# Supplementary Materials

Title: Whole genome sequence analysis of rice genotypes with contrasting response to salinity stress

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This file includes Supplementary Tables S1-S5 and Supplementary Figures S1-S8.

Supplementary Tables S6, S7, and S8 were uploaded separately.

**Supplementary Table S1.** Distribution and frequency of SNPs (per 100 kb) between different rice cultivars on individual rice chromosome.

**Supplementary Table S2.** Distribution and frequency of InDels (per 100 kb) between different rice cultivars on individual rice chromosome.

**Supplementary Table S3.** List of SNPs and InDels detected in rice genotypes with respect to reference genome based on impact on mRNA and proteins.

**Supplementary Table S4.** List of SNPs and InDels detected in rice genotypes with respect to reference genome based on variant type and functional role.

**Supplementary Table S5.** Large-effect single-nucleotide polymorphisms (SNPs) and InDels detected in all six pair-wise combinations of rice genotypes.

**Supplementary Table S6.** List of salt tolerant QTLs identified in three mapping populations involving Pokkali and Nona Bokra as salt tolerant donors (De Leon et al. 2016; Puram et al. 2017, 2018)[17-19] to identify large effect variants in CDS and promoter regions of genes present in the QTL intervals (uploaded separately).

**Supplementary Table S7.** Differentially expressed genes harboring SNPs and/or InDels in promoter present in QTLs listed in Supplementary Table S6 (uploaded separately).

**Supplementary Table S8.** Differentially expressed genes harboring large effect SNPs and/or InDels in the promoter regions present in QTLs listed in Supplementary Table S6 (uploaded separately).

**Supplementary Figure S1.** Distribution and frequency of SNPs and InDels on individual rice chromosome detected in all pair-wise analysis of rice genotypes, Pokkali, Nona Bokra, Bengal, Cocodrie, and IR64. Number and frequency (per 100 kb) of SNPs (A) and InDels (B) detected on each rice chromosome are shown in the bar graphs.

**Supplementary Figure S2.** Number of SNPs and InDels between rice genotypes with contrasting response to salinity. Number of SNPs and Indels between salt sensitive (IR64, Bengal, and Cocodrie) and salt tolerant (Pokkali and Nona Bokra) rice cultivars are shown in the bar graphs.

**Supplementary Figure S3.** (A) Number of different substitution types in the identified SNPs detected in all pair-wise analysis of rice genotypes, Pokkali, Nona Bokra, Bengal, Cocodrie, and IR64. (B) Length distribution of InDels. Number of insertions and deletions (y-axis) of various lengths (x-axis, in bp) are shown in the bar graphs.

**Supplementary Figure S4.** Annotation of SNPs and InDels detected in all pair-wise analysis of rice genotypes, Pokkali, Nona Bokra, Bengal, Cocodrie, and IR64. (A) Distribution of SNPs and InDels in different genomic regions. (B) Distribution of SNPs (top) and InDels (bottom) in different genic regions. The number of synonymous (syn) and nonsynonymous (non-syn) SNPs and number of frameshift mutations are shown for SNPs and InDels, respectively.

**Supplementary Figure S5.** Functional categorization of genes identified with nonsynonymous/large-effect single-nucleotide polymorphisms (SNPs)/InDels. (A) Distribution of the eukaryotic orthologous group (KOG) classes in the genes identified with nonsynonymous SNPs in Bengal/Nona Bokra, Cocodrie/Nona Bokra, and IR64/Nona Bokra, (B) Distribution of the KOG classes in the genes identified with nonsynonymous SNPs in Bengal/Pokkali, Cocodrie/Pokkali, and IR64/Pokkali. Different KOG classes are listed on the right. P-value <0.05 is indicated by *.

**Supplementary Figure S6.** Gene ontology enrichment analysis for the genes harboring large effect/nonsynonymous SNPs and InDels (All SNPs/InDels detected in all pair-wise analysis of rice genotypes, Pokkali, Nona Bokra, Bengal, Cocodrie, and IR64).

**Supplementary Figure S7.** Gene ontology enrichment analysis for the genes harboring SNPs/InDels in the promoter regions (All SNPs/InDels detected in all pair-wise analysis of rice genotypes, Pokkali, Nona Bokra, Bengal, Cocodrie, and IR64).

**Supplementary Figure S8.** Gene ontology enrichment analysis for the differentially expressed genes (DEGs) harboring large effect SNPs/InDels and/or nonsynymous SNPs/InDels in the promoter regions (All SNPs/InDels detected in all pair-wise analysis of rice genotypes, Pokkali, Nona Bokra, Bengal, Cocodrie, and IR64 were included in this analysis).

**Supplementary Table S1.** Distribution and frequency of SNPs (per 100 kb) between different rice cultivars on individual rice chromosome.

