572_5394 | sce_4519 | 0.00E+00 | 0.00E+00 |
| SCE1572_54 | sce_9403 | 2.00E-39 | 3.00E-48 |
| SCE1572_540 | sce_346 | 0.00E+00 | 0.00E+00 |
| SCE1572_5400 | sce_4522 | 0.00E+00 | 0.00E+00 |
| SCE1572_5401 | sce_4523 | 8.00E-38 | 1.00E-30 |
| SCE1572_5402 | sce_4524 | 7.00E-106 | 9.00E-105 |
| SCE1572_5404 | sce_4537 | 4.00E-60 | 4.00E-60 |
| SCE1572_5405 | sce_4538 | 2.00E-128 | 2.00E-128 |
| SCE1572_5406 | sce_4539 | 5.00E-62 | 9.00E-61 |
| SCE1572_5408 | sce_4540 | 6.00E-120 | 4.00E-103 |
| SCE1572_541 | sce_347 | 6.00E-90 | 1.00E-86 |
| SCE1572_5412 | sce_4562 | 0.00E+00 | 1.00E-176 |
| SCE1572_5414 | sce_4564 | 2.00E-122 | 3.00E-128 |
| SCE1572_5415 | sce_4565 | 0.00E+00 | 0.00E+00 |
| SCE1572_5416 | sce_4566 | 2.00E-113 | 6.00E-107 |
| SCE1572_5417 | sce_4567 | 3.00E-161 | 2.00E-159 |
| SCE1572_5418 | sce_10011 | 9.00E-38 | 2.00E-47 |
| SCE1572_5419 | sce_9329 | 6.00E-76 | 1.00E-62 |
| SCE1572_542 | sce_348 | 9.00E-120 | 7.00E-119 |
| SCE1572_5420 | sce_4568 | 7.00E-131 | 5.00E-139 |
| SCE1572_5421 | sce_4569 | 3.00E-76 | 1.00E-79 |
| SCE1572_5423 | sce_4573 | 0.00E+00 | 0.00E+00 |
| SCE1572_5426 | sce_1600 | 5.00E-13 | 3.00E-18 |
| SCE1572_5427 | sce_3045 | 1.00E-58 | 2.00E-59 |
| SCE1572_5429 | sce_4574 | 0.00E+00 | 0.00E+00 |
| SCE1572_543 | sce_349 | 4.00E-120 | 3.00E-100 |
| SCE1572_5430 | sce_7563 | 0.00E+00 | 0.00E+00 |
| SCE1572_5434 | sce_4578 | 0.00E+00 | 0.00E+00 |
| SCE1572_544 | sce_350 | 3.00E-57 | 3.00E-57 |
| SCE1572_545 | sce_352 | 4.00E-144 | 2.00E-145 |
| SCE1572_5451 | sce_5278 | 0.00E+00 | 0.00E+00 |

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| SCE1572_5452 | sce_5276 | 0.00E+00 | 0.00E+00 |
| SCE1572_5452 | sce_2161 | 0.00E+00 | 0.00E+00 |
| SCE1572_5452 | sce_225 | 0.00E+00 | 0.00E+00 |
| SCE1572_5452 | sce_8357 | 0.00E+00 | 0.00E+00 |
| SCE1572_5452 | sce_6235 | 0.00E+00 | 0.00E+00 |
| SCE1572_5468 | sce_388 | 0.00E+00 | 0.00E+00 |
| SCE1572_5468 | sce_5835 | 0.00E+00 | 0.00E+00 |
| SCE1572_5468 | sce_7640 | 0.00E+00 | 0.00E+00 |
| SCE1572_5468 | sce_10204 | 0.00E+00 | 0.00E+00 |
| SCE1572_5468 | sce_9920 | 0.00E+00 | 0.00E+00 |
| SCE1572_5468 | sce_7661 | 0.00E+00 | 0.00E+00 |
| SCE1572_5468 | sce_3085 | 0.00E+00 | 0.00E+00 |
| SCE1572_5468 | sce_9557 | 0.00E+00 | 0.00E+00 |
| SCE1572_5468 | sce_3003 | 0.00E+00 | 0.00E+00 |
| SCE1572_5468 | sce_6092 | 0.00E+00 | 0.00E+00 |
| SCE1572_5468 | sce_4513 | 0.00E+00 | 0.00E+00 |
| SCE1572_5468 | sce_6095 | 0.00E+00 | 0.00E+00 |
| SCE1572_5468 | sce_7109 | 0.00E+00 | 0.00E+00 |
| SCE1572_5468 | sce_6094 | 0.00E+00 | 0.00E+00 |
| SCE1572_5468 | sce_6535 | 0.00E+00 | 0.00E+00 |
| SCE1572_5468 | sce_2065 | 0.00E+00 | 0.00E+00 |
| SCE1572_5468 | sce_6093 | 0.00E+00 | 0.00E+00 |
| SCE1572_5468 | sce_3917 | 0.00E+00 | 0.00E+00 |
| SCE1572_5468 | sce_6107 | 0.00E+00 | 0.00E+00 |
| SCE1572_5468 | sce_1398 | 0.00E+00 | 0.00E+00 |
| SCE1572_5468 | sce_8602 | 0.00E+00 | 0.00E+00 |
| SCE1572_547 | sce_353 | 2.00E-107 | 3.00E-115 |
| SCE1572_5470 | sce_4595 | 2.00E-52 | 1.00E-53 |
| SCE1572_5475 | sce_8779 | 5.00E-101 | 2.00E-84 |
| SCE1572_5476 | sce_8781 | 0.00E+00 | 0.00E+00 |
| SCE1572_5477 | sce_8782 | 2.00E-128 | 6.00E-153 |
| SCE1572_548 | sce_355 | 0.00E+00 | 0.00E+00 |
| SCE1572_5480 | sce_7640 | 0.00E+00 | 0.00E+00 |
| SCE1572_5480 | sce_388 | 0.00E+00 | 0.00E+00 |
| SCE1572_5480 | sce_5835 | 0.00E+00 | 0.00E+00 |
| SCE1572_5480 | sce_10204 | 0.00E+00 | 0.00E+00 |
| SCE1572_5480 | sce_3085 | 0.00E+00 | 0.00E+00 |
| SCE1572_5480 | sce_4513 | 0.00E+00 | 0.00E+00 |
| SCE1572_5480 | sce_9557 | 0.00E+00 | 0.00E+00 |
| SCE1572_5480 | sce_7109 | 0.00E+00 | 0.00E+00 |
| SCE1572_5480 | sce_9920 | 0.00E+00 | 0.00E+00 |
| SCE1572_5480 | sce_6107 | 0.00E+00 | 0.00E+00 |
| SCE1572_5480 | sce_3003 | 0.00E+00 | 0.00E+00 |
| SCE1572_5480 | sce_6535 | 0.00E+00 | 0.00E+00 |
| SCE1572_5480 | sce_6092 | 0.00E+00 | 0.00E+00 |
| SCE1572_5480 | sce_6093 | 0.00E+00 | 0.00E+00 |
| SCE1572_5480 | sce_7661 | 0.00E+00 | 0.00E+00 |
| SCE1572_5480 | sce_3917 | 0.00E+00 | 0.00E+00 |
| SCE1572_5480 | sce_6095 | 0.00E+00 | 0.00E+00 |
| SCE1572_5480 | sce_6094 | 0.00E+00 | 0.00E+00 |
| SCE1572_5480 | sce_2065 | 0.00E+00 | 0.00E+00 |
| SCE1572_5480 | sce_8618 | 0.00E+00 | 0.00E+00 |
| SCE1572_5482 | sce_5502 | 0.00E+00 | 0.00E+00 |
| SCE1572_5482 | sce_2641 | 0.00E+00 | 0.00E+00 |
| SCE1572_5483 | sce_5480 | 7.00E-121 | 5.00E-109 |
| SCE1572_5484 | sce_5479 | 3.00E-179 | 0.00E+00 |
| SCE1572_5485 | sce_7637 | 0.00E+00 | 0.00E+00 |
| SCE1572_5485 | sce_389 | 0.00E+00 | 0.00E+00 |
| SCE1572_5485 | sce_2666 | 0.00E+00 | 0.00E+00 |
| SCE1572_5485 | sce_9230 | 0.00E+00 | 0.00E+00 |
| SCE1572_5485 | sce_9237 | 0.00E+00 | 0.00E+00 |
| SCE1572_5487 | sce_4598 | 1.00E-112 | 2.00E-121 |
| SCE1572_5488 | sce_4599 | 2.00E-111 | 2.00E-110 |
| SCE1572_55 | sce_8347 | 0.00E+00 | 0.00E+00 |
| SCE1572_55 | sce_4610 | 0.00E+00 | 0.00E+00 |
| SCE1572_5504 | sce_2328 | 1.00E-21 | 3.00E-10 |
| SCE1572_551 | sce_357 | 2.00E-68 | 2.00E-67 |
| SCE1572_5510 | sce_2321 | 1.00E-14 | 1.00E-15 |
| SCE1572_5512 | sce_2319 | 4.00E-60 | 8.00E-62 |
| SCE1572_552 | sce_358 | 0.00E+00 | 0.00E+00 |
| SCE1572_5522 | sce_6361 | 6.00E-47 | 9.00E-56 |
| SCE1572_5528 | sce_7463 | 2.00E-37 | 6.00E-31 |
| SCE1572_5529 | sce_3646 | 9.00E-179 | 4.00E-179 |
| SCE1572_5533 | sce_3598 | 0.00E+00 | 0.00E+00 |
| SCE1572_5536 | sce_3597 | 0.00E+00 | 0.00E+00 |
| SCE1572_5537 | sce_3596 | 0.00E+00 | 0.00E+00 |

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| SCE1572_5538 | sce_3595 | 0.00E+00 | 0.00E+00 |
| SCE1572_5539 | sce_3594 | 0.00E+00 | 0.00E+00 |
| SCE1572_5540 | sce_3593 | 4.00E-121 | 2.00E-128 |
| SCE1572_5541 | sce_3592 | 5.00E-89 | 5.00E-89 |
| SCE1572_5542 | sce_3590 | 0.00E+00 | 0.00E+00 |
| SCE1572_5543 | sce_3589 | 5.00E-38 | 5.00E-38 |
| SCE1572_5544 | sce_3588 | 9.00E-179 | 5.00E-179 |
| SCE1572_556 | sce_359 | 5.00E-93 | 7.00E-101 |
| SCE1572_557 | sce_360 | 0.00E+00 | 0.00E+00 |
| SCE1572_5570 | sce_7637 | 0.00E+00 | 0.00E+00 |
| SCE1572_5570 | sce_9230 | 0.00E+00 | 0.00E+00 |
| SCE1572_5570 | sce_389 | 0.00E+00 | 0.00E+00 |
| SCE1572_5570 | sce_2666 | 0.00E+00 | 0.00E+00 |
| SCE1572_5570 | sce_9237 | 0.00E+00 | 0.00E+00 |
| SCE1572_5570 | sce_9231 | 0.00E+00 | 0.00E+00 |
| SCE1572_5571 | sce_9230 | 0.00E+00 | 0.00E+00 |
| SCE1572_5571 | sce_7637 | 0.00E+00 | 0.00E+00 |
| SCE1572_5571 | sce_389 | 0.00E+00 | 0.00E+00 |
| SCE1572_5571 | sce_2666 | 0.00E+00 | 0.00E+00 |
| SCE1572_5571 | sce_9237 | 0.00E+00 | 0.00E+00 |
| SCE1572_5571 | sce_9231 | 0.00E+00 | 0.00E+00 |
| SCE1572_5572 | sce_9230 | 0.00E+00 | 0.00E+00 |
| SCE1572_5572 | sce_389 | 0.00E+00 | 0.00E+00 |
| SCE1572_5572 | sce_2666 | 0.00E+00 | 0.00E+00 |
| SCE1572_5572 | sce_7637 | 0.00E+00 | 0.00E+00 |
| SCE1572_5572 | sce_9237 | 0.00E+00 | 0.00E+00 |
| SCE1572_5572 | sce_9231 | 0.00E+00 | 0.00E+00 |
| SCE1572_5579 | sce_4645 | 0.00E+00 | 0.00E+00 |
| SCE1572_558 | sce_361 | 1.00E-106 | 2.00E-103 |
| SCE1572_5580 | sce_4646 | 1.00E-159 | 6.00E-165 |
| SCE1572_5581 | sce_4647 | 3.00E-144 | 1.00E-139 |
| SCE1572_5582 | sce_1162 | 3.00E-98 | 4.00E-104 |
| SCE1572_5583 | sce_1161 | 3.00E-133 | 4.00E-140 |
| SCE1572_5584 | sce_1160 | 1.00E-149 | 4.00E-160 |
| SCE1572_5585 | sce_4648 | 3.00E-111 | 2.00E-102 |
| SCE1572_5587 | sce_4650 | 1.00E-91 | 3.00E-95 |
| SCE1572_559 | sce_362 | 1.00E-52 | 1.00E-52 |
| SCE1572_5592 | sce_4656 | 0.00E+00 | 0.00E+00 |
| SCE1572_5594 | sce_4657 | 6.00E-142 | 7.00E-142 |
| SCE1572_5596 | sce_4658 | 0.00E+00 | 0.00E+00 |
| SCE1572_5597 | sce_4660 | 0.00E+00 | 0.00E+00 |
| SCE1572_5598 | sce_4661 | 2.00E-160 | 3.00E-171 |
| SCE1572_5599 | sce_5147 | 0.00E+00 | 0.00E+00 |
| SCE1572_5599 | sce_4662 | 0.00E+00 | 0.00E+00 |
| SCE1572_560 | sce_363 | 6.00E-176 | 6.00E-176 |
| SCE1572_5600 | sce_4663 | 0.00E+00 | 0.00E+00 |
| SCE1572_5600 | sce_5148 | 0.00E+00 | 0.00E+00 |
| SCE1572_5601 | sce_4665 | 0.00E+00 | 0.00E+00 |
| SCE1572_5602 | sce_4671 | 0.00E+00 | 0.00E+00 |
| SCE1572_5606 | sce_4684 | 4.00E-139 | 1.00E-147 |
| SCE1572_5607 | sce_6014 | 0.00E+00 | 0.00E+00 |
| SCE1572_5608 | sce_4685 | 6.00E-69 | 8.00E-63 |
| SCE1572_5609 | sce_4686 | 0.00E+00 | 0.00E+00 |
| SCE1572_561 | sce_364 | 1.00E-142 | 1.00E-143 |
| SCE1572_5612 | sce_5882 | 9.00E-60 | 6.00E-60 |
| SCE1572_5614 | sce_4701 | 2.00E-79 | 7.00E-78 |
| SCE1572_5617 | sce_4702 | 0.00E+00 | 1.00E-176 |
| SCE1572_5619 | sce_4704 | 1.00E-87 | 5.00E-90 |
| SCE1572_562 | sce_365 | 6.00E-130 | 9.00E-122 |
| SCE1572_5622 | sce_4705 | 0.00E+00 | 0.00E+00 |
| SCE1572_5623 | sce_4706 | 0.00E+00 | 0.00E+00 |
| SCE1572_5625 | sce_4707 | 2.00E-34 | 3.00E-27 |
| SCE1572_563 | sce_366 | 3.00E-96 | 1.00E-85 |
| SCE1572_5630 | sce_7538 | 0.00E+00 | 0.00E+00 |
| SCE1572_5635 | sce_8649 | 0.00E+00 | 0.00E+00 |
| SCE1572_5635 | sce_6571 | 0.00E+00 | 0.00E+00 |
| SCE1572_5636 | sce_8648 | 1.00E-141 | 1.00E-141 |
| SCE1572_5637 | sce_4709 | 0.00E+00 | 0.00E+00 |
| SCE1572_5639 | sce_4710 | 1.00E-92 | 5.00E-104 |
| SCE1572_5640 | sce_7661 | 0.00E+00 | 0.00E+00 |
| SCE1572_5640 | sce_8602 | 0.00E+00 | 0.00E+00 |
| SCE1572_5640 | sce_3917 | 0.00E+00 | 0.00E+00 |
| SCE1572_5640 | sce_6107 | 0.00E+00 | 0.00E+00 |
| SCE1572_5640 | sce_6092 | 0.00E+00 | 0.00E+00 |
| SCE1572_5640 | sce_6093 | 0.00E+00 | 0.00E+00 |
| SCE1572_5640 | sce_6094 | 0.00E+00 | 0.00E+00 |

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| SCE1572_5640 | sce_6095 | 0.00E+00 | 0.00E+00 |
| SCE1572_5640 | sce_6535 | 0.00E+00 | 0.00E+00 |
| SCE1572_5640 | sce_388 | 0.00E+00 | 0.00E+00 |
| SCE1572_5640 | sce_10204 | 0.00E+00 | 0.00E+00 |
| SCE1572_5640 | sce_9920 | 0.00E+00 | 0.00E+00 |
| SCE1572_5640 | sce_3003 | 0.00E+00 | 0.00E+00 |
| SCE1572_5640 | sce_9557 | 0.00E+00 | 0.00E+00 |
| SCE1572_5640 | sce_5835 | 0.00E+00 | 0.00E+00 |
| SCE1572_5640 | sce_7640 | 0.00E+00 | 0.00E+00 |
| SCE1572_5640 | sce_2065 | 0.00E+00 | 0.00E+00 |
| SCE1572_5640 | sce_8618 | 0.00E+00 | 0.00E+00 |
| SCE1572_5640 | sce_4513 | 0.00E+00 | 0.00E+00 |
| SCE1572_5640 | sce_3085 | 0.00E+00 | 0.00E+00 |
| SCE1572_5640 | sce_7109 | 0.00E+00 | 0.00E+00 |
| SCE1572_5649 | sce_4711 | 0.00E+00 | 0.00E+00 |
| SCE1572_5649 | sce_3376 | 0.00E+00 | 0.00E+00 |
| SCE1572_565 | sce_368 | 7.00E-73 | 7.00E-73 |
| SCE1572_5652 | sce_9774 | 3.00E-134 | 8.00E-150 |
| SCE1572_5654 | sce_9776 | 0.00E+00 | 0.00E+00 |
| SCE1572_5654 | sce_5358 | 0.00E+00 | 0.00E+00 |
| SCE1572_5655 | sce_9777 | 0.00E+00 | 0.00E+00 |
| SCE1572_5655 | sce_5359 | 0.00E+00 | 0.00E+00 |
| SCE1572_5656 | sce_1130 | 5.00E-22 | 5.00E-55 |
| SCE1572_5658 | sce_4713 | 0.00E+00 | 0.00E+00 |
| SCE1572_5659 | sce_9663 | 0.00E+00 | 0.00E+00 |
| SCE1572_5663 | sce_4714 | 0.00E+00 | 0.00E+00 |
| SCE1572_5664 | sce_4715 | 2.00E-166 | 1.00E-155 |
| SCE1572_5665 | sce_4716 | 2.00E-62 | 2.00E-67 |
| SCE1572_5666 | sce_4717 | 5.00E-122 | 3.00E-130 |
| SCE1572_5668 | sce_4718 | 9.00E-29 | 9.00E-28 |
| SCE1572_5669 | sce_4719 | 4.00E-134 | 3.00E-139 |
| SCE1572_567 | sce_370 | 0.00E+00 | 0.00E+00 |
| SCE1572_567 | sce_41 | 0.00E+00 | 0.00E+00 |
| SCE1572_5670 | sce_4720 | 3.00E-176 | 5.00E-164 |
| SCE1572_5671 | sce_4721 | 1.00E-130 | 1.00E-130 |
| SCE1572_5673 | sce_4722 | 1.00E-103 | 7.00E-111 |
| SCE1572_5675 | sce_4727 | 1.00E-170 | 1.00E-152 |
| SCE1572_5676 | sce_4728 | 8.00E-45 | 1.00E-37 |
| SCE1572_5677 | sce_4729 | 5.00E-129 | 1.00E-125 |
| SCE1572_5678 | sce_4730 | 0.00E+00 | 4.00E-175 |
| SCE1572_5679 | sce_4731 | 0.00E+00 | 0.00E+00 |
| SCE1572_568 | sce_371 | 5.00E-48 | 3.00E-48 |
| SCE1572_5680 | sce_4732 | 0.00E+00 | 0.00E+00 |
| SCE1572_5681 | sce_4733 | 8.00E-30 | 9.00E-30 |
| SCE1572_5682 | sce_4734 | 8.00E-66 | 1.00E-62 |
| SCE1572_5683 | sce_4735 | 0.00E+00 | 0.00E+00 |
| SCE1572_5684 | sce_4736 | 1.00E-89 | 1.00E-89 |
| SCE1572_5685 | sce_4738 | 3.00E-66 | 3.00E-60 |
| SCE1572_5686 | sce_4739 | 1.00E-48 | 1.00E-48 |
| SCE1572_5688 | sce_4740 | 7.00E-99 | 7.00E-99 |
| SCE1572_5689 | sce_4741 | 1.00E-119 | 1.00E-119 |
| SCE1572_569 | sce_372 | 6.00E-20 | 5.00E-22 |
| SCE1572_5690 | sce_4742 | 8.00E-70 | 3.00E-77 |
| SCE1572_5691 | sce_4743 | 7.00E-149 | 3.00E-163 |
| SCE1572_5692 | sce_4744 | 0.00E+00 | 0.00E+00 |
| SCE1572_5693 | sce_4745 | 4.00E-96 | 7.00E-89 |
| SCE1572_5694 | sce_4746 | 0.00E+00 | 2.00E-173 |
| SCE1572_5695 | sce_9269 | 1.00E-46 | 1.00E-46 |
| SCE1572_5697 | sce_4750 | 0.00E+00 | 0.00E+00 |
| SCE1572_5699 | sce_4751 | 1.00E-92 | 5.00E-92 |
| SCE1572_57 | sce_6254 | 6.00E-92 | 5.00E-89 |
| SCE1572_570 | sce_804 | 2.00E-138 | 2.00E-141 |
| SCE1572_5700 | sce_4752 | 2.00E-64 | 2.00E-60 |
| SCE1572_5701 | sce_4753 | 3.00E-37 | 7.00E-44 |
| SCE1572_5702 | sce_4754 | 0.00E+00 | 0.00E+00 |
| SCE1572_5703 | sce_4755 | 0.00E+00 | 0.00E+00 |
| SCE1572_5704 | sce_4756 | 7.00E-146 | 7.00E-146 |
| SCE1572_5705 | sce_4757 | 9.00E-72 | 4.00E-58 |
| SCE1572_5706 | sce_4758 | 2.00E-97 | 2.00E-94 |
| SCE1572_5707 | sce_4759 | 6.00E-102 | 2.00E-102 |
| SCE1572_5708 | sce_4761 | 0.00E+00 | 0.00E+00 |
| SCE1572_5709 | sce_4762 | 0.00E+00 | 0.00E+00 |
| SCE1572_5710 | sce_4763 | 3.00E-11 | 1.00E-15 |
| SCE1572_5711 | sce_4764 | 0.00E+00 | 0.00E+00 |
| SCE1572_5712 | sce_4765 | 2.00E-55 | 2.00E-55 |
| SCE1572_5713 | sce_4766 | 4.00E-56 | 2.00E-56 |

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| SCE1572_5714 | sce_4767 | 1.00E-104 | 4.00E-110 |
| SCE1572_5715 | sce_4768 | 1.00E-48 | 8.00E-49 |
| SCE1572_5716 | sce_4769 | 0.00E+00 | 0.00E+00 |
| SCE1572_5716 | sce_1353 | 0.00E+00 | 0.00E+00 |
| SCE1572_5717 | sce_4770 | 1.00E-48 | 1.00E-47 |
| SCE1572_5718 | sce_4771 | 4.00E-160 | 7.00E-160 |
| SCE1572_5719 | sce_4772 | 2.00E-115 | 2.00E-115 |
| SCE1572_5720 | sce_4773 | 2.00E-159 | 3.00E-159 |
| SCE1572_5721 | sce_4774 | 3.00E-166 | 3.00E-164 |
| SCE1572_5722 | sce_4775 | 8.00E-127 | 2.00E-129 |
| SCE1572_5726 | sce_4776 | 0.00E+00 | 0.00E+00 |
| SCE1572_5727 | sce_4778 | 0.00E+00 | 0.00E+00 |
| SCE1572_5728 | sce_4779 | 8.00E-106 | 4.00E-103 |
| SCE1572_5729 | sce_4780 | 1.00E-46 | 1.00E-50 |
| SCE1572_573 | sce_375 | 0.00E+00 | 0.00E+00 |
| SCE1572_5731 | sce_4781 | 6.00E-38 | 5.00E-46 |
| SCE1572_5732 | sce_4782 | 7.00E-94 | 2.00E-104 |
| SCE1572_5733 | sce_4783 | 8.00E-167 | 2.00E-169 |
| SCE1572_5734 | sce_4784 | 0.00E+00 | 0.00E+00 |
| SCE1572_5735 | sce_4785 | 0.00E+00 | 0.00E+00 |
| SCE1572_5736 | sce_4786 | 8.00E-48 | 2.00E-54 |
| SCE1572_5737 | sce_4788 | 1.00E-58 | 4.00E-54 |
| SCE1572_5738 | sce_4789 | 6.00E-45 | 2.00E-45 |
| SCE1572_5739 | sce_4790 | 2.00E-69 | 2.00E-70 |
| SCE1572_574 | sce_376 | 9.00E-108 | 1.00E-115 |
| SCE1572_5740 | sce_4791 | 4.00E-87 | 4.00E-87 |
| SCE1572_5741 | sce_4792 | 4.00E-137 | 6.00E-135 |
| SCE1572_5742 | sce_4793 | 2.00E-129 | 1.00E-116 |
| SCE1572_5744 | sce_4794 | 0.00E+00 | 0.00E+00 |
| SCE1572_5745 | sce_4795 | 2.00E-52 | 2.00E-52 |
| SCE1572_5746 | sce_4796 | 0.00E+00 | 0.00E+00 |
| SCE1572_5747 | sce_4797 | 1.00E-65 | 6.00E-91 |
| SCE1572_5748 | sce_4798 | 2.00E-165 | 3.00E-165 |
| SCE1572_5749 | sce_4799 | 0.00E+00 | 0.00E+00 |
| SCE1572_575 | sce_377 | 5.00E-22 | 5.00E-22 |
| SCE1572_5750 | sce_4800 | 2.00E-61 | 3.00E-72 |
| SCE1572_5751 | sce_4801 | 0.00E+00 | 0.00E+00 |
| SCE1572_5752 | sce_4803 | 1.00E-124 | 2.00E-112 |
| SCE1572_5754 | sce_4805 | 7.00E-121 | 4.00E-121 |
| SCE1572_5755 | sce_4806 | 0.00E+00 | 0.00E+00 |
| SCE1572_5759 | sce_4807 | 5.00E-147 | 6.00E-169 |
| SCE1572_576 | sce_381 | 0.00E+00 | 0.00E+00 |
| SCE1572_5760 | sce_4808 | 8.00E-134 | 7.00E-122 |
| SCE1572_5761 | sce_4809 | 2.00E-155 | 2.00E-154 |
| SCE1572_5762 | sce_4810 | 5.00E-125 | 2.00E-114 |
| SCE1572_5764 | sce_4811 | 8.00E-147 | 3.00E-146 |
| SCE1572_5765 | sce_4812 | 0.00E+00 | 0.00E+00 |
| SCE1572_5766 | sce_4813 | 0.00E+00 | 0.00E+00 |
| SCE1572_5767 | sce_4814 | 0.00E+00 | 0.00E+00 |
| SCE1572_5768 | sce_4815 | 0.00E+00 | 0.00E+00 |
| SCE1572_5769 | sce_4816 | 4.00E-177 | 4.00E-177 |
| SCE1572_5770 | sce_4817 | 0.00E+00 | 0.00E+00 |
| SCE1572_5770 | sce_9407 | 0.00E+00 | 0.00E+00 |
| SCE1572_5770 | sce_8451 | 0.00E+00 | 0.00E+00 |
| SCE1572_5770 | sce_3765 | 0.00E+00 | 0.00E+00 |
| SCE1572_5772 | sce_4818 | 0.00E+00 | 0.00E+00 |
| SCE1572_5774 | sce_4820 | 3.00E-13 | 1.00E-15 |
| SCE1572_5775 | sce_4821 | 0.00E+00 | 0.00E+00 |
| SCE1572_5776 | sce_4822 | 0.00E+00 | 0.00E+00 |
| SCE1572_5777 | sce_4823 | 9.00E-56 | 1.00E-55 |
| SCE1572_5778 | sce_4824 | 2.00E-108 | 2.00E-108 |
| SCE1572_5779 | sce_4825 | 5.00E-100 | 8.00E-135 |
| SCE1572_5780 | sce_4826 | 5.00E-117 | 1.00E-117 |
| SCE1572_5781 | sce_4827 | 0.00E+00 | 0.00E+00 |
| SCE1572_5782 | sce_4828 | 2.00E-30 | 6.00E-31 |
| SCE1572_5783 | sce_4830 | 4.00E-141 | 2.00E-160 |
| SCE1572_5784 | sce_4831 | 3.00E-73 | 1.00E-100 |
| SCE1572_5785 | sce_4832 | 1.00E-68 | 1.00E-70 |
| SCE1572_5786 | sce_4833 | 3.00E-47 | 8.00E-48 |
| SCE1572_5787 | sce_4834 | 5.00E-86 | 5.00E-86 |
| SCE1572_5788 | sce_4835 | 6.00E-98 | 3.00E-104 |
| SCE1572_5789 | sce_4836 | 0.00E+00 | 0.00E+00 |
| SCE1572_579 | sce_384 | 2.00E-57 | 1.00E-58 |
| SCE1572_5790 | sce_4837 | 1.00E-176 | 1.00E-176 |
| SCE1572_5791 | sce_4838 | 0.00E+00 | 0.00E+00 |
| SCE1572_5792 | sce_4839 | 7.00E-52 | 4.00E-54 |

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| SCE1572_5793 | sce_4840 | 3.00E-108 | 9.00E-122 |
| SCE1572_5794 | sce_4841 | 1.00E-119 | 2.00E-121 |
| SCE1572_5795 | sce_4842 | 9.00E-80 | 1.00E-78 |
| SCE1572_5796 | sce_4843 | 2.00E-104 | 3.00E-110 |
| SCE1572_5797 | sce_4844 | 2.00E-146 | 3.00E-158 |
| SCE1572_5798 | sce_4846 | 6.00E-107 | 4.00E-103 |
| SCE1572_5799 | sce_4847 | 5.00E-137 | 2.00E-136 |
| SCE1572_58 | sce_6262 | 3.00E-124 | 9.00E-129 |
| SCE1572_580 | sce_385 | 1.00E-116 | 1.00E-125 |
| SCE1572_5800 | sce_4848 | 7.00E-180 | 0.00E+00 |
| SCE1572_5801 | sce_4849 | 8.00E-109 | 5.00E-120 |
| SCE1572_5802 | sce_4850 | 2.00E-124 | 3.00E-126 |
| SCE1572_5803 | sce_4851 | 2.00E-88 | 6.00E-84 |
| SCE1572_5804 | sce_4852 | 2.00E-41 | 2.00E-42 |
| SCE1572_5806 | sce_4854 | 2.00E-31 | 2.00E-31 |
| SCE1572_5807 | sce_4855 | 2.00E-73 | 2.00E-80 |
| SCE1572_5808 | sce_4856 | 4.00E-163 | 2.00E-163 |
| SCE1572_5809 | sce_4857 | 0.00E+00 | 0.00E+00 |
| SCE1572_581 | sce_386 | 3.00E-159 | 6.00E-174 |
| SCE1572_5810 | sce_4858 | 3.00E-64 | 3.00E-73 |
| SCE1572_5811 | sce_4859 | 0.00E+00 | 0.00E+00 |
| SCE1572_5812 | sce_4861 | 0.00E+00 | 0.00E+00 |
| SCE1572_5812 | sce_4106 | 0.00E+00 | 0.00E+00 |
| SCE1572_5813 | sce_4862 | 2.00E-170 | 4.00E-167 |
| SCE1572_5814 | sce_4863 | 3.00E-111 | 0.00E+00 |
| SCE1572_5815 | sce_4864 | 0.00E+00 | 0.00E+00 |
| SCE1572_5816 | sce_4865 | 2.00E-176 | 3.00E-169 |
| SCE1572_5818 | sce_9910 | 7.00E-118 | 6.00E-106 |
| SCE1572_582 | sce_392 | 0.00E+00 | 2.00E-180 |
| SCE1572_5820 | sce_10365 | 0.00E+00 | 0.00E+00 |
| SCE1572_5820 | sce_9503 | 0.00E+00 | 0.00E+00 |
| SCE1572_5820 | sce_9908 | 0.00E+00 | 0.00E+00 |
| SCE1572_5823 | sce_4866 | 2.00E-58 | 1.00E-58 |
| SCE1572_5825 | sce_4867 | 0.00E+00 | 0.00E+00 |
| SCE1572_5826 | sce_4868 | 3.00E-133 | 6.00E-142 |
| SCE1572_5827 | sce_4869 | 0.00E+00 | 2.00E-171 |
| SCE1572_5828 | sce_4870 | 4.00E-150 | 1.00E-156 |
| SCE1572_583 | sce_393 | 1.00E-104 | 2.00E-120 |
| SCE1572_5831 | sce_4872 | 8.00E-99 | 1.00E-76 |
| SCE1572_5832 | sce_4873 | 1.00E-147 | 6.00E-163 |
| SCE1572_5833 | sce_4874 | 0.00E+00 | 0.00E+00 |
| SCE1572_5834 | sce_4875 | 2.00E-45 | 2.00E-45 |
| SCE1572_5835 | sce_4876 | 1.00E-135 | 2.00E-135 |
| SCE1572_5837 | sce_4878 | 0.00E+00 | 0.00E+00 |
| SCE1572_5838 | sce_4879 | 1.00E-94 | 4.00E-88 |
| SCE1572_584 | sce_394 | 1.00E-168 | 6.00E-161 |
| SCE1572_585 | sce_395 | 0.00E+00 | 0.00E+00 |
| SCE1572_5850 | sce_160 | 2.00E-112 | 5.00E-108 |
| SCE1572_5853 | sce_2040 | 4.00E-08 | 1.00E-07 |
| SCE1572_5854 | sce_7025 | 3.00E-15 | 2.00E-26 |
| SCE1572_5855 | sce_3173 | 4.00E-59 | 4.00E-59 |
| SCE1572_586 | sce_396 | 0.00E+00 | 0.00E+00 |
| SCE1572_5868 | sce_4880 | 1.00E-112 | 2.00E-102 |
| SCE1572_5869 | sce_4881 | 7.00E-102 | 4.00E-102 |
| SCE1572_587 | sce_398 | 8.00E-180 | 0.00E+00 |
| SCE1572_5870 | sce_4882 | 1.00E-62 | 2.00E-63 |
| SCE1572_5871 | sce_4883 | 0.00E+00 | 0.00E+00 |
| SCE1572_5872 | sce_4885 | 0.00E+00 | 0.00E+00 |
| SCE1572_5873 | sce_4887 | 0.00E+00 | 0.00E+00 |
| SCE1572_5874 | sce_4888 | 5.00E-51 | 5.00E-51 |
| SCE1572_5875 | sce_4889 | 3.00E-41 | 1.00E-43 |
| SCE1572_5876 | sce_4890 | 7.00E-138 | 6.00E-143 |
| SCE1572_5879 | sce_4891 | 4.00E-68 | 7.00E-75 |
| SCE1572_588 | sce_399 | 2.00E-75 | 6.00E-83 |
| SCE1572_5883 | sce_7152 | 8.00E-69 | 7.00E-69 |
| SCE1572_5884 | sce_7151 | 0.00E+00 | 0.00E+00 |
| SCE1572_5886 | sce_7494 | 1.00E-83 | 7.00E-71 |
| SCE1572_5887 | sce_4892 | 4.00E-130 | 4.00E-133 |
| SCE1572_5889 | sce_4893 | 6.00E-15 | 4.00E-15 |
| SCE1572_5890 | sce_4895 | 3.00E-176 | 5.00E-177 |
| SCE1572_5893 | sce_4896 | 2.00E-150 | 1.00E-152 |
| SCE1572_5894 | sce_7535 | 9.00E-52 | 1.00E-47 |
| SCE1572_5895 | sce_7536 | 0.00E+00 | 0.00E+00 |
| SCE1572_5896 | sce_7537 | 0.00E+00 | 0.00E+00 |
| SCE1572_5898 | sce_4908 | 2.00E-28 | 1.00E-34 |
| SCE1572_5899 | sce_2489 | 4.00E-89 | 8.00E-87 |

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|--------------|----------|-----------|-----------|
| SCE1572_59 | sce_6258 | 3.00E-74 | 1.00E-90 |
| SCE1572_5900 | sce_2490 | 2.00E-98 | 2.00E-105 |
| SCE1572_5906 | sce_4909 | 0.00E+00 | 0.00E+00 |
| SCE1572_5907 | sce_4911 | 6.00E-58 | 6.00E-58 |
| SCE1572_5908 | sce_4912 | 0.00E+00 | 0.00E+00 |
| SCE1572_5909 | sce_4913 | 9.00E-70 | 9.00E-70 |
| SCE1572_591 | sce_400 | 5.00E-158 | 8.00E-146 |
| SCE1572_5910 | sce_4914 | 2.00E-121 | 4.00E-106 |
| SCE1572_5911 | sce_4915 | 0.00E+00 | 0.00E+00 |
| SCE1572_5912 | sce_4916 | 2.00E-71 | 5.00E-73 |
| SCE1572_5913 | sce_4917 | 2.00E-136 | 8.00E-141 |
| SCE1572_5914 | sce_4918 | 3.00E-130 | 5.00E-140 |
| SCE1572_5915 | sce_4919 | 0.00E+00 | 0.00E+00 |
| SCE1572_5916 | sce_4920 | 6.00E-68 | 1.00E-66 |
| SCE1572_5917 | sce_4921 | 0.00E+00 | 5.00E-173 |
| SCE1572_5919 | sce_4923 | 1.00E-178 | 1.00E-178 |
| SCE1572_592 | sce_401 | 4.00E-105 | 2.00E-112 |
| SCE1572_5920 | sce_4924 | 0.00E+00 | 0.00E+00 |
| SCE1572_5922 | sce_4925 | 3.00E-133 | 9.00E-155 |
| SCE1572_5923 | sce_4926 | 0.00E+00 | 0.00E+00 |
| SCE1572_5924 | sce_4927 | 4.00E-39 | 2.00E-58 |
| SCE1572_5925 | sce_4928 | 0.00E+00 | 0.00E+00 |
| SCE1572_5926 | sce_4929 | 0.00E+00 | 0.00E+00 |
| SCE1572_5927 | sce_4930 | 0.00E+00 | 0.00E+00 |
| SCE1572_5928 | sce_6137 | 9.00E-85 | 1.00E-84 |
| SCE1572_5929 | sce_6138 | 4.00E-63 | 7.00E-55 |
| SCE1572_593 | sce_402 | 0.00E+00 | 0.00E+00 |
| SCE1572_5931 | sce_4931 | 0.00E+00 | 0.00E+00 |
| SCE1572_5932 | sce_4932 | 0.00E+00 | 0.00E+00 |
| SCE1572_5940 | sce_2546 | 1.00E-08 | 7.00E-07 |
| SCE1572_595 | sce_404 | 2.00E-137 | 1.00E-138 |
| SCE1572_596 | sce_405 | 0.00E+00 | 0.00E+00 |
| SCE1572_5973 | sce_4934 | 9.00E-142 | 9.00E-133 |
| SCE1572_5975 | sce_4935 | 2.00E-132 | 2.00E-139 |
| SCE1572_5976 | sce_4936 | 2.00E-122 | 9.00E-141 |
| SCE1572_5977 | sce_4937 | 2.00E-113 | 1.00E-110 |
| SCE1572_5978 | sce_4938 | 0.00E+00 | 0.00E+00 |
| SCE1572_5979 | sce_4939 | 1.00E-116 | 1.00E-116 |
| SCE1572_598 | sce_406 | 6.00E-75 | 4.00E-83 |
| SCE1572_5980 | sce_4941 | 4.00E-169 | 3.00E-170 |
| SCE1572_5981 | sce_4942 | 2.00E-43 | 4.00E-43 |
| SCE1572_5983 | sce_2441 | 1.00E-06 | 2.00E-07 |
| SCE1572_5990 | sce_9404 | 0.00E+00 | 0.00E+00 |
| SCE1572_5991 | sce_4943 | 2.00E-151 | 2.00E-154 |
| SCE1572_5992 | sce_4944 | 1.00E-137 | 4.00E-149 |
| SCE1572_5993 | sce_4945 | 2.00E-101 | 3.00E-92 |
| SCE1572_5994 | sce_4946 | 0.00E+00 | 0.00E+00 |
| SCE1572_5995 | sce_4947 | 9.00E-155 | 9.00E-148 |
| SCE1572_5996 | sce_4948 | 7.00E-75 | 4.00E-74 |
| SCE1572_5997 | sce_4949 | 6.00E-137 | 3.00E-152 |
| SCE1572_5998 | sce_4950 | 5.00E-153 | 7.00E-162 |
| SCE1572_5999 | sce_4951 | 1.00E-154 | 1.00E-154 |
| SCE1572_6 | sce_6 | 0.00E+00 | 0.00E+00 |
| SCE1572_60 | sce_50 | 0.00E+00 | 0.00E+00 |
| SCE1572_6000 | sce_4952 | 3.00E-103 | 4.00E-117 |
| SCE1572_6001 | sce_4953 | 9.00E-37 | 2.00E-37 |
| SCE1572_6002 | sce_4954 | 8.00E-77 | 3.00E-79 |
| SCE1572_6003 | sce_4955 | 4.00E-124 | 2.00E-104 |
| SCE1572_6004 | sce_4956 | 2.00E-135 | 7.00E-136 |
| SCE1572_6005 | sce_4957 | 9.00E-160 | 5.00E-166 |
| SCE1572_6007 | sce_4958 | 2.00E-107 | 2.00E-109 |
| SCE1572_6008 | sce_4959 | 9.00E-83 | 2.00E-74 |
| SCE1572_6009 | sce_4960 | 8.00E-32 | 8.00E-32 |
| SCE1572_601 | sce_407 | 0.00E+00 | 0.00E+00 |
| SCE1572_6010 | sce_4961 | 3.00E-40 | 3.00E-40 |
| SCE1572_6011 | sce_4963 | 0.00E+00 | 0.00E+00 |
| SCE1572_6012 | sce_4964 | 5.00E-151 | 5.00E-170 |
| SCE1572_6013 | sce_4965 | 0.00E+00 | 0.00E+00 |
| SCE1572_6014 | sce_4966 | 1.00E-126 | 4.00E-120 |
| SCE1572_6016 | sce_4969 | 2.00E-90 | 2.00E-90 |
| SCE1572_6017 | sce_4970 | 0.00E+00 | 0.00E+00 |
| SCE1572_6018 | sce_4971 | 0.00E+00 | 0.00E+00 |
| SCE1572_6019 | sce_4972 | 1.00E-29 | 5.00E-29 |
| SCE1572_602 | sce_410 | 0.00E+00 | 0.00E+00 |
| SCE1572_6020 | sce_4973 | 3.00E-125 | 4.00E-125 |
| SCE1572_6021 | sce_4974 | 0.00E+00 | 0.00E+00 |

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| SCE1572_6023 | sce_4976 | 0.00E+00 | 0.00E+00 |
| SCE1572_6024 | sce_4977 | 0.00E+00 | 0.00E+00 |
| SCE1572_6025 | sce_4978 | 1.00E-39 | 8.00E-57 |
| SCE1572_6026 | sce_4979 | 3.00E-121 | 4.00E-120 |
| SCE1572_6027 | sce_4980 | 2.00E-42 | 6.00E-51 |
| SCE1572_6028 | sce_4981 | 3.00E-73 | 2.00E-70 |
| SCE1572_6029 | sce_4982 | 0.00E+00 | 0.00E+00 |
| SCE1572_603 | sce_411 | 2.00E-117 | 5.00E-114 |
| SCE1572_6030 | sce_4983 | 1.00E-144 | 1.00E-136 |
| SCE1572_6031 | sce_4984 | 0.00E+00 | 0.00E+00 |
| SCE1572_6032 | sce_4985 | 3.00E-23 | 3.00E-23 |
| SCE1572_6033 | sce_4986 | 0.00E+00 | 0.00E+00 |
| SCE1572_6034 | sce_4987 | 0.00E+00 | 0.00E+00 |
| SCE1572_6036 | sce_4988 | 1.00E-14 | 9.00E-11 |
| SCE1572_6037 | sce_4989 | 9.00E-22 | 5.00E-14 |
| SCE1572_6038 | sce_4990 | 3.00E-146 | 4.00E-162 |
| SCE1572_6039 | sce_4991 | 8.00E-150 | 9.00E-161 |
| SCE1572_604 | sce_413 | 0.00E+00 | 0.00E+00 |
| SCE1572_6040 | sce_4992 | 0.00E+00 | 0.00E+00 |
| SCE1572_6041 | sce_4993 | 0.00E+00 | 0.00E+00 |
| SCE1572_6042 | sce_4994 | 4.00E-118 | 7.00E-117 |
| SCE1572_6044 | sce_4995 | 1.00E-42 | 2.00E-35 |
| SCE1572_6045 | sce_4996 | 2.00E-177 | 2.00E-178 |
| SCE1572_6046 | sce_4997 | 0.00E+00 | 0.00E+00 |
| SCE1572_6047 | sce_4999 | 3.00E-38 | 3.00E-39 |
| SCE1572_6048 | sce_5000 | 1.00E-109 | 5.00E-89 |
| SCE1572_6049 | sce_5001 | 1.00E-82 | 3.00E-70 |
| SCE1572_605 | sce_414 | 1.00E-69 | 8.00E-70 |
| SCE1572_6051 | sce_5002 | 2.00E-173 | 5.00E-174 |
| SCE1572_6052 | sce_5003 | 0.00E+00 | 0.00E+00 |
| SCE1572_6053 | sce_5004 | 2.00E-136 | 2.00E-144 |
| SCE1572_6054 | sce_5005 | 0.00E+00 | 0.00E+00 |
| SCE1572_6055 | sce_5006 | 0.00E+00 | 0.00E+00 |
| SCE1572_6056 | sce_5007 | 0.00E+00 | 0.00E+00 |
| SCE1572_6057 | sce_5008 | 2.00E-33 | 2.00E-25 |
| SCE1572_6058 | sce_5009 | 8.00E-106 | 5.00E-128 |
| SCE1572_6059 | sce_4871 | 3.00E-81 | 1.00E-89 |
| SCE1572_606 | sce_415 | 0.00E+00 | 0.00E+00 |
| SCE1572_6061 | sce_5011 | 4.00E-94 | 1.00E-92 |
| SCE1572_6062 | sce_5012 | 0.00E+00 | 0.00E+00 |
| SCE1572_6064 | sce_5013 | 2.00E-84 | 3.00E-91 |
| SCE1572_6065 | sce_5014 | 8.00E-17 | 4.00E-14 |
| SCE1572_6066 | sce_5015 | 4.00E-86 | 4.00E-70 |
| SCE1572_6067 | sce_5016 | 0.00E+00 | 0.00E+00 |
| SCE1572_6068 | sce_5017 | 5.00E-169 | 8.00E-174 |
| SCE1572_6069 | sce_5018 | 7.00E-81 | 1.00E-82 |
| SCE1572_607 | sce_416 | 1.00E-20 | 1.00E-20 |
| SCE1572_6070 | sce_5019 | 1.00E-61 | 7.00E-73 |
| SCE1572_6074 | sce_5020 | 0.00E+00 | 0.00E+00 |
| SCE1572_6075 | sce_5022 | 0.00E+00 | 0.00E+00 |
| SCE1572_6076 | sce_5023 | 7.00E-15 | 7.00E-15 |
| SCE1572_6077 | sce_5024 | 8.00E-35 | 8.00E-35 |
| SCE1572_608 | sce_418 | 0.00E+00 | 0.00E+00 |
| SCE1572_6082 | sce_244 | 6.00E-53 | 5.00E-52 |
| SCE1572_6083 | sce_3006 | 2.00E-126 | 3.00E-144 |
| SCE1572_6086 | sce_1876 | 7.00E-13 | 8.00E-13 |
| SCE1572_6087 | sce_5033 | 0.00E+00 | 0.00E+00 |
| SCE1572_6087 | sce_5602 | 0.00E+00 | 0.00E+00 |
| SCE1572_6087 | sce_3185 | 0.00E+00 | 0.00E+00 |
| SCE1572_6088 | sce_5035 | 3.00E-127 | 2.00E-118 |
| SCE1572_6089 | sce_5036 | 3.00E-39 | 8.00E-39 |
| SCE1572_6090 | sce_5037 | 2.00E-71 | 1.00E-66 |
| SCE1572_6091 | sce_5039 | 1.00E-32 | 1.00E-16 |
| SCE1572_6094 | sce_835 | 2.00E-128 | 7.00E-126 |
| SCE1572_6096 | sce_9920 | 0.00E+00 | 0.00E+00 |
| SCE1572_6096 | sce_7640 | 0.00E+00 | 0.00E+00 |
| SCE1572_6097 | sce_5042 | 1.00E-86 | 5.00E-77 |
| SCE1572_6098 | sce_5043 | 8.00E-140 | 5.00E-146 |
| SCE1572_6099 | sce_5045 | 1.00E-175 | 6.00E-174 |
| SCE1572_61 | sce_51 | 0.00E+00 | 0.00E+00 |
| SCE1572_6100 | sce_5047 | 0.00E+00 | 0.00E+00 |
| SCE1572_6100 | sce_8489 | 0.00E+00 | 0.00E+00 |
| SCE1572_6101 | sce_5048 | 0.00E+00 | 0.00E+00 |
| SCE1572_6102 | sce_5049 | 3.00E-83 | 3.00E-83 |
| SCE1572_6103 | sce_5050 | 9.00E-86 | 3.00E-83 |
| SCE1572_6104 | sce_5051 | 7.00E-153 | 6.00E-161 |

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|--------------|----------|-----------|-----------|
| SCE1572_6105 | sce_5052 | 1.00E-42 | 6.00E-43 |
| SCE1572_6106 | sce_5053 | 2.00E-101 | 1.00E-93 |
| SCE1572_6107 | sce_5054 | 7.00E-169 | 3.00E-159 |
| SCE1572_6108 | sce_5055 | 0.00E+00 | 0.00E+00 |
| SCE1572_6109 | sce_5056 | 3.00E-82 | 5.00E-81 |
| SCE1572_611 | sce_420 | 6.00E-99 | 1.00E-107 |
| SCE1572_6110 | sce_5057 | 3.00E-23 | 2.00E-22 |
| SCE1572_6111 | sce_5058 | 6.00E-94 | 6.00E-99 |
| SCE1572_6112 | sce_5059 | 4.00E-42 | 3.00E-63 |
| SCE1572_6113 | sce_5060 | 8.00E-107 | 2.00E-111 |
| SCE1572_6114 | sce_6885 | 1.00E-30 | 1.00E-28 |
| SCE1572_6116 | sce_2459 | 2.00E-97 | 6.00E-96 |
| SCE1572_6118 | sce_6665 | 7.00E-08 | 7.00E-08 |
| SCE1572_6119 | sce_5062 | 2.00E-112 | 2.00E-112 |
| SCE1572_612 | sce_421 | 1.00E-94 | 9.00E-95 |
| SCE1572_6120 | sce_5063 | 1.00E-81 | 2.00E-77 |
| SCE1572_6121 | sce_5064 | 2.00E-91 | 2.00E-130 |
| SCE1572_6122 | sce_5066 | 0.00E+00 | 0.00E+00 |
| SCE1572_6123 | sce_5068 | 0.00E+00 | 0.00E+00 |
| SCE1572_6123 | sce_5637 | 0.00E+00 | 0.00E+00 |
| SCE1572_6124 | sce_5069 | 3.00E-84 | 3.00E-84 |
| SCE1572_6125 | sce_5070 | 4.00E-133 | 4.00E-120 |
| SCE1572_6126 | sce_5071 | 1.00E-121 | 2.00E-118 |
| SCE1572_6127 | sce_5072 | 2.00E-172 | 0.00E+00 |
| SCE1572_6128 | sce_5073 | 0.00E+00 | 0.00E+00 |
| SCE1572_6129 | sce_5074 | 0.00E+00 | 0.00E+00 |
| SCE1572_613 | sce_422 | 4.00E-112 | 2.00E-103 |
| SCE1572_6131 | sce_5076 | 8.00E-44 | 8.00E-44 |
| SCE1572_6133 | sce_5077 | 0.00E+00 | 0.00E+00 |
| SCE1572_6134 | sce_5078 | 4.00E-42 | 2.00E-41 |
| SCE1572_6135 | sce_5079 | 0.00E+00 | 0.00E+00 |
| SCE1572_6136 | sce_5080 | 0.00E+00 | 0.00E+00 |
| SCE1572_6137 | sce_5081 | 2.00E-71 | 3.00E-72 |
| SCE1572_6138 | sce_7381 | 1.00E-120 | 1.00E-120 |
| SCE1572_6139 | sce_5082 | 0.00E+00 | 0.00E+00 |
| SCE1572_614 | sce_423 | 5.00E-78 | 8.00E-79 |
| SCE1572_6140 | sce_5083 | 0.00E+00 | 0.00E+00 |
| SCE1572_6142 | sce_5084 | 1.00E-120 | 9.00E-129 |
| SCE1572_6145 | sce_5088 | 7.00E-103 | 2.00E-116 |
| SCE1572_6146 | sce_1290 | 1.00E-37 | 3.00E-30 |
| SCE1572_6151 | sce_5091 | 0.00E+00 | 0.00E+00 |
| SCE1572_6154 | sce_5638 | 3.00E-69 | 4.00E-69 |
| SCE1572_6155 | sce_5094 | 2.00E-135 | 1.00E-136 |
| SCE1572_6156 | sce_5123 | 1.00E-75 | 2.00E-83 |
| SCE1572_6158 | sce_5128 | 8.00E-149 | 3.00E-137 |
| SCE1572_6159 | sce_5129 | 1.00E-169 | 2.00E-126 |
| SCE1572_616 | sce_424 | 0.00E+00 | 0.00E+00 |
| SCE1572_6161 | sce_5130 | 0.00E+00 | 0.00E+00 |
| SCE1572_6162 | sce_5131 | 0.00E+00 | 0.00E+00 |
| SCE1572_6164 | sce_5160 | 3.00E-100 | 2.00E-122 |
| SCE1572_6165 | sce_5161 | 0.00E+00 | 0.00E+00 |
| SCE1572_6166 | sce_5162 | 0.00E+00 | 3.00E-177 |
| SCE1572_6167 | sce_5163 | 1.00E-46 | 4.00E-51 |
| SCE1572_6168 | sce_5164 | 2.00E-161 | 3.00E-175 |
| SCE1572_617 | sce_425 | 8.00E-100 | 8.00E-100 |
| SCE1572_6170 | sce_5165 | 2.00E-76 | 2.00E-76 |
| SCE1572_6171 | sce_5166 | 0.00E+00 | 0.00E+00 |
| SCE1572_6173 | sce_335 | 4.00E-71 | 2.00E-64 |
| SCE1572_6174 | sce_336 | 7.00E-109 | 6.00E-115 |
| SCE1572_6175 | sce_5250 | 1.00E-138 | 8.00E-139 |
| SCE1572_6176 | sce_5171 | 2.00E-115 | 4.00E-124 |
| SCE1572_6178 | sce_5176 | 3.00E-102 | 7.00E-96 |
| SCE1572_6179 | sce_5177 | 5.00E-83 | 3.00E-101 |
| SCE1572_618 | sce_426 | 3.00E-116 | 8.00E-119 |
| SCE1572_6180 | sce_5178 | 0.00E+00 | 0.00E+00 |
| SCE1572_6181 | sce_5179 | 1.00E-101 | 1.00E-101 |
| SCE1572_6184 | sce_5320 | 5.00E-09 | 8.00E-10 |
| SCE1572_6185 | sce_5195 | 0.00E+00 | 0.00E+00 |
| SCE1572_6186 | sce_5196 | 2.00E-06 | 1.00E-18 |
| SCE1572_6187 | sce_5197 | 2.00E-67 | 3.00E-81 |
| SCE1572_6188 | sce_5199 | 2.00E-110 | 6.00E-109 |
| SCE1572_619 | sce_427 | 5.00E-89 | 4.00E-44 |
| SCE1572_6191 | sce_5200 | 7.00E-79 | 9.00E-83 |
| SCE1572_6192 | sce_5206 | 6.00E-77 | 9.00E-83 |
| SCE1572_6195 | sce_5207 | 6.00E-57 | 1.00E-54 |
| SCE1572_6196 | sce_5208 | 2.00E-35 | 3.00E-25 |

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| SCE1572_6197 | sce_5209 | 7.00E-14 | 8.00E-18 |
| SCE1572_6198 | sce_5211 | 1.00E-116 | 2.00E-122 |
| SCE1572_620 | sce_428 | 0.00E+00 | 0.00E+00 |
| SCE1572_6200 | sce_5224 | 4.00E-144 | 2.00E-154 |
| SCE1572_6201 | sce_5225 | 0.00E+00 | 0.00E+00 |
| SCE1572_6202 | sce_5226 | 0.00E+00 | 0.00E+00 |
| SCE1572_6202 | sce_5403 | 0.00E+00 | 0.00E+00 |
| SCE1572_6202 | sce_1803 | 0.00E+00 | 0.00E+00 |
| SCE1572_6202 | sce_7969 | 0.00E+00 | 0.00E+00 |
| SCE1572_6202 | sce_7154 | 0.00E+00 | 0.00E+00 |
| SCE1572_6202 | sce_9665 | 0.00E+00 | 0.00E+00 |
| SCE1572_6202 | sce_5751 | 0.00E+00 | 0.00E+00 |
| SCE1572_6202 | sce_4073 | 0.00E+00 | 0.00E+00 |
| SCE1572_6202 | sce_5746 | 0.00E+00 | 0.00E+00 |
| SCE1572_6202 | sce_2053 | 0.00E+00 | 0.00E+00 |
| SCE1572_6202 | sce_9757 | 0.00E+00 | 0.00E+00 |
| SCE1572_6202 | sce_9954 | 0.00E+00 | 0.00E+00 |
| SCE1572_6202 | sce_3750 | 0.00E+00 | 0.00E+00 |
| SCE1572_6202 | sce_6712 | 0.00E+00 | 0.00E+00 |
| SCE1572_6202 | sce_5229 | 0.00E+00 | 0.00E+00 |
| SCE1572_6203 | sce_5228 | 4.00E-144 | 3.00E-135 |
| SCE1572_6205 | sce_2524 | 0.00E+00 | 0.00E+00 |
| SCE1572_6206 | sce_2525 | 0.00E+00 | 0.00E+00 |
| SCE1572_621 | sce_430 | 0.00E+00 | 0.00E+00 |
| SCE1572_6210 | sce_8592 | 0.00E+00 | 0.00E+00 |
| SCE1572_6210 | sce_3937 | 0.00E+00 | 0.00E+00 |
| SCE1572_6213 | sce_10331 | 4.00E-83 | 8.00E-81 |
| SCE1572_6215 | sce_5242 | 2.00E-135 | 1.00E-134 |
| SCE1572_6217 | sce_9321 | 2.00E-16 | 6.00E-18 |
| SCE1572_6222 | sce_2729 | 4.00E-51 | 5.00E-58 |
| SCE1572_6224 | sce_5247 | 1.00E-114 | 3.00E-121 |
| SCE1572_6225 | sce_5248 | 3.00E-82 | 1.00E-91 |
| SCE1572_6227 | sce_8772 | 4.00E-33 | 4.00E-42 |
| SCE1572_623 | sce_431 | 0.00E+00 | 0.00E+00 |
| SCE1572_6231 | sce_3674 | 3.00E-126 | 1.00E-128 |
| SCE1572_6232 | sce_3675 | 3.00E-165 | 2.00E-163 |
| SCE1572_6234 | sce_8040 | 8.00E-10 | 9.00E-11 |
| SCE1572_6235 | sce_10194 | 4.00E-48 | 1.00E-42 |
| SCE1572_6236 | sce_2008 | 2.00E-115 | 1.00E-115 |
| SCE1572_6238 | sce_5252 | 9.00E-122 | 1.00E-140 |
| SCE1572_6241 | sce_5253 | 2.00E-57 | 6.00E-58 |
| SCE1572_6242 | sce_5254 | 0.00E+00 | 8.00E-173 |
| SCE1572_6246 | sce_7862 | 5.00E-167 | 5.00E-165 |
| SCE1572_6247 | sce_614 | 9.00E-120 | 1.00E-109 |
| SCE1572_6248 | sce_7861 | 4.00E-56 | 4.00E-56 |
| SCE1572_6252 | sce_5264 | 0.00E+00 | 0.00E+00 |
| SCE1572_6253 | sce_5265 | 2.00E-97 | 1.00E-90 |
| SCE1572_6254 | sce_5266 | 0.00E+00 | 0.00E+00 |
| SCE1572_6259 | sce_5270 | 5.00E-47 | 2.00E-46 |
| SCE1572_6260 | sce_5271 | 9.00E-132 | 1.00E-132 |
| SCE1572_6261 | sce_5272 | 1.00E-58 | 1.00E-63 |
| SCE1572_6262 | sce_5273 | 0.00E+00 | 0.00E+00 |
| SCE1572_6263 | sce_5274 | 3.00E-179 | 0.00E+00 |
| SCE1572_6264 | sce_5275 | 3.00E-118 | 5.00E-121 |
| SCE1572_6265 | sce_5282 | 1.00E-75 | 1.00E-75 |
| SCE1572_6266 | sce_5284 | 2.00E-07 | 2.00E-06 |
| SCE1572_6269 | sce_5285 | 2.00E-56 | 4.00E-57 |
| SCE1572_627 | sce_10425 | 0.00E+00 | 0.00E+00 |
| SCE1572_627 | sce_7361 | 0.00E+00 | 0.00E+00 |
| SCE1572_627 | sce_3520 | 0.00E+00 | 0.00E+00 |
| SCE1572_6270 | sce_5287 | 3.00E-109 | 3.00E-109 |
| SCE1572_6272 | sce_5289 | 7.00E-169 | 2.00E-173 |
| SCE1572_6273 | sce_3740 | 0.00E+00 | 0.00E+00 |
| SCE1572_6274 | sce_3739 | 3.00E-71 | 3.00E-71 |
| SCE1572_6275 | sce_3738 | 0.00E+00 | 0.00E+00 |
| SCE1572_6276 | sce_3737 | 8.00E-96 | 6.00E-90 |
| SCE1572_6278 | sce_3669 | 2.00E-53 | 5.00E-60 |
| SCE1572_6279 | sce_5294 | 1.00E-43 | 6.00E-47 |
| SCE1572_628 | sce_436 | 2.00E-66 | 8.00E-74 |
| SCE1572_6280 | sce_5297 | 2.00E-66 | 1.00E-66 |
| SCE1572_6281 | sce_1108 | 0.00E+00 | 0.00E+00 |
| SCE1572_6281 | sce_9028 | 0.00E+00 | 0.00E+00 |
| SCE1572_6283 | sce_5305 | 7.00E-161 | 3.00E-174 |
| SCE1572_6284 | sce_5310 | 3.00E-108 | 3.00E-108 |
| SCE1572_6285 | sce_5311 | 1.00E-115 | 1.00E-115 |
| SCE1572_6286 | sce_5312 | 3.00E-81 | 1.00E-81 |

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| SCE1572_6287 | sce_5313 | 1.00E-93 | 1.00E-99 |
| SCE1572_6289 | sce_5318 | 8.00E-84 | 1.00E-78 |
| SCE1572_629 | sce_437 | 0.00E+00 | 0.00E+00 |
| SCE1572_6291 | sce_5319 | 3.00E-73 | 1.00E-102 |
| SCE1572_6292 | sce_5321 | 9.00E-127 | 1.00E-131 |
| SCE1572_6293 | sce_5150 | 3.00E-148 | 5.00E-148 |
| SCE1572_6296 | sce_5322 | 4.00E-73 | 8.00E-69 |
| SCE1572_6298 | sce_5323 | 2.00E-123 | 4.00E-128 |
| SCE1572_63 | sce_54 | 0.00E+00 | 0.00E+00 |
| SCE1572_630 | sce_438 | 1.00E-134 | 1.00E-134 |
| SCE1572_6300 | sce_5324 | 2.00E-78 | 2.00E-80 |
| SCE1572_6301 | sce_7403 | 2.00E-43 | 1.00E-42 |
| SCE1572_6302 | sce_5329 | 0.00E+00 | 0.00E+00 |
| SCE1572_6304 | sce_5331 | 3.00E-39 | 3.00E-39 |
| SCE1572_6305 | sce_5332 | 6.00E-99 | 9.00E-100 |
| SCE1572_6306 | sce_5333 | 1.00E-116 | 1.00E-118 |
| SCE1572_6307 | sce_5334 | 5.00E-158 | 1.00E-163 |
| SCE1572_6308 | sce_5335 | 3.00E-133 | 3.00E-141 |
| SCE1572_6309 | sce_5336 | 7.00E-135 | 7.00E-135 |
| SCE1572_631 | sce_439 | 0.00E+00 | 0.00E+00 |
| SCE1572_6310 | sce_5337 | 3.00E-144 | 4.00E-145 |
| SCE1572_6311 | sce_5338 | 7.00E-141 | 7.00E-141 |
| SCE1572_6313 | sce_2034 | 2.00E-101 | 5.00E-105 |
| SCE1572_6318 | sce_5340 | 3.00E-62 | 8.00E-83 |
| SCE1572_6319 | sce_5341 | 3.00E-76 | 1.00E-74 |
| SCE1572_632 | sce_440 | 3.00E-162 | 2.00E-162 |
| SCE1572_6321 | sce_5342 | 3.00E-90 | 7.00E-94 |
| SCE1572_6322 | sce_5343 | 6.00E-65 | 1.00E-64 |
| SCE1572_6323 | sce_5344 | 0.00E+00 | 0.00E+00 |
| SCE1572_6324 | sce_5345 | 2.00E-147 | 2.00E-156 |
| SCE1572_6325 | sce_5346 | 1.00E-57 | 6.00E-43 |
| SCE1572_6326 | sce_5348 | 5.00E-51 | 5.00E-51 |
| SCE1572_6327 | sce_5349 | 1.00E-32 | 3.00E-33 |
| SCE1572_6328 | sce_5350 | 2.00E-113 | 2.00E-113 |
| SCE1572_6329 | sce_5351 | 0.00E+00 | 0.00E+00 |
| SCE1572_633 | sce_441 | 2.00E-135 | 8.00E-140 |
| SCE1572_6330 | sce_5352 | 0.00E+00 | 0.00E+00 |
| SCE1572_6331 | sce_5353 | 1.00E-64 | 1.00E-64 |
| SCE1572_6332 | sce_5354 | 7.00E-130 | 9.00E-140 |
| SCE1572_6333 | sce_5355 | 2.00E-142 | 3.00E-142 |
| SCE1572_6334 | sce_5357 | 2.00E-154 | 2.00E-164 |
| SCE1572_6335 | sce_5358 | 0.00E+00 | 0.00E+00 |
| SCE1572_6335 | sce_9776 | 0.00E+00 | 0.00E+00 |
| SCE1572_6336 | sce_5359 | 0.00E+00 | 0.00E+00 |
| SCE1572_6336 | sce_9777 | 0.00E+00 | 0.00E+00 |
| SCE1572_6337 | sce_5360 | 4.00E-96 | 4.00E-96 |
| SCE1572_6338 | sce_5361 | 2.00E-72 | 8.00E-64 |
| SCE1572_6339 | sce_5373 | 1.00E-147 | 1.00E-147 |
| SCE1572_634 | sce_442 | 0.00E+00 | 0.00E+00 |
| SCE1572_6340 | sce_5374 | 6.00E-46 | 3.00E-79 |
| SCE1572_6341 | sce_5375 | 6.00E-141 | 6.00E-141 |
| SCE1572_6342 | sce_5377 | 1.00E-172 | 0.00E+00 |
| SCE1572_6343 | sce_5378 | 0.00E+00 | 0.00E+00 |
| SCE1572_6344 | sce_5379 | 0.00E+00 | 0.00E+00 |
| SCE1572_6345 | sce_5380 | 2.00E-45 | 2.00E-50 |
| SCE1572_6346 | sce_5382 | 1.00E-150 | 1.00E-153 |
| SCE1572_6347 | sce_5383 | 3.00E-85 | 3.00E-85 |
| SCE1572_635 | sce_443 | 5.00E-95 | 5.00E-83 |
| SCE1572_6351 | sce_5387 | 3.00E-146 | 3.00E-139 |
| SCE1572_6352 | sce_5388 | 1.00E-63 | 9.00E-58 |
| SCE1572_6353 | sce_5389 | 7.00E-124 | 7.00E-124 |
| SCE1572_6354 | sce_5506 | 1.00E-56 | 2.00E-52 |
| SCE1572_6356 | sce_6038 | 1.00E-173 | 2.00E-170 |
| SCE1572_6357 | sce_5390 | 6.00E-158 | 6.00E-177 |
| SCE1572_6359 | sce_5391 | 7.00E-80 | 4.00E-69 |
| SCE1572_636 | sce_444 | 1.00E-97 | 1.00E-104 |
| SCE1572_6360 | sce_5392 | 3.00E-56 | 8.00E-50 |
| SCE1572_6363 | sce_5393 | 0.00E+00 | 0.00E+00 |
| SCE1572_6364 | sce_5394 | 5.00E-110 | 2.00E-126 |
| SCE1572_6365 | sce_5395 | 1.00E-168 | 6.00E-171 |
| SCE1572_6366 | sce_5396 | 2.00E-124 | 5.00E-74 |
| SCE1572_6367 | sce_5397 | 3.00E-79 | 7.00E-74 |
| SCE1572_6368 | sce_5398 | 0.00E+00 | 0.00E+00 |
| SCE1572_637 | sce_446 | 4.00E-90 | 4.00E-90 |
| SCE1572_6370 | sce_5400 | 9.00E-42 | 2.00E-45 |
| SCE1572_6377 | sce_5401 | 4.00E-95 | 7.00E-99 |

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| SCE1572_6378 | sce_7567 | 3.00E-96 | 2.00E-96 |
| SCE1572_638 | sce_447 | 4.00E-108 | 1.00E-108 |
| SCE1572_6381 | sce_5402 | 4.00E-46 | 4.00E-46 |
| SCE1572_6382 | sce_5403 | 0.00E+00 | 0.00E+00 |
| SCE1572_6382 | sce_5226 | 0.00E+00 | 0.00E+00 |
| SCE1572_6382 | sce_7969 | 0.00E+00 | 0.00E+00 |
| SCE1572_6382 | sce_7154 | 0.00E+00 | 0.00E+00 |
| SCE1572_6382 | sce_5751 | 0.00E+00 | 0.00E+00 |
| SCE1572_6382 | sce_4073 | 0.00E+00 | 0.00E+00 |
| SCE1572_6382 | sce_9665 | 0.00E+00 | 0.00E+00 |
| SCE1572_6382 | sce_5746 | 0.00E+00 | 0.00E+00 |
| SCE1572_6382 | sce_2053 | 0.00E+00 | 0.00E+00 |
| SCE1572_6382 | sce_9954 | 0.00E+00 | 0.00E+00 |
| SCE1572_6382 | sce_1803 | 0.00E+00 | 0.00E+00 |
| SCE1572_6382 | sce_6712 | 0.00E+00 | 0.00E+00 |
| SCE1572_6382 | sce_3750 | 0.00E+00 | 0.00E+00 |
| SCE1572_6382 | sce_5229 | 0.00E+00 | 0.00E+00 |
| SCE1572_6383 | sce_5404 | 8.00E-12 | 8.00E-12 |
| SCE1572_6384 | sce_5405 | 7.00E-142 | 4.00E-140 |
| SCE1572_6386 | sce_5406 | 0.00E+00 | 0.00E+00 |
| SCE1572_6387 | sce_5407 | 0.00E+00 | 0.00E+00 |
| SCE1572_6388 | sce_5408 | 0.00E+00 | 0.00E+00 |
| SCE1572_6389 | sce_5409 | 0.00E+00 | 0.00E+00 |
| SCE1572_639 | sce_448 | 0.00E+00 | 0.00E+00 |
| SCE1572_6390 | sce_5410 | 1.00E-139 | 1.00E-139 |
| SCE1572_6392 | sce_5412 | 1.00E-110 | 1.00E-110 |
| SCE1572_6393 | sce_5413 | 5.00E-129 | 5.00E-129 |
| SCE1572_6394 | sce_5414 | 3.00E-58 | 6.00E-58 |
| SCE1572_6396 | sce_5415 | 0.00E+00 | 0.00E+00 |
| SCE1572_6397 | sce_5416 | 0.00E+00 | 0.00E+00 |
| SCE1572_6398 | sce_5417 | 3.00E-124 | 1.00E-130 |
| SCE1572_6399 | sce_5418 | 0.00E+00 | 0.00E+00 |
| SCE1572_64 | sce_55 | 1.00E-110 | 4.00E-103 |
| SCE1572_640 | sce_449 | 5.00E-50 | 8.00E-79 |
| SCE1572_6400 | sce_5419 | 0.00E+00 | 0.00E+00 |
| SCE1572_6401 | sce_5420 | 9.00E-07 | 9.00E-07 |
| SCE1572_6402 | sce_5422 | 0.00E+00 | 0.00E+00 |
| SCE1572_6403 | sce_5423 | 1.00E-123 | 7.00E-120 |
| SCE1572_6404 | sce_5424 | 2.00E-13 | 1.00E-27 |
| SCE1572_6405 | sce_5425 | 1.00E-98 | 4.00E-101 |
| SCE1572_6406 | sce_5426 | 2.00E-56 | 5.00E-75 |
| SCE1572_6407 | sce_5427 | 5.00E-140 | 7.00E-146 |
| SCE1572_6408 | sce_5428 | 4.00E-142 | 3.00E-134 |
| SCE1572_6409 | sce_5429 | 2.00E-13 | 3.00E-12 |
| SCE1572_641 | sce_450 | 3.00E-116 | 2.00E-112 |
| SCE1572_6412 | sce_5430 | 7.00E-103 | 8.00E-103 |
| SCE1572_6413 | sce_5431 | 1.00E-83 | 2.00E-83 |
| SCE1572_6415 | sce_5433 | 5.00E-128 | 2.00E-128 |
| SCE1572_6416 | sce_5434 | 3.00E-68 | 4.00E-51 |
| SCE1572_6418 | sce_5435 | 0.00E+00 | 0.00E+00 |
| SCE1572_6419 | sce_4723 | 3.00E-11 | 4.00E-18 |
| SCE1572_642 | sce_451 | 0.00E+00 | 0.00E+00 |
| SCE1572_6420 | sce_4725 | 0.00E+00 | 0.00E+00 |
| SCE1572_6420 | sce_5308 | 0.00E+00 | 0.00E+00 |
| SCE1572_6422 | sce_7652 | 1.00E-32 | 4.00E-24 |
| SCE1572_6423 | sce_3067 | 2.00E-134 | 2.00E-138 |
| SCE1572_6425 | sce_1172 | 5.00E-85 | 7.00E-76 |
| SCE1572_6426 | sce_1171 | 1.00E-47 | 7.00E-43 |
| SCE1572_6428 | sce_7206 | 1.00E-129 | 4.00E-145 |
| SCE1572_6429 | sce_2031 | 1.00E-144 | 8.00E-141 |
| SCE1572_643 | sce_452 | 4.00E-111 | 1.00E-98 |
| SCE1572_6430 | sce_6181 | 0.00E+00 | 0.00E+00 |
| SCE1572_6431 | sce_7564 | 8.00E-76 | 2.00E-73 |
| SCE1572_6432 | sce_2123 | 4.00E-75 | 3.00E-84 |
| SCE1572_6433 | sce_2124 | 2.00E-59 | 6.00E-58 |
| SCE1572_6436 | sce_3639 | 1.00E-109 | 9.00E-112 |
| SCE1572_6437 | sce_3640 | 8.00E-97 | 8.00E-97 |
| SCE1572_644 | sce_453 | 7.00E-56 | 2.00E-65 |
| SCE1572_6445 | sce_5449 | 5.00E-101 | 7.00E-106 |
| SCE1572_6451 | sce_8592 | 0.00E+00 | 0.00E+00 |
| SCE1572_6451 | sce_3937 | 0.00E+00 | 0.00E+00 |
| SCE1572_6452 | sce_3937 | 0.00E+00 | 0.00E+00 |
| SCE1572_6452 | sce_8592 | 0.00E+00 | 0.00E+00 |
| SCE1572_6457 | sce_5452 | 0.00E+00 | 0.00E+00 |
| SCE1572_6464 | sce_5437 | 7.00E-43 | 5.00E-40 |
| SCE1572_6465 | sce_5438 | 6.00E-93 | 3.00E-97 |

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| SCE1572_6466 | sce_5439 | 7.00E-108 | 1.00E-107 |
| SCE1572_6467 | sce_5440 | 6.00E-150 | 6.00E-141 |
| SCE1572_6468 | sce_5441 | 0.00E+00 | 0.00E+00 |
| SCE1572_6469 | sce_5442 | 1.00E-174 | 7.00E-179 |
| SCE1572_6470 | sce_5443 | 2.00E-140 | 2.00E-140 |
| SCE1572_6471 | sce_5444 | 0.00E+00 | 2.00E-178 |
| SCE1572_6472 | sce_5445 | 2.00E-127 | 3.00E-127 |
| SCE1572_6478 | sce_2488 | 1.00E-61 | 7.00E-62 |
| SCE1572_648 | sce_455 | 0.00E+00 | 0.00E+00 |
| SCE1572_6482 | sce_5451 | 5.00E-170 | 2.00E-161 |
| SCE1572_6484 | sce_5454 | 5.00E-164 | 0.00E+00 |
| SCE1572_6485 | sce_5455 | 7.00E-93 | 5.00E-94 |
| SCE1572_6486 | sce_5456 | 4.00E-46 | 5.00E-43 |
| SCE1572_6487 | sce_5457 | 4.00E-59 | 9.00E-43 |
| SCE1572_6488 | sce_5458 | 2.00E-16 | 5.00E-13 |
| SCE1572_6490 | sce_2076 | 1.00E-67 | 2.00E-81 |
| SCE1572_6492 | sce_2078 | 1.00E-103 | 9.00E-124 |
| SCE1572_6493 | sce_2079 | 1.00E-101 | 2.00E-107 |
| SCE1572_6498 | sce_5461 | 0.00E+00 | 0.00E+00 |
| SCE1572_6499 | sce_9818 | 5.00E-08 | 4.00E-10 |
| SCE1572_65 | sce_56 | 2.00E-106 | 2.00E-102 |
| SCE1572_650 | sce_945 | 0.00E+00 | 0.00E+00 |
| SCE1572_650 | sce_457 | 0.00E+00 | 0.00E+00 |
| SCE1572_6509 | sce_3727 | 4.00E-59 | 2.00E-60 |
| SCE1572_651 | sce_458 | 3.00E-26 | 3.00E-26 |
| SCE1572_6511 | sce_9988 | 1.00E-85 | 4.00E-84 |
| SCE1572_6512 | sce_5465 | 0.00E+00 | 0.00E+00 |
| SCE1572_6514 | sce_5467 | 0.00E+00 | 0.00E+00 |
| SCE1572_6515 | sce_5468 | 4.00E-53 | 2.00E-74 |
| SCE1572_6516 | sce_5469 | 0.00E+00 | 0.00E+00 |
| SCE1572_6517 | sce_5471 | 3.00E-46 | 2.00E-62 |
| SCE1572_652 | sce_459 | 1.00E-55 | 2.00E-39 |
| SCE1572_6520 | sce_5493 | 2.00E-125 | 8.00E-100 |
| SCE1572_6521 | sce_5494 | 9.00E-28 | 9.00E-28 |
| SCE1572_6524 | sce_5495 | 7.00E-142 | 1.00E-141 |
| SCE1572_6525 | sce_1706 | 7.00E-67 | 2.00E-58 |
| SCE1572_653 | sce_460 | 6.00E-99 | 6.00E-99 |
| SCE1572_6530 | sce_9960 | 0.00E+00 | 0.00E+00 |
| SCE1572_6531 | sce_9961 | 0.00E+00 | 0.00E+00 |
| SCE1572_6535 | sce_9435 | 3.00E-73 | 2.00E-81 |
| SCE1572_6541 | sce_5497 | 1.00E-121 | 7.00E-118 |
| SCE1572_6542 | sce_5498 | 2.00E-141 | 2.00E-149 |
| SCE1572_6543 | sce_5499 | 1.00E-118 | 1.00E-118 |
| SCE1572_6544 | sce_5500 | 0.00E+00 | 0.00E+00 |
| SCE1572_6545 | sce_5501 | 2.00E-171 | 2.00E-143 |
| SCE1572_6547 | sce_9557 | 3.00E-169 | 0.00E+00 |
| SCE1572_655 | sce_461 | 2.00E-80 | 2.00E-80 |
| SCE1572_6551 | sce_5511 | 4.00E-170 | 0.00E+00 |
| SCE1572_6556 | sce_7099 | 1.00E-61 | 7.00E-66 |
| SCE1572_6557 | sce_5514 | 1.00E-134 | 1.00E-120 |
| SCE1572_6559 | sce_6328 | 4.00E-70 | 1.00E-69 |
| SCE1572_656 | sce_462 | 9.00E-111 | 2.00E-111 |
| SCE1572_657 | sce_463 | 1.00E-94 | 6.00E-85 |
| SCE1572_6570 | sce_6017 | 2.00E-64 | 4.00E-50 |
| SCE1572_6572 | sce_9878 | 2.00E-86 | 2.00E-86 |
| SCE1572_6574 | sce_8429 | 0.00E+00 | 0.00E+00 |
| SCE1572_6575 | sce_5136 | 3.00E-22 | 8.00E-23 |
| SCE1572_6576 | sce_9599 | 2.00E-108 | 2.00E-108 |
| SCE1572_6577 | sce_9598 | 5.00E-142 | 2.00E-141 |
| SCE1572_6578 | sce_1328 | 7.00E-162 | 3.00E-164 |
| SCE1572_6579 | sce_9849 | 9.00E-64 | 3.00E-65 |
| SCE1572_658 | sce_464 | 4.00E-47 | 5.00E-47 |
| SCE1572_6581 | sce_6235 | 0.00E+00 | 0.00E+00 |
| SCE1572_6581 | sce_2161 | 0.00E+00 | 0.00E+00 |
| SCE1572_6581 | sce_225 | 0.00E+00 | 0.00E+00 |
| SCE1572_6581 | sce_8357 | 0.00E+00 | 0.00E+00 |
| SCE1572_6581 | sce_5276 | 0.00E+00 | 0.00E+00 |
| SCE1572_6582 | sce_5517 | 1.00E-111 | 2.00E-120 |
| SCE1572_6585 | sce_7661 | 0.00E+00 | 0.00E+00 |
| SCE1572_6585 | sce_6093 | 0.00E+00 | 0.00E+00 |
| SCE1572_6585 | sce_6092 | 0.00E+00 | 0.00E+00 |
| SCE1572_6585 | sce_6095 | 0.00E+00 | 0.00E+00 |
| SCE1572_6585 | sce_3917 | 0.00E+00 | 0.00E+00 |
| SCE1572_6585 | sce_6107 | 0.00E+00 | 0.00E+00 |
| SCE1572_6585 | sce_6094 | 0.00E+00 | 0.00E+00 |
| SCE1572_6585 | sce_10204 | 0.00E+00 | 0.00E+00 |

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|--------------|-----------|-----------|-----------|
| SCE1572_6585 | sce_9920 | 0.00E+00 | 0.00E+00 |
| SCE1572_6585 | sce_6535 | 0.00E+00 | 0.00E+00 |
| SCE1572_6585 | sce_388 | 0.00E+00 | 0.00E+00 |
| SCE1572_6585 | sce_3003 | 0.00E+00 | 0.00E+00 |
| SCE1572_6585 | sce_7640 | 0.00E+00 | 0.00E+00 |
| SCE1572_6585 | sce_9557 | 0.00E+00 | 0.00E+00 |
| SCE1572_6585 | sce_5835 | 0.00E+00 | 0.00E+00 |
| SCE1572_6585 | sce_4513 | 0.00E+00 | 0.00E+00 |
| SCE1572_6585 | sce_8618 | 0.00E+00 | 0.00E+00 |
| SCE1572_6587 | sce_9236 | 0.00E+00 | 0.00E+00 |
| SCE1572_6587 | sce_389 | 0.00E+00 | 0.00E+00 |
| SCE1572_6588 | sce_389 | 0.00E+00 | 0.00E+00 |
| SCE1572_6588 | sce_7637 | 0.00E+00 | 0.00E+00 |
| SCE1572_6588 | sce_2666 | 0.00E+00 | 0.00E+00 |
| SCE1572_6588 | sce_9237 | 0.00E+00 | 0.00E+00 |
| SCE1572_659 | sce_465 | 4.00E-24 | 4.00E-24 |
| SCE1572_6596 | sce_5518 | 4.00E-23 | 2.00E-38 |
| SCE1572_6597 | sce_5519 | 4.00E-52 | 2.00E-56 |
| SCE1572_6598 | sce_5520 | 2.00E-107 | 5.00E-107 |
| SCE1572_6599 | sce_5522 | 0.00E+00 | 0.00E+00 |
| SCE1572_66 | sce_58 | 0.00E+00 | 0.00E+00 |
| SCE1572_660 | sce_466 | 0.00E+00 | 0.00E+00 |
| SCE1572_6600 | sce_5523 | 0.00E+00 | 0.00E+00 |
| SCE1572_6601 | sce_5524 | 0.00E+00 | 0.00E+00 |
| SCE1572_6601 | sce_9469 | 0.00E+00 | 0.00E+00 |
| SCE1572_6602 | sce_5526 | 3.00E-72 | 3.00E-97 |
| SCE1572_6603 | sce_5527 | 3.00E-121 | 3.00E-126 |
| SCE1572_6605 | sce_2518 | 4.00E-26 | 5.00E-23 |
| SCE1572_6609 | sce_8361 | 3.00E-09 | 8.00E-10 |
| SCE1572_661 | sce_467 | 3.00E-09 | 4.00E-15 |
| SCE1572_6610 | sce_803 | 6.00E-37 | 1.00E-47 |
| SCE1572_6614 | sce_5529 | 3.00E-152 | 1.00E-148 |
| SCE1572_6616 | sce_5530 | 0.00E+00 | 0.00E+00 |
| SCE1572_6617 | sce_7059 | 2.00E-47 | 9.00E-53 |
| SCE1572_6619 | sce_7066 | 2.00E-19 | 2.00E-29 |
| SCE1572_662 | sce_468 | 0.00E+00 | 0.00E+00 |
| SCE1572_6624 | sce_169 | 2.00E-22 | 1.00E-24 |
| SCE1572_6625 | sce_9401 | 3.00E-41 | 2.00E-43 |
| SCE1572_6629 | sce_3602 | 8.00E-63 | 6.00E-61 |
| SCE1572_6630 | sce_3603 | 9.00E-63 | 1.00E-63 |
| SCE1572_6634 | sce_9373 | 0.00E+00 | 0.00E+00 |
| SCE1572_6634 | sce_4062 | 0.00E+00 | 0.00E+00 |
| SCE1572_6637 | sce_5710 | 0.00E+00 | 0.00E+00 |
| SCE1572_664 | sce_469 | 0.00E+00 | 0.00E+00 |
| SCE1572_6640 | sce_5538 | 0.00E+00 | 0.00E+00 |
| SCE1572_6641 | sce_5539 | 6.00E-122 | 2.00E-116 |
| SCE1572_6642 | sce_5540 | 4.00E-73 | 1.00E-77 |
| SCE1572_6643 | sce_5541 | 2.00E-177 | 1.00E-177 |
| SCE1572_6645 | sce_1705 | 3.00E-86 | 6.00E-98 |
| SCE1572_6646 | sce_2536 | 7.00E-93 | 8.00E-93 |
| SCE1572_665 | sce_470 | 1.00E-78 | 3.00E-93 |
| SCE1572_6650 | sce_1704 | 2.00E-133 | 2.00E-134 |
| SCE1572_6652 | sce_7114 | 3.00E-48 | 8.00E-49 |
| SCE1572_6654 | sce_5546 | 0.00E+00 | 0.00E+00 |
| SCE1572_6654 | sce_10036 | 0.00E+00 | 0.00E+00 |
| SCE1572_6655 | sce_5551 | 1.00E-20 | 2.00E-44 |
| SCE1572_6657 | sce_3612 | 0.00E+00 | 0.00E+00 |
| SCE1572_666 | sce_471 | 8.00E-147 | 4.00E-150 |
| SCE1572_6663 | sce_5556 | 2.00E-116 | 2.00E-101 |
| SCE1572_6665 | sce_5554 | 7.00E-176 | 1.00E-154 |
| SCE1572_6666 | sce_5555 | 0.00E+00 | 0.00E+00 |
| SCE1572_6668 | sce_9809 | 2.00E-154 | 2.00E-171 |
| SCE1572_6669 | sce_9810 | 3.00E-96 | 7.00E-97 |
| SCE1572_667 | sce_472 | 0.00E+00 | 0.00E+00 |
| SCE1572_6670 | sce_9811 | 1.00E-56 | 9.00E-43 |
| SCE1572_6671 | sce_5917 | 5.00E-62 | 3.00E-62 |
| SCE1572_6673 | sce_5558 | 1.00E-30 | 7.00E-38 |
| SCE1572_6676 | sce_5560 | 7.00E-88 | 5.00E-95 |
| SCE1572_6677 | sce_5181 | 2.00E-94 | 1.00E-82 |
| SCE1572_6678 | sce_5561 | 2.00E-92 | 8.00E-93 |
| SCE1572_668 | sce_473 | 1.00E-116 | 2.00E-112 |
| SCE1572_6680 | sce_5562 | 2.00E-84 | 5.00E-90 |
| SCE1572_6681 | sce_5563 | 7.00E-103 | 8.00E-128 |
| SCE1572_6683 | sce_5564 | 2.00E-166 | 2.00E-159 |
| SCE1572_6684 | sce_5568 | 2.00E-172 | 2.00E-179 |
| SCE1572_6687 | sce_5569 | 2.00E-66 | 2.00E-66 |

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|--------------|-----------|-----------|-----------|
| SCE1572_6688 | sce_5086 | 0.00E+00 | 0.00E+00 |
| SCE1572_6688 | sce_5085 | 0.00E+00 | 0.00E+00 |
| SCE1572_6688 | sce_6701 | 0.00E+00 | 0.00E+00 |
| SCE1572_6688 | sce_3793 | 0.00E+00 | 0.00E+00 |
| SCE1572_669 | sce_474 | 0.00E+00 | 0.00E+00 |
| SCE1572_6691 | sce_10016 | 3.00E-24 | 3.00E-24 |
| SCE1572_6694 | sce_2414 | 3.00E-131 | 1.00E-122 |
| SCE1572_6695 | sce_5574 | 5.00E-162 | 2.00E-171 |
| SCE1572_6696 | sce_5575 | 3.00E-89 | 1.00E-100 |
| SCE1572_6697 | sce_5576 | 9.00E-102 | 9.00E-102 |
| SCE1572_67 | sce_60 | 1.00E-133 | 8.00E-122 |
| SCE1572_670 | sce_475 | 3.00E-160 | 4.00E-164 |
| SCE1572_6700 | sce_2475 | 7.00E-145 | 1.00E-152 |
| SCE1572_6701 | sce_3424 | 0.00E+00 | 0.00E+00 |
| SCE1572_6704 | sce_5577 | 2.00E-66 | 1.00E-77 |
| SCE1572_6705 | sce_5578 | 0.00E+00 | 0.00E+00 |
| SCE1572_6705 | sce_1392 | 0.00E+00 | 0.00E+00 |
| SCE1572_6706 | sce_5579 | 7.00E-89 | 7.00E-89 |
| SCE1572_6708 | sce_5580 | 1.00E-132 | 1.00E-130 |
| SCE1572_6709 | sce_5581 | 9.00E-180 | 8.00E-180 |
| SCE1572_671 | sce_476 | 2.00E-145 | 8.00E-167 |
| SCE1572_6710 | sce_5582 | 0.00E+00 | 0.00E+00 |
| SCE1572_6710 | sce_8116 | 0.00E+00 | 0.00E+00 |
| SCE1572_6711 | sce_5583 | 2.00E-101 | 2.00E-101 |
| SCE1572_6712 | sce_5584 | 0.00E+00 | 0.00E+00 |
| SCE1572_6713 | sce_5585 | 4.00E-94 | 3.00E-96 |
| SCE1572_6714 | sce_5586 | 0.00E+00 | 0.00E+00 |
| SCE1572_6715 | sce_5587 | 0.00E+00 | 0.00E+00 |
| SCE1572_6716 | sce_5588 | 0.00E+00 | 0.00E+00 |
| SCE1572_6717 | sce_5589 | 9.00E-105 | 1.00E-97 |
| SCE1572_6719 | sce_5590 | 3.00E-145 | 3.00E-140 |
| SCE1572_672 | sce_478 | 7.00E-53 | 2.00E-83 |
| SCE1572_6720 | sce_5592 | 8.00E-78 | 3.00E-69 |
| SCE1572_6721 | sce_5593 | 1.00E-60 | 3.00E-60 |
| SCE1572_6722 | sce_5594 | 9.00E-74 | 9.00E-74 |
| SCE1572_6723 | sce_5595 | 0.00E+00 | 0.00E+00 |
| SCE1572_6724 | sce_5596 | 9.00E-172 | 0.00E+00 |
| SCE1572_6725 | sce_5597 | 4.00E-103 | 2.00E-102 |
| SCE1572_6726 | sce_5598 | 4.00E-85 | 3.00E-85 |
| SCE1572_6727 | sce_5599 | 5.00E-82 | 3.00E-86 |
| SCE1572_6728 | sce_5600 | 8.00E-54 | 2.00E-38 |
| SCE1572_6729 | sce_5601 | 6.00E-13 | 5.00E-15 |
| SCE1572_6730 | sce_5602 | 0.00E+00 | 0.00E+00 |
| SCE1572_6730 | sce_3185 | 0.00E+00 | 0.00E+00 |
| SCE1572_6730 | sce_5033 | 0.00E+00 | 0.00E+00 |
| SCE1572_6732 | sce_5604 | 6.00E-124 | 2.00E-127 |
| SCE1572_6733 | sce_5605 | 7.00E-152 | 2.00E-145 |
| SCE1572_6734 | sce_5606 | 3.00E-114 | 1.00E-102 |
| SCE1572_6735 | sce_5607 | 0.00E+00 | 0.00E+00 |
| SCE1572_6736 | sce_5608 | 1.00E-153 | 1.00E-153 |
| SCE1572_6737 | sce_5609 | 4.00E-84 | 1.00E-83 |
| SCE1572_6738 | sce_5610 | 4.00E-96 | 8.00E-112 |
| SCE1572_6740 | sce_1003 | 0.00E+00 | 0.00E+00 |
| SCE1572_6742 | sce_5614 | 4.00E-130 | 2.00E-140 |
| SCE1572_6743 | sce_5615 | 5.00E-12 | 3.00E-14 |
| SCE1572_6744 | sce_5616 | 5.00E-80 | 3.00E-66 |
| SCE1572_6750 | sce_5627 | 4.00E-169 | 3.00E-178 |
| SCE1572_6755 | sce_10428 | 4.00E-43 | 9.00E-43 |
| SCE1572_6756 | sce_10429 | 4.00E-54 | 9.00E-54 |
| SCE1572_6757 | sce_10430 | 5.00E-116 | 5.00E-116 |
| SCE1572_6759 | sce_5628 | 2.00E-54 | 3.00E-62 |
| SCE1572_676 | sce_480 | 4.00E-78 | 8.00E-81 |
| SCE1572_6760 | sce_1338 | 0.00E+00 | 0.00E+00 |
| SCE1572_6760 | sce_9335 | 0.00E+00 | 0.00E+00 |
| SCE1572_6764 | sce_5629 | 0.00E+00 | 0.00E+00 |
| SCE1572_6768 | sce_5447 | 7.00E-20 | 2.00E-14 |
| SCE1572_6769 | sce_5632 | 0.00E+00 | 0.00E+00 |
| SCE1572_677 | sce_481 | 0.00E+00 | 0.00E+00 |
| SCE1572_6770 | sce_5634 | 2.00E-06 | 1.00E-06 |
| SCE1572_6771 | sce_5635 | 4.00E-23 | 3.00E-08 |
| SCE1572_6773 | sce_5637 | 0.00E+00 | 0.00E+00 |
| SCE1572_6776 | sce_5639 | 0.00E+00 | 0.00E+00 |
| SCE1572_6776 | sce_9625 | 0.00E+00 | 0.00E+00 |
| SCE1572_6776 | sce_5292 | 0.00E+00 | 0.00E+00 |
| SCE1572_6777 | sce_5640 | 9.00E-10 | 8.00E-10 |
| SCE1572_6778 | sce_5641 | 2.00E-90 | 6.00E-100 |

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|--------------|----------|-----------|-----------|
| SCE1572_6779 | sce_5642 | 7.00E-87 | 1.00E-87 |
| SCE1572_678 | sce_482 | 0.00E+00 | 0.00E+00 |
| SCE1572_6781 | sce_5643 | 3.00E-50 | 1.00E-41 |
| SCE1572_6782 | sce_5644 | 1.00E-42 | 3.00E-40 |
| SCE1572_6783 | sce_5645 | 1.00E-73 | 1.00E-73 |
| SCE1572_6787 | sce_5646 | 4.00E-111 | 3.00E-113 |
| SCE1572_6788 | sce_5647 | 9.00E-129 | 2.00E-126 |
| SCE1572_6789 | sce_5648 | 0.00E+00 | 0.00E+00 |
| SCE1572_679 | sce_483 | 8.00E-72 | 8.00E-72 |
| SCE1572_6792 | sce_5650 | 0.00E+00 | 0.00E+00 |
| SCE1572_6793 | sce_5652 | 0.00E+00 | 0.00E+00 |
| SCE1572_6794 | sce_5653 | 1.00E-113 | 4.00E-117 |
| SCE1572_6795 | sce_5654 | 0.00E+00 | 0.00E+00 |
| SCE1572_6796 | sce_5655 | 1.00E-35 | 2.00E-22 |
| SCE1572_6797 | sce_5656 | 1.00E-169 | 1.00E-169 |
| SCE1572_6798 | sce_5657 | 0.00E+00 | 0.00E+00 |
| SCE1572_6799 | sce_5658 | 5.00E-50 | 3.00E-78 |
| SCE1572_68 | sce_61 | 0.00E+00 | 0.00E+00 |
| SCE1572_6800 | sce_5660 | 0.00E+00 | 0.00E+00 |
| SCE1572_6802 | sce_5662 | 0.00E+00 | 0.00E+00 |
| SCE1572_6803 | sce_5663 | 1.00E-111 | 8.00E-102 |
| SCE1572_6804 | sce_5664 | 3.00E-106 | 3.00E-110 |
| SCE1572_6806 | sce_5666 | 0.00E+00 | 0.00E+00 |
| SCE1572_6807 | sce_5667 | 2.00E-133 | 2.00E-133 |
| SCE1572_6808 | sce_5668 | 5.00E-134 | 9.00E-143 |
| SCE1572_6809 | sce_5669 | 0.00E+00 | 0.00E+00 |
| SCE1572_681 | sce_484 | 2.00E-77 | 7.00E-90 |
| SCE1572_6810 | sce_5670 | 0.00E+00 | 0.00E+00 |
| SCE1572_6811 | sce_5671 | 3.00E-134 | 5.00E-141 |
| SCE1572_6812 | sce_5672 | 4.00E-24 | 5.00E-37 |
| SCE1572_6813 | sce_5673 | 0.00E+00 | 0.00E+00 |
| SCE1572_6814 | sce_5675 | 0.00E+00 | 0.00E+00 |
| SCE1572_6815 | sce_5677 | 0.00E+00 | 0.00E+00 |
| SCE1572_6816 | sce_5678 | 0.00E+00 | 0.00E+00 |
| SCE1572_6817 | sce_5679 | 9.00E-55 | 5.00E-55 |
| SCE1572_6818 | sce_5680 | 4.00E-60 | 3.00E-60 |
| SCE1572_6819 | sce_5681 | 1.00E-97 | 4.00E-101 |
| SCE1572_682 | sce_485 | 0.00E+00 | 0.00E+00 |
| SCE1572_6820 | sce_5682 | 2.00E-35 | 3.00E-34 |
| SCE1572_6821 | sce_5683 | 1.00E-116 | 2.00E-107 |
| SCE1572_6822 | sce_5684 | 6.00E-79 | 8.00E-80 |
| SCE1572_6823 | sce_5685 | 0.00E+00 | 0.00E+00 |
| SCE1572_6824 | sce_5686 | 4.00E-124 | 4.00E-118 |
| SCE1572_6826 | sce_5687 | 4.00E-63 | 1.00E-62 |
| SCE1572_6827 | sce_5688 | 0.00E+00 | 0.00E+00 |
| SCE1572_6828 | sce_5689 | 0.00E+00 | 0.00E+00 |
| SCE1572_683 | sce_486 | 8.00E-47 | 9.00E-47 |
| SCE1572_6831 | sce_5691 | 0.00E+00 | 0.00E+00 |
| SCE1572_6832 | sce_5694 | 5.00E-87 | 8.00E-88 |
| SCE1572_6833 | sce_5695 | 1.00E-146 | 1.00E-162 |
| SCE1572_6835 | sce_5696 | 1.00E-93 | 1.00E-93 |
| SCE1572_6837 | sce_5697 | 1.00E-73 | 8.00E-74 |
| SCE1572_6838 | sce_5698 | 3.00E-69 | 4.00E-69 |
| SCE1572_6839 | sce_5699 | 2.00E-169 | 0.00E+00 |
| SCE1572_684 | sce_487 | 1.00E-156 | 2.00E-147 |
| SCE1572_6840 | sce_5700 | 2.00E-93 | 1.00E-93 |
| SCE1572_6841 | sce_5701 | 0.00E+00 | 0.00E+00 |
| SCE1572_6842 | sce_5702 | 1.00E-147 | 2.00E-146 |
| SCE1572_6843 | sce_5703 | 6.00E-104 | 2.00E-112 |
| SCE1572_6844 | sce_5704 | 0.00E+00 | 0.00E+00 |
| SCE1572_6845 | sce_5705 | 6.00E-78 | 3.00E-86 |
| SCE1572_6846 | sce_5706 | 2.00E-99 | 2.00E-99 |
| SCE1572_6847 | sce_5707 | 0.00E+00 | 1.00E-130 |
| SCE1572_6848 | sce_5709 | 0.00E+00 | 1.00E-168 |
| SCE1572_6849 | sce_5711 | 0.00E+00 | 0.00E+00 |
| SCE1572_6850 | sce_5712 | 4.00E-85 | 4.00E-66 |
| SCE1572_6851 | sce_5713 | 3.00E-27 | 2.00E-30 |
| SCE1572_6853 | sce_5714 | 0.00E+00 | 0.00E+00 |
| SCE1572_6854 | sce_5715 | 7.00E-79 | 1.00E-79 |
| SCE1572_6855 | sce_5716 | 6.00E-30 | 7.00E-30 |
| SCE1572_6856 | sce_5717 | 5.00E-94 | 5.00E-94 |
| SCE1572_6857 | sce_5718 | 1.00E-97 | 2.00E-102 |
| SCE1572_6858 | sce_5719 | 2.00E-168 | 1.00E-157 |
| SCE1572_6859 | sce_5720 | 2.00E-51 | 4.00E-51 |
| SCE1572_686 | sce_488 | 0.00E+00 | 0.00E+00 |
| SCE1572_6860 | sce_5721 | 0.00E+00 | 0.00E+00 |

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| SCE1572_6860 | sce_8732 | 0.00E+00 | 0.00E+00 |
| SCE1572_6861 | sce_5723 | 8.00E-23 | 1.00E-22 |
| SCE1572_6862 | sce_5724 | 0.00E+00 | 0.00E+00 |
| SCE1572_6863 | sce_5725 | 2.00E-165 | 6.00E-171 |
| SCE1572_6865 | sce_5728 | 0.00E+00 | 0.00E+00 |
| SCE1572_6866 | sce_5729 | 0.00E+00 | 0.00E+00 |
| SCE1572_6867 | sce_5730 | 0.00E+00 | 0.00E+00 |
| SCE1572_6868 | sce_5731 | 2.00E-95 | 3.00E-90 |
| SCE1572_6869 | sce_5732 | 9.00E-51 | 8.00E-58 |
| SCE1572_687 | sce_489 | 8.00E-53 | 1.00E-49 |
| SCE1572_6870 | sce_5733 | 7.00E-176 | 2.00E-169 |
| SCE1572_6871 | sce_5734 | 2.00E-100 | 2.00E-96 |
| SCE1572_6872 | sce_5735 | 1.00E-162 | 9.00E-163 |
| SCE1572_6873 | sce_5737 | 6.00E-148 | 1.00E-156 |
| SCE1572_6874 | sce_5738 | 7.00E-130 | 0.00E+00 |
| SCE1572_6875 | sce_5739 | 7.00E-16 | 4.00E-17 |
| SCE1572_6876 | sce_5741 | 2.00E-45 | 4.00E-41 |
| SCE1572_6877 | sce_5742 | 0.00E+00 | 0.00E+00 |
| SCE1572_6878 | sce_5743 | 4.00E-113 | 6.00E-118 |
| SCE1572_6879 | sce_5744 | 0.00E+00 | 0.00E+00 |
| SCE1572_688 | sce_490 | 6.00E-123 | 4.00E-118 |
| SCE1572_6883 | sce_5745 | 4.00E-120 | 3.00E-117 |
| SCE1572_6886 | sce_9736 | 1.00E-60 | 5.00E-61 |
| SCE1572_689 | sce_491 | 3.00E-172 | 0.00E+00 |
| SCE1572_6892 | sce_5751 | 0.00E+00 | 0.00E+00 |
| SCE1572_6892 | sce_5746 | 0.00E+00 | 0.00E+00 |
| SCE1572_6892 | sce_9665 | 0.00E+00 | 0.00E+00 |
| SCE1572_6892 | sce_5403 | 0.00E+00 | 0.00E+00 |
| SCE1572_6892 | sce_5226 | 0.00E+00 | 0.00E+00 |
| SCE1572_6892 | sce_1803 | 0.00E+00 | 0.00E+00 |
| SCE1572_6892 | sce_7154 | 0.00E+00 | 0.00E+00 |
| SCE1572_6892 | sce_7969 | 0.00E+00 | 0.00E+00 |
| SCE1572_6892 | sce_2053 | 0.00E+00 | 0.00E+00 |
| SCE1572_6893 | sce_5746 | 0.00E+00 | 0.00E+00 |
| SCE1572_6893 | sce_9665 | 0.00E+00 | 0.00E+00 |
| SCE1572_6893 | sce_5751 | 0.00E+00 | 0.00E+00 |
| SCE1572_6893 | sce_5403 | 0.00E+00 | 0.00E+00 |
| SCE1572_6893 | sce_5226 | 0.00E+00 | 0.00E+00 |
| SCE1572_6893 | sce_7969 | 0.00E+00 | 0.00E+00 |
| SCE1572_6893 | sce_2053 | 0.00E+00 | 0.00E+00 |
| SCE1572_6893 | sce_1803 | 0.00E+00 | 0.00E+00 |
| SCE1572_6893 | sce_4073 | 0.00E+00 | 0.00E+00 |
| SCE1572_6893 | sce_9954 | 0.00E+00 | 0.00E+00 |
| SCE1572_6893 | sce_3750 | 0.00E+00 | 0.00E+00 |
| SCE1572_6894 | sce_5751 | 0.00E+00 | 0.00E+00 |
| SCE1572_6894 | sce_5746 | 0.00E+00 | 0.00E+00 |
| SCE1572_6894 | sce_9665 | 0.00E+00 | 0.00E+00 |
| SCE1572_6894 | sce_5226 | 0.00E+00 | 0.00E+00 |
| SCE1572_6894 | sce_5403 | 0.00E+00 | 0.00E+00 |
| SCE1572_6894 | sce_7969 | 0.00E+00 | 0.00E+00 |
| SCE1572_6894 | sce_4073 | 0.00E+00 | 0.00E+00 |
| SCE1572_6894 | sce_7154 | 0.00E+00 | 0.00E+00 |
| SCE1572_6894 | sce_2053 | 0.00E+00 | 0.00E+00 |
| SCE1572_6894 | sce_9954 | 0.00E+00 | 0.00E+00 |
| SCE1572_6894 | sce_9757 | 0.00E+00 | 0.00E+00 |
| SCE1572_6894 | sce_6712 | 0.00E+00 | 0.00E+00 |
| SCE1572_6894 | sce_3750 | 0.00E+00 | 0.00E+00 |
| SCE1572_6894 | sce_1803 | 0.00E+00 | 0.00E+00 |
| SCE1572_6898 | sce_5752 | 0.00E+00 | 0.00E+00 |
| SCE1572_6899 | sce_5753 | 3.00E-127 | 1.00E-118 |
| SCE1572_69 | sce_62 | 3.00E-21 | 2.00E-12 |
| SCE1572_690 | sce_492 | 4.00E-58 | 1.00E-58 |
| SCE1572_6903 | sce_2563 | 5.00E-44 | 2.00E-37 |
| SCE1572_691 | sce_494 | 4.00E-151 | 8.00E-155 |
| SCE1572_6910 | sce_9236 | 0.00E+00 | 0.00E+00 |
| SCE1572_6910 | sce_389 | 0.00E+00 | 0.00E+00 |
| SCE1572_6915 | sce_5756 | 0.00E+00 | 0.00E+00 |
| SCE1572_6916 | sce_5761 | 5.00E-143 | 6.00E-143 |
| SCE1572_6917 | sce_8380 | 3.00E-64 | 3.00E-48 |
| SCE1572_6918 | sce_5762 | 5.00E-68 | 5.00E-68 |
| SCE1572_6919 | sce_8379 | 2.00E-89 | 1.00E-97 |
| SCE1572_692 | sce_495 | 6.00E-42 | 6.00E-42 |
| SCE1572_6921 | sce_2065 | 0.00E+00 | 0.00E+00 |
| SCE1572_6921 | sce_8618 | 0.00E+00 | 0.00E+00 |
| SCE1572_6921 | sce_10204 | 0.00E+00 | 0.00E+00 |
| SCE1572_6921 | sce_6092 | 0.00E+00 | 0.00E+00 |

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| SCE1572_6921 | sce_6535 | 0.00E+00 | 0.00E+00 |
| SCE1572_6921 | sce_3003 | 0.00E+00 | 0.00E+00 |
| SCE1572_6921 | sce_6095 | 0.00E+00 | 0.00E+00 |
| SCE1572_6921 | sce_7661 | 0.00E+00 | 0.00E+00 |
| SCE1572_6921 | sce_388 | 0.00E+00 | 0.00E+00 |
| SCE1572_6921 | sce_7640 | 0.00E+00 | 0.00E+00 |
| SCE1572_6921 | sce_4513 | 0.00E+00 | 0.00E+00 |
| SCE1572_6921 | sce_9557 | 0.00E+00 | 0.00E+00 |
| SCE1572_6921 | sce_5835 | 0.00E+00 | 0.00E+00 |
| SCE1572_6922 | sce_1259 | 1.00E-22 | 5.00E-27 |
| SCE1572_6923 | sce_805 | 0.00E+00 | 0.00E+00 |
| SCE1572_6923 | sce_229 | 0.00E+00 | 0.00E+00 |
| SCE1572_6929 | sce_5770 | 5.00E-15 | 1.00E-21 |
| SCE1572_693 | sce_496 | 0.00E+00 | 0.00E+00 |
| SCE1572_6932 | sce_5763 | 1.00E-76 | 1.00E-76 |
| SCE1572_6937 | sce_5766 | 4.00E-41 | 2.00E-43 |
| SCE1572_6939 | sce_5767 | 4.00E-121 | 9.00E-127 |
| SCE1572_694 | sce_9364 | 2.00E-47 | 8.00E-48 |
| SCE1572_6940 | sce_5768 | 3.00E-51 | 2.00E-53 |
| SCE1572_6941 | sce_5769 | 0.00E+00 | 0.00E+00 |
| SCE1572_6942 | sce_1680 | 0.00E+00 | 0.00E+00 |
| SCE1572_6946 | sce_5528 | 6.00E-65 | 6.00E-65 |
| SCE1572_6947 | sce_5773 | 3.00E-94 | 5.00E-113 |
| SCE1572_6948 | sce_5835 | 0.00E+00 | 0.00E+00 |
| SCE1572_6948 | sce_388 | 0.00E+00 | 0.00E+00 |
| SCE1572_6948 | sce_7640 | 0.00E+00 | 0.00E+00 |
| SCE1572_6948 | sce_3085 | 0.00E+00 | 0.00E+00 |
| SCE1572_6948 | sce_7109 | 0.00E+00 | 0.00E+00 |
| SCE1572_6948 | sce_3003 | 0.00E+00 | 0.00E+00 |
| SCE1572_6948 | sce_10204 | 0.00E+00 | 0.00E+00 |
| SCE1572_6948 | sce_4513 | 0.00E+00 | 0.00E+00 |
| SCE1572_695 | sce_9358 | 3.00E-66 | 7.00E-71 |
| SCE1572_6953 | sce_2385 | 1.00E-37 | 1.00E-38 |
| SCE1572_6955 | sce_5883 | 5.00E-75 | 5.00E-65 |
| SCE1572_6956 | sce_177 | 2.00E-15 | 4.00E-12 |
| SCE1572_6960 | sce_5775 | 0.00E+00 | 0.00E+00 |
| SCE1572_6962 | sce_5776 | 3.00E-77 | 7.00E-77 |
| SCE1572_6963 | sce_5777 | 0.00E+00 | 0.00E+00 |
| SCE1572_6964 | sce_5778 | 0.00E+00 | 0.00E+00 |
| SCE1572_6965 | sce_5779 | 2.00E-125 | 2.00E-125 |
| SCE1572_6966 | sce_5780 | 0.00E+00 | 0.00E+00 |
| SCE1572_6967 | sce_5781 | 0.00E+00 | 0.00E+00 |
| SCE1572_6968 | sce_5782 | 1.00E-147 | 2.00E-135 |
| SCE1572_6969 | sce_5783 | 1.00E-66 | 9.00E-55 |
| SCE1572_6970 | sce_5784 | 4.00E-36 | 1.00E-39 |
| SCE1572_6974 | sce_5787 | 0.00E+00 | 0.00E+00 |
| SCE1572_6974 | sce_1723 | 0.00E+00 | 0.00E+00 |
| SCE1572_6974 | sce_774 | 0.00E+00 | 0.00E+00 |
| SCE1572_6975 | sce_5788 | 4.00E-102 | 4.00E-114 |
| SCE1572_6976 | sce_5789 | 1.00E-156 | 1.00E-163 |
| SCE1572_6978 | sce_5790 | 6.00E-86 | 4.00E-85 |
| SCE1572_6980 | sce_5791 | 2.00E-123 | 1.00E-123 |
| SCE1572_6981 | sce_5794 | 2.00E-77 | 2.00E-77 |
| SCE1572_6983 | sce_5797 | 0.00E+00 | 0.00E+00 |
| SCE1572_6983 | sce_3612 | 0.00E+00 | 0.00E+00 |
| SCE1572_6983 | sce_886 | 0.00E+00 | 0.00E+00 |
| SCE1572_6983 | sce_248 | 0.00E+00 | 0.00E+00 |
| SCE1572_6984 | sce_5799 | 2.00E-40 | 1.00E-35 |
| SCE1572_6985 | sce_5800 | 0.00E+00 | 0.00E+00 |
| SCE1572_6988 | sce_5805 | 3.00E-106 | 3.00E-98 |
| SCE1572_6991 | sce_5807 | 7.00E-180 | 2.00E-170 |
| SCE1572_6992 | sce_100 | 2.00E-129 | 2.00E-136 |
| SCE1572_6993 | sce_5811 | 9.00E-108 | 3.00E-123 |
| SCE1572_6994 | sce_5812 | 3.00E-112 | 2.00E-111 |
| SCE1572_6995 | sce_5813 | 6.00E-98 | 4.00E-86 |
| SCE1572_6996 | sce_5815 | 4.00E-76 | 6.00E-76 |
| SCE1572_7 | sce_7 | 1.00E-88 | 1.00E-88 |
| SCE1572_70 | sce_63 | 2.00E-151 | 6.00E-152 |
| SCE1572_7003 | sce_3413 | 0.00E+00 | 0.00E+00 |
| SCE1572_7004 | sce_5821 | 6.00E-86 | 2.00E-89 |
| SCE1572_7005 | sce_5822 | 6.00E-64 | 2.00E-57 |
| SCE1572_7008 | sce_6818 | 4.00E-08 | 4.00E-08 |
| SCE1572_7009 | sce_9483 | 1.00E-101 | 1.00E-113 |
| SCE1572_701 | sce_497 | 0.00E+00 | 0.00E+00 |
| SCE1572_7011 | sce_9481 | 9.00E-135 | 3.00E-124 |
| SCE1572_7015 | sce_9479 | 1.00E-29 | 9.00E-34 |

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| SCE1572_702 | sce_498 | 1.00E-24 | 3.00E-23 |
| SCE1572_7022 | sce_6228 | 0.00E+00 | 0.00E+00 |
| SCE1572_7022 | sce_6833 | 0.00E+00 | 0.00E+00 |
| SCE1572_7022 | sce_6827 | 0.00E+00 | 0.00E+00 |
| SCE1572_7022 | sce_10159 | 0.00E+00 | 0.00E+00 |
| SCE1572_7022 | sce_7513 | 0.00E+00 | 0.00E+00 |
| SCE1572_7022 | sce_7408 | 0.00E+00 | 0.00E+00 |
| SCE1572_7022 | sce_6876 | 0.00E+00 | 0.00E+00 |
| SCE1572_7022 | sce_6836 | 0.00E+00 | 0.00E+00 |
| SCE1572_7022 | sce_2543 | 0.00E+00 | 0.00E+00 |
| SCE1572_7026 | sce_5823 | 0.00E+00 | 0.00E+00 |
| SCE1572_7027 | sce_5824 | 0.00E+00 | 0.00E+00 |
| SCE1572_7027 | sce_5830 | 0.00E+00 | 0.00E+00 |
| SCE1572_7027 | sce_2940 | 0.00E+00 | 0.00E+00 |
| SCE1572_7027 | sce_5827 | 0.00E+00 | 0.00E+00 |
| SCE1572_7027 | sce_2589 | 0.00E+00 | 0.00E+00 |
| SCE1572_7029 | sce_5827 | 0.00E+00 | 0.00E+00 |
| SCE1572_7029 | sce_5830 | 0.00E+00 | 0.00E+00 |
| SCE1572_7029 | sce_5824 | 0.00E+00 | 0.00E+00 |
| SCE1572_7029 | sce_2940 | 0.00E+00 | 0.00E+00 |
| SCE1572_7029 | sce_2589 | 0.00E+00 | 0.00E+00 |
| SCE1572_703 | sce_500 | 1.00E-17 | 9.00E-31 |
| SCE1572_7030 | sce_5828 | 7.00E-57 | 7.00E-57 |
| SCE1572_7032 | sce_5830 | 0.00E+00 | 0.00E+00 |
| SCE1572_7032 | sce_5827 | 0.00E+00 | 0.00E+00 |
| SCE1572_7032 | sce_5824 | 0.00E+00 | 0.00E+00 |
| SCE1572_7032 | sce_2940 | 0.00E+00 | 0.00E+00 |
| SCE1572_7032 | sce_2589 | 0.00E+00 | 0.00E+00 |
| SCE1572_7033 | sce_5831 | 2.00E-63 | 2.00E-63 |
| SCE1572_7034 | sce_5832 | 2.00E-83 | 2.00E-70 |
| SCE1572_7035 | sce_5833 | 0.00E+00 | 0.00E+00 |
| SCE1572_7036 | sce_5834 | 2.00E-97 | 2.00E-97 |
| SCE1572_704 | sce_501 | 0.00E+00 | 0.00E+00 |
| SCE1572_7041 | sce_5839 | 5.00E-70 | 4.00E-79 |
| SCE1572_7044 | sce_9896 | 3.00E-106 | 3.00E-115 |
| SCE1572_705 | sce_502 | 0.00E+00 | 0.00E+00 |
| SCE1572_706 | sce_503 | 3.00E-40 | 9.00E-50 |
| SCE1572_7063 | sce_7667 | 0.00E+00 | 0.00E+00 |
| SCE1572_7068 | sce_5840 | 0.00E+00 | 0.00E+00 |
| SCE1572_7069 | sce_1257 | 9.00E-50 | 3.00E-54 |
| SCE1572_707 | sce_504 | 0.00E+00 | 0.00E+00 |
| SCE1572_7072 | sce_5849 | 0.00E+00 | 0.00E+00 |
| SCE1572_7074 | sce_5850 | 1.00E-72 | 1.00E-72 |
| SCE1572_7075 | sce_5851 | 1.00E-117 | 8.00E-117 |
| SCE1572_7076 | sce_5854 | 0.00E+00 | 0.00E+00 |
| SCE1572_7079 | sce_5855 | 6.00E-55 | 6.00E-55 |
| SCE1572_708 | sce_505 | 2.00E-92 | 2.00E-92 |
| SCE1572_7080 | sce_5856 | 0.00E+00 | 0.00E+00 |
| SCE1572_7081 | sce_5857 | 9.00E-152 | 4.00E-153 |
| SCE1572_7082 | sce_5858 | 2.00E-81 | 3.00E-76 |
| SCE1572_7083 | sce_5859 | 5.00E-72 | 3.00E-84 |
| SCE1572_7084 | sce_5860 | 1.00E-167 | 2.00E-159 |
| SCE1572_7087 | sce_9904 | 1.00E-85 | 3.00E-80 |
| SCE1572_7091 | sce_5861 | 0.00E+00 | 0.00E+00 |
| SCE1572_7095 | sce_5863 | 4.00E-45 | 7.00E-43 |
| SCE1572_7096 | sce_1560 | 0.00E+00 | 0.00E+00 |
| SCE1572_7097 | sce_1561 | 3.00E-112 | 3.00E-105 |
| SCE1572_7098 | sce_1562 | 2.00E-115 | 2.00E-114 |
| SCE1572_71 | sce_64 | 6.00E-100 | 2.00E-102 |
| SCE1572_710 | sce_507 | 2.00E-50 | 2.00E-50 |
| SCE1572_7100 | sce_5868 | 9.00E-66 | 3.00E-58 |
| SCE1572_7101 | sce_5869 | 0.00E+00 | 0.00E+00 |
| SCE1572_7102 | sce_5870 | 0.00E+00 | 0.00E+00 |
| SCE1572_7104 | sce_5836 | 0.00E+00 | 0.00E+00 |
| SCE1572_7105 | sce_5837 | 0.00E+00 | 0.00E+00 |
| SCE1572_7109 | sce_1435 | 6.00E-36 | 6.00E-36 |
| SCE1572_711 | sce_508 | 7.00E-59 | 4.00E-67 |
| SCE1572_7114 | sce_7551 | 1.00E-115 | 5.00E-107 |
| SCE1572_7118 | sce_9883 | 4.00E-77 | 3.00E-93 |
| SCE1572_7122 | sce_5871 | 0.00E+00 | 0.00E+00 |
| SCE1572_7124 | sce_5872 | 0.00E+00 | 0.00E+00 |
| SCE1572_7125 | sce_5874 | 0.00E+00 | 0.00E+00 |
| SCE1572_713 | sce_509 | 0.00E+00 | 0.00E+00 |
| SCE1572_7131 | sce_8424 | 5.00E-23 | 7.00E-15 |
| SCE1572_7132 | sce_3684 | 5.00E-85 | 5.00E-85 |
| SCE1572_7133 | sce_5482 | 0.00E+00 | 0.00E+00 |

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|--------------|----------|-----------|-----------|
| SCE1572_7134 | sce_6324 | 5.00E-50 | 3.00E-50 |
| SCE1572_7135 | sce_5876 | 5.00E-167 | 2.00E-173 |
| SCE1572_7136 | sce_5877 | 6.00E-130 | 2.00E-140 |
| SCE1572_7143 | sce_301 | 2.00E-69 | 4.00E-66 |
| SCE1572_7144 | sce_5878 | 4.00E-66 | 7.00E-74 |
| SCE1572_7146 | sce_5879 | 2.00E-57 | 1.00E-57 |
| SCE1572_7147 | sce_5880 | 2.00E-158 | 5.00E-168 |
| SCE1572_7148 | sce_5885 | 1.00E-110 | 1.00E-73 |
| SCE1572_7149 | sce_5886 | 4.00E-67 | 1.00E-67 |
| SCE1572_7150 | sce_5887 | 4.00E-98 | 2.00E-98 |
| SCE1572_7151 | sce_5889 | 2.00E-31 | 1.00E-32 |
| SCE1572_7152 | sce_5890 | 2.00E-126 | 3.00E-122 |
| SCE1572_7153 | sce_9846 | 2.00E-115 | 2.00E-128 |
| SCE1572_7155 | sce_5893 | 3.00E-160 | 1.00E-149 |
| SCE1572_7157 | sce_1355 | 7.00E-23 | 2.00E-25 |
| SCE1572_7159 | sce_5894 | 6.00E-59 | 2.00E-59 |
| SCE1572_7161 | sce_5895 | 3.00E-73 | 4.00E-73 |
| SCE1572_7162 | sce_5896 | 3.00E-171 | 3.00E-171 |
| SCE1572_7163 | sce_5897 | 2.00E-163 | 3.00E-155 |
| SCE1572_7164 | sce_3432 | 1.00E-28 | 2.00E-37 |
| SCE1572_7170 | sce_5899 | 0.00E+00 | 0.00E+00 |
| SCE1572_7171 | sce_5900 | 3.00E-28 | 3.00E-28 |
| SCE1572_7172 | sce_5901 | 1.00E-80 | 2.00E-80 |
| SCE1572_7173 | sce_5902 | 0.00E+00 | 0.00E+00 |
| SCE1572_7175 | sce_5904 | 0.00E+00 | 0.00E+00 |
| SCE1572_7176 | sce_5905 | 1.00E-176 | 1.00E-163 |
| SCE1572_7178 | sce_2175 | 0.00E+00 | 0.00E+00 |
| SCE1572_7181 | sce_6290 | 2.00E-18 | 2.00E-18 |
| SCE1572_7182 | sce_1246 | 2.00E-159 | 6.00E-160 |
| SCE1572_7183 | sce_1245 | 2.00E-118 | 2.00E-115 |
| SCE1572_7185 | sce_5906 | 3.00E-62 | 5.00E-71 |
| SCE1572_7186 | sce_5907 | 0.00E+00 | 0.00E+00 |
| SCE1572_7187 | sce_5908 | 0.00E+00 | 0.00E+00 |
| SCE1572_7188 | sce_5909 | 0.00E+00 | 0.00E+00 |
| SCE1572_7189 | sce_1882 | 2.00E-129 | 1.00E-118 |
| SCE1572_7190 | sce_1881 | 2.00E-122 | 3.00E-114 |
| SCE1572_7191 | sce_5914 | 5.00E-117 | 9.00E-118 |
| SCE1572_7193 | sce_5915 | 0.00E+00 | 0.00E+00 |
| SCE1572_7199 | sce_8384 | 3.00E-134 | 3.00E-134 |
| SCE1572_72 | sce_65 | 2.00E-153 | 6.00E-148 |
| SCE1572_7200 | sce_5918 | 0.00E+00 | 0.00E+00 |
| SCE1572_7201 | sce_5919 | 9.00E-139 | 7.00E-138 |
| SCE1572_7206 | sce_5924 | 6.00E-101 | 3.00E-101 |
| SCE1572_7207 | sce_5926 | 4.00E-79 | 2.00E-93 |
| SCE1572_7208 | sce_5920 | 7.00E-73 | 3.00E-76 |
| SCE1572_7209 | sce_5936 | 1.00E-146 | 3.00E-147 |
| SCE1572_7210 | sce_5937 | 3.00E-37 | 2.00E-35 |
| SCE1572_7211 | sce_5938 | 8.00E-160 | 1.00E-170 |
| SCE1572_7212 | sce_5939 | 1.00E-10 | 1.00E-10 |
| SCE1572_7214 | sce_5941 | 3.00E-105 | 1.00E-110 |
| SCE1572_7216 | sce_5944 | 2.00E-133 | 2.00E-139 |
| SCE1572_7219 | sce_5945 | 2.00E-90 | 9.00E-93 |
| SCE1572_7220 | sce_5946 | 1.00E-10 | 1.00E-28 |
| SCE1572_7222 | sce_5947 | 7.00E-154 | 4.00E-152 |
| SCE1572_7223 | sce_5948 | 0.00E+00 | 0.00E+00 |
| SCE1572_7224 | sce_5950 | 6.00E-176 | 6.00E-176 |
| SCE1572_7225 | sce_5951 | 2.00E-173 | 7.00E-175 |
| SCE1572_7226 | sce_5952 | 2.00E-129 | 2.00E-112 |
| SCE1572_7227 | sce_5953 | 3.00E-56 | 7.00E-66 |
| SCE1572_7228 | sce_5954 | 3.00E-88 | 3.00E-86 |
| SCE1572_7229 | sce_5955 | 2.00E-128 | 3.00E-138 |
| SCE1572_7233 | sce_8264 | 3.00E-66 | 3.00E-78 |
| SCE1572_7234 | sce_5956 | 2.00E-77 | 5.00E-75 |
| SCE1572_7235 | sce_5957 | 0.00E+00 | 0.00E+00 |
| SCE1572_7236 | sce_5958 | 0.00E+00 | 0.00E+00 |
| SCE1572_7237 | sce_5960 | 0.00E+00 | 0.00E+00 |
| SCE1572_7238 | sce_5962 | 0.00E+00 | 0.00E+00 |
| SCE1572_7240 | sce_5963 | 4.00E-117 | 1.00E-106 |
| SCE1572_7241 | sce_7661 | 0.00E+00 | 0.00E+00 |
| SCE1572_7241 | sce_6107 | 0.00E+00 | 0.00E+00 |
| SCE1572_7241 | sce_3917 | 0.00E+00 | 0.00E+00 |
| SCE1572_7241 | sce_6093 | 0.00E+00 | 0.00E+00 |
| SCE1572_7241 | sce_3003 | 0.00E+00 | 0.00E+00 |
| SCE1572_7241 | sce_6535 | 0.00E+00 | 0.00E+00 |
| SCE1572_7241 | sce_6092 | 0.00E+00 | 0.00E+00 |
| SCE1572_7241 | sce_388 | 0.00E+00 | 0.00E+00 |

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| SCE1572_7241 | sce_6094 | 0.00E+00 | 0.00E+00 |
| SCE1572_7241 | sce_8602 | 0.00E+00 | 0.00E+00 |
| SCE1572_7241 | sce_6095 | 0.00E+00 | 0.00E+00 |
| SCE1572_7241 | sce_9920 | 0.00E+00 | 0.00E+00 |
| SCE1572_7241 | sce_7640 | 0.00E+00 | 0.00E+00 |
| SCE1572_7241 | sce_5835 | 0.00E+00 | 0.00E+00 |
| SCE1572_7241 | sce_10204 | 0.00E+00 | 0.00E+00 |
| SCE1572_7241 | sce_8618 | 0.00E+00 | 0.00E+00 |
| SCE1572_7242 | sce_5964 | 0.00E+00 | 0.00E+00 |
| SCE1572_7243 | sce_5965 | 0.00E+00 | 0.00E+00 |
| SCE1572_7245 | sce_5966 | 2.00E-47 | 2.00E-46 |
| SCE1572_7246 | sce_5968 | 6.00E-126 | 6.00E-126 |
| SCE1572_7248 | sce_5969 | 1.00E-35 | 1.00E-35 |
| SCE1572_7249 | sce_2378 | 0.00E+00 | 0.00E+00 |
| SCE1572_725 | sce_9985 | 5.00E-42 | 2.00E-27 |
| SCE1572_7250 | sce_2378 | 0.00E+00 | 0.00E+00 |
| SCE1572_7252 | sce_2379 | 6.00E-177 | 4.00E-171 |
| SCE1572_7253 | sce_2380 | 1.00E-60 | 9.00E-61 |
| SCE1572_7254 | sce_2382 | 3.00E-65 | 7.00E-34 |
| SCE1572_7255 | sce_5970 | 0.00E+00 | 0.00E+00 |
| SCE1572_7256 | sce_5971 | 1.00E-158 | 3.00E-177 |
| SCE1572_7257 | sce_5537 | 1.00E-30 | 4.00E-33 |
| SCE1572_7258 | sce_5972 | 4.00E-147 | 4.00E-147 |
| SCE1572_726 | sce_527 | 0.00E+00 | 0.00E+00 |
| SCE1572_7260 | sce_5973 | 3.00E-103 | 2.00E-111 |
| SCE1572_7263 | sce_5978 | 3.00E-97 | 4.00E-84 |
| SCE1572_7265 | sce_5979 | 0.00E+00 | 0.00E+00 |
| SCE1572_7268 | sce_5980 | 0.00E+00 | 0.00E+00 |
| SCE1572_7270 | sce_5982 | 0.00E+00 | 0.00E+00 |
| SCE1572_7271 | sce_6026 | 4.00E-68 | 3.00E-63 |
| SCE1572_7272 | sce_6025 | 1.00E-65 | 3.00E-73 |
| SCE1572_7275 | sce_6816 | 7.00E-76 | 1.00E-84 |
| SCE1572_7277 | sce_7693 | 2.00E-19 | 2.00E-19 |
| SCE1572_7279 | sce_629 | 2.00E-06 | 3.00E-06 |
| SCE1572_728 | sce_528 | 2.00E-158 | 1.00E-157 |
| SCE1572_7280 | sce_5983 | 1.00E-82 | 8.00E-65 |
| SCE1572_7281 | sce_5984 | 3.00E-79 | 1.00E-72 |
| SCE1572_7282 | sce_5986 | 7.00E-125 | 6.00E-129 |
| SCE1572_7283 | sce_5987 | 0.00E+00 | 0.00E+00 |
| SCE1572_7285 | sce_5988 | 0.00E+00 | 0.00E+00 |
| SCE1572_7286 | sce_5989 | 0.00E+00 | 0.00E+00 |
| SCE1572_7287 | sce_5990 | 3.00E-62 | 2.00E-62 |
| SCE1572_7288 | sce_6130 | 0.00E+00 | 0.00E+00 |
| SCE1572_729 | sce_529 | 3.00E-86 | 2.00E-81 |
| SCE1572_7290 | sce_5991 | 2.00E-120 | 2.00E-128 |
| SCE1572_7296 | sce_6071 | 8.00E-138 | 7.00E-142 |
| SCE1572_7297 | sce_6072 | 3.00E-34 | 5.00E-34 |
| SCE1572_7298 | sce_6074 | 0.00E+00 | 0.00E+00 |
| SCE1572_7299 | sce_3003 | 0.00E+00 | 0.00E+00 |
| SCE1572_7299 | sce_9920 | 0.00E+00 | 0.00E+00 |
| SCE1572_7299 | sce_6535 | 0.00E+00 | 0.00E+00 |
| SCE1572_7299 | sce_388 | 0.00E+00 | 0.00E+00 |
| SCE1572_7299 | sce_5835 | 0.00E+00 | 0.00E+00 |
| SCE1572_7299 | sce_9557 | 0.00E+00 | 0.00E+00 |
| SCE1572_7299 | sce_10204 | 0.00E+00 | 0.00E+00 |
| SCE1572_7299 | sce_7640 | 0.00E+00 | 0.00E+00 |
| SCE1572_7299 | sce_4513 | 0.00E+00 | 0.00E+00 |
| SCE1572_7299 | sce_3085 | 0.00E+00 | 0.00E+00 |
| SCE1572_7299 | sce_3917 | 0.00E+00 | 0.00E+00 |
| SCE1572_7299 | sce_6093 | 0.00E+00 | 0.00E+00 |
| SCE1572_7299 | sce_6092 | 0.00E+00 | 0.00E+00 |
| SCE1572_7299 | sce_6107 | 0.00E+00 | 0.00E+00 |
| SCE1572_7299 | sce_7661 | 0.00E+00 | 0.00E+00 |
| SCE1572_7299 | sce_8618 | 0.00E+00 | 0.00E+00 |
| SCE1572_7299 | sce_6095 | 0.00E+00 | 0.00E+00 |
| SCE1572_7299 | sce_2065 | 0.00E+00 | 0.00E+00 |
| SCE1572_7299 | sce_6094 | 0.00E+00 | 0.00E+00 |
| SCE1572_7299 | sce_7109 | 0.00E+00 | 0.00E+00 |
| SCE1572_73 | sce_66 | 0.00E+00 | 0.00E+00 |
| SCE1572_730 | sce_532 | 0.00E+00 | 0.00E+00 |
| SCE1572_7300 | sce_3004 | 3.00E-82 | 3.00E-82 |
| SCE1572_7302 | sce_2466 | 3.00E-09 | 1.00E-09 |
| SCE1572_7303 | sce_5169 | 1.00E-92 | 4.00E-95 |
| SCE1572_7304 | sce_5168 | 3.00E-119 | 1.00E-121 |
| SCE1572_7305 | sce_2493 | 9.00E-138 | 5.00E-144 |
| SCE1572_7308 | sce_10414 | 1.00E-14 | 7.00E-14 |

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| SCE1572_7309 | sce_4708 | 0.00E+00 | 0.00E+00 |
| SCE1572_7309 | sce_6222 | 0.00E+00 | 0.00E+00 |
| SCE1572_731 | sce_533 | 2.00E-113 | 5.00E-116 |
| SCE1572_7310 | sce_6091 | 3.00E-141 | 5.00E-155 |
| SCE1572_7311 | sce_6095 | 0.00E+00 | 0.00E+00 |
| SCE1572_7311 | sce_6093 | 0.00E+00 | 0.00E+00 |
| SCE1572_7311 | sce_6092 | 0.00E+00 | 0.00E+00 |
| SCE1572_7311 | sce_6094 | 0.00E+00 | 0.00E+00 |
| SCE1572_7311 | sce_6107 | 0.00E+00 | 0.00E+00 |
| SCE1572_7311 | sce_3917 | 0.00E+00 | 0.00E+00 |
| SCE1572_7311 | sce_7661 | 0.00E+00 | 0.00E+00 |
| SCE1572_7311 | sce_388 | 0.00E+00 | 0.00E+00 |
| SCE1572_7311 | sce_9920 | 0.00E+00 | 0.00E+00 |
| SCE1572_7311 | sce_6535 | 0.00E+00 | 0.00E+00 |
| SCE1572_7311 | sce_4513 | 0.00E+00 | 0.00E+00 |
| SCE1572_7311 | sce_3003 | 0.00E+00 | 0.00E+00 |
| SCE1572_7311 | sce_9557 | 0.00E+00 | 0.00E+00 |
| SCE1572_7311 | sce_10204 | 0.00E+00 | 0.00E+00 |
| SCE1572_7311 | sce_8602 | 0.00E+00 | 0.00E+00 |
| SCE1572_7311 | sce_7640 | 0.00E+00 | 0.00E+00 |
| SCE1572_7311 | sce_5835 | 0.00E+00 | 0.00E+00 |
| SCE1572_7319 | sce_6109 | 4.00E-70 | 7.00E-67 |
| SCE1572_732 | sce_534 | 3.00E-180 | 8.00E-179 |
| SCE1572_7321 | sce_6110 | 4.00E-18 | 4.00E-18 |
| SCE1572_7323 | sce_6111 | 5.00E-38 | 8.00E-37 |
| SCE1572_7325 | sce_6112 | 6.00E-179 | 3.00E-178 |
| SCE1572_7326 | sce_6113 | 7.00E-159 | 1.00E-145 |
| SCE1572_7327 | sce_6114 | 0.00E+00 | 0.00E+00 |
| SCE1572_7327 | sce_6541 | 0.00E+00 | 0.00E+00 |
| SCE1572_7329 | sce_6116 | 2.00E-60 | 2.00E-55 |
| SCE1572_733 | sce_536 | 3.00E-121 | 2.00E-131 |
| SCE1572_7330 | sce_6117 | 0.00E+00 | 0.00E+00 |
| SCE1572_7332 | sce_6119 | 0.00E+00 | 0.00E+00 |
| SCE1572_7334 | sce_6120 | 0.00E+00 | 0.00E+00 |
| SCE1572_7336 | sce_6121 | 0.00E+00 | 0.00E+00 |
| SCE1572_7337 | sce_6122 | 0.00E+00 | 0.00E+00 |
| SCE1572_7338 | sce_6123 | 6.00E-163 | 7.00E-164 |
| SCE1572_7339 | sce_6124 | 7.00E-47 | 7.00E-49 |
| SCE1572_734 | sce_537 | 0.00E+00 | 0.00E+00 |
| SCE1572_7340 | sce_6125 | 2.00E-102 | 2.00E-101 |
| SCE1572_7341 | sce_6126 | 0.00E+00 | 0.00E+00 |
| SCE1572_7342 | sce_6127 | 0.00E+00 | 0.00E+00 |
| SCE1572_7343 | sce_4461 | 0.00E+00 | 0.00E+00 |
| SCE1572_7348 | sce_6131 | 2.00E-88 | 3.00E-88 |
| SCE1572_7349 | sce_6132 | 3.00E-58 | 1.00E-64 |
| SCE1572_735 | sce_538 | 9.00E-88 | 4.00E-101 |
| SCE1572_7350 | sce_6133 | 4.00E-56 | 2.00E-75 |
| SCE1572_7351 | sce_6134 | 5.00E-77 | 3.00E-54 |
| SCE1572_7352 | sce_6135 | 6.00E-115 | 2.00E-116 |
| SCE1572_7357 | sce_6139 | 3.00E-113 | 3.00E-129 |
| SCE1572_7358 | sce_6140 | 8.00E-137 | 8.00E-137 |
| SCE1572_736 | sce_539 | 2.00E-102 | 7.00E-105 |
| SCE1572_7360 | sce_6141 | 0.00E+00 | 0.00E+00 |
| SCE1572_7361 | sce_6142 | 6.00E-108 | 2.00E-90 |
| SCE1572_7363 | sce_6144 | 0.00E+00 | 0.00E+00 |
| SCE1572_7364 | sce_6145 | 0.00E+00 | 0.00E+00 |
| SCE1572_7365 | sce_2350 | 0.00E+00 | 0.00E+00 |
| SCE1572_7366 | sce_6146 | 6.00E-160 | 7.00E-163 |
| SCE1572_7367 | sce_6147 | 0.00E+00 | 0.00E+00 |
| SCE1572_7368 | sce_6148 | 2.00E-74 | 1.00E-82 |
| SCE1572_7369 | sce_6149 | 1.00E-30 | 1.00E-33 |
| SCE1572_7370 | sce_6150 | 0.00E+00 | 0.00E+00 |
| SCE1572_7371 | sce_6151 | 2.00E-46 | 1.00E-52 |
| SCE1572_7372 | sce_6153 | 0.00E+00 | 0.00E+00 |
| SCE1572_7377 | sce_6154 | 0.00E+00 | 0.00E+00 |
| SCE1572_7379 | sce_7617 | 7.00E-31 | 3.00E-31 |
| SCE1572_738 | sce_540 | 1.00E-171 | 3.00E-166 |
| SCE1572_7380 | sce_868 | 1.00E-179 | 0.00E+00 |
| SCE1572_7384 | sce_2434 | 9.00E-168 | 6.00E-161 |
| SCE1572_7387 | sce_6155 | 2.00E-160 | 2.00E-160 |
| SCE1572_7388 | sce_6156 | 6.00E-155 | 8.00E-150 |
| SCE1572_739 | sce_541 | 0.00E+00 | 0.00E+00 |
| SCE1572_7390 | sce_7829 | 6.00E-49 | 3.00E-50 |
| SCE1572_7391 | sce_7831 | 1.00E-149 | 4.00E-152 |
| SCE1572_7393 | sce_7832 | 5.00E-60 | 4.00E-60 |
| SCE1572_7394 | sce_7833 | 3.00E-74 | 3.00E-76 |

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| SCE1572_7395 | sce_7834 | 1.00E-103 | 1.00E-96 |
| SCE1572_7396 | sce_6157 | 9.00E-92 | 1.00E-89 |
| SCE1572_7397 | sce_6158 | 5.00E-126 | 1.00E-125 |
| SCE1572_7398 | sce_6159 | 0.00E+00 | 0.00E+00 |
| SCE1572_7399 | sce_6161 | 1.00E-66 | 2.00E-51 |
| SCE1572_74 | sce_67 | 5.00E-119 | 4.00E-106 |
| SCE1572_740 | sce_542 | 3.00E-54 | 4.00E-42 |
| SCE1572_7400 | sce_6162 | 4.00E-141 | 9.00E-142 |
| SCE1572_7403 | sce_6163 | 5.00E-151 | 2.00E-150 |
| SCE1572_7404 | sce_6164 | 6.00E-67 | 5.00E-67 |
| SCE1572_7405 | sce_6165 | 8.00E-73 | 1.00E-72 |
| SCE1572_7406 | sce_6166 | 2.00E-88 | 2.00E-71 |
| SCE1572_7408 | sce_6167 | 7.00E-110 | 7.00E-110 |
| SCE1572_741 | sce_543 | 8.00E-85 | 1.00E-96 |
| SCE1572_7411 | sce_6169 | 4.00E-58 | 6.00E-61 |
| SCE1572_7412 | sce_6170 | 1.00E-165 | 1.00E-161 |
| SCE1572_7413 | sce_6171 | 0.00E+00 | 0.00E+00 |
| SCE1572_7416 | sce_6172 | 6.00E-140 | 8.00E-151 |
| SCE1572_7417 | sce_6173 | 0.00E+00 | 0.00E+00 |
| SCE1572_742 | sce_544 | 4.00E-156 | 4.00E-157 |
| SCE1572_7420 | sce_6175 | 1.00E-127 | 3.00E-132 |
| SCE1572_7423 | sce_6176 | 3.00E-39 | 1.00E-46 |
| SCE1572_7424 | sce_6177 | 2.00E-127 | 2.00E-127 |
| SCE1572_7425 | sce_6178 | 2.00E-76 | 2.00E-74 |
| SCE1572_7427 | sce_5086 | 0.00E+00 | 0.00E+00 |
| SCE1572_7427 | sce_5085 | 0.00E+00 | 0.00E+00 |
| SCE1572_7427 | sce_6701 | 0.00E+00 | 0.00E+00 |
| SCE1572_7427 | sce_3793 | 0.00E+00 | 0.00E+00 |
| SCE1572_7428 | sce_6179 | 0.00E+00 | 0.00E+00 |
| SCE1572_7429 | sce_6180 | 2.00E-153 | 5.00E-147 |
| SCE1572_743 | sce_545 | 5.00E-85 | 2.00E-110 |
| SCE1572_7430 | sce_3028 | 0.00E+00 | 0.00E+00 |
| SCE1572_7431 | sce_4600 | 5.00E-96 | 3.00E-109 |
| SCE1572_7432 | sce_6207 | 5.00E-66 | 5.00E-69 |
| SCE1572_7433 | sce_6208 | 1.00E-34 | 3.00E-35 |
| SCE1572_7434 | sce_6211 | 2.00E-43 | 2.00E-43 |
| SCE1572_7435 | sce_6212 | 1.00E-177 | 0.00E+00 |
| SCE1572_7436 | sce_8363 | 6.00E-29 | 2.00E-29 |
| SCE1572_7438 | sce_6218 | 4.00E-105 | 3.00E-106 |
| SCE1572_7443 | sce_5549 | 7.00E-66 | 2.00E-65 |
| SCE1572_7446 | sce_6219 | 2.00E-32 | 2.00E-32 |
| SCE1572_7448 | sce_6220 | 0.00E+00 | 0.00E+00 |
| SCE1572_7449 | sce_6221 | 0.00E+00 | 0.00E+00 |
| SCE1572_745 | sce_548 | 0.00E+00 | 0.00E+00 |
| SCE1572_7453 | sce_6235 | 0.00E+00 | 0.00E+00 |
| SCE1572_7453 | sce_2161 | 0.00E+00 | 0.00E+00 |
| SCE1572_7453 | sce_225 | 0.00E+00 | 0.00E+00 |
| SCE1572_7453 | sce_8357 | 0.00E+00 | 0.00E+00 |
| SCE1572_7453 | sce_5276 | 0.00E+00 | 0.00E+00 |
| SCE1572_7454 | sce_6238 | 4.00E-106 | 6.00E-96 |
| SCE1572_7455 | sce_6239 | 3.00E-159 | 1.00E-149 |
| SCE1572_7456 | sce_6240 | 0.00E+00 | 3.00E-174 |
| SCE1572_7457 | sce_6241 | 4.00E-73 | 8.00E-85 |
| SCE1572_7458 | sce_6242 | 4.00E-160 | 3.00E-163 |
| SCE1572_746 | sce_549 | 0.00E+00 | 0.00E+00 |
| SCE1572_746 | sce_3665 | 0.00E+00 | 0.00E+00 |
| SCE1572_7460 | sce_6244 | 4.00E-25 | 2.00E-30 |
| SCE1572_7461 | sce_6246 | 0.00E+00 | 0.00E+00 |
| SCE1572_7462 | sce_6247 | 4.00E-126 | 3.00E-126 |
| SCE1572_7463 | sce_6248 | 3.00E-150 | 1.00E-161 |
| SCE1572_7464 | sce_6249 | 1.00E-115 | 3.00E-112 |
| SCE1572_7465 | sce_6250 | 2.00E-107 | 1.00E-107 |
| SCE1572_7467 | sce_6263 | 4.00E-176 | 3.00E-176 |
| SCE1572_7468 | sce_6264 | 4.00E-23 | 5.00E-24 |
| SCE1572_7469 | sce_6265 | 8.00E-136 | 5.00E-139 |
| SCE1572_7470 | sce_6266 | 2.00E-118 | 8.00E-116 |
| SCE1572_7472 | sce_6268 | 8.00E-102 | 8.00E-102 |
| SCE1572_7473 | sce_6269 | 0.00E+00 | 0.00E+00 |
| SCE1572_7474 | sce_6270 | 5.00E-94 | 5.00E-94 |
| SCE1572_7475 | sce_6271 | 0.00E+00 | 0.00E+00 |
| SCE1572_7477 | sce_6273 | 3.00E-120 | 9.00E-136 |
| SCE1572_7478 | sce_6275 | 4.00E-67 | 5.00E-67 |
| SCE1572_7479 | sce_6276 | 0.00E+00 | 0.00E+00 |
| SCE1572_748 | sce_551 | 2.00E-75 | 8.00E-76 |
| SCE1572_7480 | sce_6278 | 4.00E-65 | 1.00E-66 |
| SCE1572_7481 | sce_6279 | 7.00E-12 | 5.00E-12 |

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| SCE1572_7482 | sce_6280 | 8.00E-18 | 1.00E-24 |
| SCE1572_7483 | sce_6281 | 0.00E+00 | 0.00E+00 |
| SCE1572_7483 | sce_9625 | 0.00E+00 | 0.00E+00 |
| SCE1572_7483 | sce_5292 | 0.00E+00 | 0.00E+00 |
| SCE1572_7485 | sce_6306 | 0.00E+00 | 0.00E+00 |
| SCE1572_7487 | sce_615 | 0.00E+00 | 0.00E+00 |
| SCE1572_749 | sce_4659 | 4.00E-105 | 2.00E-102 |
| SCE1572_7492 | sce_7123 | 1.00E-42 | 8.00E-42 |
| SCE1572_7493 | sce_6083 | 3.00E-175 | 2.00E-159 |
| SCE1572_75 | sce_68 | 1.00E-79 | 1.00E-81 |
| SCE1572_750 | sce_552 | 0.00E+00 | 0.00E+00 |
| SCE1572_7500 | sce_6307 | 2.00E-60 | 1.00E-60 |
| SCE1572_7501 | sce_6309 | 9.00E-155 | 1.00E-154 |
| SCE1572_7502 | sce_6310 | 9.00E-92 | 9.00E-95 |
| SCE1572_7503 | sce_6313 | 9.00E-157 | 1.00E-156 |
| SCE1572_7504 | sce_6314 | 3.00E-40 | 1.00E-44 |
| SCE1572_7505 | sce_6315 | 3.00E-176 | 3.00E-177 |
| SCE1572_7506 | sce_8592 | 0.00E+00 | 0.00E+00 |
| SCE1572_7506 | sce_3937 | 0.00E+00 | 0.00E+00 |
| SCE1572_7508 | sce_3937 | 0.00E+00 | 0.00E+00 |
| SCE1572_751 | sce_553 | 1.00E-85 | 2.00E-84 |
| SCE1572_7515 | sce_6331 | 3.00E-50 | 5.00E-59 |
| SCE1572_7516 | sce_6332 | 4.00E-45 | 7.00E-41 |
| SCE1572_7517 | sce_6344 | 0.00E+00 | 0.00E+00 |
| SCE1572_7518 | sce_6345 | 0.00E+00 | 0.00E+00 |
| SCE1572_7519 | sce_6346 | 5.00E-81 | 5.00E-81 |
| SCE1572_752 | sce_554 | 7.00E-25 | 9.00E-29 |
| SCE1572_7520 | sce_6347 | 4.00E-83 | 1.00E-83 |
| SCE1572_7524 | sce_6348 | 1.00E-45 | 2.00E-45 |
| SCE1572_7525 | sce_6349 | 0.00E+00 | 0.00E+00 |
| SCE1572_7527 | sce_6351 | 6.00E-173 | 2.00E-177 |
| SCE1572_7528 | sce_6352 | 0.00E+00 | 0.00E+00 |
| SCE1572_753 | sce_555 | 7.00E-126 | 3.00E-126 |
| SCE1572_7530 | sce_6375 | 3.00E-149 | 9.00E-150 |
| SCE1572_7531 | sce_6373 | 1.00E-08 | 4.00E-09 |
| SCE1572_7534 | sce_6381 | 2.00E-21 | 1.00E-20 |
| SCE1572_7535 | sce_6382 | 0.00E+00 | 0.00E+00 |
| SCE1572_7536 | sce_6383 | 0.00E+00 | 0.00E+00 |
| SCE1572_7537 | sce_6401 | 5.00E-27 | 5.00E-28 |
| SCE1572_7538 | sce_6403 | 0.00E+00 | 0.00E+00 |
| SCE1572_7539 | sce_6404 | 2.00E-23 | 3.00E-32 |
| SCE1572_754 | sce_556 | 8.00E-168 | 8.00E-168 |
| SCE1572_7540 | sce_6405 | 3.00E-177 | 8.00E-176 |
| SCE1572_7541 | sce_6406 | 1.00E-50 | 7.00E-45 |
| SCE1572_7542 | sce_6407 | 1.00E-74 | 4.00E-82 |
| SCE1572_7543 | sce_6408 | 0.00E+00 | 0.00E+00 |
| SCE1572_7544 | sce_6409 | 7.00E-78 | 3.00E-95 |
| SCE1572_7545 | sce_9213 | 0.00E+00 | 0.00E+00 |
| SCE1572_7546 | sce_9212 | 0.00E+00 | 0.00E+00 |
| SCE1572_7547 | sce_9211 | 7.00E-158 | 5.00E-153 |
| SCE1572_7548 | sce_9210 | 5.00E-147 | 8.00E-154 |
| SCE1572_7549 | sce_5154 | 0.00E+00 | 0.00E+00 |
| SCE1572_755 | sce_557 | 4.00E-37 | 2.00E-33 |
| SCE1572_7550 | sce_5153 | 0.00E+00 | 0.00E+00 |
| SCE1572_7552 | sce_6410 | 2.00E-97 | 2.00E-77 |
| SCE1572_7553 | sce_6411 | 3.00E-66 | 3.00E-66 |
| SCE1572_7554 | sce_6412 | 1.00E-94 | 8.00E-106 |
| SCE1572_7555 | sce_6413 | 8.00E-45 | 2.00E-69 |
| SCE1572_7557 | sce_6415 | 3.00E-74 | 4.00E-82 |
| SCE1572_7559 | sce_3680 | 0.00E+00 | 0.00E+00 |
| SCE1572_7560 | sce_9660 | 3.00E-165 | 2.00E-178 |
| SCE1572_7562 | sce_1286 | 2.00E-30 | 5.00E-39 |
| SCE1572_7563 | sce_5995 | 0.00E+00 | 0.00E+00 |
| SCE1572_7566 | sce_6421 | 8.00E-62 | 2.00E-62 |
| SCE1572_7567 | sce_6422 | 3.00E-103 | 7.00E-68 |
| SCE1572_7568 | sce_6423 | 2.00E-107 | 3.00E-105 |
| SCE1572_7569 | sce_6424 | 0.00E+00 | 0.00E+00 |
| SCE1572_757 | sce_558 | 1.00E-121 | 1.00E-121 |
| SCE1572_7571 | sce_6425 | 0.00E+00 | 0.00E+00 |
| SCE1572_7572 | sce_6427 | 4.00E-29 | 6.00E-20 |
| SCE1572_7573 | sce_6428 | 2.00E-111 | 1.00E-109 |
| SCE1572_7574 | sce_6429 | 1.00E-96 | 5.00E-106 |
| SCE1572_7575 | sce_6430 | 0.00E+00 | 0.00E+00 |
| SCE1572_7576 | sce_6431 | 0.00E+00 | 0.00E+00 |
| SCE1572_7577 | sce_6432 | 4.00E-76 | 4.00E-76 |
| SCE1572_7578 | sce_6433 | 2.00E-50 | 2.00E-50 |

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| SCE1572_7579 | sce_6435 | 0.00E+00 | 0.00E+00 |
| SCE1572_758 | sce_559 | 3.00E-93 | 1.00E-103 |
| SCE1572_7580 | sce_6436 | 6.00E-132 | 1.00E-145 |
| SCE1572_7581 | sce_6437 | 0.00E+00 | 0.00E+00 |
| SCE1572_7581 | sce_831 | 0.00E+00 | 0.00E+00 |
| SCE1572_7582 | sce_6438 | 2.00E-87 | 2.00E-94 |
| SCE1572_7583 | sce_6439 | 2.00E-149 | 2.00E-156 |
| SCE1572_7584 | sce_6440 | 2.00E-16 | 2.00E-16 |
| SCE1572_7585 | sce_6441 | 3.00E-46 | 3.00E-46 |
| SCE1572_7586 | sce_6442 | 9.00E-53 | 6.00E-51 |
| SCE1572_7587 | sce_6443 | 3.00E-161 | 3.00E-159 |
| SCE1572_7588 | sce_6444 | 5.00E-78 | 8.00E-79 |
| SCE1572_7589 | sce_6448 | 1.00E-138 | 1.00E-138 |
| SCE1572_759 | sce_560 | 4.00E-93 | 4.00E-93 |
| SCE1572_7590 | sce_6449 | 0.00E+00 | 0.00E+00 |
| SCE1572_7591 | sce_6450 | 0.00E+00 | 0.00E+00 |
| SCE1572_7592 | sce_6451 | 0.00E+00 | 0.00E+00 |
| SCE1572_7593 | sce_6452 | 0.00E+00 | 0.00E+00 |
| SCE1572_7594 | sce_6453 | 2.00E-43 | 2.00E-43 |
| SCE1572_7595 | sce_6454 | 6.00E-165 | 4.00E-165 |
| SCE1572_7596 | sce_6455 | 0.00E+00 | 8.00E-154 |
| SCE1572_7597 | sce_6456 | 7.00E-73 | 7.00E-73 |
| SCE1572_7599 | sce_6458 | 3.00E-51 | 4.00E-52 |
| SCE1572_760 | sce_561 | 0.00E+00 | 0.00E+00 |
| SCE1572_7600 | sce_6461 | 9.00E-124 | 4.00E-142 |
| SCE1572_7601 | sce_6462 | 6.00E-178 | 5.00E-176 |
| SCE1572_7602 | sce_6463 | 0.00E+00 | 0.00E+00 |
| SCE1572_7603 | sce_6464 | 0.00E+00 | 0.00E+00 |
| SCE1572_7604 | sce_6465 | 1.00E-64 | 6.00E-65 |
| SCE1572_7606 | sce_9946 | 1.00E-160 | 1.00E-175 |
| SCE1572_7607 | sce_6467 | 5.00E-109 | 6.00E-107 |
| SCE1572_7609 | sce_6470 | 4.00E-56 | 2.00E-49 |
| SCE1572_761 | sce_562 | 1.00E-95 | 3.00E-101 |
| SCE1572_7610 | sce_6471 | 4.00E-117 | 4.00E-117 |
| SCE1572_7611 | sce_6472 | 1.00E-61 | 2.00E-61 |
| SCE1572_7612 | sce_6473 | 0.00E+00 | 0.00E+00 |
| SCE1572_7613 | sce_6475 | 8.00E-88 | 6.00E-84 |
| SCE1572_7614 | sce_6476 | 2.00E-114 | 4.00E-117 |
| SCE1572_7617 | sce_6477 | 2.00E-134 | 2.00E-134 |
| SCE1572_7618 | sce_6478 | 5.00E-120 | 5.00E-120 |
| SCE1572_7619 | sce_6479 | 3.00E-157 | 3.00E-157 |
| SCE1572_762 | sce_92 | 0.00E+00 | 0.00E+00 |
| SCE1572_7620 | sce_6480 | 1.00E-149 | 9.00E-158 |
| SCE1572_7621 | sce_6481 | 1.00E-139 | 3.00E-127 |
| SCE1572_7622 | sce_6482 | 0.00E+00 | 0.00E+00 |
| SCE1572_7623 | sce_6483 | 1.00E-151 | 9.00E-144 |
| SCE1572_7624 | sce_6484 | 0.00E+00 | 0.00E+00 |
| SCE1572_7625 | sce_6486 | 0.00E+00 | 0.00E+00 |
| SCE1572_7626 | sce_6487 | 3.00E-78 | 1.00E-77 |
| SCE1572_7627 | sce_7919 | 1.00E-09 | 6.00E-10 |
| SCE1572_7628 | sce_6488 | 6.00E-139 | 4.00E-140 |
| SCE1572_7629 | sce_6489 | 1.00E-126 | 1.00E-126 |
| SCE1572_7630 | sce_6491 | 2.00E-56 | 8.00E-50 |
| SCE1572_7631 | sce_6492 | 2.00E-53 | 4.00E-56 |
| SCE1572_7632 | sce_6493 | 0.00E+00 | 0.00E+00 |
| SCE1572_7634 | sce_6494 | 3.00E-75 | 6.00E-74 |
| SCE1572_7635 | sce_6495 | 0.00E+00 | 0.00E+00 |
| SCE1572_7636 | sce_6496 | 1.00E-71 | 1.00E-81 |
| SCE1572_7637 | sce_6497 | 0.00E+00 | 0.00E+00 |
| SCE1572_7638 | sce_6498 | 3.00E-108 | 6.00E-116 |
| SCE1572_7639 | sce_6499 | 0.00E+00 | 0.00E+00 |
| SCE1572_764 | sce_563 | 0.00E+00 | 0.00E+00 |
| SCE1572_7640 | sce_6500 | 2.00E-72 | 9.00E-71 |
| SCE1572_7641 | sce_6501 | 0.00E+00 | 0.00E+00 |
| SCE1572_7641 | sce_736 | 0.00E+00 | 0.00E+00 |
| SCE1572_7643 | sce_6502 | 0.00E+00 | 1.00E-179 |
| SCE1572_7644 | sce_6504 | 0.00E+00 | 0.00E+00 |
| SCE1572_7645 | sce_6505 | 0.00E+00 | 0.00E+00 |
| SCE1572_7646 | sce_6506 | 0.00E+00 | 0.00E+00 |
| SCE1572_7647 | sce_9653 | 0.00E+00 | 0.00E+00 |
| SCE1572_7648 | sce_2926 | 0.00E+00 | 0.00E+00 |
| SCE1572_765 | sce_2573 | 3.00E-26 | 2.00E-26 |
| SCE1572_7654 | sce_8663 | 3.00E-12 | 7.00E-10 |
| SCE1572_7655 | sce_8662 | 1.00E-41 | 2.00E-24 |
| SCE1572_7659 | sce_9782 | 8.00E-45 | 2.00E-45 |
| SCE1572_7662 | sce_9807 | 1.00E-60 | 9.00E-69 |

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| SCE1572_7665 | sce_1677 | 3.00E-127 | 2.00E-126 |
| SCE1572_7667 | sce_2109 | 2.00E-12 | 6.00E-13 |
| SCE1572_767 | sce_565 | 4.00E-147 | 7.00E-133 |
| SCE1572_7677 | sce_6508 | 0.00E+00 | 0.00E+00 |
| SCE1572_7678 | sce_6509 | 2.00E-55 | 2.00E-55 |
| SCE1572_7679 | sce_6510 | 5.00E-81 | 4.00E-80 |
| SCE1572_768 | sce_566 | 5.00E-180 | 1.00E-163 |
| SCE1572_7680 | sce_6511 | 3.00E-127 | 1.00E-134 |
| SCE1572_7681 | sce_6512 | 7.00E-129 | 3.00E-147 |
| SCE1572_7682 | sce_6513 | 1.00E-76 | 4.00E-82 |
| SCE1572_7683 | sce_6514 | 0.00E+00 | 0.00E+00 |
| SCE1572_7685 | sce_6515 | 5.00E-34 | 4.00E-63 |
| SCE1572_7687 | sce_6516 | 3.00E-117 | 5.00E-126 |
| SCE1572_769 | sce_567 | 1.00E-52 | 7.00E-56 |
| SCE1572_7691 | sce_6517 | 3.00E-71 | 7.00E-70 |
| SCE1572_7692 | sce_6518 | 6.00E-160 | 3.00E-173 |
| SCE1572_7693 | sce_6519 | 4.00E-116 | 3.00E-120 |
| SCE1572_7694 | sce_6520 | 0.00E+00 | 0.00E+00 |
| SCE1572_7695 | sce_6521 | 7.00E-83 | 2.00E-101 |
| SCE1572_7696 | sce_6522 | 2.00E-117 | 2.00E-120 |
| SCE1572_7697 | sce_6523 | 4.00E-176 | 1.00E-172 |
| SCE1572_7698 | sce_6524 | 6.00E-145 | 3.00E-150 |
| SCE1572_7699 | sce_6525 | 1.00E-124 | 7.00E-125 |
| SCE1572_77 | sce_69 | 1.00E-169 | 9.00E-177 |
| SCE1572_770 | sce_568 | 8.00E-101 | 8.00E-101 |
| SCE1572_7700 | sce_6526 | 2.00E-165 | 7.00E-159 |
| SCE1572_7701 | sce_6527 | 5.00E-27 | 1.00E-29 |
| SCE1572_7702 | sce_6528 | 0.00E+00 | 0.00E+00 |
| SCE1572_7703 | sce_6536 | 4.00E-113 | 2.00E-121 |
| SCE1572_7704 | sce_6537 | 1.00E-37 | 3.00E-34 |
| SCE1572_7706 | sce_6538 | 0.00E+00 | 0.00E+00 |
| SCE1572_7707 | sce_6539 | 0.00E+00 | 0.00E+00 |
| SCE1572_7709 | sce_6541 | 0.00E+00 | 0.00E+00 |
| SCE1572_7709 | sce_6114 | 0.00E+00 | 0.00E+00 |
| SCE1572_771 | sce_569 | 1.00E-157 | 2.00E-139 |
| SCE1572_7710 | sce_6542 | 2.00E-84 | 2.00E-88 |
| SCE1572_7711 | sce_6543 | 1.00E-71 | 3.00E-70 |
| SCE1572_7712 | sce_6544 | 3.00E-120 | 5.00E-153 |
| SCE1572_7713 | sce_6545 | 1.00E-63 | 5.00E-62 |
| SCE1572_7718 | sce_6546 | 1.00E-139 | 1.00E-162 |
| SCE1572_7719 | sce_6547 | 4.00E-97 | 1.00E-99 |
| SCE1572_772 | sce_570 | 4.00E-129 | 2.00E-135 |
| SCE1572_7720 | sce_6548 | 1.00E-139 | 8.00E-142 |
| SCE1572_7723 | sce_6549 | 4.00E-153 | 3.00E-147 |
| SCE1572_7724 | sce_6550 | 0.00E+00 | 0.00E+00 |
| SCE1572_7725 | sce_6551 | 0.00E+00 | 0.00E+00 |
| SCE1572_7726 | sce_6552 | 2.00E-59 | 3.00E-59 |
| SCE1572_7727 | sce_6553 | 0.00E+00 | 0.00E+00 |
| SCE1572_7729 | sce_6554 | 1.00E-76 | 1.00E-85 |
| SCE1572_773 | sce_571 | 2.00E-97 | 5.00E-100 |
| SCE1572_7730 | sce_6555 | 3.00E-102 | 1.00E-99 |
| SCE1572_7731 | sce_6556 | 9.00E-51 | 9.00E-51 |
| SCE1572_7732 | sce_6557 | 5.00E-82 | 2.00E-67 |
| SCE1572_7733 | sce_6558 | 8.00E-111 | 4.00E-102 |
| SCE1572_7735 | sce_6560 | 1.00E-51 | 1.00E-51 |
| SCE1572_7736 | sce_6561 | 4.00E-107 | 2.00E-113 |
| SCE1572_7737 | sce_6562 | 6.00E-51 | 2.00E-64 |
| SCE1572_7738 | sce_6563 | 2.00E-130 | 0.00E+00 |
| SCE1572_774 | sce_572 | 0.00E+00 | 0.00E+00 |
| SCE1572_7740 | sce_6564 | 0.00E+00 | 0.00E+00 |
| SCE1572_7741 | sce_6565 | 3.00E-162 | 1.00E-158 |
| SCE1572_7742 | sce_6566 | 0.00E+00 | 0.00E+00 |
| SCE1572_7743 | sce_6567 | 9.00E-138 | 4.00E-135 |
| SCE1572_7744 | sce_6568 | 1.00E-155 | 1.00E-155 |
| SCE1572_7745 | sce_6569 | 6.00E-51 | 2.00E-48 |
| SCE1572_7746 | sce_6571 | 0.00E+00 | 0.00E+00 |
| SCE1572_7746 | sce_8649 | 0.00E+00 | 0.00E+00 |
| SCE1572_7747 | sce_6572 | 5.00E-139 | 5.00E-139 |
| SCE1572_775 | sce_573 | 6.00E-54 | 4.00E-54 |
| SCE1572_7758 | sce_6574 | 3.00E-76 | 1.00E-89 |
| SCE1572_7759 | sce_6577 | 0.00E+00 | 0.00E+00 |
| SCE1572_7760 | sce_6578 | 0.00E+00 | 0.00E+00 |
| SCE1572_7761 | sce_6579 | 1.00E-51 | 2.00E-50 |
| SCE1572_7765 | sce_6583 | 1.00E-46 | 1.00E-46 |
| SCE1572_7766 | sce_6584 | 0.00E+00 | 0.00E+00 |
| SCE1572_7768 | sce_6585 | 0.00E+00 | 0.00E+00 |

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| SCE1572_7768 | sce_900 | 0.00E+00 | 0.00E+00 |
| SCE1572_7769 | sce_6586 | 3.00E-134 | 3.00E-144 |
| SCE1572_777 | sce_574 | 6.00E-98 | 1.00E-96 |
| SCE1572_7770 | sce_6587 | 0.00E+00 | 0.00E+00 |
| SCE1572_7771 | sce_6588 | 1.00E-127 | 1.00E-115 |
| SCE1572_7772 | sce_6589 | 2.00E-47 | 7.00E-41 |
| SCE1572_7773 | sce_6590 | 1.00E-51 | 1.00E-51 |
| SCE1572_7777 | sce_512 | 1.00E-75 | 8.00E-77 |
| SCE1572_778 | sce_575 | 1.00E-150 | 3.00E-144 |
| SCE1572_7784 | sce_518 | 5.00E-155 | 7.00E-144 |
| SCE1572_779 | sce_576 | 0.00E+00 | 0.00E+00 |
| SCE1572_7790 | sce_6596 | 4.00E-19 | 3.00E-18 |
| SCE1572_7791 | sce_6597 | 3.00E-114 | 8.00E-116 |
| SCE1572_7792 | sce_6598 | 8.00E-74 | 8.00E-74 |
| SCE1572_7793 | sce_6599 | 0.00E+00 | 0.00E+00 |
| SCE1572_7794 | sce_6600 | 4.00E-64 | 8.00E-77 |
| SCE1572_7795 | sce_6601 | 8.00E-114 | 2.00E-125 |
| SCE1572_7798 | sce_6602 | 2.00E-08 | 6.00E-16 |
| SCE1572_78 | sce_70 | 2.00E-58 | 4.00E-59 |
| SCE1572_7800 | sce_6605 | 0.00E+00 | 0.00E+00 |
| SCE1572_7801 | sce_6606 | 0.00E+00 | 0.00E+00 |
| SCE1572_7802 | sce_6607 | 7.00E-106 | 4.00E-108 |
| SCE1572_7803 | sce_6608 | 8.00E-16 | 3.00E-09 |
| SCE1572_7804 | sce_6609 | 0.00E+00 | 0.00E+00 |
| SCE1572_7805 | sce_6610 | 0.00E+00 | 0.00E+00 |
| SCE1572_7806 | sce_6611 | 1.00E-164 | 5.00E-165 |
| SCE1572_7807 | sce_6612 | 0.00E+00 | 0.00E+00 |
| SCE1572_7808 | sce_6613 | 0.00E+00 | 0.00E+00 |
| SCE1572_7810 | sce_6614 | 1.00E-58 | 5.00E-58 |
| SCE1572_7811 | sce_6615 | 3.00E-108 | 3.00E-108 |
| SCE1572_7812 | sce_6616 | 2.00E-103 | 2.00E-103 |
| SCE1572_7814 | sce_6617 | 3.00E-47 | 2.00E-47 |
| SCE1572_7815 | sce_6618 | 0.00E+00 | 0.00E+00 |
| SCE1572_7815 | sce_3121 | 0.00E+00 | 0.00E+00 |
| SCE1572_7816 | sce_6619 | 3.00E-89 | 3.00E-89 |
| SCE1572_7817 | sce_6620 | 3.00E-96 | 3.00E-96 |
| SCE1572_7818 | sce_6621 | 5.00E-107 | 6.00E-123 |
| SCE1572_7819 | sce_6622 | 0.00E+00 | 0.00E+00 |
| SCE1572_782 | sce_577 | 5.00E-99 | 4.00E-97 |
| SCE1572_7820 | sce_6623 | 3.00E-141 | 1.00E-139 |
| SCE1572_7821 | sce_6624 | 1.00E-85 | 3.00E-92 |
| SCE1572_7822 | sce_6625 | 8.00E-162 | 5.00E-162 |
| SCE1572_7823 | sce_6626 | 8.00E-56 | 5.00E-56 |
| SCE1572_7824 | sce_6627 | 3.00E-169 | 0.00E+00 |
| SCE1572_7825 | sce_6628 | 6.00E-115 | 1.00E-114 |
| SCE1572_7826 | sce_6629 | 0.00E+00 | 0.00E+00 |
| SCE1572_7827 | sce_6630 | 9.00E-49 | 8.00E-38 |
| SCE1572_7828 | sce_6631 | 6.00E-151 | 6.00E-151 |
| SCE1572_7829 | sce_6632 | 1.00E-98 | 5.00E-100 |
| SCE1572_783 | sce_578 | 0.00E+00 | 0.00E+00 |
| SCE1572_7830 | sce_6633 | 0.00E+00 | 0.00E+00 |
| SCE1572_7831 | sce_6634 | 1.00E-154 | 1.00E-154 |
| SCE1572_7832 | sce_6635 | 5.00E-82 | 5.00E-82 |
| SCE1572_7833 | sce_6636 | 0.00E+00 | 0.00E+00 |
| SCE1572_7834 | sce_6637 | 1.00E-08 | 4.00E-08 |
| SCE1572_7835 | sce_6638 | 5.00E-92 | 5.00E-92 |
| SCE1572_7836 | sce_6639 | 5.00E-159 | 1.00E-151 |
| SCE1572_7837 | sce_6640 | 4.00E-35 | 4.00E-35 |
| SCE1572_7838 | sce_6641 | 4.00E-127 | 9.00E-102 |
| SCE1572_7839 | sce_6642 | 3.00E-87 | 7.00E-71 |
| SCE1572_784 | sce_579 | 4.00E-149 | 4.00E-135 |
| SCE1572_7840 | sce_6644 | 0.00E+00 | 0.00E+00 |
| SCE1572_7841 | sce_6645 | 3.00E-77 | 6.00E-77 |
| SCE1572_7842 | sce_6646 | 1.00E-94 | 1.00E-97 |
| SCE1572_7843 | sce_6647 | 0.00E+00 | 0.00E+00 |
| SCE1572_7844 | sce_6648 | 5.00E-92 | 6.00E-92 |
| SCE1572_7845 | sce_6649 | 3.00E-164 | 1.00E-159 |
| SCE1572_7846 | sce_6650 | 3.00E-36 | 5.00E-26 |
| SCE1572_7847 | sce_6651 | 3.00E-39 | 3.00E-39 |
| SCE1572_7848 | sce_6652 | 0.00E+00 | 0.00E+00 |
| SCE1572_7849 | sce_6653 | 0.00E+00 | 0.00E+00 |
| SCE1572_785 | sce_581 | 1.00E-165 | 2.00E-176 |
| SCE1572_7850 | sce_6654 | 0.00E+00 | 0.00E+00 |
| SCE1572_7851 | sce_6655 | 1.00E-98 | 1.00E-98 |
| SCE1572_7853 | sce_6656 | 3.00E-112 | 3.00E-112 |
| SCE1572_7854 | sce_6657 | 2.00E-109 | 1.00E-98 |

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| SCE1572_7855 | sce_6658 | 2.00E-79 | 4.00E-72 |
| SCE1572_7856 | sce_6659 | 0.00E+00 | 0.00E+00 |
| SCE1572_7857 | sce_6660 | 4.00E-166 | 2.00E-158 |
| SCE1572_7858 | sce_6661 | 0.00E+00 | 0.00E+00 |
| SCE1572_7862 | sce_6662 | 3.00E-170 | 1.00E-174 |
| SCE1572_7863 | sce_6663 | 7.00E-50 | 7.00E-50 |
| SCE1572_7864 | sce_6664 | 3.00E-100 | 3.00E-100 |
| SCE1572_7865 | sce_6667 | 1.00E-151 | 1.00E-165 |
| SCE1572_7866 | sce_6668 | 0.00E+00 | 7.00E-180 |
| SCE1572_7867 | sce_6669 | 1.00E-47 | 1.00E-50 |
| SCE1572_7868 | sce_6670 | 5.00E-154 | 3.00E-134 |
| SCE1572_7869 | sce_6671 | 2.00E-161 | 2.00E-160 |
| SCE1572_787 | sce_582 | 0.00E+00 | 0.00E+00 |
| SCE1572_7870 | sce_6672 | 5.00E-87 | 3.00E-90 |
| SCE1572_7871 | sce_6673 | 4.00E-123 | 3.00E-134 |
| SCE1572_7872 | sce_6674 | 0.00E+00 | 0.00E+00 |
| SCE1572_7873 | sce_6675 | 1.00E-82 | 1.00E-82 |
| SCE1572_7874 | sce_6676 | 2.00E-52 | 3.00E-54 |
| SCE1572_7875 | sce_6678 | 6.00E-125 | 3.00E-129 |
| SCE1572_7876 | sce_6679 | 2.00E-127 | 2.00E-127 |
| SCE1572_7877 | sce_6680 | 7.00E-127 | 7.00E-127 |
| SCE1572_7878 | sce_6681 | 3.00E-131 | 4.00E-137 |
| SCE1572_7879 | sce_6682 | 0.00E+00 | 0.00E+00 |
| SCE1572_788 | sce_583 | 0.00E+00 | 0.00E+00 |
| SCE1572_7880 | sce_6684 | 3.00E-42 | 2.00E-42 |
| SCE1572_7881 | sce_6685 | 0.00E+00 | 0.00E+00 |
| SCE1572_7883 | sce_6688 | 1.00E-96 | 1.00E-99 |
| SCE1572_7884 | sce_6689 | 0.00E+00 | 0.00E+00 |
| SCE1572_7884 | sce_5475 | 0.00E+00 | 0.00E+00 |
| SCE1572_7885 | sce_5474 | 0.00E+00 | 0.00E+00 |
| SCE1572_7885 | sce_6690 | 0.00E+00 | 0.00E+00 |
| SCE1572_7886 | sce_6691 | 5.00E-48 | 5.00E-48 |
| SCE1572_7887 | sce_6692 | 0.00E+00 | 0.00E+00 |
| SCE1572_7888 | sce_6693 | 0.00E+00 | 0.00E+00 |
| SCE1572_7889 | sce_6694 | 2.00E-137 | 2.00E-138 |
| SCE1572_7890 | sce_6695 | 7.00E-55 | 5.00E-40 |
| SCE1572_7893 | sce_2085 | 1.00E-14 | 9.00E-15 |
| SCE1572_7896 | sce_6697 | 3.00E-41 | 3.00E-41 |
| SCE1572_7898 | sce_6698 | 6.00E-102 | 2.00E-120 |
| SCE1572_7902 | sce_6705 | 6.00E-72 | 2.00E-72 |
| SCE1572_7903 | sce_6706 | 9.00E-70 | 2.00E-71 |
| SCE1572_7904 | sce_6707 | 6.00E-115 | 2.00E-114 |
| SCE1572_7907 | sce_4677 | 1.00E-108 | 2.00E-108 |
| SCE1572_791 | sce_584 | 0.00E+00 | 0.00E+00 |
| SCE1572_7910 | sce_4620 | 3.00E-12 | 6.00E-12 |
| SCE1572_7911 | sce_1247 | 4.00E-70 | 1.00E-68 |
| SCE1572_7912 | sce_7656 | 2.00E-32 | 6.00E-29 |
| SCE1572_7914 | sce_6714 | 1.00E-126 | 6.00E-128 |
| SCE1572_7916 | sce_6716 | 0.00E+00 | 0.00E+00 |
| SCE1572_7917 | sce_6717 | 8.00E-153 | 1.00E-161 |
| SCE1572_7918 | sce_6718 | 0.00E+00 | 0.00E+00 |
| SCE1572_7919 | sce_6718 | 0.00E+00 | 0.00E+00 |
| SCE1572_792 | sce_585 | 3.00E-53 | 7.00E-48 |
| SCE1572_7920 | sce_6718 | 0.00E+00 | 0.00E+00 |
| SCE1572_7922 | sce_6719 | 1.00E-168 | 1.00E-160 |
| SCE1572_7923 | sce_6720 | 3.00E-55 | 1.00E-49 |
| SCE1572_7924 | sce_6721 | 0.00E+00 | 0.00E+00 |
| SCE1572_7925 | sce_6722 | 7.00E-42 | 4.00E-56 |
| SCE1572_7927 | sce_6723 | 0.00E+00 | 0.00E+00 |
| SCE1572_7928 | sce_6724 | 0.00E+00 | 0.00E+00 |
| SCE1572_7929 | sce_6725 | 3.00E-109 | 3.00E-109 |
| SCE1572_793 | sce_586 | 3.00E-108 | 3.00E-108 |
| SCE1572_7930 | sce_6726 | 3.00E-158 | 8.00E-158 |
| SCE1572_7931 | sce_6729 | 0.00E+00 | 0.00E+00 |
| SCE1572_7932 | sce_6730 | 0.00E+00 | 0.00E+00 |
| SCE1572_7935 | sce_6733 | 0.00E+00 | 0.00E+00 |
| SCE1572_7936 | sce_6734 | 1.00E-112 | 6.00E-126 |
| SCE1572_7937 | sce_6735 | 1.00E-103 | 2.00E-130 |
| SCE1572_7938 | sce_6736 | 4.00E-160 | 6.00E-162 |
| SCE1572_7939 | sce_6737 | 9.00E-120 | 3.00E-103 |
| SCE1572_794 | sce_587 | 6.00E-113 | 6.00E-113 |
| SCE1572_7940 | sce_6738 | 0.00E+00 | 0.00E+00 |
| SCE1572_7941 | sce_6739 | 5.00E-122 | 9.00E-123 |
| SCE1572_7942 | sce_6742 | 0.00E+00 | 0.00E+00 |
| SCE1572_7943 | sce_6743 | 9.00E-104 | 9.00E-104 |
| SCE1572_7944 | sce_6744 | 1.00E-58 | 1.00E-63 |

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| SCE1572_7949 | sce_6745 | 2.00E-110 | 1.00E-121 |
| SCE1572_795 | sce_588 | 0.00E+00 | 0.00E+00 |
| SCE1572_7950 | sce_6746 | 4.00E-172 | 9.00E-179 |
| SCE1572_7951 | sce_6747 | 1.00E-82 | 1.00E-82 |
| SCE1572_7952 | sce_6748 | 0.00E+00 | 0.00E+00 |
| SCE1572_7953 | sce_6750 | 0.00E+00 | 0.00E+00 |
| SCE1572_7955 | sce_6751 | 2.00E-157 | 9.00E-160 |
| SCE1572_7956 | sce_6752 | 2.00E-118 | 5.00E-110 |
| SCE1572_7957 | sce_6753 | 9.00E-89 | 1.00E-100 |
| SCE1572_7958 | sce_4490 | 1.00E-74 | 1.00E-74 |
| SCE1572_7959 | sce_6754 | 2.00E-59 | 2.00E-59 |
| SCE1572_796 | sce_589 | 0.00E+00 | 0.00E+00 |
| SCE1572_7960 | sce_2029 | 9.00E-123 | 1.00E-122 |
| SCE1572_7962 | sce_6756 | 0.00E+00 | 0.00E+00 |
| SCE1572_7963 | sce_6757 | 0.00E+00 | 0.00E+00 |
| SCE1572_7965 | sce_6764 | 3.00E-33 | 2.00E-38 |
| SCE1572_7966 | sce_6765 | 6.00E-65 | 8.00E-63 |
| SCE1572_7968 | sce_6766 | 8.00E-111 | 3.00E-98 |
| SCE1572_797 | sce_590 | 0.00E+00 | 0.00E+00 |
| SCE1572_7970 | sce_6769 | 2.00E-126 | 1.00E-125 |
| SCE1572_7971 | sce_6770 | 6.00E-76 | 6.00E-86 |
| SCE1572_7972 | sce_6771 | 1.00E-76 | 5.00E-90 |
| SCE1572_7973 | sce_6772 | 1.00E-49 | 1.00E-51 |
| SCE1572_7974 | sce_6773 | 3.00E-150 | 6.00E-153 |
| SCE1572_7975 | sce_7456 | 5.00E-94 | 2.00E-97 |
| SCE1572_7976 | sce_7452 | 7.00E-29 | 1.00E-29 |
| SCE1572_7978 | sce_9166 | 1.00E-141 | 3.00E-145 |
| SCE1572_798 | sce_591 | 7.00E-125 | 7.00E-125 |
| SCE1572_7984 | sce_6787 | 2.00E-155 | 3.00E-151 |
| SCE1572_7985 | sce_6788 | 0.00E+00 | 0.00E+00 |
| SCE1572_7986 | sce_6789 | 1.00E-109 | 5.00E-106 |
| SCE1572_7987 | sce_6790 | 2.00E-99 | 3.00E-111 |
| SCE1572_799 | sce_592 | 0.00E+00 | 0.00E+00 |
| SCE1572_7991 | sce_6792 | 8.00E-102 | 3.00E-102 |
| SCE1572_7993 | sce_6793 | 6.00E-155 | 9.00E-179 |
| SCE1572_7997 | sce_6225 | 2.00E-118 | 5.00E-99 |
| SCE1572_7998 | sce_6226 | 0.00E+00 | 0.00E+00 |
| SCE1572_8 | sce_8 | 9.00E-170 | 1.00E-169 |
| SCE1572_8001 | sce_9566 | 0.00E+00 | 0.00E+00 |
| SCE1572_8003 | sce_9566 | 0.00E+00 | 0.00E+00 |
| SCE1572_8003 | sce_7530 | 0.00E+00 | 0.00E+00 |
| SCE1572_8005 | sce_6795 | 0.00E+00 | 0.00E+00 |
| SCE1572_8007 | sce_6796 | 2.00E-139 | 4.00E-138 |
| SCE1572_8008 | sce_6797 | 0.00E+00 | 0.00E+00 |
| SCE1572_8009 | sce_6798 | 3.00E-142 | 3.00E-142 |
| SCE1572_801 | sce_593 | 1.00E-127 | 2.00E-118 |
| SCE1572_8010 | sce_6800 | 2.00E-117 | 8.00E-119 |
| SCE1572_8011 | sce_6801 | 2.00E-141 | 7.00E-156 |
| SCE1572_8013 | sce_6802 | 0.00E+00 | 0.00E+00 |
| SCE1572_8014 | sce_6803 | 0.00E+00 | 0.00E+00 |
| SCE1572_8015 | sce_6804 | 3.00E-46 | 6.00E-46 |
| SCE1572_8016 | sce_6805 | 9.00E-22 | 2.00E-24 |
| SCE1572_8018 | sce_6807 | 1.00E-66 | 7.00E-67 |
| SCE1572_8019 | sce_1676 | 0.00E+00 | 0.00E+00 |
| SCE1572_802 | sce_594 | 0.00E+00 | 0.00E+00 |
| SCE1572_8020 | sce_6833 | 0.00E+00 | 0.00E+00 |
| SCE1572_8020 | sce_6827 | 0.00E+00 | 0.00E+00 |
| SCE1572_8020 | sce_6228 | 0.00E+00 | 0.00E+00 |
| SCE1572_8020 | sce_10159 | 0.00E+00 | 0.00E+00 |
| SCE1572_8020 | sce_7513 | 0.00E+00 | 0.00E+00 |
| SCE1572_8020 | sce_7408 | 0.00E+00 | 0.00E+00 |
| SCE1572_8020 | sce_6876 | 0.00E+00 | 0.00E+00 |
| SCE1572_8020 | sce_6836 | 0.00E+00 | 0.00E+00 |
| SCE1572_8020 | sce_2543 | 0.00E+00 | 0.00E+00 |
| SCE1572_8020 | sce_7036 | 0.00E+00 | 0.00E+00 |
| SCE1572_8021 | sce_7413 | 3.00E-69 | 3.00E-69 |
| SCE1572_8022 | sce_7414 | 3.00E-39 | 3.00E-45 |
| SCE1572_8030 | sce_304 | 1.00E-163 | 3.00E-165 |
| SCE1572_8034 | sce_9170 | 6.00E-53 | 1.00E-52 |
| SCE1572_8035 | sce_9171 | 2.00E-137 | 5.00E-142 |
| SCE1572_8039 | sce_9793 | 2.00E-70 | 3.00E-61 |
| SCE1572_8040 | sce_10359 | 4.00E-88 | 3.00E-86 |
| SCE1572_8041 | sce_6872 | 8.00E-80 | 2.00E-91 |
| SCE1572_8042 | sce_6877 | 6.00E-45 | 3.00E-49 |
| SCE1572_8043 | sce_6809 | 4.00E-12 | 4.00E-12 |
| SCE1572_8068 | sce_7404 | 0.00E+00 | 0.00E+00 |

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| SCE1572_8072 | sce_9803 | 1.00E-36 | 3.00E-37 |
| SCE1572_8073 | sce_9804 | 2.00E-34 | 2.00E-29 |
| SCE1572_8074 | sce_1036 | 4.00E-18 | 2.00E-16 |
| SCE1572_8082 | sce_6847 | 5.00E-13 | 5.00E-13 |
| SCE1572_8083 | sce_6849 | 2.00E-31 | 7.00E-38 |
| SCE1572_8089 | sce_5122 | 6.00E-149 | 1.00E-160 |
| SCE1572_809 | sce_225 | 0.00E+00 | 0.00E+00 |
| SCE1572_809 | sce_6235 | 0.00E+00 | 0.00E+00 |
| SCE1572_809 | sce_2161 | 0.00E+00 | 0.00E+00 |
| SCE1572_809 | sce_8357 | 0.00E+00 | 0.00E+00 |
| SCE1572_809 | sce_5276 | 0.00E+00 | 0.00E+00 |
| SCE1572_8090 | sce_5121 | 0.00E+00 | 0.00E+00 |
| SCE1572_8091 | sce_5118 | 2.00E-50 | 8.00E-50 |
| SCE1572_8092 | sce_5117 | 4.00E-45 | 1.00E-51 |
| SCE1572_8093 | sce_5116 | 0.00E+00 | 0.00E+00 |
| SCE1572_8094 | sce_5115 | 3.00E-133 | 1.00E-135 |
| SCE1572_8095 | sce_5114 | 6.00E-125 | 6.00E-125 |
| SCE1572_8096 | sce_5113 | 6.00E-72 | 6.00E-72 |
| SCE1572_8097 | sce_5112 | 0.00E+00 | 0.00E+00 |
| SCE1572_8098 | sce_9043 | 6.00E-26 | 9.00E-34 |
| SCE1572_8099 | sce_9044 | 0.00E+00 | 0.00E+00 |
| SCE1572_810 | sce_6107 | 0.00E+00 | 0.00E+00 |
| SCE1572_810 | sce_3917 | 0.00E+00 | 0.00E+00 |
| SCE1572_810 | sce_6093 | 0.00E+00 | 0.00E+00 |
| SCE1572_810 | sce_6094 | 0.00E+00 | 0.00E+00 |
| SCE1572_810 | sce_6092 | 0.00E+00 | 0.00E+00 |
| SCE1572_810 | sce_7661 | 0.00E+00 | 0.00E+00 |
| SCE1572_810 | sce_6095 | 0.00E+00 | 0.00E+00 |
| SCE1572_810 | sce_2065 | 0.00E+00 | 0.00E+00 |
| SCE1572_810 | sce_8618 | 0.00E+00 | 0.00E+00 |
| SCE1572_8100 | sce_5110 | 0.00E+00 | 0.00E+00 |
| SCE1572_8115 | sce_5109 | 2.00E-100 | 2.00E-101 |
| SCE1572_8126 | sce_5107 | 0.00E+00 | 0.00E+00 |
| SCE1572_8127 | sce_9045 | 0.00E+00 | 0.00E+00 |
| SCE1572_8133 | sce_5552 | 2.00E-23 | 7.00E-23 |
| SCE1572_8137 | sce_861 | 5.00E-10 | 1.00E-09 |
| SCE1572_8146 | sce_3042 | 4.00E-52 | 6.00E-47 |
| SCE1572_8176 | sce_5106 | 6.00E-81 | 1.00E-93 |
| SCE1572_8190 | sce_4070 | 4.00E-147 | 2.00E-147 |
| SCE1572_8203 | sce_6891 | 7.00E-28 | 3.00E-27 |
| SCE1572_8206 | sce_8351 | 3.00E-130 | 2.00E-143 |
| SCE1572_8207 | sce_8350 | 1.00E-56 | 2.00E-60 |
| SCE1572_8208 | sce_8348 | 5.00E-17 | 7.00E-18 |
| SCE1572_8209 | sce_8347 | 0.00E+00 | 0.00E+00 |
| SCE1572_8209 | sce_4610 | 0.00E+00 | 0.00E+00 |
| SCE1572_8210 | sce_8346 | 6.00E-110 | 7.00E-117 |
| SCE1572_8211 | sce_8345 | 0.00E+00 | 0.00E+00 |
| SCE1572_8212 | sce_8344 | 4.00E-54 | 8.00E-43 |
| SCE1572_8213 | sce_8343 | 0.00E+00 | 0.00E+00 |
| SCE1572_8214 | sce_8342 | 0.00E+00 | 0.00E+00 |
| SCE1572_8220 | sce_4907 | 3.00E-52 | 1.00E-48 |
| SCE1572_8222 | sce_7070 | 5.00E-169 | 6.00E-175 |
| SCE1572_8225 | sce_6785 | 6.00E-86 | 1.00E-96 |
| SCE1572_8226 | sce_6895 | 1.00E-87 | 4.00E-101 |
| SCE1572_8227 | sce_6896 | 3.00E-125 | 1.00E-123 |
| SCE1572_8228 | sce_6897 | 0.00E+00 | 0.00E+00 |
| SCE1572_8229 | sce_6899 | 2.00E-121 | 2.00E-142 |
| SCE1572_823 | sce_631 | 4.00E-68 | 8.00E-69 |
| SCE1572_8230 | sce_6900 | 5.00E-156 | 2.00E-167 |
| SCE1572_8231 | sce_6901 | 0.00E+00 | 0.00E+00 |
| SCE1572_8232 | sce_6902 | 2.00E-78 | 5.00E-74 |
| SCE1572_8233 | sce_6905 | 1.00E-175 | 1.00E-167 |
| SCE1572_8235 | sce_6906 | 6.00E-36 | 2.00E-29 |
| SCE1572_8236 | sce_6907 | 3.00E-74 | 2.00E-74 |
| SCE1572_8237 | sce_6908 | 1.00E-66 | 5.00E-62 |
| SCE1572_8238 | sce_6909 | 1.00E-96 | 4.00E-97 |
| SCE1572_8239 | sce_6910 | 5.00E-132 | 7.00E-136 |
| SCE1572_824 | sce_5835 | 0.00E+00 | 0.00E+00 |
| SCE1572_824 | sce_10204 | 0.00E+00 | 0.00E+00 |
| SCE1572_824 | sce_388 | 0.00E+00 | 0.00E+00 |
| SCE1572_824 | sce_7640 | 0.00E+00 | 0.00E+00 |
| SCE1572_824 | sce_4513 | 0.00E+00 | 0.00E+00 |
| SCE1572_824 | sce_3085 | 0.00E+00 | 0.00E+00 |
| SCE1572_824 | sce_7109 | 0.00E+00 | 0.00E+00 |
| SCE1572_824 | sce_3003 | 0.00E+00 | 0.00E+00 |
| SCE1572_824 | sce_9557 | 0.00E+00 | 0.00E+00 |

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| SCE1572_824 | sce_6535 | 0.00E+00 | 0.00E+00 |
| SCE1572_824 | sce_6092 | 0.00E+00 | 0.00E+00 |
| SCE1572_824 | sce_7661 | 0.00E+00 | 0.00E+00 |
| SCE1572_8240 | sce_6911 | 8.00E-103 | 3.00E-113 |
| SCE1572_8241 | sce_6912 | 0.00E+00 | 0.00E+00 |
| SCE1572_8242 | sce_6913 | 4.00E-44 | 2.00E-39 |
| SCE1572_8243 | sce_6914 | 1.00E-169 | 1.00E-169 |
| SCE1572_8244 | sce_6915 | 2.00E-95 | 2.00E-95 |
| SCE1572_8245 | sce_6916 | 0.00E+00 | 0.00E+00 |
| SCE1572_8246 | sce_6917 | 1.00E-73 | 3.00E-73 |
| SCE1572_8247 | sce_6918 | 4.00E-107 | 2.00E-102 |
| SCE1572_8248 | sce_6919 | 4.00E-77 | 2.00E-85 |
| SCE1572_8249 | sce_6920 | 0.00E+00 | 0.00E+00 |
| SCE1572_825 | sce_621 | 0.00E+00 | 0.00E+00 |
| SCE1572_8250 | sce_6921 | 0.00E+00 | 0.00E+00 |
| SCE1572_8251 | sce_6922 | 2.00E-45 | 5.00E-71 |
| SCE1572_8252 | sce_6923 | 0.00E+00 | 0.00E+00 |
| SCE1572_8253 | sce_6924 | 3.00E-157 | 0.00E+00 |
| SCE1572_8254 | sce_6925 | 3.00E-133 | 1.00E-139 |
| SCE1572_8255 | sce_6926 | 0.00E+00 | 0.00E+00 |
| SCE1572_8256 | sce_6927 | 3.00E-79 | 9.00E-75 |
| SCE1572_8257 | sce_6928 | 3.00E-108 | 7.00E-108 |
| SCE1572_8258 | sce_6929 | 2.00E-118 | 2.00E-118 |
| SCE1572_8259 | sce_6930 | 0.00E+00 | 0.00E+00 |
| SCE1572_826 | sce_622 | 0.00E+00 | 0.00E+00 |
| SCE1572_8260 | sce_6931 | 4.00E-136 | 2.00E-154 |
| SCE1572_8261 | sce_6932 | 2.00E-110 | 1.00E-124 |
| SCE1572_8262 | sce_6933 | 0.00E+00 | 0.00E+00 |
| SCE1572_8263 | sce_6934 | 0.00E+00 | 0.00E+00 |
| SCE1572_8264 | sce_6935 | 2.00E-104 | 1.00E-103 |
| SCE1572_8265 | sce_6936 | 2.00E-69 | 8.00E-87 |
| SCE1572_8266 | sce_6937 | 0.00E+00 | 0.00E+00 |
| SCE1572_8268 | sce_6317 | 3.00E-11 | 9.00E-11 |
| SCE1572_8269 | sce_6318 | 0.00E+00 | 0.00E+00 |
| SCE1572_827 | sce_623 | 4.00E-106 | 1.00E-112 |
| SCE1572_8270 | sce_6319 | 0.00E+00 | 0.00E+00 |
| SCE1572_8271 | sce_6940 | 1.00E-136 | 8.00E-111 |
| SCE1572_8272 | sce_6941 | 3.00E-88 | 3.00E-89 |
| SCE1572_8273 | sce_6942 | 1.00E-98 | 1.00E-98 |
| SCE1572_8274 | sce_7920 | 4.00E-19 | 4.00E-33 |
| SCE1572_8275 | sce_6944 | 0.00E+00 | 5.00E-107 |
| SCE1572_8276 | sce_6945 | 6.00E-114 | 9.00E-113 |
| SCE1572_8277 | sce_6946 | 6.00E-87 | 8.00E-85 |
| SCE1572_8278 | sce_6947 | 3.00E-149 | 4.00E-158 |
| SCE1572_8279 | sce_6948 | 3.00E-72 | 1.00E-75 |
| SCE1572_828 | sce_624 | 4.00E-42 | 1.00E-43 |
| SCE1572_8280 | sce_6949 | 0.00E+00 | 0.00E+00 |
| SCE1572_8281 | sce_6950 | 2.00E-169 | 4.00E-169 |
| SCE1572_8282 | sce_6951 | 0.00E+00 | 0.00E+00 |
| SCE1572_8283 | sce_6316 | 1.00E-49 | 5.00E-43 |
| SCE1572_8284 | sce_611 | 3.00E-07 | 8.00E-13 |
| SCE1572_8285 | sce_613 | 2.00E-54 | 6.00E-58 |
| SCE1572_8286 | sce_6953 | 9.00E-84 | 1.00E-83 |
| SCE1572_8287 | sce_6954 | 1.00E-161 | 1.00E-166 |
| SCE1572_8289 | sce_6053 | 3.00E-25 | 5.00E-31 |
| SCE1572_829 | sce_625 | 3.00E-83 | 5.00E-86 |
| SCE1572_8291 | sce_9526 | 7.00E-12 | 3.00E-13 |
| SCE1572_8294 | sce_6979 | 7.00E-91 | 6.00E-95 |
| SCE1572_8295 | sce_6980 | 4.00E-115 | 4.00E-115 |
| SCE1572_8296 | sce_6981 | 2.00E-105 | 4.00E-98 |
| SCE1572_8297 | sce_6982 | 0.00E+00 | 0.00E+00 |
| SCE1572_8298 | sce_6983 | 0.00E+00 | 0.00E+00 |
| SCE1572_830 | sce_626 | 7.00E-66 | 2.00E-67 |
| SCE1572_8301 | sce_6985 | 0.00E+00 | 0.00E+00 |
| SCE1572_8302 | sce_6986 | 7.00E-83 | 1.00E-73 |
| SCE1572_8303 | sce_6987 | 1.00E-43 | 1.00E-53 |
| SCE1572_8304 | sce_6988 | 3.00E-64 | 1.00E-68 |
| SCE1572_8305 | sce_6989 | 2.00E-106 | 2.00E-106 |
| SCE1572_8306 | sce_6990 | 4.00E-26 | 4.00E-26 |
| SCE1572_8307 | sce_1129 | 7.00E-16 | 1.00E-16 |
| SCE1572_8309 | sce_6991 | 1.00E-124 | 5.00E-150 |
| SCE1572_8310 | sce_6992 | 4.00E-159 | 2.00E-160 |
| SCE1572_8311 | sce_6993 | 0.00E+00 | 1.00E-104 |
| SCE1572_8312 | sce_6994 | 4.00E-93 | 4.00E-93 |
| SCE1572_8313 | sce_6995 | 1.00E-172 | 2.00E-169 |
| SCE1572_8314 | sce_6996 | 0.00E+00 | 0.00E+00 |

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| SCE1572_8315 | sce_6997 | 2.00E-60 | 2.00E-71 |
| SCE1572_8316 | sce_6998 | 2.00E-165 | 4.00E-173 |
| SCE1572_8317 | sce_6999 | 2.00E-111 | 2.00E-120 |
| SCE1572_8318 | sce_7000 | 7.00E-156 | 4.00E-133 |
| SCE1572_8319 | sce_7002 | 0.00E+00 | 0.00E+00 |
| SCE1572_8320 | sce_7003 | 3.00E-47 | 2.00E-61 |
| SCE1572_8321 | sce_7004 | 0.00E+00 | 0.00E+00 |
| SCE1572_8322 | sce_7006 | 1.00E-105 | 4.00E-105 |
| SCE1572_8323 | sce_7007 | 3.00E-118 | 3.00E-118 |
| SCE1572_8324 | sce_7008 | 2.00E-127 | 7.00E-118 |
| SCE1572_8325 | sce_7009 | 0.00E+00 | 1.00E-166 |
| SCE1572_8326 | sce_7010 | 0.00E+00 | 0.00E+00 |
| SCE1572_8327 | sce_7011 | 0.00E+00 | 2.00E-180 |
| SCE1572_8329 | sce_7012 | 0.00E+00 | 0.00E+00 |
| SCE1572_8330 | sce_7013 | 0.00E+00 | 0.00E+00 |
| SCE1572_8331 | sce_7014 | 9.00E-148 | 4.00E-150 |
| SCE1572_8332 | sce_7015 | 6.00E-85 | 1.00E-85 |
| SCE1572_8333 | sce_7016 | 6.00E-48 | 6.00E-48 |
| SCE1572_8336 | sce_1676 | 0.00E+00 | 0.00E+00 |
| SCE1572_8337 | sce_304 | 2.00E-155 | 3.00E-165 |
| SCE1572_8338 | sce_9167 | 7.00E-22 | 1.00E-21 |
| SCE1572_8343 | sce_3174 | 8.00E-28 | 2.00E-18 |
| SCE1572_8347 | sce_9482 | 5.00E-100 | 7.00E-129 |
| SCE1572_8349 | sce_9480 | 2.00E-49 | 2.00E-50 |
| SCE1572_835 | sce_633 | 6.00E-28 | 5.00E-29 |
| SCE1572_8355 | sce_6226 | 0.00E+00 | 0.00E+00 |
| SCE1572_836 | sce_634 | 0.00E+00 | 0.00E+00 |
| SCE1572_8367 | sce_2167 | 1.00E-126 | 2.00E-121 |
| SCE1572_8368 | sce_2165 | 4.00E-124 | 7.00E-110 |
| SCE1572_8369 | sce_7077 | 5.00E-151 | 8.00E-156 |
| SCE1572_8370 | sce_7078 | 1.00E-96 | 2.00E-112 |
| SCE1572_8371 | sce_7079 | 5.00E-84 | 1.00E-77 |
| SCE1572_8372 | sce_7080 | 7.00E-60 | 1.00E-59 |
| SCE1572_8373 | sce_7085 | 0.00E+00 | 0.00E+00 |
| SCE1572_8374 | sce_7086 | 6.00E-83 | 6.00E-83 |
| SCE1572_8375 | sce_7087 | 5.00E-93 | 3.00E-86 |
| SCE1572_8378 | sce_7088 | 2.00E-116 | 1.00E-127 |
| SCE1572_8379 | sce_7089 | 2.00E-108 | 2.00E-90 |
| SCE1572_838 | sce_635 | 1.00E-122 | 2.00E-108 |
| SCE1572_8380 | sce_7090 | 4.00E-43 | 9.00E-45 |
| SCE1572_8381 | sce_7144 | 0.00E+00 | 0.00E+00 |
| SCE1572_8385 | sce_8592 | 0.00E+00 | 0.00E+00 |
| SCE1572_8385 | sce_3937 | 0.00E+00 | 0.00E+00 |
| SCE1572_8386 | sce_1676 | 0.00E+00 | 0.00E+00 |
| SCE1572_8388 | sce_7378 | 3.00E-73 | 2.00E-86 |
| SCE1572_8389 | sce_8819 | 3.00E-73 | 1.00E-76 |
| SCE1572_839 | sce_636 | 2.00E-65 | 7.00E-57 |
| SCE1572_8391 | sce_7154 | 0.00E+00 | 0.00E+00 |
| SCE1572_8391 | sce_5403 | 0.00E+00 | 0.00E+00 |
| SCE1572_8391 | sce_7969 | 0.00E+00 | 0.00E+00 |
| SCE1572_8391 | sce_5226 | 0.00E+00 | 0.00E+00 |
| SCE1572_8391 | sce_1803 | 0.00E+00 | 0.00E+00 |
| SCE1572_8391 | sce_9665 | 0.00E+00 | 0.00E+00 |
| SCE1572_8391 | sce_5751 | 0.00E+00 | 0.00E+00 |
| SCE1572_8391 | sce_4073 | 0.00E+00 | 0.00E+00 |
| SCE1572_8391 | sce_5746 | 0.00E+00 | 0.00E+00 |
| SCE1572_8391 | sce_2053 | 0.00E+00 | 0.00E+00 |
| SCE1572_8391 | sce_9954 | 0.00E+00 | 0.00E+00 |
| SCE1572_8391 | sce_9757 | 0.00E+00 | 0.00E+00 |
| SCE1572_8391 | sce_3750 | 0.00E+00 | 0.00E+00 |
| SCE1572_8391 | sce_6712 | 0.00E+00 | 0.00E+00 |
| SCE1572_8394 | sce_7155 | 0.00E+00 | 0.00E+00 |
| SCE1572_8395 | sce_7156 | 0.00E+00 | 0.00E+00 |
| SCE1572_8396 | sce_7157 | 2.00E-45 | 2.00E-52 |
| SCE1572_8397 | sce_7158 | 0.00E+00 | 0.00E+00 |
| SCE1572_8399 | sce_7159 | 0.00E+00 | 0.00E+00 |
| SCE1572_84 | sce_71 | 4.00E-54 | 3.00E-65 |
| SCE1572_840 | sce_637 | 0.00E+00 | 0.00E+00 |
| SCE1572_8400 | sce_7160 | 0.00E+00 | 0.00E+00 |
| SCE1572_8401 | sce_7161 | 0.00E+00 | 0.00E+00 |
| SCE1572_8402 | sce_7162 | 2.00E-168 | 2.00E-168 |
| SCE1572_8403 | sce_7163 | 0.00E+00 | 0.00E+00 |
| SCE1572_8405 | sce_7164 | 1.00E-63 | 1.00E-63 |
| SCE1572_8406 | sce_7165 | 0.00E+00 | 3.00E-146 |
| SCE1572_8407 | sce_7166 | 4.00E-40 | 1.00E-49 |
| SCE1572_8408 | sce_7167 | 0.00E+00 | 0.00E+00 |

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| SCE1572_841 | sce_5488 | 2.00E-170 | 1.00E-168 |
| SCE1572_8410 | sce_7169 | 1.00E-108 | 2.00E-110 |
| SCE1572_8411 | sce_7170 | 2.00E-46 | 1.00E-47 |
| SCE1572_8412 | sce_7171 | 0.00E+00 | 0.00E+00 |
| SCE1572_8413 | sce_7172 | 5.00E-112 | 2.00E-119 |
| SCE1572_8414 | sce_7173 | 0.00E+00 | 0.00E+00 |
| SCE1572_8415 | sce_7176 | 0.00E+00 | 0.00E+00 |
| SCE1572_8416 | sce_7177 | 6.00E-102 | 4.00E-110 |
| SCE1572_8417 | sce_7178 | 7.00E-152 | 3.00E-135 |
| SCE1572_8418 | sce_7179 | 4.00E-79 | 2.00E-82 |
| SCE1572_8420 | sce_7180 | 1.00E-66 | 1.00E-66 |
| SCE1572_8421 | sce_7181 | 4.00E-178 | 3.00E-153 |
| SCE1572_8422 | sce_7182 | 4.00E-132 | 2.00E-136 |
| SCE1572_8423 | sce_7183 | 0.00E+00 | 0.00E+00 |
| SCE1572_8425 | sce_7186 | 6.00E-66 | 4.00E-66 |
| SCE1572_8427 | sce_7187 | 5.00E-12 | 5.00E-12 |
| SCE1572_8428 | sce_7189 | 4.00E-46 | 1.00E-32 |
| SCE1572_8429 | sce_7190 | 2.00E-178 | 0.00E+00 |
| SCE1572_843 | sce_639 | 0.00E+00 | 0.00E+00 |
| SCE1572_8431 | sce_7191 | 2.00E-91 | 2.00E-91 |
| SCE1572_8432 | sce_7192 | 8.00E-35 | 1.00E-37 |
| SCE1572_8434 | sce_7193 | 0.00E+00 | 0.00E+00 |
| SCE1572_8436 | sce_7196 | 1.00E-169 | 7.00E-166 |
| SCE1572_8438 | sce_7197 | 5.00E-107 | 2.00E-107 |
| SCE1572_8439 | sce_7198 | 4.00E-112 | 1.00E-111 |
| SCE1572_844 | sce_640 | 0.00E+00 | 0.00E+00 |
| SCE1572_8440 | sce_7199 | 1.00E-146 | 3.00E-138 |
| SCE1572_8441 | sce_7201 | 1.00E-177 | 1.00E-177 |
| SCE1572_8442 | sce_7202 | 1.00E-54 | 1.00E-59 |
| SCE1572_8443 | sce_7203 | 6.00E-83 | 8.00E-76 |
| SCE1572_8444 | sce_7204 | 2.00E-67 | 3.00E-60 |
| SCE1572_8445 | sce_7205 | 4.00E-37 | 7.00E-49 |
| SCE1572_8448 | sce_3793 | 0.00E+00 | 0.00E+00 |
| SCE1572_8448 | sce_7069 | 0.00E+00 | 0.00E+00 |
| SCE1572_8448 | sce_5086 | 0.00E+00 | 0.00E+00 |
| SCE1572_8448 | sce_5085 | 0.00E+00 | 0.00E+00 |
| SCE1572_8448 | sce_6701 | 0.00E+00 | 0.00E+00 |
| SCE1572_8449 | sce_7207 | 1.00E-71 | 2.00E-77 |
| SCE1572_8450 | sce_7208 | 2.00E-111 | 4.00E-105 |
| SCE1572_8451 | sce_7211 | 2.00E-96 | 6.00E-102 |
| SCE1572_8452 | sce_7212 | 7.00E-66 | 1.00E-72 |
| SCE1572_8453 | sce_7213 | 1.00E-55 | 3.00E-59 |
| SCE1572_8454 | sce_7214 | 1.00E-117 | 5.00E-128 |
| SCE1572_8455 | sce_7215 | 2.00E-122 | 4.00E-137 |
| SCE1572_8456 | sce_7216 | 2.00E-107 | 4.00E-118 |
| SCE1572_8457 | sce_7217 | 0.00E+00 | 0.00E+00 |
| SCE1572_8458 | sce_7218 | 0.00E+00 | 0.00E+00 |
| SCE1572_8459 | sce_7219 | 1.00E-84 | 3.00E-93 |
| SCE1572_8460 | sce_7220 | 4.00E-136 | 1.00E-124 |
| SCE1572_8461 | sce_7221 | 1.00E-34 | 1.00E-34 |
| SCE1572_8462 | sce_7222 | 1.00E-76 | 5.00E-82 |
| SCE1572_8463 | sce_7224 | 0.00E+00 | 0.00E+00 |
| SCE1572_8464 | sce_7225 | 6.00E-15 | 6.00E-15 |
| SCE1572_8466 | sce_7226 | 5.00E-70 | 3.00E-68 |
| SCE1572_8467 | sce_7227 | 7.00E-56 | 5.00E-73 |
| SCE1572_8468 | sce_7228 | 0.00E+00 | 0.00E+00 |
| SCE1572_8469 | sce_7230 | 4.00E-11 | 3.00E-12 |
| SCE1572_847 | sce_4968 | 0.00E+00 | 0.00E+00 |
| SCE1572_8470 | sce_7231 | 1.00E-159 | 2.00E-168 |
| SCE1572_8471 | sce_7232 | 0.00E+00 | 0.00E+00 |
| SCE1572_8472 | sce_7234 | 5.00E-93 | 6.00E-69 |
| SCE1572_8473 | sce_7236 | 7.00E-75 | 4.00E-74 |
| SCE1572_8474 | sce_7237 | 0.00E+00 | 0.00E+00 |
| SCE1572_8476 | sce_7238 | 5.00E-114 | 3.00E-124 |
| SCE1572_8477 | sce_7239 | 0.00E+00 | 0.00E+00 |
| SCE1572_8477 | sce_9431 | 0.00E+00 | 0.00E+00 |
| SCE1572_8478 | sce_7243 | 1.00E-44 | 3.00E-59 |
| SCE1572_8479 | sce_7244 | 1.00E-140 | 6.00E-155 |
| SCE1572_848 | sce_4641 | 0.00E+00 | 0.00E+00 |
| SCE1572_848 | sce_4638 | 0.00E+00 | 0.00E+00 |
| SCE1572_848 | sce_3575 | 0.00E+00 | 0.00E+00 |
| SCE1572_848 | sce_3577 | 0.00E+00 | 0.00E+00 |
| SCE1572_848 | sce_3580 | 0.00E+00 | 0.00E+00 |
| SCE1572_8480 | sce_7245 | 0.00E+00 | 0.00E+00 |
| SCE1572_8481 | sce_7246 | 7.00E-66 | 4.00E-73 |
| SCE1572_8482 | sce_7248 | 8.00E-35 | 8.00E-35 |

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|--------------|-----------|-----------|-----------|
| SCE1572_8483 | sce_7249 | 0.00E+00 | 0.00E+00 |
| SCE1572_8484 | sce_7251 | 5.00E-39 | 5.00E-46 |
| SCE1572_8485 | sce_7252 | 3.00E-121 | 2.00E-166 |
| SCE1572_8488 | sce_7254 | 0.00E+00 | 0.00E+00 |
| SCE1572_8489 | sce_7256 | 2.00E-123 | 1.00E-131 |
| SCE1572_849 | sce_4638 | 0.00E+00 | 0.00E+00 |
| SCE1572_849 | sce_4641 | 0.00E+00 | 0.00E+00 |
| SCE1572_849 | sce_4640 | 0.00E+00 | 0.00E+00 |
| SCE1572_8490 | sce_7257 | 3.00E-154 | 1.00E-149 |
| SCE1572_8491 | sce_7258 | 1.00E-106 | 9.00E-98 |
| SCE1572_8492 | sce_7260 | 0.00E+00 | 0.00E+00 |
| SCE1572_8493 | sce_7261 | 2.00E-73 | 4.00E-76 |
| SCE1572_8494 | sce_7262 | 7.00E-112 | 6.00E-83 |
| SCE1572_8495 | sce_3750 | 0.00E+00 | 0.00E+00 |
| SCE1572_8495 | sce_5229 | 0.00E+00 | 0.00E+00 |
| SCE1572_8495 | sce_6712 | 0.00E+00 | 0.00E+00 |
| SCE1572_85 | sce_73 | 0.00E+00 | 0.00E+00 |
| SCE1572_850 | sce_3577 | 0.00E+00 | 0.00E+00 |
| SCE1572_850 | sce_3575 | 0.00E+00 | 0.00E+00 |
| SCE1572_8503 | sce_4101 | 2.00E-37 | 7.00E-38 |
| SCE1572_8504 | sce_4100 | 2.00E-116 | 9.00E-124 |
| SCE1572_8505 | sce_4099 | 1.00E-98 | 1.00E-105 |
| SCE1572_8506 | sce_4098 | 1.00E-82 | 7.00E-91 |
| SCE1572_8507 | sce_7263 | 1.00E-109 | 7.00E-108 |
| SCE1572_8509 | sce_9501 | 2.00E-164 | 0.00E+00 |
| SCE1572_851 | sce_3575 | 0.00E+00 | 0.00E+00 |
| SCE1572_851 | sce_3576 | 0.00E+00 | 8.00E-172 |
| SCE1572_851 | sce_3580 | 0.00E+00 | 0.00E+00 |
| SCE1572_851 | sce_3577 | 0.00E+00 | 0.00E+00 |
| SCE1572_851 | sce_3579 | 0.00E+00 | 0.00E+00 |
| SCE1572_8510 | sce_8461 | 2.00E-67 | 2.00E-67 |
| SCE1572_8511 | sce_9502 | 2.00E-153 | 2.00E-153 |
| SCE1572_8517 | sce_10363 | 5.00E-113 | 9.00E-111 |
| SCE1572_8518 | sce_7264 | 5.00E-129 | 5.00E-129 |
| SCE1572_8519 | sce_7265 | 2.00E-39 | 5.00E-39 |
| SCE1572_8520 | sce_7266 | 8.00E-55 | 4.00E-67 |
| SCE1572_8522 | sce_7267 | 0.00E+00 | 0.00E+00 |
| SCE1572_8524 | sce_7268 | 1.00E-176 | 2.00E-147 |
| SCE1572_8525 | sce_7269 | 9.00E-50 | 9.00E-50 |
| SCE1572_8526 | sce_7270 | 2.00E-73 | 5.00E-66 |
| SCE1572_8528 | sce_7272 | 2.00E-173 | 4.00E-174 |
| SCE1572_8529 | sce_7273 | 0.00E+00 | 0.00E+00 |
| SCE1572_8530 | sce_7274 | 3.00E-169 | 1.00E-164 |
| SCE1572_8531 | sce_7275 | 6.00E-100 | 3.00E-107 |
| SCE1572_8533 | sce_7276 | 5.00E-173 | 2.00E-147 |
| SCE1572_8534 | sce_7277 | 3.00E-165 | 4.00E-165 |
| SCE1572_8535 | sce_7278 | 2.00E-173 | 2.00E-173 |
| SCE1572_8536 | sce_7279 | 1.00E-107 | 2.00E-119 |
| SCE1572_8537 | sce_7280 | 1.00E-169 | 1.00E-178 |
| SCE1572_8538 | sce_7281 | 1.00E-172 | 1.00E-171 |
| SCE1572_8539 | sce_7282 | 7.00E-116 | 1.00E-118 |
| SCE1572_8540 | sce_7283 | 0.00E+00 | 0.00E+00 |
| SCE1572_8541 | sce_7285 | 3.00E-96 | 3.00E-96 |
| SCE1572_8542 | sce_7286 | 3.00E-90 | 5.00E-99 |
| SCE1572_8543 | sce_7288 | 2.00E-146 | 1.00E-146 |
| SCE1572_8545 | sce_3427 | 0.00E+00 | 0.00E+00 |
| SCE1572_8546 | sce_3426 | 0.00E+00 | 0.00E+00 |
| SCE1572_8547 | sce_3425 | 2.00E-128 | 2.00E-135 |
| SCE1572_8548 | sce_3424 | 0.00E+00 | 0.00E+00 |
| SCE1572_8549 | sce_7289 | 0.00E+00 | 0.00E+00 |
| SCE1572_8550 | sce_7290 | 7.00E-146 | 3.00E-152 |
| SCE1572_8551 | sce_7291 | 8.00E-173 | 5.00E-166 |
| SCE1572_8552 | sce_7292 | 4.00E-75 | 4.00E-72 |
| SCE1572_8553 | sce_7293 | 3.00E-94 | 1.00E-91 |
| SCE1572_8554 | sce_7294 | 0.00E+00 | 0.00E+00 |
| SCE1572_8555 | sce_7295 | 3.00E-54 | 3.00E-54 |
| SCE1572_8556 | sce_7296 | 2.00E-123 | 8.00E-147 |
| SCE1572_8557 | sce_7297 | 0.00E+00 | 0.00E+00 |
| SCE1572_8558 | sce_7298 | 0.00E+00 | 0.00E+00 |
| SCE1572_8560 | sce_6041 | 3.00E-85 | 3.00E-85 |
| SCE1572_8561 | sce_7304 | 0.00E+00 | 0.00E+00 |
| SCE1572_8561 | sce_6101 | 0.00E+00 | 0.00E+00 |
| SCE1572_8565 | sce_4641 | 0.00E+00 | 0.00E+00 |
| SCE1572_8566 | sce_7306 | 2.00E-86 | 4.00E-82 |
| SCE1572_8567 | sce_7307 | 0.00E+00 | 0.00E+00 |
| SCE1572_8568 | sce_7308 | 4.00E-86 | 4.00E-88 |

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| SCE1572_8578 | sce_1676 | 0.00E+00 | 0.00E+00 |
| SCE1572_8581 | sce_9566 | 0.00E+00 | 0.00E+00 |
| SCE1572_8581 | sce_7530 | 0.00E+00 | 0.00E+00 |
| SCE1572_8583 | sce_9567 | 0.00E+00 | 0.00E+00 |
| SCE1572_8583 | sce_7528 | 0.00E+00 | 5.00E-175 |
| SCE1572_8585 | sce_7312 | 7.00E-56 | 4.00E-58 |
| SCE1572_8588 | sce_7314 | 1.00E-107 | 2.00E-107 |
| SCE1572_8589 | sce_7315 | 2.00E-67 | 6.00E-67 |
| SCE1572_8590 | sce_7317 | 2.00E-13 | 6.00E-20 |
| SCE1572_8594 | sce_6282 | 0.00E+00 | 0.00E+00 |
| SCE1572_860 | sce_3570 | 3.00E-10 | 3.00E-10 |
| SCE1572_8601 | sce_8200 | 9.00E-22 | 2.00E-22 |
| SCE1572_8603 | sce_7319 | 3.00E-167 | 2.00E-167 |
| SCE1572_8604 | sce_7320 | 0.00E+00 | 0.00E+00 |
| SCE1572_8605 | sce_7321 | 6.00E-101 | 2.00E-100 |
| SCE1572_8607 | sce_7322 | 0.00E+00 | 0.00E+00 |
| SCE1572_8608 | sce_7323 | 3.00E-53 | 1.00E-57 |
| SCE1572_861 | sce_3567 | 2.00E-35 | 2.00E-35 |
| SCE1572_8610 | sce_7325 | 2.00E-161 | 3.00E-161 |
| SCE1572_8611 | sce_7326 | 0.00E+00 | 0.00E+00 |
| SCE1572_8613 | sce_7332 | 8.00E-126 | 9.00E-126 |
| SCE1572_8614 | sce_7334 | 2.00E-117 | 8.00E-97 |
| SCE1572_8615 | sce_7335 | 0.00E+00 | 0.00E+00 |
| SCE1572_8616 | sce_7336 | 3.00E-136 | 3.00E-134 |
| SCE1572_8617 | sce_7337 | 4.00E-118 | 5.00E-121 |
| SCE1572_8618 | sce_7338 | 2.00E-158 | 8.00E-166 |
| SCE1572_8619 | sce_7339 | 4.00E-61 | 3.00E-55 |
| SCE1572_8620 | sce_7341 | 5.00E-76 | 8.00E-74 |
| SCE1572_8621 | sce_7343 | 0.00E+00 | 0.00E+00 |
| SCE1572_8622 | sce_7344 | 3.00E-72 | 7.00E-68 |
| SCE1572_8623 | sce_7345 | 3.00E-112 | 1.00E-117 |
| SCE1572_8624 | sce_7346 | 2.00E-24 | 2.00E-31 |
| SCE1572_8625 | sce_7347 | 0.00E+00 | 0.00E+00 |
| SCE1572_8627 | sce_7348 | 1.00E-125 | 5.00E-118 |
| SCE1572_8628 | sce_7349 | 2.00E-115 | 2.00E-115 |
| SCE1572_8629 | sce_6206 | 2.00E-48 | 2.00E-44 |
| SCE1572_8630 | sce_7350 | 3.00E-55 | 3.00E-39 |
| SCE1572_8632 | sce_7352 | 4.00E-61 | 9.00E-61 |
| SCE1572_8635 | sce_4902 | 1.00E-62 | 5.00E-58 |
| SCE1572_8637 | sce_7353 | 1.00E-180 | 0.00E+00 |
| SCE1572_8638 | sce_7355 | 3.00E-47 | 5.00E-52 |
| SCE1572_8639 | sce_7358 | 0.00E+00 | 4.00E-172 |
| SCE1572_864 | sce_3568 | 5.00E-105 | 1.00E-104 |
| SCE1572_8640 | sce_7359 | 3.00E-105 | 9.00E-107 |
| SCE1572_8641 | sce_7360 | 5.00E-108 | 6.00E-106 |
| SCE1572_8643 | sce_7362 | 4.00E-98 | 6.00E-97 |
| SCE1572_8644 | sce_7363 | 7.00E-149 | 7.00E-146 |
| SCE1572_8646 | sce_7364 | 9.00E-55 | 2.00E-47 |
| SCE1572_8650 | sce_7366 | 4.00E-161 | 5.00E-163 |
| SCE1572_8652 | sce_7367 | 1.00E-149 | 1.00E-127 |
| SCE1572_8653 | sce_7368 | 2.00E-127 | 1.00E-140 |
| SCE1572_8654 | sce_7369 | 0.00E+00 | 0.00E+00 |
| SCE1572_8655 | sce_7370 | 0.00E+00 | 0.00E+00 |
| SCE1572_8656 | sce_7371 | 5.00E-67 | 7.00E-68 |
| SCE1572_8657 | sce_7372 | 1.00E-28 | 1.00E-28 |
| SCE1572_8658 | sce_7373 | 9.00E-82 | 2.00E-80 |
| SCE1572_8659 | sce_7374 | 3.00E-51 | 5.00E-48 |
| SCE1572_8661 | sce_7375 | 0.00E+00 | 0.00E+00 |
| SCE1572_8663 | sce_7393 | 2.00E-109 | 2.00E-109 |
| SCE1572_8664 | sce_7395 | 2.00E-59 | 1.00E-65 |
| SCE1572_8668 | sce_2495 | 2.00E-71 | 1.00E-61 |
| SCE1572_8669 | sce_6970 | 6.00E-17 | 6.00E-17 |
| SCE1572_867 | sce_641 | 2.00E-98 | 2.00E-96 |
| SCE1572_8671 | sce_6971 | 1.00E-19 | 2.00E-25 |
| SCE1572_8672 | sce_3730 | 9.00E-66 | 2.00E-76 |
| SCE1572_8674 | sce_2613 | 7.00E-67 | 1.00E-63 |
| SCE1572_8676 | sce_7073 | 1.00E-28 | 2.00E-28 |
| SCE1572_868 | sce_642 | 3.00E-180 | 0.00E+00 |
| SCE1572_8680 | sce_7433 | 3.00E-118 | 3.00E-118 |
| SCE1572_8681 | sce_3735 | 4.00E-103 | 2.00E-108 |
| SCE1572_8682 | sce_6962 | 4.00E-11 | 9.00E-15 |
| SCE1572_8684 | sce_1255 | 1.00E-30 | 1.00E-30 |
| SCE1572_8685 | sce_7426 | 1.00E-165 | 1.00E-165 |
| SCE1572_8687 | sce_7428 | 3.00E-84 | 9.00E-90 |
| SCE1572_8688 | sce_4940 | 4.00E-106 | 2.00E-105 |
| SCE1572_8689 | sce_8360 | 5.00E-79 | 4.00E-76 |

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| SCE1572_8691 | sce_8694 | 0.00E+00 | 0.00E+00 |
| SCE1572_8691 | sce_9974 | 0.00E+00 | 0.00E+00 |
| SCE1572_8691 | sce_9973 | 0.00E+00 | 0.00E+00 |
| SCE1572_8691 | sce_2645 | 0.00E+00 | 0.00E+00 |
| SCE1572_8694 | sce_7435 | 0.00E+00 | 0.00E+00 |
| SCE1572_8695 | sce_7436 | 1.00E-179 | 2.00E-169 |
| SCE1572_8698 | sce_7465 | 0.00E+00 | 0.00E+00 |
| SCE1572_8698 | sce_774 | 0.00E+00 | 0.00E+00 |
| SCE1572_8698 | sce_1723 | 0.00E+00 | 0.00E+00 |
| SCE1572_8698 | sce_5787 | 0.00E+00 | 0.00E+00 |
| SCE1572_8698 | sce_9954 | 0.00E+00 | 0.00E+00 |
| SCE1572_8698 | sce_5229 | 0.00E+00 | 0.00E+00 |
| SCE1572_8698 | sce_6712 | 0.00E+00 | 0.00E+00 |
| SCE1572_8698 | sce_3750 | 0.00E+00 | 0.00E+00 |
| SCE1572_87 | sce_74 | 2.00E-102 | 9.00E-97 |
| SCE1572_870 | sce_645 | 6.00E-100 | 2.00E-94 |
| SCE1572_8700 | sce_7466 | 3.00E-150 | 9.00E-152 |
| SCE1572_8702 | sce_7467 | 6.00E-61 | 1.00E-56 |
| SCE1572_8703 | sce_7473 | 9.00E-117 | 3.00E-126 |
| SCE1572_8704 | sce_7474 | 4.00E-40 | 2.00E-43 |
| SCE1572_8709 | sce_7477 | 4.00E-33 | 4.00E-37 |
| SCE1572_871 | sce_646 | 0.00E+00 | 0.00E+00 |
| SCE1572_8710 | sce_851 | 1.00E-67 | 1.00E-67 |
| SCE1572_8711 | sce_852 | 1.00E-65 | 1.00E-65 |
| SCE1572_8712 | sce_7522 | 2.00E-148 | 2.00E-148 |
| SCE1572_8713 | sce_7523 | 4.00E-167 | 6.00E-170 |
| SCE1572_8714 | sce_7524 | 4.00E-171 | 4.00E-177 |
| SCE1572_8715 | sce_7525 | 1.00E-129 | 1.00E-129 |
| SCE1572_8716 | sce_7526 | 2.00E-134 | 2.00E-169 |
| SCE1572_8719 | sce_5999 | 3.00E-105 | 1.00E-105 |
| SCE1572_872 | sce_647 | 0.00E+00 | 0.00E+00 |
| SCE1572_8722 | sce_5994 | 5.00E-49 | 2.00E-44 |
| SCE1572_8729 | sce_7527 | 2.00E-68 | 1.00E-83 |
| SCE1572_8730 | sce_7540 | 8.00E-131 | 2.00E-130 |
| SCE1572_8731 | sce_7541 | 3.00E-70 | 7.00E-63 |
| SCE1572_8733 | sce_828 | 3.00E-110 | 2.00E-120 |
| SCE1572_8734 | sce_829 | 4.00E-84 | 6.00E-73 |
| SCE1572_8737 | sce_7545 | 4.00E-158 | 2.00E-162 |
| SCE1572_8738 | sce_7546 | 5.00E-125 | 2.00E-129 |
| SCE1572_8739 | sce_7547 | 6.00E-152 | 4.00E-171 |
| SCE1572_874 | sce_648 | 5.00E-60 | 1.00E-57 |
| SCE1572_8740 | sce_7557 | 6.00E-126 | 6.00E-122 |
| SCE1572_8741 | sce_7559 | 1.00E-152 | 4.00E-162 |
| SCE1572_8748 | sce_7571 | 0.00E+00 | 0.00E+00 |
| SCE1572_8749 | sce_7572 | 0.00E+00 | 6.00E-177 |
| SCE1572_8756 | sce_7575 | 0.00E+00 | 0.00E+00 |
| SCE1572_8757 | sce_7576 | 1.00E-50 | 8.00E-64 |
| SCE1572_8758 | sce_7578 | 0.00E+00 | 3.00E-180 |
| SCE1572_8759 | sce_7579 | 0.00E+00 | 3.00E-177 |
| SCE1572_876 | sce_649 | 2.00E-61 | 2.00E-61 |
| SCE1572_8760 | sce_2037 | 0.00E+00 | 0.00E+00 |
| SCE1572_8764 | sce_1676 | 0.00E+00 | 0.00E+00 |
| SCE1572_8766 | sce_8672 | 7.00E-40 | 4.00E-31 |
| SCE1572_8767 | sce_9806 | 6.00E-63 | 9.00E-74 |
| SCE1572_8767 | sce_6808 | 6.00E-63 | 9.00E-74 |
| SCE1572_877 | sce_651 | 1.00E-75 | 1.00E-75 |
| SCE1572_8777 | sce_7787 | 2.00E-81 | 5.00E-94 |
| SCE1572_8779 | sce_7584 | 1.00E-64 | 1.00E-64 |
| SCE1572_878 | sce_653 | 5.00E-60 | 2.00E-57 |
| SCE1572_8781 | sce_7585 | 0.00E+00 | 0.00E+00 |
| SCE1572_8782 | sce_7586 | 8.00E-155 | 2.00E-145 |
| SCE1572_8783 | sce_7587 | 0.00E+00 | 0.00E+00 |
| SCE1572_8784 | sce_7588 | 1.00E-140 | 4.00E-140 |
| SCE1572_8785 | sce_7589 | 3.00E-166 | 6.00E-169 |
| SCE1572_8786 | sce_7590 | 0.00E+00 | 0.00E+00 |
| SCE1572_8787 | sce_7591 | 3.00E-176 | 0.00E+00 |
| SCE1572_8789 | sce_7592 | 9.00E-164 | 3.00E-173 |
| SCE1572_879 | sce_654 | 9.00E-144 | 6.00E-130 |
| SCE1572_8790 | sce_2005 | 0.00E+00 | 0.00E+00 |
| SCE1572_8791 | sce_1526 | 7.00E-17 | 1.00E-16 |
| SCE1572_8792 | sce_5303 | 3.00E-97 | 3.00E-97 |
| SCE1572_8795 | sce_8795 | 2.00E-33 | 9.00E-28 |
| SCE1572_88 | sce_75 | 2.00E-152 | 2.00E-152 |
| SCE1572_880 | sce_655 | 0.00E+00 | 0.00E+00 |
| SCE1572_8803 | sce_1534 | 4.00E-65 | 5.00E-71 |
| SCE1572_8804 | sce_1535 | 6.00E-71 | 2.00E-71 |

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| SCE1572_881 | sce_656 | 1.00E-121 | 2.00E-96 |
| SCE1572_8811 | sce_2112 | 6.00E-52 | 3.00E-51 |
| SCE1572_8812 | sce_7084 | 3.00E-88 | 4.00E-88 |
| SCE1572_8814 | sce_2393 | 1.00E-16 | 7.00E-17 |
| SCE1572_8815 | sce_7043 | 6.00E-34 | 6.00E-34 |
| SCE1572_8816 | sce_9596 | 2.00E-147 | 2.00E-147 |
| SCE1572_8818 | sce_9597 | 1.00E-105 | 1.00E-105 |
| SCE1572_882 | sce_657 | 0.00E+00 | 0.00E+00 |
| SCE1572_8824 | sce_2109 | 2.00E-12 | 6.00E-13 |
| SCE1572_8826 | sce_515 | 1.00E-167 | 3.00E-168 |
| SCE1572_8834 | sce_6701 | 0.00E+00 | 0.00E+00 |
| SCE1572_8834 | sce_5086 | 0.00E+00 | 0.00E+00 |
| SCE1572_8834 | sce_5085 | 0.00E+00 | 0.00E+00 |
| SCE1572_8834 | sce_3793 | 0.00E+00 | 0.00E+00 |
| SCE1572_884 | sce_658 | 1.00E-57 | 1.00E-57 |
| SCE1572_8841 | sce_2158 | 4.00E-132 | 6.00E-129 |
| SCE1572_8845 | sce_7604 | 9.00E-145 | 1.00E-146 |
| SCE1572_8846 | sce_7605 | 4.00E-129 | 2.00E-125 |
| SCE1572_8848 | sce_7607 | 8.00E-161 | 8.00E-163 |
| SCE1572_8849 | sce_7610 | 2.00E-156 | 3.00E-152 |
| SCE1572_885 | sce_659 | 5.00E-134 | 1.00E-134 |
| SCE1572_8850 | sce_7611 | 1.00E-106 | 2.00E-86 |
| SCE1572_8852 | sce_7620 | 0.00E+00 | 0.00E+00 |
| SCE1572_8854 | sce_7621 | 8.00E-140 | 2.00E-139 |
| SCE1572_8855 | sce_7622 | 2.00E-84 | 2.00E-84 |
| SCE1572_8856 | sce_7624 | 1.00E-90 | 2.00E-90 |
| SCE1572_8857 | sce_7625 | 5.00E-69 | 5.00E-69 |
| SCE1572_8858 | sce_7626 | 0.00E+00 | 0.00E+00 |
| SCE1572_8859 | sce_7627 | 0.00E+00 | 0.00E+00 |
| SCE1572_886 | sce_660 | 0.00E+00 | 0.00E+00 |
| SCE1572_8861 | sce_8755 | 0.00E+00 | 0.00E+00 |
| SCE1572_8861 | sce_7818 | 0.00E+00 | 0.00E+00 |
| SCE1572_8861 | sce_7814 | 0.00E+00 | 0.00E+00 |
| SCE1572_8861 | sce_7815 | 0.00E+00 | 0.00E+00 |
| SCE1572_8861 | sce_8753 | 0.00E+00 | 0.00E+00 |
| SCE1572_8865 | sce_6039 | 7.00E-151 | 6.00E-151 |
| SCE1572_8866 | sce_6040 | 2.00E-166 | 2.00E-169 |
| SCE1572_8868 | sce_1251 | 4.00E-11 | 2.00E-13 |
| SCE1572_8869 | sce_7628 | 3.00E-135 | 2.00E-126 |
| SCE1572_887 | sce_661 | 3.00E-140 | 3.00E-140 |
| SCE1572_8871 | sce_7630 | 0.00E+00 | 0.00E+00 |
| SCE1572_8872 | sce_7631 | 2.00E-111 | 1.00E-111 |
| SCE1572_8873 | sce_1062 | 1.00E-171 | 0.00E+00 |
| SCE1572_8876 | sce_7661 | 0.00E+00 | 0.00E+00 |
| SCE1572_8876 | sce_6092 | 0.00E+00 | 0.00E+00 |
| SCE1572_8876 | sce_6095 | 0.00E+00 | 0.00E+00 |
| SCE1572_8876 | sce_3917 | 0.00E+00 | 0.00E+00 |
| SCE1572_8876 | sce_6107 | 0.00E+00 | 0.00E+00 |
| SCE1572_8876 | sce_6093 | 0.00E+00 | 0.00E+00 |
| SCE1572_8876 | sce_6094 | 0.00E+00 | 0.00E+00 |
| SCE1572_8876 | sce_388 | 0.00E+00 | 0.00E+00 |
| SCE1572_8876 | sce_6535 | 0.00E+00 | 0.00E+00 |
| SCE1572_8876 | sce_9920 | 0.00E+00 | 0.00E+00 |
| SCE1572_8876 | sce_10204 | 0.00E+00 | 0.00E+00 |
| SCE1572_8876 | sce_7640 | 0.00E+00 | 0.00E+00 |
| SCE1572_8876 | sce_5835 | 0.00E+00 | 0.00E+00 |
| SCE1572_8876 | sce_4513 | 0.00E+00 | 0.00E+00 |
| SCE1572_8876 | sce_9557 | 0.00E+00 | 0.00E+00 |
| SCE1572_8876 | sce_1398 | 0.00E+00 | 0.00E+00 |
| SCE1572_8876 | sce_3003 | 0.00E+00 | 0.00E+00 |
| SCE1572_8876 | sce_8602 | 0.00E+00 | 0.00E+00 |
| SCE1572_8876 | sce_8618 | 0.00E+00 | 0.00E+00 |
| SCE1572_8878 | sce_7515 | 5.00E-94 | 4.00E-57 |
| SCE1572_8880 | sce_7519 | 6.00E-117 | 3.00E-105 |
| SCE1572_8881 | sce_9791 | 4.00E-135 | 3.00E-140 |
| SCE1572_8883 | sce_10354 | 8.00E-63 | 3.00E-63 |
| SCE1572_8886 | sce_7657 | 0.00E+00 | 0.00E+00 |
| SCE1572_8886 | sce_3491 | 0.00E+00 | 0.00E+00 |
| SCE1572_8886 | sce_6712 | 0.00E+00 | 0.00E+00 |
| SCE1572_8886 | sce_9954 | 0.00E+00 | 0.00E+00 |
| SCE1572_8887 | sce_7658 | 3.00E-21 | 2.00E-19 |
| SCE1572_8888 | sce_7659 | 1.00E-144 | 1.00E-121 |
| SCE1572_889 | sce_662 | 0.00E+00 | 0.00E+00 |
| SCE1572_8890 | sce_6214 | 5.00E-96 | 1.00E-96 |
| SCE1572_8894 | sce_7664 | 0.00E+00 | 0.00E+00 |
| SCE1572_8896 | sce_7666 | 4.00E-55 | 8.00E-62 |

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| SCE1572_8897 | sce_7673 | 0.00E+00 | 0.00E+00 |
| SCE1572_8897 | sce_7667 | 0.00E+00 | 0.00E+00 |
| SCE1572_89 | sce_76 | 0.00E+00 | 0.00E+00 |
| SCE1572_890 | sce_663 | 0.00E+00 | 1.00E-179 |
| SCE1572_8900 | sce_7675 | 8.00E-170 | 1.00E-177 |
| SCE1572_8901 | sce_7677 | 0.00E+00 | 0.00E+00 |
| SCE1572_8902 | sce_3000 | 2.00E-126 | 5.00E-140 |
| SCE1572_8904 | sce_7678 | 2.00E-143 | 7.00E-144 |
| SCE1572_8905 | sce_7689 | 3.00E-78 | 2.00E-78 |
| SCE1572_8909 | sce_7691 | 2.00E-117 | 6.00E-123 |
| SCE1572_891 | sce_664 | 0.00E+00 | 0.00E+00 |
| SCE1572_8910 | sce_7692 | 8.00E-69 | 3.00E-69 |
| SCE1572_8911 | sce_7695 | 5.00E-98 | 3.00E-102 |
| SCE1572_8914 | sce_7696 | 2.00E-107 | 2.00E-103 |
| SCE1572_8917 | sce_6286 | 1.00E-94 | 4.00E-73 |
| SCE1572_8918 | sce_6287 | 5.00E-62 | 5.00E-74 |
| SCE1572_8919 | sce_6288 | 1.00E-45 | 1.00E-45 |
| SCE1572_8920 | sce_864 | 0.00E+00 | 0.00E+00 |
| SCE1572_8929 | sce_7697 | 2.00E-47 | 2.00E-47 |
| SCE1572_893 | sce_666 | 3.00E-92 | 5.00E-85 |
| SCE1572_8931 | sce_7698 | 3.00E-136 | 2.00E-120 |
| SCE1572_8932 | sce_7699 | 0.00E+00 | 0.00E+00 |
| SCE1572_8933 | sce_7700 | 7.00E-113 | 1.00E-109 |
| SCE1572_8934 | sce_7701 | 2.00E-86 | 7.00E-71 |
| SCE1572_8935 | sce_7702 | 5.00E-77 | 3.00E-78 |
| SCE1572_8937 | sce_7703 | 0.00E+00 | 0.00E+00 |
| SCE1572_8938 | sce_7704 | 1.00E-22 | 5.00E-23 |
| SCE1572_8939 | sce_7705 | 6.00E-95 | 7.00E-95 |
| SCE1572_894 | sce_667 | 0.00E+00 | 0.00E+00 |
| SCE1572_8940 | sce_7706 | 6.00E-168 | 0.00E+00 |
| SCE1572_8941 | sce_7708 | 2.00E-140 | 3.00E-149 |
| SCE1572_8942 | sce_7709 | 2.00E-168 | 2.00E-168 |
| SCE1572_8943 | sce_7710 | 1.00E-42 | 3.00E-45 |
| SCE1572_8945 | sce_7712 | 2.00E-117 | 2.00E-117 |
| SCE1572_8946 | sce_7713 | 0.00E+00 | 0.00E+00 |
| SCE1572_8947 | sce_7714 | 0.00E+00 | 0.00E+00 |
| SCE1572_8948 | sce_7715 | 6.00E-25 | 2.00E-25 |
| SCE1572_8949 | sce_7717 | 1.00E-68 | 3.00E-78 |
| SCE1572_895 | sce_668 | 7.00E-110 | 4.00E-129 |
| SCE1572_8952 | sce_7718 | 4.00E-81 | 4.00E-62 |
| SCE1572_8953 | sce_7719 | 5.00E-16 | 8.00E-15 |
| SCE1572_8954 | sce_7720 | 5.00E-142 | 4.00E-144 |
| SCE1572_8958 | sce_7721 | 0.00E+00 | 0.00E+00 |
| SCE1572_8962 | sce_309 | 3.00E-74 | 1.00E-79 |
| SCE1572_8963 | sce_7725 | 2.00E-84 | 4.00E-90 |
| SCE1572_8964 | sce_7726 | 4.00E-108 | 4.00E-116 |
| SCE1572_8965 | sce_7727 | 0.00E+00 | 0.00E+00 |
| SCE1572_8968 | sce_7729 | 0.00E+00 | 0.00E+00 |
| SCE1572_8969 | sce_7730 | 3.00E-101 | 3.00E-97 |
| SCE1572_8970 | sce_7731 | 1.00E-173 | 9.00E-167 |
| SCE1572_8971 | sce_7733 | 0.00E+00 | 0.00E+00 |
| SCE1572_8975 | sce_7734 | 2.00E-135 | 3.00E-128 |
| SCE1572_8976 | sce_7735 | 3.00E-47 | 3.00E-50 |
| SCE1572_8977 | sce_7736 | 1.00E-63 | 1.00E-63 |
| SCE1572_8978 | sce_7737 | 9.00E-176 | 8.00E-166 |
| SCE1572_8979 | sce_7738 | 6.00E-15 | 4.00E-14 |
| SCE1572_898 | sce_670 | 8.00E-99 | 3.00E-116 |
| SCE1572_8980 | sce_10099 | 9.00E-46 | 5.00E-46 |
| SCE1572_8984 | sce_7750 | 7.00E-139 | 6.00E-156 |
| SCE1572_8987 | sce_7751 | 2.00E-154 | 1.00E-173 |
| SCE1572_8989 | sce_7752 | 0.00E+00 | 0.00E+00 |
| SCE1572_8990 | sce_7753 | 6.00E-53 | 4.00E-51 |
| SCE1572_8991 | sce_7756 | 1.00E-36 | 6.00E-37 |
| SCE1572_8992 | sce_7757 | 1.00E-122 | 6.00E-123 |
| SCE1572_8993 | sce_7758 | 0.00E+00 | 0.00E+00 |
| SCE1572_8994 | sce_7759 | 4.00E-104 | 2.00E-109 |
| SCE1572_8995 | sce_7760 | 5.00E-56 | 2.00E-55 |
| SCE1572_8996 | sce_7761 | 1.00E-47 | 4.00E-41 |
| SCE1572_8997 | sce_7762 | 1.00E-129 | 1.00E-127 |
| SCE1572_8998 | sce_7763 | 0.00E+00 | 0.00E+00 |
| SCE1572_8999 | sce_7764 | 4.00E-88 | 2.00E-88 |
| SCE1572_9 | sce_9 | 3.00E-110 | 3.00E-111 |
| SCE1572_90 | sce_77 | 0.00E+00 | 0.00E+00 |
| SCE1572_900 | sce_671 | 0.00E+00 | 0.00E+00 |
| SCE1572_9000 | sce_7765 | 4.00E-118 | 4.00E-118 |
| SCE1572_9001 | sce_7766 | 2.00E-67 | 6.00E-68 |

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| SCE1572_9002 | sce_7767 | 6.00E-42 | 6.00E-42 |
| SCE1572_9003 | sce_7768 | 2.00E-78 | 2.00E-78 |
| SCE1572_9004 | sce_7769 | 1.00E-103 | 3.00E-117 |
| SCE1572_9005 | sce_7770 | 2.00E-08 | 1.00E-10 |
| SCE1572_9006 | sce_7771 | 0.00E+00 | 0.00E+00 |
| SCE1572_9007 | sce_7772 | 3.00E-39 | 2.00E-30 |
| SCE1572_9008 | sce_7773 | 0.00E+00 | 0.00E+00 |
| SCE1572_901 | sce_672 | 2.00E-128 | 3.00E-136 |
| SCE1572_9012 | sce_7774 | 2.00E-135 | 3.00E-127 |
| SCE1572_902 | sce_674 | 4.00E-25 | 1.00E-22 |
| SCE1572_9021 | sce_7776 | 4.00E-115 | 7.00E-105 |
| SCE1572_9022 | sce_7777 | 7.00E-159 | 4.00E-150 |
| SCE1572_9023 | sce_7778 | 0.00E+00 | 0.00E+00 |
| SCE1572_9024 | sce_7779 | 1.00E-40 | 1.00E-40 |
| SCE1572_9025 | sce_7780 | 8.00E-130 | 5.00E-130 |
| SCE1572_9026 | sce_7781 | 6.00E-153 | 2.00E-141 |
| SCE1572_9027 | sce_7782 | 0.00E+00 | 0.00E+00 |
| SCE1572_9028 | sce_7783 | 3.00E-165 | 2.00E-158 |
| SCE1572_9029 | sce_7784 | 7.00E-94 | 3.00E-95 |
| SCE1572_903 | sce_6084 | 6.00E-92 | 3.00E-88 |
| SCE1572_9030 | sce_7785 | 2.00E-116 | 2.00E-91 |
| SCE1572_9031 | sce_7786 | 0.00E+00 | 0.00E+00 |
| SCE1572_9032 | sce_7361 | 0.00E+00 | 0.00E+00 |
| SCE1572_9032 | sce_10425 | 0.00E+00 | 0.00E+00 |
| SCE1572_9032 | sce_3520 | 0.00E+00 | 0.00E+00 |
| SCE1572_9033 | sce_7791 | 2.00E-106 | 8.00E-90 |
| SCE1572_9034 | sce_7792 | 1.00E-80 | 6.00E-84 |
| SCE1572_9035 | sce_7793 | 7.00E-111 | 1.00E-105 |
| SCE1572_9036 | sce_7794 | 0.00E+00 | 0.00E+00 |
| SCE1572_9037 | sce_7796 | 0.00E+00 | 0.00E+00 |
| SCE1572_9038 | sce_7798 | 1.00E-48 | 2.00E-44 |
| SCE1572_9039 | sce_7799 | 2.00E-162 | 1.00E-155 |
| SCE1572_904 | sce_676 | 6.00E-145 | 5.00E-145 |
| SCE1572_9040 | sce_7800 | 9.00E-113 | 5.00E-123 |
| SCE1572_9041 | sce_7801 | 2.00E-176 | 6.00E-170 |
| SCE1572_9042 | sce_7802 | 5.00E-47 | 4.00E-50 |
| SCE1572_9043 | sce_7804 | 8.00E-76 | 2.00E-127 |
| SCE1572_9044 | sce_7805 | 0.00E+00 | 0.00E+00 |
| SCE1572_9046 | sce_7806 | 0.00E+00 | 0.00E+00 |
| SCE1572_9047 | sce_7807 | 1.00E-19 | 3.00E-20 |
| SCE1572_9048 | sce_7808 | 3.00E-54 | 2.00E-47 |
| SCE1572_9049 | sce_7809 | 0.00E+00 | 0.00E+00 |
| SCE1572_905 | sce_677 | 6.00E-124 | 3.00E-154 |
| SCE1572_9050 | sce_7810 | 5.00E-71 | 1.00E-77 |
| SCE1572_9051 | sce_7812 | 1.00E-75 | 2.00E-75 |
| SCE1572_9053 | sce_7818 | 0.00E+00 | 0.00E+00 |
| SCE1572_9053 | sce_7814 | 0.00E+00 | 0.00E+00 |
| SCE1572_9053 | sce_8755 | 0.00E+00 | 0.00E+00 |
| SCE1572_9053 | sce_7815 | 0.00E+00 | 0.00E+00 |
| SCE1572_9053 | sce_8753 | 0.00E+00 | 0.00E+00 |
| SCE1572_9054 | sce_7818 | 0.00E+00 | 0.00E+00 |
| SCE1572_9055 | sce_7819 | 5.00E-86 | 2.00E-97 |
| SCE1572_9056 | sce_1376 | 4.00E-69 | 1.00E-61 |
| SCE1572_906 | sce_678 | 3.00E-97 | 4.00E-97 |
| SCE1572_9065 | sce_7821 | 0.00E+00 | 0.00E+00 |
| SCE1572_9067 | sce_7822 | 3.00E-136 | 3.00E-157 |
| SCE1572_9068 | sce_7823 | 1.00E-111 | 6.00E-111 |
| SCE1572_9069 | sce_7824 | 4.00E-109 | 9.00E-121 |
| SCE1572_907 | sce_680 | 3.00E-89 | 3.00E-89 |
| SCE1572_9070 | sce_7825 | 0.00E+00 | 0.00E+00 |
| SCE1572_9071 | sce_7827 | 1.00E-179 | 0.00E+00 |
| SCE1572_9072 | sce_7828 | 4.00E-81 | 1.00E-88 |
| SCE1572_9073 | sce_7385 | 3.00E-169 | 2.00E-166 |
| SCE1572_9074 | sce_7837 | 3.00E-171 | 2.00E-167 |
| SCE1572_9075 | sce_3793 | 0.00E+00 | 0.00E+00 |
| SCE1572_9075 | sce_7069 | 0.00E+00 | 0.00E+00 |
| SCE1572_9075 | sce_5086 | 0.00E+00 | 0.00E+00 |
| SCE1572_9075 | sce_6701 | 0.00E+00 | 0.00E+00 |
| SCE1572_9075 | sce_5085 | 0.00E+00 | 0.00E+00 |
| SCE1572_9077 | sce_2024 | 0.00E+00 | 0.00E+00 |
| SCE1572_9078 | sce_2025 | 1.00E-65 | 1.00E-66 |
| SCE1572_908 | sce_681 | 9.00E-68 | 9.00E-78 |
| SCE1572_9082 | sce_7846 | 2.00E-79 | 1.00E-69 |
| SCE1572_9083 | sce_7847 | 9.00E-174 | 3.00E-167 |
| SCE1572_9084 | sce_7849 | 0.00E+00 | 0.00E+00 |
| SCE1572_9087 | sce_7850 | 0.00E+00 | 0.00E+00 |

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|--------------|-----------|-----------|-----------|
| SCE1572_9088 | sce_7851 | 1.00E-47 | 2.00E-47 |
| SCE1572_9089 | sce_7867 | 0.00E+00 | 0.00E+00 |
| SCE1572_9090 | sce_7869 | 1.00E-69 | 4.00E-62 |
| SCE1572_9092 | sce_7876 | 0.00E+00 | 0.00E+00 |
| SCE1572_9093 | sce_7877 | 3.00E-21 | 5.00E-08 |
| SCE1572_9094 | sce_7878 | 5.00E-102 | 2.00E-108 |
| SCE1572_9095 | sce_7879 | 2.00E-135 | 1.00E-134 |
| SCE1572_9096 | sce_7880 | 2.00E-50 | 3.00E-44 |
| SCE1572_9099 | sce_7886 | 8.00E-123 | 3.00E-133 |
| SCE1572_91 | sce_79 | 3.00E-109 | 3.00E-109 |
| SCE1572_910 | sce_2065 | 0.00E+00 | 0.00E+00 |
| SCE1572_910 | sce_8618 | 0.00E+00 | 0.00E+00 |
| SCE1572_910 | sce_3917 | 0.00E+00 | 0.00E+00 |
| SCE1572_910 | sce_6107 | 0.00E+00 | 0.00E+00 |
| SCE1572_910 | sce_6092 | 0.00E+00 | 0.00E+00 |
| SCE1572_910 | sce_6094 | 0.00E+00 | 0.00E+00 |
| SCE1572_910 | sce_6095 | 0.00E+00 | 0.00E+00 |
| SCE1572_910 | sce_6093 | 0.00E+00 | 0.00E+00 |
| SCE1572_910 | sce_7661 | 0.00E+00 | 0.00E+00 |
| SCE1572_910 | sce_6535 | 0.00E+00 | 0.00E+00 |
| SCE1572_910 | sce_3003 | 0.00E+00 | 0.00E+00 |
| SCE1572_910 | sce_10204 | 0.00E+00 | 0.00E+00 |
| SCE1572_910 | sce_4513 | 0.00E+00 | 0.00E+00 |
| SCE1572_910 | sce_388 | 0.00E+00 | 0.00E+00 |
| SCE1572_910 | sce_7640 | 0.00E+00 | 0.00E+00 |
| SCE1572_910 | sce_9557 | 0.00E+00 | 0.00E+00 |
| SCE1572_910 | sce_5835 | 0.00E+00 | 0.00E+00 |
| SCE1572_9100 | sce_7882 | 5.00E-87 | 2.00E-88 |
| SCE1572_9101 | sce_7883 | 0.00E+00 | 0.00E+00 |
| SCE1572_9103 | sce_7884 | 0.00E+00 | 0.00E+00 |
| SCE1572_9104 | sce_7887 | 0.00E+00 | 0.00E+00 |
| SCE1572_9105 | sce_7888 | 2.00E-139 | 1.00E-131 |
| SCE1572_9107 | sce_7889 | 4.00E-53 | 2.00E-55 |
| SCE1572_9108 | sce_7890 | 6.00E-50 | 3.00E-51 |
| SCE1572_9109 | sce_7891 | 7.00E-79 | 2.00E-82 |
| SCE1572_9110 | sce_7892 | 0.00E+00 | 0.00E+00 |
| SCE1572_9111 | sce_7893 | 4.00E-77 | 3.00E-79 |
| SCE1572_9112 | sce_7894 | 8.00E-137 | 7.00E-135 |
| SCE1572_9113 | sce_7895 | 5.00E-71 | 5.00E-71 |
| SCE1572_9115 | sce_7897 | 2.00E-44 | 2.00E-44 |
| SCE1572_9116 | sce_7898 | 0.00E+00 | 0.00E+00 |
| SCE1572_9117 | sce_7899 | 0.00E+00 | 0.00E+00 |
| SCE1572_912 | sce_682 | 0.00E+00 | 0.00E+00 |
| SCE1572_9123 | sce_7901 | 2.00E-100 | 2.00E-100 |
| SCE1572_9124 | sce_7902 | 0.00E+00 | 0.00E+00 |
| SCE1572_9125 | sce_7903 | 2.00E-72 | 2.00E-66 |
| SCE1572_9126 | sce_7904 | 7.00E-71 | 2.00E-58 |
| SCE1572_9127 | sce_7905 | 4.00E-116 | 2.00E-117 |
| SCE1572_9128 | sce_7906 | 2.00E-73 | 2.00E-73 |
| SCE1572_9129 | sce_7907 | 0.00E+00 | 0.00E+00 |
| SCE1572_913 | sce_683 | 8.00E-59 | 1.00E-61 |
| SCE1572_9130 | sce_7908 | 5.00E-66 | 4.00E-62 |
| SCE1572_9131 | sce_7909 | 5.00E-26 | 2.00E-27 |
| SCE1572_9132 | sce_7910 | 1.00E-131 | 8.00E-132 |
| SCE1572_9134 | sce_7912 | 8.00E-89 | 9.00E-43 |
| SCE1572_9135 | sce_7913 | 1.00E-68 | 1.00E-56 |
| SCE1572_9136 | sce_7914 | 2.00E-79 | 2.00E-68 |
| SCE1572_914 | sce_684 | 2.00E-44 | 2.00E-44 |
| SCE1572_9143 | sce_8592 | 0.00E+00 | 0.00E+00 |
| SCE1572_9143 | sce_3937 | 0.00E+00 | 0.00E+00 |
| SCE1572_9144 | sce_7942 | 1.00E-108 | 6.00E-109 |
| SCE1572_9145 | sce_7943 | 7.00E-138 | 5.00E-139 |
| SCE1572_9147 | sce_7944 | 7.00E-128 | 7.00E-128 |
| SCE1572_9148 | sce_7945 | 0.00E+00 | 0.00E+00 |
| SCE1572_9149 | sce_7946 | 1.00E-104 | 1.00E-104 |
| SCE1572_9150 | sce_7947 | 1.00E-51 | 5.00E-31 |
| SCE1572_9151 | sce_7948 | 3.00E-50 | 6.00E-45 |
| SCE1572_9152 | sce_7949 | 0.00E+00 | 0.00E+00 |
| SCE1572_9153 | sce_7951 | 6.00E-83 | 6.00E-83 |
| SCE1572_9154 | sce_7952 | 0.00E+00 | 0.00E+00 |
| SCE1572_9155 | sce_7953 | 2.00E-172 | 1.00E-165 |
| SCE1572_9156 | sce_7954 | 0.00E+00 | 0.00E+00 |
| SCE1572_9157 | sce_7955 | 0.00E+00 | 0.00E+00 |
| SCE1572_9158 | sce_7956 | 5.00E-74 | 7.00E-65 |
| SCE1572_9160 | sce_7957 | 0.00E+00 | 0.00E+00 |
| SCE1572_9161 | sce_7958 | 3.00E-114 | 7.00E-119 |

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|--------------|----------|-----------|-----------|
| SCE1572_917 | sce_685 | 0.00E+00 | 0.00E+00 |
| SCE1572_9171 | sce_7098 | 6.00E-20 | 6.00E-27 |
| SCE1572_9173 | sce_7964 | 4.00E-40 | 5.00E-43 |
| SCE1572_9174 | sce_7965 | 8.00E-148 | 2.00E-158 |
| SCE1572_9175 | sce_7967 | 1.00E-107 | 1.00E-95 |
| SCE1572_9177 | sce_7969 | 0.00E+00 | 0.00E+00 |
| SCE1572_9177 | sce_5403 | 0.00E+00 | 0.00E+00 |
| SCE1572_9178 | sce_2177 | 8.00E-44 | 2.00E-55 |
| SCE1572_9179 | sce_7971 | 2.00E-87 | 1.00E-87 |
| SCE1572_918 | sce_686 | 0.00E+00 | 0.00E+00 |
| SCE1572_9181 | sce_7972 | 0.00E+00 | 0.00E+00 |
| SCE1572_9187 | sce_7985 | 7.00E-124 | 3.00E-123 |
| SCE1572_9188 | sce_7986 | 0.00E+00 | 0.00E+00 |
| SCE1572_9189 | sce_4575 | 5.00E-12 | 1.00E-12 |
| SCE1572_919 | sce_687 | 1.00E-72 | 1.00E-72 |
| SCE1572_9190 | sce_7987 | 1.00E-112 | 9.00E-113 |
| SCE1572_9191 | sce_7988 | 5.00E-55 | 5.00E-55 |
| SCE1572_9192 | sce_7386 | 0.00E+00 | 0.00E+00 |
| SCE1572_9193 | sce_7387 | 2.00E-55 | 2.00E-52 |
| SCE1572_9194 | sce_7388 | 7.00E-72 | 1.00E-75 |
| SCE1572_9195 | sce_7389 | 4.00E-88 | 5.00E-91 |
| SCE1572_9196 | sce_7990 | 2.00E-158 | 2.00E-159 |
| SCE1572_9197 | sce_1285 | 4.00E-56 | 3.00E-52 |
| SCE1572_9198 | sce_7991 | 7.00E-128 | 4.00E-131 |
| SCE1572_9199 | sce_7992 | 3.00E-139 | 3.00E-139 |
| SCE1572_92 | sce_81 | 0.00E+00 | 0.00E+00 |
| SCE1572_9200 | sce_7998 | 3.00E-15 | 4.00E-14 |
| SCE1572_9202 | sce_8000 | 0.00E+00 | 0.00E+00 |
| SCE1572_9203 | sce_8001 | 2.00E-114 | 3.00E-112 |
| SCE1572_9204 | sce_8002 | 3.00E-118 | 1.00E-120 |
| SCE1572_9205 | sce_8003 | 6.00E-72 | 2.00E-64 |
| SCE1572_9206 | sce_8004 | 3.00E-168 | 5.00E-167 |
| SCE1572_9209 | sce_8010 | 0.00E+00 | 0.00E+00 |
| SCE1572_921 | sce_688 | 0.00E+00 | 0.00E+00 |
| SCE1572_9210 | sce_8011 | 0.00E+00 | 0.00E+00 |
| SCE1572_9211 | sce_8012 | 1.00E-157 | 2.00E-156 |
| SCE1572_9212 | sce_8013 | 6.00E-159 | 3.00E-160 |
| SCE1572_9214 | sce_8014 | 0.00E+00 | 0.00E+00 |
| SCE1572_9215 | sce_8015 | 4.00E-42 | 2.00E-44 |
| SCE1572_9216 | sce_8016 | 0.00E+00 | 0.00E+00 |
| SCE1572_9217 | sce_8019 | 2.00E-180 | 0.00E+00 |
| SCE1572_922 | sce_689 | 7.00E-39 | 9.00E-35 |
| SCE1572_9220 | sce_8022 | 0.00E+00 | 0.00E+00 |
| SCE1572_9222 | sce_9351 | 6.00E-76 | 5.00E-76 |
| SCE1572_9223 | sce_7616 | 7.00E-80 | 7.00E-80 |
| SCE1572_923 | sce_690 | 2.00E-125 | 2.00E-106 |
| SCE1572_9235 | sce_4668 | 3.00E-45 | 7.00E-38 |
| SCE1572_9236 | sce_4669 | 3.00E-20 | 4.00E-25 |
| SCE1572_924 | sce_691 | 3.00E-68 | 4.00E-68 |
| SCE1572_9248 | sce_8023 | 0.00E+00 | 0.00E+00 |
| SCE1572_9249 | sce_8024 | 2.00E-168 | 1.00E-168 |
| SCE1572_925 | sce_692 | 2.00E-113 | 1.00E-104 |
| SCE1572_9250 | sce_8026 | 0.00E+00 | 0.00E+00 |
| SCE1572_9251 | sce_8027 | 0.00E+00 | 0.00E+00 |
| SCE1572_9253 | sce_8028 | 2.00E-108 | 2.00E-121 |
| SCE1572_9254 | sce_8029 | 2.00E-175 | 0.00E+00 |
| SCE1572_9255 | sce_8030 | 2.00E-157 | 1.00E-157 |
| SCE1572_9256 | sce_8031 | 8.00E-19 | 7.00E-16 |
| SCE1572_9258 | sce_8033 | 9.00E-151 | 4.00E-153 |
| SCE1572_9259 | sce_8034 | 2.00E-175 | 9.00E-166 |
| SCE1572_926 | sce_694 | 6.00E-131 | 1.00E-132 |
| SCE1572_9260 | sce_8035 | 0.00E+00 | 6.00E-176 |
| SCE1572_9261 | sce_8039 | 7.00E-33 | 3.00E-35 |
| SCE1572_9262 | sce_8041 | 3.00E-63 | 3.00E-63 |
| SCE1572_9263 | sce_8042 | 1.00E-50 | 1.00E-50 |
| SCE1572_9264 | sce_8043 | 8.00E-124 | 9.00E-132 |
| SCE1572_9265 | sce_8044 | 0.00E+00 | 0.00E+00 |
| SCE1572_9266 | sce_8047 | 1.00E-180 | 1.00E-141 |
| SCE1572_9268 | sce_8049 | 7.00E-137 | 2.00E-143 |
| SCE1572_9269 | sce_8050 | 3.00E-96 | 4.00E-109 |
| SCE1572_927 | sce_695 | 3.00E-109 | 6.00E-124 |
| SCE1572_9272 | sce_8052 | 7.00E-105 | 1.00E-101 |
| SCE1572_9273 | sce_8053 | 2.00E-136 | 8.00E-125 |
| SCE1572_9274 | sce_8054 | 0.00E+00 | 0.00E+00 |
| SCE1572_9275 | sce_8055 | 0.00E+00 | 0.00E+00 |
| SCE1572_9276 | sce_8056 | 0.00E+00 | 0.00E+00 |

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| SCE1572_9277 | sce_8057 | 7.00E-168 | 4.00E-149 |
| SCE1572_9278 | sce_8058 | 8.00E-46 | 5.00E-25 |
| SCE1572_9279 | sce_8059 | 2.00E-89 | 3.00E-126 |
| SCE1572_928 | sce_696 | 6.00E-98 | 2.00E-105 |
| SCE1572_9280 | sce_8060 | 4.00E-22 | 2.00E-47 |
| SCE1572_9281 | sce_8061 | 2.00E-96 | 3.00E-97 |
| SCE1572_9282 | sce_8062 | 2.00E-115 | 2.00E-135 |
| SCE1572_9283 | sce_8064 | 1.00E-79 | 1.00E-79 |
| SCE1572_9285 | sce_8065 | 1.00E-58 | 3.00E-51 |
| SCE1572_9286 | sce_8067 | 2.00E-164 | 5.00E-163 |
| SCE1572_9287 | sce_8068 | 0.00E+00 | 0.00E+00 |
| SCE1572_9288 | sce_8069 | 4.00E-45 | 4.00E-45 |
| SCE1572_929 | sce_697 | 1.00E-157 | 8.00E-155 |
| SCE1572_9290 | sce_8070 | 0.00E+00 | 0.00E+00 |
| SCE1572_9291 | sce_8071 | 1.00E-104 | 1.00E-104 |
| SCE1572_9292 | sce_8072 | 0.00E+00 | 0.00E+00 |
| SCE1572_9293 | sce_8073 | 0.00E+00 | 0.00E+00 |
| SCE1572_9294 | sce_8074 | 0.00E+00 | 1.00E-179 |
| SCE1572_9295 | sce_8075 | 0.00E+00 | 0.00E+00 |
| SCE1572_9296 | sce_8076 | 4.00E-177 | 4.00E-170 |
| SCE1572_9297 | sce_8077 | 1.00E-67 | 8.00E-76 |
| SCE1572_9298 | sce_8078 | 1.00E-67 | 2.00E-71 |
| SCE1572_9299 | sce_8079 | 1.00E-92 | 2.00E-101 |
| SCE1572_93 | sce_82 | 0.00E+00 | 0.00E+00 |
| SCE1572_930 | sce_698 | 2.00E-95 | 2.00E-95 |
| SCE1572_9300 | sce_8080 | 7.00E-167 | 3.00E-166 |
| SCE1572_9301 | sce_8081 | 4.00E-42 | 8.00E-41 |
| SCE1572_9302 | sce_8082 | 5.00E-30 | 5.00E-30 |
| SCE1572_9303 | sce_8083 | 1.00E-75 | 1.00E-75 |
| SCE1572_9304 | sce_8084 | 0.00E+00 | 0.00E+00 |
| SCE1572_9305 | sce_8085 | 6.00E-118 | 2.00E-129 |
| SCE1572_9306 | sce_8086 | 7.00E-172 | 0.00E+00 |
| SCE1572_9307 | sce_8087 | 0.00E+00 | 0.00E+00 |
| SCE1572_9308 | sce_8088 | 0.00E+00 | 0.00E+00 |
| SCE1572_931 | sce_699 | 4.00E-100 | 4.00E-100 |
| SCE1572_9310 | sce_8089 | 0.00E+00 | 0.00E+00 |
| SCE1572_9311 | sce_8090 | 1.00E-163 | 6.00E-168 |
| SCE1572_9312 | sce_8092 | 2.00E-89 | 3.00E-89 |
| SCE1572_9313 | sce_8093 | 4.00E-80 | 2.00E-78 |
| SCE1572_9314 | sce_8094 | 0.00E+00 | 0.00E+00 |
| SCE1572_9315 | sce_8095 | 2.00E-113 | 8.00E-136 |
| SCE1572_9316 | sce_8096 | 1.00E-135 | 4.00E-143 |
| SCE1572_9317 | sce_8097 | 4.00E-174 | 0.00E+00 |
| SCE1572_9318 | sce_8099 | 0.00E+00 | 0.00E+00 |
| SCE1572_9318 | sce_6289 | 0.00E+00 | 0.00E+00 |
| SCE1572_9320 | sce_8101 | 2.00E-144 | 2.00E-144 |
| SCE1572_9321 | sce_8102 | 7.00E-38 | 2.00E-32 |
| SCE1572_9322 | sce_8103 | 2.00E-61 | 2.00E-61 |
| SCE1572_9323 | sce_8104 | 0.00E+00 | 0.00E+00 |
| SCE1572_9324 | sce_8105 | 0.00E+00 | 0.00E+00 |
| SCE1572_9326 | sce_8106 | 6.00E-53 | 6.00E-48 |
| SCE1572_9327 | sce_8107 | 1.00E-24 | 1.00E-24 |
| SCE1572_9328 | sce_8108 | 0.00E+00 | 0.00E+00 |
| SCE1572_933 | sce_701 | 0.00E+00 | 0.00E+00 |
| SCE1572_9330 | sce_8109 | 5.00E-89 | 5.00E-89 |
| SCE1572_9331 | sce_8110 | 3.00E-112 | 3.00E-112 |
| SCE1572_9333 | sce_8112 | 2.00E-70 | 1.00E-74 |
| SCE1572_9334 | sce_8113 | 0.00E+00 | 0.00E+00 |
| SCE1572_9335 | sce_8114 | 3.00E-158 | 3.00E-145 |
| SCE1572_9336 | sce_8115 | 5.00E-72 | 6.00E-79 |
| SCE1572_9337 | sce_8116 | 0.00E+00 | 0.00E+00 |
| SCE1572_9337 | sce_5582 | 0.00E+00 | 0.00E+00 |
| SCE1572_9338 | sce_8117 | 3.00E-66 | 2.00E-66 |
| SCE1572_9339 | sce_8118 | 5.00E-25 | 5.00E-31 |
| SCE1572_934 | sce_702 | 1.00E-148 | 2.00E-142 |
| SCE1572_9340 | sce_8119 | 1.00E-133 | 1.00E-133 |
| SCE1572_9341 | sce_8120 | 1.00E-144 | 3.00E-138 |
| SCE1572_9342 | sce_8121 | 9.00E-39 | 9.00E-39 |
| SCE1572_9343 | sce_8123 | 3.00E-131 | 2.00E-132 |
| SCE1572_9344 | sce_8124 | 7.00E-157 | 2.00E-148 |
| SCE1572_9345 | sce_8125 | 0.00E+00 | 0.00E+00 |
| SCE1572_9346 | sce_8126 | 0.00E+00 | 0.00E+00 |
| SCE1572_9349 | sce_8130 | 3.00E-18 | 1.00E-22 |
| SCE1572_935 | sce_703 | 5.00E-139 | 6.00E-139 |
| SCE1572_9350 | sce_8131 | 0.00E+00 | 0.00E+00 |
| SCE1572_9351 | sce_8132 | 7.00E-62 | 7.00E-62 |

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| SCE1572_9352 | sce_8133 | 4.00E-102 | 2.00E-109 |
| SCE1572_9353 | sce_8134 | 0.00E+00 | 0.00E+00 |
| SCE1572_9354 | sce_8135 | 1.00E-84 | 7.00E-85 |
| SCE1572_9355 | sce_8136 | 3.00E-62 | 2.00E-62 |
| SCE1572_9356 | sce_8137 | 0.00E+00 | 0.00E+00 |
| SCE1572_9357 | sce_8138 | 0.00E+00 | 0.00E+00 |
| SCE1572_9358 | sce_8139 | 1.00E-131 | 4.00E-135 |
| SCE1572_9359 | sce_8140 | 6.00E-167 | 4.00E-167 |
| SCE1572_936 | sce_704 | 2.00E-112 | 1.00E-123 |
| SCE1572_9360 | sce_8141 | 2.00E-177 | 2.00E-173 |
| SCE1572_9362 | sce_8142 | 0.00E+00 | 0.00E+00 |
| SCE1572_9364 | sce_8144 | 0.00E+00 | 0.00E+00 |
| SCE1572_9365 | sce_8145 | 0.00E+00 | 0.00E+00 |
| SCE1572_9366 | sce_8146 | 2.00E-78 | 1.00E-87 |
| SCE1572_9367 | sce_8147 | 0.00E+00 | 0.00E+00 |
| SCE1572_9368 | sce_8148 | 2.00E-64 | 1.00E-53 |
| SCE1572_9369 | sce_8149 | 8.00E-13 | 8.00E-13 |
| SCE1572_937 | sce_705 | 4.00E-71 | 4.00E-66 |
| SCE1572_9370 | sce_8150 | 8.00E-124 | 2.00E-120 |
| SCE1572_9371 | sce_8151 | 5.00E-39 | 9.00E-47 |
| SCE1572_9372 | sce_8152 | 2.00E-168 | 2.00E-169 |
| SCE1572_9373 | sce_8153 | 5.00E-89 | 1.00E-95 |
| SCE1572_9374 | sce_8155 | 2.00E-172 | 4.00E-177 |
| SCE1572_9376 | sce_8157 | 3.00E-20 | 3.00E-20 |
| SCE1572_9377 | sce_8158 | 1.00E-67 | 5.00E-78 |
| SCE1572_9379 | sce_8159 | 0.00E+00 | 0.00E+00 |
| SCE1572_938 | sce_706 | 2.00E-22 | 6.00E-14 |
| SCE1572_9380 | sce_8160 | 7.00E-27 | 4.00E-44 |
| SCE1572_9381 | sce_8161 | 0.00E+00 | 0.00E+00 |
| SCE1572_9383 | sce_8162 | 0.00E+00 | 0.00E+00 |
| SCE1572_9384 | sce_8164 | 4.00E-76 | 3.00E-83 |
| SCE1572_9385 | sce_8165 | 2.00E-15 | 2.00E-23 |
| SCE1572_9386 | sce_8166 | 2.00E-155 | 2.00E-174 |
| SCE1572_9387 | sce_8167 | 0.00E+00 | 0.00E+00 |
| SCE1572_9388 | sce_8168 | 8.00E-88 | 2.00E-87 |
| SCE1572_9389 | sce_8169 | 0.00E+00 | 0.00E+00 |
| SCE1572_939 | sce_707 | 1.00E-107 | 3.00E-111 |
| SCE1572_9390 | sce_8170 | 1.00E-155 | 4.00E-155 |
| SCE1572_9391 | sce_8171 | 1.00E-34 | 1.00E-43 |
| SCE1572_9393 | sce_8172 | 2.00E-72 | 3.00E-64 |
| SCE1572_9394 | sce_8173 | 2.00E-150 | 4.00E-164 |
| SCE1572_9395 | sce_8174 | 7.00E-22 | 7.00E-20 |
| SCE1572_9396 | sce_8175 | 0.00E+00 | 0.00E+00 |
| SCE1572_9397 | sce_8179 | 2.00E-83 | 3.00E-84 |
| SCE1572_9398 | sce_8180 | 4.00E-115 | 8.00E-108 |
| SCE1572_9399 | sce_8181 | 8.00E-150 | 6.00E-149 |
| SCE1572_94 | sce_83 | 3.00E-46 | 3.00E-46 |
| SCE1572_940 | sce_708 | 0.00E+00 | 0.00E+00 |
| SCE1572_9400 | sce_8182 | 8.00E-36 | 1.00E-44 |
| SCE1572_9401 | sce_8183 | 1.00E-58 | 2.00E-58 |
| SCE1572_9402 | sce_8184 | 0.00E+00 | 0.00E+00 |
| SCE1572_9403 | sce_8185 | 1.00E-148 | 1.00E-140 |
| SCE1572_9404 | sce_8186 | 1.00E-106 | 6.00E-102 |
| SCE1572_9407 | sce_8189 | 0.00E+00 | 0.00E+00 |
| SCE1572_9408 | sce_8190 | 1.00E-85 | 6.00E-93 |
| SCE1572_9409 | sce_8191 | 0.00E+00 | 0.00E+00 |
| SCE1572_941 | sce_709 | 5.00E-29 | 2.00E-29 |
| SCE1572_9410 | sce_8192 | 0.00E+00 | 0.00E+00 |
| SCE1572_9411 | sce_8193 | 2.00E-147 | 1.00E-144 |
| SCE1572_9412 | sce_8195 | 7.00E-150 | 2.00E-147 |
| SCE1572_9413 | sce_8196 | 1.00E-154 | 5.00E-173 |
| SCE1572_9414 | sce_8198 | 0.00E+00 | 0.00E+00 |
| SCE1572_9416 | sce_8203 | 1.00E-69 | 1.00E-69 |
| SCE1572_9417 | sce_8204 | 0.00E+00 | 0.00E+00 |
| SCE1572_9418 | sce_8205 | 2.00E-72 | 2.00E-72 |
| SCE1572_9419 | sce_8206 | 4.00E-70 | 2.00E-70 |
| SCE1572_9420 | sce_8207 | 1.00E-61 | 4.00E-66 |
| SCE1572_9421 | sce_8208 | 0.00E+00 | 0.00E+00 |
| SCE1572_9422 | sce_8209 | 6.00E-53 | 7.00E-53 |
| SCE1572_9423 | sce_8210 | 9.00E-26 | 1.00E-24 |
| SCE1572_9424 | sce_8211 | 3.00E-66 | 5.00E-73 |
| SCE1572_9425 | sce_8212 | 2.00E-82 | 7.00E-89 |
| SCE1572_9426 | sce_8213 | 2.00E-105 | 1.00E-103 |
| SCE1572_9427 | sce_8214 | 1.00E-29 | 4.00E-24 |
| SCE1572_9428 | sce_8215 | 0.00E+00 | 0.00E+00 |
| SCE1572_9430 | sce_8219 | 1.00E-113 | 1.00E-123 |

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| SCE1572_9431 | sce_8220 | 3.00E-104 | 1.00E-108 |
| SCE1572_9432 | sce_8221 | 2.00E-135 | 8.00E-126 |
| SCE1572_9433 | sce_8222 | 1.00E-24 | 1.00E-24 |
| SCE1572_9434 | sce_8223 | 1.00E-139 | 3.00E-136 |
| SCE1572_9435 | sce_8224 | 0.00E+00 | 0.00E+00 |
| SCE1572_9436 | sce_8225 | 0.00E+00 | 0.00E+00 |
| SCE1572_9437 | sce_8226 | 2.00E-35 | 2.00E-35 |
| SCE1572_9439 | sce_8227 | 2.00E-107 | 2.00E-117 |
| SCE1572_9440 | sce_8228 | 4.00E-153 | 4.00E-138 |
| SCE1572_9441 | sce_8229 | 4.00E-134 | 3.00E-133 |
| SCE1572_9442 | sce_8230 | 5.00E-53 | 4.00E-53 |
| SCE1572_9443 | sce_6393 | 2.00E-07 | 3.00E-12 |
| SCE1572_9444 | sce_1718 | 0.00E+00 | 0.00E+00 |
| SCE1572_9446 | sce_8233 | 6.00E-43 | 8.00E-50 |
| SCE1572_9448 | sce_8235 | 0.00E+00 | 5.00E-179 |
| SCE1572_9449 | sce_8236 | 8.00E-156 | 2.00E-155 |
| SCE1572_945 | sce_710 | 5.00E-72 | 3.00E-74 |
| SCE1572_9450 | sce_8237 | 5.00E-171 | 5.00E-171 |
| SCE1572_9451 | sce_8238 | 2.00E-15 | 5.00E-15 |
| SCE1572_9452 | sce_8239 | 2.00E-96 | 8.00E-86 |
| SCE1572_9458 | sce_8241 | 7.00E-58 | 4.00E-58 |
| SCE1572_946 | sce_711 | 6.00E-101 | 1.00E-91 |
| SCE1572_9460 | sce_8242 | 2.00E-138 | 2.00E-163 |
| SCE1572_9461 | sce_8243 | 6.00E-116 | 2.00E-113 |
| SCE1572_9462 | sce_8244 | 9.00E-54 | 3.00E-60 |
| SCE1572_9464 | sce_8245 | 3.00E-163 | 3.00E-161 |
| SCE1572_9466 | sce_8247 | 0.00E+00 | 9.00E-175 |
| SCE1572_9467 | sce_8248 | 3.00E-110 | 6.00E-155 |
| SCE1572_9468 | sce_8249 | 0.00E+00 | 0.00E+00 |
| SCE1572_9469 | sce_8250 | 0.00E+00 | 0.00E+00 |
| SCE1572_9470 | sce_8251 | 1.00E-67 | 2.00E-70 |
| SCE1572_9473 | sce_8252 | 3.00E-137 | 2.00E-139 |
| SCE1572_9474 | sce_8253 | 1.00E-179 | 4.00E-180 |
| SCE1572_9475 | sce_8254 | 7.00E-145 | 7.00E-149 |
| SCE1572_9476 | sce_8255 | 8.00E-77 | 1.00E-86 |
| SCE1572_9478 | sce_8265 | 6.00E-152 | 8.00E-151 |
| SCE1572_9479 | sce_8266 | 9.00E-132 | 6.00E-119 |
| SCE1572_9480 | sce_8267 | 5.00E-60 | 3.00E-47 |
| SCE1572_9481 | sce_8268 | 0.00E+00 | 0.00E+00 |
| SCE1572_9482 | sce_8269 | 1.00E-59 | 5.00E-69 |
| SCE1572_9483 | sce_8270 | 6.00E-171 | 0.00E+00 |
| SCE1572_9484 | sce_8271 | 3.00E-142 | 3.00E-142 |
| SCE1572_9485 | sce_8272 | 8.00E-73 | 7.00E-58 |
| SCE1572_9486 | sce_8273 | 2.00E-177 | 2.00E-177 |
| SCE1572_9487 | sce_2574 | 2.00E-09 | 3.00E-09 |
| SCE1572_9488 | sce_8274 | 1.00E-164 | 0.00E+00 |
| SCE1572_9489 | sce_8275 | 0.00E+00 | 0.00E+00 |
| SCE1572_949 | sce_2338 | 2.00E-62 | 4.00E-63 |
| SCE1572_9490 | sce_8276 | 4.00E-175 | 3.00E-178 |
| SCE1572_9492 | sce_8277 | 0.00E+00 | 0.00E+00 |
| SCE1572_9494 | sce_8280 | 4.00E-51 | 2.00E-62 |
| SCE1572_9495 | sce_8281 | 1.00E-172 | 2.00E-171 |
| SCE1572_9496 | sce_8282 | 3.00E-122 | 9.00E-126 |
| SCE1572_9497 | sce_8283 | 0.00E+00 | 0.00E+00 |
| SCE1572_9498 | sce_8284 | 8.00E-65 | 8.00E-65 |
| SCE1572_9499 | sce_8285 | 6.00E-69 | 6.00E-69 |
| SCE1572_95 | sce_84 | 9.00E-06 | 2.00E-06 |
| SCE1572_9500 | sce_8286 | 0.00E+00 | 0.00E+00 |
| SCE1572_9501 | sce_8287 | 0.00E+00 | 0.00E+00 |
| SCE1572_9502 | sce_8288 | 2.00E-127 | 1.00E-118 |
| SCE1572_9503 | sce_8290 | 5.00E-43 | 3.00E-43 |
| SCE1572_9504 | sce_8291 | 5.00E-156 | 1.00E-157 |
| SCE1572_9505 | sce_8292 | 3.00E-148 | 5.00E-160 |
| SCE1572_9506 | sce_8293 | 0.00E+00 | 0.00E+00 |
| SCE1572_9507 | sce_8294 | 2.00E-93 | 3.00E-102 |
| SCE1572_9508 | sce_8295 | 3.00E-149 | 6.00E-159 |
| SCE1572_9509 | sce_8296 | 5.00E-29 | 1.00E-26 |
| SCE1572_9510 | sce_8297 | 1.00E-15 | 5.00E-16 |
| SCE1572_9512 | sce_8299 | 0.00E+00 | 0.00E+00 |
| SCE1572_9513 | sce_8300 | 1.00E-114 | 3.00E-124 |
| SCE1572_9514 | sce_8301 | 4.00E-101 | 4.00E-101 |
| SCE1572_9515 | sce_8302 | 4.00E-179 | 0.00E+00 |
| SCE1572_9516 | sce_8303 | 2.00E-56 | 3.00E-50 |
| SCE1572_9517 | sce_8304 | 0.00E+00 | 0.00E+00 |
| SCE1572_9518 | sce_8305 | 1.00E-97 | 1.00E-117 |
| SCE1572_9520 | sce_3738 | 0.00E+00 | 0.00E+00 |

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| SCE1572_9523 | sce_8308 | 4.00E-65 | 2.00E-65 |
| SCE1572_9524 | sce_8309 | 2.00E-84 | 1.00E-91 |
| SCE1572_9526 | sce_8310 | 0.00E+00 | 0.00E+00 |
| SCE1572_9527 | sce_8311 | 1.00E-26 | 5.00E-29 |
| SCE1572_9528 | sce_8312 | 0.00E+00 | 0.00E+00 |
| SCE1572_9529 | sce_8313 | 0.00E+00 | 0.00E+00 |
| SCE1572_953 | sce_716 | 1.00E-36 | 7.00E-37 |
| SCE1572_9530 | sce_8314 | 0.00E+00 | 0.00E+00 |
| SCE1572_9531 | sce_8315 | 0.00E+00 | 0.00E+00 |
| SCE1572_9532 | sce_8316 | 4.00E-69 | 2.00E-69 |
| SCE1572_9533 | sce_8317 | 0.00E+00 | 0.00E+00 |
| SCE1572_9534 | sce_8318 | 0.00E+00 | 0.00E+00 |
| SCE1572_9536 | sce_8319 | 0.00E+00 | 0.00E+00 |
| SCE1572_9537 | sce_8320 | 2.00E-23 | 7.00E-25 |
| SCE1572_9538 | sce_8321 | 2.00E-63 | 3.00E-63 |
| SCE1572_9541 | sce_8323 | 9.00E-110 | 1.00E-139 |
| SCE1572_9542 | sce_8324 | 2.00E-48 | 2.00E-50 |
| SCE1572_9543 | sce_8325 | 3.00E-131 | 1.00E-119 |
| SCE1572_9547 | sce_2969 | 0.00E+00 | 0.00E+00 |
| SCE1572_9549 | sce_8328 | 1.00E-128 | 1.00E-128 |
| SCE1572_9550 | sce_8329 | 3.00E-59 | 3.00E-59 |
| SCE1572_9551 | sce_8330 | 3.00E-107 | 5.00E-98 |
| SCE1572_9554 | sce_8631 | 6.00E-14 | 1.00E-14 |
| SCE1572_9555 | sce_8332 | 7.00E-93 | 7.00E-95 |
| SCE1572_9556 | sce_8333 | 0.00E+00 | 0.00E+00 |
| SCE1572_9557 | sce_8334 | 3.00E-131 | 1.00E-130 |
| SCE1572_9560 | sce_8336 | 5.00E-134 | 6.00E-135 |
| SCE1572_9561 | sce_8337 | 0.00E+00 | 0.00E+00 |
| SCE1572_9563 | sce_8352 | 3.00E-177 | 4.00E-169 |
| SCE1572_9564 | sce_8353 | 2.00E-97 | 5.00E-92 |
| SCE1572_9565 | sce_8354 | 3.00E-149 | 5.00E-166 |
| SCE1572_9568 | sce_136 | 0.00E+00 | 0.00E+00 |
| SCE1572_957 | sce_719 | 0.00E+00 | 0.00E+00 |
| SCE1572_9570 | sce_7661 | 0.00E+00 | 0.00E+00 |
| SCE1572_9570 | sce_10204 | 0.00E+00 | 0.00E+00 |
| SCE1572_9570 | sce_3917 | 0.00E+00 | 0.00E+00 |
| SCE1572_9570 | sce_6095 | 0.00E+00 | 0.00E+00 |
| SCE1572_9570 | sce_6093 | 0.00E+00 | 0.00E+00 |
| SCE1572_9570 | sce_6092 | 0.00E+00 | 0.00E+00 |
| SCE1572_9570 | sce_6094 | 0.00E+00 | 0.00E+00 |
| SCE1572_9570 | sce_6107 | 0.00E+00 | 0.00E+00 |
| SCE1572_9570 | sce_6535 | 0.00E+00 | 0.00E+00 |
| SCE1572_9570 | sce_388 | 0.00E+00 | 0.00E+00 |
| SCE1572_9570 | sce_9920 | 0.00E+00 | 0.00E+00 |
| SCE1572_9570 | sce_9557 | 0.00E+00 | 0.00E+00 |
| SCE1572_9570 | sce_3003 | 0.00E+00 | 0.00E+00 |
| SCE1572_9570 | sce_7640 | 0.00E+00 | 0.00E+00 |
| SCE1572_9570 | sce_5835 | 0.00E+00 | 0.00E+00 |
| SCE1572_9570 | sce_8602 | 0.00E+00 | 0.00E+00 |
| SCE1572_9570 | sce_8618 | 0.00E+00 | 0.00E+00 |
| SCE1572_9570 | sce_2065 | 0.00E+00 | 0.00E+00 |
| SCE1572_9570 | sce_4513 | 0.00E+00 | 0.00E+00 |
| SCE1572_9570 | sce_3085 | 0.00E+00 | 0.00E+00 |
| SCE1572_9571 | sce_8364 | 1.00E-154 | 8.00E-174 |
| SCE1572_9572 | sce_8365 | 1.00E-18 | 2.00E-19 |
| SCE1572_9573 | sce_8366 | 9.00E-57 | 3.00E-78 |
| SCE1572_9574 | sce_8367 | 4.00E-37 | 3.00E-32 |
| SCE1572_9576 | sce_8368 | 2.00E-56 | 2.00E-53 |
| SCE1572_9577 | sce_8369 | 1.00E-85 | 1.00E-68 |
| SCE1572_9579 | sce_4341 | 2.00E-169 | 4.00E-161 |
| SCE1572_958 | sce_720 | 3.00E-71 | 2.00E-74 |
| SCE1572_959 | sce_721 | 0.00E+00 | 0.00E+00 |
| SCE1572_9597 | sce_9238 | 0.00E+00 | 0.00E+00 |
| SCE1572_9597 | sce_4347 | 0.00E+00 | 0.00E+00 |
| SCE1572_9598 | sce_4593 | 0.00E+00 | 0.00E+00 |
| SCE1572_960 | sce_722 | 6.00E-88 | 6.00E-88 |
| SCE1572_9601 | sce_9564 | 0.00E+00 | 0.00E+00 |
| SCE1572_9603 | sce_8430 | 9.00E-110 | 1.00E-108 |
| SCE1572_961 | sce_723 | 7.00E-66 | 2.00E-65 |
| SCE1572_9617 | sce_8431 | 6.00E-139 | 8.00E-138 |
| SCE1572_9618 | sce_8432 | 3.00E-92 | 4.00E-102 |
| SCE1572_962 | sce_724 | 0.00E+00 | 0.00E+00 |
| SCE1572_9621 | sce_8435 | 0.00E+00 | 0.00E+00 |
| SCE1572_9622 | sce_8435 | 3.00E-176 | 0.00E+00 |
| SCE1572_9623 | sce_8436 | 0.00E+00 | 0.00E+00 |
| SCE1572_9624 | sce_8437 | 0.00E+00 | 0.00E+00 |

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| SCE1572_9625 | sce_8438 | 0.00E+00 | 0.00E+00 |
| SCE1572_9627 | sce_2065 | 0.00E+00 | 0.00E+00 |
| SCE1572_9627 | sce_8618 | 0.00E+00 | 0.00E+00 |
| SCE1572_9628 | sce_1657 | 4.00E-159 | 2.00E-161 |
| SCE1572_9629 | sce_8441 | 0.00E+00 | 0.00E+00 |
| SCE1572_963 | sce_725 | 0.00E+00 | 0.00E+00 |
| SCE1572_9631 | sce_8443 | 6.00E-32 | 1.00E-31 |
| SCE1572_9632 | sce_8444 | 1.00E-109 | 3.00E-112 |
| SCE1572_9633 | sce_8445 | 0.00E+00 | 0.00E+00 |
| SCE1572_9634 | sce_8446 | 0.00E+00 | 0.00E+00 |
| SCE1572_9635 | sce_8447 | 3.00E-109 | 2.00E-113 |
| SCE1572_9636 | sce_8448 | 0.00E+00 | 0.00E+00 |
| SCE1572_9637 | sce_8449 | 1.00E-33 | 2.00E-28 |
| SCE1572_9638 | sce_8450 | 3.00E-80 | 1.00E-93 |
| SCE1572_964 | sce_726 | 2.00E-68 | 8.00E-71 |
| SCE1572_9640 | sce_8451 | 0.00E+00 | 0.00E+00 |
| SCE1572_9640 | sce_9407 | 0.00E+00 | 0.00E+00 |
| SCE1572_9640 | sce_4817 | 0.00E+00 | 0.00E+00 |
| SCE1572_9640 | sce_3765 | 0.00E+00 | 0.00E+00 |
| SCE1572_9641 | sce_8452 | 0.00E+00 | 0.00E+00 |
| SCE1572_9642 | sce_8453 | 5.00E-42 | 4.00E-56 |
| SCE1572_9643 | sce_8454 | 0.00E+00 | 0.00E+00 |
| SCE1572_9644 | sce_8455 | 1.00E-49 | 2.00E-50 |
| SCE1572_9645 | sce_8456 | 2.00E-41 | 2.00E-41 |
| SCE1572_9646 | sce_8457 | 0.00E+00 | 0.00E+00 |
| SCE1572_9647 | sce_8458 | 0.00E+00 | 0.00E+00 |
| SCE1572_9648 | sce_8459 | 2.00E-32 | 8.00E-25 |
| SCE1572_9652 | sce_10366 | 4.00E-92 | 3.00E-85 |
| SCE1572_9653 | sce_9503 | 0.00E+00 | 0.00E+00 |
| SCE1572_9653 | sce_10365 | 0.00E+00 | 0.00E+00 |
| SCE1572_9653 | sce_9908 | 0.00E+00 | 0.00E+00 |
| SCE1572_9656 | sce_8463 | 3.00E-101 | 8.00E-102 |
| SCE1572_9657 | sce_8464 | 3.00E-162 | 1.00E-157 |
| SCE1572_9658 | sce_8465 | 0.00E+00 | 0.00E+00 |
| SCE1572_9659 | sce_8466 | 0.00E+00 | 0.00E+00 |
| SCE1572_9660 | sce_8467 | 8.00E-121 | 3.00E-121 |
| SCE1572_9661 | sce_8469 | 2.00E-119 | 2.00E-119 |
| SCE1572_9662 | sce_8470 | 3.00E-74 | 6.00E-97 |
| SCE1572_9663 | sce_8471 | 1.00E-164 | 3.00E-157 |
| SCE1572_9664 | sce_8472 | 1.00E-42 | 4.00E-24 |
| SCE1572_9665 | sce_8473 | 3.00E-64 | 5.00E-62 |
| SCE1572_9666 | sce_8474 | 3.00E-24 | 5.00E-33 |
| SCE1572_9667 | sce_8475 | 2.00E-127 | 2.00E-127 |
| SCE1572_9668 | sce_8476 | 1.00E-139 | 3.00E-136 |
| SCE1572_9669 | sce_8477 | 2.00E-88 | 4.00E-95 |
| SCE1572_9670 | sce_8478 | 0.00E+00 | 0.00E+00 |
| SCE1572_9671 | sce_8479 | 3.00E-74 | 7.00E-73 |
| SCE1572_9672 | sce_8480 | 1.00E-166 | 4.00E-160 |
| SCE1572_9673 | sce_8481 | 1.00E-84 | 5.00E-89 |
| SCE1572_9674 | sce_8483 | 0.00E+00 | 0.00E+00 |
| SCE1572_9675 | sce_8484 | 0.00E+00 | 0.00E+00 |
| SCE1572_9676 | sce_8485 | 2.00E-28 | 8.00E-35 |
| SCE1572_9677 | sce_8486 | 3.00E-146 | 2.00E-134 |
| SCE1572_9678 | sce_8487 | 1.00E-121 | 5.00E-132 |
| SCE1572_9679 | sce_8488 | 3.00E-104 | 3.00E-103 |
| SCE1572_968 | sce_728 | 8.00E-79 | 2.00E-79 |
| SCE1572_9680 | sce_8489 | 0.00E+00 | 0.00E+00 |
| SCE1572_9681 | sce_8490 | 0.00E+00 | 0.00E+00 |
| SCE1572_9682 | sce_8491 | 4.00E-109 | 7.00E-115 |
| SCE1572_9683 | sce_8492 | 2.00E-109 | 2.00E-109 |
| SCE1572_9684 | sce_8493 | 0.00E+00 | 2.00E-172 |
| SCE1572_9685 | sce_8494 | 2.00E-32 | 3.00E-51 |
| SCE1572_9686 | sce_8495 | 2.00E-127 | 2.00E-134 |
| SCE1572_9687 | sce_8496 | 4.00E-168 | 4.00E-174 |
| SCE1572_9688 | sce_8497 | 0.00E+00 | 0.00E+00 |
| SCE1572_9689 | sce_8498 | 7.00E-129 | 9.00E-118 |
| SCE1572_969 | sce_729 | 2.00E-109 | 4.00E-117 |
| SCE1572_9690 | sce_8499 | 8.00E-49 | 7.00E-52 |
| SCE1572_9691 | sce_8500 | 0.00E+00 | 0.00E+00 |
| SCE1572_9692 | sce_8501 | 8.00E-76 | 7.00E-78 |
| SCE1572_9693 | sce_8502 | 0.00E+00 | 0.00E+00 |
| SCE1572_9694 | sce_8504 | 0.00E+00 | 0.00E+00 |
| SCE1572_9696 | sce_8505 | 0.00E+00 | 0.00E+00 |
| SCE1572_9697 | sce_8506 | 2.00E-108 | 2.00E-107 |
| SCE1572_9698 | sce_8507 | 2.00E-128 | 3.00E-129 |
| SCE1572_9699 | sce_8508 | 3.00E-145 | 8.00E-148 |

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| SCE1572_970 | sce_730 | 2.00E-30 | 1.00E-30 |
| SCE1572_9700 | sce_8509 | 9.00E-76 | 9.00E-71 |
| SCE1572_9702 | sce_8510 | 2.00E-81 | 1.00E-80 |
| SCE1572_9704 | sce_8511 | 9.00E-122 | 2.00E-133 |
| SCE1572_9705 | sce_8512 | 1.00E-68 | 2.00E-61 |
| SCE1572_9708 | sce_8513 | 0.00E+00 | 0.00E+00 |
| SCE1572_9709 | sce_8514 | 0.00E+00 | 0.00E+00 |
| SCE1572_971 | sce_731 | 6.00E-107 | 9.00E-111 |
| SCE1572_9710 | sce_8515 | 0.00E+00 | 0.00E+00 |
| SCE1572_9711 | sce_8516 | 0.00E+00 | 0.00E+00 |
| SCE1572_9713 | sce_8517 | 2.00E-86 | 9.00E-91 |
| SCE1572_9714 | sce_8518 | 1.00E-51 | 1.00E-51 |
| SCE1572_9715 | sce_8520 | 3.00E-44 | 1.00E-74 |
| SCE1572_9716 | sce_8521 | 5.00E-55 | 3.00E-60 |
| SCE1572_9717 | sce_8522 | 4.00E-160 | 4.00E-160 |
| SCE1572_9718 | sce_8523 | 0.00E+00 | 0.00E+00 |
| SCE1572_972 | sce_732 | 0.00E+00 | 0.00E+00 |
| SCE1572_9720 | sce_8524 | 0.00E+00 | 0.00E+00 |
| SCE1572_9721 | sce_8525 | 9.00E-144 | 4.00E-146 |
| SCE1572_9722 | sce_8526 | 2.00E-175 | 1.00E-175 |
| SCE1572_9725 | sce_8528 | 1.00E-96 | 2.00E-78 |
| SCE1572_9726 | sce_8529 | 4.00E-63 | 2.00E-64 |
| SCE1572_9728 | sce_8530 | 5.00E-155 | 5.00E-155 |
| SCE1572_9729 | sce_8531 | 6.00E-141 | 9.00E-162 |
| SCE1572_973 | sce_733 | 1.00E-90 | 9.00E-91 |
| SCE1572_9730 | sce_8532 | 3.00E-94 | 2.00E-103 |
| SCE1572_9731 | sce_8533 | 0.00E+00 | 0.00E+00 |
| SCE1572_9732 | sce_8534 | 0.00E+00 | 0.00E+00 |
| SCE1572_9733 | sce_8535 | 1.00E-153 | 2.00E-148 |
| SCE1572_9734 | sce_8536 | 1.00E-100 | 2.00E-100 |
| SCE1572_9735 | sce_8537 | 4.00E-171 | 0.00E+00 |
| SCE1572_9736 | sce_8538 | 6.00E-28 | 1.00E-06 |
| SCE1572_9737 | sce_8539 | 0.00E+00 | 0.00E+00 |
| SCE1572_9738 | sce_8540 | 4.00E-128 | 8.00E-123 |
| SCE1572_9740 | sce_8541 | 2.00E-126 | 1.00E-137 |
| SCE1572_9741 | sce_8542 | 0.00E+00 | 0.00E+00 |
| SCE1572_9742 | sce_8543 | 0.00E+00 | 0.00E+00 |
| SCE1572_9743 | sce_8544 | 4.00E-179 | 4.00E-179 |
| SCE1572_9744 | sce_8545 | 5.00E-105 | 2.00E-137 |
| SCE1572_9746 | sce_8547 | 3.00E-34 | 1.00E-30 |
| SCE1572_9747 | sce_8548 | 3.00E-87 | 1.00E-104 |
| SCE1572_9748 | sce_8549 | 0.00E+00 | 0.00E+00 |
| SCE1572_9749 | sce_8550 | 2.00E-109 | 2.00E-109 |
| SCE1572_975 | sce_734 | 1.00E-87 | 9.00E-80 |
| SCE1572_9750 | sce_8551 | 1.00E-140 | 1.00E-148 |
| SCE1572_9757 | sce_8552 | 3.00E-111 | 8.00E-105 |
| SCE1572_9758 | sce_8553 | 0.00E+00 | 0.00E+00 |
| SCE1572_9759 | sce_8555 | 7.00E-147 | 7.00E-158 |
| SCE1572_9760 | sce_8556 | 0.00E+00 | 0.00E+00 |
| SCE1572_9761 | sce_8557 | 7.00E-42 | 8.00E-42 |
| SCE1572_9762 | sce_8558 | 6.00E-86 | 1.00E-120 |
| SCE1572_9763 | sce_7918 | 7.00E-83 | 1.00E-83 |
| SCE1572_9764 | sce_7917 | 2.00E-82 | 8.00E-141 |
| SCE1572_9765 | sce_8560 | 4.00E-109 | 5.00E-113 |
| SCE1572_9766 | sce_8561 | 0.00E+00 | 0.00E+00 |
| SCE1572_9767 | sce_8562 | 2.00E-103 | 2.00E-103 |
| SCE1572_9768 | sce_8564 | 4.00E-134 | 8.00E-106 |
| SCE1572_9769 | sce_8565 | 3.00E-47 | 5.00E-51 |
| SCE1572_977 | sce_736 | 0.00E+00 | 0.00E+00 |
| SCE1572_977 | sce_6501 | 0.00E+00 | 0.00E+00 |
| SCE1572_9770 | sce_8566 | 0.00E+00 | 0.00E+00 |
| SCE1572_9771 | sce_8567 | 2.00E-53 | 2.00E-53 |
| SCE1572_9772 | sce_8568 | 2.00E-63 | 2.00E-63 |
| SCE1572_9773 | sce_8569 | 3.00E-178 | 3.00E-178 |
| SCE1572_9774 | sce_8570 | 0.00E+00 | 0.00E+00 |
| SCE1572_9776 | sce_8571 | 2.00E-140 | 4.00E-133 |
| SCE1572_9777 | sce_8572 | 6.00E-29 | 8.00E-33 |
| SCE1572_9778 | sce_8574 | 0.00E+00 | 0.00E+00 |
| SCE1572_9779 | sce_8575 | 2.00E-18 | 4.00E-11 |
| SCE1572_978 | sce_737 | 3.00E-100 | 6.00E-107 |
| SCE1572_9781 | sce_8576 | 2.00E-71 | 2.00E-69 |
| SCE1572_9782 | sce_8577 | 1.00E-25 | 2.00E-32 |
| SCE1572_9783 | sce_8578 | 8.00E-158 | 1.00E-154 |
| SCE1572_9784 | sce_8580 | 6.00E-79 | 4.00E-71 |
| SCE1572_9786 | sce_8584 | 6.00E-145 | 7.00E-146 |
| SCE1572_9787 | sce_8585 | 2.00E-169 | 0.00E+00 |

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|--------------|-----------|-----------|-----------|
| SCE1572_9788 | sce_8586 | 2.00E-125 | 2.00E-117 |
| SCE1572_9789 | sce_8587 | 4.00E-153 | 1.00E-149 |
| SCE1572_979 | sce_739 | 5.00E-23 | 4.00E-23 |
| SCE1572_9790 | sce_220 | 1.00E-40 | 9.00E-54 |
| SCE1572_9792 | sce_7989 | 4.00E-79 | 7.00E-82 |
| SCE1572_9793 | sce_8605 | 0.00E+00 | 0.00E+00 |
| SCE1572_9794 | sce_8606 | 0.00E+00 | 0.00E+00 |
| SCE1572_9796 | sce_8607 | 2.00E-101 | 3.00E-103 |
| SCE1572_9797 | sce_8608 | 2.00E-10 | 1.00E-10 |
| SCE1572_9798 | sce_8609 | 1.00E-21 | 5.00E-18 |
| SCE1572_9799 | sce_8610 | 1.00E-40 | 8.00E-41 |
| SCE1572_980 | sce_740 | 1.00E-123 | 1.00E-123 |
| SCE1572_9805 | sce_8612 | 1.00E-169 | 5.00E-178 |
| SCE1572_9807 | sce_8613 | 5.00E-41 | 4.00E-41 |
| SCE1572_9808 | sce_8614 | 0.00E+00 | 0.00E+00 |
| SCE1572_9809 | sce_8615 | 2.00E-85 | 5.00E-104 |
| SCE1572_981 | sce_741 | 0.00E+00 | 0.00E+00 |
| SCE1572_9810 | sce_8616 | 5.00E-170 | 1.00E-174 |
| SCE1572_9812 | sce_8618 | 0.00E+00 | 0.00E+00 |
| SCE1572_9812 | sce_2065 | 0.00E+00 | 0.00E+00 |
| SCE1572_9812 | sce_6535 | 0.00E+00 | 0.00E+00 |
| SCE1572_9812 | sce_6092 | 0.00E+00 | 0.00E+00 |
| SCE1572_9812 | sce_6095 | 0.00E+00 | 0.00E+00 |
| SCE1572_9812 | sce_3003 | 0.00E+00 | 0.00E+00 |
| SCE1572_9812 | sce_7661 | 0.00E+00 | 0.00E+00 |
| SCE1572_9812 | sce_9557 | 0.00E+00 | 0.00E+00 |
| SCE1572_9812 | sce_10204 | 0.00E+00 | 0.00E+00 |
| SCE1572_9812 | sce_5835 | 0.00E+00 | 0.00E+00 |
| SCE1572_9812 | sce_388 | 0.00E+00 | 0.00E+00 |
| SCE1572_9812 | sce_7640 | 0.00E+00 | 0.00E+00 |
| SCE1572_9812 | sce_4513 | 0.00E+00 | 0.00E+00 |
| SCE1572_9813 | sce_8619 | 5.00E-53 | 6.00E-48 |
| SCE1572_9814 | sce_8620 | 8.00E-58 | 2.00E-52 |
| SCE1572_9816 | sce_8621 | 1.00E-112 | 4.00E-122 |
| SCE1572_9819 | sce_3896 | 4.00E-08 | 5.00E-14 |
| SCE1572_9820 | sce_8622 | 4.00E-110 | 7.00E-105 |
| SCE1572_9821 | sce_8623 | 8.00E-129 | 4.00E-131 |
| SCE1572_9822 | sce_8624 | 3.00E-129 | 5.00E-132 |
| SCE1572_9823 | sce_7836 | 1.00E-66 | 2.00E-60 |
| SCE1572_983 | sce_742 | 0.00E+00 | 0.00E+00 |
| SCE1572_9835 | sce_7133 | 1.00E-84 | 4.00E-87 |
| SCE1572_9836 | sce_8655 | 2.00E-151 | 2.00E-151 |
| SCE1572_9837 | sce_8650 | 5.00E-118 | 2.00E-118 |
| SCE1572_984 | sce_744 | 1.00E-159 | 1.00E-159 |
| SCE1572_9846 | sce_7504 | 5.00E-14 | 7.00E-06 |
| SCE1572_9847 | sce_8635 | 0.00E+00 | 0.00E+00 |
| SCE1572_9849 | sce_8638 | 8.00E-156 | 4.00E-157 |
| SCE1572_985 | sce_745 | 0.00E+00 | 0.00E+00 |
| SCE1572_9850 | sce_6016 | 6.00E-14 | 5.00E-14 |
| SCE1572_9853 | sce_8645 | 2.00E-168 | 2.00E-171 |
| SCE1572_9854 | sce_8657 | 0.00E+00 | 0.00E+00 |
| SCE1572_9855 | sce_8658 | 0.00E+00 | 0.00E+00 |
| SCE1572_9856 | sce_2572 | 9.00E-90 | 8.00E-90 |
| SCE1572_9857 | sce_8667 | 0.00E+00 | 0.00E+00 |
| SCE1572_9858 | sce_8668 | 7.00E-77 | 3.00E-98 |
| SCE1572_9859 | sce_8669 | 0.00E+00 | 0.00E+00 |
| SCE1572_986 | sce_747 | 0.00E+00 | 0.00E+00 |
| SCE1572_9860 | sce_6222 | 0.00E+00 | 0.00E+00 |
| SCE1572_9860 | sce_4708 | 0.00E+00 | 0.00E+00 |
| SCE1572_9863 | sce_10287 | 1.00E-10 | 2.00E-12 |
| SCE1572_9864 | sce_8675 | 1.00E-100 | 7.00E-101 |
| SCE1572_9865 | sce_8676 | 0.00E+00 | 0.00E+00 |
| SCE1572_9866 | sce_8677 | 0.00E+00 | 0.00E+00 |
| SCE1572_9867 | sce_8678 | 2.00E-119 | 4.00E-104 |
| SCE1572_9868 | sce_8679 | 1.00E-125 | 6.00E-142 |
| SCE1572_9869 | sce_8680 | 1.00E-166 | 1.00E-164 |
| SCE1572_987 | sce_749 | 2.00E-180 | 0.00E+00 |
| SCE1572_9870 | sce_8681 | 1.00E-69 | 3.00E-68 |
| SCE1572_9871 | sce_8682 | 2.00E-161 | 0.00E+00 |
| SCE1572_9872 | sce_8685 | 2.00E-111 | 2.00E-111 |
| SCE1572_9873 | sce_9440 | 9.00E-94 | 1.00E-93 |
| SCE1572_9874 | sce_9439 | 4.00E-132 | 6.00E-123 |
| SCE1572_9876 | sce_8692 | 1.00E-34 | 1.00E-35 |
| SCE1572_9880 | sce_5093 | 2.00E-32 | 9.00E-20 |
| SCE1572_9882 | sce_2092 | 3.00E-100 | 3.00E-100 |
| SCE1572_9885 | sce_8696 | 7.00E-154 | 2.00E-154 |

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|--------------|----------|-----------|-----------|
| SCE1572_9886 | sce_8697 | 0.00E+00 | 0.00E+00 |
| SCE1572_9887 | sce_8698 | 2.00E-122 | 2.00E-118 |
| SCE1572_9888 | sce_8699 | 0.00E+00 | 0.00E+00 |
| SCE1572_9889 | sce_8700 | 0.00E+00 | 0.00E+00 |
| SCE1572_9890 | sce_8701 | 0.00E+00 | 0.00E+00 |
| SCE1572_9892 | sce_8703 | 5.00E-07 | 1.00E-11 |
| SCE1572_9893 | sce_8704 | 0.00E+00 | 0.00E+00 |
| SCE1572_9894 | sce_8705 | 2.00E-06 | 8.00E-15 |
| SCE1572_9895 | sce_8706 | 0.00E+00 | 0.00E+00 |
| SCE1572_9898 | sce_8708 | 2.00E-83 | 2.00E-83 |
| SCE1572_9899 | sce_8709 | 6.00E-79 | 8.00E-80 |
| SCE1572_990 | sce_750 | 0.00E+00 | 0.00E+00 |
| SCE1572_9900 | sce_8710 | 0.00E+00 | 0.00E+00 |
| SCE1572_9902 | sce_8712 | 4.00E-136 | 9.00E-127 |
| SCE1572_9903 | sce_8713 | 0.00E+00 | 0.00E+00 |
| SCE1572_9904 | sce_7561 | 1.00E-30 | 1.00E-31 |
| SCE1572_9907 | sce_8718 | 0.00E+00 | 0.00E+00 |
| SCE1572_9908 | sce_8719 | 0.00E+00 | 0.00E+00 |
| SCE1572_9910 | sce_8720 | 8.00E-91 | 6.00E-93 |
| SCE1572_9911 | sce_8721 | 1.00E-140 | 1.00E-142 |
| SCE1572_9912 | sce_8722 | 4.00E-47 | 5.00E-44 |
| SCE1572_9914 | sce_8724 | 8.00E-26 | 8.00E-29 |
| SCE1572_9915 | sce_8725 | 0.00E+00 | 0.00E+00 |
| SCE1572_9916 | sce_8726 | 0.00E+00 | 0.00E+00 |
| SCE1572_9917 | sce_8727 | 3.00E-97 | 7.00E-97 |
| SCE1572_992 | sce_752 | 0.00E+00 | 0.00E+00 |
| SCE1572_9920 | sce_3794 | 0.00E+00 | 0.00E+00 |
| SCE1572_9921 | sce_8730 | 0.00E+00 | 0.00E+00 |
| SCE1572_9923 | sce_8731 | 0.00E+00 | 0.00E+00 |
| SCE1572_9924 | sce_8732 | 0.00E+00 | 0.00E+00 |
| SCE1572_9924 | sce_5721 | 0.00E+00 | 0.00E+00 |
| SCE1572_9926 | sce_8733 | 1.00E-61 | 9.00E-63 |
| SCE1572_9927 | sce_8734 | 0.00E+00 | 0.00E+00 |
| SCE1572_9928 | sce_8735 | 3.00E-50 | 6.00E-40 |
| SCE1572_993 | sce_753 | 4.00E-105 | 3.00E-116 |
| SCE1572_9930 | sce_8737 | 0.00E+00 | 0.00E+00 |
| SCE1572_9931 | sce_8738 | 4.00E-64 | 5.00E-71 |
| SCE1572_9935 | sce_8739 | 1.00E-34 | 2.00E-42 |
| SCE1572_9936 | sce_8740 | 6.00E-96 | 1.00E-95 |
| SCE1572_9939 | sce_6035 | 1.00E-71 | 3.00E-80 |
| SCE1572_9942 | sce_8792 | 2.00E-167 | 2.00E-167 |
| SCE1572_9943 | sce_8791 | 3.00E-70 | 2.00E-69 |
| SCE1572_9946 | sce_3894 | 5.00E-20 | 4.00E-16 |
| SCE1572_9949 | sce_6031 | 2.00E-46 | 2.00E-46 |
| SCE1572_9950 | sce_8747 | 2.00E-160 | 3.00E-150 |
| SCE1572_9951 | sce_8748 | 1.00E-110 | 1.00E-102 |
| SCE1572_9952 | sce_8750 | 2.00E-124 | 1.00E-133 |
| SCE1572_9953 | sce_7598 | 0.00E+00 | 0.00E+00 |
| SCE1572_9954 | sce_7599 | 0.00E+00 | 0.00E+00 |
| SCE1572_9955 | sce_7600 | 5.00E-150 | 2.00E-144 |
| SCE1572_9956 | sce_7601 | 2.00E-100 | 2.00E-100 |
| SCE1572_9957 | sce_7602 | 3.00E-22 | 3.00E-22 |
| SCE1572_9958 | sce_7603 | 8.00E-62 | 1.00E-65 |
| SCE1572_9959 | sce_9664 | 0.00E+00 | 0.00E+00 |
| SCE1572_996 | sce_754 | 0.00E+00 | 0.00E+00 |
| SCE1572_9960 | sce_9662 | 0.00E+00 | 0.00E+00 |
| SCE1572_9963 | sce_8755 | 0.00E+00 | 0.00E+00 |
| SCE1572_9963 | sce_8753 | 0.00E+00 | 0.00E+00 |
| SCE1572_9963 | sce_7818 | 0.00E+00 | 0.00E+00 |
| SCE1572_9963 | sce_7815 | 0.00E+00 | 0.00E+00 |
| SCE1572_9964 | sce_8755 | 0.00E+00 | 0.00E+00 |
| SCE1572_9964 | sce_7818 | 0.00E+00 | 0.00E+00 |
| SCE1572_9964 | sce_8753 | 0.00E+00 | 0.00E+00 |
| SCE1572_9964 | sce_7814 | 0.00E+00 | 0.00E+00 |
| SCE1572_9964 | sce_7815 | 0.00E+00 | 0.00E+00 |
| SCE1572_9966 | sce_3146 | 3.00E-10 | 4.00E-12 |
| SCE1572_9967 | sce_8760 | 0.00E+00 | 8.00E-173 |
| SCE1572_9968 | sce_8762 | 2.00E-43 | 6.00E-52 |
| SCE1572_9969 | sce_8763 | 1.00E-69 | 2.00E-75 |
| SCE1572_997 | sce_755 | 3.00E-115 | 6.00E-112 |
| SCE1572_9970 | sce_8765 | 6.00E-41 | 6.00E-44 |
| SCE1572_9971 | sce_8766 | 5.00E-133 | 6.00E-133 |
| SCE1572_9972 | sce_8767 | 3.00E-111 | 2.00E-107 |
| SCE1572_9973 | sce_8768 | 0.00E+00 | 0.00E+00 |
| SCE1572_9974 | sce_8770 | 9.00E-109 | 5.00E-93 |
| SCE1572_9975 | sce_8771 | 0.00E+00 | 0.00E+00 |

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| SCE1572_9977 | sce_8773 | 8.00E-165 | 2.00E-167 |
| SCE1572_998 | sce_756 | 9.00E-149 | 3.00E-153 |
| SCE1572_9980 | sce_8776 | 4.00E-101 | 1.00E-110 |
| SCE1572_9981 | sce_8777 | 0.00E+00 | 0.00E+00 |
| SCE1572_9982 | sce_8778 | 0.00E+00 | 0.00E+00 |
| SCE1572_9983 | sce_7926 | 0.00E+00 | 0.00E+00 |
| SCE1572_9984 | sce_8784 | 9.00E-157 | 5.00E-157 |
| SCE1572_9985 | sce_5809 | 9.00E-49 | 2.00E-52 |
| SCE1572_9986 | sce_5808 | 4.00E-152 | 4.00E-146 |
| SCE1572_9987 | sce_8796 | 2.00E-137 | 7.00E-137 |
| SCE1572_9988 | sce_8797 | 1.00E-57 | 2.00E-56 |
| SCE1572_9989 | sce_8798 | 0.00E+00 | 0.00E+00 |
| SCE1572_9990 | sce_8799 | 3.00E-71 | 2.00E-109 |
| SCE1572_9991 | sce_8803 | 0.00E+00 | 0.00E+00 |
| SCE1572_9996 | sce_8812 | 0.00E+00 | 3.00E-164 |
| SCE1572_9997 | sce_8818 | 0.00E+00 | 0.00E+00 |
| SCE1572_9998 | sce_8820 | 2.00E-122 | 1.00E-124 |
| SCE1572_9999 | sce_8821 | 1.00E-127 | 5.00E-135 |

Table S8 A comparison of KEGG categories for So0157-2 and So ce56

| Presence | Category | Subcategory | Subsystem | Role | Organism A | Active in organism A | Organism B | Active in organism B |
|----------|-----------------------------|--------------------------------------|--|--|---------------|----------------------|------------|----------------------|
| A and B | Amino Acids and Derivatives | Alanine, serine, and glycine | Alanine biosynthesis | Alanine racemase (EC 5.1.1.1) | SCE1572_9334 | yes | sce_8113 | yes |
| A and B | Amino Acids and Derivatives | Alanine, serine, and glycine | Alanine biosynthesis | Branched-chain amino acid aminotransferase (EC 2.6.1.42) | SCE1572_354 | yes | sce_195 | yes |
| A and B | Amino Acids and Derivatives | Alanine, serine, and glycine | Alanine biosynthesis | Chaperone protein HscA | SCE1572_9421 | yes | sce_8208 | yes |
| A and B | Amino Acids and Derivatives | Alanine, serine, and glycine | Alanine biosynthesis | Cysteine desulfurase (EC 2.8.1.7) | SCE1572_1872 | yes | sce_1345 | yes |
| A and B | Amino Acids and Derivatives | Alanine, serine, and glycine | Alanine biosynthesis | Cysteine desulfurase (EC 2.8.1.7), lscS subfamily | SCE1572_9417 | yes | sce_8204 | yes |
| A and B | Amino Acids and Derivatives | Alanine, serine, and glycine | Alanine biosynthesis | Cysteine desulfurase (EC 2.8.1.7), SufS subfamily | SCE1572_10250 | yes | sce_5192 | yes |
| A and B | Amino Acids and Derivatives | Alanine, serine, and glycine | Alanine biosynthesis | Ferredoxin, 2Fe-2S | SCE1572_9111 | yes | sce_7893 | yes |
| A and B | Amino Acids and Derivatives | Alanine, serine, and glycine | Alanine biosynthesis | Iron binding protein IscA for iron-sulfur cluster assembly | SCE1572_9419 | yes | sce_8206 | yes |
| A and B | Amino Acids and Derivatives | Alanine, serine, and glycine | Alanine biosynthesis | Iron-sulfur cluster assembly scaffold protein IscU | SCE1572_9418 | yes | sce_8205 | yes |
| A and B | Amino Acids and Derivatives | Alanine, serine, and glycine | Alanine biosynthesis | Iron-sulfur cluster regulator IscP | SCE1572_7588 | yes | sce_6444 | yes |
| A and B | Amino Acids and Derivatives | Alanine, serine, and glycine | Alanine biosynthesis | Valine--pyruvate aminotransferase (EC 2.6.1.66) | SCE1572_1439 | yes | sce_6322 | yes |
| A and B | Amino Acids and Derivatives | Alanine, serine, and glycine | Glycine Biosynthesis | 2-amino-3-ketobutyrate coenzyme A ligase (EC 2.3.1.29) | SCE1572_9365 | yes | sce_8145 | yes |
| A and B | Amino Acids and Derivatives | Alanine, serine, and glycine | Glycine Biosynthesis | L-threonine 3-dehydrogenase (EC 1.1.1.103) | SCE1572_9364 | yes | sce_8144 | yes |
| A and B | Amino Acids and Derivatives | Alanine, serine, and glycine | Glycine Biosynthesis | Low-specificity L-threonine aldolase (EC 4.1.2.5) | SCE1572_2736 | yes | sce_2275 | yes |
| A and B | Amino Acids and Derivatives | Alanine, serine, and glycine | Glycine Biosynthesis | Serine hydroxymethyltransferase (EC 2.1.2.1) | SCE1572_8655 | yes | sce_7370 | yes |
| A and B | Amino Acids and Derivatives | Alanine, serine, and glycine | Glycine and Serine Utilization | 2-amino-3-ketobutyrate coenzyme A ligase (EC 2.3.1.29) | SCE1572_9365 | yes | sce_8145 | yes |
| A and B | Amino Acids and Derivatives | Alanine, serine, and glycine | Glycine and Serine Utilization | Aminomethyltransferase (glycine cleavage system T protein) (EC 2.1.2) | SCE1572_2704 | yes | sce_2242 | yes |
| A and B | Amino Acids and Derivatives | Alanine, serine, and glycine | Glycine and Serine Utilization | Cystathionine beta-synthase (EC 4.2.1.22) | SCE1572_693 | yes | sce_496 | yes |
| A and B | Amino Acids and Derivatives | Alanine, serine, and glycine | Glycine and Serine Utilization | Cystathionine gamma-lyase (EC 4.4.1.1) | SCE1572_164 | yes | sce_6912 | yes |
| A and B | Amino Acids and Derivatives | Alanine, serine, and glycine | Glycine and Serine Utilization | D-3-phosphoglycerate dehydrogenase (EC 1.1.1.95) | SCE1572_1389 | yes | sce_1692 | yes |
| A and B | Amino Acids and Derivatives | Alanine, serine, and glycine | Glycine and Serine Utilization | Glycine cleavage system H protein | SCE1572_2703 | yes | sce_2241 | yes |
| A and B | Amino Acids and Derivatives | Alanine, serine, and glycine | Glycine and Serine Utilization | Glycine dehydrogenase [decarboxylating] (glycine cleavage system P1) | SCE1572_2702 | yes | sce_2240 | yes |
| A and B | Amino Acids and Derivatives | Alanine, serine, and glycine | Glycine and Serine Utilization | Glycine dehydrogenase [decarboxylating] (glycine cleavage system P2) | SCE1572_8088 | yes | sce_10237 | yes |
| A and B | Amino Acids and Derivatives | Alanine, serine, and glycine | Glycine and Serine Utilization | L-serine dehydratase (EC 4.3.1.17) | SCE1572_2497 | yes | sce_2075 | yes |
| A and B | Amino Acids and Derivatives | Alanine, serine, and glycine | Glycine and Serine Utilization | Phosphoserine aminotransferase (EC 2.6.1.52) | SCE1572_5915 | yes | sce_4919 | yes |
| A and B | Amino Acids and Derivatives | Alanine, serine, and glycine | Glycine and Serine Utilization | Phosphoserine phosphatase (EC 3.1.3.3) | SCE1572_985 | yes | sce_745 | yes |
| A and B | Amino Acids and Derivatives | Alanine, serine, and glycine | Glycine and Serine Utilization | Serine hydroxymethyltransferase (EC 2.1.2.1) | SCE1572_8655 | yes | sce_7370 | yes |
| A and B | Amino Acids and Derivatives | Alanine, serine, and glycine | Glycine and Serine Utilization | Seryl-tRNA synthetase (EC 6.1.1.11) | SCE1572_10462 | yes | sce_9101 | yes |
| A and B | Amino Acids and Derivatives | Alanine, serine, and glycine | Glycine and Serine Utilization | Threonine dehydratase, catabolic (EC 4.3.1.19) | SCE1572_5116 | yes | sce_4304 | yes |
| A and B | Amino Acids and Derivatives | Alanine, serine, and glycine | Glycine cleavage system | Aminomethyltransferase (glycine cleavage system T protein) (EC 2.1.2) | SCE1572_2704 | yes | sce_2242 | yes |
| A and B | Amino Acids and Derivatives | Alanine, serine, and glycine | Glycine cleavage system | Glycine cleavage system H protein | SCE1572_2703 | yes | sce_2241 | yes |
| A and B | Amino Acids and Derivatives | Alanine, serine, and glycine | Glycine cleavage system | Glycine cleavage system transcriptional activator GcvA | SCE1572_1245 | yes | sce_5041 | yes |
| A and B | Amino Acids and Derivatives | Alanine, serine, and glycine | Glycine cleavage system | Glycine dehydrogenase [decarboxylating] (glycine cleavage system P1) | SCE1572_2702 | yes | sce_2240 | yes |
| A and B | Amino Acids and Derivatives | Alanine, serine, and glycine | Glycine cleavage system | Glycine dehydrogenase [decarboxylating] (glycine cleavage system P2) | SCE1572_8088 | yes | sce_10237 | yes |
| A and B | Amino Acids and Derivatives | Alanine, serine, and glycine | Serine Biosynthesis | D-3-phosphoglycerate dehydrogenase (EC 1.1.1.95) | SCE1572_1389 | yes | sce_1692 | yes |
| A and B | Amino Acids and Derivatives | Alanine, serine, and glycine | Serine Biosynthesis | Phosphoserine aminotransferase (EC 2.6.1.52) | SCE1572_5915 | yes | sce_4919 | yes |
| A and B | Amino Acids and Derivatives | Alanine, serine, and glycine | Serine Biosynthesis | Phosphoserine phosphatase (EC 3.1.3.3) | SCE1572_985 | yes | sce_745 | yes |
| A and B | Amino Acids and Derivatives | Alanine, serine, and glycine | Serine Biosynthesis | Serine hydroxymethyltransferase (EC 2.1.2.1) | SCE1572_8655 | yes | sce_7370 | yes |
| B | Amino Acids and Derivatives | Alanine, serine, and glycine | Glycine cleavage system | Glycine cleavage system transcriptional activator GcvR | | no | sce_9889 | yes |
| A and B | Amino Acids and Derivatives | Arginine; urea cycle, polyamines | Arginine Biosynthesis -- gjo | Acetylglutamate kinase (EC 2.7.2.8) | SCE1572_92 | yes | sce_81 | yes |
| A and B | Amino Acids and Derivatives | Arginine; urea cycle, polyamines | Arginine Biosynthesis -- gjo | Argininosuccinate lyase (EC 4.3.2.1) | SCE1572_2405 | yes | sce_1959 | yes |
| A and B | Amino Acids and Derivatives | Arginine; urea cycle, polyamines | Arginine Biosynthesis -- gjo | Argininosuccinate synthase (EC 6.3.4.5) | SCE1572_6795 | yes | sce_5654 | yes |
| A and B | Amino Acids and Derivatives | Arginine; urea cycle, polyamines | Arginine Biosynthesis -- gjo | Glutamate N-acetyltransferase (EC 2.3.1.35) | SCE1572_3887 | yes | sce_3211 | yes |
| A and B | Amino Acids and Derivatives | Arginine; urea cycle, polyamines | Arginine Biosynthesis -- gjo | N-acetyl-gamma-glutamyl-phosphate reductase (EC 1.2.1.38) | SCE1572_6683 | yes | sce_5564 | yes |
| A and B | Amino Acids and Derivatives | Arginine; urea cycle, polyamines | Arginine Biosynthesis -- gjo | N-acetylglutamate synthase (EC 2.3.1.1) | SCE1572_3887 | yes | sce_3211 | yes |
| A and B | Amino Acids and Derivatives | Arginine; urea cycle, polyamines | Arginine Biosynthesis -- gjo | N-acetylmethionine carbamoyltransferase (EC 2.1.3.9) | SCE1572_93 | yes | sce_82 | yes |
| A and B | Amino Acids and Derivatives | Arginine; urea cycle, polyamines | Arginine Biosynthesis -- gjo | N-succinyl-L,L-diaminopimelate desuccinylase (EC 3.5.1.18) | SCE1572_3985 | yes | sce_3316 | yes |
| A and B | Amino Acids and Derivatives | Arginine; urea cycle, polyamines | Arginine Biosynthesis -- gjo | Ornithine carbamoyltransferase (EC 2.1.3.3) | SCE1572_9212 | yes | sce_8013 | yes |
| A and B | Amino Acids and Derivatives | Arginine; urea cycle, polyamines | Arginine Biosynthesis extended | Acetylglutamate kinase (EC 2.7.2.8) | SCE1572_92 | yes | sce_81 | yes |
| A and B | Amino Acids and Derivatives | Arginine; urea cycle, polyamines | Arginine Biosynthesis extended | Argininosuccinate lyase (EC 4.3.2.1) | SCE1572_2405 | yes | sce_1959 | yes |
| A and B | Amino Acids and Derivatives | Arginine; urea cycle, polyamines | Arginine Biosynthesis extended | Argininosuccinate synthase (EC 6.3.4.5) | SCE1572_6795 | yes | sce_5654 | yes |
| A and B | Amino Acids and Derivatives | Arginine; urea cycle, polyamines | Arginine Biosynthesis extended | Glutamate N-acetyltransferase (EC 2.3.1.35) | SCE1572_3887 | yes | sce_3211 | yes |
| A and B | Amino Acids and Derivatives | Arginine; urea cycle, polyamines | Arginine Biosynthesis extended | N-acetyl-gamma-glutamyl-phosphate reductase (EC 1.2.1.38) | SCE1572_6683 | yes | sce_5564 | yes |
| A and B | Amino Acids and Derivatives | Arginine; urea cycle, polyamines | Arginine Biosynthesis extended | N-acetylglutamate synthase (EC 2.3.1.1) | SCE1572_3887 | yes | sce_3211 | yes |
| A and B | Amino Acids and Derivatives | Arginine; urea cycle, polyamines | Arginine Biosynthesis extended | N-acetylmethionine carbamoyltransferase (EC 2.1.3.9) | SCE1572_93 | yes | sce_82 | yes |
| A and B | Amino Acids and Derivatives | Arginine; urea cycle, polyamines | Arginine Biosynthesis extended | N-succinyl-L,L-diaminopimelate desuccinylase (EC 3.5.1.18) | SCE1572_3985 | yes | sce_3316 | yes |
| A and B | Amino Acids and Derivatives | Arginine; urea cycle, polyamines | Arginine Biosynthesis extended | Ornithine carbamoyltransferase (EC 2.1.3.3) | SCE1572_9212 | yes | sce_8013 | yes |
| A and B | Amino Acids and Derivatives | Arginine; urea cycle, polyamines | Arginine and Ornithine Degradation | Agmatinase (EC 3.5.3.11) | SCE1572_47 | yes | sce_46 | yes |
| A and B | Amino Acids and Derivatives | Arginine; urea cycle, polyamines | Arginine and Ornithine Degradation | Arginine N-succinyltransferase (EC 2.3.1.109) | SCE1572_2280 | yes | sce_1826 | yes |
| A and B | Amino Acids and Derivatives | Arginine; urea cycle, polyamines | Arginine and Ornithine Degradation | Arginine decarboxylase (EC 4.1.1.19) | SCE1572_8115 | yes | sce_93 | yes |
| A and B | Amino Acids and Derivatives | Arginine; urea cycle, polyamines | Arginine and Ornithine Degradation | Biosynthetic arginine decarboxylase (EC 4.1.1.19) | SCE1572_3252 | yes | sce_2748 | yes |
| A and B | Amino Acids and Derivatives | Arginine; urea cycle, polyamines | Arginine and Ornithine Degradation | Delta-1-pyrroline-5-carboxylate dehydrogenase (EC 1.5.1.12) | SCE1572_6031 | yes | sce_4984 | yes |
| A and B | Amino Acids and Derivatives | Arginine; urea cycle, polyamines | Arginine and Ornithine Degradation | N-carbamoylputrescine amidase (3.5.1.53) | SCE1572_8402 | yes | sce_7162 | yes |
| A and B | Amino Acids and Derivatives | Arginine; urea cycle, polyamines | Arginine and Ornithine Degradation | NADP-specific glutamate dehydrogenase (EC 1.4.1.4) | SCE1572_15044 | yes | sce_6937 | yes |
| A and B | Amino Acids and Derivatives | Arginine; urea cycle, polyamines | Arginine and Ornithine Degradation | Ornithine carbonyltransferase (EC 2.1.3.3) | SCE1572_9212 | yes | sce_8013 | yes |
| A and B | Amino Acids and Derivatives | Arginine; urea cycle, polyamines | Arginine and Ornithine Degradation | Ornithine cyclodiaminase (EC 4.3.1.12) | SCE1572_3173 | yes | sce_2667 | yes |
| A and B | Amino Acids and Derivatives | Arginine; urea cycle, polyamines | Arginine and Ornithine Degradation | Succinylglutamic semialdehyde dehydrogenase (EC 1.2.1.71) | SCE1572_1008 | yes | sce_761 | yes |
| A and B | Amino Acids and Derivatives | Arginine; urea cycle, polyamines | Arginine and Ornithine Degradation | Succinylornithine transaminase (EC 2.6.1.81) | SCE1572_5 | yes | sce_5 | yes |
| A and B | Amino Acids and Derivatives | Arginine; urea cycle, polyamines | Polyamine Metabolism | ABC transporter, periplasmic spermidine putrescine-binding protein PotA (TC SCE1572_11387) | | yes | sce_10223 | yes |
| A and B | Amino Acids and Derivatives | Arginine; urea cycle, polyamines | Polyamine Metabolism | Agmatinase (EC 3.5.3.11) | SCE1572_47 | yes | sce_46 | yes |
| A and B | Amino Acids and Derivatives | Arginine; urea cycle, polyamines | Polyamine Metabolism | Arginine decarboxylase (EC 4.1.1.19) | SCE1572_8115 | yes | sce_93 | yes |
| A and B | Amino Acids and Derivatives | Arginine; urea cycle, polyamines | Polyamine Metabolism | Biosynthetic arginine decarboxylase (EC 4.1.1.19) | SCE1572_3252 | yes | sce_2748 | yes |
| A and B | Amino Acids and Derivatives | Arginine; urea cycle, polyamines | Polyamine Metabolism | N-carbamoylputrescine amidase (3.5.1.53) | SCE1572_8402 | yes | sce_7162 | yes |
| A and B | Amino Acids and Derivatives | Arginine; urea cycle, polyamines | Polyamine Metabolism | Putrescine transport ATP-binding protein PotA (TC 3.A.1.11.1) | SCE1572_11392 | yes | sce_10231 | yes |
| A and B | Amino Acids and Derivatives | Arginine; urea cycle, polyamines | Polyamine Metabolism | S-adenosylmethionine decarboxylase proenzyme (EC 4.1.1.50), prokaryotic | SCE1572_7524 | yes | sce_6348 | yes |
| A and B | Amino Acids and Derivatives | Arginine; urea cycle, polyamines | Polyamine Metabolism | Spermidine Putrescine ABC transporter permease component PotB (TC SCE1572_11391) | | yes | sce_10230 | yes |
| A and B | Amino Acids and Derivatives | Arginine; urea cycle, polyamines | Polyamine Metabolism | Spermidine Putrescine ABC transporter permease component PotC (TC SCE1572_11390) | | yes | sce_10229 | yes |
| A and B | Amino Acids and Derivatives | Arginine; urea cycle, polyamines | Polyamine Metabolism | Spermidine synthase (EC 2.5.1.16) | SCE1572_507 | yes | sce_1673 | yes |
| A and B | Amino Acids and Derivatives | Arginine; urea cycle, polyamines | Urea carboxylase and Allophanate hydrolase cluster | Urea carboxylase (EC 6.3.4.6) | SCE1572_6544 | yes | sce_800 | yes |
| A and B | Amino Acids and Derivatives | Arginine; urea cycle, polyamines | Urea decomposition | Nickel transporter UreH | SCE1572_1803 | yes | sce_6510 | yes |
| A and B | Amino Acids and Derivatives | Arginine; urea cycle, polyamines | Urea decomposition | Urea ABC transporter, ATPase protein Urd | SCE1572_7464 | yes | sce_6249 | yes |
| A and B | Amino Acids and Derivatives | Arginine; urea cycle, polyamines | Urea decomposition | Urea ABC transporter, ATPase protein UreE | SCE1572_7465 | yes | sce_6250 | yes |
| A and B | Amino Acids and Derivatives | Arginine; urea cycle, polyamines | Urea decomposition | Urea ABC transporter, permease protein UrdB | SCE1572_7462 | yes | sce_6247 | yes |
| A and B | Amino Acids and Derivatives | Arginine; urea cycle, polyamines | Urea decomposition | Urea ABC transporter, permease protein UrdC | SCE1572_7463 | yes | sce_6248 | yes |
| A and B | Amino Acids and Derivatives | Arginine; urea cycle, polyamines | Urea decomposition | Urea ABC transporter, substrate binding protein UrdA | SCE1572_7461 | yes | sce_6246 | yes |
| A and B | Amino Acids and Derivatives | Arginine; urea cycle, polyamines | Urea decomposition | Urea carboxylase (EC 6.3.4.6) | SCE1572_6544 | yes | sce_5500 | yes |
| A and B | Amino Acids and Derivatives | Arginine; urea cycle, polyamines | Urea decomposition | Urea carboxylase-related ABC transporter, ATPase protein | SCE1572_4525 | yes | sce_3784 | yes |
| A and B | Amino Acids and Derivatives | Arginine; urea cycle, polyamines | Urea decomposition | Urea carboxylase-related ABC transporter, periplasmic substrate-binding protein | SCE1572_4524 | yes | sce_2159 | yes |
| A and B | Amino Acids and Derivatives | Arginine; urea cycle, polyamines | Urea decomposition | Urea carboxylase-related ABC transporter, permease protein | SCE1572_4526 | yes | sce_3785 | yes |
| A and B | Amino Acids and Derivatives | Arginine; urea cycle, polyamines | Urea decomposition | Urea carboxylase-related amino acid permease | SCE1572_6545 | yes | sce_5501 | yes |
| A and B | Amino Acids and Derivatives | Arginine; urea cycle, polyamines | Urea decomposition | Urea carboxylase-related aminomethyltransferase (EC 2.1.2.10) | SCE1572_6542 | yes | sce_5498 | yes |
| A and B | Amino Acids and Derivatives | Arginine; urea cycle, polyamines | Urea decomposition | Urea decomposing protein Urd | SCE1572_3069 | yes | sce_1827 | yes |
| A and B | Amino Acids and Derivatives | Arginine; urea cycle, polyamines | Urea decomposition | Urease accessory protein UreF | SCE1572_3073 | yes | sce_7330 | yes |
| A and B | Amino Acids and Derivatives | Arginine; urea cycle, polyamines | Urea decomposition | Urease accessory protein UreG | SCE1572_3074 | yes | sce_7331 | yes |
| A and B | Amino Acids and Derivatives | Arginine; urea cycle, polyamines | Urea decomposition | Urease alpha subunit (EC 3.5.1.5) | SCE1572_3071 | yes | sce_7329 | yes |
| A and B | Amino Acids and Derivatives | Arginine; urea cycle, polyamines | Urea decomposition | Urease gamma subunit (EC 3.5.1.5) | SCE1572_3070 | yes | sce_7328 | yes |
| A | Amino Acids and Derivatives | Arginine; urea cycle, polyamines | Arginine Biosynthesis -- gjo | Acetylmethionine aminotransferase (EC 2.6.1.11) | SCE1572_10277 | yes | no | no |
| A | Amino Acids and Derivatives | Arginine; urea cycle, polyamines | Arginine Biosynthesis -- gjo | Acetylmethionine decarboxylase (EC 3.5.1.16) | SCE1572_5459 | yes | no | no |
| A | Amino Acids and Derivatives | Arginine; urea cycle, polyamines | Cyanophycin Metabolism | Cyanophycin synthase (EC 6.3.2.29)(EC 6.3.2.30) | SCE1572_9183 | yes | no | no |
| A | Amino Acids and Derivatives | Arginine; urea cycle, polyamines | Cyanophycin Metabolism | Cyanophycinase (EC 3.4.15.6) | SCE1572_9182 | yes | no | no |
| B | Amino Acids and Derivatives | Arginine and Ornithine Degradation | Arginine and Ornithine Degradation | Ornithine decarboxylase (EC 4.1.1.17) | | no | sce_93 | yes |
| A and B | Amino Acids and Derivatives | Aromatic amino acids and derivatives | Aromatic amino acid degradation | 4-hydroxyphenylpyruvate dioxygenase (EC 1.13.11.27) | SCE1572_4318 | | | |

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|---------|-----------------------------|---|---|--|---------------|-----|-----------|-----|
| A and B | Amino Acids and Derivatives | Branched-chain amino acids | Branched-Chain Amino Acid Biosynthesis | Leucine dehydrogenase (EC 1.4.1.9) | SCE1572_8281 | yes | sce_6950 | yes |
| A and B | Amino Acids and Derivatives | Branched-chain amino acids | Branched-Chain Amino Acid Biosynthesis | Threonine dehydratase, catabolic (EC 4.3.1.19) | SCE1572_5116 | yes | sce_4304 | yes |
| A and B | Amino Acids and Derivatives | Branched-chain amino acids | Branched-Chain Amino Acid Biosynthesis | Valine-pyruvate aminotransferase (EC 2.6.1.66) | SCE1572_1439 | yes | sce_6322 | yes |
| A and B | Amino Acids and Derivatives | Branched-chain amino acids | HMG-CoA | Biotin carboxyl carrier protein of methylcrotonyl-CoA carboxylase | SCE1572_4933 | yes | sce_4144 | yes |
| A and B | Amino Acids and Derivatives | Branched-chain amino acids | HMG-CoA | Branched-chain alpha-keto acid dehydrogenase, E1 component, alpha | SCE1572_2201 | yes | sce_1748 | yes |
| A and B | Amino Acids and Derivatives | Branched-chain amino acids | HMG-CoA | Branched-chain alpha-keto acid dehydrogenase, E1 component, beta | SCE1572_2200 | yes | sce_1747 | yes |
| A and B | Amino Acids and Derivatives | Branched-chain amino acids | HMG-CoA | Branched-chain amino acid aminotransferase (EC 2.6.1.42) | SCE1572_354 | yes | sce_195 | yes |
| A and B | Amino Acids and Derivatives | Branched-chain amino acids | HMG-CoA | Dihydropyrimidine acyltransferase component of branched-chain alpha- | SCE1572_2199 | yes | sce_1746 | yes |
| A and B | Amino Acids and Derivatives | Branched-chain amino acids | HMG-CoA | Hydroxymethylglutaryl-CoA lyase (EC 4.1.3.4) | SCE1572_5790 | yes | sce_4837 | yes |
| A and B | Amino Acids and Derivatives | Branched-chain amino acids | HMG-CoA | Hydroxymethylglutaryl-CoA reductase (EC 1.1.1.34) | SCE1572_4053 | yes | sce_3379 | yes |
| A and B | Amino Acids and Derivatives | Branched-chain amino acids | HMG-CoA | Hydroxymethylglutaryl-CoA synthase (EC 2.3.3.10) | SCE1572_864 | yes | sce_3568 | yes |
| A and B | Amino Acids and Derivatives | Branched-chain amino acids | HMG-CoA | Isovaleryl-CoA dehydrogenase (EC 1.3.99.10) | SCE1572_8971 | yes | sce_7733 | yes |
| A and B | Amino Acids and Derivatives | Branched-chain amino acids | HMG-CoA | Leucine dehydrogenase (EC 1.4.1.9) | SCE1572_8281 | yes | sce_6950 | yes |
| A and B | Amino Acids and Derivatives | Branched-chain amino acids | HMG-CoA | Methylcrotonyl-CoA carboxylase biotin-containing subunit (EC 6.4.1.4) | SCE1572_2729 | yes | sce_2267 | yes |
| A and B | Amino Acids and Derivatives | Branched-chain amino acids | HMG-CoA | Methylcrotonyl-CoA carboxylase carboxyl transferase subunit (EC 6.4.1.4) | SCE1572_3419 | yes | sce_2906 | yes |
| A and B | Amino Acids and Derivatives | Branched-chain amino acids | HMG-CoA | Methylglutaconyl-CoA hydratase (EC 4.2.1.18) | SCE1572_861 | yes | sce_1987 | yes |
| A and B | Amino Acids and Derivatives | Branched-chain amino acids | HMG-CoA | Succinyl-CoA:3-ketoadid-coenzyme A transferase subunit A (EC 2.8.3) | SCE1572_7617 | yes | sce_6477 | yes |
| A and B | Amino Acids and Derivatives | Branched-chain amino acids | HMG-CoA | Succinyl-CoA:3-ketoadid-coenzyme A transferase subunit B (EC 2.8.3) | SCE1572_7618 | yes | sce_6478 | yes |
| A and B | Amino Acids and Derivatives | Branched-chain amino acids | HMG-CoA | Biotin carboxyl carrier protein of methylcrotonyl-CoA carboxylase | SCE1572_4933 | yes | sce_4144 | yes |
| A and B | Amino Acids and Derivatives | Branched-chain amino acids | HMG-CoA | Hydroxymethylglutaryl-CoA lyase (EC 4.1.3.4) | SCE1572_5790 | yes | sce_4837 | yes |
| A and B | Amino Acids and Derivatives | Branched-chain amino acids | HMG-CoA | Isovaleryl-CoA dehydrogenase (EC 1.3.99.10) | SCE1572_8971 | yes | sce_7733 | yes |
| A and B | Amino Acids and Derivatives | Branched-chain amino acids | HMG-CoA | Methylcrotonyl-CoA carboxylase biotin-containing subunit (EC 6.4.1.4) | SCE1572_2729 | yes | sce_2267 | yes |
| A and B | Amino Acids and Derivatives | Branched-chain amino acids | HMG-CoA | Methylcrotonyl-CoA carboxylase carboxyl transferase subunit (EC 6.4.1.4) | SCE1572_3419 | yes | sce_2906 | yes |
| A and B | Amino Acids and Derivatives | Branched-chain amino acids | HMG-CoA | Methylglutaconyl-CoA hydratase (EC 4.2.1.18) | SCE1572_861 | yes | sce_1987 | yes |
| A and B | Amino Acids and Derivatives | Branched-chain amino acids | HMG-CoA | 3-hydroxyacyl-CoA dehydrogenase (EC 1.1.1.35) | SCE1572_60 | yes | sce_50 | yes |
| A and B | Amino Acids and Derivatives | Branched-chain amino acids | HMG-CoA | 3-ketoadid-CoA thiolase (EC 2.3.1.16) | SCE1572_61 | yes | sce_51 | yes |
| A and B | Amino Acids and Derivatives | Branched-chain amino acids | Isoleucine degradation | Acyl-CoA dehydrogenase, short-chain specific (EC 1.3.99.2) | SCE1572_1837 | yes | sce_1299 | yes |
| A and B | Amino Acids and Derivatives | Branched-chain amino acids | Isoleucine degradation | Branched-chain alpha-keto acid dehydrogenase, E1 component, alpha | SCE1572_2201 | yes | sce_1748 | yes |
| A and B | Amino Acids and Derivatives | Branched-chain amino acids | Isoleucine degradation | Branched-chain alpha-keto acid dehydrogenase, E1 component, beta | SCE1572_2200 | yes | sce_1747 | yes |
| A and B | Amino Acids and Derivatives | Branched-chain amino acids | Isoleucine degradation | Branched-chain amino acid aminotransferase (EC 2.6.1.42) | SCE1572_354 | yes | sce_195 | yes |
| A and B | Amino Acids and Derivatives | Branched-chain amino acids | Isoleucine degradation | Butyryl-CoA dehydrogenase (EC 1.3.99.2) | SCE1572_1711 | yes | sce_1225 | yes |
| A and B | Amino Acids and Derivatives | Branched-chain amino acids | Isoleucine degradation | Dihydropyrimidine acyltransferase component of branched-chain alpha- | SCE1572_2199 | yes | sce_1746 | yes |
| A and B | Amino Acids and Derivatives | Branched-chain amino acids | Isoleucine degradation | Enoyl-CoA hydratase (EC 4.2.1.17) | SCE1572_60 | yes | sce_50 | yes |
| A and B | Amino Acids and Derivatives | Branched-chain amino acids | Isoleucine degradation | Enoyl-CoA hydratase [isoleucine degradation] (EC 4.2.1.17) | SCE1572_60 | yes | sce_50 | yes |
| A and B | Amino Acids and Derivatives | Branched-chain amino acids | Isoleucine degradation | Transcriptional regulator BkR of isoleucine and valine catabolism oper | SCE1572_3384 | yes | sce_2871 | yes |
| A and B | Amino Acids and Derivatives | Branched-chain amino acids | Leucine Biosynthesis | 2-isopropylmalate synthase (EC 2.3.3.13) | SCE1572_4976 | yes | sce_4185 | yes |
| A and B | Amino Acids and Derivatives | Branched-chain amino acids | Leucine Biosynthesis | 3-isopropylmalate dehydratase large subunit (EC 4.2.1.33) | SCE1572_108 | yes | sce_96 | yes |
| A and B | Amino Acids and Derivatives | Branched-chain amino acids | Leucine Biosynthesis | 3-isopropylmalate dehydratase small subunit (EC 4.2.1.33) | SCE1572_107 | yes | sce_95 | yes |
| A and B | Amino Acids and Derivatives | Branched-chain amino acids | Leucine Biosynthesis | 3-isopropylmalate dehydrogenase (EC 1.1.1.85) | SCE1572_4978 | yes | sce_4187 | yes |
| A and B | Amino Acids and Derivatives | Branched-chain amino acids | Leucine Biosynthesis | Branched-chain amino acid aminotransferase (EC 2.6.1.42) | SCE1572_354 | yes | sce_195 | yes |
| A and B | Amino Acids and Derivatives | Branched-chain amino acids | Leucine Degradation and HMG-CoA Metabolism | Biotin carboxyl carrier protein of methylcrotonyl-CoA carboxylase | SCE1572_4933 | yes | sce_4144 | yes |
| A and B | Amino Acids and Derivatives | Branched-chain amino acids | Leucine Degradation and HMG-CoA Metabolism | Branched-chain alpha-keto acid dehydrogenase, E1 component, alpha | SCE1572_2201 | yes | sce_1748 | yes |
| A and B | Amino Acids and Derivatives | Branched-chain amino acids | Leucine Degradation and HMG-CoA Metabolism | Branched-chain alpha-keto acid dehydrogenase, E1 component, beta | SCE1572_2200 | yes | sce_1747 | yes |
| A and B | Amino Acids and Derivatives | Branched-chain amino acids | Leucine Degradation and HMG-CoA Metabolism | Branched-chain amino acid aminotransferase (EC 2.6.1.42) | SCE1572_354 | yes | sce_195 | yes |
| A and B | Amino Acids and Derivatives | Branched-chain amino acids | Leucine Degradation and HMG-CoA Metabolism | Dihydropyrimidine acyltransferase component of branched-chain alpha- | SCE1572_2199 | yes | sce_1746 | yes |
| A and B | Amino Acids and Derivatives | Branched-chain amino acids | Leucine Degradation and HMG-CoA Metabolism | Hydroxymethylglutaryl-CoA lyase (EC 4.1.3.4) | SCE1572_5790 | yes | sce_4837 | yes |
| A and B | Amino Acids and Derivatives | Branched-chain amino acids | Leucine Degradation and HMG-CoA Metabolism | Hydroxymethylglutaryl-CoA reductase (EC 1.1.1.34) | SCE1572_4053 | yes | sce_3379 | yes |
| A and B | Amino Acids and Derivatives | Branched-chain amino acids | Leucine Degradation and HMG-CoA Metabolism | Hydroxymethylglutaryl-CoA synthase (EC 2.3.3.10) | SCE1572_864 | yes | sce_3568 | yes |
| A and B | Amino Acids and Derivatives | Branched-chain amino acids | Leucine Degradation and HMG-CoA Metabolism | Isovaleryl-CoA dehydrogenase (EC 1.3.99.10) | SCE1572_8971 | yes | sce_7733 | yes |
| A and B | Amino Acids and Derivatives | Branched-chain amino acids | Leucine Degradation and HMG-CoA Metabolism | Leucine dehydrogenase (EC 1.4.1.9) | SCE1572_8281 | yes | sce_6950 | yes |
| A and B | Amino Acids and Derivatives | Branched-chain amino acids | Leucine Degradation and HMG-CoA Metabolism | Methylcrotonyl-CoA carboxylase biotin-containing subunit (EC 6.4.1.4) | SCE1572_2729 | yes | sce_2267 | yes |
| A and B | Amino Acids and Derivatives | Branched-chain amino acids | Leucine Degradation and HMG-CoA Metabolism | Methylcrotonyl-CoA carboxylase carboxyl transferase subunit (EC 6.4.1.4) | SCE1572_3419 | yes | sce_2906 | yes |
| A and B | Amino Acids and Derivatives | Branched-chain amino acids | Leucine Degradation and HMG-CoA Metabolism | Methylglutaconyl-CoA hydratase (EC 4.2.1.18) | SCE1572_861 | yes | sce_1987 | yes |
| A and B | Amino Acids and Derivatives | Branched-chain amino acids | Leucine Degradation and HMG-CoA Metabolism | Succinyl-CoA:3-ketoadid-coenzyme A transferase subunit A (EC 2.8.3) | SCE1572_7617 | yes | sce_6477 | yes |
| A and B | Amino Acids and Derivatives | Branched-chain amino acids | Leucine Degradation and HMG-CoA Metabolism | Succinyl-CoA:3-ketoadid-coenzyme A transferase subunit B (EC 2.8.3) | SCE1572_7618 | yes | sce_6478 | yes |
| A and B | Amino Acids and Derivatives | Branched-chain amino acids | Valine degradation | 3-hydroxyacyl-CoA dehydrogenase (EC 1.1.1.35) | SCE1572_60 | yes | sce_50 | yes |
| A and B | Amino Acids and Derivatives | Branched-chain amino acids | Valine degradation | Branched-chain alpha-keto acid dehydrogenase, E1 component, alpha | SCE1572_2201 | yes | sce_1748 | yes |
| A and B | Amino Acids and Derivatives | Branched-chain amino acids | Valine degradation | Branched-chain alpha-keto acid dehydrogenase, E1 component, beta | SCE1572_2200 | yes | sce_1747 | yes |
| A and B | Amino Acids and Derivatives | Branched-chain amino acids | Valine degradation | Branched-chain amino acid aminotransferase (EC 2.6.1.42) | SCE1572_354 | yes | sce_195 | yes |
| A and B | Amino Acids and Derivatives | Branched-chain amino acids | Valine degradation | Butyryl-CoA dehydrogenase (EC 1.3.99.2) | SCE1572_1711 | yes | sce_1225 | yes |
| A and B | Amino Acids and Derivatives | Branched-chain amino acids | Valine degradation | Dihydropyrimidine acyltransferase component of branched-chain alpha- | SCE1572_2199 | yes | sce_1746 | yes |
| A and B | Amino Acids and Derivatives | Branched-chain amino acids | Valine degradation | Enoyl-CoA hydratase (EC 4.2.1.17) | SCE1572_60 | yes | sce_50 | yes |
| A and B | Amino Acids and Derivatives | Branched-chain amino acids | Valine degradation | Enoyl-CoA hydratase [semialdehyde dehydrogenase (EC 1.2.1.27)] | SCE1572_5449 | yes | sce_7163 | yes |
| A and B | Amino Acids and Derivatives | Branched-chain amino acids | Valine degradation | Methylmalonate-semialdehyde dehydrogenase (EC 1.2.1.27) | SCE1572_5449 | yes | sce_7163 | yes |
| A and B | Amino Acids and Derivatives | Branched-chain amino acids | Valine degradation | Transcriptional regulator BkR of isoleucine and valine catabolism oper | SCE1572_3384 | yes | sce_2871 | yes |
| B | Amino Acids and Derivatives | Branched-Chain Amino Acid Biosynthesis | Branched-Chain Amino Acid Biosynthesis | Leucine-responsive regulatory protein, regulator for leucine (or trp) regulon and high-affinity branch | SCE1572_5095 | yes | sce_6297 | yes |
| A and B | Amino Acids and Derivatives | Glutamine, glutamate, aspartate, asparagine; at Glutamate and Aspartate uptake in Bacteria | Glutamine, glutamate, aspartate, asparagine; at Glutamate and Aspartate uptake in Bacteria | Asparagine synthetase [glutamine-hydrolyzing] (EC 6.3.5.4) | SCE1572_5095 | yes | sce_2297 | yes |
| A and B | Amino Acids and Derivatives | Glutamine, glutamate, aspartate, asparagine; at Glutamine, Glutamate, Aspartate and Asparagine Biosynthesis | Glutamine, glutamate, aspartate, asparagine; at Glutamine, Glutamate, Aspartate and Asparagine Biosynthesis | Sodium/glutamate symport protein | SCE1572_4740 | yes | sce_3961 | yes |
| A and B | Amino Acids and Derivatives | Glutamine, glutamate, aspartate, asparagine; at Glutamate dehydrogenases | Glutamine, glutamate, aspartate, asparagine; at Glutamate dehydrogenases | NAD-specific glutamate dehydrogenase (EC 1.4.1.2) | SCE1572_5775 | yes | sce_4821 | yes |
| A and B | Amino Acids and Derivatives | Glutamine, glutamate, aspartate, asparagine; at Glutamate dehydrogenases | Glutamine, glutamate, aspartate, asparagine; at Glutamate dehydrogenases | NADP-specific glutamate dehydrogenase (EC 1.4.1.4) | SCE1572_1504 | yes | sce_6937 | yes |
| A and B | Amino Acids and Derivatives | Glutamine, glutamate, aspartate, asparagine; at Glutamine, Glutamate, Aspartate and Asparagine Biosynthesis | Glutamine, glutamate, aspartate, asparagine; at Glutamine, Glutamate, Aspartate and Asparagine Biosynthesis | Asparagine synthetase [glutamine-hydrolyzing] (EC 6.3.5.4) | SCE1572_5095 | yes | sce_2297 | yes |
| A and B | Amino Acids and Derivatives | Glutamine, glutamate, aspartate, asparagine; at Glutamine, Glutamate, Aspartate and Asparagine Biosynthesis | Glutamine, glutamate, aspartate, asparagine; at Glutamine, Glutamate, Aspartate and Asparagine Biosynthesis | Aspartate aminotransferase (EC 2.6.1.1) | SCE1572_689 | yes | sce_1273 | yes |
| A and B | Amino Acids and Derivatives | Glutamine, glutamate, aspartate, asparagine; at Glutamine, Glutamate, Aspartate and Asparagine Biosynthesis | Glutamine, glutamate, aspartate, asparagine; at Glutamine, Glutamate, Aspartate and Asparagine Biosynthesis | Aspartate ammonia-lyase (EC 4.3.1.1) | SCE1572_545 | yes | sce_352 | yes |
| A and B | Amino Acids and Derivatives | Glutamine, glutamate, aspartate, asparagine; at Glutamine, Glutamate, Aspartate and Asparagine Biosynthesis | Glutamine, glutamate, aspartate, asparagine; at Glutamine, Glutamate, Aspartate and Asparagine Biosynthesis | Glutamate racemase (EC 5.1.1.3) | SCE1572_284 | yes | sce_5417 | yes |
| A and B | Amino Acids and Derivatives | Glutamine, glutamate, aspartate, asparagine; at Glutamine, Glutamate, Aspartate and Asparagine Biosynthesis | Glutamine, glutamate, aspartate, asparagine; at Glutamine, Glutamate, Aspartate and Asparagine Biosynthesis | Glutamate synthase [NADPH] large chain (EC 1.4.1.13) | SCE1572_6809 | yes | sce_5669 | yes |
| A and B | Amino Acids and Derivatives | Glutamine, glutamate, aspartate, asparagine; at Glutamine, Glutamate, Aspartate and Asparagine Biosynthesis | Glutamine, glutamate, aspartate, asparagine; at Glutamine, Glutamate, Aspartate and Asparagine Biosynthesis | Glutamate synthase [NADPH] small chain (EC 1.4.1.13) | SCE1572_5280 | yes | sce_4385 | yes |
| A and B | Amino Acids and Derivatives | Glutamine, glutamate, aspartate, asparagine; at Glutamine, Glutamate, Aspartate and Asparagine Biosynthesis | Glutamine, glutamate, aspartate, asparagine; at Glutamine, Glutamate, Aspartate and Asparagine Biosynthesis | Glutamine synthetase type I (EC 6.3.1.2) | SCE1572_9287 | yes | sce_8068 | yes |
| A and B | Amino Acids and Derivatives | Glutamine, glutamate, aspartate, asparagine; at Glutamine, Glutamate, Aspartate and Asparagine Biosynthesis | Glutamine, glutamate, aspartate, asparagine; at Glutamine, Glutamate, Aspartate and Asparagine Biosynthesis | L-asparaginase (EC 3.5.1.1) | SCE1572_4078 | yes | sce_3404 | yes |
| A and B | Amino Acids and Derivatives | Glutamine, glutamate, aspartate, asparagine; at Glutamine, Glutamate, Aspartate and Asparagine Biosynthesis | Glutamine, glutamate, aspartate, asparagine; at Glutamine, Glutamate, Aspartate and Asparagine Biosynthesis | NAD-specific glutamate dehydrogenase (EC 1.4.1.2) | SCE1572_5775 | yes | sce_4821 | yes |
| A and B | Amino Acids and Derivatives | Glutamine, glutamate, aspartate, asparagine; at Glutamine, Glutamate, Aspartate and Asparagine Biosynthesis | Glutamine, glutamate, aspartate, asparagine; at Glutamine, Glutamate, Aspartate and Asparagine Biosynthesis | NADP-specific glutamate dehydrogenase (EC 1.4.1.4) | SCE1572_1504 | yes | sce_6937 | yes |
| A and B | Amino Acids and Derivatives | Glutamine, glutamate, aspartate, asparagine; at Glutamine, Glutamate, Aspartate and Asparagine Biosynthesis | Glutamine, glutamate, aspartate, asparagine; at Glutamine, Glutamate, Aspartate and Asparagine Biosynthesis | glutamine synthetase family protein | SCE1572_5267 | yes | sce_4421 | yes |
| A and B | Amino Acids and Derivatives | Glutamine, glutamate, aspartate, asparagine; at Glutamine synthetases | Glutamine, glutamate, aspartate, asparagine; at Glutamine synthetases | Glutamine synthetase type I (EC 6.3.1.2) | SCE1572_9287 | yes | sce_8068 | yes |
| A | Amino Acids and Derivatives | Glutamine, glutamate, aspartate, asparagine; at Glutamine, Glutamate, Aspartate and Asparagine Biosynthesis | Glutamine, glutamate, aspartate, asparagine; at Glutamine, Glutamate, Aspartate and Asparagine Biosynthesis | Aspartate racemase (EC 5.1.1.13) | SCE1572_8667 | yes | no | no |
| A and B | Amino Acids and Derivatives | Histidine Metabolism | Histidine Biosynthesis | ATP phosphoribosyltransferase (EC 2.4.2.17) | SCE1572_11377 | yes | sce_10213 | yes |
| A and B | Amino Acids and Derivatives | Histidine Metabolism | Histidine Biosynthesis | ATP phosphoribosyltransferase regulatory subunit (EC 2.4.2.17) | SCE1572_11192 | yes | sce_9931 | yes |
| A and B | Amino Acids and Derivatives | Histidine Metabolism | Histidine Biosynthesis | Histidinol dehydrogenase (EC 1.1.1.23) | SCE1572_3264 | yes | sce_2759 | yes |
| A and B | Amino Acids and Derivatives | Histidine Metabolism | Histidine Biosynthesis | Histidinol-phosphate aminotransferase (EC 2.6.1.9) | SCE1572_5675 | yes | sce_4727 | yes |
| A and B | Amino Acids and Derivatives | Histidine Metabolism | Histidine Biosynthesis | Imidazole glycerol phosphate synthase amidotransferase subunit (EC 2.8.2) | SCE1572_3880 | yes | sce_3168 | yes |
| A and B | Amino Acids and Derivatives | Histidine Metabolism | Histidine Biosynthesis | Imidazole glycerol phosphate synthase cyclase subunit (EC 4.1.3.-) | SCE1572_7751 | yes | sce_6588 | yes |
| A and B | Amino Acids and Derivatives | Histidine Metabolism | Histidine Biosynthesis | 5-azidothiophenylphosphate dehydrogenase (EC 4.2.1.19) | SCE1572_8281 | yes | sce_3948 | yes |
| A and B | Amino Acids and Derivatives | Histidine Metabolism | Histidine Biosynthesis | Phosphoribosyl-AMP cyclohydrolase (EC 3.5.4.19) | SCE1572_641 | yes | sce_450 | yes |
| A and B | Amino Acids and Derivatives | Histidine Metabolism | Histidine Biosynthesis | Phosphoribosyl-ATP pyrophosphatase (EC 3.6.1.31) | SCE1572_641 | yes | sce_450 | yes |
| A and B | Amino Acids and Derivatives | Histidine Metabolism | Histidine Biosynthesis | Phosphoribosylformimino-5-aminoimidazole carboxamide ribotide isom | SCE1572_3830 | yes | sce_3157 | yes |
| A and B | Amino Acids and Derivatives | Histidine Metabolism | Histidine Degradation | Forminoglutamate iminohydrolase (EC 3.5.3.13) | SCE1572_1551 | yes | sce_1078 | yes |
| A and B | Amino Acids and Derivatives | Histidine Metabolism | Histidine Degradation | Histidine ammonia-lyase (EC 4.3.1.3) | SCE1572_8014 | yes | sce_6803 | yes |
| A and B | Amino Acids and Derivatives | Histidine Metabolism | Histidine Degradation | Imidazoleonepropionase (EC 3.5.2.7) | SCE1572_5759 | yes | sce_4807 | yes |
| A and B | Amino Acids and Derivatives | Histidine Metabolism | Histidine Degradation | N-formylglutamate deformylase (EC 3.5.1.68) | SCE1572_5999 | yes | sce_4951 | yes |
| A and B | Amino Acids and Derivatives | Histidine Metabolism | Histidine Degradation | Urocanate hydratase (EC 4.2.1.49) | SCE1572_10157 | yes | sce_8960 | yes |
| A and B | Amino Acids and Derivatives | Lysine, threonine, methionine, and cysteine | Cysteine Biosynthesis | Adenylylsulfate kinase (EC 2.7.1.25) | SCE1572_7923 | yes | sce_6720 | yes |
| A and B | Amino Acids and Derivatives | Lysine, threonine, methionine, and cysteine | Cysteine Biosynthesis | Cystathionine beta-synthase (EC 4.2.1.22) | SCE1572_693 | yes | sce_496 | yes |
| A and B | Amino Acids and Derivatives | Lysine, threonine, methionine, and cysteine | Cysteine Biosynthesis | Cystathionine gamma-lyase (EC 4.4.1.1) | SCE1572_164 | yes | sce_6912 | yes |
| A and B | Amino Acids and Derivatives | Lysine, threonine, methionine, and cysteine | Cysteine Biosynthesis | Cysteine synthase (EC 2.5.1.47) | SCE1572_3174 | yes | sce_3947 | yes |
| A and B | Amino Acids and Derivatives | Lysine, threonine, methionine, and cysteine | Cysteine Biosynthesis | Phosphoenolpyruvate reductase [thioredoxin] (EC 1.8.4.8) | SCE1572_10665 | yes | sce_9273 | yes |
| A and B | Amino Acids and Derivatives | Lysine, threonine, methionine, and cysteine | Cysteine Biosynthesis | Phosphoenolpyruvate carboxyltransferase (EC 2.3.1.19) | SCE1572_8282 | yes | sce_3948 | yes |
| A and B | Amino Acids and Derivatives | Lysine, threonine, methionine, and cysteine | Cysteine Biosynthesis | Sulfate and thiosulfate binding protein CysP | SCE1572_560 | yes | sce_363 | yes |
| A and B | Amino Acids and Derivatives | Lysine, threonine, methionine, and cysteine | Cysteine Biosynthesis | Sulfate and thiosulfate import ATP-binding protein CysA (EC 3.6.3.25) | SCE1572_9474 | yes | sce_8253 | yes |

| | | | | | | | | | |
|---------|-----------------------------|---|--|--|--|---------------|----------|----------|-----|
| A and B | Amino Acids and Derivatives | Lysine, threonine, methionine, and cysteine | Threonine degradation | L-threonine 3-dehydrogenase (EC 1.1.1.103) | SCE1572_9364 | yes | sce_8144 | yes | |
| A and B | Amino Acids and Derivatives | Lysine, threonine, methionine, and cysteine | Threonine degradation | Threonine degradation | Low-specificity L-threonine aldolase (EC 4.1.2.5) | SCE1572_2736 | yes | sce_2275 | yes |
| A and B | Amino Acids and Derivatives | Lysine, threonine, methionine, and cysteine | Threonine degradation | Threonine degradation | Threonine dehydratase, catabolic (EC 4.3.1.19) | SCE1572_5116 | yes | sce_4304 | yes |
| A and B | Amino Acids and Derivatives | Lysine, threonine, methionine, and cysteine | Threonine degradation | Threonine degradation | Threonine dehydrogenase and related Zn-dependent dehydrogenases | SCE1572_42 | yes | sce_534 | yes |
| A | Amino Acids and Derivatives | Lysine, threonine, methionine, and cysteine | Cysteine Biosynthesis | Cysteine Biosynthesis | Sulfate permease | SCE1572_6929 | yes | | no |
| A | Amino Acids and Derivatives | Lysine, threonine, methionine, and cysteine | Methionine Biosynthesis | Methionine Biosynthesis | 5-methyltetrahydropteroylglutamate--homocysteine methyltransferase | SCE1572_3532 | yes | | no |
| A | Amino Acids and Derivatives | Lysine, threonine, methionine, and cysteine | Methionine Biosynthesis | Methionine Biosynthesis | Methionine ABC transporter permease protein | SCE1572_1101 | yes | | no |
| A | Amino Acids and Derivatives | Lysine, threonine, methionine, and cysteine | Methionine Biosynthesis | Methionine Biosynthesis | Methionine ABC transporter substrate-binding protein | SCE1572_1102 | yes | | no |
| B | Amino Acids and Derivatives | Lysine, threonine, methionine, and cysteine | Cysteine Biosynthesis | Cysteine Biosynthesis | Cys regulon transcriptional activator CysB | | no | sce_2533 | yes |
| B | Amino Acids and Derivatives | Lysine, threonine, methionine, and cysteine | Lysine degradation | Lysine degradation | Lysine decarboxylase (EC 4.1.1.18) | | no | sce_93 | yes |
| B | Amino Acids and Derivatives | Lysine, threonine, methionine, and cysteine | Methionine Biosynthesis | Methionine Biosynthesis | Predicted regulator of methionine metabolism, ArsR family | | no | sce_3330 | yes |
| A and B | Amino Acids and Derivatives | Proline and 4-hydroxyproline | A Hypothetical Protein Related to Proline Metabolism | Hypothetical protein YggS, proline synthase co-transcribed bacterial ho | SCE1572_10504 | yes | sce_9152 | yes | |
| A and B | Amino Acids and Derivatives | Proline and 4-hydroxyproline | A Hypothetical Protein Related to Proline Metabolism | A Hypothetical Protein Related to Proline Metabolism | Pyroline-5-carboxylate reductase (EC 1.5.1.2) | SCE1572_7743 | yes | sce_6567 | yes |
| A and B | Amino Acids and Derivatives | Proline and 4-hydroxyproline | Proline, 4-hydroxyproline uptake and utilization | Proline, 4-hydroxyproline uptake and utilization | D-amino-acid oxidase (EC 1.4.3.3) | SCE1572_7258 | yes | sce_5972 | yes |
| A and B | Amino Acids and Derivatives | Proline and 4-hydroxyproline | Proline, 4-hydroxyproline uptake and utilization | Proline, 4-hydroxyproline uptake and utilization | Delta-1-pyrroline-5-carboxylate dehydrogenase (EC 1.5.1.12) | SCE1572_6031 | yes | sce_4984 | yes |
| A and B | Amino Acids and Derivatives | Proline and 4-hydroxyproline | Proline, 4-hydroxyproline uptake and utilization | Proline, 4-hydroxyproline uptake and utilization | Ketoglutarate semialdehyde dehydrogenase (EC 1.2.1.26) | SCE1572_10398 | yes | sce_9215 | yes |
| A and B | Amino Acids and Derivatives | Proline and 4-hydroxyproline | Proline, 4-hydroxyproline uptake and utilization | Proline, 4-hydroxyproline uptake and utilization | Proline iminopeptidase (EC 3.4.11.5) | SCE1572_7176 | yes | sce_5905 | yes |
| A and B | Amino Acids and Derivatives | Proline and 4-hydroxyproline | Proline Synthesis | Proline Synthesis | Gamma-glutamyl phosphate reductase (EC 1.2.1.41) | SCE1572_4908 | yes | sce_4118 | yes |
| A and B | Amino Acids and Derivatives | Proline and 4-hydroxyproline | Proline Synthesis | Proline Synthesis | Glutamate 5-kinase (EC 2.7.2.11) | SCE1572_10703 | yes | sce_9312 | yes |
| A and B | Amino Acids and Derivatives | Proline and 4-hydroxyproline | Proline Synthesis | Proline Synthesis | NADP-specific glutamate dehydrogenase (EC 1.4.1.4) | SCE1572_1504 | yes | sce_6937 | yes |
| A and B | Amino Acids and Derivatives | Proline and 4-hydroxyproline | Proline Synthesis | Proline Synthesis | Pyroline-5-carboxylate reductase (EC 1.5.1.2) | SCE1572_7743 | yes | sce_6567 | yes |
| A and B | Amino Acids and Derivatives | Proline and 4-hydroxyproline | Proline Synthesis | Proline Synthesis | RNA-binding C-terminal domain PUA | SCE1572_10703 | yes | sce_9312 | yes |
| A | Amino Acids and Derivatives | Proline and 4-hydroxyproline | Proline, 4-hydroxyproline uptake and utilization | Proline, 4-hydroxyproline uptake and utilization | D-proline reductase, 23 kDa subunit (EC 1.2.1.4.1) | SCE1572_8108 | yes | | no |
| A | Amino Acids and Derivatives | Proline and 4-hydroxyproline | Proline, 4-hydroxyproline uptake and utilization | Proline, 4-hydroxyproline uptake and utilization | D-proline reductase, 26 kDa subunit (EC 1.2.1.4.1) | SCE1572_8107 | yes | | no |
| A | Amino Acids and Derivatives | Proline and 4-hydroxyproline | Proline, 4-hydroxyproline uptake and utilization | Proline, 4-hydroxyproline uptake and utilization | D-proline reductase, 45 kDa subunit (EC 1.2.1.4.1) | SCE1572_8108 | yes | | no |
| A and B | Amino Acids and Derivatives | no subcategory | Creatine and Creatinine Degradation | Creatine and Creatinine Degradation | Creatinine amidohydrolyase (EC 3.5.2.10) | SCE1572_2672 | yes | sce_2221 | yes |
| A and B | Amino Acids and Derivatives | no subcategory | Creatine and Creatinine Degradation | Creatine and Creatinine Degradation | N-methylhydantoinase (ATP-hydrolyzing) (EC 3.5.2.14) | SCE1572_3451 | yes | sce_2943 | yes |
| A and B | Amino Acids and Derivatives | no subcategory | Creatine and Creatinine Degradation | Creatine and Creatinine Degradation | N-methylhydantoinase A (EC 3.5.2.14) | SCE1572_3453 | yes | sce_2945 | yes |
| A and B | Amino Acids and Derivatives | no subcategory | Creatine and Creatinine Degradation | Creatine and Creatinine Degradation | N-methylhydantoinase B (EC 3.5.2.14) | SCE1572_3452 | yes | sce_2944 | yes |
| B | Amino Acids and Derivatives | no subcategory | Creatine and Creatinine Degradation | Creatine and Creatinine Degradation | Cytosine deaminase (EC 3.5.4.1) | | no | sce_4620 | yes |
| A | Carbohydrates | Aminosugars | Chitin and N-acetylglucosamine utilization | Glucosamine-6-phosphate deaminase [isomerizing], alternative (EC 3.5. | SCE1572_3562 | yes | | | no |
| A | Carbohydrates | Aminosugars | Chitin and N-acetylglucosamine utilization | N-acetylglucosamine related transporter, NagX | SCE1572_7992 | yes | | | no |
| A | Carbohydrates | Aminosugars | Chitin and N-acetylglucosamine utilization | N-acetylglucosamine-6-phosphate deacetylase (EC 3.5.1.25) | SCE1572_3561 | yes | | | no |
| A | Carbohydrates | Aminosugars | Chitin and N-acetylglucosamine utilization | PTS system, N-acetylglucosamine-specific, IIB component (EC 2.7.1.66) | SCE1572_2560 | yes | | | no |
| A | Carbohydrates | Aminosugars | Chitin and N-acetylglucosamine utilization | PTS system, N-acetylglucosamine-specific, IIC component (EC 2.7.1.65) | SCE1572_2560 | yes | | | no |
| A and B | Carbohydrates | Central carbohydrate metabolism | Dehydrogenase complexes | 2-oxoglutarate dehydrogenase E1 component (EC 1.2.4.2) | SCE1572_2352 | yes | sce_1318 | yes | |
| A and B | Carbohydrates | Central carbohydrate metabolism | Dehydrogenase complexes | Branched-chain alpha-keto acid dehydrogenase, E1 component, alpha sub | SCE1572_2201 | yes | sce_1748 | yes | |
| A and B | Carbohydrates | Central carbohydrate metabolism | Dehydrogenase complexes | Branched-chain alpha-keto acid dehydrogenase, E1 component, beta su | SCE1572_2200 | yes | sce_1747 | yes | |
| A and B | Carbohydrates | Central carbohydrate metabolism | Dehydrogenase complexes | Cytosol aminopeptidase PepA (EC 3.4.11.1) | SCE1572_3407 | yes | sce_2894 | yes | |
| A and B | Carbohydrates | Central carbohydrate metabolism | Dehydrogenase complexes | Dihydropyrimidine acetyltransferase component of pyruvate dehydrogen | SCE1572_2006 | yes | sce_1142 | yes | |
| A and B | Carbohydrates | Central carbohydrate metabolism | Dehydrogenase complexes | Dihydropyrimidine acetyltransferase component of branched-chain alpha- | SCE1572_2199 | yes | sce_1746 | yes | |
| A and B | Carbohydrates | Central carbohydrate metabolism | Dehydrogenase complexes | Dihydropyrimidine succinyltransferase component (E2) of 2-oxoglutarat | SCE1572_828 | yes | sce_1318 | yes | |
| A and B | Carbohydrates | Central carbohydrate metabolism | Dehydrogenase complexes | Pyruvate dehydrogenase E1 component alpha subunit (EC 1.2.4.1) | SCE1572_5066 | yes | sce_4255 | yes | |
| A and B | Carbohydrates | Central carbohydrate metabolism | Dehydrogenase complexes | Pyruvate dehydrogenase E1 component beta subunit (EC 1.2.4.1) | SCE1572_5067 | yes | sce_4256 | yes | |
| A and B | Carbohydrates | Central carbohydrate metabolism | Dihydroxyacetone kinases | DHA-specific E1 component | SCE1572_3297 | yes | sce_2789 | yes | |
| A and B | Carbohydrates | Central carbohydrate metabolism | Dihydroxyacetone kinases | DHA-specific IIA component | SCE1572_3297 | yes | sce_2789 | yes | |
| A and B | Carbohydrates | Central carbohydrate metabolism | Dihydroxyacetone kinases | DHA-specific phosphocarrier protein HPr | SCE1572_3297 | yes | sce_2789 | yes | |
| A and B | Carbohydrates | Central carbohydrate metabolism | Dihydroxyacetone kinases | Phosphoenolpyruvate-dihydroxyacetone phosphotransferase (EC 2.7.1. | SCE1572_3298 | yes | sce_2790 | yes | |
| A and B | Carbohydrates | Central carbohydrate metabolism | Dihydroxyacetone kinases | Phosphoenolpyruvate-dihydroxyacetone phosphotransferase (EC 2.7.1. | SCE1572_3299 | yes | sce_2791 | yes | |
| A and B | Carbohydrates | Central carbohydrate metabolism | Dihydroxyacetone kinases | Phosphoenolpyruvate-dihydroxyacetone phosphotransferase (EC 2.7.1. | SCE1572_3297 | yes | sce_2789 | yes | |
| A and B | Carbohydrates | Central carbohydrate metabolism | Entner-Doudoroff Pathway | 2,3-bisphosphoglycerate-independent phosphoglycerate mutase (EC 5.4.SCE1572_1634 | SCE1572_1634 | yes | sce_1168 | yes | |
| A and B | Carbohydrates | Central carbohydrate metabolism | Entner-Doudoroff Pathway | 2-dehydro-3-deoxygluconate kinase (EC 2.7.1.45) | SCE1572_4552 | yes | sce_1380 | yes | |
| A and B | Carbohydrates | Central carbohydrate metabolism | Entner-Doudoroff Pathway | 2-dehydro-3-deoxyphosphogluconate aldolase (EC 4.1.2.14) | SCE1572_4553 | yes | sce_1379 | yes | |
| A and B | Carbohydrates | Central carbohydrate metabolism | Entner-Doudoroff Pathway | 6-phosphogluconolactonase (EC 3.1.1.31), eukaryotic type | SCE1572_5831 | yes | sce_4872 | yes | |
| A and B | Carbohydrates | Central carbohydrate metabolism | Entner-Doudoroff Pathway | D-glycerate 2-kinase (EC 2.7.1.-) | SCE1572_4036 | yes | sce_3364 | yes | |
| A and B | Carbohydrates | Central carbohydrate metabolism | Entner-Doudoroff Pathway | Enolase (EC 4.2.1.11) | SCE1572_9808 | yes | sce_8614 | yes | |
| A and B | Carbohydrates | Central carbohydrate metabolism | Entner-Doudoroff Pathway | Glucokinase (EC 2.7.1.2) | SCE1572_5828 | yes | sce_4870 | yes | |
| A and B | Carbohydrates | Central carbohydrate metabolism | Entner-Doudoroff Pathway | Gluconokinase (EC 2.7.1.12) | SCE1572_1893 | yes | sce_1407 | yes | |
| A and B | Carbohydrates | Central carbohydrate metabolism | Entner-Doudoroff Pathway | Gluconolactonase (EC 3.1.1.17) | SCE1572_7960 | yes | sce_2029 | yes | |
| A and B | Carbohydrates | Central carbohydrate metabolism | Entner-Doudoroff Pathway | Glucose 1-dehydrogenase (EC 1.1.1.47) | SCE1572_1769 | yes | sce_1694 | yes | |
| A and B | Carbohydrates | Central carbohydrate metabolism | Entner-Doudoroff Pathway | Glucose-6-phosphate 1-dehydrogenase (EC 1.1.1.49) | SCE1572_5833 | yes | sce_4874 | yes | |
| A and B | Carbohydrates | Central carbohydrate metabolism | Entner-Doudoroff Pathway | Hexokinase (EC 2.7.1.1) | SCE1572_7950 | yes | sce_6746 | yes | |
| A and B | Carbohydrates | Central carbohydrate metabolism | Entner-Doudoroff Pathway | NAD-dependent glyceraldehyde-3-phosphate dehydrogenase (EC 1.2.1. | SCE1572_6421 | yes | sce_8225 | yes | |
| A and B | Carbohydrates | Central carbohydrate metabolism | Entner-Doudoroff Pathway | Phosphoglycerate kinase (EC 2.7.2.3) | SCE1572_6890 | yes | sce_8224 | yes | |
| A and B | Carbohydrates | Central carbohydrate metabolism | Entner-Doudoroff Pathway | Polyphosphate glucokinase (EC 2.7.1.63) | SCE1572_1006 | yes | sce_759 | yes | |
| A and B | Carbohydrates | Central carbohydrate metabolism | Entner-Doudoroff Pathway | Pyruvate kinase (EC 2.7.1.40) | SCE1572_6128 | yes | sce_5073 | yes | |
| A and B | Carbohydrates | Central carbohydrate metabolism | Glycolate, glyoxylate interconversions | Glycolate dehydrogenase (EC 1.1.99.14), subunit GkD | SCE1572_6827 | yes | sce_5688 | yes | |
| A and B | Carbohydrates | Central carbohydrate metabolism | Glycolate, glyoxylate interconversions | Glycolate oxidase (EC 1.1.3.15) | SCE1572_9787 | yes | sce_8585 | yes | |
| A and B | Carbohydrates | Central carbohydrate metabolism | Glycolate, glyoxylate interconversions | Phosphoglycolate phosphatase (EC 3.1.3.18) | SCE1572_11194 | yes | sce_8372 | yes | |
| A and B | Carbohydrates | Central carbohydrate metabolism | Glycolysis and Gluconeogenesis | 2,3-bisphosphoglycerate-independent phosphoglycerate mutase (EC 5.4.SCE1572_1634 | SCE1572_1634 | yes | sce_1168 | yes | |
| A and B | Carbohydrates | Central carbohydrate metabolism | Glycolysis and Gluconeogenesis | 6-phosphofructokinase (EC 2.7.1.11) | SCE1572_4596 | yes | sce_3833 | yes | |
| A and B | Carbohydrates | Central carbohydrate metabolism | Glycolysis and Gluconeogenesis | Enolase (EC 4.2.1.11) | SCE1572_9808 | yes | sce_8614 | yes | |
| A and B | Carbohydrates | Central carbohydrate metabolism | Glycolysis and Gluconeogenesis | Fructose-1,6-bisphosphatase, Bacillus type (EC 3.1.3.11) | SCE1572_10951 | yes | sce_9561 | yes | |
| A and B | Carbohydrates | Central carbohydrate metabolism | Glycolysis and Gluconeogenesis | Fructose-1,6-bisphosphatase, type I (EC 3.1.3.11) | SCE1572_10951 | yes | sce_2892 | yes | |
| A and B | Carbohydrates | Central carbohydrate metabolism | Glycolysis and Gluconeogenesis | Fructose-bisphosphate aldolase class I (EC 4.1.2.13) | SCE1572_2467 | yes | sce_2893 | yes | |
| A and B | Carbohydrates | Central carbohydrate metabolism | Glycolysis and Gluconeogenesis | Fructose-bisphosphate aldolase class II (EC 4.1.2.13) | SCE1572_2560 | yes | sce_2139 | yes | |
| A and B | Carbohydrates | Central carbohydrate metabolism | Glycolysis and Gluconeogenesis | Glucokinase (EC 2.7.1.2) | SCE1572_5828 | yes | sce_4870 | yes | |
| A and B | Carbohydrates | Central carbohydrate metabolism | Glycolysis and Gluconeogenesis | Glucose-6-phosphate isomerase (EC 5.3.1.9) | SCE1572_7517 | yes | sce_6344 | yes | |
| A and B | Carbohydrates | Central carbohydrate metabolism | Glycolysis and Gluconeogenesis | Hexokinase (EC 2.7.1.1) | SCE1572_7950 | yes | sce_6746 | yes | |
| A and B | Carbohydrates | Central carbohydrate metabolism | Glycolysis and Gluconeogenesis | NAD-dependent glyceraldehyde-3-phosphate dehydrogenase (EC 1.2.1. | SCE1572_6421 | yes | sce_8225 | yes | |
| A and B | Carbohydrates | Central carbohydrate metabolism | Glycolysis and Gluconeogenesis | Phosphoenolpyruvate synthase (EC 2.7.9.2) | SCE1572_1055 | yes | sce_4687 | yes | |
| A and B | Carbohydrates | Central carbohydrate metabolism | Glycolysis and Gluconeogenesis | Phosphoglycerate kinase (EC 2.7.2.3) | SCE1572_6890 | yes | sce_8224 | yes | |
| A and B | Carbohydrates | Central carbohydrate metabolism | Glycolysis and Gluconeogenesis | Polyphosphate glucokinase (EC 2.7.1.63) | SCE1572_1006 | yes | sce_759 | yes | |
| A and B | Carbohydrates | Central carbohydrate metabolism | Glycolysis and Gluconeogenesis | Pyrophosphate-fructose 6-phosphate 1-phosphotransferase, alpha sub | SCE1572_2888 | yes | sce_2511 | yes | |
| A and B | Carbohydrates | Central carbohydrate metabolism | Glycolysis and Gluconeogenesis | Pyruvate kinase (EC 2.7.1.40) | SCE1572_6128 | yes | sce_5073 | yes | |
| A and B | Carbohydrates | Central carbohydrate metabolism | Glycolysis and Gluconeogenesis | Pyruvate,phosphate dikinase (EC 2.7.9.1) | SCE1572_9634 | yes | sce_8446 | yes | |
| A and B | Carbohydrates | Central carbohydrate metabolism | Glycolysis and Gluconeogenesis | Triosephosphate isomerase (EC 5.3.1.1) | SCE1572_9434 | yes | sce_8223 | yes | |
| A and B | Carbohydrates | Central carbohydrate metabolism | Glyoxylate bypass | Aconitate hydratase (EC 4.2.1.3) | SCE1572_5235 | yes | sce_4390 | yes | |
| A and B | Carbohydrates | Central carbohydrate metabolism | Glyoxylate bypass | Citrate synthase (EC 2.3.3.1) | SCE1572_2382 | yes | sce_1933 | yes | |
| A and B | Carbohydrates | Central carbohydrate metabolism | Glyoxylate bypass | Isocitrate lyase (EC 4.1.3.1) | SCE1572_11040 | yes | sce_9752 | yes | |
| A and B | Carbohydrates | Central carbohydrate metabolism | Glyoxylate bypass | Malate dehydrogenase (EC 1.1.1.37) | SCE1572_1660 | yes | sce_1175 | yes | |
| A and B | Carbohydrates | Central carbohydrate metabolism | Glyoxylate bypass | Malate synthase (EC 2.3.3.9) | SCE1572_11039 | yes | sce_9751 | yes | |
| A and B | Carbohydrates | Central carbohydrate metabolism | Methylglyoxal Metabolism | Aldehyde dehydrogenase (EC 1.2.1.3) | SCE1572_4022 | yes | sce_2406 | yes | |
| A and B | Carbohydrates | Central carbohydrate metabolism | Methylglyoxal Metabolism | Hydroxyacylglutathione hydrolase (EC 3.1.2.6) | SCE1572_10143 | yes | sce_8946 | yes | |
| A and B | Carbohydrates | Central carbohydrate metabolism | Methylglyoxal Metabolism | Lactoylglutathione lyase (EC 4.4.1.5) | SCE1572_4796 | yes | sce_4011 | yes | |
| A and B | Carbohydrates | Central carbohydrate metabolism | Pentose phosphate pathway | 6-phosphogluconate dehydrogenase, decarboxylating (EC 1.1.1.44) | SCE1572_4750 | yes | sce_3971 | yes | |
| A and B | Carbohydrates | Central carbohydrate metabolism | Pentose phosphate pathway | 6-phosphogluconolactonase (EC 3.1.1.31), eukaryotic type | SCE1572_5831 | yes | sce_4872 | yes | |
| A and B | Carbohydrates | Central carbohydrate metabolism | Pentose phosphate pathway | Glucose-6-phosphate 1-dehydrogenase (EC 1.1.1.49) | SCE1572_5833 | yes | sce_4874 | yes | |
| A and B | Carbohydrates | Central carbohydrate metabolism | Pentose phosphate pathway | Ribose 5-phosphate isomerase A (EC 5.3.1.6) | SCE1572_2404 | yes | sce_1958 | yes | |
| A and B | Carbohydrates | Central carbohydrate metabolism | Pentose phosphate pathway | Ribose-phosphate pyrophosphokinase (EC 2.7.6.1) | SCE1572_8154 | yes | sce_7319 | yes | |
| A and B | Carbohydrates | Central carbohydrate metabolism | Pentose phosphate pathway | Ribulose-phosphate 3-epimerase (EC 5.1.3.1) | SCE1572_10509 | yes | sce_9159 | yes | |
| A and B | Carbohydrates | Central carbohydrate metabolism | Pentose phosphate pathway | Transaldolase (EC 2.2.1.2) | SCE1572_29 | yes | sce_31 | yes | |
| A and B | Carbohydrates | Central carbohydrate metabolism | Pentose phosphate pathway | Transketolase (EC 2.2.1.1) | SCE1572_27 | yes | sce_31 | yes | |
| A and B | Carbohydrates | Central carbohydrate metabolism | Pyruvate,ferredoxin oxidoreductase | Pyruvate,ferredoxin oxidoreductase (EC 1.2.7.-) | SCE1572_6058 | yes | sce_5009 | yes | |
| A and B | Carbohydrates | Central carbohydrate metabolism | Pyruvate Alanine Serine Interconversions | Alanine dehydrogenase (EC 1.4.1.1) | SCE1572_10473 | yes | sce_9118 | yes | |
| A and B | Carbohydrates | Central carbohydrate metabolism | Pyruvate Alanine Serine Interconversions | Alanine racemase (EC 5.1.1.1) | SCE1572_9334 | yes | sce_8113 | yes | |
| A and B | Carbohydrates | Central carbohydrate metabolism | Pyruvate Alanine Serine Interconversions | Branched-chain amino acid aminotransferase (EC 2.6.1.42) | SCE1572_354 | yes | sce_195 | yes | |
| A and B | Carbohydrates | Central carbohydrate metabolism | Pyruvate Alanine Serine Interconversions | L-serine dehydratase (EC 4.3.1.17) | SCE1572_2497 | yes | sce_2075 | yes | |
| A and B | Carbohydrates | Central carbohydrate metabolism | Pyruvate Alanine Serine Interconversions | Omega-amino acid--pyruvate aminotransferase (EC 2.6.1.18) | SCE1572_8423 | yes | sce_7183 | yes | |
| A and B | Carbohydrates | Central carbohydrate metabolism | Pyruvate Alanine Serine Interconversions | Valine--pyruvate aminotransferase (EC 2.6.1.66) | SCE1572_1439 | yes | sce_6322 | yes | |
| A and B | Carbohydrates | Central carbohydrate metabolism | Pyruvate metabolism I: anaplerotic reactions, PEP | Malate permease | SCE1572_5325 | yes | sce_4462 | yes | |
| A and B | Carbohydrates | Central carbohydrate metabolism | Pyruvate metabolism I: anaplerotic reactions, PEP | Phosphoenolpyruvate carboxykinase [GTP] (EC 4.1.1.32) | SCE1572_4050 | yes | sce_3376 | yes | |
| A and B | Carbohydrates | Central carbohydrate metabolism | Pyruvate metabolism I: anaplerotic reactions, PEP | Phosphoenolpyruvate carboxylase (EC 4.1.1.31) | SCE1572_4598 | yes | sce_3835 | yes | |
| A and B | Carbohydrates | Central carbohydrate metabolism | Pyruvate metabolism I: anaplerotic reactions, PEP | Phosphoenolpyruvate synthase (EC 2.7.9.2) | SCE1572_1055 | yes | sce_4687 | yes | |
| A and B | Carbohydrates | Central carbohydrate metabolism | Pyruvate metabolism I: anaplerotic reactions, PEP | Pyruvate kinase (EC 2.7.1.40) | SCE1572_6128 | yes</ | | | |

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|---------|---------------|--------------------------|--|---|---------------|-----|-----------|-----|
| A and B | Carbohydrates | Di- and oligosaccharides | Trehalose Biosynthesis | Trehalose synthase (EC 5.4.99.16) | SCE1572_601 | yes | sce_407 | yes |
| A and B | Carbohydrates | Di- and oligosaccharides | Trehalose Biosynthesis | Trehalose-6-phosphate phosphatase (EC 3.1.3.12) | SCE1572_746 | yes | sce_549 | yes |
| A and B | Carbohydrates | Di- and oligosaccharides | Trehalose Uptake and Utilization | Beta-phosphoglucosylase (EC 5.4.2.6) | SCE1572_11165 | yes | sce_9891 | yes |
| A and B | Carbohydrates | Di- and oligosaccharides | Trehalose Uptake and Utilization | Glucose/mannose/H symporter G6P | SCE1572_10391 | yes | sce_9046 | yes |
| A and B | Carbohydrates | Di- and oligosaccharides | Trehalose Uptake and Utilization | Trehalose phosphorylase (EC 2.4.1.64) | SCE1572_10442 | yes | sce_9083 | yes |
| A | Carbohydrates | Di- and oligosaccharides | Lactose and Galactose Uptake and Utilization | Galactose:methyl galactoside ABC transport system, ATP-binding protein | SCE1572_212 | yes | | no |
| A | Carbohydrates | Di- and oligosaccharides | Lactose and Galactose Uptake and Utilization | Galactose:methyl galactoside ABC transport system, permease protein I | SCE1572_211 | yes | | no |
| A | Carbohydrates | Di- and oligosaccharides | Trehalose Uptake and Utilization | PTS system, glucose-specific IIA component (EC 2.7.1.69) | SCE1572_3559 | yes | | no |
| B | Carbohydrates | Di- and oligosaccharides | Lactose and Galactose Uptake and Utilization | Allose 1-epimerase (EC 5.1.3.3) | | no | sce_9185 | yes |
| B | Carbohydrates | Di- and oligosaccharides | Maltose and Maltodextrin Utilization | Maltose/maltodextrin transport ATP-binding protein MalK (EC 3.6.3.19) | | no | sce_3429 | yes |
| B | Carbohydrates | Di- and oligosaccharides | Maltose and Maltodextrin Utilization | Multiple sugar ABC transporter, ATP-binding protein | | no | sce_3429 | yes |
| B | Carbohydrates | Di- and oligosaccharides | Maltose and Maltodextrin Utilization | Periplasmic alpha-amylase (EC 3.2.1.1) | | no | sce_7664 | yes |
| A and B | Carbohydrates | Fermentation | Acetoin, butanediol metabolism | Acetolactate synthase large subunit (EC 2.2.1.6) | SCE1572_311 | yes | sce_4182 | yes |
| A and B | Carbohydrates | Fermentation | Acetoin, butanediol metabolism | Acetolactate synthase small subunit (EC 2.2.1.6) | SCE1572_4974 | yes | sce_4183 | yes |
| A and B | Carbohydrates | Fermentation | Acetyl-CoA fermentation to Butyrate | 3-hydroxyacyl-CoA dehydrogenase (EC 1.1.1.35) | SCE1572_60 | yes | sce_50 | yes |
| A and B | Carbohydrates | Fermentation | Acetyl-CoA fermentation to Butyrate | 3-hydroxybutyryl-CoA dehydratase (EC 4.2.1.55) | SCE1572_463 | yes | sce_277 | yes |
| A and B | Carbohydrates | Fermentation | Acetyl-CoA fermentation to Butyrate | 3-hydroxybutyryl-CoA dehydrogenase (EC 1.1.1.187) | SCE1572_466 | yes | sce_278 | yes |
| A and B | Carbohydrates | Fermentation | Acetyl-CoA fermentation to Butyrate | 3-hydroxybutyryl-CoA epimerase (EC 5.1.2.3) | SCE1572_60 | yes | sce_50 | yes |
| A and B | Carbohydrates | Fermentation | Acetyl-CoA fermentation to Butyrate | Acetyl-CoA acetyltransferase (EC 2.3.1.9) | SCE1572_61 | yes | sce_51 | yes |
| A and B | Carbohydrates | Fermentation | Acetyl-CoA fermentation to Butyrate | Butyryl-CoA dehydrogenase (EC 1.3.99.2) | SCE1572_1711 | yes | sce_1225 | yes |
| A and B | Carbohydrates | Fermentation | Acetyl-CoA fermentation to Butyrate | Electron transfer flavoprotein, alpha subunit | SCE1572_934 | yes | sce_702 | yes |
| A and B | Carbohydrates | Fermentation | Acetyl-CoA fermentation to Butyrate | Electron transfer flavoprotein, beta subunit | SCE1572_935 | yes | sce_703 | yes |
| A and B | Carbohydrates | Fermentation | Acetyl-CoA fermentation to Butyrate | Enoyl-CoA hydratase (EC 4.2.1.17) | SCE1572_60 | yes | sce_50 | yes |
| A and B | Carbohydrates | Fermentation | Butanol Biosynthesis | 3-hydroxybutyryl-CoA dehydrogenase (EC 1.1.1.157) | SCE1572_466 | yes | sce_278 | yes |
| A and B | Carbohydrates | Fermentation | Butanol Biosynthesis | Acetyl-CoA acetyltransferase (EC 2.3.1.9) | SCE1572_61 | yes | sce_51 | yes |
| A and B | Carbohydrates | Fermentation | Butanol Biosynthesis | Butyryl-CoA dehydrogenase (EC 1.3.99.2) | SCE1572_1711 | yes | sce_1225 | yes |
| A and B | Carbohydrates | Fermentation | Butanol Biosynthesis | Enoyl-CoA hydratase (EC 4.2.1.17) | SCE1572_60 | yes | sce_50 | yes |
| A and B | Carbohydrates | Fermentation | Fermentations: Lactate | L-lactate dehydrogenase (EC 1.1.1.127) | SCE1572_7135 | yes | sce_5876 | yes |
| A | Carbohydrates | Fermentation | Acetoin, butanediol metabolism | Acetoin dehydrogenase E1 component alpha-subunit (EC 1.2.4.-) | SCE1572_8155 | yes | | no |
| A | Carbohydrates | Fermentation | Acetoin, butanediol metabolism | Acetoin dehydrogenase E1 component beta-subunit (EC 1.2.4.-) | SCE1572_8160 | yes | | no |
| A | Carbohydrates | Fermentation | Acetoin, butanediol metabolism | Dihydropyrimidine acetyltransferase component (E2) of acetoin dehydrogenase | SCE1572_8161 | yes | | no |
| B | Carbohydrates | Fermentation | Acetoin, butanediol metabolism | 2,3-butanediol dehydrogenase, R- and (S)-acetoin-specific (EC 1.1.1.4) | | no | sce_2886 | yes |
| A and B | Carbohydrates | Monosaccharides | D-glucanate and ketoglucanates metabolism | 2-dehydro-3-deoxyglucanate kinase (EC 2.7.1.45) | SCE1572_4552 | yes | sce_1380 | yes |
| A and B | Carbohydrates | Monosaccharides | D-glucanate and ketoglucanates metabolism | 5-keto-D-glucanate 5-reductase (EC 1.1.1.69) | SCE1572_6965 | yes | sce_3779 | yes |
| A and B | Carbohydrates | Monosaccharides | D-glucanate and ketoglucanates metabolism | 6-phosphogluconate dehydrogenase, decarboxylating (EC 1.1.1.44) | SCE1572_4750 | yes | sce_3971 | yes |
| A and B | Carbohydrates | Monosaccharides | D-glucanate and ketoglucanates metabolism | Gluconokinase (EC 2.7.1.12) | SCE1572_1893 | yes | sce_1407 | yes |
| A and B | Carbohydrates | Monosaccharides | D-glucanate and ketoglucanates metabolism | Glucose 1-dehydrogenase (EC 1.1.1.147) | SCE1572_1769 | yes | sce_1694 | yes |
| A and B | Carbohydrates | Monosaccharides | D-ribose utilization | Ribokinase (EC 2.7.1.15) | SCE1572_898 | yes | sce_670 | yes |
| A and B | Carbohydrates | Monosaccharides | D-ribose utilization | Ribose 5-phosphate isomerase A (EC 5.3.1.6) | SCE1572_2404 | yes | sce_1958 | yes |
| A and B | Carbohydrates | Monosaccharides | D-ribose utilization | Ribose ABC transport system, ATP-binding protein RbsA (TC 3.A.1.2) | SCE1572_5387 | yes | sce_2471 | yes |
| A and B | Carbohydrates | Monosaccharides | D-ribose utilization | Ribose ABC transport system, periplasmic ribose-binding protein RbsB | SCE1572_11133 | yes | sce_3723 | yes |
| A and B | Carbohydrates | Monosaccharides | D-ribose utilization | Ribose ABC transport system, permease protein RbsC (TC 3.A.1.2.1) | SCE1572_2642 | yes | sce_2472 | yes |
| A and B | Carbohydrates | Monosaccharides | Deoxyribose and Deoxynucleoside Catabolism | Deoxyribose-phosphate aldolase (EC 4.1.2.4) | SCE1572_6736 | yes | sce_5608 | yes |
| A and B | Carbohydrates | Monosaccharides | Deoxyribose and Deoxynucleoside Catabolism | Purine nucleoside phosphorylase (EC 2.4.2.1) | SCE1572_7736 | yes | sce_6561 | yes |
| A and B | Carbohydrates | Monosaccharides | Deoxyribose and Deoxynucleoside Catabolism | Putative deoxyribose-specific ABC transporter, ATP-binding protein | SCE1572_9866 | yes | sce_8677 | yes |
| A and B | Carbohydrates | Monosaccharides | Deoxyribose and Deoxynucleoside Catabolism | Pyrimidine-nucleoside phosphorylase (EC 2.4.2.2) | SCE1572_3232 | yes | sce_2724 | yes |
| A and B | Carbohydrates | Monosaccharides | Deoxyribose and Deoxynucleoside Catabolism | Ribokinase (EC 2.7.1.15) | SCE1572_898 | yes | sce_670 | yes |
| A and B | Carbohydrates | Monosaccharides | Fructose utilization | PTS system, fructose-specific IIA component (EC 2.7.1.69) | SCE1572_3318 | yes | sce_2813 | yes |
| A and B | Carbohydrates | Monosaccharides | Fructose utilization | PTS system, fructose-specific IIB component (EC 2.7.1.69) | SCE1572_3318 | yes | sce_2813 | yes |
| A and B | Carbohydrates | Monosaccharides | Fructose utilization | PTS system, fructose-specific IIC component (EC 2.7.1.69) | SCE1572_3318 | yes | sce_2813 | yes |
| A and B | Carbohydrates | Monosaccharides | Fructose utilization | Phosphoenolpyruvate-protein phosphotransferase of PTS system (EC 2.7.1.69) | SCE1572_3559 | yes | sce_6452 | yes |
| A and B | Carbohydrates | Monosaccharides | Fructose utilization | Transaldolase (EC 2.2.1.2) | SCE1572_29 | yes | sce_31 | yes |
| A and B | Carbohydrates | Monosaccharides | L-Arabinose utilization | Alpha-L-arabinofuranosidase II precursor (EC 3.2.1.55) | SCE1572_3113 | yes | sce_1386 | yes |
| A and B | Carbohydrates | Monosaccharides | L-Arabinose utilization | Arabinan endo-1,5-alpha-L-arabinosidase (EC 3.2.1.99) | SCE1572_2128 | yes | sce_1647 | yes |
| A and B | Carbohydrates | Monosaccharides | L-Arabinose utilization | Hypothetical glycoside hydrolase, family 43, similar to arabinosidase | SCE1572_4336 | yes | sce_9941 | yes |
| A and B | Carbohydrates | Monosaccharides | L-Arabinose utilization | L-arabinose isomerase (EC 5.3.1.4) | SCE1572_2638 | yes | sce_3711 | yes |
| A and B | Carbohydrates | Monosaccharides | L-Arabinose utilization | L-arabinose transport ATP-binding protein AraG (TC 3.A.1.2.2) | SCE1572_2641 | yes | sce_3708 | yes |
| A and B | Carbohydrates | Monosaccharides | L-Arabinose utilization | L-arabinose-specific 1-epimerase (mutarotase) | SCE1572_1772 | yes | sce_1086 | yes |
| A and B | Carbohydrates | Monosaccharides | L-Arabinose utilization | L-ribulose-5-phosphate 4-epimerase (EC 5.1.3.4) | SCE1572_2639 | yes | sce_3710 | yes |
| A and B | Carbohydrates | Monosaccharides | L-Arabinose utilization | Ribulokinase (EC 2.7.1.16) | SCE1572_2637 | yes | sce_3712 | yes |
| A and B | Carbohydrates | Monosaccharides | Mannose Metabolism | Endoglucanase (EC 3.2.1.4) | SCE1572_8738 | yes | sce_1536 | yes |
| A and B | Carbohydrates | Monosaccharides | Mannose Metabolism | Hexokinase (EC 2.7.1.1) | SCE1572_7950 | yes | sce_6746 | yes |
| A and B | Carbohydrates | Monosaccharides | Mannose Metabolism | Mannose-1-phosphate guanylyltransferase (EC 2.7.7.13) | SCE1572_4958 | yes | sce_4167 | yes |
| A and B | Carbohydrates | Monosaccharides | Mannose Metabolism | Mannose-1-phosphate guanylyltransferase (GDP) (EC 2.7.7.22) | SCE1572_11327 | yes | sce_10107 | yes |
| A and B | Carbohydrates | Monosaccharides | Mannose Metabolism | Mannose-6-phosphate isomerase (EC 5.3.1.8) | SCE1572_6242 | yes | sce_5254 | yes |
| A and B | Carbohydrates | Monosaccharides | Mannose Metabolism | Phosphomannomutase (EC 5.4.2.8) | SCE1572_6389 | yes | sce_9011 | yes |
| A and B | Carbohydrates | Monosaccharides | Xylose utilization | Beta-xylosidase (EC 3.2.1.37) | SCE1572_2022 | yes | sce_137 | yes |
| A and B | Carbohydrates | Monosaccharides | Xylose utilization | D-xylose transport ATP-binding protein XyG | SCE1572_7367 | yes | sce_3480 | yes |
| A and B | Carbohydrates | Monosaccharides | Xylose utilization | Endo-1,4-beta-xylanase A precursor (EC 3.2.1.8) | SCE1572_346 | yes | sce_841 | yes |
| A and B | Carbohydrates | Monosaccharides | Xylose utilization | Xylanase | SCE1572_8890 | yes | sce_1082 | yes |
| A and B | Carbohydrates | Monosaccharides | Xylose utilization | Xylose ABC transporter, periplasmic xylose-binding protein XyIF | SCE1572_5388 | yes | sce_4512 | yes |
| A and B | Carbohydrates | Monosaccharides | Xylose utilization | Xylose ABC transporter, substrate-binding component | SCE1572_1271 | yes | sce_1556 | yes |
| A and B | Carbohydrates | Monosaccharides | Xylose utilization | Xylose isomerase (EC 5.3.1.5) | SCE1572_271 | yes | sce_6076 | yes |
| A and B | Carbohydrates | Monosaccharides | Xylose utilization | Xylose-responsive transcription regulator, ROK family | SCE1572_9783 | yes | sce_3806 | yes |
| A and B | Carbohydrates | Monosaccharides | Xylose utilization | Xylose kinase (EC 2.7.1.17) | SCE1572_11535 | yes | sce_6019 | yes |
| A | Carbohydrates | Monosaccharides | Mannose Metabolism | Alpha-1,2-mannosidase | SCE1572_2166 | yes | | no |
| B | Carbohydrates | Monosaccharides | D-ribose utilization | Ribose operon repressor | | no | sce_9376 | yes |
| B | Carbohydrates | Monosaccharides | Fructose utilization | Fructokinase (EC 2.7.1.4) | | no | sce_9859 | yes |
| B | Carbohydrates | Monosaccharides | Fructose utilization | Phosphotransferase system, phosphocarrier protein HPr | | no | sce_6453 | yes |
| A and B | Carbohydrates | One-carbon Metabolism | One-carbon metabolism by tetrahydropterines | 5,10-methylenetetrahydrofolate reductase (EC 1.5.1.20) | SCE1572_7802 | yes | sce_6607 | yes |
| A and B | Carbohydrates | One-carbon Metabolism | One-carbon metabolism by tetrahydropterines | 5-formyltetrahydrofolate cyclo-ligase (EC 6.3.3.2) | SCE1572_9050 | yes | sce_7810 | yes |
| A and B | Carbohydrates | One-carbon Metabolism | One-carbon metabolism by tetrahydropterines | Formyltetrahydrofolate deformylase (EC 3.5.1.10) | SCE1572_754 | yes | sce_556 | yes |
| A and B | Carbohydrates | One-carbon Metabolism | One-carbon metabolism by tetrahydropterines | Methylenetetrahydrofolate cyclohydrolase (EC 3.5.4.9) | SCE1572_4947 | yes | sce_4161 | yes |
| A and B | Carbohydrates | One-carbon Metabolism | One-carbon metabolism by tetrahydropterines | Methylenetetrahydrofolate dehydrogenase (NADP) (EC 1.5.1.5) | SCE1572_4947 | yes | sce_4161 | yes |
| A and B | Carbohydrates | One-carbon Metabolism | Serine-glyoxylate cycle | 3-ketocetyl-CoA thiolase (EC 2.3.1.16) | SCE1572_61 | yes | sce_51 | yes |
| A and B | Carbohydrates | One-carbon Metabolism | Serine-glyoxylate cycle | 5,10-methylenetetrahydrofolate reductase (EC 1.5.1.20) | SCE1572_7802 | yes | sce_6607 | yes |
| A and B | Carbohydrates | One-carbon Metabolism | Serine-glyoxylate cycle | 5-formyltetrahydrofolate cyclo-ligase (EC 6.3.3.2) | SCE1572_9050 | yes | sce_7810 | yes |
| A and B | Carbohydrates | One-carbon Metabolism | Serine-glyoxylate cycle | Acetyl-CoA acetyltransferase (EC 2.3.1.9) | SCE1572_61 | yes | sce_51 | yes |
| A and B | Carbohydrates | One-carbon Metabolism | Serine-glyoxylate cycle | Acetoin hydratase (EC 4.2.1.3) | SCE1572_525 | yes | sce_390 | yes |
| A and B | Carbohydrates | One-carbon Metabolism | Serine-glyoxylate cycle | Citrate synthase (6s) (EC 2.3.3.1) | SCE1572_2382 | yes | sce_1933 | yes |
| A and B | Carbohydrates | One-carbon Metabolism | Serine-glyoxylate cycle | Enolase (EC 4.2.1.11) | SCE1572_9808 | yes | sce_8614 | yes |
| A and B | Carbohydrates | One-carbon Metabolism | Serine-glyoxylate cycle | Fumarate hydratase class I, aerobic (EC 4.2.1.2) | SCE1572_593 | yes | sce_402 | yes |
| A and B | Carbohydrates | One-carbon Metabolism | Serine-glyoxylate cycle | Isocitrate lyase (EC 4.1.3.1) | SCE1572_11040 | yes | sce_9752 | yes |
| A and B | Carbohydrates | One-carbon Metabolism | Serine-glyoxylate cycle | Malate dehydrogenase (EC 1.1.1.37) | SCE1572_1660 | yes | sce_1175 | yes |
| A and B | Carbohydrates | One-carbon Metabolism | Serine-glyoxylate cycle | Methylenetetrahydrofolate cyclohydrolase (EC 3.5.4.9) | SCE1572_4947 | yes | sce_4161 | yes |
| A and B | Carbohydrates | One-carbon Metabolism | Serine-glyoxylate cycle | Methylcrotonyl-CoA carboxylase biotin-containing subunit (EC 6.4.1.4) | SCE1572_2729 | yes | sce_2267 | yes |
| A and B | Carbohydrates | One-carbon Metabolism | Serine-glyoxylate cycle | Methylcrotonyl-CoA carboxylase carboxyl transferase subunit (EC 6.4.1.3) | SCE1572_3419 | yes | sce_2906 | yes |
| A and B | Carbohydrates | One-carbon Metabolism | Serine-glyoxylate cycle | Methylenetetrahydrofolate dehydrogenase (NADP) (EC 1.5.1.5) | SCE1572_4947 | yes | sce_4161 | yes |
| A and B | Carbohydrates | One-carbon Metabolism | Serine-glyoxylate cycle | Methylmalonyl-CoA mutase (EC 5.4.99.2) | SCE1572_3702 | yes | sce_3052 | yes |
| A and B | Carbohydrates | One-carbon Metabolism | Serine-glyoxylate cycle | Propionyl-CoA carboxylase beta chain (EC 6.4.1.3) | SCE1572_9348 | yes | sce_8129 | yes |
| A and B | Carbohydrates | One-carbon Metabolism | Serine-glyoxylate cycle | Propionyl-CoA carboxylase carboxyl transferase subunit (EC 6.4.1.3) | SCE1572_4445 | yes | sce_3690 | yes |
| A and B | Carbohydrates | One-carbon Metabolism | Serine-glyoxylate cycle | Serine hydroxymethyltransferase (EC 2.1.2.1) | SCE1572_8655 | yes | sce_7370 | yes |
| A and B | Carbohydrates | One-carbon Metabolism | Serine-glyoxylate cycle | Serine-pyruvate aminotransferase (EC 2.6.1.51) | SCE1572_704 | yes | sce_3001 | yes |
| A and B | Carbohydrates | One-carbon Metabolism | Serine-glyoxylate cycle | Succinate dehydrogenase flavoprotein subunit (EC 1.3.99.1) | SCE1572_8615 | yes | sce_3094 | yes |
| A and B | Carbohydrates | One-carbon Metabolism | Serine-glyoxylate cycle | Succinate dehydrogenase iron-sulfur protein (EC 1.3.99.1) | SCE1572_8616 | yes | sce_7336 | yes |
| A and B | Carbohydrates | One-carbon Metabolism | Serine-glyoxylate cycle | Succinyl-CoA ligase [ADP-forming] alpha chain (EC 6.2.1.5) | SCE1572_11373 | yes | sce_10210 | yes |
| A and B | Carbohydrates | One-carbon Metabolism | Serine-glyoxylate cycle | Succinyl-CoA ligase [ADP-forming] beta chain (EC 6.2.1.5) | SCE1572_3507 | yes | sce_2990 | yes |
| A and B | Carbohydrates | One-carbon Metabolism | Serine-glyoxylate cycle | Succinyl-CoA3-ketoadid-coenzyme A transferase subunit A (EC 2.8.3.) | SCE1572_7617 | yes | sce_6477 | yes |
| A and B | Carbohydrates | One-carbon Metabolism | Serine-glyoxylate cycle | Succinyl-CoA3-ketoadid-coenzyme A transferase subunit B (EC 2.8.3.) | SCE1572_7618 | yes | sce_6478 | yes |
| A and B | Carbohydrates | One-carbon Metabolism | Serine-glyoxylate cycle | isobutyryl-CoA dehydrogenase | SCE1572_889 | yes | sce_662 | yes |
| A and B | Carbohydrates | Organic acids | Glycerate metabolism | D-glycerate 2-kinase (EC 2.7.1.-) | SCE1572_4036 | yes | sce_3364 | yes |
| A and B | Carbohydrates | Organic acids | Glycerate metabolism | Pyruvate kinase (EC 2.7.1.40) | SCE1572_6128 | yes | sce_5073 | yes |
| A and B | Carbohydrates | Organic acids | Propionyl-CoA to Succinyl-CoA Module | B12 binding domain of Methylmalonyl-CoA mutase (EC 5.4.99.2) | SCE1572_2298 | yes | sce_1845 | yes |
| A and B | Carbohydrates | Organic acids | Propionyl-CoA to Succinyl-CoA Module | Methylmalonyl-CoA decarboxylase, alpha chain (EC 4.1.1.41) | SCE1572_2434 | yes | sce_1988 | yes |
| A and B | Carbohydrates | Organic acids | Propionyl-CoA to Succinyl-CoA Module | Methylmalonyl-CoA epimerase (EC 5.1.99.1) | SCE1572_3701 | yes | sce_3051 | yes |
| A and B | Carbohydrates | Organic acids | Propionyl-CoA to Succinyl-CoA Module | Methylmalonyl-CoA mutase (EC 5.4.99.2) | SCE1572_3702 | yes | sce_3052 | yes |
| A and B | Carbohydrates | Organic acids | Propionyl-CoA to Succinyl-CoA Module | Propionyl-CoA carboxylase biotin-containing subunit (EC 6.4.1.3) | SCE1572_4444 | yes | sce_3689 | yes |
| A and B | Carbohydrates | Organic acids | Propionyl-CoA to Succinyl-CoA Module | Propionyl-CoA carboxylase carboxyl transferase subunit (EC 6.4.1.3) | SCE1572_4445 | yes | sce_3690 | yes |
| B | Carbohydrates | Organic acids | Glycerate metabolism | Glycerate kinase (EC 2.7.1.31) | | no | sce_3986 | yes |
| A and B | Carbohydrates | Polysaccharides | Alpha-Amylase locus in Streptococcus | Maltose/maltodextrin ABC transporter, substrate binding periplasmic pr | SCE1572_6789 | yes | sce_5648 | yes |
| A and B | Carbohydrates | Polys | | | | | | |

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|---------|------------------------------|---|---|---|---------------|-----|-----------|-----|
| A and B | Cell Division and Cell Cycle | no subcategory | MukBEF Chromosome Condensation | Chromosome partition protein MukE | SCE1572_4306 | yes | sce_6371 | yes |
| A and B | Cell Division and Cell Cycle | no subcategory | MukBEF Chromosome Condensation | Chromosome partition protein MukF | SCE1572_4307 | yes | sce_6372 | yes |
| A and B | Cell Division and Cell Cycle | no subcategory | MukBEF Chromosome Condensation | Membrane Protein Functionally coupled to the MukBEF Chromosome | SCE1572_1346 | yes | sce_971 | yes |
| A and B | Cell Division and Cell Cycle | no subcategory | YgD and YeaZ | Inactive homolog of metal-dependent proteases, putative molecular chaperone | SCE1572_2318 | yes | sce_1865 | yes |
| A and B | Cell Division and Cell Cycle | no subcategory | YgD and YeaZ | YgD-Kae1/Qt7 family, required for N6-threonylcarbamoyl adenosine | SCE1572_2254 | yes | sce_1799 | yes |
| A and B | Cell Wall and Capsule | Capsular and extracellular polysaccharides | Capsular heptose biosynthesis | D,D-heptose 7-phosphate kinase | SCE1572_838 | yes | sce_635 | yes |
| A and B | Cell Wall and Capsule | Capsular and extracellular polysaccharides | Capsular heptose biosynthesis | D-glycero-D-manno-heptose 1,7-bisphosphate phosphatase (EC 3.1.1.) | SCE1572_4996 | yes | sce_4200 | yes |
| A and B | Cell Wall and Capsule | Capsular and extracellular polysaccharides | Capsular heptose biosynthesis | Phosphoheptose isomerase (EC 5.3.1.) | SCE1572_4995 | yes | sce_4199 | yes |
| A and B | Cell Wall and Capsule | Capsular and extracellular polysaccharides | Exopolysaccharide Biosynthesis | Capsular polysaccharide synthesis enzyme CpsC, exopolysaccharide export | SCE1572_7842 | yes | sce_6646 | yes |
| A and B | Cell Wall and Capsule | Capsular and extracellular polysaccharides | Exopolysaccharide Biosynthesis | Capsular polysaccharide synthesis enzyme CpsD, exopolysaccharide export | SCE1572_9410 | yes | sce_8192 | yes |
| A and B | Cell Wall and Capsule | Capsular and extracellular polysaccharides | Exopolysaccharide Biosynthesis | Exopolysaccharide biosynthesis glycosyltransferase EpsF (EC 2.4.1.) | SCE1572_7325 | yes | sce_6112 | yes |
| A and B | Cell Wall and Capsule | Capsular and extracellular polysaccharides | Exopolysaccharide Biosynthesis | Glycosyl transferase, group 1 family protein | SCE1572_1609 | yes | sce_1148 | yes |
| A and B | Cell Wall and Capsule | Capsular and extracellular polysaccharides | Exopolysaccharide Biosynthesis | Glycosyl transferase, group 2 family protein | SCE1572_1345 | yes | sce_970 | yes |
| A and B | Cell Wall and Capsule | Capsular and extracellular polysaccharides | Exopolysaccharide Biosynthesis | Manganese-dependent protein-tyrosine phosphatase (EC 3.1.3.48) | SCE1572_7864 | yes | sce_6664 | yes |
| A and B | Cell Wall and Capsule | Capsular and extracellular polysaccharides | Exopolysaccharide Biosynthesis | Tyrosine-protein kinase EpsD (EC 2.7.10.2) | SCE1572_1361 | yes | sce_987 | yes |
| A and B | Cell Wall and Capsule | Capsular and extracellular polysaccharides | Exopolysaccharide Biosynthesis | Undecaprenyl-phosphate galactosylphosphotransferase (EC 2.7.8.6) | SCE1572_4803 | yes | sce_4018 | yes |
| A and B | Cell Wall and Capsule | Capsular and extracellular polysaccharides | Rhamnose containing glycans | Glucose-1-phosphate thymidyltransferase (EC 2.7.7.24) | SCE1572_11044 | yes | sce_7609 | yes |
| A and B | Cell Wall and Capsule | Capsular and extracellular polysaccharides | Rhamnose containing glycans | UDP-glucose 4-epimerase (EC 5.1.3.2) | SCE1572_1369 | yes | sce_995 | yes |
| A and B | Cell Wall and Capsule | Capsular and extracellular polysaccharides | Rhamnose containing glycans | dTDP-4-dehydrothiamine reductase (EC 1.1.1.133) | SCE1572_6699 | yes | sce_3427 | yes |
| A and B | Cell Wall and Capsule | Capsular and extracellular polysaccharides | Rhamnose containing glycans | dTDP-glucose 4,6-dehydratase (EC 4.2.1.46) | SCE1572_8789 | yes | sce_7489 | yes |
| A and B | Cell Wall and Capsule | Capsular and extracellular polysaccharides | Sialic Acid Metabolism | Glucosamine-fructose-6-phosphate aminotransferase [isomerizing] (EC 2.6.1.13) | SCE1572_5465 | yes | sce_8287 | yes |
| A and B | Cell Wall and Capsule | Capsular and extracellular polysaccharides | Sialic Acid Metabolism | Glucosamine-1-phosphate N-acetyltransferase (EC 2.3.1.157) | SCE1572_7188 | yes | sce_5909 | yes |
| A and B | Cell Wall and Capsule | Capsular and extracellular polysaccharides | Sialic Acid Metabolism | N-acetylglucosamine-1-phosphate uridylyltransferase (EC 2.7.7.23) | SCE1572_7188 | yes | sce_5909 | yes |
| A and B | Cell Wall and Capsule | Capsular and extracellular polysaccharides | Sialic Acid Metabolism | Phosphoglucosamine mutase (EC 5.4.2.10) | SCE1572_5464 | yes | sce_6482 | yes |
| A and B | Cell Wall and Capsule | Capsular and extracellular polysaccharides | Sialic Acid Metabolism | Sialic acid transporter (permease) NanT | SCE1572_2086 | yes | sce_1596 | yes |
| A and B | Cell Wall and Capsule | Capsular and extracellular polysaccharides | Sialic Acid Metabolism | UDP-N-acetylglucosamine 2-epimerase (EC 5.1.3.14) | SCE1572_2892 | yes | sce_2786 | yes |
| A and B | Cell Wall and Capsule | Capsular and extracellular polysaccharides | dTDP-rhamnose synthesis | Glucose-1-phosphate cytidylyltransferase (EC 2.7.7.33) | SCE1572_6470 | yes | sce_5443 | yes |
| A and B | Cell Wall and Capsule | Capsular and extracellular polysaccharides | dTDP-rhamnose synthesis | Glucose-1-phosphate thymidyltransferase (EC 2.7.7.24) | SCE1572_11044 | yes | sce_7609 | yes |
| A and B | Cell Wall and Capsule | Capsular and extracellular polysaccharides | dTDP-rhamnose synthesis | dTDP-4-dehydrothiamine reductase (EC 1.1.1.133) | SCE1572_6699 | yes | sce_3427 | yes |
| A and B | Cell Wall and Capsule | Capsular and extracellular polysaccharides | dTDP-rhamnose synthesis | dTDP-glucose 4,6-dehydratase (EC 4.2.1.46) | SCE1572_8789 | yes | sce_7489 | yes |
| A | Cell Wall and Capsule | Capsular and extracellular polysaccharides | Streptococcal Hyaluronic Acid Capsule | UDP-glucose-1-phosphate uridylyltransferase (EC 2.7.7.9) | SCE1572_9897 | yes | sce_1243 | no |
| A and B | Cell Wall and Capsule | Gram-Negative cell wall components | Lipoprotein sorting system | Lipoprotein releasing system ATP-binding protein LolD | SCE1572_1740 | yes | sce_1216 | yes |
| A and B | Cell Wall and Capsule | Gram-Negative cell wall components | Lipoprotein sorting system | Lipoprotein releasing system transmembrane protein LolC | SCE1572_1703 | yes | sce_1217 | yes |
| A and B | Cell Wall and Capsule | Gram-Negative cell wall components | Lipoprotein sorting system | Outer membrane lipoprotein carrier protein LolA | SCE1572_1685 | yes | sce_5686 | yes |
| A and B | Cell Wall and Capsule | Gram-Negative cell wall components | Peptidoglycan lipid II flippase | Proposed peptidoglycan lipid II flippase MurJ | SCE1572_5025 | yes | sce_4227 | yes |
| A and B | Cell Wall and Capsule | Gram-Positive cell wall components | Teichuronic acid biosynthesis | Putative teichuronic acid biosynthesis glycosyl transferase TaaC | SCE1572_2396 | yes | sce_1950 | yes |
| A and B | Cell Wall and Capsule | Gram-Positive cell wall components | Teichuronic acid biosynthesis | UDP-glucose dehydrogenase (EC 1.1.1.22) | SCE1572_1358 | yes | sce_984 | yes |
| A and B | Cell Wall and Capsule | no subcategory | Murein Hydrolases | D-alanyl-D-alanine carboxypeptidase (EC 3.4.16.4) | SCE1572_330 | yes | sce_4328 | yes |
| A and B | Cell Wall and Capsule | no subcategory | Murein Hydrolases | Membrane-bound lytic murein transglycosylase D precursor (EC 3.2.1.) | SCE1572_2236 | yes | sce_1784 | yes |
| A and B | Cell Wall and Capsule | no subcategory | Murein Hydrolases | Muramoyltetrapeptide carboxypeptidase (EC 3.4.17.13) | SCE1572_5722 | yes | sce_4775 | yes |
| A and B | Cell Wall and Capsule | no subcategory | Murein Hydrolases | N-acetylmuramoyl-L-alanine amidase (EC 3.5.1.28) | SCE1572_5042 | yes | sce_4242 | yes |
| A and B | Cell Wall and Capsule | no subcategory | Murein Hydrolases | Soluble lytic murein transglycosylase precursor (EC 3.2.1.-) | SCE1572_1540 | yes | sce_1060 | yes |
| A and B | Cell Wall and Capsule | no subcategory | Peptidoglycan Biosynthesis | Cell division protein FtsI [Peptidoglycan synthetase] (EC 2.4.1.129) | SCE1572_2302 | yes | sce_1849 | yes |
| A and B | Cell Wall and Capsule | no subcategory | Peptidoglycan Biosynthesis | D-alanine-D-alanine ligase (EC 6.3.2.4) | SCE1572_1374 | yes | sce_1000 | yes |
| A and B | Cell Wall and Capsule | no subcategory | Peptidoglycan Biosynthesis | D-alanine-D-alanine ligase A (EC 6.3.2.4) | SCE1572_836 | yes | sce_634 | yes |
| A and B | Cell Wall and Capsule | no subcategory | Peptidoglycan Biosynthesis | D-alanyl-D-alanine carboxypeptidase (EC 3.4.16.4) | SCE1572_330 | yes | sce_4328 | yes |
| A and B | Cell Wall and Capsule | no subcategory | Peptidoglycan Biosynthesis | Glucosamine-1-phosphate N-acetyltransferase (EC 2.3.1.157) | SCE1572_7188 | yes | sce_5909 | yes |
| A and B | Cell Wall and Capsule | no subcategory | Peptidoglycan Biosynthesis | Glutamate racemase (EC 5.1.1.3) | SCE1572_284 | yes | sce_5417 | yes |
| A and B | Cell Wall and Capsule | no subcategory | Peptidoglycan Biosynthesis | Glutamine synthetase type I (EC 6.3.1.2) | SCE1572_9287 | yes | sce_8068 | yes |
| A and B | Cell Wall and Capsule | no subcategory | Peptidoglycan Biosynthesis | Monofunctional biosynthetic peptidoglycan transglycosylase (EC 2.4.2.) | SCE1572_3414 | yes | sce_2900 | yes |
| A and B | Cell Wall and Capsule | no subcategory | Peptidoglycan Biosynthesis | Multimodular transpeptidase-transglycosylase (EC 2.4.1.129) (EC 3.4.) | SCE1572_39 | yes | sce_41 | yes |
| A and B | Cell Wall and Capsule | no subcategory | Peptidoglycan Biosynthesis | N-acetylglucosamine-1-phosphate uridylyltransferase (EC 2.7.7.23) | SCE1572_7188 | yes | sce_5909 | yes |
| A and B | Cell Wall and Capsule | no subcategory | Peptidoglycan Biosynthesis | N-acetylglucosamine-1-phosphate uridylyltransferase eukaryotic (EC 2.7.7.23) | SCE1572_4115 | yes | sce_3465 | yes |
| A and B | Cell Wall and Capsule | no subcategory | Peptidoglycan Biosynthesis | Penicillin-binding protein 2 (PBP-2) | SCE1572_3205 | yes | sce_2699 | yes |
| A and B | Cell Wall and Capsule | no subcategory | Peptidoglycan Biosynthesis | Phospho-N-acetylmuramoyl-pentapeptide-transferase (EC 2.7.8.13) | SCE1572_2304 | yes | sce_1851 | yes |
| A and B | Cell Wall and Capsule | no subcategory | Peptidoglycan Biosynthesis | Rod shape-determining protein RodA | SCE1572_3206 | yes | sce_2700 | yes |
| A and B | Cell Wall and Capsule | no subcategory | Peptidoglycan Biosynthesis | UDP-N-acetylenolpyruvylglucosamine reductase (EC 1.1.1.158) | SCE1572_9952 | yes | sce_8750 | yes |
| A and B | Cell Wall and Capsule | no subcategory | Peptidoglycan Biosynthesis | UDP-N-acetylglucosamine-1-carboxyvinyltransferase (EC 2.5.1.7) | SCE1572_8996 | yes | sce_10214 | yes |
| A and B | Cell Wall and Capsule | no subcategory | Peptidoglycan Biosynthesis | UDP-N-acetylglucosamine-N-acetylmuramyl-(pentapeptide) pyrophosphatase | SCE1572_2307 | yes | sce_1854 | yes |
| A and B | Cell Wall and Capsule | no subcategory | Peptidoglycan Biosynthesis | UDP-N-acetylmuramate-alanine ligase (EC 6.3.2.8) | SCE1572_2308 | yes | sce_1855 | yes |
| A and B | Cell Wall and Capsule | no subcategory | Peptidoglycan Biosynthesis | UDP-N-acetylmuramoylalanine-D-glutamate ligase (EC 6.3.2.9) | SCE1572_2305 | yes | sce_1852 | yes |
| A and B | Cell Wall and Capsule | no subcategory | Peptidoglycan Biosynthesis | UDP-N-acetylmuramoylalanine-D-glutamate-2,6-diaminopimelate ligase | SCE1572_2303 | yes | sce_1850 | yes |
| A and B | Cell Wall and Capsule | no subcategory | Peptidoglycan Biosynthesis | UDP-N-acetylmuramoylalanine-D-glutamyl-2,6-diaminopimelate-D-alanine ligase | SCE1572_9508 | yes | sce_8295 | yes |
| A and B | Cell Wall and Capsule | no subcategory | Peptidoglycan biosynthesis--go | D-alanine-D-alanine ligase (EC 6.3.2.4) | SCE1572_1374 | yes | sce_1000 | yes |
| A and B | Cell Wall and Capsule | no subcategory | Peptidoglycan biosynthesis--go | D-alanine-D-alanine ligase A (EC 6.3.2.4) | SCE1572_836 | yes | sce_634 | yes |
| A and B | Cell Wall and Capsule | no subcategory | Peptidoglycan biosynthesis--go | UDP-N-acetylmuramate-alanine ligase (EC 6.3.2.8) | SCE1572_2308 | yes | sce_1855 | yes |
| A and B | Cell Wall and Capsule | no subcategory | Peptidoglycan biosynthesis--go | UDP-N-acetylmuramate-L-alanyl-gamma-D-glutamyl-meso-diaminopimelate | SCE1572_9737 | yes | sce_8539 | yes |
| A and B | Cell Wall and Capsule | no subcategory | Peptidoglycan biosynthesis--go | UDP-N-acetylmuramoylalanine-D-glutamate ligase (EC 6.3.2.9) | SCE1572_2305 | yes | sce_1852 | yes |
| A and B | Cell Wall and Capsule | no subcategory | Peptidoglycan biosynthesis--go | UDP-N-acetylmuramoylalanine-D-glutamate-2,6-diaminopimelate ligase | SCE1572_2303 | yes | sce_1850 | yes |
| A and B | Cell Wall and Capsule | no subcategory | Peptidoglycan biosynthesis--go | UDP-N-acetylmuramoylalanine-D-glutamyl-2,6-diaminopimelate-D-alanine | SCE1572_9508 | yes | sce_8295 | yes |
| A and B | Cell Wall and Capsule | no subcategory | Recycling of Peptidoglycan Amino Acids | AmpG permease | SCE1572_1393 | yes | sce_1005 | yes |
| A and B | Cell Wall and Capsule | no subcategory | Recycling of Peptidoglycan Amino Acids | Muramoyltetrapeptide carboxypeptidase (EC 3.4.17.13) | SCE1572_5722 | yes | sce_4775 | yes |
| A and B | Cell Wall and Capsule | no subcategory | Recycling of Peptidoglycan Amino Acids | N-acetylmuramoyl-L-alanine amidase (EC 3.5.1.28) | SCE1572_5042 | yes | sce_4242 | yes |
| A and B | Cell Wall and Capsule | no subcategory | Recycling of Peptidoglycan Amino Acids | UDP-N-acetylmuramate-L-alanyl-gamma-D-glutamyl-meso-diaminopimelate | SCE1572_9737 | yes | sce_8539 | yes |
| A and B | Cell Wall and Capsule | no subcategory | UDP-N-acetylmuramate from Fructose-6-phosphate Biosynthesis | Glucosamine-fructose-6-phosphate aminotransferase [isomerizing] (EC 2.6.1.13) | SCE1572_5465 | yes | sce_8287 | yes |
| A and B | Cell Wall and Capsule | no subcategory | UDP-N-acetylmuramate from Fructose-6-phosphate Biosynthesis | Glucosamine-1-phosphate N-acetyltransferase (EC 2.3.1.157) | SCE1572_7188 | yes | sce_5909 | yes |
| A and B | Cell Wall and Capsule | no subcategory | UDP-N-acetylmuramate from Fructose-6-phosphate Biosynthesis | N-acetylglucosamine-1-phosphate uridylyltransferase (EC 2.7.7.23) | SCE1572_7188 | yes | sce_5909 | yes |
| A and B | Cell Wall and Capsule | no subcategory | UDP-N-acetylmuramate from Fructose-6-phosphate Biosynthesis | N-acetylglucosamine-1-phosphate uridylyltransferase eukaryotic (EC 2.7.7.23) | SCE1572_4115 | yes | sce_3465 | yes |
| A and B | Cell Wall and Capsule | no subcategory | UDP-N-acetylmuramate from Fructose-6-phosphate Biosynthesis | Phosphoglucosamine mutase (EC 5.4.2.10) | SCE1572_5464 | yes | sce_6482 | yes |
| A and B | Cell Wall and Capsule | no subcategory | UDP-N-acetylmuramate from Fructose-6-phosphate Biosynthesis | UDP-N-acetylenolpyruvylglucosamine reductase (EC 1.1.1.158) | SCE1572_9952 | yes | sce_8750 | yes |
| A and B | Cell Wall and Capsule | no subcategory | UDP-N-acetylmuramate from Fructose-6-phosphate Biosynthesis | UDP-N-acetylglucosamine-1-carboxyvinyltransferase (EC 2.5.1.7) | SCE1572_8996 | yes | sce_10214 | yes |
| A and B | Cell Wall and Capsule | no subcategory | YjE | ATPase YjE, predicted to have essential role in cell wall biosynthesis | SCE1572_10671 | yes | sce_9283 | yes |
| A and B | Cell Wall and Capsule | no subcategory | YjE | COG178: Predicted phosphotransferase related to Ser/Thr protein kinase | SCE1572_10884 | yes | sce_9513 | yes |
| A and B | Cell Wall and Capsule | no subcategory | YjE | Inactive homolog of metal-dependent proteases, putative molecular chaperone | SCE1572_2318 | yes | sce_1865 | yes |
| A and B | Cell Wall and Capsule | no subcategory | YjE | NAD(P)HX dehydratase | SCE1572_552 | yes | sce_358 | yes |
| A and B | Cell Wall and Capsule | no subcategory | YjE | NAD(P)HX epimerase | SCE1572_552 | yes | sce_358 | yes |
| A and B | Clustering-based subsystems | 2 proteases and a MoxR | CBSS-1140.3.peg.2017 | FIG001454: Transglutaminase-like enzymes, putative cysteine proteases | SCE1572_10642 | yes | sce_9248 | yes |
| A and B | Clustering-based subsystems | 2 proteases and a MoxR | CBSS-1140.3.peg.2017 | FIG002343: hypotential protein | SCE1572_10643 | yes | sce_9248 | yes |
| A and B | Clustering-based subsystems | 2 proteases and a MoxR | CBSS-1140.3.peg.2017 | FIG02979: MoxR-like ATPase | SCE1572_6012 | yes | sce_4964 | yes |
| A and B | Clustering-based subsystems | Biosynthesis of galactoglycans and related lipo | CBSS-258594.1.peg.3339 | Tyrosine-protein kinase Wzc (EC 2.7.10.2) | SCE1572_2318 | no | sce_3722 | no |
| A and B | Clustering-based subsystems | Cell Division | Bacterial cell division cluster | Cell division topological specificity factor MinE | SCE1572_4515 | yes | sce_3732 | yes |
| A and B | Clustering-based subsystems | Cell Division | Bacterial cell division cluster | DNA repair protein RadC | SCE1572_140 | yes | sce_512 | yes |
| A and B | Clustering-based subsystems | Cell Division | Bacterial cell division cluster | Penicillin-binding protein 2 (PBP-2) | SCE1572_3205 | yes | sce_2699 | yes |
| A and B | Clustering-based subsystems | Cell Division | Bacterial cell division cluster | Rod shape-determining protein MreB | SCE1572_3202 | yes | sce_2696 | yes |
| A and B | Clustering-based subsystems | Cell Division | Bacterial cell division cluster | Rod shape-determining protein MreC | SCE1572_3203 | yes | sce_2697 | yes |
| A and B | Clustering-based subsystems | Cell Division | Bacterial cell division cluster | Rod shape-determining protein RodA | SCE1572_3206 | yes | sce_2700 | yes |
| A and B | Clustering-based subsystems | Cell Division | Bacterial cell division cluster | Septum formation protein Maf | SCE1572_748 | yes | sce_551 | yes |
| A and B | Clustering-based subsystems | Cell Division | Bacterial cell division cluster | Septum site-determining protein MinC | SCE1572_4501 | yes | sce_3764 | yes |
| A and B | Clustering-based subsystems | Cell Division | Bacterial cell division cluster | Septum site-determining protein MinD | SCE1572_4514 | yes | sce_3771 | yes |
| A and B | Clustering-based subsystems | Cell Division | Septum site-determining cluster Min | Cell division topological specificity factor MinE | SCE1572_4515 | yes | sce_3772 | yes |
| A and B | Clustering-based subsystems | Cell Division | Septum site-determining cluster Min | Septum site-determining protein MinC | SCE1572_4501 | yes | sce_3764 | yes |
| A and B | Clustering-based subsystems | Cell Division | Septum site-determining cluster Min | Septum site-determining protein MinD | SCE1572_4514 | yes | sce_3771 | yes |
| A and B | Clustering-based subsystems | Cell Division | cell division cluster containing FtsQ | Cell division protein FtsA | SCE1572_2309 | yes | sce_1856 | yes |
| A and B | Clustering-based subsystems | Cell Division | cell division cluster containing FtsQ | Cell division protein FtsW | SCE1572_2306 | yes | sce_1853 | yes |
| A and B | Clustering-based subsystems | Cell Division | cell division cluster containing FtsQ | Cell division protein FtsZ (EC 3.4.24.-) | SCE1572_2311 | yes | sce_1403 | yes |
| A and B | Clustering-based subsystems | Cell Division | cell division cluster containing FtsQ | D-alanine-D-alanine ligase (EC 6.3.2.4) | SCE1572_1374 | yes | sce_1000 | yes |
| A and B | Clustering-based subsystems | Cell Division | cell division cluster containing FtsQ | D-alanine-D-alanine ligase A (EC 6.3.2.4) | SCE1572_836 | yes | sce_634 | yes |
| A and B | Clustering-based subsystems | Cell Division | cell division cluster containing FtsQ | UDP-N-acetylmuramate-alanine ligase (EC 6.3.2.8) | SCE1572_2308 | yes | sce_1855 | yes |
| A and B | Clustering-based subsystems | Cell Division | cell division core of larger cluster | Cell division protein FtsA | SCE1572_2310 | yes | sce_1857 | yes |
| A and B | Clustering-based subsystems | Cell Division | cell division core of larger cluster | Cell division protein FtsQ | SCE1572_2309 | yes | sce_1856 | yes |
| A and B | Clustering-based subsystems | Cell Division | cell division core of larger cluster | Cell division protein FtsZ (EC 3.4.24.-) | SCE1572_2311 | yes | sce_1403 | yes |
| A and B | Clustering-based subsystems | Cell Division | cell division core of larger cluster | UDP-N-acetylglucosamine-N-acetylmuramyl-(pentapeptide) pyrophosphatase | SCE1572_2307 | yes | sce_1854 | yes |
| A and B | Clustering-based subsystems | Central carbohydrate metabolism | Glyoxylate bypass cluster | Isocitrate lyase (EC 4.1.3.1) | SCE1572_11040 | yes | sce_9752 | yes |
| A and B | Clustering-based subsystems | Central carbohydrate metabolism | Glyoxylate bypass cluster | Malate synthase (EC 2.3.3.9) | SCE1572_11039 | yes | sce_9751 | yes |
| A and B | Clustering-based subsystems | Cofactors | Riboflavin synthesis cluster | 3,4-dihydroxy-2-butanone 4-phosphate synthase (EC 4.1.99.12) | SCE1572_2917 | yes | sce_2550 | yes |
| A and B | Clustering-based subsystems | Cofactors | Riboflavin synthesis cluster | 5-amino-6-5-phosphoribosylaminoimidazole reductase (EC 1.1.1.193) | SCE1572_403 | yes | sce_267 | yes |
| A and B | Clustering-based subsystems | Cofactors | Riboflavin synthesis | | | | | |

| | | | | | | | |
|---------|-----------------------------|---|--|--|------------------|----------|----------|
| A and B | Clustering-based subsystems | May be related to ADP-phosphoribose and NACBSS-216591.1.p.168 | Aspartokinase (EC 2.7.2.4) | SCE1572_3345 | yes | sce_2841 | yes |
| A and B | Clustering-based subsystems | May be related to ADP-phosphoribose and NACBSS-216591.1.p.168 | Competence protein F homolog, phosphoribosyltransferase domain | SCE1572_3377 | yes | sce_8158 | yes |
| A and B | Clustering-based subsystems | May be related to ADP-phosphoribose and NACBSS-216591.1.p.168 | Histone acetyltransferase HPA2 and related acetyltransferases | SCE1572_1899 | yes | sce_1411 | yes |
| A and B | Clustering-based subsystems | May be related to ADP-phosphoribose and NACBSS-216591.1.p.168 | Predicted aminoglycoside phosphotransferase | SCE1572_6531 | yes | sce_9961 | yes |
| A | Clustering-based subsystems | May be related to ADP-phosphoribose and NACBSS-216591.1.p.168 | NTP pyrophosphorylhydrolases including oxidative damage repair enzyme | SCE1572_7134 | yes | | no |
| A and B | Clustering-based subsystems | Phosphate metabolism | Phosphate ABC transporter, periplasmic phosphate-binding protein PstA | SCE1572_3980 | yes | sce_3309 | yes |
| A and B | Clustering-based subsystems | Phosphate metabolism | Phosphate regulon sensor protein PhoR (SphS) (EC 2.7.13.3) | SCE1572_783 | yes | sce_437 | yes |
| A and B | Clustering-based subsystems | Phosphate metabolism | Phosphate regulon transcriptional regulatory protein PhoB (SphR) | SCE1572_1238 | yes | sce_3311 | yes |
| B | Clustering-based subsystems | Probably GTP or GMP signaling related | Ribonuclease III (EC 3.1.26.3) | | no | sce_1892 | yes |
| A and B | Clustering-based subsystems | Probably organic hydroperoxide resistance re | Homoserine kinase (EC 2.7.1.39) | SCE1572_633 | yes | sce_441 | yes |
| A and B | Clustering-based subsystems | Probably organic hydroperoxide resistance re | Organic hydroperoxide resistance protein | SCE1572_360 | yes | sce_201 | yes |
| A and B | Clustering-based subsystems | Probably organic hydroperoxide resistance re | Organic hydroperoxide resistance transcriptional regulator | SCE1572_5122 | yes | sce_4310 | yes |
| A and B | Clustering-based subsystems | Putative Isoquinoline 1-oxidoreductase subunit | Isoquinoline 1-oxidoreductase alpha subunit (EC 1.3.99.16) | SCE1572_6274 | yes | sce_3739 | yes |
| A and B | Clustering-based subsystems | Putative Isoquinoline 1-oxidoreductase subunit | Isoquinoline 1-oxidoreductase beta subunit (EC 1.3.99.16) | SCE1572_6275 | yes | sce_3738 | yes |
| A and B | Clustering-based subsystems | Putative Isoquinoline 1-oxidoreductase subunit | Putative Isoquinoline 1-oxidoreductase subunit, MI3835 protein | SCE1572_8375 | yes | sce_7087 | yes |
| A | Clustering-based subsystems | Putative associate of RNA polymerase sigma-54 | Sigma-70 region 2/Sigma-70 region 4 | SCE1572_10133 | yes | | no |
| A | Clustering-based subsystems | Putative associate of RNA polymerase sigma-54 | Transmembrane regulator protein PrtR | SCE1572_2450 | yes | | no |
| A and B | Clustering-based subsystems | Sulfatases and sulfatase modifying factor 1 (an Sulfatases and sulfatase modifying factor 1 | Arylsulfatase (EC 3.1.6.1) | SCE1572_277 | yes | sce_3154 | yes |
| A and B | Clustering-based subsystems | Sulfatases and sulfatase modifying factor 1 (an Sulfatases and sulfatase modifying factor 1 | Choline-sulfatase (EC 3.1.6.6) | SCE1572_2802 | yes | sce_8713 | yes |
| A and B | Clustering-based subsystems | Sulfatases and sulfatase modifying factor 1 (an Sulfatases and sulfatase modifying factor 1 | Sulfatase | SCE1572_4815 | yes | sce_1066 | yes |
| A and B | Clustering-based subsystems | Sulfatases and sulfatase modifying factor 1 (an Sulfatases and sulfatase modifying factor 1 | Sulfatase modifying factor 1 precursor (C-alpha-formylglycine- generat | SCE1572_5072 | yes | sce_4261 | yes |
| A and B | Clustering-based subsystems | TLD cluster | Cytoplasmic axial filament protein CafA and Ribonuclease G (EC 3.1.4. | SCE1572_9350 | yes | sce_8131 | yes |
| A and B | Clustering-based subsystems | TLD cluster | Rod shape-determining protein MreC | SCE1572_3203 | yes | sce_2697 | yes |
| A and B | Clustering-based subsystems | TLD cluster | Septum formation protein Maf | SCE1572_748 | yes | sce_551 | yes |
| A and B | Clustering-based subsystems | TLD cluster | TLD protein, part of proposed TME/TMD proteolytic complex (PM | SCE1572_8457 | yes | sce_7217 | yes |
| A and B | Clustering-based subsystems | Translation | Transcription accessory protein (S1 RNA-binding domain) | SCE1572_5755 | yes | sce_4806 | yes |
| A and B | Clustering-based subsystems | Translation | Transcription elongation factor GreB | SCE1572_4795 | yes | sce_4010 | yes |
| B | Clustering-based subsystems | heat shock, cell division, proteases, and a meth | Heat shock Cell division Proteases and a Methyltransferase | FIG015287: Zinc protease | no | sce_4289 | yes |
| A and B | Clustering-based subsystems | no category | Aerotolerance operon in Bacteroides and potentially orthologou | BatA (Bacteroides aerotolerance operon) | yes | sce_7280 | yes |
| A and B | Clustering-based subsystems | no category | Aerotolerance operon in Bacteroides and potentially orthologou | BatB | yes | sce_7281 | yes |
| A and B | Clustering-based subsystems | no category | Aerotolerance operon in Bacteroides and potentially orthologou | BatD | yes | sce_7283 | yes |
| A and B | Clustering-based subsystems | no category | Aerotolerance operon in Bacteroides and potentially orthologou | MoxR-like ATPase in aerotolerance operon | yes | sce_6634 | yes |
| A and B | Clustering-based subsystems | no category | Aerotolerance operon in Bacteroides and potentially orthologou | hypothetical protein PA3071 | yes | sce_7278 | yes |
| A and B | Clustering-based subsystems | no category | Bacterial Cell Division | Cell division protein BofA | yes | sce_3877 | yes |
| A and B | Clustering-based subsystems | no category | Bacterial Cell Division | Cell division protein FtsA | yes | sce_1857 | yes |
| A and B | Clustering-based subsystems | no category | Bacterial Cell Division | Cell division protein FtsH (EC 3.4.24.-) | yes | sce_474 | yes |
| A and B | Clustering-based subsystems | no category | Bacterial Cell Division | Cell division protein FtsI [Peptidoglycan synthetase] (EC 2.4.1.129) | yes | sce_1849 | yes |
| A and B | Clustering-based subsystems | no category | Bacterial Cell Division | Cell division protein FtsJ | yes | sce_2217 | yes |
| A and B | Clustering-based subsystems | no category | Bacterial Cell Division | Cell division protein FtsK | yes | sce_1797 | yes |
| A and B | Clustering-based subsystems | no category | Bacterial Cell Division | Cell division protein FtsQ | yes | sce_1856 | yes |
| A and B | Clustering-based subsystems | no category | Bacterial Cell Division | Cell division protein FtsW | yes | sce_1853 | yes |
| A and B | Clustering-based subsystems | no category | Bacterial Cell Division | Cell division protein FtsX | yes | sce_8086 | yes |
| A and B | Clustering-based subsystems | no category | Bacterial Cell Division | Cell division protein FtsZ (EC 3.4.24.-) | yes | sce_1403 | yes |
| A and B | Clustering-based subsystems | no category | Bacterial Cell Division | Cell division protein MraZ | yes | sce_1846 | yes |
| A and B | Clustering-based subsystems | no category | Bacterial Cell Division | Cell division topological specificity factor MinE | yes | sce_3772 | yes |
| A and B | Clustering-based subsystems | no category | Bacterial Cell Division | Cell division transporter, ATP-binding protein FtsE (TC 3.A.5.1.1) | yes | sce_1125 | yes |
| A and B | Clustering-based subsystems | no category | Bacterial Cell Division | Cell division trigger factor (EC 5.2.1.8) | yes | sce_3529 | yes |
| A and B | Clustering-based subsystems | no category | Bacterial Cell Division | Chromosome (plasmid) partitioning protein ParA | yes | sce_1641 | yes |
| A and B | Clustering-based subsystems | no category | Bacterial Cell Division | Cytoplasmic axial filament protein CafA and Ribonuclease G (EC 3.1.4. | SCE1572_9350 | yes | sce_8131 |
| A and B | Clustering-based subsystems | no category | Bacterial Cell Division | GTP-binding protein Era | yes | sce_6660 | yes |
| A and B | Clustering-based subsystems | no category | Bacterial Cell Division | Rod shape-determining protein MreB | yes | sce_2696 | yes |
| A and B | Clustering-based subsystems | no category | Bacterial Cell Division | Rod shape-determining protein MreC | yes | sce_2697 | yes |
| A and B | Clustering-based subsystems | no category | Bacterial Cell Division | Septum formation protein Maf | yes | sce_551 | yes |
| A and B | Clustering-based subsystems | no category | Bacterial Cell Division | Septum site-determining protein MinC | yes | sce_3764 | yes |
| A and B | Clustering-based subsystems | no category | Bacterial Cell Division | Septum site-determining protein MinD | yes | sce_3771 | yes |
| A and B | Clustering-based subsystems | no category | Bacterial Cell Division | Signal recognition particle receptor protein FtsY (=alpha subunit) (TC 3 | SCE1572_3933 | yes | sce_3267 |
| A and B | Clustering-based subsystems | no category | Bacterial Cell Division | rRNA small subunit methyltransferase H | yes | sce_1847 | yes |
| A and B | Clustering-based subsystems | no category | Bacterial RNA-metabolizing Zn-dependent hydrolases | Cell division protein FtsK | yes | sce_1797 | yes |
| A and B | Clustering-based subsystems | no category | Bacterial RNA-metabolizing Zn-dependent hydrolases | Ferric uptake regulation protein FUR | yes | sce_7 | yes |
| A and B | Clustering-based subsystems | no category | Bacterial RNA-metabolizing Zn-dependent hydrolases | Inactive homolog of metal-dependent proteases, putative molecular ch | SCE1572_2318 | yes | sce_1865 |
| A and B | Clustering-based subsystems | no category | Bacterial RNA-metabolizing Zn-dependent hydrolases | Peptidyl deaminase (EC 3.5.1.88) | yes | sce_4266 | yes |
| A and B | Clustering-based subsystems | no category | Bacterial RNA-metabolizing Zn-dependent hydrolases | Polyhydroxynucleotide nucleotidyltransferase (EC 2.7.7.8) | yes | sce_5974 | yes |
| A and B | Clustering-based subsystems | no category | Bacterial RNA-metabolizing Zn-dependent hydrolases | Ribonuclease J2 (endoribonuclease in RNA processing) | SCE1572_620 | yes | sce_428 |
| A and B | Clustering-based subsystems | no category | Bacterial RNA-metabolizing Zn-dependent hydrolases | Ribosomal-protein-S18p-alanine acetyltransferase (EC 2.3.1.-) | SCE1572_7710 | yes | sce_6542 |
| A and B | Clustering-based subsystems | no category | Bacterial RNA-metabolizing Zn-dependent hydrolases | Trk system potassium uptake protein TrkA | yes | sce_3654 | yes |
| A and B | Clustering-based subsystems | no category | Bacterial RNA-metabolizing Zn-dependent hydrolases | YggD/Kae1 Qri7 family, required for N6-threonylcarbamoyl adenosine | SCE1572_2254 | yes | sce_1799 |
| A and B | Clustering-based subsystems | no category | Butyrate metabolism cluster | 3-hydroxyacyl-CoA dehydrogenase (EC 1.1.1.35) | SCE1572_60 | yes | sce_50 |
| A and B | Clustering-based subsystems | no category | Butyrate metabolism cluster | Acetyl-CoA acetyltransferase (EC 2.3.1.9) | SCE1572_61 | yes | sce_51 |
| A and B | Clustering-based subsystems | no category | Butyrate metabolism cluster | Enoyl-CoA hydratase (EC 4.2.1.17) | SCE1572_60 | yes | sce_50 |
| A and B | Clustering-based subsystems | no category | CBSS-1352.1.p.856 | Transcriptional regulator, PadR family | SCE1572_4122 | yes | sce_3467 |
| A and B | Clustering-based subsystems | no category | CBSS-138119.3.p.2719 | Ribosome-binding factor A | SCE1572_7630 | yes | sce_6491 |
| A and B | Clustering-based subsystems | no category | CBSS-138119.3.p.2719 | Translation initiation factor 2 | SCE1572_7632 | yes | sce_3829 |
| A and B | Clustering-based subsystems | no category | CBSS-138119.3.p.2719 | rRNA pseudouridine synthase B (EC 4.2.1.70) | yes | sce_4800 | yes |
| A and B | Clustering-based subsystems | no category | CBSS-176279.3.p.868 | GTP-binding protein Obg | SCE1572_2454 | yes | sce_2000 |
| A and B | Clustering-based subsystems | no category | CBSS-176279.3.p.868 | LSU ribosomal protein L21p | SCE1572_10045 | yes | sce_8861 |
| A and B | Clustering-based subsystems | no category | CBSS-176279.3.p.868 | LSU ribosomal protein L27p | SCE1572_10044 | yes | sce_8860 |
| A and B | Clustering-based subsystems | no category | CBSS-176299.4.p.1996A | Endoribonuclease L-PSF | SCE1572_472 | yes | sce_283 |
| A and B | Clustering-based subsystems | no category | CBSS-176299.4.p.1996A | Glycerophosphoryl diester phosphodiesterase (EC 3.1.4.46) | SCE1572_1970 | yes | sce_5734 |
| A and B | Clustering-based subsystems | no category | CBSS-176299.4.p.1996B | ATP-dependent Clp protease ATP-binding subunit ClpA | SCE1572_571 | yes | sce_373 |
| A and B | Clustering-based subsystems | no category | CBSS-176299.4.p.1996B | Ribosome recycling factor | SCE1572_8244 | yes | sce_6915 |
| A and B | Clustering-based subsystems | no category | CBSS-176299.4.p.1996B | SSU ribosomal protein S2p (SAe) | SCE1572_4193 | yes | sce_3515 |
| A and B | Clustering-based subsystems | no category | CBSS-176299.4.p.1996B | Translation elongation factor Ts | SCE1572_4194 | yes | sce_3516 |
| A and B | Clustering-based subsystems | no category | CBSS-176299.4.p.1996B | Uridylate kinase (EC 2.7.4.-) | SCE1572_9343 | yes | sce_8123 |
| A and B | Clustering-based subsystems | no category | CBSS-188.1.p.6720 | Serine protein kinase (prkA protein), P-loop containing | SCE1572_9023 | yes | sce_7778 |
| A and B | Clustering-based subsystems | no category | CBSS-188.1.p.6720 | Stage V sporulation protein involved in spore cortex synthesis (SpoVR) | SCE1572_2420 | yes | sce_1974 |
| A and B | Clustering-based subsystems | no category | CBSS-188.1.p.6720 | UPF0229 protein YeaH | SCE1572_2419 | yes | sce_1973 |
| A and B | Clustering-based subsystems | no category | CBSS-211586.1.p.2832 | Preprotein translocase subunit YajC (TC 3.A.5.1.1) | SCE1572_6057 | yes | sce_5008 |
| A and B | Clustering-based subsystems | no category | CBSS-211586.1.p.2832 | Protein-export membrane protein SecD (TC 3.A.5.1.1) | SCE1572_6056 | yes | sce_5007 |
| A and B | Clustering-based subsystems | no category | CBSS-211586.1.p.2832 | Protein-export membrane protein SecE (TC 3.A.5.1.1) | SCE1572_6055 | yes | sce_5006 |
| A and B | Clustering-based subsystems | no category | CBSS-211586.1.p.2832 | S-adenosylmethionine:RNA ribosyltransferase-isomerase (EC 5.-.-) | SCE1572_2293 | yes | sce_1841 |
| A and B | Clustering-based subsystems | no category | CBSS-211586.1.p.2832 | rRNA-guanine transglycosylase (EC 2.4.2.29) | SCE1572_2294 | yes | sce_1842 |
| A and B | Clustering-based subsystems | no category | CBSS-228410.1.p.134 | DNA polymerase III epsilon subunit (EC 2.7.7.7) | SCE1572_2355 | yes | sce_1906 |
| A and B | Clustering-based subsystems | no category | CBSS-228410.1.p.134 | Hydroxyacylglutathione hydrolase (EC 3.1.2.6) | SCE1572_10143 | yes | sce_8946 |
| A and B | Clustering-based subsystems | no category | CBSS-228410.1.p.134 | Membrane-bound lytic murein transglycosylase D precursor (EC 3.2.1. | SCE1572_2236 | yes | sce_1784 |
| A and B | Clustering-based subsystems | no category | CBSS-228410.1.p.134 | Ribonuclease HI (EC 3.1.26.4) | SCE1572_1626 | yes | sce_1164 |
| A and B | Clustering-based subsystems | no category | CBSS-266117.6.p.1260 | Phosphatantennine adenylyltransferase (EC 2.7.7.3) | SCE1572_2357 | yes | sce_1908 |
| A and B | Clustering-based subsystems | no category | CBSS-266117.6.p.1260 | Ribosomal RNA small subunit methyltransferase D (EC 2.1.1.-) | SCE1572_10320 | yes | sce_9013 |
| A and B | Clustering-based subsystems | no category | CBSS-269801.1.p.1715 | Phosphatantennine adenylyltransferase (EC 2.7.7.3) | SCE1572_2357 | yes | sce_1908 |
| A and B | Clustering-based subsystems | no category | CBSS-269801.1.p.1715 | Ribosomal RNA small subunit methyltransferase D (EC 2.1.1.-) | SCE1572_10320 | yes | sce_9013 |
| A and B | Clustering-based subsystems | no category | CBSS-272943.3.p.1367 | DNA topoisomerase I (EC 5.99.1.2) | SCE1572_6867 | yes | sce_5730 |
| A and B | Clustering-based subsystems | no category | CBSS-272943.3.p.1367 | Rossmann fold nucleotide-binding protein Smf possibly involved in DN | SCE1572_6868 | yes | sce_5731 |
| A and B | Clustering-based subsystems | no category | CBSS-281090.3.p.464 | Alanyl-RNA synthetase (EC 6.1.1.7) | SCE1572_6877 | yes | sce_5742 |
| A and B | Clustering-based subsystems | no category | CBSS-281090.3.p.464 | Alanyl-RNA synthetase beta chain (EC 6.1.1.14) | SCE1572_9746 | yes | sce_8547 |
| A and B | Clustering-based subsystems | no category | CBSS-281090.3.p.464 | Putative Holliday junction resolvase (EC 3.1.-) | SCE1572_6134 | yes | sce_5078 |
| A and B | Clustering-based subsystems | no category | CBSS-281090.3.p.464 | Shikimate 5-dehydrogenase I alpha (EC 1.1.1.25) | SCE1572_3015 | yes | sce_2476 |
| A and B | Clustering-based subsystems | no category | CBSS-312309.3.p.1965 | Methionine aminopeptidase (EC 3.4.11.18) | SCE1572_1680 | yes | sce_1195 |
| A and B | Clustering-based subsystems | no category | CBSS-312309.3.p.1965 | SSU ribosomal protein S2p (SAe) | SCE1572_4193 | yes | sce_3515 |
| A and B | Clustering-based subsystems | no category | CBSS-312309.3.p.1965 | Translation elongation factor Ts | SCE1572_4194 | yes | sce_3516 |
| A and B | Clustering-based subsystems | no category | CBSS-312309.3.p.1965 | Uridylate kinase (EC 2.7.4.-) | SCE1572_9343 | yes | sce_8123 |
| A and B | Clustering-based subsystems | no category | CBSS-312309.3.p.1965 | [Protein-Pil] uridylyltransferase (EC 2.7.7.59) | SCE1572_4206 | yes | sce_3524 |
| A and B | Clustering-based subsystems | no category | CBSS-316057.3.p.3521 | Glutamate-ammonia-lyase adenylyltransferase (EC 2.7.7.42) | SCE1572_2412 | yes | sce_1966 |
| A and B | Clustering-based subsystems | no category | CBSS-316057.3.p.3521 | Large exoproteins involved in heme utilization or adhesion | SCE1572_4644 | yes | sce_3741 |
| A and B | Clustering-based subsystems | no category | CBSS-316057.3.p.3521 | Thiol peroxidase, Bcp-type (EC 1.11.1.15) | SCE1572_6737 | yes | sce_5609 |
| A and B | Clustering-based subsystems | no category | CBSS-316057.3.p.563 | Cytochrome c oxidase polypeptide II (EC 1.9.3.1) | SCE1572_6107 | yes | sce_5054 |
| A and B | Clustering-based subsystems | no category | CBSS-316057.3.p.563 | Cytochrome c oxidase polypeptide III (EC 1.9.3.1) | SCE1572_6109 | yes | sce_5056 |
| A and B | Clustering-based subsystems | no category | CBSS-316057.3.p.563 | Heme O synthase, prothotheme IX farnesyltransferase (EC 2.5.1.-) | COX SCE1572_3921 | yes | sce_3254 |
| A and B | Clustering-based subsystems | no category | CBSS-323097.3.p.2594 | TMD protein, part of proposed TME/TMD proteolytic complex (PM | SCE1572_8457 | yes | sce_7217 |
| A and B | Clustering-based subsystems | no category | CBSS-323097.3.p.2594 | FIG04453: protein YccG like | SCE1572_5816 | yes | sce_4865 |
| A and B | Clustering-based subsystems | no category | CBSS-323097.3.p.2594 | Guanlylate kinase (EC 2.7.4.8) | SCE1572 | | |

| | | | | | | | | |
|---------|-------------------------------------|-----------------|--|--|---------------|----------|----------|-----|
| A and B | Clustering-based subsystems | no subcategory | Conserved gene cluster associated with Met-tRNA formyltransferase | SCE1572_530 | yes | sce_333 | yes | |
| A and B | Clustering-based subsystems | no subcategory | Conserved gene cluster associated with Met-tRNA formyltransferase YgiD/Kae1/Qri7 family, required for N6-threonylcarbamoyl adenosine | SCE1572_2254 | yes | sce_1799 | yes | |
| A and B | Clustering-based subsystems | no subcategory | Conserved gene cluster associated with Met-tRNA formyltransferase | SCE1572_6866 | yes | sce_5729 | yes | |
| A and B | Clustering-based subsystems | no subcategory | DNA gyrase subunits | DNA gyrase subunit A (EC 5.99.1.3) | SCE1572_4963 | yes | sce_4070 | yes |
| A and B | Clustering-based subsystems | no subcategory | DNA gyrase subunits | DNA gyrase subunit B (EC 5.99.1.3) | SCE1572_10487 | yes | sce_9133 | yes |
| A and B | Clustering-based subsystems | no subcategory | DNA replication cluster 1 | Chromosomal replication initiator protein DnaA | SCE1572_1 | yes | sce_1 | yes |
| A and B | Clustering-based subsystems | no subcategory | DNA replication cluster 1 | DNA gyrase subunit B (EC 5.99.1.3) | SCE1572_10487 | yes | sce_9133 | yes |
| A and B | Clustering-based subsystems | no subcategory | DNA replication cluster 1 | DNA polymerase III beta subunit (EC 2.7.7.7) | SCE1572_10485 | yes | sce_9130 | yes |
| A and B | Clustering-based subsystems | no subcategory | DNA replication cluster 1 | DNA recombination and repair protein RecF | SCE1572_10486 | yes | sce_9131 | yes |
| A and B | Clustering-based subsystems | no subcategory | EC5IG4-SIG7 | 4-hydroxythreonine-4-phosphate dehydrogenase (EC 1.1.1.262) | SCE1572_8455 | yes | sce_7215 | yes |
| A and B | Clustering-based subsystems | no subcategory | EC5IG4-SIG7 | Dimethyladenosine transferase (EC 2.1.1.-) | SCE1572_6014 | yes | sce_4966 | yes |
| A and B | Clustering-based subsystems | no subcategory | EC5IG4-SIG7 | Survival protein SurA precursor (Peptidyl-prolyl cis-trans isomerase SurA) | SCE1572_1628 | yes | sce_1165 | yes |
| A and B | Clustering-based subsystems | no subcategory | Glycogen metabolism cluster | 1,4-alpha-glucan (glycogen) branching enzyme, GH-13-type (EC 2.4.1.1) | SCE1572_6074 | yes | sce_5020 | yes |
| A and B | Clustering-based subsystems | no subcategory | Glycogen metabolism cluster | 4-alpha-glucanotransferase (amylomaltase) (EC 2.4.1.25) | SCE1572_586 | yes | sce_396 | yes |
| A and B | Clustering-based subsystems | no subcategory | Glycogen metabolism cluster | Glucose-1-phosphate adenylyltransferase (EC 2.7.7.27) | SCE1572_7285 | yes | sce_5988 | yes |
| A and B | Clustering-based subsystems | no subcategory | Glycogen metabolism cluster | Glycogen debranching enzyme (EC 3.2.1.-) | SCE1572_1926 | yes | sce_1444 | yes |
| A and B | Clustering-based subsystems | no subcategory | Glycogen metabolism cluster | Glycogen phosphorylase (EC 2.4.1.1) | SCE1572_5906 | yes | sce_4909 | yes |
| A and B | Clustering-based subsystems | no subcategory | Glycogen metabolism cluster | Glycogen synthase, ADP-glucose transglycosylase (EC 2.4.1.21) | SCE1572_1673 | yes | sce_1189 | yes |
| A and B | Clustering-based subsystems | no subcategory | KH domain RNA binding protein Yj4C | 16S rRNA processing protein RlmM | SCE1572_6008 | yes | sce_4959 | yes |
| A and B | Clustering-based subsystems | no subcategory | KH domain RNA binding protein Yj4C | KH domain RNA binding protein Yj4C | SCE1572_6009 | yes | sce_4960 | yes |
| A and B | Clustering-based subsystems | no subcategory | KH domain RNA binding protein Yj4C | SSU ribosomal protein S16p | SCE1572_6010 | yes | sce_4961 | yes |
| A and B | Clustering-based subsystems | no subcategory | LSU ribosomal proteins cluster | LSU ribosomal protein L10p (P0) | SCE1572_657 | yes | sce_463 | yes |
| A and B | Clustering-based subsystems | no subcategory | LSU ribosomal proteins cluster | LSU ribosomal protein L11p (L12e) | SCE1572_655 | yes | sce_461 | yes |
| A and B | Clustering-based subsystems | no subcategory | LSU ribosomal proteins cluster | LSU ribosomal protein L1p (L10Ae) | SCE1572_656 | yes | sce_462 | yes |
| A and B | Clustering-based subsystems | no subcategory | LSU ribosomal proteins cluster | LSU ribosomal protein L7/L12 (P1/P2) | SCE1572_658 | yes | sce_464 | yes |
| A and B | Clustering-based subsystems | no subcategory | LSU ribosomal proteins cluster | Preprotein translocase subunit SecE (TC 3.A.5.1.1) | SCE1572_652 | yes | sce_459 | yes |
| A and B | Clustering-based subsystems | no subcategory | LSU ribosomal proteins cluster | Transcription antitermination protein NusG | SCE1572_653 | yes | sce_460 | yes |
| A and B | Clustering-based subsystems | no subcategory | Lipoic acid synthesis cluster | Lipoic acid synthase | SCE1572_2203 | yes | sce_1750 | yes |
| A and B | Clustering-based subsystems | no subcategory | Lipoic acid synthesis cluster | Octanoate-[acyl-carrier-protein]-protein-N-octanoyltransferase | SCE1572_3366 | yes | sce_2855 | yes |
| A and B | Clustering-based subsystems | no subcategory | NusA-TFI Cluster | COG2740: Predicted nucleic-acid-binding protein implicated in transcription | SCE1572_7634 | yes | sce_6494 | yes |
| A and B | Clustering-based subsystems | no subcategory | NusA-TFI Cluster | FIG000325: clustered with transcription termination protein NusA | SCE1572_7636 | yes | sce_6496 | yes |
| A and B | Clustering-based subsystems | no subcategory | NusA-TFI Cluster | Ribosome-binding factor A | SCE1572_7630 | yes | sce_6491 | yes |
| A and B | Clustering-based subsystems | no subcategory | NusA-TFI Cluster | Transcription termination protein NusA | SCE1572_7635 | yes | sce_6495 | yes |
| A and B | Clustering-based subsystems | no subcategory | NusA-TFI Cluster | Translation initiation factor 2 | SCE1572_7632 | yes | sce_3829 | yes |
| A and B | Clustering-based subsystems | no subcategory | NusA-TFI Cluster | YjP-like protein | SCE1572_7631 | yes | sce_6492 | yes |
| A and B | Clustering-based subsystems | no subcategory | Purine salvage cluster | Exodeoxyribonuclease VII large subunit (EC 3.1.11.6) | SCE1572_3278 | yes | sce_2773 | yes |
| A and B | Clustering-based subsystems | no subcategory | Purine salvage cluster | Exodeoxyribonuclease VII small subunit (EC 3.1.11.6) | SCE1572_8519 | yes | sce_6045 | yes |
| A and B | Clustering-based subsystems | no subcategory | Purine salvage cluster | GMP synthase [glutamine-hydrolyzing], ATP pyrophosphatase subunit | SCE1572_4911 | yes | sce_4121 | yes |
| A and B | Clustering-based subsystems | no subcategory | Purine salvage cluster | GMP synthase [glutamine-hydrolyzing], amidotransferase subunit (EC 3.6.1.15) | SCE1572_4911 | yes | sce_4121 | yes |
| A and B | Clustering-based subsystems | no subcategory | Purine salvage cluster | Inosine-5'-monophosphate dehydrogenase (EC 1.1.1.205) | SCE1572_110 | yes | sce_98 | yes |
| A and B | Clustering-based subsystems | no subcategory | RNA modification cluster | Inner membrane protein translocase component YidC, long form | SCE1572_3329 | yes | sce_2824 | yes |
| A and B | Clustering-based subsystems | no subcategory | RNA modification cluster | LSU ribosomal protein L34p | SCE1572_3332 | yes | sce_2828 | yes |
| A and B | Clustering-based subsystems | no subcategory | RNA modification cluster | Protein YidD | SCE1572_3330 | yes | sce_2826 | yes |
| A and B | Clustering-based subsystems | no subcategory | RNA modification cluster | Ribonuclease P protein component (EC 3.1.26.5) | SCE1572_3331 | yes | sce_2827 | yes |
| A and B | Clustering-based subsystems | no subcategory | Sigma-B stress response cluster 1 | Anti-sigma B factor RsbT | SCE1572_4836 | yes | sce_4048 | yes |
| A and B | Clustering-based subsystems | no subcategory | Sigma-B stress response cluster 1 | Anti-sigma B factor antagonist RsbV | SCE1572_1363 | yes | sce_989 | yes |
| A and B | Clustering-based subsystems | no subcategory | Sigma-B stress response cluster 1 | Phosphoserine phosphatase RsbX (EC 3.1.3.3) | SCE1572_4836 | yes | sce_4048 | yes |
| A and B | Clustering-based subsystems | no subcategory | Sigma-B stress response cluster 1 | RNA polymerase sigma factor RpoD | SCE1572_379 | yes | sce_211 | yes |
| A and B | Clustering-based subsystems | no subcategory | Sigma-B stress response cluster 1 | RNA polymerase sigma factor SigH | SCE1572_3441 | yes | sce_2933 | yes |
| A and B | Clustering-based subsystems | no subcategory | Sigma-B stress response cluster 1 | RsbR, positive regulator of sigma-B | SCE1572_203 | yes | sce_202 | yes |
| A and B | Clustering-based subsystems | no subcategory | Sigma-B stress response cluster 1 | RsbS, negative regulator of sigma-B | SCE1572_4838 | yes | sce_4050 | yes |
| A and B | Clustering-based subsystems | no subcategory | Sigma-B stress response cluster 1 | Serine phosphatase RsbU, regulator of sigma subunit | SCE1572_1359 | yes | sce_985 | yes |
| A and B | Clustering-based subsystems | no subcategory | Sigma-B stress response cluster 1 | Serine-protein kinase RsbW (EC 2.7.11.1) | SCE1572_1364 | yes | sce_990 | yes |
| A and B | Clustering-based subsystems | no subcategory | Stress related cluster | Arsenical pump-driving ATPase (EC 3.6.3.16) | SCE1572_1021 | yes | sce_6662 | yes |
| A and B | Clustering-based subsystems | no subcategory | Stress related cluster | Carbon starvation protein A | SCE1572_8282 | yes | sce_6951 | yes |
| A and B | Clustering-based subsystems | no subcategory | Transcription repair cluster | Arsenate reductase (EC 1.20.4.1) | SCE1572_1030 | yes | sce_6285 | yes |
| A and B | Clustering-based subsystems | no subcategory | Transcription repair cluster | Glucosamine-1-phosphate N-acetyltransferase (EC 2.3.1.157) | SCE1572_7188 | yes | sce_5909 | yes |
| A and B | Clustering-based subsystems | no subcategory | Transcription repair cluster | LSU ribosomal protein L25p | SCE1572_8999 | yes | sce_7764 | yes |
| A and B | Clustering-based subsystems | no subcategory | Transcription repair cluster | N-acetylglucosamine-1-phosphate uridylyltransferase (EC 2.7.7.23) | SCE1572_7188 | yes | sce_5909 | yes |
| A and B | Clustering-based subsystems | no subcategory | Transcription repair cluster | Peptidyl-tRNA hydrolase (EC 3.1.1.29) | SCE1572_9000 | yes | sce_7765 | yes |
| A and B | Clustering-based subsystems | no subcategory | Transcription repair cluster | Ribose-phosphate pyrophosphokinase (EC 2.7.6.1) | SCE1572_8154 | yes | sce_7319 | yes |
| A and B | Clustering-based subsystems | no subcategory | Transcription repair cluster | Short-chain dehydrogenase/reductase SDR | SCE1572_2326 | yes | sce_1873 | yes |
| A and B | Clustering-based subsystems | no subcategory | Transcription repair cluster | Transcription-repair coupling factor | SCE1572_3464 | yes | sce_2957 | yes |
| A and B | Clustering-based subsystems | no subcategory | USS-DB-7 | CtpB protein | SCE1572_6714 | yes | sce_5586 | yes |
| A and B | Clustering-based subsystems | no subcategory | USS-DB-7 | Protein ImpG/VasA | SCE1572_6723 | yes | sce_5595 | yes |
| A and B | Clustering-based subsystems | no subcategory | USS-DB-7 | Uncharacterized protein ImpA | SCE1572_6708 | yes | sce_5580 | yes |
| A and B | Clustering-based subsystems | no subcategory | USS-DB-7 | Uncharacterized protein ImpB | SCE1572_6706 | yes | sce_638 | yes |
| A and B | Clustering-based subsystems | no subcategory | USS-DB-7 | Uncharacterized protein ImpC | SCE1572_1876 | yes | sce_1392 | yes |
| A and B | Clustering-based subsystems | no subcategory | USS-DB-7 | Uncharacterized protein ImpH/VasB | SCE1572_6724 | yes | sce_5596 | yes |
| A and B | Clustering-based subsystems | no subcategory | USS-DB-7 | Uncharacterized protein ImpI/VasC | SCE1572_6716 | yes | sce_5588 | yes |
| A and B | Clustering-based subsystems | no subcategory | USS-DB-7 | Uncharacterized protein ImpJ/VasE | SCE1572_6712 | yes | sce_5584 | yes |
| A and B | Clustering-based subsystems | no subcategory | USS-DB-7 | Uncharacterized protein similar to VCA0109 | SCE1572_6722 | yes | sce_5594 | yes |
| A and B | Clustering-based subsystems | no subcategory | USS-DB-7 | VgrG protein | SCE1572_53 | yes | sce_117 | yes |
| A and B | Clustering-based subsystems | no subcategory | RNA-methyltransferase containing cluster | Apollipoprotein N-acyltransferase (EC 2.3.1.-) | SCE1572_26 | yes | sce_28 | yes |
| A and B | Clustering-based subsystems | no subcategory | RNA-methyltransferase containing cluster | Copper homeostasis protein CufE | SCE1572_26 | yes | sce_28 | yes |
| A and B | Clustering-based subsystems | no subcategory | RNA-methyltransferase containing cluster | Magnesium and cobalt efflux protein CusC | SCE1572_5751 | yes | sce_4801 | yes |
| A and B | Clustering-based subsystems | no subcategory | RNA-methyltransferase containing cluster | Metal-dependent hydrolase YbeY, involved in rRNA and/or ribosome maturation | SCE1572_28 | yes | sce_30 | yes |
| A and B | Clustering-based subsystems | no subcategory | RNA-methyltransferase containing cluster | Phosphate starvation-inducible protein PhoH, predicted ATPase | SCE1572_10090 | yes | sce_8907 | yes |
| A and B | Clustering-based subsystems | no subcategory | RNA-methyltransferase containing cluster | RNA-4(6)A37 methyltransferase | SCE1572_7173 | yes | sce_5902 | yes |
| A | Clustering-based subsystems | no subcategory | CBSS-176299.4.peg.1996A | Bis(5'-nucleosyl)-tetraphosphate (asymmetrical) (EC 3.6.1.17) | SCE1572_11295 | yes | no | no |
| A | Clustering-based subsystems | no subcategory | CBSS-36873.1.peg.4752 | Cd(II)/Pb(II)-responsive transcriptional regulator | SCE1572_9416 | yes | no | no |
| A | Clustering-based subsystems | no subcategory | CBSS-393124.3.peg.2657 | ADA regulatory protein | SCE1572_9552 | yes | no | no |
| A | Clustering-based subsystems | no subcategory | CBSS-393124.3.peg.2657 | Probable carboxyvinyl-carboxyphosphonate phosphorilymutase (EC 2.7.1.1) | SCE1572_1901 | yes | no | no |
| B | Clustering-based subsystems | no subcategory | CBSS-159087.4.peg.2189 | FIG014574: hypothetical protein | no | sce_6822 | yes | |
| B | Clustering-based subsystems | no subcategory | CBSS-159087.4.peg.2189 | Phage T7 exclusion protein | no | sce_6820 | yes | |
| B | Clustering-based subsystems | no subcategory | CBSS-159087.4.peg.2189 | Phage T7 exclusion protein associated hypothetical protein | no | sce_6821 | yes | |
| B | Clustering-based subsystems | no subcategory | CBSS-159087.4.peg.2189 | Putative deoxyribonuclease similar to YcH1, type 4 | no | sce_6823 | yes | |
| B | Clustering-based subsystems | no subcategory | CBSS-235909.3.peg.1769 | FIG087842: Hypothetical protein | no | sce_2362 | yes | |
| B | Clustering-based subsystems | no subcategory | CBSS-235909.3.peg.1769 | FIG094048: Hypothetical protein | no | sce_2363 | yes | |
| B | Clustering-based subsystems | no subcategory | CBSS-235909.3.peg.1769 | FIG100068: Hypothetical protein | no | sce_2361 | yes | |
| B | Clustering-based subsystems | no subcategory | CBSS-235909.3.peg.1769 | FIG124585: Hypothetical protein | no | sce_2360 | yes | |
| A and B | Cofactors, Vitamins, Prosthetic Gro | Biotin | Biotin biosynthesis | 3-ketocacyl-CoA thiolase (EC 2.3.1.16) | SCE1572_61 | yes | sce_51 | yes |
| A and B | Cofactors, Vitamins, Prosthetic Gro | Biotin | Biotin biosynthesis | 8-amino-7-oxononanoate synthase (EC 2.3.1.47) | SCE1572_3903 | yes | sce_3232 | yes |
| A and B | Cofactors, Vitamins, Prosthetic Gro | Biotin | Biotin biosynthesis | Adenosylmethionine-8-amino-7-oxononanoate aminotransferase (EC 2.3.1.47) | SCE1572_1046 | yes | sce_782 | yes |
| A and B | Cofactors, Vitamins, Prosthetic Gro | Biotin | Biotin biosynthesis | Biotin operon repressor | SCE1572_3403 | yes | sce_2890 | yes |
| A and B | Cofactors, Vitamins, Prosthetic Gro | Biotin | Biotin biosynthesis | Biotin synthesis protein bioC | SCE1572_6412 | yes | sce_5430 | yes |
| A and B | Cofactors, Vitamins, Prosthetic Gro | Biotin | Biotin biosynthesis | Biotin-protein ligase (EC 6.3.4.15) | SCE1572_3403 | yes | sce_2890 | yes |
| A and B | Cofactors, Vitamins, Prosthetic Gro | Biotin | Biotin biosynthesis | Dethiobiotin synthetase (EC 6.3.3.3) | SCE1572_10482 | yes | sce_9127 | yes |
| A and B | Cofactors, Vitamins, Prosthetic Gro | Biotin | Biotin biosynthesis | Long-chain-fatty-acid-CoA ligase (EC 6.2.1.3) | SCE1572_267 | yes | sce_389 | yes |
| A and B | Cofactors, Vitamins, Prosthetic Gro | Biotin | Biotin biosynthesis Experimental | 8-amino-7-oxononanoate synthase (EC 2.3.1.47) | SCE1572_3903 | yes | sce_3232 | yes |
| A and B | Cofactors, Vitamins, Prosthetic Gro | Biotin | Biotin biosynthesis Experimental | Adenosylmethionine-8-amino-7-oxononanoate aminotransferase (EC 2.3.1.47) | SCE1572_1046 | yes | sce_782 | yes |
| A and B | Cofactors, Vitamins, Prosthetic Gro | Biotin | Biotin biosynthesis Experimental | Biotin synthesis protein bioC | SCE1572_6412 | yes | sce_5430 | yes |
| A and B | Cofactors, Vitamins, Prosthetic Gro | Biotin | Biotin biosynthesis Experimental | Competence protein F homolog, phosphoribosyltransferase domain | SCE1572_9486 | yes | sce_4158 | yes |
| A and B | Cofactors, Vitamins, Prosthetic Gro | Biotin | Biotin biosynthesis Experimental | Dethiobiotin synthetase (EC 6.3.3.3) | SCE1572_10482 | yes | sce_9127 | yes |
| A and B | Cofactors, Vitamins, Prosthetic Gro | Coenzyme A | Coenzyme A Biosynthesis | 2-dehydropanoate 2-reductase (EC 1.1.1.169) | SCE1572_308 | yes | sce_2028 | yes |
| A and B | Cofactors, Vitamins, Prosthetic Gro | Coenzyme A | Coenzyme A Biosynthesis | 3-methyl-2-oxobutanate hydroxymethyltransferase (EC 2.1.2.11) | SCE1572_666 | yes | sce_471 | yes |
| A and B | Cofactors, Vitamins, Prosthetic Gro | Coenzyme A | Coenzyme A Biosynthesis | Aspartate 1-decarboxylase (EC 4.1.1.11) | SCE1572_1532 | yes | sce_1053 | yes |
| A and B | Cofactors, Vitamins, Prosthetic Gro | Coenzyme A | Coenzyme A Biosynthesis | Dephospho-CoA kinase (EC 2.7.1.24) | SCE1572_4942 | yes | sce_4156 | yes |
| A and B | Cofactors, Vitamins, Prosthetic Gro | Coenzyme A | Coenzyme A Biosynthesis | FIG173306: hypothetical protein | SCE1572_3257 | yes | sce_2753 | yes |
| A and B | Cofactors, Vitamins, Prosthetic Gro | Coenzyme A | Coenzyme A Biosynthesis | Ketol-acid reductoisomerase (EC 1.1.1.86) | SCE1572_4975 | yes | sce_4184 | yes |
| A and B | Cofactors, Vitamins, Prosthetic Gro | Coenzyme A | Coenzyme A Biosynthesis | Pantoate-beta-alanine ligase (EC 6.3.2.1) | SCE1572_1303 | yes | sce_938 | yes |
| A and B | Cofactors, Vitamins, Prosthetic Gro | Coenzyme A | Coenzyme A Biosynthesis | Pantothenate kinase type III, CoA-like (EC 2.7.1.33) | SCE1572_523 | yes | sce_326 | yes |
| A and B | Cofactors, Vitamins, Prosthetic Gro | Coenzyme A | Coenzyme A Biosynthesis | Pantothenate:Na symporter (TC 2.A.21.1.1) | SCE1572_3579 | yes | sce_6216 | yes |
| A and B | Cofactors, Vitamins, Prosthetic Gro | Coenzyme A | Coenzyme A Biosynthesis | Phosphopantetheine adenylyltransferase (EC 2.7.7.3) | SCE1572_2387 | yes | sce_1908 | yes |
| A and B | Cofactors, Vitamins, Prosthetic Gro | Coenzyme A | Coenzyme A Biosynthesis | Phosphopantetheinoylcysteine decarboxylase (EC 4.1.1.36) | SCE1572_9486 | yes | sce_8273 | yes |
| A and B | Cofactors, Vitamins, Prosthetic Gro | Coenzyme A | Coenzyme A Biosynthesis | Phosphopantetheinoylcysteine synthetase (EC 6.3.2.5) | SCE1572_9486 | yes | sce_8273 | yes |
| A and B | Cofactors, Vitamins, Prosthetic Gro | Coenzyme A | Coenzyme A Biosynthesis cluster | 3-methyl-2-oxobutanate hydroxymethyltransferase (EC 2.1.2.11) | SCE1572_666 | yes | sce_471 | yes |
| A and B | Cofactors, Vitamins, Prosthetic Gro | Coenzyme A | Coenzyme A Biosynthesis cluster | Aspartate 1-decarboxylase (EC 4.1.1.11) | SCE1572_1532 | yes | sce_1053 | yes |
| A and B | Cofactors, Vitamins, Prosthetic Gro | Coenzyme A | Coenzyme A Biosynthesis cluster | FIG173306: hypothetical protein | SCE1572_3257 | yes | sce_2753 | yes |
| A and B | Cofactors, Vitamins, Prosthetic Gro | Coenzyme A | Coenzyme A Biosynthesis cluster | Pantoate-beta-alanine ligase (EC 6.3.2.1) | SCE1572_1303 | yes | sce_938 | yes |
| A and B | Cofactors, Vitamins, Prosthetic Gro | Coenzyme A | Coenzyme A Biosynthesis cluster | Pantothenate kinase type III, CoA-like (EC 2.7.1.33) | SCE1572_523 | yes | sce_326 | yes |
| A and B | Cofactors, Vitamins, Prosthetic Gro | Coenzyme A | Coenzyme A Biosynthesis | Pantothenate kinase (EC 2.7.1.33) | no | sce_5774 | yes | |
| A and B | Cofactors, Vitamins, Prosthetic Gro | Fe-S clusters | Chaperone protein HscA | SCE1572_9421 | yes | sce_8208 | yes | |
| A and B | Cofactors, Vitamins, Prosthetic Gro | Fe-S clusters | Chaperone protein HscB | SCE1572_9420 | yes | sce_8207 | yes | |
| A and B | Cofactors, Vitamins, Prosthetic Gro | Fe-S clusters | Fe-S cluster assembly | Cysteine desulfurase (EC 2.8.1.7), IscS subfamily | SCE1572_1872 | yes | sce_1345 | yes |
| A and B | Cofactors, Vitamins, Prosthetic Gro | Fe-S clusters</ | | | | | | |

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|---------|---|--------------------------------|---|--|---------------|-----------|----------|-----|
| A and B | Cofactors, Vitamins, Prosthetic Groo Tetrapyrroles | Heme and Siroheme Biosynthesis | Ferrochelatase, protoheme ferro-lyase (EC 4.99.1.1) | SCE1572_2325 | yes | sce_1872 | yes | |
| A and B | Cofactors, Vitamins, Prosthetic Groo Tetrapyrroles | Heme and Siroheme Biosynthesis | Glutamate-1-semialdehyde aminotransferase (EC 5.4.3.8) | SCE1572_11399 | yes | sce_4351 | yes | |
| A and B | Cofactors, Vitamins, Prosthetic Groo Tetrapyrroles | Heme and Siroheme Biosynthesis | Glutamyl-tRNA reductase (EC 1.2.1.70) | SCE1572_2266 | yes | sce_1810 | yes | |
| A and B | Cofactors, Vitamins, Prosthetic Groo Tetrapyrroles | Heme and Siroheme Biosynthesis | Glutamyl-tRNA synthetase (EC 6.1.1.17) | SCE1572_871 | yes | sce_646 | yes | |
| A and B | Cofactors, Vitamins, Prosthetic Groo Tetrapyrroles | Heme and Siroheme Biosynthesis | Hypothetical radical SAM family enzyme, NOT coproporphyrinogen III synthase | SCE1572_5115 | yes | sce_4303 | yes | |
| A and B | Cofactors, Vitamins, Prosthetic Groo Tetrapyrroles | Heme and Siroheme Biosynthesis | Porphobilinogen deaminase (EC 2.5.1.61) | SCE1572_2267 | yes | sce_1811 | yes | |
| A and B | Cofactors, Vitamins, Prosthetic Groo Tetrapyrroles | Heme and Siroheme Biosynthesis | Porphobilinogen synthase (EC 4.2.1.24) | SCE1572_16 | yes | sce_16 | yes | |
| A and B | Cofactors, Vitamins, Prosthetic Groo Tetrapyrroles | Heme and Siroheme Biosynthesis | Protoporphyrinogen IX oxidase, aerobic, HemY (EC 1.3.3.4) | SCE1572_7477 | yes | sce_6273 | yes | |
| A and B | Cofactors, Vitamins, Prosthetic Groo Tetrapyrroles | Heme and Siroheme Biosynthesis | Uroporphyrinogen III decarboxylase (EC 4.1.1.37) | SCE1572_10274 | yes | sce_9639 | yes | |
| A and B | Cofactors, Vitamins, Prosthetic Groo Tetrapyrroles | Heme and Siroheme Biosynthesis | Uroporphyrinogen-III methyltransferase (EC 2.1.1.107) | SCE1572_14 | yes | sce_14 | yes | |
| A and B | Cofactors, Vitamins, Prosthetic Groo Tetrapyrroles | Heme and Siroheme Biosynthesis | Uroporphyrinogen-III synthase (EC 4.2.1.75) | SCE1572_14 | yes | sce_14 | yes | |
| A | Cofactors, Vitamins, Prosthetic Groo Tetrapyrroles | B12-Du71 | CobN component of cobalt chelatase involved in B12 biosynthesis | SCE1572_4715 | yes | | no | |
| A | Cofactors, Vitamins, Prosthetic Groo Tetrapyrroles | Heme and Siroheme Biosynthesis | Precorrin-2 oxidase (EC 1.3.1.76) | SCE1572_637 | yes | | no | |
| A | Cofactors, Vitamins, Prosthetic Groo Tetrapyrroles | Heme and Siroheme Biosynthesis | Sirohydrochlorin ferrochelatase (EC 4.99.1.4) | SCE1572_637 | yes | | no | |
| B | Cofactors, Vitamins, Prosthetic Groo Tetrapyrroles | B12-Du71 | Cob(D)lamina adenosyltransferase PduO (EC 2.5.1.17) | | no | sce_4313 | yes | |
| A and B | Cofactors, Vitamins, Prosthetic Groo no subcategory | Thiamin biosynthesis | Cysteine desulfurase (EC 2.8.1.7), lscS subfamily | SCE1572_9417 | yes | sce_8204 | yes | |
| A and B | Cofactors, Vitamins, Prosthetic Groo no subcategory | Thiamin biosynthesis | Glycine oxidase ThiO (EC 1.4.3.19) | SCE1572_10901 | yes | sce_9534 | yes | |
| A and B | Cofactors, Vitamins, Prosthetic Groo no subcategory | Thiamin biosynthesis | Hydroxymethylpyrimidine ABC transporter, substrate-binding component | SCE1572_7412 | yes | sce_2167 | yes | |
| A and B | Cofactors, Vitamins, Prosthetic Groo no subcategory | Thiamin biosynthesis | Hydroxymethylpyrimidine ABC transporter, transmembrane component | SCE1572_7411 | yes | sce_6169 | yes | |
| A and B | Cofactors, Vitamins, Prosthetic Groo no subcategory | Thiamin biosynthesis | Phosphomethylpyrimidine kinase (EC 2.7.4.7) | SCE1572_978 | yes | sce_737 | yes | |
| A and B | Cofactors, Vitamins, Prosthetic Groo no subcategory | Thiamin biosynthesis | Sulfur carrier protein ThiS | SCE1572_7171 | yes | sce_5900 | yes | |
| A and B | Cofactors, Vitamins, Prosthetic Groo no subcategory | Thiamin biosynthesis | Sulfur carrier protein adenylyltransferase ThiF | SCE1572_5128 | yes | sce_4315 | yes | |
| A and B | Cofactors, Vitamins, Prosthetic Groo no subcategory | Thiamin biosynthesis | Thiamin biosynthesis protein ThiC | SCE1572_5711 | yes | sce_4764 | yes | |
| A and B | Cofactors, Vitamins, Prosthetic Groo no subcategory | Thiamin biosynthesis | Thiamin-phosphate pyrophosphorylase (EC 2.5.1.3) | SCE1572_2436 | yes | sce_1990 | yes | |
| A and B | Cofactors, Vitamins, Prosthetic Groo no subcategory | Thiamin biosynthesis | Thiamine-monophosphate kinase (EC 2.7.4.16) | SCE1572_628 | yes | sce_436 | yes | |
| A and B | Cofactors, Vitamins, Prosthetic Groo no subcategory | Thiamin biosynthesis | Thiazole biosynthesis protein ThiG | SCE1572_5704 | yes | sce_4756 | yes | |
| A and B | DNA Metabolism | CRISPRs | CRISPR-associated helicase Cas3 | SCE1572_482 | yes | sce_293 | yes | |
| A and B | DNA Metabolism | CRISPRs | CRISPR-associated protein Cas1 | SCE1572_485 | yes | sce_296 | yes | |
| A and B | DNA Metabolism | CRISPRs | CRISPR-associated protein Cas2 | SCE1572_486 | yes | sce_297 | yes | |
| B | DNA Metabolism | CRISPRs | CRISPR repeat RNA endonuclease Cas6 | | no | sce_6381 | yes | |
| B | DNA Metabolism | CRISPRs | CRISPR-associated RecB family exonuclease CasB | | no | sce_10250 | yes | |
| B | DNA Metabolism | CRISPRs | CRISPR-associated RAMP Cmr1 | | no | sce_6355 | yes | |
| B | DNA Metabolism | CRISPRs | CRISPR-associated RAMP Cmr2 | | no | sce_6356 | yes | |
| B | DNA Metabolism | CRISPRs | CRISPR-associated RAMP Cmr3 | | no | sce_6357 | yes | |
| B | DNA Metabolism | CRISPRs | CRISPR-associated RAMP Cmr4 | | no | sce_6358 | yes | |
| B | DNA Metabolism | CRISPRs | CRISPR-associated RAMP Cmr5 | | no | sce_6359 | yes | |
| B | DNA Metabolism | CRISPRs | CRISPR-associated RAMP Cmr6 | | no | sce_6360 | yes | |
| A and B | DNA Metabolism | DNA recombination | RuvABC plus a hypothetical | Crossover junction endonuclease RuvC (EC 3.1.22.4) | SCE1572_6826 | yes | sce_5687 | yes |
| A and B | DNA Metabolism | DNA recombination | RuvABC plus a hypothetical | FlgG00859: hypothetical protein YecB | SCE1572_9484 | yes | sce_8271 | yes |
| A and B | DNA Metabolism | DNA recombination | RuvABC plus a hypothetical | Holliday junction DNA helicase RuvA | SCE1572_527 | yes | sce_330 | yes |
| A and B | DNA Metabolism | DNA recombination | RuvABC plus a hypothetical | Holliday junction DNA helicase RuvB | SCE1572_9294 | yes | sce_8074 | yes |
| A and B | DNA Metabolism | DNA repair | 2-phosphoglycolate salvage | Phosphoglycolate phosphatase (EC 3.1.3.18) | SCE1572_11194 | yes | sce_8372 | yes |
| A and B | DNA Metabolism | DNA repair | 2-phosphoglycolate salvage | Putative phosphatase YqaB | SCE1572_1585 | yes | sce_7900 | yes |
| A and B | DNA Metabolism | DNA repair | DNA Repair Base Excision | ATP-dependent DNA ligase (EC 6.5.1.1) LigC | SCE1572_8901 | yes | sce_7677 | yes |
| A and B | DNA Metabolism | DNA repair | DNA Repair Base Excision | ATP-dependent DNA ligase (EC 6.5.1.1) clustered with Ku protein, Lig | SCE1572_2124 | yes | sce_3945 | yes |
| A and B | DNA Metabolism | DNA repair | DNA Repair Base Excision | DNA ligase (EC 6.5.1.2) | SCE1572_6029 | yes | sce_4982 | yes |
| A and B | DNA Metabolism | DNA repair | DNA Repair Base Excision | DNA polymerase I (EC 2.7.7.7) | SCE1572_10576 | yes | sce_9687 | yes |
| A and B | DNA Metabolism | DNA repair | DNA Repair Base Excision | DNA polymerase II (EC 2.7.7.7) | SCE1572_7372 | yes | sce_6153 | yes |
| A and B | DNA Metabolism | DNA repair | DNA Repair Base Excision | DNA-3-methyladenine glycosylase II (EC 3.2.2.21) | SCE1572_8247 | yes | sce_6918 | yes |
| A and B | DNA Metabolism | DNA repair | DNA Repair Base Excision | Endonuclease III (EC 4.2.99.18) | SCE1572_5224 | yes | sce_4579 | yes |
| A and B | DNA Metabolism | DNA repair | DNA Repair Base Excision | Formamidopyrimidine-DNA glycosylase (EC 3.2.2.23) | SCE1572_4699 | yes | sce_3926 | yes |
| A and B | DNA Metabolism | DNA repair | DNA Repair Base Excision | Ku domain protein | SCE1572_3505 | yes | sce_2988 | yes |
| A and B | DNA Metabolism | DNA repair | DNA Repair Base Excision | Single-stranded-DNA-specific exonuclease RecJ (EC 3.1.-.-) | SCE1572_6054 | yes | sce_5005 | yes |
| A and B | DNA Metabolism | DNA repair | DNA Repair Base Excision | Uracil-DNA glycosylase, family 1 | SCE1572_6285 | yes | sce_5311 | yes |
| A and B | DNA Metabolism | DNA repair | DNA repair, UvrABC system | Excinuclease ABC subunit A | SCE1572_5037 | yes | sce_4238 | yes |
| A and B | DNA Metabolism | DNA repair | DNA repair, UvrABC system | Excinuclease ABC subunit A paralog of unknown function | SCE1572_1785 | yes | sce_7067 | yes |
| A and B | DNA Metabolism | DNA repair | DNA repair, UvrABC system | Excinuclease ABC subunit A, dimeric form | SCE1572_3397 | yes | sce_2884 | yes |
| A and B | DNA Metabolism | DNA repair | DNA repair, UvrABC system | Excinuclease ABC subunit B | SCE1572_986 | yes | sce_747 | yes |
| A and B | DNA Metabolism | DNA repair | DNA repair, UvrABC system | Excinuclease ABC subunit C | SCE1572_9492 | yes | sce_8277 | yes |
| A and B | DNA Metabolism | DNA repair | DNA repair, bacterial | A/G-specific adenine glycosylase (EC 3.2.2.-) | SCE1572_5244 | yes | sce_4399 | yes |
| A and B | DNA Metabolism | DNA repair | DNA repair, bacterial | Alkylated DNA repair protein ABB | SCE1572_9443 | yes | sce_6393 | yes |
| A and B | DNA Metabolism | DNA repair | DNA repair, bacterial | DNA mismatch repair endonuclease MutH | SCE1572_4044 | yes | sce_3370 | yes |
| A and B | DNA Metabolism | DNA repair | DNA repair, bacterial | DNA polymerase IV (EC 2.7.7.7) | SCE1572_2024 | yes | sce_1510 | yes |
| A and B | DNA Metabolism | DNA repair | DNA repair, bacterial | DNA polymerase-like protein PA0670 | SCE1572_2385 | yes | sce_1938 | yes |
| A and B | DNA Metabolism | DNA repair | DNA repair, bacterial | DNA repair protein RadC | SCE1572_140 | yes | sce_512 | yes |
| A and B | DNA Metabolism | DNA repair | DNA repair, bacterial | DNA repair protein RecN | SCE1572_1678 | yes | sce_1193 | yes |
| A and B | DNA Metabolism | DNA repair | DNA repair, bacterial | Exodeoxyribonuclease III (EC 3.1.11.2) | SCE1572_10436 | yes | sce_9077 | yes |
| A and B | DNA Metabolism | DNA repair | DNA repair, bacterial | Exodeoxyribonuclease VII large subunit (EC 3.1.11.6) | SCE1572_3278 | yes | sce_2773 | yes |
| A and B | DNA Metabolism | DNA repair | DNA repair, bacterial | Exodeoxyribonuclease VII small subunit (EC 3.1.11.6) | SCE1572_8519 | yes | sce_6045 | yes |
| A and B | DNA Metabolism | DNA repair | DNA repair, bacterial | Exonuclease SbcC | SCE1572_6457 | yes | sce_3501 | yes |
| A and B | DNA Metabolism | DNA repair | DNA repair, bacterial | GTU mismatch-specific uracil/thymine DNA-glycosylase | SCE1572_6850 | yes | sce_5712 | yes |
| A and B | DNA Metabolism | DNA repair | DNA repair, bacterial | Methylated-DNA-protein-cysteine methyltransferase (EC 2.1.1.63) | SCE1572_1428 | yes | sce_6948 | yes |
| A and B | DNA Metabolism | DNA repair | DNA repair, bacterial | RecA protein | SCE1572_2384 | yes | sce_1937 | yes |
| A and B | DNA Metabolism | DNA repair | DNA repair, bacterial | SOS-response repressor and protease LexA (EC 3.4.21.88) | SCE1572_6042 | yes | sce_4994 | yes |
| A and B | DNA Metabolism | DNA repair | DNA repair, bacterial | Single-stranded-DNA-binding protein | SCE1572_2458 | yes | sce_2948 | yes |
| A and B | DNA Metabolism | DNA repair | DNA repair, bacterial | DnaG family ATP-dependent helicase YoaA | SCE1572_4006 | yes | sce_3336 | yes |
| A and B | DNA Metabolism | DNA repair | DNA repair, bacterial | DNA mismatch repair protein MutL | SCE1572_6791 | yes | sce_9496 | yes |
| A and B | DNA Metabolism | DNA repair | DNA repair, bacterial | DNA mismatch repair protein MutS | SCE1572_4190 | yes | sce_3512 | yes |
| A and B | DNA Metabolism | DNA repair | DNA repair, bacterial | MutS-related protein, family 1 | SCE1572_2103 | yes | sce_1619 | yes |
| A and B | DNA Metabolism | DNA repair | DNA repair, bacterial | Recombination inhibitory protein MutS2 | SCE1572_2121 | yes | sce_1634 | yes |
| A and B | DNA Metabolism | DNA repair | DNA repair, bacterial | RecD-like DNA helicase YrrC | SCE1572_10040 | yes | sce_8856 | yes |
| A and B | DNA Metabolism | DNA repair | DNA repair, bacterial | RecQ | SCE1572_3180 | yes | sce_3239 | yes |
| A and B | DNA Metabolism | DNA repair | DNA repair, bacterial | DNA recombination and repair protein RecF | SCE1572_10486 | yes | sce_9131 | yes |
| A and B | DNA Metabolism | DNA repair | DNA repair, bacterial | DNA recombination and repair protein RecO | SCE1572_2322 | yes | sce_1869 | yes |
| A and B | DNA Metabolism | DNA repair | DNA repair, bacterial | RecA protein | SCE1572_2384 | yes | sce_1937 | yes |
| A and B | DNA Metabolism | DNA repair | DNA repair, bacterial | Recombination protein RecR | SCE1572_473 | yes | sce_284 | yes |
| A and B | DNA Metabolism | DNA repair | DNA repair, bacterial | Single-stranded-DNA-binding protein | SCE1572_3458 | yes | sce_2948 | yes |
| A and B | DNA Metabolism | DNA repair | DNA repair, bacterial | Single-stranded-DNA-specific exonuclease RecJ (EC 3.1.-.-) | SCE1572_6054 | yes | sce_5005 | yes |
| A and B | DNA Metabolism | DNA repair | DNA repair, bacterial | ATP-dependent DNA helicase Rgp | SCE1572_2458 | yes | sce_2948 | yes |
| A and B | DNA Metabolism | DNA repair | DNA repair, bacterial | ATP-dependent DNA helicase UvrD/PcrA | SCE1572_1375 | yes | sce_1002 | yes |
| A and B | DNA Metabolism | DNA repair | DNA repair, bacterial | Deoxyribodipyrimidine photolyase, type II (EC 4.1.99.3) | SCE1572_8415 | yes | sce_7176 | yes |
| A and B | DNA Metabolism | DNA repair | DNA repair system including RecA, MutS and a hypothetical p | DNA mismatch repair protein MutS | SCE1572_4190 | yes | sce_3512 | yes |
| A and B | DNA Metabolism | DNA repair | DNA repair system including RecA, MutS and a hypothetical p | RecA protein | SCE1572_2384 | yes | sce_1937 | yes |
| A and B | DNA Metabolism | DNA repair | Nonhomologous End-Joining in Bacteria | ATP-dependent DNA ligase (EC 6.5.1.1) LigC | SCE1572_8901 | yes | sce_7677 | yes |
| A and B | DNA Metabolism | DNA repair | Nonhomologous End-Joining in Bacteria | ATP-dependent DNA ligase (EC 6.5.1.1) clustered with Ku protein, Lig | SCE1572_2124 | yes | sce_3945 | yes |
| A and B | DNA Metabolism | DNA repair | Nonhomologous End-Joining in Bacteria | Ku domain protein | SCE1572_3505 | yes | sce_2988 | yes |
| A and B | DNA Metabolism | DNA repair | Nonhomologous End-Joining in Bacteria | Uracil-DNA glycosylase | SCE1572_6850 | yes | sce_5712 | yes |
| A and B | DNA Metabolism | DNA repair | Uracil-DNA glycosylase | Uracil-DNA glycosylase, family 1 | SCE1572_6285 | yes | sce_5311 | yes |
| A and B | DNA Metabolism | DNA repair | Uracil-DNA glycosylase | Uracil-DNA glycosylase, family 4 | SCE1572_9744 | yes | sce_8545 | yes |
| A and B | DNA Metabolism | DNA repair | Uracil-DNA glycosylase | Uracil-DNA glycosylase, family 5 | SCE1572_4017 | yes | sce_3345 | yes |
| A and B | DNA Metabolism | DNA repair | Uracil-DNA glycosylase | Uracil-DNA glycosylase, putative family 6 | SCE1572_2224 | yes | sce_1931 | yes |
| A | DNA Metabolism | DNA repair | DNA Repair Base Excision | DNA-3-methyladenine glycosylase (EC 3.2.2.20) | SCE1572_1611 | yes | | no |
| A | DNA Metabolism | DNA repair | DNA repair, bacterial | Endonuclease IV (EC 3.1.21.1) | SCE1572_10158 | yes | | no |
| A | DNA Metabolism | DNA repair | DNA repair, bacterial | ATP-dependent DNA helicase, RecQ family | SCE1572_2832 | yes | | no |
| A | DNA Metabolism | DNA repair | Uracil-DNA glycosylase | Domain often clustered or fused with uracil-DNA glycosylase | SCE1572_2224 | yes | | no |
| A and B | DNA Metabolism | DNA replication | DNA replication | ATP-dependent DNA helicase RecQ | SCE1572_3180 | yes | sce_3239 | yes |
| A and B | DNA Metabolism | DNA replication | DNA replication | Chromosomal replication initiator protein DnaA | SCE1572_1 | yes | sce_1 | yes |
| A and B | DNA Metabolism | DNA replication | DNA replication | Crossover junction endonuclease RuvC (EC 3.1.22.4) | SCE1572_6826 | yes | sce_5687 | yes |
| A and B | DNA Metabolism | DNA replication | DNA replication | DNA polymerase I (EC 2.7.7.7) | SCE1572_10576 | yes | sce_9687 | yes |
| A and B | DNA Metabolism | DNA replication | DNA replication | DNA polymerase II (EC 2.7.7.7) | SCE1572_7372 | yes | sce_6153 | yes |
| A and B | DNA Metabolism | DNA replication | DNA replication | DNA polymerase III alpha subunit (EC 2.7.7.7) | SCE1572_2386 | yes | sce_1939 | yes |
| A and B | DNA Metabolism | DNA replication | DNA replication | DNA polymerase III beta subunit (EC 2.7.7.7) | SCE1572_10485 | yes | sce_9130 | yes |
| A and B | DNA Metabolism | DNA replication | DNA replication | DNA polymerase III delta prime subunit (EC 2.7.7.7) | SCE1572_2438 | yes | sce_1992 | yes |
| A and B | DNA Metabolism | DNA replication | DNA replication | DNA polymerase III delta subunit (EC 2.7.7.7) | SCE1572_7209 | yes | sce_5936 | yes |
| A and B | DNA Metabolism | DNA replication | DNA replication | DNA polymerase III epsilon subunit (EC 2.7.7.7) | SCE1572_2355 | yes | sce_1906 | yes |
| A and B | DNA Metabolism | DNA replication | DNA replication | DNA polymerase III subunits gamma and tau (EC 2.7.7.7) | SCE1572_475 | yes | sce_286 | yes |
| A and B | DNA Metabolism | DNA replication | DNA replication | DNA primase (EC 2.7.7.-) | SCE1572_6017 | yes | sce_4970 | yes |
| A and B | DNA Metabolism | DNA replication | DNA replication | DNA repair protein RecN | SCE1572_1678 | yes | sce_1193 | yes |
| A and B | DNA Metabolism | DNA replication | DNA replication | Helicase PrgA essential for oriC/DnaA-independent DNA replication | SCE1572_9110 | yes | sce_7892 | yes |
| A and B | DNA Metabolism | DNA replication | DNA replication | Holliday junction DNA helicase RuvA | SCE1572_527 | yes | sce_330 | yes |
| A and B | DNA Metabolism | DNA replication | DNA replication | Holliday junction DNA helicase RuvB | SCE1572_9294 | yes | sce_8074 | yes |
| A and B | DNA Metabolism | DNA replication | DNA replication | RecA protein | SCE1572_2384 | yes | sce_1937 | yes |
| A and B | DNA Metabolism | DNA replication | DNA replication | Recombination protein RecR | SCE1572_473 | yes | sce_284 | yes |
| A and B | DNA Metabolism | DNA replication | DNA replication | Replicative DNA helicase (EC 3.6.1.-) | SCE1572_9006 | yes | sce_7771 | yes |
| A and B | DNA Metabolism | DNA replication | DNA replication | Single-stranded-DNA-specific exonuclease RecJ (EC 3.1.-.-) | SCE1572_6054 | yes | sce_5005 | yes |
| A and B | DNA Metabolism | DNA replication | DNA replication | Transcription-repair coupling factor | SCE1572_3464 | yes | sce_2957 | yes |
| A and B | DNA Metabolism | DNA replication | DNA Helicase of Unknown Function | DNA helicase (Rad25 homolog) | SCE1572_8858 | yes | sce_7626 | yes |
| A and B | DNA Metabolism | DNA replication | DNA Helicase of Unknown Function | Hypothetical protein (associated with DNA helicase - Rad25 homolog) | SCE1572_8859 | yes | sce_7627 | yes |
| A and B | DNA Metabolism | DNA replication | DNA topoisomerases, Type II, ATP-dependent | DNA gyrase subunit A (EC 5.99.1.3) | SCE1572_4963 | yes | sce_4070 | yes |
| A and B | DNA Metabolism | DNA replication | DNA topoisomerases, Type II, ATP-dependent | DNA gyrase subunit B (EC 5.99.1.3) | SCE1572_10487 | yes | sce_9133 | yes |
| A and B | DNA Metabolism | DNA replication | DNA topoisomerases, Type II, ATP-dependent | Topoisomerase IV subunit A (EC 5.99.1.-) | SCE1572_6023 | yes | sce_4972 | yes |
| A and B | DNA Metabolism | DNA replication | DNA topoisomerases, Type II, ATP-dependent | Topoisomerase IV subunit B (EC 5.99.1.-) | SCE1572_6024 | yes | sce_4977 | yes |
| B | DNA Metabolism | DNA replication | DNA replication | Exodeoxyribonuclease V beta chain (EC 3.1.11.5) | SCE1572_475 | | | |

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|---------|--------------------------------------|---|---|---|---------------|-----|-----------|-----|
| A and B | Fatty Acids, Lipids, and Isoprenoids | Fatty acids | Fatty Acid Biosynthesis FASII | Enoyl-[acyl-carrier-protein] reductase [NADPH] (EC 1.3.1.10) | SCE1572_3437 | yes | sce_2931 | yes |
| A and B | Fatty Acids, Lipids, and Isoprenoids | Fatty acids | Fatty Acid Biosynthesis FASII | Holo-[acyl-carrier-protein] synthase (EC 2.7.8.7) | SCE1572_551 | yes | sce_357 | yes |
| A and B | Fatty Acids, Lipids, and Isoprenoids | Fatty acids | Fatty Acid Biosynthesis FASII | Malonyl-CoA-acyl carrier protein transacylase (EC 2.3.1.39) | SCE1572_592 | yes | sce_401 | yes |
| A and B | Fatty Acids, Lipids, and Isoprenoids | Fatty acids | Fatty acid metabolism cluster | 3-hydroxyacyl-CoA dehydrogenase (EC 1.1.1.35) | SCE1572_60 | yes | sce_50 | yes |
| A and B | Fatty Acids, Lipids, and Isoprenoids | Fatty acids | Fatty acid metabolism cluster | 3-hydroxybutyryl-CoA epimerase (EC 5.1.2.3) | SCE1572_60 | yes | sce_50 | yes |
| A and B | Fatty Acids, Lipids, and Isoprenoids | Fatty acids | Fatty acid metabolism cluster | 3-ketoacyl-CoA thiolase (EC 2.3.1.16) | SCE1572_61 | yes | sce_51 | yes |
| A and B | Fatty Acids, Lipids, and Isoprenoids | Fatty acids | Fatty acid metabolism cluster | Enoyl-CoA hydratase (EC 4.2.1.17) | SCE1572_60 | yes | sce_50 | yes |
| A and B | Fatty Acids, Lipids, and Isoprenoids | Fatty acids | Fatty acid metabolism cluster | Long-chain-fatty-acyl-CoA ligase (EC 6.2.1.3) | SCE1572_267 | yes | sce_389 | yes |
| A and B | Fatty Acids, Lipids, and Isoprenoids | Fatty acids | Polysaturated Fatty Acids synthesis | Enoyl-[acyl-carrier-protein] reductase [FMN] (EC 1.3.1.9), inferred for | SCE1572_1284 | yes | sce_920 | yes |
| A and B | Fatty Acids, Lipids, and Isoprenoids | Fatty acids | Polysaturated Fatty Acids synthesis | omega-3 polysaturated fatty acid synthase subunit, PfaA | SCE1572_1285 | yes | sce_921 | yes |
| A and B | Fatty Acids, Lipids, and Isoprenoids | Fatty acids | Polysaturated Fatty Acids synthesis | omega-3 polysaturated fatty acid synthase subunit, PfaC | SCE1572_1286 | yes | sce_922 | yes |
| A and B | Fatty Acids, Lipids, and Isoprenoids | Isoprenoids | Isoprenoid Biosynthesis | Acetyl-CoA acetyltransferase (EC 2.3.1.9) | SCE1572_61 | yes | sce_51 | yes |
| A and B | Fatty Acids, Lipids, and Isoprenoids | Isoprenoids | Isoprenoid Biosynthesis | Dimethylallyltransferase (EC 2.5.1.1) | SCE1572_329 | yes | sce_661 | yes |
| A and B | Fatty Acids, Lipids, and Isoprenoids | Isoprenoids | Isoprenoid Biosynthesis | Diphosphomevalonate decarboxylase (EC 4.1.1.33) | SCE1572_5666 | yes | sce_4717 | yes |
| A and B | Fatty Acids, Lipids, and Isoprenoids | Isoprenoids | Isoprenoid Biosynthesis | Hydroxymethylglutaryl-CoA reductase (EC 1.1.1.34) | SCE1572_4053 | yes | sce_3379 | yes |
| A and B | Fatty Acids, Lipids, and Isoprenoids | Isoprenoids | Isoprenoid Biosynthesis | Hydroxymethylglutaryl-CoA synthase (EC 2.3.3.10) | SCE1572_864 | yes | sce_3568 | yes |
| A and B | Fatty Acids, Lipids, and Isoprenoids | Isoprenoids | Isoprenoid Biosynthesis | Isopentenyl-diphosphate delta-isomerase, FMN-dependent (EC 5.3.3.2) | SCE1572_2407 | yes | sce_1961 | yes |
| A and B | Fatty Acids, Lipids, and Isoprenoids | Isoprenoids | Isoprenoid Biosynthesis | Mevalonate kinase (EC 2.7.1.36) | SCE1572_5665 | yes | sce_4716 | yes |
| A and B | Fatty Acids, Lipids, and Isoprenoids | Isoprenoids | Isoprenoid Biosynthesis | Undecaprenyl diphosphate synthase (EC 2.5.1.31) | SCE1572_8264 | yes | sce_2864 | yes |
| A and B | Fatty Acids, Lipids, and Isoprenoids | Isoprenoids | Isoprenoids for Quinones | Undecaprenyl diphosphate synthase (EC 2.5.1.31) | SCE1572_8264 | yes | sce_2864 | yes |
| A and B | Fatty Acids, Lipids, and Isoprenoids | Isoprenoids | Mevalonate Branch of Isoprenoid Biosynthesis | Acetyl-CoA acetyltransferase (EC 2.3.1.9) | SCE1572_61 | yes | sce_51 | yes |
| A and B | Fatty Acids, Lipids, and Isoprenoids | Isoprenoids | Mevalonate Branch of Isoprenoid Biosynthesis | Diphosphomevalonate decarboxylase (EC 4.1.1.33) | SCE1572_5666 | yes | sce_4717 | yes |
| A and B | Fatty Acids, Lipids, and Isoprenoids | Isoprenoids | Mevalonate Branch of Isoprenoid Biosynthesis | Hydroxymethylglutaryl-CoA reductase (EC 1.1.1.34) | SCE1572_4053 | yes | sce_3379 | yes |
| A and B | Fatty Acids, Lipids, and Isoprenoids | Isoprenoids | Mevalonate Branch of Isoprenoid Biosynthesis | Hydroxymethylglutaryl-CoA synthase (EC 2.3.3.10) | SCE1572_864 | yes | sce_3568 | yes |
| A and B | Fatty Acids, Lipids, and Isoprenoids | Isoprenoids | Mevalonate Branch of Isoprenoid Biosynthesis | Mevalonate kinase (EC 2.7.1.36) | SCE1572_5665 | yes | sce_4716 | yes |
| A and B | Fatty Acids, Lipids, and Isoprenoids | Isoprenoids | Myxoxanthophyll biosynthesis in Cyanobacteria | Beta-carotene hydroxylase | SCE1572_884 | yes | sce_658 | yes |
| B | Fatty Acids, Lipids, and Isoprenoids | Isoprenoids | Isoprenoid Biosynthesis | Phosphomevalonate kinase (EC 2.7.4.2) | | no | sce_4718 | yes |
| B | Fatty Acids, Lipids, and Isoprenoids | Isoprenoids | Myxoxanthophyll biosynthesis in Cyanobacteria | Lycopene cyclase, CruA type | | no | sce_657 | yes |
| A and B | Fatty Acids, Lipids, and Isoprenoids | Phospholipids | Cardiolipin synthesis | Cardiolipin synthetase (EC 2.7.8.-) | SCE1572_6566 | yes | sce_5725 | yes |
| A and B | Fatty Acids, Lipids, and Isoprenoids | Phospholipids | Glycerolipid and Glycerophospholipid Metabolism in Bacteria | 1-acyl-sn-glycerol-3-phosphate acyltransferase (EC 2.3.1.51) | SCE1572_48 | yes | sce_47 | yes |
| A and B | Fatty Acids, Lipids, and Isoprenoids | Phospholipids | Glycerolipid and Glycerophospholipid Metabolism in Bacteria | Acyl carrier protein | SCE1572_860 | yes | sce_3570 | yes |
| A and B | Fatty Acids, Lipids, and Isoprenoids | Phospholipids | Glycerolipid and Glycerophospholipid Metabolism in Bacteria | Acyl-phosphatidylglycerol-3-phosphate O-acyltransferase PkY | SCE1572_7399 | yes | sce_6161 | yes |
| A and B | Fatty Acids, Lipids, and Isoprenoids | Phospholipids | Glycerolipid and Glycerophospholipid Metabolism in Bacteria | Alcohol dehydrogenase (EC 1.1.1.1) | SCE1572_1248 | yes | sce_1248 | yes |
| A and B | Fatty Acids, Lipids, and Isoprenoids | Phospholipids | Glycerolipid and Glycerophospholipid Metabolism in Bacteria | Aldehyde dehydrogenase (EC 1.2.1.3) | SCE1572_4022 | yes | sce_2406 | yes |
| A and B | Fatty Acids, Lipids, and Isoprenoids | Phospholipids | Glycerolipid and Glycerophospholipid Metabolism in Bacteria | Anaerobic glycerol-3-phosphate dehydrogenase subunit A (EC 1.1.5.3) | SCE1572_10981 | yes | sce_9703 | yes |
| A and B | Fatty Acids, Lipids, and Isoprenoids | Phospholipids | Glycerolipid and Glycerophospholipid Metabolism in Bacteria | Anaerobic glycerol-3-phosphate dehydrogenase subunit B (EC 1.1.5.3) | SCE1572_10980 | yes | sce_9702 | yes |
| A and B | Fatty Acids, Lipids, and Isoprenoids | Phospholipids | Glycerolipid and Glycerophospholipid Metabolism in Bacteria | CDP-diacylglycerol-glycerol-3-phosphate 3-phosphatidyltransferase (EC 1.1.5.3) | SCE1572_1690 | yes | sce_1204 | yes |
| A and B | Fatty Acids, Lipids, and Isoprenoids | Phospholipids | Glycerolipid and Glycerophospholipid Metabolism in Bacteria | CDP-diacylglycerol-serine O-phosphatidyltransferase (EC 2.7.8.8) | SCE1572_2263 | yes | sce_1807 | yes |
| A and B | Fatty Acids, Lipids, and Isoprenoids | Phospholipids | Glycerolipid and Glycerophospholipid Metabolism in Bacteria | Cardiolipin synthetase (EC 2.7.8.-) | SCE1572_6566 | yes | sce_5725 | yes |
| A and B | Fatty Acids, Lipids, and Isoprenoids | Phospholipids | Glycerolipid and Glycerophospholipid Metabolism in Bacteria | Glycerol kinase (EC 2.7.1.30) | SCE1572_9720 | yes | sce_8524 | yes |
| A and B | Fatty Acids, Lipids, and Isoprenoids | Phospholipids | Glycerolipid and Glycerophospholipid Metabolism in Bacteria | Glycerol-3-phosphate acyltransferase (EC 2.3.1.15) | SCE1572_10142 | yes | sce_8945 | yes |
| A and B | Fatty Acids, Lipids, and Isoprenoids | Phospholipids | Glycerolipid and Glycerophospholipid Metabolism in Bacteria | Glycerol-3-phosphate dehydrogenase (EC 1.1.5.3) | SCE1572_1855 | yes | sce_1309 | yes |
| A and B | Fatty Acids, Lipids, and Isoprenoids | Phospholipids | Glycerolipid and Glycerophospholipid Metabolism in Bacteria | Glycerol-3-phosphate dehydrogenase [NAD(P)] (EC 1.1.1.94) | SCE1572_9359 | yes | sce_8140 | yes |
| A and B | Fatty Acids, Lipids, and Isoprenoids | Phospholipids | Glycerolipid and Glycerophospholipid Metabolism in Bacteria | Phosphatidate cytidyltransferase (EC 2.7.7.41) | SCE1572_8265 | yes | sce_6936 | yes |
| A and B | Fatty Acids, Lipids, and Isoprenoids | Phospholipids | Glycerolipid and Glycerophospholipid Metabolism in Bacteria | Phosphatidylglycerophosphatase B (EC 3.1.3.27) | SCE1572_11249 | yes | sce_10035 | yes |
| A and B | Fatty Acids, Lipids, and Isoprenoids | Phospholipids | Glycerolipid and Glycerophospholipid Metabolism in Bacteria | Phosphatidylserine decarboxylase (EC 4.1.1.65) | SCE1572_11298 | yes | sce_10081 | yes |
| A and B | Fatty Acids, Lipids, and Isoprenoids | Triacylglycerols | Triacylglycerol metabolism | Lysophospholipase (EC 3.1.1.5) | SCE1572_1412 | yes | sce_1009 | yes |
| A and B | Fatty Acids, Lipids, and Isoprenoids | Triacylglycerols | Triacylglycerol metabolism | Monoglyceride lipase (EC 3.1.1.23) | SCE1572_1412 | yes | sce_1009 | yes |
| A and B | Fatty Acids, Lipids, and Isoprenoids | no subcategory | Polyhydroxybutyrate metabolism | 3-hydroxyacyl-CoA dehydrogenase (EC 1.1.1.35) | SCE1572_60 | yes | sce_50 | yes |
| A and B | Fatty Acids, Lipids, and Isoprenoids | no subcategory | Polyhydroxybutyrate metabolism | 3-hydroxybutyryl-CoA dehydratase (EC 4.2.1.55) | SCE1572_463 | yes | sce_277 | yes |
| A and B | Fatty Acids, Lipids, and Isoprenoids | no subcategory | Polyhydroxybutyrate metabolism | 3-hydroxybutyryl-CoA dehydrogenase (EC 1.1.1.157) | SCE1572_466 | yes | sce_278 | yes |
| A and B | Fatty Acids, Lipids, and Isoprenoids | no subcategory | Polyhydroxybutyrate metabolism | 3-hydroxybutyryl-CoA epimerase (EC 5.1.2.3) | SCE1572_60 | yes | sce_50 | yes |
| A and B | Fatty Acids, Lipids, and Isoprenoids | no subcategory | Polyhydroxybutyrate metabolism | 3-ketoacyl-CoA thiolase (EC 2.3.1.16) | SCE1572_61 | yes | sce_51 | yes |
| A and B | Fatty Acids, Lipids, and Isoprenoids | no subcategory | Polyhydroxybutyrate metabolism | Acetyl-CoA acetyltransferase (EC 2.3.1.9) | SCE1572_61 | yes | sce_51 | yes |
| A and B | Fatty Acids, Lipids, and Isoprenoids | no subcategory | Polyhydroxybutyrate metabolism | D-beta-hydroxybutyrate dehydrogenase (EC 1.1.1.30) | SCE1572_2679 | yes | sce_2228 | yes |
| A and B | Fatty Acids, Lipids, and Isoprenoids | no subcategory | Polyhydroxybutyrate metabolism | Enoyl-CoA hydratase (EC 4.2.1.17) | SCE1572_60 | yes | sce_50 | yes |
| A and B | Fatty Acids, Lipids, and Isoprenoids | no subcategory | Polyhydroxybutyrate metabolism | Polyhydroxyalkanoic acid synthase | SCE1572_537 | yes | sce_343 | yes |
| A and B | Iron acquisition and metabolism | no subcategory | Hemin transport system | Ferric siderophore transport system, periplasmic binding protein TonB | SCE1572_5715 | yes | sce_4768 | yes |
| A and B | Iron acquisition and metabolism | no subcategory | Hemin transport system | Outer membrane receptor proteins, mostly Fe transport | SCE1572_1518 | yes | sce_1041 | yes |
| B | Iron acquisition and metabolism | no subcategory | Encapsulating protein for DYP-type peroxidase and ferritin-like | Uncharacterized protein COG3461 | | no | sce_5912 | yes |
| A and B | Membrane Transport | ABC transporters | ABC transporter branched-chain amino acid (TC 3.A.1.4.1) | ABC transporter branched-chain amino acid ABC transporter, amino acid-binding protein | SCE1572_1724 | yes | sce_1236 | yes |
| A and B | Membrane Transport | ABC transporters | ABC transporter branched-chain amino acid (TC 3.A.1.4.1) | Branched-chain amino acid ABC transporter, amino acid-binding protein | SCE1572_1280 | yes | sce_1280 | yes |
| A and B | Membrane Transport | ABC transporters | ABC transporter branched-chain amino acid (TC 3.A.1.4.1) | Branched-chain amino acid transport ATP-binding protein LpF (TC 3.A.1.4.1) | SCE1572_151 | yes | sce_9615 | yes |
| A and B | Membrane Transport | ABC transporters | ABC transporter branched-chain amino acid (TC 3.A.1.4.1) | Branched-chain amino acid transport ATP-binding protein LpG (TC 3.A.1.4.1) | SCE1572_4484 | yes | sce_9614 | yes |
| A and B | Membrane Transport | ABC transporters | ABC transporter branched-chain amino acid (TC 3.A.1.4.1) | Branched-chain amino acid transport system permease protein LpmT (TC 3.A.1.4.1) | SCE1572_4483 | yes | sce_9613 | yes |
| A and B | Membrane Transport | ABC transporters | ABC transporter branched-chain amino acid (TC 3.A.1.4.1) | High-affinity branched-chain amino acid transport system permease protein LpmU (TC 3.A.1.4.1) | SCE1572_153 | yes | sce_9290 | yes |
| A and B | Membrane Transport | ABC transporters | ABC transporter dipeptide (TC 3.A.1.5.2) | Dipeptide transport system permease protein DppB (TC 3.A.1.5.2) | SCE1572_4877 | yes | sce_4091 | yes |
| A and B | Membrane Transport | ABC transporters | ABC transporter dipeptide (TC 3.A.1.5.2) | Dipeptide-binding ABC transporter, periplasmic substrate-binding component DppA (TC 3.A.1.5.2) | SCE1572_4054 | yes | sce_3765 | yes |
| A and B | Membrane Transport | ABC transporters | ABC transporter oligopeptide (TC 3.A.1.5.1) | Oligopeptide ABC transporter, periplasmic oligopeptide-binding protein OgpA (TC 3.A.1.5.1) | SCE1572_4629 | yes | sce_3859 | yes |
| A and B | Membrane Transport | ABC transporters | ABC transporter oligopeptide (TC 3.A.1.5.1) | Oligopeptide transport ATP-binding protein OgpD (TC 3.A.1.5.1) | SCE1572_4652 | yes | sce_3874 | yes |
| A and B | Membrane Transport | ABC transporters | ABC transporter oligopeptide (TC 3.A.1.5.1) | Oligopeptide transport ATP-binding protein OgpE (TC 3.A.1.5.1) | SCE1572_4653 | yes | sce_3875 | yes |
| A and B | Membrane Transport | ABC transporters | ABC transporter oligopeptide (TC 3.A.1.5.1) | Oligopeptide transport system permease protein OgpH (TC 3.A.1.5.1) | SCE1572_2728 | yes | sce_2266 | yes |
| A and B | Membrane Transport | ABC transporters | ABC transporter oligopeptide (TC 3.A.1.5.1) | Oligopeptide transport system permease protein OgpI (TC 3.A.1.5.1) | SCE1572_2727 | yes | sce_2265 | yes |
| B | Membrane Transport | ABC transporters | ABC transporter branched-chain amino acid (TC 3.A.1.4.1) | ABC transporter branched-chain amino acid ABC transporter, periplasmic-binding protein LpK (TC 3.A.1.4.1) | SCE1572_1518 | yes | sce_10187 | yes |
| A and B | Membrane Transport | Cation transporters | Magnesium transport | Magnesium and cobalt transport protein CorA | SCE1572_8871 | yes | sce_7630 | yes |
| B | Membrane Transport | Cation transporters | Magnesium transport | Mg/Co/Ni transporter MgfE | | no | sce_3950 | yes |
| A and B | Membrane Transport | Protein secretion system, Type VI | Type VI secretion systems | CtpB protein | SCE1572_6714 | yes | sce_5586 | yes |
| A and B | Membrane Transport | Protein secretion system, Type VI | Type VI secretion systems | IcnF-related protein | SCE1572_6710 | yes | sce_5582 | yes |
| A and B | Membrane Transport | Protein secretion system, Type VI | Type VI secretion systems | Protein ImpG/VasA | SCE1572_6723 | yes | sce_5595 | yes |
| A and B | Membrane Transport | Protein secretion system, Type VI | Type VI secretion systems | Sigma-54 dependent transcriptional regulator | SCE1572_9885 | yes | sce_8696 | yes |
| A and B | Membrane Transport | Protein secretion system, Type VI | Type VI secretion systems | Type VI secretion lipoprotein/VasD | SCE1572_6713 | yes | sce_5585 | yes |
| A and B | Membrane Transport | Protein secretion system, Type VI | Type VI secretion systems | Uncharacterized protein ImpA | SCE1572_6708 | yes | sce_5580 | yes |
| A and B | Membrane Transport | Protein secretion system, Type VI | Type VI secretion systems | Uncharacterized protein ImpB | SCE1572_6706 | yes | sce_638 | yes |
| A and B | Membrane Transport | Protein secretion system, Type VI | Type VI secretion systems | Uncharacterized protein ImpC | SCE1572_1876 | yes | sce_1392 | yes |
| A and B | Membrane Transport | Protein secretion system, Type VI | Type VI secretion systems | Uncharacterized protein ImpH/VasB | SCE1572_6724 | yes | sce_5596 | yes |
| A and B | Membrane Transport | Protein secretion system, Type VI | Type VI secretion systems | Uncharacterized protein ImpI/VasE | SCE1572_6712 | yes | sce_5588 | yes |
| A and B | Membrane Transport | Protein secretion system, Type VI | Type VI secretion systems | Uncharacterized protein ImpJ/VasF | SCE1572_6716 | yes | sce_5584 | yes |
| A and B | Membrane Transport | Protein secretion system, Type VI | Type VI secretion systems | Uncharacterized protein similar to VCA0109 | SCE1572_6722 | yes | sce_5594 | yes |
| A and B | Membrane Transport | Protein secretion system, Type VI | Type VI secretion systems | VgrG protein | SCE1572_53 | yes | sce_117 | yes |
| B | Membrane Transport | Protein secretion system, Type VI | Type VI secretion systems | Uncharacterized protein ImpF | | no | sce_10433 | yes |
| A and B | Membrane Transport | Protein translocation across cytoplasmic membrane | Bacterial signal recognition particle (SRP) | Signal recognition particle receptor protein FtsY (=alpha subunit) (TC 3.A.1.5.1) | SCE1572_3933 | yes | sce_3267 | yes |
| A and B | Membrane Transport | Protein translocation across cytoplasmic membrane | Bacterial signal recognition particle (SRP) | Signal recognition particle, subunit FtsY SRP54 (TC 3.A.1.5.1) | SCE1572_4739 | yes | sce_9541 | yes |
| A and B | Membrane Transport | Protein translocation across cytoplasmic membrane | Twin-arginine translocation system | Twin-arginine translocation protein TatB | SCE1572_2968 | yes | sce_4361 | yes |
| A and B | Membrane Transport | Protein translocation across cytoplasmic membrane | Twin-arginine translocation system | Twin-arginine translocation protein TatC | SCE1572_5204 | yes | sce_4362 | yes |
| A | Membrane Transport | TRAP transporters | TRAP Transporter collection | TRAP-type C4-dicarboxylate transport system, large permease component | SCE1572_4547 | yes | | no |
| A | Membrane Transport | TRAP transporters | TRAP Transporter collection | TRAP-type C4-dicarboxylate transport system, periplasmic component | SCE1572_4545 | yes | | no |
| A | Membrane Transport | TRAP transporters | TRAP Transporter collection | TRAP-type C4-dicarboxylate transport system, small permease component | SCE1572_4546 | yes | | no |
| A and B | Membrane Transport | Uni-Sym- and Antiporters | Multi-subunit cation antiporter | Na(I) H(i) antiporter subunit A | SCE1572_3619 | yes | sce_2155 | yes |
| A and B | Membrane Transport | Uni-Sym- and Antiporters | Multi-subunit cation antiporter | Na(I) H(i) antiporter subunit B | SCE1572_3620 | yes | sce_2154 | yes |
| A and B | Membrane Transport | Uni-Sym- and Antiporters | Multi-subunit cation antiporter | Na(I) H(i) antiporter subunit C | SCE1572_3621 | yes | sce_2153 | yes |
| A and B | Membrane Transport | Uni-Sym- and Antiporters | Multi-subunit cation antiporter | Na(I) H(i) antiporter subunit D | SCE1572_3622 | yes | sce_2152 | yes |
| A and B | Membrane Transport | Uni-Sym- and Antiporters | Multi-subunit cation antiporter | Na(I) H(i) antiporter subunit E | SCE1572_3623 | yes | sce_2151 | yes |
| A and B | Membrane Transport | Uni-Sym- and Antiporters | Multi-subunit cation antiporter | Na(I) H(i) antiporter subunit F | SCE1572_3624 | yes | sce_2150 | yes |
| A and B | Membrane Transport | Uni-Sym- and Antiporters | Multi-subunit cation antiporter | Na(I) H(i) antiporter subunit G | SCE1572_3625 | yes | sce_2149 | yes |
| A and B | Membrane Transport | Uni-Sym- and Antiporters | NhaA, NhaD and Sodium-dependent phosphate transporters | Na ₂ H antiporter NhaA type | SCE1572_4429 | yes | sce_3666 | yes |
| A and B | Membrane Transport | no subcategory | Proton-dependent Peptide Transporters | Di-tripeptide transporter | SCE1572_3305 | yes | sce_6349 | yes |
| A and B | Membrane Transport | no subcategory | Ton and Tol transport systems | 4-hydroxybenzoyl-CoA thioesterase family active site | SCE1572_2810 | yes | sce_3385 | yes |
| A and B | Membrane Transport | no subcategory | Ton and Tol transport systems | Biopolymer transport protein ExbD/TolR | SCE1572_970 | yes | sce_730 | yes |
| A and B | Membrane Transport | no subcategory | Ton and Tol transport systems | Ferric siderophore transport system, periplasmic binding protein TonB | SCE1572_5715 | yes | sce_4768 | yes |
| A and B | Membrane Transport | no subcategory | Ton and Tol transport systems | MotA/TolQ/ExbB proton channel family protein | SCE1572_969 | yes | sce_729 | yes |
| A and B | Membrane Transport | no subcategory | Ton and Tol transport systems | Outer membrane lipoprotein omp16 precursor | SCE1572_7219 | yes | sce_1206 | yes |
| A and B | Membrane Transport | no subcategory | Ton and Tol transport systems | Peptidoglycan-associated lipoprotein precursor | SCE1572_968 | yes | sce_728 | yes |
| A and B | Membrane Transport | no subcategory | Ton and Tol transport systems | Protein-L-isospartate O-methyltransferase (EC 2.1.1.77) | SCE1572_903 | yes | sce_6084 | yes |
| A and B | Membrane Transport | no subcategory | Ton and Tol transport systems | TPR domain protein, putative component of TonB system | | yes | sce_279 | yes |
| A and B | Membrane Transport | no subcategory | Ton and Tol transport systems | Tol biopolymer transport system, TolR protein | SCE1572_4617 | yes | sce_3679 | yes |
| A and B | Membrane Transport | no subcategory | Ton and Tol transport systems | TolA protein | SCE1572_20 | yes | sce_20 | yes |