| Chr | Chr length (bp) | IR64/Pokkali | | IR64/Nona Bokra | | Bengal/Pokkali | | Bengal/Nona Bokra | | Cocodrie/Pokkali | | Cocodrie/Nona Bokra | |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| | | Count | Frequency | Count | Frequency | Count | Frequency | Count | Frequency | Count | Frequency | Count | Frequency |
| 1 | 43270923 | 70987 | 164.1 | 63165 | 146.0 | 134354 | 310.5 | 149635 | 345.8 | 95019 | 219.6 | 102929 | 237.9 |
| 2 | 35937250 | 46650 | 129.8 | 58686 | 163.3 | 137742 | 383.3 | 131351 | 365.5 | 81750 | 227.5 | 80242 | 223.3 |
| 3 | 36413819 | 36282 | 99.6 | 47031 | 129.2 | 134359 | 369.0 | 138954 | 381.6 | 83002 | 227.9 | 85611 | 235.1 |
| 4 | 35502694 | 46433 | 130.8 | 39311 | 110.7 | 96234 | 271.1 | 107861 | 303.8 | 60714 | 171.0 | 70697 | 199.1 |
| 5 | 29958434 | 46060 | 153.7 | 50567 | 168.8 | 112318 | 374.9 | 109802 | 366.5 | 67603 | 225.7 | 66520 | 222.0 |
| 6 | 31248787 | 53029 | 169.7 | 51623 | 165.2 | 120597 | 385.9 | 113854 | 364.3 | 78115 | 250.0 | 73731 | 235.9 |
| 7 | 29697621 | 33090 | 111.4 | 32181 | 108.4 | 114496 | 385.5 | 113359 | 381.7 | 72735 | 244.9 | 72182 | 243.1 |
| 8 | 28443022 | 38737 | 136.2 | 64957 | 228.4 | 96643 | 339.8 | 96804 | 340.3 | 62644 | 220.2 | 61038 | 214.6 |
| 9 | 23012720 | 30454 | 132.3 | 24120 | 104.8 | 92155 | 400.5 | 89210 | 387.7 | 57032 | 247.8 | 55521 | 241.3 |
| 10 | 23207287 | 29266 | 126.1 | 33768 | 145.5 | 75077 | 323.5 | 84102 | 362.4 | 45904 | 197.8 | 52922 | 228.0 |
| 11 | 29021106 | 39541 | 136.2 | 46147 | 159.0 | 91703 | 316.0 | 92437 | 318.5 | 66010 | 227.5 | 64230 | 221.3 |
| 12 | 27531856 | 65792 | 239.0 | 37267 | 135.4 | 94840 | 344.5 | 86114 | 312.8 | 53606 | 194.7 | 48909 | 177.6 |
| Sy[$] | 633585 | 133 | 22.5 | 117 | 19.8 | 859 | 145.1 | 833 | 140.7 | 553 | 93.4 | 554 | 93.6 |
| Un[$] | 592136 | 409 | 64.6 | 357 | 56.3 | 457 | 72.1 | 395 | 62.3 | 259 | 40.9 | 237 | 37.4 |
| Total | 374471240 | 536,863 | 129.7 | 549,297 | 131.5 | 1,301,834 | 315.8 | 1,314,711 | 316.7 | 824,946 | 199.2 | 835,323 | 200.7 |

[$] Sy and Un represent the Syngenta and unanchored BAC pseudomolecules, respectively, as included in the MSU7 rice genome.

**Supplementary Table S2.** Distribution and frequency of InDels (per 100 kb) between different rice cultivars on individual rice chromosome.

| Chr | Chromosome Length (bp) | IR64/Pokkali | | IR64/Nona Bokra | | Bengal/Pokkali | | Bengal/Nona Bokra | | Cocodrie/Pokkali | | Cocodrie/Nona Bokra | |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| | | Count | Frequency | Count | Frequency | Count | Frequency | Count | Frequency | Count | Frequency | Count | Frequency |
| 1 | 43270923 | 6382 | 14.7 | 5709 | 13.2 | 11663 | 27.0 | 13288 | 30.7 | 7945 | 18.4 | 8801 | 20.3 |
| 2 | 35937250 | 4114 | 11.4 | 5430 | 15.1 | 11499 | 32.0 | 11433 | 31.8 | 6393 | 17.8 | 6464 | 18.0 |
| 3 | 36413819 | 3031 | 8.3 | 4118 | 11.3 | 11134 | 30.6 | 11968 | 32.9 | 6800 | 18.7 | 7307 | 20.1 |
| 4 | 35502694 | 3633 | 10.2 | 3131 | 8.8 | 7498 | 21.1 | 8587 | 24.2 | 4575 | 12.9 | 5355 | 15.1 |
| 5 | 29958434 | 3300 | 11.0 | 3724 | 12.4 | 8786 | 29.3 | 8818 | 29.4 | 4983 | 16.6 | 5070 | 16.9 |
| 6 | 31248787 | 4313 | 13.8 | 4437 | 14.2 | 9558 | 30.6 | 9278 | 29.7 | 5871 | 18.8 | 5669 | 18.1 |
| 7 | 29697621 | 2665 | 9.0 | 2819 | 9.5 | 9263 | 31.2 | 9432 | 31.8 | 5643 | 19.0 | 5661 | 19.1 |
| 8 | 28443022 | 3090 | 10.9 | 5149 | 18.1 | 7468 | 26.3 | 7940 | 27.9 | 4601 | 16.2 | 4854 | 17.1 |
| 9 | 23012720 | 2322 | 10.1 | 2047 | 8.9 | 7057 | 30.7 | 7159 | 31.1 | 4257 | 18.5 | 4246 | 18.5 |
| 10 | 23207287 | 2179 | 9.4 | 2602 | 11.2 | 5949 | 25.6 | 6802 | 29.3 | 3742 | 16.1 | 4248 | 18.3 |
| 11 | 29021106 | 3457 | 11.9 | 3915 | 13.5 | 7529 | 25.9 | 7941 | 27.4 | 4780 | 16.5 | 4690 | 16.2 |
| 12 | 27531856 | 5088 | 18.5 | 3372 | 12.2 | 7538 | 27.4 | 6897 | 25.1 | 4082 | 14.8 | 3906 | 14.2 |
| Sy[$] | 633585 | 9 | 1.5 | 8 | 1.4 | 53 | 9.0 | 60 | 10.1 | 30 | 5.1 | 29 | 4.9 |
| Un[$] | 592136 | 21 | 3.3 | 21 | 3.3 | 32 | 5.1 | 23 | 3.6 | 7 | 1.1 | 5 | 0.8 |
| Total | 374471240 | 43,604 | 10.3 | 46,482 | 10.9 | 105,027 | 25.1 | 109,626 | 26.1 | 63,709 | 15 | 66,305 | 15.5 |

[$] Sy and Un represent the Syngenta and unanchored BAC pseudomolecules, respectively, as included in the MSU7 rice genome.