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|---------|---------------|-----------------------------|--------------------------------------|---|---------------|-----|-----------|-----|
| A and B | Miscellaneous | Plant-Prkaryote DOE project | At3g21300 | Glutamyl-tRNA(Gln) amidotransferase subunit C (EC 6.3.5.7) | SCE1572_5745 | yes | sce_4795 | yes |
| A and B | Miscellaneous | Plant-Prkaryote DOE project | At3g21300 | RNA methyltransferase, TrmA family | SCE1572_3368 | yes | sce_2857 | yes |
| A and B | Miscellaneous | Plant-Prkaryote DOE project | At3g21300 | Transcription regulator [contains diacylglycerol kinase catalytic domain | SCE1572_1549 | yes | sce_1075 | yes |
| A and B | Miscellaneous | Plant-Prkaryote DOE project | At5g04520 AT1G06240 | Amidophosphoribosyltransferase (EC 2.4.2.14) | SCE1572_5789 | yes | sce_4836 | yes |
| A and B | Miscellaneous | Plant-Prkaryote DOE project | At5g04520 AT1G06240 | COG2833: uncharacterized protein | SCE1572_1561 | yes | sce_1091 | yes |
| A and B | Miscellaneous | Plant-Prkaryote DOE project | At5g04520 AT1G06240 | COGs COG3146 | SCE1572_5923 | yes | sce_4926 | yes |
| A and B | Miscellaneous | Plant-Prkaryote DOE project | At5g04520 AT1G06240 | Glutamate-ammonia-lyase adenylyltransferase (EC 2.7.7.42) | SCE1572_2412 | yes | sce_1966 | yes |
| A and B | Miscellaneous | Plant-Prkaryote DOE project | At5g04520 AT1G06240 | Large exoproteins involved in home utilization or adhesion | SCE1572_4644 | yes | sce_3741 | yes |
| A and B | Miscellaneous | Plant-Prkaryote DOE project | At5g04520 AT1G06240 | Peptide methionine sulfide reductase MsrB (EC 1.8.4.12) | SCE1572_10145 | yes | sce_6036 | yes |
| A and B | Miscellaneous | Plant-Prkaryote DOE project | At5g04520 AT1G06240 | Thiol peroxidase, Bcp-type (EC 1.11.1.15) | SCE1572_6737 | yes | sce_5609 | yes |
| A and B | Miscellaneous | Plant-Prkaryote DOE project | At5g37530 | Aspartyl-tRNA synthetase (EC 6.1.1.12) | SCE1572_10640 | yes | sce_9245 | yes |
| A and B | Miscellaneous | Plant-Prkaryote DOE project | At5g37530 | Cysteine desulfurase (EC 2.8.1.7) | SCE1572_1872 | yes | sce_1345 | yes |
| A and B | Miscellaneous | Plant-Prkaryote DOE project | At5g37530 | Cysteine desulfurase (EC 2.8.1.7), lscS subfamily | SCE1572_9417 | yes | sce_8204 | yes |
| A and B | Miscellaneous | Plant-Prkaryote DOE project | At5g37530 | Cysteine desulfurase (EC 2.8.1.7), SuS subfamily | SCE1572_10250 | yes | sce_5192 | yes |
| A and B | Miscellaneous | Plant-Prkaryote DOE project | At5g37530 | Histidyl-tRNA synthetase (EC 6.1.1.21) | SCE1572_6135 | yes | sce_5079 | yes |
| A and B | Miscellaneous | Plant-Prkaryote DOE project | At5g37530 | Iron-sulfur cluster regulator lscR | SCE1572_7588 | yes | sce_6444 | yes |
| A and B | Miscellaneous | Plant-Prkaryote DOE project | At5g37530 | tRNA (5-methylaminomethyl-2-thiouridylyl)-methyltransferase (EC 2. | SCE1572_9389 | yes | sce_8169 | yes |
| A and B | Miscellaneous | Plant-Prkaryote DOE project | At5g38900 | 2-hydroxycyromene-2-carboxylate isomerase/Dsba-like thioredoxin do | SCE1572_2043 | yes | sce_1523 | yes |
| A and B | Miscellaneous | Plant-Prkaryote DOE project | At5g48545 and At3g56490 At1g31160 | Foldase protein-PrsA precursor (EC 5.2.1.8) | SCE1572_9344 | yes | sce_8124 | yes |
| A and B | Miscellaneous | Plant-Prkaryote DOE project | At5g48545 and At3g56490 At1g31160 | Histidine triad (HTT) nucleotide-binding protein, similarity with At5g485 | SCE1572_8943 | yes | sce_7710 | yes |
| A and B | Miscellaneous | Plant-Prkaryote DOE project | At5g48545 and At3g56490 At1g31160 | Integration host factor alpha subunit | SCE1572_10292 | yes | sce_9620 | yes |
| A and B | Miscellaneous | Plant-Prkaryote DOE project | At5g63420 | Cell division protein Psk | SCE1572_4011 | yes | sce_1797 | yes |
| A and B | Miscellaneous | Plant-Prkaryote DOE project | At5g63420 | Ferric uptake regulation protein FUR | SCE1572_7 | yes | sce_7 | yes |
| A and B | Miscellaneous | Plant-Prkaryote DOE project | At5g63420 | Inactive homolog of metal-dependent proteases, putative molecular chap | SCE1572_2318 | yes | sce_1865 | yes |
| A and B | Miscellaneous | Plant-Prkaryote DOE project | At5g63420 | Peptide deformylase (EC 3.5.1.88) | SCE1572_5077 | yes | sce_4266 | yes |
| A and B | Miscellaneous | Plant-Prkaryote DOE project | At5g63420 | Polyribonucleotide nucleotidyltransferase (EC 2.7.7.8) | SCE1572_6129 | yes | sce_5074 | yes |
| A and B | Miscellaneous | Plant-Prkaryote DOE project | At5g63420 | Ribonuclease J2 (endoribonuclease in RNA processing) | SCE1572_620 | yes | sce_428 | yes |
| A and B | Miscellaneous | Plant-Prkaryote DOE project | At5g63420 | Ribosomal-protein-S18p-alanine acetyltransferase (EC 2.3.1.-) | SCE1572_7710 | yes | sce_6542 | yes |
| A and B | Miscellaneous | Plant-Prkaryote DOE project | At5g63420 | Ygd/Kae1/Qu7 family, required for N6-threonylcarbamoyl adenosine | SCE1572_2254 | yes | sce_1799 | yes |
| A and B | Miscellaneous | Plant-Prkaryote DOE project | COG0277 | D-2-hydroxyglutarate dehydrogenase | SCE1572_5592 | yes | sce_4656 | yes |
| A and B | Miscellaneous | Plant-Prkaryote DOE project | COG0277 | D-3-phosphoglycerate dehydrogenase (EC 1.1.1.95) | SCE1572_1389 | yes | sce_1692 | yes |
| A and B | Miscellaneous | Plant-Prkaryote DOE project | COG0277 | Fumarylacetoacetate hydrolase family protein | SCE1572_3892 | yes | sce_3221 | yes |
| A and B | Miscellaneous | Plant-Prkaryote DOE project | COG0451 | Glyoxyltransferase | SCE1572_681 | yes | sce_484 | yes |
| A and B | Miscellaneous | Plant-Prkaryote DOE project | COG0451 | Mucin endopeptidase | SCE1572_10435 | yes | sce_9076 | yes |
| A and B | Miscellaneous | Plant-Prkaryote DOE project | COG0451 | Nucleoside-diphosphate-sugar epimerases | SCE1572_1129 | yes | sce_1996 | yes |
| A and B | Miscellaneous | Plant-Prkaryote DOE project | COG0451 | Undecaprenyl-diphosphate (EC 3.6.1.27) | SCE1572_7898 | yes | sce_6698 | yes |
| A and B | Miscellaneous | Plant-Prkaryote DOE project | COG0523 | S0S ribosomal subunit maturation GTPase RbgA (B. subtilis Y1qF) | SCE1572_2042 | yes | sce_1522 | yes |
| A and B | Miscellaneous | Plant-Prkaryote DOE project | COG0523 | C4-type zinc finger protein, DksA/TrAR family | SCE1572_5038 | yes | sce_4239 | yes |
| A and B | Miscellaneous | Plant-Prkaryote DOE project | COG0523 | Carbon starvation protein A | SCE1572_8282 | yes | sce_6951 | yes |
| A and B | Miscellaneous | Plant-Prkaryote DOE project | COG0523 | Creatinine amidohydrolase (EC 3.5.2.10) | SCE1572_2672 | yes | sce_2221 | yes |
| A and B | Miscellaneous | Plant-Prkaryote DOE project | COG0523 | D-alanyl-D-alanine carboxypeptidase (EC 3.4.16.4) | SCE1572_330 | yes | sce_4328 | yes |
| A and B | Miscellaneous | Plant-Prkaryote DOE project | COG0523 | Dihydroorotase (EC 3.5.2.3) | SCE1572_5734 | yes | sce_4784 | yes |
| A and B | Miscellaneous | Plant-Prkaryote DOE project | COG0523 | GTP cyclohydrolase I (EC 3.5.4.16) type 1 | SCE1572_11540 | yes | sce_10389 | yes |
| A and B | Miscellaneous | Plant-Prkaryote DOE project | COG0523 | High-affinity carbon uptake protein Hat/HatR | SCE1572_324 | yes | sce_254 | yes |
| A and B | Miscellaneous | Plant-Prkaryote DOE project | COG0523 | LSU ribosomal protein L21p | SCE1572_10045 | yes | sce_8861 | yes |
| A and B | Miscellaneous | Plant-Prkaryote DOE project | COG0523 | LSU ribosomal protein L27p | SCE1572_10044 | yes | sce_8860 | yes |
| A and B | Miscellaneous | Plant-Prkaryote DOE project | COG0523 | LSU ribosomal protein L29p | SCE1572_6001 | yes | sce_4953 | yes |
| A and B | Miscellaneous | Plant-Prkaryote DOE project | COG0523 | LSU ribosomal protein L31p | SCE1572_11291 | yes | sce_10074 | yes |
| A and B | Miscellaneous | Plant-Prkaryote DOE project | COG0523 | LSU ribosomal protein L32p | SCE1572_5086 | yes | sce_4274 | yes |
| A and B | Miscellaneous | Plant-Prkaryote DOE project | COG0523 | LSU ribosomal protein L33p | SCE1572_651 | yes | sce_458 | yes |
| A and B | Miscellaneous | Plant-Prkaryote DOE project | COG0523 | LSU ribosomal protein L36p | SCE1572_10064 | yes | sce_8881 | yes |
| A and B | Miscellaneous | Plant-Prkaryote DOE project | COG0523 | Phosphoribosyl-AMP cyclohydrolase (EC 3.5.4.19) | SCE1572_641 | yes | sce_450 | yes |
| A and B | Miscellaneous | Plant-Prkaryote DOE project | COG0523 | Phosphoribosyl-ATP pyrophosphatase (EC 3.6.1.31) | SCE1572_641 | yes | sce_450 | yes |
| A and B | Miscellaneous | Plant-Prkaryote DOE project | COG0523 | Putative metal chaperone, involved in Zn homeostasis, GTPase of COG | SCE1572_10351 | yes | sce_9219 | yes |
| A and B | Miscellaneous | Plant-Prkaryote DOE project | COG0523 | SSU ribosomal protein S14p (S29e) | SCE1572_10074 | yes | sce_8891 | yes |
| A and B | Miscellaneous | Plant-Prkaryote DOE project | COG0523 | Uracil phosphoribosyltransferase (EC 2.4.2.9) | SCE1572_3269 | yes | sce_2764 | yes |
| A and B | Miscellaneous | Plant-Prkaryote DOE project | COG0523 | Zinc uptake regulation protein ZUR | SCE1572_9283 | yes | sce_8064 | yes |
| A and B | Miscellaneous | Plant-Prkaryote DOE project | COG1565 | 2-amino-4-hydroxy-6-hydroxymethylhydropteridine pyrophosphokin | SCE1572_9665 | yes | sce_8473 | yes |
| A and B | Miscellaneous | Plant-Prkaryote DOE project | COG1565 | COG1565: Uncharacterized conserved protein | SCE1572_4934 | yes | sce_4145 | yes |
| A and B | Miscellaneous | Plant-Prkaryote DOE project | COG1565 | Dihydroneopterin adolase (EC 4.1.2.25) | SCE1572_9262 | yes | sce_8041 | yes |
| A and B | Miscellaneous | Plant-Prkaryote DOE project | COG1565 | FolM Alternative dihydrofolate reductase 1 | SCE1572_10968 | yes | sce_9682 | yes |
| A and B | Miscellaneous | Plant-Prkaryote DOE project | COG1565 | GTP cyclohydrolase I (EC 3.5.4.16) type 1 | SCE1572_11540 | yes | sce_10389 | yes |
| A and B | Miscellaneous | Plant-Prkaryote DOE project | COG1565 | Prolipropin diacylglyceryl transferase (EC 2.4.99.-) | SCE1572_642 | yes | sce_451 | yes |
| A and B | Miscellaneous | Plant-Prkaryote DOE project | COG1565 | Pterin-4-alpha-carbinolamine dehydratase (EC 4.2.1.96) | SCE1572_2342 | yes | sce_1891 | yes |
| A and B | Miscellaneous | Plant-Prkaryote DOE project | COG1565 | Queuosine biosynthesis QueD, PTPS-1 | SCE1572_10281 | yes | sce_9631 | yes |
| A and B | Miscellaneous | Plant-Prkaryote DOE project | COG2363 | COG2363 | SCE1572_3822 | yes | sce_3149 | yes |
| A and B | Miscellaneous | Plant-Prkaryote DOE project | COG2363 | Cysteine desulfurase (EC 2.8.1.7) | SCE1572_1872 | yes | sce_1345 | yes |
| A and B | Miscellaneous | Plant-Prkaryote DOE project | COG2363 | Cysteine desulfurase (EC 2.8.1.7), lscS subfamily | SCE1572_9417 | yes | sce_8204 | yes |
| A and B | Miscellaneous | Plant-Prkaryote DOE project | COG2363 | Cysteine desulfurase (EC 2.8.1.7), SuS subfamily | SCE1572_10250 | yes | sce_5192 | yes |
| A and B | Miscellaneous | Plant-Prkaryote DOE project | COG2363 | Hydroxymethylpyrimidine ABC transporter, substrate-binding compone | SCE1572_7412 | yes | sce_2167 | yes |
| A and B | Miscellaneous | Plant-Prkaryote DOE project | COG2363 | Phosphomethylpyrimidine kinase (EC 2.7.4.7) | SCE1572_978 | yes | sce_737 | yes |
| A and B | Miscellaneous | Plant-Prkaryote DOE project | COG2363 | Sulfur carrier protein ThiS | SCE1572_7171 | yes | sce_5900 | yes |
| A and B | Miscellaneous | Plant-Prkaryote DOE project | COG2363 | ThiJ/PilJ family protein | SCE1572_500 | yes | sce_1070 | yes |
| A and B | Miscellaneous | Plant-Prkaryote DOE project | COG2363 | Thiamin biosynthesis protein ThiC | SCE1572_5711 | yes | sce_4764 | yes |
| A and B | Miscellaneous | Plant-Prkaryote DOE project | COG2363 | Thiamin-phosphate pyrophosphatase (EC 5.2.1.2) | SCE1572_2456 | yes | sce_1990 | yes |
| A and B | Miscellaneous | Plant-Prkaryote DOE project | COG2363 | Thiazole biosynthesis protein ThiG | SCE1572_5704 | yes | sce_2756 | yes |
| A and B | Miscellaneous | Plant-Prkaryote DOE project | COG2509 | Glucosamine-fructose-6-phosphate aminotransferase [isomerizing] (E | SCE1572_5465 | yes | sce_8287 | yes |
| A and B | Miscellaneous | Plant-Prkaryote DOE project | COG2509 | Hypothetical protein YhbP, contains nucleotide-binding domain of Dks | SCE1572_9729 | yes | sce_8531 | yes |
| A and B | Miscellaneous | Plant-Prkaryote DOE project | COG3146 experimental | 2-amino-4-hydroxy-6-hydroxymethylhydropteridine pyrophosphokin | SCE1572_9665 | yes | sce_8473 | yes |
| A and B | Miscellaneous | Plant-Prkaryote DOE project | COG3146 experimental | 4-hydroxyphenylpyruvate dioxygenase (EC 1.13.11.27) | SCE1572_4318 | yes | sce_5475 | yes |
| A and B | Miscellaneous | Plant-Prkaryote DOE project | COG3146 experimental | COGs COG3146 | SCE1572_5923 | yes | sce_4926 | yes |
| A and B | Miscellaneous | Plant-Prkaryote DOE project | COG3146 experimental | Dihydroneopterin adolase (EC 4.1.2.25) | SCE1572_9262 | yes | sce_8041 | yes |
| A and B | Miscellaneous | Plant-Prkaryote DOE project | COG3146 experimental | FolM Alternative dihydrofolate reductase 1 | SCE1572_10968 | yes | sce_9682 | yes |
| A and B | Miscellaneous | Plant-Prkaryote DOE project | COG3146 experimental | Fumarylacetoacetase (EC 3.7.1.2) | SCE1572_7163 | yes | sce_5897 | yes |
| A and B | Miscellaneous | Plant-Prkaryote DOE project | COG3146 experimental | GTP cyclohydrolase I (EC 3.5.4.16) type 1 | SCE1572_11540 | yes | sce_10389 | yes |
| A and B | Miscellaneous | Plant-Prkaryote DOE project | COG3146 experimental | Gutathione S-transferase (EC 2.5.1.18) | SCE1572_220 | yes | sce_558 | yes |
| A and B | Miscellaneous | Plant-Prkaryote DOE project | COG3146 experimental | Homogentisate 1,2-dioxygenase (EC 1.13.11.5) | SCE1572_4319 | yes | sce_5474 | yes |
| A and B | Miscellaneous | Plant-Prkaryote DOE project | COG3146 experimental | Maleylacetoacetate isomerase (EC 5.2.1.2) | SCE1572_7883 | yes | sce_6399 | yes |
| A and B | Miscellaneous | Plant-Prkaryote DOE project | COG3146 experimental | Nitric oxide synthase (EC 1.11.1.2) | SCE1572_2418 | yes | sce_1762 | yes |
| A and B | Miscellaneous | Plant-Prkaryote DOE project | COG3146 experimental | Pterin-4-alpha-carbinolamine dehydratase (EC 4.2.1.96) | SCE1572_2342 | yes | sce_1891 | yes |
| A and B | Miscellaneous | Plant-Prkaryote DOE project | COG3146 experimental | Queuosine biosynthesis QueD, PTPS-1 | SCE1572_10281 | yes | sce_9631 | yes |
| A and B | Miscellaneous | Plant-Prkaryote DOE project | COG3533 | Alpha-L-arabinofuranosidase II precursor (EC 3.2.1.55) | SCE1572_3113 | yes | sce_1386 | yes |
| A and B | Miscellaneous | Plant-Prkaryote DOE project | COG3533 | Arabinan endo-1,5-alpha-L-arabinosidase (EC 3.2.1.99) | SCE1572_2128 | yes | sce_1647 | yes |
| A and B | Miscellaneous | Plant-Prkaryote DOE project | COG3533 | COG3866 Pectate lyase | SCE1572_841 | yes | sce_5488 | yes |
| A and B | Miscellaneous | Plant-Prkaryote DOE project | COG3533 | Endo-1,4-beta-xylanase A precursor (EC 3.2.1.8) | SCE1572_346 | yes | sce_841 | yes |
| A and B | Miscellaneous | Plant-Prkaryote DOE project | COG3533 | Hypothetical glycoside hydrolase, family 43, similar to arabinosidase | SCE1572_4336 | yes | sce_9941 | yes |
| A and B | Miscellaneous | Plant-Prkaryote DOE project | COG3533 | L-arabinose isomerase (EC 5.3.1.4) | SCE1572_2638 | yes | sce_3711 | yes |
| A and B | Miscellaneous | Plant-Prkaryote DOE project | COG3533 | L-arabinose transport ATP-binding protein AraG (TC 3.A.1.2.2) | SCE1572_2641 | yes | sce_3708 | yes |
| A and B | Miscellaneous | Plant-Prkaryote DOE project | COG3533 | L-arabinose-specific 1-epimerase (mutarotase) | SCE1572_1772 | yes | sce_1086 | yes |
| A and B | Miscellaneous | Plant-Prkaryote DOE project | COG3533 | L-ribulose-5-phosphate 4-epimerase (EC 5.1.3.4) | SCE1572_2639 | yes | sce_3710 | yes |
| A and B | Miscellaneous | Plant-Prkaryote DOE project | COG3533 | N-Acetyl-D-glucosamine ABC transport system, sugar-binding protein | SCE1572_1169 | yes | sce_858 | yes |
| A and B | Miscellaneous | Plant-Prkaryote DOE project | COG3533 | Ribulokinase (EC 2.7.1.16) | SCE1572_2637 | yes | sce_3712 | yes |
| A and B | Miscellaneous | Plant-Prkaryote DOE project | COG3533 | Gamma-glutamyl acetyltransferase | SCE1572_2132 | yes | sce_1762 | yes |
| A and B | Miscellaneous | Plant-Prkaryote DOE project | Experimental-COG2515 | D-cysteine desulfhydrase (EC 4.4.1.15) | SCE1572_7567 | yes | sce_6422 | yes |
| A and B | Miscellaneous | Plant-Prkaryote DOE project | Experimental-COG2515 | pyridoxal phosphate-dependent deaminase, putative | SCE1572_5913 | yes | sce_4917 | yes |
| A and B | Miscellaneous | Plant-Prkaryote DOE project | Experimental-PTPS | 2-amino-4-hydroxy-6-hydroxymethylhydropteridine pyrophosphokin | SCE1572_9665 | yes | sce_8473 | yes |
| A and B | Miscellaneous | Plant-Prkaryote DOE project | Experimental-PTPS | COG1565: Uncharacterized conserved protein | SCE1572_4934 | yes | sce_4145 | yes |
| A and B | Miscellaneous | Plant-Prkaryote DOE project | Experimental-PTPS | Dihydroneopterin adolase (EC 4.1.2.25) | SCE1572_9262 | yes | sce_8041 | yes |
| A and B | Miscellaneous | Plant-Prkaryote DOE project | Experimental-PTPS | Dihydroterate synthase (EC 2.5.1.15) | SCE1572_9730 | yes | sce_8532 | yes |
| A and B | Miscellaneous | Plant-Prkaryote DOE project | Experimental-PTPS | FolM Alternative dihydrofolate reductase 1 | SCE1572_10968 | yes | sce_9682 | yes |
| A and B | Miscellaneous | Plant-Prkaryote DOE project | Experimental-PTPS | GTP cyclohydrolase I (EC 3.5.4.16) type 1 | SCE1572_11540 | yes | sce_10389 | yes |
| A and B | Miscellaneous | Plant-Prkaryote DOE project | Experimental-PTPS | PTPS-like type 4 | SCE1572_7553 | yes | sce_6411 | yes |
| A and B | Miscellaneous | Plant-Prkaryote DOE project | Experimental-PTPS | Queuosine Biosynthesis QueE Radical SAM | SCE1572_3404 | yes | sce_2891 | yes |
| A and B | Miscellaneous | Plant-Prkaryote DOE project | Experimental-PTPS | Queuosine biosynthesis QueD, PTPS-1 | SCE1572_10281 | yes | sce_9631 | yes |
| A and B | Miscellaneous | Plant-Prkaryote DOE project | Experimental - Histidine Degradation | 5-formyltetrahydrofolate cyclo-lyase (EC 6.3.3.2) | SCE1572_9050 | yes | sce_7810 | yes |
| A and B | Miscellaneous | Plant-Prkaryote DOE project | Experimental - Histidine Degradation | Forminoglutamic iminohydrolase (EC 3.5.3.13) | SCE1572_1551 | yes | sce_1078 | yes |
| A and B | Miscellaneous | Plant-Prkaryote DOE project | Experimental - Histidine Degradation | Histidine ammonia-lyase (EC 4.3.1.3) | SCE1572_8014 | yes | sce_6803 | yes |
| A and B | Miscellaneous | Plant-Prkaryote DOE project | Experimental - Histidine Degradation | Imidazolonepropiolase (EC 3.5.2.7) | SCE1572_5759 | yes | sce_4807 | yes |
| A and B | Miscellaneous | Plant-Prkaryote DOE project | Experimental - Histidine Degradation | Methylenetetrahydrofolate cyclohydrolase (EC 3.5.4.9) | SCE1572_4947 | yes | sce_4161 | yes |
| A and B | | | | | | | | |

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|---------|-----------------------------|--|--|---|---------------|-----|-----------|-----|
| A and B | Miscellaneous | Plant-Prokaryote DOE project | YrdC-Yco-Sua5 protein family | Serine hydroxymethyltransferase (EC 2.1.2.1) | SCE1572_8655 | yes | sce_7370 | yes |
| A and B | Miscellaneous | Plant-Prokaryote DOE project | YrdC-Yco-Sua5 protein family | YgdKae1 Qrr7 family, required for N6-threonylcarbamoyl adenosine | SCE1572_2254 | yes | sce_1799 | yes |
| A | Miscellaneous | Plant-Prokaryote DOE project | At3g50560 | Short-chain dehydrogenase, associated with 2-hydroxychromene-2-carb | SCE1572_389 | yes | | no |
| A | Miscellaneous | Plant-Prokaryote DOE project | COG3533 | Alpha-xylosidase (EC 3.2.1.-) | SCE1572_2924 | yes | | no |
| A | Miscellaneous | Plant-Prokaryote DOE project | COG3533 | L-arabinose transport system permease protein (TC 3.A.1.2.2) | SCE1572_3121 | yes | | no |
| A | Miscellaneous | Plant-Prokaryote DOE project | COG3533 | L-arabinose-binding periplasmic protein precursor AraF (TC 3.A.1.2.2) | SCE1572_80 | yes | | no |
| A | Miscellaneous | Plant-Prokaryote DOE project | COG3533 | Putative glycosyl hydrolase of unknown function (DUF1680) | SCE1572_2866 | yes | | no |
| B | Miscellaneous | Plant-Prokaryote DOE project | At1g52510 AT4G12830 (COG0596) | 3-beta hydroxysteroid dehydrogenase/isomerase family protein in hypothetical gene cluster | | no | sce_2397 | yes |
| B | Miscellaneous | Plant-Prokaryote DOE project | At5g63420 | Metallo-beta-lactamase family protein, RNA-specific | | no | sce_4676 | yes |
| B | Miscellaneous | Plant-Prokaryote DOE project | COG0523 | Zinc ABC transporter, inner membrane permease protein ZnuB | | no | sce_8066 | yes |
| B | Miscellaneous | Plant-Prokaryote DOE project | COG4319 | Alternative dihydrofolate reductase 3 | | no | sce_5172 | yes |
| B | Miscellaneous | Plant-Prokaryote DOE project | lojap | LSU m3Psi915 methyltransferase RlmH | | no | sce_4116 | yes |
| B | Miscellaneous | Plant-Prokaryote DOE project | | Scaffold proteins for [4Fe-4S] cluster assembly (MRP family) | | no | sce_8089 | yes |
| A and B | Miscellaneous | no subcategory | Broadly distributed proteins not in subsystems | UPH0225 protein YchJ | SCE1572_960 | yes | sce_722 | yes |
| A and B | Miscellaneous | no subcategory | Broadly distributed proteins not in subsystems | YpfJ protein, zinc metalloprotease superfamily | SCE1572_9557 | yes | sce_8334 | yes |
| A and B | Miscellaneous | no subcategory | DedA family of inner membrane proteins | DedA protein | SCE1572_8416 | yes | sce_7177 | yes |
| A and B | Miscellaneous | no subcategory | Muconate lactonizing enzyme family | Muconate cycloisomerase (EC 5.5.1.1) | SCE1572_3882 | yes | sce_3206 | yes |
| A and B | Miscellaneous | no subcategory | Muconate lactonizing enzyme family | O-succinylbenzoate synthase (EC 4.2.1.113) | SCE1572_4058 | yes | sce_3383 | yes |
| A and B | Miscellaneous | no subcategory | Phosphoglycerate mutase protein family | 2,3-bisphosphoglycerate-independent phosphoglycerate mutase (EC 5.4.5) | SCE1572_1634 | yes | sce_1168 | yes |
| A and B | Miscellaneous | no subcategory | Phosphoglycerate mutase protein family | Alpha-ribazole-5'-phosphatase (EC 3.1.3.73) | SCE1572_8977 | yes | sce_7736 | yes |
| A and B | Miscellaneous | no subcategory | Phosphoglycerate mutase protein family | Carboxyl-terminal protease (EC 3.4.21.102) | SCE1572_4325 | yes | sce_7224 | yes |
| A and B | Miscellaneous | no subcategory | YbbK | Inner membrane protein YbbK | SCE1572_7101 | yes | sce_5869 | yes |
| A and B | Miscellaneous | no subcategory | YbbK | Putative membrane-bound CtpP-class protease associated with aq_911 | SCE1572_4393 | yes | sce_5976 | yes |
| A and B | Miscellaneous | no subcategory | YbbK | Putative stomatin/prohibitin-family membrane protease subunit aq_911 | SCE1572_9441 | yes | sce_8229 | yes |
| A and B | Miscellaneous | no subcategory | ZZ_gjo need homes | Lipid A export ATP-binding/permease protein MsbA | SCE1572_19 | yes | sce_19 | yes |
| A and B | Miscellaneous | no subcategory | ZZ_gjo need homes | Na _v 1 antiporter | SCE1572_9565 | yes | sce_8354 | yes |
| A and B | Miscellaneous | no subcategory | ZZ_gjo need homes | Phosphocarrier protein kinase/phosphorylase, nitrogen regulation associ | SCE1572_10280 | yes | sce_9633 | yes |
| A and B | Miscellaneous | no subcategory | ZZ_gjo need homes | Proton/glutamate symport protein | SCE1572_4740 | yes | sce_3961 | yes |
| A and B | Miscellaneous | no subcategory | ZZ_gjo need homes | Putative heat shock protein YegD | SCE1572_10346 | yes | sce_9037 | yes |
| A and B | Miscellaneous | no subcategory | ZZ_gjo need homes | Sodium/glutamate symport protein | SCE1572_4740 | yes | sce_3961 | yes |
| A | Miscellaneous | no subcategory | Broadly distributed proteins not in subsystems | Putative oxidoreductase YncB | SCE1572_859 | yes | | no |
| A | Miscellaneous | no subcategory | ZZ_gjo need homes 2 | UPH0182 protein AF1421 | SCE1572_3617 | yes | | no |
| A and B | Motility and Chemotaxis | Social motility and nonflagellar swimming in b | Bacterial motility-Glding | Acetylornithine decarboxylase/Succinyl-diaminopimelate desuccinylase an | SCE1572_581 | yes | sce_386 | yes |
| A and B | Motility and Chemotaxis | Social motility and nonflagellar swimming in b | Bacterial motility-Glding | Cell division protein FtsX | SCE1572_9306 | yes | sce_8086 | yes |
| A and B | Motility and Chemotaxis | Social motility and nonflagellar swimming in b | Bacterial motility-Glding | Twitching motility protein PflT | SCE1572_5709 | yes | sce_4762 | yes |
| A and B | Motility and Chemotaxis | Social motility and nonflagellar swimming in b | Bacterial motility-Glding | Two-component sensor PflS | SCE1572_8313 | yes | sce_6995 | yes |
| A and B | Motility and Chemotaxis | Social motility and nonflagellar swimming in b | Bacterial motility-Glding | Type IV fimbrial assembly protein PIC | SCE1572_8314 | yes | sce_6996 | yes |
| A and B | Motility and Chemotaxis | Social motility and nonflagellar swimming in b | Bacterial motility-Glding | Type IV fimbrial assembly, ATPase PilB | SCE1572_3272 | yes | sce_2767 | yes |
| A and B | Motility and Chemotaxis | Social motility and nonflagellar swimming in b | Bacterial motility-Glding | Type IV fimbrial biogenesis protein PilY1 | SCE1572_2706 | yes | sce_2244 | yes |
| A and B | Motility and Chemotaxis | Social motility and nonflagellar swimming in b | Bacterial motility-Glding | Type IV pilin PilA | SCE1572_3293 | yes | sce_2787 | yes |
| A and B | Motility and Chemotaxis | Social motility and nonflagellar swimming in b | Bacterial motility-Glding | gliding motility protein GldF | SCE1572_3226 | yes | sce_2718 | yes |
| A and B | Motility and Chemotaxis | Social motility and nonflagellar swimming in b | Bacterial motility-Glding | gliding motility protein GldG | SCE1572_3342 | yes | sce_2838 | yes |
| A and B | Motility and Chemotaxis | Social motility and nonflagellar swimming in b | Bacterial motility-Glding | gliding motility protein MglA | SCE1572_630 | yes | sce_438 | yes |
| A and B | Motility and Chemotaxis | Social motility and nonflagellar swimming in b | Bacterial motility-Glding | twitching motility protein PilH | SCE1572_3219 | yes | sce_2451 | yes |
| A and B | Motility and Chemotaxis | Social motility and nonflagellar swimming in b | Bacterial motility-Glding | type 4 fimbrial biogenesis protein FimU | SCE1572_2710 | yes | sce_2249 | yes |
| B | Motility and Chemotaxis | Social motility and nonflagellar swimming in b | Bacterial motility-Glding | Type II secretory pathway, ATPase PulE/Tlp pilus assembly pathway, ATPase PilB | | no | sce_5100 | yes |
| A and B | Motility and Chemotaxis | no subcategory | Bacterial Chemotaxis | Chemotaxis protein CheD | SCE1572_2796 | yes | sce_2449 | yes |
| A and B | Motility and Chemotaxis | no subcategory | Bacterial Chemotaxis | Chemotaxis protein CheY (EC 2.7.3.-) | SCE1572_3987 | yes | sce_3318 | yes |
| A and B | Motility and Chemotaxis | no subcategory | Bacterial Chemotaxis | Chemotaxis protein methyltransferase CheR (EC 2.1.1.80) | SCE1572_374 | yes | sce_206 | yes |
| A and B | Motility and Chemotaxis | no subcategory | Bacterial Chemotaxis | Chemotaxis regulator - transmits chemoreceptor signals to flagellar mot | SCE1572_1254 | yes | sce_904 | yes |
| A and B | Motility and Chemotaxis | no subcategory | Bacterial Chemotaxis | Chemotaxis response regulator protein-glutamate methyltransferase CheB | SCE1572_2235 | yes | sce_1783 | yes |
| A and B | Motility and Chemotaxis | no subcategory | Bacterial Chemotaxis | Dipeptide-binding ABC transporter, periplasmic substrate-binding comp | SCE1572_4504 | yes | sce_3765 | yes |
| A and B | Motility and Chemotaxis | no subcategory | Bacterial Chemotaxis | Maltose/maltodextrin ABC transporter, substrate binding periplasmic pr | SCE1572_6789 | yes | sce_5648 | yes |
| A and B | Motility and Chemotaxis | no subcategory | Bacterial Chemotaxis | Positive regulator of CheA protein activity (CheW) | SCE1572_2231 | yes | sce_1365 | yes |
| A and B | Motility and Chemotaxis | no subcategory | Bacterial Chemotaxis | Ribose ABC transporter, periplasmic ribose-binding protein RbsB (TC :SCE1572_7545 | | yes | sce_9213 | yes |
| A and B | Motility and Chemotaxis | no subcategory | Bacterial Chemotaxis | Signal transduction histidine kinase CheA (EC 2.7.3.-) | SCE1572_824 | yes | sce_871 | yes |
| A | Motility and Chemotaxis | no subcategory | Bacterial Chemotaxis | Galactose/methyl galactoside ABC transport system, D-galactose-bindin | SCE1572_213 | yes | | no |
| A | Motility and Chemotaxis | no subcategory | Bacterial Chemotaxis | Methyl-accepting chemotaxis protein I (serine chemoreceptor protein) | SCE1572_2800 | yes | | no |
| B | Motility and Chemotaxis | no subcategory | Bacterial Chemotaxis | Flagellar motor switch protein Flin | | no | sce_6182 | yes |
| A and B | Nitrogen Metabolism | no subcategory | Ammonia assimilation | Ammonium transporter family | SCE1572_3159 | yes | sce_2654 | yes |
| A and B | Nitrogen Metabolism | no subcategory | Ammonia assimilation | Ammonium transporter family | SCE1572_9483 | yes | sce_2670 | yes |
| A and B | Nitrogen Metabolism | no subcategory | Ammonia assimilation | Ammonia synthase [NADPH] large chain (EC 1.4.1.13) | SCE1572_6809 | yes | sce_8270 | yes |
| A and B | Nitrogen Metabolism | no subcategory | Ammonia assimilation | Glutamate synthase [NADPH] small chain (EC 1.4.1.13) | SCE1572_5230 | yes | sce_4385 | yes |
| A and B | Nitrogen Metabolism | no subcategory | Ammonia assimilation | Glutamate-ammonia-lyase adenylyltransferase (EC 2.7.7.42) | SCE1572_2412 | yes | sce_1966 | yes |
| A and B | Nitrogen Metabolism | no subcategory | Ammonia assimilation | Glutamine synthetase type I (EC 6.3.1.2) | SCE1572_9287 | yes | sce_8068 | yes |
| A and B | Nitrogen Metabolism | no subcategory | Ammonia assimilation | Nitrogen regulation protein NRI | SCE1572_429 | yes | sce_2532 | yes |
| A and B | Nitrogen Metabolism | no subcategory | Ammonia assimilation | Nitrogen regulatory protein P-II | SCE1572_9288 | yes | sce_8069 | yes |
| A and B | Nitrogen Metabolism | no subcategory | Ammonia assimilation | [Protein-Pil] uridylyltransferase (EC 2.7.7.59) | SCE1572_4206 | yes | sce_3524 | yes |
| A and B | Nitrogen Metabolism | no subcategory | Denitrification | Copper-containing nitrite reductase (EC 1.7.2.1) | SCE1572_4092 | yes | sce_3418 | yes |
| A and B | Nitrogen Metabolism | no subcategory | Denitrification | Nitric-oxide reductase (EC 1.7.99.7), quinol-dependent | SCE1572_1862 | yes | sce_3679 | yes |
| A and B | Nitrogen Metabolism | no subcategory | Denitrification | Nitrous oxide reductase maturation protein NosF (ATPase) | SCE1572_1950 | yes | sce_848 | yes |
| A and B | Nitrogen Metabolism | no subcategory | Nitrate and nitrite ammonification | Assimilatory nitrate reductase large subunit (EC:1.7.99.4) | SCE1572_4421 | yes | sce_1282 | yes |
| A and B | Nitrogen Metabolism | no subcategory | Nitrate and nitrite ammonification | Cytochrome c nitrite reductase, small subunit NrfH | SCE1572_2082 | yes | sce_1594 | yes |
| A and B | Nitrogen Metabolism | no subcategory | Nitrate and nitrite ammonification | Cytochrome c552 precursor (EC 1.7.2.2) | SCE1572_2081 | yes | sce_1593 | yes |
| A and B | Nitrogen Metabolism | no subcategory | Nitrate and nitrite ammonification | Nitrate ABC transporter, ATP-binding protein | SCE1572_5391 | yes | sce_4516 | yes |
| A and B | Nitrogen Metabolism | no subcategory | Nitrate and nitrite ammonification | Nitrate ABC transporter, nitrate-binding protein | SCE1572_5394 | yes | sce_4519 | yes |
| A and B | Nitrogen Metabolism | no subcategory | Nitrate and nitrite ammonification | Nitrate ABC transporter, permease protein | SCE1572_5393 | yes | sce_4518 | yes |
| A and B | Nitrogen Metabolism | no subcategory | Nitrate and nitrite ammonification | Nitrate/nitrite response regulator protein | SCE1572_7300 | yes | sce_3004 | yes |
| A and B | Nitrogen Metabolism | no subcategory | Nitrate and nitrite ammonification | Nitrate/nitrite transporter | SCE1572_4983 | yes | sce_3009 | yes |
| A and B | Nitrogen Metabolism | no subcategory | Nitrate and nitrite ammonification | Nitrite reductase [NAD(P)H] large subunit (EC 1.7.1.4) | SCE1572_4684 | yes | sce_1283 | yes |
| A and B | Nitrogen Metabolism | no subcategory | Nitrate and nitrite ammonification | Nitrite reductase [NAD(P)H] small subunit (EC 1.7.1.4) | SCE1572_10860 | yes | sce_9488 | yes |
| A and B | Nitrogen Metabolism | no subcategory | Nitric oxide synthase | Nitric oxide synthase oxygenase (EC 1.-.-.-) | SCE1572_2218 | yes | sce_1762 | yes |
| A and B | Nitrogen Metabolism | no subcategory | Nitric oxide synthase | putative cytochrome P450 hydroxylase | SCE1572_137 | yes | sce_133 | yes |
| A and B | Nitrogen Metabolism | no subcategory | Nitrosative stress | Anaerobic nitric oxide reductase transcription regulator NorR | SCE1572_1974 | yes | sce_608 | yes |
| A and B | Nitrogen Metabolism | no subcategory | Nitrosative stress | Hydroxylamine reductase (EC 1.7.-.-) | SCE1572_1192 | yes | sce_866 | yes |
| A and B | Nitrogen Metabolism | no subcategory | Nitrosative stress | Nitric-oxide reductase (EC 1.7.99.7), quinol-dependent | SCE1572_1862 | yes | sce_3679 | yes |
| A | Nitrogen Metabolism | no subcategory | Allantoin Utilization | 2-hydroxy-3-oxopropionate reductase (EC 1.1.1.60) | SCE1572_5693 | yes | | no |
| A | Nitrogen Metabolism | no subcategory | Allantoin Utilization | Allantoinase (EC 3.5.3.4) | SCE1572_7760 | yes | | no |
| A | Nitrogen Metabolism | no subcategory | Cyanate hydrolysis | Cyanate hydratase (EC 4.2.1.104) | SCE1572_2062 | yes | | no |
| A | Nitrogen Metabolism | no subcategory | Nitrate and nitrite ammonification | Nitrate transporter from formate/nitrite family | SCE1572_2834 | yes | | no |
| B | Nitrogen Metabolism | no subcategory | Nitrate and nitrite ammonification | Nitrate reductase cytochrome c550-type subunit | | no | sce_5256 | yes |
| B | Nitrogen Metabolism | no subcategory | Nitrate and nitrite ammonification | Periplasmic nitrate reductase precursor (EC 1.7.99.4) | | no | sce_5257 | yes |
| B | Nitrogen Metabolism | no subcategory | Nitrosative stress | Nitric oxide-dependent regulator DnrN or Nora | | no | sce_7685 | yes |
| A and B | Nucleosides and Nucleotides | Detoxification | Housecleaning nucleoside triphosphate pyrophosphatases | 5-nucleotidase SurE (EC 3.1.3.5) | SCE1572_4021 | yes | sce_3349 | yes |
| A and B | Nucleosides and Nucleotides | Detoxification | Housecleaning nucleoside triphosphate pyrophosphatases | Deoxyuridine 5'-triphosphate nucleotidohydrolase (EC 3.6.1.23) | SCE1572_4602 | yes | sce_3838 | yes |
| A and B | Nucleosides and Nucleotides | Detoxification | Housecleaning nucleoside triphosphate pyrophosphatases | Nucleoside 5-triphosphatase RdgB (dHAPTP, dTTP, XTP-specific) (EC:SCE1572_10103 | | yes | sce_8921 | yes |
| A and B | Nucleosides and Nucleotides | Detoxification | Nucleoside triphosphate pyrophosphohydrolase MazG | Nucleoside triphosphate pyrophosphohydrolase MazG | SCE1572_6339 | yes | sce_5373 | yes |
| A and B | Nucleosides and Nucleotides | Detoxification | Nudix proteins (nucleoside triphosphate hydrolases) | 5-methyl-dCTP pyrophosphohydrolase (EC 3.6.1.-) | SCE1572_10894 | yes | sce_9529 | yes |
| A and B | Nucleosides and Nucleotides | Detoxification | Nudix proteins (nucleoside triphosphate hydrolases) | ADP-ribose pyrophosphatase (EC 3.6.1.13) | SCE1572_3103 | yes | sce_2621 | yes |
| A and B | Nucleosides and Nucleotides | Detoxification | Nudix proteins (nucleoside triphosphate hydrolases) | Deoxyuridine 5'-triphosphate nucleotidohydrolase (EC 3.6.1.23) | SCE1572_4602 | yes | sce_3838 | yes |
| A and B | Nucleosides and Nucleotides | Detoxification | Nudix proteins (nucleoside triphosphate hydrolases) | Hypothetical nudix hydrolase YeaB | SCE1572_6253 | yes | sce_5265 | yes |
| A and B | Nucleosides and Nucleotides | Detoxification | Nudix proteins (nucleoside triphosphate hydrolases) | Nucleoside diphosphate kinase (7,8-dihydro-8-oxoguanine-triphosphatase) (EC :SCE1572_8608 | | yes | sce_2454 | yes |
| A and B | Nucleosides and Nucleotides | Detoxification | Nudix proteins (nucleoside triphosphate hydrolases) | NADH pyrophosphatase (EC 3.6.1.22) | SCE1572_1391 | yes | sce_4892 | yes |
| A and B | Nucleosides and Nucleotides | Detoxification | Nudix proteins (nucleoside triphosphate hydrolases) | NADH hydrolase family protein YihH | SCE1572_7287 | yes | sce_5990 | yes |
| A and B | Nucleosides and Nucleotides | Detoxification | Nudix proteins (nucleoside triphosphate hydrolases) | Putative Nudix hydrolase YfcD (EC 3.6.-.-) | SCE1572_3784 | yes | sce_3119 | yes |
| A and B | Nucleosides and Nucleotides | Purines | De Novo Purine Biosynthesis | Adenylosuccinate lyase (EC 4.3.2.2) | SCE1572_10661 | yes | sce_9266 | yes |
| A and B | Nucleosides and Nucleotides | Purines | De Novo Purine Biosynthesis | Amidophosphoribosyltransferase (EC 2.4.2.14) | SCE1572_5789 | yes | sce_4836 | yes |
| A and B | Nucleosides and Nucleotides | Purines | De Novo Purine Biosynthesis | IMP cyclohydrolase (EC 3.5.4.10) | SCE1572_4217 | yes | sce_3535 | yes |
| A and B | Nucleosides and Nucleotides | Purines | De Novo Purine Biosynthesis | Phosphoribosylamine-glycine lyase (EC 6.3.4.13) | SCE1572_11277 | yes | sce_10061 | yes |
| A and B | Nucleosides and Nucleotides | Purines | De Novo Purine Biosynthesis | Phosphoribosylaminoimidazole carboxylase ATPase subunit (EC 4.1.1.)SCE1572_2474 | | yes | sce_2015 | yes |
| A and B | Nucleosides and Nucleotides | Purines | De Novo Purine Biosynthesis | Phosphoribosylaminoimidazole carboxylase catalytic subunit (EC 4.1.1.)SCE1572_2473 | | yes | sce_2014 | yes |
| A and B | Nucleosides and Nucleotides | Purines | De Novo Purine Biosynthesis | Phosphoribosylaminoimidazole-succinocarboxamide synthase (EC 6.3.3.)SCE1572_1661 | | yes | sce_1176 | yes |
| A and B | Nucleosides and Nucleotides | Purines | De Novo Purine Biosynthesis | Phosphoribosylaminoimidazolecarboxamide formyltransferase (EC 2.1.)SCE1572_4217 | | yes | sce_3535 | yes |
| A and B | Nucleosides and Nucleotides | Purines | De Novo Purine Biosynthesis | Phosphoribosylformylglycinamide cyclo-lyase (EC 6.3.3.1) | SCE1572_10893 | yes | sce_9525 | yes |
| A and B | Nucleosides and Nucleotides | Purines | De Novo Purine Biosynthesis | Phosphoribosylformylglycinamide synthase, glutamine amidotransferase | SCE1572_9392 | yes | sce_264 | yes |
| A and B | Nucleosides and Nucleotides | Purines | De Novo Purine Biosynthesis | Phosphoribosylformylglycinamide synthase, synthetase subunit (EC 6.SCE1572_8608 | | yes | sce_2454 | yes |
| A and B | Nucleosides and Nucleotides | Purines | De Novo Purine Biosynthesis | Phosphoribosylglycinamide formyltransferase (EC 2.1.2.2) | SCE1572_10890 | yes | sce_9522 | yes |
| A and B | Nucleosides and Nucleotides | Purines | De Novo Purine Biosynthesis | Ribose-phosphate pyrophosphokinase (EC 2.7.6.1) | SCE1572_8154 | yes | sce_7319 | yes |
| A and B | Nucleosides and Nucleotides | Purines | GMP synthase | GMP synthase [glutamine-hydrolyzing], ATP pyrophosphatase subunit | SCE1572_4911 | yes | sce_4121 | yes |
| A and B | Nucleosides and Nucleotides | Purines | GMP synthase | GMP synthase [glutamine-hydrolyzing], amidotransferase subunit (EC :SCE1572_4911 | | yes | sce_4121 | yes |
| A and B | Nucleosides and Nucleotides | Purines | Purine Utilization | Cytosine/purine/uracil/thiamine/allantoin permease family protein | SCE1572_3449 | yes | sce_2941 | yes |
| A and B | Nucleosides and Nucleotides | Purines | Purine Utilization | Guanine deaminase (EC 3.5.4.3) | SCE1572_1709 | yes | sce_1223 | yes |
| A and B | Nucleosides and Nucleotides | Purines | Purine Utilization | Xanthine and CO dehydrogenases maturation factor, XdhC/CoxF fami | SCE1572_6273 | yes | sce_3740 | yes |
| A and B | Nucleosides and Nucleotides | Purines | Purine Utilization | Xanthine dehydrogenase, FAD binding subunit (EC 1.17.1.4) | SCE1572_7791 | yes | sce_ | |

| | | | | | | | | |
|---------|--|---------------------------|--|---|---------------|-----|-----------|-----|
| A and B | Nucleosides and Nucleotides | Pyrimidines | pyrimidine conversions | Thioredoxin reductase (EC 1.8.1.9) | SCE1572_1090 | yes | sce_2388 | yes |
| A and B | Nucleosides and Nucleotides | Pyrimidines | pyrimidine conversions | Thymidylate kinase (EC 2.7.4.9) | SCE1572_1302 | yes | sce_937 | yes |
| A and B | Nucleosides and Nucleotides | Pyrimidines | pyrimidine conversions | Uracil phosphoribosyltransferase (EC 2.4.2.9) | SCE1572_3269 | yes | sce_2764 | yes |
| A | Nucleosides and Nucleotides | Pyrimidines | Pyrimidine utilization | Predicted reductase RufeE in novel pyrimidine catabolism pathway | SCE1572_6620 | yes | no | no |
| A and B | Nucleosides and Nucleotides | no subcategory | Adenosyl nucleosidases | Purine nucleoside phosphorylase (EC 2.4.2.1) | SCE1572_7736 | yes | sce_6561 | yes |
| A and B | Nucleosides and Nucleotides | no subcategory | Hydantoin metabolism | Deacetylases, including yeast histone deacetylase and acetoin utilization | SCE1572_8232 | yes | sce_6902 | yes |
| A and B | Nucleosides and Nucleotides | no subcategory | Hydantoin metabolism | Dihydropyrimidinase (EC 3.5.2.2) | SCE1572_8401 | yes | sce_7161 | yes |
| A and B | Nucleosides and Nucleotides | no subcategory | Hydantoin metabolism | N-methylhydantoinase (ATP-hydrolyzing) (EC 3.5.2.14) | SCE1572_3451 | yes | sce_2943 | yes |
| A and B | Nucleosides and Nucleotides | no subcategory | Hydantoin metabolism | N-methylhydantoinase A (EC 3.5.2.14) | SCE1572_3453 | yes | sce_2945 | yes |
| A and B | Nucleosides and Nucleotides | no subcategory | Hydantoin metabolism | N-methylhydantoinase B (EC 3.5.2.14) | SCE1572_3452 | yes | sce_2944 | yes |
| A and B | Nucleosides and Nucleotides | no subcategory | Ribonucleotide reduction | Ribonucleotide reductase of class II (coenzyme B12-dependent) (EC 1. SCE1572_623 | SCE1572_623 | yes | sce_431 | yes |
| A and B | Nucleosides and Nucleotides | no subcategory | Ribonucleotide reduction | Ribonucleotide reductase of class Ia (aerobic), alpha subunit (EC 1.17.4.SCE1572_5170 | SCE1572_5170 | yes | sce_4336 | yes |
| A and B | Nucleosides and Nucleotides | no subcategory | Ribonucleotide reduction | Ribonucleotide reductase of class Ia (aerobic), beta subunit (EC 1.17.4.SCE1572_5171 | SCE1572_5171 | yes | sce_4337 | yes |
| A and B | Nucleosides and Nucleotides | no subcategory | Ribonucleotide reduction | Ribonucleotide reductase transcriptional regulator NrdR | SCE1572_5079 | yes | sce_4268 | yes |
| A and B | Phages, Prophages, Transposable ek Phages, Prophages | Phage tail fiber proteins | Phage tail fiber proteins | Phage tail fiber protein | SCE1572_3192 | yes | sce_2684 | yes |
| A | Phages, Prophages, Transposable ek Phages, Prophages | Phage tail fiber proteins | Phage tail fibers | Phage tail fiber protein | SCE1572_5948 | yes | no | no |
| A | Phages, Prophages, Transposable ek Phages, Prophages | Phage tail proteins | Phage minor tail protein | Phage minor tail protein | SCE1572_10420 | yes | no | no |
| B | Phages, Prophages, Transposable ek Phages, Prophages | Phage replication | DNA primase/helicase, phage-associated | DNA primase/helicase, phage-associated | SCE1572_247 | no | sce_4552 | yes |
| A and B | Phages, Prophages, Transposable ek Phages, Prophages | Integrations | Integron integrase IntPac | Integron integrase IntPac | SCE1572_247 | yes | sce_515 | yes |
| A and B | Phosphorus Metabolism | no subcategory | High affinity phosphate transporter and control of PHO regulon Phosphate ABC transporter, periplasmic phosphate-binding protein PhoA | Phosphate ABC transporter, periplasmic phosphate-binding protein PhoA | SCE1572_3980 | yes | sce_3309 | yes |
| A and B | Phosphorus Metabolism | no subcategory | High affinity phosphate transporter and control of PHO regulon Phosphate regulon sensor protein PhoR (SphS) (EC 2.7.13.3) | Phosphate regulon sensor protein PhoR (SphS) (EC 2.7.13.3) | SCE1572_783 | yes | sce_437 | yes |
| A and B | Phosphorus Metabolism | no subcategory | High affinity phosphate transporter and control of PHO regulon Phosphate regulon transcriptional regulatory protein PhoB (SphR) | Phosphate regulon transcriptional regulatory protein PhoB (SphR) | SCE1572_1238 | yes | sce_3311 | yes |
| A and B | Phosphorus Metabolism | no subcategory | High affinity phosphate transporter and control of PHO regulon Phosphate transport ATP-binding protein PstB (TC 3.A.1.7.1) | Phosphate transport ATP-binding protein PstB (TC 3.A.1.7.1) | SCE1572_3977 | yes | sce_3306 | yes |
| A and B | Phosphorus Metabolism | no subcategory | High affinity phosphate transporter and control of PHO regulon Phosphate transport system permease protein PstA (TC 3.A.1.7.1) | Phosphate transport system permease protein PstA (TC 3.A.1.7.1) | SCE1572_3978 | yes | sce_3307 | yes |
| A and B | Phosphorus Metabolism | no subcategory | High affinity phosphate transporter and control of PHO regulon Phosphate transport system permease protein PstC (TC 3.A.1.7.1) | Phosphate transport system permease protein PstC (TC 3.A.1.7.1) | SCE1572_3979 | yes | sce_3308 | yes |
| A and B | Phosphorus Metabolism | no subcategory | High affinity phosphate transporter and control of PHO regulon Phosphate transport system regulatory protein PhoU | Phosphate transport system regulatory protein PhoU | SCE1572_3976 | yes | sce_3305 | yes |
| A and B | Phosphorus Metabolism | no subcategory | High affinity phosphate transporter and control of PHO regulon Polyphosphate kinase (EC 2.7.4.1) | Polyphosphate kinase (EC 2.7.4.1) | SCE1572_1304 | yes | sce_939 | yes |
| A and B | Phosphorus Metabolism | no subcategory | Phosphate metabolism | Inorganic pyrophosphatase (EC 3.6.1.1) | SCE1572_1440 | yes | sce_6323 | yes |
| A and B | Phosphorus Metabolism | no subcategory | Phosphate metabolism | Phosphatase, Ppx/GppA family | SCE1572_2348 | yes | sce_1898 | yes |
| A and B | Phosphorus Metabolism | no subcategory | Phosphate metabolism | Phosphate ABC transporter, periplasmic phosphate-binding protein PstA | SCE1572_3980 | yes | sce_3309 | yes |
| A and B | Phosphorus Metabolism | no subcategory | Phosphate metabolism | Phosphate regulon sensor protein PhoR (SphS) (EC 2.7.13.3) | SCE1572_783 | yes | sce_437 | yes |
| A and B | Phosphorus Metabolism | no subcategory | Phosphate metabolism | Phosphate regulon transcriptional regulatory protein PhoB (SphR) | SCE1572_1238 | yes | sce_3311 | yes |
| A and B | Phosphorus Metabolism | no subcategory | Phosphate metabolism | Phosphate starvation-inducible regulatory protein PhoH, predicted ATPase | SCE1572_1090 | yes | sce_8907 | yes |
| A and B | Phosphorus Metabolism | no subcategory | Phosphate metabolism | Phosphate transport ATP-binding protein PstB (TC 3.A.1.7.1) | SCE1572_3977 | yes | sce_3306 | yes |
| A and B | Phosphorus Metabolism | no subcategory | Phosphate metabolism | Phosphate transport regulator (distant homolog of PhoU) | SCE1572_4593 | yes | sce_3732 | yes |
| A and B | Phosphorus Metabolism | no subcategory | Phosphate metabolism | Phosphate transport system permease protein PstA (TC 3.A.1.7.1) | SCE1572_3978 | yes | sce_3307 | yes |
| A and B | Phosphorus Metabolism | no subcategory | Phosphate metabolism | Phosphate transport system permease protein PstC (TC 3.A.1.7.1) | SCE1572_3979 | yes | sce_3308 | yes |
| A and B | Phosphorus Metabolism | no subcategory | Phosphate metabolism | Phosphate transport system regulatory protein PhoU | SCE1572_3976 | yes | sce_3305 | yes |
| A and B | Phosphorus Metabolism | no subcategory | Phosphate metabolism | Polyphosphate kinase (EC 2.7.4.1) | SCE1572_1304 | yes | sce_939 | yes |
| A and B | Phosphorus Metabolism | no subcategory | Phosphate metabolism | Predicted ATPase related to phosphate starvation-inducible protein Pho | SCE1572_3906 | yes | sce_3235 | yes |
| A and B | Phosphorus Metabolism | no subcategory | Phosphate metabolism | Probable low-affinity inorganic phosphate transporter | SCE1572_4594 | yes | sce_3731 | yes |
| A and B | Phosphorus Metabolism | no subcategory | Phosphate metabolism | Pyrophosphate-energized proton pump (EC 3.6.1.1) | SCE1572_1526 | yes | sce_1048 | yes |
| A and B | Phosphorus Metabolism | no subcategory | Phosphate metabolism | Soluble pyridine nucleotide transhydrogenase (EC 1.6.1.1) | SCE1572_2691 | yes | sce_2231 | yes |
| A and B | Phosphorus Metabolism | no subcategory | Polyphosphate | Polyphosphate glucokinase (EC 2.7.1.63) | SCE1572_1006 | yes | sce_759 | yes |
| A and B | Phosphorus Metabolism | no subcategory | Polyphosphate | Polyphosphate kinase (EC 2.7.4.1) | SCE1572_1304 | yes | sce_939 | yes |
| B | Phosphorus Metabolism | no subcategory | Phosphate metabolism | Exopolyphosphatase (EC 3.6.1.11) | SCE1572_1238 | no | sce_6277 | yes |
| A and B | Potassium metabolism | no subcategory | Potassium homeostasis | FKBP-type peptidyl-prolyl cis-trans isomerase SlyD (EC 5.2.1.8) | SCE1572_9203 | yes | sce_8083 | yes |
| A and B | Potassium metabolism | no subcategory | Potassium homeostasis | Guanidium-regulated potassium-efflux system protein KefC | SCE1572_7336 | yes | sce_6121 | yes |
| A and B | Potassium metabolism | no subcategory | Potassium homeostasis | Kup system potassium uptake protein | SCE1572_2381 | yes | sce_1932 | yes |
| A and B | Potassium metabolism | no subcategory | Potassium homeostasis | Large-conductance mechanosensitive channel | SCE1572_9051 | yes | sce_7812 | yes |
| A and B | Potassium metabolism | no subcategory | Potassium homeostasis | Osmosensitive K channel histidine kinase KdpD (EC 2.7.3.-) | SCE1572_497 | yes | sce_1499 | yes |
| A and B | Potassium metabolism | no subcategory | Potassium homeostasis | Potassium efflux system KefA protein | SCE1572_3426 | yes | sce_1600 | yes |
| A and B | Potassium metabolism | no subcategory | Potassium homeostasis | Potassium-transporting ATPase A chain (EC 3.6.3.12) (TC 3.A.3.7.1) | SCE1572_2016 | yes | sce_1496 | yes |
| A and B | Potassium metabolism | no subcategory | Potassium homeostasis | Potassium-transporting ATPase B chain (EC 3.6.3.12) (TC 3.A.3.7.1) | SCE1572_2017 | yes | sce_1497 | yes |
| A and B | Potassium metabolism | no subcategory | Potassium homeostasis | Potassium-transporting ATPase C chain (EC 3.6.3.12) (TC 3.A.3.7.1) | SCE1572_2018 | yes | sce_1498 | yes |
| A and B | Potassium metabolism | no subcategory | Potassium homeostasis | Trk system potassium uptake protein TrkA | SCE1572_4368 | yes | sce_3654 | yes |
| B | Potassium metabolism | no subcategory | Hyperosmotic potassium uptake | Potassium uptake protein TrkH | SCE1572_4368 | no | sce_3655 | yes |
| A and B | Protein biosynthesis | Protein biosynthesis | Programmed frameshift | Peptide chain release factor 2 | SCE1572_2275 | yes | sce_1820 | yes |
| A and B | Protein Metabolism | Protein biosynthesis | Ribosome LSU bacterial | LSU ribosomal protein L10p (P0) | SCE1572_657 | yes | sce_463 | yes |
| A and B | Protein Metabolism | Protein biosynthesis | Ribosome LSU bacterial | Ribosome LSU bacterial | SCE1572_657 | yes | sce_461 | yes |
| A and B | Protein Metabolism | Protein biosynthesis | Ribosome LSU bacterial | LSU ribosomal protein L13p (L13Ae) | SCE1572_9499 | yes | sce_8285 | yes |
| A and B | Protein Metabolism | Protein biosynthesis | Ribosome LSU bacterial | LSU ribosomal protein L14p (L23e) | SCE1572_10077 | yes | sce_8904 | yes |
| A and B | Protein Metabolism | Protein biosynthesis | Ribosome LSU bacterial | LSU ribosomal protein L15p (L27Ae) | SCE1572_10068 | yes | sce_8885 | yes |
| A and B | Protein Metabolism | Protein biosynthesis | Ribosome LSU bacterial | LSU ribosomal protein L16p (L10e) | SCE1572_10080 | yes | sce_8897 | yes |
| A and B | Protein Metabolism | Protein biosynthesis | Ribosome LSU bacterial | LSU ribosomal protein L17p | SCE1572_10058 | yes | sce_8875 | yes |
| A and B | Protein Metabolism | Protein biosynthesis | Ribosome LSU bacterial | LSU ribosomal protein L18p (L5e) | SCE1572_10071 | yes | sce_8888 | yes |
| A and B | Protein Metabolism | Protein biosynthesis | Ribosome LSU bacterial | LSU ribosomal protein L19p | SCE1572_3327 | yes | sce_2822 | yes |
| A and B | Protein Metabolism | Protein biosynthesis | Ribosome LSU bacterial | LSU ribosomal protein L1p (L10Ae) | SCE1572_656 | yes | sce_462 | yes |
| A and B | Protein Metabolism | Protein biosynthesis | Ribosome LSU bacterial | LSU ribosomal protein L20p | SCE1572_9326 | yes | sce_8106 | yes |
| A and B | Protein Metabolism | Protein biosynthesis | Ribosome LSU bacterial | LSU ribosomal protein L21p | SCE1572_10045 | yes | sce_8861 | yes |
| A and B | Protein Metabolism | Protein biosynthesis | Ribosome LSU bacterial | LSU ribosomal protein L22p (L17e) | SCE1572_10082 | yes | sce_8899 | yes |
| A and B | Protein Metabolism | Protein biosynthesis | Ribosome LSU bacterial | LSU ribosomal protein L23p (L23Ae) | SCE1572_1312 | yes | sce_948 | yes |
| A and B | Protein Metabolism | Protein biosynthesis | Ribosome LSU bacterial | LSU ribosomal protein L24p (L26e) | SCE1572_10076 | yes | sce_8893 | yes |
| A and B | Protein Metabolism | Protein biosynthesis | Ribosome LSU bacterial | LSU ribosomal protein L25p | SCE1572_8999 | yes | sce_7764 | yes |
| A and B | Protein Metabolism | Protein biosynthesis | Ribosome LSU bacterial | LSU ribosomal protein L27p | SCE1572_10044 | yes | sce_8860 | yes |
| A and B | Protein Metabolism | Protein biosynthesis | Ribosome LSU bacterial | LSU ribosomal protein L28p | SCE1572_6001 | yes | sce_6053 | yes |
| A and B | Protein Metabolism | Protein biosynthesis | Ribosome LSU bacterial | LSU ribosomal protein L29p (L35e) | SCE1572_10079 | yes | sce_8896 | yes |
| A and B | Protein Metabolism | Protein biosynthesis | Ribosome LSU bacterial | LSU ribosomal protein L2p (L8e) | SCE1572_1313 | yes | sce_949 | yes |
| A and B | Protein Metabolism | Protein biosynthesis | Ribosome LSU bacterial | LSU ribosomal protein L30p (L7e) | SCE1572_10069 | yes | sce_8886 | yes |
| A and B | Protein Metabolism | Protein biosynthesis | Ribosome LSU bacterial | LSU ribosomal protein L31p | SCE1572_11291 | yes | sce_10074 | yes |
| A and B | Protein Metabolism | Protein biosynthesis | Ribosome LSU bacterial | LSU ribosomal protein L32p | SCE1572_5086 | yes | sce_4274 | yes |
| A and B | Protein Metabolism | Protein biosynthesis | Ribosome LSU bacterial | LSU ribosomal protein L33p | SCE1572_651 | yes | sce_458 | yes |
| A and B | Protein Metabolism | Protein biosynthesis | Ribosome LSU bacterial | LSU ribosomal protein L34p | SCE1572_3332 | yes | sce_2828 | yes |
| A and B | Protein Metabolism | Protein biosynthesis | Ribosome LSU bacterial | LSU ribosomal protein L35p | SCE1572_9327 | yes | sce_8107 | yes |
| A and B | Protein Metabolism | Protein biosynthesis | Ribosome LSU bacterial | LSU ribosomal protein L36p | SCE1572_10064 | yes | sce_8881 | yes |
| A and B | Protein Metabolism | Protein biosynthesis | Ribosome LSU bacterial | LSU ribosomal protein L3p (L3e) | SCE1572_2664 | yes | sce_2216 | yes |
| A and B | Protein Metabolism | Protein biosynthesis | Ribosome LSU bacterial | LSU ribosomal protein L4p (L1e) | SCE1572_1311 | yes | sce_947 | yes |
| A and B | Protein Metabolism | Protein biosynthesis | Ribosome LSU bacterial | LSU ribosomal protein L5p (L11e) | SCE1572_10075 | yes | sce_8892 | yes |
| A and B | Protein Metabolism | Protein biosynthesis | Ribosome LSU bacterial | LSU ribosomal protein L6p (L12e) | SCE1572_10072 | yes | sce_8889 | yes |
| A and B | Protein Metabolism | Protein biosynthesis | Ribosome LSU bacterial | LSU ribosomal protein L7L12 (P1-P2) | SCE1572_658 | yes | sce_464 | yes |
| A and B | Protein Metabolism | Protein biosynthesis | Ribosome LSU bacterial | LSU ribosomal protein L9p | SCE1572_9003 | yes | sce_7768 | yes |
| A and B | Protein Metabolism | Protein biosynthesis | Ribosome SSU bacterial | SSU ribosomal protein S10p (S20e) | SCE1572_1310 | yes | sce_946 | yes |
| A and B | Protein Metabolism | Protein biosynthesis | Ribosome SSU bacterial | SSU ribosomal protein S11p (S14e) | SCE1572_10062 | yes | sce_8879 | yes |
| A and B | Protein Metabolism | Protein biosynthesis | Ribosome SSU bacterial | SSU ribosomal protein S12p (S23e) | SCE1572_1306 | yes | sce_942 | yes |
| A and B | Protein Metabolism | Protein biosynthesis | Ribosome SSU bacterial | SSU ribosomal protein S13p (S18e) | SCE1572_10063 | yes | sce_8880 | yes |
| A and B | Protein Metabolism | Protein biosynthesis | Ribosome SSU bacterial | SSU ribosomal protein S14p (S29e) | SCE1572_10074 | yes | sce_8891 | yes |
| A and B | Protein Metabolism | Protein biosynthesis | Ribosome SSU bacterial | SSU ribosomal protein S15p (S13e) | SCE1572_6131 | yes | sce_5076 | yes |
| A and B | Protein Metabolism | Protein biosynthesis | Ribosome SSU bacterial | SSU ribosomal protein S16p | SCE1572_6010 | yes | sce_4961 | yes |
| A and B | Protein Metabolism | Protein biosynthesis | Ribosome SSU bacterial | SSU ribosomal protein S17p (S11e) | SCE1572_10078 | yes | sce_8895 | yes |
| A and B | Protein Metabolism | Protein biosynthesis | Ribosome SSU bacterial | SSU ribosomal protein S18p | SCE1572_9002 | yes | sce_7767 | yes |
| A and B | Protein Metabolism | Protein biosynthesis | Ribosome SSU bacterial | SSU ribosomal protein S19p (S15e) | SCE1572_1314 | yes | sce_950 | yes |
| A and B | Protein Metabolism | Protein biosynthesis | Ribosome SSU bacterial | SSU ribosomal protein S1p | SCE1572_4258 | yes | sce_3559 | yes |
| A and B | Protein Metabolism | Protein biosynthesis | Ribosome SSU bacterial | SSU ribosomal protein S20p | SCE1572_10075 | yes | sce_8896 | yes |
| A and B | Protein Metabolism | Protein biosynthesis | Ribosome SSU bacterial | SSU ribosomal protein S21p | SCE1572_2397 | yes | sce_1951 | yes |
| A and B | Protein Metabolism | Protein biosynthesis | Ribosome SSU bacterial | SSU ribosomal protein S2p (SAe) | SCE1572_4193 | yes | sce_3515 | yes |
| A and B | Protein Metabolism | Protein biosynthesis | Ribosome SSU bacterial | SSU ribosomal protein S3p (S3e) | SCE1572_10081 | yes | sce_8898 | yes |
| A and B | Protein Metabolism | Protein biosynthesis | Ribosome SSU bacterial | SSU ribosomal protein S4p (S9e) | SCE1572_4119 | yes | sce_3469 | yes |
| A and B | Protein Metabolism | Protein biosynthesis | Ribosome SSU bacterial | SSU ribosomal protein S5p (S2e) | SCE1572_10070 | yes | sce_8887 | yes |
| A and B | Protein Metabolism | Protein biosynthesis | Ribosome SSU bacterial | SSU ribosomal protein S6p | SCE1572_9001 | yes | sce_282 | yes |
| A and B | Protein Metabolism | Protein biosynthesis | Ribosome SSU bacterial | SSU ribosomal protein S7p (S5e) | SCE1572_1307 | yes | sce_943 | yes |
| A and B | Protein Metabolism | Protein biosynthesis | Ribosome SSU bacterial | SSU ribosomal protein S8p (S15Ae) | SCE1572_10073 | yes | sce_8890 | yes |
| A and B | Protein Metabolism | Protein biosynthesis | Ribosome SSU bacterial | SSU ribosomal protein S9p (S16e) | SCE1572_9498 | yes | sce_8284 | yes |
| A and B | Protein Metabolism | Protein biosynthesis | Ribosome activity modulation | Ribosomal subunit interface protein | SCE1572_7599 | yes | sce_6458 | yes |
| A and B | Protein Metabolism | Protein biosynthesis | Ribosome biogenesis bacterial | 16S rRNA processing protein RimM | SCE1572_6008 | yes | sce_4959 | yes |
| A and B | Protein Metabolism | Protein biosynthesis | Ribosome biogenesis bacterial | Dimethyladenosine transferase (EC 2.1.1.1.-) | SCE1572_6014 | yes | sce_4966 | yes |
| A and B | Protein Metabolism | Protein biosynthesis | Ribosome biogenesis bacterial | Inactive homolog of metal-dependent proteases, putative molecular chaperone | SCE1572_2318 | yes | sce_1865 | yes |
| A and B | Protein Metabolism | Protein biosynthesis | Ribosome biogenesis bacterial | LSU mSCL92 methyltransferase RimD | SCE1572_24 | yes | sce_25 | yes |
| A and B | Protein Metabolism | Protein biosynthesis | Ribosome biogenesis bacterial | Ribosome E (EC 3.1.26.12) | SCE1572_8450 | yes | sce_59 | yes |
| A and B | Protein Metabolism | Protein biosynthesis | Ribosome biogenesis bacterial | Ribosomal large subunit pseudouridine synthase D (EC 4.2.1.70) | SCE1572_11 | yes | sce_11 | yes |
| A and B | Protein Metabolism | Protein biosynthesis | Ribosome biogenesis bacterial | Ribosomal protein L11 methyltransferase (EC 2.1.1.-) | SCE1572_9145 | yes | sce_4521 | yes |
| A and B | Protein Metabolism | Protein biosynthesis | Ribosome biogenesis bacterial | Ribosomal protein S6 glutaminyl transferase | SCE1572_8970 | yes | sce_7731 | yes |
| A and B | Protein Metabolism | Protein biosynthesis | Ribosome biogenesis bacterial | Ribosomal-protein-L7p-serine acetyltransferase | SCE1572_1813 | yes | sce_1271 | yes |
| A and B | Protein Metabolism | Protein biosynthesis | Ribosome biogenesis bacterial | Ribosomal-protein-S18p-alanine acetyltransferase (EC 2.3.1.-) | SCE1572_7710 | yes | sce_6542 | yes |
| A and B | Protein Metabolism | Protein biosynthesis | Ribosome biogenesis bacterial | Ribosomal-protein-S5p-alanine acetyltransferase | SCE1572_665 | yes | sce_470 | yes |
| A and B | Protein Metabolism | Protein biosynthesis | Ribosome biogenesis bacterial | tRNA (Guanine37-N | | | | |

| | | | | | | | | |
|---------|--------------------|-------------------------------------|---|---|---------------|-----|-----------|-----|
| A and B | Protein Metabolism | Protein biosynthesis | IRNA aminoacylation, Asp and Asn | Asparaginyl-tRNA synthetase (EC 6.1.1.22) | SCE1572_7819 | yes | sce_6622 | yes |
| A and B | Protein Metabolism | Protein biosynthesis | IRNA aminoacylation, Asp and Asn | Asparaginyl-tRNA synthetase (EC 6.1.1.12) | SCE1572_10640 | yes | sce_9245 | yes |
| A and B | Protein Metabolism | Protein biosynthesis | IRNA aminoacylation, Asp and Asn | Asparaginyl-tRNA synthetase (EC 6.1.1.12) | SCE1572_2395 | yes | sce_127 | yes |
| A and B | Protein Metabolism | Protein biosynthesis | IRNA aminoacylation, Asp and Asn | Asparaginyl-tRNA synthetase (EC 6.1.1.12) | SCE1572_799 | yes | sce_592 | yes |
| A and B | Protein Metabolism | Protein biosynthesis | IRNA aminoacylation, Asp and Asn | Asparaginyl-tRNA synthetase (EC 6.1.1.12) | SCE1572_5745 | yes | sce_4795 | yes |
| A and B | Protein Metabolism | Protein biosynthesis | IRNA aminoacylation, Cys | Cysteinylyl-tRNA synthetase (EC 6.1.1.16) | SCE1572_7237 | yes | sce_693 | yes |
| A and B | Protein Metabolism | Protein biosynthesis | IRNA aminoacylation, Glu and Gln | Glutaminylyl-tRNA synthetase (EC 6.1.1.18) | SCE1572_11041 | yes | sce_9753 | yes |
| A and B | Protein Metabolism | Protein biosynthesis | IRNA aminoacylation, Glu and Gln | Glutaminylyl-tRNA synthetase (EC 6.1.1.17) | SCE1572_871 | yes | sce_646 | yes |
| A and B | Protein Metabolism | Protein biosynthesis | IRNA aminoacylation, Glu and Gln | Glutaminylyl-tRNA synthetase (EC 6.1.1.17) | SCE1572_2395 | yes | sce_127 | yes |
| A and B | Protein Metabolism | Protein biosynthesis | IRNA aminoacylation, Glu and Gln | Glutaminylyl-tRNA synthetase (EC 6.1.1.17) | SCE1572_799 | yes | sce_592 | yes |
| A and B | Protein Metabolism | Protein biosynthesis | IRNA aminoacylation, Glu and Gln | Glutaminylyl-tRNA synthetase (EC 6.1.1.17) | SCE1572_5745 | yes | sce_4795 | yes |
| A and B | Protein Metabolism | Protein biosynthesis | IRNA aminoacylation, Glu and Gln | Glutaminylyl-tRNA synthetase (EC 6.1.1.24) | SCE1572_871 | yes | sce_646 | yes |
| A and B | Protein Metabolism | Protein biosynthesis | IRNA aminoacylation, Gly | Glycyl-tRNA synthetase alpha chain (EC 6.1.1.14) | SCE1572_707 | yes | sce_504 | yes |
| A and B | Protein Metabolism | Protein biosynthesis | IRNA aminoacylation, Gly | Glycyl-tRNA synthetase beta chain (EC 6.1.1.14) | SCE1572_9746 | yes | sce_8547 | yes |
| A and B | Protein Metabolism | Protein biosynthesis | IRNA aminoacylation, His | Histidyl-tRNA synthetase (EC 6.1.1.21) | SCE1572_6135 | yes | sce_5079 | yes |
| A and B | Protein Metabolism | Protein biosynthesis | IRNA aminoacylation, Ile | Isoleucyl-tRNA synthetase (EC 6.1.1.5) | SCE1572_5697 | yes | sce_4750 | yes |
| A and B | Protein Metabolism | Protein biosynthesis | IRNA aminoacylation, Leu | Leucyl-tRNA synthetase (EC 6.1.1.4) | SCE1572_9512 | yes | sce_8299 | yes |
| A and B | Protein Metabolism | Protein biosynthesis | IRNA aminoacylation, Lys | Lysyl-tRNA synthetase (class II) (EC 6.1.1.6) | SCE1572_2276 | yes | sce_1821 | yes |
| A and B | Protein Metabolism | Protein biosynthesis | IRNA aminoacylation, Met | Methionyl-tRNA synthetase (EC 6.1.1.10) | SCE1572_155 | yes | sce_140 | yes |
| A and B | Protein Metabolism | Protein biosynthesis | IRNA aminoacylation, Phe | Phenylalanyl-tRNA synthetase alpha chain (EC 6.1.1.20) | SCE1572_4544 | yes | sce_3798 | yes |
| A and B | Protein Metabolism | Protein biosynthesis | IRNA aminoacylation, Phe | Phenylalanyl-tRNA synthetase beta chain (EC 6.1.1.20) | SCE1572_4543 | yes | sce_3797 | yes |
| A and B | Protein Metabolism | Protein biosynthesis | IRNA aminoacylation, Pro | Prolyl-tRNA synthetase (EC 6.1.1.15), archaeal/eukaryal type | SCE1572_5018 | yes | sce_4220 | yes |
| A and B | Protein Metabolism | Protein biosynthesis | IRNA aminoacylation, Ser | Archaeal seryl-tRNA synthetase-related sequence | SCE1572_8625 | yes | sce_7347 | yes |
| A and B | Protein Metabolism | Protein biosynthesis | IRNA aminoacylation, Ser | Seryl-tRNA synthetase (EC 6.1.1.11) | SCE1572_10462 | yes | sce_9101 | yes |
| A and B | Protein Metabolism | Protein biosynthesis | IRNA aminoacylation, Thr | Threonyl-tRNA synthetase (EC 6.1.1.3) | SCE1572_6059 | yes | sce_4871 | yes |
| A and B | Protein Metabolism | Protein biosynthesis | IRNA aminoacylation, Trp | Tryptophanyl-tRNA synthetase (EC 6.1.1.2) | SCE1572_8267 | yes | sce_8274 | yes |
| A and B | Protein Metabolism | Protein biosynthesis | IRNA aminoacylation, Val | Valyl-tRNA synthetase (EC 6.1.1.9) | SCE1572_6241 | yes | sce_5752 | yes |
| A and B | Protein Metabolism | Protein biosynthesis | IRNAs | tRNA-Ala-CGC | SCE1572_ma.3 | yes | sce_ma.3 | yes |
| A and B | Protein Metabolism | Protein biosynthesis | IRNAs | tRNA-Ala-GGC | SCE1572_ma.60 | yes | sce_ma.60 | yes |
| A and B | Protein Metabolism | Protein biosynthesis | IRNAs | tRNA-Arg-ACG | SCE1572_ma.29 | yes | sce_ma.29 | yes |
| A and B | Protein Metabolism | Protein biosynthesis | IRNAs | tRNA-Arg-CCG | SCE1572_ma.13 | yes | sce_ma.13 | yes |
| A and B | Protein Metabolism | Protein biosynthesis | IRNAs | tRNA-Cys-GCA | SCE1572_ma.2 | yes | sce_ma.2 | yes |
| A and B | Protein Metabolism | Protein biosynthesis | IRNAs | tRNA-Cys-GCC | SCE1572_ma.38 | yes | sce_ma.38 | yes |
| A and B | Protein Metabolism | Protein biosynthesis | IRNAs | tRNA-Gly-CCC | SCE1572_ma.37 | yes | sce_ma.37 | yes |
| A and B | Protein Metabolism | Protein biosynthesis | IRNAs | tRNA-Leu-CAA | SCE1572_ma.20 | yes | sce_ma.20 | yes |
| A and B | Protein Metabolism | Protein biosynthesis | IRNAs | tRNA-Leu-CAG | SCE1572_ma.43 | yes | sce_ma.43 | yes |
| A and B | Protein Metabolism | Protein biosynthesis | IRNAs | tRNA-Leu-GAG | SCE1572_ma.48 | yes | sce_ma.48 | yes |
| A and B | Protein Metabolism | Protein biosynthesis | IRNAs | tRNA-Phe-GAA | SCE1572_ma.19 | yes | sce_ma.19 | yes |
| A and B | Protein Metabolism | Protein biosynthesis | IRNAs | tRNA-Pro-CGG | SCE1572_ma.11 | yes | sce_ma.11 | yes |
| A and B | Protein Metabolism | Protein biosynthesis | IRNAs | tRNA-Pro-GGG | SCE1572_ma.14 | yes | sce_ma.14 | yes |
| A and B | Protein Metabolism | Protein biosynthesis | IRNAs | tRNA-Ser-CGA | SCE1572_ma.62 | yes | sce_ma.62 | yes |
| A and B | Protein Metabolism | Protein biosynthesis | IRNAs | tRNA-Ser-GGA | SCE1572_ma.61 | yes | sce_ma.61 | yes |
| A and B | Protein Metabolism | Protein biosynthesis | IRNAs | tRNA-Trp-CCA | SCE1572_ma.8 | yes | sce_ma.8 | yes |
| A and B | Protein Metabolism | Protein biosynthesis | IRNAs | tRNA-Val-CAC | SCE1572_ma.44 | yes | sce_ma.44 | yes |
| A and B | Protein Metabolism | Protein biosynthesis | IRNAs | tRNA-Val-GAC | SCE1572_ma.45 | yes | sce_ma.45 | yes |
| B | Protein Metabolism | Protein biosynthesis | IRNA aminoacylation, Tyr | Tyrosyl-tRNA synthetase (EC 6.1.1.1) | SCE1572_2080 | no | sce_572 | yes |
| A and B | Protein Metabolism | Protein degradation | Aminopeptidases (EC 3.4.11.-) | Aminopeptidase Y (Arg, Lys, Leu preference) (EC 3.4.11.15) | SCE1572_3407 | yes | sce_1592 | yes |
| A and B | Protein Metabolism | Protein degradation | Aminopeptidases (EC 3.4.11.-) | Cytosolic aminopeptidase PcpA (EC 3.4.11.1) | SCE1572_3033 | yes | sce_2894 | yes |
| A and B | Protein Metabolism | Protein degradation | Aminopeptidases (EC 3.4.11.-) | Membrane alanine aminopeptidase N (EC 3.4.11.2) | SCE1572_10969 | yes | sce_2602 | yes |
| A and B | Protein Metabolism | Protein degradation | Aminopeptidases (EC 3.4.11.-) | Xaa-Pro aminopeptidase (EC 3.4.11.9) | SCE1572_330 | yes | sce_9683 | yes |
| A and B | Protein Metabolism | Protein degradation | Metalloproteases (EC 3.4.17.-) | D-alanyl-D-alanine carboxypeptidase (EC 3.4.16.4) | SCE1572_5722 | yes | sce_4328 | yes |
| A and B | Protein Metabolism | Protein degradation | Metalloproteases (EC 3.4.17.-) | Muramoyltetrapeptide carboxypeptidase (EC 3.4.17.13) | SCE1572_5019 | yes | sce_4775 | yes |
| A and B | Protein Metabolism | Protein degradation | Omega peptidases (EC 3.4.19.-) | Isospartyl aminopeptidase (EC 3.4.19.5) | SCE1572_5019 | yes | sce_4221 | yes |
| A and B | Protein Metabolism | Protein degradation | Protein degradation | Asp-X dipeptidase | SCE1572_7629 | yes | sce_4221 | yes |
| A and B | Protein Metabolism | Protein degradation | Protein degradation | Leucylphenylalanyl-tRNA-protein transferase (EC 2.3.2.6) | SCE1572_9044 | yes | sce_6489 | yes |
| A and B | Protein Metabolism | Protein degradation | Protein degradation | Oligopeptidase A (EC 3.4.24.70) | SCE1572_6034 | yes | sce_7805 | yes |
| A and B | Protein Metabolism | Protein degradation | Protein degradation | Thimet oligopeptidase (EC 3.4.24.15) | SCE1572_571 | yes | sce_4987 | yes |
| A and B | Protein Metabolism | Protein degradation | Protein degradation | ATP-dependent Clp protease ATP-binding subunit ClpA | SCE1572_4215 | yes | sce_373 | yes |
| A and B | Protein Metabolism | Protein degradation | Protein degradation | ATP-dependent Clp protease ATP-binding subunit ClpX | SCE1572_5907 | yes | sce_3533 | yes |
| A and B | Protein Metabolism | Protein degradation | Protein degradation | ATP-dependent Clp protease adaptor protein ClpS | SCE1572_4213 | yes | sce_836 | yes |
| A and B | Protein Metabolism | Protein degradation | Protein degradation | ATP-dependent Clp protease proteolytic subunit (EC 3.4.21.92) | SCE1572_1411 | yes | sce_2489 | yes |
| A and B | Protein Metabolism | Protein degradation | Protein degradation | ATP-dependent protease La (EC 3.4.21.53) Type I | SCE1572_10444 | yes | sce_1008 | yes |
| A and B | Protein Metabolism | Protein degradation | Protein degradation | ATP-dependent protease La (EC 3.4.21.53) Type II | SCE1572_6714 | yes | sce_9085 | yes |
| A and B | Protein Metabolism | Protein degradation | Protein degradation | ClpB protein | SCE1572_8457 | yes | sce_5586 | yes |
| A and B | Protein Metabolism | Protein degradation | Protein degradation | TiD protein, part of proposed TlE/TlD proteolytic complex (PMID 1572_2722) | SCE1572_2722 | yes | sce_7217 | yes |
| A and B | Protein Metabolism | Protein degradation | Protein degradation | TlE-TlD protein, part of proposed TlE/TlD proteolytic complex (PMID 1572_1165) | SCE1572_1165 | yes | sce_2260 | yes |
| A and B | Protein Metabolism | Protein degradation | Protein degradation | Serine endopeptidase (EC 3.4.21.-) | SCE1572_5228 | yes | sce_856 | yes |
| A | Protein Metabolism | Protein degradation | Protein degradation | Arginine-tRNA-protein transferase (EC 2.3.2.8) | SCE1572_3786 | yes | sce_10315 | no |
| B | Protein Metabolism | Protein folding | Serine endopeptidase (EC 3.4.21.-) | Glutamyl endopeptidase precursor (EC 3.4.21.19), blaSE | SCE1572_3785 | yes | sce_2479 | yes |
| A and B | Protein Metabolism | Protein folding | GroEL, GroES | Heat shock protein 60 family chaperone GroEL | SCE1572_3785 | yes | sce_3121 | yes |
| A and B | Protein Metabolism | Protein folding | GroEL, GroES | Heat shock protein 60 family co-chaperone GroES | SCE1572_9303 | yes | sce_3120 | yes |
| A and B | Protein Metabolism | Protein folding | Peptidyl-prolyl cis-trans isomerase | FKBP-type peptidyl-prolyl cis-trans isomerase SlyD (EC 5.2.1.8) | SCE1572_6322 | yes | sce_8083 | yes |
| A and B | Protein Metabolism | Protein folding | Peptidyl-prolyl cis-trans isomerase | FKBP-type peptidyl-prolyl cis-trans isomerase RfB (EC 5.2.1.8) | SCE1572_9344 | yes | sce_8447 | yes |
| A and B | Protein Metabolism | Protein folding | Peptidyl-prolyl cis-trans isomerase | Foldase protein PrsA precursor (EC 5.2.1.8) | SCE1572_2712 | yes | sce_8124 | yes |
| A and B | Protein Metabolism | Protein folding | Peptidyl-prolyl cis-trans isomerase | Peptidyl-prolyl cis-trans isomerase ppfB (EC 5.2.1.8) | SCE1572_10897 | yes | sce_2251 | yes |
| A and B | Protein Metabolism | Protein folding | Peptidyl-prolyl cis-trans isomerase | Survival protein SurA precursor (Peptidyl-prolyl cis-trans isomerase SurA) (EC 5.2.1.8) | SCE1572_10897 | yes | sce_1165 | yes |
| A and B | Protein Metabolism | Protein folding | Periplasmic disulfide interchange | Cytochrome c-type biogenesis protein CcdA (DshD analog) | SCE1572_8993 | yes | sce_9530 | yes |
| A and B | Protein Metabolism | Protein folding | Periplasmic disulfide interchange | Cytochrome c-type biogenesis protein DshD, DshD-disulfide reductase | SCE1572_9668 | yes | sce_7758 | yes |
| A and B | Protein Metabolism | Protein folding | Periplasmic disulfide interchange | Periplasmic thioldisulfide interchange protein DshA | SCE1572_2243 | yes | sce_8476 | yes |
| A and B | Protein Metabolism | Protein folding | Chaperone protein DnaJ | Chaperone protein DnaJ | SCE1572_3 | yes | sce_1795 | yes |
| A and B | Protein Metabolism | Protein folding | Chaperone protein DnaK | Chaperone protein DnaK | SCE1572_9421 | yes | sce_3 | yes |
| A and B | Protein Metabolism | Protein folding | Chaperone protein HscA | Chaperone protein HscA | SCE1572_9420 | yes | sce_8208 | yes |
| A and B | Protein Metabolism | Protein folding | Chaperone protein HscB | Chaperone protein HscB | SCE1572_11480 | yes | sce_8207 | yes |
| A and B | Protein Metabolism | Protein folding | Chaperone protein HtpG | Chaperone protein HtpG | SCE1572_6714 | yes | sce_10315 | yes |
| A and B | Protein Metabolism | Protein folding | ClpB protein | ClpB protein | SCE1572_926 | yes | sce_5586 | yes |
| A and B | Protein Metabolism | Protein folding | Protein chaperones | DnaJ-class molecular chaperone CbpA | SCE1572_4 | yes | sce_694 | yes |
| A | Protein Metabolism | Protein folding | Peptidyl-prolyl cis-trans isomerase | Heat shock protein GrpE | SCE1572_5061 | yes | sce_4 | no |
| A and B | Protein Metabolism | Protein processing and modification | G3E family of P-loop GTPases (metallocenter biosynthesis) | FKBP-type peptidyl-prolyl cis-trans isomerase FkpA precursor (EC 5.2.1.8) | SCE1572_2298 | yes | sce_1845 | yes |
| A and B | Protein Metabolism | Protein processing and modification | G3E family of P-loop GTPases (metallocenter biosynthesis) | B1HIE family of Methylmalonyl-CoA mutase (EC 5.4.99.2) | SCE1572_9303 | yes | sce_8083 | yes |
| A and B | Protein Metabolism | Protein processing and modification | G3E family of P-loop GTPases (metallocenter biosynthesis) | FKBP-type peptidyl-prolyl cis-trans isomerase SlyD (EC 5.2.1.8) | SCE1572_3702 | yes | sce_3052 | yes |
| A and B | Protein Metabolism | Protein processing and modification | G3E family of P-loop GTPases (metallocenter biosynthesis) | Methylmalonyl-CoA mutase (EC 5.4.99.2) | SCE1572_10351 | yes | sce_9219 | yes |
| A and B | Protein Metabolism | Protein processing and modification | G3E family of P-loop GTPases (metallocenter biosynthesis) | Putative metal chaperone, involved in Zn homeostasis, GTPase of COG | SCE1572_3069 | yes | sce_7327 | yes |
| A and B | Protein Metabolism | Protein processing and modification | G3E family of P-loop GTPases (metallocenter biosynthesis) | Urease accessory protein UreD | SCE1572_3073 | yes | sce_7330 | yes |
| A and B | Protein Metabolism | Protein processing and modification | G3E family of P-loop GTPases (metallocenter biosynthesis) | Urease accessory protein UreF | SCE1572_3074 | yes | sce_7331 | yes |
| A and B | Protein Metabolism | Protein processing and modification | G3E family of P-loop GTPases (metallocenter biosynthesis) | Urease accessory protein UreG | SCE1572_3071 | yes | sce_7329 | yes |
| A and B | Protein Metabolism | Protein processing and modification | G3E family of P-loop GTPases (metallocenter biosynthesis) | Urease alpha subunit (EC 3.5.1.5) | SCE1572_3070 | yes | sce_7328 | yes |
| A and B | Protein Metabolism | Protein processing and modification | G3E family of P-loop GTPases (metallocenter biosynthesis) | Urease gamma subunit (EC 3.5.1.5) | SCE1572_8090 | yes | sce_5121 | yes |
| A and B | Protein Metabolism | Protein processing and modification | G3E family of P-loop GTPases (metallocenter biosynthesis) | [NiFe] hydrogenase metallocenter assembly protein HypD | SCE1572_3170 | yes | sce_5122 | yes |
| A and B | Protein Metabolism | Protein processing and modification | G3E family of P-loop GTPases (metallocenter biosynthesis) | [NiFe] hydrogenase metallocenter assembly protein HypE | SCE1572_3169 | yes | sce_5119 | yes |
| A and B | Protein Metabolism | Protein processing and modification | G3E family of P-loop GTPases (metallocenter biosynthesis) | [NiFe] hydrogenase metallocenter assembly protein HypF | SCE1572_8091 | yes | sce_5118 | yes |
| A and B | Protein Metabolism | Protein processing and modification | G3E family of P-loop GTPases (metallocenter biosynthesis) | [NiFe] hydrogenase nickel incorporation protein HypA | SCE1572_3703 | yes | sce_3053 | yes |
| A and B | Protein Metabolism | Protein processing and modification | G3E family of P-loop GTPases (metallocenter biosynthesis) | putative periplasmic protein kinase ArgK and related GTPases of G3E family | SCE1572_2306 | yes | sce_29 | yes |
| A and B | Protein Metabolism | Protein processing and modification | Lipoprotein Biosynthesis | Apolipoprotein A-II (EC 3.4.23.1.-) | SCE1572_5206 | yes | sce_4364 | yes |
| A and B | Protein Metabolism | Protein processing and modification | Lipoprotein Biosynthesis | Lipoprotein signal peptidase (EC 3.4.23.36) | SCE1572_642 | yes | sce_451 | yes |
| A and B | Protein Metabolism | Protein processing and modification | Lipoprotein Biosynthesis | Prolipoprotein diacylglyceryl transferase (EC 2.9.9.-) | SCE1572_10897 | yes | sce_9530 | yes |
| A and B | Protein Metabolism | Protein processing and modification | Methionine sulfoxide reductases | Cytochrome c-type biogenesis protein CcdA (DshD analog) | SCE1572_10145 | yes | sce_8948 | yes |
| A and B | Protein Metabolism | Protein processing and modification | Methionine sulfoxide reductases | Peptide methionine sulfoxide reductase MsrA (EC 1.8.4.11) | SCE1572_10145 | yes | sce_6036 | yes |
| A and B | Protein Metabolism | Protein processing and modification | Methionine sulfoxide reductases | Peptide methionine sulfoxide reductase MsrB (EC 1.8.4.12) | SCE1572_3630 | yes | sce_6065 | yes |
| A and B | Protein Metabolism | Protein processing and modification | Methionine sulfoxide reductases | Peptide methionine sulfoxide reductase MsrC (EC 1.8.4.11) | SCE1572_10145 | yes | sce_8948 | yes |
| A and B | Protein Metabolism | Protein processing and modification | Methionine sulfoxide reductases | Peptide methionine sulfoxide reductase MsrD (EC 1.8.4.12) | SCE1572_10145 | yes | sce_6036 | yes |
| A and B | Protein Metabolism | Protein processing and modification | Protein-L-isoaspartate O-methyltransferase | Protein-L-isoaspartate O-methyltransferase (EC 2.1.1.77) | SCE1572_5735 | yes | sce_6084 | yes |
| A and B | Protein Metabolism | Protein processing and modification | Ribosomal protein S12p Asp methyltransferase | Ribosomal protein S12p Asp88 (E. coli) methyltransferase | SCE1572_1306 | yes | sce_4785 | yes |
| A and B | Protein Metabolism | Protein processing and modification | Ribosomal protein S12p Asp methyltransferase | SSU ribosomal protein S12p (S23e) | SCE1572_665 | yes | sce_942 | yes |
| A and B | Protein Metabolism | Protein processing and modification | Ribosomal protein S5p acylation | Ribosomal protein-S5p-alanine acetyltransferase | SCE1572_10070 | yes | sce_470 | yes |
| A and B | Protein Metabolism | Protein processing and modification | Signal peptidase | RSU ribosomal protein S5p (S2e) | SCE1572_2282 | yes | sce_8887 | yes |
| A and B | Protein Metabolism | Protein processing and modification | Signal peptidase | Lipoprotein signal peptidase (EC 3.4.23.36) | SCE1572_2282 | yes | sce_1828 | yes |
| A and B | Protein Metabolism | Protein processing and modification | Signal peptidase | Signal peptidase I (EC 3.4.21.89) | SCE1572_11483 | yes | sce_10318 | yes |
| A and B | Protein Metabolism | Protein processing and modification | Translation elongation factor P lysislation | Translation elongation factor P | SCE1572_3824 | yes | sce_3152 | yes |
| A and B | Protein Metabolism | Protein processing and modification | Translation elongation factor P lysislation | Translation elongation factor P Lys34:lysine transferase | SCE1572_3072 | yes | sce_1120 | yes |
| A | Protein Metabolism | Protein processing and modification | G3E family of P-loop GTPases (metallocenter biosynthesis) | Urease accessory protein UreE | SCE1572_3630 | yes | sce_6065 | yes |
| B | Protein Metabolism | Protein processing and modification | G3E family of P-loop GTPases (metallocenter biosynthesis) | [NiFe | | | | |

| | | | | | | | | |
|---------|-------------------------------|---|--|--|---------------|-----|-----------|-------|
| A and B | RNA Metabolism | RNA processing and modification | RNA processing and degradation, bacterial | Cytoplasmic axial filament protein CafA and Ribonuclease G (EC 3.1.4.) | SCE1572_9350 | yes | sce_8131 | yes |
| A and B | RNA Metabolism | RNA processing and modification | RNA processing and degradation, bacterial | Ribonuclease E (EC 3.1.26.12) | RCE1572_8450 | yes | sce_59 | yes |
| A and B | RNA Metabolism | RNA processing and modification | RNA processing and degradation, bacterial | Ribonuclease E inhibitor RraA | SCE1572_8481 | yes | sce_7246 | yes |
| A and B | RNA Metabolism | RNA processing and modification | RNA processing orphans | 2'5'-RNA ligase | SCE1572_6840 | yes | sce_5700 | yes |
| A and B | RNA Metabolism | RNA processing and modification | RNA pseudouridine synthases | Ribosomal large subunit pseudouridine synthase D (EC 4.2.1.70) | SCE1572_11 | yes | sce_11 | yes |
| A and B | RNA Metabolism | RNA processing and modification | RNA pseudouridine synthases | RNA pseudouridine synthase A (EC 4.2.1.70) | SCE1572_533 | yes | sce_1685 | yes |
| A and B | RNA Metabolism | RNA processing and modification | RNA pseudouridine synthases | RNA pseudouridine synthase B (EC 4.2.1.70) | SCE1572_5750 | yes | sce_4800 | yes |
| A and B | RNA Metabolism | RNA processing and modification | Ribonuclease H | Ribonuclease HII (EC 3.1.26.4) | SCE1572_1626 | yes | sce_1164 | yes |
| A and B | RNA Metabolism | RNA processing and modification | Ribonucleases in Bacillus | Ribonuclease J2 (endoribonuclease in RNA processing) | SCE1572_620 | yes | sce_428 | yes |
| A and B | RNA Metabolism | RNA processing and modification | mm5U34 biosynthesis bacteria | Cysteine desulfurase (EC 2.8.1.7) | SCE1572_1872 | yes | sce_1345 | yes |
| A and B | RNA Metabolism | RNA processing and modification | mm5U34 biosynthesis bacteria | Cysteine desulfurase (EC 2.8.1.7), IscS subfamily | SCE1572_9417 | yes | sce_8204 | yes |
| A and B | RNA Metabolism | RNA processing and modification | mm5U34 biosynthesis bacteria | Cysteine desulfurase (EC 2.8.1.7), SufS subfamily | SCE1572_10250 | yes | sce_5192 | yes |
| A and B | RNA Metabolism | RNA processing and modification | mm5U34 biosynthesis bacteria | iRNA (5-methylaminomethyl-2-thiouridylylate)-methyltransferase (EC 2.2.1.1.22) | SCE1572_9389 | yes | sce_8169 | yes |
| A and B | RNA Metabolism | RNA processing and modification | iRNA modification Archaea | Asparaginyl-tRNA synthetase (EC 6.1.1.22) | SCE1572_7819 | yes | sce_6622 | yes |
| A and B | RNA Metabolism | RNA processing and modification | iRNA modification Archaea | COG009 Sua5 subfamily, required for N6-threonylcarbamoyl adenosine | SCE1572_9021 | yes | sce_7776 | yes |
| A and B | RNA Metabolism | RNA processing and modification | iRNA modification Archaea | COG1180: Radical SAM, Pyruvate-formate lyase-activating enzyme like | SCE1572_408 | yes | sce_227 | yes |
| A and B | RNA Metabolism | RNA processing and modification | iRNA modification Archaea | COG1720: Uncharacterized conserved protein | SCE1572_1715 | yes | sce_2673 | yes |
| A and B | RNA Metabolism | RNA processing and modification | iRNA modification Archaea | Cysteine desulfurase (EC 2.8.1.7) | SCE1572_1872 | yes | sce_1345 | yes |
| A and B | RNA Metabolism | RNA processing and modification | iRNA modification Archaea | Cysteine desulfurase (EC 2.8.1.7), IscS subfamily | SCE1572_9417 | yes | sce_8204 | yes |
| A and B | RNA Metabolism | RNA processing and modification | iRNA modification Archaea | Cysteine desulfurase (EC 2.8.1.7), SufS subfamily | SCE1572_10250 | yes | sce_5192 | yes |
| A and B | RNA Metabolism | RNA processing and modification | iRNA modification Archaea | GTP-binding protein Era | SCE1572_7857 | yes | sce_6660 | yes |
| A and B | RNA Metabolism | RNA processing and modification | iRNA modification Archaea | Iron-sulfur cluster assembly scaffold protein IscU | SCE1572_9418 | yes | sce_8205 | yes |
| A and B | RNA Metabolism | RNA processing and modification | iRNA modification Archaea | Protein-L-isoaspartate O-methyltransferase (EC 2.1.1.77) | SCE1572_903 | yes | sce_6084 | yes |
| A and B | RNA Metabolism | RNA processing and modification | iRNA modification Archaea | RNA-2'3'-PO4:RNA-5'-OH ligase | SCE1572_1930 | yes | sce_1448 | yes |
| A and B | RNA Metabolism | RNA processing and modification | iRNA modification Archaea | Rhodanese-like domain protein | SCE1572_332 | yes | sce_180 | yes |
| A and B | RNA Metabolism | RNA processing and modification | iRNA modification Archaea | iRNA (Guanine37-N1)-methyltransferase (EC 2.1.1.31) | SCE1572_6006 | yes | sce_4958 | yes |
| A and B | RNA Metabolism | RNA processing and modification | iRNA modification Archaea | iRNA dihydrouridine synthase B (EC 1.-.-.-) | SCE1572_4986 | yes | sce_4190 | yes |
| A and B | RNA Metabolism | RNA processing and modification | iRNA modification Archaea | iRNA pseudouridine 13 synthase (EC 4.2.1.-) | SCE1572_5783 | yes | sce_4830 | yes |
| A and B | RNA Metabolism | RNA processing and modification | iRNA modification Archaea | iRNA pseudouridine synthase A (EC 4.2.1.70) | SCE1572_533 | yes | sce_1685 | yes |
| A and B | RNA Metabolism | RNA processing and modification | iRNA modification Archaea | iRNA (Cytosine32)-2-thiocytidine synthetase | SCE1572_3408 | yes | sce_2895 | yes |
| A and B | RNA Metabolism | RNA processing and modification | iRNA modification Archaea | iRNA-(6)A37 methylthiotransferase | SCE1572_7173 | yes | sce_5902 | yes |
| A and B | RNA Metabolism | RNA processing and modification | iRNA modification Bacteria | COG1720: Uncharacterized conserved protein | SCE1572_1715 | yes | sce_2673 | yes |
| A and B | RNA Metabolism | RNA processing and modification | iRNA modification Bacteria | Chaperone protein HscA | SCE1572_9421 | yes | sce_8208 | yes |
| A and B | RNA Metabolism | RNA processing and modification | iRNA modification Bacteria | Chaperone protein HscB | SCE1572_9420 | yes | sce_8207 | yes |
| A and B | RNA Metabolism | RNA processing and modification | iRNA modification Bacteria | Cysteine desulfurase (EC 2.8.1.7) | SCE1572_1872 | yes | sce_1345 | yes |
| A and B | RNA Metabolism | RNA processing and modification | iRNA modification Bacteria | Cysteine desulfurase (EC 2.8.1.7), IscS subfamily | SCE1572_9417 | yes | sce_8204 | yes |
| A and B | RNA Metabolism | RNA processing and modification | iRNA modification Bacteria | Cysteine desulfurase (EC 2.8.1.7), SufS subfamily | SCE1572_10250 | yes | sce_5192 | yes |
| A and B | RNA Metabolism | RNA processing and modification | iRNA modification Bacteria | Cytidine deaminase (EC 3.5.4.5) | SCE1572_7737 | yes | sce_6562 | yes |
| A and B | RNA Metabolism | RNA processing and modification | iRNA modification Bacteria | FIG004453: protein YecG like | SCE1572_5816 | yes | sce_4865 | yes |
| A and B | RNA Metabolism | RNA processing and modification | iRNA modification Bacteria | FIG137478: Hypothetical protein | SCE1572_5033 | yes | sce_4235 | yes |
| A and B | RNA Metabolism | RNA processing and modification | iRNA modification Bacteria | Ferredoxin, 2Fe-2S | SCE1572_9111 | yes | sce_7893 | yes |
| A and B | RNA Metabolism | RNA processing and modification | iRNA modification Bacteria | GTP cyclohydrolase I (EC 3.5.4.16) type 1 | SCE1572_11540 | yes | sce_10389 | yes |
| A and B | RNA Metabolism | RNA processing and modification | iRNA modification Bacteria | Iron binding protein IscA for iron-sulfur cluster assembly | SCE1572_9419 | yes | sce_8206 | yes |
| A and B | RNA Metabolism | RNA processing and modification | iRNA modification Bacteria | Iron-sulfur cluster assembly scaffold protein IscU | SCE1572_9418 | yes | sce_8205 | yes |
| A and B | RNA Metabolism | RNA processing and modification | iRNA modification Bacteria | Queuosine Biosynthesis QueE Radical SAM | SCE1572_3404 | yes | sce_2891 | yes |
| A and B | RNA Metabolism | RNA processing and modification | iRNA modification Bacteria | Queuosine biosynthesis QueD, PTPS-I | SCE1572_10281 | yes | sce_9631 | yes |
| A and B | RNA Metabolism | RNA processing and modification | iRNA modification Bacteria | RNA binding methyltransferase FtsI like | SCE1572_10681 | yes | sce_9292 | yes |
| A and B | RNA Metabolism | RNA processing and modification | iRNA modification Bacteria | S-adenosylmethionine:RNA ribosyltransferase-isomerase (EC 5.-.-.-) | SCE1572_2293 | yes | sce_1841 | yes |
| A and B | RNA Metabolism | RNA processing and modification | iRNA modification Bacteria | glutamylyl-Q-RNA synthetase | SCE1572_870 | yes | sce_645 | yes |
| A and B | RNA Metabolism | RNA processing and modification | iRNA modification Bacteria | iRNA (5-methylaminomethyl-2-thiouridylylate)-methyltransferase (EC 2.2.1.1.22) | SCE1572_9389 | yes | sce_8169 | yes |
| A and B | RNA Metabolism | RNA processing and modification | iRNA modification Bacteria | iRNA (Guanine37-N1)-methyltransferase (EC 2.1.1.31) | SCE1572_6006 | yes | sce_4958 | yes |
| A and B | RNA Metabolism | RNA processing and modification | iRNA modification Bacteria | iRNA (Guanosine18-2'-O)-methyltransferase (EC 2.1.1.34) | SCE1572_611 | yes | sce_420 | yes |
| A and B | RNA Metabolism | RNA processing and modification | iRNA modification Bacteria | iRNA (cytosine34-2'-O)-methyltransferase (EC 2.1.1.-) | SCE1572_2345 | yes | sce_1895 | yes |
| A and B | RNA Metabolism | RNA processing and modification | iRNA modification Bacteria | iRNA (guanine46-N7)-methyltransferase (EC 2.1.1.33) | SCE1572_1219 | yes | sce_879 | yes |
| A and B | RNA Metabolism | RNA processing and modification | iRNA modification Bacteria | iRNA delta(2)-isopentenylpyrophosphate transferase (EC 2.5.1.8) | SCE1572_11322 | yes | sce_10101 | yes |
| A and B | RNA Metabolism | RNA processing and modification | iRNA modification Bacteria | iRNA dihydrouridine synthase B (EC 1.-.-.-) | SCE1572_4986 | yes | sce_4190 | yes |
| A and B | RNA Metabolism | RNA processing and modification | iRNA modification Bacteria | iRNA pseudouridine 13 synthase (EC 4.2.1.-) | SCE1572_5783 | yes | sce_4830 | yes |
| A and B | RNA Metabolism | RNA processing and modification | iRNA modification Bacteria | iRNA pseudouridine synthase A (EC 4.2.1.70) | SCE1572_533 | yes | sce_1685 | yes |
| A and B | RNA Metabolism | RNA processing and modification | iRNA modification Bacteria | iRNA pseudouridine synthase B (EC 4.2.1.70) | SCE1572_5780 | yes | sce_4800 | yes |
| A and B | RNA Metabolism | RNA processing and modification | iRNA modification Bacteria | iRNA (Cytosine32)-2-thiocytidine synthetase | SCE1572_3408 | yes | sce_2895 | yes |
| A and B | RNA Metabolism | RNA processing and modification | iRNA modification Bacteria | iRNA (6e)-lysine synthetase | SCE1572_9384 | yes | sce_8164 | yes |
| A and B | RNA Metabolism | RNA processing and modification | iRNA modification Bacteria | iRNA-specific adenosine-34 deaminase (EC 3.5.4.29) | SCE1572_2294 | yes | sce_1842 | yes |
| A and B | RNA Metabolism | RNA processing and modification | iRNA modification Bacteria | iRNA-(6)A37 methylthiotransferase | SCE1572_7173 | yes | sce_5902 | yes |
| A and B | RNA Metabolism | RNA processing and modification | iRNA modification Bacteria | iRNA-specific adenosine-34 deaminase (EC 3.5.4.-) | SCE1572_3415 | yes | sce_2901 | yes |
| A and B | RNA Metabolism | RNA processing and modification | iRNA modification Bacteria | iRNAmt5U-54 MTase gid | SCE1572_6866 | yes | sce_5729 | yes |
| A and B | RNA Metabolism | RNA processing and modification | iRNA nucleotidyltransferase | iRNA nucleotidyltransferase (EC 2.7.7.21) (EC 2.7.7.25) | SCE1572_1432 | yes | sce_1024 | yes |
| A and B | RNA Metabolism | RNA processing and modification | iRNA nucleotidyltransferase | iRNA nucleotidyltransferase, A-adding (EC 2.7.7.25) | SCE1572_4448 | yes | sce_3692 | yes |
| A and B | RNA Metabolism | RNA processing and modification | iRNA processing | Ribonuclease D (EC 3.1.26.3) | SCE1572_5707 | yes | sce_4759 | yes |
| A and B | RNA Metabolism | RNA processing and modification | iRNA processing | Ribonuclease P protein component (EC 3.1.26.5) | SCE1572_3331 | yes | sce_2827 | yes |
| A and B | RNA Metabolism | RNA processing and modification | iRNA processing | Ribonuclease PH (EC 2.7.7.56) | SCE1572_10102 | yes | sce_8920 | yes |
| A and B | RNA Metabolism | RNA processing and modification | iRNA processing | iRNA delta(2)-isopentenylpyrophosphate transferase (EC 2.5.1.8) | SCE1572_11322 | yes | sce_10101 | yes |
| A and B | RNA Metabolism | RNA processing and modification | iRNA processing | iRNA pseudouridine 13 synthase (EC 4.2.1.-) | SCE1572_5783 | yes | sce_4830 | yes |
| A and B | RNA Metabolism | RNA processing and modification | iRNA processing | iRNA pseudouridine synthase A (EC 4.2.1.70) | SCE1572_533 | yes | sce_1685 | yes |
| A and B | RNA Metabolism | RNA processing and modification | iRNA processing | iRNA pseudouridine synthase B (EC 4.2.1.70) | SCE1572_5780 | yes | sce_4800 | yes |
| A and B | RNA Metabolism | RNA processing and modification | iRNA processing | iRNA (6e)-lysine synthetase | SCE1572_9384 | yes | sce_8164 | yes |
| A and B | RNA Metabolism | RNA processing and modification | iRNA processing | iRNA-(6)A37 methylthiotransferase | SCE1572_7173 | yes | sce_5902 | yes |
| A and B | RNA Metabolism | RNA processing and modification | iRNA processing | iRNA-specific adenosine-34 deaminase (EC 3.5.4.-) | SCE1572_3415 | yes | sce_2901 | yes |
| A and B | RNA Metabolism | RNA processing and modification | iRNA splicing | ADP-ribose 1'-phosphate phosphatase | SCE1572_4147 | yes | sce_7614 | yes |
| A and B | RNA Metabolism | RNA processing and modification | iRNA splicing | RNA 3'-terminal phosphate cyclase (EC 6.5.1.4) | SCE1572_9211 | yes | sce_8012 | yes |
| A and B | RNA Metabolism | RNA processing and modification | iRNA splicing | RNA-2'3'-PO4:RNA-5'-OH ligase | SCE1572_1930 | yes | sce_1448 | yes |
| A and B | RNA Metabolism | RNA processing and modification | iRNA splicing | RNA-NAD 2'-phosphotransferase | SCE1572_2604 | yes | sce_2186 | yes |
| A | RNA Metabolism | RNA processing and modification | iRNA methylation | 23S rRNA (guanine-N-2)-methyltransferase rmlE (EC 2.1.1.-) | SCE1572_7706 | yes | no | no |
| A | RNA Metabolism | RNA processing and modification | iRNA modification Archaea | Predicted N6-adenine-specific RNA methylase containing THUMP domain | SCE1572_7798 | yes | no | no |
| B | RNA Metabolism | RNA processing and modification | iRNA modification Archaea | rRNA small subunit 7-methylguanosine (m7G) methyltransferase GddB | no | no | sce_6774 | yes |
| B | RNA Metabolism | RNA processing and modification | iRNA modification Archaea | 5-carboxymethyl uridine and 5-carboxymethyl-2-thiouridine methyltransferase | no | no | sce_8197 | yes |
| B | RNA Metabolism | RNA processing | iRNA processing | iRNAH5-8'-guanylyltransferase | no | no | sce_6780 | yes |
| A and B | RNA Metabolism | Transcription | RNA polymerase bacterial | DNA-directed RNA polymerase alpha subunit (EC 2.7.7.6) | SCE1572_10059 | yes | sce_8876 | yes |
| A and B | RNA Metabolism | Transcription | RNA polymerase bacterial | DNA-directed RNA polymerase beta subunit (EC 2.7.7.6) | SCE1572_660 | yes | sce_466 | yes |
| A and B | RNA Metabolism | Transcription | RNA polymerase bacterial | DNA-directed RNA polymerase beta' subunit (EC 2.7.7.6) | SCE1572_963 | yes | sce_468 | yes |
| A and B | RNA Metabolism | Transcription | RNA polymerase bacterial | DNA-directed RNA polymerase omega subunit (EC 2.7.7.6) | SCE1572_9342 | yes | sce_8121 | yes |
| A and B | RNA Metabolism | Transcription | Rrf2 family transcriptional regulators | Iron-sulfur cluster regulator IscR | SCE1572_7588 | yes | sce_6444 | yes |
| A and B | RNA Metabolism | Transcription | Rrf2 family transcriptional regulators | Rrf2 family transcriptional regulator, group III | SCE1572_1737 | yes | sce_6432 | yes |
| A and B | RNA Metabolism | Transcription | Transcription factors bacterial | COG2740: Predicted nucleic-acid-binding protein implicated in transcription | SCE1572_7634 | yes | sce_6494 | yes |
| A and B | RNA Metabolism | Transcription | Transcription factors bacterial | FIG000325: clustered with transcription termination protein NusA | SCE1572_7636 | yes | sce_6496 | yes |
| A and B | RNA Metabolism | Transcription | Transcription factors bacterial | Regulator of nucleoside diphosphate kinase | SCE1572_5427 | yes | sce_3045 | yes |
| A and B | RNA Metabolism | Transcription | Transcription factors bacterial | Transcription accessory protein (S1 RNA-binding domain) | SCE1572_5755 | yes | sce_4806 | yes |
| A and B | RNA Metabolism | Transcription | Transcription factors bacterial | Transcription antitermination protein NusG | SCE1572_653 | yes | sce_460 | yes |
| A and B | RNA Metabolism | Transcription | Transcription factors bacterial | Transcription elongation factor GreA | SCE1572_4817 | yes | sce_4031 | yes |
| A and B | RNA Metabolism | Transcription | Transcription factors bacterial | Transcription elongation factor GreB | SCE1572_4795 | yes | sce_4010 | yes |
| A and B | RNA Metabolism | Transcription | Transcription factors bacterial | Transcription termination factor Rho | SCE1572_10055 | yes | sce_8872 | yes |
| A and B | RNA Metabolism | Transcription | Transcription factors bacterial | Transcription termination protein NusA | SCE1572_7635 | yes | sce_6495 | yes |
| A and B | RNA Metabolism | Transcription | Transcription factors bacterial | Transcription termination protein NusB | SCE1572_9355 | yes | sce_8136 | yes |
| A and B | RNA Metabolism | Transcription | Transcription factors bacterial | Transcription-repair coupling factor | SCE1572_3466 | yes | sce_2957 | yes |
| A and B | RNA Metabolism | Transcription | Transcription initiation, bacterial sigma factors | RNA polymerase sigma factor RpoD | SCE1572_379 | yes | sce_211 | yes |
| A and B | RNA Metabolism | Transcription | Transcription initiation, bacterial sigma factors | RNA polymerase sigma factor RpoE | SCE1572_380 | yes | sce_625 | yes |
| A and B | RNA Metabolism | Transcription | Transcription initiation, bacterial sigma factors | RNA polymerase sigma factor RpoH | SCE1572_1341 | yes | sce_965 | yes |
| A and B | RNA Metabolism | Transcription | Transcription initiation, bacterial sigma factors | RNA polymerase sigma factor SigB | SCE1572_3441 | yes | sce_2933 | yes |
| A and B | RNA Metabolism | Transcription | Transcription initiation, bacterial sigma factors | RNA polymerase sigma factor SigW | SCE1572_1464 | yes | sce_6812 | yes |
| A and B | RNA Metabolism | Transcription | Transcription initiation, bacterial sigma factors | RNA polymerase sigma factor for flagellar operon | SCE1572_2286 | yes | sce_1833 | yes |
| A and B | RNA Metabolism | Transcription | Transcription initiation, bacterial sigma factors | RNA polymerase sigma-54 factor RpoN | SCE1572_33 | yes | sce_35 | yes |
| A and B | RNA Metabolism | Transcription | Transcription initiation, bacterial sigma factors | RNA polymerase sigma-70 factor | SCE1572_8559 | yes | sce_9825 | yes |
| A and B | RNA Metabolism | Transcription | Transcription initiation, bacterial sigma factors | Serine protease precursor MucD/AlgY associated with sigma factor Rpo | SCE1572_2316 | yes | sce_1863 | yes |
| A | RNA Metabolism | Transcription | Transcription initiation, bacterial sigma factors | RNA polymerase sigma factor SigZ | SCE1572_1023 | yes | no | no |
| B | Regulation and Cell signaling | Programmed Cell Death and Toxin-antitoxin S | Phd-Doc, YdcE-YdcD toxin-antitoxin (programmed cell death) | Death on curing protein, Doc toxin | no | no | sce_434 | yes |
| B | Regulation and Cell signaling | Programmed Cell Death and Toxin-antitoxin S | Phd-Doc, YdcE-YdcD toxin-antitoxin (programmed cell death) | Prevent host death protein, Phd antitoxin | no | no | sce_435 | yes |
| B | Regulation and Cell signaling | Programmed Cell Death and Toxin-antitoxin S | Phd-Doc, YdcE-YdcD toxin-antitoxin (programmed cell death) | Programmed cell death toxin YdcE | no | no | sce_6022 | yes |
| A and B | Regulation and Cell signaling | no subcategory | Global Two-component Regulator PrfA in Proteobacteria | Global Two-component Regulator PrfA (RegA) | SCE1572_10200 | yes | sce_7139 | yes |
| A and B | Regulation and Cell signaling | no subcategory | Global Two-component Regulator PrfBA in Proteobacteria | Sensor histidine kinase PrfB (RegB) (EC 2.7.3.-) | SCE1572_10201 | yes | sce_9006 | yes |
| A and B | Regulation and Cell signaling | no subcategory | HPr catabolic repression system | Catabolic control protein A | SCE1572_3157 | yes | sce_2645 | yes |
| A and B | Regulation and Cell signaling | no subcategory | HPr catabolic repression system | HPr kinase/phosphorylase (EC 2.7.1.-) (EC 2.7.4.-) | SCE1572_7596 | yes | sce_6455 | yes |
| A and B | Regulation and Cell signaling | no subcategory | LysR-family proteins in Escherichia coli | Glycine cleavage system transcriptional activator GcvA | SCE1572_1245 | yes | sce_5041 | yes |
| A and B | Regulation and Cell signaling | no subcategory | LysR-family proteins in Escherichia coli | LysR family transcriptional regulator YbhD | SCE1572_2605 | yes | sce_2180 | yes |
| A and B | Regulation and Cell signaling | no subcategory | LysR-family proteins in Escherichia coli | LysR family transcriptional regulator YnfL | SCE1572_4744 | yes | sce_1246 | yes |
| A and B | Regulation and Cell signaling | no subcategory | LysR-family proteins in Salmonella enterica Typhimurium | LysR family transcriptional regulator STM3121 | SCE1572_2067 | yes | sce_1578 | yes |
| A and B | Regulation and Cell signaling | no subcategory | LysR-family proteins in Salmonella enterica Typhimurium | LysR family transcriptional regulator YnfL | SCE1572_4744 | yes | sce_1246 | yes |
| A and B | Regulation and Cell signaling | no subcategory | Orphan regulatory proteins | Copper sensory histidine kinase CpxA | SCE1572_7189 | yes | sce_1882 | yes</ |

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|---------|----------------------|----------------------------------|--|--|------------------|-----|-----------|-----|
| A and B | Respiration | Electron accepting reactions | Anaerobic respiratory reductases | Fe-S-cluster-containing hydrogenase components 1 | SCE1572_5192 | yes | sce_5047 | yes |
| A and B | Respiration | Electron accepting reactions | Anaerobic respiratory reductases | Flavodoxin reductases (ferredoxin-NADPH reductases) family 1 | SCE1572_117 | yes | sce_105 | yes |
| A and B | Respiration | Electron accepting reactions | Anaerobic respiratory reductases | Vanilate O-demethylase oxidoreductase (EC 1.14.13.-) | SCE1572_451 | yes | sce_267 | yes |
| A and B | Respiration | Electron accepting reactions | Cytochrome c oxidases d@O copy | putative Cytochrome bd2, subunit I | SCE1572_3233 | yes | sce_2726 | yes |
| A and B | Respiration | Electron accepting reactions | Cytochrome c oxidases d@O copy | putative Cytochrome bd2, subunit II | SCE1572_3234 | yes | sce_2727 | yes |
| A and B | Respiration | Electron accepting reactions | Terminal cytochrome C oxidases | Cytochrome c oxidase polypeptide I (EC 1.9.3.1) | SCE1572_6108 | yes | sce_5055 | yes |
| A and B | Respiration | Electron accepting reactions | Terminal cytochrome C oxidases | Cytochrome c oxidase polypeptide II (EC 1.9.3.1) | SCE1572_6107 | yes | sce_5054 | yes |
| A and B | Respiration | Electron accepting reactions | Terminal cytochrome C oxidases | Cytochrome c oxidase polypeptide III (EC 1.9.3.1) | SCE1572_6109 | yes | sce_5056 | yes |
| A and B | Respiration | Electron accepting reactions | Terminal cytochrome C oxidases | Cytochrome c oxidase polypeptide IV (EC 1.9.3.1) | SCE1572_9690 | yes | sce_8499 | yes |
| A and B | Respiration | Electron accepting reactions | Terminal cytochrome d ubiquinol oxidases | putative Cytochrome bd2, subunit I | SCE1572_3233 | yes | sce_2726 | yes |
| A and B | Respiration | Electron accepting reactions | Terminal cytochrome d ubiquinol oxidases | putative Cytochrome bd2, subunit II | SCE1572_3234 | yes | sce_2727 | yes |
| A and B | Respiration | Electron accepting reactions | Terminal cytochrome oxidases | putative Cytochrome bd2, subunit I | SCE1572_3233 | yes | sce_2726 | yes |
| A and B | Respiration | Electron accepting reactions | Terminal cytochrome oxidases | putative Cytochrome bd2, subunit II | SCE1572_3234 | yes | sce_2727 | yes |
| A and B | Respiration | Electron accepting reactions | Ubiquinone Menaquinone-cytochrome c reductase complexes | Ubiquinol-cytochrome c reductase, cytochrome B subunit (EC 1.10.2.2) | SCE1572_604 | yes | sce_413 | yes |
| A and B | Respiration | Electron accepting reactions | Ubiquinone Menaquinone-cytochrome c reductase complexes | Ubiquinol-cytochrome C reductase iron-sulfur subunit (EC 1.10.2.2) | SCE1572_605 | yes | sce_414 | yes |
| A | Respiration | Electron accepting reactions | Cytochrome c oxidases d@O copy | Transport ATP-binding protein CydC | SCE1572_5692 | yes | | no |
| A and B | Respiration | Electron donating reactions | Hydrogenases | Fe-S-cluster-containing hydrogenase components 1 | SCE1572_5192 | yes | sce_5047 | yes |
| A and B | Respiration | Electron donating reactions | Hydrogenases | hydrogenase/sulfur reductase, alpha subunit | SCE1572_8093 | yes | sce_5116 | yes |
| A and B | Respiration | Electron donating reactions | Hydrogenases | hydrogenase/sulfur reductase, delta subunit | SCE1572_8094 | yes | sce_5115 | yes |
| A and B | Respiration | Electron donating reactions | NiFe hydrogenase maturation | [NiFe] hydrogenase metallocenter assembly protein HypD | SCE1572_3170 | yes | sce_5121 | yes |
| A and B | Respiration | Electron donating reactions | NiFe hydrogenase maturation | [NiFe] hydrogenase metallocenter assembly protein HypE | SCE1572_3170 | yes | sce_5122 | yes |
| A and B | Respiration | Electron donating reactions | NiFe hydrogenase maturation | [NiFe] hydrogenase metallocenter assembly protein HypF | SCE1572_3169 | yes | sce_5119 | yes |
| A and B | Respiration | Electron donating reactions | NiFe hydrogenase maturation | [NiFe] hydrogenase nickel incorporation protein HypA | SCE1572_8091 | yes | sce_5118 | yes |
| A and B | Respiration | Electron donating reactions | Respiratory Complex I | Hypothetical transmembrane protein coupled to NADH-ubiquinone oxidoreductase chain I | SCE1572_9659 | yes | sce_8466 | yes |
| A and B | Respiration | Electron donating reactions | Respiratory Complex I | NAD(P)H-quinone oxidoreductase chain I | SCE1572_10178 | yes | sce_8977 | yes |
| A and B | Respiration | Electron donating reactions | Respiratory Complex I | NAD(P)H-quinone oxidoreductase chain I (EC 1.6.5.2) | SCE1572_10177 | yes | sce_8976 | yes |
| A and B | Respiration | Electron donating reactions | Respiratory Complex I | NADH ubiquinone oxidoreductase chain A (EC 1.6.5.3) | SCE1572_792 | yes | sce_585 | yes |
| A and B | Respiration | Electron donating reactions | Respiratory Complex I | NADH-ubiquinone oxidoreductase chain B (EC 1.6.5.3) | SCE1572_793 | yes | sce_586 | yes |
| A and B | Respiration | Electron donating reactions | Respiratory Complex I | NADH-ubiquinone oxidoreductase chain C (EC 1.6.5.3) | SCE1572_794 | yes | sce_587 | yes |
| A and B | Respiration | Electron donating reactions | Respiratory Complex I | NADH-ubiquinone oxidoreductase chain D (EC 1.6.5.3) | SCE1572_795 | yes | sce_588 | yes |
| A and B | Respiration | Electron donating reactions | Respiratory Complex I | NADH-ubiquinone oxidoreductase chain E (EC 1.6.5.3) | SCE1572_5683 | yes | sce_4736 | yes |
| A and B | Respiration | Electron donating reactions | Respiratory Complex I | NADH-ubiquinone oxidoreductase chain F (EC 1.6.5.3) | SCE1572_5683 | yes | sce_4735 | yes |
| A and B | Respiration | Electron donating reactions | Respiratory Complex I | NADH-ubiquinone oxidoreductase chain G (EC 1.6.5.3) | SCE1572_796 | yes | sce_590 | yes |
| A and B | Respiration | Electron donating reactions | Respiratory Complex I | NADH-ubiquinone oxidoreductase chain H (EC 1.6.5.3) | SCE1572_797 | yes | sce_591 | yes |
| A and B | Respiration | Electron donating reactions | Respiratory Complex I | NADH-ubiquinone oxidoreductase chain I (EC 1.6.5.3) | SCE1572_798 | yes | sce_591 | yes |
| A and B | Respiration | Electron donating reactions | Respiratory Complex I | NADH-ubiquinone oxidoreductase chain J (EC 1.6.5.3) | SCE1572_5682 | yes | sce_1234 | yes |
| A and B | Respiration | Electron donating reactions | Respiratory Complex I | NADH-ubiquinone oxidoreductase chain K (EC 1.6.5.3) | SCE1572_5681 | yes | sce_4733 | yes |
| A and B | Respiration | Electron donating reactions | Respiratory Complex I | NADH-ubiquinone oxidoreductase chain L (EC 1.6.5.3) | SCE1572_5653 | yes | sce_4732 | yes |
| A and B | Respiration | Electron donating reactions | Respiratory Complex I | NADH-ubiquinone oxidoreductase chain M (EC 1.6.5.3) | SCE1572_5652 | yes | sce_4731 | yes |
| A and B | Respiration | Electron donating reactions | Respiratory Complex I | NADH-ubiquinone oxidoreductase chain N (EC 1.6.5.3) | SCE1572_5678 | yes | sce_4730 | yes |
| A and B | Respiration | Electron donating reactions | Respiratory dehydrogenases 1 | Anaerobic glycerol-3-phosphate dehydrogenase subunit A (EC 1.1.5.3) | SCE1572_10981 | yes | sce_9703 | yes |
| A and B | Respiration | Electron donating reactions | Respiratory dehydrogenases 1 | Anaerobic glycerol-3-phosphate dehydrogenase subunit B (EC 1.1.5.3) | SCE1572_10980 | yes | sce_9702 | yes |
| A and B | Respiration | Electron donating reactions | Respiratory dehydrogenases 1 | Glycerol dehydrogenase (EC 1.1.1.6) | SCE1572_6356 | yes | sce_6038 | yes |
| A and B | Respiration | Electron donating reactions | Respiratory dehydrogenases 1 | Glycerol-3-phosphate dehydrogenase (EC 1.1.5.3) | SCE1572_1855 | yes | sce_1309 | yes |
| A and B | Respiration | Electron donating reactions | Respiratory dehydrogenases 1 | NADH dehydrogenase (EC 1.6.99.3) | SCE1572_557 | yes | sce_360 | yes |
| A and B | Respiration | Electron donating reactions | Succinate dehydrogenase | Succinate dehydrogenase cytochrome b subunit | SCE1572_8614 | yes | sce_7334 | yes |
| A and B | Respiration | Electron donating reactions | Succinate dehydrogenase | Succinate dehydrogenase cytochrome b558 subunit | SCE1572_10674 | yes | sce_9286 | yes |
| A and B | Respiration | Electron donating reactions | Succinate dehydrogenase | Succinate dehydrogenase flavoprotein subunit (EC 1.3.99.1) | SCE1572_8615 | yes | sce_3094 | yes |
| A and B | Respiration | Electron donating reactions | Succinate dehydrogenase | Succinate dehydrogenase iron-sulfur protein (EC 1.3.99.1) | SCE1572_8616 | yes | sce_7336 | yes |
| B | Respiration | Electron donating reactions | Hydrogenases | Ni-Fe hydrogenase III large subunit | | no | sce_5367 | yes |
| A and B | Respiration | no subcategory | Biogenesis of c-type cytochromes | ABC transporter involved in cytochrome c biogenesis, ATPase component | SCE1572_10483 | yes | sce_9128 | yes |
| A and B | Respiration | no subcategory | Biogenesis of c-type cytochromes | ABC transporter involved in cytochrome c biogenesis, CcmB subunit | SCE1572_3253 | yes | sce_2749 | yes |
| A and B | Respiration | no subcategory | Biogenesis of c-type cytochromes | Cytochrome c heme lyase subunit CcmF | SCE1572_10493 | yes | sce_9141 | yes |
| A and B | Respiration | no subcategory | Biogenesis of c-type cytochromes | Cytochrome c-type biogenesis protein CcdA (DsbD analog) | SCE1572_10897 | yes | sce_9530 | yes |
| A and B | Respiration | no subcategory | Biogenesis of c-type cytochromes | Cytochrome c-type biogenesis protein CcmC, putative heme lyase for CcmB | SCE1572_3875 | yes | sce_3198 | yes |
| A and B | Respiration | no subcategory | Biogenesis of c-type cytochromes | Cytochrome c-type biogenesis protein CcmE, heme chaperone | SCE1572_11505 | yes | sce_10337 | yes |
| A and B | Respiration | no subcategory | Biogenesis of c-type cytochromes | Cytochrome c-type biogenesis protein DsbD, protein-disulfide reductase | SCE1572_8993 | yes | sce_7758 | yes |
| A and B | Respiration | no subcategory | Biogenesis of c-type cytochromes | Periplasmic thioldisulfide interchange protein DsbA | SCE1572_9668 | yes | sce_8476 | yes |
| A and B | Respiration | no subcategory | Biogenesis of c-type cytochromes | Thioldisulfide oxidoreductase related to ResA | SCE1572_9313 | yes | sce_8093 | yes |
| A and B | Respiration | no subcategory | Biogenesis of cytochrome c oxidases | Cytochrome oxidase biogenesis protein CcoI, SenCPnC, putative copper | SCE1572_2790 | yes | sce_2380 | yes |
| A and B | Respiration | no subcategory | Biogenesis of cytochrome c oxidases | Frataxin homolog CyoY, facilitates iron supply for heme A synthesis or | SCE1572_3370 | yes | sce_2860 | yes |
| A and B | Respiration | no subcategory | Biogenesis of cytochrome c oxidases | Heme A synthase, cytochrome oxidase biogenesis protein CcoA5-CcoA | SCE1572_3871 | yes | sce_3194 | yes |
| A and B | Respiration | no subcategory | Biogenesis of cytochrome c oxidases | Heme O synthase, protoheme IX farnesyltransferase (EC 2.5.1.-) | COX SCE1572_3921 | yes | sce_3254 | yes |
| A and B | Respiration | no subcategory | Formate hydrogenase | Formate dehydrogenase chain D (EC 1.2.1.2) | SCE1572_11416 | yes | sce_10274 | yes |
| A and B | Respiration | no subcategory | Formate hydrogenase | Formate hydrogenase subunit 2 | SCE1572_5811 | yes | sce_4859 | yes |
| A and B | Respiration | no subcategory | Formate hydrogenase | Formate hydrogenase transcriptional activator | SCE1572_2333 | yes | sce_1883 | yes |
| A and B | Respiration | no subcategory | Formate hydrogenase | Putative formate dehydrogenase oxidoreductase protein | SCE1572_11420 | yes | sce_10275 | yes |
| A and B | Respiration | no subcategory | Quinone oxidoreductase family | Quinone oxidoreductase (EC 1.6.5.5) | SCE1572_1070 | yes | sce_2411 | yes |
| A and B | Respiration | no subcategory | Soluble cytochromes and functionally related electron carriers | Soluble cytochrome c552 precursor (EC 1.7.2.2) | SCE1572_2081 | yes | sce_1593 | yes |
| A and B | Respiration | no subcategory | Soluble cytochromes and functionally related electron carriers | Ferredoxin | SCE1572_114 | yes | sce_1214 | yes |
| A and B | Respiration | no subcategory | Soluble cytochromes and functionally related electron carriers | Ferredoxin, 2Fe-2S | SCE1572_9111 | yes | sce_7893 | yes |
| A | Respiration | no subcategory | Carbon monoxide dehydrogenase maturation factors | Carbon monoxide oxidation accessory protein CoxE | SCE1572_3418 | yes | | no |
| A | Respiration | no subcategory | Formate hydrogenase | Formate dehydrogenase-O, major subunit (EC 1.2.1.2) | SCE1572_3017 | yes | | no |
| A | Respiration | no subcategory | Biogenesis of cytochrome c oxidases | Ferredoxin-NAD(P) reductase (EC 1.18.1.2) | | no | sce_8046 | yes |
| B | Respiration | no subcategory | Formate hydrogenase | Formate hydrogenase subunit 3 | | no | sce_5371 | yes |
| B | Respiration | no subcategory | Formate hydrogenase | Formate hydrogenase subunit 4 | | no | sce_5370 | yes |
| B | Respiration | no subcategory | Formate hydrogenase | Formate hydrogenase subunit 7 | | no | sce_5366 | yes |
| B | Respiration | no subcategory | Formate hydrogenase | Hydrogenase-4 component B (EC 1.-.-.-) | | no | sce_5371 | yes |
| B | Respiration | no subcategory | Formate hydrogenase | Hydrogenase-4 component F (EC 1.-.-.-) | | no | sce_5368 | yes |
| A and B | Secondary Metabolism | Biosynthesis of phenylpropanoids | Apigenin derivatives | Isoflavone reductase homolog P3 (EC 1.3.1.-) | SCE1572_5607 | yes | sce_6014 | yes |
| A and B | Secondary Metabolism | Plant Alkaloids | Alkaloid biosynthesis from L-lysine | Deoxyhypusine synthase | SCE1572_5057 | yes | sce_6692 | yes |
| A and B | Secondary Metabolism | no subcategory | Thiazole-oxazole-modified microcin (TOMM) synthesis | AknN | SCE1572_437 | yes | sce_251 | yes |
| A and B | Secondary Metabolism | no subcategory | Thiazole-oxazole-modified microcin (TOMM) synthesis | TOMM biosynthesis cyclodehydratase (protein C) | SCE1572_7935 | yes | sce_6733 | yes |
| A and B | Secondary Metabolism | no subcategory | Thiazole-oxazole-modified microcin (TOMM) synthesis | TOMM biosynthesis dehydrogenase (protein B) | SCE1572_7936 | yes | sce_6734 | yes |
| A and B | Secondary Metabolism | no subcategory | Thiazole-oxazole-modified microcin (TOMM) synthesis | TOMM biosynthesis docking scaffold (protein D) | SCE1572_7935 | yes | sce_6733 | yes |
| B | Secondary Metabolism | no subcategory | Lanthionine Synthetases | Lanthionine biosynthesis protein LanB | | no | sce_10124 | yes |
| A and B | Stress Response | Heat shock | Thiazole-oxazole-modified microcin (TOMM) synthesis | SagD family docking scaffold | | no | sce_10126 | yes |
| A and B | Stress Response | Heat shock | Cold shock, CspA family, of proteins | Cold shock protein CspG | SCE1572_5074 | yes | sce_4833 | yes |
| A and B | Stress Response | Detoxification | D-tyrosyl-tRNA(Tyr) deacylase | D-tyrosyl-tRNA(Tyr) deacylase | SCE1572_8453 | yes | sce_7213 | yes |
| A and B | Stress Response | Detoxification | Glutathione-dependent pathway of formaldehyde detoxification | S-(hydroxymethyl)glutathione dehydrogenase (EC 1.1.1.24) | SCE1572_3773 | yes | sce_3109 | yes |
| A and B | Stress Response | Detoxification | Uptake of selenate and selenite | DedA protein | SCE1572_8416 | yes | sce_7177 | yes |
| A and B | Stress Response | Detoxification | Uptake of selenate and selenite | Sulfate and thiosulfate import ATP-binding protein CysA (EC 3.6.3.25) | SCE1572_9474 | yes | sce_8253 | yes |
| A and B | Stress Response | Heat shock | Heat shock dnaK gene cluster extended | Chaperone protein DnaJ | SCE1572_2243 | yes | sce_1795 | yes |
| A and B | Stress Response | Heat shock | Heat shock dnaK gene cluster extended | Chaperone protein DnaK | SCE1572_3 | yes | sce_3 | yes |
| A and B | Stress Response | Heat shock | Heat shock dnaK gene cluster extended | FIG001341: Probable Fet(2)-trafficking protein YggX | SCE1572_8333 | yes | sce_7016 | yes |
| A and B | Stress Response | Heat shock | Heat shock dnaK gene cluster extended | Glutathione synthetase (EC 6.3.2.3) | SCE1572_9663 | yes | sce_8471 | yes |
| A and B | Stress Response | Heat shock | Heat shock dnaK gene cluster extended | Heat shock protein GrpE | SCE1572_4 | yes | sce_4 | yes |
| A and B | Stress Response | Heat shock | Heat shock dnaK gene cluster extended | Heat-inducible transcription repressor HrcA | SCE1572_10 | yes | sce_10 | yes |
| A and B | Stress Response | Heat shock | Heat shock dnaK gene cluster extended | Hypothetical radical SAM family enzyme, NOT coproporphyrinogen III | SCE1572_5115 | yes | sce_4303 | yes |
| A and B | Stress Response | Heat shock | Heat shock dnaK gene cluster extended | Nucleoside 5-triphosphatase RdgB (dHATP, dITP, XTP-specific) | SCE1572_10103 | yes | sce_8921 | yes |
| A and B | Stress Response | Heat shock | Heat shock dnaK gene cluster extended | RNA polymerase sigma factor RpoH | SCE1572_1341 | yes | sce_965 | yes |
| A and B | Stress Response | Heat shock | Heat shock dnaK gene cluster extended | Ribonuclease PH (EC 2.7.7.56) | SCE1572_6854 | yes | sce_3920 | yes |
| A and B | Stress Response | Heat shock | Heat shock dnaK gene cluster extended | Ribosomal RNA small subunit methyltransferase E (EC 2.1.1.-) | SCE1572_9144 | yes | sce_7942 | yes |
| A and B | Stress Response | Heat shock | Heat shock dnaK gene cluster extended | Ribosomal protein L11 methyltransferase (EC 2.1.1.-) | SCE1572_9145 | yes | sce_4521 | yes |
| A and B | Stress Response | Heat shock | Heat shock dnaK gene cluster extended | Translation elongation factor LepA | SCE1572_5105 | yes | sce_4292 | yes |
| A and B | Stress Response | Heat shock | Heat shock dnaK gene cluster extended | Xanthosine/inosine triphosphate pyrophosphatase | SCE1572_3840 | yes | sce_3163 | yes |
| A and B | Stress Response | Heat shock | Heat shock dnaK gene cluster extended | rRNA small subunit methyltransferase I | SCE1572_11326 | yes | sce_10106 | yes |
| A and B | Stress Response | Heat shock | Heat shock dnaK gene cluster extended | mRNA-binding protein SmpB | SCE1572_2190 | yes | sce_2564 | yes |
| B | Stress Response | Heat shock | Heat shock dnaK gene cluster extended | MiaB family protein, possibly involved in tRNA or rRNA modification | | no | sce_6292 | yes |
| A and B | Stress Response | Osmotic stress | Choline and Betaine Uptake and Betaine Biosynthesis | Choline dehydrogenase (EC 1.1.99.1) | SCE1572_4673 | yes | sce_3906 | yes |
| A and B | Stress Response | Osmotic stress | Choline and Betaine Uptake and Betaine Biosynthesis | Choline-sulfatase (EC 3.1.6.6) | SCE1572_2802 | yes | sce_8713 | yes |
| A and B | Stress Response | Osmotic stress | Choline and Betaine Uptake and Betaine Biosynthesis | L-proline glycine betaine binding ABC transporter protein ProX (TC 3) | SCE1572_9764 | yes | sce_7917 | yes |
| A and B | Stress Response | Osmotic stress | Choline and Betaine Uptake and Betaine Biosynthesis | Sarcosine oxidase beta subunit (EC 1.5.3.1) | SCE1572_966 | yes | sce_754 | yes |
| A and B | Stress Response | Osmotic stress | Osmoregulation | Aquaporin Z | SCE1572_1029 | yes | sce_2197 | yes |
| A and B | Stress Response | Osmotic stress | Osmoregulation | Outer membrane protein A precursor | SCE1572_4720 | yes | sce_4354 | yes |
| A and B | Stress Response | Osmotic stress | Synthesis of osmoregulated periplasmic glucans | Cyclic beta-1,2-glycan synthase (EC 2.4.1.-) | SCE1572_4710 | yes | sce_3935 | no |
| A | Stress Response | Osmotic stress | Choline and Betaine Uptake and Betaine Biosynthesis | L-proline glycine betaine ABC transport system permease protein ProV | SCE1572_9763 | yes | | no |
| A and B | Stress Response | Oxidative stress | Glutaredoxins | Glutaredoxin 3 | SCE1572_10047 | yes | sce_8863 | yes |
| A and B | Stress Response | Oxidative stress | Glutaredoxins | Glutaredoxin-related protein | SCE1572_4016 | yes | sce_3870 | yes |
| A and B | Stress Response | Oxidative stress | Glutathione: Biosynthesis and gamma-glutamyl cycle | Gamma-glutamyltranspeptidase (EC 2.3.2.2) | SCE1572_1873 | yes | sce_1347 | yes |
| A and B | Stress Response | Oxidative stress | Glutathione: Biosynthesis and gamma-glutamyl cycle | Glutamate-cysteine ligase (EC 6.3.2.2) | SCE1572_7801 | yes | sce_6606 | yes |
| A and B | Stress Response | Oxidative stress | Glutathione: Biosynthesis and gamma-glutamyl cycle | Glutathione synthetase (EC 6.3.2.3) | SCE1572_9663 | yes | sce_8471 | yes |
| A and B | Stress Response | Oxidative stress | Glutathione: Biosynthesis and gamma-glutamyl cycle | Similar to 5-oxoprolinase (EC 3.5.2.9) and Methylhydantoinsase A, B | SCE1572_5423 | yes | sce_4573 | yes |
| A and B | Stress Response | Oxidative stress | Glutathione: Non-redox reactions | Glutathione S-transferase (EC 2.5.1.18) | SCE1572_220 | yes | sce_558 | yes |
| A and B | Stress Response | Oxidative stress | Glutathione: Non-redox reactions | Glutathione S-transferase family protein | SCE1572_6610 | yes | sce_679 | yes |
| A and B | Stress Response | Oxidative stress | Glutathione: Non-redox reactions | Glutathione S-transferase, phi (EC 2.5.1.18) | SCE1572_6287 | yes | sce_5313 | yes |
| A and B | Stress Response | Oxidative stress | Glutathione: Non-redox reactions | Glutathione S-transferase, unnamed subgroup (EC 2 | | | | |

TableS9 A comparison of sequence similarity for So0157.2 and So ce56

| Locus tag (<i>Sorangium cellulosum</i> So0157.2) | Function | Hit | Locus tag (<i>S. cellulosum</i> So ce56) | percent identity | Function |
|---|---|-----|---|------------------|---|
| SCE1572_1 | Chromosomal replication initiator protein DnaA | bi | sce_1 | 98.73 | Chromosomal replication initiator protein DnaA |
| SCE1572_2 | Serine/threonine protein kinase PrkC, regulator of stationary phase | bi | sce_2 | 93.42 | Serine/threonine protein kinase PrkC, regulator of stationary phase |
| SCE1572_3 | Chaperone protein DnaK | bi | sce_3 | 95.97 | Chaperone protein DnaK |
| SCE1572_4 | Heat shock protein GrpE | bi | sce_4 | 91.75 | Heat shock protein GrpE |
| SCE1572_5 | Succinylornithine transaminase (EC 2.6.1.81) | bi | sce_5 | 94.52 | Succinylornithine transaminase (EC 2.6.1.81) |
| SCE1572_6 | Lead, cadmium, zinc and mercury transporting ATPase (EC 3.6.3.3) (EC 3.6.3.5); Copper-translocating P-type ATPase (EC 3.6.3.4) | bi | sce_6 | 91.41 | Lead, cadmium, zinc and mercury transporting ATPase (EC 3.6.3.3) (EC 3.6.3.5); Copper-translocating P-type ATPase (EC 3.6.3.4) |
| SCE1572_7 | Ferric uptake regulation protein FUR | bi | sce_7 | 90 | Ferric uptake regulation protein FUR |
| SCE1572_8 | FIG01089057: hypothetical protein | bi | sce_8 | 89.89 | FIG01089057: hypothetical protein |
| SCE1572_9 | FIG01085619: hypothetical protein | bi | sce_9 | 88.3 | FIG01085619: hypothetical protein |
| SCE1572_10 | Heat-inducible transcription repressor HrcA | bi | sce_10 | 95.68 | Heat-inducible transcription repressor HrcA |
| SCE1572_11 | Ribosomal large subunit pseudouridine synthase D (EC 4.2.1.70) | bi | sce_11 | 91.85 | Ribosomal large subunit pseudouridine synthase D (EC 4.2.1.70) |
| SCE1572_12 | response regulator receiver protein | bi | sce_12 | 94.83 | response regulator receiver protein |
| SCE1572_13 | Polymyxin resistance protein ArnT, undecaprenyl phosphate-alpha-L-Ara4N transferase; Melittin resistance protein PqdB | bi | sce_13 | 86.39 | Polymyxin resistance protein ArnT, undecaprenyl phosphate-alpha-L-Ara4N transferase; Melittin resistance protein PqdB |
| SCE1572_14 | Uroporphyrinogen-III methyltransferase (EC 2.1.1.107) / Uroporphyrinogen-III synthase (EC 4.2.1.75) | bi | sce_14 | 90.56 | Uroporphyrinogen-III methyltransferase (EC 2.1.1.107) / Uroporphyrinogen-III synthase (EC 4.2.1.75) |
| SCE1572_15 | hypothetical protein | bi | sce_15 | 73.33 | hypothetical protein |
| SCE1572_16 | Porphobilinogen synthase (EC 4.2.1.24) | bi | sce_16 | 96.94 | Porphobilinogen synthase (EC 4.2.1.24) |
| SCE1572_17 | hypothetical protein | bi | sce_17 | 72.73 | hypothetical protein |
| SCE1572_18 | ABC transporter, ATP-binding protein | bi | sce_18 | 92.19 | ABC transporter, ATP-binding protein |
| SCE1572_19 | Lipid A export ATP-binding/permease protein MsbA | bi | sce_19 | 92.64 | Lipid A export ATP-binding/permease protein MsbA |
| SCE1572_20 | TolA protein | bi | sce_20 | 92.39 | TolA protein |
| SCE1572_21 | conserved hypothetical protein | bi | sce_22 | 81.13 | hypothetical protein |
| SCE1572_22 | serine/threonine protein kinase | bi | sce_23 | 96.2 | serine/threonine protein kinase |
| SCE1572_23 | conserved hypothetical protein | bi | sce_24 | 87.68 | HAD-superfamily hydrolase, subfamily IIB |
| SCE1572_24 | LSU m5C1962 methyltransferase RlmI | bi | sce_25 | 97.1 | LSU m5C1962 methyltransferase RlmI |
| SCE1572_25 | hypothetical protein | bi | sce_27 | 79.42 | BH4862 protein |
| SCE1572_26 | Apolipoprotein N-acyltransferase (EC 2.3.1.-) / Copper homeostasis protein CutE | bi | sce_28 | 87.31 | Apolipoprotein N-acyltransferase (EC 2.3.1.-) / Copper homeostasis protein CutE |
| SCE1572_27 | DNA-binding protein BphI2 | bi | sce_29 | 98.04 | histone-like DNA-binding protein |
| SCE1572_28 | Metal-dependent hydrolase YbeY, involved in rRNA and/or ribosome maturation and assembly | bi | sce_30 | 88.06 | Metal-dependent hydrolase YbeY, involved in rRNA and/or ribosome maturation and assembly |
| SCE1572_29 | Transaldolase (EC 2.2.1.2) | bi | sce_31 | 91.67 | Transaldolase (EC 2.2.1.2) |
| SCE1572_30 | Protein export cytoplasm protein SecA ATPase RNA helicase (TC 3.A.5.1.1) | bi | sce_32 | 96.24 | Protein export cytoplasm protein SecA ATPase RNA helicase (TC 3.A.5.1.1) |
| SCE1572_31 | hypothetical protein | bi | sce_33 | 74.3 | hypothetical protein |
| SCE1572_32 | cAMP-binding proteins - catabolite gene activator and regulatory subunit of cAMP-dependent protein kinases | bi | sce_34 | 81.55 | cAMP-binding proteins - catabolite gene activator and regulatory subunit of cAMP-dependent protein kinases |
| SCE1572_33 | RNA polymerase sigma-54 factor RpoN | bi | sce_35 | 98.42 | RNA polymerase sigma-54 factor RpoN |
| SCE1572_34 | hypothetical protein | bi | sce_36 | 87.88 | hypothetical protein |
| SCE1572_35 | hypothetical protein | bi | sce_37 | 93.37 | hypothetical protein |
| SCE1572_36 | Fructose-6-phosphate-2-kinase/fructose-2, 6-bisphosphatase | bi | sce_38 | 97.86 | 6-phosphofructo-2-kinase/fructose-2,6-bisphosphatase 3 |
| SCE1572_37 | UPF0124 protein Rv2149c/MT208 | bi | sce_39 | 90.74 | UPF0124 protein Rv2149c/MT208 |
| SCE1572_38 | Serine/threonine protein kinase PrkC, regulator of stationary phase | bi | sce_40 | 95.51 | Serine/threonine protein kinase PrkC, regulator of stationary phase |
| SCE1572_39 | Multimodular transpeptidase-transglycosylase (EC 2.4.1.129) (EC 3.4.-.-) | bi | sce_41 | 86.83 | Multimodular transpeptidase-transglycosylase (EC 2.4.1.129) (EC 3.4.-.-) |
| SCE1572_40 | hypothetical protein | - | | 0 | |
| SCE1572_41 | PE_PGRS family protein | bi | sce_42 | 85.53 | PE_PGRS family protein |
| SCE1572_42 | Threonine dehydrogenase and related Zn-dependent dehydrogenases | umi | sce_6150 | 70.18 | Threonine dehydrogenase and related Zn-dependent dehydrogenases |
| SCE1572_43 | COG5637: Predicted integral membrane protein | umi | sce_6149 | 29.41 | cyclase/dehydrase |
| SCE1572_44 | hypothetical protein | bi | sce_43 | 85.8 | hypothetical protein |
| SCE1572_45 | serine/threonine protein kinase | bi | sce_44 | 78.34 | serine/threonine protein kinase |
| SCE1572_46 | zinc carboxypeptidase-related protein | bi | sce_45 | 85.45 | Carboxypeptidase A1 precursor (EC 3.4.17.1) |
| SCE1572_47 | Agmatinase (EC 3.5.3.11) | bi | sce_46 | 93.67 | Agmatinase (EC 3.5.3.11) |
| SCE1572_48 | 1-acyl-sn-glycerol-3-phosphate acyltransferase (EC 2.3.1.51) | bi | sce_47 | 86.1 | 1-acyl-sn-glycerol-3-phosphate acyltransferase (EC 2.3.1.51) |
| SCE1572_49 | ribosomal-protein-alanine acetyltransferase | bi | sce_48 | 92.47 | ribosomal-protein-alanine acetyltransferase |
| SCE1572_50 | Oxidoreductase | bi | sce_49 | 83.74 | Oxidoreductase |
| SCE1572_51 | hypothetical protein | umi | sce_5213 | 41.96 | FIG01089581: hypothetical protein |
| SCE1572_52 | hypothetical protein | - | | 0 | |
| SCE1572_53 | VgrG protein | umi | sce_9404 | 56.54 | VgrG protein |
| SCE1572_54 | hypothetical protein | umi | sce_116 | 36.86 | FIG01088201: hypothetical protein |
| SCE1572_55 | Rhs family protein | umi | sce_8347 | 41.96 | Rhs family protein |
| SCE1572_56 | hypothetical protein | - | | 0 | |
| SCE1572_57 | LOC432261 protein | bi | sce_6260 | 54.82 | LOC432261 protein |
| SCE1572_58 | Probable serine/threonine-protein kinase pknH (EC 2.7.11.1) | umi | sce_6257 | 61.9 | Probable serine/threonine-protein kinase pknH (EC 2.7.11.1) |
| SCE1572_59 | RD1 region associated protein Rv3879c | bi | sce_6258 | 64.96 | RD1 region associated protein Rv3879c |
| SCE1572_60 | Enoyl-CoA hydratase (EC 4.2.1.17) / Delta(3)-cis-delta(2)-trans-enoyl-CoA isomerase (EC 5.3.3.8) / 3-hydroxyacyl-CoA dehydrogenase (EC 1.1.1.1) | bi | sce_50 | 89.64 | Enoyl-CoA hydratase (EC 4.2.1.17) / Delta(3)-cis-delta(2)-trans-enoyl-CoA isomerase (EC 5.3.3.8) / 3-hydroxyacyl-CoA dehydrogenase (EC 1.1.1.1) |
| SCE1572_61 | 3-ketoacyl-CoA thiolase (EC 2.3.1.16) @ Acetyl-CoA acetyltransferase (EC 2.3.1.9) | bi | sce_51 | 94.5 | 3-ketoacyl-CoA thiolase (EC 2.3.1.16) @ Acetyl-CoA acetyltransferase (EC 2.3.1.9) |
| SCE1572_62 | hypothetical protein | - | | 0 | |
| SCE1572_63 | hypothetical protein | bi | sce_54 | 87.96 | hypothetical protein |
| SCE1572_64 | FIG01089490: hypothetical protein | bi | sce_55 | 73.4 | FIG01089490: hypothetical protein |
| SCE1572_65 | FIG01087520: hypothetical protein | bi | sce_56 | 77.57 | FIG01087520: hypothetical protein |
| SCE1572_66 | FIG01086441: hypothetical protein | bi | sce_58 | 86.35 | FIG01086441: hypothetical protein |
| SCE1572_67 | hypothetical protein | bi | sce_60 | 73.68 | hypothetical protein |
| SCE1572_68 | Thrombospondin | bi | sce_61 | 68.84 | Thrombospondin |
| SCE1572_69 | FIG01084899: hypothetical protein | bi | sce_62 | 63.18 | FIG01084899: hypothetical protein |
| SCE1572_70 | Gli4200 protein | bi | sce_63 | 58.8 | Gli4200 protein |
| SCE1572_71 | hypothetical protein | bi | sce_64 | 78.25 | hypothetical protein |
| SCE1572_72 | Serine-threonine protein kinase | bi | sce_65 | 71.11 | Serine-threonine protein kinase |
| SCE1572_73 | cyclic nucleotide-binding domain protein | bi | sce_66 | 94.68 | cyclic nucleotide-binding domain protein |
| SCE1572_74 | Dienelactone hydrolase family | bi | sce_67 | 91.48 | Dienelactone hydrolase family |
| SCE1572_75 | hypothetical protein | bi | sce_68 | 89.62 | hypothetical protein |
| SCE1572_76 | hypothetical protein | - | | 0 | |
| SCE1572_77 | aminotransferase, class I and II | bi | sce_69 | 83.82 | Transcriptional regulator, GntR family domain |
| SCE1572_78 | putative lipoprotein | bi | sce_70 | 70.78 | endoglucanase A (EC:3.2.1.4) |
| SCE1572_79 | DNA polymerase, beta domain protein region | - | | 0 | |
| SCE1572_80 | L-arabinose-binding periplasmic protein precursor AraF (TC 3.A.1.2.2) | umi | sce_6717 | 43.8 | Xylose ABC transporter, periplasmic xylose-binding protein XylF |
| SCE1572_81 | ABC transporter related | umi | sce_4511 | 57.14 | Ribose ABC transport system, ATP-binding protein RbsA (TC 3.A.1.2.1) |
| SCE1572_82 | hypothetical protein | - | | 0 | |
| SCE1572_83 | ribose transport system permease protein RbsC(EC:3.6.3.17) | umi | sce_3725 | 41.32 | Ribose ABC transport system, permease protein RbsC (TC 3.A.1.2.1) |
| SCE1572_84 | hypothetical protein | bi | sce_71 | 84.97 | hypothetical protein |
| SCE1572_85 | 2-polypropenyl-6-methoxyphenol hydroxylase and related FAD-dependent oxidoreductases | bi | sce_73 | 79.16 | 2-polypropenyl-6-methoxyphenol hydroxylase and related FAD-dependent oxidoreductases |
| SCE1572_86 | hypothetical protein | - | | 0 | |
| SCE1572_87 | Transcriptional regulator, TetR family | bi | sce_74 | 85.78 | Transcriptional regulator, TetR family |
| SCE1572_88 | Chaperonin (heat shock protein 33) | bi | sce_75 | 92.36 | Chaperonin (heat shock protein 33) |
| SCE1572_89 | internalin, putative | bi | sce_76 | 78.34 | internalin, putative |
| SCE1572_90 | outer membrane protein OmpA | bi | sce_77 | 89.64 | outer membrane protein OmpA |
| SCE1572_91 | Superoxide dismutase [Mn] (EC 1.15.1.1) | bi | sce_79 | 92.96 | Superoxide dismutase [Mn] (EC 1.15.1.1) |
| SCE1572_92 | Acetylglutamate kinase (EC 2.7.2.8) | bi | sce_81 | 94.36 | Acetylglutamate kinase (EC 2.7.2.8) |
| SCE1572_93 | N-acetylmethionine carbamoyltransferase (EC 2.1.3.9) | bi | sce_82 | 96.1 | N-acetylmethionine carbamoyltransferase (EC 2.1.3.9) |
| SCE1572_94 | hypothetical protein | bi | sce_83 | 89.9 | hypothetical protein |
| SCE1572_95 | acetyltransferase | bi | sce_84 | 84.62 | hypothetical protein |
| SCE1572_96 | hypothetical protein | bi | sce_2027 | 70.45 | hypothetical protein |
| SCE1572_97 | hypothetical protein | umi | sce_5129 | 37.91 | serine/threonine protein kinase |
| SCE1572_98 | hypothetical protein | - | | 0 | |
| SCE1572_99 | hypothetical protein | umi | sce_1997 | 60.34 | FIG01087771: hypothetical protein |
| SCE1572_100 | UvrD/REP helicase | bi | sce_87 | 91.04 | UvrD/REP helicase |
| SCE1572_101 | hypothetical protein | - | | 0 | |
| SCE1572_102 | hypothetical protein | bi | sce_88 | 85.85 | hypothetical protein |
| SCE1572_103 | hypothetical protein | bi | sce_89 | 87.04 | hypothetical protein |
| SCE1572_104 | 1,4-dihydroxy-2-naphthoate octaprenyltransferase (EC 2.5.1.74) | bi | sce_90 | 87.87 | 1,4-dihydroxy-2-naphthoate octaprenyltransferase (EC 2.5.1.74) |
| SCE1572_105 | hypothetical protein | bi | sce_91 | 80.95 | hypothetical protein |
| SCE1572_106 | Proline-rich protein | umi | sce_6423 | 32.66 | Proline-rich protein |
| SCE1572_107 | 3-isopropylmalate dehydratase small subunit (EC 4.2.1.33) | bi | sce_95 | 91.22 | 3-isopropylmalate dehydratase small subunit (EC 4.2.1.33) |
| SCE1572_108 | 3-isopropylmalate dehydratase large subunit (EC 4.2.1.33) | bi | sce_96 | 96.59 | 3-isopropylmalate dehydratase large subunit (EC 4.2.1.33) |
| SCE1572_109 | transcriptional regulator, LysR family | bi | sce_97 | 95.36 | transcriptional regulator, LysR family |
| SCE1572_110 | Inosine-5-'-monophosphate dehydrogenase (EC 1.1.1.205) | bi | sce_98 | 96.1 | Inosine-5-'-monophosphate dehydrogenase (EC 1.1.1.205) |
| SCE1572_111 | Transcriptional regulator, AraC family | bi | sce_99 | 84.42 | Transcriptional regulator, AraC family |
| SCE1572_112 | FIG01087827: hypothetical protein | umi | sce_7999 | 84.64 | FIG01087827: hypothetical protein |
| SCE1572_113 | FIG01087441: hypothetical protein | bi | sce_101 | 82.71 | FIG01087441: hypothetical protein |
| SCE1572_114 | Ferredoxin | bi | sce_102 | 84.72 | hypothetical protein |
| SCE1572_115 | hypothetical protein | bi | sce_103 | 92.66 | hypothetical protein |
| SCE1572_116 | hypothetical protein | bi | sce_104 | 87.08 | hypothetical protein |
| SCE1572_117 | Flavodoxin reductases (ferredoxin-NADPH reductases) family 1 | bi | sce_105 | 87.59 | Flavodoxin reductases (ferredoxin-NADPH reductases) family 1 |
| SCE1572_118 | BiI7875 protein | bi | sce_106 | 90.51 | hypothetical protein |
| SCE1572_119 | hydrolase, alpha/beta fold family | bi | sce_107 | 87.41 | hydrolase, alpha/beta fold family |
| SCE1572_120 | Putative carboxymethylglutaminase (EC 3.1.1.45) | bi | sce_108 | 88.52 | dienelactone hydrolase(EC:3.1.1.45) |
| SCE1572_121 | probable dienelactone hydrolase protein | bi | sce_109 | 86.97 | dienelactone hydrolase family protein |
| SCE1572_122 | Alpha-ketoglutarate-dependent taurine dioxygenase (EC 1.14.11.17) | bi | sce_110 | 95.72 | Alpha-ketoglutarate-dependent taurine dioxygenase (EC 1.14.11.17) |
| SCE1572_123 | hypothetical protein | - | | 0 | |
| SCE1572_124 | hypothetical protein | - | | 0 | |
| SCE1572_125 | hypothetical protein | bi | sce_125 | 83.19 | hypothetical protein |
| SCE1572_126 | Glutamyl-tRNA(Gln) amidotransferase subunit A-like protein | bi | sce_127 | 85.87 | Aspartyl-tRNA(Asn) amidotransferase subunit A (EC 6.3.5.6) @ Glutamyl-tRNA(Gln) amidotransferase subunit A (EC 6.3.5.7) |
| SCE1572_127 | FIG01088941: hypothetical protein | bi | sce_128 | 83.33 | FIG01088941: hypothetical protein |
| SCE1572_128 | hypothetical protein | - | | 0 | |
| SCE1572_129 | Methyltransferase | umi | sce_2123 | 46.15 | Methyltransferase |
| SCE1572_130 | hypothetical protein | - | | 0 | |
| SCE1572_131 | hypothetical protein | bi | sce_129 | 92.7 | hypothetical protein |
| SCE1572_132 | internalin, putative | bi | sce_130 | 80.38 | internalin, putative |
| SCE1572_133 | outer membrane protein OmpA | bi | sce_131 | 91.65 | outer membrane protein OmpA |
| SCE1572_134 | hypothetical protein | - | | 0 | |
| SCE1572_135 | hypothetical protein | bi | sce_9966 | 81.23 | Endo-1,4-beta-xylanase A precursor (EC 3.2.1.8) |
| SCE1572_136 | hypothetical protein | bi | sce_9965 | 87.83 | Cellulase (EC:3.2.1.4) |
| SCE1572_137 | putative cytochrome P450 hydroxylase | bi | sce_133 | 82.43 | putative cytochrome P450 hydroxylase |
| SCE1572_138 | FIG01089623: hypothetical protein | umi | sce_220 | 78.72 | FIG01089623: hypothetical protein |
| SCE1572_139 | FIG01089623: hypothetical protein | umi | sce_220 | 78.4 | FIG01089623: hypothetical protein |
| SCE1572_140 | DNA repair protein RadC | umi | sce_8397 | 55 | DNA repair protein RadC |
| SCE1572_141 | hypothetical protein | umi | sce_513 | 76.96 | FIG01087636: hypothetical protein |
| SCE1572_142 | hypothetical protein | bi | sce_3623 | 88.58 | FIG01085486: hypothetical protein |
| SCE1572_143 | Gsr1690 protein | umi | sce_1297 | 54.93 | hypothetical protein |
| SCE1572_144 | Plasmid stabilization system protein | bi | sce_1298 | 48.28 | hypothetical protein |
| SCE1572_145 | hypothetical protein | bi | sce_6050 | 69.94 | hypothetical protein |
| SCE1572_146 | hypothetical protein | bi | sce_6051 | 89.96 | hypothetical protein |
| SCE1572_147 | hypothetical protein | bi | sce_6052 | 91.3 | hypothetical protein |
| SCE1572_148 | Phage shock protein A | umi | sce_6125 | 50.72 | Phage shock protein A |
| SCE1572_149 | conserved hypothetical protein | bi | sce_1469 | 49.86 | FIG01086976: hypothetical protein |
| SCE1572_150 | antenna complex, alpha/beta subunit | bi | sce_138 | 80.25 | FIG01088764: hypothetical protein |
| SCE1572_151 | Branched-chain amino acid transport ATP-binding protein LivF (TC 3.A.1.4.1) | umi | sce_9572 | 43.04 | Oligopeptide transport ATP-binding protein OppF (TC 3.A.1.5.1) |
| SCE1572_152 | ABC transporter ATP-binding protein | umi | sce_6248 | 28.69 | Urea ABC transporter, permease protein UrtC |
| SCE1572_153 | High-affinity branched-chain amino acid transport system permease protein LivH (TC 3.A.1.4.1) | umi | sce_3979 | 35.57 | RIBOSE TRANSPORT SYSTEM PERMEASE PROTEIN RBSC |
| SCE1572_154 | hypothetical protein | umi | sce_6246 | 27.05 | Urea ABC transporter, substrate binding protein UrtA |
| SCE1572_155 | Methionyl-tRNA synthetase (EC 6.1.1.10) | bi | sce_140 | 88.51 | Methionyl-tRNA synthetase (EC 6.1.1.10) |
| SCE1572_156 | putative lipoprotein | bi | sce_141 | 78.4 | hypothetical protein |
| SCE1572_157 | serine/threonine protein kinase | umi | sce_5982 | 75.05 | serine/threonine protein kinase |
| SCE1572_158 | hypothetical protein | bi | sce_3489 | 70.94 | hypothetical protein |
| SCE1572_159 | FIG01085038: hypothetical protein | bi | sce_5980 | 85.69 | FIG01085038: hypothetical protein |
| SCE1572_160 | hypothetical protein | - | | 0 | |
| SCE1572_161 | hypothetical protein | bi | sce_8630 | 81.19 | hypothetical protein |

| | | | | |
|-------------|---|-----|-----------|--|
| SCE1572_162 | metallophosphoesterase | bi | sce_8629 | 91.55 metallophosphoesterase |
| SCE1572_163 | EBNA-1 | uni | sce_6758 | 38.47 FIG01086116: hypothetical protein |
| SCE1572_164 | Cystathionine gamma-lyase (EC 4.4.1.1) | uni | sce_6912 | 45.55 Cystathionine gamma-lyase (EC 4.4.1.1) |
| SCE1572_165 | Bifunctional protein: zinc-containing alcohol dehydrogenase; quinone oxidoreductase (NADPH:quinone reductase) (EC 1.1.1.-) | bi | sce_147 | 85.5 Bifunctional protein: zinc-containing alcohol dehydrogenase; quinone oxidoreductase (NADPH:quinone reductase) (EC 1.1.1.-); Sin |
| SCE1572_166 | hypothetical protein | - | - | 0 |
| SCE1572_167 | hypothetical protein | - | - | 0 |
| SCE1572_168 | SSU ribosomal protein S24e | bi | sce_148 | 61.46 FIG01086802: hypothetical protein |
| SCE1572_169 | gnl[WGS:AAAB]agCPI3423[gb]EAA06237 | bi | sce_149 | 71.43 hypothetical protein |
| SCE1572_170 | conserved hypothetical protein | bi | sce_151 | 87.69 conserved hypothetical protein |
| SCE1572_171 | Msl3173 protein | bi | sce_152 | 85.71 Msl3173 protein |
| SCE1572_172 | hypothetical protein | - | - | 0 |
| SCE1572_173 | FIG01086777: hypothetical protein | bi | sce_153 | 61.24 FIG01086777: hypothetical protein |
| SCE1572_174 | hypothetical protein | bi | sce_154 | 84.5 hypothetical protein |
| SCE1572_175 | hypothetical protein | bi | sce_155 | 93.33 conserved hypothetical protein |
| SCE1572_176 | predicted protein | bi | sce_156 | 87.74 predicted protein |
| SCE1572_177 | short-chain dehydrogenase/reductase SDR | bi | sce_7124 | 85.88 short-chain dehydrogenase/reductase SDR |
| SCE1572_178 | hypothetical protein | - | - | 0 |
| SCE1572_179 | hypothetical protein | bi | sce_159 | 84.59 hypothetical protein |
| SCE1572_180 | hypothetical protein | - | - | 0 |
| SCE1572_181 | probable oxygenase | bi | sce_1372 | 93.78 probable oxygenase |
| SCE1572_182 | FIG01087706: hypothetical protein | bi | sce_868 | 75.55 FIG01087706: hypothetical protein |
| SCE1572_183 | F5/8 type C domain protein | bi | sce_9533 | 85.14 F5/8 type C domain protein |
| SCE1572_184 | hypothetical protein | - | - | 0 |
| SCE1572_185 | PE-PGRS family protein | bi | sce_7864 | 68.93 1,4-beta-cellobiosidase |
| SCE1572_186 | Transcriptional regulator, AraC family | bi | sce_7863 | 83.85 Transcriptional regulator, AraC family |
| SCE1572_187 | NAD(P)H oxidoreductase YRKL (EC 1.6.99.-) @ Putative NADPH-quinone reductase (modulator of drug activity B) @ Flavou | uni | sce_9440 | 28.04 NAD(P)H dehydrogenase (quinone) |
| SCE1572_188 | integral membrane protein | bi | sce_171 | 84.36 integral membrane protein |
| SCE1572_189 | Erythrocyte membrane protein 1 | bi | sce_172 | 76.13 FIG01086900: hypothetical protein |
| SCE1572_190 | putative lipoprotein | bi | sce_3728 | 86.86 putative lipoprotein |
| SCE1572_191 | Nodulation protein noIO (EC 2.1.3.-) | uni | sce_2688 | 40.64 Nodulation protein noIO (EC 2.1.3.-) |
| SCE1572_192 | hypothetical protein | - | - | 0 |
| SCE1572_193 | Fe-S oxidoreductase | uni | sce_7488 | 24.38 Coenzyme PQQ synthesis protein E (Pyroloquinoline quinone biosynthesis protein E) |
| SCE1572_194 | hypothetical protein | - | - | 0 |
| SCE1572_195 | hypothetical protein | - | - | 0 |
| SCE1572_196 | Twin-arginine translocation pathway signal | - | - | 0 |
| SCE1572_197 | COG3899. Predicted ATPase | uni | sce_919 | 40 Response regulator receiver:ATP-binding region, ATPase-like:Histidine kinase A, N-terminal |
| SCE1572_198 | sensor histidine kinase with multiple PAS and a response regulator receiver domain | uni | sce_229 | 40.05 FOG: PAS/PAC domain |
| SCE1572_199 | succinyl-diaminopimelate desuccinylase | bi | sce_173 | 90.93 Succinyl-diaminopimelate desuccinylase |
| SCE1572_200 | hypothetical protein; putative Lanthionine synthetase C-like protein | bi | sce_6011 | 44.29 hypothetical protein; putative Lanthionine synthetase C-like protein |
| SCE1572_201 | hypothetical protein | - | - | 0 |
| SCE1572_202 | hypothetical protein | - | - | 0 |
| SCE1572_203 | RsbR, positive regulator of sigma-B | bi | sce_1460 | 80.48 RsbR, positive regulator of sigma-B |
| SCE1572_204 | cell surface protein | - | - | 0 |
| SCE1572_205 | FIG01086206: hypothetical protein | bi | sce_6005 | 85.9 FIG01086206: hypothetical protein |
| SCE1572_206 | hypothetical protein | - | - | 0 |
| SCE1572_207 | hypothetical protein | - | - | 0 |
| SCE1572_208 | hypothetical protein | - | - | 0 |
| SCE1572_209 | transcriptional activator domain | uni | sce_8789 | 30.74 Adenylate cyclase (EC 4.6.1.1) / Guanylate cyclase (EC 4.6.1.2) |
| SCE1572_210 | putative oxidoreductase | uni | sce_4749 | 35.76 Oxidoreductase |
| SCE1572_211 | Galactose/methyl galactoside ABC transport system, permease protein MglC (TC 3.A.1.2.3) | uni | sce_6146 | 34.12 Ribose ABC transport system, permease protein RbsC (TC 3.A.1.2.1) |
| SCE1572_212 | Galactose/methyl galactoside ABC transport system, ATP-binding protein MglA (EC 3.6.3.17) | uni | sce_3480 | 44.95 D-xylose transport ATP-binding protein XylG |
| SCE1572_213 | Galactose/methyl galactoside ABC transport system, D-galactose-binding periplasmic protein MglB (TC 3.A.1.2.3) | uni | sce_3709 | 27.21 Putative sugar ABC transport system, periplasmic binding protein YtFQ precursor |
| SCE1572_214 | FIG01088228: hypothetical protein | bi | sce_2528 | 97.56 FIG01088228: hypothetical protein |
| SCE1572_215 | NAD binding oxidoreductase | bi | sce_6003 | 89.39 NAD binding oxidoreductase |
| SCE1572_216 | hypothetical protein | - | - | 0 |
| SCE1572_217 | membrane-bound metal-dependent hydrolase | - | - | 0 |
| SCE1572_218 | conserved hypothetical protein | - | - | 0 |
| SCE1572_219 | hypothetical protein | bi | sce_5881 | 91.13 hypothetical protein |
| SCE1572_220 | Glutathione S-transferase (EC 2.5.1.18) | uni | sce_7306 | 45.5 Glutathione S-transferase (EC 2.5.1.18) |
| SCE1572_221 | AAA ATPase, central region | uni | sce_3102 | 34.51 Cell division protein FtsH (EC 3.4.24.-) |
| SCE1572_222 | Glutathione S-transferase | bi | sce_10163 | 97.38 Glutathione S-transferase |
| SCE1572_223 | Transcriptional regulator, LysR family | bi | sce_9852 | 85.86 Transcriptional regulator, LysR family |
| SCE1572_224 | Beta-lactamase-like precursor | bi | sce_9851 | 82.76 Beta-lactamase-like precursor |
| SCE1572_225 | hypothetical protein | - | - | 0 |
| SCE1572_226 | hypothetical protein | uni | sce_2494 | 49.76 metal dependent phosphohydrolase |
| SCE1572_227 | Transcriptional regulator, AraC family | uni | sce_9866 | 50 Transcriptional regulator, AraC family |
| SCE1572_228 | hypothetical protein | - | - | 0 |
| SCE1572_229 | hypothetical protein | bi | sce_3088 | 37.61 hypothetical protein |
| SCE1572_230 | hypothetical protein | bi | sce_3089 | 44.14 hypothetical protein |
| SCE1572_231 | hypothetical protein | - | - | 0 |
| SCE1572_232 | hypothetical protein | - | - | 0 |
| SCE1572_233 | hypothetical protein | uni | sce_1297 | 37.7 hypothetical protein |
| SCE1572_234 | FIG01087333: hypothetical protein | bi | sce_5301 | 84.62 FIG01087333: hypothetical protein |
| SCE1572_235 | hypothetical protein | bi | sce_5302 | 90.36 hypothetical protein |
| SCE1572_236 | DNA repair protein RadC | uni | sce_8397 | 89.13 DNA repair protein RadC |
| SCE1572_237 | hypothetical protein | bi | sce_5613 | 40 hypothetical protein |
| SCE1572_238 | hypothetical protein | bi | sce_5612 | 54.93 FIG01086888: hypothetical protein |
| SCE1572_239 | hypothetical protein | - | - | 0 |
| SCE1572_240 | DNA repair protein RadC | bi | sce_8397 | 93.9 DNA repair protein RadC |
| SCE1572_241 | Rhs-family protein | uni | sce_10193 | 40.69 Rhs family carbohydrate-binding protein |
| SCE1572_242 | hypothetical protein | uni | sce_4560 | 34.34 FIG01088881: hypothetical protein |
| SCE1572_243 | hypothetical protein | - | - | 0 |
| SCE1572_244 | DNA repair protein RadC | bi | sce_8398 | 94.31 DNA repair protein RadC |
| SCE1572_245 | hypothetical protein | uni | sce_513 | 81.57 FIG01087636: hypothetical protein |
| SCE1572_246 | Transcriptional regulator Cro/CI family | uni | sce_514 | 50.59 hypothetical protein |
| SCE1572_247 | Integron integrase IntIPac | uni | sce_515 | 96.2 Integron integrase IntIPac |
| SCE1572_248 | putative hydrolase/lactonase | - | - | 0 |
| SCE1572_249 | hypothetical protein | - | - | 0 |
| SCE1572_250 | hypothetical protein | uni | sce_6975 | 91.41 hypothetical protein |
| SCE1572_251 | Tat (Twin-arginine translocation) pathway signal sequence domain protein | bi | sce_7318 | 89.49 Tat (Twin-arginine translocation) pathway signal sequence domain protein |
| SCE1572_252 | hypothetical protein | - | - | 0 |
| SCE1572_253 | hypothetical protein | bi | sce_5453 | 62.18 hypothetical protein |
| SCE1572_254 | hypothetical protein | - | - | 0 |
| SCE1572_255 | hypothetical protein | bi | sce_8414 | 92.68 hypothetical protein |
| SCE1572_256 | PE-PGRS FAMILY PROTEIN | bi | sce_8408 | 80.6 PE-PGRS FAMILY PROTEIN |
| SCE1572_257 | hypothetical protein | - | - | 0 |
| SCE1572_258 | hypothetical protein | bi | sce_8407 | 82.02 hypothetical protein |
| SCE1572_259 | PE-PGRS FAMILY PROTEIN | uni | sce_6815 | 63.87 PE-PGRS FAMILY PROTEIN |
| SCE1572_260 | hypothetical protein | uni | sce_6878 | 75.08 hypothetical protein |
| SCE1572_261 | hypothetical protein | - | - | 0 |
| SCE1572_262 | Dihydrofolate reductase (EC 1.5.1.3) | bi | sce_4682 | 87.33 Dihydrofolate reductase (EC 1.5.1.3) |
| SCE1572_263 | hypothetical protein | - | - | 0 |
| SCE1572_264 | hypothetical protein | bi | sce_1106 | 62.75 hypothetical protein |
| SCE1572_265 | Para-aminobenzoate synthase, aminase component (EC 2.6.1.85) # PabAa | uni | sce_5651 | 36.49 Para-aminobenzoate synthase, amidotransferase component (EC 2.6.1.85) / Para-aminobenzoate synthase, aminase component (EC 2 |
| SCE1572_266 | Anthranilate synthase, amidotransferase component (EC 4.1.3.27) | bi | sce_5651 | 43.39 Para-aminobenzoate synthase, amidotransferase component (EC 2.6.1.85) / Para-aminobenzoate synthase, aminase component (EC 2 |
| SCE1572_267 | Long-chain-fatty-acid--CoA ligase (EC 6.2.1.3) | uni | sce_9237 | 37.14 Long-chain-fatty-acid--CoA ligase (EC 6.2.1.3) |
| SCE1572_268 | hypothetical protein | - | - | 0 |
| SCE1572_269 | hypothetical protein | bi | sce_9355 | 69.23 hypothetical protein |
| SCE1572_270 | Glutathione S-transferase (EC 2.5.1.18) | uni | sce_1670 | 33.67 Glutathione S-transferase (EC 2.5.1.18) |
| SCE1572_271 | Xylose isomerase (EC 5.3.1.5) | uni | sce_6076 | 94.36 Xylose isomerase (EC 5.3.1.5) |
| SCE1572_272 | hypothetical protein | - | - | 0 |
| SCE1572_273 | FIG01088530: hypothetical protein | bi | sce_9375 | 77.76 FIG01088530: hypothetical protein |
| SCE1572_274 | hypothetical protein | - | - | 0 |
| SCE1572_275 | conserved hypothetical protein | bi | sce_8423 | 93.53 conserved hypothetical protein |
| SCE1572_276 | putative glyoxalase/bleomycin resistance protein/dioxygenase superfamily protein | - | - | 0 |
| SCE1572_277 | Arylsulfatase (EC 3.1.6.1) | uni | sce_8647 | 32.33 Arylsulfatase (EC 3.1.6.1) |
| SCE1572_278 | hypothetical protein | - | - | 0 |
| SCE1572_279 | hypothetical protein | - | - | 0 |
| SCE1572_280 | hypothetical protein | - | - | 0 |
| SCE1572_281 | hypothetical abductin-like protein | bi | sce_6002 | 79.34 hypothetical abductin-like protein |
| SCE1572_282 | hypothetical protein | - | - | 0 |
| SCE1572_283 | Bifunctional protein: zinc-containing alcohol dehydrogenase; quinone oxidoreductase (NADPH:quinone reductase) (EC 1.1.1.-) | bi | sce_1702 | 56.52 Bifunctional protein: zinc-containing alcohol dehydrogenase; quinone oxidoreductase (NADPH:quinone reductase) (EC 1.1.1.-); Sin |
| SCE1572_284 | Glutamate racemase (EC 5.1.1.3) | bi | sce_9986 | 82.22 Glutamate racemase (EC 5.1.1.3) |
| SCE1572_285 | hypothetical protein | - | - | 0 |
| SCE1572_286 | hypothetical protein | - | - | 0 |
| SCE1572_287 | hypothetical protein | uni | sce_5705 | 40.45 FIG01088991: hypothetical protein |
| SCE1572_288 | dienelactone hydrolase family protein | bi | sce_9362 | 82.93 hypothetical protein |
| SCE1572_289 | Penicillin amidase (EC:3.5.1.11) | uni | sce_9234 | 29.29 Penicillin acylase II (EC 3.5.1.11) |
| SCE1572_290 | hypothetical protein | - | - | 0 |
| SCE1572_291 | hypothetical protein | - | - | 0 |
| SCE1572_292 | hypothetical protein | uni | sce_6470 | 44.83 Lactoylglutathione lyase (EC 4.4.1.5) |
| SCE1572_293 | hypothetical protein | - | - | 0 |
| SCE1572_294 | hypothetical protein | - | - | 0 |
| SCE1572_295 | hypothetical protein | - | - | 0 |
| SCE1572_296 | YegF | - | - | 0 |
| SCE1572_297 | Reductase | bi | sce_8687 | 85.49 Reductase |
| SCE1572_298 | Transcriptional regulator | bi | sce_8686 | 88.16 Transcriptional regulator |
| SCE1572_299 | FIG01085860: hypothetical protein | bi | sce_9374 | 58.82 FIG01085860: hypothetical protein |
| SCE1572_300 | methyltransferase, UbiE/COQ5 family | uni | sce_9010 | 37.8 Methylase of polypeptide chain release factors |
| SCE1572_301 | serine/threonine protein kinase | uni | sce_10233 | 34.77 protein kinase domain |
| SCE1572_302 | hypothetical protein | - | - | 0 |
| SCE1572_303 | hypothetical protein | - | - | 0 |
| SCE1572_304 | hypothetical protein | - | - | 0 |
| SCE1572_305 | hypothetical protein | uni | sce_1333 | 42.38 FIG01085833: hypothetical protein |
| SCE1572_306 | hypothetical protein | uni | sce_10267 | 49.42 hypothetical protein |
| SCE1572_307 | hypothetical protein | uni | sce_10267 | 56.14 hypothetical protein |
| SCE1572_308 | 2-dehydropantoate 2-reductase (EC 1.1.1.169) | bi | sce_2028 | 92.02 2-dehydropantoate 2-reductase (EC 1.1.1.169) |
| SCE1572_309 | FAD-binding monooxygenase, PheA/TfDB family, similarity to 2,4-dichlorophenol 6-monoxygenase | bi | sce_7865 | 72.98 FAD-binding monooxygenase, PheA/TfDB family, similarity to 2,4-dichlorophenol 6-monoxygenase |
| SCE1572_310 | Transcriptional regulator, TetR family | bi | sce_7866 | 87.84 Transcriptional regulator, TetR family |
| SCE1572_311 | Acetoactolactate synthase large subunit (EC 2.2.1.6) | bi | sce_9786 | 34.71 FIG01089071: hypothetical protein |
| SCE1572_312 | 3-oxoacyl-[acyl-carrier-protein] synthase, KASIII (EC 2.3.1.41) | bi | sce_9787 | 30.6 3-oxoacyl-[acyl-carrier-protein] synthase, KASIII (EC 2.3.1.41) |
| SCE1572_313 | hypothetical protein | - | - | 0 |
| SCE1572_314 | Predicted membrane protein/domain | bi | sce_2561 | 85.23 Predicted membrane protein/domain |
| SCE1572_315 | NHL repeat protein | bi | sce_616 | 66.06 NHL repeat protein |
| SCE1572_316 | hypothetical protein | bi | sce_619 | 69.25 hypothetical protein |
| SCE1572_317 | Transcriptional regulator, AraC family | bi | sce_620 | 65.96 Transcriptional regulator, AraC family |
| SCE1572_318 | hypothetical protein | uni | sce_3777 | 55.17 FIG01087231: hypothetical protein |
| SCE1572_319 | hypothetical protein | uni | sce_198 | 57.2 hypothetical protein |
| SCE1572_320 | protein of unknown function DUF1568 | uni | sce_207 | 42.09 FIG01088682: hypothetical protein |
| SCE1572_321 | hypothetical protein | - | - | 0 |
| SCE1572_322 | hypothetical protein | bi | sce_4699 | 70.65 FIG01087239: hypothetical protein |
| SCE1572_323 | hypothetical protein | uni | sce_2128 | 40.95 hypothetical protein |
| SCE1572_324 | High-affinity carbon uptake protein Hat/HatR | uni | sce_5086 | 34.45 toIB protein precursor, periplasmic protein involved in the tonB-independent uptake of group A colicins |
| SCE1572_325 | hypothetical protein | - | - | 0 |

| | | | |
|-------------|--|-----|--|
| SCE1572_326 | hypothetical protein | - | 0 |
| SCE1572_327 | hypothetical protein | - | 0 |
| SCE1572_328 | hypothetical protein | - | 0 |
| SCE1572_329 | Octaprenyl-diphosphate synthase (EC 2.5.1.-) / Dimethylallyltransferase (EC 2.5.1.1) / Geranyltransferase (farnesylidiphosphate | uni | 34.63 Octaprenyl-diphosphate synthase (EC 2.5.1.-) / Dimethylallyltransferase (EC 2.5.1.1) / Geranyltransferase (farnesylidiphosphate |
| SCE1572_330 | D-alanyl-D-alanine carboxypeptidase (EC 3.4.16.4) | uni | 78.12 D-alanyl-D-alanine carboxypeptidase (EC 3.4.16.4) |
| SCE1572_331 | Beta-lactamase class C and other penicillin binding proteins | bi | 75.31 Beta-lactamase class C and other penicillin binding proteins |
| SCE1572_332 | Rhodanese-like domain protein | bi | 87.67 Rhodanese-like domain protein |
| SCE1572_333 | Putative cytoplasmic protein | bi | 87.59 Putative cytoplasmic protein |
| SCE1572_334 | Probable transcription regulator protein | bi | 87.12 Probable transcription regulator protein |
| SCE1572_335 | Alkanesulfonates-binding protein | bi | 80.43 Alkanesulfonates-binding protein |
| SCE1572_336 | Alkanesulfonates transport system permease protein | bi | 88.19 Alkanesulfonates transport system permease protein |
| SCE1572_337 | Nitrioltriacetate monooxygenase | bi | 92.44 Nitrioltriacetate monooxygenase |
| SCE1572_338 | FIG01124324: hypothetical protein | bi | 49.7 FIG01124324: hypothetical protein |
| SCE1572_339 | Transcriptional regulator, AraC family | bi | 79.27 Transcriptional regulator, AraC family |
| SCE1572_340 | Glutathione S-transferase (EC 2.5.1.18) | bi | 80.8 Glutathione S-transferase (EC 2.5.1.18) |
| SCE1572_341 | carboxyl-terminal protease | bi | 78 carboxyl-terminal protease |
| SCE1572_342 | Alkyl hydroperoxide reductase subunit C-like protein | bi | 96.23 Alkyl hydroperoxide reductase subunit C-like protein |
| SCE1572_343 | hypothetical protein | bi | 87.56 hypothetical protein |
| SCE1572_344 | hypothetical protein | bi | 38.25 hypothetical protein |
| SCE1572_345 | Transcriptional regulator, LysR family | bi | 61.17 Transcriptional regulator, LysR family |
| SCE1572_346 | Endo-1,4-beta-xylanase A precursor (EC 3.2.1.8) | bi | 84.54 Endo-1,4-beta-xylanase A precursor (EC 3.2.1.8) |
| SCE1572_347 | Transcriptional regulator, AraC family | bi | 81.09 Transcriptional regulator, AraC family |
| SCE1572_348 | putative glycosyl transferase | uni | 50.66 putative glycosyl transferase |
| SCE1572_349 | glycosyl transferase, group 1 | uni | 45.92 glycosyl transferase, group 1 family protein |
| SCE1572_350 | glycosyl transferase, group 1 | bi | 82.19 glycosyl transferase, group 1 |
| SCE1572_351 | aminoglycoside N(3')-acetyltransferase IV (ACC(3)-IV)(EC:2.3.1.81) | - | 0 |
| SCE1572_352 | FIG01085969: hypothetical protein | bi | 79.51 FIG01085969: hypothetical protein |
| SCE1572_353 | Transcriptional regulator, IclR family | bi | 91.88 Transcriptional regulator, IclR family |
| SCE1572_354 | Branched-chain amino acid aminotransferase (EC 2.6.1.42) | bi | 90.51 Branched-chain amino acid aminotransferase (EC 2.6.1.42) |
| SCE1572_355 | Transcriptional regulator, LysR family | bi | 89 Transcriptional regulator, LysR family |
| SCE1572_356 | hypothetical protein | - | 0 |
| SCE1572_357 | hypothetical protein | bi | 76.91 hypothetical protein |
| SCE1572_358 | Lipid A export ATP-binding/permease protein MsbA | bi | 88.14 Lipid A export ATP-binding/permease protein MsbA |
| SCE1572_359 | Lipid A export ATP-binding/permease protein MsbA | bi | 90.32 Lipid A export ATP-binding/permease protein MsbA |
| SCE1572_360 | Organic hydroperoxide resistance protein | bi | 94.33 Organic hydroperoxide resistance protein |
| SCE1572_361 | hypothetical protein | - | 0 |
| SCE1572_362 | hypothetical protein | - | 0 |
| SCE1572_363 | hypothetical protein | - | 0 |
| SCE1572_364 | hypothetical protein | uni | 37.5 Gll0645 protein |
| SCE1572_365 | FIG01086339: hypothetical protein | uni | 58.21 PE-PGRS FAMILY PROTEIN |
| SCE1572_366 | Transcriptional regulator, AraC family | uni | 57.51 Transcriptional regulator, AraC family |
| SCE1572_367 | hypothetical protein | bi | 86.22 hypothetical protein |
| SCE1572_368 | Serine-threonine protein kinase | bi | 84.47 Serine-threonine protein kinase |
| SCE1572_369 | Probable transmembrane protein | - | 0 |
| SCE1572_370 | Branched-chain amino acid transport protein aziC | - | 0 |
| SCE1572_371 | Transcriptional regulator, TetR family | uni | 39.13 Transcriptional regulator, TetR family |
| SCE1572_372 | putative cytochrome P450 hydroxylase | uni | 44.39 putative cytochrome P450 hydroxylase |
| SCE1572_373 | FIG01211180: hypothetical protein | bi | 88.78 FIG01211180: hypothetical protein |
| SCE1572_374 | Chemotaxis protein methyltransferase CheR (EC 2.1.1.80) | bi | 78.79 Chemotaxis protein methyltransferase CheR (EC 2.1.1.80) |
| SCE1572_375 | Catalase (EC 1.11.1.6) | - | 0 |
| SCE1572_376 | putative glucose-fructose oxidoreductase oxidoreductase protein | uni | 32.84 NAD binding oxidoreductase |
| SCE1572_377 | FIG01087827: hypothetical protein | bi | 84.97 FIG01087827: hypothetical protein |
| SCE1572_378 | Probable glutathione S-transferase-related transmembrane protein (EC 2.5.1.18) | bi | 47.44 Probable glutathione S-transferase-related transmembrane protein (EC 2.5.1.18) |
| SCE1572_379 | RNA polymerase sigma factor RpoD | bi | 90.83 RNA polymerase sigma factor RpoD |
| SCE1572_380 | RNA polymerase sigma factor RpoE | bi | 74.44 RNA polymerase sigma factor RpoE |
| SCE1572_381 | hypothetical protein | bi | 48.89 FIG01088162: hypothetical protein |
| SCE1572_382 | hypothetical protein | bi | 89.92 Arsenate reductase and related proteins, glutaredoxin family |
| SCE1572_383 | Response regulator of zinc sigma-54-dependent two-component system | bi | 61.2 Response regulator of zinc sigma-54-dependent two-component system |
| SCE1572_384 | hypothetical protein | - | 0 |
| SCE1572_385 | hypothetical protein | - | 0 |
| SCE1572_386 | hypothetical protein | - | 0 |
| SCE1572_387 | Similarities with trjQ12218 Saccharomyces cerevisiae YOR009w | bi | 68.44 Similarities with trjQ12218 Saccharomyces cerevisiae YOR009w |
| SCE1572_388 | hypothetical protein | bi | 79.29 hypothetical protein |
| SCE1572_389 | Short-chain dehydrogenase, associated with 2-hydroxychromene-2-carboxylate isomerase family protein | bi | 73.33 short-chain dehydrogenase/reductase SDR |
| SCE1572_390 | hypothetical protein | bi | 89.78 hypothetical protein |
| SCE1572_391 | hypothetical protein | - | 0 |
| SCE1572_392 | hypothetical protein | bi | 63.4 conserved hypothetical protein |
| SCE1572_393 | FIG01086155: hypothetical protein | bi | 73.03 FIG01086155: hypothetical protein |
| SCE1572_394 | two-component sensor histidine kinase | bi | 85.28 two-component sensor histidine kinase |
| SCE1572_395 | FIG01086972: hypothetical protein | bi | 77.89 FIG01086972: hypothetical protein |
| SCE1572_396 | hypothetical protein | - | 0 |
| SCE1572_397 | hypothetical protein | uni | 33.64 Gfa-like protein |
| SCE1572_398 | Long-chain-fatty-acid-CoA ligase (EC 6.2.1.3) | bi | 87.73 ATP-dependent nuclease subunit B-like protein |
| SCE1572_399 | hypothetical protein | - | 0 |
| SCE1572_400 | hypothetical protein | bi | 95.79 hypothetical protein |
| SCE1572_401 | hypothetical protein | bi | 97.67 hypothetical protein |
| SCE1572_402 | hypothetical protein | - | 0 |
| SCE1572_403 | Diaminohydroxyphosphoribosylaminopyrimidine deaminase (EC 3.5.4.26) / 5-amino-6-(5-phosphoribosylamino)uracil reducta | bi | 48.48 Diaminohydroxyphosphoribosylaminopyrimidine deaminase (EC 3.5.4.26) / 5-amino-6-(5-phosphoribosylamino)uracil reductase (EC |
| SCE1572_404 | peptidase, S1 (chymotrypsin) family(EC:3.4.21.-) | bi | 86.73 FIG01085761: hypothetical protein |
| SCE1572_405 | FIG00841528: hypothetical protein | bi | 88.89 FIG00841528: hypothetical protein |
| SCE1572_406 | hypothetical protein | - | 0 |
| SCE1572_407 | hypothetical protein | bi | 74.04 hypothetical protein |
| SCE1572_408 | COG1180: Radical SAM, Pyruvate-formate lyase-activating enzyme like | bi | 90 COG1180: Radical SAM, Pyruvate-formate lyase-activating enzyme like |
| SCE1572_409 | putative LpqP (Hydrolase/esterase) | bi | 83.85 LpqP protein |
| SCE1572_410 | Signal transduction protein containing GAF and PtsI domains | bi | 92.75 Signal transduction protein containing GAF and PtsI domains |
| SCE1572_411 | FOG: PAS/PAC domain | bi | 85.13 FOG: PAS/PAC domain |
| SCE1572_412 | Regulatory protein recX | bi | 89.2 Regulatory protein recX |
| SCE1572_413 | Iron-sulfur cluster-binding protein | bi | 86.1 Iron-sulfur cluster-binding protein |
| SCE1572_414 | hypothetical protein | bi | 52.09 hypothetical protein |
| SCE1572_415 | UV-endonuclease uvde | - | 0 |
| SCE1572_416 | hypothetical protein | uni | 33.28 Adenosylhomocysteinase (EC 3.3.1.1) |
| SCE1572_417 | Streptococcal hemagglutinin protein | uni | 33.52 Streptococcal hemagglutinin protein |
| SCE1572_418 | High-affinity carbon uptake protein Hat/HatR | uni | 51.82 NB-ARC domain protein |
| SCE1572_419 | Cobryric acid synthase | bi | 91.24 Cobryric acid synthase |
| SCE1572_420 | Adenosylcobinamide-phosphate synthase | bi | 90.13 Adenosylcobinamide-phosphate synthase |
| SCE1572_421 | Adenosylcobinamide-phosphate guanylyltransferase (EC 2.7.7.62) | bi | 89.29 Adenosylcobinamide-phosphate guanylyltransferase (EC 2.7.7.62) |
| SCE1572_422 | Cobrynic acid A,C-diamide synthase | bi | 86.77 Cobrynic acid A,C-diamide synthase |
| SCE1572_423 | Cob(II)alamin adenosyltransferase (EC 2.5.1.17) | bi | 90.53 Cob(II)alamin adenosyltransferase (EC 2.5.1.17) |
| SCE1572_424 | Cobalt-precorrin-4 C11-methyltransferase (EC 2.1.1.133) | bi | 94.32 Cobalt-precorrin-4 C11-methyltransferase (EC 2.1.1.133) |
| SCE1572_425 | Transcriptional regulator, TetR family | bi | 89.35 Transcriptional regulator, TetR family |
| SCE1572_426 | FIG01087864: hypothetical protein | bi | 81.17 FIG01087864: hypothetical protein |
| SCE1572_427 | hypothetical protein | bi | 85.56 hypothetical protein |
| SCE1572_428 | hypothetical protein | bi | 61.96 FIG01088944: hypothetical protein |
| SCE1572_429 | Nitrogen regulation protein NR(I) | bi | 78.98 Nitrogen regulation protein NR(I) |
| SCE1572_430 | Adenylate cyclase (EC 4.6.1.1) | bi | 84.95 Adenylate cyclase (EC 4.6.1.1) |
| SCE1572_431 | adenylate cyclase 2(EC:4.6.1.1) | bi | 83.39 two-component sensor histidine kinase |
| SCE1572_432 | NtrC | bi | 92.14 NtrC |
| SCE1572_433 | Adenylate cyclase (EC 4.6.1.1) / Guanylate cyclase (EC 4.6.1.2) | bi | 69.33 Adenylate cyclase (EC 4.6.1.1) / Guanylate cyclase (EC 4.6.1.2) |
| SCE1572_434 | hypothetical protein | - | 0 |
| SCE1572_435 | conserved hypothetical protein | bi | 69.5 hypothetical protein |
| SCE1572_436 | hypothetical protein | bi | 64.42 hypothetical protein |
| SCE1572_437 | AknN | bi | 90.42 AknN |
| SCE1572_438 | hypothetical protein | - | 0 |
| SCE1572_439 | hypothetical protein | - | 0 |
| SCE1572_440 | Alpha-glucosidase (EC 3.2.1.20) | uni | 30.67 Alpha-glucosidase (EC 3.2.1.20) |
| SCE1572_441 | hypothetical protein | - | 0 |
| SCE1572_442 | Transcriptional regulator, LysR family | uni | see_7791 |
| SCE1572_443 | Alcohol dehydrogenase (EC 1.1.1.1) | uni | 42.64 Alcohol dehydrogenase (EC 1.1.1.1) |
| SCE1572_444 | Cobalt-precorrin-3b C17-methyltransferase | bi | 86.52 Cobalt-precorrin-3b C17-methyltransferase |
| SCE1572_445 | Cobalt-precorrin-3b C17-methyltransferase | bi | 96.44 Cobalt-precorrin-3b C17-methyltransferase |
| SCE1572_446 | Cobalamin biosynthesis protein CbiG | bi | 93.67 Cobalamin biosynthesis protein CbiG |
| SCE1572_447 | Cobalt-precorrin-2 C20-methyltransferase (EC 2.1.1.130) | bi | 92.88 Cobalt-precorrin-2 C20-methyltransferase (EC 2.1.1.130) |
| SCE1572_448 | Cobalt-precorrin-6y C5-methyltransferase (EC 2.1.1.-) / Cobalt-precorrin-6y C15-methyltransferase [decarboxylating] (EC 2.1.1.-) | bi | 96.06 Cobalt-precorrin-6y C5-methyltransferase (EC 2.1.1.-) / Cobalt-precorrin-6y C15-methyltransferase [decarboxylating] (EC 2.1.1.-) |
| SCE1572_449 | Cobalt-precorrin-8x methylmutase (EC 5.4.1.2) | bi | 95.07 Cobalt-precorrin-8x methylmutase (EC 5.4.1.2) |
| SCE1572_450 | Cobalt-precorrin-6 synthase, anaerobic | bi | 95.64 Cobalt-precorrin-6 synthase, anaerobic |
| SCE1572_451 | Flavodoxin reductases (ferredoxin-NADPH reductases) family 1; Vanillate O-demethylase oxidoreductase (EC 1.14.13.-) | bi | 80.74 Flavodoxin reductases (ferredoxin-NADPH reductases) family 1; Vanillate O-demethylase oxidoreductase (EC 1.14.13.-) |
| SCE1572_452 | unknown protein confirmed by proteomics | bi | 91.94 unknown protein confirmed by proteomics |
| SCE1572_453 | probable secreted protein | bi | 91.17 probable secreted protein |
| SCE1572_454 | hypothetical protein | uni | 30.57 Membrane protein involved in colicin uptake-like protein |
| SCE1572_455 | hypothetical protein | - | 0 |
| SCE1572_456 | ABC-type multidrug transport system, ATPase component | uni | see_848 |
| SCE1572_457 | Transcriptional regulator, TetR family | uni | see_8359 |
| SCE1572_458 | Sirohydrochlorin cobaltochelatae (EC 4.99.1.3) / Putative 2Fe-2S ferredoxin CbiW involved in B12 biosynthesis | bi | see_270 |
| SCE1572_459 | ATPase component CbiO of energizing module of cobalt ECF transporter | bi | see_271 |
| SCE1572_460 | Transmembrane component NikQ of energizing module of nickel ECF transporter | bi | see_272 |
| SCE1572_461 | cobalamin biosynthesis protein CbiM | bi | see_273 |
| SCE1572_462 | Substrate-specific component CbiM of cobalt ECF transporter | bi | see_274 |
| SCE1572_463 | 3-hydroxybutyryl-CoA dehydratase (EC 4.2.1.55) | bi | see_277 |
| SCE1572_464 | hypothetical protein | - | 0 |
| SCE1572_465 | hypothetical membrane protein | - | 0 |
| SCE1572_466 | 3-hydroxybutyryl-CoA dehydrogenase (EC 1.1.1.157); 3-hydroxyacyl-CoA dehydrogenase (EC 1.1.1.155) | bi | see_278 |
| SCE1572_467 | TPR domain protein, putative component of TonB system | bi | see_279 |
| SCE1572_468 | Branched-chain amino acid aminotransferase (EC 2.6.1.42) | bi | see_280 |
| SCE1572_469 | hypothetical protein | bi | see_281 |
| SCE1572_470 | conserved hypothetical protein | bi | see_282 |
| SCE1572_471 | collagen-like protein | uni | see_2882 |
| SCE1572_472 | Endoribonuclease L-PSP | bi | see_283 |
| SCE1572_473 | Recombination protein RecR | bi | see_284 |
| SCE1572_474 | FIG000557: hypothetical protein co-occurring with RecR | bi | see_285 |
| SCE1572_475 | DNA polymerase III subunits gamma and tau (EC 2.7.7.7) | bi | see_286 |
| SCE1572_476 | hypothetical protein | bi | see_287 |
| SCE1572_477 | FIG01086270: hypothetical protein | bi | see_288 |
| SCE1572_478 | expressed protein | bi | see_289 |
| SCE1572_479 | Molybdenum cofactor biosynthesis protein MoaA | bi | see_290 |
| SCE1572_480 | Molybdenum cofactor biosynthesis protein MoaA | bi | see_291 |
| SCE1572_481 | hypothetical protein | bi | see_292 |
| SCE1572_482 | CRISPR-associated helicase Cas3 | bi | see_293 |
| SCE1572_483 | conserved hypothetical protein | bi | see_294 |
| SCE1572_484 | hypothetical protein | bi | see_295 |
| SCE1572_485 | CRISPR-associated protein Cas1 | bi | see_296 |
| SCE1572_486 | CRISPR-associated protein Cas2 | bi | see_297 |
| SCE1572_487 | FIG01087436: hypothetical protein | bi | see_298 |
| SCE1572_488 | HlyD family secretion protein | - | 0 |
| SCE1572_489 | HlyD family secretion protein | uni | see_3858 |
| | | | 26.12 Adenosylhomocysteinase (EC 3.3.1.1) |

| | | | | |
|-------------|--|-----|----------|--|
| SCE1572_490 | HlyD family secretion protein | - | | 0 |
| SCE1572_491 | FIG01087249: hypothetical protein | uni | sce_2338 | 95 Transposase |
| SCE1572_492 | hypothetical protein | - | | 0 |
| SCE1572_493 | FIG01089651: hypothetical protein | uni | sce_5846 | 61.95 FIG01089651: hypothetical protein |
| SCE1572_494 | FIG01087210: hypothetical protein | bi | sce_5847 | 51.65 FIG01087210: hypothetical protein |
| SCE1572_495 | hypothetical protein | - | | 0 |
| SCE1572_496 | FIG01086383: hypothetical protein | bi | sce_5848 | 80.43 FIG01086383: hypothetical protein |
| SCE1572_497 | Osmosensitive K channel histidine kinase KdpD (EC 2.7.3.-) | bi | sce_2515 | 42.92 Osmosensitive K channel histidine kinase KdpD (EC 2.7.3.-) |
| SCE1572_498 | COG3899: Predicted ATPase | uni | sce_8618 | 66.19 Signal transduction histidine kinase CheA (EC 2.7.3.-) |
| SCE1572_499 | D-threo-aldose 1-dehydrogenase (EC 1.1.1.122) | uni | sce_5656 | 27.6 Aldo-keto reductase |
| SCE1572_500 | Thi/PfpI family protein | bi | sce_1070 | 45.33 Thi/PfpI family protein |
| SCE1572_501 | hypothetical protein | - | | 0 |
| SCE1572_502 | hypothetical protein | - | | 0 |
| SCE1572_503 | FIG01086144: hypothetical protein | bi | sce_8663 | 33.63 hypothetical protein |
| SCE1572_504 | RNA polymerase sigma factor RpoE | bi | sce_8662 | 54.88 RNA polymerase sigma factor RpoE |
| SCE1572_505 | hypothetical protein | uni | sce_1483 | 39.29 Serine-threonine protein kinase |
| SCE1572_506 | hypothetical protein | uni | sce_7367 | 49.12 Maltose/maltodextrin ABC transporter, substrate binding periplasmic protein MalE |
| SCE1572_507 | Spermidine synthase (EC 2.5.1.16) | bi | sce_1673 | 89.85 Spermidine synthase (EC 2.5.1.16) |
| SCE1572_508 | Spermine synthase | bi | sce_1674 | 90.25 putative spermidine synthase |
| SCE1572_509 | hypothetical protein | bi | sce_312 | 81.59 hypothetical protein |
| SCE1572_510 | FIG01088788: hypothetical protein | bi | sce_313 | 70.92 FIG01088788: hypothetical protein |
| SCE1572_511 | Large protein containing transglutaminase-like domain | bi | sce_315 | 91.07 Large protein containing transglutaminase-like domain |
| SCE1572_512 | hypothetical protein | bi | sce_317 | 83.33 hypothetical protein |
| SCE1572_513 | unknown | bi | sce_318 | 65.7 unknown |
| SCE1572_514 | hypothetical protein | bi | sce_319 | 86.98 hypothetical protein |
| SCE1572_515 | Oxidoreductase, short chain dehydrogenase/reductase family | bi | sce_321 | 88.26 Oxidoreductase, short chain dehydrogenase/reductase family |
| SCE1572_516 | hypothetical protein | - | | 0 |
| SCE1572_517 | Esterase/hydrolase | uni | sce_107 | 25.75 hydrolase, alpha/beta fold family |
| SCE1572_518 | hypothetical protein | - | | 0 |
| SCE1572_519 | Gfa-like protein | bi | sce_2023 | 88.81 Gfa-like protein |
| SCE1572_520 | hypothetical protein | bi | sce_322 | 60.87 FIG01086035: hypothetical protein |
| SCE1572_521 | EBNA-1 | bi | sce_323 | 68.18 hypothetical protein |
| SCE1572_522 | O-methyltransferase | bi | sce_325 | 84.98 O-methyltransferase |
| SCE1572_523 | Pantothenate kinase type III, CoaX-like (EC 2.7.1.33) | bi | sce_326 | 91.95 Pantothenate kinase type III, CoaX-like (EC 2.7.1.33) |
| SCE1572_524 | Vitamin B12 ABC transporter, permease component BtuC | bi | sce_327 | 89.38 Vitamin B12 ABC transporter, permease component BtuC |
| SCE1572_525 | Mutator mutT protein (7,8-dihydro-8-oxoguanine-triphosphatase) (EC 3.6.1.-) | bi | sce_328 | 97.73 Mutator mutT protein (7,8-dihydro-8-oxoguanine-triphosphatase) (EC 3.6.1.-) |
| SCE1572_526 | FHA domain containing protein | bi | sce_329 | 90.51 FHA domain containing protein |
| SCE1572_527 | Holliday junction DNA helicase RuvA | bi | sce_330 | 91.83 Holliday junction DNA helicase RuvA |
| SCE1572_528 | hypothetical protein | bi | sce_331 | 83.82 hypothetical protein |
| SCE1572_529 | hypothetical protein | bi | sce_332 | 80.74 hypothetical protein |
| SCE1572_530 | Uncharacterized protein with LysM domain, COG1652 | bi | sce_333 | 88.99 Uncharacterized protein with LysM domain, COG1652 |
| SCE1572_531 | FIG01087344: hypothetical protein | bi | sce_334 | 86.87 FIG01087344: hypothetical protein |
| SCE1572_532 | Rhs family protein | uni | sce_121 | 38.68 Putative membrane protein |
| SCE1572_533 | RNA pseudouridine synthase A (EC 4.2.1.70) | bi | sce_339 | 79.49 hypothetical protein |
| SCE1572_534 | hypothetical protein | - | | 0 |
| SCE1572_535 | two component, sigma54 specific, transcriptional regulator, Fis family | bi | sce_341 | 92.1 two component, sigma54 specific, transcriptional regulator, Fis family |
| SCE1572_536 | Copper resistance protein B | bi | sce_342 | 71.7 Copper resistance protein B |
| SCE1572_537 | Polyhydroxyalkanoic acid synthase | bi | sce_343 | 90.96 Polyhydroxyalkanoic acid synthase |
| SCE1572_538 | UPF0256 protein SAV4024 | bi | sce_344 | 83.5 UPF0256 protein SAV4024 |
| SCE1572_539 | hypothetical protein | bi | sce_345 | 90.17 hypothetical protein |
| SCE1572_540 | Probable serine/threonine-protein kinase pknB (EC 2.7.1.-) | bi | sce_346 | 81.65 Probable serine/threonine-protein kinase pknB (EC 2.7.1.-) |
| SCE1572_541 | Thiol-specific antioxidant family (AhpC/TSA) protein associated with thiol:disulfide interchange protein | bi | sce_347 | 86.32 Thiol-specific antioxidant family (AhpC/TSA) protein associated with thiol:disulfide interchange protein |
| SCE1572_542 | hypothetical protein | bi | sce_348 | 85.19 hypothetical protein |
| SCE1572_543 | phosphoesterase PA-phosphatase related | bi | sce_349 | 80.17 hypothetical protein |
| SCE1572_544 | hypothetical protein | bi | sce_350 | 87.29 hypothetical protein |
| SCE1572_545 | Aspartate ammonia-lyase (EC 4.3.1.1) | bi | sce_352 | 90.06 Aspartate ammonia-lyase (EC 4.3.1.1) |
| SCE1572_546 | hypothetical protein | - | | 0 |
| SCE1572_547 | hypothetical protein | bi | sce_354 | 77.53 hypothetical protein |
| SCE1572_548 | Modification methylase XhoI (EC 2.1.1.72) (Adenine-specific methyltransferase XhoI) (M.XhoI) | bi | sce_355 | 87.39 Modification methylase XhoI (EC 2.1.1.72) (Adenine-specific methyltransferase XhoI) (M.XhoI) |
| SCE1572_549 | hypothetical protein | - | | 0 |
| SCE1572_550 | hypothetical protein | - | | 0 |
| SCE1572_551 | Holo-[acyl-carrier protein] synthase (EC 2.7.8.7) | bi | sce_357 | 84.24 Holo-[acyl-carrier protein] synthase (EC 2.7.8.7) |
| SCE1572_552 | NAD(P)HX epimerase / NAD(P)HX dehydratase | bi | sce_358 | 89.72 NAD(P)HX epimerase / NAD(P)HX dehydratase |
| SCE1572_553 | NADP oxidoreductase, coenzyme F420-dependent | - | | 0 |
| SCE1572_554 | hypothetical protein | - | | 0 |
| SCE1572_555 | Cytochrome c551 peroxidase (EC 1.11.1.5) | uni | sce_3352 | 50.78 Cytochrome c551 peroxidase (EC 1.11.1.5) |
| SCE1572_556 | RNA polymerase sigma factor | bi | sce_359 | 86.84 RNA polymerase sigma factor |
| SCE1572_557 | NADH dehydrogenase (EC 1.6.99.3) | bi | sce_360 | 89.33 NADH dehydrogenase (EC 1.6.99.3) |
| SCE1572_558 | Probable transcriptional regulator | bi | sce_361 | 91.96 Probable transcriptional regulator |
| SCE1572_559 | FIG01086996: hypothetical protein | bi | sce_362 | 92.52 FIG01086996: hypothetical protein |
| SCE1572_560 | Sulfate and thiosulfate binding protein CysP | bi | sce_363 | 90.42 Sulfate and thiosulfate binding protein CysP |
| SCE1572_561 | Sulfate transport system permease protein CysT | bi | sce_364 | 92.36 Sulfate transport system permease protein CysT |
| SCE1572_562 | Sulfate transport system permease protein CysW | bi | sce_365 | 92.69 Sulfate transport system permease protein CysW |
| SCE1572_563 | FIG01088797: hypothetical protein | bi | sce_366 | 73.36 FIG01088797: hypothetical protein |
| SCE1572_564 | putative acetyltransferase | uni | sce_8115 | 40.43 Ribosomal-protein-S18p-alanine acetyltransferase (EC 2.3.1.-) |
| SCE1572_565 | conserved hypothetical protein | bi | sce_368 | 91.18 conserved hypothetical protein |
| SCE1572_566 | hypothetical protein | uni | sce_4075 | 29.97 hypothetical protein |
| SCE1572_567 | Multimodular transpeptidase-transglycosylase (EC 2.4.1.129) (EC 3.4.-) | bi | sce_370 | 87.33 Multimodular transpeptidase-transglycosylase (EC 2.4.1.129) (EC 3.4.-) |
| SCE1572_568 | hypothetical protein | bi | sce_371 | 85.95 hypothetical protein |
| SCE1572_569 | hypothetical protein | bi | sce_372 | 80.39 hypothetical protein |
| SCE1572_570 | LuxR family transcriptional regulator | bi | sce_804 | 75 LuxR family transcriptional regulator |
| SCE1572_571 | ATP-dependent Clp protease ATP-binding subunit ClpA | - | | 0 |
| SCE1572_572 | FIG01087436: hypothetical protein | uni | sce_8636 | 58.18 FIG01087436: hypothetical protein |
| SCE1572_573 | Cytochrome c551 peroxidase (EC 1.11.1.5) | bi | sce_375 | 88.71 Cytochrome c551 peroxidase (EC 1.11.1.5) |
| SCE1572_574 | Probable short-chain dehydrogenase | bi | sce_376 | 89.96 Probable short-chain dehydrogenase |
| SCE1572_575 | Rubredoxin | bi | sce_377 | 83.33 Rubredoxin |
| SCE1572_576 | FIG01085894: hypothetical protein | bi | sce_381 | 85.08 FIG01085894: hypothetical protein |
| SCE1572_577 | hypothetical protein | bi | sce_382 | 65.22 hypothetical protein |
| SCE1572_578 | hypothetical protein | bi | sce_383 | 73.85 FIG01086543: hypothetical protein |
| SCE1572_579 | conserved hypothetical protein | bi | sce_384 | 76.1 conserved hypothetical protein |
| SCE1572_580 | Acetylglutamate kinase (EC 2.7.2.8) | bi | sce_385 | 93.09 Acetylglutamate kinase (EC 2.7.2.8) |
| SCE1572_581 | Acetylmethine deacetylase/Succinyl-diaminopimelate desuccinylase and related deacetylases | bi | sce_386 | 90.41 Acetylmethine deacetylase/Succinyl-diaminopimelate desuccinylase and related deacetylases |
| SCE1572_582 | LSU m5C1962 methyltransferase RlmI | bi | sce_392 | 89.67 LSU m5C1962 methyltransferase RlmI |
| SCE1572_583 | hypothetical protein | bi | sce_393 | 77.13 hypothetical protein |
| SCE1572_584 | FIG01087934: hypothetical protein | bi | sce_394 | 95 FIG01087934: hypothetical protein |
| SCE1572_585 | FIG01088190: hypothetical protein | bi | sce_395 | 91.17 FIG01088190: hypothetical protein |
| SCE1572_586 | 4-alpha-glucanotransferase (amylomaltase) (EC 2.4.1.25) | bi | sce_396 | 86.75 4-alpha-glucanotransferase (amylomaltase) (EC 2.4.1.25) |
| SCE1572_587 | serine/threonine protein kinase | bi | sce_398 | 65.8 serine/threonine protein kinase |
| SCE1572_588 | hypothetical protein | bi | sce_399 | 69.05 S-layer protein |
| SCE1572_589 | hypothetical protein | uni | sce_397 | 43.18 FIG01086142: hypothetical protein |
| SCE1572_590 | hypothetical protein | - | | 0 |
| SCE1572_591 | FIG01087489: hypothetical protein | bi | sce_400 | 82.35 FIG01087489: hypothetical protein |
| SCE1572_592 | Malonyl CoA-acyl carrier protein transacylase (EC 2.3.1.39) | bi | sce_401 | 80.78 Malonyl CoA-acyl carrier protein transacylase (EC 2.3.1.39) |
| SCE1572_593 | Fumarate hydratase class I, aerobic (EC 4.2.1.2) | bi | sce_402 | 97.26 Fumarate hydratase class I, aerobic (EC 4.2.1.2) |
| SCE1572_594 | hypothetical protein | - | | 0 |
| SCE1572_595 | alpha/beta hydrolase fold | bi | sce_404 | 84.52 alpha/beta hydrolase fold |
| SCE1572_596 | serine/threonine protein kinase | bi | sce_405 | 85.11 serine/threonine protein kinase |
| SCE1572_597 | erythrocyte membrane protein 1 (PEMP1) | uni | sce_4564 | 70.64 endo-alpha-1,4 polygalactosaminidase precursor |
| SCE1572_598 | FIG01087914: hypothetical protein | bi | sce_406 | 81.68 FIG01087914: hypothetical protein |
| SCE1572_599 | hypothetical protein | uni | sce_5241 | 46.08 FIG01086664: hypothetical protein |
| SCE1572_600 | hypothetical protein | - | | 0 |
| SCE1572_601 | Trehalose synthase (EC 5.4.99.16) | bi | sce_407 | 93.18 Trehalose synthase (EC 5.4.99.16) |
| SCE1572_602 | Serine/threonine-protein kinase pkn3 (EC 2.7.11.1) | bi | sce_410 | 87.52 Serine/threonine-protein kinase pkn3 (EC 2.7.11.1) |
| SCE1572_603 | General secretion pathway protein C | bi | sce_411 | 82.13 General secretion pathway protein C |
| SCE1572_604 | Ubiquinol-cytochrome c reductase, cytochrome B subunit (EC 1.10.2.2) | bi | sce_413 | 87.94 Ubiquinol-cytochrome c reductase, cytochrome B subunit (EC 1.10.2.2) |
| SCE1572_605 | Ubiquinol-cytochrome c reductase iron-sulfur subunit (EC 1.10.2.2) | bi | sce_414 | 91.4 Ubiquinol-cytochrome c reductase iron-sulfur subunit (EC 1.10.2.2) |
| SCE1572_606 | Outer membrane protein assembly factor YaeT precursor | bi | sce_415 | 81.81 Outer membrane protein assembly factor YaeT precursor |
| SCE1572_607 | hypothetical protein | bi | sce_416 | 85.19 hypothetical protein |
| SCE1572_608 | Fe-S oxidoreductase | bi | sce_418 | 92.29 Fe-S oxidoreductase |
| SCE1572_609 | hypothetical protein | - | | 0 |
| SCE1572_610 | TRNA (Guanosine-2'-O)-methyltransferase (EC 2.1.1.34) | bi | sce_420 | 86.02 tRNA (Guanosine18-2'-O)-methyltransferase (EC 2.1.1.34) |
| SCE1572_611 | tRNA (Guanosine18-2'-O)-methyltransferase (EC 2.1.1.34) | uni | sce_420 | 80 tRNA (Guanosine18-2'-O)-methyltransferase (EC 2.1.1.34) |
| SCE1572_612 | Ureidoglycolate hydrolase (EC 3.5.3.19) | bi | sce_421 | 94.25 Ureidoglycolate hydrolase (EC 3.5.3.19) |
| SCE1572_613 | LemA family protein | bi | sce_422 | 94.2 LemA family protein |
| SCE1572_614 | Beta-propeller domains of methanol dehydrogenase type | bi | sce_423 | 86.64 Beta-propeller domains of methanol dehydrogenase type |
| SCE1572_615 | hypothetical protein | - | | 0 |
| SCE1572_616 | 3-ketoacyl-CoA thiolase (EC 2.3.1.16) @ Acetyl-CoA acetyltransferase (EC 2.3.1.9) | bi | sce_424 | 96.03 3-ketoacyl-CoA thiolase (EC 2.3.1.16) @ Acetyl-CoA acetyltransferase (EC 2.3.1.9) |
| SCE1572_617 | Peptidyl-prolyl cis-trans isomerase (EC 5.2.1.8) | bi | sce_425 | 88.89 Peptidyl-prolyl cis-trans isomerase (EC 5.2.1.8) |
| SCE1572_618 | FIG01085502: hypothetical protein | bi | sce_426 | 77.84 FIG01085502: hypothetical protein |
| SCE1572_619 | hypothetical protein; putative Adenylate cyclase domain | bi | sce_427 | 74.53 chad domain family |
| SCE1572_620 | Ribonuclease J2 (endoribonuclease in RNA processing) | bi | sce_428 | 96.42 Ribonuclease J2 (endoribonuclease in RNA processing) |
| SCE1572_621 | signal peptide peptidase SppA, 36K type (EC:3.1.3.2) | bi | sce_430 | 90.03 peptidase S49, protease IV:Peptidase S49, SppA |
| SCE1572_622 | hypothetical protein | - | | 0 |
| SCE1572_623 | Ribonucleotide reductase of class II (coenzyme B12-dependent) (EC 1.17.4.1) | bi | sce_431 | 94.3 Ribonucleotide reductase of class II (coenzyme B12-dependent) (EC 1.17.4.1) |
| SCE1572_624 | hypothetical protein | - | | 0 |
| SCE1572_625 | hypothetical protein | - | | 0 |
| SCE1572_626 | hypothetical protein | uni | sce_5162 | 36.36 Serine-threonine protein kinase |
| SCE1572_627 | AAA ATPase | uni | sce_3520 | 70.91 AAA ATPase |
| SCE1572_628 | Thiamine-monophosphate kinase (EC 2.7.4.16) | bi | sce_436 | 86.93 Thiamine-monophosphate kinase (EC 2.7.4.16) |
| SCE1572_629 | Sensor protein | bi | sce_437 | 87.29 Phosphate regulon sensor protein Phor (SphS) (EC 2.7.13.3) |
| SCE1572_630 | gliding motility protein MglA | bi | sce_438 | 96.69 gliding motility protein MglA |
| SCE1572_631 | Putative ATP /GTP binding protein | bi | sce_439 | 96.69 Dynamins family protein |
| SCE1572_632 | Zn-dependent protease with chaperone function | bi | sce_440 | 97.98 Zn-dependent protease with chaperone function |
| SCE1572_633 | Homoserine kinase (EC 2.7.1.39) | bi | sce_441 | 87.25 Homoserine kinase (EC 2.7.1.39) |
| SCE1572_634 | GTP-binding protein HlX | bi | sce_442 | 94.22 GTP-binding protein HlX |
| SCE1572_635 | hypothetical protein | bi | sce_443 | 69.18 FIG01089529: hypothetical protein |
| SCE1572_636 | OmpA/MotB | bi | sce_444 | 86.88 FIG01086993: hypothetical protein |
| SCE1572_637 | Siroheme synthase / Precorrin-2 oxidase (EC 1.3.1.76) / Sirohydrochlorin ferrochelatase (EC 4.99.1.4) / Uroporphyrinogen-III | bi | sce_446 | 88.61 siroheme synthase-like protein |
| SCE1572_638 | FIG01089624: hypothetical protein | bi | sce_447 | 87.94 FIG01089624: hypothetical protein |
| SCE1572_639 | Outer membrane protein assembly factor YaeT precursor | bi | sce_448 | 92.46 Outer membrane protein assembly factor YaeT precursor |
| SCE1572_640 | FIG01089580: hypothetical protein | bi | sce_449 | 78.69 FIG01089580: hypothetical protein |
| SCE1572_641 | Phosphoribosyl-AMP cyclohydrolase (EC 3.5.4.19) / Phosphoribosyl-ATP pyrophosphatase (EC 3.6.1.31) | bi | sce_450 | 93.45 Phosphoribosyl-AMP cyclohydrolase (EC 3.5.4.19) / Phosphoribosyl-ATP pyrophosphatase (EC 3.6.1.31) |
| SCE1572_642 | Prolipoprotein diacylglyceryl transferase (EC 2.4.99.-) | bi | sce_451 | 85.17 Prolipoprotein diacylglyceryl transferase (EC 2.4.99.-) |
| SCE1572_643 | hypothetical protein | bi | sce_452 | 80.26 hypothetical protein |
| SCE1572_644 | hypothetical protein | uni | sce_453 | 66.85 hypothetical protein |
| SCE1572_645 | hypothetical protein | bi | sce_453 | 89.93 hypothetical protein |
| SCE1572_646 | hypothetical protein | - | | 0 |
| SCE1572_647 | hypothetical protein | - | | 0 |
| SCE1572_648 | Serine/threonine-protein kinase pkn3 (EC 2.7.11.1) | bi | sce_455 | 85.48 Serine/threonine-protein kinase pkn3 (EC 2.7.11.1) |
| SCE1572_649 | hypothetical protein | - | | 0 |
| SCE1572_650 | Translation elongation factor Tu | uni | sce_457 | 98.74 Translation elongation factor Tu |
| SCE1572_651 | LSU ribosomal protein L33p | bi | sce_458 | 96.43 LSU ribosomal protein L33p |
| SCE1572_652 | Preprotein translocase subunit SecE (TC 3.A.5.1.1) | bi | sce_459 | 81.82 Preprotein translocase subunit SecE (TC 3.A.5.1.1) |
| SCE1572_653 | Transcription antitermination protein NusG | bi | sce_460 | 98.3 Transcription antitermination protein NusG |

| | | | | |
|-------------|---|-----|-----------|---|
| SCE1572_654 | hypothetical protein | - | | 0 |
| SCE1572_655 | LSU ribosomal protein L11p (L12e) | bi | sce_461 | 96.6 LSU ribosomal protein L11p (L12e) |
| SCE1572_656 | LSU ribosomal protein L1p (L10Ae) | bi | sce_462 | 97.03 LSU ribosomal protein L1p (L10Ae) |
| SCE1572_657 | LSU ribosomal protein L10p (P0) | bi | sce_463 | 95.38 LSU ribosomal protein L10p (P0) |
| SCE1572_658 | LSU ribosomal protein L7/L12 (P1/P2) | bi | sce_464 | 96.12 LSU ribosomal protein L7/L12 (P1/P2) |
| SCE1572_659 | hypothetical protein | bi | sce_465 | 92.98 hypothetical protein |
| SCE1572_660 | DNA-directed RNA polymerase beta subunit (EC 2.7.7.6) | bi | sce_466 | 99.13 DNA-directed RNA polymerase beta subunit (EC 2.7.7.6) |
| SCE1572_661 | hypothetical protein | bi | sce_467 | 78 hypothetical protein |
| SCE1572_662 | DNA-directed RNA polymerase beta' subunit (EC 2.7.7.6) | bi | sce_468 | 99.3 DNA-directed RNA polymerase beta' subunit (EC 2.7.7.6) |
| SCE1572_663 | hypothetical protein | - | | 0 |
| SCE1572_664 | GSPII_E domain/HD domain/response regulator | bi | sce_469 | 90.66 Response regulator receiver: Metal-dependent phosphohydrolase, HD subdomain |
| SCE1572_665 | Ribosomal-protein-S5p-alanine acetyltransferase | bi | sce_470 | 87.56 Ribosomal-protein-S5p-alanine acetyltransferase |
| SCE1572_666 | 3-methyl-2-oxobutanoate hydroxymethyltransferase (EC 2.1.2.11) | bi | sce_471 | 97.46 3-methyl-2-oxobutanoate hydroxymethyltransferase (EC 2.1.2.11) |
| SCE1572_667 | conserved hypothetical protein, double-transmembrane region | bi | sce_472 | 90.3 conserved hypothetical protein, double-transmembrane region |
| SCE1572_668 | hypothetical protein | bi | sce_473 | 94.04 hypothetical protein |
| SCE1572_669 | Cell division protein FtsH (EC 3.4.24.-) | bi | sce_474 | 90.34 Cell division protein FtsH (EC 3.4.24.-) |
| SCE1572_670 | FIG01085043: hypothetical protein | bi | sce_475 | 78.3 FIG01085043: hypothetical protein |
| SCE1572_671 | serine/threonine protein kinase(EC:2.7.11.1) | bi | sce_476 | 76.81 Protein kinase:PASTA:Serine/threonine protein kinase, active site |
| SCE1572_672 | Flagellar motor rotation protein MotB | bi | sce_478 | 65.23 Flagellar motor rotation protein MotB |
| SCE1572_673 | FIG01088809: hypothetical protein | bi | sce_479 | 91.3 FIG01088809: hypothetical protein |
| SCE1572_674 | hypothetical protein | - | | 0 |
| SCE1572_675 | hypothetical protein | - | | 0 |
| SCE1572_676 | hypothetical protein | bi | sce_480 | 87.71 probable O-linked GlcNAc transferase-putative TPR-containing transmembrane protein |
| SCE1572_677 | Heat shock protein DnaJ-like | bi | sce_481 | 96.38 ATP-binding protein |
| SCE1572_678 | FIG00675759: hypothetical protein | bi | sce_482 | 93.37 FIG00675759: hypothetical protein |
| SCE1572_679 | Rhodanese-related sulfurtransferase | bi | sce_483 | 87.59 Rhodanese-related sulfurtransferase |
| SCE1572_680 | hypothetical protein | umi | sce_9648 | 63.16 hypothetical protein |
| SCE1572_681 | Glycosyltransferase | bi | sce_484 | 90.68 Glycosyltransferase |
| SCE1572_682 | two-component hybrid sensor and regulator | bi | sce_485 | 92.86 two-component hybrid sensor and regulator |
| SCE1572_683 | Copper-sensing two-component system response regulator CpxR | bi | sce_486 | 96.72 Copper-sensing two-component system response regulator CpxR |
| SCE1572_684 | FIG01084951: hypothetical protein | bi | sce_487 | 85 FIG01084951: hypothetical protein |
| SCE1572_685 | hypothetical protein | - | | 0 |
| SCE1572_686 | Serine/threonine protein kinase (EC 2.7.11.1) | bi | sce_488 | 85.48 Serine/threonine protein kinase (EC 2.7.11.1) |
| SCE1572_687 | hypothetical protein | bi | sce_489 | 71.53 hypothetical protein |
| SCE1572_688 | hypothetical protein | bi | sce_490 | 89.66 FIG01088316: hypothetical protein |
| SCE1572_689 | Transcriptional regulator, GntR family domain / Aspartate aminotransferase (EC 2.6.1.1) | bi | sce_491 | 88.27 Transcriptional regulator, GntR family domain |
| SCE1572_690 | 4-carboxymuconolactone decarboxylase domain/alkylhydroperoxidase AhpD family core domain protein | bi | sce_492 | 69.03 4-carboxymuconolactone decarboxylase domain/alkylhydroperoxidase AhpD family core domain protein |
| SCE1572_691 | Long-chain-fatty-acid-CoA ligase (EC 6.2.1.3) | bi | sce_494 | 85.82 Long-chain-fatty-acid-CoA ligase (EC 6.2.1.3) |
| SCE1572_692 | FIG01086587: hypothetical protein | bi | sce_495 | 92.13 FIG01086587: hypothetical protein |
| SCE1572_693 | Cystathionine beta-synthase (EC 4.2.1.22) | bi | sce_496 | 95.01 Cystathionine beta-synthase (EC 4.2.1.22) |
| SCE1572_694 | hypothetical protein | bi | sce_9364 | 89.9 hypothetical protein |
| SCE1572_695 | putative ring-cleaving dioxygenase | bi | sce_9358 | 89.93 putative ring-cleaving dioxygenase |
| SCE1572_696 | hypothetical protein | umi | sce_923 | 54.55 hypothetical protein |
| SCE1572_697 | Gill1489 protein | umi | sce_924 | 48.41 Gill1489 protein |
| SCE1572_698 | Gill1489 protein | umi | sce_924 | 62.96 Gill1489 protein |
| SCE1572_699 | Neurosporene desaturase (EC 1.-.-.) | umi | sce_688 | 30.07 Phytoene desaturase, neurosporene or lycopene producing (EC 1.3.-.) |
| SCE1572_700 | hypothetical protein | - | | 0 |
| SCE1572_701 | Response regulator of zinc sigma-54-dependent two-component system | bi | sce_497 | 93.39 Response regulator of zinc sigma-54-dependent two-component system |
| SCE1572_702 | CsbD-like | bi | sce_498 | 83.84 UPF0337 protein PSPTO_1596 |
| SCE1572_703 | Transglycosylase-associated protein | bi | sce_500 | 94.12 putative membrane protein |
| SCE1572_704 | Serine-pyruvate aminotransferase (EC 2.6.1.51) | bi | sce_501 | 97.52 Serine-pyruvate aminotransferase (EC 2.6.1.51) |
| SCE1572_705 | Chloride channel protein | bi | sce_502 | 86.58 Chloride channel protein |
| SCE1572_706 | transcriptional regulator | bi | sce_503 | 88.2 transcriptional regulator |
| SCE1572_707 | Glycyl-tRNA synthetase alpha chain (EC 6.1.1.14) | bi | sce_504 | 97.14 Glycyl-tRNA synthetase alpha chain (EC 6.1.1.14) |
| SCE1572_708 | Orotate phosphoribosyltransferase (EC 2.4.2.10) | bi | sce_505 | 96.35 Orotate phosphoribosyltransferase (EC 2.4.2.10) |
| SCE1572_709 | hypothetical protein | umi | sce_9938 | 42.11 EBNA-1 |
| SCE1572_710 | hypothetical protein | bi | sce_507 | 98.08 hypothetical protein |
| SCE1572_711 | hypothetical protein | bi | sce_508 | 92.25 hypothetical protein |
| SCE1572_712 | hypothetical protein | umi | sce_9445 | 38.26 hypothetical protein |
| SCE1572_713 | styrene monooxygenase component 1-like protein | bi | sce_509 | 85.23 styrene monooxygenase component 1-like protein |
| SCE1572_714 | hypothetical protein | - | | 0 |
| SCE1572_715 | hypothetical protein | - | | 0 |
| SCE1572_716 | FIG01086549: hypothetical protein | umi | sce_5307 | 56.42 FIG01086549: hypothetical protein |
| SCE1572_717 | DNA repair protein RadC | umi | sce_512 | 78.85 DNA repair protein RadC |
| SCE1572_718 | hypothetical protein | umi | sce_513 | 76.5 FIG01087636: hypothetical protein |
| SCE1572_719 | FIG01087953: hypothetical protein | bi | sce_518 | 92.7 FIG01087953: hypothetical protein |
| SCE1572_720 | FIG01087372: hypothetical protein | bi | sce_522 | 93.68 FIG01087372: hypothetical protein |
| SCE1572_721 | FIG01087372: hypothetical protein | umi | sce_522 | 91.15 FIG01087372: hypothetical protein |
| SCE1572_722 | Adenosylhomocysteinase (EC 3.3.1.1) | - | | 0 |
| SCE1572_723 | hypothetical protein | umi | sce_7460 | 36.52 hydrolase, alpha/beta fold family |
| SCE1572_724 | alpha/beta hydrolase fold | umi | sce_9985 | 39.45 Transcriptional regulator, AraC family |
| SCE1572_725 | Transcriptional regulator, AraC family | bi | sce_527 | 87.79 conserved hypothetical protein-putative chloride channel |
| SCE1572_726 | Periplasmic protein TonB links inner and outer membranes-like | bi | sce_527 | 0 |
| SCE1572_727 | hypothetical protein | - | | 0 |
| SCE1572_728 | Serine/threonine-protein kinase pkn2 (EC 2.7.11.1) | bi | sce_528 | 84.66 Serine/threonine-protein kinase pkn2 (EC 2.7.11.1) |
| SCE1572_729 | hypothetical protein | bi | sce_529 | 94.36 hypothetical protein |
| SCE1572_730 | hypothetical protein | bi | sce_532 | 88.45 hypothetical protein |
| SCE1572_731 | protein of unknown function DUF58 | bi | sce_533 | 91.78 hypothetical protein |
| SCE1572_732 | Threonine dehydrogenase and related Zn-dependent dehydrogenases | bi | sce_534 | 85.45 Threonine dehydrogenase and related Zn-dependent dehydrogenases |
| SCE1572_733 | hypothetical protein | bi | sce_535 | 86.62 hypothetical protein |
| SCE1572_734 | Putative membrane protein precursor | bi | sce_537 | 88.38 Putative membrane protein precursor |
| SCE1572_735 | similar to NF-X1 type zinc finger containing protein (ZJ511) (predicted) | bi | sce_538 | 79.36 similar to NF-X1 type zinc finger containing protein (ZJ511) (predicted) |
| SCE1572_736 | hypothetical protein | bi | sce_539 | 72.76 hypothetical protein |
| SCE1572_737 | hypothetical protein | - | | 0 |
| SCE1572_738 | BNR/Asp-box repeat domain protein | bi | sce_540 | 73.48 FIG01089269: hypothetical protein |
| SCE1572_739 | hypothetical protein | bi | sce_541 | 80.68 hypothetical protein |
| SCE1572_740 | Phosphoesterase | bi | sce_542 | 71.57 Phosphoesterase |
| SCE1572_741 | FIG01088764: hypothetical protein | bi | sce_543 | 81.58 FIG01088764: hypothetical protein |
| SCE1572_742 | FIG01086707: hypothetical protein | bi | sce_544 | 75.82 FIG01086707: hypothetical protein |
| SCE1572_743 | FIG01089121: hypothetical protein | bi | sce_545 | 84.62 FIG01089121: hypothetical protein |
| SCE1572_744 | hypothetical protein | - | | 0 |
| SCE1572_745 | serine/threonine protein kinase | bi | sce_548 | 89.91 serine/threonine protein kinase |
| SCE1572_746 | Alpha,alpha-trehalose-phosphate synthase [UDP-forming] (EC 2.4.1.15) / Trehalose-6-phosphate phosphatase (EC 3.1.3.12) | bi | sce_549 | 86.47 Alpha,alpha-trehalose-phosphate synthase [UDP-forming] (EC 2.4.1.15) / Trehalose-6-phosphate phosphatase (EC 3.1.3.12) |
| SCE1572_747 | hypothetical protein | umi | sce_8748 | 33.02 Adenosylhomocysteinase (EC 3.3.1.1) |
| SCE1572_748 | Septum formation protein Maf | bi | sce_551 | 88.29 Septum formation protein Maf |
| SCE1572_749 | Transcriptional (co)regulator CytR | bi | sce_4659 | 58.51 LacI-family transcriptional regulator |
| SCE1572_750 | Magnesium transporter | bi | sce_552 | 88.96 Magnesium transporter |
| SCE1572_751 | hypothetical protein | bi | sce_553 | 80.1 hypothetical protein |
| SCE1572_752 | FIG01085612: hypothetical protein | bi | sce_554 | 72.28 FIG01085612: hypothetical protein |
| SCE1572_753 | FIG01085873: hypothetical protein | bi | sce_555 | 93.47 FIG01085873: hypothetical protein |
| SCE1572_754 | Formyltetrahydrofolate deformylase (EC 3.5.1.10) | bi | sce_556 | 94.35 Formyltetrahydrofolate deformylase (EC 3.5.1.10) |
| SCE1572_755 | Flagelliform silk protein | bi | sce_557 | 48.63 Flagelliform silk protein |
| SCE1572_756 | hypothetical protein | - | | 0 |
| SCE1572_757 | Glutathione S-transferase (EC 2.5.1.18) | bi | sce_558 | 88.7 Glutathione S-transferase (EC 2.5.1.18) |
| SCE1572_758 | Homocysteine S-methyltransferase (EC 2.1.1.10) | bi | sce_559 | 86.44 Homocysteine S-methyltransferase (EC 2.1.1.10) |
| SCE1572_759 | FIG01089040: hypothetical protein | bi | sce_560 | 77.67 FIG01089040: hypothetical protein |
| SCE1572_760 | Family S53 non-peptidase homologue | bi | sce_561 | 82.59 Kumamolysin |
| SCE1572_761 | Tropomyosin-1, isoforms 33/34 (Tropomyosin II) | bi | sce_562 | 80.57 Tropomyosin-1, isoforms 33/34 (Tropomyosin II) |
| SCE1572_762 | Maltodextrin glucosidase (EC 3.2.1.20) | bi | sce_92 | 83.37 Maltodextrin glucosidase (EC 3.2.1.20) |
| SCE1572_763 | hypothetical protein | - | | 0 |
| SCE1572_764 | FIG01085945: hypothetical protein | bi | sce_563 | 88.95 FIG01085945: hypothetical protein |
| SCE1572_765 | hypothetical protein | bi | sce_2567 | 61.54 putative orphan protein |
| SCE1572_766 | hypothetical protein | bi | sce_564 | 72.58 hypothetical protein |
| SCE1572_767 | Copper tolerance protein | bi | sce_565 | 82.96 Copper tolerance protein |
| SCE1572_768 | Multicopper oxidase | bi | sce_566 | 90.77 Multicopper oxidase |
| SCE1572_769 | FIG01088333: hypothetical protein | bi | sce_567 | 77.95 FIG01088333: hypothetical protein |
| SCE1572_770 | FIG01088012: hypothetical protein | bi | sce_568 | 86.57 FIG01088012: hypothetical protein |
| SCE1572_771 | metallophosphoesterase | bi | sce_569 | 83.44 metallophosphoesterase |
| SCE1572_772 | hypothetical protein | bi | sce_570 | 76.78 hypothetical protein |
| SCE1572_773 | FIG01088987: hypothetical protein | bi | sce_571 | 89.52 FIG01088987: hypothetical protein |
| SCE1572_774 | tyrosyl-tRNA synthetase(EC:6.1.1.1) | bi | sce_572 | 92.91 Tyrosyl-tRNA synthetase (EC 6.1.1.1) ## cluster 2 |
| SCE1572_775 | Integration host factor beta subunit | bi | sce_573 | 96.49 Integration host factor beta subunit |
| SCE1572_776 | hypothetical protein | - | | 0 |
| SCE1572_777 | tRNA pseudouridine synthase A (EC 4.2.1.70) | bi | sce_574 | 78.92 Membrane protein involved in colicin uptake-like protein |
| SCE1572_778 | FIG01089647: hypothetical protein | bi | sce_575 | 81.61 FIG01089647: hypothetical protein |
| SCE1572_779 | post-translocation molecular chaperone | bi | sce_576 | 75.76 DsbA oxidoreductase |
| SCE1572_780 | hypothetical protein | - | | 0 |
| SCE1572_781 | CG2839-PA | umi | sce_3858 | 37.23 Adenosylhomocysteinase (EC 3.3.1.1) |
| SCE1572_782 | hypothetical protein | bi | sce_577 | 93.56 zinc finger/histone putative |
| SCE1572_783 | Phosphate regulon sensor protein PhoR (SphS) (EC 2.7.13.3) | bi | sce_578 | 93.95 Phosphate regulon sensor protein PhoR (SphS) (EC 2.7.13.3) |
| SCE1572_784 | conserved hypothetical protein TIGR02757 | bi | sce_579 | 94.2 hypothetical protein |
| SCE1572_785 | Polyhydroxyalkanoic acid synthase | bi | sce_581 | 91.96 Polyhydroxyalkanoic acid synthase |
| SCE1572_786 | hypothetical protein | - | | 0 |
| SCE1572_787 | hypothetical protein | bi | sce_582 | 64.67 hypothetical protein |
| SCE1572_788 | hypothetical protein | bi | sce_583 | 66.43 hypothetical protein |
| SCE1572_789 | hypothetical protein | - | | 0 |
| SCE1572_790 | hypothetical protein | - | | 0 |
| SCE1572_791 | FIG01087057: hypothetical protein | bi | sce_584 | 96.74 FIG01087057: hypothetical protein |
| SCE1572_792 | NADH ubiquinone oxidoreductase chain A (EC 1.6.5.3) | bi | sce_585 | 94.07 NADH ubiquinone oxidoreductase chain A (EC 1.6.5.3) |
| SCE1572_793 | NADH-ubiquinone oxidoreductase chain B (EC 1.6.5.3) | bi | sce_586 | 96.34 NADH-ubiquinone oxidoreductase chain B (EC 1.6.5.3) |
| SCE1572_794 | NADH-ubiquinone oxidoreductase chain C (EC 1.6.5.3) | bi | sce_587 | 88.05 NADH-ubiquinone oxidoreductase chain C (EC 1.6.5.3) |
| SCE1572_795 | NADH-ubiquinone oxidoreductase chain D (EC 1.6.5.3) | bi | sce_588 | 96.53 NADH-ubiquinone oxidoreductase chain D (EC 1.6.5.3) |
| SCE1572_796 | NADH-ubiquinone oxidoreductase chain G (EC 1.6.5.3) | bi | sce_589 | 94.86 NADH-ubiquinone oxidoreductase chain G (EC 1.6.5.3) |
| SCE1572_797 | NADH-ubiquinone oxidoreductase chain H (EC 1.6.5.3) | bi | sce_590 | 88.78 NADH-ubiquinone oxidoreductase chain H (EC 1.6.5.3) |
| SCE1572_798 | NADH-ubiquinone oxidoreductase chain I (EC 1.6.5.3) | bi | sce_591 | 94.64 NADH-ubiquinone oxidoreductase chain I (EC 1.6.5.3) |
| SCE1572_799 | Aspartyl-tRNA(Asn) amidotransferase subunit B (EC 6.3.5.6) @ Glutamyl-tRNA(Gln) amidotransferase subunit B (EC 6.3.5.7) | bi | sce_592 | 94.21 Aspartyl-tRNA(Asn) amidotransferase subunit B (EC 6.3.5.6) @ Glutamyl-tRNA(Gln) amidotransferase subunit B (EC 6.3.5.7) |
| SCE1572_800 | hypothetical protein | - | | 0 |
| SCE1572_801 | phospholipid/glycerol acyltransferase | bi | sce_593 | 85.82 phospholipid/glycerol acyltransferase |
| SCE1572_802 | two-component hybrid sensor and regulator | bi | sce_594 | 92.77 two-component hybrid sensor and regulator |
| SCE1572_803 | hypothetical protein | - | | 0 |
| SCE1572_804 | hypothetical protein | - | | 0 |
| SCE1572_805 | Adenylate cyclase (EC 4.6.1.1) / Guanylate cyclase (EC 4.6.1.2) | umi | sce_6158 | 65.59 Adenylate cyclase (EC 4.6.1.1) / Guanylate cyclase (EC 4.6.1.2) |
| SCE1572_806 | hypothetical protein | - | | 0 |
| SCE1572_807 | Dihydrodipicolinate synthase (EC 4.2.1.52) | umi | sce_8978 | 34.48 Dihydrodipicolinate synthase (EC 4.2.1.52) |
| SCE1572_808 | Transcriptional regulator, GntR family domain / Aspartate aminotransferase (EC 2.6.1.1) | umi | sce_1410 | 45.71 Transcriptional regulator, GntR family domain / Aspartate aminotransferase (EC 2.6.1.1) |
| SCE1572_809 | FIG00841528: hypothetical protein | umi | sce_225 | 68.88 FIG00841528: hypothetical protein |
| SCE1572_810 | RsbR, positive regulator of sigma-B | umi | sce_6107 | 43.88 Signal transduction histidine kinase CheA (EC 2.7.3.-) |
| SCE1572_811 | hypothetical protein | umi | sce_10334 | 49.44 FIG01087636: hypothetical protein |
| SCE1572_812 | hypothetical protein | - | | 0 |
| SCE1572_813 | RNA polymerase sigma factor RpoE | umi | sce_6134 | 35.29 RNA polymerase sigma factor RpoE |
| SCE1572_814 | FIG01089478: hypothetical protein | umi | sce_6133 | 48.25 Twin-arginine translocation protein TatB |
| SCE1572_815 | FIG01086383: hypothetical protein | umi | sce_6132 | 36.86 FIG01089345: hypothetical protein |
| SCE1572_816 | FIG01086383: hypothetical protein | umi | sce_2804 | 30 FIG01086383: hypothetical protein |
| SCE1572_817 | hypothetical protein | - | | 0 |

| | | | | | |
|--------------|---|-----|-----------|-------|--|
| SCE1572_982 | Extensin-like | umi | see_1463 | 53.62 | FIG01085728: hypothetical protein |
| SCE1572_983 | FIG01122936: hypothetical protein | bi | see_742 | 92.51 | FIG01122936: hypothetical protein |
| SCE1572_984 | Regulatory protein, LacI | bi | see_744 | 92.92 | Regulatory protein, LacI |
| SCE1572_985 | Phosphoserine phosphatase (EC 3.1.3.3) | bi | see_745 | 96.16 | Phosphoserine phosphatase (EC 3.1.3.3) |
| SCE1572_986 | Excinuclease ABC subunit B | bi | see_747 | 93.78 | Excinuclease ABC subunit B |
| SCE1572_987 | Probable GTPase related to EngC | umi | see_749 | 87.5 | Probable GTPase related to EngC |
| SCE1572_988 | RsbR, positive regulator of sigma-B | bi | see_5156 | 46.88 | RsbR, positive regulator of sigma-B |
| SCE1572_989 | hypothetical protein | - | - | 0 | |
| SCE1572_990 | Response regulator of zinc sigma-54-dependent two-component system | bi | see_750 | 95.99 | Response regulator of zinc sigma-54-dependent two-component system |
| SCE1572_991 | hypothetical protein | - | - | 0 | |
| SCE1572_992 | hypothetical protein | bi | see_752 | 92.64 | hypothetical protein |
| SCE1572_993 | short-chain dehydrogenase/reductase SDR | bi | see_753 | 91.43 | 3-oxoacyl-[acyl-carrier protein] reductase (EC 1.1.1.100) |
| SCE1572_994 | hypothetical protein | - | - | 0 | |
| SCE1572_995 | hypothetical protein | - | - | 0 | |
| SCE1572_996 | Sarcosine oxidase beta subunit (EC 1.5.3.1) | bi | see_754 | 95.03 | Sarcosine oxidase beta subunit (EC 1.5.3.1) |
| SCE1572_997 | 3'(2'),5'-bisphosphate nucleotidase (EC 3.1.3.7) | bi | see_755 | 90.78 | 3'(2'),5'-bisphosphate nucleotidase (EC 3.1.3.7) |
| SCE1572_998 | Aldo-keto reductase | bi | see_756 | 85.58 | Aldo-keto reductase |
| SCE1572_999 | kelch domain protein | umi | see_7673 | 45.22 | FIG01085006: hypothetical protein |
| SCE1572_1000 | Thrombospondin | umi | see_7158 | 50 | Streptococcal hemagglutinin protein |
| SCE1572_1001 | hypothetical protein | - | - | 0 | |
| SCE1572_1002 | FIG01086989: hypothetical protein | bi | see_757 | 90.55 | FIG01086989: hypothetical protein |
| SCE1572_1003 | putative esterase | bi | see_758 | 78.42 | putative esterase |
| SCE1572_1004 | Tat (Twin-arginine translocation) pathway signal sequence domain protein | bi | see_5158 | 84.41 | Tat (Twin-arginine translocation) pathway signal sequence domain protein |
| SCE1572_1005 | Cellulose-binding domain protein | bi | see_1115 | 78.97 | Cellulose-binding domain protein |
| SCE1572_1006 | Polyphosphate glucokinase (EC 2.7.1.63) | bi | see_759 | 92.24 | Polyphosphate glucokinase (EC 2.7.1.63) |
| SCE1572_1007 | putative cytochrome P450 hydroxylase | bi | see_760 | 89.64 | putative cytochrome P450 hydroxylase |
| SCE1572_1008 | Succinylglutamic semialdehyde dehydrogenase (EC 1.2.1.71) | bi | see_761 | 89.75 | Succinylglutamic semialdehyde dehydrogenase (EC 1.2.1.71) |
| SCE1572_1009 | FIG01088242: hypothetical protein | bi | see_763 | 89.41 | FIG01088242: hypothetical protein |
| SCE1572_1010 | FIG00496687: hypothetical protein | umi | see_7493 | 39.63 | Branched-chain amino acid ABC transporter, amino acid-binding protein (TC 3.A.1.4.1) |
| SCE1572_1011 | histidine kinase | bi | see_9659 | 47.35 | Response Regulator Receiver Signal Transduction Histidine Kinase |
| SCE1572_1012 | hypothetical protein | - | - | 0 | |
| SCE1572_1013 | Serine/threonine protein kinase PrkC, regulator of stationary phase | bi | see_768 | 88.37 | Serine/threonine protein kinase PrkC, regulator of stationary phase |
| SCE1572_1014 | FIG01086311: hypothetical protein | bi | see_769 | 63.68 | FIG01086311: hypothetical protein |
| SCE1572_1015 | Adenylate cyclase (EC 4.6.1.1) / Guanylate cyclase (EC 4.6.1.2) | umi | see_3750 | 46.46 | serine/threonine protein kinase with WD40 repeats |
| SCE1572_1016 | hypothetical protein | - | - | 0 | |
| SCE1572_1017 | FIG01087426: hypothetical protein | bi | see_772 | 85.86 | FIG01087426: hypothetical protein |
| SCE1572_1018 | Flagellar regulatory protein FleQ | bi | see_773 | 82.28 | Flagellar regulatory protein FleQ |
| SCE1572_1019 | hypothetical protein | - | - | 0 | |
| SCE1572_1020 | hypothetical protein | bi | see_7608 | 45.33 | Methyltransferase type 11 |
| SCE1572_1021 | Arsenical pump-driving ATPase (EC 3.6.3.16) | umi | see_9274 | 28.52 | Arsenical pump-driving ATPase (EC 3.6.3.16) |
| SCE1572_1022 | SAM-dependent methyltransferase DSY4148 (UbiE paralog) | bi | see_6293 | 42.61 | SAM-dependent methyltransferase |
| SCE1572_1023 | RNA polymerase sigma factor SigZ | bi | see_5566 | 34.21 | RNA polymerase sigma-70 factor, ECF subfamily |
| SCE1572_1024 | hypothetical protein | umi | see_5645 | 30.52 | Cell division inhibitor |
| SCE1572_1025 | Arsenical resistance operon repressor | umi | see_7064 | 40.85 | Transcriptional regulator, ArsR family |
| SCE1572_1026 | Arsenical resistance operon trans-acting repressor ArsD | - | - | 0 | |
| SCE1572_1027 | Arsenical pump-driving ATPase (EC 3.6.3.16) | umi | see_9274 | 28.23 | Arsenical pump-driving ATPase (EC 3.6.3.16) |
| SCE1572_1028 | hypothetical protein | umi | see_6287 | 74.51 | Lactoylglutathione lyase (EC 4.4.1.5) @ Cadmium-induced protein CadI |
| SCE1572_1029 | Aquaporin Z | umi | see_6286 | 92.02 | Aquaporin Z |
| SCE1572_1030 | Arsenate reductase (EC 1.20.4.1) | bi | see_6285 | 87.31 | Arsenate reductase (EC 1.20.4.1) |
| SCE1572_1031 | Arsenate reductase (EC 1.20.4.1) | umi | see_6285 | 29.6 | Arsenate reductase (EC 1.20.4.1) |
| SCE1572_1032 | hypothetical protein | umi | see_6572 | 34.57 | FIG01085864: hypothetical protein |
| SCE1572_1033 | CAAX amino terminal protease family protein | bi | see_9382 | 51.88 | CAAX amino terminal protease family protein |
| SCE1572_1034 | BchE/P-methylase family protein | umi | see_778 | 89.84 | BchE/P-methylase family protein |
| SCE1572_1035 | FIG01086169: hypothetical protein | bi | see_10117 | 84.08 | FIG01086169: hypothetical protein |
| SCE1572_1036 | hypothetical protein | bi | see_7392 | 33.33 | FIG01089338: hypothetical protein |
| SCE1572_1037 | hypothetical protein | - | - | 0 | |
| SCE1572_1038 | hypothetical protein | bi | see_6088 | 62.32 | hypothetical protein |
| SCE1572_1039 | Twin-arginine translocation pathway signal(EC:1.11.1.10) | umi | see_9708 | 29.55 | Beta-ketoadipate enol-lactone hydrolase (EC 3.1.1.24) |
| SCE1572_1040 | FIG01087426: hypothetical protein | bi | see_775 | 82.55 | FIG01087426: hypothetical protein |
| SCE1572_1041 | serine/threonine protein kinase | umi | see_1995 | 56.82 | serine/threonine protein kinase |
| SCE1572_1042 | FIG01085121: hypothetical protein | bi | see_780 | 77.27 | FIG01085121: hypothetical protein |
| SCE1572_1043 | FIG01085121: hypothetical protein | umi | see_780 | 67.61 | FIG01085121: hypothetical protein |
| SCE1572_1044 | hypothetical protein | umi | see_780 | 73.05 | FIG01085121: hypothetical protein |
| SCE1572_1045 | hypothetical protein | bi | see_781 | 78.81 | hypothetical protein |
| SCE1572_1046 | Adenosylmethionine-8-amino-7-oxononanoate aminotransferase (EC 2.6.1.62) | bi | see_782 | 89.93 | Adenosylmethionine-8-amino-7-oxononanoate aminotransferase (EC 2.6.1.62) |
| SCE1572_1047 | EstC | bi | see_784 | 86.22 | hydrolase, alpha/beta fold family protein / similar to ethylene-induced esterase [Citrus sinensis] GI:14279437, polynucleotide aldehyd |
| SCE1572_1048 | RNA polymerase sigma factor RpoE | bi | see_785 | 83.6 | RNA polymerase sigma factor RpoE |
| SCE1572_1049 | hypothetical protein | bi | see_786 | 91.25 | hypothetical protein |
| SCE1572_1050 | hypothetical protein | - | - | 0 | |
| SCE1572_1051 | 3-oxoacyl-[acyl-carrier protein] reductase (EC 1.1.1.100) | bi | see_3616 | 84.21 | 3-oxoacyl-[acyl-carrier protein] reductase (EC 1.1.1.100) |
| SCE1572_1052 | FIG01089703: hypothetical protein | bi | see_8827 | 63.64 | FIG01089703: hypothetical protein |
| SCE1572_1053 | FIG01087894: hypothetical protein | bi | see_8826 | 88.5 | FIG01087894: hypothetical protein |
| SCE1572_1054 | Serine/threonine-protein kinase (EC 2.7.1.-) | bi | see_8825 | 77.56 | Serine/threonine-protein kinase (EC 2.7.1.-) |
| SCE1572_1055 | Phosphoenolpyruvate synthase (EC 2.7.9.2) | bi | see_4687 | 85.78 | Phosphoenolpyruvate synthase (EC 2.7.9.2) |
| SCE1572_1056 | BchE/P-methylase family protein | bi | see_778 | 89.94 | BchE/P-methylase family protein |
| SCE1572_1057 | Cold-shock DEAD-box protein A | bi | see_792 | 82.91 | Cold-shock DEAD-box protein A |
| SCE1572_1058 | hypothetical protein | bi | see_793 | 91.22 | hypothetical protein |
| SCE1572_1059 | Pressure-regulated protein | bi | see_4898 | 79.74 | Pressure-regulated protein |
| SCE1572_1060 | hypothetical protein | - | - | 0 | |
| SCE1572_1061 | putative dipeptidase | bi | see_794 | 65.27 | putative dipeptidase |
| SCE1572_1062 | hypothetical protein | - | - | 0 | |
| SCE1572_1063 | hypothetical protein | - | - | 0 | |
| SCE1572_1064 | two-component hybrid sensor and regulator | umi | see_7642 | 49.53 | Chemotaxis protein methyltransferase CheR (EC 2.1.1.80) |
| SCE1572_1065 | FIG01085111: hypothetical protein | bi | see_9451 | 92.8 | FIG01085111: hypothetical protein |
| SCE1572_1066 | Long-chain-fatty-acid-CoA ligase (EC 6.2.1.3) / long-chain acyl-CoA synthetase | bi | see_9453 | 96.98 | Long-chain-fatty-acid-CoA ligase (EC 6.2.1.3) / long-chain acyl-CoA synthetase |
| SCE1572_1067 | 3-oxoacyl-[acyl-carrier-protein] synthase III (EC 2.3.1.41) | bi | see_9454 | 96.01 | 3-oxoacyl-[acyl-carrier-protein] synthase III (EC 2.3.1.41) |
| SCE1572_1068 | hypothetical protein | - | - | 0 | |
| SCE1572_1069 | Mobile element protein | umi | see_6934 | 24.62 | 3-aminobutyryl-CoA ammonia-lyase (EC 4.3.1.14) / 3-keto-5-aminohexanoate cleavage enzyme |
| SCE1572_1070 | Quinone oxidoreductase (EC 1.6.5.5) | umi | see_3869 | 47.83 | Quinone oxidoreductase (EC 1.6.5.5) |
| SCE1572_1071 | Probable taurine catabolism dioxygenase | umi | see_8413 | 37.04 | Alpha-ketoglutarate-dependent taurine dioxygenase (EC 1.14.11.17) |
| SCE1572_1072 | Cytochrome c family protein | bi | see_795 | 82.97 | Cytochrome c family protein |
| SCE1572_1073 | putative Dehydrogenase (partial) | umi | see_3971 | 28.87 | 6-phosphogluconate dehydrogenase, decarboxylating (EC 1.1.1.44) |
| SCE1572_1074 | hypothetical protein | - | - | 0 | |
| SCE1572_1075 | Na-Ca exchanger/integrin-beta4 | umi | see_8443 | 34.52 | hypothetical protein |
| SCE1572_1076 | hypothetical protein | - | - | 0 | |
| SCE1572_1077 | transporter, putative | bi | see_5210 | 57.86 | transporter, putative |
| SCE1572_1078 | putative lipoprotein | bi | see_5665 | 77.37 | putative lipoprotein |
| SCE1572_1079 | hypothetical protein | - | - | 0 | |
| SCE1572_1080 | membrane protein, MarC family | bi | see_796 | 92.38 | membrane protein, MarC family |
| SCE1572_1081 | putative sensory transduction histidine kinase | bi | see_798 | 71.9 | putative sensory transduction histidine kinase |
| SCE1572_1082 | Oxidoreductase | bi | see_799 | 78.81 | YesF |
| SCE1572_1083 | conserved hypothetical protein | bi | see_800 | 78.15 | conserved hypothetical protein |
| SCE1572_1084 | FIG01086697: hypothetical protein | bi | see_801 | 84.35 | FIG01086697: hypothetical protein |
| SCE1572_1085 | Rab family protein | bi | see_7119 | 65.52 | hypothetical protein |
| SCE1572_1086 | Parallel beta-helix repeat | umi | see_802 | 86.08 | Parallel beta-helix repeat |
| SCE1572_1087 | Kazal domain protein | umi | see_7094 | 63.93 | Transposase |
| SCE1572_1088 | hypothetical protein | - | - | 0 | |
| SCE1572_1089 | Bicyclomycin resistance protein | umi | see_9993 | 26.61 | Permeases of the major facilitator superfamily |
| SCE1572_1090 | Thioredoxin reductase (EC 1.8.1.9) | umi | see_9822 | 38.31 | Thioredoxin reductase (EC 1.8.1.9) |
| SCE1572_1091 | Endo-1,4-beta-xylanase A precursor (EC 3.2.1.8) | umi | see_5146 | 68.26 | Endo-1,4-beta-xylanase A precursor (EC 3.2.1.8) |
| SCE1572_1092 | hypothetical protein | - | - | 0 | |
| SCE1572_1093 | putative RNA polymerase sigma factor | umi | see_7651 | 59.66 | putative RNA polymerase sigma factor |
| SCE1572_1094 | Multimeric flavodoxin WrbA | - | - | 0 | |
| SCE1572_1095 | hypothetical protein | bi | see_5295 | 77.44 | DNA gyrase subunit B |
| SCE1572_1096 | hypothetical protein | - | - | 0 | |
| SCE1572_1097 | MSHA biogenesis protein MshQ | umi | see_171 | 33.1 | integral membrane protein |
| SCE1572_1098 | FIG01087003: hypothetical protein | umi | see_3750 | 56.57 | serine/threonine protein kinase with WD40 repeats |
| SCE1572_1099 | Multiple EGF-like-domain protein 3 precursor | umi | see_3405 | 56.67 | Endo-1,4-beta-xylanase A precursor (EC 3.2.1.8) |
| SCE1572_1100 | Methionine ABC transporter ATP-binding protein | umi | see_1243 | 41.09 | Lipoprotein releasing system ATP-binding protein LolD |
| SCE1572_1101 | Methionine ABC transporter permease protein | umi | see_7917 | 31.09 | L-proline glycine betaine binding ABC transporter protein ProX (TC 3.A.1.12.1) / Osmotic adaptation |
| SCE1572_1102 | Methionine ABC transporter substrate-binding protein | - | - | 0 | |
| SCE1572_1103 | hypothetical protein | - | - | 0 | |
| SCE1572_1104 | Putative metal-dependent phosphohydrolase(EC:3.1.7.2) | bi | see_6782 | 36.27 | GTP pyrophosphokinase (EC 2.7.6.5) |
| SCE1572_1105 | Aromatic-L-amino-acid decarboxylase (EC 4.1.1.28) | bi | see_2563 | 33.94 | Aromatic-L-amino-acid decarboxylase (EC 4.1.1.28) |
| SCE1572_1106 | Cystathionine gamma-synthase(EC:2.5.1.48) | umi | see_6912 | 39.64 | Cystathionine gamma-lyase (EC 4.4.1.1) |
| SCE1572_1107 | Inosamine-phosphate amidinotransferase 1 (EC 2.1.4.2) (Inosamine-phosphate amidinotransferase 1) (Aminocycitol amidinotr- | umi | see_5973 | 27.14 | Beta-carotene hydroxylase |
| SCE1572_1108 | fatty acid desaturase family protein, putative | umi | see_5973 | 0 | |
| SCE1572_1109 | hypothetical protein | - | - | 0 | |
| SCE1572_1110 | hypothetical protein | - | - | 0 | |
| SCE1572_1111 | hypothetical protein | - | - | 0 | |
| SCE1572_1112 | Transcriptional regulator, AraC family | umi | see_1358 | 44.44 | Transcriptional regulator, AraC family |
| SCE1572_1113 | hypothetical protein | - | - | 0 | |
| SCE1572_1114 | Dipeptidyl aminopeptidases/acylaminoacyl-peptidases-like | bi | see_7128 | 35.08 | unknown |
| SCE1572_1115 | hypothetical protein | umi | see_180 | 27.89 | Rhodanese-like domain protein |
| SCE1572_1116 | hypothetical protein | - | - | 0 | |
| SCE1572_1117 | Transcriptional regulator, LysR family | umi | see_9329 | 45.17 | Transcriptional regulator, LysR family |
| SCE1572_1118 | Rhs-family protein | umi | see_10193 | 26.59 | Rhs family carbohydrate-binding protein |
| SCE1572_1119 | hypothetical protein | - | - | 0 | |
| SCE1572_1120 | hypothetical protein | - | - | 0 | |
| SCE1572_1121 | hypothetical protein | - | - | 0 | |
| SCE1572_1122 | hypothetical protein | - | - | 0 | |
| SCE1572_1123 | hypothetical protein | - | - | 0 | |
| SCE1572_1124 | hypothetical protein | - | - | 0 | |
| SCE1572_1125 | hypothetical protein | - | - | 0 | |
| SCE1572_1126 | hypothetical protein | - | - | 0 | |
| SCE1572_1127 | aldo/keto reductase Tas | bi | see_807 | 94.32 | aldo/keto reductase |
| SCE1572_1128 | Pyoverdinin biosynthesis protein PvdN, putative aminotransferase, class V | bi | see_808 | 81.29 | Pyoverdinin biosynthesis protein PvdN, putative aminotransferase, class V |
| SCE1572_1129 | Nucleoside-diphosphate-sugar epimerases | - | - | 0 | |
| SCE1572_1130 | hypothetical protein | - | - | 0 | |
| SCE1572_1131 | Transcriptional regulator, LysR family | umi | see_862 | 41.81 | Transcriptional regulator, LysR family |
| SCE1572_1132 | 3-demethylubiquinone-9 3-methyltransferase | umi | see_809 | 76.1 | 3-demethylubiquinone-9 3-methyltransferase |
| SCE1572_1133 | hypothetical protein | bi | see_810 | 68.22 | hypothetical protein |
| SCE1572_1134 | hypothetical protein | bi | see_8742 | 66.67 | Flavoredoxin |
| SCE1572_1135 | hypothetical protein | - | - | 0 | |
| SCE1572_1136 | hypothetical protein | - | - | 0 | |
| SCE1572_1137 | FIG01086053: hypothetical protein | umi | see_9398 | 83.05 | FIG01086053: hypothetical protein |
| SCE1572_1138 | Transcriptional regulator, TetR family | umi | see_5426 | 36.36 | Transcriptional regulator, TetR family |
| SCE1572_1139 | Lignostilbene-alpha,beta-dioxygenase and related enzymes | bi | - | 0 | |
| SCE1572_1140 | hypothetical protein | - | - | 0 | |
| SCE1572_1141 | RNA ligase 2 | - | - | 0 | |
| SCE1572_1142 | Sensor protein | bi | see_815 | 86.1 | Sensor protein |
| SCE1572_1143 | hypothetical protein | bi | see_816 | 74.46 | hypothetical protein |
| SCE1572_1144 | hypothetical protein | umi | see_5962 | 38.13 | Similarity |
| SCE1572_1145 | hypothetical protein | umi | see_3858 | 33.51 | Adenosylhomocysteinase (EC 3.3.1.1) |

| | | | | | |
|--------------|---|-----|-----------|-------|---|
| SCE1572_1146 | conserved hypothetical protein | bi | sce_817 | 83.13 | hypothetical protein |
| SCE1572_1147 | FIG01089218: hypothetical protein | umi | sce_3880 | 55.34 | FIG01089218: hypothetical protein |
| SCE1572_1148 | FIG01085391: hypothetical protein | bi | sce_3879 | 66.62 | FIG01085391: hypothetical protein |
| SCE1572_1149 | hypothetical protein | - | - | 0 | 0 |
| SCE1572_1150 | hypothetical protein | - | - | 0 | 0 |
| SCE1572_1151 | conserved hypothetical protein | bi | sce_7978 | 68.25 | conserved hypothetical protein |
| SCE1572_1152 | hypothetical protein | umi | sce_10127 | 33.91 | hypothetical protein |
| SCE1572_1153 | Aromatic hydrocarbon utilization transcriptional regulator CatR (LysR family) | umi | sce_3966 | 55.42 | LysR family transcriptional regulator YnFL |
| SCE1572_1154 | hypothetical protein | - | - | 0 | 0 |
| SCE1572_1155 | HupE-UreJ family metal transporter | - | - | 0 | 0 |
| SCE1572_1156 | hypothetical protein | - | - | 0 | 0 |
| SCE1572_1157 | probable transcriptional regulator | umi | sce_196 | 40.26 | Transcriptional regulator, LysR family |
| SCE1572_1158 | Quinone oxidoreductase (EC 1.6.5.5) | umi | sce_10217 | 37.99 | Quinone oxidoreductase (EC 1.6.5.5) |
| SCE1572_1159 | putative lipoprotein | umi | sce_6522 | 30.62 | hypothetical protein |
| SCE1572_1160 | TonB family protein / TonB-dependent receptor | umi | sce_10401 | 50.89 | TonB family protein / TonB-dependent receptor |
| SCE1572_1161 | oxidoreductase | - | - | 0 | 0 |
| SCE1572_1162 | Inositol-1-monophosphatase (EC 3.1.3.25) | umi | sce_8540 | 27.82 | Inositol-1-monophosphatase (EC 3.1.3.25) |
| SCE1572_1163 | LysR-family transcriptional regulator | umi | sce_1249 | 45.21 | Transcriptional regulator, LysR family |
| SCE1572_1164 | FIG01088080: hypothetical protein | bi | sce_854 | 76.19 | FIG01088080: hypothetical protein |
| SCE1572_1165 | Prolyl endopeptidase (EC 3.4.21.26) | bi | sce_856 | 84.14 | Prolyl endopeptidase (EC 3.4.21.26) |
| SCE1572_1166 | Secreted trypsin-like serine protease | bi | sce_857 | 85.21 | Secreted trypsin-like serine protease |
| SCE1572_1167 | hypothetical protein | - | - | 0 | 0 |
| SCE1572_1168 | Anaerobic dimethyl sulfoxide reductase chain B (EC 1.8.99.-) | bi | sce_4696 | 51.04 | Anaerobic dimethyl sulfoxide reductase chain B (EC 1.8.99.-) |
| SCE1572_1169 | N-Acetyl-D-glucosamine ABC transport system, sugar-binding protein | bi | sce_858 | 84.8 | N-Acetyl-D-glucosamine ABC transport system, sugar-binding protein |
| SCE1572_1170 | sugar ABC transporter permease protein | umi | sce_10351 | 34.39 | N-Acetyl-D-glucosamine ABC transport system, permease protein 1 |
| SCE1572_1171 | Maltose/maltodextrin ABC transporter, permease protein MalG | umi | sce_5646 | 40.07 | Maltose/maltodextrin ABC transporter, permease protein MalG |
| SCE1572_1172 | hypothetical protein | umi | sce_5999 | 35.29 | FIG01088071: hypothetical protein |
| SCE1572_1173 | probable transcriptional regulator | umi | sce_196 | 40.4 | Transcriptional regulator, LysR family |
| SCE1572_1174 | hypothetical protein | - | - | 0 | 0 |
| SCE1572_1175 | Conserved domain protein | bi | sce_5251 | 77.84 | hypothetical protein |
| SCE1572_1176 | hypothetical protein | bi | sce_2435 | 72.61 | Uncharacterized protein MJ1396 |
| SCE1572_1177 | hypothetical protein | bi | sce_860 | 78.32 | hypothetical protein |
| SCE1572_1178 | hypothetical protein | bi | sce_2432 | 82.57 | hypothetical protein |
| SCE1572_1179 | hypothetical protein | bi | sce_2431 | 82.57 | Outer membrane protein |
| SCE1572_1180 | RNA polymerase sigma factor RpoE | bi | sce_2430 | 85.53 | RNA polymerase sigma factor RpoE |
| SCE1572_1181 | Transcriptional regulator, TetR family | bi | sce_5268 | 79.08 | transcriptional regulator, TetR family |
| SCE1572_1182 | hypothetical protein | - | - | 0 | 0 |
| SCE1572_1183 | RsbR, positive regulator of sigma-B | umi | sce_10290 | 46.46 | Sensor protein |
| SCE1572_1184 | tolB protein precursor, periplasmic protein involved in the tonb-independent uptake of group A colicins | umi | sce_5085 | 68.21 | tolB protein precursor, periplasmic protein involved in the tonb-independent uptake of group A colicins |
| SCE1572_1185 | hypothetical protein | bi | sce_2391 | 79.03 | hypothetical protein |
| SCE1572_1186 | Transcriptional regulator, LysR family | bi | sce_862 | 95 | Transcriptional regulator, LysR family |
| SCE1572_1187 | putative membrane protein | bi | sce_863 | 88.57 | putative membrane protein |
| SCE1572_1188 | hypothetical protein | bi | sce_9528 | 76.63 | hypothetical protein |
| SCE1572_1189 | RsbR, positive regulator of sigma-B | bi | sce_202 | 69.6 | RsbR, positive regulator of sigma-B |
| SCE1572_1190 | Alpha-glucuronidase (EC 3.2.1.139) | bi | sce_1118 | 84.28 | Alpha-glucuronidase (EC 3.2.1.139) |
| SCE1572_1191 | hypothetical protein | - | - | 0 | 0 |
| SCE1572_1192 | Hydroxylamine reductase (EC 1.7.-.-) | bi | sce_866 | 91.49 | Hydroxylamine reductase (EC 1.7.-.-) |
| SCE1572_1193 | FG-GAP repeat protein | bi | sce_867 | 73.77 | Hemolysin-type calcium-binding region |
| SCE1572_1194 | FIG01086900: hypothetical protein | umi | sce_7579 | 62.72 | FIG01086900: hypothetical protein |
| SCE1572_1195 | hypothetical protein | - | - | 0 | 0 |
| SCE1572_1196 | Transcriptional regulator, TetR family | umi | sce_5339 | 33.54 | putative transcriptional regulator, TetR family |
| SCE1572_1197 | Signal transduction histidine kinase CheA (EC 2.7.3.-) | umi | sce_6094 | 73.13 | Signal transduction histidine kinase CheA (EC 2.7.3.-) |
| SCE1572_1198 | FIG01087706: hypothetical protein | umi | sce_868 | 74.7 | FIG01087706: hypothetical protein |
| SCE1572_1199 | hypothetical protein | umi | sce_8766 | 72.5 | hypothetical protein |
| SCE1572_1200 | MSHA biogenesis protein MshL | bi | sce_6199 | 70.82 | MSHA biogenesis protein MshL |
| SCE1572_1201 | PE_PGRS family protein | umi | sce_1120 | 51.56 | Endo-1,4-beta-xylanase A precursor (EC 3.2.1.8) |
| SCE1572_1202 | FIG01084975: hypothetical protein | bi | sce_869 | 72.14 | FIG01084975: hypothetical protein |
| SCE1572_1203 | Flagellar motor rotation protein MotB | bi | sce_870 | 73.15 | Flagellar motor rotation protein MotB |
| SCE1572_1204 | hypothetical protein | bi | sce_6397 | 39.19 | TPR domain protein, putative component of TonB system |
| SCE1572_1205 | Chemotaxis protein methyltransferase CheR (EC 2.1.1.80) | umi | sce_3523 | 35.27 | Chemotaxis protein methyltransferase CheR (EC 2.1.1.80) |
| SCE1572_1206 | Chemotaxis response regulator protein-glutamate methyltransferase of group 2 operon (EC 3.1.1.61) | umi | sce_9080 | 30.28 | Two-component response regulator |
| SCE1572_1207 | Signal transduction histidine kinase CheA (EC 2.7.3.-) | bi | sce_871 | 83.92 | Signal transduction histidine kinase CheA (EC 2.7.3.-) |
| SCE1572_1208 | FIG01085293: hypothetical protein | bi | sce_872 | 90.53 | FIG01085293: hypothetical protein |
| SCE1572_1209 | FIG01084954: hypothetical protein | bi | sce_873 | 84.21 | FIG01084954: hypothetical protein |
| SCE1572_1210 | hypothetical protein | - | - | 0 | 0 |
| SCE1572_1211 | PAA subfamily | bi | sce_874 | 89.08 | hypothetical protein |
| SCE1572_1212 | hypothetical protein | bi | sce_875 | 75.46 | hypothetical protein |
| SCE1572_1213 | hypothetical protein | - | - | 0 | 0 |
| SCE1572_1214 | protein of unknown function DUF417 | - | - | 0 | 0 |
| SCE1572_1215 | RNA polymerase sigma factor, sigma-70 family protein | umi | sce_9699 | 30.87 | RNA polymerase sigma factor RpoE |
| SCE1572_1216 | FIG01087191: hypothetical protein | bi | sce_2569 | 87.01 | FIG01087191: hypothetical protein |
| SCE1572_1217 | hypothetical protein | bi | sce_9399 | 81.48 | FIG01086053: hypothetical protein |
| SCE1572_1218 | nuclear antigen EBNA1 | umi | sce_5536 | 53.42 | hypothetical protein |
| SCE1572_1219 | tRNA (guanine46-N7-)-methyltransferase (EC 2.1.1.33) | bi | sce_879 | 90.75 | tRNA (guanine46-N7-)-methyltransferase (EC 2.1.1.33) |
| SCE1572_1220 | hypothetical protein | - | - | 0 | 0 |
| SCE1572_1221 | Chitinase (EC 3.2.1.14) | - | - | 0 | 0 |
| SCE1572_1222 | Collagen triple helix repeat | bi | sce_881 | 78.67 | Collagen triple helix repeat |
| SCE1572_1223 | hypothetical protein | umi | sce_4424 | 38.71 | hypothetical protein |
| SCE1572_1224 | Beta-lactamase class C and other penicillin binding proteins | umi | sce_5987 | 34.58 | Beta-lactamase (EC 3.5.2.6) |
| SCE1572_1225 | Transcriptional regulator, TetR family | umi | sce_9844 | 51.92 | Transcriptional regulator, TetR family |
| SCE1572_1226 | protein of unknown function DUF6, transmembrane | bi | sce_10032 | 28.47 | FIG01289198: hypothetical protein |
| SCE1572_1227 | RsbR, positive regulator of sigma-B | bi | sce_3085 | 50.22 | putative PAS/PAC sensor protein |
| SCE1572_1228 | Multi-sensor Hybrid Histidine Kinase | umi | sce_7643 | 56.32 | Sensor protein |
| SCE1572_1229 | Serine/Threonine protein kinase and Signal Transduction Histidine Kinase (EC:2.7.1.112) | umi | sce_7643 | 34.83 | Sensor protein |
| SCE1572_1230 | High-affinity carbon uptake protein Hat/HatR | umi | sce_4062 | 44.79 | High-affinity carbon uptake protein Hat/HatR |
| SCE1572_1231 | PROBABLE CHOLESTEROL OXIDASE CHOD (CHOLESTEROL-O2 OXIDOREDUCTASE) (EC 1.1.3.6) | bi | sce_885 | 92.44 | PROBABLE CHOLESTEROL OXIDASE CHOD (CHOLESTEROL-O2 OXIDOREDUCTASE) (EC 1.1.3.6) |
| SCE1572_1232 | hypothetical protein | - | - | 0 | 0 |
| SCE1572_1233 | FIG01086049: hypothetical protein | bi | sce_895 | 90 | FIG01086049: hypothetical protein |
| SCE1572_1234 | Cellulose-binding domain protein | bi | sce_896 | 84.67 | Cellulose-binding domain protein |
| SCE1572_1235 | hypothetical protein | - | - | 0 | 0 |
| SCE1572_1236 | Sheath polysaccharide-degrading enzyme precursor | bi | sce_898 | 81.8 | Sheath polysaccharide-degrading enzyme precursor |
| SCE1572_1237 | hypothetical protein | umi | sce_3278 | 40.62 | hypothetical abductin-like protein |
| SCE1572_1238 | Phosphate regulon transcriptional regulatory protein PhoB (SphR) | umi | sce_2722 | 49.13 | Response regulator receiver:Transcriptional regulatory protein, C- terminal precursor |
| SCE1572_1239 | periplasmic sensor signal transduction histidine kinase | umi | sce_578 | 41.95 | Phosphate regulon sensor protein PhoR (SphS) (EC 2.7.13.3) |
| SCE1572_1240 | predicted protein | - | - | 0 | 0 |
| SCE1572_1241 | Ribokinase (EC 2.7.1.15) | umi | sce_9859 | 32.14 | Fructokinase (EC 2.7.1.4) |
| SCE1572_1242 | FIG01086124: hypothetical protein | bi | sce_900 | 76.75 | FIG01086124: hypothetical protein |
| SCE1572_1243 | FMN-dependent NADH-azoreductase | bi | sce_9368 | 29.63 | FMN-dependent NADH-azoreductase |
| SCE1572_1244 | hypothetical protein | - | - | 0 | 0 |
| SCE1572_1245 | Glycine cleavage system transcriptional activator GcvA | bi | sce_5041 | 37.21 | Glycine cleavage system transcriptional activator GcvA |
| SCE1572_1246 | hypothetical protein | - | - | 0 | 0 |
| SCE1572_1247 | hypothetical protein | umi | sce_4377 | 25.88 | FIG00706509: hypothetical protein |
| SCE1572_1248 | FIG01088524: hypothetical protein | bi | sce_901 | 81.66 | FIG01088524: hypothetical protein |
| SCE1572_1249 | TonB-dependent receptor, plug | umi | sce_1403 | 62 | Cell division protein FtsZ (EC 3.4.24.-) |
| SCE1572_1250 | hypothetical protein | bi | sce_1317 | 36.3 | ABC-type phosphate transport system, periplasmic component |
| SCE1572_1251 | ADAM 28 precursor (EC 3.4.24.-) | umi | sce_1142 | 47.11 | Dihydroipoamide acetyltransferase component of pyruvate dehydrogenase complex (EC 2.3.1.12) |
| SCE1572_1252 | Signal transduction histidine kinase CheA (EC 2.7.3.-) | bi | sce_902 | 82.63 | Signal transduction histidine kinase CheA (EC 2.7.3.-) |
| SCE1572_1253 | hypothetical protein | bi | sce_903 | 88.2 | hypothetical protein |
| SCE1572_1254 | Chemotaxis regulator - transmits chemoreceptor signals to flagellar motor components CheY | bi | sce_904 | 90.4 | Chemotaxis regulator - transmits chemoreceptor signals to flagellar motor components CheY |
| SCE1572_1255 | serine/threonine protein kinase | umi | sce_5835 | 46.32 | putative PAS/PAC sensor protein |
| SCE1572_1256 | Endo-1,4-beta-xylanase A precursor (EC 3.2.1.8) | umi | sce_841 | 34.74 | Endo-1,4-beta-xylanase A precursor (EC 3.2.1.8) |
| SCE1572_1257 | probable glycolate oxidase FAD-linked subunit | bi | sce_846 | 91.11 | FAD-binding oxidoreductase |
| SCE1572_1258 | Bil4390 protein | bi | sce_1687 | 86.29 | Bil4390 protein |
| SCE1572_1259 | hypothetical protein | bi | sce_1688 | 92.05 | hypothetical protein |
| SCE1572_1260 | Glycogen debranching enzyme | bi | sce_1689 | 94.71 | Glycogen debranching enzyme |
| SCE1572_1261 | putative aldo/keto reductase | bi | sce_1690 | 92.21 | putative aldo/keto reductase |
| SCE1572_1262 | Mobile element protein | bi | sce_10368 | 66.46 | Mobile element protein |
| SCE1572_1263 | FIG01086369: hypothetical protein | bi | sce_909 | 79.84 | FIG01086369: hypothetical protein |
| SCE1572_1264 | hypothetical protein | - | - | 0 | 0 |
| SCE1572_1265 | hypothetical protein | bi | sce_910 | 83.96 | hypothetical protein |
| SCE1572_1266 | hypothetical protein | bi | sce_911 | 75.47 | hypothetical protein |
| SCE1572_1267 | Transglutaminase-like domain | umi | sce_914 | 65.31 | Transglutaminase-like domain |
| SCE1572_1268 | Metallo-beta-lactamase superfamily protein | bi | sce_916 | 77.28 | Metallo-beta-lactamase superfamily protein |
| SCE1572_1269 | Mlr6493 protein | bi | sce_917 | 84.95 | Mlr6493 protein |
| SCE1572_1270 | RsbR, positive regulator of sigma-B | bi | sce_1557 | 79.05 | RsbR, positive regulator of sigma-B |
| SCE1572_1271 | Xylose ABC transporter, substrate-binding component | bi | sce_1556 | 81.11 | Xylose ABC transporter, substrate-binding component |
| SCE1572_1272 | conserved hypothetical protein; putative PE_PGRS motifs | bi | sce_1553 | 62.16 | conserved hypothetical protein, PE_PGRS |
| SCE1572_1273 | Outer membrane vitamin B12 receptor BtuB | bi | sce_1552 | 81.83 | Outer membrane vitamin B12 receptor BtuB |
| SCE1572_1274 | hypothetical protein | bi | sce_1551 | 83.25 | hypothetical protein |
| SCE1572_1275 | Hypothetical protein | bi | sce_1550 | 89.63 | Hypothetical protein |
| SCE1572_1276 | Chemotaxis protein cheA (EC 2.7.3.-) | bi | sce_1549 | 83.36 | Chemotaxis protein cheA (EC 2.7.3.-) |
| SCE1572_1277 | hypothetical protein | - | - | 0 | 0 |
| SCE1572_1278 | hypothetical protein | bi | sce_7038 | 72.13 | hypothetical protein |
| SCE1572_1279 | hypothetical protein | umi | sce_3770 | 43.35 | sugar ABC transporter, periplasmic sugar-binding protein |
| SCE1572_1280 | Branched-chain amino acid ABC transporter, amino acid-binding protein (TC 3.A.1.4.1) | umi | sce_1493 | 62.67 | Branched-chain amino acid ABC transporter, amino acid-binding protein (TC 3.A.1.4.1) |
| SCE1572_1281 | Response regulator receiver:ATP-binding region, ATPase-like:Histidine kinase A, N-terminal | bi | sce_919 | 79.68 | Response regulator receiver:ATP-binding region, ATPase-like:Histidine kinase A, N-terminal |
| SCE1572_1282 | 3-oxoacyl-[acyl-carrier protein] reductase (EC 1.1.1.100) | umi | sce_3759 | 38.27 | 3-oxoacyl-[acyl-carrier protein] reductase (EC 1.1.1.100) |
| SCE1572_1283 | hypothetical protein | - | - | 0 | 0 |
| SCE1572_1284 | Enoyl-[acyl-carrier-protein] reductase [FMN] (EC 1.3.1.9), inferred for PFA pathway | bi | sce_920 | 93.53 | Enoyl-[acyl-carrier-protein] reductase [FMN] (EC 1.3.1.9), inferred for PFA pathway |
| SCE1572_1285 | omega-3 polyunsaturated fatty acid synthase subunit, PfaA | bi | sce_921 | 68.49 | omega-3 polyunsaturated fatty acid synthase subunit, PfaA |
| SCE1572_1286 | omega-3 polyunsaturated fatty acid synthase subunit, PfaC | bi | sce_922 | 81.53 | omega-3 polyunsaturated fatty acid synthase subunit, PfaC |
| SCE1572_1287 | hypothetical protein | bi | sce_923 | 78.6 | hypothetical protein |
| SCE1572_1288 | Gll1489 protein | bi | sce_924 | 66.04 | Gll1489 protein |
| SCE1572_1289 | hypothetical protein | - | - | 0 | 0 |
| SCE1572_1290 | FIG01085670: hypothetical protein | bi | sce_925 | 85.47 | FIG01085670: hypothetical protein |
| SCE1572_1291 | FIG01088460: hypothetical protein | bi | sce_926 | 71.92 | hypothetical protein |
| SCE1572_1292 | hypothetical protein | bi | sce_927 | 80.74 | LOC432261 protein |
| SCE1572_1293 | FIG01087208: hypothetical protein | bi | sce_928 | 80.65 | FIG01087208: hypothetical protein |
| SCE1572_1294 | serine/threonine protein kinase with TPR repeats | bi | sce_929 | 76.2 | serine/threonine protein kinase |
| SCE1572_1295 | Serine/threonine-protein kinase pkn3 (EC 2.7.11.1) | umi | sce_930 | 82.84 | Serine/threonine-protein kinase pkn3 (EC 2.7.11.1) |
| SCE1572_1296 | hypothetical protein | bi | sce_930 | 68.33 | Serine/threonine-protein kinase pkn3 (EC 2.7.11.1) |
| SCE1572_1297 | hypothetical protein | bi | sce_931 | 88.44 | hypothetical protein |
| SCE1572_1298 | hypothetical protein | bi | sce_932 | 94.52 | hypothetical protein |
| SCE1572_1299 | FIG01085618: hypothetical protein | bi | sce_933 | 92.01 | FIG01085618: hypothetical protein |
| SCE1572_1300 | FIG01086321: hypothetical protein | bi | sce_934 | 77.17 | FIG01086321: hypothetical protein |
| SCE1572_1301 | hypothetical protein | bi | sce_936 | 87.53 | hypothetical protein |
| SCE1572_1302 | Thymidylate kinase (EC 2.7.4.9) | bi | sce_937 | 83.76 | Thymidylate kinase (EC 2.7.4.9) |
| SCE1572_1303 | Pantoate-beta-alanine ligase (EC 6.3.2.1) | bi | sce_938 | 89.01 | Pantoate-beta-alanine ligase (EC 6.3.2.1) |
| SCE1572_1304 | Polyphosphate kinase (EC 2.7.4.1) | bi | sce_939 | 94.3 | Polyphosphate kinase (EC 2.7.4.1) |
| SCE1572_1305 | Serine/threonine-protein kinase pkn3 (EC 2.7.11.1) | bi | sce_940 | 78.32 | VgrG protein |
| SCE1572_1306 | SSU ribosomal protein S12p (S23e) | bi | sce_942 | 100 | SSU ribosomal protein S12p (S23e) |
| SCE1572_1307 | SSU ribosomal protein S7p (S5e) | bi | sce_943 | 100 | SSU ribosomal protein S7p (S5e) |
| SCE1572_1308 | Translation elongation factor G | bi | sce_944 | 97.02 | Translation elongation factor G |
| SCE1572_1309 | Translation elongation factor Tu | bi | sce_457 | 98.99 | Translation elongation factor Tu |

| | | | | |
|--------------|---|-----|-----------|---|
| SCE1572_1310 | SSU ribosomal protein S10p (S20e) | bi | sce_946 | 100 SSU ribosomal protein S10p (S20e) |
| SCE1572_1311 | LSU ribosomal protein L4p (L1e) | bi | sce_947 | 97.58 LSU ribosomal protein L4p (L1e) |
| SCE1572_1312 | LSU ribosomal protein L23p (L23Ae) | bi | sce_948 | 97.96 LSU ribosomal protein L23p (L23Ae) |
| SCE1572_1313 | LSU ribosomal protein L2p (L8e) | bi | sce_949 | 98.55 LSU ribosomal protein L2p (L8e) |
| SCE1572_1314 | SSU ribosomal protein S19p (S15e) | bi | sce_950 | 98.99 SSU ribosomal protein S19p (S15e) |
| SCE1572_1315 | FIG01086337: hypothetical protein | bi | sce_951 | 81.03 FIG01086337: hypothetical protein |
| SCE1572_1316 | Serine/threonine-protein kinase (EC 2.7.1.-) | bi | sce_952 | 72.7 serine/threonine protein kinase |
| SCE1572_1317 | hypothetical protein | umi | sce_3858 | 31.65 Adenosylhomocysteinase (EC 3.3.1.1) |
| SCE1572_1318 | FIG01089061: hypothetical protein | bi | sce_953 | 79.23 FIG01089061: hypothetical protein |
| SCE1572_1319 | Protein kinase | bi | sce_954 | 76.02 Ribonuclease E (EC 3.1.26.12) |
| SCE1572_1320 | hypothetical protein | bi | sce_956 | 81.56 hypothetical protein |
| SCE1572_1321 | oxidoreductase, short-chain dehydrogenase/reductase family | bi | sce_957 | 92.11 oxidoreductase, short-chain dehydrogenase/reductase family |
| SCE1572_1322 | Serine/threonine protein kinase | umi | sce_9757 | 42.41 Serine/threonine protein kinase |
| SCE1572_1323 | Autotransporter adhesin | bi | sce_959 | 80.61 Autotransporter adhesin |
| SCE1572_1324 | Skin secretory protein xP2 precursor (Protein APEG) | bi | sce_960 | 93.57 Skin secretory protein xP2 precursor (Protein APEG) |
| SCE1572_1325 | hypothetical protein | umi | sce_710 | 38.1 hypothetical protein |
| SCE1572_1326 | hypothetical protein | - | - | 0 |
| SCE1572_1327 | hypothetical protein | - | - | 0 |
| SCE1572_1328 | Protein serine/threonine phosphatase PrpC, regulation of stationary phase | umi | sce_4001 | 52.45 Protein serine/threonine phosphatase PrpC, regulation of stationary phase |
| SCE1572_1329 | hypothetical protein | bi | sce_717 | 67.39 hypothetical protein |
| SCE1572_1330 | FIG01085829: hypothetical protein | umi | sce_711 | 68.52 FIG01085829: hypothetical protein |
| SCE1572_1331 | hypothetical protein | umi | sce_1796 | 38.63 hypothetical protein |
| SCE1572_1332 | hypothetical protein | umi | sce_705 | 31.2 FIG01089428: hypothetical protein |
| SCE1572_1333 | hypothetical protein | umi | sce_1832 | 41.1 hypothetical protein |
| SCE1572_1334 | hypothetical protein | umi | sce_9337 | 30.53 hypothetical protein |
| SCE1572_1335 | hypothetical protein | umi | sce_1486 | 39.58 VgrG protein |
| SCE1572_1336 | FIG01086577: hypothetical protein | umi | sce_2302 | 70.73 hypothetical protein |
| SCE1572_1337 | serine/threonine protein kinase | bi | sce_961 | 93.63 serine/threonine-protein kinase |
| SCE1572_1338 | hypothetical protein | bi | sce_962 | 86.73 heat shock protein DnaJ domain protein |
| SCE1572_1339 | Carboxyl-terminal protease (EC 3.4.21.-) | bi | sce_963 | 90.75 Carboxyl-terminal protease (EC 3.4.21.-) |
| SCE1572_1340 | LiPid Depleted | bi | sce_9445 | 42.96 hypothetical protein |
| SCE1572_1341 | RNA polymerase sigma factor RpoH | bi | sce_965 | 95.27 RNA polymerase sigma factor RpoH |
| SCE1572_1342 | FIG01087452: hypothetical protein | bi | sce_967 | 99.64 FIG01087452: hypothetical protein |
| SCE1572_1343 | conserved hypothetical protein | bi | sce_968 | 85.87 FIG01087584: hypothetical protein |
| SCE1572_1344 | Peptidyl-prolyl cis-trans isomerase (EC 5.2.1.8) | bi | sce_969 | 85.98 Peptidyl-prolyl cis-trans isomerase (EC 5.2.1.8) |
| SCE1572_1345 | Glycosyl transferase, group 2 family protein | bi | sce_970 | 94.39 Glycosyl transferase, group 2 family protein |
| SCE1572_1346 | Membrane Protein Functionally coupled to the MukBEF Chromosome Partitioning Mechanism | bi | sce_971 | 80.63 Membrane Protein Functionally coupled to the MukBEF Chromosome Partitioning Mechanism |
| SCE1572_1347 | cytochrome c family protein | bi | sce_972 | 74.07 cytochrome c family protein |
| SCE1572_1348 | hypothetical protein | bi | sce_973 | 79.2 hypothetical protein |
| SCE1572_1349 | hypothetical protein | bi | sce_1433 | 52.27 FIG01087100: hypothetical protein |
| SCE1572_1350 | FIG01087958: hypothetical protein | bi | sce_974 | 81.94 FIG01087958: hypothetical protein |
| SCE1572_1351 | FIG00964846: hypothetical protein | bi | sce_975 | 93.88 FIG00964846: hypothetical protein |
| SCE1572_1352 | hypothetical protein | bi | sce_976 | 89.65 hypothetical protein |
| SCE1572_1353 | FIG01086412: hypothetical protein | bi | sce_978 | 92.33 FIG01086412: hypothetical protein |
| SCE1572_1354 | hypothetical protein | bi | sce_979 | 82.39 hypothetical protein |
| SCE1572_1355 | 3-dehydroquinate synthase (EC 4.2.3.4) | bi | sce_980 | 90.64 3-dehydroquinate synthase (EC 4.2.3.4) |
| SCE1572_1356 | polysaccharide export protein | bi | sce_981 | 94.5 polysaccharide export protein |
| SCE1572_1357 | polysaccharide biosynthesis protein | bi | sce_982 | 90.67 polysaccharide biosynthesis protein |
| SCE1572_1358 | UDP-glucose dehydrogenase (EC 1.1.1.22) | bi | sce_984 | 93.69 UDP-glucose dehydrogenase (EC 1.1.1.22) |
| SCE1572_1359 | Serine phosphatase RsbU, regulator of sigma subunit | bi | sce_985 | 98.61 Serine phosphatase RsbU, regulator of sigma subunit |
| SCE1572_1360 | FIG01086903: hypothetical protein | bi | sce_986 | 81.62 FIG01086903: hypothetical protein |
| SCE1572_1361 | Tyrosine-protein kinase EpsD (EC 2.7.10.2) | bi | sce_987 | 80.9 Tyrosine-protein kinase EpsD (EC 2.7.10.2) |
| SCE1572_1362 | Lipopolysaccharide biosynthesis | bi | sce_988 | 88.87 Chain length determinant protein, Wzz-like protein |
| SCE1572_1363 | Anti-sigma F factor antagonist (spoIIAA-2); Anti-sigma B factor antagonist RsbV | bi | sce_989 | 98.84 Anti-sigma F factor antagonist (spoIIAA-2); Anti-sigma B factor antagonist RsbV |
| SCE1572_1364 | Serine-protein kinase RsbW (EC 2.7.11.1) | bi | sce_990 | 96.92 Serine-protein kinase RsbW (EC 2.7.11.1) |
| SCE1572_1365 | FIG01088236: hypothetical protein | bi | sce_991 | 97.53 FIG01088236: hypothetical protein |
| SCE1572_1366 | Putative membrane protein of ExoQ family, involved in exopolysaccharide production | bi | sce_992 | 93.23 O-antigen polymerase family protein |
| SCE1572_1367 | hypothetical protein | bi | sce_993 | 87.23 hypothetical protein |
| SCE1572_1368 | Heparinase II protein precursor | bi | sce_994 | 85.63 Heparinase II protein precursor |
| SCE1572_1369 | UDP-glucose 4-epimerase (EC 5.1.3.2) | bi | sce_995 | 94.64 UDP-glucose 4-epimerase (EC 5.1.3.2) |
| SCE1572_1370 | Oxidoreductase-like | bi | sce_996 | 96.41 Oxidoreductase-like |
| SCE1572_1371 | Glycosyl transferase, group 1 | bi | sce_998 | 92.98 Glycosyl transferase, group 1 |
| SCE1572_1372 | FIG01086181: hypothetical protein | bi | sce_999 | 94.4 FIG01086181: hypothetical protein |
| SCE1572_1373 | D-aminopeptidase (EC 3.4.11.9) | umi | sce_1000 | 91.98 D-alanine--D-alanine ligase (EC 6.3.2.4) |
| SCE1572_1374 | D-alanine--D-alanine ligase (EC 6.3.2.4) | bi | sce_1000 | 92.04 D-alanine--D-alanine ligase (EC 6.3.2.4) |
| SCE1572_1375 | ATP-dependent DNA helicase UvrD/PerA | bi | sce_1002 | 89.56 ATP-dependent DNA helicase UvrD/PerA |
| SCE1572_1376 | FIG01089158: hypothetical protein | umi | sce_6082 | 54.52 FIG01089158: hypothetical protein |
| SCE1572_1377 | hypothetical protein | umi | sce_5241 | 60.41 FIG01086664: hypothetical protein |
| SCE1572_1378 | FIG01085364: hypothetical protein | umi | sce_8038 | 60.43 FIG01085364: hypothetical protein |
| SCE1572_1379 | hypothetical protein | bi | sce_1428 | 62.5 hypothetical protein |
| SCE1572_1380 | Anaerobic dimethyl sulfoxide reductase chain B (EC 1.8.99.-) | umi | sce_4696 | 43.74 Anaerobic dimethyl sulfoxide reductase chain B (EC 1.8.99.-) |
| SCE1572_1381 | possible helicase | bi | sce_6188 | 94.51 Helicase, SNF2/RAD54 family |
| SCE1572_1382 | hypothetical protein | umi | sce_3673 | 48.98 Protein of unknown function DUF11 |
| SCE1572_1383 | hypothetical protein | - | - | 0 |
| SCE1572_1384 | FIG01086874: hypothetical protein | bi | sce_8656 | 76.45 FIG01086874: hypothetical protein |
| SCE1572_1385 | EBNA-1 | bi | sce_6414 | 82.66 Cellulase (EC 3.2.1.4) |
| SCE1572_1386 | hypothetical protein | - | - | 0 |
| SCE1572_1387 | Endo-1,4-beta-xylanase A precursor (EC 3.2.1.8) | bi | sce_9995 | 86.98 secreted protein |
| SCE1572_1388 | regulator of chromosome condensation, RCC1 | umi | sce_6010 | 33.53 Collagen triple helix repeat |
| SCE1572_1389 | D-3-phosphoglycerate dehydrogenase (EC 1.1.1.95) | bi | sce_1692 | 35.51 D-3-phosphoglycerate dehydrogenase (EC 1.1.1.95) |
| SCE1572_1390 | ABC-type nitrate/sulfonate/bicarbonate transport systems, periplasmic components | bi | sce_4602 | 86.87 ABC-type nitrate/sulfonate/bicarbonate transport systems, periplasmic components |
| SCE1572_1391 | NADH pyrophosphatase (EC 3.6.1.22) | umi | sce_4892 | 44.89 NADH pyrophosphatase (EC 3.6.1.22) |
| SCE1572_1392 | hypothetical protein | bi | sce_1004 | 92.31 secreted protein |
| SCE1572_1393 | AmpG permease | bi | sce_1005 | 90.42 AmpG permease |
| SCE1572_1394 | probable oxidoreductase/Short-chain dehydrogenase | bi | sce_6012 | 43.06 Retinol dehydrogenase 13 (EC 1.1.1.-) |
| SCE1572_1395 | FIG01085227: hypothetical protein | bi | sce_1006 | 82.58 FIG01085227: hypothetical protein |
| SCE1572_1396 | putative N-acetylmuramoyl-L-alanine amidase | bi | sce_1007 | 90.44 putative N-acetylmuramoyl-L-alanine amidase |
| SCE1572_1397 | hypothetical protein | bi | sce_1333 | 45.12 FIG01085833: hypothetical protein |
| SCE1572_1398 | hypothetical protein | bi | sce_1331 | 31.85 hypothetical protein |
| SCE1572_1399 | hypothetical protein | bi | sce_1330 | 45.98 hypothetical protein |
| SCE1572_1400 | hypothetical protein | bi | sce_1341 | 83.42 hypothetical protein |
| SCE1572_1401 | FIG01089095: hypothetical protein | bi | sce_1340 | 71.95 FIG01089095: hypothetical protein |
| SCE1572_1402 | hypothetical protein | umi | sce_7383 | 33.15 Cell surface protein |
| SCE1572_1403 | hypothetical protein | umi | sce_3673 | 56.41 Protein of unknown function DUF11 |
| SCE1572_1404 | hypothetical protein | umi | sce_1677 | 27.75 PE-PGRS FAMILY PROTEIN |
| SCE1572_1405 | FOG: HEAT repeat | bi | sce_1339 | 87.74 FOG: HEAT repeat |
| SCE1572_1406 | VgrG protein | bi | sce_1338 | 88.33 VgrG protein |
| SCE1572_1407 | Mir2351 protein | bi | sce_1337 | 91.2 hypothetical protein |
| SCE1572_1408 | FIG01087519: hypothetical protein | bi | sce_1336 | 81.25 FIG01087519: hypothetical protein |
| SCE1572_1409 | hypothetical protein | bi | sce_1335 | 80.45 hypothetical protein |
| SCE1572_1410 | hypothetical protein | bi | sce_1334 | 84.77 hypothetical protein |
| SCE1572_1411 | ATP-dependent protease La (EC 3.4.21.53) Type I | bi | sce_1008 | 94.15 ATP-dependent protease La (EC 3.4.21.53) Type I |
| SCE1572_1412 | Lysophospholipase (EC 3.1.1.5); Monoglyceride lipase (EC 3.1.1.23); putative | bi | sce_1009 | 83.18 Lysophospholipase (EC 3.1.1.5); Monoglyceride lipase (EC 3.1.1.23); putative |
| SCE1572_1413 | Fibronectin/fibrinogen-binding protein | bi | sce_1010 | 93.6 fibronectin-binding protein homolog |
| SCE1572_1414 | hypothetical protein | bi | sce_1011 | 62.69 hypothetical protein |
| SCE1572_1415 | hypothetical protein | umi | sce_5240 | 32.65 hypothetical protein |
| SCE1572_1416 | Similarity | umi | sce_5962 | 64.89 Similarity |
| SCE1572_1417 | AhaI domain protein | bi | sce_4679 | 47.71 AhaI domain protein |
| SCE1572_1418 | Transcriptional regulator, ArsR family | bi | sce_4680 | 67.92 Transcriptional regulator, ArsR family |
| SCE1572_1419 | hypothetical protein | - | - | 0 |
| SCE1572_1420 | Response regulator of zinc sigma-54-dependent two-component system | umi | sce_9770 | 52.75 Response regulator of zinc sigma-54-dependent two-component system |
| SCE1572_1421 | protein kinase domain | umi | sce_7729 | 42.29 eukaryotic-type protein kinase |
| SCE1572_1422 | serine/threonine protein kinase | umi | sce_10233 | 45.58 protein kinase domain |
| SCE1572_1423 | Long-chain-fatty-acid--CoA ligase (EC 6.2.1.3) | bi | sce_1015 | 91.43 Long-chain-fatty-acid--CoA ligase (EC 6.2.1.3) |
| SCE1572_1424 | Uncharacterized PE-PGRS family protein PE_PGRS3 precursor | bi | sce_3601 | 80.12 Uncharacterized PE-PGRS family protein PE_PGRS3 precursor |
| SCE1572_1425 | Cytochrome c551 peroxidase (EC 1.11.1.5) | bi | sce_3600 | 88.22 Cytochrome c551 peroxidase (EC 1.11.1.5) |
| SCE1572_1426 | Peroxioredoxin family protein/glutaredoxin | bi | sce_1017 | 90 Peroxioredoxin family protein/glutaredoxin |
| SCE1572_1427 | hypothetical protein | - | - | 0 |
| SCE1572_1428 | Methylated-DNA--protein-cysteine methyltransferase (EC 2.1.1.63) | bi | sce_1018 | 80.65 methylated-DNA--protein-cysteine methyltransferase |
| SCE1572_1429 | L-rhamnose operon transcriptional activator RhaR | bi | sce_1019 | 82.14 L-rhamnose operon transcriptional activator RhaR |
| SCE1572_1430 | predicted nucleotidyltransferase | bi | sce_1022 | 91.1 predicted nucleotidyltransferase |
| SCE1572_1431 | hypothetical protein | bi | sce_1023 | 77.04 hypothetical protein |
| SCE1572_1432 | tRNA nucleotidyltransferase (EC 2.7.7.21) (EC 2.7.7.25) | bi | sce_1024 | 90.12 tRNA nucleotidyltransferase (EC 2.7.7.21) (EC 2.7.7.25) |
| SCE1572_1433 | hypothetical protein | - | - | 0 |
| SCE1572_1434 | Rhs family carbohydrate-binding protein | umi | sce_3970 | 42.47 Rhs family carbohydrate-binding protein |
| SCE1572_1435 | hypothetical protein | bi | sce_4560 | 39.22 FIG01088881: hypothetical protein |
| SCE1572_1436 | hypothetical protein | - | - | 0 |
| SCE1572_1437 | Endoribonuclease L-PSP | bi | sce_6320 | 90.37 Endoribonuclease L-PSP |
| SCE1572_1438 | Transcriptional regulator, LysR family | bi | sce_6321 | 91.39 Transcriptional regulator, LysR family |
| SCE1572_1439 | Valine--pyruvate aminotransferase (EC 2.6.1.66) | bi | sce_6322 | 93.4 Valine--pyruvate aminotransferase (EC 2.6.1.66) |
| SCE1572_1440 | Inorganic pyrophosphatase (EC 3.6.1.1) | bi | sce_6323 | 97.36 Inorganic pyrophosphatase (EC 3.6.1.1) |
| SCE1572_1441 | Sortilin-related receptor precursor | bi | sce_6330 | 79.4 Sortilin-related receptor precursor |
| SCE1572_1442 | hypothetical protein | bi | sce_6326 | 85.4 hypothetical protein |
| SCE1572_1443 | Endo-beta-1,6-galactanase | bi | sce_1084 | 80.7 Endo-beta-1,6-galactanase |
| SCE1572_1444 | beta-lactamase | umi | sce_8748 | 30.96 Adenosylhomocysteinase (EC 3.3.1.1) |
| SCE1572_1445 | Catalase (EC 1.11.1.6) | bi | sce_2350 | 90.74 Catalase (EC 1.11.1.6) |
| SCE1572_1446 | hypothetical protein | umi | sce_5793 | 45.61 hypothetical protein |
| SCE1572_1447 | FIG01085592: hypothetical protein | bi | sce_6187 | 91.59 FIG01085592: hypothetical protein |
| SCE1572_1448 | Transcriptional regulator, HxIR family | bi | sce_2658 | 57.49 Transcriptional regulator, HxIR family |
| SCE1572_1449 | hypothetical protein | bi | sce_2659 | 52.75 Dihydrofolate reductase (EC 1.5.1.3) |
| SCE1572_1450 | LysR family transcriptional regulator | bi | sce_9885 | 91.85 LysR family transcriptional regulator |
| SCE1572_1451 | Quinone oxidoreductase (EC 1.6.5.5) | bi | sce_9884 | 91.54 Quinone oxidoreductase (EC 1.6.5.5) |
| SCE1572_1452 | hypothetical protein | umi | sce_1036 | 65.12 hypothetical protein |
| SCE1572_1453 | Mobile element protein | bi | sce_1675 | 96.77 ISLp1 |
| SCE1572_1454 | hypothetical protein | umi | sce_3190 | 50.79 large tegument protein |
| SCE1572_1455 | Integrase Int | bi | sce_7521 | 86.71 FIG01087954: hypothetical protein |
| SCE1572_1456 | hypothetical protein | umi | sce_6807 | 87.37 hypothetical protein |
| SCE1572_1457 | hypothetical protein | umi | sce_6807 | 81.65 hypothetical protein |
| SCE1572_1458 | hypothetical protein | - | - | 0 |
| SCE1572_1459 | FIG01085109: hypothetical protein | umi | sce_8592 | 82.94 FIG01085109: hypothetical protein |
| SCE1572_1460 | hypothetical protein | - | - | 0 |
| SCE1572_1461 | PE-PGRS FAMILY PROTEIN | umi | sce_6815 | 67.74 PE-PGRS FAMILY PROTEIN |
| SCE1572_1462 | hypothetical protein | - | - | 0 |
| SCE1572_1463 | FIG01089478: hypothetical protein | bi | sce_9794 | 70.43 FIG01089478: hypothetical protein |
| SCE1572_1464 | RNA polymerase sigma factor SigW | bi | sce_9902 | 76.06 RNA polymerase sigma factor SigW |
| SCE1572_1465 | hypothetical protein | bi | sce_10361 | 74.5 hypothetical protein |
| SCE1572_1466 | hypothetical protein | - | - | 0 |
| SCE1572_1467 | Bacteriophage protein gp37 | - | - | 0 |
| SCE1572_1468 | hypothetical protein | - | - | 0 |
| SCE1572_1469 | Putative bacterial haemoglobin | umi | sce_5698 | 46.74 Putative bacterial haemoglobin |
| SCE1572_1470 | nitrogen metabolism transcriptional regulator, NtrC, Fis Family | umi | sce_9871 | 38.64 Response regulator of zinc sigma-54-dependent two-component system |
| SCE1572_1471 | hypothetical protein | - | - | 0 |
| SCE1572_1472 | hypothetical protein | - | - | 0 |
| SCE1572_1473 | hypothetical protein | - | - | 0 |

| | | | | |
|--------------|---|-----|-----------|--|
| SCE1572_1474 | hypothetical protein | - | - | 0 |
| SCE1572_1475 | POSSIBLE TRANSPOSASE | uni | sce_2392 | 84.62 hypothetical protein |
| SCE1572_1476 | similar to O-linked GlcNAc transferase | - | - | 0 |
| SCE1572_1477 | hypothetical protein | - | - | 0 |
| SCE1572_1478 | glycosyl transferase | uni | sce_7824 | 32.2 glycosyltransferase |
| SCE1572_1479 | expressed protein | uni | sce_7489 | 29.69 dTDP-glucose 4,6-dehydratase (EC 4.2.1.46) |
| SCE1572_1480 | tolB protein precursor, periplasmic protein involved in the tonb-independent uptake of group A colicins | - | - | 0 |
| SCE1572_1481 | predicted nucleoside-diphosphate-sugar epimerase | uni | sce_10011 | 30.35 Oxidoreductase |
| SCE1572_1482 | hypothetical protein | - | - | 0 |
| SCE1572_1483 | Probable poly(beta-D-mannuronate) O-acetylase (EC 2.3.1.-) | uni | sce_9390 | 38.07 Probable poly(beta-D-mannuronate) O-acetylase (EC 2.3.1.-) |
| SCE1572_1484 | hypothetical protein | bi | sce_4697 | 45.83 PASTA domain containing protein |
| SCE1572_1485 | hypothetical protein | - | - | 0 |
| SCE1572_1486 | hypothetical protein | - | - | 0 |
| SCE1572_1487 | hypothetical protein | - | - | 0 |
| SCE1572_1488 | hypothetical protein | uni | sce_8653 | 80.43 hypothetical protein |
| SCE1572_1489 | Mobile element protein | bi | sce_7680 | 31.98 POSSIBLE TRANSPOSASE |
| SCE1572_1490 | transposase | - | - | 0 |
| SCE1572_1491 | hypothetical protein | - | - | 0 |
| SCE1572_1492 | Tat (Twin-arginine translocation) pathway signal sequence domain protein | uni | sce_7318 | 87.25 Tat (Twin-arginine translocation) pathway signal sequence domain protein |
| SCE1572_1493 | hypothetical protein | - | - | 0 |
| SCE1572_1494 | 2-polypropenyl-6-methoxyphenol hydroxylase and related FAD-dependent oxidoreductases | uni | sce_2498 | 74.79 2-polypropenyl-6-methoxyphenol hydroxylase and related FAD-dependent oxidoreductases |
| SCE1572_1495 | hypothetical protein | - | - | 0 |
| SCE1572_1496 | alkylhydroperoxidase like protein, AhpD family | bi | sce_8802 | 98.21 alkylhydroperoxidase like protein, AhpD family |
| SCE1572_1497 | Transcriptional regulator, ArsR family | bi | sce_8801 | 94.23 FIG016027: protein of unknown function YeaO |
| SCE1572_1498 | Probable glutathione S-transferase-related transmembrane protein (EC 2.5.1.18) | uni | sce_9878 | 96.18 hypothetical protein |
| SCE1572_1499 | hypothetical protein | - | - | 0 |
| SCE1572_1500 | Probable transcriptional regulator IrfA | uni | sce_1329 | 35.71 Transcriptional regulator, LysR family |
| SCE1572_1501 | hypothetical protein | - | - | 0 |
| SCE1572_1502 | RabR, positive regulator of sigma-B | uni | sce_5782 | 56.83 RabR, positive regulator of sigma-B |
| SCE1572_1503 | Lignostilbene-alpha,beta-dioxygenase and related enzymes | - | - | 0 |
| SCE1572_1504 | NADP-specific glutamate dehydrogenase (EC 1.4.1.4) | bi | sce_10169 | 96.35 NADP-specific glutamate dehydrogenase (EC 1.4.1.4) |
| SCE1572_1505 | hypothetical protein | - | - | 0 |
| SCE1572_1506 | hypothetical protein | - | - | 0 |
| SCE1572_1507 | hypothetical protein | - | - | 0 |
| SCE1572_1508 | Endo-1,4-beta-xylanase A precursor (EC 3.2.1.8) | bi | sce_7495 | 85.57 Endo-1,4-beta-xylanase A precursor (EC 3.2.1.8) |
| SCE1572_1509 | Serine protease inhibitor precursor | uni | sce_4594 | 67.28 Serine protease inhibitor precursor |
| SCE1572_1510 | Probable oxidoreductase | uni | sce_6012 | 30.28 Retinol dehydrogenase 13 (EC 1.1.1.-) |
| SCE1572_1511 | FIG01085393: hypothetical protein | bi | sce_7061 | 76.8 FIG01085393: hypothetical protein |
| SCE1572_1512 | Transcriptional regulator, AraC family | bi | sce_9866 | 83.6 Transcriptional regulator, AraC family |
| SCE1572_1513 | hypothetical protein | uni | sce_9865 | 38.57 Transcriptional regulator, AraC family |
| SCE1572_1514 | haloacid dehalogenase, type II (EC:3.8.1.2) | bi | sce_1037 | 83.46 haloacid dehalogenase, type II (EC:3.8.1.2) |
| SCE1572_1515 | hypothetical protein | bi | sce_1039 | 48 hypothetical protein |
| SCE1572_1516 | GTP-binding protein TypA/BipA | bi | sce_1040 | 97.06 GTP-binding protein TypA/BipA |
| SCE1572_1517 | hypothetical protein | - | - | 0 |
| SCE1572_1518 | Outer membrane receptor proteins, mostly Fe transport | bi | sce_1041 | 81.13 Outer membrane receptor proteins, mostly Fe transport |
| SCE1572_1519 | Type I restriction-modification system, DNA-methyltransferase subunit M (EC 2.1.1.72) | uni | sce_9268 | 28.42 hypothetical protein |
| SCE1572_1520 | hypothetical protein | - | - | 0 |
| SCE1572_1521 | hypothetical protein | bi | sce_1044 | 77.78 hypothetical protein |
| SCE1572_1522 | Transcriptional regulator, MerR family | uni | sce_9675 | 37.5 MerR family transcriptional regulatory protein |
| SCE1572_1523 | COG4251: Bacteriophytochrome (light-regulated signal transduction histidine kinase) | bi | sce_1045 | 86.9 hypothetical protein |
| SCE1572_1524 | hypothetical protein | - | - | 0 |
| SCE1572_1525 | serine/threonine protein kinase | bi | sce_1047 | 98.9 serine/threonine protein kinase |
| SCE1572_1526 | Pyrophosphate-energized proton pump (EC 3.6.1.1) | bi | sce_1048 | 94.09 Pyrophosphate-energized proton pump (EC 3.6.1.1) |
| SCE1572_1527 | hypothetical protein | bi | sce_1049 | 80.33 hypothetical protein |
| SCE1572_1528 | Phosphatase | bi | sce_1051 | 81.53 Phosphatase |
| SCE1572_1529 | Uncharacterized lipoprotein aq_1262 precursor | bi | sce_1052 | 90.31 Uncharacterized lipoprotein aq_1262 precursor |
| SCE1572_1530 | hypothetical protein | - | - | 0 |
| SCE1572_1531 | MATE efflux family protein | uni | sce_4895 | 26.85 MATE efflux family protein |
| SCE1572_1532 | Aspartate 1-decarboxylase (EC 4.1.1.11) | bi | sce_1053 | 95.16 Aspartate 1-decarboxylase (EC 4.1.1.11) |
| SCE1572_1533 | FIG01086776: hypothetical protein | bi | sce_1054 | 67.8 FIG01086776: hypothetical protein |
| SCE1572_1534 | At1g18480/F15H18_1 | bi | sce_1056 | 86.46 At1g18480/F15H18_1 |
| SCE1572_1535 | FIG01088905: hypothetical protein | bi | sce_1057 | 94.48 FIG01088905: hypothetical protein |
| SCE1572_1536 | FG-GAP repeat domain protein | - | - | 0 |
| SCE1572_1537 | Prion-like-(Q/n-rich)-domain-bearing protein protein 54 | uni | sce_7801 | 32.38 Prion-like-(Q/n-rich)-domain-bearing protein protein 54 |
| SCE1572_1538 | Uncharacterized protein in pqqA 5'region (ORF X) (Fragment) | bi | sce_1058 | 89.26 peptidase M19, renal dipeptidase |
| SCE1572_1539 | serine/threonine-protein kinase PknI (EC:2.7.1.1) | bi | sce_1059 | 81.08 serine/threonine protein kinase |
| SCE1572_1540 | Soluble lytic murein transglycosylase precursor (EC 3.2.1.-) | bi | sce_1060 | 88.48 Soluble lytic murein transglycosylase precursor (EC 3.2.1.-) |
| SCE1572_1541 | hypothetical protein | - | - | 0 |
| SCE1572_1542 | hypothetical protein | uni | sce_9062 | 46.27 Hypothetical protein |
| SCE1572_1543 | hypothetical protein | bi | sce_1061 | 54.96 FIG01089630: hypothetical protein |
| SCE1572_1544 | hypothetical protein | bi | sce_1063 | 91.56 hypothetical protein |
| SCE1572_1545 | hypothetical protein | bi | sce_1065 | 93.31 sulfatase |
| SCE1572_1546 | Sulfatase (EC 3.1.6.-) | bi | sce_1066 | 87.2 Sulfatase |
| SCE1572_1547 | FIG01086453: hypothetical protein | bi | sce_1071 | 87.57 FIG01086453: hypothetical protein |
| SCE1572_1548 | FIG01084974: hypothetical protein | bi | sce_1074 | 78.32 FIG01084974: hypothetical protein |
| SCE1572_1549 | Transcription regulator [contains diacylglycerol kinase catalytic domain] | bi | sce_1075 | 88.27 Transcription regulator [contains diacylglycerol kinase catalytic domain] |
| SCE1572_1550 | hypothetical protein | bi | sce_1076 | 56.63 hypothetical protein |
| SCE1572_1551 | Formiminoglutamic aminohydrolase (EC 3.5.3.13) | bi | sce_1078 | 93.94 Formiminoglutamic aminohydrolase (EC 3.5.3.13) |
| SCE1572_1552 | hypothetical protein | bi | sce_9982 | 85.19 hypothetical protein |
| SCE1572_1553 | hypothetical protein | bi | sce_1080 | 76.09 hypothetical protein |
| SCE1572_1554 | FIG01085942: hypothetical protein | bi | sce_1081 | 82.27 FIG01085942: hypothetical protein |
| SCE1572_1555 | hypothetical protein | - | - | 0 |
| SCE1572_1556 | FOG: WD40-like repeat | bi | sce_4904 | 50.23 FOG: WD40-like repeat |
| SCE1572_1557 | hypothetical protein | - | - | 0 |
| SCE1572_1558 | hypothetical protein | bi | sce_1087 | 83.97 hypothetical protein |
| SCE1572_1559 | Kazal-type serine protease inhibitor domain | bi | sce_1088 | 62.19 Kazal-type serine protease inhibitor domain |
| SCE1572_1560 | hypothetical protein | bi | sce_1090 | 88.82 hypothetical protein |
| SCE1572_1561 | COG2833: uncharacterized protein | bi | sce_1091 | 77.65 COG2833: uncharacterized protein |
| SCE1572_1562 | FIG01089238: hypothetical protein | bi | sce_1092 | 96.33 FIG01089238: hypothetical protein |
| SCE1572_1563 | FIG01087205: hypothetical protein | bi | sce_1094 | 94.92 FIG01087205: hypothetical protein |
| SCE1572_1564 | hypothetical protein | bi | sce_1095 | 88.83 hypothetical protein |
| SCE1572_1565 | hypothetical protein | uni | sce_666 | 31.91 hypothetical protein |
| SCE1572_1566 | Phytoene dehydrogenase and related proteins | uni | sce_4222 | 39.16 Phytoene dehydrogenase and related proteins |
| SCE1572_1567 | GIY-YIG catalytic domain protein | bi | sce_1096 | 87.21 COG2827: putative endonuclease containing a URI domain |
| SCE1572_1568 | Tetratricopeptide TPR_2 repeat protein | bi | sce_1097 | 89.27 hypothetical protein |
| SCE1572_1569 | Citronellol and citronellal dehydrogenase | bi | sce_1098 | 89.36 oxidoreductase, short-chain dehydrogenase/reductase family |
| SCE1572_1570 | Oxidoreductase, short chain dehydrogenase/reductase family | uni | sce_3648 | 40.31 PUTATIVE OXIDOREDUCTASE PROTEIN |
| SCE1572_1571 | hypothetical protein | bi | sce_1122 | 87.62 hypothetical protein |
| SCE1572_1572 | hypothetical protein | bi | sce_1123 | 84.08 hypothetical protein |
| SCE1572_1573 | Rhamnogalacturonides degradation protein RhiN | bi | sce_1124 | 83.91 Rhamnogalacturonides degradation protein RhiN |
| SCE1572_1574 | Cell division transporter, ATP-binding protein FtsE (TC 3.A.5.1.1) | bi | sce_1125 | 90.94 Cell division transporter, ATP-binding protein FtsE (TC 3.A.5.1.1) |
| SCE1572_1575 | Probable Co/Zn/Cd efflux system membrane fusion protein | bi | sce_1126 | 88.47 Probable Co/Zn/Cd efflux system membrane fusion protein |
| SCE1572_1576 | Macrolide export ATP-binding/permease protein MacB (EC 3.6.3.-) | bi | sce_1127 | 87.01 protein of unknown function DUF214 |
| SCE1572_1577 | FIG01087495: hypothetical protein | bi | sce_1128 | 90.6 FIG01087495: hypothetical protein |
| SCE1572_1578 | MFS permease | bi | sce_1131 | 71.94 MFS permease |
| SCE1572_1579 | GCNS-related N-acetyltransferase | - | - | 0 |
| SCE1572_1580 | hypothetical protein | - | - | 0 |
| SCE1572_1581 | FIG00841076: hypothetical protein | bi | sce_1132 | 88 FIG00841076: hypothetical protein |
| SCE1572_1582 | alpha/beta hydrolase fold | bi | sce_1133 | 82.13 hydrolase |
| SCE1572_1583 | hypothetical protein | - | - | 0 |
| SCE1572_1584 | hypothetical protein | bi | sce_1604 | 92.57 hypothetical protein |
| SCE1572_1585 | Putative phosphatase YqaB | bi | sce_7900 | 84 Putative phosphatase YqaB |
| SCE1572_1586 | hypothetical protein | - | - | 0 |
| SCE1572_1587 | hypothetical protein | - | - | 0 |
| SCE1572_1588 | hypothetical protein | uni | sce_3766 | 57.23 hypothetical protein |
| SCE1572_1589 | hypothetical protein | uni | sce_7501 | 75 hypothetical protein |
| SCE1572_1590 | Mir2351 protein | uni | sce_1020 | 45.81 Mir2351 protein |
| SCE1572_1591 | VgrG protein | uni | sce_118 | 54.6 VgrG protein |
| SCE1572_1592 | hypothetical protein | - | - | 0 |
| SCE1572_1593 | hypothetical protein | - | - | 0 |
| SCE1572_1594 | pentapeptide repeat family protein | uni | sce_115 | 43.64 FIG01089519: hypothetical protein |
| SCE1572_1595 | hypothetical protein | uni | sce_114 | 30.41 FIG01085979: hypothetical protein |
| SCE1572_1596 | hypothetical protein | uni | sce_113 | 50 hypothetical protein |
| SCE1572_1597 | hypothetical protein | uni | sce_116 | 35.03 FIG01088201: hypothetical protein |
| SCE1572_1598 | FIG01086191: hypothetical protein | uni | sce_1675 | 96.08 ISLpI |
| SCE1572_1599 | hypothetical protein | - | - | 0 |
| SCE1572_1600 | 2-polypropenyl-6-methoxyphenol hydroxylase and related FAD-dependent oxidoreductases | bi | sce_8426 | 89 2-polypropenyl-6-methoxyphenol hydroxylase and related FAD-dependent oxidoreductases |
| SCE1572_1601 | hypothetical protein | uni | sce_9602 | 31.33 Heavy metal RND efflux outer membrane protein, CzcC family |
| SCE1572_1602 | Putative membrane protein with von Willebrand (VWA) domain | uni | sce_6508 | 35.81 hypothetical protein |
| SCE1572_1603 | hypothetical protein | - | - | 0 |
| SCE1572_1604 | hypothetical protein | bi | sce_1140 | 64.53 FIG01085859: hypothetical protein |
| SCE1572_1605 | Tat (twin-arginine translocation) pathway signal sequence domain protein | bi | sce_1143 | 85 Tat (Twin-arginine translocation) pathway signal sequence domain protein |
| SCE1572_1606 | Cellulose-binding domain protein | bi | sce_1144 | 86.93 Cellulose-binding domain protein |
| SCE1572_1607 | hypothetical protein | bi | sce_1145 | 76.33 FIG01086282: hypothetical protein |
| SCE1572_1608 | hypothetical protein | bi | sce_1146 | 79.53 Gll0645 protein |
| SCE1572_1609 | Glycosyl transferase, group 1 family protein | bi | sce_1148 | 85.08 Glycosyl transferase, group 1 family protein |
| SCE1572_1610 | serine/threonine protein kinase | bi | sce_1149 | 96.02 serine/threonine protein kinase |
| SCE1572_1611 | DNA-3-methyladenine glycosylase (EC 3.2.2.20) | - | - | 0 |
| SCE1572_1612 | Glycosyltransferase (EC 2.4.1.-) | bi | sce_1151 | 76.29 Glycosyltransferase (EC 2.4.1.-) |
| SCE1572_1613 | hypothetical protein | - | - | 0 |
| SCE1572_1614 | Glycosyltransferase | bi | sce_1152 | 90.32 Glycosyltransferase |
| SCE1572_1615 | exporters of the RND superfamily | bi | sce_1153 | 86.75 exporters of the RND superfamily |
| SCE1572_1616 | Glycosyl transferase, group 1 family protein | bi | sce_1154 | 91.03 Glycosyl transferase, group 1 family protein |
| SCE1572_1617 | TPR/glycosyl transferase domain protein | bi | sce_1155 | 81.4 TPR/glycosyl transferase domain protein |
| SCE1572_1618 | Inosine-5'-monophosphate dehydrogenase (EC 1.1.1.205) | bi | sce_1156 | 95.02 Inosine-5'-monophosphate dehydrogenase (EC 1.1.1.205) |
| SCE1572_1619 | Acyltransferase family protein | bi | sce_1157 | 85.38 Acyltransferase family protein |
| SCE1572_1620 | FIG01088859: hypothetical protein | bi | sce_1158 | 87.1 FIG01088859: hypothetical protein |
| SCE1572_1621 | hypothetical protein | bi | sce_1159 | 89.78 hypothetical protein |
| SCE1572_1622 | hypothetical protein | uni | sce_631 | 29.73 hypothetical protein |
| SCE1572_1623 | hypothetical protein | - | - | 0 |
| SCE1572_1624 | hypothetical protein | uni | sce_8407 | 37.74 hypothetical protein |
| SCE1572_1625 | hypothetical protein | bi | sce_8406 | 39.73 hypothetical protein |
| SCE1572_1626 | Ribonuclease HI (EC 3.1.26.4) | bi | sce_1164 | 90.51 Ribonuclease HI (EC 3.1.26.4) |
| SCE1572_1627 | Isocitrate dehydrogenase [NADP] (EC 1.1.1.42); Monomeric isocitrate dehydrogenase [NADP] (EC 1.1.1.42) | bi | sce_7633 | 96.23 Isocitrate dehydrogenase [NADP] (EC 1.1.1.42); Monomeric isocitrate dehydrogenase [NADP] (EC 1.1.1.42) |
| SCE1572_1628 | Survival protein SurA precursor (Peptidyl-prolyl cis-trans isomerase SurA) (EC 5.2.1.8) | bi | sce_1165 | 90.53 Survival protein SurA precursor (Peptidyl-prolyl cis-trans isomerase SurA) (EC 5.2.1.8) |
| SCE1572_1629 | hypothetical protein | bi | sce_1166 | 83.76 hypothetical protein |
| SCE1572_1630 | hypothetical protein | - | - | 0 |
| SCE1572_1631 | hypothetical protein | - | - | 0 |
| SCE1572_1632 | hypothetical protein | - | - | 0 |
| SCE1572_1633 | serine/threonine protein kinase | bi | sce_1167 | 86.82 serine/threonine protein kinase |
| SCE1572_1634 | 2,3-bisphosphoglycerate-independent phosphoglycerate mutase (EC 5.4.2.1) | bi | sce_1168 | 92.82 2,3-bisphosphoglycerate-independent phosphoglycerate mutase (EC 5.4.2.1) |
| SCE1572_1635 | probable dioxygenase | - | - | 0 |
| SCE1572_1636 | FIG01085270: hypothetical protein | bi | sce_1170 | 94.15 FIG01085270: hypothetical protein |
| SCE1572_1637 | hypothetical protein | bi | sce_3038 | 45.7 hypothetical protein |

| | | | | | |
|--------------|---|-----|-----------|-------|---|
| SCE1572_1638 | hypothetical protein | bi | sce_4585 | 57.25 | hypothetical protein |
| SCE1572_1639 | hypothetical protein | uni | sce_9112 | 31.85 | FIG01089486: hypothetical protein |
| SCE1572_1640 | Mir2351 protein | uni | sce_9338 | 32.57 | hypothetical protein |
| SCE1572_1641 | hypothetical protein | - | - | 0 | 0 |
| SCE1572_1642 | hypothetical protein | - | - | 0 | 0 |
| SCE1572_1643 | Rhs family protein | uni | sce_8347 | 40.88 | Rhs family protein |
| SCE1572_1644 | conserved hypothetical protein | uni | sce_9338 | 30.32 | hypothetical protein |
| SCE1572_1645 | VgrG protein | bi | sce_4581 | 59.17 | VgrG protein |
| SCE1572_1646 | hypothetical protein | - | - | 0 | 0 |
| SCE1572_1647 | Fimh-like protein | uni | sce_4372 | 70.05 | Fimh-like protein |
| SCE1572_1648 | PE-PGRS FAMILY PROTEIN | uni | sce_1215 | 66.86 | conserved hypothetical protein |
| SCE1572_1649 | BNR repeat domain protein | uni | sce_6171 | 74.9 | BNR repeat domain protein |
| SCE1572_1650 | Transposase | uni | sce_7292 | 48.76 | FIG01086976: hypothetical protein |
| SCE1572_1651 | hypothetical protein | bi | sce_5536 | 60.62 | hypothetical protein |
| SCE1572_1652 | TolA protein, putative | bi | sce_9536 | 42.31 | extracellular protein, putative |
| SCE1572_1653 | hypothetical protein | - | - | 0 | 0 |
| SCE1572_1654 | hypothetical protein | uni | sce_9684 | 26.77 | Protease |
| SCE1572_1655 | hypothetical protein | - | - | 0 | 0 |
| SCE1572_1656 | cDNA sequence BC036718 | uni | sce_4892 | 36.7 | NADH pyrophosphatase (EC 3.6.1.22) |
| SCE1572_1657 | hypothetical protein | - | - | 0 | 0 |
| SCE1572_1658 | GCN5-related N-acetyltransferase | bi | sce_1173 | 90.45 | GCN5-related N-acetyltransferase |
| SCE1572_1659 | Uncharacterized protein RP592 | bi | sce_1174 | 77.56 | Uncharacterized protein RP592 |
| SCE1572_1660 | Malate dehydrogenase (EC 1.1.1.37) | bi | sce_1175 | 96.49 | Malate dehydrogenase (EC 1.1.1.37) |
| SCE1572_1661 | Phosphoribosylaminoimidazole-succinocarboxamide synthase (EC 6.3.2.6) | bi | sce_1176 | 95.3 | Phosphoribosylaminoimidazole-succinocarboxamide synthase (EC 6.3.2.6) |
| SCE1572_1662 | Phosphoribosylformylglycinamide synthase, PurS subunit (EC 6.3.5.3) | - | - | 0 | 0 |
| SCE1572_1663 | FIG01087635: hypothetical protein | bi | sce_1177 | 73.17 | FIG01087635: hypothetical protein |
| SCE1572_1664 | hypothetical protein | bi | sce_1178 | 95.07 | hypothetical protein |
| SCE1572_1665 | hypothetical protein | bi | sce_1180 | 88.64 | hypothetical protein |
| SCE1572_1666 | hypothetical protein | bi | sce_1181 | 89.64 | Membrane protein involved in colicin uptake-like protein |
| SCE1572_1667 | hypothetical protein | bi | sce_1183 | 91.47 | hypothetical protein |
| SCE1572_1668 | hypothetical protein | bi | sce_1184 | 89.84 | predicted ATPase |
| SCE1572_1669 | FIG01087795: hypothetical protein | bi | sce_1185 | 84.21 | FIG01087795: hypothetical protein |
| SCE1572_1670 | Benzoyl-CoA oxygenase component B | bi | sce_1186 | 93.4 | Benzoyl-CoA oxygenase component B |
| SCE1572_1671 | benzoyl-CoA-dihydrodiol lyase (BoxC) | bi | sce_1187 | 90.61 | benzoyl-CoA-dihydrodiol lyase (BoxC) |
| SCE1572_1672 | Regulatory protein of benzoate catabolism | bi | sce_1188 | 88.17 | Regulatory protein of benzoate catabolism |
| SCE1572_1673 | Glycogen synthase, ADP-glucose transglucosylase (EC 2.4.1.21) | bi | sce_1189 | 87.96 | Glycogen synthase, ADP-glucose transglucosylase (EC 2.4.1.21) |
| SCE1572_1674 | putative lipoprotein | bi | sce_1190 | 84.58 | putative lipoprotein |
| SCE1572_1675 | FIG01086112: hypothetical protein | bi | sce_1191 | 91.08 | FIG01086112: hypothetical protein |
| SCE1572_1676 | EBNA-1 | uni | sce_7119 | 33.82 | hypothetical protein |
| SCE1572_1677 | FIG01087540: hypothetical protein | bi | sce_1192 | 80.38 | FIG01087540: hypothetical protein |
| SCE1572_1678 | DNA repair protein RecN | bi | sce_1193 | 98.05 | DNA repair protein RecN |
| SCE1572_1679 | Thymidylate synthase thyX (EC 2.1.1.-) | bi | sce_1194 | 93.75 | Thymidylate synthase thyX (EC 2.1.1.-) |
| SCE1572_1680 | Methionine aminopeptidase (EC 3.4.11.18) | bi | sce_1195 | 95.59 | Methionine aminopeptidase (EC 3.4.11.18) |
| SCE1572_1681 | FIG01085851: hypothetical protein | bi | sce_1196 | 87.63 | FIG01085851: hypothetical protein |
| SCE1572_1682 | FIG01088694: hypothetical protein | bi | sce_1197 | 85.56 | FIG01088694: hypothetical protein |
| SCE1572_1683 | hypothetical protein | bi | sce_1198 | 98.84 | hypothetical protein |
| SCE1572_1684 | hypothetical protein | bi | sce_1199 | 93.88 | hypothetical protein |
| SCE1572_1685 | Membrane protein involved in colicin uptake-like protein | bi | sce_1200 | 84.35 | hypothetical protein |
| SCE1572_1686 | hypothetical protein | bi | sce_1201 | 72.4 | Hypothetical protein |
| SCE1572_1687 | hypothetical protein | bi | sce_1202 | 85.62 | hypothetical protein |
| SCE1572_1688 | hypothetical protein | bi | sce_1203 | 74.02 | hypothetical protein |
| SCE1572_1689 | hypothetical protein | - | - | 0 | 0 |
| SCE1572_1690 | CDP-diaclyglycerol-glycerol-3-phosphate 3-phosphatidyltransferase (EC 2.7.8.5) | bi | sce_1204 | 92.31 | CDP-diaclyglycerol-glycerol-3-phosphate 3-phosphatidyltransferase (EC 2.7.8.5) |
| SCE1572_1691 | Universal stress protein family | bi | sce_1205 | 89.58 | Universal stress protein family |
| SCE1572_1692 | hypothetical protein | bi | sce_1206 | 83.67 | Outer membrane lipoprotein omp16 precursor |
| SCE1572_1693 | hypothetical protein | bi | sce_1207 | 81.9 | FIG01086986: hypothetical protein |
| SCE1572_1694 | FIG00546957: hypothetical protein | uni | sce_6759 | 39.54 | FIG01089529: hypothetical protein |
| SCE1572_1695 | hypothetical protein | - | - | 0 | 0 |
| SCE1572_1696 | FIG01086577: hypothetical protein | bi | sce_1209 | 86.21 | FIG01086577: hypothetical protein |
| SCE1572_1697 | hypothetical protein | bi | sce_1210 | 80.28 | hypothetical protein |
| SCE1572_1698 | hypothetical protein | bi | sce_1211 | 86.54 | hypothetical protein |
| SCE1572_1699 | Serine/threonine protein kinase with WD40 repeats precursor | bi | sce_1212 | 85.9 | serine/threonine protein kinase |
| SCE1572_1700 | Iron-sulfur cluster-binding protein | bi | sce_1213 | 96.67 | Iron-sulfur cluster-binding protein |
| SCE1572_1701 | Ferredoxin | bi | sce_1214 | 93.26 | Ferredoxin |
| SCE1572_1702 | PE-PGRS FAMILY PROTEIN | bi | sce_1215 | 69.05 | conserved hypothetical protein |
| SCE1572_1703 | Lipoprotein releasing system transmembrane protein LoIC | bi | sce_1216 | 83.15 | Lipoprotein releasing system transmembrane protein LoIC |
| SCE1572_1704 | hypothetical protein | bi | sce_1217 | 53.23 | hypothetical protein |
| SCE1572_1705 | serine/threonine protein kinase | bi | sce_1218 | 90.19 | serine/threonine protein kinase |
| SCE1572_1706 | RNA nucleotidyltransferase (EC 2.7.7.21) (EC 2.7.7.25) | bi | sce_1219 | 93.46 | RNA nucleotidyltransferase (EC 2.7.7.21) (EC 2.7.7.25) |
| SCE1572_1707 | Similarity | bi | sce_1221 | 77.23 | Similarity |
| SCE1572_1708 | conserved hypothetical protein | bi | sce_1222 | 93.1 | hypothetical protein |
| SCE1572_1709 | Guanine deaminase (EC 3.5.4.3) | bi | sce_1223 | 86.52 | Guanine deaminase (EC 3.5.4.3) |
| SCE1572_1710 | FIG01088286: hypothetical protein | bi | sce_1224 | 75.94 | FIG01088286: hypothetical protein |
| SCE1572_1711 | Butyryl-CoA dehydrogenase (EC 1.3.99.2) | bi | sce_1225 | 90.08 | Butyryl-CoA dehydrogenase (EC 1.3.99.2) |
| SCE1572_1712 | sulfatase | bi | sce_1226 | 82.58 | Sulfatase (EC 3.1.6.-) |
| SCE1572_1713 | FIG01086453: hypothetical protein | bi | sce_1227 | 89.23 | FIG01086453: hypothetical protein |
| SCE1572_1714 | response regulator receiver protein | uni | sce_9029 | 62.9 | response regulator receiver protein |
| SCE1572_1715 | COG1720: Uncharacterized conserved protein | uni | sce_2673 | 40.48 | COG1720: Uncharacterized conserved protein |
| SCE1572_1716 | hypothetical protein | - | - | 0 | 0 |
| SCE1572_1717 | Anthraniolate phosphoribosyltransferase (EC 2.4.2.18) | bi | sce_1230 | 89.66 | Anthraniolate phosphoribosyltransferase (EC 2.4.2.18) |
| SCE1572_1718 | Indole-3-glycerol phosphate synthase (EC 4.1.1.48) / Phosphoribosylanthranilate isomerase (EC 5.3.1.24) | bi | sce_1231 | 89.88 | Indole-3-glycerol phosphate synthase (EC 4.1.1.48) / Phosphoribosylanthranilate isomerase (EC 5.3.1.24) |
| SCE1572_1719 | Tryptophan synthase beta chain (EC 4.2.1.20) | bi | sce_1232 | 97.47 | Tryptophan synthase beta chain (EC 4.2.1.20) |
| SCE1572_1720 | Tryptophan synthase alpha chain (EC 4.2.1.20) | bi | sce_1233 | 92.51 | Tryptophan synthase alpha chain (EC 4.2.1.20) |
| SCE1572_1721 | hypothetical protein | uni | sce_574 | 39 | Membrane protein involved in colicin uptake-like protein |
| SCE1572_1722 | Outer membrane protein assembly factor YaeT precursor | bi | sce_1235 | 83.14 | Outer membrane protein assembly factor YaeT precursor |
| SCE1572_1723 | hypothetical protein | - | - | 0 | 0 |
| SCE1572_1724 | Phosphonate ABC transporter phosphate-binding periplasmic component (TC 3.A.1.9.1) | bi | sce_1236 | 95.85 | Phosphonate ABC transporter phosphate-binding periplasmic component (TC 3.A.1.9.1) |
| SCE1572_1725 | FIG01087640: hypothetical protein | bi | sce_1237 | 87.87 | FIG01087640: hypothetical protein |
| SCE1572_1726 | malto-oligosyltrehalose trehalohydrolase | uni | sce_7119 | 60 | hypothetical protein |
| SCE1572_1727 | ABC transporter, ATP-binding protein | bi | sce_1238 | 96.4 | ABC transporter, ATP-binding protein |
| SCE1572_1728 | Membrane protein implicated in protein export | bi | sce_1240 | 86.91 | Membrane protein implicated in protein export |
| SCE1572_1729 | hypothetical protein | - | - | 0 | 0 |
| SCE1572_1730 | hypothetical protein | - | - | 0 | 0 |
| SCE1572_1731 | RND multidrug efflux transporter: Acriflavin resistance protein | uni | sce_9222 | 58.93 | Acriflavin resistance protein |
| SCE1572_1732 | efflux transporter, RND family, MFP subunit | uni | sce_9221 | 47.83 | Probable Co/Zn/Cd efflux system membrane fusion protein |
| SCE1572_1733 | conserved domain protein | uni | sce_3810 | 26.29 | oxidoreductase of aldo/keto reductase family, subgroup I |
| SCE1572_1734 | conserved hypothetical protein | - | - | 0 | 0 |
| SCE1572_1735 | integral membrane transport protein | uni | sce_8782 | 31.1 | Probable transmembrane efflux transmembrane protein |
| SCE1572_1736 | Thioredoxin reductase (EC 1.8.1.9) | uni | sce_9822 | 39.14 | Thioredoxin reductase (EC 1.8.1.9) |
| SCE1572_1737 | Rrt2 family transcriptional regulator, group III | uni | sce_6432 | 27.5 | Rrt2 family transcriptional regulator, group III |
| SCE1572_1738 | Integron integrase IntIPac | uni | sce_8712 | 57.78 | Tyrosine recombinase XerC |
| SCE1572_1739 | Lipoprotein releasing system transmembrane protein LoIC | bi | sce_1242 | 96.86 | Lipoprotein releasing system transmembrane protein LoIC |
| SCE1572_1740 | Lipoprotein releasing system ATP-binding protein LoID | bi | sce_1243 | 93.86 | Lipoprotein releasing system ATP-binding protein LoID |
| SCE1572_1741 | putative ATP-dependent protease | uni | sce_1008 | 29.93 | ATP-dependent protease La (EC 3.4.21.53) Type I |
| SCE1572_1742 | PglZ domain | - | - | 0 | 0 |
| SCE1572_1743 | hypothetical protein | uni | sce_10208 | 43.68 | FIG01084875: hypothetical protein |
| SCE1572_1744 | hypothetical protein | uni | sce_10207 | 42.01 | hypothetical protein |
| SCE1572_1745 | COG1002: Type II restriction enzyme, methylase subunits | - | - | 0 | 0 |
| SCE1572_1746 | Type II restriction enzyme, methylase subunits | - | - | 0 | 0 |
| SCE1572_1747 | ATP-dependent DNA helicase | - | - | 0 | 0 |
| SCE1572_1748 | hypothetical protein | - | - | 0 | 0 |
| SCE1572_1749 | hypothetical protein | - | - | 0 | 0 |
| SCE1572_1750 | hypothetical protein | - | - | 0 | 0 |
| SCE1572_1751 | hypothetical protein | - | - | 0 | 0 |
| SCE1572_1752 | FIG01086577: hypothetical protein | uni | sce_2302 | 74.36 | hypothetical protein |
| SCE1572_1753 | hypothetical protein | - | - | 0 | 0 |
| SCE1572_1754 | hypothetical protein | - | - | 0 | 0 |
| SCE1572_1755 | hypothetical protein | - | - | 0 | 0 |
| SCE1572_1756 | hypothetical protein | - | - | 0 | 0 |
| SCE1572_1757 | Type III restriction-modification enzyme, helicase subunit | - | - | 0 | 0 |
| SCE1572_1758 | Possible DNA methylase | uni | sce_2039 | 22.9 | Type III restriction-modification system methylation subunit (EC 2.1.1.72) |
| SCE1572_1759 | hypothetical protein | - | - | 0 | 0 |
| SCE1572_1760 | conserved hypothetical protein | - | - | 0 | 0 |
| SCE1572_1761 | Glutathione S-transferase (EC 2.5.1.18) | bi | sce_1670 | 85.58 | Glutathione S-transferase (EC 2.5.1.18) |
| SCE1572_1762 | Tat (Twin-arginine translocation) pathway signal sequence domain protein | uni | sce_5158 | 83.52 | Tat (Twin-arginine translocation) pathway signal sequence domain protein |
| SCE1572_1763 | Cellulose-binding domain protein | uni | sce_1115 | 78.69 | Cellulose-binding domain protein |
| SCE1572_1764 | RNA polymerase sigma factor RpoE | uni | sce_3084 | 50 | RNA polymerase sigma factor RpoE |
| SCE1572_1765 | FIG01088605: hypothetical protein | uni | sce_3083 | 40.2 | FIG01088605: hypothetical protein |
| SCE1572_1766 | Flagellar hook-length control protein FlhK | uni | sce_3078 | 34.2 | Flagellar hook-length control protein FlhK |
| SCE1572_1767 | Endo-1,4-beta-xylanase A precursor (EC 3.2.1.8) | uni | sce_5134 | 56.49 | Endo-1,4-beta-xylanase A precursor (EC 3.2.1.8) |
| SCE1572_1768 | regulator of chromosome condensation, RCC1 | bi | sce_5098 | 86.44 | putative RTX family exportin |
| SCE1572_1769 | Glucose 1-dehydrogenase (EC 1.1.1.47) | uni | sce_5211 | 39.15 | 3-oxoacyl-[acyl-carrier protein] reductase (EC 1.1.1.100) |
| SCE1572_1770 | FIG01086453: hypothetical protein | uni | sce_1071 | 60.54 | FIG01086453: hypothetical protein |
| SCE1572_1771 | putative esterase | bi | sce_1085 | 92.31 | probable ferric enterobactin esterase-related protein Fes |
| SCE1572_1772 | L-arabinose-specific 1-epimerase (mutarotase) | bi | sce_1086 | 92.66 | L-arabinose-specific 1-epimerase (mutarotase) |
| SCE1572_1773 | hypothetical protein | - | - | 0 | 0 |
| SCE1572_1774 | RNA polymerase sigma factor RpoE | uni | sce_5484 | 83.58 | RNA polymerase sigma factor RpoE |
| SCE1572_1775 | hypothetical protein | bi | sce_5485 | 69.12 | hypothetical protein |
| SCE1572_1776 | hypothetical protein-transmembrane prediction | bi | sce_5486 | 86.96 | hypothetical protein-transmembrane prediction |
| SCE1572_1777 | FIG01087065: hypothetical protein | bi | sce_5487 | 94.67 | FIG01087065: hypothetical protein |
| SCE1572_1778 | Transcriptional regulator, AraC family | bi | sce_8627 | 79.66 | Transcriptional regulator, AraC family |
| SCE1572_1779 | O-methyltransferase (EC 2.1.1.-) | uni | sce_3613 | 51.06 | O-methyltransferase (EC 2.1.1.-) |
| SCE1572_1780 | Dehydrogenases with different specificities (related to short-chain alcohol dehydrogenases) | uni | sce_1565 | 89.63 | Dehydrogenases with different specificities (related to short-chain alcohol dehydrogenases) |
| SCE1572_1781 | Transcriptional regulator, AraC family | bi | sce_1564 | 89.53 | Transcriptional regulator, AraC family |
| SCE1572_1782 | Transcriptional regulator, ArsR family | bi | sce_7064 | 92.16 | Transcriptional regulator, ArsR family |
| SCE1572_1783 | conserved hypothetical protein | bi | sce_7065 | 84.14 | hypothetical protein |
| SCE1572_1784 | hypothetical membrane protein | - | - | 0 | 0 |
| SCE1572_1785 | Excinuclease ABC subunit A paralog of unknown function | bi | sce_7067 | 89.61 | Excinuclease ABC subunit A paralog of unknown function |
| SCE1572_1786 | FIG00501492: hypothetical protein | - | - | 0 | 0 |
| SCE1572_1787 | hypothetical protein | - | - | 0 | 0 |
| SCE1572_1788 | Molybdenum transport ATP-binding protein ModC (TC 3.A.1.8.1) | uni | sce_1266 | 75.34 | Molybdenum transport ATP-binding protein ModC (TC 3.A.1.8.1) |
| SCE1572_1789 | hypothetical protein | - | - | 0 | 0 |
| SCE1572_1790 | hypothetical protein | - | - | 0 | 0 |
| SCE1572_1791 | ABC-type antimicrobial peptide transport system, permease component | uni | sce_7523 | 26.01 | ABC-type antimicrobial peptide transport system, permease component |
| SCE1572_1792 | ABC transporter, ATP-binding protein, putative | uni | sce_1243 | 44.33 | Lipoprotein releasing system ATP-binding protein LoID |
| SCE1572_1793 | LSU ribosomal protein L33p | uni | sce_9218 | 85.71 | LSU ribosomal protein L33p |
| SCE1572_1794 | probable ABC transporter ATP-binding protein | uni | sce_9842 | 51.52 | probable ABC transporter ATP-binding protein |
| SCE1572_1795 | hypothetical protein | uni | sce_9840 | 38.71 | hypothetical protein |
| SCE1572_1796 | hypothetical protein | uni | sce_9840 | 29.83 | hypothetical protein |
| SCE1572_1797 | hypothetical protein | - | - | 0 | 0 |
| SCE1572_1798 | FIG01087034: hypothetical protein | uni | sce_3333 | 40.48 | FIG01087034: hypothetical protein |
| SCE1572_1799 | methyltransferase (EC 2.1.1.-) | uni | sce_3380 | 32.37 | 2-heptaprenyl-1,4-naphthoquinone methyltransferase (EC 2.1.1.163) |
| SCE1572_1800 | hypothetical protein | - | - | 0 | 0 |
| SCE1572_1801 | hypothetical protein | - | - | 0 | 0 |

| | | | | |
|--------------|--|-----|-----------|--|
| SCE1572_1802 | Similar to ferrous iron transporter protein B | - | | 0 |
| SCE1572_1803 | Nickel transporter UreH | uni | sce_6510 | 36.59 Nickel transporter UreH |
| SCE1572_1804 | Excinuclease ABC subunit A paralog of unknown function | uni | sce_7094 | 59.09 Transposase |
| SCE1572_1805 | GTP-binding protein related to HnX | bi | sce_2389 | 71.6 GTP-binding protein related to HnX |
| SCE1572_1806 | Molybdenum transport ATP-binding protein ModC (TC 3.A.1.8.1) | bi | sce_1266 | 81.63 Molybdenum transport ATP-binding protein ModC (TC 3.A.1.8.1) |
| SCE1572_1807 | Molybdenum transport system permease protein ModB (TC 3.A.1.8.1) | bi | sce_1267 | 85.98 Molybdenum transport system permease protein ModB (TC 3.A.1.8.1) |
| SCE1572_1808 | Molybdenum ABC transporter, periplasmic molybdenum-binding protein ModA (TC 3.A.1.8.1) | bi | sce_1268 | 81.75 Molybdenum ABC transporter, periplasmic molybdenum-binding protein ModA (TC 3.A.1.8.1) |
| SCE1572_1809 | Predicted molybdate-responsive regulator YvgK in bacilli | bi | sce_1269 | 85.05 Predicted molybdate-responsive regulator YvgK in bacilli |
| SCE1572_1810 | putative transcriptional regulator | bi | sce_5174 | 90.61 putative transcriptional regulator |
| SCE1572_1811 | DNA alkylation repair enzyme | bi | sce_5175 | 85.68 DNA alkylation repair enzyme |
| SCE1572_1812 | Phytochrome, two-component sensor histidine kinase (EC 2.7.3.-) | bi | sce_1270 | 66.88 Phytochrome, two-component sensor histidine kinase (EC 2.7.3.-) |
| SCE1572_1813 | Ribosomal-protein-L7p-serine acetyltransferase | bi | sce_1271 | 84.75 Ribosomal-protein-L7p-serine acetyltransferase |
| SCE1572_1814 | FIG01086118: hypothetical protein | bi | sce_1272 | 82.11 FIG01086118: hypothetical protein |
| SCE1572_1815 | Transcriptional regulator, GntR family domain / Aspartate aminotransferase (EC 2.6.1.1) | bi | sce_1273 | 84.47 Transcriptional regulator, GntR family domain / Aspartate aminotransferase (EC 2.6.1.1) |
| SCE1572_1816 | conserved hypothetical protein | bi | sce_1275 | 75 conserved hypothetical protein |
| SCE1572_1817 | two-component response regulator | uni | sce_10305 | 32.65 Response regulator of zinc sigma-54-dependent two-component system |
| SCE1572_1818 | hypothetical protein | bi | sce_9112 | 46.55 FIG01089486: hypothetical protein |
| SCE1572_1819 | hypothetical protein | - | | 0 |
| SCE1572_1820 | Protein of unknown function UPF0153 | bi | sce_1284 | 89.77 hypothetical protein |
| SCE1572_1821 | hypothetical protein | uni | sce_6260 | 30.36 LOC432261 protein |
| SCE1572_1822 | hypothetical protein | bi | sce_9371 | 25.11 Trypsin iota precursor (EC 3.4.21.4) |
| SCE1572_1823 | hypothetical protein | - | | 0 |
| SCE1572_1824 | hypothetical protein | bi | sce_2457 | 86.08 hypothetical protein |
| SCE1572_1825 | maleylacetoacetate isomerase | bi | sce_2458 | 89.66 Glutathione S-transferase (EC 2.5.1.18) |
| SCE1572_1826 | conserved hypothetical protein; putative PE_PGRS motifs | uni | sce_3154 | 69.64 Arylsulfatase (EC 3.1.6.1) |
| SCE1572_1827 | hypothetical protein | uni | sce_3421 | 33.33 FIG01086098: hypothetical protein |
| SCE1572_1828 | PE-PGRS FAMILY PROTEIN | uni | sce_2493 | 54.39 Uncharacterized protein with a C-terminal OMP (outer membrane protein) domain |
| SCE1572_1829 | Xylose isomerase (EC 5.3.1.5) | bi | sce_6076 | 94.81 Xylose isomerase (EC 5.3.1.5) |
| SCE1572_1830 | FIG01085806: hypothetical protein | bi | sce_1292 | 81.29 FIG01085806: hypothetical protein |
| SCE1572_1831 | hypothetical protein | - | | 0 |
| SCE1572_1832 | hypothetical protein | bi | sce_1293 | 70.8 hypothetical protein |
| SCE1572_1833 | DNA topoisomerase IB (poxvirus type) (EC 5.99.1.2) | bi | sce_1294 | 80.79 DNA topoisomerase IB (poxvirus type) (EC 5.99.1.2) |
| SCE1572_1834 | hypothetical protein | bi | sce_1295 | 73.21 hypothetical protein |
| SCE1572_1835 | FIG01087107: hypothetical protein | bi | sce_1296 | 86.79 FIG01087107: hypothetical protein |
| SCE1572_1836 | Gsr1690 protein | bi | sce_1297 | 93.15 hypothetical protein |
| SCE1572_1837 | Acyl-CoA dehydrogenase, short-chain specific (EC 1.3.99.2) | bi | sce_1299 | 93.3 Acyl-CoA dehydrogenase, short-chain specific (EC 1.3.99.2) |
| SCE1572_1838 | SAM-dependent methyltransferase | bi | sce_1300 | 87.89 SAM-dependent methyltransferase |
| SCE1572_1839 | hypothetical protein | bi | sce_1301 | 77.5 hypothetical protein |
| SCE1572_1840 | Alcohol dehydrogenase (EC 1.1.1.1) | bi | sce_1302 | 89.11 iron-containing alcohol dehydrogenase |
| SCE1572_1841 | Antibiotic biosynthesis monooxygenase | bi | sce_1303 | 86.67 Antibiotic biosynthesis monooxygenase |
| SCE1572_1842 | hypothetical protein | bi | sce_1304 | 77.38 hypothetical protein |
| SCE1572_1843 | putative carboxylesterase | bi | sce_1305 | 75.56 putative carboxylesterase |
| SCE1572_1844 | Histidine kinase | bi | sce_1306 | 87.34 Histidine kinase |
| SCE1572_1845 | hypothetical protein | - | | 0 |
| SCE1572_1846 | Two-component response regulator | bi | sce_1308 | 90.48 response regulator receiver protein |
| SCE1572_1847 | Branched-chain amino acid ABC transporter, amino acid-binding protein (TC 3.A.1.4.1) | bi | sce_1493 | 63.23 Branched-chain amino acid ABC transporter, amino acid-binding protein (TC 3.A.1.4.1) |
| SCE1572_1848 | Xylose ABC transporter, substrate-binding component | uni | sce_7038 | 67.21 hypothetical protein |
| SCE1572_1849 | TonB-dependent receptor; Outer membrane receptor for ferrienterochelin and colicins | bi | sce_1492 | 82.37 TonB-dependent receptor; Outer membrane receptor for ferrienterochelin and colicins |
| SCE1572_1850 | ATP-binding region, ATPase domain protein domain protein | bi | sce_1491 | 83.14 Signal transduction histidine kinase |
| SCE1572_1851 | two component transcriptional regulator, winged helix family | bi | sce_1490 | 77.78 response regulator receiver protein |
| SCE1572_1852 | FIG01084882: hypothetical protein | bi | sce_1488 | 82.61 FIG01084882: hypothetical protein |
| SCE1572_1853 | secreted protein | bi | sce_1487 | 85.71 secreted protein |
| SCE1572_1854 | hypothetical protein | - | | 0 |
| SCE1572_1855 | Glycerol-3-phosphate dehydrogenase (EC 1.1.5.3) | bi | sce_1309 | 86.63 Glycerol-3-phosphate dehydrogenase (EC 1.1.5.3) |
| SCE1572_1856 | HlyB/MsbA family ABC transporter | bi | sce_1310 | 87.91 HlyB/MsbA family ABC transporter |
| SCE1572_1857 | hypothetical protein | - | | 0 |
| SCE1572_1858 | Trp repressor binding protein | bi | sce_1312 | 71.96 Trp repressor binding protein |
| SCE1572_1859 | Two-component response regulator | bi | sce_1313 | 67.47 Two-component response regulator |
| SCE1572_1860 | Multicopper oxidase | bi | sce_1315 | 84.99 Multicopper oxidase |
| SCE1572_1861 | acetyltransferase | - | | 0 |
| SCE1572_1862 | Nitric-oxide reductase (EC 1.7.99.7), quinol-dependent | uni | sce_3679 | 59.45 Nitric-oxide reductase (EC 1.7.99.7), quinol-dependent |
| SCE1572_1863 | MATE efflux family protein | uni | sce_4895 | 27.88 MATE efflux family protein |
| SCE1572_1864 | hypothetical protein | - | | 0 |
| SCE1572_1865 | transcriptional regulator, LysR family | uni | sce_8686 | 49.21 Transcriptional regulator |
| SCE1572_1866 | GCNS-related N-acetyltransferase | bi | sce_6298 | 39.22 COG1247: Sortase and related acyltransferases |
| SCE1572_1867 | hypothetical protein | uni | sce_1730 | 34.53 hypothetical protein |
| SCE1572_1868 | Transcriptional regulator, AraC family | uni | sce_1564 | 37.06 Transcriptional regulator, AraC family |
| SCE1572_1869 | serine/threonine protein kinase | bi | sce_1342 | 92.31 serine/threonine protein kinase |
| SCE1572_1870 | hypothetical protein | bi | sce_1344 | 76.99 hypothetical protein |
| SCE1572_1871 | Cell division protein FtsH (EC 3.4.24.-) | uni | sce_3154 | 55.17 Arylsulfatase (EC 3.1.6.1) |
| SCE1572_1872 | Cysteine desulfurase (EC 2.8.1.7) | bi | sce_1345 | 89.83 Cysteine desulfurase (EC 2.8.1.7) |
| SCE1572_1873 | Gamma-glutamyltranspeptidase (EC 2.3.2.2) | bi | sce_1347 | 85.37 Gamma-glutamyltranspeptidase (EC 2.3.2.2) |
| SCE1572_1874 | Glutathione S-transferase, unnamed subgroup 2 (EC 2.5.1.18) | bi | sce_1390 | 89.1 Glutathione S-transferase, unnamed subgroup 2 (EC 2.5.1.18) |
| SCE1572_1875 | Metalloproteinase | bi | sce_1391 | 88.09 Metalloproteinase |
| SCE1572_1876 | Uncharacterized protein ImpC | bi | sce_1392 | 90.79 Uncharacterized protein ImpC |
| SCE1572_1877 | hypothetical protein | bi | sce_1393 | 70 hypothetical protein |
| SCE1572_1878 | hypothetical protein | bi | sce_1394 | 77.91 hypothetical protein |
| SCE1572_1879 | hypothetical protein | bi | sce_1395 | 79.7 hypothetical protein |
| SCE1572_1880 | Lead, cadmium, zinc and mercury transporting ATPase (EC 3.6.3.3) (EC 3.6.3.5); Copper-translocating P-type ATPase (EC 3.6.3.3) | bi | sce_1396 | 91.61 Lead, cadmium, zinc and mercury transporting ATPase (EC 3.6.3.3) (EC 3.6.3.5); Copper-translocating P-type ATPase (EC 3.6.3.4) |
| SCE1572_1881 | putative cytochrome c precursor | bi | sce_1397 | 80.98 putative cytochrome c precursor |
| SCE1572_1882 | Serine/threonine kinase with two-component sensor domain | bi | sce_1398 | 82.03 Serine/threonine kinase with two-component sensor domain |
| SCE1572_1883 | hypothetical protein | - | | 0 |
| SCE1572_1884 | Serine/threonine-protein kinase pkn3 (EC 2.7.11.1) | bi | sce_1399 | 69.44 Serine/threonine-protein kinase pkn3 (EC 2.7.11.1) |
| SCE1572_1885 | Prephenate and/or arginate dehydrogenase (unknown specificity) (EC 1.3.1.12)(EC 1.3.1.43) / Chorismate mutase 1 (EC 5.4.99.5) | bi | sce_1401 | 90.27 Prephenate and/or arginate dehydrogenase (unknown specificity) (EC 1.3.1.12)(EC 1.3.1.43) / Chorismate mutase 1 (EC 5.4.99.5) |
| SCE1572_1886 | hypothetical protein | uni | sce_3858 | 42 Adenylosylhomocysteinase (EC 3.3.1.1) |
| SCE1572_1887 | two-component sensor histidine kinase | bi | sce_1402 | 90.46 response regulator |
| SCE1572_1888 | Beta-hexosaminidase (EC 3.2.1.52) | bi | sce_1403 | 64.79 Cell division protein FtsZ (EC 3.4.24.-) |
| SCE1572_1889 | Serine/threonine kinase with two-component sensor domain | bi | sce_1404 | 75.12 Serine/threonine kinase with two-component sensor domain |
| SCE1572_1890 | NAD dependent epimerase/dehydratase family | uni | sce_1993 | 28.83 NAD-dependent epimerase/dehydratase |
| SCE1572_1891 | hypothetical protein | bi | sce_1405 | 56.36 hypothetical protein |
| SCE1572_1892 | GlI0645 protein | bi | sce_1406 | 73.62 GlI0645 protein |
| SCE1572_1893 | Gluconokinase (EC 2.7.1.12) | bi | sce_1407 | 88.2 Gluconokinase (EC 2.7.1.12) |
| SCE1572_1894 | Leukocyte elastase inhibitor (LEI) (Serpine B1) (Leukocyte neutral proteinase inhibitor) (LNPI) | bi | sce_1408 | 82.18 Leukocyte elastase inhibitor (LEI) (Serpine B1) (Leukocyte neutral proteinase inhibitor) (LNPI) |
| SCE1572_1895 | FIG01085385: hypothetical protein | bi | sce_1409 | 81.36 FIG01085385: hypothetical protein |
| SCE1572_1896 | hypothetical protein | uni | sce_8580 | 68.97 Kazal-type serine protease inhibitor domain |
| SCE1572_1897 | hypothetical protein | - | | 0 |
| SCE1572_1898 | Transcriptional regulator, GntR family domain / Aspartate aminotransferase (EC 2.6.1.1) | bi | sce_1410 | 91.75 Transcriptional regulator, GntR family domain / Aspartate aminotransferase (EC 2.6.1.1) |
| SCE1572_1899 | Histone acetyltransferase HPA2 and related acetyltransferases | bi | sce_1411 | 87.17 Histone acetyltransferase HPA2 and related acetyltransferases |
| SCE1572_1900 | 4-carboxymuconolactone decarboxylase domain/alkylhydroperoxidase AhpD family core domain protein | uni | sce_492 | 45.07 4-carboxymuconolactone decarboxylase domain/alkylhydroperoxidase AhpD family core domain protein |
| SCE1572_1901 | Probable carboxyvinyl-carboxyphosphate phosphorylmutase (EC 2.7.8.23) | uni | sce_676 | 30.38 carboxyvinyl-carboxyphosphate phosphorylmutase |
| SCE1572_1902 | FIG01086573: hypothetical protein | bi | sce_1414 | 93.74 FIG01086573: hypothetical protein |
| SCE1572_1903 | Translation elongation factor G-related protein | bi | sce_1415 | 93.63 Translation elongation factor G-related protein |
| SCE1572_1904 | hypothetical protein | - | | 0 |
| SCE1572_1905 | hypothetical protein | bi | sce_1416 | 84.91 hypothetical protein |
| SCE1572_1906 | serine/threonine protein kinase | bi | sce_1417 | 72.74 serine/threonine protein kinase |
| SCE1572_1907 | FIG01085868: hypothetical protein | bi | sce_1418 | 86.55 FIG01085868: hypothetical protein |
| SCE1572_1908 | FIG01085539: hypothetical protein | bi | sce_1419 | 94.03 FIG01085539: hypothetical protein |
| SCE1572_1909 | hypothetical protein | - | | 0 |
| SCE1572_1910 | hypothetical protein | uni | sce_8406 | 31.36 hypothetical protein |
| SCE1572_1911 | hypothetical protein | uni | sce_7594 | 46.11 hypothetical protein |
| SCE1572_1912 | FIG01085539: hypothetical protein | uni | sce_1419 | 85.11 FIG01085539: hypothetical protein |
| SCE1572_1913 | hypothetical protein | - | | 0 |
| SCE1572_1914 | Usg protein | bi | sce_1421 | 63.83 Usg protein |
| SCE1572_1915 | hypothetical protein | bi | sce_1422 | 85.99 hypothetical protein |
| SCE1572_1916 | FIG01086549: hypothetical protein | uni | sce_5307 | 58.06 FIG01086549: hypothetical protein |
| SCE1572_1917 | Chemotaxis protein methyltransferase CheR (EC 2.1.1.80) | bi | sce_1436 | 84.89 Chemotaxis protein methyltransferase CheR (EC 2.1.1.80) |
| SCE1572_1918 | FIG01087804: hypothetical protein | bi | sce_1437 | 90.13 FIG01087804: hypothetical protein |
| SCE1572_1919 | FIG01085464: hypothetical protein | bi | sce_1438 | 91.94 FIG01085464: hypothetical protein |
| SCE1572_1920 | hypothetical protein | bi | sce_1439 | 88.21 hypothetical protein |
| SCE1572_1921 | hypothetical protein | - | | 0 |
| SCE1572_1922 | Glycosyltransferase (EC 2.4.1.-) | bi | sce_1440 | 85.75 Glycosyltransferase (EC 2.4.1.-) |
| SCE1572_1923 | glycosyl transferase, group 1 family protein | bi | sce_1441 | 86.08 glycosyl transferase, group 1 family protein |
| SCE1572_1924 | FIG00704173: hypothetical protein | bi | sce_1442 | 93.37 FIG00704173: hypothetical protein |
| SCE1572_1925 | hypothetical protein | bi | sce_1443 | 84.09 hypothetical protein |
| SCE1572_1926 | Glycogen debranching enzyme (EC 3.2.1.-) | bi | sce_1444 | 93.65 Glycogen debranching enzyme (EC 3.2.1.-) |
| SCE1572_1927 | acetyltransferase | bi | sce_1445 | 94.82 acetyltransferase |
| SCE1572_1928 | Serine-threonine protein kinase | bi | sce_1446 | 82.42 Serine-threonine protein kinase |
| SCE1572_1929 | nitrite reductase (NAD(P)H), small subunit | bi | sce_1447 | 87.25 nitrite reductase (NAD(P)H), small subunit |
| SCE1572_1930 | RNA-2'-3'-PO4:RNA-5'-OH ligase | bi | sce_1448 | 93.56 RNA-2'-3'-PO4:RNA-5'-OH ligase |
| SCE1572_1931 | FIG00703100: hypothetical protein | uni | sce_2577 | 50.39 FIG00703100: hypothetical protein |
| SCE1572_1932 | FIG01087818: hypothetical protein | bi | sce_1449 | 82.19 FIG01087818: hypothetical protein |
| SCE1572_1933 | conserved hypothetical protein | uni | sce_7493 | 31.33 Branched-chain amino acid ABC transporter, amino acid-binding protein (TC 3.A.1.4.1) |
| SCE1572_1934 | putative | bi | sce_1450 | 89.92 transglutaminase-like |
| SCE1572_1935 | hypothetical protein | - | | 0 |
| SCE1572_1936 | serine/threonine protein kinase | uni | sce_5226 | 40.36 Adenylate cyclase (EC 4.6.1.1) / Guanylate cyclase (EC 4.6.1.2) |
| SCE1572_1937 | hypothetical protein | - | | 0 |
| SCE1572_1938 | Putative bacterial haemoglobin | uni | sce_5698 | 50 Putative bacterial haemoglobin |
| SCE1572_1939 | nitrogen metabolism transcriptional regulator, NtrC, Fis Family | uni | sce_9770 | 37.13 Response regulator of zinc sigma-54-dependent two-component system |
| SCE1572_1940 | putative RTX family exoprotein | uni | sce_6197 | 31.48 BNR repeat domain protein |
| SCE1572_1941 | putative RTX family exoprotein | uni | sce_6171 | 32.79 BNR repeat domain protein |
| SCE1572_1942 | hypothetical protein | - | | 0 |
| SCE1572_1943 | alpha/beta hydrolase fold | uni | sce_4657 | 40.4 epoxide hydrolase |
| SCE1572_1944 | Catalase (EC 1.11.1.6) | - | | 0 |
| SCE1572_1945 | hypothetical protein | - | | 0 |
| SCE1572_1946 | hypothetical protein | bi | sce_5198 | 27.45 FIG01089306: hypothetical protein |
| SCE1572_1947 | Long-chain-fatty-acid--CoA ligase (EC 6.2.1.3) | uni | sce_3170 | 32.63 serine/threonine kinase Pkn10 (EC-2.7.1.-) |
| SCE1572_1948 | hypothetical protein | bi | sce_1316 | 69.18 FIG01086389: hypothetical protein |
| SCE1572_1949 | hypothetical protein | - | | 0 |
| SCE1572_1950 | Nitrous oxide reductase maturation protein NosF (ATPase) | bi | sce_848 | 75 Nitrous oxide reductase maturation protein NosF (ATPase) |
| SCE1572_1951 | hypothetical protein | bi | sce_849 | 63.08 hypothetical protein |
| SCE1572_1952 | hypothetical protein | bi | sce_850 | 46.13 FIG01086100: hypothetical protein |
| SCE1572_1953 | Carbonic anhydrase (EC 4.2.1.1) | bi | sce_1455 | 90.42 Carbonic anhydrase (EC 4.2.1.1) |
| SCE1572_1954 | MII0076 protein | bi | sce_6015 | 87.5 MII0076 protein |
| SCE1572_1955 | conserved hypothetical protein | bi | sce_1456 | 85 hypothetical protein |
| SCE1572_1956 | Choline kinase (EC 2.7.1.32) | bi | sce_1457 | 82.13 Choline kinase (EC 2.7.1.32) |
| SCE1572_1957 | RNA signal recognition particle 4.5S RNA | bi | sce_6060 | 70.69 RNA signal recognition particle 4.5S RNA |
| SCE1572_1958 | RsbR, positive regulator of sigma-B | bi | sce_2565 | 82.53 RsbR, positive regulator of sigma-B |
| SCE1572_1959 | hypothetical protein | bi | sce_1461 | 61.54 hypothetical protein |
| SCE1572_1960 | Predicted metal-dependent hydrolase of the TIM-barrel fold | bi | sce_1462 | 96.46 Predicted metal-dependent hydrolase of the TIM-barrel fold |
| SCE1572_1961 | FIG01085728: hypothetical protein | bi | sce_1463 | 89.46 FIG01085728: hypothetical protein |
| SCE1572_1962 | Alkanesulfonates-binding protein | bi | sce_1464 | 91.92 Alkanesulfonates-binding protein |
| SCE1572_1963 | Alkanesulfonates transport system permease protein | bi | sce_1465 | 89.86 Alkanesulfonates transport system permease protein |
| SCE1572_1964 | Alkanesulfonates transport system permease protein | bi | sce_1466 | 88.85 Alkanesulfonates transport system permease protein |
| SCE1572_1965 | Alkanesulfonates ABC transporter ATP-binding protein / Sulfonate ABC transporter, ATP-binding subunit SsuB | bi | sce_1467 | 91.63 Alkanesulfonates ABC transporter ATP-binding protein / Sulfonate ABC transporter, ATP-binding subunit SsuB |

| | | | | |
|--------------|--|-----|-----------|---|
| SCE1572_1966 | Alkanesulfonates-binding protein | bi | see_1468 | 90.21 Alkanesulfonates-binding protein |
| SCE1572_1967 | thioredoxin 2 (EC 1.8.1.8) | bi | see_1470 | 92.79 thioredoxin |
| SCE1572_1968 | hypothetical protein | - | - | 0 |
| SCE1572_1969 | Cell division inhibitor | bi | see_1471 | 91.45 Cell division inhibitor |
| SCE1572_1970 | Glycerophosphoryl diester phosphodiesterase (EC 3.1.4.46) | - | - | 0 |
| SCE1572_1971 | hypothetical protein | bi | see_1472 | 84.27 hypothetical protein |
| SCE1572_1972 | peptidase, M16 family | bi | see_1473 | 85 peptidase M16-like |
| SCE1572_1973 | hypothetical protein | - | - | 0 |
| SCE1572_1974 | Anaerobic nitric oxide reductase transcription regulator NorR | bi | see_5699 | 93.69 Anaerobic nitric oxide reductase transcription regulator NorR |
| SCE1572_1975 | peptidase M16-like | bi | see_1474 | 81.93 peptidase M16-like |
| SCE1572_1976 | lysyl oxidase | bi | see_1475 | 73.81 lysyl oxidase |
| SCE1572_1977 | Glutathione S-transferase (EC 2.5.1.18) | umi | see_7792 | 32 Glutathione S-transferase, unnamed subgroup (EC 2.5.1.18) |
| SCE1572_1978 | Transcriptional regulator, TetR family | umi | see_7595 | 32.86 Transcriptional regulator, TetR family |
| SCE1572_1979 | hypothetical protein | - | - | 0 |
| SCE1572_1980 | hypothetical protein-transmembrane prediction | - | - | 0 |
| SCE1572_1981 | hypothetical protein | - | - | 0 |
| SCE1572_1982 | hypothetical protein | - | - | 0 |
| SCE1572_1983 | hypothetical protein | - | - | 0 |
| SCE1572_1984 | hypothetical protein | - | - | 0 |
| SCE1572_1985 | Vanadium haloperoxidase (EC 1.11.1.-) | - | - | 0 |
| SCE1572_1986 | Flagellar hook-length control protein FlkK | umi | see_3697 | 28.44 PE-PGRS FAMILY PROTEIN |
| SCE1572_1987 | FIG01085490: hypothetical protein | umi | see_9493 | 49.23 putative secreted protein |
| SCE1572_1988 | hypothetical protein | - | - | 0 |
| SCE1572_1989 | hypothetical protein | - | - | 0 |
| SCE1572_1990 | hypothetical protein | - | - | 0 |
| SCE1572_1991 | putative hydrolase | umi | see_7491 | 30.17 Bll1406 protein |
| SCE1572_1992 | hypothetical protein | - | - | 0 |
| SCE1572_1993 | probable short-chain dehydrogenase | bi | see_1476 | 87.69 probable short-chain dehydrogenase |
| SCE1572_1994 | Predicted thiol oxidoreductase | bi | see_1477 | 82.93 Predicted thiol oxidoreductase |
| SCE1572_1995 | FIG01087065: hypothetical protein | bi | see_1478 | 92.98 FIG01087065: hypothetical protein |
| SCE1572_1996 | hypothetical protein-transmembrane prediction | bi | see_1479 | 82.02 hypothetical protein-transmembrane prediction |
| SCE1572_1997 | hypothetical protein | bi | see_1480 | 64.18 hypothetical protein |
| SCE1572_1998 | putative transmembrane protein | bi | see_1481 | 81.6 hypothetical protein |
| SCE1572_1999 | FIG01087210: hypothetical protein | bi | see_1482 | 75 FIG01087210: hypothetical protein |
| SCE1572_2000 | PUTATIVE LIPOPROTEIN TRANSMEMBRANE | bi | see_1483 | 66.08 Serine-threonine protein kinase |
| SCE1572_2001 | RNA polymerase sigma factor RpoE | bi | see_1484 | 90.38 RNA polymerase sigma factor RpoE |
| SCE1572_2002 | EBNA-1 | bi | see_9154 | 51 PE-PGRS family protein |
| SCE1572_2003 | VgrG protein | umi | see_1486 | 60.54 VgrG protein |
| SCE1572_2004 | hypothetical protein | - | - | 0 |
| SCE1572_2005 | hypothetical protein | - | - | 0 |
| SCE1572_2006 | Dihydrolypoamide acetyltransferase component of pyruvate dehydrogenase complex (EC 2.3.1.12) | umi | see_8025 | 88.83 hypothetical protein |
| SCE1572_2007 | acetyltransferase, GNAT family | umi | see_9025 | 36.57 hypothetical protein |
| SCE1572_2008 | conserved hypothetical ATP-binding protein | umi | see_5653 | 30.15 FIG01088914: hypothetical protein |
| SCE1572_2009 | hypothetical protein | umi | see_8597 | 34.1 ATP binding protein |
| SCE1572_2010 | hypothetical protein | umi | see_1587 | 34.09 hypothetical protein |
| SCE1572_2011 | hypothetical protein | - | - | 0 |
| SCE1572_2012 | FIG01089158: hypothetical protein | bi | see_5518 | 60.22 NAD(P)HX epimerase / NAD(P)HX dehydratase |
| SCE1572_2013 | FIG01089158: hypothetical protein | umi | see_6082 | 56.64 FIG01089158: hypothetical protein |
| SCE1572_2014 | FIG01089158: hypothetical protein | umi | see_6082 | 59.6 FIG01089158: hypothetical protein |
| SCE1572_2015 | hypothetical protein | bi | see_6082 | 62.71 FIG01089158: hypothetical protein |
| SCE1572_2016 | Potassium-transporting ATPase A chain (EC 3.6.3.12) (TC 3.A.3.7.1) | bi | see_1496 | 93.67 Potassium-transporting ATPase A chain (EC 3.6.3.12) (TC 3.A.3.7.1) |
| SCE1572_2017 | Potassium-transporting ATPase B chain (EC 3.6.3.12) (TC 3.A.3.7.1) | bi | see_1497 | 91.64 Potassium-transporting ATPase B chain (EC 3.6.3.12) (TC 3.A.3.7.1) |
| SCE1572_2018 | Potassium-transporting ATPase C chain (EC 3.6.3.12) (TC 3.A.3.7.1) | bi | see_1498 | 92.59 Potassium-transporting ATPase C chain (EC 3.6.3.12) (TC 3.A.3.7.1) |
| SCE1572_2019 | Osmosensitive K channel histidine kinase KdpD (EC 2.7.3.-) | bi | see_1499 | 89.56 Osmosensitive K channel histidine kinase KdpD (EC 2.7.3.-) |
| SCE1572_2020 | DNA-binding response regulator KdpE | bi | see_1500 | 95.26 DNA-binding response regulator KdpE |
| SCE1572_2021 | hypothetical protein | - | - | 0 |
| SCE1572_2022 | Beta-xylosidase (EC 3.2.1.37) | bi | see_3705 | 73.04 Beta-xylosidase (EC 3.2.1.37) |
| SCE1572_2023 | hypothetical protein | bi | see_5152 | 72.66 predicted protein |
| SCE1572_2024 | DNA polymerase IV (EC 2.7.7.7) | bi | see_1510 | 89.66 DNA polymerase IV (EC 2.7.7.7) |
| SCE1572_2025 | FIG01087716: hypothetical protein | bi | see_1511 | 75.3 FIG01087716: hypothetical protein |
| SCE1572_2026 | Putative oxidoreductase YncB | bi | see_9276 | 48.38 Quinone oxidoreductase (EC 1.6.5.5) |
| SCE1572_2027 | hypothetical protein | - | - | 0 |
| SCE1572_2028 | Dihydrofolate reductase (EC 1.5.1.3) | bi | see_1517 | 80.11 Dihydrofolate reductase (EC 1.5.1.3) |
| SCE1572_2029 | hypothetical protein | bi | see_1512 | 86.7 Transport protein |
| SCE1572_2030 | hypothetical protein | bi | see_8774 | 61.25 hypothetical protein |
| SCE1572_2031 | FIG01087529: hypothetical protein | bi | see_1513 | 86.54 FIG01087529: hypothetical protein |
| SCE1572_2032 | PE-PGRS family protein | umi | see_1514 | 59.28 putative immediate early protein |
| SCE1572_2033 | Mobile element protein | umi | see_1675 | 96.77 ISLp1 |
| SCE1572_2034 | FIG01085909: hypothetical protein | umi | see_7667 | 45.16 FIG01085909: hypothetical protein |
| SCE1572_2035 | hypothetical protein | - | - | 0 |
| SCE1572_2036 | Collagen triple helix repeat | umi | see_1518 | 58.15 FIG01087054: hypothetical protein |
| SCE1572_2037 | FIG00660906: hypothetical protein | umi | see_4839 | 32.76 FIG01088196: hypothetical protein |
| SCE1572_2038 | FIG01085825: hypothetical protein | bi | see_1519 | 85.32 FIG01085825: hypothetical protein |
| SCE1572_2039 | hypothetical protein | bi | see_1520 | 87.32 hypothetical protein |
| SCE1572_2040 | Membrane protein, putative | bi | see_1521 | 87.13 Membrane protein, putative |
| SCE1572_2041 | NAD(P)H dehydrogenase (quinone):NADPH-dependent FMN reductase | bi | see_1679 | 76.5 NAD(P)H dehydrogenase (quinone):NADPH-dependent FMN reductase |
| SCE1572_2042 | 50S ribosomal subunit maturation GTPase RbgA (B. subtilis Y1qF) | bi | see_1522 | 92.08 50S ribosomal subunit maturation GTPase RbgA (B. subtilis Y1qF) |
| SCE1572_2043 | 2-hydroxychromene-2-carboxylate isomerase/DsbA-like thioredoxin domain | bi | see_1523 | 85.71 2-hydroxychromene-2-carboxylate isomerase/DsbA-like thioredoxin domain |
| SCE1572_2044 | hypothetical protein | - | - | 0 |
| SCE1572_2045 | possible rhomboid family protein | bi | see_1527 | 81.14 Rhomboid family protein |
| SCE1572_2046 | hypothetical protein | bi | see_1529 | 88.85 hypothetical protein |
| SCE1572_2047 | hypothetical protein | - | - | 0 |
| SCE1572_2048 | GNAT family acetyltransferase YjcF | bi | see_1530 | 83.92 GNAT family acetyltransferase YjcF |
| SCE1572_2049 | hypothetical protein | umi | see_8963 | 38.6 Dihydroflavonol-4-reductase (EC 1.1.1.219) |
| SCE1572_2050 | conserved hypothetical protein | - | - | 0 |
| SCE1572_2051 | hypothetical protein | umi | see_3844 | 39.71 Uncharacterized protein conserved in bacteria, NMA0228-like |
| SCE1572_2052 | hypothetical protein | - | - | 0 |
| SCE1572_2053 | hypothetical protein | - | - | 0 |
| SCE1572_2054 | UDP-galactose-lipid carrier transferase (EC 2.-.-) | bi | see_1546 | 90.75 UDP-galactose-lipid carrier transferase (EC 2.-.-) |
| SCE1572_2055 | PROBABLE TREHALOSE-6-PHOSPHATE PHOSPHATASE OTS1 (TREHALOSE- PHOSPHATASE) (TPP) (EC 3.2.1.2) | bi | see_1567 | 77.24 PROBABLE TREHALOSE-6-PHOSPHATE PHOSPHATASE OTS1 (TREHALOSE- PHOSPHATASE) (TPP) (EC 3.2.1.2) |
| SCE1572_2056 | D-alanine--D-alanine ligase (EC 6.3.2.4) | umi | see_3103 | 38.59 D-alanine--D-alanine ligase (EC 6.3.2.4) |
| SCE1572_2057 | hypothetical protein | - | - | 0 |
| SCE1572_2058 | hypothetical protein | - | - | 0 |
| SCE1572_2059 | Permeases of the major facilitator superfamily | bi | see_1569 | 86.8 Permeases of the major facilitator superfamily |
| SCE1572_2060 | ABC-type nitrate/sulfonate/bicarbonate transport systems, periplasmic components | umi | see_1570 | 69.62 ABC-type nitrate/sulfonate/bicarbonate transport systems, periplasmic components |
| SCE1572_2061 | ABC-type nitrate/sulfonate/bicarbonate transport systems, periplasmic components | bi | see_1570 | 86.34 ABC-type nitrate/sulfonate/bicarbonate transport systems, periplasmic components |
| SCE1572_2062 | Cyanate hydratase (EC 4.2.1.104) | - | - | 0 |
| SCE1572_2063 | RsbR, positive regulator of sigma-B | umi | see_4461 | 50.89 RsbR, positive regulator of sigma-B |
| SCE1572_2064 | hypothetical protein | bi | see_3848 | 33.81 hypothetical protein |
| SCE1572_2065 | Probable Co/Zn/Cd efflux system membrane fusion protein | bi | see_1576 | 89.31 Probable Co/Zn/Cd efflux system membrane fusion protein |
| SCE1572_2066 | Cobalt-zinc-cadmium resistance protein CzcA; Cation efflux system protein CusA | bi | see_1577 | 93.66 Cobalt-zinc-cadmium resistance protein CzcA; Cation efflux system protein CusA |
| SCE1572_2067 | LysR family transcriptional regulator STM3121 | bi | see_1578 | 89.1 LysR family transcriptional regulator STM3121 |
| SCE1572_2068 | hypothetical protein | - | - | 0 |
| SCE1572_2069 | RsbR, positive regulator of sigma-B | bi | see_1579 | 77.18 positive regulator |
| SCE1572_2070 | hypothetical protein | - | - | 0 |
| SCE1572_2071 | hypothetical protein | bi | see_1583 | 72.14 hypothetical protein |
| SCE1572_2072 | sigma-54 dependent DNA-binding response regulator | bi | see_1588 | 89.76 sigma-54 dependent DNA-binding response regulator |
| SCE1572_2073 | sigma-54 dependent DNA-binding response regulator | umi | see_1588 | 82.75 sigma-54 dependent DNA-binding response regulator |
| SCE1572_2074 | FIG01084914: hypothetical protein | bi | see_1589 | 69.96 FIG01084914: hypothetical protein |
| SCE1572_2075 | hypothetical protein | bi | see_1590 | 67.86 hypothetical protein |
| SCE1572_2076 | Transcriptional regulator, LacI family | bi | see_1591 | 70.92 Transcriptional regulator, LacI family |
| SCE1572_2077 | Agmatinase (EC 3.5.3.11) | bi | see_10225 | 71.2 Agmatinase (EC 3.5.3.11) |
| SCE1572_2078 | hydrolase, alpha/beta fold family | bi | see_7460 | 89.96 hydrolase, alpha/beta fold family |
| SCE1572_2079 | Similar to F420-dependent glucose-6-phosphate dehydrogenase, Mext_1273 family | - | - | 0 |
| SCE1572_2080 | Aminopeptidase Y (Arg, Lys, Leu preference) (EC 3.4.11.15) | bi | see_1592 | 76.19 Aminopeptidase Y (Arg, Lys, Leu preference) (EC 3.4.11.15) |
| SCE1572_2081 | Cytochrome c552 precursor (EC 1.7.2.2) | bi | see_1593 | 90.76 Cytochrome c552 precursor (EC 1.7.2.2) |
| SCE1572_2082 | Cytochrome c nitrite reductase, small subunit NrfH | bi | see_1594 | 82.66 Cytochrome c nitrite reductase, small subunit NrfH |
| SCE1572_2083 | hypothetical protein | - | - | 0 |
| SCE1572_2084 | hypothetical protein | - | - | 0 |
| SCE1572_2085 | hypothetical protein | umi | see_8056 | 29.95 FIG01085335: hypothetical protein |
| SCE1572_2086 | Sialic acid transporter (permease) NanT | bi | see_1596 | 86.47 Sialic acid transporter (permease) NanT |
| SCE1572_2087 | hypothetical protein | - | - | 0 |
| SCE1572_2088 | putative cytochrome P450 hydroxylase | umi | see_7075 | 60.89 putative cytochrome P450 hydroxylase |
| SCE1572_2089 | putative immediate early protein | bi | see_5892 | 59.31 erythrocyte membrane protein 1 (PIEMP1) |
| SCE1572_2090 | hypothetical protein | - | - | 0 |
| SCE1572_2091 | hypothetical protein | - | - | 0 |
| SCE1572_2092 | Gfa-like protein | bi | see_7399 | 73.85 Gfa-like protein |
| SCE1572_2093 | hypothetical protein | - | - | 0 |
| SCE1572_2094 | dioxygenase | - | - | 0 |
| SCE1572_2095 | Hydrolase, alpha/beta fold family | bi | see_1609 | 74.73 Hydrolase, alpha/beta fold family |
| SCE1572_2096 | FIG01088506: hypothetical protein | bi | see_1610 | 77.42 FIG01088506: hypothetical protein |
| SCE1572_2097 | hypothetical protein | bi | see_1611 | 94.21 hypothetical protein |
| SCE1572_2098 | PE-PGRS FAMILY PROTEIN | bi | see_1612 | 77.13 Chitinase (EC 3.2.1.14) |
| SCE1572_2099 | aldose 1-epimerase family protein | bi | see_1613 | 87.03 aldose 1-epimerase family protein |
| SCE1572_2100 | hypothetical protein | bi | see_1614 | 91.49 hypothetical protein |
| SCE1572_2101 | FIG01087944: hypothetical protein | bi | see_1617 | 83.44 FIG01087944: hypothetical protein |
| SCE1572_2102 | hydrolase, alpha/beta hydrolase fold family | bi | see_1618 | 84.36 probable hydrolase (EC 3.-) |
| SCE1572_2103 | MutS-related protein, family 1 | bi | see_1619 | 90.09 MutS-related protein, family 1 |
| SCE1572_2104 | Transaldolase (EC 2.2.1.2) | bi | see_1620 | 91.79 Transaldolase (EC 2.2.1.2) |
| SCE1572_2105 | FIG01086000: hypothetical protein | bi | see_1621 | 84.47 FIG01086000: hypothetical protein |
| SCE1572_2106 | FIG01089281: hypothetical protein | bi | see_1622 | 84.4 FIG01089281: hypothetical protein |
| SCE1572_2107 | FIG01085285: hypothetical protein | bi | see_1623 | 92.09 FIG01085285: hypothetical protein |
| SCE1572_2108 | hypothetical protein | bi | see_1624 | 84.82 hypothetical protein |
| SCE1572_2109 | hypothetical protein | bi | see_1625 | 94.39 hypothetical protein |
| SCE1572_2110 | Cyclopropane-fatty-acyl-phospholipid synthase (EC 2.1.1.79) | bi | see_1626 | 97.12 PUTATIVE CYCLOPROPANE-FATTY-ACYL-PHOSPHOLIPID SYNTHASE PROTEIN (EC 2.1.1.79) |
| SCE1572_2111 | Long-chain-fatty-acid--CoA ligase (EC 6.2.1.3) | bi | see_1627 | 93.54 Long-chain-fatty-acid--CoA ligase (EC 6.2.1.3) |
| SCE1572_2112 | hypothetical protein | - | - | 0 |
| SCE1572_2113 | PE-PGRS FAMILY PROTEIN | umi | see_4770 | 51.81 hypothetical protein |
| SCE1572_2114 | Endo-1,4-beta-xylanase A precursor (EC 3.2.1.8) | bi | see_1629 | 78.54 Endo-1,4-beta-xylanase A precursor (EC 3.2.1.8) |
| SCE1572_2115 | FIG01088155: hypothetical protein | bi | see_1630 | 84.54 FIG01088155: hypothetical protein |
| SCE1572_2116 | hypothetical protein | - | - | 0 |
| SCE1572_2117 | Na driven multidrug efflux pump | bi | see_1631 | 88.59 Na driven multidrug efflux pump |
| SCE1572_2118 | hypothetical protein | - | - | 0 |
| SCE1572_2119 | FIG01088775: hypothetical protein | bi | see_1632 | 81.64 FIG01088775: hypothetical protein |
| SCE1572_2120 | Response regulator of zinc sigma-54-dependent two-component system | bi | see_1633 | 93 Response regulator of zinc sigma-54-dependent two-component system |
| SCE1572_2121 | Recombination inhibitory protein MutS2 | bi | see_1634 | 91.11 Recombination inhibitory protein MutS2 |
| SCE1572_2122 | Malonyl CoA-acyl carrier protein transacylase (EC 2.3.1.39) | - | - | 0 |
| SCE1572_2123 | two-component hybrid sensor and regulator | bi | see_1635 | 76.38 two-component hybrid sensor and regulator |
| SCE1572_2124 | ATP-dependent DNA ligase (EC 6.5.1.1) clustered with Ku protein, LigD | umi | see_3945 | 50.58 ATP-dependent DNA ligase (EC 6.5.1.1) clustered with Ku protein, LigD |
| SCE1572_2125 | drug resistance transporter, EmrB/QacA family | bi | see_1645 | 91.33 drug resistance transporter, EmrB/QacA family |
| SCE1572_2126 | serine/threonine kinase family protein | bi | see_1646 | 77.5 hypothetical protein |
| SCE1572_2127 | hypothetical protein | - | - | 0 |
| SCE1572_2128 | Arabinan endo-1,5-alpha-L-arabinosidase (EC 3.2.1.99) | bi | see_1647 | 74.25 Arabinan endo-1,5-alpha-L-arabinosidase (EC 3.2.1.99) |
| SCE1572_2129 | FIG01089314: hypothetical protein | bi | see_1648 | 91.09 FIG01089314: hypothetical protein |

| | | | | | |
|--------------|--|-----|-----------|---------|--|
| SCE1572_2130 | hypothetical protein | bi | see_1649 | 56.01 | hypothetical protein |
| SCE1572_2131 | hypothetical protein | bi | see_1650 | 85.37 | hypothetical protein |
| SCE1572_2132 | rhamnolacturonan acetyltransferase | bi | see_1652 | 76.56 | rhamnolacturonan acetyltransferase |
| SCE1572_2133 | Predicted rhamnolacturonan lyase in rhamnose utilization cluster | umi | see_3412 | 54.61 | Predicted rhamnolacturonan lyase in rhamnose utilization cluster |
| SCE1572_2134 | hypothetical protein | - | - | 0 | 0 |
| SCE1572_2135 | hypothetical protein | - | - | 0 | 0 |
| SCE1572_2136 | gliding motility protein MglA | bi | see_1655 | 94.82 | gliding motility protein MglA |
| SCE1572_2137 | FIG01087084: hypothetical protein | bi | see_1656 | 89.63 | FIG01087084: hypothetical protein |
| SCE1572_2138 | hypothetical protein | - | - | 0 | 0 |
| SCE1572_2139 | putative cytochrome P450 hydroxylase | bi | see_7075 | 64.96 | putative cytochrome P450 hydroxylase |
| SCE1572_2140 | hypothetical protein | - | - | 0 | 0 |
| SCE1572_2141 | hypothetical protein | - | - | 0 | 0 |
| SCE1572_2142 | Beta-lactamase class C and other penicillin binding proteins | bi | see_1658 | 83.29 | Beta-lactamase class C and other penicillin binding proteins |
| SCE1572_2143 | Adenylate cyclase (EC 4.6.1.1) | bi | see_1666 | 87.96 | Adenylate cyclase (EC 4.6.1.1) |
| SCE1572_2144 | Outer membrane protein A-like protein | bi | see_1667 | 86.69 | Outer membrane protein A-like protein |
| SCE1572_2145 | hypothetical protein | bi | see_1668 | 80.51 | FIG01086036: hypothetical protein |
| SCE1572_2146 | Endo-1,4-beta-xylanase A precursor (EC 3.2.1.8) | umi | see_841 | 83.54 | Endo-1,4-beta-xylanase A precursor (EC 3.2.1.8) |
| SCE1572_2147 | hypothetical protein | umi | see_1677 | 27.38 | PE-PGRS FAMILY PROTEIN |
| SCE1572_2148 | Endo-1,4-beta-xylanase A precursor (EC 3.2.1.8) | bi | see_841 | 89.64 | Endo-1,4-beta-xylanase A precursor (EC 3.2.1.8) |
| SCE1572_2149 | Transcriptional regulator, AraC family | umi | see_2490 | 38.1 | Transcriptional regulator, AraC family |
| SCE1572_2150 | short-chain dehydrogenase/reductase SDR | umi | see_6012 | 40 | Retinol dehydrogenase 13 (EC 1.1.1.-) |
| SCE1572_2151 | Succinoglycan biosynthesis protein exoA (EC 2.-.-.-) | bi | see_1719 | 88.76 | Succinoglycan biosynthesis protein exoA (EC 2.-.-.-) |
| SCE1572_2152 | Methylthioribulose-1-phosphate dehydratase (EC 4.2.1.109) | bi | see_1720 | 86.32 | Methylthioribulose-1-phosphate dehydratase (EC 4.2.1.109) |
| SCE1572_2153 | 1,2-dihydroxy-3-keto-5-methylthiopentene dioxygenase (EC 1.13.11.54) | bi | see_1721 | 91.67 | 1,2-dihydroxy-3-keto-5-methylthiopentene dioxygenase (EC 1.13.11.54) |
| SCE1572_2154 | 2,3-diketo-5-methylthiopentyl-1-phosphate enolase-phosphatase (EC 3.1.3.77) | bi | see_1722 | 87.83 | 2,3-diketo-5-methylthiopentyl-1-phosphate enolase-phosphatase (EC 3.1.3.77) |
| SCE1572_2155 | hypothetical protein | - | - | 0 | 0 |
| SCE1572_2156 | Transcriptional regulator, HxIR family | umi | see_2658 | 42.05 | Transcriptional regulator, HxIR family |
| SCE1572_2157 | Glutathione S-transferase (EC 2.5.1.18) | umi | see_4471 | 56.06 | Glutathione S-transferase domain protein |
| SCE1572_2158 | Conserved domain protein | umi | see_5251 | 77.78 | hypothetical protein |
| SCE1572_2159 | hypothetical protein | bi | see_3770 | 64.15 | sugar ABC transporter, periplasmic sugar-binding protein |
| SCE1572_2160 | Phytanoyl-CoA dioxygenase | - | - | 0 | 0 |
| SCE1572_2161 | Long-chain-fatty-acid-CoA ligase (EC 6.2.1.3) | umi | see_389 | 45.2 | Long-chain-fatty-acid-CoA ligase (EC 6.2.1.3) |
| SCE1572_2162 | SanA protein | umi | see_968 | 32.03 | FIG01087584: hypothetical protein |
| SCE1572_2163 | FIG01088801: hypothetical protein | bi | see_175 | 78.66 | FIG01088801: hypothetical protein |
| SCE1572_2164 | hypothetical protein | - | - | 0 | 0 |
| SCE1572_2165 | putative membrane protein of unknown function with protease domain | - | - | 0 | 0 |
| SCE1572_2166 | Alpha-1,2-mannosidase | umi | see_857 | 50.75 | Secreted trypsin-like serine protease |
| SCE1572_2167 | hypothetical protein | - | - | 0 | 0 |
| SCE1572_2168 | hypothetical protein | - | - | 0 | 0 |
| SCE1572_2169 | Nitrilase (EC 3.5.5.7) | umi | see_10049 | 38.33 | Nitrilase (EC 3.5.5.7) |
| SCE1572_2170 | serine/threonine protein kinase | bi | see_5759 | 93.72 | serine/threonine protein kinase |
| SCE1572_2171 | Serine/threonine-protein kinase pkn1 (EC 2.7.11.1) | bi | see_5758 | 87.04 | Serine/threonine-protein kinase pkn1 (EC 2.7.11.1) |
| SCE1572_2172 | hypothetical protein | - | - | 0 | 0 |
| SCE1572_2173 | Thioredoxin | umi | see_6433 | 41.49 | Thioredoxin |
| SCE1572_2174 | putative membrane protein | bi | see_764 | 94.14 | putative membrane protein |
| SCE1572_2175 | FIG01086453: hypothetical protein | umi | see_1227 | 49.74 | FIG01086453: hypothetical protein |
| SCE1572_2176 | structural constituent of cell wall | bi | see_1727 | 69.96 | Prolipoprotein diacylglycerol transferase (EC 2.4.99.-) |
| SCE1572_2177 | FIG01087703: hypothetical protein | bi | see_1728 | 74.57 | FIG01087703: hypothetical protein |
| SCE1572_2178 | putative secreted hydrolase | bi | see_10158 | 34.41 | hypothetical protein |
| SCE1572_2179 | RNA polymerase, sigma-24 subunit, ECF subfamily | - | - | 0 | 0 |
| SCE1572_2180 | hypothetical protein | bi | see_1276 | 28.16 | Fibronectin type III domain protein |
| SCE1572_2181 | Putative glutathione S-transferase (EC 2.5.1.18) | bi | see_1326 | 94.78 | Putative glutathione S-transferase (EC 2.5.1.18) |
| SCE1572_2182 | protein kinase domain | umi | see_10233 | 37.7 | protein kinase domain |
| SCE1572_2183 | Serine/threonine protein kinase (EC 2.7.11.1) | umi | see_10233 | 42.32 | protein kinase domain |
| SCE1572_2184 | FIG01175415: hypothetical protein | bi | see_6334 | 34.36 | putative integrin-like protein |
| SCE1572_2185 | Uncharacterized serpin-like protein MA_2246 | bi | see_9438 | 88.99 | Uncharacterized serpin-like protein MA_2246 |
| SCE1572_2186 | hypothetical protein | - | - | 0 | 0 |
| SCE1572_2187 | hypothetical protein | bi | see_7422 | 89.45 | hypothetical protein |
| SCE1572_2188 | hypothetical protein | - | - | 0 | 0 |
| SCE1572_2189 | hypothetical protein | umi | see_4176 | 44.44 | putative membrane protein |
| SCE1572_2190 | tmRNA-binding protein SmpB | bi | see_2564 | 90.74 | tmRNA-binding protein SmpB |
| SCE1572_2191 | Dopamine beta-hydroxylase precursor (EC 1.14.17.1) (Dopamine beta-monoxygenase) | bi | see_7916 | 93.85 | Dopamine beta-hydroxylase precursor (EC 1.14.17.1) (Dopamine beta-monoxygenase) |
| SCE1572_2192 | hypothetical protein | - | - | 0 | 0 |
| SCE1572_2193 | istB transposition helper protein | bi | see_7096 | 92.45 | istB transposition helper protein |
| SCE1572_2194 | FIG01087754: hypothetical protein | umi | see_2414 | 63.25 | FIG01087754: hypothetical protein |
| SCE1572_2195 | hypothetical protein | bi | see_176 | 71.79 | hypothetical protein |
| SCE1572_2196 | serine/threonine protein kinase | bi | see_9450 | 85.04 | serine/threonine protein kinase |
| SCE1572_2197 | Signal transduction histidine kinase CheA (EC 2.7.3.-) | bi | see_3917 | 83.41 | Signal transduction histidine kinase CheA (EC 2.7.3.-) |
| SCE1572_2198 | hypothetical protein | - | - | 0 | 0 |
| SCE1572_2199 | Dihydroliipoamide acyltransferase component of branched-chain alpha-keto acid dehydrogenase complex (EC 2.3.1.168) | bi | see_1746 | 84.78 | Dihydroliipoamide acyltransferase component of branched-chain alpha-keto acid dehydrogenase complex (EC 2.3.1.168) |
| SCE1572_2200 | Branched-chain alpha-keto acid dehydrogenase, E1 component, beta subunit (EC 1.2.4.4) | bi | see_1747 | 96.57 | Branched-chain alpha-keto acid dehydrogenase, E1 component, beta subunit (EC 1.2.4.4) |
| SCE1572_2201 | Branched-chain alpha-keto acid dehydrogenase, E1 component, alpha subunit (EC 1.2.4.4) | bi | see_1748 | 92.68 | Branched-chain alpha-keto acid dehydrogenase, E1 component, alpha subunit (EC 1.2.4.4) |
| SCE1572_2202 | FIG01089395: hypothetical protein | bi | see_1749 | 85.57 | FIG01089395: hypothetical protein |
| SCE1572_2203 | Lipoate synthase | bi | see_1750 | 90.53 | Lipoate synthase |
| SCE1572_2204 | Methylthioribose-1-phosphate isomerase (EC 5.3.1.23) | bi | see_1751 | 89.92 | Methylthioribose-1-phosphate isomerase (EC 5.3.1.23) |
| SCE1572_2205 | hypothetical protein | bi | see_1752 | 87.85 | hypothetical protein |
| SCE1572_2206 | short-chain dehydrogenase/reductase SDR | bi | see_1753 | 91.73 | short-chain dehydrogenase/reductase SDR |
| SCE1572_2207 | FIG01088303: hypothetical protein | umi | see_1754 | 72.09 | FIG01088303: hypothetical protein |
| SCE1572_2208 | FIG01088303: hypothetical protein | bi | see_1754 | 82.65 | FIG01088303: hypothetical protein |
| SCE1572_2209 | putative alpha-dextrin endo-1, 6-alpha-glucosidase | bi | see_1755 | 82.77 | putative alpha-dextrin endo-1, 6-alpha-glucosidase |
| SCE1572_2210 | ATP binding protein | umi | see_9281 | 33.07 | ATP binding protein |
| SCE1572_2211 | hypothetical protein | umi | see_1587 | 29.22 | hypothetical protein |
| SCE1572_2212 | FIG01089178: hypothetical protein | bi | see_1756 | 88.27 | FIG01089178: hypothetical protein |
| SCE1572_2213 | hypothetical protein | umi | see_4997 | 33.5 | hypothetical protein |
| SCE1572_2214 | hypothetical protein | - | - | 0 | 0 |
| SCE1572_2215 | Ribosomal RNA large subunit methyltransferase N (EC 2.1.1.-) | bi | see_1759 | 90.15 | Ribosomal RNA large subunit methyltransferase N (EC 2.1.1.-) |
| SCE1572_2216 | FIG01087693: hypothetical protein | bi | see_1760 | 81.39 | FIG01087693: hypothetical protein |
| SCE1572_2217 | hypothetical protein | - | - | 0 | 0 |
| SCE1572_2218 | Nitric oxide synthase oxygenase (EC 1.-.-.-) | bi | see_1762 | 87.81 | Nitric oxide synthase oxygenase (EC 1.-.-.-) |
| SCE1572_2219 | hypothetical protein | - | - | 0 | 0 |
| SCE1572_2220 | serine/threonine protein kinase | umi | see_1342 | 72.78 | serine/threonine protein kinase |
| SCE1572_2221 | hypothetical protein | - | - | 0 | 0 |
| SCE1572_2222 | FIG01088490: hypothetical protein | bi | see_1765 | 77.78 | FIG01088490: hypothetical protein |
| SCE1572_2223 | FIG01088098: hypothetical protein | bi | see_1766 | 89.51 | FIG01088098: hypothetical protein |
| SCE1572_2224 | Domain often clustered or fused with uracil-DNA glycosylase / Uracil-DNA glycosylase, putative family 6 | umi | see_1931 | 59.42 | Uracil-DNA glycosylase, putative family 6 |
| SCE1572_2225 | Biotin synthase related domain containing protein | - | - | 0 | 0 |
| SCE1572_2226 | Membrane protein | bi | see_1775 | 76.81 | Membrane protein |
| SCE1572_2227 | FIG01086931: hypothetical protein | bi | see_787 | 82.35 | FIG01086931: hypothetical protein |
| SCE1572_2228 | hypothetical protein | bi | see_1776 | 95.65 | hypothetical protein |
| SCE1572_2229 | Chemotaxis regulator - transmits chemoreceptor signals to flagellar motor components CheY | bi | see_1777 | 81.14 | Chemotaxis regulator - transmits chemoreceptor signals to flagellar motor components CheY |
| SCE1572_2230 | Signal transduction histidine kinase CheA (EC 2.7.3.-) | bi | see_1778 | 98.54 | Signal transduction histidine kinase CheA (EC 2.7.3.-) |
| SCE1572_2231 | Positive regulator of CheA protein activity (CheW) | bi | see_1779 | 97.75 | Positive regulator of CheA protein activity (CheW) |
| SCE1572_2232 | Positive regulator of CheA protein activity (CheW) | bi | see_1780 | 96.53 | Positive regulator of CheA protein activity (CheW) |
| SCE1572_2233 | FOG: HEAT repeat | bi | see_1781 | 85.84 | FOG: HEAT repeat |
| SCE1572_2234 | Chemotaxis protein methyltransferase CheR (EC 2.1.1.80) | bi | see_1782 | 92.53 | Chemotaxis protein methyltransferase CheR (EC 2.1.1.80) |
| SCE1572_2235 | Chemotaxis response regulator protein-glutamate methyltransferase CheB (EC 3.1.1.61) | bi | see_1783 | 97.22 | Chemotaxis response regulator protein-glutamate methyltransferase CheB (EC 3.1.1.61) |
| SCE1572_2236 | Membrane-bound lytic murein transglycosylase D precursor (EC 3.2.1.-) | bi | see_1784 | 78.1 | Membrane-bound lytic murein transglycosylase D precursor (EC 3.2.1.-) |
| SCE1572_2237 | FIG00871199: hypothetical protein | bi | see_1785 | 90.27 | FIG00871199: hypothetical protein |
| SCE1572_2238 | serine/threonine protein kinase | bi | see_1786 | 65.89 | serine/threonine protein kinase |
| SCE1572_2239 | FIG01086365: hypothetical protein | bi | see_1787 | 67.6 | FIG01086365: hypothetical protein |
| SCE1572_2240 | EBNA-1 | bi | see_1515 | 61.15 | PE-PGRS FAMILY PROTEIN |
| SCE1572_2241 | serine/threonine protein kinase | umi | see_1787 | 42.83 | FIG01086365: hypothetical protein |
| SCE1572_2242 | Serine-threonine protein kinase | bi | see_1794 | 54.09 | serine/threonine protein kinase |
| SCE1572_2243 | Chaperone protein DnaJ | umi | see_1789 | 49.39 | PE-PGRS family protein |
| SCE1572_2244 | hypothetical protein | umi | see_1790 | 50.45 | hypothetical protein |
| SCE1572_2245 | PE-PGRS FAMILY PROTEIN | umi | see_1789 | 50.21 | PE-PGRS family protein |
| SCE1572_2246 | PEGA domain protein | umi | see_1793 | 42.38 | FIG01085807: hypothetical protein |
| SCE1572_2247 | hypothetical protein | - | - | 0 | 0 |
| SCE1572_2248 | PE-PGRS FAMILY PROTEIN | umi | see_1789 | 44.15 | PE-PGRS family protein |
| SCE1572_2249 | hypothetical protein | bi | see_1790 | 54.63 | hypothetical protein |
| SCE1572_2250 | PE-PGRS FAMILY PROTEIN | umi | see_4006 | 44.19 | FIG01086775: hypothetical protein |
| SCE1572_2251 | Dihydroliipoamide acetyltransferase component of pyruvate dehydrogenase complex (EC 2.3.1.12) | bi | see_1796 | 39.48 | hypothetical protein |
| SCE1572_2252 | hypothetical protein | bi | see_1797 | 59.5 | Cell division protein FtsK |
| SCE1572_2253 | FIG01087277: hypothetical protein | bi | see_1798 | 91.18 | FIG01087277: hypothetical protein |
| SCE1572_2254 | YgiD/KaeI/Qri7 family, required for N6-threonylcarbamoyl adenosine t(6)A37 modification in tRNA | bi | see_1799 | 93.54 | YgiD/KaeI/Qri7 family, required for N6-threonylcarbamoyl adenosine t(6)A37 modification in tRNA |
| SCE1572_2255 | hypothetical protein | bi | see_1800 | 86.43 | hypothetical protein |
| SCE1572_2256 | conserved hypothetical protein-containing TPR-domains | bi | see_1801 | 92.96 | conserved hypothetical protein-containing TPR-domains |
| SCE1572_2257 | Conserved protein, with a weak D-galactarate dehydratase/altronate hydrolase domain | umi | see_6222 | 47.87 | Conserved protein, with a weak D-galactarate dehydratase/altronate hydrolase domain |
| SCE1572_2258 | Adenylate cyclase (EC 4.6.1.1) / Guanylate cyclase (EC 4.6.1.2) | bi | see_1803 | 87.63 | Adenylate cyclase (EC 4.6.1.1) / Guanylate cyclase (EC 4.6.1.2) |
| SCE1572_2259 | FIG01089242: hypothetical protein | bi | see_1804 | 68.42 | FIG01089242: hypothetical protein |
| SCE1572_2260 | FIG01086453: hypothetical protein | umi | see_1071 | 63.31 | FIG01086453: hypothetical protein |
| SCE1572_2261 | WD40-like beta Propeller | bi | see_1805 | 92.31 | WD40-like beta Propeller |
| SCE1572_2262 | hypothetical protein | bi | see_1806 | 79.8 | hypothetical protein |
| SCE1572_2263 | CDP-diacylglycerol--serine O-phosphatidyltransferase (EC 2.7.8.8) | bi | see_1807 | 96.15 | CDP-diacylglycerol--serine O-phosphatidyltransferase (EC 2.7.8.8) |
| SCE1572_2264 | FIG01088615: hypothetical protein | bi | see_1808 | 96.24 | FIG01088615: hypothetical protein |
| SCE1572_2265 | cytochrome c assembly protein | bi | see_1809 | 90.1 | cytochrome c assembly protein |
| SCE1572_2266 | Glutamyl-tRNA reductase (EC 1.2.1.70) | bi | see_1810 | 87.41 | Glutamyl-tRNA reductase (EC 1.2.1.70) |
| SCE1572_2267 | Porphobilinogen deaminase (EC 2.5.1.61) | bi | see_1811 | 91.58 | Porphobilinogen deaminase (EC 2.5.1.61) |
| SCE1572_2268 | Glycogen branching enzyme, GH-57-type, archaeal (EC 2.4.1.18) | bi | see_1812 | 88.83 | Glycogen branching enzyme, GH-57-type, archaeal (EC 2.4.1.18) |
| SCE1572_2269 | Efflux transporter, RND family, MFP subunit, AcrA/E family | bi | see_1813 | 87.76 | Efflux transporter, RND family, MFP subunit, AcrA/E family |
| SCE1572_2270 | RND multidrug efflux transporter, Acriflavin resistance protein | bi | see_1814 | 93.79 | RND multidrug efflux transporter, Acriflavin resistance protein |
| SCE1572_2271 | Peptidase S1C, Do | bi | see_1815 | 89.32 | trypsin-like serine protease |
| SCE1572_2272 | protein of unknown function DUF885 | bi | see_1817 | 89.55 | hypothetical protein |
| SCE1572_2273 | protein of unknown function UPF0153 | bi | see_1818 | 86.29 | protein of unknown function UPF0153 |
| SCE1572_2274 | hypothetical protein | bi | see_1819 | 75.61 | hypothetical protein |
| SCE1572_2275 | Peptide chain release factor 2 | bi | see_1820 | 97.14 | Peptide chain release factor 2 |
| SCE1572_2276 | Lysyl-tRNA synthetase (class II) (EC 6.1.1.6) | bi | see_1821 | 95.29 | Lysyl-tRNA synthetase (class II) (EC 6.1.1.6) |
| SCE1572_2277 | Lipoprotein releasing system transmembrane protein LolC | bi | see_1822 | 83.75 | Lipoprotein releasing system transmembrane protein LolC |
| SCE1572_2278 | Lipoprotein releasing system ATP-binding protein LolD | bi | see_1823 | 95.49 | Lipoprotein releasing system ATP-binding protein LolD |
| SCE1572_2279 | PROBABLE OXIDOREDUCTASE GMC-TYPE (EC 1.-.-.-) | bi | see_1824 | 92.39 | PROBABLE OXIDOREDUCTASE GMC-TYPE (EC 1.-.-.-) |
| SCE1572_2280 | Arginine N-succinyltransferase (EC 2.3.1.109) | bi | see_1826 | 92.8 | Arginine N-succinyltransferase (EC 2.3.1.109) |
| SCE1572_2281 | Shikimate 5-dehydrogenase I gamma (EC 1.1.1.25) | bi | see_1827 | 91.9 | Shikimate 5-dehydrogenase I gamma (EC 1.1.1.25) |
| SCE1572_2282 | Signal peptidase I (EC 3.4.21.89) | bi | see_1828 | 90.16 | Signal peptidase I (EC 3.4.21.89) |
| SCE1572_2283 | Cell division protein FtsH (EC 3.4.24.-) | bi | see_1829 | 87.31 | Cell division protein FtsH (EC 3.4.24.-) |
| SCE1572_2284 | Basic proline-rich protein | bi | see_1831 | 81.76 | Basic proline-rich protein |
| SCE1572_2285 | hypothetical protein | bi | see_1832 | 96.25 | hypothetical protein |
| SCE1572_2286 | RNA polymerase sigma factor for flagellar operon | bi | see_1833 | 90.09 | RNA polymerase sigma factor for flagellar operon |
| SCE1572_2287 | Very large tegument protein | bi | see_1834 | 87.14 | Very large tegument protein |
| SCE1572_2288 | 3-oxoacyl-[acyl-carrier protein] reductase (EC 1.1.1.100) | bi | see_1835 | 96.46</ | |

| | | | | |
|--------------|---|-----|-----------|---|
| SCE1572_2294 | rRNA-guanine transglycosylase (EC 2.4.2.29) | bi | sce_1842 | 95.96 rRNA-guanine transglycosylase (EC 2.4.2.29) |
| SCE1572_2295 | hypothetical protein | - | - | 0 |
| SCE1572_2296 | response regulator receiver protein | bi | sce_1843 | 96.28 DNA-binding response regulator |
| SCE1572_2297 | putative Fe-S oxidoreductase | bi | sce_1844 | 71.16 FIG01089683: hypothetical protein |
| SCE1572_2298 | B12 binding domain of Methylmalonyl-CoA mutase (EC 5.4.99.2) | bi | sce_1845 | 97.01 B12 binding domain of Methylmalonyl-CoA mutase (EC 5.4.99.2) |
| SCE1572_2299 | Cell division protein MraZ | bi | sce_1846 | 97.37 Cell division protein MraZ |
| SCE1572_2300 | rRNA small subunit methyltransferase H | bi | sce_1847 | 92.7 rRNA small subunit methyltransferase H |
| SCE1572_2301 | hypothetical protein | bi | sce_1848 | 91.45 hypothetical protein |
| SCE1572_2302 | Cell division protein FtsI [Peptidoglycan synthetase] (EC 2.4.1.129) | bi | sce_1849 | 93.38 Cell division protein FtsI [Peptidoglycan synthetase] (EC 2.4.1.129) |
| SCE1572_2303 | UDP-N-acetylmuramoylalanine-D-glutamate-2,6-diaminopimelate ligase (EC 6.3.2.13) | bi | sce_1850 | 91.01 UDP-N-acetylmuramoylalanine-D-glutamate-2,6-diaminopimelate ligase (EC 6.3.2.13) |
| SCE1572_2304 | Phospho-N-acetylmuramoyl-pentapeptide-transferase (EC 2.7.8.13) | bi | sce_1851 | 97.87 Phospho-N-acetylmuramoyl-pentapeptide-transferase (EC 2.7.8.13) |
| SCE1572_2305 | UDP-N-acetylmuramoylalanine-D-glutamate ligase (EC 6.3.2.9) | bi | sce_1852 | 90.97 UDP-N-acetylmuramoylalanine-D-glutamate ligase (EC 6.3.2.9) |
| SCE1572_2306 | Cell division protein FtsW | bi | sce_1853 | 89.73 Cell division protein FtsW |
| SCE1572_2307 | UDP-N-acetylglucosamine-N-acetylmuramyl-(pentapeptide) pyrophosphoryl-undecaprenol N-acetylglucosamine transferase | bi | sce_1854 | 92.1 UDP-N-acetylglucosamine-N-acetylmuramyl-(pentapeptide) pyrophosphoryl-undecaprenol N-acetylglucosamine transferase (EC 2.3.1.12) |
| SCE1572_2308 | UDP-N-acetylmuramate-alanine ligase (EC 6.3.2.8) | bi | sce_1855 | 96.58 UDP-N-acetylmuramate-alanine ligase (EC 6.3.2.8) |
| SCE1572_2309 | Cell division protein FtsQ | bi | sce_1856 | 86.73 Cell division protein FtsQ |
| SCE1572_2310 | Cell division protein FtsA | bi | sce_1857 | 97.94 Cell division protein FtsA |
| SCE1572_2311 | Cell division protein FtsZ (EC 3.4.24.-) | bi | sce_1858 | 92.76 Cell division protein FtsZ (EC 3.4.24.-) |
| SCE1572_2312 | Chaperone protein DnaJ | bi | sce_1859 | 96.4 Chaperone protein DnaJ |
| SCE1572_2313 | hypothetical protein | bi | sce_1860 | 89.79 hypothetical protein |
| SCE1572_2314 | FIG01088969: hypothetical protein | bi | sce_1861 | 84.3 FIG01088969: hypothetical protein |
| SCE1572_2315 | protein of unknown function DUF329 | bi | sce_1862 | 82.22 hypothetical protein |
| SCE1572_2316 | Serine protease precursor MucD/AlgY associated with sigma factor RpoE | bi | sce_1863 | 83.54 Serine protease precursor MucD/AlgY associated with sigma factor RpoE |
| SCE1572_2317 | FIG01086853: hypothetical protein | bi | sce_1864 | 77.3 hypothetical protein |
| SCE1572_2318 | Inactive homolog of metal-dependent proteases, putative molecular chaperone | bi | sce_1865 | 83.15 Inactive homolog of metal-dependent proteases, putative molecular chaperone |
| SCE1572_2319 | cAMP-binding proteins - catabolite gene activator and regulatory subunit of cAMP-dependent protein kinases | bi | sce_1866 | 89.36 cAMP-binding proteins - catabolite gene activator and regulatory subunit of cAMP-dependent protein kinases |
| SCE1572_2320 | TPR domain protein | bi | sce_1867 | 88.68 TPR domain protein |
| SCE1572_2321 | Hypothetical protein | bi | sce_1868 | 97.92 Hypothetical protein |
| SCE1572_2322 | DNA recombination and repair protein RecO | bi | sce_1869 | 92.05 DNA recombination and repair protein RecO |
| SCE1572_2323 | FIG01088242: hypothetical protein | bi | sce_1870 | 91.54 FIG01088242: hypothetical protein |
| SCE1572_2324 | MiS389 protein | bi | sce_1871 | 84.43 MiS389 protein |
| SCE1572_2325 | Ferrochelatase, protoheme ferro-lyase (EC 4.99.1.1) | bi | sce_1872 | 90 Ferrochelatase, protoheme ferro-lyase (EC 4.99.1.1) |
| SCE1572_2326 | Short-chain dehydrogenase/reductase SDR | bi | sce_1873 | 80 Short-chain dehydrogenase/reductase SDR |
| SCE1572_2327 | TPR Domain containing protein | bi | sce_1875 | 92.21 Tetratricopeptide TPR_2 repeat protein |
| SCE1572_2328 | hypothetical protein | bi | sce_1877 | 88.82 hypothetical protein |
| SCE1572_2329 | FIG01087871: hypothetical protein | bi | sce_1878 | 85.48 FIG01087871: hypothetical protein |
| SCE1572_2330 | FIG01085537: hypothetical protein | bi | sce_1879 | 89.82 FIG01085537: hypothetical protein |
| SCE1572_2331 | hypothetical protein | bi | sce_10208 | 45.27 FIG01084875: hypothetical protein |
| SCE1572_2332 | hypothetical protein | bi | sce_10207 | 47.51 hypothetical protein |
| SCE1572_2333 | Formate hydrogenlyase transcriptional activator | bi | sce_1883 | 96.3 Formate hydrogenlyase transcriptional activator |
| SCE1572_2334 | hypothetical protein | umi | sce_8748 | 35.96 Adenosylhomocysteinase (EC 3.3.1.1) |
| SCE1572_2335 | hypothetical protein | bi | sce_1885 | 77.83 hypothetical protein |
| SCE1572_2336 | hypothetical protein | bi | sce_1886 | 83.87 hypothetical protein |
| SCE1572_2337 | hypothetical protein | bi | sce_1887 | 91.26 hypothetical protein |
| SCE1572_2338 | Cell binding factor 2 precursor | bi | sce_1888 | 91.06 Cell binding factor 2 precursor |
| SCE1572_2339 | FIG01087318: hypothetical protein | bi | sce_1889 | 86.94 FIG01087318: hypothetical protein |
| SCE1572_2340 | hypothetical protein | - | - | 0 |
| SCE1572_2341 | FIG01086761: hypothetical protein | bi | sce_1890 | 92.34 FIG01086761: hypothetical protein |
| SCE1572_2342 | Pterin-4-alpha-carbinolamine dehydratase (EC 4.2.1.96) | bi | sce_1891 | 88.66 Pterin-4-alpha-carbinolamine dehydratase (EC 4.2.1.96) |
| SCE1572_2343 | hypothetical protein | bi | sce_1893 | 95.68 hypothetical protein |
| SCE1572_2344 | FIG01089220: hypothetical protein | bi | sce_1894 | 86.32 FIG01089220: hypothetical protein |
| SCE1572_2345 | rRNA (cytosine34-2'-O)-methyltransferase (EC 2.1.1.-) | bi | sce_1895 | 96.51 rRNA (cytosine34-2'-O)-methyltransferase (EC 2.1.1.-) |
| SCE1572_2346 | hypothetical protein | bi | sce_1896 | 88.89 hypothetical protein |
| SCE1572_2347 | CarD-like transcriptional regulator | bi | sce_1897 | 100 CarD-like transcriptional regulator |
| SCE1572_2348 | Phosphatase, Ppx/GppA family | bi | sce_1898 | 90.68 Phosphatase, Ppx/GppA family |
| SCE1572_2349 | Flagellar motor rotation protein MotB | bi | sce_1899 | 97.45 Flagellar motor rotation protein MotB |
| SCE1572_2350 | hypothetical protein | bi | sce_1900 | 96.46 Histone H1 |
| SCE1572_2351 | hypothetical protein | bi | sce_1902 | 97.2 hypothetical protein |
| SCE1572_2352 | Dihydropyrimidine succinyltransferase component (E2) of 2-oxoglutarate dehydrogenase complex (EC 2.3.1.61) / 2-oxoglutarat | bi | sce_1903 | 88.24 Dihydropyrimidine acetyltransferase component of pyruvate dehydrogenase complex (EC 2.3.1.12) |
| SCE1572_2353 | hypothetical protein | bi | sce_1904 | 71.6 hypothetical protein |
| SCE1572_2354 | HNH endonuclease family protein | bi | sce_1905 | 93.21 HNH endonuclease family protein |
| SCE1572_2355 | DNA polymerase III epsilon subunit (EC 2.7.7.7) | bi | sce_1906 | 94.34 DNA polymerase III epsilon subunit (EC 2.7.7.7) |
| SCE1572_2356 | Preprotein translocase subunit SecG (TC 3.A.5.1.1) | bi | sce_1907 | 89.42 Preprotein translocase subunit SecG (TC 3.A.5.1.1) |
| SCE1572_2357 | Phosphopantetheine adenylyltransferase (EC 2.7.7.3) | bi | sce_1908 | 96.36 Phosphopantetheine adenylyltransferase (EC 2.7.7.3) |
| SCE1572_2358 | FIG01087039: hypothetical protein | bi | sce_1909 | 90.31 FIG01087039: hypothetical protein |
| SCE1572_2359 | Serine/threonine protein kinase PrkC, regulator of stationary phase | bi | sce_1910 | 87.5 Serine/threonine protein kinase PrkC, regulator of stationary phase |
| SCE1572_2360 | hypothetical protein | - | - | 0 |
| SCE1572_2361 | Poly(A) polymerase (EC 2.7.7.19) | bi | sce_1912 | 97.23 Poly(A) polymerase (EC 2.7.7.19) |
| SCE1572_2362 | FIG01085896: hypothetical protein | bi | sce_1913 | 89.14 FIG01085896: hypothetical protein |
| SCE1572_2363 | NUDIX hydrolase | bi | sce_1914 | 84.44 NUDIX hydrolase |
| SCE1572_2364 | hypothetical protein | bi | sce_1915 | 71.28 hypothetical protein |
| SCE1572_2365 | transcriptional regulator, TetR family | bi | sce_1916 | 86.04 transcriptional regulator, TetR family |
| SCE1572_2366 | Cysteine protease | bi | sce_1917 | 93.4 hypothetical protein |
| SCE1572_2367 | hypothetical protein | - | - | 0 |
| SCE1572_2368 | FIG01087505: hypothetical protein | bi | sce_1918 | 79.89 FIG01087505: hypothetical protein |
| SCE1572_2369 | hypothetical protein | bi | sce_1919 | 91.78 hypothetical protein |
| SCE1572_2370 | hypothetical protein | bi | sce_1920 | 77.68 FIG01084943: hypothetical protein |
| SCE1572_2371 | Adenylate cyclase (EC 4.6.1.1) | bi | sce_1921 | 89.6 Adenylate cyclase (EC 4.6.1.1) |
| SCE1572_2372 | FIG01086442: hypothetical protein | bi | sce_1922 | 94.02 FIG01086442: hypothetical protein |
| SCE1572_2373 | Response regulator of zinc sigma-54-dependent two-component system | bi | sce_1923 | 88.62 Response regulator of zinc sigma-54-dependent two-component system |
| SCE1572_2374 | response regulator receiver domain protein (CheY-like) | bi | sce_1925 | 96.75 response regulator receiver domain protein (CheY-like) |
| SCE1572_2375 | hypothetical protein | bi | sce_1926 | 80.87 hypothetical protein |
| SCE1572_2376 | Chemotaxis protein methyltransferase CheR (EC 2.1.1.80) | bi | sce_1927 | 82.22 Chemotaxis protein methyltransferase CheR (EC 2.1.1.80) |
| SCE1572_2377 | hypothetical protein | bi | sce_1928 | 68.3 hypothetical protein |
| SCE1572_2378 | hypothetical protein | bi | sce_1929 | 84.62 hypothetical protein |
| SCE1572_2379 | Transcriptional regulator, TetR family | bi | sce_1930 | 83.27 Transcriptional regulator, TetR family |
| SCE1572_2380 | Uracil-DNA glycosylase, putative family 6 | bi | sce_1931 | 90.54 Uracil-DNA glycosylase, putative family 6 |
| SCE1572_2381 | Kup system potassium uptake protein | bi | sce_1932 | 92.59 Kup system potassium uptake protein |
| SCE1572_2382 | Citrate synthase (si) (EC 2.3.3.1) | bi | sce_1933 | 93.08 Citrate synthase (si) (EC 2.3.3.1) |
| SCE1572_2383 | Citrate synthase (si) (EC 2.3.3.1) | bi | sce_1935 | 89.69 Citrate synthase (si) (EC 2.3.3.1) |
| SCE1572_2384 | RecA protein | bi | sce_1937 | 92.17 RecA protein |
| SCE1572_2385 | DNA polymerase-like protein PA0670 | bi | sce_1938 | 90.91 DNA polymerase-like protein PA0670 |
| SCE1572_2386 | DNA polymerase III alpha subunit (EC 2.7.7.7) | bi | sce_1939 | 92.13 DNA polymerase III alpha subunit (EC 2.7.7.7) |
| SCE1572_2387 | multi-sensor hybrid histidine kinase | bi | sce_1940 | 85.04 multi-sensor hybrid histidine kinase |
| SCE1572_2388 | hypothetical protein | - | - | 0 |
| SCE1572_2389 | hypothetical protein | bi | sce_1941 | 82.35 hypothetical protein |
| SCE1572_2390 | Chromosome partition protein smc | bi | sce_1942 | 96.11 Chromosome partition protein smc |
| SCE1572_2391 | hypothetical protein | - | - | 0 |
| SCE1572_2392 | Chorismate mutase I (EC 5.4.99.5) / Prephenate dehydratase (EC 4.2.1.51) | bi | sce_1945 | 95.32 Chorismate mutase I (EC 5.4.99.5) / Prephenate dehydratase (EC 4.2.1.51) |
| SCE1572_2393 | FIG01087408: hypothetical protein | bi | sce_1946 | 90.14 FIG01087408: hypothetical protein |
| SCE1572_2394 | ATP-dependent helicase HrpB | bi | sce_1947 | 90.95 ATP-dependent helicase HrpB |
| SCE1572_2395 | Aspartyl-tRNA(Asn) amidotransferase subunit A (EC 6.3.5.6) @ Glutamyl-tRNA(Gln) amidotransferase subunit A (EC 6.3.5.7) | bi | sce_1948 | 88.39 Aspartyl-tRNA(Asn) amidotransferase subunit A (EC 6.3.5.6) @ Glutamyl-tRNA(Gln) amidotransferase subunit A (EC 6.3.5.7) |
| SCE1572_2396 | Putative teichuronic acid biosynthesis glycosyl transferase TaaC | bi | sce_1950 | 83.1 Putative teichuronic acid biosynthesis glycosyl transferase TaaC |
| SCE1572_2397 | SSU ribosomal protein S21p | bi | sce_1951 | 100 SSU ribosomal protein S21p |
| SCE1572_2398 | Peroxide stress regulator PerR, FUR family | bi | sce_1952 | 88.76 Peroxide stress regulator PerR, FUR family |
| SCE1572_2399 | Rubryerythrin | bi | sce_1953 | 97.18 Rubryerythrin |
| SCE1572_2400 | Fe-S oxidoreductase-like protein in Rubryerythrin cluster | bi | sce_1954 | 94.46 Fe-S oxidoreductase-like protein in Rubryerythrin cluster |
| SCE1572_2401 | Hypothetical protein i Rubryerythrin cluster | bi | sce_1955 | 90.62 Hypothetical protein i Rubryerythrin cluster |
| SCE1572_2402 | Putative 4-hydroxybenzoyl CoA thioesterase (EC 3.1.2.23) | bi | sce_1956 | 89.12 thioesterase superfamily protein |
| SCE1572_2403 | phospholipase D. Active site motif domain protein | bi | sce_1957 | 94.31 phospholipase domain protein |
| SCE1572_2404 | Ribose 5-phosphate isomerase A (EC 5.3.1.6) | bi | sce_1958 | 84.48 Ribose 5-phosphate isomerase A (EC 5.3.1.6) |
| SCE1572_2405 | Argininosuccinate lyase (EC 4.3.2.1) | bi | sce_1959 | 97.35 Argininosuccinate lyase (EC 4.3.2.1) |
| SCE1572_2406 | hypothetical protein | bi | sce_1960 | 93.15 FIG01088531: hypothetical protein |
| SCE1572_2407 | Isopentenyl-diphosphate delta-isomerase, FMN-dependent (EC 5.3.3.2) | bi | sce_1961 | 91.06 Isopentenyl-diphosphate delta-isomerase, FMN-dependent (EC 5.3.3.2) |
| SCE1572_2408 | GAF domain protein | bi | sce_1962 | 98.46 GAF domain protein |
| SCE1572_2409 | Chemotaxis regulator - transmits chemoreceptor signals to flagellar motor components CheY | bi | sce_1963 | 100 Chemotaxis regulator - transmits chemoreceptor signals to flagellar motor components CheY |
| SCE1572_2410 | FHA/GGDEF domain protein | bi | sce_1964 | 95.16 hypothetical protein |
| SCE1572_2411 | Diadenosine tetraphosphatase | bi | sce_1965 | 91.97 Diadenosine tetraphosphatase |
| SCE1572_2412 | Glutamate-ammonia-lyase adenylyltransferase (EC 2.7.7.42) | bi | sce_1966 | 91.04 Glutamate-ammonia-lyase adenylyltransferase (EC 2.7.7.42) |
| SCE1572_2413 | FIG01089130: hypothetical protein | bi | sce_1967 | 80 FIG01089130: hypothetical protein |
| SCE1572_2414 | FIG01088155: hypothetical protein | bi | sce_1968 | 84.52 FIG01088155: hypothetical protein |
| SCE1572_2415 | hypothetical protein | bi | sce_1969 | 78.26 hypothetical protein |
| SCE1572_2416 | hypothetical protein | bi | sce_1970 | 59.55 hypothetical protein |
| SCE1572_2417 | hypothetical protein | - | - | 0 |
| SCE1572_2418 | keratin associated protein | bi | sce_1971 | 43.53 keratin associated protein |
| SCE1572_2419 | UPF0229 protein Yeah | bi | sce_1973 | 98.37 UPF0229 protein Yeah |
| SCE1572_2420 | Stage V sporulation protein involved in spore cortex synthesis (SpoVR) | bi | sce_1974 | 96.35 Stage V sporulation protein involved in spore cortex synthesis (SpoVR) |
| SCE1572_2421 | TPR domain protein | bi | sce_1975 | 83.09 TPR repeat:Sell-like repeat:Sell-like repeat |
| SCE1572_2422 | hypothetical protein | - | - | 0 |
| SCE1572_2423 | hypothetical protein | bi | sce_1976 | 65.25 hypothetical protein |
| SCE1572_2424 | methyltransferase type 11 | bi | sce_1977 | 66.41 methyltransferase type 11 |
| SCE1572_2425 | Serine phosphatase RsbU, regulator of sigma subunit | bi | sce_1978 | 60.79 Serine phosphatase RsbU, regulator of sigma subunit |
| SCE1572_2426 | conserved hypothetical protein | bi | sce_1979 | 100 conserved hypothetical protein |
| SCE1572_2427 | Serine phosphatase RsbU, regulator of sigma subunit | bi | sce_1980 | 98.78 Serine phosphatase RsbU, regulator of sigma subunit |
| SCE1572_2428 | hypothetical protein | bi | sce_1981 | 98.77 hypothetical protein |
| SCE1572_2429 | FIG01086628: hypothetical protein | bi | sce_1982 | 100 FIG01086628: hypothetical protein |
| SCE1572_2430 | RsbR, positive regulator of sigma-B | bi | sce_1983 | 90.02 RsbR, positive regulator of sigma-B |
| SCE1572_2431 | transcriptional regulator, MarR family | bi | sce_1985 | 96.08 transcriptional regulator, MarR family |
| SCE1572_2432 | hypothetical protein | bi | sce_1986 | 92.31 hypothetical protein |
| SCE1572_2433 | Methylglutacetyl-CoA hydratase (EC 4.2.1.18) | bi | sce_1987 | 88.89 Methylglutacetyl-CoA hydratase (EC 4.2.1.18) |
| SCE1572_2434 | Methylmalonyl-CoA decarboxylase, alpha chain (EC 4.1.1.41); Acetyl-coenzyme A carboxyl transferase alpha chain (EC 6.4.1.2) / A | bi | sce_1988 | 96.55 Methylmalonyl-CoA decarboxylase, alpha chain (EC 4.1.1.41); Acetyl-coenzyme A carboxyl transferase alpha chain (EC 6.4.1.2) / A |
| SCE1572_2435 | Large tegument protein | bi | sce_1989 | 76.52 Large tegument protein |
| SCE1572_2436 | Thiamin-phosphate pyrophosphorylase (EC 2.5.1.3) | bi | sce_1990 | 80.25 Thiamin-phosphate pyrophosphorylase (EC 2.5.1.3) |
| SCE1572_2437 | hypothetical protein | bi | sce_1991 | 83.58 hypothetical protein |
| SCE1572_2438 | DNA polymerase III delta prime subunit (EC 2.7.7.7) | bi | sce_1992 | 92.15 DNA polymerase III delta prime subunit (EC 2.7.7.7) |
| SCE1572_2439 | NAD-dependent epimerase/dehydratase | bi | sce_1993 | 86.76 NAD-dependent epimerase/dehydratase |
| SCE1572_2440 | Coenzyme F390 synthetase | bi | sce_1994 | 93.63 Coenzyme F390 synthetase |
| SCE1572_2441 | FHA domain protein | bi | sce_1995 | 88.26 serine/threonine protein kinase |
| SCE1572_2442 | FIG01087771: hypothetical protein | bi | sce_1997 | 77.89 FIG01087771: hypothetical protein |
| SCE1572_2443 | hypothetical protein | - | - | 0 |
| SCE1572_2444 | Nucleoside-diphosphate-sugar epimerases | bi | sce_1996 | 90.88 Nucleoside-diphosphate-sugar epimerases |
| SCE1572_2445 | hypothetical protein | - | - | 0 |
| SCE1572_2446 | FIG01086574: hypothetical protein | bi | sce_1998 | 78.53 FIG01086574: hypothetical protein |
| SCE1572_2447 | cytochrome B561 | - | - | 0 |
| SCE1572_2448 | Catalase (EC 1.11.1.6) | umi | sce_2350 | 25.76 Catalase (EC 1.11.1.6) |
| SCE1572_2449 | RNA polymerase sigma-54 factor RpoN | umi | sce_9532 | 35.53 RNA polymerase sigma factor RpoE |
| SCE1572_2450 | Transmembrane regulator protein PrtR | umi | sce_9531 | 31.09 PUTATIVE TRANSMEMBRANE PROTEIN |
| SCE1572_2451 | hypothetical protein | - | - | 0 |
| SCE1572_2452 | peptidase S1 and S6, chymotrypsin/Hap | umi | sce_7618 | 73.72 hydrolase |
| SCE1572_2453 | FIG01087988: hypothetical protein | bi | sce_1999 | 75.26 FIG01087988: hypothetical protein |
| SCE1572_2454 | GTP-binding protein Obg | bi | sce_2000 | 93.24 GTP-binding protein Obg |
| SCE1572_2455 | Two-component sensor histidine kinase | bi | sce_2001 | 93.89 Two-component sensor histidine kinase |
| SCE1572_2456 | hypothetical protein | bi | sce_2002 | 97.64 hypothetical protein |
| SCE1572_2457 | hypothetical protein | - | - | 0 |

| | | | | |
|--------------|--|-----|----------|---|
| SCE1572_2458 | FIG01086106: hypothetical protein | bi | sce_2003 | 94.89 FIG01086106: hypothetical protein |
| SCE1572_2459 | hemolysin-type calcium binding protein | bi | sce_2004 | 72.85 hemolysin-type calcium binding protein |
| SCE1572_2460 | erythrocyte membrane protein 1 (PEMP1) | uni | sce_4564 | 65.69 endo alpha-1,4 polygalactosaminidase precursor |
| SCE1572_2461 | hypothetical protein | bi | sce_6427 | 83.16 hypothetical protein |
| SCE1572_2462 | FIG01086728: hypothetical protein | uni | sce_6265 | 45.3 GII0995 protein |
| SCE1572_2463 | hypothetical protein | - | - | 0 |
| SCE1572_2464 | Inositol-1-phosphate synthase (EC 5.5.1.4) | bi | sce_2005 | 92.68 Inositol-1-phosphate synthase (EC 5.5.1.4) |
| SCE1572_2465 | FIG01086453: hypothetical protein | uni | sce_1227 | 65.22 FIG01086453: hypothetical protein |
| SCE1572_2466 | hypothetical protein | bi | sce_2006 | 80.05 hypothetical protein |
| SCE1572_2467 | hypothetical protein | bi | sce_2007 | 87.68 hypothetical protein |
| SCE1572_2468 | FIG01088594: hypothetical protein | bi | sce_2010 | 86.49 FIG01088594: hypothetical protein |
| SCE1572_2469 | PBS lyase HEAT domain protein repeat-containing protein | uni | sce_2011 | 71.08 PBS lyase HEAT domain protein repeat-containing protein |
| SCE1572_2470 | PBS lyase HEAT domain protein repeat-containing protein | bi | sce_2011 | 88.14 PBS lyase HEAT domain protein repeat-containing protein |
| SCE1572_2471 | FIG01086827: hypothetical protein | bi | sce_2012 | 92.52 FIG01086827: hypothetical protein |
| SCE1572_2472 | hypothetical protein | bi | sce_2013 | 92.59 hypothetical protein |
| SCE1572_2473 | Phosphoribosylaminoimidazole carboxylase catalytic subunit (EC 4.1.1.21) | bi | sce_2014 | 94.09 Phosphoribosylaminoimidazole carboxylase catalytic subunit (EC 4.1.1.21) |
| SCE1572_2474 | Phosphoribosylaminoimidazole carboxylase ATPase subunit (EC 4.1.1.21) | bi | sce_2015 | 91.04 Phosphoribosylaminoimidazole carboxylase ATPase subunit (EC 4.1.1.21) |
| SCE1572_2475 | FIG01088601: hypothetical protein | bi | sce_2016 | 79.79 Sortilin-related receptor precursor |
| SCE1572_2476 | hypothetical protein | bi | sce_2017 | 82.91 hypothetical protein |
| SCE1572_2477 | FIG01088972: hypothetical protein | bi | sce_2018 | 87.01 FIG01088972: hypothetical protein |
| SCE1572_2478 | FIG01085548: hypothetical protein | bi | sce_2019 | 83.33 FIG01085548: hypothetical protein |
| SCE1572_2479 | hypothetical protein | bi | sce_2020 | 89.82 hypothetical protein |
| SCE1572_2480 | hypothetical protein | - | - | 0 |
| SCE1572_2481 | Endo-1,4-beta-glucanase | bi | sce_7593 | 76.47 Endo-1,4-beta-glucanase |
| SCE1572_2482 | hypothetical protein | bi | sce_2042 | 84.83 FIG01085009: hypothetical protein |
| SCE1572_2483 | hypothetical protein | - | - | 0 |
| SCE1572_2484 | hypothetical protein | - | - | 0 |
| SCE1572_2485 | hypothetical protein | - | - | 0 |
| SCE1572_2486 | FIG01089507: hypothetical protein | bi | sce_2056 | 69.84 FIG01089507: hypothetical protein |
| SCE1572_2487 | FIG01085792: hypothetical protein | bi | sce_2057 | 79.94 FIG01085792: hypothetical protein |
| SCE1572_2488 | hypothetical protein | - | - | 0 |
| SCE1572_2489 | Oat5g0517900 | bi | sce_2059 | 73.03 hypothetical protein |
| SCE1572_2490 | Cytochrome P450 family protein | bi | sce_2066 | 80.85 Cytochrome P450 family protein |
| SCE1572_2491 | hypothetical protein | - | - | 0 |
| SCE1572_2492 | hypothetical protein | bi | sce_253 | 25.94 FOG: WD40 repeat |
| SCE1572_2493 | hypothetical protein | - | - | 0 |
| SCE1572_2494 | hypothetical protein | bi | sce_2073 | 85.75 glycosyl transferase, family 28 |
| SCE1572_2495 | OmpA family protein | bi | sce_2074 | 93.24 OmpA family protein |
| SCE1572_2496 | serine/threonine protein kinase | bi | sce_8756 | 39.32 1-acyl-sn-glycerol-3-phosphate acyltransferase (EC 2.3.1.51) |
| SCE1572_2497 | L-serine dehydratase (EC 4.3.1.17) | bi | sce_2075 | 93.83 L-serine dehydratase (EC 4.3.1.17) |
| SCE1572_2498 | hypothetical protein | - | - | 0 |
| SCE1572_2499 | Glycoprotein gp2 | bi | sce_2419 | 87.04 Glycoprotein gp2 |
| SCE1572_2500 | putative lipoprotein | bi | sce_2418 | 88.58 FIG00817277: hypothetical protein |
| SCE1572_2501 | putative cytochrome P450 hydroxylase | uni | sce_8024 | 47.13 putative cytochrome P450 hydroxylase |
| SCE1572_2502 | hypothetical protein | - | - | 0 |
| SCE1572_2503 | Poly(3-hydroxyalkanoate) depolymerase (EC 3.1.1.-) | bi | sce_7548 | 84.62 Poly(3-hydroxyalkanoate) depolymerase (EC 3.1.1.-) |
| SCE1572_2504 | hypothetical protein | bi | sce_3033 | 84.83 hypothetical protein |
| SCE1572_2505 | ubiquinone/menaquinone biosynthesis methyltransferase (EC 2.1.1.-) | bi | sce_3034 | 84.19 ubiquinone/menaquinone biosynthesis methyltransferase (EC 2.1.1.-) |
| SCE1572_2506 | Methionine synthase, vitamin-B12 independent | - | - | 0 |
| SCE1572_2507 | hypothetical protein | - | - | 0 |
| SCE1572_2508 | 4-hydroxybenzoate transporter | uni | sce_9046 | 27.98 Glucose/mannose:H symporter GlcP |
| SCE1572_2509 | hypothetical protein | uni | sce_3000 | 44.58 conserved hypothetical protein |
| SCE1572_2510 | L-fuconate dehydratase (EC 4.2.1.68) | bi | sce_8785 | 53.57 L-fuconate dehydratase (EC 4.2.1.68) |
| SCE1572_2511 | FIG01089335: hypothetical protein | bi | sce_2094 | 83.01 FIG01089335: hypothetical protein |
| SCE1572_2512 | Transcriptional regulator, TetR family | uni | sce_5426 | 32.42 Transcriptional regulator, TetR family |
| SCE1572_2513 | hypothetical protein | - | - | 0 |
| SCE1572_2514 | hypothetical protein | - | - | 0 |
| SCE1572_2515 | hypothetical protein | - | - | 0 |
| SCE1572_2516 | hypothetical protein | - | - | 0 |
| SCE1572_2517 | hypothetical protein | bi | sce_8744 | 78.72 hypothetical protein |
| SCE1572_2518 | serine/threonine-protein kinase PknI (EC:2.7.11.1) | uni | sce_7547 | 49.1 serine/threonine protein kinase |
| SCE1572_2519 | cytochrome P450 | bi | sce_2437 | 80.65 cytochrome P450 |
| SCE1572_2520 | Phenylpropanoate dioxygenase and related ring-hydroxylating dioxygenases, large terminal subunit | bi | sce_2097 | 88.27 Rieske (2Fe-2S) domain protein |
| SCE1572_2521 | FIG01085239: hypothetical protein | bi | sce_2098 | 78.28 FIG01085239: hypothetical protein |
| SCE1572_2522 | hypothetical protein | bi | sce_2099 | 91.13 hypothetical protein |
| SCE1572_2523 | hypothetical protein | uni | sce_2100 | 66.15 hypothetical protein |
| SCE1572_2524 | hypothetical protein | bi | sce_2100 | 71.64 hypothetical protein |
| SCE1572_2525 | hypothetical protein | bi | sce_2101 | 87.68 PPE family protein |
| SCE1572_2526 | Gamma-butyrobetaine 2-oxoglutarate dioxygenase (EC:1.14.11.1) | bi | sce_2102 | 88.56 hypothetical protein |
| SCE1572_2527 | cellulosome enzyme, dockerin type I | bi | sce_3701 | 86.5 cellulosome enzyme, dockerin type I |
| SCE1572_2528 | hypothetical protein | uni | sce_2102 | 73.21 hypothetical protein |
| SCE1572_2529 | hypothetical protein | uni | sce_924 | 54.72 GII1489 protein |
| SCE1572_2530 | hypothetical protein | - | - | 0 |
| SCE1572_2531 | hypothetical protein | - | - | 0 |
| SCE1572_2532 | Transcriptional regulator, TetR family | uni | sce_9220 | 31.35 Transcriptional regulator, TetR family |
| SCE1572_2533 | PhnB protein; putative DNA binding 3-demethylubiquinone-9 3-methyltransferase domain protein | uni | sce_7184 | 31.11 glyoxalase family protein |
| SCE1572_2534 | hypothetical protein | - | - | 0 |
| SCE1572_2535 | hypothetical protein | - | - | 0 |
| SCE1572_2536 | NADP oxidoreductase, coenzyme F420-dependent | - | - | 0 |
| SCE1572_2537 | hypothetical protein | bi | sce_2104 | 88.73 hypothetical protein |
| SCE1572_2538 | hypothetical protein | bi | sce_2118 | 88.38 FIG01085755: hypothetical protein |
| SCE1572_2539 | hypothetical protein | bi | sce_2119 | 89.37 hypothetical protein |
| SCE1572_2540 | hypothetical protein | - | - | 0 |
| SCE1572_2541 | hypothetical protein | - | - | 0 |
| SCE1572_2542 | hypothetical protein | - | - | 0 |
| SCE1572_2543 | Conserved domain protein | bi | sce_2126 | 81.5 Conserved domain protein |
| SCE1572_2544 | High-affinity carbon uptake protein Hat/HatR | uni | sce_5086 | 45.36 tolB protein precursor, periplasmic protein involved in the tonb-independent uptake of group A colicins |
| SCE1572_2545 | hypothetical protein | - | - | 0 |
| SCE1572_2546 | hypothetical protein | - | - | 0 |
| SCE1572_2547 | hypothetical protein | bi | sce_2128 | 80.58 hypothetical protein |
| SCE1572_2548 | RsbR, positive regulator of sigma-B | uni | sce_828 | 44.03 RsbR, positive regulator of sigma-B |
| SCE1572_2549 | hypothetical protein | - | - | 0 |
| SCE1572_2550 | hypothetical protein | - | - | 0 |
| SCE1572_2551 | RNA-directed DNA polymerase from retron -RT (EC:2.7.7.49) | uni | sce_2130 | 87.68 RNA-directed DNA polymerase from retron -RT (EC:2.7.7.49) |
| SCE1572_2552 | SWIM zinc finger domain protein | uni | sce_2996 | 29.07 hypothetical protein |
| SCE1572_2553 | FIG00838574: hypothetical protein | bi | sce_2131 | 83.8 FIG00838574: hypothetical protein |
| SCE1572_2554 | hypothetical protein | bi | sce_2132 | 88.12 hypothetical protein |
| SCE1572_2555 | WGR domain family | bi | sce_2133 | 86.67 WGR domain protein |
| SCE1572_2556 | hypothetical protein | uni | sce_5560 | 62.16 FIG01087606: hypothetical protein |
| SCE1572_2557 | Rhs family carbohydrate-binding protein | uni | sce_3970 | 58.86 Rhs family carbohydrate-binding protein |
| SCE1572_2558 | Membrane protein involved in colicin uptake-like protein | uni | sce_3968 | 36.5 Putative Ferredoxin |
| SCE1572_2559 | hypothetical protein | - | - | 0 |
| SCE1572_2560 | FIG01088620: hypothetical protein | bi | sce_2134 | 84.04 FIG01088620: hypothetical protein |
| SCE1572_2561 | hypothetical protein | bi | sce_2135 | 84.25 hypothetical protein |
| SCE1572_2562 | TonB family protein / TonB-dependent receptor | bi | sce_2136 | 80.75 TonB family protein / TonB-dependent receptor |
| SCE1572_2563 | sugar-non-specific nuclease NucA homolog | bi | sce_2137 | 85.58 sugar-non-specific nuclease NucA homolog |
| SCE1572_2564 | nuclease A inhibitor-like | bi | sce_2138 | 78.83 sugar-non-specific nuclease inhibitor NuiA homolog |
| SCE1572_2565 | Alpha-glucosidase (EC 3.2.1.20) | uni | sce_9663 | 55.88 FIG01085909: hypothetical protein |
| SCE1572_2566 | hypothetical protein | - | - | 0 |
| SCE1572_2567 | Fructose-bisphosphate aldolase class II (EC 4.1.2.13) | bi | sce_2139 | 94.96 Fructose-bisphosphate aldolase class II (EC 4.1.2.13) |
| SCE1572_2568 | FIG01089074: hypothetical protein | bi | sce_2140 | 72.99 FIG01089074: hypothetical protein |
| SCE1572_2569 | hypothetical protein | bi | sce_2141 | 56.25 hypothetical protein |
| SCE1572_2570 | hypothetical protein | bi | sce_2143 | 63.38 hypothetical protein |
| SCE1572_2571 | hypothetical protein | - | - | 0 |
| SCE1572_2572 | hypothetical protein | uni | sce_3976 | 30.65 TPR repeat |
| SCE1572_2573 | hypothetical protein | bi | sce_2144 | 89.68 hypothetical protein |
| SCE1572_2574 | hypothetical protein | bi | sce_2145 | 76.96 hypothetical protein |
| SCE1572_2575 | FIG01088923: hypothetical protein | bi | sce_2146 | 89.01 FIG01088923: hypothetical protein |
| SCE1572_2576 | Beta-lactamase (EC 3.5.2.6) | - | - | 0 |
| SCE1572_2577 | Trypsin-like serine proteases, typically periplasmic, contain C-terminal PDZ domain | bi | sce_2148 | 64.42 Trypsin-like serine proteases, typically periplasmic, contain C-terminal PDZ domain |
| SCE1572_2578 | Large tegument protein | bi | sce_2156 | 80.38 Large tegument protein |
| SCE1572_2579 | hypothetical protein | uni | sce_817 | 38.69 hypothetical protein |
| SCE1572_2580 | POSSIBLE TRANSPOSASE | uni | sce_7501 | 89.74 hypothetical protein |
| SCE1572_2581 | hypothetical protein | bi | sce_2162 | 82.74 hypothetical protein |
| SCE1572_2582 | hypothetical protein | - | - | 0 |
| SCE1572_2583 | hypothetical protein | uni | sce_6225 | 95.41 hypothetical protein |
| SCE1572_2584 | Mobile element protein | uni | sce_7431 | 39.84 reverse transcriptase/maturase family protein |
| SCE1572_2585 | hypothetical protein | bi | sce_6225 | 97.32 hypothetical protein |
| SCE1572_2586 | PUTATIVE TRANSPOSASE [SECOND PART] | uni | sce_6226 | 91.76 Integrase, catalytic region |
| SCE1572_2587 | hypothetical protein | bi | sce_6227 | 86.36 hypothetical protein |
| SCE1572_2588 | Serine/threonine protein kinase | bi | sce_3750 | 83.69 serine/threonine protein kinase with WD40 repeats |
| SCE1572_2589 | sigma-54 dependent DNA-binding response regulator | bi | sce_6703 | 74.9 sigma-54 dependent DNA-binding response regulator |
| SCE1572_2590 | Probable serine/threonine-protein kinase PknB | bi | sce_9769 | 50.26 serine/threonine protein kinase |
| SCE1572_2591 | hypothetical protein | uni | sce_9768 | 35.58 FIG01085203: hypothetical protein |
| SCE1572_2592 | hypothetical protein | - | - | 0 |
| SCE1572_2593 | hypothetical protein | - | - | 0 |
| SCE1572_2594 | RtcB-like protein | bi | sce_2174 | 94.04 RtcB-like protein |
| SCE1572_2595 | FIG01086549: hypothetical protein | bi | sce_5307 | 77.44 FIG01086549: hypothetical protein |
| SCE1572_2596 | Putative IS1492 transposase, TnpA1 | - | - | 0 |
| SCE1572_2597 | hypothetical protein | uni | sce_6225 | 94.32 hypothetical protein |
| SCE1572_2598 | hypothetical protein | uni | sce_6226 | 90.87 Integrase, catalytic region |
| SCE1572_2599 | Rhs protein | uni | sce_4725 | 46.06 FIG01086549: hypothetical protein |
| SCE1572_2600 | hypothetical protein | - | - | 0 |
| SCE1572_2601 | hypothetical protein | - | - | 0 |
| SCE1572_2602 | hypothetical protein | - | - | 0 |
| SCE1572_2603 | hypothetical protein | - | - | 0 |
| SCE1572_2604 | RNA:NAD 2'-phosphotransferase | bi | sce_2186 | 85.23 RNA:NAD 2'-phosphotransferase |
| SCE1572_2605 | LysR family transcriptional regulator YbhD | bi | sce_2187 | 89.74 LysR family transcriptional regulator YbhD |
| SCE1572_2606 | 1,4-alpha-glucan branching enzyme (EC 2.4.1.18) | bi | sce_2188 | 73.64 hypothetical protein |
| SCE1572_2607 | hypothetical protein | uni | sce_149 | 38.08 hypothetical protein |
| SCE1572_2608 | predicted protein | bi | sce_2189 | 81.22 hypothetical protein-transmembrane region and signal peptide prediction |
| SCE1572_2609 | hypothetical protein | bi | sce_2190 | 81.82 hypothetical protein |
| SCE1572_2610 | FIG01085708: hypothetical protein | bi | sce_2192 | 89.47 FIG01085708: hypothetical protein |
| SCE1572_2611 | hypothetical protein | bi | sce_2198 | 26.33 hypothetical protein |
| SCE1572_2612 | Cellulose biosynthesis protein | bi | sce_2195 | 84.45 Cellulose biosynthesis protein |
| SCE1572_2613 | Putative outer membrane lipoprotein | bi | sce_2196 | 87.69 hypothetical protein |
| SCE1572_2614 | protein of unknown function DUF81 | bi | sce_2199 | 90.94 protein of unknown function DUF81 |
| SCE1572_2615 | FIG01089294: hypothetical protein | bi | sce_2200 | 81.7 FIG01089294: hypothetical protein |
| SCE1572_2616 | Lipid A export ATP-binding/permease protein MsbA (EC 3.6.3.25) | uni | sce_7835 | 39.18 ABC transporter, ATP-binding protein, MsbA family |
| SCE1572_2617 | hypothetical protein | bi | sce_2202 | 77.78 hypothetical protein |
| SCE1572_2618 | hypothetical protein | - | - | 0 |
| SCE1572_2619 | conserved hypothetical protein | bi | sce_2204 | 83.63 conserved hypothetical protein |
| SCE1572_2620 | hypothetical protein-putative conserved hypothetical protein | bi | sce_3715 | 77.47 hypothetical protein-putative conserved hypothetical protein |
| SCE1572_2621 | Cellulose-binding domain protein | bi | sce_3716 | 63.04 Cellulose-binding domain protein |

| | | | | |
|--------------|--|-----|-----------|--|
| SCE1572_2622 | hypothetical protein | - | - | 0 |
| SCE1572_2623 | hypothetical protein | - | - | 0 |
| SCE1572_2624 | Endo-1,4-beta-xylanase A precursor (EC 3.2.1.8) | bi | sce_5143 | 85.64 Endo-1,4-beta-xylanase A precursor (EC 3.2.1.8) |
| SCE1572_2625 | hypothetical protein | - | - | 0 |
| SCE1572_2626 | FIG01089363: hypothetical protein | bi | sce_8582 | 78.68 FIG01089363: hypothetical protein |
| SCE1572_2627 | Endo-1,4-beta-xylanase A precursor (EC 3.2.1.8) | bi | sce_5133 | 80.95 Endo-1,4-beta-xylanase A precursor (EC 3.2.1.8) |
| SCE1572_2628 | Endo-1,4-beta-xylanase A precursor (EC 3.2.1.8) | bi | sce_5134 | 82.59 Endo-1,4-beta-xylanase A precursor (EC 3.2.1.8) |
| SCE1572_2629 | hypothetical protein | bi | sce_5147 | 91.91 Tat (Twin-arginine translocation) pathway signal sequence domain protein |
| SCE1572_2630 | Cellulose-binding domain protein | bi | sce_5148 | 83.48 Cellulose-binding domain protein |
| SCE1572_2631 | RsbR, positive regulator of sigma-B | bi | sce_5156 | 82.73 RsbR, positive regulator of sigma-B |
| SCE1572_2632 | FIG01087568: hypothetical protein | bi | sce_1664 | 86.24 FIG01087568: hypothetical protein |
| SCE1572_2633 | FIG01087568: hypothetical protein | bi | sce_5137 | 86.46 FIG01087568: hypothetical protein |
| SCE1572_2634 | Cellulose-binding domain protein | bi | sce_5138 | 80.11 Cellulose-binding domain protein |
| SCE1572_2635 | Transcriptional regulator, LacI family | bi | sce_3717 | 86.97 Transcriptional regulator, LacI family |
| SCE1572_2636 | Endo-1,4-beta-xylanase A precursor (EC 3.2.1.8) | bi | sce_3502 | 47.2 Endo-1,4-beta-xylanase A precursor (EC 3.2.1.8) |
| SCE1572_2637 | Ribulokinase (EC 2.7.1.16) | bi | sce_3712 | 84.4 Ribulokinase (EC 2.7.1.16) |
| SCE1572_2638 | L-arabinose isomerase (EC 5.3.1.4) | bi | sce_3711 | 88.6 L-arabinose isomerase (EC 5.3.1.4) |
| SCE1572_2639 | L-ribulose-5-phosphate 4-epimerase (EC 5.1.3.4) | bi | sce_3710 | 90.09 L-ribulose-5-phosphate 4-epimerase (EC 5.1.3.4) |
| SCE1572_2640 | Putative sugar ABC transport system, periplasmic binding protein YtqQ precursor | bi | sce_3709 | 89.16 Putative sugar ABC transport system, periplasmic binding protein YtqQ precursor |
| SCE1572_2641 | L-arabinose transport ATP-binding protein AraG (TC 3.A.1.2.2) | bi | sce_3708 | 80 L-arabinose transport ATP-binding protein AraG (TC 3.A.1.2.2) |
| SCE1572_2642 | Ribose ABC transport system, permease protein RbsC (TC 3.A.1.2.1) | bi | sce_3707 | 85.8 Ribose ABC transport system, permease protein RbsC (TC 3.A.1.2.1) |
| SCE1572_2643 | Putative sugar ABC transport system, permease protein Yjif | bi | sce_3706 | 85.8 Putative sugar ABC transport system, permease protein Yjif |
| SCE1572_2644 | Functional role page for Anaerobic nitric oxide reductase transcription regulator NorR | bi | sce_6530 | 68.69 Functional role page for Anaerobic nitric oxide reductase transcription regulator NorR |
| SCE1572_2645 | hypothetical protein | - | - | 0 |
| SCE1572_2646 | hypothetical protein | - | - | 0 |
| SCE1572_2647 | Adenylate cyclase (EC 4.6.1.1) | bi | sce_6531 | 72.83 Adenylate cyclase (EC 4.6.1.1) |
| SCE1572_2648 | hypothetical protein | - | - | 0 |
| SCE1572_2649 | hypothetical protein | - | - | 0 |
| SCE1572_2650 | hypothetical protein | - | - | 0 |
| SCE1572_2651 | hypothetical protein | bi | sce_6534 | 23.91 Cytochrome c family protein |
| SCE1572_2652 | Adenylate cyclase (EC 4.6.1.1) | bi | sce_9920 | 42.92 Serine/threonine kinase with two-component sensor domain |
| SCE1572_2653 | Carboxyl-terminal protease | bi | sce_2205 | 73.49 carboxyl-terminal protease (EC 3.4.21.-) |
| SCE1572_2654 | hypothetical protein | bi | sce_2206 | 80.69 hypothetical protein |
| SCE1572_2655 | Pentapeptide repeat family protein | bi | sce_2207 | 85.99 hypothetical protein |
| SCE1572_2656 | hypothetical protein | bi | sce_2208 | 83.97 hypothetical protein |
| SCE1572_2657 | Predicted cell-wall-anchored protein SasA (LPXTG motif) | bi | sce_2209 | 67.12 Predicted cell-wall-anchored protein SasA (LPXTG motif) |
| SCE1572_2658 | FIG01086828: hypothetical protein | bi | sce_2210 | 81.73 FIG01086828: hypothetical protein |
| SCE1572_2659 | FIG01085014: hypothetical protein | bi | sce_2212 | 89.28 FIG01085014: hypothetical protein |
| SCE1572_2660 | hypothetical protein | - | - | 0 |
| SCE1572_2661 | COG0670: Integral membrane protein, interacts with FtsH | bi | sce_2213 | 87.34 membrane protein |
| SCE1572_2662 | hypothetical protein | bi | sce_2214 | 83.58 hypothetical protein |
| SCE1572_2663 | FIG01087723: hypothetical protein | bi | sce_2215 | 75.74 FIG01087723: hypothetical protein |
| SCE1572_2664 | LSU ribosomal protein L3p (L3e) | bi | sce_2216 | 92.7 LSU ribosomal protein L3p (L3e) |
| SCE1572_2665 | Cell division protein FtsJ / Ribosomal RNA large subunit methyltransferase E (EC 2.1.1.-) ## LSU rRNA Um2552 | bi | sce_2217 | 97.56 Cell division protein FtsJ / Ribosomal RNA large subunit methyltransferase E (EC 2.1.1.-) ## LSU rRNA Um2552 |
| SCE1572_2666 | HipA-like | - | - | 0 |
| SCE1572_2667 | hypothetical protein | - | - | 0 |
| SCE1572_2668 | hypothetical protein | uni | sce_3987 | 38.96 metallophosphoesterase |
| SCE1572_2669 | Glutaryl-CoA dehydrogenase (EC 1.3.99.7) | bi | sce_2218 | 94.92 Glutaryl-CoA dehydrogenase (EC 1.3.99.7) |
| SCE1572_2670 | ErfK/YbiS/YciS/YnhG family protein | bi | sce_2219 | 81.59 Sll0670 protein |
| SCE1572_2671 | LOC432261 protein | bi | sce_2220 | 67.45 LOC432261 protein |
| SCE1572_2672 | Creatinine amidohydrolase (EC 3.5.2.10) | bi | sce_2221 | 89.15 Creatinine amidohydrolase (EC 3.5.2.10) |
| SCE1572_2673 | Benzoate-CoA ligase (EC 6.2.1.25) | bi | sce_2222 | 91.18 Benzoate-CoA ligase (EC 6.2.1.25) |
| SCE1572_2674 | NADH-dependent flavin oxidoreductase | bi | sce_2223 | 91.7 NADH-dependent flavin oxidoreductase |
| SCE1572_2675 | Butyryl-CoA dehydrogenase (EC 1.3.99.2) | bi | sce_2224 | 89.21 Butyryl-CoA dehydrogenase (EC 1.3.99.2) |
| SCE1572_2676 | Enoyl-CoA hydratase (EC 4.2.1.17) | bi | sce_2225 | 89.38 Enoyl-CoA hydratase (EC 4.2.1.17) |
| SCE1572_2677 | Transcriptional regulator, MarR family | bi | sce_2226 | 96.67 Transcriptional regulator, MarR family |
| SCE1572_2678 | Endoribonuclease L-PSP | bi | sce_2227 | 80.27 COG0251: Putative translation initiation inhibitor, yjgF family |
| SCE1572_2679 | D-beta-hydroxybutyrate dehydrogenase (EC 1.1.1.30) | bi | sce_2228 | 91.8 D-beta-hydroxybutyrate dehydrogenase (EC 1.1.1.30) |
| SCE1572_2680 | fatty acid desaturase family protein, putative | - | - | 0 |
| SCE1572_2681 | Inosamine-phosphate amidinotransferase 1 (EC 2.1.4.2) (Inosamine-phosphate amidinotransferase 1) (Aminocycitol amidinotransferase) | uni | sce_9522 | 32.79 Phosphoribosylglycinamide formyltransferase (EC 2.1.2.2) |
| SCE1572_2682 | hypothetical protein | uni | sce_6912 | 39.05 Cystathionine gamma-lyase (EC 4.4.1.1) |
| SCE1572_2683 | methionine gamma-lyase (EC 4.4.1.11) | uni | sce_2563 | 33.88 Aromatic-L-amino-acid decarboxylase (EC 4.1.1.28) |
| SCE1572_2684 | Aromatic-L-amino-acid decarboxylase (EC 4.1.1.28) | uni | sce_2563 | 33.88 Aromatic-L-amino-acid decarboxylase (EC 4.1.1.28) |
| SCE1572_2685 | hypothetical protein | - | - | 0 |
| SCE1572_2686 | hypothetical protein | - | - | 0 |
| SCE1572_2687 | hypothetical protein | - | - | 0 |
| SCE1572_2688 | hypothetical protein | bi | sce_2229 | 86.96 hypothetical protein |
| SCE1572_2689 | hypothetical protein | bi | sce_2230 | 88.32 hypothetical protein |
| SCE1572_2690 | NB-ARC domain protein | uni | sce_1995 | 55.46 serine/threonine protein kinase |
| SCE1572_2691 | Soluble pyridine nucleotide transhydrogenase (EC 1.6.1.1) | bi | sce_2231 | 93.98 Soluble pyridine nucleotide transhydrogenase (EC 1.6.1.1) |
| SCE1572_2692 | hypothetical protein | bi | sce_2232 | 96.36 TPR repeat |
| SCE1572_2693 | hypothetical protein | bi | sce_2233 | 86.41 hypothetical protein |
| SCE1572_2694 | putative secreted lipase | bi | sce_2234 | 88.24 putative secreted lipase |
| SCE1572_2695 | FIG01085228: hypothetical protein | bi | sce_2235 | 90.43 FIG01085228: hypothetical protein |
| SCE1572_2696 | hypothetical protein | - | - | 0 |
| SCE1572_2697 | FIG01086605: hypothetical protein | uni | sce_8463 | 41.37 FIG01086605: hypothetical protein |
| SCE1572_2698 | predicted protein | uni | sce_7695 | 46.02 predicted protein |
| SCE1572_2699 | hypothetical protein | uni | sce_7692 | 59.09 hypothetical protein |
| SCE1572_2700 | Putative integrase | bi | sce_1425 | 40.8 Integrase-like protein |
| SCE1572_2701 | Serine/threonine protein kinase | bi | sce_6712 | 60.36 Adenylate cyclase (EC 4.6.1.1) / Guanylate cyclase (EC 4.6.1.2) |
| SCE1572_2702 | Glycine dehydrogenase [decarboxylating] (glycine cleavage system P1 protein) (EC 1.4.4.2) | bi | sce_2240 | 95.68 Glycine dehydrogenase [decarboxylating] (glycine cleavage system P1 protein) (EC 1.4.4.2) |
| SCE1572_2703 | Glycine cleavage system H protein | bi | sce_2241 | 89.47 Glycine cleavage system H protein |
| SCE1572_2704 | Aminomethyltransferase (glycine cleavage system T protein) (EC 2.1.2.10) | bi | sce_2242 | 94.91 Aminomethyltransferase (glycine cleavage system T protein) (EC 2.1.2.10) |
| SCE1572_2705 | hypothetical protein | bi | sce_2243 | 83.51 hypothetical protein |
| SCE1572_2706 | Type IV fimbrial biogenesis protein PilY1 | bi | sce_2245 | 77.87 FIG01085186: hypothetical protein |
| SCE1572_2707 | hypothetical protein | bi | sce_2246 | 74.16 hypothetical protein |
| SCE1572_2708 | FIG01085679: hypothetical protein | bi | sce_2247 | 70.93 FIG01085679: hypothetical protein |
| SCE1572_2709 | hypothetical protein | bi | sce_2248 | 78.61 hypothetical protein |
| SCE1572_2710 | type 4 fimbrial biogenesis protein FimU | bi | sce_2249 | 79.13 type 4 fimbrial biogenesis protein FimU |
| SCE1572_2711 | FIG01087162: hypothetical protein | bi | sce_2250 | 88 FIG01087162: hypothetical protein |
| SCE1572_2712 | Peptidyl-prolyl cis-trans isomerase ppiD (EC 5.2.1.8) | bi | sce_2251 | 87.14 Peptidyl-prolyl cis-trans isomerase ppiD (EC 5.2.1.8) |
| SCE1572_2713 | 3-alpha,7-alpha,12-alpha-trihydroxy-5-beta-cholest-24-enoyl-CoA hydratase (EC 4.2.1.107) | bi | sce_2252 | 90.78 3-alpha,7-alpha,12-alpha-trihydroxy-5-beta-cholest-24-enoyl-CoA hydratase (EC 4.2.1.107) |
| SCE1572_2714 | FIG01088153: hypothetical protein | bi | sce_2253 | 81.75 FIG01088153: hypothetical protein |
| SCE1572_2715 | serine/threonine protein kinase | bi | sce_2254 | 80.56 serine/threonine protein kinase |
| SCE1572_2716 | Segregation and condensation protein A | bi | sce_2255 | 71.45 Segregation and condensation protein A |
| SCE1572_2717 | Segregation and condensation protein A | uni | sce_2255 | 58 Segregation and condensation protein A |
| SCE1572_2718 | Segregation and condensation protein B | bi | sce_2256 | 78.14 Segregation and condensation protein B |
| SCE1572_2719 | hypothetical protein | bi | sce_2257 | 77.46 FIG01088020: hypothetical protein |
| SCE1572_2720 | FIG01088901: hypothetical protein | bi | sce_2258 | 81.27 FIG01088901: hypothetical protein |
| SCE1572_2721 | FIG01088310: hypothetical protein | bi | sce_2259 | 89.16 FIG01088310: hypothetical protein |
| SCE1572_2722 | TldE/PmbA protein, part of proposed TldE/TldD proteolytic complex (PMID 12029038) | bi | sce_2260 | 92.73 TldE/PmbA protein, part of proposed TldE/TldD proteolytic complex (PMID 12029038) |
| SCE1572_2723 | FIG01089612: hypothetical protein | bi | sce_2261 | 84.8 FIG01089612: hypothetical protein |
| SCE1572_2724 | Circadian phase modifier | bi | sce_2262 | 93.6 Circadian phase modifier |
| SCE1572_2725 | hypothetical protein | bi | sce_2263 | 91.1 protein of unknown function DUF111 |
| SCE1572_2726 | Thioredoxin | bi | sce_2264 | 91.08 Thioredoxin |
| SCE1572_2727 | Oligopeptide transport system permease protein OppC (TC 3.A.1.5.1) | bi | sce_2265 | 91.24 Oligopeptide transport system permease protein OppC (TC 3.A.1.5.1) |
| SCE1572_2728 | Oligopeptide transport system permease protein OppB (TC 3.A.1.5.1) | bi | sce_2266 | 92.93 Oligopeptide transport system permease protein OppB (TC 3.A.1.5.1) |
| SCE1572_2729 | Methylcrotonyl-CoA carboxylase biotin-containing subunit (EC 6.4.1.4) | bi | sce_2267 | 84.78 Methylcrotonyl-CoA carboxylase biotin-containing subunit (EC 6.4.1.4) |
| SCE1572_2730 | Possible serine proteinase | bi | sce_2268 | 91.32 Methylcrotonyl-CoA carboxylase biotin-containing subunit (EC 6.4.1.4) |
| SCE1572_2731 | Protein serine/threonine phosphatase PtpC, regulation of stationary phase | bi | sce_2269 | 87.05 Protein serine/threonine phosphatase PtpC, regulation of stationary phase |
| SCE1572_2732 | hypothetical protein | bi | sce_2270 | 94.79 FHA domain containing protein |
| SCE1572_2733 | hypothetical protein | bi | sce_2272 | 81.29 hypothetical protein |
| SCE1572_2734 | hypothetical protein | bi | sce_2273 | 94.62 hypothetical protein |
| SCE1572_2735 | hypothetical protein | bi | sce_2274 | 86.22 hypothetical protein |
| SCE1572_2736 | Low-specificity L-threonine aldolase (EC 4.1.2.5) | bi | sce_2275 | 89.81 Low-specificity L-threonine aldolase (EC 4.1.2.5) |
| SCE1572_2737 | PROBABLE OXIDOREDUCTASE GMC-TYPE (EC 1.-.-.-) | bi | sce_2276 | 91.03 PROBABLE OXIDOREDUCTASE GMC-TYPE (EC 1.-.-.-) |
| SCE1572_2738 | hypothetical protein | bi | sce_2277 | 85.55 hypothetical protein |
| SCE1572_2739 | UL36 very large tegument protein | bi | sce_2278 | 75.84 Serine/threonine protein kinase (EC 2.7.11.1) |
| SCE1572_2740 | hypothetical protein | bi | sce_2279 | 86.81 hypothetical protein |
| SCE1572_2741 | hypothetical protein | bi | sce_2280 | 75.31 hypothetical protein |
| SCE1572_2742 | DNA-binding response regulator | bi | sce_2281 | 96.48 DNA-binding response regulator |
| SCE1572_2743 | sensor histidine kinase | bi | sce_2282 | 85.68 sensor histidine kinase |
| SCE1572_2744 | two-component response regulator | bi | sce_2283 | 90.32 two-component response regulator |
| SCE1572_2745 | hypothetical protein | bi | sce_2284 | 84.05 hypothetical protein |
| SCE1572_2746 | hypothetical protein | bi | sce_2285 | 81.65 hypothetical protein |
| SCE1572_2747 | Antifreeze glycopeptide AFGP polyprotein precursor | bi | sce_2286 | 78.72 Antifreeze glycopeptide AFGP polyprotein precursor |
| SCE1572_2748 | FIG01089119: hypothetical protein | bi | sce_2287 | 76.15 FIG01089119: hypothetical protein |
| SCE1572_2749 | serine/threonine protein kinase | bi | sce_2288 | 70.04 serine/threonine protein kinase |
| SCE1572_2750 | hypothetical protein | bi | sce_2289 | 92.33 hypothetical protein |
| SCE1572_2751 | hypothetical protein | bi | sce_2290 | 83.66 FIG01086707: hypothetical protein |
| SCE1572_2752 | hypothetical protein | bi | sce_2291 | 91.55 hypothetical protein |
| SCE1572_2753 | hypothetical protein | - | - | 0 |
| SCE1572_2754 | AmpG permease | bi | sce_2292 | 81.61 AmpG permease |
| SCE1572_2755 | hypothetical protein | uni | sce_4703 | 39.38 FIG01088187: hypothetical protein |
| SCE1572_2756 | hypothetical protein | - | - | 0 |
| SCE1572_2757 | FIG01086577: hypothetical protein | bi | sce_2302 | 75 hypothetical protein |
| SCE1572_2758 | peptidase M16-like | bi | sce_2304 | 85.07 peptidase M16-like |
| SCE1572_2759 | FIG01085406: hypothetical protein | bi | sce_2305 | 87.62 FIG01085406: hypothetical protein |
| SCE1572_2760 | FIG01085501: hypothetical protein | bi | sce_2306 | 78.2 FIG01085501: hypothetical protein |
| SCE1572_2761 | hypothetical protein | bi | sce_2307 | 67.31 hypothetical protein |
| SCE1572_2762 | hypothetical protein | - | - | 0 |
| SCE1572_2763 | FIG01085454: hypothetical protein | bi | sce_2308 | 87.55 FIG01085454: hypothetical protein |
| SCE1572_2764 | hypothetical protein | - | - | 0 |
| SCE1572_2765 | hypothetical protein | bi | sce_2310 | 60.62 Feruloyl esterase B precursor (EC 3.1.1.73) (Ferulic acid esterase B) (FAEB) (Cinnamoyl esterase) |
| SCE1572_2766 | hypothetical protein | bi | sce_2311 | 81.44 hypothetical protein |
| SCE1572_2767 | hypothetical protein | bi | sce_2312 | 80.42 hypothetical protein |
| SCE1572_2768 | Glyoxalase/bleomycin resistance protein/dioxygenase | bi | sce_2313 | 90.08 Glyoxalase/bleomycin resistance protein/dioxygenase |
| SCE1572_2769 | FIG01087685: hypothetical protein | bi | sce_2314 | 61.35 FIG01087685: hypothetical protein |
| SCE1572_2770 | hypothetical protein | bi | sce_4153 | 82.19 hypothetical protein |
| SCE1572_2771 | hypothetical protein | bi | sce_7299 | 85.53 hypothetical protein |
| SCE1572_2772 | hypothetical protein | uni | sce_167 | 54.66 hypothetical protein |
| SCE1572_2773 | hypothetical protein | - | - | 0 |
| SCE1572_2774 | FIG01084927: hypothetical protein | bi | sce_9577 | 78.97 FIG01084927: hypothetical protein |
| SCE1572_2775 | protein phosphatase homolog | uni | sce_5702 | 37.37 hypothetical protein |
| SCE1572_2776 | hypothetical protein | - | - | 0 |
| SCE1572_2777 | TonB family protein / TonB-dependent receptor | bi | sce_10401 | 82.11 TonB family protein / TonB-dependent receptor |
| SCE1572_2778 | hypothetical protein | - | - | 0 |
| SCE1572_2779 | hypothetical protein | uni | sce_5996 | 33.03 FIG01087215: hypothetical protein |
| SCE1572_2780 | hypothetical protein | - | - | 0 |
| SCE1572_2781 | transcriptional regulator, MerR family | bi | sce_2367 | 86.42 transcriptional regulator, MerR family |
| SCE1572_2782 | von Willebrand factor type A domain protein | bi | sce_2368 | 82.69 von Willebrand factor type A like domain |
| SCE1572_2783 | Flagellar motor rotation protein MotB | bi | sce_2369 | 73.65 Flagellar motor rotation protein MotB |
| SCE1572_2784 | Chloride peroxidase (EC 1.11.1.10) | bi | sce_5173 | 70.02 Chloride peroxidase (EC 1.11.1.10) |
| SCE1572_2785 | monooxygenase, FAD-binding | bi | sce_2429 | 30.89 NAD binding site |

| | | | | |
|--------------|--|-----|-----------|---|
| SCE1572_2786 | hypothetical protein | - | | 0 |
| SCE1572_2787 | Chalcone synthase (EC 2.3.1.74) | bi | sce_2372 | 33.14 Chalcone synthase (EC 2.3.1.74) |
| SCE1572_2788 | hypothetical protein | bi | sce_2375 | 89.43 hypothetical protein |
| SCE1572_2789 | Ribosomal protein S3 | bi | sce_2376 | 69.28 Ribosomal protein S3 |
| SCE1572_2790 | Cytochrome oxidase biogenesis protein Sco1/SenC/PrrC, putative copper metallochaperone | bi | sce_2381 | 71.91 Cytochrome oxidase biogenesis protein Sco1/SenC/PrrC, putative copper metallochaperone |
| SCE1572_2791 | Xylosidase/arabinosidase | umi | sce_5143 | 32.51 Endo-1,4-beta-xylanase A precursor (EC 3.2.1.8) |
| SCE1572_2792 | conserved hypothetical protein | bi | sce_2439 | 85.82 FIG01150558: hypothetical protein |
| SCE1572_2793 | hypothetical protein | umi | sce_2439 | 78.24 FIG01150558: hypothetical protein |
| SCE1572_2794 | hypothetical protein | - | | 0 |
| SCE1572_2795 | response regulator receiver domain protein (CheY-like) | bi | sce_2451 | 68.03 twitching motility protein PilH |
| SCE1572_2796 | Chemotaxis protein CheD | bi | sce_2449 | 66.2 Chemotaxis protein CheD |
| SCE1572_2797 | Signal transduction histidine kinase CheA (EC 2.7.3.-) | bi | sce_1364 | 86.73 Signal transduction histidine kinase CheA (EC 2.7.3.-) |
| SCE1572_2798 | Positive regulator of CheA protein activity (CheW) | bi | sce_1365 | 90.76 Positive regulator of CheA protein activity (CheW) |
| SCE1572_2799 | Chemotaxis protein methyltransferase CheR (EC 2.1.1.80) | bi | sce_2462 | 81.99 Chemotaxis protein methyltransferase CheR (EC 2.1.1.80) |
| SCE1572_2800 | Methyl-accepting chemotaxis protein I (serine chemoreceptor protein) | bi | sce_1367 | 89.09 methyl-accepting chemotaxis sensory transducer |
| SCE1572_2801 | PHP C-terminal domain protein | umi | sce_7628 | 50.14 Phosphoesterase PHP, N-terminal precursor |
| SCE1572_2802 | Choline-sulfatase (EC 3.1.6.6) | umi | sce_1065 | 28.79 sulfatase |
| SCE1572_2803 | hypothetical protein | bi | sce_6975 | 93.14 hypothetical protein |
| SCE1572_2804 | hypothetical protein | bi | sce_2463 | 65.91 hypothetical protein |
| SCE1572_2805 | Probable proteinase | bi | sce_2465 | 92.63 Probable proteinase |
| SCE1572_2806 | FIG00546957: hypothetical protein | umi | sce_4688 | 88.4 hypothetical protein |
| SCE1572_2807 | Probable proteinase | - | | 0 |
| SCE1572_2808 | hypothetical protein | bi | sce_4688 | 94.65 hypothetical protein |
| SCE1572_2809 | EBNA-1 | umi | sce_4688 | 71.05 hypothetical protein |
| SCE1572_2810 | 4-hydroxybenzoyl-CoA thioesterase family active site | umi | sce_9147 | 86.54 4-hydroxybenzoyl-CoA thioesterase family active site |
| SCE1572_2811 | hypothetical protein | - | | 0 |
| SCE1572_2812 | Cellulose-binding domain protein | umi | sce_1144 | 31.44 Cellulose-binding domain protein |
| SCE1572_2813 | Glyoxalase/bleomycin resistance protein/dioxygenase | bi | sce_10023 | 89.94 Glyoxalase/bleomycin resistance protein/dioxygenase |
| SCE1572_2814 | peptidase S1 and S6, chymotrypsin/Hap | bi | sce_7618 | 83.06 hydrolase |
| SCE1572_2815 | Transcriptional regulator, LysR family | bi | sce_4673 | 85.96 Transcriptional regulator, LysR family |
| SCE1572_2816 | hypothetical protein | umi | sce_7618 | 63.69 hydrolase |
| SCE1572_2817 | hypothetical protein | - | | 0 |
| SCE1572_2818 | hypothetical protein | umi | sce_940 | 25.33 VgrG protein |
| SCE1572_2819 | hypothetical protein | umi | sce_9160 | 31.95 FIG01088789: hypothetical protein |
| SCE1572_2820 | RabR, positive regulator of sigma-B | bi | sce_7859 | 82.35 RabR, positive regulator of sigma-B |
| SCE1572_2821 | Probable polyketide cyclase | bi | sce_7860 | 88.17 Probable polyketide cyclase |
| SCE1572_2822 | NAD(P)H oxidoreductase YRKL (EC 1.6.99.-) @ Putative NADPH-quinone reductase (modulator of drug activity B) @ Flavom | umi | sce_9440 | 29.3 NAD(P)H dehydrogenase (quinone) |
| SCE1572_2823 | transcriptional regulator, LysR family | umi | sce_196 | 43.9 Transcriptional regulator, LysR family |
| SCE1572_2824 | FIG01089656: hypothetical protein | bi | sce_6417 | 95.36 FIG01089656: hypothetical protein |
| SCE1572_2825 | Transcriptional regulator | bi | sce_1113 | 92.56 transcriptional regulator, LysR family |
| SCE1572_2826 | 3-oxoacyl-[acyl-carrier protein] reductase (EC 1.1.1.100) | bi | sce_1112 | 95.06 3-oxoacyl-[acyl-carrier protein] reductase (EC 1.1.1.100) |
| SCE1572_2827 | FIG01086405: hypothetical protein | bi | sce_1111 | 87.5 FIG01086405: hypothetical protein |
| SCE1572_2828 | hypothetical protein | - | | 0 |
| SCE1572_2829 | hypothetical protein | bi | sce_1110 | 69.51 hypothetical protein |
| SCE1572_2830 | hypothetical protein | - | | 0 |
| SCE1572_2831 | hypothetical protein | - | | 0 |
| SCE1572_2832 | ATP-dependent DNA helicase, RecQ family | umi | sce_3239 | 46.17 ATP-dependent DNA helicase RecQ |
| SCE1572_2833 | Ferredoxin | umi | sce_6415 | 82.14 Ferredoxin |
| SCE1572_2834 | Nitrite transporter from formate/nitrite family | - | | 0 |
| SCE1572_2835 | hypothetical protein | bi | sce_521 | 55.17 hypothetical protein |
| SCE1572_2836 | hypothetical protein | bi | sce_520 | 32.33 hypothetical protein |
| SCE1572_2837 | hypothetical protein | umi | sce_8817 | 44.54 Rhs family carbohydrate-binding protein |
| SCE1572_2838 | Mobile element protein | - | | 0 |
| SCE1572_2839 | Rhs protein | umi | sce_121 | 37.5 Putative membrane protein |
| SCE1572_2840 | hypothetical protein | - | | 0 |
| SCE1572_2841 | hypothetical protein | umi | sce_5612 | 52.11 FIG01086888: hypothetical protein |
| SCE1572_2842 | hypothetical protein | - | | 0 |
| SCE1572_2843 | DNA repair protein RadC | umi | sce_8397 | 93.9 DNA repair protein RadC |
| SCE1572_2844 | hypothetical protein | - | | 0 |
| SCE1572_2845 | hypothetical protein | umi | sce_513 | 72.35 FIG01087636: hypothetical protein |
| SCE1572_2846 | Transcriptional regulator Cro/C1 family | bi | sce_514 | 77.08 hypothetical protein |
| SCE1572_2847 | hypothetical protein | - | | 0 |
| SCE1572_2848 | Cytochrome c551 peroxidase (EC 1.11.1.5) | umi | sce_10371 | 64.03 Cytochrome c551 peroxidase (EC 1.11.1.5) |
| SCE1572_2849 | hypothetical protein | - | | 0 |
| SCE1572_2850 | Dihydrofolate reductase (EC 1.5.1.3) | bi | sce_10151 | 94.05 Dihydrofolate reductase (EC 1.5.1.3) |
| SCE1572_2851 | hypothetical protein | - | | 0 |
| SCE1572_2852 | hypothetical protein | - | | 0 |
| SCE1572_2853 | Cellulase(EC:3.2.1.4) | umi | sce_4169 | 51.89 Aspartyl-tRNA(Asn) amidotransferase subunit A (EC 6.3.5.6) @ Glutamyl-tRNA(Gln) amidotransferase subunit A (EC 6.3.5.7) |
| SCE1572_2854 | hypothetical protein | - | | 0 |
| SCE1572_2855 | hypothetical protein | bi | sce_6878 | 77.52 hypothetical protein |
| SCE1572_2856 | COG0583: Transcriptional regulator | umi | sce_2359 | 35.03 Transcriptional regulator, LysR family |
| SCE1572_2857 | Mir5572 protein | - | | 0 |
| SCE1572_2858 | FIG01084860: hypothetical protein | bi | sce_10022 | 66.58 FIG01084860: hypothetical protein |
| SCE1572_2859 | PE-PGRS FAMILY PROTEIN | bi | sce_8405 | 77.59 PE-PGRS FAMILY PROTEIN |
| SCE1572_2860 | conserved hypothetical protein | - | | 0 |
| SCE1572_2861 | Oxidoreductase | - | | 0 |
| SCE1572_2862 | Oxidoreductase | bi | sce_10011 | 54.29 Oxidoreductase |
| SCE1572_2863 | Transcriptional regulator | umi | sce_5333 | 36.07 Transcriptional regulator, LysR family |
| SCE1572_2864 | hypothetical protein | - | | 0 |
| SCE1572_2865 | hypothetical protein | - | | 0 |
| SCE1572_2866 | Putative glycosyl hydrolase of unknown function (DUF1680) | umi | sce_8647 | 45.05 Arylsulfatase (EC 3.1.6.1) |
| SCE1572_2867 | hypothetical protein | - | | 0 |
| SCE1572_2868 | Extracellular ligand-binding receptor | - | | 0 |
| SCE1572_2869 | hypothetical protein | - | | 0 |
| SCE1572_2870 | aspartyl-tRNA synthetase(EC:6.1.1.12) | - | | 0 |
| SCE1572_2871 | hypothetical protein | - | | 0 |
| SCE1572_2872 | hypothetical protein | bi | sce_2416 | 87.86 FIG01088021: hypothetical protein |
| SCE1572_2873 | hypothetical protein | bi | sce_1277 | 78.53 hypothetical protein |
| SCE1572_2874 | protein of unknown function DUF885 | umi | sce_1817 | 28.89 hypothetical protein |
| SCE1572_2875 | hypothetical protein | bi | sce_2477 | 88.85 hypothetical protein |
| SCE1572_2876 | putative phosphoesterase | bi | sce_2478 | 91.07 putative phosphoesterase |
| SCE1572_2877 | hypothetical protein | bi | sce_2483 | 87.5 hypothetical protein |
| SCE1572_2878 | Cellulase CelE ortholog; dockerin domain | bi | sce_2484 | 86.34 Cellulase CelE ortholog; dockerin domain |
| SCE1572_2879 | hypothetical protein | bi | sce_2504 | 28.15 Levansucrase (EC 3.2.1.65) |
| SCE1572_2880 | hypothetical protein | - | | 0 |
| SCE1572_2881 | hypothetical protein | - | | 0 |
| SCE1572_2882 | beta-lactamase domain protein | umi | sce_205 | 34.08 FIG01211180: hypothetical protein |
| SCE1572_2883 | hypothetical protein | bi | sce_2505 | 92.98 hypothetical protein |
| SCE1572_2884 | Predicted glutamine amidotransferase | bi | sce_2506 | 88.19 Predicted glutamine amidotransferase |
| SCE1572_2885 | protein of unknown function DUF407 | bi | sce_2507 | 75.64 protein of unknown function DUF407 |
| SCE1572_2886 | glutamate-cysteine ligase, family 2 | bi | sce_2508 | 88.42 glutamate-cysteine ligase, family 2 |
| SCE1572_2887 | hypothetical protein | bi | sce_2510 | 72.26 hypothetical protein |
| SCE1572_2888 | Pyrophosphate-fructose 6-phosphate 1-phosphotransferase, alpha subunit (EC 2.7.1.90) | bi | sce_2511 | 94.24 Pyrophosphate-fructose 6-phosphate 1-phosphotransferase, alpha subunit (EC 2.7.1.90) |
| SCE1572_2889 | hypothetical protein | - | | 0 |
| SCE1572_2890 | bacteriophage N4 adsorption protein B | - | | 0 |
| SCE1572_2891 | hypothetical protein | - | | 0 |
| SCE1572_2892 | UDP-N-acetylglucosamine 2-epimerase (EC 5.1.3.14) | umi | sce_2786 | 33.07 UDP-N-acetylglucosamine 2-epimerase (EC 5.1.3.14) |
| SCE1572_2893 | Twin-arginine translocation pathway signal | - | | 0 |
| SCE1572_2894 | conserved hypothetical transmembrane protein | - | | 0 |
| SCE1572_2895 | FIG01085316: hypothetical protein | bi | sce_2512 | 78.83 FIG01085316: hypothetical protein |
| SCE1572_2896 | hypothetical protein | - | | 0 |
| SCE1572_2897 | SAM-dependent methyltransferases | bi | sce_2548 | 93.67 hypothetical protein |
| SCE1572_2898 | hypothetical protein | - | | 0 |
| SCE1572_2899 | Alkanesulfonates-binding protein | bi | sce_2549 | 89.87 Alkanesulfonates-binding protein |
| SCE1572_2900 | hypothetical protein | - | | 0 |
| SCE1572_2901 | hypothetical protein | - | | 0 |
| SCE1572_2902 | hypothetical protein | - | | 0 |
| SCE1572_2903 | hypothetical protein | - | | 0 |
| SCE1572_2904 | Transposase | bi | sce_9024 | 78.48 Transposase |
| SCE1572_2905 | hypothetical protein | umi | sce_2135 | 31.08 hypothetical protein |
| SCE1572_2906 | hypothetical protein | - | | 0 |
| SCE1572_2907 | Transcriptional regulator, MarR family | umi | sce_8692 | 34.23 Transcriptional regulator, MarR family |
| SCE1572_2908 | protoglobin | - | | 0 |
| SCE1572_2909 | ABC transporter, ATP-binding protein | umi | sce_6239 | 52.81 ABC-type multidrug transport system, ATPase component |
| SCE1572_2910 | ABC-2 type transporter family | umi | sce_6238 | 52.25 ABC-type multidrug transport system, permease component |
| SCE1572_2911 | Long-chain-fatty-acid-CoA ligase (EC 6.2.1.3) | umi | sce_5460 | 23.87 alkanal monooxygenase |
| SCE1572_2912 | Long-chain-fatty-acid-CoA ligase (EC 6.2.1.3) | umi | sce_2666 | 47.74 Long-chain-fatty-acid-CoA ligase (EC 6.2.1.3) |
| SCE1572_2913 | Long-chain-fatty-acid-CoA ligase (EC 6.2.1.3) | umi | sce_9231 | 48.88 Long-chain-fatty-acid-CoA ligase (EC 6.2.1.3) |
| SCE1572_2914 | Malonyl CoA-acyl carrier protein transacylase (EC 2.3.1.39) | umi | sce_2666 | 47.74 Long-chain-fatty-acid-CoA ligase (EC 6.2.1.3) |
| SCE1572_2915 | Malonyl CoA-acyl carrier protein transacylase (EC 2.3.1.39) | umi | sce_4641 | 45.79 Malonyl CoA-acyl carrier protein transacylase (EC 2.3.1.39) |
| SCE1572_2916 | putative methyltransferase | bi | sce_6296 | 83.33 putative methyltransferase |
| SCE1572_2917 | 3,4-dihydroxy-2-butanone 4-phosphate synthase (EC 4.1.99.12) / GTP cyclohydrolase II (EC 3.5.4.25) | bi | sce_2550 | 83.19 3,4-dihydroxy-2-butanone 4-phosphate synthase (EC 4.1.99.12) / GTP cyclohydrolase II (EC 3.5.4.25) |
| SCE1572_2918 | regulatory protein, MarR | umi | sce_6851 | 25.18 FIG01085217: hypothetical protein |
| SCE1572_2919 | hypothetical protein | umi | sce_8363 | 35.85 Transcriptional regulator, MerR family |
| SCE1572_2920 | PE_PGRS family protein | umi | sce_6265 | 40.63 Gll0995 protein |
| SCE1572_2921 | extracellular solute-binding protein, family 1 | umi | sce_3430 | 23.23 N-Acetyl-D-glucosamine ABC transport system, sugar-binding protein |
| SCE1572_2922 | N-Acetyl-D-glucosamine ABC transport system, permease protein 1 | umi | sce_10351 | 34.78 N-Acetyl-D-glucosamine ABC transport system, permease protein 1 |
| SCE1572_2923 | Multiple sugar ABC transporter, membrane-spanning permease protein MsmG | umi | sce_8698 | 30.63 Maltose/maltodextrin ABC transporter, permease protein MalG |
| SCE1572_2924 | Alpha-xylosidase (EC 3.2.1.-) | umi | sce_3862 | 28.61 Alpha-glucosidase (EC 3.2.1.20) |
| SCE1572_2925 | Beta-glucosidase (EC 3.2.1.21) | umi | sce_3502 | 39.09 Endo-1,4-beta-xylanase A precursor (EC 3.2.1.8) |
| SCE1572_2926 | hypothetical protein | bi | sce_6392 | 50.46 hypothetical protein |
| SCE1572_2927 | Methyltransferase type 12 | umi | sce_5920 | 44.78 Methyltransferase |
| SCE1572_2928 | hypothetical protein | - | | 0 |
| SCE1572_2929 | hypothetical protein | - | | 0 |
| SCE1572_2930 | hypothetical protein | - | | 0 |
| SCE1572_2931 | hypothetical protein | - | | 0 |
| SCE1572_2932 | TonB-dependent receptor; Outer membrane receptor for ferrienterochelin and colicins | bi | sce_2553 | 85.24 TonB-dependent receptor; Outer membrane receptor for ferrienterochelin and colicins |
| SCE1572_2933 | hypothetical protein | - | | 0 |
| SCE1572_2934 | Serine/threonine-protein kinase pkn3 (EC 2.7.11.1) | bi | sce_2554 | 67.86 Serine/threonine-protein kinase pkn3 (EC 2.7.11.1) |
| SCE1572_2935 | Probable transmembrane protein | bi | sce_2555 | 83.33 Probable transmembrane protein |
| SCE1572_2936 | protein of unknown function DUF395, YeeE/YedE | bi | sce_2556 | 71.43 GENE II AND X PROTEINS |
| SCE1572_2937 | probable cell surface glycoprotein | - | | 0 |
| SCE1572_2938 | FIG01090715: hypothetical protein | - | | 0 |
| SCE1572_2939 | Oxygenase reductase-like protein | umi | sce_1372 | 46.51 probable oxygenase |
| SCE1572_2940 | probable oxygenase | umi | sce_7151 | 59.76 putative flavodoxin monooxygenase |
| SCE1572_2941 | Transcriptional regulator, TetR family | umi | sce_9220 | 28.83 Transcriptional regulator, TetR family |
| SCE1572_2942 | EBNA-1 | umi | sce_3674 | 45.35 hypothetical protein |
| SCE1572_2943 | hypothetical protein | umi | sce_577 | 48.44 zinc finger/ferredoxin putative |
| SCE1572_2944 | Gil2764 protein | umi | sce_5157 | 50 Gil2764 protein |
| SCE1572_2945 | hypothetical protein | umi | sce_8653 | 89.13 hypothetical protein |
| SCE1572_2946 | hypothetical protein | umi | sce_6896 | 33.95 hypothetical protein |
| SCE1572_2947 | hypothetical protein | - | | 0 |
| SCE1572_2948 | hypothetical protein | umi | sce_8368 | 43.51 EBNA-1 |
| SCE1572_2949 | FIG01088881: hypothetical protein | - | | 0 |

| | | | | | |
|--------------|--|--------|----------|-------|---|
| SCE1572_2950 | POSSIBLE TRANSPOSASE | bi | sce_7501 | 91.84 | hypothetical protein |
| SCE1572_2951 | RabR, positive regulator of sigma-B | bi | sce_6236 | 72.97 | RabR, positive regulator of sigma-B |
| SCE1572_2952 | putative transposase | - | - | 0 | 0 |
| SCE1572_2953 | hypothetical protein | umi | sce_8653 | 92.59 | hypothetical protein |
| SCE1572_2954 | IstB transposition helper protein | bi | sce_3807 | 92.31 | IstB helper protein C-terminal domain |
| SCE1572_2955 | hypothetical protein | - | - | 0 | 0 |
| SCE1572_2956 | alginate regulatory protein AlgP | bi | sce_2576 | 58.49 | hypothetical protein |
| SCE1572_2957 | hypothetical protein | bi | sce_2577 | 82.94 | FIG00703100: hypothetical protein |
| SCE1572_2958 | Sensor histidine kinase | umi | sce_1882 | 41.22 | Copper sensory histidine kinase CpxA |
| SCE1572_2959 | regulatory protein | umi | sce_1881 | 46.97 | two component, sigma54 specific, transcriptional regulator, Fis family |
| SCE1572_2960 | Beta-xylosidase (EC 3.2.1.37) | bi | sce_137 | 50.09 | Beta-xylosidase (EC 3.2.1.37) |
| SCE1572_2961 | Signal transduction histidine kinase | bi | sce_2578 | 88.89 | Signal transduction histidine kinase |
| SCE1572_2962 | hypothetical protein | - | - | 0 | 0 |
| SCE1572_2963 | Serine/threonine kinase | bi | sce_2579 | 91.58 | Serine/threonine kinase |
| SCE1572_2964 | Serine/threonine kinase | - | - | 0 | 0 |
| SCE1572_2965 | FIG01089186: hypothetical protein | umi | sce_1502 | 75.7 | FIG01085594: hypothetical protein |
| SCE1572_2966 | Adenylylate cyclase (EC 4.6.1.1) / Guanylate cyclase (EC 4.6.1.2) | umi | sce_8507 | 32.29 | serine/threonine protein kinase |
| SCE1572_2967 | - | umi | sce_1486 | 46.28 | VgrG protein |
| SCE1572_2968 | Twin-arginine translocation protein TatB | 24 umi | sce_1796 | 35.28 | hypothetical protein |
| SCE1572_2969 | FIG01085829: hypothetical protein | umi | sce_711 | 59.71 | FIG01085829: hypothetical protein |
| SCE1572_2970 | hypothetical protein | bi | sce_8259 | 46.84 | hypothetical protein |
| SCE1572_2971 | Protein serine/threonine phosphatase PrpC, regulation of stationary phase | umi | sce_4001 | 51.94 | Protein serine/threonine phosphatase PrpC, regulation of stationary phase |
| SCE1572_2972 | VgrG protein | umi | sce_3035 | 48.55 | VgrG protein |
| SCE1572_2973 | hypothetical protein | - | - | 0 | 0 |
| SCE1572_2974 | hypothetical protein | - | - | 0 | 0 |
| SCE1572_2975 | PE-PGRS FAMILY PROTEIN | umi | sce_711 | 59.75 | FIG01085829: hypothetical protein |
| SCE1572_2976 | hypothetical protein | umi | sce_8259 | 40.21 | hypothetical protein |
| SCE1572_2977 | Protein serine/threonine phosphatase PrpC, regulation of stationary phase | umi | sce_4001 | 51.94 | Protein serine/threonine phosphatase PrpC, regulation of stationary phase |
| SCE1572_2978 | hypothetical protein | bi | sce_4652 | 38.96 | FIG01085963: hypothetical protein |
| SCE1572_2979 | MutT/nudix family protein | bi | sce_2583 | 91.54 | MutT/nudix family protein |
| SCE1572_2980 | hypothetical protein | bi | sce_2584 | 87.11 | hypothetical protein |
| SCE1572_2981 | Phenazine biosynthesis protein PhzF like | - | - | 0 | 0 |
| SCE1572_2982 | hypothetical protein | - | - | 0 | 0 |
| SCE1572_2983 | rRNA (adenine37-N(6)-)-methyltransferase TrmN6 | bi | sce_2585 | 89.53 | rRNA (adenine37-N(6)-)-methyltransferase TrmN6 |
| SCE1572_2984 | hypothetical protein | bi | sce_2586 | 55.51 | FIG01084968: hypothetical protein |
| SCE1572_2985 | Protein of unknown function DUF541 | bi | sce_2587 | 74.36 | Protein of unknown function DUF541 |
| SCE1572_2986 | hypothetical protein | - | - | 0 | 0 |
| SCE1572_2987 | Probable serine/threonine-protein kinase pknB (EC 2.7.11.1) | bi | sce_2588 | 90.96 | Probable serine/threonine-protein kinase pknB (EC 2.7.11.1) |
| SCE1572_2988 | hypothetical protein | - | - | 0 | 0 |
| SCE1572_2989 | 4-hydroxyphenylacetate 3-monooxygenase (EC 1.14.13.3) | - | - | 0 | 0 |
| SCE1572_2990 | hypothetical protein | - | - | 0 | 0 |
| SCE1572_2991 | Serine phosphatase RsbU, regulator of sigma subunit | bi | sce_2589 | 80.85 | Serine phosphatase RsbU, regulator of sigma subunit |
| SCE1572_2992 | FIG01089073: hypothetical protein | bi | sce_2590 | 75.81 | FIG01089073: hypothetical protein |
| SCE1572_2993 | FIG01085827: hypothetical protein | bi | sce_2591 | 96.55 | FIG01085827: hypothetical protein |
| SCE1572_2994 | hypothetical protein | - | - | 0 | 0 |
| SCE1572_2995 | FIG01087338: hypothetical protein | bi | sce_2593 | 80.81 | FIG01087338: hypothetical protein |
| SCE1572_2996 | serine/threonine protein kinase | bi | sce_2596 | 83.64 | serine/threonine protein kinase |
| SCE1572_2997 | hypothetical protein | - | - | 0 | 0 |
| SCE1572_2998 | hypothetical protein | bi | sce_2597 | 90.58 | hypothetical protein |
| SCE1572_2999 | predicted protein | bi | sce_3447 | 25.6 | FIG01088771: hypothetical protein |
| SCE1572_3000 | FIG01086549: hypothetical protein | umi | sce_8347 | 35.25 | Rhs family protein |
| SCE1572_3001 | hypothetical protein | umi | sce_3858 | 37.29 | Adenosylhomocysteinase (EC 3.3.1.1) |
| SCE1572_3002 | hypothetical protein | bi | sce_6068 | 75.86 | hypothetical protein |
| SCE1572_3003 | RNA polymerase sigma factor RpoE | bi | sce_9937 | 85.64 | RNA polymerase sigma factor RpoE |
| SCE1572_3004 | Epstein-Barr nuclear antigen 1 (EBV nuclear antigen 1) (EBNA-1) | umi | sce_9938 | 57.43 | EBNA-1 |
| SCE1572_3005 | Cucumis sativus mRNA expressed in cucumber hypocotyls, complete cds | bi | sce_9938 | 66.22 | EBNA-1 |
| SCE1572_3006 | hypothetical protein | - | - | 0 | 0 |
| SCE1572_3007 | GCN5-related N-acetyltransferase | bi | sce_2598 | 87.08 | GCN5-related N-acetyltransferase |
| SCE1572_3008 | putative signal transduction protein with CBS domains | bi | sce_2600 | 82.98 | putative signal-transduction protein with CBS domains |
| SCE1572_3009 | FIG01088135: hypothetical protein | bi | sce_6056 | 90.24 | FIG01088135: hypothetical protein |
| SCE1572_3010 | FIG01086674: hypothetical protein | bi | sce_2938 | 57.55 | FIG01086674: hypothetical protein |
| SCE1572_3011 | Cytochrome c peroxidase (EC 1.11.1.5) | bi | sce_2937 | 71.35 | Cytochrome c peroxidase (EC 1.11.1.5) |
| SCE1572_3012 | FIG01085516: hypothetical protein | bi | sce_1454 | 84.21 | FIG01085516: hypothetical protein |
| SCE1572_3013 | putative acetyltransferase | - | - | 0 | 0 |
| SCE1572_3014 | FIG01084854: hypothetical protein | bi | sce_2467 | 79.18 | FIG01084854: hypothetical protein |
| SCE1572_3015 | Shikimate 5-dehydrogenase I alpha (EC 1.1.1.25) | bi | sce_2476 | 89.05 | Shikimate 5-dehydrogenase I alpha (EC 1.1.1.25) |
| SCE1572_3016 | hypothetical protein | - | - | 0 | 0 |
| SCE1572_3017 | Formate dehydrogenase-O, major subunit (EC 1.2.1.2) | umi | sce_1282 | 29.23 | Assimilatory nitrate reductase large subunit (EC 1.7.99.4) |
| SCE1572_3018 | hypothetical protein | umi | sce_224 | 31.45 | FIG01085761: hypothetical protein |
| SCE1572_3019 | hypothetical protein | umi | sce_5527 | 70.42 | hypothetical protein |
| SCE1572_3020 | FIG01087954: hypothetical protein | umi | sce_7521 | 76.55 | FIG01087954: hypothetical protein |
| SCE1572_3021 | hypothetical protein | umi | sce_6807 | 80.7 | hypothetical protein |
| SCE1572_3022 | PE-PGRS FAMILY PROTEIN | bi | sce_6869 | 85.71 | hypothetical protein |
| SCE1572_3023 | PE_PGRS family protein | umi | sce_6869 | 76.72 | hypothetical protein |
| SCE1572_3024 | PE-PGRS family protein | bi | sce_6870 | 77.88 | PE-PGRS FAMILY PROTEIN |
| SCE1572_3025 | hypothetical protein | umi | sce_9794 | 65.53 | FIG01089478: hypothetical protein |
| SCE1572_3026 | RNA polymerase sigma factor SigW | umi | sce_6872 | 54.45 | RNA polymerase sigma factor SigW |
| SCE1572_3027 | putative amine oxidase (EC 1.4.3.4) | - | - | 0 | 0 |
| SCE1572_3028 | hypothetical protein | - | - | 0 | 0 |
| SCE1572_3029 | hypothetical protein | - | - | 0 | 0 |
| SCE1572_3030 | Integrase, catalytic region | umi | sce_9803 | 29.81 | Mobile element protein |
| SCE1572_3031 | hypothetical protein | - | - | 0 | 0 |
| SCE1572_3032 | CmnU | bi | sce_2601 | 92.38 | CmnU |
| SCE1572_3033 | Membrane alanine aminopeptidase N (EC 3.4.11.2) | bi | sce_2602 | 91.73 | Membrane alanine aminopeptidase N (EC 3.4.11.2) |
| SCE1572_3034 | hypothetical protein | bi | sce_2603 | 89.73 | hypothetical protein |
| SCE1572_3035 | FIG01086200: hypothetical protein | bi | sce_2604 | 83.87 | FIG01086200: hypothetical protein |
| SCE1572_3036 | hypothetical protein | bi | sce_2606 | 89.89 | FIG01087050: hypothetical protein |
| SCE1572_3037 | Protein rarD | bi | sce_2607 | 86.04 | Protein rarD |
| SCE1572_3038 | hypothetical protein | bi | sce_2347 | 44.55 | Mlr6568 protein |
| SCE1572_3039 | hypothetical protein | bi | sce_7068 | 33.61 | WD-40 repeat protein |
| SCE1572_3040 | sigma54 specific transcriptional regulator with PAS sensor, Fis family | umi | sce_1588 | 47.25 | sigma-54 dependent DNA-binding response regulator |
| SCE1572_3041 | AAA ATPase, central region | umi | sce_2324 | 36.64 | ATPase, AAA family |
| SCE1572_3042 | exonuclease SbcC | umi | sce_6493 | 28.96 | Translation initiation factor 2 |
| SCE1572_3043 | hypothetical protein | - | - | 0 | 0 |
| SCE1572_3044 | hypothetical protein | umi | sce_5640 | 29.39 | FIG01089683: hypothetical protein |
| SCE1572_3045 | hypothetical protein | - | - | 0 | 0 |
| SCE1572_3046 | hypothetical protein | - | - | 0 | 0 |
| SCE1572_3047 | BclA protein | - | - | 0 | 0 |
| SCE1572_3048 | NHL repeat domain protein | umi | sce_1060 | 27.78 | Soluble lytic murein transglycosylase precursor (EC 3.2.1.-) |
| SCE1572_3049 | hypothetical protein | umi | sce_2333 | 26.73 | FIG00500935: hypothetical protein |
| SCE1572_3050 | hypothetical protein | umi | sce_2331 | 35.63 | hypothetical protein |
| SCE1572_3051 | hypothetical protein | umi | sce_2329 | 30.26 | VgrG protein |
| SCE1572_3052 | hypothetical protein | umi | sce_2328 | 27.78 | hypothetical protein |
| SCE1572_3053 | hypothetical protein | - | - | 0 | 0 |
| SCE1572_3054 | hypothetical protein | - | - | 0 | 0 |
| SCE1572_3055 | hypothetical protein | - | - | 0 | 0 |
| SCE1572_3056 | Phage tail sheath protein FI | umi | sce_9511 | 36.13 | Mir2351 protein |
| SCE1572_3057 | hypothetical protein | umi | sce_2320 | 27.63 | FIG01131549: hypothetical protein |
| SCE1572_3058 | Phage tail sheath protein FI | umi | sce_2319 | 43.93 | Phage tail sheath protein FI |
| SCE1572_3059 | hypothetical protein | - | - | 0 | 0 |
| SCE1572_3060 | hypothetical protein | bi | sce_2323 | 26.27 | conserved hypothetical protein; putative secreted protein |
| SCE1572_3061 | hypothetical protein | bi | sce_7454 | 61.88 | FIG01089015: hypothetical protein |
| SCE1572_3062 | RNA polymerase sigma factor RpoE | bi | sce_7455 | 88.76 | RNA polymerase sigma factor RpoE |
| SCE1572_3063 | Flagellar regulatory protein FleQ | bi | sce_5710 | 72.9 | Flagellar regulatory protein FleQ |
| SCE1572_3064 | hypothetical protein | bi | sce_2609 | 67.77 | hypothetical protein |
| SCE1572_3065 | thioredoxin | bi | sce_2610 | 81.3 | thioredoxin |
| SCE1572_3066 | putative RNA polymerase ECF-subfamily sigma factor | bi | sce_2611 | 91.53 | putative RNA polymerase ECF-subfamily sigma factor |
| SCE1572_3067 | FIG01086884: hypothetical protein | bi | sce_2612 | 90.73 | FIG01086884: hypothetical protein |
| SCE1572_3068 | hypothetical protein | bi | sce_2614 | 85.23 | FIG00485988: hypothetical protein |
| SCE1572_3069 | Urease accessory protein UreD | bi | sce_7327 | 31.7 | Urease accessory protein UreD |
| SCE1572_3070 | Urease gamma subunit (EC 3.5.1.5) | bi | sce_7328 | 50.89 | Urease gamma subunit (EC 3.5.1.5) |
| SCE1572_3071 | Urease alpha subunit (EC 3.5.1.5) | bi | sce_7329 | 64 | Urease alpha subunit (EC 3.5.1.5) |
| SCE1572_3072 | Urease accessory protein UreE | bi | sce_8793 | 68 | hypothetical protein |
| SCE1572_3073 | Urease accessory protein UreF | bi | sce_7330 | 31.22 | Urease accessory protein UreF |
| SCE1572_3074 | Urease accessory protein UreG | bi | sce_7331 | 65.61 | Urease accessory protein UreG |
| SCE1572_3075 | hypothetical protein | - | - | 0 | 0 |
| SCE1572_3076 | Peptidyl-prolyl cis-trans isomerase (EC 5.2.1.8) | umi | sce_425 | 39.23 | Peptidyl-prolyl cis-trans isomerase (EC 5.2.1.8) |
| SCE1572_3077 | PE-PGRS FAMILY PROTEIN | umi | sce_2972 | 64.71 | FIG01086339: hypothetical protein |
| SCE1572_3078 | WD-repeat protein | umi | sce_3016 | 27.33 | High-affinity carbon uptake protein Hat/HatR |
| SCE1572_3079 | WD-40 repeat protein | umi | sce_3016 | 27.72 | High-affinity carbon uptake protein Hat/HatR |
| SCE1572_3080 | hypothetical protein | bi | sce_157 | 85.84 | hypothetical protein |
| SCE1572_3081 | FIG01086383: hypothetical protein | umi | sce_3918 | 82.63 | FIG01086383: hypothetical protein |
| SCE1572_3082 | contains ESTs D41575(S4159),AU097348(S4159) / putative extensin-like protein | bi | sce_1504 | 66.85 | hypothetical protein |
| SCE1572_3083 | Glycoprotein gp2 | bi | sce_1503 | 60.96 | Glycoprotein gp2 |
| SCE1572_3084 | FIG01089186: hypothetical protein | bi | sce_3936 | 80 | FIG01089186: hypothetical protein |
| SCE1572_3085 | hypothetical protein | umi | sce_7299 | 53.85 | hypothetical protein |
| SCE1572_3086 | DNA repair protein RadC | umi | sce_8398 | 53.85 | DNA repair protein RadC |
| SCE1572_3087 | hypothetical protein | - | - | 0 | 0 |
| SCE1572_3088 | hypothetical protein | umi | sce_514 | 37.65 | hypothetical protein |
| SCE1572_3089 | hypothetical protein | - | - | 0 | 0 |
| SCE1572_3090 | FIG01084927: hypothetical protein | bi | sce_160 | 62.38 | hypothetical protein |
| SCE1572_3091 | hypothetical protein | - | - | 0 | 0 |
| SCE1572_3092 | hypothetical protein | - | - | 0 | 0 |
| SCE1572_3093 | FIG01088041: hypothetical protein | bi | sce_2615 | 86.57 | FIG01088041: hypothetical protein |
| SCE1572_3094 | sigma-B regulator RabR | umi | sce_7786 | 42.22 | FIG00502110: hypothetical protein |
| SCE1572_3095 | conserved hypothetical protein | umi | sce_394 | 29.32 | FIG01087934: hypothetical protein |
| SCE1572_3096 | hypothetical protein | - | - | 0 | 0 |
| SCE1572_3097 | predicted nucleoside-diphosphate-sugar epimerase | umi | sce_8057 | 33.33 | UDP-glucose 4-epimerase (EC 5.1.3.2) |
| SCE1572_3098 | hypothetical protein | - | - | 0 | 0 |
| SCE1572_3099 | hypothetical protein | bi | sce_9462 | 42.39 | hypothetical protein |
| SCE1572_3100 | hypothetical protein | umi | sce_116 | 40.81 | FIG01088201: hypothetical protein |
| SCE1572_3101 | Hypothetical protein YaeJ with similarity to translation release factor | bi | sce_2618 | 90 | Hypothetical protein YaeJ with similarity to translation release factor |
| SCE1572_3102 | hypothetical protein | bi | sce_2619 | 80.49 | Mobile element protein |
| SCE1572_3103 | ADP-ribose pyrophosphatase (EC 3.6.1.13) | bi | sce_2621 | 93.41 | ADP-ribose pyrophosphatase (EC 3.6.1.13) |
| SCE1572_3104 | transcriptional regulator, AraC family | umi | sce_9985 | 39.45 | Transcriptional regulator, AraC family |
| SCE1572_3105 | lipase family protein | bi | sce_6302 | 50.49 | lipase family protein |
| SCE1572_3106 | hypothetical protein | - | - | 0 | 0 |
| SCE1572_3107 | FIG01087007: hypothetical protein | bi | sce_2623 | 87.58 | FIG01087007: hypothetical protein |
| SCE1572_3108 | FIG01088780: hypothetical protein | bi | sce_2624 | 90.84 | FIG01088780: hypothetical protein |
| SCE1572_3109 | Nicotinamidase (EC 3.5.1.19) | bi | sce_2625 | 94.17 | Nicotinamidase (EC 3.5.1.19) |
| SCE1572_3110 | Putative chaperonin | bi | sce_2626 | 88.73 | Putative chaperonin |
| SCE1572_3111 | Serine/threonine protein phosphatase | bi | sce_2627 | 84.86 | Serine/threonine protein phosphatase |
| SCE1572_3112 | FIG01086405: hypothetical protein | umi | sce_1111 | 76.19 | FIG01086405: hypothetical protein |
| SCE1572_3113 | Alpha-L-arabinofuranosidase II precursor (EC 3.2.1.55) | bi | sce_1386 | 90.59 | Alpha-L-arabinofuranosidase II precursor (EC 3.2.1.55) |

| | | | | | |
|--------------|--|-----|-----------|-------|--|
| SCE1572_3114 | COG5492: Bacterial surface proteins containing Ig-like domains | bi | sce_1387 | 91.88 | COG5492: Bacterial surface proteins containing Ig-like domains |
| SCE1572_3115 | Nudix-related transcriptional regulator NtrR | bi | sce_2628 | 94.32 | Nudix-related transcriptional regulator NtrR |
| SCE1572_3116 | RsbR, positive regulator of sigma-B | bi | sce_2629 | 71.17 | RsbR, positive regulator of sigma-B |
| SCE1572_3117 | Sll0670 protein | bi | sce_2630 | 79.37 | Erk/YbiS/Ycs/YnhG family protein, putative |
| SCE1572_3118 | D-aminoacylase (EC 3.5.1.81) | bi | sce_2631 | 93.02 | D-aminoacylase (EC 3.5.1.81) |
| SCE1572_3119 | RNA polymerase sigma-70 factor, ECF subfamily | bi | sce_2632 | 88.89 | RNA polymerase sigma-70 factor, ECF subfamily |
| SCE1572_3120 | FIG01085649: hypothetical protein | bi | sce_2633 | 93.37 | FIG01085649: hypothetical protein |
| SCE1572_3121 | L-arabinose transport system permease protein (TC 3.A.1.2.2) | umi | sce_6146 | 34.49 | Ribose ABC transport system, permease protein RbsC (TC 3.A.1.2.1) |
| SCE1572_3122 | L-arabinose transport ATP-binding protein AraG (TC 3.A.1.2.2) | umi | sce_6147 | 46.52 | D-xylose transport ATP-binding protein XylG |
| SCE1572_3123 | L-arabinose-binding periplasmic protein precursor AraF (TC 3.A.1.2.2) | umi | sce_6717 | 35.38 | Xylose ABC transporter, periplasmic xylose-binding protein XylF |
| SCE1572_3124 | hypothetical protein | bi | sce_2634 | 83.85 | hypothetical protein |
| SCE1572_3125 | Gfa-like protein | bi | sce_2636 | 91.73 | Gfa-like protein |
| SCE1572_3126 | thioredoxin | bi | sce_2637 | 89.39 | Thioredoxin |
| SCE1572_3127 | hypothetical protein | bi | sce_6335 | 42.28 | hypothetical protein |
| SCE1572_3128 | hypothetical protein | umi | sce_6336 | 71.54 | hypothetical protein |
| SCE1572_3129 | hypothetical protein | umi | sce_6337 | 57.14 | hypothetical protein |
| SCE1572_3130 | pentapeptide repeat family protein | umi | sce_6338 | 53.76 | Pentapeptide repeat family protein |
| SCE1572_3131 | FIG01088856: hypothetical protein | umi | sce_6339 | 57.71 | FIG01088856: hypothetical protein |
| SCE1572_3132 | FIG01089519: hypothetical protein | umi | sce_6339 | 45.1 | FIG01088856: hypothetical protein |
| SCE1572_3133 | VgrG protein | umi | sce_6341 | 52.93 | VgrG protein |
| SCE1572_3134 | FIG01085998: hypothetical protein | umi | sce_6342 | 60.58 | FIG01085998: hypothetical protein |
| SCE1572_3135 | Transcriptional regulator, DeoR family | umi | sce_9911 | 44.59 | Transcriptional regulator, DeoR family |
| SCE1572_3136 | Oxidoreductase | umi | sce_10011 | 40.99 | Oxidoreductase |
| SCE1572_3137 | Serine/threonine protein kinase | umi | sce_3750 | 48.03 | serine/threonine protein kinase with WD40 repeats |
| SCE1572_3138 | hypothetical protein | bi | sce_2638 | 90.28 | hypothetical protein |
| SCE1572_3139 | hypothetical protein | bi | sce_2639 | 68.42 | hypothetical protein |
| SCE1572_3140 | Aminobenzoyl-glutamate transport protein | bi | sce_1537 | 85.25 | Aminobenzoyl-glutamate transport protein |
| SCE1572_3141 | RsbR, positive regulator of sigma-B | umi | sce_7640 | 51.81 | RsbR, positive regulator of sigma-B |
| SCE1572_3142 | HemK related protein | - | - | 0 | |
| SCE1572_3143 | predicted protein | - | - | 0 | |
| SCE1572_3144 | hypothetical protein | umi | sce_6789 | 28.18 | hypothetical protein |
| SCE1572_3145 | Coenzyme F420-dependent N5,N10-methylene tetrahydromethanopterin reductase and related flavin-dependent oxidoreductase | bi | sce_2643 | 87.06 | RNA polymerase sigma factor RpoE |
| SCE1572_3146 | Butyryl-CoA dehydrogenase (EC 1.3.99.2) | bi | sce_9834 | 34.48 | Acyl-CoA dehydrogenase, short-chain specific (EC 1.3.99.2) |
| SCE1572_3147 | putative Acyl-CoA dehydrogenase (EC 1.3.99.3) | - | - | 0 | |
| SCE1572_3148 | Acyl-CoA dehydrogenase, probable dibenzothiothiophene desulfurization enzyme | umi | sce_677 | 24.62 | Acyl-CoA dehydrogenases |
| SCE1572_3149 | Alkanesulfonate monooxygenase (EC 1.14.14.5) | bi | sce_5504 | 86.81 | Alkanesulfonate monooxygenase (EC 1.14.14.5) |
| SCE1572_3150 | sigma54 specific transcriptional regulator, Fis family | umi | sce_1468 | 49.76 | Alkanesulfonates-binding protein |
| SCE1572_3151 | FMN reductase (EC 1.5.1.29) | bi | sce_2640 | 87.23 | FMN reductase (EC 1.5.1.29) |
| SCE1572_3152 | BlI2291 protein | bi | sce_2641 | 58.55 | BlI2291 protein |
| SCE1572_3153 | hypothetical protein | - | - | 0 | |
| SCE1572_3154 | Dihydroliipoamide succinyltransferase component (E2) of 2-oxoglutarate dehydrogenase complex (EC 2.3.1.61) | bi | sce_2642 | 73.79 | Dihydroliipoamide succinyltransferase component (E2) of 2-oxoglutarate dehydrogenase complex (EC 2.3.1.61) |
| SCE1572_3155 | RNA polymerase sigma factor RpoE | bi | sce_2643 | 87.06 | RNA polymerase sigma factor RpoE |
| SCE1572_3156 | FIG01087210: hypothetical protein | bi | sce_2644 | 74.93 | FIG01087210: hypothetical protein |
| SCE1572_3157 | Catabolite control protein A | bi | sce_2645 | 75.48 | Catabolite control protein A |
| SCE1572_3158 | Adenylate cyclase (EC 4.6.1.1) / Guanylate cyclase (EC 4.6.1.2) | umi | sce_5229 | 47.14 | Serine/threonine protein kinase |
| SCE1572_3159 | Ammonium transporter | bi | sce_2654 | 93.35 | Ammonium transporter |
| SCE1572_3160 | hypothetical protein | bi | sce_10130 | 30.32 | Transcriptional regulator, ArsR family |
| SCE1572_3161 | Transcriptional regulator, ArsR family | bi | sce_10131 | 57.14 | Transcriptional regulator, ArsR family |
| SCE1572_3162 | 4-alpha-glucanotransferase (amylomaltase) (EC 2.4.1.25) | bi | sce_2655 | 88.18 | 4-alpha-glucanotransferase (amylomaltase) (EC 2.4.1.25) |
| SCE1572_3163 | Glycogen debranching enzyme (EC 3.2.1.-) | bi | sce_2656 | 93.08 | Glycogen debranching enzyme (EC 3.2.1.-) |
| SCE1572_3164 | putative lipoprotein | bi | sce_9942 | 84.24 | putative lipoprotein |
| SCE1572_3165 | hypothetical protein | bi | sce_9943 | 86.37 | hypothetical protein |
| SCE1572_3166 | hypothetical protein | bi | sce_9944 | 87.02 | hypothetical protein |
| SCE1572_3167 | Glutathione S-transferase (EC 2.5.1.18) | umi | sce_4136 | 54.55 | Glutathione S-transferase (EC 2.5.1.18) |
| SCE1572_3168 | COG4615: ABC-type siderophore export system, fused ATPase and permease components | umi | sce_9235 | 47.38 | putative ABC transporter (ATP-binding protein) |
| SCE1572_3169 | [NiFe] hydrogenase metalcenter assembly protein HypF | bi | sce_5119 | 42.36 | [NiFe] hydrogenase metalcenter assembly protein HypF |
| SCE1572_3170 | [NiFe] hydrogenase metalcenter assembly protein HypE | umi | sce_5122 | 44.01 | [NiFe] hydrogenase metalcenter assembly protein HypE |
| SCE1572_3171 | Nicotinamide (EC 3.5.1.19) | umi | sce_4937 | 32.05 | Isochorismatase (EC 3.3.2.1) |
| SCE1572_3172 | Long-chain-fatty-acid-CoA ligase (EC 6.2.1.3) | bi | sce_2666 | 44.05 | Long-chain-fatty-acid-CoA ligase (EC 6.2.1.3) |
| SCE1572_3173 | Ornithine cyclodeaminase (EC 4.3.1.12) | umi | sce_2667 | 54.6 | Ornithine cyclodeaminase (EC 4.3.1.12) |
| SCE1572_3174 | Cysteine synthase (EC 2.5.1.47) | bi | sce_2668 | 56.55 | Putative siderophore biosynthesis protein, related to cysteine synthase |
| SCE1572_3175 | Nodulation protein noO (EC 2.1.3.-) | umi | sce_2688 | 36.16 | Nodulation protein noO (EC 2.1.3.-) |
| SCE1572_3176 | hypothetical protein | umi | sce_7804 | 25.93 | Butyryl-CoA dehydrogenase (EC 1.3.99.2) |
| SCE1572_3177 | NODULATION PROTEIN NOLO | umi | sce_2688 | 30.07 | Nodulation protein noO (EC 2.1.3.-) |
| SCE1572_3178 | hypothetical protein | - | - | 0 | |
| SCE1572_3179 | transcriptional regulator, Fis family | umi | sce_2871 | 48.44 | Transcriptional regulator BkdR of isoleucine and valine catabolism operon |
| SCE1572_3180 | ATP-dependent DNA helicase RecQ | umi | sce_3239 | 42.6 | ATP-dependent DNA helicase RecQ |
| SCE1572_3181 | Malto-oligosyltrehalose synthase (EC 5.4.99.15) | bi | sce_2671 | 84.78 | Malto-oligosyltrehalose synthase (EC 5.4.99.15) |
| SCE1572_3182 | Malto-oligosyltrehalose trehalohydrolase (EC 3.2.1.141) | bi | sce_2672 | 89.44 | Malto-oligosyltrehalose trehalohydrolase (EC 3.2.1.141) |
| SCE1572_3183 | COG1720: Uncharacterized conserved protein | bi | sce_2673 | 86.62 | COG1720: Uncharacterized conserved protein |
| SCE1572_3184 | hypothetical protein | - | - | 0 | |
| SCE1572_3185 | Chemotaxis protein methyltransferase CheR (EC 2.1.1.80) | umi | sce_3006 | 46.85 | Chemotaxis protein methyltransferase CheR (EC 2.1.1.80) |
| SCE1572_3186 | 3-oxoacyl-[acyl-carrier protein] reductase (EC 1.1.1.100) | umi | sce_5211 | 45.12 | 3-oxoacyl-[acyl-carrier protein] reductase (EC 1.1.1.100) |
| SCE1572_3187 | hypothetical protein | bi | sce_2677 | 71.05 | hypothetical protein |
| SCE1572_3188 | Cation-transporting ATPase | bi | sce_2679 | 77.48 | Cation-transporting ATPase |
| SCE1572_3189 | hypothetical protein | bi | sce_2680 | 79.79 | hypothetical protein |
| SCE1572_3190 | amino acid permease family protein | bi | sce_2681 | 78.46 | amino acid permease family protein |
| SCE1572_3191 | hypothetical protein | bi | sce_2683 | 91.67 | hypothetical protein |
| SCE1572_3192 | Phage tail fiber protein | bi | sce_2684 | 61.96 | Phage tail fiber protein |
| SCE1572_3193 | Carbamoyl-phosphate synthase large chain (EC 6.3.5.5) | bi | sce_2685 | 96.51 | Carbamoyl-phosphate synthase large chain (EC 6.3.5.5) |
| SCE1572_3194 | Carbamoyl-phosphate synthase small chain (EC 6.3.5.5) | bi | sce_2686 | 95.36 | Carbamoyl-phosphate synthase small chain (EC 6.3.5.5) |
| SCE1572_3195 | hypothetical protein | bi | sce_2687 | 65.79 | hypothetical protein |
| SCE1572_3196 | Nodulation protein noO (EC 2.1.3.-) | bi | sce_2688 | 92.97 | Nodulation protein noO (EC 2.1.3.-) |
| SCE1572_3197 | Molybdopterin biosynthesis protein MoeA | bi | sce_2689 | 91.36 | Molybdopterin biosynthesis protein MoeA |
| SCE1572_3198 | Molybdenum cofactor biosynthesis protein MoaB | bi | sce_2690 | 88.14 | Molybdenum cofactor biosynthesis protein MoaB |
| SCE1572_3199 | Prolipoprotein diacylglycerol transferase (EC 2.4.99.-) | bi | sce_2692 | 90.4 | Prolipoprotein diacylglycerol transferase (EC 2.4.99.-) |
| SCE1572_3200 | RNA-binding protein | bi | sce_2694 | 96.92 | RNA-binding region RNP-1 (RNA recognition motif) |
| SCE1572_3201 | LSU ribosomal protein L33p | bi | sce_2695 | 100 | LSU ribosomal protein L33p |
| SCE1572_3202 | Rod shape-determining protein MreB | bi | sce_2696 | 99.42 | Rod shape-determining protein MreB |
| SCE1572_3203 | Rod shape-determining protein MreC | bi | sce_2697 | 98.6 | Rod shape-determining protein MreC |
| SCE1572_3204 | hypothetical protein | bi | sce_2698 | 97.7 | hypothetical protein |
| SCE1572_3205 | Penicillin-binding protein 2 (PBP-2) | bi | sce_2699 | 97.7 | Penicillin-binding protein 2 (PBP-2) |
| SCE1572_3206 | Rod shape-determining protein RodA | bi | sce_2700 | 97.09 | Rod shape-determining protein RodA |
| SCE1572_3207 | gliding motility protein MglA | bi | sce_2701 | 89.53 | gliding motility protein MglA |
| SCE1572_3208 | PA14 domain protein | bi | sce_2702 | 88.46 | PA14 domain protein |
| SCE1572_3209 | Rhomboid family membrane protein | bi | sce_2703 | 82.77 | Rhomboid family membrane protein |
| SCE1572_3210 | sigma-24 | bi | sce_2704 | 91.96 | putative RNA polymerase sigma factor |
| SCE1572_3211 | hypothetical protein | bi | sce_2705 | 80.61 | hypothetical protein |
| SCE1572_3212 | hypothetical protein | bi | sce_2706 | 86.34 | hypothetical protein |
| SCE1572_3213 | tetratricopeptide repeat protein | bi | sce_2707 | 74.04 | DnaJ domain protein |
| SCE1572_3214 | hypothetical protein | - | - | 0 | |
| SCE1572_3215 | Chaperone protein DnaK | bi | sce_2708 | 99.67 | Chaperone protein DnaK |
| SCE1572_3216 | Tetratricopeptide TPR_2 repeat protein | bi | sce_2709 | 83.93 | hypothetical protein |
| SCE1572_3217 | putative metalloproteinase | bi | sce_2710 | 82.15 | Zn-dependent aminopeptidase, putative |
| SCE1572_3218 | hypothetical protein | bi | sce_2711 | 80.13 | Conjugative transfer protein TrbL |
| SCE1572_3219 | twitching motility protein PilH | bi | sce_2712 | 95.03 | twitching motility protein PilH |
| SCE1572_3220 | hypothetical protein | bi | sce_2713 | 77.48 | hypothetical protein |
| SCE1572_3221 | FIG01087708: hypothetical protein | bi | sce_2714 | 71.43 | FIG01087708: hypothetical protein |
| SCE1572_3222 | hypothetical protein | bi | sce_2715 | 92.48 | hypothetical protein |
| SCE1572_3223 | hypothetical protein | bi | sce_2716 | 78.01 | hypothetical protein |
| SCE1572_3224 | LigA | umi | sce_3858 | 38.22 | Adenylylhomocysteinase (EC 3.3.1.1) |
| SCE1572_3225 | FIG01088928: hypothetical protein | bi | sce_2717 | 85.22 | FIG01088928: hypothetical protein |
| SCE1572_3226 | gliding motility protein GldF | bi | sce_2718 | 97.58 | gliding motility protein GldF |
| SCE1572_3227 | ABC transporter, ATP-binding protein | bi | sce_2719 | 87.15 | ABC transporter |
| SCE1572_3228 | hypothetical protein | bi | sce_2720 | 98.71 | hypothetical protein |
| SCE1572_3229 | FIG01089310: hypothetical protein | bi | sce_2721 | 95.89 | FIG01089310: hypothetical protein |
| SCE1572_3230 | Response regulator receiver:Transcriptional regulatory protein, C- terminal precursor | bi | sce_2722 | 96.71 | Response regulator receiver:Transcriptional regulatory protein, C- terminal precursor |
| SCE1572_3231 | Phosphate regulon sensor protein PhoR (SphS) (EC 2.7.13.3) | bi | sce_2723 | 87.1 | sensor histidine kinase |
| SCE1572_3232 | Pyrimidine-nucleoside phosphorylase (EC 2.4.2.2) | bi | sce_2724 | 94.27 | Pyrimidine-nucleoside phosphorylase (EC 2.4.2.2) |
| SCE1572_3233 | putative Cytochrome bd2, subunit I | bi | sce_2726 | 92.29 | putative Cytochrome bd2, subunit I |
| SCE1572_3234 | putative Cytochrome bd2, subunit II | bi | sce_2727 | 91.81 | putative Cytochrome bd2, subunit II |
| SCE1572_3235 | Muc19 precursor | bi | sce_2728 | 74.41 | bacterial Ig-like domain protein |
| SCE1572_3236 | OmpA domain protein | bi | sce_2732 | 87.32 | OmpA domain protein |
| SCE1572_3237 | hypothetical protein | - | - | 0 | |
| SCE1572_3238 | hypothetical protein | bi | sce_2733 | 89.51 | hypothetical protein |
| SCE1572_3239 | hypothetical protein | bi | sce_2734 | 81.56 | hypothetical protein |
| SCE1572_3240 | hypothetical protein | - | - | 0 | |
| SCE1572_3241 | BlI3113 protein | bi | sce_2735 | 82.16 | BlI3113 protein |
| SCE1572_3242 | hypothetical protein | bi | sce_2736 | 65.41 | hypothetical protein |
| SCE1572_3243 | FIG01086461: hypothetical protein | bi | sce_2737 | 79.3 | FIG01086461: hypothetical protein |
| SCE1572_3244 | hypothetical protein | bi | sce_2738 | 87.23 | hypothetical protein |
| SCE1572_3245 | GntR family transcriptional regulator | bi | sce_2740 | 93.43 | putative Fe-S oxidoreductase |
| SCE1572_3246 | Lysine 2,3-aminomutase (EC 5.4.3.2) | bi | sce_2741 | 96.31 | Lysine 2,3-aminomutase (EC 5.4.3.2) |
| SCE1572_3247 | Lytic transglycosylase, catalytic | bi | sce_2742 | 90.6 | soluble lytic murein transglycosylase |
| SCE1572_3248 | hypothetical protein | bi | sce_2744 | 92.55 | hypothetical protein |
| SCE1572_3249 | FIG01085742: hypothetical protein | bi | sce_2745 | 91.18 | FIG01085742: hypothetical protein |
| SCE1572_3250 | hypothetical protein | bi | sce_2746 | 91.2 | hypothetical protein |
| SCE1572_3251 | hypothetical protein | bi | sce_2747 | 71.43 | hypothetical protein |
| SCE1572_3252 | Biosynthetic arginine decarboxylase (EC 4.1.1.19) | bi | sce_2748 | 97.98 | Biosynthetic arginine decarboxylase (EC 4.1.1.19) |
| SCE1572_3253 | ABC transporter involved in cytochrome c biogenesis, CcmB subunit | bi | sce_2749 | 93 | ABC transporter involved in cytochrome c biogenesis, CcmB subunit |
| SCE1572_3254 | sarcosine oxidase, subunit alpha | bi | sce_2750 | 89.39 | pyridine nucleotide-disulphide oxidoreductase |
| SCE1572_3255 | FIG01087618: hypothetical protein | bi | sce_2751 | 92.34 | FIG01087618: hypothetical protein |
| SCE1572_3256 | nicotinate-nucleotide adenyltransferase | bi | sce_2752 | 85.14 | nicotinate-nucleotide adenyltransferase |
| SCE1572_3257 | FIG173306: hypothetical protein | bi | sce_2753 | 87.2 | FIG173306: hypothetical protein |
| SCE1572_3258 | Flagellar regulatory protein FleQ | umi | sce_2754 | 75.37 | Flagellar regulatory protein FleQ |
| SCE1572_3259 | Flagellar regulatory protein FleQ | bi | sce_2754 | 82.11 | Flagellar regulatory protein FleQ |
| SCE1572_3260 | hypothetical protein | bi | sce_2755 | 42.11 | hypothetical protein |
| SCE1572_3261 | Sensor protein of zinc sigma-54-dependent two-component system | bi | sce_2756 | 96.77 | Sensor protein of zinc sigma-54-dependent two-component system |
| SCE1572_3262 | 3,5-diaminohexanoate dehydrogenase (EC 1.4.1.11) | bi | sce_2757 | 89.3 | 3,5-diaminohexanoate dehydrogenase (EC 1.4.1.11) |
| SCE1572_3263 | FHA domain protein | bi | sce_2758 | 97.62 | FHA domain protein |
| SCE1572_3264 | Histidinol dehydrogenase (EC 1.1.1.23) | bi | sce_2759 | 94.58 | Histidinol dehydrogenase (EC 1.1.1.23) |
| SCE1572_3265 | hypothetical protein | - | - | 0 | |
| SCE1572_3266 | hypothetical protein | bi | sce_2760 | 91.32 | hypothetical protein |
| SCE1572_3267 | Serine/threonine protein kinase PrkC, regulator of stationary phase | bi | sce_2761 | 85.58 | Serine/threonine protein kinase PrkC, regulator of stationary phase |
| SCE1572_3268 | hypothetical protein | bi | sce_2762 | 97.53 | hypothetical protein |
| SCE1572_3269 | Uracil phosphoribosyltransferase (EC 2.4.2.9) | bi | sce_2764 | 94.35 | Uracil phosphoribosyltransferase (EC 2.4.2.9) |
| SCE1572_3270 | hypothetical protein | bi | sce_2765 | 94.15 | FIG00841391: hypothetical protein |
| SCE1572_3271 | Serine/threonine-protein kinase pkn3 (EC 2.7.11.1) | bi | sce_2766 | 94.83 | Serine/threonine-protein kinase pkn3 (EC 2.7.11.1) |
| SCE1572_3272 | Type IV fimbrial assembly, ATPase PilB | - | - | 0 | |
| SCE1572_3273 | Type IV fimbrial assembly, ATPase PilB | bi | sce_2767 | 80.99 | Type IV fimbrial assembly, ATPase PilB |
| SCE1572_3274 | Alpha-methylacyl-CoA racemase (EC 5.1.99.4) | bi | sce_2768 | 88.97 | Alpha-methylacyl-CoA racemase (EC 5.1.99.4) |
| SCE1572_3275 | putative sterol carrier protein | bi | sce_2769 | 91.23 | Short chain dehydrogenase</ |