**Supplementary Table S3.** List of SNPs and InDels detected in rice genotypes with respect to reference genome based on impact on mRNA and proteins.

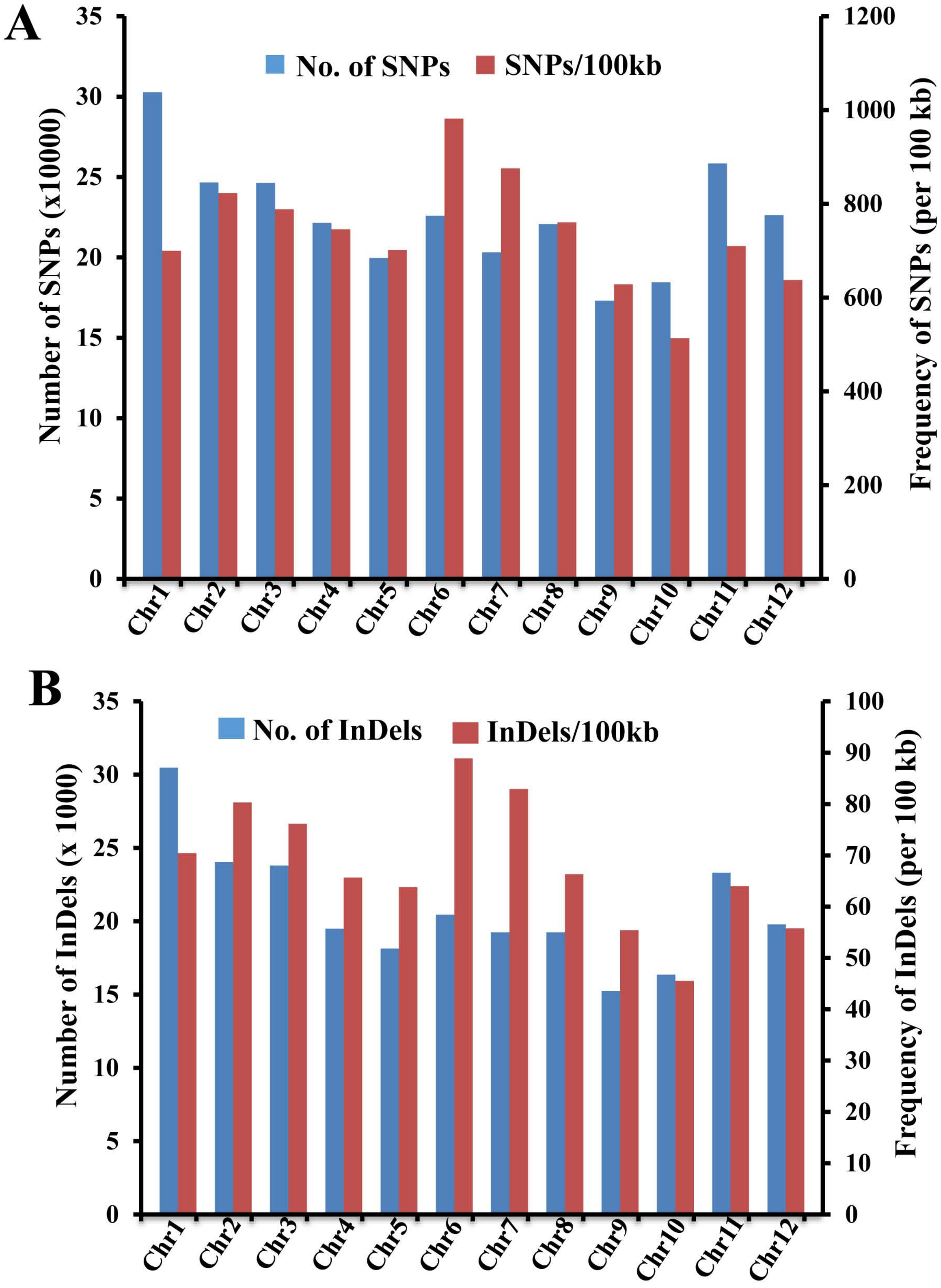
| **Impact** | **SNPs** | **InDels** |
|---|---|---|
| **High** | 282 (0.23%) | 95 (1.13%) |
| **Moderate** | 4237 (3.52%) | 13 (0.15%) |
| **Modifier** | 112679 (93.51%) | 8275 (98.31%) |
| **Low** | 3296 (2.74%) | 34 (0.40%) |

**Supplementary Table S4.** List of SNPs and InDels detected in rice genotypes with respect to reference genome based on variant type and functional role.