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|--------------|---|-----|-----------|---|
| SCE1572_3442 | Ribonuclease J2 (endoribonuclease in RNA processing) | bi | sce_2934 | 94.52 beta-lactamase domain protein |
| SCE1572_3443 | hypothetical protein | bi | sce_2935 | 75 hypothetical protein |
| SCE1572_3444 | RabR, positive regulator of sigma-B | uni | sce_5835 | 47.11 putative PAS/PAC sensor protein |
| SCE1572_3445 | FIG00841528: hypothetical protein | uni | sce_225 | 67.06 FIG00841528: hypothetical protein |
| SCE1572_3446 | hypothetical protein | - | - | 0 |
| SCE1572_3447 | FIG01087229: hypothetical protein | bi | sce_2939 | 81.67 hypothetical protein |
| SCE1572_3448 | Serine phosphatase RsbU, regulator of sigma subunit | bi | sce_2940 | 82.55 Serine phosphatase RsbU, regulator of sigma subunit |
| SCE1572_3449 | Cytosine/purine/uracil/thiamine/allantoin permease family protein | bi | sce_2941 | 88.07 Cytosine/purine/uracil/thiamine/allantoin permease family protein |
| SCE1572_3450 | Conservative hypothetical protein probably involved in hydantoin, pyrimidine utilization | bi | sce_2942 | 87.29 Conservative hypothetical protein probably involved in hydantoin, pyrimidine utilization |
| SCE1572_3451 | N-methylhydantoinase (ATP-hydrolyzing) (EC 3.5.2.14) | bi | sce_2943 | 84.96 N-methylhydantoinase (ATP-hydrolyzing) (EC 3.5.2.14) |
| SCE1572_3452 | N-methylhydantoinase B (EC 3.5.2.14) | bi | sce_2944 | 92.13 N-methylhydantoinase B (EC 3.5.2.14) |
| SCE1572_3453 | N-methylhydantoinase A (EC 3.5.2.14) | bi | sce_2945 | 89.78 N-methylhydantoinase A (EC 3.5.2.14) |
| SCE1572_3454 | conserved hypothetical protein | uni | sce_1469 | 49.85 FIG1086976: hypothetical protein |
| SCE1572_3455 | MG(2) CHELATASE FAMILY PROTEIN / ComM-related protein | bi | sce_2946 | 92.32 MG(2) CHELATASE FAMILY PROTEIN / ComM-related protein |
| SCE1572_3456 | RecA protein | bi | sce_2947 | 97.95 RecA protein |
| SCE1572_3457 | hypothetical protein | - | - | 0 |
| SCE1572_3458 | Single-stranded DNA-binding protein | bi | sce_2948 | 92.41 Single-stranded DNA-binding protein |
| SCE1572_3459 | hypothetical protein | bi | sce_2952 | 47.53 hypothetical protein |
| SCE1572_3460 | hypothetical protein | bi | sce_2953 | 55.29 FIG1086872: hypothetical protein |
| SCE1572_3461 | conserved hypothetical protein | bi | sce_2954 | 86.39 hypothetical protein |
| SCE1572_3462 | hypothetical protein | bi | sce_2955 | 83.15 hypothetical protein |
| SCE1572_3463 | hypothetical protein | bi | sce_2956 | 86.13 hypothetical protein |
| SCE1572_3464 | Transcription-repair coupling factor | bi | sce_2957 | 91.72 Transcription-repair coupling factor |
| SCE1572_3465 | hypothetical protein | - | - | 0 |
| SCE1572_3466 | hypothetical protein | - | - | 0 |
| SCE1572_3467 | hypothetical protein | bi | sce_2958 | 86.36 Uncharacterized conserved protein |
| SCE1572_3468 | hypothetical protein | bi | sce_2960 | 74.42 hypothetical protein |
| SCE1572_3469 | EBNA-1 | bi | sce_2962 | 75.46 Uncharacterized protein with a C-terminal OMP (outer membrane protein) domain |
| SCE1572_3470 | FIG1089305: hypothetical protein | bi | sce_2963 | 86.24 FIG1089305: hypothetical protein |
| SCE1572_3471 | hypothetical protein | - | - | 0 |
| SCE1572_3472 | putative lipoprotein | bi | sce_2964 | 76.83 lorierin |
| SCE1572_3473 | hypothetical protein | bi | sce_2965 | 70.06 FIG1089285: hypothetical protein |
| SCE1572_3474 | Gli0645 protein | bi | sce_2966 | 80.83 Gli0645 protein |
| SCE1572_3475 | FIG1086691: hypothetical protein | bi | sce_2967 | 81.59 FIG1086691: hypothetical protein |
| SCE1572_3476 | putative oxidoreductase protein | bi | sce_2969 | 85.19 putative oxidoreductase protein |
| SCE1572_3477 | hypothetical protein | - | - | 0 |
| SCE1572_3478 | hypothetical protein | bi | sce_2970 | 53.93 hypothetical protein |
| SCE1572_3479 | hypothetical protein | - | - | 0 |
| SCE1572_3480 | FIG1086339: hypothetical protein | bi | sce_2972 | 66.14 FIG1086339: hypothetical protein |
| SCE1572_3481 | hypothetical protein | bi | sce_2973 | 82.11 General stress protein |
| SCE1572_3482 | hypothetical protein | uni | sce_3858 | 32.39 Adenosylhomocysteinase (EC 3.3.1.1) |
| SCE1572_3483 | FIG1088545: hypothetical protein | bi | sce_2974 | 86.8 FIG1088545: hypothetical protein |
| SCE1572_3484 | ABC transporter, fused permease and ATPase domains | bi | sce_2975 | 90.85 ABC transporter, fused permease and ATPase domains |
| SCE1572_3485 | PKD domain containing protein | - | - | 0 |
| SCE1572_3486 | D-AMINOPEPTIDASE (EC 3.4.11.19) | uni | sce_1000 | 44.52 D-alanine--D-alanine ligase (EC 6.3.2.4) |
| SCE1572_3487 | Periplasmic aromatic aldehyde oxidoreductase, molybdenum binding subunit YagR | uni | sce_7082 | 36.52 Isoquinoline 1-oxidoreductase beta subunit (EC 1.3.99.16) |
| SCE1572_3488 | Periplasmic aromatic aldehyde oxidoreductase, FAD binding subunit YagS | uni | sce_6597 | 23 Xanthine dehydrogenase, FAD binding subunit (EC 1.17.1.4) |
| SCE1572_3489 | Periplasmic aromatic aldehyde oxidoreductase, iron-sulfur subunit YagT | uni | sce_3739 | 48.61 Isoquinoline 1-oxidoreductase alpha subunit (EC 1.3.99.16) |
| SCE1572_3490 | COG0583: Transcriptional regulator | bi | sce_1329 | 66.89 Transcriptional regulator, LysR family |
| SCE1572_3491 | putative cytochrome P450 hydroxylase | uni | sce_5180 | 39.24 putative cytochrome P450 hydroxylase |
| SCE1572_3492 | hypothetical protein | - | - | 0 |
| SCE1572_3493 | FIG1088435: hypothetical protein | bi | sce_2976 | 81.14 FIG1088435: hypothetical protein |
| SCE1572_3494 | Two component response regulator | bi | sce_2977 | 85.6 Two component response regulator |
| SCE1572_3495 | FIG1085803: hypothetical protein | bi | sce_7153 | 46.67 Flagellar motor switch protein FlhN |
| SCE1572_3496 | Chemotaxis protein methyltransferase CheR (EC 2.1.1.80) | bi | sce_2978 | 84.96 Chemotaxis protein methyltransferase CheR (EC 2.1.1.80) |
| SCE1572_3497 | Chemotaxis regulator - transmits chemoreceptor signals to flagellar motor components CheY | bi | sce_2980 | 91.34 Chemotaxis regulator - transmits chemoreceptor signals to flagellar motor components CheY |
| SCE1572_3498 | Signal transduction histidine kinase CheA (EC 2.7.3.-) | bi | sce_2981 | 84.67 Signal transduction histidine kinase CheA (EC 2.7.3.-) |
| SCE1572_3499 | Positive regulator of CheA protein activity (CheW) | bi | sce_2982 | 89.21 Positive regulator of CheA protein activity (CheW) |
| SCE1572_3500 | Methyl accepting chemotaxis protein | bi | sce_2983 | 82.9 Methyl accepting chemotaxis protein |
| SCE1572_3501 | FOG: HEAT repeat | bi | sce_2984 | 84.5 conserved hypothetical protein |
| SCE1572_3502 | Chemotaxis protein methyltransferase CheR (EC 2.1.1.80) | bi | sce_2985 | 84.93 Chemotaxis protein methyltransferase CheR (EC 2.1.1.80) |
| SCE1572_3503 | Chemotaxis response regulator protein-glutamate methyltransferase CheB (EC 3.1.1.61) | bi | sce_2986 | 80.83 Chemotaxis response regulator protein-glutamate methyltransferase CheB (EC 3.1.1.61) |
| SCE1572_3504 | hypothetical protein | bi | sce_2987 | 76.77 hypothetical protein |
| SCE1572_3505 | Ku domain protein | bi | sce_2988 | 82.19 Ku domain protein |
| SCE1572_3506 | Nicotinamidase (EC 3.5.1.19) | bi | sce_2989 | 92.46 Nicotinamidase (EC 3.5.1.19) |
| SCE1572_3507 | Succinyl-CoA ligase [ADP-forming] beta chain (EC 6.2.1.5) | bi | sce_2990 | 93.92 Succinyl-CoA ligase [ADP-forming] beta chain (EC 6.2.1.5) |
| SCE1572_3508 | putative hyperosmotically inducible periplasmic protein | bi | sce_2991 | 86.49 putative hyperosmotically inducible periplasmic protein |
| SCE1572_3509 | Adenosylhomocysteinase (EC 3.3.1.1) | bi | sce_2992 | 82.88 sigma-54 dependent DNA-binding response regulator |
| SCE1572_3510 | FIG1084914: hypothetical protein | bi | sce_2993 | 65.43 FIG1084914: hypothetical protein |
| SCE1572_3511 | Xanthine permease | bi | sce_2994 | 71.54 Xanthine permease |
| SCE1572_3512 | Major facilitator superfamily (MFS_1) transporter | uni | sce_9993 | 45 Permeases of the major facilitator superfamily |
| SCE1572_3513 | Dopamine beta-hydroxylase | bi | sce_7498 | 83.37 Dopamine beta-hydroxylase |
| SCE1572_3514 | Transcriptional regulator, TetR family | bi | sce_7500 | 82.69 Transcriptional regulator, TetR family |
| SCE1572_3515 | tetratricopeptide repeat domain protein | - | - | 0 |
| SCE1572_3516 | FIG1085542: hypothetical protein | bi | sce_7492 | 83.64 FIG1085542: hypothetical protein |
| SCE1572_3517 | putative hydrolase | bi | sce_8421 | 37.09 FIG1085520: hypothetical protein |
| SCE1572_3518 | hypothetical protein | bi | sce_5238 | 44.95 hypothetical protein |
| SCE1572_3519 | FIG1086458: hypothetical protein | uni | sce_5638 | 36.24 FIG1086458: hypothetical protein |
| SCE1572_3520 | hypothetical protein | - | - | 0 |
| SCE1572_3521 | PAS/PAC sensor hybrid histidine kinase | bi | sce_1043 | 47.77 Signal transduction histidine kinase |
| SCE1572_3522 | hypothetical protein | - | - | 0 |
| SCE1572_3523 | FIG1088655: hypothetical protein | bi | sce_3138 | 83.58 FIG1088655: hypothetical protein |
| SCE1572_3524 | Osmosensitive K channel histidine kinase KdpD (EC 2.7.3.-) | uni | sce_5554 | 42.86 PAS |
| SCE1572_3525 | BIll1406 protein | bi | sce_7491 | 76.7 BIll1406 protein |
| SCE1572_3526 | Transcriptional regulator, TetR family | uni | sce_7925 | 41.38 Transcriptional regulator, TetR family |
| SCE1572_3527 | hypothetical protein | - | - | 0 |
| SCE1572_3528 | OmpA/MotB | bi | sce_2106 | 62.16 Extensin-like protein precursor |
| SCE1572_3529 | Excinuclease ABC subunit A paralog of unknown function | uni | sce_7067 | 50.91 Excinuclease ABC subunit A paralog of unknown function |
| SCE1572_3530 | hypothetical protein | - | - | 0 |
| SCE1572_3531 | Transcriptional regulator, TetR family | uni | sce_9220 | 34.64 Transcriptional regulator, TetR family |
| SCE1572_3532 | 5-methyltetrahydropteroylglutamate--homocysteine methyltransferase (EC 2.1.1.14) | - | - | 0 |
| SCE1572_3533 | Pectin lyase like protein | bi | sce_7120 | 80.35 Pectin lyase like protein |
| SCE1572_3534 | hypothetical protein | bi | sce_8653 | 93.48 hypothetical protein |
| SCE1572_3535 | Oxidoreductase | uni | sce_10011 | 40.99 Oxidoreductase |
| SCE1572_3536 | hypothetical protein | - | - | 0 |
| SCE1572_3537 | hypothetical protein | - | - | 0 |
| SCE1572_3538 | hypothetical protein | - | - | 0 |
| SCE1572_3539 | hypothetical protein | bi | sce_5183 | 30.82 Uncharacterized protein y4kT |
| SCE1572_3540 | hypothetical protein | uni | sce_3728 | 30.47 putative lipoprotein |
| SCE1572_3541 | hypothetical protein | - | - | 0 |
| SCE1572_3542 | hypothetical protein | - | - | 0 |
| SCE1572_3543 | hypothetical protein | - | - | 0 |
| SCE1572_3544 | OsD1g0793100 | - | - | 0 |
| SCE1572_3545 | hypothetical protein | - | - | 0 |
| SCE1572_3546 | hypothetical protein | - | - | 0 |
| SCE1572_3547 | hypothetical protein | uni | sce_2402 | 85 hypothetical protein |
| SCE1572_3548 | PE-PGRS FAMILY PROTEIN | bi | sce_5572 | 60.4 Flagellar hook-length control protein FlhK |
| SCE1572_3549 | Endo-1,4-beta-xylanase A precursor (EC 3.2.1.8) | uni | sce_5143 | 76.25 Endo-1,4-beta-xylanase A precursor (EC 3.2.1.8) |
| SCE1572_3550 | hypothetical protein | bi | sce_1370 | 87.18 hypothetical protein |
| SCE1572_3551 | hypothetical protein | - | - | 0 |
| SCE1572_3552 | conserved hypothetical protein | bi | sce_6024 | 34.72 conserved hypothetical protein |
| SCE1572_3553 | hypothetical protein | bi | sce_6183 | 68.53 similar to GRound-Like (grd related) family member (grl-25) |
| SCE1572_3554 | hypothetical protein | bi | sce_10012 | 88.44 hypothetical protein |
| SCE1572_3555 | Adenylate cyclase (EC 4.6.1.1) / Guanylate cyclase (EC 4.6.1.2) | uni | sce_5751 | 72.06 Adenylate cyclase (EC 4.6.1.1) / Guanylate cyclase (EC 4.6.1.2) |
| SCE1572_3556 | hypothetical protein | - | - | 0 |
| SCE1572_3557 | Chitinase (EC 3.2.1.14) | uni | sce_1403 | 59.68 Cell division protein FtsZ (EC 3.4.24.-) |
| SCE1572_3558 | hypothetical protein | - | - | 0 |
| SCE1572_3559 | PTS system, glucose-specific IIA component (EC 2.7.1.69) / Phosphocarrier protein of PTS system / Phosphoenolpyruvate-pro uni | - | sce_2789 | 38.63 Phosphoenolpyruvate-dihydroxyacetone phosphotransferase (EC 2.7.1.121), subunit DhaM; DHA-specific IIA component / DHA-sp |
| SCE1572_3560 | PTS system, N-acetylglucosamine-specific IIB component (EC 2.7.1.69) / PTS system, N-acetylglucosamine-specific IIC com | - | - | 0 |
| SCE1572_3561 | N-acetylglucosamine-6-phosphate deacetylase (EC 3.5.1.25) | uni | sce_6730 | 26.25 Xaa-Pro dipeptidase (EC 3.4.13.9) |
| SCE1572_3562 | Glucosamine-6-phosphate deaminase [isomerizing], alternative (EC 3.5.99.6) | uni | sce_8287 | 34.18 Glucosamine--fructose-6-phosphate aminotransferase [isomerizing] (EC 2.6.1.16) |
| SCE1572_3563 | Beta-hexosaminidase (EC 3.2.1.52) | - | - | 0 |
| SCE1572_3564 | Serine/threonine protein kinase | bi | sce_5229 | 48.13 Serine/threonine protein kinase |
| SCE1572_3565 | Serine/threonine protein kinase | uni | sce_6712 | 55.65 Adenylate cyclase (EC 4.6.1.1) / Guanylate cyclase (EC 4.6.1.2) |
| SCE1572_3566 | Acyl-CoA dehydrogenase, type 2-like | uni | sce_677 | 32.89 Acyl-CoA dehydrogenases |
| SCE1572_3567 | hypothetical protein | uni | sce_8336 | 32.31 hypothetical protein |
| SCE1572_3568 | Adenylate cyclase (EC 4.6.1.1) / Guanylate cyclase (EC 4.6.1.2) | uni | sce_6712 | 48.38 Adenylate cyclase (EC 4.6.1.1) / Guanylate cyclase (EC 4.6.1.2) |
| SCE1572_3569 | hypothetical protein | - | - | 0 |
| SCE1572_3570 | hypothetical protein | - | - | 0 |
| SCE1572_3571 | Transcriptional regulator BkdR of isoleucine and valine catabolism operon | uni | sce_3816 | 62.23 Transcriptional regulator BkdR of isoleucine and valine catabolism operon |
| SCE1572_3572 | hypothetical protein | - | - | 0 |
| SCE1572_3573 | Low-density lipoprotein receptor-related protein 1 precursor | uni | sce_149 | 29.07 hypothetical protein |
| SCE1572_3574 | hypothetical protein | uni | sce_4089 | 28.96 Alpha/beta hydrolase fold (EC 3.8.1.5) |
| SCE1572_3575 | hypothetical protein | - | - | 0 |
| SCE1572_3576 | FIG1085859: hypothetical protein | bi | sce_6709 | 50.21 FIG1085859: hypothetical protein |
| SCE1572_3577 | beta-mannanase | bi | sce_170 | 87.84 beta-mannanase |
| SCE1572_3578 | Methylated-DNA-(protein)-cysteine S-methyltransferase | - | - | 0 |
| SCE1572_3579 | Pantothenate:Na symporter (TC 2.A.21.1.1) | bi | sce_6216 | 69.67 Pantothenate:Na symporter (TC 2.A.21.1.1) |
| SCE1572_3580 | hypothetical protein | uni | sce_2007 | 33.15 hypothetical protein |
| SCE1572_3581 | von Willebrand factor C and EGF domains | bi | sce_4603 | 77 Kielin |
| SCE1572_3582 | High-affinity carbon uptake protein Hat/HatR | - | - | 0 |
| SCE1572_3583 | hypothetical protein | uni | sce_2126 | 62.11 Conserved domain protein |
| SCE1572_3584 | hypothetical protein | - | - | 0 |
| SCE1572_3585 | POSSIBLE TRANSMEMBRANE PROTEIN | bi | sce_9857 | 87.92 hypothetical protein |
| SCE1572_3586 | hypothetical protein | uni | sce_7354 | 51.77 hypothetical protein |
| SCE1572_3587 | hypothetical protein | - | - | 0 |
| SCE1572_3588 | hypothetical protein | - | - | 0 |
| SCE1572_3589 | hypothetical protein | bi | sce_10265 | 88.68 hypothetical protein |
| SCE1572_3590 | hypothetical protein | - | - | 0 |
| SCE1572_3591 | hypothetical protein | - | - | 0 |
| SCE1572_3592 | hypothetical protein | bi | sce_7649 | 84 Alkylhydroperoxidase AhpD core domain |
| SCE1572_3593 | Metallo-beta-lactamase superfamily protein | bi | sce_7648 | 87.18 Metallo-beta-lactamase superfamily protein |
| SCE1572_3594 | putative RNA polymerase sigma factor | bi | sce_7651 | 87.8 putative RNA polymerase sigma factor |
| SCE1572_3595 | hypothetical protein | - | - | 0 |
| SCE1572_3596 | hypothetical protein | - | - | 0 |
| SCE1572_3597 | hypothetical protein | - | - | 0 |
| SCE1572_3598 | Cell division transporter, ATP-binding protein FtsE (TC 3.A.5.1.1) | uni | sce_8566 | 30.49 Lipid A export ATP-binding/permease protein MsbA |
| SCE1572_3599 | Transcriptional regulator, ArsR family | bi | sce_1701 | 85.19 transcriptional regulator (ArsR family) |
| SCE1572_3600 | hypothetical protein | - | - | 0 |
| SCE1572_3601 | hypothetical protein | uni | sce_4539 | 42 FIG1086337: hypothetical protein |
| SCE1572_3602 | serine/Threonine protein kinase | uni | sce_3801 | 47.48 protein kinase |
| SCE1572_3603 | cAMP-binding proteins - catabolite gene activator and regulatory subunit of cAMP-dependent protein kinases | uni | sce_1598 | 69.54 cAMP-binding proteins - catabolite gene activator and regulatory subunit of cAMP-dependent protein kinases |
| SCE1572_3604 | Germaacridinol/germacrene D synthase (EC 4.2.3.22) | bi | sce_1597 | 62.71 FIG1120759: hypothetical protein |
| SCE1572_3605 | cAMP-binding proteins - catabolite gene activator and regulatory subunit of cAMP-dependent protein kinases | bi | sce_1598 | 71.34 cAMP-binding proteins - catabolite gene activator and regulatory subunit of cAMP-dependent protein kinases |

| | | | | |
|--------------|--|-----|-----------|--|
| SCE1572_3606 | hypothetical protein | - | | 0 |
| SCE1572_3607 | Response regulator of zinc sigma-54-dependent two-component system | bi | sce_4487 | 84.12 Response regulator of zinc sigma-54-dependent two-component system |
| SCE1572_3608 | FIG01085495: hypothetical protein | bi | sce_3024 | 73.66 FIG01085495: hypothetical protein |
| SCE1572_3609 | Two-component sensor CbrB: intracellular carbon:nitrogen balance | bi | sce_3025 | 81.58 Two-component sensor CbrB: intracellular carbon:nitrogen balance |
| SCE1572_3610 | hypothetical protein | - | | 0 |
| SCE1572_3611 | protein kinase domain | uni | sce_7729 | 39.86 eukaryotic-type protein kinase |
| SCE1572_3612 | hypothetical protein | uni | sce_3894 | 29.79 Gli0642 protein |
| SCE1572_3613 | hypothetical protein | - | | 0 |
| SCE1572_3614 | hypothetical protein | bi | sce_6533 | 33.43 FIG1086595: hypothetical protein |
| SCE1572_3615 | FAD linked oxidase, C-terminal:FAD linked oxidase, N-terminal | uni | sce_10079 | 30.81 Alkylldihydroxyacetonephosphate synthase |
| SCE1572_3616 | Putative cytoplasmic protein | - | | 0 |
| SCE1572_3617 | UPF0182 protein AF1421 | - | | 0 |
| SCE1572_3618 | hypothetical protein | - | | 0 |
| SCE1572_3619 | Na(I) H) antiporter subunit A | bi | sce_2155 | 91.78 Na(I) H) antiporter subunit A |
| SCE1572_3620 | Na(I) H) antiporter subunit B | bi | sce_2154 | 92.09 Na(I) H) antiporter subunit B |
| SCE1572_3621 | Na(I) H) antiporter subunit C | bi | sce_2153 | 93.04 Na(I) H) antiporter subunit C |
| SCE1572_3622 | Na(I) H) antiporter subunit D | bi | sce_2152 | 91.12 Na(I) H) antiporter subunit D |
| SCE1572_3623 | Na(I) H) antiporter subunit E | bi | sce_2151 | 91.08 Na(I) H) antiporter subunit E |
| SCE1572_3624 | Na(I) H) antiporter subunit F | bi | sce_2150 | 94.19 Na(I) H) antiporter subunit F |
| SCE1572_3625 | Na(I) H) antiporter subunit G | bi | sce_2149 | 91.62 Na(I) H) antiporter subunit G |
| SCE1572_3626 | FIG01086300: hypothetical protein | bi | sce_6850 | 81.02 FIG1086300: hypothetical protein |
| SCE1572_3627 | FIG01085217: hypothetical protein | bi | sce_6851 | 81.11 FIG1085217: hypothetical protein |
| SCE1572_3628 | hypothetical protein | bi | sce_1042 | 71.88 hypothetical protein |
| SCE1572_3629 | hypothetical protein | bi | sce_7856 | 81.4 hypothetical protein |
| SCE1572_3630 | Selenoprotein O and cysteine-containing homologs | bi | sce_6065 | 88.64 Selenoprotein O and cysteine-containing homologs |
| SCE1572_3631 | oxidoreductase, FAD/FMN-binding | bi | sce_6047 | 91.99 oxidoreductase |
| SCE1572_3632 | Polyvinylalcohol dehydrogenase | bi | sce_6048 | 86.63 Polyvinylalcohol dehydrogenase |
| SCE1572_3633 | FIG01087588: hypothetical protein | bi | sce_6046 | 83.61 FIG1087588: hypothetical protein |
| SCE1572_3634 | hypothetical protein | bi | sce_2425 | 83.75 hypothetical protein |
| SCE1572_3635 | Histone acetyltransferase HPA2 and related acetyltransferases | uni | sce_2495 | 37.5 Histone acetyltransferase HPA2/related acetyltransferase |
| SCE1572_3636 | hypothetical protein | - | | 0 |
| SCE1572_3637 | hypothetical protein | - | | 0 |
| SCE1572_3638 | hypothetical protein | - | | 0 |
| SCE1572_3639 | hypothetical protein | bi | sce_6070 | 77.78 hypothetical protein |
| SCE1572_3640 | hypothetical protein | - | | 0 |
| SCE1572_3641 | Alcohol dehydrogenase, zinc-binding domain protein | bi | sce_6018 | 85.76 Alcohol dehydrogenase (EC 1.1.1.1) |
| SCE1572_3642 | putative oxidoreductase | uni | sce_5691 | 34.21 Cellulase (EC:3.2.1.4) |
| SCE1572_3643 | hypothetical protein | - | | 0 |
| SCE1572_3644 | RsbR, positive regulator of sigma-B | uni | sce_5334 | 51.88 RsbR, positive regulator of sigma-B |
| SCE1572_3645 | hypothetical protein | - | | 0 |
| SCE1572_3646 | hypothetical protein | bi | sce_4691 | 83.27 hypothetical protein |
| SCE1572_3647 | FIG01086973: hypothetical protein | bi | sce_4692 | 82.83 FIG1086973: hypothetical protein |
| SCE1572_3648 | FIG01089683: hypothetical protein | bi | sce_4693 | 70.68 FIG1089683: hypothetical protein |
| SCE1572_3649 | hypothetical protein | - | | 0 |
| SCE1572_3650 | Bil0118 protein | bi | sce_2436 | 73.64 Bil0118 protein |
| SCE1572_3651 | hypothetical protein | uni | sce_8637 | 42.75 FIG1087436: hypothetical protein |
| SCE1572_3652 | hypothetical protein | uni | sce_6039 | 31.01 hypothetical protein |
| SCE1572_3653 | hypothetical protein | - | | 0 |
| SCE1572_3654 | hypothetical protein | bi | sce_3043 | 86.03 hypothetical protein |
| SCE1572_3655 | hypothetical protein | - | | 0 |
| SCE1572_3656 | hypothetical protein | bi | sce_5240 | 37 hypothetical protein |
| SCE1572_3657 | hypothetical protein | bi | sce_5239 | 34.07 FIG1086776: hypothetical protein |
| SCE1572_3658 | COG0457: FOG: TPR repeat | bi | sce_5235 | 48.7 hypothetical protein |
| SCE1572_3659 | hypothetical protein | - | | 0 |
| SCE1572_3660 | hypothetical protein | - | | 0 |
| SCE1572_3661 | Flagellar regulatory protein FleQ | uni | sce_773 | 49.71 Flagellar regulatory protein FleQ |
| SCE1572_3662 | HlyD family secretion protein | uni | sce_8030 | 43.19 HlyD family secretion protein |
| SCE1572_3663 | ABC transporter, ATP-binding protein | uni | sce_8029 | 47.72 ABC transporter, ATP-binding protein |
| SCE1572_3664 | ABC transporter, ATP-binding protein | uni | sce_8028 | 46.04 transport ATP-binding protein MsbA |
| SCE1572_3665 | hypothetical protein | - | | 0 |
| SCE1572_3666 | hypothetical protein | - | | 0 |
| SCE1572_3667 | hypothetical protein | uni | sce_3858 | 34.76 Adenosylhomocysteinase (EC 3.3.1.1) |
| SCE1572_3668 | hypothetical protein | - | | 0 |
| SCE1572_3669 | hypothetical protein | - | | 0 |
| SCE1572_3670 | FIG01087249: hypothetical protein | uni | sce_2337 | 92.74 FIG1087249: hypothetical protein |
| SCE1572_3671 | hypothetical protein | - | | 0 |
| SCE1572_3672 | hypothetical protein | uni | sce_6700 | 65.31 hypothetical protein |
| SCE1572_3673 | alpha/beta hydrolase fold | - | | 0 |
| SCE1572_3674 | D-alanyl-D-alanine carboxypeptidase (EC 3.4.16.4) | uni | sce_4326 | 39.71 Beta-lactamase class C and other penicillin binding proteins |
| SCE1572_3675 | hypothetical protein | - | | 0 |
| SCE1572_3676 | Xylose ABC transporter, substrate-binding component | uni | sce_7038 | 58.06 hypothetical protein |
| SCE1572_3677 | hypothetical protein | bi | sce_7357 | 88.16 hypothetical protein |
| SCE1572_3678 | hypothetical protein | bi | sce_7356 | 92.36 hypothetical protein |
| SCE1572_3679 | Endo-1,4-beta-xylanase A precursor (EC 3.2.1.8) (Xylanase A) (1,4-beta-D-xylan xylanohydrolase A) (XYLA) | uni | sce_5891 | 40.45 unknown |
| SCE1572_3680 | hypothetical protein | bi | sce_6700 | 71.72 hypothetical protein |
| SCE1572_3681 | FIG01085648: hypothetical protein | uni | sce_10332 | 56.29 FIG1087210: hypothetical protein |
| SCE1572_3682 | Extensin-like protein | uni | sce_10332 | 50 FIG1087210: hypothetical protein |
| SCE1572_3683 | FIG01086383: hypothetical protein | uni | sce_10333 | 62.18 hypothetical protein |
| SCE1572_3684 | hypothetical protein | - | | 0 |
| SCE1572_3685 | RNA polymerase sigma factor RpoE | uni | sce_10335 | 50.32 RNA polymerase sigma factor RpoE |
| SCE1572_3686 | hypothetical protein | uni | sce_10334 | 52.17 FIG1087636: hypothetical protein |
| SCE1572_3687 | cytochrome P450 | uni | sce_7190 | 42.56 Cytochrome P450 |
| SCE1572_3688 | FIG01088284: hypothetical protein | bi | sce_1325 | 84.78 FIG1088284: hypothetical protein |
| SCE1572_3689 | Metalloid methyltransferase | bi | sce_3046 | 83.64 Metalloid methyltransferase |
| SCE1572_3690 | hypothetical protein | uni | sce_2128 | 44.12 hypothetical protein |
| SCE1572_3691 | putative lipoprotein | bi | sce_3794 | 56.39 Type IV fimbrial biogenesis protein PilY1 |
| SCE1572_3692 | hypothetical protein | uni | sce_3796 | 56.69 hypothetical protein |
| SCE1572_3693 | TolA protein, putative | uni | sce_3793 | 28.86 WD-40 repeat protein |
| SCE1572_3694 | Conserved domain protein | uni | sce_2126 | 54.76 Conserved domain protein |
| SCE1572_3695 | hypothetical protein | - | | 0 |
| SCE1572_3696 | hypothetical protein | bi | sce_3047 | 75.96 hypothetical protein |
| SCE1572_3697 | Hypothetical protein VC0266 (sugar utilization related?) | uni | sce_1931 | 33.09 Uracil-DNA glycosylase, putative family 6 |
| SCE1572_3698 | Rhomboid family protein | - | | 0 |
| SCE1572_3699 | Malonyl CoA-acyl carrier protein transacylase (EC 2.3.1.39) | - | | 0 |
| SCE1572_3700 | hypothetical protein | bi | sce_3049 | 90.81 peptidase M14, carboxypeptidase A |
| SCE1572_3701 | Methylmalonyl-CoA epimerase (EC 5.1.99.1) | bi | sce_3051 | 90.67 Methylmalonyl-CoA epimerase (EC 5.1.99.1) |
| SCE1572_3702 | Methylmalonyl-CoA mutase (EC 5.4.99.2) | bi | sce_3052 | 90.48 Methylmalonyl-CoA mutase (EC 5.4.99.2) |
| SCE1572_3703 | putative periplasmic protein kinase ArgK and related GTPases of G3E family | bi | sce_3053 | 86.9 putative periplasmic protein kinase ArgK and related GTPases of G3E family |
| SCE1572_3704 | FIG1089097: hypothetical protein | bi | sce_2116 | 88.89 FIG1089097: hypothetical protein |
| SCE1572_3705 | Endo-1,4-beta-xylanase 2 precursor (EC 3.2.1.8) (Xylanase 2) (1,4-beta-D-xylan xylanohydrolase 2) | bi | sce_10408 | 89.19 hypothetical protein (EC:3.2.1.8) |
| SCE1572_3706 | hypothetical protein | - | | 0 |
| SCE1572_3707 | FIG01087489: hypothetical protein | bi | sce_7655 | 78.78 hypothetical protein |
| SCE1572_3708 | hypothetical protein | - | | 0 |
| SCE1572_3709 | hypothetical protein | - | | 0 |
| SCE1572_3710 | RNA-binding protein | uni | sce_6697 | 86.14 RNA-binding protein |
| SCE1572_3711 | hypothetical protein | bi | sce_8388 | 86.67 hypothetical protein |
| SCE1572_3712 | DTW domain protein | bi | sce_3061 | 83.61 DTW domain protein |
| SCE1572_3713 | hypothetical protein | uni | sce_6519 | 44.52 FIG1085716: hypothetical protein |
| SCE1572_3714 | Parallel beta-helix repeat | - | | 0 |
| SCE1572_3715 | Cytochrome c551 peroxidase (EC 1.11.1.5) | uni | sce_6518 | 53.91 Methylamine utilization protein mauG |
| SCE1572_3716 | FIG01088601: hypothetical protein | uni | sce_3879 | 30.84 FIG1085391: hypothetical protein |
| SCE1572_3717 | group II decarboxylase family protein | uni | sce_2563 | 31.84 Aromatic-L-amino-acid decarboxylase (EC 4.1.1.28) |
| SCE1572_3718 | hypothetical protein | - | | 0 |
| SCE1572_3719 | FIG01088133: hypothetical protein | bi | sce_3062 | 80.8 FIG1088133: hypothetical protein |
| SCE1572_3720 | Two-component sensor CbrA: intracellular carbon:nitrogen balance | bi | sce_3065 | 88.57 histidine kinase |
| SCE1572_3721 | hypothetical protein | - | | 0 |
| SCE1572_3722 | putative sugar transport protein | bi | sce_3066 | 92.14 putative sugar transport protein |
| SCE1572_3723 | membrane protein, putative | - | | 0 |
| SCE1572_3724 | hypothetical protein | - | | 0 |
| SCE1572_3725 | PE-PGRS FAMILY PROTEIN | bi | sce_7838 | 64.23 hypothetical protein |
| SCE1572_3726 | hypothetical protein | - | | 0 |
| SCE1572_3727 | LamG domain protein jellyroll fold domain protein | uni | sce_5962 | 32.69 Similarity |
| SCE1572_3728 | hypothetical protein | - | | 0 |
| SCE1572_3729 | hypothetical protein | - | | 0 |
| SCE1572_3730 | hypothetical protein | - | | 0 |
| SCE1572_3731 | Protein serine-threonine phosphatase | bi | sce_3071 | 93.92 Protein serine-threonine phosphatase |
| SCE1572_3732 | HEN1 C-terminal domain; double-stranded RNA 3''-methylase | bi | sce_3072 | 89.44 HEN1 C-terminal domain; double-stranded RNA 3''-methylase |
| SCE1572_3733 | hypothetical protein | - | | 0 |
| SCE1572_3734 | PE-PGRS family protein | uni | sce_5891 | 64.33 unknown |
| SCE1572_3735 | RsbR, positive regulator of sigma-B | uni | sce_5334 | 56.46 RsbR, positive regulator of sigma-B |
| SCE1572_3736 | PE-PGRS FAMILY PROTEIN | uni | sce_1495 | 75 Collagen triple helix repeat |
| SCE1572_3737 | hypothetical protein | uni | sce_8542 | 46.38 hypothetical protein |
| SCE1572_3738 | Flagellar hook-length control protein FliK | bi | sce_3078 | 79.68 Flagellar hook-length control protein FliK |
| SCE1572_3739 | hypothetical protein | - | | 0 |
| SCE1572_3740 | NtrC | uni | sce_2052 | 53.98 NtrC |
| SCE1572_3741 | Gli2764 protein | uni | sce_7864 | 31.76 1,4-beta-cellobiosidase |
| SCE1572_3742 | serine/threonine protein kinase | uni | sce_7475 | 38.39 serine/threonine protein kinase |
| SCE1572_3743 | hypothetical protein | - | | 0 |
| SCE1572_3744 | hypothetical protein | uni | sce_7392 | 29.89 FIG1089338: hypothetical protein |
| SCE1572_3745 | FIG1088605: hypothetical protein | bi | sce_3083 | 83.2 FIG1088605: hypothetical protein |
| SCE1572_3746 | RNA polymerase sigma factor RpoE | bi | sce_3084 | 91.08 RNA polymerase sigma factor RpoE |
| SCE1572_3747 | hypothetical protein | - | | 0 |
| SCE1572_3748 | RsbR, positive regulator of sigma-B | bi | sce_3085 | 91.88 putative PAS/PAC sensor protein |
| SCE1572_3749 | hypothetical protein | bi | sce_3086 | 87.5 hypothetical protein |
| SCE1572_3750 | hypothetical protein | uni | sce_3087 | 77.5 hypothetical protein |
| SCE1572_3751 | Proteophosphoglycan 5 | bi | sce_3087 | 81.15 hypothetical protein |
| SCE1572_3752 | putative cytochrome P450 hydroxylase | uni | sce_8803 | 35.05 putative cytochrome P450 hydroxylase |
| SCE1572_3753 | Putative SAM-dependent methyltransferases | - | | 0 |
| SCE1572_3754 | hypothetical protein | - | | 0 |
| SCE1572_3755 | Malonyl CoA-acyl carrier protein transacylase (EC 2.3.1.39) | uni | sce_4641 | 45.82 Malonyl CoA-acyl carrier protein transacylase (EC 2.3.1.39) |
| SCE1572_3756 | Malonyl CoA-acyl carrier protein transacylase (EC 2.3.1.39) | bi | sce_3575 | 46.38 Malonyl CoA-acyl carrier protein transacylase (EC 2.3.1.39) |
| SCE1572_3757 | Malonyl CoA-acyl carrier protein transacylase (EC 2.3.1.39) | uni | sce_4641 | 44.54 Malonyl CoA-acyl carrier protein transacylase (EC 2.3.1.39) |
| SCE1572_3758 | FIG1085109: hypothetical protein | uni | sce_3939 | 75.29 FIG1085109: hypothetical protein |
| SCE1572_3759 | FIG1085109: hypothetical protein | uni | sce_8592 | 67.9 FIG1085109: hypothetical protein |
| SCE1572_3760 | Adenosylhomocysteinase (EC 3.3.1.1) | - | | 0 |
| SCE1572_3761 | Patatin | bi | sce_3092 | 96.5 hypothetical protein |
| SCE1572_3762 | serine/threonine-protein kinase Pkn6 (EC:2.7.11.1) | bi | sce_3093 | 93.31 serine/threonine protein kinase |
| SCE1572_3763 | Membrane protein, distant similarity to thiosulphate quinone oxidoreductase DoxD | bi | sce_3100 | 80.85 Membrane protein, distant similarity to thiosulphate:quinone oxidoreductase DoxD |
| SCE1572_3764 | PAS/PAC sensor signal transduction histidine kinase (EC:2.7.13.3) | bi | sce_3101 | 77.67 PAS/PAC sensor signal transduction histidine kinase |
| SCE1572_3765 | Cell division protein FtsH (EC 3.4.24.-) | bi | sce_3102 | 94.27 Cell division protein FtsH (EC 3.4.24.-) |
| SCE1572_3766 | D-alanine--D-alanine ligase (EC 6.3.2.4) | bi | sce_3103 | 92.59 D-alanine--D-alanine ligase (EC 6.3.2.4) |
| SCE1572_3767 | putative acetyltransferase | bi | sce_3104 | 86.67 putative acetyltransferase |
| SCE1572_3768 | YihE protein, a ser/thr kinase implicated in LPS synthesis and Cpx signalling | bi | sce_3105 | 91.35 YihE protein, a ser/thr kinase implicated in LPS synthesis and Cpx signalling |
| SCE1572_3769 | hypothetical protein | bi | sce_3106 | 89.29 hypothetical protein |

| | | | | |
|--------------|--|-----|----------|--|
| SCE1572_3770 | hypothetical protein | - | | 0 |
| SCE1572_3771 | Serine/threonine protein kinase PknB (EC 2.7.11.1) | bi | sce_3107 | 84.41 Serine/threonine protein kinase PknB (EC 2.7.11.1) |
| SCE1572_3772 | hypothetical protein | bi | sce_3108 | 74.45 hypothetical protein |
| SCE1572_3773 | S-(hydroxymethyl)glutathione dehydrogenase (EC 1.1.1.284) | bi | sce_3109 | 97.3 S-(hydroxymethyl)glutathione dehydrogenase (EC 1.1.1.284) |
| SCE1572_3774 | Cytosol aminopeptidase PepA (EC 3.4.11.1) | bi | sce_3110 | 94.05 Cytosol aminopeptidase PepA (EC 3.4.11.1) |
| SCE1572_3775 | FIGO1087857: hypothetical protein | bi | sce_3111 | 79.68 FIGO1087857: hypothetical protein |
| SCE1572_3776 | hypothetical protein | bi | sce_3112 | 85.79 hypothetical protein |
| SCE1572_3777 | Glycine cleavage system transcriptional activator | bi | sce_3113 | 92.59 Glycine cleavage system transcriptional activator |
| SCE1572_3778 | FIGO1086569: hypothetical protein | bi | sce_3114 | 79.14 FIGO1086569: hypothetical protein |
| SCE1572_3779 | putative Fe-S oxidoreductase | bi | sce_3115 | 76.55 Predicted membrane protein |
| SCE1572_3780 | FIGO1087567: hypothetical protein | bi | sce_3116 | 88.64 FIGO1087567: hypothetical protein |
| SCE1572_3781 | DNA adenine methylase(EC:2.1.1.72) | bi | sce_3117 | 91.86 DNA adenine methylase(EC:2.1.1.72) |
| SCE1572_3782 | hypothetical protein | bi | sce_3118 | 87.93 FIGO1085157: hypothetical protein |
| SCE1572_3783 | hypothetical protein | - | | 0 |
| SCE1572_3784 | Putative Nudix hydrolase YfcD (EC 3.6.-.-) | bi | sce_3119 | 77.97 Putative Nudix hydrolase YfcD (EC 3.6.-.-) |
| SCE1572_3785 | Heat shock protein 60 family co-chaperone GroES | bi | sce_3120 | 98.98 Heat shock protein 60 family co-chaperone GroES |
| SCE1572_3786 | Heat shock protein 60 family chaperone GroEL | bi | sce_3121 | 95.73 Heat shock protein 60 family chaperone GroEL |
| SCE1572_3787 | cAMP-binding proteins - catabolite gene activator and regulatory subunit of cAMP-dependent protein kinases | bi | sce_3122 | 87.16 cAMP-binding proteins - catabolite gene activator and regulatory subunit of cAMP-dependent protein kinases |
| SCE1572_3788 | putative cAMP phosphodiesterases class-II | bi | sce_3123 | 94.9 putative cAMP phosphodiesterases class-II |
| SCE1572_3789 | Protein serine/threonine phosphatase PtpC, regulation of stationary phase | bi | sce_3124 | 99.24 Protein serine/threonine phosphatase PtpC, regulation of stationary phase |
| SCE1572_3790 | hypothetical protein | bi | sce_3126 | 91.94 hypothetical protein |
| SCE1572_3791 | Spermidine synthase (EC 2.5.1.16) | bi | sce_3127 | 94.82 Spermidine synthase (EC 2.5.1.16) |
| SCE1572_3792 | hypothetical protein | bi | sce_3128 | 84.31 hypothetical protein |
| SCE1572_3793 | hypothetical protein-transmembrane prediction | bi | sce_3129 | 91.84 hypothetical protein-transmembrane prediction |
| SCE1572_3794 | hypothetical protein | bi | sce_3130 | 91.18 FIGO1085339: hypothetical protein |
| SCE1572_3795 | hypothetical protein | bi | sce_3131 | 88.14 hypothetical protein |
| SCE1572_3796 | FIGO1086618: hypothetical protein | bi | sce_3132 | 81.87 FIGO1086618: hypothetical protein |
| SCE1572_3797 | Sensor protein of zinc sigma-54-dependent two-component system | bi | sce_3133 | 88.44 Sensor protein of zinc sigma-54-dependent two-component system |
| SCE1572_3798 | Response regulator of zinc sigma-54-dependent two-component system | bi | sce_3134 | 95.91 Response regulator of zinc sigma-54-dependent two-component system |
| SCE1572_3799 | UDP-glucose dehydrogenase (EC 1.1.1.22) | bi | sce_3135 | 97 UDP-glucose dehydrogenase (EC 1.1.1.22) |
| SCE1572_3800 | hypothetical protein | - | | 0 |
| SCE1572_3801 | hypothetical protein | bi | sce_5620 | 36.62 Predicted ATPase |
| SCE1572_3802 | hypothetical protein | uni | sce_5400 | 50 hypothetical protein |
| SCE1572_3803 | hypothetical protein | bi | sce_3137 | 77.67 hypothetical protein |
| SCE1572_3804 | hypothetical protein | uni | sce_3968 | 30.1 Putative Ferredoxin |
| SCE1572_3805 | hypothetical protein | bi | sce_3139 | 92.43 hypothetical protein |
| SCE1572_3806 | hypothetical protein | - | | 0 |
| SCE1572_3807 | Metalloprotease MEP2 | uni | sce_5178 | 48.23 Metalloprotease MEP2 |
| SCE1572_3808 | Serine/threonine-protein kinase pkn1 (EC 2.7.11.1) | bi | sce_3140 | 85.68 Serine/threonine-protein kinase pkn1 (EC 2.7.11.1) |
| SCE1572_3809 | hypothetical protein | bi | sce_3141 | 81.6 hypothetical protein |
| SCE1572_3810 | hypothetical protein | - | | 0 |
| SCE1572_3811 | transcriptional regulator, AraC family | uni | sce_3459 | 43.21 transcriptional regulator, AraC family protein |
| SCE1572_3812 | Histone acetyltransferase HPA2 and related acetyltransferases | - | | 0 |
| SCE1572_3813 | hypothetical protein | - | | 0 |
| SCE1572_3814 | Major facilitator family transporter | uni | sce_1384 | 27.92 D-galactonate transporter |
| SCE1572_3815 | Endo-1,4-beta-xylanase A precursor (EC 3.2.1.8) | bi | sce_2107 | 62.05 Endo-1,4-beta-xylanase A precursor (EC 3.2.1.8) |
| SCE1572_3816 | hypothetical protein | - | | 0 |
| SCE1572_3817 | hypothetical protein | bi | sce_4644 | 73.46 hypothetical protein |
| SCE1572_3818 | Probable ATP-dependent DNA helicase | bi | sce_3145 | 88.19 Probable ATP-dependent DNA helicase |
| SCE1572_3819 | PE-PGRS family protein | uni | sce_1146 | 37.08 GII0645 protein |
| SCE1572_3820 | Efflux transporter, RND family, MFP subunit, AcrA/E family | bi | sce_3147 | 84.5 Efflux transporter, RND family, MFP subunit, AcrA/E family |
| SCE1572_3821 | RND multidrug efflux transporter, Acriflavin resistance protein | bi | sce_3148 | 90.2 RND multidrug efflux transporter, Acriflavin resistance protein |
| SCE1572_3822 | COG2363 | bi | sce_3149 | 81.54 COG2363 |
| SCE1572_3823 | FIGO1087789: hypothetical protein | bi | sce_3151 | 85.31 FIGO1087789: hypothetical protein |
| SCE1572_3824 | Translation elongation factor P Lys34:lysine transferase | bi | sce_3152 | 92.23 Translation elongation factor P Lys34:lysine transferase |
| SCE1572_3825 | hypothetical protein | - | | 0 |
| SCE1572_3826 | FIGO1088368: hypothetical protein | bi | sce_3153 | 75.23 FIGO1088368: hypothetical protein |
| SCE1572_3827 | PE_PGRS family protein | bi | sce_3154 | 76.81 Arylsulfatase (EC 3.1.6.1) |
| SCE1572_3828 | CDP-diacylglycerol-glycerol-3-phosphate 3-phosphatidyltransferase (EC 2.7.8.5) | bi | sce_3155 | 96.77 CDP-diacylglycerol-glycerol-3-phosphate 3-phosphatidyltransferase (EC 2.7.8.5) |
| SCE1572_3829 | Very large tegument protein | bi | sce_3156 | 85.49 Very large tegument protein |
| SCE1572_3830 | Phosphoribosylformimino-5-aminoimidazole carboxamide ribotide isomerase (EC 5.3.1.16) | bi | sce_3157 | 95.85 Phosphoribosylformimino-5-aminoimidazole carboxamide ribotide isomerase (EC 5.3.1.16) |
| SCE1572_3831 | FIGO1084962: hypothetical protein | bi | sce_3158 | 81.52 FIGO1084962: hypothetical protein |
| SCE1572_3832 | Probable serine/threonine-protein kinase pknH (EC 2.7.11.1) | bi | sce_3159 | 83.94 Probable serine/threonine-protein kinase pknH (EC 2.7.11.1) |
| SCE1572_3833 | LOC432261 protein | bi | sce_3161 | 79.14 LOC432261 protein |
| SCE1572_3834 | hypothetical protein | - | | 0 |
| SCE1572_3835 | histidine kinase | uni | sce_7642 | 55.25 Chemotaxis protein methyltransferase CheR (EC 2.1.1.80) |
| SCE1572_3836 | hypothetical protein | - | | 0 |
| SCE1572_3837 | RsbR, positive regulator of sigma-B | uni | sce_7990 | 39.15 RsbR, positive regulator of sigma-B |
| SCE1572_3838 | hypothetical protein | - | | 0 |
| SCE1572_3839 | NAD-dependent protein deacetylase, SIR2 family | bi | sce_3162 | 92.83 putative Sir2-like transcriptional silencer protein |
| SCE1572_3840 | Xanthosine/inosine triphosphate pyrophosphatase | bi | sce_3163 | 85 Xanthosine/inosine triphosphate pyrophosphatase |
| SCE1572_3841 | Oxidoreductase | bi | sce_3164 | 90.14 Oxidoreductase |
| SCE1572_3842 | 2-hydroxy-3-keto-5-methylthiopentyl-1-phosphate phosphatase related protein | bi | sce_3165 | 79.04 2-hydroxy-3-keto-5-methylthiopentyl-1-phosphate phosphatase related protein |
| SCE1572_3843 | hypothetical protein | - | | 0 |
| SCE1572_3844 | Penicillin amidase(EC:3.5.1.11) | uni | sce_9234 | 29.93 Penicillin acylase II (EC 3.5.1.11) |
| SCE1572_3845 | Protein serine/threonine phosphatase PtpC, regulation of stationary phase | uni | sce_2269 | 37.55 Protein serine/threonine phosphatase PtpC, regulation of stationary phase |
| SCE1572_3846 | hypothetical protein | bi | sce_2595 | 29.96 Hydrolase (HAD superfamily) |
| SCE1572_3847 | probable conserved lipoprotein lppf | - | | 0 |
| SCE1572_3848 | probable general stress protein 26 | bi | sce_3166 | 89.24 General stress protein |
| SCE1572_3849 | Serine/threonine kinase with two-component sensor domain | bi | sce_3167 | 75.08 protein kinase |
| SCE1572_3850 | Imidazole glycerol phosphate synthase amidotransferase subunit (EC 2.4.2.-) | bi | sce_3168 | 88 Imidazole glycerol phosphate synthase amidotransferase subunit (EC 2.4.2.-) |
| SCE1572_3851 | Imidazoleglycerol-phosphate dehydratase (EC 4.2.1.19) | bi | sce_3169 | 96.92 Imidazoleglycerol-phosphate dehydratase (EC 4.2.1.19) |
| SCE1572_3852 | Serine/threonine-protein kinase pkn3 (EC 2.7.11.1) | bi | sce_3170 | 82.38 serine/threonine kinase Pkn10(EC:2.7.11.-) |
| SCE1572_3853 | Mucin 2 precursor | uni | sce_3170 | 50.45 serine/threonine kinase Pkn10(EC:2.7.11.-) |
| SCE1572_3854 | Dihydrolipoamide acetyltransferase component of pyruvate dehydrogenase complex (EC 2.3.1.12) | bi | sce_3171 | 76.96 Dihydrolipoamide acetyltransferase component of pyruvate dehydrogenase complex (EC 2.3.1.12) |
| SCE1572_3855 | Low-density lipoprotein receptor-related protein 1 precursor | bi | sce_3172 | 62.01 Low-density lipoprotein receptor-related protein 1 precursor |
| SCE1572_3856 | Thrombospondin-2 precursor (Corticotropin-induced secreted protein) (CISP) | bi | sce_3180 | 65.37 FIGO1089285: hypothetical protein |
| SCE1572_3857 | Outer membrane protein A-like protein | bi | sce_3181 | 84.5 Outer membrane protein A-like protein |
| SCE1572_3858 | S-layer protein | bi | sce_3182 | 84.82 S-layer protein |
| SCE1572_3859 | Low-density lipoprotein receptor-related protein 1 precursor | bi | sce_3183 | 78.4 Low-density lipoprotein receptor-related protein 1 precursor |
| SCE1572_3860 | FIGO1084940: hypothetical protein | bi | sce_3184 | 90.11 FIGO1084940: hypothetical protein |
| SCE1572_3861 | ATP-dependent protease La (EC 3.4.21.53) Type I | bi | sce_3185 | 98.38 ATP-dependent protease La (EC 3.4.21.53) Type I |
| SCE1572_3862 | 3-oxoacyl-[acyl-carrier protein] reductase (EC 1.1.1.100) | uni | sce_6012 | 34.38 Retinol dehydrogenase 13 (EC 1.1.1.-) |
| SCE1572_3863 | UvrD/REP helicase | bi | sce_3186 | 85.14 ATP-dependent nuclease, subunit A, putative |
| SCE1572_3864 | ATP-dependent nuclease subunit B-like | bi | sce_3187 | 86.62 Chromosome partition protein smc |
| SCE1572_3865 | hypothetical protein | - | | 0 |
| SCE1572_3866 | FIGO1087857: hypothetical protein | bi | sce_3188 | 78.4 FIGO1087857: hypothetical protein |
| SCE1572_3867 | protein of unknown function DUF583 | bi | sce_3189 | 86.67 protein of unknown function DUF583 |
| SCE1572_3868 | large tegument protein | bi | sce_3190 | 73.4 large tegument protein |
| SCE1572_3869 | protein of unknown function DUF99 | bi | sce_3191 | 87.96 protein of unknown function DUF99 |
| SCE1572_3870 | FIGO1088554: hypothetical protein | bi | sce_3192 | 77.09 FIGO1088554: hypothetical protein |
| SCE1572_3871 | Heme A synthase, cytochrome oxidase biogenesis protein Cox15-CtaA | bi | sce_3194 | 89.72 Heme A synthase, cytochrome oxidase biogenesis protein Cox15-CtaA |
| SCE1572_3872 | GGDEF/response regulator receiver domain protein | bi | sce_3195 | 89.51 GGDEF/response regulator receiver domain protein |
| SCE1572_3873 | Response regulator of zinc sigma-54-dependent two-component system | bi | sce_3196 | 82.42 Response regulator of zinc sigma-54-dependent two-component system |
| SCE1572_3874 | outer membrane efflux protein, putative | bi | sce_3197 | 91.79 outer membrane efflux protein, putative |
| SCE1572_3875 | Cytochrome c-type biogenesis protein CcmC, putative heme lyase for CcmE | bi | sce_3198 | 90.4 Cytochrome c-type biogenesis protein CcmC, putative heme lyase for CcmE |
| SCE1572_3876 | FIGO1087957: hypothetical protein | bi | sce_3199 | 89.13 FIGO1087957: hypothetical protein |
| SCE1572_3877 | hypothetical protein | bi | sce_3200 | 95.74 hypothetical protein |
| SCE1572_3878 | Butyryl-CoA dehydrogenase (EC 1.3.99.2) | bi | sce_3201 | 96.04 Butyryl-CoA dehydrogenase (EC 1.3.99.2) |
| SCE1572_3879 | hypothetical protein | bi | sce_3202 | 92.83 hypothetical protein |
| SCE1572_3880 | Protein serine/threonine phosphatase PtpC, regulation of stationary phase | bi | sce_3204 | 95.29 Protein serine/threonine phosphatase PtpC, regulation of stationary phase |
| SCE1572_3881 | pseudouridine synthase | bi | sce_3205 | 93.72 pseudouridine synthase |
| SCE1572_3882 | Muconate cycloisomerase (EC 5.5.1.1) | bi | sce_3206 | 92.33 Muconate cycloisomerase (EC 5.5.1.1) |
| SCE1572_3883 | thioredoxin family protein | bi | sce_3207 | 82.38 thioredoxin family protein |
| SCE1572_3884 | (3R)-hydroxymyristoyl-[acyl carrier protein] dehydratase (EC 4.2.1.-) | bi | sce_3208 | 94.84 (3R)-hydroxymyristoyl-[acyl carrier protein] dehydratase (EC 4.2.1.-) |
| SCE1572_3885 | Outer membrane protein H precursor | bi | sce_3209 | 93.23 Outer membrane protein H precursor |
| SCE1572_3886 | FIGO1088229: hypothetical protein | bi | sce_3210 | 79.73 FIGO1088229: hypothetical protein |
| SCE1572_3887 | Glutamate N-acetyltransferase (EC 2.3.1.35) / N-acetylglutamate synthase (EC 2.3.1.1) | bi | sce_3211 | 92.84 Glutamate N-acetyltransferase (EC 2.3.1.35) / N-acetylglutamate synthase (EC 2.3.1.1) |
| SCE1572_3888 | hypothetical protein | bi | sce_3212 | 81.23 hypothetical protein |
| SCE1572_3889 | FIGO1086572: hypothetical protein | bi | sce_3213 | 83.22 FIGO1086572: hypothetical protein |
| SCE1572_3890 | Mlr2351 protein | bi | sce_3215 | 73.63 hypothetical protein |
| SCE1572_3891 | Serine/threonine protein kinase (EC 2.7.11.1) | bi | sce_3216 | 92.23 Serine/threonine protein kinase (EC 2.7.11.1) |
| SCE1572_3892 | Fumarylacetoacetate hydrolase family protein | bi | sce_3221 | 90.33 Fumarylacetoacetate hydrolase family protein |
| SCE1572_3893 | Methyltransferase type 12 | bi | sce_3222 | 95.79 Methyltransferase type 12 |
| SCE1572_3894 | FIG00597249: hypothetical protein | bi | sce_3223 | 94.14 FIG00597249: hypothetical protein |
| SCE1572_3895 | Haloacid dehalogenase-like hydrolase | bi | sce_3224 | 85.49 Haloacid dehalogenase-like hydrolase |
| SCE1572_3896 | Similarity | bi | sce_3225 | 77.36 Similarity |
| SCE1572_3897 | phosphatidylinositol transfer protein | bi | sce_3226 | 87.75 Retinal degeneration B protein |
| SCE1572_3898 | hypothetical protein | bi | sce_3227 | 86.18 hypothetical protein |
| SCE1572_3899 | Serine protease inhibitor (serpin family) | bi | sce_3228 | 80.13 proteinase inhibitor I4, serpin |
| SCE1572_3900 | FIGO1085013: hypothetical protein | bi | sce_3229 | 72.91 FIGO1085013: hypothetical protein |
| SCE1572_3901 | hypothetical protein | bi | sce_3230 | 85.96 hypothetical protein |
| SCE1572_3902 | Glutathione S-transferase family protein SII1545 | uni | sce_5703 | 33.21 hypothetical protein |
| SCE1572_3903 | 8-amino-7-oxononanoate synthase (EC 2.3.1.47) | bi | sce_3232 | 92.61 8-amino-7-oxononanoate synthase (EC 2.3.1.47) |
| SCE1572_3904 | hypothetical protein | - | | 0 |
| SCE1572_3905 | Type IV fimbriae expression regulatory protein PilR | bi | sce_3234 | 98.01 Type IV fimbriae expression regulatory protein PilR |
| SCE1572_3906 | Predicted ATPase related to phosphate starvation-inducible protein PhoH | bi | sce_3235 | 97.72 Predicted ATPase related to phosphate starvation-inducible protein PhoH |
| SCE1572_3907 | FIGO1088085: hypothetical protein | bi | sce_3236 | 92.31 FIGO1088085: hypothetical protein |
| SCE1572_3908 | hypothetical protein | bi | sce_3238 | 90 hypothetical protein |
| SCE1572_3909 | ATP-dependent DNA helicase RecQ | bi | sce_3239 | 88.67 ATP-dependent DNA helicase RecQ |
| SCE1572_3910 | conserved unknownl protein | bi | sce_3240 | 93.39 Oxidoreductase (EC 1.1.1.-) |
| SCE1572_3911 | hypothetical protein | bi | sce_3241 | 89.53 hypothetical protein |
| SCE1572_3912 | FxsA protein | bi | sce_3242 | 83.5 FxsA protein |
| SCE1572_3913 | L-beta-lysine 5,6-aminomutase alpha subunit (EC 5.4.3.3) | bi | sce_3243 | 95.47 L-beta-lysine 5,6-aminomutase alpha subunit (EC 5.4.3.3) |
| SCE1572_3914 | L-beta-lysine 5,6-aminomutase beta subunit (EC 5.4.3.3) | bi | sce_3245 | 95.88 L-beta-lysine 5,6-aminomutase beta subunit (EC 5.4.3.3) |
| SCE1572_3915 | heat shock protein DnaJ-like protein | bi | sce_3246 | 84.5 hypothetical protein |
| SCE1572_3916 | Oxidoreductase, short chain dehydrogenase/reductase family | bi | sce_3247 | 95.73 Oxidoreductase, short chain dehydrogenase/reductase family |
| SCE1572_3917 | Splicing factor, proline- and glutamine-rich (Polypyrimidine tract-binding protein-associated-splicing factor) (PTB-associated)-bi | bi | sce_3249 | 91.42 Splicing factor, proline- and glutamine-rich (Polypyrimidine tract-binding protein-associated-splicing factor) (PTB-associated)-bi |
| SCE1572_3918 | conserved hypothetical protein | bi | sce_3250 | 97.45 hypothetical protein |
| SCE1572_3919 | hypothetical protein | bi | sce_3251 | 87.23 putative minor tail protein |
| SCE1572_3920 | conserved hypothetical protein | bi | sce_3252 | 86.53 conserved hypothetical protein |
| SCE1572_3921 | Heme O synthase, protoheme IX farnesyltransferase (EC 2.5.1.-) COX10-CtaB | bi | sce_3254 | 85.03 Heme O synthase, protoheme IX farnesyltransferase (EC 2.5.1.-) COX10-CtaB |
| SCE1572_3922 | Cytochrome oxidase biogenesis protein Sco1/SenC/PrrC, putative copper metallochaperone | bi | sce_3255 | 76.67 Cytochrome oxidase biogenesis protein Sco1/SenC/PrrC, putative copper metallochaperone |
| SCE1572_3923 | Response regulator of zinc sigma-54-dependent two-component system | bi | sce_3256 | 87.02 sigma-54 dependent DNA-binding response regulator |
| SCE1572_3924 | Putative membrane protein | bi | sce_3257 | 74.27 conserved hypothetical protein |
| SCE1572_3925 | FHA domain/GGDEF domain protein | bi | sce_3258 | 94.3 FHA domain/GGDEF domain protein |
| SCE1572_3926 | hypothetical protein | bi | sce_3259 | 72.18 hypothetical protein |
| SCE1572_3927 | hypothetical protein | bi | sce_3260 | 98.81 hypothetical protein |
| SCE1572_3928 | Cytochrome c family protein | bi | sce_3261 | 89.3 Cytochrome c family protein |
| SCE1572_3929 | FIGO1088576: hypothetical protein | bi | sce_3262 | 83.19 FIGO1088576: hypothetical protein |
| SCE1572_3930 | FIGO1087893: hypothetical protein | bi | sce_3263 | 90.51 FIGO1087893: hypothetical protein |
| SCE1572_3931 | hypothetical protein | bi | sce_3264 | 89.63 hypothetical protein |
| SCE1572_3932 | FIGO1085140: hypothetical protein | bi | sce_3265 | 91.99 FIGO1085140: hypothetical protein |
| SCE1572_3933 | Signal recognition particle receptor protein FtsY (=alpha subunit) (TC 3.A.5.1.1) | bi | sce_3267 | 91.03 Signal recognition particle receptor protein FtsY (=alpha subunit) (TC 3.A.5.1.1) |

| | | | | |
|--------------|---|-----|-----------|--|
| SCE1572_3934 | hypothetical protein | - | | 0 |
| SCE1572_3935 | hypothetical protein | bi | sce_3268 | 84.12 hypothetical protein |
| SCE1572_3936 | hypothetical protein | - | | 0 |
| SCE1572_3937 | FIGO1088207: hypothetical protein | bi | sce_3270 | 91.35 FIGO1088207: hypothetical protein |
| SCE1572_3938 | FIGO1086869: hypothetical protein | bi | sce_3271 | 92.73 FIGO1086869: hypothetical protein |
| SCE1572_3939 | UPF0102 protein SCO5602 | bi | sce_3272 | 88.79 UPF0102 protein SCO5602 |
| SCE1572_3940 | MEGF11 protein | bi | sce_3273 | 72.01 MEGF11 protein |
| SCE1572_3941 | FIGO1089532: hypothetical protein | bi | sce_3274 | 95.07 FIGO1089532: hypothetical protein |
| SCE1572_3942 | TPR domain protein, putative component of TonB system | bi | sce_3275 | 96.28 TPR domain protein, putative component of TonB system |
| SCE1572_3943 | FOG: TPR repeat | bi | sce_3276 | 93.31 COG0457: FOG: TPR repeat |
| SCE1572_3944 | hypothetical protein | bi | sce_3277 | 91.67 hypothetical protein |
| SCE1572_3945 | hypothetical abductin-like protein | bi | sce_3278 | 80.84 hypothetical abductin-like protein |
| SCE1572_3946 | TPR Domain containing protein | bi | sce_3279 | 96.01 TPR Domain containing protein |
| SCE1572_3947 | TPR domain protein, putative component of TonB system | bi | sce_3281 | 95.79 TPR domain protein, putative component of TonB system |
| SCE1572_3948 | serine/threonine protein kinase | bi | sce_3282 | 89.11 serine/threonine protein kinase |
| SCE1572_3949 | Adenylate cyclase (EC 4.6.1.1) / Guanylate cyclase (EC 4.6.1.2) | bi | sce_3283 | 93.44 Adenylate cyclase (EC 4.6.1.1) / Guanylate cyclase (EC 4.6.1.2) |
| SCE1572_3950 | hypothetical protein | bi | sce_3284 | 78.38 hypothetical protein |
| SCE1572_3951 | hypothetical protein | bi | sce_3285 | 92.19 hypothetical protein |
| SCE1572_3952 | hypothetical protein | bi | sce_3286 | 89.7 hypothetical protein |
| SCE1572_3953 | FIGO1087100: hypothetical protein | bi | sce_3287 | 80.31 GTP-binding protein EngA |
| SCE1572_3954 | hypothetical protein | - | | 0 |
| SCE1572_3955 | Rhs-family protein | bi | sce_121 | 39.54 Putative membrane protein |
| SCE1572_3956 | Rhs-family protein | umi | sce_10193 | 38.33 Rhs family carbohydrate-binding protein |
| SCE1572_3957 | hypothetical protein | - | | 0 |
| SCE1572_3958 | hypothetical protein | bi | sce_8665 | 38.03 hypothetical protein |
| SCE1572_3959 | Nitrogen regulation protein NR(I) | bi | sce_3289 | 92.38 Nitrogen regulation protein NR(I) |
| SCE1572_3960 | GI0645 protein | bi | sce_3290 | 49.5 Exoglucanase 3 precursor (EC 3.2.1.91) (Exocellobiohydrolase 3) (1,4-beta-cellobiohydrolase 3) |
| SCE1572_3961 | FIGO1086282: hypothetical protein | bi | sce_2530 | 77.09 FIGO1086282: hypothetical protein |
| SCE1572_3962 | Cellulose-binding domain protein | bi | sce_3292 | 86.42 Cellulose-binding domain protein |
| SCE1572_3963 | Tat (Twin-arginine translocation) pathway signal sequence domain protein | bi | sce_3293 | 85.68 Tat (Twin-arginine translocation) pathway signal sequence domain protein |
| SCE1572_3964 | SII0670 protein | bi | sce_3294 | 89.39 SII0670 protein |
| SCE1572_3965 | FIGO1086360: hypothetical protein | bi | sce_3295 | 83.9 FIGO1086360: hypothetical protein |
| SCE1572_3966 | hypothetical protein | umi | sce_5560 | 30.4 FIGO1087606: hypothetical protein |
| SCE1572_3967 | Proline-rich protein | bi | sce_10164 | 81.65 Proline-rich protein |
| SCE1572_3968 | Adenylate cyclase (EC 4.6.1.1) / Guanylate cyclase (EC 4.6.1.2) | bi | sce_3296 | 85.28 Adenylate cyclase (EC 4.6.1.1) / Guanylate cyclase (EC 4.6.1.2) |
| SCE1572_3969 | RsbR, positive regulator of sigma-B | bi | sce_3297 | 83.23 RsbR, positive regulator of sigma-B |
| SCE1572_3970 | hypothetical protein | bi | sce_3299 | 90 hypothetical protein |
| SCE1572_3971 | serine/threonine protein kinase | bi | sce_3300 | 95.23 serine/threonine protein kinase |
| SCE1572_3972 | Molybdenum cofactor biosynthesis protein MoaD | bi | sce_3301 | 95.18 Molybdenum cofactor biosynthesis protein MoaD |
| SCE1572_3973 | Molybdenum cofactor biosynthesis protein MoaA | bi | sce_3302 | 91.64 Molybdenum cofactor biosynthesis protein MoaA |
| SCE1572_3974 | Molybdenum cofactor biosynthesis protein MoaC | bi | sce_3303 | 94.15 Molybdenum cofactor biosynthesis protein MoaC |
| SCE1572_3975 | Molybdenum cofactor biosynthesis protein MoeE | bi | sce_3304 | 80 Molybdenum cofactor biosynthesis protein MoeE |
| SCE1572_3976 | Phosphate transport system regulatory protein PhoU | bi | sce_3305 | 94.61 Phosphate transport system regulatory protein PhoU |
| SCE1572_3977 | Phosphate transport ATP-binding protein PstB (TC 3.A.1.7.1) | bi | sce_3306 | 91.99 Phosphate transport ATP-binding protein PstB (TC 3.A.1.7.1) |
| SCE1572_3978 | Phosphate transport system permease protein PstA (TC 3.A.1.7.1) | bi | sce_3307 | 91.45 Phosphate transport system permease protein PstA (TC 3.A.1.7.1) |
| SCE1572_3979 | Phosphate transport system permease protein PstC (TC 3.A.1.7.1) | bi | sce_3308 | 89.69 Phosphate transport system permease protein PstC (TC 3.A.1.7.1) |
| SCE1572_3980 | Phosphate ABC transporter, periplasmic phosphate-binding protein PstS (TC 3.A.1.7.1) | bi | sce_3309 | 91.6 Phosphate ABC transporter, periplasmic phosphate-binding protein PstS (TC 3.A.1.7.1) |
| SCE1572_3981 | Phosphate regulon sensor protein PhoR (SphS) (EC 2.7.13.3) | bi | sce_3310 | 89.94 Phosphate regulon sensor protein PhoR (SphS) (EC 2.7.13.3) |
| SCE1572_3982 | Phosphate regulon transcriptional regulatory protein PhoB (SphR) | bi | sce_3311 | 98.24 Phosphate regulon transcriptional regulatory protein PhoB (SphR) |
| SCE1572_3983 | hypothetical protein | bi | sce_3314 | 88.89 hypothetical protein |
| SCE1572_3984 | 2,3,4,5-tetrahydropyridine-2,6-dicarboxylate N-succinyltransferase (EC 2.3.1.117) | bi | sce_3315 | 96.91 2,3,4,5-tetrahydropyridine-2,6-dicarboxylate N-succinyltransferase (EC 2.3.1.117) |
| SCE1572_3985 | N-succinyl-L,L-diaminopimelate desuccinylase (EC 3.5.1.18) | bi | sce_3316 | 93.19 N-succinyl-L,L-diaminopimelate desuccinylase (EC 3.5.1.18) |
| SCE1572_3986 | Phytochrome, two-component sensor histidine kinase (EC 2.7.3.-) | bi | sce_3317 | 87.42 Phytochrome, two-component sensor histidine kinase (EC 2.7.3.-) |
| SCE1572_3987 | Chemotaxis protein CheV (EC 2.7.3.-) | bi | sce_3318 | 93.06 Chemotaxis protein CheV (EC 2.7.3.-) |
| SCE1572_3988 | twitching motility protein PilH | bi | sce_3319 | 96.73 twitching motility protein PilH |
| SCE1572_3989 | sensor histidine kinase | bi | sce_3320 | 82.56 sensor histidine kinase |
| SCE1572_3990 | FrgA | bi | sce_3321 | 69.04 FrgA |
| SCE1572_3991 | DsbA oxidoreductase | bi | sce_3322 | 93.77 putative lipoprotein |
| SCE1572_3992 | hypothetical protein | bi | sce_3323 | 64.77 hypothetical protein |
| SCE1572_3993 | FIGO1086203: hypothetical protein | bi | sce_3324 | 76.54 FIGO1086203: hypothetical protein |
| SCE1572_3994 | hypothetical protein | bi | sce_3325 | 45.26 hypothetical protein |
| SCE1572_3995 | hypothetical protein | umi | sce_3858 | 38.34 Adenosylhomocysteinase (EC 3.3.1.1) |
| SCE1572_3996 | FIGO1089076: hypothetical protein | bi | sce_3326 | 66.47 FIGO1089076: hypothetical protein |
| SCE1572_3997 | FIGO1086567: hypothetical protein | bi | sce_3327 | 94.16 FIGO1086567: hypothetical protein |
| SCE1572_3998 | short chain dehydrogenase (EC 1.1.1.-) | bi | sce_3328 | 91.16 short chain dehydrogenase |
| SCE1572_3999 | Adenosylhomocysteinase (EC 3.3.1.1) | bi | sce_3329 | 97.49 Adenosylhomocysteinase (EC 3.3.1.1) |
| SCE1572_4000 | transcriptional regulator, ArsR family/methyltransferase, UbiE/COQ5 family | bi | sce_3330 | 92.68 Predicted regulator of methionine metabolism, ArsR family |
| SCE1572_4001 | peptidase, M16 (pitriylsin) family(EC:3.4.24.-) | bi | sce_3331 | 94.43 peptidase, M16 (pitriylsin) family(EC:3.4.24.-) |
| SCE1572_4002 | Peptidyl-prolyl cis-trans isomerase ppiD (EC 5.2.1.8) | bi | sce_3332 | 87.68 Peptidyl-prolyl cis-trans isomerase ppiD (EC 5.2.1.8) |
| SCE1572_4003 | FIGO1087034: hypothetical protein | bi | sce_3333 | 93.71 FIGO1087034: hypothetical protein |
| SCE1572_4004 | hypothetical protein | bi | sce_3334 | 66.67 hypothetical protein |
| SCE1572_4005 | hypothetical protein | bi | sce_3335 | 92.24 hypothetical protein |
| SCE1572_4006 | DinG family ATP-dependent helicase YoaA | bi | sce_3336 | 92.19 DinG family ATP-dependent helicase YoaA |
| SCE1572_4007 | FIGO1086441: hypothetical protein | bi | sce_3337 | 83.12 FIGO1086441: hypothetical protein |
| SCE1572_4008 | hypothetical protein | bi | sce_3338 | 84.34 hypothetical protein |
| SCE1572_4009 | PROBABLE OXIDOREDUCTASE GMC-TYPE (EC 1.-.-) | bi | sce_3339 | 91.24 Uncharacterized GMC-type oxidoreductase y4nJ (EC 1.1.-.-) |
| SCE1572_4010 | Response regulator of zinc sigma-54-dependent two-component system | bi | sce_3340 | 93.44 Response regulator of zinc sigma-54-dependent two-component system |
| SCE1572_4011 | Cell division protein FtsK | bi | sce_3341 | 84.34 Cell division protein FtsK |
| SCE1572_4012 | FIGO1089524: hypothetical protein | bi | sce_3342 | 86.06 FIGO1089524: hypothetical protein |
| SCE1572_4013 | hypothetical protein | bi | sce_3343 | 80.29 hypothetical protein |
| SCE1572_4014 | hypothetical protein | - | | 0 |
| SCE1572_4015 | putative lipoprotein | bi | sce_3344 | 93.83 FIGO0998302: hypothetical protein |
| SCE1572_4016 | Glutaredoxin-related protein | umi | sce_7244 | 53.76 Uncharacterized monothiol glutaredoxin ycf64-like |
| SCE1572_4017 | Uracyl-DNA glycosylase, family 5 | bi | sce_3345 | 88.1 Uracyl-DNA glycosylase, family 5 |
| SCE1572_4018 | Lipase precursor (EC 3.1.1.3) | bi | sce_3346 | 90.6 Lipase precursor (EC 3.1.1.3) |
| SCE1572_4019 | FIGO1086560: hypothetical protein | bi | sce_3347 | 82.43 FIGO1086560: hypothetical protein |
| SCE1572_4020 | Adenine phosphoribosyltransferase (EC 2.4.2.7) | bi | sce_3348 | 93.5 Adenine phosphoribosyltransferase (EC 2.4.2.7) |
| SCE1572_4021 | 5-nucleotidase SurE (EC 3.1.3.5) | bi | sce_3349 | 93.73 5-nucleotidase SurE (EC 3.1.3.5) |
| SCE1572_4022 | Aldehyde dehydrogenase (EC 1.2.1.3) | bi | sce_3350 | 88.59 Aldehyde dehydrogenase (EC 1.2.1.3) |
| SCE1572_4023 | alginate regulatory protein AlgP | bi | sce_3351 | 70.11 FIGO1087540: hypothetical protein |
| SCE1572_4024 | Cytochrome c551 peroxidase (EC 1.11.1.5) | bi | sce_3352 | 79.17 Cytochrome c551 peroxidase (EC 1.11.1.5) |
| SCE1572_4025 | outer membrane efflux protein | bi | sce_3353 | 60.14 outer membrane efflux protein |
| SCE1572_4026 | Pyrophosphate-energized proton pump (EC 3.6.1.1) | bi | sce_3354 | 97.15 Pyrophosphate-energized proton pump (EC 3.6.1.1) |
| SCE1572_4027 | Helicase, SNF2/RAD54 family | bi | sce_3355 | 98.02 Helicase, SNF2/RAD54 family |
| SCE1572_4028 | hypothetical protein | bi | sce_3356 | 95.02 hypothetical protein |
| SCE1572_4029 | hypothetical protein | bi | sce_3357 | 96.81 transport energizing protein, ExbD/TolR family |
| SCE1572_4030 | MotA/TolQ/ExbB proton channel family protein | bi | sce_3358 | 99.09 MotA/TolQ/ExbB proton channel family protein |
| SCE1572_4031 | MotA/TolQ/ExbB proton channel family protein | bi | sce_3360 | 100 MotA/TolQ/ExbB proton channel family protein |
| SCE1572_4032 | TolR protein | bi | sce_3361 | 96.3 TolR protein |
| SCE1572_4033 | Adventurous gliding motility protein S | umi | sce_3362 | 95.24 adventurous gliding motility protein S |
| SCE1572_4034 | adventurous gliding motility protein S | bi | sce_3362 | 99.44 adventurous gliding motility protein S |
| SCE1572_4035 | hypothetical protein | bi | sce_3363 | 95.48 hypothetical protein |
| SCE1572_4036 | D-glycerate 2-kinase (EC 2.7.1.-) | bi | sce_3364 | 87.26 D-glycerate 2-kinase (EC 2.7.1.-) |
| SCE1572_4037 | hypothetical protein | bi | sce_3365 | 73.44 hypothetical protein |
| SCE1572_4038 | Deoxyguanosinetriphosphate triphosphohydrolase (EC 3.1.5.1) | bi | sce_3366 | 95.03 Deoxyguanosinetriphosphate triphosphohydrolase (EC 3.1.5.1) |
| SCE1572_4039 | hypothetical protein | - | | 0 |
| SCE1572_4040 | hypothetical protein | - | | 0 |
| SCE1572_4041 | FIGO1085049: hypothetical protein | bi | sce_3368 | 98.17 FIGO1085049: hypothetical protein |
| SCE1572_4042 | hypothetical protein | - | | 0 |
| SCE1572_4043 | serine/threonine-protein kinase Pkn3 (EC:2.7.11.1) | bi | sce_3369 | 81.74 Serine/threonine-protein kinase pkn3 (EC 2.7.11.1) |
| SCE1572_4044 | DNA mismatch repair endonuclease Muth | bi | sce_3370 | 92.38 DNA mismatch repair endonuclease Muth |
| SCE1572_4045 | serine/threonine protein kinase | bi | sce_3372 | 92.67 serine/threonine protein kinase |
| SCE1572_4046 | hypothetical protein | - | | 0 |
| SCE1572_4047 | Kynureninase (EC 3.7.1.3) homolog | bi | sce_3374 | 87.5 Kynureninase (EC 3.7.1.3) homolog |
| SCE1572_4048 | iron permease FTR1 | bi | sce_5533 | 42.23 Cytochrome c family protein |
| SCE1572_4049 | FIGO1084932: hypothetical protein | bi | sce_3375 | 91.55 FIGO1084932: hypothetical protein |
| SCE1572_4050 | Phosphoenolpyruvate carboxykinase [GTP] (EC 4.1.1.32) | bi | sce_3376 | 90.58 Phosphoenolpyruvate carboxykinase [GTP] (EC 4.1.1.32) |
| SCE1572_4051 | regulatory protein, ArsR | bi | sce_3377 | 94.59 regulatory protein, ArsR |
| SCE1572_4052 | Octaprenyl-diphosphate synthase (EC 2.5.1.-) / Dimethylallyltransferase (EC 2.5.1.1) / Geranyltransferase (farnesyl)diphosphate | bi | sce_3378 | 93.3 Octaprenyl-diphosphate synthase (EC 2.5.1.-) / Dimethylallyltransferase (EC 2.5.1.1) / Geranyltransferase (farnesyl)diphosphate |
| SCE1572_4053 | Hydroxymethylglutaryl-CoA reductase (EC 1.1.1.34) | bi | sce_3379 | 91.15 Hydroxymethylglutaryl-CoA reductase (EC 1.1.1.34) |
| SCE1572_4054 | 2-heptaprenyl-1,4-naphthoquinone methyltransferase (EC 2.1.1.163) | bi | sce_3380 | 91.77 2-heptaprenyl-1,4-naphthoquinone methyltransferase (EC 2.1.1.163) |
| SCE1572_4055 | 2-succinyl-5-enolpyruvyl-6-hydroxy-3-cyclohexene-1-carboxylic-acid synthase (EC 2.2.1.9) | bi | sce_3381 | 89.38 2-succinyl-5-enolpyruvyl-6-hydroxy-3-cyclohexene-1-carboxylic-acid synthase (EC 2.2.1.9) |
| SCE1572_4056 | 1,4-dihydroxy-2-naphthoate octaprenyltransferase (EC 2.5.1.74) | bi | sce_3382 | 87.05 1,4-dihydroxy-2-naphthoate octaprenyltransferase (EC 2.5.1.74) |
| SCE1572_4057 | hypothetical protein | umi | sce_3383 | 68.42 O-succinylbenzoate synthase (EC 4.2.1.113) |
| SCE1572_4058 | O-succinylbenzoate synthase (EC 4.2.1.113) | bi | sce_3383 | 84.25 O-succinylbenzoate synthase (EC 4.2.1.113) |
| SCE1572_4059 | O-succinylbenzoic acid-CoA ligase (EC 6.2.1.26) | bi | sce_3384 | 88.05 O-succinylbenzoic acid-CoA ligase (EC 6.2.1.26) |
| SCE1572_4060 | 4-hydroxybenzoyl-CoA thioesterase family active site | bi | sce_3385 | 94.44 4-hydroxybenzoyl-CoA thioesterase family active site |
| SCE1572_4061 | FIGO1086129: hypothetical protein | bi | sce_3386 | 84.99 FIGO1086129: hypothetical protein |
| SCE1572_4062 | 1-acyl-sn-glycerol-3-phosphate acyltransferase (EC 2.3.1.51) | bi | sce_3387 | 89.71 1-acyl-sn-glycerol-3-phosphate acyltransferase (EC 2.3.1.51) |
| SCE1572_4063 | hypothetical protein | bi | sce_3388 | 80.1 hypothetical protein |
| SCE1572_4064 | hypothetical protein | - | | 0 |
| SCE1572_4065 | serine/threonine protein kinase with CHASE2 sensor | bi | sce_3390 | 76.53 putative serine/threonine protein kinase |
| SCE1572_4066 | TPR domain protein, putative component of TonB system | bi | sce_3391 | 92.56 TPR domain protein, putative component of TonB system |
| SCE1572_4067 | Twin-arginine translocation protein TatB | bi | sce_3392 | 89.05 integral membrane protein |
| SCE1572_4068 | NADH dehydrogenase (EC 1.6.99.3) | bi | sce_3393 | 85.17 NADH dehydrogenase (EC 1.6.99.3) |
| SCE1572_4069 | hypothetical protein | - | | 0 |
| SCE1572_4070 | FIGO1087510: hypothetical protein | bi | sce_3394 | 92.77 FIGO1087510: hypothetical protein |
| SCE1572_4071 | Chemotaxis regulator - transmits chemoreceptor signals to flagellar motor components CheY | bi | sce_3396 | 90.44 Chemotaxis regulator - transmits chemoreceptor signals to flagellar motor components CheY |
| SCE1572_4072 | Serine/threonine protein kinase PrkC, regulator of stationary phase | bi | sce_3397 | 69.8 serine/threonine-protein kinase Pkn6 (EC:2.7.11.1) |
| SCE1572_4073 | Biosynthetic Aromatic amino acid aminotransferase beta (EC 2.6.1.57) | bi | sce_3398 | 90.55 Biosynthetic Aromatic amino acid aminotransferase beta (EC 2.6.1.57) |
| SCE1572_4074 | FIGO1088642: hypothetical protein | bi | sce_3399 | 91.58 FIGO1088642: hypothetical protein |
| SCE1572_4075 | hypothetical protein | bi | sce_3401 | 91.43 hypothetical protein |
| SCE1572_4076 | hypothetical protein | - | | 0 |
| SCE1572_4077 | FIGO1089039: hypothetical protein | bi | sce_3403 | 75 FIGO1089039: hypothetical protein |
| SCE1572_4078 | L-asparaginase (EC 3.5.1.1) | bi | sce_3404 | 89.44 L-asparaginase (EC 3.5.1.1) |
| SCE1572_4079 | hypothetical protein | - | | 0 |
| SCE1572_4080 | 5-Enolpyruvylshikimate-3-phosphate synthase (EC 2.5.1.19) | bi | sce_3406 | 93.46 5-Enolpyruvylshikimate-3-phosphate synthase (EC 2.5.1.19) |
| SCE1572_4081 | hypothetical protein | umi | sce_1971 | 35.31 keratin associated protein |
| SCE1572_4082 | hypothetical protein | - | | 0 |
| SCE1572_4083 | hypothetical protein | - | | 0 |
| SCE1572_4084 | FIGO1085676: hypothetical protein | bi | sce_3407 | 82.7 FIGO1085676: hypothetical protein |
| SCE1572_4085 | Ferredoxin | bi | sce_3410 | 87.25 Ferredoxin |
| SCE1572_4086 | Predicted rhamnogalacturonan lyase in rhamnose utilization cluster | bi | sce_3412 | 83.99 Predicted rhamnogalacturonan lyase in rhamnose utilization cluster |
| SCE1572_4087 | Transcriptional regulator, AraC family | umi | sce_9985 | 37.69 Transcriptional regulator, AraC family |
| SCE1572_4088 | LamG domain protein jellyroll fold domain protein | umi | sce_615 | 35.52 peptidase, M19 family |
| SCE1572_4089 | FIGO1085103: hypothetical protein | bi | sce_3415 | 76.44 FIGO1085103: hypothetical protein |
| SCE1572_4090 | Ubiquinone/menaquinone biosynthesis methyltransferase | bi | sce_3416 | 89.3 Ubiquinone/menaquinone biosynthesis methyltransferase |
| SCE1572_4091 | Alpha-ketoglutarate-dependent taurine dioxygenase (EC 1.14.11.17) | bi | sce_3417 | 89.44 Alpha-ketoglutarate-dependent taurine dioxygenase (EC 1.14.11.17) |
| SCE1572_4092 | Copper-containing nitrite reductase (EC 1.7.2.1) | bi | sce_3418 | 85.86 Copper-containing nitrite reductase (EC 1.7.2.1) |
| SCE1572_4093 | hypothetical protein | umi | sce_3419 | 85.58 hypothetical protein |
| SCE1572_4094 | hypothetical protein | bi | sce_3419 | 90.61 hypothetical protein |
| SCE1572_4095 | hypothetical protein | bi | sce_3420 | 89.35 hypothetical protein |
| SCE1572_4096 | hypothetical protein | - | | 0 |
| SCE1572_4097 | hypothetical protein | - | | 0 |

| | | | | | |
|--------------|---|-----|----------|-------|---|
| SCE1572_4098 | putative lyase | bi | sce_3422 | 92.65 | putative lyase |
| SCE1572_4099 | O-methyltransferase | umi | sce_325 | 42.2 | O-methyltransferase |
| SCE1572_4100 | alpha amylase catalytic region | bi | sce_3438 | 78.59 | alpha amylase catalytic region |
| SCE1572_4101 | Cytochrome P450 | bi | sce_3439 | 86.94 | Cytochrome P450 |
| SCE1572_4102 | hypothetical protein | - | - | 0 | |
| SCE1572_4103 | periplasmic ATP/GTP-binding protein | umi | sce_1486 | 57.14 | VgrG protein |
| SCE1572_4104 | hypothetical protein | - | - | 0 | |
| SCE1572_4105 | Transcriptional regulator, AraC family | bi | sce_3459 | 81.42 | transcriptional regulator, AraC family protein |
| SCE1572_4106 | 5-aminopentanamide (EC 3.5.1.30) | umi | sce_4305 | 33.97 | 5-aminopentanamide (EC 3.5.1.30) |
| SCE1572_4107 | EBNA-1 | bi | sce_1137 | 60.29 | Uncharacterized protein with a C-terminal OMP (outer membrane protein) domain |
| SCE1572_4108 | hypothetical protein | - | - | 0 | |
| SCE1572_4109 | hypothetical protein | - | - | 0 | |
| SCE1572_4110 | FIG01085519: hypothetical protein | bi | sce_3461 | 78.75 | FIG01085519: hypothetical protein |
| SCE1572_4111 | polysaccharide export protein | bi | sce_3462 | 91.63 | polysaccharide export protein |
| SCE1572_4112 | Putative membrane protein of ExoQ family, involved in exopolysaccharide production | bi | sce_3463 | 85.94 | Putative membrane protein of ExoQ family, involved in exopolysaccharide production |
| SCE1572_4113 | hypothetical protein | bi | sce_3464 | 83.44 | hypothetical protein |
| SCE1572_4114 | Glutathione S-transferase (EC 2.5.1.18) | umi | sce_1670 | 37.26 | Glutathione S-transferase (EC 2.5.1.18) |
| SCE1572_4115 | N-acetylglucosamine-1-phosphate uridylyltransferase eukaryotic (EC 2.7.7.23) | bi | sce_3465 | 93.09 | N-acetylglucosamine-1-phosphate uridylyltransferase eukaryotic (EC 2.7.7.23) |
| SCE1572_4116 | PE_PGRS family protein | bi | sce_4897 | 69.14 | FIG01086098: hypothetical protein |
| SCE1572_4117 | hypothetical protein | umi | sce_9559 | 27.35 | Exonuclease SbcC |
| SCE1572_4118 | O-methyltransferase-related protein | bi | sce_3468 | 85.38 | O-methyltransferase-related protein |
| SCE1572_4119 | SSU ribosomal protein S4p (S9e) | bi | sce_3469 | 88.67 | SSU ribosomal protein S4p (S9e) |
| SCE1572_4120 | Cholesterol oxidase (EC 1.1.3.6) | umi | sce_581 | 31.67 | Polyhydroxyalkanoic acid synthase |
| SCE1572_4121 | phosphoesterase | bi | sce_8009 | 37.84 | Phosphoesterase family protein [EC:3.1.4.3] |
| SCE1572_4122 | Transcriptional regulator, PadR family | bi | sce_3467 | 93.59 | Transcriptional regulator, PadR family |
| SCE1572_4123 | hypothetical protein | - | - | 0 | |
| SCE1572_4124 | PIN (Pit N terminus) domain | - | - | 0 | |
| SCE1572_4125 | Tyrosine-protein kinase EpsD (EC 2.7.10.2) | bi | sce_3471 | 78.87 | tyrosine kinase(EC:2.7.1.112) |
| SCE1572_4126 | hypothetical protein | - | - | 0 | |
| SCE1572_4127 | hypothetical protein | - | - | 0 | |
| SCE1572_4128 | Lactoylglutathione lyase and related lyases | bi | sce_3472 | 84.51 | Lactoylglutathione lyase and related lyases |
| SCE1572_4129 | FIG00964757: hypothetical protein | bi | sce_3473 | 93.06 | FIG00964757: hypothetical protein |
| SCE1572_4130 | Protein serine/threonine phosphatase PrpC, regulation of stationary phase | bi | sce_3474 | 95.06 | Protein serine/threonine phosphatase PrpC, regulation of stationary phase |
| SCE1572_4131 | hypothetical protein | bi | sce_3475 | 89.87 | hypothetical protein |
| SCE1572_4132 | Glycosyltransferase (EC 2.4.1.-) | bi | sce_3476 | 95.25 | Glycosyltransferase (EC 2.4.1.-) |
| SCE1572_4133 | FIG01088564: hypothetical protein | bi | sce_3477 | 83.38 | FIG01088564: hypothetical protein |
| SCE1572_4134 | metallophosphoesterase | umi | sce_1117 | 26.16 | FIG01088538: hypothetical protein |
| SCE1572_4135 | hypothetical protein | - | - | 0 | |
| SCE1572_4136 | hypothetical protein | - | - | 0 | |
| SCE1572_4137 | hypothetical protein | bi | sce_3478 | 84.21 | hypothetical protein |
| SCE1572_4138 | PE-PGRS FAMILY PROTEIN | bi | sce_3483 | 89.59 | Fimh-like protein |
| SCE1572_4139 | hypothetical protein | bi | sce_3484 | 85.19 | hypothetical protein |
| SCE1572_4140 | conserved hypothetical protein | bi | sce_3485 | 88.92 | conserved hypothetical protein |
| SCE1572_4141 | 3-oxoacyl-(acyl-carrier-protein) synthase | bi | sce_3486 | 85.88 | 3-oxoacyl-(acyl-carrier-protein) synthase |
| SCE1572_4142 | hypothetical protein | - | - | 0 | |
| SCE1572_4143 | hypothetical protein | - | - | 0 | |
| SCE1572_4144 | hypothetical protein | umi | sce_2271 | 32.02 | hypothetical protein |
| SCE1572_4145 | FIG01085227: hypothetical protein | umi | sce_1006 | 69.75 | FIG01085227: hypothetical protein |
| SCE1572_4146 | hypothetical protein | - | - | 0 | |
| SCE1572_4147 | ADP-ribose 1"-phosphate phosphatase | bi | sce_7614 | 94.81 | ADP-ribose 1"-phosphate phosphatase |
| SCE1572_4148 | hypothetical protein | bi | sce_7615 | 96.05 | conserved hypothetical protein |
| SCE1572_4149 | hypothetical protein | - | - | 0 | |
| SCE1572_4150 | Transcriptional regulator, GntR family domain / Aspartate aminotransferase (EC 2.6.1.1) | umi | sce_1410 | 54.66 | Transcriptional regulator, GntR family domain / Aspartate aminotransferase (EC 2.6.1.1) |
| SCE1572_4151 | Outer membrane protein romA | bi | sce_3080 | 87.9 | Outer membrane protein romA |
| SCE1572_4152 | Transcriptional regulator, TetR family | bi | sce_8359 | 73.11 | Transcriptional regulator, TetR family |
| SCE1572_4153 | hypothetical protein | - | - | 0 | |
| SCE1572_4154 | hypothetical protein | - | - | 0 | |
| SCE1572_4155 | metallophosphoesterase | bi | sce_2035 | 76.12 | hypothetical protein |
| SCE1572_4156 | Tetratricopeptide TPR_2 repeat protein | bi | sce_3492 | 90.29 | Large extracellular alpha-helical protein |
| SCE1572_4157 | hypothetical protein | - | - | 0 | |
| SCE1572_4158 | hypothetical protein | bi | sce_2442 | 83.33 | hypothetical protein |
| SCE1572_4159 | GCNS-related N-acetyltransferase | - | - | 0 | |
| SCE1572_4160 | Transcriptional regulator, AraC family | umi | sce_7055 | 37.86 | Transcriptional regulator, AraC family |
| SCE1572_4161 | hypothetical protein | - | - | 0 | |
| SCE1572_4162 | 3-oxoacyl-[acyl-carrier protein] reductase (EC 1.1.1.100) | umi | sce_5211 | 44.27 | 3-oxoacyl-[acyl-carrier protein] reductase (EC 1.1.1.100) |
| SCE1572_4163 | putative cytochrome P450 hydroxylase | umi | sce_7075 | 48.22 | putative cytochrome P450 hydroxylase |
| SCE1572_4164 | Transcriptional regulator, LysR family | umi | sce_9329 | 38.7 | Transcriptional regulator, LysR family |
| SCE1572_4165 | 3-oxoacyl-[acyl-carrier protein] reductase (EC 1.1.1.100) | umi | sce_8328 | 38.65 | 3-oxoacyl-[acyl-carrier protein] reductase (EC 1.1.1.100) |
| SCE1572_4166 | hypothetical protein | bi | sce_9855 | 39.47 | FIG01088188: hypothetical protein |
| SCE1572_4167 | transcriptional regulator, AraC/XylS family | umi | sce_2490 | 37.86 | Transcriptional regulator, AraC family |
| SCE1572_4168 | hypothetical protein | - | - | 0 | |
| SCE1572_4169 | hypothetical protein | - | - | 0 | |
| SCE1572_4170 | hypothetical protein | - | - | 0 | |
| SCE1572_4171 | VgrG protein | bi | sce_3495 | 91.77 | VgrG protein |
| SCE1572_4172 | VgrG protein | bi | sce_3496 | 90.75 | VgrG protein |
| SCE1572_4173 | VgrG protein | bi | sce_3497 | 87.51 | VgrG protein |
| SCE1572_4174 | hypothetical protein | bi | sce_3498 | 71.36 | hypothetical protein |
| SCE1572_4175 | hypothetical protein | - | - | 0 | |
| SCE1572_4176 | hypothetical protein | - | - | 0 | |
| SCE1572_4177 | hypothetical protein | - | - | 0 | |
| SCE1572_4178 | hypothetical protein | - | - | 0 | |
| SCE1572_4179 | hypothetical protein | bi | sce_3503 | 59.2 | VgrG protein |
| SCE1572_4180 | hypothetical protein | bi | sce_3504 | 84 | hypothetical protein |
| SCE1572_4181 | hypothetical protein | bi | sce_3505 | 80.11 | FIG01087379: hypothetical protein |
| SCE1572_4182 | hypothetical protein | umi | sce_8826 | 37.15 | FIG01087894: hypothetical protein |
| SCE1572_4183 | hypothetical protein | - | - | 0 | |
| SCE1572_4184 | Outer membrane protein H precursor | bi | sce_3506 | 83.67 | Outer membrane protein H precursor |
| SCE1572_4185 | serine/threonine protein kinase | bi | sce_3507 | 83.48 | Serine/threonine protein kinase (EC 2.7.11.1) |
| SCE1572_4186 | hypothetical protein | bi | sce_3508 | 49.15 | FIG01089183: hypothetical protein |
| SCE1572_4187 | Protein serine/threonine phosphatase PrpC, regulation of stationary phase | bi | sce_3509 | 91.89 | Protein serine/threonine phosphatase PrpC, regulation of stationary phase |
| SCE1572_4188 | FIG01086348: hypothetical protein | bi | sce_3510 | 69.31 | FIG01086348: hypothetical protein |
| SCE1572_4189 | hypothetical protein | bi | sce_3511 | 70.61 | hypothetical protein |
| SCE1572_4190 | DNA mismatch repair protein MutS | bi | sce_3512 | 92.18 | DNA mismatch repair protein MutS |
| SCE1572_4191 | Hemagglutinin/hemolysin-related protein | bi | sce_3513 | 82.41 | Hemagglutinin/hemolysin-related protein |
| SCE1572_4192 | hypothetical protein | bi | sce_3514 | 86.38 | hypothetical protein |
| SCE1572_4193 | SSU ribosomal protein S2p (SAe) | bi | sce_3515 | 96.61 | SSU ribosomal protein S2p (SAe) |
| SCE1572_4194 | Translation elongation factor Ts | bi | sce_3516 | 86.39 | Translation elongation factor Ts |
| SCE1572_4195 | polysaccharide deacetylase domain protein | bi | sce_3517 | 90.42 | polysaccharide deacetylase domain protein |
| SCE1572_4196 | hypothetical protein | - | - | 0 | |
| SCE1572_4197 | hypothetical protein | - | - | 0 | |
| SCE1572_4198 | hypothetical protein | - | - | 0 | |
| SCE1572_4199 | hypothetical protein | bi | sce_3518 | 86.31 | hypothetical protein |
| SCE1572_4200 | conserved hypothetical protein | umi | sce_479 | 72.52 | FIG01088809: hypothetical protein |
| SCE1572_4201 | Protein crcB homolog | bi | sce_3519 | 88.89 | CrcB protein |
| SCE1572_4202 | AAA ATPase | bi | sce_3520 | 93.89 | AAA ATPase |
| SCE1572_4203 | Methionine ABC transporter ATP-binding protein | bi | sce_3521 | 95.42 | Methionine ABC transporter ATP-binding protein |
| SCE1572_4204 | hypothetical protein | bi | sce_3522 | 92.63 | hypothetical protein |
| SCE1572_4205 | Chemotaxis protein methyltransferase CheR (EC 2.1.1.80) | bi | sce_3523 | 90.58 | Chemotaxis protein methyltransferase CheR (EC 2.1.1.80) |
| SCE1572_4206 | [Protein-Pil] uridylyltransferase (EC 2.7.7.59) | bi | sce_3524 | 91.4 | [Protein-Pil] uridylyltransferase (EC 2.7.7.59) |
| SCE1572_4207 | Adenylate cyclase (EC 4.6.1.1) | bi | sce_3525 | 84.12 | Adenylate cyclase (EC 4.6.1.1) |
| SCE1572_4208 | Chromosome (plasmid) partitioning protein ParB / Stage 0 sporulation protein J | bi | sce_3526 | 96.69 | Chromosome (plasmid) partitioning protein ParB / Stage 0 sporulation protein J |
| SCE1572_4209 | Chromosome (plasmid) partitioning protein ParA | bi | sce_3527 | 90.68 | Chromosome (plasmid) partitioning protein ParA / Sporulation initiation inhibitor protein Soj |
| SCE1572_4210 | hypothetical protein | bi | sce_3528 | 90.74 | hypothetical protein |
| SCE1572_4211 | Cell division trigger factor (EC 5.2.1.8) | bi | sce_3529 | 96.21 | Cell division trigger factor (EC 5.2.1.8) |
| SCE1572_4212 | hypothetical protein | - | - | 0 | |
| SCE1572_4213 | ATP-dependent Clp protease proteolytic subunit (EC 3.4.21.92) | bi | sce_3531 | 99.53 | ATP-dependent Clp protease proteolytic subunit (EC 3.4.21.92) |
| SCE1572_4214 | hypothetical protein | - | - | 0 | |
| SCE1572_4215 | ATP-dependent Clp protease ATP-binding subunit ClpX | bi | sce_3533 | 99.28 | ATP-dependent Clp protease ATP-binding subunit ClpX |
| SCE1572_4216 | ATP-dependent protease La (EC 3.4.21.53) Type I | bi | sce_3534 | 99.28 | ATP-dependent protease La (EC 3.4.21.53) Type I |
| SCE1572_4217 | IMP cyclohydrolase (EC 3.5.4.10) / Phosphoribosylaminoimidazolecarboxamide formyltransferase (EC 2.1.2.3) | bi | sce_3535 | 91.68 | IMP cyclohydrolase (EC 3.5.4.10) / Phosphoribosylaminoimidazolecarboxamide formyltransferase (EC 2.1.2.3) |
| SCE1572_4218 | ParA family protein | bi | sce_3536 | 91.59 | ParA family protein |
| SCE1572_4219 | ParA family protein | umi | sce_3536 | 88.41 | ParA family protein |
| SCE1572_4220 | FIG01085099: hypothetical protein | bi | sce_3537 | 92.98 | FIG01085099: hypothetical protein |
| SCE1572_4221 | Putative membrane protein | bi | sce_3538 | 87.33 | Putative membrane protein |
| SCE1572_4222 | endoglucanase | umi | sce_1629 | 30.56 | Endo-1,4-beta-xylanase A precursor (EC 3.2.1.8) |
| SCE1572_4223 | FIG01088066: hypothetical protein | bi | sce_3539 | 79.17 | FIG01088066: hypothetical protein |
| SCE1572_4224 | hypothetical protein | - | - | 0 | |
| SCE1572_4225 | FIG01087393: hypothetical protein | bi | sce_3540 | 84.05 | FIG01087393: hypothetical protein |
| SCE1572_4226 | hypothetical protein | umi | sce_4880 | 30.8 | Gli0726 protein |
| SCE1572_4227 | Anaerobic dehydrogenases, typically selenocysteine-containing | bi | sce_3542 | 88.99 | Anaerobic dehydrogenases, typically selenocysteine-containing |
| SCE1572_4228 | Mtr2351 protein | bi | sce_1020 | 83.8 | Mtr2351 protein |
| SCE1572_4229 | VgrG protein | bi | sce_118 | 65.14 | VgrG protein |
| SCE1572_4230 | hypothetical protein | umi | sce_5081 | 41.5 | hypothetical protein |
| SCE1572_4231 | hypothetical protein | umi | sce_117 | 24.8 | VgrG protein |
| SCE1572_4232 | pentapeptide repeat family protein | umi | sce_116 | 43.23 | FIG01088201: hypothetical protein |
| SCE1572_4233 | hypothetical protein | umi | sce_115 | 44.73 | FIG01089519: hypothetical protein |
| SCE1572_4234 | hypothetical protein | bi | sce_114 | 43.05 | FIG01085979: hypothetical protein |
| SCE1572_4235 | hypothetical protein | bi | sce_113 | 65.44 | hypothetical protein |
| SCE1572_4236 | FIG01086136: hypothetical protein | bi | sce_3543 | 79.57 | FIG01086136: hypothetical protein |
| SCE1572_4237 | Ribosomal large subunit pseudouridine synthase D (EC 4.2.1.70) | bi | sce_3544 | 94 | Ribosomal large subunit pseudouridine synthase D (EC 4.2.1.70) |
| SCE1572_4238 | hypothetical protein | - | - | 0 | |
| SCE1572_4239 | putative secreted protein | bi | sce_3545 | 72.54 | putative secreted protein |
| SCE1572_4240 | FIG01086686: hypothetical protein | bi | sce_1034 | 71.13 | FIG01086686: hypothetical protein |
| SCE1572_4241 | hypothetical protein | - | - | 0 | |
| SCE1572_4242 | hypothetical protein | - | - | 0 | |
| SCE1572_4243 | hypothetical protein | umi | sce_4905 | 28.84 | FIG01086791: hypothetical protein |
| SCE1572_4244 | Glycogen synthase, ADP-glucose transglucosylase (EC 2.4.1.21) | bi | sce_3546 | 94.2 | Glycogen synthase, ADP-glucose transglucosylase (EC 2.4.1.21) |
| SCE1572_4245 | Conjugative transfer protein TrbI | bi | sce_3547 | 65.18 | Conjugative transfer protein TrbI |
| SCE1572_4246 | FIG01087712: hypothetical protein | bi | sce_3548 | 60.26 | FIG01087712: hypothetical protein |
| SCE1572_4247 | FIG01088142: hypothetical protein | bi | sce_3549 | 74.26 | FIG01088142: hypothetical protein |
| SCE1572_4248 | two-component sensor histidine kinase | bi | sce_3550 | 85.31 | sensory box histidine kinase |
| SCE1572_4249 | hypothetical protein | - | - | 0 | |
| SCE1572_4250 | GTP-binding protein related to HflX | bi | sce_3551 | 93.99 | GTP-binding protein related to HflX |
| SCE1572_4251 | hypothetical protein | bi | sce_3553 | 72.14 | hypothetical protein |
| SCE1572_4252 | response regulator receiver protein | bi | sce_3554 | 95.38 | CheY homolog |
| SCE1572_4253 | hypothetical protein | bi | sce_3555 | 60 | FIG01089493: hypothetical protein |
| SCE1572_4254 | Tail fiber protein | - | - | 0 | |
| SCE1572_4255 | hypothetical protein | bi | sce_3556 | 91.96 | hypothetical protein |
| SCE1572_4256 | FIG01085945: hypothetical protein | bi | sce_3557 | 90 | FIG01085945: hypothetical protein |
| SCE1572_4257 | hypothetical protein | bi | sce_3558 | 45.1 | hypothetical protein |
| SCE1572_4258 | SSU ribosomal protein S1p | bi | sce_3559 | 88.89 | SSU ribosomal protein S1p |
| SCE1572_4259 | hypothetical protein | - | - | 0 | |
| SCE1572_4260 | type III restriction enzyme, res subunit | bi | sce_9165 | 92.6 | helicase, DEAD/DEAH family |
| SCE1572_4261 | glycosyltransferase | - | - | 0 | |

| | | | | |
|--------------|---|-----|-----------|--|
| SCE1572_4262 | hypothetical protein | - | | 0 |
| SCE1572_4263 | Carbamoyltransferase | uni | sce_2688 | 28.48 Nodulation protein nolO (EC 2.1.3.-) |
| SCE1572_4264 | ArgE/DapE/Acy1 family protein | - | | 0 |
| SCE1572_4265 | Polysaccharide deacetylase | uni | sce_7862 | 29.94 FIG01086488: hypothetical protein |
| SCE1572_4266 | FIG00707640: hypothetical protein | uni | sce_8003 | 44.17 FIG01088889: hypothetical protein |
| SCE1572_4267 | hypothetical protein | - | | 0 |
| SCE1572_4268 | InterPro IPR000694:IPR006665 COGs COG2885 | uni | sce_4615 | 33.4 FIG01085999: hypothetical protein |
| SCE1572_4269 | 3-oxoacyl-(acyl-carrier-protein) synthase | uni | sce_10429 | 33.14 hypothetical protein |
| SCE1572_4270 | hypothetical protein | - | | 0 |
| SCE1572_4271 | hypothetical protein | - | | 0 |
| SCE1572_4272 | hypothetical protein | - | | 0 |
| SCE1572_4273 | hypothetical protein | uni | sce_4652 | 29.79 FIG01085963: hypothetical protein |
| SCE1572_4274 | Conserved domain protein | uni | sce_113 | 49.44 hypothetical protein |
| SCE1572_4275 | hypothetical protein | uni | sce_8351 | 38.51 hypothetical protein |
| SCE1572_4276 | VgrG protein | uni | sce_1338 | 34.88 VgrG protein |
| SCE1572_4277 | VgrG protein | uni | sce_3496 | 36.39 VgrG protein |
| SCE1572_4278 | VgrG protein | uni | sce_3496 | 33.94 VgrG protein |
| SCE1572_4279 | hypothetical protein | uni | sce_3498 | 30.94 hypothetical protein |
| SCE1572_4280 | hypothetical protein | uni | sce_3503 | 31.82 VgrG protein |
| SCE1572_4281 | hypothetical protein | uni | sce_3215 | 35 hypothetical protein |
| SCE1572_4282 | hypothetical protein | bi | sce_3583 | 93.91 hypothetical protein |
| SCE1572_4283 | hypothetical protein | - | | 0 |
| SCE1572_4284 | RsbR, positive regulator of sigma-B | uni | sce_2629 | 70.74 RsbR, positive regulator of sigma-B |
| SCE1572_4285 | hypothetical protein | uni | sce_3858 | 30.15 Adenosylhomocysteinase (EC 3.3.1.1) |
| SCE1572_4286 | hypothetical protein | - | | 0 |
| SCE1572_4287 | PBS lyase HEAT domain protein repeat-containing protein | bi | sce_2984 | 29.6 conserved hypothetical protein |
| SCE1572_4288 | FIG01085486: hypothetical protein | bi | sce_3587 | 89.12 FIG01088294: hypothetical protein |
| SCE1572_4289 | hypothetical protein | bi | sce_2038 | 82.39 FIG01084927: hypothetical protein |
| SCE1572_4290 | hypothetical protein | uni | sce_2040 | 36.54 hypothetical protein |
| SCE1572_4291 | hypothetical protein | uni | sce_2041 | 63.04 FIG01087636: hypothetical protein |
| SCE1572_4292 | Conserved domain protein | bi | sce_3630 | 93.77 Conserved domain protein |
| SCE1572_4293 | hypothetical protein | bi | sce_3631 | 96.97 hypothetical protein |
| SCE1572_4294 | Superfamily II DNA and RNA helicase | bi | sce_3632 | 96 Superfamily II DNA and RNA helicase |
| SCE1572_4295 | hypothetical protein | bi | sce_3633 | 92.41 conserved hypothetical protein |
| SCE1572_4296 | SMC domain protein | bi | sce_3634 | 91.25 hypothetical protein |
| SCE1572_4297 | hypothetical protein | - | | 0 |
| SCE1572_4298 | hypothetical protein | uni | sce_8407 | 46.15 hypothetical protein |
| SCE1572_4299 | FIG01150558: hypothetical protein | bi | sce_3635 | 86.31 FIG01150558: hypothetical protein |
| SCE1572_4300 | ATP-dependent RNA helicase, DEAD/DEAH box family | bi | sce_3636 | 97.69 ATP-dependent RNA helicase, DEAD/DEAH box family |
| SCE1572_4301 | Adenylate cyclase (EC 4.6.1.1) | bi | sce_3637 | 86.16 Adenylate cyclase (EC 4.6.1.1) |
| SCE1572_4302 | hypothetical protein | - | | 0 |
| SCE1572_4303 | Family with sequence similarity 118, member B | bi | sce_1742 | 36.84 hypothetical protein |
| SCE1572_4304 | hypothetical protein | bi | sce_6369 | 56.23 hypothetical protein |
| SCE1572_4305 | Chromosome partition protein MukB | bi | sce_6370 | 46.86 Chromosome partition protein MukB |
| SCE1572_4306 | Chromosome partition protein MukE | bi | sce_6371 | 59.21 Chromosome partition protein MukE |
| SCE1572_4307 | Chromosome partition protein MukF | bi | sce_6372 | 63.92 Chromosome partition protein MukF |
| SCE1572_4308 | hypothetical protein | - | | 0 |
| SCE1572_4309 | predicted protein | - | | 0 |
| SCE1572_4310 | hypothetical protein | uni | sce_4297 | 40.21 Putative 2-component regulator |
| SCE1572_4311 | 5-methylcytosine-specific restriction related enzyme | bi | sce_3642 | 87.24 5-methylcytosine-specific restriction related enzyme |
| SCE1572_4312 | Conserved domain protein | bi | sce_3643 | 89.96 Conserved domain protein |
| SCE1572_4313 | hypothetical protein | - | | 0 |
| SCE1572_4314 | 2-polypropyl-6-methoxyphenol hydroxylase and related FAD-dependent oxidoreductases | bi | sce_5479 | 92.65 2-polypropyl-6-methoxyphenol hydroxylase and related FAD-dependent oxidoreductases |
| SCE1572_4315 | hypothetical protein | bi | sce_5478 | 85.82 hypothetical protein |
| SCE1572_4316 | FmdC precursor | bi | sce_5477 | 85.07 FmdC precursor |
| SCE1572_4317 | Fumarylacetoacetate hydrolase family protein | bi | sce_5476 | 94.46 Fumarylacetoacetate hydrolase family protein |
| SCE1572_4318 | 4-hydroxyphenylpyruvate dioxygenase (EC 1.13.11.27) | uni | sce_5475 | 92.82 4-hydroxyphenylpyruvate dioxygenase (EC 1.13.11.27) |
| SCE1572_4319 | Homogentisate 1,2-dioxygenase (EC 1.13.11.5) | uni | sce_5474 | 90.13 Homogentisate 1,2-dioxygenase (EC 1.13.11.5) |
| SCE1572_4320 | VgrG protein | uni | sce_9510 | 50.74 VgrG protein |
| SCE1572_4321 | Predicted cell-wall-anchored protein SasA (LPXTG motif) | uni | sce_9301 | 41.12 Predicted cell-wall-anchored protein SasA (LPXTG motif) |
| SCE1572_4322 | pentapeptide repeat family protein | uni | sce_3055 | 49.69 hypothetical protein |
| SCE1572_4323 | hypothetical protein | uni | sce_9303 | 47.13 hypothetical protein |
| SCE1572_4324 | hypothetical protein | bi | sce_3057 | 56.98 hypothetical protein |
| SCE1572_4325 | Carboxyl-terminal protease (EC 3.4.21.102) | bi | sce_9304 | 46.22 carboxyl-terminal protease (EC 3.4.21.102) |
| SCE1572_4326 | Transcriptional regulator, LysR family | bi | sce_1249 | 49 Transcriptional regulator, LysR family |
| SCE1572_4327 | O-methyltransferase (EC 2.1.1.-) | bi | sce_3613 | 91.5 O-methyltransferase (EC 2.1.1.-) |
| SCE1572_4328 | Alcohol dehydrogenase (EC 1.1.1.1) | bi | sce_3644 | 83.24 Alcohol dehydrogenase (EC 1.1.1.1) |
| SCE1572_4329 | Transcriptional regulator, LysR family | bi | sce_3645 | 86.5 Transcriptional regulator, LysR family |
| SCE1572_4330 | hypothetical protein | - | | 0 |
| SCE1572_4331 | hypothetical protein | bi | sce_1730 | 89.86 hypothetical protein |
| SCE1572_4332 | Transcriptional regulator, LysR family | bi | sce_1731 | 93.25 Transcriptional regulator, LysR family |
| SCE1572_4333 | hypothetical protein | - | | 0 |
| SCE1572_4334 | Kynurenine formamidase, bacterial (EC 3.5.1.9) | bi | sce_1451 | 72.49 Kynurenine formamidase, bacterial (EC 3.5.1.9) |
| SCE1572_4335 | kelch domain protein | uni | sce_7673 | 40.17 FIG01085006: hypothetical protein |
| SCE1572_4336 | Hypothetical glycoside hydrolase, family 43, similar to arabinosidase | bi | sce_9941 | 73.59 Hypothetical glycoside hydrolase, family 43, similar to arabinosidase |
| SCE1572_4337 | hypothetical protein | - | | 0 |
| SCE1572_4338 | Transcriptional regulator, GntR family domain / Aspartate aminotransferase (EC 2.6.1.1) | bi | sce_3614 | 93.08 Transcriptional regulator, GntR family domain / Aspartate aminotransferase (EC 2.6.1.1) |
| SCE1572_4339 | Transporter, LysE family | bi | sce_3615 | 87.18 Transporter, LysE family |
| SCE1572_4340 | hypothetical protein | bi | sce_3617 | 82.83 putative protease |
| SCE1572_4341 | Response regulator of zinc sigma-54-dependent two-component system | bi | sce_3618 | 91.3 Response regulator of zinc sigma-54-dependent two-component system |
| SCE1572_4342 | Serine/threonine protein kinase | bi | sce_3619 | 80.57 Serine/threonine protein kinase PrkC, regulator of stationary phase |
| SCE1572_4343 | hypothetical protein | bi | sce_3620 | 42.33 FIG01086967: hypothetical protein |
| SCE1572_4344 | hypothetical protein | - | | 0 |
| SCE1572_4345 | ABC transporter, ATP-binding protein | bi | sce_6956 | 76.64 ABC transporter, ATP-binding protein |
| SCE1572_4346 | hypothetical protein | - | | 0 |
| SCE1572_4347 | FIG01089544: hypothetical protein | bi | sce_3647 | 80 FIG01089544: hypothetical protein |
| SCE1572_4348 | PUTATIVE OXIDOREDUCTASE PROTEIN | bi | sce_3648 | 88.46 PUTATIVE OXIDOREDUCTASE PROTEIN |
| SCE1572_4349 | sensor histidine kinase | uni | sce_7661 | 30.96 Signal transduction histidine kinase CheA (EC 2.7.3.-) |
| SCE1572_4350 | Serine/threonine protein kinase | bi | sce_8789 | 89.31 Adenylate cyclase (EC 4.6.1.1) / Guanylate cyclase (EC 4.6.1.2) |
| SCE1572_4351 | FIG01089454: hypothetical protein | bi | sce_8790 | 86.12 FIG01089454: hypothetical protein |
| SCE1572_4352 | hypothetical protein | - | | 0 |
| SCE1572_4353 | Glycine-rich cell wall structural protein 1 precursor | bi | sce_10400 | 80.37 Collagen triple helix repeat |
| SCE1572_4354 | hypothetical protein | - | | 0 |
| SCE1572_4355 | hypothetical protein | - | | 0 |
| SCE1572_4356 | Transcriptional regulator, TetR family | bi | sce_6224 | 42.2 Transcriptional regulator, TetR family |
| SCE1572_4357 | FIG01086876: hypothetical protein | bi | sce_4503 | 77.6 FIG01086876: hypothetical protein |
| SCE1572_4358 | FIG01089333: hypothetical protein | bi | sce_4502 | 80.47 FIG01089333: hypothetical protein |
| SCE1572_4359 | hypothetical protein | bi | sce_3650 | 72.46 hypothetical protein |
| SCE1572_4360 | FIG01085189: hypothetical protein | bi | sce_3651 | 91.44 FIG01085189: hypothetical protein |
| SCE1572_4361 | Hypothetical MbtH-like protein, PA2412 homolog | uni | sce_9233 | 80.95 Hypothetical MbtH-like protein, PA2412 homolog |
| SCE1572_4362 | hypothetical protein | - | | 0 |
| SCE1572_4363 | hypothetical protein | - | | 0 |
| SCE1572_4364 | lipoygenase family protein | - | | 0 |
| SCE1572_4365 | hypothetical protein | uni | sce_133 | 24.86 putative cytochrome P450 hydroxylase |
| SCE1572_4366 | Cell division protein FtsH (EC 3.4.24.-) | bi | sce_3652 | 60.68 Cell division protein FtsH (EC 3.4.24.-) |
| SCE1572_4367 | TonB family protein / TonB-dependent receptor | bi | sce_3653 | 87.86 TonB family protein / TonB-dependent receptor |
| SCE1572_4368 | Trk system potassium uptake protein TrkA | bi | sce_3654 | 94.71 Trk system potassium uptake protein TrkA |
| SCE1572_4369 | Inner spore coat protein H | bi | sce_3656 | 83.27 Inner spore coat protein H |
| SCE1572_4370 | transporter, major facilitator family | uni | sce_5480 | 30.06 3-hydroxyphenylpropionic acid transporter |
| SCE1572_4371 | hypothetical protein | - | | 0 |
| SCE1572_4372 | TPR repeat protein | bi | sce_1774 | 43.42 GIL2226 protein |
| SCE1572_4373 | hypothetical protein | - | | 0 |
| SCE1572_4374 | hypothetical protein | - | | 0 |
| SCE1572_4375 | Serine/threonine-protein kinase pkn2 (EC 2.7.11.1) | bi | sce_1768 | 50.93 Serine/threonine-protein kinase pkn2 (EC 2.7.11.1) |
| SCE1572_4376 | hypothetical protein | bi | sce_1773 | 40.68 FIG01086855: hypothetical protein |
| SCE1572_4377 | RsbR, positive regulator of sigma-B | uni | sce_202 | 69.36 RsbR, positive regulator of sigma-B |
| SCE1572_4378 | MbtH-like | bi | sce_7961 | 79.75 MbtH-like |
| SCE1572_4379 | hypothetical protein | bi | sce_2664 | 41.3 FIG01085004: hypothetical protein |
| SCE1572_4380 | Long-chain-fatty-acid-CoA ligase (EC 6.2.1.3) | uni | sce_9237 | 45.98 Long-chain-fatty-acid-CoA ligase (EC 6.2.1.3) |
| SCE1572_4381 | Malonyl CoA-acyl carrier protein transacylase (EC 2.3.1.39) | uni | sce_9236 | 53.45 Malonyl CoA-acyl carrier protein transacylase (EC 2.3.1.39) |
| SCE1572_4382 | Long-chain-fatty-acid-CoA ligase (EC 6.2.1.3) | uni | sce_9237 | 38.96 Long-chain-fatty-acid-CoA ligase (EC 6.2.1.3) |
| SCE1572_4383 | coproporphyrinogen III oxidase | uni | sce_4303 | 30 Hypothetical radical SAM family enzyme, NOT coproporphyrinogen III oxidase, oxygen-independent |
| SCE1572_4384 | SyrP-like protein | uni | sce_9232 | 47.16 syrP protein, putative |
| SCE1572_4385 | Long-chain-fatty-acid-CoA ligase (EC 6.2.1.3) | uni | sce_9231 | 36.13 Long-chain-fatty-acid-CoA ligase (EC 6.2.1.3) |
| SCE1572_4386 | Potassium channel beta chain | uni | sce_2194 | 44.51 putative oxidoreductase |
| SCE1572_4387 | Peptidyl-glycine alpha-amidating monooxygenase precursor (EC 1.14.17.3) | bi | sce_3657 | 81.26 Peptidyl-glycine alpha-amidating monooxygenase precursor (EC 1.14.17.3) |
| SCE1572_4388 | acetyltransferase, GNAT family | bi | sce_5785 | 80.12 Histone acetyltransferase HPA2 and related acetyltransferases |
| SCE1572_4389 | hypothetical protein | - | | 0 |
| SCE1572_4390 | RsbR, positive regulator of sigma-B | bi | sce_8231 | 68.94 RsbR, positive regulator of sigma-B |
| SCE1572_4391 | Potassium uptake protein, integral membrane component, KtrB | bi | sce_3655 | 79.54 Potassium uptake protein TrkH |
| SCE1572_4392 | Osmosensitive K channel histidine kinase KdpD (EC 2.7.3.-) | bi | sce_7959 | 79.43 Osmosensitive K channel histidine kinase KdpD (EC 2.7.3.-) |
| SCE1572_4393 | Putative membrane-bound ClpP-class protease associated with aq_911 | bi | sce_5977 | 45.63 Putative membrane-bound ClpP-class protease associated with aq_911 |
| SCE1572_4394 | DUF1432 domain-containing protein | bi | sce_5975 | 69.03 DUF1432 domain-containing protein |
| SCE1572_4395 | hypothetical protein | - | | 0 |
| SCE1572_4396 | Cell division protein FtsH (EC 3.4.24.-) | bi | sce_1708 | 80.95 hypothetical protein |
| SCE1572_4397 | Response regulator of zinc sigma-54-dependent two-component system | bi | sce_3659 | 94.31 Response regulator of zinc sigma-54-dependent two-component system |
| SCE1572_4398 | sensor histidine kinase | bi | sce_3660 | 93.06 sensor histidine kinase |
| SCE1572_4399 | hypothetical protein | uni | sce_9725 | 32.88 Fibrillin 1 precursor |
| SCE1572_4400 | General secretion pathway protein C | bi | sce_3662 | 83.94 General secretion pathway protein C |
| SCE1572_4401 | hypothetical protein | bi | sce_3663 | 90.13 hypothetical protein |
| SCE1572_4402 | Transcriptional regulator, AraC family | uni | sce_9883 | 34.07 FIG01086649: hypothetical protein |
| SCE1572_4403 | conserved hypothetical protein | - | | 0 |
| SCE1572_4404 | hypothetical protein | - | | 0 |
| SCE1572_4405 | Dihydrofolate reductase (EC 1.5.1.3) | uni | sce_10151 | 33.17 Dihydrofolate reductase (EC 1.5.1.3) |
| SCE1572_4406 | putative signal-transduction protein with CBS domains | uni | sce_2600 | 48.57 putative signal-transduction protein with CBS domains |
| SCE1572_4407 | hypothetical protein | - | | 0 |
| SCE1572_4408 | unknown | - | | 0 |
| SCE1572_4409 | hypothetical protein | - | | 0 |
| SCE1572_4410 | hypothetical protein | - | | 0 |
| SCE1572_4411 | hypothetical protein | uni | sce_3929 | 27.9 Putative transport protein |
| SCE1572_4412 | hypothetical protein | - | | 0 |
| SCE1572_4413 | monovalent cation/proton antiporter, MnhG/PhaG subunit | uni | sce_2149 | 41.57 Na() H() antiporter subunit G |
| SCE1572_4414 | multiple resistance and pH regulation related protein MrpF | uni | sce_2150 | 34.57 Na() H() antiporter subunit F |
| SCE1572_4415 | Na() H() antiporter subunit E | uni | sce_2151 | 33.33 Na() H() antiporter subunit E |
| SCE1572_4416 | Na() H() antiporter subunit D | uni | sce_2152 | 44.4 Na() H() antiporter subunit D |
| SCE1572_4417 | Na() H() antiporter subunit C | uni | sce_2153 | 48.51 Na() H() antiporter subunit C |
| SCE1572_4418 | Na? antiporter MnhB subunit-related protein | uni | sce_9585 | 38.1 Na() H() antiporter subunit A; Na() H() antiporter subunit B |
| SCE1572_4419 | Na() H() antiporter subunit A; Na() H() antiporter subunit B | uni | sce_2155 | 38.55 Na() H() antiporter subunit A |
| SCE1572_4420 | hypothetical protein | - | | 0 |
| SCE1572_4421 | Assimilatory nitrate reductase large subunit (EC:1.7.99.4) | - | | 0 |
| SCE1572_4422 | hypothetical protein | uni | sce_1292 | 25 FIG01085806: hypothetical protein |
| SCE1572_4423 | hypothetical protein | - | | 0 |
| SCE1572_4424 | Alpha, alpha-trehalose-phosphate synthase [UDP-forming] (EC 2.4.1.15) / Trehalose-6-phosphate phosphatase (EC 3.1.3.12) | bi | sce_3665 | 85.9 Alpha, alpha-trehalose-phosphate synthase [UDP-forming] (EC 2.4.1.15) / Trehalose-6-phosphate phosphatase (EC 3.1.3.12) |
| SCE1572_4425 | hypothetical protein | - | | 0 |

| | | | | |
|--------------|--|----|-----------|---|
| SCE1572_4426 | possible methyltransferase | bi | see_7566 | 92.34 possible methyltransferase |
| SCE1572_4427 | Transcriptional regulator, LysR family | bi | see_7565 | 92.43 transcriptional regulator, LysR family |
| SCE1572_4428 | hypothetical protein | - | - | 0 |
| SCE1572_4429 | Na ⁺ antiporter NhaA type | bi | see_3666 | 91.2 Na ⁺ antiporter NhaA type |
| SCE1572_4430 | hypothetical protein | bi | see_3667 | 87.32 hypothetical protein |
| SCE1572_4431 | Phosphoglycerate mutase | bi | see_3668 | 91.1 Phosphoglycerate mutase |
| SCE1572_4432 | anti-sigma-factor antagonist | um | see_5951 | 37.44 RsbK, positive regulator of sigma-B |
| SCE1572_4433 | RsbR, positive regulator of sigma-B | um | see_7990 | 51.32 RsbR, positive regulator of sigma-B |
| SCE1572_4434 | Tat (Twin-arginine translocation) pathway signal sequence domain protein | um | see_7318 | 85.94 Tat (Twin-arginine translocation) pathway signal sequence domain protein |
| SCE1572_4435 | tRNA pseudouridine synthase A (EC 4.2.1.70) | bi | see_1685 | 44.78 tRNA pseudouridine synthase A (EC 4.2.1.70) |
| SCE1572_4436 | hypothetical protein | um | see_3858 | 28.65 Adenosylhomocysteinase (EC 3.3.1.1) |
| SCE1572_4437 | hypothetical protein | um | see_6493 | 41.44 Translation initiation factor 2 |
| SCE1572_4438 | integrins alpha chain | bi | see_5548 | 27.44 probable aggregation factor core protein MAFp3, isoform C |
| SCE1572_4439 | probable tonB-dependent receptor signal peptide protein, putative | um | see_6504 | 31.5 TonB-dependent receptor; Outer membrane receptor for ferrienterochelin and colicins |
| SCE1572_4440 | L-sorbose dehydrogenase | bi | see_3676 | 90.6 L-sorbose dehydrogenase |
| SCE1572_4441 | transcriptional regulator, Fis family | bi | see_3678 | 87.14 Anaerobic nitric oxide reductase transcription regulator NorR |
| SCE1572_4442 | Nitric-oxide reductase (EC 1.7.99.7), quinol-dependent | bi | see_3679 | 92.75 Nitric-oxide reductase (EC 1.7.99.7), quinol-dependent |
| SCE1572_4443 | FIG01089063: hypothetical protein | bi | see_6978 | 69.29 FIG01089063: hypothetical protein |
| SCE1572_4444 | Propionyl-CoA carboxylase biotin-containing subunit (EC 6.4.1.3) | bi | see_3689 | 89.6 Propionyl-CoA carboxylase biotin-containing subunit (EC 6.4.1.3) |
| SCE1572_4445 | Propionyl-CoA carboxylase carboxyl transferase subunit (EC 6.4.1.3) | bi | see_3690 | 95.76 Propionyl-CoA carboxylase carboxyl transferase subunit (EC 6.4.1.3) |
| SCE1572_4446 | hypothetical protein | - | - | 0 |
| SCE1572_4447 | 4-hydroxybutyrate coenzyme A transferase | bi | see_3691 | 93.3 4-hydroxybutyrate coenzyme A transferase |
| SCE1572_4448 | tRNA nucleotidyltransferase, A-adding (EC 2.7.7.25) | bi | see_3692 | 89.55 tRNA nucleotidyltransferase, A-adding (EC 2.7.7.25) |
| SCE1572_4449 | hypothetical protein | bi | see_4170 | 88.06 hypothetical protein |
| SCE1572_4450 | hypothetical protein | um | see_4542 | 82.01 hypothetical protein |
| SCE1572_4451 | hypothetical protein | - | - | 0 |
| SCE1572_4452 | hypothetical protein | bi | see_9472 | 71.53 hypothetical protein |
| SCE1572_4453 | Inosine-5-'-monophosphate dehydrogenase (EC 1.1.1.205) | bi | see_3693 | 72.76 Inosine-5-'-monophosphate dehydrogenase (EC 1.1.1.205) |
| SCE1572_4454 | Universal stress protein family | bi | see_3694 | 86.49 Universal stress protein family |
| SCE1572_4455 | EBN-1 | bi | see_3696 | 77.21 Aspartyl-tRNA(Asn) amidotransferase subunit A (EC 6.3.5.6) @ Glutamyl-tRNA(Gln) amidotransferase subunit A (EC 6.3.5.7) |
| SCE1572_4456 | FIG01088460: hypothetical protein | bi | see_3699 | 63.19 FIG01088460: hypothetical protein |
| SCE1572_4457 | hypothetical protein | - | - | 0 |
| SCE1572_4458 | Phenylpropanoate dioxygenase and related ring-hydroxylating dioxygenases, large terminal subunit | bi | see_3700 | 89.39 Phenylpropanoate dioxygenase and related ring-hydroxylating dioxygenases, large terminal subunit |
| SCE1572_4459 | FIG01089697: hypothetical protein | bi | see_3702 | 88.6 FIG01089697: hypothetical protein |
| SCE1572_4460 | hypothetical protein | bi | see_7662 | 59.57 Transcriptional regulator |
| SCE1572_4461 | beta-1,3-1,4-glucanase | bi | see_3220 | 54.17 Xylanase |
| SCE1572_4462 | hypothetical protein | - | - | 0 |
| SCE1572_4463 | serine/threonine protein kinase | bi | see_7475 | 64.77 serine/threonine protein kinase |
| SCE1572_4464 | beta-lactamase | um | see_1658 | 35.44 Beta-lactamase class C and other penicillin binding proteins |
| SCE1572_4465 | Phytochrome, two-component sensor histidine kinase (EC 2.7.3.-); Cyanobacterial phytochrome B | um | see_10379 | 55.46 Two-component sensor histidine kinase |
| SCE1572_4466 | FIG01088674: hypothetical protein | bi | see_3703 | 90.06 FIG01088674: hypothetical protein |
| SCE1572_4467 | conserved hypothetical protein | um | see_2593 | 43.03 FIG01087338: hypothetical protein |
| SCE1572_4468 | transcriptional regulator, LysR family | um | see_8721 | 37.5 LysR-family transcriptional regulator |
| SCE1572_4469 | FIG01085379: hypothetical protein | um | see_7563 | 58.92 FIG01085379: hypothetical protein |
| SCE1572_4470 | hypothetical protein | bi | see_3713 | 75.39 hypothetical protein |
| SCE1572_4471 | FIG01086929: hypothetical protein | bi | see_3714 | 83.69 FIG01086929: hypothetical protein |
| SCE1572_4472 | transcriptional regulator, LysR family | um | see_3645 | 40.48 Transcriptional regulator, LysR family |
| SCE1572_4473 | 4-oxalocrotonate tautomerase | - | - | 0 |
| SCE1572_4474 | hypothetical protein | bi | see_5993 | 76.03 Endo-1,4-beta-xylanase A precursor (EC 3.2.1.8) |
| SCE1572_4475 | Endo-1,4-beta-xylanase A precursor (EC 3.2.1.8) | - | - | 0 |
| SCE1572_4476 | Transcriptional regulator, AraC family | bi | see_1358 | 45.02 Transcriptional regulator, AraC family |
| SCE1572_4477 | Oxidoreductase | um | see_4749 | 43.48 Oxidoreductase |
| SCE1572_4478 | RNA polymerase sigma factor RpoE | um | see_6103 | 63.96 RNA polymerase sigma factor RpoE |
| SCE1572_4479 | FIG01088605: hypothetical protein | um | see_4099 | 45.15 FIG01086011: hypothetical protein |
| SCE1572_4480 | Flagellar hook-length control protein FlkK | bi | see_6105 | 41.32 Extensin-like protein precursor |
| SCE1572_4481 | MEGF11 protein | um | see_3273 | 48.28 MEGF11 protein |
| SCE1572_4482 | High-affinity branched-chain amino acid transport system permease protein LivH (TC 3.A.1.4.1) | um | see_9290 | 34.25 High-affinity branched-chain amino acid transport system permease protein LivH (TC 3.A.1.4.1) |
| SCE1572_4483 | Branched-chain amino acid transport system permease protein LivM (TC 3.A.1.4.1) | um | see_9613 | 31.82 Branched-chain amino acid transport system permease protein LivM (TC 3.A.1.4.1) |
| SCE1572_4484 | Branched-chain amino acid transport ATP-binding protein LivG (TC 3.A.1.4.1) | um | see_9614 | 42 Branched-chain amino acid transport ATP-binding protein LivG (TC 3.A.1.4.1) |
| SCE1572_4485 | Branched-chain amino acid transport ATP-binding protein LivF (TC 3.A.1.4.1) | um | see_9615 | 47.41 Branched-chain amino acid transport ATP-binding protein LivF (TC 3.A.1.4.1) |
| SCE1572_4486 | FIG01087458: hypothetical protein | bi | see_7885 | 87.35 FIG01087458: hypothetical protein |
| SCE1572_4487 | FIG01086607: hypothetical protein | bi | see_3726 | 82.24 FIG01086607: hypothetical protein |
| SCE1572_4488 | Endo-1,4-beta-xylanase A precursor (EC 3.2.1.8) | um | see_5146 | 73.9 Endo-1,4-beta-xylanase A precursor (EC 3.2.1.8) |
| SCE1572_4489 | Similarity | bi | see_3719 | 67.91 Similarity |
| SCE1572_4490 | Pirin-like protein | bi | see_7400 | 64.26 Pirin, N-terminal:Pirin, C-terminal |
| SCE1572_4491 | DNA-binding response regulator, AraC family | bi | see_6061 | 67.42 Transcriptional regulator, AraC family |
| SCE1572_4492 | 3-oxoacyl-[acyl-carrier protein] reductase (EC 1.1.1.100) | um | see_2920 | 37.4 short-chain dehydrogenase |
| SCE1572_4493 | serine/threonine protein kinase | bi | see_2657 | 66.97 serine/threonine protein kinase |
| SCE1572_4494 | methyltransferase | um | see_7608 | 38.82 Methyltransferase type 11 |
| SCE1572_4495 | Similarity with glutathionylspermidine synthase (EC 6.3.1.8), group 2 | bi | see_3745 | 92.75 Similarity with glutathionylspermidine synthase (EC 6.3.1.8), group 2 |
| SCE1572_4496 | FIG01086440: hypothetical protein | bi | see_3746 | 95.76 FIG01086440: hypothetical protein |
| SCE1572_4497 | hypothetical protein | bi | see_3747 | 84.39 FIG01089697: hypothetical protein |
| SCE1572_4498 | hypothetical protein | bi | see_3748 | 85.62 hypothetical protein |
| SCE1572_4499 | hypothetical protein | bi | see_3749 | 86.84 hypothetical protein |
| SCE1572_4500 | FIG01085602: hypothetical protein | bi | see_3763 | 84.47 FIG01085602: hypothetical protein |
| SCE1572_4501 | Septum site-determining protein MinC | bi | see_3764 | 92.17 Septum site-determining protein MinC |
| SCE1572_4502 | hypothetical protein | - | - | 0 |
| SCE1572_4503 | conserved hypothetical protein SCD8A_23 | um | see_10344 | 51.49 Invasin |
| SCE1572_4504 | Dipeptide-binding ABC transporter, periplasmic substrate-binding component (TC 3.A.1.5.2) | bi | see_3765 | 84.34 Dipeptide-binding ABC transporter, periplasmic substrate-binding component (TC 3.A.1.5.2) |
| SCE1572_4505 | hypothetical protein | - | - | 0 |
| SCE1572_4506 | Kynurenine formamidase, bacterial (EC 3.5.1.9) | um | see_1451 | 32.98 Kynurenine formamidase, bacterial (EC 3.5.1.9) |
| SCE1572_4507 | hypothetical protein | bi | see_3766 | 93.46 hypothetical protein |
| SCE1572_4508 | hypothetical protein | bi | see_3767 | 50.68 hypothetical protein |
| SCE1572_4509 | Uncharacterized domain COG3236 / GTP cyclohydrolase II (EC 3.5.4.25) | um | see_3769 | 93.1 Uncharacterized domain COG3236 / GTP cyclohydrolase II (EC 3.5.4.25) |
| SCE1572_4510 | Xylose ABC transporter, substrate-binding component | bi | see_7038 | 72.13 hypothetical protein |
| SCE1572_4511 | peptidase, S1 (chymotrypsin) family(EC:3.4.21.-) | um | see_8300 | 32.17 Trypsin-2 precursor (EC 3.4.21.4) |
| SCE1572_4512 | hypothetical protein | - | - | 0 |
| SCE1572_4513 | hypothetical protein | - | - | 0 |
| SCE1572_4514 | Septum site-determining protein MinD | bi | see_3771 | 93.43 Septum site-determining protein MinD |
| SCE1572_4515 | Cell division topological specificity factor MinE | bi | see_3772 | 96.12 Cell division topological specificity factor MinE |
| SCE1572_4516 | SWIM zinc finger domain protein | bi | see_3773 | 82.24 SWIM Zn-finger |
| SCE1572_4517 | Helicase, SNF2/RAD54 family | bi | see_3774 | 85.33 Helicase, SNF2/RAD54 family |
| SCE1572_4518 | hypothetical protein | um | see_1971 | 35 keratin associated protein |
| SCE1572_4519 | Putative gluconolactonase (EC:3.1.1.17) | bi | see_3778 | 86.44 Putative gluconolactonase(EC:3.1.1.17) |
| SCE1572_4520 | Putative preQ0 transporter | bi | see_8632 | 88.34 Putative preQ0 transporter |
| SCE1572_4521 | L-asparaginase (EC 3.5.1.1) | bi | see_3779 | 88.69 L-asparaginase (EC 3.5.1.1) |
| SCE1572_4522 | Predicted metal-dependent hydrolase of the TIM-barrel fold | bi | see_3780 | 95.52 Predicted metal-dependent hydrolase of the TIM-barrel fold |
| SCE1572_4523 | tRNA-specific adenosine-34 deaminase (EC 3.5.4.-) | bi | see_3782 | 86.09 tRNA-specific adenosine-34 deaminase (EC 3.5.4.-) |
| SCE1572_4524 | Urea carboxylase-related ABC transporter, periplasmic substrate-binding protein | bi | see_3783 | 78.22 Urea carboxylase-related ABC transporter, periplasmic substrate-binding protein |
| SCE1572_4525 | Urea carboxylase-related ABC transporter, ATPase protein | bi | see_3784 | 78.18 Urea carboxylase-related ABC transporter, ATPase protein |
| SCE1572_4526 | Urea carboxylase-related ABC transporter, permease protein | bi | see_3785 | 82.85 Urea carboxylase-related ABC transporter, permease protein |
| SCE1572_4527 | RsbR, positive regulator of sigma-B | bi | see_3787 | 75.24 RsbR, positive regulator of sigma-B |
| SCE1572_4528 | hypothetical protein | - | - | 0 |
| SCE1572_4529 | periplasmic ATP/GTP-binding protein | bi | see_3788 | 77.56 periplasmic ATP/GTP-binding protein |
| SCE1572_4530 | Transcriptional regulator, AraC family | bi | see_3789 | 87.2 transcriptional regulator, AraC family |
| SCE1572_4531 | Beta-lactamase (EC 3.5.2.6) | um | see_5987 | 40.49 Beta-lactamase (EC 3.5.2.6) |
| SCE1572_4532 | hypothetical protein | - | - | 0 |
| SCE1572_4533 | Pirin, N-terminal:Pirin, C-terminal | bi | see_3790 | 90.08 Pirin, N-terminal:Pirin, C-terminal |
| SCE1572_4534 | Arabinose efflux permease | bi | see_3791 | 90.59 Arabinose efflux permease |
| SCE1572_4535 | hypothetical protein | bi | see_3792 | 82.91 FIG01088068: hypothetical protein |
| SCE1572_4536 | Response regulator of zinc sigma-54-dependent two-component system | bi | see_9770 | 61.86 Response regulator of zinc sigma-54-dependent two-component system |
| SCE1572_4537 | hypothetical protein | um | see_3796 | 55.73 hypothetical protein |
| SCE1572_4538 | putative lipoprotein | um | see_3794 | 54.32 Type IV fimbrial biogenesis protein PilY1 |
| SCE1572_4539 | hypothetical protein | um | see_3796 | 56 hypothetical protein |
| SCE1572_4540 | WD-40 repeat protein | um | see_7069 | 78.06 WD-40 repeat protein |
| SCE1572_4541 | Type IV fimbrial biogenesis protein PilY1 | um | see_3794 | 51.02 Type IV fimbrial biogenesis protein PilY1 |
| SCE1572_4542 | hypothetical protein | - | - | 0 |
| SCE1572_4543 | Phenylalanyl-tRNA synthetase beta chain (EC 6.1.1.20) | bi | see_3797 | 87.71 Phenylalanyl-tRNA synthetase beta chain (EC 6.1.1.20) |
| SCE1572_4544 | Phenylalanyl-tRNA synthetase alpha chain (EC 6.1.1.20) | bi | see_3798 | 97.71 Phenylalanyl-tRNA synthetase alpha chain (EC 6.1.1.20) |
| SCE1572_4545 | TRAP-type C4-dicarboxylate transport system, periplasmic component | - | - | 0 |
| SCE1572_4546 | TRAP-type C4-dicarboxylate transport system, small permease component | - | - | 0 |
| SCE1572_4547 | TRAP-type C4-dicarboxylate transport system, large permease component | - | - | 0 |
| SCE1572_4548 | hypothetical protein | - | - | 0 |
| SCE1572_4549 | hypothetical protein | um | see_4778 | 40.86 Serine/threonine-protein kinase pkn3 (EC 2.7.11.1) |
| SCE1572_4550 | Hexuronate transporter | um | see_5778 | 43.4 Hexuronate transporter |
| SCE1572_4551 | 2-deoxy-D-gluconate 3-dehydrogenase (EC 1.1.1.125) | um | see_8328 | 42.68 3-oxoacyl-[acyl-carrier protein] reductase (EC 1.1.1.100) |
| SCE1572_4552 | 2-dehydro-3-deoxygluconate kinase (EC 2.7.1.45) | bi | see_1380 | 92.54 2-dehydro-3-deoxygluconate kinase (EC 2.7.1.45) |
| SCE1572_4553 | 4-Hydroxy-2-oxoglutarate aldolase (EC 4.1.3.16) / 2-dehydro-3-deoxyphosphoglucuronate aldolase (EC 4.1.2.14) | bi | see_1379 | 91.48 4-Hydroxy-2-oxoglutarate aldolase (EC 4.1.3.16) / 2-dehydro-3-deoxyphosphoglucuronate aldolase (EC 4.1.2.14) |
| SCE1572_4554 | hypothetical protein | - | - | 0 |
| SCE1572_4555 | FIG00483917: hypothetical protein | - | - | 0 |
| SCE1572_4556 | Pectate lyase precursor (EC 4.2.2.2) | um | see_9562 | 47.01 Collagen triple helix repeat |
| SCE1572_4557 | Endo-1,4-beta-glucanase | bi | see_3799 | 86.26 Endo-1,4-beta-glucanase |
| SCE1572_4558 | serine/threonine protein kinase | bi | see_3801 | 77.22 protein kinase |
| SCE1572_4559 | FIG01088311: hypothetical protein | bi | see_3802 | 80.9 FIG01088311: hypothetical protein |
| SCE1572_4560 | hypothetical protein | - | - | 0 |
| SCE1572_4561 | Transcriptional regulator BkdR of isoleucine and valine catabolism operon | um | see_3527 | 32.61 Chromosome (plasmid) partitioning protein ParA / Sporulation initiation inhibitor protein Soj |
| SCE1572_4562 | Cobyrinic acid a,c-diamide synthase | um | see_3527 | 91.36 hypothetical protein |
| SCE1572_4563 | hypothetical protein | bi | see_3813 | 95.12 hypothetical protein |
| SCE1572_4564 | hypothetical protein | bi | see_3814 | 94.33 Transcriptional regulator BkdR of isoleucine and valine catabolism operon |
| SCE1572_4565 | Transcriptional regulator BkdR of isoleucine and valine catabolism operon | bi | see_3816 | 84.79 conserved hypothetical protein |
| SCE1572_4566 | hypothetical protein | bi | see_3818 | 95.55 probable pectate lyase |
| SCE1572_4567 | probable pectate lyase | bi | see_3819 | 70.27 hypothetical protein |
| SCE1572_4568 | putative minor tail protein | bi | see_3820 | 30.31 CglB |
| SCE1572_4569 | Similarity | um | see_4514 | 62.65 endo-alpha-1,4 polygalactosaminidase precursor |
| SCE1572_4570 | COG3866 Pectate lyase | um | see_4564 | 49.23 Prolipoprotein diacylglycerol transferase (EC 2.4.99.-) |
| SCE1572_4571 | hypothetical protein | um | see_2821 | 43.33 PAS/PAC sensor signal transduction histidine kinase |
| SCE1572_4572 | two-component system sensor histidine kinase/response regulator, hybrid ('one component system') | um | see_9087 | 38.17 Chemotaxis response regulator protein-glutamate methyltransferase CheB (EC 3.1.1.61) |
| SCE1572_4573 | Chemotaxis response regulator protein-glutamate methyltransferase CheB (EC 3.1.1.61) | um | see_2986 | 33.76 Signal transduction histidine kinase CheA (EC 2.7.3.-) |
| SCE1572_4574 | Signal transduction histidine kinase CheA (EC 2.7.3.-) | um | see_2981 | 28.02 Methyl accepting chemotaxis protein |
| SCE1572_4575 | methyl-accepting chemotaxis sensory transducer | um | see_2983 | 0 |
| SCE1572_4576 | conserved hypothetical protein | - | - | 0 |
| SCE1572_4577 | Chemotaxis protein methyltransferase CheR (EC 2.1.1.80) | um | see_3523 | 35.98 Chemotaxis protein methyltransferase CheR (EC 2.1.1.80) |
| SCE1572_4578 | CheW protein | um | see_2982 | 31.13 Positive regulator of CheA protein activity (CheW) |
| SCE1572_4579 | hypothetical protein | - | - | 0 |
| SCE1572_4580 | ABC transporter substrate-binding protein | bi | see_3097 | 61.52 ABC transporter substrate-binding protein |
| SCE1572_4581 | hypothetical protein | - | - | 0 |
| SCE1572_4582 | DNA topoisomerase III (EC 5.99.1.2) | bi | see_3821 | 84.18 DNA topoisomerase III (EC 5.99.1.2) |
| SCE1572_4583 | hypothetical protein | bi | see_3822 | 95.24 hypothetical protein |
| SCE1572_4584 | Gil0645 protein | bi | see_3823 | 55.82 Gil0645 protein |
| SCE1572_4585 | short-chain dehydrogenase/reductase SDR | bi | see_3824 | 86.76 short-chain dehydrogenase/reductase SDR |
| SCE1572_4586 | hypothetical protein | bi | see_3825 | 71.8 hypothetical protein |
| SCE1572_4587 | OmpA | bi | see_3826 | 90.62 OmpA |
| SCE1572_4588 | Transcriptional regulatory protein algP | bi | see_3827 | 80.63 Possible CheA Signal Transduction Histidine Kinases (STHK) |
| SCE1572_4589 | Peptidyl-prolyl cis-trans isomerase ppiD (EC 5.2.1.8) | bi | see_3828 | 83.14 Peptidyl-prolyl cis-trans isomerase ppiD (EC 5.2.1.8) |

| | | | | |
|--------------|---|-----|-----------|---|
| SCE1572_4590 | hypothetical protein | - | | 0 |
| SCE1572_4591 | hypothetical protein | bi | see_3829 | 72.56 Translation initiation factor 2 |
| SCE1572_4592 | Phosphate regulon sensor protein PhoR (SphS) (EC 2.7.13.3) | bi | see_3830 | 87.71 Phosphate regulon sensor protein PhoR (SphS) (EC 2.7.13.3) |
| SCE1572_4593 | Phosphate transport regulator (distant homolog of PhoU) | bi | see_3831 | 87.32 Phosphate transport regulator (distant homolog of PhoU) |
| SCE1572_4594 | Probable low-affinity inorganic phosphate transporter | bi | see_3832 | 93.73 Probable low-affinity inorganic phosphate transporter |
| SCE1572_4595 | hypothetical protein | umi | see_2397 | 38.94 3-beta-hydroxysteroid dehydrogenase/isomerase family protein in hypothetical gene cluster |
| SCE1572_4596 | 6-phosphofructokinase (EC 2.7.1.11) | bi | see_3833 | 93.98 6-phosphofructokinase (EC 2.7.1.11) |
| SCE1572_4597 | hypothetical protein | bi | see_3834 | 52.94 hypothetical protein |
| SCE1572_4598 | Phosphoenolpyruvate carboxylase (EC 4.1.1.31) | bi | see_3835 | 94.19 Phosphoenolpyruvate carboxylase (EC 4.1.1.31) |
| SCE1572_4599 | hypothetical protein | bi | see_6186 | 47.06 hypothetical protein |
| SCE1572_4600 | Serine/threonine-protein kinase pkn1 (EC 2.7.11.1) | bi | see_3837 | 84.74 Serine/threonine-protein kinase pkn1 (EC 2.7.11.1) |
| SCE1572_4601 | Transcriptional regulator, LysR family | umi | see_9852 | 38.21 Transcriptional regulator, LysR family |
| SCE1572_4602 | Deoxyuridine 5-'-triphosphate nucleotidohydrolase (EC 3.6.1.23) | bi | see_3838 | 92.67 Deoxyuridine 5-'-triphosphate nucleotidohydrolase (EC 3.6.1.23) |
| SCE1572_4603 | Miscellaneous; Hypothetical/Global homology | bi | see_3839 | 88.29 hypothetical protein |
| SCE1572_4604 | FIG01088557: hypothetical protein | bi | see_3840 | 89.67 FIG01088557: hypothetical protein |
| SCE1572_4605 | 1-acyl-sn-glycerol-3-phosphate acyltransferase (EC 2.3.1.51) | bi | see_3841 | 95.16 1-acyl-sn-glycerol-3-phosphate acyltransferase (EC 2.3.1.51) |
| SCE1572_4606 | FIG00008365: hypothetical protein | bi | see_3842 | 94.33 FIG00008365: hypothetical protein |
| SCE1572_4607 | hypothetical protein | bi | see_3843 | 79.87 hypothetical protein |
| SCE1572_4608 | Uncharacterized protein conserved in bacteria, NMA0228-like | bi | see_3844 | 90.11 Uncharacterized protein conserved in bacteria, NMA0228-like |
| SCE1572_4609 | FIG01085170: hypothetical protein | bi | see_3845 | 75.47 FIG01085170: hypothetical protein |
| SCE1572_4610 | FIG01088029: hypothetical protein | bi | see_3846 | 85.54 FIG01088029: hypothetical protein |
| SCE1572_4611 | FIG01086529: hypothetical protein | bi | see_3847 | 86.86 FIG01086529: hypothetical protein |
| SCE1572_4612 | hypothetical protein | - | | 0 |
| SCE1572_4613 | Permease of the drug/metabolite transporter (DMT) superfamily | umi | see_10032 | 24.53 FIG01289198: hypothetical protein |
| SCE1572_4614 | hypothetical protein | - | | 0 |
| SCE1572_4615 | hypothetical protein | umi | see_2361 | 28.72 FIG100068: Hypothetical protein |
| SCE1572_4616 | hypothetical protein | - | | 0 |
| SCE1572_4617 | hypothetical protein | - | | 0 |
| SCE1572_4618 | FIG01087382: hypothetical protein | bi | see_3850 | 91.19 FIG01087382: hypothetical protein |
| SCE1572_4619 | hypothetical protein | - | | 0 |
| SCE1572_4620 | hypothetical protein | - | | 0 |
| SCE1572_4621 | putative fatty acid desaturase | umi | see_4921 | 40.71 Beta-carotene hydroxylase |
| SCE1572_4622 | hypothetical protein | umi | see_5973 | 25.68 Beta-carotene hydroxylase |
| SCE1572_4623 | Dihydropyrimidine acetyltransferase component of pyruvate dehydrogenase complex (EC 2.3.1.12) | bi | see_3852 | 70.47 hypothetical protein |
| SCE1572_4624 | Protein of unknown function DUF55 | bi | see_3853 | 92.91 Protein of unknown function DUF55 |
| SCE1572_4625 | hypothetical protein | bi | see_3855 | 72.07 hypothetical protein |
| SCE1572_4626 | alginate regulatory protein AlgP | bi | see_3856 | 80.69 methyl-accepting chemotaxis sensory transducer |
| SCE1572_4627 | hypothetical protein | bi | see_3857 | 77.29 hypothetical protein |
| SCE1572_4628 | hypothetical protein | umi | see_3858 | 39.86 Adenosylhomocysteinase (EC 3.3.1.1) |
| SCE1572_4629 | Oligopeptide ABC transporter, periplasmic oligopeptide-binding protein OppA (TC 3.A.1.5.1) | bi | see_3859 | 85.19 Oligopeptide ABC transporter, periplasmic oligopeptide-binding protein OppA (TC 3.A.1.5.1) |
| SCE1572_4630 | VgrG protein | umi | see_6341 | 48.97 VgrG protein |
| SCE1572_4631 | hypothetical protein | umi | see_6339 | 42.12 FIG01088856: hypothetical protein |
| SCE1572_4632 | hypothetical protein | - | | 0 |
| SCE1572_4633 | UDP-glucose 4-epimerase (EC 5.1.3.2) | bi | see_3860 | 95.27 UDP-glucose 4-epimerase (EC 5.1.3.2) |
| SCE1572_4634 | Oligopeptide ABC transporter, periplasmic oligopeptide-binding protein OppA (TC 3.A.1.5.1) | bi | see_3861 | 86.12 Oligopeptide ABC transporter, periplasmic oligopeptide-binding protein OppA (TC 3.A.1.5.1) |
| SCE1572_4635 | Uncharacterized domain COG3236 / GTP cyclohydrolase II (EC 3.5.4.25) | umi | see_3769 | 58.74 Uncharacterized domain COG3236 / GTP cyclohydrolase II (EC 3.5.4.25) |
| SCE1572_4636 | hypothetical protein | - | | 0 |
| SCE1572_4637 | Alpha-glucosidase (EC 3.2.1.20) | bi | see_3862 | 89.32 Alpha-glucosidase (EC 3.2.1.20) |
| SCE1572_4638 | Transcriptional regulator, LysR family | bi | see_3863 | 89.35 Transcriptional regulator, LysR family |
| SCE1572_4639 | short-chain dehydrogenase/reductase SDR | bi | see_3864 | 82.4 short-chain dehydrogenase/reductase SDR |
| SCE1572_4640 | hypothetical protein | bi | see_3865 | 71.7 hypothetical protein |
| SCE1572_4641 | FIG01086874: hypothetical protein | umi | see_1320 | 52.07 FIG01086874: hypothetical protein |
| SCE1572_4642 | aldo/keto reductase | umi | see_5289 | 36.75 Oxidoreductase |
| SCE1572_4643 | Transcriptional regulator, GntR family domain / Aspartate aminotransferase (EC 2.6.1.1) | umi | see_1410 | 36.25 Transcriptional regulator, GntR family domain / Aspartate aminotransferase (EC 2.6.1.1) |
| SCE1572_4644 | Large exoproteins involved in heme utilization or adhesion | bi | see_10174 | 50.67 Large exoproteins involved in heme utilization or adhesion |
| SCE1572_4645 | Beta-glucosidase (EC 3.2.1.21) | bi | see_3868 | 86.14 Beta-glucosidase (EC 3.2.1.21) |
| SCE1572_4646 | Quinone oxidoreductase (EC 1.6.5.5) | bi | see_3869 | 90.06 Quinone oxidoreductase (EC 1.6.5.5) |
| SCE1572_4647 | hypothetical protein | - | | 0 |
| SCE1572_4648 | Glutaredoxin-related protein | bi | see_3870 | 88.43 Glutaredoxin-related protein |
| SCE1572_4649 | PE-PGRS FAMILY PROTEIN | umi | see_1320 | 40.76 FIG01086874: hypothetical protein |
| SCE1572_4650 | Oligopeptide transport system permease protein OppB (TC 3.A.1.5.1) | bi | see_3872 | 97.39 Oligopeptide transport system permease protein OppB (TC 3.A.1.5.1) |
| SCE1572_4651 | Oligopeptide transport system permease protein OppC (TC 3.A.1.5.1) | bi | see_3873 | 93.95 Oligopeptide transport system permease protein OppC (TC 3.A.1.5.1) |
| SCE1572_4652 | Oligopeptide transport ATP-binding protein OppD (TC 3.A.1.5.1) | bi | see_3874 | 96.74 Oligopeptide transport ATP-binding protein OppD (TC 3.A.1.5.1) |
| SCE1572_4653 | Oligopeptide transport ATP-binding protein OppF (TC 3.A.1.5.1) | bi | see_3875 | 95.86 Oligopeptide transport ATP-binding protein OppF (TC 3.A.1.5.1) |
| SCE1572_4654 | FIG01086263: hypothetical protein | bi | see_3876 | 56.25 FIG01086263: hypothetical protein |
| SCE1572_4655 | FIG01088883: hypothetical protein | bi | see_7308 | 94.79 hypothetical protein |
| SCE1572_4656 | hypothetical protein | umi | see_8901 | 60.38 putative secreted protein |
| SCE1572_4657 | Cell division protein BofA | bi | see_3877 | 84.38 Cell division protein BofA |
| SCE1572_4658 | hypothetical protein | bi | see_3878 | 92.22 hypothetical protein |
| SCE1572_4659 | Transposase | umi | see_4570 | 46.27 Mobile element protein |
| SCE1572_4660 | Inosine-5-'-monophosphate dehydrogenase (EC 1.1.1.205) | bi | see_3881 | 87.68 Inosine-5-'-monophosphate dehydrogenase (EC 1.1.1.205) |
| SCE1572_4661 | FIG01085153: hypothetical protein | bi | see_3882 | 70.55 FIG01085153: hypothetical protein |
| SCE1572_4662 | Adenylate cyclase (EC 4.6.1.1) / Guanylate cyclase (EC 4.6.1.2) | bi | see_3883 | 81.97 FIG01087003: hypothetical protein |
| SCE1572_4663 | hypothetical protein | bi | see_3884 | 68.29 hypothetical protein |
| SCE1572_4664 | Lipase precursor (EC 3.1.1.3) | bi | see_3885 | 86.14 lactonizing lipase |
| SCE1572_4665 | lipase chaperone | bi | see_3886 | 76.33 lipase chaperone |
| SCE1572_4666 | hypothetical protein | bi | see_3887 | 70.07 hypothetical protein |
| SCE1572_4667 | hypothetical protein | - | | 0 |
| SCE1572_4668 | FIG01087065: hypothetical protein | umi | see_1478 | 88 FIG01087065: hypothetical protein |
| SCE1572_4669 | hypothetical protein | umi | see_2935 | 57.32 hypothetical protein |
| SCE1572_4670 | EBNA-1 | umi | see_7871 | 49.42 FIG01124324: hypothetical protein |
| SCE1572_4671 | hypothetical protein | - | | 0 |
| SCE1572_4672 | hypothetical protein | - | | 0 |
| SCE1572_4673 | Choline dehydrogenase (EC 1.1.99.1) | bi | see_3906 | 91.95 Choline dehydrogenase (EC 1.1.99.1) |
| SCE1572_4674 | FIG01088405: hypothetical protein | bi | see_3907 | 87.62 FIG01088405: hypothetical protein |
| SCE1572_4675 | Serine/threonine-protein kinase pkn1 (EC 2.7.11.1) | bi | see_3910 | 78.73 Serine/threonine-protein kinase pkn1 (EC 2.7.11.1) |
| SCE1572_4676 | hypothetical protein | - | | 0 |
| SCE1572_4677 | hypothetical protein | bi | see_1142 | 58.14 Dihydropyrimidine acetyltransferase component of pyruvate dehydrogenase complex (EC 2.3.1.12) |
| SCE1572_4678 | hypothetical protein | - | | 0 |
| SCE1572_4679 | polyphenol oxidase A | - | | 0 |
| SCE1572_4680 | hypothetical protein | - | | 0 |
| SCE1572_4681 | hypothetical protein | umi | see_9109 | 31.76 hypothetical protein |
| SCE1572_4682 | hypothetical protein | - | | 0 |
| SCE1572_4683 | predicted protein | umi | see_10081 | 32.48 Phosphatidylserine decarboxylase (EC 4.1.1.65) |
| SCE1572_4684 | Nitrite reductase [NAD(P)H] large subunit (EC 1.7.1.4) | umi | see_1283 | 86.34 Nitrite reductase [NAD(P)H] large subunit (EC 1.7.1.4) |
| SCE1572_4685 | Assimilatory nitrate reductase large subunit (EC:1.7.99.4) | bi | see_1282 | 89.09 Assimilatory nitrate reductase large subunit (EC:1.7.99.4) |
| SCE1572_4686 | FIG01088161: hypothetical protein | bi | see_8439 | 79.15 FIG01088161: hypothetical protein |
| SCE1572_4687 | hypothetical protein | umi | see_1502 | 77.51 FIG01085594: hypothetical protein |
| SCE1572_4688 | hypothetical protein | - | | 0 |
| SCE1572_4689 | FIG01088161: hypothetical protein | umi | see_8439 | 65.02 FIG01088161: hypothetical protein |
| SCE1572_4690 | hypothetical protein | umi | see_312 | 41.36 hypothetical protein |
| SCE1572_4691 | RNA polymerase, sigma-24 subunit, ECF subfamily | - | | 0 |
| SCE1572_4692 | serine/threonine protein kinase | umi | see_5043 | 45.17 Serine/threonine-protein kinase pkn3 (EC 2.7.11.1) |
| SCE1572_4693 | FIG00890145: hypothetical protein | bi | see_1662 | 87.11 FIG00890145: hypothetical protein |
| SCE1572_4694 | hypothetical protein | umi | see_1486 | 40.26 VgrG protein |
| SCE1572_4695 | hypothetical protein | - | | 0 |
| SCE1572_4696 | Endo-1,4-beta-xylanase A precursor (EC 3.2.1.8) | bi | see_7939 | 77.19 Endo-1,4-beta-xylanase A precursor (EC 3.2.1.8) |
| SCE1572_4697 | hypothetical protein | bi | see_5765 | 83.05 hypothetical protein |
| SCE1572_4698 | hypothetical protein | bi | see_9111 | 37.18 Mir2351 protein |
| SCE1572_4699 | Formamidopyrimidine-DNA glycosylase (EC 3.2.2.23) | bi | see_3926 | 89.82 Formamidopyrimidine-DNA glycosylase (EC 3.2.2.23) |
| SCE1572_4700 | hypothetical protein | bi | see_3927 | 74.7 hypothetical protein |
| SCE1572_4701 | hypothetical protein | umi | see_5100 | 24.83 Type II secretory pathway, ATPase Pule/Tip pilus assembly pathway, ATPase PilB |
| SCE1572_4702 | TPR repeat | umi | see_7657 | 32.93 Adenylate cyclase (EC 4.6.1.1) / Guanylate cyclase (EC 4.6.1.2) |
| SCE1572_4703 | Putative transport protein | bi | see_3929 | 87.97 Putative transport protein |
| SCE1572_4704 | probable general stress protein 26 | bi | see_3930 | 84.09 probable general stress protein 26 |
| SCE1572_4705 | hypothetical protein | bi | see_3931 | 85.29 hypothetical protein |
| SCE1572_4706 | Primosomal protein N'39; (replication factor Y) - superfamily II helicase | bi | see_3932 | 88.6 Primosomal protein N'39; (replication factor Y) - superfamily II helicase |
| SCE1572_4707 | possible hydrolase | bi | see_3933 | 83.76 alpha/beta hydrolase fold |
| SCE1572_4708 | hypothetical protein | - | | 0 |
| SCE1572_4709 | Von Willebrand factor type A domain protein | bi | see_9357 | 79.25 Von Willebrand factor type A domain protein |
| SCE1572_4710 | Cyclic beta-1,2-glucan synthase (EC 2.4.1.-) | bi | see_3935 | 73.12 Cyclic beta-1,2-glucan synthase (EC 2.4.1.-) |
| SCE1572_4711 | FIG01086361: hypothetical protein | bi | see_8816 | 83.06 FIG01086361: hypothetical protein |
| SCE1572_4712 | Rhs family carbohydrate-binding protein | bi | see_8817 | 87.24 Rhs family carbohydrate-binding protein |
| SCE1572_4713 | peptidase M14, carboxypeptidase A | umi | see_3939 | 84.42 FIG01085109: hypothetical protein |
| SCE1572_4714 | secreted protein | bi | see_3940 | 88 putative secreted protein |
| SCE1572_4715 | CobN component of cobalt chelatase involved in B12 biosynthesis | umi | see_2882 | 41.55 Phage tail fiber protein |
| SCE1572_4716 | FIG01089085: hypothetical protein | bi | see_3941 | 75.18 FIG01089085: hypothetical protein |
| SCE1572_4717 | hypothetical protein | bi | see_3942 | 87.44 hypothetical protein |
| SCE1572_4718 | hypothetical protein | bi | see_3943 | 90.87 hypothetical protein |
| SCE1572_4719 | ATP-dependent DNA ligase (EC 6.5.1.1) clustered with Ku protein, LigD | bi | see_3945 | 84.2 ATP-dependent DNA ligase (EC 6.5.1.1) clustered with Ku protein, LigD |
| SCE1572_4720 | FIG01087739: hypothetical protein | bi | see_3946 | 82.84 FIG01087739: hypothetical protein |
| SCE1572_4721 | Cysteine synthase (EC 2.5.1.47) | bi | see_3947 | 90 Cysteine synthase (EC 2.5.1.47) |
| SCE1572_4722 | Serine acetyltransferase (EC 2.3.1.30) | bi | see_3948 | 91.54 Serine acetyltransferase (EC 2.3.1.30) |
| SCE1572_4723 | SeIT/seIW/seIH selenoprotein | bi | see_3949 | 87.5 SeIT/seIW/seIH selenoprotein |
| SCE1572_4724 | Magnesium transporter | bi | see_3950 | 90.53 Mg/Co/Ni transporter MgtE / CBS domain |
| SCE1572_4725 | Putative beta-lactamase hcpC precursor (EC 3.5.2.6) (Cysteine-rich protein C) | bi | see_3951 | 85.11 Putative beta-lactamase hcpC precursor (EC 3.5.2.6) (Cysteine-rich protein C) |
| SCE1572_4726 | ATP-dependent DNA helicase UvrD/PcrA | bi | see_3952 | 89.2 ATP-dependent DNA helicase UvrD/PcrA |
| SCE1572_4727 | FIG01085998: hypothetical protein | bi | see_6342 | 62.94 FIG01085998: hypothetical protein |
| SCE1572_4728 | VgrG protein | bi | see_6341 | 80.22 VgrG protein |
| SCE1572_4729 | hypothetical protein | bi | see_6340 | 65.25 FIG01087556: hypothetical protein |
| SCE1572_4730 | FIG01088856: hypothetical protein | bi | see_6339 | 80.61 FIG01088856: hypothetical protein |
| SCE1572_4731 | Pentapeptide repeat family protein | bi | see_6338 | 82.52 Pentapeptide repeat family protein |
| SCE1572_4732 | hypothetical protein | bi | see_6337 | 87.76 hypothetical protein |
| SCE1572_4733 | hypothetical protein | bi | see_6336 | 96.15 hypothetical protein |
| SCE1572_4734 | FIG01087400: hypothetical protein | bi | see_3954 | 81.75 FIG01087400: hypothetical protein |
| SCE1572_4735 | ATP-dependent RNA helicase RhlE | bi | see_3956 | 87.27 ATP-dependent RNA helicase RhlE |
| SCE1572_4736 | Peptidase | bi | see_3957 | 85.09 Peptidase |
| SCE1572_4737 | 2-hydroxy-6-oxo-6-phenylhexa-2,4-dienoate hydrolase (EC 3.7.1.-) | umi | see_3912 | 40.2 Epoxide hydrolase (EC 3.3.2.9) |
| SCE1572_4738 | conserved hypothetical protein | bi | see_3958 | 84.96 conserved hypothetical protein |
| SCE1572_4739 | Signal recognition particle, subunit Fih SRP54 (TC 3.A.5.1.1) | umi | see_8051 | 32.19 hypothetical protein |
| SCE1572_4740 | Proton/glutamate symport protein @ Sodium/glutamate symport protein | bi | see_3961 | 95.22 Proton/glutamate symport protein @ Sodium/glutamate symport protein |
| SCE1572_4741 | FIG01088916: hypothetical protein | bi | see_3962 | 86.52 FIG01088916: hypothetical protein |
| SCE1572_4742 | hypothetical protein | bi | see_3963 | 88.34 hypothetical protein |
| SCE1572_4743 | Methionine aminopeptidase (EC 3.4.11.18) | bi | see_3965 | 94.35 Methionine aminopeptidase (EC 3.4.11.18) |
| SCE1572_4744 | LysR family transcriptional regulator YnfL | bi | see_3966 | 92.38 LysR family transcriptional regulator YnfL |
| SCE1572_4745 | ADP-ribosylglycohydrolase | bi | see_3967 | 90.86 Inositol-phosphate phosphatase(EC:3.1.3.25) |
| SCE1572_4746 | Putative Ferredoxin | bi | see_3968 | 79.47 Putative Ferredoxin |
| SCE1572_4747 | YD repeat | bi | see_3969 | 91.8 hypothetical protein |
| SCE1572_4748 | Mobile element protein | - | | 0 |
| SCE1572_4749 | Rhs family carbohydrate-binding protein | bi | see_3970 | 88.38 Rhs family carbohydrate-binding protein |
| SCE1572_4750 | 6-phosphogluconate dehydrogenase, decarboxylating (EC 1.1.1.44) | bi | see_3971 | 92.75 6-phosphogluconate dehydrogenase, decarboxylating (EC 1.1.1.44) |
| SCE1572_4751 | RabR, positive regulator of sigma-B | bi | see_3972 | 89.71 RabR, positive regulator of sigma-B |
| SCE1572_4752 | hypothetical protein | bi | see_3974 | 97.26 hypothetical protein |
| SCE1572_4753 | hypothetical protein | - | | 0 |

| | | | | |
|--------------|---|-----|----------|--|
| SCE1572_4754 | conserved hypothetical protein | umi | sce_7978 | 55.99 conserved hypothetical protein |
| SCE1572_4755 | conserved hypothetical protein | umi | sce_605 | 50.43 hypothetical protein |
| SCE1572_4756 | FIG01087953: hypothetical protein | umi | sce_6129 | 43.14 FIG01088173: hypothetical protein |
| SCE1572_4757 | hypothetical protein | - | - | 0 |
| SCE1572_4758 | hypothetical protein | bi | sce_3976 | 75.48 TPR repeat |
| SCE1572_4759 | FIG01087953: hypothetical protein | umi | sce_3977 | 71.74 hypothetical protein |
| SCE1572_4760 | hypothetical protein | umi | sce_5449 | 40 FIG01088294: hypothetical protein |
| SCE1572_4761 | hypothetical protein | - | - | 0 |
| SCE1572_4762 | Thrombospondin-1 precursor | bi | sce_3978 | 74.58 Thrombospondin-1 precursor |
| SCE1572_4763 | RIBOSE TRANSPORT SYSTEM PERMEASE PROTEIN RBSC | bi | sce_3979 | 87.91 RIBOSE TRANSPORT SYSTEM PERMEASE PROTEIN RBSC |
| SCE1572_4764 | Probable transmembrane abc transporter protein | bi | sce_3980 | 85.47 Probable transmembrane abc transporter protein |
| SCE1572_4765 | sugar ABC transporter, ATP-binding protein | bi | sce_3981 | 83.55 Ribose ABC transport system, ATP-binding protein RbsA (TC 3.A.1.2.1) |
| SCE1572_4766 | bmp family protein | bi | sce_3982 | 84.76 bmp family protein |
| SCE1572_4767 | Similarity | bi | sce_3983 | 73.24 Similarity |
| SCE1572_4768 | Alcohol dehydrogenase, zinc-binding domain protein | umi | sce_6316 | 35.95 Bifunctional protein: zinc-containing alcohol dehydrogenase; quinone oxidoreductase (NADPH:quinone reductase) (EC 1.1.1.-); Sin |
| SCE1572_4769 | COG4118: Antitoxin of toxin-antitoxin stability system | - | - | 0 |
| SCE1572_4770 | hypothetical protein | umi | sce_4893 | 31.03 FIG00501228: hypothetical protein |
| SCE1572_4771 | metallophosphoesterase | bi | sce_3987 | 89.81 metallophosphoesterase |
| SCE1572_4772 | hypothetical protein | bi | sce_3988 | 78.08 hypothetical protein |
| SCE1572_4773 | probable oxidoreductase | bi | sce_7233 | 88.89 probable oxidoreductase |
| SCE1572_4774 | Flagelliform silk protein | bi | sce_3989 | 49.3 (MTV044.05), len: 923. Unknown glycine richprotein, similar to other PGRS-type sequences e.g. gp/AL0091/MTV004_1M. tubercu |
| SCE1572_4775 | hypothetical protein | - | - | 0 |
| SCE1572_4776 | serine/threonine protein kinase | bi | sce_3991 | 83.93 serine/threonine protein kinase |
| SCE1572_4777 | S-layer-like array protein | bi | sce_3992 | 82.89 S-layer-like array protein |
| SCE1572_4778 | Branched-chain amino acid ABC transporter, amino acid-binding protein (TC 3.A.1.4.1) | umi | sce_3993 | 79.31 Aspartyl-tRNA(Asn) amidotransferase subunit A (EC 6.3.5.6) @ Glutamyl-tRNA(Gln) amidotransferase subunit A (EC 6.3.5.7) |
| SCE1572_4779 | hypothetical protein | - | - | 0 |
| SCE1572_4780 | EBNA-1 | bi | sce_3993 | 81.62 Aspartyl-tRNA(Asn) amidotransferase subunit A (EC 6.3.5.6) @ Glutamyl-tRNA(Gln) amidotransferase subunit A (EC 6.3.5.7) |
| SCE1572_4781 | FIG01089285: hypothetical protein | bi | sce_3995 | 61.69 FIG01089285: hypothetical protein |
| SCE1572_4782 | RNA-binding protein, RRM domain | bi | sce_7494 | 62.93 FIG01087054: hypothetical protein |
| SCE1572_4783 | Mobile element protein | umi | sce_299 | 94.61 Mobile element protein |
| SCE1572_4784 | hypothetical protein | - | - | 0 |
| SCE1572_4785 | Outer membrane protein A-like protein | bi | sce_3999 | 87.21 Outer membrane protein A-like protein |
| SCE1572_4786 | hypothetical protein | bi | sce_4000 | 90.91 FIG01088242: hypothetical protein |
| SCE1572_4787 | Protein serine/threonine phosphatase PrpC, regulation of stationary phase | bi | sce_4001 | 88.54 Protein serine/threonine phosphatase PrpC, regulation of stationary phase |
| SCE1572_4788 | hypothetical protein | bi | sce_4002 | 83 hypothetical protein |
| SCE1572_4789 | conserved hypothetical protein; putative signal peptide | bi | sce_4004 | 89.27 hypothetical protein |
| SCE1572_4790 | FIG01085814: hypothetical protein | bi | sce_4005 | 84.29 FIG01085814: hypothetical protein |
| SCE1572_4791 | FIG01086775: hypothetical protein | bi | sce_4006 | 67.95 FIG01086775: hypothetical protein |
| SCE1572_4792 | hypothetical protein | - | - | 0 |
| SCE1572_4793 | hypothetical protein | bi | sce_4007 | 86.88 hypothetical protein |
| SCE1572_4794 | Acyl-CoA dehydrogenase (EC 1.3.99.3) | bi | sce_4008 | 94.51 Acyl-CoA dehydrogenase (EC 1.3.99.3) |
| SCE1572_4795 | Transcription elongation factor GreB | bi | sce_4010 | 95.54 Transcription elongation factor GreB |
| SCE1572_4796 | Lactoylglutathione lyase (EC 4.4.1.5) | bi | sce_4011 | 93.89 Lactoylglutathione lyase (EC 4.4.1.5) |
| SCE1572_4797 | hypothetical protein | bi | sce_4012 | 92.46 FIG01089186: hypothetical protein |
| SCE1572_4798 | YCII-like protein | bi | sce_4013 | 87.13 YCII-like protein |
| SCE1572_4799 | Serine/threonine kinase associate protein KapC | bi | sce_4014 | 82.42 Serine/threonine kinase associate protein KapC |
| SCE1572_4800 | hypothetical protein | bi | sce_4015 | 76.24 hypothetical protein |
| SCE1572_4801 | Putative teichuronic acid biosynthesis glycosyl transferase TaaC | bi | sce_4016 | 85.96 Putative teichuronic acid biosynthesis glycosyl transferase TaaC |
| SCE1572_4802 | FIG01086330: hypothetical protein | bi | sce_4017 | 83.85 FIG01086330: hypothetical protein |
| SCE1572_4803 | Undecaprenyl-phosphate galactosephosphotransferase (EC 2.7.8.6) | bi | sce_4018 | 91.39 Undecaprenyl-phosphate galactosephosphotransferase (EC 2.7.8.6) |
| SCE1572_4804 | Transglutaminase elicitor M81D | umi | sce_4444 | 61.94 Transglutaminase elicitor M81D |
| SCE1572_4805 | PA14 domain protein | umi | sce_2702 | 44.27 PA14 domain protein |
| SCE1572_4806 | Chemotaxis protein methyltransferase CheR (EC 2.1.1.80) | umi | sce_1927 | 36.28 Chemotaxis protein methyltransferase CheR (EC 2.1.1.80) |
| SCE1572_4807 | Enzymatic protein of unknown function | bi | sce_4021 | 92.27 Enzymatic protein of unknown function |
| SCE1572_4808 | FIG01085591: hypothetical protein | bi | sce_4022 | 88.38 FIG01085591: hypothetical protein |
| SCE1572_4809 | Serine/threonine-protein kinase (EC 2.7.1.-) | bi | sce_4023 | 88.08 Serine/threonine-protein kinase (EC 2.7.1.-) |
| SCE1572_4810 | hypothetical protein | - | - | 0 |
| SCE1572_4811 | OmpA/MotB domain protein | bi | sce_4025 | 67.3 OmpA/MotB |
| SCE1572_4812 | acetyltransferase, GNAT family | bi | sce_4026 | 71.58 acetyltransferase, GNAT family |
| SCE1572_4813 | PQQ enzyme repeat family protein | bi | sce_4027 | 91.99 PQQ enzyme repeat family protein |
| SCE1572_4814 | TolA protein | bi | sce_4028 | 87.44 TolA protein |
| SCE1572_4815 | Sulfatase | bi | sce_4029 | 92.09 Sulfatase |
| SCE1572_4816 | hypothetical protein | bi | sce_4030 | 68.42 hypothetical protein |
| SCE1572_4817 | Transcription elongation factor GreA | bi | sce_4031 | 99.34 Transcription elongation factor GreA |
| SCE1572_4818 | hypothetical protein | bi | sce_4032 | 96.15 hypothetical protein |
| SCE1572_4819 | Competence protein ComL precursor | bi | sce_4033 | 90.59 Competence protein ComL precursor |
| SCE1572_4820 | Response regulator of zinc sigma-54-dependent two-component system | bi | sce_4034 | 94.86 Response regulator of zinc sigma-54-dependent two-component system |
| SCE1572_4821 | Sensory box histidine kinase/response regulator | bi | sce_4035 | 84.45 Sensory box histidine kinase/response regulator |
| SCE1572_4822 | hypothetical protein | - | - | 0 |
| SCE1572_4823 | Transaldolase (EC 2.2.1.2) | bi | sce_4036 | 93.98 Transaldolase (EC 2.2.1.2) |
| SCE1572_4824 | O-antigen biosynthesis protein rfbC | bi | sce_4037 | 90.67 O-antigen biosynthesis protein rfbC |
| SCE1572_4825 | hypothetical protein | bi | sce_4038 | 76.31 hypothetical protein |
| SCE1572_4826 | hypothetical protein | bi | sce_4039 | 85.06 hypothetical protein |
| SCE1572_4827 | FIG01085829: hypothetical protein | bi | sce_4040 | 72.63 FIG01085829: hypothetical protein |
| SCE1572_4828 | hypothetical protein | bi | sce_4041 | 88.75 hypothetical protein |
| SCE1572_4829 | hypothetical protein | bi | sce_4042 | 87 FIG01087124: hypothetical protein |
| SCE1572_4830 | PE-PGRS FAMILY PROTEIN | bi | sce_4043 | 85.65 FIG01087036: hypothetical protein |
| SCE1572_4831 | hypothetical protein | bi | sce_4045 | 89.6 hypothetical protein |
| SCE1572_4832 | hypothetical protein | - | - | 0 |
| SCE1572_4833 | Hypothetical protein | bi | sce_4046 | 98.24 Hypothetical protein |
| SCE1572_4834 | hypothetical protein | - | - | 0 |
| SCE1572_4835 | ATP-binding region, ATPase-like | bi | sce_4047 | 89.31 hypothetical protein |
| SCE1572_4836 | Anti-sigma B factor RsbT / Phosphoserine phosphatase RsbX (EC 3.1.3.3) | bi | sce_4048 | 93.23 Anti-sigma B factor RsbT / Phosphoserine phosphatase RsbX (EC 3.1.3.3) |
| SCE1572_4837 | anti-sigma B factor RsbT | bi | sce_4049 | 95.02 anti-sigma B factor RsbT |
| SCE1572_4838 | RsbS, negative regulator of sigma-B | bi | sce_4050 | 97.84 RsbS, negative regulator of sigma-B |
| SCE1572_4839 | RsbR, positive regulator of sigma-B | bi | sce_4051 | 85.3 RsbR, positive regulator of sigma-B |
| SCE1572_4840 | Protein flbA | bi | sce_4052 | 96.94 Protein flbA |
| SCE1572_4841 | Cold-shock DEAD-box protein A | bi | sce_4053 | 90.86 Cold-shock DEAD-box protein A |
| SCE1572_4842 | FIG01085327: hypothetical protein | bi | sce_4054 | 92.18 FIG01085327: hypothetical protein |
| SCE1572_4843 | FIG01089152: hypothetical protein | bi | sce_4055 | 83.47 FIG01089152: hypothetical protein |
| SCE1572_4844 | hypothetical protein | bi | sce_4056 | 84.94 hypothetical protein |
| SCE1572_4845 | outer membrane efflux protein | bi | sce_4057 | 72.88 efflux transporter, HAEI family, outer membrane efflux protein |
| SCE1572_4846 | Aldehyde dehydrogenase (EC 1.2.1.3), PaaZ | bi | sce_4058 | 93.03 Aldehyde dehydrogenase (EC 1.2.1.3), PaaZ |
| SCE1572_4847 | Serine/threonine protein kinase PrkC, regulator of stationary phase | bi | sce_4059 | 82.85 Serine/threonine protein kinase PrkC, regulator of stationary phase |
| SCE1572_4848 | GTP-binding protein | bi | sce_4060 | 91.09 GTP-binding protein |
| SCE1572_4849 | hypothetical protein | umi | sce_3628 | 27.01 ABC transport protein, ATP-binding subunit |
| SCE1572_4850 | hypothetical protein | - | - | 0 |
| SCE1572_4851 | High-affinity carbon uptake protein Hat/HatR | bi | sce_4062 | 76.85 High-affinity carbon uptake protein Hat/HatR |
| SCE1572_4852 | hypothetical protein | umi | sce_529 | 65.1 hypothetical protein |
| SCE1572_4853 | conserved hypothetical protein | bi | sce_4064 | 82.08 hypothetical protein |
| SCE1572_4854 | Transcriptional regulator, AraC family | bi | sce_4066 | 83.27 Transcriptional regulator, AraC family |
| SCE1572_4855 | hypothetical protein | bi | sce_4067 | 88.82 hypothetical protein |
| SCE1572_4856 | hypothetical protein | bi | sce_4069 | 86.32 hypothetical protein |
| SCE1572_4857 | FIG01087953: hypothetical protein | bi | sce_3977 | 75.76 hypothetical protein |
| SCE1572_4858 | WD domain, G-beta repeat protein | bi | sce_7974 | 46.15 High-affinity carbon uptake protein Hat/HatR |
| SCE1572_4859 | hypothetical protein | bi | sce_4071 | 66.38 FIG01086827: hypothetical protein |
| SCE1572_4860 | hypothetical protein | umi | sce_1975 | 31.85 TPR repeat-Sell-like repeat-Sell-like repeat |
| SCE1572_4861 | Adenylate cyclase (EC 4.6.1.1) / Guanylate cyclase (EC 4.6.1.2) | bi | sce_4073 | 79.42 Adenylate cyclase (EC 4.6.1.1) / Guanylate cyclase (EC 4.6.1.2) |
| SCE1572_4862 | hypothetical protein | bi | sce_4075 | 88.99 hypothetical protein |
| SCE1572_4863 | FIG01089327: hypothetical protein | bi | sce_4077 | 96.31 FIG01089327: hypothetical protein |
| SCE1572_4864 | FIG01087716: hypothetical protein | bi | sce_4078 | 77.46 putative serine/threonine protein kinase |
| SCE1572_4865 | FIG01089354: hypothetical protein | umi | sce_6904 | 84.1 FIG01089354: hypothetical protein |
| SCE1572_4866 | CDP-diacylglycerol--serine O-phosphatidyltransferase (EC 2.7.8.8) | bi | sce_4080 | 97.6 CDP-diacylglycerol--serine O-phosphatidyltransferase (EC 2.7.8.8) |
| SCE1572_4867 | hypothetical protein | - | - | 0 |
| SCE1572_4868 | WD40-like repeat protein | bi | sce_4081 | 95.79 WD40-like repeat protein |
| SCE1572_4869 | Rare lipoprotein A | bi | sce_4082 | 75.26 Rare lipoprotein A |
| SCE1572_4870 | hypothetical protein | bi | sce_4083 | 84.15 hypothetical protein |
| SCE1572_4871 | hypothetical protein | bi | sce_4084 | 88.95 hypothetical protein |
| SCE1572_4872 | Membrane protein involved in colicin uptake-like protein | bi | sce_4086 | 85.61 Antifreeze glycopeptide AFGP polyprotein precursor |
| SCE1572_4873 | hypothetical protein | bi | sce_4087 | 89.92 hypothetical protein |
| SCE1572_4874 | FIG01086790: hypothetical protein | bi | sce_4088 | 96.51 FIG01086790: hypothetical protein |
| SCE1572_4875 | Alpha/beta hydrolase fold (EC 3.8.1.5) | bi | sce_4089 | 96.2 Alpha/beta hydrolase fold (EC 3.8.1.5) |
| SCE1572_4876 | Oligopeptide transport system permease protein OppC (TC 3.A.1.5.1) | bi | sce_4090 | 83.46 Oligopeptide transport system permease protein OppC (TC 3.A.1.5.1) |
| SCE1572_4877 | Dipeptide transport system permease protein DppB (TC 3.A.1.5.2) | bi | sce_4091 | 86.29 Dipeptide transport system permease protein DppB (TC 3.A.1.5.2) |
| SCE1572_4878 | OmpA/MotB domain protein | umi | sce_4092 | 65.75 response regulator |
| SCE1572_4879 | Serine/threonine-protein kinase pkn3 (EC 2.7.11.1) | bi | sce_4092 | 89.02 response regulator |
| SCE1572_4880 | hypothetical protein | bi | sce_4094 | 94.8 hypothetical protein |
| SCE1572_4881 | hypothetical protein | - | - | 0 |
| SCE1572_4882 | FIG01087877: hypothetical protein | bi | sce_4095 | 93.01 FIG01087877: hypothetical protein |
| SCE1572_4883 | Nickel responsive regulator NikR | bi | sce_4096 | 89.29 Nickel responsive regulator NikR |
| SCE1572_4884 | adventurous gliding motility protein AgmI | bi | sce_4097 | 91.64 hypothetical protein |
| SCE1572_4885 | hypothetical protein | - | - | 0 |
| SCE1572_4886 | hypothetical protein | - | - | 0 |
| SCE1572_4887 | hypothetical protein | - | - | 0 |
| SCE1572_4888 | Kup system potassium uptake protein | umi | sce_1932 | 53.56 Kup system potassium uptake protein |
| SCE1572_4889 | hypothetical protein | bi | sce_4102 | 83.19 hypothetical protein |
| SCE1572_4890 | Transglutaminase-like domain | bi | sce_914 | 87.27 Transglutaminase-like domain |
| SCE1572_4891 | hypothetical protein | - | - | 0 |
| SCE1572_4892 | Fatty acid desaturase (EC 1.14.19.1); Delta-9 fatty acid desaturase (EC 1.14.19.1) | umi | sce_6798 | 80.54 Fatty acid desaturase (EC 1.14.19.1); Delta-9 fatty acid desaturase (EC 1.14.19.1) |
| SCE1572_4893 | Two-component sensor histidine kinase | umi | sce_6757 | 44 FIG01087941: hypothetical protein |
| SCE1572_4894 | Carbonic anhydrase (EC 4.2.1.1) | umi | sce_5179 | 51.64 Carbonic anhydrase (EC 4.2.1.1) |
| SCE1572_4895 | hypothetical protein | umi | sce_2477 | 40.51 hypothetical protein |
| SCE1572_4896 | 4-carboxymuconolactone decarboxylase (EC 4.1.1.44) | - | - | 0 |
| SCE1572_4897 | Phosphate transport regulator (distant homolog of PhoU) | umi | sce_3831 | 73.66 Phosphate transport regulator (distant homolog of PhoU) |
| SCE1572_4898 | hypothetical protein | - | - | 0 |
| SCE1572_4899 | hypothetical protein | - | - | 0 |
| SCE1572_4900 | hypothetical protein | umi | sce_1995 | 52.94 serine/threonine protein kinase |
| SCE1572_4901 | FIG01087767: hypothetical protein | bi | sce_4105 | 75.76 Chitodextrinase precursor (EC 3.2.1.14) |
| SCE1572_4902 | Transcriptional regulator, DeoR family | bi | sce_4107 | 83.29 Transcriptional regulator, DeoR family |
| SCE1572_4903 | 3-oxoacyl-[acyl-carrier protein] reductase (EC 1.1.1.100) | bi | sce_4108 | 88.96 3-oxoacyl-[acyl-carrier protein] reductase (EC 1.1.1.100) |
| SCE1572_4904 | hypothetical protein | umi | sce_5560 | 34.18 FIG01087606: hypothetical protein |
| SCE1572_4905 | Transcriptional regulator, TetR family | umi | sce_6665 | 40.48 Transcriptional regulator, TetR family |
| SCE1572_4906 | protein of unknown function DUF163 | bi | sce_4116 | 93.79 LSU m3Psi1915 methyltransferase RimH # ybeA |
| SCE1572_4907 | lojap protein | bi | sce_4117 | 86.58 lojap protein |
| SCE1572_4908 | Gamma-glutamyl phosphate reductase (EC 1.2.1.41) | bi | sce_4118 | 92.49 Gamma-glutamyl phosphate reductase (EC 1.2.1.41) |
| SCE1572_4909 | hypothetical protein | bi | sce_4119 | 70.08 hypothetical protein |
| SCE1572_4910 | hypothetical protein | bi | sce_4120 | 75 hypothetical protein |
| SCE1572_4911 | GMP synthase [glutamine-hydrolyzing], amidotransferase subunit (EC 6.3.5.2) / GMP synthase [glutamine-hydrolyzing], ATP | bi | sce_4121 | 96.92 GMP synthase [glutamine-hydrolyzing], amidotransferase subunit (EC 6.3.5.2) / GMP synthase [glutamine-hydrolyzing], ATP pyro |
| SCE1572_4912 | FIG01085182: hypothetical protein | bi | sce_4122 | 85.05 FIG01085182: hypothetical protein |
| SCE1572_4913 | hypothetical protein | bi | sce_4123 | 82.31 hypothetical protein |
| SCE1572_4914 | hypothetical protein | bi | sce_4124 | 79.03 hypothetical protein |
| SCE1572_4915 | hypothetical protein | bi | sce_4126 | 84.91 hypothetical protein |
| SCE1572_4916 | serine/threonine protein kinase | bi | sce_4127 | 84.97 serine/threonine protein kinase |
| SCE1572_4917 | FIG01085782: hypothetical protein | bi | sce_4128 | 82.33 FIG01085782: hypothetical protein |

| | | | | |
|--------------|---|-----|----------|--|
| SCE1572_4918 | 2-keto-3-deoxy-D-arabino-heptulosonate-7-phosphate synthase II (EC 2.5.1.54) | bi | see_4129 | 91.74 2-keto-3-deoxy-D-arabino-heptulosonate-7-phosphate synthase II (EC 2.5.1.54) |
| SCE1572_4919 | FIG01087720: hypothetical protein | bi | see_4130 | 69.57 FIG01087720: hypothetical protein |
| SCE1572_4920 | FIG01088212: hypothetical protein | bi | see_4131 | 91.34 FIG01088212: hypothetical protein |
| SCE1572_4921 | RNA-2'-3'-PO4:RNA-5'-OH ligase | bi | see_4132 | 90.43 RNA-2'-3'-PO4:RNA-5'-OH ligase |
| SCE1572_4922 | hypothetical protein | bi | see_4134 | 89.86 hypothetical protein |
| SCE1572_4923 | UDP-glucose 4-epimerase (EC 5.1.3.2) | bi | see_4135 | 96.24 UDP-glucose 4-epimerase (EC 5.1.3.2) |
| SCE1572_4924 | Glutathione S-transferase (EC 2.5.1.18) | bi | see_4136 | 88.79 Glutathione S-transferase (EC 2.5.1.18) |
| SCE1572_4925 | FIG00925933: hypothetical protein | bi | see_4137 | 86.16 FIG00925933: hypothetical protein |
| SCE1572_4926 | Permease of the drug/metabolite transporter (DMT) superfamily | bi | see_4138 | 88.46 Permease of the drug/metabolite transporter (DMT) superfamily |
| SCE1572_4927 | hypothetical protein | - | - | 0 |
| SCE1572_4928 | hypothetical protein | bi | see_4139 | 62 hypothetical protein |
| SCE1572_4929 | protein of unknown function DUF140 | bi | see_4140 | 97.63 ABC transporter, permease |
| SCE1572_4930 | hypothetical protein | bi | see_4141 | 93.68 hypothetical protein |
| SCE1572_4931 | ABC transporter, ATP-binding protein | bi | see_4142 | 96.54 ABC-type organic solvent resistance transport system ATP-binding protein |
| SCE1572_4932 | FIG01087177: hypothetical protein | bi | see_4143 | 93.53 FIG01087177: hypothetical protein |
| SCE1572_4933 | Biotin carboxyl carrier protein of methylcrotonyl-CoA carboxylase | bi | see_4144 | 94.37 Biotin carboxyl carrier protein of methylcrotonyl-CoA carboxylase |
| SCE1572_4934 | COG1565: Uncharacterized conserved protein | bi | see_4145 | 85 COG1565: Uncharacterized conserved protein |
| SCE1572_4935 | Orotidine 5'-phosphate decarboxylase (EC 4.1.1.23) | bi | see_4146 | 87.64 Orotidine 5'-phosphate decarboxylase (EC 4.1.1.23) |
| SCE1572_4936 | TrmH family tRNA/rRNA methyltransferase YacO (EC 2.1.1.-) | bi | see_4147 | 96.77 TrmH family tRNA/rRNA methyltransferase YacO (EC 2.1.1.-) |
| SCE1572_4937 | Cysteine desulfurase (EC 2.8.1.7) | bi | see_4149 | 87.81 Cysteine desulfurase (EC 2.8.1.7) |
| SCE1572_4938 | hypothetical protein | - | - | 0 |
| SCE1572_4939 | Apolipoprotein N-acyltransferase (EC 2.3.1.-) / Copper homeostasis protein CutE | bi | see_4152 | 88.2 Apolipoprotein N-acyltransferase (EC 2.3.1.-) / Copper homeostasis protein CutE |
| SCE1572_4940 | hypothetical protein | bi | see_4154 | 97.69 hypothetical protein |
| SCE1572_4941 | hypothetical protein | bi | see_4155 | 84.04 hypothetical protein |
| SCE1572_4942 | Dephospho-CoA kinase (EC 2.7.1.24) | bi | see_4156 | 87.86 Dephospho-CoA kinase (EC 2.7.1.24) |
| SCE1572_4943 | diguanylate cyclase/phosphodiesterase (GGDEF & EAL domains) with PAS/PAC sensor(s) | bi | see_4157 | 93.28 diguanylate cyclase/phosphodiesterase (GGDEF & EAL domains) with PAS/PAC sensor(s) |
| SCE1572_4944 | Nicotinamidase (EC 3.5.1.19) | bi | see_4158 | 90.22 Nicotinamidase (EC 3.5.1.19) |
| SCE1572_4945 | Nicotinate phosphoribosyltransferase (EC 2.4.2.11) | bi | see_4159 | 89.3 Nicotinate phosphoribosyltransferase (EC 2.4.2.11) |
| SCE1572_4946 | hypothetical protein | - | - | 0 |
| SCE1572_4947 | Methylenetetrahydrofolate dehydrogenase (NADP) (EC 1.5.1.5) / Methylenetetrahydrofolate cyclohydrolase (EC 3.5.4.9) | bi | see_4161 | 87.11 Methylenetetrahydrofolate dehydrogenase (NADP) (EC 1.5.1.5) / Methylenetetrahydrofolate cyclohydrolase (EC 3.5.4.9) |
| SCE1572_4948 | putative esterase | uni | see_1755 | 26.56 putative alpha-dextrin endo-1, 6-alpha-glucosidase |
| SCE1572_4949 | SAM-dependent methyltransferases | bi | see_4162 | 82.64 SAM-dependent methyltransferases |
| SCE1572_4950 | hypothetical protein | bi | see_4899 | 49.14 hypothetical protein |
| SCE1572_4951 | putative ABC transporter ATP-binding protein | bi | see_4163 | 78.77 branched-chain amino acid transport ATP-binding protein livG |
| SCE1572_4952 | Membrane glycoprotein | bi | see_4164 | 76.92 Membrane protein involved in colicin uptake-like protein |
| SCE1572_4953 | peptidase S8 and S53, subtilisin, kexin, sedolisin | uni | see_1234 | 42.94 NADH-ubiquinone oxidoreductase chain J (EC 1.6.5.3) |
| SCE1572_4954 | hypothetical protein | - | - | 0 |
| SCE1572_4955 | Conserved domain protein | bi | see_4165 | 86.29 Conserved domain protein |
| SCE1572_4956 | Phytoene dehydrogenase (EC 1.14.99.-) | bi | see_4166 | 93.28 Phytoene dehydrogenase (EC 1.14.99.-) |
| SCE1572_4957 | EBNA-1 | uni | see_7119 | 55.56 hypothetical protein |
| SCE1572_4958 | Mannose-1-phosphate guanylyltransferase (EC 2.7.7.13) | bi | see_4167 | 87.09 Mannose-1-phosphate guanylyltransferase (EC 2.7.7.13) |
| SCE1572_4959 | hypothetical protein | - | - | 0 |
| SCE1572_4960 | Probable serine/threonine-protein kinase pknH (EC 2.7.11.1) | bi | see_4168 | 83.65 Probable serine/threonine-protein kinase pknH (EC 2.7.11.1) |
| SCE1572_4961 | EBNA-1 | uni | see_1376 | 57.95 Gli0995 protein |
| SCE1572_4962 | FIG01085474: hypothetical protein | bi | see_4173 | 61.93 FIG01085474: hypothetical protein |
| SCE1572_4963 | DNA gyrase subunit A (EC 5.99.1.3) | bi | see_4174 | 97.82 DNA gyrase subunit A (EC 5.99.1.3) |
| SCE1572_4964 | Cation transport protein chaC | bi | see_4175 | 81.48 Cation transport regulator-like protein |
| SCE1572_4965 | WD-40 repeat protein | uni | see_7069 | 69.81 WD-40 repeat protein |
| SCE1572_4966 | hypothetical protein | - | - | 0 |
| SCE1572_4967 | putative membrane protein | bi | see_4176 | 84.71 putative membrane protein |
| SCE1572_4968 | Glutamyl-tRNA(Gln) amidotransferase subunit A (EC 6.3.5.7) | bi | see_4177 | 91.98 Glutamyl-tRNA(Gln) amidotransferase subunit A (EC 6.3.5.7) |
| SCE1572_4969 | hypothetical protein | bi | see_4178 | 70.09 hypothetical protein |
| SCE1572_4970 | hypothetical protein | bi | see_4179 | 53.15 hypothetical protein |
| SCE1572_4971 | hypothetical protein | - | - | 0 |
| SCE1572_4972 | hypothetical protein | bi | see_4181 | 82.67 hypothetical protein |
| SCE1572_4973 | Acetolactate synthase large subunit (EC 2.2.1.6) | bi | see_4182 | 94.55 Acetolactate synthase large subunit (EC 2.2.1.6) |
| SCE1572_4974 | Acetolactate synthase small subunit (EC 2.2.1.6) | bi | see_4183 | 92.86 Acetolactate synthase small subunit (EC 2.2.1.6) |
| SCE1572_4975 | Ketol-acid reductoisomerase (EC 1.1.1.86) | bi | see_4184 | 96.74 Ketol-acid reductoisomerase (EC 1.1.1.86) |
| SCE1572_4976 | 2-isopropylmalate synthase (EC 2.3.3.13) | bi | see_4185 | 97 2-isopropylmalate synthase (EC 2.3.3.13) |
| SCE1572_4977 | (R)-citramalate synthase (EC 2.3.1.182) | bi | see_4186 | 94.16 (R)-citramalate synthase (EC 2.3.1.182) |
| SCE1572_4978 | 3-isopropylmalate dehydrogenase (EC 1.1.1.85) | bi | see_4187 | 96.32 3-isopropylmalate dehydrogenase (EC 1.1.1.85) |
| SCE1572_4979 | hypothetical protein | - | - | 0 |
| SCE1572_4980 | RsbR, positive regulator of sigma-B | uni | see_5835 | 40.96 putative PAS/PAC sensor protein |
| SCE1572_4981 | hypothetical protein | - | - | 0 |
| SCE1572_4982 | hypothetical glycine-rich protein | bi | see_4188 | 55.29 Glycine-rich protein GRP22-like |
| SCE1572_4983 | Nitrate/nitrite transporter | uni | see_3009 | 24.22 Nitrate/nitrite transporter |
| SCE1572_4984 | serine/threonine protein kinase | bi | see_4189 | 89.66 serine/threonine protein kinase |
| SCE1572_4985 | hypothetical protein | - | - | 0 |
| SCE1572_4986 | tRNA dihydrouridine synthase B (EC 1.-.-.) | bi | see_4190 | 95.07 tRNA dihydrouridine synthase B (EC 1.-.-.) |
| SCE1572_4987 | HAD superfamily (Subfamily IG) hydrolase, 5'-nucleotidase | bi | see_4191 | 95.41 HAD superfamily (Subfamily IG) hydrolase, 5'-nucleotidase |
| SCE1572_4988 | RsbS, negative regulator of sigma-B | bi | see_4192 | 90.96 RsbS, negative regulator of sigma-B |
| SCE1572_4989 | Phosphoserine phosphatase RsbX (EC 3.1.3.3) | bi | see_4193 | 89.89 Phosphoserine phosphatase RsbX (EC 3.1.3.3) |
| SCE1572_4990 | anti-sigma B factor RsbT | bi | see_4194 | 95.22 anti-sigma B factor RsbT |
| SCE1572_4991 | hypothetical protein | bi | see_4195 | 63.26 5'-nucleotidase (EC 3.1.3.5) |
| SCE1572_4992 | hypothetical protein | bi | see_4196 | 84.44 hypothetical protein |
| SCE1572_4993 | Mannose-1-phosphate guanylyltransferase | bi | see_4197 | 87.1 Mannose-1-phosphate guanylyltransferase |
| SCE1572_4994 | D,D-heptose 7-phosphate kinase | bi | see_4198 | 96.07 D,D-heptose 7-phosphate kinase |
| SCE1572_4995 | Phosphoheptose isomerase (EC 5.3.1.-) | bi | see_4199 | 96.12 Phosphoheptose isomerase (EC 5.3.1.-) |
| SCE1572_4996 | D-glycero-D-manno-heptose 1,7-bisphosphate phosphatase (EC 3.1.1.-) | bi | see_4200 | 92.61 D-glycero-D-manno-heptose 1,7-bisphosphate phosphatase (EC 3.1.1.-) |
| SCE1572_4997 | hypothetical protein | uni | see_9244 | 28.69 Two-component response regulator |
| SCE1572_4998 | FIG00901899: hypothetical protein | bi | see_4201 | 93.69 FIG00901899: hypothetical protein |
| SCE1572_4999 | DNA polymerase III alpha subunit (EC 2.7.7.7) | bi | see_4202 | 95.13 DNA polymerase III alpha subunit (EC 2.7.7.7) |
| SCE1572_5000 | hypothetical protein | - | - | 0 |
| SCE1572_5001 | FIG01088773: hypothetical protein | bi | see_4203 | 81.34 FIG01088773: hypothetical protein |
| SCE1572_5002 | Putative outer membrane lipoprotein | bi | see_4204 | 88.04 Putative outer membrane lipoprotein |
| SCE1572_5003 | FIG01086127: hypothetical protein | bi | see_4205 | 80.82 FIG01086127: hypothetical protein |
| SCE1572_5004 | hypothetical protein | bi | see_4206 | 76.35 hypothetical protein |
| SCE1572_5005 | hypothetical protein | bi | see_4207 | 98.31 hypothetical protein |
| SCE1572_5006 | hypothetical protein | bi | see_4208 | 97.8 hypothetical protein |
| SCE1572_5007 | Cyclic AMP receptor protein | bi | see_4209 | 98.42 Cyclic AMP receptor protein |
| SCE1572_5008 | FIG01088052: hypothetical protein | bi | see_4210 | 93.53 FIG01088052: hypothetical protein |
| SCE1572_5009 | FIG01088898: hypothetical protein | bi | see_4211 | 98.2 FIG01088898: hypothetical protein |
| SCE1572_5010 | UDP-glucose 4-epimerase (EC 5.1.3.2) | bi | see_4212 | 93.1 UDP-glucose 4-epimerase (EC 5.1.3.2) |
| SCE1572_5011 | Protein YicC | bi | see_4213 | 96.92 Protein YicC |
| SCE1572_5012 | Guanylate kinase (EC 2.7.4.8) | bi | see_4214 | 99.53 Guanylate kinase (EC 2.7.4.8) |
| SCE1572_5013 | 5'-methylthioadenosine phosphorylase (EC 2.4.2.28) | bi | see_4215 | 89.15 5'-methylthioadenosine phosphorylase (EC 2.4.2.28) |
| SCE1572_5014 | Ribokinase (EC 2.7.1.15) | bi | see_4216 | 94.81 Ribokinase (EC 2.7.1.15) |
| SCE1572_5015 | hypothetical protein | bi | see_4217 | 94.01 hypothetical protein |
| SCE1572_5016 | Serine/threonine-protein kinase (EC 2.7.1.-) | bi | see_4218 | 77.26 Serine/threonine-protein kinase (EC 2.7.1.-) |
| SCE1572_5017 | hypothetical protein | bi | see_4219 | 83.64 WW domain binding protein 11 |
| SCE1572_5018 | Prolyl-tRNA synthetase (EC 6.1.1.15), archaeal/eukaryal type | bi | see_4220 | 95.95 Prolyl-tRNA synthetase (EC 6.1.1.15), archaeal/eukaryal type |
| SCE1572_5019 | Isospartyl aminopeptidase (EC 3.4.19.5) @ Asp-X dipeptidase | bi | see_4221 | 87.92 Isospartyl aminopeptidase (EC 3.4.19.5) @ Asp-X dipeptidase |
| SCE1572_5020 | Phytoene dehydrogenase and related proteins | bi | see_4222 | 91.33 Phytoene dehydrogenase and related proteins |
| SCE1572_5021 | sigma-54 dependent transcriptional regulator | bi | see_4223 | 86.37 sigma-54 dependent transcriptional regulator |
| SCE1572_5022 | hypothetical protein | bi | see_4225 | 88.42 hypothetical protein |
| SCE1572_5023 | hypothetical protein | - | - | 0 |
| SCE1572_5024 | FIG01086339: hypothetical protein | bi | see_4226 | 83.27 COG3511: Phospholipase C |
| SCE1572_5025 | Proposed peptidoglycan lipid II flippase MurJ | bi | see_4227 | 90.74 Proposed peptidoglycan lipid II flippase MurJ |
| SCE1572_5026 | FIG01087105: hypothetical protein | bi | see_4228 | 85.86 FIG01087105: hypothetical protein |
| SCE1572_5027 | Sil0670 protein | bi | see_4229 | 85.49 Sil0670 protein |
| SCE1572_5028 | FIG01088567: hypothetical protein | bi | see_4230 | 83.48 FIG01088567: hypothetical protein |
| SCE1572_5029 | Putative deoxyribonuclease YefH | bi | see_4231 | 95.79 Putative deoxyribonuclease YefH |
| SCE1572_5030 | putative serine protein kinase, PrkA | bi | see_4232 | 97.09 putative serine protein kinase, PrkA |
| SCE1572_5031 | hypothetical protein | bi | see_4233 | 88.05 hypothetical protein |
| SCE1572_5032 | serine/threonine protein kinase | bi | see_4234 | 86.54 serine/threonine protein kinase |
| SCE1572_5033 | FIG137478: Hypothetical protein | bi | see_4235 | 93.23 FIG137478: Hypothetical protein |
| SCE1572_5034 | Butyryl-CoA dehydrogenase (EC 1.3.99.2) | bi | see_4236 | 91.19 putative serine/threonine protein kinase |
| SCE1572_5035 | Sulfatase-modifying factor 2 precursor (C-alpha-formylglycine-generating enzyme 2) | bi | see_4237 | 83.38 Butyryl-CoA dehydrogenase (EC 1.3.99.2) |
| SCE1572_5036 | hypothetical protein | - | - | 0 |
| SCE1572_5037 | Excinuclease ABC subunit A | bi | see_4238 | 96.49 Excinuclease ABC subunit A |
| SCE1572_5038 | C4-type zinc finger protein, DksA/TrpR family | bi | see_4239 | 96.67 C4-type zinc finger protein, DksA/TrpR family |
| SCE1572_5039 | hypothetical protein | - | - | 0 |
| SCE1572_5040 | BIl5330 protein | bi | see_4240 | 87.88 BIl5330 protein |
| SCE1572_5041 | FIG01088310: hypothetical protein | bi | see_4241 | 97.95 FIG01088310: hypothetical protein |
| SCE1572_5042 | N-acetylmuramoyl-L-alanine amidase (EC 3.5.1.28) | bi | see_4242 | 88.61 N-acetylmuramoyl-L-alanine amidase (EC 3.5.1.28) |
| SCE1572_5043 | hypothetical protein | bi | see_4243 | 92.75 hypothetical protein |
| SCE1572_5044 | hypothetical protein | bi | see_4244 | 57.14 Serine/threonine-protein kinase pkn3 (EC 2.7.11.1) |
| SCE1572_5045 | Dihydroliipoamide acetyltransferase component of pyruvate dehydrogenase complex (EC 2.3.1.12) | bi | see_4245 | 75.78 Dihydroliipoamide acetyltransferase component of pyruvate dehydrogenase complex (EC 2.3.1.12) |
| SCE1572_5046 | hypothetical protein | - | - | 0 |
| SCE1572_5047 | hypothetical protein | bi | see_6904 | 86.22 FIG01089354: hypothetical protein |
| SCE1572_5048 | DNA repair protein RadC | uni | see_512 | 81.25 DNA repair protein RadC |
| SCE1572_5049 | hypothetical protein | uni | see_513 | 78.34 FIG01087636: hypothetical protein |
| SCE1572_5050 | Transcriptional regulator Cro/Cl family | uni | see_514 | 52.44 hypothetical protein |
| SCE1572_5051 | FIG01087953: hypothetical protein | uni | see_6129 | 33.56 FIG01088173: hypothetical protein |
| SCE1572_5052 | FIG01087372: hypothetical protein | uni | see_522 | 92.2 FIG01087372: hypothetical protein |
| SCE1572_5053 | Probable serine/threonine-protein kinase pknH (EC 2.7.11.1) | uni | see_3991 | 56.25 serine/threonine protein kinase |
| SCE1572_5054 | Probable serine/threonine-protein kinase pknH (EC 2.7.11.1) | uni | see_8864 | 35.53 serine/threonine protein kinase |
| SCE1572_5055 | S-layer protein | uni | see_3992 | 41.99 S-layer-like array protein |
| SCE1572_5056 | Branched-chain amino acid ABC transporter, amino acid-binding protein (TC 3.A.1.4.1) | uni | see_7667 | 51.6 FIG01085006: hypothetical protein |
| SCE1572_5057 | Deoxyhypusine synthase | bi | see_7841 | 95.65 Deoxyhypusine synthase |
| SCE1572_5058 | Response regulator of zinc sigma-54-dependent two-component system | bi | see_4246 | 81.74 Response regulator of zinc sigma-54-dependent two-component system |
| SCE1572_5059 | hypothetical protein | bi | see_4247 | 77.49 hypothetical protein |
| SCE1572_5060 | Protein serine/threonine phosphatase PrpC, regulation of stationary phase | bi | see_4248 | 82.31 Protein serine/threonine phosphatase PrpC, regulation of stationary phase |
| SCE1572_5061 | FKBP-type peptidyl-prolyl cis-trans isomerase FkpA precursor (EC 5.2.1.8) | bi | see_4250 | 93.58 probable FkpB-type peptidyl-prolyl cis-trans isomerase (EC 5.2.1.8) |
| SCE1572_5062 | hypothetical protein | bi | see_4251 | 93.1 hypothetical protein |
| SCE1572_5063 | hypothetical protein | bi | see_4252 | 71.73 hypothetical protein |
| SCE1572_5064 | hypothetical protein | bi | see_4253 | 87.75 FIG01085462: hypothetical protein |
| SCE1572_5065 | serine/threonine protein kinase | bi | see_4254 | 80.24 serine/threonine protein kinase |
| SCE1572_5066 | Pyruvate dehydrogenase E1 component alpha subunit (EC 1.2.4.1) | bi | see_4255 | 95.69 Pyruvate dehydrogenase E1 component alpha subunit (EC 1.2.4.1) |
| SCE1572_5067 | Pyruvate dehydrogenase E1 component beta subunit (EC 1.2.4.1) | bi | see_4256 | 96.18 Pyruvate dehydrogenase E1 component beta subunit (EC 1.2.4.1) |
| SCE1572_5068 | Dihydroliipoamide acetyltransferase component of pyruvate dehydrogenase complex (EC 2.3.1.12) | bi | see_4257 | 91.67 Dihydroliipoamide acetyltransferase component of pyruvate dehydrogenase complex (EC 2.3.1.12) |
| SCE1572_5069 | FIG01089217: hypothetical protein | bi | see_4258 | 94.82 FIG01089217: hypothetical protein |
| SCE1572_5070 | Putative ATP/GTP-binding protein | bi | see_4259 | 91.22 Putative ATP/GTP-binding protein |
| SCE1572_5071 | ATPase involved in DNA repair | bi | see_4260 | 89.7 ATPase involved in DNA repair |
| SCE1572_5072 | Sulfatase modifying factor 1 precursor (C-alpha-formylglycine-generating enzyme 1) | bi | see_4261 | 88.25 Sulfatase modifying factor 1 precursor (C-alpha-formylglycine-generating enzyme 1) |
| SCE1572_5073 | Metallophosphoesterase | bi | see_4262 | 89.49 Metallophosphoesterase |
| SCE1572_5074 | Cold shock protein CspG | bi | see_4263 | 100 Cold shock protein CspG |
| SCE1572_5075 | PE-PGRS family protein | uni | see_3858 | 34.96 Adenosylhomocysteinase (EC 3.3.1.1) |
| SCE1572_5076 | Type II/IV secretion system ATP hydrolase TadaA/VirB11/CpaF, TadaA subfamily | bi | see_4265 | 86.66 Type II/IV secretion system ATP hydrolase TadaA/VirB11/CpaF, TadaA subfamily |
| SCE1572_5077 | Peptide deformylase (EC 3.5.1.88) | bi | see_4266 | 94.05 Peptide deformylase (EC 3.5.1.88) |
| SCE1572_5078 | Diaminohydroxyphosphoribosylaminopyrimidine deaminase (EC 3.5.4.26) / 5-amino-6-(5-phosphoribosylamino)uracil reductase | bi | see_4267 | 95.54 Diaminohydroxyphosphoribosylaminopyrimidine deaminase (EC 3.5.4.26) / 5-amino-6-(5-phosphoribosylamino)uracil reductase (EC 3.5.1.8) |
| SCE1572_5079 | Ribonucleotide reductase transcriptional regulator NrdR | bi | see_4268 | 98.04 Ribonucleotide reductase transcriptional regulator NrdR |
| SCE1572_5080 | 3-oxoacyl-[acyl-carrier-protein] synthase, KASII (EC 2.3.1.41) | bi | see_4269 | 96.14 3-oxoacyl-[acyl-carrier-protein] synthase, KASII (EC 2. |

| | | | | |
|--------------|---|-----|-----------|--|
| SCE1572_5082 | 3-oxoacyl-[acyl-carrier protein] reductase (EC 1.1.1.100) | bi | see_4271 | 95.16 3-oxoacyl-[acyl-carrier protein] reductase (EC 1.1.1.100) |
| SCE1572_5083 | Malonyl CoA-acyl carrier protein transacylase (EC 2.3.1.39) | bi | see_4272 | 92.26 Malonyl CoA-acyl carrier protein transacylase (EC 2.3.1.39) |
| SCE1572_5084 | 3-oxoacyl-[acyl-carrier-protein] synthase, KASIII (EC 2.3.1.41) | bi | see_4273 | 91.54 3-oxoacyl-[acyl-carrier-protein] synthase, KASIII (EC 2.3.1.41) |
| SCE1572_5085 | hypothetical protein | - | - | 0 |
| SCE1572_5086 | LSU ribosomal protein L32p | bi | see_4274 | 98.44 LSU ribosomal protein L32p |
| SCE1572_5087 | COG1399 protein in cluster with ribosomal protein L32p, putative divergent | bi | see_4275 | 88.57 COG1399 protein in cluster with ribosomal protein L32p, putative divergent |
| SCE1572_5088 | hypothetical protein | bi | see_4276 | 90.09 hypothetical protein |
| SCE1572_5089 | Uracil phosphoribosyltransferase (EC 2.4.2.9) / Pyrimidine operon regulatory protein PyrR | bi | see_4277 | 96.26 Uracil phosphoribosyltransferase (EC 2.4.2.9) / Pyrimidine operon regulatory protein PyrR |
| SCE1572_5090 | Aspartate carbamoyltransferase (EC 2.1.3.2) | bi | see_4278 | 97.19 Aspartate carbamoyltransferase (EC 2.1.3.2) |
| SCE1572_5091 | NAD synthetase (EC 6.3.1.5) | bi | see_4279 | 95.37 NAD synthetase (EC 6.3.1.5) |
| SCE1572_5092 | hypothetical protein | - | - | 0 |
| SCE1572_5093 | Acyl carrier protein | bi | see_4280 | 96.51 conserved hypothetical protein |
| SCE1572_5094 | Long-chain-fatty-acid--CoA ligase (EC 6.2.1.3) | bi | see_4281 | 94.52 Long-chain-fatty-acid--CoA ligase (EC 6.2.1.3) |
| SCE1572_5095 | Asparagine synthetase [glutamine-hydrolyzing] (EC 6.3.5.4) | bi | see_4282 | 95.24 Asparagine synthetase [glutamine-hydrolyzing] (EC 6.3.5.4) |
| SCE1572_5096 | FIG01088601: hypothetical protein | umi | see_4283 | 64.95 FIG01088601: hypothetical protein |
| SCE1572_5097 | FIG01086664: hypothetical protein | bi | see_4284 | 84.8 FIG01086664: hypothetical protein |
| SCE1572_5098 | Probable serine/threonine-protein kinase pknH (EC 2.7.11.1) | bi | see_4285 | 79.48 Probable serine/threonine-protein kinase pknH (EC 2.7.11.1) |
| SCE1572_5099 | TPR domain protein, putative component of TonB system | bi | see_4286 | 84.02 TPR domain protein, putative component of TonB system |
| SCE1572_5100 | hypothetical protein | bi | see_4287 | 67.6 hypothetical protein |
| SCE1572_5101 | FIG01086678: hypothetical protein | bi | see_4288 | 77.25 FIG01086678: hypothetical protein |
| SCE1572_5102 | putative zinc protease | bi | see_4289 | 93.61 FIG015287: Zinc protease |
| SCE1572_5103 | Protease precursor | bi | see_4290 | 92.5 Protease precursor |
| SCE1572_5104 | Possible N-terminal part of IF-2 | bi | see_4291 | 86.51 Possible N-terminal part of IF-2 |
| SCE1572_5105 | Translation elongation factor LepA | bi | see_4292 | 97.17 Translation elongation factor LepA |
| SCE1572_5106 | hypothetical protein | bi | see_4293 | 95.65 hypothetical protein |
| SCE1572_5107 | putative lipoprotein | bi | see_4294 | 76.07 putative lipoprotein |
| SCE1572_5108 | conserved hypothetical protein | bi | see_4295 | 88.76 putative lipoprotein |
| SCE1572_5109 | hypothetical protein | umi | see_4297 | 35.34 GTP-binding protein EngA |
| SCE1572_5110 | Putative 2-component regulator | bi | see_4297 | 98.56 Putative 2-component regulator |
| SCE1572_5111 | anaerobic nitric oxide reductase transcription regulator NorR | bi | see_4298 | 97.57 anaerobic nitric oxide reductase transcription regulator NorR |
| SCE1572_5112 | UPF0103 protein TTHA0924 | bi | see_4299 | 89.74 UPF0103 protein TTHA0924 |
| SCE1572_5113 | hypothetical protein | bi | see_4300 | 85.96 Dsr1 |
| SCE1572_5114 | GTP pyrophosphokinase (EC 2.7.6.5) / Guanosine-3'-5'-bis(diphosphate) 3'-pyrophosphohydrolase (EC 3.1.1.7) | bi | see_4301 | 97.79 GTP pyrophosphokinase (EC 2.7.6.5) / Guanosine-3'-5'-bis(diphosphate) 3'-pyrophosphohydrolase (EC 3.1.1.7) |
| SCE1572_5115 | Hypothetical radical SAM family enzyme, NOT coproporphyrinogen III oxidase, oxygen-independent | bi | see_4303 | 89.81 Hypothetical radical SAM family enzyme, NOT coproporphyrinogen III oxidase, oxygen-independent |
| SCE1572_5116 | Threonine dehydratase, catabolic (EC 4.3.1.19) | bi | see_4304 | 86.54 Threonine dehydratase, catabolic (EC 4.3.1.19) |
| SCE1572_5117 | 5-aminopentanamide (EC 3.5.1.30) | bi | see_4305 | 82.06 5-aminopentanamide (EC 3.5.1.30) |
| SCE1572_5118 | Response regulator receiver domain protein | bi | see_4306 | 94.96 Response regulator receiver domain protein |
| SCE1572_5119 | Adenylate cyclase (EC 4.6.1.1) / Guanylate cyclase (EC 4.6.1.2) | bi | see_4307 | 86.11 Adenylate cyclase (EC 4.6.1.1) / Guanylate cyclase (EC 4.6.1.2) |
| SCE1572_5120 | FIG01086499: hypothetical protein | bi | see_4308 | 70.86 FIG01086499: hypothetical protein |
| SCE1572_5121 | Membrane-bound lytic murein transglycosylase D precursor (EC 3.2.1.-) | bi | see_4309 | 88.84 Membrane-bound lytic murein transglycosylase D precursor (EC 3.2.1.-) |
| SCE1572_5122 | Organic hydroperoxide resistance transcriptional regulator | bi | see_4310 | 91.19 Organic hydroperoxide resistance transcriptional regulator |
| SCE1572_5123 | RTX toxins and related Ca ²⁺ -binding proteins | bi | see_4311 | 74.68 FIG01088538: hypothetical protein |
| SCE1572_5124 | CDP-alcohol phosphatidyltransferase | - | - | 0 |
| SCE1572_5125 | PAP2 family protein | - | - | 0 |
| SCE1572_5126 | hypothetical protein | - | - | 0 |
| SCE1572_5127 | hypothetical protein | bi | see_4314 | 81.2 hypothetical protein |
| SCE1572_5128 | Sulfur carrier protein adenylyltransferase ThiF | bi | see_4315 | 94.06 Sulfur carrier protein adenylyltransferase ThiF |
| SCE1572_5129 | hypothetical protein | - | - | 0 |
| SCE1572_5130 | hypothetical protein | bi | see_4317 | 86.36 hypothetical protein |
| SCE1572_5131 | hypothetical protein | bi | see_4318 | 92 hypothetical protein |
| SCE1572_5132 | TPR domain protein, putative component of TonB system | bi | see_4319 | 94.97 TPR domain protein, putative component of TonB system |
| SCE1572_5133 | annexin VII | umi | see_8512 | 54.81 hypothetical protein |
| SCE1572_5134 | hypothetical protein | bi | see_4320 | 91.89 hypothetical protein |
| SCE1572_5135 | histone protein | bi | see_4321 | 80.16 conserved hypothetical protein |
| SCE1572_5136 | hypothetical protein | bi | see_4322 | 87.7 hypothetical protein |
| SCE1572_5137 | hypothetical protein | bi | see_4323 | 86.93 hypothetical protein |
| SCE1572_5138 | hypothetical protein | - | - | 0 |
| SCE1572_5139 | hypothetical protein | - | - | 0 |
| SCE1572_5140 | hypothetical protein | - | - | 0 |
| SCE1572_5141 | Nudix hydrolase 3 (EC 3.6.1.-) | bi | see_4324 | 85.43 hypothetical protein |
| SCE1572_5142 | metallophosphoesterase | bi | see_4325 | 81.01 metallophosphoesterase |
| SCE1572_5143 | hypothetical protein | - | - | 0 |
| SCE1572_5144 | hypothetical protein | - | - | 0 |
| SCE1572_5145 | FIG01086383: hypothetical protein | bi | see_3918 | 85.79 FIG01086383: hypothetical protein |
| SCE1572_5146 | Diaphanous protein homolog 2 | umi | see_1504 | 52.88 hypothetical protein |
| SCE1572_5147 | Glycoprotein gp2 | umi | see_1503 | 52.18 Glycoprotein gp2 |
| SCE1572_5148 | FIG01089660: hypothetical protein | bi | see_4330 | 85.71 FIG01089660: hypothetical protein |
| SCE1572_5149 | TPR repeat | umi | see_4258 | 33.56 FIG01089217: hypothetical protein |
| SCE1572_5150 | FIG01088065: hypothetical protein | bi | see_4331 | 81.73 FIG01088065: hypothetical protein |
| SCE1572_5151 | hypothetical protein | umi | see_577 | 52.31 zinc finger/thioredoxin putative |
| SCE1572_5152 | hypothetical protein | - | - | 0 |
| SCE1572_5153 | hypothetical protein | - | - | 0 |
| SCE1572_5154 | Oligonucleotide cyclase/lipid transport protein | bi | see_4332 | 94.27 hypothetical protein |
| SCE1572_5155 | hypothetical protein | umi | see_7119 | 45.07 hypothetical protein |
| SCE1572_5156 | hypothetical protein | - | - | 0 |
| SCE1572_5157 | FIG01087380: hypothetical protein | bi | see_4333 | 84.19 FIG01087380: hypothetical protein |
| SCE1572_5158 | hypothetical protein | - | - | 0 |
| SCE1572_5159 | hypothetical protein | bi | see_4334 | 82.45 oxidoreductase, 2OG-Fe(II) oxygenase family |
| SCE1572_5160 | NAD-dependent protein deacetylase of SIR2 family | bi | see_4335 | 89.75 NAD-dependent protein deacetylase of SIR2 family |
| SCE1572_5161 | hypothetical protein | - | - | 0 |
| SCE1572_5162 | hypothetical protein | - | - | 0 |
| SCE1572_5163 | hypothetical protein | - | - | 0 |
| SCE1572_5164 | hypothetical | bi | see_7843 | 82.49 hypothetical |
| SCE1572_5165 | hypothetical protein | umi | see_3180 | 42.31 FIG01089285: hypothetical protein |
| SCE1572_5166 | erythrocyte membrane protein 1 (PEMP1) | umi | see_8647 | 51.02 Arylsulfatase (EC 3.1.6.1) |
| SCE1572_5167 | FIG01085964: hypothetical protein | bi | see_5858 | 66.67 FIG01085964: hypothetical protein |
| SCE1572_5168 | putative lipoprotein | - | - | 0 |
| SCE1572_5169 | hypothetical protein | - | - | 0 |
| SCE1572_5170 | Ribonucleotide reductase of class Ia (aerobic), alpha subunit (EC 1.17.4.1) | bi | see_4336 | 88.19 Ribonucleotide reductase of class Ia (aerobic), alpha subunit (EC 1.17.4.1) |
| SCE1572_5171 | Ribonucleotide reductase of class Ia (aerobic), beta subunit (EC 1.17.4.1) | bi | see_4337 | 92.26 Ribonucleotide reductase of class Ia (aerobic), beta subunit (EC 1.17.4.1) |
| SCE1572_5172 | hypothetical protein | - | - | 0 |
| SCE1572_5173 | hypothetical protein | - | - | 0 |
| SCE1572_5174 | periplasmic binding protein | - | - | 0 |
| SCE1572_5175 | ABC transport protein, ATP-binding component | umi | see_10231 | 37.38 Putrescine transport ATP-binding protein PotA (TC 3.A.1.11.1) |
| SCE1572_5176 | Vitamin B12 ABC transporter, permease component BtuC | bi | see_327 | 38.29 Vitamin B12 ABC transporter, permease component BtuC |
| SCE1572_5177 | hypothetical protein | bi | see_4338 | 81.2 hypothetical protein |
| SCE1572_5178 | Outer membrane vitamin B12 receptor BtuB | bi | see_4339 | 80.49 Outer membrane vitamin B12 receptor BtuB |
| SCE1572_5179 | hypothetical protein | umi | see_3858 | 36.31 Adenosylhomocysteinase (EC 3.3.1.1) |
| SCE1572_5180 | Isochorismate synthase (EC 5.4.4.2) of siderophore biosynthesis | bi | see_4340 | 83.41 Isochorismate synthase (EC 5.4.4.2) of siderophore biosynthesis |
| SCE1572_5181 | Isochorismatase (EC 3.3.2.1) of siderophore biosynthesis | bi | see_4342 | 78.12 Isochorismatase (EC 3.3.2.1) of siderophore biosynthesis |
| SCE1572_5182 | iron-chelator utilization protein | bi | see_4343 | 77.42 iron-chelator utilization protein |
| SCE1572_5183 | 2,3-dihydro-2,3-dihydroxybenzoate dehydrogenase (EC 1.3.1.28) [bacillibactin] siderophore @ 2,3-dihydro-2,3-dihydroxybenzoate | bi | see_4344 | 81.4 2,3-dihydro-2,3-dihydroxybenzoate dehydrogenase (EC 1.3.1.28) [bacillibactin] siderophore @ 2,3-dihydro-2,3-dihydroxybenzoate |
| SCE1572_5184 | hypothetical protein | bi | see_4345 | 72.29 hypothetical protein |
| SCE1572_5185 | MxcI | bi | see_4346 | 67.06 MxcI |
| SCE1572_5186 | TonB-dependent receptor | bi | see_4347 | 61.57 TonB-dependent receptor |
| SCE1572_5187 | hypothetical protein | - | - | 0 |
| SCE1572_5188 | non-ribosomal peptide synthase MxcG | bi | see_4350 | 37.5 Non-ribosomal peptide synthase MxcG |
| SCE1572_5189 | Arabinose efflux permease | bi | see_4352 | 78.8 Arabinose efflux permease |
| SCE1572_5190 | major facilitator superfamily MFS_1 | - | - | 0 |
| SCE1572_5191 | Assimilatory nitrate reductase large subunit (EC:1.7.99.4) | umi | see_1282 | 45.3 Assimilatory nitrate reductase large subunit (EC:1.7.99.4) |
| SCE1572_5192 | Fe-S-cluster-containing hydrogenase components 1 | umi | see_5260 | 30.23 Fe-S-cluster-containing hydrogenase components 1 |
| SCE1572_5193 | Rieske (2Fe-2S) region | - | - | 0 |
| SCE1572_5194 | hypothetical protein | - | - | 0 |
| SCE1572_5195 | C4-dicarboxylate transporter/malic acid transport protein | - | - | 0 |
| SCE1572_5196 | Redoxin | - | - | 0 |
| SCE1572_5197 | hypothetical protein | - | - | 0 |
| SCE1572_5198 | HRC protein | - | - | 0 |
| SCE1572_5199 | 3-oxoacyl-[acyl-carrier protein] reductase (EC 1.1.1.100) | umi | see_8328 | 44.53 3-oxoacyl-[acyl-carrier protein] reductase (EC 1.1.1.100) |
| SCE1572_5200 | long-chain fatty acid transport protein | bi | see_4359 | 85.26 hypothetical protein |
| SCE1572_5201 | hypothetical protein | umi | see_5640 | 29.19 FIG01089683: hypothetical protein |
| SCE1572_5202 | Ribosomal RNA large subunit methyltransferase N (EC 2.1.1.-) | bi | see_4360 | 91.02 Ribosomal RNA large subunit methyltransferase N (EC 2.1.1.-) |
| SCE1572_5203 | Twin-arginine translocation protein TatB | bi | see_4361 | 51.11 Twin-arginine translocation protein TatB |
| SCE1572_5204 | Twin-arginine translocation protein TatC | bi | see_4362 | 90.17 Twin-arginine translocation protein TatC |
| SCE1572_5205 | Prolipoprotein diacylglycerol transferase (EC 2.4.99.-) | bi | see_4363 | 93.91 Prolipoprotein diacylglycerol transferase (EC 2.4.99.-) |
| SCE1572_5206 | Lipoprotein signal peptidase (EC 3.4.23.36) | bi | see_4364 | 88.05 Lipoprotein signal peptidase (EC 3.4.23.36) |
| SCE1572_5207 | Lipoprotein signal peptidase (EC 3.4.23.36) | bi | see_4365 | 84.14 Lipoprotein signal peptidase (EC 3.4.23.36) |
| SCE1572_5208 | OmpA family protein | bi | see_4366 | 70.62 Outer membrane lipoprotein omp16 precursor |
| SCE1572_5209 | FIG01086986: hypothetical protein | bi | see_4367 | 72.65 FIG01086986: hypothetical protein |
| SCE1572_5210 | hypothetical protein | - | - | 0 |
| SCE1572_5211 | ATP-dependent RNA helicase | bi | see_4368 | 95.51 ATP-dependent RNA helicase |
| SCE1572_5212 | Short chain dehydrogenase | bi | see_9054 | 86.54 Short chain dehydrogenase |
| SCE1572_5213 | serine/threonine protein kinase | bi | see_4370 | 78.3 serine/threonine protein kinase |
| SCE1572_5214 | Mir5283 protein | bi | see_4371 | 89.47 Mir5283 protein |
| SCE1572_5215 | Fimh-like protein | bi | see_4372 | 76.98 Fimh-like protein |
| SCE1572_5216 | hypothetical protein | - | - | 0 |
| SCE1572_5217 | Serine protease precursor | bi | see_4373 | 82.2 Serine protease precursor |
| SCE1572_5218 | hypothetical protein | - | - | 0 |
| SCE1572_5219 | hypothetical protein | - | - | 0 |
| SCE1572_5220 | FIG01087528: hypothetical protein | bi | see_4374 | 83.42 FIG01087528: hypothetical protein |
| SCE1572_5221 | FIG01085600: hypothetical protein | bi | see_4375 | 94.85 FIG01085600: hypothetical protein |
| SCE1572_5222 | FIG00706509: hypothetical protein | bi | see_4377 | 91.5 FIG00706509: hypothetical protein |
| SCE1572_5223 | Huntingtin interacting protein E-like protein | bi | see_4378 | 87.84 Huntingtin interacting protein E-like protein |
| SCE1572_5224 | Endonuclease III (EC 4.2.99.18) | bi | see_4379 | 85.19 Endonuclease III (EC 4.2.99.18) |
| SCE1572_5225 | hypothetical protein | bi | see_4380 | 72.04 hypothetical protein |
| SCE1572_5226 | putative periplasmic protein kinase ArgK and related GTPases of G3E family | bi | see_4381 | 91.34 putative periplasmic protein kinase ArgK and related GTPases of G3E family |
| SCE1572_5227 | hypothetical protein | bi | see_4382 | 71.23 PE-PGRS FAMILY PROTEIN |
| SCE1572_5228 | Arginine-tRNA-protein transferase (EC 2.3.2.8) | bi | see_4383 | 91.67 arginine-tRNA-protein transferase |
| SCE1572_5229 | RNA binding protein | bi | see_4384 | 94 RNA binding protein |
| SCE1572_5230 | Glutamate synthase [NADPH] small chain (EC 1.4.1.13) | bi | see_4385 | 93.54 Glutamate synthase [NADPH] small chain (EC 1.4.1.13) |
| SCE1572_5231 | Biotin carboxylase of acetyl-CoA carboxylase (EC 6.3.4.14) | bi | see_4386 | 95.76 Biotin carboxylase of acetyl-CoA carboxylase (EC 6.3.4.14) |
| SCE1572_5232 | Biotin carboxyl carrier protein of acetyl-CoA carboxylase | bi | see_4387 | 88.7 Biotin carboxyl carrier protein of acetyl-CoA carboxylase |
| SCE1572_5233 | 3-dehydroquinate dehydratase I (EC 4.2.1.10) | bi | see_4388 | 93.75 3-dehydroquinate dehydratase I (EC 4.2.1.10) |
| SCE1572_5234 | hypothetical protein | bi | see_4389 | 98.32 hypothetical protein |
| SCE1572_5235 | Aconitate hydratase (EC 4.2.1.3) | bi | see_4390 | 95.58 Aconitate hydratase (EC 4.2.1.3) |
| SCE1572_5236 | hypothetical protein | bi | see_4391 | 85.21 hypothetical protein |
| SCE1572_5237 | FIG01089373: hypothetical protein | bi | see_4392 | 92.35 FIG01089373: hypothetical protein |
| SCE1572_5238 | Sulfatase | bi | see_4393 | 83.99 Sulfatase |
| SCE1572_5239 | FIG01087844: hypothetical protein | bi | see_4394 | 81.4 FIG01087844: hypothetical protein |
| SCE1572_5240 | hypothetical protein | bi | see_4395 | 83.82 hypothetical protein |
| SCE1572_5241 | FIG01087817: hypothetical protein | bi | see_4396 | 84.89 FIG01087817: hypothetical protein |
| SCE1572_5242 | hypothetical protein | bi | see_4397 | 86.43 hypothetical protein |
| SCE1572_5243 | hypothetical protein | bi | see_4398 | 100 hypothetical protein |
| SCE1572_5244 | A/G-specific adenine glycosylase (EC 3.2.2.-) | bi | see_4399 | 89.77 A/G-specific adenine glycosylase (EC 3.2.2.-) |
| SCE1572_5245 | hypothetical protein | bi | see_4400 | 84.35 hypothetical protein |

| | | | | |
|--------------|--|-----|----------|--|
| SCE1572_5246 | conserved hypothetical protein | bi | sce_4402 | 98.81 conserved hypothetical protein |
| SCE1572_5247 | hypothetical protein | bi | sce_4403 | 93.28 hypothetical protein |
| SCE1572_5248 | FIG01085847: hypothetical protein | bi | sce_4404 | 86.65 FIG01085847: hypothetical protein |
| SCE1572_5249 | FIG01088685: hypothetical protein | bi | sce_4405 | 78.83 FIG01088685: hypothetical protein |
| SCE1572_5250 | hypothetical protein with 50bp hit to Dihydrolypoamide acetyltransferase | bi | sce_4406 | 90.63 hypothetical protein with 50bp hit to Dihydrolypoamide acetyltransferase |
| SCE1572_5251 | serine/threonine protein kinase Pkn1 | bi | sce_4407 | 78.28 serine/threonine protein kinase Pkn1 |
| SCE1572_5252 | hypothetical protein | bi | sce_4408 | 83.61 hypothetical protein |
| SCE1572_5253 | hypothetical protein | - | - | 0 |
| SCE1572_5254 | serine/threonine protein kinase Pkn9(EC:2.7.1.-) | bi | sce_4409 | 74.43 serine/threonine protein kinase Pkn9(EC:2.7.1.-) |
| SCE1572_5255 | hypothetical protein | bi | sce_4410 | 58.62 hypothetical protein |
| SCE1572_5256 | hypothetical protein | bi | sce_4411 | 90.8 transglycosylase-associated protein |
| SCE1572_5257 | hypothetical protein | bi | sce_4412 | 77.74 FIG01088464: hypothetical protein |
| SCE1572_5258 | hypothetical protein | - | - | 0 |
| SCE1572_5259 | serine/threonine protein kinase | bi | sce_4413 | 86.09 serine/threonine protein kinase |
| SCE1572_5260 | Membrane protein involved in the export of O-antigen, teichoic acid lipoteichoic acids | bi | sce_4415 | 91.25 O-antigen transporter related protein |
| SCE1572_5261 | FIG01087063: hypothetical protein | bi | sce_4416 | 86.67 FIG01087063: hypothetical protein |
| SCE1572_5262 | Signal recognition particle receptor protein FtsY (=alpha subunit) (TC 3.A.5.1.1) | - | - | 0 |
| SCE1572_5263 | hypothetical protein | - | - | 0 |
| SCE1572_5264 | Fatty acid hydroxylase | bi | sce_4418 | 91.98 Fatty acid hydroxylase |
| SCE1572_5265 | hypothetical protein | - | - | 0 |
| SCE1572_5266 | Alcohol dehydrogenase (EC 1.1.1.1) | bi | sce_4420 | 96.87 Alcohol dehydrogenase (EC 1.1.1.1) |
| SCE1572_5267 | glutamine synthetase family protein | bi | sce_4421 | 92.05 glutamine synthetase family protein |
| SCE1572_5268 | hypothetical protein | bi | sce_4422 | 89.22 hypothetical protein |
| SCE1572_5269 | Serine/threonine kinase | bi | sce_4423 | 88.59 Serine/threonine kinase |
| SCE1572_5270 | hypothetical protein | bi | sce_4424 | 92 hypothetical protein |
| SCE1572_5271 | hypothetical protein | - | - | 0 |
| SCE1572_5272 | Adenylate cyclase (EC 4.6.1.1) | uni | sce_3976 | 36.61 TPR repeat |
| SCE1572_5273 | hypothetical protein | bi | sce_4427 | 83.12 hypothetical protein |
| SCE1572_5274 | hypothetical protein | - | - | 0 |
| SCE1572_5275 | hypothetical protein | - | - | 0 |
| SCE1572_5276 | hypothetical protein | bi | sce_4428 | 68.83 hypothetical protein |
| SCE1572_5277 | hypothetical protein | - | - | 0 |
| SCE1572_5278 | hypothetical protein | bi | sce_4431 | 91.4 hypothetical protein |
| SCE1572_5279 | Tyrosine protein kinase:Serine/threonine protein kinase:PASTA | bi | sce_4432 | 90 hypothetical protein |
| SCE1572_5280 | Methionine ABC transporter ATP-binding protein | bi | sce_4433 | 97.96 Methionine ABC transporter ATP-binding protein |
| SCE1572_5281 | hypothetical protein | - | - | 0 |
| SCE1572_5282 | hypothetical protein | uni | sce_3634 | 50 hypothetical protein |
| SCE1572_5283 | lipid A biosynthesis lauroyl acyltransferase | bi | sce_4434 | 88.69 lipid A biosynthesis lauroyl acyltransferase |
| SCE1572_5284 | two-component response regulator | bi | sce_4435 | 93.4 two-component response regulator |
| SCE1572_5285 | FIG01087180: hypothetical protein | bi | sce_4436 | 88 FIG01087180: hypothetical protein |
| SCE1572_5286 | putative lipoprotein | bi | sce_4439 | 84.01 putative lipoprotein |
| SCE1572_5287 | General stress protein | bi | sce_4440 | 79.81 General stress protein |
| SCE1572_5288 | Probable ATP-dependent helicase Ihr (EC 3.6.1.-) | bi | sce_4441 | 91.06 Probable ATP-dependent helicase Ihr (EC 3.6.1.-) |
| SCE1572_5289 | hypothetical protein | - | - | 0 |
| SCE1572_5290 | Transglutaminase elicitor M81D | bi | sce_4444 | 82.69 Transglutaminase elicitor M81D |
| SCE1572_5291 | hypothetical protein | - | - | 0 |
| SCE1572_5292 | hypothetical protein | bi | sce_4448 | 81.92 hypothetical protein |
| SCE1572_5293 | Transcriptional regulator, LysR family | uni | sce_9885 | 50.74 LysR family transcriptional regulator |
| SCE1572_5294 | Hydrolase, alpha/beta fold family protein, At1g52510/AT4G12830 homolog 2 | uni | sce_3912 | 34.78 Epoxide hydrolase (EC 3.3.2.9) |
| SCE1572_5295 | FIG01086489: hypothetical protein | bi | sce_4451 | 80.44 FIG01086489: hypothetical protein |
| SCE1572_5296 | conserved hypothetical protein | bi | sce_9863 | 65.26 conserved hypothetical membrane spanning protein |
| SCE1572_5297 | FIG01086743: hypothetical protein | bi | sce_4452 | 58.56 FIG01086743: hypothetical protein |
| SCE1572_5298 | acetyltransferase, GNAT family | bi | sce_4454 | 75.76 acetyltransferase, GNAT family |
| SCE1572_5299 | Peptidyl-dipeptidase A precursor (EC 3.4.15.1) | bi | sce_4455 | 83.96 Peptidyl-dipeptidase A precursor (EC 3.4.15.1) |
| SCE1572_5300 | Arabinan endo-1,5-alpha-L-arabinosidase (EC 3.2.1.99) | uni | sce_5529 | 61.29 Type III effector HrpW, hairpin with pectate lyase domain |
| SCE1572_5301 | hypothetical protein | - | - | 0 |
| SCE1572_5302 | hypothetical protein | uni | sce_5645 | 36.13 Cell division inhibitor |
| SCE1572_5303 | hypothetical protein | - | - | 0 |
| SCE1572_5304 | FIG00822188: hypothetical protein | bi | sce_4456 | 86.61 Glyoxalase/bleomycin resistance protein/dioxygenase |
| SCE1572_5305 | hypothetical protein | - | - | 0 |
| SCE1572_5306 | FIG01088446: hypothetical protein | bi | sce_1644 | 86.11 FIG01088446: hypothetical protein |
| SCE1572_5307 | FIG01085317: hypothetical protein | bi | sce_1643 | 84.55 FIG01085317: hypothetical protein |
| SCE1572_5308 | FIG01087668: hypothetical protein | bi | sce_1642 | 89.69 FIG01087668: hypothetical protein |
| SCE1572_5309 | Chromosome (plasmid) partitioning protein ParA / Sporulation initiation inhibitor protein Soj | bi | sce_1641 | 96.25 Chromosome (plasmid) partitioning protein ParA / Sporulation initiation inhibitor protein Soj |
| SCE1572_5310 | FIG01085974: hypothetical protein | bi | sce_1640 | 82.12 FIG01085974: hypothetical protein |
| SCE1572_5311 | FIG01089084: hypothetical protein | bi | sce_1639 | 94.21 FIG01089084: hypothetical protein |
| SCE1572_5312 | amidohydrolase 2 | - | - | 0 |
| SCE1572_5313 | hypothetical protein | - | - | 0 |
| SCE1572_5314 | hypothetical protein | - | - | 0 |
| SCE1572_5315 | FOG: WD40 repeat | bi | sce_4457 | 81.34 FOG: WD40 repeat |
| SCE1572_5316 | FIG01087827: hypothetical protein | uni | sce_207 | 78.36 FIG01087827: hypothetical protein |
| SCE1572_5317 | hypothetical protein | - | - | 0 |
| SCE1572_5318 | 3-oxoacyl-[acyl-carrier protein] reductase (EC 1.1.1.100) | uni | sce_5211 | 36.47 3-oxoacyl-[acyl-carrier protein] reductase (EC 1.1.1.100) |
| SCE1572_5319 | 6-phosphogluconate dehydrogenase, NAD-binding | - | - | 0 |
| SCE1572_5320 | probable transcriptional regulator | uni | sce_5984 | 40.91 FIG01086592: hypothetical protein |
| SCE1572_5321 | RNA polymerase sigma-70 factor, ECF subfamily | bi | sce_9369 | 44.48 putative RNA polymerase sigma factor |
| SCE1572_5322 | Mil1641 protein | uni | sce_492 | 42.96 4-carboxymuconolactone decarboxylase domain/alkylhydroperoxidase AhpD family core domain protein |
| SCE1572_5323 | hypothetical protein | - | - | 0 |
| SCE1572_5324 | putative heat shock protein | bi | sce_4460 | 92.1 putative heat shock protein |
| SCE1572_5325 | Malate permease | bi | sce_4462 | 88.1 Malate permease |
| SCE1572_5326 | hypothetical protein | - | - | 0 |
| SCE1572_5327 | Transketolase (EC 2.2.1.1) | bi | sce_4463 | 93.83 Transketolase (EC 2.2.1.1) |
| SCE1572_5328 | hypothetical protein | uni | sce_1320 | 42.4 FIG01086874: hypothetical protein |
| SCE1572_5329 | FIG01086874: hypothetical protein | uni | sce_1320 | 40.4 FIG01086874: hypothetical protein |
| SCE1572_5330 | serine/threonine kinase family protein | uni | sce_1646 | 60 hypothetical protein |
| SCE1572_5331 | RsbR, positive regulator of sigma-B | bi | sce_4465 | 83.18 RsbR, positive regulator of sigma-B |
| SCE1572_5332 | serine/threonine kinase with two-component sensor domain | bi | sce_4466 | 84.88 Serine/threonine protein kinase PrkC, regulator of stationary phase |
| SCE1572_5333 | acyl-CoA dehydrogenase family protein | bi | sce_4467 | 84.44 acyl-CoA dehydrogenase family protein |
| SCE1572_5334 | Circumsporozoite protein | bi | sce_2438 | 84.92 Circumsporozoite protein |
| SCE1572_5335 | Glu-tRNA-Gln amidotransferase A subunit | bi | sce_6710 | 74.26 Glu-tRNA-Gln amidotransferase A subunit |
| SCE1572_5336 | Methanol oxidation genes, glmU-like | bi | sce_4472 | 83.63 hypothetical protein |
| SCE1572_5337 | FIG01085490: hypothetical protein | bi | sce_3082 | 80.98 FIG01085490: hypothetical protein |
| SCE1572_5338 | Protein of unknown function UPF0060 | - | - | 0 |
| SCE1572_5339 | putative cation efflux system protein czcB | bi | sce_3073 | 74.78 Probable Co/Zn/Cd efflux system membrane fusion protein |
| SCE1572_5340 | Probable Co/Zn/Cd efflux system membrane fusion protein | bi | sce_3074 | 87.47 Probable Co/Zn/Cd efflux system membrane fusion protein |
| SCE1572_5341 | Cobalt-zinc-cadmium resistance protein CzcA; Cation efflux system protein CusA | bi | sce_3075 | 94.47 Cobalt-zinc-cadmium resistance protein CzcA; Cation efflux system protein CusA |
| SCE1572_5342 | thioredoxin | bi | sce_3076 | 69.74 thioredoxin |
| SCE1572_5343 | hypothetical protein | bi | sce_4470 | 82.86 hypothetical protein |
| SCE1572_5344 | hypothetical protein | - | - | 0 |
| SCE1572_5345 | Glutathione S-transferase domain protein | bi | sce_4471 | 86.93 Glutathione S-transferase domain protein |
| SCE1572_5346 | FIG01086763: hypothetical protein | bi | sce_4473 | 89.39 FIG01086763: hypothetical protein |
| SCE1572_5347 | Transcriptional regulator, XRE family | bi | sce_4474 | 85.32 MII704 protein |
| SCE1572_5348 | Serine-threonine protein kinase | bi | sce_4475 | 70.12 Serine-threonine protein kinase |
| SCE1572_5349 | hypothetical protein | - | - | 0 |
| SCE1572_5350 | S-adenosylmethionine decarboxylase proenzyme | - | - | 0 |
| SCE1572_5351 | hypothetical protein | - | - | 0 |
| SCE1572_5352 | Adenylate cyclase (EC 4.6.1.1) | bi | sce_4477 | 87.72 Adenylate cyclase (EC 4.6.1.1) |
| SCE1572_5353 | Conserved domain protein | uni | sce_8776 | 46.67 hypothetical protein |
| SCE1572_5354 | hydrolase | bi | sce_4479 | 82.61 hydrolase |
| SCE1572_5355 | SAM-dependent methyltransferases | bi | sce_4481 | 90.43 SAM-dependent methyltransferases |
| SCE1572_5356 | hypothetical protein | - | - | 0 |
| SCE1572_5357 | Catalase (EC 1.11.1.6) | - | - | 0 |
| SCE1572_5358 | hypothetical protein-transmembrane prediction | - | - | 0 |
| SCE1572_5359 | putative integral membrane transport protein | bi | sce_4482 | 83.86 putative integral membrane transport protein |
| SCE1572_5360 | hypothetical protein | - | - | 0 |
| SCE1572_5361 | Galactitol utilization operon repressor | bi | sce_4484 | 91.73 Galactitol utilization operon repressor |
| SCE1572_5362 | hypothetical protein | bi | sce_6192 | 41.11 FIG01089550: hypothetical protein |
| SCE1572_5363 | serine/threonine protein kinase | uni | sce_6193 | 53.28 serine/threonine protein kinase |
| SCE1572_5364 | hypothetical protein | - | - | 0 |
| SCE1572_5365 | Serine/threonine-protein kinase pkn1 (EC 2.7.11.1) | bi | sce_6194 | 56.73 Serine/threonine-protein kinase pkn1 (EC 2.7.11.1) |
| SCE1572_5366 | Response regulator of zinc sigma-54-dependent two-component system | uni | sce_497 | 68.78 Response regulator of zinc sigma-54-dependent two-component system |
| SCE1572_5367 | hypothetical protein | - | - | 0 |
| SCE1572_5368 | Cadmium resistance transporter | bi | sce_4493 | 78.04 Cadmium resistance transporter |
| SCE1572_5369 | Lead, cadmium, zinc and mercury transporting ATPase (EC 3.6.3.3) (EC 3.6.3.5); Copper-translocating P-type ATPase (EC 3.6.3.3) (EC 3.6.3.5); Copper-translocating P-type ATPase (EC 3.6.3.4) | bi | sce_4494 | 84.24 Lead, cadmium, zinc and mercury transporting ATPase (EC 3.6.3.3) (EC 3.6.3.5); Copper-translocating P-type ATPase (EC 3.6.3.3) (EC 3.6.3.5); Copper-translocating P-type ATPase (EC 3.6.3.4) |
| SCE1572_5370 | hypothetical protein | - | - | 0 |
| SCE1572_5371 | FIG01088200: hypothetical protein | bi | sce_4495 | 67.79 FIG01088200: hypothetical protein |
| SCE1572_5372 | FIG01085222: hypothetical protein | bi | sce_7583 | 95.72 FIG01085222: hypothetical protein |
| SCE1572_5373 | FIG00501689: hypothetical protein | bi | sce_7582 | 89.62 FIG00501689: hypothetical protein |
| SCE1572_5374 | FIG01134227: hypothetical protein | bi | sce_4496 | 79 Ricin B lectin |
| SCE1572_5375 | Nucleoside-diphosphate-sugar epimerases | bi | sce_4497 | 92.86 NAD-dependent epimerase/dehydratase |
| SCE1572_5376 | Tat (twin-arginine translocation) pathway signal sequence domain protein | bi | sce_4498 | 87.17 Tat (twin-arginine translocation) pathway signal sequence domain protein |
| SCE1572_5377 | Cellulose-binding domain protein | bi | sce_4499 | 81.71 Cellulose-binding domain protein |
| SCE1572_5378 | integral membrane protein | - | - | 0 |
| SCE1572_5379 | Urate oxidase(EC:1.7.3.3) | bi | sce_4505 | 87.14 Urate oxidase(EC:1.7.3.3) |
| SCE1572_5380 | FIG01088504: hypothetical protein | bi | sce_4506 | 70.72 FIG01088504: hypothetical protein |
| SCE1572_5381 | Probable two-component sensor | bi | sce_4507 | 78.79 Probable two-component sensor |
| SCE1572_5382 | Osmosensitive K channel histidine kinase kdpD (EC 2.7.3.-) | bi | sce_4508 | 80.93 response regulator receiver modulated serine phosphatase with GAF sensor |
| SCE1572_5383 | peptidase M1, membrane alanine aminopeptidase | uni | sce_5948 | 51.9 Chitinase (EC 3.2.1.14) |
| SCE1572_5384 | Enoyl-[acyl-carrier-protein] reductase [FMN] (EC 1.3.1.9) | bi | sce_2062 | 43.48 Enoyl-[acyl-carrier-protein] reductase [FMN] (EC 1.3.1.9) |
| SCE1572_5385 | Glucosylase (EC 3.2.1.3) | bi | sce_4509 | 80.31 Glucosylase (EC 3.2.1.3) |
| SCE1572_5386 | Ribose ABC transport system, permease protein RbsC (TC 3.A.1.2.1) | bi | sce_4510 | 89.53 Ribose ABC transport system, permease protein RbsC (TC 3.A.1.2.1) |
| SCE1572_5387 | Ribose ABC transport system, ATP-binding protein RbsA (TC 3.A.1.2.1) | bi | sce_4511 | 92.13 Ribose ABC transport system, ATP-binding protein RbsA (TC 3.A.1.2.1) |
| SCE1572_5388 | Xylose ABC transporter, periplasmic xylose-binding protein XylF | bi | sce_4512 | 90.17 Xylose ABC transporter, periplasmic xylose-binding protein XylF |
| SCE1572_5389 | RsbR, positive regulator of sigma-B | bi | sce_4513 | 89.38 RsbR, positive regulator of sigma-B |
| SCE1572_5390 | hypothetical protein | - | - | 0 |
| SCE1572_5391 | Nitrate ABC transporter, ATP-binding protein | bi | sce_4516 | 92.15 Nitrate ABC transporter, ATP-binding protein |
| SCE1572_5392 | Nitrate ABC transporter, ATP-binding protein | bi | sce_4517 | 88.41 Nitrate ABC transporter, ATP-binding protein |
| SCE1572_5393 | Nitrate ABC transporter, permease protein | bi | sce_4518 | 98.48 Nitrate ABC transporter, permease protein |
| SCE1572_5394 | Nitrate ABC transporter, nitrate-binding protein | bi | sce_4519 | 90.89 Nitrate ABC transporter, nitrate-binding protein |
| SCE1572_5395 | hypothetical protein | - | - | 0 |
| SCE1572_5396 | FIG01087334: hypothetical protein | uni | sce_5952 | 52.9 FIG01087334: hypothetical protein |
| SCE1572_5397 | putative cytochrome P450 hydroxylase | uni | sce_7075 | 50.88 putative cytochrome P450 hydroxylase |
| SCE1572_5398 | probable hydrolase protein, putative | - | - | 0 |
| SCE1572_5399 | hypothetical protein | - | - | 0 |
| SCE1572_5400 | Cytochrome c peroxidase (EC 1.11.1.5) | bi | sce_4522 | 89.26 Cytochrome c peroxidase (EC 1.11.1.5) |
| SCE1572_5401 | FIG01086674: hypothetical protein | bi | sce_4523 | 58.92 Sporulation domain protein |
| SCE1572_5402 | hypothetical protein | bi | sce_4524 | 79.19 protein of unknown function DUF323 |
| SCE1572_5403 | hypothetical protein | uni | sce_8637 | 49.06 FIG01087436: hypothetical protein |
| SCE1572_5404 | glyoxalase family protein | bi | sce_4537 | 92.31 glyoxalase family protein |
| SCE1572_5405 | serine/threonine protein kinase | bi | sce_4538 | 69.78 serine/threonine protein kinase |
| SCE1572_5406 | hypothetical protein | uni | sce_4539 | 78.07 FIG01086337: hypothetical protein |
| SCE1572_5407 | hypothetical protein | bi | sce_4539 | 79.57 FIG01086337: hypothetical protein |
| SCE1572_5408 | protein kinase domain protein | bi | sce_4540 | 80 protein kinase domain protein |
| SCE1572_5409 | hypothetical protein | - | - | 0 |

| | | | | |
|--------------|---|----------|-----------|---|
| SCE1572_5574 | Siderophore biosynthesis diaminobutyrate--2-oxoglutarate aminotransferase (EC 2.6.1.76) | umi | see_9228 | 52.47 Pyoverdinin biosynthesis protein PvdH, L-2,4-diaminobutyrate-2-oxoglutarate aminotransferase (EC 2.6.1.76) |
| SCE1572_5575 | ISLp1 | umi | see_1675 | 82.26 ISLp1 |
| SCE1572_5576 | hypothetical protein | - | - | 0 |
| SCE1572_5577 | hypothetical protein | - | - | 0 |
| SCE1572_5578 | hypothetical protein | umi | see_5196 | 39.24 hypothetical protein |
| SCE1572_5579 | TonB-dependent receptor | bi | see_4645 | 78.52 TonB-dependent receptor |
| SCE1572_5580 | FIG01088105: hypothetical protein | bi | see_4646 | 80.99 FIG01088105: hypothetical protein |
| SCE1572_5581 | FIG01086505: hypothetical protein | bi | see_4647 | 66.72 FIG01086505: hypothetical protein |
| SCE1572_5582 | Glycosyl transferase, group 1 family protein | bi | see_1162 | 78.86 Glycosyl transferase, group 1 family protein |
| SCE1572_5583 | UDP-glucose 4-epimerase (EC 5.1.3.2) | bi | see_1161 | 82.42 UDP-glucose 4-epimerase (EC 5.1.3.2) |
| SCE1572_5584 | glycosyl transferase, group 1 | bi | see_1160 | 84.42 glycosyl transferase, group 1 |
| SCE1572_5585 | CBS domain-containing protein | bi | see_4648 | 92.34 CBS domain-containing protein |
| SCE1572_5586 | hypothetical protein | bi | see_4649 | 46.41 hypothetical protein |
| SCE1572_5587 | PE-PGRS FAMILY PROTEIN | bi | see_4650 | 77.64 glycine-rich protein |
| SCE1572_5588 | acetyltransferase, GNAT family | - | - | 0 |
| SCE1572_5589 | ATPase involved in DNA repair | umi | see_9772 | 43.62 hypothetical protein |
| SCE1572_5590 | protein kinase | umi | see_1788 | 44.09 serine/threonine protein kinase |
| SCE1572_5591 | Serine/threonine-protein kinase pkn3 (EC 2.7.11.1) | - | - | 0 |
| SCE1572_5592 | D-2-hydroxyglutarate dehydrogenase | bi | see_4656 | 95.73 D-2-hydroxyglutarate dehydrogenase |
| SCE1572_5593 | hypothetical protein | - | - | 0 |
| SCE1572_5594 | epoxide hydrolase | bi | see_4657 | 83.45 epoxide hydrolase |
| SCE1572_5595 | hypothetical protein | - | - | 0 |
| SCE1572_5596 | Transporter, MFS superfamily | bi | see_4658 | 86.49 General substrate transporter:Major facilitator superfamily MFS_1 |
| SCE1572_5597 | D-3-phosphoglycerate dehydrogenase (EC 1.1.1.95) | bi | see_4660 | 93.99 D-3-phosphoglycerate dehydrogenase (EC 1.1.1.95) |
| SCE1572_5598 | DegP protease | bi | see_4661 | 86.19 DegP protease |
| SCE1572_5599 | hypothetical protein | umi | see_5147 | 88.43 Tat (Twin-arginine translocation) pathway signal sequence domain protein |
| SCE1572_5600 | Cellulose-binding domain protein | umi | see_5148 | 80.71 Cellulose-binding domain protein |
| SCE1572_5601 | TPR domain protein | bi | see_4665 | 75.13 TPR domain protein |
| SCE1572_5602 | Response regulator of zinc sigma-54-dependent two-component system | bi | see_4671 | 92.57 Response regulator of zinc sigma-54-dependent two-component system |
| SCE1572_5603 | hypothetical protein | - | - | 0 |
| SCE1572_5604 | hypothetical protein | umi | see_4102 | 31.63 hypothetical protein |
| SCE1572_5605 | hypothetical protein | - | - | 0 |
| SCE1572_5606 | FIG01085636: hypothetical protein | bi | see_4684 | 86.9 FIG01085636: hypothetical protein |
| SCE1572_5607 | Isoflavone reductase homolog P3 (EC 1.3.1.-) | bi | see_6014 | 68.14 Isoflavone reductase homolog P3 (EC 1.3.1.-) |
| SCE1572_5608 | hypothetical protein | bi | see_4685 | 43.56 FIG01089242: hypothetical protein |
| SCE1572_5609 | serine/threonine protein kinase | bi | see_4686 | 83.17 serine/threonine protein kinase |
| SCE1572_5610 | predicted protein | umi | see_4820 | 37.18 hypothetical protein |
| SCE1572_5611 | hypothetical protein | umi | see_7270 | 31.48 acetyltransferase, GNAT family |
| SCE1572_5612 | hypothetical protein | bi | see_5882 | 70.51 hypothetical protein |
| SCE1572_5613 | Collagen triple helix repeat | umi | see_9583 | 56.67 Glycoprotein gp2 |
| SCE1572_5614 | FIG01087566: hypothetical protein | bi | see_4701 | 81.84 FIG01087566: hypothetical protein |
| SCE1572_5615 | conserved hypothetical protein-putative response regulator | umi | see_10290 | 32.85 Sensor protein |
| SCE1572_5616 | hypothetical protein | - | - | 0 |
| SCE1572_5617 | RsbR, positive regulator of sigma-B | bi | see_4702 | 81.84 RsbR, positive regulator of sigma-B |
| SCE1572_5618 | FIG01085516: hypothetical protein | umi | see_1454 | 67.44 FIG01085516: hypothetical protein |
| SCE1572_5619 | Putative heme iron utilization protein | bi | see_4704 | 88.6 pyridoxamine 5'-phosphate oxidase-related, FMN-binding |
| SCE1572_5620 | hypothetical protein | umi | see_4437 | 37.6 Serine protease precursor |
| SCE1572_5621 | hypothetical protein | umi | see_4437 | 39.69 Serine protease precursor |
| SCE1572_5622 | TPR domain/radical SAM/B12 binding domain protein | bi | see_4705 | 91.94 TPR domain/radical SAM/B12 binding domain protein |
| SCE1572_5623 | Beta-glucosidase (EC 3.2.1.21) | bi | see_4706 | 94.38 Beta-glucosidase (EC 3.2.1.21) |
| SCE1572_5624 | hypothetical protein | umi | see_3858 | 35.29 Adenylosuccinylase (EC 3.3.1.1) |
| SCE1572_5625 | hypothetical protein | bi | see_4707 | 87.08 hypothetical protein |
| SCE1572_5626 | hypothetical protein | - | - | 0 |
| SCE1572_5627 | Conserved protein, with a weak D-galactarate dehydratase/altronate hydrolase domain | umi | see_4708 | 81.89 hypothetical protein |
| SCE1572_5628 | hypothetical protein | bi | see_4708 | 93.57 hypothetical protein |
| SCE1572_5629 | Conserved protein, with a weak D-galactarate dehydratase/altronate hydrolase domain | umi | see_4708 | 84 hypothetical protein |
| SCE1572_5630 | FIG01087049: hypothetical protein | bi | see_7538 | 82.87 FIG01087049: hypothetical protein |
| SCE1572_5631 | Oxidoreductase | umi | see_3164 | 43.68 Oxidoreductase |
| SCE1572_5632 | hypothetical protein | - | - | 0 |
| SCE1572_5633 | hypothetical protein | - | - | 0 |
| SCE1572_5634 | FIG00686302: hypothetical protein | - | - | 0 |
| SCE1572_5635 | 5-methyltetrahydrofolate--homocysteine methyltransferase (EC 2.1.1.13) | bi | see_8649 | 95.08 5-methyltetrahydrofolate--homocysteine methyltransferase (EC 2.1.1.13) |
| SCE1572_5636 | Transcriptional regulator, ArsR family / Methyltransferase fusion | bi | see_8648 | 92.09 Transcriptional regulator, ArsR family / Methyltransferase fusion |
| SCE1572_5637 | Threonine dehydrogenase and related Zn-dependent dehydrogenases | bi | see_4709 | 92.23 Threonine dehydrogenase and related Zn-dependent dehydrogenases |
| SCE1572_5638 | acetyltransferase (GNAT) family protein | umi | see_6542 | 36.92 Ribosomal-protein-S18p-alanine acetyltransferase (EC 2.3.1.-) |
| SCE1572_5639 | Cobalt-zinc-cadmium resistance protein | bi | see_4710 | 82.47 Cobalt-zinc-cadmium resistance protein |
| SCE1572_5640 | Signal transduction histidine kinase CheA (EC 2.7.3.-) | bi | see_8602 | 73.65 Signal transduction histidine kinase CheA (EC 2.7.3.-) |
| SCE1572_5641 | response regulator/sensory box histidine kinase | bi | see_1532 | 62.69 FIG01089498: hypothetical protein |
| SCE1572_5642 | serine/threonine kinase with two-component sensor domain | - | - | 0 |
| SCE1572_5643 | hypothetical protein | - | - | 0 |
| SCE1572_5644 | Serine/threonine kinase with two-component sensor domain | - | - | 0 |
| SCE1572_5645 | Signal transduction histidine kinase CheA (EC 2.7.3.-) | - | - | 0 |
| SCE1572_5646 | hypothetical protein | - | - | 0 |
| SCE1572_5647 | Adenylate cyclase (EC 4.6.1.1) / Guanylate cyclase (EC 4.6.1.2) | umi | see_5226 | 51.18 Adenylate cyclase (EC 4.6.1.1) / Guanylate cyclase (EC 4.6.1.2) |
| SCE1572_5648 | Adenylate cyclase (EC 4.6.1.1) / Guanylate cyclase (EC 4.6.1.2) | umi | see_5746 | 33.48 Adenylate cyclase (EC 4.6.1.1) / Guanylate cyclase (EC 4.6.1.2) |
| SCE1572_5649 | Phosphoenolpyruvate carboxykinase [GTP] (EC 4.1.1.32) | bi | see_4711 | 95.17 Phosphoenolpyruvate carboxykinase [GTP] (EC 4.1.1.32) |
| SCE1572_5650 | hypothetical protein | - | - | 0 |
| SCE1572_5651 | hypothetical protein | - | - | 0 |
| SCE1572_5652 | NADH-ubiquinone oxidoreductase chain M (EC 1.6.5.3) | bi | see_9774 | 82.16 NADH-ubiquinone oxidoreductase chain M (EC 1.6.5.3) |
| SCE1572_5653 | NADH-ubiquinone oxidoreductase chain L (EC 1.6.5.3) | bi | see_9775 | 82.92 NADH-ubiquinone oxidoreductase chain L (EC 1.6.5.3) |
| SCE1572_5654 | Hypothetical transmembrane protein coupled to NADH-ubiquinone oxidoreductase chain 5 homolog | bi | see_9776 | 84.77 Hypothetical transmembrane protein coupled to NADH-ubiquinone oxidoreductase chain 5 homolog |
| SCE1572_5655 | anion transporters (Cl(-), SO4(2-), PO4(3-), etc.) | bi | see_9777 | 87.48 anion transporters (Cl(-), SO4(2-), PO4(3-), etc.) |
| SCE1572_5656 | YidE/YbjL duplication | umi | see_1130 | 43.09 YidE/YbjL duplication |
| SCE1572_5657 | hypothetical protein | umi | see_6734 | 30.65 TOMM biosynthesis dehydrogenase (protein B) |
| SCE1572_5658 | serine/threonine protein kinase | see_4713 | see_4713 | 82.84 serine/threonine protein kinase |
| SCE1572_5659 | FIG01085909: hypothetical protein | bi | see_9663 | 81.71 FIG01085909: hypothetical protein |
| SCE1572_5660 | FIG01086053: hypothetical protein | bi | see_10019 | 83.82 FIG01086053: hypothetical protein |
| SCE1572_5661 | protein containing glyoxalase/bleomycin resistance protein/dioxygenase superfamily domain | - | - | 0 |
| SCE1572_5662 | hypothetical protein | - | - | 0 |
| SCE1572_5663 | FIG01086593: hypothetical protein | bi | see_4714 | 76.88 FIG01086593: hypothetical protein |
| SCE1572_5664 | Octaprenyl-diphosphate synthase (EC 2.5.1.-) / Dimethylallyltransferase (EC 2.5.1.1) / Geranyltransferase (farnesyl)diphosphate | bi | see_4715 | 90.54 Octaprenyl-diphosphate synthase (EC 2.5.1.-) / Dimethylallyltransferase (EC 2.5.1.1) / Geranyltransferase (farnesyl)diphosphate |
| SCE1572_5665 | Mevalonate kinase (EC 2.7.1.36) | bi | see_4716 | 82.03 Mevalonate kinase (EC 2.7.1.36) |
| SCE1572_5666 | Diphosphomevalonate decarboxylase (EC 4.1.1.33) | bi | see_4717 | 94.33 Diphosphomevalonate decarboxylase (EC 4.1.1.33) |
| SCE1572_5667 | hypothetical protein | umi | see_4718 | 84.87 Phosphomevalonate kinase (EC 2.7.4.2) |
| SCE1572_5668 | phosphomevalonate kinase | see_4718 | see_4718 | 89.03 Phosphomevalonate kinase (EC 2.7.4.2) |
| SCE1572_5669 | FIG01087491: hypothetical protein | bi | see_4719 | 91.22 FIG01087491: hypothetical protein |
| SCE1572_5670 | hypothetical protein | bi | see_4720 | 79.1 hypothetical protein |
| SCE1572_5671 | hypothetical protein | bi | see_4721 | 84.15 hypothetical protein |
| SCE1572_5672 | Excinuclease ABC subunit A, dimeric form | - | - | 0 |
| SCE1572_5673 | hypothetical protein | - | - | 0 |
| SCE1572_5674 | hypothetical protein | - | - | 0 |
| SCE1572_5675 | Aspartate aminotransferase (EC 2.6.1.1) @ Histidinol-phosphate aminotransferase (EC 2.6.1.9) | bi | see_4727 | 89.81 Aspartate aminotransferase (EC 2.6.1.1) @ Histidinol-phosphate aminotransferase (EC 2.6.1.9) |
| SCE1572_5676 | FIG01085737: hypothetical protein | bi | see_4728 | 76.55 FIG01085737: hypothetical protein |
| SCE1572_5677 | Homeobox protein HB9 | bi | see_4729 | 82.19 Homeobox protein HB9 |
| SCE1572_5678 | NADH-ubiquinone oxidoreductase chain N (EC 1.6.5.3) | bi | see_4730 | 96.65 NADH-ubiquinone oxidoreductase chain N (EC 1.6.5.3) |
| SCE1572_5679 | NADH-ubiquinone oxidoreductase chain M (EC 1.6.5.3) | bi | see_4731 | 91.46 NADH-ubiquinone oxidoreductase chain M (EC 1.6.5.3) |
| SCE1572_5680 | NADH-ubiquinone oxidoreductase chain L (EC 1.6.5.3) | bi | see_4732 | 93.33 NADH-ubiquinone oxidoreductase chain L (EC 1.6.5.3) |
| SCE1572_5681 | NADH-ubiquinone oxidoreductase chain K (EC 1.6.5.3) | bi | see_4733 | 97.09 NADH-ubiquinone oxidoreductase chain K (EC 1.6.5.3) |
| SCE1572_5682 | NADH-ubiquinone oxidoreductase chain J (EC 1.6.5.3) | bi | see_4734 | 85.39 NADH-ubiquinone oxidoreductase chain J (EC 1.6.5.3) |
| SCE1572_5683 | NADH-ubiquinone oxidoreductase chain F (EC 1.6.5.3) | bi | see_4735 | 96.89 NADH-ubiquinone oxidoreductase chain F (EC 1.6.5.3) |
| SCE1572_5684 | NADH-ubiquinone oxidoreductase chain E (EC 1.6.5.3) | bi | see_4736 | 92.12 NADH-ubiquinone oxidoreductase chain E (EC 1.6.5.3) |
| SCE1572_5685 | annexin VII | bi | see_4738 | 79.05 PE-PGRS virulence associated protein |
| SCE1572_5686 | hypothetical protein | bi | see_4739 | 84.13 hypothetical protein |
| SCE1572_5687 | hypothetical protein | - | - | 0 |
| SCE1572_5688 | hemerythrin HHE cation binding region | bi | see_4740 | 94.15 hemerythrin HHE cation binding region |
| SCE1572_5689 | serine/threonine protein kinase | see_4741 | see_4741 | 91.39 serine/threonine protein kinase |
| SCE1572_5690 | exonuclease | bi | see_4742 | 91.3 Exonuclease |
| SCE1572_5691 | hypothetical protein | bi | see_4743 | 77.44 Long-chain-fatty-acid--CoA ligase (EC 6.2.1.3) |
| SCE1572_5692 | Transport ATP-binding protein CydC | bi | see_4744 | 88.98 hypothetical protein |
| SCE1572_5693 | 2-hydroxy-3-oxopropionate reductase (EC 1.1.1.60) | bi | see_4745 | 78.6 HAD-superfamily hydrolase, subfamily 1A, variant 3 |
| SCE1572_5694 | hypothetical protein | bi | see_4746 | 84.73 GIII843 protein |
| SCE1572_5695 | hypothetical protein | bi | see_9269 | 47.17 hypothetical protein |
| SCE1572_5696 | hypothetical protein | umi | see_4746 | 43.53 GIII843 protein |
| SCE1572_5697 | Isoleucyl-tRNA synthetase (EC 6.1.1.5) | bi | see_4750 | 90.78 Isoleucyl-tRNA synthetase (EC 6.1.1.5) |
| SCE1572_5698 | FIG01085270: hypothetical protein | umi | see_4751 | 89.34 hypothetical protein |
| SCE1572_5699 | hypothetical protein | bi | see_4751 | 90.36 hypothetical protein |
| SCE1572_5700 | Thiamin-phosphate pyrophosphorylase (EC 2.5.1.3) | bi | see_4752 | 94.09 Thiamin-phosphate pyrophosphorylase (EC 2.5.1.3) |
| SCE1572_5701 | FIG01086571: hypothetical protein | bi | see_4753 | 77.39 FIG01086571: hypothetical protein |
| SCE1572_5702 | Glycosyl transferase, group 1 family protein | bi | see_4754 | 83.96 Glycosyl transferase, group 1 family protein |
| SCE1572_5703 | Glycosyl transferase, group 1 | bi | see_4755 | 91.23 putative glycosyl transferase |
| SCE1572_5704 | Thiazole biosynthesis protein ThiG | bi | see_4756 | 97.69 Thiazole biosynthesis protein ThiG |
| SCE1572_5705 | FIG01085173: hypothetical protein | bi | see_4757 | 81.96 FIG01085173: hypothetical protein |
| SCE1572_5706 | hypothetical protein | bi | see_4758 | 71.08 Membrane type-3 matrix metalloproteinase |
| SCE1572_5707 | Ribonuclease D (EC 3.1.26.3) | bi | see_4759 | 83.29 Ribonuclease D (EC 3.1.26.3) |
| SCE1572_5708 | Potassium efflux system KefA protein / Small-conductance mechanosensitive channel | bi | see_4761 | 85.21 Potassium efflux system KefA protein / Small-conductance mechanosensitive channel |
| SCE1572_5709 | Twitching motility protein PII | bi | see_4762 | 92.29 Twitching motility protein PII |
| SCE1572_5710 | hypothetical protein | bi | see_4763 | 67.69 hypothetical protein |
| SCE1572_5711 | Thiamin biosynthesis protein ThiC | bi | see_4764 | 97.2 Thiamin biosynthesis protein ThiC |
| SCE1572_5712 | Biopolymer transport protein ExbD/TolR | bi | see_4765 | 92.47 Biopolymer transport protein ExbD/TolR |
| SCE1572_5713 | Biopolymer transport protein ExbD/TolR | bi | see_4766 | 93.48 Biopolymer transport protein ExbD/TolR |
| SCE1572_5714 | MotA/TolQ/ExbB proton channel family protein | bi | see_4767 | 89.92 MotA/TolQ/ExbB proton channel family protein |
| SCE1572_5715 | Ferric siderophore transport system, periplasmic binding protein TonB | bi | see_4768 | 84.77 Ferric siderophore transport system, periplasmic binding protein TonB |
| SCE1572_5716 | TonB-dependent receptor | see_4769 | see_4769 | 79.17 TonB-dependent receptor |
| SCE1572_5717 | FIG01086900: hypothetical protein | umi | see_881 | 68.52 Collagen triple helix repeat |
| SCE1572_5718 | FIG01088815: hypothetical protein | bi | see_4771 | 83.53 FIG01088815: hypothetical protein |
| SCE1572_5719 | hypothetical protein | bi | see_4772 | 90.5 hypothetical protein |
| SCE1572_5720 | UDP-glucose 4-epimerase (EC 5.1.3.2) | bi | see_4773 | 96.79 UDP-glucose 4-epimerase (EC 5.1.3.2) |
| SCE1572_5721 | 1-acyl-sn-glycerol-3-phosphate acyltransferase (EC 2.3.1.51) | bi | see_4774 | 97.08 1-acyl-sn-glycerol-3-phosphate acyltransferase (EC 2.3.1.51) |
| SCE1572_5722 | Muramoyltetrapeptide carboxypeptidase (EC 3.4.17.13) | bi | see_4775 | 90.55 Muramoyltetrapeptide carboxypeptidase (EC 3.4.17.13) |
| SCE1572_5723 | PE-PGRS family protein | umi | see_6814 | 60.26 PE-PGRS FAMILY PROTEIN |
| SCE1572_5724 | PE-PGRS FAMILY PROTEIN | umi | see_9483 | 72.71 FIG01086339: hypothetical protein |
| SCE1572_5725 | FIG01089478: hypothetical protein | bi | see_9482 | 77.46 hypothetical protein |
| SCE1572_5726 | Adventurous gliding motility protein K | bi | see_4776 | 80.66 Adventurous gliding motility protein K |
| SCE1572_5727 | Serine/threonine-protein kinase pkn3 (EC 2.7.11.1) | bi | see_4778 | 85.32 Serine/threonine-protein kinase pkn3 (EC 2.7.11.1) |
| SCE1572_5728 | hypothetical protein | bi | see_4779 | 66.76 FIG01089119: hypothetical protein |
| SCE1572_5729 | Putative hydroxyproline-rich glycoprotein | bi | see_4780 | 67.57 Putative hydroxyproline-rich glycoprotein |
| SCE1572_5730 | hypothetical protein</ | | | |