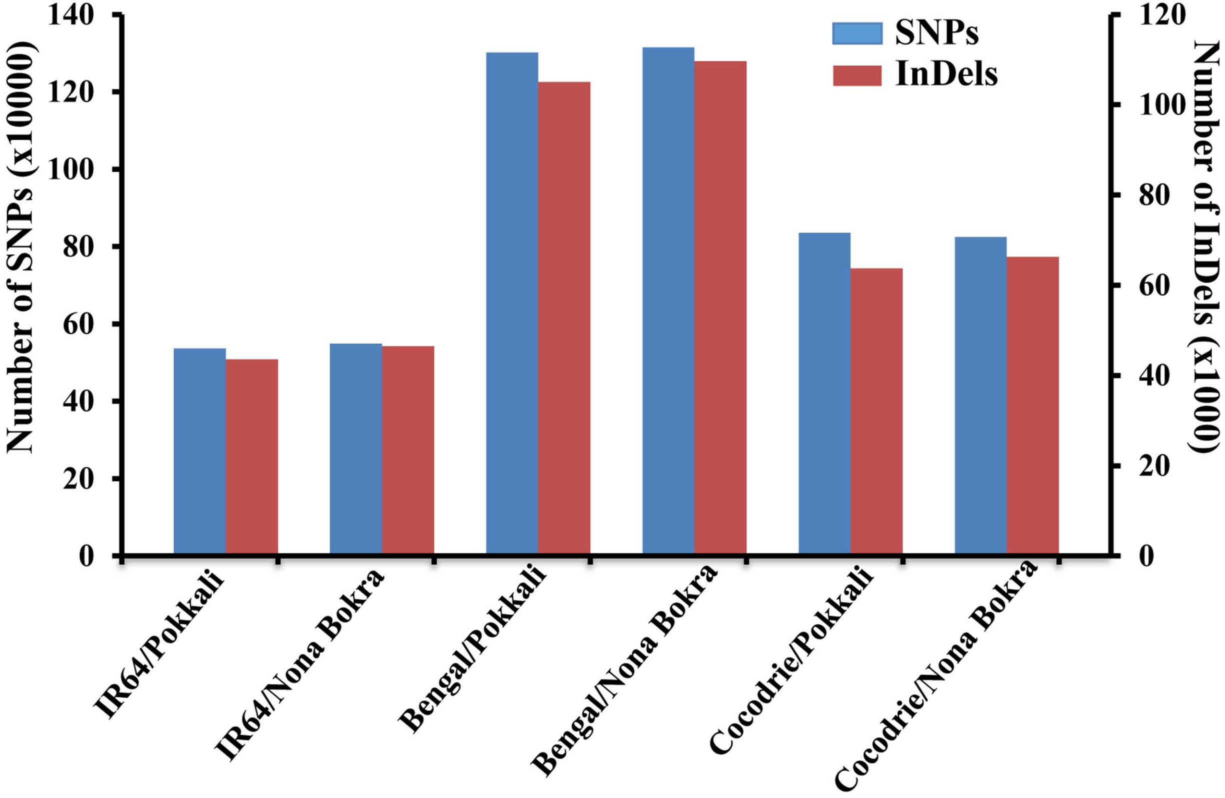
| | **SNPs** | | **InDels** | |
|---|---|---|---|---|
| **Type of variants** | **Count** | **Percentage** | **Count** | **Percentage** |
| Missense variants | 4,267 | 58.05% | 0 | 0 |
| Nonsense variants | 197 | 2.68% | 0 | 0 |
| Silent variants | 2,886 | 39.27% | 0 | 0 |
| splice_acceptor_variant | 32 | 0.026% | 1 | 0.012% |
| splice_donor_variant | 23 | 0.019% | 0 | 0 |
| splice_region_variant | 499 | 0.412% | 38 | 0.449% |
| start_lost | 10 | 0.008% | 0 | 0 |
| stop_gained | 197 | 0.163% | 0 | 0 |
| stop_lost | 20 | 0.017% | 5 | 0.06% |
| stop_retained_variant | 12 | 0.01% | 0 | 0 |
| conservative_inframe_deletion | 0 | 0 | 5 | 0.059% |
| conservative_inframe_insertion | 0 | 0 | 7 | 0.083% |
| disruptive_inframe_insertion | 0 | 0 | 1 | 0.012% |
| frameshift_variant | 0 | 0 | 94 | 1.111% |

**Supplementary Table S5.** Large-effect single-nucleotide polymorphisms (SNPs) and InDels detected in all six pair-wise combinations of rice genotypes.

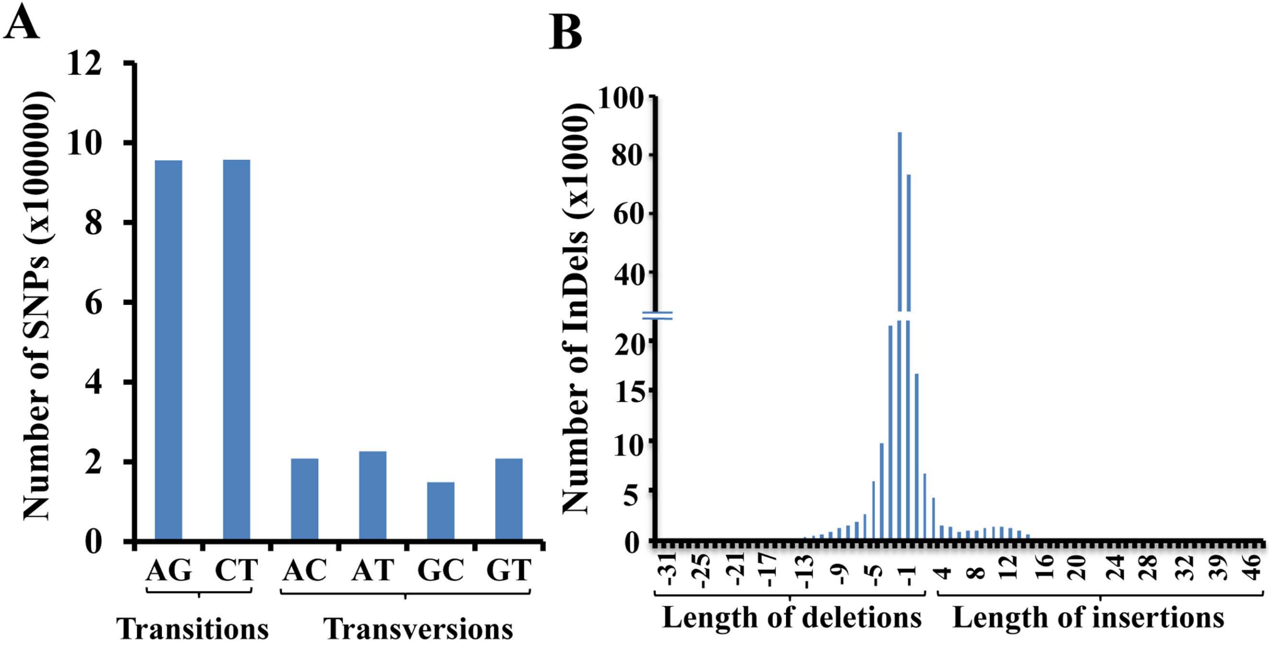
| Type | Bengal vs Pokkali | | IR64 vs Pokkali | | Cocodrie vs Pokkali | | Bengal vs Nona Bokra | | IR64 vs Nona Bokra | | Cocodrie vs Nona Bokra | |
|---|---|---|---|---|---|---|---|---|---|---|---|---|
| | InDels | SNPs | InDels | SNPs | InDels | SNPs | InDels | SNPs | InDels | SNPs | InDels | SNPs |
| Splice site acceptor | 28 | 621 | 8 | 232 | 18 | 399 | 26 | 585 | 11 | 221 | 15 | 392 |
| Splice site donor | 32 | 515 | 13 | 206 | 16 | 297 | 28 | 500 | 9 | 199 | 19 | 293 |
| Start lost | 0 | 265 | 0 | 78 | 0 | 154 | 1 | 257 | 2 | 70 | 0 | 66 |
| Stop lost | 1 | 535 | 1 | 125 | 0 | 288 | 3 | 494 | 1 | 113 | 1 | 296 |
| Stop gained | 4 | 3476 | 4 | 1613 | 1 | 2163 | 3 | 3405 | 3 | 1613 | 1 | 2135 |
| Frameshift | 1800 | 0 | 842 | 0 | 955 | 0 | 1748 | 0 | 824 | 0 | 950 | 0 |
| Total | 1865 | 5412 | 868 | 2254 | 990 | 3301 | 1809 | 5241 | 850 | 2216 | 986 | 3182 |



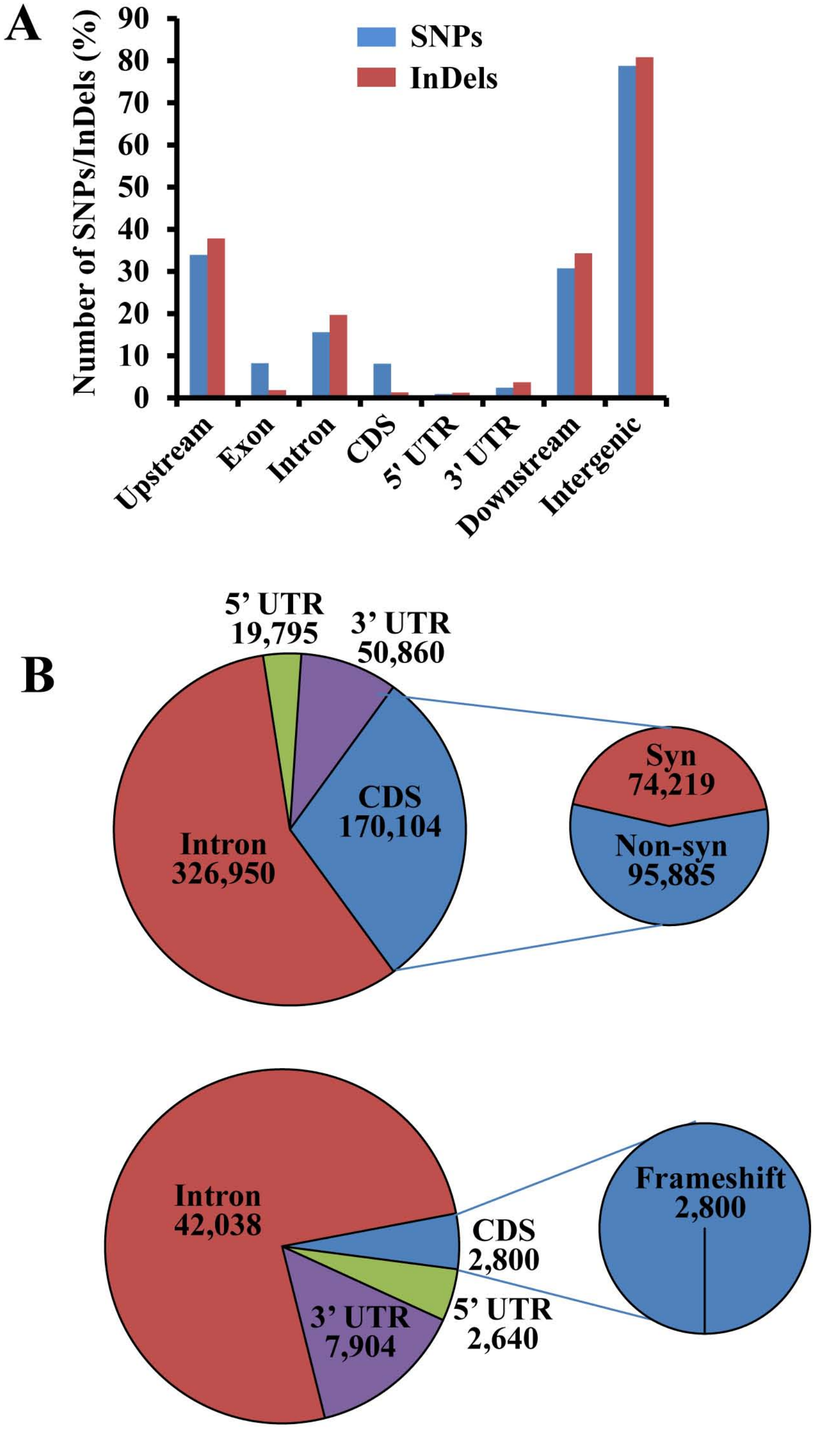
**Supplementary Fig. S1** Distribution and frequency of SNPs and InDels on individual rice chromosome detected in all pair-wise analysis of rice genotypes, Pokkali, Nona Bokra, Bengal, Cocodrie, and IR64. Number and frequency (per 100 kb) of SNPs (A) and InDels (B) detected on each rice chromosome are shown in the bar graphs.