| | | | | |
|--------------|---|-----|-----------|--|
| SCE1572_5738 | Type IV pilin PilA | bi | sce_4789 | 70.42 Type IV pilin PilA |
| SCE1572_5739 | Type IV pilin PilA | bi | sce_4790 | 70.1 Type IV pilin PilA |
| SCE1572_5740 | hypothetical protein | bi | sce_4791 | 95.76 hypothetical protein |
| SCE1572_5741 | hypothetical protein | bi | sce_4792 | 86.59 hypothetical protein |
| SCE1572_5742 | FIG01085470: hypothetical protein | bi | sce_4793 | 75.79 FIG01085470: hypothetical protein |
| SCE1572_5743 | PE-PGRS family protein | umi | sce_8647 | 40.26 Arylsulfatase (EC 3.1.6.1) |
| SCE1572_5744 | XL-ALEX protein | bi | sce_4794 | 88.26 XL-ALEX protein |
| SCE1572_5745 | Aspartyl-tRNA(Asn) amidotransferase subunit C (EC 6.3.5.6) @ Glutamyl-tRNA(Gln) amidotransferase subunit C (EC 6.3.5.7) | bi | sce_4795 | 99.03 Aspartyl-tRNA(Asn) amidotransferase subunit C (EC 6.3.5.6) @ Glutamyl-tRNA(Gln) amidotransferase subunit C (EC 6.3.5.7) |
| SCE1572_5746 | Aspartyl-tRNA(Asn) amidotransferase subunit A (EC 6.3.5.6) @ Glutamyl-tRNA(Gln) amidotransferase subunit A (EC 6.3.5.7) | bi | sce_4796 | 93.98 Aspartyl-tRNA(Asn) amidotransferase subunit A (EC 6.3.5.6) @ Glutamyl-tRNA(Gln) amidotransferase subunit A (EC 6.3.5.7) |
| SCE1572_5747 | Histone acetyltransferase HPA2 and related acetyltransferases | bi | sce_4797 | 88.89 Histone acetyltransferase HPA2 and related acetyltransferases |
| SCE1572_5748 | NAD dependent epimerase/dehydratase family | bi | sce_4798 | 86.1 NAD dependent epimerase/dehydratase family |
| SCE1572_5749 | acyltransferase family protein | bi | sce_4799 | 85.81 acyltransferase family protein |
| SCE1572_5750 | tRNA pseudouridine synthase B (EC 4.2.1.70) | bi | sce_4800 | 71.63 tRNA pseudouridine synthase B (EC 4.2.1.70) |
| SCE1572_5751 | Magnesium and cobalt efflux protein CorC | bi | sce_4801 | 96.98 Magnesium and cobalt efflux protein CorC |
| SCE1572_5752 | Protein diaphanous homolog 2 (Diaphanous-related formin-2) (DRF2) (mDia3) | bi | sce_4803 | 85.37 Protein diaphanous homolog 2 (Diaphanous-related formin-2) (DRF2) (mDia3) |
| SCE1572_5753 | hypothetical protein | - | - | 0 |
| SCE1572_5754 | Alpha/beta hydrolase fold-1 | bi | sce_4805 | 83.22 Alpha/beta hydrolase fold-1 |
| SCE1572_5755 | Transcription accessory protein (S1 RNA-binding domain) | bi | sce_4806 | 93.77 Transcription accessory protein (S1 RNA-binding domain) |
| SCE1572_5756 | hypothetical protein | umi | sce_4012 | 36.13 FIG01089186: hypothetical protein |
| SCE1572_5757 | FIG00559100: hypothetical protein | umi | sce_1878 | 41.32 FIG01087871: hypothetical protein |
| SCE1572_5758 | hypothetical protein | - | - | 0 |
| SCE1572_5759 | Imidazolonepropionase (EC 3.5.2.7) | bi | sce_4807 | 92.94 Imidazolonepropionase (EC 3.5.2.7) |
| SCE1572_5760 | Beta-hexosaminidase (EC 3.2.1.52) | bi | sce_4808 | 86.52 Beta-hexosaminidase (EC 3.2.1.52) |
| SCE1572_5761 | Alcohol dehydrogenase (EC 1.1.1.1) | bi | sce_4809 | 83.09 Alcohol dehydrogenase (EC 1.1.1.1) |
| SCE1572_5762 | putative membrane protein | bi | sce_4810 | 88.71 conserved hypothetical membrane protein |
| SCE1572_5763 | hypothetical protein | - | - | 0 |
| SCE1572_5764 | FIG01088840: hypothetical protein | bi | sce_4811 | 81.15 FIG01088840: hypothetical protein |
| SCE1572_5765 | Type IV fimbrial assembly, ATPase PilB | bi | sce_4812 | 93.18 Type IV fimbrial assembly, ATPase PilB |
| SCE1572_5766 | Beta-glucosidase (EC 3.2.1.21) | bi | sce_4813 | 92.44 Beta-glucosidase (EC 3.2.1.21) |
| SCE1572_5767 | Oligopeptide/dipeptide ABC transporter, ATP-binding protein-like | bi | sce_4814 | 93.71 Oligopeptide/dipeptide ABC transporter, ATP-binding protein-like |
| SCE1572_5768 | Oligopeptide transport ATP-binding protein OppD (TC 3.A.1.5.1) | bi | sce_4815 | 94.69 Oligopeptide transport ATP-binding protein OppD (TC 3.A.1.5.1) |
| SCE1572_5769 | (GlcNAc)2 ABC transporter, permease component 1 | bi | sce_4816 | 94.46 (GlcNAc)2 ABC transporter, permease component 1 |
| SCE1572_5770 | Oligopeptide ABC transporter, periplasmic oligopeptide-binding protein OppA (TC 3.A.1.5.1) | bi | sce_4817 | 92.52 Oligopeptide ABC transporter, periplasmic oligopeptide-binding protein OppA (TC 3.A.1.5.1) |
| SCE1572_5771 | hypothetical protein | - | - | 0 |
| SCE1572_5772 | FIG01086557: hypothetical protein | bi | sce_4818 | 74.93 FIG01086557: hypothetical protein |
| SCE1572_5773 | hypothetical protein | - | - | 0 |
| SCE1572_5774 | hypothetical protein | umi | sce_3989 | 47.56 (MTV044.05), len: 923. Unknown glycine richprotein, similar to other PGRS-type sequences e.g. gp[AL0091]MTV004_1M. tubercul |
| SCE1572_5775 | NAD-specific glutamate dehydrogenase (EC 1.4.1.2) | bi | sce_4821 | 95.71 NAD-specific glutamate dehydrogenase (EC 1.4.1.2) |
| SCE1572_5776 | Acetoacetate metabolism regulatory protein atoC (Ornithine/arginine decarboxylase inhibitor) (Ornithine decarboxylase antizyme) | bi | sce_4822 | 89.74 Acetoacetate metabolism regulatory protein atoC (Ornithine/arginine decarboxylase inhibitor) (Ornithine decarboxylase antizyme) |
| SCE1572_5777 | hypothetical protein | bi | sce_4823 | 95.19 hypothetical protein |
| SCE1572_5778 | short-chain dehydrogenase/reductase SDR | bi | sce_4824 | 91.35 putative oxidoreductase |
| SCE1572_5779 | Response regulator receiver:ATP-binding region, ATPase-like:Histidine kinase, HAMP region:Histidine kinase A, N-terminal: | bi | sce_4825 | 55.56 Response regulator receiver:ATP-binding region, ATPase-like:Histidine kinase, HAMP region:Histidine kinase A, N-terminal: Hpt pr |
| SCE1572_5780 | FIG01089017: hypothetical protein | bi | sce_4826 | 95.02 FIG01089017: hypothetical protein |
| SCE1572_5781 | HAD superfamily (subfamily IG) hydrolase, 5'-nucleotidase (EC:3.1.3.5) | bi | sce_4827 | 95.57 HAD superfamily (subfamily IG) hydrolase, 5'-nucleotidase (EC:3.1.3.5) |
| SCE1572_5782 | hypothetical protein | bi | sce_4828 | 73.53 hypothetical protein |
| SCE1572_5783 | tRNA pseudouridine 13 synthase (EC 4.2.1.-) | bi | sce_4830 | 83.85 tRNA pseudouridine 13 synthase (EC 4.2.1.-) |
| SCE1572_5784 | MotA/TolQ/ExbB proton channel family protein | bi | sce_4831 | 92.94 MotA/TolQ/ExbB proton channel family protein |
| SCE1572_5785 | Biopolymer transport protein ExhD/TolR | bi | sce_4832 | 95.21 Biopolymer transport protein ExhD/TolR |
| SCE1572_5786 | Ferric siderophore transport system, periplasmic binding protein TonB | bi | sce_4833 | 83.87 Ferric siderophore transport system, periplasmic binding protein TonB |
| SCE1572_5787 | cAMP-binding proteins - catabolite gene activator and regulatory subunit of cAMP-dependent protein kinases | bi | sce_4834 | 98.73 cAMP-binding proteins - catabolite gene activator and regulatory subunit of cAMP-dependent protein kinases |
| SCE1572_5788 | FIG01086310: hypothetical protein | bi | sce_4835 | 89.04 FIG01086310: hypothetical protein |
| SCE1572_5789 | Amidophosphoribosyltransferase (EC 2.4.2.14) | bi | sce_4836 | 93.95 Amidophosphoribosyltransferase (EC 2.4.2.14) |
| SCE1572_5790 | Hydroxymethylglutaryl-CoA lyase (EC 4.1.3.4) | bi | sce_4837 | 94.48 Hydroxymethylglutaryl-CoA lyase (EC 4.1.3.4) |
| SCE1572_5791 | RTX toxins and related Ca2+ proteins | bi | sce_4838 | 84.2 RTX toxins and related Ca2+ proteins |
| SCE1572_5792 | FIG01088196: hypothetical protein | bi | sce_4839 | 86.89 FIG01088196: hypothetical protein |
| SCE1572_5793 | EsV-1-144 | bi | sce_4840 | 83.13 EsV-1-144 |
| SCE1572_5794 | Peptidyl-prolyl cis-trans isomerase (EC 5.2.1.8) | bi | sce_4841 | 91.39 Peptidyl-prolyl cis-trans isomerase (EC 5.2.1.8) |
| SCE1572_5795 | DUF192 precursor | bi | sce_4842 | 74.7 DUF192 precursor |
| SCE1572_5796 | Metal-dependent hydrolases of the beta-lactamase superfamily 1 | bi | sce_4843 | 89.05 Metal-dependent hydrolases of the beta-lactamase superfamily 1 |
| SCE1572_5797 | Flagellar hook-length control protein FliK | bi | sce_4844 | 81.17 hypothetical protein |
| SCE1572_5798 | hypothetical protein | bi | sce_4846 | 72.97 protein kinase domain protein |
| SCE1572_5799 | FIG01088183: hypothetical protein | bi | sce_4847 | 93.98 FIG01088183: hypothetical protein |
| SCE1572_5800 | serine/threonine protein kinase | bi | sce_4848 | 85.63 serine/threonine protein kinase |
| SCE1572_5801 | Rubisco activation protein CbbO | bi | sce_4849 | 82.61 hypothetical protein |
| SCE1572_5802 | gnl WGS:AAAblagCP13423 gb EAA06237 | bi | sce_4850 | 72.91 gnl WGS:AAAblagCP13423 gb EAA06237 |
| SCE1572_5803 | Very large tegument protein | bi | sce_4851 | 79.34 Very large tegument protein |
| SCE1572_5804 | Liga | bi | sce_4852 | 60.55 FIG01088333: hypothetical protein |
| SCE1572_5805 | hypothetical protein | - | - | 0 |
| SCE1572_5806 | FIG01089709: hypothetical protein | bi | sce_4854 | 93.33 FIG01089709: hypothetical protein |
| SCE1572_5807 | hypothetical protein-transmembrane prediction | bi | sce_4855 | 81.22 hypothetical protein-transmembrane prediction |
| SCE1572_5808 | serine/threonine protein kinase | bi | sce_4856 | 83.41 serine/threonine protein kinase |
| SCE1572_5809 | serine/threonine protein kinase | bi | sce_4857 | 83.59 Serine/threonine-protein kinase pkn1 (EC 2.7.11.1) |
| SCE1572_5810 | FIG01085198: hypothetical protein | bi | sce_4858 | 61.75 FIG01085198: hypothetical protein |
| SCE1572_5811 | Formate hydrogenlyase subunit 2 | bi | sce_4859 | 86.73 Formate hydrogenlyase subunit 2 |
| SCE1572_5812 | FIG01087767: hypothetical protein | bi | sce_4861 | 67.43 FIG01087767: hypothetical protein |
| SCE1572_5813 | Uncharacterized PE-PGRS family protein PE_PGRS54 precursor | bi | sce_4862 | 68.62 Uncharacterized PE-PGRS family protein PE_PGRS54 precursor |
| SCE1572_5814 | Thioredoxin reductase (EC 1.8.1.9) | bi | sce_4863 | 77.56 Thioredoxin reductase (EC 1.8.1.9) |
| SCE1572_5815 | hypothetical protein | bi | sce_4864 | 87.67 von Willebrand factor type A domain protein |
| SCE1572_5816 | FIG004453: protein YeeG like | bi | sce_4865 | 88.6 FIG004453: protein YeeG like |
| SCE1572_5817 | hypothetical protein | - | - | 0 |
| SCE1572_5818 | FIG01088755: hypothetical protein | bi | sce_9910 | 67.89 FIG01088755: hypothetical protein |
| SCE1572_5819 | FIG01086239: hypothetical protein | umi | sce_10366 | 54.93 FIG01086239: hypothetical protein |
| SCE1572_5820 | hypothetical protein | umi | sce_9503 | 72.27 hypothetical protein |
| SCE1572_5821 | hypothetical protein | umi | sce_10364 | 79.55 hypothetical protein |
| SCE1572_5822 | hypothetical protein | - | - | 0 |
| SCE1572_5823 | Dihydroloamide succinyltransferase component (E2) of 2-oxoglutarate dehydrogenase complex (EC 2.3.1.61) / 2-oxoglutarate de | bi | sce_4866 | 74.89 Dihydroloamide succinyltransferase component (E2) of 2-oxoglutarate dehydrogenase complex (EC 2.3.1.61) / 2-oxoglutarate dehy |
| SCE1572_5824 | FIG01086453: hypothetical protein | umi | sce_2384 | 64.1 FIG01086453: hypothetical protein |
| SCE1572_5825 | sodium/hydrogen exchanger | bi | sce_4867 | 88.13 transporter, monovalent cation:proton antiporter-2 (CPA2) family |
| SCE1572_5826 | Na(H) antiporter, homolog | bi | sce_4868 | 91.08 hypothetical protein |
| SCE1572_5827 | hypothetical protein | bi | sce_4869 | 75.07 |
| SCE1572_5828 | Glucokinase (EC 2.7.1.2) | bi | sce_4870 | 87.77 Glucokinase (EC 2.7.1.2) |
| SCE1572_5829 | two-component hybrid sensor and regulator | umi | sce_1532 | 38.24 FIG01089498: hypothetical protein |
| SCE1572_5830 | 5-methyltetrahydrofolate--homocysteine methyltransferase (EC 2.1.1.13) | umi | sce_4506 | 35.09 FIG01088504: hypothetical protein |
| SCE1572_5831 | 6-phosphogluconolactonase (EC 3.1.1.31), eukaryotic type | bi | sce_4872 | 89.63 6-phosphogluconolactonase (EC 3.1.1.31), eukaryotic type |
| SCE1572_5832 | Putative glucose 6-phosphate dehydrogenase effector OpeA | bi | sce_4873 | 92.63 Putative glucose 6-phosphate dehydrogenase effector OpeA |
| SCE1572_5833 | Glucose-6-phosphate 1-dehydrogenase (EC 1.1.1.49) | bi | sce_4874 | 94.25 Glucose-6-phosphate 1-dehydrogenase (EC 1.1.1.49) |
| SCE1572_5834 | hypothetical protein | bi | sce_4875 | 92.47 hypothetical protein |
| SCE1572_5835 | Flagellar hook-length control protein FliK | bi | sce_4876 | 92.89 Flagellar hook-length control protein FliK |
| SCE1572_5836 | hypothetical protein | - | - | 0 |
| SCE1572_5837 | serine/threonine protein kinase | bi | sce_4878 | 88.43 serine/threonine protein kinase |
| SCE1572_5838 | 1-acyl-sn-glycerol-3-phosphate acyltransferase (EC 2.3.1.51) | bi | sce_4879 | 87.08 1-acyl-sn-glycerol-3-phosphate acyltransferase (EC 2.3.1.51) |
| SCE1572_5839 | serine/threonine protein kinase | umi | sce_1787 | 37.62 FIG01086365: hypothetical protein |
| SCE1572_5840 | hypothetical protein | umi | sce_6133 | 23.77 Twin-arginine translocation protein TatB |
| SCE1572_5841 | hypothetical protein | umi | sce_1797 | 41.32 Cell division protein FtsK |
| SCE1572_5842 | FIG01087277: hypothetical protein | umi | sce_1798 | 55.89 FIG01087277: hypothetical protein |
| SCE1572_5843 | hypothetical protein | - | - | 0 |
| SCE1572_5844 | hypothetical protein | - | - | 0 |
| SCE1572_5845 | hypothetical protein | umi | sce_6361 | 34.25 FIG01088774: hypothetical protein |
| SCE1572_5846 | COG0457: FOG: TPR repeat | umi | sce_5129 | 27.26 serine/threonine protein kinase |
| SCE1572_5847 | hypothetical protein | umi | sce_7913 | 24.29 serine/threonine protein kinase |
| SCE1572_5848 | hypothetical protein | - | - | 0 |
| SCE1572_5849 | FIG01085594: hypothetical protein | bi | sce_1502 | 80.42 FIG01085594: hypothetical protein |
| SCE1572_5850 | hypothetical protein | umi | sce_160 | 60.98 hypothetical protein |
| SCE1572_5851 | hypothetical protein | - | - | 0 |
| SCE1572_5852 | hypothetical protein | - | - | 0 |
| SCE1572_5853 | hypothetical protein | bi | sce_2040 | 38.32 hypothetical protein |
| SCE1572_5854 | hypothetical protein | bi | sce_7025 | 72.73 hypothetical protein |
| SCE1572_5855 | FIG01087636: hypothetical protein | bi | sce_3173 | 70.49 hypothetical protein |
| SCE1572_5856 | hypothetical protein | umi | sce_7299 | 52.63 hypothetical protein |
| SCE1572_5857 | hypothetical protein | - | - | 0 |
| SCE1572_5858 | hypothetical protein | - | - | 0 |
| SCE1572_5859 | hypothetical protein | umi | sce_2602 | 29.69 Membrane alanine aminopeptidase N (EC 3.4.11.2) |
| SCE1572_5860 | hypothetical protein | - | - | 0 |
| SCE1572_5861 | Internalin A (LPXTG motif) | umi | sce_7314 | 38.16 Leucine-rich repeat |
| SCE1572_5862 | phosphorylase | umi | sce_3976 | 44.74 TPR repeat |
| SCE1572_5863 | Chemotaxis protein methyltransferase CheR (EC 2.1.1.80) | umi | sce_7642 | 42.67 Chemotaxis protein methyltransferase CheR (EC 2.1.1.80) |
| SCE1572_5864 | hypothetical protein | - | - | 0 |
| SCE1572_5865 | Chemotaxis protein methyltransferase CheR (EC 2.1.1.80) | umi | sce_3830 | 33.85 Phosphate regulon sensor protein PhoR (SphS) (EC 2.7.13.3) |
| SCE1572_5866 | Response regulator of zinc sigma-54-dependent two-component system | umi | sce_1923 | 41.23 Response regulator of zinc sigma-54-dependent two-component system |
| SCE1572_5867 | Chemotaxis response regulator protein-glutamate methyltransferase CheB (EC 3.1.1.61) | umi | sce_4700 | 31.96 Chemotaxis protein methyltransferase CheR (EC 2.1.1.80) |
| SCE1572_5868 | Gli0726 protein | bi | sce_4880 | 87.24 Gli0726 protein |
| SCE1572_5869 | FIG01086583: hypothetical protein | bi | sce_4881 | 77.54 FIG01086583: hypothetical protein |
| SCE1572_5870 | hypothetical protein, INTERPRO-suggestion: probable ferritin-like | bi | sce_4882 | 76.8 conserved hypothetical protein |
| SCE1572_5871 | Dipeptidyl peptidase IV | bi | sce_4883 | 85.99 Dipeptidyl peptidase IV |
| SCE1572_5872 | Helicase, C-terminal:DEAD/DEAH box helicase, N-terminal | bi | sce_4885 | 93.19 Helicase, C-terminal:DEAD/DEAH box helicase, N-terminal |
| SCE1572_5873 | Multi-sensor Hybrid Histidine Kinase | bi | sce_4887 | 74.95 Multi-sensor Hybrid Histidine Kinase |
| SCE1572_5874 | Rhodanese-related sulfurtransferase | bi | sce_4888 | 87.96 Rhodanese-related sulfurtransferase |
| SCE1572_5875 | hypothetical protein | bi | sce_4889 | 90.65 hypothetical protein |
| SCE1572_5876 | serine/threonine protein kinase | bi | sce_4890 | 52.05 serine/threonine protein kinase |
| SCE1572_5877 | hypothetical protein | - | - | 0 |
| SCE1572_5878 | Ssl5025 protein | umi | sce_3858 | 29.87 Adenosylhomocysteinase (EC 3.3.1.1) |
| SCE1572_5879 | putative exported protein of unknown function with OmpA family domain | bi | sce_4891 | 74.2 hypothetical protein |
| SCE1572_5880 | hypothetical protein | - | - | 0 |
| SCE1572_5881 | two-component signal transduction histidine kinase | - | - | 0 |
| SCE1572_5882 | response regulator of the LytR/AlgR family | umi | sce_4465 | 40.83 RsbR, positive regulator of sigma-B |
| SCE1572_5883 | Transcriptional regulator, MarR family | bi | sce_7152 | 87.97 Transcriptional regulator, MarR family |
| SCE1572_5884 | putative flavodoxin monooxygenase | bi | sce_7151 | 90.3 putative flavodoxin monooxygenase |
| SCE1572_5885 | FIG01087506: hypothetical protein | umi | sce_6785 | 52.24 FIG01087506: hypothetical protein |
| SCE1572_5886 | erythrocyte membrane protein 1 (PEMP1) | umi | sce_1146 | 38.6 Gli0645 protein |
| SCE1572_5887 | NADH pyrophosphatase (EC 3.6.1.22) | bi | sce_4892 | 89.93 NADH pyrophosphatase (EC 3.6.1.22) |
| SCE1572_5888 | hypothetical protein | - | - | 0 |
| SCE1572_5889 | hypothetical protein | bi | sce_4893 | 41.3 FIG00501228: hypothetical protein |
| SCE1572_5890 | MATE efflux family protein | bi | sce_4895 | 84.36 MATE efflux family protein |
| SCE1572_5891 | hypothetical protein | - | - | 0 |
| SCE1572_5892 | hypothetical protein | - | - | 0 |
| SCE1572_5893 | UPF0135 protein Bsu YqfO @ Bsu YqfO NIF3/CutA domain | bi | sce_4896 | 91.78 UPF0135 protein Bsu YqfO @ Bsu YqfO NIF3/CutA domain |
| SCE1572_5894 | mosc domain protein | bi | sce_7535 | 93.33 hypothetical protein |
| SCE1572_5895 | protein containing QXW lectin repeats | bi | sce_7536 | 87.8 Putative secretion accessory protein EsaA/VueB |
| SCE1572_5896 | glycosyl hydrolase, BNR repeat-containing protein | bi | sce_7537 | 89.39 Glycosyl hydrolase, BNR repeat precursor |
| SCE1572_5897 | FIG00660906: hypothetical protein | umi | sce_926 | 35.24 hypothetical protein |
| SCE1572_5898 | FIG01089542: hypothetical protein | umi | sce_4908 | 82.69 FIG01089542: hypothetical protein |
| SCE1572_5899 | ATP-dependent Clp protease proteolytic subunit (EC 3.4.21.92) | bi | sce_2489 | 90.72 ATP-dependent Clp protease proteolytic subunit (EC 3.4.21.92) |
| SCE1572_5900 | Transcriptional regulator, ArnC family | bi | sce_2490 | 84.84 Transcriptional regulator, ArnC family |
| SCE1572_5901 | hypothetical protein | - | - | 0 |

| | | | | | |
|--------------|--|-----|-----------|-------|---|
| SCE1572_5902 | TonB-dependent receptor | umi | sce_3939 | 31.72 | FIG01085109: hypothetical protein |
| SCE1572_5903 | hypothetical protein | umi | sce_4330 | 42.86 | FIG01089660: hypothetical protein |
| SCE1572_5904 | hypothetical protein | umi | sce_3993 | 30 | Aspartyl-tRNA(Asn) amidotransferase subunit A (EC 6.3.5.6) @ Glutamyl-tRNA(Gln) amidotransferase subunit A (EC 6.3.5.7) |
| SCE1572_5905 | hypothetical protein | - | - | 0 | 0 |
| SCE1572_5906 | Glycogen phosphorylase (EC 2.4.1.1) | bi | sce_4909 | 94.84 | Glycogen phosphorylase (EC 2.4.1.1) |
| SCE1572_5907 | ATP-dependent Clp protease adaptor protein ClpS | bi | sce_4911 | 99.07 | ATP-dependent Clp protease adaptor protein ClpS |
| SCE1572_5908 | ATP-dependent Clp protease ATP-binding subunit ClpA | bi | sce_4912 | 94.47 | ATP-dependent Clp protease ATP-binding subunit ClpA |
| SCE1572_5909 | ApaG protein | bi | sce_4913 | 97.64 | ApaG protein |
| SCE1572_5910 | rhomboid family protein | bi | sce_4914 | 86.57 | rhomboid family protein |
| SCE1572_5911 | FIG01087968: hypothetical protein | bi | sce_4915 | 88.37 | FIG01087968: hypothetical protein |
| SCE1572_5912 | hypothetical protein | bi | sce_4916 | 84.29 | hypothetical protein |
| SCE1572_5913 | pyridoxal phosphate-dependent deaminase, putative | bi | sce_4917 | 88.63 | pyridoxal phosphate-dependent deaminase, putative |
| SCE1572_5914 | hypothetical protein | bi | sce_4918 | 92.99 | hypothetical protein |
| SCE1572_5915 | Phosphoserine aminotransferase (EC 2.6.1.52) | bi | sce_4919 | 95.56 | Phosphoserine aminotransferase (EC 2.6.1.52) |
| SCE1572_5916 | hypothetical protein | bi | sce_4920 | 96.08 | hypothetical protein |
| SCE1572_5917 | Beta-carotene hydroxylase | bi | sce_4921 | 96.17 | Beta-carotene hydroxylase |
| SCE1572_5918 | hypothetical protein | - | - | 0 | 0 |
| SCE1572_5919 | Agmatinase (EC 3.5.3.11) | bi | sce_4923 | 91.04 | Agmatinase (EC 3.5.3.11) |
| SCE1572_5920 | Aspartyl aminopeptidase | bi | sce_4924 | 91.96 | Aspartyl aminopeptidase |
| SCE1572_5921 | hypothetical protein | - | - | 0 | 0 |
| SCE1572_5922 | Dihydroorotate dehydrogenase (EC 1.3.3.1) | bi | sce_4925 | 91.29 | Dihydroorotate dehydrogenase (EC 1.3.3.1) |
| SCE1572_5923 | COGs COG3146 | bi | sce_4926 | 89.38 | COGs COG3146 |
| SCE1572_5924 | FIG01089566: hypothetical protein | bi | sce_4927 | 77.87 | FIG01089566: hypothetical protein |
| SCE1572_5925 | Response regulator of zinc sigma-54-dependent two-component system | bi | sce_4928 | 94.91 | Response regulator of zinc sigma-54-dependent two-component system |
| SCE1572_5926 | Cellulose-binding domain protein | bi | sce_4929 | 88.35 | Cellulose-binding domain protein |
| SCE1572_5927 | FIG01087019: hypothetical protein | bi | sce_4930 | 89.39 | FIG01087019: hypothetical protein |
| SCE1572_5928 | Transcriptional regulatory protein prrA | bi | sce_6137 | 51.38 | Transcriptional regulatory protein prrA |
| SCE1572_5929 | Sensor protein | bi | sce_6138 | 40.75 | sensory box histidine kinase |
| SCE1572_5930 | hypothetical protein | - | - | 0 | 0 |
| SCE1572_5931 | Multimodular transpeptidase-transglycosylase (EC 2.4.1.129) (EC 3.4.-.-) | bi | sce_4931 | 85.43 | Multimodular transpeptidase-transglycosylase (EC 2.4.1.129) (EC 3.4.-.-) |
| SCE1572_5932 | Large extracellular alpha-helical protein | bi | sce_4932 | 87.73 | Large extracellular alpha-helical protein |
| SCE1572_5933 | Signal transduction histidine kinase | umi | sce_815 | 34.6 | Sensor protein |
| SCE1572_5934 | regulatory protein, LuxR-Response regulator receiver | umi | sce_3234 | 37.98 | Type IV fimbriae expression regulatory protein PilR |
| SCE1572_5935 | hypothetical protein | umi | sce_2128 | 52.24 | hypothetical protein |
| SCE1572_5936 | Conserved domain protein | umi | sce_2126 | 60.12 | Conserved domain protein |
| SCE1572_5937 | Tetratricopeptide repeat-containing protein | umi | sce_7678 | 41.35 | transcriptional regulator, winged helix family |
| SCE1572_5938 | hypothetical protein | - | - | 0 | 0 |
| SCE1572_5939 | hypothetical protein | umi | sce_2128 | 47.66 | hypothetical protein |
| SCE1572_5940 | hypothetical protein | umi | sce_1870 | 26.46 | FIG01088242: hypothetical protein |
| SCE1572_5941 | hypothetical protein | - | - | 0 | 0 |
| SCE1572_5942 | Erk/Ybs/YciS/YnhG family | umi | sce_9660 | 48.24 | Carboxypeptidase |
| SCE1572_5943 | hypothetical protein | umi | sce_6493 | 38.6 | Translation initiation factor 2 |
| SCE1572_5944 | hypothetical protein | bi | sce_2045 | 50 | Mlr6568 protein |
| SCE1572_5945 | hypothetical protein | umi | sce_9495 | 28.7 | hypothetical protein |
| SCE1572_5946 | hypothetical protein | - | - | 0 | 0 |
| SCE1572_5947 | hypothetical protein | - | - | 0 | 0 |
| SCE1572_5948 | Phage tail fibers | - | - | 0 | 0 |
| SCE1572_5949 | hypothetical protein | - | - | 0 | 0 |
| SCE1572_5950 | hypothetical protein | - | - | 0 | 0 |
| SCE1572_5951 | GPW/gp25 family protein | - | - | 0 | 0 |
| SCE1572_5952 | hypothetical protein | - | - | 0 | 0 |
| SCE1572_5953 | Rhs element Vgr protein | umi | sce_2329 | 27.72 | VgrG protein |
| SCE1572_5954 | hypothetical protein | - | - | 0 | 0 |
| SCE1572_5955 | hypothetical protein | - | - | 0 | 0 |
| SCE1572_5956 | hypothetical protein | - | - | 0 | 0 |
| SCE1572_5957 | hypothetical protein | - | - | 0 | 0 |
| SCE1572_5958 | Afp1 | - | - | 0 | 0 |
| SCE1572_5959 | Phage tail sheath protein FI | umi | sce_2319 | 36.28 | Phage tail sheath protein FI |
| SCE1572_5960 | hypothetical protein | - | - | 0 | 0 |
| SCE1572_5961 | hypothetical protein | - | - | 0 | 0 |
| SCE1572_5962 | hypothetical protein | - | - | 0 | 0 |
| SCE1572_5963 | Cell division protein FtsH (EC 3.4.24.-) | bi | sce_2324 | 47.04 | ATPase, AAA family |
| SCE1572_5964 | hypothetical protein | - | - | 0 | 0 |
| SCE1572_5965 | hypothetical protein | - | - | 0 | 0 |
| SCE1572_5966 | hypothetical protein | umi | sce_3858 | 28.24 | Adenosylhomocysteinase (EC 3.3.1.1) |
| SCE1572_5967 | WD-40 repeat protein | umi | sce_5086 | 52.19 | tolB protein precursor, periplasmic protein involved in the tonb-independent uptake of group A colicins |
| SCE1572_5968 | serine/threonine protein kinase | umi | sce_3991 | 35.61 | serine/threonine protein kinase |
| SCE1572_5969 | S-layer-like array protein | umi | sce_8317 | 36.77 | FIG01085807: hypothetical protein |
| SCE1572_5970 | hypothetical protein | - | - | 0 | 0 |
| SCE1572_5971 | hypothetical protein | - | - | 0 | 0 |
| SCE1572_5972 | hypothetical protein | - | - | 0 | 0 |
| SCE1572_5973 | FIG01088786: hypothetical protein | bi | sce_4934 | 74.09 | FIG01088786: hypothetical protein |
| SCE1572_5974 | hypothetical protein | - | - | 0 | 0 |
| SCE1572_5975 | ABC transporter permease protein | bi | sce_4935 | 84.41 | ABC transporter permease protein |
| SCE1572_5976 | ABC transporter permease protein | bi | sce_4936 | 94.84 | Ribose ABC transport system, permease protein RbsC (TC 3.A.1.2.1) |
| SCE1572_5977 | Isochorismatase (EC 3.3.2.1) | bi | sce_4937 | 94.78 | Isochorismatase (EC 3.3.2.1) |
| SCE1572_5978 | Ribose ABC transport system, ATP-binding protein RbsA (TC 3.A.1.2.1) | bi | sce_4938 | 86.69 | Ribose ABC transport system, ATP-binding protein RbsA (TC 3.A.1.2.1) |
| SCE1572_5979 | Nicotinamide/isochorismatase family protein | bi | sce_4939 | 91.52 | Nicotinamide/isochorismatase family protein |
| SCE1572_5980 | Bmp family protein | bi | sce_4941 | 87.03 | Bmp family protein |
| SCE1572_5981 | hypothetical protein | bi | sce_4942 | 86.41 | hypothetical protein |
| SCE1572_5982 | hypothetical protein | - | - | 0 | 0 |
| SCE1572_5983 | putative lipoprotein | bi | sce_2441 | 42.65 | hypothetical protein |
| SCE1572_5984 | Phospholipase A1 | umi | sce_6336 | 41.11 | hypothetical protein |
| SCE1572_5985 | conserved hypothetical protein | umi | sce_10430 | 32.13 | Mir2351 protein |
| SCE1572_5986 | hypothetical protein | - | - | 0 | 0 |
| SCE1572_5987 | hypothetical protein | umi | sce_3038 | 37.85 | hypothetical protein |
| SCE1572_5988 | hypothetical protein | - | - | 0 | 0 |
| SCE1572_5989 | hypothetical protein | bi | sce_9405 | 62.92 | FIG01088026: hypothetical protein |
| SCE1572_5990 | VgrG protein | bi | sce_9404 | 72.23 | VgrG protein |
| SCE1572_5991 | hypothetical protein | bi | sce_4943 | 95.61 | hypothetical protein |
| SCE1572_5992 | ABC transporter, ATP-binding protein | bi | sce_4944 | 92.76 | ABC-type multidrug transport system, ATPase component |
| SCE1572_5993 | putative membrane spanning protein | bi | sce_4945 | 96.62 | ABC-type transport system involved in multi-copper enzyme maturation, permease component, putative |
| SCE1572_5994 | hypothetical protein | bi | sce_4946 | 85.8 | hypothetical protein |
| SCE1572_5995 | FIG01087481: hypothetical protein | bi | sce_4947 | 87.94 | FIG01087481: hypothetical protein |
| SCE1572_5996 | hypothetical protein | bi | sce_4948 | 85.51 | hypothetical protein |
| SCE1572_5997 | serine/threonine protein kinase | bi | sce_4949 | 76.9 | serine/threonine protein kinase |
| SCE1572_5998 | tyrosine recombinase XerD | bi | sce_4950 | 95.61 | tyrosine recombinase XerD |
| SCE1572_5999 | N-formylglutamate deformylase (EC 3.5.1.68) | bi | sce_4951 | 92.41 | N-formylglutamate deformylase (EC 3.5.1.68) |
| SCE1572_6000 | FIG01086988: hypothetical protein | bi | sce_4952 | 81.84 | FIG01086988: hypothetical protein |
| SCE1572_6001 | LSU ribosomal protein L28p | bi | sce_4953 | 98.65 | LSU ribosomal protein L28p |
| SCE1572_6002 | hypothetical protein | bi | sce_4954 | 89.68 | hypothetical protein |
| SCE1572_6003 | 235aa long hypothetical protein | bi | sce_4955 | 92.53 | 235aa long hypothetical protein |
| SCE1572_6004 | FIG01085758: hypothetical protein | bi | sce_4956 | 93.29 | FIG01085758: hypothetical protein |
| SCE1572_6005 | Epoxyqueuosine (oQ) reductase QueG | bi | sce_4957 | 84.21 | Epoxyqueuosine (oQ) reductase QueG |
| SCE1572_6006 | rRNA (Guanine37-N1)-methyltransferase (EC 2.1.1.31) / protein of unknown function aq_054 | bi | sce_4958 | 91.1 | rRNA (Guanine37-N1)-methyltransferase (EC 2.1.1.31) |
| SCE1572_6007 | rRNA (Guanine37-N1)-methyltransferase (EC 2.1.1.31) | umi | sce_4958 | 87.5 | rRNA (Guanine37-N1)-methyltransferase (EC 2.1.1.31) |
| SCE1572_6008 | 16S rRNA processing protein RimM | bi | sce_4959 | 86.47 | 16S rRNA processing protein RimM |
| SCE1572_6009 | KH domain RNA binding protein YlqC | bi | sce_4960 | 100 | KH domain RNA binding protein YlqC |
| SCE1572_6010 | SSU ribosomal protein S16p | bi | sce_4961 | 100 | SSU ribosomal protein S16p |
| SCE1572_6011 | FIG01086863: hypothetical protein | bi | sce_4963 | 81.93 | FIG01086863: hypothetical protein |
| SCE1572_6012 | FIG022979: MoxR-like ATPases | bi | sce_4964 | 96 | FIG022979: MoxR-like ATPases |
| SCE1572_6013 | hypothetical protein | bi | sce_4965 | 92.1 | hypothetical protein |
| SCE1572_6014 | Dimethyladenosine transferase (EC 2.1.1.-) | bi | sce_4966 | 91.67 | Dimethyladenosine transferase (EC 2.1.1.-) |
| SCE1572_6015 | ATP synthase beta chain (EC 3.6.3.14) | bi | sce_4968 | 95.77 | ATP synthase beta chain (EC 3.6.3.14) |
| SCE1572_6016 | ATP synthase epsilon chain (EC 3.6.3.14) | bi | sce_4969 | 95.14 | ATP synthase epsilon chain (EC 3.6.3.14) |
| SCE1572_6017 | DNA primase (EC 2.7.7.-) | bi | sce_4970 | 93.68 | DNA primase (EC 2.7.7.-) |
| SCE1572_6018 | RNA polymerase sigma factor RpoD | bi | sce_4971 | 99.53 | RNA polymerase sigma factor RpoD |
| SCE1572_6019 | hypothetical protein | bi | sce_4972 | 74 | hypothetical protein |
| SCE1572_6020 | rhomboid family protein | bi | sce_4973 | 92.09 | rhomboid family protein |
| SCE1572_6021 | Outer membrane protein assembly factor YaeT precursor | bi | sce_4974 | 92.22 | Outer membrane protein assembly factor YaeT precursor |
| SCE1572_6022 | hypothetical protein | - | - | 0 | 0 |
| SCE1572_6023 | Topoisomerase IV subunit A (EC 5.99.1.-) | bi | sce_4976 | 97 | Topoisomerase IV subunit A (EC 5.99.1.-) |
| SCE1572_6024 | Topoisomerase IV subunit B (EC 5.99.1.-) | bi | sce_4977 | 96.74 | Topoisomerase IV subunit B (EC 5.99.1.-) |
| SCE1572_6025 | hypothetical protein | bi | sce_4978 | 89.92 | hypothetical protein |
| SCE1572_6026 | Omega amidase (Nit2 homolog) | bi | sce_4979 | 92.16 | Omega amidase (Nit2 homolog) |
| SCE1572_6027 | EBNA-1 | bi | sce_4980 | 72.36 | Epstein-Barr nuclear antigen 1 (EBV nuclear antigen 1) (EBNA-1) |
| SCE1572_6028 | NUDIX hydrolase | bi | sce_4981 | 91.23 | mutator MutT homolog |
| SCE1572_6029 | DNA ligase (EC 6.5.1.2) | bi | sce_4982 | 94.08 | DNA ligase (EC 6.5.1.2) |
| SCE1572_6030 | hypothetical protein | bi | sce_4983 | 84.73 | hypothetical protein |
| SCE1572_6031 | Delta-1-pyrroline-5-carboxylate dehydrogenase (EC 1.5.1.12) | bi | sce_4984 | 95.24 | Delta-1-pyrroline-5-carboxylate dehydrogenase (EC 1.5.1.12) |
| SCE1572_6032 | hypothetical protein | bi | sce_4985 | 69.57 | hypothetical protein |
| SCE1572_6033 | Serine protease, subtilase family | bi | sce_4986 | 73.44 | Serine protease, subtilase family |
| SCE1572_6034 | Thimet oligopeptidase (EC 3.4.24.15) | bi | sce_4987 | 88.67 | Thimet oligopeptidase (EC 3.4.24.15) |
| SCE1572_6035 | TPR domain protein, putative component of TonB system | umi | sce_3281 | 30.57 | TPR domain protein, putative component of TonB system |
| SCE1572_6036 | hypothetical protein | - | - | 0 | 0 |
| SCE1572_6037 | hypothetical protein | bi | sce_4989 | 75.81 | hypothetical protein |
| SCE1572_6038 | protein kinase | bi | sce_4990 | 87.75 | protein kinase |
| SCE1572_6039 | Trypsin-like serine proteases, typically periplasmic, contain C-terminal PDZ domain | bi | sce_4991 | 87.25 | Trypsin-like serine proteases, typically periplasmic, contain C-terminal PDZ domain |
| SCE1572_6040 | Type IV fimbrial assembly, ATPase PilB | bi | sce_4992 | 98.23 | Type IV fimbrial assembly, ATPase PilB |
| SCE1572_6041 | Twitching motility protein PilT | bi | sce_4993 | 96.83 | Twitching motility protein PilT |
| SCE1572_6042 | SOS-response repressor and protease LexA (EC 3.4.21.88) | bi | sce_4994 | 97.83 | SOS-response repressor and protease LexA (EC 3.4.21.88) |
| SCE1572_6043 | hypothetical protein | - | - | 0 | 0 |
| SCE1572_6044 | FIG01088921: hypothetical protein | bi | sce_4995 | 93.41 | FIG01088921: hypothetical protein |
| SCE1572_6045 | OmpA | bi | sce_4996 | 94.21 | OmpA |
| SCE1572_6046 | hypothetical protein | bi | sce_4997 | 82.53 | hypothetical protein |
| SCE1572_6047 | hypothetical protein | bi | sce_4999 | 94.21 | hypothetical protein |
| SCE1572_6048 | Transcriptional regulatory protein algP | bi | sce_5000 | 78.86 | Transcriptional regulatory protein algP |
| SCE1572_6049 | Flagellar assembly protein FliH | bi | sce_5001 | 70.61 | Flagellar assembly protein FliH |
| SCE1572_6050 | hypothetical protein | - | - | 0 | 0 |
| SCE1572_6051 | Aspartate aminotransferase (EC 2.6.1.1) | bi | sce_5002 | 92.11 | Aspartate aminotransferase (EC 2.6.1.1) |
| SCE1572_6052 | Virulence factor Mce family protein | bi | sce_5003 | 93.98 | Virulence factor Mce family protein |
| SCE1572_6053 | Methionine ABC transporter ATP-binding protein | bi | sce_5004 | 95.37 | Methionine ABC transporter ATP-binding protein |
| SCE1572_6054 | Single-stranded-DNA-specific exonuclease RecJ (EC 3.1.-.-) | bi | sce_5005 | 91.69 | Single-stranded-DNA-specific exonuclease RecJ (EC 3.1.-.-) |
| SCE1572_6055 | Protein-export membrane protein SecF (TC 3.A.5.1.1) | bi | sce_5006 | 90.8 | Protein-export membrane protein SecF (TC 3.A.5.1.1) |
| SCE1572_6056 | Protein-export membrane protein SecD (TC 3.A.5.1.1) | bi | sce_5007 | 94.28 | Protein-export membrane protein SecD (TC 3.A.5.1.1) |
| SCE1572_6057 | Preprotein translocase subunit YajC (TC 3.A.5.1.1) | bi | sce_5008 | 89.19 | Preprotein translocase subunit YajC (TC 3.A.5.1.1) |
| SCE1572_6058 | Pyruvate-flavodoxin oxidoreductase (EC 1.2.7.-) | bi | sce_5009 | 93.68 | Pyruvate-flavodoxin oxidoreductase (EC 1.2.7.-) |
| SCE1572_6059 | Threonyl-tRNA synthetase (EC 6.1.1.3) | umi | sce_4871 | 36.46 | Threonyl-tRNA synthetase (EC 6.1.1.3) |
| SCE1572_6060 | hypothetical protein | - | - | 0 | 0 |
| SCE1572_6061 | Translation initiation factor 3 | bi | sce_5011 | 95.8 | Translation initiation factor 3 |
| SCE1572_6062 | serine/threonine protein kinase | bi | sce_5012 | 83.21 | Serine/threonine protein kinase PrkC, regulator of stationary phase |
| SCE1572_6063 | hypothetical protein | - | - | 0 | 0 |
| SCE1572_6064 | hypothetical protein | bi | sce_5013 | 86.84 | hypothetical protein |
| SCE1572_6065 | hypothetical protein | bi | sce_5014 | 90.48 | hypothetical protein |

| | | | | | |
|--------------|---|-----|-----------|-------|---|
| SCE1572_6066 | hypothetical protein | bi | sce_5015 | 84.75 | hypothetical protein |
| SCE1572_6067 | FIG01086293: hypothetical protein | bi | sce_5016 | 86.57 | FIG01086293: hypothetical protein |
| SCE1572_6068 | hypothetical protein | bi | sce_5017 | 92.34 | hypothetical protein |
| SCE1572_6069 | FMN-binding domain protein | bi | sce_5018 | 92.43 | FMN-binding |
| SCE1572_6070 | Conserved domain protein | bi | sce_5019 | 90.82 | Conserved domain protein |
| SCE1572_6071 | hypothetical protein | - | - | 0 | 0 |
| SCE1572_6072 | hypothetical protein | uni | sce_10290 | 42.41 | Sensor protein |
| SCE1572_6073 | hypothetical protein | - | - | 0 | 0 |
| SCE1572_6074 | 1,4-alpha-glucan (glycogen) branching enzyme, GH-13-type (EC 2.4.1.18) | bi | sce_5020 | 90.62 | 1,4-alpha-glucan (glycogen) branching enzyme, GH-13-type (EC 2.4.1.18) |
| SCE1572_6075 | Aldehyde dehydrogenase (EC 1.2.1.3) | bi | sce_5022 | 95.08 | Aldehyde dehydrogenase (EC 1.2.1.3) |
| SCE1572_6076 | hypothetical protein | bi | sce_5023 | 84.44 | FIG01085073: hypothetical protein |
| SCE1572_6077 | hypothetical protein | bi | sce_5024 | 88.31 | hypothetical protein |
| SCE1572_6078 | FIG01087372: hypothetical protein | uni | sce_522 | 84.62 | FIG01087372: hypothetical protein |
| SCE1572_6079 | hypothetical protein | - | - | 0 | 0 |
| SCE1572_6080 | FIG01086922: hypothetical protein | uni | sce_7361 | 54.36 | AAA ATPase |
| SCE1572_6081 | Prophage Lp2 protein 6 | uni | sce_244 | 80.95 | Prophage Lp2 protein 6 |
| SCE1572_6082 | Prophage Lp2 protein 6 | bi | sce_244 | 91.43 | Prophage Lp2 protein 6 |
| SCE1572_6083 | Chemotaxis protein methyltransferase CheR (EC 2.1.1.80) | uni | sce_9491 | 47.87 | Chemotaxis protein methyltransferase CheR (EC 2.1.1.80) |
| SCE1572_6084 | hypothetical protein | - | - | 0 | 0 |
| SCE1572_6085 | Endonuclease/exonuclease/phosphatase | - | - | 0 | 0 |
| SCE1572_6086 | hypothetical protein | bi | sce_1876 | 67.24 | hypothetical protein |
| SCE1572_6087 | ATP-dependent protease La (EC 3.4.21.53) Type I | bi | sce_5033 | 94.49 | ATP-dependent protease La (EC 3.4.21.53) Type I |
| SCE1572_6088 | ICE-like protease (caspase) p20 domain protein | bi | sce_5035 | 68.71 | peptidase C14, caspase catalytic subunit p20 |
| SCE1572_6089 | putative exported protein of unknown function with OmpA family domain | bi | sce_5036 | 75.76 | hypothetical protein |
| SCE1572_6090 | RNA polymerase sigma factor RpoE | bi | sce_5037 | 89 | RNA polymerase sigma factor RpoE |
| SCE1572_6091 | hypothetical protein | bi | sce_5039 | 67.46 | hypothetical protein |
| SCE1572_6092 | serine/threonine protein kinase | uni | sce_1794 | 48.91 | serine/threonine protein kinase |
| SCE1572_6093 | probable secreted protease | - | - | 0 | 0 |
| SCE1572_6094 | FIG01085119: hypothetical protein | bi | sce_835 | 77.35 | FIG01085119: hypothetical protein |
| SCE1572_6095 | PAS fold-3 | uni | sce_6175 | 49.66 | RsbR, positive regulator of sigma-B |
| SCE1572_6096 | Signal transduction histidine kinase CheA (EC 2.7.3.-) | uni | sce_3917 | 39.95 | Signal transduction histidine kinase CheA (EC 2.7.3.-) |
| SCE1572_6097 | Transcriptional regulator, TetR family | bi | sce_5042 | 89.76 | Transcriptional regulator, TetR family |
| SCE1572_6098 | Serine/threonine-protein kinase pkn3 (EC 2.7.11.1) | bi | sce_5044 | 75.13 | hypothetical protein |
| SCE1572_6099 | FIG01085909: hypothetical protein | bi | sce_5045 | 72.98 | FIG01087200: hypothetical protein |
| SCE1572_6100 | Fe-S-cluster-containing hydrogenase components 1 | bi | sce_5047 | 84.47 | Fe-S-cluster-containing hydrogenase components 1 |
| SCE1572_6101 | Molybdopterin oxidoreductase membrane subunit | bi | sce_5048 | 86.55 | Molybdopterin oxidoreductase membrane subunit |
| SCE1572_6102 | ABC-type Fe3 transport system protein, Molybdenum transport protein, putative | bi | sce_5049 | 84.48 | ABC-type Fe3 transport system protein, Molybdenum transport protein, putative |
| SCE1572_6103 | hypothetical protein | bi | sce_5050 | 77.99 | hypothetical protein |
| SCE1572_6104 | hypothetical protein | bi | sce_5051 | 83.54 | hypothetical protein |
| SCE1572_6105 | hypothetical protein | bi | sce_5052 | 73.08 | hypothetical protein |
| SCE1572_6106 | SCO1/SenC family protein | bi | sce_5053 | 82.37 | hypothetical protein |
| SCE1572_6107 | Cytochrome c oxidase polypeptide II (EC 1.9.3.1) | bi | sce_5054 | 83.7 | Cytochrome c oxidase polypeptide II (EC 1.9.3.1) |
| SCE1572_6108 | Cytochrome c oxidase polypeptide I (EC 1.9.3.1) | bi | sce_5055 | 90.35 | Cytochrome c oxidase polypeptide I (EC 1.9.3.1) |
| SCE1572_6109 | Cytochrome c oxidase polypeptide III (EC 1.9.3.1) | bi | sce_5056 | 86.1 | Cytochrome c oxidase polypeptide III (EC 1.9.3.1) |
| SCE1572_6110 | Caa(3)-type oxidase, subunit IV | bi | sce_5057 | 79.09 | caa(3)-type oxidase, subunit IV |
| SCE1572_6111 | Mobile element protein | bi | sce_5058 | 82.98 | putative lipoprotein |
| SCE1572_6112 | Putative ATP-dependent DNA helicase | bi | sce_5059 | 49.27 | Putative ATP-dependent DNA helicase |
| SCE1572_6113 | FIG01086098: hypothetical protein | bi | sce_5060 | 87.59 | FIG01086489: hypothetical protein |
| SCE1572_6114 | TeiR | bi | sce_6885 | 39.82 | TeiR |
| SCE1572_6115 | hypothetical protein | - | - | 0 | 0 |
| SCE1572_6116 | Endo-1,4-beta-xylanase A precursor (EC 3.2.1.8) | uni | sce_6214 | 62.56 | Xylanase |
| SCE1572_6117 | iron-sulfur cluster-binding protein, Rieske family | uni | sce_7799 | 33.14 | C3: similar to Vanillate O-demethylase oxygenase |
| SCE1572_6118 | Transcription repressor of multidrug efflux pump acrAB operon, TetR (AcrR) family | uni | sce_6665 | 34.18 | Transcriptional regulator, TetR family |
| SCE1572_6119 | FIG01086131: hypothetical protein | bi | sce_5062 | 98.98 | FIG01086131: hypothetical protein |
| SCE1572_6120 | contains protein kinase domain, Pfam:PF00669; go_function: kinase activity [goid 0016301] / protein kinase family protein | bi | sce_5063 | 73.07 | contains protein kinase domain, Pfam:PF00669; go_function: kinase activity [goid 0016301] / protein kinase family protein |
| SCE1572_6121 | Phytoene dehydrogenase (EC 1.14.99.-) | bi | sce_5064 | 80.39 | Phytoene dehydrogenase (EC 1.14.99.-) |
| SCE1572_6122 | serine/threonine protein kinase | bi | sce_5066 | 95.6 | serine/threonine protein kinase |
| SCE1572_6123 | FIG01086778: hypothetical protein | bi | sce_5068 | 71.36 | FIG01086778: hypothetical protein |
| SCE1572_6124 | hypothetical protein | bi | sce_5069 | 90.85 | hypothetical protein |
| SCE1572_6125 | Methyltransferase type 11 | bi | sce_5070 | 88.4 | Methyltransferase type 11 |
| SCE1572_6126 | FIG01087980: hypothetical protein | bi | sce_5071 | 84.7 | FIG01087980: hypothetical protein |
| SCE1572_6127 | serine/threonine protein kinase | bi | sce_5072 | 82.98 | serine/threonine protein kinase |
| SCE1572_6128 | Pyruvate kinase (EC 2.7.1.40) | bi | sce_5073 | 98.55 | Pyruvate kinase (EC 2.7.1.40) |
| SCE1572_6129 | Polyribonucleotide nucleotidyltransferase (EC 2.7.7.8) | bi | sce_5074 | 95.78 | Polyribonucleotide nucleotidyltransferase (EC 2.7.7.8) |
| SCE1572_6130 | hypothetical protein | bi | sce_5075 | 88.64 | hypothetical protein |
| SCE1572_6131 | SSU ribosomal protein S15p (S13e) | bi | sce_5076 | 95.45 | SSU ribosomal protein S15p (S13e) |
| SCE1572_6132 | hypothetical protein | - | - | 0 | 0 |
| SCE1572_6133 | serine/threonine protein kinase | bi | sce_5077 | 92.9 | serine/threonine protein kinase |
| SCE1572_6134 | Putative Holliday junction resolvase (EC 3.1.-.-) | bi | sce_5078 | 94.37 | Putative Holliday junction resolvase (EC 3.1.-.-) |
| SCE1572_6135 | Histidyl-tRNA synthetase (EC 6.1.1.21) | bi | sce_5079 | 92.86 | Histidyl-tRNA synthetase (EC 6.1.1.21) |
| SCE1572_6136 | hypothetical protein | bi | sce_5080 | 90.57 | hypothetical protein |
| SCE1572_6137 | hypothetical protein | bi | sce_5081 | 94.55 | hypothetical protein |
| SCE1572_6138 | hypothetical protein | bi | sce_7381 | 93.75 | hypothetical protein |
| SCE1572_6139 | putative sensory box histidine kinase/response regulator | bi | sce_5082 | 88.8 | Histidine kinase |
| SCE1572_6140 | hypothetical protein | bi | sce_5083 | 87.42 | putative vgr-related protein |
| SCE1572_6141 | hypothetical protein | - | - | 0 | 0 |
| SCE1572_6142 | FIG01087734: hypothetical protein | bi | sce_5084 | 82.65 | FIG01087734: hypothetical protein |
| SCE1572_6143 | Ribose ABC transport system, permease protein RbsC (TC 3.A.1.2.1) | - | - | 0 | 0 |
| SCE1572_6144 | hypothetical protein | - | - | 0 | 0 |
| SCE1572_6145 | hypothetical protein | bi | sce_5088 | 78.88 | hypothetical protein |
| SCE1572_6146 | Multi antimicrobial extrusion protein (Na)/drug antiporter, MATE family of MDR efflux pumps | uni | sce_1290 | 31.79 | MATE efflux family protein |
| SCE1572_6147 | Carbonic anhydrase (EC:4.2.1.1) | uni | sce_7712 | 26.06 | Carbonic anhydrase (EC 4.2.1.1) |
| SCE1572_6148 | FIG01086657: hypothetical protein | uni | sce_6904 | 76.41 | FIG01089354: hypothetical protein |
| SCE1572_6149 | hypothetical protein | - | - | 0 | 0 |
| SCE1572_6150 | hypothetical protein | - | - | 0 | 0 |
| SCE1572_6151 | COG0553: Superfamily II DNA/RNA helicases, SNF2 family | bi | sce_5091 | 84.26 | COG0553: Superfamily II DNA/RNA helicases, SNF2 family |
| SCE1572_6152 | xenobiotic reductase, putative | bi | sce_4458 | 96.15 | xenobiotic reductase, putative |
| SCE1572_6153 | hypothetical protein | - | - | 0 | 0 |
| SCE1572_6154 | FIG01086458: hypothetical protein | uni | sce_5638 | 71.5 | FIG01086458: hypothetical protein |
| SCE1572_6155 | serine/threonine protein kinase | bi | sce_5094 | 77.88 | serine/threonine protein kinase |
| SCE1572_6156 | FIG01087783: hypothetical protein | bi | sce_5123 | 82.81 | FIG01087783: hypothetical protein |
| SCE1572_6157 | hypothetical protein | - | - | 0 | 0 |
| SCE1572_6158 | Serine/threonine-protein kinase pkn1 (EC 2.7.11.1) | bi | sce_5128 | 75.74 | Serine/threonine-protein kinase pkn1 (EC 2.7.11.1) |
| SCE1572_6159 | serine/threonine protein kinase | uni | sce_5129 | 74.63 | serine/threonine protein kinase |
| SCE1572_6160 | serine/threonine kinase family protein (EC:2.7.1.-) | bi | sce_5129 | 83.33 | serine/threonine protein kinase |
| SCE1572_6161 | conserved hypothetical protein | bi | sce_5130 | 63.9 | conserved hypothetical protein |
| SCE1572_6162 | Transcriptional activator of acetoin/glycerol metabolism | bi | sce_5131 | 89.52 | Transcriptional activator of acetoin/glycerol metabolism |
| SCE1572_6163 | hypothetical protein | - | - | 0 | 0 |
| SCE1572_6164 | Serine-threonine protein kinase | bi | sce_5160 | 80.71 | Serine-threonine protein kinase |
| SCE1572_6165 | Adenylate cyclase (EC 4.6.1.1) / Guanylate cyclase (EC 4.6.1.2) | bi | sce_5161 | 88.13 | serine/threonine protein kinase |
| SCE1572_6166 | Serine-threonine protein kinase | bi | sce_5162 | 77.69 | Serine-threonine protein kinase |
| SCE1572_6167 | hypothetical protein | bi | sce_5163 | 76.1 | Succinyl-CoA ligase [ADP-forming] beta chain (EC 6.2.1.5) |
| SCE1572_6168 | hypothetical protein | bi | sce_5164 | 88.86 | hypothetical protein |
| SCE1572_6169 | hypothetical protein | - | - | 0 | 0 |
| SCE1572_6170 | Alkyl hydroperoxide reductase subunit C-like protein | bi | sce_5165 | 84.38 | Alkyl hydroperoxide reductase subunit C-like protein |
| SCE1572_6171 | FIG01086485: hypothetical protein | bi | sce_5166 | 81.64 | FIG01086485: hypothetical protein |
| SCE1572_6172 | hypothetical protein | - | - | 0 | 0 |
| SCE1572_6173 | FIG01086810: hypothetical protein | bi | sce_335 | 77.89 | FIG01086810: hypothetical protein |
| SCE1572_6174 | Similarity | bi | sce_336 | 71.6 | zonadhesin, putative |
| SCE1572_6175 | Butyryl-CoA dehydrogenase (EC 1.3.99.2) | bi | sce_5250 | 81.85 | Butyryl-CoA dehydrogenase (EC 1.3.99.2) |
| SCE1572_6176 | Small-conductance mechanosensitive channel | bi | sce_5171 | 84.67 | Small-conductance mechanosensitive channel |
| SCE1572_6177 | MscS Mechanosensitive ion channel | bi | sce_10374 | 34.73 | MscS Mechanosensitive ion channel |
| SCE1572_6178 | FIG01085444: hypothetical protein | bi | sce_5176 | 91.51 | FIG01085444: hypothetical protein |
| SCE1572_6179 | phytol kinase | bi | sce_5177 | 91.54 | phytol kinase |
| SCE1572_6180 | Metalloprotease MEP2 | bi | sce_5178 | 82.96 | Metalloprotease MEP2 |
| SCE1572_6181 | Carbonic anhydrase (EC 4.2.1.1) | bi | sce_5179 | 84.47 | Carbonic anhydrase (EC 4.2.1.1) |
| SCE1572_6182 | serine/threonine protein kinase | uni | sce_4890 | 45.39 | serine/threonine protein kinase |
| SCE1572_6183 | Arachidonate 15-lipoxygenase precursor (EC 1.13.11.33) | - | - | 0 | 0 |
| SCE1572_6184 | PE_PGRS family protein | uni | sce_3675 | 44.35 | Feruloyl esterase B precursor (EC 3.1.1.73) (Ferulic acid esterase B) (FAEB) (Cinnamoyl esterase) |
| SCE1572_6185 | FIG01088641: hypothetical protein | bi | sce_5195 | 87.04 | FIG01088641: hypothetical protein |
| SCE1572_6186 | hypothetical protein | bi | sce_5196 | 65 | hypothetical protein |
| SCE1572_6187 | FIG01086463: hypothetical protein | bi | sce_5197 | 84.97 | FIG01086463: hypothetical protein |
| SCE1572_6188 | putative esterase | bi | sce_5199 | 88.61 | putative esterase |
| SCE1572_6189 | hypothetical protein | uni | sce_2163 | 46.55 | ABC transporter substrate-binding protein |
| SCE1572_6190 | Ubiquinone biosynthesis monooxygenase UbiB | uni | sce_8312 | 37.36 | hypothetical protein |
| SCE1572_6191 | YbaK family protein | bi | sce_5200 | 94.44 | YbaK family protein |
| SCE1572_6192 | FIG01084969: hypothetical protein | bi | sce_5206 | 79.06 | FIG01084969: hypothetical protein |
| SCE1572_6193 | hypothetical protein | - | - | 0 | 0 |
| SCE1572_6194 | serine/threonine protein kinase | uni | sce_7827 | 51.68 | Cytochrome c551 peroxidase (EC 1.11.1.5) |
| SCE1572_6195 | hypothetical protein | bi | sce_5207 | 83.93 | hypothetical protein |
| SCE1572_6196 | Tropomyosin-1, isoforms 33/34 (Tropomyosin II) | bi | sce_5208 | 75.19 | Tropomyosin-1, isoforms 33/34 (Tropomyosin II) |
| SCE1572_6197 | FIG01089605: hypothetical protein | bi | sce_5209 | 67.54 | FIG01089605: hypothetical protein |
| SCE1572_6198 | 3-oxoacyl-[acyl-carrier protein] reductase (EC 1.1.1.100) | bi | sce_5211 | 83.21 | 3-oxoacyl-[acyl-carrier protein] reductase (EC 1.1.1.100) |
| SCE1572_6199 | hypothetical protein | - | - | 0 | 0 |
| SCE1572_6200 | hypothetical protein | bi | sce_5224 | 84.39 | hypothetical protein |
| SCE1572_6201 | hypothetical protein | bi | sce_5225 | 82.06 | hypothetical protein |
| SCE1572_6202 | Adenylate cyclase (EC 4.6.1.1) / Guanylate cyclase (EC 4.6.1.2) | bi | sce_5226 | 90.4 | Adenylate cyclase (EC 4.6.1.1) / Guanylate cyclase (EC 4.6.1.2) |
| SCE1572_6203 | RIBITOL TYPE DEHYDROGENASE PROTEIN | bi | sce_5228 | 94.89 | short-chain dehydrogenase/reductase SDR |
| SCE1572_6204 | Universal stress protein family | bi | sce_135 | 60.38 | Universal stress protein family 4 |
| SCE1572_6205 | Tat (twin-arginine translocation) pathway signal sequence domain protein | bi | sce_2524 | 88.94 | Tat (twin-arginine translocation) pathway signal sequence domain protein |
| SCE1572_6206 | Cellulose-binding domain protein | bi | sce_2525 | 84.33 | Cellulose-binding domain protein |
| SCE1572_6207 | putative transposase | - | - | 0 | 0 |
| SCE1572_6208 | hypothetical protein | - | - | 0 | 0 |
| SCE1572_6209 | FIG01085109: hypothetical protein | uni | sce_8592 | 59.57 | FIG01085109: hypothetical protein |
| SCE1572_6210 | FIG01085109: hypothetical protein | uni | sce_8592 | 62.59 | FIG01085109: hypothetical protein |
| SCE1572_6211 | Splicing factor, proline- and glutamine-rich (Polypyrimidine tract-binding protein-associated-splicing factor) (PTB-associated- | uni | sce_3249 | 42.86 | Splicing factor, proline- and glutamine-rich (Polypyrimidine tract-binding protein-associated-splicing factor) (PTB-associated-splicing |
| SCE1572_6212 | PREDICTED: hypothetical protein, partial | uni | sce_3858 | 29.49 | Adenosylhomocysteinase (EC 3.3.1.1) |
| SCE1572_6213 | hypothetical protein | uni | sce_10331 | 80 | hypothetical protein |
| SCE1572_6214 | hypothetical protein | bi | sce_5241 | 77.42 | FIG01086664: hypothetical protein |
| SCE1572_6215 | FIG01085364: hypothetical protein | bi | sce_5242 | 71.73 | FIG01085364: hypothetical protein |
| SCE1572_6216 | hypothetical protein | uni | sce_7083 | 37.5 | hypothetical protein |
| SCE1572_6217 | Flavodoxin | bi | sce_9321 | 83.05 | Flavodoxin |
| SCE1572_6218 | BlI2291 protein | uni | sce_2641 | 50.29 | BlI2291 protein |
| SCE1572_6219 | hypothetical protein | - | - | 0 | 0 |
| SCE1572_6220 | erythrocyte membrane protein 1 (PEMP1) | uni | sce_6314 | 44.87 | putative lipoprotein |
| SCE1572_6221 | hypothetical protein | uni | sce_2591 | 87.12 | FIG01088827: hypothetical protein |
| SCE1572_6222 | Phosphatidylinositol-glycan-specific phospholipase D precursor (EC 3.1.4.50) (PI-G PLD) (Glycoprotein phospholipase D) (Glumi | uni | sce_867 | 43.43 | Hemolysin-type calcium-binding region |
| SCE1572_6223 | hypothetical protein | uni | sce_171 | 66.29 | integral membrane protein |
| SCE1572_6224 | hypothetical protein | bi | sce_5247 | 79.39 | FIG01086104: hypothetical protein |
| SCE1572_6225 | FIG01088230: hypothetical protein | bi | sce_5248 | 90.79 | FIG01088230: hypothetical protein |
| SCE1572_6226 | secretion protein HlyD | uni | sce_8771 | 50.67 | Fusaric acid resistance protein |
| SCE1572_6227 | outer membrane efflux protein | bi | sce_8772 | 49.02 | Heavy metal RND efflux outer membrane protein, CzcC family |
| SCE1572_6228 | Endo-1,4-beta-xylanase A precursor (EC 3.2.1.8) | uni | sce_1629 | 54.55 | Endo-1,4-beta-xylanase A precursor (EC 3.2.1.8) |
| SCE1572_6229 | hypothetical protein | uni | sce_6965 | 32.55 | FIG01088986: hypothetical protein |

| | | | | |
|--------------|---|-----|-----------|---|
| SCE1572_6230 | hypothetical protein | - | | 0 |
| SCE1572_6231 | hypothetical protein | bi | sce_3674 | 90.57 hypothetical protein |
| SCE1572_6232 | Feruloyl esterase B precursor (EC 3.1.1.73) (Ferulic acid esterase B) (FAEB) (Cinnamoyl esterase) | bi | sce_3675 | 86.18 Feruloyl esterase B precursor (EC 3.1.1.73) (Ferulic acid esterase B) (FAEB) (Cinnamoyl esterase) |
| SCE1572_6233 | RsbR, positive regulator of sigma-B | uni | sce_6175 | 62.58 RsbR, positive regulator of sigma-B |
| SCE1572_6234 | Nitrate reductase (NADH) (EC:1.7.1.1) | uni | sce_8040 | 25.64 molybdopterin-binding oxidoreductase |
| SCE1572_6235 | PASTA domain containing protein | bi | sce_10194 | 49.49 hypothetical protein |
| SCE1572_6236 | Probable lipoprotein signal peptide | bi | sce_2008 | 76.89 Probable lipoprotein signal peptide |
| SCE1572_6237 | Transcriptional regulator, AraC family | uni | sce_1019 | 40.4 L-rhamnose operon transcriptional activator RhaR |
| SCE1572_6238 | FIG01086207: hypothetical protein | bi | sce_5252 | 75.96 FIG01086207: hypothetical protein |
| SCE1572_6239 | hypothetical protein | - | | 0 |
| SCE1572_6240 | hypothetical protein | uni | sce_6334 | 30.15 putative integrin-like protein |
| SCE1572_6241 | Valyl-tRNA synthetase (EC 6.1.1.9) | bi | sce_5253 | 69.35 DifB protein |
| SCE1572_6242 | Mannose-6-phosphate isomerase (EC 5.3.1.8) | bi | sce_5254 | 88.97 Mannose-6-phosphate isomerase (EC 5.3.1.8) |
| SCE1572_6243 | Protein involved in cellulose biosynthesis (CelD)-like protein | uni | sce_2195 | 28.96 Cellulose biosynthesis protein |
| SCE1572_6244 | probable phosphatase | uni | sce_1965 | 29.81 Diadenosine tetraphosphatase |
| SCE1572_6245 | hypothetical protein | - | | 0 |
| SCE1572_6246 | FIG01086488: hypothetical protein | bi | sce_7862 | 82.8 FIG01086488: hypothetical protein |
| SCE1572_6247 | Glycosyl transferase, group 1 | bi | sce_614 | 66.59 Glycosyl transferase, group 1 |
| SCE1572_6248 | hypothetical protein | bi | sce_7861 | 79.26 hypothetical protein |
| SCE1572_6249 | hypothetical protein | - | | 0 |
| SCE1572_6250 | hypothetical protein | - | | 0 |
| SCE1572_6251 | Chemotaxis protein methyltransferase CheR (EC 2.1.1.80) | uni | sce_9491 | 50.25 Chemotaxis protein methyltransferase CheR (EC 2.1.1.80) |
| SCE1572_6252 | carboxylesterase | bi | sce_5264 | 81.33 carboxylesterase |
| SCE1572_6253 | Hypothetical nudix hydrolase YeaB | bi | sce_5265 | 86.26 Hypothetical nudix hydrolase YeaB |
| SCE1572_6254 | TonB family protein / TonB-dependent receptor | bi | sce_5266 | 89.37 TonB family protein / TonB-dependent receptor |
| SCE1572_6255 | Epoxide hydrolase (EC 3.3.2.9) | - | | 0 |
| SCE1572_6256 | Histone acetyltransferase HPA2 and related acetyltransferases | - | | 0 |
| SCE1572_6257 | hypothetical protein | - | | 0 |
| SCE1572_6258 | hypothetical protein | - | | 0 |
| SCE1572_6259 | hypothetical protein | bi | sce_5270 | 60.71 FIG01086383: hypothetical protein |
| SCE1572_6260 | FIG01087506: hypothetical protein | bi | sce_5271 | 80.24 hypothetical protein |
| SCE1572_6261 | FIG01085123: hypothetical protein | bi | sce_5272 | 80.2 FIG01085123: hypothetical protein |
| SCE1572_6262 | MoxR-like ATPases | bi | sce_5273 | 95.17 MoxR-like ATPases |
| SCE1572_6263 | FIG01085640: hypothetical protein | bi | sce_5274 | 91.91 FIG01085640: hypothetical protein |
| SCE1572_6264 | hypothetical protein | bi | sce_5275 | 74.75 hypothetical protein |
| SCE1572_6265 | FIG01087582: hypothetical protein | bi | sce_5282 | 64.86 FIG01087582: hypothetical protein |
| SCE1572_6266 | hypothetical protein | bi | sce_5284 | 54.72 hypothetical protein |
| SCE1572_6267 | hypothetical protein | - | | 0 |
| SCE1572_6268 | hypothetical protein | - | | 0 |
| SCE1572_6269 | FIG01087638: hypothetical protein | bi | sce_5285 | 82.82 FIG01087638: hypothetical protein |
| SCE1572_6270 | FIG01088450: hypothetical protein | bi | sce_5287 | 87.61 FIG01088450: hypothetical protein |
| SCE1572_6271 | transcriptional regulator, MerR family | uni | sce_9675 | 36.92 MerR family transcriptional regulatory protein |
| SCE1572_6272 | Oxidoreductase | bi | sce_5289 | 90.83 Oxidoreductase |
| SCE1572_6273 | Xanthine and CO dehydrogenases maturation factor, XdhC/CoxF family | bi | sce_3740 | 90.43 Xanthine and CO dehydrogenases maturation factor, XdhC/CoxF family |
| SCE1572_6274 | Isoquinoline 1-oxidoreductase alpha subunit (EC 1.3.99.16) | bi | sce_3739 | 91.5 Isoquinoline 1-oxidoreductase alpha subunit (EC 1.3.99.16) |
| SCE1572_6275 | Isoquinoline 1-oxidoreductase beta subunit (EC 1.3.99.16) | bi | sce_3738 | 89.45 Isoquinoline 1-oxidoreductase beta subunit (EC 1.3.99.16) |
| SCE1572_6276 | FIG01086323: hypothetical protein | bi | sce_3737 | 90.36 FIG01086323: hypothetical protein |
| SCE1572_6277 | Short-chain dehydrogenase/reductase SDR | uni | sce_1873 | 41.8 Short-chain dehydrogenase/reductase SDR |
| SCE1572_6278 | Transcriptional regulator, AraC family | bi | sce_3669 | 43.37 Transcriptional regulator, AraC family |
| SCE1572_6279 | hypothetical protein | bi | sce_5294 | 77.47 Probable calcium-binding signal peptide protein |
| SCE1572_6280 | FIG01085124: hypothetical protein | bi | sce_5297 | 80.79 FIG01085124: hypothetical protein |
| SCE1572_6281 | protein of unknown function DUF11 | uni | sce_1108 | 83.53 hypothetical protein |
| SCE1572_6282 | hypothetical protein | - | | 0 |
| SCE1572_6283 | FIG01085332: hypothetical protein | bi | sce_5305 | 89.56 FIG01085332: hypothetical protein |
| SCE1572_6284 | Endonuclease III (EC 4.2.99.18) | bi | sce_5310 | 88.1 Endonuclease III (EC 4.2.99.18) |
| SCE1572_6285 | Uracil-DNA glycosylase, family 1 | bi | sce_5311 | 85.33 Uracil-DNA glycosylase, family 1 |
| SCE1572_6286 | hypothetical protein | bi | sce_5312 | 91.3 hypothetical protein |
| SCE1572_6287 | Glutathione S-transferase, phi (EC 2.5.1.18) | bi | sce_5313 | 81.95 Glutathione S-transferase, phi (EC 2.5.1.18) |
| SCE1572_6288 | hypothetical protein | bi | sce_142 | 87.5 FIG01087231: hypothetical protein |
| SCE1572_6289 | FIG01088078: hypothetical protein | bi | sce_5318 | 78.04 FIG01088078: hypothetical protein |
| SCE1572_6290 | hypothetical protein | - | | 0 |
| SCE1572_6291 | POSSIBLE SERINE/THREONINE PHOSPHATASE PPP (EC 3.1.3.16) | bi | sce_5319 | 87 Protein serine/threonine phosphatase PpC, regulation of stationary phase |
| SCE1572_6292 | oxidoreductase, aldo/keto reductase family | bi | sce_5321 | 89.32 InterPro IPR001395 COGs COG0656 |
| SCE1572_6293 | LpqC | bi | sce_5150 | 80.8 LpqC |
| SCE1572_6294 | Transcriptional regulator, TetR family | uni | sce_5339 | 36.36 putative transcriptional regulator, TetR family |
| SCE1572_6295 | short-chain dehydrogenase/reductase SDR | uni | sce_5575 | 30 Oxidoreductase, short chain dehydrogenase/reductase family |
| SCE1572_6296 | Kazal-type serine protease inhibitor domain | bi | sce_5322 | 57.54 Kazal-type serine protease inhibitor domain |
| SCE1572_6297 | Kazal-type serine protease inhibitor domain | uni | sce_5322 | 39.26 Kazal-type serine protease inhibitor domain |
| SCE1572_6298 | UL36 very large tegument protein | bi | sce_5323 | 84.99 Chromosome partition protein smc |
| SCE1572_6299 | hypothetical protein | uni | sce_7356 | 33.94 hypothetical protein |
| SCE1572_6300 | hypothetical protein | bi | sce_5324 | 93.56 hypothetical protein |
| SCE1572_6301 | Mobile element protein | uni | sce_6200 | 35.89 reverse transcriptase/maturase family protein |
| SCE1572_6302 | oligopeptide transporter, OPT family | bi | sce_5329 | 90.9 oligopeptide transporter, OPT family |
| SCE1572_6303 | hypothetical protein | uni | sce_1486 | 45.33 VgrG protein |
| SCE1572_6304 | hypothetical protein | bi | sce_5331 | 94.87 hypothetical protein |
| SCE1572_6305 | Nicotinamide/isochorismatase family protein | bi | sce_5332 | 82.04 Nicotinamide/isochorismatase family protein |
| SCE1572_6306 | Transcriptional Regulator, LysR family | bi | sce_5333 | 85.43 Transcriptional regulator, LysR family |
| SCE1572_6307 | RsbR, positive regulator of sigma-B | bi | sce_5334 | 73.92 RsbR, positive regulator of sigma-B |
| SCE1572_6308 | Taurine transport ATP-binding protein TauB | bi | sce_5335 | 92.68 Taurine transport ATP-binding protein TauB |
| SCE1572_6309 | Alkanesulfonates transport system permease protein | bi | sce_5336 | 92.06 Alkanesulfonates transport system permease protein |
| SCE1572_6310 | aldo/keto reductase | bi | sce_5337 | 93.2 aldo/keto reductase |
| SCE1572_6311 | Alpha/beta hydrolase | bi | sce_5338 | 81.85 carboxylesterase |
| SCE1572_6312 | Phosphoribosylaminoimidazole carboxylase ATPase subunit (EC 4.1.1.21) | uni | sce_3858 | 34.07 Adenosylhomocysteinase (EC 3.3.1.1) |
| SCE1572_6313 | heme biosynthesis protein | bi | sce_2034 | 48.63 FIG01085108: hypothetical protein |
| SCE1572_6314 | PE-PGRS family protein | uni | sce_7494 | 50 FIG01087054: hypothetical protein |
| SCE1572_6315 | RNA polymerase sigma-70 factor, ECF subfamily | uni | sce_7181 | 40.14 RNA polymerase sigma-70 factor, ECF subfamily |
| SCE1572_6316 | hypothetical protein | - | | 0 |
| SCE1572_6317 | hypothetical protein | - | | 0 |
| SCE1572_6318 | FIG01086027: hypothetical protein | bi | sce_5340 | 80.68 FIG01086027: hypothetical protein |
| SCE1572_6319 | Matrix metalloproteinase-25 precursor (EC 3.4.24.-) (MMP-25) (Membrane-type matrix metalloproteinase 6) (MT-MMP 6) (MMP-25) | bi | sce_5341 | 72.82 PE-PGRS FAMILY PROTEIN |
| SCE1572_6320 | hypothetical protein | bi | sce_5342 | 91.09 hypothetical protein |
| SCE1572_6321 | hypothetical protein | uni | sce_5342 | 90.41 hypothetical protein |
| SCE1572_6322 | FKBP-type peptidyl-prolyl cis-trans isomerase (FKBP) (EC 5.2.1.8) | bi | sce_5343 | 81 FKBP-type peptidyl-prolyl cis-trans isomerase (PPIase) |
| SCE1572_6323 | 2-aminoethylphosphonate-pyruvate aminotransferase (EC 2.6.1.37) | bi | sce_5344 | 92.99 2-aminoethylphosphonate-pyruvate aminotransferase (EC 2.6.1.37) |
| SCE1572_6324 | Ubiquinone biosynthesis monooxygenase UbiB | bi | sce_5345 | 97.19 Ubiquinone biosynthesis monooxygenase UbiB |
| SCE1572_6325 | hypothetical protein | bi | sce_5346 | 90.58 FIG01086692: hypothetical protein |
| SCE1572_6326 | FIG01085169: hypothetical protein | bi | sce_5348 | 97 FIG01085169: hypothetical protein |
| SCE1572_6327 | hypothetical protein | bi | sce_5349 | 89.13 hypothetical protein |
| SCE1572_6328 | putative mannose-1-phosphate guanylyltransferase | bi | sce_5350 | 94.31 putative mannose-1-phosphate guanylyltransferase |
| SCE1572_6329 | UDP-4-amino-4-deoxy-L-arabinose-oxoglutarate aminotransferase (EC 2.6.1.-) | bi | sce_5351 | 94.23 UDP-4-amino-4-deoxy-L-arabinose-oxoglutarate aminotransferase (EC 2.6.1.-) |
| SCE1572_6330 | UDP-glucose 4-epimerase (EC 5.1.3.2) | bi | sce_5352 | 97.59 UDP-glucose 4-epimerase (EC 5.1.3.2) |
| SCE1572_6331 | FIG01088445: hypothetical protein | bi | sce_5353 | 85.31 FIG01088445: hypothetical protein |
| SCE1572_6332 | putative secreted protein | bi | sce_5354 | 87.06 putative secreted protein |
| SCE1572_6333 | Cysteine synthase (EC 2.5.1.47) | bi | sce_5355 | 92.45 Cysteine synthase (EC 2.5.1.47) |
| SCE1572_6334 | NADH-ubiquinone oxidoreductase chain L (EC 1.6.5.3) | bi | sce_5357 | 88.45 NADH-ubiquinone oxidoreductase chain L (EC 1.6.5.3) |
| SCE1572_6335 | Hypothetical transmembrane protein coupled to NADH-ubiquinone oxidoreductase chain 5 homolog | bi | sce_5358 | 87.14 Hypothetical transmembrane protein coupled to NADH-ubiquinone oxidoreductase chain 5 homolog |
| SCE1572_6336 | anion transporters (Cl ⁻ , SO ₄ ²⁻ , PO ₄ ³⁻ , etc.) | bi | sce_5359 | 87.43 anion transporters (Cl ⁻ , SO ₄ ²⁻ , PO ₄ ³⁻ , etc.) |
| SCE1572_6337 | RNA polymerase, sigma-24 subunit, ECF subfamily | bi | sce_5360 | 89.74 putative RNA polymerase sigma factor |
| SCE1572_6338 | hypothetical protein | bi | sce_5361 | 83.17 hypothetical protein |
| SCE1572_6339 | Nucleoside triphosphate pyrophosphohydrolase MazG | bi | sce_5373 | 93.5 Nucleoside triphosphate pyrophosphohydrolase MazG |
| SCE1572_6340 | Latent membrane protein 1 | bi | sce_5374 | 71.89 hypothetical protein |
| SCE1572_6341 | FIG01087827: hypothetical protein | bi | sce_5375 | 81.54 FIG01087827: hypothetical protein |
| SCE1572_6342 | FAD-dependent monooxygenase PhzS | bi | sce_5377 | 82.09 Salicylate hydroxylase (EC 1.14.13.1) |
| SCE1572_6343 | FIG01086098: hypothetical protein | bi | sce_5378 | 74.91 hypothetical protein |
| SCE1572_6344 | Gli0645 protein | bi | sce_5379 | 77.87 Gli0645 protein |
| SCE1572_6345 | hypothetical protein | bi | sce_5380 | 73.11 FIG01087100: hypothetical protein |
| SCE1572_6346 | unknown | bi | sce_5382 | 94.46 unknown |
| SCE1572_6347 | FHA domain protein | bi | sce_5383 | 82.02 FHA domain protein |
| SCE1572_6348 | hypothetical protein | - | | 0 |
| SCE1572_6349 | Beta-xylosidase (EC 3.2.1.37) | - | | 0 |
| SCE1572_6350 | NAD-dependent epimerase/dehydratase | uni | sce_1993 | 28.86 NAD-dependent epimerase/dehydratase |
| SCE1572_6351 | Pectate lyase precursor (EC 4.2.2.2) | bi | sce_5387 | 80.7 Pectate lyase precursor (EC 4.2.2.2) |
| SCE1572_6352 | hypothetical protein | bi | sce_5388 | 66 hypothetical protein |
| SCE1572_6353 | Oxidoreductase, short chain dehydrogenase/reductase family | bi | sce_5389 | 91.91 Oxidoreductase, short chain dehydrogenase/reductase family |
| SCE1572_6354 | Alkanesulfonates-binding protein | bi | sce_5506 | 72.43 Alkanesulfonates-binding protein |
| SCE1572_6355 | Alkanesulfonates transport system permease protein | bi | sce_5507 | 87.76 Alkanesulfonates transport system permease protein |
| SCE1572_6356 | Glycerol dehydrogenase (EC 1.1.1.6) | bi | sce_6038 | 98.28 Glycerol dehydrogenase (EC 1.1.1.6) |
| SCE1572_6357 | RsbR, positive regulator of sigma-B | bi | sce_5390 | 86.15 RsbR, positive regulator of sigma-B |
| SCE1572_6358 | putative endoglucanase (EC:3.2.1.-) | uni | sce_5442 | 25.34 Endoglucanase II precursor (EC 3.2.1.4) (EgII) (Endo-1,4-beta-glucanase H) (Cellulase H) |
| SCE1572_6359 | FIG01087447: hypothetical protein | bi | sce_5391 | 84.69 FIG01087447: hypothetical protein |
| SCE1572_6360 | FIG01089037: hypothetical protein | bi | sce_5392 | 77.16 FIG01089037: hypothetical protein |
| SCE1572_6361 | hypothetical protein | uni | sce_4720 | 35.9 hypothetical protein |
| SCE1572_6362 | hypothetical protein | uni | sce_4721 | 34.62 hypothetical protein |
| SCE1572_6363 | Macrolide export ATP-binding/permease protein MacB (EC 3.6.3.-) | bi | sce_5393 | 94.79 Macrolide export ATP-binding/permease protein MacB (EC 3.6.3.-) |
| SCE1572_6364 | Cell division transporter, ATP-binding protein FtsE (TC 3.A.5.1.1) | bi | sce_5394 | 90.95 ABC transporter, ATP binding protein |
| SCE1572_6365 | Macrolide-specific efflux protein MacA | bi | sce_5395 | 87.98 Membrane fusion protein, HlyD family |
| SCE1572_6366 | Outer membrane efflux protein family | bi | sce_5396 | 75.24 Outer membrane efflux protein family |
| SCE1572_6367 | Copper-sensing two-component system response regulator CpxR | bi | sce_5397 | 92.31 Copper-sensing two-component system response regulator CpxR |
| SCE1572_6368 | Putative two-component system sensor kinase | bi | sce_5398 | 90.24 Putative two-component system sensor kinase |
| SCE1572_6369 | conserved hypothetical protein | uni | sce_6998 | 36.59 Predicted ATPase |
| SCE1572_6370 | hypothetical protein | bi | sce_5400 | 82.24 hypothetical protein |
| SCE1572_6371 | putative cytochrome P450 hydroxylase | uni | sce_7075 | 43.56 putative cytochrome P450 hydroxylase |
| SCE1572_6372 | hypothetical protein | - | | 0 |
| SCE1572_6373 | hypothetical protein | - | | 0 |
| SCE1572_6374 | FIG01127640: hypothetical protein | - | | 0 |
| SCE1572_6375 | tannase precursor | - | | 0 |
| SCE1572_6376 | ethanolamine ammonia-lyase (EC:4.3.1.7) | - | | 0 |
| SCE1572_6377 | hypothetical protein | bi | sce_5401 | 77.17 hypothetical protein |
| SCE1572_6378 | FIG01088313: hypothetical protein | bi | sce_7567 | 77.04 FIG01088313: hypothetical protein |
| SCE1572_6379 | FIG01125955: hypothetical protein | uni | sce_453 | 31.16 hypothetical protein |
| SCE1572_6380 | hypothetical protein | - | | 0 |
| SCE1572_6381 | protein of unknown function DUF1255 | bi | sce_5402 | 89.25 Uncharacterized protein conserved in bacteria |
| SCE1572_6382 | Adenylate cyclase (EC 4.6.1.1) / Guanylate cyclase (EC 4.6.1.2) | bi | sce_5403 | 90.05 Adenylate cyclase (EC 4.6.1.1) / Guanylate cyclase (EC 4.6.1.2) |
| SCE1572_6383 | hypothetical protein | bi | sce_5404 | 50.96 hypothetical protein |
| SCE1572_6384 | serine/threonine protein kinase | bi | sce_5405 | 85.95 serine/threonine protein kinase |
| SCE1572_6385 | hypothetical protein | - | | 0 |
| SCE1572_6386 | Uncharacterized protein conserved in bacteria | bi | sce_5406 | 94.52 Uncharacterized protein conserved in bacteria |
| SCE1572_6387 | Ribosomal RNA large subunit methyltransferase N (EC 2.1.1.-) | bi | sce_5407 | 97.69 Ribosomal RNA large subunit methyltransferase N (EC 2.1.1.-) |
| SCE1572_6388 | Methylcrotonyl-CoA carboxylase biotin-containing subunit (EC 6.4.1.4) | bi | sce_5408 | 92.27 Methylcrotonyl-CoA carboxylase biotin-containing subunit (EC 6.4.1.4) |
| SCE1572_6389 | Phosphomannomutase (EC 5.4.2.8) | bi | sce_5409 | 87.42 putative phosphoglucosyltransferase/phosphomannomutase |
| SCE1572_6390 | FIG01087770: hypothetical protein | bi | sce_5410 | 92.64 FIG01087770: hypothetical protein |
| SCE1572_6391 | hypothetical protein | - | | 0 |
| SCE1572_6392 | hypothetical protein | bi | sce_5412 | 92.04 hypothetical protein |
| SCE1572_6393 | Pyroloquinoline quinone (Coenzyme PQQ) biosynthesis protein C | bi | sce_5413 | 89.43 Pyroloquinoline quinone (Coenzyme PQQ) biosynthesis protein C |

| | | | | |
|--------------|--|-----|-----------|---|
| SCE1572_6394 | Two-component response regulator | bi | sce_5414 | 90.6 Two-component response regulator |
| SCE1572_6395 | hypothetical protein | - | - | 0 |
| SCE1572_6396 | Shikimate kinase I (EC 2.7.1.71) / 3-dehydroquinate synthase (EC 4.2.3.4) | bi | sce_5415 | 92.34 Shikimate kinase I (EC 2.7.1.71) / 3-dehydroquinate synthase (EC 4.2.3.4) |
| SCE1572_6397 | Chorismate synthase (EC 4.2.3.5) | bi | sce_5416 | 97.21 Chorismate synthase (EC 4.2.3.5) |
| SCE1572_6398 | Glutamate racemase (EC 5.1.1.3) | bi | sce_5417 | 82.42 Glutamate racemase (EC 5.1.1.3) |
| SCE1572_6399 | Homoserine dehydrogenase (EC 1.1.1.3) | bi | sce_5418 | 92.32 Homoserine dehydrogenase (EC 1.1.1.3) |
| SCE1572_6400 | Uncharacterized protein ImpC | bi | sce_5419 | 86.75 Uncharacterized protein ImpC |
| SCE1572_6401 | hypothetical protein | bi | sce_5420 | 75.68 hypothetical protein |
| SCE1572_6402 | Probable secreted protein | bi | sce_5422 | 86.79 Probable secreted protein |
| SCE1572_6403 | GTP cyclohydrolase II (EC 3.5.4.25) | bi | sce_5423 | 94.52 GTP cyclohydrolase II (EC 3.5.4.25) |
| SCE1572_6404 | FIG01089015: hypothetical protein | bi | sce_5424 | 74.85 FIG01089015: hypothetical protein |
| SCE1572_6405 | phosphoesterase, PA-phosphatase related | bi | sce_5425 | 80.92 phosphoesterase PA-phosphatase related |
| SCE1572_6406 | Transcriptional regulator, TetR family | bi | sce_5426 | 88.02 Transcriptional regulator, TetR family |
| SCE1572_6407 | FIG01087697: hypothetical protein | bi | sce_5427 | 89.85 FIG01087697: hypothetical protein |
| SCE1572_6408 | Homoserine kinase (EC 2.7.1.39) | bi | sce_5428 | 85.71 Homoserine kinase (EC 2.7.1.39) |
| SCE1572_6409 | hypothetical protein | bi | sce_5429 | 62.8 hypothetical protein |
| SCE1572_6410 | hypothetical protein | - | - | 0 |
| SCE1572_6411 | Glutathione S-transferase (EC 2.5.1.18) | uni | sce_7550 | 40.22 Glutathione S-transferase (EC 2.5.1.18) |
| SCE1572_6412 | Biotin synthesis protein bioC | bi | sce_5430 | 81.53 Biotin synthesis protein bioC |
| SCE1572_6413 | COGs COG3558 | bi | sce_5431 | 91.25 COGs COG3558 |
| SCE1572_6414 | hypothetical protein | - | - | 0 |
| SCE1572_6415 | conserved hypothetical protein | bi | sce_5433 | 82.35 conserved hypothetical protein |
| SCE1572_6416 | Transcriptional regulator, TetR family | bi | sce_5434 | 87.96 Transcriptional regulator, TetR family |
| SCE1572_6417 | hypothetical protein | - | - | 0 |
| SCE1572_6418 | cellulosome enzyme, dockerin type I | bi | sce_5435 | 78.14 cellulosome enzyme, dockerin type I |
| SCE1572_6419 | hypothetical protein | uni | sce_8512 | 59.18 hypothetical protein |
| SCE1572_6420 | FIG01086549: hypothetical protein | uni | sce_5307 | 73.86 FIG01086549: hypothetical protein |
| SCE1572_6421 | NAD-dependent glyceraldehyde-3-phosphate dehydrogenase (EC 1.2.1.12) | uni | sce_8225 | 67.26 NAD-dependent glyceraldehyde-3-phosphate dehydrogenase (EC 1.2.1.12) |
| SCE1572_6422 | conserved hypothetical protein | bi | sce_7652 | 52.74 hypothetical protein |
| SCE1572_6423 | Endo-1,4-beta-xylanase A precursor (EC 3.2.1.8) | bi | sce_3067 | 70.19 Xylanase |
| SCE1572_6424 | hypothetical protein | - | - | 0 |
| SCE1572_6425 | hypothetical protein | uni | sce_1172 | 64.98 hypothetical protein |
| SCE1572_6426 | hypothetical protein | bi | sce_9434 | 56.21 FIG01086661: hypothetical protein |
| SCE1572_6427 | annexin VII | bi | sce_4820 | 51.47 hypothetical protein |
| SCE1572_6428 | D-alanyl-D-alanine carboxypeptidase (EC 3.4.16.4) | bi | sce_7206 | 74.63 D-alanyl-D-alanine carboxypeptidase (EC 3.4.16.4) |
| SCE1572_6429 | FIG01089505: hypothetical protein | bi | sce_2031 | 84.14 FIG01089505: hypothetical protein |
| SCE1572_6430 | P-methylase | bi | sce_6181 | 96.57 Radical SAM domain protein |
| SCE1572_6431 | Endo-1,4-beta-xylanase A precursor (EC 3.2.1.8) | bi | sce_7564 | 44.79 Putative galactosidase |
| SCE1572_6432 | Methyltransferase | bi | sce_2123 | 81.85 Methyltransferase |
| SCE1572_6433 | Transcriptional regulator, MerR family | bi | sce_2124 | 83.33 Transcriptional regulator, MerR family |
| SCE1572_6434 | hypothetical protein | - | - | 0 |
| SCE1572_6435 | hypothetical protein | - | - | 0 |
| SCE1572_6436 | hypothetical protein | bi | sce_3639 | 89.54 hypothetical protein |
| SCE1572_6437 | hypothetical protein | bi | sce_3640 | 82.5 hypothetical protein |
| SCE1572_6438 | hypothetical protein | - | - | 0 |
| SCE1572_6439 | Isochorismatase (EC 3.3.2.1) | uni | sce_2989 | 36.07 Nicotinamidase (EC 3.5.1.19) |
| SCE1572_6440 | hypothetical protein | - | - | 0 |
| SCE1572_6441 | hypothetical protein | - | - | 0 |
| SCE1572_6442 | Fimh-like protein | uni | sce_4372 | 66.86 Fimh-like protein |
| SCE1572_6443 | hypothetical protein | uni | sce_160 | 58.06 hypothetical protein |
| SCE1572_6444 | hypothetical protein | - | - | 0 |
| SCE1572_6445 | hypothetical protein | bi | sce_5449 | 82.31 FIG01088294: hypothetical protein |
| SCE1572_6446 | DNA repair protein RadC | uni | sce_8398 | 55.34 DNA repair protein RadC |
| SCE1572_6447 | Transcriptional regulator Cro/C1 family | uni | sce_514 | 51.85 hypothetical protein |
| SCE1572_6448 | Type I restriction-modification system, DNA-methyltransferase subunit M (EC 2.1.1.72) | uni | sce_6179 | 26.84 Type I restriction-modification system, DNA-methyltransferase subunit M (EC 2.1.1.72) |
| SCE1572_6449 | Type I restriction-modification system, specificity subunit S (EC 3.1.21.3) | uni | - | 0 |
| SCE1572_6450 | Type I restriction-modification system, restriction subunit R (EC 3.1.21.3) | uni | - | 0 |
| SCE1572_6451 | FIG01085109: hypothetical protein | bi | sce_8592 | 83.74 FIG01085109: hypothetical protein |
| SCE1572_6452 | FIG01085109: hypothetical protein | uni | sce_3939 | 84.5 FIG01085109: hypothetical protein |
| SCE1572_6453 | hypothetical protein | - | - | 0 |
| SCE1572_6454 | Mobile element protein | uni | sce_1676 | 89.64 Mobile element protein |
| SCE1572_6455 | hypothetical protein | - | - | 0 |
| SCE1572_6456 | hypothetical protein | - | - | 0 |
| SCE1572_6457 | Exonuclease SbcC | bi | sce_5452 | 85.47 Exonuclease SbcC |
| SCE1572_6458 | hypothetical protein | uni | sce_9562 | 56.03 Collagen triple helix repeat |
| SCE1572_6459 | hypothetical protein | uni | sce_4539 | 35.77 FIG01086337: hypothetical protein |
| SCE1572_6460 | hypothetical protein | uni | sce_5572 | 59.15 Flagellar hook-length control protein FlhK |
| SCE1572_6461 | Arabinan endo-1,5-alpha-L-arabinosidase (EC 3.2.1.99) | uni | sce_1647 | 45.25 Arabinan endo-1,5-alpha-L-arabinosidase (EC 3.2.1.99) |
| SCE1572_6462 | serine/threonine protein kinase | uni | sce_3282 | 47.27 serine/threonine protein kinase |
| SCE1572_6463 | hypothetical protein | - | - | 0 |
| SCE1572_6464 | Extensin-like protein precursor | bi | sce_5437 | 71.29 Extensin-like protein precursor |
| SCE1572_6465 | FIG01086011: hypothetical protein | bi | sce_5438 | 84.18 FIG01086011: hypothetical protein |
| SCE1572_6466 | RNA polymerase sigma factor RpoE | bi | sce_5439 | 91.52 RNA polymerase sigma factor RpoE |
| SCE1572_6467 | FIG01085133: hypothetical protein | bi | sce_5440 | 81.87 FIG01085133: hypothetical protein |
| SCE1572_6468 | Cellulose synthase catalytic subunit | bi | sce_5441 | 89.5 Cellulose synthase catalytic subunit |
| SCE1572_6469 | Endoglucanase H precursor (EC 3.2.1.4) (EgH) (Endo-1,4-beta-glucanase H) (Cellulase H) | bi | sce_5442 | 88.4 Endoglucanase H precursor (EC 3.2.1.4) (EgH) (Endo-1,4-beta-glucanase H) (Cellulase H) |
| SCE1572_6470 | Glucose-1-phosphate cytidylyltransferase (EC 2.7.7.33) | bi | sce_5443 | 94.49 Glucose-1-phosphate cytidylyltransferase (EC 2.7.7.33) |
| SCE1572_6471 | Similar to CDP-glucose 4,6-dehydratase (EC 4.2.1.45) | bi | sce_5444 | 91.27 Similar to CDP-glucose 4,6-dehydratase (EC 4.2.1.45) |
| SCE1572_6472 | UDP-glucose 4-epimerase (EC 5.1.3.2) | bi | sce_5445 | 88.06 UDP-glucose 4-epimerase (EC 5.1.3.2) |
| SCE1572_6473 | RsbR, positive regulator of sigma-B | uni | sce_8231 | 50.66 RsbR, positive regulator of sigma-B |
| SCE1572_6474 | hypothetical protein | - | - | 0 |
| SCE1572_6475 | cytochrome P450 | uni | sce_2437 | 34.29 cytochrome P450 |
| SCE1572_6476 | hypothetical protein | - | - | 0 |
| SCE1572_6477 | hypothetical protein | - | - | 0 |
| SCE1572_6478 | FIG01088963: hypothetical protein | bi | sce_2488 | 80 FIG01088963: hypothetical protein |
| SCE1572_6479 | hydrophobic amino acid ABC transporter (HAAT) family, amino acid-binding protein | uni | - | 0 |
| SCE1572_6480 | TonB-dependent receptor; Outer membrane receptor for ferrienterochelin and colicins | uni | sce_10228 | 30.57 TonB-dependent receptor; Outer membrane receptor for ferrienterochelin and colicins |
| SCE1572_6481 | hypothetical protein | uni | sce_4904 | 29.52 FOG: WD40-like repeat |
| SCE1572_6482 | Probable ATP-binding protein NMA0346 | bi | sce_5451 | 86.67 Probable ATP-binding protein NMA0346 |
| SCE1572_6483 | hypothetical protein | - | - | 0 |
| SCE1572_6484 | Two-component sensor histidine kinase | bi | sce_5454 | 86.69 Two-component sensor histidine kinase |
| SCE1572_6485 | two-component response regulator | bi | sce_5455 | 94.44 two-component transcriptional regulator (OmpR family), BaeR/ChvL/OmpR-like protein |
| SCE1572_6486 | hypothetical protein | bi | sce_5456 | 89.36 hypothetical protein |
| SCE1572_6487 | hypothetical protein | bi | sce_5457 | 78.4 hypothetical protein |
| SCE1572_6488 | FIG01085949: hypothetical protein | bi | sce_5458 | 76.38 FIG01085949: hypothetical protein |
| SCE1572_6489 | FIG01086453: hypothetical protein | uni | sce_1071 | 66.3 FIG01086453: hypothetical protein |
| SCE1572_6490 | FIG01085939: hypothetical protein | bi | sce_2076 | 94.97 FIG01085939: hypothetical protein |
| SCE1572_6491 | hypothetical protein | - | - | 0 |
| SCE1572_6492 | transcriptional regulator, AraC family | bi | sce_2078 | 90.07 transcriptional regulator, AraC family |
| SCE1572_6493 | Glyoxalase: bleomycin resistance protein/dioxygenase | bi | sce_2079 | 82.25 hypothetical protein, bleomycin resistance protein family |
| SCE1572_6494 | hypothetical protein | - | - | 0 |
| SCE1572_6495 | hypothetical protein | - | - | 0 |
| SCE1572_6496 | bacterial Ig-like domain protein | uni | sce_7612 | 44.44 FIG01086551: hypothetical protein |
| SCE1572_6497 | Twin-arginine translocation protein TatB | uni | sce_3392 | 40.44 integral membrane protein |
| SCE1572_6498 | 2-isopropylmalate synthase (EC 2.3.3.13) | bi | sce_5461 | 87.57 2-isopropylmalate synthase (EC 2.3.3.13) |
| SCE1572_6499 | hypothetical protein | uni | sce_4382 | 50 PE-PGRS FAMILY PROTEIN |
| SCE1572_6500 | hypothetical protein | uni | sce_10425 | 49.54 AAA ATPase |
| SCE1572_6501 | hypothetical protein | uni | sce_10425 | 57.78 AAA ATPase |
| SCE1572_6502 | Chemotaxis protein methyltransferase CheR (EC 2.1.1.80) | bi | sce_3006 | 54.5 Chemotaxis protein methyltransferase CheR (EC 2.1.1.80) |
| SCE1572_6503 | hypothetical protein | - | - | 0 |
| SCE1572_6504 | Short-chain dehydrogenase/reductase SDR | uni | sce_1873 | 39.69 Short-chain dehydrogenase/reductase SDR |
| SCE1572_6505 | Hypothetical transcriptional regulator YqhC | uni | sce_1564 | 37.5 Transcriptional regulator, AraC family |
| SCE1572_6506 | hypothetical protein | - | - | 0 |
| SCE1572_6507 | succinoglycan biosynthesis | uni | sce_6084 | 26.37 Protein-L-isoaspartate O-methyltransferase (EC 2.1.1.77) |
| SCE1572_6508 | hypothetical protein | - | - | 0 |
| SCE1572_6509 | hypothetical protein | bi | sce_3727 | 78.57 hypothetical protein |
| SCE1572_6510 | hypothetical protein | - | - | 0 |
| SCE1572_6511 | acetyltransferase, GNAT family | bi | sce_9988 | 84.23 acetyltransferase, GNAT family |
| SCE1572_6512 | cytochrome P450 | bi | sce_5465 | 90.54 cytochrome P450 |
| SCE1572_6513 | hypothetical protein | - | - | 0 |
| SCE1572_6514 | Enoyl-[acyl-carrier-protein] reductase [NADPH] (EC 1.3.1.10) | bi | sce_5467 | 79.2 Enoyl-[acyl-carrier-protein] reductase [NADPH] (EC 1.3.1.10) |
| SCE1572_6515 | 4'-phosphopantetheinyl transferase family protein | bi | sce_5468 | 90.16 4'-phosphopantetheinyl transferase family protein |
| SCE1572_6516 | FIG01088651: hypothetical protein | bi | sce_5469 | 75.16 FIG01088651: hypothetical protein |
| SCE1572_6517 | COG1846: Transcriptional regulators | bi | sce_5471 | 77.17 transcriptional regulator, MarR family |
| SCE1572_6518 | Superoxide dismutase [Fe] (EC 1.15.1.1) | uni | sce_4677 | 52.53 Superoxide dismutase [Fe] (EC 1.15.1.1) |
| SCE1572_6519 | sigma-B regulator RsbR | uni | sce_7786 | 42.6 FIG0050210: hypothetical protein |
| SCE1572_6520 | Mir5400 protein | bi | sce_5493 | 81.17 Mir5400 protein |
| SCE1572_6521 | FIG01087331: hypothetical protein | bi | sce_5494 | 86.15 FIG01087331: hypothetical protein |
| SCE1572_6522 | hypothetical protein | - | - | 0 |
| SCE1572_6523 | Heat shock protein 60 family chaperone GroEL | uni | sce_1495 | 77.05 Collagen triple helix repeat |
| SCE1572_6524 | Endo-1,4-beta-xylanase A precursor (EC 3.2.1.8) | bi | sce_5495 | 73.52 Endo-1,4-beta-xylanase A precursor (EC 3.2.1.8) |
| SCE1572_6525 | DGPFATKE family protein | bi | sce_1706 | 81.76 PtnB protein |
| SCE1572_6526 | oxidoreductase, short chain dehydrogenase/reductase family superfamily | uni | sce_3864 | 38.75 short-chain dehydrogenase/reductase SDR |
| SCE1572_6527 | 3-oxoacyl-[acyl-carrier protein] reductase (EC 1.1.1.100) | uni | - | 0 |
| SCE1572_6528 | Transcriptional regulator, AraC family | - | - | 0 |
| SCE1572_6529 | AttM/AttB family protein | uni | sce_1358 | 40.19 Transcriptional regulator, AraC family |
| SCE1572_6530 | Butyryl-CoA dehydrogenase (EC 1.3.99.2) | uni | sce_9851 | 25 Beta-lactamase-like precursor |
| SCE1572_6531 | Predicted aminoglycoside phosphotransferase | bi | sce_9960 | 93.73 Butyryl-CoA dehydrogenase (EC 1.3.99.2) |
| SCE1572_6532 | D-alanyl-D-alanine carboxypeptidase (EC 3.4.16.4) | uni | sce_7206 | 90.28 Predicted aminoglycoside phosphotransferase |
| SCE1572_6533 | hypothetical protein | - | - | 0 |
| SCE1572_6534 | hypothetical protein | uni | sce_1171 | 49.16 FIG01089390: hypothetical protein |
| SCE1572_6535 | hypothetical protein | bi | sce_1172 | 66.45 hypothetical protein |
| SCE1572_6536 | 2'-cyclic-nucleotide 2'-phosphodiesterase (EC 3.1.4.16) | uni | sce_7884 | 24.95 5'-nucleotidase (EC 3.1.3.5) |
| SCE1572_6537 | aminoglycoside N3-acetyltransferase | - | - | 0 |
| SCE1572_6538 | Inositol oxygenase (EC 1.13.99.1) | - | - | 0 |
| SCE1572_6539 | hypothetical protein | - | - | 0 |
| SCE1572_6540 | hypothetical protein | - | - | 0 |
| SCE1572_6541 | TetR-family transcriptional regulator | bi | sce_5497 | 81.75 TetR-family transcriptional regulator |
| SCE1572_6542 | Urea carboxylase-related aminomethyltransferase (EC 2.1.2.10) | bi | sce_5498 | 92.91 Urea carboxylase-related aminomethyltransferase (EC 2.1.2.10) |
| SCE1572_6543 | Urea carboxylase-related aminomethyltransferase (EC 2.1.2.10) | bi | sce_5499 | 94.64 Urea carboxylase-related aminomethyltransferase (EC 2.1.2.10) |
| SCE1572_6544 | Urea carboxylase (EC 6.3.4.6) | bi | sce_5500 | 90.95 Urea carboxylase (EC 6.3.4.6) |
| SCE1572_6545 | Urea carboxylase-related amino acid permease | bi | sce_5501 | 88.48 Urea carboxylase-related amino acid permease |
| SCE1572_6546 | Chemotaxis protein methyltransferase CheR (EC 2.1.1.80) | uni | sce_7642 | 56.52 Chemotaxis protein methyltransferase CheR (EC 2.1.1.80) |
| SCE1572_6547 | serine/threonine protein kinase | uni | sce_6094 | 37.65 Signal transduction histidine kinase CheA (EC 2.7.3.-) |
| SCE1572_6548 | hypothetical protein | - | - | 0 |
| SCE1572_6549 | InterPro IPR000792:IPR001789 COGs COG2197 | uni | sce_6078 | 40.09 DNA-binding response regulator, LuxR family |
| SCE1572_6550 | FIG01085516: hypothetical protein | uni | sce_1454 | 82.37 FIG01085516: hypothetical protein |
| SCE1572_6551 | Basic proline-rich protein | bi | sce_5511 | 72.97 hypothetical protein |
| SCE1572_6552 | HlyD family secretion protein | bi | sce_5843 | 70.27 hypothetical protein |
| SCE1572_6553 | hypothetical protein | - | - | 0 |
| SCE1572_6554 | hypothetical protein | - | - | 0 |
| SCE1572_6555 | PE-PGRS FAMILY PROTEIN | uni | sce_6870 | 67.37 PE-PGRS FAMILY PROTEIN |
| SCE1572_6556 | hypothetical protein | uni | sce_6813 | 54.68 hypothetical protein |
| SCE1572_6557 | FIG01088083: hypothetical protein | bi | sce_5514 | 81.92 FIG01088083: hypothetical protein |

| | | | | |
|--------------|---|-----|-----------|---|
| SCE1572_6558 | Predicted membrane protein/domain | umi | sce_2561 | 28.02 Predicted membrane protein/domain |
| SCE1572_6559 | hypothetical protein | bi | sce_6328 | 51.21 RTX family exoprotein |
| SCE1572_6560 | hypothetical protein | - | - | 0 |
| SCE1572_6561 | hypothetical protein | - | - | 0 |
| SCE1572_6562 | hypothetical protein | umi | sce_2034 | 47.75 FIG01085108: hypothetical protein |
| SCE1572_6563 | 3-oxoacyl-[acyl-carrier protein] reductase (EC 1.1.1.100) | umi | sce_8328 | 38.74 3-oxoacyl-[acyl-carrier protein] reductase (EC 1.1.1.100) |
| SCE1572_6564 | hypothetical protein | - | - | 0 |
| SCE1572_6565 | transcriptional regulator, AraC-family | umi | sce_9866 | 42.15 Transcriptional regulator, AraC family |
| SCE1572_6566 | Cardiolipin synthetase (EC 2.7.8.-) | umi | sce_7289 | 38.19 Cardiolipin synthetase (EC 2.7.8.-) |
| SCE1572_6567 | putative oxidoreductase, mmyg | umi | sce_6003 | 27.81 NAD binding oxidoreductase |
| SCE1572_6568 | Transcriptional regulator, TetR family | umi | sce_7595 | 32.48 Transcriptional regulator, TetR family |
| SCE1572_6569 | putative RNA polymerase sigma factor | umi | sce_8821 | 37.36 RNA polymerase sigma-70 factor, ECF subfamily |
| SCE1572_6570 | hypothetical protein | bi | sce_6017 | 57.96 Putative secreted protein |
| SCE1572_6571 | Transcriptional regulator, ArsR family | bi | sce_9879 | 100 Transcriptional regulator, ArsR family |
| SCE1572_6572 | Probable glutathione S-transferase-related transmembrane protein (EC 2.5.1.18) | bi | sce_9878 | 96.82 hypothetical protein |
| SCE1572_6573 | conserved hypothetical protein-putative thiol-disulfide isomerase or thioredoxin | umi | sce_5870 | 52.24 hypothetical protein |
| SCE1572_6574 | aldo/keto reductase | bi | sce_8429 | 94.34 hydrolase, HAD-superfamily, subfamily IIIA |
| SCE1572_6575 | hypothetical protein | bi | sce_5136 | 56.44 hypothetical protein |
| SCE1572_6576 | Transcriptional regulator, AraC family | bi | sce_9599 | 87.15 Transcriptional regulator, AraC family |
| SCE1572_6577 | Nucleoside-diphosphate-sugar epimerases | bi | sce_9598 | 88.47 Nucleoside-diphosphate-sugar epimerases |
| SCE1572_6578 | Aldo-keto reductase | bi | sce_1328 | 91.34 Aldo-keto reductase |
| SCE1572_6579 | FIG01085734: hypothetical protein | bi | sce_9849 | 60.1 FIG01085734: hypothetical protein |
| SCE1572_6580 | Collagen triple helix repeat | umi | sce_5892 | 57.44 erythrocyte membrane protein 1 (PIEMP1) |
| SCE1572_6581 | conserved hypothetical protein | umi | sce_6235 | 69.04 FIG00841528: hypothetical protein |
| SCE1572_6582 | CTP synthase (EC 6.3.4.2) | bi | sce_5517 | 89.32 CTP synthase (EC 6.3.4.2) |
| SCE1572_6583 | putative membrane protein | umi | sce_5539 | 82.23 putative membrane protein |
| SCE1572_6584 | hypothetical protein | - | - | 0 |
| SCE1572_6585 | Signal transduction histidine kinase CheA (EC 2.7.3.-) | umi | sce_6095 | 41.31 Signal transduction histidine kinase CheA (EC 2.7.3.-) |
| SCE1572_6586 | hypothetical protein | - | - | 0 |
| SCE1572_6587 | Malonyl CoA-acyl carrier protein transacylase (EC 2.3.1.39) | umi | sce_9236 | 53.98 Malonyl CoA-acyl carrier protein transacylase (EC 2.3.1.39) |
| SCE1572_6588 | Long-chain-fatty-acid-CoA ligase (EC 6.2.1.3) | umi | sce_389 | 44.28 Long-chain-fatty-acid-CoA ligase (EC 6.2.1.3) |
| SCE1572_6589 | hypothetical protein | - | - | 0 |
| SCE1572_6590 | isrA17-transposase protein | - | - | 0 |
| SCE1572_6591 | Kazal domain protein | umi | sce_2393 | 89.13 Kazal domain protein |
| SCE1572_6592 | Rrf2 family transcriptional regulator, group III | umi | sce_6432 | 28.36 Rrf2 family transcriptional regulator, group III |
| SCE1572_6593 | integral membrane transport protein | - | - | 0 |
| SCE1572_6594 | conserved domain protein | bi | sce_3810 | 27.5 oxidoreductase of aldo/keto reductase family, subgroup 1 |
| SCE1572_6595 | hypothetical protein | - | - | 0 |
| SCE1572_6596 | hypothetical protein | umi | sce_5518 | 55.12 NAD(P)HX epimerase / NAD(P)HX dehydratase |
| SCE1572_6597 | hypothetical protein | bi | sce_5519 | 94.62 hypothetical protein |
| SCE1572_6598 | hypothetical protein | bi | sce_5520 | 92.53 conserved hypothetical protein |
| SCE1572_6599 | Pentapeptide repeat | bi | sce_5522 | 91.48 hypothetical protein |
| SCE1572_6600 | High-affinity carbon uptake protein Hat/HatR | bi | sce_5523 | 90.45 Pentapeptide repeat |
| SCE1572_6601 | VgrG protein | bi | sce_5524 | 86.93 VgrG protein |
| SCE1572_6602 | N-formylglutamate amidohydrolase | bi | sce_5526 | 83.02 N-formylglutamate amidohydrolase |
| SCE1572_6603 | hypothetical protein | bi | sce_5527 | 70.8 hypothetical protein |
| SCE1572_6604 | Putative hydroxylase | - | - | 0 |
| SCE1572_6605 | Aspartyl-tRNA(Asn) amidotransferase subunit A (EC 6.3.5.6) @ Glutamyl-tRNA(Gln) amidotransferase subunit A (EC 6.3.5.7) | umi | sce_2518 | 32.38 Aspartyl-tRNA(Asn) amidotransferase subunit A (EC 6.3.5.6) @ Glutamyl-tRNA(Gln) amidotransferase subunit A (EC 6.3.5.7) |
| SCE1572_6606 | Chemotaxis protein methyltransferase CheR (EC 2.1.1.80) | umi | sce_9491 | 50.98 Chemotaxis protein methyltransferase CheR (EC 2.1.1.80) |
| SCE1572_6607 | hypothetical protein | - | - | 0 |
| SCE1572_6608 | hypothetical protein | umi | sce_1045 | 41.1 hypothetical protein |
| SCE1572_6609 | hypothetical protein | bi | sce_8361 | 67.92 hypothetical protein |
| SCE1572_6610 | Glutathione S-transferase family protein | bi | sce_803 | 51.76 Glutathione S-transferase family protein |
| SCE1572_6611 | hypothetical protein | - | - | 0 |
| SCE1572_6612 | hypothetical protein | umi | sce_9009 | 41.88 hypothetical protein |
| SCE1572_6613 | Serine/threonine-protein kinase pkn1 (EC 2.7.11.1) | umi | sce_5953 | 31.41 Serine/threonine-protein kinase pkn1 (EC 2.7.11.1) |
| SCE1572_6614 | Type III effector HrpW, hairpin with pectate lyase domain | bi | sce_5529 | 80.42 Type III effector HrpW, hairpin with pectate lyase domain |
| SCE1572_6615 | glyoxalase/bleomycin resistance protein/dioxygenase | umi | sce_5762 | 64.71 Glyoxalase/bleomycin resistance protein/dioxygenase |
| SCE1572_6616 | Asparagine synthetase [glutamine-hydrolyzing] (EC 6.3.5.4) | bi | sce_5530 | 80.03 Asparagine synthetase [glutamine-hydrolyzing] (EC 6.3.5.4) |
| SCE1572_6617 | Endoribonuclease L-PSP | bi | sce_7059 | 88.37 Endoribonuclease L-PSP |
| SCE1572_6618 | Transcriptional regulator, LysR family | umi | sce_6071 | 36.43 Transcriptional regulator, LysR family |
| SCE1572_6619 | hypothetical protein | bi | sce_7066 | 58.33 hypothetical protein |
| SCE1572_6620 | Predicted reductase RutE in novel pyrimidine catabolism pathway | - | - | 0 |
| SCE1572_6621 | hypothetical protein | - | - | 0 |
| SCE1572_6622 | hypothetical protein | - | - | 0 |
| SCE1572_6623 | hypothetical protein | - | - | 0 |
| SCE1572_6624 | endonuclease/exonuclease/phosphatase family | bi | sce_169 | 36.87 endonuclease/exonuclease/phosphatase family |
| SCE1572_6625 | hypothetical protein | umi | sce_9401 | 35.96 FIG01087747: hypothetical protein |
| SCE1572_6626 | hypothetical protein | bi | sce_9402 | 34.69 hypothetical protein |
| SCE1572_6627 | hypothetical protein | bi | sce_9402 | 41.07 hypothetical protein |
| SCE1572_6628 | conserved hypothetical protein | umi | sce_9338 | 30.36 hypothetical protein |
| SCE1572_6629 | hypothetical protein | bi | sce_3602 | 49.67 hypothetical protein |
| SCE1572_6630 | Transcriptional regulator, TetR family | bi | sce_3603 | 72.16 Transcriptional regulator, TetR family |
| SCE1572_6631 | Ferredoxin | - | - | 0 |
| SCE1572_6632 | putative cytochrome P450 hydroxylase | umi | sce_8024 | 33.84 putative cytochrome P450 hydroxylase |
| SCE1572_6633 | hypothetical protein | - | - | 0 |
| SCE1572_6634 | High-affinity carbon uptake protein Hat/HatR | bi | sce_9373 | 68.96 NB-ARC domain protein |
| SCE1572_6635 | hypothetical protein | umi | sce_3858 | 39.5 Adenosylhomocysteinase (EC 3.3.1.1) |
| SCE1572_6636 | hypothetical protein | - | - | 0 |
| SCE1572_6637 | Flagellar regulatory protein FleQ | umi | sce_5710 | 71.31 Flagellar regulatory protein FleQ |
| SCE1572_6638 | serine/threonine protein kinase | umi | sce_7827 | 42.23 Cytochrome c551 peroxidase (EC 1.11.1.5) |
| SCE1572_6639 | hypothetical protein | - | - | 0 |
| SCE1572_6640 | Cyclohexanone monooxygenase (EC 1.14.13.22) | bi | sce_5538 | 84.83 Cyclohexanone monooxygenase (EC 1.14.13.22) |
| SCE1572_6641 | putative membrane protein | bi | sce_5539 | 83.85 putative membrane protein |
| SCE1572_6642 | FIG01086315: hypothetical protein | bi | sce_5540 | 86.21 FIG01086315: hypothetical protein |
| SCE1572_6643 | hypothetical protein | bi | sce_5541 | 80.52 FIG01087323: hypothetical protein |
| SCE1572_6644 | hypothetical protein | - | - | 0 |
| SCE1572_6645 | Very large tegument protein | bi | sce_1705 | 64.6 Very large tegument protein |
| SCE1572_6646 | FIG01087241: hypothetical protein | bi | sce_2523 | 92.59 hypothetical protein |
| SCE1572_6647 | hypothetical protein | - | - | 0 |
| SCE1572_6648 | hypothetical protein | - | - | 0 |
| SCE1572_6649 | hypothetical protein | - | - | 0 |
| SCE1572_6650 | putative dioxygenase | bi | sce_1704 | 74.39 putative dioxygenase |
| SCE1572_6651 | hypothetical protein | bi | sce_7113 | 57.89 FIG01089302: hypothetical protein |
| SCE1572_6652 | sensor histidine kinase | bi | sce_7114 | 48.48 Osmosensitive K channel histidine kinase KdpD (EC 2.7.3.-) |
| SCE1572_6653 | hypothetical protein | bi | sce_5545 | 89.66 hypothetical protein |
| SCE1572_6654 | Multiple EGF-like-domain protein 3 precursor | bi | sce_5546 | 73.93 Multiple EGF-like-domain protein 3 precursor |
| SCE1572_6655 | Permeases of the major facilitator superfamily | bi | sce_5551 | 78.8 Permeases of the major facilitator superfamily |
| SCE1572_6656 | EBNA-1 | umi | sce_4770 | 52.5 hypothetical protein |
| SCE1572_6657 | Adenylate cyclase (EC 4.6.1.1) / Guanylate cyclase (EC 4.6.1.2) | umi | sce_248 | 37.36 Adenylate cyclase (EC 4.6.1.1) / Guanylate cyclase (EC 4.6.1.2) |
| SCE1572_6658 | hypothetical protein | - | - | 0 |
| SCE1572_6659 | Phytanoyl-CoA dioxygenase | umi | sce_8487 | 26.82 FIG00840231: hypothetical protein |
| SCE1572_6660 | probable methyltransferase | umi | sce_10042 | 40.48 NADH-FMN oxidoreductase |
| SCE1572_6661 | AknN | umi | sce_5801 | 41.35 AknN |
| SCE1572_6662 | serine/threonine kinase with two-component sensor domain | umi | sce_6535 | 30.92 Signal transduction histidine kinase CheA (EC 2.7.3.-) |
| SCE1572_6663 | FIG1044843: hypothetical protein | bi | sce_5556 | 83 FIG1044843: hypothetical protein |
| SCE1572_6664 | Adenylate cyclase (EC 4.6.1.1) | umi | sce_6236 | 49.12 RsbR, positive regulator of sigma-B |
| SCE1572_6665 | multi-sensor hybrid histidine kinase | bi | sce_5554 | 90.71 PAS |
| SCE1572_6666 | PAS | bi | sce_5555 | 81.38 PAS |
| SCE1572_6667 | epoxide hydrolase | umi | sce_3912 | 32.6 Epoxide hydrolase (EC 3.3.2.9) |
| SCE1572_6668 | Na ⁺ antiporter NhaD and related arsenite permease | bi | sce_9809 | 94.38 hypothetical protein |
| SCE1572_6669 | putative carboxylesterase | bi | sce_9810 | 86.02 putative carboxylesterase |
| SCE1572_6670 | hypothetical protein | bi | sce_9811 | 91.33 hypothetical protein |
| SCE1572_6671 | NHL repeat protein | bi | sce_5917 | 39.9 FIG01086804: hypothetical protein |
| SCE1572_6672 | hypothetical protein | - | - | 0 |
| SCE1572_6673 | hypothetical protein | bi | sce_5558 | 81.56 hypothetical protein |
| SCE1572_6674 | transcriptional regulator | umi | sce_1100 | 29.09 Transcriptional regulator, GntR family / Transcriptional regulator, TetR family |
| SCE1572_6675 | hypothetical protein | bi | sce_5570 | 60 Oxygenase |
| SCE1572_6676 | FIG01087606: hypothetical protein | bi | sce_5560 | 71 FIG01087606: hypothetical protein |
| SCE1572_6677 | RsbR, positive regulator of sigma-B | bi | sce_5181 | 48.55 RsbR, positive regulator of sigma-B |
| SCE1572_6678 | FIG01086953: hypothetical protein | bi | sce_5561 | 72.58 FIG01089423: hypothetical protein |
| SCE1572_6679 | hypothetical protein | - | - | 0 |
| SCE1572_6680 | Glutathione S-transferase (EC 2.5.1.18) | bi | sce_5562 | 78.97 Glutathione S-transferase (EC 2.5.1.18) |
| SCE1572_6681 | transcriptional regulator (LysR family) | bi | sce_5563 | 86.02 transcriptional regulator, LysR family |
| SCE1572_6682 | hypothetical protein | umi | sce_1706 | 50 PnB protein |
| SCE1572_6683 | N-acetyl-gamma-glutamyl-phosphate reductase (EC 1.2.1.38) | bi | sce_5564 | 93.33 N-acetyl-gamma-glutamyl-phosphate reductase (EC 1.2.1.38) |
| SCE1572_6684 | N-acetyl-L,L-diaminopimelate deacetylase (EC 3.5.1.47) | bi | sce_5568 | 95.35 N-acetyl-L,L-diaminopimelate deacetylase (EC 3.5.1.47) |
| SCE1572_6685 | proton/sodium-glutamate symport protein | umi | sce_3961 | 25.61 Proton/glutamate symport protein @ Sodium/glutamate symport protein |
| SCE1572_6686 | hypothetical protein | - | - | 0 |
| SCE1572_6687 | Hemoglobin-like protein HbO | bi | sce_5569 | 92.48 Hemoglobin-like protein HbO |
| SCE1572_6688 | tolB protein precursor, periplasmic protein involved in the tonb-independent uptake of group A colicins | bi | sce_5086 | 70.73 tolB protein precursor, periplasmic protein involved in the tonb-independent uptake of group A colicins |
| SCE1572_6689 | hypothetical protein | - | - | 0 |
| SCE1572_6690 | conserved hypothetical protein | - | - | 0 |
| SCE1572_6691 | Asr9028 protein | bi | sce_10016 | 85.94 hypothetical protein |
| SCE1572_6692 | DNA repair protein RadC | umi | sce_8398 | 62.86 DNA repair protein RadC |
| SCE1572_6693 | hypothetical protein | - | - | 0 |
| SCE1572_6694 | FIG01087754: hypothetical protein | bi | sce_2414 | 82.98 FIG01087754: hypothetical protein |
| SCE1572_6695 | S-adenosylmethionine:tRNA ribosyltransferase-isomerase (EC 5.-.-.-) | bi | sce_5574 | 92.35 S-adenosylmethionine:tRNA ribosyltransferase-isomerase (EC 5.-.-.-) |
| SCE1572_6696 | Oxidoreductase, short chain dehydrogenase/reductase family | bi | sce_5575 | 88.3 Oxidoreductase, short chain dehydrogenase/reductase family |
| SCE1572_6697 | DNA-binding protein | bi | sce_5576 | 96.77 DNA-binding protein |
| SCE1572_6698 | hypothetical protein | umi | sce_1612 | 42.11 Chitinase (EC 3.2.1.14) |
| SCE1572_6699 | dTDP-4-dehydrohamnose reductase (EC 1.1.1.133) | umi | sce_3427 | 63.41 dTDP-4-dehydrohamnose reductase (EC 1.1.1.133) |
| SCE1572_6700 | Galactokinase (EC 2.7.1.6) | bi | sce_2475 | 88.3 Galactokinase (EC 2.7.1.6) |
| SCE1572_6701 | Beta-galactosidase (EC 3.2.1.23) | umi | sce_3424 | 67.41 Beta-galactosidase (EC 3.2.1.23) |
| SCE1572_6702 | UDP-galactopyranose mutase (EC 5.4.99.9) | umi | sce_3426 | 69.47 UDP-galactopyranose mutase (EC 5.4.99.9) |
| SCE1572_6703 | Glycosyltransferase | umi | sce_3425 | 58.92 Glycosyltransferase |
| SCE1572_6704 | Lysine decarboxylase family | bi | sce_5577 | 85.2 Lysine decarboxylase family |
| SCE1572_6705 | Uncharacterized protein ImpC | bi | sce_5578 | 97.57 Uncharacterized protein ImpC |
| SCE1572_6706 | Uncharacterized protein ImpB | bi | sce_5579 | 98.77 Uncharacterized protein ImpB |
| SCE1572_6707 | hypothetical protein | - | - | 0 |
| SCE1572_6708 | Uncharacterized protein ImpA | bi | sce_5580 | 78.23 Uncharacterized protein ImpA |
| SCE1572_6709 | hypothetical protein | bi | sce_5581 | 94.44 hypothetical protein |
| SCE1572_6710 | IcmF-related protein | bi | sce_5582 | 91.53 IcmF-related protein |
| SCE1572_6711 | Probable transmembrane protein | bi | sce_5583 | 98.67 Probable transmembrane protein |
| SCE1572_6712 | Uncharacterized protein ImpJ/VasE | bi | sce_5584 | 91.61 Uncharacterized protein ImpJ/VasE |
| SCE1572_6713 | Type VI secretion lipoprotein/VasD | bi | sce_5585 | 88.51 Type VI secretion lipoprotein/VasD |
| SCE1572_6714 | CtpB protein | bi | sce_5586 | 96.88 CtpB protein |
| SCE1572_6715 | Membrane-bound lytic murein transglycosylase D precursor (EC 3.2.1.-) | bi | sce_5587 | 81.98 Membrane-bound lytic murein transglycosylase D precursor (EC 3.2.1.-) |
| SCE1572_6716 | Uncharacterized protein ImpL/VasC | bi | sce_5588 | 94.88 Uncharacterized protein ImpL/VasC |
| SCE1572_6717 | hypothetical protein | bi | sce_5589 | 90.91 hypothetical protein |
| SCE1572_6718 | hypothetical protein | - | - | 0 |
| SCE1572_6719 | putative lipoprotein | bi | sce_5590 | 94.32 hypothetical protein |
| SCE1572_6720 | Hcp protein | bi | sce_5592 | 81.55 Hcp protein |
| SCE1572_6721 | hep protein | bi | sce_5593 | 89.66 hep protein |

| | | | | |
|--------------|---|-----|-----------|--|
| SCE1572_6722 | Uncharacterized protein similar to VCA0109 | bi | see_5594 | 93.57 Uncharacterized protein similar to VCA0109 |
| SCE1572_6723 | Protein ImpG/VasA | bi | see_5595 | 96.77 Protein ImpG/VasA |
| SCE1572_6724 | Uncharacterized protein ImpH/VasB | bi | see_5596 | 92.57 Uncharacterized protein ImpH/VasB |
| SCE1572_6725 | FIG01086198: hypothetical protein | bi | see_5597 | 89.91 FIG01086198: hypothetical protein |
| SCE1572_6726 | hypothetical protein | bi | see_5598 | 86.39 hypothetical protein |
| SCE1572_6727 | hypothetical protein | bi | see_5599 | 57.98 hypothetical protein |
| SCE1572_6728 | Adenosylmethionine-8-amino-7-oxononanoate aminotransferase (EC 2.6.1.62) | bi | see_5600 | 67.72 hypothetical protein |
| SCE1572_6729 | hypothetical protein | bi | see_5601 | 69.57 hypothetical protein |
| SCE1572_6730 | ATP-dependent protease La (EC 3.4.21.53) Type I | bi | see_5602 | 98.78 ATP-dependent protease La (EC 3.4.21.53) Type I |
| SCE1572_6731 | hypothetical protein | bi | see_5603 | 69.09 hypothetical protein |
| SCE1572_6732 | Sulfatase modifying factor 2 precursor (C-alpha-formylglycine-generating enzyme 2) | bi | see_5604 | 87.81 Sulfatase-modifying factor 2 precursor (C-alpha-formylglycine-generating enzyme 2) |
| SCE1572_6733 | Methionyl-tRNA formyltransferase (EC 2.1.2.9) | bi | see_5605 | 90.03 Methionyl-tRNA formyltransferase (EC 2.1.2.9) |
| SCE1572_6734 | Aldehyde dehydrogenase (EC 1.2.1.3) | bi | see_5606 | 94.54 Aldehyde dehydrogenase (EC 1.2.1.3) |
| SCE1572_6735 | Aldehyde dehydrogenase (EC 1.2.1.3) | bi | see_5607 | 94.2 Aldehyde dehydrogenase (EC 1.2.1.3) |
| SCE1572_6736 | Deoxyribose-phosphate aldolase (EC 4.1.2.4) | bi | see_5608 | 94.7 Deoxyribose-phosphate aldolase (EC 4.1.2.4) |
| SCE1572_6737 | Thiol peroxidase, Bcp-type (EC 1.11.1.15) | bi | see_5609 | 86.29 Thiol peroxidase, Bcp-type (EC 1.11.1.15) |
| SCE1572_6738 | Alpha/beta hydrolase fold | see | see_5610 | 84.69 Alpha/beta hydrolase fold |
| SCE1572_6739 | hypothetical protein | - | - | 0 |
| SCE1572_6740 | FIG01087377: hypothetical protein | bi | see_1003 | 84.94 FIG01087377: hypothetical protein |
| SCE1572_6741 | hypothetical protein | uni | see_10158 | 25 hypothetical protein |
| SCE1572_6742 | putative eukaryotic-type serine/threonine protein kinase | bi | see_5614 | 70.17 putative eukaryotic-type serine/threonine protein kinase |
| SCE1572_6743 | FIG01088996: hypothetical protein | bi | see_5615 | 88.54 FIG01088996: hypothetical protein |
| SCE1572_6744 | RNA polymerase sigma factor for flagellar operon | bi | see_5616 | 81.15 RNA polymerase sigma factor for flagellar operon |
| SCE1572_6745 | protein of unknown function DUF433 | - | - | 0 |
| SCE1572_6746 | conserved hypothetical protein | - | - | 0 |
| SCE1572_6747 | hypothetical protein | - | - | 0 |
| SCE1572_6748 | hypothetical protein | - | - | 0 |
| SCE1572_6749 | hypothetical protein | - | - | 0 |
| SCE1572_6750 | Alcohol dehydrogenase (EC 1.1.1.1) | bi | see_5627 | 90.67 Alcohol dehydrogenase (EC 1.1.1.1) |
| SCE1572_6751 | hypothetical protein | - | - | 0 |
| SCE1572_6752 | hypothetical protein | - | - | 0 |
| SCE1572_6753 | hypothetical protein | - | - | 0 |
| SCE1572_6754 | hypothetical protein | - | - | 0 |
| SCE1572_6755 | hypothetical protein | bi | see_10428 | 79.67 hypothetical protein |
| SCE1572_6756 | hypothetical protein | bi | see_10429 | 56.36 hypothetical protein |
| SCE1572_6757 | Mir2351 protein | bi | see_10430 | 59.94 Mir2351 protein |
| SCE1572_6758 | FOG: HEAT repeat | uni | see_1339 | 55.21 FOG: HEAT repeat |
| SCE1572_6759 | Mil2356 protein | bi | see_5628 | 83.1 Mil2356 protein |
| SCE1572_6760 | VgrG protein | uni | see_1338 | 64.86 VgrG protein |
| SCE1572_6761 | FIG01089095: hypothetical protein | uni | see_1340 | 48.8 FIG01089095: hypothetical protein |
| SCE1572_6762 | hypothetical protein | - | - | 0 |
| SCE1572_6763 | Beta-xylosidase (EC 3.2.1.37) | uni | see_137 | 36.13 Beta-xylosidase (EC 3.2.1.37) |
| SCE1572_6764 | radical SAM/B12 binding domain protein | bi | see_5629 | 93.7 hypothetical protein |
| SCE1572_6765 | HNH endonuclease | - | - | 0 |
| SCE1572_6766 | hypothetical protein | - | - | 0 |
| SCE1572_6767 | hypothetical protein | - | - | 0 |
| SCE1572_6768 | hypothetical protein | bi | see_5447 | 44.17 FIG01084967: hypothetical protein |
| SCE1572_6769 | Ferredoxin | bi | see_5632 | 95.4 Ferredoxin |
| SCE1572_6770 | protein of unknown function DUF1328 | bi | see_5634 | 96.3 Protein of unknown function DUF1328 |
| SCE1572_6771 | Autotransporter subtilisin-like protease | bi | see_5635 | 63.81 Autotransporter subtilisin-like protease |
| SCE1572_6772 | hypothetical protein | - | - | 0 |
| SCE1572_6773 | Mil1661 protein | bi | see_5637 | 82.11 hypothetical protein |
| SCE1572_6774 | FIG01086458: hypothetical protein | bi | see_5638 | 78.67 FIG01086458: hypothetical protein |
| SCE1572_6775 | hypothetical protein | - | - | 0 |
| SCE1572_6776 | FIG01088413: hypothetical protein | bi | see_5639 | 66.27 FIG01088413: hypothetical protein |
| SCE1572_6777 | Collagen triple helix repeat | bi | see_5640 | 46.11 FIG01089683: hypothetical protein |
| SCE1572_6778 | RNA polymerase sigma factor RpoE | bi | see_5641 | 81.38 RNA polymerase sigma factor RpoE |
| SCE1572_6779 | Dihydropyrimidine acetyltransferase component of pyruvate dehydrogenase complex (EC 2.3.1.12) | bi | see_5642 | 61.63 Dihydropyrimidine acetyltransferase component of pyruvate dehydrogenase complex (EC 2.3.1.12) |
| SCE1572_6780 | hypothetical protein | - | - | 0 |
| SCE1572_6781 | hypothetical protein | bi | see_5643 | 85.48 hypothetical protein |
| SCE1572_6782 | hypothetical protein | bi | see_5644 | 80.51 hypothetical protein |
| SCE1572_6783 | Cell division inhibitor | bi | see_5645 | 92.7 Cell division inhibitor |
| SCE1572_6784 | hypothetical protein | uni | see_7568 | 27.58 FIG01087433: hypothetical protein |
| SCE1572_6785 | hypothetical protein | - | - | 0 |
| SCE1572_6786 | HipA protein | - | - | 0 |
| SCE1572_6787 | Maltose/maltodextrin ABC transporter, permease protein MalG | bi | see_5646 | 91.07 Maltose/maltodextrin ABC transporter, permease protein MalG |
| SCE1572_6788 | Maltose/maltodextrin ABC transporter, permease protein MalF | bi | see_5647 | 88.03 Maltose/maltodextrin ABC transporter, permease protein MalF |
| SCE1572_6789 | Maltose/maltodextrin ABC transporter, substrate binding periplasmic protein MalE | bi | see_5648 | 89.72 Maltose/maltodextrin ABC transporter, substrate binding periplasmic protein MalE |
| SCE1572_6790 | hypothetical protein | - | - | 0 |
| SCE1572_6791 | DNA mismatch repair protein MutL | uni | see_6428 | 46.58 Cellulase (EC:3.2.1.4) |
| SCE1572_6792 | Isochorismate synthase (EC 5.4.4.2) of siderophore biosynthesis | bi | see_5650 | 91.31 Isochorismate synthase (EC 5.4.4.2) of siderophore biosynthesis |
| SCE1572_6793 | Anthraniolate synthase, aminase component (EC 4.1.3.27) / Anthranilate synthase, amidotransferase component (EC 4.1.3.27) | bi | see_5652 | 91.74 Anthranilate synthase, aminase component (EC 4.1.3.27) / Anthranilate synthase, amidotransferase component (EC 4.1.3.27) |
| SCE1572_6794 | FIG01088914: hypothetical protein | bi | see_5653 | 82.85 FIG01088914: hypothetical protein |
| SCE1572_6795 | Argininosuccinate synthase (EC 6.3.4.5) | bi | see_5654 | 97.78 Argininosuccinate synthase (EC 6.3.4.5) |
| SCE1572_6796 | putative membrane protein | bi | see_5655 | 89.08 putative membrane protein |
| SCE1572_6797 | Aldo-keto reductase | bi | see_5656 | 93.27 Aldo-keto reductase |
| SCE1572_6798 | DNA mismatch repair protein MutS | bi | see_5657 | 90.19 DNA mismatch repair protein MutS |
| SCE1572_6799 | large Ala/Glu-rich protein | bi | see_5658 | 60.53 large Ala/Glu-rich protein |
| SCE1572_6800 | serine/threonine protein kinase | bi | see_5660 | 81 serine/threonine protein kinase |
| SCE1572_6801 | ubiquinone/menaquinone biosynthesis methyltransferases | uni | see_10042 | 39.5 NADH-FMN oxidoreductase |
| SCE1572_6802 | 3-oxoacyl-[acyl-carrier-protein] synthase, KASIII (EC 2.3.1.41) | bi | see_5662 | 95.75 3-oxoacyl-[acyl-carrier-protein] synthase, KASIII (EC 2.3.1.41) |
| SCE1572_6803 | Endonuclease III (EC 4.2.99.18) | bi | see_5663 | 93.27 Endonuclease III (EC 4.2.99.18) |
| SCE1572_6804 | putative lipoprotein | bi | see_5664 | 83.74 putative lipoprotein |
| SCE1572_6805 | collagen triple helix repeat domain protein, putative | uni | see_5665 | 69.78 putative lipoprotein |
| SCE1572_6806 | FIG01086887: hypothetical protein | bi | see_5666 | 84.97 FIG01086887: hypothetical protein |
| SCE1572_6807 | 4'-phosphopantetheinyl transferase (EC 2.7.8.-) | bi | see_5667 | 93.06 4'-phosphopantetheinyl transferase (EC 2.7.8.-) |
| SCE1572_6808 | putative SimX4 homolog | bi | see_5668 | 90.94 putative SimX4 homolog |
| SCE1572_6809 | Glutamate synthase [NADPH] large chain (EC 1.4.1.13) | bi | see_5669 | 95.24 Glutamate synthase [NADPH] large chain (EC 1.4.1.13) |
| SCE1572_6810 | Glutamate synthase [NADPH] small chain (EC 1.4.1.13) | bi | see_5670 | 94.36 Glutamate synthase [NADPH] small chain (EC 1.4.1.13) |
| SCE1572_6811 | Threonine dehydrogenase and related Zn-dependent dehydrogenases | bi | see_5671 | 89.76 Threonine dehydrogenase and related Zn-dependent dehydrogenases |
| SCE1572_6812 | hypothetical protein | bi | see_5672 | 63.04 hypothetical protein |
| SCE1572_6813 | SCARECROW gene regulator-like | bi | see_5673 | 94.72 SCARECROW gene regulator-like |
| SCE1572_6814 | Two-component system regulatory protein | bi | see_5675 | 92.24 Two-component system regulatory protein |
| SCE1572_6815 | FIG01089275: hypothetical protein | bi | see_5677 | 85.68 FIG01089275: hypothetical protein |
| SCE1572_6816 | TonB-dependent receptor | bi | see_5678 | 81.34 TonB-dependent receptor |
| SCE1572_6817 | Tol biopolymer transport system, TolR protein | bi | see_5679 | 91.03 Tol biopolymer transport system, TolR protein |
| SCE1572_6818 | Biopolymer transport protein ExbD/TolR | bi | see_5680 | 95.27 Biopolymer transport protein ExbD/TolR |
| SCE1572_6819 | MotA/TolQ/ExbB proton channel family protein | bi | see_5681 | 94.47 MotA/TolQ/ExbB proton channel family protein |
| SCE1572_6820 | Ferric siderophore transport system, periplasmic binding protein TonB | bi | see_5682 | 80.54 Ferric siderophore transport system, periplasmic binding protein TonB |
| SCE1572_6821 | Phosphate regulon transcriptional regulatory protein PhoB (SphR) | bi | see_5683 | 96.54 Phosphate regulon transcriptional regulatory protein PhoB (SphR) |
| SCE1572_6822 | Serine acetyltransferase (EC 2.3.1.30) | bi | see_5684 | 93.65 Serine acetyltransferase (EC 2.3.1.30) |
| SCE1572_6823 | putative membrane protein | bi | see_5685 | 94.96 putative membrane protein |
| SCE1572_6824 | Outer membrane lipoprotein carrier protein LolA | bi | see_5686 | 92.67 Outer membrane lipoprotein carrier protein LolA |
| SCE1572_6825 | hypothetical protein | - | - | 0 |
| SCE1572_6826 | Crossover junction endodeoxyribonuclease RuvC (EC 3.1.22.4) | bi | see_5687 | 97.21 Crossover junction endodeoxyribonuclease RuvC (EC 3.1.22.4) |
| SCE1572_6827 | Glycolate dehydrogenase (EC 1.1.99.14), subunit GldD | bi | see_5688 | 95.22 Glycolate dehydrogenase (EC 1.1.99.14), subunit GldD |
| SCE1572_6828 | FIG01086522: hypothetical protein | bi | see_5689 | 85.95 FIG01086522: hypothetical protein |
| SCE1572_6829 | hypothetical protein | bi | see_5690 | 76.67 hypothetical protein |
| SCE1572_6830 | hypothetical protein | - | - | 0 |
| SCE1572_6831 | conserved hypothetical protein | see | see_5691 | 75.96 Cellulase (EC:3.2.1.4) |
| SCE1572_6832 | FIG01087100: hypothetical protein | bi | see_5694 | 79.22 FIG01087100: hypothetical protein |
| SCE1572_6833 | Serine/threonine-protein kinase pkn3 (EC 2.7.11.1) | bi | see_5695 | 75.95 Serine/threonine-protein kinase pkn3 (EC 2.7.11.1) |
| SCE1572_6834 | hypothetical protein | - | - | 0 |
| SCE1572_6835 | Pyridoxamine 5'-phosphate oxidase (EC 1.4.3.5) | bi | see_5696 | 91.79 Pyridoxamine 5'-phosphate oxidase (EC 1.4.3.5) |
| SCE1572_6836 | HNH endonuclease domain protein | uni | see_1905 | 44.74 HNH endonuclease family protein |
| SCE1572_6837 | FIG01166001: hypothetical protein | bi | see_5697 | 94.16 FIG01166001: hypothetical protein |
| SCE1572_6838 | Putative bacterial haemoglobin | bi | see_5698 | 86.84 Putative bacterial haemoglobin |
| SCE1572_6839 | two component, sigma54 specific, transcriptional regulator, Fis family | uni | see_5699 | 85.28 Anaerobic nitric oxide reductase transcription regulator NorR |
| SCE1572_6840 | 2'-5'-RNA ligase | bi | see_5700 | 94.36 2'-5'-RNA ligase |
| SCE1572_6841 | Peptidyl-dipeptidase A precursor (EC 3.4.15.1) | bi | see_5701 | 84.06 Peptidyl-dipeptidase A precursor (EC 3.4.15.1) |
| SCE1572_6842 | Dual specificity protein phosphatase 23 (EC 3.1.3.48) (EC 3.1.3.16) (Low molecular mass dual specificity phosphatase 3) (LDI) | bi | see_5702 | 85.76 hypothetical protein |
| SCE1572_6843 | Glutathione S-transferase family protein | bi | see_5703 | 85.71 hypothetical protein |
| SCE1572_6844 | Alpha-amylase family protein | bi | see_5704 | 94.07 Alpha-amylase family protein |
| SCE1572_6845 | FIG01088991: hypothetical protein | bi | see_5705 | 78.95 FIG01088991: hypothetical protein |
| SCE1572_6846 | FIG01087265: hypothetical protein | bi | see_5706 | 89.95 FIG01087265: hypothetical protein |
| SCE1572_6847 | Mir2412 protein | bi | see_5707 | 65.37 Mir2412 protein |
| SCE1572_6848 | Mir2412 protein | bi | see_5709 | 72.2 FIG01086591: hypothetical protein |
| SCE1572_6849 | Flagellar hook-length control protein FliK | bi | see_5711 | 75.76 Flagellar hook-length control protein FliK |
| SCE1572_6850 | G:T/U mismatch-specific uracil/thymine DNA-glycosylase | bi | see_5712 | 86.63 G:T/U mismatch-specific uracil/thymine DNA-glycosylase |
| SCE1572_6851 | hypothetical protein | bi | see_5713 | 73.21 hypothetical protein |
| SCE1572_6852 | hypothetical protein | - | - | 0 |
| SCE1572_6853 | Phytochrome, two-component sensor histidine kinase (EC 2.7.3.-); Cyanobacterial phytochrome B | bi | see_5714 | 94.49 Phytochrome, two-component sensor histidine kinase (EC 2.7.3.-); Cyanobacterial phytochrome B |
| SCE1572_6854 | Outer membrane protein A precursor | bi | see_5715 | 82.11 Outer membrane protein A precursor |
| SCE1572_6855 | hypothetical protein | bi | see_5716 | 80.92 hypothetical protein |
| SCE1572_6856 | hypothetical protein | bi | see_5717 | 88.46 hypothetical protein |
| SCE1572_6857 | FIG01087803: hypothetical protein | bi | see_5718 | 79.89 FIG01087803: hypothetical protein |
| SCE1572_6858 | MscS Mechanosensitive ion channel | bi | see_5719 | 88.24 Membrane protein |
| SCE1572_6859 | RNA binding protein | bi | see_5720 | 56.45 RNA binding protein |
| SCE1572_6860 | Two-component hybrid sensor and regulator | bi | see_5721 | 86.96 Two-component hybrid sensor and regulator |
| SCE1572_6861 | hypothetical protein | bi | see_5723 | 66.22 hypothetical protein |
| SCE1572_6862 | Serine/threonine protein kinase PknB (EC 2.7.11.1) | bi | see_5724 | 71.59 Serine/threonine protein kinase PknB (EC 2.7.11.1) |
| SCE1572_6863 | Cardiolipin synthase (EC 2.7.8.-) | bi | see_5725 | 85.03 Cardiolipin synthase (EC 2.7.8.-) |
| SCE1572_6864 | hypothetical protein | - | - | 0 |
| SCE1572_6865 | conserved hypothetical protein | bi | see_5728 | 85.54 conserved hypothetical protein |
| SCE1572_6866 | tRNA.m(5)U-54 MTase gid | bi | see_5729 | 94.58 tRNA.m(5)U-54 MTase gid |
| SCE1572_6867 | DNA topoisomerase I (EC 5.99.1.2) | bi | see_5730 | 93.43 DNA topoisomerase I (EC 5.99.1.2) |
| SCE1572_6868 | Rossmann fold nucleotide-binding protein Smf possibly involved in DNA uptake | bi | see_5731 | 87.31 Rossmann fold nucleotide-binding protein Smf possibly involved in DNA uptake |
| SCE1572_6869 | Dihydropyrimidine acetyltransferase component of pyruvate dehydrogenase complex (EC 2.3.1.12) | bi | see_5732 | 74.9 Dihydropyrimidine acetyltransferase component of pyruvate dehydrogenase complex (EC 2.3.1.12) |
| SCE1572_6870 | Exopolyphosphatase-related protein | bi | see_5733 | 94.31 Exopolyphosphatase-related protein |
| SCE1572_6871 | Glycerophosphoryl diester phosphodiesterase (EC 3.1.4.46) | bi | see_5734 | 87.27 Glycerophosphoryl diester phosphodiesterase (EC 3.1.4.46) |
| SCE1572_6872 | serine/threonine-protein kinase PknI (EC:2.7.11.1) | bi | see_5735 | 75.45 serine/threonine protein kinase |
| SCE1572_6873 | FIG01086974: hypothetical protein | bi | see_5737 | 89.83 FIG01086974: hypothetical protein |
| SCE1572_6874 | transcription termination factor Rho | bi | see_5738 | 88.34 hypothetical protein |
| SCE1572_6875 | hypothetical protein | bi | see_5739 | 89.89 hypothetical protein |
| SCE1572_6876 | hypothetical protein | bi | see_5741 | 85.6 hypothetical protein |
| SCE1572_6877 | Alanyl-tRNA synthetase (EC 6.1.1.7) | bi | see_5742 | 94.55 Alanyl-tRNA synthetase (EC 6.1.1.7) |
| SCE1572_6878 | hypothetical protein | bi | see_5743 | 86.07 FIG01088207: hypothetical protein |
| SCE1572_6879 | Tropomyosin-1, isoforms 33/34 (Tropomyosin II) | bi | see_5744 | 84.16 Tropomyosin-1, isoforms 33/34 (Tropomyosin II) |
| SCE1572_6880 | hypothetical protein | - | - | 0 |
| SCE1572_6881 | outer membrane protein, OmpA/MotB family | uni | see_77 | 34.32 outer membrane protein OmpA |
| SCE1572_6882 | hypothetical protein | - | - | 0 |
| SCE1572_6883 | Flagellar motor rotation protein MotB | bi | see_5745 | 91.79 Flagellar motor rotation protein MotB |
| SCE1572_6884 | FIG01086922: hypothetical protein | uni | see_7361 | 54.79 AAA ATPase |
| SCE1572_6885 | RNA polymerase sigma-70 factor, ECF subfamily | uni | see_9225 | 39.78 DNA-directed RNA polymerase specialized sigma subunit, sigma24-like |

| | | | | |
|--------------|---|-----|-----------|---|
| SCE1572_6886 | Putative protein-S-isoprenylcysteine methyltransferase | uni | see_9736 | 79.9 Putative protein-S-isoprenylcysteine methyltransferase |
| SCE1572_6887 | Adenylate cyclase (EC 4.6.1.1) / Guanylate cyclase (EC 4.6.1.2) | bi | see_5746 | 73.58 Adenylate cyclase (EC 4.6.1.1) / Guanylate cyclase (EC 4.6.1.2) |
| SCE1572_6888 | Mobile element protein | uni | see_9804 | 33.04 Mobile element protein |
| SCE1572_6889 | hypothetical protein | - | - | 0 |
| SCE1572_6890 | Phosphoglycerate kinase (EC 2.7.2.3) | uni | see_8224 | 44.12 Phosphoglycerate kinase (EC 2.7.2.3) |
| SCE1572_6891 | Phosphoglycerate kinase (EC 2.7.2.3) | uni | see_8224 | 40 Phosphoglycerate kinase (EC 2.7.2.3) |
| SCE1572_6892 | Adenylate cyclase (EC 4.6.1.1) / Guanylate cyclase (EC 4.6.1.2) | bi | see_5751 | 85.68 Adenylate cyclase (EC 4.6.1.1) / Guanylate cyclase (EC 4.6.1.2) |
| SCE1572_6893 | Adenylate cyclase (EC 4.6.1.1) / Guanylate cyclase (EC 4.6.1.2) | bi | see_5746 | 81.24 Adenylate cyclase (EC 4.6.1.1) / Guanylate cyclase (EC 4.6.1.2) |
| SCE1572_6894 | Adenylate cyclase (EC 4.6.1.1) / Guanylate cyclase (EC 4.6.1.2) | uni | see_5751 | 80.11 Adenylate cyclase (EC 4.6.1.1) / Guanylate cyclase (EC 4.6.1.2) |
| SCE1572_6895 | hypothetical protein | - | - | 0 |
| SCE1572_6896 | hypothetical protein | uni | see_3489 | 62.44 hypothetical protein |
| SCE1572_6897 | Valyl-tRNA synthetase (EC 6.1.1.9) | - | - | 0 |
| SCE1572_6898 | Valyl-tRNA synthetase (EC 6.1.1.9) | bi | see_5752 | 92.86 Valyl-tRNA synthetase (EC 6.1.1.9) |
| SCE1572_6899 | Flavodoxin reductases (ferredoxin-NADPH reductases) family 1 | bi | see_5753 | 92.65 Flavodoxin reductases (ferredoxin-NADPH reductases) family 1 |
| SCE1572_6900 | hypothetical protein | - | - | 0 |
| SCE1572_6901 | hypothetical protein | - | - | 0 |
| SCE1572_6902 | Aspartate aminotransferase (EC 2.6.1.1) | uni | see_9835 | 36.16 Aspartate aminotransferase (EC 2.6.1.1) |
| SCE1572_6903 | Aromatic-L-amino-acid decarboxylase (EC 4.1.1.28) | uni | see_2563 | 32.06 Aromatic-L-amino-acid decarboxylase (EC 4.1.1.28) |
| SCE1572_6904 | hypothetical protein | - | - | 0 |
| SCE1572_6905 | B3/4 domain protein | - | - | 0 |
| SCE1572_6906 | hypothetical protein | - | - | 0 |
| SCE1572_6907 | 3-oxoacyl-[acyl-carrier protein] reductase (EC 1.1.1.100) | uni | see_5941 | 41.2 3-oxoacyl-[acyl-carrier protein] reductase (EC 1.1.1.100) |
| SCE1572_6908 | hypothetical protein | - | - | 0 |
| SCE1572_6909 | hypothetical protein | - | - | 0 |
| SCE1572_6910 | Malonyl CoA-acyl carrier protein transacylase (EC 2.3.1.39) | uni | see_9236 | 54.74 Malonyl CoA-acyl carrier protein transacylase (EC 2.3.1.39) |
| SCE1572_6911 | Long-chain-fatty-acid-CoA ligase (EC 6.2.1.3) | bi | see_2666 | 52.81 Long-chain-fatty-acid-CoA ligase (EC 6.2.1.3) |
| SCE1572_6912 | Long-chain-fatty-acid-CoA ligase (EC 6.2.1.3) | uni | see_9229 | 57.14 FIG01085400: hypothetical protein |
| SCE1572_6913 | D-alanyl-D-alanine carboxypeptidase (EC 3.4.16.4) | uni | see_7206 | 54.71 D-alanyl-D-alanine carboxypeptidase (EC 3.4.16.4) |
| SCE1572_6914 | large tegument protein | bi | see_5755 | 50.6 hypothetical protein |
| SCE1572_6915 | hypothetical protein | bi | see_5756 | 92.5 hypothetical protein |
| SCE1572_6916 | RNA polymerase sigma factor | bi | see_5761 | 89.35 RNA polymerase sigma factor |
| SCE1572_6917 | membrane protein | bi | see_8380 | 79.75 membrane protein |
| SCE1572_6918 | Glyoxalase/bleomycin resistance protein/dioxygenase | bi | see_5762 | 81.75 Glyoxalase/bleomycin resistance protein/dioxygenase |
| SCE1572_6919 | Glutathione S-transferase (EC 2.5.1.18) | bi | see_8379 | 84.16 Glutathione S-transferase (EC 2.5.1.18) |
| SCE1572_6920 | hypothetical protein | - | - | 0 |
| SCE1572_6921 | Serine/threonine kinase with two-component sensor domain | bi | see_2065 | 94.27 putative sensory box histidine kinase |
| SCE1572_6922 | Transcriptional regulator, ArsR family | bi | see_1259 | 52.94 Transcriptional regulator, ArsR family |
| SCE1572_6923 | Chemotaxis protein methyltransferase CheR (EC 2.1.1.80) | uni | see_229 | 49.74 FOG: PAS/PAC domain |
| SCE1572_6924 | hypothetical protein | - | - | 0 |
| SCE1572_6925 | Transcriptional regulator, LysR family | uni | see_9329 | 47.65 Transcriptional regulator, LysR family |
| SCE1572_6926 | hypothetical protein | - | - | 0 |
| SCE1572_6927 | two component, sigma54 specific, transcriptional regulator, Fis family | uni | see_3234 | 47.89 Type IV fimbriae expression regulatory protein PiIR |
| SCE1572_6928 | turgor pressure sensor | uni | see_1499 | 31.7 Osmosensitive K channel histidine kinase KdpD (EC 2.7.3.-) |
| SCE1572_6929 | Sulfate permease | bi | see_5770 | 32.52 Putative sulfate permease |
| SCE1572_6930 | hypothetical protein | uni | see_2639 | 41.38 hypothetical protein |
| SCE1572_6931 | hypothetical protein | - | - | 0 |
| SCE1572_6932 | Probable glutathione S-transferase-related transmembrane protein (EC 2.5.1.18) | bi | see_5763 | 77.84 Probable glutathione S-transferase-related transmembrane protein (EC 2.5.1.18) |
| SCE1572_6933 | hypothetical protein | - | - | 0 |
| SCE1572_6934 | hypothetical protein | uni | see_8806 | 25.93 hypothetical protein |
| SCE1572_6935 | hypothetical protein | - | - | 0 |
| SCE1572_6936 | hypothetical protein | bi | see_5309 | 27.99 FIG01086732: hypothetical protein |
| SCE1572_6937 | hypothetical protein | bi | see_5766 | 76.15 hypothetical protein |
| SCE1572_6938 | D-aminopeptidase | - | - | 0 |
| SCE1572_6939 | FIG01087559: hypothetical protein | bi | see_5767 | 76.05 FIG01087559: hypothetical protein |
| SCE1572_6940 | DGPF domain protein | bi | see_5768 | 88.19 DGPF domain protein |
| SCE1572_6941 | RNA polymerase sigma-70 factor, ECF subfamily | bi | see_5769 | 86.67 RNA polymerase sigma-70 factor, ECF subfamily |
| SCE1572_6942 | V8-like Glu-specific endopeptidase | bi | see_1680 | 74.16 V8-like Glu-specific endopeptidase |
| SCE1572_6943 | Alcohol dehydrogenase, zinc-binding domain protein(EC:1.6.5.5) | uni | see_9569 | 35.29 Quinone oxidoreductase (EC 1.6.5.5) |
| SCE1572_6944 | hypothetical protein | - | - | 0 |
| SCE1572_6945 | hypothetical protein | uni | see_9883 | 40 FIG01086649: hypothetical protein |
| SCE1572_6946 | hypothetical protein | bi | see_5528 | 65.2 Conserved hypothetical protein 481 |
| SCE1572_6947 | hypothetical protein | bi | see_5773 | 75.69 hypothetical protein |
| SCE1572_6948 | RsbR, positive regulator of sigma-B | bi | see_5835 | 49.82 putative PAS/PAC sensor protein |
| SCE1572_6949 | Cellulase(EC:3.2.1.4) | uni | see_3609 | 24.09 Endo-1,4-beta-xylanase A precursor (EC 3.2.1.8) |
| SCE1572_6950 | conserved domain protein | - | - | 0 |
| SCE1572_6951 | putative cytochrome P450 hydroxylase | uni | see_8024 | 34.79 putative cytochrome P450 hydroxylase |
| SCE1572_6952 | FIG01134227: hypothetical protein | uni | see_4496 | 61.59 Ricin B lectin |
| SCE1572_6953 | NmrA family protein | bi | see_2385 | 89.16 hypothetical protein |
| SCE1572_6954 | transcriptional regulator, AraC family | uni | see_2078 | 39.03 transcriptional regulator, AraC family |
| SCE1572_6955 | Long-chain-fatty-acid-CoA ligase (EC 6.2.1.3) | bi | see_5883 | 60.91 hypothetical protein |
| SCE1572_6956 | Catechol 1,2-dioxygenase(EC:1.13.11.1) | bi | see_177 | 38.73 dioxygenase |
| SCE1572_6957 | hypothetical protein | - | - | 0 |
| SCE1572_6958 | hypothetical protein | - | - | 0 |
| SCE1572_6959 | hypothetical protein | - | - | 0 |
| SCE1572_6960 | Dihydroipoamide acetyltransferase component of pyruvate dehydrogenase complex (EC 2.3.1.12) | bi | see_5775 | 76.21 Dihydroipoamide acetyltransferase component of pyruvate dehydrogenase complex (EC 2.3.1.12) |
| SCE1572_6961 | hypothetical protein | - | - | 0 |
| SCE1572_6962 | 4-Hydroxy-2-oxoglutarate aldolase (EC 4.1.3.16) / 2-dehydro-3-deoxyphosphogluconate aldolase (EC 4.1.2.14) | bi | see_5776 | 89.81 4-Hydroxy-2-oxoglutarate aldolase (EC 4.1.3.16) / 2-dehydro-3-deoxyphosphogluconate aldolase (EC 4.1.2.14) |
| SCE1572_6963 | 2-dehydro-3-deoxygluconate kinase (EC 2.7.1.45) | bi | see_5777 | 90.41 2-dehydro-3-deoxygluconate kinase (EC 2.7.1.45) |
| SCE1572_6964 | Hexuronate transporter | bi | see_5778 | 87.94 Hexuronate transporter |
| SCE1572_6965 | 5-keto-D-gluconate 5-reductase (EC 1.1.1.69) | bi | see_5779 | 87.16 5-keto-D-gluconate 5-reductase (EC 1.1.1.69) |
| SCE1572_6966 | Uronate isomerase, family BH0493 (EC 5.3.1.12) | bi | see_5780 | 89.25 Uronate isomerase, family BH0493 (EC 5.3.1.12) |
| SCE1572_6967 | Glucarate dehydratase (EC 4.2.1.40) | bi | see_5781 | 92.95 Glucarate dehydratase (EC 4.2.1.40) |
| SCE1572_6968 | RsbR, positive regulator of sigma-B | bi | see_5782 | 87.02 RsbR, positive regulator of sigma-B |
| SCE1572_6969 | hypothetical protein | bi | see_5783 | 66.35 hypothetical protein |
| SCE1572_6970 | hypothetical protein | bi | see_5784 | 78.91 hypothetical protein |
| SCE1572_6971 | lysophospholipase-like family protein | - | - | 0 |
| SCE1572_6972 | oligopeptide transporter, OPT family | uni | see_5329 | 32.18 oligopeptide transporter, OPT family |
| SCE1572_6973 | hypothetical protein | - | - | 0 |
| SCE1572_6974 | FIG01087003: hypothetical protein | bi | see_5787 | 74.29 FIG01087003: hypothetical protein |
| SCE1572_6975 | Two component response regulator | bi | see_5788 | 87.1 Two component response regulator |
| SCE1572_6976 | RedC | bi | see_5789 | 75.1 sensor histidine kinase |
| SCE1572_6977 | hypothetical protein | - | - | 0 |
| SCE1572_6978 | Sensory histidine kinase CreB | bi | see_5790 | 82.72 Sensory histidine kinase CreB |
| SCE1572_6979 | RedD | uni | see_6705 | 60.51 RedD |
| SCE1572_6980 | rhamnogalacturonan acetyltransferase | bi | see_5791 | 74.58 rhamnogalacturonan acetyltransferase |
| SCE1572_6981 | EBNA-1 | bi | see_5794 | 73.63 RTX toxins and related Ca ²⁺ proteins |
| SCE1572_6982 | hypothetical protein | bi | see_5796 | 43.3 hypothetical protein |
| SCE1572_6983 | Adenylate cyclase (EC 4.6.1.1) / Guanylate cyclase (EC 4.6.1.2) | bi | see_5797 | 78.76 Adenylate cyclase (EC 4.6.1.1) / Guanylate cyclase (EC 4.6.1.2) |
| SCE1572_6984 | hypothetical protein | bi | see_5799 | 71.82 hypothetical protein |
| SCE1572_6985 | BarH | bi | see_5800 | 86.15 BarH |
| SCE1572_6986 | hypothetical protein | - | - | 0 |
| SCE1572_6987 | Acetoacetate metabolism regulatory protein atnC (Ornithine/arginine decarboxylase inhibitor) (Ornithine decarboxylase antizyme) | uni | see_4822 | 51.07 Acetoacetate metabolism regulatory protein atnC (Ornithine/arginine decarboxylase inhibitor) (Ornithine decarboxylase antizyme) |
| SCE1572_6988 | FIG01085581: hypothetical protein | bi | see_5805 | 76.49 FIG01085581: hypothetical protein |
| SCE1572_6989 | bacterial transcription activator family protein | - | - | 0 |
| SCE1572_6990 | hypothetical protein | - | - | 0 |
| SCE1572_6991 | hypothetical protein | bi | see_5807 | 89.26 hypothetical protein |
| SCE1572_6992 | FIG01087827: hypothetical protein | uni | see_100 | 82.67 FIG01087827: hypothetical protein |
| SCE1572_6993 | flagellar motor protein | bi | see_5811 | 78.18 Tetratricopeptide TPR_2 repeat protein |
| SCE1572_6994 | SB protease | bi | see_5812 | 84.86 SB protease |
| SCE1572_6995 | hypothetical protein | bi | see_5813 | 73.55 hypothetical protein |
| SCE1572_6996 | hypothetical protein | bi | see_5815 | 84 hypothetical protein |
| SCE1572_6997 | hypothetical protein | - | - | 0 |
| SCE1572_6998 | hypothetical protein | - | - | 0 |
| SCE1572_6999 | hypothetical protein | - | - | 0 |
| SCE1572_7000 | hypothetical protein | - | - | 0 |
| SCE1572_7001 | Beta-glucosidase (EC 3.2.1.21) | uni | see_7721 | 38.36 FIG01087134: hypothetical protein |
| SCE1572_7002 | hypothetical protein | - | - | 0 |
| SCE1572_7003 | Similarity | bi | see_3413 | 77.78 Similarity |
| SCE1572_7004 | putative ABC transporter ATP-binding protein | bi | see_5821 | 74.87 ABC transporter, permease/ATP-binding protein, putative |
| SCE1572_7005 | hypothetical protein | bi | see_5822 | 83.93 hypothetical protein |
| SCE1572_7006 | hypothetical protein | - | - | 0 |
| SCE1572_7007 | hypothetical protein | - | - | 0 |
| SCE1572_7008 | hypothetical protein | bi | see_6818 | 86.21 hypothetical protein |
| SCE1572_7009 | PE-PGRS FAMILY PROTEIN | uni | see_9483 | 72.71 FIG01086339: hypothetical protein |
| SCE1572_7010 | FIG01089478: hypothetical protein | uni | see_9482 | 75.77 hypothetical protein |
| SCE1572_7011 | RNA polymerase sigma-H factor | bi | see_9481 | 83.51 RNA polymerase sigma-H factor |
| SCE1572_7012 | hypothetical protein | - | - | 0 |
| SCE1572_7013 | hypothetical protein | - | - | 0 |
| SCE1572_7014 | hypothetical protein | - | - | 0 |
| SCE1572_7015 | hypothetical protein | bi | see_9479 | 72.9 hypothetical protein |
| SCE1572_7016 | hypothetical protein | - | - | 0 |
| SCE1572_7017 | hypothetical protein | - | - | 0 |
| SCE1572_7018 | hypothetical protein, aspartate-rich | uni | see_3180 | 57.14 FIG01089285: hypothetical protein |
| SCE1572_7019 | FIG01089285: hypothetical protein | uni | see_3995 | 52 FIG01089285: hypothetical protein |
| SCE1572_7020 | hypothetical protein | uni | see_10161 | 84.82 hypothetical protein |
| SCE1572_7021 | Transposase | bi | see_10160 | 88.03 Transposase |
| SCE1572_7022 | Mobile element protein | uni | see_6228 | 71.04 Mobile element protein |
| SCE1572_7023 | hypothetical protein | - | - | 0 |
| SCE1572_7024 | hypothetical protein | uni | see_5849 | 38.5 putative secreted protein |
| SCE1572_7025 | hypothetical protein | - | - | 0 |
| SCE1572_7026 | Pyruvate kinase family protein | bi | see_5823 | 83.9 Pyruvate kinase family protein |
| SCE1572_7027 | Serine phosphatase RsbU, regulator of sigma subunit | bi | see_5824 | 82.89 Serine phosphatase RsbU, regulator of sigma subunit |
| SCE1572_7028 | FIG01089073: hypothetical protein | uni | see_5825 | 79.84 FIG01089073: hypothetical protein |
| SCE1572_7029 | Serine phosphatase RsbU, regulator of sigma subunit | bi | see_5827 | 81.6 Serine phosphatase RsbU, regulator of sigma subunit |
| SCE1572_7030 | FIG01087229: hypothetical protein | bi | see_5828 | 83.06 hypothetical protein |
| SCE1572_7031 | FIG01087678: hypothetical protein | bi | see_5829 | 92.72 FIG01087678: hypothetical protein |
| SCE1572_7032 | Serine phosphatase RsbU, regulator of sigma subunit | bi | see_5830 | 80.63 Serine phosphatase RsbU, regulator of sigma subunit |
| SCE1572_7033 | FIG01087229: hypothetical protein | uni | see_5831 | 92.74 FIG01087229: hypothetical protein |
| SCE1572_7034 | FIG01085827: hypothetical protein | bi | see_2591 | 88.96 FIG01085827: hypothetical protein |
| SCE1572_7035 | serine/threonine protein kinase | bi | see_5833 | 86.9 Long-chain-fatty-acid-CoA ligase (EC 6.2.1.3) |
| SCE1572_7036 | FIG01085659: hypothetical protein | bi | see_5834 | 88.6 FIG01085659: hypothetical protein |
| SCE1572_7037 | two component, sigma54 specific, transcriptional regulator, Fis family | uni | see_773 | 55.28 Flagellar regulatory protein FleQ |
| SCE1572_7038 | two component, sigma54 specific, transcriptional regulator, Fis family | uni | see_4034 | 48.66 Response regulator of zinc sigma-54-dependent two-component system |
| SCE1572_7039 | FIG01089256: hypothetical protein | uni | see_9939 | 33.77 FIG01089423: hypothetical protein |
| SCE1572_7040 | hypothetical protein | - | - | 0 |
| SCE1572_7041 | hypothetical protein | bi | see_5839 | 66.98 hypothetical protein |
| SCE1572_7042 | hypothetical protein | - | - | 0 |
| SCE1572_7043 | hypothetical protein | bi | see_9895 | 73.74 hypothetical protein |
| SCE1572_7044 | Gli2764 protein | bi | see_9896 | 95.19 Gli2764 protein |
| SCE1572_7045 | protein kinase | uni | see_7782 | 40.3 serine/threonine protein kinase |
| SCE1572_7046 | hypothetical protein | - | - | 0 |
| SCE1572_7047 | hypothetical protein | - | - | 0 |
| SCE1572_7048 | hypothetical protein | - | - | 0 |
| SCE1572_7049 | response regulator receiver domain/DnaJ domain protein | uni | see_157 | 46.26 hypothetical protein |

| | | | |
|--------------|---|---------------|--|
| SCE1572_7050 | hypothetical protein | - | 0 |
| SCE1572_7051 | hypothetical protein | - | 0 |
| SCE1572_7052 | hypothetical protein | - | 0 |
| SCE1572_7053 | hypothetical protein | - | 0 |
| SCE1572_7054 | hypothetical protein | - | 0 |
| SCE1572_7055 | Chitodextrinase precursor (EC 3.2.1.14) | uni sce_4105 | 33.55 Chitodextrinase precursor (EC 3.2.1.14) |
| SCE1572_7056 | hypothetical protein | - | 0 |
| SCE1572_7057 | hypothetical protein | - | 0 |
| SCE1572_7058 | hypothetical protein | - | 0 |
| SCE1572_7059 | two component, sigma54 specific, transcriptional regulator, Fis family | uni sce_2168 | 51.45 two component, sigma54 specific, transcriptional regulator, Fis family |
| SCE1572_7060 | hypothetical protein | - | 0 |
| SCE1572_7061 | hypothetical protein | - | 0 |
| SCE1572_7062 | hypothetical protein | - | 0 |
| SCE1572_7063 | Branched-chain amino acid ABC transporter, amino acid-binding protein (TC 3.A.1.4.1) | uni sce_7667 | 52.08 FIGO1085006: hypothetical protein |
| SCE1572_7064 | S-layer protein | uni sce_3992 | 42.24 S-layer-like array protein |
| SCE1572_7065 | Serine/threonine-protein kinase pkn3 (EC 2.7.11.1) | uni sce_7827 | 49.67 Cytochrome c551 peroxidase (EC 1.11.1.5) |
| SCE1572_7066 | hypothetical protein | uni sce_7404 | 48.68 Mobile element protein |
| SCE1572_7067 | hypothetical protein | - | 0 |
| SCE1572_7068 | hypothetical protein | bi sce_5840 | 85.17 hypothetical protein |
| SCE1572_7069 | Uncharacterized glutathione S-transferase-like protein | bi sce_1257 | 52.05 Uncharacterized glutathione S-transferase-like protein |
| SCE1572_7070 | hypothetical protein | - | 0 |
| SCE1572_7071 | Transcriptional regulator, HxIR family | uni sce_2658 | 33.04 Transcriptional regulator, HxIR family |
| SCE1572_7072 | putative secreted protein | bi sce_5849 | 83.18 putative secreted protein |
| SCE1572_7073 | hypothetical protein | - | 0 |
| SCE1572_7074 | glutathione-dependent formaldehyde-activating, GFA | bi sce_5850 | 82.12 glutathione-dependent formaldehyde-activating, GFA |
| SCE1572_7075 | Transcriptional regulator, DeoR family | bi sce_5851 | 84.88 Transcriptional regulator, DeoR family |
| SCE1572_7076 | FIGO1085614: hypothetical protein | bi sce_5854 | 83.8 FIGO1085614: hypothetical protein |
| SCE1572_7077 | hypothetical protein | - | 0 |
| SCE1572_7078 | hypothetical protein | - | 0 |
| SCE1572_7079 | hypothetical protein | bi sce_5855 | 94.23 hypothetical protein |
| SCE1572_7080 | FIGO1088289: hypothetical protein | bi sce_5856 | 82.45 FIGO1088289: hypothetical protein |
| SCE1572_7081 | peptidase C14, caspase catalytic subunit p20 | bi sce_5857 | 83.65 hypothetical protein |
| SCE1572_7082 | FIGO1085964: hypothetical protein | uni sce_5858 | 66.45 FIGO1085964: hypothetical protein |
| SCE1572_7083 | FIGO1087316: hypothetical protein | bi sce_5859 | 88.82 FIGO1087316: hypothetical protein |
| SCE1572_7084 | Endo-1,4-beta-glucanase | bi sce_5860 | 74.19 Endo-1,4-beta-glucanase |
| SCE1572_7085 | Beta-glucosidase (EC 3.2.1.21) | uni sce_4706 | 32.69 Beta-glucosidase (EC 3.2.1.21) |
| SCE1572_7086 | PE-PGRS FAMILY PROTEIN [SECOND PART] | bi sce_9905 | 86.52 PE-PGRS FAMILY PROTEIN |
| SCE1572_7087 | Collagen triple helix repeat | uni sce_6814 | 67.49 PE-PGRS FAMILY PROTEIN |
| SCE1572_7088 | hypothetical protein | uni sce_9794 | 63.66 FIGO1089478: hypothetical protein |
| SCE1572_7089 | RNA polymerase sigma factor SigW | uni sce_9902 | 56.91 RNA polymerase sigma factor SigW |
| SCE1572_7090 | hypothetical protein | - | 0 |
| SCE1572_7091 | conserved hypothetical protein | bi sce_5861 | 89.1 conserved hypothetical protein |
| SCE1572_7092 | hypothetical protein | - | 0 |
| SCE1572_7093 | Methyltransferase type 11 | uni sce_6296 | 40.95 putative methyltransferase |
| SCE1572_7094 | hypothetical protein | - | 0 |
| SCE1572_7095 | Single-stranded DNA-binding protein | bi sce_5863 | 69.23 Single-stranded DNA-binding protein |
| SCE1572_7096 | FIGO1088501: hypothetical protein | bi sce_1560 | 79.41 FIGO1088501: hypothetical protein |
| SCE1572_7097 | hypothetical protein | bi sce_1561 | 82.9 hypothetical protein |
| SCE1572_7098 | serine/threonine protein kinase | bi sce_1562 | 75 Serine/threonine-protein kinase pkn3 (EC 2.7.11.1) |
| SCE1572_7099 | hypothetical protein | uni sce_7807 | 72 hypothetical protein |
| SCE1572_7100 | hypothetical protein | bi sce_5868 | 80.47 hypothetical protein |
| SCE1572_7101 | Inner membrane protein YqiK | bi sce_5869 | 94.05 Inner membrane protein YqiK |
| SCE1572_7102 | conserved hypothetical protein-putative thiol-disulfide isomerase or thioredoxin | bi sce_5870 | 79.91 hypothetical protein |
| SCE1572_7103 | hypothetical protein | - | 0 |
| SCE1572_7104 | Tat (Twin-arginine translocation) pathway signal sequence domain protein | bi sce_5836 | 90.69 Tat (Twin-arginine translocation) pathway signal sequence domain protein |
| SCE1572_7105 | Cellulose-binding domain protein | bi sce_5837 | 88.3 Cellulose-binding domain protein |
| SCE1572_7106 | hypothetical protein | - | 0 |
| SCE1572_7107 | PE-PGRS FAMILY PROTEIN | uni sce_8050 | 39.22 FIGO1087571: hypothetical protein |
| SCE1572_7108 | hypothetical protein | - | 0 |
| SCE1572_7109 | hypothetical protein | bi sce_1435 | 72.83 hypothetical protein |
| SCE1572_7110 | hypothetical protein | - | 0 |
| SCE1572_7111 | outer membrane protein OmpA | uni sce_77 | 41.72 outer membrane protein OmpA |
| SCE1572_7112 | hypothetical protein | - | 0 |
| SCE1572_7113 | Amidohydrolase 3 | uni sce_3442 | 32.3 Amidohydrolase 3 |
| SCE1572_7114 | Indigoidine synthase A-like protein, uncharacterized enzyme involved in pigment biosynthesis | bi sce_7551 | 89.14 Indigoidine synthase A-like protein, uncharacterized enzyme involved in pigment biosynthesis |
| SCE1572_7115 | Ribokinase (EC 2.7.1.15) | uni sce_4216 | 39.62 Ribokinase (EC 2.7.1.15) |
| SCE1572_7116 | acetoin utilization protein AcuB | uni sce_54 | 36.36 hypothetical protein |
| SCE1572_7117 | FIGO1043599: hypothetical protein | uni sce_2008 | 30.52 Probable lipoprotein signal peptide |
| SCE1572_7118 | FIGO1086649: hypothetical protein | bi sce_9883 | 71.49 FIGO1086649: hypothetical protein |
| SCE1572_7119 | Tenascin-X | uni sce_7238 | 57.75 Tenascin-X |
| SCE1572_7120 | Band 7 protein | - | 0 |
| SCE1572_7121 | hypothetical protein | - | 0 |
| SCE1572_7122 | Multiple EGF-like-domain protein 3 precursor | bi sce_5871 | 82.3 Multiple EGF-like-domain protein 3 precursor |
| SCE1572_7123 | hypothetical protein | uni sce_9036 | 38.67 200 kDa antigen p200, putative |
| SCE1572_7124 | hypothetical protein | bi sce_5872 | 90.38 hypothetical protein |
| SCE1572_7125 | unknown | bi sce_5874 | 91.44 hypothetical protein |
| SCE1572_7126 | hypothetical protein | - | 0 |
| SCE1572_7127 | hypothetical protein | - | 0 |
| SCE1572_7128 | hypothetical protein | - | 0 |
| SCE1572_7129 | hypothetical protein | - | 0 |
| SCE1572_7130 | peptidase S8 and S53, subtilisin, kexin, sedolisin | uni sce_9684 | 33.04 Protease |
| SCE1572_7131 | hypothetical protein | bi sce_8424 | 84.51 hypothetical protein |
| SCE1572_7132 | hypothetical protein | bi sce_3684 | 85.38 hypothetical protein |
| SCE1572_7133 | RsbR, positive regulator of sigma-B | bi sce_5482 | 85.85 RsbR, positive regulator of sigma-B |
| SCE1572_7134 | NTP pyrophosphohydrolases including oxidative damage repair enzymes | bi sce_6324 | 85.85 hypothetical protein |
| SCE1572_7135 | L-lactate dehydrogenase (EC 1.1.1.27) | bi sce_5876 | 93.75 L-lactate dehydrogenase (EC 1.1.1.27) |
| SCE1572_7136 | probable integral membrane protein | bi sce_5877 | 82.4 hypothetical protein |
| SCE1572_7137 | hypothetical protein | - | 0 |
| SCE1572_7138 | FIGO1086383: hypothetical protein | uni sce_2804 | 39.27 FIGO1086383: hypothetical protein |
| SCE1572_7139 | hypothetical protein | - | 0 |
| SCE1572_7140 | hypothetical protein | - | 0 |
| SCE1572_7141 | Glucokinase (EC 2.7.1.2) | uni sce_5843 | 62.86 hypothetical protein |
| SCE1572_7142 | HlyD family secretion protein | - | 0 |
| SCE1572_7143 | FIGO1086605: hypothetical protein | bi sce_301 | 61.64 FIGO1086605: hypothetical protein |
| SCE1572_7144 | O-acetylhomoserine sulphydrylase (EC 2.5.1.49) / O-succinylhomoserine sulphydrylase (EC 2.5.1.48) | bi sce_5878 | 92.57 O-acetylhomoserine sulphydrylase (EC 2.5.1.49) / O-succinylhomoserine sulphydrylase (EC 2.5.1.48) |
| SCE1572_7145 | hypothetical protein | uni sce_8433 | 28.43 GII1489 protein |
| SCE1572_7146 | hypothetical protein | bi sce_5879 | 73.91 hypothetical protein |
| SCE1572_7147 | Radical SAM domain protein | bi sce_5880 | 92.67 radical SAM domain protein |
| SCE1572_7148 | HAMP domain protein | bi sce_5885 | 91.51 HAMP domain protein |
| SCE1572_7149 | FIGO1089025: hypothetical protein | bi sce_5886 | 94 FIGO1089025: hypothetical protein |
| SCE1572_7150 | Fibronectin/fibrinogen-binding protein | bi sce_5887 | 88.74 Fibronectin/fibrinogen-binding protein |
| SCE1572_7151 | hypothetical protein | bi sce_5889 | 49.61 NADH-ubiquinone oxidoreductase chain J (EC 1.6.5.3) |
| SCE1572_7152 | Sulfatase modifying factor 2 precursor (C-alpha-formylglycine- generating enzyme 2) | uni sce_5890 | 95.53 putative serine/threonine protein kinase |
| SCE1572_7153 | FIGO1085516: hypothetical protein | bi sce_1454 | 84.19 FIGO1085516: hypothetical protein |
| SCE1572_7154 | hypothetical protein | - | 0 |
| SCE1572_7155 | FIGO1088355: hypothetical protein | bi sce_5893 | 70.11 FIGO1088355: hypothetical protein |
| SCE1572_7156 | hypothetical protein | uni sce_157 | 48.64 hypothetical protein |
| SCE1572_7157 | O-methyltransferase, family 2 | bi sce_1355 | 28.48 O-methyltransferase, family 2 |
| SCE1572_7158 | Peptidyl-prolyl cis-trans isomerase (EC 5.2.1.8) | uni sce_8326 | 47.27 putative secreted protein |
| SCE1572_7159 | lipoprotein, putative | bi sce_5894 | 87.8 lipoprotein, putative |
| SCE1572_7160 | transcriptional regulator, LysR family | uni sce_3645 | 41.89 Transcriptional regulator, LysR family |
| SCE1572_7161 | FIGO1087828: hypothetical protein | bi sce_5895 | 70.37 FIGO1087828: hypothetical protein |
| SCE1572_7162 | putative oxidoreductase | bi sce_5896 | 91.33 putative oxidoreductase |
| SCE1572_7163 | Fumarylacetoacetase (EC 3.7.1.2) | bi sce_5897 | 90.94 Fumarylacetoacetase (EC 3.7.1.2) |
| SCE1572_7164 | N-Acetyl-D-glucosamine ABC transport system, permease protein 2 | bi sce_3432 | 40.77 N-Acetyl-D-glucosamine ABC transport system, permease protein 2 |
| SCE1572_7165 | FIGO0816855: hypothetical protein | uni sce_10351 | 36.1 N-Acetyl-D-glucosamine ABC transport system, permease protein 1 |
| SCE1572_7166 | ABC transporter, sugar binding protein | uni sce_858 | 26.41 N-Acetyl-D-glucosamine ABC transport system, sugar-binding protein |
| SCE1572_7167 | Transcriptional regulator, TetR family | uni sce_9220 | 59.62 Transcriptional regulator, TetR family |
| SCE1572_7168 | hypothetical protein | bi sce_5100 | 27.55 Type II secretory pathway, ATPase Pule/Tif pilus assembly pathway, ATPase PilB |
| SCE1572_7169 | TPR repeat | uni sce_2 | 27.7 Serine/threonine protein kinase PrkC, regulator of stationary phase |
| SCE1572_7170 | Vancomycin B-type resistance protein VanW | bi sce_5899 | 85.36 Vancomycin B-type resistance protein VanW |
| SCE1572_7171 | Sulfur carrier protein ThiS | bi sce_5900 | 90.91 Sulfur carrier protein ThiS |
| SCE1572_7172 | carbonic anhydrase, family 3 | bi sce_5901 | 84 carbonic anhydrase, family 3 |
| SCE1572_7173 | tRNA-(i(6)A37 methylthio)transferase | bi sce_5902 | 93.98 tRNA-(i(6)A37 methylthio)transferase |
| SCE1572_7174 | hypothetical protein | - | 0 |
| SCE1572_7175 | Long-chain-fatty-acid-CoA ligase (EC 6.2.1.3) | bi sce_5904 | 87.46 Long-chain-fatty-acid-CoA ligase (EC 6.2.1.3) |
| SCE1572_7176 | Proline iminopeptidase (EC 3.4.11.5) | bi sce_5905 | 91.88 Proline iminopeptidase (EC 3.4.11.5) |
| SCE1572_7177 | hypothetical protein | - | 0 |
| SCE1572_7178 | Endo-1,4-beta-xylanase A precursor (EC 3.2.1.8) | bi sce_2175 | 83.02 Endo-1,4-beta-xylanase A precursor (EC 3.2.1.8) |
| SCE1572_7179 | signal transduction histidine kinase, LysS | - | 0 |
| SCE1572_7180 | two-component response regulator LysR | uni sce_5455 | 33.09 two-component transcriptional regulator (OmpR family), BaeR/ChvL/OmpR-like protein |
| SCE1572_7181 | beta-lactamase | bi sce_6290 | 29.71 FIGO1086026: hypothetical protein |
| SCE1572_7182 | LysR family transcriptional regulator YnfL | bi sce_1246 | 91.51 LysR family transcriptional regulator YnfL |
| SCE1572_7183 | O-methyltransferase (EC 2.1.1.-) | bi sce_1245 | 80.42 O-methyltransferase (EC 2.1.1.-) |
| SCE1572_7184 | hypothetical protein | - | 0 |
| SCE1572_7185 | FIGO1087280: hypothetical protein | bi sce_5906 | 90.91 FIGO1087280: hypothetical protein |
| SCE1572_7186 | Putative fatty acid transport system, membrane protein | bi sce_5907 | 83.57 Putative fatty acid transport system, membrane protein |
| SCE1572_7187 | FIGO1087195: hypothetical protein | bi sce_5908 | 77.02 FIGO1087195: hypothetical protein |
| SCE1572_7188 | N-acetylglucosamine-1-phosphate uridylyltransferase (EC 2.7.7.23) / Glucosamine-1-phosphate N-acetyltransferase (EC 2.3.1.15) | bi sce_5909 | 91.7 N-acetylglucosamine-1-phosphate uridylyltransferase (EC 2.7.7.23) / Glucosamine-1-phosphate N-acetyltransferase (EC 2.3.1.15) |
| SCE1572_7189 | Copper sensory histidine kinase CpxA | bi sce_1882 | 50.46 Copper sensory histidine kinase CpxA |
| SCE1572_7190 | two component, sigma54 specific, transcriptional regulator, Fis family | bi sce_1881 | 71.24 two component, sigma54 specific, transcriptional regulator, Fis family |
| SCE1572_7191 | GTP cyclohydrolase II (EC 3.5.4.25) | bi sce_5914 | 91.27 GTP cyclohydrolase II (EC 3.5.4.25) |
| SCE1572_7192 | hypothetical protein | - | 0 |
| SCE1572_7193 | Acyl-CoA dehydrogenase (EC 1.3.99.3) | bi sce_5915 | 86 Acyl-CoA dehydrogenase (EC 1.3.99.3) |
| SCE1572_7194 | hypothetical protein | - | 0 |
| SCE1572_7195 | COG3391: Uncharacterized conserved protein | - | 0 |
| SCE1572_7196 | Acyl-CoA dehydrogenase (EC 1.3.99.3) | - | 0 |
| SCE1572_7197 | 2-polypropenyl-6-methoxyphenol hydroxylase and related FAD-dependent oxidoreductases | uni sce_2498 | 79.91 2-polypropenyl-6-methoxyphenol hydroxylase and related FAD-dependent oxidoreductases |
| SCE1572_7198 | (MTV023.15), len: 1901. Member of Mycobacterium tuberculosis PE protein family, Gly-rich PGRS subfamily, most similar to | uni sce_8582 | 40.88 FIGO1089363: hypothetical protein |
| SCE1572_7199 | Hydrolase (HAD superfamily) | bi sce_8384 | 89.43 Hydrolase (HAD superfamily) |
| SCE1572_7200 | RND multidrug efflux transporter, Acriflavin resistance protein | bi sce_5918 | 93.9 RND multidrug efflux transporter, Acriflavin resistance protein |
| SCE1572_7201 | Probable RND efflux membrane fusion protein | bi sce_5919 | 82.37 Probable RND efflux membrane fusion protein |
| SCE1572_7202 | FIGO1086577: hypothetical protein | uni sce_1209 | 39.25 FIGO1086577: hypothetical protein |
| SCE1572_7203 | hypothetical protein | uni sce_10265 | 81.48 hypothetical protein |
| SCE1572_7204 | hypothetical protein | uni sce_5242 | 50 FIGO1085364: hypothetical protein |
| SCE1572_7205 | hypothetical protein | uni sce_8568 | 43.83 hypothetical protein |
| SCE1572_7206 | FIGO1087763: hypothetical protein | bi sce_5924 | 76.57 FIGO1087763: hypothetical protein |
| SCE1572_7207 | hydrolase, haloacid dehalogenase-like family | bi sce_5926 | 88.34 hydrolase, haloacid dehalogenase-like family |
| SCE1572_7208 | putative methyltransferase | bi sce_5920 | 63.75 Methyltransferase |
| SCE1572_7209 | DNA polymerase III delta subunit (EC 2.7.7.7) | bi sce_5936 | 90.25 DNA polymerase III delta subunit (EC 2.7.7.7) |
| SCE1572_7210 | hypothetical protein | bi sce_5937 | 70.59 hypothetical protein |
| SCE1572_7211 | Arsenical pump membrane protein | bi sce_5938 | 88 arsenical pump membrane protein |
| SCE1572_7212 | hypothetical protein | bi sce_5939 | 77.59 FIGO1087896: hypothetical protein |
| SCE1572_7213 | hypothetical protein | - | 0 |

| | | | | |
|--------------|--|-----|-----------|--|
| SCE1572_7214 | 3-oxoacyl-[acyl-carrier protein] reductase (EC 1.1.1.100) | bi | sce_5941 | 81.42 3-oxoacyl-[acyl-carrier protein] reductase (EC 1.1.1.100) |
| SCE1572_7215 | hypothetical protein | umi | sce_9755 | 56.19 Large exoproteins involved in heme utilization or adhesion |
| SCE1572_7216 | hypothetical protein | bi | sce_5944 | 87.14 hypothetical protein |
| SCE1572_7217 | Enoyl-[acyl-carrier-protein] reductase [FMN] (EC 1.3.1.9) | umi | sce_2062 | 28.76 Enoyl-[acyl-carrier-protein] reductase [FMN] (EC 1.3.1.9) |
| SCE1572_7218 | hypothetical protein | umi | sce_1644 | 25.97 FIG01088446: hypothetical protein |
| SCE1572_7219 | Outer membrane lipoprotein omp16 precursor | bi | sce_5945 | 84.55 Outer membrane lipoprotein omp16 precursor |
| SCE1572_7220 | FIG01086986: hypothetical protein | bi | sce_5946 | 80 FIG01086986: hypothetical protein |
| SCE1572_7221 | ATP-dependent RNA helicase, DEAD/DEAH box family | umi | sce_5947 | 85.47 ATP-dependent RNA helicase, DEAD/DEAH box family |
| SCE1572_7222 | ATP-dependent RNA helicase, DEAD/DEAH box family | bi | sce_5947 | 92.44 ATP-dependent RNA helicase, DEAD/DEAH box family |
| SCE1572_7223 | Chitinase (EC 3.2.1.14) | bi | sce_5948 | 84.19 Chitinase (EC 3.2.1.14) |
| SCE1572_7224 | Naphthoate synthase (EC 4.1.3.36) | bi | sce_5950 | 97.99 Naphthoate synthase (EC 4.1.3.36) |
| SCE1572_7225 | RsbR, positive regulator of sigma-B | bi | sce_5951 | 80.73 RsbR, positive regulator of sigma-B |
| SCE1572_7226 | FIG01087334: hypothetical protein | bi | sce_5952 | 71.9 FIG01087334: hypothetical protein |
| SCE1572_7227 | hypothetical protein | bi | sce_5953 | 83.03 Serine/threonine-protein kinase pknI (EC 2.7.11.1) |
| SCE1572_7228 | hypothetical protein | bi | sce_5954 | 84.26 hypothetical protein |
| SCE1572_7229 | serine/threonine protein kinase | bi | sce_5955 | 77.81 serine/threonine protein kinase |
| SCE1572_7230 | hypothetical protein | - | - | 0 |
| SCE1572_7231 | hypothetical protein | - | - | 0 |
| SCE1572_7232 | hypothetical protein | umi | sce_8433 | 30 GII489 protein |
| SCE1572_7233 | FIG01085539: hypothetical protein | umi | sce_1419 | 65.04 FIG01085539: hypothetical protein |
| SCE1572_7234 | FIG01088874: hypothetical protein | bi | sce_5956 | 65.81 FIG01088874: hypothetical protein |
| SCE1572_7235 | serine/threonine protein kinase | bi | sce_5957 | 82.13 serine/threonine protein kinase |
| SCE1572_7236 | serine/threonine protein kinase | bi | sce_5958 | 80.31 serine/threonine protein kinase |
| SCE1572_7237 | CysteinyI-rRNA synthetase (EC 6.1.1.16) | bi | sce_5960 | 91.41 CysteinyI-rRNA synthetase (EC 6.1.1.16) |
| SCE1572_7238 | Similarity | bi | sce_5962 | 76.34 Similarity |
| SCE1572_7239 | Fumarate hydratase class II (EC 4.2.1.2) | umi | sce_10196 | 83.05 Fumarate hydratase class II (EC 4.2.1.2) |
| SCE1572_7240 | N-hydroxyarylamine O-acetyltransferase (EC 2.3.1.118) | bi | sce_5963 | 75.93 N-hydroxyarylamine O-acetyltransferase (EC 2.3.1.118) |
| SCE1572_7241 | Signal transduction histidine kinase CheA (EC 2.7.3.-) | umi | sce_6107 | 46.69 Signal transduction histidine kinase CheA (EC 2.7.3.-) |
| SCE1572_7242 | Twitching motility protein PII | bi | sce_5964 | 96.07 Twitching motility protein PII |
| SCE1572_7243 | Twitching motility protein PII | bi | sce_5965 | 84.05 Twitching motility protein PII |
| SCE1572_7244 | hypothetical protein | - | - | 0 |
| SCE1572_7245 | FIG01087216: hypothetical protein | bi | sce_5966 | 76.7 FIG01087216: hypothetical protein |
| SCE1572_7246 | hypothetical protein | bi | sce_5968 | 90.12 hypothetical protein |
| SCE1572_7247 | hypothetical protein | - | - | 0 |
| SCE1572_7248 | FIG01088842: hypothetical protein | bi | sce_5969 | 90.91 FIG01088842: hypothetical protein |
| SCE1572_7249 | Conserved domain protein | umi | sce_2378 | 59.88 Conserved domain protein |
| SCE1572_7250 | Conserved domain protein | bi | sce_2378 | 61.94 Conserved domain protein |
| SCE1572_7251 | hypothetical protein | - | - | 0 |
| SCE1572_7252 | FIG01088157: hypothetical protein | bi | sce_2379 | 56.82 FIG01088157: hypothetical protein |
| SCE1572_7253 | Cytochrome oxidase biogenesis protein Sco1/SenC/PrrC, putative copper metallochaperone | bi | sce_2380 | 63.11 Cytochrome oxidase biogenesis protein Sco1/SenC/PrrC, putative copper metallochaperone |
| SCE1572_7254 | cytochrome c, putative | bi | sce_2382 | 51.64 Fibronin |
| SCE1572_7255 | Dihydroxy-acid dehydratase (EC 4.2.1.9) | bi | sce_5970 | 95.52 Dihydroxy-acid dehydratase (EC 4.2.1.9) |
| SCE1572_7256 | LOC432261 protein | bi | sce_5971 | 75 LOC432261 protein |
| SCE1572_7257 | Cobalamin biosynthesis protein BluB @ 5,6-dimethylbenzimidazole synthase, flavin destructase family | bi | sce_5537 | 44.2 Cobalamin biosynthesis protein BluB @ 5,6-dimethylbenzimidazole synthase, flavin destructase family / Nicotinate-nucleotide-dim |
| SCE1572_7258 | D-amino-acid oxidase (EC 1.4.3.3) | bi | sce_5972 | 84.74 D-amino-acid oxidase (EC 1.4.3.3) |
| SCE1572_7259 | hypothetical protein | - | - | 0 |
| SCE1572_7260 | Beta-carotene hydroxylase | bi | sce_5973 | 88.15 Beta-carotene hydroxylase |
| SCE1572_7261 | hypothetical protein | - | - | 0 |
| SCE1572_7262 | glutathione S-transferase (EC 2.5.1.18) | umi | sce_2458 | 30.94 Glutathione S-transferase (EC 2.5.1.18) |
| SCE1572_7263 | alpha/beta hydrolase fold | bi | sce_5978 | 77.59 Alpha/beta hydrolase fold |
| SCE1572_7264 | hypothetical protein | - | - | 0 |
| SCE1572_7265 | FIG01086694: hypothetical protein | bi | sce_5979 | 82.28 FIG01086694: hypothetical protein |
| SCE1572_7266 | hypothetical protein | - | - | 0 |
| SCE1572_7267 | Thrombospondin 4 precursor | umi | sce_3978 | 54.17 Thrombospondin-1 precursor |
| SCE1572_7268 | FIG01085038: hypothetical protein | umi | sce_5980 | 77.36 FIG01085038: hypothetical protein |
| SCE1572_7269 | hypothetical protein | umi | sce_3489 | 50.76 hypothetical protein |
| SCE1572_7270 | serine/threonine protein kinase | bi | sce_5982 | 79.7 serine/threonine protein kinase |
| SCE1572_7271 | Macrophage infectivity potentiator-related protein | bi | sce_6026 | 91.53 COG2128: Uncharacterized conserved protein |
| SCE1572_7272 | Transcriptional regulator, MarR family | bi | sce_6025 | 93.51 Transcriptional regulator, MarR family |
| SCE1572_7273 | hypothetical protein | - | - | 0 |
| SCE1572_7274 | hypothetical protein | umi | sce_7696 | 86.96 FIG01087243: hypothetical protein |
| SCE1572_7275 | hypothetical protein | bi | sce_6816 | 79.68 hypothetical protein |
| SCE1572_7276 | predicted protein | umi | sce_7695 | 68.06 predicted protein |
| SCE1572_7277 | hypothetical protein | bi | sce_7693 | 84.31 hypothetical protein |
| SCE1572_7278 | hypothetical protein | umi | sce_7692 | 62.93 hypothetical protein |
| SCE1572_7279 | hypothetical protein | bi | sce_629 | 66.67 hypothetical protein |
| SCE1572_7280 | Permease of the drug/metabolite transporter (DMT) superfamily | bi | sce_5983 | 81.43 Permease of the drug/metabolite transporter (DMT) superfamily |
| SCE1572_7281 | FIG01086592: hypothetical protein | bi | sce_5984 | 82.73 FIG01086592: hypothetical protein |
| SCE1572_7282 | hypothetical protein | bi | sce_5986 | 87.55 FIG01103339: hypothetical protein |
| SCE1572_7283 | Beta-lactamase (EC 3.5.2.6) | bi | sce_5987 | 83.88 Beta-lactamase (EC 3.5.2.6) |
| SCE1572_7284 | hypothetical protein | umi | sce_8804 | 38.6 FIG01086715: hypothetical protein |
| SCE1572_7285 | Glucose-1-phosphate adenyltransferase (EC 2.7.7.27) | bi | sce_5988 | 93.81 Glucose-1-phosphate adenyltransferase (EC 2.7.7.27) |
| SCE1572_7286 | Aspartate-semialdehyde dehydrogenase (EC 1.2.1.11) | bi | sce_5989 | 92.15 Aspartate-semialdehyde dehydrogenase (EC 1.2.1.11) |
| SCE1572_7287 | Nudix hydrolase family protein YfH | bi | sce_5990 | 97.41 Nudix hydrolase family protein YfH |
| SCE1572_7288 | hypothetical protein | bi | sce_6130 | 91.97 hypothetical protein |
| SCE1572_7289 | hypothetical protein | umi | sce_1421 | 30.63 Usg protein |
| SCE1572_7290 | FIG01089430: hypothetical protein | bi | sce_5991 | 88.06 FIG01089430: hypothetical protein |
| SCE1572_7291 | hypothetical protein | - | - | 0 |
| SCE1572_7292 | hypothetical protein | umi | sce_10035 | 30.23 Phosphatidylglycerophosphatase B (EC 3.1.3.27) |
| SCE1572_7293 | glucose-fructose oxidoreductase | - | - | 0 |
| SCE1572_7294 | hypothetical protein | umi | sce_6851 | 53.15 FIG01085217: hypothetical protein |
| SCE1572_7295 | putative cytochrome P450 hydroxylase | umi | sce_8803 | 35.66 putative cytochrome P450 hydroxylase |
| SCE1572_7296 | Transcriptional regulator, LysR family | bi | sce_6071 | 85.21 Transcriptional regulator, LysR family |
| SCE1572_7297 | hypothetical protein | bi | sce_6072 | 86.09 hypothetical protein |
| SCE1572_7298 | hypothetical protein | bi | sce_6074 | 87.88 probable conserved hypothetical protein |
| SCE1572_7299 | High-affinity carbon uptake protein Hat/HatR | bi | sce_3003 | 87.26 High-affinity carbon uptake protein Hat/HatR |
| SCE1572_7300 | Nitrate/nitrite response regulator protein | bi | sce_3004 | 89.57 Nitrate/nitrite response regulator protein |
| SCE1572_7301 | hypothetical protein | - | - | 0 |
| SCE1572_7302 | hypothetical protein | bi | sce_2466 | 47.27 hypothetical protein |
| SCE1572_7303 | cAMP-binding proteins - catabolite gene activator and regulatory subunit of cAMP-dependent protein kinases | bi | sce_5169 | 89.16 cAMP-binding proteins - catabolite gene activator and regulatory subunit of cAMP-dependent protein kinases |
| SCE1572_7304 | ThiJ/Pfj family protein | bi | sce_5168 | 86.35 ThiJ/Pfj family protein |
| SCE1572_7305 | Uncharacterized protein with a C-terminal OMP (outer membrane protein) domain | bi | sce_2493 | 80.87 Uncharacterized protein with a C-terminal OMP (outer membrane protein) domain |
| SCE1572_7306 | hypothetical protein | - | - | 0 |
| SCE1572_7307 | GIY-YIG catalytic domain protein | umi | sce_8277 | 34.31 Excinuclease ABC subunit C |
| SCE1572_7308 | FIG01086542: hypothetical protein | bi | sce_10414 | 87.5 FIG01086542: hypothetical protein |
| SCE1572_7309 | Conserved protein, with a weak D-galactarate dehydratase/alttronate hydrolase domain | umi | sce_4708 | 62.72 hypothetical protein |
| SCE1572_7310 | D-AMINOPEPTIDASE (EC 3.4.11.19) | bi | sce_6091 | 85.6 D-AMINOPEPTIDASE (EC 3.4.11.19) |
| SCE1572_7311 | Signal transduction histidine kinase CheA (EC 2.7.3.-) | bi | sce_6095 | 75.87 Signal transduction histidine kinase CheA (EC 2.7.3.-) |
| SCE1572_7312 | phosphoglycerate mutase | umi | sce_3668 | 35.58 Phosphoglycerate mutase |
| SCE1572_7313 | PEBP family protein | bi | sce_3000 | 59.55 conserved hypothetical protein |
| SCE1572_7314 | AmpG permease | umi | sce_1005 | 43.75 AmpG permease |
| SCE1572_7315 | transcriptional regulator, TetR family | umi | sce_1534 | 40 Transcriptional regulator, TetR family |
| SCE1572_7316 | hypothetical protein | - | - | 0 |
| SCE1572_7317 | putative immediate early protein | umi | sce_9154 | 48.31 PE-PGRS family protein |
| SCE1572_7318 | Trypsin domain protein | - | - | 0 |
| SCE1572_7319 | Ribosomal-protein-S5p-alanine acetyltransferase | bi | sce_6109 | 80.98 acetyltransferase, GNAT family protein |
| SCE1572_7320 | putative lipoprotein | bi | sce_6418 | 40.41 FIG01088727: hypothetical protein |
| SCE1572_7321 | Potassium efflux system KefA protein / Small-conductance mechanosensitive channel | bi | sce_6110 | 46.88 Potassium efflux system KefA protein / Small-conductance mechanosensitive channel |
| SCE1572_7322 | ribonuclease E | umi | sce_3858 | 36.43 Adenosylhomocysteinase (EC 3.3.1.1) |
| SCE1572_7323 | Collagen triple helix repeat domain protein | bi | sce_6111 | 84.62 Phage tail fiber protein |
| SCE1572_7324 | hypothetical protein | - | - | 0 |
| SCE1572_7325 | Exopolysaccharide biosynthesis glycosyltransferase EpsF (EC 2.4.1.-) | bi | sce_6112 | 91.58 Exopolysaccharide biosynthesis glycosyltransferase EpsF (EC 2.4.1.-) |
| SCE1572_7326 | serine/threonine protein kinase | bi | sce_6113 | 77.89 serine/threonine protein kinase |
| SCE1572_7327 | FIG01088683: hypothetical protein | bi | sce_6114 | 87.11 FIG01088683: hypothetical protein |
| SCE1572_7328 | hypothetical protein | - | - | 0 |
| SCE1572_7329 | FIG01087912: hypothetical protein | bi | sce_6116 | 82.66 FIG01087912: hypothetical protein |
| SCE1572_7330 | FIG01089567: hypothetical protein | bi | sce_6117 | 77.88 FIG01089567: hypothetical protein |
| SCE1572_7331 | hypothetical protein | - | - | 0 |
| SCE1572_7332 | FIG01089567: hypothetical protein | bi | sce_6119 | 71.18 FIG01089567: hypothetical protein |
| SCE1572_7333 | hypothetical protein | - | - | 0 |
| SCE1572_7334 | BchE/P-methylase family protein | bi | sce_6120 | 95.74 BchE/P-methylase family protein |
| SCE1572_7335 | Extensin-like protein | umi | sce_2189 | 36.63 hypothetical protein-transmembrane region and signal peptide prediction |
| SCE1572_7336 | Glutathione-regulated potassium-efflux system protein KefC | bi | sce_6121 | 89.33 Glutathione-regulated potassium-efflux system protein KefC |
| SCE1572_7337 | Response regulator of zinc sigma-54-dependent two-component system | bi | sce_6122 | 96.56 Response regulator of zinc sigma-54-dependent two-component system |
| SCE1572_7338 | Serine/threonine protein kinase (EC 2.7.11.1) | bi | sce_6123 | 80.08 Serine/threonine protein kinase (EC 2.7.11.1) |
| SCE1572_7339 | hypothetical protein | bi | sce_6124 | 97.67 hypothetical protein |
| SCE1572_7340 | Phage shock protein A | bi | sce_6125 | 96.76 Phage shock protein A |
| SCE1572_7341 | calcium-transporting ATPase | bi | sce_6126 | 94.78 cation-transporting ATPase, E1-E2 family |
| SCE1572_7342 | PREDICTED: similar to drug sensory protein A, partial | bi | sce_6127 | 85.84 hypothetical protein |
| SCE1572_7343 | RabR, positive regulator of sigma-B | bi | sce_4461 | 89.15 RabR, positive regulator of sigma-B |
| SCE1572_7344 | hypothetical protein | - | - | 0 |
| SCE1572_7345 | hypothetical protein | - | - | 0 |
| SCE1572_7346 | hypothetical protein | - | - | 0 |
| SCE1572_7347 | best DB hits: PFAM: PF00009; Elongation factor Tu family; E=0.29 | - | - | 0 |
| SCE1572_7348 | hypothetical protein | bi | sce_6131 | 50.53 FIG01086383: hypothetical protein |
| SCE1572_7349 | hypothetical protein | bi | sce_6132 | 48.92 FIG01089345: hypothetical protein |
| SCE1572_7350 | Twin-arginine translocation protein TatB | bi | sce_6133 | 72.81 Twin-arginine translocation protein TatB |
| SCE1572_7351 | RNA polymerase sigma factor RpoE | bi | sce_6134 | 63.88 RNA polymerase sigma factor RpoE |
| SCE1572_7352 | FIG01089237: hypothetical protein | bi | sce_6135 | 87.04 FIG01089237: hypothetical protein |
| SCE1572_7353 | MICRONEME PROTEIN 4 | umi | sce_1376 | 30.55 GII0995 protein |
| SCE1572_7354 | hypothetical protein | umi | sce_2287 | 32.7 FIG01089119: hypothetical protein |
| SCE1572_7355 | hypothetical protein | umi | sce_7678 | 27.06 transcriptional regulator, winged helix family |
| SCE1572_7356 | hypothetical protein | - | - | 0 |
| SCE1572_7357 | D-3-phosphoglycerate dehydrogenase (EC 1.1.1.95) | bi | sce_6139 | 87.96 D-3-phosphoglycerate dehydrogenase (EC 1.1.1.95) |
| SCE1572_7358 | oxidoreductases of the aldo/keto reductase family-like | bi | sce_6140 | 91.57 aldo/keto reductase |
| SCE1572_7359 | hypothetical protein | - | - | 0 |
| SCE1572_7360 | Sulfatase modifying factor 1 precursor (C-alpha-formylglycine- generating enzyme 1) | bi | sce_6141 | 92.62 Sulfatase modifying factor 1 precursor (C-alpha-formylglycine- generating enzyme 1) |
| SCE1572_7361 | ABC-type nitrate/sulfonate/bicarbonate transport system, ATPase component | bi | sce_6142 | 89.13 ABC-type nitrate/sulfonate/bicarbonate transport system, ATPase component |
| SCE1572_7362 | hypothetical protein | - | - | 0 |
| SCE1572_7363 | Hemolysin-related protein RbmC | bi | sce_6144 | 76.26 Hemolysin-related protein Vcp |
| SCE1572_7364 | COG0488: ATPase components of ABC transporters with duplicated ATPase domains | bi | sce_6145 | 95.32 COG0488: ATPase components of ABC transporters with duplicated ATPase domains |
| SCE1572_7365 | Catalase (EC 1.11.1.6) | umi | sce_2350 | 54.37 Catalase (EC 1.11.1.6) |
| SCE1572_7366 | Ribose ABC transport system, permease protein RbsC (TC 3.A.1.2.1) | bi | sce_6146 | 92.35 Ribose ABC transport system, permease protein RbsC (TC 3.A.1.2.1) |
| SCE1572_7367 | D-xylose transport ATP-binding protein XylG | bi | sce_6147 | 92.11 D-xylose transport ATP-binding protein XylG |
| SCE1572_7368 | Flagellar hook-length control protein FliK | bi | sce_6148 | 71.03 Flagellar hook-length control protein FliK |
| SCE1572_7369 | cyclase/dehydrase | bi | sce_6149 | 65.35 cyclase/dehydrase |
| SCE1572_7370 | Threonine dehydrogenase and related Zn-dependent dehydrogenases | bi | sce_6150 | 89.2 Threonine dehydrogenase and related Zn-dependent dehydrogenases |
| SCE1572_7371 | hypothetical protein | bi | sce_6151 | 63.72 hypothetical protein |
| SCE1572_7372 | DNA polymerase II (EC 2.7.7.7) | bi | sce_6153 | 91.13 DNA polymerase II (EC 2.7.7.7) |
| SCE1572_7373 | hypothetical protein | umi | sce_7389 | 32.74 hypothetical protein |
| SCE1572_7374 | RNA polymerase, sigma-24 subunit, ECF subfamily | umi | sce_7388 | 56.55 RNA polymerase sigma-70 factor, group 3 |
| SCE1572_7375 | hypothetical protein | umi | sce_7387 | 48.71 ActD |
| SCE1572_7376 | ActD | umi | sce_7386 | 56.93 ActD |
| SCE1572_7377 | Phosphoglucosyltransferase (EC 5.4.2.2) | bi | sce_6154 | 93.82 Phosphoglucosyltransferase (EC 5.4.2.2) |

| | | | | |
|--------------|---|-----|----------|---|
| SCE1572_7378 | BioH protein, putative | - | | 0 |
| SCE1572_7379 | SAM-dependent methyltransferases | bi | sce_7617 | 79.01 hypothetical protein |
| SCE1572_7380 | FIG01087706: hypothetical protein | uni | sce_868 | 72.16 FIG01087706: hypothetical protein |
| SCE1572_7381 | hypothetical protein | - | | 0 |
| SCE1572_7382 | hypothetical protein | - | | 0 |
| SCE1572_7383 | hypothetical protein | - | | 0 |
| SCE1572_7384 | Endo-1,4-beta-xylanase A precursor (EC 3.2.1.8) | bi | sce_2434 | 75.06 Endo-1,4-beta-xylanase A precursor (EC 3.2.1.8) |
| SCE1572_7385 | Transcriptional regulator, LysR family | bi | sce_9581 | 46.94 Regulatory protein, LysR: LysR, substrate-binding |
| SCE1572_7386 | Oxidoreductase | uni | sce_4749 | 52.23 Oxidoreductase |
| SCE1572_7387 | FIG01085966: hypothetical protein | bi | sce_6155 | 88 FIG01085966: hypothetical protein |
| SCE1572_7388 | hypothetical protein | bi | sce_6156 | 81.77 hypothetical protein |
| SCE1572_7389 | hypothetical protein | - | | 0 |
| SCE1572_7390 | Epstein-Barr nuclear antigen 1 (EBV nuclear antigen 1) (EBNA-1) | bi | sce_7829 | 62.55 endo alpha-1,4 polygalactosaminidase precursor |
| SCE1572_7391 | Gli0645 protein | bi | sce_7831 | 69.05 Gli0645 protein |
| SCE1572_7392 | FIG01089651: hypothetical protein | bi | sce_5846 | 66.97 FIG01089651: hypothetical protein |
| SCE1572_7393 | Extensin-like protein precursor | bi | sce_7832 | 75.29 Flagellar hook-length control protein FliK |
| SCE1572_7394 | FIG01088605: hypothetical protein | bi | sce_7833 | 81.94 FIG01088605: hypothetical protein |
| SCE1572_7395 | RNA polymerase sigma factor RpoE | bi | sce_7834 | 87.62 RNA polymerase sigma factor RpoE |
| SCE1572_7396 | RsbR, positive regulator of sigma-B | bi | sce_6157 | 92 RsbR, positive regulator of sigma-B |
| SCE1572_7397 | Adenylate cyclase (EC 4.6.1.1) / Guanylate cyclase (EC 4.6.1.2) | bi | sce_6158 | 83.55 Adenylate cyclase (EC 4.6.1.1) / Guanylate cyclase (EC 4.6.1.2) |
| SCE1572_7398 | patatin, putative | bi | sce_6159 | 94.34 patatin, putative |
| SCE1572_7399 | Acyl-phosphate:glycerol-3-phosphate O-acyltransferase PlsY | bi | sce_6161 | 86.45 Acyl-phosphate:glycerol-3-phosphate O-acyltransferase PlsY |
| SCE1572_7400 | Acid phosphatase(EC:3.1.3.2) | bi | sce_6162 | 74.32 predicted protein |
| SCE1572_7401 | hypothetical protein | - | | 0 |
| SCE1572_7402 | tetracenomycin C synthesis protein homolog | uni | sce_3468 | 37.85 O-methyltransferase-related protein |
| SCE1572_7403 | Endo-1,4-beta-xylanase A precursor (EC 3.2.1.8) | bi | sce_6163 | 66.5 Endo-1,4-beta-xylanase A precursor (EC 3.2.1.8) |
| SCE1572_7404 | Flagellar hook-length control protein FliK | bi | sce_6164 | 78.76 Flagellar hook-length control protein FliK |
| SCE1572_7405 | RNA polymerase sigma factor RpoE | bi | sce_6165 | 93 RNA polymerase sigma factor RpoE |
| SCE1572_7406 | hypothetical protein | bi | sce_6166 | 71.08 hypothetical protein |
| SCE1572_7407 | hypothetical protein | - | | 0 |
| SCE1572_7408 | HAD-superfamily hydrolase, subfamily IA, variant 3 | bi | sce_6167 | 92.49 HAD-superfamily hydrolase, subfamily IA, variant 1 |
| SCE1572_7409 | hypothetical protein | - | | 0 |
| SCE1572_7410 | hypothetical protein | bi | sce_6168 | 90.7 hypothetical protein |
| SCE1572_7411 | Hydroxymethylpyrimidine ABC transporter, transmembrane component | bi | sce_6169 | 91.92 Hydroxymethylpyrimidine ABC transporter, transmembrane component |
| SCE1572_7412 | Hydroxymethylpyrimidine ABC transporter, substrate-binding component | bi | sce_6170 | 89.42 Hydroxymethylpyrimidine ABC transporter, substrate-binding component |
| SCE1572_7413 | BNR repeat domain protein | bi | sce_6171 | 80.54 BNR repeat domain protein |
| SCE1572_7414 | NADH dehydrogenase (EC 1.6.99.3) | uni | sce_7160 | 29.23 Pyridine nucleotide-disulphide oxidoreductase associated with reductive pyrimidine catabolism |
| SCE1572_7415 | RNA polymerase ECF-subfamily sigma factor | uni | sce_9369 | 39.26 putative RNA polymerase sigma factor |
| SCE1572_7416 | hypothetical protein | bi | sce_6172 | 80.3 hypothetical protein |
| SCE1572_7417 | Threonine dehydrogenase and related Zn-dependent dehydrogenases | bi | sce_6173 | 89.14 Threonine dehydrogenase and related Zn-dependent dehydrogenases |
| SCE1572_7418 | hypothetical protein | - | | 0 |
| SCE1572_7419 | Signal peptidase I (EC 3.4.21.89) | uni | sce_1142 | 47.3 Dihydroipoamide acetyltransferase component of pyruvate dehydrogenase complex (EC 2.3.1.12) |
| SCE1572_7420 | RsbR, positive regulator of sigma-B | bi | sce_6175 | 77.6 RsbR, positive regulator of sigma-B |
| SCE1572_7421 | hypothetical protein | uni | sce_6904 | 60.53 FIG01089354: hypothetical protein |
| SCE1572_7422 | hypothetical protein | bi | sce_5090 | 62.71 hypothetical protein |
| SCE1572_7423 | hypothetical protein | bi | sce_6176 | 60.29 FIG01086220: hypothetical protein |
| SCE1572_7424 | hypothetical protein | bi | sce_6177 | 88.04 hypothetical protein |
| SCE1572_7425 | FIG01084940: hypothetical protein | bi | sce_6178 | 92.38 FIG01084940: hypothetical protein |
| SCE1572_7426 | FIG01089566: hypothetical protein | uni | sce_4927 | 42.92 FIG01089566: hypothetical protein |
| SCE1572_7427 | tolB protein precursor, periplasmic protein involved in the tonB-independent uptake of group A colicins | uni | sce_5086 | 66.19 tolB protein precursor, periplasmic protein involved in the tonB-independent uptake of group A colicins |
| SCE1572_7428 | Type I restriction-modification system, DNA-methyltransferase subunit M (EC 2.1.1.72) | bi | sce_6179 | 87.68 Type I restriction-modification system, DNA-methyltransferase subunit M (EC 2.1.1.72) |
| SCE1572_7429 | Type I restriction-modification system, specificity subunit S (EC 3.1.21.3) | bi | sce_6180 | 82.84 Type I restriction-modification system, specificity subunit S (EC 3.1.21.3) |
| SCE1572_7430 | Similarity | bi | sce_3028 | 77.84 Similarity |
| SCE1572_7431 | Polysaccharide deacetylase | bi | sce_4600 | 74.17 Polysaccharide deacetylase |
| SCE1572_7432 | transcriptional regulator | bi | sce_6207 | 92.95 putative MerR-family transcriptional regulator |
| SCE1572_7433 | FIG01087541: hypothetical protein | bi | sce_6208 | 84.42 FIG01087541: hypothetical protein |
| SCE1572_7434 | 4Fe-4S ferredoxin, iron-sulfur binding | bi | sce_6211 | 84.31 4Fe-4S ferredoxin, iron-sulfur binding |
| SCE1572_7435 | Formate hydrogenlyase transcriptional activator | bi | sce_6212 | 91.45 Formate hydrogenlyase transcriptional activator |
| SCE1572_7436 | Protein of unknown function Mtu_121 | uni | sce_8363 | 40.95 Transcriptional regulator, MerR family |
| SCE1572_7437 | cysteine proteinase | - | | 0 |
| SCE1572_7438 | Cell division protein FtsZ (EC 3.4.24.-) | bi | sce_6218 | 73.83 RhoGEF Guanine nucleotide exchange factor for Rho/Rac/Cdc42-like GTPases-like |
| SCE1572_7439 | hypothetical protein | - | | 0 |
| SCE1572_7440 | hypothetical protein | - | | 0 |
| SCE1572_7441 | hypothetical protein | - | | 0 |
| SCE1572_7442 | hypothetical protein | uni | sce_6737 | 38.56 FIG01086993: hypothetical protein |
| SCE1572_7443 | serine/threonine protein kinase | uni | sce_5549 | 38.24 serine/threonine protein kinase |
| SCE1572_7444 | hypothetical protein | - | | 0 |
| SCE1572_7445 | similar to keratin associated protein 5-4 | uni | sce_2794 | 31.61 putative lipoprotein |
| SCE1572_7446 | hypothetical protein | bi | sce_6219 | 82.19 hypothetical protein |
| SCE1572_7447 | hypothetical protein | - | | 0 |
| SCE1572_7448 | Transcriptional regulator containing an amidase domain and an AraC-type DNA-binding HTH domain | bi | sce_6220 | 90.16 phospholipase D/Transphosphatidylase |
| SCE1572_7449 | Diaminopimelate decarboxylase (EC 4.1.1.20) | bi | sce_6221 | 91.49 Diaminopimelate decarboxylase (EC 4.1.1.20) |
| SCE1572_7450 | hypothetical protein | - | | 0 |
| SCE1572_7451 | Nitriolotriacetate monooxygenase component A (EC 1.14.13.-) | bi | sce_6233 | 95.34 Nitriolotriacetate monooxygenase component A (EC 1.14.13.-) |
| SCE1572_7452 | Nitriolotriacetate monooxygenase component A (EC 1.14.13.-) | uni | sce_6233 | 93.59 Nitriolotriacetate monooxygenase component A (EC 1.14.13.-) |
| SCE1572_7453 | FIG00841528: hypothetical protein | bi | sce_6235 | 88.83 FIG00841528: hypothetical protein |
| SCE1572_7454 | ABC-type multidrug transport system, permease component | bi | sce_6238 | 81.25 ABC-type multidrug transport system, permease component |
| SCE1572_7455 | ABC transporter, ATP-binding protein | bi | sce_6239 | 90.76 ABC-type multidrug transport system, ATPase component |
| SCE1572_7456 | serine/threonine-protein kinase PknI(EC:2.7.11.1) | bi | sce_6240 | 69.04 serine/threonine protein kinase |
| SCE1572_7457 | hypothetical protein | bi | sce_6241 | 78.59 hypothetical protein |
| SCE1572_7458 | hypothetical protein | bi | sce_6242 | 69.95 Gli0645 protein |
| SCE1572_7459 | FIG00817182: hypothetical protein | bi | sce_6243 | 48.77 FIG01087868: hypothetical protein |
| SCE1572_7460 | FIG01089493: hypothetical protein | bi | sce_6244 | 68.97 FIG01089493: hypothetical protein |
| SCE1572_7461 | Urea ABC transporter, substrate binding protein UrtA | bi | sce_6246 | 92.4 Urea ABC transporter, substrate binding protein UrtA |
| SCE1572_7462 | Urea ABC transporter, permease protein UrtB | bi | sce_6247 | 97.32 Urea ABC transporter, permease protein UrtB |
| SCE1572_7463 | Urea ABC transporter, permease protein UrtC | bi | sce_6248 | 90.11 Urea ABC transporter, permease protein UrtC |
| SCE1572_7464 | Urea ABC transporter, ATPase protein UrtD | bi | sce_6249 | 91.14 Urea ABC transporter, ATPase protein UrtD |
| SCE1572_7465 | Urea ABC transporter, ATPase protein UrtE | bi | sce_6250 | 95.28 Urea ABC transporter, ATPase protein UrtE |
| SCE1572_7466 | FIG01088098: hypothetical protein | bi | sce_6251 | 80.52 FIG01088098: hypothetical protein |
| SCE1572_7467 | LOC432261 protein | bi | sce_6263 | 85.14 LOC432261 protein |
| SCE1572_7468 | Ornithine cyclodeaminase (EC 4.3.1.12) | bi | sce_6264 | 91.67 Ornithine cyclodeaminase (EC 4.3.1.12) |
| SCE1572_7469 | cell surface receptor IPT/ITG domain protein | bi | sce_6265 | 67.11 Gli0995 protein |
| SCE1572_7470 | hypothetical protein | bi | sce_6266 | 73.96 hypothetical protein |
| SCE1572_7471 | hypothetical protein | - | | 0 |
| SCE1572_7472 | cold shock domain family protein | bi | sce_6268 | 92.59 cold shock domain family protein |
| SCE1572_7473 | serine/threonine protein kinase | bi | sce_6269 | 82.54 serine/threonine protein kinase |
| SCE1572_7474 | HNH endonuclease family protein | bi | sce_6270 | 94.19 HNH endonuclease family protein |
| SCE1572_7475 | 60 kDa SS-A/Ro ribonucleoprotein homolog (Ro sixty-related protein) | bi | sce_6271 | 93.02 60 kDa SS-A/Ro ribonucleoprotein homolog (Ro sixty-related protein) |
| SCE1572_7476 | hypothetical protein | - | | 0 |
| SCE1572_7477 | Protoporphyrinogen IX oxidase, aerobic, HemY (EC 1.3.3.4) | bi | sce_6273 | 88.83 Protoporphyrinogen IX oxidase, aerobic, HemY (EC 1.3.3.4) |
| SCE1572_7478 | hypothetical protein | bi | sce_6275 | 95.97 hypothetical protein |
| SCE1572_7479 | hypothetical protein | bi | sce_6276 | 88.51 FIG01086190: hypothetical protein |
| SCE1572_7480 | FIG01088599: hypothetical protein | bi | sce_6278 | 86.34 FIG01088599: hypothetical protein |
| SCE1572_7481 | hypothetical protein | bi | sce_6279 | 75 hypothetical protein |
| SCE1572_7482 | hypothetical protein | bi | sce_6280 | 87.93 hypothetical protein |
| SCE1572_7483 | FIG01088413: hypothetical protein | bi | sce_6281 | 75.53 FIG01088413: hypothetical protein |
| SCE1572_7484 | phyhd1 protein | - | | 0 |
| SCE1572_7485 | ABC transporter ATP-binding protein uup | bi | sce_6306 | 94.62 ABC transporter ATP-binding protein uup |
| SCE1572_7486 | Transcriptional regulator, AraC family | uni | sce_620 | 36.62 Transcriptional regulator, AraC family |
| SCE1572_7487 | peptidase, M19 family | bi | sce_615 | 84.01 peptidase, M19 family |
| SCE1572_7488 | hypothetical protein | - | | 0 |
| SCE1572_7489 | hypothetical protein | - | | 0 |
| SCE1572_7490 | hypothetical protein | bi | sce_1486 | 61.43 VgrG protein |
| SCE1572_7491 | small membrane hydrophobic protein | bi | sce_7440 | 33.6 putative membrane protein |
| SCE1572_7492 | Transcriptional regulator, AraC family | bi | sce_7441 | 40.07 Transcriptional regulator, AraC family |
| SCE1572_7493 | hypothetical protein | bi | sce_6083 | 95.45 hypothetical protein |
| SCE1572_7494 | hypothetical protein | - | | 0 |
| SCE1572_7495 | hypothetical protein | - | | 0 |
| SCE1572_7496 | hypothetical protein | - | | 0 |
| SCE1572_7497 | hypothetical protein | uni | sce_6867 | 76.32 hypothetical protein |
| SCE1572_7498 | hypothetical protein | bi | sce_6863 | 80.77 hypothetical protein |
| SCE1572_7499 | hypothetical protein | - | | 0 |
| SCE1572_7500 | hypothetical protein | bi | sce_6307 | 65.52 hypothetical protein |
| SCE1572_7501 | serine/threonine protein kinase | bi | sce_6309 | 79.12 serine/threonine protein kinase |
| SCE1572_7502 | FIG01087536: hypothetical protein | bi | sce_6310 | 82.48 FIG01087536: hypothetical protein |
| SCE1572_7503 | Gli0645 protein | bi | sce_6313 | 59.46 Cell division protein FtsZ (EC 3.4.24.-) |
| SCE1572_7504 | EBNA-1 | bi | sce_6314 | 57.74 putative lipoprotein |
| SCE1572_7505 | Surface protein from Gram-positive cocci, anchor region | bi | sce_6315 | 68.8 PASTA domain containing protein |
| SCE1572_7506 | FIG01085109: hypothetical protein | uni | sce_8592 | 67.23 FIG01085109: hypothetical protein |
| SCE1572_7507 | FIG01085109: hypothetical protein | uni | sce_8592 | 66.88 FIG01085109: hypothetical protein |
| SCE1572_7508 | FIG01085109: hypothetical protein | uni | sce_3937 | 74.73 FIG01085109: hypothetical protein |
| SCE1572_7509 | hypothetical protein | - | | 0 |
| SCE1572_7510 | FIG01085109: hypothetical protein | - | | 0 |
| SCE1572_7511 | FIG01085109: hypothetical protein | - | | 0 |
| SCE1572_7512 | hypothetical protein | - | | 0 |
| SCE1572_7513 | hypothetical protein | uni | sce_6493 | 30.47 Translation initiation factor 2 |
| SCE1572_7514 | Twin-arginine translocation protein TatB | uni | sce_6331 | 52.63 Twin-arginine translocation protein TatB |
| SCE1572_7515 | Twin-arginine translocation protein TatB | bi | sce_6331 | 75.29 Twin-arginine translocation protein TatB |
| SCE1572_7516 | ABC transporter, ATP-binding component | bi | sce_6332 | 69.58 Twin-arginine translocation protein TatB |
| SCE1572_7517 | Glucose-6-phosphate isomerase (EC 5.3.1.9) | bi | sce_6344 | 93.21 Glucose-6-phosphate isomerase (EC 5.3.1.9) |
| SCE1572_7518 | 2-oxoglutarate dehydrogenase E1 component (EC 1.2.4.2) | bi | sce_6345 | 94.68 2-oxoglutarate dehydrogenase E1 component (EC 1.2.4.2) |
| SCE1572_7519 | thioesterase family protein | bi | sce_6346 | 92.95 thioesterase family protein |
| SCE1572_7520 | LigA | bi | sce_6347 | 65.88 hypothetical protein |
| SCE1572_7521 | putative histidine kinase protein | uni | sce_2157 | 44.35 Sensor protein |
| SCE1572_7522 | two-component hybrid sensor and regulator | uni | sce_4477 | 39.53 Adenylate cyclase (EC 4.6.1.1) |
| SCE1572_7523 | Two-component hybrid sensor and regulator | uni | sce_7643 | 39.8 Sensor protein |
| SCE1572_7524 | S-adenosylmethionine decarboxylase proenzyme (EC 4.1.1.50), prokaryotic class 1B | bi | sce_6348 | 88.89 S-adenosylmethionine decarboxylase proenzyme (EC 4.1.1.50), prokaryotic class 1B |
| SCE1572_7525 | Di-/tripeptide transporter | bi | sce_6349 | 93.04 Di-/tripeptide transporter |
| SCE1572_7526 | hypothetical protein | - | | 0 |
| SCE1572_7527 | FIG01087746: hypothetical protein | bi | sce_6351 | 81.94 FIG01087746: hypothetical protein |
| SCE1572_7528 | AAA ATPase | bi | sce_6352 | 92.02 AAA ATPase |
| SCE1572_7529 | transposase, IS4 | - | | 0 |
| SCE1572_7530 | FIG01087975: hypothetical protein | bi | sce_6375 | 82.8 FIG01087975: hypothetical protein |
| SCE1572_7531 | hypothetical protein | bi | sce_6373 | 50.85 hypothetical protein |
| SCE1572_7532 | FIG01087249: hypothetical protein | uni | sce_2337 | 87.55 FIG01087249: hypothetical protein |
| SCE1572_7533 | hypothetical protein | - | | 0 |
| SCE1572_7534 | possible A. fulgidus predicted coding region AF1859 | bi | sce_6381 | 94.12 CRISPR repeat RNA endoribonuclease Cas6 |
| SCE1572_7535 | hypothetical protein | bi | sce_6382 | 86.08 hypothetical protein |
| SCE1572_7536 | EBNA-1 | bi | sce_6383 | 76.15 FIG01086339: hypothetical protein |
| SCE1572_7537 | FIG01085566: hypothetical protein | bi | sce_6401 | 75.82 FIG01085566: hypothetical protein |
| SCE1572_7538 | Cellulase(EC:3.2.1.4) | bi | sce_6403 | 80.7 Cellulase(EC:3.2.1.4) |
| SCE1572_7539 | GCNS-related N-acetyltransferase | bi | sce_6404 | 54.92 Single-stranded DNA-binding protein |
| SCE1572_7540 | lipolytic enzyme, G-D-S-L | bi | sce_6405 | 82.07 Acetylxlanyl esterase, acyl-CoA esterase or GDSL lipase family, strong similarity to C-terminal region of endoglucanase E precursor |
| SCE1572_7541 | hypothetical protein | bi | sce_6406 | 76.23 hypothetical protein |

| | | | | |
|--------------|--|-----|-----------|--|
| SCE1572_7542 | Thiol peroxidase, Tpx-type (EC 1.11.1.15) | bi | see_6407 | 87.8 Thiol peroxidase, Tpx-type (EC 1.11.1.15) |
| SCE1572_7543 | Cytochrome P450 | bi | see_6408 | 88.34 Cytochrome P450 |
| SCE1572_7544 | phospholipid:glycerol acyltransferase | bi | see_6409 | 85.96 phospholipid:glycerol acyltransferase |
| SCE1572_7545 | Ribose ABC transporter, periplasmic ribose-binding protein RbsB (TC 3.A.1.2.1) | bi | see_9213 | 93.51 Ribose ABC transporter, periplasmic ribose-binding protein RbsB (TC 3.A.1.2.1) |
| SCE1572_7546 | Ribose ABC transport system, ATP-binding protein RbsA (TC 3.A.1.2.1) | bi | see_9212 | 92.86 Ribose ABC transport system, ATP-binding protein RbsA (TC 3.A.1.2.1) |
| SCE1572_7547 | Ribose ABC transport system, permease protein RbsC (TC 3.A.1.2.1) | bi | see_9211 | 94.3 Ribose ABC transport system, permease protein RbsC (TC 3.A.1.2.1) |
| SCE1572_7548 | Ribose ABC transport system, permease protein RbsC (TC 3.A.1.2.1) | bi | see_9210 | 92.86 Ribose ABC transport system, permease protein RbsC (TC 3.A.1.2.1) |
| SCE1572_7549 | Tat (Twin-arginine translocation) pathway signal sequence domain protein | bi | see_5154 | 88.98 Tat (Twin-arginine translocation) pathway signal sequence domain protein |
| SCE1572_7550 | Cellulose-binding domain protein | bi | see_5153 | 86 Cellulose-binding domain protein |
| SCE1572_7551 | hypothetical protein | umi | see_8674 | 30.71 hypothetical protein |
| SCE1572_7552 | Glycosyl transferase, group 1 | bi | see_6410 | 88.12 Glycosyl transferase, group 1 family protein |
| SCE1572_7553 | PTPS-like type 4 | bi | see_6411 | 90.91 PTPS-like type 4 |
| SCE1572_7554 | Threonine dehydrogenase and related Zn-dependent dehydrogenases | bi | see_6412 | 91.09 Threonine dehydrogenase and related Zn-dependent dehydrogenases |
| SCE1572_7555 | Riboflavin-specific deaminase-like protein(EC:1.1.1.193) | bi | see_6413 | 75.97 2, 5-diamino-6-hydroxy-4-(5-phosphoribosylamino)pyrimidine 1-reductase(EC:1.1.1.193) |
| SCE1572_7556 | hypothetical protein | - | | 0 |
| SCE1572_7557 | Ferredoxin | bi | see_6415 | 82.49 Ferredoxin |
| SCE1572_7558 | Signal peptidase I (EC 3.4.21.89) | umi | see_8142 | 33.62 Signal peptidase I (EC 3.4.21.89) |
| SCE1572_7559 | monooxygenase, flavin-binding family | bi | see_3680 | 89.29 monooxygenase, flavin-binding family |
| SCE1572_7560 | Carboxypeptidase | bi | see_9660 | 83.84 Carboxypeptidase |
| SCE1572_7561 | hypothetical protein | - | | 0 |
| SCE1572_7562 | RD1 region associated protein Rv3876 | bi | see_1286 | 67 RD1 region associated protein Rv3876 |
| SCE1572_7563 | putative lipoprotein | bi | see_5995 | 79.34 putative lipoprotein |
| SCE1572_7564 | hypothetical protein | - | | 0 |
| SCE1572_7565 | putative glutathione S-transferase | - | | 0 |
| SCE1572_7566 | ComA operon protein 2 | bi | see_6421 | 87.58 ComA operon protein 2 |
| SCE1572_7567 | D-cysteine desulphydrase (EC 4.4.1.15) | bi | see_6422 | 86.38 D-cysteine desulphydrase (EC 4.4.1.15) |
| SCE1572_7568 | Proline-rich protein | bi | see_6423 | 79.56 Proline-rich protein |
| SCE1572_7569 | FIG01087451: hypothetical protein | bi | see_6424 | 83.09 FIG01087451: hypothetical protein |
| SCE1572_7570 | Transcriptional regulator, DeoR family | umi | see_9911 | 52.78 Transcriptional regulator, DeoR family |
| SCE1572_7571 | FIG01089165: hypothetical protein | bi | see_6425 | 85.1 FIG01089165: hypothetical protein |
| SCE1572_7572 | hypothetical protein | umi | see_6427 | 83.16 hypothetical protein |
| SCE1572_7573 | erythrocyte membrane protein 1 (PEMP1) | bi | see_6428 | 70.2 Cellulase(EC:3.2.1.4) |
| SCE1572_7574 | Permease of the drug/metabolite transporter (DMT) superfamily | bi | see_6429 | 85.54 Permease of the drug/metabolite transporter (DMT) superfamily |
| SCE1572_7575 | Transcriptional regulator, GntR family domain / Aspartate aminotransferase (EC 2.6.1.1) | bi | see_6430 | 94.21 Transcriptional regulator, GntR family domain / Aspartate aminotransferase (EC 2.6.1.1) |
| SCE1572_7576 | Nuclease sbcCD subunit C | bi | see_6431 | 87.77 hypothetical protein |
| SCE1572_7577 | Rrt2 family transcriptional regulator, group III | bi | see_6432 | 95.27 Rrt2 family transcriptional regulator, group III |
| SCE1572_7578 | Thioredoxin | bi | see_6433 | 85.05 Thioredoxin |
| SCE1572_7579 | Serine/threonine protein kinase PrkC, regulator of stationary phase | bi | see_6435 | 92.23 serine/threonine protein kinase |
| SCE1572_7580 | Flagellar hook-length control protein FliK | bi | see_6436 | 78.83 Flagellar hook-length control protein FliK |
| SCE1572_7581 | Sulfate adenylyltransferase, dissimilatory-type (EC 2.7.7.4) | bi | see_6437 | 96.21 Sulfate adenylyltransferase, dissimilatory-type (EC 2.7.7.4) |
| SCE1572_7582 | Sulfur carrier protein adenylyltransferase ThiF | bi | see_6438 | 90 Sulfur carrier protein adenylyltransferase ThiF |
| SCE1572_7583 | Cysteine synthase (EC 2.5.1.47) | bi | see_6439 | 94.94 Cysteine synthase (EC 2.5.1.47) |
| SCE1572_7584 | hypothetical protein | bi | see_6440 | 82.76 hypothetical protein |
| SCE1572_7585 | FIG038648: MoadA and/or ThiS families | bi | see_6441 | 98.91 FIG038648: MoadA and/or ThiS families |
| SCE1572_7586 | Sulfur carrier protein adenylyltransferase ThiF | bi | see_6442 | 87.25 Sulfur carrier protein adenylyltransferase ThiF |
| SCE1572_7587 | Cysteine synthase (EC 2.5.1.47) | bi | see_6443 | 89.86 Cysteine synthase (EC 2.5.1.47) |
| SCE1572_7588 | Iron-sulfur cluster regulator IscR | bi | see_6444 | 94.04 Iron-sulfur cluster regulator IscR |
| SCE1572_7589 | hypothetical protein | bi | see_6448 | 88.81 hypothetical protein |
| SCE1572_7590 | predicted protein | bi | see_6449 | 73.26 hypothetical protein |
| SCE1572_7591 | FIG01084907: hypothetical protein | bi | see_6450 | 77.46 FIG01084907: hypothetical protein |
| SCE1572_7592 | 5'-nucleotidase (EC 3.1.3.5) | bi | see_6451 | 89.04 5'-nucleotidase (EC 3.1.3.5) |
| SCE1572_7593 | Phosphoenolpyruvate-protein phosphotransferase of PTS system (EC 2.7.3.9) | bi | see_6452 | 94.83 Phosphoenolpyruvate-protein phosphotransferase of PTS system (EC 2.7.3.9) |
| SCE1572_7594 | Phosphocarrier protein, nitrogen regulation associated | bi | see_6453 | 92.13 Phosphotransferase system, phosphocarrier protein HPr |
| SCE1572_7595 | FIG000506: Predicted P-loop-containing kinase | bi | see_6454 | 89.35 Uncharacterised P-loop ATPase protein UPF0042 |
| SCE1572_7596 | HPr kinase/phosphorylase (EC 2.7.1.-) (EC 2.7.4.-) | bi | see_6455 | 92.17 HPr kinase/phosphorylase (EC 2.7.1.-) (EC 2.7.4.-) |
| SCE1572_7597 | PTS IIA-like nitrogen-regulatory protein PtsN | bi | see_6456 | 93.71 PTS IIA-like nitrogen-regulatory protein PtsN |
| SCE1572_7598 | hypothetical protein | - | | 0 |
| SCE1572_7599 | Ribosomal subunit interface protein | bi | see_6458 | 91.13 Ribosomal subunit interface protein |
| SCE1572_7600 | hypothetical protein | bi | see_6461 | 84.72 hypothetical protein |
| SCE1572_7601 | serine/threonine protein kinase | bi | see_6462 | 90.34 serine/threonine protein kinase |
| SCE1572_7602 | Isocitrate dehydrogenase [NAD] (EC 1.1.1.41) | bi | see_6463 | 95.92 Isocitrate dehydrogenase [NAD] (EC 1.1.1.41) |
| SCE1572_7603 | Osmosensitive K channel histidine kinase KdpD (EC 2.7.3.-) | bi | see_6464 | 74.62 Osmosensitive K channel histidine kinase KdpD (EC 2.7.3.-) |
| SCE1572_7604 | hypothetical protein | bi | see_6465 | 89.66 hypothetical protein |
| SCE1572_7605 | hypothetical protein | bi | see_10331 | 82.59 hypothetical protein |
| SCE1572_7606 | RabR, positive regulator of sigma-B | bi | see_9946 | 82.74 RabR, positive regulator of sigma-B |
| SCE1572_7607 | FIG01087122: hypothetical protein | bi | see_6467 | 90.19 FIG01087122: hypothetical protein |
| SCE1572_7608 | hypothetical protein | - | | 0 |
| SCE1572_7609 | Lactoylglutathione lyase (EC 4.4.1.5) | bi | see_6470 | 80.65 Lactoylglutathione lyase (EC 4.4.1.5) |
| SCE1572_7610 | FIG01085689: hypothetical protein | bi | see_6471 | 91.29 FIG01085689: hypothetical protein |
| SCE1572_7611 | acyl-CoA thioester hydrolase | bi | see_6472 | 89.51 Acyl-CoA thioester hydrolase(EC:3.1.2.-) |
| SCE1572_7612 | Adenylate cyclase (EC 4.6.1.1) / Guanylate cyclase (EC 4.6.1.2) | bi | see_6473 | 90.38 Adenylate cyclase (EC 4.6.1.1) / Guanylate cyclase (EC 4.6.1.2) |
| SCE1572_7613 | FIG01086043: hypothetical protein | bi | see_6475 | 78.57 FIG01086043: hypothetical protein |
| SCE1572_7614 | penicillin-insensitive murein endopeptidase | bi | see_6476 | 74.03 penicillin-insensitive murein endopeptidase |
| SCE1572_7615 | hypothetical protein | umi | see_3256 | 29.43 sigma-54 dependent DNA-binding response regulator |
| SCE1572_7616 | COG4928: Predicted P-loop ATPase | - | | 0 |
| SCE1572_7617 | Succinyl-CoA:3-ketoacid-coenzyme A transferase subunit A (EC 2.8.3.5) | bi | see_6477 | 96.43 Succinyl-CoA:3-ketoacid-coenzyme A transferase subunit A (EC 2.8.3.5) |
| SCE1572_7618 | Succinyl-CoA:3-ketoacid-coenzyme A transferase subunit B (EC 2.8.3.5) | bi | see_6478 | 96.83 Succinyl-CoA:3-ketoacid-coenzyme A transferase subunit B (EC 2.8.3.5) |
| SCE1572_7619 | Acetyl-coenzyme A carboxyl transferase beta chain (EC 6.4.1.2) | bi | see_6479 | 93.33 Acetyl-coenzyme A carboxyl transferase beta chain (EC 6.4.1.2) |
| SCE1572_7620 | Dihydrofolate synthase (EC 6.3.2.12) / Folylpolylglutamate synthase (EC 6.3.2.17) | bi | see_6480 | 86.14 Dihydrofolate synthase (EC 6.3.2.12) / Folylpolylglutamate synthase (EC 6.3.2.17) |
| SCE1572_7621 | Ketoacyl reductase | bi | see_6481 | 89.44 Ketoacyl reductase |
| SCE1572_7622 | Phosphoglucosamine mutase (EC 5.4.2.10) | bi | see_6482 | 97.08 Phosphoglucosamine mutase (EC 5.4.2.10) |
| SCE1572_7623 | probable ABC transporter ATP-binding protein | bi | see_6483 | 90.75 ATP-binding protein of ABC transporter |
| SCE1572_7624 | Response regulator of zinc sigma-54-dependent two-component system | bi | see_6484 | 97.89 Response regulator of zinc sigma-54-dependent two-component system |
| SCE1572_7625 | hypothetical protein | bi | see_6486 | 91.18 COLLAGEN |
| SCE1572_7626 | hypothetical protein | bi | see_6487 | 70.36 hypothetical protein |
| SCE1572_7627 | protein of unknown function DUF323 | umi | see_6141 | 32.23 Sulfatase modifying factor 1 precursor (C-alpha-formylglycine- generating enzyme 1) |
| SCE1572_7628 | Glycosyl transferase, group 2 family protein | bi | see_6488 | 91.3 Glycosyl transferase, group 2 family protein |
| SCE1572_7629 | Leucyl/phenylalanyl-tRNA--protein transferase (EC 2.3.2.6) | bi | see_6489 | 93.22 Leucyl/phenylalanyl-tRNA--protein transferase (EC 2.3.2.6) |
| SCE1572_7630 | Ribosome-binding factor A | bi | see_6491 | 92.5 Ribosome-binding factor A |
| SCE1572_7631 | YlxP-like protein | bi | see_6492 | 92.37 YlxP-like protein |
| SCE1572_7632 | Translation initiation factor 2 | bi | see_6493 | 92.9 Translation initiation factor 2 |
| SCE1572_7633 | Translation initiation factor 2 | umi | see_6493 | 79.55 Translation initiation factor 2 |
| SCE1572_7634 | COG2740: Predicted nucleic-acid-binding protein implicated in transcription termination / domain of unknown function | bi | see_6494 | 78.85 COG2740: Predicted nucleic-acid-binding protein implicated in transcription termination / domain of unknown function |
| SCE1572_7635 | Transcription termination protein NusA | bi | see_6495 | 98.52 Transcription termination protein NusA |
| SCE1572_7636 | FIG000325: clustered with transcription termination protein NusA | bi | see_6496 | 88.12 FIG000325: clustered with transcription termination protein NusA |
| SCE1572_7637 | D-3-phosphoglycerate dehydrogenase (EC 1.1.1.195) | bi | see_6497 | 95.69 D-3-phosphoglycerate dehydrogenase (EC 1.1.1.195) |
| SCE1572_7638 | FIG01085861: hypothetical protein | bi | see_6498 | 78.45 FIG01085861: hypothetical protein |
| SCE1572_7639 | FIG01087419: hypothetical protein | bi | see_6499 | 82.3 FIG01087419: hypothetical protein |
| SCE1572_7640 | FIG01088444: hypothetical protein | bi | see_6500 | 93.99 FIG01088444: hypothetical protein |
| SCE1572_7641 | serine/threonine protein kinase | bi | see_6501 | 99.29 serine/threonine protein kinase |
| SCE1572_7642 | hypothetical protein | - | | 0 |
| SCE1572_7643 | Serine/threonine protein kinase PrkC, regulator of stationary phase | bi | see_6502 | 76.29 Serine/threonine protein kinase PrkC, regulator of stationary phase |
| SCE1572_7644 | TonB-dependent receptor: Outer membrane receptor for ferrienterochelin and colicins | bi | see_6504 | 86.43 TonB-dependent receptor: Outer membrane receptor for ferrienterochelin and colicins |
| SCE1572_7645 | hypothetical protein | bi | see_6505 | 85.01 hypothetical protein |
| SCE1572_7646 | Serine proteases, subtilase family | bi | see_6506 | 79.64 Serine proteases, subtilase family |
| SCE1572_7647 | hypothetical protein | bi | see_9653 | 80.94 hypothetical protein |
| SCE1572_7648 | glycosyl hydrolase, BNR repeat-containing protein | bi | see_2926 | 74.41 hypothetical protein |
| SCE1572_7649 | Streptococcal hemagglutinin protein | umi | see_7564 | 39.25 Putative galactosidase |
| SCE1572_7650 | hypothetical protein | umi | see_1486 | 46.88 VgrG protein |
| SCE1572_7651 | Pectate lyase | - | | 0 |
| SCE1572_7652 | Beta-xylosidase (EC 3.2.1.37) | umi | see_5463 | 33.44 Beta-xylosidase (EC 3.2.1.37) |
| SCE1572_7653 | hypothetical protein | umi | see_9025 | 29.73 hypothetical protein |
| SCE1572_7654 | XL | umi | see_8663 | 33.5 hypothetical protein |
| SCE1572_7655 | RNA polymerase sigma factor RpoE | umi | see_8662 | 50.53 RNA polymerase sigma factor RpoE |
| SCE1572_7656 | Epstein-Barr nuclear antigen 1 (EBV nuclear antigen 1) (EBNA-1) | umi | see_8661 | 35.76 OmpA/MotB |
| SCE1572_7657 | OmpA family protein | umi | see_3697 | 30.03 PE-PGRS FAMILY PROTEIN |
| SCE1572_7658 | hypothetical protein | - | | 0 |
| SCE1572_7659 | hypothetical protein(EC:3.2.1.18) | bi | see_9782 | 44.44 serine/threonine protein kinase, putative |
| SCE1572_7660 | Collagen triple helix repeat | umi | see_1320 | 41.07 FIG01086874: hypothetical protein |
| SCE1572_7661 | FIG01087754: hypothetical protein | - | | 0 |
| SCE1572_7662 | hypothetical protein | bi | see_9807 | 84 hypothetical protein |
| SCE1572_7663 | hypothetical protein | - | | 0 |
| SCE1572_7664 | Mobile element protein | - | | 0 |
| SCE1572_7665 | hypothetical protein | bi | see_1677 | 98.78 PE-PGRS FAMILY PROTEIN |
| SCE1572_7666 | Ankyrin | - | | 0 |
| SCE1572_7667 | hypothetical protein | bi | see_2109 | 31.58 FIG01089134: hypothetical protein |
| SCE1572_7668 | FIG01087249: hypothetical protein | umi | see_2338 | 95 Transposase |
| SCE1572_7669 | serine/threonine protein kinase | umi | see_5751 | 38.23 Adenylate cyclase (EC 4.6.1.1) / Guanylate cyclase (EC 4.6.1.2) |
| SCE1572_7670 | hypothetical protein | - | | 0 |
| SCE1572_7671 | hypothetical protein | - | | 0 |
| SCE1572_7672 | hypothetical protein | - | | 0 |
| SCE1572_7673 | FIG01085109: hypothetical protein | umi | see_3937 | 26.59 FIG01085109: hypothetical protein |
| SCE1572_7674 | Rhs family protein | umi | see_3937 | 29.7 FIG01085109: hypothetical protein |
| SCE1572_7675 | Rhs family protein-like protein | umi | see_3939 | 31.58 FIG01085109: hypothetical protein |
| SCE1572_7676 | hypothetical protein | umi | see_3858 | 30.77 Adenosylhomocysteinase (EC 3.3.1.1) |
| SCE1572_7677 | hypothetical protein | bi | see_6508 | 82.08 hypothetical protein |
| SCE1572_7678 | FIG01087525: hypothetical protein | bi | see_6509 | 91.89 FIG01087525: hypothetical protein |
| SCE1572_7679 | Nickel transporter UreH | bi | see_6510 | 80.47 Nickel transporter UreH |
| SCE1572_7680 | sensor histidine kinase/response regulator | bi | see_6511 | 94.05 sensor histidine kinase/response regulator |
| SCE1572_7681 | Signal transduction histidine kinase | bi | see_6512 | 83.91 Signal transduction histidine kinase |
| SCE1572_7682 | Small GTP-binding protein domain | bi | see_6513 | 87.28 Small GTP-binding protein domain |
| SCE1572_7683 | hypothetical protein | bi | see_6514 | 79.63 OmpA/MotB |
| SCE1572_7684 | hypothetical protein | - | | 0 |
| SCE1572_7685 | hypothetical protein | bi | see_6515 | 76.02 hypothetical protein |
| SCE1572_7686 | hypothetical protein | - | | 0 |
| SCE1572_7687 | hypothetical protein | bi | see_6516 | 77.16 hypothetical protein |
| SCE1572_7688 | hypothetical protein | - | | 0 |
| SCE1572_7689 | FIG01087249: hypothetical protein | umi | see_2338 | 93.48 Transposase |
| SCE1572_7690 | FIG01087249: hypothetical protein | umi | see_2338 | 92.86 Transposase |
| SCE1572_7691 | hypothetical protein | bi | see_6517 | 78.35 hypothetical protein |
| SCE1572_7692 | Methylamine utilization protein mauG | bi | see_6518 | 80.67 Methylamine utilization protein mauG |
| SCE1572_7693 | FIG01085716: hypothetical protein | bi | see_6519 | 67.44 FIG01085716: hypothetical protein |
| SCE1572_7694 | Outer membrane receptor proteins, mostly Fe transport | bi | see_6520 | 84.99 Outer membrane receptor proteins, mostly Fe transport |
| SCE1572_7695 | putative lipoprotein | bi | see_6521 | 79.53 hypothetical protein |
| SCE1572_7696 | putative lipoprotein | bi | see_6522 | 88.53 hypothetical protein |
| SCE1572_7697 | Serine/threonine-protein kinase pkn1 (EC 2.7.11.1) | bi | see_6523 | 73.41 Serine/threonine-protein kinase pkn1 (EC 2.7.11.1) |
| SCE1572_7698 | monooxygenase, FAD-binding | bi | see_6524 | 90.07 hypothetical protein |
| SCE1572_7699 | Methyltransferase | bi | see_6525 | 90.94 methyltransferase type 11 |
| SCE1572_7700 | peptidase M19, renal dipeptidase | bi | see_6526 | 88.56 peptidase, M19 (membrane dipeptidase) family(EC:3.4.-) |
| SCE1572_7701 | Quaternary ammonium compound-resistance protein sugE | bi | see_6527 | 84.62 Quaternary ammonium compound-resistance protein sugE |
| SCE1572_7702 | COG3866 Pectate lyase | bi | see_6528 | 86.11 COG3866 Pectate lyase |
| SCE1572_7703 | Pyridoxine 5'-phosphate synthase (EC 2.6.99.2) | bi | see_6536 | 94.26 Pyridoxine 5'-phosphate synthase (EC 2.6.99.2) |
| SCE1572_7704 | hypothetical protein | bi | see_6537 | 68.52 hypothetical protein |
| SCE1572_7705 | hypothetical protein | - | | 0 |

| | | | | |
|--------------|---|-----|----------|---|
| SCE1572_7706 | 23S rRNA (guanine-N-2)-methyltransferase rlmL (EC 2.1.1.-) | bi | see_6538 | 95.12 putative RNA methylase |
| SCE1572_7707 | serine/threonine protein kinase | bi | see_6539 | 78.12 serine/threonine protein kinase |
| SCE1572_7708 | hypothetical protein | bi | see_6540 | 55.34 hypothetical protein |
| SCE1572_7709 | FIG01088683: hypothetical protein | bi | see_6541 | 81.88 FIG01088683: hypothetical protein |
| SCE1572_7710 | Ribosomal-protein-S18p-alanine acetyltransferase (EC 2.3.1.-) | bi | see_6542 | 82.14 Ribosomal-protein-S18p-alanine acetyltransferase (EC 2.3.1.-) |
| SCE1572_7711 | major facilitator superfamily MFS_1 | bi | see_6543 | 88.31 multidrug-efflux transporter |
| SCE1572_7712 | Carboxypeptidase A1 precursor (EC 3.4.17.1) | bi | see_6544 | 77.2 carboxypeptidase B |
| SCE1572_7713 | FIG01084923: hypothetical protein | bi | see_6545 | 90.5 FIG01084923: hypothetical protein |
| SCE1572_7714 | hypothetical protein | umi | see_529 | 68.34 hypothetical protein |
| SCE1572_7715 | ABC transporter, permease protein | umi | see_3979 | 34.59 RIBOSE TRANSPORT SYSTEM PERMEASE PROTEIN RBSC |
| SCE1572_7716 | inner-membrane translocator | umi | see_8679 | 37.89 inner-membrane translocator |
| SCE1572_7717 | sugar transport ATP-binding protein | umi | see_8677 | 41.63 Putative deoxyribose-specific ABC transporter, ATP-binding protein |
| SCE1572_7718 | conserved domain protein | bi | see_6546 | 89.96 conserved domain protein |
| SCE1572_7719 | peptidoglycan-associated lipoprotein | bi | see_6547 | 84.52 OmpA/MotB |
| SCE1572_7720 | GMP synthase [glutamine-hydrolyzing] (EC 6.3.5.2) | bi | see_6548 | 94.41 GMP synthase [glutamine-hydrolyzing] (EC 6.3.5.2) |
| SCE1572_7721 | hypothetical protein | - | - | 0 |
| SCE1572_7722 | hypothetical protein | - | - | 0 |
| SCE1572_7723 | ATP/GTP-binding protein, SA1392 homolog | bi | see_6549 | 95.02 ATP/GTP-binding protein, SA1392 homolog |
| SCE1572_7724 | Chaperone protein DnaJ | bi | see_6550 | 93.04 Chaperone protein DnaJ |
| SCE1572_7725 | Long-chain-fatty-acid-CoA ligase (EC 6.2.1.3) | bi | see_6551 | 84.92 Long-chain-fatty-acid-CoA ligase (EC 6.2.1.3) |
| SCE1572_7726 | hypothetical protein | bi | see_6552 | 92.31 type IV pilus assembly PilZ |
| SCE1572_7727 | DNA double-strand break repair Rad50 ATPase | bi | see_6553 | 88.76 TPR domain protein, putative component of TonB system |
| SCE1572_7728 | hypothetical protein | - | - | 0 |
| SCE1572_7729 | FIG01086521: hypothetical protein | bi | see_6554 | 85.98 FIG01086521: hypothetical protein |
| SCE1572_7730 | FIG01086093: hypothetical protein | bi | see_6555 | 79.14 FIG01086093: hypothetical protein |
| SCE1572_7731 | hypothetical protein | bi | see_6556 | 90.1 hypothetical protein |
| SCE1572_7732 | PROBABLE GSPD-RELATED PROTEIN | bi | see_6557 | 73.52 FIG01088605: hypothetical protein |
| SCE1572_7733 | RNA polymerase sigma factor RpoE | bi | see_6558 | 86.77 RNA polymerase sigma factor RpoE |
| SCE1572_7734 | hypothetical protein | bi | see_6559 | 91.67 hypothetical protein |
| SCE1572_7735 | hypothetical protein | bi | see_6560 | 93.89 hypothetical protein |
| SCE1572_7736 | Purine nucleoside phosphorylase (EC 2.4.2.1) | bi | see_6561 | 90.31 Purine nucleoside phosphorylase (EC 2.4.2.1) |
| SCE1572_7737 | Cytidine deaminase (EC 3.5.4.5) | bi | see_6562 | 86.36 Cytidine deaminase (EC 3.5.4.5) |
| SCE1572_7738 | plectin 1 isoform 8 | bi | see_6563 | 74.47 plectin 1 isoform 8 |
| SCE1572_7739 | hypothetical protein | - | - | 0 |
| SCE1572_7740 | 6-phosphofructokinase (EC 2.7.1.11) | bi | see_6564 | 95.98 6-phosphofructokinase (EC 2.7.1.11) |
| SCE1572_7741 | integral membrane protein | bi | see_6565 | 86.12 hypothetical protein |
| SCE1572_7742 | Serine protease precursor MucD/AlgY associated with sigma factor RpoE | bi | see_6566 | 86.9 Serine protease precursor MucD/AlgY associated with sigma factor RpoE |
| SCE1572_7743 | Pyroline-5-carboxylate reductase (EC 1.5.1.2) | bi | see_6567 | 95.44 Pyroline-5-carboxylate reductase (EC 1.5.1.2) |
| SCE1572_7744 | RNA polymerase sigma factor RpoH | bi | see_6568 | 99.65 RNA polymerase sigma factor RpoH |
| SCE1572_7745 | probable iron binding protein from the HesB_IscA_SufA family | bi | see_6569 | 99.07 probable iron binding protein from the HesB_IscA_SufA family |
| SCE1572_7746 | 5-methyltetrahydrofolate-homocysteine methyltransferase (EC 2.1.1.13) | bi | see_6571 | 91.98 5-methyltetrahydrofolate-homocysteine methyltransferase (EC 2.1.1.13) |
| SCE1572_7747 | FIG01085864: hypothetical protein | bi | see_6572 | 87.97 FIG01085864: hypothetical protein |
| SCE1572_7748 | OmpA/MotB domain protein | umi | see_577 | 33.01 zinc finger/thioredoxin putative |
| SCE1572_7749 | hypothetical protein | - | - | 0 |
| SCE1572_7750 | hypothetical protein | - | - | 0 |
| SCE1572_7751 | VgrG protein | umi | see_9404 | 32.49 VgrG protein |
| SCE1572_7752 | hypothetical protein | - | - | 0 |
| SCE1572_7753 | hypothetical protein | - | - | 0 |
| SCE1572_7754 | PAAR repeat-containing protein | umi | see_5221 | 46.97 hypothetical protein |
| SCE1572_7755 | hypothetical protein | - | - | 0 |
| SCE1572_7756 | Glutathione S-transferase (EC 2.5.1.18) | umi | see_4136 | 57.01 Glutathione S-transferase (EC 2.5.1.18) |
| SCE1572_7757 | Transcriptional regulator, LysR family | umi | see_7565 | 40.91 transcriptional regulator, LysR family |
| SCE1572_7758 | probable putative transmembrane protein | bi | see_6574 | 81.68 hypothetical protein |
| SCE1572_7759 | Allantoicase (EC 3.5.2.5) | bi | see_6577 | 94.24 Allantoicase (EC 3.5.2.5) |
| SCE1572_7760 | Allantoicase (EC 3.5.3.4) | bi | see_6578 | 88.63 allantoicase (EC 3.5.3.4) |
| SCE1572_7761 | hypothetical protein | bi | see_6579 | 80.69 hypothetical protein |
| SCE1572_7762 | Transcriptional regulator, TetR family | umi | see_5497 | 36.47 TetR-family transcriptional regulator |
| SCE1572_7763 | hypothetical protein | bi | see_6581 | 78.95 hypothetical protein |
| SCE1572_7764 | putative lipoprotein | bi | see_6582 | 71.21 putative lipoprotein |
| SCE1572_7765 | 5-Hydroxyisourate Hydrolase (HIUase) (EC 3.5.2.17) | bi | see_6583 | 89.38 5-Hydroxyisourate Hydrolase (HIUase) (EC 3.5.2.17) |
| SCE1572_7766 | FIG00841714: hypothetical protein | bi | see_6584 | 88.68 hypothetical protein |
| SCE1572_7767 | hypothetical protein | - | - | 0 |
| SCE1572_7768 | FIG01086124: hypothetical protein | bi | see_6585 | 69.17 FIG01086124: hypothetical protein |
| SCE1572_7769 | FOG: PKD repeat | bi | see_6586 | 89.28 FOG: PKD repeat |
| SCE1572_7770 | COLIagen | bi | see_6587 | 81.73 General secretory system II, protein E-like |
| SCE1572_7771 | Imidazole glycerol phosphate synthase cyclase subunit (EC 4.1.3.-) | bi | see_6588 | 95.93 Imidazole glycerol phosphate synthase cyclase subunit (EC 4.1.3.-) |
| SCE1572_7772 | hypothetical protein | bi | see_6589 | 57.09 OmpA/MotB |
| SCE1572_7773 | putative membrane protein | bi | see_6590 | 90.16 putative membrane protein |
| SCE1572_7774 | DNA repair protein RadC | umi | see_8397 | 84.48 DNA repair protein RadC |
| SCE1572_7775 | Rhs-family protein | umi | see_3584 | 46.46 Probable Rhs-family protein |
| SCE1572_7776 | FIG01087953: hypothetical protein | umi | see_4592 | 85.47 FIG01086445: hypothetical protein |
| SCE1572_7777 | DNA repair protein RadC | bi | see_512 | 87.02 DNA repair protein RadC |
| SCE1572_7778 | hypothetical protein | bi | see_513 | 82.49 FIG01087636: hypothetical protein |
| SCE1572_7779 | Transcriptional regulator Cro/CI family | umi | see_514 | 48.78 hypothetical protein |
| SCE1572_7780 | Integron integrase IntIPac | umi | see_515 | 84.29 Integron integrase IntIPac |
| SCE1572_7781 | hypothetical protein | - | - | 0 |
| SCE1572_7782 | hypothetical protein | - | - | 0 |
| SCE1572_7783 | hypothetical protein | - | - | 0 |
| SCE1572_7784 | FIG01087953: hypothetical protein | umi | see_518 | 92.43 FIG01087953: hypothetical protein |
| SCE1572_7785 | hypothetical protein | - | - | 0 |
| SCE1572_7786 | FIG01087372: hypothetical protein | umi | see_522 | 90.97 FIG01087372: hypothetical protein |
| SCE1572_7787 | Adenosylhomocysteinase (EC 3.3.1.1) | - | - | 0 |
| SCE1572_7788 | hypothetical protein | - | - | 0 |
| SCE1572_7789 | hypothetical protein | - | - | 0 |
| SCE1572_7790 | hypothetical protein | bi | see_6596 | 77.61 hypothetical protein |
| SCE1572_7791 | Xanthine dehydrogenase, FAD binding subunit (EC 1.17.1.4) | bi | see_6597 | 86.08 Xanthine dehydrogenase, FAD binding subunit (EC 1.17.1.4) |
| SCE1572_7792 | 4-hydroxybenzoyl-CoA reductase, gamma subunit (EC 1.3.99.20) | bi | see_6598 | 94.38 4-hydroxybenzoyl-CoA reductase, gamma subunit (EC 1.3.99.20) |
| SCE1572_7793 | Xanthine dehydrogenase, molybdenum binding subunit (EC 1.17.1.4) | bi | see_6599 | 92.57 Xanthine dehydrogenase, molybdenum binding subunit (EC 1.17.1.4) |
| SCE1572_7794 | hypothetical protein | bi | see_6600 | 91.79 hypothetical protein |
| SCE1572_7795 | XdhC protein (assists in molybdopterin insertion into xanthine dehydrogenase) | bi | see_6601 | 85.27 XdhC protein (assists in molybdopterin insertion into xanthine dehydrogenase) |
| SCE1572_7796 | ATPase | umi | see_9281 | 30.85 ATP binding protein |
| SCE1572_7797 | hypothetical protein | bi | see_1587 | 41.51 hypothetical protein |
| SCE1572_7798 | Predicted N6-adenine-specific RNA methylase containing THUMP domain | bi | see_6602 | 59.28 hypothetical protein |
| SCE1572_7799 | hypothetical protein | bi | see_6604 | 66.67 hypothetical protein |
| SCE1572_7800 | Magnesium and cobalt efflux protein CorC | bi | see_6605 | 96.57 Magnesium and cobalt efflux protein CorC |
| SCE1572_7801 | Glutamate-cysteine ligase (EC 6.3.2.2) | bi | see_6606 | 92.33 Glutamate-cysteine ligase (EC 6.3.2.2) |
| SCE1572_7802 | 5,10-methylenetetrahydrofolate reductase (EC 1.5.1.20) / Homolog of homocysteine-binding domain | bi | see_6607 | 93.52 5,10-methylenetetrahydrofolate reductase (EC 1.5.1.20) / Homolog of homocysteine-binding domain |
| SCE1572_7803 | hypothetical protein | bi | see_6608 | 73.58 hypothetical protein |
| SCE1572_7804 | FIG01086517: hypothetical protein | bi | see_6609 | 96.49 FIG01086517: hypothetical protein |
| SCE1572_7805 | Double-transmembrane region-like | bi | see_6610 | 93.7 hypothetical protein |
| SCE1572_7806 | hypothetical protein | bi | see_6611 | 95.58 hypothetical protein |
| SCE1572_7807 | Methanol dehydrogenase regulator (MoxR) homolog | bi | see_6612 | 95.51 Methanol dehydrogenase regulator (MoxR) homolog |
| SCE1572_7808 | hypothetical protein | bi | see_6613 | 94.27 hypothetical protein |
| SCE1572_7809 | hypothetical protein | - | - | 0 |
| SCE1572_7810 | hypothetical protein | bi | see_6614 | 73.86 Exonuclease SbcC |
| SCE1572_7811 | hypothetical protein | bi | see_6615 | 90.5 hypothetical protein |
| SCE1572_7812 | hypothetical protein | bi | see_6616 | 95.81 hypothetical protein |
| SCE1572_7813 | hypothetical protein | - | - | 0 |
| SCE1572_7814 | Heat shock protein 60 family co-chaperone GroES | bi | see_6617 | 97.92 Heat shock protein 60 family co-chaperone GroES |
| SCE1572_7815 | Heat shock protein 60 family chaperone GroEL | bi | see_6618 | 98.34 Heat shock protein 60 family chaperone GroEL |
| SCE1572_7816 | Ribosomal-protein-alanine acetyltransferase (EC 2.3.1.128) | bi | see_6619 | 93.22 Ribosomal-protein-alanine acetyltransferase (EC 2.3.1.128) |
| SCE1572_7817 | POSSIBLE RNA METHYLTRANSFERASE (RNA METHYLASE) | bi | see_6620 | 95.98 rRNA/rRNA methyltransferase |
| SCE1572_7818 | hypothetical protein | bi | see_6621 | 79.7 hypothetical protein |
| SCE1572_7819 | Asparaginyl-tRNA synthetase (EC 6.1.1.22) | bi | see_6622 | 93.72 Asparaginyl-tRNA synthetase (EC 6.1.1.22) |
| SCE1572_7820 | Glutamine amidotransferases class-II | bi | see_6623 | 97.12 Glutamine amidotransferases class-II |
| SCE1572_7821 | FIG01087965: hypothetical protein | bi | see_6624 | 86.47 FIG01087965: hypothetical protein |
| SCE1572_7822 | FIG01087972: hypothetical protein | bi | see_6625 | 99.01 FIG01087972: hypothetical protein |
| SCE1572_7823 | hypothetical protein | bi | see_6626 | 90.7 hypothetical protein |
| SCE1572_7824 | 3-oxoacyl-[acyl-carrier-protein] synthase, KASII (EC 2.3.1.41) | bi | see_6627 | 90.39 3-oxoacyl-[acyl-carrier-protein] synthase, KASII (EC 2.3.1.41) |
| SCE1572_7825 | hypothetical protein | bi | see_6628 | 84.15 hypothetical protein |
| SCE1572_7826 | 3-oxoacyl-[acyl-carrier-protein] synthase, KASII (EC 2.3.1.41) | bi | see_6629 | 91.64 3-oxoacyl-[acyl-carrier-protein] synthase, KASII (EC 2.3.1.41) |
| SCE1572_7827 | Acyl carrier protein | bi | see_6630 | 97.92 Acyl carrier protein |
| SCE1572_7828 | Enoyl-CoA hydratase (EC 4.2.1.17) | bi | see_6631 | 97.34 Enoyl-CoA hydratase (EC 4.2.1.17) |
| SCE1572_7829 | FIG01089576: hypothetical protein | bi | see_6632 | 77.55 FIG01089576: hypothetical protein |
| SCE1572_7830 | FIG01087330: hypothetical protein | bi | see_6633 | 92.8 FIG01087330: hypothetical protein |
| SCE1572_7831 | MoxR-like ATPase in aerotolerance operon | bi | see_6634 | 96.22 MoxR-like ATPase in aerotolerance operon |
| SCE1572_7832 | phosphohistidine phosphatase, SixA | bi | see_6635 | 88.57 phosphohistidine phosphatase, SixA |
| SCE1572_7833 | FIG01086953: hypothetical protein | bi | see_6636 | 80.06 FIG01086953: hypothetical protein |
| SCE1572_7834 | hypothetical protein | bi | see_6637 | 79.69 hypothetical protein |
| SCE1572_7835 | hypothetical protein | bi | see_6638 | 95.7 hypothetical protein |
| SCE1572_7836 | Ribosomal large subunit pseudouridine synthase D (EC 4.2.1.70) | bi | see_6639 | 91.59 Ribosomal large subunit pseudouridine synthase D (EC 4.2.1.70) |
| SCE1572_7837 | hypothetical protein | bi | see_6640 | 100 hypothetical protein |
| SCE1572_7838 | Conserved membrane protein | bi | see_6641 | 86.18 probable O-linked GlcNAc transferase-putative TPR-containing transmembrane protein |
| SCE1572_7839 | Septum formation protein Maf | bi | see_6642 | 89.95 Septum formation protein Maf |
| SCE1572_7840 | OmpA | bi | see_6644 | 84.47 OmpA |
| SCE1572_7841 | FIG01087550: hypothetical protein | bi | see_6645 | 83.67 FIG01087550: hypothetical protein |
| SCE1572_7842 | Capsular polysaccharide synthesis enzyme CpsC, polysaccharide export | bi | see_6646 | 93.01 Capsular polysaccharide synthesis enzyme CpsC, polysaccharide export |
| SCE1572_7843 | FIG01086724: hypothetical protein | bi | see_6647 | 83.15 FIG01086724: hypothetical protein |
| SCE1572_7844 | FIG01087823: hypothetical protein | bi | see_6648 | 93.72 FIG01087823: hypothetical protein |
| SCE1572_7845 | hypothetical protein | bi | see_6649 | 94.61 NADH-ubiquinone oxidoreductase chain J (EC 1.6.5.3) |
| SCE1572_7846 | hypothetical protein | bi | see_6650 | 79.13 hypothetical protein |
| SCE1572_7847 | FIG01086734: hypothetical protein | bi | see_6651 | 96.34 FIG01086734: hypothetical protein |
| SCE1572_7848 | FIG01088890: hypothetical protein | bi | see_6652 | 90.47 FIG01088890: hypothetical protein |
| SCE1572_7849 | tetratricopeptide repeat domain protein | bi | see_6653 | 92.13 tetratricopeptide repeat protein |
| SCE1572_7850 | hypothetical protein | bi | see_6654 | 93.42 tetratricopeptide repeat domain protein |
| SCE1572_7851 | Dihydropyridine acetyltransferase component of pyruvate dehydrogenase complex (EC 2.3.1.12) | bi | see_6655 | 85.32 Dihydropyridine acetyltransferase component of pyruvate dehydrogenase complex (EC 2.3.1.12) |
| SCE1572_7852 | hypothetical protein | - | - | 0 |
| SCE1572_7853 | RNA polymerase sigma-70 factor, ECF subfamily | bi | see_6656 | 95.63 RNA polymerase sigma-70 factor, ECF subfamily |
| SCE1572_7854 | Fe-S oxidoreductase | bi | see_6657 | 79.58 Hypothetical protein |
| SCE1572_7855 | FIG01087628: hypothetical protein | bi | see_6658 | 87.95 FIG01087628: hypothetical protein |
| SCE1572_7856 | glycosyl transferase, family 39, putative | bi | see_6659 | 83.75 hypothetical protein |
| SCE1572_7857 | GTP-binding protein Era | bi | see_6660 | 93.87 GTP-binding protein Era |
| SCE1572_7858 | GTP-binding protein EngA | bi | see_6661 | 88.31 GTP-binding protein EngA |
| SCE1572_7859 | hypothetical protein | - | - | 0 |
| SCE1572_7860 | hypothetical protein | - | - | 0 |
| SCE1572_7861 | GTP-binding protein EngA | - | - | 0 |
| SCE1572_7862 | Arsenical pump-driving ATPase (EC 3.6.3.16) | bi | see_6662 | 94.91 Arsenical pump-driving ATPase (EC 3.6.3.16) |
| SCE1572_7863 | hypothetical protein | bi | see_6663 | 83.8 hypothetical protein |
| SCE1572_7864 | Manganese-dependent protein-tyrosine phosphatase (EC 3.1.3.48) | bi | see_6664 | 90.12 Manganese-dependent protein-tyrosine phosphatase (EC 3.1.3.48) |
| SCE1572_7865 | serine/threonine protein kinase | bi | see_6667 | 87.93 serine/threonine protein kinase |
| SCE1572_7866 | RecA protein | bi | see_6668 | 94.92 RecA protein |
| SCE1572_7867 | phosphohistidine phosphatase SixA | bi | see_6669 | 80.24 Uncharacterized protein all0400 (EC 3.1.3.-) |
| SCE1572_7868 | FIG01086717: hypothetical protein | bi | see_6670 | 93.36 FIG01086717: hypothetical protein |
| SCE1572_7869 | rRNA nucleotidyltransferase (EC 2.7.7.21) (EC 2.7.7.25) | bi | see_6671 | 91.95 rRNA nucleotidyltransferase (EC 2.7.7.21) (EC 2.7.7.25) |