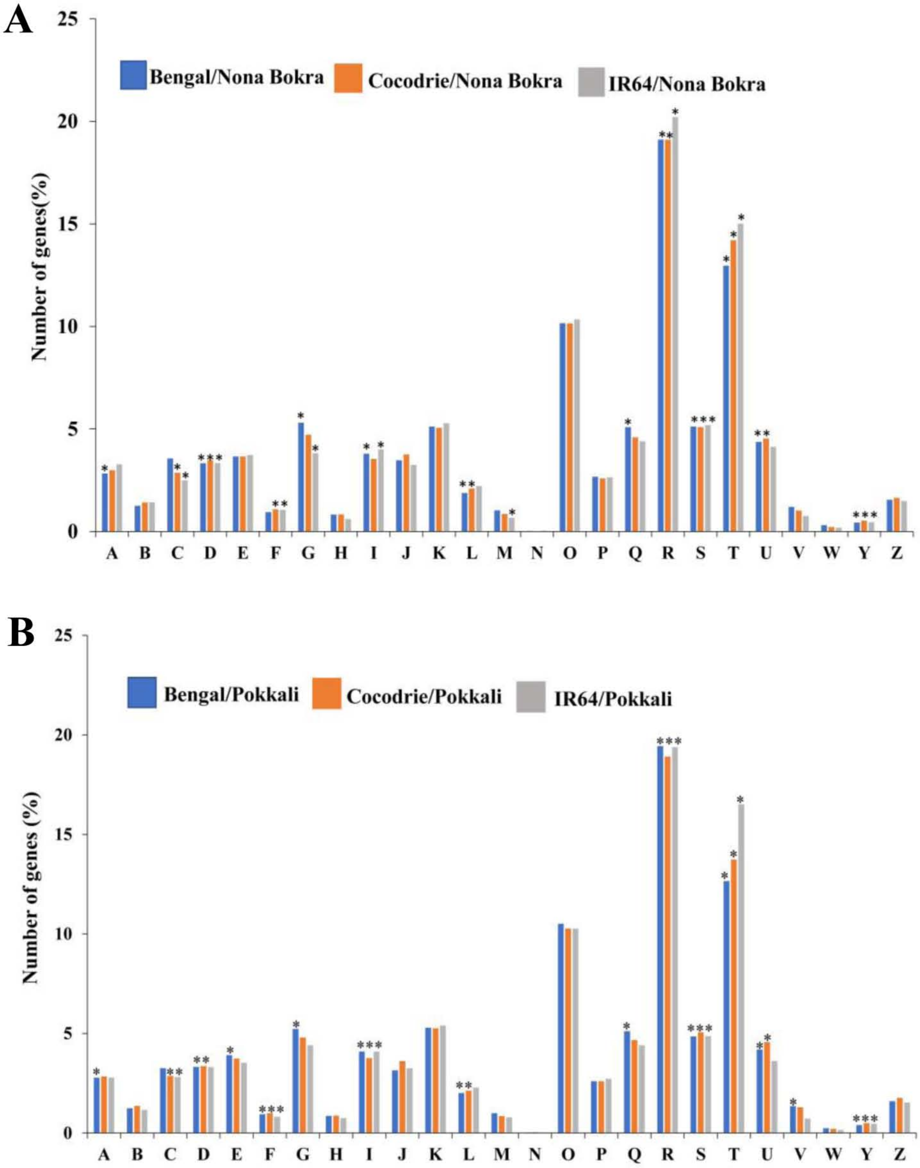
**Supplementary Fig. S2** Number of SNPs and InDels between rice genotypes with contrasting response to salinity. Number of SNPs and Indels between salt sensitive (IR64, Bengal, and Cocodrie) and salt tolerant (Pokkali and Nona Bokra) rice cultivars are shown in the bar graphs.



**Supplementary Fig. S3** (A) Number of different substitution types in the identified SNPs detected in all pair-wise analysis of rice genotypes, Pokkali, Nona Bokra, Bengal, Cocodrie, and IR64. (B) Length distribution of InDels. Number of insertions and deletions (y-axis) of various lengths (x-axis, in bp) are shown in the bar graphs.

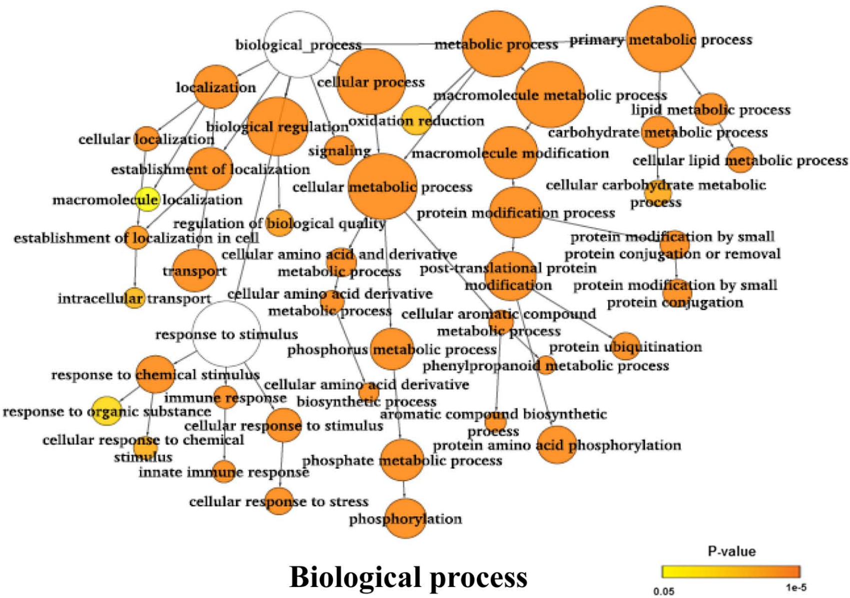


**Supplementary Fig. S4** Annotation of SNPs and InDels detected in all pair-wise analysis of rice genotypes, Pokkali, Nona Bokra, Bengal, Cocodrie, and IR64. (A) Distribution of SNPs and InDels in different genomic regions. (B) Distribution of SNPs and InDels in different genic regions. The number of synonymous (syn) and non-synonymous (non-syn) SNPs and number of frameshift mutations are shown for SNPs and InDels, respectively.

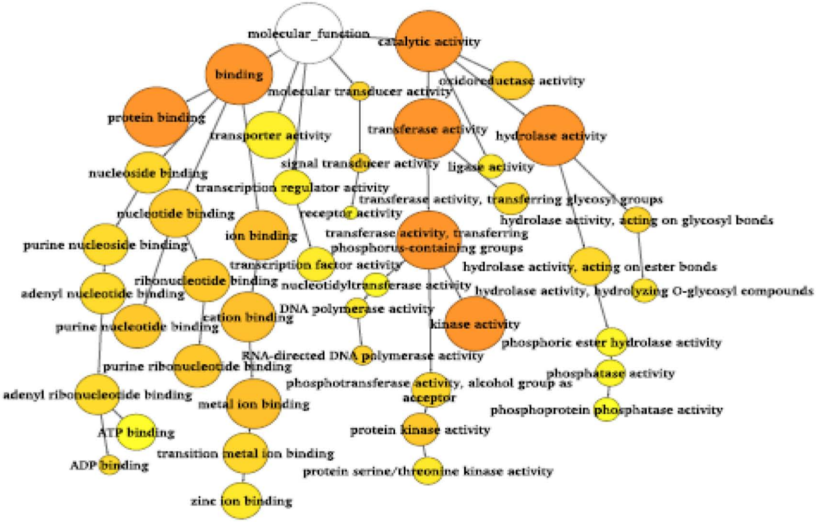


| KOG ids | Description |
|---|---|
| J | Translation, ribosomal structure and biogenesis |
| A | RNA processing and modification |
| K | Transcription |
| L | Replication, recombination and repair |
| B | Chromatin structure and dynamics |
| D | Cell cycle control, cell division, chromosome partitioning |
| Y | Nuclear structure |
| V | Defense mechanisms |
| T | Signal transduction mechanisms |
| M | Cell wall/membrane/envelope biogenesis |
| N | Cell motility |
| Z | Cytoskeleton |
| W | Extracellular structures |
| U | Intracellular trafficking, secretion, and vesicular transport |
| O | Posttranslational modification, protein turnover, chaperones |
| C | Energy production and conversion |
| G | Carbohydrate transport and metabolism |
| E | Amino acid transport and metabolism |
| F | Nucleotide transport and metabolism |
| H | Coenzyme transport and metabolism |
| I | Lipid transport and metabolism |
| P | Inorganic ion transport and metabolism |
| Q | Secondary metabolites biosynthesis, transport and catabolism |
| R | General function prediction only |
| S | Function unknown |

**Supplementary Fig. S5** Functional categorization of genes identified with nonsynonymous/large-effect single-nucleotide polymorphisms (SNPs)/InDels. (A) Distribution of the eukaryotic orthologous group (KOG) classes in the genes identified with nonsynonymous SNPs in Bengal/Nona Bokra, Cocodrie/Nona Bokra, and IR64/Nona bokra, (B) Distribution of the KOG classes in the genes identified with nonsynonymous SNPs in Bengal/Pokkali, Cocodrie/Pokkali, and IR64/Pokkali. Different KOG classes are listed on the right. P-value <0.05 is indicated by *.