| | | | | |
|--------------|---|-----|-----------|---|
| SCE1572_7870 | hypothetical protein | bi | see_6672 | 86.89 hypothetical protein |
| SCE1572_7871 | hypothetical protein | bi | see_6673 | 77.64 hypothetical protein |
| SCE1572_7872 | serine/threonine-protein kinase Pkn6 (EC:2.7.1.1.1) | bi | see_6674 | 93.53 serine/threonine protein kinase |
| SCE1572_7873 | Thiol peroxidase, Bcp-type (EC 1.11.1.15) | bi | see_6675 | 92.86 Thiol peroxidase, Bcp-type (EC 1.11.1.15) |
| SCE1572_7874 | hypothetical protein | bi | see_6676 | 76.98 hypothetical protein |
| SCE1572_7875 | similar to 2,3-bisphosphoglycerate-independent phosphoglycerate mutase | bi | see_6678 | 90.3 similar to 2,3-bisphosphoglycerate-independent phosphoglycerate mutase |
| SCE1572_7876 | hydrolase of the alpha/beta superfamily N | bi | see_6679 | 80.88 temperature sensitive suppressor-like protein |
| SCE1572_7877 | Predicted phosphoesterases, related to the lcc protein | bi | see_6680 | 89.88 Predicted phosphoesterases, related to the lcc protein |
| SCE1572_7878 | FIG01089313: hypothetical protein | bi | see_6681 | 82.49 FIG01089313: hypothetical protein |
| SCE1572_7879 | Succinate-semialdehyde dehydrogenase [NAD] (EC 1.2.1.24); Succinate-semialdehyde dehydrogenase [NADP] (EC 1.2.1.16) | bi | see_6682 | 93.38 Succinate-semialdehyde dehydrogenase [NAD] (EC 1.2.1.24); Succinate-semialdehyde dehydrogenase [NADP] (EC 1.2.1.16) |
| SCE1572_7880 | FIG01086235: hypothetical protein | bi | see_6684 | 82.05 FIG01086235: hypothetical protein |
| SCE1572_7881 | Xylose ABC transporter, substrate-binding component | bi | see_6685 | 76.74 Xylose ABC transporter, substrate-binding component |
| SCE1572_7882 | Fumarylacetoacetate hydrolase family protein | uni | see_5476 | 94.15 Fumarylacetoacetate hydrolase family protein |
| SCE1572_7883 | Maleylacetoacetate isomerase (EC 5.2.1.2) / Glutathione S-transferase | bi | see_6688 | 92.63 Maleylacetoacetate isomerase (EC 5.2.1.2) / Glutathione S-transferase |
| SCE1572_7884 | 4-hydroxyphenylpyruvate dioxygenase (EC 1.13.11.27) | bi | see_5475 | 93.62 4-hydroxyphenylpyruvate dioxygenase (EC 1.13.11.27) |
| SCE1572_7885 | Homogentisate 1,2-dioxygenase (EC 1.13.11.5) | bi | see_5474 | 91.95 Homogentisate 1,2-dioxygenase (EC 1.13.11.5) |
| SCE1572_7886 | hypothetical protein | bi | see_6691 | 59.12 hypothetical protein |
| SCE1572_7887 | Deoxyhypusine synthase | bi | see_6692 | 96.19 Deoxyhypusine synthase |
| SCE1572_7888 | FIG01086591: hypothetical protein | bi | see_6693 | 74.95 FIG01086591: hypothetical protein |
| SCE1572_7889 | hypothetical protein | bi | see_6694 | 80.69 hypothetical protein |
| SCE1572_7890 | FIG01085668: hypothetical protein | bi | see_6695 | 85.82 FIG01085668: hypothetical protein |
| SCE1572_7891 | FIG01087636: hypothetical protein | uni | see_10334 | 48.48 FIG01087636: hypothetical protein |
| SCE1572_7892 | hypothetical protein | - | - | 0 |
| SCE1572_7893 | hypothetical protein | bi | see_2085 | 78.26 hypothetical protein |
| SCE1572_7894 | SRp25 nuclear protein, isoform 3, putative | bi | see_6696 | 87.04 hypothetical protein |
| SCE1572_7895 | hypothetical protein | - | - | 0 |
| SCE1572_7896 | RNA-binding protein | bi | see_2087 | 92.22 RNA-binding protein |
| SCE1572_7897 | hypothetical protein | - | - | 0 |
| SCE1572_7898 | Undecaprenyl-diphosphatase (EC 3.6.1.27) | bi | see_6698 | 90.23 Undecaprenyl-diphosphatase (EC 3.6.1.27) |
| SCE1572_7899 | hypothetical protein | bi | see_1016 | 33.08 FIG01085492: hypothetical protein |
| SCE1572_7900 | hypothetical protein, INTERPRO-suggestion: probable ferritin-like | uni | see_7172 | 48.97 hypothetical protein, INTERPRO-suggestion: probable ferritin-like |
| SCE1572_7901 | FIG01089058: hypothetical protein | uni | see_7173 | 69.59 FIG01089058: hypothetical protein |
| SCE1572_7902 | RedD | bi | see_6705 | 73.82 RedD |
| SCE1572_7903 | Glyoxalase family protein | bi | see_6706 | 89.54 Glyoxalase family protein |
| SCE1572_7904 | transcriptional regulator | bi | see_6707 | 86.93 transcriptional regulator |
| SCE1572_7905 | Tat (twin-arginine translocation) pathway signal sequence domain protein | uni | see_3293 | 39.49 Tat (Twin-arginine translocation) pathway signal sequence domain protein |
| SCE1572_7906 | hypothetical protein | - | - | 0 |
| SCE1572_7907 | Superoxide dismutase [Fe] (EC 1.15.1.1) | bi | see_4677 | 95.83 Superoxide dismutase [Fe] (EC 1.15.1.1) |
| SCE1572_7908 | hypothetical protein | - | - | 0 |
| SCE1572_7909 | hypothetical protein | - | - | 0 |
| SCE1572_7910 | Cytidine/deoxycytidylic deaminase, zinc-binding region | uni | see_2901 | 40.2 rRNA-specific adenosine-34 deaminase (EC 3.5.4.-) |
| SCE1572_7911 | hypothetical protein | bi | see_1247 | 91.41 hypothetical protein |
| SCE1572_7912 | hypothetical protein | uni | see_4564 | 48.39 endo alpha-1,4 polygalactosaminidase precursor |
| SCE1572_7913 | hypothetical protein | - | - | 0 |
| SCE1572_7914 | Sterol desaturase | bi | see_6714 | 86.25 Sterol desaturase |
| SCE1572_7915 | hypothetical protein | - | - | 0 |
| SCE1572_7916 | mannanase, putative | bi | see_6716 | 83.57 FIG01085495: hypothetical protein |
| SCE1572_7917 | Xylose ABC transporter, periplasmic xylose-binding protein XylF | bi | see_6717 | 88.67 Xylose ABC transporter, periplasmic xylose-binding protein XylF |
| SCE1572_7918 | Multicopper oxidase | bi | see_6718 | 87.78 Bilirubin oxidase (EC:1.3.3.5) |
| SCE1572_7919 | Multicopper oxidase | uni | see_6718 | 62.34 Bilirubin oxidase (EC:1.3.3.5) |
| SCE1572_7920 | Spore coat protein A | uni | see_6718 | 59.4 Bilirubin oxidase (EC:1.3.3.5) |
| SCE1572_7921 | hypothetical protein | - | - | 0 |
| SCE1572_7922 | FIG01089645: hypothetical protein | bi | see_6719 | 87.1 FIG01089645: hypothetical protein |
| SCE1572_7923 | Adenylylsulfate kinase (EC 2.7.1.25) | bi | see_6720 | 83.05 Adenylylsulfate kinase (EC 2.7.1.25) |
| SCE1572_7924 | Sensor protein of zinc sigma-54-dependent two-component system | bi | see_6721 | 88.18 Sensor protein of zinc sigma-54-dependent two-component system |
| SCE1572_7925 | Response regulator of zinc sigma-54-dependent two-component system | bi | see_6722 | 77.4 Response regulator of zinc sigma-54-dependent two-component system |
| SCE1572_7926 | putative signal-transduction protein with CBS domains | uni | see_3693 | 40.35 Inosine-5'-monophosphate dehydrogenase (EC 1.1.1.205) |
| SCE1572_7927 | Response regulator of zinc sigma-54-dependent two-component system | bi | see_6723 | 93.3 Response regulator of zinc sigma-54-dependent two-component system |
| SCE1572_7928 | Branched-chain amino acid aminotransferase (EC 2.6.1.42) | bi | see_6724 | 91.69 Branched-chain amino acid aminotransferase (EC 2.6.1.42) |
| SCE1572_7929 | Hypothetical metal-binding enzyme, YcbL homolog | bi | see_6725 | 90.95 Hypothetical metal-binding enzyme, YcbL homolog |
| SCE1572_7930 | FIG01088601: hypothetical protein | bi | see_6726 | 75.29 FIG01088601: hypothetical protein |
| SCE1572_7931 | serine/threonine protein kinase | bi | see_6729 | 89.81 serine/threonine protein kinase |
| SCE1572_7932 | Xaa-Pro dipeptidase (EC 3.4.13.9) | bi | see_6730 | 77.81 Xaa-Pro dipeptidase (EC 3.4.13.9) |
| SCE1572_7933 | hypothetical protein | - | - | 0 |
| SCE1572_7934 | FIG01225684: hypothetical protein | uni | see_4876 | 37.5 Flagellar hook-length control protein FlhK |
| SCE1572_7935 | TOMM biosynthesis cyclodehydratase (protein C) / TOMM biosynthesis docking scaffold (protein D) | bi | see_6733 | 80 TOMM biosynthesis cyclodehydratase (protein C) / TOMM biosynthesis docking scaffold (protein D) |
| SCE1572_7936 | TOMM biosynthesis dehydrogenase (protein B) | bi | see_6734 | 83.2 TOMM biosynthesis dehydrogenase (protein B) |
| SCE1572_7937 | Molybdopterin biosynthesis protein MoeB | bi | see_6735 | 77.36 Molybdopterin biosynthesis protein MoeB |
| SCE1572_7938 | Probable serine/threonine-protein kinase pknH (EC 2.7.1.1.1) | bi | see_6736 | 82.3 Serine/threonine-protein kinase pkn3 (EC 2.7.1.1.1) |
| SCE1572_7939 | FIG01086993: hypothetical protein | bi | see_6737 | 85.96 FIG01086993: hypothetical protein |
| SCE1572_7940 | Flagellar motor rotation protein MotB | bi | see_6738 | 89.75 Flagellar motor rotation protein MotB |
| SCE1572_7941 | hypothetical protein | bi | see_6739 | 75.12 FIG01089703: hypothetical protein |
| SCE1572_7942 | aminopeptidase N (EC:3.4.11.2) | bi | see_6742 | 85.45 aminopeptidase N (EC:3.4.11.2) |
| SCE1572_7943 | hypothetical protein | bi | see_6743 | 88.12 hypothetical protein |
| SCE1572_7944 | hypothetical protein | bi | see_6744 | 91.03 hypothetical protein |
| SCE1572_7945 | hypothetical protein | - | - | 0 |
| SCE1572_7946 | Chemotaxis protein methyltransferase CheR (EC 2.1.1.80) | uni | see_1927 | 33.37 Chemotaxis protein methyltransferase CheR (EC 2.1.1.80) |
| SCE1572_7947 | hypothetical protein | - | - | 0 |
| SCE1572_7948 | two component transcriptional regulator, winged helix family | uni | see_919 | 30.15 Response regulator receiver:ATP-binding region, ATPase-like:Histidine kinase A, N-terminal |
| SCE1572_7949 | hypothetical abductin-like protein | bi | see_6745 | 72.28 FIG01089658: hypothetical protein |
| SCE1572_7950 | Hexokinase (EC 2.7.1.1) | bi | see_6746 | 93.68 Hexokinase (EC 2.7.1.1) |
| SCE1572_7951 | FIG01088471: hypothetical protein | bi | see_6747 | 92.9 FIG01088471: hypothetical protein |
| SCE1572_7952 | 6-phosphogluconate dehydrogenase, decarboxylating (EC 1.1.1.44) | bi | see_6748 | 97.06 6-phosphogluconate dehydrogenase, decarboxylating (EC 1.1.1.44) |
| SCE1572_7953 | antifreeze glycoprotein | bi | see_6750 | 83.85 FIG01086205: hypothetical protein |
| SCE1572_7954 | hypothetical protein | - | - | 0 |
| SCE1572_7955 | Serine/threonine protein kinase (EC 2.7.1.1.1) | bi | see_6751 | 67.23 Serine/threonine protein kinase (EC 2.7.1.1.1) |
| SCE1572_7956 | FIG01086789: hypothetical protein | bi | see_6752 | 72.07 FIG01086789: hypothetical protein |
| SCE1572_7957 | FIG01086435: hypothetical protein | bi | see_6753 | 82.43 FIG01086435: hypothetical protein |
| SCE1572_7958 | FIG01088944: hypothetical protein | bi | see_4490 | 53.8 FIG01088944: hypothetical protein |
| SCE1572_7959 | Arsenate reductase (EC 1.20.4.1) | bi | see_6754 | 92.37 Arsenate reductase (EC 1.20.4.1) |
| SCE1572_7960 | Glucanotactonase (EC 3.1.1.17) | bi | see_2029 | 64.43 Glucanotactonase (EC 3.1.1.17) |
| SCE1572_7961 | hypothetical protein | - | - | 0 |
| SCE1572_7962 | ATP-binding protein of ABC transporter | bi | see_6756 | 97.78 ATP-binding protein of ABC transporter |
| SCE1572_7963 | FIG01087941: hypothetical protein | bi | see_6757 | 81.13 FIG01087941: hypothetical protein |
| SCE1572_7964 | hypothetical protein | - | - | 0 |
| SCE1572_7965 | hypothetical protein | bi | see_6764 | 76 hypothetical protein |
| SCE1572_7966 | hypothetical protein | bi | see_6765 | 80.57 hypothetical protein |
| SCE1572_7967 | hypothetical protein | - | - | 0 |
| SCE1572_7968 | hypothetical protein | bi | see_6766 | 87.96 hypothetical protein |
| SCE1572_7969 | Twin-arginine translocation protein TatB | bi | see_6768 | 75.18 Twin-arginine translocation protein TatB |
| SCE1572_7970 | hypothetical protein | bi | see_6769 | 89.76 FIG023677: hypothetical protein |
| SCE1572_7971 | hypothetical protein | bi | see_6770 | 75.44 hypothetical protein |
| SCE1572_7972 | RNA polymerase sigma-70 factor, ECF subfamily | bi | see_6771 | 79.76 RNA polymerase sigma-70 factor, ECF subfamily |
| SCE1572_7973 | FIG01088275: hypothetical protein | bi | see_6772 | 82.74 FIG01088275: hypothetical protein |
| SCE1572_7974 | Putative hemagglutinin-related protein | bi | see_6773 | 73.07 Putative hemagglutinin-related protein |
| SCE1572_7975 | FIG01087210: hypothetical protein | bi | see_7456 | 85.39 FIG01087210: hypothetical protein |
| SCE1572_7976 | Cellulase(EC:3.2.1.4) | bi | see_7452 | 42.78 putative lipoprotein |
| SCE1572_7977 | hypothetical protein | bi | see_6775 | 84.38 Glyoxalase family protein |
| SCE1572_7978 | VgrG protein | bi | see_9166 | 40.27 VgrG protein |
| SCE1572_7979 | hypothetical protein | uni | see_3673 | 33.63 Protein of unknown function DUF11 |
| SCE1572_7980 | hypothetical protein | - | - | 0 |
| SCE1572_7981 | hypothetical protein | uni | see_9170 | 80.43 hypothetical protein |
| SCE1572_7982 | OmpA/MotB domain protein | uni | see_9171 | 57.43 FIG01085999: hypothetical protein |
| SCE1572_7983 | hypothetical protein | uni | see_5449 | 35.93 FIG01088294: hypothetical protein |
| SCE1572_7984 | FIG01087276: hypothetical protein | bi | see_6787 | 83.15 FIG01087276: hypothetical protein |
| SCE1572_7985 | hypothetical protein | bi | see_6788 | 95.57 hypothetical protein |
| SCE1572_7986 | hypothetical protein | bi | see_6789 | 78.09 hypothetical protein |
| SCE1572_7987 | RsbR, positive regulator of sigma-B | bi | see_6790 | 84.48 RsbR, positive regulator of sigma-B |
| SCE1572_7988 | hypothetical protein | uni | see_4254 | 29.86 serine/threonine protein kinase |
| SCE1572_7989 | hypothetical protein | - | - | 0 |
| SCE1572_7990 | hypothetical protein | - | - | 0 |
| SCE1572_7991 | PPO candidate 1 | bi | see_6792 | 91.19 hypothetical protein |
| SCE1572_7992 | N-acetylglucosamine related transporter, NagX | - | - | 0 |
| SCE1572_7993 | spore peptidoglycan hydrolase | bi | see_6793 | 78.66 peptidoglycan hydrolase |
| SCE1572_7994 | hypothetical protein | - | - | 0 |
| SCE1572_7995 | Insecticidal toxin complex protein TcdB1 | bi | see_9566 | 88.62 Insecticidal toxin complex protein TcdB1 |
| SCE1572_7996 | Insecticidal toxin complex protein TcdB1 | uni | see_6225 | 95.57 hypothetical protein |
| SCE1572_7997 | hypothetical protein | bi | see_6226 | 93.32 Integrase, catalytic region |
| SCE1572_7998 | transposase for IS481 element | uni | see_6227 | 84.09 hypothetical protein |
| SCE1572_7999 | hypothetical protein | - | - | 0 |
| SCE1572_8000 | Insecticidal toxin complex protein TcdB1 | uni | see_9566 | 88 Insecticidal toxin complex protein TcdB1 |
| SCE1572_8001 | Insecticidal toxin complex protein TcdB1 | - | - | 0 |
| SCE1572_8002 | Mobile element protein | uni | see_9566 | 76.85 Insecticidal toxin complex protein TcdB1 |
| SCE1572_8003 | Insecticidal toxin complex protein TcdB1 | - | - | 0 |
| SCE1572_8004 | hypothetical protein | bi | see_6795 | 94.22 hypothetical protein |
| SCE1572_8005 | hypothetical protein | - | - | 0 |
| SCE1572_8006 | hypothetical protein | bi | see_6796 | 88.74 Cell division inhibitor |
| SCE1572_8007 | Cell division inhibitor | bi | see_6797 | 92.6 Short-chain alcohol dehydrogenase |
| SCE1572_8008 | Short-chain alcohol dehydrogenase | bi | see_6798 | 93 Fatty acid desaturase (EC 1.14.19.1); Delta-9 fatty acid desaturase (EC 1.14.19.1) |
| SCE1572_8009 | Fatty acid desaturase (EC 1.14.19.1); Delta-9 fatty acid desaturase (EC 1.14.19.1) | bi | see_6800 | 91.02 hypothetical protein |
| SCE1572_8010 | putative nucleotide sugar-1-phosphate transferase | bi | see_6801 | 93.31 pyridoxal phosphate-dependent deaminase, putative |
| SCE1572_8011 | pyridoxal phosphate-dependent deaminase, putative | - | - | 0 |
| SCE1572_8012 | hypothetical protein | bi | see_6802 | 85.19 hypothetical protein |
| SCE1572_8013 | hypothetical protein | bi | see_6803 | 90.22 Histidine ammonia-lyase (EC 4.3.1.3) |
| SCE1572_8014 | Histidine ammonia-lyase (EC 4.3.1.3) | bi | see_6804 | 87.83 FIG01088805: hypothetical protein |
| SCE1572_8015 | FIG01088805: hypothetical protein | bi | see_6805 | 93.94 hypothetical protein |
| SCE1572_8016 | hypothetical protein | bi | see_6807 | 89.31 hypothetical protein |
| SCE1572_8017 | hypothetical protein | uni | see_1675 | 96.77 ISLp1 |
| SCE1572_8018 | Mobile element protein | bi | see_6827 | 87.36 Mobile element protein |
| SCE1572_8019 | Mobile element protein | bi | see_7413 | 87.86 Transposase |
| SCE1572_8020 | Transposase | bi | see_10161 | 89.29 hypothetical protein |
| SCE1572_8021 | hypothetical protein | - | - | 0 |
| SCE1572_8022 | hypothetical protein | uni | see_9479 | 64.49 hypothetical protein |
| SCE1572_8023 | hypothetical protein | - | - | 0 |
| SCE1572_8024 | hypothetical protein | - | - | 0 |
| SCE1572_8025 | hypothetical protein | uni | see_513 | 40.28 FIG01087636: hypothetical protein |
| SCE1572_8026 | hypothetical protein | - | - | 0 |
| SCE1572_8027 | hypothetical protein | - | - | 0 |
| SCE1572_8028 | hypothetical protein | bi | see_304 | 40.94 VgrG protein |
| SCE1572_8029 | hypothetical protein | uni | see_9167 | 35.47 FIG01088662: hypothetical protein |
| SCE1572_8030 | VgrG protein | - | - | 0 |
| SCE1572_8031 | hypothetical protein | - | - | 0 |
| SCE1572_8032 | hypothetical protein | - | - | 0 |
| SCE1572_8033 | hypothetical protein | - | - | 0 |
| SCE1572_8034 | hypothetical protein | uni | see_9170 | 90 hypothetical protein |

| | | | | | |
|--------------|--|-----|-----------|-------|--|
| SCE1572_8035 | hypothetical protein | bi | sce_9171 | 68.6 | FIG01085999: hypothetical protein |
| SCE1572_8036 | hypothetical protein | uni | sce_9479 | 61.25 | hypothetical protein |
| SCE1572_8037 | hypothetical protein | - | - | 0 | 0 |
| SCE1572_8038 | hypothetical protein | uni | sce_6869 | 71.65 | hypothetical protein |
| SCE1572_8039 | PE-PGRS FAMILY PROTEIN | uni | sce_6870 | 69.28 | PE-PGRS FAMILY PROTEIN |
| SCE1572_8040 | FIG01089478: hypothetical protein | bi | sce_7516 | 60.89 | FIG01089478: hypothetical protein |
| SCE1572_8041 | RNA polymerase sigma factor SigW | bi | sce_6872 | 66.78 | RNA polymerase sigma factor SigW |
| SCE1572_8042 | RNA polymerase sigma factor | bi | sce_6877 | 68.67 | RNA polymerase sigma factor |
| SCE1572_8043 | hypothetical protein | bi | sce_6809 | 70.45 | hypothetical protein |
| SCE1572_8044 | hypothetical protein | - | - | 0 | 0 |
| SCE1572_8045 | hypothetical protein | uni | sce_8035 | 24.67 | Chromosome partition protein smc |
| SCE1572_8046 | hypothetical protein | - | - | 0 | 0 |
| SCE1572_8047 | hypothetical protein | - | - | 0 | 0 |
| SCE1572_8048 | FIG01088450: hypothetical protein | uni | sce_1463 | 47.62 | FIG01085728: hypothetical protein |
| SCE1572_8049 | putative peptidoglycan bound protein (LPXTG motif) | uni | sce_3180 | 32.69 | FIG01089285: hypothetical protein |
| SCE1572_8050 | hypothetical protein | - | - | 0 | 0 |
| SCE1572_8051 | hypothetical protein | - | - | 0 | 0 |
| SCE1572_8052 | hypothetical protein | - | - | 0 | 0 |
| SCE1572_8053 | hypothetical protein | - | - | 0 | 0 |
| SCE1572_8054 | hypothetical protein | - | - | 0 | 0 |
| SCE1572_8055 | hypothetical protein | - | - | 0 | 0 |
| SCE1572_8056 | hypothetical protein | - | - | 0 | 0 |
| SCE1572_8057 | hypothetical protein | - | - | 0 | 0 |
| SCE1572_8058 | hypothetical protein | bi | sce_7416 | 48.84 | hypothetical protein |
| SCE1572_8059 | hypothetical protein | - | - | 0 | 0 |
| SCE1572_8060 | hypothetical protein | - | - | 0 | 0 |
| SCE1572_8061 | hypothetical protein | - | - | 0 | 0 |
| SCE1572_8062 | hypothetical protein | - | - | 0 | 0 |
| SCE1572_8063 | hypothetical protein | - | - | 0 | 0 |
| SCE1572_8064 | RNA polymerase sigma factor RpoE | uni | sce_6165 | 59.72 | RNA polymerase sigma factor RpoE |
| SCE1572_8065 | HK97 major tail subunit | uni | sce_616 | 38.19 | NHL repeat protein |
| SCE1572_8066 | hypothetical protein | - | - | 0 | 0 |
| SCE1572_8067 | hypothetical protein | - | - | 0 | 0 |
| SCE1572_8068 | Mobile element protein | uni | sce_7404 | 80.75 | Mobile element protein |
| SCE1572_8069 | Transposase | uni | sce_10160 | 66.67 | Transposase |
| SCE1572_8070 | hypothetical protein | uni | sce_10161 | 89.29 | hypothetical protein |
| SCE1572_8071 | putative transposase | - | - | 0 | 0 |
| SCE1572_8072 | Mobile element protein | uni | sce_9803 | 35.19 | Mobile element protein |
| SCE1572_8073 | Mobile element protein | bi | sce_9804 | 33.59 | Mobile element protein |
| SCE1572_8074 | Mobile element protein | bi | sce_1036 | 85 | hypothetical protein |
| SCE1572_8075 | bil2159; putative transposase | uni | sce_6228 | 71.64 | Mobile element protein |
| SCE1572_8076 | Transposase | uni | sce_10160 | 87.93 | Transposase |
| SCE1572_8077 | hypothetical protein | uni | sce_10161 | 86.61 | hypothetical protein |
| SCE1572_8078 | hypothetical protein | - | - | 0 | 0 |
| SCE1572_8079 | hypothetical protein | - | - | 0 | 0 |
| SCE1572_8080 | RNA polymerase sigma factor RpoE | uni | sce_6165 | 59.72 | RNA polymerase sigma factor RpoE |
| SCE1572_8081 | hypothetical protein | - | - | 0 | 0 |
| SCE1572_8082 | hypothetical protein | bi | sce_6847 | 62 | hypothetical protein |
| SCE1572_8083 | FIG01087954: hypothetical protein | uni | sce_6849 | 80.85 | FIG01087954: hypothetical protein |
| SCE1572_8084 | hypothetical protein | - | - | 0 | 0 |
| SCE1572_8085 | hypothetical protein | - | - | 0 | 0 |
| SCE1572_8086 | hypothetical protein | - | - | 0 | 0 |
| SCE1572_8087 | Glycine dehydrogenase [decarboxylating] (glycine cleavage system P1 protein) (EC 1.4.4.2) | uni | sce_2240 | 43.22 | Glycine dehydrogenase [decarboxylating] (glycine cleavage system P1 protein) (EC 1.4.4.2) |
| SCE1572_8088 | Glycine dehydrogenase [decarboxylating] (glycine cleavage system P2 protein) (EC 1.4.4.2) | uni | sce_10237 | 45.57 | Glycine dehydrogenase [decarboxylating] (glycine cleavage system P2 protein) (EC 1.4.4.2) |
| SCE1572_8089 | [NiFe] hydrogenase metalcenter assembly protein HypE | bi | sce_5122 | 93.77 | [NiFe] hydrogenase metalcenter assembly protein HypE |
| SCE1572_8090 | [NiFe] hydrogenase metalcenter assembly protein HypD | bi | sce_5121 | 92.41 | [NiFe] hydrogenase metalcenter assembly protein HypD |
| SCE1572_8091 | [NiFe] hydrogenase nickel incorporation protein HypA | bi | sce_5118 | 94.69 | [NiFe] hydrogenase nickel incorporation protein HypA |
| SCE1572_8092 | Hydrogenase maturation protease (EC 3.4.24.-) | bi | sce_5117 | 80.84 | hypothetical protein |
| SCE1572_8093 | hydrogenase/sulfur reductase, alpha subunit | bi | sce_5116 | 91.28 | hydrogenase/sulfur reductase, alpha subunit |
| SCE1572_8094 | hydrogenase/sulfur reductase, delta subunit | bi | sce_5115 | 98.06 | hydrogenase/sulfur reductase, delta subunit |
| SCE1572_8095 | 2-polyphenylphenol hydroxylase and related flavodoxin oxidoreductases | bi | sce_5114 | 93.56 | 2-polyphenylphenol hydroxylase and related flavodoxin oxidoreductases |
| SCE1572_8096 | cAMP-binding proteins - catabolite gene activator and regulatory subunit of cAMP-dependent protein kinases | bi | sce_5113 | 85.44 | cAMP-binding proteins - catabolite gene activator and regulatory subunit of cAMP-dependent protein kinases |
| SCE1572_8097 | Ferredoxin | bi | sce_5112 | 84.65 | Ferredoxin |
| SCE1572_8098 | hypothetical protein | bi | sce_9043 | 84.09 | hypothetical protein |
| SCE1572_8099 | Ferrous iron transport protein B | bi | sce_9044 | 88.86 | Ferrous iron transport protein B |
| SCE1572_8100 | Phosphoenolpyruvate synthase (EC 2.7.9.2) | bi | sce_5110 | 91.37 | Phosphoenolpyruvate synthase (EC 2.7.9.2) |
| SCE1572_8101 | Endoglucanase Y (EC 3.2.1.4) | uni | sce_1998 | 46.34 | FIG01086574: hypothetical protein |
| SCE1572_8102 | hypothetical protein | uni | sce_3292 | 37.57 | Cellulose-binding domain protein |
| SCE1572_8103 | Cellulose-binding domain protein | uni | sce_4499 | 37.63 | Cellulose-binding domain protein |
| SCE1572_8104 | Tat (twin-arginine translocation) pathway signal sequence domain protein | uni | sce_3293 | 30.62 | Tat (Twin-arginine translocation) pathway signal sequence domain protein |
| SCE1572_8105 | hypothetical protein | - | - | 0 | 0 |
| SCE1572_8106 | 5-aminopentanamide (EC 3.5.1.30) | uni | sce_4305 | 29.71 | 5-aminopentanamide (EC 3.5.1.30) |
| SCE1572_8107 | D-proline reductase, 26 kDa subunit (EC 1.21.4.1) @ selenocysteine-containing | - | - | 0 | 0 |
| SCE1572_8108 | D-proline reductase, 45 kDa subunit (EC 1.21.4.1) / D-proline reductase, 23 kDa subunit (EC 1.21.4.1) | - | - | 0 | 0 |
| SCE1572_8109 | proline racemase | - | - | 0 | 0 |
| SCE1572_8110 | hypothetical protein | - | - | 0 | 0 |
| SCE1572_8111 | High-affinity branched-chain amino acid transport system permease protein LivH (TC 3.A.1.4.1) | uni | sce_9290 | 38.94 | High-affinity branched-chain amino acid transport system permease protein LivH (TC 3.A.1.4.1) |
| SCE1572_8112 | Branched-chain amino acid transport system permease protein LivM (TC 3.A.1.4.1) | uni | sce_9613 | 34.48 | Branched-chain amino acid transport system permease protein LivM (TC 3.A.1.4.1) |
| SCE1572_8113 | Branched-chain amino acid transport ATP-binding protein LivG (TC 3.A.1.4.1) | uni | sce_9614 | 45.67 | Branched-chain amino acid transport ATP-binding protein LivG (TC 3.A.1.4.1) |
| SCE1572_8114 | Branched-chain amino acid transport ATP-binding protein LivF (TC 3.A.1.4.1) | uni | sce_9615 | 44.92 | Branched-chain amino acid transport ATP-binding protein LivF (TC 3.A.1.4.1) |
| SCE1572_8115 | Arginine decarboxylase (EC 4.1.1.19) | bi | sce_5109 | 95.43 | Arginine decarboxylase (EC 4.1.1.19) |
| SCE1572_8116 | hypothetical protein | - | - | 0 | 0 |
| SCE1572_8117 | hypothetical protein | - | - | 0 | 0 |
| SCE1572_8118 | FIG01087249: hypothetical protein | uni | sce_2338 | 92.86 | Transposase |
| SCE1572_8119 | FIG01087249: hypothetical protein | uni | sce_2337 | 87.95 | FIG01087249: hypothetical protein |
| SCE1572_8120 | hypothetical protein | - | - | 0 | 0 |
| SCE1572_8121 | Glutamate decarboxylase | - | - | 0 | 0 |
| SCE1572_8122 | hypothetical protein | uni | sce_4578 | 32.41 | Acetyl-CoA synthetase (ADP-forming) alpha and beta chains, putative |
| SCE1572_8123 | hypothetical protein | - | - | 0 | 0 |
| SCE1572_8124 | Mannose-6-phosphate isomerase | - | - | 0 | 0 |
| SCE1572_8125 | hypothetical protein | - | - | 0 | 0 |
| SCE1572_8126 | cation-transporting ATPase, E1-E2 family | bi | sce_5107 | 94.25 | cation-transporting ATPase, E1-E2 family |
| SCE1572_8127 | Chemotaxis protein methyltransferase CheR (EC 2.1.1.80) | bi | sce_9045 | 78.91 | Chemotaxis protein methyltransferase CheR (EC 2.1.1.80) |
| SCE1572_8128 | hypothetical protein | - | - | 0 | 0 |
| SCE1572_8129 | hypothetical protein | - | - | 0 | 0 |
| SCE1572_8130 | Dihydroliipoamide acyltransferase component of branched-chain alpha-keto acid dehydrogenase complex (EC 2.3.1.168) | uni | sce_1746 | 24.79 | Dihydroliipoamide acyltransferase component of branched-chain alpha-keto acid dehydrogenase complex (EC 2.3.1.168) |
| SCE1572_8131 | hypothetical protein | - | - | 0 | 0 |
| SCE1572_8132 | dienolactone hydrolase | uni | sce_10090 | 62.28 | Hydrolases of the alpha/beta superfamily |
| SCE1572_8133 | heat shock protein, HSP20 family | uni | sce_8620 | 44.57 | Molecular chaperone (small heat shock protein) |
| SCE1572_8134 | Heat shock protein 60 family chaperone GroEL | uni | sce_3121 | 55.33 | Heat shock protein 60 family chaperone GroEL |
| SCE1572_8135 | DNA polymerase X | uni | sce_9813 | 38.09 | phosphoesterase, PHP-like |
| SCE1572_8136 | hypothetical protein | - | - | 0 | 0 |
| SCE1572_8137 | Glucosylase GLA1 precursor (EC 3.2.1.3) (Glucan 1,4-alpha-glucosidase) (1,4-alpha-D-glucan glucohydrolase) | bi | sce_861 | 30 | putative glucosylase protein (EC:3.2.1.3) |
| SCE1572_8138 | hypothetical protein | uni | sce_3694 | 36.89 | Universal stress protein family |
| SCE1572_8139 | COG1801: Uncharacterized conserved protein | bi | sce_6416 | 42.86 | protein of unknown function DUF72 |
| SCE1572_8140 | RNA polymerase sigma factor RpoD | uni | sce_2933 | 46.77 | RNA polymerase sigma factor SigB |
| SCE1572_8141 | transport-associated | - | - | 0 | 0 |
| SCE1572_8142 | protein of unknown function DUF294, nucleotidyltransferase putative | uni | sce_8964 | 38.66 | CBS domain protein |
| SCE1572_8143 | CBS domain protein | uni | sce_8964 | 34.55 | CBS domain protein |
| SCE1572_8144 | cold shock domain family protein | uni | sce_6268 | 39.56 | cold shock domain family protein |
| SCE1572_8145 | Transcription antitermination protein NusG | uni | sce_460 | 55.43 | Transcription antitermination protein NusG |
| SCE1572_8146 | Inosine-5-phosphatase (EC 3.1.1.205) | bi | sce_3042 | 81.15 | Inosine-5-phosphatase (EC 3.1.1.205) |
| SCE1572_8147 | Magnesium and cobalt efflux protein CorC | uni | sce_4801 | 28.57 | Magnesium and cobalt efflux protein CorC |
| SCE1572_8148 | Capsule biosynthesis protein capA | uni | sce_10411 | 32.05 | FIG01089659: hypothetical protein |
| SCE1572_8149 | Ribonucleotide reductase of class Ia (coenzyme B12-dependent) (EC 1.17.4.1) | uni | sce_4336 | 30.72 | Ribonucleotide reductase of class Ia (aerobic), alpha subunit (EC 1.17.4.1) |
| SCE1572_8150 | hypothetical protein | uni | sce_10090 | 64.73 | Hydrolases of the alpha/beta superfamily |
| SCE1572_8151 | CBS domain protein | uni | sce_8964 | 31.3 | CBS domain protein |
| SCE1572_8152 | hypothetical protein | uni | sce_2973 | 70.18 | General stress protein |
| SCE1572_8153 | Heat shock protein Hsp20 | uni | sce_5552 | 46.97 | Molecular chaperone (small heat shock protein)-like |
| SCE1572_8154 | Ribose-phosphate pyrophosphokinase (EC 2.7.6.1) | uni | sce_7763 | 42.72 | Ribose-phosphate pyrophosphokinase (EC 2.7.6.1) |
| SCE1572_8155 | Acetoin dehydrogenase E1 component alpha-subunit (EC 1.2.4.-) | uni | sce_4255 | 46.3 | Pyruvate dehydrogenase E1 component alpha subunit (EC 1.2.4.1) |
| SCE1572_8156 | magnesium-translocating P-type ATPase | uni | sce_6126 | 32.31 | cation-transporting ATPase, E1-E2 family |
| SCE1572_8157 | hypothetical protein | - | - | 0 | 0 |
| SCE1572_8158 | hypothetical protein | - | - | 0 | 0 |
| SCE1572_8159 | hypothetical protein | - | - | 0 | 0 |
| SCE1572_8160 | Acetoin dehydrogenase E1 component beta-subunit (EC 1.2.4.-) | uni | sce_4256 | 49.84 | Pyruvate dehydrogenase E1 component beta subunit (EC 1.2.4.1) |
| SCE1572_8161 | Dihydroliipoamide acetyltransferase component (E2) of acetoin dehydrogenase complex (EC 2.3.1.-) | uni | sce_4257 | 36.51 | Dihydroliipoamide acetyltransferase component of pyruvate dehydrogenase complex (EC 2.3.1.12) |
| SCE1572_8162 | similar to acyl carrier protein | - | - | 0 | 0 |
| SCE1572_8163 | Acetyl-coenzyme A synthetase (EC 6.2.1.1) | uni | sce_8866 | 40.24 | Acetyl-coenzyme A synthetase (EC 6.2.1.1) |
| SCE1572_8164 | hypothetical protein | - | - | 0 | 0 |
| SCE1572_8165 | hypothetical protein | bi | sce_6970 | 82.98 | hypothetical protein |
| SCE1572_8166 | hypothetical protein | bi | sce_8358 | 86.84 | COGs COG0840 |
| SCE1572_8167 | hypothetical protein | - | - | 0 | 0 |
| SCE1572_8168 | hydroxylase | - | - | 0 | 0 |
| SCE1572_8169 | membrane protein-like protein | - | - | 0 | 0 |
| SCE1572_8170 | Phosphate ABC transporter, periplasmic phosphate-binding protein PstS (TC 3.A.1.7.1) | uni | sce_3309 | 23.2 | Phosphate ABC transporter, periplasmic phosphate-binding protein PstS (TC 3.A.1.7.1) |
| SCE1572_8171 | Phosphate transport system permease protein PstC (TC 3.A.1.7.1) | uni | sce_3308 | 37.71 | Phosphate transport system permease protein PstC (TC 3.A.1.7.1) |
| SCE1572_8172 | Phosphate transport ATP-binding protein PstB (TC 3.A.1.7.1) | uni | sce_3306 | 48.93 | Phosphate transport ATP-binding protein PstB (TC 3.A.1.7.1) |
| SCE1572_8173 | Phosphate transport ATP-binding protein PstB (TC 3.A.1.7.1) | uni | sce_3306 | 52.17 | Phosphate transport ATP-binding protein PstB (TC 3.A.1.7.1) |
| SCE1572_8174 | Phosphate transport system regulatory protein PhoU | uni | sce_3305 | 33.08 | Phosphate transport system regulatory protein PhoU |
| SCE1572_8175 | Amino acid permease | bi | sce_5106 | 93.15 | Amino acid permease |
| SCE1572_8176 | Amino acid permease | uni | sce_5106 | 92.61 | Amino acid permease |
| SCE1572_8177 | putative oxidoreductase | uni | sce_5114 | 33.33 | 2-polyphenylphenol hydroxylase and related flavodoxin oxidoreductases |
| SCE1572_8178 | hypothetical protein | - | - | 0 | 0 |
| SCE1572_8179 | hypothetical protein | - | - | 0 | 0 |
| SCE1572_8180 | Lead, cadmium, zinc and mercury transporting ATPase (EC 3.6.3.3) (EC 3.6.3.5); Copper-translocating P-type ATPase (EC 3.6.3.4) | uni | sce_9067 | 39.85 | Lead, cadmium, zinc and mercury transporting ATPase (EC 3.6.3.3) (EC 3.6.3.5); Copper-translocating P-type ATPase (EC 3.6.3.4) |
| SCE1572_8181 | hypothetical protein | - | - | 0 | 0 |
| SCE1572_8182 | hypothetical protein | uni | sce_1205 | 40.24 | Universal stress protein family |
| SCE1572_8183 | hypothetical protein | - | - | 0 | 0 |
| SCE1572_8184 | FIG01087954: hypothetical protein | bi | sce_6849 | 81.82 | FIG01087954: hypothetical protein |
| SCE1572_8185 | hypothetical protein | - | - | 0 | 0 |
| SCE1572_8186 | hypothetical protein | - | - | 0 | 0 |
| SCE1572_8187 | hypothetical protein | - | - | 0 | 0 |
| SCE1572_8188 | ADL187Wp | uni | sce_6679 | 75.51 | temperature sensitive suppressor-like protein |
| SCE1572_8189 | hypothetical protein | uni | sce_7509 | 29.26 | Oligopeptide ABC transporter, periplasmic oligopeptide-binding protein OppA (TC 3.A.1.5.1) |
| SCE1572_8190 | NB-ARC domain protein | uni | sce_4070 | 44.51 | DNA gyrase subunit A (EC 5.99.1.3) |
| SCE1572_8191 | hypothetical protein | uni | sce_6052 | 30.21 | hypothetical protein |
| SCE1572_8192 | hypothetical protein | uni | sce_3606 | 32.14 | Protein kinase |
| SCE1572_8193 | response regulator receiver | uni | sce_2361 | 28.73 | FIG100068: Hypothetical protein |
| SCE1572_8194 | DNA double-strand break repair protein Mre11 | uni | sce_8023 | 24.87 | DNA double-strand break repair protein Mre11 |
| SCE1572_8195 | transcriptional regulator, LuxR family protein | - | - | 0 | 0 |
| SCE1572_8196 | hypothetical protein | - | - | 0 | 0 |
| SCE1572_8197 | hypothetical protein | - | - | 0 | 0 |
| SCE1572_8198 | hypothetical protein | - | - | 0 | 0 |

| | | | | | |
|--------------|--|-----|-----------|-------|--|
| SCE1572_8199 | sigma54 specific transcriptional regulator with PAS sensor, Fis family | umi | sce_2992 | 49.51 | sigma-54 dependent DNA-binding response regulator |
| SCE1572_8200 | hypothetical protein | - | - | 0 | |
| SCE1572_8201 | hypothetical protein | - | - | 0 | |
| SCE1572_8202 | hypothetical protein | - | - | 0 | |
| SCE1572_8203 | hypothetical protein | bi | sce_6891 | 93.44 | hypothetical protein |
| SCE1572_8204 | hypothetical protein | - | - | 0 | |
| SCE1572_8205 | Serine/arginine repetitive matrix protein 2 | bi | sce_6848 | 82.54 | Flagellar hook-length control protein FliK |
| SCE1572_8206 | hypothetical protein | bi | sce_8351 | 82.98 | hypothetical protein |
| SCE1572_8207 | FIG01085999: hypothetical protein | bi | sce_8350 | 55.09 | FIG01085999: hypothetical protein |
| SCE1572_8208 | hypothetical protein | bi | sce_8348 | 51.95 | hypothetical protein |
| SCE1572_8209 | FIG01085109: hypothetical protein | bi | sce_8347 | 74.88 | Rhs family protein |
| SCE1572_8210 | FIG01087149: hypothetical protein | bi | sce_8346 | 70.21 | FIG01087149: hypothetical protein |
| SCE1572_8211 | VgrG protein | bi | sce_8345 | 77.83 | VgrG protein |
| SCE1572_8212 | FIG01087791: hypothetical protein | bi | sce_8344 | 80.29 | FIG01087791: hypothetical protein |
| SCE1572_8213 | VgrG protein | bi | sce_8343 | 74.14 | VgrG protein |
| SCE1572_8214 | VgrG protein | bi | sce_8342 | 76.44 | VgrG protein |
| SCE1572_8215 | hypothetical protein | - | - | 0 | |
| SCE1572_8216 | hypothetical protein | - | - | 0 | |
| SCE1572_8217 | hypothetical protein | - | - | 0 | |
| SCE1572_8218 | two-component sensor histidine kinase | umi | sce_229 | 52.96 | FOG: PAS/PAC domain |
| SCE1572_8219 | hypothetical protein | - | - | 0 | |
| SCE1572_8220 | Uncharacterized protein conserved in bacteria | bi | sce_4907 | 46.54 | hypothetical protein |
| SCE1572_8221 | unknown protein | bi | sce_4905 | 45.07 | FIG01086791: hypothetical protein |
| SCE1572_8222 | N-succinyl-L,L-diaminopimelate desuccinylase (EC 3.5.1.18) | bi | sce_7070 | 85.96 | N-succinyl-L,L-diaminopimelate desuccinylase (EC 3.5.1.18) |
| SCE1572_8223 | hypothetical protein | - | - | 0 | |
| SCE1572_8224 | hypothetical protein | - | - | 0 | |
| SCE1572_8225 | FIG01087506: hypothetical protein | bi | sce_6785 | 62.16 | FIG01087506: hypothetical protein |
| SCE1572_8226 | hypothetical protein | bi | sce_6895 | 90.56 | hypothetical protein |
| SCE1572_8227 | hypothetical protein | bi | sce_6896 | 83.79 | hypothetical protein |
| SCE1572_8228 | Soluble lytic murein transglycosylase precursor (EC 3.2.1.-) | bi | sce_6897 | 87.64 | Soluble lytic murein transglycosylase precursor (EC 3.2.1.-) |
| SCE1572_8229 | hypothetical protein | bi | sce_6899 | 89.3 | hypothetical protein |
| SCE1572_8230 | hypothetical protein | bi | sce_6900 | 88.83 | hypothetical protein |
| SCE1572_8231 | hypothetical protein | bi | sce_6901 | 93.36 | hypothetical protein |
| SCE1572_8232 | Acetylsermidine deacetylase (EC 3.5.1.48); Deacetylases, including yeast histone deacetylase and acetoin utilization protein | bi | sce_6902 | 88.29 | Acetylsermidine deacetylase (EC 3.5.1.48); Deacetylases, including yeast histone deacetylase and acetoin utilization protein |
| SCE1572_8233 | FIG01085396: hypothetical protein | bi | sce_6905 | 81.3 | FIG01085396: hypothetical protein |
| SCE1572_8234 | hypothetical protein | - | - | 0 | |
| SCE1572_8235 | hypothetical protein | bi | sce_6906 | 83.87 | hypothetical protein |
| SCE1572_8236 | Nitrate/nitrite response regulator protein | bi | sce_6907 | 88.02 | Nitrate/nitrite response regulator protein |
| SCE1572_8237 | dedA protein | bi | sce_6908 | 83.33 | Uncharacterized protein MJ0374 |
| SCE1572_8238 | FIG01087842: hypothetical protein | bi | sce_6909 | 95.02 | FIG01087842: hypothetical protein |
| SCE1572_8239 | hypothetical protein | bi | sce_6910 | 82.55 | hypothetical protein |
| SCE1572_8240 | protein kinase | bi | sce_6911 | 82.03 | serine/threonine protein kinase |
| SCE1572_8241 | Cystathionine gamma-lyase (EC 4.4.1.1) | bi | sce_6912 | 93.38 | Cystathionine gamma-lyase (EC 4.4.1.1) |
| SCE1572_8242 | hypothetical protein | bi | sce_6913 | 53.44 | hypothetical protein |
| SCE1572_8243 | Protein serine/threonine phosphatase PrpC, regulation of stationary phase | bi | sce_6914 | 97.28 | Protein serine/threonine phosphatase PrpC, regulation of stationary phase |
| SCE1572_8244 | Ribosome recycling factor | bi | sce_6915 | 93.51 | Ribosome recycling factor |
| SCE1572_8245 | Response regulator of zinc sigma-54-dependent two-component system | bi | sce_6916 | 93.71 | Response regulator of zinc sigma-54-dependent two-component system |
| SCE1572_8246 | Alkyl hydroperoxide reductase subunit C-like protein | bi | sce_6917 | 81.17 | Alkyl hydroperoxide reductase subunit C-like protein |
| SCE1572_8247 | DNA-3-methyladenine glycosylase II (EC 3.2.2.21) | bi | sce_6918 | 90.45 | DNA-3-methyladenine glycosylase II (EC 3.2.2.21) |
| SCE1572_8248 | FIG00578842: hypothetical protein | bi | sce_6919 | 59.34 | putative lipoprotein |
| SCE1572_8249 | hypothetical protein | bi | sce_6920 | 85.33 | hypothetical protein |
| SCE1572_8250 | Peptide chain release factor 3 | bi | sce_6921 | 97.55 | Peptide chain release factor 3 |
| SCE1572_8251 | hypothetical protein | bi | sce_6922 | 78.32 | hypothetical protein |
| SCE1572_8252 | Halogenase | bi | sce_6923 | 90.66 | Halogenase |
| SCE1572_8253 | hypothetical protein | bi | sce_6924 | 89.44 | hypothetical protein |
| SCE1572_8254 | probable transcriptional regulator | bi | sce_6925 | 79.74 | transcriptional regulator, LysR family |
| SCE1572_8255 | Type IV pilus biogenesis protein PilQ | bi | sce_6926 | 90.91 | Type IV pilus biogenesis protein PilQ |
| SCE1572_8256 | hypothetical protein | bi | sce_6927 | 84.86 | hypothetical protein |
| SCE1572_8257 | Type IV pilus biogenesis protein PilO | bi | sce_6928 | 93.87 | Type IV pilus biogenesis protein PilO |
| SCE1572_8258 | Type IV pilus biogenesis protein PilN | bi | sce_6929 | 97.2 | Type IV pilus biogenesis protein PilN |
| SCE1572_8259 | Type IV pilus biogenesis protein PilM | bi | sce_6930 | 98.56 | Type IV pilus biogenesis protein PilM |
| SCE1572_8260 | FIG01086474: hypothetical protein | bi | sce_6931 | 81.63 | FIG01086474: hypothetical protein |
| SCE1572_8261 | RNA polymerase sigma factor for flagellar operon | bi | sce_6932 | 77.12 | RNA polymerase sigma factor for flagellar operon |
| SCE1572_8262 | hypothetical protein | bi | sce_6933 | 82.09 | hypothetical protein |
| SCE1572_8263 | 3-aminobutryl-CoA ammonia-lyase (EC 4.3.1.14) / 3-keto-5-aminohexanoate cleavage enzyme | bi | sce_6934 | 94.13 | 3-aminobutryl-CoA ammonia-lyase (EC 4.3.1.14) / 3-keto-5-aminohexanoate cleavage enzyme |
| SCE1572_8264 | Undecaprenyl diphosphate synthase (EC 2.5.1.31) | bi | sce_6935 | 89.63 | Undecaprenyl diphosphate synthase (EC 2.5.1.31) |
| SCE1572_8265 | Phosphatidate cytidyltransferase (EC 2.7.7.41) | bi | sce_6936 | 93.75 | Phosphatidate cytidyltransferase (EC 2.7.7.41) |
| SCE1572_8266 | NAD-specific glutamate dehydrogenase (EC 1.4.1.2); NADP-specific glutamate dehydrogenase (EC 1.4.1.4) | bi | sce_6937 | 95.92 | NAD-specific glutamate dehydrogenase (EC 1.4.1.2); NADP-specific glutamate dehydrogenase (EC 1.4.1.4) |
| SCE1572_8267 | Tryptophanyl-tRNA synthetase (EC 6.1.1.2) | umi | sce_8274 | 31.34 | Tryptophanyl-tRNA synthetase (EC 6.1.1.2) |
| SCE1572_8268 | hypothetical protein | bi | sce_6317 | 72.5 | Transcriptional regulator, TetR family |
| SCE1572_8269 | Lipid A export ATP-binding/permease protein MsbA | bi | sce_6318 | 94.84 | Lipid A export ATP-binding/permease protein MsbA |
| SCE1572_8270 | Lipid A export ATP-binding/permease protein MsbA | bi | sce_6319 | 93.95 | Lipid A export ATP-binding/permease protein MsbA |
| SCE1572_8271 | Folate-dependent protein for Fe/S cluster synthesis/repair in oxidative stress | bi | sce_6940 | 86.79 | Folate-dependent protein for Fe/S cluster synthesis/repair in oxidative stress |
| SCE1572_8272 | hypothetical protein | bi | sce_6941 | 91.87 | hypothetical protein |
| SCE1572_8273 | S-adenosylmethionine decarboxylase | bi | sce_6942 | 97.18 | S-adenosylmethionine decarboxylase |
| SCE1572_8274 | conserved hypothetical protein | bi | sce_7920 | 36.98 | FIG01086882: hypothetical protein |
| SCE1572_8275 | Vitamin K epoxide reductase | bi | sce_6944 | 91.07 | Vitamin K epoxide reductase |
| SCE1572_8276 | hypothetical protein | bi | sce_6945 | 94.83 | hypothetical protein |
| SCE1572_8277 | Thioredoxin | bi | sce_6946 | 87.39 | Thioredoxin |
| SCE1572_8278 | FIG01088185: hypothetical protein | bi | sce_6947 | 88.32 | FIG01088185: hypothetical protein |
| SCE1572_8279 | Methylated-DNA--protein-cysteine methyltransferase (EC 2.1.1.63) | bi | sce_6948 | 89.71 | Methylated-DNA--protein-cysteine methyltransferase (EC 2.1.1.63) |
| SCE1572_8280 | DNA-3-methyladenine glycosylase II (EC 3.2.2.21) | bi | sce_6949 | 92.02 | DNA-3-methyladenine glycosylase II (EC 3.2.2.21) |
| SCE1572_8281 | Leucine dehydrogenase (EC 1.4.1.9) | bi | sce_6950 | 89.5 | Leucine dehydrogenase (EC 1.4.1.9) |
| SCE1572_8282 | Carbon starvation protein A | bi | sce_6951 | 93.4 | Carbon starvation protein A |
| SCE1572_8283 | Bifunctional protein: zinc-containing alcohol dehydrogenase; quinone oxidoreductase (NADPH:quinone reductase) (EC 1.1.1.-); | bi | sce_6316 | 41.21 | Bifunctional protein: zinc-containing alcohol dehydrogenase; quinone oxidoreductase (NADPH:quinone reductase) (EC 1.1.1.-); |
| SCE1572_8284 | hypothetical protein | bi | sce_611 | 59.62 | COG1937: Uncharacterized protein conserved in bacteria |
| SCE1572_8285 | hypothetical protein | bi | sce_613 | 78.84 | hypothetical protein |
| SCE1572_8286 | Protein ThiJ | bi | sce_6953 | 92.9 | Protein ThiJ |
| SCE1572_8287 | Adenylate cyclase (EC 4.6.1.1) / Guanylate cyclase (EC 4.6.1.2) | bi | sce_6954 | 87.16 | Adenylate cyclase (EC 4.6.1.1) / Guanylate cyclase (EC 4.6.1.2) |
| SCE1572_8288 | putative signal transduction protein with Nacht domain | bi | sce_6964 | 90.31 | serine/threonine protein kinase |
| SCE1572_8289 | hypothetical protein | bi | sce_6053 | 58.88 | FIG01086409: hypothetical protein |
| SCE1572_8290 | Rhs-family protein | umi | sce_8817 | 39.24 | Rhs family carbohydrate-binding protein |
| SCE1572_8291 | hypothetical protein | bi | sce_9526 | 28.88 | hypothetical protein |
| SCE1572_8292 | major facilitator superfamily MFS_1 | umi | sce_4482 | 45.15 | putative integral membrane transport protein |
| SCE1572_8293 | conserved hypothetical protein | umi | sce_3882 | 38.75 | FIG01085153: hypothetical protein |
| SCE1572_8294 | FIG01085721: hypothetical protein | bi | sce_6979 | 90.32 | FIG01085721: hypothetical protein |
| SCE1572_8295 | glutamine amidotransferase class-I | bi | sce_6980 | 86.36 | GMP synthase (EC 6.3.5.2) |
| SCE1572_8296 | transcriptional regulator (TetR/AcrR family) | bi | sce_6981 | 85.53 | transcriptional regulator (TetR/AcrR family) |
| SCE1572_8297 | FIG01087738: hypothetical protein | bi | sce_6982 | 96.51 | FIG01087738: hypothetical protein |
| SCE1572_8298 | Activator of (R)-2-hydroxyglutaryl-CoA dehydratase | bi | sce_6983 | 93.15 | Activator of (R)-2-hydroxyglutaryl-CoA dehydratase |
| SCE1572_8299 | serine esterase, putative | umi | sce_5625 | 29.14 | LpqP protein |
| SCE1572_8300 | hypothetical protein | - | - | 0 | |
| SCE1572_8301 | Aspartate transaminase (EC 2.6.1.1) | bi | sce_6985 | 90.93 | Aspartate transaminase (EC 2.6.1.1) |
| SCE1572_8302 | hypothetical protein | bi | sce_6986 | 83.93 | hypothetical protein |
| SCE1572_8303 | hypothetical protein | bi | sce_6987 | 88.1 | hypothetical protein |
| SCE1572_8304 | Thiol:disulfide interchange protein, thioredoxin family protein precursor | bi | sce_6988 | 83.6 | hypothetical protein |
| SCE1572_8305 | hypothetical protein | bi | sce_6989 | 92.95 | hypothetical protein |
| SCE1572_8306 | hypothetical protein | bi | sce_6990 | 85.51 | hypothetical protein |
| SCE1572_8307 | photoactive yellow protein | bi | sce_1129 | 50.56 | Photoactive yellow protein (PYP) |
| SCE1572_8308 | hypothetical protein | - | - | 0 | |
| SCE1572_8309 | Flagellar hook-length control protein FliK | bi | sce_6991 | 85.38 | Flagellar hook-length control protein FliK |
| SCE1572_8310 | Aspartokinase (EC 2.7.2.4) | bi | sce_6992 | 89.7 | Aspartokinase (EC 2.7.2.4) |
| SCE1572_8311 | hypothetical protein | bi | sce_6993 | 85.53 | hypothetical protein |
| SCE1572_8312 | ABC-type transport system involved in resistance to organic solvents, auxiliary component | bi | sce_6994 | 89.05 | Toluene tolerance |
| SCE1572_8313 | Two-component sensor PilS | bi | sce_6995 | 87.95 | Two-component sensor PilS |
| SCE1572_8314 | Type IV fimbrial assembly protein PilC | bi | sce_6996 | 94.81 | Type IV fimbrial assembly protein PilC |
| SCE1572_8315 | hypothetical protein | bi | sce_6997 | 83.02 | hypothetical protein |
| SCE1572_8316 | hypothetical protein | bi | sce_6998 | 87.34 | Predicted ATPase |
| SCE1572_8317 | Protein-L-isoaspartate O-methyltransferase (EC 2.1.1.77) | bi | sce_6999 | 85.57 | Protein-L-isoaspartate O-methyltransferase (EC 2.1.1.77) |
| SCE1572_8318 | Beta-lactamase class C and other penicillin binding proteins | bi | sce_7000 | 88.68 | Beta-lactamase class C and other penicillin binding proteins |
| SCE1572_8319 | Ubiquinone biosynthesis monoxygenase UbiB | bi | sce_7002 | 93.17 | Ubiquinone biosynthesis monoxygenase UbiB |
| SCE1572_8320 | hypothetical protein | bi | sce_7003 | 88.37 | hypothetical protein |
| SCE1572_8321 | serine/threonine-protein kinase Pkn3 (EC:2.7.11.1) | bi | sce_7004 | 88.09 | serine/threonine protein kinase with TPR repeats |
| SCE1572_8322 | conserved hypothetical protein | bi | sce_7006 | 90.48 | DUF124 domain-containing protein |
| SCE1572_8323 | conserved hypothetical protein | bi | sce_7007 | 92.79 | conserved hypothetical protein |
| SCE1572_8324 | hypothetical protein | bi | sce_7008 | 95.61 | hypothetical protein |
| SCE1572_8325 | FHA domain containing protein | bi | sce_7009 | 83.73 | FHA domain/tetratricopeptide repeat protein |
| SCE1572_8326 | putative transmembrane protein | bi | sce_7010 | 92.47 | hypothetical protein |
| SCE1572_8327 | ATP/ADP translocase-like | bi | sce_7011 | 89.24 | Major facilitator superfamily MFS_1 |
| SCE1572_8328 | hypothetical protein | - | - | 0 | |
| SCE1572_8329 | Chromosome undetermined SCAF14611, whole genome shotgun sequence | bi | sce_7012 | 79.61 | Chromosome undetermined SCAF14611, whole genome shotgun sequence |
| SCE1572_8330 | hypothetical protein | bi | sce_7013 | 89.34 | hypothetical protein |
| SCE1572_8331 | Lipase precursor (EC 3.1.1.3) | bi | sce_7014 | 84.33 | Lipase precursor (EC 3.1.1.3) |
| SCE1572_8332 | hypothetical protein | bi | sce_7015 | 82.88 | hypothetical protein |
| SCE1572_8333 | FIG001341: Probable Fe(2)-trafficking protein YggX | bi | sce_7016 | 90.62 | FIG001341: Probable Fe(2)-trafficking protein YggX |
| SCE1572_8334 | hypothetical protein | - | - | 0 | |
| SCE1572_8335 | hypothetical protein | - | - | 0 | |
| SCE1572_8336 | Mobile element protein | umi | sce_1675 | 96.77 | ISLp1 |
| SCE1572_8337 | VgrG protein | umi | sce_304 | 40.82 | VgrG protein |
| SCE1572_8338 | hypothetical protein | bi | sce_305 | 37.42 | FIG01088662: hypothetical protein |
| SCE1572_8339 | hypothetical protein | - | - | 0 | |
| SCE1572_8340 | hypothetical protein | - | - | 0 | |
| SCE1572_8341 | predicted protein | bi | sce_9170 | 90.29 | hypothetical protein |
| SCE1572_8342 | OmpA/MotB | umi | sce_9171 | 68.39 | FIG01085999: hypothetical protein |
| SCE1572_8343 | hypothetical protein | bi | sce_3174 | 71.6 | hypothetical protein |
| SCE1572_8344 | hypothetical protein | umi | sce_163 | 59.63 | FIG01087636: hypothetical protein |
| SCE1572_8345 | hypothetical protein | - | - | 0 | |
| SCE1572_8346 | PE-PGRS family protein | bi | sce_9483 | 72.84 | FIG01086339: hypothetical protein |
| SCE1572_8347 | FIG01089478: hypothetical protein | umi | sce_9482 | 76.69 | hypothetical protein |
| SCE1572_8348 | RNA polymerase sigma-H factor | umi | sce_9481 | 78.06 | RNA polymerase sigma-H factor |
| SCE1572_8349 | hypothetical protein | bi | sce_9480 | 72.97 | hypothetical protein |
| SCE1572_8350 | hypothetical protein | - | - | 0 | |
| SCE1572_8351 | hypothetical protein | - | - | 0 | |
| SCE1572_8352 | hypothetical protein | umi | sce_9479 | 68.22 | hypothetical protein |
| SCE1572_8353 | TPR domain protein | - | - | 0 | |
| SCE1572_8354 | integron integrase | umi | sce_8403 | 70.21 | Integron integrase IntIPac |
| SCE1572_8355 | transposase | umi | sce_6226 | 89.76 | Integrase, catalytic region |
| SCE1572_8356 | hypothetical protein | umi | sce_6227 | 86.05 | hypothetical protein |
| SCE1572_8357 | hypothetical protein | - | - | 0 | |
| SCE1572_8358 | transposase IS66 family | umi | sce_7404 | 37.85 | Mobile element protein |
| SCE1572_8359 | hypothetical protein | - | - | 0 | |
| SCE1572_8360 | hypothetical protein | umi | sce_10160 | 37.5 | Transposase |
| SCE1572_8361 | hypothetical protein | - | - | 0 | |
| SCE1572_8362 | hypothetical protein | umi | sce_10265 | 87.8 | hypothetical protein |

| | | | | | |
|--------------|---|-----|-----------|-------|---|
| SCE1572_8363 | FIGO1086053: hypothetical protein | umi | sce_10019 | 81.29 | FIGO1086053: hypothetical protein |
| SCE1572_8364 | conserved hypothetical protein-putative thiol-disulfide isomerase or thioredoxin | umi | sce_5870 | 53.81 | hypothetical protein |
| SCE1572_8365 | Transcriptional regulator, TetR family | umi | sce_1930 | 41.33 | Transcriptional regulator, TetR family |
| SCE1572_8366 | acetyltransferase (GNAT) family | - | - | 0 | |
| SCE1572_8367 | Hydroxymethylpyrimidine ABC transporter, substrate-binding component | bi | sce_2167 | 66.36 | Hydroxymethylpyrimidine ABC transporter, substrate-binding component |
| SCE1572_8368 | transcriptional regulator, AraC family | bi | sce_2165 | 69.44 | Transcriptional regulator, AraC family |
| SCE1572_8369 | FIG00481795: hypothetical protein | bi | sce_7077 | 87.61 | FIG00481795: hypothetical protein |
| SCE1572_8370 | FIG001614: Membrane protein | bi | sce_7078 | 88.05 | FIG001614: Membrane protein |
| SCE1572_8371 | FIG015373: Membrane protein | bi | sce_7079 | 86.84 | FIG015373: Membrane protein |
| SCE1572_8372 | Histone acetyltransferase HPA2 and related acetyltransferases | bi | sce_7080 | 88.28 | Histone acetyltransferase HPA2 and related acetyltransferases |
| SCE1572_8373 | Isoquinoline 1-oxidoreductase beta subunit (EC 1.3.99.16) | bi | sce_7082 | 90.19 | Isoquinoline 1-oxidoreductase beta subunit (EC 1.3.99.16) |
| SCE1572_8374 | Isoquinoline 1-oxidoreductase alpha subunit (EC 1.3.99.16) | bi | sce_7086 | 96.05 | Isoquinoline 1-oxidoreductase alpha subunit (EC 1.3.99.16) |
| SCE1572_8375 | Putative Isoquinoline 1-oxidoreductase subunit, MII3835 protein | bi | sce_7087 | 91.2 | Putative Isoquinoline 1-oxidoreductase subunit, MII3835 protein |
| SCE1572_8376 | hypothetical protein | - | - | 0 | |
| SCE1572_8377 | hypothetical protein | - | - | 0 | |
| SCE1572_8378 | Serine/threonine-protein kinase pkn1 (EC 2.7.11.1) | bi | sce_7088 | 73.29 | Serine/threonine-protein kinase pkn1 (EC 2.7.11.1) |
| SCE1572_8379 | hypothetical protein | bi | sce_7089 | 77.17 | FIG01086691: hypothetical protein |
| SCE1572_8380 | FIG01087735: hypothetical protein | bi | sce_7090 | 60.71 | FIG01087735: hypothetical protein |
| SCE1572_8381 | ATP-dependent helicase hrpA | bi | sce_7144 | 92.6 | ATP-dependent helicase hrpA |
| SCE1572_8382 | FIG01087763: hypothetical protein | umi | sce_5241 | 34.12 | FIG01086664: hypothetical protein |
| SCE1572_8383 | serine/threonine protein kinase | umi | sce_8564 | 31.08 | serine/threonine protein kinase |
| SCE1572_8384 | gamma-aminobutyric acid (GABA-A) receptor, subunit epsilon | umi | sce_527 | 32.33 | conserved hypothetical protein-putative chloride channel |
| SCE1572_8385 | FIG01085109: hypothetical protein | umi | sce_8592 | 82.68 | FIG01085109: hypothetical protein |
| SCE1572_8386 | Mobile element protein | umi | sce_1675 | 96.77 | ISLp1 |
| SCE1572_8387 | hypothetical protein | - | - | 0 | |
| SCE1572_8388 | Enoyl-CoA hydratase/isomerase | bi | sce_7378 | 76.38 | Enoyl-CoA hydratase (EC 4.2.1.17) |
| SCE1572_8389 | Non-specific DNA-binding protein Dps / Iron-binding ferritin-like antioxidant protein / Ferroxidase (EC 1.16.3.1) | bi | sce_8819 | 68 | Non-specific DNA-binding protein Dps / Iron-binding ferritin-like antioxidant protein / Ferroxidase (EC 1.16.3.1) |
| SCE1572_8390 | hypothetical protein | - | - | 0 | |
| SCE1572_8391 | Adenylate cyclase (EC 4.6.1.1) / Guanylate cyclase (EC 4.6.1.2) | bi | sce_7154 | 88.18 | Adenylate cyclase (EC 4.6.1.1) / Guanylate cyclase (EC 4.6.1.2) |
| SCE1572_8392 | hypothetical protein | - | - | 0 | |
| SCE1572_8393 | putative antibiotic resistance membrane protein | umi | sce_8038 | 43.97 | FIG01085364: hypothetical protein |
| SCE1572_8394 | endo-1,4-beta-glucanase | bi | sce_7155 | 87.59 | endo-1,4-beta-glucanase |
| SCE1572_8395 | Hydroxymethylglutaryl-CoA synthase (EC 2.3.3.10) | bi | sce_7156 | 93.86 | Hydroxymethylglutaryl-CoA synthase (EC 2.3.3.10) |
| SCE1572_8396 | hypothetical protein | bi | sce_7157 | 77.78 | hypothetical protein |
| SCE1572_8397 | Streptococcal hemagglutinin protein | bi | sce_7158 | 77.27 | Streptococcal hemagglutinin protein |
| SCE1572_8398 | Cytosine/purine/uracil/thiamine/allantoin permease family protein | umi | sce_5278 | 56.49 | Cytosine/purine/uracil/thiamine/allantoin permease family protein |
| SCE1572_8399 | Dihydropyrimidine dehydrogenase [NADP] (EC 1.3.1.2) | bi | sce_7159 | 95.67 | Dihydropyrimidine dehydrogenase [NADP] (EC 1.3.1.2) |
| SCE1572_8400 | Pyridine nucleotide-disulphide oxidoreductase associated with reductive pyrimidine catabolism | bi | sce_7160 | 88.3 | Pyridine nucleotide-disulphide oxidoreductase associated with reductive pyrimidine catabolism |
| SCE1572_8401 | Dihydropyrimidase (EC 3.5.2.2) | bi | sce_7161 | 94.85 | Dihydropyrimidase (EC 3.5.2.2) |
| SCE1572_8402 | N-carbamoylputrescine amidase (3.5.1.53) | bi | sce_7162 | 95.52 | N-carbamoylputrescine amidase (3.5.1.53) |
| SCE1572_8403 | Methylmalonate-semialdehyde dehydrogenase (EC 1.2.1.27) | bi | sce_7163 | 92.08 | Methylmalonate-semialdehyde dehydrogenase (EC 1.2.1.27) |
| SCE1572_8404 | hypothetical protein | - | - | 0 | |
| SCE1572_8405 | hypothetical protein | bi | sce_7164 | 79.56 | hypothetical protein |
| SCE1572_8406 | POSSIBLE MOLYBDOPROTEIN BIOSYNTHESIS PROTEIN MOEY | bi | sce_7165 | 76.63 | POSSIBLE MOLYBDOPROTEIN BIOSYNTHESIS PROTEIN MOEY |
| SCE1572_8407 | hypothetical protein | bi | sce_7166 | 84.13 | hypothetical protein |
| SCE1572_8408 | hypothetical protein | bi | sce_7167 | 76.91 | hypothetical protein |
| SCE1572_8409 | hypothetical protein | - | - | 0 | |
| SCE1572_8410 | Integral membrane protein TerC | bi | sce_7169 | 89.66 | Integral membrane protein TerC |
| SCE1572_8411 | FIG01087362: hypothetical protein | bi | sce_7170 | 85.23 | FIG01087362: hypothetical protein |
| SCE1572_8412 | Dipeptidyl aminopeptidase | bi | sce_7171 | 89.47 | Dipeptidyl aminopeptidase |
| SCE1572_8413 | hypothetical protein, INTERPRO-suggestion: probable ferritin-like | bi | sce_7172 | 86.9 | hypothetical protein, INTERPRO-suggestion: probable ferritin-like |
| SCE1572_8414 | FIG01089058: hypothetical protein | bi | sce_7173 | 92.98 | FIG01089058: hypothetical protein |
| SCE1572_8415 | Deoxyribodipyrimidine photolyase, type II (EC 4.1.99.3) | bi | sce_7176 | 92.09 | Deoxyribodipyrimidine photolyase, type II (EC 4.1.99.3) |
| SCE1572_8416 | DedA protein | bi | sce_7177 | 93.75 | DedA protein |
| SCE1572_8417 | serine/threonine protein kinase | bi | sce_7178 | 72.25 | serine/threonine protein kinase |
| SCE1572_8418 | FIG01086020: hypothetical protein | bi | sce_7179 | 73.12 | FIG01086020: hypothetical protein |
| SCE1572_8419 | hypothetical protein | - | - | 0 | |
| SCE1572_8420 | PhnB protein | bi | sce_7180 | 92.91 | PhnB protein |
| SCE1572_8421 | RNA polymerase sigma-70 factor, ECF subfamily | bi | sce_7181 | 94.12 | RNA polymerase sigma-70 factor, ECF subfamily |
| SCE1572_8422 | hypothetical protein | bi | sce_7182 | 92 | hypothetical protein |
| SCE1572_8423 | Omega-amino acid-pyruvate aminotransferase (EC 2.6.1.18) | bi | sce_7183 | 96.38 | Omega-amino acid-pyruvate aminotransferase (EC 2.6.1.18) |
| SCE1572_8424 | hypothetical protein | - | - | 0 | |
| SCE1572_8425 | Transcriptional regulator, MarR family | bi | sce_7186 | 93.42 | Transcriptional regulator, MarR family |
| SCE1572_8426 | hypothetical protein | - | - | 0 | |
| SCE1572_8427 | hypothetical protein | bi | sce_7187 | 75 | hypothetical protein |
| SCE1572_8428 | FIG01085592: hypothetical protein | bi | sce_7189 | 84.21 | Cytochrome P450 |
| SCE1572_8429 | Cytochrome P450 | bi | sce_7190 | 83.44 | Cytochrome P450 |
| SCE1572_8430 | Threonyl-tRNA synthetase (EC 6.1.1.3) | bi | sce_4871 | 42.02 | Threonyl-tRNA synthetase (EC 6.1.1.3) |
| SCE1572_8431 | FIG01089260: hypothetical protein | bi | sce_7191 | 82.41 | FIG01089260: hypothetical protein |
| SCE1572_8432 | Exonuclease SbcC | bi | sce_7192 | 75.9 | Exonuclease SbcC |
| SCE1572_8433 | hypothetical protein | - | - | 0 | |
| SCE1572_8434 | putative serine/threonine protein kinase | bi | sce_7193 | 83.24 | putative serine/threonine protein kinase |
| SCE1572_8435 | hypothetical protein | - | - | 0 | |
| SCE1572_8436 | FIG01089129: hypothetical protein | umi | sce_7196 | 69.25 | FIG01089129: hypothetical protein |
| SCE1572_8437 | FIG01089129: hypothetical protein | bi | sce_7196 | 82.29 | FIG01089129: hypothetical protein |
| SCE1572_8438 | SAM-dependent methyltransferase | bi | sce_7197 | 93.33 | Methyltransferase type 11 |
| SCE1572_8439 | helix-turn-helix, AraC type | bi | sce_7198 | 87.21 | helix-turn-helix, AraC type |
| SCE1572_8440 | Flagellar motor rotation protein MotB | bi | sce_7199 | 91.81 | Flagellar motor rotation protein MotB |
| SCE1572_8441 | Iso citrate dehydrogenase [NAD] (EC 1.1.1.141) | bi | sce_7201 | 94.38 | Iso citrate dehydrogenase [NAD] (EC 1.1.1.141) |
| SCE1572_8442 | hypothetical protein | bi | sce_7202 | 83.09 | hypothetical protein |
| SCE1572_8443 | hypothetical protein | bi | sce_7203 | 80.57 | hypothetical protein |
| SCE1572_8444 | Smr domain protein | bi | sce_7204 | 95.32 | Smr domain protein |
| SCE1572_8445 | hypothetical protein | bi | sce_7205 | 84.8 | hypothetical protein |
| SCE1572_8446 | Internalin-like protein (LPXTG motif) Lmo1136 homolog | umi | sce_9433 | 38.26 | Annexin max4 |
| SCE1572_8447 | hypothetical protein | - | - | 0 | |
| SCE1572_8448 | WD-40 repeat protein | umi | sce_7069 | 73.55 | WD-40 repeat protein |
| SCE1572_8449 | ADP-ribose pyrophosphatase (EC 3.6.1.13) homolog | bi | sce_7207 | 85.39 | ADP-ribose pyrophosphatase (EC 3.6.1.13) |
| SCE1572_8450 | Ribonuclease E (EC 3.1.26.12) | bi | sce_7208 | 73.44 | Ribonuclease E (EC 3.1.26.12) |
| SCE1572_8451 | hypothetical protein | bi | sce_7211 | 84.52 | hypothetical protein |
| SCE1572_8452 | hypothetical protein | bi | sce_7212 | 90.91 | hypothetical protein |
| SCE1572_8453 | D-tyrosyl-tRNA(Tyr) deacylase | bi | sce_7213 | 93.33 | D-tyrosyl-tRNA(Tyr) deacylase |
| SCE1572_8454 | 2-dehydropanoate 2-reductase (EC 1.1.1.169) | bi | sce_7214 | 76.97 | 2-dehydropanoate 2-reductase (EC 1.1.1.169) |
| SCE1572_8455 | 4-hydroxythreonine-4-phosphate dehydrogenase (EC 1.1.1.262) | bi | sce_7215 | 92.13 | 4-hydroxythreonine-4-phosphate dehydrogenase (EC 1.1.1.262) |
| SCE1572_8456 | Hypothetical protein | bi | sce_7216 | 89.78 | Hypothetical protein |
| SCE1572_8457 | TldD protein, part of proposed TldE/TldD proteolytic complex (PMID 12029038) | bi | sce_7217 | 95.43 | TldD protein, part of proposed TldE/TldD proteolytic complex (PMID 12029038) |
| SCE1572_8458 | TPR domain protein | bi | sce_7218 | 90.89 | TPR domain protein, putative |
| SCE1572_8459 | hypothetical protein | bi | sce_7219 | 82.85 | hypothetical protein |
| SCE1572_8460 | FIG01085025: hypothetical protein | bi | sce_7220 | 83.9 | FIG01085025: hypothetical protein |
| SCE1572_8461 | FIG01087052: hypothetical protein | bi | sce_7221 | 90.48 | FIG01087052: hypothetical protein |
| SCE1572_8462 | hypothetical protein | bi | sce_7222 | 92.39 | hypothetical protein |
| SCE1572_8463 | Carboxyl-terminal protease (EC 3.4.21.102) | bi | sce_7224 | 94.4 | Carboxyl-terminal protease (EC 3.4.21.102) |
| SCE1572_8464 | hypothetical protein | bi | sce_7225 | 90 | hypothetical protein |
| SCE1572_8465 | hypothetical protein | - | - | 0 | |
| SCE1572_8466 | FIG01086374: hypothetical protein | bi | sce_7226 | 88.18 | FIG01086374: hypothetical protein |
| SCE1572_8467 | hypothetical protein | bi | sce_7227 | 87.91 | hypothetical protein |
| SCE1572_8468 | DnaK-related protein | bi | sce_7228 | 95.04 | DnaK-related protein |
| SCE1572_8469 | FIG01087868: hypothetical protein | bi | sce_7230 | 60.26 | FIG01087868: hypothetical protein |
| SCE1572_8470 | amidohydrolase | bi | sce_7231 | 78.4 | similar to Xaa-Pro dipeptidase |
| SCE1572_8471 | Cellobiose phosphorylase (EC 2.4.1.-) | bi | sce_7232 | 97.17 | Cellobiose phosphorylase (EC 2.4.1.-) |
| SCE1572_8472 | hypothetical protein | bi | sce_7234 | 77.69 | hypothetical protein |
| SCE1572_8473 | Outer membrane protein A precursor | bi | sce_7236 | 92.94 | Outer membrane protein A precursor |
| SCE1572_8474 | DnaK-related protein | bi | sce_7237 | 89.64 | DnaK-related protein |
| SCE1572_8475 | COG4748: Uncharacterized conserved protein | umi | sce_244 | 29.26 | Prophage Lp2 protein 6 |
| SCE1572_8476 | Tenascin-X | bi | sce_7238 | 79.22 | Tenascin-X |
| SCE1572_8477 | hypothetical protein | bi | sce_7239 | 71.11 | Secreted protein containing C-terminal beta-propeller domain distantly related to WD-40 repeats |
| SCE1572_8478 | FIG01087397: hypothetical protein | bi | sce_7243 | 85.47 | FIG01087397: hypothetical protein |
| SCE1572_8479 | Glutaredoxin | bi | sce_7244 | 86.36 | Uncharacterized monothiol glutaredoxin ycf64-like |
| SCE1572_8480 | Two-component system regulatory protein | bi | sce_7245 | 83.44 | Two-component system regulatory protein |
| SCE1572_8481 | Ribonuclease E inhibitor RraA | bi | sce_7246 | 82.91 | Ribonuclease E inhibitor RraA |
| SCE1572_8482 | hypothetical protein | bi | sce_7248 | 86.59 | hypothetical protein |
| SCE1572_8483 | FIG01089146: hypothetical protein | bi | sce_7249 | 80.23 | FIG01089146: hypothetical protein |
| SCE1572_8484 | hypothetical protein | bi | sce_7251 | 75.66 | Annexin A7 (Annexin-7) (Annexin VII) (Synexin) |
| SCE1572_8485 | Leishmania major strain Friedlin hypothetical protein LMJ_0963 | bi | sce_7252 | 79.22 | Tetratricopeptide TPR_2 repeat protein |
| SCE1572_8486 | Thrombospondin-1 precursor | umi | sce_4105 | 69.76 | Chitodextrinase precursor (EC 3.2.1.14) |
| SCE1572_8487 | hypothetical protein | - | - | 0 | |
| SCE1572_8488 | Capsule biosynthesis protein capA | bi | sce_7254 | 85.64 | Capsule biosynthesis protein capA |
| SCE1572_8489 | Membrane proteins related to metalloendopeptidases | bi | sce_7256 | 85.82 | Membrane proteins related to metalloendopeptidases |
| SCE1572_8490 | Ribosomal large subunit pseudouridine synthase D (EC 4.2.1.70) | bi | sce_7257 | 97.12 | Ribosomal large subunit pseudouridine synthase D (EC 4.2.1.70) |
| SCE1572_8491 | Elastin precursor (Tropoelastin) | bi | sce_7258 | 82.46 | FIG01086165: hypothetical protein |
| SCE1572_8492 | Protein serine/threonine phosphatase PpC, regulation of stationary phase | bi | sce_7260 | 96.85 | Protein serine/threonine phosphatase PpC, regulation of stationary phase |
| SCE1572_8493 | hypothetical protein | bi | sce_7261 | 80.8 | hypothetical protein |
| SCE1572_8494 | TPR domain protein | bi | sce_7262 | 84.33 | TPR repeat-containing protein |
| SCE1572_8495 | Adenylate cyclase (EC 4.6.1.1) / Guanylate cyclase (EC 4.6.1.2) | umi | sce_3750 | 47.42 | serine/threonine protein kinase with WD40 repeats |
| SCE1572_8496 | serine/threonine-protein kinase Pkn3 (EC:2.7.11.1) | umi | sce_5226 | 39.35 | Adenylate cyclase (EC 4.6.1.1) / Guanylate cyclase (EC 4.6.1.2) |
| SCE1572_8497 | endoglucanase (EC:3.2.1.4) | umi | sce_1662 | 30.56 | FIG00890145: hypothetical protein |
| SCE1572_8498 | hypothetical protein | - | - | 0 | |
| SCE1572_8499 | Serine/threonine protein kinase | umi | sce_3750 | 45.83 | serine/threonine protein kinase with WD40 repeats |
| SCE1572_8500 | hypothetical protein | umi | sce_1566 | 34.33 | conserved repeat domain protein |
| SCE1572_8501 | hypothetical protein | umi | sce_3858 | 27.67 | Adenosylhomocysteinase (EC 3.3.1.1) |
| SCE1572_8502 | LigA | umi | sce_8748 | 30.73 | Adenosylhomocysteinase (EC 3.3.1.1) |
| SCE1572_8503 | hypothetical protein | bi | sce_4101 | 81.4 | hypothetical protein |
| SCE1572_8504 | Extensin-like protein precursor | bi | sce_4100 | 76.58 | Flagellar hook-length control protein FliK |
| SCE1572_8505 | FIG01086011: hypothetical protein | bi | sce_4099 | 82.24 | FIG01086011: hypothetical protein |
| SCE1572_8506 | RNA polymerase sigma factor RpoE | bi | sce_4098 | 92.54 | RNA polymerase sigma factor RpoE |
| SCE1572_8507 | DNA repair protein RadC | bi | sce_7263 | 89.43 | DNA repair protein RadC |
| SCE1572_8508 | FIG01086239: hypothetical protein | umi | sce_9500 | 76.47 | hypothetical protein |
| SCE1572_8509 | hypothetical protein | umi | sce_9501 | 79.35 | hypothetical protein |
| SCE1572_8510 | FIG01087109: hypothetical protein | bi | sce_8461 | 89.93 | FIG01087109: hypothetical protein |
| SCE1572_8511 | FIG01086239: hypothetical protein | bi | sce_9502 | 94.35 | FIG01086239: hypothetical protein |
| SCE1572_8512 | hypothetical protein | bi | sce_9503 | 93.08 | hypothetical protein |
| SCE1572_8513 | hypothetical protein | umi | sce_9503 | 87.87 | hypothetical protein |
| SCE1572_8514 | hypothetical protein | umi | sce_10365 | 73.76 | hypothetical protein |
| SCE1572_8515 | Methyltransferase type 11 | umi | sce_10364 | 77.61 | hypothetical protein |
| SCE1572_8516 | hypothetical protein | - | - | 0 | |
| SCE1572_8517 | hypothetical protein | bi | sce_10363 | 94.46 | hypothetical protein |
| SCE1572_8518 | Molybdopter binding motif, ClnA N-terminal domain | bi | sce_7264 | 93.39 | Molybdopter binding motif, ClnA N-terminal domain |
| SCE1572_8519 | Exodeoxyribonuclease VII small subunit (EC 3.1.11.6) | bi | sce_7265 | 77.78 | Exodeoxyribonuclease VII small subunit (EC 3.1.11.6) |
| SCE1572_8520 | Chromosome partition protein smc | bi | sce_7266 | 86.93 | Chromosome partition protein smc |
| SCE1572_8521 | hypothetical protein | - | - | 0 | |
| SCE1572_8522 | Molybdenum cofactor biosynthesis protein MoaA | bi | sce_7267 | 94.41 | Molybdenum cofactor biosynthesis protein MoaA |
| SCE1572_8523 | hypothetical protein | - | - | 0 | |
| SCE1572_8524 | serine/threonine protein kinase | bi | sce_7268 | 74.75 | serine/threonine protein kinase |
| SCE1572_8525 | FIG01087802: hypothetical protein | bi | sce_7269 | 87.74 | FIG01087802: hypothetical protein |

| | | | | |
|--------------|--|-----|----------|---|
| SCE1572_8527 | hypothetical protein | - | | 0 |
| SCE1572_8528 | UDP-glucose 4-epimerase (EC 5.1.3.2) | bi | sce_7272 | 95.18 UDP-glucose 4-epimerase (EC 5.1.3.2) |
| SCE1572_8529 | Nudix hydrolase 3 (EC 3.6.1.-) | bi | sce_7273 | 91.36 Nudix hydrolase 3 (EC 3.6.1.-) |
| SCE1572_8530 | GI0645 protein | bi | sce_7274 | 71.88 GI0645 protein |
| SCE1572_8531 | hypothetical protein | bi | sce_7275 | 75.12 FIG01087536: hypothetical protein |
| SCE1572_8532 | Flagellar motor rotation protein MotA | bi | sce_8933 | 51.22 Electron transfer flavoprotein, alpha subunit |
| SCE1572_8533 | serine/threonine protein kinase | bi | sce_7276 | 88.3 Serine/threonine-protein kinase (EC 2.7.1.-) |
| SCE1572_8534 | MoxR-like ATPase in aerotolerance operon | bi | sce_7277 | 98.17 MoxR-like ATPase in aerotolerance operon |
| SCE1572_8535 | hypothetical protein PA3071 | bi | sce_7278 | 98.68 hypothetical protein PA3071 |
| SCE1572_8536 | hypothetical protein | bi | sce_7279 | 85.6 hypothetical protein |
| SCE1572_8537 | BatA (Bacteroides aerotolerance operon) | bi | sce_7280 | 95.28 BatA (Bacteroides aerotolerance operon) |
| SCE1572_8538 | BatB | bi | sce_7281 | 96.35 BatB |
| SCE1572_8539 | hypothetical protein | bi | sce_7282 | 84.64 Ser-Asp rich fibrinogen-binding, bone sialoprotein-binding protein |
| SCE1572_8540 | BatD | bi | sce_7283 | 87.82 BatD |
| SCE1572_8541 | FIG01088673: hypothetical protein | bi | sce_7285 | 99.44 FIG01088673: hypothetical protein |
| SCE1572_8542 | TolR protein | bi | sce_7286 | 91.98 TolR protein |
| SCE1572_8543 | transcriptional regulator, XRE family | bi | sce_7288 | 75.7 Probable transcriptional regulator |
| SCE1572_8544 | hypothetical protein | - | | 0 |
| SCE1572_8545 | dTDP-4-dehydrohamnose reductase (EC 1.1.1.133) | bi | sce_3427 | 73.61 dTDP-4-dehydrohamnose reductase (EC 1.1.1.133) |
| SCE1572_8546 | UDP-galactopyranose mutase (EC 5.4.99.9) | bi | sce_3426 | 85.75 UDP-galactopyranose mutase (EC 5.4.99.9) |
| SCE1572_8547 | Glycosyltransferase | bi | sce_3425 | 71.09 Glycosyltransferase |
| SCE1572_8548 | Beta-galactosidase (EC 3.2.1.23) | bi | sce_3424 | 74.96 Beta-galactosidase (EC 3.2.1.23) |
| SCE1572_8549 | Cardiolipin synthetase (EC 2.7.8.-) | bi | sce_7289 | 91.28 Cardiolipin synthetase (EC 2.7.8.-) |
| SCE1572_8550 | ATPase associated with various cellular activities, AAA_5 | bi | sce_7290 | 93.19 ATPase associated with various cellular activities, AAA_5 |
| SCE1572_8551 | Thioredoxin reductase (EC 1.8.1.9) | bi | sce_7291 | 91.23 Thioredoxin reductase (EC 1.8.1.9) |
| SCE1572_8552 | Transposase | bi | sce_7292 | 84.28 FIG01086976: hypothetical protein |
| SCE1572_8553 | histidine kinase | bi | sce_7293 | 90.79 periplasmic sensor signal transduction histidine kinase |
| SCE1572_8554 | FIG092679: Fe-S oxidoreductase | bi | sce_7294 | 89.97 FIG092679: Fe-S oxidoreductase |
| SCE1572_8555 | hypothetical protein | bi | sce_7295 | 96.19 hypothetical protein |
| SCE1572_8556 | Inner membrane protein YihY, formerly thought to be RNase BN | bi | sce_7296 | 86.16 Inner membrane protein YihY, formerly thought to be RNase BN |
| SCE1572_8557 | FIG01087472: hypothetical protein | bi | sce_7297 | 84.46 FIG01087472: hypothetical protein |
| SCE1572_8558 | hypothetical protein | bi | sce_7298 | 85.77 FIG01087472: hypothetical protein |
| SCE1572_8559 | RNA polymerase sigma-70 factor | uni | sce_5761 | 43.89 RNA polymerase sigma factor |
| SCE1572_8560 | putative glutathione S-transferase protein | bi | sce_2394 | 91.43 putative glutathione S-transferase protein |
| SCE1572_8561 | FIG01088113: hypothetical protein | bi | sce_7304 | 78.57 FIG01088113: hypothetical protein |
| SCE1572_8562 | RsbR, positive regulator of sigma-B | uni | sce_5156 | 47.85 RsbR, positive regulator of sigma-B |
| SCE1572_8563 | hypothetical protein | - | | 0 |
| SCE1572_8564 | Malonyl CoA-acyl carrier protein transacylase (EC 2.3.1.39) | uni | sce_4641 | 44.67 Malonyl CoA-acyl carrier protein transacylase (EC 2.3.1.39) |
| SCE1572_8565 | Malonyl CoA-acyl carrier protein transacylase (EC 2.3.1.39) | uni | sce_4641 | 45.61 Malonyl CoA-acyl carrier protein transacylase (EC 2.3.1.39) |
| SCE1572_8566 | Glutathione S-transferase (EC 2.5.1.18) | bi | sce_7306 | 77.29 Glutathione S-transferase (EC 2.5.1.18) |
| SCE1572_8567 | ABC transporter, ATP-binding protein | bi | sce_7307 | 90 ABC transporter ATP-binding protein |
| SCE1572_8568 | hypothetical protein | uni | sce_7308 | 91.37 hypothetical protein |
| SCE1572_8569 | hypothetical protein | - | | 0 |
| SCE1572_8570 | hypothetical protein | - | | 0 |
| SCE1572_8571 | hypothetical protein | - | | 0 |
| SCE1572_8572 | hypothetical protein | - | | 0 |
| SCE1572_8573 | hypothetical protein | - | | 0 |
| SCE1572_8574 | Insecticidal toxin complex protein TcdB1 | - | | 0 |
| SCE1572_8575 | Insecticidal toxin complex protein TcdB1 | - | | 0 |
| SCE1572_8576 | transposase IS116/IS110/IS902 family protein | - | | 0 |
| SCE1572_8577 | Mobile element protein | uni | sce_299 | 94.19 Mobile element protein |
| SCE1572_8578 | Mobile element protein | uni | sce_1675 | 96.77 ISLp1 |
| SCE1572_8579 | hypothetical protein | - | | 0 |
| SCE1572_8580 | Insecticidal toxin complex protein TcdB1 | uni | sce_8753 | 33.18 YD repeat protein |
| SCE1572_8581 | Insecticidal toxin complex protein TcdB1 | uni | sce_9566 | 77.28 Insecticidal toxin complex protein TcdB1 |
| SCE1572_8582 | hypothetical protein | - | | 0 |
| SCE1572_8583 | Insecticidal toxin complex protein TccB1 | bi | sce_9567 | 37.53 Insecticidal toxin complex protein TccB1 |
| SCE1572_8584 | hypothetical protein | - | | 0 |
| SCE1572_8585 | FIG01088568: hypothetical protein | bi | sce_7312 | 76.65 FIG01088568: hypothetical protein |
| SCE1572_8586 | LigA | uni | sce_3858 | 38.36 Adenosylhomocysteinase (EC 3.3.1.1) |
| SCE1572_8587 | hypothetical protein | bi | sce_7313 | 54.24 peptidase, M23/M37 family protein |
| SCE1572_8588 | Leucine-rich repeat | bi | sce_7314 | 91.57 Leucine-rich repeat |
| SCE1572_8589 | hypothetical protein | bi | sce_7315 | 89.74 hypothetical protein |
| SCE1572_8590 | hypothetical protein | bi | sce_7317 | 90.91 hypothetical protein |
| SCE1572_8591 | hypothetical protein | - | | 0 |
| SCE1572_8592 | hypothetical protein | - | | 0 |
| SCE1572_8593 | hypothetical protein | - | | 0 |
| SCE1572_8594 | putative thioredoxin | bi | sce_6282 | 84.3 putative thioredoxin |
| SCE1572_8595 | hypothetical protein | - | | 0 |
| SCE1572_8596 | hypothetical protein | - | | 0 |
| SCE1572_8597 | regulator of chromosome condensation, RCC1 | uni | sce_6010 | 36.46 Collagen triple helix repeat |
| SCE1572_8598 | hypothetical protein | - | | 0 |
| SCE1572_8599 | hypothetical protein | - | | 0 |
| SCE1572_8600 | hypothetical protein | - | | 0 |
| SCE1572_8601 | Serine acetyltransferase (EC 2.3.1.30) | uni | sce_8200 | 43.51 serine O-acetyltransferase (serine acetyltransferase)(EC:2.3.1.30) |
| SCE1572_8602 | glycosyl transferase, group 1 | uni | sce_1162 | 35.53 Glycosyl transferase, group 1 family protein |
| SCE1572_8603 | Ribose-phosphate pyrophosphokinase (EC 2.7.6.1) | bi | sce_7319 | 95.36 Ribose-phosphate pyrophosphokinase (EC 2.7.6.1) |
| SCE1572_8604 | LSU m5C1962 methyltransferase RlmI | bi | sce_7320 | 86.35 LSU m5C1962 methyltransferase RlmI |
| SCE1572_8605 | Outer membrane lipoprotein carrier protein LolA | bi | sce_7321 | 94.27 Translation initiation factor 2 |
| SCE1572_8606 | hypothetical protein | - | | 0 |
| SCE1572_8607 | Serine phosphatase RsbU, regulator of sigma subunit | bi | sce_7322 | 95.49 sigma factor regulatory protein |
| SCE1572_8608 | Phosphoribosylformylglycinamide synthase, synthetase subunit (EC 6.3.5.3) | bi | sce_7323 | 90.32 Phosphoribosylformylglycinamide synthase, synthetase subunit (EC 6.3.5.3) |
| SCE1572_8609 | Phytochrome, two-component sensor histidine kinase (EC 2.7.3.-) | uni | sce_217 | 33.46 two-component sensor histidine kinase |
| SCE1572_8610 | PUTATIVE ZINC PROTEASE PROTEIN | bi | sce_7325 | 84.75 PUTATIVE ZINC PROTEASE PROTEIN |
| SCE1572_8611 | Cyclopropane-fatty-acyl-phospholipid synthase (EC 2.1.1.79) | bi | sce_7326 | 88.25 Cyclopropane-fatty-acyl-phospholipid synthase (EC 2.1.1.79) |
| SCE1572_8612 | hypothetical protein | uni | sce_2131 | 31.25 FIG00838574: hypothetical protein |
| SCE1572_8613 | Response regulator of zinc sigma-54-dependent two-component system | bi | sce_7332 | 89.16 Response regulator of zinc sigma-54-dependent two-component system |
| SCE1572_8614 | Succinate dehydrogenase cytochrome b subunit | bi | sce_7334 | 88.74 Succinate dehydrogenase cytochrome b subunit |
| SCE1572_8615 | Succinate dehydrogenase flavoprotein subunit (EC 1.3.99.1) | bi | sce_7335 | 96.7 Succinate dehydrogenase flavoprotein subunit (EC 1.3.99.1) |
| SCE1572_8616 | Succinate dehydrogenase iron-sulfur protein (EC 1.3.99.1) | bi | sce_7336 | 93.77 Succinate dehydrogenase iron-sulfur protein (EC 1.3.99.1) |
| SCE1572_8617 | FIG01088091: hypothetical protein | bi | sce_7337 | 84.03 hypothetical protein |
| SCE1572_8618 | Sulfite oxidase and related enzymes | bi | sce_7338 | 86.36 Sulfite oxidase and related enzymes |
| SCE1572_8619 | FIG001196: putative membrane protein | bi | sce_7339 | 87.21 FIG001196: putative membrane protein |
| SCE1572_8620 | FIG01086216: hypothetical protein | bi | sce_7341 | 95.11 FIG01086216: hypothetical protein |
| SCE1572_8621 | Glutathione reductase (EC 1.8.1.7) | bi | sce_7343 | 89.05 Glutathione reductase (EC 1.8.1.7) |
| SCE1572_8622 | FIG01086997: hypothetical protein | bi | sce_7344 | 87.36 FIG01086997: hypothetical protein |
| SCE1572_8623 | Maltose O-acetyltransferase (EC 2.3.1.79) | bi | sce_7345 | 81.72 Maltose O-acetyltransferase (EC 2.3.1.79) |
| SCE1572_8624 | hypothetical protein | bi | sce_7346 | 85.33 hypothetical protein |
| SCE1572_8625 | Archaeal seryl-ARN synthetase-related sequence | bi | sce_7347 | 93.35 Archaeal seryl-ARN synthetase-related sequence |
| SCE1572_8626 | Lactoylglutathione lyase (EC 4.4.1.5) | uni | sce_7063 | 43.33 Glyoxalase family protein |
| SCE1572_8627 | FIG01088001: hypothetical protein | bi | sce_7348 | 79.94 FIG01088001: hypothetical protein |
| SCE1572_8628 | Pirin-like protein YhhW, possibly qercetin 2,3-dioxygenase activity | bi | sce_7349 | 87.3 Pirin-like protein YhhW, possibly qercetin 2,3-dioxygenase activity |
| SCE1572_8629 | Transcriptional regulator | bi | sce_6206 | 50.71 Transcriptional regulator |
| SCE1572_8630 | Hemerythrin HHE cation binding domain protein | bi | sce_7350 | 83.02 Hemerythrin HHE cation binding protein |
| SCE1572_8631 | hypothetical protein | - | | 0 |
| SCE1572_8632 | hypothetical protein | bi | sce_7352 | 81.02 hypothetical protein |
| SCE1572_8633 | 6-phosphogluconolactonase (EC 3.1.1.31) | uni | sce_6773 | 36.29 Putative hemagglutinin-related protein |
| SCE1572_8634 | Tat (Twin-arginine translocation) pathway signal sequence domain protein | - | | 0 |
| SCE1572_8635 | Tat (Twin-arginine translocation) pathway signal sequence domain protein | bi | sce_4902 | 82.24 Tat (Twin-arginine translocation) pathway signal sequence domain protein |
| SCE1572_8636 | Cellulose-binding domain protein | bi | sce_4903 | 87.01 Cellulose-binding domain protein |
| SCE1572_8637 | Thermophilic serine proteinase precursor (EC 3.4.21.-) (Ak.1 protease) | bi | sce_7353 | 78.89 subtilase family peptidase |
| SCE1572_8638 | FIG01086376: hypothetical protein | bi | sce_7355 | 72.66 FIG01086376: hypothetical protein |
| SCE1572_8639 | FIG00840944: hypothetical protein | bi | sce_7358 | 79.35 hypothetical protein |
| SCE1572_8640 | hypothetical protein | bi | sce_7359 | 75.53 hypothetical protein |
| SCE1572_8641 | 1,4-alpha-glucan (glycogen) branching enzyme, GH-13-type (EC 2.4.1.18) | bi | sce_7360 | 81.76 1,4-alpha-glucan (glycogen) branching enzyme, GH-13-type (EC 2.4.1.18) |
| SCE1572_8642 | AAA ATPase | bi | sce_7361 | 90.41 AAA ATPase |
| SCE1572_8643 | hypothetical protein | bi | sce_7362 | 91.88 hypothetical protein |
| SCE1572_8644 | 4-amino-4-deoxy-L-arabinose transferase and related glycosyltransferases of PMT family | bi | sce_7363 | 87.44 4-amino-4-deoxy-L-arabinose transferase and related glycosyltransferases of PMT family |
| SCE1572_8645 | hypothetical protein | uni | sce_4778 | 47.14 Serine/threonine-protein kinase pkn3 (EC 2.7.11.1) |
| SCE1572_8646 | hypothetical Membrane Spanning Protein | bi | sce_7364 | 87.61 hypothetical abductin-like protein |
| SCE1572_8647 | hypothetical protein | - | | 0 |
| SCE1572_8648 | Methyltransferase type 11 | uni | sce_4134 | 40.62 hypothetical protein |
| SCE1572_8649 | hypothetical protein | uni | sce_7596 | 36.49 FIG01087864: hypothetical protein |
| SCE1572_8650 | glycosyl transferase group 1 | bi | sce_7366 | 87.93 glycosyl transferase, group 1 |
| SCE1572_8651 | hypothetical protein | - | | 0 |
| SCE1572_8652 | erythrocyte membrane protein 1 (PfEMP1) | bi | sce_7367 | 66.79 Maltose/maltodextrin ABC transporter, substrate binding periplasmic protein MalE |
| SCE1572_8653 | hypothetical protein | bi | sce_7368 | 83.58 hypothetical protein |
| SCE1572_8654 | Dihydrolipamide acyltransferase component of branched-chain alpha-keto acid dehydrogenase complex (EC 2.3.1.168) | bi | sce_7369 | 90.11 Dihydrolipamide acyltransferase component of branched-chain alpha-keto acid dehydrogenase complex (EC 2.3.1.168) |
| SCE1572_8655 | Serine hydroxymethyltransferase (EC 2.1.2.1) | bi | sce_7370 | 95.98 Serine hydroxymethyltransferase (EC 2.1.2.1) |
| SCE1572_8656 | hypothetical protein | bi | sce_7371 | 89.22 FIG00995724: hypothetical protein |
| SCE1572_8657 | hypothetical protein | bi | sce_7372 | 89.71 hypothetical protein |
| SCE1572_8658 | Dihydrolipamide acetyltransferase component of pyruvate dehydrogenase complex (EC 2.3.1.12) | bi | sce_7373 | 90.05 FIG00995724: hypothetical protein |
| SCE1572_8659 | histone-like DNA-binding protein | bi | sce_7374 | 99.11 histone-like DNA-binding protein |
| SCE1572_8660 | hypothetical protein | - | | 0 |
| SCE1572_8661 | hypothetical protein | bi | sce_7375 | 86.69 TPR domain protein, putative component of TonB system |
| SCE1572_8662 | hypothetical protein | uni | sce_2131 | 30.98 FIG00838574: hypothetical protein |
| SCE1572_8663 | hypothetical protein | bi | sce_7393 | 88.5 hypothetical protein |
| SCE1572_8664 | hypothetical protein | bi | sce_7395 | 67.98 hypothetical protein |
| SCE1572_8665 | Urea carboxylase-related ABC transporter, periplasmic substrate-binding protein | uni | sce_2159 | 30.19 Urea carboxylase-related ABC transporter, periplasmic substrate-binding protein |
| SCE1572_8666 | Urea carboxylase-related ABC transporter, permease protein | - | | 0 |
| SCE1572_8667 | Aspartate racemase (EC 5.1.1.13) | - | | 0 |
| SCE1572_8668 | putative acetyltransferase | bi | sce_2495 | 88.74 Histone acetyltransferase HPA2/related acetyltransferase |
| SCE1572_8669 | glycoside hydrolase, family 43 | uni | sce_6970 | 77.36 hypothetical protein |
| SCE1572_8670 | putative nitrotriacetate monooxygenase | bi | sce_7122 | 94.44 Coenzyme F420-dependent N5,N10-methylene tetrahydromethanopterin reductase and related flavin-dependent oxidoreductases |
| SCE1572_8671 | hypothetical protein | bi | sce_6971 | 78.57 hypothetical protein |
| SCE1572_8672 | hypothetical protein | bi | sce_7370 | 70.62 hypothetical protein |
| SCE1572_8673 | FIG01085364: hypothetical protein | uni | sce_7367 | 36.68 Maltose/maltodextrin ABC transporter, substrate binding periplasmic protein MalE |
| SCE1572_8674 | Predicted transcriptional regulators | bi | sce_2613 | 73.2 Predicted transcriptional regulators |
| SCE1572_8675 | Activator of Hsp90 ATPase 1 family protein | uni | sce_2614 | 50.18 FIG00485988: hypothetical protein |
| SCE1572_8676 | RsbR, positive regulator of sigma-B | uni | sce_5782 | 37.87 RsbR, positive regulator of sigma-B |
| SCE1572_8677 | hypothetical protein | - | | 0 |
| SCE1572_8678 | Transcriptional regulator, LysR family | uni | sce_6321 | 44.3 Transcriptional regulator, LysR family |
| SCE1572_8679 | oxidoreductase | uni | sce_1565 | 45.85 Dehydrogenases with different specificities (related to short-chain alcohol dehydrogenases) |
| SCE1572_8680 | FIG01089157: hypothetical protein | bi | sce_7433 | 93.85 FIG01089157: hypothetical protein |
| SCE1572_8681 | FIG01089570: hypothetical protein | bi | sce_3735 | 92.52 FIG01089570: hypothetical protein |
| SCE1572_8682 | hypothetical protein | bi | sce_6962 | 56.86 hypothetical protein |
| SCE1572_8683 | short-chain dehydrogenase/reductase SDR | uni | sce_376 | 40.25 Probable short-chain dehydrogenase |
| SCE1572_8684 | Transcriptional regulator, LysR family | bi | sce_1255 | 36.88 Transcriptional regulator, LysR family |
| SCE1572_8685 | hypothetical protein | bi | sce_7426 | 86.27 jmjC domain protein |
| SCE1572_8686 | hypothetical protein | bi | sce_7427 | 69.3 predicted protein |
| SCE1572_8687 | hypothetical protein | bi | sce_7428 | 63.7 hypothetical protein |
| SCE1572_8688 | putative lipoprotein | bi | sce_7434 | 73.94 Similarity |
| SCE1572_8689 | UPF0043 membrane protein YdjX | bi | sce_8360 | 73.15 UPF0043 membrane protein YdjX |
| SCE1572_8690 | hypothetical protein | - | | 0 |

| | | | | |
|--------------|---|-----|----------|---|
| SCE1572_8691 | Catabolite control protein A | bi | sce_8694 | 82.33 Catabolite control protein A |
| SCE1572_8692 | FIG01088161: hypothetical protein | uni | sce_1321 | 62.16 FIG01085514: hypothetical protein |
| SCE1572_8693 | FIG01085514: hypothetical protein | uni | sce_1321 | 66.84 FIG01085514: hypothetical protein |
| SCE1572_8694 | Beta-lactamase class C and other penicillin binding proteins | bi | sce_7435 | 76.05 Beta-lactamase class C and other penicillin binding proteins |
| SCE1572_8695 | Nif-specific regulatory protein | uni | sce_7436 | 82.38 Nif-specific regulatory protein |
| SCE1572_8696 | hypothetical protein | uni | sce_5150 | 44.44 LpqC |
| SCE1572_8697 | Nif-specific regulatory protein | bi | sce_7436 | 86.21 Nif-specific regulatory protein |
| SCE1572_8698 | FIG01087003: hypothetical protein | bi | sce_7465 | 91.43 FIG01087003: hypothetical protein |
| SCE1572_8699 | similarity to galactose oxidase from Dactylium dendroides | bi | sce_9318 | 29.88 RTX toxins and related Ca ²⁺ proteins |
| SCE1572_8700 | FIG01087098: hypothetical protein | bi | sce_7466 | 79.94 FIG01087098: hypothetical protein |
| SCE1572_8701 | FIG00840613: hypothetical protein | - | - | 0 |
| SCE1572_8702 | transcriptional regulator, TetR family | bi | sce_7467 | 80.1 Transcriptional regulator, TetR family |
| SCE1572_8703 | FIG01086489: hypothetical protein | bi | sce_7473 | 91.8 hypothetical protein |
| SCE1572_8704 | hypothetical protein | bi | sce_7474 | 58.06 hypothetical protein |
| SCE1572_8705 | hypothetical protein | - | - | 0 |
| SCE1572_8706 | Transcriptional regulator, TetR family | uni | sce_1534 | 28.57 Transcriptional regulator, TetR family |
| SCE1572_8707 | FIG01087827: hypothetical protein | uni | sce_100 | 81.44 FIG01087827: hypothetical protein |
| SCE1572_8708 | Transcriptional regulator, AraC family | uni | sce_1358 | 38.51 Transcriptional regulator, AraC family |
| SCE1572_8709 | FIG01088376: hypothetical protein | bi | sce_7477 | 79.05 FIG01088376: hypothetical protein |
| SCE1572_8710 | Lactoylglutathione lyase and related lyases | bi | sce_851 | 92.97 Lactoylglutathione lyase and related lyases |
| SCE1572_8711 | Transcriptional regulator, AraC family | bi | sce_852 | 89.8 Transcriptional regulator, AraC family |
| SCE1572_8712 | hypothetical protein | bi | sce_7522 | 84.59 COG1306 predicted glycoside hydrolase |
| SCE1572_8713 | ABC-type antimicrobial peptide transport system, permease component | bi | sce_7523 | 88.92 ABC-type antimicrobial peptide transport system, permease component |
| SCE1572_8714 | ABC-type antimicrobial peptide transport system, permease component | bi | sce_7524 | 88.66 ABC-type antimicrobial peptide transport system, permease component |
| SCE1572_8715 | Methionine ABC transporter ATP-binding protein | bi | sce_7525 | 96.98 Methionine ABC transporter ATP-binding protein |
| SCE1572_8716 | Acriflavin resistance protein | bi | sce_7526 | 88.26 Acriflavin resistance protein |
| SCE1572_8717 | hypothetical protein | - | - | 0 |
| SCE1572_8718 | Nucleoside-diphosphate-sugar epimerase | uni | sce_7592 | 38.82 putative dTDP-glucose 4,6-dehydratase protein(EC:4.2.1.46) |
| SCE1572_8719 | FIG01088071: hypothetical protein | bi | sce_5999 | 75.2 FIG01088071: hypothetical protein |
| SCE1572_8720 | hypothetical protein | uni | sce_331 | 42.33 hypothetical protein |
| SCE1572_8721 | putative cytochrome P450 hydroxylase | uni | sce_7075 | 40.53 putative cytochrome P450 hydroxylase |
| SCE1572_8722 | FIG01087435: hypothetical protein | bi | sce_5994 | 84 FIG01087435: hypothetical protein |
| SCE1572_8723 | hypothetical protein | - | - | 0 |
| SCE1572_8724 | Beta-lactamase class C and other penicillin binding proteins | uni | sce_4328 | 30.99 D-alanyl-D-alanine carboxypeptidase (EC 3.4.16.4) |
| SCE1572_8725 | hypothetical protein | - | - | 0 |
| SCE1572_8726 | hypothetical protein | - | - | 0 |
| SCE1572_8727 | hypothetical protein | uni | sce_3292 | 28.57 Cellulose-binding domain protein |
| SCE1572_8728 | putative transcriptional regulator (AraC family) | uni | sce_7800 | 35.2 Transcriptional regulator, AraC family |
| SCE1572_8729 | FIG01086984: hypothetical protein | bi | sce_7527 | 78.37 FIG01086984: hypothetical protein |
| SCE1572_8730 | Matrix metalloproteinase-25 precursor (EC 3.4.24.-) (MMP-25) (Membrane-type matrix metalloproteinase 6) (MT-MMP 6) (M | bi | sce_7540 | 80.36 Matrix metalloproteinase-25 precursor (EC 3.4.24.-) (MMP-25) (Membrane-type matrix metalloproteinase 6) (MT-MMP 6) (Membr |
| SCE1572_8731 | protein of unknown function DUF82 | bi | sce_7541 | 76.44 protein of unknown function DUF82 |
| SCE1572_8732 | FIG01086246: hypothetical protein | bi | sce_7544 | 67.8 hypothetical protein |
| SCE1572_8733 | RsbR, positive regulator of sigma-B | bi | sce_828 | 83.59 RsbR, positive regulator of sigma-B |
| SCE1572_8734 | FIG01089631: hypothetical protein | bi | sce_829 | 92.64 FIG01089631: hypothetical protein |
| SCE1572_8735 | hypothetical protein | - | - | 0 |
| SCE1572_8736 | hypothetical protein | - | - | 0 |
| SCE1572_8737 | FIG01086608: hypothetical protein | bi | sce_7545 | 91.37 FIG01086608: hypothetical protein |
| SCE1572_8738 | Endoglucanase (EC 3.2.1.4) | bi | sce_7546 | 69.39 Endoglucanase (EC 3.2.1.4) |
| SCE1572_8739 | serine/threonine protein kinase | bi | sce_7547 | 69.83 serine/threonine protein kinase |
| SCE1572_8740 | ABC transporter permease protein | bi | sce_7557 | 90.84 protein of unknown function DUF990 |
| SCE1572_8741 | ABC transporter, ATP-binding protein | bi | sce_7559 | 95.4 ABC transporter, ATP-binding protein |
| SCE1572_8742 | putative phosphotransferase | bi | sce_7560 | 73.68 hypothetical protein |
| SCE1572_8743 | hypothetical protein | - | - | 0 |
| SCE1572_8744 | BlI2291 protein | uni | sce_5502 | 35.97 BlI2291 protein |
| SCE1572_8745 | hypothetical protein | bi | sce_8644 | 48.98 hypothetical protein |
| SCE1572_8746 | hypothetical protein | bi | sce_162 | 61.97 hypothetical protein |
| SCE1572_8747 | hypothetical protein | - | - | 0 |
| SCE1572_8748 | FIG01086696: hypothetical protein | bi | sce_7571 | 83.06 FIG01086696: hypothetical protein |
| SCE1572_8749 | serine/threonine kinase | bi | sce_7572 | 83.71 protein of unknown function DUF323 |
| SCE1572_8750 | hypothetical protein | - | - | 0 |
| SCE1572_8751 | Malonyl CoA-acyl carrier protein transacylase (EC 2.3.1.39) | bi | sce_4639 | 44.61 Malonyl CoA-acyl carrier protein transacylase (EC 2.3.1.39) |
| SCE1572_8752 | hypothetical protein | - | - | 0 |
| SCE1572_8753 | hypothetical protein | uni | sce_289 | 25.11 expressed protein |
| SCE1572_8754 | FIG01085697: hypothetical protein | uni | sce_7575 | 66.67 FIG01085697: hypothetical protein |
| SCE1572_8755 | COG2124: Cytochrome P450 | bi | sce_7574 | 64.44 hypothetical protein |
| SCE1572_8756 | FIG01085697: hypothetical protein | bi | sce_7575 | 76.08 FIG01085697: hypothetical protein |
| SCE1572_8757 | FIG01085898: hypothetical protein | bi | sce_7576 | 76.73 FIG01085898: hypothetical protein |
| SCE1572_8758 | RsbR, positive regulator of sigma-B | bi | sce_7578 | 84.26 RsbR, positive regulator of sigma-B |
| SCE1572_8759 | FIG01086900: hypothetical protein | bi | sce_7579 | 71.62 FIG01086900: hypothetical protein |
| SCE1572_8760 | Glycosyl hydrolase, family 30 | bi | sce_2037 | 74.14 Glycosyl hydrolase, family 30 |
| SCE1572_8761 | Redoxin | uni | sce_4916 | 45.71 hypothetical protein |
| SCE1572_8762 | Serine/threonine protein kinase | uni | sce_774 | 55.47 FIG01087003: hypothetical protein |
| SCE1572_8763 | hypothetical protein | - | - | 0 |
| SCE1572_8764 | Mobile element protein | uni | sce_1675 | 96.77 ISLp1 |
| SCE1572_8765 | serine/threonine protein kinase | uni | sce_1432 | 45.28 Serine/threonine protein kinase PpkA |
| SCE1572_8766 | predicted protein | uni | sce_7695 | 42.47 predicted protein |
| SCE1572_8767 | hypothetical protein | bi | sce_6808 | 91.77 hypothetical protein |
| SCE1572_8768 | hypothetical protein | - | - | 0 |
| SCE1572_8769 | FIG01003647: hypothetical protein | - | - | 0 |
| SCE1572_8770 | hypothetical protein | - | - | 0 |
| SCE1572_8771 | hypothetical protein | - | - | 0 |
| SCE1572_8772 | Bacteriophage protein gp37 | - | - | 0 |
| SCE1572_8773 | hypothetical protein | - | - | 0 |
| SCE1572_8774 | Resolvase, N-terminal domain | - | - | 0 |
| SCE1572_8775 | Serine/threonine protein kinase | uni | sce_5787 | 40.3 FIG01087003: hypothetical protein |
| SCE1572_8776 | FIG01087754: hypothetical protein | uni | sce_2414 | 65.57 FIG01087754: hypothetical protein |
| SCE1572_8777 | integral membrane protein | bi | sce_7787 | 90.22 integral membrane protein |
| SCE1572_8778 | CDP-diacetylglucosyl-serine O-phosphatidyltransferase (EC 2.7.8.8) | bi | sce_7581 | 69.13 CDP-diacetylglucosyl-serine O-phosphatidyltransferase (EC 2.7.8.8) |
| SCE1572_8779 | Antibiotic biosynthesis monooxygenase | bi | sce_7584 | 96.61 Antibiotic biosynthesis monooxygenase |
| SCE1572_8780 | Predicted membrane protein | - | - | 0 |
| SCE1572_8781 | UDP-glucose 4-epimerase (EC 5.1.3.2) | bi | sce_7585 | 88.44 UDP-glucose 4-epimerase (EC 5.1.3.2) |
| SCE1572_8782 | Nucleoside-diphosphate-sugar epimerases | bi | sce_7586 | 84.04 Nucleoside-diphosphate-sugar epimerases |
| SCE1572_8783 | Fe-S oxidoreductase | bi | sce_7587 | 87.99 Fe-S oxidoreductase |
| SCE1572_8784 | Glycosyltransferase | bi | sce_7588 | 83.03 Glycosyltransferase |
| SCE1572_8785 | Glycosyltransferase (EC 2.4.1.-) | bi | sce_7589 | 88.31 Glycosyltransferase (EC 2.4.1.-) |
| SCE1572_8786 | Uncharacterized protein conserved in bacteria | bi | sce_7590 | 90.26 Uncharacterized protein conserved in bacteria |
| SCE1572_8787 | Uncharacterized protein conserved in bacteria | bi | sce_7591 | 86.18 Uncharacterized protein conserved in bacteria |
| SCE1572_8788 | hypothetical protein | - | - | 0 |
| SCE1572_8789 | dTDP-glucose 4,6-dehydratase (EC 4.2.1.46) | bi | sce_7592 | 87.8 putative dTDP-glucose 4,6-dehydratase protein(EC:4.2.1.46) |
| SCE1572_8790 | Inositol-1-phosphate synthase (EC 5.5.1.4) | uni | sce_2005 | 79.86 Inositol-1-phosphate synthase (EC 5.5.1.4) |
| SCE1572_8791 | N-acetylglutamate synthase (EC 2.3.1.1) | bi | sce_1526 | 32.99 Acetyltransferase, GNAT family |
| SCE1572_8792 | hypothetical protein | bi | sce_5303 | 83.66 hypothetical protein |
| SCE1572_8793 | hypothetical protein | - | - | 0 |
| SCE1572_8794 | LOC432261 protein | bi | sce_6254 | 57.29 LOC432261 protein |
| SCE1572_8795 | protein of unknown function DUF541 | bi | sce_8795 | 43.89 Outer membrane protein |
| SCE1572_8796 | hypothetical protein | uni | sce_867 | 33.42 Hemolysin-type calcium-binding region |
| SCE1572_8797 | putative ISXo8 transposase | - | - | 0 |
| SCE1572_8798 | hypothetical protein | - | - | 0 |
| SCE1572_8799 | hypothetical protein | - | - | 0 |
| SCE1572_8800 | hypothetical protein | - | - | 0 |
| SCE1572_8801 | hypothetical protein | - | - | 0 |
| SCE1572_8802 | hypothetical protein | uni | sce_6222 | 46.45 Conserved protein, with a weak D-galactarate dehydratase/altronate hydrolase domain |
| SCE1572_8803 | Transcriptional regulator, TetR family | bi | sce_1534 | 89.7 Transcriptional regulator, TetR family |
| SCE1572_8804 | Galactoside O-acetyltransferase (EC 2.3.1.18) | bi | sce_1535 | 88.83 Galactoside O-acetyltransferase (EC 2.3.1.18) |
| SCE1572_8805 | hypothetical protein | - | - | 0 |
| SCE1572_8806 | hypothetical protein | - | - | 0 |
| SCE1572_8807 | hypothetical protein | - | - | 0 |
| SCE1572_8808 | membrane protein | - | - | 0 |
| SCE1572_8809 | cytochrome P460 precursor | - | - | 0 |
| SCE1572_8810 | RsbR, positive regulator of sigma-B | - | - | 0 |
| SCE1572_8811 | POSSIBLE TRANSPOSASE | bi | sce_2112 | 100 POSSIBLE TRANSPOSASE |
| SCE1572_8812 | POSSIBLE TRANSPOSASE | bi | sce_2111 | 100 POSSIBLE TRANSPOSASE |
| SCE1572_8813 | RsbR, positive regulator of sigma-B | uni | sce_6236 | 72.97 RsbR, positive regulator of sigma-B |
| SCE1572_8814 | Kazal domain protein | bi | sce_2393 | 93.48 Kazal domain protein |
| SCE1572_8815 | IS, phage, Tn, Transposon-related functions | bi | sce_7043 | 100 IS, phage, Tn, Transposon-related functions |
| SCE1572_8816 | LysR family transcriptional regulator YnfL | bi | sce_9596 | 94.98 LysR family transcriptional regulator YnfL |
| SCE1572_8817 | hypothetical protein | - | - | 0 |
| SCE1572_8818 | hypothetical protein | bi | sce_9597 | 90.31 hypothetical protein |
| SCE1572_8819 | hypothetical protein | - | - | 0 |
| SCE1572_8820 | tetratricopeptide repeat domain protein | - | - | 0 |
| SCE1572_8821 | Transcriptional regulator, TetR family | - | - | 0 |
| SCE1572_8822 | 3-oxoacyl-[acyl-carrier protein] reductase (EC 1.1.1.100) | uni | sce_4271 | 42.17 3-oxoacyl-[acyl-carrier protein] reductase (EC 1.1.1.100) |
| SCE1572_8823 | hypothetical protein | - | - | 0 |
| SCE1572_8824 | hypothetical protein | uni | sce_2109 | 31.58 FIG01089134: hypothetical protein |
| SCE1572_8825 | hypothetical protein | - | - | 0 |
| SCE1572_8826 | Integron integrase IntIPac | bi | sce_515 | 96.83 Integron integrase IntIPac |
| SCE1572_8827 | hypothetical protein | uni | sce_513 | 80.65 FIG01087636: hypothetical protein |
| SCE1572_8828 | DNA repair protein RadC | uni | sce_8398 | 92.89 DNA repair protein RadC |
| SCE1572_8829 | transcriptional regulator, LysR family | - | - | 0 |
| SCE1572_8830 | BlI2291 protein | uni | sce_2641 | 37.21 BlI2291 protein |
| SCE1572_8831 | hypothetical protein | bi | sce_9916 | 36.62 hypothetical protein |
| SCE1572_8832 | putative DNA-binding regulatory protein | - | - | 0 |
| SCE1572_8833 | putative DNA-binding regulatory protein | uni | sce_2704 | 35.71 putative RNA polymerase sigma factor |
| SCE1572_8834 | tolB protein precursor, periplasmic protein involved in the tonB-independent uptake of group A colicins | uni | sce_5085 | 60.2 tolB protein precursor, periplasmic protein involved in the tonB-independent uptake of group A colicins |
| SCE1572_8835 | hypothetical protein | uni | sce_5098 | 50.82 putative RTX family exoprotein |
| SCE1572_8836 | hypothetical protein | - | - | 0 |
| SCE1572_8837 | hypothetical protein | uni | sce_6072 | 69.7 hypothetical protein |
| SCE1572_8838 | POSSIBLE TRANSPOSASE | uni | sce_7501 | 87.76 hypothetical protein |
| SCE1572_8839 | hypothetical protein | - | - | 0 |
| SCE1572_8840 | hypothetical protein | uni | sce_858 | 23.63 N-Acetyl-D-glucosamine ABC transport system, sugar-binding protein |
| SCE1572_8841 | COG0642: Signal transduction histidine kinase | uni | sce_2158 | 47.33 Sensor protein |
| SCE1572_8842 | two-component hybrid sensor and regulator | uni | sce_4465 | 55.97 RsbR, positive regulator of sigma-B |
| SCE1572_8843 | hypothetical protein | - | - | 0 |
| SCE1572_8844 | metal dependent phosphohydrolase | bi | sce_2494 | 93.94 metal dependent phosphohydrolase |
| SCE1572_8845 | Glycosyltransferase | bi | sce_7604 | 89.17 Glycosyltransferase |
| SCE1572_8846 | FIG00804978: hypothetical protein | bi | sce_7605 | 85.76 FIG00804978: hypothetical protein |
| SCE1572_8847 | hypothetical protein | - | - | 0 |
| SCE1572_8848 | Beta-xylosidase (EC 3.2.1.37) | bi | sce_7607 | 91.13 Beta-xylosidase (EC 3.2.1.37) |
| SCE1572_8849 | Uncharacterized protein conserved in bacteria | bi | sce_7610 | 85.2 Uncharacterized protein conserved in bacteria |
| SCE1572_8850 | hypothetical protein | bi | sce_7611 | 82.8 hypothetical protein |
| SCE1572_8851 | hypothetical protein | - | - | 0 |
| SCE1572_8852 | hypothetical protein | bi | sce_7620 | 77.49 Cell division protein FtsK |
| SCE1572_8853 | hypothetical protein | - | - | 0 |
| SCE1572_8854 | S1 RNA binding domain | bi | sce_7621 | 84.54 S1 RNA binding domain |

| | | | | |
|--------------|---|-----|-----------|---|
| SCE1572_8855 | Non-specific DNA-binding protein Dps / Iron-binding ferritin-like antioxidant protein / Ferroxidase (EC 1.16.3.1) | bi | see_7622 | 93.55 Non-specific DNA-binding protein Dps / Iron-binding ferritin-like antioxidant protein / Ferroxidase (EC 1.16.3.1) |
| SCE1572_8856 | protein of unknown function DUF179 | bi | see_7624 | 94.44 hypothetical protein |
| SCE1572_8857 | PTPS-like type 4 | bi | see_7625 | 90.44 PTPS-like type 4 |
| SCE1572_8858 | DNA helicase (Rad25 homolog) | bi | see_7626 | 93.6 DNA helicase (Rad25 homolog) |
| SCE1572_8859 | Hypothetical protein (associated with DNA helicase - Rad25 homolog) | bi | see_7627 | 94.62 Hypothetical protein (associated with DNA helicase - Rad25 homolog) |
| SCE1572_8860 | hypothetical protein | - | - | 0 |
| SCE1572_8861 | YD repeat protein | uni | see_7815 | 47.21 wall-associated protein |
| SCE1572_8862 | hypothetical protein | - | - | 0 |
| SCE1572_8863 | FIG01089478: hypothetical protein | uni | see_7516 | 43.29 FIG01089478: hypothetical protein |
| SCE1572_8864 | hypothetical protein | - | - | 0 |
| SCE1572_8865 | hypothetical protein | bi | see_6039 | 80.86 hypothetical protein |
| SCE1572_8866 | Multi antimicrobial extrusion protein (Na ⁺ /drug antiporter), MATE family of MDR efflux pumps | bi | see_6040 | 80.57 Multi antimicrobial extrusion protein (Na ⁺ /drug antiporter), MATE family of MDR efflux pumps |
| SCE1572_8867 | transcriptional regulator, LysR family | uni | see_6853 | 30.86 Transcriptional regulator, LysR family |
| SCE1572_8868 | Putative transport protein | uni | see_1251 | 31.21 drug resistance transporter, EmrB/QacA family |
| SCE1572_8869 | Phosphoesterase PHP, N-terminal precursor | bi | see_7628 | 83.33 Phosphoesterase PHP, N-terminal precursor |
| SCE1572_8870 | hypothetical protein | uni | see_9036 | 37.8 200 kDa antigen p200, putative |
| SCE1572_8871 | Magnesium and cobalt transport protein CorA | bi | see_7630 | 90.1 Magnesium and cobalt transport protein CorA |
| SCE1572_8872 | FIG01085382: hypothetical protein | bi | see_7631 | 69.2 FIG01085382: hypothetical protein |
| SCE1572_8873 | FIG01085954: hypothetical protein | bi | see_1062 | 80.37 FIG01085954: hypothetical protein |
| SCE1572_8874 | hypothetical protein | uni | see_9653 | 58.89 hypothetical protein |
| SCE1572_8875 | Serine/threonine protein kinase (EC 2.7.1.1) | uni | see_7661 | 47.1 Signal transduction histidine kinase CheA (EC 2.7.3.-) |
| SCE1572_8876 | Signal transduction histidine kinase CheA (EC 2.7.3.-) | uni | - | 0 |
| SCE1572_8877 | Serine/threonine protein kinase (EC 2.7.1.1) | bi | see_7515 | 62.65 RNA polymerase sigma factor SigW |
| SCE1572_8878 | RNA polymerase sigma factor SigW | bi | see_6813 | 70.09 hypothetical protein |
| SCE1572_8879 | hypothetical protein | bi | see_7519 | 79.05 PE-PGRS family protein |
| SCE1572_8880 | Collagen triple helix repeat | uni | see_6868 | 75.65 hypothetical protein |
| SCE1572_8881 | hypothetical protein | - | - | 0 |
| SCE1572_8882 | hypothetical protein | bi | see_10354 | 67.21 hypothetical protein |
| SCE1572_8883 | FIG01089660: hypothetical protein | uni | see_4330 | 69.7 FIG01089660: hypothetical protein |
| SCE1572_8884 | hypothetical protein | uni | see_3287 | 42.59 GTP-binding protein EngA |
| SCE1572_8885 | Adenylate cyclase (EC 4.6.1.1) / Guanylate cyclase (EC 4.6.1.2) | bi | see_7657 | 88.94 Adenylate cyclase (EC 4.6.1.1) / Guanylate cyclase (EC 4.6.1.2) |
| SCE1572_8886 | hypothetical protein | bi | see_7658 | 82.3 hypothetical protein |
| SCE1572_8887 | sigma54 specific transcriptional regulator, Fis family | bi | see_7659 | 84.68 sigma-54 dependent response regulator |
| SCE1572_8888 | putative cytochrome P450 hydroxylase | uni | see_7075 | 49.35 putative cytochrome P450 hydroxylase |
| SCE1572_8889 | Xylanase | uni | see_1082 | 76.11 Xylanase |
| SCE1572_8890 | Xylanase | bi | see_1082 | 76.37 Xylanase |
| SCE1572_8891 | Glutathione S-transferase (EC 2.5.1.18) | uni | see_558 | 49.3 Glutathione S-transferase (EC 2.5.1.18) |
| SCE1572_8892 | hypothetical protein | - | - | 0 |
| SCE1572_8893 | Possible glucoamylase (Diverged) , 15 family | bi | see_7664 | 81.77 Periplasmic alpha-amylase (EC 3.2.1.1) |
| SCE1572_8894 | Putative oxidoreductase YncB | uni | see_9276 | 46.49 Quinone oxidoreductase (EC 1.6.5.5) |
| SCE1572_8895 | FIG01088760: hypothetical protein | bi | see_7666 | 81.99 FIG01088760: hypothetical protein |
| SCE1572_8896 | FIG01085006: hypothetical protein | bi | see_7673 | 72.11 FIG01085006: hypothetical protein |
| SCE1572_8897 | peptidase M16-like | uni | see_2304 | 57.26 peptidase M16-like |
| SCE1572_8898 | hypothetical protein | - | - | 0 |
| SCE1572_8899 | D-alanine--D-alanine ligase (EC 6.3.2.4) | bi | see_7675 | 95.82 D-alanine--D-alanine ligase (EC 6.3.2.4) |
| SCE1572_8900 | ATP-dependent DNA ligase (EC 6.5.1.1) LigC | bi | see_7677 | 82.39 ATP-dependent DNA ligase (EC 6.5.1.1) LigC |
| SCE1572_8901 | conserved hypothetical protein | uni | see_3000 | 58.59 conserved hypothetical protein |
| SCE1572_8902 | Possible glucoamylase (Diverged) , 15 family | uni | see_7119 | 52.44 hypothetical protein |
| SCE1572_8903 | AfsR-like regulatory protein | bi | see_7678 | 89.26 transcriptional regulator, winged helix family |
| SCE1572_8904 | hypothetical protein | bi | see_7689 | 81.82 FIG01085226: hypothetical protein |
| SCE1572_8905 | hypothetical protein | uni | see_9963 | 51.52 hypothetical protein |
| SCE1572_8906 | hypothetical protein | uni | see_7691 | 60.22 FIG01089506: hypothetical protein |
| SCE1572_8907 | hypothetical protein | uni | see_10330 | 33.67 hypothetical protein |
| SCE1572_8908 | FIG01089506: hypothetical protein | bi | see_7691 | 66.32 FIG01089506: hypothetical protein |
| SCE1572_8909 | hypothetical protein | bi | see_7692 | 74.1 hypothetical protein |
| SCE1572_8910 | predicted protein | bi | see_7695 | 76.45 predicted protein |
| SCE1572_8911 | hypothetical protein | - | - | 0 |
| SCE1572_8912 | response regulator | uni | see_6723 | 42.97 Response regulator of zinc sigma-54-dependent two-component system |
| SCE1572_8913 | hypothetical protein | bi | see_7696 | 89.01 FIG01087243: hypothetical protein |
| SCE1572_8914 | hypothetical protein | uni | see_283 | 39.53 Endoribonuclease L-PSP |
| SCE1572_8915 | Arsenate reductase (EC 1.20.4.1) | uni | see_6285 | 82.86 Arsenate reductase (EC 1.20.4.1) |
| SCE1572_8916 | Aquaporin Z | bi | see_6286 | 93.25 Aquaporin Z |
| SCE1572_8917 | Lactoylglutathione lyase (EC 4.4.1.5) @ Cadmium-induced protein CadI | bi | see_6287 | 88.54 Lactoylglutathione lyase (EC 4.4.1.5) @ Cadmium-induced protein CadI |
| SCE1572_8918 | Transcriptional regulator, ArsR family | bi | see_6288 | 82.18 Transcriptional regulator, ArsR family |
| SCE1572_8919 | hypothetical protein | bi | see_864 | 81.18 hypothetical protein |
| SCE1572_8920 | hypothetical protein | uni | see_7697 | 89.47 Predicted enzyme of the cupin superfamily |
| SCE1572_8921 | FIG01088601: hypothetical protein | bi | see_4283 | 66.32 FIG01085391: hypothetical protein |
| SCE1572_8922 | Hydroxylamine reductase (EC 1.7.-.-) | uni | see_866 | 81.73 Hydroxylamine reductase (EC 1.7.-.-) |
| SCE1572_8923 | hypothetical protein | - | - | 0 |
| SCE1572_8924 | Asr1714 protein | uni | see_7697 | 89.47 Predicted enzyme of the cupin superfamily |
| SCE1572_8925 | Collagen alpha 1(I) chain precursor | uni | see_4283 | 66.32 FIG01085391: hypothetical protein |
| SCE1572_8926 | Hydroxylamine reductase (EC 1.7.-.-) | uni | see_866 | 81.73 Hydroxylamine reductase (EC 1.7.-.-) |
| SCE1572_8927 | hypothetical protein | - | - | 0 |
| SCE1572_8928 | Predicted enzyme of the cupin superfamily | bi | see_7697 | 94.62 Predicted enzyme of the cupin superfamily |
| SCE1572_8929 | ATP-dependent DNA helicase recG (EC 3.6.1.-) | bi | see_7698 | 87.33 nucleotidyltransferase domain protein |
| SCE1572_8930 | nucleotidyltransferase domain protein | bi | see_7699 | 91.76 5-Enolpyruvylshikimate-3-phosphate synthase (EC 2.5.1.19) |
| SCE1572_8931 | 5-Enolpyruvylshikimate-3-phosphate synthase (EC 2.5.1.19) | bi | see_7700 | 83.87 Cytidylate kinase (EC 2.7.4.14) |
| SCE1572_8932 | Cytidylate kinase (EC 2.7.4.14) | bi | see_7701 | 80.3 hypothetical protein |
| SCE1572_8933 | hypothetical protein | bi | see_7702 | 75.88 FIG01086947: hypothetical protein |
| SCE1572_8934 | FIG01086947: hypothetical protein | - | - | 0 |
| SCE1572_8935 | hypothetical protein | bi | see_7703 | 98.44 SSU ribosomal protein S1p |
| SCE1572_8936 | SSU ribosomal protein S1p | bi | see_7704 | 81.72 Putative lipoprotein |
| SCE1572_8937 | Putative lipoprotein | bi | see_7705 | 93.3 histidine triad (HIT) protein |
| SCE1572_8938 | HIT family protein | bi | see_7706 | 86.15 UPF0118 membrane protein YrrI |
| SCE1572_8939 | UPF0118 membrane protein YrrI | bi | see_7708 | 94.92 hypothetical protein |
| SCE1572_8940 | hypothetical protein | bi | see_7709 | 88.01 hypothetical protein |
| SCE1572_8941 | hypothetical protein | bi | see_7710 | 82.46 Histidine triad (HIT) nucleotide-binding protein, similarity with At5g48545 and yeast YDL125C (HNT1) |
| SCE1572_8942 | Histidine triad (HIT) nucleotide-binding protein, similarity with At5g48545 and yeast YDL125C (HNT1) | - | - | 0 |
| SCE1572_8943 | hypothetical protein | bi | see_7712 | 90.05 Carbonic anhydrase (EC 4.2.1.1) |
| SCE1572_8944 | Carbonic anhydrase (EC 4.2.1.1) | bi | see_7713 | 88.81 Carbonic anhydrase (EC 4.2.1.1) |
| SCE1572_8945 | Carbonic anhydrase (EC 4.2.1.1) | bi | see_7714 | 82.77 putative oxidoreductase |
| SCE1572_8946 | putative oxidoreductase | bi | see_7715 | 79.52 FIG01088741: hypothetical protein |
| SCE1572_8947 | FIG01088741: hypothetical protein | bi | see_7717 | 74.36 Type II/IV secretion system secretin RcpA/CpaC, associated with Flp pilus assembly |
| SCE1572_8948 | Type II/IV secretion system secretin RcpA/CpaC, associated with Flp pilus assembly | uni | see_5999 | 28.67 FIG01088071: hypothetical protein |
| SCE1572_8949 | hypothetical protein | - | - | 0 |
| SCE1572_8950 | hypothetical protein | bi | see_7718 | 72.9 FIG01084939: hypothetical protein |
| SCE1572_8951 | FIG01084939: hypothetical protein | uni | see_7719 | 42.95 Cellulase (EC 3.2.1.4) |
| SCE1572_8952 | putative lipoprotein | bi | see_7720 | 67.51 serine/threonine protein kinase |
| SCE1572_8953 | serine/threonine protein kinase | - | - | 0 |
| SCE1572_8954 | hypothetical protein | - | - | 0 |
| SCE1572_8955 | hypothetical protein | uni | see_5675 | 51.38 Two-component system regulatory protein |
| SCE1572_8956 | Two-component system regulatory protein | uni | see_7721 | 87.24 FIG01087134: hypothetical protein |
| SCE1572_8957 | FIG01087134: hypothetical protein | - | - | 0 |
| SCE1572_8958 | hypothetical protein | - | - | 0 |
| SCE1572_8959 | phenazine biosynthesis protein PhzF family | bi | see_2361 | 34.88 FIG100068: Hypothetical protein |
| SCE1572_8960 | phenazine biosynthesis protein PhzF family | bi | see_309 | 80 hypothetical protein |
| SCE1572_8961 | hypothetical protein | bi | see_7725 | 90.59 hypothetical protein |
| SCE1572_8962 | OB-fold nucleic acid binding domain protein | bi | see_7726 | 90.67 FIG01085229: hypothetical protein |
| SCE1572_8963 | hypothetical protein | bi | see_7727 | 91.76 hypothetical protein |
| SCE1572_8964 | FIG01085229: hypothetical protein | uni | see_4880 | 80.74 GII0726 protein |
| SCE1572_8965 | hypothetical protein | - | - | 0 |
| SCE1572_8966 | GII0726 protein | bi | see_7729 | 83.35 eukaryotic-type protein kinase |
| SCE1572_8967 | phosphotransferase (aminonucleoside antibiotic resistance) | bi | see_7730 | 87.65 Enoyl-CoA hydratase (EC 4.2.1.17) |
| SCE1572_8968 | protein kinase domain | bi | see_7731 | 97.29 Ribosomal protein S6 glutaminyl transferase |
| SCE1572_8969 | Enoyl-CoA hydratase (EC 4.2.1.17) | bi | see_7733 | 94.6 Isolevaleryl-CoA dehydrogenase (EC 1.3.99.10) |
| SCE1572_8970 | Ribosomal protein S6 glutaminyl transferase | uni | see_4338 | 37.2 hypothetical protein |
| SCE1572_8971 | Isolevaleryl-CoA dehydrogenase (EC 1.3.99.10) | uni | see_4339 | 38.98 Outer membrane vitamin B12 receptor BtuB |
| SCE1572_8972 | hypothetical protein | uni | see_4980 | 55.56 Epstein-Barr nuclear antigen 1 (EBV nuclear antigen 1) (EBNA-1) |
| SCE1572_8973 | Outer membrane vitamin B12 receptor BtuB | bi | see_7734 | 89.2 Nicotinate-nucleotide--dimethylbenzimidazole phosphoribosyltransferase (EC 2.4.2.21) |
| SCE1572_8974 | putative lipoprotein | bi | see_7735 | 84.25 Cobalamin synthase |
| SCE1572_8975 | Nicotinate-nucleotide--dimethylbenzimidazole phosphoribosyltransferase (EC 2.4.2.21) | bi | see_7736 | 76.92 Alpha-ribazole-5-'-phosphate phosphatase (EC 3.1.3.73) |
| SCE1572_8976 | Cobalamin synthase | bi | see_7737 | 93.37 Agmatinase (EC 3.5.3.11) |
| SCE1572_8977 | Alpha-ribazole-5-'-phosphate phosphatase (EC 3.1.3.73) | bi | see_7738 | 86.05 Thiosulfate sulfurtransferase, rhodanese (EC 2.8.1.1) |
| SCE1572_8978 | Agmatinase (EC 3.5.3.11) | bi | see_10099 | 75 hypothetical protein, mmyy |
| SCE1572_8979 | Thiosulfate sulfurtransferase, rhodanese (EC 2.8.1.1) | uni | see_7083 | 59.46 hypothetical protein |
| SCE1572_8980 | MII046 protein | - | - | 0 |
| SCE1572_8981 | hypothetical protein | - | - | 0 |
| SCE1572_8982 | hypothetical protein | - | - | 0 |
| SCE1572_8983 | hypothetical protein | bi | see_7750 | 80.52 Bipolar DNA helicase |
| SCE1572_8984 | Bipolar DNA helicase | uni | see_1227 | 63.35 FIG01086453: hypothetical protein |
| SCE1572_8985 | FIG01086453: hypothetical protein | - | - | 0 |
| SCE1572_8986 | hypothetical protein | bi | see_7751 | 73.48 Probable serine/threonine-protein kinase pknJ (EC 2.7.11.1) |
| SCE1572_8987 | Probable serine/threonine-protein kinase pknJ (EC 2.7.11.1) | - | - | 0 |
| SCE1572_8988 | hypothetical protein | bi | see_7752 | 92.31 hypothetical protein |
| SCE1572_8989 | hypothetical protein | bi | see_7753 | 83.07 FIG00840272: hypothetical protein |
| SCE1572_8990 | FIG00840272: hypothetical protein | bi | see_7756 | 89.01 hypothetical protein |
| SCE1572_8991 | hypothetical protein | bi | see_7757 | 94.81 hypothetical protein |
| SCE1572_8992 | hypothetical protein | bi | see_7758 | 88.63 Cytochrome c-type biogenesis protein DsbD, protein-disulfide reductase (EC 1.8.1.8) |
| SCE1572_8993 | Cytochrome c-type biogenesis protein DsbD, protein-disulfide reductase (EC 1.8.1.8) | bi | see_7759 | 79.03 hypothetical protein |
| SCE1572_8994 | hypothetical protein | bi | see_7760 | 83.04 Hypothetical protein |
| SCE1572_8995 | putative exported protein of unknown function with OmpA family domain | bi | see_7761 | 58.38 serine/threonine protein kinase |
| SCE1572_8996 | UDP-N-acetylglucosamine 1-carboxyvinyltransferase (EC 2.5.1.7) | bi | see_7762 | 92.49 Riboflavin kinase (EC 2.7.1.26) / FMN adenylyltransferase (EC 2.7.7.2) |
| SCE1572_8997 | UDP-N-acetylglucosamine 1-carboxyvinyltransferase (EC 2.5.1.7) | bi | see_7763 | 98.41 Ribose-phosphate pyrophosphokinase (EC 2.7.6.1) |
| SCE1572_8998 | Riboflavin kinase (EC 2.7.1.26) / FMN adenylyltransferase (EC 2.7.7.2) | bi | see_7764 | 92.17 LSU ribosomal protein L25p |
| SCE1572_8999 | Ribose-phosphate pyrophosphokinase (EC 2.7.6.1) | bi | see_7765 | 93.27 Peptidyl-tRNA hydrolase (EC 3.1.1.29) |
| SCE1572_9000 | LSU ribosomal protein L25p | bi | see_7766 | 91.62 SSU ribosomal protein S6p |
| SCE1572_9001 | Peptidyl-tRNA hydrolase (EC 3.1.1.29) | bi | see_7767 | 100 SSU ribosomal protein S18p |
| SCE1572_9002 | SSU ribosomal protein S6p | bi | see_7768 | 94.67 LSU ribosomal protein L9p |
| SCE1572_9003 | SSU ribosomal protein S18p | bi | see_7769 | 84.36 2-keto-3-deoxy-gluconate kinase |
| SCE1572_9004 | LSU ribosomal protein L9p | bi | see_7770 | 74.19 hypothetical protein |
| SCE1572_9005 | 2-keto-3-deoxy-gluconate kinase | bi | see_7771 | 96.6 Replicative DNA helicase (EC 3.6.1.-) |
| SCE1572_9006 | hypothetical protein | bi | see_7772 | 78.91 hypothetical protein |
| SCE1572_9007 | Replicative DNA helicase (EC 3.6.1.-) | bi | see_7773 | 79.78 FIG01086555: hypothetical protein |
| SCE1572_9008 | protein of unknown function DUF6, transmembrane | - | - | 0 |
| SCE1572_9009 | FIG01086555: hypothetical protein | - | - | 0 |
| SCE1572_9010 | hypothetical protein | - | - | 0 |
| SCE1572_9011 | hypothetical protein | uni | see_6904 | 83.16 FIG01089354: hypothetical protein |
| SCE1572_9012 | hypothetical protein | bi | see_7774 | 86.28 FIG01089060: hypothetical protein |
| SCE1572_9013 | FIG01089060: hypothetical protein | - | - | 0 |
| SCE1572_9014 | hypothetical protein | - | - | 0 |
| SCE1572_9015 | hypothetical protein | - | - | 0 |
| SCE1572_9016 | hypothetical protein | - | - | 0 |
| SCE1572_9017 | hypothetical protein | - | - | 0 |
| SCE1572_9018 | putative transposase | - | - | 0 |

| | | | |
|--------------|---|-----|-----------|
| SCE1572_9019 | hypothetical protein | - | 0 |
| SCE1572_9020 | hypothetical protein | - | 0 |
| SCE1572_9021 | COG0009 Sua5 subfamily, required for N6-threonylcarbamoyl adenosine t(6)A37 modification in tRNA | bi | sce_7776 |
| SCE1572_9022 | putative exported protein | bi | sce_7777 |
| SCE1572_9023 | Serine protein kinase (prkA protein), P-loop containing | bi | sce_7778 |
| SCE1572_9024 | hypothetical protein | bi | sce_7779 |
| SCE1572_9025 | putative protein phosphatase | bi | sce_7780 |
| SCE1572_9026 | FIG01085338: hypothetical protein | bi | sce_7781 |
| SCE1572_9027 | serine/threonine protein kinase | bi | sce_7782 |
| SCE1572_9028 | ABC transporter, ATP-binding protein | bi | sce_7783 |
| SCE1572_9029 | protein of unknown function DUF990 | bi | sce_7784 |
| SCE1572_9030 | ABC transporter permease protein | bi | sce_7785 |
| SCE1572_9031 | FIG00502110: hypothetical protein | bi | sce_7786 |
| SCE1572_9032 | AAA ATPase | uni | sce_7361 |
| SCE1572_9033 | Transcriptional regulator, LysR family | uni | sce_7791 |
| SCE1572_9034 | Glutathione S-transferase, unnamed subgroup (EC 2.5.1.18) | bi | sce_7792 |
| SCE1572_9035 | probable iron-sulfur binding protein YPO1417 | bi | sce_7793 |
| SCE1572_9036 | sensor histidine kinase | bi | sce_7794 |
| SCE1572_9037 | Response regulator of zinc sigma-54-dependent two-component system | bi | sce_7796 |
| SCE1572_9038 | Acetoacetate metabolism regulatory protein atOC (Ornithine/arginine decarboxylase inhibitor) (Ornithine decarboxylase antizyme) | bi | sce_7798 |
| SCE1572_9039 | C3: similar to Vanillate O-demethylase oxygenase | bi | sce_7799 |
| SCE1572_9040 | Transcriptional regulator, AraC family | bi | sce_7800 |
| SCE1572_9041 | Prion-like-(Q/n-rich)-domain-bearing protein protein 54 | bi | sce_7801 |
| SCE1572_9042 | Pathogenesis-related protein 1A precursor (PR-1A) | bi | sce_7802 |
| SCE1572_9043 | Butyryl-CoA dehydrogenase (EC 1.3.99.2) | bi | sce_7804 |
| SCE1572_9044 | Oligopeptidase A (EC 3.4.24.70) | bi | sce_7805 |
| SCE1572_9045 | BlI2291 protein | uni | sce_2641 |
| SCE1572_9046 | Putative peptidoglycan bound protein (LPXTG motif) Lmo1799 homolog | bi | sce_7806 |
| SCE1572_9047 | hypothetical protein | bi | sce_7807 |
| SCE1572_9048 | hypothetical protein | bi | sce_7808 |
| SCE1572_9049 | putative inner membrane protein | bi | sce_7809 |
| SCE1572_9050 | 5-formyltetrahydrofolate cyclo-ligase (EC 6.3.3.2) | bi | sce_7810 |
| SCE1572_9051 | Large-conductance mechanosensitive channel | bi | sce_7812 |
| SCE1572_9052 | YD repeat protein | bi | sce_7816 |
| SCE1572_9053 | YD repeat protein | bi | sce_7814 |
| SCE1572_9054 | Rhs family protein | uni | sce_7818 |
| SCE1572_9055 | FIG01089649: hypothetical protein | bi | sce_7819 |
| SCE1572_9056 | Na-Ca exchanger/integrin-beta4 | bi | sce_4532 |
| SCE1572_9057 | hypothetical protein | - | 0 |
| SCE1572_9058 | conserved hypothetical protein | uni | sce_3992 |
| SCE1572_9059 | hypothetical protein | uni | sce_3991 |
| SCE1572_9060 | High-affinity carbon uptake protein Hat/HatR | uni | sce_8704 |
| SCE1572_9061 | hypothetical protein | uni | sce_2126 |
| SCE1572_9062 | S-layer-like array protein | uni | sce_3992 |
| SCE1572_9063 | hypothetical protein | - | 0 |
| SCE1572_9064 | VCBS | uni | sce_4532 |
| SCE1572_9065 | Adenylate cyclase (EC 4.6.1.1) | bi | sce_7821 |
| SCE1572_9066 | Glucan endo-1,3-beta-glucosidase A1 ((1->3)-beta-glucan endohydrolase) ((1->3)-beta-glucanase A1) (EC 3.2.1.39) | uni | sce_1518 |
| SCE1572_9067 | hypothetical protein | bi | sce_7822 |
| SCE1572_9068 | major facilitator superfamily MFS_1 | bi | sce_7823 |
| SCE1572_9069 | Dolichyl-phosphate mannose synthase related protein | bi | sce_7824 |
| SCE1572_9070 | hypothetical protein | bi | sce_7825 |
| SCE1572_9071 | Cytochrome c551 peroxidase (EC 1.11.1.5) | bi | sce_7827 |
| SCE1572_9072 | FIG01088064: hypothetical protein | bi | sce_7828 |
| SCE1572_9073 | Internalin-like protein (LPXTG motif) Lmo0333 homolog | bi | sce_7385 |
| SCE1572_9074 | Butyryl-CoA dehydrogenase (EC 1.3.99.2) | bi | sce_7837 |
| SCE1572_9075 | WD-40 repeat protein | bi | sce_3793 |
| SCE1572_9076 | hypothetical protein | uni | sce_3796 |
| SCE1572_9077 | hypothetical protein | bi | sce_2024 |
| SCE1572_9078 | COG3005: Nitrate/TMAO reductases, membrane-bound tetraheme cytochrome c subunit | bi | sce_2025 |
| SCE1572_9079 | hypothetical protein | - | 0 |
| SCE1572_9080 | Similarities with trjQ12218 Saccharomyces cerevisiae YOR009w | uni | sce_8998 |
| SCE1572_9081 | hypothetical protein | uni | sce_8997 |
| SCE1572_9082 | Peptide chain release factor homolog | bi | sce_7846 |
| SCE1572_9083 | Protein with similarity to RtcB | bi | sce_7847 |
| SCE1572_9084 | nitrogen fixation positive regulatory protein | bi | sce_7849 |
| SCE1572_9085 | hypothetical protein | uni | sce_3767 |
| SCE1572_9086 | hypothetical protein | - | 0 |
| SCE1572_9087 | Threonine dehydrogenase and related Zn-dependent dehydrogenases | bi | sce_7850 |
| SCE1572_9088 | hypothetical protein | uni | sce_7851 |
| SCE1572_9089 | Cytochrome c Snr1 | bi | sce_7867 |
| SCE1572_9090 | nuclease (SNase-like) | bi | sce_7869 |
| SCE1572_9091 | hypothetical protein | uni | sce_3858 |
| SCE1572_9092 | FIG01086277: hypothetical protein | bi | sce_7876 |
| SCE1572_9093 | FIG01088782: hypothetical protein | bi | sce_7877 |
| SCE1572_9094 | FIG01085916: hypothetical protein | bi | sce_7878 |
| SCE1572_9095 | Dienelactone hydrolase family | bi | sce_7879 |
| SCE1572_9096 | Chemotaxis regulator - transmits chemoreceptor signals to flagellar motor components CheY | bi | sce_7880 |
| SCE1572_9097 | hypothetical protein | uni | sce_709 |
| SCE1572_9098 | hypothetical protein | uni | sce_1120 |
| SCE1572_9099 | EBNA-1 | bi | sce_7886 |
| SCE1572_9100 | Protocatechuate 3,4-Dioxygenase beta chain (EC 1.13.11.3) | bi | sce_7882 |
| SCE1572_9101 | Diaminopimelate decarboxylase (EC 4.1.1.20) | bi | sce_7883 |
| SCE1572_9102 | hypothetical protein | - | 0 |
| SCE1572_9103 | 5'-nucleotidase (EC 3.1.3.5) | bi | sce_7884 |
| SCE1572_9104 | FIG01089636: hypothetical protein | bi | sce_7887 |
| SCE1572_9105 | Chorismate mutase I (EC 5.4.99.5) / Prephenate dehydratase (EC 4.2.1.51) | bi | sce_7888 |
| SCE1572_9106 | hypothetical protein | - | 0 |
| SCE1572_9107 | ECF subfamily sigma subunit | bi | sce_7889 |
| SCE1572_9108 | Transcriptional regulator, Cro/CI family | bi | sce_7890 |
| SCE1572_9109 | FIG01085414: hypothetical protein | bi | sce_7891 |
| SCE1572_9110 | Helicase PriA essential for oriC/DnaA-independent DNA replication | bi | sce_7892 |
| SCE1572_9111 | Ferredoxin, 2Fe-2S | bi | sce_7893 |
| SCE1572_9112 | Serine/threonine kinase PKN11 | bi | sce_7894 |
| SCE1572_9113 | Vitamin B12 ABC transporter, B12-binding component BtuF | bi | sce_7895 |
| SCE1572_9114 | hypothetical protein | bi | sce_7896 |
| SCE1572_9115 | FIG01088646: hypothetical protein | bi | sce_7897 |
| SCE1572_9116 | Long-chain-fatty-acid-CoA ligase (EC 6.2.1.3) | bi | sce_7898 |
| SCE1572_9117 | Glycerol-3-phosphate transporter | bi | sce_7899 |
| SCE1572_9118 | Proline-rich protein | uni | sce_6423 |
| SCE1572_9119 | putative multi-domain protein | - | 0 |
| SCE1572_9120 | hypothetical protein | - | 0 |
| SCE1572_9121 | hypothetical protein | - | 0 |
| SCE1572_9122 | Putative ATP/GTP-binding protein | uni | sce_9664 |
| SCE1572_9123 | FIG01088065: hypothetical protein | bi | sce_7901 |
| SCE1572_9124 | hypothetical protein | bi | sce_7902 |
| SCE1572_9125 | FIG01088131: hypothetical protein | bi | sce_7903 |
| SCE1572_9126 | hypothetical protein | bi | sce_7904 |
| SCE1572_9127 | Chromosome (plasmid) partitioning protein ParA / Sporulation initiation inhibitor protein Soj | bi | sce_7905 |
| SCE1572_9128 | hypothetical protein | bi | sce_7906 |
| SCE1572_9129 | Outer membrane receptor proteins, mostly Fe transport | bi | sce_7907 |
| SCE1572_9130 | hypothetical protein | bi | sce_7908 |
| SCE1572_9131 | hypothetical protein | bi | sce_7909 |
| SCE1572_9132 | putative lipoprotein | bi | sce_7910 |
| SCE1572_9133 | hypothetical protein | uni | sce_8647 |
| SCE1572_9134 | Flagellar hook-length control protein FliK | bi | sce_7912 |
| SCE1572_9135 | FIG01088605: hypothetical protein | bi | sce_7913 |
| SCE1572_9136 | RNA polymerase sigma factor nccH | bi | sce_7914 |
| SCE1572_9137 | hypothetical protein | - | 0 |
| SCE1572_9138 | hypothetical protein | bi | sce_10329 |
| SCE1572_9139 | hypothetical protein | - | 0 |
| SCE1572_9140 | hypothetical protein | uni | sce_5088 |
| SCE1572_9141 | hypothetical protein | uni | sce_5924 |
| SCE1572_9142 | FIG01085109: hypothetical protein | - | 0 |
| SCE1572_9143 | FIG01085109: hypothetical protein | uni | sce_3939 |
| SCE1572_9144 | Ribosomal RNA small subunit methyltransferase E (EC 2.1.1.-) | bi | sce_7942 |
| SCE1572_9145 | Ribosomal protein L11 methyltransferase (EC 2.1.1.-) | bi | sce_7943 |
| SCE1572_9146 | hypothetical protein | - | 0 |
| SCE1572_9147 | metallophosphoesterase | bi | sce_7944 |
| SCE1572_9148 | Glucose-1-phosphate adenyltransferase (EC 2.7.7.27) | bi | sce_7945 |
| SCE1572_9149 | hypothetical protein | bi | sce_7946 |
| SCE1572_9150 | FIG01086998: hypothetical protein | bi | sce_7947 |
| SCE1572_9151 | FIG01088345: hypothetical protein | bi | sce_7948 |
| SCE1572_9152 | Chloride channel protein | bi | sce_7949 |
| SCE1572_9153 | response regulator receiver protein | bi | sce_7951 |
| SCE1572_9154 | Protein containing domains DUF404, DUF407 | bi | sce_7952 |
| SCE1572_9155 | Protein containing domains DUF403 | bi | sce_7953 |
| SCE1572_9156 | Protein containing transglutaminase-like domain, putative cysteine protease | bi | sce_7954 |
| SCE1572_9157 | FIG01086465: hypothetical protein | bi | sce_7955 |
| SCE1572_9158 | Thiol peroxidase, Bcp-type (EC 1.11.1.15) | bi | sce_7956 |
| SCE1572_9159 | hypothetical protein | - | 0 |
| SCE1572_9160 | 3-ketoacyl-CoA thiolase (EC 2.3.1.16) @ Acetyl-CoA acetyltransferase (EC 2.3.1.9) | bi | sce_7957 |
| SCE1572_9161 | Metallo-beta-lactamase family protein | bi | sce_7958 |
| SCE1572_9162 | hypothetical protein | - | 0 |
| SCE1572_9163 | hypothetical protein | uni | sce_2576 |
| SCE1572_9164 | FIG01086577: hypothetical protein | uni | sce_1209 |
| SCE1572_9165 | hypothetical protein | - | 0 |
| SCE1572_9166 | hypothetical protein | uni | sce_8406 |
| SCE1572_9167 | hypothetical protein | - | 0 |
| SCE1572_9168 | hypothetical protein | uni | sce_8407 |
| SCE1572_9169 | PE-PGRS FAMILY PROTEIN | uni | sce_10357 |
| SCE1572_9170 | hypothetical protein | - | 0 |
| SCE1572_9171 | hypothetical protein | bi | sce_7098 |
| SCE1572_9172 | hypothetical protein | uni | sce_9480 |
| SCE1572_9173 | hypothetical protein | bi | sce_7964 |
| SCE1572_9174 | transcriptional regulator, LysR family | bi | sce_7965 |
| SCE1572_9175 | FIG01088750: hypothetical protein | bi | sce_7967 |
| SCE1572_9176 | hypothetical protein | - | 0 |
| SCE1572_9177 | Adenylate cyclase (EC 4.6.1.1) / Guanylate cyclase (EC 4.6.1.2) | bi | sce_7969 |
| SCE1572_9178 | FIG01088228: hypothetical protein | uni | sce_2528 |
| SCE1572_9179 | hypothetical protein-putative transmembrane protein | bi | sce_7971 |
| SCE1572_9180 | hypothetical protein | - | 0 |
| SCE1572_9181 | Putative adhesin | bi | sce_7972 |
| SCE1572_9182 | Cyanophycinase (EC 3.4.15.6) | - | 0 |

| | | | | | |
|----------------|---|-----|----------|-------|---|
| SCE1572_9183 | Cyanophycin synthase (EC 6.3.2.29)(EC 6.3.2.30) | umi | sce_1850 | 25.71 | UDP-N-acetylmuramoylanyl-D-glutamate--2,6-diaminopimelate ligase (EC 6.3.2.13) |
| SCE1572_9184 | Cyanophycinase (EC 3.4.15.6) | - | - | 0 | 0 |
| SCE1572_9185 | hypothetical protein | bi | sce_7851 | 80 | hypothetical protein |
| SCE1572_9186 | hypothetical protein | - | - | 0 | 0 |
| SCE1572_9187 | Formamidopyrimidine-DNA glycosylase (EC 3.2.2.23) | bi | sce_7985 | 85.17 | Formamidopyrimidine-DNA glycosylase (EC 3.2.2.23) |
| SCE1572_9188 | FIG01087869: hypothetical protein | bi | sce_7986 | 76.05 | FIG01087869: hypothetical protein |
| SCE1572_9189 | rhamnogalacturonan acetyltransferase | umi | sce_8647 | 43.48 | Arylsulfatase (EC 3.1.6.1) |
| SCE1572_9190 | Phytanoyl-CoA dioxygenase | bi | sce_7987 | 81.56 | Phytanoyl-CoA dioxygenase |
| SCE1572_9191 | hypothetical protein | bi | sce_7988 | 86.96 | hypothetical protein |
| SCE1572_9192 | ActD | bi | sce_7386 | 85.71 | ActD |
| SCE1572_9193 | hypothetical protein | bi | sce_7387 | 74.62 | ActD |
| SCE1572_9194 | RNA polymerase sigma-70 factor, group 3 | bi | sce_7388 | 87.57 | RNA polymerase sigma-70 factor, group 3 |
| SCE1572_9195 | hypothetical protein | bi | sce_7389 | 77.22 | hypothetical protein |
| SCE1572_9196 | RsbR, positive regulator of sigma-B | bi | sce_7990 | 79.47 | RsbR, positive regulator of sigma-B |
| SCE1572_9197 | FIG01089256: hypothetical protein | bi | sce_1285 | 60.61 | FIG01089256: hypothetical protein |
| SCE1572_9198 | transcriptional regulator, LysR family | bi | sce_7991 | 82.78 | transcriptional regulator, LysR family |
| SCE1572_9199 | NmrA-like | bi | sce_7992 | 88.47 | NADPH:quinone oxidoreductase 2 |
| SCE1572_9200 | hypothetical protein | bi | sce_7998 | 68.52 | hypothetical protein |
| SCE1572_9201 | FIG01087827: hypothetical protein | umi | sce_7999 | 81.76 | FIG01087792: hypothetical protein |
| SCE1572_9202 | hypothetical protein | bi | sce_8000 | 89.12 | hypothetical protein |
| SCE1572_9203 | FIG01088267: hypothetical protein | bi | sce_8001 | 85.88 | FIG01088267: hypothetical protein |
| SCE1572_9204 | Serine/threonine-protein kinase pkn1 (EC 2.7.11.1) | bi | sce_8002 | 75.44 | Serine/threonine-protein kinase pkn1 (EC 2.7.11.1) |
| SCE1572_9205 | FIG01088889: hypothetical protein | bi | sce_8003 | 88.83 | FIG01088889: hypothetical protein |
| SCE1572_9206 | FIG01085803: hypothetical protein | bi | sce_8004 | 83.25 | FIG01085803: hypothetical protein |
| SCE1572_9207 | FIG01086053: hypothetical protein | umi | sce_9398 | 80.7 | FIG01086053: hypothetical protein |
| SCE1572_9208 | hypothetical protein | - | - | 0 | 0 |
| SCE1572_9209 | Transcriptional regulatory protein RtcR | bi | sce_8010 | 90.94 | Transcriptional regulatory protein RtcR |
| SCE1572_9210 | RNA-2'-3'-PO4:RNA-5'-OH ligase | bi | sce_8011 | 92.4 | RNA-2'-3'-PO4:RNA-5'-OH ligase |
| SCE1572_9211 | RNA 3'-terminal phosphate cyclase (EC 6.5.1.4) | bi | sce_8012 | 92.04 | RNA 3'-terminal phosphate cyclase (EC 6.5.1.4) |
| SCE1572_9212 | Ornithine carbamoyltransferase (EC 2.1.3.3) | bi | sce_8013 | 92.28 | Ornithine carbamoyltransferase (EC 2.1.3.3) |
| SCE1572_9213 | transport-associated | umi | sce_5863 | 34.39 | Single-stranded DNA-binding protein |
| SCE1572_9214 | two-component hybrid sensor and regulator | bi | sce_8014 | 75.33 | two-component hybrid sensor and regulator |
| SCE1572_9215 | hypothetical protein | bi | sce_8015 | 89.73 | hypothetical protein |
| SCE1572_9216 | hypothetical protein | bi | sce_8016 | 81.01 | hypothetical protein |
| SCE1572_9217 | FIG01085014: hypothetical protein | bi | sce_8019 | 87.84 | FIG01085014: hypothetical protein |
| SCE1572_9218 | hypothetical protein | bi | sce_8021 | 81.63 | hypothetical protein |
| SCE1572_9219 | putative exported protein of unknown function with OmpA family domain | umi | sce_3858 | 37.17 | Adenosylhomocysteinase (EC 3.3.1.1) |
| SCE1572_9220 | FIG01089013: hypothetical protein | bi | sce_8022 | 64.74 | FIG01089013: hypothetical protein |
| SCE1572_9221 | FIG01089013: hypothetical protein | - | - | 0 | 0 |
| SCE1572_9222 | FIG01088758: hypothetical protein | bi | sce_9351 | 72.87 | FIG01088758: hypothetical protein |
| SCE1572_9223 | FIG01087800: hypothetical protein | bi | sce_7616 | 95.27 | FIG01087800: hypothetical protein |
| SCE1572_9224 | PE-PGRS FAMILY PROTEIN | umi | sce_6815 | 69.42 | PE-PGRS FAMILY PROTEIN |
| SCE1572_9225 | hypothetical protein | - | - | 0 | 0 |
| SCE1572_9226 | hypothetical protein | umi | sce_6813 | 52.49 | hypothetical protein |
| SCE1572_9227 | RNA polymerase sigma factor SigW | umi | sce_6872 | 55.26 | RNA polymerase sigma factor SigW |
| SCE1572_9228 | hypothetical protein | - | - | 0 | 0 |
| SCE1572_9229 | hypothetical protein | - | - | 0 | 0 |
| SCE1572_9230 | kelch domain protein | umi | sce_9663 | 43.66 | FIG01085909: hypothetical protein |
| SCE1572_9231 | Branched-chain amino acid ABC transporter, amino acid-binding protein (TC 3.A.1.4.1) | umi | sce_7667 | 51.22 | FIG01085006: hypothetical protein |
| SCE1572_9232 | FIG01085006: hypothetical protein | - | - | 0 | 0 |
| SCE1572_9233 | Functional role page for Anaerobic nitric oxide reductase transcription regulator NorR | umi | sce_6530 | 49.82 | Functional role page for Anaerobic nitric oxide reductase transcription regulator NorR |
| SCE1572_9234 | FIG00840401: hypothetical protein | umi | sce_774 | 39.54 | FIG01087003: hypothetical protein |
| SCE1572_9235 | Dihydrolypoamide acetyltransferase | bi | sce_4668 | 53.6 | hypothetical protein |
| SCE1572_9236 | hypothetical protein | bi | sce_4669 | 42.86 | FIG01089212: hypothetical protein |
| SCE1572_9237 | hypothetical protein | - | - | 0 | 0 |
| SCE1572_9238 | hypothetical protein | - | - | 0 | 0 |
| SCE1572_9239 | hypothetical protein | - | - | 0 | 0 |
| SCE1572_9240 | hypothetical protein | umi | sce_8653 | 91.3 | hypothetical protein |
| SCE1572_9241 | hypothetical protein | - | - | 0 | 0 |
| SCE1572_9242 | hypothetical protein | - | - | 0 | 0 |
| SCE1572_9243 | hypothetical protein | - | - | 0 | 0 |
| SCE1572_9244 | hypothetical protein | - | - | 0 | 0 |
| SCE1572_9245 | Kazal domain protein | - | - | 0 | 0 |
| SCE1572_9246 | POSSIBLE TRANSPOSASE | umi | sce_2392 | 87.18 | hypothetical protein |
| SCE1572_9247 | major facilitator superfamily MFS_1 | umi | sce_7011 | 34.77 | Major facilitator superfamily MFS_1 |
| SCE1572_9248 | DNA double-strand break repair protein Mre11 | bi | sce_8023 | 92.6 | DNA double-strand break repair protein Mre11 |
| SCE1572_9249 | putative cytochrome P450 hydroxylase | bi | sce_8024 | 74.26 | putative cytochrome P450 hydroxylase |
| SCE1572_9250 | Putative glycogen debranching enzyme, archaical type, TIGR01561 | bi | sce_8026 | 90 | Putative glycogen debranching enzyme, archaical type, TIGR01561 |
| SCE1572_9251 | Malto-oligosyltrehalose trehalohydrolase (EC 3.2.1.141) | bi | sce_8027 | 89.01 | Malto-oligosyltrehalose trehalohydrolase (EC 3.2.1.141) |
| SCE1572_9252 | transport ATP-binding protein MsbA | bi | sce_8028 | 95.05 | transport ATP-binding protein MsbA |
| SCE1572_9253 | transport ATP-binding protein MsbA | umi | sce_8028 | 77.7 | transport ATP-binding protein MsbA |
| SCE1572_9254 | ABC transporter, ATP-binding protein | bi | sce_8029 | 84.64 | ABC transporter, ATP-binding protein |
| SCE1572_9255 | HlyD family secretion protein | bi | sce_8030 | 89.46 | HlyD family secretion protein |
| SCE1572_9256 | hypothetical protein | bi | sce_8032 | 64.94 | hypothetical protein |
| SCE1572_9257 | hypothetical protein | umi | sce_8032 | 64.1 | hypothetical protein |
| SCE1572_9258 | FIG01086237: hypothetical protein | bi | sce_8033 | 88.48 | FIG01086237: hypothetical protein |
| SCE1572_9259 | Integrase | bi | sce_8034 | 88.34 | Integrase |
| SCE1572_9260 | Chromosome partition protein smc | bi | sce_8035 | 87.68 | Chromosome partition protein smc |
| SCE1572_9261 | hypothetical protein | bi | sce_8039 | 81.4 | FIG01088134: hypothetical protein |
| SCE1572_9262 | Dihydroneopterin aldolase (EC 4.1.2.25) | bi | sce_8041 | 94.44 | Dihydroneopterin aldolase (EC 4.1.2.25) |
| SCE1572_9263 | FIG01086078: hypothetical protein | bi | sce_8042 | 87.25 | FIG01086078: hypothetical protein |
| SCE1572_9264 | cAMP-binding proteins - catabolite gene activator and regulatory subunit of cAMP-dependent protein kinases | bi | sce_8043 | 95.53 | cAMP-binding proteins - catabolite gene activator and regulatory subunit of cAMP-dependent protein kinases |
| SCE1572_9265 | FIG01085033: hypothetical protein | bi | sce_8044 | 87.42 | FIG01085033: hypothetical protein |
| SCE1572_9266 | response regulator receiver | bi | sce_8047 | 85.53 | Methyltransferase type 11 |
| SCE1572_9267 | hypothetical protein | bi | sce_8048 | 60.87 | hypothetical protein |
| SCE1572_9268 | FIG01086923: hypothetical protein | bi | sce_8049 | 82.08 | FIG01086923: hypothetical protein |
| SCE1572_9269 | FIG01087571: hypothetical protein | bi | sce_8050 | 77.91 | FIG01087571: hypothetical protein |
| SCE1572_9270 | hypothetical protein | - | - | 0 | 0 |
| SCE1572_9271 | GL13382 gene product from transcript GL13382-RA | bi | sce_8051 | 40.96 | hypothetical protein |
| SCE1572_9272 | Probable transcriptional regulator | bi | sce_8052 | 89.73 | Probable transcriptional regulator |
| SCE1572_9273 | serine/threonine protein kinase | bi | sce_8053 | 80.75 | serine/threonine protein kinase |
| SCE1572_9274 | Probable serine/threonine-protein kinase pknH (EC 2.7.11.1) | bi | sce_8054 | 82.3 | Probable serine/threonine-protein kinase pknH (EC 2.7.11.1) |
| SCE1572_9275 | cAMP-binding proteins - catabolite gene activator and regulatory subunit of cAMP-dependent protein kinases | bi | sce_8055 | 93.98 | cAMP-binding proteins - catabolite gene activator and regulatory subunit of cAMP-dependent protein kinases |
| SCE1572_9276 | FIG01085335: hypothetical protein | bi | sce_8056 | 92.06 | FIG01085335: hypothetical protein |
| SCE1572_9277 | UDP-glucose 4-epimerase (EC 5.1.3.2) | bi | sce_8057 | 90.06 | UDP-glucose 4-epimerase (EC 5.1.3.2) |
| SCE1572_9278 | putative Fe-S oxidoreductase | bi | sce_8058 | 73.97 | hypothetical protein |
| SCE1572_9279 | conserved hypothetical protein | bi | sce_8059 | 77.33 | hypothetical protein |
| SCE1572_9280 | Glycoprotein gp2 | bi | sce_8060 | 82.31 | Glycoprotein gp2 |
| SCE1572_9281 | FIG01087898: hypothetical protein | bi | sce_8061 | 81.12 | FIG01087898: hypothetical protein |
| SCE1572_9282 | GIII663 protein | bi | sce_8062 | 74.67 | GIII663 protein |
| SCE1572_9283 | Zinc uptake regulation protein ZUR | bi | sce_8064 | 94.63 | Zinc uptake regulation protein ZUR |
| SCE1572_9284 | hypothetical protein | - | - | 0 | 0 |
| SCE1572_9285 | conserved hypothetical protein | bi | sce_8065 | 68.78 | permease |
| SCE1572_9286 | serine/threonine protein kinase | bi | sce_8067 | 89.75 | serine/threonine protein kinase |
| SCE1572_9287 | Glutamine synthetase type I (EC 6.3.1.2) | bi | sce_8068 | 94.68 | Glutamine synthetase type I (EC 6.3.1.2) |
| SCE1572_9288 | Nitrogen regulatory protein P-II | bi | sce_8069 | 99.11 | Nitrogen regulatory protein P-II |
| SCE1572_9289 | hypothetical protein | - | - | 0 | 0 |
| SCE1572_9290 | serine/threonine protein kinase | bi | sce_8070 | 90.55 | serine/threonine protein kinase |
| SCE1572_9291 | Ribosomal-protein-L7p-serine acetyltransferase | bi | sce_8071 | 96.86 | Ribosomal-protein-L7p-serine acetyltransferase |
| SCE1572_9292 | Two component sensor kinase | bi | sce_8072 | 86.45 | Two component sensor kinase |
| SCE1572_9293 | FIG01087721: hypothetical protein | bi | sce_8073 | 94.05 | FIG01087721: hypothetical protein |
| SCE1572_9294 | Holliday junction DNA helicase RuvB | bi | sce_8074 | 95.59 | Holliday junction DNA helicase RuvB |
| SCE1572_9295 | sensory transduction histidine kinase | bi | sce_8075 | 96.59 | sensory transduction histidine kinase |
| SCE1572_9296 | sensory box sensor histidine kinase | bi | sce_8076 | 88.86 | sensory box sensor histidine kinase |
| SCE1572_9297 | FIG01088088: hypothetical protein | bi | sce_8077 | 88.95 | FIG01088088: hypothetical protein |
| SCE1572_9298 | Putative mitochondrial protein, with 2 coiled coil-4 domains, of bilateral origin, Nuclear Pore complex Protein NPP-11 (77.2 kDa) (n) | kbi | sce_8078 | 80.91 | Putative mitochondrial protein, with 2 coiled coil-4 domains, of bilateral origin, Nuclear Pore complex Protein NPP-11 (77.2 kDa) (n) |
| SCE1572_9299 | RNA polymerase sigma factor RpoE | bi | sce_8079 | 92.91 | RNA polymerase sigma factor RpoE |
| SCE1572_9300 | Serine protease precursor MucD/AlgY associated with sigma factor RpoE | bi | sce_8080 | 96.88 | Serine protease precursor MucD/AlgY associated with sigma factor RpoE |
| SCE1572_9301 | hypothetical protein | bi | sce_8081 | 93 | hypothetical protein |
| SCE1572_9302 | hypothetical protein | bi | sce_8082 | 84.21 | hypothetical protein |
| SCE1572_9303 | FKBP-type peptidyl-prolyl cis-trans isomerase SlyD (EC 5.2.1.8) | bi | sce_8083 | 83.94 | FKBP-type peptidyl-prolyl cis-trans isomerase SlyD (EC 5.2.1.8) |
| SCE1572_9304 | Macrolide-specific efflux protein MacA | bi | sce_8084 | 90.7 | Macrolide-specific efflux protein MacA |
| SCE1572_9305 | Macrolide export ATP-binding/permease protein MacB (EC 3.6.3.-) | bi | sce_8085 | 92.83 | Macrolide export ATP-binding/permease protein MacB (EC 3.6.3.-) |
| SCE1572_9306 | Cell division protein FtsX | bi | sce_8086 | 91.38 | Cell division protein FtsX |
| SCE1572_9307 | Cell division protein FtsX | bi | sce_8087 | 93.66 | Cell division protein FtsX |
| SCE1572_9308 | SSU ribosomal protein S1p | bi | sce_8088 | 90.52 | SSU ribosomal protein S1p |
| SCE1572_9309 | hypothetical protein | - | - | 0 | 0 |
| SCE1572_9310 | mnp protein | bi | sce_8089 | 96.17 | Scaffold protein for [4Fe-4S] cluster assembly ApbC, MRP-like |
| SCE1572_9311 | hypothetical protein | bi | sce_8090 | 76.81 | hypothetical protein |
| SCE1572_9312 | Thiol-disulfide oxidoreductase | bi | sce_8092 | 87.43 | Thiol-disulfide oxidoreductase |
| SCE1572_9313 | Thiol-disulfide oxidoreductase related to ResA | bi | sce_8093 | 91.91 | Thiol-disulfide oxidoreductase related to ResA |
| SCE1572_9314 | FIG01089261: hypothetical protein | bi | sce_8094 | 67.17 | FIG01089261: hypothetical protein |
| SCE1572_9315 | hypothetical protein | bi | sce_8095 | 81.32 | probable tail fiber protein |
| SCE1572_9316 | hypothetical protein | bi | sce_8096 | 85.89 | hypothetical protein |
| SCE1572_9317 | Fatty acid desaturase (EC 1.14.19.1); Delta-9 fatty acid desaturase (EC 1.14.19.1) | bi | sce_8097 | 93.69 | Fatty acid desaturase (EC 1.14.19.1); Delta-9 fatty acid desaturase (EC 1.14.19.1) |
| SCE1572_9318 | CTP synthase (EC 6.3.4.2) | bi | sce_8099 | 97.15 | CTP synthase (EC 6.3.4.2) |
| SCE1572_9319 | hypothetical protein | - | - | 0 | 0 |
| SCE1572_9320 | Fumarylacetoacetase (EC 3.7.1.2) | bi | sce_8101 | 86.01 | Fumarylacetoacetase (EC 3.7.1.2) |
| SCE1572_9321 | hypothetical protein | bi | sce_8102 | 84.38 | hypothetical protein |
| SCE1572_9322 | hypothetical protein | bi | sce_8103 | 84.75 | hypothetical protein |
| SCE1572_9323 | D-alanyl-D-alanine carboxypeptidase (EC 3.4.16.4) | bi | sce_8104 | 84.16 | D-alanyl-D-alanine carboxypeptidase (EC 3.4.16.4) |
| SCE1572_9324 | RNA polymerase sigma factor RpoD | bi | sce_8105 | 97.6 | RNA polymerase sigma factor RpoD |
| SCE1572_9325 | hypothetical protein | - | - | 0 | 0 |
| SCE1572_9326 | LSU ribosomal protein L20p | bi | sce_8106 | 96.64 | LSU ribosomal protein L20p |
| SCE1572_9327 | LSU ribosomal protein L35p | bi | sce_8107 | 98.46 | LSU ribosomal protein L35p |
| SCE1572_9328 | FIG01087985: hypothetical protein | bi | sce_8108 | 91.57 | FIG01087985: hypothetical protein |
| SCE1572_9329 | hypothetical protein | - | - | 0 | 0 |
| SCE1572_9330 | gliding motility protein MglA | bi | sce_8109 | 100 | gliding motility protein MglA |
| SCE1572_9331 | gliding motility protein MglA | bi | sce_8110 | 99.49 | gliding motility protein MglA |
| SCE1572_9332 | hypothetical protein | bi | sce_8111 | 100 | hypothetical protein |
| SCE1572_9333</ | | | | | |

| | | | | |
|--------------|--|-----|----------|--|
| SCE1572_9347 | hypothetical protein | umi | see_2307 | 31.64 hypothetical protein |
| SCE1572_9348 | Acetyl-coenzyme A carboxyl transferase alpha chain (EC 6.4.1.2) / Acetyl-coenzyme A carboxyl transferase beta chain (EC 6.4.1.3) | bi | see_8128 | 92.86 Methylcrotonyl-CoA carboxylase carboxyl transferase subunit (EC 6.4.1.4) |
| SCE1572_9349 | PE_PGRS family protein | bi | see_8130 | 57.99 hypothetical protein |
| SCE1572_9350 | Cytoplasmic axial filament protein CafA and Ribonuclease G (EC 3.1.4.-) | bi | see_8131 | 85.28 Cytoplasmic axial filament protein CafA and Ribonuclease G (EC 3.1.4.-) |
| SCE1572_9351 | FIG01088548: hypothetical protein | bi | see_8132 | 96.58 FIG01088548: hypothetical protein |
| SCE1572_9352 | Riboflavin synthase eubacterial/eukaryotic (EC 2.5.1.9) | bi | see_8133 | 88.26 Riboflavin synthase eubacterial/eukaryotic (EC 2.5.1.9) |
| SCE1572_9353 | 3,4-dihydroxy-2-butanone 4-phosphate synthase (EC 4.1.99.12) / GTP cyclohydrolase II (EC 3.5.4.25) | bi | see_8134 | 92.1 3,4-dihydroxy-2-butanone 4-phosphate synthase (EC 4.1.99.12) / GTP cyclohydrolase II (EC 3.5.4.25) |
| SCE1572_9354 | 6,7-dimethyl-8-ribityllumazine synthase (EC 2.5.1.78) | bi | see_8135 | 96.45 6,7-dimethyl-8-ribityllumazine synthase (EC 2.5.1.78) |
| SCE1572_9355 | Transcription termination protein NusB | bi | see_8136 | 92.13 Transcription termination protein NusB |
| SCE1572_9356 | Recombination inhibitory protein MutS2 | bi | see_8137 | 93.89 Recombination inhibitory protein MutS2 |
| SCE1572_9357 | Response regulatory protein | bi | see_8138 | 97.07 sigma-54 dependent transcriptional regulator, Fis family |
| SCE1572_9358 | PE_PGRS | bi | see_8139 | 85.83 PE_PGRS |
| SCE1572_9359 | Glycerol-3-phosphate dehydrogenase [NAD(P)] (EC 1.1.1.94) | bi | see_8140 | 92.97 Glycerol-3-phosphate dehydrogenase [NAD(P)] (EC 1.1.1.94) |
| SCE1572_9360 | hypothetical protein | bi | see_8141 | 91.88 FIG01089057: hypothetical protein |
| SCE1572_9361 | hypothetical protein | - | - | 0 |
| SCE1572_9362 | Signal peptidase I (EC 3.4.21.89) | bi | see_8142 | 90.52 Signal peptidase I (EC 3.4.21.89) |
| SCE1572_9363 | Circumsporozoite protein precursor (CS) | umi | see_5794 | 43.82 RTX toxins and related Ca ²⁺ proteins |
| SCE1572_9364 | L-threonine 3-dehydrogenase (EC 1.1.1.103) | bi | see_8144 | 94.6 L-threonine 3-dehydrogenase (EC 1.1.1.103) |
| SCE1572_9365 | 2-amino-3-ketobutyrate coenzyme A ligase (EC 2.3.1.29) | bi | see_8145 | 93.92 2-amino-3-ketobutyrate coenzyme A ligase (EC 2.3.1.29) |
| SCE1572_9366 | hypothetical protein | bi | see_8146 | 83.59 hypothetical protein |
| SCE1572_9367 | hypothetical protein | bi | see_8147 | 90.85 hypothetical protein |
| SCE1572_9368 | FIG01088555: hypothetical protein | bi | see_8148 | 78.31 FIG01088555: hypothetical protein |
| SCE1572_9369 | hypothetical protein | bi | see_8149 | 75.61 hypothetical protein |
| SCE1572_9370 | hypothetical protein | bi | see_8150 | 84.13 hypothetical protein |
| SCE1572_9371 | hypothetical protein | bi | see_8151 | 90.2 hypothetical protein |
| SCE1572_9372 | endonuclease/exonuclease/phosphatase family protein | bi | see_8152 | 88.14 endonuclease/exonuclease/phosphatase family protein |
| SCE1572_9373 | hypothetical protein | bi | see_8153 | 85.96 hypothetical protein |
| SCE1572_9374 | polysaccharide deacetylase | bi | see_8155 | 91.77 polysaccharide deacetylase |
| SCE1572_9375 | hypothetical protein | - | - | 0 |
| SCE1572_9376 | hypothetical protein | bi | see_8157 | 79.25 hypothetical protein |
| SCE1572_9377 | Competence protein F homolog, phosphoribosyltransferase domain, protein YhgH required for utilization of DNA as sole source of | bi | see_8158 | 78.46 Competence protein F homolog, phosphoribosyltransferase domain, protein YhgH required for utilization of DNA as sole source of |
| SCE1572_9378 | hypothetical protein | - | - | 0 |
| SCE1572_9379 | hypothetical protein | bi | see_8159 | 76.12 peptidase C14, caspase catalytic subunit p20 |
| SCE1572_9380 | Membrane protein involved in colicin uptake-like protein | bi | see_8160 | 75 hypothetical protein |
| SCE1572_9381 | Unknown protein | bi | see_8161 | 88.34 Unknown protein |
| SCE1572_9382 | hypothetical protein | - | - | 0 |
| SCE1572_9383 | Cell division protein FtsH (EC 3.4.24.-) | bi | see_8162 | 98.15 Cell division protein FtsH (EC 3.4.24.-) |
| SCE1572_9384 | tRNA(Ile)-lysine synthetase | bi | see_8164 | 86.22 tRNA(Ile)-lysine synthetase |
| SCE1572_9385 | hypothetical protein | bi | see_8165 | 75.95 hypothetical protein |
| SCE1572_9386 | FIG00431633: hypothetical protein | bi | see_8166 | 87.74 FIG00431633: hypothetical protein |
| SCE1572_9387 | serine/threonine protein kinase | bi | see_8167 | 79.95 serine/threonine protein kinase |
| SCE1572_9388 | hypothetical protein | bi | see_8168 | 88.02 hypothetical protein |
| SCE1572_9389 | tRNA (5-methylaminomethyl-2-thiouridylate)-methyltransferase (EC 2.1.1.61) | bi | see_8169 | 89.95 tRNA (5-methylaminomethyl-2-thiouridylate)-methyltransferase (EC 2.1.1.61) |
| SCE1572_9390 | DNA-binding response regulator KdpE | bi | see_8170 | 80.5 DNA-binding response regulator KdpE |
| SCE1572_9391 | FIG01088964: hypothetical protein | bi | see_8171 | 87.06 FIG01088964: hypothetical protein |
| SCE1572_9392 | Phosphoribosylformylglycinamide synthase, glutamine amidotransferase subunit (EC 6.3.5.3) | bi | see_264 | 31.91 Phosphoribosylformylglycinamide synthase, synthetase subunit (EC 6.3.5.3) / Phosphoribosylformylglycinamide synthase, glutar |
| SCE1572_9393 | FIG01085655: hypothetical protein | bi | see_8172 | 81.72 FIG01085655: hypothetical protein |
| SCE1572_9394 | modification methylase, putative | bi | see_8173 | 87.8 modification methylase, putative |
| SCE1572_9395 | hypothetical protein | bi | see_8174 | 76.11 hypothetical protein |
| SCE1572_9396 | FIG022199: FAD-binding protein | bi | see_8175 | 88.58 FIG022199: FAD-binding protein |
| SCE1572_9397 | Sulfolpyruvate decarboxylase - beta subunit (EC 4.1.1.79) | bi | see_8179 | 94.65 Sulfolpyruvate decarboxylase - beta subunit (EC 4.1.1.79) |
| SCE1572_9398 | Cholinephosphate cytidylyltransferase (EC 2.7.7.15) | bi | see_8180 | 92.77 Cholinephosphate cytidylyltransferase (EC 2.7.7.15) |
| SCE1572_9399 | FIG01087394: hypothetical protein | bi | see_8181 | 91.72 FIG01087394: hypothetical protein |
| SCE1572_9400 | D1 protease precursor | bi | see_8182 | 86.07 hypothetical protein |
| SCE1572_9401 | FIG01087662: hypothetical protein | bi | see_8183 | 93.98 FIG01087662: hypothetical protein |
| SCE1572_9402 | S-adenosylmethionine synthetase (EC 2.5.1.6) | bi | see_8184 | 93.13 S-adenosylmethionine synthetase (EC 2.5.1.6) |
| SCE1572_9403 | FIG01088440: hypothetical protein | bi | see_8185 | 72.11 FIG01088440: hypothetical protein |
| SCE1572_9404 | FIG01088015: hypothetical protein | bi | see_8186 | 92.42 FIG01088015: hypothetical protein |
| SCE1572_9405 | hypothetical protein | - | - | 0 |
| SCE1572_9406 | hypothetical protein | - | - | 0 |
| SCE1572_9407 | Bil2366 protein | bi | see_8189 | 82.07 Bil2366 protein |
| SCE1572_9408 | hypothetical protein | bi | see_8190 | 75.95 hypothetical protein |
| SCE1572_9409 | FIG01088883: hypothetical protein | bi | see_8191 | 67.46 FIG01088883: hypothetical protein |
| SCE1572_9410 | Capsular polysaccharide synthesis enzyme CpsD, exopolysaccharide synthesis | bi | see_8192 | 81.95 Capsular polysaccharide synthesis enzyme CpsD, exopolysaccharide synthesis |
| SCE1572_9411 | hypothetical protein | bi | see_8193 | 61.52 hypothetical protein |
| SCE1572_9412 | putative glycosyl transferase | bi | see_8195 | 83.15 Glycosyl transferase, group 1 |
| SCE1572_9413 | Heparinase II/III-like | bi | see_8196 | 79.92 Heparinase II/III-like |
| SCE1572_9414 | Undecaprenyl-phosphate N-acetylglucosaminyl 1-phosphate transferase (EC 2.7.8.-) | bi | see_8198 | 85.49 Undecaprenyl-phosphate N-acetylglucosaminyl 1-phosphate transferase (EC 2.7.8.-) |
| SCE1572_9415 | hypothetical protein | - | - | 0 |
| SCE1572_9416 | Cd(II)/Pb(II)-responsive transcriptional regulator | bi | see_8203 | 89.93 mercuric resistance operon regulatory protein (MerR) |
| SCE1572_9417 | Cysteine desulfurase (EC 2.8.1.7), IscS subfamily | bi | see_8204 | 97.05 Cysteine desulfurase (EC 2.8.1.7), IscS subfamily |
| SCE1572_9418 | Iron-sulfur cluster assembly scaffold protein IscU | bi | see_8205 | 92.62 Iron-sulfur cluster assembly scaffold protein IscU |
| SCE1572_9419 | Iron binding protein IscA for iron-sulfur cluster assembly | bi | see_8206 | 87.34 Iron binding protein IscA for iron-sulfur cluster assembly |
| SCE1572_9420 | Chaperone protein HscB | bi | see_8207 | 88.07 Chaperone protein HscB |
| SCE1572_9421 | Chaperone protein HscA | bi | see_8208 | 91.48 Chaperone protein HscA |
| SCE1572_9422 | Ferredoxin, 2Fe-2S | bi | see_8209 | 94.07 Ferredoxin, 2Fe-2S |
| SCE1572_9423 | hypothetical protein | bi | see_8210 | 86.67 hypothetical protein |
| SCE1572_9424 | putative outer membrane protein | bi | see_8211 | 73.91 putative outer membrane protein |
| SCE1572_9425 | hypothetical protein | bi | see_8212 | 93.75 hypothetical protein |
| SCE1572_9426 | FIG01085962: hypothetical protein | bi | see_8213 | 93.4 FIG01085962: hypothetical protein |
| SCE1572_9427 | FIG01089442: hypothetical protein | bi | see_8214 | 73.13 FIG01089442: hypothetical protein |
| SCE1572_9428 | GTP-binding and nucleic acid-binding protein YchF | bi | see_8215 | 95.04 GTP-binding and nucleic acid-binding protein YchF |
| SCE1572_9429 | Transcriptional regulator, LysR family | umi | see_5333 | 44.63 Transcriptional regulator, LysR family |
| SCE1572_9430 | DegT/DnrJ/EryC1/StrS family protein | bi | see_8219 | 85.44 DegT/DnrJ/EryC1/StrS family protein |
| SCE1572_9431 | 2,3,4,5-tetrahydropyridine-2,6-dicarboxylate N-acetyltransferase (EC 2.3.1.89) | bi | see_8220 | 90.58 2,3,4,5-tetrahydropyridine-2,6-dicarboxylate N-acetyltransferase (EC 2.3.1.89) |
| SCE1572_9432 | hypothetical protein | bi | see_8221 | 85.9 hypothetical protein |
| SCE1572_9433 | Preprotein translocase subunit SecG (TC 3.A.5.1.1) | bi | see_8222 | 94.44 Preprotein translocase subunit SecG (TC 3.A.5.1.1) |
| SCE1572_9434 | Triosephosphate isomerase (EC 5.3.1.1) | bi | see_8223 | 95.36 Triosephosphate isomerase (EC 5.3.1.1) |
| SCE1572_9435 | Phosphoglycerate kinase (EC 2.7.2.3) | bi | see_8224 | 96.59 Phosphoglycerate kinase (EC 2.7.2.3) |
| SCE1572_9436 | NAD-dependent glyceraldehyde-3-phosphate dehydrogenase (EC 1.2.1.12) | bi | see_8225 | 97.65 NAD-dependent glyceraldehyde-3-phosphate dehydrogenase (EC 1.2.1.12) |
| SCE1572_9437 | Thioredoxin | bi | see_8226 | 59.81 putative thioredoxin |
| SCE1572_9438 | hypothetical protein | - | - | 0 |
| SCE1572_9439 | Glycosyl transferase, group 2 family protein | bi | see_8227 | 93.33 Glycosyl transferase, group 2 family protein |
| SCE1572_9440 | serine/threonine kinase | bi | see_8228 | 81.16 serine/threonine kinase |
| SCE1572_9441 | Putative stomatin/prohibitin-family membrane protease subunit aq_911 | bi | see_8229 | 91 Putative stomatin/prohibitin-family membrane protease subunit aq_911 |
| SCE1572_9442 | hypothetical protein | bi | see_8230 | 80.5 hypothetical protein |
| SCE1572_9443 | Alkylated DNA repair protein AlkB | bi | see_6393 | 32.41 Alkylated DNA repair protein AlkB |
| SCE1572_9444 | d-aminoacylase (separatase, glutamate etc) | bi | see_1718 | 91.14 N-acyl-D-amino acid deacylase family protein (EC:3.5.1.81) |
| SCE1572_9445 | Multidrug resistance transporter, Bcr/CfIA family | umi | see_1251 | 29.74 drug resistance transporter, EmrB/QacA family |
| SCE1572_9446 | hypothetical protein | bi | see_8233 | 83.33 hypothetical protein |
| SCE1572_9447 | hypothetical protein | - | - | 0 |
| SCE1572_9448 | Amino acid permease | bi | see_8235 | 85.32 Amino acid permease |
| SCE1572_9449 | FIG002813: LPPG:FO 2-phospho-L-lactate transferase like, CoFD-like | bi | see_8236 | 93.42 FIG002813: LPPG:FO 2-phospho-L-lactate transferase like, CoFD-like |
| SCE1572_9450 | Site-specific DNA methyltransferase (EC 2.1.1.72) | bi | see_8237 | 92.83 Site-specific DNA methyltransferase (EC 2.1.1.72) |
| SCE1572_9451 | hypothetical protein | bi | see_8238 | 92.11 hypothetical protein |
| SCE1572_9452 | FIG01086943: hypothetical protein | bi | see_8239 | 70.47 FIG01086943: hypothetical protein |
| SCE1572_9453 | serine/threonine protein kinase | umi | see_6194 | 49.01 Serine/threonine-protein kinase pkn1 (EC 2.7.11.1) |
| SCE1572_9454 | serine/threonine protein kinase | umi | see_6193 | 51.22 serine/threonine protein kinase |
| SCE1572_9455 | hypothetical protein | umi | see_2054 | 37.72 BNR repeat domain protein |
| SCE1572_9456 | hypothetical protein | - | - | 0 |
| SCE1572_9457 | Threonine dehydrogenase and related Zn-dependent dehydrogenases | umi | see_534 | 69.81 Threonine dehydrogenase and related Zn-dependent dehydrogenases |
| SCE1572_9458 | hypothetical protein | bi | see_8241 | 76.26 hypothetical protein |
| SCE1572_9459 | hypothetical protein | - | - | 0 |
| SCE1572_9460 | hypothetical protein-putative transmembrane protein | bi | see_8242 | 82.04 hypothetical protein-putative transmembrane protein |
| SCE1572_9461 | hypothetical protein | bi | see_8243 | 80.77 FIG01089478: hypothetical protein |
| SCE1572_9462 | putative exported protein of unknown function with OmpA family domain | bi | see_8244 | 70.19 OmpA/MotB |
| SCE1572_9463 | Anchorage subunit of a-agglutinin of a-cells, highly O-glycosylated protein with N-terminal secretion signal and C-terminal signal | bi | see_5532 | 41.51 FIG01085490: hypothetical protein |
| SCE1572_9464 | Serine/threonine protein kinase pkn3 (EC 2.7.11.1) | bi | see_8245 | 85.3 Serine/threonine-protein kinase pkn3 (EC 2.7.11.1) |
| SCE1572_9465 | hypothetical protein | - | - | 0 |
| SCE1572_9466 | hypothetical protein | bi | see_8247 | 82.99 hypothetical protein |
| SCE1572_9467 | ABC transporter, ATP-binding protein | bi | see_8248 | 87.44 ABC transporter, ATP-binding protein |
| SCE1572_9468 | FIG01086004: hypothetical protein | bi | see_8249 | 83.57 FIG01086004: hypothetical protein |
| SCE1572_9469 | FIG017823: ATPase, MoxR family | bi | see_8250 | 93.22 methanol dehydrogenase regulatory protein |
| SCE1572_9470 | FIG01086883: hypothetical protein | bi | see_8251 | 78.29 FIG01086883: hypothetical protein |
| SCE1572_9471 | hypothetical protein | - | - | 0 |
| SCE1572_9472 | Response regulator receiver | umi | see_4145 | 43.14 COG1565: Uncharacterized conserved protein |
| SCE1572_9473 | Cysteine synthase (EC 2.5.1.47) | bi | see_8252 | 94.01 Cysteine synthase (EC 2.5.1.47) |
| SCE1572_9474 | Sulfate and thiosulfate import ATP-binding protein CysA (EC 3.6.3.25) | bi | see_8253 | 94.1 Sulfate and thiosulfate import ATP-binding protein CysA (EC 3.6.3.25) |
| SCE1572_9475 | UDP-glucose 4-epimerase (EC 5.1.3.2) | bi | see_8254 | 89.42 UDP-glucose 4-epimerase (EC 5.1.3.2) |
| SCE1572_9476 | Uncharacterized protein MJ0935 | bi | see_8255 | 84.55 Uncharacterized conserved protein |
| SCE1572_9477 | hypothetical protein | - | - | 0 |
| SCE1572_9478 | Glycosyltransferase | bi | see_8265 | 92.52 Glycosyltransferase |
| SCE1572_9479 | FIG01088584: hypothetical protein | bi | see_8266 | 92.9 BII5419 protein |
| SCE1572_9480 | Antifreeze glycopeptide AFGP polyprotein precursor | bi | see_8267 | 84.43 hypothetical protein |
| SCE1572_9481 | FIG01086688: hypothetical protein | bi | see_8268 | 84.67 FIG01086688: hypothetical protein |
| SCE1572_9482 | Universal stress protein family | bi | see_8269 | 88.36 Universal stress protein family |
| SCE1572_9483 | Ammonium transporter family | bi | see_8270 | 94.55 Ammonium transporter family |
| SCE1572_9484 | FIG000859: hypothetical protein YebC | bi | see_8271 | 97.59 FIG000859: hypothetical protein YebC |
| SCE1572_9485 | hypothetical protein | bi | see_8272 | 85.29 hypothetical protein |
| SCE1572_9486 | Phosphopantothenoylecysteine decarboxylase (EC 4.1.1.36) / Phosphopantothenoylecysteine synthetase (EC 6.3.2.5) | bi | see_8273 | 90.78 Phosphopantothenoylecysteine decarboxylase (EC 4.1.1.36) / Phosphopantothenoylecysteine synthetase (EC 6.3.2.5) |
| SCE1572_9487 | hypothetical protein | bi | see_2574 | 35.76 hypothetical protein |
| SCE1572_9488 | Tryptophanyl-tRNA synthetase (EC 6.1.1.2) | bi | see_8274 | 89.18 Tryptophanyl-tRNA synthetase (EC 6.1.1.2) |
| SCE1572_9489 | Vancomycin B-type resistance protein VanW | bi | see_8275 | 92.04 Vancomycin B-type resistance protein VanW |
| SCE1572_9490 | Serine/threonine-protein kinase (EC 2.7.1.-) | bi | see_8276 | 81.72 Serine/threonine-protein kinase (EC 2.7.1.-) |
| SCE1572_9491 | hypothetical protein | - | - | 0 |
| SCE1572_9492 | Excinuclease ABC subunit C | bi | see_8277 | 88.77 Excinuclease ABC subunit C |
| SCE1572_9493 | hypothetical protein | - | - | 0 |
| SCE1572_9494 | FIG01088182: hypothetical protein | bi | see_8280 | 95.33 FIG01088182: hypothetical protein |
| SCE1572_9495 | Conserved domain protein | bi | see_8281 | 90.19 Conserved domain protein |
| SCE1572_9496 | TPR repeat | bi | see_8282 | 85.86 TPR repeat |
| SCE1572_9497 | FIG01088962: hypothetical protein | bi | see_8283 | 80.97 FIG01088962: hypothetical protein |
| SCE1572_9498 | SSU ribosomal protein S9p (S16e) | bi | see_8284 | 96.15 SSU ribosomal protein S9p (S16e) |
| SCE1572_9499 | LSU ribosomal protein L13p (L13Ae) | bi | see_8285 | 98.43 LSU ribosomal protein L13p (L13Ae) |
| SCE1572_9500 | Nitrogen regulation protein ntrY (EC 2.7.3.-) | bi | see_8286 | 86.48 Nitrogen regulation protein ntrY (EC 2.7.3.-) |
| SCE1572_9501 | Glucosamine--fructose-6-phosphate aminotransferase [isomerizing] (EC 2.6.1.16) | bi | see_8287 | 96.56 Glucosamine--fructose-6-phosphate aminotransferase [isomerizing] (EC 2.6.1.16) |
| SCE1572_9502 | Major facilitator superfamily MFS_1 | bi | see_8288 | 82.27 COG0477: Permeases of the major facilitator superfamily |
| SCE1572_9503 | RNA-binding protein | bi | see_8290 | 92.37 RNA-binding protein |
| SCE1572_9504 | extracellular solute-binding protein, family 5 | bi | see_8291 | 90.44 PERIPLASMIC DIPEPTIDE TRANSPORT PROTEIN PRECURSOR |
| SCE1572_9505 | hypothetical protein | bi | see_8292 | 89.74 hypothetical protein |
| SCE1572_9506 | Transport protein | bi | see_8293 | 92.8 Transport protein |
| SCE1572_9507 | Peptide deformylase (EC 3.5.1.88) | bi | see_8294 | 82.87 Peptide deformylase (EC 3.5.1.88) |
| SCE1572_9508 | UDP-N-acetylmuramoylalanine-D-glutamate-2,6-diaminopimelate--D-alanyl-D-alanine ligase (EC 6.3.2.10) | bi | see_8295 | 90.78 UDP-N-acetylmuramoylalanine-D-glutamate-2,6-diaminopimelate--D-alanyl-D-alanine ligase (EC 6.3.2.10) |
| SCE1572_9509 | InterPro IPR000694.IPR006665 COGs COG2885 | bi | see_8296 | 84.09 hypothetical protein |
| SCE1572_9510 | hypothetical protein | bi | see_8297 | 74.19 hypothetical protein |

| | | | | |
|--------------|--|-----|-----------|--|
| SCE1572_9511 | hypothetical protein | - | | 0 |
| SCE1572_9512 | Leucyl-tRNA synthetase (EC 6.1.1.4) | bi | sce_8299 | 92.93 Leucyl-tRNA synthetase (EC 6.1.1.4) |
| SCE1572_9513 | Trypsin-2 precursor (EC 3.4.21.4) | bi | sce_8300 | 79.51 Trypsin-2 precursor (EC 3.4.21.4) |
| SCE1572_9514 | Putative lipoprotein | bi | sce_8301 | 88.73 Putative lipoprotein |
| SCE1572_9515 | hypothetical protein | bi | sce_8302 | 89.11 hypothetical protein |
| SCE1572_9516 | Peptidyl-prolyl cis-trans isomerase ppiD (EC 5.2.1.8) | bi | sce_8303 | 88 Peptidyl-prolyl cis-trans isomerase ppiD (EC 5.2.1.8) |
| SCE1572_9517 | FIG00706878: hypothetical protein | bi | sce_8304 | 92.12 FIG00706878: hypothetical protein |
| SCE1572_9518 | hypothetical protein | bi | sce_8305 | 88.73 Zinc transporter ZupT |
| SCE1572_9520 | Isoquinoline 1-oxidoreductase beta subunit (EC 1.3.99.16) | umi | sce_3738 | 89.45 Isoquinoline 1-oxidoreductase beta subunit (EC 1.3.99.16) |
| SCE1572_9521 | FIG01086323: hypothetical protein | umi | sce_3737 | 88.89 FIG01086323: hypothetical protein |
| SCE1572_9522 | hypothetical protein | - | | 0 |
| SCE1572_9523 | hypothetical protein | bi | sce_8308 | 86.81 hypothetical protein |
| SCE1572_9524 | hypothetical protein | bi | sce_8309 | 74.72 hypothetical protein |
| SCE1572_9525 | hypothetical protein | umi | sce_9076 | 44.3 Murein endopeptidase |
| SCE1572_9526 | Quinolinate synthetase (EC 2.5.1.72) | bi | sce_8310 | 96.87 Quinolinate synthetase (EC 2.5.1.72) |
| SCE1572_9527 | FIG01086785: hypothetical protein | bi | sce_8311 | 91.96 FIG01086785: hypothetical protein |
| SCE1572_9528 | ABC1 family protein | bi | sce_8312 | 94.17 hypothetical protein |
| SCE1572_9529 | Serine/threonine protein kinase PknB (EC 2.7.11.1) | bi | sce_8313 | 73.31 Serine/threonine protein kinase PknB (EC 2.7.11.1) |
| SCE1572_9530 | GlI0645 protein | bi | sce_8314 | 77.56 GlI0645 protein |
| SCE1572_9531 | 3'-to-5'; exoribonuclease RNase R | bi | sce_8315 | 91.5 3'-to-5'; exoribonuclease RNase R |
| SCE1572_9532 | FIG01088398: hypothetical protein | bi | sce_8316 | 87.8 FIG01088398: hypothetical protein |
| SCE1572_9533 | FIG01085807: hypothetical protein | bi | sce_8317 | 83.33 FIG01085807: hypothetical protein |
| SCE1572_9534 | serine/threonine protein kinase | - | sce_8318 | 85.94 serine/threonine protein kinase |
| SCE1572_9535 | hypothetical protein | - | | 0 |
| SCE1572_9536 | Di-haem cytochrome c peroxidase | bi | sce_8319 | 86.88 Di-haem cytochrome c peroxidase |
| SCE1572_9537 | hypothetical protein | bi | sce_8320 | 73.91 hypothetical protein |
| SCE1572_9538 | hypothetical protein | bi | sce_8321 | 81.62 hypothetical protein |
| SCE1572_9539 | Oo6g0254700 | - | | 0 |
| SCE1572_9540 | integral membrane protein | - | | 0 |
| SCE1572_9541 | hypothetical protein | bi | sce_8323 | 78.91 hypothetical protein |
| SCE1572_9542 | hypothetical protein | bi | sce_8324 | 86.67 hypothetical protein |
| SCE1572_9543 | hypothetical protein, INTERPRO suggestion: probable carbohydrate kinase | bi | sce_8325 | 79.46 hypothetical protein, INTERPRO suggestion: probable carbohydrate kinase |
| SCE1572_9544 | hypothetical protein | - | | 0 |
| SCE1572_9545 | Aldo/keto reductase family | umi | sce_1690 | 33.79 putative aldo/keto reductase |
| SCE1572_9546 | Phytochrome, two-component sensor histidine kinase (EC 2.7.3.-); Cyanobacterial phytochrome B | umi | sce_229 | 55.34 FOG: PAS/PAC domain |
| SCE1572_9547 | putative oxidoreductase protein | umi | sce_2969 | 71.93 putative oxidoreductase protein |
| SCE1572_9548 | hypothetical protein | - | | 0 |
| SCE1572_9549 | 3-oxoacyl-[acyl-carrier protein] reductase (EC 1.1.1.100) | bi | sce_8328 | 92.55 3-oxoacyl-[acyl-carrier protein] reductase (EC 1.1.1.100) |
| SCE1572_9550 | Gla-like protein | bi | sce_8329 | 87.39 hypothetical protein |
| SCE1572_9551 | NAD-dependent protein deacetylase of SIR2 family | bi | sce_8330 | 90.4 NAD-dependent protein deacetylase of SIR2 family |
| SCE1572_9552 | ADA regulatory protein / Methylated-DNA--protein-cysteine methyltransferase (EC 2.1.1.63) | umi | sce_6948 | 47.78 Methylated-DNA--protein-cysteine methyltransferase (EC 2.1.1.63) |
| SCE1572_9553 | FIG0045822: hypothetical protein | - | | 0 |
| SCE1572_9554 | hypothetical protein | bi | sce_4770 | 68.42 hypothetical protein |
| SCE1572_9555 | hypothetical protein | bi | sce_8332 | 88.72 hypothetical protein |
| SCE1572_9556 | Poly-gamma-glutamate synthase subunit PgsB/CapB (EC 6.3.2.-) | bi | sce_8333 | 92.37 Poly-gamma-glutamate synthase subunit PgsB/CapB (EC 6.3.2.-) |
| SCE1572_9557 | YpfJ protein, zinc metalloprotease superfamily | bi | sce_8334 | 89.21 YpfJ protein, zinc metalloprotease superfamily |
| SCE1572_9558 | hypothetical protein | - | | 0 |
| SCE1572_9559 | Thiol peroxidase, Bcp-type (EC 1.11.1.15) | umi | sce_5609 | 39.13 Thiol peroxidase, Bcp-type (EC 1.11.1.15) |
| SCE1572_9560 | hypothetical protein | bi | sce_8336 | 71.55 hypothetical protein |
| SCE1572_9561 | Probable serine/threonine-protein kinase PknB | bi | sce_8337 | 84.48 Probable serine/threonine-protein kinase PknB |
| SCE1572_9562 | hypothetical protein | - | | 0 |
| SCE1572_9563 | conserved hypothetical protein-putative thiol-disulfide isomerase or thioredoxin | bi | sce_8352 | 80.5 conserved hypothetical protein-putative thiol-disulfide isomerase or thioredoxin |
| SCE1572_9564 | Trk system potassium uptake protein TrkA | bi | sce_8353 | 89.32 Trk system potassium uptake protein TrkA |
| SCE1572_9565 | Na? antiporter | bi | sce_8354 | 83.56 Na? antiporter |
| SCE1572_9566 | hypothetical protein | - | | 0 |
| SCE1572_9567 | hypothetical protein | - | | 0 |
| SCE1572_9568 | FIG01020577: hypothetical protein | bi | sce_136 | 80.72 FIG01020577: hypothetical protein |
| SCE1572_9569 | Transcriptional regulator, MerR family | bi | sce_8363 | 79.59 Transcriptional regulator, MerR family |
| SCE1572_9570 | Signal transduction histidine kinase CheA (EC 2.7.3.-) | umi | sce_7661 | 50.35 Signal transduction histidine kinase CheA (EC 2.7.3.-) |
| SCE1572_9571 | hypothetical protein | bi | sce_8364 | 86.31 hypothetical protein |
| SCE1572_9572 | FIG01088723: hypothetical protein | bi | sce_8365 | 77.5 FIG01088723: hypothetical protein |
| SCE1572_9573 | Regulator of cell morphogenesis and NO signaling | bi | sce_8366 | 83.63 Regulator of cell morphogenesis and NO signaling |
| SCE1572_9574 | hypothetical protein | bi | sce_8367 | 72.83 FIG01089257: hypothetical protein |
| SCE1572_9575 | HNH endonuclease family protein | umi | sce_6270 | 88.33 HNH endonuclease family protein |
| SCE1572_9576 | hypothetical protein | bi | sce_8368 | 88.46 EBNA-1 |
| SCE1572_9577 | DTW domain containing protein | bi | sce_8369 | 85.34 COG3148: Uncharacterized conserved protein |
| SCE1572_9578 | iron acquisition yersiniabactin synthesis enzyme (YbtT, resembles thioesterases) | umi | sce_401 | 29.82 Malonyl CoA-acyl carrier protein transacylase (EC 2.3.1.39) |
| SCE1572_9579 | 2,3-dihydroxybenzoate-AMP ligase (EC 2.7.7.58) | bi | sce_4341 | 59.2 2,3-dihydroxybenzoate-AMP ligase (EC 2.7.7.58) |
| SCE1572_9580 | FIG00855540: hypothetical protein | - | | 0 |
| SCE1572_9581 | hypothetical protein | - | | 0 |
| SCE1572_9582 | putative cytochrome P450 hydroxylase | umi | sce_9951 | 38.12 putative cytochrome P450 hydroxylase |
| SCE1572_9583 | pyochelin synthetase F | umi | sce_4641 | 26.19 Malonyl CoA-acyl carrier protein transacylase (EC 2.3.1.39) |
| SCE1572_9584 | pyochelin synthetase F | - | | 0 |
| SCE1572_9585 | Putative reductoisomerase in siderophore biosynthesis gene cluster | - | | 0 |
| SCE1572_9586 | ABC transporter component | umi | sce_7835 | 33.27 ABC transporter, ATP-binding protein, MsbA family |
| SCE1572_9587 | Inner membrane ABC-transporter YbtQ | umi | sce_2975 | 41.38 ABC transporter, fused permease and ATPase domains |
| SCE1572_9588 | Long-chain-fatty-acid--CoA ligase (EC 6.2.1.3) | umi | sce_4639 | 37.53 Malonyl CoA-acyl carrier protein transacylase (EC 2.3.1.39) |
| SCE1572_9589 | iron acquisition yersiniabactin synthesis enzyme (Irp2) | umi | sce_2666 | 33.58 Long-chain-fatty-acid--CoA ligase (EC 6.2.1.3) |
| SCE1572_9590 | iron acquisition 2,3-dihydroxybenzoate-AMP ligase (EC 2.7.7.58,Irp5) | umi | sce_5650 | 32.17 Isochorismate synthase (EC 5.4.4.2) of siderophore biosynthesis |
| SCE1572_9591 | hypothetical protein | - | | 0 |
| SCE1572_9592 | ABC transporter, ATP-binding protein | umi | sce_2719 | 39.13 ABC transporter |
| SCE1572_9593 | hypothetical protein | umi | sce_4346 | 28.68 MxcI |
| SCE1572_9594 | Ferric siderophore transport system, periplasmic binding protein TonB | umi | sce_1486 | 34.75 VgrG protein |
| SCE1572_9595 | Biopolymer transport protein ExhD/TolR | umi | sce_4832 | 49.26 Biopolymer transport protein ExhD/TolR |
| SCE1572_9596 | MotA/TolQ/ExbB proton channel family protein | umi | sce_4831 | 48.24 MotA/TolQ/ExbB proton channel family protein |
| SCE1572_9597 | TonB-dependent receptor | umi | sce_9238 | 53.71 TonB-dependent receptor |
| SCE1572_9598 | Multi antimicrobial extrusion protein (Na)/(drug antiporter), MATE family of MDR efflux pumps | bi | sce_4593 | 76.03 Multi antimicrobial extrusion protein (Na)/(drug antiporter), MATE family of MDR efflux pumps |
| SCE1572_9599 | 4-deoxy-L-threo-5-hexosulose-uronate ketol-isomerase (EC 5.3.1.17) | - | | 0 |
| SCE1572_9600 | hypothetical protein | - | | 0 |
| SCE1572_9601 | Periplasmic beta-glucosidase (EC 3.2.1.21) | umi | sce_9564 | 62.06 Periplasmic beta-glucosidase (EC 3.2.1.21) |
| SCE1572_9602 | Endo-1,4-beta-xylanase A precursor (EC 3.2.1.8) | umi | sce_7864 | 54.2 1,4-beta-cellobiosidase |
| SCE1572_9603 | Large low complexity protein with proline/alanine-rich repeat | bi | sce_8430 | 84.85 putative Fe-S oxidoreductase |
| SCE1572_9604 | hypothetical protein | umi | sce_8430 | 72.18 putative Fe-S oxidoreductase |
| SCE1572_9605 | Y25C1A.3 | umi | sce_6240 | 30.13 serine/threonine protein kinase |
| SCE1572_9606 | hypothetical protein | umi | sce_8430 | 62.32 putative Fe-S oxidoreductase |
| SCE1572_9607 | Transposase | umi | sce_7292 | 56.85 FIG01086976: hypothetical protein |
| SCE1572_9608 | hypothetical protein | umi | sce_9281 | 33.08 ATP binding protein |
| SCE1572_9609 | hypothetical protein | - | | 0 |
| SCE1572_9610 | hypothetical protein | - | | 0 |
| SCE1572_9611 | hypothetical protein | - | | 0 |
| SCE1572_9612 | DNA repair protein RadC | umi | sce_7263 | 50 DNA repair protein RadC |
| SCE1572_9613 | hypothetical protein | - | | 0 |
| SCE1572_9614 | hypothetical protein | - | | 0 |
| SCE1572_9615 | hypothetical protein | - | | 0 |
| SCE1572_9616 | hypothetical protein | - | | 0 |
| SCE1572_9617 | LOC432261 protein | bi | sce_8431 | 84.92 LOC432261 protein |
| SCE1572_9618 | hypothetical protein | bi | sce_8432 | 81.03 hypothetical protein |
| SCE1572_9619 | hypothetical protein | umi | sce_3096 | 27.17 FOG: HEAT repeat |
| SCE1572_9620 | hypothetical protein | - | | 0 |
| SCE1572_9621 | hypothetical protein | bi | sce_8435 | 91.96 hypothetical protein |
| SCE1572_9622 | hypothetical protein | umi | sce_8435 | 83.11 hypothetical protein |
| SCE1572_9623 | hypothetical protein | bi | sce_8436 | 85.73 membrane protein |
| SCE1572_9624 | peptidase S8 and S53, subtilisin, kexin, sedolisin | bi | sce_8437 | 84.09 Kumamolysin |
| SCE1572_9625 | Hypothetical protein | bi | sce_8438 | 89.01 Hypothetical protein |
| SCE1572_9626 | hypothetical protein | - | | 0 |
| SCE1572_9627 | serine/threonine kinase with two-component sensor domain | umi | sce_2065 | 64.57 putative sensory box histidine kinase |
| SCE1572_9628 | FIG01085590: hypothetical protein | umi | sce_2065 | 75.52 putative sensory box histidine kinase |
| SCE1572_9629 | SNF2-related,Helicase-like:SWIM Zn-finger:DEAD/DEAH box helicase-like | bi | sce_8441 | 78.21 SWF/SNF family helicase |
| SCE1572_9630 | hypothetical protein | - | | 0 |
| SCE1572_9631 | PE-PGRS FAMILY PROTEIN | bi | sce_8443 | 62.11 hypothetical protein |
| SCE1572_9632 | COG1842: Phage shock protein A (IM30), suppresses sigma54-dependent transcription | bi | sce_8444 | 96.71 COG1842: Phage shock protein A (IM30), suppresses sigma54-dependent transcription |
| SCE1572_9633 | FIG01089567: hypothetical protein | bi | sce_8445 | 82.3 FIG01089567: hypothetical protein |
| SCE1572_9634 | Pyruvate,phosphate dikinase (EC 2.7.9.1) | bi | sce_8446 | 92.93 Pyruvate,phosphate dikinase (EC 2.7.9.1) |
| SCE1572_9635 | FKBP-type peptidyl-prolyl cis-trans isomerase fklB (EC 5.2.1.8) | bi | sce_8447 | 84.49 FKBP-type peptidyl-prolyl cis-trans isomerase fklB (EC 5.2.1.8) |
| SCE1572_9636 | hypothetical protein | bi | sce_8448 | 93.63 hypothetical protein |
| SCE1572_9637 | cellulose-binding, family II | bi | sce_8449 | 53.1 RNA-binding protein |
| SCE1572_9638 | FIG01089533: hypothetical protein | bi | sce_8450 | 83.64 FIG01089533: hypothetical protein |
| SCE1572_9639 | hypothetical protein | - | | 0 |
| SCE1572_9640 | (GlcNAc)2 ABC transporter, periplasmic substrate-binding protein | bi | sce_8451 | 91.88 putative oligopeptide/dipeptide ABC transporter, periplasmic oligopeptide/dipeptide-binding protein |
| SCE1572_9641 | Methylmalonyl-CoA mutase (EC 5.4.99.2) | bi | sce_8452 | 92.85 Methylmalonyl-CoA mutase (EC 5.4.99.2) |
| SCE1572_9642 | FIG01085148: hypothetical protein | bi | sce_8453 | 79.17 FIG01085148: hypothetical protein |
| SCE1572_9643 | Flagellar motor rotation protein MotB | bi | sce_8454 | 84.25 Flagellar motor rotation protein MotB |
| SCE1572_9644 | putative lipoprotein | bi | sce_8455 | 57.32 putative lipoprotein |
| SCE1572_9645 | Cell division protein BolA | bi | sce_8456 | 92.94 Cell division protein BolA |
| SCE1572_9646 | 3-ketoacyl-CoA thiolase (EC 2.3.1.16) @ Acetyl-CoA acetyltransferase (EC 2.3.1.9) | bi | sce_8457 | 92.93 3-ketoacyl-CoA thiolase (EC 2.3.1.16) @ Acetyl-CoA acetyltransferase (EC 2.3.1.9) |
| SCE1572_9647 | Enoyl-CoA hydratase [isoleucine degradation] (EC 4.2.1.17) / 3-hydroxyacyl-CoA dehydrogenase (EC 1.1.1.35) | bi | sce_8458 | 94.58 Enoyl-CoA hydratase [isoleucine degradation] (EC 4.2.1.17) / 3-hydroxyacyl-CoA dehydrogenase (EC 1.1.1.35) |
| SCE1572_9648 | FIG01089010: hypothetical protein | bi | sce_8459 | 80.81 FIG01089010: hypothetical protein |
| SCE1572_9649 | hypothetical protein | umi | sce_5241 | 66.28 FIG01086664: hypothetical protein |
| SCE1572_9650 | FIG01085364: hypothetical protein | umi | sce_5242 | 66.27 FIG01085364: hypothetical protein |
| SCE1572_9651 | FIG01088755: hypothetical protein | umi | sce_9910 | 67.04 FIG01088755: hypothetical protein |
| SCE1572_9652 | hypothetical protein | umi | sce_10366 | 64.24 FIG01086239: hypothetical protein |
| SCE1572_9653 | hypothetical protein | umi | sce_9503 | 71.61 hypothetical protein |
| SCE1572_9654 | hypothetical protein | bi | sce_10364 | 87.6 hypothetical protein |
| SCE1572_9655 | hypothetical protein | umi | sce_10364 | 61.69 hypothetical protein |
| SCE1572_9656 | FIG01086605: hypothetical protein | umi | sce_8463 | 80.68 FIG01086605: hypothetical protein |
| SCE1572_9657 | hypothetical protein | bi | sce_8464 | 89.12 hypothetical protein |
| SCE1572_9658 | FIG01087820: hypothetical protein | bi | sce_8465 | 81.26 FIG01087820: hypothetical protein |
| SCE1572_9659 | NAD(P)H-quinone oxidoreductase chain 1 | bi | sce_8466 | 92.71 NAD(P)H-quinone oxidoreductase chain 1 |
| SCE1572_9660 | Vitamin B12 ABC transporter, ATPase component BtuD | bi | sce_8467 | 93.13 Vitamin B12 ABC transporter, ATPase component BtuD |
| SCE1572_9661 | RNA polymerase sigma factor | bi | sce_8469 | 96.93 RNA polymerase sigma factor |
| SCE1572_9662 | putative transmembrane anti-sigma factor | bi | sce_8470 | 81.88 putative transmembrane anti-sigma factor |
| SCE1572_9663 | Glutathione synthetase (EC 6.3.2.3) | bi | sce_8471 | 94.38 Glutathione synthetase (EC 6.3.2.3) |
| SCE1572_9664 | hypothetical protein | bi | sce_8472 | 80.47 hypothetical protein |
| SCE1572_9665 | 2-amino-4-hydroxy-6-hydroxymethylidihydropteridine pyrophosphokinase (EC 2.7.6.3) | bi | sce_8473 | 87.9 2-amino-4-hydroxy-6-hydroxymethylidihydropteridine pyrophosphokinase (EC 2.7.6.3) |
| SCE1572_9666 | hypothetical protein | bi | sce_8474 | 80.93 hypothetical protein |
| SCE1572_9667 | DNA polymerase III alpha subunit (EC 2.7.7.7) | bi | sce_8475 | 94.19 DNA polymerase III alpha subunit (EC 2.7.7.7) |
| SCE1572_9668 | Periplasmic thiol-disulfide interchange protein DsbA | bi | sce_8476 | 84.47 Periplasmic thiol-disulfide interchange protein DsbA |
| SCE1572_9669 | Hypothetical protein | bi | sce_8477 | 81.13 Hypothetical protein |
| SCE1572_9670 | Probable outer membrane protein | bi | sce_8478 | 83.77 Probable outer membrane protein |
| SCE1572_9671 | FIG01087493: hypothetical protein | bi | sce_8479 | 72.25 FIG01087493: hypothetical protein |
| SCE1572_9672 | Cytoplasmic membrane protein | bi | sce_8480 | 91.71 Cytoplasmic membrane protein |
| SCE1572_9673 | Xaa-Pro dipeptidase (EC 3.4.13.9) | bi | sce_8481 | 75.21 hypothetical protein |
| SCE1572_9674 | FIG01088940: hypothetical protein | bi | sce_8483 | 91.73 FIG01088940: hypothetical protein |
| SCE1572_9675 | hypothetical protein | bi | sce_8484 | 89.45 hypothetical protein |

| | | | | | |
|--------------|--|----------|-----------|-------|--|
| SCE1572_9676 | hypothetical protein | bi | see_8485 | 91.25 | hypothetical protein |
| SCE1572_9677 | Oxidoreductase, aldo/keto reductase family | bi | see_8486 | 85.02 | Oxidoreductase, aldo/keto reductase family |
| SCE1572_9678 | FIG00840231: hypothetical protein | bi | see_8487 | 91.89 | FIG00840231: hypothetical protein |
| SCE1572_9679 | Molybdopterin oxidoreductase subunit, predicted; chaperone protein HipG | bi | see_8488 | 92.69 | Molybdopterin oxidoreductase subunit, predicted; chaperone protein HipG |
| SCE1572_9680 | Fe-S-cluster-containing hydrogenase components 1 | bi | see_8489 | 90.02 | Fe-S-cluster-containing hydrogenase components 1 |
| SCE1572_9681 | Molybdopterin oxidoreductase (EC 1.2.7.-) | bi | see_8490 | 94.46 | Molybdopterin oxidoreductase (EC 1.2.7.-) |
| SCE1572_9682 | ABC-type Fe3 transport system protein; Molybdenum transport protein, putative | bi | see_8491 | 79.3 | ABC-type Fe3 transport system protein; Molybdenum transport protein, putative |
| SCE1572_9683 | ABC-type Fe3 transport system protein; Molybdenum transport protein, putative | bi | see_8492 | 92.54 | hypothetical protein |
| SCE1572_9684 | FIG01086031: hypothetical protein | bi | see_8493 | 93.02 | FIG01086031: hypothetical protein |
| SCE1572_9685 | Virulence-associated cell-wall-anchored protein SasG (LPXTG motif), binding to squamous nasal epithelial cells | bi | see_8494 | 66.38 | Virulence-associated cell-wall-anchored protein SasG (LPXTG motif), binding to squamous nasal epithelial cells |
| SCE1572_9686 | SCO1/SenC family protein | bi | see_8495 | 90.71 | SCO1/SenC family protein |
| SCE1572_9687 | Cytochrome c oxidase polypeptide II (EC 1.9.3.1) | bi | see_8496 | 90.51 | Cytochrome c oxidase polypeptide II (EC 1.9.3.1) |
| SCE1572_9688 | Cytochrome c oxidase polypeptide I (EC 1.9.3.1) | bi | see_8497 | 93.21 | Cytochrome c oxidase polypeptide I (EC 1.9.3.1) |
| SCE1572_9689 | Cytochrome c oxidase polypeptide III (EC 1.9.3.1) | bi | see_8498 | 95.61 | Cytochrome c oxidase polypeptide III (EC 1.9.3.1) |
| SCE1572_9690 | Cytochrome c oxidase polypeptide IV (EC 1.9.3.1) | bi | see_8499 | 86.71 | Cytochrome c oxidase polypeptide IV (EC 1.9.3.1) |
| SCE1572_9691 | Signal transduction histidine kinase | bi | see_8500 | 88.78 | Signal transduction histidine kinase |
| SCE1572_9692 | response regulator receiver sensor signal transduction histidine kinase | bi | see_8501 | 96.79 | sigma-54 dependent DNA-binding response regulator FrgC |
| SCE1572_9693 | Cystathionine gamma-synthase (EC 2.5.1.48) | bi | see_8502 | 94.29 | Cystathionine gamma-synthase (EC 2.5.1.48) |
| SCE1572_9694 | Sulfite reductase [NADPH] hemoprotein beta-component (EC 1.8.1.2) | bi | see_8504 | 95.12 | Sulfite reductase [NADPH] hemoprotein beta-component (EC 1.8.1.2) |
| SCE1572_9695 | hypothetical protein | - | - | 0 | 0 |
| SCE1572_9696 | ATP-dependent DNA helicase Rep | bi | see_8505 | 96.06 | ATP-dependent DNA helicase Rep |
| SCE1572_9697 | hypothetical protein | bi | see_8506 | 81.31 | hypothetical protein |
| SCE1572_9698 | serine/threonine protein kinase | bi | see_8507 | 70.22 | serine/threonine protein kinase |
| SCE1572_9699 | serine/threonine protein kinase | bi | see_8508 | 86.36 | serine/threonine protein kinase |
| SCE1572_9700 | Cyclic beta-1,2-glucan synthase (EC 2.4.1.-) | bi | see_8509 | 75.37 | Cyclic beta-1,2-glucan synthase (EC 2.4.1.-) |
| SCE1572_9701 | hypothetical protein | - | - | 0 | 0 |
| SCE1572_9702 | caax amino terminal protease family | bi | see_8510 | 84.98 | caax amino terminal protease family |
| SCE1572_9703 | Phosphoserine phosphatase (EC 3.1.3.3) | uni | see_9272 | 29.72 | Phosphoserine phosphatase (EC 3.1.3.3) |
| SCE1572_9704 | FIG01086044: hypothetical protein | bi | see_8511 | 90.62 | FIG01086044: hypothetical protein |
| SCE1572_9705 | hypothetical protein | bi | see_8512 | 86.9 | hypothetical protein |
| SCE1572_9706 | hypothetical protein | - | - | 0 | 0 |
| SCE1572_9707 | hypothetical protein | - | - | 0 | 0 |
| SCE1572_9708 | FIG01085105: hypothetical protein | bi | see_8513 | 92.37 | FIG01085105: hypothetical protein |
| SCE1572_9709 | NADH-ubiquinone oxidoreductase chain N (EC 1.6.5.3) | bi | see_8514 | 87.55 | NADH-ubiquinone oxidoreductase chain N (EC 1.6.5.3) |
| SCE1572_9710 | NADH-ubiquinone oxidoreductase chain M (EC 1.6.5.3) | bi | see_8515 | 91.67 | NADH-ubiquinone oxidoreductase chain M (EC 1.6.5.3) |
| SCE1572_9711 | NADH-ubiquinone oxidoreductase chain L (EC 1.6.5.3) | bi | see_8516 | 91.31 | NADH-ubiquinone oxidoreductase chain L (EC 1.6.5.3) |
| SCE1572_9712 | hypothetical protein | - | - | 0 | 0 |
| SCE1572_9713 | GTP-binding protein EngB | bi | see_8517 | 88.58 | GTP-binding protein EngB |
| SCE1572_9714 | COG3536: Uncharacterized protein conserved in bacteria | bi | see_8518 | 98.91 | COG3536: Uncharacterized protein conserved in bacteria |
| SCE1572_9715 | putative oxidoreductase | bi | see_8520 | 83.82 | oxidoreductase domain protein |
| SCE1572_9716 | hypothetical protein | bi | see_8521 | 84.96 | hypothetical protein |
| SCE1572_9717 | Acetyl-coenzyme A carboxyl transferase alpha chain (EC 6.4.1.2) | bi | see_8522 | 97.79 | Acetyl-coenzyme A carboxyl transferase alpha chain (EC 6.4.1.2) |
| SCE1572_9718 | Adenylate cyclase (EC 4.6.1.1) | bi | see_8523 | 94.78 | Adenylate cyclase (EC 4.6.1.1) |
| SCE1572_9719 | Adenylate cyclase (EC 4.6.1.1) | uni | see_8523 | 75.27 | Adenylate cyclase (EC 4.6.1.1) |
| SCE1572_9720 | Glycerol kinase (EC 2.7.1.30) | bi | see_8524 | 93.63 | Glycerol kinase (EC 2.7.1.30) |
| SCE1572_9721 | FIG01087592: hypothetical protein | bi | see_8525 | 94 | FIG01087592: hypothetical protein |
| SCE1572_9722 | FIG01086935: hypothetical protein | bi | see_8526 | 75.05 | FIG01086935: hypothetical protein |
| SCE1572_9723 | hypothetical protein | bi | see_8527 | 33.97 | Putative ATP-dependent DNA helicase |
| SCE1572_9724 | Beta-lactamase class C and other penicillin binding proteins | uni | see_1658 | 70.18 | Beta-lactamase class C and other penicillin binding proteins |
| SCE1572_9725 | hypothetical protein | bi | see_8528 | 87.28 | hypothetical protein |
| SCE1572_9726 | hypothetical protein | bi | see_8529 | 87.58 | hypothetical protein |
| SCE1572_9727 | Basic membrane protein A | uni | see_8680 | 34.29 | FIG01089215: hypothetical protein |
| SCE1572_9728 | YbbR-like | bi | see_8530 | 89.1 | YbbR-like |
| SCE1572_9729 | Hypothetical protein YbbP, contains nucleotide-binding domain of DisA bacterial checkpoint controller | bi | see_8531 | 89.72 | Hypothetical protein YbbP, contains nucleotide-binding domain of DisA bacterial checkpoint controller |
| SCE1572_9730 | Dihydropterate synthase (EC 2.5.1.15) | bi | see_8532 | 84.08 | Dihydropterate synthase (EC 2.5.1.15) |
| SCE1572_9731 | Membrane protein containing HD superfamily hydrolase domain, YQFF ortholog | bi | see_8533 | 88.29 | Membrane protein containing HD superfamily hydrolase domain, YQFF ortholog |
| SCE1572_9732 | Acyl-CoA dehydrogenase, short-chain specific (EC 1.3.99.2) | bi | see_8534 | 95.48 | Acyl-CoA dehydrogenase, short-chain specific (EC 1.3.99.2) |
| SCE1572_9733 | serine/threonine protein kinase | bi | see_8535 | 82.81 | serine/threonine protein kinase |
| SCE1572_9734 | hypothetical protein | bi | see_8536 | 84.69 | hypothetical protein |
| SCE1572_9735 | hypothetical protein | bi | see_8537 | 92.9 | hypothetical protein |
| SCE1572_9736 | late competence protein (DNA binding and uptake) | bi | see_8538 | 76.79 | putative DNA-binding protein |
| SCE1572_9737 | UDP-N-acetylmuramate-1-alanyl-gamma-D-glutamyl-meso-diaminopimelate ligase (EC 6.3.2.-) | bi | see_8539 | 90.89 | UDP-N-acetylmuramate-1-alanyl-gamma-D-glutamyl-meso-diaminopimelate ligase (EC 6.3.2.-) |
| SCE1572_9738 | Inositol-1-monophosphatase (EC 3.1.3.25) | bi | see_8540 | 87.68 | Inositol-1-monophosphatase (EC 3.1.3.25) |
| SCE1572_9739 | hypothetical protein | - | - | 0 | 0 |
| SCE1572_9740 | hypothetical protein | bi | see_8541 | 83.93 | hypothetical protein |
| SCE1572_9741 | hypothetical protein | bi | see_8542 | 90.74 | hypothetical protein |
| SCE1572_9742 | FIG01085306: hypothetical protein | bi | see_8543 | 87.57 | FIG01085306: hypothetical protein |
| SCE1572_9743 | Thioredoxin reductase (EC 1.8.1.9) | bi | see_8544 | 97.49 | Thioredoxin reductase (EC 1.8.1.9) |
| SCE1572_9744 | Uracil-DNA glycosylase, family 4 | bi | see_8545 | 78.53 | Uracil-DNA glycosylase, family 4 |
| SCE1572_9745 | hypothetical protein | bi | see_8546 | 81.58 | hypothetical protein |
| SCE1572_9746 | Glycyl-tRNA synthetase beta chain (EC 6.1.1.14) | bi | see_8547 | 64.9 | Glycyl-tRNA synthetase beta chain (EC 6.1.1.14) |
| SCE1572_9747 | hypothetical protein | bi | see_8548 | 87.5 | hypothetical protein |
| SCE1572_9748 | Long-chain-fatty-acid-CoA ligase (EC 6.2.1.3) | bi | see_8549 | 89.43 | Long-chain-fatty-acid-CoA ligase (EC 6.2.1.3) |
| SCE1572_9749 | FIG01087035: hypothetical protein | bi | see_8550 | 95.38 | FIG01087035: hypothetical protein |
| SCE1572_9750 | Thymidylate kinase (EC 2.7.4.9) | bi | see_8551 | 77.41 | response regulator receiver domain protein (CheY-like) |
| SCE1572_9751 | putative signal transduction protein with Nacht domain | - | - | 0 | 0 |
| SCE1572_9752 | hypothetical protein | - | - | 0 | 0 |
| SCE1572_9753 | hypothetical protein | uni | see_9445 | 35.45 | hypothetical protein |
| SCE1572_9754 | unknown | see_2587 | - | 35.87 | Protein of unknown function DUF541 |
| SCE1572_9755 | hypothetical protein | - | - | 0 | 0 |
| SCE1572_9756 | RNA polymerase, sigma-24 subunit, ECF subfamily | uni | see_10335 | 33.09 | RNA polymerase sigma factor RpoE |
| SCE1572_9757 | hydrolase, alpha/beta fold family | bi | see_8552 | 90.1 | putative hydrolase |
| SCE1572_9758 | cytochrome c-554 precursor | bi | see_8553 | 88.85 | Cytochrome c family protein |
| SCE1572_9759 | FIG01088561: hypothetical protein | bi | see_8555 | 91.78 | FIG01088561: hypothetical protein |
| SCE1572_9760 | Chaperone protein DnaK | bi | see_8556 | 93.8 | Chaperone protein DnaK |
| SCE1572_9761 | hypothetical protein | bi | see_8557 | 98.43 | hypothetical protein |
| SCE1572_9762 | hypothetical protein | bi | see_8558 | 75.32 | hypothetical protein |
| SCE1572_9763 | L-proline glycine betaine ABC transport system permease protein ProV (TC 3.A.1.12.1) | bi | see_7918 | 75.6 | glycine/betaine transport ATP-binding protein |
| SCE1572_9764 | L-proline glycine betaine binding ABC transporter protein ProX (TC 3.A.1.12.1) / Osmotic adaptation | bi | see_7917 | 65.54 | L-proline glycine betaine binding ABC transporter protein ProX (TC 3.A.1.12.1) / Osmotic adaptation |
| SCE1572_9765 | Cobalt-zinc-cadmium resistance protein CzeD | bi | see_8560 | 86.56 | Cobalt-zinc-cadmium resistance protein CzeD |
| SCE1572_9766 | 3-ketoacyl-CoA thiolase (EC 2.3.1.16) @ Acetyl-CoA acetyltransferase (EC 2.3.1.9) | bi | see_8561 | 95.12 | 3-ketoacyl-CoA thiolase (EC 2.3.1.16) @ Acetyl-CoA acetyltransferase (EC 2.3.1.9) |
| SCE1572_9767 | 3'-to-5' oligoribonuclease (orm) | bi | see_8562 | 95.72 | 3'-to-5' oligoribonuclease (orm) |
| SCE1572_9768 | Putative two component sensor serine/threonine kinase (EC:2.7.1.-) | bi | see_8564 | 72.11 | serine/threonine protein kinase |
| SCE1572_9769 | Transcriptional regulator, Cro/CI family | bi | see_8565 | 90.07 | Transcriptional regulator, Cro/CI family |
| SCE1572_9770 | Lipid A export ATP-binding/permease protein MsbA | bi | see_8566 | 91.95 | Lipid A export ATP-binding/permease protein MsbA |
| SCE1572_9771 | FIG01085938: hypothetical protein | bi | see_8567 | 84.68 | FIG01085938: hypothetical protein |
| SCE1572_9772 | FIG01085364: hypothetical protein | bi | see_8568 | 82.64 | hypothetical protein |
| SCE1572_9773 | FIG01086569: hypothetical protein | bi | see_8569 | 84.15 | FIG01086569: hypothetical protein |
| SCE1572_9774 | Arginyl-tRNA synthetase (EC 6.1.1.19) | bi | see_8570 | 93.07 | Arginyl-tRNA synthetase (EC 6.1.1.19) |
| SCE1572_9775 | Putative CDP-glycosylpolyol phosphate:glycosylpolyol glycosylpolyolphosphotransferase | uni | see_9036 | 34.86 | 200 kDa antigen p200, putative |
| SCE1572_9776 | serine/threonine protein kinase | bi | see_8571 | 76.88 | serine/threonine protein kinase |
| SCE1572_9777 | hypothetical protein | bi | see_8572 | 84.91 | hypothetical protein |
| SCE1572_9778 | Beta-glucosidase (EC 3.2.1.21) | bi | see_8574 | 94.18 | Beta-glucosidase (EC 3.2.1.21) |
| SCE1572_9779 | heavy metal binding protein | bi | see_8575 | 86.44 | heavy metal binding protein |
| SCE1572_9780 | putative lipoprotein | uni | see_8568 | 52.67 | hypothetical protein |
| SCE1572_9781 | Transcriptional regulator, AraC family | bi | see_8576 | 79.51 | Transcriptional regulator, AraC family |
| SCE1572_9782 | hypothetical protein | bi | see_8577 | 88.73 | hypothetical protein |
| SCE1572_9783 | Xylose-responsive transcription regulator, ROK family | bi | see_8578 | 92.16 | Xylose-responsive transcription regulator, ROK family |
| SCE1572_9784 | Kazal-type serine protease inhibitor domain | bi | see_8580 | 84.21 | Kazal-type serine protease inhibitor domain |
| SCE1572_9785 | hypothetical protein | uni | see_1158 | 41.33 | FIG01088859: hypothetical protein |
| SCE1572_9786 | FIG01086002: hypothetical protein | bi | see_8584 | 96.36 | FIG01086002: hypothetical protein |
| SCE1572_9787 | Glycolate oxidase (EC 1.1.3.15) | bi | see_8585 | 92.37 | Glycolate oxidase (EC 1.1.3.15) |
| SCE1572_9788 | unknown | bi | see_8586 | 79.94 | unknown |
| SCE1572_9789 | Hypothetical protein | bi | see_8587 | 81.3 | Hypothetical protein |
| SCE1572_9790 | hypothetical protein | bi | see_220 | 82.78 | FIG01089623: hypothetical protein |
| SCE1572_9791 | hypothetical protein | - | - | 0 | 0 |
| SCE1572_9792 | GlI2422 protein | bi | see_7989 | 85.51 | GlI2422 protein |
| SCE1572_9793 | FIG01086797: hypothetical protein | bi | see_8605 | 91.98 | FIG01086797: hypothetical protein |
| SCE1572_9794 | FIG01086088: hypothetical protein | bi | see_8606 | 88.63 | FIG01086088: hypothetical protein |
| SCE1572_9795 | hypothetical protein | - | - | 0 | 0 |
| SCE1572_9796 | hypothetical protein | bi | see_8607 | 77.46 | hypothetical protein |
| SCE1572_9797 | hypothetical protein | bi | see_8608 | 58.02 | hypothetical protein |
| SCE1572_9798 | hypothetical protein | bi | see_8609 | 79.1 | hypothetical protein |
| SCE1572_9799 | hypothetical protein | bi | see_8610 | 91.67 | hypothetical protein |
| SCE1572_9800 | RsbR, positive regulator of sigma-B | uni | see_5390 | 48.13 | RsbR, positive regulator of sigma-B |
| SCE1572_9801 | hypothetical protein | uni | see_800 | 28.21 | conserved hypothetical protein |
| SCE1572_9802 | hypothetical protein | uni | see_10099 | 34.31 | hypothetical protein, mmyy |
| SCE1572_9803 | probable transcriptional regulator, AraC family | uni | see_9866 | 37.96 | Transcriptional regulator, AraC family |
| SCE1572_9804 | hypothetical protein | - | - | 0 | 0 |
| SCE1572_9805 | alkaline serine protease | bi | see_8612 | 91.71 | alkaline serine protease |
| SCE1572_9806 | hypothetical protein | uni | see_4576 | 27.6 | Glycine-rich cell wall structural protein 1.8 precursor |
| SCE1572_9807 | RNA-binding protein | bi | see_8613 | 90.7 | RNA-binding protein |
| SCE1572_9808 | Enolase (EC 4.2.1.11) | bi | see_8614 | 95.82 | Enolase (EC 4.2.1.11) |
| SCE1572_9809 | hypothetical protein | bi | see_8615 | 86.32 | hypothetical protein |
| SCE1572_9810 | IcmF-related protein | bi | see_8616 | 87.26 | IcmF domain protein |
| SCE1572_9811 | hypothetical protein | - | - | 0 | 0 |
| SCE1572_9812 | Signal transduction histidine kinase CheA (EC 2.7.3.-) | bi | see_8618 | 78.38 | Signal transduction histidine kinase CheA (EC 2.7.3.-) |
| SCE1572_9813 | Phytochrome, two-component sensor histidine kinase (EC 2.7.3.-) | bi | see_8619 | 83.2 | putative response regulator |
| SCE1572_9814 | small heat shock protein | bi | see_8620 | 78.49 | Molecular chaperone (small heat shock protein) |
| SCE1572_9815 | FIG01086053: hypothetical protein | bi | see_9398 | 84.75 | FIG01086053: hypothetical protein |
| SCE1572_9816 | Periplasmic thiol:disulfide interchange protein DsbA | bi | see_8621 | 85.37 | Periplasmic thiol:disulfide interchange protein DsbA |
| SCE1572_9817 | D-alanine-D-alanine ligase (EC 6.3.2.4) | uni | see_940 | 45.83 | VgrG protein |
| SCE1572_9818 | Putative protein-S-isoprenylcysteine methyltransferase | - | - | 0 | 0 |
| SCE1572_9819 | Transcriptional regulator, TetR family | bi | see_6665 | 51.11 | Transcriptional regulator, TetR family |
| SCE1572_9820 | FIG01086385: hypothetical protein | bi | see_8622 | 73.01 | FIG01086385: hypothetical protein |
| SCE1572_9821 | hypothetical protein | bi | see_8623 | 87.68 | Uncharacterized protein conserved in bacteria, NMA0228-like |
| SCE1572_9822 | Conserved domain protein | bi | see_8624 | 81.09 | Conserved domain protein |
| SCE1572_9823 | penicillin G acylase, putative | uni | see_1477 | 32.39 | Predicted thiol oxidoreductase |
| SCE1572_9824 | hypothetical protein | uni | see_3766 | 57.23 | hypothetical protein |
| SCE1572_9825 | hypothetical protein | - | - | 0 | 0 |
| SCE1572_9826 | hypothetical protein | - | - | 0 | 0 |
| SCE1572_9827 | hypothetical protein | - | - | 0 | 0 |
| SCE1572_9828 | hypothetical protein | - | - | 0 | 0 |
| SCE1572_9829 | hypothetical protein | - | - | 0 | 0 |
| SCE1572_9830 | hypothetical protein | - | - | 0 | 0 |
| SCE1572_9831 | RNA polymerase sigma-70 factor, ECF subfamily | uni | see_6097 | 35.45 | RNA polymerase sigma factor RpoE |
| SCE1572_9832 | hypothetical protein | uni | see_5955 | 36.96 | serine/threonine protein kinase |
| SCE1572_9833 | Periplasmic thiol:disulfide interchange protein DsbA | uni | see_576 | 43.68 | DsbA oxidoreductase |
| SCE1572_9834 | Mobile element protein | uni | see_1676 | 74.65 | Mobile element protein |
| SCE1572_9835 | carboxylesterase, putative | bi | see_7133 | 92.27 | phospholipase/carboxylesterase family protein |
| SCE1572_9836 | hypothetical protein | bi | see_8655 | 95.4 | hypothetical protein |
| SCE1572_9837 | Glutathione S-transferase (EC 2.5.1.18) | bi | see_8650 | 97.14 | Glutathione S-transferase (EC 2.5.1.18) |
| SCE1572_9838 | ATP-DEPENDENT DNA HELICASE | uni | see_8635 | | |

| | | | |
|---------------|---|-----|--|
| SCE1572_9840 | hypothetical protein | - | 0 |
| SCE1572_9841 | hypothetical protein | - | 0 |
| SCE1572_9842 | FIG01087249: hypothetical protein | uni | 93.48 Transposase |
| SCE1572_9843 | FIG01087249: hypothetical protein | uni | 92.86 Transposase |
| SCE1572_9844 | hypothetical protein | - | 0 |
| SCE1572_9845 | Fibroin heavy chain precursor (Fib-H) (H-fibroin) | bi | 20.99 FG-GAP repeat domain protein |
| SCE1572_9846 | hypothetical protein | bi | 64.58 hypothetical protein |
| SCE1572_9847 | ATP-DEPENDENT DNA HELICASE | bi | 90.77 ATP-DEPENDENT DNA HELICASE |
| SCE1572_9848 | hypothetical protein | - | 0 |
| SCE1572_9849 | Serine-threonine protein kinase | bi | 73.63 Serine-threonine protein kinase |
| SCE1572_9850 | hypothetical protein | bi | 72.92 hypothetical protein |
| SCE1572_9851 | hypothetical protein | uni | 71.11 Bifunctional protein: zinc-containing alcohol dehydrogenase; quinone oxidoreductase (NADPH:quinone reductase) (EC 1.1.1.-); Sin |
| SCE1572_9852 | hypothetical protein | - | 0 |
| SCE1572_9853 | Oxidoreductase (EC 1.1.1.-) | bi | 84.97 Oxidoreductase (EC 1.1.1.-) |
| SCE1572_9854 | Tat (Twin-arginine translocation) pathway signal sequence domain protein | bi | 85.12 hypothetical protein |
| SCE1572_9855 | Cellulose-binding domain protein | bi | 85.19 Cellulose-binding domain protein |
| SCE1572_9856 | Tissue factor pathway inhibitor 2 precursor (TFPI-2) | bi | 70.31 Tissue factor pathway inhibitor 2 precursor (TFPI-2) |
| SCE1572_9857 | predicted protein | bi | 90 Ser/Thr protein phosphatase, putative |
| SCE1572_9858 | putative minor silk ampullate protein | bi | 78.52 putative minor silk ampullate protein |
| SCE1572_9859 | Tat (twin-arginine translocation) pathway signal sequence domain protein | bi | 89.09 Tat (twin-arginine translocation) pathway signal sequence domain protein |
| SCE1572_9860 | Conserved protein, with a weak D-galactarate dehydratase/altronate hydrolase domain | uni | 66.18 Conserved protein, with a weak D-galactarate dehydratase/altronate hydrolase domain |
| SCE1572_9861 | hypothetical protein | uni | 48.25 AAA ATPase |
| SCE1572_9862 | hypothetical protein | bi | 26.53 hypothetical protein |
| SCE1572_9863 | hypothetical protein | - | 0 |
| SCE1572_9864 | FIG01089571: hypothetical protein | bi | 89.55 FIG01089571: hypothetical protein |
| SCE1572_9865 | hypothetical protein | bi | 88.09 hypothetical protein |
| SCE1572_9866 | Putative deoxyribose-specific ABC transporter, ATP-binding protein | bi | 93.32 Putative deoxyribose-specific ABC transporter, ATP-binding protein |
| SCE1572_9867 | Ribose ABC transport system, permease protein RbsC (TC 3.A.1.2.1) | bi | 92.5 nucleoside transport system permease protein |
| SCE1572_9868 | inner-membrane translocator | bi | 91.74 inner-membrane translocator |
| SCE1572_9869 | FIG01089215: hypothetical protein | bi | 93.26 FIG01089215: hypothetical protein |
| SCE1572_9870 | hypothetical protein | bi | 82.47 hypothetical protein |
| SCE1572_9871 | Putative cytochrome c oxidase subunit II (EC 1.9.3.1) | bi | 85.97 Putative cytochrome c oxidase subunit II (EC 1.9.3.1) |
| SCE1572_9872 | FIG01088846: hypothetical protein | bi | 92.68 FIG01088846: hypothetical protein |
| SCE1572_9873 | NAD(P)H dehydrogenase (quinone) | bi | 84.62 NAD(P)H dehydrogenase (quinone) |
| SCE1572_9874 | FIG01089066: hypothetical protein | bi | 86.73 FIG01089066: hypothetical protein |
| SCE1572_9875 | hypothetical protein | - | 0 |
| SCE1572_9876 | Transcriptional regulator, MarR family | bi | 95.35 Transcriptional regulator, MarR family |
| SCE1572_9877 | hypothetical protein | - | 0 |
| SCE1572_9878 | 3-oxoacyl-[acyl-carrier protein] reductase (EC 1.1.1.100) | uni | 46 3-oxoacyl-[acyl-carrier protein] reductase (EC 1.1.1.100) |
| SCE1572_9879 | transcriptional regulator, MerR family | uni | 37.68 methyltransferase type 11 |
| SCE1572_9880 | hypothetical protein | bi | 79.45 hypothetical protein |
| SCE1572_9881 | Predicted membrane protein/domain | uni | 28.74 keratin associated protein |
| SCE1572_9882 | NADPH-dependent FMN reductase | bi | 93.48 NADPH-dependent FMN reductase |
| SCE1572_9883 | hypothetical protein | - | 0 |
| SCE1572_9884 | Enterochelin esterase and related enzymes | - | 0 |
| SCE1572_9885 | Sigma-54 dependent transcriptional regulator; Response regulator receiver domain / Serine-protein kinase RsbW (EC 2.7.11.1) | bi | 91.21 Sigma-54 dependent transcriptional regulator; Response regulator receiver domain / Serine-protein kinase RsbW (EC 2.7.11.1) |
| SCE1572_9886 | Sensory box histidine kinase/response regulator | bi | 84.74 Sensory box histidine kinase/response regulator |
| SCE1572_9887 | Maltose/maltodextrin ABC transporter, permease protein MalG | bi | 91.26 Maltose/maltodextrin ABC transporter, permease protein MalG |
| SCE1572_9888 | Maltose/maltodextrin ABC transporter, permease protein MalF | bi | 86.72 Maltose/maltodextrin ABC transporter, permease protein MalF |
| SCE1572_9889 | SN-glycerol-3-phosphate transport ATP-binding protein ugpC (TC 3.A.1.1.3) | bi | 92.37 SN-glycerol-3-phosphate transport ATP-binding protein ugpC (TC 3.A.1.1.3) |
| SCE1572_9890 | Maltodextrin glucosidase (EC 3.2.1.20) | bi | 79.39 Maltodextrin glucosidase (EC 3.2.1.20) |
| SCE1572_9891 | FIG01085109: hypothetical protein | uni | 33.48 Adenosylhomocysteinase (EC 3.3.1.1) |
| SCE1572_9892 | hypothetical protein | bi | 84.21 hypothetical protein |
| SCE1572_9893 | WD-40 repeat protein | bi | 83.44 WD-40 repeat protein |
| SCE1572_9894 | hypothetical protein | bi | 82.61 hypothetical protein |
| SCE1572_9895 | Serine/threonine-protein kinase pksC (EC 2.7.11.1) | bi | 83.1 Serine/threonine-protein kinase pksC (EC 2.7.11.1) |
| SCE1572_9896 | Serine/threonine-protein kinase pksC (EC 2.7.11.1) | uni | 80.47 Serine/threonine-protein kinase pksC (EC 2.7.11.1) |
| SCE1572_9897 | UTP-glucose-1-phosphate uridylyltransferase (EC 2.7.7.9) | uni | 43.1 hypothetical protein |
| SCE1572_9898 | hypothetical protein | bi | 80.88 hypothetical protein |
| SCE1572_9899 | FIG01088098: hypothetical protein | bi | 87.28 FIG01088098: hypothetical protein |
| SCE1572_9900 | Di-/tripeptide transporter | bi | 91.72 Di-/tripeptide transporter |
| SCE1572_9901 | hypothetical protein | uni | 43.16 Adenosylhomocysteinase (EC 3.3.1.1) |
| SCE1572_9902 | Tyrosine recombinase XerC | bi | 86.93 Tyrosine recombinase XerC |
| SCE1572_9903 | sulfatase(EC:3.1.6.6) | bi | 91.04 Choline-sulfatase (EC 3.1.6.6) |
| SCE1572_9904 | hypothetical protein | bi | 51.66 hypothetical protein |
| SCE1572_9905 | hypothetical protein | - | 0 |
| SCE1572_9906 | Homoserine/homoserine lactone efflux protein | uni | 28.9 Transporter, LysE family |
| SCE1572_9907 | MoxR-like ATPases | bi | 98.06 MoxR-like ATPases |
| SCE1572_9908 | hypothetical protein | bi | 88.39 hypothetical protein |
| SCE1572_9909 | FIG01087827: hypothetical protein | uni | 76.64 FIG01087827: hypothetical protein |
| SCE1572_9910 | FIG01085607: hypothetical protein | bi | 64.5 FIG01085607: hypothetical protein |
| SCE1572_9911 | LysR-family transcriptional regulator | bi | 85.13 LysR-family transcriptional regulator |
| SCE1572_9912 | Hemoglobin-like protein HbO | bi | 83.96 Hemoglobin-like protein HbO |
| SCE1572_9913 | hypothetical protein | - | 0 |
| SCE1572_9914 | hypothetical protein | bi | 80.77 hypothetical protein |
| SCE1572_9915 | sensor histidine kinase | bi | 88.02 sensor histidine kinase |
| SCE1572_9916 | Response regulator of zinc sigma-54-dependent two-component system | bi | 97.83 Response regulator of zinc sigma-54-dependent two-component system |
| SCE1572_9917 | FIG01086248: hypothetical protein | bi | 80.69 FIG01086248: hypothetical protein |
| SCE1572_9918 | Inner membrane protein YrbG, predicted calcium/sodium/proton antiporter | - | 0 |
| SCE1572_9919 | hypothetical protein | bi | 62.7 hypothetical protein |
| SCE1572_9920 | cysteine-rich repeat protein | uni | 53.44 Type IV fimbrial biogenesis protein PilY1 |
| SCE1572_9921 | Mg-chelatase subunit ChID | bi | 94.19 Mg-chelatase subunit ChID |
| SCE1572_9922 | hypothetical protein | - | 0 |
| SCE1572_9923 | response regulator | bi | 90.95 two-component regulator |
| SCE1572_9924 | Two-component hybrid sensor and regulator | bi | 95.37 Two-component hybrid sensor and regulator |
| SCE1572_9925 | Two-component hybrid sensor and regulator | uni | 94.44 Two-component hybrid sensor and regulator |
| SCE1572_9926 | Response regulator of zinc sigma-54-dependent two-component system | bi | 91.78 Response regulator of zinc sigma-54-dependent two-component system |
| SCE1572_9927 | Sensor histidine kinase | bi | 80.78 Sensor histidine kinase |
| SCE1572_9928 | Transcriptional regulator, HxIR family | bi | 86.15 Transcriptional regulator, HxIR family |
| SCE1572_9929 | hypothetical protein | - | 0 |
| SCE1572_9930 | FOG: HEAT repeat | bi | 88.35 FOG: HEAT repeat |
| SCE1572_9931 | Two-component response regulator | bi | 94.29 Two-component response regulator |
| SCE1572_9932 | hypothetical protein | - | 0 |
| SCE1572_9933 | Multi-sensor Hybrid Histidine Kinase(EC:3.1.1.61) | uni | 68.8 Phytochrome, two-component sensor histidine kinase (EC 2.7.3.-); Cyanobacterial phytochrome B |
| SCE1572_9934 | hypothetical protein | - | 0 |
| SCE1572_9935 | hypothetical protein | bi | 75.11 hypothetical protein |
| SCE1572_9936 | Chromosome (plasmid) partitioning protein Para | bi | 94.71 Chromosome (plasmid) partitioning protein Para |
| SCE1572_9937 | hypothetical protein | - | 0 |
| SCE1572_9938 | hypothetical protein | - | 0 |
| SCE1572_9939 | hypothetical protein | bi | 78.8 hypothetical protein |
| SCE1572_9940 | hypothetical protein | - | 0 |
| SCE1572_9941 | Alkanesulfonate monooxygenase (EC 1.14.14.5) | uni | 50.69 Alkanesulfonate monooxygenase (EC 1.14.14.5) |
| SCE1572_9942 | hypothetical protein | bi | 91.38 hypothetical protein |
| SCE1572_9943 | hypothetical protein | bi | 84.34 hypothetical protein |
| SCE1572_9944 | hypothetical protein | - | 0 |
| SCE1572_9945 | hypothetical protein | - | 0 |
| SCE1572_9946 | Gli0642 protein | bi | 84.13 Gli0642 protein |
| SCE1572_9947 | hypothetical protein | - | 0 |
| SCE1572_9948 | hypothetical protein | - | 0 |
| SCE1572_9949 | hypothetical protein | bi | 61.43 FIG01088619: hypothetical protein |
| SCE1572_9950 | RsbR, positive regulator of sigma-B | bi | 80.96 RsbR, positive regulator of sigma-B |
| SCE1572_9951 | Adenosylhomocysteinase (EC 3.3.1.1) | bi | 86.12 hypothetical protein |
| SCE1572_9952 | UDP-N-acetylenolpyruvylglucosamine reductase (EC 1.1.1.158) | bi | 86.25 UDP-N-acetylenolpyruvylglucosamine reductase (EC 1.1.1.158) |
| SCE1572_9953 | VgrG protein | bi | 72.44 VgrG protein |
| SCE1572_9954 | pentapeptide repeat family protein | bi | 73.07 hypothetical protein |
| SCE1572_9955 | pentapeptide repeat family protein | bi | 80.11 pentapeptide repeat |
| SCE1572_9956 | FIG01088521: hypothetical protein | bi | 81.94 FIG01088521: hypothetical protein |
| SCE1572_9957 | conserved hypothetical protein | bi | 62.96 hypothetical protein |
| SCE1572_9958 | hypothetical protein | bi | 76.92 hypothetical protein |
| SCE1572_9959 | Serine/threonine protein kinase (EC 2.7.11.1) | bi | 70.71 Serine/threonine protein kinase (EC 2.7.11.1) |
| SCE1572_9960 | Response regulator of zinc sigma-54-dependent two-component system | bi | 80.28 Response regulator of zinc sigma-54-dependent two-component system |
| SCE1572_9961 | hypothetical protein | - | 0 |
| SCE1572_9962 | hypothetical protein | - | 0 |
| SCE1572_9963 | YD repeat protein | bi | 86.05 hypothetical protein |
| SCE1572_9964 | hypothetical protein | bi | 80.56 YD repeat protein |
| SCE1572_9965 | hypothetical protein | - | 0 |
| SCE1572_9966 | Ser/Arg-related nuclear matrix protein | bi | 37.57 FIG1085660: hypothetical protein |
| SCE1572_9967 | Chorismate mutase I (EC 5.4.99.5) / Prephenate dehydratase (EC 4.2.1.51) | bi | 92.2 Chorismate mutase I (EC 5.4.99.5) / Prephenate dehydratase (EC 4.2.1.51) |
| SCE1572_9968 | Uil36 very large tegument protein | bi | 67.8 hypothetical protein |
| SCE1572_9969 | RNA polymerase sigma-70 factor, ECF subfamily | bi | 83.7 RNA polymerase sigma-70 factor, ECF subfamily |
| SCE1572_9970 | OmpA/MotB | bi | 69.7 Exonuclease SbcC |
| SCE1572_9971 | hypothetical protein | bi | 77.58 hypothetical protein |
| SCE1572_9972 | MSHA biogenesis protein MshL | bi | 77.54 MSHA biogenesis protein MshL |
| SCE1572_9973 | hypothetical protein | bi | 87.97 hypothetical protein |
| SCE1572_9974 | FIG01089539: hypothetical protein | bi | 83.7 FIG01089539: hypothetical protein |
| SCE1572_9975 | Fusaric acid resistance protein | bi | 77.32 Fusaric acid resistance protein |
| SCE1572_9976 | hypothetical protein | - | 0 |
| SCE1572_9977 | lectin C-type domain protein | bi | 74.7 lectin C-type domain protein |
| SCE1572_9978 | Chitodextrinase precursor (EC 3.2.1.14) | uni | 43.48 Chitodextrinase precursor (EC 3.2.1.14) |
| SCE1572_9979 | hypothetical protein | - | 0 |
| SCE1572_9980 | 3-demethylubiquinone-9 3-O-methyltransferase(EC:2.1.1.64) | bi | 92 hypothetical protein |
| SCE1572_9981 | Coenzyme F390 synthetase | bi | 93.31 Phenylacetate--CoA ligase(EC:6.2.1.30) |
| SCE1572_9982 | Iron-sulfur cluster-binding protein | bi | 92.46 Iron-sulfur cluster-binding protein |
| SCE1572_9983 | FIG01088113: hypothetical protein | bi | 54.43 FIG01088113: hypothetical protein |
| SCE1572_9984 | Endo-1,4-beta-xylanase A precursor (EC 3.2.1.8) | bi | 74.53 Endo-1,4-beta-xylanase A precursor (EC 3.2.1.8) |
| SCE1572_9985 | Regulatory protein, LysR-LysR, substrate-binding | bi | 83.97 Regulatory protein, LysR-LysR, substrate-binding |
| SCE1572_9986 | FIG01086158: hypothetical protein | bi | 74.74 FIG01086158: hypothetical protein |
| SCE1572_9987 | Similarity | bi | 81.14 Similarity |
| SCE1572_9988 | hypothetical protein | bi | 68.48 hypothetical protein |
| SCE1572_9989 | Response regulator of zinc sigma-54-dependent two-component system | bi | 93.93 Response regulator of zinc sigma-54-dependent two-component system |
| SCE1572_9990 | FIG01088423: hypothetical protein | bi | 81.61 FIG01088423: hypothetical protein |
| SCE1572_9991 | putative cytochrome P450 hydroxylase | bi | 90.02 putative cytochrome P450 hydroxylase |
| SCE1572_9992 | hypothetical protein | - | 0 |
| SCE1572_9993 | Endo-1,4-beta-xylanase A precursor (EC 3.2.1.8) | uni | 72.15 Endo-1,4-beta-xylanase A precursor (EC 3.2.1.8) |
| SCE1572_9994 | Carbohydrate binding family 6 | uni | 58.82 Endo-1,4-beta-xylanase A precursor (EC 3.2.1.8) |
| SCE1572_9995 | hypothetical protein | uni | 37.34 Similarity |
| SCE1572_9996 | sensor histidine kinase | bi | 89.08 sensor histidine kinase |
| SCE1572_9997 | Methionyl-tRNA synthetase (EC 6.1.1.10) | bi | 94.81 Methionyl-tRNA synthetase (EC 6.1.1.10) |
| SCE1572_9998 | Dehydrogenase | bi | 82.87 Dehydrogenase |
| SCE1572_9999 | RNA polymerase sigma-70 factor, ECF subfamily | bi | 83.49 RNA polymerase sigma-70 factor, ECF subfamily |
| SCE1572_10000 | hypothetical protein | bi | 93.52 hypothetical protein |
| SCE1572_10001 | hypothetical protein | - | 0 |
| SCE1572_10002 | Intramembrane protease RasP/YluC, implicated in cell division based on FtsL cleavage | bi | 96.94 Intramembrane protease RasP/YluC, implicated in cell division based on FtsL cleavage |
| SCE1572_10003 | Ribosomal RNA small subunit methyltransferase B (EC 2.1.1.-) | bi | 87.9 Ribosomal RNA small subunit methyltransferase B (EC 2.1.1.-) |