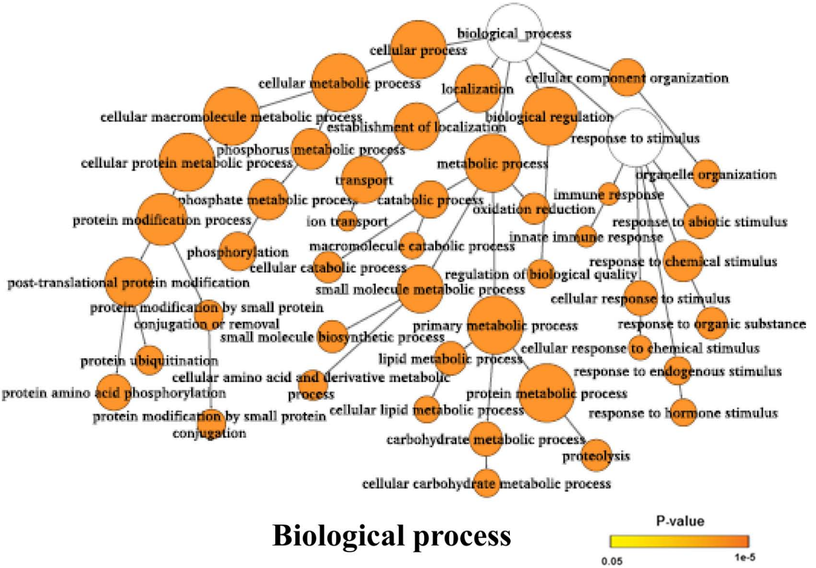


Biological process

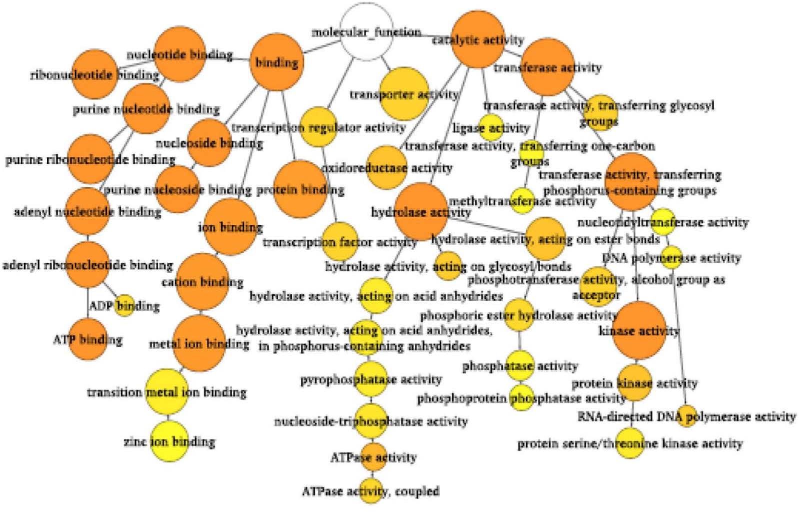


Molecular function

**Supplementary Fig. S6** Gene ontology enrichment analysis for the genes harboring large effect/nonsynonymous SNPs and InDels (All SNPs/InDels detected in all pair-wise analysis of rice genotypes, Pokkali, Nona Bokra, Bengal, Cocodrie, and IR64).

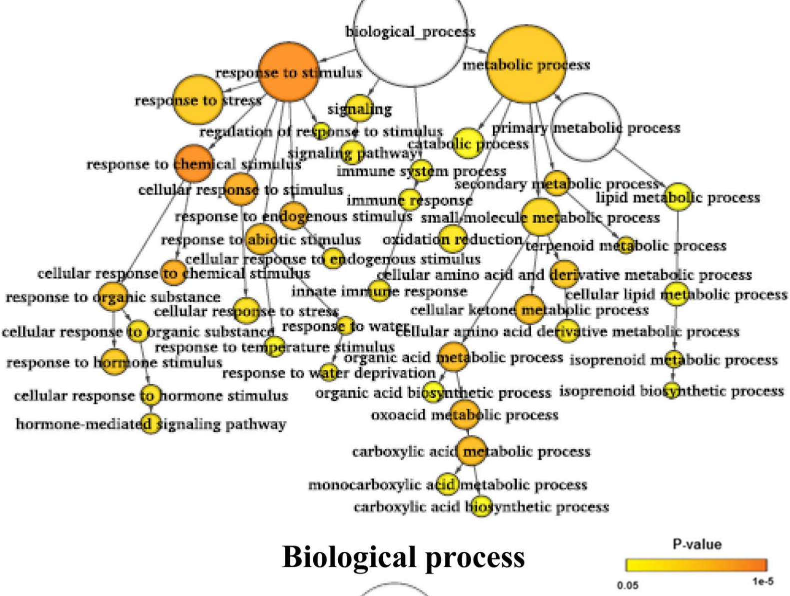


**Biological process**

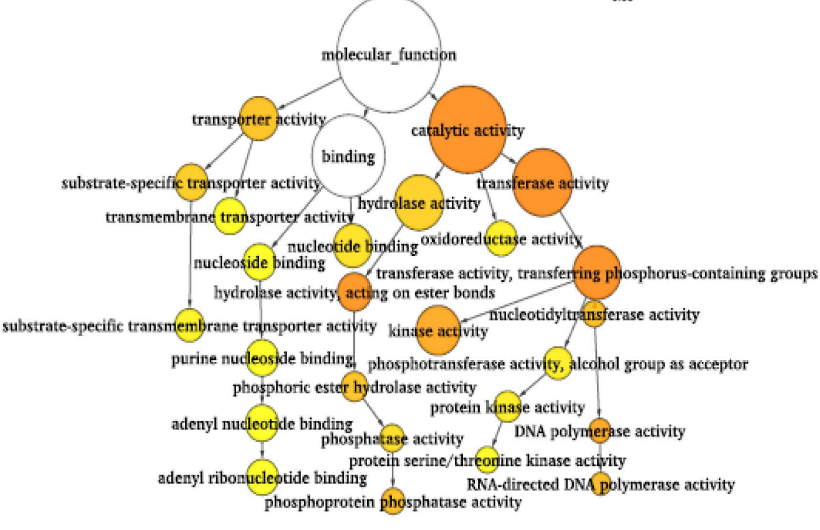


**Molecular function**

**Supplementary Fig. S7** Gene ontology enrichment analysis for the genes harboring SNPs/InDels in promoter regions (All SNPs/InDels detected in all pair-wise analysis of rice genotypes, Pokkali, Nona Bokra, Bengal, Cocodrie, and IR64).



**Biological process**



**Molecular function**

**Supplementary Fig. S8** Gene ontology enrichment analysis for the differentially expressed genes (DEGs) harboring large effect SNPs/InDels and/or nonsynonymous SNPs/InDels in the promoter regions (All SNPs/InDels detected in all pair-wise analysis of rice genotypes, Pokkali, Nona Bokra, Bengal, Cocodrie, and IR64).