| | | | | |
|---------------|---|-----|----------|---|
| SCE1572_10004 | AAA ATPase | umi | see_7361 | 68.54 AAA ATPase |
| SCE1572_10005 | AAA ATPase | umi | see_7361 | 72.46 AAA ATPase |
| SCE1572_10006 | hypothetical protein | bi | see_8830 | 87.13 hypothetical protein |
| SCE1572_10007 | RD1 region associated protein Rv3879c | bi | see_8831 | 75.22 RD1 region associated protein Rv3879c |
| SCE1572_10008 | blr2149; hypothetical protein | bi | see_8832 | 65.56 Serine/threonine protein kinase PpkA |
| SCE1572_10009 | RNA polymerase sigma factor RpoE | bi | see_8833 | 78.55 RNA polymerase sigma factor RpoE |
| SCE1572_10010 | hypothetical protein | bi | see_8834 | 75.32 hypothetical protein |
| SCE1572_10011 | Protein serine/threonine phosphatase PrpC, regulation of stationary phase | bi | see_8835 | 97.67 Protein serine/threonine phosphatase PrpC, regulation of stationary phase |
| SCE1572_10012 | HtrA family serine protease | bi | see_8836 | 83.86 HtrA family serine protease |
| SCE1572_10013 | RNA polymerase sigma factor RpoE | bi | see_8837 | 95.31 RNA polymerase sigma factor RpoE |
| SCE1572_10014 | Outer membrane protein | bi | see_8838 | 79.4 Outer membrane protein |
| SCE1572_10015 | Hypothetical protein | bi | see_8839 | 90.07 Hypothetical protein |
| SCE1572_10016 | Serine-threonine protein kinase | bi | see_8840 | 65.61 hypothetical protein |
| SCE1572_10017 | 3-hydroxybutyryl-CoA dehydrogenase (EC 1.1.1.157); 3-hydroxyacyl-CoA dehydrogenase (EC 1.1.1.35) | bi | see_8841 | 91.75 3-hydroxybutyryl-CoA dehydrogenase (EC 1.1.1.157); 3-hydroxyacyl-CoA dehydrogenase (EC 1.1.1.35) |
| SCE1572_10018 | FIG01088755: hypothetical protein | bi | see_9498 | 94.4 FIG01088755: hypothetical protein |
| SCE1572_10019 | FIG01086239: hypothetical protein | bi | see_9499 | 95.44 FIG01086239: hypothetical protein |
| SCE1572_10020 | FIG01088755: hypothetical protein | bi | see_9500 | 88.15 hypothetical protein |
| SCE1572_10021 | hypothetical protein | bi | see_9501 | 91.77 hypothetical protein |
| SCE1572_10022 | hypothetical protein | umi | see_9503 | 87.87 hypothetical protein |
| SCE1572_10023 | hypothetical protein | umi | see_9503 | 77.23 hypothetical protein |
| SCE1572_10024 | hypothetical protein | umi | see_9504 | 72.38 hypothetical protein |
| SCE1572_10025 | FIG01086605: hypothetical protein | bi | see_8463 | 81.78 FIG01086605: hypothetical protein |
| SCE1572_10026 | Circumsporozoite protein | bi | see_8842 | 85.23 Circumsporozoite protein |
| SCE1572_10027 | Seroreactive antigen BMN1-7 | bi | see_8843 | 84.18 Seroreactive antigen BMN1-7 |
| SCE1572_10028 | pseudouridylyl synthase | bi | see_8844 | 86.54 pseudouridylyl synthase, RluA family (EC 4.2.1.70) |
| SCE1572_10029 | Phosphoenolpyruvate synthase (EC 2.7.9.2) | bi | see_8845 | 82.89 Phosphoenolpyruvate synthase (EC 2.7.9.2) |
| SCE1572_10030 | hypothetical protein | bi | see_8846 | 83.76 putative esterase |
| SCE1572_10031 | putative amino-acid permease protein | umi | see_5501 | 30.42 Urea carboxylase-related amino acid permease |
| SCE1572_10032 | Lignostilbene-alpha,beta-dioxygenase and related enzymes | - | - | 0 |
| SCE1572_10033 | hypothetical abductin-like protein | bi | see_8847 | 80.86 hypothetical abductin-like protein |
| SCE1572_10034 | serine/threonine protein kinase | bi | see_8851 | 77.51 serine/threonine protein kinase |
| SCE1572_10035 | TonB protein | umi | see_4768 | 58.62 Ferric siderophore transport system, periplasmic binding protein TonB |
| SCE1572_10036 | hypothetical protein | bi | see_8852 | 88.82 hypothetical protein |
| SCE1572_10037 | conserved hypothetical protein | bi | see_8853 | 84 conserved hypothetical protein |
| SCE1572_10038 | Penicillin-insensitive murein endopeptidase A | bi | see_8854 | 85.27 Penicillin-insensitive murein endopeptidase A |
| SCE1572_10039 | Formamidopyrimidine-DNA glycosylase (EC 3.2.2.23) | umi | see_3926 | 34.22 Formamidopyrimidine-DNA glycosylase (EC 3.2.2.23) |
| SCE1572_10040 | RecD-like DNA helicase YrrC | bi | see_8856 | 94.25 RecD-like DNA helicase YrrC |
| SCE1572_10041 | hypothetical protein | - | - | 0 |
| SCE1572_10042 | TPR repeat | bi | see_8858 | 95.76 TPR repeat |
| SCE1572_10043 | Cof-like hydrolase | bi | see_8859 | 91.4 hypothetical protein |
| SCE1572_10044 | LSU ribosomal protein L27p | bi | see_8860 | 100 LSU ribosomal protein L27p |
| SCE1572_10045 | LSU ribosomal protein L21p | bi | see_8861 | 98.04 LSU ribosomal protein L21p |
| SCE1572_10046 | ClpB protein | bi | see_8862 | 97.01 ClpB protein |
| SCE1572_10047 | Glutaredoxin 3 | bi | see_8863 | 79.8 Glutaredoxin 3 |
| SCE1572_10048 | serine/threonine protein kinase | bi | see_8864 | 85.19 serine/threonine protein kinase |
| SCE1572_10049 | tetratricopeptide repeat protein | bi | see_8865 | 86.92 Dihydroipoamide acetyltransferase component of pyruvate dehydrogenase complex (EC 2.3.1.12) |
| SCE1572_10050 | Acetyl-coenzyme A synthetase (EC 6.2.1.1) | bi | see_8866 | 95.42 Acetyl-coenzyme A synthetase (EC 6.2.1.1) |
| SCE1572_10051 | serine/threonine protein kinase | bi | see_8868 | 79.92 serine/threonine protein kinase |
| SCE1572_10052 | integral membrane sensor signal transduction histidine kinase | bi | see_8869 | 90.83 sensor histidine kinase |
| SCE1572_10053 | Iron-sulphur-binding reductase | bi | see_8870 | 90.66 protein of unknown function DUF224, cysteine-rich region domain protein |
| SCE1572_10054 | Adenylate cyclase (EC 4.6.1.1) | bi | see_8871 | 85.65 Adenylate cyclase (EC 4.6.1.1) |
| SCE1572_10055 | Transcription termination factor Rho | bi | see_8872 | 99.76 Transcription termination factor Rho |
| SCE1572_10056 | Acylphosphate phosphohydrolase (EC 3.6.1.7), putative | bi | see_8873 | 100 Acylphosphate phosphohydrolase (EC 3.6.1.7), putative |
| SCE1572_10057 | AGR138Wp | bi | see_8874 | 71.93 putative membrane protein |
| SCE1572_10058 | LSU ribosomal protein L17p | bi | see_8875 | 97.39 LSU ribosomal protein L17p |
| SCE1572_10059 | DNA-directed RNA polymerase alpha subunit (EC 2.7.7.6) | bi | see_8876 | 99.71 DNA-directed RNA polymerase alpha subunit (EC 2.7.7.6) |
| SCE1572_10060 | hypothetical protein | - | - | 0 |
| SCE1572_10061 | SSU ribosomal protein S4p (S9c) | bi | see_8878 | 98.56 SSU ribosomal protein S4p (S9c) |
| SCE1572_10062 | SSU ribosomal protein S11p (S14e) | bi | see_8879 | 99.26 SSU ribosomal protein S11p (S14e) |
| SCE1572_10063 | SSU ribosomal protein S13p (S18e) | bi | see_8880 | 96.03 SSU ribosomal protein S13p (S18e) |
| SCE1572_10064 | LSU ribosomal protein L36p | bi | see_8881 | 100 LSU ribosomal protein L36p |
| SCE1572_10065 | Translation initiation factor I | bi | see_8882 | 96.39 Translation initiation factor I |
| SCE1572_10066 | Adenylate kinase (EC 2.7.4.3) | bi | see_8883 | 93.02 Adenylate kinase (EC 2.7.4.3) |
| SCE1572_10067 | Preprotein translocase secY subunit (TC 3.A.5.1.1) | bi | see_8884 | 97.51 Preprotein translocase secY subunit (TC 3.A.5.1.1) |
| SCE1572_10068 | LSU ribosomal protein L15p (L27Ac) | bi | see_8885 | 90.71 LSU ribosomal protein L15p (L27Ac) |
| SCE1572_10069 | LSU ribosomal protein L30p (L7e) | bi | see_8886 | 91.04 LSU ribosomal protein L30p (L7e) |
| SCE1572_10070 | SSU ribosomal protein S5p (S2e) | bi | see_8887 | 95.1 SSU ribosomal protein S5p (S2e) |
| SCE1572_10071 | LSU ribosomal protein L18p (L5e) | bi | see_8888 | 97.48 LSU ribosomal protein L18p (L5e) |
| SCE1572_10072 | LSU ribosomal protein L6p (L9e) | bi | see_8889 | 94.74 LSU ribosomal protein L6p (L9e) |
| SCE1572_10073 | SSU ribosomal protein S8p (S15Ae) | bi | see_8890 | 96.95 SSU ribosomal protein S8p (S15Ae) |
| SCE1572_10074 | SSU ribosomal protein S14p (S29e) | bi | see_8891 | 98.36 SSU ribosomal protein S14p (S29e) |
| SCE1572_10075 | LSU ribosomal protein L5p (L11e) | bi | see_8892 | 94.65 LSU ribosomal protein L5p (L11e) |
| SCE1572_10076 | LSU ribosomal protein L24p (L26e) | bi | see_8893 | 96.19 LSU ribosomal protein L24p (L26e) |
| SCE1572_10077 | LSU ribosomal protein L14p (L23e) | bi | see_8894 | 98.36 LSU ribosomal protein L14p (L23e) |
| SCE1572_10078 | SSU ribosomal protein S17p (S11e) | bi | see_8895 | 96.49 SSU ribosomal protein S17p (S11e) |
| SCE1572_10079 | LSU ribosomal protein L29p (L35e) | bi | see_8896 | 100 LSU ribosomal protein L29p (L35e) |
| SCE1572_10080 | LSU ribosomal protein L16p (L10e) | bi | see_8897 | 97.08 LSU ribosomal protein L16p (L10e) |
| SCE1572_10081 | SSU ribosomal protein S3p (S3e) | bi | see_8898 | 99.57 SSU ribosomal protein S3p (S3e) |
| SCE1572_10082 | LSU ribosomal protein L22p (L17e) | bi | see_8899 | 100 LSU ribosomal protein L22p (L17e) |
| SCE1572_10083 | putative secreted protein | bi | see_8901 | 61.63 putative secreted protein |
| SCE1572_10084 | FIG01085003: hypothetical protein | bi | see_8902 | 83.11 FIG01085003: hypothetical protein |
| SCE1572_10085 | unknown | bi | see_8903 | 81.89 unknown |
| SCE1572_10086 | Histone-like protein | bi | see_8904 | 94.38 Histone-like protein |
| SCE1572_10087 | hypothetical protein | - | - | 0 |
| SCE1572_10088 | hypothetical protein | - | - | 0 |
| SCE1572_10089 | FIG01087145: hypothetical protein | bi | see_8905 | 87.33 FIG01087145: hypothetical protein |
| SCE1572_10090 | Phosphate starvation-inducible protein PhoH, predicted ATPase | bi | see_8907 | 97.99 Phosphate starvation-inducible protein PhoH, predicted ATPase |
| SCE1572_10091 | FIG01089318: hypothetical protein | bi | see_8909 | 76.6 FIG01089318: hypothetical protein |
| SCE1572_10092 | Cell division protein FtsI [Peptidoglycan synthetase] (EC 2.4.1.129) | bi | see_8910 | 94.33 Cell division protein FtsI [Peptidoglycan synthetase] (EC 2.4.1.129) |
| SCE1572_10093 | hypothetical protein | bi | see_8911 | 100 hypothetical protein |
| SCE1572_10094 | hypothetical protein | bi | see_8912 | 86.67 hypothetical protein |
| SCE1572_10095 | FIG01086079: hypothetical protein | bi | see_8913 | 84.21 FIG01086079: hypothetical protein |
| SCE1572_10096 | FOG: WD40 repeat | bi | see_8914 | 87.72 FOG: WD40 repeat |
| SCE1572_10097 | hypothetical protein | bi | see_8915 | 82.43 Serine/threonine-protein kinase pkn3 (EC 2.7.11.1) |
| SCE1572_10098 | Methionyl-tRNA formyltransferase (EC 2.1.2.9) | bi | see_8916 | 92.55 Methionyl-tRNA formyltransferase (EC 2.1.2.9) |
| SCE1572_10099 | Cell division transporter, ATP-binding protein FtsE (TC 3.A.5.1.1) | bi | see_8917 | 96.34 Cell division transporter, ATP-binding protein FtsE (TC 3.A.5.1.1) |
| SCE1572_10100 | Cell division protein FtsX | bi | see_8918 | 95.96 Cell division protein FtsX |
| SCE1572_10101 | Periplasmic septal ring factor with murein hydrolase activity EnvC/YibP | bi | see_8919 | 91.72 peptidase M23B |
| SCE1572_10102 | Ribonuclease PH (EC 2.7.7.56) | bi | see_8920 | 93.77 Ribonuclease PH (EC 2.7.7.56) |
| SCE1572_10103 | Nucleoside 5-triphosphatase RdgB (dHAPTP, dTTP, XTP-specific) (EC 3.6.1.15) | bi | see_8921 | 86.47 Nucleoside 5-triphosphatase RdgB (dHAPTP, dTTP, XTP-specific) (EC 3.6.1.15) |
| SCE1572_10104 | ATP synthase protein I | bi | see_8922 | 76.61 ATP synthase protein I |
| SCE1572_10105 | FIG048548: ATP synthase protein I2 | bi | see_8923 | 86.36 FIG048548: ATP synthase protein I2 |
| SCE1572_10106 | ATP synthase A chain (EC 3.6.3.14) | bi | see_8924 | 97.25 ATP synthase A chain (EC 3.6.3.14) |
| SCE1572_10107 | ATP synthase C chain (EC 3.6.3.14) | bi | see_8925 | 100 ATP synthase C chain (EC 3.6.3.14) |
| SCE1572_10108 | hypothetical protein | bi | see_8926 | 89.18 hypothetical protein |
| SCE1572_10109 | Gb AAD23008.1 | bi | see_8927 | 83.33 Gb AAD23008.1 |
| SCE1572_10110 | Gb AAD23008.1 | umi | see_4432 | 86.84 hypothetical protein |
| SCE1572_10111 | FIG01089283: hypothetical protein | bi | see_8928 | 92.18 FIG01089283: hypothetical protein |
| SCE1572_10112 | hypothetical protein | - | - | 0 |
| SCE1572_10113 | predicted tail fiber protein | umi | see_3821 | 30.1 DNA topoisomerase III (EC 5.99.1.2) |
| SCE1572_10114 | hypothetical protein | umi | see_3858 | 41.82 Adenosylhomocysteinase (EC 3.3.1.1) |
| SCE1572_10115 | Cell division protein FtsK | bi | see_8930 | 80.85 Cell division protein FtsK |
| SCE1572_10116 | putative exported protein of unknown function with OmpA family domain | umi | see_1486 | 37.55 VgrG protein |
| SCE1572_10117 | RD1 region associated protein Rv3876 | bi | see_8934 | 67.89 RD1 region associated protein Rv3876 |
| SCE1572_10118 | hypothetical membrane protein | bi | see_8935 | 87.87 hypothetical membrane protein |
| SCE1572_10119 | hypothetical protein | bi | see_8937 | 83.38 hypothetical protein |
| SCE1572_10120 | Intramembrane protease RasP/YluC, implicated in cell division based on FtsL cleavage | bi | see_8938 | 89.95 Intramembrane protease RasP/YluC, implicated in cell division based on FtsL cleavage |
| SCE1572_10121 | hypothetical protein | bi | see_8939 | 86.7 hypothetical protein |
| SCE1572_10122 | hypothetical protein | bi | see_8940 | 87.46 hypothetical protein |
| SCE1572_10123 | unknown | bi | see_8941 | 66.52 hypothetical protein |
| SCE1572_10124 | Gli0645 protein | umi | see_1146 | 32.49 Gli0645 protein |
| SCE1572_10125 | Single-stranded DNA-binding protein | umi | see_7913 | 53.62 serine/threonine protein kinase |
| SCE1572_10126 | Cell division protein FtsH (EC 3.4.24.-) | umi | see_1829 | 57.14 Cell division protein FtsH (EC 3.4.24.-) |
| SCE1572_10127 | Cell division protein FtsH (EC 3.4.24.-) | umi | see_1829 | 54.12 Cell division protein FtsH (EC 3.4.24.-) |
| SCE1572_10128 | hypothetical protein | - | - | 0 |
| SCE1572_10129 | hypothetical protein | - | - | 0 |
| SCE1572_10130 | Chromosome undetermined SCAF14611, whole genome shotgun sequence | bi | see_8942 | 90.76 Chromosome undetermined SCAF14611, whole genome shotgun sequence |
| SCE1572_10131 | hypothetical protein | umi | see_6133 | 43.49 Twin-arginine translocation protein TatB |
| SCE1572_10132 | Heat shock protein 60 family chaperone GroEL | umi | see_4006 | 42.19 FIG01086775: hypothetical protein |
| SCE1572_10133 | Sigma-70 region 2.Sigma-70 region 4 | umi | see_2800 | 39.9 RNA polymerase sigma factor RpoE |
| SCE1572_10134 | DNA polymerase, beta-like region | - | - | 0 |
| SCE1572_10135 | hypothetical protein | umi | see_3936 | 53.06 FIG01089186: hypothetical protein |
| SCE1572_10136 | hypothetical protein | - | - | 0 |
| SCE1572_10137 | hypothetical protein | umi | see_5854 | 27.44 FIG01085614: hypothetical protein |
| SCE1572_10138 | hypothetical protein | - | - | 0 |
| SCE1572_10139 | hypothetical protein | - | - | 0 |
| SCE1572_10140 | Cobyrinic acid a,c-diamide synthase | - | - | 0 |
| SCE1572_10141 | Glycerol-3-phosphate dehydrogenase [NAD(P)] (EC 1.1.1.94) | bi | see_8944 | 93.15 Glycerol-3-phosphate dehydrogenase [NAD(P)] (EC 1.1.1.94) |
| SCE1572_10142 | Glycerol-3-phosphate acyltransferase (EC 2.3.1.15) | bi | see_8945 | 91 Glycerol-3-phosphate acyltransferase (EC 2.3.1.15) |
| SCE1572_10143 | Hydroxyacylglutathione hydrolase (EC 3.1.2.6) | bi | see_8946 | 88.84 Hydroxyacylglutathione hydrolase (EC 3.1.2.6) |
| SCE1572_10144 | best DB hits: PFAM: PF01351; Ribonuclease HII; E=0.11 | bi | see_8947 | 85.59 best DB hits: PFAM: PF01351; Ribonuclease HII; E=0.11 |
| SCE1572_10145 | Peptide methionine sulfoxide reductase MsrB (EC 1.8.4.12) / Peptide methionine sulfoxide reductase MsrA (EC 1.8.4.11) | bi | see_8948 | 86.55 Peptide methionine sulfoxide reductase MsrB (EC 1.8.4.12) / Peptide methionine sulfoxide reductase MsrA (EC 1.8.4.11) |
| SCE1572_10146 | Dihydroipoamide dehydrogenase of pyruvate dehydrogenase complex (EC 1.8.1.4) | bi | see_8949 | 92.52 Dihydroipoamide dehydrogenase of pyruvate dehydrogenase complex (EC 1.8.1.4) |
| SCE1572_10147 | Branched-chain alpha-keto acid dehydrogenase, E1 component, alpha subunit (EC 1.2.4.4) | bi | see_8950 | 92.8 Branched-chain alpha-keto acid dehydrogenase, E1 component, alpha subunit (EC 1.2.4.4) |
| SCE1572_10148 | FIG01085819: hypothetical protein | bi | see_8951 | 95.6 FIG01085819: hypothetical protein |
| SCE1572_10149 | hypothetical protein | bi | see_8952 | 89.22 hypothetical protein |
| SCE1572_10150 | FOG: HEAT repeat | bi | see_8953 | 87.61 FOG: HEAT repeat |
| SCE1572_10151 | hypothetical protein | bi | see_8954 | 73.88 PE_PGRS family protein |
| SCE1572_10152 | 4Fe-4S ferredoxin, iron-sulfur binding | bi | see_8955 | 93.07 4Fe-4S ferredoxin, iron-sulfur binding |
| SCE1572_10153 | FIG01087345: hypothetical protein | bi | see_8956 | 82.28 FIG01087345: hypothetical protein |
| SCE1572_10154 | FIG01088198: hypothetical protein | bi | see_8957 | 87.67 FIG01088198: hypothetical protein |
| SCE1572_10155 | serine/threonine protein kinase | bi | see_8958 | 89.1 serine/threonine protein kinase |
| SCE1572_10156 | hypothetical protein | bi | see_8959 | 74.19 hypothetical protein |
| SCE1572_10157 | Urocanate hydratase (EC 4.2.1.49) | bi | see_8960 | 96.34 Urocanate hydratase (EC 4.2.1.49) |
| SCE1572_10158 | Endonuclease IV (EC 3.1.21.2) | - | - | 0 |
| SCE1572_10159 | hypothetical protein | bi | see_8961 | 63.16 hypothetical protein |
| SCE1572_10160 | Long-chain-fatty-acid-CoA ligase (EC 6.2.1.3) | bi | see_8962 | 92.45 Long-chain-fatty-acid-CoA ligase (EC 6.2.1.3) |
| SCE1572_10161 | Dihydroflavonol-4-reductase (EC 1.1.1.219) | bi | see_8963 | 91.57 Dihydroflavonol-4-reductase (EC 1.1.1.219) |
| SCE1572_10162 | multi-sensor signal transduction histidine kinase | umi | see_1532 | 46.58 FIG01089498: hypothetical protein |
| SCE1572_10163 | Circadian clock protein KaiC | - | - | 0 |
| SCE1572_10164 | Response regulator receiver:CheW-like protein:ATP-binding region, ATPase-like:Hpt | umi | see_1925 | 40.87 response regulator receiver domain protein (CheY-like) |
| SCE1572_10165 | CBS domain protein | bi | see_8964 | 92.51 CBS domain protein |
| SCE1572_10166 | hypothetical protein | - | - | 0 |
| SCE1572_10167 | FIG01086833: hypothetical protein | bi | see_8966 | 89.4 FIG01086833: hypothetical protein |

| | | | | | |
|---------------|---|-----|-----------|-------|---|
| SCE1572_10168 | hypothetical protein | bi | sce_8967 | 90.68 | FIG01087342: hypothetical protein |
| SCE1572_10169 | FIG01084921: hypothetical protein | bi | sce_8968 | 86.23 | FIG01084921: hypothetical protein |
| SCE1572_10170 | Serine-threonine protein kinase | bi | sce_8969 | 85.71 | Serine/threonine-protein kinase pkn3 (EC 2.7.11.1) |
| SCE1572_10171 | hypothetical protein | umi | sce_8969 | 58.03 | Serine/threonine-protein kinase pkn3 (EC 2.7.11.1) |
| SCE1572_10172 | Methyltransferase type 11 | bi | sce_8970 | 94.33 | Methyltransferase type 11 |
| SCE1572_10173 | hypothetical protein | bi | sce_8972 | 29.93 | hypothetical protein |
| SCE1572_10174 | hypothetical protein | - | - | 0 | 0 |
| SCE1572_10175 | hypothetical protein | bi | sce_8974 | 94.44 | hypothetical protein |
| SCE1572_10176 | NADH-ubiquinone oxidoreductase chain K (EC 1.6.5.3) | bi | sce_8975 | 92.08 | NADH-ubiquinone oxidoreductase chain K (EC 1.6.5.3) |
| SCE1572_10177 | NAD(P)H-quinone oxidoreductase chain J (EC 1.6.5.2) | bi | sce_8976 | 95.32 | NAD(P)H-quinone oxidoreductase chain J (EC 1.6.5.2) |
| SCE1572_10178 | NAD(P)H-quinone oxidoreductase chain I (EC 1.6.5.2) | bi | sce_8977 | 91.74 | NAD(P)H-quinone oxidoreductase chain I (EC 1.6.5.2) |
| SCE1572_10179 | Dihydrodipicolinate synthase (EC 4.2.1.52) | bi | sce_8978 | 93.36 | Dihydrodipicolinate synthase (EC 4.2.1.52) |
| SCE1572_10180 | Dihydrodipicolinate reductase (EC 1.3.1.26) | bi | sce_8979 | 93.54 | Dihydrodipicolinate reductase (EC 1.3.1.26) |
| SCE1572_10181 | possible OmpA family member | bi | sce_8980 | 58.29 | large tegument protein |
| SCE1572_10182 | Glycyl-tRNA synthetase beta chain (EC 6.1.1.14) | bi | sce_8981 | 93.71 | Glycyl-tRNA synthetase beta chain (EC 6.1.1.14) |
| SCE1572_10183 | Enoyl-[acyl-carrier-protein] reductase [NADPH] (EC 1.3.1.10) | bi | sce_9845 | 81.71 | Enoyl-[acyl-carrier-protein] reductase [NADPH] (EC 1.3.1.10) |
| SCE1572_10184 | Transcriptional regulator, TetR family | bi | sce_9844 | 87.63 | Transcriptional regulator, TetR family |
| SCE1572_10185 | hypothetical protein | - | - | 0 | 0 |
| SCE1572_10186 | Peptidase M48, Ste24p precursor | bi | sce_8992 | 93.36 | Peptidase M48, Ste24p precursor |
| SCE1572_10187 | FIG01087569: hypothetical protein | bi | sce_8993 | 89.4 | FIG01087569: hypothetical protein |
| SCE1572_10188 | hypothetical protein | bi | sce_8994 | 91.94 | hypothetical protein |
| SCE1572_10189 | FIG01085362: hypothetical protein | bi | sce_8995 | 86.65 | FIG01085362: hypothetical protein |
| SCE1572_10190 | FIG01089091: hypothetical protein | bi | sce_8996 | 95.37 | FIG01089091: hypothetical protein |
| SCE1572_10191 | hypothetical protein | bi | sce_8997 | 60.69 | hypothetical protein |
| SCE1572_10192 | FIG01088552: hypothetical protein | bi | sce_8998 | 78.26 | FIG01088552: hypothetical protein |
| SCE1572_10193 | Putative zinc metalloprotease MJ0392 (EC 3.4.24.-) | bi | sce_8999 | 86.29 | Putative zinc metalloprotease MJ0392 (EC 3.4.24.-) |
| SCE1572_10194 | hypothetical protein | bi | sce_9000 | 90.43 | hypothetical protein |
| SCE1572_10195 | 3-oxoacyl-[acyl-carrier-protein] synthase, KASIII (EC 2.3.1.41) | bi | sce_9001 | 74.6 | 3-oxoacyl-[acyl-carrier-protein] synthase, KASIII (EC 2.3.1.41) |
| SCE1572_10196 | hypothetical protein | - | - | 0 | 0 |
| SCE1572_10197 | hypothetical protein | - | - | 0 | 0 |
| SCE1572_10198 | Flagelliform silk protein | bi | sce_9003 | 62.93 | FIG01086917: hypothetical protein |
| SCE1572_10199 | Glucosylase (EC 3.2.1.3) | bi | sce_9004 | 91.3 | Glucosylase (EC 3.2.1.3) |
| SCE1572_10200 | Dna binding response regulator PrrA (RegA) | bi | sce_9005 | 89.56 | Dna binding response regulator PrrA (RegA) |
| SCE1572_10201 | Sensor histidine kinase PrrB (RegB) (EC 2.7.3.-) | bi | sce_9006 | 90.51 | Sensor histidine kinase PrrB (RegB) (EC 2.7.3.-) |
| SCE1572_10202 | Rhs family protein | umi | sce_3937 | 36.81 | FIG01085109: hypothetical protein |
| SCE1572_10203 | FIG01087249: hypothetical protein | umi | sce_2338 | 92.86 | Transposase |
| SCE1572_10204 | hypothetical protein | - | - | 0 | 0 |
| SCE1572_10205 | Rhs family protein | - | - | 0 | 0 |
| SCE1572_10206 | YD repeat protein | umi | sce_3939 | 36.97 | FIG01085109: hypothetical protein |
| SCE1572_10207 | POSSIBLE BENZOQUINONE METHYLTRANSFERASE (METHYLASE) | umi | sce_3222 | 45.31 | Methyltransferase type 12 |
| SCE1572_10208 | NADH:flavin oxidoreductase/NADH oxidase | bi | sce_9676 | 92.51 | NADH:flavin oxidoreductase/NADH oxidase |
| SCE1572_10209 | hypothetical protein | - | - | 0 | 0 |
| SCE1572_10210 | MerR family transcriptional regulatory protein | bi | sce_9675 | 89.12 | MerR family transcriptional regulatory protein |
| SCE1572_10211 | RsbR, positive regulator of sigma-B | umi | sce_9946 | 50.72 | RsbR, positive regulator of sigma-B |
| SCE1572_10212 | Inner membrane protein YihY, formerly thought to be RNase BN | bi | sce_9674 | 83.38 | Inner membrane protein YihY, formerly thought to be RNase BN |
| SCE1572_10213 | hypothetical protein | bi | sce_9673 | 61.54 | FIG01088899: hypothetical protein |
| SCE1572_10214 | Mil2607 protein | bi | sce_9672 | 81.65 | Mil2607 protein |
| SCE1572_10215 | hypothetical protein | - | - | 0 | 0 |
| SCE1572_10216 | putative ABC transporter ATP-binding protein | bi | sce_9670 | 83.33 | ATP binding protein |
| SCE1572_10217 | 2-dehydropanoate 2-reductase (EC 1.1.1.169) | bi | sce_9669 | 84.78 | 2-dehydropanoate 2-reductase (EC 1.1.1.169) |
| SCE1572_10218 | FIG01087423: hypothetical protein | bi | sce_9668 | 87.54 | FIG01087423: hypothetical protein |
| SCE1572_10219 | hypothetical protein | bi | sce_9667 | 86.51 | FIG01087423: hypothetical protein |
| SCE1572_10220 | Probable outer membrane protein | bi | sce_9666 | 86.52 | Probable outer membrane protein |
| SCE1572_10221 | Blue copper oxidase CueO precursor | bi | sce_2358 | 86.79 | Blue copper oxidase CueO precursor |
| SCE1572_10222 | Methionine ABC transporter ATP-binding protein | bi | sce_9656 | 97.17 | Methionine ABC transporter ATP-binding protein |
| SCE1572_10223 | ABC transporter associated permease | bi | sce_9655 | 91.36 | protein of unknown function DUF214 |
| SCE1572_10224 | hypothetical protein | bi | sce_7438 | 22.13 | FIG01088128: hypothetical protein |
| SCE1572_10225 | hypothetical protein | - | - | 0 | 0 |
| SCE1572_10226 | transposase | - | - | 0 | 0 |
| SCE1572_10227 | hypothetical protein | - | - | 0 | 0 |
| SCE1572_10228 | hypothetical protein | umi | sce_10160 | 36.46 | Transposase |
| SCE1572_10229 | hypothetical protein | - | - | 0 | 0 |
| SCE1572_10230 | transposase IS66 family | umi | sce_7404 | 37.85 | Mobile element protein |
| SCE1572_10231 | Mobile element protein | bi | sce_4534 | 43.74 | Mobile element protein |
| SCE1572_10232 | probable transposase | - | - | 0 | 0 |
| SCE1572_10233 | hypothetical protein | - | - | 0 | 0 |
| SCE1572_10234 | hypothetical protein | - | - | 0 | 0 |
| SCE1572_10235 | Mobile element protein | bi | sce_7404 | 81.22 | Mobile element protein |
| SCE1572_10236 | hypothetical protein | - | - | 0 | 0 |
| SCE1572_10237 | putative dipeptidyl-peptidase III | umi | sce_4371 | 39.74 | Mir5283 protein |
| SCE1572_10238 | hypothetical protein | - | - | 0 | 0 |
| SCE1572_10239 | hypothetical protein | bi | sce_6868 | 88 | hypothetical protein |
| SCE1572_10240 | hypothetical protein | - | - | 0 | 0 |
| SCE1572_10241 | hypothetical protein | umi | sce_7695 | 43.75 | predicted protein |
| SCE1572_10242 | Serine/threonine protein kinase PpkA | bi | sce_1432 | 46.59 | Serine/threonine protein kinase PpkA |
| SCE1572_10243 | hypothetical protein | bi | sce_8673 | 35.14 | FIG01086383: hypothetical protein |
| SCE1572_10244 | hypothetical protein | - | - | 0 | 0 |
| SCE1572_10245 | hypothetical protein | bi | sce_6866 | 83.89 | hypothetical protein |
| SCE1572_10246 | hypothetical protein | - | - | 0 | 0 |
| SCE1572_10247 | hypothetical protein | - | - | 0 | 0 |
| SCE1572_10248 | Transcription-repair coupling factor | bi | sce_7083 | 68.32 | hypothetical protein |
| SCE1572_10249 | hypothetical protein | - | - | 0 | 0 |
| SCE1572_10250 | Cysteine desulfurase (EC 2.8.1.7), SufS subfamily | bi | sce_5192 | 54.57 | Cysteine desulfurase (EC 2.8.1.7), SufS subfamily |
| SCE1572_10251 | hypothetical protein | - | - | 0 | 0 |
| SCE1572_10252 | hypothetical protein | - | - | 0 | 0 |
| SCE1572_10253 | hypothetical protein | - | - | 0 | 0 |
| SCE1572_10254 | hypothetical protein | - | - | 0 | 0 |
| SCE1572_10255 | phosphodiesterase/alkaline phosphatase D (EC:3.1.3.1) | umi | sce_1314 | 24.75 | Phosphodiesterase/alkaline phosphatase D |
| SCE1572_10256 | Na ⁺ antiporter NhaP | bi | sce_1659 | 96.88 | Na ⁺ antiporter NhaP |
| SCE1572_10257 | putative RecF protein | bi | sce_6864 | 94.75 | RecF/RecN/SMC N terminal domain, putative |
| SCE1572_10258 | hypothetical protein | - | - | 0 | 0 |
| SCE1572_10259 | acetyltransferase | umi | sce_9277 | 41.53 | GCN5-related N-acetyltransferase |
| SCE1572_10260 | FIG01088058: hypothetical protein | bi | sce_9652 | 72.94 | FIG01088058: hypothetical protein |
| SCE1572_10261 | Radical SAM domain protein | bi | sce_9651 | 95.99 | Radical SAM domain protein |
| SCE1572_10262 | Cysteine desulfurase (EC 2.8.1.7) | bi | sce_9650 | 92.61 | Cysteine desulfurase (EC 2.8.1.7) |
| SCE1572_10263 | hypothetical protein | - | - | 0 | 0 |
| SCE1572_10264 | SMC domain protein | umi | sce_924 | 45.9 | Gli1489 protein |
| SCE1572_10265 | hypothetical protein | bi | sce_9648 | 88.6 | hypothetical protein |
| SCE1572_10266 | FIG01085066: hypothetical protein | bi | sce_9647 | 82.59 | FIG01085066: hypothetical protein |
| SCE1572_10267 | 5,10-methylenetetrahydrofolate reductase (EC 1.5.1.20) | bi | sce_9646 | 95.97 | 5,10-methylenetetrahydrofolate reductase (EC 1.5.1.20) |
| SCE1572_10268 | FIG01087936: hypothetical protein | bi | sce_9645 | 93.13 | FIG01087936: hypothetical protein |
| SCE1572_10269 | Methylglutaconyl-CoA hydratase (EC 4.2.1.18) | bi | sce_9644 | 96.09 | Methylglutaconyl-CoA hydratase (EC 4.2.1.18) |
| SCE1572_10270 | hypothetical protein | umi | sce_6252 | 52.17 | FIG01088254: hypothetical protein |
| SCE1572_10271 | Thiamin biosynthesis lipoprotein ApbE | bi | sce_9643 | 85.68 | Thiamin biosynthesis lipoprotein ApbE |
| SCE1572_10272 | Amidohydrolase | bi | sce_9642 | 94.92 | Amidohydrolase |
| SCE1572_10273 | FIG01088011: hypothetical protein | bi | sce_9641 | 91.22 | FIG01088011: hypothetical protein |
| SCE1572_10274 | Uroporphyrinogen III decarboxylase (EC 4.1.1.37) | bi | sce_9639 | 98.57 | Uroporphyrinogen III decarboxylase (EC 4.1.1.37) |
| SCE1572_10275 | Predicted glutamine amidotransferase | bi | sce_9638 | 93.05 | Predicted glutamine amidotransferase |
| SCE1572_10276 | GGDEF family protein | bi | sce_9637 | 99.67 | GGDEF family protein |
| SCE1572_10277 | Acetylmethionine aminotransferase (EC 2.6.1.11) | bi | sce_9636 | 90.71 | acetylmethionine and succinylmethionine aminotransferases (EC:2.6.1.11) |
| SCE1572_10278 | Long-chain-fatty-acid-luciferin-component ligase (EC 6.2.1.19) | bi | sce_9635 | 88.12 | possible acyl protein synthase/acyl-CoA reductase-like protein |
| SCE1572_10279 | putative acyl-CoA reductase | bi | sce_9634 | 88.68 | hypothetical protein |
| SCE1572_10280 | Phosphocarrier protein kinase/phosphorylase, nitrogen regulation associated | bi | sce_9633 | 88.76 | Phosphocarrier protein kinase/phosphorylase, nitrogen regulation associated |
| SCE1572_10281 | Queuosine biosynthesis QueD, PTPS-1 | bi | sce_9631 | 95.2 | Queuosine biosynthesis QueD, PTPS-1 |
| SCE1572_10282 | FAD dependent oxidoreductase | bi | sce_9630 | 95.6 | sarcosine oxidase, beta subunit family protein |
| SCE1572_10283 | Biotin synthesis protein bioC | bi | sce_9629 | 93.8 | Biotin synthesis protein bioC |
| SCE1572_10284 | hypothetical protein | bi | sce_9628 | 93.36 | hypothetical protein |
| SCE1572_10285 | FIG01088095: hypothetical protein | bi | sce_9627 | 86.99 | FIG01088095: hypothetical protein |
| SCE1572_10286 | Phosphate regulon transcriptional regulatory protein PhoB | bi | sce_9626 | 98.7 | Phosphate regulon transcriptional regulatory protein PhoB |
| SCE1572_10287 | FIG01088413: hypothetical protein | bi | sce_9625 | 76.75 | FIG01088413: hypothetical protein |
| SCE1572_10288 | Magnesium transporter | bi | sce_9624 | 97.4 | Magnesium transporter |
| SCE1572_10289 | Single-stranded DNA-binding protein | bi | sce_9623 | 87.32 | Single-stranded DNA-binding protein |
| SCE1572_10290 | FIG01085931: hypothetical protein | bi | sce_9622 | 81.9 | FIG01085931: hypothetical protein |
| SCE1572_10291 | Transcriptional regulator, MerR family | bi | sce_9621 | 95.12 | Transcriptional regulator, MerR family |
| SCE1572_10292 | Integration host factor alpha subunit | bi | sce_9620 | 100 | Integration host factor alpha subunit |
| SCE1572_10293 | hypothetical protein | - | - | 0 | 0 |
| SCE1572_10294 | Glycosyltransferase | bi | sce_9619 | 93.12 | Glycosyltransferase |
| SCE1572_10295 | hypothetical protein | bi | sce_9617 | 90.46 | hypothetical protein |
| SCE1572_10296 | hypothetical protein | bi | sce_9616 | 94.35 | hypothetical protein |
| SCE1572_10297 | Branched-chain amino acid transport ATP-binding protein LivF (TC 3.A.1.4.1) | bi | sce_9615 | 96.83 | Branched-chain amino acid transport ATP-binding protein LivF (TC 3.A.1.4.1) |
| SCE1572_10298 | Branched-chain amino acid transport ATP-binding protein LivG (TC 3.A.1.4.1) | bi | sce_9614 | 92.16 | Branched-chain amino acid transport ATP-binding protein LivG (TC 3.A.1.4.1) |
| SCE1572_10299 | Branched-chain amino acid transport system permease protein LivM (TC 3.A.1.4.1) | bi | sce_9613 | 87.86 | Branched-chain amino acid transport system permease protein LivM (TC 3.A.1.4.1) |
| SCE1572_10300 | Stringent starvation protein B | bi | sce_9612 | 86.59 | Stringent starvation protein B |
| SCE1572_10301 | FIG01089093: hypothetical protein | bi | sce_9611 | 89.72 | FIG01089093: hypothetical protein |
| SCE1572_10302 | protein of unknown function DUF6, transmembrane | bi | sce_9610 | 86.15 | protein of unknown function DUF6, transmembrane |
| SCE1572_10303 | Hemagglutinin/hemolysin-related protein | bi | sce_9609 | 80.87 | Hemagglutinin/hemolysin-related protein |
| SCE1572_10304 | Excinuclease ABC subunit A | bi | sce_9607 | 92.97 | Excinuclease ABC subunit A |
| SCE1572_10305 | Protein serine/threonine phosphatase PrcC, regulation of stationary phase | bi | sce_9606 | 92.28 | Protein serine/threonine phosphatase PrcC, regulation of stationary phase |
| SCE1572_10306 | hypothetical protein, glycine-rich | bi | sce_9605 | 84.46 | hypothetical protein |
| SCE1572_10307 | conserved hypothetical protein | bi | sce_9604 | 86.2 | hypothetical protein |
| SCE1572_10308 | conserved hypothetical outer membrane protein | bi | sce_9603 | 95.71 | outer membrane protein, OmpA/MotB family |
| SCE1572_10309 | Response regulator receiver | bi | sce_9602 | 91.46 | Heavy metal RND efflux outer membrane protein, CzcC family |
| SCE1572_10310 | Methyl-accepting chemotaxis protein | umi | sce_9602 | 50.31 | Heavy metal RND efflux outer membrane protein, CzcC family |
| SCE1572_10311 | hypothetical protein | bi | sce_9601 | 85.13 | hypothetical protein |
| SCE1572_10312 | Prolyl endopeptidase (EC 3.4.21.26) | bi | sce_9600 | 92.25 | Prolyl endopeptidase (EC 3.4.21.26) |
| SCE1572_10313 | hypothetical protein | bi | sce_9007 | 65.69 | hypothetical protein |
| SCE1572_10314 | hypothetical protein | bi | sce_9008 | 73.79 | hypothetical protein |
| SCE1572_10315 | hypothetical protein | bi | sce_9009 | 83.74 | hypothetical protein |
| SCE1572_10316 | hypothetical protein | - | - | 0 | 0 |
| SCE1572_10317 | Methylase of polypeptide chain release factors | bi | sce_9010 | 90.82 | Methylase of polypeptide chain release factors |
| SCE1572_10318 | Phosphomannomutase (EC 5.4.2.8) | bi | sce_9011 | 89.96 | Phosphomannomutase (EC 5.4.2.8) |
| SCE1572_10319 | hypothetical protein | bi | sce_9012 | 79.37 | hypothetical protein |
| SCE1572_10320 | Ribosomal RNA small subunit methyltransferase D (EC 2.1.1.-) | bi | sce_9013 | 92.74 | Ribosomal RNA small subunit methyltransferase D (EC 2.1.1.-) |
| SCE1572_10321 | hypothetical protein | bi | sce_9015 | 91.67 | hypothetical protein |
| SCE1572_10322 | endo-1,4-beta-glucanase | umi | sce_4564 | 67.21 | endo alpha-1,4 polygalactosaminidase precursor |
| SCE1572_10323 | tRNA pseudouridine synthase A (EC 4.2.1.70) | bi | sce_9017 | 89.73 | tRNA pseudouridine synthase A (EC 4.2.1.70) |
| SCE1572_10324 | Peptidase S1, chymotrypsin:PDZ/DHR/GLGF domain | umi | sce_8080 | 39.41 | Serine protease precursor MucD/AlgY associated with sigma factor RpoE |
| SCE1572_10325 | alternate gene name: yzdB | bi | sce_9018 | 90.98 | alternate gene name: yzdB |
| SCE1572_10326 | conserved hypothetical protein | bi | sce_9019 | 78.12 | hypothetical protein |
| SCE1572_10327 | hypothetical protein | umi | sce_506 | 43.02 | FIG01086293: hypothetical protein |
| SCE1572_10328 | FAD-linked oxidoreductase family | - | - | 0 | 0 |
| SCE1572_10329 | metal dependent phosphohydrolase | bi | sce_9020 | 93.41 | RelA/SpoT protein (EC:2.7.6.5) |
| SCE1572_10330 | hypothetical protein | - | - | 0 | 0 |
| SCE1572_10331 | outer membrane protein OmpA | bi | sce_9022 | 84.9 | outer membrane protein OmpA |

| | | | | | |
|---------------|--|-----|-----------|-------|--|
| SCE1572_10332 | internalin, putative | bi | sce_9023 | 90.26 | internalin, putative |
| SCE1572_10333 | hypothetical protein | - | - | 0 | 0 |
| SCE1572_10334 | hypothetical protein | umi | sce_9025 | 76.7 | hypothetical protein |
| SCE1572_10335 | MJ0042 family finger-like domain protein | bi | sce_9025 | 83.82 | hypothetical protein |
| SCE1572_10336 | hypothetical protein | bi | sce_9027 | 84.63 | hypothetical protein |
| SCE1572_10337 | hypothetical protein | - | - | 0 | 0 |
| SCE1572_10338 | protein of unknown function DUF11 | bi | sce_1108 | 89.24 | hypothetical protein |
| SCE1572_10339 | response regulator receiver protein | bi | sce_9029 | 89.86 | response regulator receiver protein |
| SCE1572_10340 | FIG01086268: hypothetical protein | bi | sce_9030 | 82.36 | FIG01086268: hypothetical protein |
| SCE1572_10341 | DSBA oxidoreductase | bi | sce_9031 | 79.03 | thiol:disulfide interchange protein |
| SCE1572_10342 | transcriptional regulator, SARP family | bi | sce_9032 | 92.2 | transcriptional regulator, SARP family |
| SCE1572_10343 | Transcriptional regulator, LysR family | bi | sce_9033 | 89.51 | Transcriptional regulator, LysR family |
| SCE1572_10344 | Exoglucanase 3 precursor (EC 3.2.1.91) (Exocellobiohydrolase 3) (1,4-beta-cellobiohydrolase 3) | bi | sce_9034 | 65.29 | Exoglucanase 3 precursor (EC 3.2.1.91) (Exocellobiohydrolase 3) (1,4-beta-cellobiohydrolase 3) |
| SCE1572_10345 | Phosphoesterase (EC 3.1.-.-) | bi | sce_9035 | 81.32 | metallophosphoesterase |
| SCE1572_10346 | Putative heat shock protein YegD | bi | sce_9037 | 93.93 | Putative heat shock protein YegD |
| SCE1572_10347 | serine/threonine protein kinase | bi | sce_9038 | 88.54 | serine/threonine protein kinase |
| SCE1572_10348 | Catalase (EC 1.11.1.6) | umi | sce_2350 | 71.21 | Catalase (EC 1.11.1.6) |
| SCE1572_10349 | hypothetical protein | - | - | 0 | 0 |
| SCE1572_10350 | Nickel transporter UreH | umi | sce_6510 | 39.66 | Nickel transporter UreH |
| SCE1572_10351 | Putative metal chaperone, involved in Zn homeostasis, GTPase of COG0523 family | umi | sce_9219 | 39 | Putative metal chaperone, involved in Zn homeostasis, GTPase of COG0523 family |
| SCE1572_10352 | High-affinity carbon uptake protein Hat/HatR | umi | sce_3016 | 34.37 | High-affinity carbon uptake protein Hat/HatR |
| SCE1572_10353 | hypothetical protein | bi | sce_8066 | 73.68 | Zinc ABC transporter, inner membrane permease protein ZnuB |
| SCE1572_10354 | LSU ribosomal protein L33p | bi | sce_9218 | 89.29 | LSU ribosomal protein L33p |
| SCE1572_10355 | Putative metal chaperone, involved in Zn homeostasis, GTPase of COG0523 family | umi | sce_9219 | 81.23 | Putative metal chaperone, involved in Zn homeostasis, GTPase of COG0523 family |
| SCE1572_10356 | hypothetical protein | - | - | 0 | 0 |
| SCE1572_10357 | putative lipoprotein | - | - | 0 | 0 |
| SCE1572_10358 | hypothetical protein | umi | sce_6522 | 30.58 | hypothetical protein |
| SCE1572_10359 | hypothetical protein | umi | sce_7908 | 30.08 | hypothetical protein |
| SCE1572_10360 | TonB-dependent receptor | umi | sce_6520 | 37.65 | Outer membrane receptor proteins, mostly Fe transport |
| SCE1572_10361 | putative lipoprotein | - | - | 0 | 0 |
| SCE1572_10362 | hypothetical protein | - | - | 0 | 0 |
| SCE1572_10363 | LamG domain protein jellyroll fold domain protein | umi | sce_4576 | 32.5 | Glycine-rich cell wall structural protein 1.8 precursor |
| SCE1572_10364 | hypothetical protein | - | - | 0 | 0 |
| SCE1572_10365 | hypothetical protein | umi | sce_6758 | 34.87 | FIG01086116: hypothetical protein |
| SCE1572_10366 | hypothetical protein | - | - | 0 | 0 |
| SCE1572_10367 | Lead, cadmium, zinc and mercury transporting ATPase (EC 3.6.3.3) (EC 3.6.3.5); Copper-translocating P-type ATPase (EC 3.6.3.4) | umi | sce_4494 | 69.28 | Lead, cadmium, zinc and mercury transporting ATPase (EC 3.6.3.3) (EC 3.6.3.5); Copper-translocating P-type ATPase (EC 3.6.3.4) |
| SCE1572_10368 | Ferredoxin | bi | sce_9055 | 81.68 | Ferredoxin |
| SCE1572_10369 | Cobalt-zinc-cadmium resistance protein CzcA; Cation efflux system protein CusA | bi | sce_9056 | 95.15 | Cobalt-zinc-cadmium resistance protein CzcA; Cation efflux system protein CusA |
| SCE1572_10370 | Probable Co/Zn/Cd efflux system membrane fusion protein | bi | sce_9057 | 93.49 | Probable Co/Zn/Cd efflux system membrane fusion protein |
| SCE1572_10371 | Heavy metal RND efflux outer membrane protein, CzcC family | bi | sce_9058 | 92.79 | Heavy metal RND efflux outer membrane protein, CzcC family |
| SCE1572_10372 | Protein of unknown function DUF305 | bi | sce_9059 | 87.43 | Protein of unknown function DUF305 |
| SCE1572_10373 | Multicopper oxidase | bi | sce_9061 | 95.5 | Multicopper oxidase |
| SCE1572_10374 | Hypothetical protein | bi | sce_9062 | 88.61 | Hypothetical protein |
| SCE1572_10375 | Transcriptional regulator, TetR family | bi | sce_9065 | 91.55 | transcriptional regulator, TetR family |
| SCE1572_10376 | sterol desaturase-like protein | bi | sce_9066 | 95.33 | sterol desaturase-like protein |
| SCE1572_10377 | MI1645 protein | - | - | 0 | 0 |
| SCE1572_10378 | Lead, cadmium, zinc and mercury transporting ATPase (EC 3.6.3.3) (EC 3.6.3.5); Copper-translocating P-type ATPase (EC 3.6.3.4) | bi | sce_9067 | 91.02 | Lead, cadmium, zinc and mercury transporting ATPase (EC 3.6.3.3) (EC 3.6.3.5); Copper-translocating P-type ATPase (EC 3.6.3.4) |
| SCE1572_10379 | hypothetical protein | - | - | 0 | 0 |
| SCE1572_10380 | Response regulator of zinc sigma-54-dependent two-component system | bi | sce_9069 | 97.03 | Response regulator of zinc sigma-54-dependent two-component system |
| SCE1572_10381 | Sensor histidine kinase | bi | sce_9070 | 91.57 | Sensor histidine kinase |
| SCE1572_10382 | FIG01087616: hypothetical protein | bi | sce_9071 | 91.81 | FIG01087616: hypothetical protein |
| SCE1572_10383 | Heavy metal RND efflux outer membrane protein, CzcC family | bi | sce_9072 | 90.76 | Heavy metal RND efflux outer membrane protein, CzcC family |
| SCE1572_10384 | hypothetical protein | bi | sce_9073 | 94.84 | hypothetical protein |
| SCE1572_10385 | COG0845: Membrane-fusion protein | bi | sce_9074 | 92.91 | COG0845: Membrane-fusion protein |
| SCE1572_10386 | Cobalt-zinc-cadmium resistance protein CzcA; Cation efflux system protein CusA | bi | sce_9075 | 96.61 | Cobalt-zinc-cadmium resistance protein CzcA; Cation efflux system protein CusA |
| SCE1572_10387 | CBS domain containing protein | umi | sce_2797 | 64.43 | CBS domain containing protein |
| SCE1572_10388 | hypothetical protein | - | - | 0 | 0 |
| SCE1572_10389 | Type I restriction-modification system, specificity subunit S (EC 3.1.21.3) | - | - | 0 | 0 |
| SCE1572_10390 | Type I restriction-modification system, DNA-methyltransferase subunit M (EC 2.1.1.72) | umi | sce_6179 | 24.27 | Type I restriction-modification system, DNA-methyltransferase subunit M (EC 2.1.1.72) |
| SCE1572_10391 | Glucose/mannose:H symporter GlcP | bi | sce_9046 | 90.45 | Glucose/mannose:H symporter GlcP |
| SCE1572_10392 | LysE-family efflux protein | bi | sce_2299 | 32.34 | Lysine exporter protein (LYSE/YGGA) |
| SCE1572_10393 | Alpha-L-arabinofuranosidase II precursor (EC 3.2.1.55) | bi | sce_3027 | 83.48 | Alpha-L-arabinofuranosidase II precursor (EC 3.2.1.55) |
| SCE1572_10394 | hypothetical protein | bi | sce_9047 | 73.81 | hypothetical protein |
| SCE1572_10395 | hypothetical protein | - | - | 0 | 0 |
| SCE1572_10396 | Erythromycin esterase | umi | sce_10090 | 42.27 | Hydrolases of the alpha/beta superfamily |
| SCE1572_10397 | Fumarylacetoacetate hydrolase family protein | bi | sce_9216 | 91.32 | Fumarylacetoacetate hydrolase family protein |
| SCE1572_10398 | Ketoglutarate semialdehyde dehydrogenase (EC 1.2.1.26) | bi | sce_9215 | 92.02 | Ketoglutarate semialdehyde dehydrogenase (EC 1.2.1.26) |
| SCE1572_10399 | Dihydroxy-acid dehydratase (EC 4.2.1.9) | bi | sce_9214 | 95.65 | Dihydroxy-acid dehydratase (EC 4.2.1.9) |
| SCE1572_10400 | Gluconolactonase (EC 3.1.1.17) | bi | sce_9209 | 93.14 | Gluconolactonase (EC 3.1.1.17) |
| SCE1572_10401 | hypothetical protein | umi | sce_5580 | 33.68 | Uncharacterized protein ImpA |
| SCE1572_10402 | conserved hypothetical protein, secreted | umi | sce_2173 | 26.28 | FIG01089269: hypothetical protein |
| SCE1572_10403 | hypothetical protein | - | - | 0 | 0 |
| SCE1572_10404 | Na-Ca exchanger/integrin-beta4 | umi | sce_3180 | 43.33 | FIG01089285: hypothetical protein |
| SCE1572_10405 | collagen triple helix repeat protein | umi | sce_2684 | 55.97 | Phage tail fiber protein |
| SCE1572_10406 | hypothetical protein | - | - | 0 | 0 |
| SCE1572_10407 | hypothetical protein | - | - | 0 | 0 |
| SCE1572_10408 | hypothetical protein | - | - | 0 | 0 |
| SCE1572_10409 | hypothetical protein | - | - | 0 | 0 |
| SCE1572_10410 | hypothetical protein | umi | sce_2694 | 47.44 | RNA-binding region RNP-1 (RNA recognition motif) |
| SCE1572_10411 | hypothetical protein | - | - | 0 | 0 |
| SCE1572_10412 | hypothetical protein | - | - | 0 | 0 |
| SCE1572_10413 | hypothetical protein | - | - | 0 | 0 |
| SCE1572_10414 | hypothetical protein | umi | sce_304 | 26.23 | VgrG protein |
| SCE1572_10415 | hypothetical protein | - | - | 0 | 0 |
| SCE1572_10416 | hypothetical protein | umi | sce_6493 | 33.49 | Translation initiation factor 2 |
| SCE1572_10417 | hypothetical protein | - | - | 0 | 0 |
| SCE1572_10418 | hypothetical protein | - | - | 0 | 0 |
| SCE1572_10419 | hypothetical protein | - | - | 0 | 0 |
| SCE1572_10420 | Phage minor tail protein | umi | sce_2319 | 21.87 | Phage tail sheath protein F1 |
| SCE1572_10421 | hypothetical protein | - | - | 0 | 0 |
| SCE1572_10422 | hypothetical protein | umi | sce_921 | 21.41 | omega-3 polyunsaturated fatty acid synthase subunit, PfaA |
| SCE1572_10423 | hypothetical protein | - | - | 0 | 0 |
| SCE1572_10424 | hypothetical protein | - | - | 0 | 0 |
| SCE1572_10425 | hypothetical protein | - | - | 0 | 0 |
| SCE1572_10426 | hypothetical protein | umi | sce_10308 | 45.83 | Ferredoxin, 2Fe-2S |
| SCE1572_10427 | hypothetical protein | - | - | 0 | 0 |
| SCE1572_10428 | hypothetical protein | - | - | 0 | 0 |
| SCE1572_10429 | hypothetical protein | - | - | 0 | 0 |
| SCE1572_10430 | hypothetical protein | - | - | 0 | 0 |
| SCE1572_10431 | hypothetical protein | bi | sce_5028 | 28.17 | conserved hypothetical protein, putative DNA helicase |
| SCE1572_10432 | hypothetical protein | - | - | 0 | 0 |
| SCE1572_10433 | hypothetical protein | - | - | 0 | 0 |
| SCE1572_10434 | WD-40 repeat protein | umi | sce_9769 | 28.45 | serine/threonine protein kinase |
| SCE1572_10435 | Murein endopeptidase | bi | sce_9076 | 84.07 | Murein endopeptidase |
| SCE1572_10436 | Exodeoxyribonuclease III (EC 3.1.11.2) | bi | sce_9077 | 92.94 | Exodeoxyribonuclease III (EC 3.1.11.2) |
| SCE1572_10437 | contains Interpro entry IPR000379 / expressed protein | bi | sce_9078 | 87.21 | contains Interpro entry IPR000379 / expressed protein |
| SCE1572_10438 | hypothetical protein | bi | sce_9079 | 62.86 | hypothetical protein |
| SCE1572_10439 | Two-component response regulator | bi | sce_9080 | 100 | Two-component response regulator |
| SCE1572_10440 | hypothetical protein | - | - | 0 | 0 |
| SCE1572_10441 | Two-component response regulator | bi | sce_9082 | 86.23 | Two-component response regulator |
| SCE1572_10442 | Maltose phosphorylase (EC 2.4.1.8) / Trehalose phosphorylase (EC 2.4.1.64) | bi | sce_9083 | 82.9 | Maltose phosphorylase (EC 2.4.1.8) / Trehalose phosphorylase (EC 2.4.1.64) |
| SCE1572_10443 | FIG01088575: hypothetical protein | bi | sce_9084 | 71.21 | FIG01088575: hypothetical protein |
| SCE1572_10444 | ATP-dependent protease La (EC 3.4.21.53) Type II | bi | sce_9085 | 96.06 | ATP-dependent protease La (EC 3.4.21.53) Type II |
| SCE1572_10445 | hypothetical protein | - | - | 0 | 0 |
| SCE1572_10446 | hypothetical protein | bi | sce_9086 | 74.48 | hypothetical protein |
| SCE1572_10447 | PAS/PAC sensor signal transduction histidine kinase | bi | sce_9087 | 93.46 | PAS/PAC sensor signal transduction histidine kinase |
| SCE1572_10448 | FIG01086305: hypothetical protein | bi | sce_9088 | 93.06 | FIG01086305: hypothetical protein |
| SCE1572_10449 | COG0028: Thiamine pyrophosphate-requiring enzymes | bi | sce_9089 | 95.21 | COG0028: Thiamine pyrophosphate-requiring enzymes |
| SCE1572_10450 | hypothetical protein | - | - | 0 | 0 |
| SCE1572_10451 | hypothetical protein | bi | sce_9093 | 90 | hypothetical protein |
| SCE1572_10452 | Urea ABC transporter, permease protein UrtC | bi | sce_9094 | 68.21 | hypothetical protein |
| SCE1572_10453 | Cysteine desulfurase (EC 2.8.1.7) | bi | sce_9095 | 87.44 | Cysteine desulfurase (EC 2.8.1.7) |
| SCE1572_10454 | hypothetical protein | - | - | 0 | 0 |
| SCE1572_10455 | Putative membrane protein precursor | bi | sce_9096 | 77.71 | Putative membrane protein precursor |
| SCE1572_10456 | hypothetical protein | bi | sce_9097 | 82.35 | FIG01089086: hypothetical protein |
| SCE1572_10457 | hypothetical protein | - | - | 0 | 0 |
| SCE1572_10458 | hypothetical protein | - | - | 0 | 0 |
| SCE1572_10459 | Universal stress protein family | bi | sce_9098 | 89.93 | Universal stress protein family |
| SCE1572_10460 | hypothetical protein | bi | sce_9099 | 88.53 | hypothetical protein |
| SCE1572_10461 | periplasmic sensor signal transduction histidine kinase | bi | sce_9100 | 92.32 | integral membrane sensor signal transduction histidine kinase |
| SCE1572_10462 | Seryl-tRNA synthetase (EC 6.1.1.11) | bi | sce_9101 | 94 | Seryl-tRNA synthetase (EC 6.1.1.11) |
| SCE1572_10463 | Aconitate hydratase (EC 4.2.1.3) | bi | sce_9102 | 95.42 | Aconitate hydratase (EC 4.2.1.3) |
| SCE1572_10464 | Gli2498 protein | bi | sce_9103 | 77.32 | Gli2498 protein |
| SCE1572_10465 | Regulator of cell morphogenesis and NO signaling | bi | sce_9104 | 76.32 | hypothetical protein |
| SCE1572_10466 | sulfatase | bi | sce_9105 | 89.45 | hypothetical protein |
| SCE1572_10467 | hypothetical protein | - | - | 0 | 0 |
| SCE1572_10468 | hypothetical protein | - | - | 0 | 0 |
| SCE1572_10469 | FIG01088596: hypothetical protein | bi | sce_9115 | 89.04 | FIG01088596: hypothetical protein |
| SCE1572_10470 | FIG01085488: hypothetical protein | - | - | 0 | 0 |
| SCE1572_10471 | FIG01085488: hypothetical protein | bi | sce_9116 | 79.15 | FIG01085488: hypothetical protein |
| SCE1572_10472 | 3-isopropylmalate dehydrogenase (EC 1.1.1.85) | bi | sce_9117 | 96.14 | 3-isopropylmalate dehydrogenase (EC 1.1.1.85) |
| SCE1572_10473 | Alanine dehydrogenase (EC 1.4.1.1) | bi | sce_9118 | 94.32 | Alanine dehydrogenase (EC 1.4.1.1) |
| SCE1572_10474 | FIG01087650: hypothetical protein | bi | sce_9119 | 84.87 | FIG01087650: hypothetical protein |
| SCE1572_10475 | response regulator/GGDEF/GAF domain protein | bi | sce_9120 | 89.49 | response regulator/GGDEF/GAF domain protein |
| SCE1572_10476 | Diaminopimelate epimerase (EC 5.1.1.7) | bi | sce_9121 | 93.28 | Diaminopimelate epimerase (EC 5.1.1.7) |
| SCE1572_10477 | UPF0235 protein CT1832 | bi | sce_9122 | 91.96 | UPF0235 protein CT1832 |
| SCE1572_10478 | FIG01089150: hypothetical protein | bi | sce_9123 | 71.43 | FIG01089150: hypothetical protein |
| SCE1572_10479 | FIG01088827: hypothetical protein | bi | sce_9124 | 79.49 | FIG01088827: hypothetical protein |
| SCE1572_10480 | FIG01084956: hypothetical protein | bi | sce_9125 | 91.18 | FIG01084956: hypothetical protein |
| SCE1572_10481 | 8-amino-7-oxononanoate synthase (EC 2.3.1.47) | bi | sce_9126 | 83.25 | 8-amino-7-oxononanoate synthase (EC 2.3.1.47) |
| SCE1572_10482 | Dethiobiotin synthetase (EC 6.3.3.3) | bi | sce_9127 | 81.07 | Dethiobiotin synthetase (EC 6.3.3.3) |
| SCE1572_10483 | ABC transporter involved in cytochrome c biogenesis, ATPase component CcmA | bi | sce_9128 | 88.53 | ABC transporter involved in cytochrome c biogenesis, ATPase component CcmA |
| SCE1572_10484 | serine/threonine protein kinase | bi | sce_9129 | 68.94 | serine/threonine protein kinase |
| SCE1572_10485 | DNA polymerase III beta subunit (EC 2.7.7.7) | bi | sce_9130 | 97.87 | DNA polymerase III beta subunit (EC 2.7.7.7) |
| SCE1572_10486 | DNA recombination and repair protein RecF | bi | sce_9131 | 90.58 | DNA recombination and repair protein RecF |
| SCE1572_10487 | DNA gyrase subunit B (EC 5.99.1.3) | bi | sce_9133 | 96.36 | DNA gyrase subunit B (EC 5.99.1.3) |
| SCE1572_10488 | ClpB protein | bi | sce_9135 | 97.12 | ClpB protein |
| SCE1572_10489 | Molybdopter binding motif, ClnA N-terminal domain / C-terminal domain of ClnA type S | bi | sce_9136 | 94.92 | Molybdopter binding motif, ClnA N-terminal domain / C-terminal domain of ClnA type S |
| SCE1572_10490 | hypothetical protein | bi | sce_9137 | 84.27 | hypothetical protein |
| SCE1572_10491 | putative Fe-S oxidoreductase | bi | sce_9139 | 84.32 | hypothetical protein |
| SCE1572_10492 | putative cytochrome c biogenesis protein | bi | sce_9140 | 87.83 | putative cytochrome c biogenesis protein |
| SCE1572_10493 | Cytochrome c heme lyase subunit CcmF | bi | sce_9141 | 92.9 | Cytochrome c heme lyase subunit CcmF |
| SCE1572_10494 | 2-isopropylmalate synthase (EC 2.3.3.13) | bi | sce_9142 | 94.76 | 2-isopropylmalate synthase (EC 2.3.3.13) |
| SCE1572_10495 | hypothetical protein | bi | sce_9143 | 93.13 | hypothetical protein |

| | | | | | |
|---------------|---|-----|----------|-------|--|
| SCE1572_10496 | hypothetical protein | bi | sce_9144 | 89.23 | hypothetical protein |
| SCE1572_10497 | FIG01088467: hypothetical protein | bi | sce_9145 | 92.03 | FIG01088467: hypothetical protein |
| SCE1572_10498 | FIG01086588: hypothetical protein | bi | sce_9146 | 85.25 | FIG01086588: hypothetical protein |
| SCE1572_10499 | 4-hydroxybenzoyl-CoA thioesterase family active site | bi | sce_9147 | 92.36 | 4-hydroxybenzoyl-CoA thioesterase family active site |
| SCE1572_10500 | Hyoxanthine-guanine phosphoribosyltransferase (EC 2.4.2.8) | bi | sce_9148 | 96.53 | Hyoxanthine-guanine phosphoribosyltransferase (EC 2.4.2.8) |
| SCE1572_10501 | hypothetical protein | bi | sce_9149 | 90.57 | hypothetical protein |
| SCE1572_10502 | Holliday junction DNA helicase RuvB | bi | sce_9150 | 95.86 | Holliday junction DNA helicase RuvB |
| SCE1572_10503 | hypothetical protein | bi | sce_9151 | 87.56 | Redoxin domain protein |
| SCE1572_10504 | Hypothetical protein YggS, proline synthase co-transcribed bacterial homolog PROSC | bi | sce_9152 | 90.09 | Hypothetical protein YggS, proline synthase co-transcribed bacterial homolog PROSC |
| SCE1572_10505 | Glycyl-tRNA synthetase beta chain (EC 6.1.1.14) | uni | sce_5518 | 37.93 | NAD(P)HX epimerase / NAD(P)HX dehydratase |
| SCE1572_10506 | FIG01086900: hypothetical protein | bi | sce_1495 | 77.78 | Collagen triple helix repeat |
| SCE1572_10507 | Conserved Hypothetical protein; putative cAMP-binding protein | bi | sce_9156 | 92.22 | Conserved Hypothetical protein; putative cAMP-binding protein |
| SCE1572_10508 | GCNS-related N-acetyltransferase | bi | sce_9157 | 99.31 | COG0454: Histone acetyltransferase HPA2 and related acetyltransferases |
| SCE1572_10509 | Ribulose-phosphate 3-epimerase (EC 5.1.3.1) | bi | sce_9159 | 85.45 | Ribulose-phosphate 3-epimerase (EC 5.1.3.1) |
| SCE1572_10510 | FIG01088789: hypothetical protein | bi | sce_9160 | 84.52 | FIG01088789: hypothetical protein |
| SCE1572_10511 | hypothetical protein | - | - | 0 | |
| SCE1572_10512 | hypothetical protein | - | - | 0 | |
| SCE1572_10513 | hypothetical protein | - | - | 0 | |
| SCE1572_10514 | FIG01089091: hypothetical protein | uni | sce_8996 | 91.28 | FIG01089091: hypothetical protein |
| SCE1572_10515 | hypothetical protein | - | - | 0 | |
| SCE1572_10516 | EBNA-1 | uni | sce_2045 | 31.34 | Mlr6568 protein |
| SCE1572_10517 | hypothetical protein | - | - | 0 | |
| SCE1572_10518 | hypothetical protein | bi | sce_2335 | 25.32 | FIG01086312: hypothetical protein |
| SCE1572_10519 | hypothetical protein | uni | sce_7454 | 28.97 | FIG01089015: hypothetical protein |
| SCE1572_10520 | hypothetical protein | bi | sce_2333 | 34.2 | FIG00500935: hypothetical protein |
| SCE1572_10521 | hypothetical protein | bi | sce_2332 | 30.86 | hypothetical protein |
| SCE1572_10522 | hypothetical protein | bi | sce_2331 | 42.2 | hypothetical protein |
| SCE1572_10523 | hypothetical protein | uni | sce_9938 | 37.38 | EBNA-1 |
| SCE1572_10524 | hypothetical protein | uni | sce_2329 | 39.68 | VgrG protein |
| SCE1572_10525 | hypothetical protein | uni | sce_2328 | 29.41 | hypothetical protein |
| SCE1572_10526 | hypothetical protein | bi | sce_2327 | 37.89 | hypothetical protein |
| SCE1572_10527 | conserved hypothetical protein; putative signal peptide | bi | sce_2326 | 32.43 | conserved hypothetical protein; putative signal peptide |
| SCE1572_10528 | hypothetical protein | - | - | 0 | |
| SCE1572_10529 | ATPase, AAA family | uni | sce_2324 | 36.54 | ATPase, AAA family |
| SCE1572_10530 | hypothetical protein | - | - | 0 | |
| SCE1572_10531 | ZK84.1 | uni | sce_6493 | 34.04 | Translation initiation factor 2 |
| SCE1572_10532 | hypothetical protein | - | - | 0 | |
| SCE1572_10533 | hypothetical protein | bi | sce_2321 | 32.3 | hypothetical protein |
| SCE1572_10534 | FIG01131549: hypothetical protein | bi | sce_2320 | 58.68 | FIG01131549: hypothetical protein |
| SCE1572_10535 | Phage tail sheath protein F1 | bi | sce_2319 | 55.92 | Phage tail sheath protein F1 |
| SCE1572_10536 | hypothetical protein | - | - | 0 | |
| SCE1572_10537 | hypothetical protein | - | - | 0 | |
| SCE1572_10538 | hypothetical protein | - | - | 0 | |
| SCE1572_10539 | Two Component, Sigma-54 Specific, Transcriptional Regulator, Fis family | uni | sce_7436 | 46.78 | Nif-specific regulatory protein |
| SCE1572_10540 | hypothetical protein | - | - | 0 | |
| SCE1572_10541 | stringent starvation protein B | - | - | 0 | |
| SCE1572_10542 | hypothetical protein | - | - | 0 | |
| SCE1572_10543 | hypothetical protein | - | - | 0 | |
| SCE1572_10544 | hypothetical protein | - | - | 0 | |
| SCE1572_10545 | DNA repair protein RadC | uni | sce_7263 | 40.78 | DNA repair protein RadC |
| SCE1572_10546 | hypothetical protein | - | - | 0 | |
| SCE1572_10547 | hypothetical protein | - | - | 0 | |
| SCE1572_10548 | MoxR-like ATPase | uni | sce_4297 | 31.77 | Putative 2-component regulator |
| SCE1572_10549 | VWA containing CoxE-like | - | - | 0 | |
| SCE1572_10550 | conserved hypothetical protein | - | - | 0 | |
| SCE1572_10551 | hypothetical protein | uni | sce_163 | 48.78 | FIG01087636: hypothetical protein |
| SCE1572_10552 | hypothetical protein | - | - | 0 | |
| SCE1572_10553 | hypothetical protein | - | - | 0 | |
| SCE1572_10554 | RecA protein | uni | sce_2947 | 75.61 | RecA protein |
| SCE1572_10555 | SMC domain protein | uni | sce_6864 | 48.98 | RecF/RecN/SMC N terminal domain, putative |
| SCE1572_10556 | hypothetical protein | - | - | 0 | |
| SCE1572_10557 | MG(2) CHELATASE FAMILY PROTEIN / ComM-related protein | uni | sce_2946 | 55.66 | MG(2) CHELATASE FAMILY PROTEIN / ComM-related protein |
| SCE1572_10558 | hypothetical protein | - | - | 0 | |
| SCE1572_10559 | hypothetical protein | - | - | 0 | |
| SCE1572_10560 | hypothetical protein | - | - | 0 | |
| SCE1572_10561 | hypothetical protein | - | - | 0 | |
| SCE1572_10562 | hypothetical protein | - | - | 0 | |
| SCE1572_10563 | HYPOTHETICAL PROTEIN | - | - | 0 | |
| SCE1572_10564 | hypothetical protein | bi | sce_9181 | 40.24 | FIG00970516: hypothetical protein |
| SCE1572_10565 | conserved hypothetical protein | bi | sce_9180 | 29.6 | FIG01089090: hypothetical protein |
| SCE1572_10566 | Cardiolipin synthase (EC 2.7.8.-) | bi | sce_9179 | 40.1 | hypothetical membrane associated protein |
| SCE1572_10567 | Response regulator of zinc sigma-54-dependent two-component system | bi | sce_9178 | 39.83 | Response regulator of zinc sigma-54-dependent two-component system |
| SCE1572_10568 | Type I restriction-modification system, DNA-methyltransferase subunit M (EC 2.1.1.72) | uni | sce_6179 | 30.94 | Type I restriction-modification system, DNA-methyltransferase subunit M (EC 2.1.1.72) |
| SCE1572_10569 | Type I restriction-modification system, specificity subunit S (EC 3.1.21.3) | - | - | 0 | |
| SCE1572_10570 | Putative DNA-binding protein in cluster with Type I restriction-modification system | - | - | 0 | |
| SCE1572_10571 | Type I restriction-modification system, restriction subunit R (EC 3.1.21.3) | - | - | 0 | |
| SCE1572_10572 | Putative predicted metal-dependent hydrolase | - | - | 0 | |
| SCE1572_10573 | hypothetical protein | - | - | 0 | |
| SCE1572_10574 | hypothetical protein | - | - | 0 | |
| SCE1572_10575 | hypothetical protein | - | - | 0 | |
| SCE1572_10576 | DNA polymerase I (EC 2.7.7.7) | uni | sce_9687 | 30.1 | DNA polymerase I (EC 2.7.7.7) |
| SCE1572_10577 | hypothetical protein | - | - | 0 | |
| SCE1572_10578 | hypothetical protein | - | - | 0 | |
| SCE1572_10579 | hypothetical protein | - | - | 0 | |
| SCE1572_10580 | hypothetical protein | - | - | 0 | |
| SCE1572_10581 | hypothetical protein | - | - | 0 | |
| SCE1572_10582 | hypothetical protein | - | - | 0 | |
| SCE1572_10583 | hypothetical protein | - | - | 0 | |
| SCE1572_10584 | phage integrase family protein | uni | sce_7521 | 26.36 | FIG01087954: hypothetical protein |
| SCE1572_10585 | hypothetical protein | bi | sce_3805 | 98.84 | hypothetical protein |
| SCE1572_10586 | FIG01089646: hypothetical protein | bi | sce_3806 | 97.5 | FIG01089646: hypothetical protein |
| SCE1572_10587 | hypothetical protein | uni | sce_6225 | 61.25 | hypothetical protein |
| SCE1572_10588 | hypothetical protein | uni | sce_6227 | 43.61 | hypothetical protein |
| SCE1572_10589 | hypothetical protein | - | - | 0 | |
| SCE1572_10590 | hypothetical protein | - | - | 0 | |
| SCE1572_10591 | ATPase associated with various cellular activities, AAA_5 | uni | sce_3642 | 28.57 | 5-methylcytosine-specific restriction related enzyme |
| SCE1572_10592 | helicase, DEAD/DEAH family | uni | sce_9165 | 91 | helicase, DEAD/DEAH family |
| SCE1572_10593 | hypothetical protein | - | - | 0 | |
| SCE1572_10594 | Cellulose-binding domain protein | bi | sce_7746 | 78.57 | Cellulose-binding domain protein |
| SCE1572_10595 | FIG01087231: hypothetical protein | bi | sce_7745 | 85.64 | FIG01087231: hypothetical protein |
| SCE1572_10596 | FIG01087070: hypothetical protein | bi | sce_7744 | 85.21 | FIG01087070: hypothetical protein |
| SCE1572_10597 | hypothetical protein | bi | sce_7743 | 67.31 | hypothetical protein |
| SCE1572_10598 | hypothetical protein | - | - | 0 | |
| SCE1572_10599 | drug resistance transporter, EmrB/QacA subfamily | bi | sce_1251 | 35 | drug resistance transporter, EmrB/QacA family |
| SCE1572_10600 | Coenzyme PQQ synthesis protein E | bi | sce_7488 | 35.16 | Coenzyme PQQ synthesis protein E (Pyrroloquinoline quinone biosynthesis protein E) |
| SCE1572_10601 | Coenzyme PQQ synthesis protein C | - | - | 0 | |
| SCE1572_10602 | Coenzyme PQQ synthesis protein B | - | - | 0 | |
| SCE1572_10603 | hypothetical protein | - | - | 0 | |
| SCE1572_10604 | Putative metal chaperone, involved in Zn homeostasis, GTPase of COG0523 family | bi | sce_9219 | 88.94 | Putative metal chaperone, involved in Zn homeostasis, GTPase of COG0523 family |
| SCE1572_10605 | hypothetical protein | - | - | 0 | |
| SCE1572_10606 | Na ⁺ /multidrug efflux protein | uni | sce_4895 | 29.53 | MATE efflux family protein |
| SCE1572_10607 | Transcriptional regulator, TetR family | bi | sce_9220 | 85.17 | Transcriptional regulator, TetR family |
| SCE1572_10608 | Probable Co/Zn/Cd efflux system membrane fusion protein | bi | sce_9221 | 83.15 | Probable Co/Zn/Cd efflux system membrane fusion protein |
| SCE1572_10609 | Acriflavin resistance protein | bi | sce_9222 | 91.85 | Acriflavin resistance protein |
| SCE1572_10610 | Heavy metal transport/detoxification protein | bi | sce_9042 | 84.72 | mercury ion binding protein |
| SCE1572_10611 | hypothetical protein | - | - | 0 | |
| SCE1572_10612 | hypothetical protein | - | - | 0 | |
| SCE1572_10613 | Transcriptional regulator, LysR family | uni | sce_3645 | 50.34 | Transcriptional regulator, LysR family |
| SCE1572_10614 | hypothetical protein | uni | sce_6854 | 44.38 | hypothetical protein |
| SCE1572_10615 | hypothetical protein | bi | sce_9224 | 77.52 | hypothetical protein |
| SCE1572_10616 | DNA-directed RNA polymerase specialized sigma subunit, sigma24-like | bi | sce_9225 | 83.56 | DNA-directed RNA polymerase specialized sigma subunit, sigma24-like |
| SCE1572_10617 | hypothetical protein | - | - | 0 | |
| SCE1572_10618 | FIG01086053: hypothetical protein | uni | sce_9398 | 84.62 | FIG01086053: hypothetical protein |
| SCE1572_10619 | hypothetical protein | uni | sce_7426 | 24.8 | jmjC domain protein |
| SCE1572_10620 | 2,4-diaminobutyrate 4-transaminase(EC:2.6.1.76) | bi | sce_9228 | 86.67 | Pyoverdinin biosynthesis protein PvdH, L-2,4-diaminobutyrate:2-oxoglutarate aminotransferase (EC 2.6.1.76) |
| SCE1572_10621 | non-ribosomal peptide synthetase | bi | sce_9229 | 81.31 | FIG01085400: hypothetical protein |
| SCE1572_10622 | Long-chain-fatty-acid-CoA ligase (EC 6.2.1.3) | bi | sce_9230 | 53.65 | Long-chain-fatty-acid-CoA ligase (EC 6.2.1.3) |
| SCE1572_10623 | Long-chain-fatty-acid-CoA ligase (EC 6.2.1.3) | bi | sce_9231 | 73.65 | Long-chain-fatty-acid-CoA ligase (EC 6.2.1.3) |
| SCE1572_10624 | syfP protein, putative | bi | sce_9232 | 80.18 | syfP protein, putative |
| SCE1572_10625 | Hypothetical MbtH-like protein, PA2412 homolog | bi | sce_9233 | 88 | Hypothetical MbtH-like protein, PA2412 homolog |
| SCE1572_10626 | Penicillin acylase II (EC 3.5.1.11) | bi | sce_9234 | 78.18 | Penicillin acylase II (EC 3.5.1.11) |
| SCE1572_10627 | COG4615: ABC-type siderophore export system, fused ATPase and permease components | bi | sce_9235 | 80.14 | putative ABC transporter (ATP-binding protein) |
| SCE1572_10628 | Malonyl CoA-acyl carrier protein transacylase (EC 2.3.1.39) | bi | sce_9236 | 79.96 | Malonyl CoA-acyl carrier protein transacylase (EC 2.3.1.39) |
| SCE1572_10629 | Long-chain-fatty-acid-CoA ligase (EC 6.2.1.3) | bi | sce_9237 | 81.73 | Long-chain-fatty-acid-CoA ligase (EC 6.2.1.3) |
| SCE1572_10630 | hypothetical protein | - | - | 0 | |
| SCE1572_10631 | hypothetical protein | - | - | 0 | |
| SCE1572_10632 | hypothetical protein | - | - | 0 | |
| SCE1572_10633 | putative iron-regulated membrane protein | bi | sce_9240 | 83.24 | FIG138928: iron-regulated membrane protein |
| SCE1572_10634 | TomB-dependent receptor | bi | sce_9238 | 75.44 | TomB-dependent receptor |
| SCE1572_10635 | FIG01089420: hypothetical protein | bi | sce_9239 | 83.06 | FIG01089420: hypothetical protein |
| SCE1572_10636 | putative iron-regulated membrane protein | - | - | 0 | |
| SCE1572_10637 | hypothetical protein | bi | sce_9241 | 73.04 | hypothetical protein |
| SCE1572_10638 | hypothetical protein | bi | sce_9242 | 73.91 | hypothetical protein |
| SCE1572_10639 | Two-component response regulator | bi | sce_9244 | 95.35 | Two-component response regulator |
| SCE1572_10640 | Aspartyl-tRNA synthetase (EC 6.1.1.12) | bi | sce_9245 | 94.92 | Aspartyl-tRNA synthetase (EC 6.1.1.12) |
| SCE1572_10641 | Glycoprotein gp2 | bi | sce_9246 | 86.03 | Glycoprotein gp2 |
| SCE1572_10642 | FIG001454: Transglutaminase-like enzymes, putative cysteine proteases | bi | sce_9247 | 91.71 | FIG001454: Transglutaminase-like enzymes, putative cysteine proteases |
| SCE1572_10643 | FIG002343: hypothetical protein | bi | sce_9248 | 90 | FIG002343: hypothetical protein |
| SCE1572_10644 | FIG022979: MoxR-like ATPases | bi | sce_9249 | 98.75 | FIG022979: MoxR-like ATPases |
| SCE1572_10645 | hypothetical protein | bi | sce_9250 | 92.68 | integral membrane protein |
| SCE1572_10646 | FIG01085681: hypothetical protein | bi | sce_9251 | 93.13 | FIG01085681: hypothetical protein |
| SCE1572_10647 | ADP-ribose pyrophosphatase (EC 3.6.1.13) homolog | bi | sce_9252 | 89.95 | ADP-ribose pyrophosphatase (EC 3.6.1.13) homolog |
| SCE1572_10648 | NAD kinase (EC 2.7.1.23) | bi | sce_9253 | 89.84 | NAD kinase (EC 2.7.1.23) |
| SCE1572_10649 | hypothetical protein | uni | sce_3858 | 30.81 | Adenosylhomocysteinase (EC 3.3.1.1) |
| SCE1572_10650 | Histone-like protein | bi | sce_9254 | 98.2 | Histone-like protein |
| SCE1572_10651 | Ubiquinone biosynthesis monooxygenase UbiB | bi | sce_9255 | 93.07 | Ubiquinone biosynthesis monooxygenase UbiB |
| SCE1572_10652 | FIG01088181: hypothetical protein | bi | sce_9256 | 89.24 | FIG01088181: hypothetical protein |
| SCE1572_10653 | Citrate synthase (si) (EC 2.3.3.1) | bi | sce_9257 | 96.3 | Citrate synthase (si) (EC 2.3.3.1) |
| SCE1572_10654 | serine/threonine protein kinase | bi | sce_9258 | 91.5 | serine/threonine protein kinase |
| SCE1572_10655 | hypothetical protein | bi | sce_9259 | 91.78 | hypothetical protein |
| SCE1572_10656 | hypothetical protein | bi | sce_9260 | 84.68 | FIG01087363: hypothetical protein |
| SCE1572_10657 | BNR repeat domain protein | bi | sce_9261 | 86 | BNR repeat domain protein |
| SCE1572_10658 | Prion-like-(Q)-n-rich)-domain-bearing protein protein 54 | bi | sce_9263 | 89.31 | similar to NF-X1 type zinc finger containing protein (2f511) (predicted) |
| SCE1572_10659 | Gamma-glutamyltranspeptidase (EC 2.3.2.2) | bi | sce_9264 | 88.35 | Gamma-glutamyltranspeptidase (EC 2.3.2.2) |

| | | | | |
|---------------|---|-----|-----------|---|
| SCE1572_10660 | Universal stress protein family | bi | see_9265 | 96.06 Universal stress protein family |
| SCE1572_10661 | Adenylosuccinate lyase (EC 4.3.2.2) | bi | see_9266 | 94.43 Adenylosuccinate lyase (EC 4.3.2.2) |
| SCE1572_10662 | Protein of unknown function DUF885 | bi | see_9267 | 87.42 protein of unknown function DUF885 |
| SCE1572_10663 | Transcriptional regulator | bi | see_9271 | 96.67 Transcriptional regulator |
| SCE1572_10664 | Phosphoserine phosphatase (EC 3.1.3.3) | bi | see_9272 | 95.91 Phosphoserine phosphatase (EC 3.1.3.3) |
| SCE1572_10665 | Phosphoadenylyl-sulfate reductase [thioredoxin] (EC 1.8.4.8) / Adenylyl-sulfate reductase [thioredoxin] (EC 1.8.4.10) | bi | see_9273 | 94.12 Phosphoadenylyl-sulfate reductase [thioredoxin] (EC 1.8.4.8) / Adenylyl-sulfate reductase [thioredoxin] (EC 1.8.4.10) |
| SCE1572_10666 | Arsenical pump-driving ATPase (EC 3.6.3.16) | bi | see_9274 | 89.94 Arsenical pump-driving ATPase (EC 3.6.3.16) |
| SCE1572_10667 | Nicotinate phosphoribosyltransferase (EC 2.4.2.11) | bi | see_9275 | 85.57 Nicotinate phosphoribosyltransferase (EC 2.4.2.11) |
| SCE1572_10668 | hypothetical protein | - | - | 0 |
| SCE1572_10669 | ABC-type transport system involved in resistance to organic solvents, permease component | bi | see_9279 | 97.74 ABC-type transport system involved in resistance to organic solvents, permease component |
| SCE1572_10670 | hypothetical protein | - | - | 0 |
| SCE1572_10671 | ATPase YjeE, predicted to have essential role in cell wall biosynthesis | bi | see_9283 | 92.86 ATPase YjeE, predicted to have essential role in cell wall biosynthesis |
| SCE1572_10672 | conserved hypothetical protein SCG11A.16 | bi | see_9284 | 85.49 conserved hypothetical protein SCG11A.16 |
| SCE1572_10673 | Nuclease sbcCD subunit C | bi | see_9285 | 81.76 Nuclease sbcCD subunit C |
| SCE1572_10674 | Succinate dehydrogenase cytochrome b558 subunit | bi | see_9286 | 89.71 Succinate dehydrogenase cytochrome b558 subunit |
| SCE1572_10675 | Succinate dehydrogenase flavoprotein subunit (EC 1.3.99.1) | bi | see_9287 | 95.83 Succinate dehydrogenase flavoprotein subunit (EC 1.3.99.1) |
| SCE1572_10676 | Succinate dehydrogenase iron-sulfur protein (EC 1.3.99.1) | bi | see_9288 | 94.87 Succinate dehydrogenase iron-sulfur protein (EC 1.3.99.1) |
| SCE1572_10677 | FIG01085965: hypothetical protein | bi | see_9289 | 73.94 FIG01085965: hypothetical protein |
| SCE1572_10678 | High-affinity branched-chain amino acid transport system permease protein LivH (TC 3.A.1.4.1) | bi | see_9290 | 96.21 High-affinity branched-chain amino acid transport system permease protein LivH (TC 3.A.1.4.1) |
| SCE1572_10679 | Branched-chain amino acid ABC transporter, amino acid-binding protein (TC 3.A.1.4.1) | bi | see_9291 | 92.71 Branched-chain amino acid ABC transporter, amino acid-binding protein (TC 3.A.1.4.1) |
| SCE1572_10680 | hypothetical protein | - | - | 0 |
| SCE1572_10681 | RNA binding methyltransferase FtsJ like | bi | see_9292 | 95.18 RNA binding methyltransferase FtsJ like |
| SCE1572_10682 | Vitamin B12 ABC transporter, B12-binding component BtuF | bi | see_9293 | 78.43 Vitamin B12 ABC transporter, B12-binding component BtuF |
| SCE1572_10683 | Trypsin-2 precursor (EC 3.4.21.4) | bi | see_9294 | 81.2 Trypsin-2 precursor (EC 3.4.21.4) |
| SCE1572_10684 | hypothetical protein | - | - | 0 |
| SCE1572_10685 | DNA internalization-related competence protein ComEC/Rec2 | bi | see_9295 | 88.42 DNA internalization-related competence protein ComEC/Rec2 |
| SCE1572_10686 | Radical SAM domain protein | bi | see_9296 | 94.56 Radical SAM domain protein |
| SCE1572_10687 | hypothetical protein | bi | see_9297 | 96.34 hypothetical protein |
| SCE1572_10688 | thioredoxin | bi | see_9298 | 89.81 thioredoxin |
| SCE1572_10689 | hypothetical protein | - | - | 0 |
| SCE1572_10690 | conserved hypothetical protein NMA0935 | uni | see_5451 | 32.51 Probable ATP-binding protein NMA0346 |
| SCE1572_10691 | hypothetical protein | - | - | 0 |
| SCE1572_10692 | hypothetical protein | bi | see_9299 | 93.97 hypothetical protein |
| SCE1572_10693 | VgrG protein | bi | see_9300 | 88.41 VgrG protein |
| SCE1572_10694 | hypothetical protein | - | - | 0 |
| SCE1572_10695 | hypothetical protein | bi | see_9306 | 89.62 FIG01088994: hypothetical protein |
| SCE1572_10696 | DUF2242 domain-containing protein | bi | see_9307 | 70.55 Mir2351 protein |
| SCE1572_10697 | FHA domain containing protein | bi | see_9308 | 96.06 FHA domain protein |
| SCE1572_10698 | Signal peptidase I (EC 3.4.21.89) | bi | see_9309 | 85.38 Signal peptidase I (EC 3.4.21.89) |
| SCE1572_10699 | Trypsin-2 precursor (EC 3.4.21.4) | bi | see_9310 | 89.93 Trypsin-2 precursor (EC 3.4.21.4) |
| SCE1572_10700 | hypothetical protein | - | - | 0 |
| SCE1572_10701 | hypothetical protein | - | - | 0 |
| SCE1572_10702 | hypothetical protein | bi | see_9311 | 86.03 hypothetical protein |
| SCE1572_10703 | Glutamate 5-kinase (EC 2.7.2.11) / RNA-binding C-terminal domain PUA | bi | see_9312 | 92.25 Glutamate 5-kinase (EC 2.7.2.11) / RNA-binding C-terminal domain PUA |
| SCE1572_10704 | hypothetical protein | bi | see_9313 | 90 hypothetical protein |
| SCE1572_10705 | hypothetical protein | uni | see_4117 | 36.05 lojap protein |
| SCE1572_10706 | large ATP-binding protein | - | - | 0 |
| SCE1572_10707 | hypothetical protein | - | - | 0 |
| SCE1572_10708 | hypothetical protein | - | - | 0 |
| SCE1572_10709 | hypothetical protein | - | - | 0 |
| SCE1572_10710 | hypothetical protein | bi | see_9505 | 91.89 hypothetical protein |
| SCE1572_10711 | putative ABC transporter ATP-binding protein | bi | see_9314 | 85.08 putative ABC transporter ATP-binding protein |
| SCE1572_10712 | signal peptide peptidase SppA, 67k type | bi | see_9315 | 85.6 peptidase S49, protease IV:Peptidase S49, SppA |
| SCE1572_10713 | hypothetical protein | bi | see_9316 | 93.94 hypothetical protein |
| SCE1572_10714 | hypothetical protein | uni | see_2984 | 26.32 conserved hypothetical protein |
| SCE1572_10715 | hypothetical protein | uni | see_2045 | 43.75 Mlr6568 protein |
| SCE1572_10716 | hypothetical protein | - | - | 0 |
| SCE1572_10717 | FOG: WD40-like repeat | bi | see_9370 | 81.51 FOG: WD40-like repeat |
| SCE1572_10718 | FIG01089663: hypothetical protein | bi | see_9378 | 83.05 FIG01089663: hypothetical protein |
| SCE1572_10719 | FOG: GGDEF domain | bi | see_9379 | 88.39 FOG: GGDEF domain |
| SCE1572_10720 | Functional role page for Anaerobic nitric oxide reductase transcription regulator NorR | uni | see_6530 | 47.93 Functional role page for Anaerobic nitric oxide reductase transcription regulator NorR |
| SCE1572_10721 | YD repeat protein | uni | see_3939 | 31.61 FIG01085109: hypothetical protein |
| SCE1572_10722 | hypothetical protein | - | - | 0 |
| SCE1572_10723 | sensory box histidine kinase | uni | see_6094 | 51.34 Signal transduction histidine kinase CheA (EC 2.7.3.-) |
| SCE1572_10724 | hypothetical protein | bi | see_9383 | 83.49 Sensor histidine kinase |
| SCE1572_10725 | Sensor histidine kinase | - | - | 0 |
| SCE1572_10726 | hypothetical protein | - | - | 0 |
| SCE1572_10727 | MaoC family protein | - | - | 0 |
| SCE1572_10728 | hypothetical protein | bi | see_9384 | 92.78 hypothetical protein |
| SCE1572_10729 | hypothetical protein | bi | see_9385 | 93.12 hypothetical protein |
| SCE1572_10730 | polysaccharide deacetylase | bi | see_9387 | 90.33 polysaccharide deacetylase |
| SCE1572_10731 | hypothetical protein | bi | see_9388 | 94.62 FIG01087725: hypothetical protein |
| SCE1572_10732 | Probable poly(beta-D-mannuronate) O-acetylase (EC 2.3.1.-) | bi | see_9390 | 93.48 Probable poly(beta-D-mannuronate) O-acetylase (EC 2.3.1.-) |
| SCE1572_10733 | hypothetical protein | bi | see_9391 | 81.42 hypothetical protein |
| SCE1572_10734 | hypothetical protein | bi | see_9392 | 60.98 hypothetical protein |
| SCE1572_10735 | hypothetical protein | bi | see_9393 | 87.33 hypothetical protein |
| SCE1572_10736 | Tryptophan 2,3-dioxygenase (EC 1.13.11.11) | bi | see_9394 | 93.44 Tryptophan 2,3-dioxygenase (EC 1.13.11.11) |
| SCE1572_10737 | FIG01087757: hypothetical protein | bi | see_9395 | 85.84 FIG01087757: hypothetical protein |
| SCE1572_10738 | hypothetical protein | bi | see_9396 | 80.91 FIG01085894: hypothetical protein |
| SCE1572_10739 | hypothetical protein | - | - | 0 |
| SCE1572_10740 | 3-oxoacyl-[acyl-carrier protein] reductase (EC 1.1.1.100) | uni | see_4271 | 40.96 3-oxoacyl-[acyl-carrier protein] reductase (EC 1.1.1.100) |
| SCE1572_10741 | Transcriptional regulator, TetR family | uni | - | 0 |
| SCE1572_10742 | FIG01085516: hypothetical protein | uni | see_9846 | 82.04 FIG01086622: hypothetical protein |
| SCE1572_10743 | hypothetical protein | - | - | 0 |
| SCE1572_10744 | Endo-1,4-beta-xylanase A precursor (EC 3.2.1.8) | uni | see_1120 | 53.69 Endo-1,4-beta-xylanase A precursor (EC 3.2.1.8) |
| SCE1572_10745 | hypothetical protein | bi | see_10010 | 86.7 hypothetical protein |
| SCE1572_10746 | FIG01085453: hypothetical protein | bi | see_9987 | 95.24 FIG01085453: hypothetical protein |
| SCE1572_10747 | Transcriptional regulator, LysR family | bi | see_9992 | 90.82 Transcriptional regulator, LysR family |
| SCE1572_10748 | Permeases of the major facilitator superfamily | bi | see_9993 | 87.95 Permeases of the major facilitator superfamily |
| SCE1572_10749 | aldo/keto reductase | bi | see_10027 | 72.73 Oxidoreductase |
| SCE1572_10750 | Integration host factor beta subunit | bi | see_10004 | 75.81 Integration host factor beta subunit |
| SCE1572_10751 | LigA | bi | see_827 | 86.48 hypothetical protein |
| SCE1572_10752 | FIG00486916: hypothetical protein | bi | see_5142 | 77.66 FIG00486916: hypothetical protein |
| SCE1572_10753 | Polyvinylalcohol dehydrogenase | uni | see_6048 | 76.74 Polyvinylalcohol dehydrogenase |
| SCE1572_10754 | Gamma-glutamyltranspeptidase (EC 2.3.2.2) | uni | see_1347 | 41.74 Gamma-glutamyltranspeptidase (EC 2.3.2.2) |
| SCE1572_10755 | putative DEAD box family helicase, phage associated | bi | see_10007 | 93.78 putative DEAD box family helicase, phage associated |
| SCE1572_10756 | hypothetical protein | bi | see_9959 | 84.93 Cellulose-binding domain protein |
| SCE1572_10757 | Tat (Twin-arginine translocation) pathway signal sequence domain protein | bi | see_9958 | 87.04 Tat (Twin-arginine translocation) pathway signal sequence domain protein |
| SCE1572_10758 | hypothetical protein | bi | see_10009 | 67.76 hypothetical protein |
| SCE1572_10759 | hypothetical protein | - | - | 0 |
| SCE1572_10760 | hypothetical protein | - | - | 0 |
| SCE1572_10761 | Nitriolotriacetate monooxygenase component A (EC 1.14.13.-) | - | - | 0 |
| SCE1572_10762 | putative monooxygenase | bi | see_10003 | 85.97 putative monooxygenase |
| SCE1572_10763 | hypothetical protein | - | - | 0 |
| SCE1572_10764 | hypothetical protein | - | - | 0 |
| SCE1572_10765 | Putative cytoplasmic protein | bi | see_10018 | 91.27 Putative cytoplasmic protein |
| SCE1572_10766 | hypothetical protein | bi | see_10002 | 33.33 hypothetical protein |
| SCE1572_10767 | possible glycosyltransferase | bi | see_10013 | 86.52 possible glycosyltransferase |
| SCE1572_10768 | Gill1708 protein | bi | see_8396 | 86.36 Gill1708 protein |
| SCE1572_10769 | hypothetical protein | bi | see_8395 | 85.71 hypothetical protein |
| SCE1572_10770 | hypothetical protein | uni | see_4751 | 78.07 hypothetical protein |
| SCE1572_10771 | hypothetical protein | - | - | 0 |
| SCE1572_10772 | hypothetical protein | bi | see_10029 | 92.17 hypothetical protein |
| SCE1572_10773 | hypothetical protein | bi | see_10030 | 92.98 hypothetical protein |
| SCE1572_10774 | hypothetical protein | bi | see_10031 | 90.42 hypothetical protein |
| SCE1572_10775 | hypothetical protein | - | - | 0 |
| SCE1572_10776 | Dipeptide-binding ABC transporter, periplasmic substrate-binding component (TC 3.A.1.5.2) | bi | see_9407 | 85.46 Dipeptide-binding ABC transporter, periplasmic substrate-binding component (TC 3.A.1.5.2) |
| SCE1572_10777 | Mannanase | bi | see_9040 | 79.01 Mannanase |
| SCE1572_10778 | putative lipoprotein | bi | see_2922 | 80.38 putative lipoprotein |
| SCE1572_10779 | hypothetical protein | - | - | 0 |
| SCE1572_10780 | hypothetical protein | - | - | 0 |
| SCE1572_10781 | hypothetical protein | - | - | 0 |
| SCE1572_10782 | hypothetical protein | bi | see_9409 | 90.3 hypothetical protein |
| SCE1572_10783 | serine phosphatase | bi | see_9410 | 84.91 Serine phosphatase RsbU, regulator of sigma subunit |
| SCE1572_10784 | hypothetical protein | bi | see_9411 | 76.5 hypothetical protein |
| SCE1572_10785 | serine/threonine protein kinase | bi | see_9412 | 79.71 serine/threonine protein kinase Pkn6 |
| SCE1572_10786 | hypothetical protein | uni | see_9413 | 74.46 serine/threonine protein kinase Pkn6 |
| SCE1572_10787 | Serine-threonine protein kinase | bi | see_9413 | 64.67 Serine-threonine protein kinase |
| SCE1572_10788 | RbR, positive regulator of sigma-B | uni | see_9946 | 43.6 RbR, positive regulator of sigma-B |
| SCE1572_10789 | Superoxide dismutase [Cu-Zn] (EC 1.15.1.1) | bi | see_9414 | 85.32 Superoxide dismutase [Cu-Zn] (EC 1.15.1.1) |
| SCE1572_10790 | cellulose-binding, family II | bi | see_9415 | 68.93 cellulose-binding, family II |
| SCE1572_10791 | Adenylate cyclase (EC 4.6.1.1) | bi | see_9416 | 90.56 Adenylate cyclase (EC 4.6.1.1) |
| SCE1572_10792 | FIG01088745: hypothetical protein | bi | see_9417 | 86.62 FIG01088745: hypothetical protein |
| SCE1572_10793 | Sulfate adenylyltransferase, dissimilatory-type (EC 2.7.7.4) / Adenylylsulfate kinase (EC 2.7.1.25) | bi | see_9418 | 81.63 Sulfate adenylyltransferase, dissimilatory-type (EC 2.7.7.4) / Adenylylsulfate kinase (EC 2.7.1.25) |
| SCE1572_10794 | hypothetical protein | bi | see_9419 | 86.49 conserved hypothetical protein |
| SCE1572_10795 | hypothetical protein | bi | see_9420 | 77.61 hypothetical protein |
| SCE1572_10796 | hypothetical protein | bi | see_9421 | 54.55 hypothetical protein |
| SCE1572_10797 | hypothetical protein | bi | see_9422 | 82.02 Atherin (Sterile alpha motif domain-containing protein 1) |
| SCE1572_10798 | hypothetical protein | bi | see_9424 | 83.46 hypothetical protein |
| SCE1572_10799 | ABC-type nitrate/sulfonate/bicarbonate transport system protein | uni | see_3783 | 33.04 Urea carboxylase-related ABC transporter, periplasmic substrate-binding protein |
| SCE1572_10800 | Serine/threonine-protein kinase pkn3 (EC 2.7.11.1) | uni | see_3170 | 49 serine/threonine kinase Pkn10 (EC:2.7.1.-) |
| SCE1572_10801 | hypothetical protein | - | - | 0 |
| SCE1572_10802 | ATP-dependent Clp protease ATP-binding subunit ClpA | bi | see_9425 | 85.96 ATP-dependent Clp protease ATP-binding subunit ClpA |
| SCE1572_10803 | hypothetical protein | - | - | 0 |
| SCE1572_10804 | hypothetical protein | - | - | 0 |
| SCE1572_10805 | Chitinase | bi | see_4489 | 78.04 Chitinase |
| SCE1572_10806 | hypothetical protein | uni | see_2965 | 34.82 FIG01089285: hypothetical protein |
| SCE1572_10807 | FIG01086214: hypothetical protein | bi | see_2093 | 86.94 FIG01086214: hypothetical protein |
| SCE1572_10808 | hypothetical protein | bi | see_9441 | 69.01 hypothetical protein |
| SCE1572_10809 | hypothetical protein | bi | see_9442 | 87.93 hypothetical protein |
| SCE1572_10810 | response regulator | bi | see_9443 | 93.44 response regulator |
| SCE1572_10811 | hypothetical protein | - | - | 0 |
| SCE1572_10812 | hypothetical protein | bi | see_9444 | 89.37 hypothetical protein-putative transmembrane protein |
| SCE1572_10813 | hypothetical protein | bi | see_9446 | 90.41 hypothetical protein |
| SCE1572_10814 | FIG01089050: hypothetical protein | bi | see_9447 | 67.28 FIG01089050: hypothetical protein |
| SCE1572_10815 | FIG01088479: hypothetical protein | bi | see_9448 | 79.93 FIG01088479: hypothetical protein |
| SCE1572_10816 | hypothetical protein | bi | see_9449 | 77.09 hypothetical protein |
| SCE1572_10817 | hypothetical protein | bi | see_2995 | 87.7 hypothetical protein |
| SCE1572_10818 | hypothetical protein | bi | see_2996 | 85.15 hypothetical protein |
| SCE1572_10819 | Retron-type reverse transcriptase | bi | see_2998 | 85.96 RNA-directed DNA polymerase from retron Mx65 (EC 2.7.7.49) (Reverse transcriptase) (Mx65-RT) |
| SCE1572_10820 | hypothetical protein | bi | see_9459 | 94.77 hypothetical protein |
| SCE1572_10821 | hypothetical protein | - | - | 0 |
| SCE1572_10822 | Diadenosine tetraphosphatase | bi | see_9460 | 88.84 Diadenosine tetraphosphatase |
| SCE1572_10823 | FIG01088986: hypothetical protein | bi | see_6965 | 75.13 FIG01088986: hypothetical protein |

| | | | | |
|---------------|---|-----|-----------|---|
| SCE1572_10824 | FIG01085387: hypothetical protein | bi | see_8729 | 68.03 FIG01085387: hypothetical protein |
| SCE1572_10825 | Outer membrane protein A precursor | bi | see_8728 | 66.67 Outer membrane protein A precursor |
| SCE1572_10826 | hypothetical protein | - | - | 0 |
| SCE1572_10827 | FIG01124780: hypothetical protein | bi | see_3440 | 91 FIG01124780: hypothetical protein |
| SCE1572_10828 | hypothetical protein | bi | see_3441 | 84.25 hypothetical protein |
| SCE1572_10829 | HAD-superfamily hydrolase, subfamily IA, variant 1 family protein | - | - | 0 |
| SCE1572_10830 | hypothetical protein | bi | see_3442 | 88.14 Amidohydrolase 3 |
| SCE1572_10831 | ABC transporter substrate-binding protein | umi | see_2163 | 79.37 ABC transporter substrate-binding protein |
| SCE1572_10832 | Neurocan core protein precursor (Chondroitin sulfate proteoglycan 3) | umi | see_8773 | 35.19 lectin C-type domain protein |
| SCE1572_10833 | hypothetical protein | - | - | 0 |
| SCE1572_10834 | aminopeptidase N (EC:3.4.11.2) | bi | see_1601 | 82.36 aminopeptidase N (EC:3.4.11.2) |
| SCE1572_10835 | Sulfate transport system permease protein CysW | umi | see_365 | 53.51 Sulfate transport system permease protein CysW |
| SCE1572_10836 | Sulfate transport system permease protein CysT | umi | see_364 | 50.17 Sulfate transport system permease protein CysT |
| SCE1572_10837 | sulfate-binding protein | umi | see_363 | 43.38 Sulfate and thiosulfate binding protein CysP |
| SCE1572_10838 | BNR repeat domain protein | bi | see_9473 | 72.67 BNR repeat domain protein |
| SCE1572_10839 | hypothetical protein | - | - | 0 |
| SCE1572_10840 | hypothetical protein | bi | see_5249 | 48.31 FIG01085181: hypothetical protein |
| SCE1572_10841 | 2-isopropylmalate synthase (EC 2.3.3.13) | bi | see_9475 | 85.45 2-isopropylmalate synthase (EC 2.3.3.13) |
| SCE1572_10842 | hypothetical protein | bi | see_9476 | 92.66 FIG01088805: hypothetical protein |
| SCE1572_10843 | hypothetical protein | bi | see_9477 | 82.46 hypothetical protein |
| SCE1572_10844 | hypothetical protein | - | - | 0 |
| SCE1572_10845 | Beta-galactosidase (EC 3.2.1.23) | umi | see_4770 | 41.67 hypothetical protein |
| SCE1572_10846 | Altronate hydrolase (EC 4.2.1.7) | bi | see_1385 | 89.29 Altronate hydrolase (EC 4.2.1.7) |
| SCE1572_10847 | D-galactonate transporter | bi | see_1384 | 92.74 D-galactonate transporter |
| SCE1572_10848 | Altronate oxidoreductase (EC 1.1.1.58) | bi | see_1383 | 87.23 Altronate oxidoreductase (EC 1.1.1.58) |
| SCE1572_10849 | Oxidoreductase, zinc-binding dehydrogenase family (EC 1.1.1.-) | bi | see_1382 | 93.23 Oxidoreductase, zinc-binding dehydrogenase family (EC 1.1.1.-) |
| SCE1572_10850 | hypothetical protein | bi | see_1381 | 86.88 amidohydrolase 2 |
| SCE1572_10851 | Galactokinase (EC 2.7.1.6) | umi | see_2475 | 86.52 Galactokinase (EC 2.7.1.6) |
| SCE1572_10852 | UDP-glucose 4-epimerase (EC 5.1.3.2) | bi | see_2474 | 89.09 UDP-glucose 4-epimerase (EC 5.1.3.2) |
| SCE1572_10853 | Putative sugar ABC transport system, permease protein YjFf | bi | see_2473 | 87.38 Putative sugar ABC transport system, permease protein YjFf |
| SCE1572_10854 | ABC transporter, membrane spanning protein (ribose) | bi | see_2472 | 91.94 Ribose ABC transport system, permease protein RhsC (TC 3.A.1.2.1) |
| SCE1572_10855 | Ribose ABC transport system, ATP-binding protein RbsA (TC 3.A.1.2.1) | bi | see_2471 | 90.12 Ribose ABC transport system, ATP-binding protein RbsA (TC 3.A.1.2.1) |
| SCE1572_10856 | ABC transporter periplasmic binding protein YjQ precursor | bi | see_2470 | 88.89 ABC transporter periplasmic binding protein YjQ precursor |
| SCE1572_10857 | Endo-1,4-beta-xylanase A precursor (EC 3.2.1.8) | bi | see_5146 | 79.9 Endo-1,4-beta-xylanase A precursor (EC 3.2.1.8) |
| SCE1572_10858 | Assimilatory nitrate reductase large subunit (EC:1.7.99.4) | bi | see_9486 | 93.79 Assimilatory nitrate reductase large subunit (EC:1.7.99.4) |
| SCE1572_10859 | Molybdopterine oxidoreductase, iron sulfur subunit | bi | see_9487 | 90.43 Molybdopterine oxidoreductase, iron sulfur subunit |
| SCE1572_10860 | Nitrite reductase [NAD(P)H] small subunit (EC 1.7.1.4) | bi | see_9488 | 81.06 Nitrite reductase [NAD(P)H] small subunit (EC 1.7.1.4) |
| SCE1572_10861 | Nitrite reductase [NAD(P)H] large subunit (EC 1.7.1.4) | bi | see_9489 | 92.32 Nitrite reductase [NAD(P)H] large subunit (EC 1.7.1.4) |
| SCE1572_10862 | Chemotaxis protein methyltransferase CheR (EC 2.1.1.80) | bi | see_9491 | 77.62 Chemotaxis protein methyltransferase CheR (EC 2.1.1.80) |
| SCE1572_10863 | 2-dehydropantoate 2-reductase (EC 1.1.1.169) | bi | see_9492 | 87.95 2-dehydropantoate 2-reductase (EC 1.1.1.169) |
| SCE1572_10864 | hypothetical protein | umi | see_3392 | 30.17 integral membrane protein |
| SCE1572_10865 | putative secreted protein | umi | see_9562 | 65.93 Collagen triple helix repeat |
| SCE1572_10866 | rRNA small subunit methyltransferase, glucose inhibited division protein GidB | bi | see_6774 | 31.77 rRNA small subunit 7-methylguanosine (m7G) methyltransferase GidB |
| SCE1572_10867 | motif=eukaryotic putative RNA-binding region RNP-1 signature | bi | see_9494 | 87.19 motif=eukaryotic putative RNA-binding region RNP-1 signature |
| SCE1572_10868 | tetratricopeptide repeat protein | bi | see_9495 | 73.7 hypothetical protein |
| SCE1572_10869 | hypothetical protein | bi | see_9496 | 84.34 DNA mismatch repair protein MutL |
| SCE1572_10870 | FIG01089649: hypothetical protein | umi | see_7819 | 41.04 FIG01089649: hypothetical protein |
| SCE1572_10871 | FIG01085109: hypothetical protein | bi | see_3939 | 88.6 FIG01085109: hypothetical protein |
| SCE1572_10872 | Type I restriction-modification system, restriction subunit R (EC 3.1.21.3) | - | - | 0 |
| SCE1572_10873 | Type I restriction-modification system, specificity subunit S (EC 3.1.21.3) | umi | see_6180 | 36.04 Type I restriction-modification system, specificity subunit S (EC 3.1.21.3) |
| SCE1572_10874 | hypothetical protein | - | - | 0 |
| SCE1572_10875 | hypothetical protein | - | - | 0 |
| SCE1572_10876 | Type I restriction-modification system, DNA-methyltransferase subunit M (EC 2.1.1.72) | bi | see_9506 | 94.97 Type I restriction-modification system, DNA-methyltransferase subunit M (EC 2.1.1.72) |
| SCE1572_10877 | probable ATP-binding protein | umi | see_5451 | 34.83 Probable ATP-binding protein NMA0346 |
| SCE1572_10878 | hypothetical protein | - | - | 0 |
| SCE1572_10879 | RsbR, positive regulator of sigma-B | bi | see_9509 | 85.64 RsbR, positive regulator of sigma-B |
| SCE1572_10880 | VgrG protein | bi | see_9510 | 82.81 VgrG protein |
| SCE1572_10881 | hypothetical protein | - | - | 0 |
| SCE1572_10882 | Mir2351 protein | bi | see_9511 | 74.96 Mir2351 protein |
| SCE1572_10883 | FIG01089299: hypothetical protein | bi | see_9512 | 85.84 FIG01089299: hypothetical protein |
| SCE1572_10884 | COG3178: Predicted phosphotransferase related to Ser/Thr protein kinases | bi | see_9513 | 85.55 COG3178: Predicted phosphotransferase related to Ser/Thr protein kinases |
| SCE1572_10885 | hypothetical protein | bi | see_9514 | 83.92 hypothetical protein |
| SCE1572_10886 | Xylanase | bi | see_9515 | 76 LOC432261 protein |
| SCE1572_10887 | ABC transporter, ATP-binding protein | bi | see_9517 | 90.87 ABC transporter, ATP-binding protein |
| SCE1572_10888 | hypothetical protein | - | - | 0 |
| SCE1572_10889 | Lycopene beta cyclase (EC 1.14.--) | bi | see_9521 | 95.95 Lycopene beta cyclase (EC 1.14.--) |
| SCE1572_10890 | Phosphoribosylglycinamide formyltransferase (EC 2.1.2.2) | bi | see_9522 | 88.21 Phosphoribosylglycinamide formyltransferase (EC 2.1.2.2) |
| SCE1572_10891 | hypothetical protein | umi | see_287 | 57.14 hypothetical protein |
| SCE1572_10892 | serine/threonine protein kinase | bi | see_9524 | 69.15 serine/threonine protein kinase |
| SCE1572_10893 | Phosphoribosylformylglycinamide cyclo-ligase (EC 6.3.3.1) | bi | see_9525 | 91.67 Phosphoribosylformylglycinamide cyclo-ligase (EC 6.3.3.1) |
| SCE1572_10894 | 5-methyl-dCTP pyrophosphohydrolase (EC 3.6.1.-) | bi | see_9529 | 87.86 5-methyl-dCTP pyrophosphohydrolase (EC 3.6.1.-) |
| SCE1572_10895 | DoxX family protein | umi | see_863 | 31.29 putative membrane protein |
| SCE1572_10896 | hypothetical protein | umi | see_8874 | 39.58 putative membrane protein |
| SCE1572_10897 | Cytochrome c-type biogenesis protein CcdA (DsbD analog) | bi | see_9530 | 88.28 Cytochrome c-type biogenesis protein CcdA (DsbD analog) |
| SCE1572_10898 | PUTATIVE TRANSMEMBRANE PROTEIN | bi | see_9531 | 88.89 PUTATIVE TRANSMEMBRANE PROTEIN |
| SCE1572_10899 | hypothetical protein | - | - | 0 |
| SCE1572_10900 | hypothetical protein | - | - | 0 |
| SCE1572_10901 | Glycine oxidase ThiO (EC 1.4.3.19) | bi | see_9534 | 88.47 Glycine oxidase ThiO (EC 1.4.3.19) |
| SCE1572_10902 | hypothetical protein | - | - | 0 |
| SCE1572_10903 | VapC toxin protein | bi | - | 0 |
| SCE1572_10904 | hypothetical protein | bi | see_9537 | 89.29 hypothetical protein |
| SCE1572_10905 | hypothetical protein | bi | see_9539 | 95.03 hypothetical protein |
| SCE1572_10906 | HYpothetical protein | bi | see_9540 | 77.64 HYpothetical protein |
| SCE1572_10907 | Signal recognition particle, subunit Fh SRP54 (TC 3.A.5.1.1) | bi | see_9541 | 94.69 Signal recognition particle, subunit Fh SRP54 (TC 3.A.5.1.1) |
| SCE1572_10908 | FIG01087002: hypothetical protein | bi | see_9542 | 76.01 FIG01087002: hypothetical protein |
| SCE1572_10909 | transport-associated | umi | see_5863 | 30.55 Single-stranded DNA-binding protein |
| SCE1572_10910 | periplasmic binding protein/LacI transcriptional regulator | umi | see_7038 | 62.3 hypothetical protein |
| SCE1572_10911 | hypothetical protein | umi | see_3858 | 36.89 Adenosylhomocysteinase (EC 3.3.1.1) |
| SCE1572_10912 | COG0488: ATPase components of ABC transporters with duplicated ATPase domains | bi | see_9548 | 93.5 COG0488: ATPase components of ABC transporters with duplicated ATPase domains |
| SCE1572_10913 | hypothetical protein | bi | see_9550 | 75.9 FIG01087760: hypothetical protein |
| SCE1572_10914 | Modification methylase PstI (EC 2.1.1.72) | bi | see_8717 | 63.01 Modification methylase PstI (EC 2.1.1.72) |
| SCE1572_10915 | hypothetical protein | - | - | 0 |
| SCE1572_10916 | FIG01088550: hypothetical protein | bi | see_9551 | 88.86 FIG01088550: hypothetical protein |
| SCE1572_10917 | FIG00623084: hypothetical protein | bi | see_9552 | 89.17 FIG00623084: hypothetical protein |
| SCE1572_10918 | ThiJ/PpfI | umi | see_7653 | 44.79 ThiJ/PpfI family protein |
| SCE1572_10919 | FIG01086905: hypothetical protein | bi | see_9553 | 87.01 FIG01086905: hypothetical protein |
| SCE1572_10920 | Transcriptional regulator, TetR family | bi | see_9554 | 87.84 Transcriptional regulator, TetR family |
| SCE1572_10921 | beta-lactamase | bi | see_8693 | 38.34 Beta-lactamase class C and other penicillin binding proteins |
| SCE1572_10922 | putative cytochrome P450 hydroxylase | bi | see_9555 | 67.68 putative cytochrome P450 hydroxylase |
| SCE1572_10923 | Pentalene synthase (EC 4.2.3.7) (PS) (Sesquiterpene synthase) (Sesquiterpene cyclase) | bi | see_9556 | 70.4 Pentalene synthase (EC 4.2.3.7) (PS) (Sesquiterpene synthase) (Sesquiterpene cyclase) |
| SCE1572_10924 | RsbR, positive regulator of sigma-B | bi | see_9557 | 77.96 Signal transduction histidine kinase CheA (EC 2.7.3.-) |
| SCE1572_10925 | hypothetical protein | - | - | 0 |
| SCE1572_10926 | hypothetical protein | - | - | 0 |
| SCE1572_10927 | Gamma-glutamyltranspeptidase (EC 2.3.2.2) | bi | see_9558 | 93.08 Gamma-glutamyltranspeptidase (EC 2.3.2.2) |
| SCE1572_10928 | Exonuclease SbcC | bi | see_9559 | 75.55 Exonuclease SbcC |
| SCE1572_10929 | conserved hypothetical protein | bi | see_2568 | 43.8 FIG01088499: hypothetical protein |
| SCE1572_10930 | TolA protein | umi | see_9559 | 39.47 Exonuclease SbcC |
| SCE1572_10931 | conserved hypothetical protein | umi | see_2954 | 41.01 hypothetical protein |
| SCE1572_10932 | hypothetical protein | - | - | 0 |
| SCE1572_10933 | hypothetical protein | - | - | 0 |
| SCE1572_10934 | RNA polymerase sigma factor RpoE | umi | see_10335 | 47.79 RNA polymerase sigma factor RpoE |
| SCE1572_10935 | FIG01086383: hypothetical protein | umi | see_3918 | 53.16 FIG01086383: hypothetical protein |
| SCE1572_10936 | hypothetical protein | - | - | 0 |
| SCE1572_10937 | FIG01086383: hypothetical protein | umi | see_10333 | 54.86 hypothetical protein |
| SCE1572_10938 | hypothetical protein | umi | see_10332 | 48.59 FIG01087210: hypothetical protein |
| SCE1572_10939 | FIG01086053: hypothetical protein | umi | see_9398 | 65.54 FIG01086053: hypothetical protein |
| SCE1572_10940 | hypothetical protein | bi | see_8783 | 55.78 hypothetical protein |
| SCE1572_10941 | FIG00445893: hypothetical protein | umi | see_6987 | 45.16 hypothetical protein |
| SCE1572_10942 | Type I restriction-modification system, specificity subunit S (EC 3.1.21.3) | umi | see_6180 | 35.64 Type I restriction-modification system, specificity subunit S (EC 3.1.21.3) |
| SCE1572_10943 | Type I restriction-modification system, DNA-methyltransferase subunit M (EC 2.1.1.72) | umi | see_9506 | 48 Type I restriction-modification system, DNA-methyltransferase subunit M (EC 2.1.1.72) |
| SCE1572_10944 | hypothetical protein | - | - | 0 |
| SCE1572_10945 | hypothetical protein | - | - | 0 |
| SCE1572_10946 | Type I restriction-modification system, restriction subunit R (EC 3.1.21.3) | umi | see_10007 | 25.49 putative DEAD box family helicase, phage associated |
| SCE1572_10947 | hypothetical protein | bi | see_9423 | 81.5 hypothetical protein |
| SCE1572_10948 | aculeacin A acylase (EC:3.5.1.-) | umi | see_7836 | 30.09 putative penicillin acylase (EC:3.5.1.11) |
| SCE1572_10949 | Two-component response regulator | bi | see_9560 | 87.74 Two-component response regulator |
| SCE1572_10950 | GGDEF domain | umi | see_3917 | 45.83 Signal transduction histidine kinase CheA (EC 2.7.3.-) |
| SCE1572_10951 | Fructose-1,6-bisphosphatase, Bacillus type (EC 3.1.3.11) | bi | see_9561 | 91.89 Fructose-1,6-bisphosphatase, Bacillus type (EC 3.1.3.11) |
| SCE1572_10952 | hypothetical protein | umi | see_9562 | 45.61 Collagen triple helix repeat |
| SCE1572_10953 | Collagen triple helix repeat | umi | see_5863 | 53.64 Single-stranded DNA-binding protein |
| SCE1572_10954 | Putative outer membrane or secreted lipoprotein | - | - | 0 |
| SCE1572_10955 | Periplasmic beta-glucosidase (EC 3.2.1.21) | bi | see_9564 | 83.04 Periplasmic beta-glucosidase (EC 3.2.1.21) |
| SCE1572_10956 | Quinone oxidoreductase (EC 1.6.5.5) | bi | see_9569 | 88.6 Quinone oxidoreductase (EC 1.6.5.5) |
| SCE1572_10957 | FIG01085846: hypothetical protein | bi | see_9570 | 77.51 FIG01085846: hypothetical protein |
| SCE1572_10958 | Oligopeptide transport ATP-binding protein OppF (TC 3.A.1.5.1) | bi | see_9572 | 89.7 Oligopeptide transport ATP-binding protein OppF (TC 3.A.1.5.1) |
| SCE1572_10959 | Oligopeptide transport ATP-binding protein OppD (TC 3.A.1.5.1) | bi | see_9573 | 84.03 Oligopeptide transport ATP-binding protein OppD (TC 3.A.1.5.1) |
| SCE1572_10960 | FIG01087673: hypothetical protein | bi | see_9574 | 87.77 FIG01087673: hypothetical protein |
| SCE1572_10961 | FIG01089145: hypothetical protein | bi | see_9575 | 87.41 FIG01089145: hypothetical protein |
| SCE1572_10962 | hypothetical protein | - | - | 0 |
| SCE1572_10963 | Methyltransferase type 11 | umi | see_10042 | 36.84 NADH-FMN oxidoreductase |
| SCE1572_10964 | Cellulose-binding domain protein | bi | see_9678 | 84.83 Cellulose-binding domain protein |
| SCE1572_10965 | FIG01086083: hypothetical protein | bi | see_9679 | 91.96 FIG01086083: hypothetical protein |
| SCE1572_10966 | putative membrane protein | bi | see_9680 | 73.74 putative membrane protein |
| SCE1572_10967 | Very large tegument protein | bi | see_9681 | 84.13 hypothetical protein |
| SCE1572_10968 | FolM Alternative dihydrofolate reductase 1 | bi | see_9682 | 90.24 FolM Alternative dihydrofolate reductase 1 |
| SCE1572_10969 | Xaa-Pro aminopeptidase (EC 3.4.11.9) | bi | see_9683 | 91.02 Xaa-Pro aminopeptidase (EC 3.4.11.9) |
| SCE1572_10970 | Protease | bi | see_9684 | 89.6 Protease |
| SCE1572_10971 | hypothetical protein | bi | see_9685 | 80.28 hypothetical protein |
| SCE1572_10972 | hypothetical protein | bi | see_9686 | 78.97 hypothetical protein |
| SCE1572_10973 | DNA polymerase I (EC 2.7.7.7) | bi | see_9687 | 94.78 DNA polymerase I (EC 2.7.7.7) |
| SCE1572_10974 | hypothetical protein | - | - | 0 |
| SCE1572_10975 | SSU ribosomal protein S20p | bi | see_9696 | 94.62 SSU ribosomal protein S20p |
| SCE1572_10976 | hypothetical protein | bi | see_9697 | 95.16 hypothetical protein |
| SCE1572_10977 | Proteoglycophaglycan ppg4 | bi | see_9698 | 91.79 Alginate regulatory protein AlgP |
| SCE1572_10978 | RNA polymerase sigma factor RpoE | bi | see_9699 | 95.24 RNA polymerase sigma factor RpoE |
| SCE1572_10979 | Carboxy-terminal processing protease (EC 3.4.21.102) | bi | see_9701 | 91.51 Carboxy-terminal processing protease (EC 3.4.21.102) |
| SCE1572_10980 | Anaerobic glycerol-3-phosphate dehydrogenase subunit B (EC 1.1.5.3) | bi | see_9702 | 91.33 Anaerobic glycerol-3-phosphate dehydrogenase subunit B (EC 1.1.5.3) |
| SCE1572_10981 | Anaerobic glycerol-3-phosphate dehydrogenase subunit A (EC 1.1.5.3) | bi | see_9703 | 94.44 Anaerobic glycerol-3-phosphate dehydrogenase subunit A (EC 1.1.5.3) |
| SCE1572_10982 | glycosyl transferase, group 2 family protein | bi | see_9704 | 93.12 glycosyl transferase, group 2 family protein |
| SCE1572_10983 | amine oxidase, putative | bi | see_9705 | 93.78 hypothetical protein |
| SCE1572_10984 | 3-isopropylmalate dehydratase large subunit (EC 4.2.1.33) | bi | see_9706 | 95.3 3-isopropylmalate dehydratase large subunit (EC 4.2.1.33) |
| SCE1572_10985 | hypothetical protein | bi | see_9707 | 100 hypothetical protein |
| SCE1572_10986 | Beta-ketoadipate enol-lactone hydrolase (EC 3.1.1.24) | bi | see_9708 | 86.74 Beta-ketoadipate enol-lactone hydrolase (EC 3.1.1.24) |
| SCE1572_10987 | hypothetical protein | bi | see_9709 | 79.43 hypothetical protein |

| | | | | | |
|---------------|--|-----|-----------|-------|---|
| SCE1572_10988 | hypothetical protein | bi | see_9710 | 85.23 | hypothetical protein |
| SCE1572_10989 | putative serine/threonine protein kinase | bi | see_9711 | 89.33 | hypothetical protein |
| SCE1572_10990 | FIG01088725: hypothetical protein | bi | see_9712 | 95.6 | FIG01088725: hypothetical protein |
| SCE1572_10991 | Leader peptidase (Prepilin peptidase) (EC 3.4.23.43) / N-methyltransferase (EC 2.1.1.-) | bi | see_9713 | 90.03 | Leader peptidase (Prepilin peptidase) (EC 3.4.23.43) / N-methyltransferase (EC 2.1.1.-) |
| SCE1572_10992 | hypothetical protein | bi | see_9714 | 82.35 | hypothetical protein |
| SCE1572_10993 | hypothetical protein | - | - | 0 | 0 |
| SCE1572_10994 | FIG01087646: hypothetical protein | bi | see_9715 | 91.34 | FIG01087646: hypothetical protein |
| SCE1572_10995 | serine/threonine protein kinase | bi | see_9716 | 78.54 | serine/threonine protein kinase |
| SCE1572_10996 | hypothetical protein | umi | see_3858 | 34 | Adenosylhomocysteinase (EC 3.3.1.1) |
| SCE1572_10997 | Long-chain-fatty-acid-CoA ligase (EC 6.2.1.3) | bi | see_9718 | 85.36 | Long-chain-fatty-acid-CoA ligase (EC 6.2.1.3) |
| SCE1572_10998 | hypothetical protein | bi | see_9719 | 86.08 | predicted protein |
| SCE1572_10999 | hypothetical protein | bi | see_9721 | 76.47 | hypothetical protein |
| SCE1572_11000 | hypothetical protein | bi | see_9722 | 78.64 | hypothetical protein |
| SCE1572_11001 | Hypothetical protein | bi | see_9723 | 92.98 | Hypothetical protein |
| SCE1572_11002 | hypothetical protein | bi | see_9724 | 74.77 | hypothetical protein |
| SCE1572_11003 | Fibrillin 1 precursor | bi | see_9725 | 87.83 | Fibrillin 1 precursor |
| SCE1572_11004 | OmpA/MotB | bi | see_9726 | 80 | hypothetical protein |
| SCE1572_11005 | FIG01089681: hypothetical protein | bi | see_9727 | 90.02 | FIG01089681: hypothetical protein |
| SCE1572_11006 | hypothetical protein | bi | see_9728 | 69.23 | hypothetical protein |
| SCE1572_11007 | Flagellar hook-length control protein FliK | bi | see_9729 | 86.51 | Flagellar hook-length control protein FliK |
| SCE1572_11008 | hypothetical protein | - | - | 0 | 0 |
| SCE1572_11009 | FIG01089665: hypothetical protein | bi | see_9730 | 74.07 | FIG01089665: hypothetical protein |
| SCE1572_11010 | Sensor histidine kinase | bi | see_9731 | 82.78 | sensor histidine kinase |
| SCE1572_11011 | hypothetical protein | - | - | 0 | 0 |
| SCE1572_11012 | hypothetical protein | umi | see_6133 | 34.46 | Twin-arginine translocation protein TatB |
| SCE1572_11013 | PE-PGRS FAMILY PROTEIN | umi | see_6870 | 41.56 | PE-PGRS FAMILY PROTEIN |
| SCE1572_11014 | hypothetical protein | - | - | 0 | 0 |
| SCE1572_11015 | hypothetical protein | - | - | 0 | 0 |
| SCE1572_11016 | hypothetical protein | - | - | 0 | 0 |
| SCE1572_11017 | hypothetical protein | - | - | 0 | 0 |
| SCE1572_11018 | hypothetical protein | - | - | 0 | 0 |
| SCE1572_11019 | hypothetical protein | bi | see_9732 | 76.85 | hypothetical protein |
| SCE1572_11020 | Heavy metal RND efflux outer membrane protein, CzcC family | bi | see_9733 | 86.47 | Heavy metal RND efflux outer membrane protein, CzcC family |
| SCE1572_11021 | Cobalt/zinc/cadmium efflux RND transporter, membrane fusion protein, CzcB family | bi | see_9734 | 82.55 | Cobalt/zinc/cadmium efflux RND transporter, membrane fusion protein, CzcB family |
| SCE1572_11022 | Cobalt-zinc-cadmium resistance protein CzcA, Cation efflux system protein CusA | bi | see_9735 | 92.66 | Cobalt-zinc-cadmium resistance protein CzcA, Cation efflux system protein CusA |
| SCE1572_11023 | GAF sensor signal transduction histidine kinase | bi | see_9737 | 93.94 | sensor histidine kinase |
| SCE1572_11024 | Two-component response regulator | bi | see_9738 | 96.38 | Two-component response regulator |
| SCE1572_11025 | Two-component hybrid sensor and regulator | bi | see_9739 | 87.13 | two-component hybrid sensor and regulator |
| SCE1572_11026 | protein of unknown function DUF1328 | bi | see_9740 | 94.12 | Putative exported protein |
| SCE1572_11027 | hypothetical protein | bi | see_9741 | 80.54 | hypothetical protein |
| SCE1572_11028 | hypothetical protein | bi | see_9742 | 80.56 | hypothetical protein |
| SCE1572_11029 | hypothetical protein | bi | see_9743 | 80.85 | hypothetical protein |
| SCE1572_11030 | Regulator of cell morphogenesis and NO signaling | bi | see_9744 | 84.91 | Regulator of cell morphogenesis and NO signaling |
| SCE1572_11031 | hypothetical protein | - | - | 0 | 0 |
| SCE1572_11032 | hypothetical protein | - | - | 0 | 0 |
| SCE1572_11033 | hypothetical protein | bi | see_9745 | 48 | hypothetical protein |
| SCE1572_11034 | Response regulator of zinc sigma-54-dependent two-component system | bi | see_9746 | 98.53 | Response regulator of zinc sigma-54-dependent two-component system |
| SCE1572_11035 | Sensor histidine kinase | bi | see_9747 | 78.7 | Sensor histidine kinase |
| SCE1572_11036 | Two component Transcriptional regulator, Winged helix family | bi | see_9748 | 82.79 | Two-component response regulator |
| SCE1572_11037 | Transcriptional regulator, XRE family | bi | see_9749 | 98.53 | Transcriptional regulator, XRE family |
| SCE1572_11038 | hypothetical protein | bi | see_9750 | 94.74 | hypothetical protein |
| SCE1572_11039 | Malate synthase (EC 2.3.3.9) | bi | see_9751 | 93.28 | Malate synthase (EC 2.3.3.9) |
| SCE1572_11040 | Isocitrate lyase (EC 4.1.3.1) | bi | see_9752 | 95.83 | Isocitrate lyase (EC 4.1.3.1) |
| SCE1572_11041 | Glutamyl-tRNA synthetase (EC 6.1.1.18) | bi | see_9754 | 48.67 | hypothetical protein |
| SCE1572_11042 | Large exoproteins involved in heme utilization or adhesion | bi | see_9755 | 66.31 | Large exoproteins involved in heme utilization or adhesion |
| SCE1572_11043 | FIG01088331: hypothetical protein | bi | see_9757 | 91.56 | Serine/threonine protein kinase |
| SCE1572_11044 | Glucose-1-phosphate thymidyltransferase (EC 2.7.7.24) | bi | see_7609 | 64.71 | Glucose-1-phosphate thymidyltransferase (EC 2.7.7.24) |
| SCE1572_11045 | hypothetical protein | - | - | 0 | 0 |
| SCE1572_11046 | FIG01085038: hypothetical protein | bi | see_9758 | 85.65 | FIG01085038: hypothetical protein |
| SCE1572_11047 | FIG01089141: hypothetical protein | bi | see_9760 | 74.79 | FIG01089141: hypothetical protein |
| SCE1572_11048 | FIG01084877: hypothetical protein | bi | see_9761 | 87.79 | FIG01084877: hypothetical protein |
| SCE1572_11049 | FIG01088528: hypothetical protein | bi | see_9762 | 93.98 | FIG01088528: hypothetical protein |
| SCE1572_11050 | hypothetical protein | bi | see_9763 | 71.31 | hypothetical protein |
| SCE1572_11051 | RNA polymerase sigma factor RpoE | bi | see_9765 | 90.17 | RNA polymerase sigma factor RpoE |
| SCE1572_11052 | ZK84.1 | bi | see_9766 | 85.42 | ZK84.1 |
| SCE1572_11053 | Methylcrotonyl-CoA carboxylase biotin-containing subunit (EC 6.4.1.4) | bi | see_9767 | 90.53 | Methylcrotonyl-CoA carboxylase biotin-containing subunit (EC 6.4.1.4) |
| SCE1572_11054 | hypothetical protein | bi | see_9771 | 85.03 | hypothetical protein |
| SCE1572_11055 | Uncharacterized protein y4IF | bi | see_9772 | 85.68 | hypothetical protein |
| SCE1572_11056 | hypothetical protein | bi | see_9773 | 86.57 | hypothetical protein |
| SCE1572_11057 | hypothetical protein | - | - | 0 | 0 |
| SCE1572_11058 | hypothetical protein | umi | see_4583 | 37.41 | FIG01085899: hypothetical protein |
| SCE1572_11059 | transposase IS116/IS110/IS902 family protein | - | - | 0 | 0 |
| SCE1572_11060 | Rhs protein | umi | see_10193 | 32.65 | Rhs family carbohydrate-binding protein |
| SCE1572_11061 | Rhs family protein | bi | see_4583 | 43.75 | FIG01085899: hypothetical protein |
| SCE1572_11062 | VgrG protein | umi | see_4581 | 58.65 | VgrG protein |
| SCE1572_11063 | hypothetical protein | umi | see_1181 | 28.78 | Membrane protein involved in colicin uptake-like protein |
| SCE1572_11064 | hypothetical protein | umi | see_9779 | 81.88 | hypothetical protein |
| SCE1572_11065 | hypothetical protein | bi | see_9779 | 83.81 | hypothetical protein |
| SCE1572_11066 | Collagen alpha 1(I) chain precursor | bi | see_9780 | 89.06 | Collagen alpha 1(I) chain precursor |
| SCE1572_11067 | hypothetical protein | - | - | 0 | 0 |
| SCE1572_11068 | phosphoesterase, PHP-like | bi | see_9813 | 86.09 | phosphoesterase, PHP-like |
| SCE1572_11069 | Cystathionine beta-synthase (EC 4.2.1.22) | bi | see_9814 | 94.82 | Cystathionine beta-synthase (EC 4.2.1.22) |
| SCE1572_11070 | Metal-dependent hydrolase | bi | see_9815 | 86.44 | Metal-dependent hydrolase |
| SCE1572_11071 | hypothetical protein | umi | see_9760 | 52.92 | FIG01089141: hypothetical protein |
| SCE1572_11072 | Thioredoxin reductase (EC 1.8.1.9) | bi | see_9822 | 84.64 | Thioredoxin reductase (EC 1.8.1.9) |
| SCE1572_11073 | hypothetical protein | bi | see_9823 | 89.73 | hypothetical protein |
| SCE1572_11074 | hypothetical protein | bi | see_9824 | 82.17 | hypothetical protein |
| SCE1572_11075 | RNA polymerase sigma-70 factor | bi | see_9825 | 95.6 | RNA polymerase sigma-70 factor |
| SCE1572_11076 | collagen-like protein SclB | bi | see_9826 | 73.82 | collagen-like protein SclB |
| SCE1572_11077 | Transcription elongation factor | bi | see_9827 | 90.18 | Transcription elongation factor |
| SCE1572_11078 | hypothetical protein | - | - | 0 | 0 |
| SCE1572_11079 | Response regulator | bi | see_9829 | 70.94 | Response regulator |
| SCE1572_11080 | Sensory histidine kinase CreB | bi | see_9830 | 81.7 | Sensory histidine kinase CreB |
| SCE1572_11081 | sensor histidine kinase | bi | see_9831 | 78.18 | sensor histidine kinase |
| SCE1572_11082 | Two component response regulator | bi | see_9832 | 86.97 | Two component response regulator |
| SCE1572_11083 | response regulator | bi | see_9833 | 77.12 | response regulator |
| SCE1572_11084 | hypothetical protein | - | - | 0 | 0 |
| SCE1572_11085 | Aspartyl/Asparaginyl beta-hydroxylase | - | - | 0 | 0 |
| SCE1572_11086 | hypothetical protein | - | - | 0 | 0 |
| SCE1572_11087 | Methylthioribulose-1-phosphate dehydratase (EC 4.2.1.109) | umi | see_1720 | 46.6 | Methylthioribulose-1-phosphate dehydratase (EC 4.2.1.109) |
| SCE1572_11088 | 1,2-dihydroxy-3-keto-5-methylthiopentene dioxigenase (EC 1.13.11.54) | umi | see_1721 | 50 | 1,2-dihydroxy-3-keto-5-methylthiopentene dioxigenase (EC 1.13.11.54) |
| SCE1572_11089 | Methylthioribose-1-phosphate isomerase (EC 5.3.1.23) | umi | see_1751 | 45.88 | Methylthioribose-1-phosphate isomerase (EC 5.3.1.23) |
| SCE1572_11090 | Aspartate aminotransferase (EC 2.6.1.1) | bi | see_9835 | 90.86 | Aspartate aminotransferase (EC 2.6.1.1) |
| SCE1572_11091 | putative nicotianamine synthase | bi | see_9836 | 90.44 | nicotianamine synthase 3 |
| SCE1572_11092 | hypothetical protein | - | - | 0 | 0 |
| SCE1572_11093 | Asparagine synthetase [glutamine-hydrolyzing] (EC 6.3.5.4) | bi | see_9837 | 89.85 | Asparagine synthetase [glutamine-hydrolyzing] (EC 6.3.5.4) |
| SCE1572_11094 | DNA-damage-inducible protein | bi | see_9838 | 84.14 | DNA-damage-inducible protein |
| SCE1572_11095 | putative methylase of polypeptide chain release factor | - | - | 0 | 0 |
| SCE1572_11096 | Gill1302 protein | bi | see_9839 | 87.06 | Gill1302 protein |
| SCE1572_11097 | conserved hypothetical protein | bi | see_9840 | 89.52 | hypothetical protein |
| SCE1572_11098 | TonB-dependent receptor | bi | see_9841 | 86.18 | TonB-dependent receptor |
| SCE1572_11099 | probable ABC transporter ATP-binding protein | bi | see_9842 | 89.15 | probable ABC transporter ATP-binding protein |
| SCE1572_11100 | FIG00559100: hypothetical protein | umi | see_1878 | 47.62 | FIG01087871: hypothetical protein |
| SCE1572_11101 | hypothetical protein | - | - | 0 | 0 |
| SCE1572_11102 | COG1028: Dehydrogenases with different specificities (related to short-chain alcohol dehydrogenases) | bi | see_9843 | 93.36 | short-chain dehydrogenase/reductase SDR |
| SCE1572_11103 | hypothetical protein | bi | see_6096 | 70.67 | FIG01085366: hypothetical protein |
| SCE1572_11104 | RNA polymerase sigma factor RpoE | bi | see_6097 | 88.1 | RNA polymerase sigma factor RpoE |
| SCE1572_11105 | hypothetical protein | bi | see_6098 | 79.06 | hypothetical protein |
| SCE1572_11106 | FIG01087202: hypothetical protein | bi | see_6099 | 72.4 | FIG01087202: hypothetical protein |
| SCE1572_11107 | hydrolase, alpha/beta fold family | - | - | 0 | 0 |
| SCE1572_11108 | HupE-UreJ family metal transporter | - | - | 0 | 0 |
| SCE1572_11109 | hypothetical protein | - | - | 0 | 0 |
| SCE1572_11110 | Aromatic hydrocarbon utilization transcriptional regulator CatR (LysR family) | umi | see_3966 | 55.42 | LysR family transcriptional regulator YnfL |
| SCE1572_11111 | FIG01088103: hypothetical protein | bi | see_311 | 56.35 | FIG01088103: hypothetical protein |
| SCE1572_11112 | Putative methyltransferase | bi | see_1119 | 44.75 | Methyltransferase |
| SCE1572_11113 | cytochrome c Hsc | bi | see_9847 | 77.17 | Cytochrome c peroxidase (EC 1.11.1.5) |
| SCE1572_11114 | Beta-lactamase class C and other penicillin binding proteins | bi | see_7062 | 95.42 | Beta-lactamase class C and other penicillin binding proteins |
| SCE1572_11115 | Type III effector HrpW, hairpin with peptate lyase domain | umi | see_5529 | 62.86 | Type III effector HrpW, hairpin with peptate lyase domain |
| SCE1572_11116 | Transcriptional regulator, TetR family | umi | see_1100 | 35.53 | Transcriptional regulator, GntR family / Transcriptional regulator, TetR family |
| SCE1572_11117 | FIG00814846: hypothetical protein | bi | see_6854 | 59.34 | hypothetical protein |
| SCE1572_11118 | RsbR, positive regulator of sigma-B | bi | see_8356 | 76.2 | RsbR, positive regulator of sigma-B |
| SCE1572_11119 | FIG00841528: hypothetical protein | bi | see_8357 | 84.04 | FIG00841528: hypothetical protein |
| SCE1572_11120 | Transcriptional regulator, ArsR family | bi | see_6777 | 88 | Transcriptional regulator, ArsR family |
| SCE1572_11121 | hypothetical protein | bi | see_6778 | 90.3 | hypothetical protein |
| SCE1572_11122 | hypothetical protein | umi | see_540 | 37.61 | FIG01089269: hypothetical protein |
| SCE1572_11123 | FIG01086874: hypothetical protein | umi | see_1320 | 70.35 | FIG01086874: hypothetical protein |
| SCE1572_11124 | FIG01086874: hypothetical protein | bi | see_1320 | 76.22 | FIG01086874: hypothetical protein |
| SCE1572_11125 | FIG01089035: hypothetical protein | bi | see_3466 | 77.84 | FIG01089035: hypothetical protein |
| SCE1572_11126 | 5'-nucleotidase (EC 3.1.3.5) | bi | see_9853 | 83.62 | 5'-nucleotidase (EC 3.1.3.5) |
| SCE1572_11127 | transcriptional regulator, LuxR family protein | umi | see_4598 | 42.42 | Response regulator |
| SCE1572_11128 | hypothetical protein | - | - | 0 | 0 |
| SCE1572_11129 | conserved hypothetical protein-putative thiol-disulfide isomerase or thioredoxin | bi | see_9861 | 71.81 | hypothetical protein |
| SCE1572_11130 | FIG01088894: hypothetical protein | bi | see_3722 | 82.12 | FIG01088894: hypothetical protein |
| SCE1572_11131 | Ribose ABC transport system, permease protein RbsC (TC 3.A.1.2.1) | bi | see_3725 | 93.61 | Ribose ABC transport system, permease protein RbsC (TC 3.A.1.2.1) |
| SCE1572_11132 | Ribose ABC transport system, ATP-binding protein RbsA (TC 3.A.1.2.1) | bi | see_3724 | 84.78 | Ribose ABC transport system, ATP-binding protein RbsA (TC 3.A.1.2.1) |
| SCE1572_11133 | Ribose ABC transport system, periplasmic ribose-binding protein RbsB (TC 3.A.1.2.1) | bi | see_3723 | 82.94 | Ribose ABC transport system, periplasmic ribose-binding protein RbsB (TC 3.A.1.2.1) |
| SCE1572_11134 | Endo alpha-1,4 polygalactosaminidase precursor precursor | bi | see_8378 | 82.87 | Endo alpha-1,4 polygalactosaminidase precursor precursor |
| SCE1572_11135 | domain of unknown function DUF1745 | umi | see_9411 | 26.63 | hypothetical protein |
| SCE1572_11136 | PAS/PAC sensor signal transduction histidine kinase | umi | see_9831 | 30.41 | sensor histidine kinase |
| SCE1572_11137 | FIG01087499: hypothetical protein | bi | see_8625 | 70.05 | FIG01087499: hypothetical protein |
| SCE1572_11138 | hypothetical protein | - | - | 0 | 0 |
| SCE1572_11139 | Malonyl CoA-acyl carrier protein transacylase (EC 2.3.1.39) | umi | see_3858 | 33.8 | Adenosylhomocysteinase (EC 3.3.1.1) |
| SCE1572_11140 | hypothetical protein | - | - | 0 | 0 |
| SCE1572_11141 | Internalin-like protein (LPXTG motif) Lmo0333 homolog | umi | see_7385 | 55.69 | Internalin-like protein (LPXTG motif) Lmo0333 homolog |
| SCE1572_11142 | hypothetical protein | - | - | 0 | 0 |
| SCE1572_11143 | Enoyl-[acyl-carrier-protein] reductase [NADPH] (EC 1.3.1.10) | umi | see_9845 | 54.07 | Enoyl-[acyl-carrier-protein] reductase [NADPH] (EC 1.3.1.10) |
| SCE1572_11144 | Transcriptional regulator, TetR family | umi | see_9844 | 54.4 | Transcriptional regulator, TetR family |
| SCE1572_11145 | Azoreductase | bi | see_9872 | 83.74 | Azoreductase |
| SCE1572_11146 | Chemotaxis protein methyltransferase CheR (EC 2.1.1.80) | umi | see_9491 | 47.34 | Chemotaxis protein methyltransferase CheR (EC 2.1.1.80) |
| SCE1572_11147 | Long-chain-fatty-acid-CoA ligase (EC 6.2.1.3) | umi | see_4350 | 26.72 | Non-ribosomal peptide synthase MxG |
| SCE1572_11148 | hypothetical protein | umi | see_4745 | 41.41 | HAD-superfamily hydrolase, subfamily 1A, variant 3 |
| SCE1572_11149 | hypothetical protein | - | - | 0 | 0 |
| SCE1572_11150 | Probable lipoprotein | - | - | 0 | 0 |
| SCE1572_11151 | Trans-aconitate 2-methyltransferase (EC 2.1.1.144) | bi | see_9873 | 89.11 | Trans-aconitate 2-methyltransferase (EC 2.1.1.144) |

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|---------------|--|-----|-----------|---|
| SCE1572_11152 | hypothetical protein | bi | sce_9874 | 85.88 hypothetical protein |
| SCE1572_11153 | 3-oxoacyl-[acyl-carrier protein] reductase (EC 1.1.1.100) | bi | sce_8393 | 58.91 3-oxoacyl-[acyl-carrier protein] reductase (EC 1.1.1.100) |
| SCE1572_11154 | hypothetical protein | - | - | 0 |
| SCE1572_11155 | Transcriptional regulator, LysR family | uni | sce_6321 | 44.2 Transcriptional regulator, LysR family |
| SCE1572_11156 | hypothetical protein | bi | sce_7817 | 75.61 hypothetical protein |
| SCE1572_11157 | FIG01087249: hypothetical protein | bi | sce_2338 | 95 Transposase |
| SCE1572_11158 | FIG01087249: hypothetical protein | uni | sce_2337 | 87.95 FIG01087249: hypothetical protein |
| SCE1572_11159 | putative transcriptional regulator | bi | sce_9876 | 87.43 transcriptional regulator, MarR family |
| SCE1572_11160 | Methanol oxidation genes, glmU-like | bi | sce_9877 | 79.11 Methanol oxidation genes, glmU-like |
| SCE1572_11161 | Endoglucanase (EC 3.2.1.4) | bi | sce_9887 | 77.92 Endoglucanase (EC 3.2.1.4) |
| SCE1572_11162 | Histidinol-phosphate aminotransferase (EC 2.6.1.9) | bi | sce_9888 | 91.69 Histidinol-phosphate aminotransferase (EC 2.6.1.9) |
| SCE1572_11163 | FIG01089677: hypothetical protein | bi | sce_9890 | 94.25 FIG01089677: hypothetical protein |
| SCE1572_11164 | Helix-turn-helix motif | - | - | 0 |
| SCE1572_11165 | Beta-phosphoglucomutase (EC 5.4.2.6) | bi | sce_9891 | 84.31 Beta-phosphoglucomutase (EC 5.4.2.6) |
| SCE1572_11166 | hypothetical protein | bi | sce_9892 | 91.15 hypothetical protein |
| SCE1572_11167 | COGs COG0840 | uni | sce_8358 | 65.52 COGs COG0840 |
| SCE1572_11168 | Xylose ABC transporter, substrate-binding component | uni | sce_6685 | 54 Xylose ABC transporter, substrate-binding component |
| SCE1572_11169 | Gli0645 protein | uni | sce_7494 | 41.2 FIG01087054: hypothetical protein |
| SCE1572_11170 | FIG01087915: hypothetical protein | bi | sce_10020 | 93.06 FIG01087915: hypothetical protein |
| SCE1572_11171 | hypothetical protein | bi | sce_10021 | 77.48 hypothetical protein |
| SCE1572_11172 | Transcriptional regulator, DeoR family | bi | sce_9911 | 86.02 Transcriptional regulator, DeoR family |
| SCE1572_11173 | Blf7849 protein | bi | sce_9912 | 84.71 Blf7849 protein |
| SCE1572_11174 | FIG01086704: hypothetical protein | bi | sce_9913 | 71.58 FIG01086704: hypothetical protein |
| SCE1572_11175 | FIG01087821: hypothetical protein | bi | sce_9914 | 84.51 FIG01087821: hypothetical protein |
| SCE1572_11176 | hypothetical protein | - | - | 0 |
| SCE1572_11177 | FIG01087702: hypothetical protein | bi | sce_9915 | 88.93 FIG01087702: hypothetical protein |
| SCE1572_11178 | hypothetical protein | - | - | 0 |
| SCE1572_11179 | hypothetical protein | bi | sce_9922 | 94.61 FIG01086687: hypothetical protein |
| SCE1572_11180 | hypothetical protein | bi | sce_9924 | 76.11 cell wall surface anchor family protein |
| SCE1572_11181 | FIG01089161: hypothetical protein | bi | sce_9925 | 95.5 FIG01089161: hypothetical protein |
| SCE1572_11182 | hypothetical protein | bi | sce_9926 | 56.36 Predicted outer membrane protein |
| SCE1572_11183 | putative methyltransferase | bi | sce_9927 | 89.67 putative methyltransferase |
| SCE1572_11184 | Thi/PpfJ family protein | uni | sce_6953 | 30.86 Protein ThiJ |
| SCE1572_11185 | oxidoreductase, short chain dehydrogenase/reductase family | uni | sce_49 | 54.39 Oxidoreductase |
| SCE1572_11186 | Collagen triple helix repeat | bi | sce_9928 | 60.77 PE-PGRS FAMILY PROTEIN |
| SCE1572_11187 | hypothetical protein | - | - | 0 |
| SCE1572_11188 | hypothetical protein | - | - | 0 |
| SCE1572_11189 | hypothetical protein | bi | sce_2238 | 67.36 hypothetical protein |
| SCE1572_11190 | hypothetical protein | - | - | 0 |
| SCE1572_11191 | Adenylosuccinate synthetase (EC 6.3.4.4) | bi | sce_9930 | 97.42 Adenylosuccinate synthetase (EC 6.3.4.4) |
| SCE1572_11192 | ATP phosphoribosyltransferase regulatory subunit (EC 2.4.2.17) | bi | sce_9931 | 90.09 ATP phosphoribosyltransferase regulatory subunit (EC 2.4.2.17) |
| SCE1572_11193 | RNA polymerase sigma-54 factor RpoN | bi | sce_9932 | 97.94 RNA polymerase sigma-54 factor RpoN |
| SCE1572_11194 | Phosphoglycolate phosphatase (EC 3.1.3.18) | bi | sce_9933 | 83.98 Phosphoglycolate phosphatase (EC 3.1.3.18) |
| SCE1572_11195 | hypothetical protein | bi | sce_9948 | 70.23 hypothetical protein |
| SCE1572_11196 | conserved protein with diacylglycerol kinase catalytic domain | bi | sce_9947 | 83.22 conserved protein with diacylglycerol kinase catalytic domain |
| SCE1572_11197 | hypothetical protein | uni | sce_5889 | 28.57 NADH-ubiquinone oxidoreductase chain J (EC 1.6.5.3) |
| SCE1572_11198 | Cysteine desulfurase (EC 2.8.1.7) | bi | sce_9949 | 93.33 Cysteine desulfurase (EC 2.8.1.7) |
| SCE1572_11199 | FIG01089170: hypothetical protein | bi | sce_9950 | 84.57 FIG01089170: hypothetical protein |
| SCE1572_11200 | putative cytochrome P450 hydroxylase | bi | sce_9951 | 81.38 putative cytochrome P450 hydroxylase |
| SCE1572_11201 | FIG01086948: hypothetical protein | bi | sce_9952 | 63.28 FIG01086948: hypothetical protein |
| SCE1572_11202 | histidinol-phosphate aminotransferase | bi | sce_9953 | 87.68 Biosynthetic Aromatic amino acid aminotransferase beta (EC 2.6.1.57) |
| SCE1572_11203 | hypothetical protein | - | - | 0 |
| SCE1572_11204 | ATPase | - | - | 0 |
| SCE1572_11205 | hypothetical protein | - | - | 0 |
| SCE1572_11206 | Adenylate cyclase (EC 4.6.1.1) / Guanylate cyclase (EC 4.6.1.2) | bi | sce_9954 | 93.53 Adenylate cyclase (EC 4.6.1.1) / Guanylate cyclase (EC 4.6.1.2) |
| SCE1572_11207 | hypothetical protein | bi | sce_3482 | 51.11 Adenylosuccinate synthetase (EC 6.3.4.4) |
| SCE1572_11208 | Coenzyme F390 synthetase | bi | sce_9956 | 88.82 Coenzyme F390 synthetase |
| SCE1572_11209 | Poly(glycerol-phosphate) alpha-glucosyltransferase (EC 2.4.1.52) | bi | sce_9957 | 89.95 Poly(glycerol-phosphate) alpha-glucosyltransferase (EC 2.4.1.52) |
| SCE1572_11210 | hypothetical protein | bi | sce_9963 | 82.71 hypothetical protein |
| SCE1572_11211 | FIG01089506: hypothetical protein | bi | sce_9964 | 78.13 FIG01089506: hypothetical protein |
| SCE1572_11212 | putative sigma-54 dependent transcriptional regulator | uni | sce_5675 | 51.31 Two-component system regulatory protein |
| SCE1572_11213 | hypothetical protein | - | - | 0 |
| SCE1572_11214 | Type IV fimbrial biogenesis protein PilY1 | uni | sce_3794 | 50.66 Type IV fimbrial biogenesis protein PilY1 |
| SCE1572_11215 | WD-40 repeat protein | uni | sce_7069 | 65.61 WD-40 repeat protein |
| SCE1572_11216 | hypothetical protein | uni | sce_3796 | 52.79 hypothetical protein |
| SCE1572_11217 | FIG01085128: hypothetical protein | bi | sce_9972 | 71.28 FIG01085128: hypothetical protein |
| SCE1572_11218 | Catabolite control protein A | bi | sce_9973 | 82.58 Catabolite control protein A |
| SCE1572_11219 | hypothetical protein | - | - | 0 |
| SCE1572_11220 | transcriptional regulator, LysR family | uni | sce_3645 | 38.74 Transcriptional regulator, LysR family |
| SCE1572_11221 | hypothetical protein | - | - | 0 |
| SCE1572_11222 | 3-oxoacyl-[acyl-carrier protein] reductase (EC 1.1.1.100) | uni | sce_5211 | 46.18 3-oxoacyl-[acyl-carrier protein] reductase (EC 1.1.1.100) |
| SCE1572_11223 | hypothetical protein | bi | sce_4542 | 91.3 hypothetical protein |
| SCE1572_11224 | Kazal domain protein | uni | sce_2393 | 86.67 Kazal domain protein |
| SCE1572_11225 | Putative outer membrane protein | bi | sce_2399 | 98.02 Putative outer membrane protein |
| SCE1572_11226 | FIG01089115: hypothetical protein | bi | sce_2398 | 97.42 FIG01089115: hypothetical protein |
| SCE1572_11227 | NAD dependent epimerase/dehydratase family protein | bi | sce_2397 | 98.53 3-beta hydroxysteroid dehydrogenase/isomerase family protein in hypothetical gene cluster |
| SCE1572_11228 | Transcriptional regulator, TetR family | bi | sce_2396 | 98.65 Transcriptional regulator, TetR family |
| SCE1572_11229 | hypothetical protein | - | - | 0 |
| SCE1572_11230 | endo-1, 4-beta-xylanase | bi | sce_4485 | 85.32 Endo-1,4-beta-xylanase C precursor (EC 3.2.1.8) (Xylanase C) (1,4-beta-D-xylan xylanohydrolase C) |
| SCE1572_11231 | Catabolite control protein A | bi | sce_9974 | 81.76 Catabolite control protein A |
| SCE1572_11232 | hypothetical protein | bi | sce_9975 | 84.11 hypothetical protein |
| SCE1572_11233 | hypothetical protein | bi | sce_9976 | 76.6 conserved hypothetical protein |
| SCE1572_11234 | UDP-glucose 4-epimerase (EC 5.1.3.2) | uni | sce_7585 | 69.35 UDP-glucose 4-epimerase (EC 5.1.3.2) |
| SCE1572_11235 | NAD-dependent epimerase/dehydratase | bi | sce_9977 | 83.01 NAD-dependent epimerase/dehydratase |
| SCE1572_11236 | Radical SAM domain protein | bi | sce_9978 | 83.68 Radical SAM domain protein |
| SCE1572_11237 | Glycosyltransferase | bi | sce_9979 | 87.22 Glycosyltransferase |
| SCE1572_11238 | Uncharacterized protein conserved in bacteria | bi | sce_9980 | 85.96 Uncharacterized protein conserved in bacteria |
| SCE1572_11239 | dTDP-glucose 4,6-dehydratase (EC 4.2.1.46) | bi | sce_9981 | 84.52 dTDP-glucose 4,6-dehydratase (EC 4.2.1.46) |
| SCE1572_11240 | hypothetical protein | bi | sce_3744 | 80.41 hypothetical protein |
| SCE1572_11241 | Oxidoreductase | uni | sce_5896 | 45.99 putative oxidoreductase |
| SCE1572_11242 | Endoglucanase B precursor (EC 3.2.1.4) (Endo-1,4-beta-glucanase B) (Cellulase B) | bi | sce_1013 | 85.58 Endoglucanase B precursor (EC 3.2.1.4) (Endo-1,4-beta-glucanase B) (Cellulase B) |
| SCE1572_11243 | Ribosomal protein L11 methyltransferase (EC 2.1.1.-) | bi | sce_4521 | 85.86 Ribosomal protein L11 methyltransferase (EC 2.1.1.-) |
| SCE1572_11244 | FIG01085402: hypothetical protein | bi | sce_10033 | 86.92 FIG01085402: hypothetical protein |
| SCE1572_11245 | hypothetical protein | - | - | 0 |
| SCE1572_11246 | Patatin | bi | sce_5205 | 64.22 Patatin |
| SCE1572_11247 | hypothetical protein | - | - | 0 |
| SCE1572_11248 | vitamin K-dependent protein C (Autoproteolysin IIA) (Anticoagulant protein C) (Blood coagulation factor XIV) (EC 3.4.21.6) | bi | sce_597 | 32.2 Secreted trypsin-like serine protease |
| SCE1572_11249 | Phosphatidylglycerophosphate B (EC 3.1.3.27) | bi | sce_10035 | 81.23 Phosphatidylglycerophosphate B (EC 3.1.3.27) |
| SCE1572_11250 | TOBE domain protein | - | - | 0 |
| SCE1572_11251 | Outer membrane stress sensor protease DegS | uni | sce_4661 | 39.5 DegP protease |
| SCE1572_11252 | hypothetical protein | - | - | 0 |
| SCE1572_11253 | Multiple EGF-like-domain protein 3 precursor | bi | sce_10036 | 81.03 Multiple EGF-like-domain protein 3 precursor |
| SCE1572_11254 | Sensor protein | bi | sce_10037 | 88.74 Sensor protein |
| SCE1572_11255 | methyl-accepting chemotaxis sensory transducer | bi | sce_10038 | 92.68 methyl-accepting chemotaxis sensory transducer |
| SCE1572_11256 | FIG01088757: hypothetical protein | bi | sce_10039 | 80.47 FIG01088757: hypothetical protein |
| SCE1572_11257 | acireductone dioxygenase enzyme ARD and ARD#39; | bi | sce_10040 | 83.01 acireductone dioxygenase enzyme ARD and ARD#39; |
| SCE1572_11258 | hypothetical protein | bi | sce_10041 | 91.74 hypothetical protein |
| SCE1572_11259 | NADH-FMN oxidoreductase | bi | sce_10042 | 92.88 NADH-FMN oxidoreductase |
| SCE1572_11260 | 5,10-methylenetetrahydrofolate reductase (EC 1.5.1.20) | bi | sce_10043 | 94.39 5,10-methylenetetrahydrofolate reductase (EC 1.5.1.20) |
| SCE1572_11261 | NAD/NADP transhydrogenase alpha subunit | bi | sce_10044 | 90.53 NAD/NADP transhydrogenase alpha subunit |
| SCE1572_11262 | Glycosyltransferase | bi | sce_10045 | 87.71 glycosyl transferase, group 1 |
| SCE1572_11263 | Selenophosphate synthetase-related proteins | bi | sce_10046 | 89.15 Selenophosphate synthetase-related proteins |
| SCE1572_11264 | Histone acetyltransferase HPA2 and related acetyltransferases | bi | sce_10047 | 89.8 hypothetical protein |
| SCE1572_11265 | Biotin synthase-related enzyme | bi | sce_10048 | 92.99 Biotin synthase-related enzyme |
| SCE1572_11266 | Nitrilase (EC 3.5.5.7) | bi | sce_10049 | 96.77 Nitrilase (EC 3.5.5.7) |
| SCE1572_11267 | FIG00452614: hypothetical protein | bi | sce_10050 | 99.38 FIG00452614: hypothetical protein |
| SCE1572_11268 | 3'-to-5'-exoribonuclease RNase R | bi | sce_10051 | 93.54 3'-to-5'-exoribonuclease RNase R |
| SCE1572_11269 | DSBA oxidoreductase | bi | sce_10052 | 79.01 DsbA oxidoreductase |
| SCE1572_11270 | Adenosine deaminase (EC 3.5.4.4) | bi | sce_10053 | 92.44 Adenosine deaminase (EC 3.5.4.4) |
| SCE1572_11271 | NAD synthetase (EC 6.3.1.5) / Glutamine amidotransferase chain of NAD synthetase | bi | sce_10054 | 94.21 NAD synthetase (EC 6.3.1.5) / Glutamine amidotransferase chain of NAD synthetase |
| SCE1572_11272 | PE-PGRS FAMILY PROTEIN | bi | sce_10055 | 85.02 FIG01087036: hypothetical protein |
| SCE1572_11273 | hypothetical protein | bi | sce_10056 | 94.08 hypothetical protein |
| SCE1572_11274 | Response regulator of zinc sigma-54-dependent two-component system | bi | sce_10057 | 97.52 diguanylate cyclase (GGDEF domain) |
| SCE1572_11275 | FHA domain protein | bi | sce_10058 | 95.14 FHA domain protein |
| SCE1572_11276 | hypothetical protein | bi | sce_10060 | 83.89 hypothetical protein |
| SCE1572_11277 | Phosphoribosylamine-glycine ligase (EC 6.3.4.13) | bi | sce_10061 | 94.13 Phosphoribosylamine-glycine ligase (EC 6.3.4.13) |
| SCE1572_11278 | hypothetical protein | - | - | 0 |
| SCE1572_11279 | dCMP deaminase (EC 3.5.4.12); Late competence protein ComEB | bi | sce_10062 | 96.3 dCMP deaminase (EC 3.5.4.12); Late competence protein ComEB |
| SCE1572_11280 | Flagellar regulatory protein FleQ | bi | sce_10063 | 88.22 Flagellar regulatory protein FleQ |
| SCE1572_11281 | Adenylate cyclase (EC 4.6.1.1) / Guanylate cyclase (EC 4.6.1.2) | bi | sce_10064 | 84.03 Adenylate cyclase (EC 4.6.1.1) / Guanylate cyclase (EC 4.6.1.2) |
| SCE1572_11282 | conserved hypothetical protein SCD8A.23 | bi | sce_10065 | 82.24 hypothetical protein |
| SCE1572_11283 | hypothetical protein | bi | sce_10067 | 89.69 FIG01084893: hypothetical protein |
| SCE1572_11284 | FIG01087187: hypothetical protein | bi | sce_10068 | 85.34 FIG01087187: hypothetical protein |
| SCE1572_11285 | Peptide deformylase (EC 3.5.1.88) | bi | sce_10069 | 90.65 Peptide deformylase (EC 3.5.1.88) |
| SCE1572_11286 | 5'-nucleotidase (EC 3.1.3.5) | bi | sce_1373 | 46.33 5'-nucleotidase (EC 3.1.3.5) |
| SCE1572_11287 | C4-type zinc finger protein, DksA/TrfR family | bi | sce_10070 | 94.85 C4-type zinc finger protein, DksA/TrfR family |
| SCE1572_11288 | FIG01086802: hypothetical protein | bi | sce_10071 | 84.59 FIG01086802: hypothetical protein |
| SCE1572_11289 | hypothetical protein | - | - | 0 |
| SCE1572_11290 | Chaperone protein DnaK | bi | sce_10072 | 96.87 Chaperone protein DnaK |
| SCE1572_11291 | LSU ribosomal protein L31p | bi | sce_10074 | 100 LSU ribosomal protein L31p |
| SCE1572_11292 | hypothetical protein | bi | sce_10075 | 90.72 FIG069887: hypothetical protein |
| SCE1572_11293 | Peptide chain release factor 1 | bi | sce_10076 | 95.37 Peptide chain release factor 1 |
| SCE1572_11294 | hypothetical protein | bi | sce_10077 | 84.95 hypothetical protein |
| SCE1572_11295 | Bis(5'-nucleosyl)-tetraphosphate (asymmetrical) (EC 3.6.1.17) | bi | sce_10078 | 91.07 HIT family hydrolase |
| SCE1572_11296 | FAD linked oxidase domain protein | bi | sce_10079 | 92.34 Alkylhydroxyacetonephosphate synthase |
| SCE1572_11297 | methyltransferase, putative | bi | sce_10080 | 77.94 hypothetical protein |
| SCE1572_11298 | Phosphatidylserine decarboxylase (EC 4.1.1.65) | bi | sce_10081 | 92.95 Phosphatidylserine decarboxylase (EC 4.1.1.65) |
| SCE1572_11299 | Metal-dependent hydrolases of the beta-lactamase superfamily 1 | bi | sce_10082 | 89.19 Metal-dependent hydrolases of the beta-lactamase superfamily 1 |
| SCE1572_11300 | Response regulator of zinc sigma-54-dependent two-component system | bi | sce_10083 | 94.92 Response regulator of zinc sigma-54-dependent two-component system |
| SCE1572_11301 | hypothetical protein | bi | sce_10084 | 52.74 FIG01085160: hypothetical protein |
| SCE1572_11302 | TPR domain protein | bi | sce_10085 | 90.63 TPR domain protein |
| SCE1572_11303 | Response regulator receiver | bi | sce_10086 | 88.88 Methyl-accepting chemotaxis protein |
| SCE1572_11304 | hypothetical protein | bi | sce_10087 | 90.89 hypothetical protein |
| SCE1572_11305 | hypothetical protein | - | - | 0 |
| SCE1572_11306 | DsbA oxidoreductase | bi | sce_10088 | 84.58 DsbA oxidoreductase |
| SCE1572_11307 | histone protein | bi | sce_10089 | 74.88 hypothetical protein |
| SCE1572_11308 | diene lactone hydrolase | bi | sce_10090 | 89.84 Hydrolases of the alpha/beta superfamily |
| SCE1572_11309 | Fibronin 1 | bi | sce_10091 | 84.32 Fibronin 1 |
| SCE1572_11310 | Tat (twin-arginine translocation) pathway signal sequence domain protein | uni | sce_3293 | 34.53 Tat (Twin-arginine translocation) pathway signal sequence domain protein |
| SCE1572_11311 | Cellulose-binding domain protein | uni | sce_3292 | 42.54 Cellulose-binding domain protein |
| SCE1572_11312 | hypothetical protein | - | - | 0 |
| SCE1572_11313 | Inorganic pyrophosphatase (EC 3.6.1.1) | bi | sce_10092 | 99.44 Inorganic pyrophosphatase (EC 3.6.1.1) |
| SCE1572_11314 | hypothetical protein | - | - | 0 |
| SCE1572_11315 | Cellulose-binding domain protein | bi | sce_10095 | 79.2 Cellulose-binding domain protein |

| | | | | | |
|---------------|--|-----|-----------|-------|---|
| SCE1572_11316 | Tat (twin-arginine translocation) pathway signal sequence domain protein | bi | see_10096 | 82.39 | Tat (twin-arginine translocation) pathway signal sequence domain protein |
| SCE1572_11317 | Tat (Twin-arginine translocation) pathway signal sequence domain protein | bi | see_10097 | 87.41 | Tat (Twin-arginine translocation) pathway signal sequence domain protein |
| SCE1572_11318 | Trans-aconitate 2-methyltransferase (EC 2.1.1.144) | bi | see_10098 | 85.47 | Trans-aconitate 2-methyltransferase (EC 2.1.1.144) |
| SCE1572_11319 | hypothetical protein | - | - | 0 | 0 |
| SCE1572_11320 | hypothetical protein | bi | see_10100 | 70.85 | hypothetical protein |
| SCE1572_11321 | FIG01086074: hypothetical protein | bi | see_4678 | 92.59 | FIG01086074: hypothetical protein |
| SCE1572_11322 | rRNA delta(2)-isopentenylpyrophosphate transferase (EC 2.5.1.8) | bi | see_10101 | 88.82 | rRNA delta(2)-isopentenylpyrophosphate transferase (EC 2.5.1.8) |
| SCE1572_11323 | DNA mismatch repair protein MutL | bi | see_10102 | 85.26 | DNA mismatch repair protein MutL |
| SCE1572_11324 | hypothetical protein | bi | see_10103 | 92.35 | hypothetical protein |
| SCE1572_11325 | RNA polymerase sigma factor RpoH | bi | see_10105 | 85.27 | RNA polymerase sigma factor RpoH |
| SCE1572_11326 | rRNA small subunit methyltransferase I | bi | see_10106 | 94.79 | rRNA small subunit methyltransferase I |
| SCE1572_11327 | Mannose-1-phosphate guanylyltransferase (GDP) (EC 2.7.7.22) | bi | see_10107 | 86.39 | Mannose-1-phosphate guanylyltransferase (GDP) (EC 2.7.7.22) |
| SCE1572_11328 | hypothetical protein | - | - | 0 | 0 |
| SCE1572_11329 | hypothetical protein | - | - | 0 | 0 |
| SCE1572_11330 | NADH ubiquinone oxidoreductase chain A (EC 1.6.5.3) | bi | see_10110 | 87.13 | NADH ubiquinone oxidoreductase chain A (EC 1.6.5.3) |
| SCE1572_11331 | NADH-ubiquinone oxidoreductase chain B (EC 1.6.5.3) | bi | see_10111 | 98.35 | NADH-ubiquinone oxidoreductase chain B (EC 1.6.5.3) |
| SCE1572_11332 | NADH-ubiquinone oxidoreductase chain C (EC 1.6.5.3) | bi | see_10112 | 90.66 | NADH (or F420H2) dehydrogenase, subunit C |
| SCE1572_11333 | NADH-ubiquinone oxidoreductase chain D (EC 1.6.5.3) | bi | see_10113 | 96.65 | NADH-ubiquinone oxidoreductase chain D (EC 1.6.5.3) |
| SCE1572_11334 | putative PE-PGRS family protein | bi | see_10114 | 69 | putative PE-PGRS family protein |
| SCE1572_11335 | hypothetical protein | - | - | 0 | 0 |
| SCE1572_11336 | hypothetical protein | bi | see_10135 | 56 | hypothetical protein |
| SCE1572_11337 | O-methyltransferase, family 2 | uni | see_1355 | 24.41 | O-methyltransferase, family 2 |
| SCE1572_11338 | hypothetical protein | - | - | 0 | 0 |
| SCE1572_11339 | ATPase involved in DNA repair | uni | see_1995 | 49.25 | serine/threonine protein kinase |
| SCE1572_11340 | Transcriptional regulator, AraC family | bi | see_10140 | 85.42 | Transcriptional regulator, AraC family |
| SCE1572_11341 | hypothetical protein | - | - | 0 | 0 |
| SCE1572_11342 | FIG01088430: hypothetical protein | bi | see_10141 | 81.68 | FIG01088430: hypothetical protein |
| SCE1572_11343 | Redoxin domain protein | bi | see_10142 | 91.71 | Redoxin domain protein |
| SCE1572_11344 | Phycocyanin alpha-subunit phycocyanobilin lyase | bi | see_10143 | 92.39 | hypothetical protein |
| SCE1572_11345 | FIG01088124: hypothetical protein | bi | see_10144 | 92.7 | FIG01088124: hypothetical protein |
| SCE1572_11346 | Probable aminopeptidase (EC 3.4.11.-) | bi | see_10145 | 81.9 | Aminopeptidase Y (Arg, Lys, Leu preference) (EC 3.4.11.15) |
| SCE1572_11347 | Butyryl-CoA dehydrogenase (EC 1.3.99.2) | bi | see_10146 | 74.1 | Butyryl-CoA dehydrogenase (EC 1.3.99.2) |
| SCE1572_11348 | Single-stranded DNA-binding protein | bi | see_10147 | 88.44 | Single-stranded DNA-binding protein |
| SCE1572_11349 | hypothetical protein | - | - | 0 | 0 |
| SCE1572_11350 | hypothetical protein | - | - | 0 | 0 |
| SCE1572_11351 | FIG01085109: hypothetical protein | uni | see_3937 | 48.13 | FIG01085109: hypothetical protein |
| SCE1572_11352 | hypothetical protein | - | - | 0 | 0 |
| SCE1572_11353 | hypothetical protein | - | - | 0 | 0 |
| SCE1572_11354 | 2-dehydropanoate 2-reductase (EC 1.1.1.169) homolog | bi | see_10188 | 84.17 | 2-dehydropanoate 2-reductase (EC 1.1.1.169) homolog |
| SCE1572_11355 | 2,4-dienoyl-CoA reductase [NADPH] (EC 1.3.1.34) | uni | see_6300 | 40 | putative FMN oxidoreductase |
| SCE1572_11356 | Transcriptional regulator, TetR family | bi | see_10189 | 79.06 | Transcriptional regulator, TetR family |
| SCE1572_11357 | endonuclease/exonuclease/phosphatase family protein | uni | see_10339 | 29.93 | hypothetical protein |
| SCE1572_11358 | hypothetical protein | uni | see_1495 | 58.33 | Collagen triple helix repeat |
| SCE1572_11359 | rRNA nucleotidyltransferase, A-adding (EC 2.7.7.25) | uni | see_3692 | 56.39 | rRNA nucleotidyltransferase, A-adding (EC 2.7.7.25) |
| SCE1572_11360 | PUTATIVE OMEGA-3 FATTY ACID DESATURASE TRANSMEMBRANE PROTEIN | bi | see_10195 | 90.99 | PUTATIVE OMEGA-3 FATTY ACID DESATURASE TRANSMEMBRANE PROTEIN |
| SCE1572_11361 | Fumarate hydratase class II (EC 4.2.1.2) | bi | see_10196 | 92.67 | Fumarate hydratase class II (EC 4.2.1.2) |
| SCE1572_11362 | OmpA/MotB | bi | see_10202 | 74.32 | hypothetical protein |
| SCE1572_11363 | hypothetical protein | bi | see_10203 | 90.52 | hypothetical protein |
| SCE1572_11364 | RsbR, positive regulator of sigma-B | bi | see_10204 | 87.13 | Signal transduction histidine kinase CheA (EC 2.7.3.-) |
| SCE1572_11365 | Vitamin K-dependent gamma-carboxylase | uni | see_10205 | 78.85 | Vitamin K-dependent gamma-carboxylase |
| SCE1572_11366 | N-hydroxyarylamine O-acetyltransferase | uni | see_5963 | 48.8 | N-hydroxyarylamine O-acetyltransferase (EC 2.3.1.118) |
| SCE1572_11367 | transcriptional regulator, LysR family | uni | see_9329 | 38.82 | Transcriptional regulator, LysR family |
| SCE1572_11368 | hypothetical protein | - | - | 0 | 0 |
| SCE1572_11369 | hypothetical protein | - | - | 0 | 0 |
| SCE1572_11370 | Vitamin K-dependent gamma-carboxylase | bi | see_10205 | 86.3 | Vitamin K-dependent gamma-carboxylase |
| SCE1572_11371 | hypothetical protein | bi | see_10206 | 84.27 | FIG01088316: hypothetical protein |
| SCE1572_11372 | Uncharacterized oxidoreductase ydgJ (EC 1.-.-.-) | bi | see_10209 | 93.31 | Uncharacterized oxidoreductase ydgJ (EC 1.-.-.-) |
| SCE1572_11373 | Succinyl-CoA ligase [ADP-forming] alpha chain (EC 6.2.1.5) | bi | see_10210 | 97.95 | Succinyl-CoA ligase [ADP-forming] alpha chain (EC 6.2.1.5) |
| SCE1572_11374 | Succinyl-CoA ligase [ADP-forming] beta chain (EC 6.2.1.5) | bi | see_10211 | 97.96 | Succinyl-CoA ligase [ADP-forming] beta chain (EC 6.2.1.5) |
| SCE1572_11375 | hypothetical protein | - | - | 0 | 0 |
| SCE1572_11376 | hypothetical protein | bi | see_10212 | 88.61 | hypothetical protein |
| SCE1572_11377 | ATP phosphoribosyltransferase (EC 2.4.2.17) | bi | see_10213 | 95.26 | ATP phosphoribosyltransferase (EC 2.4.2.17) |
| SCE1572_11378 | UDP-N-acetylglucosamine 1-carboxyvinyltransferase (EC 2.5.1.7) | bi | see_10214 | 98.58 | UDP-N-acetylglucosamine 1-carboxyvinyltransferase (EC 2.5.1.7) |
| SCE1572_11379 | OmpA domain protein | bi | see_10215 | 89.34 | OmpA |
| SCE1572_11380 | ENSANGP0000016745 | bi | see_10216 | 90.68 | ENSANGP0000016745 |
| SCE1572_11381 | Quinone oxidoreductase (EC 1.6.5.5) | bi | see_10217 | 89.6 | Quinone oxidoreductase (EC 1.6.5.5) |
| SCE1572_11382 | serine/threonine protein kinase | bi | see_10218 | 94.13 | serine/threonine protein kinase |
| SCE1572_11383 | hypothetical protein | - | - | 0 | 0 |
| SCE1572_11384 | serine/threonine protein kinase | bi | see_10219 | 93.58 | serine/threonine protein kinase |
| SCE1572_11385 | Hypothetical protein | bi | see_10220 | 98.74 | Hypothetical protein |
| SCE1572_11386 | Sulfate transporter family protein | bi | see_10221 | 76.95 | Sulfate transporter family protein |
| SCE1572_11387 | ABC transporter, periplasmic spermidine putrescine-binding protein PotD (TC 3.A.1.11.1) | bi | see_10223 | 72.59 | ABC transporter, periplasmic spermidine putrescine-binding protein PotD (TC 3.A.1.11.1) |
| SCE1572_11388 | hypothetical protein | uni | see_1271 | 37.18 | Ribosomal-protein-L7p-serine acetyltransferase |
| SCE1572_11389 | TonB-dependent receptor; Outer membrane receptor for ferrienterochelin and colicins | bi | see_10228 | 64.72 | TonB-dependent receptor; Outer membrane receptor for ferrienterochelin and colicins |
| SCE1572_11390 | Spermidine Putrescine ABC transporter permease component potC (TC_3.A.1.11.1) | bi | see_10229 | 84.42 | Spermidine Putrescine ABC transporter permease component potC (TC_3.A.1.11.1) |
| SCE1572_11391 | Spermidine Putrescine ABC transporter permease component potB (TC 3.A.1.11.1) | bi | see_10230 | 91.25 | Spermidine Putrescine ABC transporter permease component potB (TC 3.A.1.11.1) |
| SCE1572_11392 | Putrescine transport ATP-binding protein PotA (TC 3.A.1.11.1) | bi | see_10231 | 93.53 | Putrescine transport ATP-binding protein PotA (TC 3.A.1.11.1) |
| SCE1572_11393 | Serine/threonine protein kinase (EC 2.7.11.1) | bi | see_10233 | 93.2 | protein kinase domain |
| SCE1572_11394 | hypothetical protein | bi | see_10235 | 99.02 | hypothetical protein |
| SCE1572_11395 | Glycine dehydrogenase [decarboxylating] (glycine cleavage system P2 protein) (EC 1.4.4.2) | bi | see_10237 | 97.38 | Glycine dehydrogenase [decarboxylating] (glycine cleavage system P2 protein) (EC 1.4.4.2) |
| SCE1572_11396 | hypothetical protein | bi | see_10238 | 81.48 | hypothetical protein |
| SCE1572_11397 | hypothetical protein | - | - | 0 | 0 |
| SCE1572_11398 | Gll1450 protein | bi | see_10239 | 86.85 | Gll1450 protein |
| SCE1572_11399 | Glutamate-1-semialdehyde aminotransferase (EC 5.4.3.8) | bi | see_10240 | 94.75 | Glutamate-1-semialdehyde aminotransferase (EC 5.4.3.8) |
| SCE1572_11400 | serine/threonine protein kinase | bi | see_10241 | 89.29 | serine/threonine protein kinase |
| SCE1572_11401 | hypothetical protein | uni | see_1271 | 36.21 | Ribosomal-protein-L7p-serine acetyltransferase |
| SCE1572_11402 | FIG01086562: hypothetical protein | bi | see_10242 | 75.95 | FIG01086562: hypothetical protein |
| SCE1572_11403 | hypothetical glutathione S-transferase like protein | uni | see_7306 | 34.86 | Glutathione S-transferase (EC 2.5.1.18) |
| SCE1572_11404 | hypothetical protein | bi | see_10243 | 86.55 | FIG01089416: hypothetical protein |
| SCE1572_11405 | FIG01085109: hypothetical protein | uni | see_3937 | 57.34 | FIG01085109: hypothetical protein |
| SCE1572_11406 | FIG01085109: hypothetical protein | uni | see_3939 | 45.12 | FIG01085109: hypothetical protein |
| SCE1572_11407 | FIG01085109: hypothetical protein | uni | see_3937 | 50.27 | FIG01085109: hypothetical protein |
| SCE1572_11408 | FIG01085109: hypothetical protein | - | - | 0 | 0 |
| SCE1572_11409 | FIG01085109: hypothetical protein | uni | see_3937 | 46.29 | FIG01085109: hypothetical protein |
| SCE1572_11410 | hypothetical protein | bi | see_10267 | 82.45 | hypothetical protein |
| SCE1572_11411 | RsbR, positive regulator of sigma-B | uni | see_8231 | 54.41 | RsbR, positive regulator of sigma-B |
| SCE1572_11412 | hypothetical protein | bi | see_10269 | 76.38 | hypothetical protein |
| SCE1572_11413 | 5-carboxymethyl-2-hydroxymuconate semialdehyde dehydrogenase (EC 1.2.1.60) | bi | see_10270 | 95.2 | 5-carboxymethyl-2-hydroxymuconate semialdehyde dehydrogenase (EC 1.2.1.60) |
| SCE1572_11414 | hypothetical protein | bi | see_10271 | 92.81 | hypothetical protein |
| SCE1572_11415 | hypothetical protein | bi | see_10272 | 86.36 | hypothetical protein |
| SCE1572_11416 | Formate dehydrogenase chain D (EC 1.2.1.2) | bi | see_10274 | 85.33 | Formate dehydrogenase chain D (EC 1.2.1.2) |
| SCE1572_11417 | hypothetical protein | - | - | 0 | 0 |
| SCE1572_11418 | hypothetical protein | uni | see_1878 | 43.86 | FIG01087871: hypothetical protein |
| SCE1572_11419 | hypothetical protein | - | - | 0 | 0 |
| SCE1572_11420 | Putative formate dehydrogenase oxidoreductase protein | bi | see_10275 | 92.76 | Putative formate dehydrogenase oxidoreductase protein |
| SCE1572_11421 | hypothetical protein (EC:2.6.1.19) | bi | see_10276 | 93.16 | hypothetical protein (EC:2.6.1.19) |
| SCE1572_11422 | hypothetical protein | bi | see_10277 | 91.75 | Deacetylases, including yeast histone deacetylase and acetoin utilization protein |
| SCE1572_11423 | FIG00807932: hypothetical protein | uni | see_529 | 52.81 | hypothetical protein |
| SCE1572_11424 | Mlr5400 protein | bi | see_10283 | 74.2 | Mlr5400 protein |
| SCE1572_11425 | VgrG protein | uni | see_3035 | 47.03 | VgrG protein |
| SCE1572_11426 | hypothetical protein | - | - | 0 | 0 |
| SCE1572_11427 | YD repeat protein | - | - | 0 | 0 |
| SCE1572_11428 | hypothetical protein | - | - | 0 | 0 |
| SCE1572_11429 | hypothetical protein | uni | see_3038 | 42.54 | hypothetical protein |
| SCE1572_11430 | FIG01085200: hypothetical protein | bi | see_10284 | 92.06 | FIG01085200: hypothetical protein |
| SCE1572_11431 | Oxidoreductase (EC 1.1.1.-) | bi | see_10285 | 90.89 | Oxidoreductase (EC 1.1.1.-) |
| SCE1572_11432 | serine/threonine protein kinase | bi | see_10288 | 91.97 | serine/threonine protein kinase |
| SCE1572_11433 | Threonine synthase (EC 4.2.3.1) | bi | see_10289 | 96.19 | Threonine synthase (EC 4.2.3.1) |
| SCE1572_11434 | sensor histidine kinase | uni | see_4507 | 29.39 | Probable two-component sensor |
| SCE1572_11435 | Sensor protein | bi | see_10290 | 85.81 | Sensor protein |
| SCE1572_11436 | hypothetical protein | bi | see_10291 | 84.72 | hypothetical protein |
| SCE1572_11437 | hypothetical protein | bi | see_10292 | 88.32 | hypothetical protein |
| SCE1572_11438 | Putative general secretion pathway protein L | bi | see_10293 | 93.48 | putative general secretion pathway protein L |
| SCE1572_11439 | FIG01085599: hypothetical protein | bi | see_10294 | 80.84 | FIG01085599: hypothetical protein |
| SCE1572_11440 | General secretion pathway protein J | bi | see_10295 | 88.02 | General secretion pathway protein J |
| SCE1572_11441 | hypothetical protein | bi | see_10296 | 84.82 | hypothetical protein |
| SCE1572_11442 | prepilin-type N-terminal cleavage/methylation domain protein | bi | see_10297 | 89.08 | hypothetical protein |
| SCE1572_11443 | general secretion pathway protein G | bi | see_10298 | 74.5 | hypothetical protein |
| SCE1572_11444 | FIG01087598: hypothetical protein | bi | see_10299 | 96.35 | FIG01087598: hypothetical protein |
| SCE1572_11445 | Type IV fimbrial assembly protein PilC | bi | see_10300 | 92.16 | Type IV fimbrial assembly protein PilC |
| SCE1572_11446 | Type IV fimbrial assembly, ATPase PilB | bi | see_10301 | 96.11 | Type IV fimbrial assembly, ATPase PilB |
| SCE1572_11447 | General secretion pathway protein D / Type II secretion outer membrane pore forming protein (PulD) | bi | see_10302 | 86.71 | General secretion pathway protein D / Type II secretion outer membrane pore forming protein (PulD) |
| SCE1572_11448 | hypothetical protein | bi | see_10303 | 74.07 | hypothetical protein |
| SCE1572_11449 | General secretion pathway protein C | bi | see_10304 | 90.83 | General secretion pathway protein C |
| SCE1572_11450 | Response regulator of zinc sigma-54-dependent two-component system | bi | see_10305 | 98.72 | Response regulator of zinc sigma-54-dependent two-component system |
| SCE1572_11451 | Isochorismatase (EC 3.3.2.1) | bi | see_10306 | 84.04 | Isochorismatase (EC 3.3.2.1) |
| SCE1572_11452 | FIG01088145: hypothetical protein | bi | see_10307 | 91.22 | FIG01088145: hypothetical protein |
| SCE1572_11453 | Ferredoxin, 2Fe-2S | bi | see_10308 | 92.91 | Ferredoxin, 2Fe-2S |
| SCE1572_11454 | hypothetical protein | bi | see_5213 | 50 | FIG01089581: hypothetical protein |
| SCE1572_11455 | LysM domain protein | - | - | 0 | 0 |
| SCE1572_11456 | hypothetical protein | - | - | 0 | 0 |
| SCE1572_11457 | VgrG protein | uni | see_5222 | 55.56 | VgrG protein |
| SCE1572_11458 | hypothetical protein | bi | see_5220 | 46.08 | hypothetical protein |
| SCE1572_11459 | FIG01200031: hypothetical protein | bi | see_5221 | 65.35 | hypothetical protein |
| SCE1572_11460 | VgrG protein | bi | see_5222 | 65.22 | VgrG protein |
| SCE1572_11461 | hypothetical protein | - | - | 0 | 0 |
| SCE1572_11462 | hypothetical protein | bi | see_1332 | 27.75 | hypothetical protein |
| SCE1572_11463 | EBNA-1 | uni | see_3993 | 39.09 | Aspartyl-tRNA(Asn) amidotransferase subunit A (EC 6.3.5.6) @ Glutamyl-tRNA(Gln) amidotransferase subunit A (EC 6.3.5.7) |
| SCE1572_11464 | FIG01089285: hypothetical protein | uni | see_2965 | 39.96 | FIG01089285: hypothetical protein |
| SCE1572_11465 | OmpA domain protein | uni | see_3999 | 51.6 | Outer membrane protein A-like protein |
| SCE1572_11466 | S-layer-like array protein | uni | see_3992 | 48.94 | S-layer-like array protein |
| SCE1572_11467 | Probable serine/threonine-protein kinase kPhn (EC 2.7.11.1) | uni | see_3991 | 48.72 | serine/threonine protein kinase |
| SCE1572_11468 | hypothetical protein | bi | see_10309 | 78.47 | hypothetical protein |
| SCE1572_11469 | Transcriptional regulator, TetR family | bi | see_10310 | 87.07 | Transcriptional regulator, TetR family |
| SCE1572_11470 | Inositol-1-monophosphatase (EC 3.1.3.25) | bi | see_10311 | 87.88 | COG0483: Archaeal fructose-1,6-bisphosphatase and related enzymes of inositol monophosphatase family |
| SCE1572_11471 | Lipase/esterase | bi | see_10312 | 83.79 | Lipase/esterase |
| SCE1572_11472 | Transcriptional regulator, AraC family | uni | see_7800 | 34.92 | Transcriptional regulator, AraC family |
| SCE1572_11473 | FIG01086239: hypothetical protein | uni | see_10366 | 60.49 | FIG01086239: hypothetical protein |
| SCE1572_11474 | hypothetical protein | uni | see_9503 | 78.06 | hypothetical protein |
| SCE1572_11475 | hypothetical protein | uni | see_10364 | 73.13 | |

| | | | | |
|---------------|---|-----|-----------|---|
| SCE1572_11480 | Chaperone protein HtpG | bi | sce_10315 | 93.67 Chaperone protein HtpG |
| SCE1572_11481 | Mil2626 protein | bi | sce_10316 | 86.05 Mil2626 protein |
| SCE1572_11482 | hypothetical protein | bi | sce_10317 | 99.3 hypothetical protein |
| SCE1572_11483 | Translational elongation factor P | bi | sce_10318 | 96.77 Translational elongation factor P |
| SCE1572_11484 | Antifreeze glycopeptide AFGP polyprotein precursor | bi | sce_10319 | 88.63 Antifreeze glycopeptide AFGP polyprotein precursor |
| SCE1572_11485 | Thrombospondin type 3 repeat family protein/Calx-beta domain protein | bi | sce_10321 | 75.86 Thrombospondin type 3 repeat family protein/Calx-beta domain protein |
| SCE1572_11486 | Chromate transport protein ChrA | bi | sce_10322 | 85.75 Chromate transport protein ChrA |
| SCE1572_11487 | hypothetical protein | - | - | 0 |
| SCE1572_11488 | putative transposase | - | - | 0 |
| SCE1572_11489 | hypothetical protein | - | - | 0 |
| SCE1572_11490 | putative IS4 family transposase | bi | sce_299 | 97.5 Mobile element protein |
| SCE1572_11491 | glycosyltransferase | bi | sce_10323 | 86.62 glycosyltransferase |
| SCE1572_11492 | Isovaleryl-CoA dehydrogenase (EC 1.3.99.10) | bi | sce_10324 | 96.58 Isovaleryl-CoA dehydrogenase (EC 1.3.99.10) |
| SCE1572_11493 | Cell division protein FtsK | bi | sce_10326 | 88.91 Cell division protein FtsK |
| SCE1572_11494 | Cell division protein FtsK | uni | sce_10326 | 76.64 Cell division protein FtsK |
| SCE1572_11495 | hypothetical protein | - | - | 0 |
| SCE1572_11496 | hypothetical protein | - | - | 0 |
| SCE1572_11497 | hypothetical protein | - | - | 0 |
| SCE1572_11498 | hypothetical protein | - | - | 0 |
| SCE1572_11499 | FIG00840272: hypothetical protein | bi | sce_10332 | 79.42 FIG01087210: hypothetical protein |
| SCE1572_11500 | FIG01086383: hypothetical protein | bi | sce_10333 | 80.6 hypothetical protein |
| SCE1572_11501 | hypothetical protein | - | - | 0 |
| SCE1572_11502 | hypothetical protein | bi | sce_10334 | 80.86 FIG01087636: hypothetical protein |
| SCE1572_11503 | RNA polymerase sigma factor RpoE | bi | sce_10335 | 76.58 RNA polymerase sigma factor RpoE |
| SCE1572_11504 | hypothetical protein | - | - | 0 |
| SCE1572_11505 | Cytochrome c-type biogenesis protein CcmE, heme chaperone | bi | sce_10337 | 88.83 Cytochrome c-type biogenesis protein CcmE, heme chaperone |
| SCE1572_11506 | phospholipase D/Transphosphatidylase | bi | sce_10338 | 85.05 Cardiolipin synthetase (EC 2.7.8.-) |
| SCE1572_11507 | Metal-dependent hydrolase | bi | sce_10339 | 91.44 hypothetical protein |
| SCE1572_11508 | Flavin reductase (EC 1.5.1.30) | bi | sce_10340 | 81.73 putative nucleoside-diphosphate-sugar epimerases |
| SCE1572_11509 | Uncharacterized PE-PGRS family protein PE_PGRS54 precursor | bi | sce_10341 | 77.03 Uncharacterized PE-PGRS family protein PE_PGRS54 precursor |
| SCE1572_11510 | hypothetical protein | bi | sce_10342 | 54.4 FIG1088359: hypothetical protein |
| SCE1572_11511 | conserved hypothetical protein SCD8A_23 | bi | sce_10344 | 79.48 Invasin |
| SCE1572_11512 | FIG1086728: hypothetical protein | bi | sce_10345 | 62.33 FIG1086728: hypothetical protein |
| SCE1572_11513 | FIG1085729: hypothetical protein | bi | sce_10346 | 86.01 FIG1085729: hypothetical protein |
| SCE1572_11514 | Aspartokinase (EC 2.7.2.4) | bi | sce_10347 | 92.55 Aspartokinase (EC 2.7.2.4) |
| SCE1572_11515 | hydrolase, haloacid dehalogenase-like family | bi | sce_10348 | 87.31 hydrolase, haloacid dehalogenase-like family |
| SCE1572_11516 | Glycerol-3-phosphate ABC transporter, ATP-binding protein UgpC (TC 3.A.1.1.3) | bi | sce_10349 | 89.42 Glycerol-3-phosphate ABC transporter, ATP-binding protein UgpC (TC 3.A.1.1.3) |
| SCE1572_11517 | Glycerol-3-phosphate ABC transporter, periplasmic glycerol-3-phosphate-binding protein (TC 3.A.1.1.3) | bi | sce_10350 | 88.69 Glycerol-3-phosphate ABC transporter, periplasmic glycerol-3-phosphate-binding protein (TC 3.A.1.1.3) |
| SCE1572_11518 | N-Acetyl-D-glucosamine ABC transport system, permease protein 1 | bi | sce_10351 | 94.88 N-Acetyl-D-glucosamine ABC transport system, permease protein 1 |
| SCE1572_11519 | Sugar ABC transporter, sugar permease protein 2 USSDB1D | bi | sce_10352 | 92.01 Sugar ABC transporter, sugar permease protein 2 USSDB1D |
| SCE1572_11520 | hypothetical protein | bi | sce_10353 | 85.19 hypothetical protein |
| SCE1572_11521 | hypothetical protein | uni | sce_10363 | 83.33 hypothetical protein |
| SCE1572_11522 | hypothetical protein | - | - | 0 |
| SCE1572_11523 | hypothetical protein | uni | sce_7057 | 51.65 hypothetical protein |
| SCE1572_11524 | hypothetical protein | bi | sce_7056 | 46.28 FIG1087585: hypothetical protein |
| SCE1572_11525 | Transcriptional regulator, AraC family | bi | sce_7055 | 67.3 Transcriptional regulator, AraC family |
| SCE1572_11526 | Transcription-repair coupling factor | uni | sce_10265 | 87.04 hypothetical protein |
| SCE1572_11527 | FIG01085364: hypothetical protein | uni | sce_8038 | 51.73 FIG1085364: hypothetical protein |
| SCE1572_11528 | hypothetical protein | uni | sce_5241 | 50.14 FIG1086664: hypothetical protein |
| SCE1572_11529 | Cytochrome c551 peroxidase (EC 1.11.1.5) | bi | sce_10371 | 78.66 Cytochrome c551 peroxidase (EC 1.11.1.5) |
| SCE1572_11530 | blr7652; hypothetical protein | bi | sce_10372 | 68.39 hypothetical protein |
| SCE1572_11531 | FIG1089001: hypothetical protein | bi | sce_10373 | 75.69 FIG1089001: hypothetical protein |
| SCE1572_11532 | hypothetical protein | - | - | 0 |
| SCE1572_11533 | Transcription regulator [contains diacylglycerol kinase catalytic domain] | bi | sce_10380 | 80.62 Transcription regulator [contains diacylglycerol kinase catalytic domain] |
| SCE1572_11534 | 3'-5'-cyclic-nucleotide phosphodiesterase | bi | sce_10381 | 88.1 3'-5'-cyclic-nucleotide phosphodiesterase |
| SCE1572_11535 | Xylulose kinase (EC 2.7.1.17) | bi | sce_10384 | 95.75 Xylulose kinase (EC 2.7.1.17) |
| SCE1572_11536 | Sorbitol dehydrogenase (EC 1.1.1.14) | bi | sce_10385 | 95.54 Sorbitol dehydrogenase (EC 1.1.1.14) |
| SCE1572_11537 | hypothetical protein | bi | sce_10386 | 91.57 hypothetical protein |
| SCE1572_11538 | Uncharacterized protein, similar to the N-terminal domain of Lon protease | bi | sce_10387 | 94.12 Uncharacterized protein, similar to the N-terminal domain of Lon protease |
| SCE1572_11539 | 3-oxoacyl-[acyl-carrier protein] reductase (EC 1.1.1.100) | bi | sce_10388 | 89.47 3-oxoacyl-[acyl-carrier protein] reductase (EC 1.1.1.100) |
| SCE1572_11540 | GTP cyclohydrolase I (EC 3.5.4.16) type 1 | bi | sce_10389 | 90.58 GTP cyclohydrolase I (EC 3.5.4.16) type 1 |
| SCE1572_11541 | hypothetical protein | bi | sce_10390 | 89.93 hypothetical protein |
| SCE1572_11542 | Spermidine Putrescine ABC transporter permease component potC (TC_3.A.1.11.1) | bi | sce_10391 | 95.27 Spermidine Putrescine ABC transporter permease component potC (TC_3.A.1.11.1) |
| SCE1572_11543 | ABC transporter, periplasmic spermidine putrescine-binding protein PotD (TC 3.A.1.11.1) | bi | sce_10392 | 91.76 ABC transporter, periplasmic spermidine putrescine-binding protein PotD (TC 3.A.1.11.1) |
| SCE1572_11544 | Spermidine Putrescine ABC transporter permease component PotB (TC 3.A.1.11.1) | bi | sce_10393 | 94.5 Spermidine Putrescine ABC transporter permease component PotB (TC 3.A.1.11.1) |
| SCE1572_11545 | Putrescine transport ATP-binding protein PotA (TC 3.A.1.11.1) | bi | sce_10394 | 91.97 Putrescine transport ATP-binding protein PotA (TC 3.A.1.11.1) |
| SCE1572_11546 | Shell matrix protein | bi | sce_10396 | 79.19 Shell matrix protein |
| SCE1572_11547 | Shell matrix protein | uni | sce_10396 | 74.4 Shell matrix protein |
| SCE1572_11548 | FIG1088065: hypothetical protein | bi | sce_10397 | 90.67 FIG1088065: hypothetical protein |
| SCE1572_11549 | Molybdopterin biosynthesis protein MoeA | bi | sce_10398 | 88.41 Molybdopterin biosynthesis protein MoeA |
| SCE1572_11550 | hypothetical protein | uni | sce_6700 | 34.44 hypothetical protein |
| SCE1572_11551 | hypothetical protein | - | - | 0 |
| SCE1572_11552 | hypothetical protein | - | - | 0 |
| SCE1572_11553 | FIG1089513: hypothetical protein | bi | sce_10402 | 82.27 FIG1089513: hypothetical protein |
| SCE1572_11554 | General secretion pathway protein C | bi | sce_10403 | 79.63 General secretion pathway protein C |
| SCE1572_11555 | FIG00840539: hypothetical protein | bi | sce_6028 | 84.91 FIG00840539: hypothetical protein |
| SCE1572_11556 | Branched-chain amino acid ABC transporter, amino acid-binding protein (TC 3.A.1.4.1) | - | - | 0 |
| SCE1572_11557 | COG2319: FOG: WD40 repeat | uni | sce_7667 | 45.42 FIG1085006: hypothetical protein |
| SCE1572_11558 | Branched-chain amino acid ABC transporter, amino acid-binding protein (TC 3.A.1.4.1) | uni | sce_7667 | 46.76 FIG1085006: hypothetical protein |
| SCE1572_11559 | kelch domain protein | uni | sce_7667 | 46.48 FIG1085006: hypothetical protein |
| SCE1572_11560 | Branched-chain amino acid ABC transporter, amino acid-binding protein (TC 3.A.1.4.1) | uni | sce_7667 | 48.98 FIG1085006: hypothetical protein |
| SCE1572_11561 | serine/threonine protein kinase | uni | sce_3991 | 42.88 serine/threonine protein kinase |
| SCE1572_11562 | hypothetical protein | - | - | 0 |
| SCE1572_11563 | hypothetical protein | bi | sce_10404 | 86.01 von Willebrand factor, type A |
| SCE1572_11564 | hypothetical protein | bi | sce_10405 | 86.79 hypothetical protein |
| SCE1572_11565 | hypothetical protein | bi | sce_8641 | 70.45 hypothetical protein |
| SCE1572_11566 | hypothetical protein | uni | sce_7302 | 51.13 FIG1084927: hypothetical protein |
| SCE1572_11567 | hypothetical protein | - | - | 0 |
| SCE1572_11568 | ATPase involved in chromosome partitioning-like protein | - | - | 0 |
| SCE1572_11569 | hypothetical protein | bi | sce_167 | 95.65 hypothetical protein |
| SCE1572_11570 | hypothetical protein | - | - | 0 |
| SCE1572_11571 | Transcriptional regulator, TetR family | bi | sce_7925 | 93.85 Transcriptional regulator, TetR family |
| SCE1572_11572 | Epoxide hydrolase (EC 3.3.2.9) | uni | sce_4089 | 30.7 Alpha/beta hydrolase fold (EC 3.8.1.5) |
| SCE1572_11573 | Epoxide hydrolase (EC 3.3.2.9) | - | - | 0 |
| SCE1572_11574 | FIG1086246: hypothetical protein | bi | sce_9347 | 91.96 FIG1086246: hypothetical protein |
| SCE1572_11575 | alcohol dehydrogenase, zinc-containing | bi | sce_10410 | 86.71 alcohol dehydrogenase, zinc-containing |
| SCE1572_11576 | FIG1087153: hypothetical protein | bi | sce_8743 | 85.28 FIG1087153: hypothetical protein |
| SCE1572_11577 | FIG1089659: hypothetical protein | bi | sce_10411 | 88.02 FIG1089659: hypothetical protein |
| SCE1572_11578 | Molybdopterin-guanine dinucleotide biosynthesis protein MobA | bi | sce_10415 | 83.18 Molybdopterin-guanine dinucleotide biosynthesis protein MobA |
| SCE1572_11579 | Putative outer membrane protein | bi | sce_10416 | 84.89 Putative outer membrane protein |
| SCE1572_11580 | FIG1086226: hypothetical protein | bi | sce_10417 | 78.74 FIG1086226: hypothetical protein |
| SCE1572_11581 | serine/threonine protein kinase | bi | sce_10418 | 89.92 serine/threonine protein kinase |
| SCE1572_11582 | serine/threonine protein kinase | bi | sce_10419 | 77.63 serine/threonine protein kinase |
| SCE1572_11583 | FIG1086379: hypothetical protein | bi | sce_10447 | 86.27 FIG1086379: hypothetical protein |
| SCE1572_11584 | Serine/threonine protein kinase (EC 2.7.1.-) | bi | sce_10448 | 76.41 Serine/threonine protein kinase (EC 2.7.1.-) |
| SCE1572_11585 | hypothetical protein | - | - | 0 |
| SCE1572_11586 | FIG1087469: hypothetical protein | bi | sce_10450 | 90.7 FIG1087469: hypothetical protein |
| SCE1572_11587 | EBNA-1 | uni | sce_7493 | 35.06 Branched-chain amino acid ABC transporter, amino acid-binding protein (TC 3.A.1.4.1) |
| SCE1572_11588 | Chromosome 17 SCAF15006, whole genome shotgun sequence | bi | sce_10452 | 80.85 Chromosome 17 SCAF15006, whole genome shotgun sequence |
| SCE1572_11589 | Murein endopeptidase | bi | sce_10454 | 85.76 penicillin-insensitive murein endopeptidase |
| SCE1572_11590 | adenine specific DNA-methyltransferase | bi | sce_10455 | 91.67 DNA methyltransferase |
| SCE1572_11591 | hypothetical protein | uni | sce_5620 | 26.9 Predicted ATPase |
| SCE1572_11592 | hypothetical protein | - | - | 0 |
| SCE1572_11593 | Sua5/YciO/YrdC/YwC | bi | sce_10456 | 94.53 Sua5/YciO/YrdC/YwC |
| SCE1572_11594 | ATP synthase gamma chain (EC 3.6.3.14) | bi | sce_10457 | 89.85 ATP synthase gamma chain (EC 3.6.3.14) |
| SCE1572_11595 | ATP synthase alpha chain (EC 3.6.3.14) | bi | sce_10458 | 94.76 ATP synthase alpha chain (EC 3.6.3.14) |
| SCE1572_11596 | ATP synthase delta chain (EC 3.6.3.14) | bi | sce_10459 | 91.11 ATP synthase delta chain (EC 3.6.3.14) |
| SCE1572_11597 | ATP synthase B chain (EC 3.6.3.14) | bi | sce_10460 | 79.71 ATP synthase B chain (EC 3.6.3.14) |
| SCE1572_11598 | ATP synthase B chain (EC 3.6.3.14) | bi | sce_10461 | 97.5 ATP synthase B chain (EC 3.6.3.14) |
| SCE1572_11599 | conserved hypothetical protein | bi | sce_10462 | 84.36 conserved hypothetical protein |
| SCE1572_11600 | TRNA (Ms[2]jo[6]A)-hydroxylase (EC 1.-.-) | bi | sce_10463 | 97.28 TRNA (Ms[2]jo[6]A)-hydroxylase (EC 1.-.-) |
| SCE1572_11601 | FIG1089661: hypothetical protein | bi | sce_10464 | 81.09 FIG1089661: hypothetical protein |

TableS11 All annotated polysaccharide-degrading enzymes and related CBM motifs in So0157-2

| Locus tag | Score | E-value | Subject ID* | Family |
|--------------|-------|---------|-------------------------------------|--------|
| SCE1572_6228 | 60.14 | 2e-103 | YP_001612106.1;CAN91626.1; | GH5 |
| SCE1572_6231 | 90.2 | 8e-130 | YP_001613915.1;CAN93435.1; | CE1 |
| SCE1572_6232 | 91.49 | 3e-172 | YP_001613916.1;CAN93436.1; | CE1 |
| SCE1572_6246 | 41.57 | 2e-12 | CAZ88575.1; | CE4 |
| SCE1572_6247 | 66.59 | 1e-139 | YP_001611186.1;CAN90706.1; | GT4 |
| SCE1572_6252 | 41.63 | 1e-39 | AAF26731.1; | CE10 |
| SCE1572_6349 | 43.72 | 8e-161 | ADI16745.1; | GH52 |
| SCE1572_6351 | 86.14 | 5e-147 | YP_001615459.1;CAN94979.1; | PL1 |
| SCE1572_6364 | 44.55 | 4e-38 | YP_002479972.1;ACL49294.1; | GT4 |
| SCE1572_6367 | 42.48 | 5e-15 | YP_001360086.1;ABS01822.1; | GT2 |
| SCE1572_6382 | 41.7 | 4e-30 | NP_628653.1;CAB92109.1; | CBM13 |
| SCE1572_6394 | 40 | 2e-09 | YP_003849847.1;ADL58534.1; | GT2 |
| SCE1572_6418 | 60.53 | 7e-143 | YP_001039270.1;ABN54077.1; | CE0 |
| SCE1572_6423 | 68.02 | 3e-172 | YP_001613368.1;CAN92888.1; | CBM2 |
| SCE1572_6423 | 68.02 | 3e-172 | YP_001613368.1;CAN92888.1; | CE4 |
| SCE1572_6431 | 57.18 | 3e-114 | YP_003073756.1;ACR12691.1; | CBM10 |
| SCE1572_6431 | 57.18 | 3e-114 | YP_003073756.1;ACR12691.1; | GH53 |
| SCE1572_6458 | 44.55 | 3e-32 | YP_003844012.1;ADL52248.1; | GH43 |
| SCE1572_6458 | 44.55 | 3e-32 | YP_003844012.1;ADL52248.1; | GH51 |
| SCE1572_6461 | 54.51 | 6e-89 | YP_001612123.1;CAN91643.1; | GH43 |
| SCE1572_6468 | 88.48 | | 0 YP_001615509.1;CAN95029.1; | GT2 |
| SCE1572_6469 | 88.4 | | 0 YP_001615510.1;CAN95030.1; | GH26 |
| SCE1572_6485 | 41.6 | 2e-16 | YP_001360086.1;ABS01822.1; | GT2 |
| SCE1572_6524 | 78.93 | 7e-144 | YP_001615553.1;CAN95073.1; | GH5 |
| SCE1572_6536 | 40.06 | 2e-127 | YP_003014630.1;ACT04544.1; | CBM50 |
| SCE1572_6574 | 44.66 | 2e-11 | YP_003835341.1;ADL45765.1; | GT9 |
| SCE1572_6580 | 42.68 | 6e-06 | BAA05832.1; | CBM20 |
| SCE1572_6580 | 42.68 | 6e-06 | BAA05832.1; | CBM34 |
| SCE1572_6580 | 42.68 | 6e-06 | BAA05832.1; | CBM48 |
| SCE1572_6580 | 42.68 | 6e-06 | BAA05832.1; | GH13 |
| SCE1572_6587 | 41.98 | 5e-07 | ACX49739.1; | GH4 |
| SCE1572_6614 | 80.42 | 1e-164 | YP_001615581.1;CAN95101.1; | CBM0 |
| SCE1572_6614 | 80.42 | 1e-164 | YP_001615581.1;CAN95101.1; | PL3 |
| SCE1572_6660 | 40 | 1e-10 | YP_002782993.1;BAH54048.1; | GT4 |
| SCE1572_6664 | 40 | 5e-17 | YP_001360086.1;ABS01822.1; | GT2 |
| SCE1572_6665 | 43.48 | 6e-18 | YP_001360086.1;ABS01822.1; | GT2 |
| SCE1572_6688 | 51.28 | | 0 YP_003270912.1;ACY19019.1; | CBM48 |
| SCE1572_6699 | 63.12 | 1e-160 | YP_001863952.1;ACC79009.1; | GH1 |
| SCE1572_6701 | 67.41 | | 0 YP_001613691.1;CAN93211.1; | GH2 |
| SCE1572_6702 | 71.94 | 2e-158 | YP_002482744.1;ACL44383.1; | GT4 |
| SCE1572_6703 | 57.77 | 4e-123 | YP_001863951.1;ACC79008.1; | GT4 |
| SCE1572_6715 | 81.45 | | 0 YP_001615633.1;CAN95153.1; | GH23 |
| SCE1572_6760 | 40.78 | 6e-102 | YP_003466227.1;CBJ79429.1; | GH24 |
| SCE1572_6763 | 57.36 | 9e-179 | YP_002131318.1;ACG78889.1; | GH43 |
| SCE1572_6800 | 42.05 | 8e-11 | NP_628653.1;CAB92109.1; | CBM13 |
| SCE1572_6844 | 93.86 | | 0 YP_001615734.1;CAN95254.1; | GH13 |
| SCE1572_6881 | 40.52 | 9e-08 | YP_526867.1;ABD80655.1; | CBM6 |
| SCE1572_6881 | 40.52 | 9e-08 | YP_526867.1;ABD80655.1; | CBM56 |
| SCE1572_6881 | 40.52 | 9e-08 | YP_526867.1;ABD80655.1; | GH16 |
| SCE1572_6893 | 40 | 9e-30 | YP_715463.1;CAJ63931.1; | CBM13 |
| SCE1572_6894 | 41.04 | 3e-27 | NP_733639.1;CAD55485.1; | CBM13 |
| SCE1572_6912 | 50.96 | 9e-49 | ACX49739.1; | GH4 |
| SCE1572_6923 | 45.05 | 4e-15 | YP_001360086.1;ABS01822.1; | GT2 |
| SCE1572_6942 | 77.14 | | 0 YP_001612153.1;CAN91673.1; | CBM3 |
| SCE1572_6949 | 62.66 | 4e-138 | BAE86850.1; | GH8 |
| SCE1572_6952 | 67.58 | 6e-66 | NP_823285.1;BAC69820.1; | CBM13 |
| SCE1572_6952 | 67.58 | 6e-66 | NP_823285.1;BAC69820.1; | GH43 |
| SCE1572_6974 | 40 | 1e-33 | YP_715463.1;CAJ63931.1; | CBM13 |
| SCE1572_6980 | 86.42 | 3e-123 | YP_001615812.1;CAN95332.1; | CE12 |
| SCE1572_6981 | 53.75 | 3e-46 | YP_002506838.1;ACL76858.1; | CBM13 |
| SCE1572_7001 | 40.13 | 2e-44 | YP_203062.1;YP_453195.1;AAW77677.1 | GH3 |
| SCE1572_7019 | 44.7 | 5e-06 | YP_003911717.1;ADN74643.1; | CBM13 |
| SCE1572_7044 | 95 | 2e-125 | YP_001619514.1;CAN99034.1; | CE3 |
| SCE1572_7045 | 40.99 | 1e-34 | YP_003765393.1;ADJ44991.1; | CBM2 |
| SCE1572_7063 | 42.22 | 1e-06 | YP_002896761.1;ZP_04886356.1;EDU07. | CE3 |
| SCE1572_7072 | 46.11 | 2e-77 | YP_003485873.1;CBG67294.1; | CBM13 |
| SCE1572_7178 | 82.62 | | 0 YP_001612594.1;CAN92114.1; | CBM6 |
| SCE1572_7178 | 82.62 | | 0 YP_001612594.1;CAN92114.1; | GH43 |
| SCE1572_7223 | 82.13 | | 0 YP_001615952.1;CAN95472.1; | GH9 |
| SCE1572_7229 | 41.92 | 2e-29 | YP_001106030.1;ZP_06565633.1;CAM03 | CBM6 |
| SCE1572_7241 | 40.45 | 9e-07 | YP_003765392.1;ADJ44990.1; | CBM2 |
| SCE1572_7267 | 42.28 | 4e-06 | YP_003911717.1;ADN74643.1; | CBM13 |
| SCE1572_7270 | 40.48 | 2e-09 | EEC68331.1; | CBM50 |
| SCE1572_7299 | 40.28 | 3e-06 | NP_810096.1;AAO76290.1; | GT2 |
| SCE1572_7305 | 90 | 8e-145 | YP_001612881.1;CAN92401.1; | GH16 |
| SCE1572_7325 | 91.15 | | 0 YP_001616104.1;CAN95624.1; | GT4 |
| SCE1572_7338 | 40.27 | 3e-07 | AAF71700.1; | CE10 |
| SCE1572_7360 | 41.95 | 2e-43 | YP_715463.1;CAJ63931.1; | CBM13 |

| | | | |
|--------------|--------------|---|-------|
| SCE1572_7384 | 81.01 1e-168 | YP_001612827.1;CAN92347.1; | GH10 |
| SCE1572_7403 | 66.49 2e-144 | YP_001616149.1;CAN95669.1; | GH8 |
| SCE1572_7427 | 52.2 | 0 YP_003270912.1;ACY19019.1; | CBM48 |
| SCE1572_7431 | 42.67 8e-45 | YP_003955230.1;ADO73403.1; | CE4 |
| SCE1572_7473 | 40.62 6e-07 | YP_003838689.1;ADL49113.1; | CBM2 |
| SCE1572_7484 | 46.07 9e-65 | XP_003080455.1;CAL54622.1; | GH2 |
| SCE1572_7490 | 50 6e-06 | YP_002930693.1;ACR72246.1; | PL1 |
| SCE1572_7490 | 50 6e-06 | YP_002930693.1;ACR72246.1; | PL9 |
| SCE1572_7493 | 95.19 | 0 YP_001616079.1;CAN95599.1; | CE15 |
| SCE1572_7538 | 92.22 | 0 YP_001616363.1;CAN95883.1; | GH5 |
| SCE1572_7540 | 79.49 | 0 YP_001616365.1;CAN95885.1; | CE2 |
| SCE1572_7552 | 88.25 2e-145 | YP_001616370.1;CAN95890.1; | GT4 |
| SCE1572_7559 | 56.99 4e-158 | NP_051574.1;AAF12585.1; | CE10 |
| SCE1572_7628 | 91.3 2e-172 | YP_001616437.1;CAN95957.1; | GT2 |
| SCE1572_7649 | 58.26 3e-164 | YP_001980577.1;ACE86114.1; | PL1 |
| SCE1572_7651 | 70.47 3e-150 | YP_001982505.1;ACE84005.1; | PL10 |
| SCE1572_7652 | 77.61 | 0 YP_003003776.1;ACT06297.1; | GH43 |
| SCE1572_7673 | 45.45 3e-09 | YP_001981082.1;ACE84184.1; | CBM35 |
| SCE1572_7674 | 42.19 1e-22 | YP_001981082.1;ACE84184.1; | CBM35 |
| SCE1572_7702 | 76.77 | 0 YP_001616475.1;CAN95995.1; | PL1 |
| SCE1572_7840 | 40.19 1e-07 | ADD17064.1; | CBM5 |
| SCE1572_7840 | 40.19 1e-07 | ADD17064.1; | GH5 |
| SCE1572_7896 | 46.43 6e-14 | CAN61133.1; | GH36 |
| SCE1572_7912 | 64 3e-119 | YP_003250632.1;ACX76150.1;ADL2603(CBM35 | |
| SCE1572_7912 | 64 3e-119 | YP_003250632.1;ACX76150.1;ADL2603(PL1 | |
| SCE1572_7916 | 86.37 | 0 YP_001616651.1;CAN96171.1; | GH5 |
| SCE1572_7932 | 45.31 6e-07 | YP_003151067.1;ACU94385.1; | CE9 |
| SCE1572_7940 | 45.59 5e-07 | Q9LAP7.1;AAF26838.1; | CBM6 |
| SCE1572_7940 | 45.59 5e-07 | Q9LAP7.1;AAF26838.1; | GH96 |
| SCE1572_7952 | 51.74 4e-105 | CBA03971.1; | GT30 |
| SCE1572_7993 | 78.66 | 0 YP_001616718.1;CAN96238.1; | GH18 |
| SCE1572_8101 | 55.38 | 0 YP_526034.1;ABD79822.1; | GH9 |
| SCE1572_8103 | 40 3e-27 | YP_003267712.1;ACY15819.1; | CBM2 |
| SCE1572_8165 | 80.85 3e-15 | YP_001616872.1;CAN96392.1; | GH43 |
| SCE1572_8228 | 87.47 | 0 YP_001616802.1;CAN96322.1; | GH23 |
| SCE1572_8260 | 40.62 4e-07 | YP_002126278.1;ACG66284.1; | CBM50 |
| SCE1572_8260 | 40.62 4e-07 | YP_002126278.1;ACG66284.1; | GH23 |
| SCE1572_8321 | 40 2e-26 | YP_003767779.1;ADJ47377.1; | CBM2 |
| SCE1572_8401 | 44.26 9e-06 | YP_003676076.1;ADH60065.1; | CE9 |
| SCE1572_8430 | 43.17 4e-89 | CAN65674.1; | GH28 |
| SCE1572_8434 | 41.06 2e-16 | YP_003766420.1;ADJ46018.1; | CBM2 |
| SCE1572_8448 | 53.99 | 0 YP_003270912.1;ACY19019.1; | CBM48 |
| SCE1572_8471 | 97.17 | 0 YP_001617109.1;CAN96629.1; | GH94 |
| SCE1572_8489 | 42.11 6e-14 | YP_604980.1;ABF45811.1; | CBM50 |
| SCE1572_8496 | 41.18 3e-08 | NP_628976.1;CAB97423.1; | GH23 |
| SCE1572_8497 | 50.55 1e-142 | ADI12317.1; | CBM2 |
| SCE1572_8497 | 50.55 1e-142 | ADI12317.1; | GH44 |
| SCE1572_8499 | 42.96 4e-20 | NP_733639.1;CAD55485.1; | CBM13 |
| SCE1572_8546 | 74.03 2e-164 | YP_002482744.1;ACL44383.1; | GT4 |
| SCE1572_8545 | 73.3 | 0 YP_001613694.1;CAN93214.1; | GH1 |
| SCE1572_8547 | 71.39 1e-147 | YP_001613692.1;CAN93212.1; | GT4 |
| SCE1572_8548 | 74.96 | 0 YP_001613691.1;CAN93211.1; | GH2 |
| SCE1572_8602 | 43.6 4e-28 | YP_001132770.1;ABP43982.1; | GT4 |
| SCE1572_8648 | 42.47 6e-10 | YP_002942693.1;ACS17427.1; | GT2 |
| SCE1572_8648 | 42.47 6e-10 | YP_002942693.1;ACS17427.1; | GT4 |
| SCE1572_8650 | 87.93 2e-169 | YP_001617232.1;CAN96752.1; | GT4 |
| SCE1572_8669 | 45.76 2e-103 | YP_615806.1;ABF52473.1; | GH43 |
| SCE1572_8715 | 41 9e-36 | YP_002479972.1;ACL49294.1; | GT4 |
| SCE1572_8724 | 40.48 5e-59 | YP_003630753.1;ADG68554.1; | CE1 |
| SCE1572_8748 | 82.18 | 0 YP_001617409.1;CAN96929.1; | GT4 |
| SCE1572_8760 | 78.4 | 0 YP_001612470.1;CAN91990.1; | GH30 |
| SCE1572_8762 | 41.42 3e-25 | YP_003766420.1;ADJ46018.1; | CBM2 |
| SCE1572_8782 | 57.97 2e-113 | YP_002538685.1;ACM21584.1; | GH0 |
| SCE1572_8784 | 83.55 2e-160 | YP_001617423.1;CAN96943.1; | GT4 |
| SCE1572_8785 | 88.71 | 0 YP_001617424.1;CAN96944.1; | GT0 |
| SCE1572_8786 | 70.45 1e-128 | YP_002296781.1;ACI97968.1; | GT0 |
| SCE1572_8787 | 40.91 4e-06 | YP_002786856.1;ACO47102.1; | GT4 |
| SCE1572_8834 | 51.54 | 0 YP_003270912.1;ACY19019.1; | CBM48 |
| SCE1572_8842 | 44.35 1e-18 | YP_001360086.1;ABS01822.1; | GT2 |
| SCE1572_8845 | 88.83 3e-171 | YP_001617439.1;CAN96959.1; | GT4 |
| SCE1572_8848 | 90.82 9e-160 | YP_001617441.1;CAN96961.1; | GH0 |
| SCE1572_8886 | 40.22 1e-36 | YP_715463.1;CAJ63931.1; | CBM13 |
| SCE1572_8890 | 69.48 6e-144 | YP_001616194.1;CAN95714.1; | CBM2 |
| SCE1572_8890 | 69.48 6e-144 | YP_001616194.1;CAN95714.1; | GH11 |
| SCE1572_8891 | 79.59 2e-96 | YP_001616194.1;CAN95714.1; | CBM2 |
| SCE1572_8891 | 79.59 2e-96 | YP_001616194.1;CAN95714.1; | GH11 |
| SCE1572_8894 | 81.15 | 0 YP_001617496.1;CAN97016.1; | GH13 |
| SCE1572_8920 | 47.81 2e-138 | YP_003100976.1;ACU37130.1; | CBM2 |
| SCE1572_8954 | 43.38 8e-31 | YP_003765392.1;ADJ44990.1; | CBM2 |
| SCE1572_8958 | 87.24 | 0 YP_001617546.1;CAN97066.1; | GH3 |

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|---------------|--------------|------------------------------|-------|
| SCE1572_9027 | 42.44 1e-30 | YP_003767779.1;ADJ47377.1; | CBM2 |
| SCE1572_9037 | 41.07 8e-12 | YP_001360086.1;ABS01822.1; | GT2 |
| SCE1572_9046 | 48.91 2e-99 | YP_001547794.1;ABX07666.1; | PL9 |
| SCE1572_9056 | 42.42 2e-61 | YP_821916.1;ABJ81631.1; | CBM47 |
| SCE1572_9064 | 41.18 7e-59 | YP_821916.1;ABJ81631.1; | CBM47 |
| SCE1572_9066 | 66.52 3e-177 | YP_632978.1;ABF93028.1; | CBM61 |
| SCE1572_9066 | 66.52 3e-177 | YP_632978.1;ABF93028.1; | GH16 |
| SCE1572_9069 | 89.89 6e-131 | YP_001617638.1;CAN97158.1; | GT2 |
| SCE1572_9075 | 49.77 | 0 YP_003270912.1;ACY19019.1; | CBM48 |
| SCE1572_6116 | 43.09 8e-38 | YP_003074845.1;ACR11863.1; | CBM57 |
| SCE1572_6116 | 43.09 8e-38 | YP_003074845.1;ACR11863.1; | CE15 |
| SCE1572_9119 | 47.15 4e-41 | CAB45032.1; | CBM35 |
| SCE1572_9157 | 81.08 | 0 YP_001617752.1;CAN97272.1; | GH81 |
| SCE1572_9189 | 49.73 6e-91 | YP_003747345.1;CBJ52922.1; | CE8 |
| SCE1572_9200 | 68.52 2e-14 | YP_001617792.1;CAN97311.1; | GH0 |
| SCE1572_9251 | 89.01 | 0 YP_001617819.1;CAN97339.1; | CBM48 |
| SCE1572_9251 | 89.01 | 0 YP_001617819.1;CAN97339.1; | GH13 |
| SCE1572_9305 | 43.87 1e-41 | YP_002479972.1;ACL49294.1; | GT4 |
| SCE1572_9374 | 42.24 2e-11 | YP_003643224.1;ADG30894.1; | CE4 |
| SCE1572_9412 | 84.29 | 0 YP_001617970.1;CAN97490.1; | GT4 |
| SCE1572_9413 | 79.92 | 0 YP_001617971.1;CAN97491.1; | PL0 |
| SCE1572_9439 | 93.33 6e-117 | YP_001618001.1;CAN97521.1; | GT2 |
| SCE1572_9478 | 92.52 3e-169 | YP_001618034.1;CAN97554.1; | GT2 |
| SCE1572_9497 | 40.38 1e-24 | NP_103730.1;BAB49516.1; | GH23 |
| SCE1572_9503 | 47.56 2e-17 | CAN61133.1; | GH36 |
| SCE1572_9517 | 92.12 | 0 YP_001618071.1;CAN97591.1; | GH0 |
| SCE1572_9534 | 42.03 1e-21 | YP_715463.1;CAJ63931.1; | CBM13 |
| SCE1572_9601 | 64.11 | 0 YP_003266510.1;ACY14617.1; | GH3 |
| SCE1572_9602 | 56.95 1e-64 | YP_001617670.1;CAN97190.1; | CE3 |
| SCE1572_9643 | 41.9 1e-09 | ACN62172.1; | CBM5 |
| SCE1572_9643 | 41.9 1e-09 | ACN62172.1; | GH5 |
| SCE1572_9669 | 41.32 2e-17 | YP_001360086.1;ABS01822.1; | GT2 |
| SCE1572_9685 | 46.02 3e-16 | AAC98688.2; | GH33 |
| SCE1572_9708 | 92.35 | 0 YP_001618257.1;CAN97777.1; | GH35 |
| SCE1572_9715 | 41.18 4e-09 | YP_822037.1;ABJ81752.1; | GH0 |
| SCE1572_9719 | 42.42 1e-06 | NP_440565.1;BAA17245.1; | GT51 |
| SCE1572_9778 | 94.18 | 0 YP_001618312.1;CAN97832.1; | GH1 |
| SCE1572_9788 | 51.24 3e-66 | YP_001615903.1;CAN95423.1; | CBM2 |
| SCE1572_9807 | 40.48 2e-10 | CAN61133.1; | GH36 |
| SCE1572_9813 | 42.5 1e-06 | YP_003849847.1;ADL58534.1; | GT2 |
| SCE1572_9836 | 93.24 2e-175 | YP_001618385.1;CAN97905.1; | CE1 |
| SCE1572_8890 | 64.82 4e-64 | ABL11222.1; | GH11 |
| SCE1572_9885 | 40.65 3e-12 | YP_001360086.1;ABS01822.1; | GT2 |
| SCE1572_9890 | 80.76 | 0 YP_001618429.1;CAN97949.1; | GH13 |
| SCE1572_9903 | 40.34 1e-07 | YP_002890225.1;ACR01848.1; | GT2 |
| SCE1572_9959 | 44.57 5e-07 | NP_628976.1;CAB97423.1; | GH23 |
| SCE1572_9964 | 40.28 9e-06 | YP_001536176.1;ABV97185.1; | CBM13 |
| SCE1572_9980 | 47.27 5e-06 | YP_001363592.1;ABS05328.1; | GT4 |
| SCE1572_9981 | 93.18 | 0 YP_001618494.1;CAN98014.1; | GT2 |
| SCE1572_9984 | 71.06 2e-167 | YP_001618500.1;CAN98020.1; | GH62 |
| SCE1572_9993 | 81.57 9e-150 | ABC94557.1; | GH10 |
| SCE1572_9994 | 65.29 4e-122 | YP_002505570.1;ACL75590.1; | CBM6 |
| SCE1572_9994 | 65.29 4e-122 | YP_002505570.1;ACL75590.1; | GH62 |
| SCE1572_10038 | 45.21 1e-07 | YP_002431094.1;ACL03626.1; | CBM50 |
| SCE1572_10038 | 45.21 1e-07 | YP_002431094.1;ACL03626.1; | GH23 |
| SCE1572_10056 | 44.16 5e-07 | YP_003148898.1;ACV06133.1; | GT2 |
| SCE1572_10089 | 47.62 3e-06 | YP_002782993.1;BAH54048.1; | GT4 |
| SCE1572_10099 | 41.67 3e-35 | YP_002479972.1;ACL49294.1; | GT4 |
| SCE1572_10199 | 91.3 | 0 YP_001618700.1;CAN98220.1; | GH15 |
| SCE1572_10205 | 49.18 6e-24 | YP_001981082.1;ACE84184.1; | CBM35 |
| SCE1572_10294 | 93.27 | 0 YP_001619258.1;CAN98778.1; | GT2 |
| SCE1572_10344 | 65.55 6e-177 | YP_001618727.1;CAN98247.1; | GH6 |
| SCE1572_10393 | 89.68 | 0 YP_001613332.1;CAN92852.1; | GH43 |
| SCE1572_10400 | 41.76 3e-08 | YP_001818156.1;ACB74556.1; | GH55 |
| SCE1572_10442 | 82.7 | 0 YP_001618771.1;CAN98291.1; | GH65 |
| SCE1572_10447 | 44.44 7e-15 | YP_001360086.1;ABS01822.1; | GT2 |
| SCE1572_10471 | 40.54 4e-11 | YP_001360086.1;ABS01822.1; | GT2 |
| SCE1572_10516 | 42.24 2e-11 | YP_003266604.1;ACY14711.1; | CBM50 |
| SCE1572_10516 | 42.24 2e-11 | YP_003266604.1;ACY14711.1; | GH46 |
| SCE1572_10621 | 41 1e-93 | ACX49739.1; | GH4 |
| SCE1572_10623 | 42.61 3e-103 | ACX49739.1; | GH4 |
| SCE1572_10730 | 90.33 2e-125 | YP_001619056.1;CAN98576.1; | CE4 |
| SCE1572_10744 | 54.21 1e-93 | YP_001615235.1;CAN94755.1; | CBM13 |
| SCE1572_10744 | 54.21 1e-93 | YP_001615235.1;CAN94755.1; | GH62 |
| SCE1572_10752 | 75.77 6e-123 | YP_001615240.1;CAN94760.1; | GH16 |
| SCE1572_10767 | 85.33 4e-162 | YP_001619622.1;CAN99142.1; | GT1 |
| SCE1572_10777 | 87.99 4e-162 | YP_001618732.1;CAN98252.1; | GH5 |
| SCE1572_10805 | 77.81 4e-149 | YP_001614648.1;CAN94168.1; | CBM12 |
| SCE1572_10805 | 77.81 4e-149 | YP_001614648.1;CAN94168.1; | GH18 |
| SCE1572_10806 | 54 5e-06 | YP_736718.1;ABI41661.1; | CE1 |

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| SCE1572_10845 | 65.13 5e-94 | YP_002505576.1;ACL75596.1; | CBM6 |
| SCE1572_10845 | 65.13 5e-94 | YP_002505576.1;ACL75596.1; | CE6 |
| SCE1572_10845 | 65.13 5e-94 | YP_002505576.1;ACL75596.1; | GH62 |
| SCE1572_10857 | 76.52 4e-169 | ABC94557.1; | GH10 |
| SCE1572_10871 | 40 9e-13 | YP_001536176.1;ABV97185.1; | CBM13 |
| SCE1572_10886 | 86.39 1e-159 | YP_001619166.1;CAN98686.1; | CBM2 |
| SCE1572_10892 | 43.37 4e-11 | P23253.1;AAA30255.1; | GH33 |
| SCE1572_10894 | 42.34 3e-12 | YP_003274139.1;ACY22246.1; | GT87 |
| SCE1572_10908 | 75.47 1e-135 | YP_001619191.1;CAN98711.1; | CBM9 |
| SCE1572_10955 | 84.78 | 0 YP_001619209.1;CAN98729.1; | GH3 |
| SCE1572_10963 | 42.27 7e-12 | YP_001278382.1;ABQ92432.1; | GT2 |
| SCE1572_10970 | 40 3e-33 | ACX42259.1; | CBM12 |
| SCE1572_10982 | 58.3 6e-76 | YP_003265049.1;ACY13156.1; | GT2 |
| SCE1572_11024 | 40 1e-06 | YP_003583586.1;ADF51390.1; | GT2 |
| SCE1572_11115 | 62.01 1e-130 | YP_001615581.1;CAN95101.1; | CBM0 |
| SCE1572_11115 | 62.01 1e-130 | YP_001615581.1;CAN95101.1; | PL3 |
| SCE1572_11134 | 82.87 4e-148 | YP_001618138.1;CAN97658.1; | GH114 |
| SCE1572_11191 | 43.47 3e-99 | CAN80640.1; | GT47 |
| SCE1572_11206 | 41.83 6e-33 | NP_628653.1;CAB92109.1; | CBM13 |
| SCE1572_11209 | 89.37 | 0 YP_001619570.1;CAN99090.1; | GT4 |
| SCE1572_11215 | 49.89 | 0 YP_003270912.1;ACY19019.1; | CBM48 |
| SCE1572_11230 | 88.99 4e-121 | YP_001614645.1;CAN94165.1; | GH11 |
| SCE1572_11235 | 54.85 4e-103 | YP_002538685.1;ACM21584.1; | GH0 |
| SCE1572_11237 | 88.1 1e-176 | YP_001619589.1;CAN99109.1; | GT4 |
| SCE1572_11238 | 85.96 1e-180 | YP_001619590.1;CAN99110.1; | GT0 |
| SCE1572_11242 | 91.99 | 0 YP_001611539.1;CAN91059.1; | GH5 |
| SCE1572_11262 | 86.8 | 0 YP_001619650.1;CAN99170.1; | GT4 |
| SCE1572_11274 | 43.55 5e-06 | YP_730767.1;ABI45390.1; | GT51 |
| SCE1572_11281 | 40 2e-06 | YP_001640271.1;ABY31200.1; | GT41 |
| SCE1572_11311 | 42.62 2e-167 | YP_003267712.1;ACY15819.1; | CBM2 |
| SCE1572_11351 | 46.15 8e-08 | YP_001536176.1;ABV97185.1; | CBM13 |
| SCE1572_11393 | 49.4 1e-10 | YP_003765392.1;ADJ44990.1; | CBM2 |
| SCE1572_11465 | 40.31 2e-10 | A1IGV8.1;BAF44076.1; | CBM6 |
| SCE1572_11465 | 40.31 2e-10 | A1IGV8.1;BAF44076.1; | GH96 |
| SCE1572_11471 | 46.64 5e-35 | NP_250788.1;YP_002440812.1;AAG0548 | CE10 |
| SCE1572_11491 | 86.62 | 0 YP_001619891.1;CAN99411.1; | GT21 |
| SCE1572_11503 | 45.98 2e-06 | AAA21932.1; | GH33 |
| SCE1572_11559 | 45.21 9e-07 | YP_108308.1;CAH35705.1; | CE3 |
| SCE1572_11581 | 40.55 1e-30 | YP_001106030.1;ZP_06565633.1;CAM03 | CBM6 |
| SCE1572_11582 | 41.74 3e-28 | YP_003765392.1;ADJ44990.1; | CBM2 |
| SCE1572_13 | 86.3 | 0 YP_001610649.1;CAN90169.1; | GT83 |
| SCE1572_22 | 40 4e-08 | EEC68331.1; | CBM50 |
| SCE1572_39 | 89.31 | 0 YP_001610675.1;CAN90195.1; | GT51 |
| SCE1572_66 | 86.85 | 0 YP_001610690.1;CAN90210.1; | GT89 |
| SCE1572_68 | 43.43 2e-06 | YP_003911717.1;ADN74643.1; | CBM13 |
| SCE1572_78 | 70.39 2e-59 | YP_001610700.1;CAN90220.1; | CBM3 |
| SCE1572_90 | 40.16 6e-12 | YP_526867.1;ABD80655.1; | CBM6 |
| SCE1572_90 | 40.16 6e-12 | YP_526867.1;ABD80655.1; | CBM56 |
| SCE1572_90 | 40.16 6e-12 | YP_526867.1;ABD80655.1; | GH16 |
| SCE1572_133 | 43.93 5e-12 | YP_526867.1;ABD80655.1; | CBM6 |
| SCE1572_133 | 43.93 5e-12 | YP_526867.1;ABD80655.1; | CBM56 |
| SCE1572_133 | 43.93 5e-12 | YP_526867.1;ABD80655.1; | GH16 |
| SCE1572_135 | 75.63 4e-134 | YP_001619579.1;CAN99099.1; | CE1 |
| SCE1572_159 | 41.11 2e-11 | NP_628653.1;CAB92109.1; | CBM13 |
| SCE1572_182 | 40.83 1e-22 | ADI10340.1; | CBM35 |
| SCE1572_183 | 85.14 | 0 YP_001619183.1;CAN98703.1; | CBM32 |
| SCE1572_185 | 67.66 9e-109 | YP_001617670.1;CAN97190.1; | CE3 |
| SCE1572_301 | 40.13 3e-16 | YP_715463.1;CAJ63931.1; | CBM13 |
| SCE1572_330 | 46.55 6e-07 | ADD62001.1; | GH3 |
| SCE1572_342 | 43.96 1e-42 | YP_001087934.1;CAJ68298.1; | GH18 |
| SCE1572_346 | 84.68 | 0 YP_001613859.1;CAN93379.1; | GH8 |
| SCE1572_348 | 50.93 3e-81 | YP_001614884.1;CAN94404.1; | GT4 |
| SCE1572_349 | 41.26 5e-35 | YP_001619570.1;CAN99090.1; | GT4 |
| SCE1572_350 | 82.09 | 0 YP_001619609.1;CAN99129.1; | GT4 |
| SCE1572_409 | 82.21 3e-145 | YP_001615664.1;CAN95184.1; | CE1 |
| SCE1572_411 | 42.61 7e-15 | YP_001360086.1;ABS01822.1; | GT2 |
| SCE1572_413 | 86.23 | 0 YP_001610845.1;CAN90365.1; | CBM0 |
| SCE1572_417 | 41.75 1e-09 | ADO77294.1; | CBM32 |
| SCE1572_530 | 88.99 | 0 YP_001610936.1;CAN90456.1; | CBM50 |
| SCE1572_567 | 91.22 | 0 YP_001610968.1;CAN90488.1; | GT51 |
| SCE1572_586 | 86.75 | 0 YP_001610988.1;CAN90508.1; | GH77 |
| SCE1572_592 | 45.73 1e-46 | YP_825958.1;ABJ85673.1; | GT4 |
| SCE1572_601 | 93.18 | 0 YP_001610998.1;CAN90518.1; | GH13 |
| SCE1572_671 | 41.61 1e-45 | YP_715463.1;CAJ63931.1; | CBM13 |
| SCE1572_681 | 90.68 7e-100 | YP_001611064.1;CAN90584.1; | GT2 |
| SCE1572_686 | 42.27 1e-10 | YP_003765392.1;ADJ44990.1; | CBM2 |
| SCE1572_726 | 42.15 2e-08 | AAA21932.1; | GH33 |
| SCE1572_728 | 40.08 1e-31 | YP_001106030.1;ZP_06565633.1;CAM03 | CBM6 |
| SCE1572_746 | 86.83 | 0 YP_001611125.1;CAN90645.1; | GT20 |
| SCE1572_762 | 83.37 | 0 YP_001610719.1;CAN90240.1; | GH31 |

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| SCE1572_841 | 79.45 | 0 YP_001615547.1;CAN95067.1; | PL1 |
| SCE1572_909 | 42.37 6e-20 | YP_001360086.1;ABS01822.1; | GT2 |
| SCE1572_966 | 58 | 0 YP_635253.1;ABF90989.1; | GH15 |
| SCE1572_983 | 92.51 | 0 YP_001611298.1;CAN90818.1; | GH5 |
| SCE1572_999 | 42.5 3e-06 | ACN30267.1; | CBM32 |
| SCE1572_1000 | 41.77 9e-07 | YP_001222417.1;CAN01726.1; | CBM22 |
| SCE1572_1000 | 41.77 9e-07 | YP_001222417.1;CAN01726.1; | GH10 |
| SCE1572_1003 | 78.42 5e-174 | YP_001611310.1;CAN90830.1; | CE13 |
| SCE1572_1015 | 40.23 1e-28 | YP_003838689.1;ADL49113.1; | CBM2 |
| SCE1572_1064 | 40.74 4e-06 | YP_003849847.1;ADL58534.1; | GT2 |
| SCE1572_1085 | 41.56 3e-07 | BAA05832.1; | CBM20 |
| SCE1572_1085 | 41.56 3e-07 | BAA05832.1; | CBM34 |
| SCE1572_1085 | 41.56 3e-07 | BAA05832.1; | CBM48 |
| SCE1572_1085 | 41.56 3e-07 | BAA05832.1; | GH13 |
| SCE1572_1091 | 86.01 4e-158 | ABC94557.1; | GH10 |
| SCE1572_1098 | 40.1 1e-26 | YP_003101875.1;ACU38029.1; | CBM2 |
| SCE1572_1184 | 52.03 | 0 YP_003270912.1;ACY19019.1; | CBM48 |
| SCE1572_1190 | 83.03 | 0 YP_001611633.1;CAN91153.1; | GH67 |
| SCE1572_1207 | 44.92 3e-13 | YP_001360086.1;ABS01822.1; | GT2 |
| SCE1572_1221 | 40.83 4e-13 | YP_003954374.1;ADO72547.1; | CBM12 |
| SCE1572_1221 | 40.83 4e-13 | YP_003954374.1;ADO72547.1; | GH18 |
| SCE1572_1227 | 46.85 7e-21 | YP_003408615.1;ADB74244.1; | GT2 |
| SCE1572_1229 | 40.12 1e-19 | YP_003838689.1;ADL49113.1; | CBM2 |
| SCE1572_1236 | 80.27 | 0 YP_001611434.1;CAN90954.1; | PL9 |
| SCE1572_1238 | 42.86 8e-18 | YP_001360086.1;ABS01822.1; | GT2 |
| SCE1572_1256 | 44.34 2e-63 | ZP_01464504.1;YP_003955390.1;EAU64' | CBM13 |
| SCE1572_1260 | 94.88 | 0 YP_001612161.1;CAN91681.1; | GH0 |
| SCE1572_1275 | 41.25 7e-06 | YP_003408615.1;ADB74244.1; | GT2 |
| SCE1572_1281 | 47.41 5e-20 | YP_001360086.1;ABS01822.1; | GT2 |
| SCE1572_1324 | 46.38 1e-07 | YP_003588908.1;ADG05764.1; | CBM50 |
| SCE1572_1345 | 94.39 | 0 YP_001611499.1;CAN91019.1; | GT2 |
| SCE1572_1365 | 44.21 4e-48 | YP_128593.1;CAG18791.1; | GT2 |
| SCE1572_1371 | 92.65 | 0 YP_001611525.1;CAN91045.1; | GT4 |
| SCE1572_1385 | 79.05 7e-145 | YP_001616374.1;CAN95894.1; | GH12 |
| SCE1572_1387 | 86.98 | 0 YP_001619605.1;CAN99125.1; | CBM2 |
| SCE1572_1395 | 41.89 6e-07 | YP_736718.1;ABI41661.1; | CE1 |
| SCE1572_1406 | 42.05 1e-105 | YP_003466227.1;CBJ79429.1; | GH24 |
| SCE1572_1421 | 43.38 1e-13 | NP_733639.1;CAD55485.1; | CBM13 |
| SCE1572_1422 | 46.08 9e-16 | ADI07346.1; | CBM13 |
| SCE1572_1443 | 89.85 | 0 YP_001611603.1;CAN91123.1; | GH30 |
| SCE1572_1476 | 40.26 3e-06 | YP_003846893.1;ADL55129.1; | GT41 |
| SCE1572_1478 | 43.98 7e-48 | YP_003250378.1;ACX75896.1;ADL27148 | GT2 |
| SCE1572_1508 | 70.16 1e-44 | YP_001617342.1;CAN96862.1; | GH10 |
| SCE1572_1525 | 40.21 2e-29 | YP_003101875.1;ACU38029.1; | CBM2 |
| SCE1572_1540 | 86.94 | 0 YP_001611582.1;CAN91102.1; | GH23 |
| SCE1572_1573 | 84.52 | 0 YP_001611639.1;CAN91159.1; | GH105 |
| SCE1572_1574 | 48.39 1e-46 | YP_002479972.1;ACL49294.1; | GT4 |
| SCE1572_1606 | 45.19 6e-105 | YP_003267712.1;ACY15819.1; | CBM2 |
| SCE1572_1609 | 85.08 | 0 YP_001611662.1;CAN91182.1; | GT4 |
| SCE1572_1612 | 76.29 9e-130 | YP_001611664.1;CAN91184.1; | GT0 |
| SCE1572_1614 | 90.48 | 0 YP_001611665.1;CAN91185.1; | GT4 |
| SCE1572_1616 | 91.03 2e-180 | YP_001611667.1;CAN91187.1; | GT4 |
| SCE1572_1617 | 81.02 3e-159 | YP_001611668.1;CAN91188.1; | GT4 |
| SCE1572_1656 | 41.35 8e-06 | YP_003274139.1;ACY22246.1; | GT87 |
| SCE1572_1673 | 92.62 | 0 YP_001611700.1;CAN91220.1; | GT5 |
| SCE1572_1694 | 40.48 1e-10 | YP_003324485.1;ACZ43662.1; | CBM57 |
| SCE1572_1720 | 52.63 9e-14 | YP_002928937.1;ACR62057.1; | GH2 |
| SCE1572_1767 | 89.14 3e-158 | AAK19891.1; | CBM13 |
| SCE1572_1771 | 51.91 3e-89 | NP_870096.1;CAD79251.1; | CE1 |
| SCE1572_1884 | 41.33 8e-19 | YP_003765392.1;ADJ44990.1; | CBM2 |
| SCE1572_1893 | 46.75 1e-30 | YP_830004.1;ABK01904.1; | GH3 |
| SCE1572_1907 | 96.37 | 0 YP_001611914.1;CAN91434.1; | GH113 |
| SCE1572_1922 | 85.75 3e-167 | YP_001611938.1;CAN91458.1; | GT4 |
| SCE1572_1923 | 84.11 1e-61 | YP_001611939.1;CAN91459.1; | GT4 |
| SCE1572_1926 | 93.65 | 0 YP_001611941.1;CAN91461.1; | CBM48 |
| SCE1572_1926 | 93.65 | 0 YP_001611941.1;CAN91461.1; | GH13 |
| SCE1572_1965 | 47.17 2e-06 | YP_191885.1;AAW61229.1; | CE1 |
| SCE1572_1994 | 42.6 5e-136 | ZP_01460104.1;YP_003955802.1;EAU69' | CBM56 |
| SCE1572_2002 | 59.52 2e-86 | ZP_01461172.1;YP_003953282.1;EAU68' | CBM32 |
| SCE1572_2011 | 40.48 2e-06 | CAD48195.1; | GH68 |
| SCE1572_2020 | 41.74 3e-18 | NP_810096.1;AAO76290.1; | GT2 |
| SCE1572_2022 | 77.99 | 0 YP_001613943.1;CAN93463.1; | CBM6 |
| SCE1572_2022 | 77.99 | 0 YP_001613943.1;CAN93463.1; | GH43 |
| SCE1572_2023 | 85.45 9e-144 | YP_001615249.1;CAN94769.1; | CE1 |
| SCE1572_2089 | 52.11 4e-33 | YP_001616194.1;CAN95714.1; | CBM2 |
| SCE1572_2089 | 52.11 4e-33 | YP_001616194.1;CAN95714.1; | GH11 |
| SCE1572_2105 | 52.27 1e-06 | YP_961238.1;ABM30050.1; | GT2 |
| SCE1572_2114 | 73.84 8e-164 | YP_001612106.1;CAN91626.1; | GH5 |
| SCE1572_2128 | 82.69 5e-155 | YP_001612123.1;CAN91643.1; | GH43 |
| SCE1572_2132 | 86.84 5e-117 | YP_001612127.1;CAN91647.1; | CE12 |

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| SCE1572_2133 | 50.13 | 0 YP_003652627.1;ADG88734.1; | CBM2 |
| SCE1572_2133 | 50.13 | 0 YP_003652627.1;ADG88734.1; | PL11 |
| SCE1572_2146 | 88.24 5e-95 | YP_001611385.1;CAN90905.1; | CBM13 |
| SCE1572_2146 | 88.24 5e-95 | YP_001611385.1;CAN90905.1; | CE1 |
| SCE1572_2148 | 89.43 | 0 YP_001611385.1;CAN90905.1; | CBM13 |
| SCE1572_2148 | 89.43 | 0 YP_001611385.1;CAN90905.1; | CE1 |
| SCE1572_2151 | 88.76 4e-154 | YP_001612186.1;CAN91706.1; | GT2 |
| SCE1572_2166 | 40.71 3e-21 | YP_003585679.1;ADF53483.1; | CBM32 |
| SCE1572_2178 | 41.32 5e-16 | NP_828618.1;BAC75153.1; | CBM13 |
| SCE1572_2178 | 41.32 5e-16 | NP_828618.1;BAC75153.1; | GH16 |
| SCE1572_2196 | 41.36 2e-22 | YP_003767779.1;ADJ47377.1; | CBM2 |
| SCE1572_2207 | 45.68 7e-19 | BAD91082.1; | GH35 |
| SCE1572_2236 | 76.53 | 0 YP_001612238.1;CAN91758.1; | GH23 |
| SCE1572_2239 | 40.59 8e-32 | YP_001106030.1;ZP_06565633.1;CAM03 | CBM6 |
| SCE1572_2241 | 40.09 4e-31 | YP_003101875.1;ACU38029.1; | CBM2 |
| SCE1572_2268 | 88.83 | 0 YP_001612264.1;CAN91784.1; | GH57 |
| SCE1572_2278 | 41.55 6e-35 | YP_002479972.1;ACL49294.1; | GT4 |
| SCE1572_2307 | 92.1 3e-178 | YP_001612302.1;A9FI55.1;CAN91822.1; | GT28 |
| SCE1572_2308 | 42.49 4e-70 | YP_003636693.1;ADG74494.1; | GT28 |
| SCE1572_2333 | 44.92 8e-24 | YP_002721447.1;ACN83743.1; | CE11 |
| SCE1572_2363 | 53.06 4e-06 | YP_003274139.1;ACY22246.1; | GT87 |
| SCE1572_2375 | 51.22 6e-13 | YP_001716461.1;ACA58829.1; | GT4 |
| SCE1572_2396 | 83.11 5e-144 | YP_001612388.1;CAN91908.1; | GT4 |
| SCE1572_2452 | 42.03 9e-07 | YP_434263.1;ABC29838.1; | CBM12 |
| SCE1572_2452 | 42.03 9e-07 | YP_434263.1;ABC29838.1; | CBM32 |
| SCE1572_2494 | 85.75 | 0 YP_001612504.1;CAN92024.1; | GT1 |
| SCE1572_2499 | 92.6 | 0 YP_001612814.1;CAN92334.1; | CE15 |
| SCE1572_2503 | 86.56 8e-162 | YP_001617388.1;CAN96908.1; | CE1 |
| SCE1572_2565 | 52.07 | 0 YP_001105474.1;ZP_06564125.1;CAM02 | GH97 |
| SCE1572_2588 | 42.25 3e-30 | YP_003766420.1;ADJ46018.1; | CBM2 |
| SCE1572_2590 | 43.71 3e-20 | YP_003766420.1;ADJ46018.1; | CBM2 |
| SCE1572_2612 | 45.14 1e-46 | YP_464228.1;ABC80791.1; | GT4 |
| SCE1572_2624 | 83.27 | 0 YP_001615241.1;CAN94761.1; | CBM6 |
| SCE1572_2624 | 83.27 | 0 YP_001615241.1;CAN94761.1; | GH43 |
| SCE1572_2627 | 87.55 1e-145 | YP_001615234.1;CAN94754.1; | GH10 |
| SCE1572_2628 | 82.04 | 0 YP_001615235.1;CAN94755.1; | CBM13 |
| SCE1572_2628 | 82.04 | 0 YP_001615235.1;CAN94755.1; | GH62 |
| SCE1572_2636 | 47.19 7e-107 | YP_529079.1;ABD82867.1; | CBM2 |
| SCE1572_2636 | 47.19 7e-107 | YP_529079.1;ABD82867.1; | CBM6 |
| SCE1572_2636 | 47.19 7e-107 | YP_529079.1;ABD82867.1; | CBM22 |
| SCE1572_2636 | 47.19 7e-107 | YP_529079.1;ABD82867.1; | GH10 |
| SCE1572_2636 | 47.19 7e-107 | YP_529079.1;ABD82867.1; | GH43 |
| SCE1572_2647 | 40.47 5e-27 | YP_003766420.1;ADJ46018.1; | CBM2 |
| SCE1572_2652 | 40.15 5e-13 | YP_003767779.1;ADJ47377.1; | CBM2 |
| SCE1572_2690 | 40.59 1e-06 | NP_628976.1;CAB97423.1; | GH23 |
| SCE1572_2701 | 45.58 5e-23 | NP_733639.1;CAD55485.1; | CBM13 |
| SCE1572_2742 | 41.88 3e-17 | YP_001360086.1;ABS01822.1; | GT2 |
| SCE1572_2791 | 69.21 1e-126 | YP_526296.1;ABD80084.1; | GH43 |
| SCE1572_2816 | 41.1 2e-08 | YP_003266068.1;ACY14175.1; | CBM13 |
| SCE1572_2866 | 56.66 | 0 YP_002505572.1;ABG76968.1;ACL75592 | CBM22 |
| SCE1572_2878 | 89.13 | 0 YP_001612873.1;CAN92393.1; | CBM4 |
| SCE1572_2878 | 89.13 | 0 YP_001612873.1;CAN92393.1; | GH9 |
| SCE1572_2890 | 62.39 3e-157 | YP_002134508.1;ACG73379.1; | GT0 |
| SCE1572_2924 | 93.24 | 0 AAY32973.1;CAI43941.1; | GH31 |
| SCE1572_2925 | 92.73 | 0 AAY32974.1; | CBM6 |
| SCE1572_2925 | 92.73 | 0 AAY32974.1; | GH3 |
| SCE1572_2942 | 46.59 8e-54 | YP_001613915.1;CAN93435.1; | CE1 |
| SCE1572_2944 | 48.71 1e-54 | YP_001619514.1;CAN99034.1; | CE3 |
| SCE1572_2960 | 57.04 2e-164 | YP_003506087.1;ADD27067.1; | GH43 |
| SCE1572_2967 | 46.88 3e-06 | AAC98688.2; | GH33 |
| SCE1572_3038 | 42.99 6e-18 | YP_002505894.1;ACL75914.1; | GH73 |
| SCE1572_3053 | 43 5e-42 | NP_952035.1;AAR34308.1;ADI83822.1; | CBM50 |
| SCE1572_3113 | 90.59 | 0 YP_001611883.1;CAN91403.1; | CBM42 |
| SCE1572_3113 | 90.59 | 0 YP_001611883.1;CAN91403.1; | GH43 |
| SCE1572_3114 | 91.48 | 0 YP_001611884.1;CAN91404.1; | GH43 |
| SCE1572_3137 | 40.37 2e-35 | YP_715463.1;CAJ63931.1; | CBM13 |
| SCE1572_3162 | 88.18 | 0 YP_001613016.1;CAN92536.1; | GH77 |
| SCE1572_3163 | 93.08 | 0 YP_001613017.1;CAN92537.1; | CBM48 |
| SCE1572_3163 | 93.08 | 0 YP_001613017.1;CAN92537.1; | GH13 |
| SCE1572_3165 | 40.8 5e-131 | YP_002942297.1;ACS17031.1; | CBM13 |
| SCE1572_3181 | 84.41 | 0 YP_001613030.1;CAN92550.1; | GH13 |
| SCE1572_3182 | 89.44 | 0 YP_001613031.1;CAN92551.1; | CBM48 |
| SCE1572_3182 | 89.44 | 0 YP_001613031.1;CAN92551.1; | GH13 |
| SCE1572_3208 | 46.27 2e-11 | ADI12636.1; | CBM35 |
| SCE1572_3236 | 40.91 5e-08 | ACN62172.1; | CBM5 |
| SCE1572_3236 | 40.91 5e-08 | ACN62172.1; | GH5 |
| SCE1572_3247 | 90.6 9e-112 | YP_001613088.1;CAN92609.1; | GH23 |
| SCE1572_3285 | 95.25 4e-166 | YP_001613123.1;CAN92643.1; | GT2 |
| SCE1572_3369 | 44.19 2e-08 | YP_003446640.1;CBJ22778.1; | CBM32 |
| SCE1572_3369 | 44.19 2e-08 | YP_003446640.1;CBJ22778.1; | GH101 |

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| SCE1572_3384 | 41.53 1e-13 | YP_001360086.1;ABS01822.1; | GT2 |
| SCE1572_3414 | 85.3 | 0 YP_001613224.1;CAN92744.1; | GT51 |
| SCE1572_3415 | 41.96 8e-30 | YP_003960686.1;ADO37723.1; | GH13 |
| SCE1572_3434 | 89.73 | 0 YP_001613240.1;CAN92760.1; | GH3 |
| SCE1572_3467 | 42.86 6e-13 | YP_002465840.1;ACL16117.1; | CBM6 |
| SCE1572_3493 | 44.07 3e-15 | YP_003408615.1;ADB74244.1; | GT2 |
| SCE1572_3496 | 40.48 7e-13 | YP_003408615.1;ADB74244.1; | GT2 |
| SCE1572_3521 | 40.48 1e-10 | YP_001360086.1;ABS01822.1; | GT2 |
| SCE1572_3533 | 81.21 | 0 YP_001617007.1;CAN96527.1; | PL9 |
| SCE1572_3549 | 73.82 | 0 YP_001615241.1;CAN94761.1; | CBM6 |
| SCE1572_3549 | 73.82 | 0 YP_001615241.1;CAN94761.1; | GH43 |
| SCE1572_3555 | 40.65 2e-27 | NP_733639.1;CAD55485.1; | CBM13 |
| SCE1572_3557 | 64.53 | 0 YP_001545516.1;ABX05388.1; | CBM12 |
| SCE1572_3557 | 64.53 | 0 YP_001545516.1;ABX05388.1; | GH18 |
| SCE1572_3559 | 42.5 3e-20 | ACX31135.1; | GH0 |
| SCE1572_3561 | 61.26 3e-125 | ACF93778.1; | CE9 |
| SCE1572_3563 | 49.94 | 0 BAA92145.1; | GH20 |
| SCE1572_3564 | 41.91 6e-36 | YP_715463.1;CAJ63931.1; | CBM13 |
| SCE1572_3565 | 41.7 1e-36 | YP_715463.1;CAJ63931.1; | CBM13 |
| SCE1572_3568 | 41.91 7e-36 | YP_715463.1;CAJ63931.1; | CBM13 |
| SCE1572_3577 | 51.3 2e-51 | ZP_01464504.1;YP_003955390.1;EAU64' | CBM13 |
| SCE1572_3579 | 43.42 8e-07 | BAA05832.1; | CBM20 |
| SCE1572_3579 | 43.42 8e-07 | BAA05832.1; | CBM34 |
| SCE1572_3579 | 43.42 8e-07 | BAA05832.1; | CBM48 |
| SCE1572_3579 | 43.42 8e-07 | BAA05832.1; | GH13 |
| SCE1572_3580 | 46.99 3e-81 | YP_677834.1;ABG58494.1; | CBM9 |
| SCE1572_3611 | 43.75 1e-12 | YP_003101875.1;ACU38029.1; | CBM2 |
| SCE1572_3642 | 76.9 8e-161 | ZP_01466799.1;YP_003955347.1;EAU62 | CBM13 |
| SCE1572_3648 | 41.59 6e-32 | YP_715463.1;CAJ63931.1; | CBM13 |
| SCE1572_3679 | 45 1e-12 | YP_003074740.1;ACR13005.1; | CBM2 |
| SCE1572_3679 | 45 1e-12 | YP_003074740.1;ACR13005.1; | CBM10 |
| SCE1572_3679 | 45 1e-12 | YP_003074740.1;ACR13005.1; | GH45 |
| SCE1572_8890 | 93.52 1e-120 | YP_001619971.1;CAN99491.1; | CBM57 |
| SCE1572_8890 | 93.52 1e-120 | YP_001619971.1;CAN99491.1; | GH11 |
| SCE1572_3709 | 48.39 9e-13 | YP_003115974.1;ACU74133.1; | GH78 |
| SCE1572_3710 | 48.75 6e-15 | CAN61133.1; | GH36 |
| SCE1572_3725 | 68.63 4e-124 | YP_001617650.1;CAN97170.1; | CE4 |
| SCE1572_3734 | 63.47 7e-144 | YP_001615903.1;CAN95423.1; | CBM2 |
| SCE1572_3773 | 51.45 3e-111 | XP_002500812.1;ACO62070.1; | CE1 |
| SCE1572_3772 | 73.51 4e-171 | YP_001613407.1;CAN92927.1; | GH5 |
| SCE1572_3815 | 67.18 3e-116 | YP_001612531.1;CAN92051.1; | CE1 |
| SCE1572_3835 | 40.34 7e-17 | YP_003408615.1;ADB74244.1; | GT2 |
| SCE1572_3856 | 43.15 2e-08 | YP_003911717.1;ADN74643.1; | CBM13 |
| SCE1572_3884 | 47.97 3e-35 | YP_002761100.1;BAH38630.1; | CE11 |
| SCE1572_3945 | 47.31 9e-09 | AAC98688.2; | GH33 |
| SCE1572_3947 | 40.43 9e-16 | AAA21932.1; | GH33 |
| SCE1572_3962 | 41.36 5e-104 | YP_003267712.1;ACY15819.1; | CBM2 |
| SCE1572_4007 | 83.55 | 0 YP_001613610.1;CAN93130.1; | GT89 |
| SCE1572_4072 | 40.29 5e-11 | P23253.1;AAA30255.1; | GH33 |
| SCE1572_4086 | 89.49 | 0 YP_001613679.1;CAN93199.1; | PL11 |
| SCE1572_4088 | 46.6 9e-14 | YP_003770756.1;ADJ50354.1; | CBM32 |
| SCE1572_4088 | 46.6 9e-14 | YP_003770756.1;ADJ50354.1; | CBM35 |
| SCE1572_4088 | 46.6 9e-14 | YP_003770756.1;ADJ50354.1; | GH29 |
| SCE1572_4100 | 78.94 | 0 YP_001613703.1;CAN93223.1; | GH13 |
| SCE1572_4132 | 95.25 | 0 YP_001613737.1;CAN93257.1; | GT1 |
| SCE1572_4195 | 40.91 2e-07 | YP_822029.1;ABJ81744.1; | CE4 |
| SCE1572_4222 | 50.78 4e-74 | YP_003744163.1;CBJ41515.1; | GH5 |
| SCE1572_4244 | 94.2 | 0 YP_001613800.1;CAN93320.1; | GT5 |
| SCE1572_4261 | 62.57 | 0 YP_003267346.1;ACY15453.1; | GT2 |
| SCE1572_4265 | 44.3 1e-05 | YP_003590781.1;ADG07637.1; | CE4 |
| SCE1572_4336 | 88.69 | 0 YP_001619556.1;CAN99076.1; | GH43 |
| SCE1572_4342 | 42.46 2e-27 | YP_003766420.1;ADJ46018.1; | CBM2 |
| SCE1572_4350 | 40.08 1e-31 | YP_715463.1;CAJ63931.1; | CBM13 |
| SCE1572_4353 | 76.3 6e-132 | YP_001619964.1;CAN99484.1; | CE6 |
| SCE1572_4424 | 85.45 | 0 YP_001613907.1;CAN93427.1; | GT20 |
| SCE1572_4461 | 54.08 9e-67 | YP_003073663.1;ACR13114.1; | CBM2 |
| SCE1572_4461 | 54.08 9e-67 | YP_003073663.1;ACR13114.1; | CBM10 |
| SCE1572_4461 | 54.08 9e-67 | YP_003073663.1;ACR13114.1; | GH16 |
| SCE1572_4463 | 40.28 3e-26 | YP_003767779.1;ADJ47377.1; | CBM2 |
| SCE1572_4469 | 64.4 | 0 YP_003650973.1;ADG87080.1; | GH115 |
| SCE1572_4475 | 81.69 | 0 YP_001615994.1;CAN95514.1; | GH5 |
| SCE1572_4488 | 79.6 6e-176 | ABC94557.1; | GH10 |
| SCE1572_4493 | 43.5 2e-30 | YP_003765393.1;ADJ44991.1; | CBM2 |
| SCE1572_4540 | 49.89 | 0 YP_003270912.1;ACY19019.1; | CBM48 |
| SCE1572_4555 | 54.97 9e-177 | YP_002943270.1;ACS18004.1; | PL10 |
| SCE1572_4556 | 44.79 2e-58 | YP_001546225.1;ABX06097.1; | CBM2 |
| SCE1572_4556 | 44.79 2e-58 | YP_001546225.1;ABX06097.1; | PL1 |
| SCE1572_4567 | 95.55 3e-138 | YP_001614053.1;CAN93573.1; | PL3 |
| SCE1572_4570 | 58.79 1e-134 | YP_003884903.1;ADN00347.1; | PL1 |
| SCE1572_4574 | 42.37 2e-12 | YP_001360086.1;ABS01822.1; | GT2 |

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| SCE1572_4587 | 41.54 1e-05 | YP_526867.1;ABD80655.1; | CBM6 |
| SCE1572_4587 | 41.54 1e-05 | YP_526867.1;ABD80655.1; | CBM56 |
| SCE1572_4587 | 41.54 1e-05 | YP_526867.1;ABD80655.1; | GH16 |
| SCE1572_4633 | 41.14 2e-67 | YP_003899706.1;ADN17640.1; | GT2 |
| SCE1572_4637 | 89.32 | 0 YP_001614089.1;CAN93609.1; | GH31 |
| SCE1572_4645 | 89.29 | 0 YP_001614095.1;CAN93615.1; | GH1 |
| SCE1572_4662 | 40.76 5e-16 | YP_003767779.1;ADJ47377.1; | CBM2 |
| SCE1572_4670 | 44.66 6e-10 | YP_028446.1;AAT54497.1; | GT51 |
| SCE1572_4692 | 40 1e-30 | YP_003101875.1;ACU38029.1; | CBM2 |
| SCE1572_4693 | 88.8 | 0 YP_001612136.1;CAN91656.1; | GH44 |
| SCE1572_4696 | 80.07 8e-138 | YP_001617738.1;CAN97258.1; | GH10 |
| SCE1572_4736 | 40.68 2e-14 | ADO76962.1; | CBM50 |
| SCE1572_4741 | 41.3 4e-42 | YP_003270912.1;ACY19019.1; | CBM48 |
| SCE1572_4762 | 65.71 3e-06 | YP_736718.1;ABI41661.1; | CE1 |
| SCE1572_4785 | 43.4 2e-11 | YP_526867.1;ABD80655.1; | CBM6 |
| SCE1572_4785 | 43.4 2e-11 | YP_526867.1;ABD80655.1; | CBM56 |
| SCE1572_4785 | 43.4 2e-11 | YP_526867.1;ABD80655.1; | GH16 |
| SCE1572_4801 | 87.67 | 0 YP_001614222.1;CAN93742.1; | GT4 |
| SCE1572_4803 | 44.12 9e-42 | YP_128593.1;CAG18791.1; | GT2 |
| SCE1572_4805 | 43.94 3e-09 | YP_003121612.1;ACU59411.1; | GH20 |
| SCE1572_4815 | 45 4e-08 | YP_314064.1;AAZ96259.1; | GT2 |
| SCE1572_4820 | 40.18 3e-15 | YP_003785142.1;ADK30641.1; | CE11 |
| SCE1572_4824 | 91.91 | 0 YP_001614240.1;CAN93760.1; | GT2 |
| SCE1572_4861 | 43.5 5e-22 | NP_628653.1;CAB92109.1; | CBM13 |
| SCE1572_4869 | 62.03 5e-18 | YP_003685414.1;ADH63906.1; | CBM50 |
| SCE1572_4879 | 40.17 4e-17 | YP_001360086.1;ABS01822.1; | GT2 |
| SCE1572_3807 | 50.79 3e-08 | ACX42259.1; | CBM12 |
| SCE1572_629 | 40.78 4e-13 | YP_003408615.1;ADB74244.1; | GT2 |
| SCE1572_4965 | 48.14 | 0 YP_003270912.1;ACY19019.1; | CBM48 |
| SCE1572_5042 | 43.02 8e-09 | YP_003800599.1;ADK67719.1; | GH73 |
| SCE1572_5045 | 46.15 5e-06 | YP_063040.1;AAT89935.1; | CBM2 |
| SCE1572_5045 | 46.15 5e-06 | YP_063040.1;AAT89935.1; | GH5 |
| SCE1572_5056 | 40.34 2e-10 | YP_003324485.1;ACZ43662.1; | CBM57 |
| SCE1572_5065 | 40.87 2e-30 | YP_003101875.1;ACU38029.1; | CBM2 |
| SCE1572_5121 | 88.44 | 0 YP_001614492.1;CAN94012.1; | GH23 |
| SCE1572_5132 | 41.38 8e-14 | YP_003523228.1;ADE10841.1; | GT41 |
| SCE1572_5300 | 64.1 4e-115 | YP_001612123.1;CAN91643.1; | GH43 |
| SCE1572_5331 | 44.14 1e-19 | YP_001360086.1;ABS01822.1; | GT2 |
| SCE1572_5337 | 88.24 | 0 YP_001613382.1;CAN92902.1; | CBM13 |
| SCE1572_5363 | 40 2e-22 | NP_628653.1;CAB92109.1; | CBM13 |
| SCE1572_5374 | 75.89 | 0 YP_001614655.1;CAN94175.1; | CBM13 |
| SCE1572_5374 | 75.89 | 0 YP_001614655.1;CAN94175.1; | GH43 |
| SCE1572_5377 | 41.98 2e-95 | YP_003267712.1;ACY15819.1; | CBM2 |
| SCE1572_5385 | 81.8 | 0 YP_001614668.1;CAN94188.1; | CBM20 |
| SCE1572_5385 | 81.8 | 0 YP_001614668.1;CAN94188.1; | GH15 |
| SCE1572_5389 | 40 3e-20 | YP_003838689.1;ADL49113.1; | CBM2 |
| SCE1572_5414 | 91.45 2e-131 | YP_001614713.1;CAN94233.1; | GH114 |
| SCE1572_5430 | 78.99 | 0 YP_001617401.1;CAN96921.1; | GH115 |
| SCE1572_5454 | 45.76 2e-09 | YP_002928937.1;ACR62057.1; | GH2 |
| SCE1572_5472 | 41.41 8e-14 | YP_001615903.1;CAN95423.1; | CBM2 |
| SCE1572_5488 | 71.68 6e-141 | YP_001614743.1;CAN94263.1; | CE1 |
| SCE1572_5498 | 48.62 8e-10 | AAA21932.1; | GH33 |
| SCE1572_5512 | 40.62 1e-06 | YP_001814235.1;ACB61218.1; | GT51 |
| SCE1572_5517 | 42.19 2e-07 | ZP_02618969.1;YP_002862279.1;EDT84 | CBM50 |
| SCE1572_5527 | 42.27 1e-46 | ACT97502.1; | GH78 |
| SCE1572_5582 | 79.61 7e-138 | YP_001611675.1;CAN91195.1; | GT4 |
| SCE1572_5584 | 84.42 | 0 YP_001611673.1;CAN91193.1; | GT4 |
| SCE1572_5590 | 42.11 1e-07 | YP_003765393.1;ADJ44991.1; | CBM2 |
| SCE1572_5623 | 94.38 | 0 YP_001614839.1;CAN94360.1; | GH1 |
| SCE1572_5692 | 46.59 4e-06 | ACO87651.1; | GH33 |
| SCE1572_5702 | 83.96 | 0 YP_001614883.1;CAN94403.1; | GT4 |
| SCE1572_5703 | 91.23 | 0 YP_001614884.1;CAN94404.1; | GT4 |
| SCE1572_5760 | 86.63 2e-165 | YP_001614935.1;CAN94455.1; | GH3 |
| SCE1572_5766 | 92.44 | 0 YP_001614940.1;CAN94460.1; | GH1 |
| SCE1572_5801 | 51.02 4e-06 | YP_001612238.1;CAN91758.1; | GH23 |
| SCE1572_5873 | 40.77 3e-10 | YP_003408615.1;ADB74244.1; | GT2 |
| SCE1572_5876 | 40.27 5e-26 | YP_715463.1;CAJ63931.1; | CBM13 |
| SCE1572_5895 | 87.46 | 0 YP_001617375.1;CAN96895.1; | CBM13 |
| SCE1572_5906 | 94.84 | 0 YP_001615031.1;CAN94551.1; | GT35 |
| SCE1572_5931 | 83.7 | 0 YP_001615051.1;CAN94571.1; | GT51 |
| SCE1572_5942 | 47.3 3e-09 | YP_003597479.1;ADF39129.1; | GH25 |
| SCE1572_5944 | 46.43 8e-20 | YP_002505894.1;ACL75914.1; | GH73 |
| SCE1572_6059 | 41.64 2e-121 | CAN65674.1; | GH28 |
| SCE1572_6074 | 90.62 | 0 YP_001615137.1;CAN94657.1; | CBM48 |
| SCE1572_6074 | 90.62 | 0 YP_001615137.1;CAN94657.1; | GH13 |
| SCE1572_6094 | 78.75 2e-127 | YP_001611380.1;CAN90900.1; | CBM5 |
| SCE1572_6116 | 67.37 1e-145 | ADI11428.1; | CE15 |
| SCE1572_6125 | 41.07 4e-10 | YP_003637447.1;ADG75248.1; | GT4 |
| SCE1572_6133 | 41.06 2e-23 | YP_003767779.1;ADJ47377.1; | CBM2 |
| SCE1572_6155 | 45.45 1e-34 | YP_003765393.1;ADJ44991.1; | CBM2 |

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|--------------|-------------|----------------------------|-------|
| SCE1572_6158 | 41.73 1e-31 | YP_003838689.1;ADL49113.1; | CBM2 |
| SCE1572_6165 | 40.24 6e-28 | NP_628653.1;CAB92109.1; | CBM13 |
| SCE1572_6180 | 43.69 2e-12 | AAT81212.1; | CBM5 |
| SCE1572_6180 | 43.69 2e-12 | AAT81212.1; | GH18 |

* Blastp analysis based on CAZy database in 2011-05.